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**Herbicide targets and detoxification proteins in sugarcane: From
gene assembly to structure modelling.**

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Abstract

In a genome context, sugarcane is a classic orphan crop, in that no genome and only very few genes have been assembled. We have devised a novel exome assembly methodology that has allowed us to assemble and characterize 49 genes that serve as herbicide targets, safener interacting proteins and members of herbicide detoxification pathways within the sugarcane genome. We have structurally modelled the products of each of these genes, as well as determining allelic, genomic and RNA-Seq based polymorphisms for each gene. This study provides the largest collection of sugarcane structures modelled to date. We demonstrate that sugarcane genes are highly polymorphic revealing that each genotype is evolving both uniquely and independently. In addition, we present an exome assembly system for orphan crops that can be executed on commodity infrastructure, making exome assembly practical for any group. In terms of knowledge about herbicide modes of action and detoxification, we have advanced sugarcane from a crop where no information about any herbicide-associated gene was available to the situation, where sugarcane is now a species with the single largest collection of known and annotated herbicide associated genes.

Keywords:

Herbicide Clearance, Herbicide Target, Molecular Modelling, Phylogenetics, Polymorphisms

Introduction

Sugarcane is a major crop in the tropical and subtropical regions of the world; indeed, it ranks amongst the top ten crop species world-wide. Sugarcane also provides between 60 and 70% of total world sugar output and is a major source of bioethanol (Reddy et al. 2008).

Herbicides are a key component of crop management systems. In commercial cultivation, sugarcane is typically propagated vegetatively by means of stem cuttings known as 'seed pieces' or 'setts', each containing one or more (typically three) buds. As a crop, sugarcane is unusual as it is typically planted with relatively wide row spacing compared to other grass family crops (eg. wheat, rice). Sugarcane growth is slow in its initial stages and it can take between 20 and 26 weeks before the cane forms a complete leaf canopy. As a result, herbicide application is important in terms of weed management, and it is typical to apply herbicide pre-emergence of the germinating setts, followed by one or two post-emergence applications until complete canopy closure (Seeruttun 2008). The crop is typically grown in rainfed areas as well as under irrigation (i.e. abundant water) with abundant nitrogen supply. In the ratoon crop (after first harvesting), little preparatory tillage is undertaken, so established weeds have a chance to flourish. Along with weed control, herbicides are also employed as chemical ripeners in sugarcane (James 2004).

Given the key role of herbicides in sugarcane production, it is surprising that very little is known about the modes of action of these chemicals within the crop. Indeed, of all the genes known to be herbicide targets, or which are responsible for herbicide detoxification only the transcript sequences of sugarcane glutathione S-transferase and glucosyl transferase have been deposited in EMBL/GenBank.

Though some herbicide interactions and detoxification pathways remain unknown, in species apart from sugarcane, quite a lot is now known about herbicide targets, the action of herbicide safeners and the mechanisms of herbicide detoxification. A summary of these data is given below:

Herbicide Modes of Action

Herbicides are classified in terms of their site of action. The list given in Table 1 is based on the Weed Science Society of America (WSSA) and Herbicide Resistance Action Committee (HRAC) joint classification

(<http://www.hracglobal.com/pages/classificationofherbicidesiteofaction.aspx>) where numbers refer to WSSA and letters refer to HRAC classifications, respectively. In addition, the potential new class of herbicides, histidine biosynthesis inhibitors, (Mori et al. 2009) are also categorized in Table 1.

Safener Modes of Action

Herbicide safeners are chemical entities that protect crop plants from herbicide damage without reducing activity in target weed species. As such they improve the discriminatory power of certain herbicides between crop and weed. Many safeners are structurally similar to herbicides, but few safeners act by directly competing with herbicides at target enzyme active sites. Indeed, many safeners work by up-regulating herbicide detoxification pathways (Jablonaki 2013; Riechers et al. 2010).

Herbicide Detoxification in plants

Unlike animals, plants have no excretory mechanisms. As such, when exposed to xenobiotic toxins (including herbicides) they need to either completely metabolize the chemicals, or they must render the chemicals inactive and then sequester them safely in cellular compartments. This is why we refer to herbicide ‘detoxification’ in plants whilst we would refer to toxin ‘clearance’ in animals.

It is generally accepted that plants employ a three-phase process (Shimabukuro 1985) to convert pesticides (and other xenobiotics, such as bacterial toxins) into intermediates with reduced phytotoxicity, which can ultimately be sequestered into vacuoles or be stably

incorporated into the plant's cell walls. The following summary is based on the references: Hall et al. (2001), Hatzios (1997), Kreuz et al. (1996), Sandeman (1992), Shimabukuro (1985), Riechers et al. (2010), Cummins et al. (2013), Yu and Powles (2014) and Kirkwood (2013).

Phase I is typically characterized by simple enzymatic reactions that introduce polar reactive substituent groups not already present in the herbicide. The major reactions in Phase I conversions being oxidation, reduction and hydrolysis. These reactions typically predispose the xenobiotic molecule to Phase II reactions.

Oxidation reactions: cytochrome P450 mediated reactions (*N*-dealkylation or *N*-demethylation; *O*-dealkylation; Aromatic hydroxylation, Thioether oxidation); and β -oxidation (enzymes involved in fatty acid metabolism).

Reduction reactions: Aryl nitroreduction by aryl nitroreductase; deamination by deaminase and photochemical reduction (electron transfer from photosystem I).

Hydrolysis reactions: Ester hydrolysis (de-esterification), typically catalyzed by esterases; though nonenzymatic conversion is possible at pH 6.0.

Amide hydrolysis by acyl arylamidase.

Benzoxazinone-mediated hydrolysis this is a non-enzymatic reaction involving the natural product, DIMBOA with water where there is a nucleophilic substitution at the Cl in position 2 of the triazine ring. This non-enzymatic reaction replaces the Cl⁻ with an OH⁻ at the same position resulting in hydroxyl-atrazine.

Hydrolysis of cyano groups: The cyano group (C=N) of herbicides can be metabolized via hydrolysis. The enzyme CYN (cyanate hydrolase) is the native hydrolase in plants.

Phase II reactions are typically classed as *conjugation reactions* — anabolic processes that, in general, form compounds of higher molecular weight with greatly reduced biological activity, increased water solubility and usually reduced mobility. In plants, the main classes of conjugates are: simple and complex glucosides, glutathione conjugates and amino acid conjugates. In terms of herbicides the same phenomena apply.

Glutathione conjugation is a major phase II reaction, catalyzed by Glutathione S-transferase (particularly the tau and phi classes). Pumps recognize these glutathione conjugates and transport them to the vacuole. Some safeners function by up-regulating the expression of Glutathione S-transferases.

Sugar conjugation: Herbicides containing phenolic, *N*-arylamine, or carboxylic acid groups as well as those metabolized to phenols, anilines or acids during Phase I can be catalyzed into sugar conjugates with uridine diphosphoglucose (UDPG) being the most common sugar donor. Glucosyl transferase and UDP-glucosyl transferase are the commonest enzymes catalyzing these reactions. Glucosyl transferases can also catalyze the formation of glucose esters in herbicides possessing acid groups.

Amino acid conjugates: Conjugation with amino acids is particularly common with the phenoxyacetic acid herbicides like 2,4-D. A peptide bond is formed between the herbicide's carboxylic acid residue and the amino acid's amino group. Though these reactions are undoubtedly catalyzed by enzymes, the specific enzymes responsible for these biochemical processes have currently not been identified.

Phase III reactions are unique to plants, as plants do not have excretory systems. There are three main parts to phase III reactions: additional conjugation of phase II conjugates (secondary conjugation); sequestration of conjugates in vacuoles for storage, and incorporating herbicide metabolites into cell walls.

Secondary conjugation includes reactions such as the addition of a malonyl group from malonyl-CoA to a glucose-herbicide conjugate catalyzed by malonyl-CoA-transferase.

Incorporation of conjugates into the cell wall, typically by irreversible binding to lignin.

Transport of conjugates into vacuoles for storage.

Detoxification by transport: Multidrug resistance proteins (MRPs) are involved in the detoxification of many toxins (endogenous and exogenous) as well as herbicides. They function by direct transport. These are particularly effective for auxin analogue transport.

Rare detoxification mechanisms: Among the less frequently observed biotransformations of herbicides are, to name but a few, oxidations at nitrogen or sulfur atoms; reductions of nitro groups, aldehydes, ketones, and α,β -unsaturated carbonyl compounds; and isomerizations (not all the enzymes associated with these reactions have been identified).

Using the processes above it is possible to derive a list of proteins that are directly affected by herbicides, proteins that interact with safeners and proteins involved in herbicide detoxification. As the majority of these proteins are enzymes, it is likely that they can be structurally modelled by homology or by mapping to known fold families.

Indeed, structure-function relationships are a key component in terms of understanding herbicide mechanisms of action and herbicide detoxification pathways, as the majority of interactions involve enzymes and membrane transporters. This presents a major problem in terms of understanding herbicide action and detoxification mechanisms in orphan plants, as the sequence for the majority of genes is unknown, and without sequence it is not possible to structurally model the protein.

- In a genomic context, sugarcane can be considered a typical example of an orphan crop (Varshney et al. 2012), where though a genome sequencing and assembly project is underway, its outputs are not yet available (De Setta et al. 2014). Indeed, a current search of GenBank reveals a total of only 1261 sugarcane genes, with an additional 679 “genes” derived from first-pass annotation of genomic contigs (based on our current analyses). However, many of these genes represent duplicated fragments and when they are made unique that leaves only 893 genes. Excluding partial sequences leaves only 637 genes with complete CDses, of which only 237 are known coding genes (the remainder are putative genes based on automated annotation of genomic contigs). A search of UniGene reveals an additional 266 unigene clusters (which reduces to 89 when duplicated transcripts, transposons and partial transcripts are eliminated), representing full length transcripts, primarily derived from EST assembly. This means that, even with the most optimistic counting scheme, the

current sampling of sugarcane genes and transcripts represents less than 2.15% of the entire gene complement of sugarcane (assuming a conservative 34 000 genes in total).

However, sugarcane is in a unique position as a test case for exome assembly in the absence of a reference genome. A closely-related genome, that of *Sorghum bicolor* (about 7.2 million years divergent, Estep et al. (2014)) has been assembled (Paterson et al. 2009). The Joint Genome Institute (JGI) has also released a high depth short read sequence dataset for the sugarcane cultivar LCP 85-834 (SRA: SRR427145). This means that it is possible to use sorghum gene sequences to bait out equivalent sugarcane reads that can then be assembled *de novo*.

We mapped all known herbicide target proteins, all known safener up-regulated or interacting proteins and all known herbicide detoxification genes to the sorghum genome and employed these genes to construct the cognate sugarcane genes. We took the protein translation from these genes and threaded onto known structures. This allowed us to construct every gene (exome sequence) for the known herbicide pathways in sugarcane and to predict the three-dimensional structures for all the proteins. Moreover, a quick scan of the EnSEMBL Sorghum pages (http://plants.ensembl.org/Sorghum_bicolor/Info/Index) reveals that 93.5% of sorghum genes had not functional annotation. We wanted to examine whether structural mapping studies could aid in gene annotation, as the sugarcane genes were built on unannotated sorghum references.

From a starting point where none of the sequence or structural data were available, sugarcane now has one of the best data collections for determining herbicide modes of action and herbicide detoxification mechanisms in any plant. We also demonstrate the utility of whole genome short read data for gene mining in orphan crops and present a method whereby the majority of genes in any species can be assembled without the need for whole genome assembly. With exemplar genes it is also possible to perform gene expression analysis in crops where it would not have been possible previously.

Results:

Target genes involved in herbicide modes of action, safener modes of action and herbicide detoxification were identified based on a combination of exhaustive literature searches, EnsEMBL keyword searches (against the EnsEMBL plants database), (Kersey et al. 2015) and NCBI keyword searches against the green plant datasets. This revealed 45 target genes, derived from 8 plant species, the orthologues of which were identified in *Sorghum bicolor* and which are listed in Table 2. In addition, we identified the β -oxidation (enzymes involved in fatty acid metabolism) pathway as corresponding to the Arabidopsis BioCyc pathway: PWY-5136. This pathway is known to be involved in herbicide detoxification (Trenkamp et al. 2004), and the two key enzymes from this pathway were mapped to sorghum cognates, yielding a total of 47 genes. The mapped sorghum genes were used to bait reads from the sugarcane short reads dataset prior to assembly with SPAdes. We also identified a potential misassembly in the genomic form of sorghum ALS (acetolactate synthase) and instead used the maize cognate as an alternate template. In addition, the known sequence of the sugarcane plastid photosystem II gene psbA was used for structural modelling — yielding a total of 49 genes. An additional gene, HM2 was identified from *Zea mays* (but which is absent from the current *Sorghum* assembly). This gene has long been known to confer resistance to the fungal pathogen, *Cochliobolus carbonum*. Domain analysis revealed that HM2 is an epimerase involved in the reduction of toxins. As the same processes are involved in the detoxification of both exogenous herbicides and toxins, HM2 was also added to the list of herbicide detoxification enzymes, yielding a grand total of 50 genes for further study. We have therefore identified three novel genes (HM2, AIM1, LACS7), which are all involved in herbicide detoxification (Table 2).

Of the 49 non-sugarcane genes identified for sequence assembly, 42 (85.7%) were constructed in their entirety on the first round of assembly. A further two genes had long introns which had significantly evolved away from the sorghum template and were built in two halves, but these halves were connected after a second round of baiting and assembly.

The MFP2 gene had a variant first exon (as compared with sorghum) and several long internal introns and took four iterations of baiting and assembly (using the best scaffolds from the previous build as bait) to construct the full-length gene. The genes, LACS7 and LACS8 proved to be by far the more problematic to build. LACS8 was constructed by increasing the baiting k-mer to 29 and the complete gene was assembled in five iterations.

Assembly of LACS7 displayed an additional complication, due to a confounding alternate copy. This could be due to the presence of either a duplicate copy in the sugarcane genome, or as sugarcane is a hybrid, the *Saccharum spontaneum* minor parental version of the gene is at sufficiently high copy number to confound assembly. One copy of the gene (at a higher copy number) is much more similar to the sorghum baiting gene than the other. Reads that were specific to the more distant version of the gene were excluded using BLAT and the primary copy of the gene was constructed using an iterative baiting approach. In this case, due to lower coverage it took 10 iterations for the gene to be constructed in its entirety.

Despite a few assembly problems, for each target gene, we managed to obtain the complete coding sequence from its sugarcane cognate, validating our methodology as a means of constructing exome sequences in orphan crops.

For exon calling we employed a pipeline based on a combination of FGENESH (Salamov and Solovyev 2000) exon calls (using both the sorghum and maize models), sugarcane EST mapping, sugarcane transcriptomic short read mapping and mapping exons from the original sorghum genome sequence. In each case, all exons had 100% coverage and we were able to call UTRs as well as alternate transcripts. Genes ranged from 801bp to 12040bp in total length, with the number of exons ranging from 1 to 30, and with five genes having more than a single transcript. In the majority of cases, sugarcane splice junctions resembled sorghum splice junctions, with type 1 splice sites predominating (type 2 splice junctions were not observed).

Closely-related genes belonging to multigene families are often difficult to annotate. We performed phylogenetic analyses at the transcript level, comparing our gene assemblies for sugarcane tau- and phi-class glutathione S-transferases with cognates in other species. The

phylogram (Figure 1), using *Chlamydomonas reinhardtii*, an unicellular green alga, glutathione S-transferase (GST) as an outgroup revealed the sister relationship between the tau and phi class GSTs. In all cases, the sugarcane protein is sister to its cognate sorghum protein, but evolutionarily divergent from it. This indicates that our assembly methodology had yielded valid sugarcane genes rather than simply mapping sugarcane reads to the sorghum template.

For each gene, a file containing every possible protein translation from each transcript was submitted to the Phyre² server for homology modelling. Each submitted transcript mapped to a single best PDB entry (Table 2) and the functions of these structural models corresponded to the function of the assembled sugarcane gene validating our functional annotation (Table 2). The final models from Phyre² were downloaded and refined by energy minimization. Images of a representative sample of the final structures are shown in Figure 2 and Figure 3. The Phyre² intensive modelling mode uses multiple PDB models to create the best possible structural model for an input protein sequence. A total of 55 protein sequences were submitted to Phyre², covering all the genes and alternate transcripts discovered in this study. All Phyre² models had 100% Phyre² confidence (Table 3) and each model had between 63% and 100% of all residues modelled with >90% confidence. Indeed, all but two models had 80% or greater of all residues modelled at >90% confidence. These two structures (ShLCY1 and ShMAT1) were modelled on cognate or orthologous genes (Table 3), however both structures were modelled on templates of the same fold family.

After molecular dynamics and energy minimizations, protein models were submitted to the ProFunc server to determine the new best-fit model along with its percentage identity and its main fold's RMSD to our final structural model. In all cases but two (ShLCY1 and ShPDS1), ProFunc analysis revealed that our model best fit a PDB entry file with cognate function (Table 3), showing that our modelling was robust and that structural modelling could be used to potentially predict the function of unknown proteins. The two outliers were shown to have similar structures to the closest matching PDB model, as defined by InterPro (Mitchell et al. 2015) for ShPDS1 and NCBI VAST (Madej et al. 2013) for ShLCY1. Therefore, all our

models retained the same predicted function as our initial gene builds, or, in the case of two models, were predicted to belong to the same fold family.

All models had RMSD $<1.49\text{\AA}$ as compared to their ProFunc best fit matching fold, with the majority of structures having an RMSD $<0.4\text{\AA}$. Thus both predicted structure and predicted function was maintained throughout our modelling process.

Though percentage identity cannot be directly used as a measure of modelling fitness with Phyre² as it under-estimates the identity between the model and the multiple templates used in its construction, percentage identity scores were captured from ProFunc. From this analysis, 39 of our 55 protein structures had $>30\%$ identity with the best matching PDB file, which is typically considered as a robust model, as long as the proteins are homologous (ie evolutionarily related), (Fiser 2010). A further 15 models lay in the >25 and $<30\%$ identity range. In all cases, identities were distributed across the model and not clustered in a specific region or fold and all modelled proteins had the same predicted function as their best PDB template as well as being predicted to be orthologues or cognate genes of the template. These findings, in conjunction with the functional and evolutionary conservation of template and model makes it likely that these models are at least useful for further structural studies and should be sufficiently robust for use in docking and predictive studies.

Of all our models, a single protein, ShNIT4 matched a different template in the ProFunc round-robin analysis with a significantly lower percentage identity than the initial Phyre² analysis. We checked our model against both the Phyre² PDB model (3WUY) and the ProFunc PDB model (5h8i). On re-checking the data, we found that ShNIT4 matched 3WUY with 34.92% identity and displayed an RMSD of $0.73\text{\AA}$. Thus, in this case, Phyre² gives a better template than ProFunc. As a result, this model should be promoted to the 'high quality' dataset.

A single model fell below the 25% identity mark, as determined by ProFunc, but even here the target and template models were of functionally equivalent and evolutionarily related proteins. Though this is the lowest quality model, it may still be useful for further modelling studies. It should be noted, however, that even in the low percentage identity models, the

aggregate percentage identity determined across all Phyre2 models is significantly higher than the standard 30% identity cutoff. The only exception to this being the model of ShLCY1. In this case, no reliable orthologous template could be found and the best matches were from similar fold families rather than functionally orthologous genes.

For global estimations of model qualities, the structures were analysed with the ProSA (Wiederstein and Sippl 2007) and Verify_3D (Eisenberg 1997) web servers. For ProSA, all models had Z-scores within the range of scores typically found for native proteins of similar size. Local residue scores were good, with few problem residues that could be fixed by manually tweaking the structural models. Verify_3D revealed that all models had a minimum of 65% of amino acids that scored ≥ 0.2 in the 3D/1D profile. The three poorest scoring models, those of ShLCY1, ShPDS1 and ShGDSL all had the most distantly related templates and Verify_3D analyses indicated that they had helices that should be beta-strand elements or strands that would better be modelled as helices. When the problem areas were re-modelled, scores improved. This shows that issues with the models, where they exist, are relatively minor, and easily remedied.

Identification of Variants

A total of 3762 high-quality genomic SNPs/MNPs were identified using our GTK-based allelic pipeline. Of these, 3256 polymorphisms were within genes and 506 outside gene boundaries. Of the gene-associated polymorphisms, 220 were in UTRs, 1169 were in coding regions and 1867 were in introns. Of the coding polymorphisms, 797 yielded potential alternate coding sequences. When sorted on the basis of cultivars, mapping of RNAseq data to the genomic backbone yielded a total of 1289 transcriptomic SNPs/MNPs, all of which were discriminative between one or more cultivars¹. Of these, 1088 were within coding region, with 551 variants being synonymous (silent) and 537 being non-synonymous (i.e. altering the protein sequence).

¹ Allelic SNPs are given in Table S1; RNA-based SNPs are given in Table S2 and genomic SNPs are given in Table S3.

Of the SP80-3280 genomic data, reads could only be mapped to 17 genes (ACC1, ALS, CYN, CYP709B3, CYP71E1, DTX1, EPSPS, GDSL, GPOX, GSH2, LACS7, LACS8, MAT1, MATE, MFP2, OEP64, PDS1), with the ACC1, ALS, CYP709B3, GSH2 and LACS8 mappings having insufficient depth of coverage to be informative. Thus SP80-3280 genomic data only mapped well to 12 of our 49 genes. This indicates that though the SP80-3280 genomic data has good read depth it does not have good genomic coverage and shows that our method can be used to confirm the genomic coverage of BAC-based samplings. For the mapped genes, a total of 1591 polymorphisms were identified between LCP 85-384 and SP80-3280, of which 87 were outside gene bounds, 68 were UTR variants and 1073 were intronic variants. Of the remaining 363 coding variants, 182 were synonymous and 181 were non-synonymous.

Combining the SNP data from all three datasets gave a total of 6370 unique SNPs/MNPs with 361 (5.4% of the total) duplicated SNPs (numbers here are higher than previous totals, as alternate SNPs in the same location are treated individually).

Analysis of short sequence repeats yielded a total of 37 simple or interspersed repeats (repeats separated by an intervening, non-repetitive sequence)².

² See Table S4

Discussion

The ability to bait sequence reads from a whole genome short read archive based on the sequence of a gene from a related species, with assembly of those reads into the sequence of the gene from the target species, represents a revolution in gene-hunting. The ability to run these applications on commodity hardware (any laptop or desktop with 16Gb memory and 1Tb storage running *NIX) also places gene assembly within the reach of everyone. In fact, most gene assemblies in the current study took <2Gb memory, which means that a small Beowulf cluster with most CPUs having 4Gb memory and a few CPUs having 16Gb memory would efficiently and cheaply assemble a complete plant exome. In our tests, an Apple MacBook Pro with a four-core (eight thread) 2.6GHz Intel Core I7 processor and 16Gib memory, running four staggered assemblies on 2 threads apiece could assemble 3.68 genes per hour (over a 72 hour assembly run), with the major computational bottleneck being concurrent disk access.

This means that, for the first time, it is possible to easily build specific genes from orphan crops as long as a whole genome short read dataset of good depth is available (about 18 Gbases) and there is a gene set from a related species to use as a reference for baiting out sequence reads from the total read pool. Sugarcane is such a crop, in that the genome has not yet been assembled, but the JGI have published a short read dataset for a sugarcane cultivar (LCP 85-384). In addition, the genomes of two close relatives, *Sorghum bicolor* (7.2 million years divergent from sugarcane) and *Zea mays* (12.8 million years divergent from sugarcane), (Estep et al. 2014) have both been published. Our prior studies (D Lloyd Evans, unpublished results) revealed that genes from both genomes could be used as templates to construct sugarcane genes. However, using templates from *Sorghum biocolor* gave the best results, as introns shared greater identity with sugarcane, meaning that fewer gene build iterations were required to construct complete exome sequences.

Herbicide action in plants is complex, as each herbicide has different sites and modes of action as well as methods of detoxification. In, addition, use of safeners as herbicide

protection agents means that additional targets can be involved in up-regulating herbicide detoxification mechanism in target plants. We identified 15 genes (Table 2 and Figure 2) acting as known herbicide targets and 3 genes known to either be involved in safener binding or to be up-regulated in the presence of safeners (however, as many safeners are analogues of herbicides, safeners will also be active in up-regulating many of the genes identified in herbicide detoxification). An additional 31 genes (Table 2 and Figure 3) were identified as either directly involved in herbicide detoxification or which were control genes up-regulated in the presence of herbicides. In addition to the 31 genes involved in herbicide detoxification, we were able to identify two novel genes from the β -oxidation fatty acid metabolism pathway of Arabidopsis, which was identified from the paper of Trenkamp et al. (2004) as a key detoxification pathway.

From the set of 50 herbicide associated genes, 48 could be reliably mapped to the sorghum cognates. ALS could only be reliably mapped to a maize gene (the gene is truncated in the sorghum assembly). The photosystem II protein D₁ (psbA) has already been assembled as part of the sugarcane plastid genome (Asano et al. 2004). These sorghum genes (plus one maize gene), detailed in Table 2, were used as bait for assembling the cognate sugarcane genes. All coding exons from all sugarcane genes were built and five genes were shown to have alternate transcripts.

Phylogenetic analyses were performed on the glutathione S-transferase genes, for three reasons: firstly, to aid with the annotation of these very closely related genes; secondly, to demonstrate that all the constructed genes were distinct and lastly to demonstrate that the genes were distinct from the original sorghum templates. The phylogram (Figure 1) employed *Chlamydomonas reinhardtii* glutathione S-transferase as an outgroup. It can clearly be seen that the tau and phi classes of GSTs are distinct families (Figure 1) and occur early in the evolutionary history of land plants. There are examples from monocots and dicots in both groups and both tau and phi families have members from the spikemoss, *Selaginella moellendorffii*, a terrestrial non-seed plant that is ancestral to monocots and dicots.

In all cases the sugarcane protein is sister to the sorghum protein, but branch lengths reveal that the two genes are divergent (the lineages diverged about 7.2 million years ago), clear evidence that our assembly method is robust. Where annotation on the sugarcane gene was ambiguous, it could be confirmed by near neighbours.

It is also clear that Arabidopsis GSTFs 2–8 and 16 represent separate lineages to the monocot GSTFs. Dicot GSTF13s are sister to monocot GSTF1 and 4. *Selaginella* GSTFs and Glycine max GSTFs (along with Arabidopsis GSTFs 11 and 12) are sister to monocot GSTFs 6 and 12. Thus, there was an early divergence of GSTF and GSTU lineages, with a subsequent complex evolution, involving gene duplication and divergence as well as gene loss, of both the phi (F) and tau (U) lineages. Despite being a smaller lineage, we show that the tau class proteins demonstrates as complex an evolutionary history as their phi class sisters.

Structural Modelling

All the CDSes derived from our set of 50 genes were translated and these proteins were all submitted to the Phyre² homology search server for homology mapping. Initially batch processing was employed, to check that each protein could be modelled, before each CDS was submitted to Phyre² as individual ‘intensive’ modelling jobs. We obtained good quality PDB structure hits for each protein (hardly surprising as the majority are enzymes) and the PDB models for the sugarcane transcripts were downloaded from the server and energy minimized locally.

To determine how robust our models were we performed a round-robin analysis, taking our models from Phyre² and after molecular dynamics and energy minimization subjecting them to analysis using the ProFunc server. However, as Phyre² uses multiple models and standard quality scores for models (eg percentage identity and RMSD between template and predicted structures) rely on single templates it is hard to find scores that do justice to the model as a whole. However, we were able to show that 39 out of our 55 protein sequences had identities of >30% as compared to the best PDB match and that they differed by an RMSD of < 1.16Å with the equivalent fold. Moreover, all these structures had a predicted function that was equivalent to the function initially determined for the parent gene. Given that all these models

had Phyre² prediction scores of 100% and all their functional cores were modelled with 100% confidence (Table 3) this gives a strong indication of the suitability of these models for further structural studies. Amongst these models, the properties of ShALS in terms of its structure, herbicide binding, inhibition of herbicide binding and interaction with its activator/inhibitor, VAT1 have been discussed previously (Lloyd Evans and Joshi 2016b).

The remaining 16 models are more problematic. All but two of the models had predicted functions that were equivalent to the starting gene. Of these, ShNIT4 was predicted to belong to the same functional (nitrilase) family, whilst ShLCY1 was predicted to belong to the same structural class. For all these models, (except for ShLCY1) the aggregate identity, as determined across all templates used by Phyre² was >32%. Thus, combining the data from Phyre² and ProFunc, we can confirm that all but one of our models pass the threshold to be structurally informative. However, despite being the poorest quality model, that of ShLCY1, may still be useful as it is the first model of an aromatic hydroxylase created to date.

Both Verify_3D and ProSA results for our models were good, indicating that the structures are robust, with relatively minor problems that will be easy to correct before performing further structural analyses. However, these structural tweaks need to be performed manually and are beyond the scope of an automated pipeline.

We have shown that bulk structural models obtained from newly assembled genes is a possibility. Of course, the majority of our genes were enzymes, so it is not that surprising that 71% of our predicted structures were of high quality. Using the multi-template modelling mode of Phyre² we can show that all but one of remaining models were of more than acceptable quality for further structural studies. Even our most poorly modelled structure, that of ShLCY1 may prove of value in functional studies. Moreover, the structural models, using ProFunc analyses helped confirm the expected functions of our assembled genes, thus linking exome assembly and three-dimensional structural prediction in a single pipeline.

We can see that our modelling pipeline, particularly cross-checking models with ProFunc can be of significant use in helping to annotate gene products of unknown function and can aid in confirming the correctness of assembled exome sequences.

For the first time we have both the gene sequences and high quality structural models for the key genes acting as herbicide targets and herbicide detoxification mechanisms in sugarcane. This will enable rational design of novel herbicides for sugarcane and *in-silico* testing of existing herbicides as the models are of sufficient resolution for docking studies. In addition, the data presented in this paper will enable the knowledge-based hunt for herbicide resistant mutations within the world's sugarcane collections.

Along with providing three-dimensional structures, which can be used to elucidate herbicide modes of action and modes of detoxification, the sugarcane genes identified and assembled in this study are also potential targets for breeding programmes. A classic example would be cytochrome p450 72A31, which is implicated in tolerance to acetolactate synthase-inhibiting herbicides (Saika et al. 2014) and identification of sugarcane plants up-regulating expression of this gene could introduce ALS herbicide tolerance without the need to mutate ALS. To aid these studies, a pipeline was produced based on read mapping with BWA, mapped alignment optimization with GATK, SNP calling with GATK and SSR variant calling with MISA. This pipeline yields high quality mapping of genomic short reads and transcriptomic RNAseq data to genomic reference sequence (our gene sequences in this case). Using GATK, high quality SNPs can be called from these mapped reads. These are allelic SNPs in the case of genomic reads (sugarcane is ~ decaploid) and cultivar (population) based SNPs in terms of RNAseq data.

In all we obtained 6642 unique SNPs from a combination of allelic, genomic and RNA-seq data (3762 total allelic SNPs, 1591 total genomic SNPs [but only from 363 gene coding regions] and 1289 transcriptomic SNPs [from 6 transcriptomic datasets]).

Using BioPerl, our base EMBL flatfiles and the application SnpEff, we developed a variant effect prediction pipeline that can map a SNP and MNP's potential effects onto UTRs, exon splice sites and protein variants. This means that not only can SNPs and MNPs be used in

selective breeding programmes as potential markers; we can also predict non-silent SNP effects and actively select SNP populations with advantageous phenotypes (eg if a single SNP within a population potentially confers herbicide resistance, as determined by three dimensional docking studies). The large number of allelic polymorphisms obtained in this study also indicate that the various alleles for the genes assembled by us are rapidly and independently evolving away from each other. This means that allelic variation within the sugarcane genome is a major source of variability. When all the gene calls are aggregated, we were able to call 6370 unique SNPs/MNPs with 361 duplicated. The majority of polymorphisms were revealed from allelic variants and there was little conservation of SNPs between cultivars. This would indicate that the sugarcane genome is highly dynamic and that, due to human selection and different local growing conditions, each cultivar is evolving independently. This is potentially problematic, as a single reference genome may have little applicability to a given cultivar in a given locale.

The short sequence repeats identified in the current study represents the first pool of known gene-associated SSRs described in sugarcane and forms the foundation of a pool of SSR-based markers that will grow as more genes are assembled and annotated.

The methodologies developed for RNAseq mapping and SNP detection can also be employed for differential expression analyses by mapping differential RNA pools (e.g. herbicide treated and untreated) to the target gene sequences as described herein. Removal of poorly mapped reads would yield high quality mappings to the gene of interest and read counts would allow for differential expression analysis. Thus, the bioinformatics systems developed in this project can readily be re-used in the future for differential expression analyses. Mapping of RNAseq data to reference genes can also be utilized for calling alternate transcripts (as we have in our pipelines) but can also lead to the discovery of alleles with alternate start codons, exon skipping due to changes in splice sites and premature stop codons³.

In common with most orphan crops, very few complete genes and transcripts have been sequenced and assembled in sugarcane. Of all the herbicide target genes and herbicide

³ See supplementary tables S1, S2 and S3.

detoxification genes identified in this study, only the transcript sequences and not the full-length genes of glutathione S-transferase and glucosyl transferase had previously been deposited in EMBL/GenBank.

In this paper we present the assembly of 49 complete sugarcane genes, for all the proteins currently known to be involved in herbicide action, safener binding and herbicide detoxification with their alternate transcripts. Moreover, each protein translated from these genes has been homology modelled onto a three dimensional structure before optimization of the derived sugarcane structural model.

Conclusion and future directions

From a position of having little or no knowledge of how herbicides function or are detoxified in sugarcane, we now have the sequences of a large number of genes and structural models for the proteins derived from those genes. For the first time, it is possible to hunt for herbicide resistant mutants in sugarcane using known genes as a basis for variant discovery. We also have structures that will enable us to perform knowledge-based herbicide design in sugarcane. Considering that, as of April 2016 there are only 237 complete and fully-annotated sugarcane gene sequences of known function deposited in EMBL/GenBank, we have increased the sum total of assembled and annotated sugarcane genes by 21%.

Knowing genes involved in herbicide detoxification can help with the search for plants where these genes are up-regulated (potentially making the plant more herbicide tolerant). These genes and structures also provide us with a toolkit for gene mutation and transgenics in sugarcane using sugarcane genes as templates.

Moreover, the current study acts as a template for sequence assembly in any orphan crop or species. Using our protocols, the exome of any species can be assembled as long as a genomic high-depth short read dataset is available along with a related reference assembly or gene set from a species about 4–8Myears divergent. With Illumina HiSeq sequencing typically costing \$40 per Gigabase of data, and with a single run yielding 30 GiB data, just one Illumina run is

more than sufficient for exome assembly. We also demonstrate that exome assembly itself can be performed on commodity infrastructure (three parallel job instances on a 16Gb, four-core (eight thread) laptop takes 13.5 hours to assemble 40 genes). No longer does exome assembly have to be the province of experienced assembly labs with ‘large dedicated infrastructure’.

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Materials and Methods:

Genes responsible for herbicide modes of action, safener modes of action and herbicide detoxification were identified by literature searching and text-based searches of GenBank and EnSEMBL. These searches resulted in 50 genes from 6 plant species being identified, which are listed in Table 2.

As all these genes were identified from different target species we employed a combination of BLAST and orthologue searching at the EnSEMBL website to identify the best orthologue for each gene in the *Sorghum bicolor* genome. As the majority of sorghum genes are unannotated, the best annotation from a close paralogue was used to annotate the sorghum gene (with this annotation being transferred to the sugarcane version of the gene, when assembled).

The short read archive was downloaded from the NCBI (SRA: SRR427145).

To construct the equivalent sugarcane gene, we employed MiraBait with a k-mer of 21 to extract sugarcane reads corresponding to the sorghum target gene. Using the baited reads, the sugarcane gene was constructed *de novo* with SPAdes using a k-mer series of 21, 25, 35, 45, 55, 65 and 75, this being a modification of the pipeline previously developed for plastid assembly (Lloyd Evans and Joshi 2016a).

The length of each gene (and its orthology) was checked by comparing it against the original sorghum gene using EnSEMBL BLAST (sorghum accessions are given in Table 2). Exons and alternate transcripts were called using a combination of sugarcane EST mapping, sugarcane transcript read mapping, FGENESH exon calling (Salamov and Soleyev 2000) and mapping to the exons in the original sorghum gene. Assembled genes were annotated with CDSes, UTRs and alternate transcripts before being submitted to the EMBL gene database. The assembled genes can be accessed via the EMBL/GenBank project accession PRJEB14492.

Phylogenetics

To verify the gene assembly methodologies and to aid in annotation of closely-related genes, phylogenetic analyses were performed. The largest set of closely related genes was the glutathione S-transferases (phi and tau classes). Orthologues to the protein sequences derived from genes constructed as above, as well as similar genes in other species (sorghum, maize, rice, Arabidopsis, soybean and the spikemoss, *Selaginella*) were derived from BLAST searches at the NCBI and EnSEMBL orthologue searches. A glutathione S-transferase from *Chlamydomonas reinhardtii* was used as an outgroup.

Transcript sequences were aligned with SATÉ (Liu et al. 2009) prior to performing maximum likelihood analyses with RAxML (version 8.1.17) (Stamatakis 2014).

For phylogenetics analyses, RAxML was used to determine the most parsimonious tree from 100 replicates using the GTRGAMMA nucleotide substitution model. After the most likely tree was determined, 5000 bootstrap replicates were performed with RAxML, again under the GTRGAMMA nucleotide substitution model. Bootstrap replicates were mapped to the most likely tree using SumTrees (part of the DendroPy package) (Sukurman and Holder 2010).

Phylogenetic trees were drawn with FigTree (v 1.4.2)

(<http://tree.bio.ed.ac.uk/software/figtree/>) prior to finishing with Adobe Illustrator.

Structural Modelling

Protein sequences for each transcript (53 in total), these representing all the alternate protein coding transcript from our assembled gene sets, were extracted from the final EMBL gene files with a custom BioPerl script prior to submission to the Phyre² protein homology recognition batch server (Kelley et al. 2015).

The best structural model from each Phyre² run was re-submitted as an intensive analysis job which models the protein sequence against multiple templates to achieve

the best optimal structure. PDB files corresponding to the final modelled structures were downloaded and prepared for molecular dynamics simulation using the Protein Preparation Wizard of the Maestro molecular modelling software (v.9.6; Schrödinger, Inc). The model included all hydrogen atoms from the start, but the polar interactions of the Histidine residues were manually checked and the protonation states selected to optimize the hydrogen bond network.

Molecular dynamics (MD) simulations were performed to confirm that the 3D structure was stable without unfolding or any significant changes in secondary structure. We employed GROMACS (Abraham et al. 2015) with the CHARMM forcefield for this purpose and solvated our model in a cubic box with TIP3P water. The system was charge equilibrated with sodium or chlorine ions before being energy minimized. After energy minimization, the systems were equilibrated by Position restrained molecular dynamics at constant temperature of 300K and a constant pressure of 1atm for about 100ps before running a 200ns molecular dynamics simulation using the CHARMM forcefield. The final model was compared with the original threaded model to ensure conformational stability. Final structural images were drawn with UCSF Chimera (Pettersen et al. 2004) and rendered with Pixar's RenderMan®.

Optimal Template Percentage Identity Determination

Rather than employing a single template for threading, Phyre² employs a multi-template approach. This means that the percentage identity value for any single template is an under-estimation of that for the model as a whole. In an attempt to overcome this limitation, the sequences from all the PDB templates used to construct the model were extracted and aligned to the input sequence with Psi-BLAST (Altschul et al. 1997). The multiple sequence alignment was input into a custom Perl script which compared the aligned sequences nucleotide by nucleotide to the initial input sequence. For each position, the best matching amino acid (by identity or synonymy) was chosen to construct an aggregate model template.

The aggregate model template was re-aligned to the protein being modelled using Smith–Waterman. The final alignment was input into a PERL wrapper around the Fasta3 package application, ggsearch (Pearson 2000) to calculate the aggregate percentage identity across all template models. This aggregate percentage identity was captured in Table 3.

Analysis of Modelled Structures

The final structural models, generated, as above, were analysed by submission to the ProFunc server (Laskowski et al. 2005). Optimal models, percentage identity and root mean square deviations from the best-fit template were determined from the ProFunc results and are given in Table 3. Overall quality of the structures were analysed with the ProSA (Wiederstein and Sippl 2007) and Verify_3D (Eisenberg 1997) web servers.

Variant Detection

To aid future gene selection efforts for plant breeding variants, (SNPs, MNPs, indels and SSRs) were determined from the genes assembled as above. Prior to variant detection, the assembled gene sequences were re-baited against the global *Saccharum* hybrid LCP 85-384 read pool with MiraBait using a k-mer of 21. Reads were mapped to the assembled reference with BWA (Li and Durbin 2009), yielding a SAM file. Separately, the recently published SP80-3280 (SRA: SRR2891265; SRR2891588 and SRR2891587) genomic reads were also mapped to our reference genes. The SAM files were converted to BAM with SAMTOOLS (Li et al. 2009) and all unmapped reads were eliminated. The BAM files' read groups were corrected prior to merging and indexing. The Broad Institute's Genome Analysis Toolkit (GATK: McKenna et al. (2010)) was employed to optimize the BAM alignment file by optimizing poorly aligned regions, particularly around indels.

SNPs, MNPs and indels were called using variations on the methods detailed by the Palumbi Lab's Simple Fool's Guide (<http://sfg.stanford.edu/SNP.html>), using the latest version (3.5) of GATK. The scripts given in the Simple Fool's Guide were re-implemented in PERL, to allow

more control and parallel processing so that all files in a given directory could be processed automatically. The methodology was adjusted for high coverage (>10-fold) and high stringency but with an option to alternately process genes with <10-fold coverage). In addition, parameters were adjusted for a decaploid genome. A high quality good confidence SNP file was created with a call confidence of 20 and an emit confidence of 10. SNPs were discovered with a call confidence of 30 and an emit confidence of 10. As we are attempting to discover SNPs in a highly polyploid crop, and we are analyzing individual genes, there is insufficient coverage to run GATK's automated SNP verification modules. For transcript-based SNP detection we mapped existing sugarcane RNA-seq datasets (for the cultivars: Co7805, Q117, RB867515, SP70-1143 and SP80-3280) to our gene calls using HISAT2 version 2.0.3-beta (Kim et al. 2015) as the read aligner. HISAT2 mapping calls of 255 were converted to 60 for GATK compatibility. All SNPs predicted by GATK that were confirmed by RNA-seq data (called with the above GATK pipeline and confirmed by visualization in IGV; Robinson et al. (2011)) were marked as 'true' SNPs. This yielded the following empirical filter for GATK: $QD < 2 \parallel FS > 60 \parallel SOR > 4 \parallel MQ < 40 \parallel MQRankSum < -6 \parallel ReadPosRankSum < -4 \&\& QUAL > 55$ that corresponded to confirmed true SNP calls. This filter was used in all subsequent analyses to extract true SNPs and MNPs from the global variant call pool for each gene. Indels were treated as a subclass of MNPs and were included in the MNP calling steps.

SSRs were called with a modification of MISA (the Microsatellite Identification Tool: <http://pgrc.ipk-gatersleben.de/misa/>) with the code re-written to allow parallel processing and the automated processing of all fasta entries in a given directory.

All high quality and in-silico validated SNP-type variants and SSR-type variants were concatenated and exported to separate EXCEL files using a custom PERL script.

Variant Effect Prediction

Our EMBL files were converted to GenBank file format with a custom BioPerl (Stajich et al. 2002) script. Each gene was treated as a pseudo chromosome and all genes were used to

create a *Saccharum* database in SnpEff (Cingolani et al. 2012). A PERL wrapper around SnpEff automatically called the program against all our gene-based SNP calls, allowing them to be annotated against the parent gene. SNP effects were merged with data from the original SNP calls and output into a tab-delimited file for further processing or importing into Excel.

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Author Contributions

DLIE and SVJ conceived the initial experiment. DLIE refined and extended the experimental design, performed the analyses, developed the software scripts and pipelines, analyzed and interpreted the data and wrote the paper. SVJ helped proofread the final version of the manuscript.

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Tables

Table 1

Herbicide Classification	Mode of Action	Chemical Family
1/A	Inhibition of acetyl CoA carboxylase (ACCase)	Aryloxyphenoxy-propionate 'FOPs' / Cyclohexanedione 'DIMs'
2/B	Inhibition of acetolactate synthase (ALS)	Sulfonylurea / Imidazolinone / Triazolopyrimidine / Pyrimidinyl(thio)benzoate / Sulfonylaminocarbonyl-triazolinone
3/K1	Microtubule assembly inhibition	Dinitroaniline / Phosphoroamidate / Pyridine / Benzamide / Benzoic acid
4/O	Action like indole acetic acid (synthetic auxins)	Phenoxy-carboxylic-acid / Benzoic acid / Pyridine carboxylic acid / Quinoline carboxylic acid
5,6,7/C	Inhibition of photosynthesis at photosystem II (psbA)	Triazine / Triazinone / Triazolinone / Uracil / Pyridazinone / Phenyl-carbamate / Urea / Amide / Nitrile / Benzothiadiazinone / Phenyl-pyridazine / Bipyridylum
8,26/N	Inhibition of lipid synthesis - not ACCase inhibition	Thiocarbamate / Phosphorodithioate / Benzofuran / Chloro-Carbonic-acid
9/G	Inhibition of EPSP synthase	Glycine
10/H	Inhibition of glutamine synthetase	Phosphinic acid
11,13/F3	Bleaching: Inhibition of carotenoid biosynthesis (unknown target)	Triazole / Isoxazolidinone / Urea / Diphenylether
12/F1	Bleaching: Inhibition of carotenoid biosynthesis at the phytoene desaturase step (PDS)	Pyridazinone / Pyridinecarboxamide
14/E	Inhibition of protoporphyrinogen oxidase (PPO)	Diphenylether / Phenylpyrazole / N-phenylphthalimide / Thiadiazole / Oxadiazole / Triazolinone / Oxazolidinedione / Pyrimidindione
15/K3	Inhibition of VLCFAs (LACS8 is the only target)	Chloroacetamide / Acetamide / Oxyacetamide / Tetrazolinone

	confirmed thus far [Trenkamp et al, 2004])	
18/I	Inhibition of DHP (dihydropteroate) synthase	Carbamate
19/P	Inhibition of auxin (indoleacetic acid) transport	Phthalamate Semicarbazone
20/L	Inhibition of cell wall (cellulose) synthesis (one target is CESA1)	Nitrile / Benzamide / Triazolocarboxamide / Quinoline carboxylic acid
22/D	Photosystem-I-electron diversion	Bipyridylum
23/K2	Inhibition of mitosis / microtubule organization	Carbamate
27/F2	Bleaching: Inhibition of 4-hydroxyphenyl-pyruvate-dioxygenase (4-HPPD)	Triketone / Isoxazole / Pyrazole
N/A	Inhibition of histidine synthesis, inhibition of Ithidazole Glycerol Phosphate Dehydratase (IGPD)	Triazole

Herbicide classes with known mechanisms of action.

Listing of all the herbicide classes (based on the Weed Science Society of America (WSSA) and Herbicide Resistance Action Committee (HRAC) joint classification) with known modes of action. Also given are the chemical families that are active against a given classification.

Table 2

Gene Name	Sorghum Identifier	Sugarcane Gene Name	Best Annotation	Gene Length (bp)	# Exons	# Transcripts	Best PDB Match	Target Type
GPOX	Sb01g041770	ShGPOX	gaiacol peroxidase	2313	4	1	1PA2 Arabidopsis thaliana	S
IN2	Sb01g038900	ShIN2	safener induced gene 2 (glutathione transferase lambda)	2059	9	1	4PQI Populus trichocarpa	S
SBP1	Sb05g008830	ShSBP1	Herbicide safener binding protein (O-methyltransferase)	1511	2	1	1ZGA Medicago truncatula	S
ACC1	Sb08g016820 GRMZM2G143008 (Sorghum ALS is misassembled)	ShACC1	Acetyl-CoA carboxylase 1	11561	30	1	3MFM Streptomyces coelicolor	T
ALS		ShALS	Acetolactate synthase	2284	1	1	1YBH Arabidopsis thaliana	T
CESA1	Sb03g004320	ShCESA1	cellulose synthase A catalytic subunit 1 like	3129	5	1	4HG6 Rhodobacter sphaeroides	T
DHPS	Sb02g039380	ShDHPS	Dihydropteroate synthase	1719	3	1	2BMB Saccharomyces cerevisiae	T
EPSPS	Sb10g002230	ShEPSPS	5-enolpyruvylshikimate-3-phosphate (EPSP) synthase	3900	8	1	1G6S Escherichia coli	T
GLN1	Sb01g042450	ShGLN1	glutamine synthetase, isoform 1	3298	11	2	2D3A Zea	T

							mays	
HPPD	Sb04g004560	ShHPPD	4-hydroxyphenylpyruvate dioxxygenase	1926	2	1	1SP8 Zea mays 2F1D	T
IGPD	Sb06g028690	ShIGPD	Imidazoleglycerol-phosphate dehydratase 1	3393	8	1	Arabidopsis thaliana 5ES8	T
LACS8	Sb05g001740	ShLACS8	Long chain acyl-CoA synthetase 8	7496	13	3	Brevibacillus parabrevis 2QA1	T
LCY1	Sb04g006120	ShLCY1	Lycopene beta cyclase, chloroplastic	1478	1	1	Streptomyces sp. PGA64	T
LFNR	Sb03g046340	ShLFNR	Ferredoxin-NADP reductase, leaf isozyme	3673	7	2	1FNC Spinacia oleracea	T
PDS1	Sb06g030030	ShPDS1	Phytoene desaturase	5495	14	1	1S3B Homo sapiens	T
PPO	Sb03g011670	ShPPO	Protoporphyrinogen IX oxidase	5831	9	1	2IVD Myxococcus xanthus	T
psbA	NC_005878.2	psbA	photosystem II protein D1	1062	1	1	1IZL Thermosynecho coccus elongatus	T
TIR1	Sb09g003870	ShTIR1	transcript inhibitor response 1, auxin binding receptor	5473	3	1	2P1N Arabidopsis thaliana	T
ABCC1	Sb06g028880	ShABCC1	ABC transporter C family member 1 multidrug resistance associated	12040	28	1	4F4C Caenorhabditis	D

			protein			elegans 4F4C	
ABCC4	Sb03g014130	ShABCC4L	ABC transporter C family member 4, xenobiotic inducible	3845	10	Caenorhabditis elegans 2D3T	D
AIM1	Sb04g010370	ShAIM1	Peroxisomal fatty acid beta- oxidation multifunctional protein	7478	18	Pseudomonas fragi	D
ALF5	Sb02g000770	ShALF5	ALF5, a multidrug efflux transporter gene family	2633	6	EMKU Vibrio cholerae 2QPU	D
AML1	Sb02g026610	ShAML1	alpha-amylase	1758	2	Hordeum vulgare 207V Actinidia	D
CXE12	Sb02g026816	ShCXE12	carboxylesterase 12	1249	1	eriantha 2IV1	D
CYN	Sb01g019580	ShCYN	cyanate hydrolase (cyanase)	2850	4	Escherichia coli	D
CYP709		ShCYP709	cytochrome P450 monooxygenase			1TQN Homo	
B3	Sb01g034340	B3	gene, salt tolerance responsive	2486	5	sapiens 2X2N	D
CYP71E		ShCYP71E	oxime monooxygenase			Trypanosoma	
1	Sb01g001180	1	(Cytochrome P450 71E1)	2073	1	brucei	D
CYP72		ShCYP72A	cytochrome p450 72A31, tolerance			3NA0 Homo	
A31	Sb03g028680	31	to acetolactate synthase-inhibiting herbicides	1982	4	sapiens 3MKU Vibrio	D
DTX1	Sb03g031420	ShDTX1	detoxifying efflux carrier	4512	7	cholerae 3KVN	D
ESR1	Sb05g018910	ShESR1	esterase	2709	5	Pseudomonas	D

						aeruginosa	
						3KVN	
						Pseudomonas	
GDSL	Sb01g011850	ShGDSL	Esterase/Lipase	3580	5	1 aeruginosa	D
			Glutathione synthetase,			3KAL Glycine	
GSH2	Sb05g025630	ShGSH2	chloroplastic	4934	13	2 max	D
GSTF1	Sb03g035420	ShGSTF1	glutathione S-transferase phi 1	2494	3	1 1BYE Zea mays	D
GSTF12	Sb01g048000	ShGSTF12	glutathione S-transferase phi 12	1657	3	1 1BYE Zea mays	D
GSTF3	Sb03g044980	ShGSTF3	glutathione S-transferase phi 3	1147	3	1 1BYE Zea mays	D
GSTF4	Sb09g003690	ShGSTF4	glutathione S-transferase phi 4	1624	3	1 1BYE Zea mays	D
GSTF6	Sb01g047980	ShGSTF6	glutathione S-transferase phi 6	1193	3	1 1BYE Zea mays	D
						1GWC	
						Aegilops	
GSTU1	Sb01g030890	ShGSTU1	glutathione S-transferase tau 1	1139	2	1 tauschii	D
						1GWC	
						Aegilops	
GSTU3	Sb01g030950	ShGSTU3	glutathione S-transferase tau 3	871	2	1 tauschii	D
						1Z45	
						Saccharomyces	
HM2	Sb10g025740	ShHM2	HC toxin reductase (hm2), Rossman fold epimerase	1869	5	1 cerevisiae	D
						5ES8	
						Brevibacillus	
LACS7	Sb08g001010	ShLACS7	Long chain acyl-CoA synthetase 7, peroxisomal	9931	23	1 parabrevis	D
						2XR7	
						Nicotiana	
MAT1	Sb07g006100	ShMAT1	Malonyl-CoA:isoflavone 7-O- glucoside-6''-O-malonyltransferase	4464	2	1 tabacum	D
MATE	Sb03g012960	ShMATE	efflux family protein 3, chloroplastic	7036	14	2 3MKU Vibrio	D

MFP2	Sb03g013790	ShMFP2	Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2	6303	18	3	cholerae 2D3T Pseudomonas fragi 2VHI Drosophila	D
NIT4	Sb04g026930	ShNIT4	Nitirase 4 (cyanide hydratase) chloroplast outer membrane	3451	5	1	melanogaster 3KFU Thermus	D
OEP64	Sb01g010650	ShOEP64	amylase	10241	13	1	thermophilus 1JU2 Prunus	D
ONL1	Sb10g026110	ShONL1	(R)-mandelonitrile lyase, putative / (R)-oxynitrilase	2269	3	1	dulcis 2WUA Helianthus	D
PED1	Sb01g020150	ShPED1	3-ketoacyl-CoA thiolase	3849	14	1	annuus 3D22 Populus trichocarpa x Populus	D
TRX	Sb06g029490	ShTRX	Thioredoxin, salt tolerance responsive	1638	3	1	deltoides 2VCH Arabidopsis	D
UGT73 C6	Sb03g004130	ShUGT73C 6	UDP-glycosyltransferase 73C6-like	2143	3	1	thaliana	D

Templates, gene descriptions, gene properties and structure templates for each sugarcane gene assembled in this study.

This table lists all the gene names, with the sorghum or maize gene identifier used as a template in the gene build. Also given are the sugarcane gene names and EMBL identifier for the gene sequence. In addition, the best annotation for the gene is given along with the total gene length,

the number of exons and the number of alternate transcripts. The final column gives the best matching PDB entry (and species of origin) for the structure identified in the initial Phyre² batch analysis.

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Table 3

Sugarcane Gene Name	Phyre2 Confidence	% of residues at >90% confidence	Residues modelled at 100% confidence	Best PDB Template	Function of PDB Template	% identity with Best PDB template	Aggregate %id	Source and Template Same Function/Structure?	ProFunc Predicted Function	Best ProFunc %id	Matching Fold RMSD (Å)
psbA	100	95%	10–344	2AXT chain A	Bacterial photosystem II reaction centre, L and M subunits	88		Y (orthologue)	spinach psii-lhcii supercomplex	99.7	1.14
ShLFNR	100	100%	70–346	1FNC chain A	spinach ferredoxin reductase	84		Y (orthologue)	leaf ferredoxin-NADP+ reductase	94.576	0.66
ShGSTF1	100	100%	2–214	1BYE chain A	maize glutathione s-transferase i	93		Y (orthologue)	Glutathione s-transferase i	93.427	0.31
ShHPPD	100	90%	34–428	1SP8 chain A	4-hydroxyphenylpyruvate dioxygenase	94		Y (orthologue)	4-hydroxyphenylpyruvate dioxygenase	90.657	0.33
ShGSTF3	100	99%	2–216	1AW9 chain A	maize glutathione s-transferase iii in apo	87		Y (orthologue)	glutathione s-transferase iii	88.426	0.33
ShGLN1	100	99%	4–355	2D3A	maize	87		Y (orthologue)	glutamine	86.932	0.41

				chain J	glutamine synthetase imidazolegly cerol-			synthetase		
ShIGPD	100	67%	75–256	2F1D chain P	phosphate dehydratase Sunflower peroxisomal	87	Y (orthologue)	igpd2	85.93	0.29
ShPED1	100	88%	47–437	2WUA chain A	3-ketoacyl- coa thiolase	77	Y (orthologue)	peroxisomal 3- ketoacyl-coa thiolase 2 Arabidopsis thaliana	78.803	0.6
ShALS	100	89%	61–573	1YI1 chain A	acetolactate synthase lpha-	76	Y (Orthologue)	acetohydroxyacid synthase	76.562	0.3
ShAML1	100	92%	27–431	2QPU chain B	amylase type a isozyme arabidopsis thaliana	67	Y (orthologue)	alpha-amylase	70.443	0.47
ShMFP2- 3	100	96%	1–594	2WTB chain A	multifunction al protein, mfp2 arabidopsis thaliana	72	Y (orthologue)	multifunctional protein, mfp2	70.401	0.72
ShMFP2	100	94%	5–717	2WTB chain A	multifunction al protein, mfp2 spinach	72	Y (orthologue)	multifunctional protein, mfp2	69.944	0.39
ShLFNR- 1	100	99%	12–281	1FNC chain A	ferredoxin reductase	82	Y (orthologue)	leaf ferredoxin- NADP+ reductase	67.119	0.98
ShGSH2- 1	100	94%	21–488	3KAL chain B	glycine max homoglutath	66	Y (orthologue)	homoglutathione synthetase	65.948	0.44

ShGSH2	100	96%	21–488	3KAL chain B	ione synthetase glycine max homoglutath ione synthetase arabidopsis thaliana multifunction al protein, mfp2	66	Y (orthologue)	homoglutathione synthetase	65.948	0.4
ShMFP2- 1	100	94%	5–617	2WTB chain A	wheat tau class glutathione s-transferase transport inhibitor response 1 protein	65	Y (orthologue)	multifunctional protein, mfp2	64.326	0.87
ShGSTU3	100	94%	6–226	1GWC chain C	wheat tau class glutathione s-transferase	63	Y (Cognate gene)	tau class glutathione s- transferase	63.063	0.19
ShTIR1	100	98%	20–591	2P1N chain E	transport inhibitor response 1 protein wheat tau class glutathione s-transferase	62	Y (orthologue)	tir1 ubiquitin ligase	62.742	0.27
ShGSTU1	100	95%	4–255	1GWC chain C	CCP-like haeme dependent peroxidases	60	Y (Cognate gene)	tau class glutathione s- transferase	60.538	0.8
ShGPOX	100	90%	33–336	1pa2 chain A	maize GLUTATHI ONE S- TRANSFER ASE I	57	Y (Cognate gene)	Banyan peroxidase with glycosylation	59.868	0.49
ShGSTF4	100	94%	6-215	1BYE chain A		57	Y (Cognate gene)	glutathione s- transferase-i	57.488	0.35

ShAIM1	100	94%	1–713	2D3T chain B	fatty acid oxidation complex alpha subunit	59	Y (Cognate gene)	Arabidopsis thaliana multifunctional protein, mfp2 (Fatty acid beta-oxidation multienzyme complex)	56.135	0.81
ShEPSPS	100	98%	1–389	1g6s chain A	Enolpyruvate transferase, EPT	55	Y (Cognate gene)	epsp synthase	53.506	1.12
ShIN2	100	96%	8–240	4PQI chain A	glutathione transferase lambda 3	55	Y (orthologue)	glutathione transferase lambda 3	52.557	0.3
ShACC1	100	96%	16–2191	5CSL chain A	yeast acetyl-coa carboxylase 2	43	Y (Cognate gene)	Acetyl-coa carboxylase carboxyltransferase	51.52	0
ShONL1	100	98%	2–414	1JU2 chain A	hydroxynitrile lyase from almond phi class	43	Y (Cognate gene)	hydroxynitrile lyase phi class	42.718	0.4
ShGSTF12	100	98%	2–220	4RI7 chain A	glutathione transferase gstf1 Populus phi class	42	Y (Cognate gene)	glutathione s transferase (Atgstf2)	40.391	0.81
ShGSTF6	100	98%	2–221	4RI7 chain A	glutathione transferase gstf1	43	Y (Cognate gene)	Atgstf2 from arabidopsis thaliana	39.904	0.85
ShOEP64	100	97%	16–477	3KFU chain E	trna-dependent amidotransferase	24	37% Y (Cognate gene)	tRNA-dependent amidotransferase	39.548	1.13

					rase (Amidase signature (AS) enzymes)						
ShLACS7	100	87%	61–675	5ES8 chain A	acetyl-coa synthetase	19	41%	Y (Cognate gene)	luciferase (acetyl- coa synthase family)	39.073	1.04
ShCYN	100	89%	5–151	2IV1 chain J	cyanate hydratase bifunctional 6- hydroxymet hyl-7,8-2 dihydroxypt erin pyrophospho kinase	36	42%	Y (Cognate gene)	cyanase	38.971	0.78
ShDHPS	100	99%	72-498	2BMB chain A	dihydroptero ate synthase poplar	38	37%	Y (Cognate gene)	ternary complex of e. Coli dihydropte synthase	37.868	0.86
ShTRX	100	95%	8–126	3D22 chain A	thioredoxin h mutant gibberellin (ga3)	32		Y (orthologue)	thioredoxin h mutant	36.634	0.61
ShCXE12	100	96%	23–326	2ZSH chain A	receptor isoflavanone 4'-o- methyltransf erase	31	39%	Y (Cognate gene)	gibberellin receptor	34.615	0.64
SBP1	100	98%	11–365	1ZGA chain A	protoporphyr inogen	34		Y (Cognate gene)	isoflavanone 4'-o- methyltransferase	34.435	1.17
ShPPO	100	92%	57–528	2IVD chain A	protoporphyr inogen	33		Y (Cognate gene)	protoporphyrinogen ix oxidase	32.839	1.1

oxidase											
gal10 fusion protein galactose mutarotase/udp-galactose 4-epimerase from saccharomyces cerevisiae phytoene desaturase crt1											
ShHM2	100	98%	7–284	1Z45 chain A	16	39%	Y (same fold family [Rossmann fold Reductases])	dihydroflavonol reductase (epimerase fold family)	31.488	1.03	
ShPDS1	100	100%	1–406	4DGK chain A	16	32%	Y (orthologue)	l-amino acid oxidase	30.323	1.16	
ShUGT73 C6	100	97%	20–494	4RIE chain B	26	44%	Y (Cognate gene)	multifunctional (iso) flavonoid glycosyltransferase	29.039	1.06	
ShCYP71 E1	100	85%	117–595	3NA0 chain B	22	44%	Y (Cognate gene)	cytochrome p450 1a1	28.694	1.03	
ShCYP72 A31	100	98%	41–531	3NA0 chain B	17	44%	Y (Cognate gene)	microsomal p450 3a4	28.082	0.96	
ShCYP70 9B3	100	97%	1–483	1izo chain A	23	37%	Y (Cognate gene)	Cytochrome p450 3a4	27.195	1.14	
CESA1L	100	63%	10–450	4HG6 chain A	24		Y (Cognate gene)	cellulose synthase	26.974	N/A	
ESR1	100	87%	36–370	3KVN chain A	17	38%	Y (Cognate gene)	electron transfer flavoprotein (esterase)	26.957	0.66	
ShLACS8	100	93%	15–713	5ES8 chain A	19	41%	Y (Cognate gene)	luciferase (acetyl-coa synthase family)	26.931	1.4	

ShNIT4	100	94%	15–324	3WUY chain A	nitrilase	35		Y (Cognate gene)	n-carbamoylputresci amidohydrolase (nitrilase family)	26.384	1.18
ShGDSL	100	89%	26–353	3KVN chain A	esterase esta autotransport er	20	35%	Y (Cognate gene)	glutathione-binding protein a	26.19	0.46
ShABCC 1	100	82%	252– 1469	1YQT chain A	multi-drug transporter	18	44%	Y (Cognate gene)	multi-drug transporter	26.112 (core: 50)	0.62
ShABCC 4L	100	94%	1–762	4MRN chain B	multi-drug transporter	22	45%	Y (Cognate gene) Y (same fold family [Flavoprotein family])	heterodimeric abc transporter	25.958	1.23
ShLCY1	100	97%	68–442	2QA1 chain A	aromatic hydroxylase cation-bound multidrug and toxin compound extrusion (MATE)	12	27%		Thiazole synthase thi4	25.926	1.37
ShALF5	100	65%	57–389	3MKU chain B	transporter sorghum hydroxycinn amoyltransfe rase	21	37%	Y (Cognate gene)	Mate transporter norm-ng	25.588	1.45
ShMAT1	100	92%	22–469	4KE4 chain A	cation-bound multidrug and toxin compound extrusion (MATE)	20	36%	Y (same fold family [Acyltransferase family])	hydroxycinnamoylt ransferase	25.182	1.28
ShDTX1	100	94%	22–479	3MKU chain B		22	34%	Y (Cognate gene)	cation-bound multidrug and toxin compound ext (mate) transporter	25	1.49

transporter

ShMATE	100	80%	98–453	2MHK chain A	multidrug and toxin compound extrusion transporter	17	33%	Y (Cognate gene)	mate multidrug transporter dinf-bh	22.188	1.39
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Template Modelling Statistics and ProFunc Analyses for the Modelled Proteins.

For each sugarcane gene and transcript, information is given about the Phyre² intensive modelling statistics (Phyre score, % of high confidence residues, residue ranges modelled at 100% confidence, function of best matched PDB template, percentage identity with PDB template, aggregate % id and the functional relationship of source and template). In addition, the predicted structure function, best % id and matching fold RMSD are given for the ProFunc analyses. Table entries are arranged by ProFunc %ids and horizontal lines demarcate structures modelled at >30% identity as well as structures modelled at >25% identity.

Figures

Figure 1

Phylogram for sugarcane tau and phi class glutathione S-transferases with cognates from: Sb — *Sorghum bicolor*; Zm — *Zea mays*; OsJ — *Oryza sativa* Japonica; Ma — *Musa acuminta*; At — *Arabidopsis thaliana*; Gm — *Glycine max*; Sm — *Selaginella moellendorffii* and *Chlamydomonas* — *Chlamydomonas reinhardtii*. The scale bar represents expected number of substitutions per site. Numbers above branches represent Maximum Likelihood bootstrap branch support.

Figure 2

Thumbnails of structures that are herbicide targets or which interact with safeners. Thumbnail images of modelled structures for all the proteins that are herbicide targets. The three boxed images are the model structures for proteins that bind to safeners. In all cases, images were drawn with UCSC Chimera. Rainbow colouring is employed from N-terminus to C-terminus. Protein codes are the same as used in Table 2. Only a single example of each major structural type is given.

Figure 3

Thumbnails of protein structures that are known to be involved in herbicide detoxification. Representative structures of proteins identified in this study that are known to act as herbicide detoxifiers. Structures were homology modelled and final cartoon representations were drawn with UCSC Chimera. Rainbow colouring is employed from N-terminus to C-terminus. Protein codes are the same as used in Table 2. Only a single example of each major structural type is given.

Supplementary Tables

Supplementary Table 1

Allelic polymorphisms

Allelic polymorphisms determined within the assembled gene sequence from LCP 85-834 based on short reads mapped back to our assembled genes and a decaploid genome. All polymorphisms have been functionally characterized.

Supplementary Table 2

Gemomic Polymorphisms

SNPs and MNPs determined from a comparison of LCP 85-834 and SP80-3280 genomic reads mapped to 12 of our assembled genes. All polymorphisms have been functionally characterized.

Supplementary Table 3

RNA-seq Polymorphisms

SNPs and MNPs determined by mapping RNA-seq data for the following sugarcane cultivars: Co7805, Q117, RB867515, SP70-1143 and SP80-3280 onto our assembled genes. All polymorphisms have been functionally characterized.

Supplementary Table 4

SSR variants

SSR variants as determined by MISA (the Microsatellite Identification Tool) for all our assembled herbicide-associated genes.

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Phylogram for sugarcane tau and phi class glutathione S-transferases with cognates from: Sb — Sorghum bicolor; Zm — Zea mays; OsJ — Oryza sativa Japonica; Ma — Musa acuminta; At — Arabidopsis thaliana; Gm — Glycine max; Sm — Selaginella moellendorffii and Chlamydomonas — Chlamydomonas reinhardtii. The scale bar represents expected number of substitutions per site. Numbers above branches represent Maximum Likelihood bootstrap branch support.

199x272mm (300 x 300 DPI)

Thumbnails of structures that are herbicide targets or which interact with safeners. Thumbnail images of modelled structures for all the proteins that are herbicide targets. The three boxed images are the model structures for proteins that bind to safeners. In all cases, images were drawn with UCS Chimera. Rainbow colouring is employed from N-terminus to C-terminus. Protein codes are the same as used in Table 2. Only a single example of each major structural type is given.

332x276mm (300 x 300 DPI)

Thumbnails of protein structures that are known to be involved in herbicide detoxification. Representative structures of proteins identified in this study that are known to act as herbicide detoxifiers. Structures were homology modelled and final cartoon representations were drawn with UCSC Chimera. Rainbow colouring is employed from N-terminus to C-terminus. Protein codes are the same as used in Table 2. Only a single example of each major structural type is given.

312x329mm (300 x 300 DPI)

Gene	Start	End	Ref	Alt	QD	MQ
ABCC1	12142	12142	C	A	5.7	60
ABCC1	12243	12243	T	A	21.04	57.27
ABCC4L	4087	4087	T	A	8.89	60
ACC1	11469	11469	T	G	10.93	60
ACC1	11601	11601	A	C	5.62	58.54
ACC1	11652	11652	T	TA	7.6	58.51
ACC1	11692	11692	G	A	11.6	60
ACC1	11765	11765	G	GTGTGTA	9.45	60
ACC1	11768	11768	C	T	15.2	60
AIM1	7385	7385	A	ACT	8.16	60
AIM1	7441	7441	G	A	5.68	60
AIM1	7453	7460	GCTATCAC	G	19	60
AML1	1523	1523	C	A	16.22	60
AML1	1524	1524	G	C	16.22	60
AML1	1530	1530	T	C	15.86	60
AML1	1531	1531	T	TCA	15.36	60
AML1	1549	1549	T	TTCAA	14.71	60
AML1	1579	1579	T	A	16.8	60
AML1	1582	1582	A	T	16.8	60
AML1	1589	1589	C	T	21.89	60
AML1	1610	1610	G	C	24.55	60
AML1	1612	1612	A	G	24.55	60
AML1	1638	1641	AAAG	A	27.63	60
AML1	1654	1654	A	T	28.62	60
AML1	1660	1660	G	C	27.96	60
CESA1	3052	3052	A	G	7.18	60
CESA1	3141	3141	A	AG	7.32	60
CYN	2757	2757	T	C	10.57	60
CYN	2758	2758	T	C	10.57	60
CYN	2854	2854	T	C	25.64	60
CYN	2954	2954	C	T	18.51	60
CYN	3009	3010	TA	T	14.47	60
CYP709B3	2317	2317	A	T	8.03	60
CYP709B3	2395	2395	A	T	6.34	60
CYP709B3	2452	2452	G	A	8.02	60
CYP709B3	2460	2460	C	CTTT	17.31	60
DHPS	1864	1864	C	G	8.66	59.85
DHPS	1867	1867	G	A	8.34	59.86
DTX1	4730	4730	A	AG	6.97	60
EPSPS	3840	3840	A	G	19.42	61.58
EPSPS	3891	3891	G	T	9.74	62.73
EPSPS	3900	3900	C	CT	9.79	62.82
EPSPS	3901	3901	A	T	12.35	62.82

EPSPS	3981	3981 G	A	34.58	61.08
EPSPS	4004	4004 T	C	21.56	60.49
EPSPS	4049	4049 T	C	27.27	60
ESR1	2710	2710 C	T	8.76	60
ESR1	2738	2738 T	C	8.94	60
ESR1	2766	2766 G	A	14.52	60
GDSL	3846	3850 TTCCC	T	6.05	60
GDSL	3851	3853 AAT	A	6.05	60
GPOX	2463	2463 C	T	6.14	60
GSL1-1	3307	3307 C	G	9.7	60
GSL1-1	3361	3361 G	A	15.92	60
GSTF1	2451	2451 G	A	18.22	60
GSTF1	2494	2494 A	G	19.12	60
GSTF1	2540	2540 A	C	22.74	60
GSTF3	1299	1299 C	A	25	59.24
GSTF3	1303	1303 T	A	28.37	59.24
GSTF3	1309	1309 T	G	31.59	59.3
GSTF3	1326	1326 G	C	28.7	57.3
GSTF3	1334	1335 GT	G	30.29	57.67
GSTF3	1338	1338 T	G	32.34	57.5
GSTF3	1342	1342 A	G	27.35	57.5
GSTF3	1346	1346 G	A	30.93	57.3
GSTF3	1348	1348 C	CA	17.23	57.3
GSTF3	1352	1352 G	T	17.93	57.3
GSTF3	1357	1357 G	C	17.93	57.3
GSTF3	1358	1358 C	T	33.68	57.3
GSTF4	1867	1867 G	A	12.42	60
GSTF4	1873	1873 A	G	28.27	60
GSTF4	1876	1876 G	C	27.54	60
GSTF4	1907	1907 A	G	25.22	60
GSTF4	1922	1922 T	C	8.85	60
GSTF6	1309	1309 T	C	9.61	60
GSTF6	1470	1470 A	T	8.63	60
HM2	1915	1915 C	T	11.17	60
HPPD	1927	1927 A	G	13.41	60
HPPD	1969	1969 T	TAACGA,TAA	31.32	60
HPPD	1972	1972 A	G	17.53	60
IGPD	3685	3685 G	A	10.22	60
IGPD	3719	3719 A	G	10.65	60
IGPD	3770	3770 G	C	14.99	60
IGPD	3806	3806 C	T	3.83	60
IGPD	3839	3839 A	T	7.53	60
IGPD	3921	3921 C	A	9.9	60
IGPD	3934	3934 G	A	8.75	60

IGPD	3949	3949 A	G	14.37	60
IGPD	3952	3952 T	A	14.37	60
IGPD	3958	3958 A	C	14.32	60
IGPD	3982	3982 G	A	15.37	60
IGPD	4021	4021 C	T	11.99	60
IGPD	4112	4112 G	T	10.1	60
IGPD	4113	4113 A	T	10.56	60
IN2	1916	1916 C	T	12.16	60
IN2	1954	1954 A	T	11.32	60
IN2	1994	1998 CTATA	C	14.39	60
IN2	1999	1999 T	C	9.87	60
IN2	2013	2013 G	T	14.72	60
IN2	2036	2037 CA	C	13.33	60
IN2	2039	2039 C	A	13.14	60
IN2	2044	2044 T	C	20.82	60
IN2	2059	2059 G	A	11.94	60
IN2	2102	2102 G	C	14.15	60
IN2	2116	2116 C	CA	15.03	60
IN2	2147	2147 T	C	13.31	60
IN2	2152	2152 C	T	12.86	60
IN2	2198	2198 A	T	8.65	60
IN2	2213	2213 T	TGGACCGAA ⁺	10.52	60
IN2	2214	2214 G	GGACCGA	10.58	60
IN2	2235	2235 G	T	24.69	60
IN2	2239	2239 T	C	9.22	60
IN2	2282	2282 T	G	9.16	60
IN2	2323	2323 G	A	19.45	59.56
LACS7	9540	9540 C	T	13.59	60
LACS7	9541	9541 C	A	13.59	60
LACS7	9552	9552 T	C	8.38	60
LACS7	9579	9581 TTA	T	15.21	60
LACS7	9610	9610 A	G	9.31	60
LACS7	9623	9623 C	CGCA	10.46	60
LACS7	9664	9664 C	G	15.33	59.41
LACS7	9665	9665 A	ACTTATAC	14.9	59.41
LACS7	9699	9699 T	C	18.17	58.53
LACS7	9710	9710 C	CGTTATGAAC	17.46	58.53
LACS7	9727	9727 A	C	20.83	58.32
LACS7	9733	9733 G	GAGT	17.42	58.32
LACS7	9736	9736 C	T	17.83	58.04
LACS7	9739	9739 A	G	9.34	58.04
LACS7	9763	9763 T	C	14.85	58.79
LACS7	9773	9773 G	T	20.01	58.44
LACS8	7058	7058 A	G	12.84	60

LACS8	7060	7060 C	CA	12.14	60
LACS8	7079	7079 T	C	13.4	60
LACS8	7326	7326 A	G	10.8	60
LACS8	7339	7339 C	G	12.7	60
LACS8	7473	7473 T	C	21.79	60
LACS8	7516	7516 C	T	32.06	60
LACS8	7517	7517 C	G	13.52	60
MATE	6969	6969 A	G	13.85	60
MATE	6974	6974 C	T	12.41	60
MATE	7018	7018 C	T	11.27	60
MATE	7026	7026 G	A	11.96	60
MATE	7051	7051 A	T	9.47	60
MATE	7053	7058 CATTAT	C	8.79	60
MATE	7074	7074 C	T	20.2	60
MATE	7076	7087 AAGATGTTTCA		9	60
MATE	7102	7102 G	A	10.72	60
MATE	7110	7110 A	G	25.31	60
MATE	7162	7162 C	CT	20.76	60
MATE	7175	7175 T	C	21.15	60
MATE	7225	7225 T	G	10.05	60
MFP2	6269	6269 T	C	13.49	60
MFP2	6274	6274 G	A	13.39	60
MFP2	6280	6280 A	G	12.02	60
MFP2	6293	6293 A	G	12.64	60
OEP64	10071	10071 T	TC	10.6	60
OEP64	10077	10077 C	CCCCCAAAA ^A	8.52	60
OEP64	10130	10130 C	CA	9.31	60
OEP64	10164	10164 G	T	8.11	60
PDS1	5994	6000 ATTTCAT	A	23.38	60
PDS1	6070	6070 T	A	7.33	60
PDS1	6079	6079 A	G	12.82	60
PED1	3883	3885 ACT	A	8.44	60
PPO	5633	5633 C	T	24.84	60
PPO	5697	5697 T	G	23.32	60
PPO	5732	5732 C	T	28.94	60
TRX	1733	1733 C	CGT	6.89	60
CESA1	258	258 A	T	8.95	59.72
GSTU3	288	288 G	C	7.85	60
OEP64	39	39 G	C	28.2	60
AIM1	74	74 A	G	19.81	60
AIM1	85	85 G	GCCGCGGAA ₁	28.07	60
AML1	81	81 G	A	26.79	61.53
AML1	85	85 C	G	26.79	61.53
AML1	105	105 A	C	31.98	61.19

CESA1	82	82 G	A	8.73	59.95
CESA1	88	88 G	T	11.23	59.95
CESA1	94	94 T	C	11.33	59.82
CESA1	100	100 T	C	10.27	59.84
CESA1	121	121 T	C	14.23	59.84
CESA1	124	124 C	T	13.44	59.83
CESA1	148	148 C	A	9.66	59.62
CESA1	157	157 T	A	10.25	59.76
CESA1	252	252 C	T	9.87	59.72
GDSL	345	345 T	C	15.03	60
GDSL	347	350 GTTT	G	9.22	60
GPOX	340	340 T	G	9.53	60
GPOX	403	403 A	G	6.64	60
GSTF12	226	226 G	A	5.88	60
GSTF12	235	235 C	T	8.28	60
GSTF12	264	264 A	G	14.06	60
GSTF4	324	324 G	GGAAAA	8.74	60
GSTU1	119	119 G	A	8.7	60.77
HM2	215	215 A	G	8.02	60
IGPD	243	243 C	A	27.79	60
LACS8	1814	1814 G	A	11.27	60
LFNR	430	430 C	CT	22.45	60
LFNR	431	431 C	CTCCTCATCG	22.45	60
LFNR	474	474 A	AAATCC	7.89	60
LFNR	492	492 C	T	7.87	60
MAT1	122	122 A	C	33.48	62.65
MATE	286	286 G	T	16.34	60
MATE	381	381 A	G	10.46	60
MATE	447	447 G	T	32.6	61.34
MATE	460	460 G	A	12.23	61.07
MFP2	260	260 T	G	15.67	60
NIT4	442	442 G	A	26.52	60
OEP64	56	56 G	C	34.9	60
PED1	135	135 C	T	28.03	60
PED1	148	148 C	A	29.08	60
PED1	168	168 G	A	11.51	60
TRX	263	263 T	C	13.42	60
TRX	331	331 G	A	11.31	60
TRX	337	337 C	G	13.55	59.91
TRX	338	338 A	G	12.98	59.92
TRX	387	387 C	T	13.18	59.89
TRX	389	389 C	T	12.48	59.9
ALF5	194	197 TGAG	T	18.94	59.14
ALF5	239	242 TGAC	T	18.94	57.13

CESA1	1616	1619 GGAA	G	11.77	58.99
CYP71E1	332	335 TGTC	T	9.51	60
GSH2	3522	3525 AAGG	A	25.27	60
PDS1	922	925 TTCC	T	15.6	60
CESA1	1622	1622 C	CGAT	13.24	59.01
DHPS	233	233 T	TACAATCACG	23.85	60
GSTU1	126	126 T	TGGA	24	60.77
GSTU1	630	630 G	GGCA	21.03	60
LACS7	2061	2061 T	TAAG	29.6	60
ONL1	1863	1863 T	TTAGGAC	8.81	60
ABCC4L	4171	4171 G	GTA	12.14	60
ABCC4L	4185	4185 T	C	14.83	60
ABCC4L	4197	4197 A	G	26.11	60
ABCC4L	4198	4198 A	C	23.15	60
ABCC4L	4212	4212 T	C	11.72	60
ABCC4L	4238	4238 T	C	11.08	60
ABCC4L	4271	4271 T	C	13.47	60
ACC1	11943	11943 A	G	6.59	60
AIM1	7634	7634 T	G	27.92	60
AIM1	7650	7650 T	C	26.64	60
AIM1	7653	7653 T	C	33.4	60
AIM1	7674	7674 G	A	26.72	59.22
ALF5	2866	2866 T	C	13.64	60
ALF5	2890	2890 A	C	12.18	60
ALF5	2969	2971 CTG	C	8.34	60
ALF5	2971	2971 G	GT	27.07	60
ALF5	3009	3009 C	T	12.45	60
ALF5	3029	3029 C	G	12.98	60
ALS	2300	2300 A	AG	13.53	60.33
ALS	2425	2425 T	G	18.73	60.39
ALS	2426	2426 C	T	18.73	60.39
ALS	2489	2489 G	C	16.42	60
ALS	2506	2506 A	AAT	8.86	60
ALS	2749	2749 A	AT	7.2	60
ALS	2779	2779 A	T	9.79	60
AML1	1816	1816 G	A	11.79	59.64
AML1	1819	1819 C	A	10.08	59.71
AML1	1824	1824 G	A	10.08	59.69
AML1	1856	1856 A	G	13.63	59.66
AML1	1882	1882 C	T	23.54	59.86
AML1	1889	1889 G	A	7.85	59.88
AML1	1993	1993 G	A	24.94	59.83
AML1	2007	2007 C	T	7.94	60
AML1	2037	2037 A	G	23.94	60

AML1	2046	2046 T	C	7.85	60
AML1	2069	2069 T	C	6.28	60
AML1	2125	2125 T	C	11.9	60
AML1	2133	2133 T	A	12.45	60
AML1	2147	2147 G	T	13.11	60
AML1	2192	2192 T	C	22.31	55.79
AML1	2197	2197 C	T	22.31	55.79
AML1	2199	2199 G	A	22.31	55.79
AML1	2207	2207 T	A	25.29	55.21
AML1	2218	2218 T	A	31.94	60
AML1	2219	2219 C	T	26.03	60
CESA1	3192	3192 T	G	7.38	60
CESA1	3219	3219 G	A	11.84	59.25
CESA1	3358	3361 ATCT	A	4.11	59.31
CXE12	1338	1338 T	G	29.9	60
CXE12	1358	1358 G	A	24.85	60
CXE12	1385	1385 C	T	13.79	60
CXE12	1508	1508 T	G	12.45	60
CXE12	1519	1519 C	T	12.91	60
CXE12	1523	1523 A	T	15.36	60
CXE12	1556	1556 A	G,C	24.09	60
CXE12	1564	1564 T	C	7.47	60
CXE12	1575	1575 C	T	9.11	60
CXE12	1593	1593 T	C	19.69	60
CXE12	1606	1606 G	A	10.68	60
CXE12	1614	1614 G	A	9.6	60
CXE12	1626	1626 C	T	8.66	60
CXE12	1678	1678 C	CTT	7.59	60
CXE12	1713	1713 T	A	6.56	60
CXE12	1724	1724 G	A	22.68	60
CYN	3037	3037 T	C	8.54	60
CYN	3127	3127 A	G	5.41	60
CYN	3165	3165 G	A	8.17	60
CYP709B3	2587	2587 G	A	6.79	60
CYP709B3	2839	2842 CAAT	C	12.13	60
CYP709B3	2852	2852 C	T	13.23	60
CYP709B3	2865	2865 C	G	10.29	60
CYP71E1	1848	1848 G	A	17.24	60
CYP71E1	1851	1855 GACGT	G	23.2	60
CYP71E1	1884	1884 A	G	10.05	59.57
CYP71E1	1912	1912 T	C	19.52	59.45
CYP72A31	2382	2382 A	C	13.89	60
CYP72A31	2387	2387 C	T	8	60
EPSPS	4108	4110 TAA	T	15.95	60

EPSPS	4123	4123 T	C	16.7	60
EPSPS	4131	4144 CGTCTGTGACC		16.62	60
EPSPS	4143	4143 T	C	17.24	60
EPSPS	4152	4152 C	T	15.43	60
EPSPS	4154	4154 C	T	14.15	60
EPSPS	4185	4185 C	A	17.52	60
ESR1	2958	2958 A	G	6.67	60
GDSL	4047	4047 C	T	12.29	60
GDSL	4286	4286 A	ACACCAC,AC,	28.89	59.42
GPOX	2681	2681 A	G	6.97	60
GPOX	2713	2713 A	G	9.85	60
GPOX	2737	2739 ACT	A	12.07	60
GSH2	4287	4288 AT	A	10.75	60
GSH2	4406	4406 A	G	11.49	60
GSH2	4460	4460 G	T	25.16	60
GSH2	4517	4519 GAC	G	8.56	60
GSH2	4544	4544 C	T	16.81	60
GSH2	4554	4554 A	C	5.09	60
GSH2	4730	4730 A	T	13.2	60
GSH2	4731	4731 C	G	12.38	60
GSH2	4800	4800 C	CATCAT	14.84	60
GSH2	4808	4808 T	C	18.72	60
GSH2	4947	4947 T	TTTCTGTCCC	14.62	60
GSH2	4954	4954 G	A	6.41	60
GSH2	5034	5046 TACTGTGTAGT		10.27	60
GSH2	5065	5065 G	GTAC	15.8	60
GSH2	5089	5089 A	ATATATATAT	14.66	60
GSH2	5091	5091 A	C	15.8	60
GSH2	5197	5197 G	A	10.38	60
GSH2	5264	5264 A	C	22.75	60
GSH2	5272	5272 A	ACGT	20.92	60
GSH2	5273	5273 A	AGACAAACA	26.15	60
GSH2	5274	5274 A	G	7.91	60
GSTF12	1610	1617 CTTGTGAG	C	18.13	60
GSTF1	2642	2642 T	C	8.38	60
GSTF1	2643	2643 G	C	19.09	60
GSTF1	2678	2678 T	C	19.09	60
GSTF1	2680	2680 A	G	16.79	60
GSTF1	2788	2788 C	T	17.52	60
GSTF1	2879	2879 G	A	22.71	58.24
GSTF1	2947	2948 CG	C	5.95	58.24
GSTF1	3077	3077 T	C	9.63	56.09
GSTF1	3085	3085 T	A	26.91	55.76
GSTF1	3089	3089 T	A	31.77	55.62

GSTF1	3099	3099 A	T	20.91	55.19
GSTF1	3100	3100 T	A,TA	30.66	55.19
GSTF1	3107	3107 A	AT	16.4	55.29
GSTF1	3108	3108 G	A	17.52	55.7
GSTF1	3121	3121 A	G	12.5	55.7
GSTF1	3123	3123 A	G	7.61	55.7
GSTF1	3124	3124 T	C	14.22	55.7
GSTF1	3127	3127 G	A	14.22	55.7
GSTU1	959	960 GA	G	7.84	60
GSTU1	971	971 T	A	22.11	60
GSTU1	973	973 T	A	20.73	60
GSTU1	993	993 C	A	29.66	59
GSTU1	1017	1017 C	A	8.69	58.18
GSTU1	1021	1021 A	G	17.71	58.25
GSTU1	1024	1024 G	C	9.15	58.31
HPPD	2020	2020 G	C	15.13	60
HPPD	2092	2092 T	A	19.82	60
HPPD	2211	2211 A	C	6.04	59.79
HPPD	2257	2257 C	T	15.86	59.81
HPPD	2514	2514 A	T	6.78	60
HPPD	2750	2750 A	G	22.89	60
HPPD	2762	2762 T	G	7.73	60
HPPD	2823	2823 A	G	21.76	60
HPPD	2887	2887 G	A	14.02	60
IGPD	4145	4145 T	G	11.87	60
IGPD	4175	4175 T	C	18.89	60
IGPD	4711	4711 G	T	33.32	59.95
IN2	2330	2330 C	CT	17.42	59.59
IN2	2350	2350 T	C	15.31	59.56
IN2	2360	2360 C	T	14.15	59.52
LACS8	7555	7555 T	G	18.17	60
LACS8	7559	7564 CTCAAG	C	17.85	60
LACS8	7573	7573 T	G,C	20.7	60
LACS8	7594	7594 T	C	20.87	60
LACS8	7597	7597 C	G	10.53	60
LACS8	7602	7602 G	C	23.94	60
LACS8	7608	7608 T	C	12.53	60
LACS8	7657	7657 C	T	14.06	60
LACS8	7664	7664 A	G	15.58	60
LACS8	7920	7920 A	G	24.24	56.28
LCY1	1782	1782 C	T	7.68	60
LCY1	1787	1787 A	G	8.45	60
LCY1	1854	1854 C	T	13.73	60
LCY1	1917	1917 A	C	11.34	60

LCY1	2451	2451 T	C	27.71	60
LFNR	3436	3436 A	T	6.73	60
MAT1	4571	4571 A	ATGATCTTGC	21.48	60
MAT1	4705	4705 A	G	14.62	60
MAT1	4722	4722 C	T,A	34.22	60
MATE	7272	7272 C	T	12.16	60
MFP2	6542	6542 G	C	11.35	60
MFP2	6587	6587 A	C	14.64	60
MFP2	6616	6616 C	T	9.89	60
MFP2	6640	6640 A	G	15.37	60
MFP2	6690	6690 T	TGA	16.73	60
MFP2	6704	6704 A	G	15.11	60
MFP2	6722	6722 T	C	17.57	59.89
MFP2	6731	6731 C	T	15.99	59.89
MFP2	6734	6736 GTT	G	16.8	59.88
MFP2	6953	6953 G	A	7.58	58.3
NIT4	3709	3709 T	G	8.34	60
NIT4	3718	3718 G	A	9.6	60
NIT4	3777	3779 GGA	G	11.85	60
NIT4	3811	3811 C	CCTCCT	12.02	60
NIT4	3817	3817 C	CTCCTT	7.18	60
NIT4	3892	3892 A	G	10.42	60
NIT4	3909	3909 A	G	18.12	60
OEP64	10285	10285 C	CT	4.58	60
OEP64	10443	10443 A	G	12.51	60
OEP64	10658	10658 G	C	11.09	60
OEP64	10737	10737 T	A	12.14	60
ONL1	2594	2594 C	CCT	13.86	60
ONL1	2642	2642 C	T	11.36	60
ONL1	2664	2664 C	A	7.67	60
ONL1	2731	2731 G	A	8.26	60
ONL1	2740	2745 GAATTA	G	10.74	60
ONL1	2777	2777 C	T	10.62	60
ONL1	2880	2880 G	A	8.34	60
ONL1	2925	2928 TGTC	T	16.6	60
ONL1	2926	2926 G	C	17.87	60
PDS1	6437	6437 C	A	7.35	60
PDS1	6488	6488 G	C	9.73	60
PED1	4015	4018 TATA	T	8.28	60
PED1	4019	4019 A	G	8.78	60
PED1	4032	4032 G	A	9.94	60
PED1	4034	4034 G	C	7.82	60
PED1	4066	4066 C	T	18.07	60
PED1	4079	4079 G	C	28.9	60

PED1	4086	4086 T	C	21.01	60
PPO	5846	5846 G	T	19.89	60
PPO	5943	5943 C	T	16.22	60
PPO	5948	5948 A	T	15.21	60
PPO	6156	6156 A	C	12.34	60
PPO	6176	6176 C	G	17.84	60
PPO	6220	6225 CTCCCA	C	17.62	60
PPO	6241	6241 G	A	23.62	60
PPO	6255	6255 A	G	21.73	59.92
PPO	6357	6357 C	G	17	60
PPO	6361	6361 A	G	12.45	60
PPO	6546	6548 TAA	T,TA	30.58	56.77
PPO	6549	6549 A	G	6.46	56.52
SBP1	1783	1783 A	G	16.99	60
SBP1	1978	1978 T	C	20.66	50.6
SBP1	2012	2012 A	ACAGTGTTTT	30.84	57.93
SBP1	2070	2070 G	GACCGTCAGC	11.53	60
TIR1	5183	5183 C	T	11.45	60
TIR1	5392	5392 C	T	5.89	60
TIR1	5464	5464 C	G	8.11	60
TIR1	5482	5484 GTC	G	11.5	60
TRX	1895	1895 C	T	19.34	59.84
TRX	1899	1899 A	T	10.77	59.84
TRX	1906	1906 C	T	8.93	59.84
UGT73C6-like	2471	2471 T	C	12.35	60
UGT73C6-like	2482	2482 C	T	11.99	60
UGT73C6-like	2501	2501 T	C	10.89	60
UGT73C6-like	2516	2516 C	G	12	60
UGT73C6-like	2521	2521 C	A	12.3	60
UGT73C6-like	2657	2657 G	C	13.99	59.86
ABCC1	2594	2595 CT	C	8.67	60
ABCC1	11263	11263 A	AT	18.81	60
ACC1	2054	2054 G	GGC	10.57	57.68
ACC1	2057	2057 T	TGG	10.21	57.77
ACC1	2060	2062 TCA	T	9.15	57.68
ACC1	2064	2066 TAC	T	9.15	57.68
ALF5	1265	1265 T	TCACTG	7.89	60
AML1	199	199 C	CCAGGTACG	28.66	60
AML1	516	517 GC	G	18.08	60
AML1	521	523 GGC	G	12.29	60
CYP709B3	1043	1043 C	CA	10.12	60
CYP709B3	1048	1049 CT	C	7.72	60
CYP71E1	784	788 GAGGC	G	12.14	58.03
CYP71E1	804	804 C	CAATTGCG	18.15	57.13

DHPS	1816	1816 G	GGT	14.82	59.85
DHPS	1817	1819 TAC	T	14.82	59.85
DTX1	595	596 TG	T	7.48	60
ESR1	2478	2478 T	TC	32.24	60
GPOX	686	686 G	GTCCAGGTAC	7.5	60
GSH2	3605	3605 G	GA	12.64	59.94
GSTF4	1481	1481 G	GGT	26.62	50.75
GSTF4	1483	1485 CCA	C	20.89	51.59
GSTU1	572	574 CAG	C	26.71	60
GSTU1	671	671 G	GTT	17.07	59.7
GSTU1	673	673 G	GCT	17.07	59.68
GSTU1	677	687 GCGTGGGGT,G		7.76	59.61
GSTU1	682	686 GGGTA	G	7.76	59.61
GSTU1	688	689 CT	C	7.15	59.65
GSTU1	707	707 G	GCA	7.05	59.65
GSTU1	709	711 TTC	T,CTC	21.64	59.65
GSTU1	899	900 CG	C	28.47	60
HM2	1448	1452 CTGGT	C	27.09	55.69
HM2	1455	1457 AGG	A	20.89	56.06
HM2	1463	1463 C	CA	19	56.38
HM2	1473	1473 A	ATCGCT	18.63	57.3
LCY1	703	704 GC	G	28.59	58.74
LCY1	710	710 A	AT	30.63	58.74
MFP2	4700	4700 A	ATAAAATATA	18.1	60
PDS1	1155	1156 TA	T	18.05	60
PDS1	1187	1188 GT	G	22.32	60
PDS1	1565	1565 T	TG	19.28	60
PDS1	2446	2447 TG	T	15.58	60
CYP71E1	27	27 A	AAT	16.42	60
GSH2	3608	3608 G	A,GTGAGAAA	31.58	59.94
AML1	714	717 TCAC	T	18.84	60
CYP72A31	1522	1525 CGAT	C	12.09	60
HM2	1438	1441 GTTC	G	17.82	60
CESA1	688	688 A	AAAG	13.69	60
CYP72A31	1578	1578 A	ACGG	12.88	59.79
HM2	1471	1471 C	CTGG	17.07	56.06
GDSL	3427	3427 T	C	26.51	56.82
TRX	843	872 ATTAGTCTGAA		18.34	60.32
ABCC1	642	655 ATGATCACTAA		13.04	60.35
ABCC1	2156	2156 T	C	12.88	60
ABCC1	2218	2218 C	T	24.04	60
ABCC1	2679	2679 T	G	15.82	59.98
ABCC1	2680	2680 T	C	14.56	59.98
ABCC1	2691	2692 CT	C	9.19	59.98

ABCC1	2697	2697 T	C	9.63	59.98
ABCC1	2700	2700 T	C	10.07	59.98
ABCC1	2707	2707 G	GT	10.33	59.98
ABCC1	3021	3021 G	A	7.38	60
ABCC1	3940	3940 T	G	24.45	58.47
ABCC1	4025	4025 G	A	32.17	59.79
ABCC1	4118	4118 T	C	15.47	60
ABCC1	4143	4143 T	C	26.33	60
ABCC1	4204	4204 A	G	32.48	1.358
ABCC1	4653	4653 C	A	17.43	60
ABCC1	4675	4675 T	TACATAATGT	28.74	60
ABCC1	4972	4972 T	C	7.73	60
ABCC1	4976	4976 G	T	13.62	60
ABCC1	5608	5608 C	T	15.36	60
ABCC1	5701	5701 T	A	12.68	60
ABCC1	5728	5728 G	A	24.62	60
ABCC1	6668	6668 G	T	8.32	60
ABCC1	6876	6877 TA	T,TAA	16.66	60
ABCC1	6938	6938 C	T	19.5	60
ABCC1	7319	7319 C	T	34.19	60
ABCC1	7340	7340 A	T	12.58	60
ABCC1	8599	8599 G	A	7.78	60
ABCC1	10210	10210 G	GAGGACTTG/	10	60
ABCC1	10671	10671 G	GTT	11.93	60
ABCC1	11090	11090 T	C	13.49	60
ABCC1	11091	11091 G	A	13.53	60
ABCC1	11093	11093 G	T	13.53	60
ABCC1	11104	11104 A	ATTT	13.49	60
ABCC1	11107	11107 C	G	13.44	60
ABCC1	11138	11138 G	A	24.44	60
ABCC1	11153	11153 T	C	10.66	60
ABCC1	11198	11198 C	A	11.88	60
ABCC1	11233	11233 G	A	9.42	60
ABCC1	11597	11597 C	CT	3.41	60.8
ABCC1	11788	11788 C	T	18.35	60
ABCC1	11900	11901 GA	G	10.03	60
ABCC4L	538	538 A	G	11.34	60
ABCC4L	1666	1666 C	T	14.8	60
ABCC4L	2433	2433 T	G	30.94	60
ABCC4L	2443	2443 A	T	32.54	60
ABCC4L	2492	2492 T	C	22.32	60
ABCC4L	3564	3564 A	ATT	10.81	60
ACC1	984	984 T	C	9.61	60
ACC1	1909	1909 A	ATT	8.66	60

ACC1	2840	2840 T	C	19.68	60
ACC1	2979	2979 T	A	6.19	60
ACC1	3578	3578 T	C	20.43	60
ACC1	3918	3920 CCT	C	11.64	60
ACC1	4033	4033 C	G	32.26	57.36
ACC1	4039	4039 T	G	28.54	57.23
ACC1	4060	4060 T	C	22.99	56.82
ACC1	4062	4062 A	G	33.65	56.71
ACC1	4071	4071 T	C	12.96	58.48
ACC1	4180	4180 T	G	14.26	53.14
ACC1	4246	4246 T	G	19.17	59.73
ACC1	4475	4475 T	C	13.04	60
ACC1	4591	4591 G	C	5.36	60
ACC1	5124	5124 G	GTTCTCTCT	14.61	60
ACC1	5576	5576 G	T	9.79	60
ACC1	5794	5794 G	A	10.58	60
ACC1	6674	6674 T	TAA	18.03	60
ACC1	7012	7012 G	C	7.94	60
ACC1	7033	7033 A	AT	3.89	60.6
ACC1	8631	8631 T	A	10.84	60
ACC1	8705	8705 C	CT	13.54	60
AIM1	214	214 T	C	14.42	60
AIM1	274	274 C	CT	16.78	60
AIM1	281	281 G	C	5.26	60
AIM1	470	470 T	C	13.79	60
AIM1	553	553 G	A	7.93	59.87
AIM1	555	555 A	G	8.66	59.87
AIM1	568	568 A	G	8.28	59.87
AIM1	603	603 C	T	10.36	60
AIM1	611	611 C	CT	9.89	60
AIM1	612	612 G	GGAAACA	9.89	60
AIM1	666	666 C	T	8.81	60
AIM1	730	730 A	ACT	12.34	60
AIM1	736	736 G	A	11.06	60
AIM1	745	745 A	G	8.2	60
AIM1	746	747 CA	C	7.72	60
AIM1	897	897 A	AT	14.53	60
AIM1	902	902 T	A	14.82	60
AIM1	936	936 G	A	14.37	60
AIM1	944	944 T	C	11.52	60
AIM1	945	945 T	G	11.72	60
AIM1	963	963 C	T	10.52	60
AIM1	975	979 CTGAT	C	8	60
AIM1	1018	1018 G	A	7.86	60

AIM1	1288	1288 T	TTC,TTG	11.3	60.43
AIM1	1319	1319 T	C	5.1	60.35
AIM1	1452	1452 T	TTTCTG	8.31	60
AIM1	1520	1520 T	C	23.18	60
AIM1	1667	1667 T	C	10.21	60
AIM1	1671	1671 A	T,G	19.46	60
AIM1	1699	1699 A	T	7.59	60
AIM1	1809	1809 T	C	10.06	60
AIM1	1842	1842 A	G	8.97	60
AIM1	1851	1851 G	C	24.45	60
AIM1	1866	1867 TC	T	19.14	60
AIM1	2062	2062 A	G	13.93	60
AIM1	2088	2088 G	C	8.75	60
AIM1	2108	2108 T	C	12.1	60
AIM1	2219	2219 G	A	10.85	60
AIM1	2229	2229 G	A	12.31	60
AIM1	2250	2250 T	A	14.84	60
AIM1	2253	2253 T	A	7.82	60
AIM1	2422	2422 A	G	18.93	60
AIM1	2451	2451 G	T	30.26	60
AIM1	2482	2482 G	C	24.07	60
AIM1	2532	2532 A	G	8.57	60
AIM1	2538	2538 T	A	9.12	60
AIM1	2539	2539 G	GT	8	60
AIM1	2563	2563 T	TCTAG	8.73	60
AIM1	2576	2576 C	T	8.28	60
AIM1	2938	2938 C	T	13.51	60
AIM1	2958	2958 T	C	13.44	60
AIM1	3051	3051 T	A	20.56	59.67
AIM1	3430	3430 T	G	8.45	60
AIM1	3449	3449 T	G	12.51	60
AIM1	3515	3516 GA	G,GAAAA	11.98	60
AIM1	3522	3522 A	AT	9.45	60
AIM1	3824	3824 T	C	10.1	60
AIM1	3871	3871 A	C	17.12	60
AIM1	4063	4063 T	C	16.33	60
AIM1	4064	4064 G	GT	15.55	60
AIM1	4080	4080 G	A	7.19	60
AIM1	4110	4110 C	G	14.3	60
AIM1	4166	4166 A	G	24.06	60
AIM1	4177	4177 T	C	4.89	60
AIM1	4440	4440 G	A	4.65	60
AIM1	4844	4844 C	T	5.77	60
AIM1	4875	4875 C	T	13.3	60

AIM1	5084	5084 G	A	15.95	60
AIM1	5115	5115 G	A	11.27	60
AIM1	5172	5172 C	T	21.29	60
AIM1	5210	5210 C	A	20.16	60
AIM1	5231	5231 A	T	5.94	60
AIM1	5365	5365 G	A	18.51	60
AIM1	5559	5559 T	TTA	20.98	60
AIM1	5855	5855 C	T	25.58	60
AIM1	6161	6161 T	A	7.41	60
AIM1	6178	6178 G	A	17.07	60
AIM1	6224	6224 G	A	22.66	60
AIM1	6337	6337 A	T	13.08	60
AIM1	6394	6394 A	G	31.8	1.136
AIM1	6420	6420 C	T	9.21	60
AIM1	6483	6483 G	A	24.89	60
AIM1	6533	6533 A	G	27.93	60
AIM1	6561	6561 A	C	31.08	60
AIM1	6581	6581 A	G	12.62	59.76
AIM1	6642	6642 G	A	23.94	59.77
AIM1	6709	6709 C	T	8.79	60
AIM1	6891	6891 G	T	11.49	60
AIM1	6903	6903 T	C	15.33	60
AIM1	6908	6908 T	C	20.72	60
AIM1	7018	7018 G	A	10.67	60
AIM1	7045	7045 G	A	12.71	60
AIM1	7049	7049 A	G	12.71	60
ALF5	665	665 C	CA	16.07	57.64
ALF5	843	843 T	C	11.75	60
ALF5	846	846 A	G	12.92	60
ALF5	919	919 T	TCTTTACACC	20.79	60
ALF5	1102	1106 CATAT	C	13.39	60
ALF5	1135	1135 A	AAACTTTTTT	17.25	60
ALF5	1239	1239 A	AATGCATGCA	20.61	60
ALF5	1844	1844 A	T	16.38	60
ALF5	1994	1995 CA	C	9.96	60
ALF5	2008	2008 T	A	11.86	60
ALF5	2009	2009 C	A	11.82	60
ALF5	2025	2027 CTT	C	9.17	60
ALF5	2031	2033 AAT	A	9.22	60
ALF5	2510	2510 A	ATCTGCGGTC	12.95	59.17
ALF5	2521	2521 C	CACAATGCTT	13.35	59.17
ALF5	2538	2538 T	C	12.09	59.38
ALF5	2593	2593 T	C	30.7	60
AML1	1165	1165 G	A	10.31	60

AML1	1169	1169 C	T	11.86	60
AML1	1188	1188 T	C	12.5	60
AML1	1205	1205 T	C	14.72	60
AML1	1214	1216 CAT	C	13.86	60
AML1	1218	1218 T	G	14.22	60
AML1	1222	1222 T	TTG	14.97	60
AML1	1226	1226 A	G	16.26	60
AML1	1227	1227 A	T	14.39	60
CESA1	234	234 T	G,A	17.4	59.76
CESA1	484	484 A	G	18.4	60
CESA1	1224	1224 A	G	7.61	60
CESA1	1881	1881 G	GT	4.12	60
CESA1	1898	1898 G	A	8.48	60
CYN	666	666 C	G	13.4	60
CYN	700	700 A	ATT	23.2	60
CYN	716	716 A	T	24.77	60
CYN	777	777 G	A	9.99	60
CYN	819	819 A	G	9.44	60
CYN	866	866 C	T	19.96	60
CYN	883	883 C	T	12.33	60
CYN	888	888 G	A	21.26	60
CYN	949	949 C	T	11.29	60
CYN	966	966 T	A	27.54	60
CYN	968	968 T	TA	28.51	60
CYN	983	983 C	G	15.33	60
CYN	1069	1069 G	T	9.36	59.56
CYN	1080	1080 T	C	10.09	59.53
CYN	1158	1158 G	A	6.89	59.37
CYN	1176	1176 A	AAATTTGTGT	31.05	59.74
CYN	1238	1238 A	G	19.15	59.82
CYN	1277	1277 C	A	24.79	59.63
CYN	1287	1287 T	G	27.68	59.61
CYN	1296	1298 CTA	C	25.03	59.61
CYN	1313	1315 CAA	C	30.91	59.85
CYN	1322	1322 A	G	32.55	59.83
CYN	1358	1358 A	G	32.97	60
CYN	1363	1363 T	C	34.99	60
CYN	1374	1374 A	G	30.73	59.81
CYN	1386	1393 TAAGGTAA	T	27.65	59.81
CYN	1458	1458 A	G	31	60
CYN	1467	1467 C	T	29.04	60
CYN	1504	1504 C	T	27.74	59.71
CYN	1637	1637 A	G,ACGGCAGT	10.53	59.98
CYN	1645	1645 C	CAG,CTAAGC	10.79	59.98

CYN	1647	1649 CTT	C	13.68	60
CYN	1693	1693 G	A	15.36	60
CYN	1761	1761 C	T	11.31	60
CYN	1770	1770 T	C	11.66	60
CYN	1900	1900 T	C	11.44	60
CYN	1959	1959 A	AT	10.01	60
CYN	1988	1988 C	T	8.02	60
CYN	2065	2065 T	C	8.08	60
CYN	2076	2076 A	G	8.08	60
CYN	2121	2121 T	C	6.64	60
CYN	2173	2173 C	G	30.28	60
CYN	2226	2226 T	A	33.5	60
CYN	2273	2273 C	T	4.79	60
CYN	2282	2284 CTG	C	8.32	60
CYN	2626	2626 A	G	11.77	60
CYN	2632	2632 A	T	10.94	60
CYN	2647	2647 A	C	7.19	60
CYN	2679	2679 G	A	10.47	60
CYN	2690	2690 T	C	12.02	60
CYP709B3	296	296 T	C	20.98	60
CYP709B3	313	313 G	C	18.32	60
CYP709B3	346	346 A	G	22.61	60.36
CYP709B3	357	357 T	C	23.41	60.36
CYP709B3	431	431 T	A	25.56	60.42
CYP709B3	438	438 A	G	24.77	60.43
CYP709B3	488	490 TAG	T	16.22	60.42
CYP709B3	511	511 T	C	15.02	60
CYP709B3	535	535 A	T	10.31	60
CYP709B3	536	536 C	A	10.31	60
CYP709B3	579	579 C	T	14.57	60
CYP709B3	600	600 G	GCGCTTTCGT	33.3	60
CYP709B3	614	614 A	C	9.42	60
CYP709B3	630	630 G	T	9.47	60
CYP709B3	916	916 T	C	9.01	60
CYP709B3	917	917 T	C	8.88	60
CYP709B3	919	919 C	G	7.56	60
CYP709B3	953	953 C	A	11.42	60
CYP709B3	954	957 TGCC	T	11.09	60
CYP709B3	959	959 T	TATA	11.09	60
CYP709B3	961	961 G	A	17.68	60
CYP709B3	1712	1712 G	A	12.96	60
CYP709B3	1718	1718 C	A	12.53	60
CYP709B3	1780	1780 T	A	10.41	60
CYP72A31	980	980 C	T	9.28	60

DHPS	852	852 C	G	20.74	60.35
DHPS	853	853 A	T	20.74	60.35
DHPS	856	856 T	C	20.85	60.4
DHPS	857	857 A	G	21.91	60.42
DHPS	861	861 C	G	18.68	60.42
DHPS	874	874 C	T	17.75	60
DHPS	888	888 T	C	15.43	60
DHPS	889	889 G	A	15.6	60
DHPS	894	894 C	G	13.46	60
DHPS	896	896 A	G	5.95	60
DHPS	901	901 T	A	14.37	60
DHPS	904	904 G	T	15.27	60
DHPS	943	943 A	G	9.79	59.79
DTX1	1091	1091 A	G	9.8	60
DTX1	1296	1296 A	AT	8.67	60
DTX1	1574	1574 A	G	8.8	60
DTX1	1579	1579 C	T	14.33	60
DTX1	1630	1632 CGG	C	14.9	60
DTX1	1661	1661 T	C	8.66	60
DTX1	1761	1761 C	CTCTTGTTTA(	19.66	60
DTX1	1790	1790 A	G	19.13	60
DTX1	1864	1864 T	A	25.28	60
DTX1	1876	1876 C	CT	15.51	60
DTX1	1908	1908 G	T	26.52	60
DTX1	1909	1909 G	A	26.96	60
DTX1	1924	1924 A	G	27.32	60
DTX1	1957	1957 T	G	27.29	60
DTX1	1961	1961 A	C	27.73	60
DTX1	1979	1979 T	C	27.01	60
DTX1	1981	1981 G	A	26.5	60
DTX1	1985	1985 T	C	26.92	60
DTX1	1994	1994 A	AT	9.91	60
DTX1	2004	2004 A	T	26.05	60
DTX1	2011	2011 A	G	27.33	60
DTX1	2014	2014 A	G	25.09	60
DTX1	2050	2050 G	C	20.14	60
DTX1	2057	2057 A	G	14.65	60
DTX1	2079	2081 CAG	C	21.61	60
DTX1	2084	2084 G	T	21.19	60
DTX1	2090	2090 A	C	19.91	60
DTX1	2102	2102 G	A	9.03	60
DTX1	2107	2107 A	G	19.91	60
DTX1	2169	2169 G	T	13.42	60
DTX1	2358	2358 G	GAATTAAAC/	8.11	60

DTX1	2545	2545 C	T	6.82	60
DTX1	2549	2549 G	C	10.74	60
DTX1	3228	3228 A	ATGCTC	8.86	59.93
DTX1	3240	3241 CT	C,TT	14.61	59.94
DTX1	3244	3246 TCG	T	11.13	59.93
DTX1	3246	3246 G	A	11.55	59.93
DTX1	3249	3251 ATG	A	10.77	59.94
DTX1	3258	3258 T	TGGCC	13.39	59.94
DTX1	3259	3260 TC	T	13.45	59.94
DTX1	3270	3270 C	CA	10.13	60
DTX1	3276	3276 G	T	10.52	60
DTX1	3297	3297 G	C,T	15.73	60
DTX1	3512	3512 T	C	28.37	59.91
DTX1	3537	3537 A	G	23.98	59.88
DTX1	3628	3631 GTAT	G	22.64	60
DTX1	3639	3639 G	A	27.96	59.87
DTX1	3657	3657 C	T	20.4	59.87
DTX1	3659	3659 G	A	26.97	59.87
DTX1	3661	3661 G	A	26.4	59.88
DTX1	3663	3663 T	C	27.33	59.88
DTX1	3674	3674 A	T	28.08	59.88
DTX1	3695	3695 C	G	28.58	59.89
DTX1	3774	3774 C	T	31.05	60
DTX1	3798	3798 C	G	29.69	60
DTX1	3802	3804 CTT	C	30.26	60
DTX1	3807	3810 ACTC	A	33.01	60
DTX1	3823	3823 G	T	30.2	59.44
DTX1	3828	3828 C	T	31.13	59.46
DTX1	3837	3837 T	G	32.34	59.44
DTX1	3848	3848 T	C	30.12	58.98
DTX1	3849	3849 C	T	29.87	58.94
DTX1	4121	4121 A	T	14.09	60
DTX1	4122	4122 T	G	12.85	60
DTX1	4129	4129 A	G	13.68	60
DTX1	4134	4134 A	T	13.74	60
DTX1	4137	4141 AAATT	A	12.61	60
DTX1	4144	4144 G	GGCAA	16.62	60
DTX1	4150	4150 T	A	16.13	60
DTX1	4152	4152 A	G	17.29	59.51
DTX1	4160	4160 G	A	13.62	58.71
DTX1	4188	4189 CT	C	11.84	58.55
DTX1	4190	4193 GATA	G	11.42	58.61
DTX1	4199	4199 C	T	11.96	58.5
DTX1	4211	4211 T	TC	12.58	58.55

DTX1	4212	4212 G	GA	14.07	58.55
DTX1	4213	4213 T	TC	14.62	58.5
DTX1	4217	4217 A	C	12.98	58.14
DTX1	4219	4219 A	C	23.5	58.14
DTX1	4535	4535 G	GCT,C	20.27	57.97
EPSPS	428	428 G	A	14.24	60
EPSPS	520	520 C	T	23.56	60
EPSPS	566	566 A	AAAG,AAAAA	23.62	60
EPSPS	583	583 T	TA	14.54	60.63
EPSPS	614	614 A	T	14.59	60.45
EPSPS	755	755 A	C	10.07	60
EPSPS	782	782 T	G	26.81	60
EPSPS	802	802 C	G	27.66	60
EPSPS	846	846 G	C	20.17	60
EPSPS	896	896 G	A	27.28	60
EPSPS	907	907 A	T	9.7	60
EPSPS	916	916 C	T	9.31	58.39
EPSPS	934	934 C	A	14.59	58.44
EPSPS	936	936 G	A	14.15	58.49
EPSPS	937	937 A	G	14.15	58.49
EPSPS	945	945 T	A	14.15	58.49
EPSPS	946	948 TTC	T	13.82	58.49
EPSPS	974	977 GTTT	G	15.84	56.59
EPSPS	978	982 GGTGA	G	16.29	57.23
EPSPS	986	986 C	A	15.73	56.98
EPSPS	1004	1004 G	A	15.08	56.87
EPSPS	1006	1006 A	G	15.44	56.79
EPSPS	1008	1008 C	A	14.89	56.79
EPSPS	1030	1030 T	C	11.44	56.7
EPSPS	1037	1037 C	T	26.72	60
EPSPS	1038	1038 T	A	16.31	60
EPSPS	1058	1058 C	T	6.78	60
EPSPS	1079	1079 A	T	13.18	60
EPSPS	1170	1170 G	T,GA	17.9	59.58
EPSPS	1542	1542 G	GT	8.29	60
EPSPS	1786	1786 A	G	15.92	60
EPSPS	1918	1918 A	T	25.68	60
EPSPS	1926	1926 G	A	26.25	60
EPSPS	1967	1967 A	G	7.94	60
EPSPS	2380	2380 G	A	7.25	60
EPSPS	2484	2484 C	T	7.31	60
EPSPS	2526	2526 C	CATAG,CGTA	21.03	60
EPSPS	2553	2553 C	T	7.52	60
EPSPS	2558	2558 C	T	13.79	60

EPSPS	2562	2562 C	T	13.79	60
EPSPS	3028	3029 AC	A	6.9	60
EPSPS	3551	3551 C	T	10.99	60
EPSPS	3585	3585 G	A	9.15	60
ESR1	908	908 A	G	9.51	60
ESR1	1198	1199 AC	A	30.33	60
ESR1	1226	1226 G	GATT	8.79	60
ESR1	1276	1276 T	TTA	28.33	58.87
ESR1	1279	1279 C	T	29.52	58.11
ESR1	1294	1294 A	C	28.7	57.32
ESR1	1298	1298 G	A	29.02	57.01
ESR1	1299	1299 T	A	29.02	57.01
ESR1	1300	1300 T	A	12.1	57.01
ESR1	1305	1305 A	G	29.9	56.9
ESR1	1306	1306 T	G	29.6	56.9
ESR1	1311	1311 A	C	31.5	56.77
ESR1	1314	1316 CTT	C	32.87	56.77
ESR1	1324	1324 A	T	28.2	56.13
ESR1	1325	1325 G	T	27.41	56.13
ESR1	1326	1326 A	T	33.78	56.13
ESR1	1331	1331 A	T	31.57	56.31
ESR1	1333	1333 T	C	28.62	56.31
ESR1	1344	1344 C	T	34.71	55.71
ESR1	1351	1351 A	T	27.56	55.46
ESR1	1353	1353 A	T	6.25	55.71
ESR1	1362	1362 G	A	32.46	54.51
ESR1	1375	1375 T	TG	31.69	56.6
ESR1	1376	1376 T	TTGGGAGGC	31.03	56.6
ESR1	1391	1391 C	A	24.12	56.8
ESR1	1397	1397 A	G	28.48	56.97
ESR1	1398	1398 C	CCATG	26.81	56.97
ESR1	1412	1412 T	C	29.25	59.08
ESR1	1428	1428 A	G	30.51	60
ESR1	1705	1705 A	T	19.51	60
ESR1	1706	1706 T	G	20.7	60
ESR1	1769	1769 C	T	10.88	60
ESR1	1851	1851 A	G	26.07	60
ESR1	1957	1958 AG	A	13.56	60.47
ESR1	1967	1967 G	C	31.35	60.47
ESR1	1969	1969 G	C	27.35	60.47
ESR1	2019	2019 A	G	30.43	60.51
ESR1	2056	2056 C	CCA	8.34	60.57
ESR1	2402	2402 A	C	12.76	60
GDSL	1369	1387 ACACATATAT A		26.92	60

GDSL	2408	2412 GGCGC	G	24.48	57.26
GDSL	2415	2423 GGCCGGCCCC	G	32.28	56
GDSL	2427	2427 C	CAGCT	31.1	55.49
GDSL	2438	2439 TC	T	31.21	56.42
GDSL	2468	2468 C	G	9.51	60
GDSL	2510	2510 C	T	11.13	60
GDSL	2582	2584 TAG	T	7.56	60
GDSL	2636	2636 T	C	13.23	60
GDSL	2670	2674 TAGGC	T	11.32	60
GDSL	2685	2685 T	A	15.41	60
GDSL	2691	2691 A	C	15.91	60
GDSL	2744	2744 C	CGCCG	14.07	60
GDSL	2927	2927 A	G	20.75	60
GDSL	3093	3093 C	T	8.8	60
GDSL	3100	3120 CCATTGCATC	C	7.99	60
GDSL	3120	3120 A	AC	21.89	60
GDSL	3421	3421 A	G	26.72	56.82
GDSL	3441	3441 T	A	31.25	56.82
GPOX	737	773 GCGCGCGCG	G	27.98	60
GPOX	783	783 G	A	30.15	60
GPOX	1314	1314 T	TC	26.05	55.85
GPOX	1339	1339 C	T	26.64	57.59
GPOX	1554	1554 T	C	16.26	60
GPOX	1557	1560 CTGG	C	9.12	60
GPOX	1596	1599 GAAA	G	14.85	60
GPOX	1679	1679 G	GCTGTCATCA	33.1	57.71
GPOX	1681	1681 G	GA	31.64	55.27
GPOX	1683	1686 GTTC	G	29.75	54.44
GPOX	1694	1694 G	GC	24.81	55.27
GPOX	1716	1716 C	A	22.84	55.88
GPOX	1717	1717 C	CGT	21.71	55.88
GPOX	1726	1728 TTA	T	18.71	55.27
GPOX	1730	1735 TCCAAC	T	18.71	55.27
GPOX	1956	1956 C	T	7.65	60
GPOX	1963	1965 CAG	C	15.36	60
GPOX	1966	1966 C	T	15.86	60
GSH2	214	214 G	C	29.72	60
GSH2	249	249 A	G	9.51	60
GSH2	251	277 GAAAAGTTTC	G	21.48	60
GSH2	451	451 G	A	10.65	60
GSH2	481	481 C	T	14.78	60
GSH2	493	493 G	A	13.14	60
GSH2	506	506 G	A	30.38	60
GSH2	512	512 C	T	14.97	60

GSH2	553	553 A	G	23.57	60
GSH2	589	589 A	T	5.17	60
GSH2	885	885 T	C	31.71	60
GSH2	912	912 C	G	28.37	60
GSH2	940	940 C	T	7.33	60
GSH2	1164	1164 C	T	9.71	60
GSH2	1431	1431 T	C	23.44	59.27
GSH2	1433	1433 G	T	24.32	59.2
GSH2	1444	1444 T	C	21.92	58.87
GSH2	1449	1449 G	T	11.5	58.77
GSH2	1456	1456 C	T	10.34	58.58
GSH2	1457	1457 T	G,TTTG	15.64	58.58
GSH2	1468	1468 A	G	6.41	58.37
GSH2	1470	1470 T	A	9.9	58.37
GSH2	1472	1472 T	C	9.9	58.37
GSH2	1477	1477 C	T	9.29	58.46
GSH2	1508	1508 G	C	13.13	58.67
GSH2	1611	1611 C	G	9.02	60
GSH2	1664	1664 G	C	11.12	60
GSH2	1715	1715 C	A	7.81	60
GSH2	1907	1907 C	A	15.14	60
GSH2	1913	1913 T	C	15.42	60
GSH2	1924	1924 T	A	13.3	60
GSH2	1928	1928 A	G	12.02	60
GSH2	1935	1935 A	G	30.52	60
GSH2	1942	1942 C	G	13.49	60
GSH2	1946	1946 T	G	14.73	60
GSH2	1956	1956 A	T	10.46	60
GSH2	1970	1970 T	C	9.33	60
GSH2	1974	1974 A	T	9.1	60
GSH2	1976	1976 G	A	9.04	60
GSH2	2198	2201 TCTC	T	8	60.39
GSH2	2365	2365 G	GA	3.89	60.45
GSH2	2513	2513 A	T	22.68	60
GSH2	2515	2515 T	C,G	22	60
GSH2	2779	2779 T	A	8.07	59.76
GSH2	2924	2924 G	A	29.26	60
GSH2	3013	3013 T	C	18.09	59.93
GSH2	3028	3028 T	G	23.33	59.94
GSH2	3066	3066 A	G	26.42	59.94
GSH2	3069	3069 T	C	4.41	59.94
GSH2	3499	3499 C	T	23.08	59.78
GSH2	3658	3658 C	G	14.13	59.85
GSH2	3662	3662 A	G	31.54	59.96

GSH2	3667	3667 T	TC	27.46	59.96
GSH2	3684	3684 A	G	34.77	59.7
GSH2	3694	3694 C	A	18.16	59.68
GSH2	3700	3700 A	G	18.88	59.67
GSH2	3705	3705 G	A	17.95	59.66
GSH2	3710	3710 T	C	29.91	59.67
GSH2	3711	3711 C	G	16.64	59.67
GSH2	3713	3713 C	T	16.64	59.67
GSL1-1	558	558 T	C	6.54	60
GSL1-1	608	608 A	G	6.9	60
GSL1-1	993	993 A	T	30.73	60
GSL1-1	1170	1170 G	A	10.15	60
GSL1-1	1193	1193 T	TAA,A	21.92	60
GSL1-1	1194	1194 A	T	9.89	60
GSL1-1	1204	1204 A	C	11.63	60
GSL1-1	1324	1324 T	TA	6.1	60
GSL1-1	1354	1355 AT	A,ATT	18.59	60
GSL1-1	1650	1650 G	C	7.54	60
GSL1-1	2064	2064 G	GTT	10.1	60
GSL1-1	2066	2066 T	TA	6.72	60
GSL1-1	2102	2103 AG	A	18.86	60
GSL1-1	2109	2110 CT	C	12.47	60
GSL1-1	2120	2120 C	CA	16.11	60
GSL1-1	2207	2208 CA	C	7.45	60
GSL1-1	2254	2258 CATT	C	26.01	60
GSL1-1	2759	2759 G	T	7.2	60
GSTF12	495	495 T	C	8.78	60
GSTF12	498	498 T	A	8.78	60
GSTF12	526	526 A	AAG	8.06	60
GSTF12	531	533 GAA	G	14.11	60
GSTF1	412	412 T	C	10.76	60
GSTF1	856	856 G	C	9.21	60
GSTF1	904	904 A	T	11.85	60.35
GSTF1	920	920 G	A	10.24	60.4
GSTF1	991	996 GCAAAC	G	23.51	60.47
GSTF1	998	998 A	T	11.8	60.47
GSTF1	1005	1005 A	G	16.63	60.45
GSTF1	1024	1024 C	T	14.91	60
GSTF1	1032	1032 G	A	14.82	60
GSTF1	1033	1033 C	T	15.46	60
GSTF1	1036	1036 C	CTATT	6.98	60
GSTF1	1114	1114 C	T	6.86	60
GSTF1	1128	1128 T	A	6.71	60
GSTF1	1222	1222 T	TTGTATGCAC	11.38	60

GSTF1	1389	1389 G	A	8.88	60
GSTF1	1497	1500 TTTG	T	9.55	60
GSTF1	1525	1525 T	A	9.52	60
GSTF1	1581	1581 T	TC	12.47	60
GSTF1	1697	1697 A	T	6.58	60
GSTF1	1755	1755 C	T	6.15	60
GSTF1	1785	1785 A	T	8.74	60
GSTF1	1800	1800 G	C	8.74	60
GSTF1	1818	1818 G	T	28.46	60
GSTF3	559	559 T	C	6.99	60
GSTF3	643	643 T	A	8.47	60
GSTF3	644	644 T	A	8	60
GSTF3	645	645 T	A,TAA	24.88	60
GSTF4	692	692 G	A	13.97	57
GSTF4	697	697 G	A	24.65	56.96
GSTF4	705	705 G	A	28.45	57.11
GSTF4	706	706 T	A	13.59	57.22
GSTF4	726	726 A	T	16.13	60
GSTF4	727	727 T	TTA,TATA	16.33	60
GSTF4	743	743 G	A	21.72	60
GSTF4	764	764 T	C	26.12	60
GSTF4	789	789 A	C	28.83	60
GSTF4	843	843 C	G	6.33	59.42
GSTF4	877	877 T	TA	12.8	59.3
GSTF4	883	883 A	T	16.13	59.3
GSTF4	889	898 CTAATATTG C,TTAATATTT		30.32	59.2
GSTF4	904	908 TCCGC	T	12.62	59.56
GSTF4	912	912 G	C	11.8	59.6
GSTF4	929	933 ATCTG	A	9.55	59.66
GSTF4	938	938 A	C	9.89	59.66
GSTF4	939	941 AGC	A	9.92	59.65
GSTF4	967	968 TA	T	18.94	59.65
GSTF4	978	978 G	A	7.08	59.66
GSTF4	1012	1012 C	T	8.3	59.3
GSTF4	1027	1027 C	T	9.53	59.32
GSTF4	1048	1048 A	G	13.54	58.78
GSTF4	1101	1101 C	G	14.46	59.1
GSTU1	464	464 T	C	12.48	60
GSTU1	466	477 GCGCAAGCG`G		10.8	60
GSTU1	478	478 A	AT	13.44	60
GSTU1	481	481 G	A,C	19.34	59.69
GSTU1	502	502 T	C	14.91	59.05
GSTU1	503	503 T	A	14.91	59.05
GSTU1	514	516 TTG	T	9.89	58.8

GSTU1	520	520 T	G	11.58	58.66
GSTU1	522	524 GTA	G	8.81	58.66
HM2	379	380 AC	A	17.53	56.84
HM2	398	398 C	T	15.96	55.62
HM2	406	407 TC	T	15.5	55.62
HM2	408	410 TCC	T	13.86	55.62
HM2	412	412 C	T	14.82	55.43
HM2	426	426 C	T	16.26	55
HM2	437	438 GT	G	12.05	55
HM2	441	441 T	G	9.21	55.74
HM2	442	442 T	TAA	8.78	55.74
HM2	452	452 A	T	9.79	55.52
HM2	453	453 C	G	9.67	55.52
HM2	468	474 GCATGAT	G	8.76	57.69
HM2	1124	1124 T	G	11.26	60
HM2	1125	1125 C	T	11.26	60
HM2	1155	1155 C	A	12.54	60
HM2	1209	1209 A	G	10.61	60
HM2	1218	1218 T	C	6.3	60
HM2	1678	1678 C	A	4.34	60
HPPD	1528	1528 A	G	7.5	60
IGPD	571	571 G	A	31.66	60
IGPD	605	605 C	G	13.92	60
IGPD	987	987 T	TA	4.93	60
IGPD	1083	1084 AT	A	10.12	60.93
IGPD	1218	1218 A	G	17.24	60.63
IGPD	1327	1327 T	A	19.44	60
IGPD	1572	1572 T	G	28.74	60.31
IGPD	1755	1755 A	T	18.01	60
IGPD	1806	1806 T	G	17.33	60
IGPD	1870	1870 C	T	33.55	60
IGPD	1891	1891 A	G	27.12	60
IGPD	1913	1913 C	T	7.99	60
IGPD	1975	1975 C	T	7.49	60
IGPD	1987	1987 C	T	13.61	60
IGPD	2221	2221 A	G	21.14	60
IGPD	2366	2366 A	G	34.26	60
IGPD	2438	2438 T	C	27.55	60
IGPD	2537	2537 T	C	20.22	60
IGPD	2551	2551 C	A	20.3	60
IGPD	2590	2590 G	GT	8.29	60
IGPD	2773	2782 ATGTTTTCTT	A	6.35	60
IGPD	2785	2791 TGCTTAG	T	7.58	60
IGPD	2847	2847 A	ACATTCATTT	13.94	60

IGPD	2875	2875 A	AAC	25.7	60
IGPD	2924	2925 CA	C,CAAA	9.61	60
IGPD	3506	3506 A	C	22.69	60
IGPD	3514	3514 T	G	21.81	60
IGPD	3553	3553 T	G	20.61	60
IN2	456	456 C	G	10.22	60
IN2	576	582 ATACTCC	A	8.4	60
IN2	582	582 C	T	9.38	60
IN2	598	598 C	CT	8.89	60
IN2	620	620 A	G	10.76	60
IN2	621	621 T	A	10.76	60
IN2	772	773 GT	G	14.05	60
IN2	778	778 G	A	14.69	60
IN2	974	974 T	C	11.07	60
IN2	1000	1002 TAG	T	13.84	60
IN2	1168	1168 G	T	18.19	60
IN2	1367	1367 T	G	10.28	60
IN2	1379	1379 C	A	13.98	60
IN2	1528	1528 C	A	31.8	60
IN2	1587	1587 T	C	14.48	60
IN2	1589	1589 C	T	15.2	60
IN2	1821	1821 T	C	16.64	60
IN2	1823	1823 C	T	25.88	60
IN2	1858	1858 T	A	8.71	60
IN2	1866	1867 GC	G	13.26	60
IN2	1886	1886 T	C	11.55	60
LACS7	330	330 T	C	24.27	59.38
LACS7	406	406 T	G	14.59	60
LACS7	455	455 G	GT	10.29	59.12
LACS7	464	464 T	C	10.3	59.16
LACS7	498	499 TG	T	15.99	59.26
LACS7	1222	1222 C	T	22.92	60
LACS7	1257	1257 G	A	6.78	60
LACS7	1270	1270 G	A	8.71	60
LACS7	1327	1327 T	C	31.11	59.57
LACS7	1795	1795 A	T	18.02	59.64
LACS7	1804	1804 C	T	18.23	59.64
LACS7	1810	1810 G	C	20.84	60
LACS7	1811	1811 T	C	20.84	60
LACS7	1816	1816 G	A	20.44	60
LACS7	1820	1832 CCAAAAAAAAA/C	C	14.9	60
LACS7	1835	1835 A	C	17.22	60
LACS7	1843	1843 T	TCCA	17.83	60
LACS7	1855	1855 G	C	19.59	60

LACS7	1858	1858 G	T	19.41	60
LACS7	1861	1861 T	C	22.49	60
LACS7	1862	1862 G	A	21.42	60
LACS7	1878	1881 CGAA	C	19.06	60
LACS7	1967	1967 C	T	18.4	59.85
LACS7	1971	1971 C	T	17.87	59.86
LACS7	1974	1974 A	G	18.55	59.85
LACS7	1977	1977 C	CTATG	8.35	59.85
LACS7	1993	1993 C	T	32.87	59.85
LACS7	2004	2004 C	A	16.59	59.84
LACS7	2005	2005 C	T	12.5	59.85
LACS7	2006	2006 C	G	34.31	59.84
LACS7	2011	2011 G	A	14.04	59.81
LACS7	2014	2014 A	G	14.04	59.81
LACS7	2015	2015 T	C	14.04	59.81
LACS7	2024	2024 C	T	16.1	59.81
LACS7	2025	2025 C	T	28.06	59.82
LACS7	2119	2119 C	G	17.29	59.91
LACS7	2125	2125 G	A,C	25.11	59.92
LACS7	2132	2132 C	A	15.96	59.92
LACS7	2142	2143 AC	A	13.51	59.93
LACS7	2147	2147 T	C	10.44	59.93
LACS7	2148	2151 TATC	T	11.09	59.94
LACS7	2155	2170 TTATTTTACA	T	9.29	59.95
LACS7	2172	2172 C	G,T	15.38	59.94
LACS7	2180	2180 A	T,G	17.35	59.94
LACS7	2189	2189 G	C	8.99	59.95
LACS7	2192	2192 G	C,T	17.88	59.58
LACS7	2202	2202 C	T	15.28	59.57
LACS7	2218	2218 T	G	15.78	58.97
LACS7	2222	2222 C	G	14.75	58.97
LACS7	2346	2346 C	CTGTCTA	9.37	60
LACS7	2352	2352 T	C	13.81	60
LACS7	2353	2353 G	A	13.81	60
LACS7	2356	2356 T	G	14.27	60
LACS7	2358	2358 A	G	10.44	60
LACS7	2364	2364 G	T	10.09	60
LACS7	2369	2369 C	T	10.44	60
LACS7	2372	2372 C	A	9.43	60
LACS7	2377	2377 T	G	15.52	60
LACS7	2406	2406 C	CA	8.47	60
LACS7	2513	2513 G	A	26.97	60
LACS7	2528	2528 T	A	27.36	60
LACS7	2531	2531 T	TG	16.24	60

LACS7	2561	2561 T	C	8.51	60
LACS7	2565	2565 A	G	33.17	60
LACS7	2573	2573 C	T	18.71	60
LACS7	2575	2575 A	G	34.19	60
LACS7	2580	2580 G	T	18.61	60
LACS7	2583	2583 A	G	32.95	60
LACS7	2591	2591 T	C	22.84	60
LACS7	2726	2726 A	AAC	29.42	60
LACS7	2746	2746 G	C	5.71	60
LACS7	2763	2763 G	T	30.12	60
LACS7	2774	2774 G	T	11.52	60
LACS7	2787	2789 TTC	T	8.78	59.94
LACS7	2792	2792 T	TG	13.52	59.94
LACS7	2794	2794 G	GTA,A	29.36	59.94
LACS7	2932	2932 T	TTCCTAAAAT	20.32	58.58
LACS7	2946	2946 A	C	17.52	58.12
LACS7	2961	2961 C	T	9.55	58.04
LACS7	2964	2964 A	C	15.25	58.19
LACS7	2970	2970 C	CGTAA	10.36	58.12
LACS7	2971	2971 C	G	10.31	58.19
LACS7	3000	3000 A	G	16.69	58.89
LACS7	3004	3004 C	T	18.17	58.83
LACS7	3005	3005 A	G	17.22	58.89
LACS7	3017	3017 T	A	19.57	59
LACS7	3026	3026 A	G	21.63	60
LACS7	3030	3030 A	T	20.45	60
LACS7	3054	3056 GAA	G	18.41	60
LACS7	3057	3057 T	C	18.62	60
LACS7	3068	3068 A	T	19.31	60
LACS7	3088	3088 G	GGCA	14.9	59.76
LACS7	3092	3094 AAG	A	14.03	59.75
LACS7	3096	3096 G	GCCAACTTTT	15.4	59.75
LACS7	3097	3097 G	T	16.53	59.76
LACS7	3101	3101 A	G	15.2	59.76
LACS7	3105	3105 A	C	14.33	59.75
LACS7	3111	3111 G	A	15.7	59.75
LACS7	3119	3119 T	G	17.99	59.77
LACS7	3121	3121 G	T	18.76	59.78
LACS7	3130	3130 T	G	15.62	59.79
LACS7	3237	3237 T	C	10.78	59.53
LACS7	3243	3243 T	C	15.2	59.58
LACS7	3245	3245 T	C	16.79	59.58
LACS7	3252	3252 A	G	8.07	59.64
LACS7	3271	3271 G	C	18.76	59.65

LACS7	3283	3283 G	A	16.16	60
LACS7	3285	3285 C	A	17.32	60
LACS7	3289	3289 G	T	17.82	60
LACS7	3416	3416 T	TAACAGTCAT	15.74	60
LACS7	3447	3447 C	CCTT	30.93	58.33
LACS7	3451	3452 TG	T	17.2	58.44
LACS7	3454	3454 C	A	16	58.57
LACS7	3569	3572 ATTT	A	19.33	60
LACS7	3606	3610 GTTTT	G,GTT	20.52	60
LACS7	3611	3611 T	A	13.27	60
LACS7	3638	3638 G	A	23.44	60
LACS7	3655	3655 A	G	26.81	60
LACS7	3680	3680 A	T	19.96	60
LACS7	3692	3692 A	T	18.45	60
LACS7	3699	3699 C	T	26.86	60
LACS7	3718	3718 G	A	30.46	60
LACS7	3730	3730 A	G	18.15	60
LACS7	3748	3748 A	G	29.1	60
LACS7	3758	3758 T	C	27.74	60
LACS7	3768	3768 G	C	7.62	60
LACS7	3784	3784 T	G	26.95	60
LACS7	3785	3785 A	G	27.64	60
LACS7	3793	3794 CA	C	19.18	60
LACS7	3817	3817 T	A	31.98	60
LACS7	3836	3836 T	C	17.16	60
LACS7	3841	3841 A	T	31.63	60
LACS7	3848	3851 TTAC	T	9	60
LACS7	3850	3850 A	T	17.29	60
LACS7	3857	3857 G	A	14.62	60
LACS7	3859	3860 TC	T	29.43	60
LACS7	3903	3903 A	AG	17.7	60
LACS7	3906	3906 T	G	29.58	60
LACS7	3928	3928 G	A	18.79	60
LACS7	3934	3935 AT	A	16.33	60
LACS7	3935	3935 T	C	9.58	60
LACS7	3939	3940 CT	C	29.46	60
LACS7	3955	3955 G	A	15.73	60
LACS7	3957	3957 G	C	10.7	60
LACS7	3959	3959 T	C	15.68	60
LACS7	3971	3971 A	T	28.95	60
LACS7	3972	3972 A	G	10.44	60
LACS7	3976	3976 A	G	29.08	60
LACS7	3991	3991 T	C	29.86	60
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LACS7	4032	4032 G	A	23.84	60
LACS7	4035	4035 C	CA	22.73	60
LACS7	4062	4062 T	C	21.33	60
LACS7	4081	4081 G	T	21.47	60
LACS7	4082	4082 G	T	14.7	60
LACS7	4104	4104 G	C	14.95	60
LACS7	4136	4137 GT	G	23.37	60
LACS7	4149	4154 AATTTT	A	24.57	60
LACS7	4170	4170 A	G	18.42	60
LACS7	4185	4185 T	C	15.04	60
LACS7	4186	4186 G	A	15.11	60
LACS7	4210	4210 C	T	8	60
LACS7	4246	4246 C	T	9.77	60
LACS7	4252	4252 G	C	21.19	60
LACS7	4255	4255 T	C	26.15	60
LACS7	4280	4282 CAT	C	10.75	60
LACS7	4295	4295 A	C	18.86	60
LACS7	4334	4334 T	A	8.08	60
LACS7	4342	4342 A	C	12.22	60
LACS7	4347	4347 T	C	8.83	60
LACS7	4400	4400 A	G	13.96	60
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LACS7	4438	4438 G	C	18.14	60
LACS7	4442	4442 T	C	7.44	60
LACS7	4458	4458 T	G	16.76	60
LACS7	4459	4459 G	A	16.76	60
LACS7	4462	4462 C	T	27.51	60
LACS7	4480	4480 T	C	16.41	60
LACS7	4481	4481 G	T	15.47	60
LACS7	4632	4632 C	T	25.88	57.55
LACS7	4670	4670 C	G	23.86	60
LACS7	4681	4681 T	C	12.38	59.6
LACS7	4683	4683 G	C	13.32	59.57
LACS7	4689	4689 C	T	8.94	59.57
LACS7	4800	4800 G	A	31.02	59.64
LACS7	5006	5006 C	T	25.95	60
LACS7	5018	5018 G	T	24.37	59.8
LACS7	5030	5030 T	C	14.09	59.8
LACS7	5068	5068 G	T	21.64	59.18
LACS7	5070	5070 A	T	9.98	59.18
LACS7	5071	5071 T	C	9.98	59.18
LACS7	5099	5099 A	G	11.21	59.09
LACS7	5103	5103 A	G	31.24	59.12
LACS7	5110	5110 T	C	23.2	59.12

LACS7	5113	5113 G	A	10.69	59.09
LACS7	5141	5142 CA	C	16.63	60
LACS7	5145	5145 A	T	10.2	60
LACS7	5147	5147 T	A	16.84	60
LACS7	5159	5159 T	C	32.26	60
LACS7	5203	5235 CAATTCAAAGC		12.91	59.79
LACS7	5267	5267 A	T	8.77	59.76
LACS7	5282	5282 T	C	10.89	59.73
LACS7	5325	5325 G	C	26.22	59.69
LACS7	5343	5344 TC	T	14.52	59.75
LACS7	5348	5348 C	T	15.43	59.74
LACS7	5390	5390 T	C	27.67	59.77
LACS7	5396	5396 T	TG	20.13	60
LACS7	5420	5420 A	G	20.5	60
LACS7	5435	5435 A	G	15.85	60
LACS7	5461	5461 C	T	13.29	60
LACS7	5472	5472 T	C	13.12	60
LACS7	5667	5667 C	T	9.83	60.32
LACS7	5668	5668 A	G	10.11	60.33
LACS7	5672	5673 TA	T	9.01	60.3
LACS7	5693	5693 A	G	14.46	60.27
LACS7	5696	5696 C	T	14.11	60.26
LACS7	5705	5712 CTGCTAAG	C	13.41	60.48
LACS7	5736	5736 A	G	21.25	60.33
LACS7	5890	5890 A	G	22	60
LACS7	5892	5892 C	T	22	60
LACS7	5894	5894 G	GTTAT	31.31	60
LACS7	5922	5922 G	A	7.84	60
LACS7	5967	5967 A	T	6.42	60
LACS7	5997	5997 A	AATGGTAT	10.46	60
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LACS7	6060	6060 C	CATTTATTCA	26.62	60
LACS7	6075	6075 C	A	25.8	60
LACS7	6085	6085 C	A	31.01	60
LACS7	6099	6099 G	A	14.04	60
LACS7	6101	6101 C	T	28.87	60
LACS7	6177	6177 A	G	18.11	59.92
LACS7	6214	6214 A	G	19.43	60
LACS7	6218	6218 A	T	19.31	60
LACS7	6219	6219 C	T	19.31	60
LACS7	6226	6226 C	G	21.91	60
LACS7	6246	6246 G	A	21.4	60
LACS7	6259	6261 ATT	A	11.32	60
LACS7	6285	6285 C	T	18.44	60

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LACS7	6491	6491 T	C	12.07	60
LACS7	6517	6517 G	A	15.25	60
LACS7	6519	6519 G	T	15.86	60
LACS7	6536	6536 C	T	18.33	60
LACS7	6676	6676 G	A	12.66	60
LACS7	6683	6683 A	T	30.11	60
LACS7	6694	6694 T	C	22.45	60
LACS7	6703	6703 T	C	21.94	60
LACS7	6727	6727 G	T	14.93	60
LACS7	6753	6754 CT	C	21.62	60
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LACS7	6781	6781 A	G	29.84	60
LACS7	6799	6799 G	T	14.94	60
LACS7	6802	6802 T	C	29.08	60
LACS7	6810	6811 GT	G	16.64	60
LACS7	6818	6818 T	TC	17.78	60
LACS7	6827	6827 C	A	27.67	60
LACS7	6836	6841 ATCTTG	A	28.85	60
LACS7	6871	6871 G	C	10.92	60
LACS7	6943	6943 C	T	29.23	60.83
LACS7	6947	6947 T	C	22.41	60.8
LACS7	6960	6960 A	G	27.59	60.74
LACS7	6964	6964 C	T	27.59	60.74
LACS7	6986	6986 C	T	25.51	60.69
LACS7	6987	6987 A	G	25.51	60.69
LACS7	6995	6995 T	A	26.05	60.67
LACS7	7042	7042 C	T	17.34	60.63
LACS7	7047	7048 CT	C	10.12	60.62
LACS7	7080	7080 A	C	26.92	60
LACS7	7089	7089 C	T	24.9	60
LACS7	7139	7139 G	T	15.84	60
LACS7	7168	7168 T	A	23.49	60
LACS7	7174	7174 C	T	22.88	60
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LACS7	7527	7527 A	C	14.37	60
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LACS7	7545	7546 TA	T	11.13	60
LACS7	7548	7548 G	T	12.84	60
LACS7	7596	7596 A	T	24.54	60
LACS7	7605	7605 A	C	23.94	60
LACS7	7617	7617 C	T	21.8	60

LACS7	7620	7623 CACA	C	10.37	60
LACS7	7632	7632 G	T	21.73	60
LACS7	7640	7640 T	A	23.57	60
LACS7	7657	7657 C	G	23.73	60
LACS7	7665	7665 T	C	22.99	60
LACS7	7685	7685 G	A	18.42	60
LACS7	7686	7686 C	A	19.44	60
LACS7	7703	7703 T	C	19.11	60
LACS7	7707	7707 T	C	18.82	60
LACS7	7740	7740 T	A	28.33	60
LACS7	7746	7750 TGGAC	T	27.67	60
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LACS7	7756	7756 T	C	29.85	60
LACS7	7798	7800 TCC	T	6.57	60
LACS7	7805	7805 C	T	33.23	60
LACS7	7826	7826 T	TTATAATG	25.94	60
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LACS7	7870	7873 TAAA	T	21.72	60
LACS7	7874	7874 A	G	17.84	60
LACS7	7879	7879 G	GA	13.39	60
LACS7	7883	7886 AAAT	A	12.14	60
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LACS7	7994	7994 G	T	16.64	59.49
LACS7	8012	8012 T	C	17.88	59.46
LACS7	8015	8015 C	T	17.03	59.44
LACS7	8028	8028 C	T	14.83	59.46
LACS7	8029	8033 CAAGG	C	16.58	59.48
LACS7	8056	8056 C	CAGA	12.41	59.48
LACS7	8058	8058 C	CTTGTGTTCT	17.07	59.46
LACS7	8080	8080 T	C	11.9	59.47
LACS7	8095	8095 T	A	10.27	59.6
LACS7	8309	8309 G	A	31.85	60
LACS7	8334	8334 G	GC	31.11	60
LACS7	8470	8470 T	C	22.66	57.78
LACS7	8471	8471 G	A	23.74	57.69
LACS7	8476	8476 A	G	22.85	57.59
LACS7	8480	8493 GCCACCTATT	G	18.11	57.95
LACS7	8497	8498 TC	T	19.74	58.56
LACS7	8500	8514 TTAGAATTCT	T	23.56	58.56
LACS7	8523	8523 C	G	22.18	56.11
LACS7	8536	8536 A	T	17.88	56.22
LACS7	8537	8541 AATGT	A	19	56.22
LACS7	8552	8552 C	T	20.99	56.47
LACS7	8580	8580 G	A	10.75	57

LACS7	8586	8586 A	G	11.81	58.56
LACS7	8589	8589 G	A	17.88	58.61
LACS7	8591	8591 T	C	15.81	58.66
LACS7	8593	8594 AT	A	16.89	58.66
LACS7	8627	8627 C	T	18.81	58.75
LACS7	8629	8629 A	T	18.81	58.75
LACS7	8641	8641 T	G	25.31	58.56
LACS7	8666	8666 G	A	22.41	59.47
LACS7	8691	8691 G	A	24.45	59.76
LACS7	8696	8696 C	G	21.56	60
LACS7	8703	8703 A	G	26.65	60
LACS7	8727	8727 T	G	26.96	60
LACS7	8749	8749 T	C	7.6	60
LACS7	8758	8758 A	G	28.42	60
LACS7	8773	8773 A	T	28.45	60
LACS7	8787	8787 T	G	28.76	59.52
LACS7	8817	8817 C	T	26.21	59.34
LACS7	8827	8827 T	G	27.07	59.28
LACS7	8831	8831 T	C	28.04	59.22
LACS7	8841	8841 T	C	16.46	59.24
LACS7	8843	8843 A	G	12.94	59.22
LACS7	8844	8844 C	CT	26.4	59.2
LACS7	8850	8851 AT	A	26.13	59.2
LACS7	8858	8858 A	G	19.52	59.2
LACS7	8860	8860 A	G	19.52	59.2
LACS7	8862	8862 T	G	24.43	59.17
LACS7	8873	8873 A	G	17.64	58.95
LACS7	8891	8891 T	G	25.79	59.11
LACS7	8896	8896 A	T	25.13	59.11
LACS7	8899	8899 G	T	25.13	59.11
LACS7	8909	8911 TTG	T	23.38	58.96
LACS7	8912	8912 C	CCT	23.38	58.96
LACS7	8932	8932 T	G	24.26	59.15
LACS7	8933	8933 G	A	25	59.15
LACS7	8938	8938 A	C	23.36	59.15
LACS7	8988	8988 C	T	14.37	59.31
LACS7	9131	9133 TTA	T	17.53	59.37
LACS7	9133	9133 A	C	12.46	59.37
LACS7	9135	9135 C	G	11.38	59.37
LACS7	9136	9136 T	TGC	19.7	59.35
LACS7	9143	9162 CTACGTAGCAC		16.13	59.42
LACS7	9145	9145 A	G	12.92	59.42
LACS7	9146	9146 C	T	11.95	59.42
LACS7	9163	9163 T	C	12.91	59.37

LACS7	9185	9185 T	C	13.11	59.88
LACS7	9190	9190 T	C,G	33.61	59.87
LACS7	9191	9191 G	T	30.84	59.87
LACS7	9195	9195 A	G	31.65	59.88
LACS7	9200	9200 A	T	31.48	59.88
LACS7	9205	9205 A	T	23.53	60
LACS7	9207	9207 T	C	17.31	60
LACS7	9217	9217 G	A	14.77	60
LACS7	9337	9337 A	G	10.47	59.66
LACS7	9351	9351 C	A	11.08	60
LACS7	9354	9390 AAATGCTGAC	A	11.52	60
LACS7	9361	9361 G	T	9.17	60
LACS7	9368	9371 TTGC	T	9.71	60
LACS7	9372	9402 ATCCTTTACA	A	7.89	59.04
LACS7	9400	9400 A	G	14.48	58.99
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LACS7	9424	9424 T	TC	17.99	58.89
LACS7	9425	9425 T	C	30.25	58.89
LACS7	9430	9430 T	C	17.07	58.83
LACS7	9431	9431 A	G	18.02	58.77
LACS8	177	177 G	C	20.33	60
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LACS8	446	446 G	T	19.66	60
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LACS8	660	660 T	TTACTAC	7.83	59.06
LACS8	688	688 G	T	9.14	60.13
LACS8	872	872 T	C	9.2	60
LACS8	913	913 T	A	10.89	60
LACS8	1118	1118 T	C	15.87	59.07
LACS8	1173	1173 A	C	6.7	59.25
LACS8	1752	1752 A	G	10.82	60
LACS8	2436	2436 C	CT	13.8	59.94
LACS8	2646	2646 C	T	4.16	60
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LACS8	2719	2719 G	A	10.04	60
LACS8	2781	2781 G	A	9.51	60
LACS8	2794	2794 T	C	9.66	60
LACS8	3129	3129 C	T	16.01	60
LACS8	3132	3132 A	G	10.08	59.66
LACS8	3165	3165 A	G	18.42	60

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LACS8	3236	3236 G	A	11.99	60
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LACS8	4060	4060 C	G	10.87	60
LACS8	4126	4126 A	G	7.9	60
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LFNR	945	945 G	A	6.33	60
LFNR	967	969 ACT	A	8.73	60
LFNR	1002	1002 G	GTACTAA	8.98	60
LFNR	1008	1008 G	A	12.39	60
LFNR	1012	1015 GGAC	G	8.16	60
LFNR	1036	1036 A	T	8.08	60
LFNR	1088	1088 A	T	13.92	59.5
LFNR	1118	1119 GT	G	15.45	59.53
LFNR	1120	1123 GTGT	G	15.45	59.53
LFNR	1125	1125 T	TACACAC	18.83	59.46
LFNR	1127	1127 T	C	21.07	59.42
LFNR	1576	1576 A	G	15.19	60
LFNR	1601	1601 T	C	8.39	60
LFNR	1654	1654 G	T	29.1	60
LFNR	1762	1764 CCT	C,CCTCT	18.46	59.34
MAT1	760	760 T	C	20.12	60
MAT1	805	805 A	ATGCATGAT	14.2	60
MAT1	938	938 A	G	6.35	60
MAT1	1005	1005 T	C	9.53	60
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MAT1	1121	1121 T	C	25.49	60

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MAT1	1274	1274 T	C	8.2	60
MAT1	1315	1315 G	A	16.1	60
MAT1	1317	1317 A	G	15.33	60
MAT1	1330	1330 A	G	15.33	60
MAT1	1378	1378 G	T	17.4	60
MAT1	1391	1391 G	A	10.71	60
MAT1	1519	1519 T	A	33.37	59.94
MAT1	1624	1624 A	G	8.93	59.42
MAT1	1706	1706 A	G	6.19	60
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MAT1	2048	2048 G	GT	20.7	60
MAT1	2053	2053 A	G	19.76	60
MAT1	2063	2064 CA	C	9.84	60
MAT1	2154	2154 T	G	29.33	59.88
MAT1	2155	2155 G	C	34.28	59.88
MAT1	2159	2159 T	C	20.17	59.88
MAT1	2162	2162 G	A	16.44	59.88
MAT1	2196	2196 G	T	15.99	59.9
MAT1	2202	2202 G	A	19.04	59.9
MAT1	2219	2219 G	A	9.97	60
MAT1	2260	2260 A	G	14.91	59.7
MAT1	2266	2266 T	C	14.22	59.71
MAT1	2275	2275 G	A	8.64	59.7
MAT1	2290	2290 G	T	10.31	59.72
MAT1	2292	2292 A	G	10.31	59.72
MAT1	2338	2338 T	TA	7.81	59.7
MAT1	2368	2370 AAT	A	9.96	60
MAT1	2578	2578 T	C	9.36	60
MAT1	2615	2615 C	G	8.77	60
MAT1	2637	2637 T	TG	33.91	60
MAT1	2664	2664 G	A	12.48	60
MAT1	2704	2704 A	AT	8	60
MAT1	3122	3122 A	G	3.02	60
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MAT1	3254	3255 CT	C,CTT	14.61	60
MAT1	3278	3278 C	T	15	60
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MATE	617	617 T	C	8.67	60.4
MATE	646	646 T	C	26.89	60.39
MATE	665	665 A	T	7.46	60.39
MATE	683	683 C	T	5.97	60.43

MATE	1342	1342 C	CT	9.15	60
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MATE	1362	1362 A	C	11.5	60
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MATE	2503	2503 A	T	19.45	60
MATE	2818	2818 T	A	9.55	60
MATE	2964	2964 T	G	8.81	60
MATE	2965	2965 T	G	8.81	60
MATE	2996	2996 T	C	7.51	60
MATE	3019	3019 T	G	5.35	60
MATE	3106	3106 T	C	28.25	60
MATE	3127	3127 T	G	8.41	60
MATE	3136	3136 G	A	21.12	60
MATE	3152	3152 G	A	9.74	60
MATE	3155	3155 T	C	12.54	60
MATE	3170	3170 A	T	11.92	60
MATE	3273	3273 C	T	9.46	59.4
MATE	3286	3286 C	T	10.47	59.3
MATE	3318	3318 T	G	11.68	60
MATE	3320	3320 C	A	10.62	60
MATE	3327	3327 T	A	11.23	60
MATE	3412	3424 GACTCTCCTC G		8.35	55.21
MATE	3446	3446 C	A	8.66	56
MATE	3622	3622 T	C	22.55	60
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MATE	4192	4192 T	C	18.54	60
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MATE	4255	4255 C	T	32.9	60
MATE	4258	4258 T	C	23.9	60
MATE	4269	4269 C	A	29.35	60
MATE	4270	4270 A	G	29.77	60
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MATE	4343	4343 C	G	6.86	60
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MATE	4482	4482 A	G	13.23	60
MATE	4497	4497 C	T	13.51	60
MATE	4552	4552 C	A	11.99	60
MATE	4648	4648 A	G	13.42	60
MATE	4708	4708 A	G	20.02	60
MATE	4818	4820 CTT	C	10.38	60
MATE	6136	6139 TGAC	T	26.58	60

MATE	6137	6137 G	GT	10.38	60
MATE	6139	6139 C	CCTT	10.38	60
MATE	6229	6229 A	C	13.1	60
MATE	6296	6296 G	A	6.76	60
MATE	6354	6354 G	A	8.2	60
MATE	6355	6355 T	A	9.16	60
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MATE	6542	6542 C	CA	9.46	60
MATE	6598	6598 G	A	11.95	60
MATE	6651	6651 T	C	30.25	60
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MFP2	2539	2539 T	A	20.84	60
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MFP2	2723	2723 A	T	33.24	60
MFP2	3058	3058 T	TTA	14.13	60
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MFP2	3566	3567 TC	T	11.61	60
MFP2	3569	3572 CTAT	C	13.15	60
MFP2	3726	3726 C	T	16.7	60
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MFP2	3749	3749 G	A	17.65	60
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MFP2	3762	3762 T	A	13.37	60
MFP2	3767	3767 G	A	18.22	60
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MFP2	3780	3780 A	C	21.26	60
MFP2	3783	3783 A	G	20.52	60
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MFP2	4405	4405 C	T	10.09	60
MFP2	4409	4409 T	A	9.77	60
MFP2	4561	4561 A	C	23.95	59.85
MFP2	4564	4564 C	T	26.31	59.86
MFP2	4571	4571 A	G	23.29	59.86
MFP2	4576	4576 T	C	22.16	59.86
MFP2	4595	4595 G	A	24.13	59.85
MFP2	4606	4606 T	G	21.38	59.85
MFP2	4814	4817 AGTT	A	20.75	59.72
MFP2	4818	4818 T	C	21.33	59.72
MFP2	4830	4830 T	C	20.52	59.73
MFP2	4902	4902 A	T	13.16	60.19
MFP2	4929	4929 T	A	14.98	60.19
MFP2	4949	4949 C	T	17.48	60.19
MFP2	4956	4956 G	A	17.79	60.2
MFP2	4963	4963 A	G	17.23	60.21
MFP2	4965	4965 G	A	12.11	60.21
MFP2	4968	4968 G	A	16.55	60.2

MFP2	4983	4983 A	T	27.54	60.21
MFP2	4992	4992 G	A	14.27	60.23
MFP2	5002	5003 CT	C	13.26	60.24
MFP2	5037	5037 T	G	10.09	60
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MFP2	5186	5196 CTGAAGTATAC		14.08	60
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MFP2	5215	5215 T	C	14.64	60
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MFP2	5249	5249 A	C	19.55	60
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MFP2	5308	5308 T	C	13.56	60
MFP2	5333	5335 AAC	A	17.31	60
MFP2	5337	5337 T	TGC	17.31	60
MFP2	5344	5344 C	A	7.2	60
MFP2	5346	5346 C	T	17.76	60
MFP2	5796	5803 AGTCATTT	A	21.36	60
MFP2	5814	5814 C	T	23.48	60
MFP2	5816	5816 T	TCA	10.41	60
MFP2	5821	5821 T	A	20.61	60
MFP2	5822	5822 G	T	9.78	60
MFP2	5831	5831 G	C	22.66	60
MFP2	5839	5841 CCA	C	20.83	60
MFP2	5846	5846 A	T	22.12	60
MFP2	5850	5850 T	A	21.6	60
MFP2	5891	5891 A	G	18.16	60
MFP2	5911	5911 G	A	16.96	60
MFP2	5918	5918 G	T	17.54	60
MFP2	5940	5940 G	GCACCTCTTG	11.02	60
MFP2	5960	5981 CAAAATGCTAC		10.59	60
MFP2	5977	5977 A	T	10.42	60
MFP2	5997	5997 C	A	10.91	60
MFP2	6009	6011 TTA	T	10.43	60.26
MFP2	6030	6030 C	A	12.2	60.28
MFP2	6050	6050 A	G	10.49	60
MFP2	6067	6067 G	A	13.44	60
NIT4	949	949 C	G	27.31	60
NIT4	959	959 G	T	9.99	60
NIT4	961	961 T	A	25.94	60
NIT4	965	965 G	T	10.06	60
NIT4	1036	1036 C	CCTA,T	17.14	59.74
NIT4	1301	1302 TG	T	4.09	60
NIT4	1372	1372 C	A	7.93	60

NIT4	1387	1387 A	T	5.36	60
NIT4	1714	1714 A	G	10.56	60
NIT4	1719	1720 TA	T	9.37	60
NIT4	1730	1730 A	T	12.1	60
NIT4	1761	1761 A	G	8.88	60
NIT4	1782	1782 C	A	15.67	60
NIT4	1834	1834 A	G	6.26	60
NIT4	2197	2197 C	T	10.39	60
NIT4	2225	2225 A	C	7.5	60
NIT4	2252	2252 C	T	8.36	60
NIT4	2404	2404 C	G	8.94	60
NIT4	2484	2484 A	G	8.97	60
NIT4	2501	2501 T	C	9.96	60
NIT4	2517	2517 T	C	9.18	60
NIT4	2886	2886 A	ACTG	9.49	60
NIT4	2901	2901 G	T	8.34	60.4
NIT4	2903	2903 T	C	9.38	60.45
NIT4	2906	2906 A	C	10.01	60.47
NIT4	3269	3269 G	A	18.47	59.81
NIT4	3299	3299 G	A	27.79	59.81
NIT4	3300	3300 G	T	27.79	59.81
NIT4	3305	3305 C	T	22.85	59.81
NIT4	3313	3313 G	T	11.17	59.81
NIT4	3357	3357 G	A	5.71	60
NIT4	3379	3379 G	A	8.47	60
OEP64	387	387 C	CG	7.49	60
OEP64	428	428 A	G	10.9	60
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OEP64	691	691 T	C	7.11	60
OEP64	710	710 G	C	20.92	60
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OEP64	803	803 G	T	7.77	60
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OEP64	1133	1133 C	T	11.84	60
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OEP64	1573	1573 C	T	27.51	60

OEP64	1593	1593 G	A	26.48	60
OEP64	1726	1730 GGGGT	G	7.07	59.27
OEP64	1731	1733 GGT	G	10.27	59.79
OEP64	1732	1732 G	GT	3.3	59.79
OEP64	1767	1767 T	C	16.78	59.78
OEP64	1788	1788 G	A	9.18	60
OEP64	1865	1865 A	G	14.53	58.53
OEP64	1943	1943 C	T	7.35	60
OEP64	2031	2031 G	A	14.97	60
OEP64	2109	2109 T	G	19.5	60
OEP64	2234	2234 C	T	9.75	60
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OEP64	2493	2493 A	ATTATAGATT	8.78	59.01
OEP64	2494	2494 T	TATA	7.46	58.91
OEP64	2495	2495 G	GATTTA	7.46	58.91
OEP64	2520	2523 CAAA	C	13.84	58.79
OEP64	2526	2526 A	G	16.7	58.63
OEP64	2585	2585 T	G	19.2	60
OEP64	2640	2643 CTGT	C	16.64	60.51
OEP64	2677	2677 G	A	25	60.42
OEP64	2758	2758 C	G	17.64	60.33
OEP64	2782	2782 A	T	20.47	60
OEP64	2829	2830 GA	G	11.15	60.29
OEP64	3165	3165 C	T	8.25	60
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OEP64	3454	3454 T	A	4.66	60
OEP64	3722	3722 G	A	28.3	60
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OEP64	3794	3794 C	T	24.47	60
OEP64	3831	3831 G	A	13.26	60
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OEP64	4001	4002 GA	G	11.25	60.23
OEP64	4050	4050 A	T	11.94	60
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OEP64	4152	4152 G	A	11.3	60
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OEP64	4309	4309 T	G	15.92	60
OEP64	4317	4317 G	A	6.62	60
OEP64	4421	4421 T	C	6.68	60
OEP64	4474	4474 T	A	7.81	60
OEP64	4574	4576 CCA	C	12.74	60
OEP64	4654	4654 A	G	31.17	60
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OEP64	4737	4737 T	C	34.03	60
OEP64	4882	4882 T	C	15.81	60
OEP64	4929	4929 G	GA	9.49	60
OEP64	4969	4969 T	C	30.08	60
OEP64	4970	4970 G	A	11.27	60
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OEP64	5091	5091 G	GAA	9.11	60
OEP64	5123	5123 A	G	6.87	60
OEP64	5137	5137 A	AT	5.93	60
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OEP64	5410	5410 T	C	31.81	60
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OEP64	6039	6039 G	A	14.6	60
OEP64	6085	6085 G	C	17.88	60
OEP64	6105	6105 C	G	20.36	60
OEP64	6126	6126 C	T	6.54	60
OEP64	6245	6245 A	C	18.99	60
OEP64	6341	6341 T	A	18.61	60
OEP64	6386	6386 C	CT	8.35	60.74
OEP64	6740	6740 A	G	19.93	60
OEP64	6853	6855 CTA	C	14.7	60
OEP64	6858	6858 G	T	26.64	60
OEP64	6902	6902 A	T	9.98	60
OEP64	6910	6910 C	G	9.98	60
OEP64	7115	7116 AT	A	4.56	60
OEP64	7491	7491 G	T	5.9	60
OEP64	7513	7513 A	G	6.12	60
OEP64	7727	7727 C	T	6.78	60
OEP64	7768	7768 T	C	15.84	60
OEP64	7861	7861 T	A	18.12	60
OEP64	7891	7891 G	A	20.3	60
OEP64	7950	7950 A	G	22.66	60
OEP64	7960	7960 G	A	14.72	60
OEP64	8037	8037 T	TC	9.99	60
OEP64	8160	8160 C	T	14.5	60.49
OEP64	8183	8183 C	G	15.63	60.49
OEP64	8194	8195 GC	G	13.2	60.51
OEP64	8247	8247 A	G	19.48	60
OEP64	8347	8347 C	T	17.98	60
OEP64	8387	8387 G	C	16.6	60
OEP64	8388	8388 A	G	22.62	60
OEP64	8649	8649 T	TA	9.34	60
OEP64	8659	8659 A	G	9.36	60

OEP64	8774	8774 T	TGTCA	23.51	60
OEP64	8897	8897 T	A	7.95	60
OEP64	8918	8918 C	T	24.18	60
OEP64	9141	9142 CT	C	6.09	60.34
OEP64	9154	9154 T	A	26.64	60.33
OEP64	9187	9187 A	T	21.67	60.33
OEP64	9310	9310 T	G	22.02	60
OEP64	9347	9347 T	A	18.05	60
OEP64	9402	9402 C	A	12.61	60.37
OEP64	9441	9441 T	C	9.29	60.3
OEP64	9443	9443 A	T	29.02	60.29
OEP64	9467	9467 C	T	5.94	60.28
OEP64	9529	9529 T	A	6.34	60
OEP64	9743	9743 G	GTGACCAAC	8.47	60
ONL1	703	703 A	C	13.25	60
ONL1	891	891 A	C	13.01	60.24
ONL1	903	919 ATCGACAATA	A	9.38	60.25
ONL1	1019	1019 T	TA	8.05	60
ONL1	1035	1035 A	G	30.7	60
ONL1	1106	1106 A	G	17.97	59.49
ONL1	1107	1107 C	T	17.39	59.5
ONL1	1140	1141 TA	T	16.25	59.43
ONL1	1143	1144 TA	T	16.25	59.43
ONL1	1145	1145 T	C	17.91	59.39
ONL1	1161	1161 C	T	4.01	59.41
ONL1	2145	2145 G	A	28.75	60
ONL1	2183	2183 T	C	9.97	60
ONL1	2211	2211 C	T	19.03	60
ONL1	2232	2232 T	A	9.54	60
ONL1	2247	2247 A	AT,ACCATGT	26.96	60
ONL1	2271	2271 C	T	15.78	60
ONL1	2511	2511 A	AT	6.12	60
PDS1	1052	1052 A	C	20.46	60
PDS1	1058	1058 T	C	25	60
PDS1	1059	1059 G	C	20.21	60
PDS1	1063	1063 T	C	20.21	60
PDS1	1093	1093 T	C	23.56	60
PDS1	1097	1097 T	A	23.3	60
PDS1	1100	1101 CT	C	22.85	60
PDS1	1255	1255 T	G	21.13	60
PDS1	1257	1257 G	A	21.06	60
PDS1	1270	1271 GT	G	16.26	60
PDS1	1277	1277 A	T	16.76	60
PDS1	1287	1287 T	C	22.41	60

PDS1	1298	1298 G	A	22.06	60
PDS1	1309	1309 C	T	21.2	60
PDS1	1324	1324 T	C	21.63	60
PDS1	1334	1334 C	T	18.82	60
PDS1	1336	1336 T	A	17.23	60
PDS1	1350	1350 C	G	14.23	60
PDS1	1352	1352 G	T	20.17	60
PDS1	1355	1355 G	A	19.35	60
PDS1	1474	1474 T	A	13.25	60
PDS1	1484	1484 A	G	18.15	60
PDS1	1518	1518 A	G	15.9	60
PDS1	1537	1537 T	TTC	18.12	60
PDS1	1538	1538 A	C	18.81	60
PDS1	1542	1542 T	TG	19.83	60
PDS1	1635	1635 G	A	27.46	60
PDS1	1669	1669 C	A	14.22	60
PDS1	1679	1679 G	GA	12.78	60
PDS1	1706	1706 G	C	11.61	59.73
PDS1	1741	1741 A	G	12.53	59.63
PDS1	1745	1770 AAACGTCTAA	A	12.58	59.65
PDS1	1801	1801 G	GCA	9.23	60
PDS1	1856	1856 A	AG	13.49	59.8
PDS1	1860	1860 A	C	15.8	59.79
PDS1	1865	1865 T	C	14.88	59.8
PDS1	1878	1878 G	A	15.22	59.81
PDS1	1882	1882 G	A	15.95	59.81
PDS1	1887	1887 A	G	17.41	59.81
PDS1	1890	1890 A	G	16.83	59.82
PDS1	1909	1909 T	C	16.02	59.84
PDS1	1942	1942 T	C	18.83	59.84
PDS1	1961	1992 CATAGACCATC		16.45	59.86
PDS1	1997	1997 G	T	18.63	59.81
PDS1	1999	1999 C	T	18.65	59.81
PDS1	2010	2010 T	C	18.6	59.81
PDS1	2014	2014 A	ATGAGCAGT	18.02	59.81
PDS1	2033	2033 C	T	22.41	59.26
PDS1	2055	2055 C	A	21.32	59.39
PDS1	2064	2064 A	G	17.09	59.34
PDS1	2066	2066 G	T	17.28	59.36
PDS1	2068	2068 G	A	17.28	59.36
PDS1	2273	2276 ACGT	A	17.37	59.73
PDS1	2280	2280 A	AAT	17.75	59.72
PDS1	2290	2290 T	G	18.31	59.71
PDS1	2291	2291 T	C	18.31	59.71

PDS1	2327	2327 C	T	16.96	60
PDS1	2359	2359 A	AC	17.04	59.93
PDS1	2361	2361 T	A	17.2	59.93
PDS1	2362	2362 T	C	17.2	59.93
PDS1	2372	2372 A	G	8.25	60
PDS1	2375	2375 T	G	16.36	60
PDS1	2377	2377 C	G	16.36	60
PDS1	2379	2379 A	T	18.1	60
PDS1	2389	2389 T	A	18.2	60
PDS1	2416	2420 TAACA	T	9.72	60
PDS1	2420	2420 A	ATGTG	9.72	60
PDS1	2423	2423 A	T	9.27	60
PDS1	2428	2428 A	G	17.13	60
PDS1	2614	2614 T	G	13.21	60
PDS1	2621	2621 T	C	12.98	60
PDS1	2654	2654 C	T	9.41	60
PDS1	2680	2680 T	A	8.13	60
PDS1	2844	2844 C	T	23.79	55.84
PDS1	2923	2923 C	G	34.38	59.18
PDS1	2984	2984 T	G	10.34	57.81
PDS1	3106	3106 G	A	16.7	60
PDS1	3154	3154 G	A	8.89	58.73
PDS1	3156	3156 G	T	9.27	58.78
PDS1	3175	3175 G	A	12.51	58.82
PDS1	3194	3194 C	T	11.78	58.82
PDS1	3196	3196 C	T	11.57	58.84
PDS1	3197	3197 A	G	11.57	58.84
PDS1	3296	3296 A	G	24.97	60
PDS1	3353	3353 G	A	10.04	60
PDS1	3389	3389 T	C	8.43	58.96
PDS1	3407	3407 C	G	16.43	58.42
PDS1	3409	3409 C	A	14.6	58.42
PDS1	3413	3415 CCT	C	8.73	58.36
PDS1	3418	3418 A	AC	19.24	58.05
PDS1	3642	3642 T	C	16.41	60
PDS1	3647	3647 G	A	15.68	60
PDS1	3650	3650 C	T	14.98	60
PDS1	3655	3655 A	T	15.9	60
PDS1	3663	3663 C	T	14.08	60
PDS1	3700	3700 T	C	13.89	60
PDS1	3708	3708 T	G	29.05	60
PDS1	3710	3710 T	C	15.74	60
PDS1	3719	3719 C	T	15.2	60
PDS1	3735	3736 CT	C	15.22	60

PDS1	3755	3755 G	A	27.76	60
PDS1	3792	3792 G	A	15.08	60
PDS1	3795	3796 CT	C	14.65	60
PDS1	4056	4056 C	CAATAAAG	22.52	60
PDS1	4067	4067 G	C	8.14	60
PDS1	4091	4091 T	A	17.34	60
PDS1	4304	4304 A	C	19.28	60
PDS1	4442	4442 A	G	8.34	60
PDS1	4452	4452 G	A	31.78	60
PDS1	4603	4603 C	T	17.9	59.98
PDS1	4608	4608 C	T	19.03	59.98
PDS1	4614	4614 T	C	20.16	59.98
PDS1	4617	4617 G	T	19.81	59.98
PDS1	4633	4633 C	T	19.02	59.96
PDS1	4635	4635 A	G	20.5	59.96
PDS1	4651	4651 C	G	17.91	59.85
PDS1	4657	4661 TCTCA	T	20.16	59.85
PDS1	4666	4669 TACA	T	17.99	59.86
PDS1	4671	4707 TTTCCACCTT/T		15.68	59.88
PDS1	4713	4713 G	A	21.87	59.84
PDS1	4744	4744 T	G	18.54	59.86
PDS1	4746	4750 CATT	CA,C	18.22	59.86
PDS1	4762	4762 C	T	20.75	59.86
PDS1	4765	4765 C	T	20.77	59.86
PDS1	4771	4771 C	T	22	59.87
PDS1	4772	4772 C	G	21.51	59.87
PDS1	4838	4847 TGCGCACATAT		10.24	58.14
PDS1	4888	4888 T	C	30.34	57.34
PDS1	4972	4972 T	A	33.69	58.18
PDS1	4977	4977 A	C	33.99	58.1
PDS1	5026	5026 C	T	16.39	58.68
PDS1	5033	5033 C	T	33.3	58.45
PDS1	5056	5056 T	C	31	54.6
PDS1	5140	5140 A	G	27.24	55.28
PDS1	5147	5147 A	G	32.87	55.14
PDS1	5177	5177 G	A	16.24	57.68
PDS1	5234	5237 CCTT	C	7.89	60
PDS1	5248	5248 T	C	34.84	60
PDS1	5494	5494 T	A	18.03	59.82
PDS1	5504	5504 T	A	17.65	59.82
PDS1	5514	5515 GT	G	6.6	59.83
PDS1	5517	5517 T	G	20.61	59.82
PDS1	5518	5518 T	G	6.69	59.82
PDS1	5520	5520 T	TCC	18.41	59.82

PDS1	5522	5525 TCTA	T	17.56	59.83
PDS1	5528	5528 A	G	18.59	59.82
PDS1	5531	5531 T	C	18.9	59.82
PDS1	5753	5753 A	C	20.94	59.22
PDS1	5756	5756 A	C	23.53	59.19
PDS1	5757	5757 T	A	22.82	59.19
PDS1	5774	5774 G	A	21.3	58.46
PDS1	5788	5788 T	C	8.96	58.48
PDS1	5794	5794 G	A	20.54	58.44
PDS1	5798	5798 T	C	9.42	58.41
PDS1	5802	5842 CATCTAATGAC		16.34	58.45
PDS1	5842	5842 T	C	18.13	58.19
PDS1	5843	5843 G	A	18.13	58.19
PDS1	5853	5853 T	TTA	17.65	57.94
PED1	791	791 C	T	7.36	60
PED1	919	919 G	T	6.99	60
PED1	1033	1033 A	G	10.89	60
PED1	1035	1035 T	A	11.5	60
PED1	1049	1049 T	C	9.37	60
PED1	1504	1504 A	G	17.49	60
PED1	1518	1518 T	C	6.89	60
PED1	1846	1846 T	TA	8.16	60
PED1	2116	2116 C	A	9.15	60.32
PED1	2529	2529 G	C	15.36	60
PED1	2736	2736 A	C	7.72	60
PED1	3016	3016 T	C	11.2	60
PED1	3292	3292 T	C	7.08	60
PPO	1329	1329 T	C	20.39	60
PPO	1385	1385 C	T	7.42	60
PPO	1440	1440 C	T	6.25	60
PPO	1510	1510 G	A	24.84	60
PPO	1702	1702 A	G	23.44	60
PPO	1706	1706 C	G	8.48	60
PPO	1708	1708 G	A	8.48	60
PPO	1754	1755 TA	T	8.79	60
PPO	2171	2171 C	A	6.27	60
PPO	2436	2436 G	A	6.85	60
PPO	2687	2687 T	TAGTAGCCTA	8.69	60
PPO	3070	3070 T	C	27.37	60
PPO	3255	3255 T	C	6.66	60
PPO	3672	3672 G	A	8.71	60
PPO	3701	3701 G	A	10.92	60
PPO	3703	3703 A	T	10.92	60
PPO	3709	3709 G	A	13.64	60

PPO	3775	3775 A	G	26.21	60
PPO	3780	3780 C	T	30.76	60
PPO	3783	3783 T	C	33.79	60
PPO	3974	3974 G	T	32.23	58.74
PPO	4018	4018 A	C	27.25	60
PPO	4733	4733 A	G	25.53	60
PPO	4735	4735 T	G	21.48	60
PPO	5091	5091 G	C	6.23	60
SBP1	1303	1303 G	T	12.23	60
SBP1	1360	1360 C	T	9.98	60
TIR1	598	598 A	G	17.7	60
TIR1	627	627 A	G	8.17	60
TIR1	630	630 C	A	6.89	60
TIR1	906	906 T	C	9.77	60
TIR1	969	971 TAC	T	8.2	60
TIR1	972	972 T	G	8.45	60
TIR1	1312	1312 T	A	11.57	60
TIR1	1313	1314 GC	G	11.01	60
TIR1	1626	1626 T	TA	6.81	60.42
TIR1	1657	1657 T	C	10.1	60.65
TIR1	1901	1901 A	AT	10.97	60
TIR1	2087	2087 T	C	8.19	60.42
TIR1	2187	2187 T	TACGATTGG/	32.22	60.4
TIR1	2244	2244 C	T	10.19	60
TIR1	2320	2320 A	AT	7.38	60
TIR1	2327	2327 T	TA	4.41	60
TIR1	2367	2367 G	T	14.51	60
TIR1	2369	2369 A	T	14.51	60
TIR1	2941	2941 A	T	8.69	60.43
TIR1	3069	3069 G	T	6.18	60
TIR1	3150	3150 G	T	10.52	60
TIR1	3152	3152 A	T	10.89	60
TIR1	3818	3818 T	C	25.02	60
TIR1	3905	3905 A	AT	5.18	60
TIR1	3999	3999 T	G	22.31	60
TIR1	4187	4187 T	TTTTCTAAAC/	12.78	60
TRX	538	538 C	T	13.31	59.56
TRX	565	565 A	G	16.02	59.39
TRX	679	679 T	C	12.03	60
TRX	1131	1131 A	C	12.76	60
TRX	1178	1178 G	A	7.73	60
TRX	1302	1303 AT	A,ATT	19.02	60
TRX	1307	1307 T	A	9.83	60
UGT73C6-like	944	944 T	C	22.86	59.81

UGT73C6-like	1062	1062 G	A	21.79	60
UGT73C6-like	1177	1178 GA	G	4.45	60
UGT73C6-like	1240	1240 G	A	11.34	60
UGT73C6-like	1273	1276 TACG	T	16.95	60.23
UGT73C6-like	2289	2289 G	A	14.03	59.59
UGT73C6-like	2297	2297 A	C	14.32	59.63
UGT73C6-like	2320	2320 C	CTGGG	11.82	59.63
UGT73C6-like	2321	2321 C	CAAATGCATC	12.54	59.91
UGT73C6-like	2324	2324 A	ATTAAGCTCC	13.54	59.91
UGT73C6-like	2342	2342 T	G	13.59	59.92
UGT73C6-like	2346	2346 C	A	12.09	59.92
UGT73C6-like	2369	2369 T	A	9.94	59.92
LCY1	700	700 C	T	27.62	58.74
DHPS	956	956 G	A	23.84	59.76
LACS7	4781	4781 G	T	10.82	59.64
MFP2	1961	1961 A	G	14.34	60
MFP2	2072	2072 C	A	22.75	60
MFP2	2074	2074 T	A	22.22	60
ONL1	661	661 T	C	11.38	60
ABCC1	4610	4610 G	A	8.73	60
ABCC1	9482	9482 C	T	20.88	60
ABCC1	11021	11021 G	C	10.96	60
ABCC1	11022	11022 A	T	10.96	60
ABCC1	11025	11025 G	A	10.42	60
ABCC1	11026	11026 C	T	10.67	60
ABCC1	11064	11064 G	A	14.34	60
ABCC1	11262	11262 C	T	18.62	60
ABCC1	11288	11288 C	T	11.53	60
ABCC1	11292	11292 G	A	14.15	60
ABCC1	11343	11343 G	A	13.05	60
ABCC1	11408	11408 T	G	10.94	59.38
ABCC4L	629	629 A	G	14.94	60
ABCC4L	1092	1092 G	C	17.29	60
ACC1	5373	5373 T	G	13.72	60
ACC1	8377	8377 T	C	14.39	60
ACC1	8872	8872 T	C	10.37	60
ACC1	10752	10752 G	A	8.25	60
ACC1	10917	10917 G	A	10.4	60
AIM1	1601	1601 G	A	23.07	60
AIM1	1775	1775 G	A	15.82	60
AIM1	2630	2630 C	T	8.66	60
AIM1	2732	2732 A	G	12.72	60
AIM1	2747	2747 A	G	16.8	60
AIM1	7160	7160 G	C	18.15	60

ALF5	201	201 G	C	19.76	59.14
ALF5	222	222 C	G	17.83	59.21
ALF5	225	225 C	G	17.83	59.21
ALF5	234	234 A	G	22.11	56.87
ALF5	252	252 C	G	22.11	56.87
ALF5	255	255 G	C	22.11	56.87
ALF5	258	258 G	T	11.12	56.87
ALF5	1413	1413 C	T	29.97	2.093
ALF5	1419	1419 C	A	31.49	3.056
ALF5	1423	1423 G	C	33.12	2.303
ALF5	1629	1629 G	C	17.08	60
ALF5	1697	1697 T	G	21.14	60
ALF5	2486	2486 G	C	20.02	60
ALF5	2645	2645 C	G	10.81	60
ALF5	2723	2723 G	C	18.88	60
ALF5	2799	2799 C	T	5.14	60
ALS	1178	1178 C	T	18.75	60
AML1	143	143 C	G	32.31	60.83
AML1	519	519 C	A	15.45	60
AML1	531	531 G	A	15.45	60
AML1	668	668 C	G	9.77	60
AML1	669	669 G	A	9.77	60
AML1	681	681 A	G	22.33	60
AML1	699	699 G	A	19.07	60
AML1	700	700 C	G	15.87	60
AML1	701	701 G	T	15.87	60
AML1	707	707 G	C	15.87	60
AML1	720	720 G	A	27.37	60
AML1	745	745 A	G,C	32.36	55.14
AML1	1252	1252 T	C	16.22	60
AML1	1507	1507 G	C	13.23	60
CESA1	2433	2433 A	T	18.12	59.63
CESA1	2441	2441 T	G	19.41	59.64
CESA1	2484	2484 C	T	18.86	59.83
CESA1	2531	2531 A	G	22.12	59.67
CESA1	2541	2541 G	A	22.81	59.49
CESA1	2604	2604 G	T	8.44	59.73
CXE12	354	354 G	A	11.55	60
CXE12	356	356 G	A	10.59	60
CXE12	1206	1206 C	T	9.83	60
CXE12	1224	1224 C	T	9.69	60
CXE12	1236	1236 C	T	16.5	60
CXE12	1251	1251 C	T	13.64	60
CYN	2368	2368 A	C	21.11	60

CYP709B3	153	153 C	A	34.13	60
CYP709B3	182	182 G	C	30.54	60
CYP709B3	766	766 C	T	11.43	60
CYP709B3	804	804 A	G	13.52	60
CYP709B3	844	844 G	T	35.14	60
CYP709B3	982	982 T	C	8.88	60
CYP709B3	1508	1508 C	G	27.73	59.3
CYP709B3	1606	1606 G	T	10.29	60
CYP709B3	1642	1642 A	C	10.06	60
CYP709B3	1644	1644 C	G	11.03	60
CYP709B3	1659	1659 T	G	9.36	60
CYP709B3	1661	1661 C	A	9.36	60
CYP709B3	1679	1679 C	T	10.79	60
CYP709B3	1955	1955 A	G	8.71	60
CYP709B3	1960	1960 T	G	14.73	60
CYP709B3	2065	2065 G	A	11.52	60
CYP71E1	58	58 A	T	31.96	60
CYP71E1	94	94 A	C	27.08	60
CYP71E1	248	248 C	T	8.8	60
CYP71E1	250	250 C	A	8.8	60
CYP71E1	325	325 G	C	22.44	60
CYP71E1	403	403 G	A	16.28	58.87
CYP71E1	404	404 C	T	16.28	58.87
CYP71E1	409	409 C	G	16.33	60
CYP71E1	415	415 A	G	11.59	60
CYP71E1	454	454 A	C	17.52	60
CYP71E1	455	455 A	G	17.52	60
CYP71E1	464	464 G	A	18.68	60
CYP71E1	466	466 G	C	17.35	60
CYP71E1	625	625 A	G	20.6	60
CYP71E1	629	629 T	A	9.17	60
CYP71E1	634	634 A	G	11.74	60
CYP71E1	641	641 C	G	9.79	60
CYP71E1	652	652 C	T	24.26	60
CYP71E1	706	706 A	G	10.84	60
CYP71E1	707	707 T	G	10.84	60
CYP71E1	719	719 A	G	13.18	60
CYP71E1	755	755 G	A	9.29	58.5
CYP71E1	767	767 A	T	11.52	58.17
CYP71E1	785	785 A	C	12.84	58.03
CYP71E1	787	787 G	T	12.84	58.03
CYP71E1	791	794 GAGC	AAGC,G	27.84	58.17
CYP71E1	797	797 C	T	13.91	57.86
CYP71E1	800	800 T	G	15.43	57.66

CYP71E1	803	803 T	C	19.15	57.13
CYP71E1	817	817 G	A	19.76	57.66
CYP71E1	823	823 G	A	23.28	57.66
CYP71E1	856	856 T	C	22.66	60
CYP71E1	877	877 A	G	24.99	60
CYP71E1	893	893 A	G	23.52	60
CYP71E1	899	899 G	A	21.54	60
CYP71E1	934	934 T	A	6.52	60
CYP71E1	1149	1149 C	G	12.84	60
CYP71E1	1156	1156 C	A	18.17	60
CYP71E1	1174	1174 C	T	20.01	60
CYP71E1	1204	1204 C	A	18.26	59.61
CYP71E1	1235	1235 G	A	19.61	59.61
CYP71E1	1272	1272 G	C	29.79	58.98
CYP71E1	1283	1283 A	G	26.5	58.98
CYP71E1	1328	1328 A	G	24.33	58.1
CYP71E1	1334	1334 A	T	24.57	57.77
CYP71E1	1353	1353 A	C	24.33	58.1
CYP71E1	1355	1355 A	C	21.06	58.1
CYP71E1	1471	1471 G	C	18.31	58.93
CYP71E1	1485	1485 C	G	22.66	58.93
CYP71E1	1498	1498 G	C	16.46	59.7
CYP71E1	1548	1548 T	G	16.1	60
CYP71E1	1570	1570 C	G	8.08	60
CYP71E1	1571	1571 A	T	8.08	60
CYP71E1	1603	1603 T	A	8.72	59.71
CYP71E1	1673	1673 C	T	9.37	59.57
CYP71E1	1721	1721 A	C	14.86	57.31
CYP71E1	1730	1730 A	C	22.18	56.99
CYP71E1	1763	1763 C	T	8.66	57.78
CYP72A31	539	539 A	C	24.36	55.97
CYP72A31	704	704 A	C	21.73	57.48
CYP72A31	1419	1419 G	A	25.62	60
CYP72A31	1452	1452 C	T	28.78	60
CYP72A31	1499	1499 A	G	12.07	60
CYP72A31	1513	1513 A	C	12.42	60
CYP72A31	1559	1559 A	G	13.47	60
DHPS	620	620 G	A	9.66	59.38
DHPS	663	663 A	T	17.48	60
DHPS	764	764 G	A	23.52	60.28
DHPS	765	765 C	A	22.91	60.28
DHPS	768	768 C	G	22.25	60.27
DHPS	809	809 C	T	21.36	60.23
DHPS	977	977 A	G	27.73	59.58

DHPS	983	983 A	G	26.16	59.59
DHPS	992	992 C	T	26.66	59.39
DHPS	1002	1002 C	G	29.49	59.37
DHPS	1016	1016 A	G	27.43	59.46
DHPS	1025	1025 A	G	28.88	59.43
DHPS	1074	1074 C	A	25.44	59.49
DHPS	1091	1091 G	T	31.06	59.75
DHPS	1167	1167 G	A	25.92	60
DHPS	1181	1181 T	A	25.63	60
DHPS	1220	1220 G	A	22.56	60
DHPS	1224	1224 C	T	22.56	60
DHPS	1248	1248 G	A	18.68	60
DHPS	1274	1274 T	G	25.94	60
DHPS	1287	1287 T	G	20.41	60
DHPS	1308	1308 T	C	17.71	60
DHPS	1433	1433 A	C	8.42	60
DHPS	1449	1449 G	A	10.89	60
DHPS	1473	1473 C	T	16.94	60
DHPS	1487	1487 A	C	20.99	60
DHPS	1490	1490 T	G	22.33	60
DHPS	1514	1514 G	A	22.42	60
DHPS	1529	1529 A	C	24.01	60
DHPS	1535	1535 A	C	23.13	60
DHPS	1565	1565 A	T	25.03	60
DHPS	1568	1568 A	G	25.03	60
DHPS	1583	1583 A	G	26.17	60
DHPS	1590	1590 A	T	23.56	60
DHPS	1618	1618 T	G	24.1	60
DHPS	1664	1664 A	C	23.12	60
DHPS	1678	1678 T	A	16.12	59.89
DHPS	1701	1701 A	G	20.78	59.89
DHPS	1703	1703 A	G	21.63	59.89
DHPS	1706	1706 G	A	21.58	59.89
DHPS	1728	1728 T	C	22.32	58.45
DHPS	1734	1734 C	T	22.16	58.35
DHPS	1736	1736 A	G	22.93	58.35
DHPS	1737	1737 T	C	22.93	58.35
DHPS	1745	1745 G	A	24.05	57.83
DHPS	1749	1749 A	C	21.82	57.78
DHPS	1757	1757 A	T	21.15	57.1
DHPS	1791	1791 T	C	24.7	56.13
DHPS	1799	1799 A	G	24.48	56.02
DHPS	1812	1812 T	C	28.54	59.86
DHPS	1824	1824 C	A	15.77	59.85

DHPS	1830	1830 C	T	13.59	59.85
DHPS	1842	1842 T	G	14.13	59.85
DHPS	1846	1846 A	T	12.5	59.85
DHPS	1849	1849 G	C	11.8	59.83
DHPS	1850	1850 G	A	11.8	59.83
DHPS	1854	1854 C	A	11.17	59.84
DTX1	598	598 C	A	8.08	60
DTX1	607	607 T	C	8.66	60
DTX1	616	616 T	G	8.66	60
DTX1	2711	2711 T	C	17.08	60
DTX1	2736	2736 A	G	7.14	60
DTX1	2840	2840 C	G	14.95	60
DTX1	3052	3052 A	G	7.35	60
DTX1	3089	3089 G	A	19.67	60
DTX1	3122	3122 A	G	10.56	60
DTX1	3134	3134 G	A	12.69	60
DTX1	3140	3140 A	G	9.67	60
DTX1	3159	3159 C	T	10.68	60
DTX1	3718	3718 T	G	32.63	60
DTX1	3905	3905 A	G	8	60
DTX1	3931	3931 T	C	12.91	60
DTX1	3953	3953 C	G	12.98	60
DTX1	3967	3967 G	A	15.36	60
DTX1	4056	4056 A	G	17.58	60
DTX1	4094	4094 C	T	24.88	60
DTX1	4102	4102 A	G	23.71	60
DTX1	4335	4335 A	G	7.2	60
DTX1	4432	4432 G	C	9.3	59.96
DTX1	4603	4603 A	G	9.34	58.81
DTX1	4624	4624 G	A	6.43	59.58
DTX1	4639	4639 A	C	8.58	59.47
EPSPS	2854	2854 A	G	17.75	60
ESR1	218	218 T	G	12.84	59.85
ESR1	219	219 T	C	12.84	59.85
ESR1	432	432 A	T	19.4	60
ESR1	783	783 T	C	18.01	60
GDSL	3188	3188 A	C	8.39	60
GPOX	546	546 A	C	28.62	52.55
GPOX	558	558 C	G	30.83	54.13
GPOX	1821	1821 C	A	18.75	60
GPOX	1857	1857 G	T	30.14	60
GPOX	1889	1889 G	C	30.29	60
GPOX	2066	2066 C	G	28.9	60
GPOX	2067	2067 G	T	23.43	60

GPOX	2130	2130 G	A	21.43	60
GPOX	2370	2370 A	G	8.58	60
GPOX	2383	2383 A	G	11.84	60
GSH2	1304	1304 T	A	11.52	59.23
GSH2	1381	1381 G	T	8.33	59.59
GSH2	2064	2064 T	C	20.4	60
GSH2	2664	2664 G	T	10.85	60
GSH2	3747	3747 A	T	14.04	59.55
GSH2	3782	3782 T	A	28.87	60
GSH2	4109	4109 A	G	19.5	50.86
GSTF12	839	839 A	C	8.43	60
GSTF12	927	927 C	G	15.63	59.07
GSTF12	951	951 C	G	15.11	59.11
GSTF12	953	953 T	C	14.53	59.07
GSTF12	964	964 A	C	14.01	59.11
GSTF12	967	967 G	A	13.89	59.11
GSTF12	969	969 G	C	14.01	59.11
GSTF12	987	987 C	A,G	22.55	59.04
GSTF1	1298	1298 A	C	19.91	60
GSTF1	1998	1998 A	G	24.29	60
GSTF1	2076	2076 G	A	28.26	60
GSTF1	2240	2240 C	G	7.78	60
GSTF1	2256	2256 T	C	12.12	60
GSTF4	364	364 T	A	16.72	60
GSTF4	446	446 A	C	17.22	60
GSTF4	620	620 C	G	15.22	57.11
GSTF4	1417	1417 A	G	22	57.96
GSTF4	1434	1434 C	A	26.39	57.63
GSTF4	1443	1443 G	A	21.65	53.51
GSTF4	1497	1497 G	C	21.65	51.59
GSTF4	1509	1509 T	G	23.22	51.86
GSTF4	1512	1512 A	G	23.22	51.86
GSTF4	1521	1521 C	T	18.06	50.38
GSTF4	1522	1522 T	A	17.84	50.38
GSTF4	1606	1606 G	C	11.52	57.41
GSTF4	1607	1607 T	C,G	31.18	57.31
GSTF4	1667	1667 C	G	11.31	57.45
GSTF4	1715	1715 G	C	14.13	57.17
GSTF4	1795	1795 T	C	5.87	58.35
GSTU1	368	368 C	G	12.53	60
GSTU1	373	373 A	C	11.8	60
GSTU1	421	421 T	C	24.33	60
GSTU1	640	640 C	G	13.63	60
GSTU1	712	712 G	A	11.75	59.65

GSTU1	713	713 T	A	11.75	59.65
GSTU1	850	850 T	C	10.94	59.95
GSTU1	852	852 T	G	19.57	59.95
GSTU1	865	865 A	G	11.8	59.96
GSTU1	869	869 C	T	20.41	59.96
GSTU1	872	872 A	G	10.31	59.96
GSTU3	463	463 C	G	14.83	56.53
HM2	333	333 A	G	13.23	59.31
HM2	349	349 C	A	6.38	59.28
HM2	1423	1423 G	C	23.34	60
HM2	1427	1427 T	G	16.73	60
HM2	1428	1428 T	C	16.36	60
HM2	1431	1431 C	A	16.36	60
HM2	1436	1436 A	G	16.36	60
HM2	1437	1437 T	G	16.36	60
HM2	1446	1446 G	C	27.92	55.69
HM2	1458	1458 G	T	21.34	56.06
HM2	1464	1464 G	T	10.07	56.06
HM2	1466	1466 G	A	19.19	55.69
HM2	1572	1572 G	C	13.11	60
HM2	1583	1583 A	G	9.43	60
IGPD	448	448 G	A	6.67	60
IGPD	449	449 G	C	7.18	60
IGPD	1670	1670 A	C	19.75	60
IN2	705	705 T	G	8.57	60
IN2	914	914 G	C	13.14	60
IN2	1094	1094 A	G	10.38	60
IN2	1471	1471 C	T	22.58	60
IN2	1656	1656 G	A	7.89	60
IN2	1699	1699 A	G	14.81	60
IN2	1726	1726 A	T	19.49	60
LACS7	2043	2043 G	A	22	60
LACS7	2289	2289 G	C	9.25	59.02
LACS7	2292	2292 G	A	13.44	59.02
LACS7	2477	2477 G	C	12.8	60
LACS7	3499	3499 A	G	30	60
LACS7	4551	4551 A	G	11.33	58.16
LACS7	4924	4924 T	A	8.87	59
LACS7	4948	4948 T	G	28.17	58.98
LACS7	5631	5631 A	G	22.54	59.95
LACS7	8396	8396 G	C	31.51	59.94
LACS7	9104	9104 G	T	10.11	59.87
LACS7	9105	9105 T	G	10.1	59.87
LACS7	9472	9472 C	T	14.51	58.99

LACS7	9510	9510 A	G	20.55	60
LACS8	1935	1935 G	A	17.86	60
LACS8	2113	2113 C	T	9.4	60
LACS8	2944	2944 A	T	6.84	60
LACS8	2958	2958 C	A	8.61	60
LACS8	2979	2979 G	A	7.84	60
LACS8	3063	3063 A	G	5.14	59.57
LACS8	3710	3710 G	A	9	60
LACS8	4648	4648 C	A	8.19	60
LCY1	716	716 G	A	29.35	58.74
LCY1	779	779 C	G	7.87	60
LCY1	1217	1217 C	T	29.38	60
LCY1	1310	1310 G	T	24.17	60
LCY1	1313	1313 C	T	28.84	60
LCY1	1337	1337 C	T	25.1	60
LCY1	1343	1343 C	A	29.57	60
LFNR	1193	1193 G	A	16.89	60
MAT1	285	285 G	T	27.25	60
MAT1	301	301 G	A	32.67	60
MAT1	349	349 G	A	31.17	60
MAT1	4058	4058 C	G	30.32	60
MATE	890	890 A	G	12.36	60
MATE	903	903 T	G	9.98	60
MATE	1022	1022 G	A	13.85	60
MATE	1037	1037 G	C	9.67	60
MATE	1047	1047 C	T	14.95	60
MATE	1050	1050 T	C	10.72	60
MATE	2346	2346 T	G	15.92	60
MATE	4099	4099 G	A	9.15	62.32
MATE	4117	4117 T	C	23.06	61.38
MATE	5685	5685 A	G	7.36	60
MFP2	276	276 A	G	22.63	60
MFP2	1724	1724 C	T	16.43	60
MFP2	1927	1927 T	G	15.4	60
MFP2	1946	1946 G	A	13.96	60
MFP2	2107	2107 A	C	22.3	60
MFP2	2122	2122 G	A	20.96	60
MFP2	2258	2258 C	T	19.43	60
MFP2	2602	2602 A	C	14.22	60
MFP2	2889	2889 C	A	12.91	60
MFP2	2999	2999 G	A	13.03	60
MFP2	3189	3189 A	C	21.32	60
MFP2	3214	3214 A	G	21.05	60
MFP2	3601	3601 A	G	13.86	60

MFP2	3607	3607 T	A	13.71	60
MFP2	3847	3847 G	T	18.61	60
MFP2	3935	3935 G	A	11.98	60
MFP2	4075	4075 T	C	17.27	60
MFP2	4450	4450 G	A	10.99	60
MFP2	5484	5484 A	G	17.68	60
NIT4	1576	1576 T	A	13.03	60
NIT4	2559	2559 T	G	16.5	56.03
NIT4	2562	2562 G	T	17.01	55.91
NIT4	2587	2587 A	T	11.69	56.64
NIT4	2597	2597 A	G	10.7	57.04
NIT4	2604	2604 G	A	11.31	57.36
NIT4	2982	2982 G	C	7.24	60
NIT4	3238	3238 C	G	6.75	60
OEP64	2912	2912 T	C	15.73	60.25
OEP64	2950	2950 G	A	25.92	60.26
OEP64	3259	3259 C	A	7.56	60
OEP64	6629	6629 A	G	18.7	60
OEP64	6647	6647 G	A	13.68	60
OEP64	9041	9041 C	T	15.53	60
ONL1	435	435 A	C	13.97	60
ONL1	649	649 G	A	11.36	60
ONL1	1691	1691 T	G	11	60
ONL1	1743	1743 A	G	10.87	60
ONL1	1848	1848 C	G	33.91	60
ONL1	1892	1892 G	A	8.08	60
ONL1	2575	2575 T	C	11.31	60
PDS1	901	901 A	C	9.06	60
PDS1	949	949 G	C	17.63	60
PDS1	957	957 G	T	17.54	60
PDS1	976	976 T	A	14.99	60
PDS1	988	988 A	G	20	60
PDS1	991	991 G	A	20.27	60
PDS1	1011	1011 T	C	31.83	60
PDS1	1162	1162 G	A	19.99	60
PDS1	1186	1186 A	C	20.58	60
PDS1	1558	1558 G	A	18.9	60
PDS1	1587	1587 G	T	20.3	60
PDS1	2223	2223 T	C	17.48	60
PDS1	2229	2229 T	G	17.9	60
PDS1	2248	2248 G	C	17.79	59.7
PDS1	2257	2257 C	T	18.61	59.7
PDS1	2504	2504 C	A	15.93	60
PDS1	2567	2567 A	G	10.3	60

PDS1	3855	3855 G	T	17.38	60
PDS1	4349	4349 A	C	7.66	60
PDS1	4562	4562 T	C	9.62	60
PDS1	5300	5300 T	C	9.69	60
PDS1	5591	5591 C	T	14.42	60
PDS1	5627	5627 G	C	17.42	60
PDS1	5657	5657 C	T	18.47	60
PDS1	5698	5698 T	C	11.24	59.92
PDS1	5930	5930 T	C	18.44	60
PED1	1611	1611 A	G	25.03	60
PED1	3597	3597 G	A	6.75	60
PPO	68	68 T	G	33.43	60
PPO	97	97 A	C	28.02	60
PPO	4630	4630 A	G	24.19	60
SBP1	589	589 A	T	11.75	60
SBP1	591	591 A	G	11.75	60
SBP1	603	603 T	G	10.59	60
SBP1	814	814 T	G	8.5	60
SBP1	829	829 G	A	13.71	60
SBP1	838	838 G	C	13.9	60
SBP1	839	839 C	T	14.77	60
SBP1	905	905 A	G	8.78	60
SBP1	953	953 G	A	14.85	60
SBP1	1420	1420 C	G	9.64	58.76
SBP1	1672	1672 C	T	13.52	60
TIR1	3390	3390 T	G	6.88	60
TIR1	4507	4507 C	G	8.35	60
TRX	403	403 A	G	14.04	59.9
TRX	406	406 G	A	14.04	59.9
TRX	1604	1604 T	G	8.18	60
UGT73C6-like	334	334 C	G	13.66	60
UGT73C6-like	358	358 G	A	17.13	60
UGT73C6-like	364	364 T	C	17.98	60
UGT73C6-like	365	365 G	A	17.98	60
UGT73C6-like	454	454 A	G	18.68	60
UGT73C6-like	477	477 C	G	11.79	60
UGT73C6-like	517	517 A	C	15.73	60
UGT73C6-like	522	522 T	G	17.05	60
UGT73C6-like	564	564 G	C	13.96	60
UGT73C6-like	598	598 C	T	14.78	60
UGT73C6-like	616	616 A	G	20.09	60
UGT73C6-like	628	628 A	G	25.35	60
UGT73C6-like	636	636 T	A	26.32	60
UGT73C6-like	690	690 T	C	23.96	60

UGT73C6-like	720	720 A	T	5.22	60
UGT73C6-like	724	724 T	G	20.18	60
UGT73C6-like	725	725 G	C	20.18	60
UGT73C6-like	1352	1352 C	A	27.92	60.2
UGT73C6-like	1460	1460 C	A	10.61	60
UGT73C6-like	1466	1466 G	A	13.63	60
UGT73C6-like	1485	1485 T	C	11.79	60
UGT73C6-like	1498	1498 G	C	16.76	60
UGT73C6-like	1521	1521 A	G	16.3	60
UGT73C6-like	1728	1728 T	C	13.22	60
UGT73C6-like	1842	1842 G	A	16.53	60
UGT73C6-like	1895	1895 A	G	17.17	60
UGT73C6-like	2021	2021 T	A	12.29	60
UGT73C6-like	2122	2122 A	T	6.59	60
UGT73C6-like	2129	2129 C	T	12.59	60
UGT73C6-like	2145	2145 C	T	15.05	60
UGT73C6-like	2184	2184 A	G	15.11	60
UGT73C6-like	2196	2196 C	A,T	21.35	60
UGT73C6-like	2224	2224 G	C	11.96	60
UGT73C6-like	2440	2440 T	C	15.47	59.91
UGT73C6-like	2441	2441 G	A	15.7	59.91
UGT73C6-like	2447	2447 C	A	16.28	59.91
GPOX	540	540 C	CCGG	34.46	49.83
DTX1	3870	3870 A	C,AC	29.14	58.72
PED1	2336	2336 G	T	5.91	60
LACS8	7382	7494 TTGGTAATCT	T	9.31	60
HM2	625	646 TCGCCACGCCT		7.05	60
ABCC1	2667	2667 T	C	16.26	59.98
DTX1	4112	4112 G	T	15.74	60
LACS7	7314	7314 A	G	29.36	60
PDS1	3633	3633 T	G	18.47	60
LACS8	3769	3777 GGTGATAAT	G	13.52	60
MFP2	1761	1765 GTATA	G	20.34	60
IN2	2327	2327 T	TATA	23.2	59.56
IN2	2328	2328 G	A	19.45	59.56
LACS8	7551	7553 CTT	C	24.49	60
ABCC1	2401	2406 CTTTTT	C	7.83	59.31
ABCC1	2672	2672 G	GTT	16.46	59.98
ABCC1	9565	9565 A	G	26	60.3
ABCC1	11252	11252 C	T	9.94	60
ACC1	3553	3553 G	GAT	11.65	60.26
AIM1	3777	3778 CA	C	8.57	60
AIM1	5384	5384 G	C	21.97	60
AIM1	5517	5517 C	T	9.05	60

ALF5	1984	1984 A	AAGCT	12.19	60
ALF5	1989	1989 C	T,CGCTTGAG	26.17	60
ALF5	2503	2503 G	GT	10.76	59.17
CESA1	165	165 A	C	9.71	59.77
CYP709B3	971	971 A	G	10.97	60
DTX1	3768	3768 C	T	32.74	60
DTX1	4119	4119 A	G	14.88	60
DTX1	4573	4573 T	C	21.78	57.71
EPSPS	2206	2206 C	T	20.96	60
EPSPS	3506	3506 T	TA	6.31	60
GDSL	1350	1354 ACGGT	A	26.26	60
GPOX	1021	1021 G	GT	6.38	60
GSH2	3721	3721 C	T	16.47	59.54
GSH2	3723	3723 T	A	16.39	59.53
GSTF12	567	567 T	C	15.15	60
GSTF1	1251	1251 T	C	22.58	60
GSTF4	630	631 AG	A	12.06	56.94
GSTU1	454	454 C	CTGAT	15.77	60
HM2	371	371 T	A	18.44	57.25
HM2	375	378 ACTC	A	18.21	56.72
IN2	1352	1352 G	A	14.83	60
IN2	1353	1353 C	A	15.97	60
IN2	1615	1615 C	A	13.38	60
IN2	1616	1616 C	T	6.31	60
LACS7	1883	1883 T	TACC	20.13	60
LACS7	2030	2030 T	C	15.17	59.82
LACS7	2510	2510 A	G	17.91	60
LACS7	2605	2605 C	A	32.28	60
LACS7	3383	3383 A	C	8.08	60
LACS7	4699	4699 C	T	9.45	59.59
LACS7	4785	4785 T	G	21.72	59.64
LACS7	7399	7399 A	C	27.28	60
LACS7	7499	7500 AG	A	15.28	60
LACS7	8362	8362 A	G	30.8	60
LACS7	8462	8462 T	A	24.59	57.07
LACS7	9017	9028 CTGTCCTTTC	C	14.7	59.35
LACS7	9433	9433 T	A	17.22	58.83
LACS7	9435	9435 C	T	8.65	58.77
LACS8	7487	7487 C	T	10.68	60
LFNR	1146	1148 CAT	C	24.84	59.42
MATE	6704	6704 A	C	8.76	60
MATE	6705	6705 A	C	8.76	60
MFP2	2131	2131 A	AT	16.21	60
MFP2	2209	2209 T	C	29.44	60

MFP2	2291	2291 C	T	26.55	60
MFP2	3235	3235 A	G	17.46	60
MFP2	3475	3475 T	G	10.31	60
MFP2	3579	3579 T	C	12.85	60
MFP2	4033	4033 T	TAA	10.98	60
MFP2	4038	4038 T	C	16.76	60
MFP2	4627	4627 A	C	21.43	60
NIT4	2969	2969 T	C	7.83	60.47
OEP64	5877	5879 ATG	A	11.63	59.28
OEP64	8622	8622 A	T	18.9	60
OEP64	9591	9591 A	G	16	60
PDS1	1034	1034 C	T	16.35	60
PDS1	1253	1253 T	C	20.67	60
PDS1	1361	1361 T	C	7.14	59.7
PDS1	2437	2439 AGG	A	32.83	60
PDS1	4581	4581 G	T	17.45	60
PDS1	5719	5719 C	A	21.14	59.69
PDS1	5866	5867 CT	C	29.41	57.9
PED1	1123	1124 GC	G	7.65	60
PED1	1223	1223 G	A	6.97	60
SBP1	1395	1395 G	A	7.25	60
TIR1	3757	3757 C	T	20.31	60
TIR1	4213	4213 T	C	8.76	60.36
TRX	984	984 G	C	11.3	60
TRX	1464	1464 A	C	13.33	60
AIM1	5510	5510 A	G	9.33	60
DHPS	841	841 G	A	20.15	60.32
GSH2	3160	3160 G	A	6.74	60
LACS7	2035	2035 G	A	5.58	60
LACS7	5651	5651 C	T	14.24	59.95
MFP2	1691	1691 T	C	13.37	60
PDS1	5715	5715 T	A	21.19	59.69
MFP2	265	265 T	C	10.21	60
ABCC1	2615	2615 C	T	8.13	59.97
ABCC1	11067	11067 G	T	14.29	60
ABCC1	11297	11297 G	T	9.52	60
CXE12	326	326 C	T	13.58	60
DTX1	4631	4631 T	G	25.1	59.49
GSH2	1330	1330 C	T	15.12	59.87
PDS1	1586	1586 G	A	20.3	60
PDS1	5381	5381 C	T	28.99	60
UGT73C6-like	2396	2396 C	G	9.41	60
AML1	333	333 A	AAGGTGCGC	25.41	60
ESR1	2707	2707 T	A	8.76	60

PDS1	5393	5393 T	C	17.56	60
LACS7	9535	9535 A	G	21.23	60
PDS1	5328	5328 A	G	10.84	60
LCY1	717	717 A	C	31.58	58.74
ABCC1	2596	2596 T	G	7.59	60
ABCC1	2629	2629 C	T	11.1	59.97
ABCC1	5990	5990 C	A	30.87	1.022
ABCC1	6026	6026 T	A	10.58	60
ABCC1	8845	8845 G	A	20.56	60
ABCC1	8935	8935 T	C	21.27	60
ABCC1	11051	11051 T	A	7.57	60
ABCC1	11305	11305 G	A	17.23	60
ABCC1	11308	11308 G	A	11.31	60
ABCC1	11344	11344 G	A	17.21	60
ABCC1	11362	11362 G	A	10.57	59.88
ABCC1	11516	11516 T	C	9.76	60.39
ABCC4L	2275	2275 T	C	23.3	60
ABCC4L	2530	2530 G	A	24.66	60
ABCC4L	2593	2593 T	A	21.08	60
ABCC4L	2605	2605 A	G	9.13	60
ABCC4L	2985	2985 C	T	11.9	60
ABCC4L	3234	3234 G	A	23.06	60
ACC1	414	414 G	C	8.9	60
ACC1	774	774 A	G	10.92	60
ACC1	2081	2081 G	T	10.68	56.91
ACC1	2084	2084 A	T	11.45	57.01
ACC1	2087	2087 A	G	10.79	56.72
ACC1	2093	2093 G	T	11.17	56.62
ACC1	2108	2108 G	T	10.29	57.32
ACC1	2111	2111 C	A	10.61	57.24
ACC1	2142	2142 T	C	11.31	60
ACC1	4297	4297 G	A	9.48	60
ACC1	5042	5042 T	C	12.99	60
ACC1	6190	6190 G	A	14.08	59.6
ACC1	8957	8957 C	T	8.91	60
ACC1	9211	9211 C	T	19.53	60
ACC1	9232	9232 T	C	19.19	60
ACC1	10252	10252 T	A	6.46	60
ACC1	10576	10576 C	T	8.65	60
ACC1	10594	10594 G	C	8.91	60
AIM1	1250	1250 C	T	6.47	60
AIM1	1736	1736 T	C	23.04	60
AIM1	2898	2898 C	T	7.53	60
AIM1	4319	4319 C	T	9.68	60

AIM1	4806	4806 C	T	7.77	60
AIM1	5671	5671 C	T	10.74	60
AIM1	5686	5686 T	C	11.57	60
AIM1	5749	5749 T	C	12.33	60
AIM1	5905	5905 T	C	9.39	60
AIM1	6825	6825 G	C	6.72	60
ALF5	209	209 T	C	17.52	59.05
ALF5	224	224 G	A	17.83	59.21
ALF5	236	236 T	C	22.11	56.87
ALF5	344	344 G	A	26.64	60
ALF5	365	365 G	C	23.58	60
ALF5	374	374 C	G	25.13	60
ALF5	1399	1399 G	A	8.95	60
ALF5	1402	1402 G	A	10.06	60
ALF5	1636	1636 G	C	17.08	60
ALF5	1639	1639 A	C	22.02	60
ALF5	2219	2219 G	C	31.67	60
ALF5	2761	2761 A	G	6.89	60
ALS	1249	1249 C	T	17.32	60
ALS	1420	1420 A	G	20.8	60
ALS	2113	2113 T	C	9.21	60
AML1	346	346 A	G	28.85	60
AML1	400	400 A	G	30.04	60
AML1	496	496 G	C	21.97	59.09
AML1	598	598 G	C	24.12	60
AML1	712	712 G	C	19.85	60
AML1	886	886 C	G	10.85	60
AML1	1066	1066 T	C	11.27	58.87
AML1	1247	1247 C	T	16.22	60
AML1	1349	1349 G	T	19.62	60
AML1	1460	1460 C	G	10.27	60
AML1	1505	1505 A	G	13.23	60
CESA1	1591	1591 C	T	10.44	59.52
CESA1	1624	1624 A	G	12.98	58.68
CESA1	1631	1631 C	T	12.09	58.36
CESA1	1639	1639 A	G	13.04	58.24
CESA1	1645	1645 A	T	13.02	58.14
CESA1	1672	1672 T	C	10.02	57.91
CESA1	1678	1678 T	C	9.27	58.04
CESA1	1690	1690 A	C	8.71	57.95
CESA1	2261	2261 C	T	23.85	58.28
CESA1	2273	2273 T	A	23.41	58.36
CESA1	2282	2282 T	C	23.59	58.45
CESA1	2283	2283 C	A	23.24	58.47

CESA1	2306	2306 G	A	23.32	58.42
CESA1	2309	2309 C	T	23.32	58.42
CESA1	2324	2324 A	G	18.18	59.36
CESA1	2336	2336 C	T	17.11	59.54
CESA1	2354	2354 G	C	22.45	59.61
CESA1	2363	2363 T	C	23.07	59.58
CESA1	2366	2366 T	G	21.44	59.56
CESA1	2375	2375 A	G	19.92	59.57
CESA1	2381	2381 C	G	19.94	59.55
CESA1	2382	2382 T	C	21.78	59.55
CESA1	2384	2384 A	G	19.5	59.58
CESA1	2390	2390 T	G	20.33	59.59
CESA1	2396	2396 A	T	22.57	59.57
CESA1	2402	2402 C	T	19.01	59.57
CESA1	2405	2405 C	T	19.01	59.57
CESA1	2408	2408 A	C	18.92	59.55
CESA1	2423	2423 A	C	17.59	59.67
CESA1	2426	2426 A	G	18.01	59.67
CESA1	2435	2435 C	T	18.85	59.62
CESA1	2447	2447 T	C	19.41	59.62
CESA1	2450	2450 T	C	19.86	59.62
CESA1	2480	2480 A	C	19.28	59.83
CESA1	2486	2486 T	G	18.93	59.83
CESA1	2489	2489 G	C	19.5	59.83
CESA1	2495	2495 C	T	20.64	59.82
CESA1	2507	2507 G	T	22.56	59.81
CESA1	2513	2513 G	C	22.01	59.67
CESA1	2516	2516 C	T	22.12	59.67
CESA1	2525	2525 T	C	22.88	59.66
CESA1	2528	2528 T	A	22.77	59.66
CESA1	2537	2537 T	A	24.73	59.58
CESA1	2543	2543 A	T	20.3	59.47
CESA1	2552	2552 T	C	17.43	59.45
CESA1	2555	2555 C	T	17.29	59.45
CESA1	2561	2561 T	C	17.22	59.39
CESA1	2573	2573 A	C	11.38	59.72
CESA1	2603	2603 T	C	8.44	59.73
CESA1	2606	2606 A	G	8.94	59.72
CXE12	337	337 C	G	14.85	60
CXE12	367	367 C	T	11.3	60
CXE12	1240	1240 T	C	16.67	60
CYP709B3	176	176 G	A	11.81	60
CYP709B3	690	690 A	C	21.78	60
CYP709B3	734	734 T	C	17.16	60

CYP709B3	780	780 C	T	11.87	60
CYP709B3	1515	1515 T	C	16.8	59.11
CYP709B3	1524	1524 A	C	18.12	59.05
CYP709B3	1563	1563 G	C	16.87	60
CYP709B3	1690	1690 C	T	11.17	60
CYP71E1	324	324 C	G	8.08	60
CYP71E1	330	330 A	G	21.04	60
CYP71E1	345	345 G	C	15.82	60
CYP71E1	369	369 G	A	8.46	60
CYP71E1	393	393 G	T	13.02	59.04
CYP71E1	447	447 G	T	15.67	60
CYP71E1	492	492 G	C	15.27	60
CYP71E1	501	501 G	C	15.55	60
CYP71E1	504	504 A	G	13.46	60
CYP71E1	522	522 C	G	12.48	60
CYP71E1	525	525 G	C	11.86	60
CYP71E1	540	540 T	G	12.71	60
CYP71E1	549	549 G	C	11.61	60
CYP71E1	594	594 C	G	15.42	60
CYP71E1	603	603 C	G	16.65	60
CYP71E1	609	609 T	C	20.55	60
CYP71E1	639	639 G	C	25.36	60
CYP71E1	651	651 T	C	24.47	60
CYP71E1	723	723 C	T	10.18	60
CYP71E1	726	726 G	T	9.67	60
CYP71E1	753	753 C	T	8.78	58.58
CYP71E1	765	765 C	T	10.84	58.3
CYP71E1	777	777 C	T	11.78	58.17
CYP71E1	780	780 C	A	11.78	58.17
CYP71E1	792	792 A	G	12.84	58.03
CYP71E1	825	825 C	G	21.65	57.86
CYP71E1	846	846 A	C	21.64	60
CYP71E1	855	855 G	C	22.66	60
CYP71E1	861	861 G	C	22.34	60
CYP71E1	885	885 C	T	25.89	60
CYP71E1	951	951 A	C	9.8	60
CYP71E1	999	999 G	A	12.36	60
CYP71E1	1146	1146 G	T	10.59	60
CYP71E1	1206	1206 C	G	34.46	59.59
CYP71E1	1233	1233 C	G	19.61	59.61
CYP71E1	1239	1239 G	C	16.96	59.61
CYP71E1	1242	1242 C	G	17.61	59.53
CYP71E1	1257	1257 C	G	28.09	59.06
CYP71E1	1312	1312 C	A	21.52	59.22

CYP71E1	1320	1320 C	G	24.33	58.1
CYP71E1	1344	1344 C	G	22.31	58.44
CYP71E1	1380	1380 G	A	13.46	59.31
CYP71E1	1449	1449 G	A	21.95	58.76
CYP71E1	1542	1542 A	G	13.33	60
CYP71E1	1557	1557 T	C	12.63	60
CYP71E1	1611	1611 C	G	7.78	59.74
CYP71E1	1680	1680 C	T	10.13	59.58
CYP71E1	1683	1683 G	C	16.81	58.93
CYP71E1	1743	1743 C	G	21.76	56.25
CYP72A31	522	522 G	C	23.68	60
CYP72A31	531	531 T	G	22.88	57.05
CYP72A31	552	552 C	G	34.93	60
CYP72A31	576	576 G	C	20.01	54.95
CYP72A31	579	579 C	T	20.01	54.95
CYP72A31	714	714 T	G	10.56	57.95
CYP72A31	1465	1465 A	G	10.73	60
CYP72A31	1612	1612 T	C	15.55	59.77
CYP72A31	1742	1742 T	C	31.75	60
CYP72A31	1978	1978 T	A	14.08	60
CYP72A31	2149	2149 T	G	10.44	60
CYP72A31	2155	2155 A	C	10.66	60
DHPS	607	607 C	T	9.04	59.36
DHPS	610	610 G	T	9.99	59.36
DHPS	628	628 T	C	12.91	59.28
DHPS	631	631 G	A	12.45	59.31
DHPS	640	640 G	C	11.96	60
DHPS	643	643 A	G	12.5	60
DHPS	646	646 G	A	13.02	60
DHPS	655	655 G	T	15.55	60
DHPS	661	661 G	A	16.76	60
DHPS	691	691 G	C	7.99	60
DHPS	718	718 T	G	17.76	60.4
DHPS	724	724 A	T	17.76	60.4
DHPS	727	727 T	C	18.62	60.39
DHPS	745	745 G	T	20.07	60.36
DHPS	751	751 C	T	22.03	60.35
DHPS	754	754 T	C	20.14	60.3
DHPS	757	757 T	C	20.14	60.3
DHPS	769	769 C	T	22.25	60.27
DHPS	778	778 G	A	21.6	60.25
DHPS	787	787 T	A	23.15	60.25
DHPS	793	793 A	G	23.06	60.25
DHPS	811	811 T	A	20.46	60.23

DHPS	976	976 C	T	26.94	59.59
DHPS	982	982 A	G	26.92	59.58
DHPS	989	989 C	T	26.22	59.37
DHPS	994	994 T	G	27.36	59.37
DHPS	1003	1003 T	C	27.64	59.39
DHPS	1009	1009 A	G	29.44	59.42
DHPS	1012	1012 G	C	29.53	59.45
DHPS	1015	1015 C	T	28.07	59.45
DHPS	1024	1024 C	G	29.59	59.42
DHPS	1030	1030 C	T	27.06	59.4
DHPS	1036	1036 C	G	29.73	59.4
DHPS	1048	1048 C	T	18.98	59.4
DHPS	1063	1063 A	T	25.22	59.46
DHPS	1072	1072 G	A	31.17	59.46
DHPS	1087	1087 C	T	24.69	59.76
DHPS	1099	1099 C	T	27.76	59.75
DHPS	1103	1103 C	T	27.88	59.75
DHPS	1106	1106 C	T	30.4	59.75
DHPS	1117	1117 G	A	27.96	59.89
DHPS	1126	1126 C	T	27.07	59.9
DHPS	1129	1129 A	C	27.82	59.89
DHPS	1138	1138 C	T	27.68	59.89
DHPS	1171	1171 G	A	25.92	60
DHPS	1183	1183 T	C	23.33	60
DHPS	1186	1186 A	G	23.33	60
DHPS	1222	1222 C	T	21.81	60
DHPS	1246	1246 A	C	18.55	60
DHPS	1252	1252 G	A	19.48	60
DHPS	1261	1261 A	G	18.83	60
DHPS	1282	1282 C	T	21.23	60
DHPS	1330	1330 T	C	18.36	60
DHPS	1342	1342 T	C	15.7	60
DHPS	1345	1345 C	T	16.24	60
DHPS	1360	1360 A	G	16.24	60
DHPS	1378	1378 T	A	18.91	60
DHPS	1429	1429 T	C	8.42	60
DHPS	1435	1435 G	A	8.7	60
DHPS	1450	1450 C	T	11.38	60
DHPS	1453	1453 C	T	13.02	60
DHPS	1474	1474 T	G	16.36	60
DHPS	1483	1483 T	C	18.07	60
DHPS	1505	1505 C	T	20.63	60
DHPS	1520	1520 C	T	21.85	60
DHPS	1552	1552 T	G	26.49	60

DHPS	1567	1567 C	T	25.03	60
DHPS	1594	1594 C	A	24.78	60
DHPS	1666	1666 C	T	23.12	60
DHPS	1699	1699 C	T	20.78	59.89
DHPS	1795	1795 G	A	24.48	56.02
DHPS	1804	1804 A	G	22.52	56.13
DHPS	1825	1825 A	T	16.21	59.84
DHPS	1834	1834 A	T	13.59	59.85
DHPS	1840	1840 T	A	13.48	59.85
DHPS	1843	1843 T	A	21.65	59.85
DTX1	2665	2665 A	G	4.75	60
DTX1	2689	2689 C	G	14.22	59.91
DTX1	2707	2707 A	G	16.95	59.9
DTX1	2743	2743 G	A	13.91	60
DTX1	2776	2776 C	G	9.79	60
DTX1	2782	2782 C	T	8.74	60
DTX1	2821	2821 G	C	11.03	60
DTX1	2839	2839 G	C	14.95	60
DTX1	2842	2842 A	G	10.75	60
DTX1	2998	2998 C	G	8.28	60
DTX1	3118	3118 G	C	14.02	60
DTX1	3124	3124 A	G	10.62	60
DTX1	3358	3358 A	G	14.8	59.97
DTX1	3723	3723 G	A	30.97	60
DTX1	3726	3726 G	A	30.97	60
DTX1	3909	3909 T	C	16.55	60
DTX1	3924	3924 C	A	13.36	60
DTX1	3927	3927 A	G	12.91	60
DTX1	3951	3951 A	G	14.41	60
DTX1	3969	3969 C	A	15.47	60
DTX1	4086	4086 C	T	15.36	60
DTX1	4107	4107 C	T	15.33	60
DTX1	4321	4321 T	C	17.38	60
DTX1	4420	4420 G	C	8.33	60
EPSPS	2073	2073 C	A	12.19	60
EPSPS	2136	2136 C	T	6.02	60
EPSPS	3700	3700 T	C	13.72	60
ESR1	668	668 T	C	6.87	60
ESR1	2628	2628 G	T	14.71	60
ESR1	2667	2667 C	T	8.69	60
GDSL	3199	3199 C	G	8.02	60
GPOX	670	670 C	T	10.11	59.94
GPOX	1912	1912 T	C	31.83	60
GPOX	2108	2108 G	C	15.22	59.91

GPOX	2123	2123 G	C	14.2	60
GPOX	2129	2129 A	C	22.01	60
GSH2	737	737 G	A	10.76	60
GSH2	1305	1305 G	A	11.57	59.23
GSH2	1329	1329 T	A	13.96	59.87
GSH2	3599	3599 G	A	33.84	59.94
GSH2	3624	3624 T	C	28.1	59.93
GSH2	3644	3644 C	T	27.72	59.88
GSH2	3741	3741 T	C	10.25	59.55
GSH2	3858	3858 G	A	16.05	60
GSH2	4060	4060 A	C	7.45	60
GSH2	4090	4090 C	A	17.34	52.79
GSH2	4093	4093 C	G	18.44	51.48
GSH2	4105	4105 T	A	20.32	50.86
GSH2	4114	4114 G	A	19.01	51.08
GSH2	4123	4123 T	A	19.43	50.86
GSL1-1	1575	1575 T	G	16.38	60
GSL1-1	2717	2717 A	G	6.82	58.28
GSL1-1	2945	2945 C	G	9.49	60
GSL1-1	2948	2948 G	C	8.81	60
GSTF12	799	799 T	C	11.04	59.8
GSTF12	957	957 C	G	15.55	59.11
GSTF12	975	975 C	G	13.48	59.04
GSTF12	1005	1005 C	G	14.82	58.96
GSTF12	1014	1014 G	C	15.96	59
GSTF12	1017	1017 A	C	16.76	58.96
GSTF1	2089	2089 T	C	27.26	60
GSTF1	2125	2125 T	C	14.9	60
GSTF1	2233	2233 C	G	10.27	60
GSTF3	1029	1029 G	C	26.12	60
GSTF4	396	396 G	C	10.27	60
GSTF4	619	619 G	C	15.29	57.11
GSTF4	1433	1433 A	C	24.84	57.71
GSTF4	1439	1439 G	A	26.8	56.53
GSTF4	1445	1445 G	A	27.44	54.89
GSTF4	1454	1454 G	A	24.02	51.02
GSTF4	1470	1470 C	T	26.8	49.73
GSTF4	1487	1487 C	T	21.65	51.59
GSTF4	1499	1499 A	G	25.16	51.59
GSTF4	1526	1526 C	T	17.02	51.08
GSTF4	1532	1532 A	G	16.15	52.42
GSTF4	1544	1544 C	G	15.65	51.51
GSTF4	1583	1583 G	C	14.58	56.6
GSTF4	1598	1598 A	G	26.25	56.76

GSTF4	1610	1610 G	A	13.74	56.67
GSTF4	1619	1619 T	C	29.37	56.85
GSTF4	1628	1628 C	T	12.74	57.02
GSTF4	1631	1631 T	C	26.58	56.85
GSTF4	1637	1637 T	C	12.68	56.94
GSTF4	1643	1643 C	T	10.23	57.77
GSTF4	1685	1685 T	C	24.28	56.79
GSTF4	1688	1688 C	A	9.41	56.69
GSTF4	1706	1706 C	T	17.4	57.37
GSTF4	1713	1713 T	C	13.59	57.27
GSTF4	1745	1745 T	C	12.33	57.42
GSTF6	834	834 C	T	20.81	60
GSTF6	969	969 A	T	15.42	60
GSTU1	216	216 T	C	29.33	60.9
GSTU1	225	225 C	G	24.02	58.59
GSTU1	435	435 G	C	18.44	60
GSTU1	441	441 T	C	18.44	60
GSTU1	708	708 T	C	11.75	59.65
GSTU1	759	759 T	C	15.31	60
GSTU1	768	768 T	C	13.11	60
GSTU1	771	771 G	A	14.57	60
GSTU1	837	837 G	A	7.74	59.93
GSTU1	849	849 A	G	20.55	59.95
GSTU1	897	897 A	C	12.49	60
GSTU3	397	397 G	C,T	22.32	58.58
GSTU3	448	448 T	C	12.85	58.62
GSTU3	478	478 A	C	9.79	56.23
GSTU3	502	502 C	G	28.95	55.95
GSTU3	565	565 A	G	10.83	60
HM2	280	280 G	C	7.09	60
HM2	596	596 C	A	8.81	60
HM2	1384	1384 G	A	20.38	60
HM2	1411	1411 G	C	24.04	60
HM2	1420	1420 G	C	20.01	60
HM2	1507	1507 A	G	13.86	60
HM2	1546	1546 C	T	15.58	60
HPPD	597	597 C	G	33.67	60
IGPD	1672	1672 G	A	19.29	60
IGPD	3363	3363 A	T	23.82	60
IGPD	3666	3666 T	C	13.32	60
IN2	747	747 G	A	5.1	60
IN2	1339	1339 T	C	9.84	60
IN2	1503	1503 C	G	29.25	60
IN2	1784	1784 A	G	24.2	60

LACS7	1908	1908 C	T	23.48	60
LACS7	1917	1917 T	A,G	21.59	60
LACS7	1932	1932 T	C	29.14	59.91
LACS7	2047	2047 A	T	11.78	60
LACS7	2057	2057 T	C	21.38	60
LACS7	2071	2071 C	T	26.61	60
LACS7	2083	2083 C	T	20.81	60
LACS7	2092	2092 G	A	19.89	60
LACS7	2266	2266 C	T	12.65	59.04
LACS7	2275	2275 A	G	21.53	59.08
LACS7	2302	2302 A	G	10.42	59.13
LACS7	2329	2329 T	C	16.32	60
LACS7	2442	2442 A	C	13.43	60
LACS7	2451	2451 C	T	14.53	60
LACS7	2454	2454 G	C	13.67	60
LACS7	2463	2463 T	A	13.61	60
LACS7	2615	2615 A	T	7.67	60
LACS7	2690	2690 A	G	5.84	60
LACS7	2814	2814 A	T	12.03	59.9
LACS7	2850	2850 T	G	20.7	60
LACS7	3487	3487 T	C	22.54	60
LACS7	3520	3520 T	C	19.27	60
LACS7	4532	4532 C	T	28.24	58.01
LACS7	4541	4541 A	G	10.13	57.91
LACS7	4562	4562 T	C	20.13	57.99
LACS7	4580	4580 A	T	25.39	57.79
LACS7	4583	4583 T	G	8.71	57.65
LACS7	4589	4589 A	G	27.34	57.69
LACS7	4777	4777 T	C	28.2	59.66
LACS7	4929	4929 A	G	31.75	59.02
LACS7	4951	4951 T	C	19.7	58.95
LACS7	4956	4956 T	C	32.2	59.55
LACS7	4968	4968 T	C	32.74	59.57
LACS7	6379	6379 G	A	21.73	59.89
LACS7	6548	6548 T	C	26.18	60
LACS7	6584	6584 A	G	13.5	60
LACS7	6635	6635 T	G	10.16	60
LACS7	7227	7227 A	T,C	24.63	59.53
LACS7	7296	7296 T	C	21.07	59.59
LACS7	7308	7308 T	C	29.05	59.58
LACS7	7421	7421 T	C	21.36	60
LACS7	8192	8192 A	G	11.92	60
LACS7	8195	8195 T	C	11.92	60
LACS7	8198	8198 C	T	12.34	60

LACS7	8204	8204 G	A	11.31	60
LACS7	8448	8448 A	G	22.49	57.9
LACS7	9086	9086 T	C	24.41	59.41
LACS7	9268	9268 T	G	21.24	60
LACS7	9304	9304 G	A	27.54	59.66
LACS7	9464	9464 G	A	22.19	58.89
LACS7	9470	9470 C	T	20.95	58.94
LACS7	9482	9482 T	C	14.04	60
LACS7	9512	9512 A	G	12.67	60
LACS8	2234	2234 C	T	12.84	60
LACS8	5366	5366 T	A	8.8	60
LACS8	5393	5393 T	C	8.18	60
LCY1	300	300 C	T	10.53	60
LCY1	705	705 C	T	27.36	58.74
LCY1	804	804 T	C	23.58	60
LFNR	806	806 G	C	13.58	59.17
LFNR	809	809 C	G	13.58	59.17
LFNR	839	839 G	C	7.51	60
LFNR	2538	2538 G	C	10.7	60
MAT1	278	278 G	T	28.71	60
MAT1	4049	4049 G	C	37.35	60
MAT1	4062	4062 A	C	29.74	60
MATE	994	994 C	T	5.47	60
MFP2	1909	1909 G	A	14.69	60
MFP2	2106	2106 T	C	22.81	60
MFP2	2221	2221 A	G	20.7	60
MFP2	2402	2402 T	A	26.68	60
MFP2	2411	2411 A	G	26.12	60
MFP2	2833	2833 G	A	10.96	60
MFP2	2845	2845 T	C	17.89	60
MFP2	2854	2854 G	A	16.78	60
MFP2	2956	2956 G	A	12.6	60
MFP2	3224	3224 G	A	18.35	60
MFP2	3408	3408 T	C	15.76	60
MFP2	3417	3417 T	G	15.57	60
MFP2	3441	3441 G	A	13.53	60
MFP2	3447	3447 A	G	14.36	60
MFP2	3614	3614 T	G	13.96	60
MFP2	3626	3626 A	G	12.42	60
MFP2	3653	3653 C	T	12.94	60
MFP2	3849	3849 G	T	18	60
MFP2	4047	4047 A	G	17.3	60
MFP2	4059	4059 A	T	18.33	60
MFP2	4491	4491 A	G	14.82	60

MFP2	4536	4536 G	A	22.13	59.84
MFP2	4642	4642 T	C	19.01	60
MFP2	4648	4648 G	A	19.43	60
MFP2	5429	5429 C	T	20.02	60
MFP2	5430	5430 A	C	20.74	60
MFP2	5498	5498 T	G	28.1	60
NIT4	1680	1680 T	C	19.28	60
NIT4	2570	2570 T	C	11.91	56.16
NIT4	2579	2579 T	C	12.74	56.37
NIT4	2588	2588 C	T	21.8	56.64
NIT4	2609	2609 G	A	11.28	57.36
NIT4	2618	2618 A	C	10.12	58.15
NIT4	2627	2627 T	C	8.45	59.17
NIT4	2729	2729 C	T	6.96	60
NIT4	3002	3002 A	G	5.3	60
NIT4	3038	3038 G	A	10.31	60
NIT4	3065	3065 T	C	10.58	60
OEP64	5245	5245 T	G	21.05	60
OEP64	5254	5254 A	G	17.51	60
OEP64	5284	5284 C	G	20.84	60
OEP64	5476	5476 A	G	22.3	60
OEP64	5806	5806 G	A	7.58	59.22
OEP64	8578	8578 A	G	19.82	60
OEP64	9789	9789 A	G	5.3	60
ONL1	641	641 C	A	11.27	60
ONL1	1507	1507 C	T	18.1	60
ONL1	1906	1906 T	C	18.81	60
ONL1	2041	2041 G	T	19.76	60
PDS1	944	944 A	G	15.77	60
PDS1	1164	1164 C	T	31.58	60
PDS1	1379	1379 T	C	19.36	59.68
PDS1	1450	1450 A	C,T	16.59	60
PDS1	1581	1581 A	G	20.8	60
PDS1	2141	2141 C	T	19.66	60
PDS1	2150	2150 G	A	20.75	60
PDS1	2183	2183 A	C	16.87	60
PDS1	2192	2192 C	T	16.73	60
PDS1	2252	2252 A	C	18.22	59.7
PDS1	2452	2452 T	C	16.14	60
PDS1	2503	2503 A	G	15.93	60
PDS1	2521	2521 A	G	16.13	60
PDS1	2527	2527 T	G	14.79	60
PDS1	2587	2587 A	G	23.87	60
PDS1	3533	3533 C	T	24.53	60

PDS1	3536	3536 C	T	24	60
PDS1	3545	3545 T	C	21.33	60
PDS1	3560	3560 A	G	17.78	60
PDS1	3593	3593 T	C	16.33	60
PDS1	3620	3620 T	C	19	60
PDS1	3621	3621 A	C	16.13	60
PDS1	3869	3869 G	A	17.29	60
PDS1	3930	3930 C	T	21.9	60
PDS1	3947	3947 A	G	23.53	60
PDS1	3992	3992 C	T	20.3	60
PDS1	4157	4157 A	T	22.76	60
PDS1	4163	4163 T	C	8.61	60
PDS1	5377	5377 T	C	19.2	60
PDS1	5595	5595 T	C	20.98	60
PDS1	5610	5610 G	C	18.8	60
PDS1	5923	5923 G	A	18.54	60
PED1	1379	1379 T	C	14.78	60
PED1	1577	1577 A	G	25.56	60
PPO	36	36 G	C	29.5	60
PPO	90	90 A	C	26.69	60
PPO	2085	2085 G	C	10	60
PPO	5472	5472 C	T	11.19	60
SBP1	225	225 C	T	15.17	60
SBP1	595	595 T	C	11.75	60
SBP1	600	600 C	T	10.38	60
SBP1	627	627 G	A	8.3	60
SBP1	765	765 T	C	10.79	60
SBP1	906	906 A	G	8.78	60
SBP1	975	975 T	A	6.45	60
SBP1	1421	1421 C	T	16.38	58.76
SBP1	1679	1679 C	T	15.7	60
SBP1	1691	1691 G	A	6.03	60
TIR1	180	180 T	C	33.42	60
TIR1	3417	3417 T	C	20.74	60
TIR1	3561	3561 A	G	25.38	60
TIR1	3723	3723 C	T	19.38	60
TRX	1566	1566 C	T	13.72	60
UGT73C6-like	356	356 C	T	18.44	60
UGT73C6-like	437	437 A	C,T	13.95	60
UGT73C6-like	476	476 A	G	5.98	60
UGT73C6-like	515	515 A	G	12.98	60
UGT73C6-like	521	521 G	A	17.9	60
UGT73C6-like	539	539 G	A	19.21	60
UGT73C6-like	578	578 G	A	18.53	60

UGT73C6-like	599	599 C	T	20.61	60
UGT73C6-like	650	650 A	T	24.33	60
UGT73C6-like	662	662 G	A	20.44	60
UGT73C6-like	683	683 C	T	26.08	60
UGT73C6-like	692	692 T	C	23.96	60
UGT73C6-like	773	773 G	C	13.53	60
UGT73C6-like	788	788 T	C	9.86	60
UGT73C6-like	1507	1507 G	A	17.33	60
UGT73C6-like	1753	1753 C	A	13.55	60
UGT73C6-like	1793	1793 T	C	18.59	60
UGT73C6-like	1810	1810 G	A	14.7	60
UGT73C6-like	1870	1870 G	A	24.77	60
UGT73C6-like	1873	1873 T	C	24.56	60
UGT73C6-like	1879	1879 C	T	22.45	60
UGT73C6-like	2002	2002 T	C	14.67	60
UGT73C6-like	2053	2053 T	C	12.71	60
UGT73C6-like	2095	2095 A	G	12.26	60
UGT73C6-like	2155	2155 A	G	6.11	60
UGT73C6-like	2173	2173 T	A	16.22	60
UGT73C6-like	2179	2179 G	T	15.78	60
UGT73C6-like	2206	2206 T	A	17.87	60
GSTF3	176	216 ACTTGTGCGA	A	13.19	60
ABCC1	96	96 G	A	5.61	60
ABCC1	164	164 T	G	10.27	60
ABCC4L	48	48 T	A	8.48	60
ALF5	51	51 C	T	25.91	58.35
ALF5	53	57 AGGAG	A	26.83	58.35
ALF5	81	82 GA	G	25.28	58.63
ALF5	84	84 C	T	25.78	58.63
ALF5	92	92 G	A	26.66	58.46
ALF5	114	115 TA	T	20.47	60
ALF5	118	126 GTTCTATAC	G	19.05	60
ALF5	128	130 GAC	G	19.05	60
ALF5	161	161 A	ATCTGTCCAT	14.85	59.32
ALF5	165	165 G	C	15.67	59.27
ALF5	168	171 GCAA	G	17.26	59.27
ALF5	174	180 GCAATAA	G	14.85	59.27
CESA1	20	21 CT	C	13.77	60
CXE12	67	67 T	G	22.93	62.97
CXE12	69	69 C	G	11.55	62.97
CXE12	73	74 CT	C	9.84	62.73
CXE12	74	75 TG	T	15.16	62.73
CXE12	75	75 G	C	10.59	62.73
CYN	32	35 CGTT	C	18.84	59.67

CYN	52	55 GCTC	G	21.2	59.63
CYN	124	124 G	A	34.7	60
CYN	127	127 C	A	34.79	60
CYP72A31	28	28 C	T	28.2	60
CYP72A31	31	31 C	T	25	60
CYP72A31	34	34 A	AGG	29.82	60
CYP72A31	53	53 G	C	14.67	56.12
CYP72A31	54	54 T	A	29.29	56.12
CYP72A31	61	61 A	T	21.96	55.07
CYP72A31	87	88 CA	C	15.95	58.06
CYP72A31	88	88 A	G	11.59	58.06
CYP72A31	89	89 T	G	17.08	58.06
CYP72A31	93	96 TCCA	T	10.46	58.06
CYP72A31	95	95 C	T	17.08	58.06
CYP72A31	102	102 T	A	33.74	58.06
CYP72A31	121	121 T	TA	12.73	58.71
CYP72A31	137	137 C	T	21.44	59.09
CYP72A31	138	138 G	A	20.25	59.14
CYP72A31	199	199 C	CG	28.38	60
CYP72A31	213	213 A	G	24.83	60.42
CYP72A31	216	216 C	T	22.9	60.39
CYP72A31	288	288 C	G	8.2	60
CYP72A31	295	295 G	T	14	60
CYP72A31	319	319 G	C	11.71	60
CYP72A31	332	332 C	CTATGTTA	7.18	60
CYP72A31	333	333 C	CAAGTGTGTT	7.98	60
DTX1	74	74 C	T	31.8	59.87
DTX1	95	95 T	C	31.48	59.94
DTX1	130	130 T	C	28.74	59.95
DTX1	184	186 TCA	GCA,ACA,T	30.25	59.87
DTX1	213	213 C	T	13.91	59.82
DTX1	217	217 T	C	33.09	59.78
DTX1	221	225 TGCTC	TATAGCTC,T	28.06	59.68
DTX1	222	225 GCTC	G	19.88	59.64
DTX1	227	227 C	G,CAGAG,CA	29.08	59.56
DTX1	238	238 A	G	30.6	59.07
DTX1	242	242 T	A	24.22	58.83
DTX1	273	273 A	G	25.75	59.38
DTX1	281	281 G	A	29.26	59.73
DTX1	295	295 T	C	26.93	59.86
ESR1	16	22 CTAGGAG	C	21.02	60
ESR1	17	22 TAGGAG	T	7.89	60
ESR1	22	22 G	GTACC	7.89	60
ESR1	173	173 T	C	8.32	60

GDSL	28	28 T	G	34.25	60
GDSL	141	141 T	G	28.39	60
GDSL	144	144 A	G	30.06	60
GDSL	284	284 G	C	14.13	60
GDSL	294	294 A	G	15.46	60
GDSL	300	300 A	C	10.11	60
GPOX	29	29 A	G	10.05	60
GPOX	30	30 T	C	10.05	60
GPOX	74	74 A	G	8.6	60
GPOX	192	192 G	A	16.35	60
GSTF1	41	43 TAA	T	16.21	60
GSTF1	79	79 G	T	26.8	60
GSTF1	80	80 C	A	26.8	60
GSTF1	86	89 CGCG	C	10.17	60
GSTF1	89	89 G	GA	21.71	60
GSTF1	92	92 C	T	11.59	60
GSTF3	83	83 C	A	28.2	60
GSTF3	169	169 C	T	16.4	60
GSTF3	183	183 C	T	7.01	60
GSTF4	35	35 C	G	7.44	60
GSTF4	164	164 C	G	15.17	58.37
GSTF4	165	165 T	G	13.59	58.37
GSTF4	183	183 C	CA	7.94	56.02
GSTF4	210	210 G	GTCAA	19.11	54.48
GSTF4	214	214 T	TCC	20.17	54.16
GSTF4	223	223 T	TATAA	9.36	54.56
GSTF4	227	227 T	TC	15.95	54.86
GSTF4	241	241 T	C	10.07	56.97
GSTF4	266	266 T	C	10.08	58.1
GSTF4	283	283 T	C	9.79	58.49
GSTF4	295	295 A	ACATCCT	10.21	58.63
GSTF4	297	297 C	CATCGTCGG/	12.62	59.81
GSTF4	299	299 A	C	11.06	59.91
GSTF4	301	301 A	ATCTT	10.15	59.91
GSTF4	304	304 G	GC	10.06	59.91
GSTF4	305	305 G	GTAGATTAC	10.15	59.91
GSTF4	308	309 AG	A	9.71	59.91
GSTF4	311	312 GC	G	9.71	59.91
GSTF4	314	314 G	A	12.34	59.91
GSTF4	318	318 A	ACACTCGCT	12.05	60
GSTF4	322	322 C	CT	8.78	60
GSTF6	31	31 C	T	15.16	60
GSTF6	86	86 C	T	7.75	60
GSTF6	97	97 G	T	10.04	60

GSTF6	121	121 G	A	10.92	60
GSTF6	127	127 C	A	16.39	60
GSTF6	184	184 A	T	8.48	60
GSTF6	232	232 T	C	9.24	60
GSTF6	247	247 G	A	13.78	60
GSTF6	277	277 T	C	16.09	60
GSTF6	280	280 C	T	10.25	60
GSTF6	308	308 T	C	10.46	59.68
GSTF6	312	312 C	A	13.28	59.67
GSTF6	323	323 T	G	6.82	59.67
GSTU1	57	57 T	C	19.91	60
GSTU1	86	86 G	A	15.97	60
GSTU1	87	87 C	CAAA	16.55	60
GSTU1	94	94 T	C	16.24	60
GSTU3	26	26 T	C	19.31	60
GSTU3	152	152 T	G	7.2	60
HM2	66	66 A	C	24.8	60
HM2	187	187 G	GTC	24.56	60
HM2	188	188 C	T	9.38	60
IGPD	9	9 G	GA	4.53	58.67
IGPD	35	35 A	C	15.47	59.42
IGPD	36	36 C	T	5.37	59.42
IGPD	89	89 G	T	8.91	60
IGPD	110	110 T	C	9.42	60
IGPD	231	231 C	A	32.83	60
IGPD	233	233 C	T	31.47	60
IN2	84	84 G	A	27.08	60
IN2	138	138 T	A	15.74	60
IN2	197	197 T	TAAAACACC	28.74	60
IN2	202	202 C	G	32.2	60
IN2	206	206 A	ATCC	21.2	60
IN2	208	208 C	CTCGTATT	28.36	60
IN2	212	216 AAGGT	A	21.22	60
LCY1	80	81 GC	G	20.75	60
LCY1	135	136 CA	C	5.26	60
LFNR	208	208 A	C	12.13	60
LFNR	221	221 C	G	19.76	60
LFNR	227	227 G	C	17.83	60
LFNR	255	256 GT	G	20.89	60
LFNR	257	257 G	A	21.65	60
MAT1	86	93 TACACGGC	T	5.75	63.51
MAT1	95	95 G	T	6.51	63.51
MATE	61	61 T	C	23.85	59.34
MATE	69	69 C	T	28.33	59.22

MATE	112	112 C	T	11.78	60
MFP2	81	81 T	C	19.89	58.6
MFP2	91	91 A	G	32.67	58.34
MFP2	96	96 A	AT	34.23	58.29
MFP2	115	115 A	G	33.82	57.94
MFP2	122	122 A	G	26.61	58.48
MFP2	735	735 A	T	11.42	60
MFP2	740	740 G	T	11.42	60
MFP2	804	804 G	T	9.44	60
MFP2	836	837 TC	T	6.93	60
MFP2	854	854 G	A	11.8	60
MFP2	899	899 C	T	11.18	60
MFP2	1067	1067 G	A	11.56	60
MFP2	1093	1093 G	C	13.22	58.69
MFP2	1103	1103 G	GTA	15.66	58.66
MFP2	1108	1110 TTG	T	15.66	58.61
MFP2	1137	1137 A	G	11.52	60
MFP2	1161	1161 C	G	11.11	59.84
MFP2	1260	1260 G	A	6.12	59.81
MFP2	1315	1315 C	T	7.96	60
MFP2	1407	1408 AT	A	9.98	59.63
MFP2	1423	1423 G	A	12.92	59.28
MFP2	1428	1428 T	C	15.22	59.3
MFP2	1441	1441 T	A	18.38	59.35
MFP2	1453	1453 G	T	15.41	59.35
MFP2	1460	1460 A	G	8.27	59.35
MFP2	1477	1479 GCA	G	15.92	59.38
MFP2	1491	1491 G	A	13.97	59.38
MFP2	1493	1493 T	C	14.23	59.37
MFP2	1494	1494 G	T	13.89	59.38
MFP2	1504	1504 T	C	15.54	59.37
MFP2	1506	1506 C	G	15.48	59.37
MFP2	1511	1511 T	C	15.73	59.4
MFP2	1526	1526 C	A	15.47	59.58
MFP2	1528	1528 T	A	15.47	59.58
MFP2	1542	1542 A	G	18.71	59.6
MFP2	1565	1565 A	G	12.33	59.94
MFP2	1571	1571 A	G	13.29	60
MFP2	1602	1602 A	T	7.44	60
MFP2	1793	1793 G	A	14.32	60
MFP2	1822	1822 C	T	17.97	60
MFP2	1824	1824 A	G	18.4	60
MFP2	1853	1853 G	C	23.52	60
MFP2	1873	1873 T	A	14.59	60

MFP2	1883	1883 C	T	14.17	60
MFP2	1975	1975 A	T	17.51	60
MFP2	1976	1976 C	A	17.44	60
MFP2	1980	1980 C	T	17.06	60
MFP2	1992	1992 C	T	17.06	60
MFP2	2016	2016 T	C	19.61	59.74
MFP2	2030	2030 T	C	19.89	59.74
MFP2	2044	2044 T	C	24.72	59.72
MFP2	2053	2053 A	G	32.04	59.75
MFP2	2060	2060 A	AT	12.59	59.76
MFP2	2143	2144 AG	A	17.91	60
MFP2	2147	2147 T	TC	18.22	60
MFP2	2154	2154 T	C	17.9	60
MFP2	2185	2185 C	T	18.78	60
MFP2	2191	2191 A	AT	15.87	60
NIT4	29	29 C	A	34.73	57.54
NIT4	41	41 G	A	14.16	57.68
NIT4	54	54 A	AC	10.11	58.22
NIT4	57	57 A	T,AT	17.99	58.22
NIT4	65	65 T	TA	5.73	58.7
NIT4	78	78 C	T	7.89	58.81
NIT4	192	192 A	G	8.61	60
ONL1	166	166 A	G	13.17	58.14
ONL1	192	192 C	G	9.54	58.32
ONL1	199	199 C	A	10.07	58.24
ONL1	200	200 A	C	10.07	58.24
ONL1	292	292 G	C	12.99	60
PDS1	118	118 A	C	12.01	60
PDS1	149	149 C	T	16.16	56.77
PDS1	151	151 T	C	11.75	56.72
PDS1	169	169 T	G	11.75	56.72
PDS1	172	172 A	T	35.88	56.98
PDS1	175	175 C	CA	8.79	57.2
PDS1	212	213 GC	G	19.31	57.7
PDS1	222	222 G	GT	11.99	57.2
PDS1	224	224 T	TC,TTCTCTC	31.78	57.94
PDS1	237	237 G	T	10.84	58.22
PDS1	238	238 C	CT	10.24	58.22
PDS1	250	253 CCTT	C	14.18	60
PDS1	254	258 GCTGC	G	15.13	60
PDS1	260	260 T	TCACA	11.99	60
PDS1	268	268 T	C	17.83	60
PDS1	272	272 C	T	17.83	60
PDS1	283	283 A	T	12.74	60

PDS1	285	285 G	A	17.83	60
PDS1	302	302 C	T	21.27	60
PDS1	331	331 G	C	16.22	60
PDS1	401	401 G	A	11.8	60
SBP1	130	130 G	A	8.05	57.04
TRX	78	78 G	A	11.51	57.15
TRX	84	84 G	C	11.43	57.15
TRX	94	94 G	T	13.48	56.7
TRX	101	102 TA	T	10.8	58.14
TRX	105	105 C	T	11.23	58.14
TRX	241	241 T	A	8.11	60
UGT73C6-like	83	83 C	CTGGGG	9.18	60
UGT73C6-like	102	102 C	G	10.1	60
UGT73C6-like	122	122 T	C	15.18	59.9
UGT73C6-like	179	179 G	C	17.94	60
UGT73C6-like	189	189 A	G	19.36	60
UGT73C6-like	194	194 G	A	17.25	60
UGT73C6-like	208	208 C	CAT	22.35	60
UGT73C6-like	214	214 C	CCTCAGCTG	21.28	60
UGT73C6-like	227	227 C	G	19.41	60
UGT73C6-like	229	235 TCAAACA	T	17.99	60
UGT73C6-like	298	298 T	G	14.06	60
UGT73C6-like	300	302 CTG	C	14.27	60

FS	SOR	MQRankSum	ReadPosRank	QUAL
1.833	1.23	-0.634	1.38	119.79
0	0.368	0.72	-0.72	126.27
12.42	2.225	-1.009	-0.57	168.88
1.283	0.446	1.375	0.808	437.31
0	0.813	0.749	1.004	196.58
3.073	0.58	1.529	0.718	250.87
0	0.745	0.817	-0.323	371.36
1.523	0.768	1.545	-0.196	292.82
0	0.836	0.02	0.861	471.06
6.008	2.621	1.626	-1.485	114.27
0	0.941	0.457	-1.763	85.24
0	0.941	-0.935	0.101	247.06
0	0.777	-0.076	0.076	324.35
0	0.777	-0.152	-0.076	324.35
1.778	1.179	0.311	-0.044	285.52
1.778	1.179	-1.999	-0.133	276.48
0	0.814	2.435	-0.847	235.29
1.957	0.729	-1.22	-1.122	285.52
4.598	0.946	1.588	-1.684	285.52
4.598	0.946	-1.01	-1.876	372.12
1.744	0.283	2.047	-1.669	564.73
0	0.446	-1.775	-2.356	564.73
1.55	0.668	-0.242	0.872	828.83
5.447	0.343	-1.807	1.588	1001.55
3.178	0.439	-2.267	2.37	1006.43
0	1.038	0.67	-0.087	179.53
8.82	2.24	-0.653	1.055	124.49
5.422	0.184	1.019	0.837	412.4
5.422	0.184	0.259	0.654	412.4
0	0.468	-0.11	2.268	846.09
1.427	1.106	0.844	0.153	592.19
1.58	1.179	-0.897	-0.626	361.69
0	0.713	0.487	0.28	321.13
0	0.627	-1.282	0.804	234.51
0	0.693	-0.455	-0.33	304.61
1.412	0.446	0.462	-0.334	623.09
12.063	3.611	-0.058	0.405	225.13
12.27	3.816	-1.411	-0.028	225.13
0	0.735	1.759	-0.271	118.5
3.488	1.08	1.312	-0.797	524.37
6.625	0.476	3.503	-0.196	301.86
6.475	0.489	3.53	-0.181	293.63
6.995	0.462	3.765	-0.651	370.5

13.406	0.433	-1.661	-0.986	1106.7
1.737	0.846	0.265	0	603.57
2.103	0.317	-1.66	-0.043	599.92
5.315	1.919	-0.264	-0.474	148.91
0	0.941	-0.56	-1.231	187.79
1.58	1.104	0.103	0.051	377.6
8.195	0.838	-0.566	-0.382	66.56
8.195	0.838	0.382	-0.382	66.56
4.06	0.643	-0.953	0.381	147.3
5.756	0.651	0.667	-0.267	135.87
0	0.495	-1.22	-0.652	238.84
5.523	1.127	-0.153	0.307	582.99
5.093	0.223	0.387	0.571	630.92
5.979	0.793	-0.102	0.468	727.81
0	2.494 -	-	-	471.2
0	2.494 -	-	-	471.2
0	1.981 -	-	-	560.86
0	2.147 -	-	-	560.86
0	1.473 -	-	-	641.56
0	1.329 -	-	-	650.6
0	1.329 -	-	-	605.81
0	1.609 -	-	-	560.86
0	1.802	-0.296	-1.48	224.03
0	1.802	-1.086	-1.283	233.07
0	1.802	-1.875	-0.296	233.07
0	1.802 -	-	-	531.77
1.74	0.925	0.495	-1.484	273.17
1.808	0.83	1.231	-1.902	593.65
1.922	1.061	1.426	-1.743	550.79
5.035	0.383	0.887	-0.197	454.01
0	0.765	1.63	0.453	159.24
1.364	0.412	0.302	0.27	355.46
1.527	0.883	-0.07	-1.277	241.55
2.158	0.223	0.556	-0.872	167.61
8.202	1.502	0.783	2.58	375.55
0	0.495	-1.809	-0.637	908.41
1.455	0.563	0.332	0	526.03
0	0.527	0.143	-1.031	112.39
0	0.883	-1.573	0.488	170.34
0	0.412	0.491	-0.567	299.84
0	1.022	-1.157	0.694	72.82
0	0.693	1.139	0.163	120.44
0	0.476	0.725	1.177	178.24
1.82	0.33	0.95	0.784	166.22

1.913	0.33	-0.732	1.122	244.34
1.913	0.33	0.537	1.025	244.34
1.82	0.33	-0.95	0.537	272.08
1.603	0.412	-0.363	-1.286	338.17
1.648	0.654	-0.339	-1.016	275.85
1.824	0.33	0.835	-0.234	232.36
0	0.382	0.141	0.987	232.36
0	0.627	-1.653	0.025	328.33
3.192	0.944	0.604	0.151	362.31
1.364	0.412	-1.5	0.513	532.57
0	0.582	1.146	-1.445	365.31
0	0.714	-0.665	-0.211	544.64
1.377	1.061	0.461	1.843	453.06
1.324	0.96	-1.349	0.905	460.03
2.958	1.292	0.182	1.705	728.53
1.377	1.061	0.78	-0.39	405.94
1.317	1.112	0.387	-0.211	523.64
0	0.61	0.32	-0.419	526.03
1.44	0.392	0.214	1.724	426
0	0.569	-1.076	2.09	385.66
0	0.859	0.977	0.302	302.76
0	0.818	0.558	0.027	283.91
0	0.593	-0.443	-2.263	296.23
0	0.498	0.471	-2.579	617.33
0	0.818	0.254	-1.207	221.3
0	1.022	0.264	0.791	155.76
0	0.892	-2.074	2.074	252.87
1.653	1.27	0.343	-1.976	353.33
1.653	1.27	0.606	-2.029	353.33
0	1.038	-0.029	-1.66	209.53
4.216	2.066	-0.465	0.837	349.75
9.751	1.188	1.862	-0.89	270
4.099	0.952	-0.262	-1.019	261.48
1.74	0.694	0.32	-1.102	322.02
1.74	0.694	-0.604	-1.173	312.98
0	0.693	0.578	-1.628	290.65
0	0.412	-0.106	-0.423	279.36
1.987	0.33	-1.276	0.068	291.65
1.987	0.33	0.068	0.068	243.82
0	0.693	-1.191	0.259	213.93
2.616	0.169	-0.536	-0.929	112.08
0	0.495	-0.361	0.361	133.62
0	0.223	0	-1.3	140.04
0	0.283	0.817	-0.437	166.88

0	0.283	-0.817	-0.696	157.84
2.817	0.136	1.461	-0.529	160.78
0	0.743	0.47	-0.47	302.3
1.617	0.34	-0.659	-1.186	330.33
1.871	0.799	-1.427	-0.061	435.85
5.959	0.058	-0.298	0.736	705.26
1.792	0.307	-0.334	2.165	297.54
3.771	1.317	1.106	1.723	374.05
8.464	1.727	0.516	0.646	372.41
14.753	2.798	0.153	-0.704	270.52
10.139	2.008	-0.808	-0.916	310.85
6.805	1.779	0.076	-0.687	265.18
9.64	1.768	2.22	-0.737	254.89
1.484	1.179	0.191	1.842	605.97
0	0.839	-0.743	-0.265	252.03
3.909	1.609	1.785	0.1	268.06
7.04	0.982	-0.478	0.968	708.57
7.949	0.126	1.439	-0.931	685.17
5.555	0.18	0.237	-0.817	697.89
1.739	1.306	0.59	-0.344	281.27
1.32	0.999	0.986	0.36	499.08
1.32	0.999	0.047	-0.36	495.31
1.298	1.042	-0.069	0.756	492.87
1.383	1.009	0.52	0.822	454.87
0	0.446	0.731	-0.296	106.02
0	1.179	0.322	-1.396	102.27
4.561	1.518	-0.887	0.042	176.94
0	0.859	-0.394	0.789	146
0	0.57	0.892	-0.817	1052.27
0	0.619	1.717	1.091	498.67
4.806	0.703	0.297	-0.082	858.77
0	1.085	0.705	0.775	185.61
0	0.399	-1.173	-0.817	645.86
0	0.776	-1.319	-0.027	676.32
0	0.693	-0.223	1.918	810.24
12.539	2.225	-0.848	-0.479	151.59
0	0.737	0.198	-3.795	402.62
2.671	2.11	0.111	-0.7	172.63
0	0.693	-	-	225.58
0	1.329	0.741	0.365	198.15
0	0.223	0.742	-0.742	268.87
0	1.022	-0.922	-1.495	187.51
0	1.022	-1.495	-1.495	187.51
0	0.33	0.747	0.747	255.83

0	0.627	-0.812	0.215	331.86
0	0.582	-0.074	0.103	449.22
0	0.896	-1.283	0.143	487.12
1.231	0.941	0.337	0.943	482.69
1.16	1.026	-0.907	-1.268	683.28
0	0.83	-1.198	-0.925	685.36
0	0.823	-0.623	-0.969	541.14
1.212	0.431	0.444	0.341	522.76
0	0.836	0.563	-4.519	444.07
0	0.473	0.637	0.232	360.7
1.851	1.445	0.254	-0.318	221.25
0	0.582	-0.212	-1.991	123.88
9.971	1.858	2.161	-0.58	112.89
0	0.473	-1.361	1.526	117.7
2.077	1.206	-0.421	-1.077	149.01
0	0.33	1.406	0.545	196.9
1.808	1.162	0.039	-1.051	183.59
0	0.458	-0.8	2	121.87
5.021	1.506	-0.354	-0.071	112.31
0	1.802 -	-	-	449.2
2.817	0.518	-0.93	0.109	450.62
0	0.446	-1.256	-1.545	291.84
0	0.446	0.978	-1.855	291.84
3.01	0.916	0.296	-0.296	78.92
3.09	0.889	0	-1.106	86.61
0	2.833 -	-	-	267.83
4.593	0.595	-0.91	-0.91	228.81
0	0.818	0.956	0.322	83.71
0	1.179 -	-	-	260.83
7.202	2.225	-0.365	-0.365	122.29
3.424	2.636	0.825	0.717	172.39
0	0.223	0.731	0.731	132.6
0	0.941 -	-	-	244.27
0	1.329 -	-	-	247.58
0	0.941 -	-	-	283.27
2.808	1.518	0.729	-0.876	103.62
10.182	3.056	0.157	-0.472	389.05
11.02	2.812	-2.786	-1.072	271.49
4.216	1.83	0.549	-2.098	311.59
4.117	1.863	0.153	-1.437	311.59
0	0.859	-2.07	-0.197	237.17
1.984	1.609	-0.211	-1.395	237.17
0	0.446	0.143	0.421	208.35
0	0.446	-0.717	0.741	208.35

9.213	1.561	-1.851	0.53	765.37
2.307	1.721	0.227	-1.926	152.22
17.45	2.14	-2.562	0.92	2552.5
2.277	1.022	0.033	-0.682	873.71
9.733	1.406	-1.966	0.478	807.41
0	0.693	-0.579	-1.35	476.99
0	1.179	0.929	-0.929	288.04
7.782	0.598	0	-0.729	189.24
0	0.859	0.411	-0.411	873.12
0	1.022	-0.369	0.264	149.84
0	1.022	-0.212	-1.092	157.84
0	0.693	-0.065	-2.001	207.63
0	0.446	0	-1.256	339.47
0	0.446	-0.978	-1.256	300.9
0	0.941	-0.289	-0.752	175.84
0	0.586	-0.732	-0.049	188.34
4.359	1.863	1.111	-0.755	242.52
0	0.627	0.717	1.832	177.96
3.979	1.447	0.731	0.731	139.59
0	0.916	0.727	0.727	106.57
0	0.916	0.727	-0.727	133.59
0	0.223	-0.731	-0.731	133.59
5.46	1.911	-0.018	-1.681	450.22
0	0.582	0.361	-0.915	304.62
1.897	1.329	0.037	0.627	183.59
1.897	0.307	0.627	-1.069	595.59
1.562	0.368	0.12	-0.599	348.69
5.907	0.833	-1.331	-0.276	350.45
0	0.49	0.396	-0.32	432.92
1.51	0.814	0.758	0.482	524.53
1.51	0.814	-0.207	0.482	524.53
3.352	0.897	0.421	-0.996	476.09
0	0.829	-0.461	-1.215	283.55
3.485	0.877	-1.508	-0.607	237.62
1.377	0.432	-0.638	0.425	332.94
0	0.905	-0.4	-0.4	165
2.246	0.774	0.793	-0.227	161.26
2.246	0.774	0.34	-0.566	161.26
0	0.693	1.027	0.201	190.88
0	0.368	0.715	-1.708	258.91
2.158	1.245	-0.53	0.059	117.78
0	0.76	-2.659	0.867	648.34
0	0.675	-0.334	1.723	214.46
0	0.776	0.188	0.619	694.32

0	0.602	0.398	1.301	211.96
3.757	1.049	1.536	-0.239	138.13
2.363	0.169	0.581	2.13	166.59
2.48	1.981	0.978	-0.696	161.88
2.43	1.609	0.633	-0.741	131.15
7.911	2.266	-1.805	-1.22	379.34
7.911	2.266	-2.196	-0.927	379.34
7.911	2.266	-1.903	-0.927	379.34
6.008	2.258	-1.286	-2.388	379.34
0	0.892	0.296	0.296	379.34
3.01	1.911	-0.762	0.762	379.34
3.332	2.833	-0.248	-2.054	66.43
5.441	0.662	0.676	0.103	118.4
9.971	1.858	-1.528	-3.004	69.88
3.183	2.093	0.4	0.4	816.08
1.757	1.23	-0.25	2.083	646.06
12.676	2.819	0.103	1.128	358.6
2.032	1.329	0.12	2.421	348.69
0	1.022	1.23	1.983	348.69
0	1.148	-1.223	1.364	429.95
3.713	1.721	0.022	-0.022	722.8
0	0.551	-0.37	-0.239	231.62
0	0.527	0.286	-0.99	273.22
3.442	0.269	-0.643	-0.694	511.96
0	0.569	-1.544	0.553	267.06
0	0.859	-0.064	1.969	230.3
0	0.527	-0.848	2.322	190.41
6.113	1.447	0.778	-0.495	106.32
6.532	1.431	0.289	1.239	78.73
0	2.303	1.026	1.026	90.71
0	0.512	1.361	-0.361	222.14
0	0.602	0.186	1.407	145.96
0	0.569	0.846	0	179.65
0	0.473	0.586	0.587	224.05
1.707	1.179	0.375	0.326	266.76
1.808	1.104	-1.774	0.833	277.82
1.643	0.399	-1.259	1.259	236.62
0	0.693	1.098	0.336	172.39
0	0.33	-1.246	0	255.2
6.455	0.859	-1.001	0.248	90.43
0	0.446	0.55	-1.38	136.63
22.411	3.1	0.128	1.059	500
23.693	4.611	0.283	0.887	279.89
0	1.609	-0.421	0.55	127.6

0	1.609	0	0.421	133.62
2.808	1.919	0.47	-0.876	166.2
5.441	0.662	0.47	0.729	172.39
2.463	0.76	-0.387	1.932	169.78
2.533	0.707	-1.134	1.532	169.78
0	0.693	0.676	-1.881	175.24
10.922	2.55	-0.751	0.173	173.34
2.772	0.124	-0.543	-0.352	221.24
1.895	1.469	0.796	-1.592	808.99
0	0.582	-0.584	0.428	146.37
0	0.446	0.81	-1.427	196.9
1.685	1.23	0	-1.61	289.69
0	0.783	0.516	-0.904	322.39
1.449	0.425	0.863	0.905	333.09
0	0.906	-0.055	-0.931	880.58
1.272	0.95	0.167	-0.54	385.3
0	0.639	0.724	-0.724	638.81
0	0.553	1.688	0.029	213.75
0	0.859	1.43	1.43	396
0	0.527	-0.759	0.409	396
5.523	0.966	-0.307	0.038	474.85
3.22	1.316	-0.717	-0.227	599
2.199	0.26	1.55	-2.35	277.69
0	0.382	0.307	0.853	140.99
2.066	1.609	0.643	-1.263	246.48
1.705	0.321	1.209	-2.689	426.49
1.569	0.399	-0.356	-0.908	366.53
0	0.534	-0.146	-0.732	379.11
1.801	1.402	0.533	-0.178	218.02
2.398	1.609	-0.678	-1.034	250.24
0	1.329	2.072	-1.133	209.24
0	0.693	0.922	-0.421	209.24
0	0.307	-1.036	1.133	79.08
3.757	1.552	-1.248	0.394	398.78
0	1.179	-0.248	1.203	75.43
0	0.368	0.573	-1.001	171.84
8.796	1.431	-0.058	0.058	286.35
8.141	0.872	-0.529	-0.048	285.4
2.43	0.223	-0.365	0.365	175.16
0	0.446	0.306	1.344	340.58
2.363	0.223	1.061	-0.077	83.27
0	0.603	-1.692	0.692	673.91
0	0.525	-0.346	-3.112	2534.79
2.54	1.112	-1.827	-5.034	2001.5

4.269	1.911	-1.712	-1.196	627.41
6.631	2.453	-3.05	-1.488	1233.57
6.641	2.28	-3.425	0.467	426.49
6.402	2.093	-3.19	0.749	437.96
3.965	1.714	-3.765	2.463	312.59
4.5	2.219	-2.754	2.693	190.21
6.402	2.093	-3.3	1.636	355.62
6.402	2.093	-3.3	1.525	355.62
0	1.075	-0.412	-1.12	117.66
5.497	0.078	-0.15	1.555	331.6
5.119	0.111	1.059	1.059	331.6
2.522	0.12	-0.201	1.668	415.24
1.757	1.23	-2.25	-3.583	226.07
6.455	0.124	0.734	1.496	442.73
11.073	0.859	-0.139	1.083	256.18
3.192	1.182	-0.534	0.257	469.07
0	0.735	1.217	0.255	495.59
1.459	1.085	-0.283	0.019	205.37
0	0.639	-0.251	-0.399	602.77
0	0.871	-0.751	-1.098	176.34
0	0.773	-0.234	1.639	412.01
0	0.368	-0.395	0.833	146.88
1.862	1.27	-0.475	0.792	435.17
0	0.976	-2.203	-0.456	280.5
1.623	1.247	0.517	0.571	296.73
1.657	1.179	0.417	0.139	491.07
0	0.693	-	-	733.13
0	0.693	-0.78	2.654	243.82
2.522	0.204	-1.954	-0.312	199.07
2.817	0.136	-0.529	0.529	169.78
0	0.765	1.2	0.184	327.12
0	0.446	2.811	-0.38	356.91
0	0.804	1.03	0.706	434.78
1.719	1.179	-0.178	0.618	438.17
4.242	0.627	0.296	0.328	199.98
1.871	0.883	0.127	0.272	454.85
0	0.551	2.518	-0.815	238.08
0	0.76	1.309	0.135	168.78
2.463	0.76	0.143	-0.387	171.39
0.991	0.54	0.926	2.113	1551.43
7.144	1.483	-0.768	-0.702	176.57
4.801	1.123	2.608	-0.584	177.48
1.603	1.085	-0.297	0.429	302.17
1.74	0.694	-1.173	-1.03	238.05

0	0.498	-0.467	0.027	886.7
10.925	3.236	0.289	-0.929	80.79
4.534	0.435	0.289	-1.445	408.04
0	0.941	-0.211	-1.225	277.82
0	0.353	1.589	0	821.29
1.871	0.754	-1.479	-0.042	231.04
8.852	1.033	1.456	0.567	306.33
11.243	0.577	0.337	-1.211	453.82
10.481	0.803	-0.193	-1.38	355.96
6.637	0.76	0.196	0.34	630.02
0	0.551	0.436	-0.247	736.31
1.096	0.606	0.72	-0.934	755.73
1.093	0.748	-0.087	-2.398	878.73
0	0.846	-0.542	-0.029	815.36
1.16	1.026	0.654	0.126	806.32
1.421	1.218	0.487	0.419	272.96
6.903	2.252	-0.47	1.079	225.13
4.533	2.012	-0.254	0.191	230.3
0	0.569	0.76	0.872	248.78
4.56	0.595	0.244	-1.805	204.29
0	0.859	-1.873	-0.493	143.55
6.56	3.258	-1.6	0.933	145.87
4.415	1.75	1.216	1.14	362.35
2.218	0.25	0.474	0.053	77.84
7.761	0.88	0.347	-0.27	250.21
1.999	0.26	0.76	0.398	232.84
0	0.941	0.722	-0.529	206.39
0	0.582	0.305	-0.25	346.57
0	1.022	-0.972	-0.694	215.79
0	0.473	0.206	-0.949	153.37
1.808	1.162	1.285	1.207	173.37
1.808	1.162	0.506	1.207	225.58
0	0.804	0.634	-0.775	233.65
3.674	1.354	0.108	0	216.85
0	0.473	-0.026	-3.163	431.61
0	0.693	0.359	2.718	464.6
1.987	1.329	-0.813	1.03	117.54
0	0.76	-1	-1.977	116.78
0	0.859	1.971	-1.084	148.96
0	0.859	-0.394	1.38	158
1.952	1.329	-0.702	0.421	179.01
2.077	0.85	-0.685	0.474	132.89
0	1.022	-0.876	-1.307	162.62
0	0.693	-	-	284.83

0	0.991	0.406	-1.537	126.04
7.231	1.773	0.028	0.694	517.07
3.558	1.394	1.244	-1.83	437.96
5.59	1.356	-0.859	-1.137	426
11.938	2.462	0.074	-2.43	419.43
9.155	1.246	-0.717	-1.291	731.42
4.519	1.483	-1.39	0.569	739.93
9.551	2.2	-0.326	-0.852	968.27
20.954	3.521	-1.039	-2.702	1043.21
4.815	0.627	1.231	-1.14	628.94
2.87	0.574	-0.789	-0.943	460.64
0	1.022	2.001	0.182	519.84
0	0.832	0.453	0	116.25
0	0.418	-1.126	0.953	407.7
0	0.223	-0.736	0.736	61.99
0	0.148	-1.495	0.922	709.31
8.451	2.788	-0.55	0	80.72
0	0.437	-1.53	0.375	274.7
4.269	0.182	1.016	-0.634	141.31
1.609	0.355	-0.594	-0.55	243.23
0	0.693	-0.795	-3.267	206.95
1.477	1.078	0.043	0.258	599.61
1.594	0.668	0.283	-0.762	333.81
1.523	0.768	-0.675	-1.501	276.88
10.098	1.289	-0.17	0.17	654.66
2.388	0.832	0.442	-0.166	623.69
1.258	0.469	-0.419	-0.503	435.72
1.227	0.507	1.361	-0.316	491.87
1.321	0.676	0.491	-0.664	491.87
0	0.693	0.869	0.264	587.41
7.04	1.485	1.273	-3.077	242.63
3.918	0.85	1.052	1.583	977.87
1.606	0.392	-0.483	-1.958	296
0	0.525	-1.344	-2.098	296
1.606	0.392	0.229	-1.246	256.14
1.606	0.392	0.076	-0.941	256.14
0	1.061	-0.546	0.296	78.92
0	0.693	-	-	186.36
0	1.179	0	0.55	126.59
3.136	0.916	-0.55	0.55	86
4.419	1.527	-0.56	-0.634	212.61
5.18	1.925	0.139	0.231	146.72
5.756	1.901	-0.437	-0.437	157.84
13.222	3.225	-0.361	0.322	163.34

16.244	4.271	0.363	1.09	385.29
16.244	4.271	-0.934	1.297	385.29
2.447	1.555	-0.196	0.196	112.2
0	0.818 -	-		572.56
2.251	1.755	-1.084	-3.253	134.96
1.451	0.545	0.607	2.982	1808.18
2.463	1.206	-1.932	1.532	292.84
2.533	1.518	-1.788	1	250.73
0	1.609 -	-		464.09
0	1.329	-0.869	-0.259	204.89
0	1.329	-0.583	-0.259	204.89
7.368	0.847	0.731	-1.818	77.56
3.233	2.419	-0.895	1.214	77.56
3.09	2.093	-0.566	1.377	78.65
3.09	2.093	-0.715	0.382	77.56
6.264	0.061	0.597	-0.678	238.04
0	0.859 -	-		915.99
0	0.693	-0.278	0.278	298.04
0	1.179	-0.689	-0.365	250.73
0	0.892	-0.377	0	247.03
0	0.495	-0.717	-1.932	204.89
0	2.303 -	-		238.54
0	2.303 -	-		238.54
2.569	0.508	1.411	-4.631	832.49
7.125	0.966	-0.532	-0.653	667.9
3.012	0.658	-0.517	-2.417	848.32
0.846	0.757	0.388	0.142	1523.13
6.117	0.205	-1.294	0.42	841.26
0	1.508	0.336	-0.676	164.2
0	0.654	-3.086	1.342	4484.74
2.808	0.707	-2.219	1.307	169.58
0	0.489	-0.27	0.222	447.3
0	1.609	-0.358	-1.231	89.12
3.556	0.531	0.329	0.188	383.22
5.153	1.015	0.119	-1.349	450.7
0	0.693	-1.378	-1.408	204.89
0	1.329 -	-		247.58
0	0.551	0	-0.288	550.32
3.448	0.223	1.764	0.106	404.18
1.527	1.329	-0.069	0.482	360.53
0	0.627	0.484	-1.155	552.91
2.713	1.278	1.038	-1.11	696.23
2.652	1.187	-0.336	-0.985	655.31
1.316	1.112	0.345	0.122	431.97

2.821	1.179	-0.512	-0.488	442.89
1.335	1.154	-1.286	-1.415	442.89
5.692	1.888	-0.487	-0.812	433.85
1.55	0.758	0.448	-0.448	214.04
0	0.576	-0.95	-2.115	1026.83
1.684	0.404	0.424	0.018	1318.91
1.317	0.473	-1.032	-0.682	526.01
0	0.88	-	-	1361.82
1	1.358	-	-	950.03
0	0.538	-1.403	-2.378	557.81
3.233	2.303	0.714	-2.302	639.11
4.947	0.124	0.132	-0.57	146.88
1.808	1.371	0.106	0.035	286
3.192	0.719	0.929	-2.391	476.05
5.391	0.894	0.731	-0.81	393.07
4.738	0.277	0.278	-0.167	738.49
1.585	0.321	-0.298	-0.528	241.34
1.702	1.426	-0.339	0.068	516.32
1.377	1.127	-0.367	-0.367	662.97
13.9	0.829	0.99	0.239	923.14
0	0.775	0.188	-0.423	352.32
0	0.765	0.454	-0.091	311.18
7.203	1.477	-0.462	-2.89	259.91
1.808	1.14	-0.658	-0.57	226.74
1.157	0.821	1.075	0.032	647.39
1.157	0.821	-1.182	0.075	649.49
1.157	0.821	0.713	0.032	649.49
3.887	0.694	0.982	0.211	714.99
2.507	0.531	0.847	0.321	685.36
3.66	0.914	0.684	1.464	1515.51
0.974	0.941	-0.317	-0.411	692.73
0	0.758	0.413	-0.923	878.99
1.078	0.848	0.38	-0.799	584.31
0	0.716	0.757	-1.785	85.33
6.107	0.881	2.003	0.825	532.05
1.507	0.399	0.024	1.299	270.92
0	0.714	0.406	2.202	272.13
2.115	1.309	0.423	-0.741	236.75
7.437	0.278	-0.35	-0.604	773.56
4.678	0.148	-0.849	-0.51	813.53
1.523	0.738	-0.892	2.111	691.86
0	0.495	-0.337	-0.521	259.44
12.7	3.912	-0.89	-0.328	173.01
0	0.368	-1.479	1.281	155.89

1.399	0.74	1.937	1.013	688.76
1.459	1.085	-0.472	0.208	210.37
1.258	0.495	-0.334	-0.398	735.5
6.107	1.518	1.629	1.675	337.58
0	0.564	-0.24	-2.525	2158.95
4.701	0.864	-1.335	-2.428	1541.41
0	0.512	-3.927	-0.906	735.78
1.398	0.425	-2.282	-0.695	1043.21
1.077	0.74	-0.38	-2.718	648.07
1.957	0.729	-0.439	-0.049	242.34
0	1.022	1.975	-1.266	383.34
2.742	1.005	-1.38	-0.44	495.5
0	0.693	1.873	2.171	203.86
1.913	0.33	-0.653	-0.955	321.4
3.565	0.912	-0.427	0.879	264.45
10.253	1.118	-0.862	-0.711	402.08
0	0.917	-0.589	-0.031	414.8
7.761	0.88	-1.196	-1.736	158.85
0	0.859	0.887	-0.296	70
1.412	0.681	0.42	0.5	336.07
0	0.706	1.057	-0.869	433.25
2.808	1.518	0.361	0.361	129.81
2.808	0.148	-1.881	-0.361	167.84
2.92	0.916	-0.761	-2.113	68.37
5.497	0.061	-0.473	-0.263	220.67
1.837	0.34	1.29	-1.115	174.41
1.837	0.34	0.479	-0.479	190.41
0	0.593	-0.595	-0.553	190.41
0	0.804	-1.184	-0.833	196.88
0	0.804	0.745	-0.57	187.83
0	0.804	0.57	-0.57	187.83
2.363	0.223	0.212	-0.212	123.31
2.003	0.669	1.63	-0.906	222.19
2.029	0.269	1.358	-0.234	199
0	0.495	-0.972	0.324	155.76
0	0.495	0.88	0.231	146.72
1.674	0.942	0.556	-0.146	348.72
1.706	0.658	-0.298	-0.06	355.62
1.657	0.313	0.54	0.18	373.65
0	0.566	0.156	0.986	299.57
1.655	0.349	-0.678	0.527	316.51
1.585	1.14	-0.354	-0.024	305.05
6.903	2.252	0.415	-0.138	216.09
1.573	1.161	-0.022	-2.368	243.66

0	0.755	-0.463	1.159	282.38
1.643	1.132	1.557	0.835	158.08
0	0.473	-1.126	-1.187	216.09
0	0.495	-2.15	-1.488	718.45
6.107	1.265	0.212	-1.391	296.04
3.471	0.828	-1.032	-0.023	564.22
4.31	1.51	1.016	0	182.04
10.139	1.755	-0.553	0.437	251.52
16.72	2.52	0.514	0.393	224.21
1.804	0.368	-1.155	1.015	562.44
0	0.527	0.277	-0.4	440.23
3.892	0.842	0.263	-0.029	334.42
0	0.941	0.992	1.246	244.91
0	0.793	-0.738	0.018	399.4
1.412	0.901	0.576	-1.568	336.36
5.792	1.327	-0.509	0.465	356.95
3.473	1.008	-0.322	-0.415	415.55
13.786	1.996	0.738	0.197	219.04
0	0.77	0.406	-0.438	700.55
2.21	0.547	0.532	-1.346	998.71
0	0.667	-1.758	-0.057	818.36
1.564	0.412	-0.868	1.758	257.09
0	0.675	-0.694	-1.466	246.27
0	0.735	1.245	1.688	216.09
0	0.941	0.575	1.301	218.27
4.31	1.196	0.245	1.295	190.44
9.616	2.266	-1.66	1.397	351.33
6.779	2.303	-0.146	-0.556	322.5
5.076	0.544	0.289	0.289	431.8
16.564	3.036	-1.113	-1.755	295.89
1.497	1.136	-1.162	-0.301	375.41
3.682	0.223	-1.55	0.087	299.61
1.897	1.329	0.258	-1.069	236.24
0	0.512	-1.122	0.233	302.97
0	0.793	1.142	-0.811	599.15
0	0.483	-0.664	1.161	490.03
1.507	0.399	-0.708	1	450.99
0	0.467	-0.136	-0.95	215.68
1.471	1.022	1.774	-0.9	371.67
0	1.244	-0.614	-0.992	481.12
5.815	0.636	0.139	-0.509	92.82
1.556	0.721	0.168	-0.084	148.73
0	0.892	0.892	0.936	178.86
0	0.495	-1.672	-0.54	345.67

1.648	0.85	-1.992	-1.184	382.7
3.963	1.561	-0.589	0	259.14
4.06	1.275	-0.064	0.064	511.04
0	0.673	0.298	-0.817	483.73
0	0.593	1.486	0.398	148.53
10.139	0.322	0.299	0.354	462.73
0	0.693	-0.243	-0.624	713.18
2.066	1.739	0.245	-0.105	588.44
1.702	1.119	0.611	-0.133	199.96
0	0.859	-0.323	1.159	546.36
4.192	1.424	1.008	-0.743	634.57
6.239	1.072	-0.246	1.615	327.11
1	1.136	-	-	795.03
0	0.662	0.682	-0.418	276.23
0	0.495	-1.411	1.079	672.15
0	1.051	-1.299	-0.337	952.59
0	0.287	0.578	-0.835	839.13
5.649	1.158	-0.686	-0.52	378.46
9.454	0.889	-0.203	0.655	742.08
6.897	1.8	-1.672	1.126	202.21
4.415	0.939	-0.733	-0.733	229.85
1.801	1.402	-0.746	0.533	322.02
1.848	1.18	-0.076	-0.076	414.35
0	1.112	-0.439	-1.025	181.39
1.987	1.329	-1.681	0.922	203.33
1.987	1.329	-0.163	1.681	203.33
0	0.693	0	0.72	128.58
0	0.495	0.278	0.278	129.24
0	0.693	-1.036	0	129.24
0	0.693	0.406	0.406	124.74
0	0.883	0.529	0.244	160.73
0	0.495	0.678	-1.663	189.73
4.593	0.959	0.715	0.386	288.59
0	0.836	-0.387	-0.951	343.95
1.657	1.179	0.361	0.083	259.02
0	0.811	-0.377	-0.755	308.46
0	0.811	-1.078	-0.701	307.27
1.641	0.864	-0.889	-0.191	220.17
1.641	0.864	-0.635	-0.381	221.25
2.158	0.828	-0.796	0.551	194.28
0	0.646	-0.551	-0.919	200.23
1.922	1.402	1.273	-2.045	241.84
3.183	2.093	-1.428	-1.656	675.34
1.721	1.071	0.528	0.75	268.06

1.721	1.071	1.083	0.694	308.46
3.624	0.612	0.708	-2.349	312.59
0	0.473	-1.61	0.381	353.33
0	0.582	1.082	0.471	346.57
0	0.582	0.416	0.582	355.62
0	0.569	-0.155	0.155	344.29
0	0.791	-0.467	0.467	357.76
0	0.791	-0.467	0.334	316.66
0	0.667	-0.429	1.343	904.68
1.352	1.022	-1.402	-0.601	607.22
0	0.681	-0.872	-0.325	281.51
0	0.859	-1.829	-0.973	86.62
0	0.382	-0.493	-0.564	186.65
0	0.446	0.876	0	120.62
0	0.33	0.597	-0.278	255.2
0	1.179	-1.041	-0.674	371.58
0	0.804	-0.133	-0.933	139.87
5.497	1.893	-1.246	-0.793	151
1.957	0.956	0.439	-1.61	339.34
0	0.412	1.356	0.38	197.33
5.569	1.759	0.471	-0.627	297.63
1.871	1.034	-1.504	-0.424	225.82
12.42	1.406	-1.981	-0.238	550.79
8.318	0.62	-2.24	-0.127	541.75
1.74	0.33	0.317	-0.387	321.95
0	0.495	-0.168	-0.042	299.59
0	0.467	1.177	-0.86	302.67
2.105	1.536	0.111	0.553	151.63
2.035	1.673	-0.1	-0.234	714.17
1.304	0.671	1.063	0.284	650.94
0	0.693	1.105	-1.105	942.08
0	0.662	-0.395	-1.68	996.34
0	0.641	0.362	-1.054	900.99
0	0.665	-1.639	-2.438	1205.38
0	0.586	0.037	-1.863	1171.66
0	0.756	-2	1.665	1285.69
1.534	0.57	2.372	1.13	1329.67
1.448	0.585	-0.141	3.3	1229.1
0	0.765	1.293	3.38	1078.36
0	0.76	1.035	-2.971	1023.09
0	0.653	-0.802	-3.112	957.45
3.96	0.204	0.437	0.087	693.46
9.879	1.844	0.474	0.239	431.85
9.829	1.856	-1.453	-1.974	431.58

0	0.495	-	-	342.11
1.957	1.015	0.222	1.159	276.52
4.117	1.863	1.378	-0.643	271.49
1.697	1.402	-0.028	-0.368	291.59
0	0.917	0.119	-0.239	274.62
2.003	0.669	0.543	0	180.19
0	1.112	-0.495	1.768	112.31
0	0.33	-0.196	-0.065	121.24
0	0.551	-0.326	1.11	121.24
2.077	0.85	-1.318	1.634	112.89
2.187	0.26	1.149	0.556	757.01
2.9	1.893	-0.88	0.787	904.43
0	0.434	-1.093	0.312	162.9
0	0.569	-1.913	0.586	282.97
13.786	1.996	0.787	-0.639	329.62
6.107	1.499	-0.99	-0.726	328.22
1.262	0.91	-0.347	0.144	287.5
7.282	0.157	-2.321	2.705	397.81
10.477	0.093	-1.54	1.176	420.53
14.893	1.938	-1.684	-0.092	503.49
9.773	1.447	-0.29	2.187	476.33
7.732	0.678	-1.011	-1.011	678.28
7.732	0.678	2.1	-1.27	702.28
6.421	1.506	0.448	-0.184	664.45
6.186	1.354	0.915	0.582	619.33
0	0.693	1.363	1.466	421.63
0	0.569	-0.364	-1.626	405.41
1.721	1.071	0.361	1.639	268.06
1.721	1.071	-0.528	1.694	268.06
1.648	0.85	-0.375	-0.953	349.7
0	0.368	-1.156	-2.161	699.38
2.017	1.265	-0.219	-0.219	178.99
1.808	0.774	-0.112	-0.336	198.79
0	0.665	1.085	0.245	207.21
0	0.665	-0.455	0.245	204.17
1.685	1.071	-1.19	0.194	204.17
3.771	1.317	0.489	-1.98	308.46
3.771	1.317	-1.209	-2.083	299.42
3.771	1.317	0.077	-2.186	299.42
5.904	1.17	-0.607	-1.674	477.41
0	0.892	-0.619	-1.086	531.23
0	0.723	-0.249	-1.529	563.82
0	0.845	-1.229	1.201	416.59
4.01	0.654	-1.007	0.485	194.79

1.451	1.085	-1.403	0.336	643
1.451	1.085	-0.889	0.336	643
0	0.804	1.092	-0.024	563.03
0	0.693	0.051	0.154	569.55
0	0.693	-2.718	-0.359	485.6
0	0.859	0.245	-0.843	443.73
0	0.832	-1.902	-0.906	277.82
0	0.832	0.272	-1.087	280.85
0	0.832	0.362	-1.811	242.24
0	0.934	-0.69	1.774	107.04
0	0.941	0.537	-2.684	244.34
1.987	1.329	-1.681	-2.44	244.34
4.533	0.711	1.216	2.312	401.39
0	0.804	-0.07	-1.339	215.65
4.01	0.207	-0.178	-1.173	181.98
0	0.459	-0.368	-1.84	219.94
0	0.73	0.18	0.129	372.65
4.123	1.288	-1.386	0.746	312.98
1.833	1.23	0.336	0.56	181.79
1.657	0.313	1.312	-1.569	511.25
1.281	0.495	0.224	0.431	650.28
1.22	1.022	0.601	0.69	1213.28
1.093	0.655	-0.871	-1.793	759.78
0	0.653	0.446	0.238	1644.46
0	0.61	0.493	0.417	1644.46
0	0.602	0.615	-0.958	1666.55
2.589	0.773	0.188	-1.576	1418.88
6.114	0.986	0.468	-0.741	1441.88
5.909	1.144	1.048	0.49	1404.59
4.156	1.037	0.686	0.366	1404.59
2.504	0.803	-0.24	0.587	1400.06
2.587	0.986	0.137	-1.052	485.59
1.238	0.817	0.594	0.743	1146.19
2.735	1.041	-0.24	0.422	1284.64
1.202	0.96	0.057	-0.194	1179.12
1.079	0.941	-0.486	-0.59	1087.7
0	0.578	1.455	1.322	747.36
6.254	0.199	0.021	0	1037.17
4.189	0.252	-0.332	-0.714	1038.41
2.304	0.433	0.476	1.85	1035.19
2.518	1.099	0.565	-0.268	469.67
2.304	0.433	-0.879	-0.275	1035.19
25.552	4.8	-0.971	-1.61	335.62
1.56	1.179	-0.99	-1.88	267.64

4.039	1.863	1.139	-0.306	177.27
7.132	0.901	-2.301	-0.495	268.52
7.732	2.264	-1.265	-1.804	256.85
3.453	1.609	-0.548	-2.785	423.65
0	0.859	-0.022	-3.235	333.89
1.536	1.27	-0.157	2.674	335.07
0	0.77	0.106	-2.176	333.83
1.503	1.27	1.135	-1.958	415.13
1.503	1.27	-0.062	-2.333	416.96
6.107	1.265	0.071	-2.758	293.63
6.107	1.265	-0.212	-2.381	305.04
8.272	1.061	0.614	-0.499	503.21
45.57	1.218	0.47	0.265	5107.02
8.629	1.387	0.078	-0.817	3501.67
2.807	0.293	1.469	0.152	928.38
2.771	0.368	-2.542	-1.841	1258.16
2.593	1.041	-0.223	-0.178	938.23
1.19	0.976	0.542	0.588	1240.68
1.202	1.044	-0.348	0.415	1240.68
1.202	1.044	-1.044	0.797	1284.64
1.228	1.082	0.076	1.157	1375.78
1.186	0.473	0.424	1.271	1457.77
11.742	0.669	-0.046	-0.273	1273.05
11.389	0.486	0.222	0.154	1098.51
11.856	0.636	-0.441	0.724	1089.47
12.439	0.993	-0.627	0.586	1089.47
9.454	0.889	-0.474	0.339	936.08
9.756	1.009	-0.805	0.519	996.28
7.043	1.033	2.055	0.071	1002.45
6.68	0.763	0.399	1.754	903.59
6.68	0.628	-0.22	1.885	866.09
1.423	0.962	0.543	0.318	464.94
1.423	0.962	-0.393	0.356	424.18
3.256	0.85	-0.02	-0.304	424.18
3.211	0.61	0.31	0.021	426
1.509	0.654	-0.861	-0.516	378.36
3.512	0.781	0.116	-1.357	465.32
1.485	0.439	0.864	-1.604	435.54
0	0.711	-0.716	-1.801	466.83
0	0.856	0.235	-1.223	381.26
1.599	1.136	-0.126	-0.577	319.65
1.531	1.022	-1.462	0.054	319.65
0	0.714	-0.162	0.755	310.85
0	0.635	-1.157	0.306	339.64

0	0.635	-0.437	-0.129	380.01
0	0.714	-1.078	-0.431	380.01
0	0.859	-0.577	-0.929	350.45
3.738	1.565	-0.797	-1.363	634.46
1.465	1.112	-0.571	-0.129	668.9
0	0.754	1.309	-1.309	170.91
6.761	0.557	-1.806	-0.582	565.49
0	0.473	0.867	-0.041	448.76
0	0.653	-0.741	0.212	232.56
0	0.714	-0.406	-0.579	350.11
8.392	1.434	0.181	2.174	181.24
0	0.693	1.449	0.315	752.75
0	0.387	-0.771	-1.735	672.81
5.315	0.88	0.099	1.183	363.01
4.151	0.718	0.321	-0.904	736.61
0	0.914	-0.39	-0.52	252.13
3.452	1.508	-0.466	-2.007	288.53
1.47	1.179	-0.192	-0.038	466.92
3.142	1.329	-0.055	0.387	466.92
3.142	1.329	-0.313	0.497	466.92
3.142	1.329	-1.971	0.976	466.92
3.142	1.329	-0.055	0.903	455.9
1.243	0.668	-1.713	-0.496	617.92
0	0.736	-1.313	-0.751	651.58
1.216	0.801	-1.716	-1.233	660.62
2.597	0.928	-1.758	-2.447	678.58
0	0.693	1.772	2.254	679.32
1.194	0.809	-2.327	-2.629	655.31
4.862	1.235	-1.608	-2.591	468.87
1.536	0.34	-0.162	-2.18	748.07
8.994	3.312	-0.606	-2.585	472.98
1.752	1.179	-1.098	0.768	176.31
9.558	1.458	-2.136	-1.304	329.62
2.522	0.877	1.606	-0.592	232.68
1.74	1.179	-1.042	-1.504	165.8
11.29	2.636	-0.099	0.033	350.17
1.55	0.542	0.023	0.344	744.62
1.583	0.557	1.23	1.331	708.69
0	0.829	-0.751	-1.503	206.31
0	0.73	0.324	-0.046	137.76
6.908	0.916	-1.01	-2.541	175.49
4.123	0.991	-0.181	-0.688	441.73
0	1.329	-0.778	-0.919	105.31
7.57	0.039	0.212	0.953	220.6

7.57	0.039	0.635	0.318	220.6
10.243	1.447	-0.636	0.867	179.27
2.276	0.799	0	0.212	142.88
0	0.446	-0.656	1.427	182.9
2.831	2.093	-1.306	-1.007	199.81
2.688	1.282	-1.043	0.562	788.64
0	0.465	0.659	-0.22	254.89
0	0.88 -	-		1495.75
0	0.957 -	-		1549.79
0	0.826 -	-		1324.85
6.532	0.515	1.898	-0.231	783.53
6.532	0.515	1.713	-0.324	783.53
0	0.653	-0.651	0.425	326.77
0	0.693 -	-		1189.96
0	0.693 -	-		1189.96
0	0.77 -	-		1100.03
0	0.77 -	-		1090.9
0	0.784 -	-		965.13
0	0.784 -	-		920.14
0	0.784 -	-		920.14
0	0.874 -	-		965.13
0	0.874 -	-		965.13
0	0.793 -	-		920.14
0	0.693 -	-		830.26
0	1.022	-0.602	-1.62	118.83
0	0.818 -	-		740.42
0	1.061 -	-		866.2
0	1.061 -	-		911.09
0	1.179 -	-		785.4
3.757	0.916	0.639	1.187	767.78
4.708	0.148	1.107	0.264	455.85
3.68	0.849	-0.413	0.413	900.39
3.203	0.499	-0.829	0.226	903.38
1.311	0.835	2.459	-1.073	682.99
0	0.779	-0.813	-1.862	682.99
2.944	1.014	0.387	0.325	402.65
2.049	0.34	0.58	0.307	945.14
1.674	1.218	0.339	-1.139	311.77
2.192	0.264	0.933	-0.287	809.69
0	0.495	0.228	-0.411	809.69
0	1.061	-0.94	-0.313	638.99
2.077	0.85	-1.107	1.845	141.84
2.276	0.799	-0.271	0.212	165.88
0	1.179 -	-		327.79

0	0.693	0.747	0.747	316.44
0	0.859	0.751	0.751	315.46
0	1.863 -	-		1.863
0	1.609 -	-		396.25
0	0.832	-0.272	-0.439	171.24
2.808	1.472	-1.866	0.633	111.29
14.211	1.85	-0.602	0.324	143.72
6.373	1.518	-0.099	0.495	291.17
0	0.735	1.055	-0.151	192.5
1.987	1.329	-0.106	-0.766	246.6
2.187	1.371	-1.355	-0.884	238.6
1.792	0.307	0.534	-0.401	309.5
0	0.657	1.294	-0.108	539.48
0	1.061	0.895	1.214	87.97
0	1.061	0.546	1.001	79.92
0	0.697	-0.731	-0.296	218.93
0	1.329 -	-		247.58
0	1.329 -	-		247.58
0	1.329 -	-		403.22
0	2.303 -	-		408.29
4.771	1.872	0.736	0.736	156.29
0	0.446	-0.727	0.727	106.57
1.574	1.27	0.024	0.756	439
0	0.426	1.778	-0.127	218.99
4.467	1.546	-1.059	-1.059	237.56
0	1.329	0.572	-1.067	264.76
0	1.981	-0.198	-0.922	264.76
0	1.609	0	-0.72	178.47
0	1.022	0	0	173.67
0	0.582	-0.684	-0.956	182.71
0	0.582	-0.684	-0.956	173.67
0	0.368	-0.55	0	131
0	0.368	-0.937	-0.55	131
0	0.859	-0.789	-0.296	137.77
0	0.412	-0.666	-0.133	276.48
0	0.412	-0.044	-0.4	285.52
0	1.085 -	-		418.2
5.497	1.911	0.184	-1.164	142.58
0	0.446	0.551	-2.051	322.24
0	0.307	0.922	0.597	170.34
2.199	0.26	-0.718	-1.31	280.85
0	0.426	-1.252	-0.298	315.47
0	1.022	-0.574	-1.244	784.69
0	0.631	-0.867	-0.289	284.52

0	0.941	-1.364	0.037	518.63
0	0.657	0.952	-0.073	149.93
8.26	0.927	-0.366	0.091	1141.46
10.966	1.627	-1.105	0.291	1049.86
1.421	1.058	-0.657	-0.8	256.48
0	0.709	-0.022	-0.892	300.86
4.534	1.225	-0.581	-1.722	1734.21
6.551	1.226	-0.206	-1.776	1653.46
4.055	1.23	-1.09	-1.07	1074.05
4.727	1.245	-0.184	-0.478	517.36
5.217	1.146	-0.39	-0.515	403.13
1.243	0.668	-1.374	-0.37	610.02
0	0.722	-0.91	1.395	211.69
1.459	1.085	-0.586	-0.472	336.58
0	0.807	0.039	-0.078	336.58
0	0.56	0.159	-0.477	334.36
15.184	2.704	0.432	-3.459	603.77
1.515	1.085	-0.983	2.086	252.47
14.428	1.99	1.102	-0.094	255.66
1.69	1.124	0.292	-0.504	210.96
0	0.84	0.178	0.312	696.23
1.158	0.91	1.298	-0.701	694.1
1.28	1.087	-1.058	0.981	571.8
2.909	1.227	0.756	1.058	492.87
1.729	1.27	-1.054	1.205	1159.68
3.089	1.383	0.799	-0.298	499.08
1.384	0.976	0.775	0.09	500.74
1.374	0.97	-0.034	0.962	376.43
1.527	1.061	-0.671	0.21	298.69
3.89	1.718	-0.61	0.122	263.93
3.89	1.718	-0.561	-0.122	262.09
0	0.735	0.526	-1.241	216.09
4.31	1.196	-0.735	0.175	89.37
0	0.848	0.321	-0.513	816.64
0	0.76	0.117	-0.35	769.86
0	0.96	0.446	0.023	242.09
0	0.693	-	-	863.13
5.988	1.022	-2.066	0.441	506.55
0	0.595	0.49	1.716	699.88
0	0.77	0.525	1.025	819.12
1.523	0.768	-0.239	0.283	136.65
35.829	2.885	1.486	-4.275	2099.86
4.457	1.255	-0.791	-0.306	1172.8
13.418	2.159	-1.609	-1.547	2334.26

7.073	1.577	-0.058	-2.432	1867
16.103	1.842	-0.83	-0.557	1843.02
14.927	2.873	1.513	-2.251	908.09
26.849	4.003	-0.731	-1.573	925.19
26.348	3.814	-0.374	-1.122	861.73
0	0.446	-1.308	-1.096	2123.21
30.833	3.705	-1.271	-0.559	815.36
34.992	3.804	-0.071	-0.919	815.36
3.722	1.571	0.025	-0.126	215.86
3.646	0.598	0.541	0.049	193.12
3.01	1.981	-0.06	-0.419	645.4
0	1.112	0.151	-0.754	172.54
0	0.693	0.893	-1.943	350.78
1.74	1.179	-0.347	1.813	197.85
0	0.473	0.307	-0.307	255.8
0	0.425	0.105	1.855	140.37
1.922	1.329	0.619	-0.041	371.75
1.725	1.329	-0.117	0.821	226.09
6.008	0.636	-1.408	0.919	151.54
1.987	1.329	-0.106	-0.423	107.49
2.158	0.842	-0.922	-1.03	301.81
0	0.814	2.646	0.212	199.51
0	0.883	1.461	0.135	241.7
0	0.582	-0.212	-1.991	96.84
0	0.697	0.731	-1.58	260.07
0	0.836	0.566	0.906	115.26
0	0.446	-1.885	-0.876	236.96
0	0.446	0.611	-0.504	236.96
0	0.425	-0.67	0.262	201.48
1.848	1.18	-1.14	0.532	352.67
9.89	1.862	0.696	-0.533	139.88
1.871	0.754	1.141	0.38	174.98
3.365	1.403	-0.507	-1.602	367.22
3.492	1.445	-0.126	-0.929	276.49
1.833	0.346	0.616	-0.253	493.78
0	0.512	-1.323	-0.109	271.49
0	0.534	0.263	-0.465	399.11
1.569	1.085	-0.205	0.556	357.76
0	0.782	1.083	1.126	355.62
0	0.917	0.527	0.905	355.62
0	1.112	-0.237	-0.829	125.59
4.075	1.574	-0.925	-2.197	178.34
1.623	0.652	-0.589	-0.165	194.73
2.248	0.215	-0.152	-1.05	296

3.326	0.25	0.917	0.917	293.18
4.262	0.148	0.186	-1.354	257.92
1.718	0.34	0.337	0.276	228.49
0	0.569	-0.76	0.253	261.78
1.935	1.278	-0.385	-0.805	151.44
0	0.904	0.735	-0.315	141.41
7.203	1.477	0.405	-0.058	227.31
4.222	1.518	1.041	-0.817	227.31
0	0.941	0.425	-1.225	882.12
0	0.941	1.007	-0.56	146.79
0	0.368	-0.623	-1.758	144
2.162	0.799	0.591	-2.161	144
2.271	1.336	-1.528	-1.473	423.03
4.561	1.053	0.039	-0.722	572.62
0	0.804	0.377	-0.427	665.45
1.68	0.368	-1.378	-0.29	682.87
1.623	0.956	-1.028	0.79	353.33
3.473	0.819	-1.195	1.605	435.54
5.904	0.959	-0.704	1.061	441.02
3.352	0.486	0.72	0.364	629.82
4.039	0.169	0.694	-0.087	679.07
0	1.708	-	-	952.04
1.705	0.321	-0.292	0.823	170.96
0	0.693	0.471	0.036	268.78
1.59	1.058	-1.773	-0.328	354.82
0	1.244	0.632	-0.211	645.8
1.922	1.609	-0.037	3.245	265.09
4.216	1.83	-0.161	2.356	271.49
6.276	1.836	0.504	1.917	257.92
6.276	1.836	-0.611	0.664	266.96
6.648	1.811	-1.806	0.361	257.92
6.085	0.381	0.778	-0.328	492.53
10.607	1.739	-1.46	-1.339	191.2
0	1.022	1.143	0.922	182.63
0	0.693	0.167	-0.1	219.21
0	0.836	1.092	-0.121	365.7
2.158	1.609	-0.637	0.637	216.84
4.775	2.066	-0.127	0.972	237.17
4.722	2.129	-0.56	1.189	226.75
4.834	2.34	-1.664	-0.317	268.78
4.561	2.303	-0.643	-0.189	386.71
0	0.473	-1.376	-1.552	357.76
0	0.473	-1.142	-1.552	357.76
0	0.569	-1.096	-0.482	187.83

0	1.022	-0.264	-1.001	196.88
0	1.022	-0.474	-1.423	149.84
13.366	2.81	-0.364	-0.952	473.37
13.779	2.44	-1.505	-1.232	399.11
13.829	2.23	-1.026	-1.083	387.53
13.829	2.23	-2.302	-0.749	346.57
17.118	2.22	-2.606	-1.039	355.62
7.168	1.198	-2.805	-1.34	357.76
4.228	0.959	-2.491	-0.745	265.09
1.999	0.26	-3.153	-0.536	193.37
1.999	0.26	-2.997	-0.619	184.32
2.128	0.188	-2.763	-0.139	195.72
2.128	0.188	-2.516	-0.046	193.37
2.336	0.223	-1.981	0.396	148.96
0	0.787	-0.158	0.475	225.17
0	0.787	0	0.555	225.17
0	0.473	0.375	-0.307	275.8
1.719	0.368	-0.398	0.036	222.8
1.808	1.162	2.374	-1.285	132.37
0	0.527	-0.396	-0.079	86.84
0	0.593	-0.377	0.427	202.45
3.736	0.861	1.2	-0.133	823.14
0	0.538	0.952	-0.171	375.96
0	0.593	-0.525	-0.175	113.37
1.674	0.351	0.092	-0.215	232.77
5.231	1.141	1.7	0.382	586.22
1.378	0.726	0.249	0.05	719.35
1.725	0.283	-2.412	1.052	1005.82
5.576	1.863	0.323	0.513	576.36
0	0.976	-0.824	2.473	381.17
5.849	0.065	-0.556	1.52	838.75
12.683	1.653	0.26	-0.548	786.35
6.306	2.093	-1.344	0.118	231.67
1.37	0.43	0.487	-0.151	269.66
6.343	0.544	-0.013	0.567	571.72
0	0.567	-0.503	0.551	591.84
3.203	0.263	-1.582	1.037	788.05
4.781	0.568	-2.033	1.915	854.08
6.429	1.088	-0.738	-0.885	566.27
6.956	0.73	0.495	-1.136	507.53
3.963	1.561	0.775	-0.961	190.77
11.139	3.234	0.196	-1.626	95.2
11.553	3.232	0.077	-1.532	98.5
0	1.518	0.736	-0.736	83.67

2.694	2.147	-0.158	-0.58	436.85
0	0.892	0.655	0.849	259.52
1.47	0.368	-0.192	1.305	725.99
3.151	0.317	-0.06	1.421	676.06
0	0.712	1.517	-0.9	556.46
0	0.892	-0.421	-0.421	184
0	0.465	-0.751	-0.578	218.27
0	0.569	0.204	0.728	234.53
3.769	1.536	-1.194	0.204	231.02
0	0.593	2.853	-0.876	301.27
0	0.593	-0.148	-0.823	301.27
5.219	1.938	-0.4	0.267	196.66
5.219	2.303	0.452	-0.71	205.71
4.561	1.492	0.158	1.823	221.33
4.752	1.506	-0.342	-0.049	235.29
0	0.495	-0.993	-1.096	272.84
0	0.551	-1.24	0.718	154.26
5.021	1.773	-0.998	-0.578	223.67
0	0.693	-1.918	1.829	986.52
0	0.593	-1.052	-1.885	448.82
3.256	1.071	-0.02	1.061	471.06
0	0.709	0.461	-0.369	465.83
3.565	0.876	-1.13	0.025	698.69
0	0.636	-0.503	-0.326	278.87
1.414	1.179	0.018	-0.729	437.72
0	0.754	1.248	0.947	346.41
1.676	0.346	-1.127	-0.056	3560.69
0	1.022	0.058	-0.868	218.84
0	0.804	-0.933	-1.6	205.87
1.808	0.774	0.112	0.187	226.5
0	0.976	0.746	0.18	415.61
3.68	1.061	-1.067	-1.589	183.35
14.211	1.85	-0.787	1.065	128.76
4.775	2.303	-0.332	-0.184	191.63
0	0.997	-	-	1038.9
1.987	1.329	-1.059	-2.223	288.4
2.158	1.863	-0.263	-1.208	291.65
2.158	1.863	0.053	0.473	333.4
2.158	1.863	-1.418	0.473	333.4
2.246	1.714	1.059	1.482	327.12
7.346	2.038	-0.604	1.905	312.98
7.701	2.031	0.612	3.307	327.12
12.465	1.981	0.53	3.002	320.95
11.563	1.421	0.041	1.429	372.12

11.563	1.421	-0.286	1.429	368.84
11.563	1.414	0.265	1.776	449.81
15.233	1.409	1.162	2.007	449.81
3.682	0.479	-0.462	-0.263	476.56
3.442	1.445	-1.209	-0.386	478.41
1.527	1.179	-0.17	-0.872	482.41
3.442	1.445	-0.952	-0.245	482.41
4.586	1.133	-0.822	0.985	217.09
1.714	0.418	0.578	0.032	854.57
1.685	0.307	-0.322	0.775	398.11
6.402	2.093	0.368	-0.459	312.59
2.114	1.402	0.503	-0.771	823.53
0	0.986	-0.193	-1.582	280.85
0	0.986	0.039	-1.582	280.85
0	0.986	-1.736	1.813	280.85
0	0.787	-0.228	1.266	322.02
2.75	1.359	-0.251	0.391	793.86
0	0.892	0.035	0.458	363.17
4.216	0.371	0.807	-0.613	577.52
0	0.859	-0.739	-0.192	399.11
1.549	0.637	0.659	-0.962	378.36
0	0.525	0.825	0.495	302.67
0	0.616	0.091	0.401	332.77
0	0.495	0.42	-0.022	325.32
1.377	0.908	-0.237	0.192	507.59
2.928	1.244	-0.017	-0.416	589.89
0	0.507	0.53	0.596	332.51
0	0.804	-1.018	-0.48	661.44
1.283	1.008	-1.911	-1.005	580.59
1.17	0.914	-1.461	-1.919	662.62
0	0.725	0.922	0.205	619.39
1.643	1.132	-0.339	0.655	290.55
5.632	1.336	-0.101	0.71	428.22
5.632	1.336	-0.831	0.71	428.22
3.471	1.139	-0.043	0.947	428.22
0	0.892	-2.333	0.306	302.67
1.584	0.709	0.226	0.86	302.67
1.657	0.346	-1.391	1.537	302.67
3.785	0.681	0.053	2.334	263.93
3.382	1.445	0.07	-0.812	434.54
0	0.859	0.062	0.062	262.62
2.612	1.143	-0.611	0.173	1240.68
1.154	0.941	0.385	0.925	1367.98
0	0.807	0.861	1.562	828.12

1.022	0.963	-1.214	-0.934	527.51
1.207	0.981	0.841	0.705	2089.66
0	0.643	1.849	0.172	1178.74
0	0.677	-0.297	1.129	2153.66
2.124	0.439	-1.01	-0.351	1172.74
1.231	1.044	-2.162	1.591	2042.81
6.603	1.068	0.02	0.859	1484.64
7.64	0.984	0.501	-1.124	1265.11
1.278	0.666	0.202	0.131	268.33
7.144	0.709	-0.085	1.696	1415.62
0	0.746	0.449	-0.41	599.19
1.183	0.794	-0.169	1.697	456.49
1.117	0.687	-0.749	-1.057	662.51
0	0.746	0.477	1.546	1438.63
0	0.495	-1.79	-2.51	650.35
1.58	0.676	0.246	-1.889	437.96
4.675	2.303	0.233	0.433	229.21
0	0.511	-0.623	-0.83	396.57
3.909	1.609	0.393	0.333	259.02
1.657	1.179	1.306	-0.139	268.06
1.829	0.668	-0.204	-1.429	317.12
1.957	1.015	-0.222	-1.2	327.12
4.32	1.273	-1.837	-1.184	327.12
4.036	1.122	-0.106	-1.14	410.95
4.32	1.546	1.102	-0.204	410.95
3.757	1.552	0.263	0.328	449.81
0	0.693	-0.804	0.85	515.48
0	0.693	-0.069	0.942	521.32
0	0.892	0.938	-0.153	560.05
1.44	1.022	-0.661	-0.901	462.02
0	0.892	-1.249	-1.164	420.91
0	0.892	0.953	-1.715	462.02
0	0.693	0.62	-2.022	512.35
3.18	0.56	0.861	-2.422	471.06
3.399	0.799	-0.402	-2.815	429.95
3.399	0.799	-1.08	-3.112	471.06
10.692	0.8	-0.271	-3.634	593.53
7.891	0.557	-0.707	-3.709	637.99
13.545	1.275	0.383	-3.95	546.78
1.882	1.251	0.028	-1.652	301.86
0	0.836	0.34	-1.701	471.06
0	0.836	0.58	-1.421	520.35
0	0.569	-0.316	-0.947	298.65
1.323	1.179	-0.73	0.817	712.87

1.236	1.071	-0.25	2.588	662.62
2.75	1.292	0.928	2.549	710.01
4.442	1.247	-1.408	2.546	712.78
0	0.54	0.604	-1.501	535.03
4.886	0.369	-0.129	-1.905	1268.11
14.239	1.575	-0.967	-2.68	791.17
12.626	1.383	-0.379	-2.107	800.21
2.814	1.262	-1.194	1.356	753.72
0	0.569	0.18	0.509	635.98
3.256	1.071	-0.3	1.799	411.25
0	0.56	0.248	-0.903	796.94
1.364	1.085	0.366	-1.607	991.98
1.216	1.11	1.66	-0.579	838.41
2.649	1.23	-0.644	0.474	793.41
0	0.855	1.058	0.026	1154.82
1.319	0.521	-2.117	1.193	1370.62
0	0.776	-0.83	0.29	889.35
9.558	0.685	-1.873	-0.849	1367.84
9.092	0.48	-1.849	-1.128	1303.69
2.78	0.55	-0.783	0.421	342.69
9.955	0.105	2.595	0.354	1077.87
15.489	0.031	0.624	-0.563	1077.87
1.356	1.022	0.19	-0.761	690.57
3.565	0.23	1.328	-1.183	1279.17
4.789	1.589	1.237	-0.313	686.21
1.462	0.368	-0.877	0.244	1360.14
5.109	0.771	0.751	0.432	396.11
2.696	1.284	0.158	0.499	743.35
2.82	1.203	0.949	1.563	599.58
0	0.665	-0.338	0.839	1206.44
13.864	1.026	-0.944	0.397	619.46
16.564	0.603	-0.019	-0.811	1035.21
24.779	0.83	0.408	-0.324	732.97
16.371	0.241	1.112	-0.682	685.83
0	0.636	0.459	0.376	402.16
14.53	0.044	-0.066	-0.224	1296.11
7.529	0.126	-1.258	-1.639	660.62
0	0.646	-0.109	1.583	449.22
7.585	0.144	0.564	-1.256	658.58
4.911	0.214	0.697	1.228	1418.68
4.498	0.249	-0.798	-0.156	511.68
2.779	0.368	1.693	1.361	1424.88
1.207	0.479	1.131	0.755	1552.47
0	0.574	0.637	0.759	1550.51

0	0.723	1.036	-0.441	1168.18
0	0.565	0.354	0.163	1159.14
0	0.719	-0.161	-2.184	1002.46
2.701	0.976	-0.894	-0.34	901.86
1.227	0.628	0.615	1.537	617.31
2.624	1.187	-0.995	0.237	657.85
3.179	1.265	-0.085	0.188	818.06
3.124	1.329	0.703	0.162	835.43
0	0.836	-1.64	0.987	571
1.515	0.392	-0.335	1.572	451.06
1.515	0.392	-0.419	1.351	453.36
1.708	0.358	-0.636	0.432	232
0	0.947	1.75	-2.972	254.06
1.721	0.307	-2.312	-2.747	529.65
1.824	0.252	1.312	-1.729	627.59
1.949	0.28	0.187	-0.792	225.75
1.744	0.283	-0.775	0.465	433.8
0	0.551	-0.457	0.457	121.24
0	1.022	0.551	-0.184	183.33
0	0.836	-0.113	-0.113	141.26
0	0.693	-1.931	-0.6	502.63
2.875	1.2	-1.842	0.528	623.62
1.264	1.042	1.7	-0.857	707.36
0	0.536	2.029	-0.242	297.48
8.85	1.53	0.354	0.051	703.87
6.548	1.579	-1.137	-0.051	703.87
5.299	1.015	0.906	-1.078	1183.14
1.192	1.085	1.008	0.753	738.46
1.192	1.085	0.753	0.614	696.23
3.969	0.283	-1.496	-1.227	1449.52
2.785	0.501	1.481	0.531	954.42
4.859	0.728	-0.326	-1.047	495.31
7.684	1.312	0.211	-0.822	492.87
1.463	1.041	-0.735	-0.804	330.75
0	0.941	1.582	1.358	1365.1
3.041	1.149	-0.998	1.773	1011.87
2.879	0.352	-0.673	1.018	901.61
1.279	0.976	-0.711	-0.499	535.59
9.276	0.793	-1.111	-1.76	887.36
7.754	1.292	1.132	-0.841	409.29
7.754	1.292	-0.33	-0.871	409.29
3.169	0.811	0.957	0.438	414.61
1.433	0.412	1.475	-0.514	1187.2
0	0.656	1.792	0.418	881.61

4.957	1.412	0.438	1.184	395.55
1.172	0.922	0.076	2.754	698.31
0	0.634	-0.68	-0.272	428.22
1.172	0.922	-0.177	2.072	707.36
0	0.749	-0.425	0.394	1322.81
1.402	0.385	-0.017	0.206	451.72
5.979	1.273	-0.239	-0.751	271.87
1.631	1.262	0.541	-0.501	305.04
1.55	0.758	0.448	-0.778	786.69
0	0.648	-1.011	0.157	421.21
0	0.76	0.812	-0.905	432.09
0	0.99	-1.669	1.331	857.81
3.155	0.518	-0.167	-0.544	603.78
0	0.569	0.417	0.767	594.46
0	0.705	-0.869	1.057	507.29
1.406	0.585	0.151	0.944	425.29
1.356	0.864	0.162	0.774	433
0	0.693	-1.531	-1.644	334.36
0	0.616	0.02	-2.84	333.51
0	0.838	-0.365	-1.227	324.47
0	0.61	0.207	0.345	578.57
0	0.553	-0.788	0.575	578.57
1.197	0.491	-0.574	0.102	603.47
5.731	0.148	0.019	1.545	679.87
4.32	1.1	2.353	-1.775	418.08
4.32	1.1	2.188	-1.693	418.08
2.017	0.796	-0.046	-1.898	594.93
0	0.569	-0.044	0.219	148.88
3.09	0.889	1.931	0	70.61
0	0.818	0.322	0.322	83.67
0	0.495	-0.736	-0.736	74.15
0	0.223	0.736	-0.736	200.64
0	1.085	-	-	426.31
0	1.022	-	-	565.81
0	0.569	1.27	1.059	224.6
0	1.609	-	-	585.57
1.641	1.075	-1.53	-0.202	434.73
6.262	2.147	-1.189	-0.752	524.53
6.262	2.147	-0.121	-0.898	521.32
6.262	2.147	-0.024	-0.849	521.32
8.463	1.492	0.667	-1.026	569.55
10.02	1.235	-0.585	-1.569	492.13
2.218	0.18	0.854	-0.854	192.49
0	0.693	1.701	0.869	368.84

0	0.892	-0.528	1.303	397.78
0	0.976	0.099	0.495	450.17
0	0.96	0.415	-0.29	362.12
0	0.511	1.09	-0.156	396.57
0	0.601	-0.301	-0.52	396.57
1.527	0.603	-0.756	-0.366	494.96
1.149	0.892	-2.027	2.103	531.59
3.405	0.455	1.776	1.12	1294.58
1.194	0.604	0.726	-0.48	965.38
0	0.575	1.982	0.111	943.58
0	0.596	1.254	1.619	641.97
1.243	0.791	0.156	0.382	843.02
0	0.58	1.503	0.074	832.55
0	0.665	1.309	-0.234	1223.48
4.658	1.609	1.948	-0.851	612.59
2.948	1.255	-1.218	-0.167	1192.08
7.16	1.838	1.986	-0.642	649.03
6.983	1.546	0.66	-1.162	693.58
1.43	0.921	0.449	-0.549	1023.61
1.36	0.713	-1.701	-0.881	1125.3
3.185	0.283	-0.597	-1.027	382.1
6.648	0.517	-0.972	-0.139	759.96
6.805	0.674	-0.664	-0.292	604.96
8.873	0.458	0.024	0.118	800.04
8.873	0.458	-0.495	0.071	800.04
5.632	0.907	-1.755	0.351	790.66
5.632	0.907	-1.59	0.31	790.66
3.325	1.149	-1.666	0.278	833.6
0	0.693	-1.526	0.555	589.6
0	0.818	-1.683	0.083	354.16
4.957	0.384	0.6	0.081	995.94
0	0.532	-1.098	0.805	970.98
1.264	0.694	-0.4	1.339	633.59
1.29	1.085	0.37	0.222	892.45
0	0.776	-0.414	-0.214	892.45
4.752	1.506	-0.439	0.439	242.24
4.752	1.506	0.244	-0.146	244.34
9.249	2.233	1.827	-1.237	194.28
9.249	2.233	1.002	-1.945	205.69
5.756	1.884	-0.933	-1.867	155.82
5.756	1.901	0.533	-2.313	166.88
1.186	0.922	-0.289	0.716	1055.36
4.351	1.071	1.699	-0.034	1101.09
6.374	1.27	-0.455	-1.145	937.38

0	0.807	0.44	-1.829	414.83
6.884	1.052	0.521	-1.231	847.42
4.655	0.589	-1.138	-2.866	895.59
4.901	1.374	-0.179	-3.573	901.61
4.901	1.374	-0.358	-4.032	873.61
2.693	0.572	0.146	-1.898	699.87
4.646	0.897	0.444	-0.539	699.87
5.023	0.781	-1.871	1.01	668.84
5.023	0.607	0.842	1.733	658.87
0	0.732	1.004	0.493	991.58
0	0.546	-0.231	0.042	996.12
1.489	0.446	1.704	-0.411	818.62
0	0.551	-2.473	-0.21	985.09
1.796	0.33	0.647	-0.377	170.81
0	1.179	-1.304	-0.767	830.69
4.416	1.863	-0.031	-0.337	622.44
4.612	1.701	-1.156	-0.112	542.79
8.141	1.447	-0.049	-1.513	369.3
12.707	2.526	-1.276	0.135	249.82
6.154	1.872	0.135	-0.831	160.73
9.89	1.862	-1.092	-1.461	157.84
6.532	1.431	-0.289	-1.106	127.08
5.449	1.196	-0.853	-0.536	515.82
3.453	1.609	-0.767	-1.294	518.46
5.969	1.981	0.441	-0.765	476.83
1.529	1.288	-1.793	-1.882	429.95
3.325	1.445	1.164	-1.926	497.31
1.497	1.136	-0.775	-2.271	372.36
3.473	1.46	-0.619	-2.455	495.17
1.55	1.025	-0.206	-2.088	345.22
0	0.693	-0.139	-1.194	266.96
1.664	0.61	-0.164	-0.305	955.36
6.332	0.415	0.67	0.345	1057.73
1.713	0.355	-0.601	-2.27	498.54
1.801	0.283	-0.036	-1.954	498.54
4.285	0.169	0.27	-2.353	457.02
1.706	0.293	-1.275	-2.279	434.69
7.025	0.769	0.387	0.035	414.51
4.075	0.819	1.022	-0.033	518.37
3.707	1.41	-1.661	-2.43	576.57
1.485	1.162	-1.157	-1.488	518.46
1.485	1.162	-0.065	-1.488	551
3.18	1.371	-1.409	-1.724	650.82
1.657	1.402	-0.231	-2.639	290.27

0	0.818	-0.394	-1.832	330.62
0	0.836	-0.504	-0.441	518.46
0	0.75	-0.377	-0.417	474.36
0	0.75	0.377	-0.285	506.78
0	0.693	0.622	1.753	601.96
0	0.693	-0.019	1.866	601.96
1.562	1.179	0.312	0.36	708.69
3.325	0.269	1.08	0.509	672.35
8.607	0.662	-0.385	-0.387	757.92
5.608	0.556	-0.861	0.332	668.35
1.475	1.085	0.915	-0.993	852.81
3.227	0.706	-0.667	0.406	997.51
0	0.892	-1.038	1.227	265.89
3.274	0.729	-1.187	-0.347	994.58
0	0.693	-0.435	0.737	967.36
0	0.693	1.404	0.657	1006.43
0	0.892	-1.47	-0.325	865.03
3.117	1.358	-1.346	-1.217	1001.55
3.235	1.093	-1.436	-1.473	953.46
1.32	1.038	0.446	-1.271	575.99
3.211	1.473	0.851	-0.851	439.89
3.211	1.037	1.012	-1.59	871.24
5.641	1.406	-0.692	-1.179	862.43
10.976	2.138	0.342	-0.991	644
10.976	2.138	0.198	-0.919	644
5.402	1.721	-1.538	-1.148	781.92
0	0.709	0.553	0.645	493.82
0	0.519	0.264	-1.277	799.42
0	0.512	-1.254	-1.254	829.18
0	0.512	0.056	-1.029	829.18
2.835	0.34	-0.99	0.517	888.41
2.835	0.34	-0.517	0.606	888.41
1.377	0.425	-0.354	-1.134	824.94
1.414	0.368	-0.792	-1.64	824.94
1.414	0.368	-1.161	-2.597	770.92
5.167	2.584	0.244	-2.586	244.34
0	0.859	-0.752	-1.466	473.37
3.783	0.577	0.701	1.047	324
3.867	0.548	0.797	0.894	307.27
1.54	1.085	-1.106	-0.79	512.28
0	0.892	0.11	-0.617	467.79
1.562	0.368	-1.558	1.607	361.68
1.585	0.321	-0.206	1.833	346.62
3.488	0.634	-0.54	2.425	348.69

0	0.534	1.968	2.564	314.73
2.521	0.929	1.141	-0.776	773.12
2.521	0.929	-0.411	0.137	838.63
2.395	0.758	-0.611	0.175	882.16
4.925	0.663	1.075	1.075	918.86
4.925	0.663	1.445	1.149	918.86
1.58	0.934	-0.952	-0.626	432.73
0	0.917	0.527	-0.589	339.8
1.971	1.229	-0.184	1.364	230.36
7.501	2.281	-0.117	0.428	232.65
1.721	1.071	-0.306	0.036	299.42
8.28	2.25	0.195	0.506	192.63
7.144	1.483	-0.367	-0.282	223.31
4.31	1.196	-0.945	0.602	181.37
0	0.743	-0.134	1.54	318.54
0	0.446	0.836	0.489	324.35
0	0.446	-0.532	0.578	324.35
0	0.693	-0.416	0.914	359.79
2.199	0.184	1.658	0.58	604.97
0	0.551	-1.511	1.01	324.35
0	0.693	0.618	0.788	324.35
0	0.223	0.736	0.736	60.99
0	1.27	-0.278	0.278	129.24
0	1.329	0.077	0.54	124.55
2.276	0.595	-1.276	-0.201	218.84
2.447	0.169	-0.993	-0.872	294.84
2.187	0.293	1.355	-0.177	331.65
2.187	0.293	-0.648	0.059	331.65
5.102	0.689	0.548	-1.175	172.37
1.734	0.307	-1.047	-1.274	228.59
4.008	0.525	0.425	1.727	229.94
17.041	2.519	-0.296	0.296	206.98
0	0.743	0.495	-2.011	349.17
1.725	1.329	1.196	-0.023	201.09
1.377	0.392	-0.367	-0.297	367.97
19.743	2.62	-0.783	-0.487	413.91
0	0.859	-0.54	-2.906	112.26
10.05	0.061	0.25	2.361	644.14
4.228	0.959	0.648	1.126	220.84
1.54	1.085	0.553	-1.239	247.33
0	0.76	-1.431	-0.596	231.73
1.74	0.925	-1.55	0.297	352.17
0	0.743	1.469	-0.067	221.79
1.74	0.991	-1.303	-0.528	386.82

1.674	0.715	-1.669	0.724	202.7
0	0.678	0.258	-0.689	387.41
0	0.547	0.913	0.159	383.6
0	0.755	-0.811	0.869	450.06
0	0.892	0.88	-0.106	344.95
3.614	0.58	0.39	-1.153	158.04
0	0.693	1.376	-0.656	325.95
1.73	0.283	0.534	-0.585	221.18
3.436	0.634	-0.126	-0.796	137.9
1.824	0.33	-0.969	-0.568	177.36
0	0.368	-1.493	-1.954	223.15
1.527	0.694	-2.344	0.814	255.33
0	0.593	-0.996	-0.244	300.09
0	0.602	-0.385	0.791	329.18
1.377	0.908	0.82	-0.055	418.22
0	0.811	-1.455	-0.108	253.85
1.494	1.085	-0.242	-0.022	296.23
0	0.821	1.027	-1.516	318.47
1.414	1.179	0.705	0.38	445.61
1.897	1.329	-0.405	-0.405	183.59
1.804	1.179	-0.175	-0.525	190.41
0	0.941	0.041	0.286	234.13
0	0.412	0.271	0.163	161.34
1.913	0.33	-0.955	-0.955	107.56
7.782	0.598	0.361	0.361	78.6
6.421	2.91	-1.157	-0.694	116.8
6.818	3.258	0	-0.929	148.72
6.008	2.621	1.485	-1.157	114.27
6.368	2.964	-0.326	-1.371	121.24
8.024	1.447	-0.663	-1.276	194.81
8.796	1.431	-0.984	-0.752	231.78
8.796	1.431	-2.257	-0.065	231.78
9.89	2.225	-0.811	0.135	244.85
15.563	3.59	-0.529	0.38	252.87
0	0.569	0.458	-2.218	318.99
2.162	0.799	0.296	0.099	151
8.751	1.17	-0.374	-0.17	727.53
0	0.646	-0.42	-0.307	424.56
0	0.43	-0.029	-0.029	482.76
3.12	1.352	-0.152	0.589	496.84
5.56	1.309	0.078	0.976	215.94
0	0.566	0	0.808	247.85
0	0.818	1.732	0.464	392.96
7.328	1.198	0.968	0.249	688.15

27.724	4.798	1.22	-0.56	277.31
7.464	1.825	0.29	1.84	577.13
12.42	2.225	-0.219	-0.658	155.88
1.74	1.179	0.152	0.076	322.02
1.801	1.402	-0.249	0.462	322.02
1.801	1.402	-0.533	0.675	322.02
0	0.693	0.456	1.244	522.03
1.533	0.327	1.547	1.666	342.6
0	0.314	0.116	1.502	1001.03
1.81	0.738	-0.762	-1.016	214.3
0	0.495	0.092	0.276	148.62
0	0.569	-0.849	1.774	276.41
0	1.609	1.159	-1.652	186.3
0	0.368	-0.387	-1.932	217.39
0	1.022	-0.289	-0.6	118.03
0	0.693	0.182	-0.303	469.3
0	0.368	-0.217	0.072	514.2
0	0.79	1.524	1.154	282.42
0	0.941	0.405	1.215	246.6
0	0.586	1.513	-0.927	271.88
0	1.085	1.91	0.489	342.69
1.922	1.402	-0.713	-0.792	199.36
0	0.473	-0.556	2.196	357.76
0	0.582	-0.915	1.969	355.62
4.853	1.957	-1.422	0.924	207.31
0	0.919	1.083	-1.361	268.06
0	0.919	0.417	-1.583	268.06
3.755	1.609	-0.088	0.439	187.41
14.055	1.726	-0.549	1.388	229.09
1.607	1.274	-0.045	-1.991	280.67
0	0.716	-0.635	1.362	219.26
2.84	0.223	-0.351	-0.15	847.7
0	0.766	0.311	-1.297	324.4
1.792	0.714	0.415	-0.249	216.09
2.066	0.193	-0.945	1.785	69.41
0	0.951	-0.577	-0.075	302.45
3.682	0.936	-1.082	-2.08	365.31
4.359	2.093	-0.604	0.107	315.02
0	0.76	-0.454	-1.858	401.08
0	0.412	1.625	-1.776	387.91
0	0.721	0.152	0.608	216.72
6.232	0.07	-1.04	1.857	753.06
0	0.512	0.216	-0.36	208.76
0	0.593	-0.379	-0.437	149.15

4.973	0.223	0.161	-0.6	356.94
5.072	0.799	0.052	0.33	379.43
7.877	1.072	0.63	1.203	379.43
1.423	0.731	-0.592	2.272	283.03
0	0.892	-1.907	0.192	641.97
0	0.836	1.481	-1.081	816.81
0	0.941	0.244	1.61	162.39
10.71	3.239	-0.354	-1.202	123.31
10.71	3.239	-1.061	-0.919	123.31
2.632	0.991	0.382	0.715	82.61
0	0.527	0.849	1.774	69.55
3.274	0.515	-0.913	1.756	648.27
1.808	1.14	0.219	1.973	159.88
0	0.693	0.589	0.465	485.8
0	0.527	-0.184	0.258	214.36
0	0.382	0.853	0.239	275.8
2.066	0.193	1.775	-1.388	274.13
4.039	1.863	0.194	1.528	245.96
7.14	2.368	-0.423	1.48	230.3
4.506	1.863	0.206	1.361	233.65
1.885	1.426	0.423	1.621	233.65
1.833	1.23	0.261	-0.336	235.79
11.633	1.426	-2.89	-1.18	217.09
7.887	1.097	-2.586	-0.046	225.13
6.205	0.124	0.275	-0.909	699.14
1.515	1.179	1.135	1.548	601.66
7.129	0.086	0.503	-0.072	765.77
0	0.711	-0.22	1.059	927.17
0	0.562	-1.055	-1.299	1248.46
0	0.804	-0.039	-0.09	1612.16
0	0.7	0.559	0.243	1218.67
0	0.681	-2.414	0.502	1584.73
0	0.681	-1.352	0.502	1607.62
0	0.608	-0.068	1.095	1521.66
4.372	0.263	-0.983	1.846	1303.08
3.083	1.36	-0.839	0.489	308.89
0	1.501	-	-	1548.73
0	0.569	-0.253	0.471	277.82
1.674	0.715	1.48	0.913	310.66
6.415	2.093	-0.724	0.787	275.66
1.279	0.946	0.45	-1.765	576.97
5.085	1.635	-0.995	-2.374	720.61
0	0.892	0.708	-1.387	259.55
0	0.61	-0.146	-0.437	664.48

0	0.784	1.777	0.437	259.48
0	0.784	-0.437	0.495	259.48
24.328	3.225	0.56	-2.539	288.17
7.908	2.266	-1.216	-0.184	148.63
0	0.73	-0.972	0.694	155.76
0	1.022	1.107	0.58	155.76
1.922	0.223	-1.007	0.858	541.75
1.922	1.609	-0.709	-0.56	198.75
6.569	1.289	-0.954	-1.385	274.84
2.128	1.445	0.175	-1.484	604.9
0	1.292	1.959	-1.197	692.35
0	1.292	0.627	-1.115	726.87
2.824	0.292	-0.347	-0.05	1175.65
4.779	0.235	0.189	-0.995	911.12
0	0.599	1.468	0.714	1761.91
5.672	0.571	-0.026	1.005	1300.85
7.561	0.316	1.486	0.782	1382.84
8.021	0.416	1.179	-0.399	1347.02
7.797	0.678	0.547	-0.602	813.61
1.106	0.96	2.103	-0.091	1095.61
2.512	1.22	1.293	0.397	1018.41
1.127	1.031	1.754	0.738	1000.43
0	0.793	1.788	0.098	694.1
0	0.733	-1.205	-0.268	696.23
2.379	0.909	1.424	-1.775	868.53
2.379	0.909	0.537	-1.568	868.53
1.154	0.525	-1.814	-0.784	1107.51
1.154	0.525	-0.105	-0.714	1107.51
2.649	1.329	0.364	-1.678	865.28
0	0.883	1.42	-1.185	871.36
0	0.883	0.951	-1.068	835.32
1.21	0.495	-0.301	1.346	700.97
1.349	0.397	-0.173	-1.299	452.5
3.575	0.258	0.355	0.017	1329.67
1.143	0.636	0.105	0.211	678.04
2.304	0.916	0.976	-2.948	688.69
1.058	0.547	1.493	1.721	669.36
0	0.509	-0.174	1.028	670.82
1.204	0.465	-1.135	1.682	793.41
2.709	0.472	0.428	1.333	793.41
2.987	1.003	-1.194	0.016	770.5
2.987	1.003	1.608	-0.08	770.5
0	0.901	0.974	-0.17	484.64
1.4	1.148	-1.098	-0.143	499.08

3.091	1.371	1.5	-1.408	541.61
1.4	1.148	1.143	-0.799	500.74
0	0.706	-0.226	0.365	406.38
0	0.593	0.667	0.054	446.99
1.03	0.904	0.016	0.923	935.06
1.03	0.904	-0.659	0.659	1017.21
1.008	0.859	0.689	-0.344	1064.89
1.041	0.895	-1.21	0.792	933.08
0	0.816	-0.599	0.438	935.7
2.595	0.368	-0.619	-0.957	637.18
2.521	0.368	-0.199	-1.223	641.87
0	0.569	0.234	-0.268	984.05
0	0.627	-1.165	-0.756	1067.85
0	0.836	-1.073	-1.09	1190.76
0	0.689	0.492	-1.476	1148.89
0	0.635	-1.078	-0.062	1023.9
8.858	1.007	-1.151	-1.057	790.56
8.858	1.007	0.564	-1.034	790.56
4.79	1.219	1.247	-0.491	411.12
4.566	1.306	0.36	0.286	617.31
4.566	1.306	1.155	0.211	617.31
1.205	0.639	0.289	-1.446	578.32
2.799	0.568	0.341	-1.181	466.86
0	0.859	-0.671	-0.421	418.06
0	0.859	-0.546	-0.453	391.13
0	0.859	0.586	-0.897	419.44
0	0.859	-1.213	-0.847	373.31
1.403	0.704	0.869	-0.714	371.34
1.101	0.764	-0.111	1.061	1173.4
8.537	0.913	0	1.366	1368.19
1.083	0.693	-0.38	0.787	1211.31
2.388	0.784	-0.409	0.808	1130.36
1.129	0.495	-0.042	-0.274	1158.07
4.043	0.316	-1.061	-0.677	1047.46
2.345	0.387	0.33	-0.413	1099.85
2.239	0.446	-1.428	-0.078	1152.03
5.291	0.413	0.476	0.098	1148.89
1.008	0.859	1.312	2.919	737.04
2.245	1.091	-0.104	-0.391	853.89
1.022	0.941	0.487	-0.344	996.27
0	0.643	1.121	-0.295	978.68
0	0.569	-2.322	0.119	896.07
0	0.671	-1.315	-0.536	617.55
0	0.596	0.717	0.735	893.66

1.255	0.815	-0.767	-1.783	1404.54
0	0.784	-2.322	-3.499	670.77
4.631	0.434	-1.006	0.666	570.27
0	0.776	-0.654	0.867	393.5
1.061	0.648	2.369	-2.369	737.18
3.699	0.796	0.289	-0.319	844.61
3.67	0.822	2.044	1.453	840.66
2.258	0.694	0.545	0.971	848.95
5.222	0.64	1.095	-0.34	1091.71
5.204	0.547	-0.235	-0.023	1122.66
2.25	0.43	1.208	-1.47	1094.83
1.033	0.469	-0.474	-1.885	1111.6
1.029	0.894	0.534	1.47	759.63
3.831	0.311	0.665	0.329	969.63
3.831	0.311	0.616	0.414	969.63
2.441	0.404	0.438	-1.159	410.65
3.707	0.348	0.248	-0.583	1012.27
0	0.754	0.163	-1.582	811.77
2.865	1.27	0.254	-0.015	962.57
2.997	1.27	0.806	-0.03	395.69
4.611	1.463	-0.353	1.111	845.01
2.909	1.227	1.448	0.663	400.97
2.883	1.392	-0.512	1.346	928.87
4.566	1.383	0.455	1.511	874.93
6.755	1.444	0.597	1.436	928.87
6.374	1.48	-0.55	1.626	928.87
13.882	2.245	1.851	-0.016	653.89
3.009	1.193	-0.878	-1.838	593.53
2.928	1.244	0.431	-2.881	596.22
6.488	1.806	0.987	-2.247	363.55
0	0.622	-0.924	1.212	423.45
0	0.776	0.35	-3.037	406.4
0	0.693	-0.173	-0.643	414.61
0	0.73	1.267	0.644	438.06
0	0.577	1.508	-0.665	475.98
0	0.586	-0.484	1.826	409.29
2.995	0.275	-1.341	1.425	537.7
10.556	2.506	-0.966	-0.071	792.04
3.654	0.243	1.267	-1.312	299.59
6.368	2.093	-1.342	-0.99	778.22
1.63	0.343	-0.543	-0.634	301.86
0	0.693	0.498	0	514.23
0	1.022	0.972	-0.972	77.78
0	0.582	1.904	0.549	182.49

0	0.693	-0.434	-1.236	123.36
5.76	1.551	-0.59	0.711	337.81
3.634	1.329	0.283	1.24	290.55
3.419	1.483	-0.176	1.038	399.43
3.074	1.27	-0.302	-0.397	310.8
0	0.582	0.458	0.196	454.32
0	0.616	0.023	0.158	194.08
0	0.738	-1.443	-0.619	425.87
1.311	0.951	1.12	-1.211	330.16
1.433	0.34	0.626	-0.598	359.64
0	0.622	-0.315	-2.331	294.89
3.581	1.061	-1.323	1.743	295.89
0	0.824	1.403	-0.226	298.69
0	0.527	-0.229	-0.788	257.09
3.891	1.609	0.581	-1.024	256.14
1.792	1.329	1.411	-0.968	225.13
1.851	1.445	0.064	-1.207	225.13
4.684	2.115	-0.945	-0.875	230.3
12.42	1.406	1.664	-0.951	369.36
0	0.693	0.949	-0.206	555.72
0	0.693	0.454	-0.124	555.72
1.871	0.799	0.116	1.196	457.02
12.42	2.225	-2.412	-1.447	212.17
0	0.368	0.394	-0.789	102.82
13.605	3.907	-0.307	-0.921	160.86
3.332	2.833	-1.203	-0.573	67.39
0	1.112	-0.495	-1.626	152.58
0	0.646	0.919	-1.898	152.58
1.725	0.973	-2.385	0.085	1107.82
1.967	0.85	0.081	-0.403	1079.92
0	0.99	-0.146	-1.254	679.69
1.451	0.641	-2.185	0.409	248.76
3.497	0.49	0.973	0.655	774.14
2.784	1.189	-1.034	-1.006	706.72
1.512	0.393	1.373	1.545	850.66
6.036	1.954	0.922	-0.042	248.62
0	0.941	0.718	-0.803	197.04
0	1.022	0.696	0.437	153.88
2.632	1.492	-0.6	1.134	127.09
0	1.329	-0.849	1.62	124.55
0	1.022	0.55	-0.55	131
8.57	1.078	-1.779	-0.843	846.38
1.527	1.14	0.801	1.529	380.41
4.977	0.223	0.849	-0.283	1072.87

2.867	0.294	0.892	-0.184	1112.23
0	0.582	-0.272	-1.752	148.41
0	0.892	0.214	1.562	246.57
4.06	0.643	1.143	0.445	79.29
1.76	1.236	0.215	1.2	385.84
8.351	0.061	-1.412	-1.123	192.82
2.158	1.609	-1.215	-1.562	217.88
0	0.859	1.058	0.102	161.59
0	0.665	1.292	0.076	299.48
3.565	0.876	-0.728	-0.879	526.45
1.402	0.446	-0.385	-1.034	302.22
0	0.866	0.195	0.693	314.76
2.515	0.18	0.196	0.326	119.24
0	1.609	0.296	-2.166	96.58
3.233	2.419	0.895	0.296	74.56
3.233	2.419	-0.296	0.296	74.56
2.808	1.518	-1.159	-0.876	124.58
3.136	1.447	-0.421	-1.638	133.62
0	1.609	-1.214	-0.296	191.97
1.871	1.402	-0.857	-1.755	316.07
0	1.22	-	-	1014.96
0	0.668	1.257	-1.767	582.28
0	0.593	-0.759	-1.499	655
5.041	1.222	0.204	-2.865	412.7
0	0.656	1.661	-0.164	288.58
8.161	2.179	-0.359	-0.222	239.51
7.501	1.108	-0.332	-0.405	102.63
0	0.732	-1.507	0.195	962.04
21.585	4.657	-0.493	-2.063	287.58
8.457	1.944	1.745	-0.349	905.35
1.235	0.465	1.817	1.225	517.07
0	0.804	1.079	-0.441	607.94
0	0.556	0.73	-1.541	506.27
1.278	0.645	-0.279	-0.782	477.71
0	0.538	-0.582	0.095	426.92
0	0.616	0.052	0.156	395.43
5.748	1.09	0.238	-0.873	404.97
2.424	0.905	0.198	0.044	732.31
2.815	1.121	-0.702	-1.027	337.54
9.968	0.332	-0.672	-1.457	340.84
1.356	0.384	0.265	2.186	328.08
1.685	1.23	-0.119	-0.157	305.69
0	0.368	-1.174	-1.174	592.26
0	0.625	0.197	0.394	374.05

1.86	0.719	0.634	1.198	120.61
0	0.487	1.617	0.809	1166.99
4.442	0.61	0.612	1.4	632.42
1.564	0.412	-0.305	-0.961	284.82
0	0.446	1.325	0.645	751.88
0	0.495	-1.439	-0.521	270.52
1.86	0.719	-1.339	0.07	232.36
1.708	0.358	-0.919	1.626	264.18
4.506	0.16	-0.895	-0.195	144.37
0	0.941	-0.902	0.434	136.31
1.606	1.127	-1.093	-0.585	688.92
10.916	0.838	1.102	0.768	1110.52
0	0.829	0.293	-0.713	226.62
0	0.711	-1.343	0.234	554.63
1.455	0.399	0.938	-0.458	518.46
3.524	0.529	0.406	-0.579	488.73
4.31	1.196	-1.155	1.015	150.41
0	0.569	-0.801	0.946	512.7
0	0.673	-0.358	1.968	446.73
3.917	0.98	0.708	-1.293	242.04
5.76	0.499	-0.549	-1.565	637.81
2.747	0.368	-1.042	0.357	573.41
0	0.722	0.343	0.401	1118.73
2.963	0.899	0.186	1.619	409.29
2.963	0.899	-0.817	1.719	409.29
1.508	0.368	1.195	-0.02	150.62
0	0.656	1.114	0.201	206.57
1.792	0.714	0.138	0.138	165.17
0	0.836	-0.636	-0.858	183.17
0	0.693	0.391	0.528	443.56
0	0.678	0	0.8	507.26
0	0.804	2.243	1.952	507.53
6.862	1.305	-0.656	1.193	543.73
1.74	1.192	-0.263	1.445	323.77
0	0.941	0.718	1.371	149.84
1.871	0.754	-0.803	1.395	304.55
1.565	0.74	-0.919	1.051	343.81
1.74	0.991	0.739	-0.176	277.13
0	0.941	-0.765	0.398	467.49
0	0.476	1.012	-0.025	485.35
3.783	1.655	-2.491	-0.882	431.57
0	0.836	-1.835	0.204	565.53
0	0.892	0.239	0.413	289.65
0	0.801	-1.09	0.629	299.59

1.489	1.292	-0.701	-3.062	728.95
0	0.536	-0.757	-0.346	357.62
7.702	0.939	1.549	-1.077	967.13
0	0.61	-1.416	-0.528	188.83
0	0.495	0.33	1.211	879.09
0	0.706	1.89	-0.745	715.03
6.107	0.707	-0.252	0.344	638.62
6.629	1.479	0.985	1.159	433.13
1.549	1.274	0.23	-2.165	353.02
1.445	1.085	-0.477	0.653	334.36
0	0.6	-1.144	1.803	1073.7
1.433	1.085	-0.315	2.238	225.86
3.062	1.341	-0.289	0.776	247.4
6.017	1.965	0.429	-0.898	287.84
0	0.941	1.185	-0.478	397.48
0	0.602	-0.602	0.67	585.38
0	0.769	0.952	-1.309	412.84
17.865	2.965	-0.736	-0.471	297.7
1.725	0.385	1.197	-0.725	1043.91
1.415	1.022	1.393	0.021	539.05
0	0.836	0.296	-0.257	539.05
3.473	0.51	0.17	-0.974	438.66
3.473	0.51	0.51	-0.18	438.66
3.682	0.223	0.082	-0.408	447.7
7.256	0.544	0.751	0.173	104.34
0	0.743	0.406	0.406	776.38
0	0.542	-0.753	-1.082	279.26
1.412	0.815	1.982	-1.741	590.07
1.779	1.222	-0.125	1.475	295.89
6.237	1.204	1.029	-2.325	889.66
0	0.665	0.251	-1.841	473.37
7.491	2.833	-0.827	1.623	165.3
5.124	1.22	0.725	-0.683	1268.74
0	0.95	-	-	2520.69
6.909	1.19	0.643	-0.44	1232.92
6.909	1.19	0.758	-0.44	1232.92
2.527	0.877	1.328	-0.68	1130.93
1.134	0.611	-0.742	-0.678	1095.22
0	0.586	1.323	-0.785	1074.18
3.809	0.346	-0.438	1.563	1119.7
3.809	0.346	0.759	1.563	1116.29
1.052	0.885	-0.276	1.603	845.61
1.114	0.996	-0.01	0.734	821.21
0	0.719	0.85	-1.318	1053.46

0	0.758	-0.23	-0.968	1080.73
1.117	0.794	-1.096	-1.208	996.21
3.917	0.953	-1.062	-1.713	1038.41
2.379	0.909	0.351	-1.734	903.41
2.34	0.913	-0.019	-1.148	861.73
0	0.784	-0.105	-1.926	725.85
0	0.641	-0.198	-0.293	1028.86
0	0.631	1.083	-0.443	986.91
1.032	0.516	0.556	0.149	781.91
0.97	0.536	-1.31	-0.268	1106.92
4.735	1.185	-0.48	-0.517	1081.48
0.889	0.88	-0.237	-1.264	1322.49
0.889	0.88	-1.816	-1.187	1373.38
0.874	0.869	-0.684	-0.628	1487.1
2.6	0.327	-0.082	1.201	1894.62
0	0.663	0.193	-0.672	924.39
1.085	0.957	0.346	-1.056	779.47
0	0.624	0.366	-4.855	615.59
7.696	1.444	-3.486	-3.994	701.92
7.342	1.233	-4.078	-5.29	729.87
0	0.631	-0.724	-0.949	378.51
2.432	1.091	0.651	-0.114	714.99
4.058	1.023	0.068	-0.3	805.85
1.064	0.936	0.678	-0.336	803.66
0	0.719	-0.747	-0.582	882.75
2.178	0.898	-0.094	-0.558	924.92
2.178	0.898	0.079	-0.154	1009.55
2.12	0.878	0.045	-1.702	1009.55
0	0.69	0.11	0.061	1089.62
0	0.7	-0.103	-1.555	1242.47
0	0.617	0.114	0.203	1217
11.963	0.661	1.109	1.117	1062.03
11.963	0.661	1.381	0.956	1063.03
7.296	0.475	-1.03	0.59	1060.03
3.765	0.436	-0.148	0.722	1009.17
6.954	0.899	3.027	-2.181	1367.19
7.487	1.044	-1.533	-2.83	1194.06
5.557	1.074	-0.626	-2.092	888.66
3.855	0.931	-0.098	-2.005	915.7
3.854	1.058	-1.541	-2.313	915.7
0	0.797	-0.634	-0.252	1041.95
1.02	0.982	-0.236	-0.555	1047.17
0	0.719	1.595	-1.579	1062.03
0	0.719	-0.132	-1.548	1062.03

5.563	1.18	0.263	1.977	932.6
11.534	0.835	0.586	0.297	1005.53
11.534	0.835	0.038	0.281	1014.57
11.534	0.835	1.194	0.251	1014.57
13.594	1.171	0.94	1.606	478.47
14.447	0.852	-0.458	0.072	932.6
14.447	0.852	-0.893	-0.024	932.6
12.339	0.861	1.978	-0.28	1013.57
12.38	0.685	0.14	-1.109	1019.27
7.361	0.14	0.808	-0.828	505.69
7.361	0.14	-1.05	-0.687	505.69
9.925	0.117	0.784	-0.123	509.8
13.435	0.092	1.242	-0.379	976.66
0	0.722	-0.46	-0.443	752.97
0	0.693	-0.319	-0.368	752.94
2.627	1.274	-0.408	0.124	545.8
0	0.656	-0.597	-0.669	471.52
0	0.709	-0.361	-2.384	2149.76
0	0.811	0.502	0.519	2801.95
9.7	0.823	0.322	0.956	82.71
0	0.536	-1.863	1.268	617.9
2.995	1.274	-2.57	-0.781	435.54
4.738	1.473	-1.524	-0.14	472.53
1.19	1.048	-2.56	0.321	675.52
2.517	1.182	-1.367	-0.725	636.16
3.96	1.262	-1.48	-0.798	636.16
3.96	1.262	-0.35	-0.26	636.16
6.022	1.116	1.2	-0.085	998.67
0	0.538	-0.823	0.623	482.07
1.452	1.215	1.133	-1.221	345.73
0	0.569	-1.444	-0.398	410.65
0	0.495	0.765	-0.395	394.33
0	0.551	-1.241	0.105	218.27
0	0.765	-0.453	0.429	346.34
7.16	0.965	0.56	-1.419	968.16
9.379	1.107	-1.767	-0.964	924.92
9.379	1.107	0.64	-0.872	883.75
5.343	0.871	1.109	-0.46	953.92
7.277	1.022	-0.692	0.101	830.66
0	0.776	-0.707	0.427	819.66
0	0.275	-1.386	-0.416	1997.85
0	0.809	0.043	-0.114	865.76
0	0.678	0.731	-0.514	805.85
1.004	0.544	0.555	-1.23	867.56

0	0.876	1.135	0.487	1415.93
0	0.662	0.286	1.444	919.66
0	0.616	1.277	1.521	908.42
3.679	0.773	-0.555	-0.743	1306.12
6.238	1.095	-1.003	-0.133	463.8
0.99	0.524	-0.038	0.22	1022.89
6.816	0.925	-0.494	0.04	790.57
6.772	2.215	1.243	0.586	250.09
0	1.688	-	-	1090.9
9.232	0.442	0.433	0.858	1056.21
9.731	0.266	0.171	-0.295	1103.89
12.147	0.506	-1.205	-0.998	1148.89
14.169	0.496	-1.866	-1.104	1148.89
12.493	0.52	0.213	-0.885	1064.89
12.755	0.674	-0.701	-0.77	1106.84
6.357	0.365	-0.64	0.485	823.77
11.459	0.718	0.557	0.535	907.32
4.037	0.751	0.934	1.645	899.35
7.438	0.825	-0.552	2.804	862.59
0	0.602	0.179	0.875	918.58
1.121	0.489	-0.755	-1.106	871.36
0	0.56	-0.561	-0.952	838.29
2.488	0.641	0.402	-1.68	996.21
5.587	0.84	-0.087	-1.995	1038.41
3.933	0.845	1.524	-2.082	1122.12
5.759	1.025	-1.918	-2.059	1118.7
0	0.646	1.041	-0.429	153.54
0	0.527	0.922	0.198	212.35
4.224	0.868	0.114	0.751	2290.62
1.343	1.126	-0.248	0.096	2141.57
10	2.776	0.406	0.406	98.36
3.979	1.447	-0.731	0.731	166.51
0	1.179	-0.736	0.736	124.27
0	1.493	-0.567	-0.567	754.75
0	1.371	-1.262	-0.332	706.45
0	1.022	0.555	0.377	211.07
0	1.061	0.296	0.296	78.92
0	1.27	-	-	383.2
2.429	0.654	0.126	-0.282	901.39
5.738	0.985	-1.479	0.556	900.39
8.297	1.243	-0.2	-1.795	349.86
7.963	0.823	-0.181	1.322	1051.33
8.8	1.522	-1.431	-1.553	340.96
7.826	0.93	1.291	1.668	939.05

7.625	0.94	1.969	1.705	930.66
3.933	1.053	0.273	1.818	948.09
1.101	1.038	-0.407	1.63	945.19
2.084	1.096	-0.498	-2.339	1402.9
4.883	1.296	-0.533	-1.967	1529.71
4.883	1.296	2.178	-1.941	1483.46
3.257	1.13	0.535	-0.739	1469.75
3.767	1.272	-1.902	1.109	627.44
0.923	0.822	-0.454	0.429	1396.76
5.365	1.251	-1.189	1.44	631.18
0	0.723	0.231	0.521	1274.8
0	0.649	2.015	1.1	1214.82
0	0.649	1.889	0.871	1214.82
0	0.787	2.822	2.583	1041.17
2.199	0.76	-0.046	0.231	139.76
2.218	1.508	1.423	0.58	118.89
0	0.941	-1.141	0.465	206.98
1.952	1.329	2.295	1.077	206.98
1.922	1.329	0.124	0.784	187.37
1.707	0.368	0.785	1.467	384.84
0	0.941	-1.007	-1.082	144.79
1.421	0.426	0.053	0.551	285.72
1.377	0.853	0.262	0.997	310.97
10.209	0.99	0.174	0.521	368.7
0	0.313	1.342	0.324	146.76
4.752	1.506	-2.098	1.317	190.34
1.657	1.179	0.083	0.139	184.07
0	0.639	-1.249	0.739	591.43
0	0.616	-0.588	0.543	222.67
3.771	1.288	0.836	-0.246	174.95
3.798	0.877	-1.337	0.915	745.09
0	0.512	-0.751	-0.347	937.5
1.524	0.368	-0.595	0.177	330.75
1.524	0.368	1.142	-0.145	330.75
0	0.541	-0.586	-0.053	307.72
1.657	1.179	-1.25	0.25	163.07
1.48	0.784	0.811	1.6	239.91
0	0.602	1.113	-2.322	217.27
0	1.179	-	-	833.04
1.412	0.446	0.936	2.031	239.66
3.332	2.303	0.322	0.684	69.71
2.363	1.675	-0.533	0.667	152.87
2.363	1.675	0.533	0.4	152.87
0	0.693	0.336	-1.453	136.39

0	1.179	-	-	336.83
0	0.892	-	-	381.66
0	0.892	-	-	381.66
0	1.022	-	-	161.16
0	0.368	-0.736	0.736	163.52
5.792	0.971	1.416	-0.607	740.41
8.557	1.16	-1.549	-1.004	644.36
3.368	1.609	0.613	0.547	236.86
0	0.814	0.423	-1.164	195.6
0	0.446	1.123	-0.76	229.55
0	0.631	-0.358	-1.371	424.76
0	0.569	0.211	0.07	179.65
0	0.446	-0.858	1.679	144.79
1.342	0.666	-1.262	-0.123	371.34
0	0.733	-0.585	-1.093	286.85
0	0.733	0.359	-0.736	295.89
3.164	0.84	-0.554	1.292	416.55
3.053	0.883	-0.406	1.444	407.5
1.643	0.399	1.388	-0.871	156.69
1.377	0.908	-1.111	1.002	333.28
0	0.804	0.02	-1.443	340.03
1.657	0.677	-1.617	0.108	212.85
0	0.892	0.213	-0.213	837.65
0	0.85	-0.318	-0.056	336.23
10.665	1.649	-0.406	1.574	265.6
5.78	1.518	0.336	-0.053	158.62
1.26	0.43	-0.317	-2.057	580.59
1.26	0.43	-1.091	-2.14	580.59
0	0.593	-0.437	0.379	217.14
0	0.61	-0.122	-0.585	179.29
0	0.892	-0.731	0.212	305.05
0	0.784	0.492	-0.098	305.05
1.476	1.136	0.42	-2.647	875.58
0	0.654	-0.333	0.454	207.13
5.639	1.082	0.373	1.937	780.76
1.76	0.293	-0.553	-0.728	319.39
0	1.112	-0.83	-0.146	226.34
5.904	0.959	-2.305	1.237	432.41
2.659	0.368	-0.101	0.96	505.36
1.471	1.022	-0.489	-0.283	331.67
0	0.773	1.779	-0.647	200.85
0	0.804	-1.18	-0.678	513.43
1.583	1.019	-1.431	0.075	265.45
0	0.852	0.518	-1.617	868.61

4.419	0.876	0.195	-0.039	457.66
0	0.941	-0.083	-1.411	120.12
1.045	0.859	-2.717	-1.218	601.06
1.133	0.46	0.714	-0.134	813.72
0	0.598	0.238	-2.161	869.82
0.938	0.859	-0.873	-2.074	988.38
0.978	0.527	-1.631	-3.929	791.83
2.325	0.589	-0.532	-3.197	789.81
1.065	0.502	-1.255	-3.157	852.81
3.567	0.673	-0.032	-3.637	937.83
0	0.641	-1.68	-3.52	894.94
1.022	0.922	-1.205	-1.124	676.15
0	2.303	-	-	247.58
0	0.611	0.585	0.475	858.21
1.199	0.902	-0.723	-0.306	487.12
4.978	0.2	-0.585	-1.299	559.45
1.218	1.051	0.623	1.614	955.58
1.174	0.941	-1.736	0.849	955.58
6.825	2.048	-0.142	1.33	284.59
3.319	0.591	-1.461	0.472	253.09
1.377	0.791	-0.755	0.424	688.92
13.496	2.833	-1.163	-0.49	449.22
13.496	2.833	-0.602	-0.49	449.22
13.852	2.82	-0.542	0.04	448.1
16.819	2.814	-0.463	-0.082	448.1
1.316	1.127	-0.298	0.468	573.55
3.828	0.891	0.756	1.859	986.91
0	0.748	-0.644	1.956	507.48
1.226	0.489	-1.312	1.181	594.36
0	0.914	-0.983	-1.014	495.98
9.064	2.274	-1.037	-0.752	350.03
7.806	0.707	-0.384	-0.23	478.03
3.68	2.494	0.55	1.754	121.04
0	0.409	-0.46	0	301.82
1.412	1.112	0.889	0.929	446.07
0	0.512	-0.072	-0.216	290.49
3.211	0.61	-0.103	-1.879	255.66
0	0.832	1.087	1.54	187.24
1.392	0.458	0.048	0.048	899.75
0	0.883	-0.894	-1.193	379.71
6.397	2.073	0.498	0.354	259.67
2.961	1.329	0	0.206	483.5
5.153	1.688	-0.347	0.809	587.99
4.359	0.169	1.288	-0.4	326.69

0	0.446	-0.387	0.361	217.39
0	1.329	-1.813	0.143	213.93
0	1.329	-0.583	0.387	213.93
0	0.693	-1.447	1.036	221.15
0	0.693	-0.741	-0.633	221.15
0	0.693	-1.866	-1.036	221.15
0	0.693	-0.633	-0.365	111.16
1	2.093	-	-	379.31
1	3.056	-	-	379.31
1	2.303	-	-	405.31
0	1.609	-1.368	-0.922	136.63
2.307	0.197	0.566	-0.68	338.22
0	1.085	0.106	-0.106	320.36
3.949	0.552	1.908	0.954	259.47
1.619	0.33	0.794	1.122	472.11
1.43	0.654	-0.814	0.282	190.34
0	0.495	-0.634	1.604	393.81
11.139	2.418	-1.283	0.888	420
0	0.991	0.406	0.406	92.71
3.979	2.225	0.72	0.72	92.71
0	1.179	0.573	0.248	87.97
2.808	0.959	0.248	0.573	87.97
0	0.223	-0.922	-0.421	178.62
2.808	0.707	-0.361	0	171.6
2.808	0.707	0.361	0	142.83
2.808	0.707	1.652	0.361	142.83
2.808	0.707	-0.876	1.307	142.83
0	0.799	-0.322	0.956	286.08
0	0.307	-1.741	1.393	323.63
0	0.777	1.292	-1.975	324.35
4.123	0.991	-0.109	1.412	277.82
0	0.569	-1.044	0.678	942.39
0	0.76	-0.774	0.792	1028.86
1.243	1.127	-0.609	3.205	754.42
13.545	1.587	0.083	-0.183	774.2
7.144	2.387	-1.139	0.892	524.53
9.425	3.352	1.676	-0.394	152
0	0.283	-2.037	1.246	127.08
0	0.223	-1.134	1.239	127.08
2.363	0.169	-0.839	-0.194	137.59
0	0.693	-1.356	0.065	135.65
1.957	0.283	-0.241	-0.818	280.52
2.003	0.223	1.466	0.133	245.52
8.471	1.363	-0.873	-0.119	675.6

0	0.693	-	-	341.31
0	0.368	0.761	0.085	397.06
4.2	1.863	-0.601	-0.067	251.54
6.186	0.45	1.232	-1.068	338.11
0	2.737	-	-	880.12
0	0.593	0.146	2.068	230.83
0	0.368	-0.567	-2.331	554.61
1.674	0.715	3.055	1.606	236.66
0	0.96	0.633	0.961	301.86
1.573	1.161	1.197	0.588	341.81
1.527	1.061	0.587	2.179	299.59
1.527	1.061	-1.76	2.179	299.59
0	0.693	-0.373	1.439	377.76
0	0.634	0.405	-0.257	391.86
0	0.627	1.022	0.764	692.46
7.205	0.397	-0.836	1.583	437.63
0	0.693	1.423	-1.423	351.61
3.31	0.105	-0.898	0.48	324.92
6.99	2.812	0.296	0.296	87.97
6.99	2.812	0.546	0.296	87.97
2.158	1.501	-1.448	-0.556	336.6
0	1.034	0.322	0.322	130.22
0	1.034	-1.517	0.322	130.22
3.31	2.303	-0.72	0	130.62
0	1.034	0.322	1.517	92.71
3.522	3.056	1.268	-0.851	175.24
3.522	3.056	-0.336	-0.47	175.24
11.553	3.905	0.101	0.377	242.87
14.564	4.169	0.201	0.068	242.87
1.603	0.412	-0.56	-1.173	453.17
4.419	1.184	0.272	0.195	192.63
4.738	1.144	-0.701	0.454	234.79
1.922	1.329	-1.691	-2.186	195.72
1.871	0.883	0.887	-0.634	460.85
0	0.941	-0.796	-1.733	162.58
0	0.941	-1.286	-1.733	162.58
0	0.619	0.421	-1.545	237.17
0	0.693	-1.528	-0.566	158
0	0.804	-0.8	-0.231	161.26
2.276	0.799	1.092	0.696	166.88
2.276	0.799	-0.437	0.533	166.88
2.522	0.877	0.761	0.085	361.96
6.154	1.872	-0.38	1.214	166.88
10.964	1.85	0.143	1.203	169.78

13.222	3.225	0.729	0.322	172.39
18.195	3.895	-0.466	-0.143	217.39
18.195	3.895	-1.749	-0.466	256.07
4.123	0.946	-1.669	0	498.54
4.415	1.304	0.579	-0.501	499.82
1.922	1.061	2.932	-0.951	470.31
1.871	0.799	-0.81	0.193	430.85
0	0.693	0.158	0.896	110.89
2.276	0.799	-1.092	-1.092	166.88
4.598	1.221	0.618	-1.766	327.12
4.359	0.169	-0.044	0.133	360.12
2.062	0.223	-0.244	-1.122	310.36
2.392	0.175	0.241	-0.529	333.4
0	0.593	0.231	0.54	387.31
0	1.802	0.694	0.386	344.55
5.569	1.759	-0.386	1.365	340.69
6.154	1.426	-0.689	1	294.82
8.616	0.859	0.965	-1.365	340.69
8.616	0.859	-1.109	-1.222	294.84
1.707	1.179	0.429	0.033	402.81
3.821	0.49	1.469	0.601	498.54
3.624	0.925	1.484	1.021	362.17
0	0.986	-0.116	0.27	322.02
0	0.551	-0.849	-0.354	121.24
0	0.551	0.457	-0.919	121.24
0	1.022	-1.528	0.324	165.72
8.806	1.218	-1.593	-0.21	299.87
3.917	0.169	0.197	0.153	430.84
1.82	0.264	-1.246	0.582	576.57
0	1.426	-0.623	-1.246	121.24
0	1.609	-0.922	-1.495	170.51
8.193	0.061	-1.2	-0.4	391.08
1.541	0.409	-0.018	1.716	947.96
3.497	0.652	0.83	2.232	1064.96
1.242	0.701	-0.663	1.394	494.92
0	0.693	1.383	0.395	447.1
4.913	0.235	1.434	-2.735	511.77
1.617	1.022	0.588	0.196	299.59
1.674	1.27	-0.769	-0.339	402.13
0	0.693	0.235	-0.169	893.62
0	0.593	-0.666	-0.399	893.62
1.183	0.685	1.012	-0.443	889.96
0	0.77	-0.48	1.546	1003.77
0	0.646	0.589	2.062	942.76

0	0.776	0.365	1.964	915.43
0	0.703	-0.7	0.819	1039.87
1.264	0.655	-2.431	0.123	1120.81
0	0.693	-0.617	-1.298	1207.12
0	0.756	0.49	-1.823	1213.1
1.204	0.957	-2.17	1.15	1144.82
0	0.693	-2.702	1.044	1180.18
3.645	1.609	0.069	-0.115	751.62
3.581	1.431	0.247	-0.292	743.22
1.483	0.368	-0.285	-0.724	654.36
0	0.527	0.373	-0.811	654.36
1.515	1.022	-0.872	-0.051	485.6
0	0.61	1.136	0.146	648.53
0	0.657	-0.952	0.694	530.65
0	0.836	0.462	0.245	442.73
6.576	1.802	0.925	-1.016	261.08
9.412	2.038	-0.59	0.197	305.04
1.527	0.883	0.859	0.859	474.36
0	0.558	1.092	0.139	650.82
0	0.558	-0.06	0.337	692.35
2.835	0.34	0.117	1.321	851.96
2.875	0.457	-0.214	-0.071	936.44
2.944	0.635	1.872	0.201	855.77
2.883	1.156	1.692	-0.42	1026.37
4.533	1.014	-0.869	0.147	1026.37
2.883	1.156	0.582	-0.203	1072.86
4.268	0.984	0.29	0.637	1060.31
1.112	0.925	-0.779	0.819	1205.17
2.448	0.392	-0.228	0.03	1156.18
3.975	0.56	-0.71	0.312	822.16
3.933	0.81	0.285	-0.174	1080.73
3.933	0.845	-0.994	-0.596	1103.12
3.855	0.82	0.458	-0.978	1143.66
3.878	0.9	-2.064	-0.63	1205.31
7.843	1.104	-0.124	-0.485	1130.36
7.843	1.104	-0.808	-0.314	1169.66
7.843	1.104	-0.029	-0.352	1169.66
8.333	1.03	-1.295	0.246	1130.36
4.04	0.627	-2.276	1.045	1003.77
4.116	0.542	-1.061	0.091	1036.46
1.279	0.473	-1.861	-2.133	938.59
3.029	0.428	-2.176	-1.957	905.74
10.392	2.925	-0.22	0.464	770.5
12.942	4.099	1.082	1.858	394.33

12.74	3.912	-1.291	1.766	353.33
12.436	3.726	0.538	1.5	353.33
12.436	3.726	-0.142	1.217	312.59
12.352	3.706	-0.161	1.065	271.49
12.352	3.706	-1.259	1.065	271.49
11.781	3.521	0.214	0.521	268.06
2.447	1.555	1.371	0.457	121.24
6.113	1.447	0.778	-0.212	121.24
10.227	1.414	-0.071	-1.061	121.24
0	0.804	-0.533	0.808	632.08
0	0.733	0.245	-0.736	249.89
0	0.921	-0.113	0.566	239.24
0	0.551	1.11	-0.979	110.24
0	0.666	0.317	-0.238	393.31
4.193	1.567	-1.057	-2.397	232.36
6.779	2.067	-0.298	-0.835	304.59
7.546	2.584	-0.1	-1.57	222.36
3.976	1.299	-0.346	1.669	245.66
10.432	0.088	-0.298	0.179	1566.46
1.871	0.677	-0.768	0.117	184.04
3.312	1.22	-0.646	-0.043	387.41
3.565	0.912	0.879	0.477	350.45
1.441	1.022	1.137	-0.255	429.95
0	0.914	-1.092	-1.376	632.87
1.323	0.576	1.268	-0.548	920.59
0	0.582	-2.006	-0.274	924.59
1.603	1.085	0.311	-1.104	180
10.588	3.047	0.485	-0.377	241.85
13.359	1.16	0.593	-0.593	242.85
3.78	1.565	0.534	0.127	180.15
0	0.804	0.352	0.141	188.65
0	0.495	0.112	0.56	372.79
0	1.022	-0.533	0.533	166.88
0	1.022	-0.817	0	166.88
19.956	2.775	1.835	0	232.83
2.251	0.19	0.091	-0.543	324.24
0	1.112	-0.495	0.231	117.41
0	1.609	-	-	141.67
0	1.022	-	-	154.16
3.68	1.108	-0.742	0.742	131.22
0	1.179	-	-	282.83
0	0.941	0.067	-0.762	272.62
0	1.609	-	-	292.27
0	1.609	-	-	292.27

0	0.223	-	-	85.71
2.757	0.132	-0.694	-0.54	111.55
0	0.283	-1.256	0.533	153.88
7.806	1.431	-0.314	0.117	633.79
4.956	0.967	-0.016	-1.88	666.29
4.084	1.069	0.092	0.153	489.49
1.562	0.368	0.024	0.935	303.69
41.491	3.475	0.238	2.437	688.17
0	0.54	-1.325	1.121	1263.9
4.246	1.087	-5.075	-0.329	877.38
2.757	0.132	-0.849	-2.237	109.55
1.632	0.293	-1.061	1.061	422.09
0	0.627	0	0.094	423.09
0	0.711	1.012	-0.123	392.26
0	0.856	-0.047	0.282	392.26
0	0.856	-0.376	0.282	389.05
0	0.856	0.423	0.282	392.26
10.77	0.442	-0.917	-0.194	586.22
1.493	0.409	-0.728	-0.8	696.76
0	0.976	1.379	1.271	923.01
5.643	0.1	0.041	-0.689	649.9
0	0.941	0.702	-0.421	140.01
0	0.368	0.839	0.194	169.63
1.808	0.238	-1.116	-1.182	367.82
0	0.941	2.003	1.135	378.8
5.138	1.4	0.85	-1.617	532.82
7.521	0.082	-1.362	-0.041	418.08
8.383	0.42	-0.423	-1.376	422.24
6.154	1.426	-1.788	-1.461	259.78
0	1.179	-2.141	0.831	259.78
0	1.402	-1.855	0.271	301.88
0	1.402	-1.991	0.212	301.88
0	0.693	-1.792	1.027	252.87
0	0.693	-1.936	1.027	249.82
2.12	1.352	-0.249	-1.149	299.59
6.825	0.532	-1.953	0.255	779.53
2.919	1.138	-2.166	-0.318	452.5
3.965	1.714	-1.783	0.425	353.33
0	0.602	-0.506	-0.584	123.37
0	0.921	-0.906	-1.473	200.53
0	0.551	0.553	-1.457	200.53
0	0.693	-1.365	-1.739	340.69
6.99	0.039	0.633	-0.365	136.29
16.154	1.39	0.896	-0.597	129.24

16.154	1.39	0.678	-0.597	129.24
7.605	2.584	-0.187	-0.485	229.79
0	0.836	0.317	0.246	410.95
4.619	2.179	-0.568	-0.234	271.49
0	0.619	-1.054	0.386	530.65
1.757	1.23	0.917	-0.25	268.06
1.796	0.33	-2.37	-2.37	385.66
5.969	1.981	-1.277	0.766	370.54
16.244	2.523	0.028	-0.802	172.17
0	0.693	0.406	0.406	140.04
0	0.693	0.406	0.406	100.38
0	0.693	0.988	-0.406	98.17
0	0.693	0.406	-0.406	98.17
0	0.693	0.406	-1.537	98.17
0	0.693	-0.406	-1.537	98.17
0	1.23	0.382	-0.895	307.08
0	1.179	-1.134	0.143	256.07
0	0.368	1.134	0.717	120.8
0	0.941	-1.408	-1.098	211.07
0	0.73	1.28	-0.289	249.08
0	0.437	-0.685	1.001	160.24
2.363	1.609	-0.778	0.778	93.37
0	1.329	-0.849	0.694	93.37
2.574	1.11	-0.327	2.239	829.41
2.218	0.18	-0.553	0.151	145.67
0	1.022	0.231	-2.143	289.17
2.216	1.432	-0.429	-0.674	155.72
3.876	0.929	1.602	-0.025	632.18
2.046	0.223	-1.511	-0.037	173.63
7.384	0.086	-0.176	-0.106	310.95
0	0.914	-0.503	-0.551	545.76
0	0.76	0.289	-0.725	418.08
3.114	1.235	0.182	2.635	370.18
6.909	1.387	-0.028	-3.073	537.7
1.302	0.877	0.241	-0.354	511.86
1.255	0.434	-0.659	-0.054	1529.94
2.294	0.435	1.435	-1.843	680.07
0	0.653	0.789	-1.759	505.42
4.161	0.367	-0.178	1.853	1577.52
1.419	0.437	-0.586	-0.628	676.06
17.148	0.088	-0.488	-0.203	4663.68
4.4	0.595	-0.234	-0.973	232.44
4.4	0.595	-1.169	-0.895	232.36
0	0.446	-1.022	-0.337	319.31

0	0.693	0.692	0.692	452.17
2.835	0.34	-1.204	-1.556	678.5
2.158	1.19	0.705	0.922	150.43
0	0.616	0.835	1.377	212.08
1.423	0.731	0.134	1.088	284.03
0	0.616	0.333	0.999	258.66
0	0.573	-0.95	1.273	169.7
0	0.859	-0.112	-0.292	261.09
0	0.77	-0.359	1.12	253.87
1	1.329 -	-		247.58
0	1.371	0.566	0.566	86.61
0	0.595	0.747	0.747	235.03
0	0.69 -	-		147.67
0	0.693 -	-		147.67
0	1.022 -	-		203.16
0	1.022 -	-		203.16
0	1.402	-0.231	-1.62	219.59
0	3.258 -	-		194.16
0	1.609 -	-		130.67
0	1.179 -	-		93.5
0	1.609 -	-		158.67
0	0.836	-0.212	0.318	197.82
0	0.646	0.674	0.551	149.72
0	0.495	-0.857	2.082	263.12
0	0.986	-0.619	0.536	193.37
1.648	0.654	1.323	0.092	343.85
1.707	1.179	0.171	0.102	235.8
0	0.644	-0.665	-1.197	509.35
3.567	1.445	-0.264	1.159	292.81
6.537	2.2	0.697	-1.458	714.94
1.378	1.038	0.801	1.335	279.61
0	0.693	1.708	-1.708	248.92
0.972	0.554	-1.397	0.371	985.55
1.145	0.449	-0.152	-0.172	754.36
6.479	0.413	0.121	0.362	614.36
0	0.559	0.931	0.264	1003.58
0	0.593	-0.117	0.535	859.56
3.772	0.914	0.18	1.142	1068.85
3.933	0.791	-0.312	-0.615	725.16
2.265	0.425	2.541	0.289	749.02
1.129	0.955	-0.471	1.035	625.22
4.3	0.431	-0.213	-2.393	938.27
2.659	0.368	0.278	-1.238	883.97
1.15	0.927	0.908	0.164	651.19

0	0.676	-0.74	0.28	685.36
0.986	0.54	-0.479	0.281	1097.92
0	0.776	-0.358	1.572	563.12
9.359	2.2	-1.907	-0.085	742.41
2.704	0.799	1.445	-0.239	472.55
8.396	0.162	-0.124	0.083	848.53
1.54	0.412	0.386	-0.026	338.67
7.825	2.279	-2.764	-1.138	626.96
7.61	2.179	-2.149	-1.905	629.5
9.664	1.691	-3.055	2.095	490.81
7.212	1.543	-2.884	1.741	449.22
4.707	1.068	-2.339	0.809	452.5
4.33	1.751	0.035	-1.085	166.44
2.447	1.555	-0.326	0.849	101.24
22.351	0.9	0.161	-1.304	676.31
0	0.573	-1.42	1.125	1062.91
5.49	0.739	0.539	1.407	264.43
1.76	0.537	-0.613	0.871	430.03
0	0.728	0.462	0.718	355.6
6.983	0.356	0.829	1.363	605.64
5.497	2.584	0.405	0.868	209.61
11.02	2.812	-0.214	1.745	272.62
0	0.73	1.054	1.157	286
0	0.787	0.238	0.475	217.36
0	0.941	-	-	542.6
1.657	1.179	1.139	0.639	210.07
0	0.693	-0.214	1.806	271.49
4.428	1.431	0.523	-2.435	416.78
0	0.737	-0.908	0.81	1128.5
0	0.797	0.511	1.043	1210.05
0.89	0.875	-0.662	1.208	1124.38
0	0.716	0.723	0.57	1459.75
2.029	1.084	0.073	0.332	1459.75
0	0.566	0.635	0.071	2100.77
6.483	0.727	-2.14	-1.76	799.42
4.763	0.392	-0.634	-2.821	802.78
0	0.648	0.378	-0.554	1493.18
4.389	0.98	0.75	0.41	1583.45
5.473	0.809	-0.682	-0.238	978.68
5.341	0.96	0.408	-0.807	1020.27
2.268	0.698	-1.34	-1.003	978.68
2.284	0.384	-0.32	-1.125	1042.03
2.169	0.446	-0.725	-0.969	939.6
0	0.789	0.242	1.117	679.89

0	0.703	-0.416	0.416	938.7
5.084	1.352	0.408	-0.619	337.16
3.568	1.362	-0.679	-0.498	288.67
0	1.022	0.817	-0.533	125.91
0	0.582	-0.725	1.081	850.6
3.461	0.375	0.923	1.472	1080.02
2.245	0.439	-0.444	1.786	1052.95
7.424	0.863	1.479	0.008	685.41
0	0.693	0.482	-0.172	626.99
1.524	1.101	-1.288	0.195	851.04
1.999	0.26	0.662	-0.35	141.71
0	1.981 -	-		167.16
0	2.303 -	-		70.57
0	0.668	2.259	1.241	604.67
2.398	0.223	0	0.597	129.24
2.398	0.223	0.896	0.597	129.24
0	0.368	0.289	0.929	127.09
0	0.446	-1.171	-0.047	153.01
0	0.646	1.473	-0.295	205.71
2.271	0.16	-0.927	-0.537	236.34
5.237	0.105	-1.356	0.054	236.34
0	0.934	-0.69	2.07	158
4.32	1.506	-1.021	-1.021	296.9
3.407	1.402	-3.503	-1.98	298.86
6.437	1.735	-0.356	0.739	338.11
7.61	1.085	-1.151	0.969	275.18
2.363	0.744	0.933	0.267	116.87
4.285	1.863	-1.504	-0.193	280.85
4.285	1.863	-1.196	-0.116	280.85
4.832	0.132	1.355	1.591	122.69
3.892	0.842	-0.439	-1.2	327.76
1.518	0.586	0.322	-0.553	479.55
1.455	0.399	0.938	-0.851	521.32
1.455	0.399	0.458	-0.807	521.32
0	0.446	0.718	0	485.65
2.128	1.402	-0.475	-1.585	235.79
8.495	0.502	-0.453	-0.996	283.08
4.419	0.162	0.176	-1.444	357.95
2.966	0.754	-0.513	1.507	488.5
0	0.678	1.07	0.466	620.58
1.377	0.425	0.638	0.886	682.94
1.384	0.473	-0.27	0.955	861.77
1.385	0.446	1.647	1.12	947.46
1.341	1.085	0.081	0.276	862.63

3.426	0.889	1.661	0.968	182.66
0	0.671	0.604	0.673	686.22
0	0.671	-0.535	1.466	686.22
3.701	0.223	0.619	1.494	1535.48
1.129	0.495	-0.491	-2.645	509.22
2.535	0.336	0.804	-1.617	667.93
1.166	0.43	-0.271	-0.726	554.1
0	0.551	1.004	-0.369	703.87
0	0.616	0.534	1.079	733.38
5.077	1.571	0.475	0.665	475.84
0	0.693	-1.036	1.338	528.96
12.161	0.956	-1.864	1.25	497.84
3.093	0.997	-0.199	0.633	405.61
6.8	0.117	-1.391	0.122	191.09
7.045	0.082	-0.382	-0.787	365.05
6.273	0.12	0.288	-1.749	436.36
2.845	1.26	1.204	1.31	619.39
0	0.608	1.159	0.891	939.19
6.673	1.235	-0.024	2.7	526.36
2.046	0.719	-0.477	0.083	1036.39
0.95	0.754	0.993	-0.136	1036.39
2.124	0.844	-0.049	-0.299	1025.5
0	1.179	-	-	105.46
9.234	0.039	-1.009	1.981	676.66
5.133	1.384	0.141	1.052	224.43
0	0.622	2.075	-0.7	288.64
2.632	0.991	0.715	0.322	77.56
1.114	0.996	-2.382	-0.774	796.74
0	0.616	0.11	0.204	582.45
7.702	0.939	0.812	-0.015	1174.29
3.565	0.513	0.084	-1.235	1089.96
0	0.904	-0.466	-0.022	419.18
0.955	0.831	-1.572	1.905	1301.87
0	1.179	-0.244	1.977	278.39
0	0.892	-0.555	2.074	252.87
2.115	1.309	-1.588	-0.101	391.89
2.251	1.755	-0.887	-1.212	140.97
0	0.749	-1.185	-0.644	790.12
0	0.826	0.7	0.573	936.02
1.086	0.727	0.695	1.649	586.32
7.514	2.19	-0.311	0.041	477.64
0	0.675	1.054	0.849	231.42
1.496	0.379	1.503	1.672	658.95
0	0.573	-0.91	0.99	298.69

0	0.743	1.458	-1.411	341.22
0	0.735	0.142	-1.387	654.2
0	0.527	-0.53	0.53	161.4
1.141	0.526	-0.543	0.464	514.73
3.617	1.358	0.541	-0.694	307.27
11.235	0.439	-0.987	-0.453	1342.14
0	0.764	0.035	-0.142	505.89
9.627	2.697	-0.691	-0.422	696.94
0	0.527	-2.001	0.182	691.69
1.808	1.14	0.132	0.044	119.83
0	1.179	-	-	327.79
2.077	1.256	-1.055	-0.553	108.5
35.456	3.701	-1.495	-1.259	774.09
36.842	3.477	-1.069	-0.191	754.09
1.623	1.179	-0.952	1.333	378.81
15.015	0.019	0.326	-0.152	699.86
6.029	1.928	0.787	-1.279	337.58
0	0.787	-0.228	-0.38	315.31
16.693	2.625	-1.054	0.18	479.55
16.477	2.8	-2.256	-0.923	473.37
0	0.368	-1.356	0.968	207.63
0	0.495	-0.66	0.811	207.63
0	0.627	0.518	-0.962	361.33
0	0.631	0.231	-0.809	164.17
3.524	0.529	-1.68	-0.394	483.09
0	0.399	-0.391	-0.609	318.54
1.115	0.899	1.323	0.11	823.77
2.746	0.364	0.09	0.646	2162.61
5.701	1.523	0.083	-0.547	306.86
5.999	2.093	-1.183	-0.517	368.48
0	0.742	-0.862	0.172	977.58
0	0.859	1.342	1.002	927.37
4.075	0.819	0.626	1.088	336.13
1.421	0.702	-3.257	-0.278	1540.18
0	0.495	-1.203	-2.646	418.08
8.141	1.739	-0.311	-0.489	264.62
0	0.892	0.367	1.203	327.12
2.392	1.527	0.584	-1.415	155.76
4.359	1.555	0.725	1.2	192.24
6.264	2.833	-0.825	-1.468	298.04
2.046	0.223	-1.069	-0.405	192.63
2.046	0.223	-1.438	-0.405	192.63
0	0.693	-0.27	0.223	713.28
0	0.599	-0.929	-1.939	1530.73

4.575	0.26	0.726	0.319	1141.74
1.377	0.392	1.145	2.254	593.53
1.323	0.713	-1.416	0.016	381.46
0	0.787	-0.056	0.393	424.18
0	0.702	-0.066	-0.595	472.07
1.172	0.922	-1.365	-0.986	703.87
4.196	0.557	0.332	-1.273	1007.21
0	0.512	0.42	-2.808	179.98
1.234	0.412	1.695	2.802	546.64
1.447	0.856	-0.626	0.736	642.73
0	0.929	0.448	0.448	543.91
4.676	1.303	1.108	-1.247	1177.43
3.901	0.314	-0.347	1.7	1116.29
0	0.573	0.331	-0.463	392.81
0	1.697	-	-	2468.65
3.84	0.574	-1.324	1.948	942.29
0.946	0.905	-0.071	0.303	1395.13
2.8	0.673	-1.315	1.438	1705.79
1.941	0.252	1.725	-0.878	191.19
1.69	1.08	0.229	-1.297	195.18
5.909	2.636	-0.231	-1.805	137.76
1.55	0.668	0.814	0.99	609.23
3.532	0.617	-0.588	-2.037	262.72
6.545	0.793	-1.209	-0.155	259.79
2.081	0.697	0.868	-0.405	199.9
0	0.495	-0.503	1.048	298.69
0	0.892	-0.742	1.018	685.22
1.451	0.641	-0.373	0.267	235.76
0	0.465	0.385	-0.536	128.41
0	0.593	1.705	0.686	413.09
2.173	0.927	0.408	0.86	829.16
0.946	0.905	1.101	0.547	1398.5
7.404	0.036	0.466	0.717	112.28
0	0.495	-1.574	-0.6	300.66
0	0.884	-0.236	-0.658	614.36
0	0.551	-0.317	0.024	437.89
3.68	2.833	0.55	0.55	95.04
0	0.495	-1.036	0.501	577.37
1.094	0.869	0.441	-1.057	741.07
4.389	0.98	-1.011	0.38	1583.45
0	0.798	-0.735	-0.188	1552.91
0.961	0.675	1.667	0.7	677.4
0	0.693	-	-	460.14
5.315	1.919	0.791	-0.58	148.91

2.561	0.814	-1.085	1.428	790.27
0	0.818	0.517	-1.169	530.65
4.752	1.153	-0.05	-2.864	184.24
0	1.329	-	-	247.58
1.792	0.346	0.029	-2.77	227.79
1.289	0.684	-0.418	0.232	410.63
1	1.022	-	-	918.96
3.757	1.049	-1.263	0.99	232.8
0	0.824	0.132	-0.337	801.98
0	0.495	0.055	-0.203	701.91
1.312	1.091	1.116	0.326	318.13
1.222	0.96	-0.367	0.911	689.01
0	0.501	-0.116	1.877	452.5
0	0.846	-0.324	-0.718	671.07
6.036	1.954	-0.335	-0.461	338.36
1.542	0.381	0.941	0.188	273.26
1.725	0.307	-1.102	0.492	699.12
1.927	0.399	-0.034	0.51	616.53
0	0.465	-0.264	1.116	716.78
0	0.804	-0.603	0.564	292
0	0.859	-0.528	-1.021	249.95
1.671	1.358	0.777	0.693	760.87
0	0.473	0.034	0.512	195.8
0	1.022	1.099	0.984	163.85
0	0.54	-1.565	0.752	341.81
0	0.616	-2.252	0.999	377.76
0	0.693	-2.505	0.48	377.76
0	0.77	-2.025	0.736	379.72
0	0.616	-1.469	0.96	339.66
0	0.54	-1.321	0.549	339.66
8.852	1.033	1.258	-0.173	305.33
1.719	0.368	-1.812	-0.888	199.02
10.02	1.001	1.077	0.769	298.85
3.312	1.41	-1.185	-0.021	422.46
1.527	0.883	-0.162	-0.395	249.54
0	0.976	-0.386	-0.746	507.65
0	0.693	-0.299	0.62	537.32
4.419	1.184	0.506	0.506	135.72
5.506	1.802	0.871	1.155	302.76
5.506	1.802	-1.546	1.084	311.76
0	0.54	0.211	-1.149	194.09
0	0.693	-0.498	-0.071	552.87
0	0.693	1.85	0.305	240.81
0	1.179	-1.272	1.973	183.89

1.515	0.392	-0.242	0.638	233.23
1.357	1.095	0.633	-1.087	386.63
1.397	1.051	-0.171	-1.652	370.36
0	0.527	0.017	-0.638	419.22
0	0.818	0.116	-0.887	187.85
0	0.653	-0.821	-2.01	167.94
0	0.85	-1.453	0.103	175.24
0	1.329	-0.467	0.466	213.93
0	0.693	-0.633	1.036	221.15
0	0.446	0.727	-0.727	106.57
3.01	0.16	0.067	0.762	212.25
3.09	0.148	-0.118	0.118	276.43
6.455	0.859	1.001	0.248	80.51
3.332	0.105	1.067	-1.067	80.51
0	1.609	-0.421	-0.421	136.63
0	0.368	-0.573	-2.054	198.15
0	0.368	0.322	-0.537	380.07
1.423	0.962	0.468	1.366	227.23
1.808	0.83	0.56	-1.306	363.79
1.475	0.412	-0.183	-0.061	665.67
0	0.612	-1.412	-0.211	331.65
0	1.329 -	-	-	173.11
0	1.609 -	-	-	210.29
4.752	1.072	-2.06	-1.558	373.53
0	0.223	0.731	-0.731	120.59
2.808	0.707	0.361	1.307	178.62
13.222	1.393	0.729	-1.307	97.62
4.06	0.643	-1.207	2.096	270.53
0	0.777	0.684	-1.444	324.35
5.434	1.472	0.312	-1.093	255.1
0	0.368	0.537	-0.784	195.08
4.123	0.991	0.688	1.485	277.82
2.148	0.986	-1.37	1.147	709.67
9.733	1.406	-0.584	0.159	791.51
9.506	1.421	-0.045	-0.074	749.46
12.584	1.363	-0.324	-1.133	756.56
15.647	1.468	-1.938	-0.858	715.99
11.441	1.492	-2.505	-1.46	490.98
5.189	1.139	-0.623	0.108	408.01
5.464	1.567	-1.285	-0.664	365.64
2.127	0.558	-0.387	-0.961	1478.51
0	0.743	-1.64	0.435	1521.47
0	0.697	-0.167	2.39	1533.55
0	0.774	-1.004	2.348	1533.55

0.923	0.823	-1.758	2.589	1562.39
0.923	0.823	-0.07	2.358	1562.39
0	0.646	-1.35	1.305	1090.66
0	0.779	-0.339	1.167	958.23
0	0.633	-2.077	-1.56	1145.18
0	0.873	-0.979	-2.27	1084.16
0	0.591	-0.921	-1.786	964.81
2.454	0.412	0.407	-1.88	916.36
4.124	0.645	0.129	-1.725	877.38
4.124	0.645	-1.537	-1.796	958.53
2.509	0.368	0.202	-2.032	916.36
1.115	0.465	-0.811	-2.534	996.21
0	0.56	-0.099	-1.704	1038.41
1.095	0.545	-0.461	-1.955	874.32
1.095	0.545	-0.154	-1.889	874.32
0	0.715	0.235	-1.363	832.38
0	0.776	-0.591	-0.13	861.73
0	0.704	0.448	0.506	900.73
1.101	0.437	-0.446	0.563	942.39
1.072	0.929	-1.592	1.291	989.86
1.096	1.022	-0.553	1.233	993.09
1.216	0.986	-0.3	2.152	790.42
1.243	1.127	-1.014	2.096	757.37
2.78	1.069	-1.812	3.133	760.62
4.815	0.961	-0.808	0.93	763.78
5.023	0.913	-0.684	0.525	812.07
5.023	0.946	-1.15	-0.217	770.5
5.023	0.946	-0.483	-0.183	774.2
7.891	1.23	-0.682	-0.367	777.97
10.84	1.458	-1.804	-0.104	774.2
9.037	1.825	-1.106	0.23	692.35
4.589	2.062	-1.352	0.429	446.7
8.28	2.964	0.387	1.162	365.95
7.991	3.056	-1.03	1.741	363.17
8.512	3.056	-1.592	0.286	327.12
9.901	3.611	0.251	0.754	193.53
9.425	3.352	0.197	-0.394	152
6.245	3.003	-0.17	0.17	152
0	1.179	0	0	133.62
8.921	0.022	-0.437	-0.271	146.88
1.957	0.283	-1.01	-0.625	283.4
0	0.883	-1.134	1.635	141.78
1.685	1.329	0.381	0.79	522.76
0	0.646	-0.85	-0.409	394.66

3.755	1.609	-0.673	-0.556	284.76
1.421	1.058	-0.85	-2.283	588.07
3.329	1.521	-0.991	-2.107	598
0	1.022	1.945	-2.077	371.17
0	0.77	0.037	0.626	379.72
6.368	2.964	-2.024	-0.718	121.24
0	1.085	0	-1.27	336.6
0	0.495	-0.811	-0.38	205.69
0	0.892	0.296	-0.573	84.61
0	0.693	0.365	1.133	130.22
0	1.179	-1.031	-0.143	172.39
2.187	0.269	0.163	0.163	244.34
0	0.476	0.091	0.543	279.85
0	0.476	0.091	1.268	242.24
0	0.941	-0.042	0.972	237.17
0	0.787	-0.872	1.109	237.17
0	0.412	-0.922	-0.648	203.43
0	0.693	-0.071	-0.071	162.58
5.119	2.252	0.423	-1.164	246.75
5.315	2.494	1.684	-1.01	283.1
1.871	1.609	-0.643	-1.247	410.95
0	0.608	1.189	-2.377	507.17
1.871	0.883	0.718	-0.887	464.98
0	0.527	-1.272	-1.447	193.37
0	0.627	-1.135	-0.436	193.37
0	0.582	0.296	-0.053	158
0	0.646	-0.674	0.212	162.58
0	0.905	1.2	1.333	164.87
5.756	1.884	-1.2	0	164.87
2.276	0.799	0.978	0.212	166.88
11.429	2.519	0.135	-0.529	259.78
4.32	1.1	0.124	0.702	411.08
4.123	0.946	-0.134	0	498.54
4.123	0.946	0	0.32	491.54
4.481	1.535	-0.555	-1.109	517.79
4.752	1.153	-0.754	-0.452	166.54
0	0.368	-1.872	1.097	173.04
0	0.368	1.468	-0.289	127.08
6.021	0.078	0	-0.269	551.32
2.392	0.175	-0.529	-0.433	333.4
2.392	0.238	-0.625	-0.053	288.4
3.68	0.105	0.452	0.101	246.6
0	0.307	-0.636	0.071	393.31
4.467	0.525	-0.423	1.482	344.36

2.363	1.288	-0.933	0.933	340.69
13.03	1.406	-0.146	-0.732	379.34
2.029	0.269	0.091	-0.543	242.24
0	1.123	0.803	-0.127	416.98
2.251	1.755	-0.815	0.634	239.98
0	0.394	-0.465	0.972	239.98
0	0.582	-1.207	0.506	163.37
0	0.793	0.607	0.529	334.36
2.87	0.339	0.046	1.448	622.14
2.197	0.269	-0.462	-0.887	457.02
0	0.693	1.026	0	94.71
0	1.329	-0.72	-1.38	137.27
0	2.303	-	-	209.58
3.68	2.494	-1.754	-0.55	140.04
3.68	2.494	-1.754	-0.937	140.04
8.77	3.037	-1.954	-1.216	232.36
0	0.741	-0.78	0.319	364.94
0	0.582	-1.482	1.324	482.1
0	0.756	0.239	0.102	857.24
0	1.609	-1.368	0.421	112.63
0	0.399	0.973	-2.219	219.26
1.922	0.307	-0.371	-1.938	213.26
4.183	1.688	-0.841	-1.147	262.09
4.269	1.911	0.399	-1.102	299.59
0	0.859	-1.13	-0.176	348.69
1.531	1.022	-1.319	0.455	348.69
0	0.963	-0.916	1.617	310.85
1.603	1.085	-1.387	1.783	312.59
1.685	1.23	1.312	2.266	312.59
1.744	1.402	-0.22	2.236	357.76
3.524	1.202	0.463	1.622	402.13
4.2	1.863	-0.58	-1.126	175.89
1.574	1.27	0.805	1.244	479.55
1.527	1.179	0.51	0.898	479.55
1.441	1.022	0.737	1.244	521.32
0	0.693	-0.145	0.436	601.96
0	0.582	0.455	0.771	682.99
0	0.703	-1.838	0.349	725.17
0	0.703	-0.158	0.317	725.17
1.183	0.685	0	-0.471	889.96
1.177	0.783	-1.357	0.061	928.87
0	0.693	-2.423	-0.704	1018.38
0	0.693	-1.874	-0.537	1014.58
0	0.77	0.416	1.588	961.46

1.399	0.74	-0.089	1.83	942.76
0	0.646	0	1.914	915.43
0	0.635	0.215	1.292	996.34
0	0.787	-0.338	1.108	1039.87
0	0.77	0.102	0.542	1077.87
0	0.693	-0.855	-0.939	1207.12
1.331	0.693	0.96	-0.626	1269.64
0	0.76	-2.086	-1.231	1207.12
0	0.693	-0.238	-1.835	1213.1
0	0.631	-1.213	-1.992	1082.5
0	0.826	-0.515	-1.796	1189.1
0	0.756	-0.625	-1.361	854.09
0	0.826	-1.046	0.164	1109.74
0	0.856	0.801	1.173	1309.14
1.333	1.085	0.14	2.878	987.7
1.397	1.092	-1.236	2.19	1082.5
0	0.749	-0.533	1.719	1087.4
0	0.602	1.367	0.466	1185.75
0	0.941	-0.309	1.477	1006.43
1.45	1.179	-0.73	1.509	1001.55
0	0.941	0.309	0.996	1001.55
1.452	1.139	0.034	0.584	996.55
3.645	1.609	-0.069	-0.298	751.62
3.39	1.493	0.529	0.191	699.95
3.39	1.493	1.037	-0.021	699.95
1.419	0.437	0.502	-1.046	654.36
1.515	1.022	0.462	0.205	482.41
1.515	1.022	0.154	0.41	506.41
0	0.657	0.489	0.231	489.67
0	0.795	0.739	0.192	530.65
1.273	0.572	-0.759	1.927	697.87
4.887	1.119	-0.169	0.874	580.77
2.846	0.862	-0.373	1.671	584.77
2.884	0.95	0.35	0.686	601.06
0	0.793	-1.7	-1.205	661.99
6.576	1.802	-0.384	-1.512	261.08
6.68	1.784	1.196	-0.727	261.08
9.864	2.022	1.672	0.18	307.27
6.262	1.51	0.477	-0.276	351.45
3.352	0.836	-0.598	1.262	474.36
0	0.818	0.652	0.613	560.05
0	0.76	1.142	0.447	721.94
1.287	0.389	1.544	1.09	851.96
8.007	1.054	-0.352	-0.654	953.46

4.533	1.014	1.269	0.094	1026.37
4.262	1.032	-2.225	-0.032	1189.49
2.449	0.385	-1.199	0.216	1156.18
3.933	0.81	1.753	-0.193	1080.73
3.029	0.428	-0.986	-1.957	905.74
2.835	0.34	-2.764	-1.227	855.77
16.221	4.307	-0.146	1.493	389.05
12.74	3.912	-0.448	1.502	353.33
12.74	3.912	-0.29	1.08	350.45
1.85	1.292	1.248	0.527	541.33
7.371	2.584	-0.194	-2.075	128.17
1.172	0.645	0.474	0.78	611.41
0	0.61	-1.254	0.775	661.07
0	0.646	-0.437	-1.872	472.97
0	0.665	1.435	-1.575	225.21
0	0.631	0.578	-0.867	227.31
1.833	1.23	-0.187	1.679	231.65
0	0.921	-1.813	0.68	239.24
0	1.022	-1.041	0.061	161.26
8.038	2.262	-0.949	0.784	165.51
0	0.473	-0.454	-1.938	280.47
4.193	1.567	0.211	-2.538	233.65
7.558	0.844	0.513	-2.022	532.78
10.494	0.079	0.174	-0.036	1517.53
7.185	0.151	1.506	0.418	1517.53
1.685	0.307	0.029	-0.205	397.11
1.55	1.025	-0.482	0.803	387.41
3.312	1.22	-1.291	-0.129	387.41
3.565	0.912	0.477	0.427	389.05
1.441	1.022	-0.766	-0.348	433.09
2.835	1.244	1.641	-0.281	583.77
0	0.75	0.657	-0.179	582.45
1.674	0.351	0.954	0.523	399.85
4.5	2.219	-0.454	-0.091	208.31
6.455	0.383	0.136	1.169	304.73
3.862	1.279	0.539	0.054	156.48
1.657	0.313	-0.746	0.746	356.67
2.808	0.148	0	0.729	61.82
2.003	0.223	-1.288	-0.933	264.69
8.038	2.262	-0.041	-0.619	173.72
0	1.112	0.354	-0.071	112.31
1.952	1.329	-1.264	-0.609	182
0	0.859	0.37	0.37	381.95
0	1.022	-0.717	0.825	167.39

3.136	1.447	0.922	-1.368	113.62
0	0.223 -	-		88.04
0	0.813	-0.259	-0.156	279.76
7.806	1.431	-1.426	0.152	636.16
0	0.804	-1.519	-0.779	697.9
0	0.74	0.9	-0.469	5041.74
0.84	0.593	-1.001	1.067	3484.66
0.949	0.866	0.723	-0.537	2660.72
53.395	5.546	1.084	1.769	481.98
1.356	0.826	-0.271	-0.813	529.61
1.573	1.161	0.544	-0.109	230.86
1.15	1.036	-4.804	-2.75	814.77
1.121	1.051	-4.98	-3.784	885.21
4.246	0.897	-5.017	-1.551	914.54
4.246	1.053	-5.426	0.352	874.32
6.235	1.015	-4.848	-0.534	874.32
1.527	0.754	-0.116	0.58	458.54
0	0.941	-2.676	-1.371	102.24
2.522	1.546	0.077	-1.003	123.31
5.021	1.506	1.485	-0.636	123.31
0	0.446	-0.039	-0.964	220.85
0	0.542	0.627	-0.58	435.54
0	0.813	-0.29	0.395	350.45
0	0.782	1.142	-0.615	355.62
0	0.936	-0.137	-0.301	399.11
0	0.76	0.695	-1.39	402.13
0	1.234	0.627	-0.627	599.63
0	0.836	0.106	0.317	312.95
0	0.735	2.462	0.653	174.53
0	0.223	-0.731	0.731	130.59
0	0.787	0.079	0.475	205.36
5.138	1.4	-0.35	-1.55	535.2
5.167	0.078	-0.439	-1.513	422.24
10.964	1.85	-1.408	-0.387	294.82
10.964	2.215	-1.408	-1.186	301.88
10.561	2.526	-1.398	-0.896	264.24
3.01	1.492	-0.895	0.296	267.97
2.533	1.518	-1.134	1.134	259.78
0	1.179	-1.134	0.831	301.88
0	0.976	-1.614	0.194	238.33
0	0.551	-1.91	0.289	242.24
0	0.877	-0.912	0.076	313.02
1.748	1.136	-1.968	1.193	349.81
6.374	0.129	-1.13	0.577	708.69

8.272	1.286	0.426	1.237	426
8.209	0.814	-0.291	-0.667	1086.51
2.859	1.222	1.683	0.834	496.98
1.28	0.963	-1.362	1.613	983.57
0	0.641	-1.545	0.805	481.81
1.328	1.022	-0.605	0.871	409.29
0	0.497	-1.187	-0.876	777
6.625	0.476	1.85	-0.065	291.69
3.492	1.445	-1.554	0.271	469.83
3.992	1.911	-0.501	-0.079	353.33
1.631	1.262	-0.59	-0.443	345.22
0	0.646	-1.469	0.401	457.77
0	0.573	-0.414	0.778	539.53
0	0.859	0.74	-1.294	351.91
2.398	1.609	-0.678	0.278	264.24
0	0.693	-0.265	0.038	368.84
0	0.693	0.189	-0.189	368.84
16.154	1.39	0.597	-0.896	129.24
6.154	1.889	0.143	-1.186	168.39
5.441	1.472	0.365	-1.036	131.15
6.854	1.426	0	-1.881	131.15
5.021	1.506	0.354	0.778	108.31
0	0.608	0.912	0.076	410.95
0	0.813	0.343	0.079	324.64
0	0.602	-0.625	0.699	1004.2
0	0.591	0.703	0.062	411.24
3.787	0.545	-3.439	-1.674	293.67
7.627	0.411	-0.308	-0.14	810.65
20.152	3.896	0.71	2.647	151.59
2.077	1.256	2.462	-1.156	120.59
6.99	2.812	-0.296	0.296	88.11
3.31	0.105	1.38	0	122.27
0	0.693	1.38	1.38	144.27
0	0.368	0.55	0.55	140.04
3.979	0.838	0.988	0.406	83.17
0	1.179	-1.656	-0.377	202.57
0	3.258	-	-	134.67
1.177	0.973	-0.377	2.175	829.41
3.41	0.223	-0.159	2.066	857.67
0	0.693	0.103	-0.336	133.24
11.553	3.229	0.778	1.202	71.45
2.171	0.223	0.813	-0.38	157.43
0	0.776	0.15	2.053	1007.53
3.565	0.876	-0.678	-0.126	653.45

5.093	0.223	0.755	1.197	774.92
7.547	0.707	-0.646	0.811	755.77
3.035	0.33	-0.265	-1.295	1136.34
0	0.804	0.395	0.394	223.79
0	0.458	-0.107	-0.391	449.02
0	0.73	2.357	-0.611	883.16
0	0.657	-1.363	0.129	540.96
1.449	1.061	-0.11	0.548	576.83
4.722	1.443	0.997	-3.343	531.23
2.527	0.694	-0.561	-2.898	947.38
1.253	0.932	0.331	0.842	469.09
8.427	0.916	-0.285	0.592	473.36
5.884	1.75	0.227	0.021	416.18
1.397	1.051	-1.458	-0.921	464.94
1.377	1.061	-1.418	-0.496	464.94
1.377	1.061	0.851	-1.028	462.77
5.229	1.38	-0.899	1.115	514.22
0	0.604	0.093	-0.693	297.84
0	0.68	-0.15	1.306	709.94
1.092	0.922	0.111	0.874	1014.21
8.545	0.757	-0.425	0.778	1104.38
13.31	1.379	0.513	0.271	944.16
1.624	0.43	-1.624	0.219	2401.95
0	0.751	1.021	-0.121	618.18
1.039	0.542	2.452	-0.56	1107.23
1.079	0.532	1.549	-1.51	1345.65
2.631	0.38	1.925	1.431	470.47
0	0.576	2.699	-1.892	1476.11
0	0.869	-0.915	-1.354	1325.5
0	0.836	-	-	2538.69
1.047	0.592	0.086	2.198	1063.85
5.356	0.569	0.334	0.605	1642.44
0	0.846	-	-	2537.69
6.956	0.889	0.806	-1.472	565.06
1.851	0.269	-0.381	-0.445	628.3
1.51	0.648	-1.043	-0.364	364.58
2.917	0.346	-1.229	0.96	355.65
1.392	1.136	0.308	-0.081	911.32
1.184	0.871	0.971	0.047	927.27
3.035	0.877	1.097	-0.284	1249.16
5.501	0.855	-1.394	0.142	705.03
0	0.582	0.097	0.032	274.13
0	0.582	0.678	0.226	274.13
0	0.693	1.263	0.239	271.49

0	0.495	-0.827	0.949	271.49
3.821	0.223	-0.099	-3.066	494.8
7.371	0.078	-0.249	-1.411	659.15
10.371	1.806	-2.803	1.014	509.73
2.262	0.223	0.724	-1.575	605.92
7.06	0.674	-0.347	-0.68	443.85
7.346	0.651	-0.107	-1.055	440.02
1.74	1.179	0.27	1.466	280.85
1.74	0.991	-1.091	-0.176	266.17
1.713	1.207	-0.401	0.868	282.54
1.44	1.022	0.475	-0.268	272.66
0	0.76	0.427	0.202	237.09
0	0.991	1.537	0.406	63.17
1	2.303 -	-		247.58
0	1.022	0.231	1.157	306.55
0	0.446	-1.754	1.3	95.04
0	0.446	0	0.937	95.04
0	1.022	-0.289	-1.239	90.08
11.83	2.804	-0.666	0.133	192.52
0	2.303 -	-		235.58
0	1.98 -	-		194.16
0	2.833 -	-		158.67
0	0.804	-0.395	0.219	103.86
0	0.622	-0.537	0.947	808.05
0	0.637	-1.516	-1.277	1003.58
1.053	0.493	0.428	-1.468	1159.01
0	0.752	0.458	-0.991	1307.25
1.114	0.941	0.394	1.241	1358.03
0	0.549	-0.111	2.04	537.21
1.148	0.473	1.273	1.273	858.73
0	0.573	0.366	1.992	889.12
7.955	0.842	0.472	0.065	655.4
1.243	0.457	-0.379	0.436	715.62
1.126	0.729	0.687	-0.853	693.27
1.205	0.639	-0.362	0.53	685.22
4.846	0.741	-0.485	0.235	500.74
3.012	0.809	0.488	-0.219	502.63
1.076	0.534	-2.154	0.367	725.9
0	0.816	0.921	0.188	621.07
1.012	0.796	1.274	-0.793	737.66
2.133	0.566	0.599	0.067	1097.92
2.696	1.284	0.67	-0.913	743.97
6.93	1.909	0.061	-1.227	788.39
4.283	0.255	-0.075	-1.29	696.46

2.499	0.931	-0.878	-0.531	1040.22
2.55	0.805	0.395	-0.461	874.32
4.246	0.947	-0.102	-0.465	874.32
3.558	0.487	0.405	-1.185	1161.21
3.67	0.35	0.994	-1.405	1161.21
5.015	0.223	-1.113	-0.138	1292.62
3.352	0.848	0.837	-0.209	578.52
3.099	1.493	-1.262	-0.062	452.5
7.134	1.741	-2.386	1.683	496.98
15.763	1.438	-0.307	0.82	915.58
4.707	1.068	-2.888	0.404	451.15
1.378	0.748	-1.911	0.15	374.33
0	0.593	0.17	-0.019	295.89
0	0.811	1.455	-1.401	180.85
0	0.859	0.35	0.506	111.37
0	0.941	-0.127	1.817	195.98
1.719	0.368	-0.543	1.485	222.09
1.447	0.46	0.652	0.292	610.38
1.402	1.022	0.298	-0.774	542.82
3.862	0.796	-0.755	-0.916	541.85
1.302	0.741	-0.372	-1.117	869.87
2.66	0.807	1.245	1.814	341.16
1.498	0.349	-1.271	-2.129	713.43
0	0.765	-0.117	1.196	159.09
14.753	2.798	1.806	0.827	270.52
3.352	0.223	0.62	-0.701	561.07
3.365	0.418	-0.75	0.466	583.22
3.393	0.605	-0.64	2.002	612.66
0	0.802	-0.811	1.55	1040.77
3.118	0.378	-1.648	1.648	1608.75
1.09	0.998	1.245	0.714	1006.86
1.07	0.599	0.879	-0.751	862.91
4.389	0.98	1.031	-0.11	1622.2
2.623	1.03	-1.373	0.595	845.56
4.363	1.08	-0.426	0.377	892.35
7.938	1.335	1.3	1.176	809.53
4.358	1.367	0.08	2.341	752.81
2.274	0.661	1.125	-0.994	1020.27
7.858	0.189	-1.332	-0.148	871.66
2.169	0.446	-0.832	-0.752	939.6
0	0.746	-0.86	-1.581	919.23
0	0.667	0.841	-0.572	872.75
1.083	0.473	0.238	0.175	1432.27
3.816	1.739	0.075	-0.778	662.26

3.581	1.739	-2.768	0.288	696.06
10.84	1.766	0.914	1.88	725.17
11.612	1.355	0.668	2.831	764.41
16.444	0.953	-0.37	0.547	979.76
7.08	0.85	1.08	-2.13	1139.75
4.084	0.794	-0.314	1.631	822.73
2.133	0.597	1.4	-0.995	1002.85
4.201	0.821	-0.965	1.702	1029.22
0	0.602	0.359	1.57	1153.08
0	0.716	-0.867	-1.471	1035.36
5.73	0.554	1.125	-1.332	1274.52
0	0.602	-0.138	-1.03	507.79
0	0.855	1.465	1.108	825.8
0	0.689	-0.841	-1.001	1195.66
2.137	0.467	-0.601	-0.326	1146.99
1.399	1.127	-0.215	-0.248	648.87
7.555	0.869	-0.283	0.95	517.21
1.71	0.815	-0.686	0.49	766.88
0	1.179	-	-	88.5
0	2.303	-	-	70.57
5.287	0.683	0.297	-0.052	340.01
2.199	1.781	-0.501	-0.501	223.85
0	0.223	0.72	0.72	91.04
2.398	0.223	-0.278	0.278	129.24
2.616	0.169	-0.825	0.6	124.58
0	0.412	-1.061	1.626	116.24
5.167	2.584	0.634	-2.001	183.36
0	0.934	-0.394	2.07	158
2.162	0.799	1.084	-1.281	116.04
0	0.85	-2.243	-2.163	507.82
3.834	0.735	-1.53	-0.491	376.7
0	0.495	0.774	0.7	132.63
0	1.609	-	-	133.67
1.316	0.473	1.257	-0.843	767.46
0	0.527	0.675	0.413	786.86
0	0.848	-0.289	0.642	697.65
2.158	0.252	-0.174	-0.289	205.84
3.653	0.76	-0.694	-0.694	479.55
1.69	1.314	-1.48	0.801	376.56
2.057	1.302	-0.973	-1.129	125.63
8.495	0.502	0.453	-1.177	233.65
4.738	0.122	0.456	-1.368	357.95
4.129	0.184	-2.028	-0.174	461.13
1.234	0.511	-1.054	0.245	722.61

0	0.672	-0.403	0.877	906.9
11.729	0.235	0.206	1.815	802.77
4.943	0.397	-0.321	2.535	735.82
1.453	1.23	-0.094	-0.43	860.63
1.341	1.085	0.633	0.211	862.63
1.325	0.392	-0.111	-0.78	487.22
1.348	0.704	1.178	-0.154	345.13
1.21	0.603	1.036	0.177	727.97
9.774	1.938	-1.138	-0.632	528.62
5.287	1.567	-0.347	-0.104	632.23
1.344	1.112	-0.48	1.474	514.53
9.16	0.072	0.402	-0.614	743.22
11.233	0.072	2.16	-1.109	786
8.564	0.486	-1.021	-0.18	696.06
5.287	1.567	0.59	0.59	498.7
7.479	1.028	-0.653	-0.589	457.5
11.051	0.889	-0.22	0.861	380.13
1.478	1.002	-0.736	-0.057	213.91
2.837	1.23	-0.696	-0.355	664.96
2.867	1.368	-0.191	0.47	662.62
4.506	0.954	-0.844	1.624	750.73
0	1.022	-1.91	-2.281	197.86
0	0.627	-0.325	3.266	207.51
0	0.582	0.68	-2.747	256.73
0	0.693	-1.202	0.354	246.05
0	1.179	-0.594	-1.613	537.11
0	1.179	-1.783	-1.444	528.07
2.077	0.76	-0.796	1.859	454.96
2.077	0.76	-0.14	1.759	464
5.119	0.419	-1.359	1.408	426.53
0	0.653	-0.212	0.627	327.56
0	0.892	-0.428	0.78	285.78
0	0.892	0.772	-0.663	285.78
0	1.022	-1.532	-2.181	163.34
0	1.022	-0.466	-1.749	172.39
0	0.693	-0.676	-1.951	207.11
0	1.022	-1.031	-1.186	163.34
0	0.941	-0.998	0.348	385.51
6.154	1.447	0.896	-0.678	252.24
2.632	1.535	2.52	0.278	127.08
2.398	1.609	2.637	0.6	118.03
0	0.307	-1.813	-1.191	181.89
2.398	1.609	2.637	0.6	127.08
2.808	1.981	-1.159	1.159	169.58

3.332	1.901	0.322	-0.937	169.58
0	0.693 -	-		69.57
0	0.693 -	-		69.57
0	2.833 -	-		114.5
0	2.833 -	-		114.5
0	2.833 -	-		149.62
0	1.179	-0.72	-0.72	88.04
0	2.093	0.406	-0.988	175.71
0	1.329	-1.221	-0.684	175.71
3.136	1.447	-0.922	-0.922	127.59
8.451	2.783	0.684	0.684	92.71
3.136	1.447	0	-0.922	136.63
8.451	2.783	0.322	0.684	83.67
3.136	1.447	-0.922	-0.922	136.63
0	0.595	0.747	-0.747	280.91
0	0.631	-0.689	-0.831	152.73
2.062	0.223	-0.439	0.146	364.52
1.778	0.368	1.377	0.578	364.52
0	0.483	0.042	-0.544	899.59
1.623	0.729	-0.132	0.237	645.45
3.565	0.825	-1.035	0.564	641.26
0	0.892	-0.643	0.077	221.46
1.507	0.399	-0.756	-0.073	377.96
1.58	0.368	1.387	-2.094	292.73
0	0.693	-0.124	-3.505	143.68
5.563	2.303	-0.584	-3.027	143.68
0	1.841 -	-		5016.68
6.783	0.292	-1.46	0.693	8199.68
0	0.992	-1.204	2.005	22739.68
0	0.691	0.405	1.264	31590.64
11.049	0.302	0.514	4.922	9386.68
11.3	1.197	-0.142	1.156	22375.68
2.858	0.507	-0.967	-0.351	11786.65
5.367	0.947	1.308	1.813	7513.75
2.707	0.539	1.315	-2.148	9973.09
0.676	0.62	-1.734	-1.739	6276.72
5.284	0.481	0.326	-0.247	3246.11
4.689	1.588	1.232	0.268	4986.69
0	2.134 -	-		6349.68
0	0.664	1.757	-0.347	3905.14
3.31	0.105	0	-1.133	210.22
0	1.609	-0.296	-0.895	78.92
0	1.609	0.296	1.214	78.92
0	0.368	0.689	0.529	99.78

0	1.27	-	-	822.03
5.035	0.383	-0.394	0	511
4.708	0.148	1.107	0.58	511
0	0.941	-0.146	-1.415	240.24
0	1.112	1.055	-0.854	262.85
0	0.693	0.421	-0.515	182.01
2.808	0.959	-0.573	1.683	90.43
2.808	0.959	-0.248	1.001	90.43
3.233	2.419	0.546	0.546	85.97
7.068	0.61	-1.221	-0.956	130.82
12.175	1.032	1.031	0.387	178.35
0	1.022	0.296	0.248	267.97
0	1.022	0.296	0.248	267.97
0	0.307	0.322	0.684	81.39
0	1.329	-1.221	-0.684	173.67
0	0.307	-0.322	1.221	92.71
0	2.303	-	-	218.58
0	0.892	-0.66	-2.424	213.14
0	0.527	-0.935	0.825	91.12
0	1.022	1.457	-0.05	126.54
1.653	1.27	-0.29	-1.186	394.33
1.653	1.27	-1.818	-0.594	353.33
6.908	0.916	-2.051	-0.888	190.58
2.017	0.243	-1.674	-2.164	363.07
2.077	0.184	-1.678	-2.031	363.07
8.903	1.068	-3.464	-1.184	177.83
9.276	1.061	-3.308	-1.681	255.27
5.237	0.681	-2.606	0.68	161.09
5.497	1.893	-1.02	-1.133	161.26
2.017	1.219	-1.856	-1.773	195.72
0	0.856	-0.634	-2.961	224.61
1.971	1.272	-0.428	-2.686	265.09
1.971	1.272	-1.051	-2.686	232.36
1.897	1.329	-1.069	-2.322	223.31
1.885	1.426	-1.128	-2.961	221.25
1.885	1.426	-1.762	-2.961	223.31
3.925	1.609	-0.1	-2.572	223.31
3.925	1.609	-0.1	-2.706	223.31
4.193	1.567	0.705	-2.89	271.49
0	0.856	-0.775	-2.538	265.09
1.808	1.162	0.817	-1.518	184.32
0	0.509	-0.58	-1.902	470.08
1.279	0.946	0.23	-2.153	333.32
2.709	0.747	0.407	1.064	411.58

1.077	0.544	-0.667	-0.479	578.59
1.054	0.941	-1.167	1.345	868.7
5.839	0.819	0.205	-0.575	432.36
2.476	1.179	0.706	2.78	499.17
0	0.569	0.615	-0.193	716.73
1.243	0.793	0.829	0.557	643.42
0	0.693	-0.133	0.959	410.13
5.525	1.577	0.021	-0.909	324.22
3.453	1.399	-1.129	-1.483	385.16
6.397	2.073	0.588	-0.86	204.67
2.158	0.925	0.429	-1.041	298.72
2.276	0.799	0.271	0.696	207.63
2.533	0.707	-0.38	0.38	198.59
2.276	0.223	-0.935	0.312	211.07
0	1.179	-0.132	0.57	366.89
0	0.818	-0.81	0.27	143.9
3.734	1.828	-0.697	0.063	768.87
2.077	0.543	0.151	-0.653	417.49
2.077	1.256	-0.955	0.151	159.53
0	0.693	-1.29	-0.037	99.59
4.036	0.855	-0.035	0.458	324.95
0	0.582	-0.195	1.596	112.67
1.748	1.136	-0.298	0.537	213.73
1.918	0.293	-0.031	1.291	216.71
0	2.303	-	-	462.2
0	2.303	-	-	462.2
0	0.859	-0.596	0.233	812.28
11.563	1.421	-1.429	2.684	299.12
0	1.179	-0.898	-1.271	287.45
0	1.022	0.922	-0.922	225.43
0	0.582	1.221	-0.684	169.58
0	0.368	0.361	-0.361	255.2
2.43	0.223	0	-1.447	212.24
8.129	3.442	-1.501	-2.938	311.2
2.881	1.721	0.825	-0.929	63.09
0	0.446	-0.466	0.387	133.4
0	0.446	0.717	0.387	217.39
0	0.307	-0.259	0.467	213.93
0	0.631	-1.134	0.135	250.73
0	0.631	0.135	-0.244	259.78
2.616	0.169	2.637	0	69.03
2.616	0.169	2.637	-0.536	78.08
4.612	2.147	0.253	-1.05	500.82
5.715	2.67	0.047	-2.201	509.88

6.41	2.833	0.648	-2.534	176.71
21.494	3.053	1.087	-0.006	1372.19
6.561	2.12	-2.876	2.012	2385.27
4.016	1.739	-0.643	2.89	2464.68
10.028	2.985	0.479	1.852	1724.89
15.789	3.903	1.061	2.758	1650.02
1.657	1.402	0.849	2.34	308.46
1.657	1.402	-2.237	2.495	308.46
0	0.512	0.742	-0.032	217.13
1.871	0.677	-0.835	0.568	159.33
6.313	1.255	-0.334	-0.668	259.54
3.981	1.643	1.702	-0.978	234.82
5.201	1.38	0.419	-0.386	416.02
14.797	2.733	-1.492	-4.145	687.69
9.063	2.149	-1.182	-3.283	767.42
9.063	2.149	-0.96	-1.97	767.42
8.696	1.999	0.497	0.516	587.37
4.54	1.427	0.058	0.15	511.19
0	0.631	-0.37	-0.595	238.75
0	0.892	0.5	0.631	246.86
8.821	2.288	-0.803	-2.487	329.32
7.88	1.96	-1.442	-1.512	452.12
1.301	0.999	0	-1.989	547.82
1.243	1.022	0.632	-2.234	716.64
7.052	1.551	-1.937	-0.517	585.77
15.093	2.447	0.359	0.109	322.34
9.489	1.802	-0.355	-0.766	652.91
9.473	2.031	-0.708	0.044	572.57
7.273	1.89	0.615	0.073	569.37
9.438	1.874	-0.176	0.269	569.37
7.257	2.049	-2.167	0.361	621.44
7.257	2.049	-0.4	0.332	619.39
6.822	1.715	-0.897	0.281	660.58
4.453	1.463	0.544	0.59	696.23
4.453	1.463	-0.336	0.217	696.23
2.488	0.998	-1.096	1.098	879.36
0	0.693	0.183	-0.125	641.03
2.365	0.835	0.376	0.156	717.59
0	0.772	-1.317	-0.146	342.34
4.895	1.112	0.243	-0.4	930.51
2.207	1.017	0.033	-2.509	1006.21
2.282	1.101	-0.328	-2.83	1012.03
1.067	0.901	2.225	-0.335	1293.66
3.541	1.179	-0.02	0.735	948.46

0	0.784	-0.505	1.344	835.9
11.235	0.635	0.171	-2.082	787.82
11.235	0.635	-0.603	-2.013	784.81
8.671	0.663	-0.044	-1.433	784.81
14.32	1.09	0.781	-0.671	784.54
4.536	0.634	0.979	0.278	745.07
1.289	0.711	0.754	0.843	755.77
0	0.807	-0.757	0.329	890.03
0	0.646	-0.659	-0.693	1281.44
1.289	1.051	0.41	1.96	465.85
0	0.569	2.002	0.31	859.49
0	0.569	-0.743	0.268	874.36
1.101	0.503	0.763	-0.424	913.09
1.062	0.892	0.718	-1.584	1013.85
3.761	1.219	1.609	-1.868	856.81
0	1.148	-	-	1408.79
1.314	1.123	-1.211	1.487	524.07
2.715	1.251	-2.395	0.973	485.21
1.148	0.976	0.114	0.197	863.7
0	0.862	-3.344	-0.393	246.3
0	0.656	-2.644	-1.717	299.75
0	0.582	1.092	0.271	111.88
2.003	0.669	-1.177	-1.359	236.98
0	0.693	-1.361	-1.608	190.72
2.199	1.426	-1.85	-1.85	191.37
2.199	1.426	-1.65	-1.95	191.37
0	0.892	0.789	1.822	324.73
8.451	2.788	-0.55	0.55	84.04
7.068	2.807	-0.956	0.322	129.24
2.632	1.535	-1.034	0.278	129.24
0	1.27	-0.278	0.597	129.24
0	0.495	-1.159	1.448	459.98
6.421	2.91	-0.386	0.54	114.27
0	1.329	-0.365	-1.133	270.35
2.757	0.132	-0.54	0	155.82
6.99	0.486	1.386	0.296	349.63
4.832	0.707	-0.061	-0.8	162.58
4.832	0.707	0.306	-0.8	153.54
2.276	1.17	-1.226	0.452	198.59
2.276	1.229	-0.312	0.377	196.64
6.154	1.872	-0.244	-0.38	143.84
2.463	1.144	0.583	0.259	213.93
2.463	1.144	-0.583	0	213.93
6.154	1.872	1.309	0.135	152.88

2.463	1.144	0.259	-0.467	213.93
3.01	0.16	-0.573	1.422	191.43
0	0.85	1.951	0.676	162.24
1.415	1.022	-0.36	0.36	353.95
0	1.179	-0.573	0.248	72.43
12.499	1.439	-1.958	-1.551	345.22
9.149	1.465	-1.474	-0.839	342.87
9.773	1.447	-0.87	-1.868	350.45
4.01	0.654	-1.306	-1.773	226.75
4.01	0.654	-0.634	-2.103	235.79
15.885	4.219	0.133	0.08	218.96
11.732	2.235	-0.775	-1.375	284.54
3.117	0.297	-0.308	-1.671	373.55
2.747	0.368	0.666	-1.629	591.96
3.696	0.233	2.204	-0.284	520.32
3.876	0.193	0.875	0.415	542.03
3.696	0.233	-0.371	0.507	500.32
0	0.582	0.579	-1.504	446.98
1.719	1.179	-0.32	-1.14	446.98
1.829	0.668	-0.531	-0.612	368.84
0	0.412	0.945	-0.718	359.79
9.558	1.458	-0.749	-1.193	351.62
6.862	1.212	-1.55	-0.775	342.57

AAchange

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[illegible]

Glu5del
Asp20del

[illegible]

[illegible]

Val357fs
Gly1494fs
Cys329fs
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Ala138fs
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Glu253fs
Leu260fs

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frameshift_variant&stop_gained	Pro371fs
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non-synonymous	Thr348Met
non-synonymous	Pro350His
non-synonymous	Val129Ile
non-synonymous	Ala36Ser
non-synonymous	Gly41Glu
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non-synonymous	Asn43Asp
non-synonymous	Leu47Trp
non-synonymous	Val87Ile
non-synonymous	Val92Leu
non-synonymous	Ala95Val
non-synonymous	Val96Ala
non-synonymous	Ser200Ala
non-synonymous	Arg312Gln
non-synonymous	Val318Ala
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non-synonymous	Leu45Phe
non-synonymous	Asp67Glu
non-synonymous	Val74Ile
non-synonymous	Ile91Leu
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non-synonymous	Cys462Arg
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non-synonymous	Leu67Met
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non-synonymous	Val131Ile
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non-synonymous	Ile77Thr
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Val446Val
Ala455Ala

[illegible]

[illegible]

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uSerAspGluProAlaAlaArgThrAsnAlaPheSerAsnTerAsnTyrSerIleTyrLeuProThrAspCysSerAsnCysVal/

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ArgAlaGly

Gene	Start	End	Ref	Alt	QD	MQ
ABCC1	8253	8253	A	AT	0.38	60
ABCC1	11256	11256	G	A	4.07	60
ABCC1	1569	1569	C	T	2.54	60
ABCC1	1847	1847	G	T	4.81	60
ABCC1	4610	4610	G	A	23.99	60
ABCC1	6000	6000	G	A	7.38	60
ABCC1	6042	6042	G	A	2.19	60
ABCC1	7593	7593	T	C	3.85	60
ABCC1	8362	8362	T	G	2.76	60
ABCC1	9270	9270	C	A	0.83	60
ABCC1	9362	9362	G	A	1.64	60
ABCC1	9482	9482	C	T	9.74	60
ABCC1	9709	9709	C	T	2.16	60
ABCC1	10333	10333	C	T	2.53	60
ABCC1	10510	10510	C	A	5.54	60
ABCC1	11423	11423	G	C	1.99	60
ABCC1	11537	11537	G	A	0.56	60
ABCC1	11567	11567	G	A	5.77	60
ABCC1	407	407	G	T	3.5	60
ABCC1	438	438	C	T	1.8	60
ABCC1	1142	1142	C	T	1.79	60
ABCC1	5330	5330	G	T	0.92	60
ABCC1	5990	5990	C	A	32.81	60
ABCC1	6026	6026	T	A	21.07	60
ABCC1	6621	6621	T	C	1.31	60
ABCC1	7537	7537	C	T	2.11	60
ABCC1	8845	8845	G	A	25.54	60
ABCC1	8935	8935	T	C	9.47	60
ABCC1	9175	9175	T	C	0.92	60
ABCC1	9178	9178	C	T	4.18	60
ABCC1	9301	9301	T	C	6.59	60
ABCC1	9436	9436	G	A	0.57	60
ABCC1	9526	9526	A	C	1.24	60
ABCC1	9728	9728	G	A	4.92	60
ABCC1	10490	10490	C	T	0.99	60
ABCC1	10514	10514	G	A	1.14	60
ABCC1	11368	11368	G	A	0.93	60
ABCC1	11516	11516	T	C	7.72	60
ABCC4L	3756	3756	G	T	2.3	60
ABCC4L	3760	3760	C	G	1.67	60
ABCC4L	3806	3806	A	G	0.9	60
ABCC4L	3807	3807	C	T	0.63	60
ABCC4L	3814	3814	G	A	3.36	60

ABCC4L	3869	3869 A	G	3.1	60
ABCC4L	3907	3907 G	T	1.92	60
ABCC4L	3921	3921 T	A	6.11	60
ABCC4L	3943	3943 G	C	0.7	60
ABCC4L	4019	4019 G	A	0.59	60
ABCC4L	4020	4020 T	A	0.6	60
ABCC4L	4036	4036 C	T	3.85	60
ABCC4L	4046	4046 C	A	2.97	60
ABCC4L	4047	4047 G	T	0.13	60
ABCC4L	4053	4053 C	A	0.17	60
ABCC4L	4060	4060 T	G	3.48	60
ABCC4L	4075	4075 A	G	1.92	60
ABCC4L	4087	4087 T	A	11.33	60
ABCC4L	288	288 G	A	1.7	60
ABCC4L	937	937 C	T	1.84	60
ABCC4L	962	962 G	A	2.03	60
ABCC4L	972	972 C	A	0.36	60
ABCC4L	1051	1051 G	C	2.42	60
ABCC4L	1092	1092 G	C	5.55	60
ABCC4L	1133	1133 C	T	0.33	60
ABCC4L	1202	1202 A	G	1.62	60
ABCC4L	1210	1210 A	G	1.84	60
ABCC4L	1211	1211 C	T	1.59	60
ABCC4L	1276	1276 G	A	0.62	60
ABCC4L	1279	1279 G	A	1.43	60
ABCC4L	1512	1512 T	C	4.57	60
ABCC4L	1882	1882 C	A	5.54	60
ABCC4L	2012	2012 G	A	0.35	60
ABCC4L	2515	2515 C	G	2.65	60
ABCC4L	2660	2660 A	G	3.11	60
ABCC4L	2666	2666 A	G	5.99	60
ABCC4L	2675	2675 A	T	4.48	60
ABCC4L	3005	3005 T	G	13.57	60
ABCC4L	3007	3007 C	T	8.47	60
ABCC4L	3349	3349 C	T	1.29	60
ABCC4L	3439	3439 A	G	1.27	60
ABCC4L	3699	3699 T	G	1.74	60
ABCC4L	2803	2803 G	A	0.63	60
ABCC4L	996	996 C	A	0.29	60
ABCC4L	1062	1062 C	T	1.97	60
ABCC4L	1107	1107 G	C	6.46	60
ABCC4L	1251	1251 C	T	4.02	60
ABCC4L	1299	1299 G	A	2.31	60
ABCC4L	1329	1329 G	A	2.21	60

ABCC4L	1834	1834 C	T	2.44	60
ABCC4L	1954	1954 C	T	0.13	60
ABCC4L	1969	1969 C	T	4.72	60
ABCC4L	2185	2185 T	C	2.62	60
ABCC4L	2275	2275 T	C	25.3	60
ABCC4L	2296	2296 C	T	2.89	60
ABCC4L	2305	2305 G	A	3.46	60
ABCC4L	2530	2530 G	A	21.83	60
ABCC4L	2531	2531 T	C	2.53	60
ABCC4L	2593	2593 T	A	32.12	60
ABCC4L	2605	2605 A	G	14.79	60
ABCC4L	2659	2659 C	A	0.41	60
ABCC4L	2952	2952 A	T	21.04	60
ABCC4L	3234	3234 G	A	30.86	60
ACC1	11374	11374 C	T	0.25	60
ACC1	11412	11412 A	G	2.49	60
ACC1	11459	11459 G	A	11.25	60
ACC1	11461	11461 T	C	1.53	60
ACC1	11469	11469 T	G	11.63	60
ACC1	11582	11582 A	G	2.57	60
ACC1	11601	11601 A	C	11.33	60
ACC1	11652	11653 TA	TAA,T,TAAA	3.53	60
ACC1	11692	11692 G	A	5.22	60
ACC1	11760	11760 C	A	0.65	60
ACC1	11768	11768 C	T	5.6	60
ACC1	11780	11780 C	T	3.79	60
ACC1	266	266 C	T	5.79	60
ACC1	842	842 C	T	17.81	60
ACC1	5373	5373 T	G	22.02	60
ACC1	7248	7248 C	A	6.87	60
ACC1	7327	7327 A	G	5.12	60
ACC1	7985	7985 A	G	1.88	60
ACC1	8036	8036 G	A	17.76	60
ACC1	8052	8052 G	A	13.46	60
ACC1	8377	8377 T	C	14.79	60
ACC1	8842	8842 C	G	2.47	60
ACC1	8872	8872 T	C	11.84	60
ACC1	9561	9561 C	T	0.87	60
ACC1	10001	10001 C	T	0.1	60
ACC1	10010	10010 C	T	1.16	60
ACC1	10029	10029 C	T	11.77	60
ACC1	10043	10043 A	T	0.88	60
ACC1	10062	10062 C	T	0.09	60
ACC1	10524	10524 C	T	0.19	60

ACC1	10752	10752 G	A	8.62	60
ACC1	10917	10917 G	A	9.11	60
ACC1	11322	11322 G	A	1.89	60
ACC1	414	414 G	C	14.16	60
ACC1	501	501 G	A	3.94	60
ACC1	519	519 C	T	5.89	60
ACC1	537	537 C	T	1.98	60
ACC1	774	774 A	G	6.6	60
ACC1	3271	3271 C	T	2.29	60
ACC1	3836	3836 T	C	20.36	60
ACC1	5042	5042 T	C	7.67	60
ACC1	5327	5327 A	G	7.27	60
ACC1	6190	6190 G	A	22.52	60
ACC1	6904	6904 A	G	2.8	60
ACC1	7298	7298 G	T	0.36	60
ACC1	7631	7631 C	T	2.44	60
ACC1	7963	7963 C	T	15.19	60
ACC1	9172	9172 G	A	2.89	60
ACC1	9211	9211 C	T	30.6	60
ACC1	9232	9232 T	C	23.6	60
ACC1	9412	9412 T	A	7.2	60
ACC1	9808	9808 G	T	1.52	60
ACC1	10030	10030 G	A	2.52	60
ACC1	10165	10165 C	T	4.87	60
ACC1	10252	10252 T	A	8.6	60
ACC1	10576	10576 C	T	1.24	60
ACC1	10588	10588 G	A	14.77	60
ACC1	10594	10594 G	C	10.79	60
ACC1	11035	11035 T	A	5.37	60
ACC1	11143	11143 G	A	6.24	60
AIM1	7221	7221 G	T	4.22	60
AIM1	7233	7233 G	A	4.08	60
AIM1	7240	7240 G	A	3.96	60
AIM1	7250	7250 A	C	1.99	60
AIM1	7267	7267 T	A	2.82	60
AIM1	7275	7275 A	G	2.88	60
AIM1	7288	7288 G	A	4.68	60
AIM1	7295	7296 GA	G,GAA	6.42	60
AIM1	7374	7374 T	C	3.13	60
AIM1	7385	7385 A	ACT	8.84	60
AIM1	7399	7399 T	G	4.31	60
AIM1	7451	7451 C	A	0.68	60
AIM1	1601	1601 G	A	29.5	60
AIM1	2630	2630 C	T	19.95	60

AIM1	2732	2732 A	G	13.48	60
AIM1	2747	2747 A	G	24.41	60
AIM1	2824	2824 A	T	2.89	60
AIM1	3636	3636 C	T	2.51	60
AIM1	3945	3945 G	T	2.26	60
AIM1	3993	3993 C	A	3.59	60
AIM1	4026	4026 A	G	1.98	60
AIM1	4681	4681 G	A	2.45	60
AIM1	5433	5433 G	A	2.06	60
AIM1	5736	5736 G	A	4.63	60
AIM1	5930	5930 G	T	2.81	60
AIM1	6832	6832 G	A	1.4	60
AIM1	7160	7160 G	C	1.73	60
AIM1	7161	7161 A	G	2.41	60
AIM1	150	150 T	C	13.02	60
AIM1	2649	2649 A	G	1.76	60
AIM1	2656	2656 T	C	1.42	60
AIM1	2667	2667 T	C	3.32	60
AIM1	2670	2670 T	C	2.29	60
AIM1	2673	2673 C	T	3.11	60
AIM1	2730	2730 C	T	2.61	60
AIM1	2811	2811 A	T	1.98	60
AIM1	2898	2898 C	T	3	60
AIM1	2901	2901 A	G	3.57	60
AIM1	2907	2907 T	C	2.21	60
AIM1	3322	3322 C	T	7.66	60
AIM1	3755	3755 G	A	1.03	60
AIM1	3944	3944 G	T	1.41	60
AIM1	3959	3959 G	T	1.3	60
AIM1	3992	3992 G	A	1.69	60
AIM1	4025	4025 C	T	2.03	60
AIM1	4211	4211 T	C	10.95	60
AIM1	4298	4298 C	A	3.9	60
AIM1	4319	4319 C	T	9.53	60
AIM1	4611	4611 G	C	2.9	60
AIM1	4614	4614 G	A	1.85	60
AIM1	4806	4806 C	T	8.32	60
AIM1	5441	5441 C	T	3.39	60
AIM1	5456	5456 A	G	4.69	60
AIM1	5671	5671 C	T	8.83	60
AIM1	5686	5686 T	C	8.76	60
AIM1	5905	5905 T	C	9.81	60
AIM1	5923	5923 C	T	3.35	60
AIM1	6738	6738 C	T	0.91	60

AIM1	6744	6744 C	T	4.09	60
AIM1	6825	6825 G	C	10.95	60
AIM1	7177	7177 G	A	2.85	60
ALF5	1367	1367 G	A	33.35	60
ALF5	1697	1697 T	G	19.98	60
ALF5	2199	2199 A	G	4.01	60
ALF5	2268	2268 G	C	5.73	60
ALF5	2315	2315 C	T	2.39	60
ALF5	2339	2339 C	G	8.97	60
ALF5	2378	2378 C	G	6.21	60
ALF5	2393	2393 G	C	4.33	60
ALF5	2442	2442 G	A	4.67	60
ALF5	2486	2486 G	C	4.65	60
ALF5	302	302 G	C	28.2	60
ALF5	1336	1336 T	G	10.71	60
ALF5	1399	1399 G	A	20.25	60
ALF5	1402	1402 G	A	20.25	60
ALF5	2186	2186 C	G	7.87	60
ALF5	2219	2219 G	C	28.06	60
AML1	855	855 G	A	6.85	60
AML1	944	944 G	A	7.88	60
AML1	1079	1079 T	A	0.69	60
AML1	745	745 A	G	27.84	60
AML1	820	820 C	T	5.9	60
AML1	868	868 C	T	7.26	60
AML1	886	886 C	G	12.02	60
AML1	916	916 C	T	11.87	60
AML1	919	919 G	T	11.93	60
AML1	955	955 G	T	2.62	60
AML1	979	979 A	G	8.13	60
AML1	1066	1066 T	C	6.99	60
CESA1	2823	2823 A	T	3.6	60
CESA1	2834	2834 A	G	1.03	60
CESA1	2836	2836 C	CGTTATTTA	0.27	60
CESA1	2837	2837 C	T,CATG	0.73	60
CESA1	2841	2841 C	G	1.11	60
CESA1	2847	2847 C	G	3.28	60
CESA1	2891	2891 T	A	2.56	60
CESA1	2951	2951 G	A	4	60
CESA1	2970	2970 A	T	3.31	60
CESA1	3018	3018 G	A	3.71	60
CESA1	3052	3052 A	G	2.92	60
CESA1	3072	3072 C	A	4.86	60
CESA1	3099	3100 AG	A	2.14	60

CESA1	3106	3106 T	C	2.21	60
CESA1	3117	3117 T	C	3.82	60
CESA1	1491	1492 GC	G	0.9	60
CESA1	688	688 A	AAAG	5.66	60
CESA1	734	734 A	G	7.08	60
CESA1	1483	1483 G	T	3.82	60
CESA1	1626	1626 A	T	1.26	60
CESA1	2230	2230 C	T	5.53	60
CESA1	2353	2353 C	T	1.39	60
CESA1	2604	2604 G	T	1.56	60
CESA1	679	679 T	C	1.76	60
CESA1	1528	1528 G	A	2.85	60
CESA1	2231	2231 G	A	4.83	60
CESA1	2354	2354 G	A	3.41	60
CESA1	2360	2360 C	T	2.4	60
CESA1	2435	2435 C	T	3.61	60
CESA1	2504	2504 T	C	4.13	60
CESA1	2522	2522 G	A	3.1	60
CESA1	2552	2552 T	C	1.34	60
CESA1	2588	2588 C	T	2.62	60
CESA1	2627	2627 C	T	2.28	60
CESA1	2669	2669 G	A	0.99	60
CXE12	717	720 CCCT	C	34.31	60
CXE12	653	653 C	G	28.37	60
CXE12	655	655 C	G	34.31	60
CXE12	722	722 C	A	30.52	60
CYN	188	188 T	C	12.85	60
CYN	206	206 A	AGGCG	9.24	60
CYN	207	211 GGCGA	G	6.34	60
CYN	338	338 G	A	2.49	60
CYN	388	388 A	C	11.03	60
CYN	458	458 T	C	3.25	60
CYN	487	487 G	C	4.72	60
CYN	2357	2357 C	G	6.69	60
CYN	2368	2368 A	C	29.95	60
CYN	2387	2387 G	A	1.5	60
CYN	477	477 C	G	3.23	60
CYN	483	483 T	C	3.5	60
CYP709B3	2276	2276 G	T	2.48	60
CYP709B3	2317	2317 A	T	4.32	60
CYP709B3	2357	2357 G	A	1.28	60
CYP709B3	2395	2395 A	T	1.44	60
CYP709B3	2424	2424 T	A	3.02	60
CYP709B3	2474	2474 A	T	16.98	60

CYP709B3	1320	1320 G	T	14.11	60
CYP709B3	60	60 C	T	1.57	60
CYP709B3	106	106 G	A	23.96	60
CYP709B3	148	148 G	C	2.77	60
CYP709B3	153	153 C	A	31.06	60
CYP709B3	182	182 G	C	32.31	60
CYP709B3	669	669 T	C	4.28	60
CYP709B3	681	681 G	A	1.16	60
CYP709B3	766	766 C	A,T	3.56	60
CYP709B3	804	804 A	G	3.53	60
CYP709B3	844	844 G	T	32.1	60
CYP709B3	982	982 T	C	15.63	60
CYP709B3	1041	1041 T	A	2.32	60
CYP709B3	1052	1052 A	T	6.42	60
CYP709B3	1060	1060 A	T	3.47	60
CYP709B3	1122	1122 G	A	0.24	60
CYP709B3	1331	1331 C	T	6.03	60
CYP709B3	1349	1349 A	C,G	2.8	60
CYP709B3	1448	1448 T	C	5.44	60
CYP709B3	1571	1571 A	T	1.05	60
CYP709B3	1606	1606 G	T	2.4	60
CYP709B3	1609	1609 C	T	1.62	60
CYP709B3	1892	1892 T	A	3.09	60
CYP709B3	1955	1955 A	G	0.73	60
CYP709B3	1960	1960 T	G	3.2	60
CYP709B3	1972	1972 C	T	1.22	60
CYP709B3	2065	2065 G	A	2.4	60
CYP709B3	2066	2066 C	T	2.17	60
CYP709B3	2225	2225 T	A	3.63	60
CYP709B3	131	131 T	C	3.83	60
CYP709B3	176	176 G	A	9.25	60
CYP709B3	690	690 A	C	33.66	60
CYP709B3	734	734 T	C	32	60
CYP709B3	780	780 C	T	3.67	60
CYP709B3	1085	1085 G	A	2.05	60
CYP709B3	1470	1470 A	G	5.8	60
CYP709B3	1479	1479 G	A	6.2	60
CYP709B3	1503	1503 C	G	4.36	60
CYP709B3	1545	1545 C	T	0.62	60
CYP709B3	1548	1548 C	T	3.79	60
CYP709B3	1563	1563 G	C	3.11	60
CYP709B3	1662	1662 A	G	5.7	60
CYP71E1	625	625 A	G	27.23	60
CYP71E1	785	785 A	C	27.7	60

CYP71E1	787	787 G	T	33.89	60
CYP71E1	791	791 G	A	33.89	60
CYP71E1	603	603 C	G	36.37	60
CYP71E1	609	609 T	C	28.02	28.02
CYP71E1	792	792 A	G	28.85	60
CYP72A31	383	383 A	C	20.06	60
CYP72A31	539	539 A	C	33.23	60
CYP72A31	704	704 A	C	27.87	60
CYP72A31	796	796 C	G	12.7	60
CYP72A31	848	848 G	A	5.87	60
CYP72A31	1214	1214 A	G	11.41	60
CYP72A31	1419	1419 G	A	25.43	60
CYP72A31	1452	1452 C	T	31.34	60
CYP72A31	1592	1592 C	A	7.36	60
CYP72A31	1612	1612 T	C	18.2	60
CYP72A31	1742	1742 T	C	27.68	60
CYP72A31	1777	1777 C	G	26.48	60
DHPS	427	428 TG	T	4.85	60
DHPS	363	363 G	C	9.35	60
DHPS	375	375 C	T	11.59	60
DHPS	440	440 G	A	7.41	60
DHPS	602	602 T	C	14.29	60
DHPS	620	620 G	A	11.64	60
DHPS	632	632 A	G	8.61	60
DHPS	750	750 G	T	8.57	60
DHPS	779	779 A	G	12.87	60
DHPS	835	835 C	G	15.2	60
DHPS	484	484 G	A	2.67	60
DHPS	619	619 C	T	6.8	60
DHPS	631	631 G	A	8.61	60
DHPS	638	638 C	T	8.18	60
DHPS	784	784 G	A	20.13	60
DTX1	4934	4934 G	T	25.25	60
DTX1	4677	4677 G	T	3.45	60
DTX1	4708	4708 C	T	5.66	60
DTX1	4726	4726 A	G	5.57	60
DTX1	4730	4730 A	AG	8.29	60
DTX1	4797	4797 T	C	4.23	60
DTX1	4813	4813 A	AT	3.14	60
DTX1	4938	4938 C	T	29.19	60
DTX1	2736	2736 A	G	7.16	60
DTX1	2894	2894 G	T	5.64	60
DTX1	2981	2981 A	T	1.25	60
DTX1	3017	3017 C	A	2.63	60

DTX1	3089	3089 G	A	25.9	60
DTX1	3122	3122 A	G	28.92	60
DTX1	4009	4009 A	G	1.33	60
DTX1	4057	4057 G	A	4.71	60
DTX1	4094	4094 C	T	8.45	60
DTX1	4432	4432 G	C	11.51	60
DTX1	4594	4594 A	T	1.77	60
DTX1	4603	4603 A	G	31.23	60
DTX1	2656	2656 C	T	17.82	60
DTX1	4631	4631 T	G	30.65	60
DTX1	476	476 C	T	6.05	60
DTX1	596	596 G	A	3.14	60
DTX1	632	632 C	T	3.1	60
DTX1	731	731 G	T	3.53	60
DTX1	2659	2659 A	G	22.07	60
DTX1	2746	2746 C	T	4.67	60
DTX1	2848	2848 C	T	1.64	60
DTX1	2989	2989 C	G	3.65	60
DTX1	3118	3118 G	C	26.34	60
DTX1	3124	3124 A	G	26.43	60
DTX1	4086	4086 C	T	2.88	60
DTX1	4321	4321 T	C	10.77	60
DTX1	4324	4324 C	T	1.61	60
DTX1	4369	4369 C	T	1.56	60
EPSPS	1229	1229 A	T	16.9	60
EPSPS	183	183 A	C	23.72	60
EPSPS	258	258 C	G	21.52	60
EPSPS	273	273 G	C	31.41	60
EPSPS	1235	1235 T	C	10.78	60
EPSPS	1380	1380 G	C	3.82	60
EPSPS	1389	1389 C	T	6.19	60
EPSPS	2068	2068 G	C	8.12	60
EPSPS	2839	2839 A	G	5.27	60
EPSPS	2854	2854 A	G	25.96	60
EPSPS	1379	1379 G	A	2.49	60
EPSPS	1421	1421 G	T	2.44	60
EPSPS	1602	1602 C	T	12.5	60
EPSPS	1605	1605 C	T	4.46	60
EPSPS	1656	1656 C	T	2.64	60
EPSPS	1998	1998 C	T	5.87	60
EPSPS	2055	2055 G	T	9.91	60
EPSPS	2073	2073 C	A	19.54	60
EPSPS	2113	2113 T	C	6.97	60
EPSPS	2136	2136 C	T	12.5	60

EPSPS	2778	2778 C	T	5.12	60
EPSPS	3163	3163 C	T	2.17	60
EPSPS	3172	3172 C	T	2.2	60
EPSPS	3175	3175 A	G	2.96	60
EPSPS	3193	3193 G	A	10.01	60
EPSPS	3208	3208 G	T	5.37	60
EPSPS	3232	3232 T	C	3.56	60
EPSPS	3259	3259 C	T	3.73	60
ESR1	218	218 T	G	8.33	60
ESR1	219	219 T	C	25.48	60
ESR1	258	258 T	C	5.83	60
ESR1	278	278 A	G	6.06	60
ESR1	347	347 G	C	3.84	60
ESR1	432	432 A	T	12.76	60
ESR1	783	783 T	C	20.26	60
ESR1	2202	2202 G	A	7.54	60
ESR1	2254	2254 C	T	3.59	60
ESR1	292	292 A	G	7.7	60
ESR1	668	668 T	C	5.6	60
ESR1	725	725 A	G	12.6	60
ESR1	1028	1028 C	G	1.68	60
ESR1	2120	2120 A	G	8.84	60
ESR1	2195	2195 C	T	5.88	60
ESR1	2201	2201 C	T	6.8	60
GDSL	409	409 C	T	9.55	60
GDSL	491	491 A	G	7.29	60
GDSL	529	529 A	T	0.58	60
GDSL	589	589 G	T	3.61	60
GDSL	697	697 G	A	29.97	60
GDSL	1306	1306 T	C	15.61	60
GDSL	3233	3233 A	G	4.63	60
GDSL	3269	3269 A	G	0.85	60
GDSL	3365	3365 G	A	3.36	60
GDSL	3376	3376 C	A	3.56	60
GDSL	3387	3387 A	G	4.13	60
GDSL	1140	1140 G	A	14.32	60
GDSL	1266	1266 C	T	5.09	60
GDSL	1317	1317 G	C	5.83	60
GDSL	3229	3229 C	G	4.63	60
GDSL	3286	3286 C	T	0.67	60
GPOX	340	340 T	G	23.53	60
GPOX	403	403 A	G	6.56	60
GPOX	433	433 G	A	9.29	60
GPOX	434	434 G	T	9.32	60

GPOX	544	546 CGA	C	26.18	60
GPOX	573	573 G	A	26.92	60
GPOX	576	576 A	G	27.22	60
GPOX	588	588 T	A	26.67	60
GPOX	603	603 C	T	32.04	60
GPOX	1821	1821 C	A	31.45	60
GPOX	1857	1857 G	T	32.42	60
GPOX	519	519 T	C	26.35	60
GPOX	525	525 G	A	0.98	60
GPOX	552	552 A	G	30.11	60
GPOX	949	949 A	C	8.57	60
GPOX	1000	1000 A	G	2.2	60
GPOX	1889	1889 G	C	7.18	60
GPOX	2066	2066 C	G	28.81	60
GPOX	2067	2067 G	T	35.22	60
GPOX	460	460 G	T	6.13	60
GPOX	508	508 C	T	4.26	60
GPOX	520	520 G	C	4.6	60
GPOX	908	908 C	A	1.34	60
GPOX	1849	1849 C	T	1.26	60
GPOX	1912	1912 T	C	31.07	60
GSH2	121	121 A	G	32.63	60
GSH2	3782	3782 T	A	28.85	60
GSH2	56	56 G	C	34.1	60
GSH2	65	65 C	G	29.79	60
GSH2	747	747 G	A	4.72	60
GSH2	815	815 G	C	3.53	60
GSH2	2046	2046 G	T	1.6	60
GSH2	2064	2064 T	C	28.72	60
GSH2	3532	3532 T	C	9.26	60
GSH2	3615	3615 C	A	1.33	60
GSH2	3776	3776 A	T	5.6	60
GSH2	3785	3785 A	G,C	5.11	60
GSH2	4168	4168 G	A	8.05	60
GSH2	132	132 G	T	30.36	60
GSH2	713	713 C	T	4.74	60
GSH2	737	737 G	A	10.98	60
GSH2	752	752 G	C	2.01	60
GSH2	767	767 A	G	4.77	60
GSH2	797	797 C	T	2.07	60
GSH2	1293	1293 G	A	3.64	60
GSH2	3220	3220 C	T	8.06	60
GSH2	3599	3599 G	A	16.68	60
GSH2	3792	3792 G	A	5.36	60

GSH2	3858	3858 G	A	13.65	60
GSH2	4060	4060 A	C	13.05	60
GSH2	4078	4078 C	T	5.02	60
GSH2	4132	4132 G	A	3.16	60
GSL1-1	381	381 T	C	1.1	60
GSL1-1	2301	2301 G	C	1.8	60
GSL1-1	2994	2994 G	A	0.21	60
GSL1-1	3007	3007 C	A	4.11	60
GSL1-1	367	367 C	T	1.56	60
GSL1-1	1557	1557 C	T	2.51	60
GSL1-1	1575	1575 T	G	18.01	60
GSL1-1	2357	2357 C	T	3.43	60
GSL1-1	2502	2502 G	A	6.02	60
GSL1-1	2915	2915 G	A	1.66	60
GSTF1	139	139 A	C	5.06	60
GSTF1	146	146 G	C	7.79	60
GSTF1	190	190 A	G	3.47	60
GSTF1	194	206 TGGAGAGGAT		0.43	60
GSTF1	214	214 T	C	1.48	60
GSTF1	232	232 T	C	1.45	60
GSTF1	283	283 C	A	5.75	60
GSTF1	298	298 A	G	5.69	60
GSTF1	310	310 A	G	3.28	60
GSTF1	313	313 G	A	1.8	60
GSTF1	1298	1298 A	C	16.6	60
GSTF12	1191	1191 T	C	3.24	60
GSTF12	1217	1217 G	A	1.87	60
GSTF12	1310	1310 G	A	2.27	60
GSTF12	1325	1329 AGCCT	A	0.86	60
GSTF12	1344	1344 A	G	1.2	60
GSTF12	226	226 G	A	2.61	60
GSTF12	235	235 C	T	9.46	60
GSTF12	264	264 A	G	11.64	60
GSTF12	764	764 C	T	15.7	60
GSTF12	814	814 C	G	8.17	60
GSTF12	893	893 A	G	5.09	60
GSTF12	905	905 C	T	4.8	60
GSTF12	961	961 A	G	1.9	60
GSTF12	987	987 C	A	12.37	60
GSTF12	1159	1159 A	G	2.02	60
GSTF12	342	342 G	A	4.38	60
GSTF12	348	348 G	T	11.86	60
GSTF12	735	735 C	G	11.87	60
GSTF12	831	831 G	A	2.96	60

GSTF12	1068	1068 C	T	12.69	60
GSTF12	1107	1107 T	C	1.74	60
GSTF3	355	355 C	G	0.5	60
GSTF3	374	374 G	A	0.53	60
GSTF3	476	476 C	G	8.1	60
GSTF3	490	490 C	T	3.73	60
GSTF3	505	505 G	C	3.51	60
GSTF3	250	250 A	G	6.61	60
GSTF3	346	346 C	T	1.67	60
GSTF6	1309	1309 T	C	14.55	60
GSTF6	1312	1312 G	C	2.29	60
GSTF6	1403	1403 T	C	3.21	60
GSTF6	1468	1471 TCAC	T	8.91	60
GSTF6	1469	1469 C	G	4.29	60
GSTF6	1470	1470 A	T	7.86	60
GSTF6	796	796 G	A	2.67	60
GSTF6	1016	1016 T	C	1.55	60
GSTF6	413	413 A	G	2.14	60
GSTF6	834	834 C	T	14.01	60
GSTF6	969	969 A	T	14.6	60
GSTF6	1017	1017 C	G	2.27	60
GSTF6	1113	1113 C	T	1.39	60
GSTF6	1140	1140 G	A	2.87	60
GSTU1	630	630 G	GGCA	30.4	60
GSTU1	899	900 CG	C	33.17	60
GSTU1	252	252 G	C	21.39	60
GSTU1	640	640 C	G	27.26	60
GSTU1	567	567 C	G	34.81	60
GSTU1	225	225 C	G	28.52	60
GSTU1	582	582 G	A	28.21	60
GSTU1	192	192 G	T	4.73	60
GSTU1	216	216 T	C	30.59	60
GSTU1	759	759 T	C	29.93	60
GSTU1	768	768 T	C	28.89	60
GSTU1	771	771 G	A	32.16	60
GSTU3	473	473 A	G	8.75	60
GSTU3	518	518 G	A	14.46	60
GSTU3	397	397 G	C	20.09	60
GSTU3	448	448 T	C	10.12	60
GSTU3	502	502 C	G	33.06	60
HM2	221	221 A	C	2.83	60
HM2	333	333 A	G	7.06	60
HM2	579	579 G	C	14.45	60
HM2	937	937 T	C	7.76	60

HM2	1324	1324 C	G	17.09	60
HM2	1326	1326 A	G	5.75	60
HM2	1416	1416 C	T	3.32	60
HM2	1464	1464 G	T	34.26	60
HM2	1544	1544 C	G	8.07	60
HM2	1583	1583 A	G	2.31	60
HM2	325	325 C	T	2.22	60
HM2	328	328 C	G	2.45	60
HM2	542	542 G	C	1.63	60
HM2	554	554 C	G	10.49	60
HM2	578	578 C	G	14.45	60
HM2	596	596 C	A	13.89	60
HM2	807	807 C	G	26.76	60
HM2	822	822 A	G	9.7	60
HM2	942	942 T	C	3.55	60
HM2	1321	1321 G	A	4.93	60
HM2	1375	1375 G	C	9.73	60
HM2	1378	1378 A	C	9.73	60
HM2	1384	1384 G	A	25.33	60
HM2	1507	1507 A	G	0.74	60
HM2	1543	1543 C	G	2.15	60
HM2	1579	1579 C	T	9	60
HM2	1588	1588 T	G	2.63	60
HPPD	1757	1757 A	C,G	7.8	60
HPPD	1775	1775 C	T,CT	9.64	60
HPPD	1797	1797 C	T	2.37	60
HPPD	1798	1798 G	A	3.29	60
HPPD	1806	1806 A	C	0.79	60
HPPD	1814	1814 A	G	2.24	60
HPPD	1843	1843 G	T	5.77	60
HPPD	1857	1857 G	A	3.57	60
HPPD	1917	1917 G	A	7.77	60
HPPD	1927	1927 A	G	30.4	60
HPPD	1940	1940 C	A	0.6	60
HPPD	1955	1955 A	G	8.75	60
HPPD	1969	1969 T	TAACAACGA	24.85	60
HPPD	1972	1972 A	G	33.73	60
HPPD	2002	2003 TA	T	11.36	60
HPPD	130	130 G	A	3.26	60
HPPD	209	209 G	T	1.28	60
HPPD	301	301 C	A	5.82	60
HPPD	304	304 T	G	18.78	60
HPPD	334	334 A	T	1.49	60
HPPD	367	367 G	T	3.46	60

HPPD	466	466 C	G	31.1	60
HPPD	485	485 C	T	29.25	60
HPPD	574	574 G	A	2.88	60
HPPD	604	604 G	A	0.32	60
HPPD	656	656 C	T	14.28	60
HPPD	839	839 C	T	1.77	60
HPPD	919	919 A	C	4.97	60
HPPD	1120	1120 T	A	22.26	60
HPPD	1623	1623 G	C	7.64	60
HPPD	1735	1735 G	A	2.56	60
HPPD	105	105 A	T	3.74	60
HPPD	141	141 G	A,T	8.58	60
HPPD	153	153 G	C	2.71	60
HPPD	237	237 G	C	26.76	60
HPPD	267	267 C	A	1.24	60
HPPD	315	315 C	T	0.98	60
HPPD	336	336 C	G	1.42	60
HPPD	387	387 G	T	7.58	60
HPPD	393	393 C	G	6.38	60
HPPD	396	396 C	T	4.63	60
HPPD	558	558 A	G	28.23	60
HPPD	597	597 C	G	30.13	60
HPPD	615	615 C	T	3.12	60
HPPD	670	670 C	T	1.2	60
HPPD	681	681 C	T	1.07	60
HPPD	786	786 C	G	10.34	60
HPPD	855	855 C	T	3.33	60
HPPD	879	879 C	G	2.16	60
HPPD	924	924 A	G	20.77	60
HPPD	948	948 C	T	2.09	60
HPPD	951	951 A	G	14.58	60
HPPD	1008	1008 T	C	19.93	60
HPPD	1017	1017 G	A	19.23	60
HPPD	1089	1089 C	T	2.53	60
HPPD	1104	1104 C	A	2.53	60
HPPD	1116	1116 G	T	1.28	60
HPPD	1140	1140 G	A	3.55	60
HPPD	1161	1161 G	A	1.52	60
HPPD	1215	1215 G	A	2.02	60
HPPD	1653	1653 C	T	12.21	60
HPPD	1662	1662 C	T	0.64	60
HPPD	1692	1692 C	A	1.22	60
IGPD	243	243 C	A	28.52	60
IGPD	305	305 C	A	2.5	60

IGPD	425	425 C	A	3.41	60
IGPD	448	448 G	A	11.22	60
IGPD	449	449 G	C	11.65	60
IGPD	1640	1640 G	A	6.36	60
IGPD	1670	1670 A	C	13.79	60
IGPD	369	369 C	T	1.88	60
IGPD	474	474 C	G	3.28	60
IGPD	699	699 G	A	2.32	60
IGPD	726	726 C	A	2.55	60
IGPD	744	744 C	T	2.52	60
IGPD	1663	1663 G	A	2.51	60
IGPD	1666	1666 C	T	7.5	60
IGPD	1672	1672 G	A	13.79	60
IGPD	1687	1687 G	A	6.83	60
IGPD	3363	3363 A	T	27.31	60
IN2	1950	1950 C	CA	19.33	60
IN2	1961	1961 C	G	24.96	60
IN2	1999	1999 T	C	18.85	60
IN2	705	705 T	G	34.1	60
IN2	1264	1264 C	A	23.88	60
IN2	1699	1699 A	G	12.08	60
IN2	1726	1726 A	T	12.88	60
IN2	1312	1312 G	C	22.47	60
IN2	1339	1339 T	C	29.79	60
IN2	1784	1784 A	G	27.29	60
LACS7	110	110 A	C	28.2	60
LACS7	239	239 G	A	20.25	60
LACS7	242	242 C	G	20.25	60
LACS7	3499	3499 A	G	28.05	60
LACS7	5631	5631 A	G	30.78	60
LACS7	7238	7238 A	T	2.16	60
LACS7	8396	8396 G	C	31.07	60
LACS7	8422	8422 T	G	33.18	60
LACS7	8437	8437 G	A	27.84	60
LACS7	5651	5651 C	T	31.35	60
LACS7	6585	6585 G	T	7.91	60
LACS7	2690	2690 A	G	37.54	60
LACS7	3487	3487 T	C	30.85	60
LACS7	4532	4532 C	T	29.92	60
LACS7	4589	4589 A	G	30.66	60
LACS7	4929	4929 A	G	30.46	60
LACS7	5766	5766 G	A	6.03	60
LACS7	6379	6379 G	A	34	60
LACS7	6409	6409 A	G	4.09	60

LACS7	6442	6442 A	C	5.57	60
LACS7	6584	6584 A	G	2.29	60
LACS7	6593	6593 C	A	2.83	60
LACS7	7227	7227 A	C	28.76	60
LACS7	7230	7230 C	T	27.61	60
LACS7	7421	7421 T	C	14.21	60
LACS7	8195	8195 T	C	27.98	60
LACS7	8430	8430 T	A	26.71	60
LACS7	4580	4580 A	T	26.09	60
LACS8	83	83 G	C	33.5	60
LACS8	124	124 T	C	28.87	60
LACS8	1814	1814 G	A	7.83	60
LACS8	4551	4551 C	CA	2.31	60
LACS8	1866	1866 G	A	3.61	60
LACS8	1869	1869 A	G	5	60
LACS8	1882	1882 A	G	3.42	60
LACS8	1935	1935 G	A	14.49	60
LACS8	1941	1941 G	A	7.06	60
LACS8	2056	2056 G	A	2.32	60
LACS8	2113	2113 C	T	3.92	60
LACS8	2149	2149 G	A	2.18	60
LACS8	2277	2277 G	A	4.53	60
LACS8	2944	2944 A	T	1.28	60
LACS8	2958	2958 C	A	18.29	60
LACS8	2979	2979 G	A	17.31	60
LACS8	3028	3028 A	T	2.97	60
LACS8	3063	3063 A	G	3.97	60
LACS8	3710	3710 G	A	17.51	60
LACS8	3988	3988 T	C	3.08	60
LACS8	4604	4604 A	C	3.26	60
LACS8	4648	4648 C	A	9.91	60
LACS8	4667	4667 C	T	1.59	60
LACS8	4728	4728 A	T	1.97	60
LACS8	5431	5431 T	C	7.33	60
LACS8	5874	5874 T	C	3.63	60
LACS8	1940	1940 C	T	4.55	60
LACS8	1947	1947 C	T	1.67	60
LACS8	1970	1970 T	C	4.68	60
LACS8	2120	2120 G	A	3.74	60
LACS8	2228	2228 G	A	2.82	60
LACS8	2234	2234 C	T	27.95	60
LACS8	2261	2261 T	C	3.17	60
LACS8	2315	2315 T	C	16.11	60
LACS8	2942	2942 T	C	2.97	60

LACS8	3044	3044 A	G	4.1	60
LACS8	3751	3751 C	A	4.05	60
LACS8	3899	3899 A	G	3.08	60
LACS8	3923	3923 G	A	0.87	60
LACS8	4603	4603 G	A	3.91	60
LACS8	4627	4627 G	A	3.76	60
LACS8	5366	5366 T	A	17.54	60
LACS8	5393	5393 T	C	5.23	60
LACS8	5414	5414 G	A	1.44	60
LACS8	6030	6030 C	T	2.47	60
LACS8	6099	6099 G	A	0.26	60
LACS8	6238	6238 G	A	5.07	60
LACS8	6430	6430 A	G	2.21	60
LCY1	1217	1217 C	T	30.03	60
LCY1	1313	1313 C	T	29.88	60
LCY1	1337	1337 C	T	28.89	60
LCY1	1343	1343 C	A	29.26	60
LCY1	420	420 G	C	30.5	60
LFNR	369	369 G	GAC	32.42	60
LFNR	400	400 T	TCC	30.48	60
LFNR	443	443 G	A	8.44	60
LFNR	458	458 A	G	1.53	60
LFNR	485	488 TCTC	T	1.92	60
LFNR	492	492 C	T	3.35	60
LFNR	511	511 T	A	1.99	60
LFNR	534	534 T	C	5.79	60
LFNR	552	552 C	T	1.75	60
LFNR	569	569 G	A	2.86	60
LFNR	697	697 A	AGCG	0.32	60
LFNR	610	610 T	TGCCCTCCTC	0.41	60
LFNR	658	658 C	T	2.11	60
LFNR	671	671 C	A	11.19	60
LFNR	694	694 C	A	2	60
LFNR	1193	1193 G	A	23.89	60
LFNR	1259	1259 G	A	2.2	60
LFNR	1283	1283 A	G	0.45	60
LFNR	599	599 G	C	7.1	60
LFNR	683	683 G	A	16.58	60
LFNR	752	752 C	T	5.49	60
LFNR	806	806 G	C	18.64	60
LFNR	809	809 C	G	18.59	60
LFNR	839	839 G	C	27.18	60
LFNR	1216	1216 C	T	1.97	60
LFNR	1684	1684 G	A	6.64	60

LFNR	2201	2201 A	G	5.14	60
LFNR	2412	2412 C	T	2.42	60
LFNR	2505	2505 G	A	3.42	60
LFNR	2538	2538 G	A	4.58	60
LFNR	2619	2619 C	T	8.56	60
MAT1	122	122 A	C	12.84	60
MAT1	142	142 T	C	10.48	60
MAT1	484	493 CCGAGGGCGC		5.47	60
MAT1	301	301 G	A	31.87	60
MAT1	349	349 G	A	26.67	60
MAT1	4062	4062 A	C,T	30.53	60
MAT1	285	285 G	T	33.94	60
MAT1	441	441 G	A	9.98	60
MAT1	522	522 G	A	7.3	60
MAT1	664	664 T	A	9.38	60
MAT1	4058	4058 C	G	28.98	60
MAT1	3848	3848 G	T	31.2	60
MAT1	203	203 C	A	15.4	60
MAT1	278	278 G	T	18.1	60
MAT1	491	491 C	T	5.44	60
MAT1	536	536 G	T	2.14	60
MAT1	3845	3845 C	A,T	25.55	60
MAT1	3866	3866 C	G	36.87	60
MATE	286	286 G	T	25.27	60
MATE	309	309 A	G	17.22	60
MATE	329	329 A	T	6.44	60
MATE	381	381 A	G	10.91	60
MATE	399	399 G	A	6.08	60
MATE	400	400 A	G	13.52	60
MATE	1019	1022 AACG	A	5.29	60
MATE	849	849 G	GTAA	1.39	60
MATE	785	785 A	T	2.07	60
MATE	800	800 C	T	5.75	60
MATE	819	819 C	T	2.02	60
MATE	864	864 G	C	1.29	60
MATE	890	890 A	G	14.92	60
MATE	893	893 A	G	1.65	60
MATE	903	903 T	G	10.19	60
MATE	1017	1017 A	G	3.27	60
MATE	1022	1022 G	A	16.3	60
MATE	1031	1031 G	T	6.56	60
MATE	1047	1047 C	T	10.37	60
MATE	2346	2346 T	G	27.54	60
MATE	4099	4099 G	A	20.32	60

MATE	4117	4117 T	C	29.36	60
MATE	5141	5141 A	T	3.2	60
MATE	5249	5249 G	T	4.05	60
MATE	5685	5685 A	G	14.73	60
MATE	5701	5701 G	A	9.82	60
MATE	5710	5710 A	G	2.05	60
MATE	6012	6012 G	A	3.74	60
MATE	6093	6093 G	A	2.23	60
MATE	877	877 T	A	2.65	60
MATE	994	994 C	T	4.95	60
MATE	2650	2650 G	A	11.27	60
MATE	2689	2689 T	C	2.85	60
MATE	3888	3888 C	T	13.22	60
MATE	3927	3927 A	T	19.49	60
MATE	5699	5699 C	T	7.76	60
MATE	6029	6029 A	G	2.71	60
MATE	6062	6062 T	C	2.1	60
MFP2	224	224 G	A	29.27	60
MFP2	231	231 A	C	35.51	60
MFP2	260	260 T	G	31.26	60
MFP2	4751	4751 G	A	2.03	60
MFP2	4752	4752 A	T	2.22	60
MFP2	276	276 A	G	32.98	60
MFP2	328	328 A	T	2.27	60
MFP2	2832	2832 A	T	1.02	60
MFP2	2886	2886 A	T	1.09	60
MFP2	2889	2889 C	A	1.71	60
MFP2	2901	2901 A	T	6.03	60
MFP2	2999	2999 G	A	3.6	60
MFP2	3325	3325 A	T	2.07	60
MFP2	3847	3847 G	T	36.55	60
MFP2	3916	3916 C	A	1.71	60
MFP2	3935	3935 G	A	28.83	60
MFP2	3941	3941 A	G	0.83	60
MFP2	4075	4075 T	C	30.4	60
MFP2	4256	4256 G	A	5.33	60
MFP2	4450	4450 G	A	2.01	60
MFP2	4510	4510 C	T	4.24	60
MFP2	4702	4702 G	A	0.45	60
MFP2	4709	4709 A	G	10.22	60
MFP2	4719	4719 C	T	0.43	60
MFP2	4724	4724 A	T	3.93	60
MFP2	5452	5452 C	T	2.59	60
MFP2	5684	5684 G	T	2.05	60

MFP2	5760	5760 C	T	1.01	60
MFP2	2833	2833 G	A	1.12	60
MFP2	2845	2845 T	C	1.93	60
MFP2	2854	2854 G	A	1.11	60
MFP2	2947	2947 A	G	1.74	60
MFP2	3037	3037 C	G	7.35	60
MFP2	3167	3167 G	T	19.4	60
MFP2	3405	3405 T	C	7.38	60
MFP2	3408	3408 T	C	24.97	60
MFP2	3417	3417 T	G	32.65	60
MFP2	3441	3441 G	A	23.51	60
MFP2	3447	3447 A	G	24.9	60
MFP2	3614	3614 T	G	23.54	60
MFP2	3626	3626 A	G	30.65	60
MFP2	3653	3653 C	T	32.38	60
MFP2	3665	3665 C	T	9.44	60
MFP2	3849	3849 G	T	32.56	60
MFP2	4251	4251 T	C	3.66	60
MFP2	4287	4287 T	C	1.72	60
MFP2	4431	4431 G	T	3.15	60
MFP2	4491	4491 A	G	12.52	60
MFP2	4645	4645 A	G	0.68	60
MFP2	4744	4744 A	T	0.93	60
MFP2	5384	5384 A	G	0.81	60
MFP2	5387	5387 C	T	0.82	60
MFP2	5429	5429 C	T	1.67	60
MFP2	5430	5430 A	C	1.67	60
MFP2	5450	5450 C	T	0.97	60
MFP2	5468	5468 C	T	1.5	60
MFP2	5489	5489 C	T	2.04	60
MFP2	5498	5498 T	G	4.38	60
MFP2	5731	5731 C	T	5.09	60
NIT4	322	322 C	A	1.67	60
NIT4	358	358 C	T	3.72	60
NIT4	428	428 C	A	1.92	60
NIT4	442	442 G	A	23.26	60
NIT4	526	526 C	T	5.6	60
NIT4	558	558 C	T	4.16	60
NIT4	644	644 G	A	3.48	60
NIT4	647	647 G	A	4.1	60
NIT4	650	650 G	T	5.08	60
NIT4	1576	1576 T	A	9.82	60
NIT4	1643	1643 G	A	1.8	60
NIT4	2554	2554 G	A	2.66	60

NIT4	2574	2574 A	C	12.24	60
NIT4	2587	2587 A	T	4.55	60
NIT4	2592	2592 G	A	1.98	60
NIT4	2982	2982 G	C	5.34	60
NIT4	3022	3022 G	T	2.07	60
NIT4	3222	3222 A	G	2.38	60
NIT4	3228	3228 G	A	4.4	60
NIT4	3238	3238 C	G	13.18	60
NIT4	670	670 A	G	11.63	60
NIT4	715	715 C	T	4.7	60
NIT4	1530	1530 A	G	5.55	60
NIT4	1554	1554 T	C	2.22	60
NIT4	1680	1680 T	C	24.68	60
NIT4	2567	2567 A	G	2.49	60
NIT4	2588	2588 C	T	14.45	60
NIT4	2589	2589 C	T	6.56	60
NIT4	2654	2654 G	A	4.26	60
NIT4	2702	2702 A	G	2.72	60
NIT4	2729	2729 C	T	13.79	60
NIT4	2756	2756 T	G	4.57	60
NIT4	2759	2759 G	A	1.26	60
NIT4	2762	2762 T	G	1.24	60
NIT4	3002	3002 A	G	4.37	60
NIT4	3038	3038 G	A	9.04	60
NIT4	3062	3062 C	T	4.21	60
NIT4	3065	3065 T	C	10.01	60
NIT4	3134	3134 C	T	2.84	60
NIT4	3173	3173 C	T	0.45	60
NIT4	3206	3206 A	G	4.68	60
NIT4	3242	3242 G	T	15.83	60
OEP64	39	39 G	C	26.27	60
OEP64	56	56 G	C	30.58	60
OEP64	67	67 C	T	4.85	60
OEP64	2912	2912 T	C	10.93	60
OEP64	2950	2950 G	A	32.66	60
OEP64	3259	3259 C	A	13.08	60
OEP64	5466	5466 A	T	4.56	60
OEP64	5511	5511 G	A	2.65	60
OEP64	5761	5761 T	A	1.02	60
OEP64	5783	5783 G	A	3.1	60
OEP64	6594	6594 G	A	1.26	60
OEP64	6627	6627 C	T	3.59	60
OEP64	6629	6629 A	G	25.61	60
OEP64	6647	6647 G	A	14.83	60

OEP64	6668	6668 T	G	2.9	60
OEP64	9028	9028 G	T	2.01	60
OEP64	9041	9041 C	T	8.38	60
OEP64	9062	9062 G	A	3.57	60
OEP64	164	164 A	G	10.28	60
OEP64	2940	2940 A	G	4.17	60
OEP64	3027	3027 C	T	7.78	60
OEP64	3228	3228 T	C	4.8	60
OEP64	5245	5245 T	A,G	26.58	60
OEP64	5254	5254 A	G	22.63	60
OEP64	5284	5284 C	G	19.05	60
OEP64	5476	5476 A	G	22.31	60
OEP64	5488	5488 T	C	4.18	60
OEP64	5512	5512 C	T	1.72	60
OEP64	5806	5806 G	A	5.38	60
OEP64	5839	5839 G	A	3.12	60
OEP64	6583	6583 T	C	0.76	60
OEP64	6652	6652 A	G	4.53	60
OEP64	8467	8467 T	C	1.35	60
OEP64	8521	8521 G	A,T	3.95	60
OEP64	8578	8578 A	G	24.57	60
OEP64	9012	9012 A	G	3.67	60
OEP64	9021	9021 A	G	3.43	60
ONL1	609	609 C	T	34.85	60
ONL1	1386	1386 C	T	8.44	60
ONL1	1691	1691 T	G	15.31	60
ONL1	1743	1743 A	G	25.56	60
ONL1	1848	1848 C	G	31.65	60
ONL1	1892	1892 G	A	7.11	60
ONL1	617	617 C	T	34.85	60
ONL1	1330	1330 C	T	5.9	60
ONL1	1393	1393 C	T	7.97	60
ONL1	1465	1465 C	A	7.52	60
ONL1	1498	1498 T	A	6.61	60
ONL1	1795	1795 G	T	16.28	60
ONL1	1816	1816 C	T	11.76	60
ONL1	1906	1906 T	C	26.3	60
ONL1	2041	2041 G	T	21.15	60
PDS1	5943	5943 T	C	0.43	60
PDS1	5972	5972 A	G	1.87	60
PDS1	5977	5977 G	C	1.05	60
PDS1	5982	5982 A	G	10.69	60
PDS1	6005	6005 A	T	9.93	60
PDS1	6026	6026 A	G	1.05	60

PDS1	6036	6036 C	T	7.77	60
PDS1	6070	6070 T	A	9.36	60
PDS1	6088	6088 G	T	2.33	60
PDS1	6109	6109 C	T	13.56	60
PDS1	6110	6110 G	A	2.65	60
PDS1	6141	6141 T	C	0.33	60
PDS1	6146	6146 G	A	0.54	60
PDS1	6159	6159 G	A	1.07	60
PDS1	6169	6169 T	TAA	28.98	60
PDS1	6180	6180 G	GA	1.04	60
PDS1	6212	6212 A	T,C	8.04	60
PDS1	823	823 G	A	8.88	60
PDS1	850	850 A	T	15.79	60
PDS1	922	925 TTCC	T	4.11	60
PDS1	913	913 T	TG	1.93	60
PDS1	901	901 A	C	17.98	60
PDS1	915	915 G	C	2.22	60
PDS1	916	916 G	T	2.2	60
PDS1	1011	1011 T	C	28.13	60
PDS1	1187	1187 G	A	4.8	60
PDS1	1213	1213 A	G	20.42	60
PDS1	2142	2142 G	A	8.83	60
PDS1	2161	2161 G	A	1.49	60
PDS1	2193	2193 G	A	0.66	60
PDS1	2504	2504 C	A	14.66	60
PDS1	2558	2558 G	A	3.19	60
PDS1	2567	2567 A	G	3.17	60
PDS1	2587	2587 A	G,T	25.12	60
PDS1	3855	3855 G	T	27.22	60
PDS1	3972	3972 A	G	0.26	60
PDS1	3987	3987 G	A	0.61	60
PDS1	4158	4158 A	T	1.72	60
PDS1	4349	4349 A	C,T	13.36	60
PDS1	4562	4562 T	C	22.4	60
PDS1	5294	5294 C	G	1.07	60
PDS1	5300	5300 T	C	1.43	60
PDS1	5591	5591 C	T	19.54	60
PDS1	5600	5600 C	G	0.88	60
PDS1	5615	5615 G	A	3.34	60
PDS1	5627	5627 G	C	25.47	60
PDS1	5657	5657 C	T	23.11	60
PDS1	5698	5698 T	C	7.77	60
PDS1	5933	5933 C	T	3.26	60
PDS1	3621	3621 A	T	31.69	60

PDS1	5381	5381 C	T	27.3	60
PDS1	5397	5397 C	A	1.17	60
PDS1	5393	5393 T	C	29.13	60
PDS1	5328	5328 A	G	32.64	60
PDS1	1164	1164 C	T	26.49	60
PDS1	1379	1379 T	C	26.62	60
PDS1	1450	1450 A	C,T	33.52	60
PDS1	2138	2138 T	C	3.87	60
PDS1	2141	2141 C	T	14.87	60
PDS1	2150	2150 G	A	14.17	60
PDS1	2183	2183 A	C	8.76	60
PDS1	2192	2192 C	T	8.54	60
PDS1	2213	2213 A	C	1.49	60
PDS1	2503	2503 A	G	14.73	60
PDS1	2521	2521 A	G	4.67	60
PDS1	2527	2527 T	G	13.42	60
PDS1	3869	3869 G	A	30.83	60
PDS1	3930	3930 C	T	26.01	60
PDS1	3947	3947 A	G	28.14	60
PDS1	3992	3992 C	T	33.85	60
PDS1	3995	3995 C	T	0.24	60
PDS1	4010	4010 A	T	0.98	60
PDS1	4013	4013 T	C	0.26	60
PDS1	4157	4157 A	T	30.93	60
PDS1	4163	4163 T	C	31.86	60
PDS1	5377	5377 T	C	34.23	60
PDS1	5595	5595 T	C	14.83	60
PDS1	5610	5610 G	C	19.98	60
PDS1	5920	5920 A	G	0.76	60
PED1	116	117 TC	T,TCC	6.21	60
PED1	135	135 C	T	36.3	60
PED1	148	148 C	A	30.39	60
PED1	168	168 G	A	25.89	60
PED1	179	179 G	T	25.92	60
PED1	223	223 C	T	5.66	60
PED1	291	291 C	CAG	4.15	60
PED1	299	299 A	G	5.09	60
PED1	326	326 A	G	2.76	60
PED1	1369	1369 G	T	2.72	60
PED1	2356	2356 G	A	5.96	60
PED1	3133	3133 G	T	9.21	60
PED1	1379	1379 T	C	29.22	60
PED1	1927	1927 A	G	1.68	60
PED1	2402	2402 G	A	1.4	60

PED1	3418	3418 C	T	17.24	60
PPO	5542	5542 G	T	4.53	60
PPO	5595	5595 G	A	1.53	60
PPO	5632	5632 C	A	0.94	60
PPO	5633	5633 C	T	28.98	60
PPO	5638	5638 G	GT	4.08	60
PPO	5647	5647 T	A	2.98	60
PPO	5652	5652 G	A	1.44	60
PPO	5653	5653 T	A	1.83	60
PPO	5697	5697 T	G	34.57	60
PPO	5732	5732 C	T	25.39	60
PPO	5744	5744 A	T	1.96	60
PPO	5796	5796 C	T	1.48	60
PPO	5802	5802 C	T	0.99	60
PPO	1157	1157 G	A	5.83	60
PPO	68	68 T	G	33.93	60
PPO	97	97 A	C	31.24	60
PPO	127	127 G	T	27.96	60
PPO	149	149 C	T	9.22	60
PPO	242	242 G	A	30.33	60
PPO	312	312 A	T	3.49	60
PPO	1047	1047 A	T	2.43	60
PPO	1048	1048 G	T	2.44	60
PPO	1069	1069 T	C	2.33	60
PPO	2026	2026 A	G	2.06	60
PPO	2042	2042 A	T	3.82	60
PPO	2075	2075 A	G	1.05	60
PPO	2076	2076 G	C	3	60
PPO	4550	4550 A	G	1.45	60
PPO	4630	4630 A	G	22.54	60
PPO	4928	4928 C	G	4.13	60
PPO	5404	5404 G	A	2.31	60
PPO	5458	5458 G	A	1.7	60
PPO	5520	5520 G	C	1.84	60
PPO	90	90 A	C	33.49	60
PPO	108	108 C	T	26.68	60
PPO	192	192 G	C	26.78	60
PPO	198	198 T	C	1.38	60
PPO	261	261 A	G	31.07	60
PPO	552	552 C	G	0.82	60
PPO	573	573 T	C	7.38	60
PPO	603	603 C	T	12.38	60
PPO	785	785 C	T	8.26	60
PPO	962	962 T	C	11.24	60

PPO	992	992 G	A	3.29	60
PPO	1998	1998 C	A	1.27	60
PPO	2067	2067 A	G	6.76	60
PPO	2085	2085 G	C,A	3.13	60
PPO	4581	4581 T	C	2.14	60
PPO	5259	5259 C	T	2.01	60
PPO	5295	5295 C	T	2.16	60
PPO	5313	5313 C	T	3.78	60
PPO	5340	5340 G	A	2.82	60
PPO	5365	5365 C	T	2.63	60
PPO	5373	5373 C	T	1.23	60
PPO	5409	5409 G	T	2.05	60
PPO	5421	5421 A	T	2.18	60
PPO	5472	5472 C	T	10.07	60
SBP1	247	247 G	A	3.78	60
SBP1	254	254 G	T	3.85	60
SBP1	301	301 G	A	12.27	60
SBP1	358	358 A	G	27.49	60
SBP1	370	370 C	G	30.27	60
SBP1	430	430 G	A	15.94	60
SBP1	442	442 T	C	7.27	60
SBP1	464	464 C	T	8.2	60
SBP1	551	551 T	C	1.08	60
SBP1	622	622 G	A	12.78	60
SBP1	642	642 G	C	4.63	60
SBP1	673	673 A	T	3.46	60
SBP1	789	789 G	T	4.95	60
SBP1	814	814 T	G	15.39	60
SBP1	820	820 G	A	0.87	60
SBP1	829	829 G	A	13.72	60
SBP1	838	838 G	C	13.56	60
SBP1	839	839 C	T	13.14	60
SBP1	891	891 G	C	5.53	60
SBP1	905	905 A	G	13.26	60
SBP1	953	953 G	A	30.56	60
SBP1	225	225 C	T	15.91	60
SBP1	231	231 G	A	2.79	60
SBP1	258	258 G	A	6.31	60
SBP1	276	276 G	C	11.39	60
SBP1	345	345 T	A	7.1	60
SBP1	354	354 T	C	22.51	60
SBP1	378	378 C	T	15.14	60
SBP1	438	438 G	C	5.15	60
SBP1	507	507 A	G	14.83	60

SBP1	534	534 C	T	5.4	60
SBP1	546	546 G	T	4.06	60
SBP1	636	636 T	C	4.59	60
SBP1	658	658 C	T	11.84	60
SBP1	717	717 C	T	4.4	60
SBP1	765	765 T	C	27.24	60
SBP1	855	855 C	T	1.45	60
SBP1	906	906 A	G	13.37	60
TIR1	59	59 C	T	32.5	60
TIR1	154	154 T	G	32.88	60
TIR1	155	155 T	C	34.29	60
TIR1	3390	3390 T	C,G	4.7	60
TIR1	3505	3505 G	A	1	60
TIR1	3545	3545 C	T	3.58	60
TIR1	3620	3620 C	A	1.57	60
TIR1	3707	3707 A	G	2.94	60
TIR1	129	129 C	G	28.94	60
TIR1	180	180 T	C	30.05	60
TIR1	321	321 A	C	7.8	60
TIR1	447	447 C	T	2.85	60
TIR1	3417	3417 T	C	27.07	60
TIR1	3561	3561 A	G	18.6	60
TIR1	3573	3573 A	G	2.08	60
TIR1	3723	3723 C	T	16.82	60
TRX	290	290 G	A	8.11	60
TRX	413	413 G	C	3.15	60
UGT73C6-like	358	358 G	A	9.58	60
UGT73C6-like	364	364 T	C	12.58	60
UGT73C6-like	365	365 G	A	12.13	60
UGT73C6-like	450	450 G	A	2.68	60
UGT73C6-like	513	513 G	A	8.37	60
UGT73C6-like	757	757 T	A	22.73	60
UGT73C6-like	1352	1352 C	A	33.71	60
UGT73C6-like	1425	1425 T	C	20.02	60
UGT73C6-like	1460	1460 C	A	32.36	60
UGT73C6-like	1466	1466 G	A	32.87	60
UGT73C6-like	1485	1485 T	C	25.52	60
UGT73C6-like	1498	1498 G	C	28.61	60
UGT73C6-like	1521	1521 A	G	26.31	60
UGT73C6-like	1589	1589 G	T	4.74	60
UGT73C6-like	1598	1598 G	A	4.46	60
UGT73C6-like	1627	1627 C	G	3.56	60
UGT73C6-like	1728	1728 T	C	6.93	60
UGT73C6-like	1842	1842 G	A	1.93	60

UGT73C6-like	1895	1895 A	G	1.73	60
UGT73C6-like	2021	2021 T	A	4.02	60
UGT73C6-like	356	356 C	T	9.58	60
UGT73C6-like	557	557 C	T	27.82	60
UGT73C6-like	659	659 G	A	10.14	60
UGT73C6-like	1507	1507 G	A	33.98	60
UGT73C6-like	1723	1723 G	A	16.84	60
UGT73C6-like	1753	1753 C	A	4.85	60
UGT73C6-like	1793	1793 T	C	4.86	60
UGT73C6-like	1810	1810 G	A	3.23	60
UGT73C6-like	2002	2002 T	C	4.41	60
UGT73C6-like	2053	2053 T	C	12.46	60
UGT73C6-like	2155	2155 A	G	2.64	60

Draft

FS	SOR	MQRankSum	ReadPosRan	QUAL	SNPType
	1.772	1.153	0.736	0.22	293.84 frameshift_variant
21.215	3.592	0.852	-1.488	101.64	missense_variant&splice_region
1.548	0.892	-1.877	1.658	696.33	non-synonymous
5.059	0.719	-0.156	2.11	832.07	non-synonymous
0	1.402	-1.473	1.591	335.8	non-synonymous
4.304	1.512	-1.345	1.127	494.28	non-synonymous
0	0.68	0.294	1.216	491.81	non-synonymous
0	0.649	1.008	1.215	5162.47	non-synonymous
0.87	0.594	0.905	2.025	3360.59	non-synonymous
0	0.784	0.033	0.635	1387.1	non-synonymous
0	0.691	-1	0.695	2112.23	non-synonymous
0.542	0.751	0.049	5.234	19687.87	non-synonymous
1.2	0.514	-1.558	0.894	701.9	non-synonymous
0	0.735	0.75	0.443	1255.95	non-synonymous
2.445	0.518	1.877	6.584	1966.4	non-synonymous
0	0.647	0.38	2.107	5987.02	non-synonymous
1.658	0.972	0.539	1.611	720.29	non-synonymous
1.052	0.499	1.156	1.648	571.41	non-synonymous
3.058	1.07	1.094	0.46	1279.1	synonymous_variant
7.278	1.457	-0.143	-0.446	803.21	synonymous_variant
3.416	0.576	0.648	-0.911	293.45	synonymous_variant
0	0.583	1.352	-0.929	313.41	synonymous_variant
0	0.806	-0.001	3.029	21094.63	synonymous_variant
0	0.698	-1.536	0.951	8365.21	synonymous_variant
4.425	1.963	0.654	-0.482	64.07	synonymous_variant
2.181	0.916	-0.115	-0.703	1869.12	synonymous_variant
0.705	0.825	-0.684	2.546	13331.52	synonymous_variant
1.169	0.577	-1.138	0.513	18276.67	synonymous_variant
0	0.699	-0.104	1.316	1397.1	synonymous_variant
2.054	0.867	-0.288	0.15	772.72	synonymous_variant
0	0.73	1.118	2.045	10818.45	synonymous_variant
0	0.772	1.044	2.238	1069.11	synonymous_variant
1.271	0.782	-0.531	1.923	1112.82	synonymous_variant
6.471	0.29	-0.065	0.907	2245.56	synonymous_variant
0	0.861	-1.376	-0.708	572.27	synonymous_variant
14.103	0.424	-1.262	-1.86	166.52	synonymous_variant
0	0.595	-0.932	0.011	3187.02	synonymous_variant
0	0.718	1.366	1.904	17615.17	synonymous_variant
0	0.639	0.742	0.177	2102.11	3_prime_UTR_variant
0	0.845	-0.009	1.939	2229.11	3_prime_UTR_variant
2.158	0.642	0.739	0.422	1341.49	3_prime_UTR_variant
0	0.585	1.294	0.83	978.49	3_prime_UTR_variant
0	0.869	1.104	-1.497	2149.87	3_prime_UTR_variant

0.779	0.611	-0.317	3.604	8433.1 3_prime_UTR_variant
0	0.676	0.152	1.318	2193.84 3_prime_UTR_variant
1.357	0.833	-1.143	0.74	16753.33 3_prime_UTR_variant
0	0.853	-0.628	-0.123	950.84 3_prime_UTR_variant
2.718	1.463	-1.532	1.166	518.49 3_prime_UTR_variant
2.647	1.368	0.1	1.099	518.49 3_prime_UTR_variant
0	0.68	-1.065	3.481	1148.02 3_prime_UTR_variant
0	0.346	-0.262	0.976	1734.26 3_prime_UTR_variant
0	0.521	0.279	0.913	94.81 3_prime_UTR_variant
0	0.73	0.518	0.431	103.53 3_prime_UTR_variant
0	0.606	-1.33	1.927	1539.27 3_prime_UTR_variant
5.065	1.379	1.433	-1.278	1552.17 3_prime_UTR_variant
0.649	0.769	0.164	-2.178	5901.41 3_prime_UTR_variant
2.641	1.207	1.111	2.579	1094.85 non-synonymous
2.525	0.75	0.415	1.237	565.47 non-synonymous
0	1.01	2.097	-0.964	397.16 non-synonymous
0	0.598	2.156	0.702	85.87 non-synonymous
0	0.654	1.028	0.118	598.23 non-synonymous
2.151	0.88	-0.597	-0.036	2902.79 non-synonymous
0	0.745	0.181	2.316	96.9 non-synonymous
4.084	0.811	1.746	0.689	1156.87 non-synonymous
0	0.883	1.239	-1.486	810.84 non-synonymous
0	0.735	1.216	-0.236	1402.33 non-synonymous
0	1.676	0.233	0.836	326.49 non-synonymous
0	0.738	0.32	-1.3	815.34 non-synonymous
6.501	0.347	-1.143	1.167	1093.24 non-synonymous
0	0.782	-1.501	1.722	2237.38 non-synonymous
0	0.402	0.445	-0.78	125.22 non-synonymous
2.904	0.713	-0.979	2.211	198.72 non-synonymous
0	0.601	0.587	2.612	3733.71 non-synonymous
0	0.727	-1.396	0.463	12976.79 non-synonymous
0	0.621	-0.54	2.189	2644.37 non-synonymous
0	0.602	-1.479	0	149.26 non-synonymous
0	0.26	-0.404	0.673	84.71 non-synonymous
1.765	0.708	0.073	0.147	1750.49 non-synonymous
0	0.408	0.706	0.158	679.92 non-synonymous
0	1.076	-0.185	1.668	1547.9 non-synonymous
0	0.366	1.94	-0.673	100.81 stop_gained
0	0.854	0.601	-0.439	69.87 synonymous_variant
0	0.679	1.41	0.508	476.95 synonymous_variant
5.386	0.603	-0.665	-1.47	1710.87 synonymous_variant
2.483	0.927	-0.288	1.588	4921.11 synonymous_variant
0	0.728	0.463	0.79	1727.6 synonymous_variant
2.046	0.971	0.28	2.108	1911.16 synonymous_variant

0.913	0.859	0.757	0.504	3138.01	synonymous_variant
0	0.913	-0.161	-0.076	101.93	synonymous_variant
0.673	0.753	-1.433	0.38	7422.45	synonymous_variant
1.455	0.847	2.027	1.115	993.72	synonymous_variant
1.266	0.728	-0.46	2.762	40275.14	synonymous_variant
0.87	0.672	0.064	-0.457	3865.24	synonymous_variant
0.902	0.746	-0.233	-0.507	3180.31	synonymous_variant
0.534	0.642	0.848	1.014	9865.38	synonymous_variant
3.478	1.85	0.832	2.025	508.34	synonymous_variant
0	0.661	0.802	2.469	63536.27	synonymous_variant
0.522	0.643	0.688	1.438	33384.39	synonymous_variant
0	0.553	0.579	1.573	418.84	synonymous_variant
0	2.303	0.322	1.92	84.15	synonymous_variant
0	1.136	-	-	921.93	synonymous_variant
0	0.666	-0.324	0.157	501.02	3_prime_UTR_variant
0	0.639	0.677	1.564	8159.94	3_prime_UTR_variant
0.594	0.775	-0.73	0.395	37876.31	3_prime_UTR_variant
0	0.642	1.694	1.542	3539.16	3_prime_UTR_variant
0	0.751	-0.622	-0.883	36919.35	3_prime_UTR_variant
0	0.721	-1.896	-0.292	1052.41	3_prime_UTR_variant
3.855	1.082	-0.462	-1.213	3105.46	3_prime_UTR_variant
4.471	1.101	-0.29	0.503	1917.75	3_prime_UTR_variant
0	0.607	-0.277	-0.909	2797.42	3_prime_UTR_variant
7.637	1.927	-2.14	2.422	119.75	3_prime_UTR_variant
0	0.706	-0.723	2.37	1412.04	3_prime_UTR_variant
6.404	0.321	-0.239	1.075	693.44	3_prime_UTR_variant
0	0.711	0.147	0.485	301.32	non-synonymous
0	0.683	0.556	-1.994	2653.41	non-synonymous
4.942	0.617	1.177	1.384	5901.87	non-synonymous
0	0.885	0.245	1.129	412.07	non-synonymous
0	0.808	1.004	2.239	588.58	non-synonymous
1.031	0.929	1.322	2.961	1405.9	non-synonymous
2.687	0.939	0.472	1.871	12056.48	non-synonymous
0	0.695	0.397	-0.683	8858.65	non-synonymous
1.099	0.611	-0.797	4.856	9065.03	non-synonymous
0.939	0.88	0.35	3.329	1348.94	non-synonymous
3.29	0.507	-0.597	5.052	12019.63	non-synonymous
0	0.675	1.133	1.049	839.8	non-synonymous
0	0.78	1.269	1.476	131.84	non-synonymous
0	0.64	0.444	-0.467	970.84	non-synonymous
4.167	1.094	0.086	0.671	15299.85	non-synonymous
0	0.492	-1.307	2.264	1220.8	non-synonymous
0	1.033	0.856	0.327	121.53	non-synonymous
2.342	0.545	1.064	2.453	205.6	non-synonymous

1.249	0.546	-0.596	2.04	22050.16 non-synonymous
0.583	0.625	-0.541	-1.598	25023 non-synonymous
5.374	1.521	0.505	-0.282	1071.8 non-synonymous
9.06	0.39	1.204	1.813	4149.17 synonymous_variant
2.039	0.982	0.267	1.191	433.01 synonymous_variant
6.939	0.908	-0.347	1.514	2178.74 synonymous_variant
0.964	0.864	0.932	2.221	404.04 synonymous_variant
0	0.783	-0.885	2.581	726.13 synonymous_variant
1.896	1.353	-1.439	-0.052	91.52 synonymous_variant
10.617	1.897	0.497	1.271	855.19 synonymous_variant
8.631	0.232	-0.561	-0.61	905.39 synonymous_variant
3.024	0.837	-0.583	1.158	2959.18 synonymous_variant
5.577	1.329	-0.255	0.42	1688.96 synonymous_variant
0	0.523	-0.067	0.535	128.7 synonymous_variant
0	1.15	-0.001	0.657	99.3 synonymous_variant
0	0.905	-1.174	2.863	844.97 synonymous_variant
1.207	0.834	0.097	2.761	8811.08 synonymous_variant
0	0.688	-0.295	-1.716	1677.8 synonymous_variant
1.287	0.609	-0.38	4.631	35312.48 synonymous_variant
3.716	0.459	1.178	2.046	27936.98 synonymous_variant
2.947	0.775	0.371	3.032	9098.48 synonymous_variant
0	0.583	1.001	1.419	960.84 synonymous_variant
0.95	0.839	1.323	1.105	4680.8 synonymous_variant
3.376	0.879	-0.538	0.156	555.66 synonymous_variant
0	0.694	-0.46	1.285	18302.22 synonymous_variant
0	0.684	0.637	2.397	892.84 synonymous_variant
1.809	0.962	1.626	0.196	9024.37 synonymous_variant
1.631	0.871	0.294	0.813	12926.3 synonymous_variant
0	1.19	1.642	-1.428	1402.39 synonymous_variant
0	0.728	0.09	1.456	16585.73 synonymous_variant
0	0.791	1.179	1.66	3954.36 3_prime_UTR_variant
3.05	0.959	0.647	2.391	4275.37 3_prime_UTR_variant
0	0.692	-0.385	0.437	7605.91 3_prime_UTR_variant
0	0.78	-1.048	0.848	2477.24 3_prime_UTR_variant
2.747	1.282	-0.731	-6.032	5859.72 3_prime_UTR_variant
2.297	0.935	-0.717	-3.595	6261.4 3_prime_UTR_variant
2.472	0.801	2.325	0.575	15434.37 3_prime_UTR_variant
1.872	0.853	-0.144	0.352	17895.47 3_prime_UTR_variant
0.878	0.528	0.615	3.799	7335.9 3_prime_UTR_variant
4.644	0.374	-1.032	0.131	18683.41 3_prime_UTR_variant
0	0.885	-0.297	0.222	430.74 3_prime_UTR_variant
4.776	0.155	0.875	-0.023	154.82 3_prime_UTR_variant
0	0.582	0.589	0.354	294.96 non-synonymous
7.089	0.903	0.828	2.602	3930.32 non-synonymous

0.525	0.75	-0.087	1.217	23436.95 non-synonymous
2.701	0.491	0.726	3.484	39907.44 non-synonymous
0	0.671	-1.23	1.649	3559.99 non-synonymous
1.228	0.439	-0.248	-1.609	1788.7 non-synonymous
1.06	0.938	-1.386	0.98	740.35 non-synonymous
0	0.993	0.498	2.086	89.86 non-synonymous
0	0.679	-0.002	0.493	808.2 non-synonymous
0	0.548	-1.397	1.099	1777.84 non-synonymous
0	0.755	-0.959	0.856	2061.94 non-synonymous
0	0.874	0.015	-1.595	115.66 non-synonymous
0	0.808	1.172	-1.288	2418.51 non-synonymous
5.318	1.619	0.328	-0.016	1780.39 non-synonymous
1.106	0.958	-1.525	7.257	1400.73 non-synonymous
0	0.992	-0.03	1.95	751.55 non-synonymous
7.692	0.385	0.456	3.252	2798.79 synonymous_variant
1.06	0.853	1.925	1.684	980.31 synonymous_variant
0	0.817	1.448	1.868	731.88 synonymous_variant
2.272	1.105	0.805	1.958	2622.16 synonymous_variant
0	0.741	-1.263	1.018	1298.79 synonymous_variant
2.236	1.02	-1.844	2.108	2669.19 synonymous_variant
0.975	0.61	-0.256	1.63	3556.97 synonymous_variant
0	0.723	0.868	2.924	2588.11 synonymous_variant
0.744	0.73	-0.078	0.448	606.43 synonymous_variant
2.316	0.941	0.515	-2.211	750.07 synonymous_variant
0	0.593	0.532	-0.19	324.22 synonymous_variant
0	0.816	-0.907	2.332	114.85 synonymous_variant
0	0.503	-1.044	1.587	607.87 synonymous_variant
1.714	0.88	1.063	0.809	492.94 synonymous_variant
1.415	1.116	0.553	-0.075	629.09 synonymous_variant
1.437	0.931	-0.379	0.703	566.59 synonymous_variant
0	0.709	-1.012	0.616	934.56 synonymous_variant
28.807	2.258	1.116	-1.611	1981.18 synonymous_variant
3.267	1.109	-0.238	1.438	4808.55 synonymous_variant
3.726	1.005	-0.491	3.801	12021.66 synonymous_variant
0.927	0.932	1.105	0.731	1582.9 synonymous_variant
0	0.737	-0.678	0.085	1122.11 synonymous_variant
1.259	0.726	0.254	0.243	5424.07 synonymous_variant
0.96	0.732	0.525	3.984	2411.85 synonymous_variant
3.277	0.848	0.44	5.328	3383.79 synonymous_variant
0	0.627	-1.844	2.171	5141.25 synonymous_variant
2.077	0.511	0.485	-0.706	5905.18 synonymous_variant
6.099	0.38	-1.095	2.405	7798.88 synonymous_variant
0	0.729	1.552	-1.713	3805.77 synonymous_variant
0	0.682	-0.32	2.977	678.66 synonymous_variant

0.878	0.521	-0.705	2.734	4335.37 synonymous_variant
0	0.733	0.727	3.275	22891.51 synonymous_variant
2.108	0.638	0.425	-0.156	2942.35 synonymous_variant
0	1.402	-0.663	0.068	166.75 non-synonymous
0	0.693	0.731	0.731	99.9 non-synonymous
9.96	1.905	0.426	-0.305	345.22 non-synonymous
0	0.779	-0.1	0.835	400.94 non-synonymous
5.505	1.009	-1.167	1.346	172.14 non-synonymous
3.398	1.135	-0.258	0.363	655.1 non-synonymous
0	0.868	0.417	1.25	68.32 non-synonymous
0.834	0.678	-0.933	0.482	520.04 non-synonymous
0	0.581	-0.29	0.004	397.25 non-synonymous
0	0.779	-0.431	-1.368	246.28 non-synonymous
0	2.303	-	-	227.62 synonymous_variant
6.117	0.625	0.453	1.359	117.77 synonymous_variant
3.31	2.303	0.72	0.72	60.75 synonymous_variant
3.31	2.303	-0.72	0.72	60.75 synonymous_variant
12.752	1.911	0.45	0.332	629.88 synonymous_variant
5.304	0.267	1.697	0.948	2609.46 synonymous_variant
0.64	0.615	-1.55	0.583	1136.31 non-synonymous
2.509	0.398	0.873	-1.452	386.05 non-synonymous
0	0.515	-2.077	2.485	110.94 non-synonymous
2.906	0.368	0.204	-1.372	1642.56 synonymous_variant
1.069	0.958	0.992	-0.251	401.53 synonymous_variant
5.767	1.031	0.223	-0.13	1096.86 synonymous_variant
1.596	0.527	0.672	-0.374	1358.29 synonymous_variant
1.827	0.492	0.783	2.082	854.29 synonymous_variant
1.863	0.487	0.054	2.986	846.77 synonymous_variant
3.988	1.19	0.976	0.291	117.89 synonymous_variant
0	0.632	0.21	0.541	1089.48 synonymous_variant
0.581	0.628	-0.178	1.71	1557.68 synonymous_variant
1.948	0.95	-0.57	1.164	3678.65 3_prime_UTR_variant
0	0.591	-1.71	0.377	1334.15 3_prime_UTR_variant
0	1.187	0.596	-4.851	247.02 3_prime_UTR_variant
3.203	1.256	-0.94	-3.204	943.01 3_prime_UTR_variant
1.706	0.844	-0.588	0.1	805.83 3_prime_UTR_variant
0	0.727	0.531	2.53	2166.5 3_prime_UTR_variant
0.969	0.54	-0.288	-0.19	2585.15 3_prime_UTR_variant
0	0.732	0.28	1.59	2653.43 3_prime_UTR_variant
0.793	0.595	-0.086	-0.49	3897.42 3_prime_UTR_variant
1.866	0.436	-1.246	2.685	2464.29 3_prime_UTR_variant
0	0.787	-1.153	-0.515	2040.8 3_prime_UTR_variant
0.882	0.5	0.494	1.085	1534.58 3_prime_UTR_variant
0	0.594	0.403	-0.194	447.83 3_prime_UTR_variant

3.56	1.431	-0.269	-2.153	161.23 3_prime_UTR_variant
4.273	1.157	-0.478	-1.527	534.45 3_prime_UTR_variant
1.648	1.24	-0.389	-2.115	332.09 frameshift_variant
1.557	0.64	-1.667	2.121	3027.33 inframe_insertion
0.982	0.48	-0.761	-1.122	417.8 non-synonymous
2.606	0.627	0.951	0.987	2133.5 non-synonymous
1.508	0.793	-1.542	1.461	593.01 non-synonymous
0	0.656	-0.154	1.802	498.03 non-synonymous
0	0.659	-0.224	0.323	853.38 non-synonymous
0	0.77	-1.644	0.839	1040.82 non-synonymous
1.205	1.133	-1.525	-1.035	609.62 synonymous_variant
1.937	0.993	0.752	2.155	1891.57 synonymous_variant
3.161	0.967	-0.438	1.414	1090.63 synonymous_variant
3.037	1.104	-0.729	0.432	2748.87 synonymous_variant
1.352	0.553	0.53	-0.166	1498.38 synonymous_variant
0	0.614	0.538	1.721	2767.12 synonymous_variant
0	0.689	1.28	2.421	3872.08 synonymous_variant
0	0.67	-1.047	0.452	2783.55 synonymous_variant
1.41	0.983	-1.077	1.968	746.37 synonymous_variant
1.806	0.881	0.606	1.774	3310.79 synonymous_variant
0	0.748	-0.583	-0.847	1533.82 synonymous_variant
0	0.517	-0.358	1.242	690.84 synonymous_variant
0	1.508 -	-	-	903.33 disruptive_inframe_deletion
0	1.445 -	-	-	821.82 non-synonymous
0	1.27 -	-	-	520.34 non-synonymous
0	1.508 -	-	-	912.38 non-synonymous
0	0.418	-0.059	1.009	77.11 5_prime_UTR_premature_stai
0	0.442	0.569	-1.321	175.61 5_prime_UTR_variant
66.227	6.272	1.824	-5.94	1362.2 5_prime_UTR_variant
0	0.573	-1.22	1.314	2589.29 non-synonymous
1.773	0.732	-0.748	2.357	13051.61 non-synonymous
0	0.672	0.719	0.857	1273.86 non-synonymous
2.124	0.985	1.054	1.259	906.44 non-synonymous
5.365	1.17	-0.894	3.669	1110.82 non-synonymous
13.51	0.602	-0.236	0.067	12893.28 non-synonymous
2.023	0.691	0.936	-0.22	375.34 non-synonymous
0	0.564	-0.777	2.241	959.88 synonymous_variant
2.65	0.551	0.408	1.514	969.93 synonymous_variant
0.971	0.97	0.294	0.35	2769.97 3_prime_UTR_variant
0	0.637	0.339	0.466	1456.63 3_prime_UTR_variant
0	0.857	0.55	-0.42	172.95 3_prime_UTR_variant
1.387	1.041	-0.432	2.402	832.32 3_prime_UTR_variant
0	0.65	0.564	0.686	1012.12 3_prime_UTR_variant
5.328	0.193	0.615	0.849	271.66 3_prime_UTR_variant

1.444	1.076	1.287	2.175	253.98 missense_variant&splice_regi
1.683	0.99	-0.293	0.293	89.3 non-synonymous
0	0.67	-0.758	-0.475	4887.37 non-synonymous
5.002	1.573	0.434	1.789	229.86 non-synonymous
0	1.321 -	-		3847.83 non-synonymous
2.046	0.333	0.206	0.289	581.64 non-synonymous
5.004	1.511	-0.55	0.529	77.12 non-synonymous
4.223	1.728	-0.553	0.351	71.62 non-synonymous
4.746	1.296	0.428	1.122	1083.69 non-synonymous
1.666	0.68	-1.116	0.043	786.92 non-synonymous
116.529	4.743	0.664	1.938	3017.67 non-synonymous
8.846	1.44	1.809	3.105	187.6 non-synonymous
2.45	1.025	0.794	0.374	697.47 non-synonymous
6.724	0.84	0.553	1.763	2559.9 non-synonymous
0.911	0.854	0.533	2.382	1301.3 non-synonymous
0	0.734	0.437	1.626	99.17 non-synonymous
5.33	1.637	1.968	2.587	199.13 non-synonymous
1.684	0.885	-0.02	-0.989	599.59 non-synonymous
0.765	0.775	-1.178	3.555	3398.77 non-synonymous
2.081	1.001	-0.476	-0.732	201.22 non-synonymous
0	0.557	-0.125	-1.955	2248.43 non-synonymous
0	0.737	-0.006	1.037	282.98 non-synonymous
0.961	0.563	-0.984	-1.402	1024.45 non-synonymous
1.492	0.92	0.578	-0.75	752.55 non-synonymous
0	0.706	0.137	1.395	3435.42 non-synonymous
1.392	0.983	-0.497	1.608	1190.14 non-synonymous
0	0.71	0.422	1.407	2757.69 non-synonymous
0	0.724	-1.15	0.872	2358.97 non-synonymous
0.83	0.57	-1.044	-0.039	3804.99 non-synonymous
0.895	0.86	0.897	-0.058	555.35 synonymous_variant
1.62	1.077	1.733	-0.193	157.31 synonymous_variant
0	0.604	-0.949	0.27	6664.26 synonymous_variant
3.024	0.49	0.626	-0.387	13631.13 synonymous_variant
0	0.841	0.998	0.533	1093.68 synonymous_variant
2.094	0.944	-0.519	0.084	318.22 synonymous_variant
0	0.643	-1	2.361	3843.91 synonymous_variant
2.82	1.175	-0.078	0.315	1537.49 synonymous_variant
1.084	0.784	-1.126	1.49	2072.72 synonymous_variant
0	0.728	-1.946	0.234	316.17 synonymous_variant
1.151	0.984	-1.407	1.296	2016.93 synonymous_variant
0	0.755	0.209	3.192	3371.59 synonymous_variant
6.282	1.141	-0.467	-0.713	1556.31 synonymous_variant
0	1.863 -	-		2588.01 non-synonymous
0	1.292 -	-		3059.43 non-synonymous

0	1.127	-	-	2857.43 non-synonymous
0	1.214	-	-	2971.29 non-synonymous
0	1.038	-	-	5742.48 synonymous_variant
0	0.973	-	-	5424.59 synonymous_variant
0	1.112	-	-	2971.29 synonymous_variant
0	0.223	-0.143	-1.932	180.58 5_prime_UTR_variant
0	1.022	-	-	365.49 non-synonymous
0	0.61	-0.932	0.261	613.17 non-synonymous
1.332	0.421	1.027	-0.064	457.21 non-synonymous
9.868	1.472	-0.535	-1.707	164.49 non-synonymous
0	0.412	-0.636	-0.071	114.05 non-synonymous
0	0.693	-0.747	0.747	260.17 non-synonymous
2.75	1.078	-0.112	0.186	658.05 non-synonymous
8.194	3.258	0.873	-1.076	220.88 non-synonymous
0	0.693	-1.563	-0.355	727.91 synonymous_variant
0	0.365	-0.63	-1.734	774.99 synonymous_variant
0	0.754	-0.529	0.244	238.33 synonymous_variant
1.524	0.399	1.022	-0.517	145.36 frameshift_variant
0	0.804	-0.567	-1.567	168.36 non-synonymous
7.574	2.279	0.7	-0.158	150.62 non-synonymous
4.134	1.938	-0.821	-0.036	177.92 non-synonymous
1.456	1.157	-0.405	1.104	314.47 non-synonymous
3.305	1.445	0.24	0.927	337.62 non-synonymous
8.074	1.905	0.825	0.778	180.75 non-synonymous
9.138	2.258	-0.441	-1.148	274.17 non-synonymous
10.328	2.809	0.076	-0.982	77.24 non-synonymous
3.432	1.375	-0.705	0.981	197.55 non-synonymous
1.727	1.278	0.254	0.496	146.71 synonymous_variant
0	0.833	0.106	2.738	135.9 synonymous_variant
8.074	1.905	0.165	0.636	180.75 synonymous_variant
10.473	2.256	-1.463	0.515	179.97 synonymous_variant
4.151	1.214	0.254	1.045	422.77 synonymous_variant
0	1.609	-	-	160.71 3_prime_UTR_varian
1.579	0.58	1.083	2.344	1615.14 3_prime_UTR_variant
2.373	0.471	-0.508	-1.234	2667.05 3_prime_UTR_variant
1.528	0.821	0.407	-0.224	2621.25 3_prime_UTR_variant
1.848	0.892	-0.198	-0.03	3663.06 3_prime_UTR_variant
1.773	0.508	0.443	0.489	1551.53 3_prime_UTR_variant
1.501	0.515	0.25	-0.52	611.6 3_prime_UTR_variant
0	1.609	-	-	160.71 3_prime_UTR_variant
0	0.722	0.434	-0.303	2133.01 non-synonymous
1.747	0.826	-0.431	1.969	1511.34 non-synonymous
4.705	1.55	0.434	1.368	217.81 non-synonymous
3.622	1.067	-0.978	-0.715	346.62 non-synonymous

3.114	0.324	-1.623	-1.732	4675.31 non-synonymous
8.451	3.901	-0.567	-2.709	702.27 non-synonymous
9.44	1.854	-0.722	1.355	249.53 non-synonymous
1.452	0.578	0.674	-1.2	881.65 non-synonymous
16.212	0.593	-0.41	2.124	126.82 non-synonymous
3.979	2.788	-1.58	0.573	69.07 non-synonymous
0	0.65	0.379	-1.029	105.95 non-synonymous
2.219	0.401	-0.033	-0.026	3841.79 non-synonymous
0	0.892	-1.062	0.839	71.29 splice_region_variant&synony
1.396	0.726	1.411	1.416	7508.26 stop_gained
16.86	0.366	-1.068	3.4	453.66 synonymous_variant
0	0.741	0.209	0.487	178.73 synonymous_variant
0	0.649	0.138	1.029	148.76 synonymous_variant
0	0.877	0.155	1.71	84.66 synonymous_variant
15.233	2.608	0.408	1.822	419.33 synonymous_variant
2.796	0.491	0.095	1.1	1199.15 synonymous_variant
11.646	1.897	0.019	-0.134	422.06 synonymous_variant
2.147	0.8	-0.419	-0.242	940.47 synonymous_variant
5.166	1.954	1.445	-2.809	860.81 synonymous_variant
8.129	3.596	0.505	-2.67	586.44 synonymous_variant
6.802	1.147	-1.563	3.074	100.74 synonymous_variant
2.782	0.825	0.547	1.216	2831.46 synonymous_variant
1.963	0.897	1.068	0.483	358.42 synonymous_variant
0	0.567	1.838	0.309	209.66 synonymous_variant
17.936	0.021	0.22	0.879	878.94 5_prime_UTR_premature_stai
0	0.223	0	-0.72	94.9 5_prime_UTR_variant
0	0.569	1.268	1.305	1140.36 5_prime_UTR_variant
3.295	1.494	0.843	-1.616	1319.36 5_prime_UTR_variant
1.316	0.39	-0.694	1.213	646.56 5_prime_UTR_variant
1.687	0.984	-0.05	-0.012	794.64 non-synonymous
0	0.714	0.646	1.486	6153.83 non-synonymous
3.024	0.471	0.627	3.551	7095.92 non-synonymous
0	0.913	-0.806	0.978	722.47 non-synonymous
1.931	0.735	-1.281	-0.925	14358.19 non-synonymous
0	0.778	0.704	2.218	2002.01 synonymous_variant
4.101	1.424	-0.608	0.985	1040.38 synonymous_variant
6.298	0.381	2.195	1.806	5499.09 synonymous_variant
0	0.683	-0.453	1.308	2306.3 synonymous_variant
1.074	0.53	0.899	-0.209	983.27 synonymous_variant
11.641	3.02	-0.427	-1.351	551.53 synonymous_variant
6.361	0.377	-0.91	1.424	6035.96 synonymous_variant
0.552	0.739	-0.284	-0.713	17549.6 synonymous_variant
2.947	1.025	1.044	0.232	7157.02 synonymous_variant
0	0.719	-0.859	-2.084	10675.96 synonymous_variant

21.47	0.905	-1.024	0.938	1084.69 synonymous_variant
2.181	0.843	0.074	1.52	2382.46 synonymous_variant
0	0.783	-1.093	-0.295	1790.71 synonymous_variant
1.096	0.707	0.809	0.432	2464.89 synonymous_variant
0	0.706	-1.533	-2.443	1321.44 synonymous_variant
0	0.693	-1.519	0.569	676.5 synonymous_variant
0	0.641	0.492	-0.684	2472.85 synonymous_variant
1.25	0.864	-1.635	2.535	1732.47 synonymous_variant
7.703	2.093	0.773	-0.215	349.8 non-synonymous
1.225	0.955	-0.938	1.036	1376.07 non-synonymous
3.58	0.712	-0.876	0.644	210 non-synonymous
3.404	1.073	0.93	2.378	236.37 non-synonymous
0	0.73	0.313	-1.143	253.17 non-synonymous
0	0.557	-1.056	0.97	523.29 non-synonymous
0	0.859	0.312	0.101	222.88 non-synonymous
0.776	0.637	0	0.821	867.48 non-synonymous
13.411	2.291	2.052	0.789	337.25 non-synonymous
0	0.929	0.465	0.578	107.76 synonymous_variant
10.957	2.388	0	2.057	403.29 synonymous_variant
5.553	0.894	0.353	-1.074	655.05 synonymous_variant
0	0.578	0.473	0.193	75.77 synonymous_variant
0	0.927	0.14	-1.652	159.21 synonymous_variant
0	0.787	0.783	-0.074	364.82 synonymous_variant
1.13	0.73	0.129	1.126	367.35 synonymous_variant
0	0.09	-0.361	0.361	76.41 5_prime_UTR_variant
3.551	0.496	-1.26	-1.108	2746.84 5_prime_UTR_variant
0	0.738	1.726	0.237	66.68 non-synonymous
1.963	1.063	0.522	-0.366	281.56 non-synonymous
1.459	0.854	-0.602	1.457	9350.37 non-synonymous
0	0.67	0.624	0.015	2513.04 non-synonymous
3.021	1.714	0.77	-0.608	226.93 non-synonymous
7.576	2.133	-0.696	-0.961	380.23 non-synonymous
6.442	0.695	-1.59	0.285	658.73 non-synonymous
0	0.813	-0.331	-0.65	60.51 non-synonymous
1.906	1.467	-0.941	-0.461	140.58 non-synonymous
0	0.595	0.321	0.539	716.2 synonymous_variant
2.573	0.515	-0.92	2.639	1258.25 synonymous_variant
5.351	0.566	0.835	1.316	151.46 synonymous_variant
3.016	1.678	1.855	-0.809	226.93 synonymous_variant
0	0.598	0.555	0.146	65.52 synonymous_variant
1.456	0.455	0.198	-1.756	1623.78 5_prime_UTR_variant
22.703	1.749	-0.572	4.037	2321.55 5_prime_UTR_variant
5.986	1.153	0.874	-1.029	3866.45 5_prime_UTR_variant
4.929	1.096	0.517	-1.265	3866.45 5_prime_UTR_variant

0	1.022	-	-	225.02 frameshift_variant
0	0.693	-	-	1100.57 non-synonymous
0	1.329	-	-	1208.51 non-synonymous
0	1.981	-	-	2552.79 non-synonymous
0	2.191	-	-	3539.23 non-synonymous
0	0.83	-	-	6794.12 non-synonymous
0	0.778	-	-	9532.92 non-synonymous
6.795	0.295	-0.117	-1.483	2950.95 non-synonymous
8.108	1.894	0.232	-1.909	75.27 non-synonymous
0	0.693	-	-	151.63 non-synonymous
5.298	0.897	-0.783	-0.875	2665.79 non-synonymous
0	0.569	0.345	0.681	230.7 non-synonymous
0.586	0.79	-0.66	-0.54	1465.36 non-synonymous
0	1.108	-	-	6177.61 non-synonymous
0	1.092	-	-	6177.61 non-synonymous
2.809	0.851	0.329	0.878	1962.13 synonymous_variant
1.888	0.995	1.183	-0.289	554.08 synonymous_variant
2.294	0.415	0.593	1.164	427.96 synonymous_variant
3.884	1.203	-1.099	0.133	91.19 synonymous_variant
0	0.608	0.857	0.439	80.64 synonymous_variant
3.085	0.32	-2.326	-0.025	3603.94 synonymous_variant
0	2.833	-	-	104.16 non-synonymous
0	1.732	-	-	6435.36 non-synonymous
0	1.981	-0.876	-0.361	227.39 non-synonymous
0	2.303	-0.633	-0.365	227.39 non-synonymous
2.228	0.388	0.176	0.81	448.57 non-synonymous
1.631	0.361	0.299	-0.737	187.07 non-synonymous
3.989	1.185	0.263	0.472	121.81 non-synonymous
6.779	0.293	-0.648	-0.048	3446.46 non-synonymous
6.469	0.3	0.15	-0.123	1101.97 non-synonymous
3.986	0.804	-0.323	-0.276	65.18 non-synonymous
0	0.589	0.319	-2.298	307.96 non-synonymous
2.259	0.369	0.511	-0.471	490.41 non-synonymous
0	1.022	0.986	1.144	96.57 splice_region_variant&synony
0	2.833	-	-	108.16 synonymous_variant
19.901	2.81	-0.426	-1.449	194.38 synonymous_variant
0.807	0.591	0.176	2.529	999.28 synonymous_variant
0	0.686	-0.535	-1.284	166.6 synonymous_variant
8.505	1.763	-1.424	1.431	581.4 synonymous_variant
0	0.73	-0.023	0.398	141.03 synonymous_variant
1.157	0.973	0.891	0.309	378.51 synonymous_variant
3.569	0.345	-1.094	1.451	661.1 synonymous_variant
3.93	0.968	-1.356	-0.127	3469.73 synonymous_variant
1.537	0.837	-0.775	2.034	1205.92 synonymous_variant

5.44	0.463	1.5	1.957	4012 synonymous_variant
8.429	1.739	-1.075	-2.421	1043.83 synonymous_variant
2.339	1.132	0.166	-0.498	537.07 synonymous_variant
3.743	1.198	0.408	-0.917	353.51 synonymous_variant
1.456	0.51	-0.226	0.744	1670.99 non-synonymous
2.329	0.908	-0.727	2.195	1612.16 non-synonymous
8.948	2.451	-0.356	-5.712	107.72 non-synonymous
6.67	0.299	-0.164	-0.178	760.72 non-synonymous
1.251	0.472	0.067	2.499	2554.83 synonymous_variant
7.972	2.742	-1.05	-0.534	120.26 synonymous_variant
2.161	0.493	-0.67	-1.537	2359.58 synonymous_variant
0	0.764	0.713	-0.781	3485.62 synonymous_variant
0	1.118	0.106	1.588	66.19 synonymous_variant
0	0.674	-0.57	3.192	3998.13 synonymous_variant
16.742	0.339	0.402	-1.214	308.87 5_prime_UTR_variant
27.876	2.446	0.591	6.911	1457.04 5_prime_UTR_variant
2.367	0.404	-0.223	-5.632	26959.96 5_prime_UTR_variant
2.395	9.126	0.532	-17.809	4050.32 5_prime_UTR_variant
0	0.721	-0.197	4.03	10624.49 5_prime_UTR_variant
0	0.847	-1.64	-1.39	14029.49 5_prime_UTR_variant
0	0.743	0.713	1.695	130008.46 non-synonymous
0	0.673	0.169	6.567	138855.45 non-synonymous
0	0.811	0.918	-0.077	12597.37 non-synonymous
0	0.781	1.058	-1.079	18514.8 non-synonymous
4.761	1.182	0.579	2.061	1793.17 non-synonymous
2.516	0.976	0.59	-0.349	4496.45 3_prime_UTR_variant
0	0.834	0.794	0.501	2651.7 3_prime_UTR_variant
0	0.663	1.031	1.477	2645.1 3_prime_UTR_variant
1.865	1.377	1.117	-4.67	862.33 3_prime_UTR_variant
1.42	1.268	0.494	-7.046	1447.89 3_prime_UTR_variant
1.029	0.981	0.499	4.335	2890.46 5_prime_UTR_variant
0.609	0.633	-0.826	1.298	12041.07 5_prime_UTR_variant
0	0.706	-0.679	2.149	19541.38 5_prime_UTR_variant
6.939	1.101	1.201	1.01	9779.41 non-synonymous
0.652	0.812	-0.838	-1.505	6361.89 non-synonymous
2.602	0.444	0.786	3.543	7195.65 non-synonymous
0.755	0.531	-0.145	2.59	7307.66 non-synonymous
0	0.662	0.991	2.055	3366.74 non-synonymous
1.743	0.798	-0.502	3.607	22769.17 non-synonymous
0.944	0.545	0.061	0.415	2874.15 non-synonymous
0	0.739	0.325	2.773	3269.21 synonymous_variant
0	0.698	0.868	4.06	15716.31 synonymous_variant
1.176	0.853	-0.663	-0.945	5271.34 synonymous_variant
0	0.518	-0.935	1.441	1840.18 synonymous_variant

0	0.655	-0.158	2.808	24012.05 synonymous_variant
0	0.57	-0.014	4.514	3094.05 synonymous_variant
0	0.658	0.213	0.822	869.88 non-synonymous
2.55	2.565	0.013	-3.443	202.94 non-synonymous
0	0.622	-0.699	2.518	291.61 non-synonymous
8.401	0.662	0.199	1.014	112.01 non-synonymous
12.685	3.217	0.698	0.318	196.59 non-synonymous
1.344	0.57	-0.194	0.39	26507.78 synonymous_variant
0	0.585	0.263	1.81	5184.46 synonymous_variant
0.518	0.74	-0.184	1.8	27514.13 3_prime_UTR_variant
0	0.624	-0.559	1.435	1888.85 3_prime_UTR_variant
3.479	1.306	-0.319	-1.142	1212.03 3_prime_UTR_variant
2.142	0.223	-1.021	0.359	285.17 3_prime_UTR_variant
5.004	2.036	-0.166	1.932	141.43 3_prime_UTR_variant
2.448	1.223	-0.078	1.911	141.43 3_prime_UTR_variant
1.947	0.92	-1.137	0.782	467.75 non-synonymous
1.326	0.723	-0.565	-1.469	1481.09 non-synonymous
0	1.574	-0.135	-2.238	64.14 synonymous_variant
0.525	0.742	0.506	0.899	13178.89 synonymous_variant
0	0.657	0.941	1.998	22284.43 synonymous_variant
0	0.67	-0.458	0.913	1976.98 synonymous_variant
0	0.76	-1.417	0.899	1940.83 synonymous_variant
2.003	0.978	0.899	1.234	4083.69 synonymous_variant
0	0.693 -	-	-	941.43 disruptive_inframe_insertion
0	0.693 -	-	-	132.66 frameshift_variant
0	0.991	0.988	0.406	85.56 non-synonymous
0	0.693 -	-	-	1060 non-synonymous
0	1.981 -	-	-	200.69 synonymous_variant
0	2.03 -	-	-	1094.09 synonymous_variant
0	1.981 -	-	-	183.69 synonymous_variant
10.915	3.15	-0.641	1.815	189.26 synonymous_variant
0	1.528 -	-	-	1206.8 synonymous_variant
0	0.859 -	-	-	426.25 synonymous_variant
0	2.833 -	-	-	222.93 synonymous_variant
0	2.833 -	-	-	116.54 synonymous_variant
2.643	0.724	-0.26	1.301	78.76 non-synonymous
2.527	1.483	0.142	-0.236	86.75 non-synonymous
1.871	0.368	1.072	0.765	482.18 synonymous_variant
1.824	1.022	0.393	0.393	172.01 synonymous_variant
0	0.491	0.087	1.222	727.4 synonymous_variant
0	0.599	-0.518	0.528	268.75 5_prime_UTR_variant
5.613	1.316	0.602	2.895	946.08 non-synonymous
3.725	0.519	-1.635	0.538	1517.72 non-synonymous
4.37	1.473	-0.236	0.86	403.5 non-synonymous

0	0.659	-0.961	0.184	854.6 non-synonymous
10.614	1.443	-0.233	0.559	183.98 non-synonymous
3.305	1.13	-0.134	0.572	156.23 non-synonymous
0	1.119	-	-	4522.89 non-synonymous
12.086	0.859	-0.697	-0.136	1517.32 non-synonymous
0	0.604	1.151	0.7	277.15 non-synonymous
0	0.476	0.077	1.437	291.36 synonymous_variant
6.881	0.192	-0.703	2.415	301.33 synonymous_variant
7.947	0.672	1.123	0.481	70.17 synonymous_variant
5.273	0.24	0.994	-0.217	765.54 synonymous_variant
3.725	0.519	0.636	0.506	1517.72 synonymous_variant
1.69	0.784	0.124	1.153	1305.44 synonymous_variant
0	0.707	0.736	0.736	133.82 synonymous_variant
0	0.148	0.303	1.152	96.97 synonymous_variant
0	0.922	-0.32	1.019	103.07 synonymous_variant
0	0.482	0.443	0.157	147.76 synonymous_variant
2.034	1.538	-0.628	-0.326	155.67 synonymous_variant
2.062	1.634	-1.765	-0.519	155.67 synonymous_variant
0	0.627	0.962	0.437	683.84 synonymous_variant
2.69	1.255	0.446	0.609	132.4 synonymous_variant
4.62	1.228	-0.442	0.654	374.24 synonymous_variant
5.64	0.361	-0.445	1.684	1223.71 synonymous_variant
0	0.675	-0.873	0.532	278.28 synonymous_variant
1.247	0.851	1.137	1.503	22952.21 3_prime_UTR_variant
1.253	0.841	-1.348	2.589	20032.03 3_prime_UTR_variant
1.947	0.896	-1.339	5.326	5079.41 3_prime_UTR_variant
0.83	0.73	-1.828	-3.518	7847.37 3_prime_UTR_variant
3.355	1.697	0.56	-6.811	1182.98 3_prime_UTR_variant
1.201	0.9	-0.032	-0.592	4503.27 3_prime_UTR_variant
6.909	1.385	-0.634	-2.085	13994.86 3_prime_UTR_variant
7.055	1.444	-1.362	9.283	8639.61 3_prime_UTR_variant
1.258	0.563	0.286	2.285	9607.01 3_prime_UTR_variant
2.349	0.757	-0.443	6.015	27234.13 3_prime_UTR_variant
7.511	1.981	-2.584	-2.408	384.2 3_prime_UTR_variant
54.87	3.851	-0.635	12.58	4023.4 3_prime_UTR_variant
92.096	5.685	0.213	6.493	4074.8 3_prime_UTR_variant
0	1.609	-0.752	0.107	3755.9 3_prime_UTR_variant
2.398	1.508	0.685	-0.369	136.33 3_prime_UTR_variant
0	1.312	1.568	2.767	355.28 non-synonymous
0	0.826	-0.147	1.149	839.85 non-synonymous
8.064	1.384	0.915	2.923	1624.74 non-synonymous
1.794	0.808	-0.334	0.849	7248.18 non-synonymous
0	0.595	-1.517	-0.888	542.6 non-synonymous
1.211	0.851	-0.486	0.72	238.42 non-synonymous

0	2.494	-	-	2209.8 non-synonymous
0	1.244	-	-	1019.88 non-synonymous
0.908	0.842	0.35	2.056	713.85 non-synonymous
0	0.492	0.097	-0.695	90.73 non-synonymous
1.774	0.569	-1.985	-0.693	12149.78 non-synonymous
1.01	0.755	-0.456	0.689	3189.78 non-synonymous
2.232	1.257	0.669	-1.228	809.56 non-synonymous
0.554	0.585	-0.371	1.648	39203.81 non-synonymous
2.183	1.16	0.39	-0.642	725.69 non-synonymous
0	0.708	-0.819	1.66	6837.05 non-synonymous
3.056	0.366	0.498	0.244	2874.68 synonymous_variant
6.622	0.362	-0.269	6.506	8844.94 synonymous_variant
14.158	0.156	1.478	-0.744	2154.27 synonymous_variant
0.683	0.808	-0.757	0.62	16779.73 synonymous_variant
2.699	0.676	0.552	-0.384	609.08 synonymous_variant
1.167	0.419	-1.024	0.066	335.45 synonymous_variant
0	0.579	1.103	-1.051	544.69 synonymous_variant
0.953	0.759	-0.289	1.259	2515.96 synonymous_variant
3.942	0.397	-1.206	-0.666	612.85 synonymous_variant
1.118	0.605	1.788	1.354	1389.73 synonymous_variant
0.93	0.943	0.133	0.557	5222.73 synonymous_variant
0.979	0.967	0.597	-1.66	12656.37 synonymous_variant
0	0.698	-2.105	1.677	761.57 synonymous_variant
0	0.95	-1.383	-0.057	684.17 synonymous_variant
1.292	1.174	-0.747	0.023	898.17 synonymous_variant
1.133	0.78	-1.104	6.306	17529.9 synonymous_variant
0	1.211	-0.171	-0.678	1308.32 synonymous_variant
0	0.716	0.093	0.447	4902.89 synonymous_variant
0	0.642	-0.577	0.904	39075.61 synonymous_variant
0	0.554	-0.252	3.869	1293.14 synonymous_variant
0	0.679	-0.329	4.404	24006.28 synonymous_variant
1.1	0.727	-0.8	0.756	26046.16 synonymous_variant
1.741	0.724	0.107	2.963	24601.13 synonymous_variant
0	0.609	-1.348	-0.044	3236.8 synonymous_variant
0	0.655	-0.643	-1.365	3410.8 synonymous_variant
0	0.777	0.336	-0.655	2043.1 synonymous_variant
1.205	0.592	2.589	-0.203	2610.22 synonymous_variant
0	0.712	-0.27	3.249	1611.8 synonymous_variant
0	0.551	-1.094	-0.932	228.68 synonymous_variant
14.832	1.054	-1.704	15.797	21302.34 synonymous_variant
5.954	2.615	-0.292	1.169	726.29 synonymous_variant
0	1.073	-0.95	-0.756	2332.34 synonymous_variant
0	4.294	-	-	2269.98 5_prime_UTR_variant
0	0.727	0.352	3.252	505.32 non-synonymous

3.048	1.076	1.635	0.533	477.67 non-synonymous
3.799	0.413	0.684	0.222	1245.29 non-synonymous
5.314	0.328	1.228	-0.155	1246.93 non-synonymous
1.677	0.941	0.175	0.915	165.45 non-synonymous
1.016	0.463	0.364	0.612	841.31 non-synonymous
0	0.772	-0.015	2.59	389.37 synonymous_variant
2.38	1.695	0.624	1.676	121.39 synonymous_variant
0	0.727	1.168	1.273	211.13 synonymous_variant
0	0.497	0.653	0.401	252 synonymous_variant
0	0.499	0.652	0.917	244.04 synonymous_variant
2.057	1.302	0.473	-0.072	85.5 synonymous_variant
2.057	1.302	0.043	-1.762	105.04 synonymous_variant
1.016	0.463	-0.51	0.685	841.31 synonymous_variant
2.057	1.302	-1.275	-0.358	95.69 synonymous_variant
0.85	0.718	-0.509	0.533	2676.12 synonymous_variant
6.474	2.349	-0.55	2.117	193.32 3_prime_UTR_variant
9.154	2.749	-0.058	3.666	299.52 3_prime_UTR_variant
8.196	2.147	-0.883	-2.498	263.95 3_prime_UTR_variant
0	0.368	-0.762	-0.762	225.01 non-synonymous
5.021	0.828	-1.164	-1.041	143.29 non-synonymous
0	0.96	1.007	2.025	507.33 non-synonymous
1.087	0.793	-0.115	-1.053	644.16 non-synonymous
5.497	1.19	-0.813	0.597	157.32 synonymous_variant
0	1.609	-0.727	0.727	95.92 synonymous_variant
2.963	0.382	0.685	1.95	123.62 synonymous_variant
0	0.707	0.736	0.736	178.26 5_prime_UTR_variant
3.31	2.303	0	0.72	60.76 non-synonymous
3.31	2.303	0.72	0.72	60.76 non-synonymous
0	1.981	0.731	0.731	156.36 non-synonymous
3.332	0.446	0.296	2.166	92.33 non-synonymous
0	0.693	-0.811	0.863	159.59 non-synonymous
44.277	3.194	1.257	1.885	3377 non-synonymous
40.21	3.334	0.822	1.073	3682.24 non-synonymous
35.087	3.428	-1.157	-0.184	3673.34 non-synonymous
0	0.223	-0.736	0.736	62.69 splice_region_variant&synony
1.209	0.478	0.029	1.344	316.39 stop_gained
0	1.109	-1.94	-0.206	598.46 synonymous_variant
0	1.981	0.731	-0.731	156.36 synonymous_variant
0	1.085 -	-		391.05 synonymous_variant
0	1.329 -	-		291.41 synonymous_variant
0	1.179 -	-		96.16 synonymous_variant
0	0.346	0.185	0.778	108.45 synonymous_variant
0	0.705	-0.028	0.068	5337.61 synonymous_variant
0	0.633	1.289	1.417	584.85 synonymous_variant

2.417	0.412	0.919	-0.594	362.02 synonymous_variant
7.432	2.425	0.322	-0.04	141.72 synonymous_variant
2.104	0.446	0.047	-1.566	517.28 synonymous_variant
0.854	0.804	0.51	-0.622	2300.45 synonymous_variant
1.807	0.96	0.363	0.355	2291.29 synonymous_variant
1.972	0.426	2.077	-4.971	1122.63 synonymous_variant
0	1.034	-0.217	-0.794	83.94 synonymous_variant
37.829	3.893	-0.991	-2.475	187 synonymous_variant
0	1.609	-	-	291.06 synonymous_variant
0	0.892	-1.954	-0.555	201 5_prime_UTR_variant
0	1.022	-0.254	2.451	333.31 5_prime_UTR_variant
17.431	0.207	1.262	2.003	1862.42 5_prime_UTR_variant
0.805	0.804	-0.297	1.511	1751.02 frameshift_variant
9.329	2.073	-0.126	0.137	2166.65 non-synonymous
0	0.628	0.065	-0.555	3777.79 non-synonymous
3.555	1.181	1.027	0.811	2513.63 non-synonymous
3.209	0.914	0.682	2.549	16716.94 non-synonymous
0	0.808	-0.902	-1.104	2217.4 non-synonymous
5.557	1.679	1.362	3.648	2134.8 non-synonymous
1.519	0.88	1.664	2.15	5883.1 non-synonymous
0	0.79	0.35	3.187	1129.39 non-synonymous
0	0.663	-1.728	1.419	1394.26 non-synonymous
0	0.896	0.525	2.39	1709.1 non-synonymous
0	0.696	-2.734	0.904	32232.14 non-synonymous
0	0.675	-1.735	-0.955	30167.74 non-synonymous
0	0.732	1.479	1.085	4220.26 non-synonymous
0.76	0.611	0.82	0.749	2320.32 non-synonymous
0.522	0.605	0.125	-1.337	15618.32 non-synonymous
0.934	0.774	3.694	2.125	2369.63 non-synonymous
0.929	0.475	1.282	2.817	4013.42 non-synonymous
1.931	0.684	0.72	0.439	15783.82 non-synonymous
1.03	1.056	-0.228	2.371	2539.47 non-synonymous
4.396	0.11	-0.043	-0.104	430.04 non-synonymous
26.508	0.184	-0.137	-5.128	798.81 non-synonymous
0.963	0.669	-0.235	5.762	3449.98 non-synonymous
1.445	0.829	1.601	2.592	5390.66 synonymous_variant
0	0.946	-0.813	1.024	1286.12 synonymous_variant
0	0.699	-0.572	0.099	2861.01 synonymous_variant
2.567	0.683	0.329	1.437	5437.14 synonymous_variant
0	0.673	1.856	0.772	1952.33 synonymous_variant
0	0.675	2.439	0.514	40925.74 synonymous_variant
0	0.71	-1.779	-0.52	2146.33 synonymous_variant
5.031	0.421	-0.792	-2.072	12923.53 synonymous_variant
0	0.764	0.781	2.5	4033.63 synonymous_variant

0.728	0.655	0.239	1.689	4199.46 synonymous_variant
0	0.775	0.063	1.868	1776.68 synonymous_variant
1.169	0.874	1.598	3.05	1302 synonymous_variant
0	0.65	-0.668	1.287	1253.4 synonymous_variant
5.186	1.171	-0.634	-2.138	6432.44 synonymous_variant
0.743	0.767	0.9	2.846	7637.52 synonymous_variant
11.396	1.46	-1.377	-2.438	9857.63 synonymous_variant
3.491	0.419	-0.514	0.866	2899.34 synonymous_variant
1.459	0.886	-0.84	1.267	504.36 synonymous_variant
0	0.737	0.658	1.06	1241.12 synonymous_variant
0	1.642	-0.879	1.73	92.32 synonymous_variant
8.039	1.272	0.865	1.196	2007.77 synonymous_variant
7.843	1.907	-0.67	1.691	81.72 synonymous_variant
0	0.942 -	-		14520.83 non-synonymous
0	1.546 -	-		11833.73 non-synonymous
0	1.421 -	-		10416.46 non-synonymous
0	1.378 -	-		10946.39 non-synonymous
0	2.67 -	-		366 synonymous_variant
0	0.307	0.956	1.221	89.02 5_prime_UTR_variant
0	0.593	-1.761	-0.202	924.98 5_prime_UTR_variant
20.017	0.194	-0.725	-1.967	1849.44 5_prime_UTR_variant
0	0.494	-1.288	-0.422	323.44 5_prime_UTR_variant
0	0.883	0.429	2.197	1507.26 5_prime_UTR_variant
0	0.61	0.159	3.4	2855.9 5_prime_UTR_variant
0	0.667	2.195	1.92	756.44 5_prime_UTR_variant
0	0.639	0.974	6.748	25611.47 5_prime_UTR_variant
0	0.564	-0.396	15.512	9798.12 5_prime_UTR_variant
0	0.522	-0.548	2.387	12572.84 5_prime_UTR_variant
0	0.752	0.144	-8.425	983 disruptive_inframe_insertion
1.839	1.198	-0.352	-23.965	2769.69 inframe_insertion
2.493	1.175	0.524	3.479	14674.99 non-synonymous
2.651	0.503	-0.402	8.644	101345.79 non-synonymous
1.141	0.528	-0.691	3.9	13711.1 non-synonymous
0	0.701	0.802	-0.755	296833.9 non-synonymous
0	0.883	0.234	1.753	18483.8 non-synonymous
5.248	2.637	-1.005	-2.821	487.96 non-synonymous
0.619	0.641	-0.304	12.644	62788.8 synonymous_variant
1.757	0.832	-0.678	3.2	141162.46 synonymous_variant
1.407	0.824	0.548	4.141	43205.95 synonymous_variant
1.113	0.768	0.917	11.143	184948.55 synonymous_variant
0	0.682	-0.088	10.245	184840.4 synonymous_variant
0.647	0.79	-1.262	-4.716	304777.73 synonymous_variant
0	0.9	0.845	11.473	13735.63 synonymous_variant
1.42	0.418	-0.064	0.321	298.89 synonymous_variant

7.488	1.466	0.602	1.714	668.43 synonymous_variant
0	0.598	0.586	2.193	9811.85 synonymous_variant
0.888	0.864	1.554	3.127	45081.05 synonymous_variant
0.699	0.584	1.045	-2.796	91671.24 synonymous_variant
0	0.685	1.107	11.002	109472.33 synonymous_variant
0	0.33	0.322	-0.956	102.68 5_prime_UTR_variant
7.562	0.075	-1.08	-1.713	261.93 5_prime_UTR_variant
0	0.941	-0.121	-2.631	169.7 inframe_deletion
0	1.251 -	-		2009.33 non-synonymous
0	0.976 -	-		1226.94 non-synonymous
0	3.258 -	-		1255.61 non-synonymous
0	1.085 -	-		2053.29 non-synonymous
1.217	1.061	-1.776	0.758	389.4 non-synonymous
1.445	1.099	-1.268	-0.703	248.33 non-synonymous
4.752	1.153	0.452	-2.261	159.52 non-synonymous
0	2.91 -	-		1329.68 non-synonymous
0	1.085 -	-		1545.4 synonymous_variant
1.24	0.438	-0.02	0	770.14 synonymous_variant
2.508	0.444	-1.202	0.274	850.58 synonymous_variant
3.304	1.244	0.098	-0.02	173.97 synonymous_variant
1.579	1.179	0.552	-0.095	77.16 synonymous_variant
0	1.284 -	-		1457.88 synonymous_variant
0	0.752 -	-		1509.4 synonymous_variant
4.393	0.39	0.437	1.059	3538.17 5_prime_UTR_variant
0.587	0.762	1.8	1.238	2703.02 5_prime_UTR_variant
0.916	0.549	0.552	1.964	489.3 5_prime_UTR_variant
4.918	0.644	0.272	1.745	1155.97 5_prime_UTR_variant
4.303	1.777	0.646	0.166	91.16 5_prime_UTR_variant
7.939	1.609	1.159	0.112	1108.98 5_prime_UTR_variant
2.844	1.163	-0.677	0.383	274.86 disruptive_inframe_deletion
4.384	1.361	-0.057	0.081	244.65 disruptive_inframe_insertion
0.964	0.846	0.747	1.135	339.08 non-synonymous
2.942	1.067	-0.112	0.34	638.51 non-synonymous
0	0.78	0.318	-0.458	211.78 non-synonymous
0	0.742	-1.978	0.927	294.71 non-synonymous
4.626	0.477	0.576	0.841	4342.03 non-synonymous
2.458	0.621	0.219	1.101	250.82 non-synonymous
3.709	0.497	0.627	-1.648	2587.06 non-synonymous
2.913	1.27	0.792	0.28	235.44 non-synonymous
12.146	1.635	-0.928	3.236	1531.96 non-synonymous
0	0.558	-0.129	1.123	223.08 non-synonymous
4.616	0.804	-0.424	0.071	103.67 non-synonymous
1.394	1.158	0.125	-0.872	3557.82 non-synonymous
6.65	1.413	-0.869	0.151	609.52 non-synonymous

0	0.931 -	-		2258.11 non-synonymous
1.651	0.648	0.229	-0.748	520.96 non-synonymous
3.981	1.215	0.03	1.577	137.7 non-synonymous
2.735	0.496	0.335	1.693	2592.62 non-synonymous
5.303	1.357	0.332	-3.234	520.47 non-synonymous
3.129	0.321	-2.454	-0.09	196.56 non-synonymous
2.719	0.419	0.733	1.101	680.83 non-synonymous
8.939	2.361	-0.837	-1.243	73.49 non-synonymous
4.508	1.05	-0.085	-0.31	403.37 synonymous_variant
11.467	1.476	-0.314	-0.834	871.75 synonymous_variant
0.572	0.641	-0.296	0.482	1972.88 synonymous_variant
2.34	0.919	0.097	0.839	321.61 synonymous_variant
1.824	0.33	-0.871	-0.484	264.32 synonymous_variant
5.076	0.33	0.517	0.136	448.32 synonymous_variant
0	0.749	-0.16	3.363	946.86 synonymous_variant
6.188	0.862	0.931	-1.097	488.23 synonymous_variant
0	0.64	0.21	-0.013	515.49 synonymous_variant
0	1.609 -	-		605.33 5_prime_UTR_variant
0	4.892 -	-		853.98 5_prime_UTR_variant
0	0.816 -	-		5433.29 5_prime_UTR_variant
0	0.545	-0.417	1.61	93.41 missense_variant&splice_regi
1.959	1.167	1.025	1.354	93.41 missense_variant&splice_regi
0	1.134 -	-		8984.81 non-synonymous
0	0.756	-0.883	1.679	427.68 non-synonymous
0	0.525	-1.063	3.108	492.84 non-synonymous
0	0.704	-0.668	-0.086	643.84 non-synonymous
1.421	1.099	0.675	-0.517	839.55 non-synonymous
1.394	0.854	-2.612	0.482	7302.5 non-synonymous
0	0.707	1.406	-1.283	1762.11 non-synonymous
2.858	0.785	0.478	2.336	519.96 non-synonymous
2.277	0.862	-0.187	1.576	36974.97 non-synonymous
0	0.629	0.138	-0.213	835.85 non-synonymous
7.577	0.838	-2.905	4.39	31766.46 non-synonymous
5.103	1.134	1.075	1.144	304.98 non-synonymous
0	0.823	-0.144	-3.336	24975.05 non-synonymous
3.357	0.641	0.342	2.82	5693.22 non-synonymous
1.767	0.952	0.408	2.835	568.85 non-synonymous
0	0.666	0.769	0.644	2619.16 non-synonymous
0	1.322	0.985	2.684	88.11 non-synonymous
2.707	0.825	-0.752	-2.7	5885.85 non-synonymous
0	1.32	-1.308	1.67	86.11 non-synonymous
1.668	0.774	0.427	0.358	369.28 non-synonymous
0	0.64	-0.146	3.066	2763.9 non-synonymous
0	0.62	-1.424	2.547	1767.05 non-synonymous

0	0.646	-1.059	1.819	398.17 non-synonymous
0	0.933	-0.837	3.995	707.94 synonymous_variant
0	0.7	1.23	-0.167	834.29 synonymous_variant
1.786	0.818	-0.146	-1.335	745 synonymous_variant
0	0.741	-0.863	1.563	972.84 synonymous_variant
12.766	1.164	0.318	2.794	646.46 synonymous_variant
6.021	2.833	-0.573	0.248	77.59 synonymous_variant
10.353	0.8	-1.682	1.523	4977.02 synonymous_variant
3.332	0.715	1.774	-2.217	23769.36 synonymous_variant
4.515	1.311	0.251	-5.691	21766.37 synonymous_variant
3.135	1.154	-0.315	-3.509	1716.09 synonymous_variant
3.47	1.179	1.109	-3.703	1593.62 synonymous_variant
56.665	5.211	-1.029	-6.209	2495.02 synonymous_variant
21.334	2.331	0.021	-6.762	4842.08 synonymous_variant
21.994	2.445	-1.352	-0.998	5667.28 synonymous_variant
8.048	0.141	0.116	-1.969	339.81 synonymous_variant
3.885	0.85	0.584	1.251	36974.97 synonymous_variant
0	0.954	0.082	1.533	1387.21 synonymous_variant
16.874	3.182	1.394	-2.293	153.19 synonymous_variant
3.569	1.25	-0.628	-0.966	832.24 synonymous_variant
0.57	0.639	-0.095	0.11	8101.31 synonymous_variant
3.569	1.301	-0.125	0.877	90.34 synonymous_variant
0	0.516	0.318	0.021	91 synonymous_variant
0	0.869	-1.108	0.922	123.49 synonymous_variant
0	0.958	-1.699	0.613	276.5 synonymous_variant
0	0.89	0.69	1.961	1356.02 synonymous_variant
0	0.89	-0.046	1.426	1356.02 synonymous_variant
0	0.865	1.491	1.373	1383.88 synonymous_variant
1.576	1.17	0.965	-0.547	1138.11 synonymous_variant
7.151	1.721	0.362	5.752	834.5 synonymous_variant
3.736	1.132	0.163	2.349	695.97 synonymous_variant
1.168	0.987	0.076	-2.685	2903.59 synonymous_variant
4.815	0.044	-0.601	1.662	76.82 5_prime_UTR_variant
1.795	0.925	0.928	0.054	830.19 5_prime_UTR_variant
1.03	0.863	0.579	0.151	575 5_prime_UTR_variant
5.218	0.448	-0.528	1.455	9070.92 5_prime_UTR_variant
3.587	1.077	-0.779	0.701	296.98 5_prime_UTR_variant
8.073	1.475	0.648	-0.961	416.14 5_prime_UTR_variant
1.376	0.547	0.211	-0.151	1062.63 non-synonymous
0.685	0.586	0.458	0.402	1048.98 non-synonymous
9.03	0.669	0.248	-0.307	904.65 non-synonymous
1.17	0.767	-0.183	2.469	4291.79 non-synonymous
0	0.797	0.373	1.317	703.8 non-synonymous
0	0.741	-1.493	0.073	330.28 non-synonymous

2.635	0.52	0.616	3.062	4969.51 non-synonymous
2.719	0.699	-0.795	0.099	764.33 non-synonymous
1.554	1.241	0.669	1.272	445.26 non-synonymous
5.799	1.495	0.444	-1.261	357.61 non-synonymous
0	0.63	1.119	-1.984	351.17 non-synonymous
0	0.731	0.254	1.946	1127.49 non-synonymous
3.355	1.681	-2.027	-0.23	475.26 non-synonymous
11.436	0.399	0.221	1.861	4454.62 non-synonymous
3.815	0.943	-2.328	2.422	2907.18 synonymous_variant
1.889	1.329	-0.962	1.321	145.57 synonymous_variant
0	1.214	0.334	0.852	94.37 synonymous_variant
6.103	1.413	0.118	-0.153	374.84 synonymous_variant
0.638	0.77	0.74	0.26	4170.98 synonymous_variant
3.169	1.102	1.045	0.603	79.71 synonymous_variant
3.326	0.488	-0.013	2.172	6979.76 synonymous_variant
0.662	0.775	0.317	1.043	2881.86 synonymous_variant
0	0.764	-0.822	0.308	978.99 synonymous_variant
0	0.685	-1.168	-1.273	908.89 synonymous_variant
0	0.703	-1.087	2.584	13929.69 synonymous_variant
0	0.582	-0.223	-1.339	853.7 synonymous_variant
5.494	1.786	-1.02	3.21	1013.79 synonymous_variant
5.516	1.682	-0.292	3.542	961.28 synonymous_variant
6.29	0.395	0.339	1.859	1384.89 synonymous_variant
1.917	0.86	0.938	0.222	6962.84 synonymous_variant
4.158	0.433	-0.16	1.329	3281.33 synonymous_variant
0	0.678	1.632	-0.28	11185.86 synonymous_variant
4.333	1.17	0.082	1.546	2614.01 synonymous_variant
0	0.425	-0.664	-0.142	343.49 synonymous_variant
0.738	0.603	-1.467	-0.173	3074.5 synonymous_variant
5.323	0.962	1.701	1.448	3830.07 synonymous_variant
0	1.997 -	-		3447.49 5_prime_UTR_premature_stai
0	1.361 -	-		4165.92 5_prime_UTR_variant
4.231	0.772	0.186	0.57	87.26 5_prime_UTR_variant
1.164	0.609	0.587	2.734	491.96 non-synonymous
0.862	0.828	-0.987	0.375	4768.66 non-synonymous
0	0.744	-0.322	1.536	1281.69 non-synonymous
0	0.582	-0.959	1.113	136.7 non-synonymous
6.588	1.139	0.449	1.38	288.59 non-synonymous
0	0.861	-0.069	-0.016	113.12 non-synonymous
0	0.706	0.434	0.105	456.38 non-synonymous
6.458	1.485	-0.742	-0.416	379.63 non-synonymous
31.009	4.046	-0.14	-0.56	390.78 non-synonymous
2.036	0.831	1.449	-0.123	8655.47 non-synonymous
0	0.684	-1.076	0.606	3738.38 non-synonymous

0	0.82	-0.293	0.927	119.07 non-synonymous
10.169	2.268	0.368	0.717	142.69 non-synonymous
1.362	0.859	-1.343	-0.646	1441.8 non-synonymous
7.057	1.39	0.222	1.779	610.94 non-synonymous
0.663	0.807	-0.689	0.191	1254.11 synonymous_variant
7.409	1.578	0.64	-1.947	395.94 synonymous_variant
2.537	1.095	-1.158	-0.252	373.33 synonymous_variant
0	0.96	0.376	-0.125	62.35 synonymous_variant
10.757	0.211	-0.261	1.987	3854.55 synonymous_variant
23.579	2.032	0.609	0.568	3258.94 synonymous_variant
14.09	1.501	1.228	1.733	1847.79 synonymous_variant
2.257	0.943	-1.263	0.15	3123.06 synonymous_variant
20.557	4.169	0.129	-1.192	213.4 synonymous_variant
0	0.793	-0.545	0.496	300.25 synonymous_variant
3.176	0.977	0.918	1.084	1145.73 synonymous_variant
3.978	1.406	-0.003	1.877	271.75 synonymous_variant
2.666	1.26	-0.374	-1.935	138.83 synonymous_variant
0	0.686	-1.242	-1.633	1091.3 synonymous_variant
4.738	1.546	-0.021	0.279	70.18 synonymous_variant
0	0.84	0.857	0.123	1019.95 synonymous_variant
6.675	0.395	0.737	0.216	6536.34 synonymous_variant
5.328	1.438	1.072	1.794	448.17 synonymous_variant
0	0.558	1.697	0.137	140.66 synonymous_variant
0	0.223	0.736	-0.736	69.69 non-synonymous
2.35	1.571	0.493	-1.926	109.67 non-synonymous
3.192	0.497	-1.526	2.185	474.71 non-synonymous
1.359	1.222	0.411	0.807	613.39 non-synonymous
0	1.445 -	-		461.6 non-synonymous
1.845	0.56	0.507	1.376	142.26 non-synonymous
0	0.223	0.736	-0.736	69.69 synonymous_variant
0	0.976	0	0.311	70.84 synonymous_variant
0	0.693	-0.298	1.49	111.61 synonymous_variant
0	0.818	-0.794	-0.217	82.71 synonymous_variant
0	1.179	-1.323	-0.945	72.7 synonymous_variant
1.485	0.569	-0.376	1.601	472.02 synonymous_variant
4.969	0.223	-0.058	-0.058	223.47 synonymous_variant
0	0.976	-0.19	3.364	578.63 synonymous_variant
0	0.871	-1.787	0.07	507.6 synonymous_variant
3.742	1.347	-0.642	8.324	792.87 3_prime_UTR_variant
0	0.733	-1.691	2.684	4447.09 3_prime_UTR_variant
2.909	0.627	-1.239	-1.619	3371.46 3_prime_UTR_variant
0	0.65	-0.649	-0.13	33055.58 3_prime_UTR_variant
2.004	0.562	-2.477	-1.491	29694.23 3_prime_UTR_variant
0	0.637	0.522	-3.75	2967.46 3_prime_UTR_variant

3.641	0.958	-0.506	-1.91	20585.44 3_prime_UTR_variant
1.162	0.805	0.29	7.547	25270.04 3_prime_UTR_variant
0	0.741	-0.03	2.633	5131.27 3_prime_UTR_variant
0.541	0.732	-1.258	7.654	32186.94 3_prime_UTR_variant
2.194	1.036	1.004	5.003	4303.84 3_prime_UTR_variant
0	0.452	2.068	-3.653	357.91 3_prime_UTR_variant
0	0.895	-0.567	-2.47	608.89 3_prime_UTR_variant
0	1.04	1.14	-0.52	1227.78 3_prime_UTR_variant
8.417	1.393	0.751	-9.144	20317.8 3_prime_UTR_variant
1.546	0.285	-0.59	-0.921	322.84 3_prime_UTR_variant
7.037	1.287	-1.247	-0.596	1157.35 3_prime_UTR_variant
1.125	0.724	0.898	0.323	453.08 5_prime_UTR_variant
1.191	0.597	0.36	-6.039	2667.84 5_prime_UTR_variant
1.116	0.862	-0.482	0.482	292.16 disruptive_inframe_deletion
3.536	1.173	0.867	2.37	279.15 frameshift_variant
0.545	0.63	0.3	-0.819	3254 non-synonymous
0	0.563	-1.683	2.289	264.3 non-synonymous
0	0.563	0.197	2.576	264.3 non-synonymous
0	0.776	-0.306	2.072	703.32 non-synonymous
8.921	0.662	-0.081	-0.188	129.73 non-synonymous
0	1.091	-0.131	1.182	347.1 non-synonymous
0	0.709	0.04	-4.485	777.37 non-synonymous
1.591	1.04	0.733	-0.509	126.31 non-synonymous
3.603	1.295	-0.465	1.039	84.24 non-synonymous
1.782	0.833	0.906	4.141	2932.26 non-synonymous
0.995	0.929	0.574	1.772	350.36 non-synonymous
1.53	1.086	-0.429	-2.586	180.64 non-synonymous
4.041	0.343	1.276	1.687	778.7 non-synonymous
3.746	0.581	0.182	2.537	30739.64 non-synonymous
0	0.576	-0.995	0.771	228.84 non-synonymous
2.057	0.586	-0.311	3.082	419.95 non-synonymous
2.59	0.328	-0.949	1.448	696.35 non-synonymous
0	0.636	-0.055	-0.037	1376.19 non-synonymous
2.463	0.595	1.154	1.276	246.36 non-synonymous
6.07	3.179	-1.379	-0.594	128.51 non-synonymous
0	0.651	0.32	6.521	928.5 non-synonymous
27.354	0.431	0.967	-5.599	6488.7 non-synonymous
14.699	1.964	-0.754	-0.618	299.18 non-synonymous
20.115	2.595	0.181	-6.822	1934.92 non-synonymous
0	0.749	-0.386	-14.319	27766.41 non-synonymous
0.551	0.739	1.126	18.636	27803.62 non-synonymous
0.629	0.579	-0.753	-7.068	7138.43 non-synonymous
0	0.752	0.01	1.633	6555.22 non-synonymous
0	0.693	-	-	172.73 stop_gained

3.647	0.958	-0.359	0.091	52562.49 stop_gained
2.867	0.846	0.414	-3.664	1083.55 stop_gained
1.421	0.869	0.15	6.651	40464.4 stop_lost
2.602	0.685	0.143	4.892	31171.22 stop_retained_variant
0	0.578	-0.05	0.941	1328.96 synonymous_variant
0	1.688	-1.005	-2.05	1140.92 synonymous_variant
0	1.802 -	-		771.07 synonymous_variant
6.012	2.552	1.355	0.043	61.97 synonymous_variant
2.688	1.012	0.362	5.331	1427.23 synonymous_variant
0.76	0.79	-1.405	5.355	1417.09 synonymous_variant
0.727	0.786	0.304	-0.38	1086.58 synonymous_variant
0	0.722	-1.182	-3.352	1049.88 synonymous_variant
0	0.581	0.937	1.111	123.75 synonymous_variant
1.137	0.812	-0.252	3.461	2932.26 synonymous_variant
10.863	1.618	0.955	4.372	919.27 synonymous_variant
0.539	0.746	-0.614	2.216	2629.39 synonymous_variant
2.011	0.844	1.902	5.571	35794.19 synonymous_variant
0	0.658	-0.833	3.522	75469.31 synonymous_variant
0	0.694	-2.958	2.578	72421.34 synonymous_variant
0.896	0.864	-0.678	-1.515	37375.61 synonymous_variant
0	0.671	0.533	-0.698	158.25 synonymous_variant
4.265	0.199	0.454	3.035	578.88 synonymous_variant
0	0.327	-1.502	0.909	109.91 synonymous_variant
0.873	0.969	0.571	4.576	15342.84 synonymous_variant
0.7	0.805	0.867	6.841	13381.03 synonymous_variant
4.803	0.979	-0.662	-1.383	45833.76 synonymous_variant
43.331	1.709	-0.956	4.517	5650.38 synonymous_variant
20.736	1.718	-1.402	-5.543	11910.06 synonymous_variant
0	0.909	-0.272	7.026	1055.84 synonymous_variant
2.532	1.105	-1.933	2.28	422.11 5_prime_UTR_variant
0	1.481 -	-		5343.59 5_prime_UTR_variant
0	1.956 -	-		6655.37 5_prime_UTR_variant
0	0.866	-1.186	-1.077	7363.52 5_prime_UTR_variant
1.517	0.522	1.653	-2.43	5105.65 5_prime_UTR_variant
4.312	1.601	0.122	1.751	90.51 5_prime_UTR_variant
7.918	1.678	0.741	-2.052	988.74 5_prime_UTR_variant
9.868	1.264	0.577	1.335	1981.51 5_prime_UTR_variant
0	0.76	0.016	-0.024	309.65 non-synonymous
0	0.728	-0.595	-0.659	782.73 non-synonymous
2.734	0.661	0.055	-0.232	1286.79 non-synonymous
0	0.599	0.811	0.639	838.08 non-synonymous
0	0.659	0.867	0.874	8678.79 synonymous_variant
2.087	1.609	-0.039	0.588	69.08 synonymous_variant
0	0.812	-0.768	2.434	607.43 synonymous_variant

2.522	1.609	0.354	1.909	86.22 synonymous_variant
0	0.769	0.61	0.512	5442.36 3_prime_UTR_variant
0	0.733	0.458	-1.734	921.41 3_prime_UTR_variant
0	0.617	-1.038	0.003	1299.58 3_prime_UTR_variant
0	0.612	0.292	2.287	51464.01 3_prime_UTR_variant
0	0.721	-0.548	1.82	7233.77 3_prime_UTR_variant
1.963	0.951	-0.335	1.537	4357.56 3_prime_UTR_variant
0	0.716	-0.636	1.638	1226.8 3_prime_UTR_variant
1.757	0.889	-0.993	0.759	1008.89 3_prime_UTR_variant
0	0.449	-0.608	-0.081	59453.72 3_prime_UTR_variant
0	0.663	-0.208	1.705	41336.79 3_prime_UTR_variant
2.572	1.214	-0.02	1.314	641.9 3_prime_UTR_variant
7.368	0.227	0.044	2.913	466.74 3_prime_UTR_variant
1.587	0.857	0.529	1.613	174.87 3_prime_UTR_variant
1.003	0.941	-0.678	1.613	402.34 missense_variant&splice_region
0	4.615 -	-	-	432.06 non-synonymous
0	6.518 -	-	-	1281.97 non-synonymous
1.48	0.393	-0.363	-0.442	1705.61 non-synonymous
12.145	0.138	-1.512	-3.346	839.32 non-synonymous
0	1.586 -	-	-	9150.89 non-synonymous
2.064	0.676	0.481	0.545	407.88 non-synonymous
4.413	1.402	-0.908	2.229	745.07 non-synonymous
4.413	1.404	0.481	2.242	745.07 non-synonymous
13.941	1.202	0.036	-0.745	430.34 non-synonymous
0	0.789	-2.125	-1.477	1496.2 non-synonymous
0	0.711	-0.145	3.93	4319.67 non-synonymous
0	0.776	-0.553	1.444	498.8 non-synonymous
1.129	0.867	0.535	-1.579	2437 non-synonymous
0	0.967	-0.592	0.022	284.98 non-synonymous
0.55	0.754	1.927	1.403	23732.32 non-synonymous
5.048	1.103	-0.521	-2.26	1090.86 non-synonymous
0	0.681	-0.166	1.844	5047.8 non-synonymous
0	0.837	-2.008	1.489	2866.37 non-synonymous
0	0.575	0.476	-0.243	2889.49 non-synonymous
0	4.615 -	-	-	1015.79 synonymous_variant
0	0.941	-0.277	-1.595	853.86 synonymous_variant
0	1.358 -	-	-	4904.42 synonymous_variant
0	0.456	-0.834	-0.569	99.46 synonymous_variant
0	0.795	1.04	0.093	7984.49 synonymous_variant
0	1.362	-0.86	-2.091	339.11 synonymous_variant
2.008	0.506	-0.069	3.704	5671.18 synonymous_variant
0.542	0.619	1.144	0.11	6423.18 synonymous_variant
0	0.804	-0.303	-1.152	107.35 synonymous_variant
1.808	0.594	0.833	0.446	4002.64 synonymous_variant

0.93	0.943	-0.212	1.988	1560.1 synonymous_variant
0.935	0.855	-0.816	2.239	368.81 synonymous_variant
2.983	0.624	1.506	-0.478	9954.33 synonymous_variant
0	0.66	-0.797	1.517	4301.1 synonymous_variant
0	0.668	-0.69	3.8	820.23 synonymous_variant
2.608	1.333	0.511	-1.079	1331.43 synonymous_variant
0	0.573	-0.63	1.053	966.41 synonymous_variant
0	0.666	-0.819	0.538	7990.35 synonymous_variant
0	0.667	0.053	2.26	6081.01 synonymous_variant
0.948	0.707	1.723	3.334	5638.2 synonymous_variant
0	0.868	-0.792	3.406	1349.8 synonymous_variant
0	0.729	-1.104	0.057	1982.8 synonymous_variant
0	0.633	-0.157	0.958	1954.82 synonymous_variant
0.545	0.743	2.201	1.652	24683.24 synonymous_variant
0.907	0.544	0.379	0.93	408.4 non-synonymous
2.087	1.037	-1.747	1.182	619.07 non-synonymous
8.111	0.303	-0.25	2.374	1828.27 non-synonymous
20.42	1.834	-0.041	-1.833	2941.72 non-synonymous
0	1.022	-	-	5881.85 non-synonymous
9.24	0.387	-0.157	1.02	4750.94 non-synonymous
7.908	0.297	1.287	2.161	1054.17 non-synonymous
9.194	0.323	0.748	1.493	1204.92 non-synonymous
3.05	1.273	-1.586	0.194	273.34 non-synonymous
0.478	0.736	-0.464	-0.832	2070.2 non-synonymous
5.964	1.356	-0.308	-0.965	1158.08 non-synonymous
5.922	1.248	2.054	-1.454	1148.7 non-synonymous
2.885	0.91	-0.759	1.072	1831.62 non-synonymous
0	0.708	0.916	-3.246	4478.52 non-synonymous
2.391	1.088	0.277	-3.596	161.74 non-synonymous
4.217	0.867	0.314	-5.456	3677.91 non-synonymous
0	0.686	1.105	-2.545	3335.79 non-synonymous
0.502	0.763	0.376	-2.777	3205.01 non-synonymous
0	0.802	0.762	-0.583	984.35 non-synonymous
1.155	0.687	-1.978	6.725	6751.32 non-synonymous
0	0.65	0.026	-0.225	7456.07 non-synonymous
6.169	1.22	-0.022	-1.383	2593.04 synonymous_variant
0	0.715	0.421	4.344	477.18 synonymous_variant
3.32	1.19	-0.604	0.66	1028.02 synonymous_variant
14.125	1.782	-0.34	-2.413	1628.83 synonymous_variant
31.617	2.948	-1.15	1.936	866.25 synonymous_variant
34.83	2.26	-1.005	-2.296	2723.32 synonymous_variant
0.6	0.62	-1.643	3.322	2286.34 synonymous_variant
17.365	1.653	0.881	2.764	1632.26 synonymous_variant
12.402	0.866	-0.314	-0.058	3575.05 synonymous_variant

4.623	1.006	0.741	1.103	1637.69	synonymous_variant
6.551	1.428	0.159	2.256	1042.95	synonymous_variant
4.613	1.351	0.121	-2.717	1147.76	synonymous_variant
0	0.625	0.977	1.392	1763.61	synonymous_variant
0	0.753	0.929	1.145	677.92	synonymous_variant
2.236	0.539	0.556	2.132	13976.49	synonymous_variant
5.391	1.322	0.584	3.163	520.5	synonymous_variant
0.542	0.709	0.91	6.697	6751.32	synonymous_variant
0	1.022	-	-	390	non-synonymous
0	3.611	-	-	548.02	non-synonymous
0	3.611	-	-	597.03	non-synonymous
1.46	0.889	0.151	1.806	2169.31	non-synonymous
0	0.623	0.284	0.817	318.97	non-synonymous
0.913	0.661	1.171	0.982	1431.62	non-synonymous
1.074	0.508	1.068	3.916	985.64	non-synonymous
0	0.801	-0.849	0.648	279	non-synonymous
0	3.056	-0.751	0.751	326.13	synonymous_variant
0	2.093	-	-	827.39	synonymous_variant
0	0.658	-0.234	0.445	647.04	synonymous_variant
6.974	1.138	-1.555	1.253	74.17	synonymous_variant
0.634	0.763	0.175	0.211	12911.32	synonymous_variant
2.457	0.88	0.625	1.48	11234.83	synonymous_variant
3.274	1.139	-0.17	0.991	625.13	synonymous_variant
1.198	0.793	1.129	0.775	2791.53	synonymous_variant
0	0.558	0.965	-0.048	519.3	5_prime_UTR_variant
0	0.971	-0.864	1.232	396.84	synonymous_variant
5.992	1.835	0.13	-3.173	258.76	non-synonymous
11.509	2.254	0.812	-2.969	339.67	non-synonymous
11.509	2.254	-0.466	-2.783	339.67	non-synonymous
1.535	1.127	-0.949	0.984	182.34	non-synonymous
2.117	1.542	-0.676	2.976	108.76	non-synonymous
5.59	1.541	0.22	1.701	409.11	non-synonymous
0	0.818	-	-	640.55	non-synonymous
1.288	0.512	0.804	-0.307	640.55	non-synonymous
1.718	1.092	1.028	-1.291	614.76	non-synonymous
1.824	1.354	-0.638	-2.025	591.61	non-synonymous
8.451	3.244	-0.278	-1.663	102.09	non-synonymous
3.68	1.108	0.101	-0.935	261.16	non-synonymous
1.584	1.08	0.964	-0.126	763.03	non-synonymous
0	0.96	-0.667	1.688	236.96	non-synonymous
0	0.544	-0.538	0.714	249.61	non-synonymous
2.421	1.027	0.081	-1.212	60.44	non-synonymous
5.494	0.656	-1.521	-1.39	429.87	non-synonymous
3.515	1.371	0.09	-0.893	148.37	non-synonymous

6.874	2.26	0.777	-0.466	126.51 non-synonymous
4.119	1.275	-0.208	0.936	425.66 non-synonymous
3.751	1.591	-0.092	-3.15	258.76 synonymous_variant
4.442	0.34	-0.102	2.009	695.41 synonymous_variant
0	0.578	-1.034	-0.654	101.39 synonymous_variant
3.31	0.588	-0.884	-1.237	339.81 synonymous_variant
0	0.867	0.388	0.018	101.06 synonymous_variant
0	0.789	0.097	0.531	368.31 synonymous_variant
0	0.792	-0.271	-0.21	369.69 synonymous_variant
1.328	0.612	-0.936	1.659	235.99 synonymous_variant
5.881	1.688	1.39	1.244	454.73 synonymous_variant
5.737	1.836	-0.14	0.498	199.35 synonymous_variant
0.983	0.7	2.024	0.371	372.7 synonymous_variant

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Draft

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Draft

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Tyr125Tyr
Leu126Leu
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Draft

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Ala349Thr
Thr382Ser
Arg403Ser
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Draft

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Glu323Gly

Glu323Asp

Lys358Arg

Lys385Glu

Thr430Arg

Asp498Asn

Val516Ile

Lys536Asn

Arg30Arg

Cys36Cys

Gly64Gly

Ser66Ser

Glu87Glu

Pro153Pro

Asp160Asp

Pro170Pro

Asn200Asn

Ser226Ser

Draft

Arg236Arg
Val297Val
Thr320Thr
Ser326Ser
Thr368Thr
Asp449Asp
Asp461Asp
Val467Val
Gln476Gln
Leu485Leu
Ala487Ala
Gly499Gly
Gly503Gly
Tyr520Tyr
Asp22Asn
Trp24Leu
Val40Met
Asn59Asp
Pro63Ala
Val83Met
Phe87Leu
Ala94Val
Val123Ala
Val147Met
Glu153Asp
Met164Leu
Gln202His
Cys211Gly
Asp213Asn
Ala216Thr
Ala219Pro
Ala219Val
Lys236Asn
Lys241Arg
Ser257Asn
Ala14Ala
Leu16Leu
Arg25Arg
Leu31Leu
Ala54Ala
Pro57Pro
Ser65Ser
Gly85Gly
Val108Val

Draft

Ile117Ile
Ser121Ser
Phe151Phe
Leu159Leu
Ala178Ala
Phe194Phe
Phe224Phe
Lys241Lys
Ala20Val
Phe52Val
Phe52Ser
Asn211Lys
Val250Ile
Pro263Leu
Ala288Asp
Glu317Gly
Ala43Ala
Leu60Leu
Pro107Pro
Leu149Leu
Thr220Thr
Lys268Lys
Ala272Ala
Ile322Ile

Gly8Gly
Gly17Glu
Met19Thr
Met19Ile
Ala48Thr
Ala69Thr
Phe150Tyr
Leu171Ile
Leu195Pro
Leu207Ile
Val209Ile
Ile215Thr
Met219Ile
Asn227Ser
Gly250Trp
Val253Ile
Cys262Trp
Ile296Thr
Arg334Lys

Draft

Asn352Asp
Leu394Met
Ser16Ser
Phe83Phe
Arg117Arg
Glu222Glu
Ser294Ser
Ala304Ala
Leu318Leu
Lys323Lys
Gly387Gly
Phe404Phe
Thr438Thr

Draft

Gene	Start	End	Ref	Alt	QD	MQ
CYN	2757	2757	T	C	10.6	60
CYN	2758	2758	T	C	10.6	60
CYN	2854	2854	T	C	25.67	60
CYN	2954	2954	C	T	18.53	60
CYN	3009	3010	TA	T	14.5	60
DTX1	4730	4730	A	AG	7.02	60
EPSPS	3840	3840	A	G	19.45	61.58
EPSPS	3891	3891	G	T	9.77	62.73
EPSPS	3900	3900	C	CT	9.82	62.82
EPSPS	3901	3901	A	T	12.38	62.82
EPSPS	3981	3981	G	A	34.61	61.08
EPSPS	4004	4004	T	C	21.59	60.49
EPSPS	4049	4049	T	C	27.31	60
GDSL	3846	3850	TTCCC	T	6.13	60
GDSL	3851	3853	AAT	A	6.13	60
GPOX	2463	2463	C	T	6.17	60
LACS7	9540	9540	C	T	13.62	60
LACS7	9541	9541	C	A	13.62	60
LACS7	9552	9552	T	C	8.42	60
LACS7	9579	9581	TTA	T	15.25	60
LACS7	9610	9610	A	G	9.34	60
LACS7	9623	9623	C	CGCA	10.49	60
LACS7	9664	9664	C	G	15.38	59.41
LACS7	9665	9665	A	ACTTATAC	14.95	59.41
LACS7	9699	9699	T	C	18.22	58.53
LACS7	9710	9710	C	CGTTATGAA	17.52	58.53
LACS7	9727	9727	A	C	20.9	58.32
LACS7	9733	9733	G	GAGT	17.48	58.32
LACS7	9736	9736	C	T	17.9	58.04
LACS7	9739	9739	A	G	9.41	58.04
LACS7	9763	9763	T	C	14.95	58.79
LACS7	9773	9773	G	T	20.13	58.44
MATE	6969	6969	A	G	13.89	60
MATE	6974	6974	C	T	12.44	60
MATE	7018	7018	C	T	11.31	60
MATE	7026	7026	G	A	11.99	60
MATE	7051	7051	A	T	9.5	60
MATE	7053	7058	CATTAT	C	8.82	60
MATE	7074	7074	C	T	20.23	60
MATE	7076	7087	AAGATGTTT	A	9.03	60
MATE	7102	7102	G	A	10.76	60
MATE	7110	7110	A	G	25.34	60
MATE	7162	7162	C	CT	20.79	60

MATE	7175	7175 T	C	21.18	60
MATE	7225	7225 T	G	10.08	60
OEP64	10071	10071 T	TC	10.69	60
OEP64	10077	10077 C	CCCCCAAAA/	8.6	60
OEP64	10130	10130 C	CA	9.36	60
OEP64	10164	10164 G	T	8.16	60
PDS1	5994	6000 ATTCAT	A	23.4	60
PDS1	6070	6070 T	A	7.35	60
PDS1	6079	6079 A	G	12.83	60
OEP64	39	39 G	C	28.2	60
EPSPS	258	258 C	G	31.96	60
EPSPS	273	273 G	C	30.41	60
GDSL	345	345 T	C	15.07	60
GDSL	347	350 GTTT	G	9.26	60
GPOX	340	340 T	G	9.6	60
GPOX	403	403 A	G	6.69	60
LACS7	177	177 G	A	29.72	59.07
MAT1	121	121 A	ACC	29.61	60.14
MAT1	122	122 A	C,AGGC	26.23	60.14
MAT1	142	142 T	C	30.5	60.15
MATE	286	286 G	T	16.41	60
MATE	381	381 A	G	10.58	60
MATE	447	447 G	T	32.72	61.34
MATE	460	460 G	A	12.32	61.07
OEP64	56	56 G	C	25	60
CYP71E1	332	335 TGTC	T	18.94	60
PDS1	922	925 TTCC	T	15.62	60
CYP71E1	347	347 T	TCACCAGCA(	34.14	60
GPOX	540	540 C	CCGG	34.46	49.83
LACS7	211	211 C	CCCG	29.49	59.52
LACS7	2061	2061 T	TAAG	32.1	60
CYN	3037	3037 T	C	8.58	60
CYN	3127	3127 A	G	5.44	60
CYN	3165	3165 G	A	8.21	60
CYP71E1	1830	1830 G	GTGACTCAC(	7.13	60
CYP71E1	1844	1844 T	A	7.95	60
CYP71E1	1848	1848 G	A	15.52	60
CYP71E1	1851	1855 GACGT	G	24.91	60
CYP71E1	1884	1884 A	G	10.15	59.57
CYP71E1	1912	1912 T	C	19.65	59.45
EPSPS	4108	4110 TAA	T	16.06	60
EPSPS	4123	4123 T	C	16.81	60
EPSPS	4131	4144 CGTCTGTGA(C	C	16.71	60
EPSPS	4143	4143 T	C	17.33	60

EPSPS	4152	4152 C	T	15.52	60
EPSPS	4154	4154 C	T	14.22	60
EPSPS	4185	4185 C	A	17.61	60
GDSL	4047	4047 C	T	12.34	60
GDSL	4286	4286 A	ACACCAC,AC	28.92	59.42
GPOX	2681	2681 A	G	7.01	60
GPOX	2713	2713 A	G	9.89	60
GPOX	2737	2739 ACT	A	12.11	60
MAT1	4571	4571 A	ATGATCTTG	21.52	60
MAT1	4705	4705 A	G	14.67	60
MAT1	4722	4722 C	T,A	34.26	60
MATE	7272	7272 C	T	12.21	60
OEP64	10285	10285 C	CT	4.63	60
OEP64	10443	10443 A	G	12.56	60
OEP64	10658	10658 G	C	11.13	60
OEP64	10737	10737 T	A	12.19	60
PDS1	6437	6437 C	A	7.4	60
PDS1	6488	6488 G	C	9.81	60
CYP71E1	784	788 GAGGC	G	25.35	59.73
CYP71E1	804	804 C	CAATTGCG	27.44	59.76
GPOX	686	686 G	GTCCAGGTA	7.55	60
LACS7	185	185 G	GCC	35.55	59.07
PDS1	1155	1156 TA	T	18.08	60
PDS1	1187	1188 GT	G	22.35	60
PDS1	1565	1565 T	TG	19.29	60
PDS1	2446	2447 TG	T	15.6	60
LACS7	186	191 AGGACG	A	31.39	59.07
CYP71E1	27	27 A	AAT	16.51	60
MAT1	484	493 CCGAGGGCGC		34.37	61.41
CYN	666	666 C	G	13.5	60
CYN	700	700 A	ATT	23.28	60
CYN	716	716 A	T	24.83	60
CYN	777	777 G	A	10.05	60
CYN	819	819 A	G	9.49	60
CYN	866	866 C	T	20.01	60
CYN	883	883 C	T	12.39	60
CYN	888	888 G	A	21.32	60
CYN	949	949 C	T	11.34	60
CYN	966	966 T	A	27.58	60
CYN	968	968 T	TA	28.56	60
CYN	983	983 C	G	15.37	60
CYN	1069	1069 G	T	9.39	59.56
CYN	1080	1080 T	C	10.12	59.53
CYN	1158	1158 G	A	6.93	59.37

CYN	1176	1176 A	AAATTTGTG1	31.09	59.74
CYN	1238	1238 A	G	19.17	59.82
CYN	1277	1277 C	A	25.52	59.63
CYN	1287	1287 T	G	27.7	59.61
CYN	1296	1298 CTA	C	25.05	59.61
CYN	1313	1315 CAA	C	30.27	59.85
CYN	1322	1322 A	G	32.57	59.83
CYN	1358	1358 A	G	32.99	60
CYN	1363	1363 T	C	32.01	60
CYN	1374	1374 A	G	30.75	59.81
CYN	1386	1393 TAAGGTAA	T	27.67	59.81
CYN	1458	1458 A	G	28.95	60
CYN	1467	1467 C	T	32.56	60
CYN	1504	1504 C	T	26.48	59.28
CYN	1567	1567 G	A	7.64	59.53
CYN	1591	1591 C	A	14.96	59.29
CYN	1693	1693 G	A	16.49	60
CYN	1761	1761 C	T	11.35	60
CYN	1770	1770 T	C	11.7	60
CYN	1900	1900 T	C	11.48	60
CYN	1959	1959 A	AT	10.06	60
CYN	1988	1988 C	T	8.09	60
CYN	2065	2065 T	C	8.14	60
CYN	2076	2076 A	G	8.14	60
CYN	2121	2121 T	C	6.69	60
CYN	2173	2173 C	G	30.32	60
CYN	2226	2226 T	A	33.53	60
CYN	2273	2273 C	T	4.82	60
CYN	2282	2284 CTG	C	8.35	60
CYN	2626	2626 A	G	11.8	60
CYN	2632	2632 A	T	10.97	60
CYN	2647	2647 A	C	7.21	60
CYN	2679	2679 G	A	10.49	60
CYN	2690	2690 T	C	12.04	60
DTX1	1091	1091 A	G	9.84	60
DTX1	1296	1296 A	AT	8.71	60
DTX1	1574	1574 A	G	8.83	60
DTX1	1579	1579 C	T	14.37	60
DTX1	1630	1632 CGG	C	14.95	60
DTX1	1661	1661 T	C	8.7	60
DTX1	1761	1761 C	CTCTGTGTTA	19.7	60
DTX1	1790	1790 A	G	19.15	60
DTX1	1864	1864 T	A	25.3	60
DTX1	1876	1876 C	CT	15.52	60

DTX1	1908	1908 G	T	26.54	60
DTX1	1909	1909 G	A	26.97	60
DTX1	1924	1924 A	G	27.34	60
DTX1	1957	1957 T	G	27.3	60
DTX1	1961	1961 A	C	27.75	60
DTX1	1979	1979 T	C	27.03	60
DTX1	1981	1981 G	A	26.52	60
DTX1	1985	1985 T	C	26.94	60
DTX1	1994	1994 A	AT	9.93	60
DTX1	2004	2004 A	T	26.07	60
DTX1	2011	2011 A	G	27.35	60
DTX1	2014	2014 A	G	25.11	60
DTX1	2050	2050 G	C	20.16	60
DTX1	2057	2057 A	G	14.67	60
DTX1	2079	2081 CAG	C	21.63	60
DTX1	2084	2084 G	T	21.21	60
DTX1	2090	2090 A	C	19.92	60
DTX1	2102	2102 G	A	9.05	60
DTX1	2107	2107 A	G	19.92	60
DTX1	2169	2169 G	T	13.46	60
DTX1	2358	2358 G	GAATTAAAC/	8.14	60
DTX1	2545	2545 C	T	6.85	60
DTX1	2549	2549 G	C	10.78	60
DTX1	3228	3228 A	ATGCTC	8.89	59.93
DTX1	3240	3241 CT	C,TT	14.64	59.94
DTX1	3244	3246 TCG	T	11.16	59.93
DTX1	3246	3246 G	A	11.58	59.93
DTX1	3249	3251 ATG	A	10.8	59.94
DTX1	3258	3258 T	TGGCC	13.42	59.94
DTX1	3259	3260 TC	T	13.48	59.94
DTX1	3270	3270 C	CA	10.16	60
DTX1	3276	3276 G	T	10.55	60
DTX1	3297	3297 G	C,T	15.75	60
DTX1	3512	3512 T	C	28.38	59.91
DTX1	3537	3537 A	G	23.99	59.88
DTX1	3628	3631 GTAT	G	22.67	60
DTX1	3639	3639 G	A	27.98	59.87
DTX1	3657	3657 C	T	20.42	59.87
DTX1	3659	3659 G	A	26.99	59.87
DTX1	3661	3661 G	A	26.42	59.88
DTX1	3663	3663 T	C	27.35	59.88
DTX1	3674	3674 A	T	28.1	59.88
DTX1	3695	3695 C	G	28.6	59.89
DTX1	3774	3774 C	T	31.07	60

DTX1	3798	3798 C	G	29.71	60
DTX1	3802	3804 CTT	C	30.29	60
DTX1	3807	3810 ACTC	A	33.04	60
DTX1	3823	3823 G	T	30.22	59.44
DTX1	3828	3828 C	T	31.16	59.46
DTX1	3837	3837 T	G	32.37	59.44
DTX1	3848	3848 T	C	30.15	58.98
DTX1	3849	3849 C	T	29.9	58.94
DTX1	4121	4121 A	T	14.12	60
DTX1	4122	4122 T	G	12.88	60
DTX1	4129	4129 A	G	13.71	60
DTX1	4134	4134 A	T	13.77	60
DTX1	4137	4141 AAATT	A	12.64	60
DTX1	4144	4144 G	GGCAA	16.65	60
DTX1	4150	4150 T	A	16.16	60
DTX1	4152	4152 A	G	17.32	59.51
DTX1	4160	4160 G	A	13.65	58.71
DTX1	4188	4189 CT	C	11.87	58.55
DTX1	4190	4193 GATA	G	11.45	58.61
DTX1	4199	4199 C	T	11.99	58.5
DTX1	4211	4211 T	TC	12.61	58.55
DTX1	4212	4212 G	GA	14.11	58.55
DTX1	4213	4213 T	TC	14.65	58.5
DTX1	4217	4217 A	C	13.01	58.14
DTX1	4219	4219 A	C	23.53	58.14
DTX1	4535	4535 G	GCT,C	20.3	57.97
EPSPS	428	428 G	A	29.22	60
EPSPS	456	456 C	G	32.42	60
EPSPS	478	478 T	C	32.25	60
EPSPS	520	520 C	T	27.96	60
EPSPS	529	529 G	A	28.76	60
EPSPS	536	536 G	T	28.69	60
EPSPS	541	541 A	T	32.95	60
EPSPS	566	566 A	AAAAG	27.46	60
EPSPS	583	583 T	TA	5.73	60.01
EPSPS	591	591 A	AG	31.96	60.9
EPSPS	614	614 A	T	13.11	60.92
EPSPS	755	755 A	C	9.46	60
EPSPS	782	782 T	G	28.55	60
EPSPS	802	802 C	G	27.75	60
EPSPS	846	846 G	C	20.22	60
EPSPS	896	896 G	A	27.32	60
EPSPS	907	907 A	T	9.73	60
EPSPS	916	916 C	T	9.34	58.39

EPSPS	934	934 C	A	14.62	58.44
EPSPS	936	936 G	A	14.18	58.49
EPSPS	937	937 A	G	14.18	58.49
EPSPS	945	945 T	A	14.18	58.49
EPSPS	946	948 TTC	T	13.84	58.49
EPSPS	974	977 GTTT	G	15.87	56.59
EPSPS	978	982 GGTGA	G	16.31	57.23
EPSPS	986	986 C	A	15.75	56.98
EPSPS	1004	1004 G	A	15.1	56.87
EPSPS	1006	1006 A	G	15.46	56.79
EPSPS	1008	1008 C	A	14.91	56.79
EPSPS	1030	1030 T	C	11.46	56.7
EPSPS	1037	1037 C	T	26.75	60
EPSPS	1038	1038 T	A	16.34	60
EPSPS	1058	1058 C	T	6.82	60
EPSPS	1079	1079 A	T	13.22	60
EPSPS	1170	1170 G	T,GA	17.97	59.58
EPSPS	1542	1542 G	GT	8.33	60
EPSPS	1786	1786 A	G	15.96	60
EPSPS	1918	1918 A	T	25.71	60
EPSPS	1926	1926 G	A	26.28	60
EPSPS	1967	1967 A	G	7.97	60
EPSPS	2380	2380 G	A	7.3	60
EPSPS	2484	2484 C	T	7.35	60
EPSPS	2526	2526 C	CATAG,CGTA	21.08	60
EPSPS	2553	2553 C	T	7.59	60
EPSPS	2558	2558 C	T	13.84	60
EPSPS	2562	2562 C	T	13.84	60
EPSPS	3028	3029 AC	A	6.93	60
EPSPS	3551	3551 C	T	11.06	60
EPSPS	3585	3585 G	A	9.19	60
GDSL	1350	1354 ACGGT	A	26.26	60
GDSL	2408	2412 GGCGC	G	26.78	57.26
GDSL	2415	2423 GGCCGGCCC	G	31.93	56
GDSL	2427	2427 C	CAGCT	30.38	55.49
GDSL	2438	2439 TC	T	31.29	56.42
GDSL	2468	2468 C	G	9.56	60
GDSL	2510	2510 C	T	11.22	60
GDSL	2582	2584 TAG	T	7.61	60
GDSL	2636	2636 T	C	13.28	60
GDSL	2670	2674 TAGGC	T	11.38	60
GDSL	2685	2685 T	A	15.47	60
GDSL	2691	2691 A	C	15.97	60
GDSL	2744	2744 C	CGCCG	14.11	60

GDSL	2927	2927 A	G	20.78	60
GDSL	3093	3093 C	T	8.89	60
GDSL	3100	3120 CCATTGCATC	C	8.08	60
GDSL	3120	3120 A	AC	21.98	60
GDSL	3421	3421 A	G	27.96	56.82
GDSL	3427	3427 T	C	29.43	56.82
GDSL	3441	3441 T	A	32.31	56.82
GPOX	737	773 GCGCGCGCGG	G	27.98	60
GPOX	783	783 G	A	30.15	60
GPOX	1179	1179 A	T	22.67	46.41
GPOX	1180	1180 C	T	34.01	46.77
GPOX	1195	1195 G	A	32.23	45.52
GPOX	1200	1200 C	G	25.75	47.19
GPOX	1314	1314 T	TC	22.69	58.73
GPOX	1339	1339 C	T	24.19	60
GPOX	1554	1554 T	C	16.29	60
GPOX	1557	1560 CTGG	C	9.16	60
GPOX	1596	1599 GAAA	G	14.9	60
GPOX	1679	1679 G	GCTGTCATC/	33.21	57.71
GPOX	1681	1681 G	GA	31.08	55.27
GPOX	1683	1686 GTTC	G	29.89	54.44
GPOX	1694	1694 G	GC	24.94	55.27
GPOX	1716	1716 C	A	22.95	55.88
GPOX	1717	1717 C	CGT	21.82	55.88
GPOX	1726	1728 TTA	T	18.84	55.27
GPOX	1730	1735 TCCAAC	T	18.84	55.27
GPOX	1956	1956 C	T	7.7	60
GPOX	1963	1965 CAG	C	15.41	60
GPOX	1966	1966 C	T	15.91	60
LACS7	330	330 T	C	29.28	59.38
LACS7	406	406 T	G	13.53	60
LACS7	455	455 G	GT	10.34	59.12
LACS7	464	464 T	C	10.34	59.16
LACS7	498	499 TG	T	16.02	59.26
LACS7	1257	1257 G	A	33.36	60
LACS7	1293	1293 G	A	27.08	59.99
LACS7	1327	1327 T	C	26.29	60
LACS7	1795	1795 A	T	17.16	59.97
LACS7	1804	1804 C	T	17.31	59.97
LACS7	1810	1810 G	C	19.87	60
LACS7	1811	1811 T	C	19.87	60
LACS7	1816	1816 G	A	19.58	60
LACS7	1820	1832 CCAAAAAA	C	14.31	60.07
LACS7	1835	1835 A	C	16.49	60.11

LACS7	1843	1843 T	TCCA	17.01	60.08
LACS7	1855	1855 G	C	18.75	60.05
LACS7	1858	1858 G	T	18.62	60.05
LACS7	1861	1861 T	C	21.69	60.05
LACS7	1862	1862 G	A	20.65	60.04
LACS7	1878	1881 CGAA	C	18.45	60.03
LACS7	1967	1967 C	T	15.44	59.99
LACS7	1971	1971 C	T	15.44	59.99
LACS7	1974	1974 A	G	16.08	59.99
LACS7	1977	1977 C	CTATG	8.84	59.99
LACS7	1993	1993 C	T	30.9	59.99
LACS7	2004	2004 C	A	13.83	59.99
LACS7	2005	2005 C	T	13.27	59.99
LACS7	2006	2006 C	G	32.18	59.99
LACS7	2011	2011 G	A	14.26	59.99
LACS7	2014	2014 A	G	14.26	59.99
LACS7	2015	2015 T	C	12.08	59.99
LACS7	2024	2024 C	T	14.18	59.99
LACS7	2025	2025 C	T	29.85	59.99
LACS7	2119	2119 C	G	16.65	60
LACS7	2125	2125 G	A,C	24.12	60
LACS7	2132	2132 C	A	15.44	60
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LACS7	2148	2151 TATC	T	10.79	60
LACS7	2155	2170 TTATTTTACA	T	9.07	60
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LACS7	2202	2202 C	T	14.96	59.97
LACS7	2218	2218 T	G	15.47	59.94
LACS7	2222	2222 C	G	14.45	59.94
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LACS7	2356	2356 T	G	12.99	60
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LACS7	2372	2372 C	A	9.53	60
LACS7	2377	2377 T	G	10.61	60
LACS7	2513	2513 G	A	23.38	60
LACS7	2528	2528 T	A	25.33	60

LACS7	2531	2531 T	TG	13.98	60
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LACS7	2565	2565 A	G	32.67	60
LACS7	2573	2573 C	T	25.74	60
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LACS7	2583	2583 A	G	32.44	60
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LACS7	2763	2763 G	T	27.17	60
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LACS7	2792	2792 T	TG	13.6	60
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LACS7	2947	2947 T	A	9.68	57.63
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LACS7	2964	2964 A	C	16.55	57.85
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LACS7	2971	2971 C	G	11.96	57.95
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LACS7	3026	3026 A	G	21.68	60
LACS7	3030	3030 A	T	20.49	60
LACS7	3054	3056 GAA	G	18.44	60
LACS7	3057	3057 T	C	18.65	60
LACS7	3068	3068 A	T	19.34	60
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LACS7	3097	3097 G	T	16.56	59.76
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LACS7	3130	3130 T	G	15.65	59.79
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LACS7	3243	3243 T	C	15.22	59.58

LACS7	3245	3245 T	C	16.81	59.58
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LACS7	3289	3289 G	T	17.84	60
LACS7	3416	3416 T	TAACAGTCA ¹	15.76	60
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LACS7	3451	3452 TG	T	17.22	58.44
LACS7	3454	3454 C	A	16.02	58.57
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LACS7	3692	3692 A	T	18.47	60
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LACS7	3785	3785 A	G	27.66	60
LACS7	3793	3794 CA	C	19.21	60
LACS7	3817	3817 T	A	32	60
LACS7	3836	3836 T	C	17.18	60
LACS7	3841	3841 A	T	31.65	60
LACS7	3848	3851 TTAC	T	9.02	60
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LACS7	3928	3928 G	A	18.82	60
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LACS7	3935	3935 T	C	9.6	60
LACS7	3939	3940 CT	C	29.48	60
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LACS7	3957	3957 G	C	10.72	60
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LACS7	4186	4186 G	A	15.14	60
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LACS7	4255	4255 T	C	26.19	60
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LACS7	4342	4342 A	C	12.28	60
LACS7	4347	4347 T	C	8.89	60
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LACS7	4481	4481 G	T	15.49	60
LACS7	4632	4632 C	T	25.9	57.55
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LACS7	4683	4683 G	C	13.34	59.57
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LACS7	4800	4800 G	A	31.05	59.64
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LACS7	5030	5030 T	C	14.12	59.8
LACS7	5068	5068 G	T	21.66	59.18
LACS7	5070	5070 A	T	10	59.18
LACS7	5071	5071 T	C	10	59.18

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LACS7	5110	5110 T	C	23.22	59.12
LACS7	5113	5113 G	A	10.71	59.09
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LACS7	5147	5147 T	A	16.86	60
LACS7	5159	5159 T	C	32.29	60
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LACS7	5267	5267 A	T	8.8	59.76
LACS7	5282	5282 T	C	10.93	59.73
LACS7	5325	5325 G	C	26.25	59.69
LACS7	5343	5344 TC	T	14.56	59.75
LACS7	5348	5348 C	T	15.46	59.74
LACS7	5390	5390 T	C	27.7	59.77
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LACS7	5472	5472 T	C	13.15	60
LACS7	5667	5667 C	T	9.86	60.32
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LACS7	5672	5673 TA	T	9.04	60.3
LACS7	5693	5693 A	G	14.49	60.27
LACS7	5696	5696 C	T	14.13	60.26
LACS7	5705	5712 CTGCTAAG	C	13.43	60.48
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LACS7	6536	6536 C	T	18.37	60
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LACS7	6799	6799 G	T	14.96	60
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LACS7	6827	6827 C	A	27.69	60
LACS7	6836	6841 ATCTTG	A	28.88	60
LACS7	6871	6871 G	C	10.94	60
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LACS7	6947	6947 T	C	22.44	60.8
LACS7	6960	6960 A	G	27.62	60.74
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LACS7	6986	6986 C	T	25.53	60.69
LACS7	6987	6987 A	G	25.53	60.69
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LACS7	7042	7042 C	T	17.37	60.63
LACS7	7047	7048 CT	C	10.14	60.62
LACS7	7080	7080 A	C	26.94	60
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LACS7	7545	7546 TA	T	11.19	60
LACS7	7548	7548 G	T	12.91	60

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LACS7	7617	7617 C	T	21.82	60
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LACS7	7632	7632 G	T	21.75	60
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LACS7	7657	7657 C	G	23.75	60
LACS7	7665	7665 T	C	23.01	60
LACS7	7685	7685 G	A	18.44	60
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LACS7	7707	7707 T	C	18.85	60
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LACS7	8309	8309 G	A	31.88	60
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LACS7	8552	8552 C	T	21.02	56.47
LACS7	8580	8580 G	A	10.78	57
LACS7	8586	8586 A	G	11.84	58.56
LACS7	8589	8589 G	A	17.91	58.61
LACS7	8591	8591 T	C	15.84	58.66
LACS7	8593	8594 AT	A	16.92	58.66
LACS7	8627	8627 C	T	18.84	58.75
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LACS7	8641	8641 T	G	25.34	58.56
LACS7	8666	8666 G	A	22.44	59.47
LACS7	8691	8691 G	A	24.48	59.76
LACS7	8696	8696 C	G	21.59	60
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LACS7	8727	8727 T	G	26.98	60
LACS7	8749	8749 T	C	7.62	60
LACS7	8758	8758 A	G	28.44	60
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LACS7	8827	8827 T	G	27.09	59.28
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LACS7	8841	8841 T	C	16.48	59.24
LACS7	8843	8843 A	G	12.96	59.22
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LACS7	8850	8851 AT	A	26.16	59.2
LACS7	8858	8858 A	G	19.54	59.2
LACS7	8860	8860 A	G	19.54	59.2
LACS7	8862	8862 T	G	24.46	59.17
LACS7	8873	8873 A	G	17.67	58.95
LACS7	8891	8891 T	G	25.82	59.11
LACS7	8896	8896 A	T	25.15	59.11
LACS7	8899	8899 G	T	25.15	59.11
LACS7	8909	8911 TTG	T	23.4	58.96
LACS7	8912	8912 C	CCT	23.4	58.96
LACS7	8932	8932 T	G	24.29	59.15
LACS7	8933	8933 G	A	25.03	59.15
LACS7	8938	8938 A	C	23.39	59.15
LACS7	8988	8988 C	T	14.43	59.31
LACS7	9131	9133 TTA	T	17.57	59.37
LACS7	9133	9133 A	C	12.5	59.37
LACS7	9135	9135 C	G	11.41	59.37
LACS7	9136	9136 T	TGC	19.74	59.35
LACS7	9143	9162 CTACGTAGC/C		16.16	59.42

LACS7	9145	9145 A	G	12.95	59.42
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LACS7	9163	9163 T	C	12.95	59.37
LACS7	9185	9185 T	C	13.15	59.88
LACS7	9190	9190 T	C,G	33.65	59.87
LACS7	9191	9191 G	T	29.08	59.87
LACS7	9195	9195 A	G	33.04	59.88
LACS7	9200	9200 A	T	30.54	59.88
LACS7	9205	9205 A	T	28.32	60
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LACS7	9217	9217 G	A	14.81	60
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LACS7	9368	9371 TTGC	T	9.75	60
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LACS7	9400	9400 A	G	14.52	58.99
LACS7	9408	9408 A	C	16.26	58.89
LACS7	9409	9409 C	T	16.26	58.89
LACS7	9424	9424 T	TC	18.03	58.89
LACS7	9425	9425 T	C	30.29	58.89
LACS7	9430	9430 T	C	17.12	58.83
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MAT1	760	760 T	C	19.43	60.04
MAT1	774	775 TC	T	26.99	60.13
MAT1	789	789 T	G	27.66	60.08
MAT1	797	797 C	A	32.87	60.08
MAT1	800	800 T	G	28.38	60.09
MAT1	805	805 A	ATGCATGAT	12.99	60.08
MAT1	938	938 A	G	6.14	60
MAT1	1005	1005 T	C	25.51	60
MAT1	1033	1033 C	T	29.05	60
MAT1	1063	1063 T	C	12.88	60
MAT1	1121	1121 T	C	33.47	60
MAT1	1141	1141 T	G	31.08	60
MAT1	1143	1143 G	A	27.38	60
MAT1	1160	1160 T	A	31.45	60
MAT1	1248	1248 G	A	30.43	60
MAT1	1274	1274 T	C	34.25	60.13
MAT1	1280	1280 G	A	27.38	60.13
MAT1	1315	1315 G	A	31.15	60.09
MAT1	1317	1317 A	G	28.08	60.06
MAT1	1330	1330 A	G	29.54	60.06

MAT1	1353	1356 AAAT	A	29.32	60.35
MAT1	1378	1378 G	T	27.67	60.21
MAT1	1391	1391 G	A	31.05	60.2
MAT1	1436	1436 G	T	30.29	60.31
MAT1	1477	1477 A	T	35.4	60
MAT1	1508	1508 T	G	23.05	60
MAT1	1519	1519 T	A	28.83	60
MAT1	1562	1562 T	G,TG	28.45	60.2
MAT1	1624	1624 A	G	31.74	59.04
MAT1	1631	1661 AAGTCGAAG A		28.29	59.12
MAT1	1706	1706 A	G	27.61	59.38
MAT1	1751	1751 G	T	29.78	60.06
MAT1	1808	1808 C	T	26.15	60.15
MAT1	1886	1917 CGTACTAGA/C		32.2	60.17
MAT1	1955	1955 T	G	16.9	60
MAT1	2048	2048 G	GT	16.8	60
MAT1	2053	2053 A	G	17.61	60
MAT1	2063	2064 CA	C	9.91	60
MAT1	2098	2098 C	T	8.14	60
MAT1	2113	2113 C	T	8.14	60
MAT1	2117	2120 CCTT	C	7.54	60
MAT1	2143	2143 C	T	8.87	60
MAT1	2154	2154 T	G	26.32	60
MAT1	2155	2155 G	C	27.21	60
MAT1	2159	2159 T	C,G	24.26	60
MAT1	2162	2162 G	A	16.5	60
MAT1	2175	2176 AG	A	32.53	60
MAT1	2190	2190 A	G	33.71	60
MAT1	2196	2196 G	A,T	31.11	60
MAT1	2202	2202 G	T,A	25.83	60
MAT1	2216	2216 A	C	30.54	60
MAT1	2219	2219 G	A	8.87	60
MAT1	2250	2250 T	C	7.5	60.28
MAT1	2260	2260 A	G	34.69	60.29
MAT1	2266	2266 T	C	27.52	60.21
MAT1	2275	2275 G	A	13.58	59.99
MAT1	2277	2277 T	TA	8.38	59.99
MAT1	2290	2290 G	T	11.49	59.99
MAT1	2292	2292 A	G	11.49	59.99
MAT1	2303	2303 G	T	29.49	59.99
MAT1	2364	2364 T	C	26.18	60
MAT1	2368	2370 AAT	A	9.92	60
MAT1	2491	2491 G	A	32.81	60
MAT1	2637	2637 T	TG	33.04	60

MAT1	2664	2664 G	A	13.34	60
MAT1	2704	2704 A	AT	8.04	60
MAT1	3122	3122 A	G	3.06	60
MAT1	3248	3248 G	C	11.24	60
MAT1	3254	3255 CT	C,CTT	14.65	60
MAT1	3278	3278 C	T	15.04	60
MAT1	3547	3547 A	T	21.16	60
MATE	549	549 T	TTCAGATGA	19.44	60.54
MATE	617	617 T	C	8.7	60.4
MATE	646	646 T	C	26.93	60.39
MATE	665	665 A	T	7.49	60.39
MATE	683	683 C	T	6	60.43
MATE	1342	1342 C	CT	9.18	60
MATE	1357	1357 T	C	10.87	60
MATE	1362	1362 A	C	11.52	60
MATE	1375	1375 A	G	8.6	60
MATE	1425	1425 A	T	18.91	60
MATE	2503	2503 A	T	19.47	60
MATE	2818	2818 T	A	9.6	60
MATE	2964	2964 T	G	8.87	60
MATE	2965	2965 T	G	8.87	60
MATE	2996	2996 T	C	7.59	60
MATE	3019	3019 T	G	5.42	60
MATE	3106	3106 T	C	28.25	60
MATE	3127	3127 T	G	8.46	60
MATE	3136	3136 G	A	21.16	60
MATE	3152	3152 G	A	9.78	60
MATE	3155	3155 T	C	12.58	60
MATE	3170	3170 A	T	11.96	60
MATE	3273	3273 C	T	9.49	59.4
MATE	3286	3286 C	T	10.51	59.3
MATE	3318	3318 T	G	11.73	60
MATE	3320	3320 C	A	10.66	60
MATE	3327	3327 T	A	11.27	60
MATE	3412	3424 GACTCTCCTC	G	8.38	55.21
MATE	3446	3446 C	A	8.69	56
MATE	3622	3622 T	C	22.58	60
MATE	3694	3694 A	G	19.44	60
MATE	3996	3996 A	ATAAATTG	27.38	61.48
MATE	4192	4192 T	C	18.56	60
MATE	4244	4244 G	A	24.5	60
MATE	4255	4255 C	T	32.92	60
MATE	4258	4258 T	C	23.91	60
MATE	4269	4269 C	A	29.36	60

MATE	4270	4270 A	G	29.79	60
MATE	4276	4276 T	C	28.73	60
MATE	4294	4296 ACT	A	26.08	60
MATE	4343	4343 C	G	6.88	60
MATE	4397	4397 A	G	34.86	60
MATE	4482	4482 A	G	13.27	60
MATE	4497	4497 C	T	13.55	60
MATE	4552	4552 C	A	12.02	60
MATE	4648	4648 A	G	13.44	60
MATE	4708	4708 A	G	20.04	60
MATE	4818	4820 CTT	C	10.42	60
MATE	6136	6139 TGAC	T	26.61	60
MATE	6137	6137 G	GT	10.41	60
MATE	6139	6139 C	CCTT	10.41	60
MATE	6229	6229 A	C	13.14	60
MATE	6296	6296 G	A	6.8	60
MATE	6354	6354 G	A	8.25	60
MATE	6355	6355 T	A	9.22	60
MATE	6475	6512 TTTGTGACACT		23	60
MATE	6517	6521 ATGCC	A	34.19	60
MATE	6522	6535 ATCTGCTGTCA		29.51	60
MATE	6537	6543 ACTGGCC	A	24.83	60
MATE	6538	6568 CTGGCCCTGC		32.23	60
MATE	6542	6542 C	CA	9.06	60
MATE	6570	6570 A	AACC	26.2	60
MATE	6574	6578 TGACG	T	31.94	60
MATE	6580	6581 TC	T	34.46	60
MATE	6588	6588 G	A	31.39	58.5
MATE	6598	6598 G	A	7.52	57.8
MATE	6613	6613 C	G	32.28	58.1
MATE	6616	6616 G	A	31.23	58.1
MATE	6617	6617 T	TATTCAA	29.5	58.1
MATE	6642	6642 C	A	29.89	49.24
MATE	6644	6644 T	A	38.28	49.47
MATE	6648	6648 T	C	23.97	49.73
MATE	6651	6651 T	C	16.97	50.04
MATE	6652	6652 T	A	33.69	50.07
MATE	6661	6661 C	G	31.37	50.17
MATE	6663	6663 A	AGGCTATGT,	22.7	50.1
OEP64	387	387 C	CG	7.59	60
OEP64	428	428 A	G	10.96	60
OEP64	429	429 T	C	10.23	60
OEP64	534	534 G	A	32.61	60
OEP64	544	544 A	G	34.86	60

OEP64	629	629 G	A	25.21	60
OEP64	691	691 T	C	7.13	60
OEP64	710	710 G	C	20.95	60
OEP64	781	781 T	G	17.69	60
OEP64	788	788 C	T	22.41	60
OEP64	803	803 G	T	7.8	60
OEP64	1112	1112 C	G	10.42	60
OEP64	1133	1133 C	T	11.91	60
OEP64	1217	1217 G	T	10.67	60
OEP64	1228	1228 T	C	9.65	60
OEP64	1312	1317 CAAGGG	C	18.84	60
OEP64	1490	1490 A	G	31.38	60
OEP64	1499	1499 C	T	14.12	60
OEP64	1573	1573 C	T	27.53	60
OEP64	1593	1593 G	A	26.5	60
OEP64	1726	1730 GGGGT	G	7.11	59.27
OEP64	1731	1733 GGT	G	10.31	59.79
OEP64	1732	1732 G	GT	3.34	59.79
OEP64	1767	1767 T	C	16.81	59.78
OEP64	1788	1788 G	A	9.22	60
OEP64	1865	1865 A	G	14.59	58.53
OEP64	1943	1943 C	T	7.39	60
OEP64	2031	2031 G	A	15.02	60
OEP64	2109	2109 T	G	19.53	60
OEP64	2234	2234 C	T	9.78	60
OEP64	2330	2330 T	C	9.02	60
OEP64	2464	2464 T	G	8.01	60
OEP64	2493	2493 A	ATTATAGATT	8.86	59.01
OEP64	2494	2494 T	TATA	7.55	58.91
OEP64	2495	2495 G	GATTTA	7.55	58.91
OEP64	2520	2523 CAAA	C	13.94	58.79
OEP64	2526	2526 A	G	16.81	58.63
OEP64	2585	2585 T	G	19.29	60
OEP64	2640	2643 CTGT	C	16.68	60.51
OEP64	2677	2677 G	A	34.78	60.42
OEP64	2758	2758 C	G	17.67	60.33
OEP64	2782	2782 A	T	20.5	60
OEP64	2829	2830 GA	G	11.18	60.29
OEP64	3165	3165 C	T	8.27	60
OEP64	3174	3174 C	T	6.5	60
OEP64	3722	3722 G	A	28.32	60
OEP64	3789	3789 C	T	8.24	60
OEP64	3794	3794 C	T	24.49	60
OEP64	3831	3831 G	A	13.28	60

OEP64	3865	3865 C	T	16.46	60
OEP64	4001	4002 GA	G	11.27	60.23
OEP64	4050	4050 A	T	11.97	60
OEP64	4071	4071 C	A	10.43	60
OEP64	4152	4152 G	A	11.32	60
OEP64	4162	4162 G	A	12.68	60
OEP64	4309	4309 T	G	15.94	60
OEP64	4317	4317 G	A	6.64	60
OEP64	4421	4421 T	C	6.7	60
OEP64	4474	4474 T	A	7.83	60
OEP64	4574	4576 CCA	C	12.77	60
OEP64	4654	4654 A	G	31.22	60
OEP64	4681	4681 A	G	20.83	60
OEP64	4709	4710 GA	G	5.52	60
OEP64	4737	4737 T	C	28.27	60
OEP64	4882	4882 T	C	15.83	60
OEP64	4929	4929 G	GA	9.52	60
OEP64	4969	4969 T	C	30.11	60
OEP64	4970	4970 G	A	11.31	60
OEP64	4978	4978 C	T	10.6	60
OEP64	5091	5091 G	GAA	9.14	60
OEP64	5123	5123 A	G	6.92	60
OEP64	5137	5137 A	AT	5.97	60
OEP64	5169	5169 A	G	24.64	60
OEP64	5410	5410 T	C	28.52	60
OEP64	5416	5416 A	G	7.11	60
OEP64	6039	6039 G	A	14.62	59.74
OEP64	6085	6085 G	C	17.91	59.67
OEP64	6105	6105 C	G	20.4	59.63
OEP64	6126	6126 C	T	6.58	59.61
OEP64	6245	6245 A	C	19.02	60
OEP64	6341	6341 T	A	18.65	60
OEP64	6386	6386 C	CT	8.38	60.74
OEP64	6740	6740 A	G	19.96	60
OEP64	6853	6855 CTA	C	14.73	60
OEP64	6858	6858 G	T	26.66	60
OEP64	6902	6902 A	T	10	60
OEP64	6910	6910 C	G	10	60
OEP64	7115	7116 AT	A	4.59	60
OEP64	7491	7491 G	T	5.93	60
OEP64	7513	7513 A	G	6.15	60
OEP64	7727	7727 C	T	6.82	60
OEP64	7768	7768 T	C	15.87	60
OEP64	7861	7861 T	A	18.15	60

OEP64	7891	7891 G	A	20.34	60
OEP64	7950	7950 A	G	22.69	60
OEP64	7960	7960 G	A	14.76	60
OEP64	8037	8037 T	TC	10.05	60
OEP64	8160	8160 C	T	14.55	60.49
OEP64	8183	8183 C	G	15.67	60.49
OEP64	8194	8195 GC	G	13.24	60.51
OEP64	8247	8247 A	G	19.52	60
OEP64	8347	8347 C	T	18.01	60
OEP64	8387	8387 G	C	16.63	60
OEP64	8388	8388 A	G	22.66	60
OEP64	8649	8649 T	TA	9.37	60
OEP64	8659	8659 A	G	9.39	60
OEP64	8774	8774 T	TGTCA	23.54	60
OEP64	8897	8897 T	A	7.97	60
OEP64	8918	8918 C	T	24.2	60
OEP64	9141	9142 CT	C	6.12	60.34
OEP64	9154	9154 T	A	26.67	60.33
OEP64	9187	9187 A	T	21.69	60.33
OEP64	9310	9310 T	G	22.05	60
OEP64	9347	9347 T	A	18.08	60
OEP64	9402	9402 C	A	12.64	60.37
OEP64	9441	9441 T	C	9.31	60.3
OEP64	9443	9443 A	T	29.04	60.29
OEP64	9467	9467 C	T	5.97	60.28
OEP64	9529	9529 T	A	6.37	60
OEP64	9743	9743 G	GTGACCAAC	8.49	60
PDS1	1052	1052 A	C	20.48	60
PDS1	1058	1058 T	C	25	60
PDS1	1059	1059 G	C	20.23	60
PDS1	1063	1063 T	C	20.23	60
PDS1	1093	1093 T	C	23.58	60
PDS1	1097	1097 T	A	23.32	60
PDS1	1100	1101 CT	C	22.87	60
PDS1	1255	1255 T	G	21.14	60
PDS1	1257	1257 G	A	21.08	60
PDS1	1270	1271 GT	G	16.28	60
PDS1	1277	1277 A	T	16.78	60
PDS1	1287	1287 T	C	22.43	60
PDS1	1298	1298 G	A	22.07	60
PDS1	1309	1309 C	T	21.21	60
PDS1	1324	1324 T	C	21.65	60
PDS1	1334	1334 C	T	18.84	60
PDS1	1336	1336 T	A	17.25	60

PDS1	1350	1350 C	G	14.25	60
PDS1	1352	1352 G	T	20.19	60
PDS1	1355	1355 G	A	19.37	60
PDS1	1474	1474 T	A	13.27	60
PDS1	1484	1484 A	G	18.16	60
PDS1	1518	1518 A	G	15.92	60
PDS1	1537	1537 T	TTC	18.13	60
PDS1	1538	1538 A	C	18.83	60
PDS1	1542	1542 T	TG	19.84	60
PDS1	1635	1635 G	A	27.47	60
PDS1	1669	1669 C	A	14.24	60
PDS1	1679	1679 G	GA	12.79	60
PDS1	1706	1706 G	C	11.63	59.73
PDS1	1741	1741 A	G	12.55	59.63
PDS1	1745	1770 AAACGTCTA/A		12.6	59.65
PDS1	1801	1801 G	GCA	9.25	60
PDS1	1856	1856 A	AG	13.51	59.8
PDS1	1860	1860 A	C	15.82	59.79
PDS1	1865	1865 T	C	14.9	59.8
PDS1	1878	1878 G	A	15.24	59.81
PDS1	1882	1882 G	A	15.96	59.81
PDS1	1887	1887 A	G	17.42	59.81
PDS1	1890	1890 A	G	16.84	59.82
PDS1	1909	1909 T	C	16.04	59.84
PDS1	1942	1942 T	C	18.84	59.84
PDS1	1961	1992 CATAGACCA`C		16.46	59.86
PDS1	1997	1997 G	T	18.65	59.81
PDS1	1999	1999 C	T	18.67	59.81
PDS1	2010	2010 T	C	18.61	59.81
PDS1	2014	2014 A	ATGAGCAGT	18.04	59.81
PDS1	2033	2033 C	T	22.43	59.26
PDS1	2055	2055 C	A	21.34	59.39
PDS1	2064	2064 A	G	17.11	59.34
PDS1	2066	2066 G	T	17.29	59.36
PDS1	2068	2068 G	A	17.29	59.36
PDS1	2273	2276 ACGT	A	17.38	59.73
PDS1	2280	2280 A	AAT	17.76	59.72
PDS1	2290	2290 T	G	18.33	59.71
PDS1	2291	2291 T	C	18.33	59.71
PDS1	2327	2327 C	T	16.97	60
PDS1	2359	2359 A	AC	17.06	59.93
PDS1	2361	2361 T	A	17.21	59.93
PDS1	2362	2362 T	C	17.21	59.93
PDS1	2372	2372 A	G	8.26	60

PDS1	2375	2375 T	G	16.38	60
PDS1	2377	2377 C	G	16.38	60
PDS1	2379	2379 A	T	18.12	60
PDS1	2389	2389 T	A	18.22	60
PDS1	2416	2420 TAACA	T	9.74	60
PDS1	2420	2420 A	ATGTG	9.74	60
PDS1	2423	2423 A	T	9.29	60
PDS1	2428	2428 A	G	17.15	60
PDS1	2614	2614 T	G	13.23	60
PDS1	2621	2621 T	C	13	60
PDS1	2654	2654 C	T	9.43	60
PDS1	2680	2680 T	A	8.15	60
PDS1	2844	2844 C	T	34	56.79
PDS1	2923	2923 C	G	28.84	59.85
PDS1	3106	3106 G	A	17.93	60
PDS1	3154	3154 G	A	8.91	58.73
PDS1	3156	3156 G	T	9.28	58.78
PDS1	3175	3175 G	A	12.53	58.82
PDS1	3194	3194 C	T	11.8	58.82
PDS1	3196	3196 C	T	11.58	58.84
PDS1	3197	3197 A	G	11.58	58.84
PDS1	3296	3296 A	G	24.96	60
PDS1	3353	3353 G	A	9.65	60
PDS1	3389	3389 T	C	10.18	50.71
PDS1	3399	3399 T	C	9.19	46.51
PDS1	3407	3407 C	G	27.58	45.9
PDS1	3409	3409 C	A	24.9	45.98
PDS1	3413	3415 CCT	C	31.23	45.9
PDS1	3418	3418 A	AC	28	45.98
PDS1	3423	3423 G	T	11.37	50.42
PDS1	3425	3425 T	G	20.9	52.2
PDS1	3642	3642 T	C	16.42	60
PDS1	3647	3647 G	A	15.69	60
PDS1	3650	3650 C	T	14.99	60
PDS1	3655	3655 A	T	15.91	60
PDS1	3663	3663 C	T	14.09	60
PDS1	3700	3700 T	C	13.91	60
PDS1	3708	3708 T	G	31.82	60
PDS1	3710	3710 T	C	15.76	60
PDS1	3719	3719 C	T	15.22	60
PDS1	3735	3736 CT	C	15.24	60
PDS1	3755	3755 G	A	27.78	60
PDS1	3792	3792 G	A	15.09	60
PDS1	3795	3796 CT	C	14.67	60

PDS1	4056	4056 C	CAATAAAG	22.53	60
PDS1	4067	4067 G	C	8.15	60
PDS1	4091	4091 T	A	17.35	60
PDS1	4304	4304 A	C	19.3	60
PDS1	4442	4442 A	G	8.37	60
PDS1	4452	4452 G	A	31.22	60
PDS1	4603	4603 C	T	18.24	59.98
PDS1	4608	4608 C	T	18.7	59.98
PDS1	4614	4614 T	C	19.78	59.98
PDS1	4617	4617 G	T	19.43	59.98
PDS1	4633	4633 C	T	19.03	59.96
PDS1	4635	4635 A	G	20.51	59.96
PDS1	4651	4651 C	G	17.93	59.85
PDS1	4657	4661 TCTCA	T	20.18	59.85
PDS1	4666	4669 TACA	T	18	59.86
PDS1	4671	4707 TTTCCACCTT	T	15.7	59.88
PDS1	4713	4713 G	A	21.89	59.84
PDS1	4744	4744 T	G	18.56	59.86
PDS1	4746	4750 CATT	CA,C	18.24	59.86
PDS1	4762	4762 C	T	19.92	59.86
PDS1	4765	4765 C	T	19.52	59.86
PDS1	4771	4771 C	T	20.82	59.86
PDS1	4772	4772 C	G	20.82	59.86
PDS1	4838	4847 TGC GCACAT	T	17.04	58.57
PDS1	4888	4888 T	C	27.96	57.57
PDS1	5015	5015 A	G	17.77	60
PDS1	5028	5028 C	T	24.77	60
PDS1	5033	5033 C	T	20.52	60
PDS1	5062	5062 A	G	11.7	58.45
PDS1	5072	5072 G	A	11.7	58
PDS1	5140	5140 A	G	33.8	53.26
PDS1	5147	5147 A	G	34.01	53.25
PDS1	5177	5177 G	A	12.76	55.88
PDS1	5248	5248 T	C	29.57	60
PDS1	5494	5494 T	A	18.05	59.82
PDS1	5504	5504 T	A	17.67	59.82
PDS1	5514	5515 GT	G	6.62	59.83
PDS1	5517	5517 T	G	20.63	59.82
PDS1	5518	5518 T	G	6.7	59.82
PDS1	5520	5520 T	TCC	18.43	59.82
PDS1	5522	5525 TCTA	T	17.58	59.83
PDS1	5528	5528 A	G	18.61	59.82
PDS1	5531	5531 T	C	18.92	59.82
PDS1	5753	5753 A	C	20.95	59.22

PDS1	5756	5756 A	C	23.55	59.19
PDS1	5757	5757 T	A	22.84	59.19
PDS1	5774	5774 G	A	21.31	58.46
PDS1	5788	5788 T	C	8.98	58.48
PDS1	5794	5794 G	A	20.55	58.44
PDS1	5798	5798 T	C	9.43	58.41
PDS1	5802	5842 CATCTAATG/C		16.36	58.45
PDS1	5842	5842 T	C	18.15	58.19
PDS1	5843	5843 G	A	18.15	58.19
PDS1	5853	5853 T	TTA	17.66	57.94
GDSL	1369	1387 ACACATATA1A		26.92	60
LACS7	4781	4781 G	T	10.84	59.64
CYN	2368	2368 A	C	21.14	60
CYP71E1	58	58 A	T	32.05	60
CYP71E1	94	94 A	C	27.15	60
CYP71E1	325	325 G	C	22.44	60
CYP71E1	386	386 G	A	33.84	59.87
CYP71E1	403	403 G	A	29.66	60
CYP71E1	404	404 C	T	31.52	60
CYP71E1	409	409 C	G	15.43	60
CYP71E1	415	415 A	G	31.44	60
CYP71E1	454	454 A	C	29.8	60
CYP71E1	455	455 A	G	26.75	60
CYP71E1	625	625 A	G	40.38	59.97
CYP71E1	629	629 T	A	26.13	59.97
CYP71E1	634	634 A	G	37.37	59.94
CYP71E1	641	641 C	G	9.37	59.95
CYP71E1	652	652 C	T	30.67	59.95
CYP71E1	688	688 G	A	26.65	59.93
CYP71E1	706	706 A	G	32.25	59.92
CYP71E1	707	707 T	G	33.06	59.91
CYP71E1	719	719 A	G	28.61	59.9
CYP71E1	767	767 A	T	30.43	59.73
CYP71E1	785	785 A	C	11.07	59.73
CYP71E1	787	787 G	T	11.07	59.73
CYP71E1	791	794 GAGC	AAGC,G	33.64	59.74
CYP71E1	797	797 C	T	28.44	59.74
CYP71E1	800	800 T	G	27.28	59.75
CYP71E1	803	803 T	C,G	26.77	59.76
CYP71E1	817	817 G	A	27.19	59.79
CYP71E1	823	823 G	A	31.46	59.79
CYP71E1	856	856 T	C	33.61	60
CYP71E1	877	877 A	G	31.36	60
CYP71E1	893	893 A	G	30.45	60

CYP71E1	899	899 G	A	29.13	60
CYP71E1	934	934 T	A	10.51	60
CYP71E1	1149	1149 C	G	25.53	60
CYP71E1	1156	1156 C	A	29.64	60
CYP71E1	1174	1174 C	T	28.35	60
CYP71E1	1204	1204 C	A	30.92	59.99
CYP71E1	1207	1207 G	A	31.85	59.99
CYP71E1	1235	1235 G	A	25.33	59.98
CYP71E1	1272	1272 G	C	29.17	59.95
CYP71E1	1283	1283 A	G	31.06	59.95
CYP71E1	1328	1328 A	G	31.66	59.93
CYP71E1	1334	1334 A	T	30.5	59.93
CYP71E1	1353	1353 A	C	29.55	59.93
CYP71E1	1355	1355 A	C	26.27	59.93
CYP71E1	1471	1471 G	C	31.87	59.94
CYP71E1	1485	1485 C	G	33.35	59.93
CYP71E1	1498	1498 G	C	28.93	59.98
CYP71E1	1548	1548 T	G	16.65	60
CYP71E1	1673	1673 C	T	28.95	59.98
CYP71E1	1721	1721 A	C	34.02	59.72
CYP71E1	1730	1730 A	C	31.15	59.52
CYP71E1	1731	1731 G	T	33.43	59.5
CYP71E1	1775	1775 A	T	8.18	60
CYP71E1	1815	1815 G	C	8.75	60
CYP71E1	1817	1817 G	A	7.95	60
DTX1	2711	2711 T	C	17.11	60
DTX1	2736	2736 A	G	7.17	60
DTX1	2840	2840 C	G	15.01	60
DTX1	3052	3052 A	G	7.41	60
DTX1	3089	3089 G	A	19.71	60
DTX1	3122	3122 A	G	10.6	60
DTX1	3134	3134 G	A	12.73	60
DTX1	3140	3140 A	G	9.71	60
DTX1	3159	3159 C	T	10.72	60
DTX1	3718	3718 T	G	32.65	60
DTX1	3905	3905 A	G	8.04	60
DTX1	3931	3931 T	C	12.94	60
DTX1	3953	3953 C	G	13.01	60
DTX1	3967	3967 G	A	15.39	60
DTX1	4056	4056 A	G	17.6	60
DTX1	4094	4094 C	T	24.91	60
DTX1	4102	4102 A	G	23.73	60
DTX1	4335	4335 A	G	7.24	60
DTX1	4432	4432 G	C	9.34	59.96

DTX1	4603	4603 A	G	9.37	58.81
DTX1	4624	4624 G	A	6.47	59.58
DTX1	4639	4639 A	C	8.62	59.47
EPSPS	2854	2854 A	G	17.79	60
GDSL	3188	3188 A	C	8.45	60
GPOX	546	546 A	C	28.62	52.55
GPOX	558	558 C	G	31.01	54.13
GPOX	1821	1821 C	A	18.87	60
GPOX	1857	1857 G	T	29.9	60
GPOX	1889	1889 G	C	30.39	60
GPOX	2066	2066 C	G	31.01	60
GPOX	2067	2067 G	T	28.91	60
GPOX	2130	2130 G	A	21.65	60
GPOX	2370	2370 A	G	8.65	60
GPOX	2383	2383 A	G	11.91	60
LACS7	194	194 G	A	28.38	59.11
LACS7	242	242 C	A	29.26	59.92
LACS7	2043	2043 G	A	19.92	60
LACS7	2289	2289 G	C	9.06	59.95
LACS7	2292	2292 G	A	13.16	59.95
LACS7	2855	2855 C	T	32.05	60
LACS7	3499	3499 A	G	30.02	60
LACS7	4551	4551 A	G	11.35	58.16
LACS7	4924	4924 T	A	8.88	59
LACS7	4948	4948 T	G	28.19	58.98
LACS7	5631	5631 A	G	22.57	59.95
LACS7	8396	8396 G	C	31.52	59.94
LACS7	9104	9104 G	T	10.15	59.87
LACS7	9105	9105 T	G	10.14	59.87
LACS7	9472	9472 C	T	14.55	58.99
LACS7	9510	9510 A	G	20.59	60
MAT1	285	285 G	T	29.28	60
MAT1	301	301 G	A	30.51	60
MAT1	349	349 G	A	32.48	60
MAT1	463	463 G	T	24.59	61.02
MAT1	477	477 G	A	25.96	61.04
MAT1	4058	4058 C	G	32.88	60
MATE	890	890 A	G	12.42	60
MATE	903	903 T	G	10.04	60
MATE	1022	1022 G	A	13.9	60
MATE	1037	1037 G	C	9.71	60
MATE	1047	1047 C	T	14.99	60
MATE	1050	1050 T	C	10.76	60
MATE	2346	2346 T	G	15.95	60

MATE	4099	4099 G	A	9.18	62.32
MATE	4117	4117 T	C	23.09	61.38
MATE	5685	5685 A	G	7.38	60
OEP64	2912	2912 T	C	15.75	60.25
OEP64	2950	2950 G	A	25.95	60.26
OEP64	3259	3259 C	A	7.58	60
OEP64	6629	6629 A	G	18.74	60
OEP64	6647	6647 G	A	13.71	60
OEP64	9041	9041 C	T	15.55	60
PDS1	901	901 A	C	9.08	60
PDS1	949	949 G	C	17.65	60
PDS1	957	957 G	T	17.55	60
PDS1	976	976 T	A	15	60
PDS1	988	988 A	G	20.01	60
PDS1	991	991 G	A	20.29	60
PDS1	1011	1011 T	C	31.84	60
PDS1	1162	1162 G	A	20.01	60
PDS1	1186	1186 A	C	20.61	60
PDS1	1558	1558 G	A	18.91	60
PDS1	1587	1587 G	T	20.31	60
PDS1	2223	2223 T	C	17.49	60
PDS1	2229	2229 T	G	17.92	60
PDS1	2248	2248 G	C	17.81	59.7
PDS1	2257	2257 C	T	18.62	59.7
PDS1	2504	2504 C	A	15.94	60
PDS1	2567	2567 A	G	10.31	60
PDS1	3855	3855 G	T	17.4	60
PDS1	4349	4349 A	C	7.68	60
PDS1	4562	4562 T	C	9.65	60
PDS1	5300	5300 T	C	8.18	60
PDS1	5591	5591 C	T	14.43	60
PDS1	5627	5627 G	C	17.43	60
PDS1	5657	5657 C	T	18.49	60
PDS1	5698	5698 T	C	11.25	59.92
PDS1	5930	5930 T	C	18.47	60
DTX1	3870	3870 A	C,AC	29.73	58.72
DTX1	4112	4112 G	T	15.77	60
LACS7	7314	7314 A	G	29.38	60
PDS1	3633	3633 T	G	18.49	60
DTX1	3768	3768 C	T	32.76	60
DTX1	4119	4119 A	G	14.91	60
DTX1	4573	4573 T	C	21.81	57.71
EPSPS	2206	2206 C	T	20.99	60
EPSPS	3506	3506 T	TA	6.35	60

GPOX	1021	1021 G	GT	6.43	60
LACS7	1883	1883 T	TACC	19.42	60.03
LACS7	2030	2030 T	C	15.48	59.99
LACS7	2510	2510 A	G	13.58	60
LACS7	2605	2605 C	A	32.74	60
LACS7	3383	3383 A	C	8.1	60
LACS7	4699	4699 C	T	9.47	59.59
LACS7	4785	4785 T	G	21.74	59.64
LACS7	7399	7399 A	C	27.3	60
LACS7	7499	7500 AG	A	15.32	60
LACS7	8362	8362 A	G	30.82	60
LACS7	8462	8462 T	A	24.65	57.07
LACS7	9017	9028 CTGTCCTTTC	C	14.75	59.35
LACS7	9433	9433 T	A	17.26	58.83
LACS7	9435	9435 C	T	8.7	58.77
MATE	6704	6704 A	C	9.25	60
MATE	6705	6705 A	C	9.25	60
OEP64	5877	5879 ATG	A	11.65	59.28
OEP64	8622	8622 A	T	18.93	60
OEP64	9591	9591 A	G	16.02	60
PDS1	1034	1034 C	T	16.37	60
PDS1	1253	1253 T	C	20.69	60
PDS1	1361	1361 T	C	7.16	59.7
PDS1	2437	2439 AGG	A	32.83	60
PDS1	4581	4581 G	T	18.16	60
PDS1	5719	5719 C	A	21.15	59.69
PDS1	5866	5867 CT	C	29.43	57.9
LACS7	5651	5651 C	T	14.28	59.95
PDS1	5715	5715 T	A	21.2	59.69
DTX1	4631	4631 T	G	25.14	59.49
PDS1	1586	1586 G	A	20.31	60
PDS1	5381	5381 C	T	32.06	60
PDS1	5393	5393 T	C	17.58	60
LACS7	9535	9535 A	G	21.26	60
CYP71E1	324	324 C	G	17.19	60
CYP71E1	330	330 A	G	19.95	60
CYP71E1	345	345 G	C	17.19	60
CYP71E1	369	369 G	A	11.29	60
CYP71E1	393	393 G	T	11.9	59.88
CYP71E1	423	423 C	T	30.88	60
CYP71E1	447	447 G	T	30.62	60
CYP71E1	492	492 G	C	16.89	60
CYP71E1	501	501 G	C	17.04	60
CYP71E1	504	504 A	G	14.63	60

CYP71E1	522	522 C	G	13.61	60
CYP71E1	525	525 G	C	12.85	60
CYP71E1	540	540 T	G	13.76	60
CYP71E1	549	549 G	C	11.92	60
CYP71E1	594	594 C	G	6.79	60
CYP71E1	603	603 C	G	30.44	59.99
CYP71E1	609	609 T	C	28.63	59.99
CYP71E1	639	639 G	C	26.78	59.95
CYP71E1	651	651 T	C	27.85	59.95
CYP71E1	690	690 G	C	31.86	59.92
CYP71E1	723	723 C	T	30.51	59.92
CYP71E1	726	726 G	T	29.18	59.92
CYP71E1	765	765 C	T	7.61	59.74
CYP71E1	777	777 C	T	10.22	59.73
CYP71E1	780	780 C	A	31.54	59.73
CYP71E1	792	792 A	G	11.07	59.73
CYP71E1	825	825 C	G	28.09	59.79
CYP71E1	846	846 A	C	26.38	60
CYP71E1	855	855 G	C	28.96	60
CYP71E1	861	861 G	C	27.58	60
CYP71E1	885	885 C	T	33.22	60
CYP71E1	951	951 A	C	10.87	60
CYP71E1	999	999 G	A	11.49	60
CYP71E1	1017	1017 T	C	28.31	60
CYP71E1	1146	1146 G	T	26.16	60
CYP71E1	1206	1206 C	G	29.37	59.99
CYP71E1	1233	1233 C	G	33.2	59.98
CYP71E1	1239	1239 G	C	31.92	59.98
CYP71E1	1242	1242 C	G	28.89	59.98
CYP71E1	1257	1257 C	G	28.49	59.96
CYP71E1	1312	1312 C	A	28.85	59.96
CYP71E1	1320	1320 C	G	32.1	59.93
CYP71E1	1344	1344 C	G	29.39	59.93
CYP71E1	1359	1359 C	A	31.89	59.97
CYP71E1	1380	1380 G	A	12.8	59.96
CYP71E1	1407	1407 G	T	30.12	60
CYP71E1	1449	1449 G	A	31.09	59.95
CYP71E1	1542	1542 A	G	14.18	60
CYP71E1	1557	1557 T	C	13.47	60
CYP71E1	1680	1680 C	T	9.31	59.98
CYP71E1	1683	1683 G	C	31.27	59.93
CYP71E1	1743	1743 C	G	32.61	59.3
CYP71E1	1824	1824 A	G	7.95	60
DTX1	2665	2665 A	G	4.78	60

DTX1	2689	2689 C	G	14.24	59.91
DTX1	2707	2707 A	G	16.97	59.9
DTX1	2743	2743 G	A	13.94	60
DTX1	2776	2776 C	G	9.83	60
DTX1	2782	2782 C	T	8.78	60
DTX1	2821	2821 G	C	11.07	60
DTX1	2839	2839 G	C	15.01	60
DTX1	2842	2842 A	G	10.81	60
DTX1	2998	2998 C	G	8.32	60
DTX1	3118	3118 G	C	14.07	60
DTX1	3124	3124 A	G	10.66	60
DTX1	3358	3358 A	G	14.82	59.97
DTX1	3723	3723 G	A	30.99	60
DTX1	3726	3726 G	A	30.99	60
DTX1	3909	3909 T	C	16.58	60
DTX1	3924	3924 C	A	13.39	60
DTX1	3927	3927 A	G	12.94	60
DTX1	3951	3951 A	G	14.44	60
DTX1	3969	3969 C	A	15.5	60
DTX1	4086	4086 C	T	15.39	60
DTX1	4107	4107 C	T	15.35	60
DTX1	4321	4321 T	C	17.42	60
DTX1	4420	4420 G	C	8.37	60
EPSPS	2073	2073 C	A	12.23	60
EPSPS	2136	2136 C	T	6.05	60
EPSPS	3700	3700 T	C	13.75	60
GDSL	3199	3199 C	G	8.09	60
GPOX	670	670 C	T	10.16	59.94
GPOX	1912	1912 T	C	31.9	60
GPOX	2108	2108 G	C	15.3	59.91
GPOX	2123	2123 G	C	14.31	60
GPOX	2129	2129 A	C	22.23	60
LACS7	1908	1908 C	T	22.88	60.02
LACS7	1917	1917 T	A,G	21.47	60
LACS7	1932	1932 T	C	26.97	59.99
LACS7	2047	2047 A	T	12.02	60
LACS7	2057	2057 T	C	19.52	60
LACS7	2071	2071 C	T	25.52	60
LACS7	2083	2083 C	T	19.27	60
LACS7	2092	2092 G	A	18.49	60
LACS7	2266	2266 C	T	12.4	59.95
LACS7	2275	2275 A	G	21.08	59.95
LACS7	2302	2302 A	G	10.22	59.95
LACS7	2329	2329 T	C	14.07	60

LACS7	2442	2442 A	C	9.79	60
LACS7	2451	2451 C	T	11.19	60
LACS7	2454	2454 G	C	10.49	60
LACS7	2463	2463 T	A	10.46	60
LACS7	2615	2615 A	T	7.54	60
LACS7	2814	2814 A	T	12.08	60
LACS7	2832	2832 T	C	27.15	60
LACS7	2850	2850 T	G	30.3	60
LACS7	3487	3487 T	C	22.56	60
LACS7	3520	3520 T	C	19.29	60
LACS7	4532	4532 C	T	29.53	58.01
LACS7	4541	4541 A	G	10.15	57.91
LACS7	4562	4562 T	C	20.15	57.99
LACS7	4580	4580 A	T	25.41	57.79
LACS7	4583	4583 T	G	8.73	57.65
LACS7	4589	4589 A	G	27.35	57.69
LACS7	4777	4777 T	C	28.22	59.66
LACS7	4929	4929 A	G	29	59.02
LACS7	4951	4951 T	C	19.72	58.95
LACS7	4956	4956 T	C	32.22	59.55
LACS7	4968	4968 T	C	27.57	59.57
LACS7	6379	6379 G	A	21.77	59.89
LACS7	6548	6548 T	C	26.22	60
LACS7	6584	6584 A	G	13.54	60
LACS7	6635	6635 T	G	10.19	60
LACS7	7227	7227 A	T,C	24.65	59.53
LACS7	7296	7296 T	C	21.09	59.59
LACS7	7308	7308 T	C	29.07	59.58
LACS7	7421	7421 T	C	21.39	60
LACS7	8192	8192 A	G	11.96	60
LACS7	8195	8195 T	C	11.96	60
LACS7	8198	8198 C	T	12.38	60
LACS7	8204	8204 G	A	11.35	60
LACS7	8448	8448 A	G	22.53	57.9
LACS7	9086	9086 T	C	24.45	59.41
LACS7	9268	9268 T	G	21.28	60
LACS7	9304	9304 G	A	27.58	59.66
LACS7	9464	9464 G	A	22.24	58.89
LACS7	9470	9470 C	T	21	58.94
LACS7	9482	9482 T	C	14.09	60
LACS7	9512	9512 A	G	12.72	60
MAT1	278	278 G	T	31.08	60
MAT1	4049	4049 G	C	27.69	60
MAT1	4062	4062 A	C	28.61	60

MATE	994	994 C	T	5.51	60
OEP64	5245	5245 T	G	21.08	60
OEP64	5254	5254 A	G	17.54	60
OEP64	5284	5284 C	G	20.87	60
OEP64	5476	5476 A	G	22.33	60
OEP64	5806	5806 G	A	7.6	59.22
OEP64	8578	8578 A	G	19.84	60
OEP64	9789	9789 A	G	5.33	60
PDS1	944	944 A	G	15.78	60
PDS1	1164	1164 C	T	31.58	60
PDS1	1379	1379 T	C	19.38	59.68
PDS1	1450	1450 A	C,T	16.61	60
PDS1	1581	1581 A	G	20.81	60
PDS1	2141	2141 C	T	19.69	60
PDS1	2150	2150 G	A	20.77	60
PDS1	2183	2183 A	C	16.88	60
PDS1	2192	2192 C	T	16.75	60
PDS1	2252	2252 A	C	18.24	59.7
PDS1	2452	2452 T	C	16.16	60
PDS1	2503	2503 A	G	15.94	60
PDS1	2521	2521 A	G	16.14	60
PDS1	2527	2527 T	G	14.81	60
PDS1	2587	2587 A	G	23.89	60
PDS1	3533	3533 C	T	24.56	60
PDS1	3536	3536 C	T	24.03	60
PDS1	3545	3545 T	C	21.33	60
PDS1	3560	3560 A	G	17.8	60
PDS1	3593	3593 T	C	16.34	60
PDS1	3620	3620 T	C	19.01	60
PDS1	3621	3621 A	C	16.15	60
PDS1	3869	3869 G	A	17.31	60
PDS1	3930	3930 C	T	21.92	60
PDS1	3947	3947 A	G	23.55	60
PDS1	3992	3992 C	T	20.32	60
PDS1	4157	4157 A	T	22.78	60
PDS1	4163	4163 T	C	8.62	60
PDS1	5377	5377 T	C	19.23	60
PDS1	5595	5595 T	C	20.99	60
PDS1	5610	5610 G	C	18.82	60
PDS1	5923	5923 G	A	18.56	60
CYN	32	35 CGTT	C	18.94	59.67
CYN	52	55 GCTC	G	21.31	59.63
CYN	124	124 G	A	27.76	60
CYN	127	127 C	A	29.09	60

DTX1	62	62 G	A	8.78	59.31
DTX1	65	65 A	G	21.99	59.3
DTX1	74	74 C	T	30.33	59.36
DTX1	95	95 T	C	31.07	59.58
DTX1	130	130 T	C	29.65	60
DTX1	184	184 T	G,A	26.68	59.79
DTX1	213	213 C	T	13.43	59.81
DTX1	217	217 T	C	30.74	59.79
DTX1	222	225 GCTC	G	19.4	59.76
DTX1	238	238 A	G	34.41	59.43
DTX1	242	242 T	A	28.2	59.2
DTX1	273	273 A	G	32.98	59.57
DTX1	281	281 G	A	35.78	59.67
DTX1	295	295 T	C	23.18	59.94
DTX1	350	351 TC	T	7.54	60
GDSL	28	28 T	G	34.29	59.55
GDSL	141	141 T	G	28.44	60
GDSL	144	144 A	G	30.11	60
GDSL	284	284 G	C	14.18	60
GDSL	294	294 A	G	15.51	60
GDSL	300	300 A	C	10.16	60
GPOX	29	29 A	G	10.15	60
GPOX	30	30 T	C	10.15	60
GPOX	74	74 A	G	8.69	60
GPOX	192	192 G	A	16.46	60
MAT1	86	93 TACACGGC	T	5.01	60.24
MAT1	88	95 CACGGCAG	C	26.23	60.25
MAT1	95	95 G	T	5.76	60.25
MATE	61	61 T	C	23.89	59.34
MATE	69	69 C	T	28.38	59.22
MATE	112	112 C	T	11.84	60
PDS1	118	118 A	C	12.13	60
PDS1	149	149 C	T	16.27	56.77
PDS1	151	151 T	C	11.83	56.72
PDS1	169	169 T	G	11.83	56.72
PDS1	172	172 A	T	35.88	56.98
PDS1	175	175 C	CA	8.86	57.2
PDS1	212	213 GC	G	19.37	57.7
PDS1	222	222 G	GT	12.06	57.2
PDS1	224	224 T	TC,TTCTCTC	31.87	57.94
PDS1	237	237 G	T	10.9	58.22
PDS1	238	238 C	CT	10.3	58.22
PDS1	250	253 CCTT	C	14.25	60
PDS1	254	258 GCTGC	G	15.19	60

PDS1	260	260 T	TCACA	12.06	60
PDS1	268	268 T	C	17.9	60
PDS1	272	272 C	T	17.9	60
PDS1	283	283 A	T	12.81	60
PDS1	285	285 G	A	17.9	60
PDS1	302	302 C	T	21.37	60
PDS1	331	331 G	C	16.31	60
PDS1	401	401 G	A	11.83	60

Draft

FS	SOR	MQRankSum	ReadPosRan	QUAL	SNPType
5.422	0.184	-0.259	0.928	413.3	3_prime_UTI
5.422	0.184	-0.715	0.593	413.3	3_prime_UTI
0	0.468	-0.594	2.356	846.99	3_prime_UTI
1.427	1.106	-1.573	0.115	593.09	3_prime_UTI
1.58	1.179	-0.136	-0.626	362.59	3_prime_UTI
0	0.735	0.251	-0.271	119.39	3_prime_UTI
3.488	1.08	0.952	-0.643	525.27	3_prime_UTI
6.625	0.476	3.895	-0.283	302.76	3_prime_UTI
6.475	0.489	3.621	-0.226	294.53	3_prime_UTI
6.995	0.462	3.425	-0.708	371.4	3_prime_UTI
13.406	0.433	1.09	-0.83	1107.6	3_prime_UTI
1.737	0.846	-0.796	0.053	604.47	3_prime_UTI
2.103	0.317	-1.745	-0.043	600.82	3_prime_UTI
8.195	0.838	0.566	-0.382	67.46	3_prime_UTI
8.195	0.838	-0.382	-0.382	67.46	3_prime_UTI
4.06	0.643	-0.381	0.445	148.19	3_prime_UTI
1.653	1.27	0.395	-1.976	354.22	3_prime_UTI
1.653	1.27	-0.606	-2.082	354.22	3_prime_UTI
0	1.038	-2.825	-1.66	210.42	3_prime_UTI
4.216	2.066	0.961	0.837	350.65	3_prime_UTI
9.751	1.188	-0.684	-0.788	270.9	3_prime_UTI
4.099	0.952	0.262	-0.903	262.37	3_prime_UTI
1.74	0.694	-1.102	-1.102	322.92	3_prime_UTI
1.74	0.694	-0.462	-1.173	313.87	3_prime_UTI
0	0.693	-0.158	-1.628	291.55	3_prime_UTI
0	0.412	-0.529	-0.212	280.25	3_prime_UTI
1.987	0.33	0.068	0.068	292.55	3_prime_UTI
1.987	0.33	0.545	0.068	244.72	3_prime_UTI
0	0.693	0	0.259	214.83	3_prime_UTI
2.616	0.169	-1.835	-0.929	112.97	3_prime_UTI
0	0.495	-0.361	0.361	134.52	3_prime_UTI
0	0.223	0	-1.3	140.94	3_prime_UTI
3.771	1.317	-0.026	1.62	374.95	3_prime_UTI
8.464	1.727	-0.516	0.559	373.3	3_prime_UTI
14.753	2.798	-1.378	-0.643	271.42	3_prime_UTI
10.139	2.008	-1.186	-0.862	311.75	3_prime_UTI
6.805	1.779	-0.28	-0.788	266.08	3_prime_UTI
9.64	1.768	-0.561	-0.687	255.78	3_prime_UTI
1.484	1.179	0.487	1.799	606.87	3_prime_UTI
0	0.839	-0.265	-0.159	252.93	3_prime_UTI
3.909	1.609	0.999	0.1	268.96	3_prime_UTI
7.04	0.982	1.539	0.968	709.47	3_prime_UTI
7.949	0.126	-0.237	-0.893	686.07	3_prime_UTI

5.555	0.18	-0.929	-0.893	698.79 3_prime_UTf
1.739	1.306	1.476	0.246	282.17 3_prime_UTf
0	0.446	0.296	-0.296	106.91 3_prime_UTf
0	1.179	-0.967	-1.396	103.16 3_prime_UTf
4.561	1.518	0.211	0.042	177.83 3_prime_UTf
0	0.859	-0.591	0.789	146.9 3_prime_UTf
0	0.57	3.232	-0.842	1053.16 3_prime_UTf
0	0.619	-1.105	1.731	499.57 3_prime_UTf
4.806	0.703	0.297	-0.373	859.66 3_prime_UTf
0	0.693 -	-		226.47 5_prime_UTf
0	4.274	2.118	0.287	23833.84 5_prime_UTf
0	3.497	-0.863	0.626	27613.2 5_prime_UTf
0	0.473	0.637	0.232	361.6 5_prime_UTf
1.851	1.445	0.254	-0.318	222.15 5_prime_UTf
0	0.582	-0.212	-1.991	124.78 5_prime_UTf
9.971	1.858	2.161	-0.58	113.78 5_prime_UTf
0	6.184 -	-		1955.62 5_prime_UTf
0	0.569	-0.878	-3.026	6431.4 5_prime_UTf
0	2.74 -	-		6884.27 5_prime_UTf
5.592	2.26	-0.441	-1.899	5643.67 5_prime_UTf
4.593	0.595	-0.91	-0.91	229.71 5_prime_UTf
0	0.818	0.956	0.322	84.61 5_prime_UTf
0	1.179 -	-		261.72 5_prime_UTf
7.202	2.225	-0.365	-0.365	123.18 5_prime_UTf
0	0.941 -	-		245.16 5_prime_UTf
0	0.941	0.876	-1.652	170.47 disruptive_in
2.277	1.022	0.033	-0.682	874.6 disruptive_in
0	0.693	-0.988	-0.988	204.82 disruptive_in
0	1.179 -	-		106.35 disruptive_in
0	5.283	0.765	0.765	3883.59 disruptive_in
10.094	1.164	-0.354	1.099	796.07 disruptive_in
0	0.512	-0.139	-0.583	223.03 downstream_
0	0.602	0.504	0.611	146.86 downstream_
0	0.569	0.282	0.564	180.55 downstream_
2.632	0.991	0.382	0	78.46 downstream_
2.632	0.991	-0.382	-0.715	87.5 downstream_
0	1.022	-0.717	-0.143	170.67 downstream_
2.398	0.223	-0.929	0	298.93 downstream_
6.455	0.859	-0.248	0.248	91.33 downstream_
0	0.446	-0.937	-1.38	137.53 downstream_
0	1.609	-0.421	0.55	128.49 downstream_
0	1.609	-0.922	0.421	134.52 downstream_
2.808	1.919	1.098	-0.729	167.09 downstream_
5.441	0.662	0.103	0.729	173.28 downstream_

2.463	0.76	-0.825	1.932	170.67 downstream
2.533	0.707	0.244	1.532	170.67 downstream
0	0.693	0.851	-1.881	176.14 downstream
2.772	0.124	0	-0.352	222.13 downstream
1.895	1.469	-2.016	-1.539	809.88 downstream
0	0.582	0.272	0.817	147.26 downstream
0	0.446	-0.579	-1.427	197.8 downstream
1.685	1.23	-1.133	-1.491	290.58 downstream
4.534	0.435	-0.95	-1.528	408.93 downstream
0	0.941	0.127	-1.141	278.71 downstream
0	0.353	0.289	0	822.18 downstream
1.871	0.754	0.211	-0.127	231.94 downstream
2.218	0.25	0.158	0.053	78.73 downstream
7.761	0.88	0.579	0.733	251.1 downstream
1.999	0.26	0.543	0.398	233.73 downstream
0	0.941	0.337	-1.491	207.29 downstream
1.987	1.329	-1.139	1.03	118.44 downstream
0	0.76	-0.244	-1.977	117.67 downstream
0	0.416	1.201	1.076	21556.71 frameshift_v
3.054	0.195	-2.273	0.149	26020.69 frameshift_v
2.251	1.755	-1.084	-3.253	135.85 frameshift_v
0	6.184	-	-	1946.57 frameshift_v
7.125	0.966	-0.532	-0.653	668.79 frameshift_v
3.012	0.658	-0.517	-2.417	849.22 frameshift_v
0.846	0.757	0.388	0.142	1524.03 frameshift_v
6.117	0.205	-1.294	0.42	842.16 frameshift_v
0	6.184	-	-	1946.57 frameshift_v
0	1.508	0.336	-0.336	165.09 frameshift_v
0	1.028	-1.123	-0.476	4197.59 inframe_dele
0	0.446	0.361	0	121.52 intron_variar
0	0.33	0.278	-0.278	256.09 intron_variar
0	1.179	-1.041	-0.674	372.48 intron_variar
0	0.804	-0.133	-0.933	140.76 intron_variar
5.497	1.893	-1.246	-0.793	151.9 intron_variar
1.957	0.956	0.439	-1.61	340.23 intron_variar
0	0.412	1.356	0.38	198.22 intron_variar
5.569	1.759	0.471	-0.627	298.52 intron_variar
1.871	1.034	-1.504	-0.424	226.71 intron_variar
12.42	1.406	-1.981	-0.238	551.69 intron_variar
8.318	0.62	-2.24	-0.127	542.64 intron_variar
1.74	0.33	0.317	-0.387	322.84 intron_variar
0	0.495	-0.168	-0.042	300.49 intron_variar
0	0.467	1.177	-0.86	303.57 intron_variar
2.105	1.536	0.111	0.553	152.53 intron_variar

2.035	1.673	-0.1	-0.234	715.07 intron_variar
1.304	0.671	1.063	0.284	651.84 intron_variar
0	0.635	0.462	-1.692	969.84 intron_variar
0	0.662	-0.494	-1.548	997.24 intron_variar
0	0.641	-1.186	-1.12	901.88 intron_variar
0	0.906	-0.941	-2.785	1180.69 intron_variar
0	0.586	-0.986	-1.9	1172.56 intron_variar
0	0.756	-0.261	1.593	1286.59 intron_variar
1.534	0.57	1.845	1.13	1330.57 intron_variar
1.448	0.585	1.609	3.266	1229.99 intron_variar
0	0.765	0.228	3.412	1079.25 intron_variar
0	0.873	0.11	-1.937	1042.12 intron_variar
0	0.776	-0.272	-1.569	976.91 intron_variar
0	0.495	1.141	0.718	503.07 intron_variar
0	0.713	2.368	4.476	802.65 intron_variar
1.823	0.966	1.381	-0.415	1182.23 intron_variar
0	0.941	-0.433	0.851	280.29 intron_variar
4.117	1.863	0.765	-1.378	272.38 intron_variar
1.697	1.402	1.33	-0.934	292.49 intron_variar
0	0.917	0.358	0.119	275.51 intron_variar
2.003	0.669	-0.091	0.091	181.09 intron_variar
0	1.112	0.778	1.768	113.21 intron_variar
0	0.33	0.849	-0.065	122.14 intron_variar
0	0.551	-0.196	0.979	122.14 intron_variar
2.077	0.85	0.474	1.95	113.78 intron_variar
2.187	0.26	0.852	0.556	757.91 intron_variar
2.9	1.893	-0.509	0.88	905.33 intron_variar
0	0.434	-0.898	0.351	163.79 intron_variar
0	0.569	0.429	0.586	283.87 intron_variar
13.786	1.996	0.59	-0.492	330.52 intron_variar
6.107	1.499	0.33	-0.374	329.12 intron_variar
1.262	0.91	-1.04	0.202	288.39 intron_variar
7.282	0.157	0.577	0.783	398.71 intron_variar
10.477	0.093	-0.944	1.54	421.42 intron_variar
0	0.804	-0.07	-1.198	216.55 intron_variar
4.01	0.207	-2.665	-1.244	182.87 intron_variar
0	0.459	0.311	-2.01	220.83 intron_variar
0	0.73	-1.106	0.077	373.55 intron_variar
4.123	1.288	0.107	0.604	313.87 intron_variar
1.833	1.23	1.604	0.634	182.69 intron_variar
1.657	0.313	-0.489	-1.569	512.15 intron_variar
1.281	0.495	-0.5	0.535	651.18 intron_variar
1.22	1.022	0.823	0.712	1214.18 intron_variar
1.093	0.655	-1.513	-1.793	760.67 intron_variar

0	0.653	-0.892	0.283	1645.35 intron_variar
0	0.61	0.417	0.387	1645.35 intron_variar
0	0.602	-1.16	-0.989	1667.44 intron_variar
2.589	0.773	0.585	-1.537	1419.77 intron_variar
6.114	0.986	-0.254	-0.722	1442.77 intron_variar
5.909	1.144	-0.991	0.49	1405.49 intron_variar
4.156	1.037	1.23	0.385	1405.49 intron_variar
2.504	0.803	0.644	0.567	1400.96 intron_variar
2.587	0.986	0.305	-1.052	486.49 intron_variar
1.238	0.817	-0.916	0.867	1147.08 intron_variar
2.735	1.041	-1.13	0.399	1285.53 intron_variar
1.202	0.96	0.308	-0.148	1180.02 intron_variar
1.079	0.941	1.804	-0.399	1088.6 intron_variar
0	0.578	0.504	1.341	748.26 intron_variar
6.254	0.199	0.54	1.767	1038.06 intron_variar
4.189	0.252	1.759	0.593	1039.3 intron_variar
2.304	0.433	0.934	1.612	1036.09 intron_variar
2.518	1.099	0.149	0.169	470.56 intron_variar
2.304	0.433	1.3	-0.275	1036.09 intron_variar
25.552	4.8	0.693	-1.61	336.51 intron_variar
1.56	1.179	0.546	-1.96	268.54 intron_variar
4.039	1.863	-0.972	-0.194	178.16 intron_variar
7.132	0.901	-0.961	-0.495	269.42 intron_variar
7.732	2.264	-0.565	-1.75	257.74 intron_variar
3.453	1.609	-0.022	-2.653	424.55 intron_variar
0	0.859	0.154	-3.281	334.79 intron_variar
1.536	1.27	0.697	2.629	335.96 intron_variar
0	0.77	-0.486	-2.134	334.72 intron_variar
1.503	1.27	-0.062	-2.002	416.03 intron_variar
1.503	1.27	0.888	-2.333	417.85 intron_variar
6.107	1.265	-0.306	-2.192	294.53 intron_variar
6.107	1.265	-1.296	-2.381	305.94 intron_variar
8.272	1.061	-0.307	-0.384	504.11 intron_variar
45.57	1.218	1.092	0.333	5107.92 intron_variar
8.629	1.387	-0.849	-0.809	3502.57 intron_variar
2.807	0.293	1.389	-0.566	929.27 intron_variar
2.771	0.368	-0.213	-1.49	1259.05 intron_variar
2.593	1.041	-0.312	-0.201	939.12 intron_variar
1.19	0.976	-0.888	0.357	1241.58 intron_variar
1.202	1.044	2.234	0.326	1241.58 intron_variar
1.202	1.044	-0.146	0.572	1285.53 intron_variar
1.228	1.082	-1.985	1.179	1376.68 intron_variar
1.186	0.473	-0.548	1.209	1458.67 intron_variar
11.742	0.669	-1.563	-0.273	1273.94 intron_variar

11.389	0.486	-0.735	0.188	1099.4 intron_variar
11.856	0.636	-1.36	0.689	1090.36 intron_variar
12.439	0.993	0.061	0.586	1090.36 intron_variar
9.454	0.889	0.158	0.384	936.97 intron_variar
9.756	1.009	1.588	0.429	997.18 intron_variar
7.043	1.033	0.969	0.024	1003.35 intron_variar
6.68	0.763	0.023	1.704	904.49 intron_variar
6.68	0.628	2.025	1.832	866.98 intron_variar
1.423	0.962	1.029	0.281	465.84 intron_variar
1.423	0.962	-0.356	0.281	425.07 intron_variar
3.256	0.85	0.507	-0.264	425.07 intron_variar
3.211	0.61	-0.392	0.103	426.9 intron_variar
1.509	0.654	-0.129	-0.43	379.26 intron_variar
3.512	0.781	1.045	-1.456	466.22 intron_variar
1.485	0.439	-0.321	-1.604	436.43 intron_variar
0	0.711	0.37	-1.801	467.73 intron_variar
0	0.856	1.599	-1.223	382.15 intron_variar
1.599	1.136	-0.126	-0.477	320.54 intron_variar
1.531	1.022	-1.031	0.054	320.54 intron_variar
0	0.714	-0.108	0.539	311.75 intron_variar
0	0.635	-1.054	0.306	340.54 intron_variar
0	0.635	-1.414	-0.18	380.9 intron_variar
0	0.714	-0.862	-0.431	380.9 intron_variar
0	0.859	-0.326	-0.929	351.35 intron_variar
3.738	1.565	-0.18	-1.414	635.35 intron_variar
1.465	1.112	-0.166	-0.129	669.79 intron_variar
0	0.639	0.097	-2.57	59250.68 intron_variar
0	1.785	-0.039	-2.134	80494.71 intron_variar
0	1.516	-0.001	-3.348	85338.33 intron_variar
0	0.373	-1.731	-2.015	87383.42 intron_variar
0	0.987	-0.844	-3.019	82422.47 intron_variar
0	0.753	-1.447	-0.658	84366.41 intron_variar
0	0.732	1.065	-0.36	82483.92 intron_variar
0	0.684	0.49	-1.578	74742.25 intron_variar
0	0.388	-0.212	2.518	91.71 intron_variar
0	1.175	-1.471	-2.09	60998.75 intron_variar
0	0.266	-0.811	0.923	301.44 intron_variar
0	1.596	0.412	3.368	170.32 intron_variar
0	0.743	2.139	-0.123	43985.57 intron_variar
0	0.283	0.241	-1.732	26667.1 intron_variar
5.315	0.88	0.69	1.577	363.91 intron_variar
4.151	0.718	-0.846	-0.962	737.51 intron_variar
0	0.914	-0.586	-0.52	253.03 intron_variar
3.452	1.508	-1.277	-2.048	289.43 intron_variar

1.47	1.179	-1.266	-0.23	467.81 intron_variar
3.142	1.329	0.755	0.313	467.81 intron_variar
3.142	1.329	-0.94	0.497	467.81 intron_variar
3.142	1.329	-1.676	0.976	467.81 intron_variar
3.142	1.329	-0.166	0.903	456.79 intron_variar
1.243	0.668	-0.949	-0.467	618.81 intron_variar
0	0.736	-3.146	-0.807	652.47 intron_variar
1.216	0.801	-2.656	-1.258	661.51 intron_variar
2.597	0.928	-1.666	-2.471	679.47 intron_variar
0	0.693	2.312	2.254	680.22 intron_variar
1.194	0.809	-2.709	-2.551	656.2 intron_variar
4.862	1.235	-1.801	-2.684	469.76 intron_variar
1.536	0.34	-0.627	-2.18	748.96 intron_variar
8.994	3.312	0.895	-2.585	473.88 intron_variar
1.752	1.179	-0.636	0.768	177.21 intron_variar
9.558	1.458	0.25	-1.359	330.51 intron_variar
2.522	0.877	-0.085	-0.592	233.58 intron_variar
1.74	1.179	0.81	-1.504	166.7 intron_variar
11.29	2.636	0.165	-0.56	351.06 intron_variar
1.55	0.542	-0.252	0.206	745.52 intron_variar
1.583	0.557	-0.226	1.28	709.58 intron_variar
0	0.829	0.116	-1.561	207.21 intron_variar
0	0.73	0.694	-0.139	138.66 intron_variar
6.908	0.916	2.419	-2.541	176.39 intron_variar
4.123	0.991	-0.036	-0.616	442.62 intron_variar
0	1.329	-0.212	-0.919	106.21 intron_variar
7.57	0.039	0	1.059	221.5 intron_variar
7.57	0.039	-0.529	0.318	221.5 intron_variar
10.243	1.447	0.578	0.809	180.17 intron_variar
2.276	0.799	0.696	0.271	143.78 intron_variar
0	0.446	0.579	1.427	183.8 intron_variar
0	1.179 -	-		328.68 intron_variar
0	0.693	-0.747	0.747	317.33 intron_variar
0	0.859	-0.751	0.751	316.36 intron_variar
0	1.863 -	-		362.51 intron_variar
0	1.609 -	-		397.14 intron_variar
0	0.832	0.725	-0.439	172.13 intron_variar
2.808	1.472	0	0.633	112.18 intron_variar
14.211	1.85	-0.787	0.324	144.61 intron_variar
6.373	1.518	-1.22	0.495	292.06 intron_variar
0	0.735	1.156	-0.151	193.39 intron_variar
1.987	1.329	-1.059	-0.766	247.5 intron_variar
2.187	1.371	1.002	-0.884	239.5 intron_variar
1.792	0.307	-0.334	-0.401	310.39 intron_variar

0	0.657	1.401	-0.108	540.37 intron_variar
0	1.061	-0.895	1.214	88.86 intron_variar
0	1.061	0.296	1.001	80.82 intron_variar
0	0.697	0.296	-0.296	219.82 intron_variar
0	1.329 -	-		248.47 intron_variar
0	1.329 -	-		248.47 intron_variar
0	1.329 -	-		248.47 intron_variar
0	1.329 -	-		404.12 intron_variar
0	2.303 -	-		409.19 intron_variar
0	0.693	0.72	-1.38	136.03 intron_variar
0	2.303	1.026	-1.026	136.03 intron_variar
0	1.981 -	-		607.71 intron_variar
0	0.793 -	-		2453.18 intron_variar
0	1.609	0	-0.72	136.12 intron_variar
0	0.368	0	0.72	145.16 intron_variar
1.574	1.27	0.366	0.61	439.9 intron_variar
0	0.426	1.397	0	219.88 intron_variar
4.467	1.546	-0.529	-1.059	238.46 intron_variar
0	1.329	-1.067	-1.067	265.66 intron_variar
0	1.981	-1.495	-0.922	265.66 intron_variar
0	1.609	0	-0.72	179.37 intron_variar
0	1.022	-0.55	0	174.56 intron_variar
0	0.582	-1.92	-0.956	183.61 intron_variar
0	0.582	-0.684	-0.956	174.56 intron_variar
0	0.368	-0.55	0	131.89 intron_variar
0	0.368	-1.754	-0.55	131.9 intron_variar
0	0.859	0.69	-0.296	138.66 intron_variar
0	0.412	0.133	-0.133	277.37 intron_variar
0	0.412	0.578	-0.311	286.41 intron_variar
1.676	0.346	-0.536	-0.872	3558.58 intron_variar
0	0.836	-0.212	-0.529	216.5 intron_variar
0	0.804	-0.4	-1.6	206.77 intron_variar
1.808	0.774	-0.187	0.187	227.39 intron_variar
0	0.976	0.797	0.231	416.51 intron_variar
11.048	0.769	0.436	0.436	3702.73 intron_variar
8.969	1.399	-0.035	0.851	6552.28 intron_variar
0	0.997 -	-		1039.8 intron_variar
15.238	1.43	-0.814	-2.79	274.57 intron_variar
18.975	1.727	-1.219	-0.369	277.02 intron_variar
18.18	1.73	1.487	2.12	317.91 intron_variar
18.082	1.73	1.051	2.447	317.91 intron_variar
19.479	1.997	0.078	2.949	313.33 intron_variar
13.834	2.03	-0.2	3.732	300.53 intron_variar
3.183	1.303	-1.235	4.631	313.33 intron_variar

1.44	1.051	-1.257	4.817	306.17 intron_variar
0	0.657	1.012	3.073	356.2 intron_variar
0	0.589	-1.512	2.915	353.83 intron_variar
0	0.611	-0.202	2.682	433.71 intron_variar
0	0.59	0.278	2.546	433.71 intron_variar
4.174	0.3	0.742	-1.398	461.2 intron_variar
4.463	1.179	-1.622	1.083	385.96 intron_variar
4.464	1.18	0.133	0.936	385.96 intron_variar
9.326	1.528	1.221	1.621	385.96 intron_variar
1.554	1.001	0.275	1.823	212.27 intron_variar
3.323	0.75	-1.429	-0.418	741.7 intron_variar
1.416	0.398	0.303	0.21	304.19 intron_variar
5.029	1.566	-1.474	-1.346	305.19 intron_variar
2.052	1.039	-0.484	-1.157	708.05 intron_variar
3.226	1.362	0.607	-1.611	270.88 intron_variar
3.229	1.368	0.299	-1.675	270.88 intron_variar
1.532	1.17	0.783	0.932	229.57 intron_variar
0	0.876	1.037	0.231	269.39 intron_variar
2.106	1.085	0.337	-0.639	718.29 intron_variar
0	0.743	0.001	1.63	349.69 intron_variar
1.842	0.606	-0.034	1.184	554.65 intron_variar
0	0.587	-0.078	0.844	385.96 intron_variar
0	0.487	1.856	0.24	367.67 intron_variar
0	0.661	-0.474	1.048	294.15 intron_variar
0	0.641	0.045	1.005	323.78 intron_variar
0	0.337	0.232	0.51	317.41 intron_variar
1.947	0.711	-1.131	1.542	494.01 intron_variar
8.3	1.033	-1.76	1.763	574.21 intron_variar
0	0.283	-0.149	2.188	324.95 intron_variar
4.456	0.596	0.344	1.856	645 intron_variar
5.338	0.852	0.922	1.336	568.46 intron_variar
2.247	0.538	-0.944	0.334	649.68 intron_variar
2.267	0.37	0.495	1.811	606.99 intron_variar
3.622	1.042	-0.933	2.049	284.56 intron_variar
2.957	1.408	-0.576	0.956	376.72 intron_variar
2.957	1.409	-0.45	0.905	376.72 intron_variar
0	1.23	-0.467	1.289	376.72 intron_variar
0	0.719	-0.886	1.871	296.25 intron_variar
0	0.742	0.294	1.925	296.25 intron_variar
0	0.5	0.689	2.661	296.25 intron_variar
3.473	0.794	0.695	3.611	257.21 intron_variar
0	1.275	-0.771	0.403	275.78 intron_variar
0	0.812	-0.841	1.739	1005.45 intron_variar
0	0.658	-0.4	2.399	1241.41 intron_variar

0	0.581	0.841	2.7	699.18 intron_variar
0	0.936	-1.095	1.079	516.86 intron_variar
1.221	0.977	-1.431	2.995	2057.94 intron_variar
1.618	0.501	-1.958	-3.04	41131.93 intron_variar
1.226	0.998	2.232	4.541	2121.92 intron_variar
1.645	0.365	1.162	-3.557	40916.93 intron_variar
1.259	1.187	1.85	5.268	2011.51 intron_variar
0	1.169	1.834	3.703	1460.61 intron_variar
0	0.308	-0.499	-2.36	36295.8 intron_variar
0	0.56	0.805	-1.681	32608.26 intron_variar
0	0.303	-0.528	-0.225	32489.08 intron_variar
0	0.703	0.192	1.68	587.54 intron_variar
1.332	0.827	0.358	-3.451	33172.5 intron_variar
1.508	0.772	1.611	-3.887	33329.03 intron_variar
0	0.535	0.124	2.858	680.19 intron_variar
0	0.885	0.595	-2.064	35197.6 intron_variar
9.321	1.56	1.358	-5.181	9465.36 intron_variar
1.848	0.605	-0.608	-1.216	364.06 intron_variar
4.964	1.952	0.786	0.524	193.53 intron_variar
4.887	2.303	0.701	0.124	236.69 intron_variar
1.768	0.269	-0.956	-0.56	364.06 intron_variar
1.885	1.426	0.423	0.211	265.98 intron_variar
0	1.022	0.226	-0.42	275.03 intron_variar
1.829	0.668	1.511	-1.429	318.01 intron_variar
1.957	1.015	-1.111	-1.111	328.01 intron_variar
4.32	1.273	0.367	-1.347	328.01 intron_variar
4.036	1.122	0.458	-1.216	411.84 intron_variar
4.32	1.546	-0.857	-0.122	411.84 intron_variar
3.757	1.552	-0.328	0.263	450.71 intron_variar
0	0.693	-0.391	1.034	516.38 intron_variar
0	0.693	0.069	0.85	522.22 intron_variar
0	0.892	1.026	-0.065	560.94 intron_variar
1.44	1.022	0.58	-0.821	462.92 intron_variar
0	0.892	1.418	-1.207	421.8 intron_variar
0	0.892	-0.783	-1.672	462.92 intron_variar
0	0.693	0.22	-2.062	513.25 intron_variar
3.18	0.56	-1.221	-2.422	471.96 intron_variar
3.399	0.799	-0.445	-2.688	430.85 intron_variar
3.399	0.799	0.529	-3.154	471.96 intron_variar
10.692	0.8	0.777	-3.67	594.42 intron_variar
7.891	0.557	0.569	-3.778	638.88 intron_variar
13.545	1.275	-1.383	-3.983	547.67 intron_variar
1.882	1.251	0.7	-1.652	302.76 intron_variar
0	0.836	-1.301	-1.781	471.96 intron_variar

0	0.836	0.38	-1.461	521.25	intron_variar
0	0.569	-0.349	-0.98	299.54	intron_variar
1.323	1.179	-1.927	0.817	713.76	intron_variar
1.236	1.071	-0.25	2.535	663.51	intron_variar
2.75	1.292	-0.118	2.549	710.91	intron_variar
4.442	1.247	0.596	2.519	713.67	intron_variar
0	0.54	0.431	-1.501	535.92	intron_variar
4.886	0.369	-1.075	-1.905	1269.01	intron_variar
14.239	1.575	-0.417	-2.658	792.06	intron_variar
12.626	1.383	-0.612	-2.126	801.11	intron_variar
2.814	1.262	1.307	1.387	754.62	intron_variar
0	0.569	-1.021	0.554	636.87	intron_variar
3.256	1.071	-0.02	1.842	412.15	intron_variar
0	0.56	0.177	-0.903	797.84	intron_variar
1.364	1.085	-0.239	-1.607	992.88	intron_variar
1.216	1.11	-0.327	-0.604	839.3	intron_variar
2.649	1.23	-0.158	0.352	794.3	intron_variar
0	0.855	-0.752	-0.052	1155.72	intron_variar
1.319	0.521	-1.681	1.424	1371.52	intron_variar
0	0.776	-1.99	0.77	890.24	intron_variar
9.558	0.685	0.221	-0.872	1368.74	intron_variar
9.092	0.48	-0.43	-1.175	1304.59	intron_variar
2.78	0.55	-1.457	0.494	343.59	intron_variar
9.955	0.105	0.723	0.298	1078.76	intron_variar
15.489	0.031	-0.533	-0.593	1078.76	intron_variar
1.356	1.022	0.317	-0.729	691.46	intron_variar
3.565	0.23	-0.583	-1.217	1280.07	intron_variar
4.789	1.589	1.482	-0.285	687.1	intron_variar
1.462	0.368	-0.647	0.244	1361.04	intron_variar
5.109	0.771	0.198	0.571	397.01	intron_variar
2.696	1.284	0.791	0.45	744.25	intron_variar
2.82	1.203	0.521	1.59	600.48	intron_variar
0	0.665	-0.074	0.897	1207.33	intron_variar
13.864	1.026	0.116	0.466	620.36	intron_variar
16.564	0.603	-0.019	-0.925	1036.1	intron_variar
24.779	0.83	-1.451	-0.324	733.86	intron_variar
16.371	0.241	-1.011	-0.708	686.72	intron_variar
0	0.636	0.348	0.32	403.06	intron_variar
14.53	0.044	1.542	-0.224	1297.01	intron_variar
7.529	0.126	-1.029	-1.741	661.51	intron_variar
0	0.646	-0.163	1.583	450.11	intron_variar
7.585	0.144	0.051	-1.204	659.48	intron_variar
4.911	0.214	0.387	1.206	1419.57	intron_variar
4.498	0.249	-1.441	-0.093	512.58	intron_variar

2.779	0.368	1.693	1.45	1425.78 intron_variar
1.207	0.479	1.192	0.755	1553.37 intron_variar
0	0.574	0.881	0.846	1551.41 intron_variar
0	0.723	-0.913	-0.954	1169.08 intron_variar
0	0.565	-0.335	-0.105	1160.04 intron_variar
0	0.719	-0.269	-2.205	1003.36 intron_variar
2.701	0.976	0.164	-0.29	902.75 intron_variar
1.227	0.628	1.947	1.537	618.21 intron_variar
2.624	1.187	-0.071	0.213	658.75 intron_variar
3.179	1.265	-0.085	0.188	818.95 intron_variar
3.124	1.329	-0.198	0.126	836.32 intron_variar
0	0.836	-0.731	0.987	571.9 intron_variar
1.515	0.392	0	1.616	451.96 intron_variar
1.515	0.392	0.67	1.218	454.26 intron_variar
1.708	0.358	-0.212	0.483	232.9 intron_variar
0	0.947	-1.028	-2.639	254.96 intron_variar
1.721	0.307	-0.517	-2.692	530.55 intron_variar
1.824	0.252	0.179	-1.908	628.49 intron_variar
1.949	0.28	0.933	-0.872	226.64 intron_variar
1.744	0.283	0.155	0.465	434.69 intron_variar
0	0.551	1.24	0.588	122.14 intron_variar
0	1.022	-1.531	-0.184	184.23 intron_variar
0	0.836	1.473	-0.34	142.16 intron_variar
0	0.693	-1.476	-0.6	503.52 intron_variar
2.875	1.2	0.385	0.357	624.52 intron_variar
1.264	1.042	0.379	-0.941	708.25 intron_variar
0	0.536	-1.454	-0.303	298.38 intron_variar
8.85	1.53	1.44	0.051	704.76 intron_variar
6.548	1.579	0.606	-0.051	704.76 intron_variar
5.299	1.015	-0.819	-1.078	1184.04 intron_variar
1.192	1.085	0.544	0.776	739.36 intron_variar
1.192	1.085	-1.448	0.66	697.12 intron_variar
3.969	0.283	-0.026	-1.317	1450.41 intron_variar
2.785	0.501	1.062	0.223	955.32 intron_variar
4.859	0.728	0.496	-0.847	496.21 intron_variar
7.684	1.312	0.438	-1.004	493.76 intron_variar
1.463	1.041	1.248	-0.585	331.65 intron_variar
0	0.941	0.994	1.414	1365.99 intron_variar
3.041	1.149	-0.164	1.773	1012.76 intron_variar
2.879	0.352	-0.705	1.08	902.51 intron_variar
1.279	0.976	-1.165	-0.469	536.49 intron_variar
9.276	0.793	0.118	-1.815	888.25 intron_variar
7.754	1.292	0.501	-0.841	410.19 intron_variar
7.754	1.292	-0.559	-0.841	410.19 intron_variar

3.169	0.811	-0.178	0.47	415.51 intron_variar
1.433	0.412	0.414	-0.381	1188.09 intron_variar
0	0.656	1.672	0.567	882.51 intron_variar
4.957	1.412	1.509	0.698	396.44 intron_variar
1.172	0.922	-1.971	2.375	699.21 intron_variar
0	0.634	0.435	-0.354	429.11 intron_variar
1.172	0.922	0.404	1.946	708.25 intron_variar
0	0.749	0.614	0.331	1323.7 intron_variar
1.402	0.385	0.734	0.243	452.62 intron_variar
5.979	1.273	-1.763	-0.694	272.77 intron_variar
1.631	1.262	1.082	-0.501	305.94 intron_variar
1.55	0.758	-0.542	-0.778	787.59 intron_variar
0	0.648	0.157	0.202	422.1 intron_variar
0	0.76	-0.348	-0.952	432.99 intron_variar
0	0.99	2.599	1.416	858.71 intron_variar
3.155	0.518	-0.963	-0.502	604.67 intron_variar
0	0.569	0.767	0.636	595.36 intron_variar
0	0.705	-0.302	0.793	508.19 intron_variar
1.406	0.585	-1.775	0.227	426.19 intron_variar
1.356	0.864	0.09	0.919	433.9 intron_variar
0	0.693	-0.397	-1.228	335.26 intron_variar
0	0.616	-0.45	-2.135	334.4 intron_variar
0	0.838	-0.767	-1.566	325.36 intron_variar
0	0.61	0.4	0.317	579.46 intron_variar
0	0.553	0.575	0.388	579.46 intron_variar
1.197	0.491	-0.129	0.077	604.36 intron_variar
5.731	0.148	1.226	1.545	680.76 intron_variar
4.32	1.1	0.784	-1.775	418.98 intron_variar
4.32	1.1	-0.454	-1.775	418.98 intron_variar
2.017	0.796	2.361	-1.898	595.82 intron_variar
0	0.569	0.307	0.395	149.77 intron_variar
3.09	0.889	0.715	0	71.5 intron_variar
0	0.818	0.322	0.322	84.56 intron_variar
0	0.495	0.736	-0.736	75.04 intron_variar
0	0.223	0.736	-0.736	201.54 intron_variar
0	1.085 -	-		427.21 intron_variar
0	1.022 -	-		566.71 intron_variar
0	0.569	-0.529	1.059	225.5 intron_variar
0	1.609 -	-		586.47 intron_variar
1.641	1.075	-0.087	-0.202	435.63 intron_variar
6.262	2.147	1.237	-0.752	525.42 intron_variar
6.262	2.147	0.073	-0.898	522.22 intron_variar
6.262	2.147	0.558	-0.849	522.22 intron_variar
8.463	1.492	0.462	-1.077	570.45 intron_variar

10.02	1.235	-0.4	-1.508	493.03 intron_variar
2.218	0.18	1.156	-0.854	193.39 intron_variar
0	0.693	0.34	1.021	369.73 intron_variar
0	0.892	-1.021	1.444	398.67 intron_variar
0	0.976	0.626	0.363	451.06 intron_variar
0	0.96	0.124	-0.29	363.02 intron_variar
0	0.511	0.934	-0.156	397.46 intron_variar
0	0.601	0.356	-0.411	397.46 intron_variar
1.527	0.603	-0.171	-0.268	495.86 intron_variar
1.149	0.892	0.038	1.775	532.49 intron_variar
3.405	0.455	-1.179	0.94	1295.48 intron_variar
1.194	0.604	-0.16	-0.357	966.28 intron_variar
0	0.575	1.612	0.16	944.48 intron_variar
0	0.596	1.863	1.595	642.86 intron_variar
1.243	0.791	0.382	0.411	843.91 intron_variar
0	0.58	0.667	0.103	833.44 intron_variar
0	0.665	-0.75	-0.265	1224.37 intron_variar
4.658	1.609	0.301	-0.851	613.49 intron_variar
2.948	1.255	1.676	-0.228	1192.98 intron_variar
7.16	1.838	-0.239	-0.674	649.92 intron_variar
6.983	1.546	-1.335	-1.162	694.48 intron_variar
1.43	0.921	0.748	-0.652	1024.51 intron_variar
1.36	0.713	0.047	-0.921	1126.19 intron_variar
3.185	0.283	-1.144	-0.955	383 intron_variar
6.648	0.517	-1.583	-0.139	760.86 intron_variar
6.805	0.674	-0.239	-0.292	605.86 intron_variar
8.873	0.458	-0.825	0.165	800.94 intron_variar
8.873	0.458	-2.616	0.071	800.94 intron_variar
5.632	0.907	-1.59	0.392	791.56 intron_variar
5.632	0.907	-1.094	0.599	791.56 intron_variar
3.325	1.149	-0.635	-0.159	834.5 intron_variar
0	0.693	-1.249	0.763	590.5 intron_variar
0	0.818	0.217	0.183	355.05 intron_variar
4.957	0.384	0.47	0.114	996.84 intron_variar
0	0.532	-1.391	0.249	971.88 intron_variar
1.264	0.694	1.008	1.339	634.49 intron_variar
1.29	1.085	-1.138	0.222	893.35 intron_variar
0	0.776	0.014	-0.186	893.35 intron_variar
4.752	1.506	-1.22	0.439	243.13 intron_variar
4.752	1.506	0.927	-0.146	245.23 intron_variar
9.249	2.233	-0.059	-1.237	195.18 intron_variar
9.249	2.233	-1.237	-1.945	206.58 intron_variar
5.756	1.884	-0.8	-1.867	156.72 intron_variar
5.756	1.901	0.533	-2.313	167.78 intron_variar

1.186	0.922	-0.992	0.616	1056.26 intron_variar
4.351	1.071	-0.822	-0.056	1101.99 intron_variar
6.374	1.27	1.489	-1.096	938.28 intron_variar
0	0.807	0.014	-1.914	415.72 intron_variar
6.884	1.052	0.099	-1.261	848.31 intron_variar
4.655	0.589	-0.015	-2.866	896.49 intron_variar
4.901	1.374	0.538	-3.604	902.51 intron_variar
4.901	1.374	0.597	-4.032	874.51 intron_variar
2.693	0.572	-2.306	-1.489	700.76 intron_variar
4.646	0.897	0.032	-0.634	700.76 intron_variar
5.023	0.781	0.281	1.01	669.73 intron_variar
5.023	0.607	-0.908	1.832	659.76 intron_variar
0	0.732	-1.114	0.493	992.48 intron_variar
0	0.546	-0.053	0.084	997.02 intron_variar
1.489	0.446	-0.529	-0.411	819.51 intron_variar
0	0.551	0.419	-0.21	985.99 intron_variar
1.796	0.33	-0.647	-0.431	171.7 intron_variar
0	1.179	1.304	-0.767	831.59 intron_variar
4.416	1.863	-0.092	-0.337	623.34 intron_variar
4.612	1.701	0.112	-0.336	543.69 intron_variar
8.141	1.447	-0.244	-1.61	370.19 intron_variar
12.707	2.526	0.201	-0.244	250.72 intron_variar
6.154	1.872	-0.529	-0.831	161.63 intron_variar
9.89	1.862	-0.533	-1.309	158.74 intron_variar
6.532	1.431	-0.6	-1.106	127.97 intron_variar
5.449	1.196	-0.615	-0.615	516.72 intron_variar
3.453	1.609	0.636	-1.425	519.36 intron_variar
5.969	1.981	0.395	-0.716	477.73 intron_variar
1.529	1.288	-1.306	-1.882	430.85 intron_variar
3.325	1.445	-0.487	-1.838	498.21 intron_variar
1.497	1.136	-0.043	-2.317	373.26 intron_variar
3.473	1.46	-0.023	-2.501	496.07 intron_variar
1.55	1.025	-0.298	-1.996	346.12 intron_variar
0	0.693	-0.639	-1.25	267.86 intron_variar
1.664	0.61	-0.117	-0.352	956.26 intron_variar
6.332	0.415	-2.091	0.345	1058.63 intron_variar
1.713	0.355	1.202	-2.27	499.44 intron_variar
1.801	0.283	-1.244	-1.954	499.44 intron_variar
4.285	0.169	0.887	-2.353	457.92 intron_variar
1.706	0.293	-0.232	-2.203	435.59 intron_variar
7.025	0.769	-0.88	0.176	415.41 intron_variar
4.075	0.819	0.495	-0.231	519.26 intron_variar
3.707	1.41	0.415	-2.495	577.46 intron_variar
1.485	1.162	-1.026	-1.391	519.36 intron_variar

1.485	1.162	-0.851	-1.683	551.9 intron_variar
3.18	1.371	-2.401	-1.889	651.72 intron_variar
1.657	1.402	0.18	-2.639	291.17 intron_variar
0	0.818	-1.771	-1.779	331.52 intron_variar
0	0.836	-1.25	-0.441	519.36 intron_variar
0	0.75	-0.293	-0.504	475.26 intron_variar
0	0.75	1.214	-0.329	507.67 intron_variar
0	0.693	0.471	1.828	602.86 intron_variar
0	0.693	0.773	1.677	602.86 intron_variar
1.562	1.179	0.072	0.36	709.58 intron_variar
3.325	0.269	-0.995	0.509	673.25 intron_variar
8.607	0.662	-0.71	-0.344	758.81 intron_variar
5.608	0.556	0.861	0.332	669.25 intron_variar
1.475	1.085	-0.63	-0.993	853.71 intron_variar
3.227	0.706	0.53	-0.124	998.4 intron_variar
0	0.892	0.208	1.189	266.78 intron_variar
3.274	0.729	-0.237	-0.639	995.48 intron_variar
0	0.693	1.493	0.775	968.26 intron_variar
0	0.693	-0.195	0.728	1007.33 intron_variar
0	0.892	0.592	-0.439	865.93 intron_variar
3.117	1.358	-0.47	-1.282	1002.44 intron_variar
3.235	1.093	-1.141	-1.473	954.36 intron_variar
1.32	1.038	0.314	-1.205	576.88 intron_variar
3.211	1.473	0.035	-0.921	440.78 intron_variar
3.211	1.037	-0.805	-1.713	872.13 intron_variar
5.641	1.406	0.168	-1.254	863.32 intron_variar
10.976	2.138	0.522	-1.027	644.9 intron_variar
10.976	2.138	0.09	-0.991	644.9 intron_variar
5.402	1.721	-1.07	-1.109	782.81 intron_variar
0	0.709	0.092	0.645	494.72 intron_variar
0	0.519	0.426	-1.359	800.31 intron_variar
0	0.512	0.692	-1.179	830.07 intron_variar
0	0.512	-0.58	-1.179	830.07 intron_variar
2.835	0.34	-1.138	0.547	889.31 intron_variar
2.835	0.34	-1.611	0.665	889.31 intron_variar
1.377	0.425	-2.41	-1.063	825.84 intron_variar
1.414	0.368	-1.087	-1.492	825.84 intron_variar
1.414	0.368	-0.276	-2.671	771.81 intron_variar
5.167	2.584	-0.146	-2.586	245.23 intron_variar
0	0.859	-0.073	-1.517	474.26 intron_variar
3.783	0.577	0.431	1.047	324.89 intron_variar
3.867	0.548	1.774	0.835	308.17 intron_variar
1.54	1.085	0.386	-0.79	513.17 intron_variar
0	0.892	-0.329	-0.617	468.68 intron_variar

1.562	0.368	0.887	1.871	362.58	intron_variar
1.585	0.321	0.574	1.582	347.52	intron_variar
3.488	0.634	2.289	2.614	349.58	intron_variar
0	0.534	-0.835	1.729	315.62	intron_variar
2.521	0.929	-1.598	-0.137	774.01	intron_variar
2.521	0.929	-0.137	-0.411	839.53	intron_variar
2.395	0.758	-1.047	0.436	883.06	intron_variar
4.925	0.663	1.445	0.927	919.75	intron_variar
4.925	0.663	-1.075	0.927	919.75	intron_variar
1.58	0.934	-0.354	-0.626	433.63	intron_variar
0	0.917	-0.961	-0.527	340.69	intron_variar
1.971	1.229	-0.774	1.438	231.25	intron_variar
7.501	2.281	-0.506	0.584	233.55	intron_variar
1.721	1.071	0.194	0.036	300.31	intron_variar
8.28	2.25	-0.195	0.506	193.53	intron_variar
7.144	1.483	-1.102	-0.211	224.21	intron_variar
4.31	1.196	0.175	0.602	182.26	intron_variar
0	0.743	-0.267	1.54	319.44	intron_variar
0	0.446	-0.456	0.489	325.24	intron_variar
0	0.446	-1.595	0.489	325.24	intron_variar
0	0.693	-0.567	0.914	360.69	intron_variar
2.199	0.184	0	0.58	605.87	intron_variar
0	0.551	-0.776	1.01	325.24	intron_variar
0	0.693	-1.148	0.893	325.24	intron_variar
0	0.482	-1.229	1.988	466.27	intron_variar
1.583	1.388	-0.226	-1.846	20945.04	intron_variar
0	0.947	-1.078	-4.182	21719.08	intron_variar
4.882	1.319	1.175	-3.766	22541.32	intron_variar
1.149	1.074	0.466	-4.197	21206.83	intron_variar
0	0.754	0.54	2.901	480.57	intron_variar
2.107	1.377	1.416	2.806	208.76	intron_variar
0	0.511	-0.048	-1.409	21841.67	intron_variar
2.887	0.92	-0.598	-2.126	20765.65	intron_variar
0	0.602	0.137	1.893	334.98	intron_variar
6.778	0.526	1.818	-1.03	20055.88	intron_variar
1.338	0.64	-0.071	-1.899	17652.25	intron_variar
4.884	0.675	0.238	-1.651	20347.25	intron_variar
2.232	0.582	-0.12	2.231	20257.98	intron_variar
5.025	0.814	0.204	-1.709	23739.45	intron_variar
2.278	0.571	-1.281	-1.106	25575.47	intron_variar
1.757	0.67	-0.264	-0.581	24135.04	intron_variar
2.278	0.803	0.68	-1.641	25104.95	intron_variar
0	0.889	0.668	-1.062	25104.95	intron_variar
0	0.789	0.751	-1.509	24339.95	intron_variar

1.291	0.684	2.025	-1.166	14045.25	intron_variar
0	0.505	0.479	-1.399	23013.19	intron_variar
1.635	0.338	-0.793	-1.859	22047.81	intron_variar
0	0.576	0.389	-1.661	19838.52	intron_variar
0	0.742	-1.848	-4.282	20553.47	intron_variar
0	0.755	1.872	-1.221	18637.17	intron_variar
0	0.422	1.378	1.479	21443.79	intron_variar
7.864	0.349	1.097	0.525	18500.09	intron_variar
0	1.17	-1.535	-2.96	25205.15	intron_variar
2.904	0.839	0.122	-4.307	23534.51	intron_variar
0	0.522	0.543	-0.759	23127.8	intron_variar
1.658	0.366	0.53	-1.157	22356.59	intron_variar
0	0.542	1.568	-0.691	20588.46	intron_variar
1.267	1.031	1.018	-0.657	10222.75	intron_variar
2.973	2.004	-1.213	-1.231	422.46	intron_variar
0	1.609	0.361	-1.652	151.21	intron_variar
0	0.693	0.103	-1.668	176.14	intron_variar
0	1.022	-1.932	-0.825	118.93	intron_variar
5.497	1.479	0.979	-1.24	122.14	intron_variar
5.497	1.479	1.11	-0.979	122.14	intron_variar
5.497	1.479	-0.718	-0.588	113.09	intron_variar
2.522	1.506	-0.636	1.202	124.21	intron_variar
0	0.569	0	-1.133	421.16	intron_variar
0	0.859	-0.457	-0.979	435.44	intron_variar
5.497	0.751	-0.796	2.021	363.96	intron_variar
2.081	0.697	0.868	0.299	247.5	intron_variar
4.166	1.487	0.877	-4.944	2980.99	intron_variar
2.21	1.044	-1.09	-5.648	6950	intron_variar
0	0.706	0.259	-3.822	8708.05	intron_variar
0	0.802	1.295	-3.591	9999.01	intron_variar
0	0.781	-1.735	-3.021	12089	intron_variar
0	0.635	1.055	1.495	150.71	intron_variar
0	0.907	1.429	1.764	165.1	intron_variar
0	0.84	-0.645	-1.284	25129.58	intron_variar
0	1.102	-0.362	-0.249	25041.69	intron_variar
2.946	2.104	-0.141	2.51	285.19	intron_variar
0	0.97	-0.051	1.419	176.05	intron_variar
0	0.953	0.919	0.06	264.26	intron_variar
0	1.009	0.429	0.034	264.26	intron_variar
0	0.462	0.01	-0.028	22642.86	intron_variar
1.648	0.381	-0.149	-3.808	23943	intron_variar
3.329	1.554	-0.618	3.539	188.53	intron_variar
0	0.639	-0.133	-2.061	20070.17	intron_variar
0	0.33	-0.818	-0.273	759.9	intron_variar

0	0.936	-0.638	-0.693	333.51 intron_variar
1.792	0.714	0.194	0.083	216.98 intron_variar
2.066	0.193	-0.175	1.785	70.31 intron_variar
0	0.951	0.628	-0.075	303.35 intron_variar
3.682	0.936	-0.416	-2.025	366.2 intron_variar
4.359	2.093	1.528	-0.036	315.92 intron_variar
0	0.76	-0.372	-1.94	401.98 intron_variar
0	0.412	1.625	-1.776	388.8 intron_variar
0	0.721	0.152	0.608	217.61 intron_variar
6.232	0.07	-1.04	1.857	753.96 intron_variar
0	0.512	0.216	-0.36	209.66 intron_variar
0	0.593	-0.379	-0.437	150.05 intron_variar
4.973	0.223	0.161	-0.6	357.83 intron_variar
5.072	0.799	0.052	0.33	380.32 intron_variar
7.877	1.072	0.63	1.203	380.32 intron_variar
1.423	0.731	-0.592	2.272	283.93 intron_variar
0	0.892	-1.907	0.192	642.86 intron_variar
0	0.836	1.481	-1.081	817.71 intron_variar
0	0.941	0.244	1.61	163.28 intron_variar
10.71	3.239	-0.354	-1.202	124.21 intron_variar
10.71	3.239	-1.061	-0.919	124.21 intron_variar
2.632	0.991	0.382	0.715	83.5 intron_variar
0	0.527	0.849	1.774	70.44 intron_variar
3.274	0.515	-0.913	1.756	649.17 intron_variar
1.808	1.14	0.219	1.973	160.77 intron_variar
0	0.693	0.589	0.465	486.69 intron_variar
0	0.527	-0.184	0.258	215.25 intron_variar
0	0.382	0.853	0.239	276.7 intron_variar
2.066	0.193	1.775	-1.388	275.03 intron_variar
4.039	1.863	0.194	1.528	246.86 intron_variar
7.14	2.368	-0.423	1.48	231.19 intron_variar
4.506	1.863	0.206	1.361	234.55 intron_variar
1.885	1.426	0.423	1.621	234.55 intron_variar
1.833	1.23	0.261	-0.336	236.69 intron_variar
11.633	1.426	-2.89	-1.18	217.98 intron_variar
7.887	1.097	-2.586	-0.046	226.03 intron_variar
6.205	0.124	0.275	-0.909	700.03 intron_variar
1.515	1.179	1.135	1.548	602.56 intron_variar
7.129	0.086	0.503	-0.072	766.66 intron_variar
0	0.711	-0.22	1.059	928.07 intron_variar
0	0.562	-1.055	-1.299	1249.35 intron_variar
0	0.804	-0.039	-0.09	1613.05 intron_variar
0	0.7	0.559	0.243	1219.56 intron_variar
0	0.681	-2.414	0.502	1585.63 intron_variar

0	0.681	-1.352	0.502	1608.51 intron_variar
0	0.608	-0.068	1.095	1522.56 intron_variar
4.372	0.263	-0.983	1.846	1303.97 intron_variar
3.083	1.36	-0.839	0.489	309.79 intron_variar
0	1.501	-	-	1549.63 intron_variar
0	0.569	-0.253	0.471	278.71 intron_variar
1.674	0.715	1.48	0.913	311.55 intron_variar
6.415	2.093	-0.724	0.787	276.55 intron_variar
1.279	0.946	0.45	-1.765	577.86 intron_variar
5.085	1.635	-0.995	-2.374	721.51 intron_variar
0	0.892	0.708	-1.387	260.44 intron_variar
0	0.61	-0.146	-0.437	665.37 intron_variar
0	0.784	1.777	0.437	260.37 intron_variar
0	0.784	-0.437	0.495	260.37 intron_variar
24.328	3.225	0.56	-2.539	289.06 intron_variar
7.908	2.266	-1.216	-0.184	149.53 intron_variar
0	0.73	0.139	1.157	156.66 intron_variar
0	1.022	-0.896	0.474	156.66 intron_variar
19.082	4.171	-0.055	-2.18	336.07 intron_variar
34.589	5.281	0.461	-2.879	644.42 intron_variar
42.658	5.668	-0.869	-3.907	955.53 intron_variar
15.003	0.052	-0.164	3.843	521.4 intron_variar
42.484	6.358	-0.483	-3.603	1088.37 intron_variar
19.569	1.403	0.289	1.316	190.23 intron_variar
41.751	6.285	-0.884	-1.419	1179.22 intron_variar
42.316	6.387	-0.045	-1.9	1527.18 intron_variar
44.858	6.698	0.422	-2.575	1817.49 intron_variar
23.35	3.317	-0.83	-3.5	2259.77 intron_variar
30.719	1.19	1.483	0.506	240.59 intron_variar
28.547	3.019	-1.277	-1.072	3195.42 intron_variar
30.37	3.044	0.094	-0.159	3992.71 intron_variar
30.37	3.044	-1.915	-0.321	3980.92 intron_variar
0.928	0.57	-2.145	-3.867	13037.9 intron_variar
1.952	0.51	-3.217	-3.948	13275.25 intron_variar
1.976	0.461	-3.407	-4.119	13815.25 intron_variar
3.686	1.157	3.674	2.935	543.02 intron_variar
3.115	0.439	-2.788	-3.808	13902.7 intron_variar
0	0.9	-1.16	-2.525	14986.74 intron_variar
0	0.873	-1.186	-2.618	16195.97 intron_variar
3.332	2.833	-1.203	-0.573	68.28 intron_variar
0	1.112	-0.495	-1.626	153.48 intron_variar
0	0.646	0.919	-1.898	153.48 intron_variar
1.725	0.973	-2.385	0.085	1108.72 intron_variar
1.967	0.85	0.081	-0.403	1080.81 intron_variar

0	0.99	-0.146	-1.254	680.59 intron_variar
1.451	0.641	-2.185	0.409	249.66 intron_variar
3.497	0.49	0.973	0.655	775.03 intron_variar
2.784	1.189	-1.034	-1.006	707.62 intron_variar
1.512	0.393	1.373	1.545	851.56 intron_variar
6.036	1.954	0.922	-0.042	249.51 intron_variar
0	0.941	0.718	-0.803	197.94 intron_variar
0	1.022	0.696	0.437	154.78 intron_variar
2.632	1.492	-0.6	1.134	127.99 intron_variar
0	1.329	-0.849	1.62	125.44 intron_variar
0	1.022	0.55	-0.55	131.89 intron_variar
8.57	1.078	-1.779	-0.843	847.28 intron_variar
1.527	1.14	0.801	1.529	381.31 intron_variar
4.977	0.223	0.849	-0.283	1073.76 intron_variar
2.867	0.294	0.892	-0.184	1113.12 intron_variar
0	0.582	-0.272	-1.752	149.3 intron_variar
0	0.892	0.214	1.562	247.47 intron_variar
4.06	0.643	1.143	0.445	80.19 intron_variar
1.76	1.236	0.215	1.2	386.74 intron_variar
8.351	0.061	-1.412	-1.123	193.71 intron_variar
2.158	1.609	-1.215	-1.562	218.78 intron_variar
0	0.859	-0.239	0.102	162.48 intron_variar
0	0.665	-2.735	-0.684	300.38 intron_variar
3.565	0.876	0.276	-0.728	527.35 intron_variar
1.402	0.446	-0.385	-0.75	303.12 intron_variar
0	0.866	0.267	0.728	315.66 intron_variar
2.515	0.18	-1.11	0.588	120.14 intron_variar
0	1.609	0.895	-2.166	97.48 intron_variar
3.233	2.419	0.296	0.296	75.46 intron_variar
3.233	2.419	0.296	-0.546	75.46 intron_variar
2.808	1.518	-0.876	-0.729	125.47 intron_variar
3.136	1.447	-0.421	-1.638	134.52 intron_variar
0	1.609	0.296	-0.546	192.86 intron_variar
1.871	1.402	1.102	-1.755	316.97 intron_variar
0	1.22	-	-	1015.85 intron_variar
0	0.668	-0.055	-1.73	583.18 intron_variar
0	0.593	0.058	-1.538	655.9 intron_variar
5.041	1.222	1.049	-2.897	413.59 intron_variar
0	0.656	0.968	-0.164	289.48 intron_variar
8.161	2.179	0.769	-0.359	240.4 intron_variar
0	0.732	-0.486	0.195	962.93 intron_variar
21.585	4.657	0.164	-2.063	288.48 intron_variar
8.457	1.944	0.116	-0.282	906.25 intron_variar
1.235	0.465	-1.789	1.141	517.97 intron_variar

0	0.804	1.291	-0.319	608.84 intron_variar
0	0.556	0.915	-1.518	507.16 intron_variar
1.278	0.645	-0.279	-0.81	478.6 intron_variar
0	0.538	-0.041	0.014	427.82 intron_variar
0	0.616	-0.122	1.234	396.32 intron_variar
5.748	1.09	1.468	-0.436	405.87 intron_variar
2.424	0.905	0.549	-0.154	733.21 intron_variar
2.815	1.121	-0.227	-0.53	338.44 intron_variar
9.968	0.332	0.424	-1.499	341.74 intron_variar
1.356	0.384	-1.128	2.269	328.98 intron_variar
1.685	1.23	-0.179	-0.283	306.58 intron_variar
0	0.368	0.95	-1.174	593.16 intron_variar
0	0.625	-0.197	0.493	374.95 intron_variar
1.86	0.719	0	1.198	121.5 intron_variar
0	0.487	0.347	0.809	1167.88 intron_variar
4.442	0.61	-0.449	1.074	633.32 intron_variar
1.564	0.412	-0.258	-1.055	285.71 intron_variar
0	0.446	-0.51	0.645	752.77 intron_variar
0	0.495	0.214	-0.398	271.42 intron_variar
1.86	0.719	1.692	0.282	233.25 intron_variar
1.708	0.358	-0.966	1.579	265.07 intron_variar
4.506	0.16	0.817	-0.117	145.26 intron_variar
0	0.941	-0.702	0.501	137.21 intron_variar
1.606	1.127	-0.381	-0.585	689.82 intron_variar
10.916	0.838	0.167	0.635	1111.41 intron_variar
0	0.829	0.503	-1.048	227.51 intron_variar
0	0.711	-1.927	0.467	555.52 intron_variar
1.455	0.399	0.415	-0.458	519.36 intron_variar
3.524	0.529	0.29	-0.695	489.63 intron_variar
4.31	1.196	-1.505	0.945	151.31 intron_variar
0	0.569	1.14	2.402	513.6 intron_variar
0	0.673	-0.775	1.848	447.63 intron_variar
3.917	0.98	1.098	-1.293	242.94 intron_variar
5.76	0.499	0.224	-1.362	638.71 intron_variar
2.747	0.368	-1.442	0.414	574.31 intron_variar
0	0.722	-0.772	0.429	1119.62 intron_variar
2.963	0.899	-1.39	0.989	410.19 intron_variar
2.963	0.899	0.33	1.628	410.19 intron_variar
1.508	0.368	-0.607	-0.02	151.52 intron_variar
0	0.656	0.602	0.42	207.47 intron_variar
1.792	0.714	0.747	-0.083	166.06 intron_variar
0	0.836	-0.581	-0.968	184.06 intron_variar
0	0.693	0.758	0.574	444.46 intron_variar
0	0.678	1.317	0.659	508.15 intron_variar

0	0.804	0.903	1.952	508.42 intron_variar
6.862	1.305	0.119	1.133	544.62 intron_variar
1.74	1.192	-1.576	1.379	324.66 intron_variar
0	0.941	-0.457	1.371	150.73 intron_variar
1.871	0.754	-1.141	1.395	305.45 intron_variar
1.565	0.74	-0.919	0.854	344.71 intron_variar
1.74	0.991	-1.514	-0.246	278.02 intron_variar
0	0.941	0.521	0.398	468.39 intron_variar
0	0.476	-2.295	0.321	486.25 intron_variar
3.783	1.655	0.519	-0.675	432.46 intron_variar
0	0.836	-0.612	1.136	566.42 intron_variar
0	0.892	-0.675	0.5	290.54 intron_variar
0	0.801	0.503	0.713	300.49 intron_variar
1.489	1.292	-2.062	-3.022	729.84 intron_variar
0	0.536	0.86	-0.346	358.52 intron_variar
7.702	0.939	-0.841	-1.048	968.02 intron_variar
0	0.61	0.486	-0.486	189.72 intron_variar
0	0.495	-0.55	1.343	879.99 intron_variar
0	0.706	1.432	-0.783	715.93 intron_variar
6.107	0.707	0.023	0.298	639.52 intron_variar
6.629	1.479	-0.463	1.159	434.03 intron_variar
1.549	1.274	-0.967	-2.211	353.92 intron_variar
1.445	1.085	-0.618	0.653	335.26 intron_variar
0	0.6	1.687	1.842	1074.6 intron_variar
1.433	1.085	-0.149	2.072	226.75 intron_variar
3.062	1.341	1.05	0.654	248.3 intron_variar
6.017	1.965	-0.937	-0.898	288.73 intron_variar
5.124	1.22	0.725	-0.683	1269.64 intron_variar
0	0.95	-	-	2521.58 intron_variar
6.909	1.19	0.643	-0.44	1233.82 intron_variar
6.909	1.19	0.758	-0.44	1233.82 intron_variar
2.527	0.877	1.328	-0.68	1131.83 intron_variar
1.134	0.611	-0.742	-0.678	1096.12 intron_variar
0	0.586	1.323	-0.785	1075.07 intron_variar
3.809	0.346	-0.438	1.563	1120.6 intron_variar
3.809	0.346	0.759	1.563	1117.19 intron_variar
1.052	0.885	-0.276	1.603	846.51 intron_variar
1.114	0.996	-0.01	0.734	822.11 intron_variar
0	0.719	0.85	-1.318	1054.36 intron_variar
0	0.758	-0.23	-0.968	1081.63 intron_variar
1.117	0.794	-1.096	-1.208	997.1 intron_variar
3.917	0.953	-1.062	-1.713	1039.3 intron_variar
2.379	0.909	0.351	-1.734	904.3 intron_variar
2.34	0.913	-0.019	-1.148	862.63 intron_variar

0	0.784	-0.105	-1.926	726.75 intron_variar
0	0.641	-0.198	-0.293	1029.76 intron_variar
0	0.631	1.083	-0.443	987.81 intron_variar
1.032	0.516	0.556	0.149	782.81 intron_variar
0.97	0.536	-1.31	-0.268	1107.82 intron_variar
4.735	1.185	-0.48	-0.517	1082.38 intron_variar
0.889	0.88	-0.237	-1.264	1323.38 intron_variar
0.889	0.88	-1.816	-1.187	1374.28 intron_variar
0.874	0.869	-0.684	-0.628	1488 intron_variar
2.6	0.327	-0.082	1.201	1895.52 intron_variar
0	0.663	0.193	-0.672	925.29 intron_variar
1.085	0.957	0.346	-1.056	780.37 intron_variar
0	0.624	0.366	-4.855	616.49 intron_variar
7.696	1.444	-3.486	-3.994	702.82 intron_variar
7.342	1.233	-4.078	-5.29	730.76 intron_variar
0	0.631	-0.724	-0.949	379.4 intron_variar
2.432	1.091	0.651	-0.114	715.88 intron_variar
4.058	1.023	0.068	-0.3	806.75 intron_variar
1.064	0.936	0.678	-0.336	804.56 intron_variar
0	0.719	-0.747	-0.582	883.65 intron_variar
2.178	0.898	-0.094	-0.558	925.82 intron_variar
2.178	0.898	0.079	-0.154	1010.45 intron_variar
2.12	0.878	0.045	-1.702	1010.45 intron_variar
0	0.69	0.11	0.061	1090.52 intron_variar
0	0.7	-0.103	-1.555	1243.36 intron_variar
0	0.617	0.114	0.203	1217.89 intron_variar
11.963	0.661	1.109	1.117	1062.93 intron_variar
11.963	0.661	1.381	0.956	1063.93 intron_variar
7.296	0.475	-1.03	0.59	1060.93 intron_variar
3.765	0.436	-0.148	0.722	1010.06 intron_variar
6.954	0.899	3.027	-2.181	1368.09 intron_variar
7.487	1.044	-1.533	-2.83	1194.96 intron_variar
5.557	1.074	-0.626	-2.092	889.55 intron_variar
3.855	0.931	-0.098	-2.005	916.6 intron_variar
3.854	1.058	-1.541	-2.313	916.6 intron_variar
0	0.797	-0.634	-0.252	1042.84 intron_variar
1.02	0.982	-0.236	-0.555	1048.06 intron_variar
0	0.719	1.595	-1.579	1062.93 intron_variar
0	0.719	-0.132	-1.548	1062.93 intron_variar
5.563	1.18	0.263	1.977	933.49 intron_variar
11.534	0.835	0.586	0.297	1006.42 intron_variar
11.534	0.835	0.038	0.281	1015.47 intron_variar
11.534	0.835	1.194	0.251	1015.47 intron_variar
13.594	1.171	0.94	1.606	479.36 intron_variar

14.447	0.852	-0.458	0.072	933.49 intron_variar
14.447	0.852	-0.893	-0.024	933.49 intron_variar
12.339	0.861	1.978	-0.28	1014.47 intron_variar
12.38	0.685	0.14	-1.109	1020.17 intron_variar
7.361	0.14	0.808	-0.828	506.59 intron_variar
7.361	0.14	-1.05	-0.687	506.59 intron_variar
9.925	0.117	0.784	-0.123	510.7 intron_variar
13.435	0.092	1.242	-0.379	977.55 intron_variar
0	0.722	-0.477	-0.527	753.86 intron_variar
0	0.693	-0.679	-0.384	753.84 intron_variar
2.627	1.274	-0.231	0.16	546.7 intron_variar
0	0.656	0.172	-0.618	472.42 intron_variar
0.884	0.85	1.093	-3.376	8346.7 intron_variar
2.676	0.384	0.136	0.255	4490.57 intron_variar
0	0.507	0.851	1.199	627.42 intron_variar
2.995	1.274	-2.434	-0.827	436.43 intron_variar
4.738	1.473	-2.691	-0.119	473.43 intron_variar
1.19	1.048	-1.294	0.431	676.41 intron_variar
2.517	1.182	-0.706	-0.651	637.06 intron_variar
3.96	1.262	-2	-0.709	637.06 intron_variar
3.96	1.262	-2.933	-0.386	637.06 intron_variar
6.022	1.116	-0.896	-0.085	998.57 intron_variar
2.652	0.603	-1.223	1.513	462.96 intron_variar
4.547	1.483	4.826	1.439	345.99 intron_variar
1.412	0.412	4.019	-0.315	257.2 intron_variar
0	0.643	-4.124	2.867	8688.99 intron_variar
0	0.64	-4.157	3.049	8629.88 intron_variar
1.291	0.419	-4.687	2.852	8611.04 intron_variar
8.675	0.818	-3.859	3.15	11661.89 intron_variar
4.439	0.987	-3.599	2.055	3205.63 intron_variar
1.342	0.614	-2.255	4.404	6665.97 intron_variar
7.16	0.965	-1.772	-1.511	969.06 intron_variar
9.379	1.107	0.841	-0.98	925.82 intron_variar
9.379	1.107	0.517	-0.856	884.65 intron_variar
5.343	0.871	-0.445	-0.521	954.82 intron_variar
7.277	1.022	0.148	0.179	831.55 intron_variar
0	0.776	-0.07	0.458	820.55 intron_variar
0	0.275	-0.139	-0.346	1998.75 intron_variar
0	0.809	-1.091	-0.167	866.66 intron_variar
0	0.678	-0.785	-0.496	806.75 intron_variar
1.004	0.544	-0.394	-1.23	868.45 intron_variar
0	0.876	-0.659	0.442	1416.82 intron_variar
0	0.662	0.726	1.474	920.55 intron_variar
0	0.616	-1.277	1.55	909.32 intron_variar

3.679	0.773	0.258	-0.758	1307.01 intron_variar
6.238	1.095	1.518	-0.044	464.7 intron_variar
0.99	0.524	1.948	0.356	1023.79 intron_variar
6.816	0.925	0.441	0.013	791.46 intron_variar
6.772	2.215	-1.618	0.586	250.98 intron_variar
0	1.688 -	-		1091.8 intron_variar
12.493	0.52	-0.098	0.705	1021.17 intron_variar
12.147	0.388	-0.646	-0.295	1065.79 intron_variar
14.437	0.639	-0.008	-0.828	1107.74 intron_variar
14.821	0.63	-0.902	-0.87	1107.74 intron_variar
12.493	0.52	0.131	-0.902	1065.79 intron_variar
12.755	0.674	-0.753	-0.84	1107.74 intron_variar
6.357	0.365	0.904	0.595	824.66 intron_variar
11.459	0.718	-0.125	0.421	908.21 intron_variar
4.037	0.751	0.701	1.692	900.24 intron_variar
7.438	0.825	-0.365	2.824	863.49 intron_variar
0	0.602	-0.436	0.908	919.48 intron_variar
1.121	0.489	1.096	-1.08	872.25 intron_variar
0	0.56	-1.242	-1.008	839.19 intron_variar
2.488	0.641	1.227	-1.707	956.24 intron_variar
4.022	0.742	0.57	-1.707	956.24 intron_variar
2.488	0.779	-0.495	-1.559	999.33 intron_variar
4.134	1.005	0.124	-1.826	999.33 intron_variar
0	0.892	1.021	-0.246	357.8 intron_variar
0	0.941	0.762	-1.666	318.37 intron_variar
10	2.78	0.358	1.231	88.86 intron_variar
6.021	2.788	0.727	0.727	99.06 intron_variar
10	2.78	-0.358	1.231	102.6 intron_variar
7.068	2.807	-0.322	1.221	93.61 intron_variar
7.068	2.807	-0.684	-1.517	93.61 intron_variar
0	0.368	-0.391	-0.727	642.16 intron_variar
0	0.537	0.592	-0.474	612.12 intron_variar
1.987	1.329	0.163	0.597	204.23 intron_variar
0	1.609 -	-		548.42 intron_variar
2.429	0.654	-0.262	-0.282	902.28 intron_variar
5.738	0.985	-0.594	0.518	901.28 intron_variar
8.297	1.243	0.962	-1.853	350.75 intron_variar
7.963	0.823	-0.276	1.322	1052.23 intron_variar
8.8	1.522	-1.167	-1.533	341.86 intron_variar
7.826	0.93	-0.085	1.611	939.94 intron_variar
7.625	0.94	0.668	1.686	931.55 intron_variar
3.933	1.053	0.292	1.799	948.99 intron_variar
1.101	1.038	-1.358	1.572	946.09 intron_variar
2.084	1.096	0.662	-2.301	1403.8 intron_variar

4.883	1.296	-0.178	-1.98	1530.61 intron_variar
4.883	1.296	-0.77	-1.901	1484.36 intron_variar
3.257	1.13	1.291	-0.823	1470.65 intron_variar
3.767	1.272	-1.519	1.123	628.33 intron_variar
0.923	0.822	-1.043	0.393	1397.66 intron_variar
5.365	1.251	-1.662	1.412	632.07 intron_variar
0	0.723	0.05	0.521	1275.69 intron_variar
0	0.649	1.513	1.083	1215.72 intron_variar
0	0.649	0.27	0.907	1215.72 intron_variar
0	0.787	1.27	2.514	1042.06 intron_variar
0	1.179	-	-	328.68 intron_variar
1.199	0.902	-0.576	-0.184	488.01 missense_va
8.471	1.363	-1.468	-0.317	676.5 non-synonymyn
0	0.693	0.158	-1.423	352.51 non-synonymyn
3.31	0.105	-0.48	0.48	325.82 non-synonymyn
0	1.981	-0.922	0	179.52 non-synonymyn
1.708	1.325	-0.78	2.198	8760.95 non-synonymyn
4.131	1.09	1.135	1.868	11361.95 non-synonymyn
4.108	1.077	-0.564	1.679	11496.95 non-synonymyn
0	0.915	1.835	-0.612	123.45 non-synonymyn
4.346	1.224	0.738	2.608	11861.51 non-synonymyn
2.055	1.544	1.937	0.336	15144.94 non-synonymyn
2.032	1.511	-0.487	0.561	15234.94 non-synonymyn
3.211	1.757	-1.76	-0.259	30414.58 non-synonymyn
0	1.435	0.053	0.856	30415.73 non-synonymyn
0	1.117	-0.87	0.495	31456.9 non-synonymyn
0	0.422	0.595	-2.04	187.5 non-synonymyn
0	1.374	-0.093	-0.209	32428.39 non-synonymyn
8.051	1.108	-0.81	0.34	23016.49 non-synonymyn
10.157	0.983	0.118	-2.19	16888.74 non-synonymyn
12.683	1.027	-0.759	-2.247	16483.74 non-synonymyn
11.84	1.123	2.014	-1.083	12606.49 non-synonymyn
0	0.678	0.25	-0.165	21646.03 non-synonymyn
0	0.913	2.354	-0.547	154.96 non-synonymyn
0	0.913	2.09	-0.781	154.96 non-synonymyn
0	0.415	0.064	1.341	22042.08 non-synonymyn
3.032	0.23	-0.231	1.485	22195.76 non-synonymyn
3.032	0.12	1.333	0.903	23145.44 non-synonymyn
0	0.175	1.339	0.267	25885.09 non-synonymyn
3.446	0.502	-0.493	0.177	27113.42 non-synonymyn
3.571	0.598	-3.081	0.569	27553.51 non-synonymyn
3.099	0.358	1.541	0.135	35724.58 non-synonymyn
0	0.547	-1.334	-2.02	41037 non-synonymyn
0	0.746	-0.997	-1.966	42374.35 non-synonymyn

0	0.57	-0.913	-0.637	40017.39 non-synonym
0	0.648	-0.672	0.993	178.61 non-synonym
12.378	2.342	-1.154	0.894	19607.88 non-synonym
12.197	2.318	0.804	1.247	20501.57 non-synonym
5.643	1.988	-0.892	0.121	21456.03 non-synonym
4.046	0.95	-1.039	-0.091	21988.96 non-synonym
6.347	0.886	0.839	0.448	18729.49 non-synonym
13.912	0.035	-1.324	0.139	17860.45 non-synonym
0	0.676	-0.143	0.181	12886.85 non-synonym
0	1.382	-0.798	0.149	12057.66 non-synonym
1.596	0.409	0.324	2.441	17609.45 non-synonym
4.212	0.192	-0.081	1.863	17156.4 non-synonym
6.338	0.154	2.029	0.437	17744.45 non-synonym
6.226	0.165	-0.314	0.213	17764.54 non-synonym
1.102	0.533	1.366	3.053	16355.71 non-synonym
0	0.613	-0.348	2.586	15115.6 non-synonym
2.728	1.262	0.314	0.013	13804.25 non-synonym
7.5	0.058	0.275	-0.028	349.69 non-synonym
1.657	0.323	-0.649	1.518	24401.81 non-synonym
30.955	0.676	1.734	-1.798	10427.36 non-synonym
54.805	3.988	2.063	-0.062	7290.73 non-synonym
135.05	5.765	2.422	-1.029	5470.51 non-synonym
13.236	1.856	0.95	1.28	89.95 non-synonym
3.522	2.245	0.48	1.271	87.5 non-synonym
2.632	0.991	0.566	0.382	87.5 non-synonym
0	0.804	-0.381	0.96	632.97 non-synonym
0	0.733	-0.472	-0.736	250.78 non-synonym
0	0.921	0.566	0.68	240.13 non-synonym
0	0.551	-2.154	-0.979	111.14 non-synonym
0	0.666	0.079	-0.079	394.2 non-synonym
4.193	1.567	0.916	-2.467	233.25 non-synonym
6.779	2.067	1.61	-1.014	305.49 non-synonym
7.546	2.584	0.167	-1.57	223.25 non-synonym
3.976	1.299	-0.031	1.669	246.55 non-synonym
10.432	0.088	0.774	0.155	1567.35 non-synonym
1.871	0.677	0.1	0.117	184.94 non-synonym
3.312	1.22	0.861	-0.387	388.3 non-synonym
3.565	0.912	-0.477	0.427	351.35 non-synonym
1.441	1.022	0.627	-0.162	430.85 non-synonym
0	0.914	0.237	-1.629	633.76 non-synonym
1.323	0.576	-0.454	-0.579	921.49 non-synonym
0	0.582	-0.014	-0.159	925.49 non-synonym
1.603	1.085	0.538	-0.991	180.9 non-synonym
10.588	3.047	-1.401	-0.377	242.75 non-synonym

13.359	1.16	0	-0.808	243.75 non-synonym
3.78	1.565	-1.093	-0.076	181.05 non-synonym
0	0.804	-0.07	0.07	189.55 non-synonym
0	0.495	-1.306	0.858	373.69 non-synonym
0	1.112	0.354	0.231	118.31 non-synonym
0	1.609 -	-		142.56 non-synonym
0	1.022 -	-		155.06 non-synonym
3.68	1.108	0.742	0.742	132.12 non-synonym
0	1.179 -	-		283.72 non-synonym
0	0.941	-0.762	-0.762	273.52 non-synonym
0	1.609 -	-		293.16 non-synonym
0	1.609 -	-		293.16 non-synonym
0	0.223 -	-		86.61 non-synonym
2.757	0.132	-1.157	-0.386	112.44 non-synonym
0	0.283	-0.817	0.533	154.78 non-synonym
0	6.273 -	-		2033.61 non-synonym
0	6.769	-0.587	-0.157	5485.64 non-synonym
1.246	1.032	-0.684	0.392	358.48 non-synonym
0	0.549	0.468	3.263	362.36 non-synonym
0	0.704	-0.008	-1.38	526.53 non-synonym
1.64	1.152	-0.281	-0.807	32531.88 non-synonym
1.255	0.434	-0.962	0.054	1530.83 non-synonym
2.294	0.435	2.062	-1.639	680.97 non-synonym
0	0.653	-0.01	-1.759	506.31 non-synonym
4.161	0.367	-0.659	1.711	1578.42 non-synonym
1.419	0.437	-0.67	-0.544	676.96 non-synonym
17.148	0.088	0.738	-1.355	4664.58 non-synonym
4.4	0.595	0.635	-1.051	233.34 non-synonym
4.4	0.595	-0.434	-0.895	233.25 non-synonym
0	0.446	-0.692	-0.433	320.2 non-synonym
0	0.693	0.56	0.758	453.06 non-synonym
0	1.303 -	-		13874.07 non-synonym
0	1.222 -	-		13112.17 non-synonym
0	0.82 -	-		8640.51 non-synonym
0	2.38	0.194	2.139	4137.5 non-synonym
0	1.219	1.322	0.428	4331.64 non-synonym
0	1.609 -	-		159.56 non-synonym
0	0.836	-0.212	0.318	198.72 non-synonym
0	0.646	0.674	0.551	150.62 non-synonym
0	0.495	-0.857	2.082	264.01 non-synonym
0	0.986	-0.619	0.536	194.26 non-synonym
1.648	0.654	1.323	0.092	344.75 non-synonym
1.707	1.179	0.171	0.102	236.7 non-synonym
0	0.644	-0.665	-1.197	510.25 non-synonym

3.567	1.445	-0.264	1.159	293.71 non-synonym
6.537	2.2	0.697	-1.458	715.83 non-synonym
1.378	1.038	0.801	1.335	280.51 non-synonym
22.351	0.9	-0.683	-1.205	677.21 non-synonym
0	0.573	-0.461	1.162	1063.8 non-synonym
5.49	0.739	0.122	1.129	265.32 non-synonym
1.76	0.537	0.484	1.84	430.92 non-synonym
0	0.728	-1.128	-0.462	356.5 non-synonym
6.983	0.356	-0.688	1.335	606.53 non-synonym
4.428	1.431	0.523	-2.435	417.68 non-synonym
0	0.737	-0.908	0.81	1129.4 non-synonym
0	0.797	0.511	1.043	1210.95 non-synonym
0.89	0.875	-0.662	1.208	1125.27 non-synonym
0	0.716	0.723	0.57	1460.64 non-synonym
2.029	1.084	0.073	0.332	1460.64 non-synonym
0	0.566	0.635	0.071	2101.67 non-synonym
6.483	0.727	-2.14	-1.76	800.31 non-synonym
4.763	0.392	-0.634	-2.821	803.67 non-synonym
0	0.648	0.378	-0.554	1494.07 non-synonym
4.389	0.98	0.75	0.41	1584.34 non-synonym
5.473	0.809	-0.682	-0.238	979.57 non-synonym
5.341	0.96	0.408	-0.807	1021.17 non-synonym
2.268	0.698	-1.34	-1.003	979.57 non-synonym
2.284	0.384	-0.32	-1.125	1042.93 non-synonym
2.169	0.446	-0.725	-0.969	940.49 non-synonym
0	0.789	0.296	1.332	680.79 non-synonym
0	0.703	0.156	0.052	939.6 non-synonym
5.084	1.352	0.092	0.25	338.05 non-synonym
3.568	1.362	-0.815	0.453	289.57 non-synonym
0	0.646	0.429	-1.164	122.67 non-synonym
0	0.582	-0.206	1.146	851.49 non-synonym
3.461	0.375	0.401	1.486	1080.92 non-synonym
2.245	0.439	-0.315	1.608	1053.84 non-synonym
7.424	0.863	0.683	0.518	686.3 non-synonym
0	0.693	0.654	-0.207	627.88 non-synonym
9.234	0.039	0.159	1.981	677.55 splice_acceptor
0	0.616	0.642	0.298	583.35 splice_donor
7.702	0.939	0.812	-0.015	1175.19 splice_donor
3.565	0.513	-0.437	-1.281	1090.86 splice_donor
11.235	0.439	1.169	-0.453	1343.04 splice_region
0	0.764	-1.701	-0.177	506.78 splice_region
9.627	2.697	-0.576	-0.384	697.83 splice_region
0	0.527	-0.869	-0.586	692.59 splice_region
1.808	1.14	-1.447	0.044	120.72 splice_region

2.077	1.256	-1.055	-0.553	109.39 splice_region
4.044	0.322	-0.173	-2.236	466.06 splice_region
1.333	1.079	-0.498	-0.317	309.58 splice_region
0	0.797	-1.359	1.184	583.84 splice_region
1.198	0.784	0.134	4.245	2193.78 splice_region
5.701	1.523	0.083	-0.514	307.75 splice_region
5.999	2.093	-0.35	-0.517	369.37 splice_region
0	0.742	-1.298	0.218	978.47 splice_region
0	0.859	-0.548	1.115	928.26 splice_region
4.075	0.819	0.033	1.088	337.02 splice_region
1.421	0.702	0.152	0.177	1541.08 splice_region
0	0.495	-1.107	-2.646	418.98 splice_region
8.141	1.739	0.133	-0.489	265.52 splice_region
0	0.892	-0.776	1.203	328.01 splice_region
2.392	1.527	0.69	-1.415	156.66 splice_region
4.506	0.16	0.428	-0.272	194.26 splice_region
4.506	0.16	-1.129	-0.195	194.26 splice_region
1.234	0.412	0.123	2.779	547.53 splice_region
1.447	0.856	-0.589	0.663	643.62 splice_region
0	0.929	0	0.689	544.81 splice_region
4.676	1.303	1.108	-1.247	1178.32 splice_region
3.901	0.314	-0.347	1.7	1117.19 splice_region
0	0.573	0.331	-0.463	393.7 splice_region
0	1.697	-	-	2469.54 splice_region
12.969	0.85	-0.009	1.649	926.09 splice_region
0.946	0.905	0.908	0.303	1396.02 splice_region
2.8	0.673	-0.106	1.438	1706.68 splice_region
0	0.593	-0.376	0.288	413.99 splice_region
0.946	0.905	1.397	0.522	1399.4 splice_region
0	0.495	-0.768	0.167	578.27 stop_gained
4.389	0.98	-1.011	0.38	1584.34 stop_gained
0	0.798	2.24	-0.53	1553.81 stop_gained
2.561	0.814	-0.423	0.674	791.17 stop_lost
0	0.818	-0.789	-1.006	531.55 stop_retaine
0	1.981	0.421	0.421	137.53 synonymous
0	0.941	-0.361	-1.159	179.52 synonymous
0	0.693	-0.922	-1.3	137.53 synonymous
0	1.034	0.684	-0.684	90.33 synonymous
1.856	0.83	-0.529	-1.153	130.94 synonymous
3.32	1.436	0.483	0.721	11480.81 synonymous
0	1.179	-0.945	1.347	13971.95 synonymous
0	0.213	-1.183	0.087	236.4 synonymous
3.398	0.184	0.244	-0.125	272.71 synonymous
3.26	0.2	-0.098	0.224	234.02 synonymous

0	0.462	-1.953	-0.141	231.32 synonymous
0	0.552	1.036	-0.184	231.32 synonymous
0	0.626	-0.943	-0.069	192.67 synonymous
0	0.532	-0.326	0.989	154.96 synonymous
0	1.629	0.431	-1.078	122.18 synonymous
4.22	2.724	-0.117	-1.301	27790.14 synonymous
4.024	2.582	-1.383	-0.625	28656.69 synonymous
0	1.482	-0.249	-1.637	32762.32 synonymous
0	1.389	-0.47	-0.479	32703.57 synonymous
8.051	1.076	-0.875	-0.321	23016.49 synonymous
14.498	1.188	0.327	-1.159	11077.02 synonymous
9.598	1.383	-1.066	-0.436	9952.02 synonymous
0	0.726	-0.319	0.605	121.71 synonymous
0	0.866	0.931	0.163	153.34 synonymous
0	0.327	1.281	1.393	21112.53 synonymous
0	0.956	0.35	-1.313	154.96 synonymous
3.622	0.739	-1.11	1.129	27558.09 synonymous
3.473	0.616	-0.033	1.487	32805.22 synonymous
3.144	0.383	0.923	0.259	35544.58 synonymous
0	0.291	0.475	-0.333	37389.58 synonymous
0	0.745	-0.62	-2.559	41821.51 synonymous
3.593	1.216	-0.053	-0.661	184.75 synonymous
0	0.46	0.175	-0.798	160.87 synonymous
0	0.474	-0.837	-0.72	20658.81 synonymous
12.378	2.343	0.813	0.9	19048.74 synonymous
3.904	0.808	-2.223	-1.199	22297.26 synonymous
14.298	0.031	-0.234	0.244	17815.45 synonymous
13.503	0.029	2.022	-0.038	17876.39 synonymous
13.444	0.033	0.858	-0.42	17324.51 synonymous
5.016	0.174	0.403	0.152	15055.64 synonymous
1.528	0.353	-0.265	2.09	16523.5 synonymous
0	0.599	0.706	1.531	17639.45 synonymous
8.869	0.101	-0.024	1.862	16927.5 synonymous
0	0.735	0.914	1.326	17140.45 synonymous
2.821	0.268	-0.526	-0.59	230.32 synonymous
12.932	2.837	-2.393	1.474	13425.6 synonymous
0	0.978	1.775	1.47	18347.57 synonymous
2.893	0.14	-1.261	0.299	269.39 synonymous
16.182	0.016	1.113	0.549	269.39 synonymous
0	1.337	0.113	-0.896	288.63 synonymous
0	0.473	0.57	2.336	24165.22 synonymous
60.061	4.183	0.438	-2.21	4487.76 synonymous
2.632	0.991	0.715	0.382	87.5 synonymous
7.371	2.584	1.245	-2.13	129.06 synonymous

1.172	0.645	0.328	1.283	612.3 synonymous
0	0.61	0.634	0.804	661.97 synonymous
0	0.646	-0.507	-1.837	473.86 synonymous
0	0.665	0.035	-1.575	226.11 synonymous
0	0.631	0.405	-0.925	228.21 synonymous
1.833	1.23	1.231	1.679	232.55 synonymous
0	0.921	-2.152	0.793	240.13 synonymous
0	1.022	-1.898	0.061	162.16 synonymous
8.038	2.262	0.949	0.784	166.4 synonymous
0	0.473	0.124	-2.021	281.37 synonymous
4.193	1.567	0.423	-2.608	234.55 synonymous
7.558	0.844	-0.866	-1.765	533.67 synonymous
10.494	0.079	-0.942	0.06	1518.43 synonymous
7.185	0.151	0.396	0.418	1518.43 synonymous
1.685	0.307	-1.259	-0.205	398 synonymous
1.55	1.025	-0.619	0.298	388.3 synonymous
3.312	1.22	-1.119	-0.559	388.3 synonymous
3.565	0.912	0.577	0.377	389.95 synonymous
1.441	1.022	0.627	-0.348	433.99 synonymous
2.835	1.244	-0.636	-0.192	584.66 synonymous
0	0.75	1.523	-0.119	583.35 synonymous
1.674	0.351	0.523	0.523	400.74 synonymous
4.5	2.219	-1.543	-0.091	209.21 synonymous
6.455	0.383	-0.354	1.169	305.63 synonymous
3.862	1.279	-0.755	-0.593	157.38 synonymous
1.657	0.313	-0.334	-0.026	357.57 synonymous
0	1.112	0.919	-0.071	113.21 synonymous
1.952	1.329	-1.264	-0.609	182.89 synonymous
0	0.859	0.185	0.74	382.85 synonymous
0	1.022	-1.532	1.031	168.28 synonymous
3.136	1.447	0.922	-0.922	114.52 synonymous
0	0.223	-	-	88.94 synonymous
3.133	0.323	-0.564	1.644	754.94 synonymous
0	0.514	0.348	1.859	708.45 synonymous
2.845	0.44	-1.1	0.145	1025 synonymous
3.587	1.296	-0.177	1.572	216.32 synonymous
2.569	0.706	-0.959	0.991	390.45 synonymous
9.608	0.95	0.012	1.663	805.11 synonymous
4.085	0.554	-0.308	1.34	481.87 synonymous
6.686	0.89	-0.963	0.85	517.85 synonymous
0	0.584	-0.383	-2.644	521 synonymous
3.886	0.29	-0.583	-1.28	927.57 synonymous
0	0.408	1.074	1.92	460.01 synonymous
0	0.767	2.103	2.111	379.83 synonymous

0	1.133	-0.394	2.661	293.61 synonymous
0	1.362	-0.262	1.263	335.65 synonymous
0	1.048	0.113	0.63	335.65 synonymous
0	1.092	-0.377	0.26	334.82 synonymous
2.208	1.454	1.086	3.533	505.12 synonymous
0	0.658	1.535	3.375	700.86 synonymous
1.264	1.017	0.891	-3.163	31318.53 synonymous
0	1.135	-0.212	-1.498	35324.68 synonymous
8.545	0.757	0.633	0.944	1105.27 synonymous
13.31	1.379	1.538	1.055	945.05 synonymous
1.624	0.43	0.426	-0.058	2402.84 synonymous
0	0.751	2.196	-0.41	619.08 synonymous
1.039	0.542	1.723	-0.42	1108.12 synonymous
1.079	0.532	1.957	-1.433	1346.54 synonymous
2.631	0.38	2.023	1.411	471.37 synonymous
0	0.576	2.789	-1.912	1477.01 synonymous
0	0.869	-1.183	-1.33	1326.4 synonymous
0	0.836	-	-	2539.58 synonymous
1.047	0.592	1.643	2.179	1064.75 synonymous
5.356	0.569	-0.976	0.605	1643.34 synonymous
0	0.846	-	-	2538.59 synonymous
6.956	0.889	-0.139	-0.917	565.96 synonymous
1.851	0.269	1.334	-0.445	629.2 synonymous
1.51	0.648	-1.334	-0.364	365.47 synonymous
2.917	0.346	-0.724	0.724	356.54 synonymous
1.392	1.136	-1.119	-0.081	912.21 synonymous
1.184	0.871	0.545	0.024	928.17 synonymous
3.035	0.877	-1.476	-0.284	1250.06 synonymous
5.501	0.855	0.057	0.142	705.93 synonymous
0	0.582	0.161	-0.032	275.03 synonymous
0	0.582	0.29	0.226	275.03 synonymous
0	0.693	0.444	0.239	272.38 synonymous
0	0.495	0.459	0.888	272.38 synonymous
3.821	0.223	-0.297	-3.066	495.69 synonymous
7.371	0.078	-1.245	-1.466	660.05 synonymous
10.371	1.806	-0.537	0.358	510.62 synonymous
2.262	0.223	-0.298	-1.575	606.82 synonymous
7.06	0.674	-0.887	-0.68	444.74 synonymous
7.346	0.651	-0.036	-1.256	440.92 synonymous
1.74	1.179	0.501	1.774	281.74 synonymous
1.74	0.991	0.176	0.106	267.06 synonymous
0	1.402	-	-	13414.8 synonymous
0	1.981	-	-	195.06 synonymous
0	2.833	-	-	159.56 synonymous

0	0.804	-0.395	0.219	104.76 synonymous
1.447	0.46	-0.112	0.292	611.28 synonymous
1.402	1.022	0.774	-0.734	543.72 synonymous
3.862	0.796	-0.485	-0.755	542.75 synonymous
1.302	0.741	1.207	-0.76	870.76 synonymous
2.66	0.807	1.079	1.838	342.06 synonymous
1.498	0.349	1.099	-2.164	714.33 synonymous
0	0.765	-0.492	1.102	159.98 synonymous
0	0.802	-0.811	1.55	1041.66 synonymous
3.118	0.378	-1.648	1.648	1609.64 synonymous
1.09	0.998	1.245	0.714	1007.76 synonymous
1.07	0.599	0.879	-0.751	863.81 synonymous
4.389	0.98	1.031	-0.11	1623.1 synonymous
2.623	1.03	-1.373	0.595	846.46 synonymous
4.363	1.08	-0.426	0.377	893.25 synonymous
7.938	1.335	1.3	1.176	810.43 synonymous
4.358	1.367	0.08	2.341	753.71 synonymous
2.274	0.661	1.125	-0.994	1021.17 synonymous
7.858	0.189	-1.332	-0.148	872.55 synonymous
2.169	0.446	-0.832	-0.752	940.49 synonymous
0	0.746	-0.86	-1.581	920.12 synonymous
0	0.667	0.841	-0.572	873.65 synonymous
1.083	0.473	-1.096	0.191	1433.17 synonymous
3.816	1.739	0.678	-0.778	663.15 synonymous
3.581	1.739	0.554	0.288	696.96 synonymous
10.84	1.766	-0.776	1.984	725.06 synonymous
11.612	1.355	-0.255	2.466	765.3 synonymous
16.444	0.953	0.251	-0.192	980.65 synonymous
7.08	0.85	0.651	-2.396	1140.64 synonymous
4.084	0.794	0.943	1.671	823.63 synonymous
2.133	0.597	-0.358	-0.964	1003.74 synonymous
4.201	0.821	0.531	1.658	1030.12 synonymous
0	0.602	-0.113	1.549	1153.97 synonymous
0	0.716	1.432	-1.451	1036.26 synonymous
5.73	0.554	-0.588	-1.644	1275.41 synonymous
0	0.602	0.057	-0.965	508.69 synonymous
0	0.855	-1.414	0.854	826.7 synonymous
0	0.689	1.29	-1.017	1196.55 synonymous
2.137	0.467	0.181	-0.384	1147.89 synonymous
1.399	1.127	0.776	-0.215	649.76 synonymous
2.808	1.981	-1.159	1.159	170.47 upstream_ge
3.332	1.901	0.322	-0.937	170.47 upstream_ge
0	0.693 -	-		70.47 upstream_ge
0	0.693 -	-		70.47 upstream_ge

4.955	0.3	-1.768	-1.131	2002.43 upstream_ge
4.282	0.231	-0.818	0.159	9131.93 upstream_ge
0	4.018 -	-		11674.68 upstream_ge
2.02	1.59	0.894	2.631	15516.77 upstream_ge
0	0.864 -	-		23513.58 upstream_ge
1.579	1.096	0.363	0.067	28852.53 upstream_ge
18.253	0.203	0.405	4.274	7491.59 upstream_ge
12.554	1.522	0.573	0.587	17697.34 upstream_ge
18.806	1.417	-0.018	0.197	6927.5 upstream_ge
3.794	0.383	0.638	-2.355	6517.56 upstream_ge
2.339	0.475	-0.548	-0.847	3863.79 upstream_ge
0	0.952	0.617	1.253	4786.58 upstream_ge
0	1.951 -	-		5526.58 upstream_ge
0	0.69	0.163	1.229	3036.21 upstream_ge
0	2.2	-0.441	-0.441	294.11 upstream_ge
0	1.27 -	-		822.93 upstream_ge
5.035	0.383	-0.394	0	511.9 upstream_ge
4.708	0.148	1.107	0.58	511.9 upstream_ge
0	0.941	-0.146	-1.415	241.13 upstream_ge
0	1.112	1.055	-0.854	263.74 upstream_ge
0	0.693	0.421	-0.515	182.9 upstream_ge
2.808	0.959	-0.573	1.683	91.33 upstream_ge
2.808	0.959	-0.248	1.001	91.33 upstream_ge
3.233	2.419	0.546	0.546	86.86 upstream_ge
7.068	0.61	-1.221	-0.956	131.72 upstream_ge
0	0.593	3.409	1.076	60.06 upstream_ge
0	0.693	-2.477	-1.1	5845.42 upstream_ge
0	0.614	3.408	0.426	69.11 upstream_ge
4.612	2.147	0.253	-1.05	501.71 upstream_ge
5.715	2.67	0.047	-2.201	510.77 upstream_ge
6.41	2.833	0.648	-2.534	177.6 upstream_ge
8.451	2.788	-0.55	0.55	84.94 upstream_ge
7.068	2.807	-0.956	0.322	130.14 upstream_ge
2.632	1.535	-1.034	0.278	130.14 upstream_ge
0	1.27	-0.278	0.597	130.14 upstream_ge
0	0.495	-1.159	1.448	460.87 upstream_ge
6.421	2.91	-0.386	0.54	115.16 upstream_ge
0	1.329	-0.365	-1.133	271.24 upstream_ge
2.757	0.132	-0.54	0	156.72 upstream_ge
6.99	0.486	1.386	0.296	350.52 upstream_ge
4.832	0.707	-0.061	-0.8	163.48 upstream_ge
4.832	0.707	0.306	-0.8	154.43 upstream_ge
2.276	1.17	-1.226	0.452	199.48 upstream_ge
2.276	1.229	-0.312	0.377	197.53 upstream_ge

6.154	1.872	-0.244	-0.38	144.74 upstream_ge
2.463	1.144	0.583	0.259	214.83 upstream_ge
2.463	1.144	-0.583	0	214.83 upstream_ge
6.154	1.872	1.309	0.135	153.78 upstream_ge
2.463	1.144	0.259	-0.467	214.83 upstream_ge
3.01	0.16	-0.573	1.422	192.33 upstream_ge
0	0.85	1.951	0.676	163.14 upstream_ge
1.415	1.022	-0.36	0.36	354.85 upstream_ge

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ABCC1		1 p1	(T)10		10	1887 1896
ABCC1		2 p1	(C)10		10	2326 2335
ABCC1		3 p1	(T)10		10	9597 9606
ACC1		1 p1	(T)11		11	4208 4218
ACC1		2 p2	(CT)8		16	5125 5140
AIM1		1 p2	(TA)6		12	3049 3060
CYN		1 p3	(ACG)5		15	545 559
CYN		2 p1	(A)10		10	1314 1323
CYP71E1		1 p1	(T)10		10	1963 1972
DTX1		1 p1	(T)10		10	1454 1463
DTX1		2 p1	(A)11		11	3564 3574
DTX1		3 p1	(A)12		12	3860 3871
EPSPS		1 p1	(T)12		12	2531 2542
EPSPS		2 p1	(A)12		12	4109 4120
GDSL		1 p3	(CGG)5		15	548 562
GPOX		1 p2	(CG)8		16	736 751
GPOX		2 p2	(AT)6		12	1129 1140
GSL1-1		1 p1	(T)10		10	2260 2269
GSTF1		1 p1	(A)10		10	42 51
GSTF1		2 p1	(T)10		10	1037 1046
IN2		1 p1	(A)10		10	2130 2139
LACS7		1 p1	(A)11		11	690 700
LACS7		2 p1	(A)11		11	910 920
LACS7		3 p1	(A)16		16	1822 1837
LACS7		4 c	(T)10gctcatcc		47	3570 3616
LACS7		5 p1	(T)10		10	8995 9004
LACS8		1 p3	(TAC)5		15	661 675
LACS8		2 p1	(T)10		10	2451 2460
LACS8		3 p1	(T)10		10	2574 2583
MAT1		1 p1	(T)10		10	1553 1562
MATE		1 p1	(T)10		10	4819 4828
OEP64		1 p1	(T)11		11	1733 1743
OEP64		2 c	(T)10ggtgtgtg		51	2527 2577
PDS1		1 p2	(TC)6		12	225 236
PDS1		2 p1	(T)11		11	5239 5249
PPO		1 c	(T)10(A)11		21	6537 6557
TIR1		1 p3	(CGC)5		15	120 134