Supplementary Appendix

Supplement to: Duncavage EJ, Jacoby MA, Chang GS, et al. Mutation clearance after transplantation for myelodysplastic syndrome. N Engl J Med 2018;379:1028-41. DOI: 10.1056/NEJMoa1804714

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Supplementary Methods

A. Study Design

All consecutive patients with adequate samples that underwent allogeneic hematopoietic cell transplant (alloHCT), from any source, at Washington University from 11/2002-05/2015 were included in the study. Adequate sample was defined as having sufficient DNA available from the bone marrow and skin pre-alloHCT, and bone marrow on at least day 30 after transplant for sequencing studies. In 58 patients, an additional bone marrow biopsy was performed within a median of 23 days prior to transplant (range, 6-61), with no intervening treatment between biopsy and transplant, and could be used to measure tumor burden at the time of transplant (i.e., pre-transplant sample). In addition, the initial banking sample for 9 patients also met the definition of the pre-transplant time-point (i.e., biopsy was performed within 60 days prior to transplant and had no intervening treatment) and were annotated in Supplementary Table S2. A bone marrow sample was available for 58 patients on day 100 post-alloHCT. The study was approved by the institutional review board at Washington University in St. Louis and was conducted in accordance with the provisions of the Declaration of Helsinki. All of the patients who were enrolled provided written informed consent that explicitly included genome sequencing and data sharing with qualified investigators.

Disease progression was defined prior to sequencing as follows: the presence of ≥5% myeloblasts in the marrow or evidence of extramedullary disease; loss of donor chimerism or re-emergence of pre-transplant morphologic abnormalities prompting any intervention by the treating physician (such as withdrawal of immunosuppression, donor lymphocyte infusion, or chemotherapy); or re-emergence of pre-transplant cytogenetic abnormalities. The reviewers were blinded to the results of the sequencing studies. Database lock was 4/16/2017. For progression-free survival, in the absence of progression, and for overall survival, patients were censored at the time they were last known to be alive. Morphologic review for all time points was provided by a board certified hematopathologist. In most cases the blast count was determined by morphological assessment of the Wright Giemsa stained bone marrow aspirate smears, however in cases where the aspirate was hemodilute or of low technical quality, the blast count was estimated by CD34 and/or CD117 immunohistochemically staining of the bone marrow core depending on the blast phenotype detected by flow cytometry.

Eight patients who had previously undergone ultra-sensitive, error-corrected sequencing prior to transplant and at day 30 post-alloHCT on a previous study were included in the outcome analyses.[1] Their UPNs were as follows: 145094, 147457, 280837, 368402, 435866, 499258, 624702, and 829970.

B. Enhanced Exome Sequencing and Somatic Variant Identification at Initial Banking

We sequenced the exome of 90 patients with a history of MDS, described above, at initial banking. HiSeq2500 sequencing systems (Illumina, CA) were used to sequence DNA, captured using SeqCap EZ Exome v3.0 Kit (Roche, CA) with additional spike-in probes targeted to 285 genes recurrently mutated (or RMGs) in myeloid malignancies, or enhanced exome sequencing (EES).[2] Exome sequencing data were aligned to the human reference sequence build GRCh37-lite-build37 using bwa[3] version 0.5.9 with "-t 4 -q 5" parameters, then merged and de-duplicated using picard version 1.46 (https://broadinstitute.github.io/picard/).

Somatic variants in tumor samples were called against normal skin samples we sequenced in EES from the same patient. In detail, single nucleotide variation (SNV) was detected using the union of four variant callers: 1) samtools[4] version r982 (params: mpileup -BuDS) filtered by var-filter-snv v1 and false-positive-vcf v1 (params: --max-mm-qualsum-diff 100 --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15), then intersected with Somatic Sniper version 1.0.4[5] (params: -F vcf -G -L -q 1 -Q 15) and processed through false-positive filter v1 (params: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15 --min-mapping-quality 40 --min-somatic-score 40), 2) VarScan[6] version 2.3.6 (params: --nobaq --version r982) filtered by varscan-high-confidence filter v1 and processed through false-positive filter v1 (params: --bam-readcount-version 0.4 --bam-readcount-min-base-quality 15), 3) Strelka[7] version 1.0.11 (params: isSkipDepthFilters = 1), and 4) MuTect version 1.1.4 (--number-of-chunks

50) with COSMIC v54.[8]

For insertions and deletions (INDELs), we used the union of four variant callers: 1) GATK[9] somatic-indel version 5336, 2) pindel[10] version 0.5 filtered with pindel-somatic-calls v1 and VAF filters v1 (params: --variant-freq-cutoff=0.08), and with pindel-read-support filter v1, 3) VarScan[6] version 2.3.6 (params: --nobaq --version r982) filtered by varscan-high-confidence-indel v1 and 4) Strelka[7] version 1.0.11 (params: isSkipDepthFilters = 1).

SNVs and INDELs were further filtered by removing artifacts found in a panel of 905 normal exomes, removing sites that exceeded 1% frequency in the Exome Aggregation Consortium (ExAC) collection,[11] and then using a Bayesian classifier (https://github.com/genome/genome/blob/master/lib/perl/Genome/Model/Tools/Validation/IdentifyOutliers.pm) and retaining variants classified as somatic with a binomial log-likelihood of at least 3 (params: --llr-cutoff 3). As a result, germline mutations, low-quality mutations, sequencing artifacts, and ambiguous variant calls owing to paralogous DNA sequences and unstable reference sequence contigs were removed.

A total 3,811 somatic variants were called from 90 patients at initial banking in the somatic variation discovery pipeline, described above, including 3,414 SNVs, 257 DELs, and 140 INSs. An average of 42 variant were called per patient (minimum 3 to maximum 644 variants called). Exome sequencing data was deposited in the dbGAP database (phs000159.v9).

C. Ultra-deep error-corrected sequencing

Probes for ultra-deep error-corrected sequencing were designed to target all somatic mutations detected by enhanced exome sequencing (or EES) using the Agilent SureDesign web interface. Genomic DNA was first digested using a mixture of restriction endonucleases found in the Agilent HaloplexHS kit (Agilent Technologies, Santa Clara, CA). Probes (designed to cover both DNA strands), 10bp degenerate barcodes, and sample-specific indexes were synthesized by Agilent Technologies. Following a 16 hour hybridization and magnetic bead enrichment, libraries were amplified for 23 PCR cycles using primers with tailed Illumina sequencing motifs.

Purified libraries were then pooled and sequenced 16 per lane (inital samples and skin) or 8 per lane (Pre, Day 30, and D100) time points on a HiSeq 4000 instrument. Pools were designed to minimize the effect of potential ‘index swapping’ by including only unique UPNs in each lane; samples from initial time points (high expected VAFs) were excluded from pools with day 30 and day 100 follow-up samples (low expected VAFs). Further, follow-up samples were pooled to avoid including samples in the same pool with the same recurrent somatic mutations when possible (e.g., only one sample with *U2AF1* S34F per pool). Samples were sequenced on an Illumina HiSeq 4000 instrument using 2x150bp reads (Illumina, Carlsbad CA).

Barcoded FASTQ data was demultiplexed using a custom UMI-aware script that merges degenerate barcode information to FASTQ files. Data was then aligned to build GRCh37-lite-build37 using bwa mem (version 7.9.a) with default parameters. Aligned BAMs were then analyzed using the Barcrawler pipeline (Duncavage and Abel, https://github.com/abelhj/gatk), a GATK locus walker implemented in Java, with the following parameters *-mmq 20 -mbq 20 -minCtBC 3 -dcov 1000000 -discardN 1 -minOffset 3 -maxNM 10*. The resulting list of variants were filtered to include only mutations present in at least 3 unique read families (each with a minimum of 3 members in which the variant was present in >90% of member reads). A background error-rate was further calculated for every targeted position by compiling the number of non-reference bases detected at that position across all cases minus the one with the mutation. For example in UPN 491309, a *TP53* p.Y243C mutation (chr17: 7577580 T->C) was detected with a VAF of 0.54% (80 variant read families out of 14,682 total). The remaining sequenced cases (all cases minus the index case) were then queried at that position and demonstrated the reference base, T, in 3,234,744 unique read families and the variant, C, in 9 total read families. A binomial distribution was then used to determine whether read counts of the observed mutation in the index case were statistically different from background. In the example, 80 out of 14,682 are statistically different from the background rate of the same mutations across all other cases (9 out of 3,234,744) with a P-value of <0.0001. P-value threshold of <0.0001 was used for all binomial comparisons. Detected mutations with a P-value >0.0001 compared to the background error were excluded from the analysis. Probes were considered validated if the SNV detected by EES was present in a marrow prior to transplant with a VAF of ≥1% and had a VAF of ≤10% in the normal skin sample and had ≥10x unique coverage at either the day 30 or day 100 time points. A total of 2,517 SNVs out of 3,414 targeted SNVs passed filter. The majority of positions that failed to validate were due to poor coverage at skin and prior to transplant time points or SNPs that were originally classified as 'somatic' variants based on lower coverage EES data. Indel calls detected by EES were not evaluated by error-corrected sequencing.

There was a wide range in unique coverage obtained across targeted positions in day 30 and day 100 samples, likely due to differences in GC content and the number of probes that could be designed to each targeted region. Therefore, a conservative VAF threshold was chosen to minimize potential variant detection bias due to differences in coverage. A maximum VAF cut-off of 0.5% resulted in >99% of day 30 and day 100 samples having a unique coverage depth that would allow detection of mutations with a VAF of ≥0.5%. A single case (day 30, 717045) had lower unique coverage due to limited available DNA. To determine whether the choice of a 0.5% maximum VAF cut-off biased the results, we compared multiple VAF cut off thresholds (2.5%, 1%, 0.1%, and no cut-off [i.e., any detected mutation]) and found that day 30 sequencing results remained a strong predictor of progression (Supplemental Figures S5-S8).

Supplementary Results

A. Treatment with a hypomethylating agent prior to alloHCT is not associated with progression

We previously reported that pre-transplant therapy with azacitidine likely influenced the mutation spectrum (e.g., C to G transversions) and evolution of emergent subclones after alloHCT.[1] This remains a potential mechanism that may affect post-alloHCT progression. We were not able to address whether putative hypomethylating agent-induced mutations influence progression in the current study because our sequencing strategy was not designed to identify emerging subclones. However, we did examine whether there was an association with therapy prior to transplant and progression in our cohort. When comparing patients who received a hypomethylating agent (e.g., azacitidine or decitabine) at any point pre-transplant versus no therapy, the hazard ratio for progression was 0.73 (95% confidence interval 0.41, 1.30; P=0.28). When compared to patients who received a hypomethylating agent at any point pre-transplant versus a therapy not containing a hypomethylating agent, the hazard ratio for progression was 0.94 (95% confidence interval 0.368, 2.40; P=0.90). While this analysis is limited by the use of non-uniform treatments, doses, and schedules, we did not observe an association with progression whether a patient received therapy prior to transplant, and if that therapy included a hypomethylating agent.

B. Post-alloHCT mutation VAF level is associated with progression

We performed an analysis using max VAF at day 30 post-alloHCT as a continuous variable (i.e., without thresholds) and it remained significantly associated with progression. For each increase of 1% in max VAF at day 30 post-alloHCT, the hazard of progression increases by about 4% (HR=1.04; 95% confidence interval, 1.02 to 1.05; P<0.001).

We also compared the cumulative incidence of progression for patients with a max VAF ≥ 0.5% versus max VAF > 0 but < 0.5%. We found that 18 patients had day 30 VAFs < 0.5% but > 0%. Six of these 18 patients progressed with a median of 195 days between detection of a day 30 post-alloHCT mutation and progression. The hazard of progression is about 2.5 times greater in patients with day 30 max VAF ≥ 0.5% versus those with detectable but lower max VAF (> 0 and < 0.5%) with a 95% confidence interval of 1.02 to 6.07 (P=0.046).

Supplementary Figure 1. Number and Distribution of Tracked Mutations at the Initial and Pre-transplant Time Points. Panel A shows the distribution of the total number of single nucleotide variant (SNV) mutations validated by error-corrected sequencing at initial sampling for patients with (n=34) or without (n=51) progression or death at one year. Panel B shows the distribution of the total number of SNV mutations validated by error-corrected sequencing at pre-transplant for patients with (n=32) or without (n=35) progression or death at one year. Panel C shows the distribution of mutation VAFs at initial sampling. Panel D shows the distribution of mutation VAFs measured pre-transplant. In Panels A-D, UPN 147457, which had 482 mutations, was omitted for clarity. Nine patients were included in both the initial sampling and pre-transplant data because they had an initial banking sample that also met the definition of the pre-transplant time-point defined in the Supplementary Appendix. They are annotated in Supplementary Table S2.

Supplementary Figure 2. Sequencing Metrics. Panels A and B show box and whiskers plot of coverage depths of non-overlapping 228,531 regions of interest targeted in enhanced exome sequencing. The line represents the median coverage depth; boxes represent upper and lower quartiles; lines represent minimum and maximum coverage values. Bone marrow samples (Panel A) and skin (Panel B, normal DNA source) are denoted by their unique patient number (UPN). Mean tumor coverage of 239x in the exomes and 1,299x over recurrently mutated genes (or RMG) in myeloid malignancies. Panel C and D show sequencing coverage depths obtained for ultra-deep error-corrected sequencing of the skin (Panel C) and bone marrow at initial sampling (Panel D). The total mean tumor coverage was 19,450x and the unique barcode coverage passing filter was 2,450x. Panels E and F show sequencing coverage depths obtained for ultra-deep error corrected sequencing at day 30 (Panel E) and bone marrow and day 100 post-allogeneic hematopoietic cell transplant (Panel F). At day 30 the total mean tumor coverage was 60,930x and the unique barcode coverage passing filter was 2,559x. At day 100 the total mean tumor coverage was 36,705x and the unique barcode coverage passing filter was 3,475x. Panel G shows sequencing coverage depths obtained for ultra-deep error-corrected sequencing for the 58 patients with pre-allogeneic hematopoietic cell transplant samples. The total mean tumor coverage was 13,926x and the unique barcode coverage passing filter was 1,569x.

Supplementary Figure 3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant.

VAF mutation clearances for recurrently mutated genes. 11 genes are shown, which were identified as mutated 4 or more times in this study including *ASXL1*, *DNMT3A*, *IDH2*, *NRAS*, *PTPN11*, *RUNX1*, *SF3B1*, *SRSF2*, *TET2*, *TP53*, and *U2AF1* (A-K). Shown are initial marrow mutation VAFs and day 30 VAFs of each gene and labeled by UPN and progression and overall day 30 maximum mutation VAF status. Plots on the right highlight mutations with VAFs < 5% at day 30 post-transplant, labeled by the same symbol and color of the patient.

Supplementary Figure 5. Association of Mutation Clearance at Day 30 post-alloHCT with Outcomes. Variant allele frequencies (VAFs) day 30 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one VAF ≥0.5% (red lines) or all VAFs <0.5% (blue lines). Risk of progression is shown in Panel A, progression free survival is shown in Panel B. Panels C and D show overall survival based on the presence of at least one VAF ≥0.5% (Panel C) and according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line) in Panel D.

Supplementary Figure 5. Association of Mutation Clearance at Day 100 Post-alloHCT with Outcomes. Variant allele frequencies (VAFs) day 100 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one VAF ≥0.5% (red lines) or all VAFs <0.5% (blue lines). Panels B, D, and F show outcomes according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line). Risk of progression (Panels A and B), progression-free survival (Panels C and D), and overall survival (Panels E and F) are shown.

Supplementary Figure 6. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 0.1%. Variant allele frequencies (VAFs) day 30 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one VAF ≥0.1% (red lines) or all VAFs <0.1% (blue lines). Panels B, D, and F show outcomes according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line). Risk of progression (Panels A and B), progression-free survival (Panels C and D), and overall survival (Panels E and F) are shown.

Supplementary Figure 7. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 1%. Variant allele frequencies (VAFs) day 30 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one VAF ≥1% (red lines) or all VAFs <1% (blue lines). Panels B, D, and F show outcomes according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line). Risk of progression (Panels A and B), progression-free survival (Panels C and D), and overall survival (Panels E and F) are shown.

Supplementary Figure 8. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 2.5%. Variant allele frequencies (VAFs) day 30 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one VAF ≥2.5% (red lines) or all VAFs <2.5% (blue lines). Panels B, D, and F show outcomes according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line). Risk of progression (Panels A and B), progression-free survival (Panels C and D), and overall survival (Panels E and F) are shown.

Supplementary Figure 9. Association of Mutation Clearance with Outcomes Using any Detectable Variant Allele Frequency. Variant allele frequencies (VAFs) day 30 post-transplant were determined using error-corrected sequencing interrogating single nucleotide variant (SNV) mutations identified by enhanced exome sequencing of samples prior to transplant. Patients are grouped by the presence of at least one detectable VAF >0% (red lines) or all VAFs =0% (blue lines). Panels B, D, and F show outcomes according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line). Risk of progression (Panels A and B), progression-free survival (Panels C and D), and overall survival (Panels E and F) are shown.

Supplementary Figure 10. Association of Mutation Clearance Determined by a 40 Gene-Panel. Only the variant allele frequencies (VAFs) of 40 genes recurrently mutated in myeloid malignancies were used to assess mutation clearance at day 30 post-transplant. VAFs were determined using error-corrected sequencing interrogating single nucleotide variants identified by enhanced exome sequencing of samples prior to transplant. Panel A shows the cumulative incidence of progression in patients grouped by the presence of at least one VAF ≥0.5% (red lines) or all VAFs <0.5% (blue lines). Panel B show progression-free survival. Panels C and D show overall survival grouped by VAF (Panel C) and according to whether the patient received reduced-intensity conditioning (RIC, solid lines) or myeloablative conditioning (MAC, dashed line) in Panel D.

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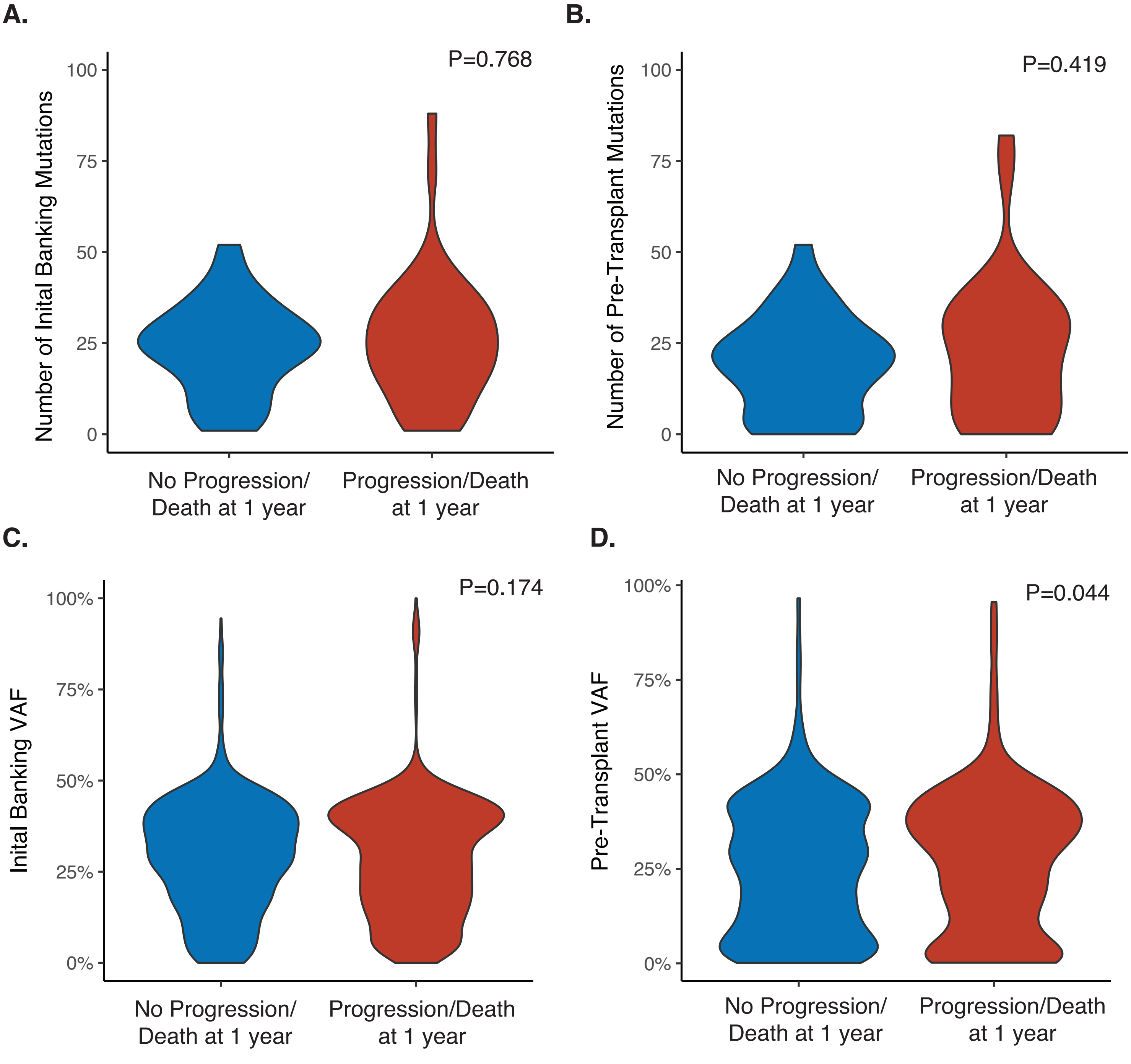
Figure S1. Number and Distribution of Tracked Mutations at the Initial and Pre-transplant Time Points



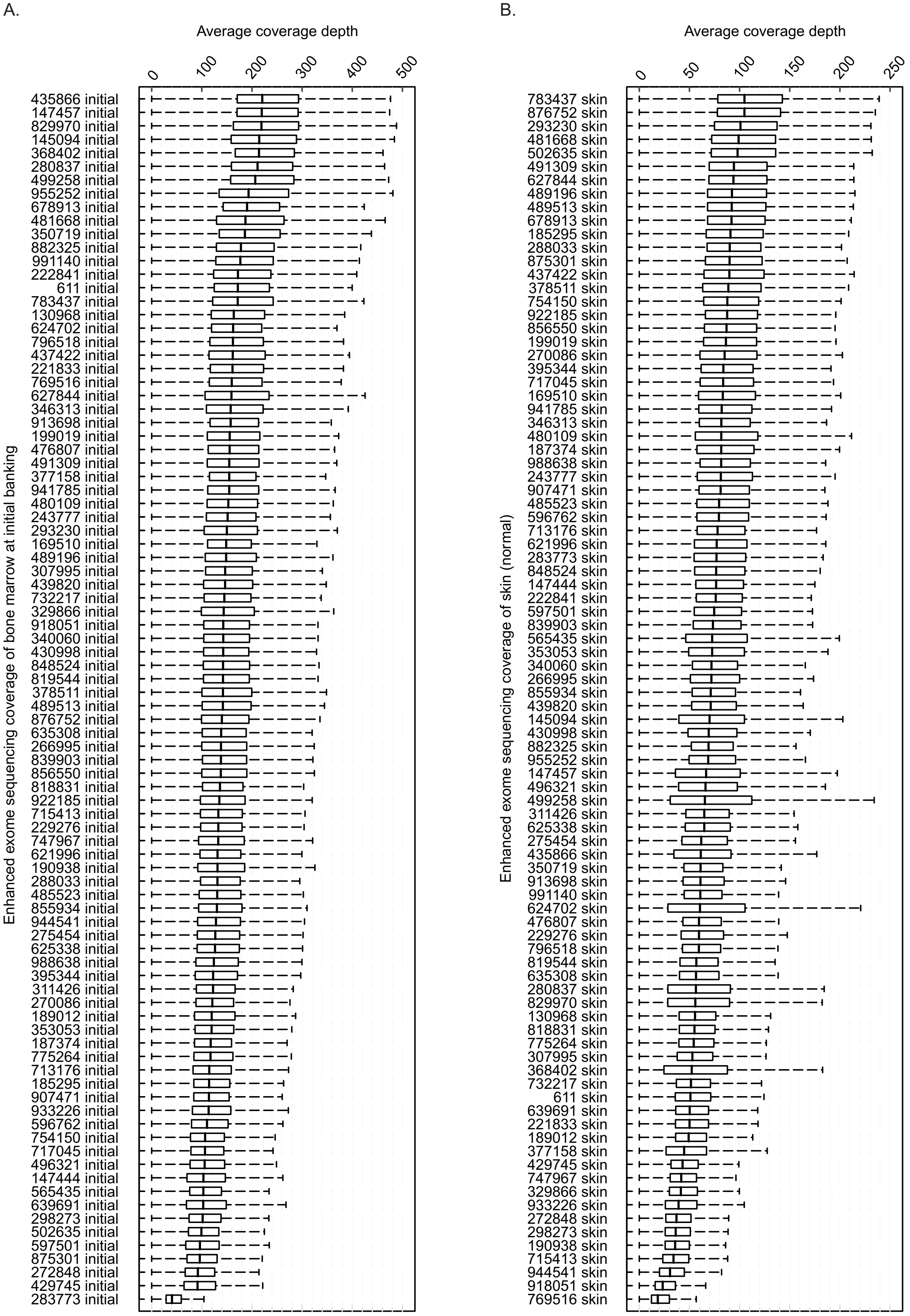


Figure S2. Sequencing Metrics

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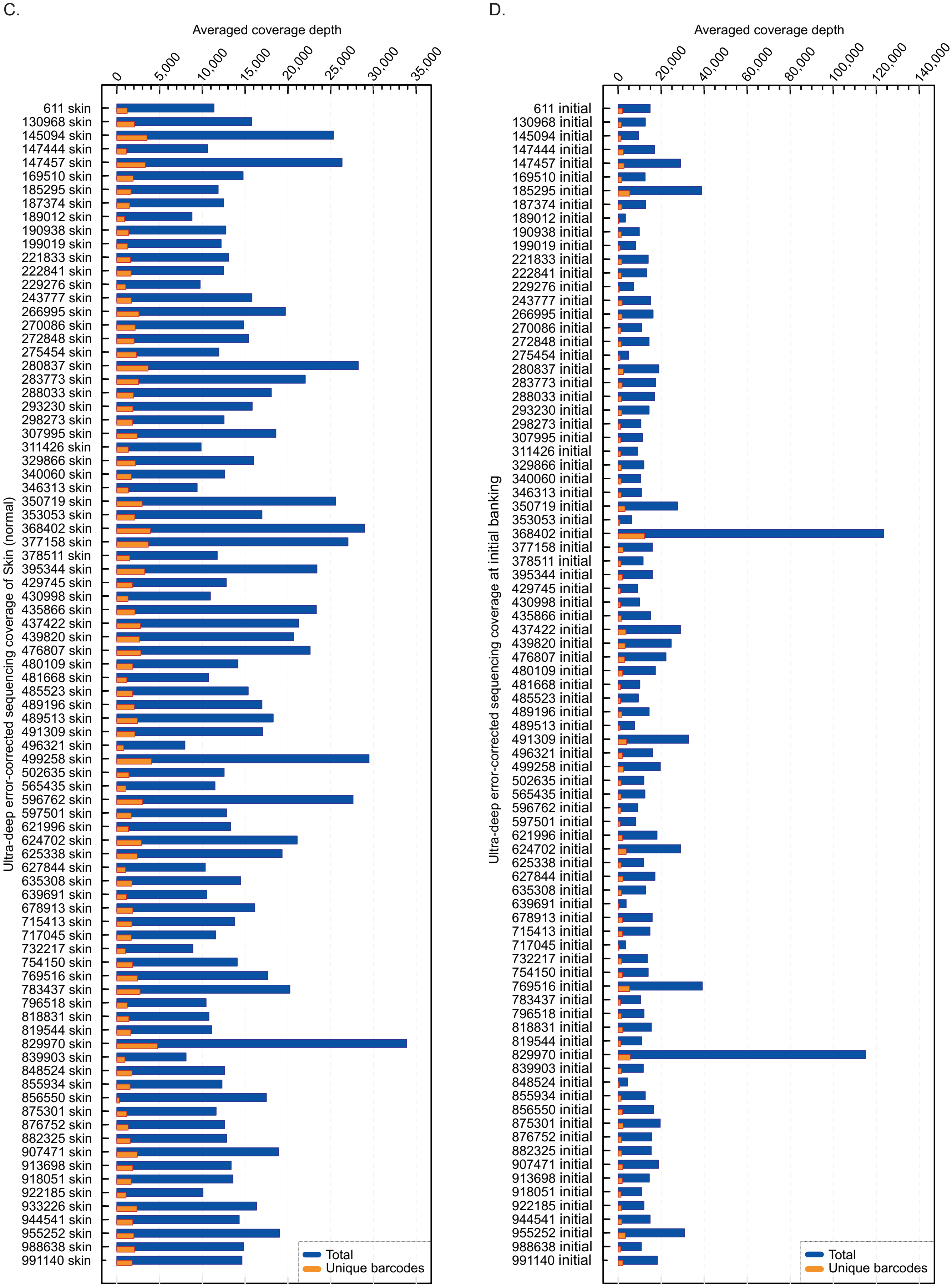

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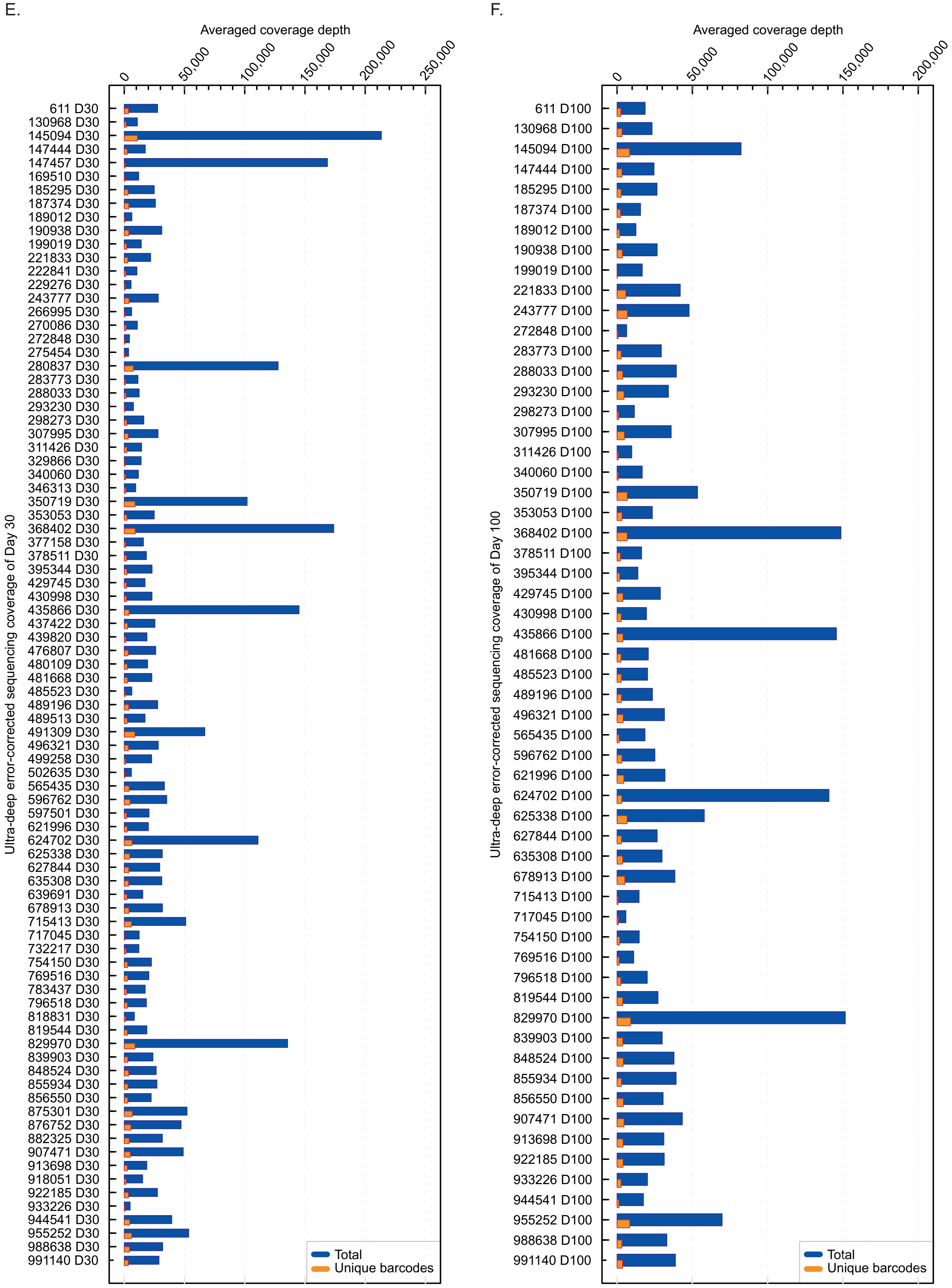

Figure S2. Sequencing Metrics

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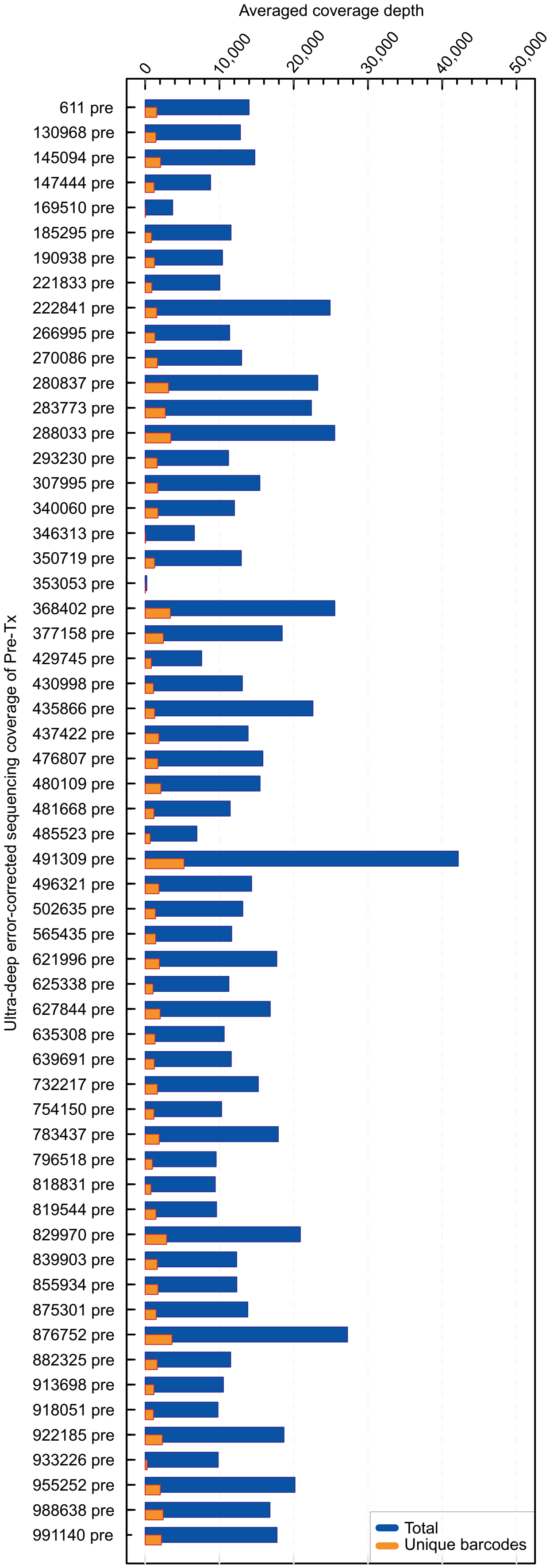
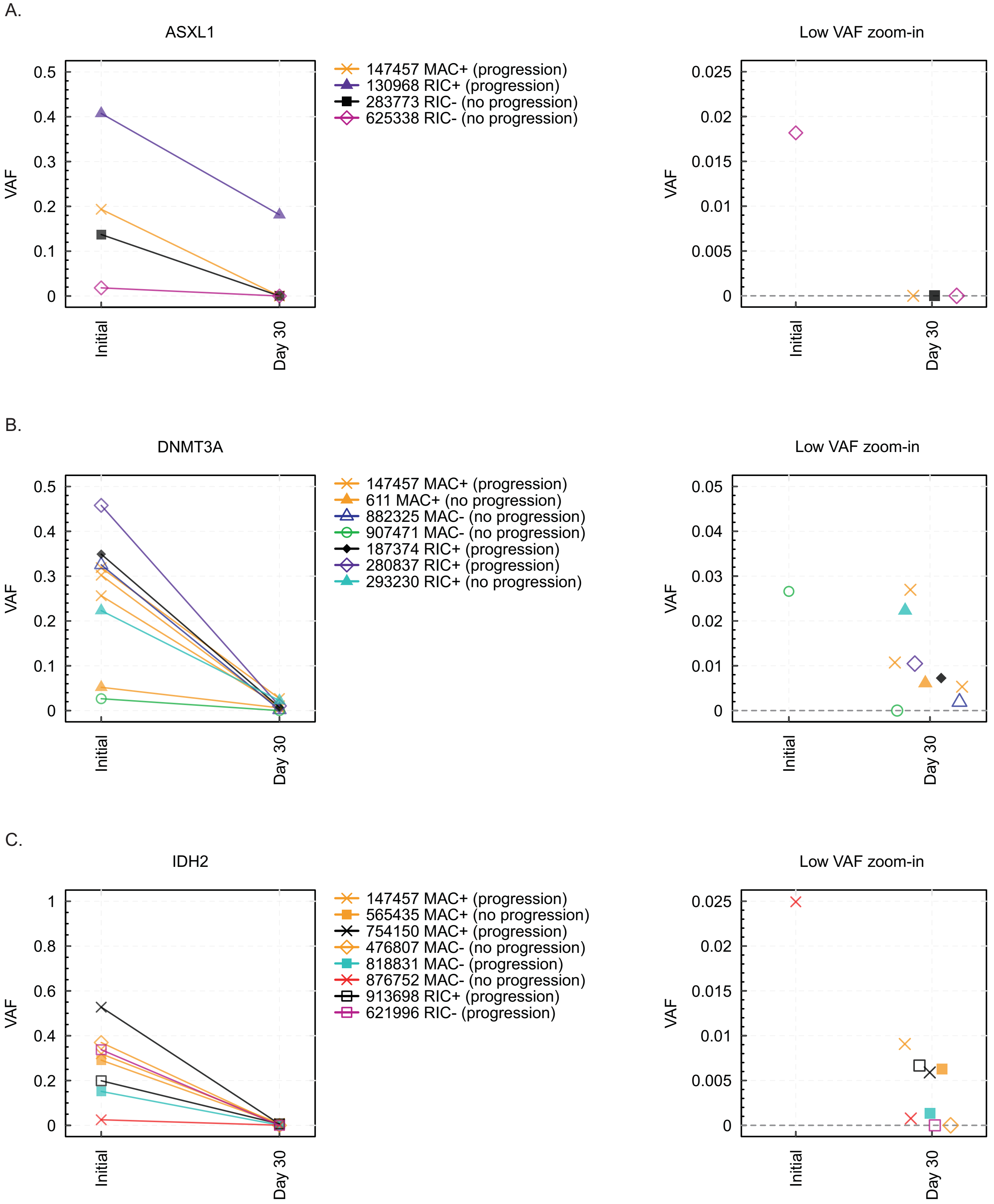


Figure S3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant



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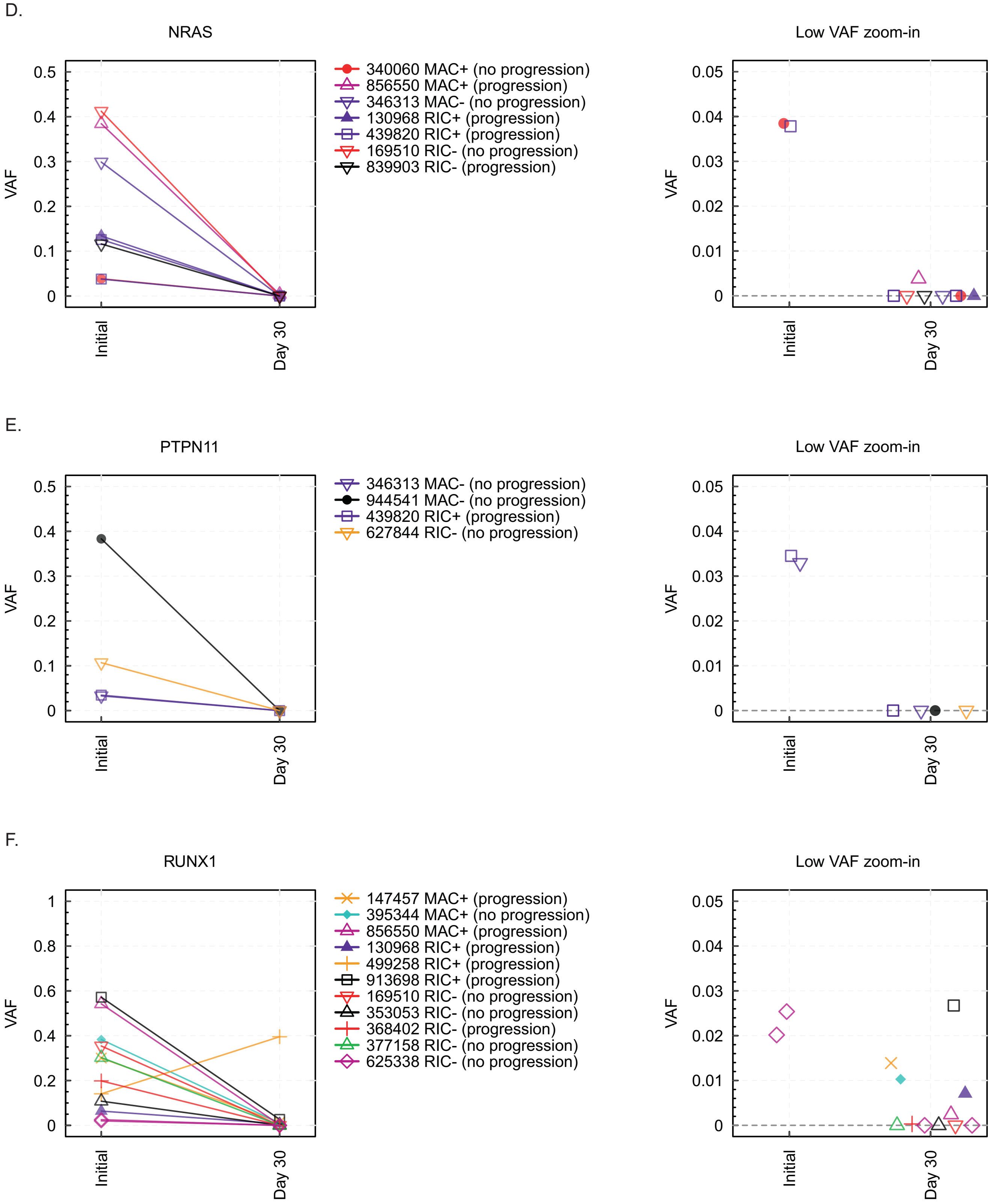

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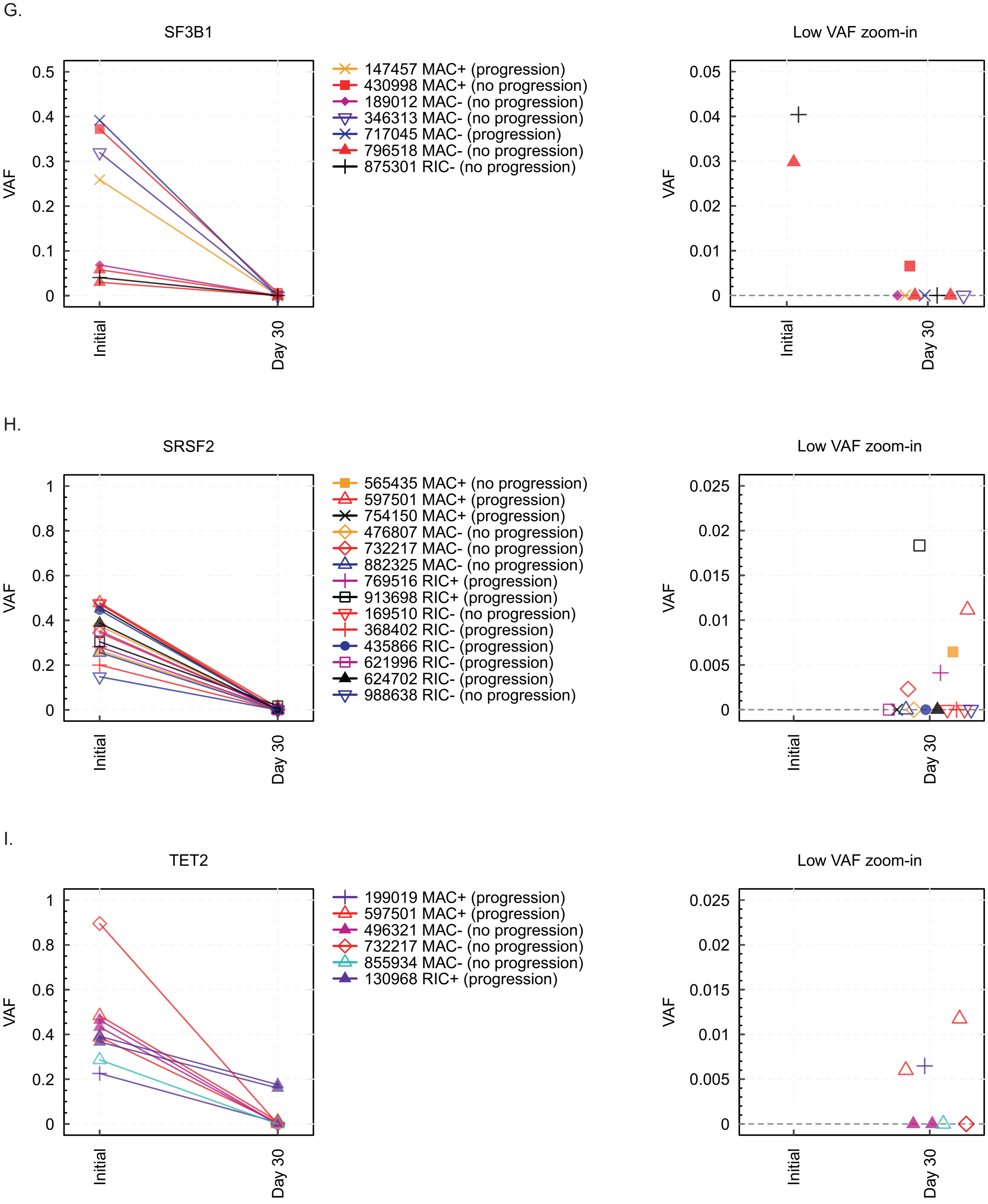

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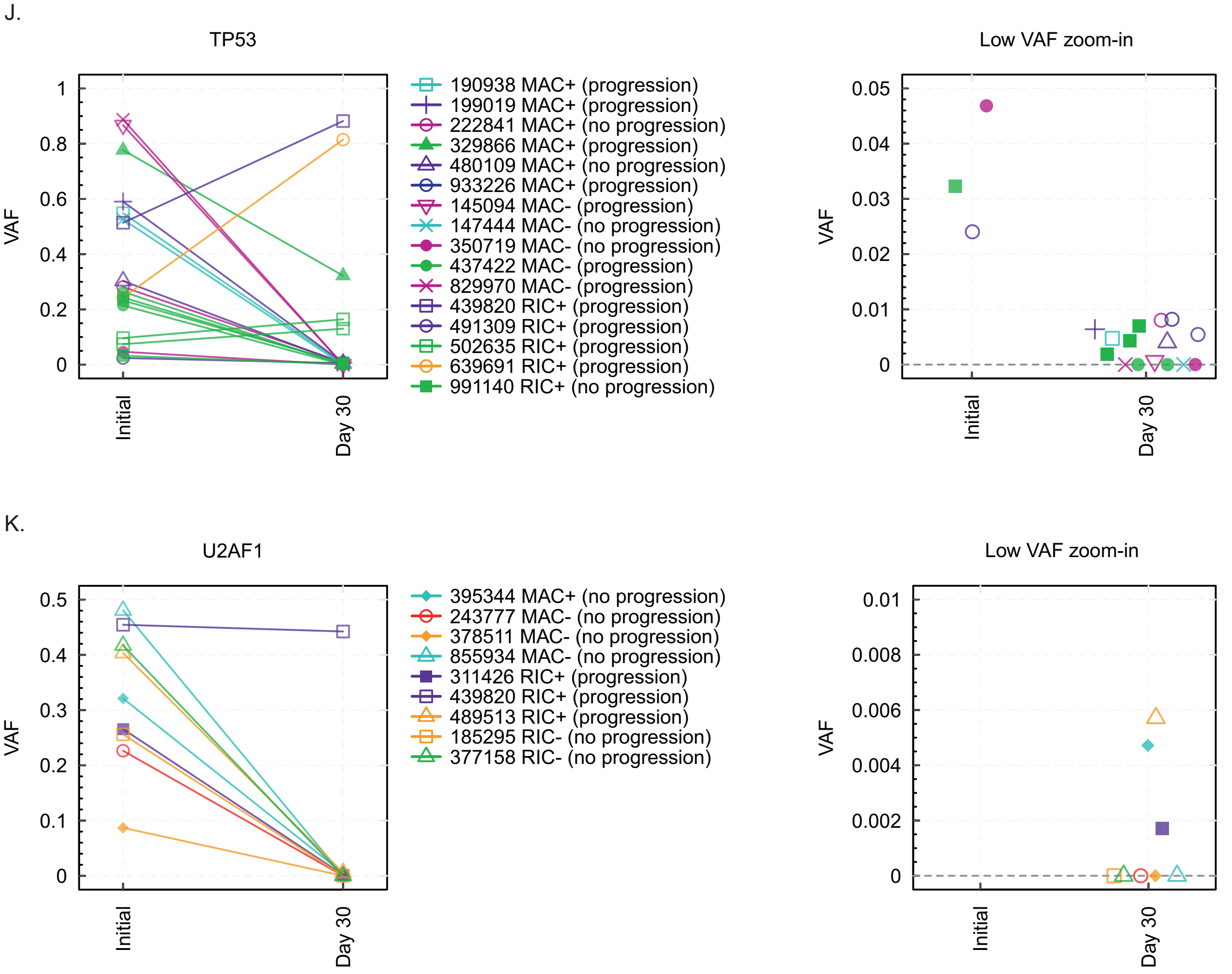


Figure S4. Association of Mutation Clearance at Day 30 post-alloHCT with Outcomes

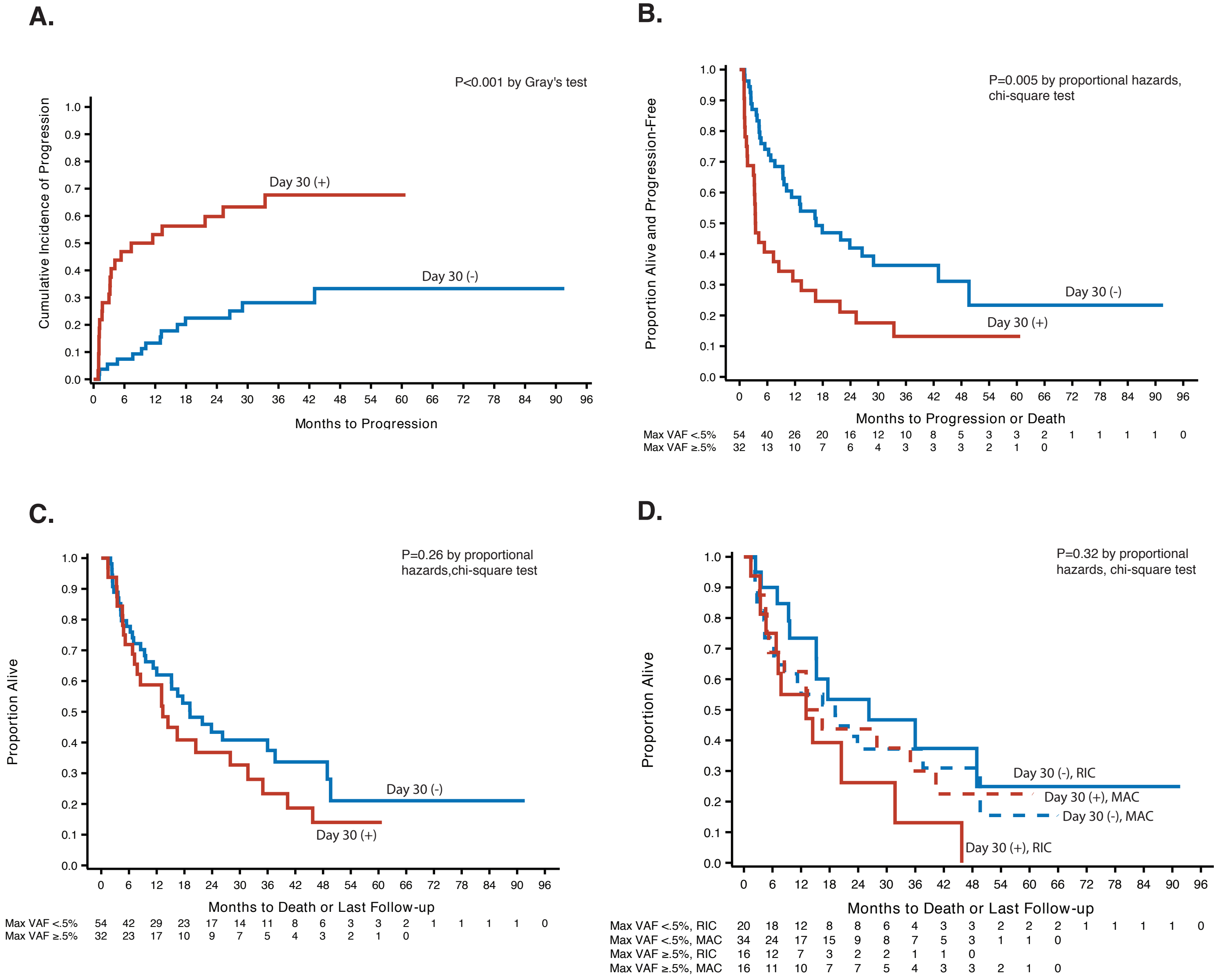


Figure S5. Association of Mutation Clearance at Day 100 post-alloHCT with Outcomes

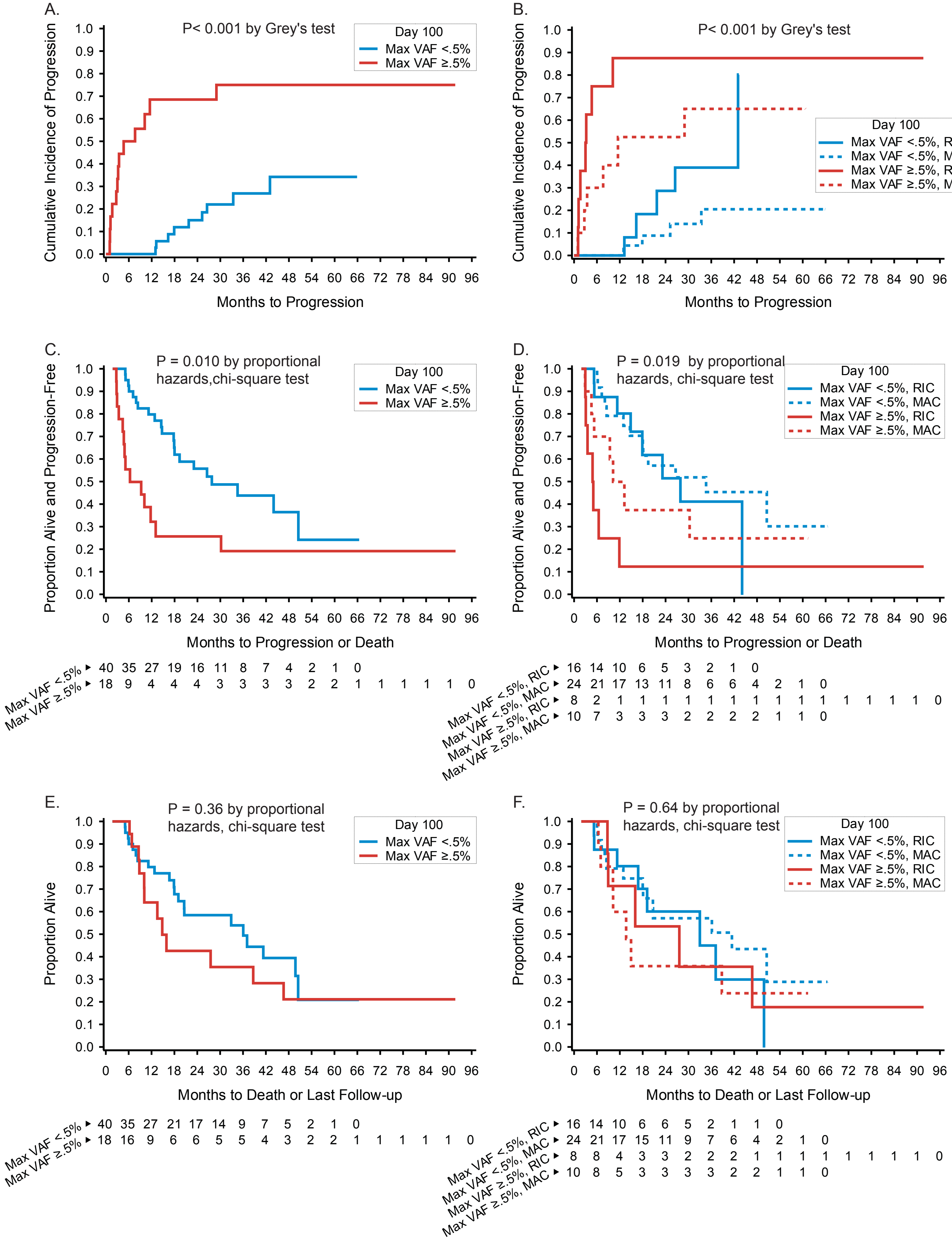
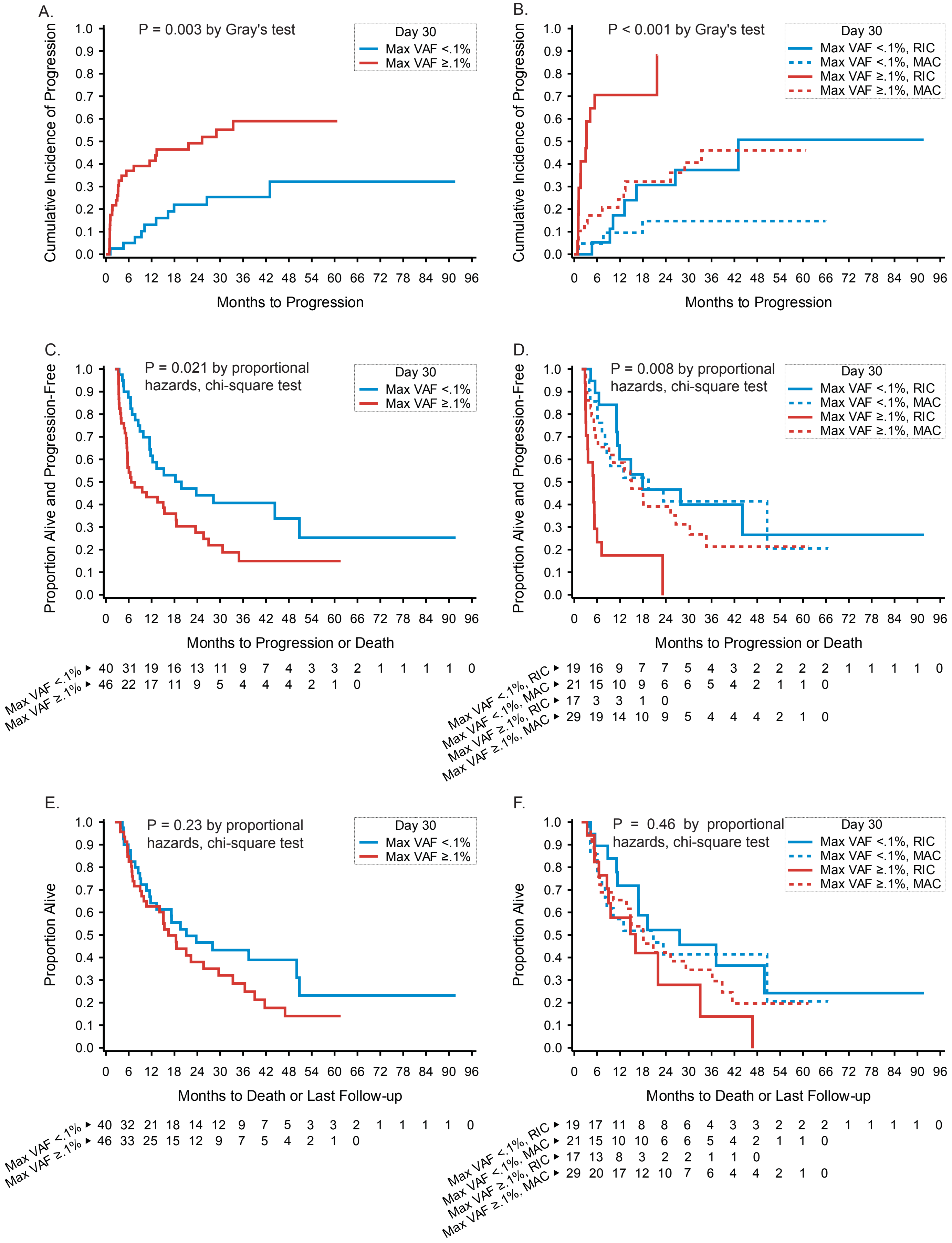


Figure S6. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 0.1%



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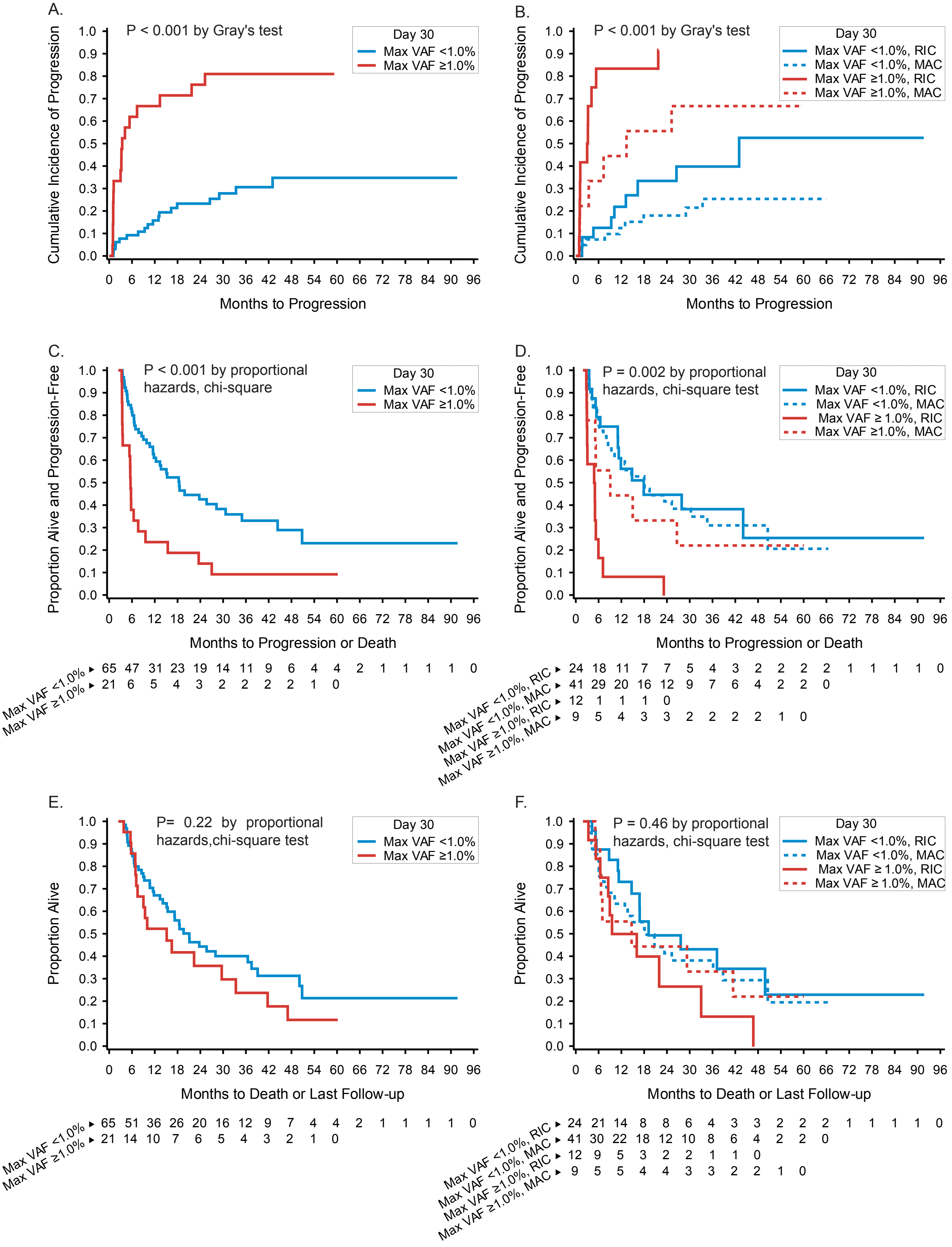

Figure S8. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 2.5%5%

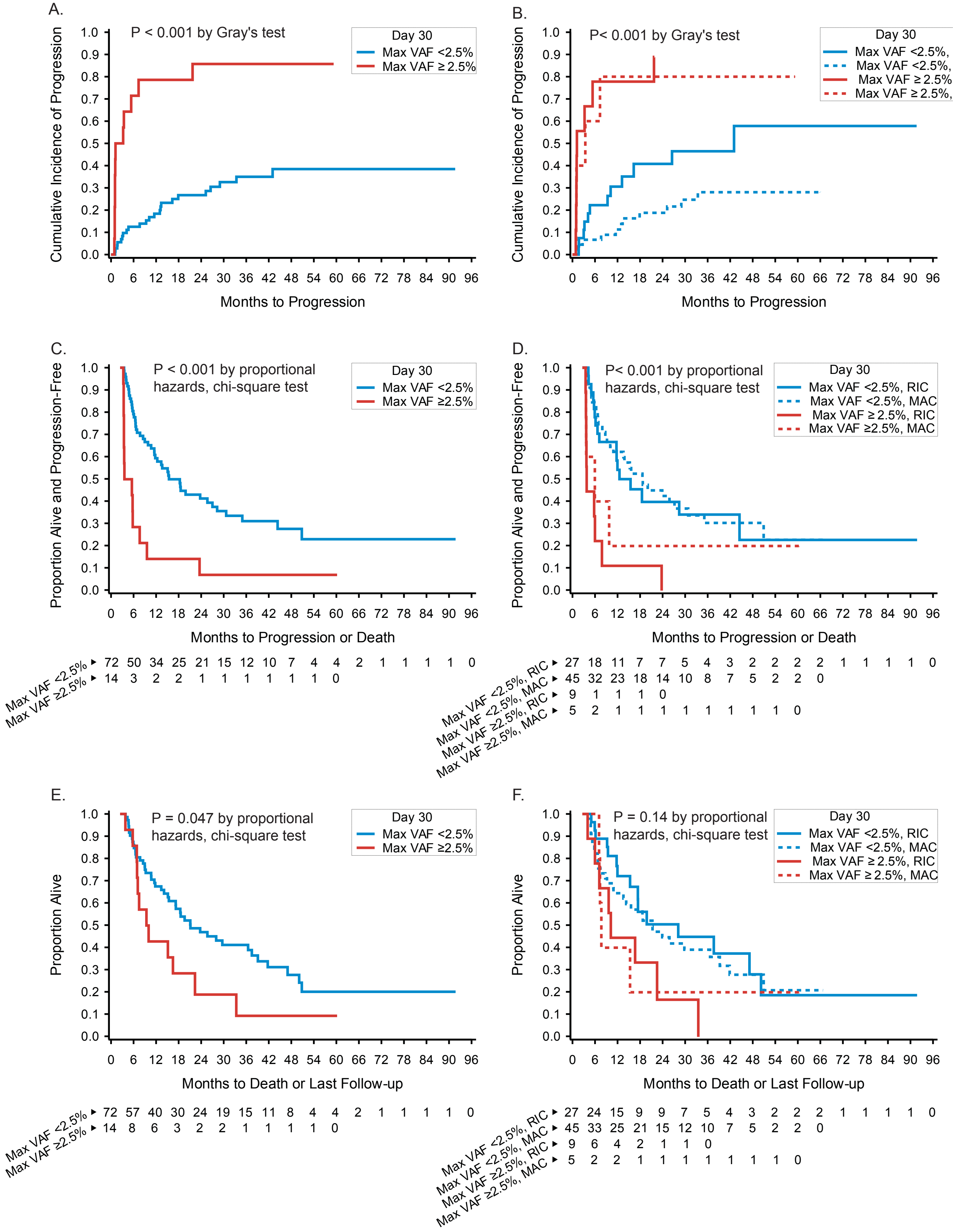

Figure S9. Association of Mutation Clearance with Outcomes Using Any Detectable Variant Allele Frequency

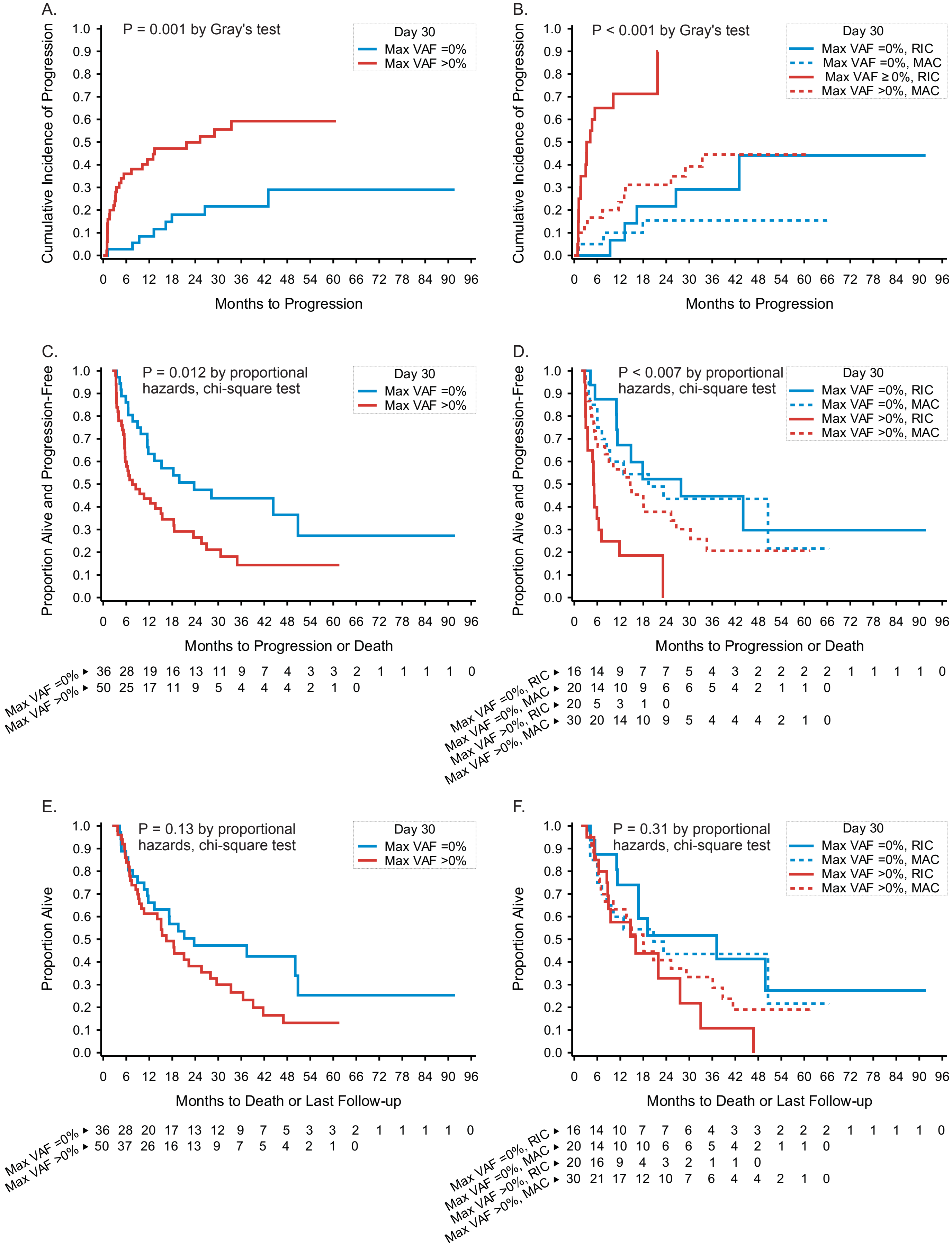

Figure S10. Association of Overall Survival with Mutation Clearance Determined by a 40 Gene-Panel

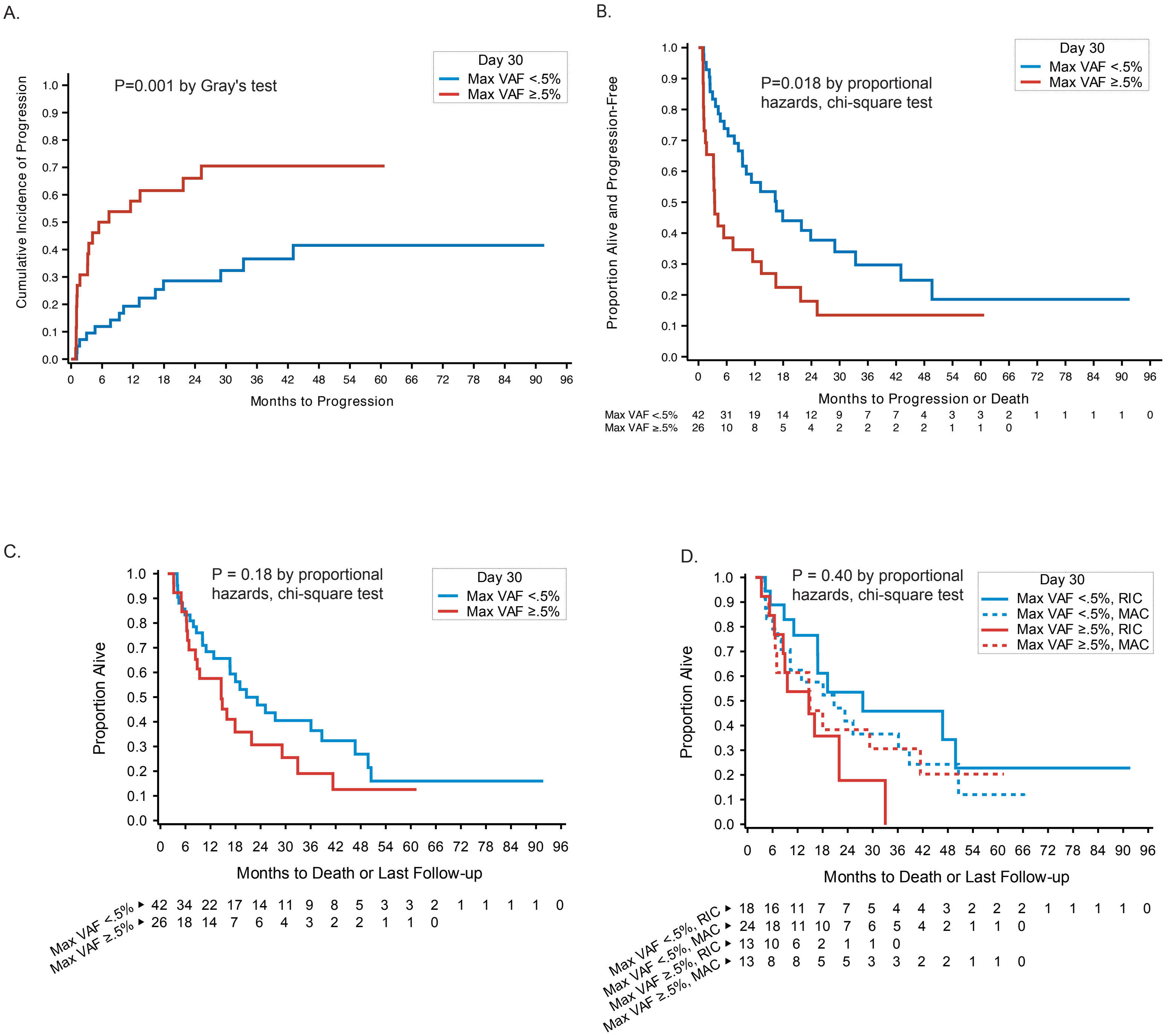

Table S1. Recurrently Mutated Genes in AML and MDS

ENSG ID	Gene symbol	Chr	Start	End	Strand
ENSG00000078369	*GNB1*	1	1716729	1822495	-
ENSG00000120952	*PRAMEF2*	1	12916941	12921764	+
ENSG00000065526	*SPEN*	1	16174359	16266955	+
ENSG00000058453	*CROCC*	1	17222232	17299474	+
ENSG00000142661	*MYOM3*	1	24382525	24438665	-
ENSG00000162521	*RBBP4*	1	33116749	33151812	+
ENSG00000188910	*GJB3*	1	35246790	35251970	+
ENSG00000054118	*THRAP3*	1	36690017	36770958	+
ENSG00000183317	*EPHA10*	1	38179561	38230824	-
ENSG00000162434	*JAK1*	1	65298906	65432187	-
ENSG00000162654	*GBP4*	1	89646831	89664633	-
ENSG00000203914	*HSP90B3P*	1	92100568	92109633	+
ENSG00000213281	*NRAS*	1	115247078	115259515	-
ENSG00000143373	*ZNF687*	1	151254094	151264381	+
ENSG00000143631	*FLG*	1	152274651	152297679	-
ENSG00000160691	*SHC1*	1	154934774	154946959	-
ENSG00000196189	*SEMA4A*	1	156117157	156147543	+
ENSG00000162733	*DDR2*	1	162601163	162750255	+
ENSG00000034971	*MYOC*	1	171604557	171621811	-
ENSG00000198216	*CACNA1E*	1	181382295	181770716	+
ENSG00000143341	*HMCN1*	1	185703683	186160085	+
ENSG00000162670	*BRINP3*	1	190066792	190446759	-
ENSG00000134369	*NAV1*	1	201592411	201796097	+
ENSG00000084674	*APOB*	2	21224301	21266945	-
ENSG00000119772	*DNMT3A*	2	25455496	25565459	-
ENSG00000091106	*NLRC4*	2	32449518	32490923	-
ENSG00000115808	*STRN*	2	37070783	37193615	-
ENSG00000068878	*PSME4*	2	54091204	54197977	-
ENSG00000135636	*DYSF*	2	71680753	71913898	+
ENSG00000168702	*LRP1B*	2	140988992	142889270	-
ENSG00000144285	*SCN1A*	2	166845670	166930149	-
ENSG00000115524	*SF3B1*	2	198256698	198299815	-
ENSG00000138413	*IDH1*	2	209100951	209130798	-
ENSG00000078018	*MAP2*	2	210288771	210598842	+
ENSG00000054356	*PTPRN*	2	220154345	220174370	-
ENSG00000072195	*SPEG*	2	220299568	220363009	+
ENSG00000204120	*GIGYF2*	2	233562009	233725287	+
ENSG00000085978	*ATG16L1*	2	234118697	234204320	+
ENSG00000168334	*XIRP1*	3	39224701	39234087	-
ENSG00000008300	*CELSR3*	3	48673896	48700348	-
ENSG00000164061	*BSN*	3	49591922	49708982	+
ENSG00000157445	*CACNA2D3*	3	54156574	55108584	+
ENSG00000163618	*CADPS*	3	62384021	62861064	-
ENSG00000114861	*FOXP1*	3	71003844	71633140	-
ENSG00000175161	*CADM2*	3	85008132	86117951	+
ENSG00000145103	*ILDR1*	3	121706170	121741051	-
ENSG00000173175	*ADCY5*	3	123001143	123168605	-
ENSG00000114626	*ABTB1*	3	127391778	127399763	+
ENSG00000179348	*GATA2*	3	128198265	128212030	-
ENSG00000118007	*STAG1*	3	136055077	136471220	-
ENSG00000090402	*SI*	3	164696686	164796283	-

ENSG00000136527	*TRA2B*	3	185632356	185655924	-
ENSG00000038219	*BOD1L1*	4	13570362	13629347	-
ENSG00000047365	*ARAP2*	4	36067620	36246131	-
ENSG00000075539	*FRYL*	4	48499378	48782339	-
ENSG00000072201	*LNX1*	4	54325468	54567572	-
ENSG00000134853	*PDGFRA*	4	55095264	55164414	+
ENSG00000157404	*KIT*	4	55524085	55606881	+
ENSG00000128052	*KDR*	4	55944426	55991762	-
ENSG00000118777	*ABCG2*	4	89011416	89152474	-
ENSG00000168769	*TET2*	4	106067032	106200973	+
ENSG00000145362	*ANK2*	4	113739239	114304896	+
ENSG00000198589	*LRBA*	4	151185594	151936879	-
ENSG00000197410	*DCHS2*	4	155155527	155412930	-
ENSG00000039139	*DNAH5*	5	13690437	13944652	-
ENSG00000131711	*MAP1B*	5	71403061	71505397	+
ENSG00000164309	*CMYA5*	5	78985659	79096063	+
ENSG00000038427	*VCAN*	5	82767284	82878122	+
ENSG00000164176	*EDIL3*	5	83236373	83680611	-
ENSG00000120733	*KDM3B*	5	137688285	137772717	+
ENSG00000081842	*PCDHA6*	5	140206816	140391929	+
ENSG00000239389	*PCDHA13*	5	140261793	140391929	+
ENSG00000171815	*PCDHB1*	5	140430961	140433547	+
ENSG00000146001	*PCDHB18*	5	140613936	140617101	+
ENSG00000182578	*CSF1R*	5	149432854	149492935	-
ENSG00000019582	*CD74*	5	149781200	149792332	-
ENSG00000132911	*NMUR2*	5	151771093	151784840	-
ENSG00000118322	*ATP10B*	5	159990127	160279219	-
ENSG00000134516	*DOCK2*	5	169064251	169510386	+
ENSG00000181163	*NPM1*	5	170814708	170838141	+
ENSG00000113739	*STC2*	5	172741716	172756506	-
ENSG00000183258	*DDX41*	5	176938578	176944470	-
ENSG00000112739	*PRPF4B*	6	4021501	4065217	+
ENSG00000095951	*HIVEP1*	6	12008995	12165232	+
ENSG00000112137	*PHACTR1*	6	12717833	13288075	+
ENSG00000137411	*VARS2*	6	30881982	30894233	+
ENSG00000197283	*SYNGAP1*	6	33387847	33421466	+
ENSG00000096433	*ITPR3*	6	33588522	33664351	+
ENSG00000112624	*GLTSCR1L*	6	42714696	42836296	+
ENSG00000146216	*TTBK1*	6	43211222	43255997	+
ENSG00000170927	*PKHD1*	6	51480098	51952423	-
ENSG00000151914	*DST*	6	56322785	56819413	-
ENSG00000079841	*RIMS1*	6	72596406	73112508	+
ENSG00000111799	*COL12A1*	6	75794042	75915767	-
ENSG00000146247	*PHIP*	6	79644136	79788011	-
ENSG00000164418	*GRIK2*	6	101846664	102517958	+
ENSG00000112333	*NR2E1*	6	108487215	108510013	+
ENSG00000213079	*SCAF8*	6	155054459	155230002	+
ENSG00000164619	*BMPER*	7	33944523	34195484	+
ENSG00000002746	*HECW1*	7	43152198	43602938	+
ENSG00000146648	*EGFR*	7	55086714	55324313	+
ENSG00000187391	*MAGI2*	7	77646374	79082890	-
ENSG00000075213	*SEMA3A*	7	83587659	84122040	-
ENSG00000198822	*GRM3*	7	86273224	86494200	+
ENSG00000066923	*STAG3*	7	99775186	99819111	+
ENSG00000154415	*PPP1R3A*	7	113516832	113715975	-

ENSG00000105976	*MET*	7	116312444	116438440	+
ENSG00000179603	*GRM8*	7	126078652	126893348	-
ENSG00000128594	*LRRC4*	7	127667124	127672160	-
ENSG00000128578	*STRIP2*	7	129073731	129128240	+
ENSG00000269955	*LUC7L2*	7	139026106	139107345	+
ENSG00000157764	*BRAF*	7	140419127	140624564	-
ENSG00000197448	*GSTK1*	7	142941186	142967947	+
ENSG00000055130	*CUL1*	7	148395006	148498202	+
ENSG00000106462	*EZH2*	7	148504475	148581414	-
ENSG00000055118	*KCNH2*	7	150642049	150675403	-
ENSG00000055609	*KMT2C*	7	151832007	152133628	-
ENSG00000183117	*CSMD1*	8	2792875	4852328	-
ENSG00000164741	*DLC1*	8	12940870	13372396	-
ENSG00000215262	*KCNU1*	8	36641842	36793643	+
ENSG00000248522	*SBF1P1*	8	56362069	56367699	-
ENSG00000121005	*CRISPLD1*	8	75896843	75946793	+
ENSG00000079102	*RUNX1T1*	8	92971152	93107443	-
ENSG00000205038	*PKHD1L1*	8	110374706	110543500	+
ENSG00000164796	*CSMD3*	8	113235157	114449328	-
ENSG00000164754	*RAD21*	8	117858173	117887105	-
ENSG00000136997	*MYC*	8	128747680	128753674	+
ENSG00000226807	*MROH5*	8	142443929	142517330	-
ENSG00000227184	*EPPK1*	8	144935822	144947434	-
ENSG00000096968	*JAK2*	9	4985033	5128183	+
ENSG00000122735	*DNAI1*	9	34457412	34520982	+
ENSG00000083067	*TRPM3*	9	73149949	74061820	-
ENSG00000165119	*HNRNPK*	9	86582998	86595569	-
ENSG00000185920	*PTCH1*	9	98205262	98279339	-
ENSG00000197816	*CCDC180*	9	100000779	100139569	+
ENSG00000041982	*TNC*	9	117782805	117880486	-
ENSG00000106804	*C5*	9	123714613	123837452	-
ENSG00000107147	*KCNT1*	9	138594031	138684992	+
ENSG00000148408	*CACNA1B*	9	140772241	141019076	+
ENSG00000095787	*WAC*	10	28821422	28911862	+
ENSG00000204176	*SYT15*	10	46955444	46971400	-
ENSG00000138336	*TET1*	10	70320117	70454239	+
ENSG00000107731	*UNC5B*	10	72972298	73062621	+
ENSG00000148602	*LRIT1*	10	85991276	86001217	-
ENSG00000182771	*GRID1*	10	87359312	88126250	-
ENSG00000171862	*PTEN*	10	89622870	89731687	+
ENSG00000138193	*PLCE1*	10	95753746	96088149	+
ENSG00000166024	*R3HCC1L*	10	99894381	100004654	+
ENSG00000107593	*PKD2L1*	10	102047903	102090243	-
ENSG00000229256	*ST13P13*	10	104975466	104976557	+
ENSG00000108055	*SMC3*	10	112327449	112364394	+
ENSG00000165813	*C10orf118*	10	115880621	115934364	-
ENSG00000117983	*MUC5B*	11	1142474	1288726	+
ENSG00000110328	*GALNT18*	11	11292421	11643561	-
ENSG00000129173	*E2F8*	11	19245614	19263389	-
ENSG00000182255	*KCNA4*	11	30031765	30038488	-
ENSG00000184937	*WT1*	11	32409321	32457176	-
ENSG00000149480	*MTA2*	11	62360675	62369303	-
ENSG00000168066	*SF1*	11	64532078	64546258	-
ENSG00000175591	*P2RY2*	11	72929344	72947397	+
ENSG00000074266	*EED*	11	85955815	85989781	+

ENSG00000165325	*CCDC67*	11	93063883	93171636	+
ENSG00000149972	*CNTN5*	11	98891871	100227473	+
ENSG00000187240	*DYNC2H1*	11	102980160	103350591	+
ENSG00000149295	*DRD2*	11	113280317	113346001	-
ENSG00000110395	*CBL*	11	119076990	119178859	+
ENSG00000149403	*GRIK4*	11	120530971	120857132	+
ENSG00000170953	*OR8B12*	11	124412618	124413550	-
ENSG00000111642	*CHD4*	12	6679248	6716551	-
ENSG00000139083	*ETV6*	12	11802788	12048336	+
ENSG00000111276	*CDKN1B*	12	12867992	12875305	+
ENSG00000133703	*KRAS*	12	25358180	25403854	-
ENSG00000013573	*DDX11*	12	31226779	31257725	+
ENSG00000167548	*KMT2D*	12	49412758	49453557	-
ENSG00000110844	*PRPF40B*	12	49962001	50038449	+
ENSG00000185640	*KRT79*	12	53215231	53228079	-
ENSG00000123411	*IKZF4*	12	56414689	56432219	+
ENSG00000139540	*SLC39A5*	12	56623820	56631630	+
ENSG00000179295	*PTPN11*	12	112856536	112947717	+
ENSG00000171435	*KSR2*	12	117890817	118406060	-
ENSG00000073060	*SCARB1*	12	125262174	125348519	-
ENSG00000198033	*TUBA3C*	13	19747910	19755992	-
ENSG00000122025	*FLT3*	13	28577411	28674729	-
ENSG00000102755	*FLT1*	13	28874489	29069265	-
ENSG00000132938	*MTUS2*	13	29598748	30080084	+
ENSG00000133119	*RFC3*	13	34392186	34540695	+
ENSG00000133083	*DCLK1*	13	36343122	36705464	-
ENSG00000150893	*FREM2*	13	39261173	39461268	+
ENSG00000139687	*RB1*	13	48877887	49056122	+
ENSG00000083520	*DIS3*	13	73329540	73356344	-
ENSG00000169508	*GPR183*	13	99946784	99959749	-
ENSG00000102452	*NALCN*	13	101706130	102068843	-
ENSG00000184497	*TMEM255B*	13	114462216	114514926	+
ENSG00000183087	*GAS6*	13	114523522	114567046	-
ENSG00000257115	*OR11H12*	14	19377594	19378574	+
ENSG00000054690	*PLEKHH1*	14	68000008	68056255	+
ENSG00000021645	*NRXN3*	14	78870093	80330762	+
ENSG00000185070	*FLRT2*	14	85996488	86094270	+
ENSG00000152315	*KCNK13*	14	90528108	90652199	+
ENSG00000211897	*IGHG3*	14	106230841	106237742	-
ENSG00000198838	*RYR3*	15	33603177	34158303	+
ENSG00000188659	*FAM154B*	15	82555140	82577268	+
ENSG00000136383	*ALPK3*	15	85359911	85416713	+
ENSG00000170776	*AKAP13*	15	85923871	86292586	+
ENSG00000140538	*NTRK3*	15	88402982	88799978	-
ENSG00000182054	*IDH2*	15	90626277	90645736	-
ENSG00000103313	*MEFV*	16	3292028	3306627	-
ENSG00000157106	*SMG1*	16	18816175	18937726	-
ENSG00000149926	*FAM57B*	16	30035748	30042194	-
ENSG00000070915	*SLC12A3*	16	56899119	56949762	+
ENSG00000067955	*CBFB*	16	67063050	67134961	+
ENSG00000039523	*FAM65A*	16	67562720	67580689	+
ENSG00000102974	*CTCF*	16	67596310	67673086	+
ENSG00000039068	*CDH1*	16	68771128	68869451	+
ENSG00000157423	*HYDIN*	16	70841289	71264569	-
ENSG00000140839	*CLEC18B*	16	74442529	74455649	-

ENSG00000152910	*CNTNAP4*	16	76311176	76593135	+
ENSG00000166473	*PKD1L2*	16	81134484	81253975	-
ENSG00000158545	*ZC3H18*	16	88636789	88698374	+
ENSG00000187741	*FANCA*	16	89803957	89883065	-
ENSG00000187624	*C17orf97*	17	260118	264367	+
ENSG00000174231	*PRPF8*	17	1553923	1588176	-
ENSG00000141510	*TP53*	17	7565257	7590863	-
ENSG00000264424	*MYH4*	17	10346607	10372876	-
ENSG00000007174	*DNAH9*	17	11501748	11873485	+
ENSG00000141027	*NCOR1*	17	15932471	16121499	-
ENSG00000196712	*NF1*	17	29421945	29705949	+
ENSG00000178691	*SUZ12*	17	30264044	30328064	+
ENSG00000171345	*KRT19*	17	39679869	39684641	-
ENSG00000073670	*ADAM11*	17	42836568	42859214	+
ENSG00000120071	*KANSL1*	17	44107282	44270166	-
ENSG00000006283	*CACNA1G*	17	48638429	48704835	+
ENSG00000141200	*KIF2B*	17	51900239	51902573	+
ENSG00000180891	*CUEDC1*	17	55940337	56032684	-
ENSG00000265206	*MIR142*	17	56408593	56408679	-
ENSG00000109066	*TMEM104*	17	72772622	72835922	+
ENSG00000161547	*SRSF2*	17	74730197	74733413	-
ENSG00000173821	*RNF213*	17	78234665	78370085	+
ENSG00000152217	*SETBP1*	18	42260138	42648475	+
ENSG00000167306	*MYO5B*	18	47349101	47721384	-
ENSG00000197561	*ELANE*	19	851014	856242	+
ENSG00000181143	*MUC16*	19	8959520	9092018	-
ENSG00000080573	*COL5A3*	19	10070237	10121147	-
ENSG00000105397	*TYK2*	19	10461204	10491248	-
ENSG00000179218	*CALR*	19	13049414	13055304	+
ENSG00000105639	*JAK3*	19	17935591	17958870	-
ENSG00000130518	*KIAA1683*	19	18367906	18385319	-
ENSG00000105701	*FKBP8*	19	18642568	18654383	-
ENSG00000245848	*CEBPA*	19	33790840	33793470	-
ENSG00000126249	*PDCD2L*	19	34895303	34917073	+
ENSG00000196218	*RYR1*	19	38924340	39078204	+
ENSG00000090920	*FCGBP*	19	40353963	40440533	-
ENSG00000105429	*MEGF8*	19	42829761	42882921	+
ENSG00000063244	*U2AF2*	19	56165512	56186081	+
ENSG00000171456	*ASXL1*	20	30946153	31027122	+
ENSG00000088305	*DNMT3B*	20	31350191	31397162	+
ENSG00000196090	*PTPRT*	20	40701392	41818610	-
ENSG00000087460	*GNAS*	20	57414773	57486247	+
ENSG00000075043	*KCNQ2*	20	62037542	62103993	-
ENSG00000159216	*RUNX1*	21	36160098	37357047	-
ENSG00000171587	*DSCAM*	21	41382926	42219065	-
ENSG00000160201	*U2AF1*	21	44513066	44527697	-
ENSG00000099954	*CECR2*	22	17840837	18033845	+
ENSG00000100038	*TOP3B*	22	21075651	22337213	-
ENSG00000099995	*SF3A1*	22	30727977	30752936	-
ENSG00000146950	*SHROOM2*	X	9754496	9917483	+
ENSG00000169249	*ZRSR2*	X	15808595	15841383	+
ENSG00000102098	*SCML2*	X	18257433	18372847	-
ENSG00000185448	*FAM47A*	X	34147873	34150428	-
ENSG00000183337	*BCOR*	X	39909068	40036582	-
ENSG00000124486	*USP9X*	X	40944888	41095832	+

ENSG00000147050	*KDM6A*	X	44732423	44971847	+
ENSG00000102145	*GATA1*	X	48644962	48652716	+
ENSG00000072501	*SMC1A*	X	53401070	53449677	-
ENSG00000102043	*MTMR8*	X	63487961	63615311	-
ENSG00000184634	*MED12*	X	70338406	70362304	+
ENSG00000215093	*EEF1A1P29*	X	85415268	85416363	-
ENSG00000204071	*TCEAL6*	X	101394933	101397942	-
ENSG00000196507	*TCEAL3*	X	102862379	102884618	+
ENSG00000177485	*ZBTB33*	X	119384607	119392251	+
ENSG00000101972	*STAG2*	X	123094062	123556514	+
ENSG00000171054	*OR13H1*	X	130677950	130679030	+
ENSG00000156531	*PHF6*	X	133507283	133562822	+
ENSG00000156920	*GPR112*	X	135383122	135499047	+
ENSG00000067842	*ATP2B3*	X	152783134	152848397	+

All genome coordinates use NCBI Build 37.

Chr, chromosome.

Supplementary Table 2. Summary of Clinical Characteristics and Sequencing Data

UPN	Initial Mutations Detected	Initial Mean VAF	Initial Max VAF	Pretransplant Mutations detected	Pretransplant Mean VAF	Pretransplant Max VAF	Day 30 Mutations Detected	Day 30 Mean VAF	Day 30 Max VAF	D30 RMG Cohort Mutations detected	Day 30 RMG Cohort Mean VAF	Day 30 RMG Cohort Max VAF	Day 100 Mutations Detected	Day 100 Mean VAF	Day 100 Max VAF	therapy-related MDS	de novo MDS	secondary AML	IPSS	IPSS-R	Conditioning	Regimen	Age at transplant	Diagnosis Cytogenetics	Cytogenetic Risk Group by IPSS-R	Diagnosis marrow blasts, %	Diagnosis Hemoglobin, g/dl	Diagnosis Platelets, K/cumm	Diagnosis absolute neutrophil count, K/cumm	Pretransplant marrow blasts, %	RAS Pathway mutation**	*TP53* mutation	*RUNX1* mutation	*ASXL1* mutation	Progression	Days from Transplant to 1st Progression	Dead	Days from transplant to death	Follow-up days if not dead	Progression Code	Cause of Death	Pre-Transplant Therapy	Transplant Type	Acute GVHD	Donor Lymphocte Infusion	Post-Progression Salvage Therapy
611	30	0.251	0.500	30	0.254	0.412	2	0.004	0.006	1	0.006	0.006	2	0.001	0.002	Y	N	N	Int-2	Int	MAC	Bu/Cy	59	nuc ish(D7Z1x2,D7S486x1)[106/200]/ (D7Z1,D7S486)x1[11/200],(EGR1x2)[200]	poor	0	12.7	70	0.71	0	Y	N	N	N	N	NA	N	NA	901	NA	NA	C	unrelated	Y	N	NA
130968	31	0.230	0.416	31	0.298	0.611	30	0.112	0.222	5	0.122	0.181	21	0.215	0.336	N	Y	N	Int-2	High	RIC	Flu/Bu2/thymo	72	46,XY[20]	good	13	8.7	233	0.5	10	Y	N	Y	Y	Y	36	Y	439	NA	B	A	A	unrelated	N	N	Y
145094	22	0.496	0.945	22	0.219	0.445	16	0.001	0.002	1	0.001	0.001	20	0.008	0.022	N	N	Y	High	Very High	MAC	Bu/Cy	62	40~44,XY,-Y,add(2)(q31),-3, add(3)(p21),add(6)(p25),add(7)(q36), del(9)(q22q32),add(10)(q26),-15,-17, +2mar[cp20]	very poor	35	9.3	40	13.97	3	Y	Y	N	N	Y	881	Y	1144	NA	A	A	A	unrelated	Y	Y	Y
147444	38	0.249	0.526	38	0.388	0.780	1	0.001	0.001	0	0.000	0.000	1	0.000	0.000	Y	N	N	Int-1	High	MAC	Bu/Cy	56	44,XX,-5,-7,-20,+mar[15]/46,XX[5]	very poor	0	9.7	105	2.832	3	N	Y	N	N	N	NA	Y	191	NA	NA	C	C	related	Y	N	NA
147457	482	0.265	0.473	NA	NA	NA	203	0.015	0.571	7	0.012	0.027	NA	NA	NA	Y	N	N	Int-1	Low	MAC	Bu/Cy	46	normal by report	good	1	11.3	85	0.483	NA	N	N	Y	Y	Y	223	Y	397	NA	A	A	C	unrelated	N	Y	Y
169510	34	0.397	0.832	13	0.360	0.571	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	Int-1	High	RIC	Flu/TBI/PTCy	59	46,XY[20]	good	9	7.7	30	0.5	NE	Y	N	Y	N	N	NA	N	NA	2106	NA	NA	A	related	Y	N	NA
185295	30	0.291	0.528	30	0.402	0.827	0	0.000	0.000	0	0.000	0.000	1	0.011	0.011	N	Y	N	missing	missing	RIC	Flu/Bu2/thymo	53	missing	missing	0	8.2	76	1.1	0	N	N	N	N	N	NA	N	NA	2786	NA	NA	C	unrelated	N	N	NA
187374	35	0.321	0.756	NA	NA	NA	34	0.008	0.018	1	0.007	0.007	35	0.058	0.157	Y	N	N	Int-2	High	RIC	Flu/Bu2/thymo	56	45,XY,-7[20]	poor	4	12.5	34	1.161	NA	N	N	N	N	Y	97	N	NA	244	C	NA	A	unrelated	N	Y	Y
189012	10	0.144	0.267	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	Int-1	Low	MAC	Bu/Cy	55	46,XY,del(5)(q15q33)[16]/ 46,XY[3] Non-clonal aberration: 46,XY,del(5)(q12q33), del(7)(q21q32)[1]	good	3	9.7	174	1.1	NA	N	N	N	N	N	NA	N	NA	2003	NA	NA	A	related	N	N	NA
190938	19	0.375	0.720	14	0.237	0.575	12	0.004	0.009	1	0.005	0.005	0	0.000	0.000	N	N	Y	High	Very High	MAC	Bu/Cy	62	46,XY,-5[17],del(7)(q32q36)[6], del(7)(q22q36)[6],-11[17],-12[17], -16[6], -17[17],-20[6],add(20)(p12)[6],+2 ~5mar[cp17]/46,XY[3]	very poor	39	8.6	35	0.143	0	N	Y	N	N	Y	1015	Y	1063	NA	A	A	B	unrelated	N	N	Y
199019	26	0.272	0.590	NA*	NA*	NA*	19	0.007	0.017	2	0.006	0.006	0	0.000	0.000	N	Y	N	Int-2	High	MAC	Bu/Cy	60	45-49,XX,+1,add(3)(p11), del(5)(q13q33),del(10)(q24q26), add(18)(q21),+19,-20,+21,+1-2mar[cp20]	very poor	0	8.3	20	1.786	NA	N	Y	N	N	Y	767	Y	1226	NA	A	A	C	unrelated	Y	Y	Y
221833	26	0.424	0.833	23	0.084	0.362	9	0.002	0.003	0	0.000	0.000	3	0.001	0.001	N	Y	N	Int-2	High	MAC	Flu/Bu4/thymo	69	47,XY+2[cp2]/48,idem,t(3;21)(q26.2;q22), +der(21)t(3;21)[18]	poor	10	11.6	33	1.62	1	N	N	N	N	N	NA	Y	503	NA	NA	C	A	unrelated	N	N	NA
222841	20	0.067	0.281	14	0.055	0.263	2	0.010	0.013	1	0.008	0.008	NA	NA	NA	N	N	Y	High	Very High	MAC	Bu/Cy	46	complex by report, including del(5q),add14,+21	very poor	17	6.1	19	2.948	12	N	Y	N	N	N	NA	Y	100	NA	NA	C	A	unrelated	Y	N	NA
229276	16	0.141	0.298	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	High	Very High	RIC	Flu/Bu2/thymo	68	46,XY[20]	good	30	8.7	22	0.039	NA	Y	N	Y	N	Y	284	Y	462	NA	B	B	A	unrelated	Y	Y	Y
243777	32	0.184	0.296	NA	NA	NA	3	0.002	0.003	0	0.000	0.000	0	0.000	0.000	N	Y	N	Int-2	Int	MAC	Cy/TBI	64	46,XX[20]	good	16	10.6	107	0.7	NA	N	N	N	Y	N	NA	N	NA	312	NA	NA	A	unrelated	N	N	NA
266995	14	0.053	0.078	12	0.291	0.469	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	Y	N	N	Int-1	Int	RIC	Flu/TBI/PTCy	54	45,XX,-7[2]/46,XX[18]	poor	1	11	151	0.3	2	Y	N	N	N	N	NA	Y	74	NA	NA	D	A	related	N	N	NA
270086	1	0.013	0.013	0	0.000	0.000	0	0.000	0.000	no RMGs	no RMGs	no RMGs	NA	NA	NA	Y	N	Y	High	Very High	MAC	Bu/Cy	25	39~43,XY,-3,add(3)(p13), der(4)t(4;11)(q31;q13),del(5)(q15q33), add(7)(q11.2),inv(9)(p12q13),-10, add(10)(q25),-11, add(12)(q14), der(12)t(12;13)(p11.2;q12),-13,-13, add(17)(p11.2),-19,-21,+1 ~3mar[cp12]/46,XY,inv(9)(p12q13)[8]	very poor	22	12.9	17	3.3	2	N	N	N	N	N	NA	Y	61	NA	NA	D	A	unrelated	Y	N	NA
272848	33	0.351	0.441	NA	NA	NA	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	Y	N	N	Int-2	Int	MAC	Bu/Cy	62	46,XX,-7,del(13)(q12q14),+mar[18] 46,XX[1]/47,XX,+15[1]	very poor	0	11.5	37	0.925	NA	N	N	N	N	N	NA	Y	205	NA	NA	C	C	unrelated	Y	N	NA
275454	2	0.031	0.044	NA*	NA*	NA*	1	0.004	0.004	no RMGs	no RMGs	no RMGs	NA	NA	NA	Y	N	N	Int-1	Int	MAC	Bu/Cy	60	46,XY[20]	good	1	6.9	65	0.016	NA	N	N	N	N	N	NA	Y	115	NA	NA	B	C	related	Y	N	NA
280837	28	0.433	0.883	28	0.394	0.878	28	0.010	0.039	2	0.016	0.022	NA	NA	NA	Y	N	N	Int-2	High	RIC	Flu/Bu2/thymo	64	45,XY,-7[17]/46,XY[3]	poor	3	10	40	1.44	9	N	N	N	N	Y	163	Y	237	NA	C	A	C	unrelated	Y	N	Y
283773	5	0.125	0.188	5	0.098	0.160	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	Low	Very Low	RIC	Fly/Cy/low dose TB	25	46, XX[20]	good	1	13.3	210	1.6	0	N	N	N	Y	N	NA	N	NA	813	NA	NA	C	unrelated	N	N	NA
288033	14	0.374	0.489	14	0.027	0.039	2	0.002	0.002	no RMGs	no RMGs	no RMGs	8	0.002	0.003	N	N	Y	Int-2	High	MAC	Cy/TBI	31	46, XX[20]	good	13	9.7	67	0.6	11	N	N	N	N	N	NA	Y	133	NA	NA	B	B	unrelated	Y	N	NA
293230	14	0.132	0.227	14	0.251	0.433	10	0.021	0.037	1	0.022	0.022	0	0.000	0.000	N	Y	N	Int-1	Low	RIC	Flu/Bu2/thymo	69	46,XY[20]	good	1	9.6	205	0.4	1	N	N	N	N	N	NA	Y	105	NA	NA	B	A	unrelated	Y	N	NA
298273	17	0.400	0.478	NA	NA	NA	2	0.002	0.004	no RMGs	no RMGs	no RMGs	11	0.082	0.187	N	N	Y	Int-2	High	MAC	Bu/Cy	27	46,XY[20]	good	18	8.5	79	2.2	NA	N	N	N	N	Y	82	Y	365	NA	A	A	A	unrelated	N	N	Y
307995	35	0.170	0.332	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	Y	N	N	Int-2	Low	RIC	Flu/Bu/Cy	61	46,XY,der(1;7)(q10;p10)[9]	intermediate	0	13.9	38	0.8	4	N	N	Y	N	N	NA	N	NA	932	NA	NA	A	related	Y	N	NA
311426	29	0.393	0.478	NA	NA	NA	19	0.004	0.008	1	0.002	0.002	24	0.248	0.390	N	Y	N	Int-1	Int	RIC	Flu/Bu2/thymo	56	46,XY[20]	good	8	9.5	57	2.3108	NA	N	N	N	N	Y	50	N	NA	208	B	NA	A	unrelated	N	Y	Y
329866	14	0.347	0.777	NA	NA	NA	11	0.144	0.322	1	0.322	0.322	NA	NA	NA	Y	N	Y	missing	missing	MAC	Cy/TBI	52	missing	missing	18	9.2	51	0.76	NA	N	Y	N	N	Y	32	Y	147	NA	A	A	B	related	Y	N	Y
340060	8	0.080	0.143	1	0.019	0.019	1	0.010	0.010	0	0.000	0.000	1	0.023	0.023	N	N	Y	missing	missing	MAC	Bu/Cy	62	missing	missing	24	7.9	9	2.34	2	Y	N	N	N	N	NA	Y	258	NA	NA	B	B	unrelated	Y	N	NA
346313	38	0.366	0.827	36	0.379	0.727	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	Int-1	Low	MAC	Bu/Cy	64	46,XY[20]	good	NE	10.4	20	0.6	83	Y	N	N	N	N	NA	Y	70	NA	NA	B	A	unrelated	Y	N	NA
350719	2	0.031	0.047	1	0.028	0.028	0	0.000	0.000	0	0.000	0.000	1	0.005	0.005	N	Y	N	Int-1	High	MAC	Bu/Cy	52	45,XX,der(5;17)(p10;q10)[11]/46,XX,del(13) (q12q22)[1]/46,XX[8]	intermediate	0	7	14	0.77	0	N	Y	N	N	N	NA	N	NA	285	NA	NA	A	related	Y	N	NA
353053	14	0.090	0.121	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	Int-2	Int	RIC	Flu/Bu2	58	46,XX,+1,der(1;7)(q10;p10)[19]/46,XX[1]	intermediate	1	10.4	67	0.782	2	N	N	Y	N	N	NA	N	NA	253	NA	NA	A	unrelated	Y	N	NA
368402	20	0.177	0.206	20	0.290	0.380	2	0.000	0.000	1	0.000	0.000	20	0.017	0.035	Y	N	N	Int-1	High	RIC	Flu/Bu2/thymo	60	46,XX[19]	good	10	10.2	27	0.2	8	N	N	Y	N	Y	141	Y	213	NA	A	A	A	unrelated	Y	N	Y
377158	32	0.352	0.430	32	0.381	0.487	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	Y	N	Int-2	High	RIC	Flu/Bu2	69	46,XX[20]. Non-clonal abnormality: del(9)(q13)[1]	good	15	8.8	14	0.89	4	N	N	Y	Y	N	NA	Y	110	NA	NA	C	A	unrelated	Y	N	NA
378511	48	0.345	0.723	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	1	0.001	0.001	Y	N	N	Int-1	Low	MAC	Bu/Cy	57	46,XY,+1,der(1;7)(q10;p10),del(13) (q12q21.3)[17]/46,XY[2]. Single cell nonclonal abnormality: 46,XY,t(2;16)(p11.2;q12.1)[1]	poor	2	11.5	332	1.188	NA	N	N	N	N	N	NA	Y	128	NA	NA	B	A	related	Y	N	NA
395344	20	0.346	0.461	NA	NA	NA	19	0.008	0.017	2	0.008	0.010	17	0.007	0.014	N	Y	N	Int-2	High	MAC	Bu/Cy	57	47,XY,+8[1]/47,idem,del(5)(q22q35)[19]	good	5	9.7	118	1.127	NA	N	N	Y	Y	N	NA	N	NA	1550	NA	NA	A	unrelated	N	N	NA
429745	35	0.375	0.508	33	0.299	0.438	34	0.106	0.183	1	0.167	0.167	34	0.109	0.196	Y	N	N	High	Very High	RIC	Flu/Bu2	68	48,XX,+8,+8,del(8)(q11.23q21.2) X3, del(12)(p13),add(17)(p13),del(22)(q13)[20]	very poor	5	9.3	27	2.135	13	N	N	Y	N	Y	32	Y	219	NA	A	A	A	related	N	Y	Y
430998	27	0.314	0.781	25	0.450	0.966	17	0.004	0.007	1	0.007	0.007	22	0.009	0.023	N	Y	N	Int-1	Low	MAC	Bu/Cy	57	47,XY,+14[5]/46,XY,i(14)(q10)[5]/46,XY[10]	intermediate	0	11.6	195	2.7	12	N	N	N	N	N	NA	N	NA	1846	NA	NA	C	related	N	N	NA
435866	25	0.400	0.481	24	0.020	0.035	1	0.001	0.001	0	0.000	0.000	23	0.002	0.005	N	Y	N	Int-2	Int	RIC	Flu/Bu2/thymo	61	46, XX[20]	good	15	10.5	253	5.36	0	N	N	N	N	Y	309	Y	798	NA	A	A	A	unrelated	N	N	Y
437422	22	0.255	0.405	22	0.316	0.610	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	High	Very High	MAC	Cy/TBI	57	42~44,XX,del(5)(q12q33),-7,-7, t(7;11)(q11.2;p15), -9,der(11)t(7;11), del(12)(p11.2),der(15;21)(q10;q10),-16, der(19)t(11;19)(q21;p11.3),-20,-21,+2 ~3mar[cp20]	very poor	15	10.5	36	0.714	10	N	Y	N	N	Y	35	Y	71	NA	A	A	B	unrelated	N	N	Y
439820	70	0.278	0.898	NA*	NA*	NA*	46	0.304	0.882	2	0.662	0.882	NA	NA	NA	N	Y	N	High	Very High	RIC	Flu/Cy/TBI	69	46,XY,del(7)(q22),del(20)(?q13.1)[12]/ 46,idem,?add(17)(p13)[4]/46,idem, add(17)(q25)[4]	very poor	7	8.5	21	1.4	NA	Y	Y	N	Y	Y	34	Y	44	NA	C	C	A	unrelated	N	N	Y
476807	30	0.308	0.413	17	0.168	0.429	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	Int-2	High	MAC	Bu/Cy	62	46,XY[20]	good	15	10	81	1.8	1	N	N	N	Y	N	NA	Y	665	NA	NA	C	A	related	N	N	NA
480109	23	0.248	0.378	0	0.000	0.000	13	0.005	0.009	2	0.005	0.006	NA	NA	NA	N	Y	N	Int-2	High	MAC	Bu/Cy	48	45~48,XX,t(1;14)(q12;q32),-2,add(5)(q11.2),dic(6;7)(q25;p15), add(12)(p11.2),-13,add(17)(q11.2),-22, +r,+2~6mar[cp15]/46,XX[7]	very poor	6	8.3	171	4.851	1	N	Y	N	N	N	NA	Y	45	NA	NA	D	A	related	N	N	NA
481668	33	0.242	0.466	33	0.196	0.369	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	Int-2	High	MAC	Flu/Bu4/thymo	63	51,XY,+der(1)t(1;9)(p?12;q?13), +8,+13,+19,+21[20]	very poor	0	9.6	14	0.9	3	N	N	N	N	N	NA	Y	166	NA	NA	C	A	related	N	N	NA
485523	8	0.066	0.095	1	0.008	0.008	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	N	Y	N	Int-2	High	RIC	Flu/Bu2/thymo	62	46,XY[20]	good	11	13.9	92	0.8	3	N	N	N	N	Y	806	Y	1094	NA	A	A	A	unrelated	Y	Y	Y
489196	50	0.267	0.469	NA*	NA*	NA*	31	0.002	0.004	no RMGs	no RMGs	no RMGs	0	0.000	0.000	Y	N	N	High	Very High	MAC	Bu/Cy	41	45,XX,t(13;17)(q25;p11.2),-20[1]/44-45,XX, del(1)(p36.1),add(2)(q33), t(3;17)(q25;p11.2),add(4)(q21), -7, add(11)(p11.2), -20,+mar[cp17]/46,XX[2]	very poor	8	8.5	96	0.1	NA	N	N	N	N	Y	395	Y	583	NA	C	A	C	related	Y	N	Y
489513	27	0.464	0.938	NA*	NA*	NA*	25	0.012	0.024	1	0.006	0.006	NA	NA	NA	Y	N	N	missing	missing	RIC	Flu/Bu2/thymo	62	missing	missing	3	12.1	42	1.5	NA	N	N	N	Y	Y	126	Y	206	NA	A	A	C	related	N	Y	Y
491309	2	0.037	0.050	2	0.051	0.078	2	0.004	0.005	1	0.005	0.005	NA	NA	NA	N	N	Y	Int-1	Low	RIC	Flu/Bu2	62	44~45,XX,der(3)t(3;12)(p25;q13), del(3)(q21q24),add(5)(q11.2), del(8)(p11.2),-12,add(15)(p11.2)[cp3]/46,XX[17]	very poor	2	11.4	386	2.475	3	N	Y	N	N	Y	52	Y	397	NA	B	A	B	related	Y	N	Y
496321	25	0.427	0.485	6	0.020	0.073	0	0.000	0.000	0	0.000	0.000	1	0.001	0.001	N	Y	N	Int-2	Int	MAC	Cy/TBI	57	46, XY [20]	good	12	10	145	7.488	0	N	N	N	N	N	NA	N	NA	1355	NA	NA	A	related	Y	N	NA
499258	21	0.171	0.405	NA	NA	NA	21	0.376	0.843	1	0.395	0.395	NA	NA	NA	N	Y	N	missing	missing	RIC	Flu/Bu2/thymo	38	missing	missing	unknown	13.2	74	0.7	NA	N	N	Y	N	Y	98	Y	622	NA	A	A	C	related	Y	N	Y
502635	12	0.069	0.103	12	0.020	0.032	12	0.128	0.164	2	0.147	0.164	NA	NA	NA	N	Y	N	High	Very High	RIC	Flu/Bu2/thymo	65	45~48,XY,-3,del(4)(q25q31),add(5)(q13), -7,add(7)(p22), -8, del(9)(q22), idic(12)(p12),add(20)(q13.3),+21,+2 ~5mar[cp12]/46,XY[8]	very poor	12	8.6	39	1	5	N	Y	N	N	Y	27	Y	141	NA	A	A	A	unrelated	N	Y	Y
565435	35	0.223	0.302	35	0.240	0.446	28	0.005	0.010	2	0.006	0.006	0	0.000	0.000	N	Y	N	Int-2	High	MAC	Bu/Cy	65	46,XY[20]	good	14	10.5	113	0.336	3	N	N	N	Y	N	NA	Y	500	NA	NA	D	A	related	Y	N	NA
596762	18	0.285	0.417	NA*	NA*	NA*	4	0.001	0.002	no RMGs	no RMGs	no RMGs	1	0.000	0.000	N	Y	N	Int-2	Very High	MAC	Bu/Cy	45	46,XY,t(6;9)(p23;q34)[4]/46,XY[16]	intermediate	6	7.6	18	1.6	NA	N	N	N	N	N	NA	N	NA	1499	NA	NA	A	related	N	N	NA
597501	40	0.396	0.512	NA	NA	NA	31	0.010	0.015	3	0.010	0.012	NA	NA	NA	N	Y	N	missing	missing	MAC	Cy/TBI	55	missing	missing	3	10.5	33	1.9	NA	Y	N	N	N	Y	406	Y	849	NA	C	A	C	related	Y	Y	Y
621996	37	0.347	0.668	37	0.433	0.870	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	Int-2	Very High	RIC	Flu/Cy/TBI/PT Cy	68	46,XY[20]	good	13	7.2	47	0.1	3	N	N	Y	Y	Y	496	Y	536	NA	A	A	A	haplo related	Y	Y	Y
624702	23	0.348	0.545	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	N	Y	Int-2	High	RIC	Flu/Bu2/thymo	67	46,XY[19]. Non clonal aberration: 46,XY,del(8)(q11.2q22)[1]	good	25	8.9	173	0.035	NA	N	N	N	N	Y	401	Y	463	NA	C	A	A	unrelated	Y	N	N
625338	3	0.021	0.025	3	0.006	0.009	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	Y	N	N	Int-1	Low	RIC	Flu/Bu2/thymo	51	46,XX[20]	good	5	12.1	194	1	1	N	N	Y	Y	N	NA	N	NA	356	NA	NA	A	unrelated	Y	N	NA
627844	26	0.264	0.682	19	0.006	0.018	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	N	Y	N	High	Very High	RIC	Flu/Bu2/thymo	54	46,XY,t(17;17)(p13;q11.2)[9]/46,XY[11]	intermediate	16	7.6	63	1.225	10	Y	N	Y	N	N	NA	N	NA	1244	NA	NA	B	unrelated	N	N	NA
635308	38	0.141	0.533	13	0.008	0.037	14	0.005	0.008	no RMGs	no RMGs	no RMGs	2	0.000	0.001	Y	N	N	Low	Int	RIC	Flu/Cy/TBI/PT Cy	67	46,XX[24]	good	0	7.4	24	0.3	1	N	N	N	N	N	NA	Y	103	NA	NA	C	A	unrelated	Y	N	NA
639691	88	0.202	0.559	82	0.150	0.609	79	0.096	0.815	1	0.815	0.815	NA	NA	NA	Y	N	N	Int-2	Very High	RIC	Flu/Bu2/thymo	70	44~46,XX,del(5)(q12q33),del(7)(q22q34), add(12)(p13),dic(12;18)(p13;p11.3), del(13)(q12q14),del(17)(p11.2), -19[cp19]/ 46,XX[1]	very poor	5	9.2	63	2.69	6	N	Y	N	N	Y	30	N	NA	441	A	NA	A	unrelated	Y	N	N
678913	13	0.359	0.460	NA*	NA*	NA*	9	0.014	0.100	no RMGs	no RMGs	no RMGs	6	0.002	0.003	Y	N	N	Low	Low	MAC	Cy/TBI	49	46,XY[18]	good	1	13.3	31	2.3	NA	N	N	N	N	N	NA	N	NA	1802	NA	NA	C	unrelated	Y	N	NA
715413	3	0.059	0.081	NA	NA	NA	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	Y	N	N	missing	missing	RIC	Flu/Bu2/thymo	56	missing	missing	0	10.2	40	2.7	NA	N	N	N	N	N	NA	Y	292	NA	NA	C	C	unrelated	Y	N	NA
717045	22	0.340	0.406	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	10	0.005	0.008	N	Y	N	Int-1	Low	MAC	Cy/TBI	48	Cytogenetic analysis showed 20 of 20 analyzed cells to have a 5q deletion	good	2	9.3	37	3.332	NA	N	N	N	N	Y	232	Y	259	NA	A	A	C	unrelated	N	N	N
732217	28	0.467	0.945	28	0.482	0.956	7	0.002	0.002	1	0.002	0.002	NA	NA	NA	N	Y	N	Int-1	Int	MAC	Bu/Cy	53	46,XY[20]	good	5	15	18	7.04	3	N	N	Y	Y	N	NA	Y	75	NA	NA	B	A	unrelated	Y	N	NA
754150	32	0.326	0.904	30	0.254	0.720	18	0.012	0.129	1	0.006	0.006	21	0.179	0.236	N	N	Y	Int-1	High	MAC	Flu/Bu2/thymo	58	46,XY[20]	good	5	8.1	17	8.772	1	N	N	N	Y	Y	104	Y	139	NA	A	A	A	unrelated	Y	N	N
769516	17	0.250	0.299	NA	NA	NA	13	0.005	0.011	1	0.004	0.004	14	0.029	0.089	N	Y	N	Int-2	Very High	RIC	Flu/Bu2	61	46,XY,-7,del(20)(q11.2),+21[3]/ 48,idem,+13,+21[9]/46,XY[8]	very poor	8	10.6	42	0.3	NA	N	N	N	N	Y	91	Y	1391	NA	C	A	A	related	Y	Y	Y
783437	2	0.021	0.026	2	0.014	0.016	0	0.000	0.000	no RMGs	no RMGs	no RMGs	NA	NA	NA	N	N	Y	High	High	MAC	Bu/Cy	65	46, XY [20]	good	24	9.5	98	0.552	NE	N	N	N	N	N	NA	Y	129	NA	NA	C	A	unrelated	Y	N	NA
796518	19	0.234	0.566	18	0.247	0.500	4	0.001	0.001	0	0.000	0.000	3	0.001	0.002	N	Y	N	Int-1	Low	MAC	Bu/Cy	57	46,XY,+1,der(1;7)(q10;p10)[20]	intermediate	1	10	149	1.3	2	N	N	N	N	N	NA	N	NA	873	NA	NA	A	unrelated	N	N	NA
818831	8	0.114	0.163	4	0.005	0.008	1	0.001	0.001	1	0.001	0.001	NA	NA	NA	N	Y	N	missing	missing	MAC	Flu/Bu4/thymo	55	missing	missing	0	8.1	7	0.1	5	N	N	N	Y	Y	33	Y	83	NA	B	B	A	related	Y	N	N
819544	4	0.029	0.045	4	0.045	0.072	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	N	Y	N	Int-2	High	MAC	Bu/Cy	61	46, XY[20]	good	16	12.4	74	0.8	11	N	N	N	N	N	NA	N	NA	1076	NA	NA	A	unrelated	Y	N	NA
829970	38	0.399	0.887	38	0.364	0.760	0	0.000	0.000	0	0.000	0.000	1	0.000	0.000	Y	N	N	Int-2	High	MAC	Flu/Bu4/thymo	65	45~46,XY,-5,del(5)(q13q33),-7, del(7)(q22?q34),+8,-17, add(17)(p11.2), -21,+22[cp20]	very poor	3	9.3	67	0.8	4	N	Y	N	N	Y	544	Y	584	NA	A	A	C	unrelated	Y	N	N
839903	47	0.302	0.470	42	0.044	0.085	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	Y	N	N	High	Very High	RIC	Flu/Bu2/thymo	69	46,XX,t(6;9)(p23;q34)[2]/46,XX[6]	intermediate	16	9.9	18	4.134	0	Y	N	N	N	Y	1308	Y	1487	NA	A	A	A	related	N	N	N
848524	28	0.371	0.554	NA	NA	NA	1	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	N	Y	N	Int-2	Very High	RIC	Flu/Bu2	63	45,XY,inv(5)(p12q22)?c,-7[5]/ 46,XY,inv(5)(p12q22)?c[10]	poor	5-7	7.7	111	7.198	NA	N	N	N	Y	N	NA	N	NA	210	NA	NA	A	unrelated	Y	N	NA
855934	26	0.450	0.908	26	0.455	0.946	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	N	Y	High	Very High	MAC	Cy/TBI	62	46,XY (by report)	good	26	7.8	40	2.173	12	N	N	N	Y	N	NA	Y	342	NA	NA	B	A	related	Y	N	NA
856550	42	0.365	0.542	NA*	NA*	NA*	33	0.011	0.121	4	0.004	0.005	21	0.002	0.008	N	Y	N	Int-2	High	MAC	Bu/Cy	53	46,XX,inv(2)(p11.2q13)c[20] con variant	intermediate	10	9.2	47	4.96	NA	Y	N	Y	N	Y	30	Y	158	NA	B	B	C	related	Y	N	N
875301	7	0.043	0.074	2	0.005	0.008	0	0.000	0.000	0	0.000	0.000	NA	NA	NA	N	N	Y	Int-2	Int	RIC	Flu/Bu2/thymo	62	46,XX[20]	good	14	11.5	125	1.4	1	N	N	N	N	N	NA	Y	285	NA	NA	C	A	unrelated	Y	N	NA
876752	13	0.326	0.464	13	0.366	0.509	7	0.001	0.001	1	0.001	0.001	NA	NA	NA	N	Y	N	Int-1	High	MAC	Bu/Cy	25	46, XX[20]	good	7	9.8	50	0.4	10	N	N	N	N	N	NA	N	NA	350	NA	NA	A	related	N	N	NA
882325	23	0.353	0.756	12	0.104	0.635	2	0.001	0.002	1	0.002	0.002	NA	NA	NA	N	N	Y	Int-2	High	MAC	Bu/Cy	59	46,XY[20]	good	15	10.7	266	0.2	1	N	N	N	N	N	NA	Y	725	NA	NA	C	A	unrelated	Y	N	NA
907471	8	0.023	0.038	NA	NA	NA	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	Y	N	Y	Int-2	High	MAC	Bu/Cy	57	46,XX,del(5)(?q12q33)[1]/46,XX[19]	good	15	12	67	0.8	NA	N	N	N	N	N	NA	N	NA	1290	NA	NA	A	unrelated	Y	N	NA
913698	24	0.280	0.572	24	0.305	0.671	22	0.018	0.040	3	0.017	0.027	3	0.001	0.001	N	Y	N	Int-1	Int	RIC	Flu/Bu2/thymo	68	46,XX[20]	good	8	12.1	26	0.98	7	N	N	Y	Y	Y	660	Y	965	NA	B	A	A	unrelated	Y	N	N
918051	20	0.384	0.433	20	0.291	0.360	0	0.000	0.000	no RMGs	no RMGs	no RMGs	NA	NA	NA	N	Y	N	Int-1	High	MAC	Bu/Cy	53	46, XY[20]	good	10	9.1	79	0.2	3	N	N	N	N	N	NA	N	NA	1136	NA	NA	A	unrelated	Y	N	NA
922185	21	0.172	0.255	21	0.136	0.238	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	Y	N	N	Int-1	Low	MAC	Bu/Cy	55	46,XY,del(20)(q11.2)[13]/46,XY[7]	good	1	12.7	83	1.5	1	N	N	N	N	N	NA	N	NA	668	NA	NA	C	related	Y	N	NA
933226	NA	NA	NA	37	0.394	0.864	10	0.005	0.008	1	0.008	0.008	16	0.002	0.011	Y	N	N	Int-1	Low	MAC	Bu/Cy	54	45, XY, -5, del (6) (p21.3) [5]	good	NE	10.8	60	2.6	2	N	Y	N	N	Y	350	Y	405	NA	B	A	C	unrelated	N	N	N
944541	23	0.332	0.423	NA*	NA*	NA*	0	0.000	0.000	0	0.000	0.000	0	0.000	0.000	N	Y	N	missing	missing	MAC	Cy/TBI	54	missing	missing	about 20	8.9	75	1.924	NA	Y	N	N	N	N	NA	Y	1509	NA	NA	NA	C	unrelated	Y	N	NA
955252	1	0.025	0.025	1	0.024	0.024	0	0.000	0.000	no RMGs	no RMGs	no RMGs	0	0.000	0.000	Y	N	N	Int-2	Very High	MAC	Bu/Cy	49	missing	missing	7	9	98	0.946	10	N	N	N	N	N	NA	N	NA	685	NA	NA	C	unrelated	Y	N	NA
988638	23	0.162	0.282	23	0.410	0.810	9	0.001	0.002	0	0.000	0.000	8	0.002	0.002	N	Y	N	Int-2	High	RIC	Flu/Bu2/thymo	67	46,XY,del(12)(q21q24.1)[13]/46,XY[7]	intermediate	14	9.6	279	4.3	15	N	N	N	Y	N	NA	N	NA	401	NA	NA	A	related	N	N	NA
991140	30	0.222	0.333	30	0.131	0.182	27	0.006	0.009	3	0.004	0.007	0	0.000	0.000	Y	N	N	Int-2	High	RIC	Flu/Bu2	61	44,XY,-7,psudic(12;15)(p13;p13),-18, +mar[13]/44,Y,t(X;19)(q11.2;p13.1), add(3)(p?23),add(5)(q13), add(7)(p13),-18[3]/46,XY[4]	very poor	1	7.9	79	0.66	NE	N	Y	N	N	N	NA	N	NA	450	NA	NA	C	unrelated	Y	N	NA

UPN, unique patient number.

VAF, variant allele frequency listed as a fraction; NE, not enumerated; NA, not available; RMG, recurrently mutated gene, 40 gene-panel data.

IPSS,International Prognostic Scoring System.

IPSS-R, International Prognostic Scoring System-Revised. A score of ≤ 1.5 indicates very low risk, >1.5-3.0 low risk, >3-4.5 intermediate risk, > 4.5-6 high risk, and >6 very high risk. Scores are calculated based on bone marrow blast percentage, cytogenetics, and cytopenias.

Int, Intermediate; Int-1, Intermediate-1; Int-2, Intermediate-2.

Progression Code: NA, not applicable; A, ≥ 5% myeloblasts or extramedullary disease; B, loss of donor chimerism or reappearance of pre-transplant morphologic abnormalities prompting an intervention by the treating physician; C= return of pre-transplant cytogenetic abnormalities. Cause of death: A, Progression; B, Graft vs Host disease; C, Infection/sepsis; D, Other.

MAC, myeloablative conditioning; RIC, reduced-intensity conditioning.

Flu, fludarabine; Bu, busulfan; thymo, thymoglobulin; Cy, cyclophosphamide; TBI, total body irradiation; PT CY, post-transplant cyclophosphamide.

Pre-Transplant therapy: A, Therapy, including a hypomethylating agent; B, Therapy, but not including a hypomethylating agent; C, No therapy.

Data is included for the 86 patients with one or more trackable somatic mutations.

* Indicates samples for which the initial timepoint was consistent with the pre-transplant banking definition in the Supplementary text.

** RAS pathway genes include tier 1 mutations that alter protein coding in *NRAS, KRAS, NF1, SOS1, PTPN11, and CBL.*

Table S3. Somatic Mutations (SNVs and indels) by Exome Sequencing

UPN	Chr	Start	Stop	Reference	Variant	Var Type	Gene Symbol	Transcript_ID	Strand	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Ref count	Normal Var Count	Normal VAF	Tumor Ref Count	Tumor Var Count	Tumor VAF
611	1	53547545	53547545	C	T	SNP	*PODN*	ENST00000312553	1	intronic	c.1806-108	e10-108	tier3	19	0	0.000	52	21	0.288
611	1	63153953	63153953	C	T	SNP	*DOCK7*	ENST00000251157	-1	5_prime_untranslated_region	c.-18	NULL	tier4	14	0	0.000	25	19	0.432
611	2	25464481	25464481	G	A	SNP	*DNMT3A*	ENST00000264709	-1	nonsense	c.2032	p.Q678*	tier1	292	4	0.014	1146	70	0.057
611	3	31495819	31495819	G	A	SNP	*THRAP3P1*	ENST00000411753	1	3_prime_untranslated_region	c.*31495819	NULL	tier3	462	0	0.000	769	311	0.288
611	3	64644370	64644370	G	A	SNP	*ADAMTS9*	ENST00000498707	-1	silent	c.777	p.S259	tier1	79	2	0.025	140	68	0.327
611	3	130720537	130720537	T	A	SNP	*ATP2C1*	ENST00000428331	1	3_prime_untranslated_region	c.*343	NULL	tier4	42	0	0.000	159	91	0.364
611	4	187540539	187540539	C	T	SNP	*FAT1*	ENST00000441802	-1	missense	c.7201	p.E2401K	tier1	33	1	0.029	94	36	0.277
611	6	33037020	33037020	G	A	SNP	*HLA-DPA1*	ENST00000419277	-1	missense	c.404	p.T135I	tier1	57	0	0.000	138	77	0.358
611	6	43206066	43206066	C	G	SNP	*TTBK1*	ENST00000259750	1	5_prime_flanking_region	c.-8333	NULL	tier4	58	0	0.000	177	49	0.217
611	7	45753309	45753309	C	T	SNP	*ADCY1*	ENST00000297323	1	silent	c.3075	p.H1025	tier1	91	2	0.021	92	56	0.378
611	7	100549883	100549883	G	A	SNP	*LOC100131514*	ENST00000379458	1	missense	c.464	p.S155N	tier1	19	0	0.000	51	28	0.350
611	8	17944578	17944578	C	T	SNP	*LOC101929066*	ENST00000499554	1	rna	NULL	NULL	tier1	85	0	0.000	182	79	0.303
611	8	72127533	72127533	C	T	SNP	*EYA1*	ENST00000340726	-1	intronic	c.1597+89	e14+89	tier3	74	2	0.026	192	62	0.244
611	8	116424437	116424437	G	C	SNP	*TRPS1*	ENST00000395715	-1	3_prime_untranslated_region	c.*1814	NULL	tier3	26	0	0.000	69	29	0.287
611	8	140768932	140768932	C	T	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-24487	e22-24487	tier3	64	1	0.015	97	35	0.263
611	9	103338826	103338826	C	T	SNP	*TMEFF1*	ENST00000374879	1	nonsense	c.1087	p.R363*	tier1	51	0	0.000	95	43	0.312
611	9	131502394	131502394	G	A	SNP	*ZER1*	ENST00000291900	-1	silent	c.1858	p.L620	tier1	31	0	0.000	76	22	0.225
611	11	6648113	6648113	C	T	SNP	*DCHS1*	ENST00000299441	-1	missense	c.6157	p.V2053M	tier1	58	0	0.000	93	32	0.254
611	11	25004690	25004690	A	G	SNP	*LUZP2*	ENST00000336930	1	missense	c.616	p.M206V	tier1	58	0	0.000	121	18	0.130
611	11	125298875	125298875	C	T	SNP	*PKNOX2*	ENST00000298282	1	intronic	c.937-33	e8-33	tier2	44	1	0.022	91	46	0.336
611	12	53553483	53553483	T	C	SNP	*CSAD*	ENST00000267085	-1	missense	c.1313	p.N438S	tier1	23	0	0.000	90	33	0.266
611	14	23072764	23072764	T	A	SNP	*ABHD4*	ENST00000539344	1	3_prime_untranslated_region	c.*23072764	NULL	tier3	86	1	0.011	160	61	0.276
611	14	104216205	104216205	G	A	SNP	*PPP1R13B*	ENST00000202556	-1	missense	c.895	p.R299C	tier1	57	0	0.000	203	67	0.248
611	15	63615709	63615709	A	-	DEL	*CA12*	ENST00000178638	-1	3_prime_untranslated_region	c.*2775	NULL	tier2	45	1	0.022	77	24	0.238
611	15	66008017	66008017	G	A	SNP	*DENND4A*	ENST00000443035	-1	intronic	c.1808-56	e12-56	tier4	34	0	0.000	99	42	0.296
611	16	3071729	3071729	G	A	SNP	*TNFRSF12A*	ENST00000326577	1	intronic	c.334+39	e3+39	tier2	27	0	0.000	76	28	0.269
611	17	3661144	3661144	G	A	SNP	*ITGAE*	ENST00000263087	-1	silent	c.876	p.I292	tier1	56	0	0.000	142	43	0.232
611	17	5077452	5077452	T	C	SNP	*USP6*	ENST00000250066	1	3_prime_untranslated_region	c.*1179	NULL	tier3	76	0	0.000	360	131	0.267
611	17	26087697	26087697	G	T	SNP	*NOS2*	ENST00000313735	-1	missense	c.2962	p.P988T	tier1	160	2	0.012	318	166	0.342
611	17	29553477	29553478	-	C	INS	*NF1*	ENST00000358273	1	frame_shift_ins	c.2026_2027	p.I679fs	tier1	207	0	0.000	653	174	0.210
611	18	42531913	42531913	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2608	p.G870S	tier1	445	4	0.009	798	358	0.310
611	19	39787541	39787541	C	T	SNP	*IFNL1*	ENST00000333625	1	intronic	c.249+19	e2+19	tier3	19	0	0.000	86	35	0.289
611	21	33684165	33684165	A	G	SNP	*MRAP*	ENST00000303645	1	missense	c.377	p.E126G	tier1	30	0	0.000	78	29	0.271
611	22	21480989	21480989	G	C	SNP	*POM121L7*	ENST00000329949	-1	missense	c.937	p.P313A	tier1	49	0	0.000	111	40	0.261
611	22	23922123	23922123	G	A	SNP	*IGLL1*	ENST00000330377	-1	intronic	c.206+49	e1+49	tier2	48	2	0.040	125	75	0.373
611	X	9757836	9757836	C	T	SNP	*SHROOM2*	ENST00000380913	1	intronic	c.165+3086	e1+3086	tier3	98	0	0.000	203	45	0.182
130968	1	6101941	6101941	T	A	SNP	*KCNAB2*	ENST00000164247	1	splice_region	c.119+9	e2+9	tier2	117	9	0.071	176	130	0.425
130968	1	115258747	115258747	C	T	SNP	*NRAS*	ENST00000369535	-1	missense	c.35	p.G12D	tier1	290	0	0.000	656	113	0.141
130968	1	154960473	154960473	C	A	SNP	*FLAD1*	ENST00000492620	1	rna	NULL	NULL	tier1	32	0	0.000	96	22	0.186
130968	1	160144523	160144523	C	T	SNP	*ATP1A4*	ENST00000368081	1	missense	c.2297	p.T766M	tier1	59	0	0.000	75	41	0.350
130968	2	76975737	76975737	G	A	SNP	*LRRTM4*	ENST00000409911	-1	3_prime_untranslated_region	c.*84	NULL	tier3	61	0	0.000	110	32	0.222
130968	2	101554339	101554339	C	T	SNP	*NPAS2*	ENST00000542504	1	intronic	c.558+35	e5+35	tier3	42	0	0.000	113	27	0.193
130968	3	121100282	121100282	C	T	SNP	*STXBP5L*	ENST00000273666	1	silent	c.2562	p.F854	tier1	89	2	0.022	233	38	0.140
130968	3	140281105	140281105	C	T	SNP	*CLSTN2*	ENST00000458420	1	nonsense	c.2167	p.R723*	tier1	55	0	0.000	159	38	0.193
130968	3	141595701	141595701	A	G	SNP	*ATP1B3*	ENST00000286371	1	missense	c.58	p.I20V	tier1	4	0	0.000	5	18	0.783
130968	3	150877579	150877579	A	G	SNP	*MED12L*	ENST00000474524	1	intronic	c.838-40	e7-40	tier3	48	0	0.000	132	21	0.137
130968	4	57389885	57389885	T	G	SNP	*ARL9*	ENST00000360096	1	missense	c.215	p.I72S	tier1	97	2	0.020	153	99	0.391
130968	4	106157023	106157023	C	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.1924	p.Q642*	tier1	413	7	0.017	712	422	0.372
130968	4	106164913	106164913	C	A	SNP	*TET2*	ENST00000380013	1	missense	c.3781	p.R1261S	tier1	214	16	0.070	378	265	0.412
130968	4	187541079	187541079	C	T	SNP	*FAT1*	ENST00000441802	-1	missense	c.6661	p.G2221R	tier1	55	0	0.000	99	28	0.221
130968	6	27840011	27840011	T	A	SNP	*HIST1H3I*	ENST00000328488	-1	missense	c.83	p.K28M	tier1	65	0	0.000	135	25	0.156
130968	6	56366476	56366476	C	T	SNP	*DST*	ENST00000370754	-1	missense	c.19489	p.A6497T	tier1	260	11	0.041	578	402	0.410
130968	6	123869713	123869713	G	A	SNP	*TRDN*	ENST00000398178	-1	missense	c.277	p.R93C	tier1	41	0	0.000	106	19	0.152
130968	7	30692952	30692953	CC	-	DEL	*CRHR2*	ENST00000348438	-1	3_prime_untranslated_region	c.*124	NULL	tier3	26	0	0.000	37	13	0.260
130968	7	30692957	30692965	CTGGAGAGC	-	DEL	*CRHR2*	ENST00000348438	-1	3_prime_untranslated_region	c.*119	NULL	tier3	28	0	0.000	38	13	0.255
130968	7	45140023	45140031	GACCTAGAA	-	DEL	*TBRG4*	ENST00000258770	-1	splice_site_del	c.1795-6_1795-1	e10-1	tier1	49	0	0.000	73	19	0.207
130968	7	135282052	135282052	A	-	DEL	*NUP205*	ENST00000462316	1	3_prime_untranslated_region	c.*135282052	NULL	tier3	49	0	0.000	141	25	0.151
130968	10	126365553	126365553	G	A	SNP	*FAM53B*	ENST00000337318	-1	intronic	c.906+4623	e3+4623	tier3	95	0	0.000	214	21	0.089
130968	11	121384952	121384952	A	G	SNP	*SORL1*	ENST00000260197	1	missense	c.1133	p.E378G	tier1	58	3	0.049	115	60	0.343
130968	12	51752848	51752848	C	T	SNP	*GALNT6*	ENST00000356317	-1	intronic	c.1368+68	e6+68	tier3	40	3	0.070	71	55	0.437
130968	14	99641862	99641862	C	T	SNP	*BCL11B*	ENST00000357195	-1	silent	c.1311	p.K437	tier1	41	1	0.024	71	24	0.253
130968	15	100272161	100272161	G	T	SNP	*LYSMD4*	ENST00000332728	-1	missense	c.44	p.A15D	tier1	83	5	0.057	125	102	0.449
130968	16	71220653	71220653	G	A	SNP	*HYDIN*	ENST00000448089	-1	intronic	c.135+11	e1+11	tier3	357	2	0.006	879	138	0.135
130968	17	7788427	7788427	C	A	SNP	*LSMD1*	ENST00000570555	-1	intronic	c.NULL	NULL	tier2	8	0	0.000	8	13	0.619
130968	17	47006371	47006372	-	T	INS	*UBE2Z*	ENST00000360943	1	3_prime_untranslated_region	c.*1875	NULL	tier2	28	1	0.035	61	27	0.307
130968	17	61790912	61790912	C	T	SNP	*STRADA*	ENST00000336174	-1	intronic	c.227-25	e5-25	tier3	58	0	0.000	179	29	0.139
130968	19	10108048	10108048	G	A	SNP	*COL5A3*	ENST00000264828	-1	missense	c.1262	p.P421L	tier1	152	0	0.000	448	72	0.138
130968	19	33793102	33793103	-	A	INS	*CEBPA*	ENST00000498907	-1	frame_shift_ins	c.219_218	p.N74fs	tier1	466	0	0.000	1259	273	0.178
130968	20	31022288	31022288	C	G	SNP	*ASXL1*	ENST00000375687	1	nonsense	c.1773	p.Y591*	tier1	528	33	0.059	880	633	0.417
130968	21	18821227	18821227	C	T	SNP	*C21orf37*	ENST00000440664	1	3_prime_untranslated_region	c.*1	NULL	tier3	42	1	0.023	58	42	0.416
130968	21	36206702	36206702	C	T	SNP	*RUNX1*	ENST00000469087	-1	5_prime_untranslated_region	c.-36206702	NULL	tier2	682	2	0.003	1546	261	0.144

130968	21	36252865	36252865	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.497	p.R166Q	tier1	743	7	0.009	1885	112	0.056
130968	21	39673268	39673268	C	T	SNP	*KCNJ15*	ENST00000328656	1	3_prime_untranslated_region	c.*957	NULL	tier3	39	1	0.025	43	40	0.482
130968	X	37028271	37028271	G	A	SNP	*FAM47C*	ENST00000358047	1	silent	c.1788	p.P596	tier1	144	1	0.007	218	83	0.276
130968	X	39913253	39913253	G	-	DEL	*BCOR*	ENST00000378444	-1	frame_shift_del	c.4862	p.P1621fs	tier1	267	6	0.022	604	232	0.278
130968	X	107512279	107512279	C	T	SNP	*COL4A6*	ENST00000461897	-1	rna	NULL	NULL	tier1	40	0	0.000	60	32	0.348
130968	X	123197009	123197015	CTCAGTA	-	DEL	*STAG2*	ENST00000218089	1	frame_shift_del	c.1775_1781	p.Q593fs	tier1	84	0	0.000	391	46	0.105
145094	1	16073346	16073346	C	T	SNP	*TMEM82*	ENST00000375782	1	intronic	c.758-16	e5-16	tier3	38	2	0.050	318	275	0.463
145094	1	186084343	186084343	G	A	SNP	*HMCN1*	ENST00000271588	1	intronic	c.11405-47	e75-47	tier3	181	1	0.006	442	331	0.428
145094	1	200880497	200880497	C	T	SNP	*C1orf106*	ENST00000367342	1	intronic	c.1215-84	e9-84	tier2	72	0	0.000	200	149	0.427
145094	1	206945563	206945563	C	G	SNP	*IL10*	ENST00000423557	-1	intronic	c.165+53	e1+53	tier3	44	0	0.000	87	63	0.420
145094	2	116520209	116520209	C	T	SNP	*DPP10*	ENST00000393147	1	intronic	c.1125+23	e12+23	tier3	63	1	0.016	93	84	0.475
145094	2	122004343	122004343	C	G	SNP	*TFCP2L1*	ENST00000263707	-1	intronic	c.657+51	e6+51	tier3	21	0	0.000	80	54	0.403
145094	2	233651863	233651863	G	A	SNP	*GIGYF2*	ENST00000373566	1	missense	c.602	p.R201K	tier1	256	0	0.000	502	463	0.479
145094	4	48563681	48563681	G	C	SNP	*FRYL*	ENST00000358350	-1	intronic	c.3697-28	e30-28	tier3	126	2	0.016	416	358	0.462
145094	4	54880073	54880073	T	C	SNP	*CHIC2*	ENST00000263921	-1	splice_region	c.388-10	e5-10	tier3	95	0	0.000	149	122	0.450
145094	5	98868390	98868390	A	G	SNP	*GUSBP8*	ENST00000502652	1	3_prime_untranslated_region	c.*98868390	NULL	tier3	204	4	0.019	38	24	0.387
145094	6	131211458	131211458	G	A	SNP	*EPB41L2*	ENST00000337057	-1	missense	c.1636	p.R546W	tier1	81	0	0.000	196	154	0.440
145094	7	2962258	2962258	G	A	SNP	*CARD11*	ENST00000396946	-1	splice_region	c.2269+10	e16+10	tier3	20	0	0.000	84	56	0.400
145094	7	128520034	128520034	G	A	SNP	*KCP*	ENST00000297801	-1	5_prime_untranslated_region	c.-128520034	NULL	tier2	30	0	0.000	60	32	0.348
145094	8	30702831	30702831	C	G	SNP	*TEX15*	ENST00000256246	-1	missense	c.3703	p.V1235L	tier1	85	0	0.000	99	70	0.414
145094	8	86573767	86573767	C	T	SNP	*REXO1L1*	ENST00000379010	-1	missense	c.1960	p.V654I	tier1	133	0	0.000	1637	135	0.076
145094	8	134239796	134239796	A	G	SNP	*WISP1*	ENST00000250160	1	missense	c.947	p.K316R	tier1	48	0	0.000	105	91	0.464
145094	9	35079180	35079180	T	G	SNP	*FANCG*	ENST00000378643	-1	missense	c.143	p.E48A	tier1	26	0	0.000	94	84	0.472
145094	9	126029252	126029252	C	-	DEL	*STRBP*	ENST00000348403	-1	intronic	c.1+1463	e0+1463	tier3	38	0	0.000	62	45	0.421
145094	9	131115881	131115881	G	A	SNP	*SLC27A4*	ENST00000300456	1	intronic	c.1324+61	e8+61	tier3	20	0	0.000	102	105	0.507
145094	10	18829133	18829133	G	C	SNP	*CACNB2*	ENST00000324631	1	3_prime_untranslated_region	c.*480	NULL	tier3	88	0	0.000	93	95	0.505
145094	10	75526485	75526485	A	G	SNP	*SEC24C*	ENST00000339365	1	intronic	c.1800-33	e12-33	tier3	78	0	0.000	100	107	0.517
145094	11	12183811	12183811	C	T	SNP	*MICAL2*	ENST00000256194	1	nonsense	c.109	p.R37*	tier1	81	0	0.000	197	165	0.456
145094	12	120638934	120638934	C	G	SNP	*RPLP0*	ENST00000228306	-1	5_prime_untranslated_region	c.-348	NULL	tier2	81	0	0.000	302	302	0.499
145094	15	45266191	45266191	A	G	SNP	*C15orf43*	ENST00000340827	1	intronic	c.523+38	e6+38	tier2	70	0	0.000	118	98	0.454
145094	17	7577120	7577120	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.818	p.R273H	tier1	195	5	0.025	66	803	0.923
145094	17	29552142	29552143	-	G	INS	*NF1*	ENST00000358273	1	frame_shift_ins	c.1875_1876	p.L625fs	tier1	163	0	0.000	91	316	0.776
145094	17	29552143	29552143	C	A	SNP	*NF1*	ENST00000358273	1	missense	c.1876	p.L626I	tier1	163	2	0.012	53	336	0.818
145094	17	45234327	45234327	C	T	SNP	*CDC27*	ENST00000531206	-1	missense	c.794	p.G265D	tier1	126	0	0.000	299	19	0.060
145094	21	44324363	44324363	G	A	SNP	*NDUFV3*	ENST00000354250	1	missense	c.1241	p.G414E	tier1	47	1	0.021	96	77	0.445
145094	X	18845595	18845595	A	T	SNP	*PPEF1*	ENST00000361511	1	missense	c.1952	p.N651I	tier1	61	1	0.016	4	106	0.964
147444	1	34164429	34164429	G	T	SNP	*CSMD2*	ENST00000373381	-1	missense	c.3849	p.S1283R	tier1	80	0	0.000	126	38	0.232
147444	1	38262323	38262323	C	A	SNP	*MANEAL*	ENST00000373045	1	intronic	c.661-93	e3-93	tier3	39	0	0.000	55	19	0.253
147444	1	89480937	89480937	G	A	SNP	*GBP3*	ENST00000370481	-1	intronic	c.318+33	e2+33	tier3	190	0	0.000	225	72	0.242
147444	1	120612014	120612014	C	A	SNP	*NOTCH2*	ENST00000256646	-1	missense	c.7	p.A3S	tier1	41	0	0.000	87	16	0.155
147444	1	163306613	163306613	C	T	SNP	*NUF2*	ENST00000271452	1	missense	c.410	p.T137M	tier1	84	1	0.012	67	17	0.202
147444	1	201016781	201016781	C	T	SNP	*CACNA1S*	ENST00000362061	-1	intronic	c.4442-27	e37-27	tier3	57	0	0.000	70	22	0.239
147444	1	226061960	226061960	G	A	SNP	*TMEM63A*	ENST00000366835	-1	intronic	c.266+28	e2+28	tier3	30	0	0.000	50	17	0.254
147444	2	21229034	21229034	T	-	DEL	*APOB*	ENST00000233242	-1	frame_shift_del	c.10706	p.N3569fs	tier1	776	0	0.000	783	262	0.251
147444	2	42119915	42119915	C	A	SNP	*LOC388942*	ENST00000398796	1	rna	NULL	NULL	tier1	39	0	0.000	45	10	0.182
147444	2	42936013	42936013	G	T	SNP	*MTA3*	ENST00000405094	1	splice_site	c.1303-1	e14-1	tier1	166	0	0.000	151	52	0.256
147444	2	128262356	128262356	T	C	SNP	*IWS1*	ENST00000295321	-1	missense	c.1123	p.M375V	tier1	89	0	0.000	70	29	0.293
147444	2	138000072	138000072	C	T	SNP	*THSD7B*	ENST00000272643	1	silent	c.2196	p.L732	tier1	157	0	0.000	217	77	0.262
147444	2	216972458	216972458	C	G	SNP	*XRCC5*	ENST00000392133	1	intronic	c.1+37	e0+37	tier2	57	0	0.000	70	21	0.231
147444	3	158306755	158306755	A	T	SNP	*MLF1*	ENST00000392822	1	intronic	c.96-3468	e2-3468	tier4	82	0	0.000	54	25	0.317
147444	4	74352793	74352793	A	-	DEL	*AFM*	ENST00000226355	1	frame_shift_del	c.592	p.V199fs	tier1	83	0	0.000	84	35	0.294
147444	4	100761543	100761543	C	A	SNP	*DAPP1*	ENST00000512369	1	missense	c.322	p.H108N	tier1	92	0	0.000	61	12	0.164
147444	4	149358015	149358015	C	T	SNP	*NR3C2*	ENST00000355292	-1	splice_site	c.1-1	e1-1	tier1	63	0	0.000	86	23	0.209
147444	5	1331845	1331845	C	T	SNP	*CLPTM1L*	ENST00000503042	-1	5_prime_untranslated_region	c.-1331845	NULL	tier3	30	0	0.000	42	14	0.246
147444	5	38464253	38464253	C	T	SNP	*EGFLAM*	ENST00000354891	1	3_prime_untranslated_region	c.*165	NULL	tier3	21	0	0.000	30	12	0.286
147444	5	39331903	39331903	C	T	SNP	*C9*	ENST00000263408	-1	missense	c.490	p.G164R	tier1	80	1	0.012	80	33	0.292
147444	6	39841127	39841127	G	A	SNP	*DAAM2*	ENST00000274867	1	missense	c.1158	p.M386I	tier1	34	0	0.000	32	16	0.333
147444	6	72086766	72086766	A	G	SNP	*LINC00472*	ENST00000413945	-1	intronic	c.NULL	NULL	tier3	80	0	0.000	79	15	0.160
147444	6	153603445	153603445	C	T	SNP	*ENSG00000218426*	ENST00000492974	-1	5_prime_untranslated_region	c.-153603445	NULL	tier2	93	0	0.000	87	36	0.293
147444	6	167571516	167571516	G	A	SNP	*GPR31*	ENST00000366834	-1	5_prime_untranslated_region	c.-197	NULL	tier3	92	0	0.000	91	31	0.254
147444	7	57522854	57522854	A	T	SNP	*ZNF716*	ENST00000420713	1	missense	c.242	p.E81V	tier1	144	0	0.000	66	23	0.258
147444	7	100190385	100190385	C	T	SNP	*FBXO24*	ENST00000427939	1	intronic	c.673-21	e5-21	tier3	102	0	0.000	89	62	0.408
147444	7	157650971	157650972	-	CT	INS	*PTPRN2*	ENST00000404321	-1	intronic	c.1857+40393_1857+4039	e12+40393	tier3	52	1	0.019	36	11	0.234
147444	9	33557962	33557962	T	C	SNP	*ANKRD18B*	ENST00000290943	1	intronic	c.2145-94	e12-94	tier3	85	0	0.000	59	14	0.192
147444	9	43628454	43628454	G	A	SNP	*SPATA31A6*	ENST00000332857	-1	intronic	c.309-76	e4-76	tier3	120	0	0.000	135	44	0.246
147444	10	24762962	24762962	C	T	SNP	*KIAA1217*	ENST00000376454	1	missense	c.1652	p.A551V	tier1	63	2	0.031	109	27	0.199
147444	10	46148449	46148449	A	T	SNP	*ZFAND4*	ENST00000344646	-1	nonsense	c.243	p.Y81*	tier1	39	0	0.000	35	10	0.222
147444	11	3687330	3687330	C	T	SNP	*CHRNA10*	ENST00000250699	-1	3_prime_untranslated_region	c.*7	NULL	tier3	30	0	0.000	50	16	0.242
147444	11	64821688	64821688	C	A	SNP	*NAALADL1*	ENST00000358658	-1	intronic	c.992+34	e6+34	tier3	80	0	0.000	84	42	0.333
147444	11	77377600	77377600	C	T	SNP	*RSF1*	ENST00000308488	-1	3_prime_untranslated_region	c.*362	NULL	tier3	106	0	0.000	101	26	0.205
147444	12	57579580	57579580	C	T	SNP	*LRP1*	ENST00000243077	1	missense	c.6730	p.R2244W	tier1	65	0	0.000	66	35	0.343
147444	12	57627594	57627594	G	T	SNP	*SHMT2*	ENST00000328923	1	missense	c.1186	p.A396S	tier1	49	0	0.000	55	17	0.236
147444	12	113444369	113444369	G	A	SNP	*OAS2*	ENST00000342315	1	silent	c.1620	p.K540	tier1	78	0	0.000	86	33	0.277
147444	14	50612016	50612016	C	G	SNP	*SOS2*	ENST00000216373	-1	missense	c.2539	p.V847L	tier1	76	0	0.000	36	16	0.308

147444	16	4384836	4384836	C	T	SNP	*GLIS2*	ENST00000262366	1	missense	c.380	p.P127L	tier1	97	0	0.000	120	35	0.224
147444	16	68721437	68721437	G	A	SNP	*CDH3*	ENST00000264012	1	silent	c.1593	p.T531	tier1	41	0	0.000	45	36	0.444
147444	17	6902088	6902088	T	A	SNP	*ALOX12*	ENST00000251535	1	missense	c.474	p.D158E	tier1	116	0	0.000	147	31	0.174
147444	17	7578212	7578212	G	A	SNP	*TP53*	ENST00000269305	-1	nonsense	c.637	p.R213*	tier1	1150	2	0.002	981	1049	0.515
147444	17	42981590	42981590	C	T	SNP	*FAM187A*	ENST00000331733	1	silent	c.393	p.D131	tier1	39	0	0.000	49	13	0.210
147444	17	67079228	67079228	T	C	SNP	*ABCA6*	ENST00000284425	-1	intronic	c.4476-74	e35-74	tier3	110	0	0.000	93	31	0.250
147444	19	15511862	15511862	A	G	SNP	*AKAP8L*	ENST00000397410	-1	splice_region	c.817-8	e6-8	tier3	41	0	0.000	80	21	0.208
147444	22	29886361	29886361	C	T	SNP	*NEFH*	ENST00000310624	1	missense	c.2732	p.P911L	tier1	39	0	0.000	46	16	0.258
147444	X	49857254	49857254	C	T	SNP	*CLCN5*	ENST00000376088	1	3_prime_untranslated_region	c.*378	NULL	tier3	70	1	0.014	33	15	0.313
147457	1	809179	809179	G	A	SNP	*ENSG00000234711*	ENST00000415481	1	3_prime_untranslated_region	c.*809179	NULL	tier2	69	0	0.000	523	203	0.279
147457	1	1275514	1275514	G	A	SNP	*DVL1*	ENST00000378888	-1	silent	c.813	p.N271	tier1	38	1	0.025	174	77	0.307
147457	1	1861568	1861568	G	A	SNP	*C1orf222*	ENST00000493964	-1	silent	c.1068	p.F356	tier1	35	0	0.000	212	88	0.293
147457	1	6021933	6021933	C	T	SNP	*NPHP4*	ENST00000378156	-1	silent	c.594	p.A198	tier1	29	0	0.000	143	57	0.285
147457	1	6532561	6532561	C	T	SNP	*PLEKHG5*	ENST00000537245	-1	intronic	c.1317+26	e11+26	tier2	23	0	0.000	110	39	0.262
147457	1	9790439	9790439	C	T	SNP	*CLSTN1*	ENST00000477264	-1	5_prime_untranslated_region	c.-9790439	NULL	tier2	35	1	0.028	270	116	0.299
147457	1	12908093	12908093	C	T	SNP	*HNRNPCL1*	ENST00000317869	-1	missense	c.50	p.R17H	tier1	490	1	0.002	1500	165	0.099
147457	1	15701093	15701093	G	A	SNP	*FHAD1*	ENST00000481324	1	missense	c.526	p.A176T	tier1	29	0	0.000	139	55	0.284
147457	1	21605671	21605671	C	T	SNP	*ECE1*	ENST00000374893	-1	intronic	c.280+13	e3+13	tier3	16	0	0.000	215	97	0.311
147457	1	22852716	22852716	G	A	SNP	*ZBTB40*	ENST00000375647	1	missense	c.3547	p.V1183M	tier1	20	0	0.000	195	75	0.278
147457	1	22902834	22902834	G	A	SNP	*EPHA8*	ENST00000166244	1	missense	c.284	p.R95Q	tier1	83	0	0.000	211	64	0.230
147457	1	24385364	24385364	G	A	SNP	*MYOM3*	ENST00000330966	-1	intronic	c.4059+50	e35+50	tier3	109	0	0.000	485	204	0.296
147457	1	24410953	24410953	C	T	SNP	*MYOM3*	ENST00000475306	-1	5_prime_untranslated_region	c.-24410953	NULL	tier3	227	3	0.013	635	306	0.325
147457	1	24671443	24671443	C	T	SNP	*GRHL3*	ENST00000350501	1	intronic	c.1454+22	e12+22	tier3	21	0	0.000	94	42	0.309
147457	1	26773790	26773790	G	A	SNP	*DHDDS*	ENST00000360009	1	intronic	c.441-260	e5-260	tier4	191	5	0.025	142	49	0.257
147457	1	27220835	27220835	G	A	SNP	*GPATCH3*	ENST00000361720	-1	missense	c.943	p.R315W	tier1	60	0	0.000	180	90	0.333
147457	1	27708286	27708286	C	T	SNP	*CD164L2*	ENST00000374030	-1	silent	c.357	p.P119	tier1	49	0	0.000	164	85	0.341
147457	1	29365837	29365837	G	A	SNP	*EPB41*	ENST00000343067	1	missense	c.1535	p.R512Q	tier1	91	0	0.000	271	103	0.275
147457	1	29609283	29609283	C	T	SNP	*PTPRU*	ENST00000345512	1	missense	c.1964	p.A655V	tier1	26	1	0.037	143	75	0.343
147457	1	31186218	31186218	G	A	SNP	*MATN1*	ENST00000373765	-1	3_prime_untranslated_region	c.*211	NULL	tier3	92	1	0.011	219	81	0.270
147457	1	32090677	32090677	G	A	SNP	*HCRTR1*	ENST00000373706	1	missense	c.1045	p.A349T	tier1	23	0	0.000	113	54	0.321
147457	1	37316001	37316001	C	T	SNP	*GRIK3*	ENST00000373091	-1	missense	c.1237	p.G413R	tier1	33	0	0.000	188	71	0.274
147457	1	43618426	43618426	C	T	SNP	*FAM183A*	ENST00000335282	1	intronic	c.194-73	e3-73	tier3	34	2	0.056	115	56	0.328
147457	1	43897426	43897426	C	T	SNP	*SZT2*	ENST00000562955	1	nonsense	c.4957	p.R1653*	tier1	24	0	0.000	107	47	0.305
147457	1	46206734	46206734	C	T	SNP	*IPP*	ENST00000396478	-1	missense	c.563	p.R188Q	tier1	101	0	0.000	175	68	0.280
147457	1	52826134	52826134	C	T	SNP	*CC2D1B*	ENST00000371586	-1	missense	c.565	p.E189K	tier1	20	0	0.000	242	128	0.344
147457	1	54670978	54670978	G	A	SNP	*MRPL37*	ENST00000360840	1	missense	c.541	p.V181M	tier1	41	0	0.000	107	48	0.310
147457	1	57085113	57085113	C	T	SNP	*ENSG00000225475*	ENST00000442812	-1	5_prime_untranslated_region	c.-57085113	NULL	tier3	233	2	0.009	451	206	0.313
147457	1	74905278	74905278	C	T	SNP	*FPGT-TNNI3K*	ENST00000370891	1	silent	c.2286	p.G762	tier1	109	0	0.000	169	76	0.309
147457	1	78031830	78031830	G	A	SNP	*ZZZ3*	ENST00000370801	-1	missense	c.2503	p.R835W	tier1	147	1	0.007	282	133	0.321
147457	1	110217523	110217523	C	T	SNP	*GSTM2*	ENST00000241337	1	3_prime_untranslated_region	c.*65	NULL	tier3	16	0	0.000	149	64	0.301
147457	1	116609238	116609238	C	T	SNP	*SLC22A15*	ENST00000369503	1	missense	c.1463	p.P488L	tier1	132	0	0.000	222	95	0.300
147457	1	149914970	149914970	C	T	SNP	*OTUD7B*	ENST00000369135	-1	3_prime_untranslated_region	c.*786	NULL	tier3	36	0	0.000	100	49	0.329
147457	1	151507600	151507600	G	A	SNP	*CGN*	ENST00000271636	1	missense	c.2987	p.R996Q	tier1	52	0	0.000	133	67	0.333
147457	1	155019719	155019719	C	T	SNP	*DCST1*	ENST00000295542	1	missense	c.1543	p.R515W	tier1	78	1	0.013	288	125	0.303
147457	1	155584452	155584452	C	T	SNP	*MSTO1*	ENST00000245564	1	3_prime_untranslated_region	c.*388	NULL	tier3	48	1	0.020	203	91	0.309
147457	1	156437379	156437379	G	A	SNP	*MEF2D*	ENST00000464356	-1	5_prime_untranslated_region	c.-156437379	NULL	tier3	58	2	0.033	382	175	0.314
147457	1	156713349	156713349	G	A	SNP	*HDGF*	ENST00000477306	-1	5_prime_untranslated_region	c.-156713349	NULL	tier3	24	1	0.040	135	75	0.356
147457	1	160604556	160604556	G	A	SNP	*SLAMF1*	ENST00000302035	-1	missense	c.547	p.H183Y	tier1	53	1	0.019	230	124	0.348
147457	1	162492585	162492585	C	T	SNP	*UHMK1*	ENST00000489294	1	3_prime_untranslated_region	c.*245	NULL	tier3	47	0	0.000	106	47	0.307
147457	1	165182958	165182958	G	A	SNP	*LMX1A*	ENST00000294816	-1	missense	c.589	p.R197C	tier1	120	0	0.000	220	83	0.273
147457	1	171308645	171308645	C	T	SNP	*TOP1P1*	ENST00000404238	1	3_prime_untranslated_region	c.*171308645	NULL	tier3	127	5	0.038	261	121	0.316
147457	1	172410952	172410952	G	A	SNP	*PIGC*	ENST00000258324	-1	missense	c.811	p.R271C	tier1	122	0	0.000	184	77	0.294
147457	1	175014844	175014844	G	A	SNP	*TNN*	ENST00000239462	1	5_prime_flanking_region	c.-31711	NULL	tier2	85	0	0.000	101	54	0.346
147457	1	186010193	186010193	G	A	SNP	*HMCN1*	ENST00000271588	1	missense	c.6229	p.D2077N	tier1	111	3	0.026	374	166	0.307
147457	1	200183198	200183198	C	T	SNP	*FAM58BP*	ENST00000424019	1	3_prime_untranslated_region	c.*200183198	NULL	tier2	34	1	0.029	242	88	0.267
147457	1	201168470	201168470	C	T	SNP	*IGFN1*	ENST00000335211	1	missense	c.376	p.R126W	tier1	40	1	0.024	144	75	0.343
147457	1	201184183	201184183	G	A	SNP	*IGFN1*	ENST00000335211	1	missense	c.8896	p.V2966M	tier1	16	0	0.000	134	56	0.293
147457	1	201983055	201983055	G	A	SNP	*ELF3*	ENST00000359651	1	missense	c.904	p.V302I	tier1	18	0	0.000	113	52	0.313
147457	1	205064086	205064086	C	T	SNP	*RBBP5*	ENST00000264515	-1	silent	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147457	1	213058620	213058620	G	A	SNP	*FLVCR1*	ENST00000366971	1	intronic	c.1093-15	e5-15	tier3	150	1	0.007	217	98	0.311
147457	1	215298011	215298011	G	A	SNP	*KCNK2*	ENST00000444842	1	silent	c.393	p.P131	tier1	103	2	0.019	216	85	0.282
147457	1	220340567	220340567	G	A	SNP	*RAB3GAP2*	ENST00000358951	-1	intronic	c.3087+68	e26+68	tier3	59	1	0.017	67	32	0.323
147457	1	228033658	228033658	G	A	SNP	*PRSS38*	ENST00000366757	1	missense	c.730	p.D244N	tier1	22	0	0.000	70	24	0.255
147457	1	232944031	232944031	G	A	SNP	*KIAA1383*	ENST00000418460	1	3_prime_untranslated_region	c.*118	NULL	tier3	115	0	0.000	187	75	0.286
147457	1	236898908	236898908	G	A	SNP	*ACTN2*	ENST00000366578	1	intronic	c.698-27	e8-27	tier3	48	0	0.000	62	29	0.319
147457	1	244230451	244230451	C	T	SNP	*ENSG00000237759*	ENST00000440148	1	5_prime_flanking_region	c.-40216	NULL	tier3	53	2	0.036	162	66	0.290
147457	2	1271318	1271318	C	T	SNP	*SNTG2*	ENST00000308624	1	missense	c.1259	p.T420M	tier1	48	0	0.000	112	46	0.291
147457	2	1652185	1652185	C	T	SNP	*PXDN*	ENST00000252804	-1	missense	c.3367	p.G1123R	tier1	22	0	0.000	153	69	0.308
147457	2	3469478	3469478	C	T	SNP	*TRAPPC12*	ENST00000416918	1	missense	c.35	p.T12M	tier1	61	0	0.000	126	41	0.246
147457	2	10059126	10059126	G	A	SNP	*TAF1B*	ENST00000263663	1	intronic	c.1272-44	e13-44	tier2	152	3	0.019	204	84	0.292
147457	2	18112379	18112379	G	A	SNP	*KCNS3*	ENST00000304101	1	missense	c.104	p.R35Q	tier1	90	2	0.022	190	80	0.295
147457	2	20845070	20845070	G	A	SNP	*HS1BP3*	ENST00000304031	-1	intronic	c.198+30	e2+30	tier2	16	0	0.000	103	44	0.295
147457	2	24255779	24255779	G	A	SNP	*C2orf44*	ENST00000295148	-1	missense	c.1856	p.A619V	tier1	89	0	0.000	194	72	0.269
147457	2	25457176	25457176	G	A	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.2711	p.P904L	tier1	127	2	0.016	368	188	0.338

147457	2	25466800	25466800	G	A	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.1903	p.R635W	tier1	165	2	0.012	704	291	0.292
147457	2	25469932	25469932	G	A	SNP	*DNMT3A*	ENST00000264709	-1	silent	c.1110	p.Y370	tier1	143	1	0.007	570	249	0.304
147457	2	26177162	26177162	G	A	SNP	*KIF3C*	ENST00000264712	-1	silent	c.1863	p.N621	tier1	25	0	0.000	165	46	0.217
147457	2	26644243	26644243	G	A	SNP	*CCDC164*	ENST00000288710	1	missense	c.331	p.E111K	tier1	120	3	0.024	190	89	0.319
147457	2	26800492	26800492	G	A	SNP	*C2orf70*	ENST00000329615	1	missense	c.457	p.V153I	tier1	28	0	0.000	185	71	0.276
147457	2	27261955	27261955	C	T	SNP	*TMEM214*	ENST00000238788	1	missense	c.1448	p.T483M	tier1	13	0	0.000	145	75	0.339
147457	2	27310227	27310227	C	T	SNP	*KHK*	ENST00000260598	1	splice_region	c.92+8	e1+8	tier2	34	0	0.000	181	60	0.248
147457	2	27592008	27592008	G	A	SNP	*EIF2B4*	ENST00000347454	-1	missense	c.283	p.R95W	tier1	25	0	0.000	83	37	0.308
147457	2	27801023	27801023	G	A	SNP	*C2orf16*	ENST00000408964	1	silent	c.1584	p.T528	tier1	120	0	0.000	263	94	0.263
147457	2	56403145	56403145	C	T	SNP	*LOC100129434*	ENST00000432793	-1	5_prime_untranslated_region	c.-56403145	NULL	tier2	94	2	0.021	157	74	0.320
147457	2	58459235	58459235	G	A	SNP	*FANCL*	ENST00000233741	-1	missense	c.109	p.H37Y	tier1	61	1	0.016	143	63	0.306
147457	2	61331050	61331050	G	A	SNP	*KIAA1841*	ENST00000356719	1	silent	c.1428	p.P476	tier1	97	1	0.010	244	104	0.298
147457	2	70504464	70504464	C	T	SNP	*PCYOX1*	ENST00000433351	1	silent	c.1458	p.N486	tier1	35	1	0.028	95	45	0.321
147457	2	73829499	73829499	C	T	SNP	*ALMS1*	ENST00000264448	1	splice_region	c.12295+4	e20+4	tier2	26	0	0.000	164	65	0.283
147457	2	74173887	74173887	G	A	SNP	*DGUOK*	ENST00000264093	1	missense	c.297	p.M99I	tier1	62	2	0.031	219	83	0.275
147457	2	74867224	74867224	C	T	SNP	*C2orf65*	ENST00000290536	-1	missense	c.179	p.R60H	tier1	58	3	0.049	178	62	0.257
147457	2	75158001	75158001	C	T	SNP	*ENSG00000204792*	ENST00000377469	1	rna	NULL	NULL	tier1	38	0	0.000	83	44	0.347
147457	2	91800800	91800800	G	A	SNP	*ENSG00000233991*	ENST00000443031	1	3_prime_untranslated_region	c.*91800800	NULL	tier2	213	0	0.000	1207	71	0.056
147457	2	98732125	98732125	G	A	SNP	*VWA3B*	ENST00000451075	1	missense	c.8	p.R3H	tier1	96	0	0.000	138	65	0.320
147457	2	99342686	99342686	G	A	SNP	*MGAT4A*	ENST00000495056	-1	5_prime_untranslated_region	c.-99342686	NULL	tier2	121	1	0.008	232	101	0.303
147457	2	120397368	120397368	C	T	SNP	*PCDP1*	ENST00000443972	1	missense	c.821	p.P274L	tier1	106	2	0.018	203	92	0.311
147457	2	131704217	131704217	C	T	SNP	*ARHGEF4*	ENST00000409359	1	missense	c.3004	p.R1002C	tier1	32	0	0.000	168	60	0.263
147457	2	132384417	132384417	G	A	SNP	*POTEKP*	ENST00000397487	1	3_prime_untranslated_region	c.*132384417	NULL	tier3	49	1	0.020	374	145	0.279
147457	2	141459402	141459402	G	A	SNP	*LRP1B*	ENST00000389484	-1	silent	c.6315	p.N2105	tier1	142	0	0.000	385	144	0.272
147457	2	160983105	160983105	G	A	SNP	*ITGB6*	ENST00000283249	-1	silent	c.1668	p.G556	tier1	16	0	0.000	106	46	0.303
147457	2	170134318	170134318	C	T	SNP	*LRP2*	ENST00000263816	-1	missense	c.1709	p.R570H	tier1	94	0	0.000	185	76	0.290
147457	2	179613743	179613743	C	T	SNP	*TTN*	ENST00000360870	-1	missense	c.13384	p.E4462K	tier1	115	1	0.009	171	79	0.316
147457	2	198274685	198274685	C	T	SNP	*SF3B1*	ENST00000335508	-1	missense	c.713	p.R238H	tier1	88	3	0.033	603	239	0.284
147457	2	201619547	201619547	C	T	SNP	*AOX2P*	ENST00000470911	1	3_prime_untranslated_region	c.*201619547	NULL	tier3	128	1	0.008	200	84	0.296
147457	2	203948117	203948117	G	A	SNP	*NBEAL1*	ENST00000449802	1	missense	c.860	p.R287H	tier1	83	0	0.000	199	89	0.309
147457	2	213886807	213886807	G	A	SNP	*IKZF2*	ENST00000434687	-1	missense	c.622	p.R208C	tier1	89	2	0.022	113	53	0.317
147457	2	215798769	215798769	C	T	SNP	*ABCA12*	ENST00000272895	-1	intronic	c.7680+33	e52+33	tier3	52	0	0.000	148	71	0.324
147457	2	216807787	216807787	C	T	SNP	*MREG*	ENST00000423087	-1	3_prime_untranslated_region	c.*1799	NULL	tier3	167	3	0.018	255	105	0.291
147457	2	218938006	218938006	C	T	SNP	*RUFY4*	ENST00000374155	1	missense	c.427	p.R143C	tier1	99	1	0.010	355	138	0.279
147457	2	219538351	219538351	G	A	SNP	*STK36*	ENST00000295709	1	missense	c.88	p.V30M	tier1	62	0	0.000	138	53	0.275
147457	2	219544699	219544699	C	T	SNP	*STK36*	ENST00000295709	1	silent	c.1032	p.L344	tier1	29	0	0.000	119	68	0.364
147457	2	220312930	220312930	C	T	SNP	*SPEG*	ENST00000312358	1	silent	c.1050	p.T350	tier1	179	1	0.006	726	274	0.274
147457	2	226447163	226447163	G	A	SNP	*NYAP2*	ENST00000272907	1	missense	c.1030	p.V344M	tier1	25	0	0.000	98	31	0.223
147457	2	226447731	226447731	G	A	SNP	*NYAP2*	ENST00000272907	1	missense	c.1598	p.R533H	tier1	16	0	0.000	174	96	0.356
147457	2	227872842	227872842	C	T	SNP	*COL4A4*	ENST00000396625	-1	silent	c.4701	p.A1567	tier1	17	0	0.000	219	81	0.270
147457	2	227915822	227915822	G	A	SNP	*COL4A4*	ENST00000396625	-1	silent	c.3021	p.Y1007	tier1	59	1	0.017	169	100	0.372
147457	2	231307770	231307770	G	A	SNP	*SP100*	ENST00000340126	1	missense	c.226	p.E76K	tier1	132	1	0.008	204	92	0.311
147457	2	238245159	238245159	C	T	SNP	*COL6A3*	ENST00000295550	-1	missense	c.8584	p.V2862I	tier1	218	4	0.018	291	115	0.283
147457	2	238461018	238461018	C	T	SNP	*MLPH*	ENST00000264605	1	nonsense	c.1714	p.R572*	tier1	89	0	0.000	194	81	0.295
147457	2	241517127	241517127	C	T	SNP	*RNPEPL1*	ENST00000270357	1	missense	c.1303	p.R435C	tier1	25	0	0.000	297	125	0.296
147457	3	3137142	3137142	C	T	SNP	*IL5RA*	ENST00000256452	-1	intronic	c.710-14	e6-14	tier3	55	0	0.000	105	34	0.245
147457	3	9768381	9768381	C	T	SNP	*CPNE9*	ENST00000273027	1	missense	c.572	p.S191L	tier1	59	0	0.000	144	70	0.326
147457	3	11468460	11468460	C	T	SNP	*ATG7*	ENST00000354449	1	intronic	c.2079+60	e17+60	tier3	128	0	0.000	191	91	0.323
147457	3	11487941	11487941	G	A	SNP	*ATG7*	ENST00000354449	1	intronic	c.2079+19541	e17+19541	tier3	127	0	0.000	202	72	0.263
147457	3	13916529	13916529	G	A	SNP	*WNT7A*	ENST00000285018	-1	silent	c.213	p.D71	tier1	35	0	0.000	94	48	0.338
147457	3	14552987	14552987	G	A	SNP	*GRIP2*	ENST00000273083	-1	5_prime_untranslated_region	c.-14552987	NULL	tier3	28	0	0.000	132	67	0.335
147457	3	14862667	14862667	C	T	SNP	*FGD5*	ENST00000285046	1	missense	c.2089	p.R697W	tier1	81	1	0.012	245	127	0.341
147457	3	16269593	16269593	C	T	SNP	*GALNTL2*	ENST00000339732	1	3_prime_untranslated_region	c.*586	NULL	tier3	60	0	0.000	123	45	0.268
147457	3	24231711	24231711	C	T	SNP	*THRB*	ENST00000356447	-1	missense	c.137	p.R46H	tier1	70	2	0.028	100	44	0.306
147457	3	32811381	32811381	G	A	SNP	*CNOT10*	ENST00000454516	1	silent	c.2187	p.A729	tier1	140	4	0.028	223	101	0.310
147457	3	46450139	46450139	C	T	SNP	*CCRL2*	ENST00000357392	1	missense	c.605	p.P202L	tier1	65	1	0.015	176	61	0.256
147457	3	48266702	48266702	C	T	SNP	*CAMP*	ENST00000296435	1	intronic	c.391-81	e4-81	tier2	70	0	0.000	266	111	0.291
147457	3	48694445	48694445	G	A	SNP	*CELSR3*	ENST00000544264	-1	missense	c.4085	p.A1362V	tier1	136	1	0.007	553	227	0.290
147457	3	49455325	49455325	C	T	SNP	*AMT*	ENST00000273588	-1	missense	c.959	p.R320H	tier1	20	0	0.000	149	60	0.287
147457	3	52559275	52559275	G	A	SNP	*NT5DC2*	ENST00000422318	-1	missense	c.1156	p.R386C	tier1	27	0	0.000	126	40	0.241
147457	3	68781240	68781240	C	T	SNP	*FAM19A4*	ENST00000295569	-1	3_prime_untranslated_region	c.*1053	NULL	tier3	47	0	0.000	88	38	0.302
147457	3	69987598	69987598	C	T	SNP	*MITF*	ENST00000394348	1	3_prime_untranslated_region	c.*69987598	NULL	tier3	133	1	0.008	290	82	0.220
147457	3	70014355	70014355	C	T	SNP	*MITF*	ENST00000448226	1	missense	c.1537	p.R513W	tier1	26	0	0.000	71	25	0.260
147457	3	101050880	101050880	C	T	SNP	*SENP7*	ENST00000394095	-1	missense	c.2647	p.V883I	tier1	163	0	0.000	270	106	0.282
147457	3	101308992	101308992	G	A	SNP	*PCNP*	ENST00000465366	1	3_prime_untranslated_region	c.*101308992	NULL	tier3	123	2	0.016	147	53	0.265
147457	3	112991437	112991437	A	G	SNP	*BOC*	ENST00000273395	1	missense	c.848	p.N283S	tier1	9	0	0.000	80	88	0.524
147457	3	122329604	122329604	G	A	SNP	*PARP15*	ENST00000464300	1	intronic	c.543+27	e3+27	tier3	51	0	0.000	156	53	0.254
147457	3	123044224	123044224	C	T	SNP	*ADCY5*	ENST00000462833	-1	missense	c.2033	p.R678H	tier1	79	0	0.000	433	186	0.300
147457	3	123210530	123210530	G	A	SNP	*PTPLB*	ENST00000383657	-1	3_prime_untranslated_region	c.*3205	NULL	tier2	189	0	0.000	325	134	0.292
147457	3	133193895	133193895	C	A	SNP	*BFSP2*	ENST00000302334	1	3_prime_untranslated_region	c.*79	NULL	tier3	59	0	0.000	96	53	0.353
147457	3	138341122	138341122	C	T	SNP	*FAIM*	ENST00000338446	1	silent	c.306	p.D102	tier1	197	4	0.020	317	133	0.296
147457	3	156431808	156431808	C	T	SNP	*METTL15P1*	ENST00000481421	-1	5_prime_untranslated_region	c.-156431808	NULL	tier3	75	1	0.013	113	51	0.309
147457	3	184289092	184289092	C	T	SNP	*EPHB3*	ENST00000330394	1	intronic	c.119-14	e2-14	tier3	109	1	0.009	227	98	0.302
147457	3	186336256	186336256	G	A	SNP	*AHSG*	ENST00000541510	1	intronic	c.772-69	e6-69	tier3	84	2	0.023	138	68	0.330

147457	3	194081495	194081495	G	A	SNP	*LRRC15*	ENST00000439944	-1	missense	c.296	p.T99M	tier1	22	0	0.000	99	39	0.281
147457	3	195509143	195509143	G	A	SNP	*MUC4*	ENST00000463781	-1	missense	c.9308	p.T3103M	tier1	226	2	0.009	1333	87	0.061
147457	3	196387275	196387275	C	T	SNP	*LRRC33*	ENST00000328557	1	missense	c.761	p.T254M	tier1	17	0	0.000	147	74	0.335
147457	3	196751232	196751232	G	A	SNP	*MFI2*	ENST00000296350	-1	silent	c.429	p.P143	tier1	24	0	0.000	175	81	0.316
147457	4	1332229	1332229	G	A	SNP	*MAEA*	ENST00000303400	1	missense	c.919	p.G307S	tier1	33	0	0.000	274	120	0.305
147457	4	2941321	2941321	G	A	SNP	*NOP14*	ENST00000416614	-1	missense	c.2251	p.R751W	tier1	18	0	0.000	116	57	0.330
147457	4	4317442	4317442	C	T	SNP	*ZBTB49*	ENST00000337872	1	nonsense	c.1456	p.R486*	tier1	73	0	0.000	124	67	0.349
147457	4	8304175	8304175	G	A	SNP	*HTRA3*	ENST00000307358	1	intronic	c.1052-15	e7-15	tier3	30	0	0.000	93	44	0.319
147457	4	9828063	9828063	G	A	SNP	*SLC2A9*	ENST00000264784	-1	silent	c.1581	p.I527	tier1	91	1	0.011	131	54	0.292
147457	4	15691400	15691400	G	A	SNP	*FAM200B*	ENST00000504137	1	3_prime_untranslated_region	c.*15691400	NULL	tier4	99	2	0.020	172	73	0.298
147457	4	17868743	17868743	C	T	SNP	*LCORL*	ENST00000326877	-1	intronic	c.776+18948	e6+18948	tier3	44	0	0.000	103	44	0.299
147457	4	42509034	42509034	G	A	SNP	*ATP8A1*	ENST00000381668	-1	silent	c.2085	p.I695	tier1	135	0	0.000	193	66	0.255
147457	4	44177057	44177057	C	T	SNP	*KCTD8*	ENST00000360029	-1	missense	c.1172	p.R391H	tier1	197	3	0.015	247	91	0.268
147457	4	48165752	48165752	G	A	SNP	*TEC*	ENST00000381501	-1	missense	c.704	p.T235M	tier1	113	3	0.026	238	85	0.262
147457	4	57384937	57384937	G	A	SNP	*ARL9*	ENST00000360096	1	missense	c.302	p.R101Q	tier1	146	0	0.000	233	87	0.271
147457	4	69048233	69048233	C	T	SNP	*FTLP10*	ENST00000503647	1	3_prime_untranslated_region	c.*69048233	NULL	tier3	48	0	0.000	281	115	0.290
147457	4	71099798	71099798	G	A	SNP	*FDCSP*	ENST00000317987	1	missense	c.152	p.R51H	tier1	190	1	0.005	161	55	0.255
147457	4	85758110	85758110	C	T	SNP	*WDFY3*	ENST00000295888	-1	missense	c.548	p.R183Q	tier1	136	3	0.022	255	124	0.326
147457	4	88293939	88293939	G	A	SNP	*HSD17B11*	ENST00000358290	-1	missense	c.479	p.T160M	tier1	195	2	0.010	302	110	0.267
147457	4	119461591	119461591	G	A	SNP	*CEP170P1*	ENST00000412784	1	intronic	c.NULL	NULL	tier3	52	1	0.019	88	48	0.353
147457	4	122846298	122846298	G	A	SNP	*TRPC3*	ENST00000379645	-1	nonsense	c.1051	p.R351*	tier1	74	0	0.000	103	64	0.383
147457	4	162421108	162421108	C	T	SNP	*FSTL5*	ENST00000306100	-1	intronic	c.1458+60	e11+60	tier3	161	0	0.000	184	84	0.313
147457	4	166009582	166009582	C	T	SNP	*TMEM192*	ENST00000306480	-1	intronic	c.574+38	e4+38	tier3	111	2	0.018	184	85	0.316
147457	4	187630302	187630302	C	T	SNP	*FAT1*	ENST00000260147	-1	missense	c.680	p.R227H	tier1	34	0	0.000	104	59	0.362
147457	4	189026057	189026057	C	T	SNP	*TRIML2*	ENST00000512729	-1	silent	c.69	p.S23	tier1	112	0	0.000	127	61	0.323
147457	5	770160	770160	C	T	SNP	*ZDHHC11*	ENST00000424784	-1	intronic	c.1239+25854	e12+25854	tier3	87	0	0.000	705	123	0.148
147457	5	1293693	1293693	C	T	SNP	*TERT*	ENST00000310581	-1	silent	c.1308	p.A436	tier1	126	0	0.000	750	334	0.307
147457	5	1338034	1338034	G	A	SNP	*CLPTM1L*	ENST00000320895	-1	silent	c.663	p.R221	tier1	31	0	0.000	118	45	0.276
147457	5	1483662	1483662	G	A	SNP	*LPCAT1*	ENST00000283415	-1	intronic	c.668-61	e6-61	tier3	48	0	0.000	233	74	0.240
147457	5	5463371	5463371	G	A	SNP	*KIAA0947*	ENST00000296564	1	silent	c.3924	p.T1308	tier1	31	0	0.000	80	31	0.279
147457	5	6602599	6602599	C	T	SNP	*NSUN2*	ENST00000264670	-1	missense	c.1972	p.V658M	tier1	84	3	0.035	162	86	0.347
147457	5	13762777	13762777	C	T	SNP	*DNAH5*	ENST00000265104	-1	intronic	c.10281+54	e60+54	tier3	76	1	0.013	294	135	0.315
147457	5	13931209	13931209	C	T	SNP	*DNAH5*	ENST00000265104	-1	splice_region	c.192+10	e2+10	tier3	223	0	0.000	660	28	0.041
147457	5	31995780	31995780	C	T	SNP	*PDZD2*	ENST00000282493	1	silent	c.1077	p.H359	tier1	77	3	0.038	236	104	0.304
147457	5	34190535	34190535	C	T	SNP	*ENSG00000215156*	ENST00000332686	1	3_prime_untranslated_region	c.*34190535	NULL	tier3	636	6	0.009	4301	196	0.043
147457	5	35910093	35910093	C	T	SNP	*CAPSL*	ENST00000397366	-1	missense	c.400	p.E134K	tier1	155	4	0.025	236	74	0.239
147457	5	41149449	41149449	G	A	SNP	*C6*	ENST00000263413	-1	silent	c.2517	p.D839	tier1	106	2	0.019	133	46	0.257
147457	5	79646877	79646877	C	T	SNP	*CRSP8P*	ENST00000514280	-1	5_prime_untranslated_region	c.-79646877	NULL	tier3	107	1	0.009	498	173	0.257
147457	5	129521471	129521471	G	A	SNP	*CHSY3*	ENST00000305031	1	missense	c.2636	p.R879Q	tier1	28	0	0.000	92	47	0.338
147457	5	140221632	140221632	C	T	SNP	*PCDHA8*	ENST00000531613	1	silent	c.726	p.F242	tier1	316	1	0.003	877	53	0.057
147457	5	140308059	140308059	C	T	SNP	*PCDHAC1*	ENST00000253807	1	missense	c.1582	p.R528W	tier1	57	0	0.000	180	69	0.277
147457	5	140720521	140720521	C	T	SNP	*PCDHGA2*	ENST00000394576	1	silent	c.1983	p.T661	tier1	42	0	0.000	432	199	0.315
147457	5	140751057	140751057	G	A	SNP	*PCDHGB3*	ENST00000576222	1	missense	c.1096	p.V366I	tier1	78	2	0.025	189	70	0.270
147457	5	145610359	145610359	C	T	SNP	*RBM27*	ENST00000265271	1	silent	c.729	p.I243	tier1	93	0	0.000	159	66	0.293
147457	5	146236055	146236055	C	T	SNP	*PPP2R2B*	ENST00000394410	-1	splice_region	c.37+7	e1+7	tier3	110	1	0.009	147	69	0.319
147457	5	147929769	147929769	G	A	SNP	*HTR4*	ENST00000360693	-1	missense	c.83	p.T28M	tier1	69	0	0.000	217	79	0.267
147457	5	149584221	149584221	C	T	SNP	*SLC6A7*	ENST00000230671	1	intronic	c.1432+27	e11+27	tier3	17	0	0.000	142	62	0.304
147457	5	153434852	153434852	C	T	SNP	*MFAP3*	ENST00000436816	1	3_prime_untranslated_region	c.*1579	NULL	tier3	89	0	0.000	119	44	0.270
147457	5	159665575	159665575	G	A	SNP	*FABP6*	ENST00000393980	1	intronic	c.481-38	e6-38	tier3	45	0	0.000	143	49	0.253
147457	5	173534383	173534383	C	T	SNP	*HMP19*	ENST00000303177	1	missense	c.391	p.R131C	tier1	75	2	0.026	253	117	0.316
147457	5	175915965	175915965	G	A	SNP	*FAF2*	ENST00000261942	1	nonsense	c.281	p.W94*	tier1	100	4	0.039	155	52	0.251
147457	5	176308809	176308809	G	A	SNP	*HK3*	ENST00000292432	-1	silent	c.2277	p.I759	tier1	38	0	0.000	172	91	0.346
147457	5	178359183	178359183	G	A	SNP	*ZFP2*	ENST00000361362	1	missense	c.869	p.R290Q	tier1	73	0	0.000	184	71	0.278
147457	6	3127540	3127540	C	T	SNP	*BPHL*	ENST00000380379	1	silent	c.276	p.V92	tier1	78	2	0.025	138	80	0.365
147457	6	25727357	25727357	G	A	SNP	*HIST1H2BA*	ENST00000274764	1	missense	c.221	p.R74H	tier1	39	2	0.049	98	41	0.295
147457	6	27217008	27217008	C	T	SNP	*PRSS16*	ENST00000230582	1	missense	c.467	p.A156V	tier1	54	1	0.018	115	46	0.286
147457	6	31555086	31555086	C	T	SNP	*LST1*	ENST00000396117	1	missense	c.10	p.R4W	tier1	59	0	0.000	173	80	0.314
147457	6	31913016	31913016	G	A	SNP	*C2*	ENST00000299367	1	missense	c.2141	p.R714H	tier1	94	1	0.011	272	126	0.314
147457	6	33554497	33554497	C	T	SNP	*GGNBP1*	ENST00000374458	1	missense	c.148	p.R50C	tier1	28	0	0.000	175	73	0.294
147457	6	33990389	33990389	C	T	SNP	*GRM4*	ENST00000374181	-1	3_prime_untranslated_region	c.*209	NULL	tier3	14	0	0.000	79	44	0.358
147457	6	42985429	42985429	C	T	SNP	*KLHDC3*	ENST00000244670	1	missense	c.41	p.T14M	tier1	58	1	0.017	162	94	0.367
147457	6	52522264	52522264	C	T	SNP	*TMEM14A*	ENST00000211314	1	5_prime_flanking_region	c.-19637	NULL	tier3	35	0	0.000	147	70	0.320
147457	6	55270421	55270421	G	A	SNP	*GFRAL*	ENST00000340465	1	3_prime_flanking_region	c.*3770	NULL	tier3	104	2	0.019	164	102	0.382
147457	6	56919602	56919602	C	T	SNP	*KIAA1586*	ENST00000370733	1	missense	c.2305	p.R769W	tier1	195	6	0.030	301	129	0.300
147457	6	75831004	75831004	G	A	SNP	*COL12A1*	ENST00000322507	-1	intronic	c.7086+14	e43+14	tier3	201	0	0.000	682	28	0.039
147457	6	105726111	105726111	C	T	SNP	*PREP*	ENST00000369110	-1	missense	c.2041	p.G681R	tier1	18	0	0.000	105	41	0.281
147457	6	108985689	108985689	G	A	SNP	*FOXO3*	ENST00000343882	1	silent	c.1653	p.S551	tier1	19	0	0.000	131	70	0.348
147457	6	136709445	136709445	C	T	SNP	*MAP7*	ENST00000454590	-1	intronic	c.592+86	e5+86	tier3	107	0	0.000	198	71	0.263
147457	6	136944051	136944051	G	A	SNP	*MAP3K5*	ENST00000359015	-1	silent	c.2085	p.Y695	tier1	115	0	0.000	246	99	0.285
147457	6	151672062	151672062	G	A	SNP	*AKAP12*	ENST00000253332	1	missense	c.2536	p.V846M	tier1	35	0	0.000	99	27	0.214
147457	6	157527582	157527582	C	T	SNP	*ARID1B*	ENST00000367148	1	silent	c.5427	p.D1809	tier1	32	1	0.030	199	76	0.276
147457	6	157529705	157529705	G	A	SNP	*ARID1B*	ENST00000367148	1	3_prime_untranslated_region	c.*680	NULL	tier3	117	3	0.025	165	60	0.266
147457	6	160481709	160481709	G	A	SNP	*IGF2R*	ENST00000356956	1	silent	c.3222	p.A1074	tier1	141	1	0.007	291	125	0.301
147457	6	170594817	170594817	C	T	SNP	*DLL1*	ENST00000366756	-1	intronic	c.732-30	e6-30	tier3	19	0	0.000	84	38	0.312

147457	7	2474107	2474107	C	T	SNP	*CHST12*	ENST00000258711	1	3_prime_untranslated_region	c.*588	NULL	tier4	56	1	0.018	90	34	0.270
147457	7	6005211	6005211	C	T	SNP	*RSPH10B*	ENST00000337579	-1	intronic	c.330+57	e2+57	tier3	15	0	0.000	59	32	0.352
147457	7	20762660	20762660	G	A	SNP	*ABCB5*	ENST00000258738	1	missense	c.1108	p.V370I	tier1	103	0	0.000	110	51	0.317
147457	7	21906048	21906048	C	T	SNP	*DNAH11*	ENST00000328843	1	intronic	c.11518-40	e72-40	tier3	47	0	0.000	124	39	0.239
147457	7	42005169	42005169	C	T	SNP	*GLI3*	ENST00000395925	-1	missense	c.3502	p.G1168R	tier1	54	1	0.018	334	108	0.244
147457	7	45813153	45813153	C	T	SNP	*ENSG00000212450*	ENST00000391148	1	5_prime_flanking_region	c.-16031	NULL	tier3	879	4	0.005	1789	86	0.046
147457	7	48139220	48139220	C	T	SNP	*UPP1*	ENST00000331803	1	intronic	c.45-47	e2-47	tier3	101	0	0.000	156	49	0.238
147457	7	51454298	51454298	G	A	SNP	*ENSG00000228897*	ENST00000444843	-1	5_prime_untranslated_region	c.-51454298	NULL	tier3	67	1	0.015	812	282	0.257
147457	7	75609676	75609676	C	T	SNP	*POR*	ENST00000461988	1	missense	c.386	p.P129L	tier1	20	0	0.000	110	40	0.265
147457	7	76610187	76610187	G	A	SNP	*ENSG00000186704*	ENST00000425797	1	3_prime_untranslated_region	c.*76610187	NULL	tier3	58	0	0.000	346	137	0.283
147457	7	92855290	92855290	C	T	SNP	*HEPACAM2*	ENST00000394468	-1	intronic	c.79+391	e1+391	tier3	59	0	0.000	69	34	0.330
147457	7	94293941	94293941	G	A	SNP	*PEG10*	ENST00000482108	1	3_prime_untranslated_region	c.*95	NULL	tier3	44	2	0.044	131	49	0.271
147457	7	97872988	97872988	C	T	SNP	*TECPR1*	ENST00000379795	-1	intronic	c.532-84	e4-84	tier3	20	0	0.000	172	60	0.259
147457	7	97920701	97920701	G	A	SNP	*BRI3*	ENST00000297290	1	3_prime_untranslated_region	c.*146	NULL	tier3	39	0	0.000	99	38	0.277
147457	7	98258817	98258817	G	A	SNP	*NPTX2*	ENST00000265634	1	3_prime_untranslated_region	c.*876	NULL	tier3	149	0	0.000	211	73	0.257
147457	7	100730606	100730606	G	A	SNP	*TRIM56*	ENST00000306085	1	missense	c.13	p.G5R	tier1	25	0	0.000	176	70	0.282
147457	7	105662648	105662648	C	T	SNP	*CDHR3*	ENST00000468477	1	missense	c.236	p.T79M	tier1	105	1	0.009	216	90	0.292
147457	7	123594538	123594538	G	A	SNP	*SPAM1*	ENST00000340011	1	missense	c.914	p.R305H	tier1	98	0	0.000	103	43	0.295
147457	7	133894966	133894966	C	T	SNP	*LRGUK*	ENST00000285928	1	intronic	c.1843+8638	e15+8638	tier3	12	0	0.000	126	77	0.379
147457	7	134632353	134632353	C	T	SNP	*CALD1*	ENST00000361388	1	missense	c.940	p.R314C	tier1	46	0	0.000	313	129	0.291
147457	7	138522637	138522637	C	T	SNP	*TMEM213*	ENST00000413208	1	nonsense	c.178	p.R60*	tier1	44	0	0.000	87	61	0.412
147457	7	139801866	139801866	C	T	SNP	*JHDM1D*	ENST00000397560	-1	missense	c.1523	p.R508Q	tier1	202	1	0.005	197	83	0.296
147457	7	140156546	140156546	G	A	SNP	*MKRN1*	ENST00000255977	-1	missense	c.892	p.R298C	tier1	46	0	0.000	134	69	0.340
147457	7	143010124	143010124	C	T	SNP	*HINT1P1*	ENST00000464866	-1	5_prime_untranslated_region	c.-143010124	NULL	tier3	36	0	0.000	79	33	0.295
147457	7	150772740	150772740	G	A	SNP	*SLC4A2*	ENST00000413384	1	missense	c.3349	p.V1117M	tier1	18	0	0.000	125	66	0.346
147457	7	150939682	150939682	C	T	SNP	*SMARCD3*	ENST00000262188	-1	missense	c.464	p.R155Q	tier1	32	0	0.000	150	65	0.302
147457	8	8185940	8185940	G	A	SNP	*SGK223*	ENST00000330777	-1	silent	c.2352	p.S784	tier1	36	0	0.000	154	78	0.336
147457	8	8235576	8235576	G	A	SNP	*SGK223*	ENST00000330777	-1	nonsense	c.343	p.R115*	tier1	153	2	0.013	363	141	0.279
147457	8	10464473	10464473	C	T	SNP	*RP1L1*	ENST00000382483	-1	missense	c.7135	p.G2379R	tier1	36	0	0.000	103	55	0.346
147457	8	11223131	11223131	G	A	SNP	*TDH*	ENST00000525246	1	3_prime_untranslated_region	c.*11223131	NULL	tier3	77	1	0.013	160	72	0.310
147457	8	12232826	12232826	G	A	SNP	*ENSG00000254423*	ENST00000532111	-1	5_prime_untranslated_region	c.-12232826	NULL	tier3	89	1	0.011	587	139	0.192
147457	8	21927047	21927047	G	A	SNP	*EPB49*	ENST00000381455	1	intronic	c.211+18	e3+18	tier3	21	0	0.000	160	75	0.319
147457	8	27094400	27094400	C	T	SNP	*STMN4*	ENST00000350889	-1	missense	c.614	p.R205Q	tier1	41	0	0.000	105	47	0.309
147457	8	32505766	32505766	G	A	SNP	*NRG1*	ENST00000520502	1	missense	c.530	p.R177H	tier1	91	0	0.000	197	92	0.317
147457	8	38109809	38109809	A	C	SNP	*DDHD2*	ENST00000397166	1	splice_region	c.1617+4	e12+4	tier3	121	1	0.008	158	58	0.267
147457	8	41791093	41791093	C	T	SNP	*KAT6A*	ENST00000265713	-1	missense	c.4645	p.G1549S	tier1	33	1	0.029	139	58	0.294
147457	8	48955608	48955608	G	A	SNP	*UBE2V2*	ENST00000523111	1	missense	c.32	p.R11H	tier1	243	1	0.004	282	91	0.244
147457	8	61192308	61192308	G	A	SNP	*CA8*	ENST00000317995	-1	nonsense	c.232	p.R78*	tier1	78	0	0.000	158	57	0.265
147457	8	88249205	88249205	C	T	SNP	*CNBD1*	ENST00000518476	1	silent	c.636	p.N212	tier1	105	2	0.019	158	81	0.339
147457	8	92998437	92998437	G	A	SNP	*RUNX1T1*	ENST00000521751	-1	missense	c.293	p.T98M	tier1	226	0	0.000	684	26	0.037
147457	8	125592809	125592809	G	A	SNP	*MTSS1*	ENST00000325064	-1	splice_region	c.461-6	e7-6	tier3	56	0	0.000	180	92	0.338
147457	8	128753030	128753030	G	A	SNP	*MYC*	ENST00000377970	1	silent	c.1191	p.P397	tier1	50	1	0.020	140	47	0.247
147457	8	130867827	130867827	G	A	SNP	*FAM49B*	ENST00000401979	-1	intronic	c.438+30	e4+30	tier3	94	2	0.021	114	54	0.321
147457	8	143618381	143618381	C	T	SNP	*BAI1*	ENST00000323289	1	missense	c.3604	p.R1202W	tier1	62	0	0.000	548	236	0.300
147457	8	143783019	143783019	C	T	SNP	*LY6K*	ENST00000561179	1	silent	c.279	p.D93	tier1	135	1	0.007	203	76	0.271
147457	8	144620573	144620573	G	A	SNP	*ZC3H3*	ENST00000262577	-1	missense	c.964	p.R322W	tier1	59	0	0.000	206	85	0.292
147457	8	144946163	144946163	C	T	SNP	*EPPK1*	ENST00000525985	-1	missense	c.1259	p.R420H	tier1	75	0	0.000	324	155	0.323
147457	9	368135	368135	G	A	SNP	*DOCK8*	ENST00000453981	1	silent	c.1797	p.P599	tier1	61	0	0.000	191	95	0.331
147457	9	34551979	34551979	G	A	SNP	*CNTFR*	ENST00000351266	-1	3_prime_untranslated_region	c.*90	NULL	tier2	105	1	0.009	312	113	0.265
147457	9	35664015	35664015	G	A	SNP	*C9orf100*	ENST00000378387	-1	missense	c.463	p.R155W	tier1	48	1	0.020	155	77	0.332
147457	9	38577921	38577921	C	T	SNP	*ANKRD18A*	ENST00000399703	-1	silent	c.2472	p.S824	tier1	266	4	0.015	513	229	0.308
147457	9	39176062	39176062	C	T	SNP	*CNTNAP3*	ENST00000297668	-1	missense	c.955	p.G319R	tier1	467	4	0.009	683	36	0.050
147457	9	43709787	43709787	C	T	SNP	*CNTNAP3B*	ENST00000377564	1	intronic	c.196+27	e2+27	tier3	255	5	0.019	628	289	0.315
147457	9	45120270	45120270	G	A	SNP	*ENSG00000231838*	ENST00000417850	1	5_prime_flanking_region	c.-44308	NULL	tier3	30	0	0.000	177	69	0.279
147457	9	66500729	66500729	G	A	SNP	*CDK2AP2P2*	ENST00000478512	1	3_prime_untranslated_region	c.*66500729	NULL	tier3	96	1	0.010	1004	101	0.091
147457	9	78973784	78973784	C	T	SNP	*PCSK5*	ENST00000545128	1	silent	c.5529	p.D1843	tier1	67	1	0.015	185	107	0.365
147457	9	82333659	82333659	G	A	SNP	*TLE4*	ENST00000376520	1	missense	c.1459	p.A487T	tier1	73	2	0.027	169	72	0.299
147457	9	95872991	95872991	C	T	SNP	*C9orf89*	ENST00000466409	1	missense	c.292	p.R98C	tier1	19	0	0.000	224	106	0.320
147457	9	97847849	97847849	G	A	SNP	*C9orf3*	ENST00000375315	1	intronic	c.2460-1115	e16-1115	tier3	43	2	0.044	89	42	0.321
147457	9	99711889	99711889	C	T	SNP	*HIATL2*	ENST00000375223	-1	missense	c.343	p.G115S	tier1	83	3	0.035	229	105	0.313
147457	9	103339628	103339628	G	A	SNP	*TMEFF1*	ENST00000374879	1	3_prime_untranslated_region	c.*746	NULL	tier2	154	1	0.007	237	85	0.263
147457	9	104124794	104124794	G	A	SNP	*BAAT*	ENST00000259407	-1	silent	c.1173	p.H391	tier1	60	0	0.000	107	65	0.376
147457	9	112017768	112017768	G	A	SNP	*EPB41L4B*	ENST00000374566	-1	intronic	c.1169+23	e11+23	tier3	54	0	0.000	154	58	0.271
147457	9	116050499	116050499	C	T	SNP	*PRPF4*	ENST00000374198	1	missense	c.980	p.A327V	tier1	78	0	0.000	160	59	0.269
147457	9	117087344	117087344	C	T	SNP	*ORM1*	ENST00000259396	1	missense	c.452	p.T151M	tier1	31	0	0.000	158	58	0.269
147457	9	117143546	117143546	C	T	SNP	*AKNA*	ENST00000307564	-1	missense	c.68	p.R23H	tier1	60	0	0.000	212	77	0.266
147457	9	123370046	123370046	C	T	SNP	*MEGF9*	ENST00000426959	-1	missense	c.1441	p.D481N	tier1	85	1	0.012	224	79	0.259
147457	9	127572232	127572232	G	A	SNP	*OLFML2A*	ENST00000373580	1	silent	c.1500	p.A500	tier1	21	0	0.000	153	51	0.249
147457	9	131394806	131394806	G	A	SNP	*SPTAN1*	ENST00000358161	1	intronic	c.7013+43	e52+43	tier3	27	0	0.000	80	41	0.339
147457	9	131893899	131893899	G	A	SNP	*PPP2R4*	ENST00000452489	1	silent	c.546	p.T182	tier1	14	0	0.000	98	56	0.364
147457	9	139616703	139616703	C	T	SNP	*FAM69B*	ENST00000371692	1	missense	c.433	p.R145W	tier1	42	0	0.000	378	141	0.272
147457	9	139996817	139996817	G	A	SNP	*MAN1B1*	ENST00000371589	1	intronic	c.1254+693	e8+693	tier3	93	0	0.000	656	60	0.083
147457	9	140807684	140807684	C	T	SNP	*CACNA1B*	ENST00000371355	1	missense	c.583	p.R195C	tier1	152	1	0.007	683	289	0.296
147457	9	140901118	140901118	G	A	SNP	*CACNA1B*	ENST00000371355	1	intronic	c.1978-101	e16-101	tier3	54	1	0.018	261	110	0.296

147457	10	11805425	11805425	C	T	SNP	*ECHDC3*	ENST00000379215	1	missense	c.794	p.T265M	tier1	26	1	0.037	214	118	0.354
147457	10	21827795	21827795	C	T	SNP	*MLLT10*	ENST00000307729	1	missense	c.194	p.P65L	tier1	109	1	0.009	172	70	0.289
147457	10	25890983	25890983	G	A	SNP	*GPR158*	ENST00000376351	1	3_prime_untranslated_region	c.*2780	NULL	tier2	80	0	0.000	123	52	0.294
147457	10	27048066	27048066	G	A	SNP	*ABI1*	ENST00000355394	-1	nonsense	c.1006	p.R336*	tier1	125	2	0.016	189	75	0.284
147457	10	28023604	28023604	G	A	SNP	*MKX*	ENST00000375790	-1	missense	c.619	p.R207W	tier1	104	1	0.010	225	78	0.257
147457	10	29773728	29773728	G	A	SNP	*SVIL*	ENST00000355867	-1	silent	c.4812	p.Y1604	tier1	202	2	0.010	287	114	0.284
147457	10	29813480	29813480	C	T	SNP	*SVIL*	ENST00000355867	-1	missense	c.2507	p.R836Q	tier1	117	4	0.033	173	71	0.290
147457	10	30654823	30654823	C	T	SNP	*ENSG00000241621*	ENST00000340929	-1	5_prime_untranslated_region	c.-30654823	NULL	tier3	96	0	0.000	546	236	0.302
147457	10	34671634	34671634	C	T	SNP	*PARD3*	ENST00000374789	-1	silent	c.1233	p.P411	tier1	142	0	0.000	132	69	0.342
147457	10	46210567	46210567	G	A	SNP	*ENSG00000237840*	ENST00000426241	-1	intronic	c.NULL	NULL	tier3	296	2	0.007	713	211	0.228
147457	10	47747160	47747160	G	A	SNP	*ENSG00000244599*	ENST00000445847	1	3_prime_untranslated_region	c.*47747160	NULL	tier3	68	1	0.015	210	90	0.300
147457	10	64967543	64967543	C	T	SNP	*JMJD1C*	ENST00000399262	-1	missense	c.3886	p.G1296R	tier1	79	0	0.000	127	52	0.291
147457	10	86004953	86004953	C	T	SNP	*RGR*	ENST00000359452	1	intronic	c.79+28	e1+28	tier3	11	0	0.000	84	56	0.397
147457	10	87379729	87379729	G	A	SNP	*GRID1*	ENST00000327946	-1	missense	c.2255	p.T752M	tier1	188	3	0.016	648	297	0.314
147457	10	87482902	87482902	C	T	SNP	*GRID1*	ENST00000327946	-1	splice_region	c.1859-4	e12-4	tier2	44	0	0.000	203	98	0.325
147457	10	87966282	87966282	G	A	SNP	*GRID1*	ENST00000327946	-1	missense	c.359	p.P120L	tier1	134	1	0.007	510	257	0.335
147457	10	99019280	99019280	C	T	SNP	*ARHGAP19*	ENST00000453547	-1	missense	c.719	p.R240H	tier1	133	0	0.000	235	116	0.331
147457	10	100022513	100022513	G	A	SNP	*LOXL4*	ENST00000260702	-1	silent	c.264	p.Y88	tier1	38	0	0.000	280	121	0.302
147457	10	103870964	103870964	G	A	SNP	*LDB1*	ENST00000425280	-1	intronic	c.173+49	e3+49	tier3	81	3	0.036	144	62	0.300
147457	10	104245343	104245343	C	T	SNP	*ACTR1A*	ENST00000369905	-1	intronic	c.440+23	e5+23	tier3	59	1	0.017	197	73	0.269
147457	10	104628872	104628872	C	T	SNP	*C10orf32*	ENST00000299353	1	intronic	c.321-690	e6-690	tier4	80	2	0.024	100	27	0.213
147457	10	106160477	106160477	C	T	SNP	*CCDC147*	ENST00000369704	1	missense	c.1855	p.R619W	tier1	56	0	0.000	121	59	0.326
147457	10	116008560	116008560	C	T	SNP	*VWA2*	ENST00000392982	1	intronic	c.52+36	e1+36	tier3	140	1	0.007	167	82	0.329
147457	10	118969094	118969094	G	A	SNP	*KCNK18*	ENST00000334549	1	missense	c.439	p.V147I	tier1	90	1	0.011	165	70	0.298
147457	10	123976222	123976222	G	A	SNP	*TACC2*	ENST00000334433	1	silent	c.7425	p.A2475	tier1	31	0	0.000	156	66	0.297
147457	10	124402685	124402685	G	A	SNP	*DMBT1*	ENST00000368915	1	missense	c.7400	p.R2467H	tier1	64	0	0.000	245	86	0.259
147457	10	135011989	135011989	C	T	SNP	*KNDC1*	ENST00000368572	1	silent	c.2055	p.N685	tier1	20	0	0.000	367	142	0.278
147457	11	1215595	1215595	G	A	SNP	*MUC5AC*	ENST00000358378	1	splice_region	c.NULL	NULL	tier2	13	0	0.000	205	106	0.339
147457	11	1316941	1316941	C	T	SNP	*TOLLIP*	ENST00000317204	-1	silent	c.117	p.A39	tier1	21	0	0.000	264	104	0.282
147457	11	1997630	1997630	C	T	SNP	*MRPL23*	ENST00000397297	1	intronic	c.497+3642	e5+3642	tier3	77	3	0.038	708	273	0.277
147457	11	6048700	6048700	C	T	SNP	*OR56A1*	ENST00000316650	-1	missense	c.235	p.V79M	tier1	49	0	0.000	301	134	0.307
147457	11	6232207	6232207	G	A	SNP	*C11orf42*	ENST00000316375	1	missense	c.937	p.D313N	tier1	36	1	0.027	199	95	0.323
147457	11	10500213	10500213	C	T	SNP	*AMPD3*	ENST00000396553	1	missense	c.362	p.T121M	tier1	34	0	0.000	131	87	0.399
147457	11	16036588	16036588	C	T	SNP	*SOX6*	ENST00000352083	-1	silent	c.1632	p.T544	tier1	152	3	0.019	154	60	0.280
147457	11	16823374	16823374	G	A	SNP	*PLEKHA7*	ENST00000448080	-1	splice_region	c.2158-10	e16-10	tier3	29	0	0.000	156	50	0.243
147457	11	17659970	17659970	C	T	SNP	*OTOG*	ENST00000399391	1	intronic	c.7832-28	e47-28	tier3	25	0	0.000	90	41	0.313
147457	11	17801160	17801160	C	T	SNP	*KCNC1*	ENST00000265969	1	silent	c.1662	p.Y554	tier1	37	0	0.000	216	84	0.280
147457	11	26558879	26558879	G	A	SNP	*ANO3*	ENST00000256737	1	intronic	c.977-74	e10-74	tier3	103	3	0.028	130	62	0.323
147457	11	43515299	43515299	C	T	SNP	*TTC17*	ENST00000039989	1	intronic	c.3295-24	e24-24	tier3	87	3	0.033	185	71	0.277
147457	11	44253924	44253924	C	T	SNP	*EXT2*	ENST00000395673	1	missense	c.1783	p.R595W	tier1	77	3	0.038	182	75	0.292
147457	11	45877647	45877647	C	T	SNP	*CRY2*	ENST00000496571	1	3_prime_untranslated_region	c.*45877647	NULL	tier3	42	1	0.023	139	85	0.380
147457	11	45950277	45950277	C	T	SNP	*GYLTL1B*	ENST00000325468	1	missense	c.2047	p.R683C	tier1	45	2	0.043	301	103	0.255
147457	11	46741344	46741344	C	T	SNP	*F2*	ENST00000311907	1	nonsense	c.172	p.R58*	tier1	47	2	0.041	243	145	0.374
147457	11	46819420	46819420	G	A	SNP	*CKAP5*	ENST00000415402	-1	missense	c.1273	p.R425C	tier1	174	1	0.006	218	77	0.260
147457	11	49897778	49897778	C	A	SNP	*OR4R3P*	ENST00000525084	1	5_prime_flanking_region	c.-46823	NULL	tier3	251	3	0.012	424	188	0.307
147457	11	55322719	55322719	C	T	SNP	*OR4C15*	ENST00000314644	1	nonsense	c.937	p.R313*	tier1	100	2	0.020	139	69	0.330
147457	11	55761663	55761663	C	T	SNP	*OR5F1*	ENST00000278409	-1	missense	c.439	p.G147R	tier1	48	0	0.000	158	74	0.319
147457	11	55839272	55839272	G	A	SNP	*OR5J1P*	ENST00000313544	1	3_prime_untranslated_region	c.*55839272	NULL	tier3	23	0	0.000	56	23	0.291
147457	11	59623312	59623312	G	A	SNP	*TCN1*	ENST00000257264	-1	intronic	c.937+30	e6+30	tier3	67	0	0.000	112	38	0.253
147457	11	61295431	61295431	C	T	SNP	*SYT7*	ENST00000263846	-1	missense	c.578	p.R193Q	tier1	60	0	0.000	151	66	0.301
147457	11	62571274	62571274	G	A	SNP	*NXF1*	ENST00000294172	-1	nonsense	c.205	p.R69*	tier1	37	0	0.000	97	41	0.297
147457	11	62751103	62751103	G	A	SNP	*SLC22A6*	ENST00000540654	-1	missense	c.511	p.R171C	tier1	19	0	0.000	199	102	0.338
147457	11	64882321	64882321	C	T	SNP	*TM7SF2*	ENST00000528026	1	3_prime_untranslated_region	c.*64882321	NULL	tier3	24	0	0.000	153	55	0.264
147457	11	64882420	64882420	C	T	SNP	*TM7SF2*	ENST00000528802	1	missense	c.242	p.T81M	tier1	20	0	0.000	128	43	0.252
147457	11	65305479	65305479	C	T	SNP	*SCYL1*	ENST00000533862	1	missense	c.2036	p.P679L	tier1	15	0	0.000	97	55	0.362
147457	11	65427692	65427692	C	T	SNP	*RELA*	ENST00000526738	-1	5_prime_untranslated_region	c.-65427692	NULL	tier3	35	0	0.000	141	49	0.258
147457	11	66103134	66103134	C	T	SNP	*RIN1*	ENST00000530745	-1	missense	c.221	p.R74Q	tier1	31	0	0.000	208	77	0.269
147457	11	66633819	66633819	C	T	SNP	*PC*	ENST00000393958	-1	missense	c.1024	p.V342I	tier1	37	0	0.000	319	115	0.263
147457	11	67209188	67209188	G	A	SNP	*CORO1B*	ENST00000545016	-1	missense	c.470	p.P157L	tier1	22	0	0.000	142	53	0.270
147457	11	67795455	67795455	C	T	SNP	*ALDH3B1*	ENST00000007633	1	3_prime_untranslated_region	c.*67795455	NULL	tier3	36	2	0.053	356	166	0.317
147457	11	68701368	68701368	G	A	SNP	*IGHMBP2*	ENST00000255078	1	silent	c.1524	p.S508	tier1	84	1	0.012	296	154	0.342
147457	11	68822767	68822767	G	A	SNP	*TPCN2*	ENST00000294309	1	missense	c.376	p.E126K	tier1	32	0	0.000	98	39	0.285
147457	11	72540399	72540399	C	T	SNP	*ATG16L2*	ENST00000540222	1	missense	c.1156	p.R386C	tier1	28	1	0.035	316	147	0.314
147457	11	74559446	74559446	G	A	SNP	*XRRA1*	ENST00000340360	-1	missense	c.1418	p.T473M	tier1	28	0	0.000	70	33	0.320
147457	11	78565287	78565287	G	A	SNP	*ODZ4*	ENST00000278550	-1	missense	c.1543	p.R515C	tier1	76	3	0.038	257	104	0.288
147457	11	99827584	99827584	G	A	SNP	*CNTN5*	ENST00000279463	1	silent	c.720	p.A240	tier1	245	4	0.016	575	250	0.303
147457	11	104872776	104872776	G	A	SNP	*CASP5*	ENST00000393141	-1	silent	c.735	p.D245	tier1	73	0	0.000	157	63	0.286
147457	11	106558472	106558472	G	A	SNP	*GUCY1A2*	ENST00000282249	-1	nonsense	c.2095	p.R699*	tier1	52	0	0.000	123	56	0.313
147457	11	111167571	111167571	C	T	SNP	*C11orf92*	ENST00000355430	-1	5_prime_untranslated_region	c.-368	NULL	tier3	27	0	0.000	158	45	0.222
147457	11	111228370	111228370	C	T	SNP	*POU2AF1*	ENST00000393067	-1	missense	c.256	p.G86S	tier1	12	0	0.000	121	72	0.373
147457	11	118362528	118362528	G	A	SNP	*MLL*	ENST00000389506	1	missense	c.4880	p.R1627Q	tier1	67	0	0.000	136	57	0.294
147457	11	122722537	122722537	G	A	SNP	*CRTAM*	ENST00000227348	1	silent	c.330	p.V110	tier1	65	1	0.015	181	79	0.304
147457	11	122828004	122828004	G	A	SNP	*C11orf63*	ENST00000227349	1	intronic	c.2011-67	e7-67	tier3	90	2	0.022	167	58	0.258
147457	11	122978373	122978373	G	A	SNP	*CLMP*	ENST00000448775	-1	intronic	c.29-9713	e2-9713	tier3	73	0	0.000	96	47	0.329

147457	11	123909293	123909293	G	A	SNP	*OR10G7*	ENST00000330487	-1	missense	c.416	p.S139L	tier1	68	0	0.000	204	117	0.363
147457	12	3390547	3390547	C	T	SNP	*TSPAN9*	ENST00000011898	1	intronic	c.564+52	e5+52	tier2	19	0	0.000	183	66	0.264
147457	12	4722773	4722773	G	A	SNP	*DYRK4*	ENST00000010132	1	missense	c.1417	p.G473R	tier1	67	2	0.029	169	82	0.323
147457	12	5154521	5154521	G	A	SNP	*KCNA5*	ENST00000252321	1	missense	c.1208	p.R403H	tier1	43	0	0.000	112	54	0.325
147457	12	7125761	7125761	G	T	SNP	*LPCAT3*	ENST00000261407	-1	5_prime_untranslated_region	c.-33	NULL	tier2	28	0	0.000	205	80	0.281
147457	12	7922788	7922788	C	T	SNP	*NANOGNB*	ENST00000382119	1	silent	c.312	p.P104	tier1	90	0	0.000	193	80	0.292
147457	12	10659128	10659128	G	A	SNP	*ENSG00000180574*	ENST00000538173	1	silent	c.627	p.A209	tier1	224	3	0.013	295	128	0.303
147457	12	16713647	16713647	G	A	SNP	*LMO3*	ENST00000541295	-1	intronic	c.261-175	e3-175	tier2	45	0	0.000	123	70	0.363
147457	12	18644489	18644489	C	T	SNP	*PIK3C2G*	ENST00000538779	1	silent	c.2790	p.H930	tier1	74	0	0.000	137	60	0.303
147457	12	31135422	31135422	C	T	SNP	*TSPAN11*	ENST00000261177	1	intronic	c.457-45	e5-45	tier2	69	1	0.014	216	85	0.282
147457	12	40758824	40758824	G	A	SNP	*LRRK2*	ENST00000298910	1	silent	c.7362	p.S2454	tier1	185	2	0.011	172	87	0.336
147457	12	40820395	40820395	C	T	SNP	*MUC19*	ENST00000425730	1	nonsense	c.1060	p.R354*	tier1	93	0	0.000	183	78	0.299
147457	12	41337805	41337805	C	T	SNP	*CNTN1*	ENST00000347616	1	nonsense	c.1516	p.R506*	tier1	45	0	0.000	30	23	0.434
147457	12	47630017	47630017	C	T	SNP	*FAM113B*	ENST00000432328	1	missense	c.1171	p.R391W	tier1	29	0	0.000	85	38	0.309
147457	12	48723716	48723716	C	T	SNP	*H1FNT*	ENST00000335017	1	silent	c.642	p.D214	tier1	15	0	0.000	204	119	0.368
147457	12	49719830	49719830	C	T	SNP	*TROAP*	ENST00000257909	1	intronic	c.634-29	e5-29	tier3	112	1	0.009	241	74	0.235
147457	12	56607793	56607793	G	A	SNP	*RNF41*	ENST00000345093	-1	silent	c.39	p.D13	tier1	47	0	0.000	174	59	0.252
147457	12	65230315	65230315	G	A	SNP	*TBC1D30*	ENST00000229088	1	missense	c.1129	p.V377I	tier1	133	1	0.007	152	77	0.336
147457	12	111345179	111345179	G	A	SNP	*CCDC63*	ENST00000308208	1	missense	c.1591	p.D531N	tier1	18	0	0.000	109	44	0.288
147457	12	117653072	117653072	C	T	SNP	*NOS1*	ENST00000317775	-1	3_prime_untranslated_region	c.*42	NULL	tier3	48	0	0.000	205	91	0.307
147457	12	119583293	119583293	G	A	SNP	*SRRM4*	ENST00000267260	1	silent	c.879	p.S293	tier1	30	1	0.032	150	98	0.392
147457	12	123001856	123001856	G	A	SNP	*RSRC2*	ENST00000331738	-1	missense	c.520	p.R174W	tier1	141	1	0.007	215	112	0.342
147457	12	123201344	123201344	G	A	SNP	*HCAR3*	ENST00000528880	-1	5_prime_untranslated_region	c.-60	NULL	tier3	55	1	0.018	174	55	0.240
147457	12	124175149	124175149	G	A	SNP	*TCTN2*	ENST00000303372	1	missense	c.961	p.V321I	tier1	86	1	0.012	150	66	0.306
147457	12	124422048	124422048	C	T	SNP	*CCDC92*	ENST00000238156	-1	missense	c.553	p.V185M	tier1	19	0	0.000	100	58	0.367
147457	12	131498748	131498748	G	A	SNP	*GPR133*	ENST00000261654	1	missense	c.1336	p.A446T	tier1	36	1	0.027	98	44	0.310
147457	12	133181273	133181273	G	A	SNP	*ENSG00000204583*	ENST00000376608	-1	intronic	c.NULL	NULL	tier2	14	0	0.000	123	62	0.330
147457	13	21562125	21562125	C	T	SNP	*LATS2*	ENST00000382592	-1	silent	c.1794	p.S598	tier1	204	2	0.010	278	143	0.339
147457	13	23928871	23928871	G	A	SNP	*SACS*	ENST00000382292	-1	missense	c.1880	p.T627M	tier1	28	0	0.000	81	44	0.349
147457	13	24410420	24410420	G	A	SNP	*MIPEP*	ENST00000382172	-1	nonsense	c.1612	p.R538*	tier1	136	4	0.029	205	104	0.337
147457	13	28133957	28133957	A	-	DEL	*LNX2*	ENST00000316334	-1	intronic	c.1368+22	e5+22	tier2	49	0	0.000	142	30	0.174
147457	13	39450219	39450219	G	A	SNP	*FREM2*	ENST00000280481	1	missense	c.8342	p.R2781H	tier1	144	0	0.000	447	175	0.280
147457	13	45857726	45857726	C	T	SNP	*GTF2F2*	ENST00000340473	1	3_prime_untranslated_region	c.*30	NULL	tier3	21	0	0.000	86	29	0.250
147457	13	58299227	58299227	C	T	SNP	*PCDH17*	ENST00000377918	1	silent	c.3279	p.S1093	tier1	50	0	0.000	116	76	0.396
147457	13	95118904	95118904	G	A	SNP	*DCT*	ENST00000446125	-1	missense	c.604	p.R202C	tier1	60	1	0.016	168	58	0.257
147457	13	111329450	111329450	G	A	SNP	*CARS2*	ENST00000257347	-1	missense	c.656	p.A219V	tier1	39	0	0.000	196	75	0.274
147457	13	113838700	113838700	G	A	SNP	*PCID2*	ENST00000246505	-1	silent	c.807	p.Y269	tier1	164	4	0.024	214	91	0.298
147457	14	21552150	21552150	C	T	SNP	*ARHGEF40*	ENST00000298694	1	missense	c.3730	p.R1244W	tier1	35	0	0.000	416	179	0.301
147457	14	21861926	21861926	C	T	SNP	*CHD8*	ENST00000399982	-1	missense	c.6028	p.E2010K	tier1	30	0	0.000	138	73	0.346
147457	14	38261600	38261600	G	A	SNP	*TTC6*	ENST00000553443	1	missense	c.3689	p.R1230Q	tier1	140	2	0.014	229	71	0.237
147457	14	45664649	45664649	G	A	SNP	*FANCM*	ENST00000267430	1	intronic	c.5341-726	e21-726	tier3	47	0	0.000	80	31	0.279
147457	14	52471285	52471285	C	T	SNP	*C14orf166*	ENST00000261700	1	3_prime_untranslated_region	c.*51	NULL	tier3	76	0	0.000	132	66	0.333
147457	14	57713531	57713531	C	T	SNP	*EXOC5*	ENST00000413566	-1	missense	c.168	p.M56I	tier1	89	1	0.011	137	51	0.271
147457	14	68047847	68047847	G	A	SNP	*PLEKHH1*	ENST00000329153	1	intronic	c.3284+92	e22+92	tier3	42	0	0.000	233	92	0.283
147457	14	76259462	76259462	G	A	SNP	*TTLL5*	ENST00000298832	1	intronic	c.3171+19	e26+19	tier3	19	0	0.000	80	51	0.389
147457	14	91211188	91211188	C	T	SNP	*TTC7B*	ENST00000357056	-1	missense	c.524	p.C175Y	tier1	71	1	0.014	171	77	0.308
147457	14	91700696	91700696	G	A	SNP	*GPR68*	ENST00000238699	-1	silent	c.729	p.T243	tier1	32	1	0.030	250	118	0.320
147457	14	92136153	92136153	C	T	SNP	*CATSPERB*	ENST00000256343	-1	splice_region	c.1287+5	e13+5	tier3	92	0	0.000	142	63	0.304
147457	14	93681299	93681299	G	A	SNP	*UBR7*	ENST00000013070	1	missense	c.466	p.V156I	tier1	104	3	0.028	181	81	0.309
147457	14	93706769	93706769	G	A	SNP	*BTBD7*	ENST00000334746	-1	3_prime_untranslated_region	c.*1850	NULL	tier2	152	1	0.007	290	24	0.076
147457	14	102801015	102801015	G	A	SNP	*ZNF839*	ENST00000442396	1	intronic	c.1509+32	e4+32	tier3	124	1	0.008	185	59	0.241
147457	14	105419206	105419206	G	A	SNP	*AHNAK2*	ENST00000333244	-1	missense	c.2582	p.P861L	tier1	160	1	0.006	778	202	0.206
147457	15	23313159	23313159	G	A	SNP	*HERC2P2*	ENST00000560464	-1	5_prime_untranslated_region	c.-23313159	NULL	tier2	81	2	0.024	386	186	0.325
147457	15	23606950	23606950	C	T	SNP	*ENSG00000261739*	ENST00000562295	1	intronic	c.1179+11	e13+11	tier2	45	0	0.000	283	132	0.317
147457	15	25349836	25349836	C	T	SNP	*SNORD116-28*	ENST00000516123	1	rna	NULL	NULL	tier1	115	0	0.000	218	102	0.319
147457	15	28517461	28517461	C	T	SNP	*HERC2*	ENST00000261609	-1	missense	c.983	p.R328H	tier1	160	1	0.006	819	61	0.069
147457	15	33358756	33358756	G	A	SNP	*FMN1*	ENST00000334528	-1	missense	c.1330	p.R444W	tier1	59	0	0.000	144	61	0.298
147457	15	33936693	33936693	C	T	SNP	*RYR3*	ENST00000389232	1	silent	c.3738	p.N1246	tier1	145	2	0.014	481	250	0.341
147457	15	40099429	40099429	C	T	SNP	*GPR176*	ENST00000561100	-1	missense	c.203	p.R68H	tier1	78	0	0.000	232	82	0.261
147457	15	40532849	40532849	C	T	SNP	*ENSG00000259288*	ENST00000558658	1	missense	c.131	p.T44M	tier1	26	0	0.000	308	135	0.304
147457	15	40583762	40583762	C	T	SNP	*PLCB2*	ENST00000558588	-1	3_prime_untranslated_region	c.*205	NULL	tier2	16	0	0.000	63	39	0.382
147457	15	40993282	40993282	C	T	SNP	*RAD51*	ENST00000382643	1	silent	c.108	p.N36	tier1	96	5	0.050	176	64	0.267
147457	15	44673070	44673070	G	A	SNP	*CASC4*	ENST00000299957	1	missense	c.968	p.R323H	tier1	208	3	0.014	298	109	0.268
147457	15	52622645	52622645	C	T	SNP	*MYO5A*	ENST00000358212	-1	missense	c.4460	p.R1487Q	tier1	146	0	0.000	252	77	0.234
147457	15	63964722	63964722	G	A	SNP	*HERC1*	ENST00000443617	-1	missense	c.8018	p.P2673L	tier1	48	0	0.000	157	66	0.296
147457	15	64218300	64218300	C	T	SNP	*DAPK2*	ENST00000557867	-1	5_prime_untranslated_region	c.-64218300	NULL	tier2	28	0	0.000	67	28	0.295
147457	15	66181422	66181422	C	T	SNP	*RAB11A*	ENST00000261890	1	3_prime_untranslated_region	c.*1244	NULL	tier3	72	0	0.000	91	35	0.273
147457	15	68480403	68480403	A	-	DEL	*PIAS1*	ENST00000563996	1	3_prime_untranslated_region	c.*474	NULL	tier4	22	0	0.000	47	24	0.338
147457	15	68603671	68603671	C	T	SNP	*ITGA11*	ENST00000315757	-1	missense	c.3044	p.S1015N	tier1	33	0	0.000	169	74	0.305
147457	15	68608000	68608000	G	A	SNP	*ITGA11*	ENST00000315757	-1	silent	c.2781	p.L927	tier1	32	0	0.000	163	51	0.237
147457	15	72454738	72454738	G	A	SNP	*GRAMD2*	ENST00000309731	-1	intronic	c.957-20	e11-20	tier3	17	0	0.000	110	56	0.337
147457	15	73889591	73889591	G	A	SNP	*NPTN*	ENST00000345330	-1	missense	c.211	p.R71W	tier1	30	0	0.000	118	35	0.229
147457	15	79069906	79069906	G	A	SNP	*ADAMTS7*	ENST00000388820	-1	silent	c.1347	p.D449	tier1	43	1	0.023	301	139	0.315
147457	15	79339147	79339147	G	A	SNP	*RASGRF1*	ENST00000419573	-1	silent	c.819	p.A273	tier1	15	0	0.000	60	30	0.333

147457	15	83931848	83931848	G	A	SNP	*BNC1*	ENST00000345382	-1	missense	c.2155	p.R719C	tier1	58	1	0.017	128	54	0.297
147457	15	85805937	85805937	C	T	SNP	*ENSG00000218052*	ENST00000561209	-1	5_prime_untranslated_region	c.-85805937	NULL	tier3	30	1	0.032	269	131	0.328
147457	15	90192982	90192982	G	A	SNP	*KIF7*	ENST00000394412	-1	silent	c.519	p.R173	tier1	18	0	0.000	62	43	0.410
147457	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	173	1	0.006	705	334	0.321
147457	15	91577490	91577490	G	A	SNP	*ENSG00000214432*	ENST00000557804	1	intronic	c.NULL	NULL	tier3	84	0	0.000	322	152	0.321
147457	15	99512919	99512919	C	T	SNP	*PGPEP1L*	ENST00000378919	-1	intronic	c.145-39	e3-39	tier3	27	0	0.000	181	82	0.311
147457	15	99671249	99671249	C	T	SNP	*SYNM*	ENST00000336292	1	missense	c.2681	p.A894V	tier1	38	0	0.000	184	66	0.264
147457	15	100821502	100821502	C	T	SNP	*ADAMTS17*	ENST00000268070	-1	missense	c.721	p.D241N	tier1	78	0	0.000	381	175	0.314
147457	15	102292626	102292626	G	A	SNP	*ENSG00000259660*	ENST00000561463	1	intronic	c.NULL	NULL	tier3	57	0	0.000	272	122	0.309
147457	16	593258	593258	C	T	SNP	*SOLH*	ENST00000219611	1	intronic	c.1-3559	e1-3559	tier3	31	0	0.000	317	152	0.324
147457	16	721798	721799	-	CCCCTG	INS	*MSLN*	ENST00000446427	1	intronic	c.1+28495_28496	e0+28495	tier4	19	0	0.000	84	33	0.282
147457	16	1255229	1255229	C	T	SNP	*CACNA1H*	ENST00000348261	1	missense	c.2567	p.P856L	tier1	47	0	0.000	170	78	0.312
147457	16	1397840	1397840	C	T	SNP	*BAIAP3*	ENST00000324385	1	intronic	c.3130+18	e31+18	tier2	25	0	0.000	161	88	0.352
147457	16	2129600	2129600	G	A	SNP	*TSC2*	ENST00000219476	1	silent	c.3327	p.P1109	tier1	26	1	0.037	318	145	0.313
147457	16	4431260	4431260	C	T	SNP	*VASN*	ENST00000304735	1	missense	c.382	p.R128C	tier1	28	0	0.000	182	74	0.289
147457	16	11001032	11001032	C	T	SNP	*CIITA*	ENST00000324288	1	silent	c.1683	p.D561	tier1	27	0	0.000	161	62	0.276
147457	16	11121344	11121344	G	A	SNP	*ENSG00000229917*	ENST00000425129	1	3_prime_untranslated_region	c.*11121344	NULL	tier3	148	2	0.013	213	97	0.312
147457	16	15457736	15457736	G	A	SNP	*LOC642778*	ENST00000360151	-1	missense	c.833	p.A278V	tier1	321	0	0.000	1467	151	0.093
147457	16	28914739	28914739	C	T	SNP	*ATP2A1*	ENST00000564112	1	missense	c.46	p.R16C	tier1	122	3	0.024	234	107	0.313
147457	16	31519174	31519174	G	A	SNP	*C16orf58*	ENST00000327237	-1	missense	c.326	p.S109F	tier1	28	0	0.000	220	80	0.266
147457	16	33740957	33740957	C	T	SNP	*ENSG00000260781*	ENST00000567025	-1	5_prime_flanking_region	c.-1323	NULL	tier3	333	2	0.006	1132	225	0.166
147457	16	46638006	46638006	G	A	SNP	*SHCBP1*	ENST00000303383	-1	missense	c.973	p.R325C	tier1	35	0	0.000	88	44	0.333
147457	16	56397961	56397961	G	A	SNP	*AMFR*	ENST00000290649	-1	silent	c.1656	p.G552	tier1	22	0	0.000	97	53	0.353
147457	16	57752349	57752349	G	A	SNP	*CCDC135*	ENST00000360716	1	missense	c.1168	p.D390N	tier1	122	1	0.008	267	112	0.296
147457	16	58550812	58550812	G	A	SNP	*SETD6*	ENST00000219315	1	missense	c.772	p.A258T	tier1	59	0	0.000	161	54	0.251
147457	16	67469912	67469912	G	A	SNP	*HSD11B2*	ENST00000326152	1	silent	c.531	p.A177	tier1	29	0	0.000	138	60	0.303
147457	16	67573993	67573993	G	A	SNP	*FAM65A*	ENST00000422602	1	missense	c.512	p.R171H	tier1	94	2	0.021	491	217	0.307
147457	16	83378566	83378566	C	T	SNP	*CDH13*	ENST00000566620	1	missense	c.736	p.R246W	tier1	43	0	0.000	141	65	0.316
147457	16	83520057	83520057	G	A	SNP	*CDH13*	ENST00000566620	1	intronic	c.782-25	e7-25	tier3	77	1	0.013	198	51	0.204
147457	16	83994327	83994327	G	A	SNP	*OSGIN1*	ENST00000361711	1	missense	c.358	p.V120M	tier1	29	0	0.000	220	79	0.264
147457	16	84529437	84529437	G	A	SNP	*KIAA1609*	ENST00000343629	-1	missense	c.236	p.A79V	tier1	25	0	0.000	106	46	0.301
147457	16	88747899	88747899	G	A	SNP	*SNAI3*	ENST00000332281	-1	silent	c.300	p.A100	tier1	66	0	0.000	440	176	0.285
147457	16	89178494	89178494	T	C	SNP	*ACSF3*	ENST00000317447	1	splice_region	c.823-6	e3-6	tier3	79	1	0.013	241	30	0.111
147457	17	3526660	3526660	G	A	SNP	*SHPK*	ENST00000225519	-1	missense	c.620	p.T207M	tier1	21	0	0.000	159	78	0.329
147457	17	6377943	6377943	G	A	SNP	*PITPNM3*	ENST00000262483	-1	intronic	c.1086-19	e10-19	tier2	15	0	0.000	251	122	0.327
147457	17	7492394	7492394	G	A	SNP	*MPDU1*	ENST00000301597	1	3_prime_untranslated_region	c.*586	NULL	tier2	16	0	0.000	135	75	0.357
147457	17	7506344	7506344	C	T	SNP	*FXR2*	ENST00000250113	-1	intronic	c.450-24	e6-24	tier2	91	0	0.000	107	58	0.352
147457	17	8216386	8216386	C	T	SNP	*ARHGEF15*	ENST00000361926	1	missense	c.748	p.R250C	tier1	26	0	0.000	306	120	0.281
147457	17	9632002	9632002	G	A	SNP	*USP43*	ENST00000285199	1	missense	c.3067	p.V1023I	tier1	20	0	0.000	172	62	0.265
147457	17	10322056	10322056	G	A	SNP	*MYH8*	ENST00000252173	-1	silent	c.417	p.P139	tier1	121	0	0.000	378	164	0.303
147457	17	10404747	10404747	G	A	SNP	*MYH1*	ENST00000226207	-1	missense	c.3418	p.R1140C	tier1	150	0	0.000	520	235	0.310
147457	17	11631100	11631100	C	T	SNP	*DNAH9*	ENST00000262442	1	intronic	c.5710-35	e28-35	tier2	123	5	0.039	306	124	0.288
147457	17	16330812	16330812	C	T	SNP	*TRPV2*	ENST00000338560	1	missense	c.1301	p.T434M	tier1	32	0	0.000	186	85	0.314
147457	17	16344404	16344404	G	A	SNP	*C17orf76-AS1*	ENST00000460249	1	3_prime_untranslated_region	c.*16344404	NULL	tier2	79	0	0.000	206	81	0.281
147457	17	16981370	16981370	C	T	SNP	*MPRIP*	ENST00000395811	1	missense	c.247	p.R83C	tier1	38	0	0.000	168	78	0.317
147457	17	18149237	18149237	C	T	SNP	*FLII*	ENST00000465046	-1	5_prime_untranslated_region	c.-18149237	NULL	tier4	21	0	0.000	186	83	0.307
147457	17	18996977	18996977	T	G	SNP	*LOC100132472*	ENST00000428928	1	missense	c.315	p.S105R	tier1	49	1	0.020	537	220	0.291
147457	17	19315938	19315938	G	A	SNP	*RNF112*	ENST00000453070	1	missense	c.79	p.D27N	tier1	14	0	0.000	110	69	0.386
147457	17	26574933	26574933	G	A	SNP	*ENSG00000197825*	ENST00000355177	-1	5_prime_flanking_region	c.-44102	NULL	tier2	23	0	0.000	101	56	0.357
147457	17	26817411	26817411	C	T	SNP	*SLC13A2*	ENST00000444914	1	silent	c.318	p.L106	tier1	50	0	0.000	172	79	0.312
147457	17	27013676	27013676	G	A	SNP	*SUPT6H*	ENST00000314616	1	missense	c.2569	p.A857T	tier1	47	1	0.021	171	59	0.257
147457	17	28395764	28395764	C	T	SNP	*EFCAB5*	ENST00000394835	1	intronic	c.2737+9045	e14+9045	tier2	51	0	0.000	212	90	0.298
147457	17	29533403	29533403	C	T	SNP	*NF1*	ENST00000358273	1	intronic	c.1392+14	e12+14	tier2	184	8	0.042	395	168	0.298
147457	17	31320043	31320043	C	T	SNP	*SPACA3*	ENST00000269053	1	intronic	c.34+1053	e1+1053	tier2	81	1	0.012	301	103	0.254
147457	17	33328217	33328217	G	A	SNP	*LIG3*	ENST00000378526	1	intronic	c.2332-59	e16-59	tier4	23	0	0.000	78	30	0.278
147457	17	34312816	34312816	G	A	SNP	*CCL14*	ENST00000435911	-1	missense	c.95	p.P32L	tier1	87	2	0.023	184	67	0.267
147457	17	36622583	36622583	G	A	SNP	*ARHGAP23*	ENST00000431231	1	missense	c.659	p.R220Q	tier1	38	0	0.000	344	161	0.318
147457	17	36689701	36689701	G	A	SNP	*SRCIN1*	ENST00000264659	-1	intronic	c.3418-35	e19-35	tier2	20	0	0.000	217	141	0.394
147457	17	37075080	37075080	C	T	SNP	*LASP1*	ENST00000318008	1	3_prime_untranslated_region	c.*49	NULL	tier2	33	0	0.000	150	58	0.279
147457	17	38146349	38146349	C	T	SNP	*PSMD3*	ENST00000264639	1	nonsense	c.880	p.R294*	tier1	49	1	0.020	224	86	0.277
147457	17	39740595	39740595	C	T	SNP	*KRT14*	ENST00000167586	-1	missense	c.679	p.E227K	tier1	116	3	0.025	419	156	0.271
147457	17	39959603	39959603	G	A	SNP	*LEPREL4*	ENST00000465097	-1	missense	c.134	p.T45M	tier1	26	0	0.000	162	69	0.299
147457	17	40063711	40063711	C	T	SNP	*ACLY*	ENST00000401700	-1	missense	c.893	p.R298Q	tier1	32	0	0.000	201	111	0.356
147457	17	41026210	41026210	C	T	SNP	*ENSG00000260105*	ENST00000570207	1	3_prime_untranslated_region	c.*41026210	NULL	tier2	109	0	0.000	322	106	0.247
147457	17	44144025	44144025	G	A	SNP	*KANSL1*	ENST00000262419	-1	nonsense	c.1726	p.R576*	tier1	196	2	0.010	616	273	0.307
147457	17	48434597	48434597	G	A	SNP	*XYLT2*	ENST00000017003	1	missense	c.1925	p.R642Q	tier1	39	0	0.000	380	161	0.296
147457	17	52993020	52993020	C	T	SNP	*TOM1L1*	ENST00000575882	1	intronic	c.604-87	e7-87	tier2	47	0	0.000	132	46	0.258
147457	17	56606542	56606542	C	T	SNP	*04.Sep*	ENST00000317268	-1	5_prime_untranslated_region	c.-7	NULL	tier2	32	0	0.000	114	58	0.337
147457	17	59668192	59668192	G	A	SNP	*NACA2*	ENST00000521764	-1	missense	c.350	p.S117L	tier1	125	0	0.000	299	127	0.297
147457	17	60754754	60754754	G	A	SNP	*MRC2*	ENST00000303375	1	silent	c.1959	p.T653	tier1	23	0	0.000	237	92	0.278
147457	17	61611215	61611215	C	T	SNP	*KCNH6*	ENST00000314672	1	intronic	c.676-32	e5-32	tier2	33	1	0.029	241	107	0.308
147457	17	64873540	64873540	C	T	SNP	*CACNG5*	ENST00000169565	1	silent	c.90	p.T30	tier1	37	0	0.000	125	59	0.321
147457	17	68171750	68171750	C	T	SNP	*KCNJ2*	ENST00000243457	1	silent	c.570	p.N190	tier1	43	0	0.000	100	49	0.329
147457	17	74900341	74900341	G	A	SNP	*MGAT5B*	ENST00000428789	1	missense	c.560	p.R187H	tier1	22	0	0.000	125	53	0.298

147457	17	76167847	76167847	C	T	SNP	*SYNGR2*	ENST00000225777	1	missense	c.505	p.R169C	tier1	18	0	0.000	148	53	0.264
147457	17	76803689	76803689	C	T	SNP	*USP36*	ENST00000312010	-1	silent	c.1437	p.P479	tier1	14	0	0.000	54	31	0.365
147457	17	77081692	77081692	C	T	SNP	*ENGASE*	ENST00000300682	1	splice_region	c.1701-10	e13-10	tier3	18	0	0.000	101	41	0.289
147457	17	77083117	77083117	G	A	SNP	*ENGASE*	ENST00000300682	1	3_prime_untranslated_region	c.*686	NULL	tier3	24	1	0.040	175	90	0.340
147457	17	78247071	78247071	G	A	SNP	*RNF213*	ENST00000508628	1	silent	c.129	p.S43	tier1	281	6	0.021	830	332	0.285
147457	18	5397381	5397381	G	A	SNP	*EPB41L3*	ENST00000341928	-1	silent	c.2517	p.P839	tier1	27	0	0.000	95	42	0.302
147457	18	6837314	6837314	C	T	SNP	*ARHGAP28*	ENST00000400091	1	silent	c.444	p.A148	tier1	89	0	0.000	243	88	0.265
147457	18	11868565	11868565	G	A	SNP	*GNAL*	ENST00000334049	1	missense	c.934	p.A312T	tier1	67	1	0.015	168	62	0.268
147457	18	13072806	13072806	C	T	SNP	*CEP192*	ENST00000506447	1	nonsense	c.5401	p.R1801*	tier1	166	2	0.012	197	98	0.332
147457	18	19024347	19024347	C	T	SNP	*GREB1L*	ENST00000424526	1	missense	c.1370	p.T457M	tier1	129	0	0.000	231	78	0.252
147457	18	19780629	19780629	C	T	SNP	*GATA6*	ENST00000269216	1	missense	c.1631	p.P544L	tier1	54	1	0.018	178	98	0.355
147457	18	24126926	24126926	G	A	SNP	*KCTD1*	ENST00000417602	-1	silent	c.1575	p.D525	tier1	20	0	0.000	97	43	0.307
147457	18	29046693	29046693	G	A	SNP	*DSG3*	ENST00000257189	1	missense	c.1612	p.V538I	tier1	53	3	0.054	124	48	0.278
147457	18	33605730	33605730	G	A	SNP	*RPRD1A*	ENST00000357384	-1	intronic	c.789+1133	e6+1133	tier2	71	0	0.000	138	55	0.285
147457	18	34340699	34340699	C	T	SNP	*FHOD3*	ENST00000257209	1	silent	c.4029	p.D1343	tier1	28	0	0.000	145	59	0.288
147457	18	47527556	47527556	C	T	SNP	*MYO5B*	ENST00000285039	-1	intronic	c.612+69	e5+69	tier2	75	0	0.000	498	212	0.298
147457	19	648900	648900	C	T	SNP	*RNF126*	ENST00000340092	-1	missense	c.652	p.V218I	tier1	94	2	0.021	333	185	0.357
147457	19	806592	806592	C	T	SNP	*PTBP1*	ENST00000356948	1	intronic	c.1119+36	e10+36	tier2	56	0	0.000	187	100	0.347
147457	19	1046266	1046266	G	A	SNP	*ABCA7*	ENST00000263094	1	missense	c.1483	p.D495N	tier1	53	0	0.000	472	164	0.257
147457	19	3976654	3976654	G	A	SNP	*EEF2*	ENST00000309311	-1	silent	c.2475	p.F825	tier1	37	0	0.000	342	124	0.264
147457	19	4491450	4491450	C	T	SNP	*HDGFRP2*	ENST00000301284	1	intronic	c.490-113	e5-113	tier3	25	0	0.000	132	59	0.309
147457	19	4511513	4511513	G	A	SNP	*PLIN4*	ENST00000301286	-1	missense	c.2417	p.T806M	tier1	54	0	0.000	368	48	0.115
147457	19	4930798	4930798	C	T	SNP	*UHRF1*	ENST00000398240	1	missense	c.518	p.T173M	tier1	29	0	0.000	169	62	0.268
147457	19	7267653	7267653	C	T	SNP	*INSR*	ENST00000302850	-1	missense	c.355	p.A119T	tier1	24	0	0.000	90	35	0.280
147457	19	7620282	7620282	G	A	SNP	*PNPLA6*	ENST00000414982	1	intronic	c.2966+29	e24+29	tier2	12	0	0.000	68	43	0.387
147457	19	8027941	8027941	C	T	SNP	*ELAVL1*	ENST00000407627	-1	3_prime_untranslated_region	c.*426	NULL	tier3	75	3	0.039	147	66	0.310
147457	19	8138001	8138001	G	A	SNP	*FBN3*	ENST00000270509	-1	missense	c.7883	p.T2628M	tier1	39	0	0.000	283	123	0.303
147457	19	8191296	8191296	C	T	SNP	*FBN3*	ENST00000270509	-1	intronic	c.2554+56	e19+56	tier3	39	1	0.025	367	147	0.285
147457	19	8617070	8617070	C	T	SNP	*MYO1F*	ENST00000338257	-1	intronic	c.505-22	e7-22	tier3	32	0	0.000	111	39	0.258
147457	19	10099957	10099957	G	A	SNP	*COL5A3*	ENST00000264828	-1	intronic	c.2091+41	e26+41	tier3	109	2	0.018	460	190	0.292
147457	19	10753529	10753529	C	T	SNP	*SLC44A2*	ENST00000335757	1	intronic	c.2014+402	e21+402	tier2	47	1	0.021	190	67	0.260
147457	19	13007031	13007031	G	A	SNP	*GCDH*	ENST00000222214	1	silent	c.648	p.S216	tier1	66	1	0.015	305	119	0.280
147457	19	13409955	13409955	C	T	SNP	*CACNA1A*	ENST00000418012	-1	missense	c.2504	p.R835H	tier1	89	4	0.043	413	140	0.253
147457	19	13441256	13441256	C	T	SNP	*CACNA1A*	ENST00000418012	-1	intronic	c.1256-106	e10-106	tier4	41	0	0.000	75	29	0.279
147457	19	13930271	13930271	G	A	SNP	*ZSWIM4*	ENST00000254323	1	silent	c.1674	p.P558	tier1	36	0	0.000	270	111	0.291
147457	19	14071785	14071785	G	A	SNP	*DCAF15*	ENST00000254337	1	missense	c.1781	p.R594Q	tier1	22	0	0.000	213	92	0.302
147457	19	14211653	14211653	C	T	SNP	*PRKACA*	ENST00000308677	-1	missense	c.404	p.R135Q	tier1	26	0	0.000	136	58	0.299
147457	19	14218255	14218255	C	T	SNP	*PRKACA*	ENST00000308677	-1	intronic	c.47-34	e2-34	tier3	105	1	0.009	172	91	0.346
147457	19	15760007	15760007	G	A	SNP	*CYP4F3*	ENST00000221307	1	missense	c.563	p.R188H	tier1	97	0	0.000	344	143	0.293
147457	19	16855367	16855367	G	A	SNP	*NWD1*	ENST00000379808	1	missense	c.334	p.E112K	tier1	39	0	0.000	180	96	0.348
147457	19	17893967	17893967	C	T	SNP	*FCHO1*	ENST00000252771	1	silent	c.2079	p.A693	tier1	32	1	0.030	124	50	0.287
147457	19	20308488	20308488	G	A	SNP	*ZNF486*	ENST00000335117	1	silent	c.969	p.T323	tier1	133	2	0.015	219	96	0.304
147457	19	23927554	23927554	C	T	SNP	*ZNF681*	ENST00000402377	-1	silent	c.798	p.S266	tier1	107	1	0.009	209	56	0.211
147457	19	33487078	33487078	C	T	SNP	*RHPN2*	ENST00000254260	-1	missense	c.1274	p.R425Q	tier1	27	0	0.000	153	66	0.301
147457	19	34925778	34925778	C	T	SNP	*UBA2*	ENST00000246548	1	nonsense	c.364	p.R122*	tier1	89	0	0.000	195	69	0.260
147457	19	38954130	38954130	C	T	SNP	*RYR1*	ENST00000359596	1	missense	c.2645	p.A882V	tier1	131	0	0.000	670	240	0.263
147457	19	40398322	40398322	G	A	SNP	*FCGBP*	ENST00000221347	-1	silent	c.6645	p.N2215	tier1	170	1	0.006	770	207	0.212
147457	19	42091848	42091848	G	A	SNP	*CEACAM21*	ENST00000401445	1	missense	c.850	p.G284S	tier1	49	0	0.000	169	75	0.305
147457	19	42525580	42525580	G	A	SNP	*GRIK5*	ENST00000301218	-1	missense	c.1744	p.R582C	tier1	72	0	0.000	332	120	0.266
147457	19	44891009	44891009	C	T	SNP	*ZFP112*	ENST00000330997	-1	silent	c.1398	p.A466	tier1	112	1	0.009	247	109	0.306
147457	19	47910756	47910756	C	T	SNP	*MEIS3*	ENST00000559524	-1	missense	c.926	p.R309Q	tier1	23	0	0.000	228	84	0.269
147457	19	48956016	48956016	G	A	SNP	*GRWD1*	ENST00000253237	1	missense	c.1075	p.V359I	tier1	34	0	0.000	248	94	0.275
147457	19	49113254	49113254	C	T	SNP	*FAM83E*	ENST00000263266	-1	missense	c.637	p.V213M	tier1	30	1	0.032	168	72	0.300
147457	19	49526129	49526129	G	A	SNP	*CGB*	ENST00000357383	-1	3_prime_untranslated_region	c.*14	NULL	tier2	34	0	0.000	185	95	0.339
147457	19	50563467	50563467	C	T	SNP	*FLJ26850*	ENST00000527209	1	intronic	c.NULL	NULL	tier3	60	0	0.000	95	38	0.286
147457	19	51128500	51128500	G	A	SNP	*SYT3*	ENST00000338916	-1	silent	c.1626	p.A542	tier1	36	0	0.000	240	137	0.363
147457	19	53208386	53208386	C	T	SNP	*ZNF611*	ENST00000319783	-1	missense	c.1922	p.R641H	tier1	173	2	0.011	393	153	0.280
147457	19	54204449	54204449	C	T	SNP	*MIR521-2*	ENST00000384818	1	5_prime_flanking_region	c.-15399	NULL	tier3	114	5	0.042	310	111	0.264
147457	19	54760964	54760964	C	T	SNP	*LILRB5*	ENST00000463460	-1	5_prime_untranslated_region	c.-54760964	NULL	tier3	32	0	0.000	191	83	0.303
147457	19	55710221	55710221	G	A	SNP	*PTPRH*	ENST00000376350	-1	missense	c.1480	p.R494C	tier1	29	0	0.000	207	95	0.315
147457	19	55870015	55870015	G	A	SNP	*FAM71E2*	ENST00000424985	-1	missense	c.2221	p.R741C	tier1	37	0	0.000	150	70	0.318
147457	19	55943894	55943894	G	A	SNP	*SHISA7*	ENST00000376325	-1	3_prime_untranslated_region	c.*629	NULL	tier3	44	0	0.000	118	44	0.272
147457	19	57133465	57133465	C	T	SNP	*ZNF71*	ENST00000328070	1	silent	c.810	p.Y270	tier1	32	0	0.000	311	142	0.313
147457	19	59061551	59061551	G	A	SNP	*TRIM28*	ENST00000253024	1	missense	c.2231	p.R744H	tier1	17	0	0.000	120	54	0.310
147457	20	2842746	2842746	G	A	SNP	*VPS16*	ENST00000380445	1	silent	c.1041	p.A347	tier1	49	0	0.000	176	64	0.266
147457	20	3147452	3147452	C	T	SNP	*ProSAPiP1*	ENST00000329152	-1	missense	c.358	p.G120R	tier1	21	0	0.000	111	53	0.321
147457	20	4705892	4705892	C	T	SNP	*PRND*	ENST00000305817	1	3_prime_untranslated_region	c.*164	NULL	tier3	31	0	0.000	114	58	0.337
147457	20	4707604	4707604	G	A	SNP	*PRND*	ENST00000305817	1	3_prime_untranslated_region	c.*1876	NULL	tier3	63	3	0.046	132	62	0.318
147457	20	18805846	18805846	C	T	SNP	*C20orf78*	ENST00000278779	-1	intronic	c.116+64	e2+64	tier3	50	1	0.020	180	79	0.305
147457	20	20152504	20152504	G	A	SNP	*C20orf26*	ENST00000377306	1	3_prime_untranslated_region	c.*52	NULL	tier3	26	0	0.000	111	42	0.273
147457	20	31023408	31023408	C	T	SNP	*ASXL1*	ENST00000358956	1	nonsense	c.2893	p.R965*	tier1	160	1	0.006	738	319	0.302
147457	20	31389203	31389203	G	A	SNP	*DNMT3B*	ENST00000328111	1	missense	c.2116	p.D706N	tier1	321	4	0.012	718	315	0.304
147457	20	35060416	35060416	G	A	SNP	*DLGAP4*	ENST00000339266	1	missense	c.296	p.R99Q	tier1	19	0	0.000	226	95	0.296
147457	20	37630380	37630380	G	A	SNP	*DHX35*	ENST00000252011	1	missense	c.650	p.R217Q	tier1	77	0	0.000	154	78	0.335

147457	20	40118424	40118424	G	A	SNP	*CHD6*	ENST00000440697	-1	missense	c.782	p.T261M	tier1	45	0	0.000	187	80	0.300
147457	20	40122259	40122259	C	T	SNP	*CHD6*	ENST00000440697	-1	missense	c.341	p.R114H	tier1	74	0	0.000	118	46	0.281
147457	20	44050134	44050134	C	T	SNP	*PIGT*	ENST00000279036	1	missense	c.1145	p.P382L	tier1	22	0	0.000	100	44	0.306
147457	20	49620923	49620923	C	T	SNP	*KCNG1*	ENST00000371571	-1	missense	c.1195	p.E399K	tier1	30	0	0.000	189	72	0.275
147457	20	53208320	53208320	C	T	SNP	*DOK5*	ENST00000262593	1	missense	c.575	p.T192M	tier1	154	2	0.013	245	133	0.352
147457	20	60704165	60704165	G	A	SNP	*LSM14B*	ENST00000253001	1	intronic	c.661-1175	e5-1175	tier3	41	0	0.000	141	76	0.347
147457	20	60910153	60910153	G	A	SNP	*LAMA5*	ENST00000252999	-1	silent	c.2406	p.H802	tier1	25	0	0.000	303	132	0.303
147457	20	62037970	62037970	G	A	SNP	*KCNQ2*	ENST00000354587	-1	3_prime_untranslated_region	c.*27	NULL	tier2	35	0	0.000	177	59	0.250
147457	20	62055538	62055538	C	T	SNP	*KCNQ2*	ENST00000354587	-1	silent	c.1209	p.P403	tier1	82	2	0.024	387	162	0.295
147457	21	31744090	31744090	G	A	SNP	*KRTAP13-2*	ENST00000399889	-1	missense	c.442	p.R148C	tier1	52	1	0.019	156	78	0.333
147457	21	33318470	33318470	G	A	SNP	*HUNK*	ENST00000270112	1	missense	c.733	p.D245N	tier1	54	0	0.000	136	58	0.297
147457	21	33696887	33696887	C	T	SNP	*URB1*	ENST00000382751	-1	missense	c.5147	p.R1716Q	tier1	104	1	0.010	249	111	0.308
147457	21	34945659	34945659	G	A	SNP	*SON*	ENST00000356577	1	missense	c.6931	p.V2311I	tier1	160	2	0.012	270	87	0.243
147457	21	36206893	36206893	G	A	SNP	*RUNX1*	ENST00000300305	-1	missense	c.619	p.R207W	tier1	134	1	0.007	755	326	0.301
147457	21	43547924	43547924	G	A	SNP	*UMODL1*	ENST00000408989	1	missense	c.4057	p.G1353R	tier1	113	0	0.000	200	91	0.313
147457	21	43984766	43984766	G	A	SNP	*SLC37A1*	ENST00000352133	1	intronic	c.1136-52	e13-52	tier3	16	0	0.000	168	75	0.309
147457	21	46363698	46363698	G	A	SNP	*FAM207A*	ENST00000291634	1	missense	c.229	p.V77I	tier1	34	0	0.000	160	74	0.315
147457	21	47766132	47766132	C	T	SNP	*PCNT*	ENST00000359568	1	splice_region	c.720+10	e4+10	tier3	43	1	0.023	149	59	0.282
147457	22	21022153	21022153	G	A	SNP	*FAM108A5P*	ENST00000411545	-1	5_prime_untranslated_region	c.-21022153	NULL	tier2	34	0	0.000	424	172	0.289
147457	22	21349265	21349265	G	A	SNP	*LZTR1*	ENST00000215739	1	missense	c.1892	p.R631Q	tier1	37	0	0.000	264	118	0.308
147457	22	23077532	23077532	C	T	SNP	*IGLV2-18*	ENST00000390310	1	silent	c.309	p.D103	tier1	37	0	0.000	233	89	0.276
147457	22	24649098	24649098	G	A	SNP	*POM121L9P*	ENST00000414583	1	3_prime_untranslated_region	c.*24649098	NULL	tier3	88	0	0.000	551	256	0.317
147457	22	25598652	25598652	C	T	SNP	*CRYBB3*	ENST00000215855	1	silent	c.87	p.Y29	tier1	49	0	0.000	172	54	0.239
147457	22	37319436	37319436	C	T	SNP	*CSF2RB*	ENST00000262825	1	intronic	c.200+27	e2+27	tier3	17	0	0.000	134	89	0.399
147457	22	37892522	37892522	C	T	SNP	*CARD10*	ENST00000251973	-1	missense	c.1993	p.E665K	tier1	15	0	0.000	114	62	0.352
147457	22	38062929	38062929	G	A	SNP	*PDXP*	ENST00000215904	1	3_prime_untranslated_region	c.*1051	NULL	tier2	97	3	0.030	148	61	0.292
147457	22	39358204	39358204	C	T	SNP	*APOBEC3A*	ENST00000249116	1	missense	c.571	p.R191W	tier1	34	0	0.000	178	80	0.309
147457	22	46125385	46125385	G	A	SNP	*ATXN10*	ENST00000252934	1	missense	c.809	p.R270Q	tier1	67	2	0.029	152	62	0.290
147457	22	50728653	50728653	C	T	SNP	*PLXNB2*	ENST00000359337	-1	missense	c.361	p.A121T	tier1	22	0	0.000	186	83	0.309
147457	22	50900128	50900128	C	T	SNP	*SBF1*	ENST00000337034	-1	missense	c.2693	p.R898H	tier1	50	0	0.000	291	131	0.309
147457	22	50962222	50962222	C	T	SNP	*SCO2*	ENST00000252785	-1	missense	c.619	p.V207M	tier1	48	2	0.040	206	80	0.280
147457	22	51182575	51182575	C	T	SNP	*ACR*	ENST00000216139	1	missense	c.652	p.R218C	tier1	59	2	0.033	273	109	0.285
147457	X	2406917	2406917	C	T	SNP	*ZBED1*	ENST00000381218	-1	missense	c.1844	p.R615H	tier1	41	0	0.000	282	118	0.293
147457	X	13765025	13765025	G	A	SNP	*OFD1*	ENST00000340096	1	missense	c.781	p.V261I	tier1	293	4	0.014	415	190	0.312
147457	X	20070889	20070889	C	T	SNP	*MAP7D2*	ENST00000379643	-1	intronic	c.595+107	e5+107	tier3	67	0	0.000	144	58	0.283
147457	X	29973688	29973688	G	A	SNP	*IL1RAPL1*	ENST00000302196	1	silent	c.1842	p.T614	tier1	98	2	0.020	185	80	0.302
147457	X	29974566	29974566	G	A	SNP	*IL1RAPL1*	ENST00000378993	1	3_prime_untranslated_region	c.*629	NULL	tier3	154	1	0.007	371	139	0.272
147457	X	34961163	34961163	G	A	SNP	*FAM47B*	ENST00000329357	1	missense	c.215	p.R72H	tier1	183	4	0.021	504	240	0.323
147457	X	41530801	41530801	C	T	SNP	*CASK*	ENST00000378163	-1	intronic	c.430-18	e6-18	tier4	231	4	0.017	520	212	0.289
147457	X	49032048	49032048	G	A	SNP	*PRICKLE3*	ENST00000376317	-1	nonsense	c.1822	p.R608*	tier1	47	2	0.041	326	129	0.283
147457	X	51639618	51639618	C	T	SNP	*MAGED1*	ENST00000375695	1	silent	c.1035	p.G345	tier1	35	0	0.000	340	138	0.288
147457	X	69595890	69595890	C	T	SNP	*KIF4A*	ENST00000374403	1	intronic	c.1924-60	e17-60	tier3	103	0	0.000	153	47	0.233
147457	X	70823895	70823895	C	T	SNP	*ACRC*	ENST00000373695	1	silent	c.768	p.D256	tier1	121	1	0.008	363	118	0.244
147457	X	70836264	70836264	C	T	SNP	*CXCR3*	ENST00000373691	-1	missense	c.1199	p.R400Q	tier1	30	1	0.032	278	116	0.292
147457	X	71427464	71427464	C	A	SNP	*ERCC6L*	ENST00000334463	-1	missense	c.1153	p.V385L	tier1	85	1	0.012	148	54	0.267
147457	X	79281277	79281277	G	A	SNP	*TBX22*	ENST00000373294	1	splice_site	c.633+1	e4+1	tier1	54	0	0.000	218	87	0.284
147457	X	84525966	84525966	C	T	SNP	*ZNF711*	ENST00000395402	1	missense	c.1442	p.P481L	tier1	119	1	0.008	236	105	0.308
147457	X	103316458	103316458	C	T	SNP	*H2BFWT*	ENST00000217926	-1	5_prime_flanking_region	c.-48226	NULL	tier3	288	4	0.014	491	187	0.275
147457	X	105144665	105144665	C	T	SNP	*NRK*	ENST00000428173	1	missense	c.766	p.P256S	tier1	123	0	0.000	125	52	0.294
147457	X	120181966	120181966	G	A	SNP	*GLUD2*	ENST00000328078	1	missense	c.428	p.R143H	tier1	168	2	0.012	398	194	0.327
147457	X	123215311	123215311	C	T	SNP	*STAG2*	ENST00000218089	1	nonsense	c.2857	p.R953*	tier1	402	0	0.000	644	273	0.297
147457	X	128929233	128929233	G	A	SNP	*ENSG00000240143*	ENST00000432513	1	intronic	c.NULL	NULL	tier3	85	0	0.000	142	57	0.286
147457	X	129190113	129190113	C	T	SNP	*BCORL1*	ENST00000303743	1	3_prime_untranslated_region	c.*2	NULL	tier3	40	0	0.000	142	42	0.228
147457	X	129318354	129318354	C	T	SNP	*RAB33A*	ENST00000257017	1	silent	c.354	p.D118	tier1	58	0	0.000	193	84	0.303
147457	X	129658059	129658059	G	A	SNP	*ENSG00000229702*	ENST00000458525	-1	5_prime_untranslated_region	c.-129658059	NULL	tier2	41	0	0.000	208	97	0.317
147457	X	135961560	135961560	C	G	SNP	*RBMX*	ENST00000320676	-1	missense	c.27	p.K9N	tier1	101	0	0.000	147	13	0.081
147457	X	138678815	138678815	G	A	SNP	*MCF2*	ENST00000370578	-1	nonsense	c.2605	p.R869*	tier1	239	1	0.004	280	112	0.285
147457	X	152808398	152808398	G	A	SNP	*ATP2B3*	ENST00000263519	1	intronic	c.791-103	e5-103	tier3	47	1	0.021	172	70	0.288
147457	X	153660704	153660704	C	T	SNP	*ATP6AP1*	ENST00000369762	1	silent	c.456	p.L152	tier1	31	0	0.000	221	109	0.329
147457	X	153696165	153696165	G	A	SNP	*PLXNA3*	ENST00000369682	1	missense	c.3641	p.R1214Q	tier1	19	0	0.000	120	56	0.316
169510	1	115258745	115258745	C	G	SNP	*NRAS*	ENST00000369535	-1	missense	c.37	p.G13R	tier1	447	15	0.033	489	323	0.397
169510	1	197168802	197168802	C	T	SNP	*ZBTB41*	ENST00000367405	-1	missense	c.802	p.D268N	tier1	51	3	0.056	40	26	0.394
169510	2	39053173	39053173	C	T	SNP	*DHX57*	ENST00000295373	-1	missense	c.2830	p.G944R	tier1	52	1	0.019	68	46	0.404
169510	2	70458050	70458051	-	A	INS	*TIA1*	ENST00000433529	-1	intronic	c.124-65_124-64	e3-64	tier3	102	0	0.000	172	15	0.080
169510	2	73316541	73316541	G	A	SNP	*RAB11FIP5*	ENST00000493523	-1	rna	NULL	NULL	tier1	60	5	0.077	54	42	0.438
169510	3	184922434	184922434	C	G	SNP	*EHHADH*	ENST00000231887	-1	missense	c.680	p.C227S	tier1	57	3	0.050	68	42	0.382
169510	3	192874515	192874515	G	A	SNP	*VEZF1P1*	ENST00000423931	-1	5_prime_untranslated_region	c.-192874515	NULL	tier2	124	9	0.068	171	131	0.434
169510	4	96044976	96044976	C	G	SNP	*BMPR1B*	ENST00000440890	1	missense	c.455	p.P152R	tier1	109	3	0.027	63	45	0.417
169510	4	170483082	170483082	C	A	SNP	*NEK1*	ENST00000507142	-1	intronic	c.1081-40	e12-40	tier3	168	11	0.062	117	83	0.411
169510	5	141236840	141236840	C	T	SNP	*PCDH1*	ENST00000287008	-1	missense	c.3296	p.G1099E	tier1	30	1	0.032	30	42	0.583
169510	6	111688892	111688892	A	T	SNP	*REV3L*	ENST00000358835	-1	silent	c.6099	p.S2033	tier1	63	4	0.060	70	51	0.422
169510	7	65257871	65257872	-	TA	INS	*ENSG00000224316*	ENST00000414608	1	intronic	c.NULL	NULL	tier3	115	1	0.009	166	20	0.108
169510	7	77585348	77585348	G	A	SNP	*PHTF2*	ENST00000248550	1	3_prime_untranslated_region	c.*1153	NULL	tier3	107	10	0.086	63	57	0.475
169510	7	89581765	89581765	C	T	SNP	*STEAP2-AS1*	ENST00000478318	-1	intronic	c.NULL	NULL	tier4	77	5	0.061	100	59	0.371

169510	8	9634628	9634628	A	G	SNP	*TNKS*	ENST00000310430	1	3_prime_untranslated_region	c.*382	NULL	tier3	90	6	0.062	73	60	0.451
169510	8	17206503	17206503	G	A	SNP	*MTMR7*	ENST00000180173	-1	missense	c.556	p.R186W	tier1	112	5	0.043	111	74	0.400
169510	9	8485187	8485187	C	T	SNP	*PTPRD*	ENST00000356435	-1	intronic	c.3153+40	e18+40	tier3	67	2	0.029	57	51	0.468
169510	9	99691238	99691238	G	C	SNP	*NUTM2G*	ENST00000354649	1	5_prime_untranslated_region	c.-69	NULL	tier3	90	0	0.000	185	41	0.181
169510	9	139848309	139848309	C	G	SNP	*LCN12*	ENST00000371633	1	missense	c.341	p.A114G	tier1	82	5	0.056	139	91	0.396
169510	10	42832502	42832503	-	TATCG	INS	*LOC441666*	ENST00000609841	-1	rna	NULL	NULL	tier1	264	1	0.004	263	14	0.051
169510	10	42832522	42832522	C	A	SNP	*LOC441666*	ENST00000609841	-1	rna	NULL	NULL	tier1	258	2	0.008	261	15	0.053
169510	10	102703909	102703909	T	G	SNP	*FAM178A*	ENST00000370269	1	intronic	c.2757+24	e12+24	tier3	57	1	0.017	44	35	0.443
169510	11	1085942	1085942	G	A	SNP	*MUC2*	ENST00000441003	1	missense	c.2782	p.E928K	tier1	45	4	0.082	41	36	0.468
169510	11	6191332	6191332	C	T	SNP	*OR52B2*	ENST00000530810	-1	silent	c.225	p.L75	tier1	91	7	0.071	97	69	0.416
169510	12	149069	149069	G	A	SNP	*FAM138D*	ENST00000320165	-1	rna	NULL	NULL	tier1	187	9	0.046	312	172	0.355
169510	12	22625197	22625197	A	T	SNP	*C2CD5*	ENST00000333957	-1	intronic	c.2169+23	e17+23	tier3	211	9	0.041	182	123	0.402
169510	12	58215300	58215300	C	T	SNP	*CTDSP2*	ENST00000398073	-1	3_prime_untranslated_region	c.*2085	NULL	tier3	27	1	0.036	38	27	0.403
169510	12	81655879	81655879	G	C	SNP	*PPFIA2*	ENST00000549396	-1	intronic	c.3716-60	e30-60	tier3	54	2	0.036	54	36	0.400
169510	12	110783211	110783211	T	A	SNP	*ATP2A2*	ENST00000539276	1	intronic	c.2741+24	e18+24	tier3	44	2	0.044	69	47	0.405
169510	14	21216226	21216226	C	G	SNP	*EDDM3A*	ENST00000326842	1	3_prime_untranslated_region	c.*43	NULL	tier3	44	0	0.000	89	39	0.305
169510	15	85383164	85383164	C	T	SNP	*ALPK3*	ENST00000258888	1	silent	c.1260	p.P420	tier1	389	36	0.084	508	424	0.453
169510	16	32070612	32070612	A	C	SNP	*IGHV1OR16-3*	ENST00000568138	1	3_prime_untranslated_region	c.*32070612	NULL	tier2	213	1	0.005	355	18	0.048
169510	16	57250830	57250830	A	T	SNP	*RSPRY1*	ENST00000394420	1	missense	c.784	p.T262S	tier1	134	5	0.036	110	105	0.486
169510	16	89597025	89597025	C	T	SNP	*SPG7*	ENST00000268704	1	intronic	c.862-66	e7-66	tier3	42	1	0.023	52	38	0.422
169510	17	7414546	7414546	G	C	SNP	*POLR2A*	ENST00000322644	1	missense	c.3826	p.V1276L	tier1	59	3	0.048	60	58	0.492
169510	17	7832533	7832533	C	T	SNP	*KCNAB3*	ENST00000303790	-1	missense	c.221	p.R74Q	tier1	77	4	0.049	73	54	0.425
169510	17	10352234	10352234	G	A	SNP	*MYH4*	ENST00000255381	-1	nonsense	c.4312	p.R1438*	tier1	667	29	0.042	704	508	0.419
169510	17	49835349	49835349	C	T	SNP	*CA10*	ENST00000340813	-1	intronic	c.298-10171	e4-10171	tier3	96	2	0.020	106	70	0.398
169510	17	73997619	73997619	A	G	SNP	*CDK3*	ENST00000425876	1	missense	c.113	p.D38G	tier1	74	3	0.039	82	55	0.402
169510	17	74733199	74733199	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.44	p.S15Y	tier1	254	23	0.083	327	310	0.486
169510	17	74733200	74733200	A	C	SNP	*SRSF2*	ENST00000359995	-1	missense	c.43	p.S15A	tier1	258	21	0.075	328	310	0.486
169510	19	15996791	15996791	C	T	SNP	*CYP4F2*	ENST00000221700	-1	missense	c.1058	p.R353H	tier1	133	9	0.063	127	96	0.431
169510	19	50753076	50753076	G	A	SNP	*MYH14*	ENST00000262269	1	missense	c.1652	p.R551Q	tier1	80	6	0.070	95	76	0.442
169510	20	48600334	48600334	C	T	SNP	*SNAI1*	ENST00000244050	1	intronic	c.83-27	e2-27	tier2	40	0	0.000	110	19	0.147
169510	20	49575622	49575622	G	T	SNP	*MOCS3*	ENST00000244051	1	silent	c.243	p.G81	tier1	18	1	0.053	19	19	0.500
169510	21	36231782	36231782	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.602	p.R201Q	tier1	719	55	0.071	843	712	0.457
169510	X	123176411	123176411	A	G	SNP	*STAG2*	ENST00000218089	1	splice_region	c.386-8	e5-8	tier3	275	37	0.119	24	240	0.899
185295	1	12032977	12032977	C	T	SNP	*PLOD1*	ENST00000376369	1	missense	c.2092	p.P698S	tier1	113	0	0.000	115	49	0.299
185295	1	167341159	167341159	A	T	SNP	*POU2F1*	ENST00000367866	1	missense	c.288	p.K96N	tier1	105	0	0.000	86	28	0.246
185295	1	176675464	176675464	G	A	SNP	*PAPPA2*	ENST00000367662	1	intronic	c.3366-31	e9-31	tier3	106	2	0.019	72	36	0.333
185295	1	220830533	220830533	C	T	SNP	*MARK1*	ENST00000366917	1	intronic	c.1989-599	e17-599	tier3	239	0	0.000	185	75	0.289
185295	1	244218466	244218466	C	A	SNP	*ZBTB18*	ENST00000358704	1	missense	c.1390	p.R464S	tier1	33	0	0.000	34	15	0.306
185295	2	56611386	56611386	C	T	SNP	*CCDC85A*	ENST00000407595	1	intronic	c.1573-15	e6-15	tier3	149	1	0.007	100	9	0.083
185295	4	20529829	20529829	G	A	SNP	*SLIT2*	ENST00000504154	1	intronic	c.1463-743	e16-743	tier3	96	0	0.000	76	25	0.248
185295	4	69344614	69344614	G	A	SNP	*TMPRSS11E*	ENST00000305363	1	missense	c.1015	p.A339T	tier1	95	0	0.000	79	25	0.238
185295	4	159618713	159618713	A	T	SNP	*ETFDH*	ENST00000511912	1	missense	c.834	p.L278F	tier1	37	1	0.026	45	16	0.262
185295	4	169195149	169195149	T	C	SNP	*DDX60*	ENST00000393743	-1	missense	c.2390	p.Y797C	tier1	99	0	0.000	68	18	0.209
185295	6	5144542	5144542	T	C	SNP	*LYRM4*	ENST00000330636	-1	intronic	c.208-34817	e3-34817	tier3	45	0	0.000	29	15	0.341
185295	6	13365713	13365713	C	T	SNP	*GFOD1*	ENST00000379287	-1	silent	c.435	p.V145	tier1	53	0	0.000	41	16	0.281
185295	6	157150512	157150512	G	A	SNP	*ARID1B*	ENST00000367148	1	missense	c.1694	p.R565Q	tier1	105	0	0.000	75	21	0.219
185295	7	124404234	124404234	C	T	SNP	*GPR37*	ENST00000303921	-1	missense	c.797	p.C266Y	tier1	77	0	0.000	85	34	0.286
185295	7	146805221	146805221	T	-	DEL	*CNTNAP2*	ENST00000361727	1	intronic	c.551-18	e5-18	tier3	72	2	0.027	73	21	0.223
185295	8	70533457	70533457	G	A	SNP	*SULF1*	ENST00000260128	1	missense	c.1565	p.R522Q	tier1	71	0	0.000	66	35	0.347
185295	8	145737271	145737271	C	G	SNP	*RECQL4*	ENST00000428558	-1	intronic	c.3393+23	e20+23	tier3	50	0	0.000	39	28	0.418
185295	9	97380079	97380079	C	T	SNP	*FBP1*	ENST00000375326	-1	missense	c.397	p.V133I	tier1	121	1	0.008	94	54	0.365
185295	10	75510973	75510973	G	-	DEL	*SEC24C*	ENST00000339365	1	frame_shift_del	c.280	p.P95fs	tier1	53	0	0.000	61	13	0.176
185295	10	88414661	88414661	C	T	SNP	*OPN4*	ENST00000372071	1	missense	c.121	p.R41W	tier1	79	0	0.000	93	40	0.301
185295	11	17663639	17663639	C	A	SNP	*OTOG*	ENST00000399391	1	intronic	c.8332-35	e52-35	tier3	59	0	0.000	64	36	0.360
185295	12	49719635	49719635	C	T	SNP	*TROAP*	ENST00000257909	1	missense	c.601	p.R201W	tier1	65	0	0.000	81	25	0.236
185295	12	65272304	65272304	C	T	SNP	*TBC1D30*	ENST00000542120	1	3_prime_untranslated_region	c.*2736	NULL	tier3	75	0	0.000	86	41	0.323
185295	12	124427322	124427322	A	C	SNP	*CCDC92*	ENST00000238156	-1	nonsense	c.192	p.Y64*	tier1	119	0	0.000	76	46	0.371
185295	13	48547335	48547335	G	A	SNP	*SUCLA2*	ENST00000378654	-1	intronic	c.663+64	e5+64	tier3	96	0	0.000	104	37	0.262
185295	13	52684711	52684711	G	T	SNP	*NEK5*	ENST00000355568	-1	silent	c.315	p.I105	tier1	84	0	0.000	84	43	0.339
185295	14	96552991	96552991	C	T	SNP	*C14orf132*	ENST00000553764	1	rna	NULL	NULL	tier1	46	0	0.000	42	22	0.344
185295	15	50926721	50926721	T	C	SNP	*TRPM7*	ENST00000313478	-1	missense	c.865	p.I289V	tier1	157	0	0.000	174	83	0.323
185295	15	78207447	78207447	T	A	SNP	*LOC645752*	ENST00000563349	-1	rna	NULL	NULL	tier1	159	0	0.000	127	60	0.321
185295	15	85343270	85343270	C	G	SNP	*ZNF592*	ENST00000299927	1	intronic	c.3273+62	e7+62	tier3	42	0	0.000	42	26	0.382
185295	17	10545798	10545798	C	T	SNP	*MYH3*	ENST00000226209	-1	silent	c.1824	p.G608	tier1	204	1	0.005	199	52	0.207
185295	17	43008929	43008929	C	T	SNP	*KIF18B*	ENST00000339151	-1	intronic	c.1553+41	e10+41	tier3	38	0	0.000	19	12	0.387
185295	17	62658267	62658267	C	A	SNP	*SMURF2*	ENST00000262435	-1	5_prime_flanking_region	c.-269	NULL	tier4	6	0	0.000	1	5	0.833
185295	18	60572437	60572437	G	T	SNP	*PHLPP1*	ENST00000262719	1	intronic	c.2648-20	e8-20	tier3	135	0	0.000	119	9	0.070
185295	21	44524456	44524456	G	A	SNP	*U2AF1*	ENST00000291552	-1	missense	c.101	p.S34F	tier1	614	2	0.003	488	302	0.382
185295	21	47680811	47680812	TT	-	DEL	*MCM3AP*	ENST00000291688	-1	frame_shift_del	c.3477_3476	p.Q1159fs	tier1	62	0	0.000	56	15	0.211
185295	21	47847509	47847509	C	T	SNP	*PCNT*	ENST00000359568	1	intronic	c.7321-27	e34-27	tier3	61	1	0.016	49	34	0.410
185295	22	21538187	21538187	A	G	SNP	*FAM230B*	ENST00000451257	1	rna	NULL	NULL	tier1	417	7	0.017	568	34	0.056
185295	22	39887386	39887386	G	A	SNP	*MGAT3*	ENST00000341184	1	3_prime_untranslated_region	c.*2432	NULL	tier3	31	0	0.000	43	19	0.307
185295	X	39921391	39921391	C	T	SNP	*BCOR*	ENST00000378444	-1	splice_site	c.4428+1	e9+1	tier1	210	0	0.000	117	149	0.560
185295	Y	4966652	4966652	G	-	DEL	*PCDH11Y*	ENST00000215473	1	frame_shift_del	c.1033	p.E345fs	tier1	19	0	0.000	11	13	0.542

187374	1	44467034	44467034	C	G	SNP	*SLC6A9*	ENST00000360584	-1	intronic	c.1419+28	e9+28	tier3	85	4	0.045	63	43	0.406
187374	1	47512254	47512254	G	A	SNP	*CYP4X1*	ENST00000371901	1	missense	c.1189	p.G397R	tier1	65	0	0.000	73	43	0.371
187374	1	176564033	176564033	C	T	SNP	*PAPPA2*	ENST00000367662	1	silent	c.1293	p.T431	tier1	79	1	0.013	59	27	0.314
187374	1	179526224	179526224	G	A	SNP	*NPHS2*	ENST00000367615	-1	silent	c.676	p.L226	tier1	120	2	0.016	127	70	0.355
187374	2	25463295	25463295	T	A	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.2198	p.E733V	tier1	514	3	0.006	499	303	0.376
187374	2	37458814	37458814	C	A	SNP	*CEBPZ*	ENST00000234170	-1	5_prime_untranslated_region	c.-104	NULL	tier2	73	0	0.000	90	42	0.316
187374	2	42280542	42280542	G	A	SNP	*PKDCC*	ENST00000485578	1	3_prime_untranslated_region	c.*42280542	NULL	tier3	39	0	0.000	37	25	0.403
187374	2	196673523	196673523	C	A	SNP	*DNAH7*	ENST00000312428	-1	missense	c.9966	p.W3322C	tier1	92	0	0.000	116	48	0.293
187374	2	207570559	207570559	G	A	SNP	*DYTN*	ENST00000452335	-1	missense	c.335	p.A112V	tier1	106	2	0.018	111	61	0.355
187374	3	49700929	49700929	C	-	DEL	*BSN*	ENST00000296452	1	frame_shift_del	c.11338	p.Q3780fs	tier1	829	4	0.005	651	329	0.336
187374	3	133667500	133667500	C	T	SNP	*SLCO2A1*	ENST00000310926	-1	missense	c.985	p.V329I	tier1	60	1	0.016	52	20	0.278
187374	4	89352470	89352470	T	-	DEL	*HERC6*	ENST00000264346	1	intronic	c.2250+13	e17+13	tier3	69	1	0.014	85	15	0.150
187374	6	49676860	49676860	A	G	SNP	*CRISP2*	ENST00000339139	-1	missense	c.50	p.L17S	tier1	102	0	0.000	76	56	0.421
187374	7	139083345	139083345	A	T	SNP	*LUC7L2*	ENST00000541515	1	nonsense	c.355	p.R119*	tier1	394	3	0.008	251	149	0.373
187374	9	101751401	101751401	C	T	SNP	*COL15A1*	ENST00000375001	1	intronic	c.724-59	e5-59	tier3	63	0	0.000	49	23	0.319
187374	9	131708388	131708388	G	A	SNP	*DOLK*	ENST00000372586	-1	nonsense	c.1195	p.R399*	tier1	37	1	0.026	30	23	0.434
187374	9	132980111	132980111	G	T	SNP	*NCS1*	ENST00000372398	1	missense	c.90	p.W30C	tier1	58	3	0.049	74	34	0.315
187374	10	25465090	25465090	C	T	SNP	*GPR158*	ENST00000376351	1	silent	c.741	p.G247	tier1	78	0	0.000	62	37	0.374
187374	11	36601073	36601073	T	C	SNP	*RAG1*	ENST00000299440	1	3_prime_untranslated_region	c.*3087	NULL	tier2	161	0	0.000	75	28	0.269
187374	11	70779207	70779207	C	T	SNP	*SHANK2*	ENST00000338508	-1	intronic	c.1072+71	e14+71	tier4	27	0	0.000	14	20	0.588
187374	11	93439939	93439939	C	A	SNP	*KIAA1731*	ENST00000411936	1	missense	c.5625	p.D1875E	tier1	95	1	0.010	102	49	0.325
187374	11	93826848	93826848	T	C	SNP	*HEPHL1*	ENST00000315765	1	intronic	c.2434+42	e13+42	tier2	46	0	0.000	27	22	0.449
187374	12	53699798	53699798	T	G	SNP	*C12orf10*	ENST00000549488	1	missense	c.107	p.V36G	tier1	70	1	0.014	68	29	0.299
187374	12	56811467	56811467	G	A	SNP	*TIMELESS*	ENST00000557589	-1	5_prime_untranslated_region	c.-56811467	NULL	tier3	45	0	0.000	86	37	0.301
187374	12	106631792	106631794	CAA	-	DEL	*CKAP4*	ENST00000378026	-1	3_prime_untranslated_region	c.*1010	NULL	tier4	51	0	0.000	53	9	0.145
187374	13	73334857	73334857	C	T	SNP	*DIS3*	ENST00000377767	-1	intronic	c.2671-68	e20-68	tier3	242	1	0.004	159	84	0.344
187374	16	32187496	32187496	A	-	DEL	*HERC2P4*	ENST00000433784	-1	5_prime_untranslated_region	c.-32187496	NULL	tier3	17	0	0.000	7	8	0.533
187374	17	8011913	8011913	G	A	SNP	*ALOXE3*	ENST00000318227	-1	splice_region	c.1959-6	e13-6	tier3	71	1	0.014	64	33	0.337
187374	17	13399643	13399643	C	T	SNP	*HS3ST3A1*	ENST00000284110	-1	silent	c.1092	p.L364	tier1	88	0	0.000	82	46	0.359
187374	17	21319856	21319856	G	A	SNP	*KCNJ12*	ENST00000331718	1	missense	c.1202	p.R401Q	tier1	87	0	0.000	94	17	0.153
187374	17	27936061	27936061	C	T	SNP	*ANKRD13B*	ENST00000394859	1	intronic	c.566-43	e6-43	tier3	64	1	0.015	46	22	0.324
187374	17	38926332	38926332	C	T	SNP	*KRT26*	ENST00000335552	-1	missense	c.724	p.V242M	tier1	119	1	0.008	121	70	0.367
187374	17	43530828	43530828	C	G	SNP	*PLEKHM1*	ENST00000430334	-1	missense	c.2390	p.C797S	tier1	80	0	0.000	63	17	0.213
187374	19	648180	648180	G	A	SNP	*RNF126*	ENST00000292363	-1	missense	c.884	p.S295L	tier1	81	0	0.000	82	57	0.407
187374	19	17471347	17471347	C	T	SNP	*PLVAP*	ENST00000252590	-1	missense	c.1312	p.A438T	tier1	51	0	0.000	85	36	0.295
187374	20	44037609	44037609	C	T	SNP	*DBNDD2*	ENST00000372717	1	missense	c.308	p.A103V	tier1	37	1	0.026	50	23	0.315
187374	21	35467626	35467626	G	A	SNP	*SLC5A3*	ENST00000381151	1	silent	c.129	p.G43	tier1	112	1	0.009	103	49	0.322
187374	21	43412853	43412853	G	C	SNP	*ZBTB21*	ENST00000310826	-1	missense	c.1352	p.A451G	tier1	27	0	0.000	33	19	0.365
187374	22	20133674	20133674	C	T	SNP	*ZDHHC8*	ENST00000334554	1	3_prime_untranslated_region	c.*751	NULL	tier3	92	1	0.011	79	32	0.288
187374	X	110489305	110489305	C	T	SNP	*CAPN6*	ENST00000324068	-1	3_prime_untranslated_region	c.*500	NULL	tier3	28	0	0.000	18	25	0.581
189012	1	16973159	16973159	A	T	SNP	*MST1P2*	ENST00000334429	1	3_prime_untranslated_region	c.*16973159	NULL	tier3	128	1	0.008	265	24	0.083
189012	2	122368824	122368824	T	G	SNP	*CLASP1*	ENST00000263710	-1	intronic	c.1-5068	e1-5068	tier4	45	0	0.000	127	27	0.175
189012	2	198266834	198266834	T	C	SNP	*SF3B1*	ENST00000335508	-1	missense	c.2098	p.K700E	tier1	251	0	0.000	598	48	0.074
189012	2	210707164	210707164	C	T	SNP	*UNC80*	ENST00000439458	1	missense	c.3454	p.R1152C	tier1	51	0	0.000	99	20	0.168
189012	3	172674651	172674651	C	T	SNP	*SPATA16*	ENST00000351008	-1	intronic	c.934-37	e5-37	tier3	26	0	0.000	68	22	0.244
189012	4	39293321	39293321	T	G	SNP	*RFC1*	ENST00000381897	-1	missense	c.3109	p.N1037H	tier1	79	0	0.000	146	27	0.156
189012	5	79095309	79095309	G	A	SNP	*CMYA5*	ENST00000446378	1	missense	c.12080	p.S4027N	tier1	397	0	0.000	933	79	0.078
189012	5	131911487	131911487	G	A	SNP	*RAD50*	ENST00000265335	1	missense	c.232	p.V78M	tier1	118	0	0.000	133	26	0.164
189012	5	170232684	170232684	C	-	DEL	*GABRP*	ENST00000265294	1	intronic	c.542-36	e6-36	tier3	65	1	0.015	147	41	0.218
189012	6	56335881	56335881	T	C	SNP	*DST*	ENST00000370754	-1	intronic	c.22228+23	e95+23	tier3	309	6	0.019	434	115	0.210
189012	6	158994487	158994487	G	A	SNP	*TMEM181*	ENST00000367090	1	missense	c.455	p.R152H	tier1	35	0	0.000	77	16	0.172
189012	8	140768641	140768641	T	G	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-24196	e22-24196	tier3	50	0	0.000	127	18	0.122
189012	11	47753670	47753670	T	C	SNP	*FNBP4*	ENST00000528388	-1	rna	NULL	NULL	tier1	47	0	0.000	60	14	0.189
189012	11	66106152	66106152	C	T	SNP	*BRMS1*	ENST00000530238	-1	5_prime_untranslated_region	c.-66106152	NULL	tier3	56	0	0.000	131	17	0.115
189012	11	119177652	119177652	A	-	DEL	*CBL*	ENST00000264033	1	3_prime_untranslated_region	c.*7161	NULL	tier2	38	0	0.000	67	14	0.173
189012	12	8376028	8376028	C	T	SNP	*FAM90A1*	ENST00000307435	-1	intronic	c.432+17	e3+17	tier3	691	1	0.001	1696	61	0.035
189012	14	20853200	20853200	T	C	SNP	*TEP1*	ENST00000262715	-1	silent	c.3051	p.Q1017	tier1	40	0	0.000	72	15	0.172
189012	18	53253420	53253420	C	G	SNP	*TCF4*	ENST00000398339	-1	intronic	c.379-837	e4-837	tier4	27	0	0.000	74	23	0.237
189012	X	20083381	20083381	A	T	SNP	*MAP7D2*	ENST00000379643	-1	intronic	c.131-458	e2-458	tier4	60	0	0.000	117	19	0.138
190938	1	17320299	17320299	A	C	SNP	*ATP13A2*	ENST00000326735	-1	missense	c.1574	p.V525G	tier1	14	0	0.000	20	17	0.460
190938	1	38510268	38510268	T	-	DEL	*POU3F1*	ENST00000373012	-1	3_prime_untranslated_region	c.*792	NULL	tier4	87	2	0.023	217	34	0.136
190938	2	61411861	61411861	A	G	SNP	*AHSA2*	ENST00000357022	1	missense	c.1	p.M1V	tier1	50	0	0.000	131	70	0.348
190938	2	97833261	97833261	T	A	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.1532-53	e21-53	tier3	75	0	0.000	582	66	0.102
190938	2	130832517	130832517	T	C	SNP	*POTEF*	ENST00000357462	-1	missense	c.2528	p.Y843C	tier1	105	0	0.000	190	86	0.311
190938	3	11406161	11406161	G	T	SNP	*ATG7*	ENST00000354449	1	missense	c.1828	p.D610Y	tier1	48	0	0.000	110	79	0.418
190938	4	79394576	79394576	G	T	SNP	*FRAS1*	ENST00000264895	1	intronic	c.7523-16	e53-16	tier3	49	0	0.000	134	68	0.337
190938	4	101386736	101386736	C	T	SNP	*EMCN*	ENST00000296420	-1	intronic	c.260-40	e4-40	tier3	19	0	0.000	96	77	0.445
190938	4	158064963	158064963	C	T	SNP	*GLRB*	ENST00000264428	1	silent	c.756	p.Y252	tier1	25	0	0.000	60	56	0.483
190938	4	186920705	186920705	G	C	SNP	*SORBS2*	ENST00000284776	-1	5_prime_flanking_region	c.-337354	NULL	tier3	160	0	0.000	390	30	0.071
190938	6	41555657	41555657	T	C	SNP	*FOXP4*	ENST00000307972	1	intronic	c.977+22	e7+22	tier3	143	2	0.014	256	24	0.085
190938	7	100648826	100648826	G	A	SNP	*MUC12*	ENST00000536621	1	intronic	c.14956+26	e2+26	tier3	28	0	0.000	40	26	0.394
190938	9	70918627	70918627	G	C	SNP	*FOXD4L3*	ENST00000342833	1	missense	c.760	p.A254P	tier1	49	1	0.020	126	28	0.182
190938	9	79985394	79985394	C	T	SNP	*VPS13A*	ENST00000360280	1	missense	c.8807	p.T2936I	tier1	50	0	0.000	114	50	0.303
190938	10	74923711	74923711	A	G	SNP	*ECD*	ENST00000430082	-1	splice_region	c.1-3	e1-3	tier3	24	0	0.000	53	27	0.338

190938	11	60230585	60230585	A	T	SNP	*MS4A1*	ENST00000345732	1	silent	c.270	p.G90	tier1	27	0	0.000	62	26	0.296
190938	13	42803590	42803590	G	A	SNP	*DGKH*	ENST00000337343	1	3_prime_untranslated_region	c.*266	NULL	tier2	28	0	0.000	68	51	0.429
190938	14	54416601	54416602	-	AT	INS	*BMP4*	ENST00000245451	-1	3_prime_untranslated_region	c.*149	NULL	tier4	66	1	0.015	276	44	0.138
190938	15	43572011	43572011	G	C	SNP	*TGM7*	ENST00000452443	-1	missense	c.1490	p.A497G	tier1	89	0	0.000	136	82	0.374
190938	17	1028614	1028614	G	A	SNP	*ABR*	ENST00000302538	-1	silent	c.150	p.I50	tier1	84	0	0.000	49	54	0.519
190938	17	7578190	7578190	T	C	SNP	*TP53*	ENST00000269305	-1	missense	c.659	p.Y220C	tier1	797	7	0.009	495	636	0.561
190938	19	50826916	50826916	C	T	SNP	*KCNC3*	ENST00000477616	-1	missense	c.1294	p.V432M	tier1	18	0	0.000	21	13	0.382
190938	19	51958846	51958846	G	A	SNP	*SIGLEC8*	ENST00000321424	-1	silent	c.877	p.L293	tier1	33	0	0.000	60	35	0.368
190938	20	58381127	58381127	C	G	SNP	*PHACTR3*	ENST00000371015	1	silent	c.1206	p.L402	tier1	76	0	0.000	106	59	0.358
190938	X	124455660	124455660	C	G	SNP	*ENSG00000263886*	ENST00000580355	1	3_prime_flanking_region	c.*33968	NULL	tier3	39	0	0.000	30	70	0.700
199019	1	1688824	1688824	A	-	DEL	*NADK*	ENST00000344463	-1	intronic	c.576-75	e5-75	tier3	123	1	0.008	182	22	0.108
199019	1	1747229	1747229	T	C	SNP	*GNB1*	ENST00000378609	-1	missense	c.169	p.K57E	tier1	636	12	0.019	623	296	0.321
199019	1	100602624	100602624	A	G	SNP	*TRMT13*	ENST00000370141	1	missense	c.244	p.R82G	tier1	104	1	0.010	176	126	0.415
199019	1	104260547	104260547	G	A	SNP	*AMYP1*	ENST00000440059	1	intronic	c.NULL	NULL	tier3	81	2	0.024	137	53	0.279
199019	1	248402867	248402867	G	T	SNP	*OR2M4*	ENST00000306687	1	missense	c.637	p.V213F	tier1	71	0	0.000	125	62	0.332
199019	2	95942786	95942786	C	T	SNP	*PROM2*	ENST00000317620	1	missense	c.749	p.A250V	tier1	51	2	0.038	48	17	0.262
199019	2	100015184	100015184	G	C	SNP	*EIF5B*	ENST00000470023	1	3_prime_untranslated_region	c.*100015184	NULL	tier3	96	3	0.030	111	38	0.255
199019	2	212288901	212288901	C	T	SNP	*ERBB4*	ENST00000342788	-1	missense	c.2845	p.V949I	tier1	136	3	0.022	188	61	0.245
199019	2	219267899	219267899	C	T	SNP	*CTDSP1*	ENST00000273062	1	intronic	c.471+49	e5+49	tier3	82	0	0.000	108	50	0.317
199019	3	154002358	154002358	T	-	DEL	*DHX36*	ENST00000496811	-1	intronic	c.2292+14	e19+14	tier3	73	0	0.000	126	15	0.106
199019	4	106156453	106156453	G	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.1354	p.E452*	tier1	640	32	0.048	846	413	0.328
199019	4	106196304	106196304	A	T	SNP	*TET2*	ENST00000380013	1	missense	c.4637	p.Q1546L	tier1	741	5	0.007	1064	110	0.093
199019	5	7302322	7302322	G	A	SNP	*ENSG00000205976*	ENST00000512854	-1	intronic	c.NULL	NULL	tier3	175	4	0.022	199	115	0.363
199019	7	57529430	57529430	A	C	SNP	*ZNF716*	ENST00000420713	1	silent	c.1263	p.S421	tier1	81	0	0.000	112	33	0.228
199019	8	38835514	38835514	C	T	SNP	*HTRA4*	ENST00000302495	1	missense	c.814	p.R272W	tier1	70	0	0.000	84	40	0.323
199019	11	46747390	46747390	C	T	SNP	*F2*	ENST00000311907	1	intronic	c.560-19	e7-19	tier4	23	0	0.000	31	20	0.392
199019	11	65062076	65062076	G	A	SNP	*POLA2*	ENST00000265465	1	silent	c.1413	p.L471	tier1	74	0	0.000	114	29	0.203
199019	11	71949104	71949104	G	A	SNP	*INPPL1*	ENST00000298229	1	missense	c.3571	p.G1191R	tier1	139	0	0.000	209	13	0.058
199019	11	89018012	89018012	G	T	SNP	*TYR*	ENST00000263321	1	missense	c.1256	p.G419V	tier1	171	2	0.012	178	71	0.285
199019	12	49426412	49426413	-	T	INS	*KMT2D*	ENST00000301067	-1	frame_shift_ins	c.12076_12075	p.Q4025fs	tier1	789	16	0.020	1091	388	0.262
199019	12	119844492	119844492	A	-	DEL	*CCDC60*	ENST00000327554	1	intronic	c.91-21996	e2-21996	tier3	53	0	0.000	77	14	0.154
199019	12	124241407	124241407	G	A	SNP	*ATP6V0A2*	ENST00000330342	1	missense	c.2339	p.R780H	tier1	93	4	0.041	107	47	0.305
199019	14	106357572	106357572	A	G	SNP	*IGHD6-19*	ENST00000390574	-1	silent	c.6	p.Y2	tier1	342	5	0.014	387	117	0.232
199019	15	50897271	50897271	C	T	SNP	*TRPM7*	ENST00000313478	-1	missense	c.2780	p.S927N	tier1	47	0	0.000	97	49	0.336
199019	16	4736332	4736332	G	A	SNP	*MGRN1*	ENST00000399577	1	3_prime_untranslated_region	c.*32	NULL	tier2	134	3	0.022	151	65	0.301
199019	17	7578445	7578445	A	T	SNP	*TP53*	ENST00000269305	-1	missense	c.485	p.I162N	tier1	987	46	0.044	601	1092	0.645
199019	17	61898424	61898424	A	G	SNP	*FTSJ3*	ENST00000427159	-1	silent	c.1938	p.D646	tier1	79	2	0.025	98	33	0.252
199019	17	72589154	72589154	T	C	SNP	*C17orf77*	ENST00000328023	1	3_prime_untranslated_region	c.*237	NULL	tier3	106	1	0.009	117	53	0.312
199019	17	75209492	75209492	G	A	SNP	*SEC14L1*	ENST00000392476	1	missense	c.1960	p.D654N	tier1	62	0	0.000	93	22	0.191
199019	X	46513121	46513121	A	T	SNP	*SLC9A7*	ENST00000328306	-1	missense	c.1067	p.F356Y	tier1	179	3	0.017	184	54	0.227
199019	X	132437274	132437274	C	T	SNP	*GPC4*	ENST00000370828	-1	missense	c.1388	p.R463H	tier1	70	0	0.000	119	52	0.304
221833	1	3566445	3566445	A	C	SNP	*WRAP73*	ENST00000270708	-1	intronic	c.69+50	e1+50	tier2	25	1	0.039	48	56	0.539
221833	2	59482372	59482372	G	A	SNP	*LOC101927285*	ENST00000409590	1	rna	NULL	NULL	tier1	103	1	0.010	281	107	0.276
221833	2	74742861	74742861	C	A	SNP	*TLX2*	ENST00000233638	1	missense	c.502	p.Q168K	tier1	55	1	0.018	64	156	0.709
221833	2	86923062	86923062	T	A	SNP	*CHMP3*	ENST00000439940	-1	intronic	c.1-7614	e1-7614	tier4	17	0	0.000	37	76	0.673
221833	2	113190918	113190918	C	G	SNP	*RGPD8*	ENST00000302558	-1	intronic	c.72+41	e1+41	tier4	51	2	0.037	111	44	0.282
221833	2	198638852	198638852	G	A	SNP	*ENSG00000222017*	ENST00000409845	1	3_prime_untranslated_region	c.*71	NULL	tier3	43	1	0.023	131	40	0.234
221833	3	38766591	38766591	C	A	SNP	*SCN10A*	ENST00000449082	-1	intronic	c.3228+74	e17+74	tier3	54	0	0.000	87	69	0.442
221833	3	57616622	57616622	G	A	SNP	*DENND6A*	ENST00000311128	-1	intronic	c.1407+30	e16+30	tier3	39	1	0.025	119	102	0.462
221833	3	97806175	97806175	C	T	SNP	*OR5AC2*	ENST00000358642	1	silent	c.159	p.N53	tier1	81	4	0.047	107	83	0.437
221833	3	195690286	195690286	C	G	SNP	*SDHAP1*	ENST00000354559	-1	rna	NULL	NULL	tier1	209	3	0.014	906	64	0.066
221833	4	6050724	6050725	-	T	INS	*JAKMIP1*	ENST00000409021	-1	intronic	c.1963-76_1963-75	e15-75	tier3	35	0	0.000	108	23	0.176
221833	4	106156548	106156548	T	-	DEL	*TET2*	ENST00000380013	1	frame_shift_del	c.1449	p.C484fs	tier1	400	4	0.010	689	497	0.419
221833	4	106164859	106164859	A	-	DEL	*TET2*	ENST00000380013	1	frame_shift_del	c.3727	p.K1243fs	tier1	276	7	0.025	392	339	0.464
221833	4	115898324	115898324	A	G	SNP	*NDST4*	ENST00000264363	-1	intronic	c.1066+19	e2+19	tier3	46	3	0.061	86	59	0.407
221833	5	13901373	13901373	C	T	SNP	*DNAH5*	ENST00000265104	-1	silent	c.2040	p.A680	tier1	370	8	0.021	569	456	0.444
221833	6	33381539	33381539	G	A	SNP	*PHF1*	ENST00000374516	1	missense	c.614	p.R205Q	tier1	53	1	0.019	69	77	0.524
221833	7	36396735	36396735	G	A	SNP	*KIAA0895*	ENST00000297063	-1	missense	c.643	p.P215S	tier1	44	0	0.000	55	49	0.471
221833	7	63032656	63032656	G	A	SNP	*TNRC18P2*	ENST00000417666	-1	intronic	c.NULL	NULL	tier2	112	0	0.000	289	86	0.229
221833	7	74482588	74482588	C	T	SNP	*WBSCR16*	ENST00000329959	-1	missense	c.472	p.V158M	tier1	15	0	0.000	35	27	0.436
221833	9	9091069	9091069	G	A	SNP	*RPS26P3*	ENST00000470205	1	3_prime_untranslated_region	c.*9091069	NULL	tier3	53	0	0.000	137	19	0.122
221833	9	138642911	138642911	G	A	SNP	*KCNT1*	ENST00000298480	1	intronic	c.434+24	e4+24	tier3	163	4	0.024	234	210	0.473
221833	11	63671439	63671439	C	T	SNP	*MARK2*	ENST00000402010	1	intronic	c.1515-19	e15-19	tier3	35	2	0.054	58	41	0.414
221833	12	53578786	53578786	C	T	SNP	*ZNF740*	ENST00000416904	1	missense	c.121	p.R41W	tier1	21	0	0.000	43	16	0.271
221833	14	60395157	60395157	C	T	SNP	*LRRC9*	ENST00000254271	1	missense	c.220	p.P74S	tier1	76	0	0.000	153	123	0.444
221833	15	29488779	29488779	G	A	SNP	*FAM189A1*	ENST00000560021	-1	5_prime_untranslated_region	c.-29488779	NULL	tier3	21	0	0.000	43	26	0.377
221833	16	67650720	67650720	G	A	SNP	*CTCF*	ENST00000264010	1	missense	c.1025	p.R342H	tier1	279	2	0.007	624	444	0.415
221833	16	82033259	82033259	G	A	SNP	*SDR42E1*	ENST00000328945	-1	silent	c.639	p.Y213	tier1	69	1	0.014	112	69	0.381
221833	17	80206875	80206875	C	T	SNP	*CSNK1D*	ENST00000314028	-1	missense	c.1073	p.R358Q	tier1	36	1	0.027	74	46	0.383
221833	18	55253819	55253819	G	A	SNP	*FECH*	ENST00000382873	-1	silent	c.34	p.L12	tier1	4	0	0.000	2	15	0.882
221833	19	54946639	54946639	G	A	SNP	*TTYH1*	ENST00000376531	1	intronic	c.1126-83	e11-83	tier4	67	2	0.029	69	63	0.477
221833	21	46913513	46913513	C	T	SNP	*SLC19A1*	ENST00000417954	-1	3_prime_untranslated_region	c.*2736	NULL	tier3	53	0	0.000	71	37	0.343
221833	X	133547689	133547689	T	C	SNP	*PHF6*	ENST00000394292	1	splice_site	c.588+2	e5+2	tier1	184	11	0.056	70	543	0.884
221833	X	155010932	155010932	A	T	SNP	*SPRY3*	ENST00000302805	1	3_prime_untranslated_region	c.*6532	NULL	tier3	37	0	0.000	77	68	0.466

222841	2	91885956	91885956	A	C	SNP	*ENSG00000230572*	ENST00000436174	-1	intronic	c.NULL	NULL	tier3	421	4	0.009	1163	50	0.041
222841	3	17418001	17418002	-	A	INS	*TBC1D5*	ENST00000253692	-1	intronic	c.701+15_701+14	e8+15	tier3	78	0	0.000	207	22	0.096
222841	3	49571621	49571621	T	-	DEL	*DAG1*	ENST00000308775	1	3_prime_untranslated_region	c.*989	NULL	tier3	46	0	0.000	63	14	0.182
222841	3	62142833	62142833	C	A	SNP	*PTPRG*	ENST00000474889	1	missense	c.775	p.P259T	tier1	85	1	0.012	206	26	0.112
222841	3	195453104	195453104	G	A	SNP	*MUC20*	ENST00000447234	1	missense	c.1630	p.V544I	tier1	152	0	0.000	234	20	0.079
222841	4	8601068	8601068	G	A	SNP	*CPZ*	ENST00000360986	1	intronic	c.89-112	e2-112	tier3	137	0	0.000	280	25	0.082
222841	4	78694321	78694321	C	T	SNP	*CNOT6L*	ENST00000264903	-1	splice_site	c.315-1	e4-1	tier1	180	0	0.000	341	53	0.134
222841	5	71496184	71496184	C	G	SNP	*MAP1B*	ENST00000296755	1	silent	c.7002	p.T2334	tier1	371	1	0.003	767	51	0.062
222841	6	101215150	101215150	G	C	SNP	*ASCC3*	ENST00000369162	-1	nonsense	c.1467	p.Y489*	tier1	199	1	0.005	489	28	0.054
222841	6	117631399	117631399	G	C	SNP	*ROS1*	ENST00000368508	-1	silent	c.6279	p.T2093	tier1	145	0	0.000	267	16	0.057
222841	7	72814623	72814623	C	T	SNP	*FZD9*	ENST00000344575	1	5_prime_flanking_region	c.-33715	NULL	tier3	210	1	0.005	345	25	0.068
222841	8	19694580	19694580	C	G	SNP	*INTS10*	ENST00000520670	1	missense	c.17	p.S6C	tier1	113	0	0.000	246	21	0.079
222841	8	22548343	22548343	C	T	SNP	*EGR3*	ENST00000317216	-1	silent	c.807	p.P269	tier1	276	0	0.000	562	25	0.043
222841	8	140768059	140768059	A	G	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-23614	e22-23614	tier3	92	1	0.011	159	22	0.122
222841	10	42949783	42949783	C	A	SNP	*CCNYL2*	ENST00000426433	-1	5_prime_untranslated_region	c.-42949783	NULL	tier3	97	4	0.039	137	38	0.216
222841	10	73497534	73497534	C	G	SNP	*C10orf105*	ENST00000398786	-1	5_prime_untranslated_region	c.-21440	NULL	tier3	294	0	0.000	505	26	0.049
222841	11	32444548	32444548	C	G	SNP	*WT1*	ENST00000332351	-1	intronic	c.872+4954	e3+4954	tier3	220	0	0.000	491	33	0.063
222841	12	49170094	49170094	G	A	SNP	*ADCY6*	ENST00000307885	-1	silent	c.1575	p.N525	tier1	412	2	0.005	742	31	0.040
222841	12	109604677	109604677	C	G	SNP	*ACACB*	ENST00000338432	1	missense	c.665	p.S222W	tier1	109	0	0.000	193	17	0.081
222841	13	36410159	36410159	A	T	SNP	*DCLK1*	ENST00000360631	-1	intronic	c.1229+11	e7+11	tier3	246	0	0.000	666	50	0.070
222841	16	81412314	81412314	G	C	SNP	*GAN*	ENST00000568107	1	3_prime_untranslated_region	c.*1113	NULL	tier3	107	0	0.000	297	21	0.066
222841	17	7577568	7577568	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.713	p.C238Y	tier1	803	19	0.023	873	482	0.355
222841	17	10350502	10350502	C	A	SNP	*MYH4*	ENST00000255381	-1	missense	c.4997	p.R1666I	tier1	417	2	0.005	927	47	0.048
222841	17	10401122	10401122	G	C	SNP	*MYH1*	ENST00000226207	-1	missense	c.4294	p.L1432V	tier1	323	0	0.000	628	21	0.032
222841	19	9176322	9176322	G	C	SNP	*OR1M1*	ENST00000429566	1	5_prime_flanking_region	c.-27599	NULL	tier3	199	0	0.000	620	26	0.040
222841	22	40055124	40055124	G	C	SNP	*CACNA1I*	ENST00000336649	1	splice_region	c.2348+3	e15+3	tier2	263	0	0.000	428	21	0.047
222841	X	137714472	137714472	A	G	SNP	*FGF13*	ENST00000315930	-1	3_prime_untranslated_region	c.*539	NULL	tier3	94	0	0.000	169	15	0.082
222841	X	152801875	152801875	G	A	SNP	*ATP2B3*	ENST00000263519	1	missense	c.170	p.S57N	tier1	500	0	0.000	883	39	0.042
229276	1	15903	15904	-	C	INS	*WASH7P*	ENST00000438504	-1	splice_site_ins	c.NULL	NULL	tier1	7	0	0.000	2	12	0.857
229276	1	17084269	17084269	G	A	SNP	*MST1L*	ENST00000455405	-1	rna	NULL	NULL	tier1	141	3	0.021	378	42	0.100
229276	1	186647324	186647324	T	-	DEL	*PTGS2*	ENST00000367468	-1	intronic	c.457+69	e4+69	tier3	33	0	0.000	73	18	0.198
229276	1	201172932	201172932	C	T	SNP	*IGFN1*	ENST00000335211	1	missense	c.814	p.R272C	tier1	71	0	0.000	116	26	0.183
229276	2	231974064	231974065	-	A	INS	*HTR2B*	ENST00000258400	-1	frame_shift_ins	c.613_612	p.I204fs	tier1	61	0	0.000	125	19	0.132
229276	3	38739967	38739967	G	A	SNP	*SCN10A*	ENST00000449082	-1	missense	c.4744	p.R1582C	tier1	74	0	0.000	195	30	0.133
229276	3	53736702	53736702	C	T	SNP	*CACNA1D*	ENST00000288139	1	missense	c.1255	p.R419W	tier1	76	2	0.026	165	33	0.167
229276	3	68684184	68684184	C	T	SNP	*ENSG00000244640*	ENST00000461635	-1	5_prime_flanking_region	c.-677	NULL	tier4	65	0	0.000	109	26	0.193
229276	4	15055756	15055756	A	G	SNP	*CPEB2*	ENST00000538197	1	silent	c.2376	p.E792	tier1	102	1	0.010	229	46	0.167
229276	4	36214995	36214995	T	C	SNP	*ARAP2*	ENST00000303965	-1	intronic	c.965-54	e3-54	tier3	173	1	0.006	256	33	0.114
229276	4	39233719	39233720	-	A	INS	*WDR19*	ENST00000399820	1	intronic	c.2143-63_2143-62	e19-62	tier3	43	0	0.000	78	14	0.152
229276	4	39928393	39928393	A	T	SNP	*PDS5A*	ENST00000303538	-1	splice_site	c.429+2	e3+2	tier1	195	1	0.005	312	20	0.059
229276	4	95202758	95202758	T	A	SNP	*SMARCAD1*	ENST00000359052	1	intronic	c.2732+17	e20+17	tier3	64	0	0.000	85	12	0.124
229276	5	55237459	55237459	A	C	SNP	*IL6ST*	ENST00000336909	-1	silent	c.2208	p.S736	tier1	77	1	0.013	162	26	0.138
229276	5	60170374	60170374	A	C	SNP	*ERCC8*	ENST00000462279	-1	rna	NULL	NULL	tier1	129	0	0.000	200	33	0.142
229276	6	30593399	30593399	C	A	SNP	*MRPS18B*	ENST00000259873	1	missense	c.602	p.P201Q	tier1	60	0	0.000	116	36	0.237
229276	6	52883236	52883236	C	T	SNP	*ICK*	ENST00000350082	-1	silent	c.555	p.A185	tier1	99	0	0.000	196	33	0.144
229276	6	76022886	76022886	G	A	SNP	*FILIP1*	ENST00000237172	-1	missense	c.2662	p.P888S	tier1	88	0	0.000	183	32	0.149
229276	6	88125414	88125414	C	T	SNP	*C6orf165*	ENST00000369562	1	silent	c.294	p.L98	tier1	169	0	0.000	273	45	0.142
229276	9	139997605	139997605	A	G	SNP	*MAN1B1*	ENST00000536349	1	3_prime_untranslated_region	c.*139997605	NULL	tier3	81	1	0.012	173	42	0.194
229276	9	139997644	139997644	A	G	SNP	*MAN1B1*	ENST00000536349	1	3_prime_untranslated_region	c.*139997644	NULL	tier3	75	3	0.039	141	50	0.254
229276	10	15177301	15177301	A	G	SNP	*NMT2*	ENST00000378165	-1	silent	c.363	p.F121	tier1	30	0	0.000	38	14	0.269
229276	12	12006417	12006418	-	T	INS	*ETV6*	ENST00000396373	1	frame_shift_ins	c.385_386	p.S131fs	tier1	379	7	0.018	618	110	0.151
229276	12	13229047	13229047	A	T	SNP	*KIAA1467*	ENST00000197268	1	missense	c.1612	p.N538Y	tier1	110	1	0.009	203	25	0.109
229276	12	64842427	64842427	T	A	SNP	*XPOT*	ENST00000332707	1	3_prime_untranslated_region	c.*516	NULL	tier4	120	0	0.000	133	27	0.169
229276	12	112657189	112657189	C	T	SNP	*HECTD4*	ENST00000377560	-1	splice_site	c.6558+1	e43+1	tier1	35	0	0.000	66	17	0.205
229276	12	124082411	124082411	G	T	SNP	*TMED2*	ENST00000262225	1	3_prime_untranslated_region	c.*1135	NULL	tier3	33	0	0.000	64	14	0.175
229276	17	29553477	29553478	-	C	INS	*NF1*	ENST00000358273	1	frame_shift_ins	c.2026_2027	p.I679fs	tier1	301	4	0.013	489	85	0.148
229276	19	36125240	36125240	G	A	SNP	*RBM42*	ENST00000262633	1	missense	c.1100	p.S367N	tier1	42	0	0.000	102	25	0.197
229276	21	36259295	36259316	CAGCGCCGGCGTCCGGGGCGCC	-	DEL	*RUNX1*	ENST00000300305	-1	frame_shift_del	c.196_175	p.G59fs	tier1	460	0	0.000	933	41	0.042
229276	X	2835999	2836007	CCACGCCGG	-	DEL	*ARSD*	ENST00000381154	-1	in_frame_del	c.709_701	p.AGV234in_frame_del	tier1	31	0	0.000	59	14	0.192
229276	X	39934092	39934092	G	-	DEL	*BCOR*	ENST00000378444	-1	frame_shift_del	c.507	p.D169fs	tier1	289	9	0.030	396	133	0.251
229276	X	123179001	123179001	A	G	SNP	*STAG2*	ENST00000218089	1	intronic	c.463-13	e6-13	tier2	158	2	0.013	184	75	0.287
243777	1	3428641	3428641	T	C	SNP	*MEGF6*	ENST00000356575	-1	missense	c.905	p.N302S	tier1	89	0	0.000	155	16	0.093
243777	1	24383863	24383863	C	T	SNP	*MYOM3*	ENST00000330966	-1	silent	c.4314	p.K1438	tier1	274	9	0.032	435	137	0.238
243777	1	152082466	152082466	A	C	SNP	*TCHH*	ENST00000368804	-1	missense	c.3227	p.L1076R	tier1	125	1	0.008	146	16	0.099
243777	1	230921753	230921753	A	G	SNP	*CAPN9*	ENST00000271971	1	missense	c.1508	p.D503G	tier1	208	0	0.000	337	16	0.045
243777	2	103124587	103124587	C	T	SNP	*SLC9A4*	ENST00000295269	1	silent	c.1248	p.F416	tier1	139	0	0.000	238	26	0.099
243777	2	152534686	152534686	C	G	SNP	*NEB*	ENST00000397345	-1	missense	c.3271	p.D1091H	tier1	67	0	0.000	82	31	0.274
243777	3	58870344	58870344	C	T	SNP	*C3orf67*	ENST00000482387	-1	silent	c.267	p.Q89	tier1	130	4	0.030	201	54	0.212
243777	4	2932778	2932778	G	A	SNP	*MFSD10*	ENST00000514800	-1	missense	c.1262	p.A421V	tier1	30	1	0.032	54	22	0.290
243777	5	82833952	82833952	C	T	SNP	*VCAN*	ENST00000265077	1	silent	c.5130	p.D1710	tier1	831	6	0.007	1350	46	0.033
243777	5	140201927	140201927	C	A	SNP	*PCDHA5*	ENST00000529859	1	missense	c.567	p.N189K	tier1	122	2	0.016	171	37	0.178
243777	5	145890610	145890610	T	-	DEL	*TCERG1*	ENST00000296702	1	3_prime_untranslated_region	c.*405	NULL	tier3	66	1	0.015	93	16	0.147
243777	6	7829666	7829666	G	A	SNP	*BMP6*	ENST00000283147	1	intronic	c.665-15707	e2-15707	tier4	42	1	0.023	50	22	0.306
243777	6	42985369	42985369	C	A	SNP	*KLHDC3*	ENST00000326974	1	silent	c.267	p.V89	tier1	59	0	0.000	132	23	0.148

243777	6	42985377	42985377	G	A	SNP	*KLHDC3*	ENST00000326974	1	nonsense	c.275	p.W92*	tier1	63	0	0.000	137	21	0.133
243777	6	64290808	64290808	G	A	SNP	*PTP4A1*	ENST00000370651	1	3_prime_untranslated_region	c.*729	NULL	tier3	100	0	0.000	158	39	0.197
243777	7	135263622	135263622	C	T	SNP	*NUP205*	ENST00000285968	1	missense	c.1001	p.A334V	tier1	151	5	0.032	216	55	0.202
243777	8	101522892	101522892	A	-	DEL	*ANKRD46*	ENST00000520552	-1	intronic	c.637-25	e4-25	tier3	38	0	0.000	48	10	0.172
243777	8	117859879	117859879	G	A	SNP	*RAD21*	ENST00000297338	-1	nonsense	c.1756	p.R586*	tier1	810	5	0.006	1188	130	0.099
243777	9	108125237	108125237	G	A	SNP	*SLC44A1*	ENST00000374720	1	missense	c.1036	p.V346I	tier1	123	0	0.000	203	50	0.198
243777	10	54076396	54076396	T	C	SNP	*DKK1*	ENST00000373970	1	silent	c.630	p.C210	tier1	71	1	0.014	75	33	0.306
243777	10	135350563	135350563	G	T	SNP	*CYP2E1*	ENST00000252945	1	splice_region	c.968-4	e7-4	tier3	51	0	0.000	85	19	0.183
243777	11	67552796	67552796	G	T	SNP	*ALG1L8P*	ENST00000533887	1	3_prime_untranslated_region	c.*67552796	NULL	tier3	97	0	0.000	146	46	0.240
243777	11	71175151	71175151	C	A	SNP	*NADSYN1*	ENST00000319023	1	missense	c.370	p.R124S	tier1	40	0	0.000	39	17	0.304
243777	11	108188267	108188267	T	-	DEL	*ATM*	ENST00000278616	1	intronic	c.6347+19	e42+19	tier3	39	0	0.000	69	13	0.159
243777	11	132081872	132081872	T	A	SNP	*NTM*	ENST00000539799	1	intronic	c.401-44	e4-44	tier3	85	2	0.023	91	25	0.216
243777	12	11992117	11992117	G	A	SNP	*ETV6*	ENST00000396373	1	nonsense	c.207	p.W69*	tier1	566	3	0.005	876	122	0.122
243777	16	12297010	12297010	T	G	SNP	*SNX29*	ENST00000306030	1	intronic	c.523+3470	e6+3470	tier3	265	3	0.011	510	36	0.066
243777	16	51175096	51175096	G	A	SNP	*SALL1*	ENST00000251020	-1	missense	c.1037	p.A346V	tier1	77	1	0.013	97	32	0.248
243777	17	10305158	10305159	-	T	INS	*MYH8*	ENST00000403437	-1	intronic	c.2689-57_2689-56	e21-56	tier3	168	2	0.012	223	46	0.171
243777	17	10451010	10451010	G	A	SNP	*MYH2*	ENST00000245503	-1	intronic	c.204+24	e1+24	tier3	156	2	0.013	268	63	0.190
243777	17	62399159	62399160	-	T	INS	*RPL31P57*	ENST00000461109	-1	5_prime_flanking_region	c.-13109	NULL	tier3	85	0	0.000	103	37	0.264
243777	17	78313118	78313118	C	G	SNP	*RNF213*	ENST00000582970	1	missense	c.4951	p.L1651V	tier1	565	18	0.031	806	234	0.225
243777	18	42531917	42531917	T	C	SNP	*SETBP1*	ENST00000282030	1	missense	c.2612	p.I871T	tier1	545	3	0.006	951	30	0.031
243777	18	77896475	77896475	A	T	SNP	*ADNP2*	ENST00000262198	1	missense	c.3179	p.D1060V	tier1	123	5	0.039	159	77	0.326
243777	19	1525633	1525633	C	T	SNP	*PLK5*	ENST00000334770	1	5_prime_untranslated_region	c.-1363	NULL	tier2	92	0	0.000	119	62	0.343
243777	19	51358189	51358189	T	A	SNP	*KLK3*	ENST00000326003	1	5_prime_untranslated_region	c.-23	NULL	tier3	81	1	0.012	100	43	0.301
243777	19	57722941	57722941	A	G	SNP	*ZNF264*	ENST00000263095	1	missense	c.476	p.D159G	tier1	89	0	0.000	143	21	0.128
243777	20	3214593	3214593	C	T	SNP	*SLC4A11*	ENST00000380059	-1	silent	c.708	p.R236	tier1	67	1	0.015	95	34	0.264
243777	20	31022762	31022762	C	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.2247	p.V751fs	tier1	718	15	0.021	939	327	0.258
243777	21	9755905	9755905	A	G	SNP	-	-	-	-	-	-	tier3	31	0	0.000	72	33	0.314
243777	21	44514777	44514777	T	G	SNP	*U2AF1*	ENST00000291552	-1	missense	c.470	p.Q157P	tier1	314	5	0.016	477	121	0.202
266995	1	24417462	24417462	C	A	SNP	*MYOM3*	ENST00000330966	-1	missense	c.1260	p.W420C	tier1	329	1	0.003	901	40	0.043
266995	1	181706618	181706618	G	A	SNP	*CACNA1E*	ENST00000367573	1	intronic	c.3423-43	e23-43	tier3	354	0	0.000	511	43	0.077
266995	2	152267722	152267722	T	-	DEL	*RIF1*	ENST00000243326	1	intronic	c.105-52	e2-52	tier2	20	0	0.000	12	7	0.368
266995	3	14239517	14239518	-	T	INS	*LSM3*	ENST00000306024	1	intronic	c.229-19_229-18	e4-18	tier2	88	0	0.000	114	13	0.102
266995	3	39230412	39230412	C	T	SNP	*XIRP1*	ENST00000340369	-1	silent	c.525	p.L175	tier1	530	2	0.004	988	64	0.061
266995	3	100463779	100463779	A	G	SNP	*TFG*	ENST00000240851	1	splice_region	c.820+4	e6+4	tier3	107	1	0.009	185	21	0.102
266995	3	137981440	137981440	A	-	DEL	*ARMC8*	ENST00000469044	1	intronic	c.1135-1141	e13-1141	tier4	58	0	0.000	60	9	0.130
266995	6	132067939	132067939	A	G	SNP	*ENPP3*	ENST00000357639	1	missense	c.2471	p.E824G	tier1	140	0	0.000	200	16	0.074
266995	7	129028858	129028858	T	-	DEL	*AHCYL2*	ENST00000491079	1	3_prime_untranslated_region	c.*129028858	NULL	tier3	86	1	0.012	104	14	0.119
266995	8	80948699	80948699	C	A	SNP	*TPD52*	ENST00000518937	-1	3_prime_untranslated_region	c.*1652	NULL	tier3	112	0	0.000	106	9	0.078
266995	8	139736829	139736829	G	A	SNP	*COL22A1*	ENST00000303045	-1	intronic	c.2247+29	e24+29	tier3	65	0	0.000	91	17	0.157
266995	10	95720906	95720906	G	A	SNP	*PIPSL*	ENST00000480546	-1	rna	NULL	NULL	tier1	161	0	0.000	270	18	0.063
266995	12	25398262	25398262	C	G	SNP	*KRAS*	ENST00000256078	-1	missense	c.57	p.L19F	tier1	478	0	0.000	750	46	0.058
266995	12	54369181	54369181	G	C	SNP	*HOXC11*	ENST00000546378	1	missense	c.899	p.G300A	tier1	184	0	0.000	339	18	0.050
266995	12	133050261	133050261	G	A	SNP	*MUC8*	ENST00000595994	-1	silent	c.183	p.L61	tier1	130	0	0.000	129	12	0.085
266995	13	101762936	101762936	G	A	SNP	*NALCN*	ENST00000251127	-1	intronic	c.2364+34	e19+34	tier2	390	2	0.005	454	47	0.094
266995	13	101910940	101910940	C	G	SNP	*NALCN*	ENST00000251127	-1	intronic	c.1135-15	e10-15	tier3	234	0	0.000	381	34	0.081
266995	15	101844339	101844339	C	G	SNP	*ENSG00000259172*	ENST00000558838	1	rna	NULL	NULL	tier1	114	0	0.000	179	17	0.087
266995	16	81941970	81941970	C	A	SNP	*PLCG2*	ENST00000359376	1	intronic	c.1558-51	e16-51	tier3	113	0	0.000	199	15	0.070
266995	18	14830201	14830201	C	G	SNP	*MIR3156-2*	ENST00000581101	1	rna	NULL	NULL	tier1	243	0	0.000	247	12	0.046
266995	19	9057573	9057573	G	A	SNP	*MUC16*	ENST00000397910	-1	missense	c.29873	p.T9958I	tier1	734	0	0.000	1536	68	0.042
266995	X	107811978	107811978	G	A	SNP	*COL4A5*	ENST00000328300	1	intronic	c.322-11	e6-11	tier3	220	0	0.000	320	28	0.080
270086	6	56473262	56473262	G	A	SNP	*DST*	ENST00000370754	-1	missense	c.6065	p.T2022I	tier1	777	0	0.000	1084	44	0.039
270086	7	114563154	114563154	C	A	SNP	*MDFIC*	ENST00000393486	1	silent	c.66	p.G22	tier1	6	0	0.000	1	8	0.889
270086	9	35906348	35906350	CTG	-	DEL	*HRCT1*	ENST00000354323	1	in_frame_del	c.64_66	p.L25in_frame_del	tier1	74	0	0.000	89	11	0.110
270086	14	23567883	23567883	A	T	SNP	*C14orf119*	ENST00000319074	1	3_prime_untranslated_region	c.*593	NULL	tier4	86	0	0.000	124	13	0.095
270086	19	633529	633530	-	GCGCCGCCGCCGCC	INS	*POLRMT*	ENST00000588649	-1	5_prime_untranslated_region	c.-17	NULL	tier2	16	0	0.000	16	10	0.385
270086	19	4817310	4817310	A	G	SNP	*TICAM1*	ENST00000248244	-1	silent	c.1080	p.P360	tier1	186	2	0.011	256	24	0.085
270086	21	14469103	14469103	G	A	SNP	*ZNF355P*	ENST00000427301	-1	5_prime_untranslated_region	c.-14469103	NULL	tier3	347	0	0.000	347	15	0.041
272848	1	145684679	145684679	G	A	SNP	*RNF115*	ENST00000369291	1	splice_site	c.667+1	e7+1	tier1	48	2	0.039	118	60	0.337
272848	2	65497525	65497525	A	G	SNP	*ACTR2*	ENST00000260641	1	3_prime_untranslated_region	c.*1657	NULL	tier3	46	0	0.000	62	43	0.410
272848	2	90109121	90109121	G	A	SNP	*IGKV1D-17*	ENST00000483379	1	5_prime_flanking_region	c.-12537	NULL	tier3	49	0	0.000	81	46	0.362
272848	2	144159094	144159094	A	T	SNP	*ARHGAP15*	ENST00000295095	1	intronic	c.475-34076	e6-34076	tier2	19	0	0.000	78	36	0.316
272848	3	37095520	37095520	A	G	SNP	*LRRFIP2*	ENST00000336686	-1	intronic	c.2056-68	e27-68	tier3	29	0	0.000	26	28	0.519
272848	3	39453515	39453515	A	G	SNP	*RPSA*	ENST00000301821	1	silent	c.756	p.V252	tier1	62	0	0.000	118	17	0.126
272848	3	41722946	41722946	G	-	DEL	*ULK4*	ENST00000301831	-1	intronic	c.2978+53	e28+53	tier3	40	0	0.000	57	32	0.360
272848	4	3891295	3891295	C	T	SNP	*OR7E163P*	ENST00000505943	-1	5_prime_untranslated_region	c.-3891295	NULL	tier3	43	0	0.000	67	35	0.343
272848	4	85654560	85654560	T	A	SNP	*WDFY3*	ENST00000295888	-1	missense	c.7196	p.E2399V	tier1	48	0	0.000	47	49	0.510
272848	4	140619263	140619263	T	A	SNP	*MGST2*	ENST00000265498	1	intronic	c.229+2842	e3+2842	tier3	50	0	0.000	105	16	0.132
272848	5	76433942	76433942	G	T	SNP	*ZBED3-AS1*	ENST00000502433	1	intronic	c.NULL	NULL	tier3	59	0	0.000	96	63	0.396
272848	5	140433285	140433285	C	A	SNP	*PCDHB1*	ENST00000306549	1	missense	c.2230	p.Q744K	tier1	343	1	0.003	554	353	0.389
272848	6	56374452	56374452	T	-	DEL	*DST*	ENST00000370754	-1	frame_shift_del	c.18907	p.I6303fs	tier1	263	0	0.000	535	290	0.352
272848	7	157509030	157509030	A	G	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1858-33401	e13-33401	tier3	44	0	0.000	14	8	0.364
272848	7	157509090	157509090	A	G	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1858-33461	e13-33461	tier3	47	2	0.041	13	14	0.519
272848	7	157509091	157509091	C	T	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1858-33462	e13-33462	tier3	48	1	0.020	13	13	0.482
272848	8	16026061	16026061	G	A	SNP	*MSR1*	ENST00000262101	-1	missense	c.536	p.S179F	tier1	40	0	0.000	42	28	0.400

272848	8	100523442	100523442	G	C	SNP	*VPS13B*	ENST00000358544	1	missense	c.4410	p.E1470D	tier1	47	0	0.000	70	59	0.457
272848	9	35480204	35480204	C	T	SNP	*ATP8B5P*	ENST00000329395	1	rna	NULL	NULL	tier1	44	0	0.000	18	23	0.561
272848	9	66457014	66457014	C	T	SNP	*LOC100996870*	ENST00000424345	1	5_prime_flanking_region	c.-275	NULL	tier4	45	0	0.000	69	14	0.169
272848	9	115932843	115932843	T	C	SNP	*FKBP15*	ENST00000238256	-1	missense	c.2725	p.N909D	tier1	55	1	0.018	84	25	0.227
272848	9	136634584	136634584	C	T	SNP	*VAV2*	ENST00000371850	-1	missense	c.2389	p.G797S	tier1	39	0	0.000	59	36	0.379
272848	10	69695996	69695996	T	C	SNP	*HERC4*	ENST00000395198	-1	splice_region	c.2596-4	e21-4	tier4	37	0	0.000	58	44	0.431
272848	10	99660362	99660362	C	T	SNP	*CRTAC1*	ENST00000370597	-1	intronic	c.1133+898	e8+898	tier3	248	2	0.008	252	256	0.503
272848	11	9081984	9081984	G	C	SNP	*SCUBE2*	ENST00000457346	-1	missense	c.938	p.T313S	tier1	50	1	0.020	54	32	0.372
272848	11	51411669	51411669	C	T	SNP	*OR4A5*	ENST00000319760	-1	missense	c.727	p.V243I	tier1	40	0	0.000	60	17	0.218
272848	11	85988219	85988219	A	G	SNP	*EED*	ENST00000525244	1	3_prime_untranslated_region	c.*85988219	NULL	tier3	62	0	0.000	169	148	0.467
272848	12	58159282	58159282	C	T	SNP	*CYP27B1*	ENST00000546609	-1	missense	c.299	p.R100Q	tier1	47	0	0.000	40	31	0.437
272848	15	41634594	41634594	T	A	SNP	*NUSAP1*	ENST00000559596	1	nonsense	c.104	p.L35*	tier1	35	0	0.000	69	44	0.389
272848	16	16272771	16272771	C	T	SNP	*ABCC6*	ENST00000205557	-1	missense	c.2299	p.V767I	tier1	50	0	0.000	80	17	0.175
272848	16	30793418	30793418	T	-	DEL	*ZNF629*	ENST00000262525	-1	frame_shift_del	c.2231	p.K744fs	tier1	45	0	0.000	43	35	0.449
272848	16	31090611	31090611	C	T	SNP	*ZNF646*	ENST00000300850	1	missense	c.2966	p.A989V	tier1	59	0	0.000	74	52	0.413
272848	16	53529201	53529201	C	T	SNP	*AKTIP*	ENST00000300245	-1	missense	c.286	p.V96M	tier1	30	0	0.000	57	41	0.418
272848	16	87870085	87870085	C	T	SNP	*SLC7A5*	ENST00000261622	-1	intronic	c.1290+19	e8+19	tier3	49	0	0.000	65	25	0.278
272848	17	33476023	33476023	C	A	SNP	*UNC45B*	ENST00000268876	1	missense	c.200	p.S67Y	tier1	32	0	0.000	41	24	0.369
272848	18	42531907	42531907	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2602	p.D868N	tier1	367	0	0.000	609	133	0.179
272848	18	42531913	42531913	G	T	SNP	*SETBP1*	ENST00000282030	1	missense	c.2608	p.G870C	tier1	367	0	0.000	527	189	0.264
272848	19	4310495	4310495	G	A	SNP	*FSD1*	ENST00000221856	1	missense	c.392	p.R131Q	tier1	36	0	0.000	56	42	0.429
272848	19	19351506	19351506	G	C	SNP	*NCAN*	ENST00000252575	1	intronic	c.3492+12	e11+12	tier3	40	0	0.000	41	29	0.414
272848	21	46957834	46957834	C	T	SNP	*SLC19A1*	ENST00000311124	-1	missense	c.40	p.V14M	tier1	53	0	0.000	58	38	0.396
272848	X	12739552	12739552	G	T	SNP	*FRMPD4*	ENST00000380682	1	3_prime_untranslated_region	c.*900	NULL	tier3	19	0	0.000	29	15	0.341
272848	X	77224984	77224984	T	C	SNP	*PGAM4*	ENST00000458128	-1	missense	c.152	p.E51G	tier1	81	0	0.000	55	36	0.391
272848	X	120008710	120008710	T	G	SNP	*CT47B1*	ENST00000371311	-1	intronic	c.775+40	e1+40	tier2	74	0	0.000	78	42	0.347
272848	X	145701712	145701712	G	A	SNP	*ENSG00000231686*	ENST00000445173	-1	5_prime_untranslated_region	c.-145701712	NULL	tier2	50	0	0.000	39	30	0.435
275454	1	1920435	1920435	A	-	DEL	*C1orf222*	ENST00000434971	-1	intronic	c.68-23	e2-23	tier3	95	0	0.000	165	18	0.098
275454	5	37212598	37212598	A	-	DEL	*C5orf42*	ENST00000425232	-1	intronic	c.2920+1063	e15+1063	tier3	43	0	0.000	82	14	0.146
275454	5	65475096	65475096	T	-	DEL	*SREK1*	ENST00000284041	1	rna	NULL	NULL	tier1	81	0	0.000	126	15	0.106
275454	5	131607200	131607200	C	T	SNP	*PDLIM4*	ENST00000462597	1	3_prime_untranslated_region	c.*131607200	NULL	tier2	131	0	0.000	234	15	0.060
275454	5	161579342	161579342	G	A	SNP	*GABRG2*	ENST00000356592	1	intronic	c.1152+583	e9+583	tier3	151	0	0.000	286	17	0.056
275454	12	107237614	107237615	-	T	INS	*RIC8B*	ENST00000392837	1	intronic	c.1066-16_1066-15	e6-15	tier3	73	1	0.014	117	23	0.164
275454	12	123107166	123107166	A	-	DEL	*KNTC1*	ENST00000333479	1	intronic	c.6515+12	e61+12	tier3	54	0	0.000	77	16	0.172
275454	14	19807134	19807134	G	T	SNP	*OR11H13P*	ENST00000359695	-1	5_prime_untranslated_region	c.-19807134	NULL	tier3	618	1	0.002	1105	29	0.026
275454	18	14809914	14809914	C	G	SNP	*ANKRD30B*	ENST00000358984	1	intronic	c.2313+1336	e25+1336	tier3	206	0	0.000	352	19	0.051
280837	1	1669668	1669668	G	C	SNP	*SLC35E2*	ENST00000246421	-1	intronic	c.586+92	e3+92	tier2	17	0	0.000	127	97	0.433
280837	1	27861349	27861349	T	G	SNP	*AHDC1*	ENST00000482400	-1	5_prime_untranslated_region	c.-27861349	NULL	tier3	32	1	0.030	96	43	0.309
280837	1	28605680	28605680	G	A	SNP	*SESN2*	ENST00000253063	1	silent	c.1284	p.V428	tier1	29	0	0.000	103	86	0.453
280837	1	71998450	71998450	C	T	SNP	*NEGR1*	ENST00000357731	-1	intronic	c.940+60050	e6+60050	tier3	63	2	0.031	123	70	0.363
280837	1	151675014	151675014	A	C	SNP	*CELF3*	ENST00000470688	-1	5_prime_untranslated_region	c.-151675014	NULL	tier2	87	2	0.022	199	35	0.150
280837	1	161976283	161976283	G	A	SNP	*OLFML2B*	ENST00000294794	-1	intronic	c.547-20	e4-20	tier3	47	4	0.078	32	37	0.507
280837	2	25467497	25467497	G	A	SNP	*DNMT3A*	ENST00000264709	-1	nonsense	c.1579	p.Q527*	tier1	122	5	0.039	622	489	0.437
280837	2	131453866	131453866	T	C	SNP	*ENSG00000240253*	ENST00000425151	1	intronic	c.NULL	NULL	tier3	42	1	0.023	74	62	0.456
280837	2	234184342	234184342	G	A	SNP	*ATG16L1*	ENST00000392017	1	intronic	c.954+918	e9+918	tier4	50	1	0.020	119	40	0.252
280837	3	118913221	118913221	C	T	SNP	*UPK1B*	ENST00000264234	1	silent	c.624	p.G208	tier1	59	0	0.000	103	100	0.490
280837	4	1949812	1949812	A	C	SNP	*WHSC1*	ENST00000398261	1	3_prime_untranslated_region	c.*5684	NULL	tier3	49	0	0.000	67	65	0.492
280837	4	71888174	71888174	G	T	SNP	*DCK*	ENST00000286648	1	missense	c.298	p.A100S	tier1	88	2	0.022	121	102	0.453
280837	4	76817552	76817552	G	C	SNP	*PPEF2*	ENST00000511880	-1	5_prime_untranslated_region	c.-74	NULL	tier2	21	0	0.000	90	71	0.438
280837	4	109769882	109769882	C	T	SNP	*COL25A1*	ENST00000399132	-1	intronic	c.1434+33	e26+33	tier3	80	0	0.000	92	58	0.384
280837	5	34190834	34190834	G	A	SNP	*ENSG00000215156*	ENST00000332686	1	3_prime_untranslated_region	c.*34190834	NULL	tier3	525	2	0.004	6549	156	0.023
280837	5	36958149	36958156	GTCTTCTT	-	DEL	*NIPBL*	ENST00000282516	1	intronic	c.231-57_231-50	e3-50	tier3	32	0	0.000	33	14	0.298
280837	5	36958159	36958178	GAATCAGTCACCATT TTAAT	-	DEL	*NIPBL*	ENST00000282516	1	intronic	c.231-47_231-28	e3-28	tier3	33	0	0.000	34	14	0.292
280837	5	74712651	74712651	C	A	SNP	*COL4A3BP*	ENST00000380494	-1	intronic	c.1221+50	e8+50	tier3	177	2	0.011	148	111	0.429
280837	6	33136506	33136506	C	T	SNP	*COL11A2*	ENST00000341947	-1	missense	c.3883	p.E1295K	tier1	31	0	0.000	192	144	0.427
280837	6	36698561	36698561	C	A	SNP	*PI16*	ENST00000536757	1	intronic	c.1+17544	e0+17544	tier4	13	0	0.000	40	40	0.500
280837	7	1055741	1055741	A	G	SNP	*C7orf50*	ENST00000357429	-1	intronic	c.130-5962	e2-5962	tier4	25	0	0.000	93	35	0.273
280837	7	1055742	1055742	G	C	SNP	*C7orf50*	ENST00000357429	-1	intronic	c.130-5963	e2-5963	tier4	26	0	0.000	91	37	0.287
280837	7	75050891	75050891	T	C	SNP	*POM121C*	ENST00000257665	-1	missense	c.3370	p.T1124A	tier1	23	0	0.000	33	31	0.477
280837	7	128553132	128553132	T	C	SNP	*ENSG00000224163*	ENST00000433622	-1	5_prime_untranslated_region	c.-128553132	NULL	tier3	23	0	0.000	23	20	0.465
280837	7	150714308	150714308	C	T	SNP	*ATG9B*	ENST00000377974	-1	5_prime_untranslated_region	c.-150714308	NULL	tier2	33	0	0.000	107	42	0.280
280837	7	157509090	157509090	A	G	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1858-33461	e13-33461	tier3	27	0	0.000	52	15	0.224
280837	7	157509091	157509091	C	T	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1858-33462	e13-33462	tier3	27	0	0.000	54	19	0.260
280837	7	157651592	157651592	C	T	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1857+39773	e12+39773	tier3	80	1	0.012	325	43	0.117
280837	8	131129068	131129068	C	T	SNP	*ASAP1*	ENST00000343135	-1	intronic	c.2005+58	e21+58	tier3	80	0	0.000	128	116	0.474
280837	9	139903977	139903977	G	A	SNP	*ABCA2*	ENST00000355090	-1	intronic	c.6824+16	e44+16	tier2	33	0	0.000	191	175	0.478
280837	10	38651191	38651191	G	A	SNP	*HSD17B7P2*	ENST00000494540	1	3_prime_untranslated_region	c.*38651191	NULL	tier3	142	2	0.014	173	151	0.466
280837	10	68139043	68139043	T	C	SNP	*CTNNA3*	ENST00000373744	-1	silent	c.1599	p.L533	tier1	96	0	0.000	141	116	0.450
280837	10	119044294	119044294	T	C	SNP	*PDZD8*	ENST00000334464	-1	silent	c.1950	p.Q650	tier1	57	1	0.017	108	78	0.419
280837	11	4107876	4107876	G	T	SNP	*STIM1*	ENST00000300737	1	intronic	c.1541+103	e11+103	tier3	28	0	0.000	81	73	0.474
280837	11	12225810	12225810	G	C	SNP	*MICAL2*	ENST00000256194	1	missense	c.278	p.G93A	tier1	48	0	0.000	98	73	0.424
280837	11	125255418	125255418	G	A	SNP	*PKNOX2*	ENST00000298282	1	intronic	c.228-29	e3-29	tier3	18	0	0.000	53	85	0.616
280837	12	12006417	12006418	-	T	INS	*ETV6*	ENST00000396373	1	frame_shift_ins	c.385_386	p.S131fs	tier1	151	1	0.007	510	293	0.365
280837	12	14689595	14689595	A	G	SNP	*PLBD1*	ENST00000240617	-1	missense	c.608	p.L203S	tier1	89	1	0.011	169	123	0.421

280837	12	50344754	50344754	G	A	SNP	*AQP2*	ENST00000199280	1	silent	c.141	p.A47	tier1	30	0	0.000	143	120	0.456
280837	17	1563288	1563288	T	A	SNP	*PRPF8*	ENST00000304992	-1	missense	c.4793	p.D1598V	tier1	87	1	0.011	479	400	0.454
280837	17	27210235	27210235	C	T	SNP	*FLOT2*	ENST00000394906	-1	silent	c.402	p.T134	tier1	19	1	0.050	125	112	0.473
280837	17	73910078	73910078	C	T	SNP	*FBF1*	ENST00000389570	-1	silent	c.3003	p.Q1001	tier1	9	0	0.000	150	123	0.447
280837	18	5891961	5891961	C	G	SNP	*TMEM200C*	ENST00000383490	-1	missense	c.102	p.R34S	tier1	23	0	0.000	84	56	0.400
280837	19	9001863	9001863	G	A	SNP	*MUC16*	ENST00000380947	-1	nonsense	c.904	p.R302*	tier1	87	1	0.011	376	334	0.468
280837	19	18553578	18553578	C	T	SNP	*ELL*	ENST00000262809	-1	3_prime_untranslated_region	c.*1984	NULL	tier3	583	0	0.000	1133	27	0.023
280837	19	51890473	51890473	C	T	SNP	*LIM2*	ENST00000221973	-1	silent	c.225	p.A75	tier1	28	0	0.000	91	58	0.389
280837	20	30409206	30409206	C	T	SNP	*MYLK2*	ENST00000375985	1	intronic	c.474-36	e3-36	tier3	18	0	0.000	80	56	0.412
280837	X	129147939	129147939	G	A	SNP	*BCORL1*	ENST00000303743	1	missense	c.1191	p.M397I	tier1	9	0	0.000	30	208	0.822
283773	1	33476435	33476435	C	A	SNP	*AK2*	ENST00000373449	-1	splice_site	c.695-1	e7-1	tier1	108	0	0.000	83	9	0.098
283773	1	89236209	89236209	G	T	SNP	*PKN2*	ENST00000370521	1	intronic	c.622+57	e4+57	tier3	53	0	0.000	22	6	0.214
283773	1	201180702	201180702	G	C	SNP	*IGFN1*	ENST00000335211	1	silent	c.6681	p.G2227	tier1	273	0	0.000	120	7	0.055
283773	1	211836204	211836204	G	A	SNP	*NEK2*	ENST00000366999	-1	3_prime_untranslated_region	c.*564	NULL	tier3	31	0	0.000	27	9	0.250
283773	2	20423047	20423048	-	A	INS	*SDC1*	ENST00000482879	-1	rna	NULL	NULL	tier1	133	1	0.008	50	7	0.123
283773	2	84668259	84668259	A	-	DEL	*SUCLG1*	ENST00000393868	-1	intronic	c.532-31	e5-31	tier3	56	0	0.000	52	10	0.161
283773	2	182399497	182399498	-	TT	INS	*ITGA4*	ENST00000397033	1	intronic	c.2884-46_2884-45	e27-45	tier3	7	0	0.000	3	7	0.700
283773	2	220082366	220082366	A	-	DEL	*ABCB6*	ENST00000265316	-1	intronic	c.687+26	e2+26	tier4	51	1	0.019	33	10	0.233
283773	5	132031958	132031958	T	-	DEL	*KIF3A*	ENST00000378735	-1	3_prime_untranslated_region	c.*368	NULL	tier3	48	0	0.000	35	9	0.205
283773	5	139905660	139905660	C	A	SNP	*ANKHD1*	ENST00000297183	1	missense	c.4572	p.F1524L	tier1	115	0	0.000	27	4	0.129
283773	6	100404004	100404004	G	T	SNP	*MCHR2*	ENST00000281806	-1	missense	c.20	p.S7Y	tier1	108	0	0.000	22	4	0.154
283773	7	86547738	86547738	A	G	SNP	*KIAA1324L*	ENST00000450689	-1	intronic	c.1593+20	e12+20	tier3	85	0	0.000	17	4	0.191
283773	7	127013340	127013340	T	-	DEL	*ZNF800*	ENST00000265827	-1	intronic	c.1994+56	e4+56	tier3	50	0	0.000	15	5	0.250
283773	8	101522892	101522892	A	-	DEL	*ANKRD46*	ENST00000520552	-1	intronic	c.637-25	e4-25	tier3	41	0	0.000	14	5	0.263
283773	9	20923717	20923717	G	A	SNP	*FOCAD*	ENST00000338382	1	missense	c.2911	p.V971I	tier1	99	0	0.000	24	6	0.200
283773	10	33619598	33619598	G	T	SNP	*NRP1*	ENST00000265371	-1	intronic	c.248+38	e2+38	tier2	139	0	0.000	33	4	0.108
283773	10	124359634	124359634	A	C	SNP	*DMBT1*	ENST00000338354	1	intronic	c.3310+25	e27+25	tier3	184	1	0.005	140	15	0.097
283773	11	559313	559313	C	-	DEL	*ENSG00000254815*	ENST00000527620	1	rna	NULL	NULL	tier1	66	0	0.000	15	4	0.211
283773	12	124144573	124144573	T	-	DEL	*GTF2H3*	ENST00000543341	1	intronic	c.821-20	e12-20	tier3	83	1	0.012	34	8	0.191
283773	14	72171435	72171435	C	T	SNP	*SIPA1L1*	ENST00000555818	1	splice_region	c.3647-3	e12-3	tier3	105	0	0.000	25	4	0.138
283773	15	42503954	42503954	A	-	DEL	*TMEM87A*	ENST00000389834	-1	splice_region_del	c.1627-7	e20-7	tier3	56	0	0.000	22	6	0.214
283773	16	4796967	4796967	G	A	SNP	*C16orf71*	ENST00000299320	1	silent	c.1221	p.E407	tier1	115	0	0.000	40	5	0.111
283773	19	2121672	2121672	C	T	SNP	*AP3D1*	ENST00000355272	-1	intronic	c.1101+61	e12+61	tier3	53	0	0.000	20	11	0.355
283773	20	31023112	31023112	T	G	SNP	*ASXL1*	ENST00000375687	1	nonsense	c.2597	p.L866*	tier1	1114	3	0.003	346	99	0.222
283773	20	31451686	31451686	G	T	SNP	*EFCAB8*	ENST00000400522	1	intronic	c.42+46	e1+46	tier3	69	0	0.000	39	6	0.133
283773	21	33919279	33919279	A	-	DEL	*RNA5SP490*	ENST00000517141	1	5_prime_flanking_region	c.-16106	NULL	tier3	54	0	0.000	34	7	0.171
283773	22	22114660	22114661	-	T	INS	*MAPK1*	ENST00000215832	-1	3_prime_untranslated_region	c.*8833	NULL	tier3	39	0	0.000	21	6	0.222
283773	22	29939380	29939380	G	T	SNP	*THOC5*	ENST00000397871	-1	intronic	c.354+38	e3+38	tier3	48	0	0.000	19	5	0.208
283773	22	50439189	50439189	C	-	DEL	*IL17REL*	ENST00000341280	-1	frame_shift_del	c.213	p.Q72fs	tier1	32	0	0.000	7	4	0.364
283773	X	70339865	70339865	T	A	SNP	*MED12*	ENST00000333646	1	missense	c.398	p.V133D	tier1	755	3	0.004	301	15	0.048
283773	X	76709731	76709731	C	T	SNP	*FGF16*	ENST00000439435	1	silent	c.84	p.S28	tier1	145	0	0.000	52	5	0.088
283773	X	106788960	106788960	T	C	SNP	*FRMPD3-AS1*	ENST00000415252	-1	rna	NULL	NULL	tier1	149	0	0.000	32	4	0.111
288033	1	146491965	146491965	G	C	SNP	*NBPF13P*	ENST00000444680	-1	intronic	c.NULL	NULL	tier3	123	2	0.016	240	27	0.101
288033	1	146492064	146492064	C	T	SNP	*NBPF13P*	ENST00000444680	-1	intronic	c.NULL	NULL	tier3	75	1	0.013	81	14	0.143
288033	2	33614218	33614218	G	T	SNP	*LTBP1*	ENST00000354476	1	intronic	c.4715-33	e32-33	tier3	91	2	0.022	81	91	0.529
288033	2	122369100	122369100	T	G	SNP	*CLASP1*	ENST00000263710	-1	intronic	c.1-5344	e1-5344	tier4	93	1	0.011	135	18	0.118
288033	2	183903211	183903211	G	A	SNP	*NCKAP1*	ENST00000360982	-1	5_prime_untranslated_region	c.-384	NULL	tier2	8	0	0.000	0	7	1.000
288033	3	126219009	126219009	C	A	SNP	*UROC1*	ENST00000290868	-1	intronic	c.1146-12	e12-12	tier3	106	3	0.028	79	63	0.444
288033	4	103611794	103611794	G	A	SNP	*MANBA*	ENST00000226578	-1	missense	c.808	p.P270S	tier1	102	3	0.029	78	74	0.484
288033	7	100839218	100839218	C	T	SNP	*MOGAT3*	ENST00000379423	-1	missense	c.832	p.A278T	tier1	83	0	0.000	90	11	0.109
288033	9	45120089	45120089	G	T	SNP	*ENSG00000231838*	ENST00000417850	1	5_prime_flanking_region	c.-44489	NULL	tier3	34	0	0.000	31	11	0.262
288033	9	90503384	90503384	G	C	SNP	*SPATA31E1*	ENST00000325643	1	missense	c.3982	p.V1328L	tier1	42	1	0.023	19	27	0.587
288033	9	136918842	136918842	T	C	SNP	*BRD3*	ENST00000433041	-1	5_prime_untranslated_region	c.-243	NULL	tier3	74	1	0.013	65	33	0.337
288033	11	1997318	1997318	T	C	SNP	*MRPL23*	ENST00000397297	1	intronic	c.497+3330	e5+3330	tier3	325	7	0.021	404	36	0.081
288033	12	64474024	64474024	A	-	DEL	*SRGAP1*	ENST00000355086	1	intronic	c.1324-42	e10-42	tier4	89	2	0.022	62	13	0.173
288033	12	85285921	85285921	A	-	DEL	*SLC6A15*	ENST00000266682	-1	5_prime_untranslated_region	c.-22	NULL	tier4	40	0	0.000	37	8	0.178
288033	12	133201355	133201355	C	T	SNP	*POLE*	ENST00000320574	-1	silent	c.6789	p.Q2263	tier1	147	0	0.000	187	16	0.079
288033	14	106330469	106330469	T	C	SNP	*IGHJ4*	ENST00000461719	-1	missense	c.2	p.Y1C	tier1	393	0	0.000	412	16	0.037
288033	15	85327071	85327071	C	T	SNP	*ZNF592*	ENST00000299927	1	missense	c.1165	p.R389W	tier1	79	0	0.000	87	13	0.130
288033	17	10350420	10350420	C	T	SNP	*MYH4*	ENST00000255381	-1	silent	c.5079	p.R1693	tier1	607	16	0.026	495	445	0.473
288033	17	67178774	67178774	A	C	SNP	*ABCA10*	ENST00000269081	-1	intronic	c.2631+42	e19+42	tier3	32	0	0.000	33	9	0.118
288033	19	13941346	13941346	C	G	SNP	*ZSWIM4*	ENST00000254323	1	missense	c.2452	p.P818A	tier1	28	0	0.000	23	27	0.540
288033	19	33793252	33793253	-	G	INS	*CEBPA*	ENST00000498907	-1	frame_shift_ins	c.69_68	p.H24fs	tier1	811	9	0.011	957	184	0.161
288033	20	43723594	43723594	A	T	SNP	*KCNS1*	ENST00000306117	-1	missense	c.1498	p.S500T	tier1	46	0	0.000	47	44	0.484
288033	20	57768618	57768618	G	A	SNP	*ZNF831*	ENST00000371030	1	silent	c.2544	p.T848	tier1	39	2	0.049	50	46	0.479
288033	21	42838094	42838094	A	-	DEL	*TMPRSS2*	ENST00000398585	-1	intronic	c.1579-14	e14-14	tier3	58	0	0.000	71	10	0.124
288033	22	41742111	41742111	C	T	SNP	*ZC3H7B*	ENST00000351589	1	missense	c.1564	p.R522C	tier1	55	2	0.035	44	47	0.517
288033	22	50960184	50960184	G	A	SNP	*NCAPH2*	ENST00000299821	1	missense	c.1015	p.V339M	tier1	76	3	0.038	66	82	0.554
288033	X	107512391	107512391	A	-	DEL	*COL4A6*	ENST00000461897	-1	splice_region_del	c.NULL	NULL	tier3	107	0	0.000	106	11	0.094
293230	1	201947766	201947766	A	G	SNP	*RNPEP*	ENST00000295640	1	5_prime_flanking_region	c.-4029	NULL	tier3	156	5	0.031	149	43	0.223
293230	2	21232014	21232014	G	A	SNP	*APOB*	ENST00000233242	-1	missense	c.7726	p.R2576C	tier1	827	3	0.004	1221	99	0.075
293230	2	25457242	25457242	C	T	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.2645	p.R882H	tier1	420	19	0.043	385	138	0.264
293230	2	133489315	133489315	G	A	SNP	*NCKAP5*	ENST00000317721	-1	missense	c.5438	p.S1813F	tier1	105	1	0.009	115	46	0.284
293230	2	170092614	170092614	G	A	SNP	*LRP2*	ENST00000263816	-1	intronic	c.4692-36	e29-36	tier3	58	1	0.017	72	18	0.200

293230	5	5462936	5462936	T	C	SNP	*KIAA0947*	ENST00000296564	1	silent	c.3489	p.T1163	tier1	108	1	0.009	156	21	0.119
293230	5	67522723	67522723	G	T	SNP	*PIK3R1*	ENST00000396611	1	missense	c.220	p.V74L	tier1	182	0	0.000	242	14	0.055
293230	6	125146129	125146129	G	T	SNP	*NKAIN2*	ENST00000368417	1	3_prime_untranslated_region	c.*1754	NULL	tier3	44	1	0.022	118	31	0.208
293230	6	159653093	159653093	G	C	SNP	*FNDC1*	ENST00000297267	1	missense	c.1549	p.G517R	tier1	87	2	0.023	87	18	0.171
293230	9	138641963	138641963	G	A	SNP	*KCNT1*	ENST00000298480	1	missense	c.274	p.V92I	tier1	651	5	0.008	771	60	0.072
293230	12	56844914	56844914	G	A	SNP	*MIP*	ENST00000257979	-1	3_prime_untranslated_region	c.*150	NULL	tier3	43	0	0.000	42	9	0.173
293230	12	133159733	133159733	C	T	SNP	*FBRSL1*	ENST00000434748	1	missense	c.2507	p.A836V	tier1	8	0	0.000	3	7	0.700
293230	15	34130377	34130377	C	T	SNP	*RYR3*	ENST00000389232	1	nonsense	c.12196	p.R4066*	tier1	1002	0	0.000	1296	74	0.054
293230	15	91044236	91044236	G	A	SNP	*IQGAP1*	ENST00000268182	1	3_prime_untranslated_region	c.*896	NULL	tier3	223	0	0.000	365	21	0.054
293230	16	1116377	1116377	C	T	SNP	*ENSG00000261720*	ENST00000564390	1	rna	NULL	NULL	tier1	82	2	0.024	55	14	0.194
293230	16	12297010	12297010	T	G	SNP	*SNX29*	ENST00000306030	1	intronic	c.523+3470	e6+3470	tier3	356	8	0.022	513	47	0.084
293230	16	67962332	67962332	G	C	SNP	*PSKH1*	ENST00000291041	1	3_prime_untranslated_region	c.*787	NULL	tier2	88	0	0.000	85	22	0.202
293230	19	7995988	7995988	A	-	DEL	*TIMM44*	ENST00000270538	-1	intronic	c.1038+35	e10+35	tier3	22	0	0.000	30	13	0.302
293230	X	72224144	72224145	-	C	INS	*PABPC1L2B*	ENST00000373521	1	3_prime_untranslated_region	c.*60	NULL	tier2	14	0	0.000	4	5	0.556
298273	1	46159297	46159297	C	T	SNP	*TMEM69*	ENST00000372025	1	missense	c.464	p.A155V	tier1	49	1	0.020	125	100	0.443
298273	1	151262327	151262328	-	C	INS	*ZNF687*	ENST00000324048	1	frame_shift_ins	c.2808_2809	p.R938fs	tier1	382	1	0.003	514	321	0.384
298273	1	183498545	183498545	G	T	SNP	*SMG7*	ENST00000507469	1	silent	c.720	p.V240	tier1	65	0	0.000	97	63	0.394
298273	2	101099723	101099723	G	A	SNP	*NMS*	ENST00000376865	1	nonsense	c.459	p.W153*	tier1	39	0	0.000	73	53	0.421
298273	3	14106117	14106117	T	C	SNP	*TPRXL*	ENST00000326972	1	silent	c.441	p.S147	tier1	48	0	0.000	94	19	0.168
298273	3	46759141	46759141	C	T	SNP	*PRSS50*	ENST00000315170	-1	intronic	c.107-14	e2-14	tier2	79	0	0.000	82	58	0.414
298273	3	50339933	50339933	C	T	SNP	*HYAL1*	ENST00000266031	-1	missense	c.455	p.R152Q	tier1	46	0	0.000	49	22	0.306
298273	3	58792080	58792081	-	T	INS	*C3orf67*	ENST00000482387	-1	intronic	c.1862+40_1862+39	e11+40	tier3	15	0	0.000	70	39	0.358
298273	3	158407931	158407931	T	-	DEL	*GFM1*	ENST00000486715	1	intronic	c.1910-21	e16-21	tier3	25	0	0.000	50	15	0.231
298273	5	31405700	31405701	-	A	INS	*DROSHA*	ENST00000344624	-1	intronic	c.3994+83_3994+82	e32+83	tier3	21	0	0.000	61	21	0.256
298273	5	140596188	140596188	G	A	SNP	*PCDHB13*	ENST00000341948	1	3_prime_untranslated_region	c.*96	NULL	tier3	24	0	0.000	54	35	0.393
298273	5	170837543	170837544	-	TCTG	INS	*NPM1*	ENST00000296930	1	frame_shift_ins	c.859_860	p.W288fs	tier1	108	2	0.018	283	133	0.320
298273	5	179150788	179150789	-	T	INS	*CANX*	ENST00000415618	1	splice_region_ins	c.1623+8_1623+7	e12+8	tier3	35	0	0.000	83	18	0.178
298273	6	10397893	10397894	-	A	INS	*TFAP2A*	ENST00000379604	-1	3_prime_untranslated_region	c.*757	NULL	tier3	16	0	0.000	26	16	0.381
298273	6	152461140	152461140	C	T	SNP	*SYNE1*	ENST00000265368	-1	missense	c.25403	p.R8468H	tier1	68	0	0.000	52	50	0.490
298273	7	64275471	64275471	T	-	DEL	*ZNF138*	ENST00000359735	1	intronic	c.1+49	e0+49	tier3	31	0	0.000	72	21	0.226
298273	7	131071805	131071805	T	G	SNP	*MKLN1*	ENST00000352689	1	intronic	c.169-74	e3-74	tier3	9	0	0.000	27	31	0.535
298273	10	94773927	94773928	-	T	INS	*EXOC6*	ENST00000371547	1	intronic	c.2144-24_2144-23	e21-23	tier3	12	0	0.000	35	29	0.453
298273	10	112340661	112340661	G	A	SNP	*SMC3*	ENST00000361804	1	splice_site	c.430-1	e8-1	tier1	196	0	0.000	654	30	0.044
298273	11	1092457	1092457	A	C	SNP	*MUC2*	ENST00000441003	1	missense	c.4276	p.T1426P	tier1	188	3	0.016	425	38	0.082
298273	11	134605529	134605529	A	G	SNP	*ENSG00000251226*	ENST00000513405	1	rna	NULL	NULL	tier1	120	1	0.008	222	35	0.136
298273	13	49073878	49073878	C	T	SNP	*RCBTB2*	ENST00000430805	-1	silent	c.1278	p.S426	tier1	41	0	0.000	50	45	0.474
298273	14	21841578	21841578	A	G	SNP	*SUPT16H*	ENST00000216297	-1	silent	c.78	p.D26	tier1	24	0	0.000	75	44	0.367
298273	17	1563288	1563288	T	C	SNP	*PRPF8*	ENST00000304992	-1	missense	c.4793	p.D1598G	tier1	266	2	0.007	432	319	0.423
298273	17	35503592	35503592	A	G	SNP	*ACACA*	ENST00000353139	-1	intronic	c.5679+3196	e45+3196	tier3	36	2	0.053	32	21	0.396
298273	17	66873661	66873661	G	A	SNP	*ABCA8*	ENST00000430352	-1	missense	c.4198	p.R1400W	tier1	91	0	0.000	93	70	0.429
298273	19	8436034	8436034	C	T	SNP	*ANGPTL4*	ENST00000301455	1	silent	c.756	p.H252	tier1	91	1	0.011	154	109	0.414
298273	19	36015866	36015866	C	A	SNP	*SBSN*	ENST00000518157	-1	intronic	c.610-40	e3-40	tier3	66	0	0.000	74	68	0.479
298273	20	1106550	1106550	G	A	SNP	*PSMF1*	ENST00000333082	1	intronic	c.282+257	e2+257	tier3	34	0	0.000	66	68	0.508
298273	21	10934043	10934043	G	A	SNP	*TPTE*	ENST00000361285	-1	silent	c.934	p.L312	tier1	244	0	0.000	810	126	0.135
298273	21	43533838	43533838	G	A	SNP	*UMODL1*	ENST00000408989	1	missense	c.2644	p.V882M	tier1	33	0	0.000	47	48	0.505
298273	22	20710809	20710809	C	G	SNP	*FAM230A*	ENST00000434783	1	silent	c.2541	p.T847	tier1	156	1	0.006	394	31	0.073
298273	X	22196368	22196370	TGT	-	DEL	*PHEX*	ENST00000379374	1	intronic	c.1483-22_1483-20	e14-20	tier2	24	0	0.000	18	49	0.731
298273	X	135761723	135761724	-	A	INS	*ARHGEF6*	ENST00000250617	-1	frame_shift_ins	c.1801_1800	p.R600fs	tier1	34	0	0.000	28	83	0.748
307995	1	34052117	34052117	G	A	SNP	*CSMD2*	ENST00000373381	-1	silent	c.7038	p.P2346	tier1	82	0	0.000	212	48	0.185
307995	1	121137613	121137613	T	A	SNP	*SRGAP2-AS1*	ENST00000437515	-1	intronic	c.NULL	NULL	tier3	47	1	0.019	67	17	0.185
307995	1	159174836	159174836	C	T	SNP	*DARC*	ENST00000368122	1	intronic	c.21+66	e1+66	tier2	35	0	0.000	95	20	0.172
307995	1	207218940	207218940	G	T	SNP	*YOD1*	ENST00000315927	-1	3_prime_untranslated_region	c.*3425	NULL	tier3	66	0	0.000	123	18	0.126
307995	2	27325149	27325149	C	G	SNP	*CGREF1*	ENST00000467539	-1	5_prime_untranslated_region	c.-27325149	NULL	tier2	30	0	0.000	82	25	0.234
307995	2	43986084	43986084	A	G	SNP	*PLEKHH2*	ENST00000490038	1	missense	c.253	p.T85A	tier1	41	0	0.000	135	23	0.144
307995	2	61510631	61510631	T	C	SNP	*USP34*	ENST00000398571	-1	intronic	c.4833-47	e36-47	tier3	103	0	0.000	179	43	0.193
307995	2	138738953	138738953	C	T	SNP	*HNMT*	ENST00000329366	1	silent	c.358	p.L120	tier1	84	0	0.000	171	37	0.178
307995	2	207310122	207310122	T	C	SNP	*ADAM23*	ENST00000264377	1	silent	c.306	p.S102	tier1	45	0	0.000	97	31	0.242
307995	3	9517257	9517257	G	T	SNP	*SETD5*	ENST00000402198	1	nonsense	c.3811	p.G1271*	tier1	32	0	0.000	84	27	0.243
307995	3	30702951	30702951	G	A	SNP	*TGFBR2*	ENST00000359013	1	intronic	c.530-10179	e5-10179	tier4	65	0	0.000	98	17	0.148
307995	3	126180517	126180517	G	A	SNP	*ZXDC*	ENST00000389709	-1	missense	c.1988	p.P663L	tier1	27	0	0.000	58	24	0.293
307995	4	107154095	107154095	C	A	SNP	*TBCK*	ENST00000273980	-1	missense	c.1639	p.G547C	tier1	59	1	0.017	67	15	0.183
307995	5	5235176	5235176	C	T	SNP	*ADAMTS16*	ENST00000274181	1	missense	c.1900	p.L634F	tier1	69	0	0.000	250	47	0.158
307995	5	14364017	14364017	C	A	SNP	*TRIO*	ENST00000344204	1	silent	c.2568	p.V856	tier1	69	0	0.000	118	34	0.222
307995	5	140174742	140174742	C	T	SNP	*PCDHA2*	ENST00000526136	1	missense	c.193	p.R65W	tier1	338	0	0.000	906	127	0.123
307995	6	32713784	32713784	C	A	SNP	*HLA-DQA2*	ENST00000374940	1	missense	c.548	p.A183D	tier1	137	5	0.035	371	81	0.178
307995	6	38743672	38743672	G	A	SNP	*DNAH8*	ENST00000359357	1	missense	c.1256	p.R419K	tier1	48	0	0.000	155	27	0.148
307995	7	29689532	29689532	T	A	SNP	*ZNRF2P2*	ENST00000442865	-1	intronic	c.NULL	NULL	tier2	69	0	0.000	187	49	0.206
307995	7	98639905	98639905	T	-	DEL	*SMURF1*	ENST00000361125	-1	intronic	c.1335-50	e13-50	tier4	29	0	0.000	53	16	0.232
307995	9	38414100	38414100	C	T	SNP	*IGFBPL1*	ENST00000377694	-1	silent	c.561	p.T187	tier1	54	0	0.000	136	39	0.223
307995	9	44109281	44109281	C	T	SNP	*ANKRD20A7P*	ENST00000402318	-1	intronic	c.NULL	NULL	tier3	105	3	0.028	116	25	0.177
307995	9	124737164	124737164	T	C	SNP	*TTLL11*	ENST00000321582	-1	missense	c.1634	p.E545G	tier1	69	0	0.000	106	13	0.109
307995	11	48387526	48387526	G	T	SNP	*OR4C5*	ENST00000319813	-1	silent	c.492	p.L164	tier1	27	1	0.036	54	33	0.375
307995	11	67049830	67049830	C	G	SNP	*ADRBK1*	ENST00000308595	1	missense	c.1046	p.A349G	tier1	120	0	0.000	346	63	0.154
307995	11	90016247	90016247	G	A	SNP	*ENSG00000214391*	ENST00000530835	1	3_prime_untranslated_region	c.*90016247	NULL	tier2	129	0	0.000	321	70	0.179

307995	12	9095076	9095076	C	G	SNP	*M6PR*	ENST00000000412	-1	missense	c.647	p.G216A	tier1	57	0	0.000	129	20	0.133
307995	12	50027356	50027356	G	A	SNP	*PRPF40B*	ENST00000548825	1	intronic	c.580+26	e8+26	tier3	496	0	0.000	1312	317	0.194
307995	12	52715016	52715016	G	T	SNP	*KRT83*	ENST00000293670	-1	missense	c.104	p.A35D	tier1	102	0	0.000	219	73	0.249
307995	12	52891238	52891238	T	A	SNP	*KRT6C*	ENST00000252250	-1	5_prime_flanking_region	c.-23717	NULL	tier3	185	0	0.000	390	106	0.213
307995	12	109519720	109519720	C	T	SNP	*USP30*	ENST00000257548	1	intronic	c.781-18	e9-18	tier3	44	0	0.000	120	22	0.155
307995	14	19378051	19378051	G	C	SNP	*OR11H12*	ENST00000550708	1	missense	c.458	p.G153A	tier1	1326	0	0.000	3626	167	0.044
307995	14	94945375	94945375	G	A	SNP	*SERPINA9*	ENST00000539349	-1	intronic	c.NULL	NULL	tier3	133	0	0.000	261	54	0.170
307995	15	45725117	45725118	-	T	INS	*C15orf48*	ENST00000344300	1	intronic	c.184-29_184-28	e4-28	tier3	73	1	0.014	114	20	0.149
307995	16	49315688	49315688	G	T	SNP	*CBLN1*	ENST00000219197	-1	5_prime_untranslated_region	c.-312	NULL	tier4	13	0	0.000	34	23	0.404
307995	17	61986092	61986092	G	C	SNP	*GH2*	ENST00000332800	-1	5_prime_flanking_region	c.-26931	NULL	tier3	135	0	0.000	233	57	0.196
307995	18	50683690	50683690	C	T	SNP	*DCC*	ENST00000442544	1	intronic	c.1262-36	e8-36	tier3	94	0	0.000	153	39	0.203
307995	20	47247205	47247205	C	T	SNP	*PREX1*	ENST00000371941	-1	intronic	c.4593+61	e36+61	tier3	42	0	0.000	147	28	0.160
307995	20	56082765	56082765	C	T	SNP	*CTCFL*	ENST00000432255	-1	silent	c.1326	p.P442	tier1	54	0	0.000	105	31	0.226
307995	20	58349240	58349240	G	A	SNP	*PHACTR3*	ENST00000371015	1	intronic	c.927-58	e7-58	tier3	83	0	0.000	159	37	0.189
307995	21	36252994	36252995	-	CC	INS	*RUNX1*	ENST00000300305	-1	frame_shift_ins	c.368_367	p.D123fs	tier1	833	0	0.000	1991	374	0.158
307995	22	20171118	20171118	C	T	SNP	*LINC00896*	ENST00000423736	1	5_prime_flanking_region	c.-22982	NULL	tier3	27	0	0.000	104	38	0.268
307995	X	39911641	39911641	C	T	SNP	*BCOR*	ENST00000378444	-1	nonsense	c.4989	p.W1663*	tier1	189	0	0.000	371	135	0.266
307995	X	53574723	53574723	G	T	SNP	*HUWE1*	ENST00000262854	-1	missense	c.10547	p.A3516D	tier1	41	0	0.000	87	36	0.293
307995	X	151336800	151336800	C	T	SNP	*GABRA3*	ENST00000370314	-1	missense	c.1379	p.R460H	tier1	75	0	0.000	158	62	0.282
311426	1	15987264	15987264	T	C	SNP	*RSC1A1*	ENST00000345034	1	silent	c.901	p.L301	tier1	31	0	0.000	54	41	0.432
311426	1	23660085	23660085	T	C	SNP	*HNRNPR*	ENST00000374616	-1	missense	c.424	p.T142A	tier1	74	2	0.026	105	69	0.397
311426	1	26795865	26795865	A	G	SNP	*DHDDS*	ENST00000360009	1	3_prime_untranslated_region	c.*243	NULL	tier3	77	3	0.038	69	67	0.489
311426	1	47904000	47904000	G	A	SNP	*FOXD2*	ENST00000334793	1	missense	c.193	p.A65T	tier1	6	0	0.000	3	9	0.750
311426	1	211433418	211433418	T	A	SNP	*RCOR3*	ENST00000367005	1	5_prime_untranslated_region	c.-40	NULL	tier4	65	1	0.015	58	38	0.392
311426	3	158380318	158380318	C	T	SNP	*GFM1*	ENST00000486715	1	intronic	c.1324-99	e11-99	tier3	28	1	0.035	34	21	0.382
311426	5	228288	228288	C	T	SNP	*SDHA*	ENST00000514027	1	3_prime_untranslated_region	c.*228288	NULL	tier3	161	0	0.000	154	10	0.061
311426	5	68849514	68849514	T	G	SNP	*OCLN*	ENST00000514370	1	rna	NULL	NULL	tier1	72	3	0.040	104	88	0.458
311426	5	108691731	108691731	A	-	DEL	*PJA2*	ENST00000361189	-1	splice_region_del	c.1653-4	e6-4	tier3	35	0	0.000	57	17	0.230
311426	5	118824832	118824832	G	A	SNP	*HSD17B4*	ENST00000256216	1	intronic	c.623-55	e9-55	tier3	55	2	0.035	52	33	0.388
311426	5	156659265	156659265	A	G	SNP	*ITK*	ENST00000422843	1	intronic	c.714-85	e8-85	tier3	51	2	0.038	59	42	0.416
311426	6	43481400	43481400	A	G	SNP	*YIPF3*	ENST00000372417	-1	5_prime_untranslated_region	c.-43481400	NULL	tier3	20	0	0.000	30	17	0.362
311426	6	75798722	75798722	C	-	DEL	*COL12A1*	ENST00000322507	-1	intronic	c.9010+100	e63+100	tier4	132	2	0.015	118	14	0.106
311426	6	96651060	96651060	G	A	SNP	*FUT9*	ENST00000302103	1	missense	c.29	p.R10H	tier1	66	0	0.000	89	54	0.375
311426	7	100643736	100643736	T	C	SNP	*MUC12*	ENST00000536621	1	missense	c.9892	p.S3298P	tier1	462	5	0.011	756	61	0.075
311426	7	120390342	120390342	C	A	SNP	*KCND2*	ENST00000331113	1	3_prime_untranslated_region	c.*2430	NULL	tier2	30	0	0.000	30	20	0.400
311426	7	141791778	141791778	G	A	SNP	*MGAM*	ENST00000475668	1	silent	c.6876	p.R2292	tier1	142	5	0.034	102	73	0.417
311426	7	151945554	151945554	G	A	SNP	*KMT2C*	ENST00000355193	-1	silent	c.1965	p.V655	tier1	318	17	0.051	467	332	0.416
311426	8	2857551	2857551	C	T	SNP	*CSMD1*	ENST00000520002	-1	missense	c.8135	p.R2712Q	tier1	703	23	0.032	607	490	0.446
311426	9	35301169	35301169	T	C	SNP	*UNC13B*	ENST00000378496	1	intronic	c.761+5242	e8+5242	tier3	57	2	0.034	95	56	0.371
311426	9	113086243	113086243	A	G	SNP	*TXNDC8*	ENST00000374507	-1	silent	c.234	p.H78	tier1	109	5	0.044	95	61	0.389
311426	10	123727090	123727090	A	T	SNP	*NSMCE4A*	ENST00000481320	-1	5_prime_untranslated_region	c.-123727090	NULL	tier3	57	0	0.000	81	62	0.434
311426	11	247379	247379	G	A	SNP	*PSMD13*	ENST00000431206	1	missense	c.505	p.G169R	tier1	145	5	0.033	152	90	0.372
311426	11	10831943	10831944	-	A	INS	*LOC101928053*	ENST00000499765	1	intronic	c.NULL	NULL	tier3	31	0	0.000	39	23	0.371
311426	11	75378554	75378554	C	T	SNP	*MAP6*	ENST00000304771	-1	silent	c.861	p.R287	tier1	16	0	0.000	2	3	0.600
311426	11	125616169	125616169	G	A	SNP	*PATE1*	ENST00000305738	1	5_prime_flanking_region	c.-31	NULL	tier3	77	5	0.061	71	50	0.413
311426	12	13714497	13714497	C	A	SNP	*GRIN2B*	ENST00000609686	-1	3_prime_untranslated_region	c.*1220	NULL	tier3	162	5	0.030	127	126	0.496
311426	12	78334060	78334060	C	T	SNP	*NAV3*	ENST00000549369	1	rna	NULL	NULL	tier1	61	2	0.032	44	39	0.470
311426	12	106853134	106853134	A	T	SNP	*POLR3B*	ENST00000228347	1	missense	c.2558	p.D853V	tier1	71	2	0.027	89	65	0.422
311426	13	26114392	26114392	T	C	SNP	*ATP8A2*	ENST00000381655	1	intronic	c.582-65	e8-65	tier3	77	0	0.000	67	51	0.432
311426	14	99988655	99988655	G	A	SNP	*CCDC85C*	ENST00000380243	-1	intronic	c.868-78	e3-78	tier3	68	2	0.029	57	47	0.452
311426	15	48065413	48065413	C	T	SNP	*SEMA6D*	ENST00000316364	1	3_prime_untranslated_region	c.*1431	NULL	tier3	48	0	0.000	63	42	0.400
311426	15	72037471	72037471	G	A	SNP	*THSD4*	ENST00000261862	1	missense	c.1933	p.V645M	tier1	67	4	0.056	40	36	0.474
311426	16	90162620	90162620	T	G	SNP	*TUBB8P7*	ENST00000564451	1	rna	NULL	NULL	tier1	190	0	0.000	263	15	0.054
311426	19	16145115	16145115	C	A	SNP	*LINC00905*	ENST00000397365	1	intronic	c.NULL	NULL	tier3	44	1	0.022	40	34	0.453
311426	19	19767521	19767521	C	T	SNP	*ATP13A1*	ENST00000357324	-1	missense	c.1031	p.R344H	tier1	34	1	0.029	50	32	0.390
311426	21	44524456	44524456	G	A	SNP	*U2AF1*	ENST00000291552	-1	missense	c.101	p.S34F	tier1	373	17	0.044	387	388	0.499
311426	X	138698653	138698653	A	-	DEL	*MCF2*	ENST00000370578	-1	intronic	c.1435-21	e12-21	tier3	79	1	0.013	113	17	0.131
329866	1	55129373	55129373	A	C	SNP	*MROH7-TTC4*	ENST00000414150	1	intronic	c.1232-1467	e2-1467	tier4	17	0	0.000	37	21	0.362
329866	1	89615249	89615249	C	T	SNP	*GBP7*	ENST00000294671	-1	missense	c.878	p.G293E	tier1	256	0	0.000	708	287	0.288
329866	1	244715862	244715862	A	G	SNP	*C1orf101*	ENST00000366531	1	missense	c.322	p.T108A	tier1	24	0	0.000	58	35	0.376
329866	2	238436052	238436052	C	T	SNP	*MLPH*	ENST00000264605	1	silent	c.913	p.L305	tier1	51	0	0.000	113	67	0.370
329866	3	56037242	56037242	A	-	DEL	*ERC2*	ENST00000288221	-1	intronic	c.2061+3967	e9+3967	tier3	24	0	0.000	73	38	0.342
329866	3	75467466	75467466	G	A	SNP	*ALG1L6P*	ENST00000515248	1	intronic	c.NULL	NULL	tier3	84	0	0.000	275	25	0.083
329866	3	112190167	112190167	C	T	SNP	*BTLA*	ENST00000334529	-1	missense	c.439	p.E147K	tier1	65	2	0.030	172	107	0.382
329866	3	127381208	127381208	G	A	SNP	*PODXL2*	ENST00000342480	1	intronic	c.1206+54	e4+54	tier3	21	0	0.000	57	32	0.356
329866	3	132363753	132363753	A	-	DEL	*ACAD11*	ENST00000264990	-1	intronic	c.150-13	e2-13	tier3	42	0	0.000	107	27	0.202
329866	3	164700861	164700861	G	A	SNP	*SI*	ENST00000264382	-1	intronic	c.5198-22	e45-22	tier3	197	0	0.000	347	154	0.307
329866	4	88536147	88536155	ACAGCAGCA	-	DEL	*DSPP*	ENST00000282478	1	in_frame_del	c.2333_2341	p.NSS781in_frame_del	tier1	107	0	0.000	309	28	0.083
329866	4	104007719	104007719	A	-	DEL	*BDH2*	ENST00000296424	-1	intronic	c.358-22	e5-22	tier3	12	0	0.000	55	38	0.409
329866	4	174447764	174447765	-	A	INS	*HAND2*	ENST00000359562	-1	3_prime_untranslated_region	c.*664	NULL	tier2	12	0	0.000	31	26	0.456
329866	7	76657407	76657408	-	CC	INS	*DTX2P1-UPK3BP1-PMS2P11*	ENST00000579700	1	intronic	c.NULL	NULL	tier3	167	18	0.097	113	119	0.513
329866	7	76657411	76657411	T	C	SNP	*DTX2P1-UPK3BP1-PMS2P11*	ENST00000579700	1	intronic	c.NULL	NULL	tier3	163	22	0.119	99	135	0.575
329866	8	81399048	81399050	GTC	-	DEL	*ZBTB10*	ENST00000430430	1	in_frame_del	c.3_5	p.S2in_frame_del	tier1	9	0	0.000	18	34	0.654
329866	8	92971169	92971170	AG	-	DEL	*RUNX1T1*	ENST00000265814	-1	3_prime_untranslated_region	c.*1301	NULL	tier3	10	0	0.000	17	15	0.469

329866	8	140768860	140768860	A	G	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-24415	e22-24415	tier3	67	0	0.000	317	32	0.091
329866	9	35076941	35076941	C	T	SNP	*FANCG*	ENST00000378643	-1	intronic	c.777+27	e6+27	tier3	40	0	0.000	100	46	0.315
329866	9	36204051	36204051	C	G	SNP	*CLTA*	ENST00000464497	1	intronic	c.374-14	e4-14	tier3	34	0	0.000	83	59	0.416
329866	9	68433510	68433510	C	G	SNP	*ENSG00000215548*	ENST00000376334	-1	5_prime_untranslated_region	c.-68433510	NULL	tier3	83	0	0.000	204	26	0.113
329866	10	112360315	112360316	-	T	INS	*SMC3*	ENST00000361804	1	intronic	c.2535+11_2535+10	e22+11	tier3	135	1	0.007	278	26	0.086
329866	11	20178072	20178072	C	T	SNP	*DBX1*	ENST00000227256	-1	silent	c.837	p.K279	tier1	67	1	0.015	203	106	0.343
329866	12	22211533	22211533	C	G	SNP	*CMAS*	ENST00000229329	1	missense	c.592	p.P198A	tier1	86	0	0.000	187	55	0.227
329866	12	22211534	22211534	C	T	SNP	*CMAS*	ENST00000229329	1	missense	c.593	p.P198L	tier1	86	0	0.000	189	55	0.225
329866	12	57037304	57037304	T	C	SNP	*ATP5B*	ENST00000552959	-1	missense	c.484	p.S162G	tier1	32	0	0.000	88	46	0.343
329866	12	114832571	114832571	G	A	SNP	*TBX5*	ENST00000310346	-1	missense	c.638	p.A213V	tier1	43	0	0.000	113	55	0.327
329866	16	50750582	50750583	-	T	INS	*NOD2*	ENST00000300589	1	splice_site_ins	c.2546+1_2546+1	e5+1	tier1	47	0	0.000	120	34	0.221
329866	16	89776108	89776108	G	A	SNP	*VPS9D1*	ENST00000389386	-1	intronic	c.1388+77	e11+77	tier3	20	0	0.000	52	40	0.435
329866	17	7577581	7577581	A	C	SNP	*TP53*	ENST00000269305	-1	missense	c.700	p.Y234D	tier1	658	0	0.000	326	1371	0.806
329866	17	40342300	40342300	C	A	SNP	*GHDC*	ENST00000436923	-1	missense	c.1366	p.V456F	tier1	63	0	0.000	88	44	0.331
329866	19	7796670	7796670	G	-	DEL	*CLEC4G*	ENST00000328853	-1	intronic	c.56-13	e2-13	tier3	25	0	0.000	49	27	0.355
329866	20	29623180	29623180	T	C	SNP	*FRG1B*	ENST00000482423	1	rna	NULL	NULL	tier1	618	3	0.005	2127	56	0.026
329866	20	62326771	62326771	G	C	SNP	*RTEL1*	ENST00000318100	1	missense	c.3590	p.G1197A	tier1	188	0	0.000	385	174	0.311
329866	21	40823790	40823790	C	T	SNP	*SH3BGR*	ENST00000333634	1	5_prime_untranslated_region	c.-44	NULL	tier3	44	0	0.000	121	69	0.363
340060	1	115258747	115258747	C	T	SNP	*NRAS*	ENST00000369535	-1	missense	c.35	p.G12D	tier1	534	5	0.009	614	32	0.050
340060	1	207888661	207888661	T	C	SNP	*CR1L*	ENST00000294997	1	nonstop	c.1165	p.*389R	tier1	223	0	0.000	354	16	0.043
340060	2	55808823	55808825	AAG	-	DEL	*SMEK2*	ENST00000272313	-1	in_frame_del	c.1245_1243	p.L415in_frame_del	tier1	44	1	0.022	86	26	0.232
340060	2	105897181	105897181	C	A	SNP	*TGFBRAP1*	ENST00000258449	-1	splice_site	c.1122-1	e5-1	tier1	42	1	0.023	55	29	0.345
340060	3	58368237	58368237	A	T	SNP	*PXK*	ENST00000356151	1	splice_region	c.202-4	e4-4	tier3	50	0	0.000	88	38	0.302
340060	4	24422954	24422954	A	T	SNP	*ENSG00000222262*	ENST00000410330	-1	5_prime_flanking_region	c.-30	NULL	tier4	70	1	0.014	162	75	0.314
340060	4	141786725	141786725	A	T	SNP	*RNF150*	ENST00000515673	-1	3_prime_untranslated_region	c.*2690	NULL	tier3	58	0	0.000	133	23	0.147
340060	5	31267727	31267727	C	A	SNP	*CDH6*	ENST00000265071	1	missense	c.147	p.N49K	tier1	102	0	0.000	164	13	0.073
340060	5	122941019	122941019	G	T	SNP	*CSNK1G3*	ENST00000360683	1	intronic	c.1290-14	e12-14	tier3	78	0	0.000	134	21	0.132
340060	5	134063500	134063500	A	-	DEL	*SEC24A*	ENST00000398844	1	3_prime_untranslated_region	c.*2716	NULL	tier3	55	0	0.000	163	21	0.114
340060	6	108882438	108882438	C	T	SNP	*FOXO3*	ENST00000343882	1	silent	c.27	p.A9	tier1	18	0	0.000	5	5	0.500
340060	7	43548582	43548582	G	A	SNP	*HECW1*	ENST00000395891	1	missense	c.3881	p.G1294D	tier1	665	1	0.002	881	43	0.047
340060	9	139997711	139997711	T	G	SNP	*MAN1B1*	ENST00000536349	1	3_prime_untranslated_region	c.*139997711	NULL	tier3	118	1	0.008	162	18	0.099
340060	10	112356156	112356156	G	T	SNP	*SMC3*	ENST00000361804	1	missense	c.1964	p.G655V	tier1	434	1	0.002	732	95	0.115
340060	11	32429666	32429666	G	A	SNP	*WT1*	ENST00000332351	-1	intronic	c.1002-8076	e6-8076	tier4	6	0	0.000	6	12	0.667
340060	12	43827516	43827516	C	A	SNP	*ADAMTS20*	ENST00000389420	-1	intronic	c.2720+532	e19+532	tier4	52	0	0.000	63	16	0.203
340060	12	72067980	72067980	A	T	SNP	*THAP2*	ENST00000308086	1	splice_region	c.72-3	e2-3	tier2	67	0	0.000	136	15	0.098
340060	13	28592642	28592642	C	A	SNP	*FLT3*	ENST00000380982	-1	missense	c.2503	p.D835Y	tier1	457	1	0.002	757	43	0.054
340060	14	58038541	58038541	A	C	SNP	*SLC35F4*	ENST00000339762	-1	intronic	c.1041+71	e5+71	tier3	41	0	0.000	80	15	0.158
340060	15	85805938	85805938	G	A	SNP	*ENSG00000218052*	ENST00000561209	-1	5_prime_untranslated_region	c.-85805938	NULL	tier3	124	0	0.000	210	16	0.071
340060	16	15227776	15227776	G	A	SNP	*PKD1P6*	ENST00000540502	-1	rna	NULL	NULL	tier1	49	1	0.020	63	29	0.315
340060	17	61995194	61995194	C	G	SNP	*GH1*	ENST00000323322	-1	missense	c.382	p.V128L	tier1	96	0	0.000	164	23	0.122
340060	18	30908069	30908069	T	G	SNP	*CCDC178*	ENST00000406524	-1	intronic	c.880-4472	e9-4472	tier4	74	0	0.000	323	31	0.088
346313	1	24294362	24294362	A	T	SNP	*SRSF10*	ENST00000374452	-1	3_prime_untranslated_region	c.*54	NULL	tier4	117	4	0.033	55	14	0.203
346313	1	89353241	89353241	G	C	SNP	*GTF2B*	ENST00000370500	-1	intronic	c.18-191	e2-191	tier3	58	0	0.000	34	155	0.816
346313	1	115258744	115258744	C	T	SNP	*NRAS*	ENST00000369535	-1	missense	c.38	p.G13D	tier1	456	2	0.004	520	253	0.327
346313	1	159038320	159038320	T	-	DEL	*AIM2*	ENST00000368130	-1	intronic	c.396+38	e2+38	tier3	100	0	0.000	114	63	0.356
346313	1	185815276	185815276	G	A	SNP	*HMCN1*	ENST00000271588	1	intronic	c.339+48	e2+48	tier3	319	1	0.003	437	286	0.395
346313	1	237494338	237494338	G	A	SNP	*RYR2*	ENST00000360064	1	intronic	c.270+52	e4+52	tier3	130	0	0.000	139	94	0.403
346313	2	79914651	79914651	C	T	SNP	*CTNNA2*	ENST00000361291	1	intronic	c.204+35867	e2+35867	tier3	116	2	0.017	124	57	0.313
346313	2	95976762	95976762	G	A	SNP	*KCNIP3*	ENST00000475491	1	3_prime_untranslated_region	c.*95976762	NULL	tier3	43	0	0.000	37	21	0.362
346313	2	97493997	97493997	C	T	SNP	*CNNM3*	ENST00000465224	1	3_prime_untranslated_region	c.*97493997	NULL	tier3	35	0	0.000	42	16	0.276
346313	2	103148926	103148926	G	A	SNP	*SLC9A4*	ENST00000295269	1	missense	c.2176	p.G726S	tier1	87	2	0.022	103	65	0.387
346313	2	130796690	130796690	C	T	SNP	*LOC440905*	ENST00000325390	-1	intronic	c.NULL	NULL	tier3	89	1	0.011	197	27	0.121
346313	2	198267359	198267359	C	A	SNP	*SF3B1*	ENST00000335508	-1	missense	c.1998	p.K666N	tier1	739	6	0.008	786	514	0.395
346313	3	124180873	124180873	A	G	SNP	*KALRN*	ENST00000360013	1	intronic	c.3915+70	e24+70	tier3	108	0	0.000	127	74	0.366
346313	3	157363624	157363624	A	T	SNP	*C3orf55*	ENST00000461040	1	nonsense	c.151	p.K51*	tier1	111	2	0.018	117	56	0.324
346313	3	185362401	185362401	C	T	SNP	*IGF2BP2*	ENST00000382199	-1	3_prime_untranslated_region	c.*918	NULL	tier3	45	0	0.000	32	23	0.397
346313	4	1389054	1389055	-	CA	INS	*CRIPAK*	ENST00000324803	1	frame_shift_ins	c.755_756	p.C254fs	tier1	107	1	0.009	126	20	0.137
346313	4	47888007	47888007	T	C	SNP	*NFXL1*	ENST00000381538	-1	missense	c.1553	p.Y518C	tier1	75	0	0.000	64	41	0.387
346313	5	128365287	128365287	G	A	SNP	*SLC27A6*	ENST00000262462	1	missense	c.1570	p.G524R	tier1	53	0	0.000	196	108	0.354
346313	5	170837545	170837546	-	TGTT	INS	*NPM1*	ENST00000296930	1	frame_shift_ins	c.861_862	p.W287fs	tier1	229	0	0.000	641	247	0.278
346313	5	180659955	180659955	C	T	SNP	*TRIM41*	ENST00000515223	1	3_prime_untranslated_region	c.*180659955	NULL	tier3	69	0	0.000	77	38	0.330
346313	7	112077307	112077307	A	C	SNP	*IFRD1*	ENST00000443101	1	5_prime_untranslated_region	c.-18567	NULL	tier4	94	0	0.000	129	100	0.435
346313	7	141794384	141794384	G	A	SNP	*MGAM*	ENST00000549489	1	intronic	c.4619-36	e38-36	tier3	46	4	0.080	27	66	0.710
346313	8	33356644	33356644	T	C	SNP	*TTI2*	ENST00000360742	-1	3_prime_untranslated_region	c.*47	NULL	tier3	98	0	0.000	120	55	0.314
346313	8	39111964	39111964	C	T	SNP	*ADAM32*	ENST00000379907	1	missense	c.1934	p.S645L	tier1	142	0	0.000	139	103	0.426
346313	8	56362027	56362027	G	A	SNP	*XKR4*	ENST00000327381	1	intronic	c.1007-73813	e3-73813	tier2	413	0	0.000	331	281	0.456
346313	9	2058252	2058252	A	T	SNP	*SMARCA2*	ENST00000349721	1	intronic	c.1348-39	e7-39	tier3	91	0	0.000	131	54	0.292
346313	9	84548900	84548900	C	A	SNP	*SPATA31D4*	ENST00000341875	1	rna	NULL	NULL	tier1	75	0	0.000	86	57	0.399
346313	9	116770653	116770653	C	T	SNP	*ZNF618*	ENST00000374126	1	missense	c.670	p.R224W	tier1	59	1	0.017	46	55	0.545
346313	9	139848263	139848263	G	C	SNP	*LCN12*	ENST00000466277	1	rna	NULL	NULL	tier1	152	0	0.000	105	54	0.340
346313	10	43612131	43612131	C	T	SNP	*RET*	ENST00000355710	1	silent	c.2236	p.L746	tier1	116	0	0.000	108	65	0.374
346313	10	71631922	71631922	C	T	SNP	*COL13A1*	ENST00000356340	1	splice_region	c.365-10	e3-10	tier3	86	0	0.000	73	68	0.479
346313	11	32413565	32413565	C	T	SNP	*WT1*	ENST00000332351	-1	missense	c.1385	p.R462Q	tier1	363	5	0.014	451	260	0.365
346313	11	66330311	66330311	C	T	SNP	*ACTN3*	ENST00000502692	1	silent	c.2562	p.N854	tier1	79	0	0.000	59	30	0.337

346313	11	74880778	74880778	C	T	SNP	*SLCO2B1*	ENST00000289575	1	silent	c.750	p.R250	tier1	50	0	0.000	39	35	0.473
346313	12	8073897	8073897	G	A	SNP	*SLC2A3*	ENST00000469295	-1	5_prime_untranslated_region	c.-8073897	NULL	tier3	135	1	0.007	213	18	0.078
346313	12	22606832	22606832	G	C	SNP	*C2CD5*	ENST00000333957	-1	missense	c.2869	p.Q957E	tier1	84	0	0.000	99	59	0.373
346313	12	112926910	112926910	G	C	SNP	*PTPN11*	ENST00000351677	1	missense	c.1530	p.Q510H	tier1	758	0	0.000	1191	33	0.027
346313	12	133384599	133384599	C	T	SNP	*GOLGA3*	ENST00000204726	-1	silent	c.1056	p.A352	tier1	102	0	0.000	85	50	0.368
346313	13	95363388	95363388	G	A	SNP	*SOX21*	ENST00000376945	-1	3_prime_untranslated_region	c.*85	NULL	tier2	52	0	0.000	53	34	0.391
346313	13	99030086	99030086	C	T	SNP	*FARP1*	ENST00000376586	1	missense	c.410	p.A137V	tier1	64	0	0.000	69	36	0.343
346313	14	38274022	38274022	A	T	SNP	*TTC6*	ENST00000478811	1	splice_region	c.357+3	e3+3	tier3	167	1	0.006	191	110	0.365
346313	14	70442537	70442537	G	A	SNP	*SMOC1*	ENST00000361956	1	splice_region	c.478+6	e4+6	tier2	107	0	0.000	94	44	0.319
346313	14	101429460	101429460	A	T	SNP	*SNORD114-7*	ENST00000362520	1	rna	NULL	NULL	tier1	30	0	0.000	67	41	0.380
346313	15	92397297	92397298	-	GT	INS	*SLCO3A1*	ENST00000318445	1	frame_shift_ins	c.159_160	p.G53fs	tier1	25	0	0.000	34	14	0.292
346313	16	790001	790001	G	A	SNP	*NARFL*	ENST00000540986	-1	5_prime_untranslated_region	c.-3603	NULL	tier3	27	0	0.000	47	34	0.420
346313	17	45664777	45664777	T	C	SNP	*NPEPPS*	ENST00000322157	1	intronic	c.1095+67	e9+67	tier3	88	0	0.000	104	61	0.370
346313	19	35991219	35991219	T	C	SNP	*DMKN*	ENST00000469960	-1	5_prime_untranslated_region	c.-35991219	NULL	tier3	50	0	0.000	51	27	0.346
346313	19	38782452	38782452	C	T	SNP	*SPINT2*	ENST00000585357	1	3_prime_untranslated_region	c.*38782452	NULL	tier3	72	0	0.000	73	34	0.315
346313	20	29633902	29633902	C	A	SNP	*FRG1B*	ENST00000278882	1	missense	c.541	p.P181T	tier1	95	0	0.000	537	41	0.071
346313	21	11039295	11039295	C	G	SNP	*BAGE2*	ENST00000470054	-1	rna	NULL	NULL	tier1	2708	1	0.000	5435	378	0.065
346313	21	45744779	45744779	T	G	SNP	*PFKL*	ENST00000403390	1	missense	c.1997	p.I666S	tier1	85	0	0.000	61	31	0.333
346313	X	19037686	19037686	A	T	SNP	*GPR64*	ENST00000479496	-1	5_prime_untranslated_region	c.-19037686	NULL	tier4	46	0	0.000	76	15	0.163
346313	X	123164976	123164977	-	T	INS	*STAG2*	ENST00000218089	1	splice_site_ins	c.288+1_288+1	e3+1	tier1	293	0	0.000	142	477	0.771
346313	Y	28654460	28654460	C	T	SNP	*TPTE2P4*	ENST00000258589	1	intronic	c.NULL	NULL	tier3	84	0	0.000	39	102	0.713
350719	17	7577568	7577568	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.713	p.C238Y	tier1	494	0	0.000	1426	85	0.056
350719	18	15272098	15272098	C	A	SNP	*BNIP3P3*	ENST00000577336	-1	5_prime_flanking_region	c.-24102	NULL	tier3	72	2	0.027	367	71	0.162
350719	19	46214702	46214702	A	T	SNP	*FBXO46*	ENST00000317683	-1	3_prime_untranslated_region	c.*240	NULL	tier2	87	1	0.011	214	28	0.114
353053	1	20881411	20881412	-	C	INS	*FAM43B*	ENST00000332947	1	3_prime_untranslated_region	c.*955	NULL	tier3	45	0	0.000	87	18	0.171
353053	1	20981993	20981993	A	G	SNP	*DDOST*	ENST00000375048	-1	missense	c.542	p.L181P	tier1	43	0	0.000	75	16	0.176
353053	1	196887311	196887311	T	C	SNP	*CFHR4*	ENST00000367416	1	intronic	c.1538-29	e10-29	tier2	68	0	0.000	83	11	0.117
353053	1	205801794	205801794	G	A	SNP	*PM20D1*	ENST00000367136	-1	missense	c.1217	p.A406V	tier1	165	0	0.000	256	29	0.102
353053	1	222833276	222833276	A	G	SNP	*MIA3*	ENST00000344441	1	missense	c.4903	p.M1635V	tier1	62	0	0.000	98	19	0.162
353053	5	14713807	14713807	G	A	SNP	*ANKH*	ENST00000284268	-1	intronic	c.1142-31	e10-31	tier3	56	0	0.000	97	20	0.171
353053	7	139094357	139094357	C	T	SNP	*LUC7L2*	ENST00000541515	1	nonsense	c.934	p.R312*	tier1	449	0	0.000	741	63	0.078
353053	9	135073547	135073547	C	T	SNP	*NTNG2*	ENST00000360670	1	silent	c.408	p.D136	tier1	88	0	0.000	111	11	0.090
353053	11	75141266	75141266	C	T	SNP	*KLHL35*	ENST00000539798	-1	missense	c.409	p.G137S	tier1	6	0	0.000	5	12	0.706
353053	12	102291646	102291646	C	T	SNP	*DRAM1*	ENST00000258534	1	missense	c.137	p.T46M	tier1	85	0	0.000	145	15	0.094
353053	12	102576308	102576308	T	-	DEL	*PARPBP*	ENST00000358383	1	intronic	c.1185-19	e8-19	tier3	55	1	0.018	112	23	0.170
353053	13	98634738	98634738	T	-	DEL	*IPO5*	ENST00000261574	1	intronic	c.145-19	e3-19	tier3	63	1	0.016	95	18	0.159
353053	13	113538580	113538580	C	A	SNP	*ATP11A*	ENST00000375630	1	3_prime_untranslated_region	c.*2202	NULL	tier2	153	0	0.000	156	12	0.071
353053	15	23689650	23689650	G	A	SNP	*GOLGA6L2*	ENST00000312015	-1	splice_region	c.214-3	e3-3	tier3	149	0	0.000	277	32	0.104
353053	15	45392025	45392025	G	A	SNP	*DUOX2*	ENST00000389039	-1	nonsense	c.3250	p.R1084*	tier1	65	0	0.000	102	16	0.136
353053	17	16723414	16723414	C	T	SNP	*ENSG00000226145*	ENST00000417510	-1	splice_site	c.NULL	NULL	tier1	190	0	0.000	221	20	0.083
353053	21	36164611	36164611	C	A	SNP	*RUNX1*	ENST00000300305	-1	nonsense	c.1264	p.E422*	tier1	706	1	0.001	833	106	0.113
353053	X	102840637	102840637	T	G	SNP	*TCEAL4*	ENST00000372629	1	missense	c.268	p.W90G	tier1	76	2	0.026	88	19	0.176
353053	X	133547986	133547986	A	G	SNP	*PHF6*	ENST00000394292	1	missense	c.722	p.Y241C	tier1	392	0	0.000	601	84	0.123
368402	1	154215669	154215669	G	A	SNP	*UBAP2L*	ENST00000466173	1	3_prime_untranslated_region	c.*154215669	NULL	tier3	79	1	0.013	228	59	0.206
368402	1	216723715	216723715	C	T	SNP	*ESRRG*	ENST00000408911	-1	intronic	c.862+13846	e5+13846	tier2	118	0	0.000	281	62	0.181
368402	2	11702607	11702607	A	G	SNP	*GREB1*	ENST00000234142	1	missense	c.176	p.N59S	tier1	27	0	0.000	206	62	0.231
368402	2	20460043	20460043	C	A	SNP	*PUM2*	ENST00000361078	-1	intronic	c.2355+55	e14+55	tier2	51	1	0.019	86	20	0.189
368402	2	179596201	179596201	T	A	SNP	*TTN*	ENST00000342992	-1	silent	c.13560	p.L4520	tier1	79	0	0.000	213	36	0.145
368402	3	38418449	38418449	T	C	SNP	*XYLB*	ENST00000207870	1	silent	c.1161	p.I387	tier1	107	2	0.018	189	47	0.198
368402	4	22421553	22421553	C	T	SNP	*GPR125*	ENST00000334304	-1	intronic	c.1809+956	e12+956	tier3	97	1	0.010	120	30	0.200
368402	4	140432050	140432050	T	C	SNP	*SETD7*	ENST00000274031	-1	3_prime_untranslated_region	c.*767	NULL	tier3	126	0	0.000	191	41	0.177
368402	4	166915437	166915437	A	T	SNP	*TLL1*	ENST00000061240	1	intronic	c.362-96	e4-96	tier3	188	0	0.000	184	48	0.206
368402	5	37239010	37239010	C	-	DEL	*C5orf42*	ENST00000425232	-1	frame_shift_del	c.887	p.S296fs	tier1	124	1	0.008	351	82	0.189
368402	5	115319116	115319116	G	A	SNP	*AQPEP*	ENST00000357872	1	missense	c.828	p.M276I	tier1	77	1	0.013	183	35	0.160
368402	5	156924056	156924056	C	T	SNP	*ADAM19*	ENST00000517374	-1	missense	c.152	p.S51N	tier1	22	0	0.000	169	57	0.252
368402	7	44105132	44105132	G	A	SNP	*PGAM2*	ENST00000297283	-1	5_prime_untranslated_region	c.-4	NULL	tier3	8	0	0.000	67	80	0.544
368402	9	78973756	78973756	G	A	SNP	*PCSK5*	ENST00000545128	1	missense	c.5501	p.R1834Q	tier1	44	0	0.000	195	52	0.210
368402	9	79319663	79319663	G	A	SNP	*PRUNE2*	ENST00000428286	-1	intronic	c.6436+14	e1+14	tier2	108	0	0.000	237	49	0.171
368402	9	79319664	79319664	G	T	SNP	*PRUNE2*	ENST00000428286	-1	intronic	c.6436+13	e1+13	tier2	107	0	0.000	236	49	0.172
368402	10	115963109	115963109	C	A	SNP	*TDRD1*	ENST00000251864	1	intronic	c.802-38	e7-38	tier3	114	0	0.000	124	40	0.244
368402	12	124826497	124826497	T	C	SNP	*NCOR2*	ENST00000356219	-1	missense	c.5081	p.N1694S	tier1	42	0	0.000	379	94	0.198
368402	12	132505857	132505857	C	T	SNP	*EP400*	ENST00000333577	1	missense	c.4789	p.R1597C	tier1	38	0	0.000	334	66	0.165
368402	16	34290568	34290568	C	G	SNP	*CCNYL3*	ENST00000407030	1	3_prime_untranslated_region	c.*34290568	NULL	tier3	88	2	0.022	138	41	0.228
368402	17	74732959	74732959	G	C	SNP	*SRSF2*	ENST00000392485	-1	missense	c.284	p.P95R	tier1	43	0	0.000	439	118	0.212
368402	17	78700994	78700994	C	T	SNP	*RPTOR*	ENST00000306801	1	intronic	c.508-3366	e5-3366	tier3	44	0	0.000	435	103	0.191
368402	17	79563240	79563240	C	T	SNP	*NPLOC4*	ENST00000374747	-1	missense	c.1022	p.C341Y	tier1	47	0	0.000	177	38	0.177
368402	19	9025669	9025669	G	A	SNP	*MUC16*	ENST00000397910	-1	intronic	c.36796-11	e15-11	tier3	204	1	0.005	1554	72	0.044
368402	21	36231802	36231802	T	A	SNP	*RUNX1*	ENST00000300305	-1	missense	c.582	p.K194N	tier1	228	1	0.004	1359	318	0.190
368402	21	36259137	36259137	T	C	SNP	*RUNX1*	ENST00000300305	-1	splice_region	c.351+3	e3+3	tier3	230	2	0.009	1400	361	0.205
368402	X	18911675	18911675	C	G	SNP	*PHKA2*	ENST00000379942	-1	missense	c.3636	p.M1212I	tier1	48	1	0.020	238	71	0.229
377158	1	16621238	16621238	C	A	SNP	*FBXO42*	ENST00000478089	-1	rna	NULL	NULL	tier1	49	0	0.000	123	29	0.191
377158	1	20471088	20471088	C	T	SNP	*PLA2G2F*	ENST00000375102	1	silent	c.330	p.H110	tier1	52	0	0.000	57	38	0.400
377158	1	78191328	78191328	A	C	SNP	*USP33*	ENST00000357428	-1	missense	c.1348	p.L450V	tier1	49	0	0.000	112	55	0.329
377158	1	215409389	215409392	ATCT	-	DEL	*KCNK2*	ENST00000444842	1	3_prime_untranslated_region	c.*901	NULL	tier4	52	0	0.000	161	22	0.120

377158	1	226413278	226413278	C	A	SNP	*MIXL1*	ENST00000366810	1	missense	c.464	p.P155Q	tier1	58	3	0.049	116	92	0.442
377158	3	1415578	1415578	C	T	SNP	*CNTN6*	ENST00000350110	1	intronic	c.1946-30	e15-30	tier3	53	0	0.000	178	110	0.382
377158	4	123260564	123260564	G	A	SNP	*KIAA1109*	ENST00000264501	1	splice_site	c.12352+1	e70+1	tier1	14	0	0.000	85	79	0.482
377158	4	156135650	156135650	C	T	SNP	*NPY2R*	ENST00000329476	1	missense	c.559	p.R187W	tier1	33	0	0.000	48	30	0.385
377158	4	186920705	186920705	G	C	SNP	*SORBS2*	ENST00000284776	-1	5_prime_flanking_region	c.-337354	NULL	tier3	199	3	0.015	432	41	0.087
377158	5	140532032	140532032	G	C	SNP	*PCDHB6*	ENST00000231136	1	missense	c.2194	p.G732R	tier1	188	1	0.005	214	172	0.444
377158	5	141233621	141233621	C	T	SNP	*PCDH1*	ENST00000287008	-1	missense	c.3700	p.E1234K	tier1	123	1	0.008	173	129	0.427
377158	7	44268486	44268486	C	T	SNP	*CAMK2B*	ENST00000395749	-1	silent	c.1377	p.R459	tier1	79	0	0.000	88	56	0.386
377158	7	76162997	76162997	C	T	SNP	*UPK3B*	ENST00000419923	1	intronic	c.963+18224	e4+18224	tier2	183	0	0.000	293	195	0.400
377158	7	100636426	100636426	C	T	SNP	*MUC12*	ENST00000536621	1	missense	c.2582	p.T861M	tier1	17	0	0.000	33	38	0.535
377158	7	102257060	102257060	G	A	SNP	*RASA4*	ENST00000462172	-1	5_prime_untranslated_region	c.-7253	NULL	tier2	191	0	0.000	490	58	0.106
377158	7	129083907	129083907	G	A	SNP	*STRIP2*	ENST00000249344	1	missense	c.242	p.R81K	tier1	160	1	0.006	530	407	0.433
377158	8	1616604	1616604	C	T	SNP	*DLGAP2*	ENST00000520901	1	missense	c.1730	p.T577M	tier1	103	4	0.037	72	65	0.471
377158	8	93029456	93029456	G	A	SNP	*RUNX1T1*	ENST00000436581	-1	missense	c.257	p.T86M	tier1	418	0	0.000	693	480	0.409
377158	9	68438490	68438490	T	C	SNP	*ENSG00000215548*	ENST00000376334	-1	intronic	c.NULL	NULL	tier3	134	2	0.015	719	65	0.083
377158	9	68438491	68438491	T	C	SNP	*ENSG00000215548*	ENST00000376334	-1	intronic	c.NULL	NULL	tier3	134	2	0.015	720	64	0.082
377158	10	125521468	125521468	C	A	SNP	*CPXM2*	ENST00000241305	-1	missense	c.1697	p.R566L	tier1	128	0	0.000	116	96	0.449
377158	11	93796883	93796883	G	C	SNP	*HEPHL1*	ENST00000315765	1	missense	c.625	p.E209Q	tier1	79	2	0.025	137	57	0.294
377158	11	132177495	132177495	A	G	SNP	*NTM*	ENST00000539799	1	intronic	c.527-88	e5-88	tier3	74	1	0.013	109	68	0.384
377158	12	2794921	2794921	G	A	SNP	*CACNA1C*	ENST00000399634	1	missense	c.5806	p.E1936K	tier1	98	1	0.010	194	21	0.097
377158	12	53439709	53439709	C	T	SNP	*LOC283335*	ENST00000546566	-1	intronic	c.NULL	NULL	tier3	87	0	0.000	176	113	0.391
377158	14	20216351	20216351	C	T	SNP	*OR4Q3*	ENST00000331723	1	silent	c.765	p.C255	tier1	27	0	0.000	48	32	0.400
377158	14	38296537	38296537	G	A	SNP	*TTC6*	ENST00000478811	1	missense	c.1457	p.G486E	tier1	11	0	0.000	97	61	0.386
377158	14	80328831	80328832	-	A	INS	*NRXN3*	ENST00000428277	1	3_prime_untranslated_region	c.*524	NULL	tier4	29	0	0.000	69	27	0.281
377158	14	94750258	94750258	A	T	SNP	*SERPINA10*	ENST00000261994	-1	3_prime_untranslated_region	c.*44	NULL	tier3	47	1	0.021	85	43	0.336
377158	15	20362902	20362902	T	-	DEL	*BMS1P15*	ENST00000554269	1	intronic	c.NULL	NULL	tier3	376	1	0.003	794	289	0.267
377158	16	67242195	67242195	C	T	SNP	*LRRC29*	ENST00000341546	-1	intronic	c.285+20	e2+20	tier3	66	0	0.000	90	68	0.430
377158	17	13399610	13399610	G	A	SNP	*HS3ST3A1*	ENST00000284110	-1	silent	c.1125	p.I375	tier1	157	0	0.000	166	134	0.447
377158	17	37901877	37901877	C	A	SNP	*GRB7*	ENST00000445327	1	intronic	c.1278+86	e11+86	tier3	47	0	0.000	103	79	0.432
377158	17	47490642	47490642	A	G	SNP	*PHB*	ENST00000300408	-1	5_prime_untranslated_region	c.-16	NULL	tier3	53	0	0.000	58	60	0.509
377158	17	48653205	48653205	G	A	SNP	*CACNA1G*	ENST00000359106	1	missense	c.1442	p.S481N	tier1	397	2	0.005	469	348	0.425
377158	19	12221114	12221114	T	C	SNP	*ENSG00000188474*	ENST00000339302	1	splice_region	c.1-6	e1-6	tier3	84	0	0.000	132	85	0.390
377158	19	16008165	16008165	G	A	SNP	*CYP4F2*	ENST00000221700	-1	intronic	c.198+59	e1+59	tier3	66	3	0.043	69	61	0.459
377158	19	33792822	33792822	C	A	SNP	*CEBPA*	ENST00000498907	-1	nonsense	c.499	p.E167*	tier1	451	1	0.002	795	70	0.081
377158	20	31022403	31022425	CACCACTGCCATAGAGAGGCGGC	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1888_1910	p.H633fs	tier1	648	5	0.008	1110	152	0.120
377158	20	31022417	31022417	A	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1902	p.E635fs	tier1	641	4	0.006	892	115	0.114
377158	20	33573852	33573852	T	C	SNP	*MYH7B*	ENST00000262873	1	intronic	c.932-51	e12-51	tier3	16	0	0.000	22	20	0.476
377158	21	36231773	36231773	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.611	p.R204Q	tier1	773	3	0.004	951	594	0.384
377158	21	39672197	39672197	T	C	SNP	*KCNJ15*	ENST00000328656	1	silent	c.1014	p.D338	tier1	19	0	0.000	39	24	0.381
377158	21	44514777	44514777	T	G	SNP	*U2AF1*	ENST00000291552	-1	missense	c.470	p.Q157P	tier1	272	1	0.004	448	282	0.386
377158	21	44838927	44838927	G	A	SNP	*SIK1*	ENST00000270162	-1	missense	c.1436	p.T479I	tier1	46	0	0.000	42	36	0.462
377158	22	34875057	34875057	C	T	SNP	-	-	-	-	-	-	tier3	25	0	0.000	50	31	0.383
377158	22	40425476	40425476	G	A	SNP	*FAM83F*	ENST00000333407	1	intronic	c.1454-44	e5-44	tier3	79	0	0.000	95	61	0.391
377158	X	54948751	54948751	G	A	SNP	*TRO*	ENST00000452830	1	5_prime_untranslated_region	c.-347	NULL	tier3	48	0	0.000	84	48	0.364
377158	X	62974526	62974526	G	A	SNP	*ARHGEF9*	ENST00000495564	-1	rna	NULL	NULL	tier1	168	0	0.000	179	93	0.341
377158	X	152826317	152826317	C	A	SNP	*ATP2B3*	ENST00000263519	1	missense	c.3023	p.T1008N	tier1	385	1	0.003	544	223	0.290
378511	1	38185727	38185727	C	T	SNP	*EPHA10*	ENST00000427468	-1	missense	c.2416	p.G806S	tier1	311	1	0.003	326	208	0.389
378511	1	103471831	103471831	T	A	SNP	*COL11A1*	ENST00000358392	-1	missense	c.1760	p.K587I	tier1	151	0	0.000	142	72	0.335
378511	1	151542094	151542095	-	TT	INS	*TUFT1*	ENST00000538902	1	intronic	c.538-39_538-38	e7-38	tier3	75	0	0.000	85	64	0.430
378511	1	159505705	159505705	G	C	SNP	*OR10J5*	ENST00000334857	-1	missense	c.93	p.F31L	tier1	77	0	0.000	105	33	0.239
378511	1	215990362	215990362	T	C	SNP	*USH2A*	ENST00000366943	-1	missense	c.9547	p.I3183V	tier1	97	0	0.000	80	112	0.583
378511	1	218458652	218458652	C	T	SNP	*RRP15*	ENST00000366932	1	5_prime_untranslated_region	c.-7	NULL	tier2	152	0	0.000	210	73	0.258
378511	2	10797867	10797867	C	T	SNP	*NOL10*	ENST00000381685	-1	splice_site	c.906+1	e11+1	tier1	112	1	0.009	121	51	0.295
378511	2	89246763	89246763	C	A	SNP	*IGKV7-3*	ENST00000357453	-1	5_prime_flanking_region	c.-31869	NULL	tier3	173	1	0.006	124	88	0.415
378511	2	127805801	127805801	G	A	SNP	*BIN1*	ENST00000462958	-1	5_prime_untranslated_region	c.-127805801	NULL	tier3	130	0	0.000	114	86	0.430
378511	2	191366422	191366422	T	A	SNP	*MFSD6*	ENST00000281416	1	3_prime_untranslated_region	c.*1478	NULL	tier3	84	0	0.000	103	57	0.356
378511	4	70826715	70826715	G	T	SNP	*CSN2*	ENST00000353151	-1	5_prime_untranslated_region	c.-2	NULL	tier3	100	0	0.000	99	60	0.377
378511	4	85562062	85562062	C	T	SNP	*CDS1*	ENST00000295887	1	silent	c.951	p.F317	tier1	93	0	0.000	67	51	0.432
378511	4	100239105	100239105	T	G	SNP	*ADH1B*	ENST00000504498	-1	rna	NULL	NULL	tier1	74	0	0.000	83	41	0.331
378511	4	150509056	150509056	A	G	SNP	*ENSG00000234828*	ENST00000511993	-1	intronic	c.NULL	NULL	tier3	94	0	0.000	159	80	0.335
378511	5	134059300	134059300	T	C	SNP	*SEC24A*	ENST00000398844	1	missense	c.3107	p.I1036T	tier1	236	0	0.000	222	119	0.347
378511	5	140033542	140033542	A	G	SNP	*IK*	ENST00000417647	1	missense	c.424	p.K142E	tier1	180	0	0.000	170	106	0.381
378511	5	140719581	140719581	A	C	SNP	*PCDHGA2*	ENST00000394576	1	missense	c.1043	p.Y348S	tier1	76	0	0.000	68	46	0.404
378511	5	145616829	145616829	T	C	SNP	*RBM27*	ENST00000265271	1	intronic	c.1145-32	e8-32	tier3	92	0	0.000	64	44	0.407
378511	6	23855602	23855602	A	G	SNP	*SPTLC1P2*	ENST00000407089	-1	3_prime_flanking_region	c.*1324	NULL	tier3	229	0	0.000	215	104	0.326
378511	6	122777603	122777603	T	C	SNP	*SERINC1*	ENST00000339697	-1	intronic	c.371+23	e3+23	tier3	109	1	0.009	120	53	0.306
378511	7	128291564	128291564	C	G	SNP	*ENSG00000243302*	ENST00000465971	1	3_prime_untranslated_region	c.*128291564	NULL	tier3	60	1	0.016	35	10	0.222
378511	8	7450151	7450151	A	T	SNP	*OR7E157P*	ENST00000494376	1	3_prime_untranslated_region	c.*7450151	NULL	tier2	311	0	0.000	442	61	0.121
378511	8	22477862	22477862	T	C	SNP	*CCAR2*	ENST00000308511	1	3_prime_untranslated_region	c.*667	NULL	tier3	128	0	0.000	130	72	0.356
378511	8	33451288	33451288	G	A	SNP	*DUSP26*	ENST00000256261	-1	intronic	c.222-23	e2-23	tier3	81	1	0.012	59	50	0.459
378511	9	23692597	23692597	T	A	SNP	*ELAVL2*	ENST00000380117	-1	silent	c.1038	p.V346	tier1	77	0	0.000	77	23	0.230
378511	9	77415313	77415313	G	T	SNP	*TRPM6*	ENST00000451710	-1	missense	c.2095	p.L699I	tier1	77	0	0.000	74	30	0.289
378511	9	116811952	116811952	G	C	SNP	*ZNF618*	ENST00000374126	1	missense	c.2370	p.E790D	tier1	45	0	0.000	44	20	0.313
378511	10	43691546	43691546	G	A	SNP	*RASGEF1A*	ENST00000395809	-1	3_prime_untranslated_region	c.*146	NULL	tier3	121	0	0.000	113	63	0.358

378511	11	18955245	18955245	C	A	SNP	*ENSG00000255244*	ENST00000528646	1	5_prime_flanking_region	c.-1287	NULL	tier3	146	0	0.000	191	21	0.099
378511	11	20805389	20805389	T	G	SNP	*NELL1*	ENST00000357134	1	intronic	c.335+13	e3+13	tier3	89	0	0.000	82	46	0.359
378511	11	34186853	34186853	G	A	SNP	*ABTB2*	ENST00000435224	-1	silent	c.1806	p.G602	tier1	52	0	0.000	63	18	0.222
378511	11	66152452	66152452	G	T	SNP	*NPAS4*	ENST00000311034	1	5_prime_flanking_region	c.-36199	NULL	tier4	42	0	0.000	75	53	0.414
378511	11	71939384	71939384	G	A	SNP	*INPPL1*	ENST00000298229	1	splice_region	c.247-8	e3-8	tier3	83	0	0.000	67	38	0.362
378511	11	72492296	72492296	C	T	SNP	*STARD10*	ENST00000334805	-1	5_prime_untranslated_region	c.-70	NULL	tier2	48	0	0.000	46	33	0.418
378511	11	119025065	119025065	T	C	SNP	*ABCG4*	ENST00000307417	1	missense	c.452	p.M151T	tier1	54	0	0.000	53	36	0.405
378511	11	129739492	129739492	G	A	SNP	*NFRKB*	ENST00000524794	-1	missense	c.3503	p.A1168V	tier1	86	0	0.000	61	36	0.371
378511	12	12038950	12038951	-	T	INS	*ETV6*	ENST00000396373	1	frame_shift_ins	c.1243_1244	p.L416fs	tier1	647	0	0.000	577	264	0.314
378511	12	52182517	52182517	T	A	SNP	*SCN8A*	ENST00000354534	1	silent	c.4266	p.A1422	tier1	71	0	0.000	68	43	0.387
378511	12	133768616	133768616	T	C	SNP	*ZNF268*	ENST00000228289	1	intronic	c.457+27	e4+27	tier3	88	0	0.000	61	32	0.344
378511	13	95361880	95361880	T	C	SNP	*LINC00391*	ENST00000433569	-1	5_prime_flanking_region	c.-6764	NULL	tier2	135	2	0.015	224	145	0.393
378511	14	73587919	73587919	A	T	SNP	*RBM25*	ENST00000261973	1	3_prime_untranslated_region	c.*1406	NULL	tier3	241	1	0.004	385	18	0.045
378511	15	25928387	25928387	G	A	SNP	*ATP10A*	ENST00000356865	-1	intronic	c.3492+46	e17+46	tier3	40	0	0.000	36	28	0.438
378511	15	44090170	44090170	G	A	SNP	*SERINC4*	ENST00000249714	-1	silent	c.60	p.S20	tier1	93	0	0.000	98	46	0.319
378511	17	7910348	7910348	T	C	SNP	*GUCY2D*	ENST00000254854	1	intronic	c.1379-30	e4-30	tier3	30	0	0.000	29	29	0.500
378511	17	39551774	39551774	A	G	SNP	*KRT31*	ENST00000251645	-1	silent	c.690	p.S230	tier1	114	0	0.000	108	43	0.285
378511	17	59557555	59557555	C	G	SNP	*TBX4*	ENST00000393853	1	missense	c.896	p.A299G	tier1	75	0	0.000	84	48	0.364
378511	17	65924700	65924700	A	C	SNP	*BPTF*	ENST00000321892	1	missense	c.6359	p.Q2120P	tier1	146	3	0.020	129	75	0.368
378511	18	60999185	60999185	T	C	SNP	*KDSR*	ENST00000406396	-1	intronic	c.880-51	e10-51	tier3	55	0	0.000	44	29	0.397
378511	18	61570598	61570598	G	T	SNP	*SERPINB2*	ENST00000299502	1	3_prime_untranslated_region	c.*59	NULL	tier3	75	0	0.000	86	43	0.333
378511	19	51648220	51648220	G	A	SNP	*SIGLEC7*	ENST00000317643	1	splice_region	c.760+4	e3+4	tier3	63	0	0.000	74	38	0.336
378511	20	11906923	11906923	T	G	SNP	*BTBD3*	ENST00000378226	1	3_prime_untranslated_region	c.*2609	NULL	tier2	96	0	0.000	140	68	0.325
378511	21	44514777	44514777	T	C	SNP	*U2AF1*	ENST00000291552	-1	missense	c.470	p.Q157R	tier1	399	1	0.003	496	38	0.071
378511	22	24401850	24401850	C	T	SNP	*GSTTP2*	ENST00000466426	-1	rna	NULL	NULL	tier1	68	0	0.000	78	59	0.431
378511	22	32162607	32162607	G	T	SNP	*DEPDC5*	ENST00000266091	1	missense	c.316	p.D106Y	tier1	246	1	0.004	271	177	0.395
378511	X	26179440	26179440	C	T	SNP	*MAGEB6P1*	ENST00000416929	1	3_prime_untranslated_region	c.*26179440	NULL	tier3	77	0	0.000	37	74	0.667
395344	1	25611201	25611201	G	A	SNP	*RHD*	ENST00000328664	1	missense	c.286	p.G96S	tier1	111	0	0.000	72	67	0.475
395344	1	53972518	53972518	C	A	SNP	*GLIS1*	ENST00000312233	-1	intronic	c.1706-69	e8-69	tier3	27	0	0.000	21	19	0.475
395344	2	3652556	3652556	T	-	DEL	*COLEC11*	ENST00000418971	1	intronic	c.172+496	e2+496	tier3	99	0	0.000	133	14	0.095
395344	2	47748558	47748558	C	A	SNP	*KCNK12*	ENST00000327876	-1	missense	c.781	p.D261Y	tier1	147	5	0.033	93	87	0.483
395344	2	131520055	131520055	C	T	SNP	*AMER3*	ENST00000321420	1	missense	c.410	p.P137L	tier1	84	1	0.012	56	28	0.333
395344	2	141130704	141130704	T	A	SNP	*LRP1B*	ENST00000389484	-1	missense	c.10641	p.R3547S	tier1	378	5	0.013	344	254	0.424
395344	2	167759975	167759975	G	A	SNP	*XIRP2*	ENST00000409195	1	5_prime_untranslated_region	c.-18	NULL	tier2	43	0	0.000	33	31	0.484
395344	4	5990869	5990870	CT	-	DEL	*C4orf50*	ENST00000531445	-1	frame_shift_del	c.630_629	p.E210fs	tier1	74	1	0.013	86	15	0.149
395344	4	134073863	134073863	C	T	SNP	*PCDH10*	ENST00000264360	1	silent	c.2568	p.I856	tier1	63	0	0.000	52	32	0.381
395344	5	140431040	140431040	G	A	SNP	*PCDHB1*	ENST00000306549	1	5_prime_untranslated_region	c.-16	NULL	tier3	475	5	0.010	418	46	0.099
395344	5	162932633	162932633	C	T	SNP	*MAT2B*	ENST00000321757	1	5_prime_untranslated_region	c.-60	NULL	tier2	265	0	0.000	207	12	0.055
395344	5	176730908	176730908	C	A	SNP	*PRELID1*	ENST00000502670	1	rna	NULL	NULL	tier1	47	0	0.000	39	27	0.409
395344	7	1056023	1056023	A	G	SNP	*C7orf50*	ENST00000357429	-1	intronic	c.130-6244	e2-6244	tier4	29	0	0.000	30	11	0.268
395344	7	1484979	1484979	G	C	SNP	*MICALL2*	ENST00000297508	-1	missense	c.727	p.P243A	tier1	191	1	0.005	133	96	0.417
395344	7	2598908	2598908	T	C	SNP	*IQCE*	ENST00000402050	1	intronic	c.36+57	e1+57	tier2	15	0	0.000	7	7	0.467
395344	8	124383531	124383531	C	T	SNP	*ATAD2*	ENST00000287394	-1	missense	c.584	p.R195H	tier1	80	0	0.000	119	36	0.232
395344	11	3041385	3041385	C	T	SNP	*CARS*	ENST00000380525	-1	intronic	c.1266+65	e11+65	tier3	48	0	0.000	39	29	0.427
395344	11	103043939	103043939	C	A	SNP	*DYNC2H1*	ENST00000398093	1	missense	c.5463	p.D1821E	tier1	494	4	0.008	522	389	0.427
395344	12	42866304	42866304	C	T	SNP	*PRICKLE1*	ENST00000345127	-1	missense	c.15	p.M5I	tier1	51	1	0.019	29	23	0.442
395344	13	95095724	95095724	G	A	SNP	*DCT*	ENST00000446125	-1	silent	c.1446	p.D482	tier1	134	4	0.029	113	74	0.394
395344	13	107822358	107822358	G	T	SNP	*FAM155A*	ENST00000375915	-1	3_prime_untranslated_region	c.*487	NULL	tier4	164	2	0.012	229	19	0.077
395344	14	59931931	59931931	T	G	SNP	*GPR135*	ENST00000395116	-1	missense	c.14	p.Q5P	tier1	6	0	0.000	1	7	0.875
395344	14	97033430	97033431	-	A	INS	*PAPOLA*	ENST00000216277	1	3_prime_untranslated_region	c.*2043	NULL	tier3	78	0	0.000	101	13	0.114
395344	16	32914951	32914951	C	A	SNP	*IGHV3OR16-15*	ENST00000565463	1	3_prime_untranslated_region	c.*32914951	NULL	tier3	168	0	0.000	125	86	0.408
395344	19	5686425	5686425	A	-	DEL	*HSD11B1L*	ENST00000423665	1	splice_site_del	c.205-2	e3-2	tier1	128	0	0.000	99	40	0.288
395344	19	36216047	36216047	T	C	SNP	*KMT2B*	ENST00000222270	1	intronic	c.3528+59	e10+59	tier3	58	0	0.000	56	28	0.333
395344	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	677	7	0.010	624	294	0.320
395344	21	36252865	36252865	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.497	p.R166Q	tier1	922	3	0.003	767	568	0.425
395344	21	44524456	44524456	G	A	SNP	*U2AF1*	ENST00000291552	-1	missense	c.101	p.S34F	tier1	456	23	0.048	457	297	0.393
395344	22	19452777	19452777	T	A	SNP	*UFD1L*	ENST00000263202	-1	missense	c.443	p.N148I	tier1	85	2	0.023	86	55	0.390
429745	1	1078202	1078202	G	A	SNP	*LOC254099*	ENST00000416774	1	rna	NULL	NULL	tier1	53	0	0.000	62	42	0.404
429745	1	78189035	78189035	T	C	SNP	*USP33*	ENST00000357428	-1	missense	c.1463	p.Q488R	tier1	42	0	0.000	29	22	0.431
429745	1	103400670	103400670	C	T	SNP	*COL11A1*	ENST00000358392	-1	splice_site	c.3475-1	e45-1	tier1	85	0	0.000	172	19	0.100
429745	1	193018974	193018974	G	T	SNP	*UCHL5*	ENST00000367451	-1	missense	c.148	p.H50N	tier1	64	0	0.000	87	76	0.466
429745	1	197021696	197021696	T	A	SNP	*F13B*	ENST00000367412	-1	intronic	c.1555+68	e9+68	tier3	34	1	0.029	37	20	0.351
429745	1	240071866	240071866	C	T	SNP	*CHRM3*	ENST00000255380	1	missense	c.1115	p.P372L	tier1	16	0	0.000	25	20	0.444
429745	2	152267897	152267898	-	T	INS	*RIF1*	ENST00000243326	1	intronic	c.183+45_183+44	e2+45	tier4	24	0	0.000	32	12	0.273
429745	2	234231616	234231616	G	A	SNP	*SAG*	ENST00000409110	1	missense	c.400	p.V134M	tier1	90	0	0.000	105	51	0.325
429745	3	38010850	38010850	G	T	SNP	*CTDSPL*	ENST00000273179	1	intronic	c.426+1477	e5+1477	tier3	54	0	0.000	99	71	0.410
429745	3	197807179	197807179	C	T	SNP	*ANKRD18DP*	ENST00000335478	-1	splice_region	c.NULL	NULL	tier2	24	0	0.000	44	22	0.333
429745	4	146046124	146046124	T	-	DEL	*ABCE1*	ENST00000296577	1	intronic	c.1641-18	e16-18	tier3	69	0	0.000	64	9	0.123
429745	5	126667153	126667153	G	A	SNP	*MEGF10*	ENST00000274473	1	intronic	c.116+37	e1+37	tier3	66	0	0.000	69	58	0.457
429745	5	134705108	134705108	G	C	SNP	*H2AFY*	ENST00000511689	-1	silent	c.465	p.A155	tier1	48	0	0.000	112	59	0.345
429745	5	139222426	139222426	G	A	SNP	*PSD2*	ENST00000274710	1	3_prime_untranslated_region	c.*367	NULL	tier3	31	0	0.000	52	34	0.395
429745	5	176008570	176008570	C	T	SNP	*CDHR2*	ENST00000261944	1	missense	c.2045	p.T682I	tier1	56	0	0.000	95	17	0.152
429745	5	176709402	176709402	A	G	SNP	*NSD1*	ENST00000439151	1	intronic	c.5893-64	e18-64	tier3	45	0	0.000	39	32	0.451
429745	6	27278373	27278373	T	C	SNP	*POM121L2*	ENST00000444565	-1	missense	c.1577	p.D526G	tier1	51	0	0.000	46	30	0.395

429745	6	32521236	32521236	C	T	SNP	*HLA-DRB6*	ENST00000411500	-1	intronic	c.NULL	NULL	tier3	35	0	0.000	74	19	0.204
429745	6	32521237	32521237	A	G	SNP	*HLA-DRB6*	ENST00000411500	-1	intronic	c.NULL	NULL	tier3	35	0	0.000	74	19	0.204
429745	7	53854870	53854870	C	T	SNP	*ENSG00000232418*	ENST00000426503	1	3_prime_untranslated_region	c.*53854870	NULL	tier2	84	0	0.000	86	56	0.394
429745	7	103206001	103206002	-	A	INS	*RELN*	ENST00000424685	-1	splice_region_ins	c.4937-4_4937-3	e34-3	tier3	19	0	0.000	27	13	0.325
429745	9	114412150	114412150	C	-	DEL	*DNAJC25*	ENST00000313525	1	frame_shift_del	c.907	p.H303fs	tier1	14	0	0.000	18	18	0.500
429745	10	11376350	11376350	T	G	SNP	*CELF2*	ENST00000450189	1	3_prime_untranslated_region	c.*5334	NULL	tier3	41	0	0.000	29	22	0.431
429745	10	35300792	35300792	T	C	SNP	*CUL2*	ENST00000537177	-1	missense	c.2147	p.N716S	tier1	56	1	0.018	62	62	0.500
429745	10	111967928	111967928	C	-	DEL	*MXI1*	ENST00000332674	1	intronic	c.274+88	e1+88	tier2	77	0	0.000	180	19	0.096
429745	11	62302518	62302518	C	T	SNP	*AHNAK*	ENST00000378024	-1	nonsense	c.299	p.W100*	tier1	50	0	0.000	53	26	0.329
429745	11	65271780	65271780	T	-	DEL	*MALAT1*	ENST00000534336	1	rna	NULL	NULL	tier1	28	0	0.000	22	11	0.333
429745	11	67020214	67020214	G	A	SNP	*KDM2A*	ENST00000529006	1	missense	c.2818	p.A940T	tier1	40	1	0.024	68	36	0.346
429745	11	67565182	67565182	C	T	SNP	*FAM86C2P*	ENST00000528684	-1	5_prime_untranslated_region	c.-67565182	NULL	tier3	138	2	0.014	149	110	0.423
429745	12	102074329	102074329	G	A	SNP	*MYBPC1*	ENST00000361466	1	intronic	c.3433+22	e29+22	tier3	27	0	0.000	28	21	0.429
429745	12	109569189	109569189	G	T	SNP	*ACACB*	ENST00000539864	1	5_prime_untranslated_region	c.-8097	NULL	tier3	38	0	0.000	23	21	0.477
429745	14	31405745	31405745	C	A	SNP	*STRN3*	ENST00000357479	-1	missense	c.802	p.G268C	tier1	71	0	0.000	76	29	0.274
429745	14	64921502	64921502	A	G	SNP	*MTHFD1*	ENST00000216605	1	missense	c.2627	p.E876G	tier1	41	0	0.000	95	17	0.152
429745	14	81950742	81950742	C	A	SNP	*SEL1L*	ENST00000336735	-1	splice_site	c.1874-1	e19-1	tier1	41	0	0.000	49	17	0.258
429745	17	26817851	26817851	C	T	SNP	*SLC13A2*	ENST00000444914	1	silent	c.648	p.N216	tier1	33	1	0.029	39	31	0.443
429745	17	45913390	45913390	T	A	SNP	*LRRC46*	ENST00000269025	1	splice_region	c.383-9	e6-9	tier3	41	0	0.000	60	47	0.439
429745	17	62924761	62924761	A	G	SNP	*ENSG00000264057*	ENST00000579873	1	3_prime_untranslated_region	c.*62924761	NULL	tier2	52	0	0.000	152	20	0.116
429745	17	65871717	65871717	T	G	SNP	*BPTF*	ENST00000321892	1	missense	c.1910	p.L637R	tier1	27	0	0.000	39	25	0.391
429745	17	74018124	74018124	C	A	SNP	*EVPL*	ENST00000301607	-1	intronic	c.646-15	e7-15	tier2	13	0	0.000	22	14	0.389
429745	18	40849590	40849590	A	T	SNP	*SYT4*	ENST00000255224	-1	3_prime_untranslated_region	c.*716	NULL	tier3	66	0	0.000	82	64	0.438
429745	19	11019894	11019894	C	T	SNP	*CARM1*	ENST00000327064	1	intronic	c.558+11	e4+11	tier3	21	0	0.000	34	20	0.370
429745	19	48643310	48643310	G	C	SNP	*LIG1*	ENST00000263274	-1	silent	c.1005	p.L335	tier1	13	0	0.000	41	39	0.488
429745	20	23860305	23860305	C	T	SNP	*CST5*	ENST00000304710	-1	nonsense	c.9	p.W3*	tier1	14	0	0.000	12	12	0.500
429745	21	36252919	36252920	-	TAGCATTTCTCAGCTC	INS	*RUNX1*	ENST00000300305	-1	frame_shift_ins	c.443_442	p.T148fs	tier1	681	0	0.000	1118	73	0.061
429745	X	39931644	39931644	A	T	SNP	*BCOR*	ENST00000378444	-1	nonsense	c.2955	p.Y985*	tier1	320	2	0.006	423	313	0.424
430998	1	24421386	24421386	C	T	SNP	*MYOM3*	ENST00000330966	-1	silent	c.888	p.S296	tier1	202	1	0.005	404	46	0.102
430998	1	32162944	32162944	T	C	SNP	*COL16A1*	ENST00000271069	-1	intronic	c.658-43	e6-43	tier4	31	1	0.031	32	24	0.429
430998	2	15533730	15533730	G	-	DEL	*NBAS*	ENST00000281513	-1	intronic	c.3257+621	e28+621	tier4	105	1	0.009	159	18	0.102
430998	2	42553171	42553171	T	G	SNP	*EML4*	ENST00000318522	1	intronic	c.2243-123	e21-123	tier3	103	2	0.019	106	42	0.284
430998	2	196851848	196851848	T	C	SNP	*DNAH7*	ENST00000312428	-1	missense	c.1696	p.I566V	tier1	72	3	0.040	84	39	0.317
430998	2	198266834	198266834	T	C	SNP	*SF3B1*	ENST00000335508	-1	missense	c.2098	p.K700E	tier1	274	4	0.014	424	268	0.386
430998	3	46486788	46486788	C	T	SNP	*LTF*	ENST00000231751	-1	silent	c.1497	p.T499	tier1	35	2	0.053	51	36	0.414
430998	3	184557400	184557400	G	T	SNP	*VPS8*	ENST00000424463	1	3_prime_untranslated_region	c.*851	NULL	tier3	104	3	0.028	102	63	0.382
430998	4	20574880	20574880	A	G	SNP	*SLIT2*	ENST00000273739	1	missense	c.3124	p.K1042E	tier1	120	0	0.000	186	13	0.065
430998	5	93217240	93217240	C	T	SNP	*FAM172A*	ENST00000395965	-1	missense	c.722	p.R241H	tier1	98	0	0.000	144	12	0.077
430998	6	123786098	123786098	G	A	SNP	*TRDN*	ENST00000398178	-1	missense	c.884	p.P295L	tier1	92	1	0.011	145	78	0.350
430998	8	11188922	11188922	T	C	SNP	*SLC35G5*	ENST00000382435	1	missense	c.307	p.W103R	tier1	80	0	0.000	182	17	0.085
430998	9	6534811	6534811	G	A	SNP	*GLDC*	ENST00000321612	-1	intronic	c.2839-23	e24-23	tier3	54	1	0.018	62	37	0.374
430998	10	105831879	105831879	C	T	SNP	*COL17A1*	ENST00000353479	-1	intronic	c.416-42	e7-42	tier3	30	0	0.000	50	38	0.432
430998	11	89606363	89606363	C	G	SNP	*TRIM64B*	ENST00000329862	-1	intronic	c.758+73	e4+73	tier3	686	7	0.010	1004	217	0.177
430998	12	3662052	3662052	C	T	SNP	*PRMT8*	ENST00000543701	1	3_prime_untranslated_region	c.*3662052	NULL	tier3	42	3	0.067	70	54	0.436
430998	12	88525006	88525006	A	-	DEL	*CEP290*	ENST00000309041	-1	intronic	c.442-11	e6-11	tier4	48	0	0.000	66	12	0.154
430998	13	79894878	79894878	A	-	DEL	*RBM26*	ENST00000438724	-1	intronic	c.2863-33	e21-33	tier4	60	1	0.016	81	19	0.190
430998	14	106391086	106391086	C	T	SNP	*KIAA0125*	ENST00000482999	1	rna	NULL	NULL	tier1	151	4	0.026	211	183	0.463
430998	16	1251965	1251965	C	T	SNP	*CACNA1H*	ENST00000348261	1	silent	c.1515	p.R505	tier1	24	1	0.040	44	26	0.371
430998	16	70044642	70044642	G	A	SNP	*PDXDC2P*	ENST00000325845	-1	intronic	c.NULL	NULL	tier3	111	0	0.000	186	21	0.101
430998	17	10403963	10403963	G	A	SNP	*MYH1*	ENST00000226207	-1	missense	c.3845	p.A1282V	tier1	74	0	0.000	198	25	0.111
430998	17	47676686	47676686	T	A	SNP	*SPOP*	ENST00000347630	-1	3_prime_untranslated_region	c.*1054	NULL	tier4	92	0	0.000	138	14	0.092
430998	17	48267657	48267657	G	A	SNP	*COL1A1*	ENST00000225964	-1	intronic	c.2451+31	e35+31	tier3	89	2	0.022	106	53	0.333
430998	17	66146458	66146458	A	G	SNP	*LRRC37A16P*	ENST00000586022	-1	5_prime_untranslated_region	c.-66146458	NULL	tier3	162	6	0.036	217	113	0.342
430998	19	1806137	1806137	C	T	SNP	*ATP8B3*	ENST00000539485	-1	missense	c.709	p.V237M	tier1	30	0	0.000	34	22	0.393
430998	19	12767474	12767474	C	T	SNP	*MAN2B1*	ENST00000593686	-1	nonsense	c.165	p.W55*	tier1	95	0	0.000	155	13	0.077
430998	19	22941441	22941441	G	T	SNP	*ZNF99*	ENST00000397104	-1	missense	c.997	p.P333T	tier1	144	6	0.040	141	80	0.362
430998	19	54722897	54722897	C	T	SNP	*LILRB3*	ENST00000407860	-1	intronic	c.1477+101	e9+101	tier3	69	0	0.000	121	16	0.116
430998	22	40719779	40719779	C	A	SNP	*TNRC6B*	ENST00000454349	1	3_prime_untranslated_region	c.*534	NULL	tier4	43	0	0.000	127	25	0.162
430998	22	47075722	47075722	T	C	SNP	*GRAMD4*	ENST00000361034	1	3_prime_flanking_region	c.*2574	NULL	tier2	36	2	0.053	49	42	0.462
430998	X	54319632	54319632	C	T	SNP	*WNK3*	ENST00000354646	-1	missense	c.1822	p.V608I	tier1	97	2	0.020	43	112	0.718
430998	X	134992384	134992384	T	C	SNP	*SAGE1*	ENST00000324447	1	intronic	c.1864+55	e14+55	tier3	21	0	0.000	16	59	0.776
435866	1	98511783	98511783	C	T	SNP	*MIR137HG*	ENST00000424528	-1	5_prime_untranslated_region	c.-98511783	NULL	tier4	89	1	0.011	243	33	0.120
435866	2	230127480	230127480	C	T	SNP	*PID1*	ENST00000392054	-1	silent	c.42	p.S14	tier1	28	0	0.000	75	35	0.318
435866	3	45718805	45718805	C	T	SNP	*LIMD1*	ENST00000273317	1	3_prime_untranslated_region	c.*254	NULL	tier3	46	2	0.042	101	70	0.409
435866	3	185978207	185978207	T	C	SNP	*DGKG*	ENST00000265022	-1	intronic	c.1424+21	e15+21	tier3	170	1	0.006	230	153	0.396
435866	4	66356333	66356333	G	A	SNP	*EPHA5*	ENST00000273854	-1	silent	c.1164	p.D388	tier1	44	0	0.000	115	110	0.489
435866	5	138658293	138658293	A	T	SNP	*MATR3*	ENST00000361059	1	missense	c.1785	p.R595S	tier1	57	0	0.000	112	78	0.411
435866	5	142254704	142254704	C	T	SNP	*ARHGAP26*	ENST00000274498	1	missense	c.280	p.L94F	tier1	109	2	0.018	168	142	0.457
435866	5	172745042	172745042	G	A	SNP	*STC2*	ENST00000265087	-1	silent	c.717	p.H239	tier1	101	3	0.029	427	384	0.473
435866	6	130504496	130504496	G	A	SNP	*SAMD3*	ENST00000524930	-1	3_prime_untranslated_region	c.*31139	NULL	tier4	53	0	0.000	283	54	0.159
435866	7	89551249	89551249	G	T	SNP	*STEAP2-AS1*	ENST00000478318	-1	intronic	c.NULL	NULL	tier3	75	0	0.000	204	129	0.387
435866	7	123269290	123269290	T	C	SNP	*ASB15*	ENST00000275699	1	silent	c.1242	p.N414	tier1	37	0	0.000	71	54	0.432
435866	7	149481922	149481922	C	T	SNP	*SSPO*	ENST00000262089	1	3_prime_untranslated_region	c.*149481922	NULL	tier3	30	2	0.063	72	59	0.450
435866	7	151882645	151882645	C	A	SNP	*MLL3*	ENST00000355193	-1	missense	c.5080	p.V1694L	tier1	164	0	0.000	767	361	0.320

435866	8	68024182	68024182	G	A	SNP	*CSPP1*	ENST00000389042	1	intronic	c.1226-25	e12-25	tier3	51	1	0.019	109	101	0.481
435866	8	139727925	139727925	C	A	SNP	*COL22A1*	ENST00000303045	-1	missense	c.2517	p.K839N	tier1	151	1	0.007	245	193	0.441
435866	10	81921715	81921715	G	T	SNP	*ANXA11*	ENST00000265447	-1	silent	c.1156	p.R386	tier1	50	0	0.000	206	143	0.410
435866	10	120810716	120810716	A	G	SNP	*EIF3A*	ENST00000369144	-1	missense	c.2314	p.Y772H	tier1	72	0	0.000	154	127	0.450
435866	12	12006446	12006447	CT	-	DEL	*ETV6*	ENST00000396373	1	frame_shift_del	c.414_415	p.S139fs	tier1	149	0	0.000	366	247	0.403
435866	14	20020000	20020000	C	T	SNP	*POTEM*	ENST00000439503	-1	missense	c.221	p.G74E	tier1	263	0	0.000	1591	170	0.096
435866	15	28420657	28420657	C	T	SNP	*HERC2*	ENST00000261609	-1	splice_site	c.9831+1	e63+1	tier1	49	0	0.000	311	260	0.455
435866	16	3341019	3341019	C	T	SNP	*ZNF263*	ENST00000219069	1	3_prime_untranslated_region	c.*461	NULL	tier2	37	0	0.000	69	41	0.373
435866	16	87870242	87870242	C	T	SNP	*SLC7A5*	ENST00000261622	-1	silent	c.1152	p.T384	tier1	40	0	0.000	95	90	0.487
435866	17	18967192	18967192	T	C	SNP	*SNORD3B-1*	ENST00000571722	-1	5_prime_untranslated_region	c.-18967192	NULL	tier2	161	0	0.000	608	148	0.195
435866	17	40049260	40049260	A	G	SNP	*ACLY*	ENST00000401700	-1	intronic	c.1763+26	e15+26	tier2	34	0	0.000	86	79	0.479
435866	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000392485	-1	missense	c.284	p.P95H	tier1	49	2	0.039	140	101	0.417
435866	18	61226995	61226995	C	G	SNP	*SERPINB12*	ENST00000269491	1	intronic	c.384+44	e3+44	tier2	37	0	0.000	73	61	0.455
435866	20	14830634	14830634	A	G	SNP	*MACROD2*	ENST00000463861	1	3_prime_untranslated_region	c.*14830634	NULL	tier3	116	0	0.000	167	126	0.430
435866	22	20715907	20715916	CAGGGCATCG	-	DEL	*ENSG00000188280*	ENST00000434783	1	intronic	c.NULL	NULL	tier2	70	0	0.000	627	79	0.112
435866	22	38884063	38884063	T	C	SNP	*DDX17*	ENST00000396821	-1	missense	c.1505	p.Y502C	tier1	42	0	0.000	85	71	0.455
435866	X	79971691	79971691	C	G	SNP	*BRWD3*	ENST00000373275	-1	missense	c.2290	p.E764Q	tier1	78	0	0.000	115	90	0.439
435866	X	105450024	105450024	C	T	SNP	*MUM1L1*	ENST00000337685	1	missense	c.599	p.S200L	tier1	60	2	0.032	102	74	0.421
437422	1	22186507	22186507	G	T	SNP	*HSPG2*	ENST00000374695	-1	intronic	c.5015-12	e41-12	tier3	38	0	0.000	51	13	0.203
437422	1	27736195	27736195	T	C	SNP	*WASF2*	ENST00000430629	-1	missense	c.1330	p.I444V	tier1	168	0	0.000	222	40	0.153
437422	1	84641417	84641417	T	-	DEL	*PRKACB*	ENST00000370685	1	intronic	c.188-3443	e2-3443	tier3	58	0	0.000	109	14	0.114
437422	1	145014784	145014784	C	G	SNP	*PDE4DIP*	ENST00000313382	-1	intronic	c.228+1076	e3+1076	tier3	75	0	0.000	121	19	0.136
437422	1	167802237	167802237	C	A	SNP	*ADCY10*	ENST00000367851	-1	missense	c.3581	p.S1194I	tier1	78	0	0.000	102	28	0.215
437422	1	190067860	190067860	C	T	SNP	*BRINP3*	ENST00000367462	-1	missense	c.1589	p.R530H	tier1	724	4	0.006	906	416	0.315
437422	1	208061976	208061976	C	T	SNP	*CD34*	ENST00000310833	-1	intronic	c.972+51	e7+51	tier3	73	3	0.040	96	37	0.278
437422	2	5838174	5838174	A	T	SNP	*SOX11*	ENST00000322002	1	3_prime_untranslated_region	c.*3995	NULL	tier2	118	0	0.000	225	17	0.070
437422	2	75105821	75105821	G	A	SNP	*HK2*	ENST00000290573	1	silent	c.1038	p.K346	tier1	43	0	0.000	60	29	0.326
437422	2	196602340	196602340	C	T	SNP	*SLC39A10*	ENST00000359634	1	3_prime_untranslated_region	c.*2575	NULL	tier3	100	0	0.000	189	16	0.078
437422	3	39453515	39453515	A	G	SNP	*RPSA*	ENST00000301821	1	silent	c.756	p.V252	tier1	130	1	0.008	200	19	0.086
437422	3	167006710	167006710	C	G	SNP	*ZBBX*	ENST00000307529	-1	missense	c.1941	p.L647F	tier1	118	1	0.008	161	75	0.314
437422	4	120327397	120327397	C	T	SNP	*LOC101926979*	ENST00000508519	1	5_prime_flanking_region	c.-48597	NULL	tier2	126	1	0.008	170	22	0.115
437422	4	166416855	166416855	C	T	SNP	*CPE*	ENST00000402744	1	intronic	c.1332+26	e8+26	tier3	67	0	0.000	118	29	0.197
437422	5	121786643	121786643	C	G	SNP	*SNCAIP*	ENST00000379533	1	missense	c.2242	p.P748A	tier1	36	1	0.027	47	18	0.277
437422	5	133898014	133898014	G	A	SNP	*PHF15*	ENST00000395003	1	missense	c.809	p.G270E	tier1	90	0	0.000	131	57	0.298
437422	6	31239544	31239544	G	T	SNP	*HLA-C*	ENST00000415537	-1	missense	c.173	p.A58E	tier1	167	2	0.012	237	26	0.099
437422	7	6193554	6193554	C	T	SNP	*USP42*	ENST00000306177	1	missense	c.2369	p.A790V	tier1	52	1	0.019	65	31	0.323
437422	7	77885784	77885784	C	T	SNP	*MAGI2*	ENST00000354212	-1	missense	c.1523	p.R508H	tier1	640	2	0.003	1123	56	0.047
437422	7	120428042	120428042	C	T	SNP	*TSPAN12*	ENST00000222747	-1	3_prime_untranslated_region	c.*604	NULL	tier2	229	1	0.004	192	138	0.417
437422	8	113299258	113299258	T	C	SNP	*CSMD3*	ENST00000297405	-1	intronic	c.9331+35	e58+35	tier3	347	2	0.006	524	228	0.302
437422	8	145754744	145754744	T	C	SNP	*ARHGAP39*	ENST00000377307	-1	3_prime_untranslated_region	c.*1062	NULL	tier4	60	0	0.000	109	52	0.321
437422	9	114341237	114341237	T	A	SNP	*PTGR1*	ENST00000309195	-1	splice_region	c.496-6	e6-6	tier3	48	0	0.000	82	14	0.146
437422	11	763314	763315	-	T	INS	*TALDO1*	ENST00000319006	1	intronic	c.462-30_462-29	e5-29	tier4	6	0	0.000	2	7	0.778
437422	11	46686904	46686904	T	G	SNP	*ATG13*	ENST00000312040	1	intronic	c.901-29	e11-29	tier3	77	0	0.000	127	58	0.312
437422	11	130067769	130067769	G	A	SNP	*ST14*	ENST00000278742	1	missense	c.1388	p.R463Q	tier1	26	0	0.000	26	18	0.409
437422	12	122091150	122091150	T	G	SNP	*MORN3*	ENST00000355329	-1	missense	c.479	p.Y160S	tier1	116	1	0.009	106	42	0.284
437422	16	10721483	10721483	C	T	SNP	*TEKT5*	ENST00000283025	-1	missense	c.1415	p.R472H	tier1	88	0	0.000	95	46	0.326
437422	17	7576851	7576851	A	C	SNP	*TP53*	ENST00000269305	-1	splice_site	c.993+2	e8+2	tier1	1059	8	0.008	1443	648	0.309
437422	17	7578431	7578431	G	A	SNP	*TP53*	ENST00000269305	-1	nonsense	c.499	p.Q167*	tier1	1051	9	0.009	1349	612	0.312
437422	17	78114602	78114603	-	T	INS	*EIF4A3*	ENST00000269349	-1	intronic	c.372+515_372+514	e4+515	tier4	114	1	0.009	190	19	0.091
437422	18	33269094	33269094	G	A	SNP	*GALNT1*	ENST00000269195	1	intronic	c.861-43	e6-43	tier3	191	0	0.000	235	88	0.272
437422	20	9360833	9360834	-	A	INS	*PLCB4*	ENST00000334005	1	intronic	c.853+24_853+23	e10+24	tier3	113	1	0.009	207	25	0.108
437422	20	33068598	33068598	G	A	SNP	*ITCH*	ENST00000262650	1	intronic	c.2075+61	e18+61	tier3	137	0	0.000	202	40	0.165
437422	X	31139616	31139616	T	A	SNP	*DMD*	ENST00000357033	-1	3_prime_untranslated_region	c.*420	NULL	tier2	213	0	0.000	416	19	0.044
437422	X	76812922	76812922	C	T	SNP	*ATRX*	ENST00000373344	-1	silent	c.6699	p.K2233	tier1	292	2	0.007	485	107	0.180
439820	1	2077399	2077399	C	G	SNP	*PRKCZ*	ENST00000378567	1	intronic	c.553-67	e7-67	tier3	49	0	0.000	106	19	0.152
439820	1	22927251	22927251	G	C	SNP	*EPHA8*	ENST00000166244	1	missense	c.2486	p.W829S	tier1	133	0	0.000	179	13	0.068
439820	1	35250948	35250948	C	T	SNP	*GJB3*	ENST00000373362	1	silent	c.585	p.S195	tier1	203	1	0.005	314	79	0.200
439820	1	91182861	91182861	A	-	DEL	*BARHL2*	ENST00000370445	-1	5_prime_flanking_region	c.-109	NULL	tier2	38	0	0.000	72	14	0.163
439820	1	97981408	97981408	G	A	SNP	*DPYD*	ENST00000370192	-1	silent	c.1614	p.A538	tier1	96	1	0.010	91	71	0.438
439820	1	115258745	115258745	C	G	SNP	*NRAS*	ENST00000369535	-1	missense	c.37	p.G13R	tier1	399	0	0.000	616	109	0.150
439820	1	115258747	115258747	C	G	SNP	*NRAS*	ENST00000369535	-1	missense	c.35	p.G12A	tier1	401	0	0.000	694	27	0.037
439820	1	145417057	145417057	C	G	SNP	*HFE2*	ENST00000336751	1	3_prime_untranslated_region	c.*121	NULL	tier3	55	0	0.000	70	69	0.496
439820	1	160090882	160090882	C	T	SNP	*ATP1A2*	ENST00000478587	1	3_prime_untranslated_region	c.*160090882	NULL	tier3	81	0	0.000	120	34	0.219
439820	1	186089086	186089086	G	C	SNP	*HMCN1*	ENST00000271588	1	intronic	c.12095-57	e80-57	tier3	317	0	0.000	549	90	0.141
439820	2	38295746	38295746	C	T	SNP	*CYP1B1*	ENST00000260630	-1	3_prime_untranslated_region	c.*2119	NULL	tier3	143	2	0.014	170	130	0.433
439820	2	89292205	89292205	C	T	SNP	*IGKV1-8*	ENST00000495489	-1	missense	c.68	p.R23Q	tier1	265	0	0.000	396	33	0.077
439820	2	91927043	91927043	T	C	SNP	*ENSG00000223703*	ENST00000445234	1	3_prime_untranslated_region	c.*91927043	NULL	tier3	43	0	0.000	35	23	0.397
439820	2	98349520	98349520	G	A	SNP	*ZAP70*	ENST00000264972	1	intronic	c.702+36	e3+36	tier3	36	2	0.053	47	26	0.356
439820	2	119739805	119739805	C	G	SNP	*MARCO*	ENST00000327097	1	silent	c.975	p.G325	tier1	57	1	0.017	44	47	0.517
439820	2	179459370	179459370	A	C	SNP	*TTN*	ENST00000342992	-1	missense	c.50147	p.V16716G	tier1	43	0	0.000	65	37	0.363
439820	3	10401760	10401760	C	T	SNP	*ATP2B2*	ENST00000352432	-1	silent	c.1707	p.T569	tier1	217	0	0.000	315	14	0.042
439820	3	12227025	12227025	C	T	SNP	*SYN2*	ENST00000432424	1	rna	NULL	NULL	tier1	100	0	0.000	113	74	0.396
439820	3	15185665	15185665	C	G	SNP	*ZFYVE20*	ENST00000253699	-1	5_prime_flanking_region	c.-48038	NULL	tier3	123	0	0.000	174	12	0.065
439820	3	53224001	53224001	C	G	SNP	*PRKCD*	ENST00000330452	1	missense	c.1856	p.P619R	tier1	56	0	0.000	109	15	0.120

439820	3	164783108	164783108	G	A	SNP	*SI*	ENST00000264382	-1	missense	c.748	p.R250C	tier1	376	1	0.003	620	99	0.138
439820	3	194146027	194146027	A	G	SNP	*ATP13A3*	ENST00000256031	-1	intronic	c.3313+44	e28+44	tier3	26	2	0.071	50	48	0.490
439820	4	23796009	23796009	G	A	SNP	*PPARGC1A*	ENST00000264867	-1	3_prime_untranslated_region	c.*1436	NULL	tier3	39	0	0.000	49	17	0.258
439820	4	159634313	159634313	C	G	SNP	*PPID*	ENST00000307720	-1	silent	c.852	p.L284	tier1	99	0	0.000	156	13	0.077
439820	5	40998245	40998245	C	T	SNP	*MROH2B*	ENST00000399564	-1	missense	c.4667	p.R1556H	tier1	80	0	0.000	93	71	0.433
439820	5	81583110	81583110	G	C	SNP	*ATP6AP1L*	ENST00000380167	1	intronic	c.1+6280	e0+6280	tier3	113	0	0.000	183	15	0.075
439820	6	131941851	131941851	C	A	SNP	*MED23*	ENST00000368058	-1	nonsense	c.514	p.E172*	tier1	100	0	0.000	122	96	0.440
439820	6	146244843	146244843	G	C	SNP	*SHPRH*	ENST00000367503	-1	missense	c.3508	p.R1170G	tier1	108	0	0.000	127	109	0.460
439820	6	168466523	168466523	G	C	SNP	*FRMD1*	ENST00000358587	-1	5_prime_untranslated_region	c.-168466523	NULL	tier3	55	0	0.000	66	13	0.165
439820	7	14217686	14217686	C	T	SNP	*DGKB*	ENST00000258767	-1	missense	c.2216	p.R739Q	tier1	64	1	0.015	49	34	0.410
439820	7	92888838	92888838	G	A	SNP	*CCDC132*	ENST00000495039	1	3_prime_untranslated_region	c.*92888838	NULL	tier3	76	0	0.000	127	102	0.444
439820	7	102427887	102427887	T	C	SNP	*FAM185A*	ENST00000413034	1	missense	c.1037	p.V346A	tier1	205	0	0.000	296	15	0.048
439820	7	139045095	139045095	T	G	SNP	*LUC7L2*	ENST00000541515	1	intronic	c.259+14728	e2+14728	tier2	150	2	0.013	123	16	0.114
439820	8	2909983	2909983	C	T	SNP	*CSMD1*	ENST00000520002	-1	splice_site	c.7663+1	e51+1	tier1	617	3	0.005	501	360	0.417
439820	8	52732287	52732287	C	T	SNP	*PCMTD1*	ENST00000360540	-1	3_prime_untranslated_region	c.*624	NULL	tier3	120	1	0.008	224	21	0.085
439820	8	102555673	102555673	C	A	SNP	*GRHL2*	ENST00000472106	1	3_prime_untranslated_region	c.*102555673	NULL	tier3	51	0	0.000	61	42	0.408
439820	8	133192501	133192501	C	T	SNP	*KCNQ3*	ENST00000388996	-1	missense	c.680	p.R227Q	tier1	105	0	0.000	129	11	0.078
439820	9	39178241	39178241	C	A	SNP	*CNTNAP3*	ENST00000297668	-1	nonsense	c.655	p.G219*	tier1	212	0	0.000	454	130	0.222
439820	10	5925962	5925962	G	A	SNP	*ANKRD16*	ENST00000380092	-1	silent	c.657	p.D219	tier1	45	0	0.000	53	35	0.398
439820	10	30316501	30316503	CTG	-	DEL	*KIAA1462*	ENST00000375377	-1	in_frame_del	c.2576_2574	p.S859in_frame_del	tier1	49	0	0.000	67	12	0.152
439820	10	46210670	46210670	G	C	SNP	*FAM21FP*	ENST00000426241	-1	5_prime_untranslated_region	c.-46210670	NULL	tier2	220	0	0.000	454	28	0.058
439820	10	71627506	71627506	C	T	SNP	*COL13A1*	ENST00000356340	1	intronic	c.365-4426	e3-4426	tier2	49	1	0.020	57	36	0.387
439820	10	105073978	105073978	C	-	DEL	*PCGF6*	ENST00000369847	-1	frame_shift_del	c.961	p.E321fs	tier1	64	1	0.015	104	72	0.409
439820	10	114925313	114925313	G	C	SNP	*TCF7L2*	ENST00000355995	1	splice_site	c.1443-1	e15-1	tier1	78	0	0.000	96	18	0.158
439820	11	2906566	2906566	C	A	SNP	*CDKN1C*	ENST00000414822	-1	nonsense	c.154	p.E52*	tier1	87	0	0.000	96	53	0.353
439820	11	4360536	4360536	C	G	SNP	*OR52B3P*	ENST00000314715	1	5_prime_flanking_region	c.-38976	NULL	tier3	57	0	0.000	120	17	0.124
439820	11	57471814	57471814	G	A	SNP	*MED19*	ENST00000431606	-1	missense	c.626	p.P209L	tier1	55	3	0.052	88	61	0.407
439820	11	62364143	62364143	T	C	SNP	*MTA2*	ENST00000278823	-1	missense	c.848	p.Y283C	tier1	446	9	0.020	476	382	0.444
439820	11	124413410	124413410	C	G	SNP	*OR8B12*	ENST00000306842	-1	silent	c.141	p.L47	tier1	654	0	0.000	1056	79	0.070
439820	11	124789263	124789263	C	G	SNP	*HEPN1*	ENST00000408930	1	5_prime_untranslated_region	c.-384	NULL	tier3	80	0	0.000	140	23	0.141
439820	12	6965657	6965657	A	G	SNP	*USP5*	ENST00000229268	1	intronic	c.584+43	e5+43	tier3	18	0	0.000	23	21	0.477
439820	12	47186868	47186868	G	A	SNP	*SLC38A4*	ENST00000266579	-1	5_prime_untranslated_region	c.-14	NULL	tier3	62	0	0.000	93	75	0.446
439820	12	50026780	50026780	C	G	SNP	*PRPF40B*	ENST00000548825	1	intronic	c.349-17	e7-17	tier3	353	4	0.010	498	26	0.046
439820	12	51844830	51844830	G	C	SNP	*SLC4A8*	ENST00000453097	1	intronic	c.277+24	e3+24	tier3	163	0	0.000	237	15	0.060
439820	12	112888165	112888165	G	C	SNP	*PTPN11*	ENST00000351677	1	missense	c.181	p.D61H	tier1	484	0	0.000	1051	46	0.042
439820	14	24518609	24518609	A	G	SNP	*DHRS4L1*	ENST00000558293	1	intronic	c.NULL	NULL	tier3	114	4	0.034	109	104	0.488
439820	14	24524337	24524337	G	T	SNP	*LRRC16B*	ENST00000342740	1	missense	c.523	p.V175F	tier1	90	0	0.000	72	66	0.475
439820	14	100792064	100792064	A	G	SNP	*SLC25A47*	ENST00000361529	1	intronic	c.29-61	e2-61	tier3	22	0	0.000	32	23	0.418
439820	15	91438809	91438809	G	C	SNP	*FES*	ENST00000328850	1	3_prime_untranslated_region	c.*21	NULL	tier3	31	1	0.031	57	33	0.367
439820	16	2098338	2098338	A	G	SNP	*TSC2*	ENST00000219476	1	intronic	c.1-250	e1-250	tier2	98	1	0.010	123	88	0.417
439820	16	7761443	7761443	G	A	SNP	*RBFOX1*	ENST00000547372	1	3_prime_untranslated_region	c.*1800	NULL	tier3	101	0	0.000	144	28	0.159
439820	16	24582766	24582766	G	A	SNP	*RBBP6*	ENST00000319715	1	missense	c.4379	p.R1460H	tier1	24	0	0.000	46	25	0.352
439820	16	29576812	29576812	T	C	SNP	*ENSG00000205534*	ENST00000447140	-1	5_prime_untranslated_region	c.-29576812	NULL	tier3	115	0	0.000	143	121	0.458
439820	16	50835415	50835415	A	G	SNP	*CYLD*	ENST00000427738	1	3_prime_untranslated_region	c.*4996	NULL	tier3	75	1	0.013	72	68	0.486
439820	16	50835731	50835731	C	G	SNP	*CYLD*	ENST00000427738	1	3_prime_untranslated_region	c.*5312	NULL	tier3	66	0	0.000	83	52	0.382
439820	17	7577538	7577538	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.743	p.R248Q	tier1	606	5	0.008	558	600	0.518
439820	17	15942836	15942836	G	C	SNP	*NCOR1*	ENST00000268712	-1	missense	c.6866	p.P2289R	tier1	591	3	0.005	690	457	0.397
439820	18	7034550	7034550	A	G	SNP	*LAMA1*	ENST00000389658	-1	missense	c.1979	p.M660T	tier1	109	0	0.000	136	102	0.427
439820	18	14752893	14752893	A	T	SNP	*ANKRD30B*	ENST00000358984	1	missense	c.392	p.D131V	tier1	111	2	0.018	161	104	0.393
439820	18	29046556	29046556	G	C	SNP	*DSG3*	ENST00000257189	1	missense	c.1475	p.C492S	tier1	74	0	0.000	127	21	0.141
439820	18	34205430	34205430	G	A	SNP	*FHOD3*	ENST00000257209	1	intronic	c.958-44	e10-44	tier3	104	0	0.000	110	55	0.331
439820	18	42531907	42531907	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2602	p.D868N	tier1	589	2	0.003	768	171	0.182
439820	19	1529504	1529504	G	T	SNP	*PLK5*	ENST00000334770	1	intronic	c.490+15	e5+15	tier3	107	0	0.000	175	90	0.338
439820	19	9007457	9007457	C	G	SNP	*MUC16*	ENST00000397910	-1	intronic	c.39481+30	e43+30	tier3	633	0	0.000	1562	76	0.046
439820	19	42401048	42401048	C	T	SNP	*ARHGEF1*	ENST00000337665	1	intronic	c.1166+493	e13+493	tier4	180	2	0.011	111	87	0.437
439820	19	53873937	53873938	-	A	INS	*ZNF525*	ENST00000474037	1	intronic	c.1-1531_1530	e1-1530	tier3	10	0	0.000	24	24	0.500
439820	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	621	15	0.024	758	356	0.320
439820	20	61291782	61291782	G	C	SNP	*SLCO4A1*	ENST00000217159	1	missense	c.906	p.E302D	tier1	70	0	0.000	61	14	0.187
439820	21	44514777	44514777	T	G	SNP	*U2AF1*	ENST00000291552	-1	missense	c.470	p.Q157P	tier1	312	1	0.003	308	229	0.425
439820	X	31462671	31462671	G	A	SNP	*DMD*	ENST00000357033	-1	missense	c.9011	p.T3004I	tier1	92	0	0.000	15	128	0.895
439820	X	110439784	110439784	G	C	SNP	*PAK3*	ENST00000360648	1	silent	c.1431	p.P477	tier1	106	0	0.000	176	20	0.101
439820	X	128781951	128781951	C	G	SNP	*APLN*	ENST00000427399	-1	intronic	c.128-57	e2-57	tier3	48	0	0.000	96	17	0.150
439820	X	133511717	133511718	AG	-	DEL	*PHF6*	ENST00000394292	1	frame_shift_del	c.70_71	p.D25fs	tier1	178	1	0.006	95	352	0.788
476807	1	26671642	26671642	C	A	SNP	*AIM1L*	ENST00000374207	-1	intronic	c.169+204	e2+204	tier3	106	0	0.000	189	50	0.209
476807	1	94342696	94342696	A	-	DEL	*DNTTIP2*	ENST00000436063	-1	frame_shift_del	c.795	p.F265fs	tier1	31	0	0.000	89	39	0.305
476807	1	176525591	176525591	T	C	SNP	*PAPPA2*	ENST00000367662	1	silent	c.133	p.L45	tier1	88	0	0.000	126	32	0.203
476807	2	97833261	97833261	T	A	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.1532-53	e21-53	tier3	159	3	0.019	555	57	0.093
476807	2	113181804	113181804	G	A	SNP	*RGPD8*	ENST00000302558	-1	intronic	c.140+13	e2+13	tier3	360	8	0.022	1468	147	0.091
476807	2	177065811	177065811	C	T	SNP	*ENSG00000218175*	ENST00000405359	-1	5_prime_untranslated_region	c.-177065811	NULL	tier2	59	1	0.017	104	49	0.318
476807	2	231906196	231906196	G	T	SNP	*C2orf72*	ENST00000373640	1	intronic	c.748+72	e2+72	tier3	31	0	0.000	40	34	0.460
476807	3	41290971	41290971	C	T	SNP	*ULK4*	ENST00000301831	-1	splice_region	c.3764+9	e35+9	tier3	86	3	0.033	124	69	0.358
476807	3	47138236	47138237	-	A	INS	*SETD2*	ENST00000409792	-1	intronic	c.5142+1208_5142+1207	e9+1208	tier4	14	0	0.000	35	30	0.462
476807	4	15937803	15937803	G	A	SNP	*FGFBP1*	ENST00000259988	-1	silent	c.453	p.V151	tier1	91	0	0.000	164	34	0.172
476807	4	66388703	66388703	G	A	SNP	*EPHA5*	ENST00000273854	-1	intronic	c.911-27442	e4-27442	tier3	29	0	0.000	71	47	0.398

476807	4	126389815	126389815	C	G	SNP	*FAT4*	ENST00000394329	1	missense	c.12048	p.D4016E	tier1	126	2	0.016	210	104	0.329
476807	4	183601392	183601392	T	C	SNP	*TENM3*	ENST00000406950	1	splice_region	c.1538-9	e8-9	tier3	54	1	0.018	105	56	0.346
476807	5	137589102	137589102	G	A	SNP	*GFRA3*	ENST00000274721	-1	intronic	c.1025-38	e7-38	tier3	151	2	0.013	160	64	0.286
476807	6	32007827	32007827	C	A	SNP	*CYP21A2*	ENST00000418967	1	missense	c.784	p.L262I	tier1	64	0	0.000	100	52	0.342
476807	7	75123378	75123378	C	A	SNP	*POM121C*	ENST00000453279	-1	5_prime_flanking_region	c.-52604	NULL	tier3	268	0	0.000	502	23	0.044
476807	7	77764563	77764563	C	T	SNP	*MAGI2*	ENST00000354212	-1	intronic	c.2846-40	e17-40	tier3	280	5	0.018	429	203	0.320
476807	7	92764778	92764778	A	C	SNP	*SAMD9L*	ENST00000318238	-1	missense	c.507	p.D169E	tier1	30	0	0.000	92	48	0.343
476807	7	100684392	100684392	C	T	SNP	*MUC17*	ENST00000306151	1	missense	c.9695	p.T3232M	tier1	130	0	0.000	237	39	0.141
476807	8	74529737	74529737	T	C	SNP	*STAU2*	ENST00000524300	-1	intronic	c.411-51	e4-51	tier3	22	0	0.000	76	36	0.321
476807	11	35016453	35016453	C	T	SNP	*PDHX*	ENST00000227868	1	splice_region	c.1248-8	e11-8	tier3	73	1	0.014	129	79	0.380
476807	11	93417105	93417105	C	T	SNP	*KIAA1731*	ENST00000411936	1	intronic	c.950-25	e8-25	tier3	69	0	0.000	152	27	0.151
476807	12	53670353	53670353	G	A	SNP	*ESPL1*	ENST00000257934	1	intronic	c.1701-51	e7-51	tier3	68	5	0.069	87	48	0.356
476807	12	85460596	85460596	A	G	SNP	*LRRIQ1*	ENST00000393217	1	missense	c.2615	p.Q872R	tier1	55	2	0.035	248	138	0.358
476807	12	114377861	114377861	G	T	SNP	*RBM19*	ENST00000261741	-1	silent	c.1842	p.G614	tier1	71	4	0.053	90	59	0.396
476807	13	19407870	19407870	G	T	SNP	*ANKRD20A9P*	ENST00000457997	-1	5_prime_untranslated_region	c.-19407870	NULL	tier3	143	0	0.000	404	215	0.346
476807	13	36347975	36347975	T	C	SNP	*DCLK1*	ENST00000360631	-1	3_prime_untranslated_region	c.*697	NULL	tier3	14	0	0.000	22	19	0.463
476807	15	21071137	21071137	G	A	SNP	*POTEB2*	ENST00000454856	-1	intronic	c.410+64	e1+64	tier3	780	5	0.006	1530	70	0.044
476807	15	38228468	38228468	A	G	SNP	*TMCO5A*	ENST00000319669	1	intronic	c.1-47	e1-47	tier3	45	1	0.022	103	63	0.375
476807	15	87097682	87097682	C	T	SNP	*AGBL1*	ENST00000441037	1	missense	c.2770	p.R924W	tier1	61	1	0.016	116	30	0.206
476807	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	555	6	0.011	597	311	0.341
476807	17	9066111	9066111	T	C	SNP	*NTN1*	ENST00000173229	1	intronic	c.1019-19	e2-19	tier3	80	0	0.000	122	51	0.295
476807	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	332	1	0.003	402	203	0.336
476807	18	14513621	14513621	T	C	SNP	*POTEC*	ENST00000358970	-1	intronic	c.1533+40	e10+40	tier3	102	0	0.000	474	32	0.063
476807	19	8654876	8654876	C	T	SNP	*ADAMTS10*	ENST00000270328	-1	splice_site	c.1798-1	e14-1	tier1	48	1	0.020	60	31	0.337
476807	19	36321785	36321785	C	T	SNP	*NPHS1*	ENST00000378910	-1	silent	c.3555	p.P1185	tier1	78	0	0.000	101	34	0.252
476807	19	56303709	56303709	G	A	SNP	*NLRP11*	ENST00000443188	-1	missense	c.2471	p.T824M	tier1	99	1	0.010	202	23	0.102
476807	20	31022403	31022425	CACCACTGCCATAGAGAGGCGGC	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1888_1910	p.H633fs	tier1	747	3	0.004	1000	114	0.102
476807	20	31531576	31531576	C	T	SNP	*EFCAB8*	ENST00000457731	1	5_prime_flanking_region	c.-16075	NULL	tier3	94	0	0.000	119	68	0.362
476807	20	48914916	48914916	G	T	SNP	*LOC284751*	ENST00000371639	1	rna	NULL	NULL	tier1	73	1	0.014	91	48	0.343
476807	22	16157940	16157940	C	T	SNP	*ENSG00000206195*	ENST00000413768	-1	intronic	c.NULL	NULL	tier2	28	0	0.000	33	10	0.233
476807	X	123181343	123181344	-	AAGCGGAAAG	INS	*STAG2*	ENST00000218089	1	frame_shift_ins	c.807_808	p.L273fs	tier1	169	0	0.000	281	34	0.108
480109	1	180789156	180789156	A	-	DEL	*XPR1*	ENST00000367590	1	intronic	c.764-4733	e8-4733	tier4	48	0	0.000	72	14	0.163
480109	2	55177887	55177887	C	T	SNP	*EML6*	ENST00000356458	1	missense	c.4184	p.A1395V	tier1	93	0	0.000	105	57	0.352
480109	2	172951837	172951837	G	T	SNP	*DLX1*	ENST00000409492	1	3_prime_untranslated_region	c.*172951837	NULL	tier2	32	0	0.000	45	18	0.286
480109	3	3099496	3099496	A	-	DEL	*CNTN4*	ENST00000397461	1	3_prime_untranslated_region	c.*1592	NULL	tier2	142	1	0.007	195	21	0.097
480109	4	106588612	106588612	T	C	SNP	*ARHGEF38*	ENST00000420470	1	missense	c.1900	p.Y634H	tier1	83	1	0.012	71	22	0.234
480109	4	153784943	153784943	A	C	SNP	*ARFIP1*	ENST00000353617	1	intronic	c.202+77	e2+77	tier3	84	1	0.012	83	49	0.371
480109	5	38489182	38489182	G	T	SNP	*LIFR*	ENST00000263409	-1	nonsense	c.2333	p.S778*	tier1	107	0	0.000	95	34	0.264
480109	5	67597268	67597268	G	A	SNP	*PIK3R1*	ENST00000396611	1	3_prime_untranslated_region	c.*3839	NULL	tier4	81	0	0.000	111	12	0.098
480109	5	118834979	118834979	A	G	SNP	*HSD17B4*	ENST00000256216	1	intronic	c.973-33	e13-33	tier3	99	0	0.000	35	37	0.514
480109	6	87969820	87969822	AAG	-	DEL	*ZNF292*	ENST00000369577	1	in_frame_del	c.6473_6475	p.E2159in_frame_del	tier1	55	0	0.000	98	26	0.210
480109	7	36671732	36671732	C	A	SNP	*AOAH*	ENST00000258749	-1	intronic	c.451-20	e6-20	tier3	95	0	0.000	157	13	0.077
480109	7	116199666	116199667	-	G	INS	*CAV1*	ENST00000341049	1	3_prime_untranslated_region	c.*325	NULL	tier3	57	0	0.000	59	11	0.157
480109	9	5073770	5073770	G	T	SNP	*JAK2*	ENST00000381652	1	missense	c.1849	p.V617F	tier1	568	2	0.004	593	251	0.297
480109	9	125282293	125282293	C	T	SNP	*OR1J4*	ENST00000340750	1	silent	c.874	p.L292	tier1	27	0	0.000	58	33	0.363
480109	11	24927450	24927450	G	C	SNP	*LUZP2*	ENST00000336930	1	intronic	c.397-87	e6-87	tier3	73	0	0.000	81	24	0.229
480109	11	65655168	65655168	C	T	SNP	*FIBP*	ENST00000338369	-1	missense	c.314	p.R105Q	tier1	71	1	0.014	138	33	0.193
480109	11	112071453	112071453	A	G	SNP	*BCO2*	ENST00000357685	1	missense	c.983	p.Q328R	tier1	100	2	0.020	160	74	0.316
480109	12	6701122	6701122	T	C	SNP	*CHD4*	ENST00000309577	-1	missense	c.3050	p.K1017R	tier1	384	2	0.005	494	174	0.260
480109	12	40689290	40689290	G	C	SNP	*LRRK2*	ENST00000298910	1	missense	c.2940	p.E980D	tier1	78	1	0.012	81	22	0.212
480109	12	122983394	122983394	C	T	SNP	*ZCCHC8*	ENST00000336229	-1	silent	c.222	p.L74	tier1	83	1	0.012	153	67	0.305
480109	14	21862072	21862072	C	T	SNP	*CHD8*	ENST00000399982	-1	missense	c.5882	p.R1961H	tier1	28	0	0.000	35	22	0.386
480109	15	85742643	85742643	A	G	SNP	*CSPG4P12*	ENST00000559989	1	intronic	c.NULL	NULL	tier3	19	1	0.050	12	12	0.500
480109	16	32956973	32956973	G	T	SNP	*ENSG00000260921*	ENST00000568904	1	5_prime_flanking_region	c.-49885	NULL	tier3	280	2	0.007	469	84	0.152
480109	16	57935363	57935363	G	C	SNP	*CNGB1*	ENST00000251102	-1	intronic	c.2893-24	e28-24	tier3	48	0	0.000	49	18	0.265
480109	17	7577114	7577114	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.824	p.C275Y	tier1	621	7	0.011	914	468	0.338
480109	17	16829225	16829225	A	C	SNP	*TBC1D27*	ENST00000261651	-1	rna	NULL	NULL	tier1	82	1	0.012	120	59	0.328
480109	19	18981487	18981487	T	-	DEL	*GDF1*	ENST00000247005	-1	intronic	c.1-59	e1-59	tier2	15	0	0.000	69	33	0.324
480109	20	43744353	43744353	G	C	SNP	*KCNS1*	ENST00000306117	-1	5_prime_flanking_region	c.-16476	NULL	tier3	119	1	0.008	117	51	0.304
480109	21	32491425	32491425	T	A	SNP	*TIAM1*	ENST00000286827	-1	3_prime_untranslated_region	c.*1261	NULL	tier4	99	0	0.000	134	12	0.082
480109	21	44010250	44010251	-	G	INS	*ENSG00000235772*	ENST00000442605	-1	5_prime_flanking_region	c.-28206	NULL	tier2	19	0	0.000	20	12	0.375
480109	21	44010254	44010255	TT	-	DEL	*ENSG00000235772*	ENST00000442605	-1	5_prime_flanking_region	c.-28210	NULL	tier2	19	0	0.000	17	12	0.414
480109	21	44010258	44010259	-	T	INS	*ENSG00000235772*	ENST00000442605	-1	5_prime_flanking_region	c.-28214	NULL	tier2	26	0	0.000	19	12	0.387
480109	22	42046726	42046726	G	C	SNP	*XRCC6*	ENST00000359308	1	splice_site	c.961-1	e7-1	tier1	112	0	0.000	168	91	0.351
480109	X	8538673	8538673	G	T	SNP	*KAL1*	ENST00000262648	-1	missense	c.929	p.T310N	tier1	55	2	0.035	67	36	0.350
480109	X	153042601	153042601	A	G	SNP	*PLXNB3*	ENST00000538966	1	intronic	c.4997-62	e29-62	tier3	29	0	0.000	52	17	0.243
481668	1	16262371	16262371	C	T	SNP	*SPEN*	ENST00000375759	1	silent	c.9636	p.A3212	tier1	726	8	0.011	901	341	0.273
481668	1	17256868	17256868	G	A	SNP	*CROCC*	ENST00000375541	1	intronic	c.683+26	e6+26	tier3	1326	12	0.009	2026	325	0.138
481668	1	46724275	46724275	A	G	SNP	*RAD54L*	ENST00000371975	1	intronic	c.211-83	e4-83	tier3	114	1	0.009	184	47	0.203
481668	1	46724283	46724283	A	C	SNP	*RAD54L*	ENST00000371975	1	intronic	c.211-75	e4-75	tier3	121	2	0.016	196	51	0.206
481668	1	46724289	46724289	A	G	SNP	*RAD54L*	ENST00000371975	1	intronic	c.211-69	e4-69	tier3	120	1	0.008	205	55	0.212
481668	1	46724300	46724300	A	C	SNP	*RAD54L*	ENST00000371975	1	intronic	c.211-58	e4-58	tier3	131	1	0.008	218	62	0.221
481668	1	152382172	152382172	G	T	SNP	*CRNN*	ENST00000271835	-1	silent	c.1386	p.T462	tier1	116	5	0.041	125	102	0.447
481668	1	182827980	182827980	A	G	SNP	*DHX9*	ENST00000367549	1	missense	c.1013	p.N338S	tier1	131	6	0.044	165	118	0.414

481668	1	247094587	247094587	T	C	SNP	*AHCTF1*	ENST00000366508	-1	5_prime_untranslated_region	c.-59	NULL	tier2	34	0	0.000	37	9	0.196
481668	2	1457512	1457512	C	G	SNP	*TPO*	ENST00000329066	1	missense	c.529	p.L177V	tier1	111	0	0.000	119	36	0.232
481668	2	61009939	61009939	T	-	DEL	*PAPOLG*	ENST00000238714	1	intronic	c.1112+34	e12+34	tier3	68	0	0.000	131	17	0.115
481668	2	98853198	98853198	A	G	SNP	*VWA3B*	ENST00000485216	1	rna	NULL	NULL	tier1	69	2	0.028	81	31	0.277
481668	4	15070967	15070968	-	A	INS	*CPEB2*	ENST00000538197	1	3_prime_untranslated_region	c.*2963	NULL	tier2	104	2	0.019	179	57	0.242
481668	4	95223388	95223388	A	G	SNP	*HPGDS*	ENST00000295256	-1	missense	c.344	p.M115T	tier1	94	1	0.011	146	46	0.240
481668	5	40959580	40959580	T	C	SNP	*C7*	ENST00000313164	1	missense	c.1519	p.S507P	tier1	92	4	0.042	130	47	0.266
481668	5	41862863	41862863	A	-	DEL	*OXCT1*	ENST00000196371	-1	intronic	c.79-11	e2-11	tier4	93	0	0.000	135	19	0.123
481668	6	325150	325150	T	C	SNP	*DUSP22*	ENST00000419235	1	intronic	c.139-9964	e4-9964	tier3	459	16	0.034	630	84	0.117
481668	6	31760727	31760727	G	C	SNP	*VARS*	ENST00000495010	-1	5_prime_untranslated_region	c.-31760727	NULL	tier3	96	2	0.020	117	46	0.281
481668	6	135513482	135513482	A	G	SNP	*MYB*	ENST00000341911	1	missense	c.548	p.N183S	tier1	122	0	0.000	131	47	0.264
481668	7	34118627	34118627	C	T	SNP	*BMPER*	ENST00000297161	1	missense	c.1237	p.R413C	tier1	738	0	0.000	1026	53	0.049
481668	7	81593304	81593304	T	G	SNP	*CACNA2D1*	ENST00000356253	-1	intronic	c.2816+68	e34+68	tier3	51	0	0.000	46	26	0.361
481668	7	100635373	100635373	C	A	SNP	*MUC12*	ENST00000536621	1	missense	c.1529	p.A510D	tier1	285	1	0.004	519	68	0.116
481668	7	148506166	148506166	T	A	SNP	*EZH2*	ENST00000320356	-1	missense	c.2192	p.Y731F	tier1	440	1	0.002	646	222	0.255
481668	9	117138957	117138957	C	T	SNP	*AKNA*	ENST00000307564	-1	missense	c.1130	p.R377H	tier1	350	0	0.000	729	24	0.032
481668	10	128933807	128933807	T	C	SNP	*FAM196A*	ENST00000522781	-1	3_prime_untranslated_region	c.*2294	NULL	tier3	167	0	0.000	214	75	0.259
481668	10	133761131	133761131	G	T	SNP	*PPP2R2D*	ENST00000455566	1	missense	c.825	p.M275I	tier1	148	1	0.007	213	57	0.211
481668	11	71903432	71903432	A	G	SNP	*FOLR1*	ENST00000312293	1	intronic	c.168+47	e1+47	tier3	63	0	0.000	70	26	0.271
481668	12	21608977	21608977	G	T	SNP	*PYROXD1*	ENST00000240651	1	missense	c.698	p.S233I	tier1	91	2	0.022	141	54	0.277
481668	12	57929244	57929245	AC	-	DEL	*DCTN2*	ENST00000551142	-1	5_prime_untranslated_region	c.-57929244	NULL	tier3	91	0	0.000	137	17	0.110
481668	12	113599210	113599210	C	A	SNP	*DDX54*	ENST00000549271	-1	rna	NULL	NULL	tier1	109	0	0.000	122	26	0.176
481668	13	33223009	33223009	C	T	SNP	*PDS5B*	ENST00000315596	1	nonsense	c.100	p.R34*	tier1	77	1	0.013	130	64	0.327
481668	14	50895475	50895476	-	A	INS	*MAP4K5*	ENST00000013125	-1	splice_region_ins	c.2234-4_2234-3	e28-3	tier3	69	0	0.000	144	16	0.100
481668	15	56704519	56704519	G	A	SNP	*TEX9*	ENST00000352903	1	missense	c.848	p.R283K	tier1	167	0	0.000	216	98	0.312
481668	15	74889854	74889855	AC	-	DEL	*ARID3B*	ENST00000346246	1	3_prime_untranslated_region	c.*1739	NULL	tier4	53	0	0.000	67	11	0.141
481668	16	30456662	30456662	C	T	SNP	*SEPHS2*	ENST00000542752	-1	silent	c.216	p.G72	tier1	82	0	0.000	84	23	0.215
481668	17	1559855	1559855	T	C	SNP	*PRPF8*	ENST00000304992	-1	missense	c.5624	p.H1875R	tier1	651	6	0.009	997	410	0.290
481668	17	37425012	37425012	A	G	SNP	*FBXL20*	ENST00000264658	-1	intronic	c.933+68	e12+68	tier3	63	2	0.031	86	46	0.349
481668	17	37879957	37879957	C	T	SNP	*ERBB2*	ENST00000269571	1	intronic	c.2208+44	e18+44	tier3	41	0	0.000	31	22	0.400
481668	19	9067438	9067438	C	T	SNP	*MUC16*	ENST00000397910	-1	missense	c.20008	p.V6670I	tier1	906	9	0.010	1848	610	0.247
481668	19	15219913	15219913	C	G	SNP	*SYDE1*	ENST00000342784	1	silent	c.135	p.P45	tier1	38	1	0.026	30	28	0.483
481668	20	2552803	2552803	T	-	DEL	*TMC2*	ENST00000358864	1	intronic	c.555-22	e5-22	tier3	100	2	0.020	167	26	0.135
481668	20	2552806	2552806	T	A	SNP	*TMC2*	ENST00000358864	1	intronic	c.555-19	e5-19	tier3	103	2	0.019	165	28	0.144
485523	1	110009655	110009655	C	-	DEL	*SYPL2*	ENST00000369872	1	intronic	c.55-26	e2-26	tier2	10	0	0.000	8	13	0.619
485523	4	39474726	39474726	G	A	SNP	*LIAS*	ENST00000261434	1	missense	c.961	p.E321K	tier1	148	0	0.000	242	17	0.066
485523	4	55976980	55976980	G	A	SNP	*KDR*	ENST00000263923	-1	intronic	c.977-45	e8-45	tier3	266	0	0.000	310	23	0.069
485523	5	23527469	23527469	C	A	SNP	*PRDM9*	ENST00000296682	1	missense	c.2272	p.R758S	tier1	165	2	0.012	207	18	0.080
485523	5	54552381	54552381	A	-	DEL	*DHX29*	ENST00000251636	-1	intronic	c.4058-13	e27-13	tier3	78	0	0.000	79	10	0.112
485523	5	176939370	176939370	C	T	SNP	*DDX41*	ENST00000507955	-1	missense	c.1574	p.R525H	tier1	524	0	0.000	677	65	0.088
485523	6	73904728	73904728	A	T	SNP	*KCNQ5*	ENST00000402622	1	missense	c.2420	p.N807I	tier1	82	0	0.000	156	18	0.103
485523	9	15472612	15472612	A	-	DEL	*PSIP1*	ENST00000495873	-1	rna	NULL	NULL	tier1	82	0	0.000	95	12	0.112
485523	14	24517447	24517447	G	A	SNP	*DHRS4L1*	ENST00000558293	1	rna	NULL	NULL	tier1	152	0	0.000	248	20	0.074
485523	15	75706652	75706652	C	T	SNP	*SIN3A*	ENST00000360439	-1	missense	c.367	p.V123M	tier1	46	0	0.000	39	10	0.204
485523	18	47462642	47462642	G	A	SNP	*MYO5B*	ENST00000285039	-1	silent	c.1983	p.N661	tier1	350	0	0.000	555	54	0.089
485523	19	7805616	7805616	G	C	SNP	*CD209*	ENST00000315599	-1	3_prime_untranslated_region	c.*2309	NULL	tier3	497	0	0.000	835	27	0.031
489196	1	1871145	1871145	G	A	SNP	*C1orf222*	ENST00000493964	-1	missense	c.614	p.P205L	tier1	103	0	0.000	48	51	0.515
489196	1	116386058	116386058	C	T	SNP	*NHLH2*	ENST00000369506	-1	5_prime_untranslated_region	c.-5065	NULL	tier4	134	0	0.000	218	78	0.262
489196	1	248651829	248651829	A	T	SNP	*OR2G6*	ENST00000343414	1	5_prime_flanking_region	c.-33119	NULL	tier3	230	1	0.004	253	52	0.171
489196	2	172930961	172930961	A	G	SNP	*METAP1D*	ENST00000315796	1	intronic	c.498-31	e5-31	tier3	37	1	0.026	62	34	0.354
489196	2	178483636	178483636	C	T	SNP	*TTC30A*	ENST00000355689	-1	5_prime_untranslated_region	c.-207	NULL	tier2	102	0	0.000	104	37	0.262
489196	2	196863801	196863801	G	T	SNP	*DNAH7*	ENST00000410072	-1	3_prime_untranslated_region	c.*13	NULL	tier4	90	0	0.000	106	29	0.215
489196	2	219501054	219501054	C	T	SNP	*PLCD4*	ENST00000417849	1	silent	c.2121	p.D707	tier1	100	0	0.000	95	36	0.275
489196	2	233407276	233407276	C	T	SNP	*CHRNG*	ENST00000389494	1	intronic	c.604+46	e6+46	tier3	32	0	0.000	26	18	0.409
489196	2	234591299	234591299	T	C	SNP	*UGT1A7*	ENST00000373426	1	missense	c.716	p.V239A	tier1	117	1	0.008	159	19	0.107
489196	3	77607305	77607305	G	A	SNP	*ROBO2*	ENST00000461745	1	splice_region	c.1437+5	e9+5	tier3	44	0	0.000	57	27	0.321
489196	3	113327118	113327118	G	T	SNP	*SIDT1*	ENST00000393830	1	intronic	c.1602+54	e16+54	tier3	67	0	0.000	49	22	0.310
489196	4	190876351	190876351	G	C	SNP	*FRG1*	ENST00000226798	1	intronic	c.432+45	e5+45	tier3	169	2	0.012	329	26	0.073
489196	5	32135733	32135733	A	G	SNP	*GOLPH3*	ENST00000265070	-1	silent	c.417	p.H139	tier1	117	0	0.000	248	39	0.135
489196	5	122713937	122713937	G	A	SNP	*CEP120*	ENST00000306467	-1	intronic	c.2196+93	e15+93	tier4	93	0	0.000	163	28	0.147
489196	5	140768657	140768657	A	T	SNP	*PCDHGB4*	ENST00000519479	1	missense	c.1206	p.L402F	tier1	82	1	0.012	79	48	0.378
489196	6	2623069	2623069	C	T	SNP	*C6orf195*	ENST00000296847	-1	3_prime_untranslated_region	c.*604	NULL	tier3	142	0	0.000	124	66	0.347
489196	6	30954600	30954600	A	C	SNP	*MUC21*	ENST00000376296	1	missense	c.648	p.R216S	tier1	172	5	0.028	213	34	0.136
489196	6	35761203	35761203	A	-	DEL	*CLPSL1*	ENST00000428710	1	intronic	c.82-62	e2-62	tier4	63	1	0.016	55	12	0.179
489196	6	36685089	36685089	G	A	SNP	*RAB44*	ENST00000229824	1	missense	c.215	p.R72K	tier1	124	1	0.008	98	40	0.290
489196	6	62611335	62611335	A	-	DEL	*KHDRBS2*	ENST00000281156	-1	intronic	c.484-59	e5-59	tier3	29	0	0.000	43	13	0.232
489196	6	112671088	112671088	G	T	SNP	*RFPL4B*	ENST00000441065	1	missense	c.178	p.A60S	tier1	99	0	0.000	77	36	0.319
489196	6	143094282	143094282	C	T	SNP	*HIVEP2*	ENST00000012134	-1	missense	c.1594	p.E532K	tier1	142	0	0.000	143	45	0.239
489196	7	23625386	23625386	G	A	SNP	*ENSG00000232553*	ENST00000416636	-1	5_prime_untranslated_region	c.-23625386	NULL	tier2	364	7	0.019	188	122	0.391
489196	7	74212351	74212351	C	T	SNP	*GTF2IRD2*	ENST00000405086	-1	silent	c.1500	p.L500	tier1	89	3	0.033	41	16	0.281
489196	7	74212352	74212352	A	G	SNP	*GTF2IRD2*	ENST00000405086	-1	missense	c.1499	p.L500S	tier1	89	3	0.033	41	18	0.305
489196	7	75070419	75070419	C	A	SNP	*POM121C*	ENST00000257665	-1	intronic	c.792-26	e3-26	tier2	156	0	0.000	171	13	0.071
489196	7	100646672	100646672	C	G	SNP	*MUC12*	ENST00000536621	1	missense	c.12828	p.H4276Q	tier1	220	2	0.009	133	54	0.287
489196	8	1857452	1857452	T	A	SNP	*ARHGEF10*	ENST00000398564	1	splice_region	c.2043-9	e18-9	tier3	83	1	0.012	92	38	0.292

489196	8	87519260	87519260	T	C	SNP	*RMDN1*	ENST00000406452	-1	missense	c.211	p.I71V	tier1	169	0	0.000	275	99	0.264
489196	8	126011647	126011647	T	C	SNP	*SQLE*	ENST00000265896	1	missense	c.2	p.M1T	tier1	79	0	0.000	80	28	0.259
489196	9	127300323	127300323	G	C	SNP	*NR6A1*	ENST00000487099	-1	intronic	c.824+48	e6+48	tier3	58	2	0.033	38	23	0.377
489196	10	23326305	23326305	G	A	SNP	*ARMC3*	ENST00000298032	1	missense	c.2516	p.G839E	tier1	139	0	0.000	98	49	0.333
489196	10	79797037	79797037	A	G	SNP	*RPS24*	ENST00000440692	1	missense	c.365	p.K122R	tier1	68	0	0.000	73	27	0.270
489196	11	20676288	20676288	G	A	SNP	*SLC6A5*	ENST00000525748	1	silent	c.2268	p.P756	tier1	128	0	0.000	118	47	0.285
489196	11	46400551	46400551	T	A	SNP	*DGKZ*	ENST00000454345	1	missense	c.2993	p.L998Q	tier1	19	0	0.000	24	18	0.429
489196	11	48454279	48454279	G	A	SNP	*OR4C10P*	ENST00000434991	-1	5_prime_untranslated_region	c.-48454279	NULL	tier3	238	0	0.000	205	87	0.298
489196	11	56000330	56000330	C	T	SNP	*OR5T2*	ENST00000313264	-1	missense	c.332	p.C111Y	tier1	33	0	0.000	72	29	0.287
489196	12	9007449	9007449	T	C	SNP	*A2ML1*	ENST00000299698	1	intronic	c.2764+22	e22+22	tier3	176	0	0.000	162	56	0.257
489196	12	52946663	52946663	C	T	SNP	*KRT71*	ENST00000267119	-1	missense	c.199	p.G67R	tier1	225	1	0.004	202	82	0.289
489196	12	54686621	54686621	C	T	SNP	*NFE2*	ENST00000312156	-1	missense	c.659	p.G220E	tier1	76	0	0.000	87	29	0.250
489196	12	56110725	56110725	A	G	SNP	*BLOC1S1*	ENST00000548925	1	missense	c.154	p.R52G	tier1	116	0	0.000	107	42	0.282
489196	12	76461257	76461258	-	A	INS	*NAP1L1*	ENST00000551524	-1	5_prime_untranslated_region	c.-24	NULL	tier3	18	0	0.000	33	17	0.340
489196	13	28009534	28009534	T	C	SNP	*GTF3A*	ENST00000419181	1	intronic	c.567-36	e6-36	tier3	31	0	0.000	57	22	0.279
489196	13	52863939	52863939	A	G	SNP	*LOC101930578*	ENST00000451298	-1	intronic	c.NULL	NULL	tier3	306	3	0.010	435	26	0.056
489196	14	59670661	59670661	G	T	SNP	*DAAM1*	ENST00000351081	1	intronic	c.1+15175	e0+15175	tier3	58	0	0.000	121	37	0.234
489196	14	106945697	106945697	G	A	SNP	*LINC00221*	ENST00000334298	1	intronic	c.NULL	NULL	tier3	62	1	0.016	42	24	0.364
489196	15	20457242	20457242	C	T	SNP	*ENSG00000258628*	ENST00000557586	-1	5_prime_untranslated_region	c.-20457242	NULL	tier3	615	3	0.005	691	51	0.069
489196	15	66191080	66191080	T	A	SNP	*MEGF11*	ENST00000409699	-1	missense	c.2960	p.N987I	tier1	66	1	0.015	41	28	0.406
489196	16	57712000	57712000	G	T	SNP	*GPR97*	ENST00000333493	1	intronic	c.346-82	e4-82	tier3	189	3	0.016	139	55	0.284
489196	16	66956068	66956068	G	A	SNP	*RRAD*	ENST00000299759	-1	missense	c.838	p.R280C	tier1	66	1	0.015	60	28	0.318
489196	17	976071	976071	C	T	SNP	*ABR*	ENST00000302538	-1	intronic	c.754-77	e8-77	tier3	81	0	0.000	71	27	0.273
489196	17	43185926	43185926	G	A	SNP	*NMT1*	ENST00000258960	1	3_prime_untranslated_region	c.*2919	NULL	tier3	146	0	0.000	131	53	0.288
489196	17	62892220	62892220	G	C	SNP	*LRRC37A3*	ENST00000319651	-1	missense	c.1156	p.P386A	tier1	374	0	0.000	512	109	0.175
489196	18	28971008	28971008	C	T	SNP	*DSG4*	ENST00000359747	1	intronic	c.685-33	e7-33	tier3	99	0	0.000	127	62	0.326
489196	19	40589158	40589158	C	T	SNP	*ZNF780A*	ENST00000455521	-1	intronic	c.10-14	e2-14	tier3	208	1	0.005	178	87	0.327
489196	19	43920107	43920107	C	T	SNP	*TEX101*	ENST00000253435	1	silent	c.90	p.L30	tier1	77	0	0.000	40	22	0.355
489196	20	9496180	9496180	G	T	SNP	*LAMP5*	ENST00000246070	1	missense	c.145	p.V49L	tier1	90	1	0.011	98	86	0.467
489196	20	29623299	29623299	G	A	SNP	*FRG1B*	ENST00000278882	1	intronic	c.66+45	e1+45	tier3	691	9	0.013	1509	65	0.041
489196	20	31073554	31073555	-	GTC	INS	*C20orf112*	ENST00000201961	-1	3_prime_untranslated_region	c.*9	NULL	tier3	76	0	0.000	74	36	0.327
489196	21	45820168	45820168	C	T	SNP	*TRPM2*	ENST00000300482	1	silent	c.2235	p.G745	tier1	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	A	SNP	*TTC38*	ENST00000445282	1	intronic	c.561+210	e6+210	tier3	53	2	0.036	54	21	0.269
489196	X	73041567	73041567	C	T	SNP	*XIST*	ENST00000429829	-1	rna	NULL	NULL	tier1	38	1	0.026	57	33	0.367
489196	X	153049418	153049418	C	G	SNP	*SRPK3*	ENST00000370101	1	intronic	c.908-11	e10-11	tier3	71	0	0.000	56	21	0.273
489196	X	153799950	153799950	G	A	SNP	*G6PD*	ENST00000369620	-1	5_prime_flanking_region	c.-25580	NULL	tier3	403	2	0.005	401	92	0.186
489513	1	71869848	71869849	-	A	INS	*NEGR1*	ENST00000357731	-1	3_prime_untranslated_region	c.*3281	NULL	tier4	172	2	0.012	156	82	0.345
489513	1	173684860	173684860	A	G	SNP	*KLHL20*	ENST00000209884	1	intronic	c.1-282	e1-282	tier2	100	4	0.039	84	84	0.500
489513	1	240351440	240351440	T	C	SNP	*FMN2*	ENST00000319653	1	intronic	c.1931-67	e4-67	tier3	137	2	0.014	79	80	0.503
489513	3	42735190	42735190	C	T	SNP	*HHATL*	ENST00000310417	-1	nonsense	c.1167	p.W389*	tier1	92	2	0.021	72	54	0.429
489513	3	46792243	46792243	C	T	SNP	*PRSS50*	ENST00000460241	-1	intronic	c.1-2102	e1-2102	tier2	30	0	0.000	16	16	0.500
489513	3	53844274	53844274	C	T	SNP	*CACNA1D*	ENST00000288139	1	silent	c.6201	p.F2067	tier1	62	0	0.000	40	43	0.518
489513	4	76570299	76570299	T	-	DEL	*G3BP2*	ENST00000359707	-1	3_prime_untranslated_region	c.*315	NULL	tier3	92	0	0.000	155	16	0.094
489513	4	152498539	152498539	G	A	SNP	*FAM160A1*	ENST00000435205	1	intronic	c.106-63	e2-63	tier3	41	1	0.024	45	40	0.471
489513	5	20304957	20304957	G	T	SNP	*ENSG00000214132*	ENST00000502634	-1	5_prime_untranslated_region	c.-20304957	NULL	tier3	155	4	0.025	159	117	0.424
489513	5	107929567	107929567	C	T	SNP	*ENSG00000244245*	ENST00000466800	1	3_prime_untranslated_region	c.*107929567	NULL	tier3	154	4	0.025	167	112	0.399
489513	5	137680472	137680472	T	C	SNP	*FAM53C*	ENST00000239906	1	intronic	c.137-42	e3-42	tier4	320	9	0.027	244	207	0.458
489513	5	140482438	140482438	G	C	SNP	*PCDHB3*	ENST00000231130	1	missense	c.2205	p.Q735H	tier1	212	2	0.009	283	67	0.191
489513	6	41011404	41011404	G	T	SNP	*TSPO2*	ENST00000373161	1	silent	c.282	p.L94	tier1	63	2	0.031	42	32	0.432
489513	7	131844359	131844359	G	C	SNP	*PLXNA4*	ENST00000321063	-1	missense	c.4533	p.N1511K	tier1	120	3	0.024	74	58	0.439
489513	8	56367730	56367730	C	T	SNP	*XKR4*	ENST00000327381	1	intronic	c.1007-68110	e3-68110	tier2	397	13	0.032	361	288	0.442
489513	8	74495119	74495119	A	-	DEL	*STAU2*	ENST00000524300	-1	intronic	c.1162-54	e9-54	tier3	58	0	0.000	65	13	0.167
489513	9	16215272	16215272	C	T	SNP	*C9orf92*	ENST00000380683	-1	missense	c.196	p.G66R	tier1	51	0	0.000	40	30	0.429
489513	9	32974446	32974446	C	T	SNP	*APTX*	ENST00000379819	-1	splice_region	c.916+10	e7+10	tier3	98	2	0.020	103	73	0.415
489513	9	101798470	101798470	G	C	SNP	*COL15A1*	ENST00000375001	1	missense	c.2308	p.G770R	tier1	112	2	0.018	119	80	0.402
489513	9	136402651	136402651	G	A	SNP	*ADAMTSL2*	ENST00000393061	1	missense	c.542	p.R181Q	tier1	167	1	0.006	126	92	0.422
489513	10	48373412	48373412	G	A	SNP	*ZNF488*	ENST00000395702	1	3_prime_untranslated_region	c.*1857	NULL	tier3	84	1	0.012	63	41	0.394
489513	10	87615842	87615842	G	A	SNP	*GRID1*	ENST00000327946	-1	missense	c.1057	p.R353W	tier1	724	2	0.003	1088	48	0.042
489513	11	32417288	32417288	G	A	SNP	*WT1*	ENST00000332351	-1	intronic	c.1249+515	e7+515	tier4	245	5	0.020	280	90	0.242
489513	12	130883190	130883190	C	A	SNP	*RIMBP2*	ENST00000261655	-1	3_prime_untranslated_region	c.*490	NULL	tier3	88	2	0.022	107	69	0.390
489513	12	133050427	133050427	A	G	SNP	*MUC8*	ENST00000595994	-1	intronic	c.148-131	e2-131	tier2	319	4	0.012	424	31	0.068
489513	15	97634474	97634474	A	G	SNP	*ENSG00000215948*	ENST00000401129	-1	3_prime_flanking_region	c.*18	NULL	tier4	128	2	0.015	127	102	0.444
489513	17	78180746	78180746	C	T	SNP	*SGSH*	ENST00000575484	-1	rna	NULL	NULL	tier1	102	2	0.019	94	61	0.394
489513	18	72113811	72113811	C	G	SNP	*FAM69C*	ENST00000343998	-1	intronic	c.876+30	e2+30	tier3	62	0	0.000	45	65	0.591
489513	19	38161162	38161162	T	-	DEL	*ZNF781*	ENST00000358582	-1	5_prime_untranslated_region	c.-113	NULL	tier3	106	1	0.009	159	16	0.091
489513	19	40834389	40834389	C	T	SNP	*C19orf47*	ENST00000582783	-1	missense	c.481	p.D161N	tier1	122	2	0.016	77	89	0.536
489513	19	59081697	59081697	G	A	SNP	*MZF1*	ENST00000595245	-1	5_prime_untranslated_region	c.-59081697	NULL	tier3	79	5	0.059	7	84	0.913
489513	20	18772588	18772588	G	A	SNP	*LINC00652*	ENST00000454749	-1	rna	NULL	NULL	tier1	172	8	0.044	133	90	0.404
489513	20	31022403	31022425	CACCACTGCCATAGAGAGGCGGC	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1888_1910	p.H633fs	tier1	991	3	0.003	1196	127	0.096
489513	21	9825838	9825838	T	C	SNP	*MIR3648*	ENST00000581792	1	rna	NULL	NULL	tier1	113	2	0.017	151	20	0.111
489513	21	31964779	31964779	C	T	SNP	*KRTAP6-3*	ENST00000391624	1	5_prime_untranslated_region	c.-7	NULL	tier3	165	0	0.000	118	100	0.459
489513	21	44524456	44524456	G	T	SNP	*U2AF1*	ENST00000291552	-1	missense	c.101	p.S34Y	tier1	592	16	0.026	543	376	0.409
489513	22	21057355	21057355	T	C	SNP	*TMEM191A*	ENST00000419950	1	rna	NULL	NULL	tier1	209	2	0.009	211	29	0.120
489513	X	118215369	118215369	G	A	SNP	*KIAA1210*	ENST00000402510	-1	missense	c.5053	p.P1685S	tier1	64	5	0.073	11	98	0.891

489513	X	119390658	119390658	G	T	SNP	*ZBTB33*	ENST00000326624	1	3_prime_untranslated_region	c.*1369	NULL	tier2	60	1	0.016	71	15	0.174
491309	1	243288182	243288182	T	-	DEL	*CEP170*	ENST00000468254	-1	rna	NULL	NULL	tier1	36	0	0.000	146	28	0.161
491309	5	179780316	179780316	T	C	SNP	*GFPT2*	ENST00000253778	-1	5_prime_untranslated_region	c.-99	NULL	tier2	12	0	0.000	11	9	0.409
491309	7	2309174	2309174	G	A	SNP	*SNX8*	ENST00000222990	-1	intronic	c.621+20	e5+20	tier3	26	0	0.000	28	9	0.231
491309	17	7577580	7577580	T	C	SNP	*TP53*	ENST00000269305	-1	missense	c.701	p.Y234C	tier1	711	3	0.004	1093	44	0.039
491309	19	16629981	16629981	C	T	SNP	*CHERP*	ENST00000546361	-1	missense	c.2740	p.E914K	tier1	99	0	0.000	156	16	0.093
496321	1	986249	986249	C	T	SNP	*AGRN*	ENST00000379370	1	intronic	c.5253+32	e30+32	tier2	27	0	0.000	22	24	0.522
496321	1	47276735	47276735	G	A	SNP	*CYP4B1*	ENST00000371923	1	intronic	c.323-77	e3-77	tier3	75	3	0.039	39	29	0.427
496321	1	114397144	114397144	C	A	SNP	*PTPN22*	ENST00000359785	-1	missense	c.699	p.R233S	tier1	29	2	0.065	59	43	0.422
496321	2	89102427	89102427	G	A	SNP	*ANKRD36BP2*	ENST00000393525	1	rna	NULL	NULL	tier1	104	2	0.019	478	69	0.126
496321	2	241513196	241513196	C	T	SNP	*RNPEPL1*	ENST00000270357	1	missense	c.133	p.R45C	tier1	69	5	0.067	48	30	0.385
496321	3	25639916	25639916	G	A	SNP	*TOP2B*	ENST00000264331	-1	missense	c.4763	p.S1588L	tier1	73	0	0.000	53	31	0.369
496321	3	38141928	38141928	G	A	SNP	*DLEC1*	ENST00000346219	1	intronic	c.2864+12	e19+12	tier3	92	6	0.061	47	40	0.460
496321	3	125643455	125643455	C	T	SNP	*FAM86JP*	ENST00000467239	1	intronic	c.NULL	NULL	tier3	56	1	0.018	29	31	0.517
496321	3	172835422	172835422	A	T	SNP	*SPATA16*	ENST00000351008	-1	missense	c.100	p.L34I	tier1	62	2	0.031	64	46	0.418
496321	3	193125021	193125021	G	A	SNP	*ATP13A4*	ENST00000342695	-1	intronic	c.3378+81	e29+81	tier3	65	2	0.030	47	33	0.413
496321	4	103822448	103822448	G	A	SNP	*SLC9B1*	ENST00000296422	-1	silent	c.1374	p.S458	tier1	435	3	0.007	605	44	0.068
496321	4	106190881	106190881	A	T	SNP	*TET2*	ENST00000380013	1	missense	c.4159	p.N1387Y	tier1	297	17	0.054	195	224	0.535
496321	4	106193892	106193892	C	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.4354	p.R1452*	tier1	702	34	0.046	568	426	0.428
496321	4	120446865	120446865	G	A	SNP	*PDE5A*	ENST00000354960	-1	intronic	c.1633-15	e12-15	tier3	53	1	0.019	40	11	0.212
496321	4	153809253	153809253	G	A	SNP	*ARFIP1*	ENST00000353617	1	intronic	c.792-32	e7-32	tier3	24	0	0.000	51	18	0.261
496321	5	140202969	140202969	C	T	SNP	*PCDHA5*	ENST00000529859	1	missense	c.1609	p.R537C	tier1	482	37	0.071	306	270	0.469
496321	6	152746604	152746604	C	T	SNP	*SYNE1*	ENST00000341594	-1	splice_site	c.5291-1	e40-1	tier1	55	1	0.018	83	63	0.429
496321	6	159660601	159660601	G	A	SNP	*FNDC1*	ENST00000329629	1	missense	c.3919	p.G1307R	tier1	160	13	0.075	91	88	0.492
496321	6	160199944	160199944	G	A	SNP	*ACAT2*	ENST00000472052	1	rna	NULL	NULL	tier1	46	2	0.041	77	67	0.465
496321	7	1132922	1132922	G	A	SNP	*GPER1*	ENST00000297469	1	3_prime_untranslated_region	c.*430	NULL	tier2	99	2	0.020	42	38	0.475
496321	7	100652450	100652450	T	C	SNP	*MUC12*	ENST00000536621	1	splice_region	c.15251+10	e5+10	tier2	59	3	0.048	67	59	0.468
496321	7	150835438	150835438	G	A	SNP	*AGAP3*	ENST00000397238	1	intronic	c.1666+38	e12+38	tier2	84	1	0.012	50	25	0.333
496321	12	48375943	48375943	C	T	SNP	*COL2A1*	ENST00000380518	-1	missense	c.2302	p.G768S	tier1	106	5	0.045	60	62	0.508
496321	13	61141522	61141522	C	T	SNP	*TDRD3*	ENST00000535286	1	intronic	c.2119-137	e13-137	tier3	70	4	0.053	107	84	0.440
496321	14	75248223	75248223	C	T	SNP	*YLPM1*	ENST00000325680	1	nonsense	c.1477	p.Q493*	tier1	61	4	0.062	67	51	0.432
496321	15	42434172	42434172	C	T	SNP	*PLA2G4F*	ENST00000397272	-1	3_prime_untranslated_region	c.*10	NULL	tier3	59	5	0.078	38	37	0.493
496321	15	72958364	72958364	C	G	SNP	*GOLGA6B*	ENST00000421285	1	missense	c.1849	p.H617D	tier1	212	0	0.000	192	32	0.143
496321	15	75219024	75219024	A	G	SNP	*COX5A*	ENST00000322347	-1	intronic	c.339+83	e3+83	tier3	15	0	0.000	29	38	0.567
496321	16	29820921	29820921	C	T	SNP	*MAZ*	ENST00000219782	1	missense	c.1340	p.P447L	tier1	48	1	0.020	18	19	0.514
496321	16	33497567	33497567	C	T	SNP	*BMS1P8*	ENST00000565156	-1	rna	NULL	NULL	tier1	354	3	0.008	573	35	0.058
496321	19	33792431	33792431	C	G	SNP	*CEBPA*	ENST00000498907	-1	missense	c.890	p.R297P	tier1	1145	61	0.050	682	577	0.458
496321	19	36727961	36727961	T	C	SNP	*ZNF146*	ENST00000443387	1	missense	c.619	p.S207P	tier1	29	2	0.065	54	46	0.455
496321	19	55697038	55697038	G	A	SNP	*PTPRH*	ENST00000376350	-1	splice_region	c.2902-8	e18-8	tier3	36	3	0.077	26	24	0.480
496321	X	49189242	49189243	-	A	INS	*GAGE13*	ENST00000381751	1	frame_shift_ins	c.27_28	p.Y9fs	tier1	14	0	0.000	3	4	0.571
496321	Y	22923114	22923114	C	T	SNP	*RPS4Y2*	ENST00000288666	1	intronic	c.263-56	e4-56	tier3	36	3	0.077	7	54	0.885
499258	1	40033490	40033490	T	C	SNP	*PABPC4*	ENST00000372858	-1	missense	c.905	p.D302G	tier1	145	1	0.007	205	51	0.199
499258	1	155028802	155028802	C	G	SNP	*ADAM15*	ENST00000525020	1	3_prime_untranslated_region	c.*155028802	NULL	tier3	34	0	0.000	138	32	0.188
499258	1	182850554	182850554	A	G	SNP	*DHX9*	ENST00000367549	1	missense	c.2780	p.D927G	tier1	109	0	0.000	161	31	0.162
499258	1	240969528	240969528	G	A	SNP	*RGS7*	ENST00000407727	-1	missense	c.1181	p.P394L	tier1	45	0	0.000	155	41	0.209
499258	2	6879873	6879873	T	-	DEL	*LINC00487*	ENST00000382045	-1	intronic	c.NULL	NULL	tier2	49	0	0.000	130	32	0.198
499258	2	43905981	43905981	A	G	SNP	*PLEKHH2*	ENST00000282406	1	intronic	c.124-21	e2-21	tier2	232	3	0.013	240	70	0.225
499258	2	88825827	88825827	C	T	SNP	*C2orf51*	ENST00000303254	1	intronic	c.28-96	e2-96	tier4	70	0	0.000	149	27	0.153
499258	2	197645323	197645323	A	G	SNP	*GTF3C3*	ENST00000263956	-1	missense	c.1178	p.M393T	tier1	81	0	0.000	93	21	0.184
499258	4	100266176	100266176	G	A	SNP	*ADH1C*	ENST00000515683	-1	missense	c.410	p.P137L	tier1	63	0	0.000	237	75	0.240
499258	7	98639905	98639905	T	-	DEL	*SMURF1*	ENST00000361125	-1	intronic	c.1335-50	e13-50	tier4	38	0	0.000	87	16	0.155
499258	7	135376425	135376425	G	A	SNP	*C7orf73*	ENST00000422968	1	3_prime_untranslated_region	c.*135376425	NULL	tier3	57	1	0.017	96	30	0.238
499258	7	144060684	144060684	G	A	SNP	*ARHGEF5*	ENST00000056217	1	missense	c.922	p.E308K	tier1	17	0	0.000	72	37	0.339
499258	9	87322805	87322805	C	T	SNP	*NTRK2*	ENST00000277120	1	missense	c.406	p.R136C	tier1	116	0	0.000	159	20	0.112
499258	10	22680773	22680773	T	C	SNP	*SPAG6*	ENST00000376603	1	missense	c.1349	p.V450A	tier1	58	0	0.000	141	32	0.185
499258	10	49291796	49291796	C	T	SNP	*ENSG00000249871*	ENST00000506185	-1	intronic	c.NULL	NULL	tier3	123	2	0.016	88	24	0.214
499258	12	100904941	100904941	A	T	SNP	*NR1H4*	ENST00000551379	1	intronic	c.475+20	e2+20	tier3	43	0	0.000	107	25	0.189
499258	15	25224990	25224990	T	C	SNP	*SNURF*	ENST00000551312	1	intronic	c.216-104	e4-104	tier2	68	0	0.000	84	25	0.229
499258	16	72821316	72821316	A	G	SNP	*ZFHX3*	ENST00000268489	-1	missense	c.10859	p.V3620A	tier1	43	0	0.000	193	49	0.203
499258	17	38450574	38450574	G	T	SNP	*CDC6*	ENST00000209728	1	intronic	c.944-42	e6-42	tier2	107	0	0.000	113	27	0.193
499258	17	42152474	42152474	G	A	SNP	*G6PC3*	ENST00000269097	1	intronic	c.535+19	e4+19	tier2	30	0	0.000	120	30	0.200
499258	19	56423693	56423693	G	A	SNP	*NLRP13*	ENST00000342929	-1	missense	c.1490	p.T497M	tier1	39	0	0.000	72	14	0.163
499258	21	16337046	16337049	TTCT	-	DEL	*NRIP1*	ENST00000318948	-1	frame_shift_del	c.3468_3465	p.K1155fs	tier1	83	1	0.012	119	17	0.125
499258	21	36252865	36252865	C	G	SNP	*RUNX1*	ENST00000300305	-1	missense	c.497	p.R166P	tier1	353	1	0.003	1294	196	0.132
499258	22	21804391	21804391	A	G	SNP	*HIC2*	ENST00000407464	1	3_prime_untranslated_region	c.*3359	NULL	tier3	84	0	0.000	189	36	0.160
499258	X	24813697	24813697	T	C	SNP	*POLA1*	ENST00000379068	1	intronic	c.2965-14318	e27-14318	tier3	55	0	0.000	61	55	0.474
502635	1	28208733	28208733	C	T	SNP	*THEMIS2*	ENST00000373921	1	missense	c.898	p.R300W	tier1	124	1	0.008	126	16	0.112
502635	1	52912122	52912122	T	A	SNP	*ZCCHC11*	ENST00000257177	-1	splice_region	c.3514-8	e21-8	tier3	120	2	0.016	78	14	0.151
502635	1	235617686	235617686	A	C	SNP	*B3GALNT2*	ENST00000366600	-1	intronic	c.1152-59	e10-59	tier3	121	1	0.008	71	13	0.155
502635	2	99685334	99685334	A	-	DEL	*TSGA10*	ENST00000355053	-1	intronic	c.1218+17	e10+17	tier3	67	0	0.000	24	5	0.172
502635	2	236480607	236480607	C	T	SNP	*ENSG00000221704*	ENST00000408777	1	rna	NULL	NULL	tier1	111	1	0.009	100	18	0.153
502635	3	111775924	111775924	C	T	SNP	*TMPRSS7*	ENST00000419127	1	missense	c.878	p.T293I	tier1	137	0	0.000	155	12	0.072
502635	4	119644046	119644046	T	C	SNP	*SEC24D*	ENST00000505134	-1	rna	NULL	NULL	tier1	353	0	0.000	126	11	0.080
502635	4	129192341	129192341	A	G	SNP	*PGRMC2*	ENST00000520121	-1	3_prime_untranslated_region	c.*130	NULL	tier3	93	0	0.000	97	10	0.094

502635	7	29546764	29546764	T	-	DEL	*CHN2*	ENST00000539406	1	intronic	c.1217-80	e12-80	tier3	43	0	0.000	33	10	0.233
502635	11	89515227	89515227	G	T	SNP	*TRIM64DP*	ENST00000529289	1	3_prime_untranslated_region	c.*89515227	NULL	tier3	305	0	0.000	323	26	0.075
502635	12	5840529	5840529	A	-	DEL	*ANO2*	ENST00000356134	-1	intronic	c.1548+1157	e16+1157	tier3	60	0	0.000	71	13	0.155
502635	12	119583250	119583250	G	A	SNP	*SRRM4*	ENST00000267260	1	missense	c.836	p.R279Q	tier1	66	0	0.000	54	8	0.129
502635	13	101881935	101881935	C	T	SNP	*NALCN*	ENST00000251127	-1	missense	c.1435	p.V479I	tier1	487	0	0.000	486	26	0.051
502635	14	106573418	106573418	T	C	SNP	*IGHV3-11*	ENST00000390601	-1	missense	c.166	p.I56V	tier1	166	7	0.040	150	36	0.194
502635	14	106573482	106573482	T	C	SNP	*IGHV3-11*	ENST00000390601	-1	silent	c.102	p.G34	tier1	195	5	0.025	164	33	0.168
502635	14	106573491	106573491	G	T	SNP	*IGHV3-11*	ENST00000390601	-1	silent	c.93	p.V31	tier1	200	5	0.024	164	33	0.168
502635	15	31086780	31086780	G	T	SNP	*GOLGA8UP*	ENST00000527159	1	3_prime_untranslated_region	c.*31086780	NULL	tier3	520	1	0.002	493	44	0.082
502635	15	43995984	43995984	C	G	SNP	*STRC*	ENST00000541030	-1	intronic	c.1+14335	e0+14335	tier3	90	0	0.000	65	8	0.110
502635	15	65715171	65715171	G	A	SNP	*IGDCC4*	ENST00000352385	-1	silent	c.30	p.R10	tier1	8	0	0.000	0	5	1.000
502635	16	9212075	9212079	TATTA	-	DEL	*C16orf72*	ENST00000327827	1	3_prime_untranslated_region	c.*1306	NULL	tier2	161	0	0.000	76	6	0.073
502635	17	1326754	1326754	G	A	SNP	*CRK*	ENST00000572145	-1	rna	NULL	NULL	tier1	106	0	0.000	120	10	0.076
502635	17	7577538	7577538	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.743	p.R248Q	tier1	1010	2	0.002	931	73	0.073
502635	17	7578551	7578551	A	T	SNP	*TP53*	ENST00000269305	-1	missense	c.379	p.S127T	tier1	1112	5	0.005	988	82	0.077
502635	18	47455964	47455964	C	A	SNP	*MYO5B*	ENST00000285039	-1	missense	c.2008	p.D670Y	tier1	197	4	0.020	200	25	0.111
502635	19	852255	852255	G	T	SNP	*ELANE*	ENST00000590230	1	5_prime_untranslated_region	c.-74	NULL	tier2	748	0	0.000	579	41	0.066
502635	21	35471902	35471903	-	T	INS	*SLC5A3*	ENST00000381151	1	3_prime_untranslated_region	c.*2248	NULL	tier3	79	0	0.000	66	8	0.108
565435	1	91402928	91402928	A	G	SNP	*ZNF644*	ENST00000337393	-1	intronic	c.3688+114	e3+114	tier3	9	0	0.000	26	37	0.587
565435	1	114641862	114641862	G	A	SNP	*SYT6*	ENST00000393296	-1	silent	c.1218	p.L406	tier1	132	0	0.000	114	50	0.303
565435	1	150246585	150246585	A	C	SNP	*C1orf54*	ENST00000369099	1	intronic	c.130+12	e2+12	tier3	81	2	0.024	110	28	0.203
565435	2	86267544	86267544	G	A	SNP	*POLR1A*	ENST00000263857	-1	silent	c.3711	p.G1237	tier1	121	2	0.016	71	32	0.311
565435	2	97849131	97849131	A	G	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.1838-65	e27-65	tier3	72	2	0.027	158	58	0.269
565435	2	130750444	130750444	C	T	SNP	*ENSG00000250207*	ENST00000511039	-1	5_prime_untranslated_region	c.-130750444	NULL	tier2	390	1	0.003	358	66	0.155
565435	2	219267322	219267322	C	A	SNP	*CTDSP1*	ENST00000273062	1	intronic	c.378+194	e4+194	tier3	63	0	0.000	58	15	0.206
565435	3	44776777	44776777	T	C	SNP	*ZNF501*	ENST00000396048	1	3_prime_untranslated_region	c.*48	NULL	tier3	39	0	0.000	76	22	0.225
565435	3	133465239	133465239	A	G	SNP	*TF*	ENST00000402696	1	5_prime_untranslated_region	c.-46	NULL	tier2	33	1	0.029	24	15	0.385
565435	3	155314188	155314188	T	C	SNP	*PLCH1*	ENST00000340059	-1	intronic	c.44-21	e2-21	tier3	25	0	0.000	13	6	0.316
565435	3	185300560	185300560	G	C	SNP	*SENP2*	ENST00000545472	1	missense	c.26	p.C9S	tier1	186	4	0.021	134	41	0.233
565435	4	73615881	73615881	G	A	SNP	-	-	-	-	-	-	tier3	87	4	0.044	133	53	0.285
565435	4	148457005	148457006	-	T	INS	*EDNRA*	ENST00000324300	1	intronic	c.748-24_748-23	e4-23	tier3	30	0	0.000	27	9	0.250
565435	5	13900350	13900350	G	A	SNP	*DNAH5*	ENST00000265104	-1	nonsense	c.2224	p.R742*	tier1	446	5	0.011	475	166	0.259
565435	5	43295963	43295963	G	A	SNP	*HMGCS1*	ENST00000325110	-1	missense	c.796	p.P266S	tier1	36	0	0.000	98	25	0.203
565435	6	31974832	31974832	G	A	SNP	*CYP21A1P*	ENST00000342991	1	3_prime_untranslated_region	c.*31974832	NULL	tier3	136	2	0.015	81	31	0.274
565435	6	54208081	54208081	C	T	SNP	*TINAG*	ENST00000259782	1	missense	c.682	p.P228S	tier1	40	0	0.000	73	37	0.336
565435	6	80774316	80774316	T	G	SNP	*ENSG00000218418*	ENST00000401578	-1	5_prime_untranslated_region	c.-80774316	NULL	tier3	135	1	0.007	117	41	0.260
565435	7	5434025	5434025	A	T	SNP	*TNRC18*	ENST00000399537	-1	intronic	c.343+46	e2+46	tier3	197	5	0.025	133	83	0.384
565435	7	122255199	122255199	A	C	SNP	*CADPS2*	ENST00000449022	-1	intronic	c.1223+36	e6+36	tier3	63	1	0.016	75	30	0.283
565435	7	150894251	150894251	C	T	SNP	*IQCA1P1*	ENST00000602757	-1	intronic	c.NULL	NULL	tier3	77	1	0.013	78	31	0.284
565435	8	144399939	144399939	G	A	SNP	*TOP1MT*	ENST00000329245	-1	silent	c.1284	p.Y428	tier1	155	3	0.019	119	36	0.232
565435	9	32631391	32631391	C	T	SNP	*TAF1L*	ENST00000242310	-1	missense	c.4187	p.R1396H	tier1	160	1	0.006	144	36	0.200
565435	9	74299332	74299332	T	C	SNP	*TMEM2*	ENST00000377057	-1	5_prime_untranslated_region	c.-74299332	NULL	tier3	41	0	0.000	75	37	0.330
565435	9	84608191	84608191	T	C	SNP	*SPATA31D1*	ENST00000344803	1	missense	c.2806	p.S936P	tier1	128	0	0.000	130	59	0.312
565435	10	95849013	95849013	G	A	SNP	*PLCE1*	ENST00000371375	1	silent	c.162	p.Q54	tier1	923	14	0.015	640	239	0.272
565435	11	27528351	27528352	-	G	INS	*LGR4*	ENST00000379214	-1	5_prime_flanking_region	c.-34502	NULL	tier2	128	3	0.023	88	22	0.200
565435	11	56738588	56738588	G	A	SNP	*OR5AK3P*	ENST00000326876	1	3_prime_untranslated_region	c.*56738588	NULL	tier3	54	0	0.000	120	18	0.130
565435	12	102140522	102140523	-	A	INS	*GNPTAB*	ENST00000299314	-1	3_prime_untranslated_region	c.*420	NULL	tier3	59	0	0.000	108	16	0.129
565435	14	19685459	19685459	C	T	SNP	*LOC440157*	ENST00000418499	1	rna	NULL	NULL	tier1	74	0	0.000	63	11	0.149
565435	14	21853909	21853909	C	T	SNP	*CHD8*	ENST00000399982	-1	missense	c.7609	p.E2537K	tier1	58	0	0.000	43	21	0.328
565435	14	56120281	56120281	C	G	SNP	*KTN1*	ENST00000395309	1	missense	c.2768	p.S923C	tier1	37	0	0.000	89	32	0.265
565435	15	79065337	79065337	C	T	SNP	*ADAMTS7*	ENST00000388820	-1	intronic	c.2131+88	e14+88	tier3	85	2	0.023	66	21	0.241
565435	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	701	10	0.014	588	212	0.265
565435	16	69738490	69738490	C	T	SNP	*ENSG00000260772*	ENST00000561622	1	rna	NULL	NULL	tier1	30	0	0.000	60	25	0.294
565435	17	10402323	10402323	C	T	SNP	*MYH1*	ENST00000226207	-1	missense	c.3952	p.E1318K	tier1	169	0	0.000	250	20	0.074
565435	17	56620367	56620367	G	T	SNP	*C17orf47*	ENST00000321691	-1	missense	c.1181	p.P394Q	tier1	139	5	0.035	101	37	0.266
565435	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	488	4	0.008	360	143	0.283
565435	19	11342899	11342899	G	A	SNP	*DOCK6*	ENST00000319867	-1	missense	c.697	p.R233W	tier1	97	0	0.000	62	35	0.357
565435	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	1055	26	0.024	802	238	0.229
565435	22	18027848	18027848	G	T	SNP	*CECR2*	ENST00000400573	1	missense	c.2805	p.L935F	tier1	421	7	0.016	531	50	0.086
565435	X	39916576	39916576	T	C	SNP	*BCOR*	ENST00000378444	-1	splice_site	c.4429-2	e10-2	tier1	214	0	0.000	208	30	0.126
565435	X	123197716	123197716	C	T	SNP	*STAG2*	ENST00000218089	1	nonsense	c.1840	p.R614*	tier1	113	0	0.000	311	64	0.170
565435	X	123220440	123220440	C	T	SNP	*STAG2*	ENST00000218089	1	nonsense	c.3097	p.R1033*	tier1	258	4	0.015	279	101	0.266
596762	1	26314633	26314634	-	T	INS	*PAFAH2*	ENST00000374282	-1	intronic	c.341+88_341+87	e3+88	tier3	50	0	0.000	69	19	0.216
596762	1	77987426	77987426	C	T	SNP	*AK5*	ENST00000354567	1	intronic	c.1312-86	e12-86	tier3	45	0	0.000	61	11	0.153
596762	1	97144881	97144881	T	C	SNP	*ENSG00000137970*	ENST00000468715	-1	5_prime_untranslated_region	c.-97144881	NULL	tier3	91	1	0.011	68	25	0.269
596762	1	177906320	177906320	A	T	SNP	*SEC16B*	ENST00000308284	-1	intronic	c.2503+29	e18+29	tier3	37	0	0.000	23	25	0.521
596762	3	114214866	114214866	T	-	DEL	*ZBTB20*	ENST00000357258	-1	intronic	c.1+4333	e0+4333	tier3	83	1	0.012	101	15	0.129
596762	4	2160973	2160973	G	A	SNP	*POLN*	ENST00000382865	-1	intronic	c.1555-35	e12-35	tier3	73	1	0.014	61	38	0.384
596762	4	17528425	17528425	C	A	SNP	*CLRN2*	ENST00000511148	1	intronic	c.434-15	e3-15	tier3	74	0	0.000	84	40	0.323
596762	5	134192331	134192338	AAATAAAT	-	DEL	*C5orf24*	ENST00000338051	1	3_prime_untranslated_region	c.*1174	NULL	tier4	23	0	0.000	40	14	0.259
596762	7	151841948	151841948	G	A	SNP	*KMT2C*	ENST00000360104	-1	missense	c.6862	p.H2288Y	tier1	460	2	0.004	415	227	0.353
596762	8	87242499	87242499	C	T	SNP	*SLC7A13*	ENST00000297524	-1	missense	c.8	p.R3K	tier1	102	3	0.029	114	43	0.274
596762	9	97426331	97426331	A	-	DEL	*FBP1*	ENST00000375326	-1	5_prime_flanking_region	c.-24739	NULL	tier3	47	0	0.000	40	10	0.200
596762	11	62496026	62496026	C	T	SNP	*TTC9C*	ENST00000513247	1	missense	c.191	p.S64F	tier1	82	0	0.000	53	24	0.312

596762	11	92531510	92531510	C	T	SNP	*FAT3*	ENST00000298047	1	silent	c.5331	p.S1777	tier1	49	0	0.000	43	16	0.267
596762	12	57850452	57850452	G	C	SNP	*INHBE*	ENST00000266646	1	missense	c.874	p.A292P	tier1	63	1	0.015	59	21	0.263
596762	12	113379563	113379563	G	T	SNP	*OAS3*	ENST00000228928	1	missense	c.366	p.E122D	tier1	31	0	0.000	37	17	0.315
596762	13	86369756	86369756	C	T	SNP	*SLITRK6*	ENST00000400286	-1	missense	c.888	p.M296I	tier1	103	0	0.000	90	43	0.323
596762	14	62547892	62547892	G	A	SNP	*SYT16*	ENST00000430451	1	missense	c.1334	p.R445Q	tier1	115	0	0.000	131	12	0.084
596762	15	85401550	85401550	G	A	SNP	*ALPK3*	ENST00000258888	1	missense	c.4187	p.R1396Q	tier1	420	1	0.002	364	201	0.353
596762	17	4109540	4109540	A	G	SNP	*ANKFY1*	ENST00000570535	-1	intronic	c.1024+76	e7+76	tier3	48	0	0.000	37	25	0.403
596762	17	38438120	38438120	G	C	SNP	*WIPF2*	ENST00000323571	1	3_prime_untranslated_region	c.*3643	NULL	tier3	88	1	0.011	86	53	0.381
596762	17	56357291	56357291	C	A	SNP	*MPO*	ENST00000340482	-1	silent	c.333	p.T111	tier1	62	2	0.031	60	29	0.326
596762	18	7774085	7774085	T	A	SNP	*PTPRM*	ENST00000400060	1	intronic	c.74-62	e2-62	tier3	76	0	0.000	72	31	0.301
596762	20	34430474	34430475	-	T	INS	*PHF20*	ENST00000374012	1	intronic	c.84-21_84-20	e2-20	tier3	92	1	0.011	119	15	0.112
596762	20	45355585	45355585	G	A	SNP	*SLC2A10*	ENST00000359271	1	silent	c.1371	p.A457	tier1	51	0	0.000	59	24	0.286
596762	20	60895795	60895795	C	G	SNP	*LAMA5*	ENST00000252999	-1	missense	c.6648	p.Q2216H	tier1	72	0	0.000	54	15	0.217
597501	2	21228297	21228297	C	T	SNP	*APOB*	ENST00000233242	-1	missense	c.11443	p.V3815M	tier1	991	7	0.007	874	56	0.060
597501	2	61006923	61006923	G	A	SNP	*PAPOLG*	ENST00000238714	1	intronic	c.833+13	e9+13	tier3	117	2	0.017	65	30	0.316
597501	2	66796098	66796099	-	T	INS	*MEIS1*	ENST00000488550	1	3_prime_untranslated_region	c.*187	NULL	tier3	87	0	0.000	66	9	0.120
597501	2	99936266	99936266	A	-	DEL	*TXNDC9*	ENST00000264255	-1	splice_region_del	c.564-4	e4-4	tier3	31	0	0.000	38	11	0.225
597501	2	121744080	121744080	G	A	SNP	*GLI2*	ENST00000361492	1	missense	c.2183	p.R728Q	tier1	60	1	0.016	49	57	0.533
597501	2	179363925	179363925	C	T	SNP	*PLEKHA3*	ENST00000234453	1	intronic	c.616-13	e6-13	tier3	67	1	0.015	59	13	0.181
597501	3	38913145	38913145	C	A	SNP	*SCN11A*	ENST00000302328	-1	missense	c.3550	p.V1184F	tier1	63	0	0.000	42	25	0.373
597501	3	138724564	138724564	C	T	SNP	*PRR23A*	ENST00000383163	-1	missense	c.547	p.A183T	tier1	178	2	0.011	193	33	0.145
597501	4	89022286	89022286	C	T	SNP	*ABCG2*	ENST00000237612	-1	intronic	c.1367+96	e10+96	tier3	196	8	0.039	176	176	0.499
597501	4	106157074	106157074	C	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.1975	p.Q659*	tier1	510	27	0.050	320	312	0.491
597501	4	106183003	106183003	C	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.4042	p.Q1348*	tier1	283	12	0.041	104	112	0.516
597501	4	109773495	109773495	C	T	SNP	*COL25A1*	ENST00000399132	-1	intronic	c.1345-59	e25-59	tier3	68	2	0.029	42	33	0.440
597501	4	115544516	115544516	T	C	SNP	*UGT8*	ENST00000310836	1	silent	c.480	p.T160	tier1	120	0	0.000	79	54	0.406
597501	5	31435975	31435975	C	A	SNP	*DROSHA*	ENST00000344624	-1	splice_region	c.2943-4	e22-4	tier3	45	1	0.021	41	13	0.241
597501	5	140203381	140203381	C	T	SNP	*PCDHA5*	ENST00000529859	1	missense	c.2021	p.A674V	tier1	489	0	0.000	598	21	0.034
597501	6	29069942	29069942	G	A	SNP	*OR2B3*	ENST00000377173	-1	5_prime_flanking_region	c.-14917	NULL	tier3	44	0	0.000	12	17	0.586
597501	6	41166075	41166075	C	T	SNP	*TREML2*	ENST00000483722	-1	missense	c.148	p.V50M	tier1	117	0	0.000	216	17	0.073
597501	6	42330640	42330640	C	T	SNP	*TRERF1*	ENST00000541110	-1	intronic	c.1+95	e0+95	tier3	57	3	0.050	55	56	0.500
597501	6	123702474	123702474	A	-	DEL	*TRDN*	ENST00000398178	-1	intronic	c.1186+41	e16+41	tier3	48	0	0.000	44	8	0.154
597501	6	136429913	136429913	C	T	SNP	*PDE7B*	ENST00000308191	1	missense	c.127	p.R43C	tier1	126	0	0.000	154	73	0.322
597501	6	139237014	139237014	C	T	SNP	*REPS1*	ENST00000450536	-1	silent	c.1701	p.R567	tier1	142	4	0.027	113	78	0.408
597501	6	163990584	163990584	A	G	SNP	*QKI*	ENST00000275262	1	3_prime_untranslated_region	c.*4842	NULL	tier3	64	1	0.015	29	37	0.561
597501	7	131122618	131122618	T	G	SNP	*MKLN1*	ENST00000352689	1	silent	c.1035	p.R345	tier1	121	6	0.047	59	58	0.496
597501	8	3045393	3045393	G	A	SNP	*CSMD1*	ENST00000520002	-1	missense	c.5621	p.S1874L	tier1	338	11	0.031	282	234	0.453
597501	8	7878120	7878120	C	T	SNP	*FAM90A24P*	ENST00000400118	-1	5_prime_untranslated_region	c.-7878120	NULL	tier3	2001	5	0.003	3019	225	0.069
597501	8	12516668	12516668	C	T	SNP	*RPS3AP35*	ENST00000478386	-1	5_prime_flanking_region	c.-29903	NULL	tier2	48	2	0.040	42	26	0.382
597501	8	99443925	99443926	-	A	INS	*KCNS2*	ENST00000287042	1	3_prime_untranslated_region	c.*2284	NULL	tier3	62	0	0.000	61	13	0.176
597501	9	116079186	116079186	C	T	SNP	*WDR31*	ENST00000374193	-1	missense	c.947	p.C316Y	tier1	59	2	0.033	59	60	0.504
597501	9	130693095	130693095	C	-	DEL	*ST6GALNAC6*	ENST00000291839	-1	5_prime_flanking_region	c.-32835	NULL	tier2	17	0	0.000	14	16	0.533
597501	10	49447649	49447649	G	A	SNP	*FRMPD2*	ENST00000374201	-1	missense	c.787	p.R263C	tier1	78	4	0.049	76	73	0.490
597501	10	135015401	135015401	C	T	SNP	*KNDC1*	ENST00000368572	1	missense	c.3392	p.P1131L	tier1	48	3	0.059	30	32	0.516
597501	11	31531364	31531364	C	T	SNP	*ELP4*	ENST00000395934	1	silent	c.33	p.A11	tier1	53	0	0.000	78	16	0.170
597501	12	117715866	117715866	C	A	SNP	*NOS1*	ENST00000317775	-1	missense	c.1562	p.R521L	tier1	111	7	0.059	119	87	0.422
597501	13	25060389	25060389	G	A	SNP	*PARP4*	ENST00000381989	-1	silent	c.1269	p.T423	tier1	109	4	0.035	59	56	0.487
597501	14	25100251	25100251	G	A	SNP	*GZMB*	ENST00000382542	-1	3_prime_untranslated_region	c.*26	NULL	tier3	131	3	0.022	95	77	0.448
597501	14	86089071	86089071	C	G	SNP	*FLRT2*	ENST00000330753	1	missense	c.1213	p.L405V	tier1	876	37	0.041	572	537	0.484
597501	15	34651895	34651895	C	T	SNP	*LPCAT4*	ENST00000314891	-1	missense	c.1294	p.G432S	tier1	96	2	0.020	94	63	0.401
597501	15	91574882	91574882	T	A	SNP	*LOC101926911*	ENST00000557804	1	intronic	c.NULL	NULL	tier3	84	4	0.046	48	18	0.273
597501	16	2522630	2522630	G	A	SNP	*NTN3*	ENST00000293973	1	missense	c.928	p.A310T	tier1	17	0	0.000	21	15	0.417
597501	17	8397209	8397209	T	-	DEL	*MYH10*	ENST00000488329	-1	5_prime_untranslated_region	c.-8397209	NULL	tier3	79	0	0.000	63	9	0.125
597501	17	11532944	11532944	C	T	SNP	*DNAH9*	ENST00000262442	1	intronic	c.1518+43	e7+43	tier3	533	1	0.002	873	42	0.046
597501	17	28900664	28900664	C	T	SNP	*LOC101927093*	ENST00000436477	-1	rna	NULL	NULL	tier1	112	3	0.026	71	81	0.533
597501	17	29422352	29422352	T	G	SNP	*NF1*	ENST00000358273	1	missense	c.25	p.W9G	tier1	339	1	0.003	323	63	0.163
597501	17	30219342	30219342	C	G	SNP	*UTP6*	ENST00000261708	-1	missense	c.361	p.A121P	tier1	138	2	0.014	58	37	0.390
597501	17	57647955	57647959	TGAAG	-	DEL	*DHX40*	ENST00000251241	1	frame_shift_del	c.357_361	p.E120fs	tier1	103	0	0.000	55	24	0.304
597501	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	335	11	0.032	292	273	0.481
597501	18	29523048	29523048	C	T	SNP	*ENSG00000263823*	ENST00000580420	1	rna	NULL	NULL	tier1	170	6	0.034	123	107	0.465
597501	19	17440815	17440815	G	A	SNP	*ANO8*	ENST00000159087	-1	missense	c.1282	p.R428W	tier1	66	0	0.000	89	17	0.160
597501	19	47884624	47884624	G	A	SNP	*DHX34*	ENST00000486327	1	3_prime_untranslated_region	c.*47884624	NULL	tier3	47	0	0.000	42	27	0.386
597501	19	54080590	54080590	T	C	SNP	*ZNF331*	ENST00000253144	1	missense	c.776	p.I259T	tier1	115	0	0.000	54	60	0.526
597501	20	48098486	48098486	G	A	SNP	*KCNB1*	ENST00000371741	-1	silent	c.532	p.L178	tier1	37	0	0.000	40	45	0.529
597501	X	10084387	10084387	T	C	SNP	*WWC3*	ENST00000380861	1	intronic	c.975-71	e9-71	tier3	143	1	0.007	82	72	0.468
597501	X	70357542	70357542	C	T	SNP	*MED12*	ENST00000333646	1	intronic	c.5836-34	e41-34	tier3	446	24	0.051	379	379	0.499
621996	1	4772000	4772000	C	A	SNP	*AJAP1*	ENST00000378190	1	missense	c.70	p.H24N	tier1	15	0	0.000	16	14	0.467
621996	1	91404719	91404719	T	C	SNP	*ZNF644*	ENST00000337393	-1	missense	c.2192	p.N731S	tier1	67	3	0.043	71	41	0.366
621996	1	152186038	152186038	A	-	DEL	*HRNR*	ENST00000368801	-1	frame_shift_del	c.8067	p.H2690fs	tier1	11	0	0.000	18	19	0.514
621996	1	152186047	152186047	A	-	DEL	*HRNR*	ENST00000368801	-1	frame_shift_del	c.8058	p.R2687fs	tier1	5	0	0.000	2	19	0.905
621996	1	154841865	154841865	G	A	SNP	*KCNN3*	ENST00000271915	-1	silent	c.576	p.S192	tier1	82	3	0.035	88	46	0.343
621996	1	176769238	176769238	C	T	SNP	*PAPPA2*	ENST00000367662	1	silent	c.5172	p.P1724	tier1	66	1	0.015	60	21	0.259
621996	2	98354060	98354060	C	T	SNP	*ZAP70*	ENST00000264972	1	missense	c.1414	p.R472W	tier1	61	0	0.000	54	12	0.182
621996	2	148716381	148716381	C	T	SNP	*ORC4*	ENST00000264169	-1	missense	c.280	p.V94I	tier1	108	1	0.009	118	64	0.352

621996	2	166223736	166223736	G	A	SNP	*SCN2A*	ENST00000283256	1	missense	c.3530	p.R1177Q	tier1	156	1	0.006	179	97	0.351
621996	2	179604342	179604342	C	T	SNP	*TTN*	ENST00000342175	-1	missense	c.13105	p.V4369M	tier1	51	3	0.056	29	34	0.540
621996	2	197709191	197709191	T	C	SNP	*PGAP1*	ENST00000354764	-1	intronic	c.2337+57	e24+57	tier3	219	0	0.000	234	111	0.320
621996	3	38291377	38291377	G	A	SNP	*OXSR1*	ENST00000311806	1	intronic	c.1323-80	e15-80	tier3	79	0	0.000	79	28	0.262
621996	3	50312255	50312255	C	G	SNP	*SEMA3B*	ENST00000416295	1	3_prime_untranslated_region	c.*50312255	NULL	tier2	46	2	0.042	58	30	0.341
621996	3	125879686	125879686	G	A	SNP	*ALDH1L1*	ENST00000393434	-1	splice_region	c.127+10	e1+10	tier3	66	0	0.000	81	36	0.308
621996	4	125592366	125592366	T	G	SNP	*ANKRD50*	ENST00000504087	-1	missense	c.2066	p.H689P	tier1	35	0	0.000	24	16	0.400
621996	5	133483867	133483867	T	G	SNP	*TCF7*	ENST00000395023	1	3_prime_untranslated_region	c.*1873	NULL	tier3	116	3	0.025	128	78	0.379
621996	5	154255096	154255096	C	A	SNP	*CNOT8*	ENST00000285896	1	3_prime_untranslated_region	c.*97	NULL	tier3	66	1	0.015	78	33	0.297
621996	5	176012012	176012012	C	A	SNP	*CDHR2*	ENST00000261944	1	missense	c.2730	p.N910K	tier1	123	4	0.031	126	65	0.340
621996	5	176016191	176016191	C	T	SNP	*CDHR2*	ENST00000261944	1	splice_region	c.3008+8	e21+8	tier3	94	0	0.000	89	69	0.437
621996	6	36569780	36569780	A	G	SNP	*SRSF3*	ENST00000373715	1	3_prime_untranslated_region	c.*14	NULL	tier3	38	0	0.000	35	17	0.321
621996	7	48964818	48964818	G	A	SNP	*ENSG00000218305*	ENST00000406468	1	3_prime_untranslated_region	c.*48964818	NULL	tier2	184	0	0.000	142	66	0.317
621996	7	100846447	100846447	C	T	SNP	*DGAT2L7P*	ENST00000379421	-1	5_prime_untranslated_region	c.-100846447	NULL	tier2	57	0	0.000	83	49	0.371
621996	7	112724366	112724366	C	T	SNP	*GPR85*	ENST00000297146	-1	silent	c.411	p.T137	tier1	60	0	0.000	61	36	0.371
621996	8	3224668	3224668	C	T	SNP	*CSMD1*	ENST00000520002	-1	missense	c.3004	p.G1002R	tier1	558	11	0.019	517	311	0.375
621996	9	141071154	141071154	T	C	SNP	*TUBBP5*	ENST00000290377	1	rna	NULL	NULL	tier1	178	1	0.006	245	19	0.072
621996	11	6243580	6243580	G	A	SNP	*FAM160A2*	ENST00000265978	-1	intronic	c.1191+92	e5+92	tier3	59	2	0.033	60	43	0.418
621996	11	24750764	24750764	C	T	SNP	*LUZP2*	ENST00000336930	1	nonsense	c.112	p.R38*	tier1	107	4	0.036	91	64	0.413
621996	11	46404356	46404356	G	A	SNP	*MDK*	ENST00000489525	1	missense	c.464	p.R155H	tier1	36	1	0.021	43	19	0.247
621996	11	116718092	116718092	C	T	SNP	*SIK3*	ENST00000375300	-1	intronic	c.3808+100	e22+100	tier3	35	0	0.000	37	21	0.362
621996	12	113405327	113405327	C	T	SNP	*OAS3*	ENST00000228928	1	missense	c.2794	p.R932W	tier1	28	1	0.035	37	24	0.393
621996	12	123005987	123005988	-	A	INS	*RSRC2*	ENST00000331738	-1	intronic	c.164-13_164-12	e3-12	tier3	53	0	0.000	57	23	0.288
621996	12	123419982	123419982	G	A	SNP	*ABCB9*	ENST00000442028	-1	splice_region	c.1744-4	e9-4	tier3	38	1	0.026	57	36	0.387
621996	14	24887568	24887568	C	G	SNP	*NYNRIN*	ENST00000382554	1	3_prime_untranslated_region	c.*916	NULL	tier3	94	1	0.011	58	37	0.390
621996	14	63269293	63269293	A	G	SNP	*KCNH5*	ENST00000322893	-1	missense	c.1576	p.S526P	tier1	38	0	0.000	44	33	0.429
621996	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	422	0	0.000	475	258	0.351
621996	15	102294753	102294753	T	C	SNP	*DNM1P47*	ENST00000561463	1	rna	NULL	NULL	tier1	34	1	0.029	41	18	0.305
621996	16	22545618	22545629	TCCACCCTCAGC	-	DEL	*NPIPB5*	ENST00000424340	1	in_frame_del	c.1314_1325	p.APPS442in_frame_del	tier1	17	0	0.000	22	12	0.353
621996	16	33585853	33585853	C	T	SNP	*ENSG00000271178*	ENST00000562905	1	5_prime_flanking_region	c.-43828	NULL	tier3	107	0	0.000	204	16	0.072
621996	16	33585887	33585887	T	C	SNP	*ENSG00000271178*	ENST00000562905	1	5_prime_flanking_region	c.-43794	NULL	tier3	134	0	0.000	240	16	0.063
621996	17	12921348	12921348	G	C	SNP	*ELAC2*	ENST00000338034	-1	5_prime_untranslated_region	c.-84	NULL	tier2	9	0	0.000	5	9	0.643
621996	17	45249355	45249355	A	G	SNP	*CDC27*	ENST00000531206	-1	missense	c.179	p.L60P	tier1	57	1	0.017	73	36	0.327
621996	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	199	5	0.025	271	169	0.384
621996	18	55024279	55024279	A	C	SNP	*ST8SIA3*	ENST00000324000	1	silent	c.438	p.S146	tier1	85	1	0.012	59	42	0.416
621996	19	52726744	52726744	G	A	SNP	*PPP2R1A*	ENST00000322088	1	intronic	c.1661+1250	e13+1250	tier4	41	2	0.047	34	20	0.370
621996	20	29623180	29623180	T	C	SNP	*FRG1B*	ENST00000482423	1	rna	NULL	NULL	tier1	1531	18	0.012	2465	72	0.028
621996	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	693	14	0.020	805	301	0.272
621996	21	36259149	36259158	GATGGGCAGG	-	DEL	*RUNX1*	ENST00000300305	-1	frame_shift_del	c.342_333	p.P113fs	tier1	795	9	0.011	772	132	0.146
621996	22	20172250	20172250	G	A	SNP	*LINC00896*	ENST00000423736	1	5_prime_flanking_region	c.-21850	NULL	tier3	82	0	0.000	59	33	0.359
621996	X	123205158	123205159	-	AT	INS	*STAG2*	ENST00000218089	1	frame_shift_ins	c.2518_2519	p.N841fs	tier1	189	0	0.000	127	180	0.586
621996	X	151092940	151092940	G	A	SNP	*MAGEA4*	ENST00000276344	1	silent	c.804	p.A268	tier1	99	2	0.020	65	43	0.398
621996	Y	14077927	14077927	C	T	SNP	*MXRA5P1*	ENST00000420610	1	3_prime_untranslated_region	c.*14077927	NULL	tier2	42	0	0.000	31	46	0.597
624702	1	143914212	143914212	T	A	SNP	*SRGAP2P2*	ENST00000494534	1	3_prime_untranslated_region	c.*143914212	NULL	tier3	23	0	0.000	117	83	0.407
624702	1	156043138	156043138	A	C	SNP	*LMNA*	ENST00000368300	1	5_prime_flanking_region	c.-41572	NULL	tier3	83	1	0.012	129	78	0.375
624702	1	158057760	158057760	G	A	SNP	*KIRREL*	ENST00000368173	1	intronic	c.768-36	e7-36	tier2	29	1	0.033	138	74	0.349
624702	1	201868536	201868536	T	G	SNP	*LMOD1*	ENST00000367288	-1	silent	c.1605	p.P535	tier1	60	0	0.000	159	21	0.115
624702	1	214204427	214204427	C	T	SNP	*PROX1*	ENST00000261454	1	intronic	c.2029-4565	e4-4565	tier3	15	0	0.000	39	23	0.365
624702	2	133403009	133403009	C	T	SNP	*GPR39*	ENST00000329321	1	missense	c.1192	p.R398C	tier1	26	0	0.000	74	34	0.315
624702	2	179454700	179454700	C	T	SNP	*TTN*	ENST00000342175	-1	silent	c.35133	p.E11711	tier1	149	4	0.026	156	102	0.394
624702	2	187627370	187627370	G	T	SNP	*FAM171B*	ENST00000304698	1	silent	c.2301	p.G767	tier1	46	0	0.000	81	39	0.325
624702	2	238287631	238287631	C	T	SNP	*COL6A3*	ENST00000295550	-1	silent	c.2145	p.S715	tier1	21	0	0.000	60	29	0.326
624702	3	9747109	9747109	A	C	SNP	*CPNE9*	ENST00000383832	1	intronic	c.261-39	e5-39	tier3	157	1	0.006	515	43	0.076
624702	3	51312620	51312620	G	A	SNP	*DOCK3*	ENST00000266037	1	missense	c.2659	p.V887I	tier1	29	0	0.000	59	33	0.355
624702	4	2951749	2951749	C	A	SNP	*NOP14*	ENST00000416614	-1	missense	c.1194	p.E398D	tier1	47	4	0.078	96	60	0.382
624702	4	76711225	76711225	T	A	SNP	*USO1*	ENST00000538159	1	intronic	c.1003-78	e11-78	tier3	50	0	0.000	22	8	0.070
624702	4	106157711	106157712	-	T	INS	*TET2*	ENST00000380013	1	frame_shift_ins	c.2612_2613	p.V872fs	tier1	57	2	0.034	39	68	0.636
624702	5	80368977	80368977	T	C	SNP	*RASGRF2*	ENST00000265080	1	intronic	c.634-41	e5-41	tier3	64	1	0.015	92	61	0.396
624702	5	102503818	102503818	G	A	SNP	*PPIP5K2*	ENST00000451606	1	missense	c.2105	p.R702H	tier1	306	9	0.029	202	123	0.379
624702	5	139505517	139505517	T	G	SNP	*CYSTM1*	ENST00000261811	1	5_prime_flanking_region	c.-68534	NULL	tier3	102	7	0.064	62	55	0.470
624702	5	140564550	140564550	C	T	SNP	*PCDHB16*	ENST00000361016	1	3_prime_untranslated_region	c.*85	NULL	tier2	64	2	0.030	99	64	0.390
624702	5	159901462	159901463	CT	-	DEL	*MIR146A*	ENST00000517927	1	intronic	c.NULL	NULL	tier3	42	0	0.000	100	25	0.200
624702	6	35936771	35936771	C	T	SNP	*SLC26A8*	ENST00000466805	-1	5_prime_untranslated_region	c.-35936771	NULL	tier3	43	0	0.000	104	72	0.409
624702	6	109830321	109830321	G	A	SNP	*AKD1*	ENST00000424296	-1	intronic	c.4481+61	e32+61	tier3	69	0	0.000	95	69	0.421
624702	7	6031678	6031678	A	G	SNP	*PMS2*	ENST00000265849	-1	missense	c.914	p.L305P	tier1	98	5	0.049	153	92	0.376
624702	7	158200082	158200082	G	A	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.232+82345	e2+82345	tier3	18	0	0.000	135	54	0.281
624702	8	7698557	7698557	G	A	SNP	*DEFB104A*	ENST00000314265	1	silent	c.60	p.V20	tier1	114	0	0.000	228	47	0.168
624702	8	10467587	10467587	T	C	SNP	*RP1L1*	ENST00000382483	-1	missense	c.4021	p.T1341A	tier1	134	1	0.007	263	22	0.076
624702	9	27610004	27610004	G	C	SNP	*CTAGE12P*	ENST00000400348	-1	5_prime_untranslated_region	c.-27610004	NULL	tier3	369	5	0.013	261	124	0.322
624702	9	101051935	101051935	T	C	SNP	*GABBR2*	ENST00000259455	-1	3_prime_untranslated_region	c.*931	NULL	tier3	103	0	0.000	281	24	0.076
624702	10	51485576	51485576	C	-	DEL	*AGAP7*	ENST00000374095	-1	intronic	c.223+403	e1+403	tier3	14	0	0.000	21	20	0.488
624702	12	104254945	104254945	T	A	SNP	*GNN*	ENST00000548527	-1	5_prime_untranslated_region	c.-104254945	NULL	tier3	155	3	0.019	195	81	0.292
624702	13	88330904	88330904	T	C	SNP	*SLITRK5*	ENST00000325089	1	3_prime_untranslated_region	c.*384	NULL	tier4	100	1	0.010	226	23	0.092
624702	14	36986274	36986274	A	T	SNP	*NKX2-1*	ENST00000354822	-1	3_prime_untranslated_region	c.*209	NULL	tier2	280	3	0.011	530	28	0.050

624702	14	50789470	50789470	G	T	SNP	*ATP5S*	ENST00000426751	1	missense	c.394	p.A132S	tier1	36	2	0.053	58	38	0.396
624702	15	93568489	93568490	-	TGT	INS	*CHD2*	ENST00000394196	1	3_prime_untranslated_region	c.*554	NULL	tier3	141	0	0.000	326	120	0.269
624702	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000392485	-1	missense	c.284	p.P95H	tier1	72	2	0.027	275	158	0.364
624702	19	6678085	6678085	A	G	SNP	*C3*	ENST00000245907	-1	intronic	c.4851-51	e41-51	tier3	16	0	0.000	68	34	0.330
624702	19	10800503	10800506	AAAT	-	DEL	*ILF3*	ENST00000449870	1	3_prime_untranslated_region	c.*515	NULL	tier3	98	2	0.020	155	60	0.279
624702	19	42861028	42861028	C	T	SNP	*MEGF8*	ENST00000251268	1	silent	c.4725	p.P1575	tier1	94	6	0.060	420	286	0.401
624702	20	1350154	1350154	T	G	SNP	*FKBP1A*	ENST00000400137	-1	3_prime_untranslated_region	c.*2602	NULL	tier3	121	2	0.016	188	30	0.136
624702	20	18744043	18744043	A	G	SNP	*DTD1*	ENST00000377452	1	3_prime_untranslated_region	c.*19147	NULL	tier3	96	3	0.030	104	69	0.390
624702	20	44505588	44505588	C	T	SNP	*ZSWIM3*	ENST00000255152	1	nonsense	c.391	p.Q131*	tier1	28	1	0.035	85	61	0.412
624702	21	27253248	27253248	T	C	SNP	*APP*	ENST00000346798	-1	3_prime_untranslated_region	c.*733	NULL	tier3	152	1	0.007	295	24	0.075
624702	22	20715828	20715828	C	G	SNP	*ENSG00000188280*	ENST00000434783	1	intronic	c.NULL	NULL	tier2	30	0	0.000	218	50	0.185
624702	22	24176559	24176559	A	C	SNP	*SMARCB1*	ENST00000263121	1	3_prime_untranslated_region	c.*192	NULL	tier3	85	0	0.000	157	18	0.102
624702	22	38341047	38341047	A	G	SNP	*C22orf23*	ENST00000249079	-1	splice_site	c.481+2	e4+2	tier1	38	0	0.000	105	56	0.348
624702	X	123176411	123176411	A	G	SNP	*STAG2*	ENST00000218089	1	splice_region	c.386-8	e5-8	tier3	142	0	0.000	117	253	0.682
624702	X	153214721	153214721	T	G	SNP	*HCFC1*	ENST00000310441	-1	3_prime_untranslated_region	c.*77	NULL	tier3	27	0	0.000	74	23	0.232
625338	17	21562303	21562303	A	T	SNP	*ENSG00000264617*	ENST00000584107	-1	5_prime_untranslated_region	c.-21562303	NULL	tier3	193	0	0.000	242	17	0.066
625338	20	31022824	31022824	C	G	SNP	*ASXL1*	ENST00000375687	1	nonsense	c.2309	p.S770*	tier1	591	1	0.002	1201	40	0.032
625338	21	36231782	36231782	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.602	p.R201Q	tier1	786	2	0.003	1092	28	0.025
625338	21	36252865	36252865	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.497	p.R166Q	tier1	984	0	0.000	1534	46	0.029
627844	1	240073885	240073885	A	-	DEL	*CHRM3*	ENST00000255380	1	3_prime_untranslated_region	c.*1361	NULL	tier3	71	0	0.000	109	16	0.128
627844	2	10224073	10224073	G	A	SNP	*ENSG00000233502*	ENST00000425235	1	splice_site	c.165+1	e1+1	tier1	120	0	0.000	119	51	0.298
627844	2	87754980	87754981	-	T	INS	*LINC00152*	ENST00000331944	1	rna	NULL	NULL	tier1	42	0	0.000	74	13	0.149
627844	3	31674390	31674390	A	T	SNP	*STT3B*	ENST00000295770	1	intronic	c.2188-37	e15-37	tier3	90	0	0.000	140	56	0.286
627844	3	49036909	49036910	-	C	INS	*P4HTM*	ENST00000343546	1	intronic	c.437-1962_437-1961	e3-1961	tier3	76	2	0.026	81	29	0.264
627844	3	122432409	122432409	A	G	SNP	*PARP14*	ENST00000474629	1	missense	c.3758	p.N1253S	tier1	97	0	0.000	169	71	0.296
627844	4	20530641	20530641	G	A	SNP	*SLIT2*	ENST00000504154	1	missense	c.1532	p.R511H	tier1	124	0	0.000	173	15	0.080
627844	6	69795034	69795034	C	T	SNP	*BAI3*	ENST00000370598	1	intronic	c.2480+9104	e15+9104	tier3	74	0	0.000	87	38	0.304
627844	6	87968388	87968395	AGTTTGGT	-	DEL	*ZNF292*	ENST00000369577	1	frame_shift_del	c.5041_5048	p.S1681fs	tier1	78	0	0.000	163	30	0.155
627844	6	135515531	135515531	G	A	SNP	*MYB*	ENST00000341911	1	missense	c.881	p.R294Q	tier1	62	1	0.016	89	17	0.160
627844	6	146719968	146719968	C	T	SNP	*GRM1*	ENST00000282753	1	missense	c.1793	p.A598V	tier1	111	1	0.009	121	59	0.326
627844	7	27236580	27236580	G	A	SNP	*HOXA13*	ENST00000222753	-1	3_prime_untranslated_region	c.*1237	NULL	tier3	169	2	0.012	441	221	0.332
627844	7	80303472	80303472	G	A	SNP	*CD36*	ENST00000309881	1	3_prime_untranslated_region	c.*9	NULL	tier2	89	0	0.000	165	104	0.387
627844	8	82373788	82373788	G	A	SNP	*FABP9*	ENST00000379071	-1	5_prime_untranslated_region	c.-30	NULL	tier3	50	0	0.000	86	29	0.252
627844	8	105503259	105503259	C	T	SNP	*LRP12*	ENST00000424843	-1	missense	c.2165	p.R722H	tier1	107	1	0.009	101	41	0.289
627844	10	120896686	120896686	A	-	DEL	*FAM45A*	ENST00000489936	1	rna	NULL	NULL	tier1	129	0	0.000	306	20	0.061
627844	11	49839389	49839389	G	A	SNP	*ENSG00000254487*	ENST00000532682	1	3_prime_untranslated_region	c.*49839389	NULL	tier2	217	0	0.000	276	25	0.083
627844	11	57268743	57268744	-	GGGT	INS	*SLC43A1*	ENST00000278426	-1	frame_shift_ins	c.214_213	p.Q71fs	tier1	69	0	0.000	60	9	0.130
627844	11	57268744	57268745	-	CT	INS	*SLC43A1*	ENST00000278426	-1	frame_shift_ins	c.213_212	p.Q72fs	tier1	69	0	0.000	60	9	0.130
627844	11	73980724	73980724	A	G	SNP	*P4HA3*	ENST00000331597	-1	silent	c.1440	p.Y480	tier1	52	0	0.000	39	20	0.339
627844	12	8186333	8186333	G	T	SNP	*FOXJ2*	ENST00000162391	1	5_prime_untranslated_region	c.-6096	NULL	tier2	81	1	0.012	90	14	0.135
627844	12	46231475	46231476	-	GACC	INS	*ARID2*	ENST00000334344	1	frame_shift_ins	c.1315_1316	p.V439fs	tier1	62	1	0.016	103	21	0.169
627844	12	64841839	64841839	A	G	SNP	*XPOT*	ENST00000332707	1	intronic	c.2863-46	e24-46	tier3	86	0	0.000	167	15	0.082
627844	12	112185009	112185009	C	T	SNP	*ACAD10*	ENST00000546647	1	3_prime_untranslated_region	c.*112185009	NULL	tier3	68	0	0.000	82	20	0.196
627844	12	112884192	112884192	C	T	SNP	*PTPN11*	ENST00000351677	1	missense	c.127	p.L43F	tier1	518	1	0.002	638	100	0.135
627844	12	133352961	133352961	A	G	SNP	*GOLGA3*	ENST00000204726	-1	intronic	c.3978+259	e20+259	tier3	144	2	0.014	144	18	0.107
627844	13	80095144	80095144	T	-	DEL	*NDFIP2*	ENST00000218652	1	intronic	c.487+34	e2+34	tier3	68	1	0.015	115	19	0.142
627844	14	21679136	21679137	-	T	INS	*HNRNPC*	ENST00000553444	-1	5_prime_untranslated_region	c.-21679136	NULL	tier3	103	2	0.019	183	50	0.215
627844	14	86088433	86088433	T	A	SNP	*FLRT2*	ENST00000330753	1	missense	c.575	p.I192N	tier1	809	3	0.004	1009	202	0.167
627844	15	28805975	28805977	AGG	-	DEL	*ENSG00000227717*	ENST00000419645	1	3_prime_untranslated_region	c.*28805975	NULL	tier4	41	0	0.000	70	15	0.177
627844	15	75798204	75798204	G	C	SNP	*PTPN9*	ENST00000306726	-1	silent	c.780	p.P260	tier1	162	1	0.006	217	23	0.096
627844	16	20563602	20563602	G	C	SNP	*ACSM2B*	ENST00000329697	-1	missense	c.758	p.A253G	tier1	127	1	0.008	164	28	0.146
627844	16	47675018	47675018	G	A	SNP	*PHKB*	ENST00000299167	1	intronic	c.1514+17	e15+17	tier3	117	3	0.025	164	66	0.287
627844	16	89836214	89836214	G	C	SNP	*FANCA*	ENST00000567205	-1	3_prime_untranslated_region	c.*27	NULL	tier3	894	8	0.009	862	422	0.328
627844	17	9282009	9282009	C	G	SNP	*STX8*	ENST00000306357	-1	intronic	c.542-39	e7-39	tier3	127	0	0.000	165	75	0.313
627844	17	11622752	11622752	G	A	SNP	*DNAH9*	ENST00000262442	1	missense	c.5654	p.R1885H	tier1	434	5	0.011	432	208	0.325
627844	17	26923218	26923218	C	A	SNP	*SPAG5*	ENST00000321765	-1	intronic	c.177+2310	e2+2310	tier4	153	0	0.000	217	16	0.068
627844	17	34894610	34894610	T	-	DEL	*PIGW*	ENST00000328396	1	3_prime_untranslated_region	c.*145	NULL	tier4	216	5	0.023	343	36	0.095
627844	18	43532461	43532462	-	ACCC	INS	*EPG5*	ENST00000282041	-1	frame_shift_ins	c.1157_1156	p.S386fs	tier1	102	0	0.000	100	20	0.167
627844	18	61323095	61323095	G	A	SNP	*SERPINB3*	ENST00000283752	-1	silent	c.969	p.L323	tier1	121	2	0.016	124	57	0.313
627844	19	20045145	20045145	G	A	SNP	*ZNF93*	ENST00000343769	1	missense	c.1381	p.A461T	tier1	76	0	0.000	128	63	0.328
627844	20	57464277	57464278	-	CGGCG	INS	*GNAS*	ENST00000469431	1	rna	NULL	NULL	tier1	13	0	0.000	6	16	0.727
627844	21	36259256	36259257	-	CA	INS	*RUNX1*	ENST00000300305	-1	frame_shift_ins	c.235_234	p.V78fs	tier1	983	10	0.010	852	354	0.294
627844	X	13337504	13337504	C	T	SNP	*ATXN3L*	ENST00000380622	-1	missense	c.550	p.E184K	tier1	46	0	0.000	34	50	0.595
627844	X	119387527	119387527	A	G	SNP	*ZBTB33*	ENST00000326624	1	missense	c.257	p.Y86C	tier1	435	16	0.035	284	472	0.624
627844	Y	13311260	13311260	A	G	SNP	*ENSG00000270570*	ENST00000603467	-1	5_prime_flanking_region	c.-47697	NULL	tier3	138	3	0.021	184	23	0.111
635308	1	65307066	65307066	C	G	SNP	*JAK1*	ENST00000342505	-1	intronic	c.2555-44	e18-44	tier3	512	6	0.012	878	124	0.123
635308	1	84394863	84394863	T	A	SNP	*TTLL7*	ENST00000260505	-1	silent	c.1098	p.V366	tier1	180	0	0.000	322	52	0.139
635308	1	86591118	86591118	C	T	SNP	*COL24A1*	ENST00000370571	-1	missense	c.901	p.V301M	tier1	73	0	0.000	129	30	0.189
635308	1	222802593	222802593	C	T	SNP	*MIA3*	ENST00000354906	1	missense	c.778	p.L260F	tier1	42	0	0.000	78	21	0.212
635308	2	88272696	88272696	G	A	SNP	*RGPD2*	ENST00000420840	-1	intronic	c.48+12550	e1+12550	tier3	69	0	0.000	174	34	0.163
635308	3	112328837	112328837	C	T	SNP	*CCDC80*	ENST00000206423	-1	missense	c.2413	p.A805T	tier1	43	0	0.000	61	11	0.153
635308	3	112530234	112530234	C	A	SNP	*ENSG00000242770*	ENST00000496067	1	intronic	c.NULL	NULL	tier4	21	0	0.000	32	12	0.235
635308	3	131217024	131217024	C	G	SNP	*MRPL3*	ENST00000264995	-1	missense	c.467	p.R156P	tier1	53	0	0.000	81	15	0.156
635308	3	196387633	196387634	-	C	INS	*NRROS*	ENST00000328557	1	frame_shift_ins	c.1119_1120	p.G375fs	tier1	26	0	0.000	39	12	0.235

635308	4	68930609	68930609	G	A	SNP	*TMPRSS11F*	ENST00000356291	-1	missense	c.809	p.P270L	tier1	75	0	0.000	156	21	0.119
635308	4	183723682	183723682	C	G	SNP	*TENM3*	ENST00000511685	1	3_prime_untranslated_region	c.*2178	NULL	tier2	87	0	0.000	177	33	0.157
635308	4	187088020	187088020	G	C	SNP	*FAM149A*	ENST00000356371	1	intronic	c.2038-102	e12-102	tier3	22	0	0.000	59	27	0.314
635308	5	60253633	60253633	A	G	SNP	*NDUFAF2*	ENST00000296597	1	intronic	c.127+12424	e1+12424	tier3	143	0	0.000	291	56	0.161
635308	5	73178364	73178364	C	A	SNP	*ARHGEF28*	ENST00000545377	1	missense	c.2882	p.A961D	tier1	131	0	0.000	234	47	0.167
635308	5	137464931	137464931	C	T	SNP	*NME5*	ENST00000265191	-1	intronic	c.335+21	e2+21	tier3	64	1	0.015	152	27	0.151
635308	5	171706385	171706385	A	C	SNP	*UBTD2*	ENST00000393792	-1	intronic	c.70+4215	e1+4215	tier4	55	0	0.000	141	25	0.150
635308	6	41575854	41575854	G	A	SNP	*MDFI*	ENST00000230321	1	5_prime_flanking_region	c.-30634	NULL	tier3	69	0	0.000	171	32	0.156
635308	6	75890933	75890933	T	A	SNP	*COL12A1*	ENST00000322507	-1	splice_region	c.1892-6	e10-6	tier3	146	3	0.020	262	74	0.220
635308	6	161565095	161565095	C	T	SNP	*AGPAT4*	ENST00000437165	-1	3_prime_untranslated_region	c.*66	NULL	tier3	58	0	0.000	131	18	0.121
635308	7	70252341	70252341	G	A	SNP	*AUTS2*	ENST00000342771	1	missense	c.2455	p.A819T	tier1	41	0	0.000	89	16	0.152
635308	7	102194790	102194790	T	A	SNP	*SPDYE2*	ENST00000507918	1	intronic	c.161-16	e2-16	tier3	170	1	0.006	454	50	0.099
635308	7	123152386	123152386	A	G	SNP	*IQUB*	ENST00000324698	-1	silent	c.9	p.N3	tier1	35	0	0.000	76	17	0.183
635308	7	157629910	157629910	T	C	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1857+61455	e12+61455	tier4	103	5	0.046	366	96	0.207
635308	8	28203295	28203295	C	T	SNP	*ZNF395*	ENST00000344423	-1	3_prime_untranslated_region	c.*2941	NULL	tier3	59	2	0.033	104	30	0.224
635308	9	124441020	124441020	C	T	SNP	*DAB2IP*	ENST00000408936	1	missense	c.188	p.P63L	tier1	78	0	0.000	178	42	0.191
635308	9	124751442	124751442	G	A	SNP	*TTLL11*	ENST00000373776	-1	missense	c.1571	p.P524L	tier1	58	1	0.017	100	19	0.160
635308	11	47364238	47364238	C	T	SNP	*MYBPC3*	ENST00000399249	-1	silent	c.1515	p.K505	tier1	52	0	0.000	80	14	0.149
635308	11	49813519	49813519	G	T	SNP	*LOC440040*	ENST00000527477	1	splice_region	c.NULL	NULL	tier4	22	0	0.000	55	25	0.305
635308	11	50379335	50379335	G	A	SNP	*ENSG00000214883*	ENST00000532521	1	3_prime_untranslated_region	c.*50379335	NULL	tier2	40	0	0.000	137	23	0.144
635308	11	56019747	56019747	A	T	SNP	*OR5T3*	ENST00000303059	1	silent	c.72	p.S24	tier1	93	2	0.021	112	45	0.283
635308	11	62327453	62327453	T	A	SNP	*MIR3654*	ENST00000496634	-1	intronic	c.1578+88	e9+88	tier3	34	0	0.000	66	14	0.175
635308	11	124189425	124189425	A	-	DEL	*OR8D2*	ENST00000357438	-1	frame_shift_del	c.669	p.S224fs	tier1	40	0	0.000	68	22	0.244
635308	11	132306614	132306614	G	A	SNP	*OPCML*	ENST00000541867	-1	silent	c.724	p.L242	tier1	65	0	0.000	86	14	0.139
635308	12	7363619	7363619	T	A	SNP	*PEX5*	ENST00000266564	1	3_prime_untranslated_region	c.*800	NULL	tier3	56	0	0.000	109	18	0.142
635308	12	21791412	21791412	A	T	SNP	*LDHB*	ENST00000470985	-1	5_prime_untranslated_region	c.-21791412	NULL	tier3	138	0	0.000	306	20	0.061
635308	12	32854280	32854280	A	G	SNP	*DNM1L*	ENST00000553257	1	intronic	c.103-69	e2-69	tier3	72	0	0.000	156	19	0.108
635308	12	52966303	52966303	C	T	SNP	*KRT74*	ENST00000305620	-1	missense	c.620	p.G207E	tier1	48	0	0.000	91	17	0.157
635308	13	29600575	29600575	G	T	SNP	*MTUS2*	ENST00000431530	1	missense	c.1770	p.L590F	tier1	594	5	0.008	1002	221	0.181
635308	14	33292181	33292181	G	A	SNP	*AKAP6*	ENST00000280979	1	missense	c.5162	p.R1721H	tier1	58	0	0.000	101	13	0.114
635308	14	63453786	63453786	T	A	SNP	*KCNH5*	ENST00000322893	-1	splice_region	c.549+4	e5+4	tier2	77	0	0.000	178	51	0.223
635308	14	70410184	70410184	G	-	DEL	*SMOC1*	ENST00000361956	1	intronic	c.100-8671	e2-8671	tier2	140	0	0.000	215	31	0.126
635308	15	102295698	102295700	GCT	-	DEL	*DNM1P47*	ENST00000561463	1	rna	NULL	NULL	tier1	27	0	0.000	32	10	0.238
635308	16	848710	848710	G	A	SNP	*GNG13*	ENST00000248150	-1	3_prime_untranslated_region	c.*9	NULL	tier3	83	0	0.000	165	39	0.191
635308	16	85145834	85145834	C	T	SNP	*FAM92B*	ENST00000539556	-1	intronic	c.20+105	e1+105	tier3	99	0	0.000	174	32	0.155
635308	17	78440948	78440948	G	T	SNP	*NPTX1*	ENST00000535681	-1	5_prime_untranslated_region	c.-78440948	NULL	tier2	29	1	0.032	45	20	0.299
635308	17	79898724	79898724	G	A	SNP	*MYADML2*	ENST00000330655	-1	silent	c.894	p.S298	tier1	103	0	0.000	182	32	0.149
635308	19	9088712	9088712	C	G	SNP	*MUC16*	ENST00000397910	-1	missense	c.3103	p.V1035L	tier1	544	8	0.015	1277	269	0.173
635308	19	49464172	49464172	G	A	SNP	*BAX*	ENST00000345358	1	splice_site	c.474+1	e5+1	tier1	53	0	0.000	112	30	0.208
635308	21	47918578	47918578	G	C	SNP	*DIP2A*	ENST00000318711	1	missense	c.487	p.V163L	tier1	64	0	0.000	117	18	0.132
635308	X	57620926	57620926	A	T	SNP	*ZXDB*	ENST00000374888	1	3_prime_untranslated_region	c.*33	NULL	tier3	72	0	0.000	146	24	0.141
635308	X	153283630	153283630	G	A	SNP	*IRAK1*	ENST00000369980	-1	intronic	c.795-59	e7-59	tier3	82	0	0.000	147	28	0.160
639691	1	45296629	45296629	C	T	SNP	*PTCH2*	ENST00000372192	-1	missense	c.704	p.R235Q	tier1	41	0	0.000	57	13	0.181
639691	1	118644343	118644343	G	A	SNP	*SPAG17*	ENST00000336338	-1	intronic	c.634+20	e5+20	tier3	62	0	0.000	95	25	0.207
639691	1	144857704	144857704	C	A	SNP	*PDE4DIP*	ENST00000369356	-1	missense	c.6350	p.R2117L	tier1	409	1	0.002	601	20	0.032
639691	1	152276933	152276933	G	T	SNP	*FLG*	ENST00000368799	-1	missense	c.10429	p.R3477S	tier1	716	1	0.001	1022	24	0.023
639691	1	152281796	152281796	G	T	SNP	*FLG*	ENST00000368799	-1	missense	c.5566	p.R1856S	tier1	790	0	0.000	1023	23	0.022
639691	1	160105026	160105026	G	A	SNP	*ATP1A2*	ENST00000361216	1	missense	c.2056	p.V686I	tier1	29	0	0.000	26	14	0.350
639691	1	205389686	205389686	T	C	SNP	*LEMD1*	ENST00000476884	-1	rna	NULL	NULL	tier1	53	0	0.000	98	15	0.133
639691	2	9558907	9558907	T	G	SNP	*ITGB1BP1*	ENST00000355346	-1	intronic	c.1-46	e1-46	tier4	37	0	0.000	50	17	0.254
639691	2	9558909	9558909	T	A	SNP	*ITGB1BP1*	ENST00000355346	-1	intronic	c.1-48	e1-48	tier4	37	0	0.000	45	14	0.237
639691	2	21238368	21238368	G	T	SNP	*APOB*	ENST00000233242	-1	missense	c.3382	p.R1128S	tier1	372	0	0.000	594	19	0.031
639691	2	71762298	71762298	C	A	SNP	*DYSF*	ENST00000413539	1	intronic	c.1446+79	e15+79	tier3	255	0	0.000	297	15	0.048
639691	2	89160377	89160377	G	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	47	0	0.000	18	30	0.625
639691	2	89160420	89160420	T	C	SNP	*IGKJ4*	ENST00000390239	-1	silent	c.15	p.G5	tier1	68	0	0.000	44	12	0.211
639691	2	89160450	89160450	T	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	72	0	0.000	45	10	0.182
639691	2	89160485	89160485	C	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	66	0	0.000	45	7	0.135
639691	2	89160500	89160500	A	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	67	0	0.000	48	7	0.127
639691	2	89160507	89160507	T	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	65	0	0.000	47	7	0.130
639691	2	89160663	89160663	T	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	78	0	0.000	41	31	0.431
639691	2	89160686	89160686	T	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	101	0	0.000	66	41	0.380
639691	2	89160714	89160714	T	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	123	0	0.000	82	53	0.393
639691	2	89160740	89160740	A	C	SNP	*IGKJ3*	ENST00000390240	-1	missense	c.31	p.Y11D	tier1	168	1	0.006	119	73	0.380
639691	2	89160789	89160789	C	T	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	222	0	0.000	161	62	0.277
639691	2	89160801	89160801	C	T	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	218	1	0.005	164	60	0.268
639691	2	89160806	89160806	A	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	220	0	0.000	159	59	0.269
639691	2	89160841	89160841	A	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	222	0	0.000	153	43	0.217
639691	2	89160860	89160860	G	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	202	0	0.000	140	26	0.156
639691	2	89160869	89160869	A	C	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	186	0	0.000	124	17	0.121
639691	2	89160962	89160962	A	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	110	0	0.000	94	23	0.197
639691	2	89160986	89160986	C	T	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	114	0	0.000	90	21	0.189
639691	2	89160999	89160999	T	A	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	115	0	0.000	88	20	0.185
639691	2	89161003	89161003	C	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	110	0	0.000	87	19	0.178
639691	2	89161026	89161026	A	G	SNP	*ENSG00000231486*	ENST00000418209	-1	intronic	c.NULL	NULL	tier3	117	0	0.000	77	16	0.172

639691	2	89185292	89185292	T	C	SNP	*IGKV4-1*	ENST00000390243	1	intronic	c.50-64	e2-64	tier3	75	0	0.000	100	11	0.099
639691	2	89185531	89185531	C	G	SNP	*IGKV4-1*	ENST00000390243	1	nonsense	c.225	p.Y75*	tier1	180	0	0.000	81	9	0.100
639691	2	89185535	89185535	G	A	SNP	*IGKV4-1*	ENST00000390243	1	missense	c.229	p.A77T	tier1	178	0	0.000	78	8	0.093
639691	2	89185568	89185568	T	G	SNP	*IGKV4-1*	ENST00000390243	1	missense	c.262	p.F88V	tier1	189	0	0.000	68	9	0.117
639691	2	89246846	89246846	A	G	SNP	*IGKV1-5*	ENST00000496168	-1	silent	c.324	p.Y108	tier1	160	0	0.000	137	11	0.074
639691	2	89246861	89246861	A	T	SNP	*IGKV1-5*	ENST00000496168	-1	missense	c.309	p.D103E	tier1	165	0	0.000	153	15	0.089
639691	2	89246918	89246918	G	A	SNP	*IGKV1-5*	ENST00000496168	-1	silent	c.252	p.F84	tier1	178	0	0.000	176	25	0.123
639691	2	89246947	89246947	T	G	SNP	*IGKV1-5*	ENST00000496168	-1	missense	c.223	p.S75R	tier1	178	1	0.006	182	26	0.125
639691	2	89246969	89246969	C	G	SNP	*IGKV1-5*	ENST00000496168	-1	missense	c.201	p.K67N	tier1	171	0	0.000	159	22	0.121
639691	2	89246970	89246970	T	C	SNP	*IGKV1-5*	ENST00000496168	-1	missense	c.200	p.K67R	tier1	170	0	0.000	157	23	0.128
639691	2	89247181	89247181	T	G	SNP	*IGKV1-5*	ENST00000496168	-1	intronic	c.55+59	e1+59	tier3	167	0	0.000	168	66	0.280
639691	2	89247195	89247195	T	C	SNP	*IGKV1-5*	ENST00000496168	-1	intronic	c.55+45	e1+45	tier3	180	0	0.000	177	64	0.265
639691	2	89247280	89247280	G	T	SNP	*IGKV1-5*	ENST00000496168	-1	silent	c.15	p.V5	tier1	187	0	0.000	172	66	0.276
639691	2	114355305	114355305	C	A	SNP	*WASH2P*	ENST00000538033	1	intronic	c.NULL	NULL	tier3	125	0	0.000	129	10	0.071
639691	2	141356343	141356343	C	A	SNP	*LRP1B*	ENST00000389484	-1	missense	c.7051	p.G2351W	tier1	452	0	0.000	954	26	0.027
639691	2	202436665	202436665	T	G	SNP	*ALS2CR11*	ENST00000286195	-1	missense	c.832	p.T278P	tier1	54	1	0.018	91	29	0.242
639691	3	15176119	15176119	G	T	SNP	*ZFYVE20*	ENST00000253699	-1	5_prime_flanking_region	c.-38492	NULL	tier3	368	0	0.000	597	19	0.031
639691	3	38592896	38592896	G	A	SNP	*SCN5A*	ENST00000333535	-1	missense	c.4967	p.A1656V	tier1	142	1	0.007	241	62	0.205
639691	3	71247370	71247370	G	T	SNP	*FOXP1*	ENST00000318789	-1	missense	c.163	p.Q55K	tier1	589	0	0.000	774	22	0.028
639691	3	193007798	193007798	G	C	SNP	*ATP13A5*	ENST00000342358	-1	missense	c.2899	p.Q967E	tier1	66	0	0.000	103	16	0.135
639691	3	193721356	193721356	C	A	SNP	*LOC647323*	ENST00000397645	-1	intronic	c.NULL	NULL	tier2	100	0	0.000	104	10	0.088
639691	4	55594015	55594015	G	T	SNP	*KIT*	ENST00000288135	1	missense	c.1801	p.G601W	tier1	338	0	0.000	610	20	0.032
639691	4	100273911	100273911	G	T	SNP	*ADH1C*	ENST00000515683	-1	5_prime_untranslated_region	c.-79	NULL	tier3	52	0	0.000	81	22	0.214
639691	4	106196822	106196822	G	T	SNP	*TET2*	ENST00000380013	1	missense	c.5155	p.G1719W	tier1	496	1	0.002	884	24	0.026
639691	4	114278785	114278785	G	T	SNP	*ANK2*	ENST00000357077	1	missense	c.9011	p.W3004L	tier1	457	0	0.000	793	22	0.027
639691	4	189013998	189013998	T	C	SNP	*TRIML2*	ENST00000503141	-1	3_prime_untranslated_region	c.*4297	NULL	tier4	72	0	0.000	96	33	0.256
639691	5	38968092	38968092	G	A	SNP	*RICTOR*	ENST00000296782	-1	missense	c.1013	p.P338L	tier1	49	0	0.000	133	29	0.178
639691	5	96248518	96248521	TAAC	-	DEL	*ERAP2*	ENST00000437043	1	intronic	c.2516+16_2516+13	e15+16	tier3	49	0	0.000	105	21	0.167
639691	5	140604754	140604754	C	A	SNP	*PCDHB14*	ENST00000239449	1	silent	c.1677	p.P559	tier1	170	0	0.000	192	11	0.054
639691	5	149808594	149808594	G	T	SNP	*CD74*	ENST00000009530	-1	5_prime_flanking_region	c.-16282	NULL	tier4	127	0	0.000	101	8	0.073
639691	6	325891	325891	G	T	SNP	*DUSP22*	ENST00000604971	1	5_prime_untranslated_region	c.-22258	NULL	tier3	264	0	0.000	245	13	0.049
639691	6	15501389	15501389	C	T	SNP	*JARID2*	ENST00000341776	1	missense	c.2197	p.R733C	tier1	57	0	0.000	69	16	0.188
639691	6	18139973	18139974	AT	-	DEL	*TPMT*	ENST00000309983	-1	intronic	c.367-26_367-25	e4-25	tier4	52	0	0.000	94	18	0.161
639691	6	52701179	52701179	A	-	DEL	*GSTA5*	ENST00000284562	-1	intronic	c.140-13	e3-13	tier3	65	0	0.000	87	35	0.287
639691	6	76343330	76343330	T	C	SNP	*SENP6*	ENST00000370014	1	missense	c.241	p.S81P	tier1	42	0	0.000	144	26	0.152
639691	6	119285878	119285878	A	C	SNP	*FAM184A*	ENST00000338891	-1	missense	c.3092	p.V1031G	tier1	38	0	0.000	135	57	0.297
639691	6	127912679	127912679	C	-	DEL	*C6orf58*	ENST00000329722	1	splice_region_del	c.914-9	e6-9	tier3	57	0	0.000	292	42	0.126
639691	7	2515372	2515372	G	T	SNP	*GRIFIN*	ENST00000417742	-1	rna	NULL	NULL	tier1	169	0	0.000	171	10	0.055
639691	7	43484053	43484053	C	A	SNP	*HECW1*	ENST00000395891	1	missense	c.1282	p.Q428K	tier1	379	3	0.008	392	157	0.286
639691	7	99795840	99795840	G	T	SNP	*STAG3*	ENST00000317296	1	intronic	c.1244+51	e11+51	tier3	268	0	0.000	311	14	0.043
639691	7	142482221	142482221	G	T	SNP	*PRSS3P2*	ENST00000603901	1	rna	NULL	NULL	tier1	58	0	0.000	24	6	0.200
639691	8	26628125	26628125	G	A	SNP	*ADRA1A*	ENST00000380586	-1	silent	c.942	p.L314	tier1	48	0	0.000	88	29	0.248
639691	8	40012484	40012484	A	C	SNP	*C8orf4*	ENST00000315792	1	3_prime_untranslated_region	c.*1112	NULL	tier2	15	0	0.000	81	40	0.331
639691	8	131073071	131073071	G	T	SNP	*ASAP1*	ENST00000524124	-1	missense	c.2407	p.Q803K	tier1	94	0	0.000	79	8	0.092
639691	8	142506437	142506437	C	A	SNP	*MROH5*	ENST00000521161	-1	missense	c.140	p.G47V	tier1	384	0	0.000	464	15	0.031
639691	8	145745801	145745801	A	C	SNP	*LRRC14*	ENST00000292524	1	missense	c.509	p.D170A	tier1	72	1	0.014	75	21	0.219
639691	9	13217161	13217161	C	T	SNP	*MPDZ*	ENST00000319217	-1	intronic	c.1201+18	e8+18	tier3	42	0	0.000	164	55	0.251
639691	9	119730785	119730787	GAG	-	DEL	*ASTN2*	ENST00000313400	-1	intronic	c.1889+6700_1889+6698	e10+6700	tier3	37	0	0.000	50	12	0.194
639691	9	140286997	140286997	G	T	SNP	*EXD3*	ENST00000465160	-1	3_prime_untranslated_region	c.*575	NULL	tier3	110	0	0.000	136	11	0.075
639691	9	141013150	141013150	G	T	SNP	*CACNA1B*	ENST00000371355	1	missense	c.5963	p.G1988V	tier1	199	0	0.000	219	12	0.052
639691	10	124458903	124458903	C	A	SNP	*C10orf120*	ENST00000329446	-1	missense	c.202	p.D68Y	tier1	164	0	0.000	177	69	0.281
639691	11	1267352	1267352	C	A	SNP	*MUC5B*	ENST00000447027	1	missense	c.9251	p.P3084Q	tier1	480	0	0.000	573	18	0.030
639691	11	1271142	1271142	C	A	SNP	*MUC5B*	ENST00000447027	1	silent	c.13041	p.P4347	tier1	577	1	0.002	580	21	0.035
639691	11	1271180	1271180	C	A	SNP	*MUC5B*	ENST00000447027	1	missense	c.13079	p.P4360Q	tier1	681	0	0.000	713	19	0.026
639691	11	6235593	6235593	T	C	SNP	*FAM160A2*	ENST00000265978	-1	intronic	c.2599+48	e10+48	tier3	57	0	0.000	90	13	0.126
639691	11	64794980	64794980	C	T	SNP	*SNX15*	ENST00000377244	1	5_prime_untranslated_region	c.-30	NULL	tier2	67	2	0.029	60	26	0.302
639691	11	118918816	118918816	A	-	DEL	*HYOU1*	ENST00000527738	-1	5_prime_untranslated_region	c.-118918816	NULL	tier3	41	0	0.000	52	21	0.288
639691	12	4920436	4920436	C	A	SNP	*KCNA6*	ENST00000280684	1	missense	c.1229	p.P410Q	tier1	91	0	0.000	72	8	0.100
639691	12	70349145	70349145	C	G	SNP	*MYRFL*	ENST00000299350	1	missense	c.473	p.S158C	tier1	62	0	0.000	192	63	0.247
639691	12	93477504	93477504	C	A	SNP	*ENSG00000257322*	ENST00000549930	-1	intronic	c.NULL	NULL	tier4	39	0	0.000	63	23	0.267
639691	12	125292397	125292397	G	T	SNP	*SCARB1*	ENST00000415380	-1	missense	c.919	p.L307M	tier1	376	0	0.000	553	20	0.035
639691	13	31002525	31002525	G	A	SNP	*UBE2L5P*	ENST00000436446	1	3_prime_untranslated_region	c.*31002525	NULL	tier2	94	0	0.000	151	31	0.170
639691	13	114530002	114530002	C	A	SNP	*GAS6*	ENST00000357389	-1	missense	c.1573	p.G525W	tier1	279	0	0.000	292	12	0.039
639691	14	20264803	20264803	G	A	SNP	*OR4N1P*	ENST00000554847	1	3_prime_untranslated_region	c.*20264803	NULL	tier3	131	0	0.000	188	48	0.203
639691	14	77844469	77844469	C	A	SNP	*SAMD15*	ENST00000216471	1	silent	c.708	p.T236	tier1	26	0	0.000	24	8	0.250
639691	14	106329350	106329350	C	G	SNP	*ENSG00000244620*	ENST00000414005	1	5_prime_flanking_region	c.-26592	NULL	tier2	31	0	0.000	14	8	0.348
639691	14	106329945	106329945	C	T	SNP	*ENSG00000244620*	ENST00000414005	1	5_prime_flanking_region	c.-25997	NULL	tier3	84	1	0.012	59	15	0.203
639691	14	106329978	106329978	C	G	SNP	*ENSG00000244620*	ENST00000414005	1	5_prime_flanking_region	c.-25964	NULL	tier3	112	1	0.009	79	17	0.177
639691	14	106330001	106330001	G	C	SNP	*ENSG00000244620*	ENST00000414005	1	5_prime_flanking_region	c.-25941	NULL	tier3	128	1	0.008	81	16	0.165
639691	14	107034793	107034793	C	A	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.287	p.S96I	tier1	71	0	0.000	55	16	0.222
639691	14	107034840	107034840	G	A	SNP	*IGHV5-51*	ENST00000390626	-1	silent	c.240	p.S80	tier1	89	0	0.000	71	25	0.260
639691	14	107034897	107034897	C	T	SNP	*IGHV5-51*	ENST00000390626	-1	silent	c.183	p.G61	tier1	117	0	0.000	81	29	0.264
639691	14	107034930	107034930	G	A	SNP	*IGHV5-51*	ENST00000390626	-1	silent	c.150	p.S50	tier1	114	1	0.009	98	28	0.222
639691	14	107034940	107034940	C	A	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.140	p.S47I	tier1	112	0	0.000	105	29	0.216

639691	14	107034956	107034956	T	C	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.124	p.K42E	tier1	109	0	0.000	96	23	0.193
639691	14	107035010	107035010	C	T	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.70	p.V24M	tier1	102	0	0.000	102	16	0.136
639691	14	107035027	107035027	C	G	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.53	p.C18S	tier1	110	0	0.000	103	19	0.155
639691	14	107035049	107035049	A	G	SNP	*IGHV5-51*	ENST00000390626	-1	intronic	c.47-16	e2-16	tier3	113	0	0.000	83	16	0.162
639691	14	107035075	107035075	A	G	SNP	*IGHV5-51*	ENST00000390626	-1	intronic	c.46+42	e1+42	tier3	108	0	0.000	85	16	0.158
639691	14	107035146	107035146	A	G	SNP	*IGHV5-51*	ENST00000390626	-1	missense	c.17	p.I6T	tier1	74	0	0.000	65	13	0.167
639691	14	107178814	107178814	C	G	SNP	*IGHV1-69*	ENST00000390633	-1	5_prime_flanking_region	c.-8447	NULL	tier3	76	0	0.000	68	15	0.181
639691	14	107178822	107178822	T	C	SNP	*IGHV2-70*	ENST00000390634	-1	missense	c.355	p.I119V	tier1	79	0	0.000	77	14	0.154
639691	14	107178861	107178861	T	C	SNP	*IGHV2-70*	ENST00000390634	-1	missense	c.316	p.M106V	tier1	102	0	0.000	139	15	0.097
639691	14	107178871	107178871	T	C	SNP	*IGHV2-70*	ENST00000390634	-1	silent	c.306	p.T102	tier1	112	0	0.000	138	28	0.169
639691	14	107178884	107178884	T	A	SNP	*IGHV2-70*	ENST00000390634	-1	missense	c.293	p.Q98L	tier1	120	0	0.000	172	17	0.090
639691	14	107178935	107178935	C	A	SNP	*IGHV2-70*	ENST00000390634	-1	missense	c.242	p.S81I	tier1	141	0	0.000	208	30	0.126
639691	14	107179009	107179009	G	A	SNP	*IGHV2-70*	ENST00000390634	-1	silent	c.168	p.S56	tier1	172	0	0.000	203	47	0.188
639691	14	107179158	107179158	C	T	SNP	*IGHV2-70*	ENST00000390634	-1	intronic	c.47-28	e2-28	tier3	186	0	0.000	256	47	0.155
639691	15	33923426	33923426	G	T	SNP	*RYR3*	ENST00000389232	1	silent	c.2799	p.L933	tier1	382	0	0.000	671	20	0.029
639691	16	1261371	1261371	G	A	SNP	*CACNA1H*	ENST00000569953	1	3_prime_untranslated_region	c.*1261371	NULL	tier3	75	1	0.013	61	12	0.164
639691	16	56652567	56652567	C	T	SNP	*MT1L*	ENST00000565768	1	rna	NULL	NULL	tier1	80	0	0.000	79	17	0.177
639691	16	67580350	67580350	C	T	SNP	*FAM65A*	ENST00000422602	1	missense	c.3704	p.A1235V	tier1	252	1	0.004	330	44	0.118
639691	17	7386234	7386234	G	A	SNP	*SLC35G6*	ENST00000412468	1	missense	c.931	p.V311M	tier1	115	3	0.025	128	26	0.169
639691	17	7579349	7579349	A	C	SNP	*TP53*	ENST00000269305	-1	missense	c.338	p.F113C	tier1	784	1	0.001	774	213	0.216
639691	17	56277172	56277172	G	A	SNP	*EPX*	ENST00000225371	1	intronic	c.1537+17	e9+17	tier3	106	1	0.009	97	45	0.317
639691	17	61972742	61972742	T	G	SNP	*CSH1*	ENST00000329882	-1	missense	c.547	p.K183Q	tier1	116	5	0.041	109	41	0.273
639691	17	79206209	79206209	C	A	SNP	*ENTHD2*	ENST00000374769	-1	silent	c.180	p.R60	tier1	181	0	0.000	172	10	0.054
639691	18	14810028	14810028	A	G	SNP	*ANKRD30B*	ENST00000358984	1	intronic	c.2313+1450	e25+1450	tier3	107	0	0.000	357	31	0.080
639691	18	20979505	20979505	T	C	SNP	*TMEM241*	ENST00000383233	-1	intronic	c.279+25	e4+25	tier3	49	0	0.000	89	33	0.271
639691	19	11564674	11564674	G	T	SNP	*ELAVL3*	ENST00000359227	-1	3_prime_untranslated_region	c.*667	NULL	tier4	41	1	0.023	57	22	0.279
639691	19	49548481	49548481	C	T	SNP	*CGB5*	ENST00000301408	1	missense	c.428	p.A143V	tier1	69	1	0.014	74	21	0.221
639691	19	54742838	54742838	G	A	SNP	*LILRA6*	ENST00000245621	-1	silent	c.1386	p.A462	tier1	187	0	0.000	276	17	0.058
639691	21	38885295	38885295	G	T	SNP	*DYRK1A*	ENST00000339659	1	3_prime_untranslated_region	c.*461	NULL	tier3	161	0	0.000	226	21	0.084
639691	22	23223246	23223246	A	T	SNP	*IGLV3-1*	ENST00000390319	1	intronic	c.47-31	e2-31	tier3	32	0	0.000	35	22	0.386
639691	22	23223346	23223346	T	C	SNP	*IGLV3-1*	ENST00000390319	1	missense	c.116	p.I39T	tier1	53	0	0.000	49	8	0.140
639691	22	23223372	23223372	G	A	SNP	*IGLV3-1*	ENST00000390319	1	missense	c.142	p.D48N	tier1	50	0	0.000	46	11	0.193
639691	22	23223397	23223397	A	C	SNP	*IGLV3-1*	ENST00000390319	1	missense	c.167	p.Q56P	tier1	58	0	0.000	58	11	0.159
639691	22	23223436	23223436	A	G	SNP	*IGLV3-1*	ENST00000390319	1	missense	c.206	p.D69G	tier1	56	0	0.000	74	14	0.159
639691	22	23223446	23223446	G	C	SNP	*IGLV3-1*	ENST00000390319	1	silent	c.216	p.R72	tier1	57	0	0.000	74	16	0.178
639691	22	23223480	23223480	A	C	SNP	*IGLV3-1*	ENST00000390319	1	missense	c.250	p.N84H	tier1	53	0	0.000	67	21	0.236
639691	22	23660791	23660791	C	T	SNP	*ENSG00000236611*	ENST00000450776	1	5_prime_flanking_region	c.-8012	NULL	tier3	93	0	0.000	133	13	0.089
639691	X	15841049	15841049	G	T	SNP	*ZRSR2*	ENST00000307771	1	missense	c.1133	p.R378L	tier1	493	0	0.000	758	22	0.028
639691	X	18323300	18323300	C	A	SNP	*SCML2*	ENST00000251900	-1	silent	c.522	p.V174	tier1	383	0	0.000	732	23	0.030
639691	X	48163116	48163116	G	T	SNP	*SSX9*	ENST00000608568	-1	5_prime_untranslated_region	c.-48163116	NULL	tier3	216	0	0.000	346	17	0.046
639691	X	62857793	62857793	G	T	SNP	*ARHGEF9*	ENST00000253401	-1	3_prime_untranslated_region	c.*115	NULL	tier4	318	4	0.012	500	37	0.069
639691	X	69455923	69455923	C	T	SNP	*AWAT1*	ENST00000374521	1	silent	c.189	p.G63	tier1	95	0	0.000	116	12	0.094
639691	X	101972409	101972409	T	C	SNP	*GPRASP2*	ENST00000332262	1	3_prime_untranslated_region	c.*95	NULL	tier3	72	1	0.014	156	67	0.300
639691	X	147031603	147031603	T	-	DEL	*FMR1*	ENST00000370475	1	3_prime_untranslated_region	c.*1239	NULL	tier3	79	0	0.000	294	30	0.093
639691	X	153134255	153134255	C	G	SNP	*L1CAM*	ENST00000543994	-1	intronic	c.1385+41	e11+41	tier3	64	0	0.000	76	21	0.217
678913	1	155884156	155884156	A	-	DEL	*KIAA0907*	ENST00000368320	-1	3_prime_untranslated_region	c.*1458	NULL	tier3	56	0	0.000	74	14	0.159
678913	2	96557526	96557526	T	A	SNP	*ANKRD36C*	ENST00000456556	-1	intronic	c.2785-41	e46-41	tier3	301	3	0.010	592	33	0.053
678913	3	78700929	78700929	C	A	SNP	*ROBO1*	ENST00000464233	-1	missense	c.2765	p.R922L	tier1	130	2	0.015	160	82	0.337
678913	3	78700930	78700930	G	T	SNP	*ROBO1*	ENST00000464233	-1	missense	c.2764	p.R922S	tier1	131	2	0.015	160	84	0.343
678913	5	150407642	150407642	T	G	SNP	*GPX3*	ENST00000388825	1	missense	c.632	p.I211S	tier1	85	1	0.012	121	66	0.353
678913	6	33261595	33261595	G	A	SNP	*RGL2*	ENST00000497454	-1	silent	c.1485	p.L495	tier1	131	2	0.015	112	79	0.414
678913	7	116166678	116166678	G	T	SNP	*CAV1*	ENST00000341049	1	missense	c.130	p.A44S	tier1	70	2	0.028	91	66	0.418
678913	7	141321598	141321598	C	A	SNP	*AGK*	ENST00000355413	1	silent	c.585	p.I195	tier1	90	2	0.022	132	75	0.359
678913	7	151945083	151945083	C	T	SNP	*KMT2C*	ENST00000355193	-1	missense	c.2436	p.M812I	tier1	2504	5	0.002	5543	178	0.031
678913	12	2912387	2912387	C	T	SNP	*FKBP4*	ENST00000001008	1	missense	c.1343	p.T448M	tier1	57	0	0.000	60	38	0.388
678913	12	39761659	39761659	T	C	SNP	*KIF21A*	ENST00000395670	-1	intronic	c.600+26	e4+26	tier3	43	0	0.000	66	44	0.400
678913	15	50784950	50784950	C	T	SNP	*USP8*	ENST00000307179	1	missense	c.2287	p.R763W	tier1	67	0	0.000	117	22	0.158
678913	16	5040788	5040788	C	T	SNP	*SEC14L5*	ENST00000251170	1	silent	c.366	p.D122	tier1	118	0	0.000	123	88	0.415
678913	17	58740533	58740533	A	-	DEL	*PPM1D*	ENST00000305921	1	frame_shift_del	c.1438	p.A481fs	tier1	63	0	0.000	82	62	0.431
678913	20	29628225	29628225	A	G	SNP	*FRG1B*	ENST00000278882	1	splice_site	c.229-2	e4-2	tier1	602	5	0.008	1566	51	0.032
678913	20	30618789	30618789	C	T	SNP	*LOC101929636*	ENST00000449519	-1	rna	NULL	NULL	tier1	133	1	0.008	147	79	0.350
678913	21	27542825	27542825	G	C	SNP	*APP*	ENST00000346798	-1	intronic	c.57+57	e1+57	tier2	39	0	0.000	52	20	0.278
715413	1	172378884	172378885	-	T	INS	*DNM3*	ENST00000358155	1	3_prime_untranslated_region	c.*1903	NULL	tier3	12	0	0.000	65	41	0.387
715413	1	201781078	201781078	A	C	SNP	*NAV1*	ENST00000367296	1	missense	c.5000	p.N1667T	tier1	315	2	0.006	977	64	0.062
715413	6	325294	325294	A	G	SNP	*DUSP22*	ENST00000604971	1	5_prime_untranslated_region	c.-22855	NULL	tier3	212	3	0.014	579	41	0.066
715413	6	32548143	32548143	T	C	SNP	*HLA-DRB1*	ENST00000360004	-1	intronic	c.764-96	e5-96	tier3	36	1	0.027	90	29	0.244
715413	6	32548146	32548146	C	T	SNP	*HLA-DRB1*	ENST00000360004	-1	intronic	c.764-99	e5-99	tier3	35	1	0.028	82	29	0.257
715413	6	75851871	75851871	C	A	SNP	*COL12A1*	ENST00000322507	-1	missense	c.4834	p.V1612L	tier1	201	2	0.010	700	41	0.055
715413	7	21828743	21828744	-	A	INS	*DNAH11*	ENST00000328843	1	intronic	c.9946-116_9946-115	e62-115	tier4	11	0	0.000	37	42	0.532
715413	8	19171376	19171376	G	T	SNP	*SH2D4A*	ENST00000265807	1	intronic	c.1+42	e0+42	tier2	14	0	0.000	18	27	0.600
715413	9	137314261	137314261	A	C	SNP	*RXRA*	ENST00000481739	1	intronic	c.910+610	e6+610	tier3	85	1	0.012	278	37	0.117
715413	10	75451844	75451844	A	-	DEL	*AGAP5*	ENST00000374094	-1	splice_region_del	c.362-9	e4-9	tier3	98	1	0.010	300	32	0.096
715413	11	109964187	109964187	G	A	SNP	*ZC3H12C*	ENST00000278590	1	intronic	c.21+29	e1+29	tier2	12	0	0.000	31	24	0.436
715413	12	50746164	50746164	A	G	SNP	*FAM186A*	ENST00000327337	-1	missense	c.4451	p.I1484T	tier1	145	2	0.014	426	48	0.101

715413	20	29612347	29612347	C	A	SNP	*FRG1B*	ENST00000482423	1	rna	NULL	NULL	tier1	250	1	0.004	815	51	0.059
715413	X	34961763	34961763	A	C	SNP	*FAM47B*	ENST00000329357	1	missense	c.815	p.H272P	tier1	422	2	0.005	1081	47	0.041
715413	X	154009603	154009603	G	A	SNP	*MPP1*	ENST00000482757	-1	5_prime_untranslated_region	c.-154009603	NULL	tier3	62	0	0.000	137	17	0.110
717045	1	32381592	32381592	T	A	SNP	*PTP4A2*	ENST00000344035	-1	splice_region	c.97-4	e2-4	tier4	122	1	0.008	141	15	0.096
717045	1	47548156	47548156	G	A	SNP	*CYP4Z1*	ENST00000334194	1	intronic	c.492+23	e4+23	tier3	89	2	0.022	80	52	0.394
717045	1	200878061	200878061	G	A	SNP	*C1orf106*	ENST00000367342	1	missense	c.1033	p.E345K	tier1	51	1	0.019	60	49	0.450
717045	1	216678795	216678796	-	T	INS	*ESRRG*	ENST00000408911	-1	3_prime_untranslated_region	c.*1486	NULL	tier3	66	0	0.000	70	9	0.114
717045	2	32666548	32666548	T	G	SNP	*BIRC6*	ENST00000421745	1	intronic	c.3944+18	e17+18	tier3	123	3	0.024	79	51	0.392
717045	2	122368248	122368248	T	G	SNP	*CLASP1*	ENST00000263710	-1	intronic	c.1-4492	e1-4492	tier4	70	1	0.014	87	17	0.160
717045	2	131947387	131947387	G	T	SNP	*PLEKHB2*	ENST00000303908	1	intronic	c.423+56823	e5+56823	tier3	463	6	0.013	412	24	0.055
717045	2	132290441	132290441	G	A	SNP	*CCDC74A*	ENST00000295171	1	missense	c.881	p.R294Q	tier1	96	0	0.000	171	16	0.086
717045	2	179481333	179481333	A	T	SNP	*TTN*	ENST00000342992	-1	nonsense	c.40481	p.L13494*	tier1	97	1	0.010	84	47	0.359
717045	2	198266834	198266834	T	C	SNP	*SF3B1*	ENST00000335508	-1	missense	c.2098	p.K700E	tier1	308	4	0.013	303	204	0.401
717045	2	217280235	217280235	T	C	SNP	*SMARCAL1*	ENST00000357276	1	missense	c.808	p.Y270H	tier1	36	1	0.027	25	19	0.432
717045	3	27208497	27208497	A	T	SNP	*NEK10*	ENST00000383771	-1	intronic	c.768-4268	e8-4268	tier3	43	0	0.000	10	19	0.655
717045	3	71355167	71355167	T	C	SNP	*FOXP1*	ENST00000318789	-1	intronic	c.1-6136	e1-6136	tier2	31	0	0.000	33	12	0.267
717045	4	25407313	25407313	G	A	SNP	*ANAPC4*	ENST00000510092	1	intronic	c.1320+69	e17+69	tier3	36	0	0.000	22	9	0.290
717045	4	105393360	105393360	C	T	SNP	*CXXC4*	ENST00000466963	-1	rna	NULL	NULL	tier1	55	0	0.000	26	15	0.357
717045	6	129475728	129475728	G	A	SNP	*LAMA2*	ENST00000421865	1	missense	c.1106	p.R369H	tier1	204	0	0.000	138	64	0.317
717045	7	73973313	73973313	G	A	SNP	*GTF2IRD1*	ENST00000265755	1	missense	c.2275	p.G759S	tier1	62	0	0.000	43	42	0.494
717045	7	151878771	151878771	T	C	SNP	*KMT2C*	ENST00000355193	-1	silent	c.6174	p.G2058	tier1	694	10	0.014	649	333	0.338
717045	8	9639151	9639151	A	G	SNP	*TNKS*	ENST00000310430	1	3_prime_untranslated_region	c.*4905	NULL	tier3	87	1	0.011	74	47	0.388
717045	10	61666207	61666207	G	A	SNP	*CCDC6*	ENST00000263102	-1	5_prime_untranslated_region	c.-25	NULL	tier2	15	0	0.000	6	6	0.500
717045	10	71620368	71620368	C	T	SNP	*COL13A1*	ENST00000356340	1	intronic	c.365-11564	e3-11564	tier3	138	4	0.028	137	81	0.370
717045	11	1770224	1770224	C	G	SNP	*IFITM10*	ENST00000482459	-1	rna	NULL	NULL	tier1	8	0	0.000	1	4	0.800
717045	12	49724201	49724201	G	A	SNP	*TROAP*	ENST00000257909	1	missense	c.1573	p.A525T	tier1	47	3	0.060	40	30	0.423
717045	14	88945999	88945999	G	A	SNP	*PTPN21*	ENST00000328736	-1	silent	c.1776	p.P592	tier1	167	1	0.006	105	83	0.442
717045	14	106805481	106805481	G	A	SNP	*IGHV4-31*	ENST00000438142	-1	missense	c.82	p.P28S	tier1	210	3	0.014	259	28	0.097
717045	14	106805485	106805485	C	G	SNP	*IGHV4-31*	ENST00000438142	-1	silent	c.78	p.S26	tier1	213	3	0.014	268	28	0.095
717045	14	106805502	106805502	C	G	SNP	*IGHV4-31*	ENST00000438142	-1	missense	c.61	p.V21L	tier1	232	2	0.009	274	27	0.090
717045	14	106805533	106805533	A	C	SNP	*IGHV4-31*	ENST00000438142	-1	intronic	c.47-17	e2-17	tier3	258	2	0.008	319	24	0.070
717045	15	101432730	101432730	G	C	SNP	*ALDH1A3*	ENST00000329841	1	missense	c.361	p.D121H	tier1	88	3	0.033	70	59	0.457
717045	16	66432084	66432084	G	T	SNP	*CDH5*	ENST00000341529	1	intronic	c.1485+75	e8+75	tier3	41	0	0.000	40	33	0.452
717045	17	40731892	40731892	C	T	SNP	*FAM134C*	ENST00000309428	-1	3_prime_untranslated_region	c.*1939	NULL	tier3	111	5	0.043	82	38	0.317
717045	17	58979988	58979988	G	T	SNP	*BCAS3*	ENST00000390652	1	missense	c.746	p.R249L	tier1	118	0	0.000	75	7	0.085
717045	19	1046259	1046259	C	G	SNP	*ABCA7*	ENST00000263094	1	silent	c.1476	p.P492	tier1	165	2	0.012	118	70	0.368
717045	20	39992390	39992390	C	T	SNP	*EMILIN3*	ENST00000332312	-1	silent	c.402	p.T134	tier1	102	1	0.010	91	74	0.449
717045	20	61444605	61444605	A	G	SNP	*OGFR*	ENST00000290291	1	silent	c.1638	p.P546	tier1	27	0	0.000	30	10	0.250
717045	22	24400302	24400302	G	A	SNP	*GSTTP2*	ENST00000389399	-1	splice_region	c.NULL	NULL	tier3	121	0	0.000	223	21	0.086
732217	1	1896486	1896486	G	A	SNP	*C1orf222*	ENST00000604159	-1	silent	c.171	p.D57	tier1	34	0	0.000	49	39	0.443
732217	1	19549161	19549161	C	T	SNP	*EMC1*	ENST00000486238	-1	missense	c.95	p.R32K	tier1	29	1	0.033	42	39	0.482
732217	1	20518895	20518895	C	T	SNP	*UBXN10*	ENST00000375099	1	3_prime_untranslated_region	c.*998	NULL	tier3	81	0	0.000	97	63	0.389
732217	1	46079781	46079781	A	G	SNP	*NASP*	ENST00000402363	1	missense	c.1526	p.N509S	tier1	82	3	0.035	144	125	0.465
732217	1	237777658	237777658	A	-	DEL	*RYR2*	ENST00000360064	1	frame_shift_del	c.5224	p.K1743fs	tier1	42	2	0.046	55	28	0.337
732217	2	112588927	112588927	C	G	SNP	*ANAPC1*	ENST00000341068	-1	missense	c.2561	p.G854A	tier1	195	8	0.039	400	328	0.451
732217	2	236949476	236949476	G	A	SNP	*AGAP1*	ENST00000304032	1	missense	c.1882	p.E628K	tier1	51	3	0.056	113	51	0.311
732217	4	106164914	106164914	G	A	SNP	*TET2*	ENST00000380013	1	missense	c.3782	p.R1261H	tier1	171	4	0.023	30	571	0.945
732217	4	125593542	125593542	A	G	SNP	*ANKRD50*	ENST00000504087	-1	missense	c.890	p.I297T	tier1	71	3	0.041	7	145	0.954
732217	5	69826356	69826356	G	A	SNP	*ENSG00000250918*	ENST00000509075	1	3_prime_untranslated_region	c.*69826356	NULL	tier3	166	4	0.023	720	87	0.107
732217	5	98109985	98109985	G	A	SNP	*RGMB*	ENST00000308234	1	intronic	c.259+75	e2+75	tier2	7	0	0.000	1	6	0.857
732217	5	171723836	171723836	G	A	SNP	*UBTD2*	ENST00000393792	-1	5_prime_flanking_region	c.-13167	NULL	tier2	73	0	0.000	140	19	0.120
732217	6	150064734	150064734	A	-	DEL	*NUP43*	ENST00000340413	-1	intronic	c.321+40	e3+40	tier4	48	0	0.000	134	26	0.163
732217	7	31378474	31378474	G	A	SNP	*NEUROD6*	ENST00000297142	-1	nonsense	c.409	p.R137*	tier1	121	3	0.024	153	97	0.388
732217	7	42003680	42003680	A	T	SNP	*GLI3*	ENST00000479210	-1	rna	NULL	NULL	tier1	71	1	0.014	251	51	0.168
732217	7	42003681	42003681	A	T	SNP	*GLI3*	ENST00000479210	-1	rna	NULL	NULL	tier1	74	0	0.000	271	25	0.084
732217	7	48545892	48545892	G	A	SNP	*ABCA13*	ENST00000435803	1	intronic	c.13292-40	e49-40	tier3	32	1	0.030	62	38	0.380
732217	7	73475359	73475359	T	C	SNP	*ELN*	ENST00000358929	1	intronic	c.1952-72	e27-72	tier4	46	0	0.000	86	70	0.449
732217	7	142223845	142223845	T	C	SNP	*TRBV11-1*	ENST00000390367	-1	missense	c.322	p.M108V	tier1	47	0	0.000	96	15	0.135
732217	8	52732382	52732382	C	T	SNP	*PCMTD1*	ENST00000360540	-1	3_prime_untranslated_region	c.*529	NULL	tier3	47	0	0.000	141	23	0.139
732217	8	77764819	77764819	C	-	DEL	*ZFHX4*	ENST00000521891	1	frame_shift_del	c.5662	p.Q1888fs	tier1	44	1	0.022	56	47	0.456
732217	8	145255402	145255402	G	A	SNP	*MROH1*	ENST00000326134	1	missense	c.1099	p.V367M	tier1	28	0	0.000	33	34	0.500
732217	9	14788	14788	G	A	SNP	*ENSG00000181404*	ENST00000330546	-1	5_prime_untranslated_region	c.-14788	NULL	tier3	397	8	0.020	655	56	0.078
732217	9	33386977	33386977	G	T	SNP	*AQP7*	ENST00000297988	-1	silent	c.258	p.G86	tier1	304	4	0.013	802	125	0.135
732217	9	130897518	130897518	A	C	SNP	*PTGES2*	ENST00000338961	-1	5_prime_flanking_region	c.-7522	NULL	tier4	139	2	0.014	267	115	0.300
732217	10	102296470	102296470	T	C	SNP	*HIF1AN*	ENST00000299163	1	intronic	c.428+52	e2+52	tier2	21	0	0.000	35	43	0.551
732217	10	119003712	119003712	C	T	SNP	*SLC18A2*	ENST00000298472	1	missense	c.352	p.P118S	tier1	41	2	0.047	44	40	0.476
732217	11	14279305	14279305	G	T	SNP	*SPON1*	ENST00000310358	1	rna	NULL	NULL	tier1	55	2	0.035	80	65	0.445
732217	11	59244984	59244984	T	C	SNP	*OR4D10*	ENST00000530162	1	missense	c.82	p.F28L	tier1	83	0	0.000	123	106	0.461
732217	12	57484814	57484814	G	T	SNP	*NAB2*	ENST00000300131	1	intronic	c.84-94	e2-94	tier2	43	0	0.000	68	47	0.409
732217	12	95926996	95926996	C	T	SNP	*USP44*	ENST00000258499	-1	missense	c.1037	p.C346Y	tier1	68	1	0.015	97	75	0.434
732217	12	102140523	102140523	A	-	DEL	*GNPTAB*	ENST00000299314	-1	3_prime_untranslated_region	c.*419	NULL	tier3	43	0	0.000	176	31	0.150
732217	12	118199039	118199039	G	A	SNP	*KSR2*	ENST00000339824	-1	missense	c.763	p.R255W	tier1	109	5	0.044	171	126	0.424
732217	14	35264956	35264956	G	T	SNP	*BAZ1A*	ENST00000360310	-1	missense	c.1144	p.R382S	tier1	25	1	0.039	38	49	0.557
732217	15	79059795	79059795	G	A	SNP	*ADAMTS7*	ENST00000388820	-1	missense	c.2785	p.R929W	tier1	122	0	0.000	151	117	0.437

732217	17	263412	263412	G	A	SNP	*C17orf97*	ENST00000360127	1	missense	c.778	p.E260K	tier1	322	6	0.018	706	59	0.077
732217	17	15984046	15984047	-	A	INS	*NCOR1*	ENST00000268712	-1	splice_region_ins	c.3178-6_3178-5	e23-5	tier2	271	5	0.018	466	219	0.320
732217	17	72363579	72363579	T	A	SNP	*GPR142*	ENST00000582579	1	5_prime_untranslated_region	c.-66	NULL	tier3	17	0	0.000	39	28	0.418
732217	17	72948180	72948180	C	T	SNP	*HID1*	ENST00000425042	-1	intronic	c.2145-22	e18-22	tier3	33	0	0.000	35	18	0.340
732217	17	74732959	74732959	G	A	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95L	tier1	164	5	0.030	254	232	0.476
732217	19	41557967	41557967	C	T	SNP	*CYP2G2P*	ENST00000594920	-1	5_prime_untranslated_region	c.-41557967	NULL	tier3	96	2	0.020	110	115	0.509
732217	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	553	14	0.025	689	347	0.335
732217	21	36164760	36164761	-	CCAT	INS	*RUNX1*	ENST00000300305	-1	frame_shift_ins	c.1115_1114	p.G372fs	tier1	764	7	0.009	691	414	0.375
732217	21	47976820	47976820	T	-	DEL	*DIP2A*	ENST00000481883	1	3_prime_untranslated_region	c.*47976820	NULL	tier3	56	0	0.000	145	20	0.121
732217	X	106482271	106482271	T	C	SNP	*PIH1D3*	ENST00000336387	1	intronic	c.515+34	e5+34	tier3	40	2	0.048	13	120	0.902
754150	1	10683092	10683092	T	C	SNP	*PEX14*	ENST00000356607	1	missense	c.401	p.L134P	tier1	160	0	0.000	154	22	0.124
754150	1	115401238	115401239	-	A	INS	*SYCP1*	ENST00000369518	1	frame_shift_ins	c.362_363	p.S122fs	tier1	65	0	0.000	98	12	0.109
754150	2	46707812	46707812	G	A	SNP	*TMEM247*	ENST00000434431	1	missense	c.386	p.R129Q	tier1	65	0	0.000	57	8	0.123
754150	2	149793838	149793838	G	A	SNP	*KIF5C*	ENST00000435030	1	missense	c.332	p.R111Q	tier1	52	0	0.000	55	10	0.154
754150	2	208394531	208394531	G	T	SNP	*CREB1*	ENST00000430624	1	5_prime_untranslated_region	c.-25829	NULL	tier2	6	0	0.000	1	5	0.833
754150	2	219221645	219221645	C	G	SNP	*C2orf62*	ENST00000289388	1	intronic	c.25+13	e1+13	tier3	171	0	0.000	119	11	0.085
754150	2	239973727	239973727	T	A	SNP	*HDAC4*	ENST00000345617	-1	3_prime_untranslated_region	c.*1066	NULL	tier3	180	4	0.022	109	73	0.401
754150	3	52012429	52012429	T	A	SNP	*ABHD14A*	ENST00000474575	1	3_prime_untranslated_region	c.*52012429	NULL	tier3	137	1	0.007	104	22	0.175
754150	3	69915190	69915190	G	A	SNP	*MITF*	ENST00000448226	1	intronic	c.105-13095	e2-13095	tier3	82	0	0.000	81	17	0.174
754150	3	182933850	182933850	G	C	SNP	*MCF2L2*	ENST00000328913	-1	missense	c.2403	p.F801L	tier1	130	0	0.000	146	11	0.070
754150	4	4190576	4190576	C	G	SNP	*OTOP1*	ENST00000296358	-1	missense	c.1793	p.R598P	tier1	62	0	0.000	97	14	0.126
754150	4	4190577	4190577	G	C	SNP	*OTOP1*	ENST00000296358	-1	missense	c.1792	p.R598G	tier1	60	0	0.000	96	14	0.127
754150	4	4190595	4190595	G	C	SNP	*OTOP1*	ENST00000296358	-1	missense	c.1774	p.P592A	tier1	63	0	0.000	90	14	0.135
754150	4	9389009	9389009	A	G	SNP	*ENSG00000219492*	ENST00000508324	-1	splice_region	c.13-8	e2-8	tier3	497	13	0.026	243	176	0.419
754150	4	20852133	20852133	G	T	SNP	*KCNIP4*	ENST00000515373	-1	5_prime_untranslated_region	c.-20852133	NULL	tier3	110	4	0.035	57	46	0.447
754150	4	25262265	25262265	C	T	SNP	*PI4K2B*	ENST00000264864	1	intronic	c.978+52	e6+52	tier4	41	1	0.024	54	17	0.239
754150	4	25677760	25677760	G	A	SNP	*SLC34A2*	ENST00000382051	1	missense	c.1462	p.A488T	tier1	54	0	0.000	59	9	0.132
754150	5	26906108	26906108	C	G	SNP	*CDH9*	ENST00000231021	-1	silent	c.771	p.T257	tier1	154	2	0.013	158	37	0.189
754150	5	55168187	55168187	C	T	SNP	*IL31RA*	ENST00000447346	1	missense	c.362	p.T121M	tier1	162	0	0.000	126	89	0.414
754150	5	115177743	115177743	G	C	SNP	*AP3S1*	ENST00000316788	1	missense	c.9	p.K3N	tier1	22	0	0.000	19	11	0.367
754150	5	139941115	139941115	T	C	SNP	*APBB3*	ENST00000356738	-1	intronic	c.762+57	e7+57	tier2	96	3	0.030	48	44	0.478
754150	5	140554370	140554370	C	T	SNP	*PCDHB7*	ENST00000231137	1	missense	c.1954	p.R652C	tier1	829	7	0.008	707	79	0.100
754150	5	178413301	178413301	C	T	SNP	*GRM6*	ENST00000231188	-1	missense	c.1954	p.A652T	tier1	83	3	0.035	65	43	0.398
754150	6	52400654	52400654	A	C	SNP	*TRAM2*	ENST00000182527	-1	splice_region	c.121-10	e2-10	tier2	87	2	0.023	73	58	0.443
754150	7	31127292	31127292	T	C	SNP	*ADCYAP1R1*	ENST00000436116	1	missense	c.85	p.C29R	tier1	108	0	0.000	99	15	0.132
754150	7	42005086	42005086	G	T	SNP	*GLI3*	ENST00000395925	-1	missense	c.3585	p.N1195K	tier1	83	4	0.046	58	42	0.420
754150	7	77584160	77584160	T	-	DEL	*PHTF2*	ENST00000248550	1	intronic	c.2338-15	e19-15	tier3	152	0	0.000	226	23	0.092
754150	11	2443297	2443297	G	A	SNP	*TRPM5*	ENST00000452833	-1	intronic	c.298+74	e2+74	tier3	25	0	0.000	14	6	0.300
754150	11	34192643	34192643	C	T	SNP	*ABTB2*	ENST00000435224	-1	intronic	c.1398-25	e5-25	tier3	71	0	0.000	62	18	0.225
754150	11	48346968	48346968	C	T	SNP	*OR4C3*	ENST00000319856	1	missense	c.476	p.T159I	tier1	85	1	0.012	98	23	0.190
754150	12	19653148	19653148	A	T	SNP	*AEBP2*	ENST00000398864	1	missense	c.1292	p.H431L	tier1	92	0	0.000	75	50	0.400
754150	12	50746672	50746672	A	G	SNP	*FAM186A*	ENST00000327337	-1	missense	c.3943	p.F1315L	tier1	285	4	0.014	283	28	0.090
754150	13	101712169	101712169	C	T	SNP	*NALCN*	ENST00000251127	-1	splice_site	c.4905+1	e41+1	tier1	606	19	0.030	313	251	0.445
754150	14	91467486	91467486	C	T	SNP	*RPS6KA5*	ENST00000261991	-1	missense	c.121	p.A41T	tier1	190	4	0.021	126	88	0.407
754150	15	76576183	76576183	A	-	DEL	*ETFA*	ENST00000557943	-1	intronic	c.665-17	e8-17	tier3	30	0	0.000	23	8	0.258
754150	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	589	12	0.020	280	269	0.490
754150	15	102295647	102295647	C	G	SNP	*DNM1P47*	ENST00000561463	1	rna	NULL	NULL	tier1	37	1	0.026	21	12	0.364
754150	16	12297294	12297294	T	G	SNP	*SNX29*	ENST00000306030	1	intronic	c.523+3754	e6+3754	tier3	572	7	0.012	619	28	0.043
754150	17	2595220	2595233	CCCGTGCCCCCGCG	-	DEL	*CLUH*	ENST00000435359	-1	intronic	c.3538-44_3538-31	e23-31	tier2	28	0	0.000	19	11	0.367
754150	17	74732959	74732959	G	C	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95R	tier1	390	20	0.049	228	138	0.377
754150	19	426497	426497	C	T	SNP	*SHC2*	ENST00000264554	-1	intronic	c.1175-1266	e10-1266	tier4	59	0	0.000	34	6	0.143
754150	19	6906516	6906516	C	T	SNP	*EMR1*	ENST00000312053	1	missense	c.1022	p.A341V	tier1	218	7	0.031	121	133	0.522
754150	19	15654862	15654862	G	A	SNP	*CYP4F22*	ENST00000269703	1	intronic	c.1006+14	e7+14	tier3	148	3	0.020	91	48	0.345
754150	19	41355820	41355820	A	G	SNP	*CYP2A6*	ENST00000301141	-1	silent	c.246	p.C82	tier1	83	0	0.000	83	13	0.135
754150	19	41355828	41355828	C	T	SNP	*CYP2A6*	ENST00000301141	-1	missense	c.238	p.V80M	tier1	78	0	0.000	83	13	0.135
754150	20	3127469	3127469	C	G	SNP	*FASTKD5*	ENST00000380266	-1	missense	c.2248	p.E750Q	tier1	70	3	0.041	33	49	0.598
754150	20	29632749	29632749	A	G	SNP	*FRG1B*	ENST00000278882	1	intronic	c.536+28	e6+28	tier3	262	3	0.011	443	27	0.057
754150	20	29652147	29652147	A	G	SNP	*MLLT10P1*	ENST00000418346	-1	5_prime_flanking_region	c.-14087	NULL	tier4	267	4	0.015	342	27	0.073
754150	20	31022403	31022425	CACCACTGCCATAGAGAGGCGGC	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1888_1910	p.H633fs	tier1	875	7	0.008	481	78	0.140
754150	20	31022417	31022417	A	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1902	p.E635fs	tier1	843	7	0.008	390	45	0.103
754150	20	55967777	55967777	G	C	SNP	*RBM38*	ENST00000356208	1	missense	c.305	p.R102P	tier1	53	3	0.054	47	31	0.397
754150	22	24094823	24094828	ATCCCC	-	DEL	*MMP11*	ENST00000215743	1	5_prime_flanking_region	c.-20235	NULL	tier3	34	1	0.029	30	19	0.388
754150	22	50903351	50903351	C	T	SNP	*SBF1*	ENST00000380817	-1	splice_region	c.1333-5	e13-5	tier2	252	10	0.038	144	107	0.423
754150	X	73064091	73064091	A	G	SNP	*XIST*	ENST00000429829	-1	rna	NULL	NULL	tier1	65	1	0.015	13	67	0.838
754150	X	123505288	123505288	T	C	SNP	*SH2D1A*	ENST00000491950	1	rna	NULL	NULL	tier1	140	6	0.041	22	143	0.867
769516	1	15046	15046	G	A	SNP	*WASH7P*	ENST00000423562	-1	splice_region	c.NULL	NULL	tier3	162	0	0.000	501	44	0.081
769516	1	116947126	116947126	C	G	SNP	*ATP1A1*	ENST00000295598	1	3_prime_untranslated_region	c.*60	NULL	tier3	28	0	0.000	140	41	0.227
769516	1	170927719	170927719	G	T	SNP	*MROH9*	ENST00000367759	1	intronic	c.152+38	e3+38	tier3	26	0	0.000	104	41	0.283
769516	1	200943970	200943970	G	A	SNP	*KIF21B*	ENST00000422435	-1	silent	c.4686	p.S1562	tier1	16	0	0.000	60	42	0.412
769516	2	179499445	179499446	-	AT	INS	*TTN*	ENST00000342992	-1	splice_region_ins	c.34447+4_34447+3	e177+4	tier3	48	0	0.000	260	102	0.282
769516	3	186288815	186288815	A	G	SNP	*DNAJB11*	ENST00000265028	1	intronic	c.68+61	e1+61	tier2	9	0	0.000	24	33	0.579
769516	4	517287	517289	CTT	-	DEL	*PIGG*	ENST00000453061	1	in_frame_del	c.1654_1656	p.L553in_frame_del	tier1	18	0	0.000	74	29	0.282
769516	4	41951461	41951461	T	G	SNP	*TMEM33*	ENST00000325094	1	intronic	c.614+59	e6+59	tier3	27	0	0.000	174	75	0.301
769516	4	74361009	74361009	C	T	SNP	*AFM*	ENST00000505794	1	3_prime_untranslated_region	c.*74361009	NULL	tier3	55	0	0.000	186	65	0.259

769516	4	187541903	187541903	C	T	SNP	*FAT1*	ENST00000441802	-1	missense	c.5837	p.S1946N	tier1	16	0	0.000	92	41	0.308
769516	5	15936967	15936967	C	T	SNP	*FBXL7*	ENST00000504595	1	missense	c.1148	p.A383V	tier1	13	0	0.000	33	30	0.476
769516	5	73168759	73168759	T	A	SNP	*ARHGEF28*	ENST00000545377	1	intronic	c.2567-65	e21-65	tier3	30	0	0.000	99	45	0.313
769516	6	56466430	56466430	A	T	SNP	*DST*	ENST00000370754	-1	silent	c.11259	p.T3753	tier1	78	0	0.000	796	310	0.280
769516	9	100137897	100137897	C	G	SNP	*CCDC180*	ENST00000526038	1	3_prime_untranslated_region	c.*100137897	NULL	tier3	57	0	0.000	405	171	0.297
769516	9	127549340	127549340	C	T	SNP	*OLFML2A*	ENST00000373580	1	silent	c.177	p.D59	tier1	22	0	0.000	133	49	0.269
769516	11	376244	376245	-	A	INS	*B4GALNT4*	ENST00000329962	1	splice_region_ins	c.1197-7_1197-6	e13-6	tier2	38	0	0.000	233	78	0.251
769516	11	68273518	68273518	T	C	SNP	*PPP6R3*	ENST00000393799	1	intronic	c.1-13451	e1-13451	tier3	47	0	0.000	216	37	0.146
769516	12	125478381	125478382	-	CTG	INS	*BRI3BP*	ENST00000341446	1	in_frame_ins	c.45_46	p.19in_frame_insL	tier1	8	0	0.000	7	10	0.588
769516	13	32783001	32783001	C	T	SNP	*FRY*	ENST00000380250	1	nonsense	c.4030	p.R1344*	tier1	28	0	0.000	135	37	0.214
769516	14	59113492	59113492	C	T	SNP	*DACT1*	ENST00000335867	1	silent	c.2151	p.Y717	tier1	30	0	0.000	149	51	0.255
769516	15	40942716	40942716	T	-	DEL	*CASC5*	ENST00000346991	1	intronic	c.6251-26	e19-26	tier3	32	0	0.000	112	34	0.233
769516	16	81208267	81208267	A	C	SNP	*PKD1L2*	ENST00000527937	-1	missense	c.604	p.C202G	tier1	181	0	0.000	693	288	0.293
769516	17	71361450	71361450	T	C	SNP	*SDK2*	ENST00000392650	-1	missense	c.5252	p.N1751S	tier1	26	0	0.000	128	43	0.250
769516	17	74732959	74732959	G	C	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95R	tier1	114	0	0.000	454	183	0.285
769516	18	14361468	14361468	G	A	SNP	*ENSG00000265437*	ENST00000584979	-1	5_prime_untranslated_region	c.-14361468	NULL	tier3	18	0	0.000	107	54	0.335
769516	22	19130308	19130308	G	A	SNP	*DGCR14*	ENST00000252137	-1	missense	c.235	p.R79W	tier1	14	0	0.000	56	31	0.356
783437	1	38488507	38488507	T	-	DEL	*UTP11L*	ENST00000373014	1	intronic	c.678+26	e7+26	tier3	68	0	0.000	114	14	0.109
783437	3	47263926	47263926	T	-	DEL	*KIF9-AS1*	ENST00000429315	1	intronic	c.NULL	NULL	tier4	75	1	0.013	124	19	0.133
783437	3	50137714	50137714	T	-	DEL	*RBM5*	ENST00000469838	1	3_prime_untranslated_region	c.*207	NULL	tier3	82	1	0.012	107	15	0.123
783437	6	31498127	31498127	T	G	SNP	*DDX39B*	ENST00000462421	-1	rna	NULL	NULL	tier1	125	1	0.008	159	20	0.107
783437	6	102516350	102516350	C	T	SNP	*GRIK2*	ENST00000421544	1	silent	c.2691	p.N897	tier1	791	2	0.003	1072	40	0.036
783437	7	95818865	95818865	A	-	DEL	*SLC25A13*	ENST00000416240	-1	intronic	c.848+28	e8+28	tier3	65	0	0.000	113	17	0.131
783437	8	143369132	143369132	G	C	SNP	*TSNARE1*	ENST00000307180	-1	intronic	c.1291-3286	e10-3286	tier3	585	4	0.007	869	28	0.031
783437	9	131104965	131104965	T	-	DEL	*TMSB4XP4*	ENST00000323496	1	3_prime_untranslated_region	c.*131104965	NULL	tier3	122	1	0.008	123	12	0.089
783437	16	85689387	85689387	A	C	SNP	*GSE1*	ENST00000253458	1	missense	c.853	p.T285P	tier1	146	3	0.020	174	26	0.129
783437	17	76001145	76001145	G	T	SNP	*TNRC6C*	ENST00000335749	1	5_prime_untranslated_region	c.-43999	NULL	tier3	266	2	0.007	626	34	0.051
783437	21	46927371	46927412	GGGAGGGCCAGGTGCTGGGGCGGGAGAGTCGGGTGCTGGGCA	-	DEL	*COL18A1*	ENST00000473212	1	3_prime_untranslated_region	c.*46927371	NULL	tier3	58	1	0.017	74	16	0.178
796518	1	55611693	55611693	C	T	SNP	*USP24*	ENST00000407756	-1	silent	c.1860	p.E620	tier1	30	1	0.032	95	48	0.336
796518	2	98846643	98846643	G	A	SNP	*VWA3B*	ENST00000477737	1	missense	c.2281	p.V761I	tier1	77	1	0.013	161	36	0.181
796518	2	171379066	171379066	T	C	SNP	*MYO3B*	ENST00000334231	1	intronic	c.3602+3016	e30+3016	tier3	50	0	0.000	101	48	0.322
796518	2	179346878	179346878	G	A	SNP	*PLEKHA3*	ENST00000234453	1	intronic	c.40+1242	e1+1242	tier3	26	0	0.000	98	38	0.279
796518	2	198266834	198266834	T	C	SNP	*SF3B1*	ENST00000335508	-1	missense	c.2098	p.K700E	tier1	239	0	0.000	664	39	0.056
796518	2	198267483	198267483	C	A	SNP	*SF3B1*	ENST00000335508	-1	missense	c.1874	p.R625L	tier1	485	1	0.002	1322	59	0.043
796518	4	151682922	151682922	T	C	SNP	*LRBA*	ENST00000357115	-1	intronic	c.5645+13	e34+13	tier4	126	0	0.000	649	54	0.077
796518	4	155254236	155254236	C	T	SNP	*DCHS2*	ENST00000357232	-1	missense	c.1627	p.G543S	tier1	334	0	0.000	514	239	0.317
796518	5	140202971	140202971	C	T	SNP	*PCDHA5*	ENST00000529859	1	silent	c.1611	p.R537	tier1	316	0	0.000	556	262	0.320
796518	6	170591580	170591580	G	A	SNP	*DLL1*	ENST00000366756	-1	3_prime_untranslated_region	c.*382	NULL	tier3	38	0	0.000	68	29	0.299
796518	7	28319235	28319235	C	G	SNP	*ENSG00000174495*	ENST00000445031	-1	5_prime_untranslated_region	c.-28319235	NULL	tier3	42	0	0.000	60	32	0.344
796518	11	55035844	55035844	T	C	SNP	*TRIM48*	ENST00000417545	1	missense	c.574	p.Y192H	tier1	46	2	0.042	0	15	1.000
796518	11	55035854	55035854	T	A	SNP	*TRIM48*	ENST00000417545	1	splice_region	c.578+6	e4+6	tier3	46	2	0.042	0	13	1.000
796518	11	55035855	55035855	A	G	SNP	*TRIM48*	ENST00000417545	1	splice_region	c.578+7	e4+7	tier3	45	2	0.042	0	12	1.000
796518	12	48179692	48179692	G	T	SNP	*ENSG00000268069*	ENST00000599515	1	3_prime_untranslated_region	c.*353	NULL	tier3	30	0	0.000	61	28	0.315
796518	13	101733940	101733940	G	A	SNP	*NALCN*	ENST00000251127	-1	nonsense	c.3823	p.R1275*	tier1	299	1	0.003	722	44	0.057
796518	14	106788772	106788772	G	A	SNP	*IGHV2-26*	ENST00000390611	-1	5_prime_flanking_region	c.-30680	NULL	tier3	22	0	0.000	47	17	0.266
796518	14	106788774	106788774	T	C	SNP	*IGHV2-26*	ENST00000390611	-1	5_prime_flanking_region	c.-30682	NULL	tier3	21	0	0.000	46	16	0.258
796518	15	32929534	32929534	C	A	SNP	*ARHGAP11A*	ENST00000361627	1	missense	c.2560	p.Q854K	tier1	92	0	0.000	181	78	0.301
796518	16	56919177	56919177	A	G	SNP	*SLC12A3*	ENST00000438926	1	missense	c.1826	p.E609G	tier1	370	0	0.000	581	264	0.312
796518	17	986858	986858	G	A	SNP	*ABR*	ENST00000302538	-1	missense	c.541	p.L181F	tier1	39	0	0.000	44	22	0.328
796518	17	51900882	51900882	G	A	SNP	*KIF2B*	ENST00000268919	1	missense	c.488	p.R163H	tier1	535	0	0.000	794	370	0.318
796518	18	47383269	47383269	A	G	SNP	*MYO5B*	ENST00000285039	-1	splice_region	c.3945-9	e30-9	tier3	243	0	0.000	461	194	0.295
796518	20	31877714	31877714	T	C	SNP	*BPIFB1*	ENST00000253354	1	missense	c.281	p.I94T	tier1	38	0	0.000	89	27	0.231
818831	1	75107026	75107026	G	A	SNP	*C1orf173*	ENST00000326665	-1	missense	c.433	p.P145S	tier1	70	0	0.000	166	37	0.182
818831	1	181706695	181706695	C	T	SNP	*CACNA1E*	ENST00000367573	1	missense	c.3457	p.R1153C	tier1	411	1	0.002	799	24	0.029
818831	2	92031582	92031582	G	A	SNP	*ABCD1P5*	ENST00000445663	1	3_prime_untranslated_region	c.*92031582	NULL	tier3	80	1	0.012	164	38	0.186
818831	2	101666881	101666881	G	A	SNP	*TBC1D8*	ENST00000409318	-1	missense	c.854	p.P285L	tier1	41	0	0.000	74	16	0.176
818831	4	175220362	175220362	G	A	SNP	*CEP44*	ENST00000426172	1	splice_site	c.89+1	e1+1	tier1	41	0	0.000	65	15	0.188
818831	4	185612642	185612642	T	A	SNP	*PRIMPOL*	ENST00000512658	1	3_prime_untranslated_region	c.*185612642	NULL	tier3	56	1	0.018	190	46	0.195
818831	5	112926812	112926812	C	A	SNP	*YTHDC2*	ENST00000161863	1	missense	c.3900	p.N1300K	tier1	72	0	0.000	138	19	0.120
818831	6	168314069	168314069	C	G	SNP	*MLLT4*	ENST00000366806	1	intronic	c.2038-779	e16-779	tier2	55	1	0.018	73	28	0.277
818831	7	74212011	74212011	C	T	SNP	*GTF2IRD2*	ENST00000405086	-1	missense	c.1840	p.V614I	tier1	99	1	0.010	195	29	0.130
818831	7	100350095	100350095	T	C	SNP	*ZAN*	ENST00000546292	1	silent	c.2367	p.I789	tier1	124	2	0.016	243	29	0.106
818831	12	133050449	133050450	-	T	INS	*MUC8*	ENST00000595994	-1	intronic	c.147+130_147+129	e1+130	tier2	6	0	0.000	1	5	0.833
818831	14	102445717	102445717	C	A	SNP	*DYNC1H1*	ENST00000360184	1	silent	c.406	p.R136	tier1	72	0	0.000	175	23	0.116
818831	15	74363428	74363428	C	T	SNP	*GOLGA6A*	ENST00000290438	-1	intronic	c.1954+37	e17+37	tier3	310	0	0.000	580	28	0.046
818831	15	89856067	89856067	T	A	SNP	*FANCI*	ENST00000310775	1	intronic	c.3652-68	e34-68	tier3	52	0	0.000	74	12	0.140
818831	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	453	4	0.009	780	128	0.141
818831	17	18334137	18334137	A	G	SNP	*KRT17P2*	ENST00000581146	1	intronic	c.NULL	NULL	tier3	58	1	0.016	140	26	0.148
818831	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	676	10	0.015	1086	150	0.121
818831	20	33577635	33577635	G	A	SNP	*MYH7B*	ENST00000262873	1	silent	c.1806	p.A602	tier1	87	0	0.000	118	27	0.186
818831	X	123215376	123215377	-	A	INS	*STAG2*	ENST00000218089	1	frame_shift_ins	c.2922_2923	p.D975fs	tier1	183	0	0.000	401	130	0.245
819544	1	1747229	1747229	T	C	SNP	*GNB1*	ENST00000378609	-1	missense	c.169	p.K57E	tier1	320	0	0.000	946	30	0.031
819544	2	141143461	141143461	C	T	SNP	*LRP1B*	ENST00000389484	-1	splice_site	c.10531+1	e67+1	tier1	311	0	0.000	766	29	0.036

819544	2	236480647	236480647	C	T	SNP	*ENSG00000221704*	ENST00000408777	1	rna	NULL	NULL	tier1	69	0	0.000	186	20	0.097
819544	5	41312207	41312207	A	T	SNP	*PLCXD3*	ENST00000328457	-1	3_prime_untranslated_region	c.*1512	NULL	tier3	100	1	0.010	261	32	0.109
819544	5	176940748	176940748	C	G	SNP	*DDX41*	ENST00000507955	-1	missense	c.1036	p.A346P	tier1	315	0	0.000	593	28	0.045
819544	6	130504496	130504496	G	A	SNP	*SAMD3*	ENST00000524930	-1	3_prime_untranslated_region	c.*31139	NULL	tier4	33	0	0.000	95	26	0.213
819544	8	110457215	110457215	A	G	SNP	*PKHD1L1*	ENST00000378402	1	missense	c.5117	p.N1706S	tier1	500	1	0.002	1136	34	0.029
819544	12	50037698	50037698	G	T	SNP	*PRPF40B*	ENST00000548825	1	nonsense	c.2497	p.E833*	tier1	498	0	0.000	1072	29	0.026
819544	15	90229787	90229787	A	-	DEL	*PEX11A*	ENST00000300056	-1	splice_region_del	c.57-10	e2-10	tier3	45	0	0.000	69	12	0.148
819544	17	30321557	30321557	T	-	DEL	*SUZ12*	ENST00000578106	1	3_prime_untranslated_region	c.*30321557	NULL	tier3	181	4	0.022	496	58	0.105
819544	17	36358189	36358189	G	T	SNP	*LOC101929950*	ENST00000312412	-1	intronic	c.947-31	e8-31	tier4	197	2	0.010	604	42	0.065
829970	1	151238730	151238730	G	T	SNP	*PSMD4*	ENST00000476855	1	3_prime_untranslated_region	c.*151238730	NULL	tier3	23	0	0.000	145	116	0.441
829970	2	1665807	1665807	T	C	SNP	*PXDN*	ENST00000252804	-1	intronic	c.1680+37	e13+37	tier2	20	0	0.000	172	124	0.418
829970	2	21238083	21238083	G	A	SNP	*APOB*	ENST00000233242	-1	silent	c.3558	p.T1186	tier1	222	0	0.000	361	277	0.434
829970	2	95944840	95944840	G	T	SNP	*PROM2*	ENST00000317620	1	nonsense	c.1222	p.E408*	tier1	13	0	0.000	114	81	0.415
829970	2	105442572	105442572	C	G	SNP	*LOC100506421*	ENST00000413121	-1	intronic	c.NULL	NULL	tier3	66	0	0.000	132	126	0.487
829970	3	38151817	38151817	G	C	SNP	*DLEC1*	ENST00000346219	1	intronic	c.3443+45	e23+45	tier3	38	0	0.000	123	92	0.426
829970	3	56766462	56766462	A	G	SNP	*ARHGEF3*	ENST00000338458	-1	splice_region	c.1138-10	e11-10	tier3	87	0	0.000	161	131	0.447
829970	3	101477008	101477008	A	T	SNP	*CEP97*	ENST00000327230	1	missense	c.1558	p.N520Y	tier1	60	0	0.000	79	83	0.512
829970	3	180320681	180320685	AAGAG	-	DEL	*TTC14*	ENST00000296015	1	frame_shift_del	c.164_168	p.K57fs	tier1	109	0	0.000	181	91	0.335
829970	3	182910694	182910694	G	C	SNP	*MCF2L2*	ENST00000488149	-1	5_prime_untranslated_region	c.-182910694	NULL	tier3	26	0	0.000	91	86	0.486
829970	4	5857824	5857824	A	T	SNP	*CRMP1*	ENST00000324989	-1	intronic	c.820+46	e4+46	tier3	42	0	0.000	88	86	0.494
829970	4	15839802	15839802	T	A	SNP	*CD38*	ENST00000226279	1	intronic	c.659+14	e5+14	tier3	107	0	0.000	105	82	0.439
829970	4	70255405	70255405	C	A	SNP	*ENSG00000215110*	ENST00000511504	1	3_prime_untranslated_region	c.*70255405	NULL	tier3	173	0	0.000	298	219	0.423
829970	5	7303612	7303612	G	A	SNP	*LOC442132*	ENST00000512854	-1	intronic	c.NULL	NULL	tier3	61	0	0.000	259	193	0.427
829970	5	149439406	149439406	C	T	SNP	*CSF1R*	ENST00000286301	-1	silent	c.1989	p.T663	tier1	57	0	0.000	26	214	0.892
829970	6	66803321	66803321	C	T	SNP	*NUFIP1P*	ENST00000402902	-1	3_prime_flanking_region	c.*3	NULL	tier3	211	0	0.000	346	65	0.158
829970	6	125231919	125231919	T	G	SNP	*STL*	ENST00000439075	-1	5_prime_untranslated_region	c.-125231919	NULL	tier3	234	0	0.000	498	20	0.039
829970	7	128292569	128292569	C	T	SNP	*FAM71F2*	ENST00000480462	1	5_prime_flanking_region	c.-19883	NULL	tier3	11	0	0.000	3	21	0.840
829970	7	138126219	138126219	C	T	SNP	*ENSG00000214815*	ENST00000399037	1	3_prime_untranslated_region	c.*138126219	NULL	tier2	54	1	0.018	211	44	0.173
829970	8	73125567	73125567	A	-	DEL	*ENSG00000250979*	ENST00000503430	-1	5_prime_untranslated_region	c.-73125567	NULL	tier2	148	0	0.000	381	150	0.283
829970	8	73125568	73125568	C	T	SNP	*ENSG00000250979*	ENST00000503430	-1	5_prime_untranslated_region	c.-73125568	NULL	tier2	147	1	0.007	361	164	0.311
829970	9	100122246	100122246	C	-	DEL	*C9orf174*	ENST00000375202	1	intronic	c.3496-18	e26-18	tier3	155	0	0.000	417	285	0.406
829970	10	82279156	82279156	A	G	SNP	*TSPAN14*	ENST00000429989	1	3_prime_untranslated_region	c.*1424	NULL	tier3	72	0	0.000	136	137	0.502
829970	10	127477858	127477858	G	T	SNP	*UROS*	ENST00000465577	-1	5_prime_untranslated_region	c.-127477858	NULL	tier3	30	0	0.000	111	116	0.511
829970	11	49897871	49897871	C	T	SNP	*ENSG00000255190*	ENST00000529746	1	3_prime_untranslated_region	c.*49897871	NULL	tier3	323	0	0.000	538	414	0.434
829970	12	5603366	5603366	C	A	SNP	*NTF3*	ENST00000423158	1	missense	c.25	p.Q9K	tier1	36	0	0.000	68	57	0.456
829970	12	18760087	18760087	T	G	SNP	*PIK3C2G*	ENST00000538779	1	intronic	c.4088-2382	e30-2382	tier2	88	0	0.000	191	33	0.147
829970	12	27919782	27919782	C	A	SNP	*MANSC4*	ENST00000381273	-1	intronic	c.230-50	e2-50	tier2	58	0	0.000	125	99	0.440
829970	13	99446895	99446895	C	T	SNP	*DOCK9*	ENST00000400228	-1	missense	c.1993	p.V665I	tier1	60	0	0.000	104	119	0.531
829970	14	60577741	60577741	A	G	SNP	*C14orf135*	ENST00000391611	1	3_prime_untranslated_region	c.*2692	NULL	tier4	45	0	0.000	82	81	0.494
829970	14	90650882	90650882	A	C	SNP	*KCNK13*	ENST00000282146	1	missense	c.762	p.Q254H	tier1	99	1	0.010	755	120	0.137
829970	15	24926165	24926165	A	T	SNP	*C15orf2*	ENST00000329468	1	3_prime_untranslated_region	c.*1680	NULL	tier4	49	0	0.000	74	48	0.393
829970	15	58007312	58007312	A	T	SNP	*POLR2M*	ENST00000299638	1	3_prime_untranslated_region	c.*435	NULL	tier3	87	0	0.000	190	31	0.140
829970	16	72829450	72829450	A	G	SNP	*ZFHX3*	ENST00000268489	-1	silent	c.7131	p.P2377	tier1	28	0	0.000	105	91	0.464
829970	17	263645	263645	C	T	SNP	*C17orf97*	ENST00000360127	1	silent	c.1011	p.P337	tier1	129	2	0.015	447	82	0.154
829970	17	7577094	7577094	G	A	SNP	*TP53*	ENST00000269305	-1	missense	c.844	p.R282W	tier1	117	1	0.008	116	696	0.857
829970	17	61995243	61995243	C	T	SNP	*GH1*	ENST00000323322	-1	silent	c.333	p.S111	tier1	39	0	0.000	213	212	0.499
829970	19	17763404	17763404	A	T	SNP	*UNC13A*	ENST00000428389	-1	intronic	c.1703+36	e13+36	tier3	38	0	0.000	83	70	0.458
829970	19	18378165	18378165	T	G	SNP	*KIAA1683*	ENST00000392413	-1	missense	c.185	p.K62T	tier1	106	0	0.000	751	111	0.129
829970	19	39214520	39214520	G	C	SNP	*ACTN4*	ENST00000252699	1	intronic	c.1552-57	e14-57	tier3	36	0	0.000	174	127	0.421
829970	19	53793213	53793213	A	T	SNP	*BIRC8*	ENST00000426466	-1	missense	c.415	p.S139T	tier1	64	0	0.000	87	69	0.442
829970	20	30785389	30785389	G	C	SNP	*PLAGL2*	ENST00000246229	-1	silent	c.357	p.T119	tier1	16	0	0.000	125	82	0.394
829970	21	31655211	31655211	C	G	SNP	*KRTAP24-1*	ENST00000340345	-1	missense	c.40	p.V14L	tier1	32	0	0.000	58	41	0.414
829970	21	42694456	42694456	G	A	SNP	*FAM3B*	ENST00000357985	1	intronic	c.20-394	e2-394	tier4	57	0	0.000	121	106	0.465
829970	21	45877697	45877697	G	A	SNP	*LRRC3*	ENST00000291592	1	3_prime_untranslated_region	c.*396	NULL	tier3	23	0	0.000	83	80	0.491
829970	22	33255649	33255649	T	C	SNP	*TIMP3*	ENST00000266085	1	3_prime_untranslated_region	c.*285	NULL	tier3	196	0	0.000	220	112	0.337
839903	1	82436028	82436028	C	T	SNP	*LPHN2*	ENST00000370717	1	missense	c.2752	p.H918Y	tier1	90	0	0.000	85	67	0.441
839903	1	115258747	115258747	C	T	SNP	*NRAS*	ENST00000369535	-1	missense	c.35	p.G12D	tier1	390	1	0.003	588	83	0.124
839903	1	144619315	144619315	G	T	SNP	*ENSG00000225241*	ENST00000421407	1	intronic	c.NULL	NULL	tier3	190	1	0.005	286	67	0.190
839903	1	177927426	177927426	C	T	SNP	*SEC16B*	ENST00000527976	-1	missense	c.136	p.A46T	tier1	72	0	0.000	43	40	0.482
839903	1	222705451	222705451	C	A	SNP	*HHIPL2*	ENST00000343410	-1	missense	c.1580	p.R527L	tier1	57	1	0.017	35	45	0.563
839903	1	223568401	223568401	G	A	SNP	*C1orf65*	ENST00000366875	1	silent	c.1584	p.K528	tier1	44	0	0.000	43	39	0.476
839903	2	26677567	26677567	G	T	SNP	*DRC1*	ENST00000288710	1	missense	c.1972	p.D658Y	tier1	74	0	0.000	42	48	0.533
839903	2	44203321	44203321	G	A	SNP	*LRPPRC*	ENST00000260665	-1	missense	c.698	p.A233V	tier1	44	0	0.000	110	23	0.172
839903	2	97784048	97784048	G	A	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.313-33	e3-33	tier3	205	3	0.014	322	25	0.072
839903	2	97817745	97817745	G	T	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.1162+69	e13+69	tier4	29	0	0.000	56	14	0.200
839903	2	187367384	187367384	G	A	SNP	*ZC3H15*	ENST00000337859	1	intronic	c.534+70	e5+70	tier3	53	0	0.000	100	41	0.289
839903	3	16217151	16217151	G	T	SNP	*GALNT15*	ENST00000339732	1	missense	c.493	p.A165S	tier1	104	0	0.000	69	45	0.395
839903	3	57447266	57447266	G	A	SNP	*DNAH12*	ENST00000351747	-1	nonsense	c.2617	p.Q873*	tier1	49	0	0.000	93	70	0.429
839903	3	78680237	78680237	A	G	SNP	*ROBO1*	ENST00000464233	-1	intronic	c.3626+74	e24+74	tier3	73	0	0.000	110	12	0.098
839903	3	130317212	130317212	G	C	SNP	*COL6A6*	ENST00000358511	1	missense	c.4537	p.A1513P	tier1	100	0	0.000	117	87	0.424
839903	3	188242334	188242334	A	-	DEL	*LPP*	ENST00000312675	1	intronic	c.307-119	e3-119	tier4	115	1	0.009	212	19	0.082
839903	4	145050305	145050305	T	A	SNP	*GYPA*	ENST00000360771	-1	intronic	c.38-8564	e2-8564	tier3	239	0	0.000	261	202	0.436
839903	5	101726657	101726657	G	A	SNP	*SLCO6A1*	ENST00000379807	-1	intronic	c.1879+28	e11+28	tier3	55	0	0.000	73	58	0.443
839903	5	131326603	131326603	A	G	SNP	*ACSL6*	ENST00000296869	-1	missense	c.328	p.Y110H	tier1	295	0	0.000	198	162	0.449

839903	5	140203552	140203552	G	T	SNP	*PCDHA5*	ENST00000529859	1	missense	c.2192	p.C731F	tier1	267	2	0.007	237	208	0.466
839903	6	30229312	30229312	G	T	SNP	*HCG17*	ENST00000453558	-1	intronic	c.NULL	NULL	tier3	127	0	0.000	82	67	0.450
839903	7	151082221	151082221	G	A	SNP	*WDR86*	ENST00000334493	-1	missense	c.815	p.T272M	tier1	66	0	0.000	84	16	0.160
839903	8	1649371	1649371	G	A	SNP	*DLGAP2*	ENST00000520901	1	missense	c.2735	p.R912H	tier1	182	0	0.000	118	108	0.478
839903	8	65496059	65496059	C	T	SNP	*BHLHE22*	ENST00000321870	1	3_prime_untranslated_region	c.*1566	NULL	tier2	106	0	0.000	156	35	0.182
839903	9	32624147	32624147	T	A	SNP	*ENSG00000223440*	ENST00000430787	1	5_prime_flanking_region	c.-9305	NULL	tier4	55	0	0.000	66	90	0.577
839903	10	5494360	5494360	G	A	SNP	*NET1*	ENST00000355029	1	missense	c.403	p.A135T	tier1	100	2	0.020	73	54	0.425
839903	10	49220302	49220302	G	A	SNP	*CTGLF12P*	ENST00000339771	-1	5_prime_untranslated_region	c.-49220302	NULL	tier3	56	0	0.000	99	53	0.349
839903	10	90582658	90582658	G	A	SNP	*ANKRD22*	ENST00000476963	-1	rna	NULL	NULL	tier1	96	0	0.000	96	79	0.451
839903	10	112356174	112356174	G	C	SNP	*SMC3*	ENST00000361804	1	missense	c.1982	p.R661P	tier1	392	1	0.003	687	160	0.189
839903	10	117486773	117486773	C	T	SNP	*ATRNL1*	ENST00000355044	1	nonsense	c.3811	p.R1271*	tier1	165	0	0.000	177	12	0.064
839903	10	131634749	131634749	C	T	SNP	*EBF3*	ENST00000368648	-1	3_prime_untranslated_region	c.*1444	NULL	tier3	345	0	0.000	314	86	0.215
839903	11	1083328	1083328	C	A	SNP	*MUC2*	ENST00000441003	1	splice_region	c.2219+9	e16+9	tier2	60	0	0.000	77	38	0.330
839903	11	46334349	46334349	C	T	SNP	*CREB3L1*	ENST00000288400	1	intronic	c.963-53	e8-53	tier3	52	0	0.000	49	37	0.430
839903	11	55322753	55322753	C	T	SNP	*OR4C15*	ENST00000314644	1	missense	c.971	p.A324V	tier1	57	0	0.000	134	38	0.221
839903	11	63997883	63997883	T	-	DEL	*DNAJC4*	ENST00000321685	1	intronic	c.1-21	e1-21	tier2	17	0	0.000	21	11	0.344
839903	11	107219570	107219570	T	G	SNP	*CWF19L2*	ENST00000462890	-1	5_prime_untranslated_region	c.-107219570	NULL	tier3	79	0	0.000	85	71	0.455
839903	12	43945607	43945607	G	T	SNP	*ADAMTS20*	ENST00000389420	-1	intronic	c.91+27	e1+27	tier2	134	0	0.000	86	63	0.417
839903	12	48360948	48360948	A	-	DEL	*TMEM106C*	ENST00000429772	1	intronic	c.603-43	e6-43	tier3	57	0	0.000	56	9	0.139
839903	12	49725038	49725038	C	T	SNP	*TROAP*	ENST00000257909	1	missense	c.2140	p.R714C	tier1	74	0	0.000	73	67	0.479
839903	13	36401953	36401953	T	G	SNP	*DCLK1*	ENST00000360631	-1	intronic	c.1288-62	e9-62	tier3	208	0	0.000	201	164	0.448
839903	14	76211445	76211445	G	A	SNP	*TTLL5*	ENST00000298832	1	missense	c.1289	p.R430H	tier1	124	1	0.008	190	20	0.095
839903	14	106135124	106135124	C	T	SNP	*IGHGP*	ENST00000390555	-1	5_prime_untranslated_region	c.-106135124	NULL	tier3	170	0	0.000	272	32	0.105
839903	15	57999148	57999148	C	T	SNP	*POLR2M*	ENST00000299638	1	silent	c.108	p.R36	tier1	113	0	0.000	134	21	0.136
839903	16	29851667	29851667	C	T	SNP	*MVP*	ENST00000357402	1	missense	c.1078	p.R360C	tier1	31	1	0.031	48	41	0.461
839903	16	30722141	30722141	G	T	SNP	*SRCAP*	ENST00000262518	1	nonsense	c.1201	p.E401*	tier1	56	0	0.000	39	36	0.480
839903	16	87160454	87160454	A	G	SNP	*C16orf95*	ENST00000562840	-1	intronic	c.NULL	NULL	tier3	77	0	0.000	104	21	0.168
839903	17	7010496	7010496	G	T	SNP	*ASGR2*	ENST00000355035	-1	intronic	c.512-26	e6-26	tier3	58	1	0.017	60	71	0.542
839903	17	39041424	39041424	C	T	SNP	*KRT20*	ENST00000167588	-1	missense	c.14	p.R5H	tier1	82	2	0.024	68	69	0.504
839903	18	21452994	21452994	C	T	SNP	*LAMA3*	ENST00000269217	1	5_prime_untranslated_region	c.-15	NULL	tier3	50	0	0.000	48	41	0.461
839903	19	13136234	13136234	G	T	SNP	*NFIX*	ENST00000585575	1	nonsense	c.403	p.E135*	tier1	114	0	0.000	143	44	0.233
839903	19	42219296	42219296	G	A	SNP	*CEACAM5*	ENST00000596606	1	3_prime_untranslated_region	c.*42219296	NULL	tier3	42	0	0.000	24	26	0.520
839903	20	16349047	16349047	C	G	SNP	*KIF16B*	ENST00000408042	-1	intronic	c.3499-576	e23-576	tier3	139	0	0.000	77	70	0.470
839903	X	48926088	48926088	C	T	SNP	*CCDC120*	ENST00000603986	1	missense	c.1985	p.A662V	tier1	96	2	0.020	67	53	0.442
839903	X	77222318	77222318	C	T	SNP	*ATP7A*	ENST00000341514	1	intronic	c.1-4800	e1-4800	tier4	38	0	0.000	49	32	0.395
839903	X	153631127	153631127	G	A	SNP	*DNASE1L1*	ENST00000014935	-1	missense	c.830	p.A277V	tier1	158	0	0.000	316	17	0.051
848524	1	99164247	99164247	T	-	DEL	*SNX7*	ENST00000306121	1	intronic	c.839-15	e6-15	tier3	46	0	0.000	93	15	0.139
848524	1	150432709	150432709	T	C	SNP	*RPRD2*	ENST00000369068	1	silent	c.1327	p.L443	tier1	59	0	0.000	82	12	0.128
848524	1	155580877	155580877	C	T	SNP	*MSTO1*	ENST00000245564	1	nonsense	c.268	p.Q90*	tier1	18	0	0.000	20	16	0.444
848524	1	168161365	168161365	C	T	SNP	*TIPRL*	ENST00000367833	1	intronic	c.516+627	e4+627	tier3	55	3	0.052	70	53	0.427
848524	1	177898245	177898245	A	-	DEL	*ENSG00000254154*	ENST00000354921	-1	rna	NULL	NULL	tier1	81	2	0.024	76	43	0.361
848524	1	243419492	243419492	A	G	SNP	*SDCCAG8*	ENST00000366541	1	missense	c.17	p.E6G	tier1	98	0	0.000	106	87	0.451
848524	2	237103618	237103618	C	T	SNP	*ASB18*	ENST00000409749	-1	missense	c.1298	p.R433H	tier1	55	2	0.035	46	50	0.521
848524	3	50138116	50138116	G	A	SNP	*RBM5*	ENST00000469838	1	3_prime_untranslated_region	c.*609	NULL	tier3	52	0	0.000	62	47	0.431
848524	3	57611690	57611690	A	G	SNP	*DENND6A*	ENST00000311128	-1	3_prime_untranslated_region	c.*2251	NULL	tier2	116	2	0.017	236	196	0.454
848524	4	1803182	1803182	C	A	SNP	*FGFR3*	ENST00000340107	1	silent	c.534	p.A178	tier1	19	0	0.000	19	24	0.558
848524	4	8234226	8234226	G	A	SNP	*SH3TC1*	ENST00000502350	1	3_prime_untranslated_region	c.*8234226	NULL	tier2	57	2	0.034	58	46	0.442
848524	4	54324769	54324769	T	C	SNP	*FIP1L1*	ENST00000507206	1	3_prime_untranslated_region	c.*54324769	NULL	tier3	35	1	0.028	57	46	0.447
848524	4	67142574	67142574	T	A	SNP	*MIR1269A*	ENST00000408636	1	rna	NULL	NULL	tier1	65	0	0.000	61	39	0.390
848524	4	165187407	165187407	T	C	SNP	*01.Mär*	ENST00000503008	-1	intronic	c.1+116932	e0+116932	tier4	232	3	0.013	318	108	0.254
848524	5	80064748	80064748	C	G	SNP	*MSH3*	ENST00000265081	1	missense	c.2179	p.R727G	tier1	161	0	0.000	280	29	0.094
848524	5	87502321	87502321	G	-	DEL	*TMEM161B*	ENST00000296595	-1	splice_region_del	c.599-5	e7-5	tier3	168	2	0.012	315	25	0.074
848524	5	140221091	140221091	G	T	SNP	*PCDHA8*	ENST00000531613	1	missense	c.185	p.R62L	tier1	548	12	0.021	577	361	0.384
848524	5	176016454	176016454	C	A	SNP	*CDHR2*	ENST00000508085	1	3_prime_untranslated_region	c.*176016454	NULL	tier3	47	1	0.021	42	43	0.506
848524	6	88757740	88757740	C	T	SNP	*SPACA1*	ENST00000237201	1	silent	c.117	p.A39	tier1	51	2	0.038	45	37	0.451
848524	7	27210530	27210530	G	A	SNP	*HOXA10*	ENST00000283921	-1	3_prime_untranslated_region	c.*988	NULL	tier2	244	1	0.004	269	15	0.053
848524	7	53103572	53103572	C	T	SNP	*POM121L12*	ENST00000408890	1	missense	c.208	p.R70C	tier1	11	0	0.000	9	15	0.625
848524	7	142353940	142353941	TG	-	DEL	*TRBV23-1*	ENST00000390396	1	frame_shift_del	c.323_324	p.Y109fs	tier1	62	1	0.016	36	46	0.561
848524	8	11189142	11189142	G	A	SNP	*SLC35G5*	ENST00000382435	1	missense	c.527	p.G176E	tier1	110	1	0.009	128	14	0.099
848524	8	51449330	51449330	G	A	SNP	*SNTG1*	ENST00000518864	1	silent	c.642	p.S214	tier1	50	0	0.000	34	40	0.541
848524	8	92982935	92982935	G	A	SNP	*RUNX1T1*	ENST00000436581	-1	missense	c.1523	p.A508V	tier1	437	13	0.029	449	398	0.469
848524	8	144800290	144800290	C	G	SNP	*MAPK15*	ENST00000475376	1	3_prime_untranslated_region	c.*144800290	NULL	tier3	79	2	0.025	58	48	0.453
848524	9	98242628	98242628	T	C	SNP	*PTCH1*	ENST00000331920	-1	intronic	c.945+44	e6+44	tier3	409	6	0.014	628	102	0.140
848524	10	75560546	75560546	C	-	DEL	*ZSWIM8*	ENST00000603195	1	rna	NULL	NULL	tier1	124	2	0.016	182	20	0.099
848524	11	69631012	69631012	C	A	SNP	*FGF3*	ENST00000334134	-1	intronic	c.324+76	e2+76	tier3	29	1	0.033	25	28	0.528
848524	11	78601098	78601098	G	A	SNP	*TENM4*	ENST00000278550	-1	intronic	c.849-33	e5-33	tier3	49	0	0.000	17	27	0.614
848524	11	102395831	102395832	-	T	INS	*MMP7*	ENST00000260227	-1	intronic	c.485-37_485-36	e4-36	tier3	79	0	0.000	101	12	0.106
848524	12	3432534	3432534	G	T	SNP	*ENSG00000236908*	ENST00000432994	1	rna	NULL	NULL	tier1	97	4	0.040	64	50	0.439
848524	12	53861637	53861637	A	-	DEL	*PCBP2*	ENST00000547048	1	3_prime_untranslated_region	c.*53861637	NULL	tier3	65	1	0.015	130	21	0.139
848524	12	122658441	122658441	G	C	SNP	*IL31*	ENST00000377035	-1	missense	c.115	p.Q39E	tier1	80	0	0.000	88	74	0.457
848524	17	40666295	40666295	C	T	SNP	*MIR5010*	ENST00000582846	1	rna	NULL	NULL	tier1	55	0	0.000	63	52	0.452
848524	17	48594960	48594960	C	T	SNP	*MYCBPAP*	ENST00000437498	1	missense	c.422	p.P141L	tier1	84	0	0.000	91	38	0.295
848524	17	75442716	75442716	A	T	SNP	*09.Sep*	ENST00000427177	1	intronic	c.722-35510	e4-35510	tier4	46	2	0.042	45	43	0.489
848524	18	42531907	42531907	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2602	p.D868N	tier1	513	4	0.008	747	248	0.249

848524	18	66344112	66344115	AATA	-	DEL	*TMX3*	ENST00000578816	-1	5_prime_untranslated_region	c.-66344112	NULL	tier3	66	3	0.044	70	40	0.364
848524	19	1043430	1043430	C	G	SNP	*ABCA7*	ENST00000263094	1	silent	c.888	p.L296	tier1	58	2	0.033	66	55	0.455
848524	19	37064363	37064363	A	T	SNP	*LOC101927599*	ENST00000448373	1	rna	NULL	NULL	tier1	111	0	0.000	145	122	0.457
848524	19	56173950	56173964	AGATTAACCAGGACA	-	DEL	*U2AF2*	ENST00000308924	1	in_frame_del	c.569_583	p.INQDK191in_frame_del	tier1	514	3	0.006	497	89	0.152
848524	20	31022403	31022425	CACCACTGCCATAGAGAGGCGGC	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1888_1910	p.H633fs	tier1	652	5	0.008	914	129	0.124
848524	20	31022417	31022417	A	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1902	p.E635fs	tier1	640	3	0.005	740	91	0.110
848524	21	14424204	14424204	C	T	SNP	*ANKRD30BP2*	ENST00000471407	1	rna	NULL	NULL	tier1	407	6	0.015	562	151	0.211
855934	1	228403429	228403429	G	A	SNP	*OBSCN*	ENST00000422127	1	missense	c.1994	p.R665Q	tier1	100	7	0.065	144	111	0.432
855934	2	81421390	81421390	G	A	SNP	*ENSG00000234429*	ENST00000378334	-1	3_prime_flanking_region	c.*71	NULL	tier2	99	0	0.000	102	87	0.456
855934	2	166611398	166611398	G	T	SNP	*GALNT3*	ENST00000392701	-1	intronic	c.1524+44	e7+44	tier3	117	0	0.000	94	73	0.437
855934	2	172231602	172231602	C	T	SNP	*ENSG00000224553*	ENST00000428525	-1	5_prime_untranslated_region	c.-172231602	NULL	tier3	68	0	0.000	105	103	0.495
855934	3	133087476	133087477	CA	-	DEL	*TMEM108*	ENST00000321871	1	intronic	c.41-11120_41-11119	e2-11119	tier3	55	0	0.000	74	11	0.129
855934	4	106157845	106157845	C	T	SNP	*TET2*	ENST00000380013	1	nonsense	c.2746	p.Q916*	tier1	50	3	0.057	49	40	0.449
855934	5	140783754	140783754	G	A	SNP	*PCDHGA9*	ENST00000573521	1	missense	c.1235	p.R412Q	tier1	44	0	0.000	56	60	0.517
855934	6	30530949	30530949	C	T	SNP	*PRR3*	ENST00000481741	1	rna	NULL	NULL	tier1	95	0	0.000	102	87	0.460
855934	6	31637272	31637272	C	T	SNP	*CSNK2B*	ENST00000375865	1	nonsense	c.544	p.Q182*	tier1	18	0	0.000	20	23	0.535
855934	6	118800974	118800974	T	C	SNP	*CEP85L*	ENST00000368488	-1	intronic	c.1923+60	e10+60	tier3	68	0	0.000	35	28	0.444
855934	7	6439714	6439714	T	C	SNP	*RAC1*	ENST00000473564	1	3_prime_untranslated_region	c.*6439714	NULL	tier3	195	0	0.000	164	134	0.450
855934	7	101758501	101758501	C	T	SNP	*CUX1*	ENST00000360264	1	nonsense	c.655	p.R219*	tier1	74	0	0.000	46	66	0.589
855934	8	139668092	139668092	C	T	SNP	*COL22A1*	ENST00000303045	-1	intronic	c.3333+48	e44+48	tier3	98	0	0.000	63	41	0.394
855934	8	140767744	140767744	T	G	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-23299	e22-23299	tier3	74	0	0.000	209	21	0.091
855934	8	145773426	145773426	C	T	SNP	*ARHGAP39*	ENST00000377307	-1	silent	c.1044	p.S348	tier1	12	0	0.000	18	15	0.455
855934	10	3183033	3183033	A	G	SNP	*PITRM1*	ENST00000380989	-1	intronic	c.2649-29	e24-29	tier3	80	0	0.000	78	55	0.410
855934	10	43651051	43651051	A	G	SNP	*CSGALNACT2*	ENST00000374466	1	missense	c.454	p.T152A	tier1	73	0	0.000	55	48	0.466
855934	10	71695049	71695049	G	A	SNP	*COL13A1*	ENST00000356340	1	intronic	c.1696-57	e30-57	tier3	66	0	0.000	62	79	0.560
855934	10	104120904	104120904	G	A	SNP	*GBF1*	ENST00000476019	1	rna	NULL	NULL	tier1	38	0	0.000	30	24	0.444
855934	10	115528652	115528652	G	A	SNP	*PLEKHS1*	ENST00000369310	1	splice_region	c.417+3	e5+3	tier2	48	0	0.000	28	26	0.482
855934	10	135292946	135292946	A	C	SNP	*SPRN*	ENST00000541506	-1	intronic	c.1-55745	e1-55745	tier3	38	0	0.000	46	11	0.193
855934	12	54796846	54796846	G	A	SNP	*ITGA5*	ENST00000551564	-1	5_prime_untranslated_region	c.-54796846	NULL	tier3	70	1	0.014	103	74	0.418
855934	12	70064230	70064230	T	G	SNP	*BEST3*	ENST00000476098	-1	missense	c.590	p.D197A	tier1	47	0	0.000	54	50	0.481
855934	16	84888372	84888372	C	T	SNP	*CRISPLD2*	ENST00000262424	1	missense	c.646	p.R216W	tier1	77	0	0.000	115	113	0.496
855934	18	30253100	30253100	C	T	SNP	*KLHL14*	ENST00000359358	-1	3_prime_untranslated_region	c.*1520	NULL	tier2	121	1	0.008	74	44	0.373
855934	18	44555207	44555207	G	A	SNP	*TCEB3C*	ENST00000330682	-1	missense	c.1007	p.T336M	tier1	574	0	0.000	1089	41	0.036
855934	19	43679576	43679576	C	T	SNP	*PSG5*	ENST00000342951	-1	missense	c.755	p.R252H	tier1	206	1	0.005	194	192	0.497
855934	19	57772501	57772501	C	G	SNP	*ZNF460*	ENST00000360338	1	5_prime_flanking_region	c.-19674	NULL	tier3	77	1	0.013	57	46	0.442
855934	20	31022442	31022443	GG	-	DEL	*ASXL1*	ENST00000375687	1	frame_shift_del	c.1927_1928	p.G645fs	tier1	732	15	0.020	990	621	0.386
855934	20	49199177	49199177	A	C	SNP	*PTPN1*	ENST00000371621	1	intronic	c.1285-52	e10-52	tier3	99	3	0.029	96	78	0.448
855934	21	44514777	44514777	T	G	SNP	*U2AF1*	ENST00000291552	-1	missense	c.470	p.Q157P	tier1	374	7	0.018	449	328	0.421
855934	X	73071895	73071895	C	A	SNP	*XIST*	ENST00000429829	-1	rna	NULL	NULL	tier1	74	4	0.051	105	41	0.281
855934	X	76888698	76888698	G	A	SNP	*ATRX*	ENST00000373344	-1	missense	c.5131	p.P1711S	tier1	25	0	0.000	2	25	0.926
855934	X	133511773	133511774	-	A	INS	*PHF6*	ENST00000394292	1	frame_shift_ins	c.126_127	p.H42fs	tier1	144	0	0.000	32	165	0.838
856550	1	26317279	26317279	G	A	SNP	*PAFAH2*	ENST00000374282	-1	missense	c.29	p.P10L	tier1	65	3	0.044	61	41	0.402
856550	1	32127089	32127089	C	A	SNP	*COL16A1*	ENST00000271069	-1	intronic	c.3727-30	e60-30	tier3	80	1	0.012	55	46	0.455
856550	1	115258747	115258747	C	T	SNP	*NRAS*	ENST00000369535	-1	missense	c.35	p.G12D	tier1	470	3	0.006	461	250	0.351
856550	1	142699411	142699412	-	T	INS	*ENSG00000203849*	ENST00000369381	-1	rna	NULL	NULL	tier1	170	1	0.006	212	77	0.266
856550	1	204960404	204960404	G	A	SNP	*NFASC*	ENST00000367172	1	intronic	c.3092+2466	e23+2466	tier2	83	0	0.000	73	51	0.411
856550	1	206941873	206941873	A	G	SNP	*IL10*	ENST00000423557	-1	3_prime_untranslated_region	c.*108	NULL	tier3	156	0	0.000	152	149	0.493
856550	2	202514343	202514343	C	T	SNP	*MPP4*	ENST00000359962	-1	missense	c.1540	p.V514I	tier1	85	2	0.023	75	40	0.348
856550	2	216967347	216967347	T	-	DEL	*TMEM169*	ENST00000295658	1	3_prime_untranslated_region	c.*2082	NULL	tier4	121	3	0.024	169	25	0.129
856550	3	57232440	57232440	A	T	SNP	*HESX1*	ENST00000295934	-1	missense	c.438	p.N146K	tier1	130	1	0.008	148	131	0.470
856550	3	141892042	141892042	A	-	DEL	*GK5*	ENST00000463349	-1	splice_region_del	c.29-3	e2-3	tier4	60	1	0.016	119	22	0.156
856550	3	178546013	178546013	C	T	SNP	*KCNMB2*	ENST00000358316	1	missense	c.275	p.T92M	tier1	98	3	0.030	72	89	0.553
856550	5	24487247	24487247	C	A	SNP	*CDH10*	ENST00000264463	-1	3_prime_untranslated_region	c.*525	NULL	tier4	262	4	0.015	282	219	0.435
856550	5	112403792	112403792	C	A	SNP	*MCC*	ENST00000302475	-1	missense	c.1444	p.V482L	tier1	47	0	0.000	36	39	0.520
856550	5	153190809	153190809	G	A	SNP	*GRIA1*	ENST00000448073	1	3_prime_untranslated_region	c.*24	NULL	tier3	49	2	0.039	34	26	0.433
856550	6	66044805	66044805	C	T	SNP	*EYS*	ENST00000342421	-1	3_prime_untranslated_region	c.*49	NULL	tier2	68	1	0.015	90	65	0.419
856550	6	131179391	131179391	G	C	SNP	*EPB41L2*	ENST00000526782	-1	5_prime_untranslated_region	c.-131179391	NULL	tier3	53	0	0.000	49	32	0.386
856550	7	131853016	131853016	A	G	SNP	*PLXNA4*	ENST00000321063	-1	intronic	c.4286+47	e21+47	tier3	53	0	0.000	32	28	0.467
856550	7	148507436	148507436	T	C	SNP	*EZH2*	ENST00000320356	-1	missense	c.2018	p.N673S	tier1	368	3	0.008	286	197	0.407
856550	9	99233221	99233221	T	C	SNP	*HABP4*	ENST00000375249	1	intronic	c.744-72	e5-72	tier3	78	1	0.013	44	31	0.408
856550	9	99233241	99233241	G	C	SNP	*HABP4*	ENST00000375249	1	intronic	c.744-52	e5-52	tier3	105	1	0.009	61	50	0.446
856550	10	89118109	89118109	T	C	SNP	*NUTM2D*	ENST00000381697	1	silent	c.87	p.L29	tier1	1001	9	0.009	1024	294	0.223
856550	11	5537218	5537218	C	T	SNP	*UBQLNL*	ENST00000380184	-1	missense	c.454	p.V152M	tier1	29	0	0.000	20	13	0.394
856550	11	72294529	72294529	G	T	SNP	*PDE2A*	ENST00000334456	-1	missense	c.1681	p.Q561K	tier1	95	0	0.000	80	65	0.448
856550	11	83770488	83770488	C	T	SNP	*DLG2*	ENST00000376104	-1	silent	c.789	p.V263	tier1	130	0	0.000	74	51	0.408
856550	11	117282559	117282559	G	A	SNP	*CEP164*	ENST00000278935	1	silent	c.4212	p.A1404	tier1	16	0	0.000	20	18	0.474
856550	12	25378647	25378647	T	A	SNP	*KRAS*	ENST00000256078	-1	missense	c.351	p.K117N	tier1	603	4	0.007	1082	59	0.052
856550	12	46205132	46205132	T	G	SNP	*ARID2*	ENST00000334344	1	intronic	c.285-69	e4-69	tier3	46	0	0.000	69	35	0.337
856550	12	48376914	48376914	G	A	SNP	*COL2A1*	ENST00000380518	-1	missense	c.2056	p.P686S	tier1	96	2	0.020	92	63	0.407
856550	12	54734318	54734318	C	T	SNP	*COPZ1*	ENST00000549043	1	silent	c.30	p.F10	tier1	167	2	0.012	116	93	0.445
856550	12	121880537	121880538	-	G	INS	*KDM2B*	ENST00000377071	-1	frame_shift_ins	c.2707_2706	p.K902fs	tier1	20	0	0.000	5	9	0.643
856550	12	125453425	125453425	C	T	SNP	*DHX37*	ENST00000308736	-1	silent	c.1281	p.P427	tier1	86	1	0.011	60	41	0.406
856550	15	43927354	43927354	T	-	DEL	*CATSPER2*	ENST00000419262	-1	splice_site_del	c.34-2	e2-2	tier1	46	0	0.000	64	12	0.158
856550	15	65496649	65496649	A	G	SNP	*CILP*	ENST00000261883	-1	silent	c.876	p.T292	tier1	151	2	0.013	101	82	0.446

856550	15	78397250	78397250	T	-	DEL	*CIB2*	ENST00000258930	-1	3_prime_untranslated_region	c.*403	NULL	tier3	111	2	0.018	139	20	0.126
856550	16	13297355	13297355	C	G	SNP	*SHISA9*	ENST00000558583	1	missense	c.919	p.Q307E	tier1	78	1	0.013	59	37	0.381
856550	17	1028517	1028517	C	A	SNP	*ABR*	ENST00000302538	-1	splice_site	c.246+1	e2+1	tier1	107	0	0.000	107	79	0.425
856550	17	11757380	11757380	G	A	SNP	*DNAH9*	ENST00000262442	1	missense	c.9568	p.A3190T	tier1	730	1	0.001	965	31	0.031
856550	17	48356336	48356336	G	A	SNP	*TMEM92*	ENST00000300433	1	silent	c.345	p.A115	tier1	154	4	0.025	139	85	0.380
856550	17	59479337	59479337	C	G	SNP	*TBX2*	ENST00000419047	1	intronic	c.441+25	e2+25	tier2	73	0	0.000	48	25	0.343
856550	17	74387223	74387223	G	C	SNP	*UBE2O*	ENST00000319380	-1	missense	c.3680	p.S1227W	tier1	54	0	0.000	46	29	0.382
856550	20	34099166	34099166	T	C	SNP	*CEP250*	ENST00000397527	1	intronic	c.7066-26	e32-26	tier3	44	0	0.000	63	11	0.126
856550	20	45052040	45052040	C	T	SNP	*ELMO2*	ENST00000445496	-1	intronic	c.1+9493	e0+9493	tier4	87	1	0.011	46	52	0.531
856550	20	57484420	57484420	C	T	SNP	*GNAS*	ENST00000354359	1	missense	c.604	p.R202C	tier1	631	6	0.009	457	358	0.439
856550	21	36252998	36252998	C	G	SNP	*RUNX1*	ENST00000300305	-1	missense	c.364	p.G122R	tier1	1222	24	0.019	206	1486	0.878
856550	22	16414079	16414079	G	A	SNP	*ENSG00000215268*	ENST00000417863	1	3_prime_untranslated_region	c.*16414079	NULL	tier3	182	9	0.047	160	73	0.312
856550	22	17029213	17029213	A	G	SNP	*ENSG00000233995*	ENST00000454360	1	5_prime_flanking_region	c.-23704	NULL	tier3	483	7	0.014	570	32	0.053
856550	22	18628675	18628675	C	T	SNP	*TUBA8*	ENST00000608634	1	missense	c.745	p.R249C	tier1	82	1	0.012	56	71	0.559
856550	22	45277142	45277142	G	A	SNP	*PHF21B*	ENST00000313237	-1	3_prime_untranslated_region	c.*1824	NULL	tier2	156	1	0.006	150	96	0.390
856550	X	41782248	41782248	G	C	SNP	*CASK*	ENST00000468986	-1	rna	NULL	NULL	tier1	96	0	0.000	69	54	0.439
856550	X	86063662	86063662	A	G	SNP	*DACH2*	ENST00000373125	1	intronic	c.1241-4197	e8-4197	tier3	136	0	0.000	146	84	0.362
856550	X	133527979	133527979	G	T	SNP	*PHF6*	ENST00000394292	1	nonsense	c.415	p.E139*	tier1	561	3	0.005	683	498	0.422
875301	1	1717243	1717243	T	-	DEL	*GNB1*	ENST00000378609	-1	3_prime_untranslated_region	c.*1527	NULL	tier2	39	0	0.000	25	7	0.219
875301	1	148887714	148887714	C	T	SNP	*ENSG00000231448*	ENST00000444424	1	3_prime_untranslated_region	c.*148887714	NULL	tier2	1927	1	0.001	2460	75	0.030
875301	2	64807082	64807082	T	G	SNP	*AFTPH*	ENST00000498706	1	3_prime_untranslated_region	c.*64807082	NULL	tier3	194	0	0.000	135	11	0.075
875301	2	179321040	179321040	A	-	DEL	*DFNB59*	ENST00000375129	1	intronic	c.549+162	e3+162	tier3	108	1	0.009	73	10	0.121
875301	2	198264776	198264776	T	G	SNP	*SF3B1*	ENST00000335508	-1	splice_region	c.3013+3	e20+3	tier3	605	0	0.000	577	42	0.068
875301	2	198267359	198267359	C	G	SNP	*SF3B1*	ENST00000335508	-1	missense	c.1998	p.K666N	tier1	828	1	0.001	926	46	0.047
875301	3	50334761	50334761	G	C	SNP	*NAT6*	ENST00000354862	-1	missense	c.200	p.P67R	tier1	64	0	0.000	64	9	0.123
875301	4	183723267	183723267	G	A	SNP	*TENM3*	ENST00000511685	1	3_prime_untranslated_region	c.*1763	NULL	tier2	94	0	0.000	57	7	0.109
875301	7	48467344	48467345	-	T	INS	*ABCA13*	ENST00000435803	1	intronic	c.12460-19_12460-18	e42-18	tier3	130	0	0.000	126	14	0.100
875301	7	50450292	50450292	A	G	SNP	*IKZF1*	ENST00000331340	1	missense	c.476	p.N159S	tier1	292	0	0.000	404	19	0.045
875301	7	104946931	104946932	-	A	INS	*SRPK2*	ENST00000465112	-1	frame_shift_ins	c.159_158	p.L53fs	tier1	108	0	0.000	75	9	0.107
875301	9	79256934	79256934	G	A	SNP	*PRUNE2*	ENST00000428286	-1	intronic	c.7654+2721	e5+2721	tier4	20	0	0.000	22	10	0.313
875301	11	33361114	33361114	A	-	DEL	*HIPK3*	ENST00000303296	1	intronic	c.1613+34	e5+34	tier3	113	2	0.017	54	9	0.143
875301	11	121475955	121475955	C	T	SNP	*SORL1*	ENST00000260197	1	splice_region	c.4778+7	e34+7	tier3	119	0	0.000	128	12	0.086
875301	12	31247676	31247676	T	A	SNP	*DDX11*	ENST00000407793	1	intronic	c.1415-13	e13-13	tier3	505	1	0.002	546	29	0.050
875301	15	60745782	60745782	A	-	DEL	*NARG2*	ENST00000561114	-1	frame_shift_del	c.1145	p.F382fs	tier1	91	1	0.011	41	7	0.146
876752	1	153190890	153190890	G	A	SNP	*PRR9*	ENST00000368744	1	silent	c.270	p.Q90	tier1	73	0	0.000	49	26	0.347
876752	1	207881643	207881643	A	G	SNP	*CR1L*	ENST00000508064	1	intronic	c.1414+35	e10+35	tier4	278	3	0.011	337	63	0.158
876752	1	207881649	207881649	C	T	SNP	*CR1L*	ENST00000508064	1	intronic	c.1414+41	e10+41	tier4	267	2	0.007	318	60	0.157
876752	1	237947039	237947039	C	T	SNP	*RYR2*	ENST00000360064	1	silent	c.12045	p.N4015	tier1	150	1	0.007	94	54	0.365
876752	2	1099077	1099077	A	T	SNP	*SNTG2*	ENST00000308624	1	intronic	c.325+4981	e4+4981	tier4	34	0	0.000	45	11	0.196
876752	2	233899445	233899445	G	A	SNP	*NEU2*	ENST00000233840	1	missense	c.821	p.G274E	tier1	50	3	0.057	35	20	0.357
876752	3	37340696	37340696	A	-	DEL	*GOLGA4*	ENST00000361924	1	intronic	c.1003-83	e9-83	tier3	144	1	0.007	144	98	0.405
876752	3	38621021	38621021	C	T	SNP	*SCN5A*	ENST00000333535	-1	intronic	c.3229-35	e17-35	tier3	40	0	0.000	20	13	0.382
876752	4	82026868	82026868	C	T	SNP	*PRKG2*	ENST00000264399	-1	intronic	c.2063+99	e15+99	tier3	106	1	0.009	82	73	0.468
876752	11	193204	193204	T	G	SNP	*SCGB1C1*	ENST00000342878	1	intronic	c.55+50	e1+50	tier3	169	4	0.023	141	22	0.133
876752	11	71373771	71373771	G	A	SNP	*ENPP7P8*	ENST00000529093	1	5_prime_flanking_region	c.-49015	NULL	tier3	630	8	0.013	504	312	0.382
876752	15	21119477	21119477	T	C	SNP	*POTEB2*	ENST00000454856	-1	5_prime_flanking_region	c.-47867	NULL	tier4	51	0	0.000	64	11	0.147
876752	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	660	0	0.000	790	29	0.035
876752	16	32890900	32890900	C	T	SNP	*SLC6A10P*	ENST00000330048	-1	intronic	c.NULL	NULL	tier3	301	0	0.000	262	11	0.040
876752	16	84227714	84227714	G	A	SNP	*ADAD2*	ENST00000268624	1	missense	c.521	p.R174H	tier1	103	0	0.000	62	54	0.466
876752	17	6703354	6703354	C	G	SNP	*TEKT1*	ENST00000338694	-1	missense	c.1249	p.V417L	tier1	40	0	0.000	19	23	0.548
876752	18	47380016	47380016	G	A	SNP	*MYO5B*	ENST00000285039	-1	silent	c.4024	p.L1342	tier1	380	6	0.016	290	209	0.418
876752	19	7944301	7944301	G	A	SNP	*FLJ22184*	ENST00000539422	-1	5_prime_flanking_region	c.-5727	NULL	tier3	73	0	0.000	50	39	0.438
876752	22	21153574	21153574	G	A	SNP	*PI4KA*	ENST00000255882	-1	splice_region	c.1821-10	e16-10	tier3	73	1	0.014	51	42	0.452
882325	1	112525116	112525116	T	G	SNP	*KCND3*	ENST00000315987	-1	missense	c.233	p.D78A	tier1	57	1	0.017	84	46	0.351
882325	1	152186038	152186038	A	-	DEL	*HRNR*	ENST00000368801	-1	frame_shift_del	c.8067	p.H2690fs	tier1	14	0	0.000	7	10	0.588
882325	1	152186047	152186047	A	-	DEL	*HRNR*	ENST00000368801	-1	frame_shift_del	c.8058	p.R2687fs	tier1	10	0	0.000	5	10	0.667
882325	1	220369746	220369746	A	-	DEL	*RAB3GAP2*	ENST00000358951	-1	splice_region_del	c.812-6	e10-6	tier3	77	1	0.013	178	24	0.119
882325	1	228464970	228464970	G	T	SNP	*OBSCN*	ENST00000422127	1	missense	c.6710	p.C2237F	tier1	35	0	0.000	50	40	0.444
882325	1	228464971	228464971	T	A	SNP	*OBSCN*	ENST00000422127	1	nonsense	c.6711	p.C2237*	tier1	37	0	0.000	51	40	0.440
882325	2	25457242	25457242	C	T	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.2645	p.R882H	tier1	270	9	0.032	370	228	0.380
882325	2	209113112	209113112	C	A	SNP	*IDH1*	ENST00000345146	-1	missense	c.395	p.R132L	tier1	301	1	0.003	564	362	0.391
882325	2	211421474	211421474	C	T	SNP	*CPS1*	ENST00000430249	1	missense	c.35	p.T12I	tier1	76	1	0.013	158	66	0.295
882325	2	238253632	238253632	T	C	SNP	*COL6A3*	ENST00000295550	-1	intronic	c.7163-37	e34-37	tier3	71	2	0.027	103	45	0.302
882325	3	38948846	38948846	T	C	SNP	*ENSG00000215941*	ENST00000401122	1	rna	NULL	NULL	tier1	19	0	0.000	31	21	0.404
882325	3	184100959	184100959	G	-	DEL	*CHRD*	ENST00000460627	1	3_prime_untranslated_region	c.*184100959	NULL	tier3	82	2	0.024	114	22	0.162
882325	4	9785355	9785355	A	-	DEL	*DRD5*	ENST00000304374	1	3_prime_untranslated_region	c.*268	NULL	tier3	53	0	0.000	143	20	0.123
882325	4	170913470	170913470	G	A	SNP	*MFAP3L*	ENST00000361618	-1	splice_region	c.299-10	e2-10	tier3	31	0	0.000	15	13	0.464
882325	5	150923971	150923971	A	G	SNP	*FAT2*	ENST00000261800	-1	silent	c.6717	p.H2239	tier1	63	0	0.000	75	36	0.321
882325	7	147335933	147335934	-	T	INS	*CNTNAP2*	ENST00000455301	1	frame_shift_ins	c.33_34	p.F15fs	tier1	32	0	0.000	68	30	0.306
882325	8	54871008	54871008	T	C	SNP	*RGS20*	ENST00000297313	1	missense	c.1157	p.I386T	tier1	55	2	0.035	103	57	0.354
882325	9	139910760	139910760	C	T	SNP	*ABCA2*	ENST00000479446	-1	missense	c.1136	p.R379Q	tier1	67	0	0.000	72	35	0.327
882325	11	56237381	56237381	A	G	SNP	*OR5M3*	ENST00000312240	-1	missense	c.593	p.I198T	tier1	100	0	0.000	183	123	0.402
882325	11	64973991	64973991	C	G	SNP	*CAPN1*	ENST00000279247	1	missense	c.1411	p.R471G	tier1	81	3	0.036	119	59	0.332
882325	11	89405200	89405200	C	A	SNP	*FOLH1B*	ENST00000525540	1	intronic	c.NULL	NULL	tier3	91	0	0.000	155	58	0.272

882325	12	21051353	21051353	C	A	SNP	*SLCO1B3*	ENST00000553473	1	intronic	c.1683-17	e12-17	tier2	110	1	0.009	246	125	0.336
882325	12	111655648	111655648	G	A	SNP	*CUX2*	ENST00000261726	1	intronic	c.175-46	e3-46	tier3	70	0	0.000	104	41	0.279
882325	14	74196463	74196464	-	G	INS	*ELMSAN1*	ENST00000286523	-1	frame_shift_ins	c.1975_1974	p.I658fs	tier1	52	1	0.019	43	25	0.368
882325	15	33833126	33833126	G	T	SNP	*RYR3*	ENST00000389232	1	intronic	c.646+35	e7+35	tier3	188	1	0.005	357	273	0.432
882325	17	74732959	74732959	G	A	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95L	tier1	320	2	0.006	427	232	0.352
882325	18	55996142	55996142	G	A	SNP	*NEDD4L*	ENST00000400345	1	intronic	c.681-85	e10-85	tier3	23	0	0.000	40	25	0.379
882325	19	2435136	2435136	G	A	SNP	*LMNB2*	ENST00000325327	-1	missense	c.718	p.R240C	tier1	15	0	0.000	21	15	0.417
882325	X	50350816	50350816	C	G	SNP	*SHROOM4*	ENST00000289292	-1	missense	c.3326	p.W1109S	tier1	25	1	0.039	9	25	0.735
882325	X	53441798	53441798	A	G	SNP	*SMC1A*	ENST00000322213	-1	missense	c.320	p.I107T	tier1	222	2	0.009	440	64	0.126
882325	X	77911875	77911875	T	C	SNP	*ZCCHC5*	ENST00000321110	-1	3_prime_untranslated_region	c.*615	NULL	tier2	32	1	0.030	37	56	0.602
907471	1	221875157	221875157	A	-	DEL	*DUSP10*	ENST00000468085	-1	rna	NULL	NULL	tier1	40	0	0.000	40	11	0.216
907471	1	237947546	237947546	C	T	SNP	*RYR2*	ENST00000360064	1	silent	c.12552	p.N4184	tier1	304	2	0.007	454	23	0.048
907471	2	25457243	25457243	G	A	SNP	*DNMT3A*	ENST00000264709	-1	missense	c.2644	p.R882C	tier1	309	1	0.003	399	18	0.043
907471	5	82817864	82817864	G	A	SNP	*VCAN*	ENST00000265077	1	missense	c.3739	p.D1247N	tier1	811	0	0.000	1203	28	0.023
907471	5	112227415	112227415	G	A	SNP	*ZRSR1*	ENST00000391338	1	missense	c.79	p.A27T	tier1	636	0	0.000	793	25	0.031
907471	5	142301123	142301123	G	T	SNP	*ARHGAP26*	ENST00000477867	1	rna	NULL	NULL	tier1	225	0	0.000	175	11	0.059
907471	5	142301124	142301124	G	T	SNP	*ARHGAP26*	ENST00000477867	1	rna	NULL	NULL	tier1	225	0	0.000	174	10	0.054
907471	7	126716306	126716306	G	A	SNP	*GRM8*	ENST00000339582	-1	intronic	c.727+30244	e2+30244	tier3	341	0	0.000	462	16	0.033
907471	12	32948971	32948971	C	T	SNP	*PKP2*	ENST00000070846	-1	intronic	c.2489+72	e12+72	tier3	72	0	0.000	121	14	0.104
907471	12	55820945	55820945	G	A	SNP	*OR6C76*	ENST00000328314	1	missense	c.908	p.R303K	tier1	29	0	0.000	23	8	0.258
907471	12	111701486	111701487	-	A	INS	*CUX2*	ENST00000261726	1	intronic	c.223-79_223-78	e4-78	tier3	76	0	0.000	121	13	0.097
907471	14	36334922	36334922	A	T	SNP	*BRMS1L*	ENST00000216807	1	splice_region	c.688-6	e8-6	tier4	47	2	0.041	35	16	0.314
907471	16	89805075	89805075	G	A	SNP	*FANCA*	ENST00000389301	-1	silent	c.4302	p.A1434	tier1	814	0	0.000	1086	27	0.024
907471	21	19628809	19628810	-	T	INS	*CHODL*	ENST00000299295	1	intronic	c.80-17_80-16	e2-16	tier3	12	0	0.000	13	13	0.500
913698	1	91973859	91973859	A	G	SNP	*CDC7*	ENST00000234626	1	silent	c.240	p.Q80	tier1	128	3	0.023	194	102	0.345
913698	1	118426264	118426264	G	A	SNP	*GDAP2*	ENST00000369443	-1	intronic	c.1108-15	e10-15	tier3	56	0	0.000	79	44	0.358
913698	1	142826527	142826527	G	A	SNP	*ANKRD20A14P*	ENST00000457776	1	3_prime_untranslated_region	c.*142826527	NULL	tier3	22	1	0.044	20	23	0.535
913698	1	182791320	182791320	G	A	SNP	*NPL*	ENST00000258317	1	missense	c.724	p.A242T	tier1	95	3	0.031	157	63	0.286
913698	2	132723935	132723935	G	A	SNP	*ENSG00000235615*	ENST00000419362	-1	rna	NULL	NULL	tier1	9	0	0.000	2	9	0.818
913698	2	196636498	196636498	G	A	SNP	*DNAH7*	ENST00000312428	-1	silent	c.11319	p.Y3773	tier1	102	0	0.000	205	40	0.162
913698	2	227924194	227924194	C	T	SNP	*COL4A4*	ENST00000396625	-1	silent	c.2310	p.P770	tier1	75	3	0.039	152	65	0.298
913698	3	47050909	47050909	G	-	DEL	*NBEAL2*	ENST00000450053	1	3_prime_untranslated_region	c.*99	NULL	tier2	6	0	0.000	8	15	0.652
913698	3	112300106	112300106	C	T	SNP	*SLC35A5*	ENST00000492406	1	missense	c.1142	p.P381L	tier1	75	4	0.051	133	51	0.276
913698	4	1656787	1656787	C	T	SNP	*FAM53A*	ENST00000308132	-1	missense	c.800	p.G267E	tier1	21	0	0.000	23	23	0.489
913698	4	184019703	184019703	C	G	SNP	*WWC2-AS2*	ENST00000506413	-1	rna	NULL	NULL	tier1	11	0	0.000	6	7	0.539
913698	5	43277155	43277155	G	A	SNP	*NIM1*	ENST00000326035	1	splice_region	c.293-4	e2-4	tier3	42	1	0.023	63	27	0.300
913698	6	26536971	26536971	A	-	DEL	*HMGN4*	ENST00000377575	1	5_prime_flanking_region	c.-8464	NULL	tier2	34	0	0.000	59	14	0.192
913698	7	100468311	100468311	C	T	SNP	*TRIP6*	ENST00000429658	1	missense	c.266	p.A89V	tier1	65	0	0.000	142	32	0.184
913698	9	119461034	119461034	C	T	SNP	*TRIM32*	ENST00000373983	1	missense	c.1013	p.A338V	tier1	41	0	0.000	52	32	0.381
913698	9	124530916	124530916	C	G	SNP	*DAB2IP*	ENST00000408936	1	splice_region	c.1899+4	e10+4	tier3	92	4	0.042	110	56	0.335
913698	11	5536564	5536564	G	A	SNP	*UBQLNL*	ENST00000380184	-1	missense	c.1108	p.H370Y	tier1	29	1	0.033	42	21	0.333
913698	11	6891758	6891758	A	T	SNP	*OR10A2*	ENST00000307322	1	missense	c.773	p.K258M	tier1	36	3	0.039	72	64	0.377
913698	11	120744937	120744937	G	A	SNP	*GRIK4*	ENST00000527524	1	splice_region	c.1059+10	e8+10	tier3	301	7	0.023	515	191	0.270
913698	12	91363823	91363823	G	A	SNP	*EPYC*	ENST00000261172	-1	nonsense	c.796	p.Q266*	tier1	130	0	0.000	241	38	0.136
913698	15	41223819	41223819	C	-	DEL	*DLL4*	ENST00000249749	1	frame_shift_del	c.513	p.R172fs	tier1	49	2	0.039	75	35	0.318
913698	15	90631934	90631934	C	T	SNP	*IDH2*	ENST00000330062	-1	missense	c.419	p.R140Q	tier1	358	3	0.008	838	203	0.195
913698	16	88808530	88808530	G	A	SNP	*ENSG00000260617*	ENST00000566114	1	rna	NULL	NULL	tier1	229	3	0.013	547	38	0.065
913698	17	39122986	39122986	G	A	SNP	*KRT39*	ENST00000355612	-1	silent	c.123	p.V41	tier1	64	3	0.045	142	57	0.286
913698	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	199	1	0.005	414	165	0.285
913698	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	590	12	0.020	1159	352	0.233
913698	20	40701696	40701696	C	T	SNP	*PTPRT*	ENST00000373198	-1	3_prime_untranslated_region	c.*7823	NULL	tier2	62	0	0.000	80	26	0.245
913698	20	60773672	60773672	G	A	SNP	*MTG2*	ENST00000370823	1	intronic	c.469-18	e4-18	tier3	52	3	0.055	95	41	0.302
913698	21	36252877	36252877	C	T	SNP	*RUNX1*	ENST00000300305	-1	missense	c.485	p.R162K	tier1	921	54	0.055	761	1152	0.602
913698	X	52679352	52679352	T	G	SNP	*SSX7*	ENST00000298181	-1	intronic	c.330+51	e4+51	tier3	254	6	0.023	486	218	0.309
913698	X	140967238	140967238	G	A	SNP	*MAGEC3*	ENST00000298296	1	intronic	c.515+21	e3+21	tier3	180	6	0.032	258	104	0.287
918051	1	94586694	94586694	A	G	SNP	*ABCA4*	ENST00000370225	-1	5_prime_flanking_region	c.-93	NULL	tier3	31	0	0.000	88	61	0.409
918051	1	94586695	94586695	C	G	SNP	*ABCA4*	ENST00000370225	-1	5_prime_flanking_region	c.-94	NULL	tier3	32	0	0.000	88	61	0.409
918051	1	150121929	150121929	C	G	SNP	*PLEKHO1*	ENST00000369126	1	5_prime_untranslated_region	c.-9109	NULL	tier2	11	0	0.000	27	36	0.571
918051	1	152186047	152186047	A	-	DEL	*HRNR*	ENST00000368801	-1	frame_shift_del	c.8058	p.R2687fs	tier1	8	0	0.000	3	6	0.667
918051	2	128621736	128621736	C	T	SNP	*AMMECR1L*	ENST00000272647	-1	3_prime_untranslated_region	c.*932	NULL	tier3	8	0	0.000	59	90	0.604
918051	3	112998095	112998095	G	A	SNP	*BOC*	ENST00000273395	1	splice_site	c.1817-1	e10-1	tier1	14	0	0.000	31	39	0.549
918051	4	7780663	7780664	-	T	INS	*AFAP1*	ENST00000505447	-1	5_prime_untranslated_region	c.-7780663	NULL	tier3	80	0	0.000	106	11	0.094
918051	5	36876937	36876937	C	-	DEL	*NIPBL*	ENST00000282516	1	5_prime_untranslated_region	c.-76862	NULL	tier2	52	1	0.019	137	51	0.271
918051	5	140232564	140232564	C	T	SNP	*PCDHA9*	ENST00000378122	1	3_prime_untranslated_region	c.*1955	NULL	tier4	36	0	0.000	13	7	0.350
918051	6	32557378	32557378	T	C	SNP	*HLA-DRB1*	ENST00000360004	-1	intronic	c.100+42	e1+42	tier3	31	0	0.000	158	37	0.190
918051	7	105668989	105668989	C	T	SNP	*CDHR3*	ENST00000468143	1	3_prime_untranslated_region	c.*105668989	NULL	tier3	45	0	0.000	82	72	0.468
918051	9	2907139	2907139	G	A	SNP	*CARM1P1*	ENST00000426329	-1	5_prime_untranslated_region	c.-2907139	NULL	tier3	14	0	0.000	82	53	0.393
918051	9	88452656	88452656	C	T	SNP	*ENSG00000165121*	ENST00000431724	1	intronic	c.NULL	NULL	tier3	48	0	0.000	126	77	0.379
918051	10	19616672	19616672	T	A	SNP	*C10orf112*	ENST00000454679	1	intronic	c.1575+70	e8+70	tier3	25	0	0.000	114	81	0.415
918051	10	47728617	47728617	T	C	SNP	*CTGLF11P*	ENST00000280961	1	3_prime_untranslated_region	c.*47728617	NULL	tier3	16	0	0.000	2	7	0.778
918051	10	55581617	55581617	A	T	SNP	*PCDH15*	ENST00000463095	-1	rna	NULL	NULL	tier1	25	0	0.000	106	76	0.415
918051	10	73492123	73492123	C	T	SNP	*CDH23*	ENST00000224721	1	silent	c.4110	p.D1370	tier1	31	0	0.000	56	43	0.434
918051	10	85968514	85968514	G	A	SNP	*CDHR1*	ENST00000372117	1	silent	c.1197	p.L399	tier1	29	0	0.000	109	78	0.417
918051	10	115985820	115985820	G	A	SNP	*TDRD1*	ENST00000251864	1	nonsense	c.3020	p.W1007*	tier1	22	0	0.000	97	54	0.358

918051	11	20696148	20696148	G	A	SNP	*NELL1*	ENST00000357134	1	intronic	c.56-3330	e2-3330	tier4	9	0	0.000	35	42	0.546
918051	11	63342376	63342376	T	C	SNP	*PLA2G16*	ENST00000394613	-1	rna	NULL	NULL	tier1	23	0	0.000	84	69	0.451
918051	11	92533422	92533422	T	C	SNP	*FAT3*	ENST00000298047	1	missense	c.7243	p.C2415R	tier1	17	0	0.000	88	59	0.401
918051	12	116446681	116446681	T	C	SNP	*MED13L*	ENST00000281928	-1	missense	c.1537	p.I513V	tier1	22	0	0.000	87	68	0.439
918051	13	42118880	42118880	A	G	SNP	*VWA8*	ENST00000379310	-1	3_prime_flanking_region	c.*23453	NULL	tier4	30	0	0.000	51	13	0.203
918051	14	57070634	57070634	A	G	SNP	*TMEM260*	ENST00000261556	1	missense	c.446	p.N149S	tier1	134	0	0.000	496	391	0.440
918051	15	62359822	62359822	C	A	SNP	*C2CD4A*	ENST00000355522	1	missense	c.10	p.L4M	tier1	22	0	0.000	63	50	0.443
918051	16	780298	780298	G	A	SNP	*NARFL*	ENST00000562862	-1	rna	NULL	NULL	tier1	25	0	0.000	96	77	0.445
918051	19	1026637	1026637	C	A	SNP	*CNN2*	ENST00000562015	1	rna	NULL	NULL	tier1	9	0	0.000	14	22	0.611
918051	19	37063218	37063219	-	A	INS	*ZNF529*	ENST00000591340	-1	intronic	c.14+16_14+15	e1+16	tier3	12	0	0.000	57	42	0.424
918051	19	39869235	39869235	G	A	SNP	*SAMD4B*	ENST00000314471	1	splice_region	c.1530+6	e7+6	tier3	23	0	0.000	35	21	0.375
918051	20	1920551	1920551	T	C	SNP	*LOC727993*	ENST00000446562	1	5_prime_flanking_region	c.-7341	NULL	tier2	49	2	0.039	60	48	0.444
918051	20	34022502	34022502	G	A	SNP	*GDF5*	ENST00000374369	-1	silent	c.711	p.A237	tier1	11	0	0.000	30	28	0.483
918051	20	44979120	44979120	G	C	SNP	*SLC35C2*	ENST00000543605	-1	silent	c.1098	p.P366	tier1	29	0	0.000	73	75	0.507
918051	22	23055600	23055600	C	T	SNP	*IGLV3-21*	ENST00000390308	1	missense	c.263	p.T88M	tier1	40	0	0.000	74	63	0.460
918051	X	123197782	123197783	-	A	INS	*STAG2*	ENST00000218089	1	frame_shift_ins	c.1906_1907	p.Y636fs	tier1	37	0	0.000	117	468	0.800
922185	1	149400471	149400471	T	C	SNP	*HIST2H3PS2*	ENST00000392948	-1	silent	c.72	p.K24	tier1	188	4	0.021	197	57	0.224
922185	2	20100829	20100829	T	A	SNP	*TTC32*	ENST00000431392	-1	silent	c.54	p.S18	tier1	85	0	0.000	115	38	0.248
922185	2	179638759	179638759	A	G	SNP	*TTN*	ENST00000342992	-1	missense	c.7136	p.V2379A	tier1	77	0	0.000	110	14	0.113
922185	4	25930000	25930000	A	-	DEL	*SMIM20*	ENST00000506197	1	splice_region_del	c.166+9	e2+9	tier3	87	0	0.000	112	15	0.118
922185	4	71463976	71463976	C	T	SNP	*AMBN*	ENST00000322937	1	intronic	c.136-97	e4-97	tier3	74	1	0.013	128	20	0.135
922185	4	100544120	100544120	T	A	SNP	*MTTP*	ENST00000265517	1	3_prime_untranslated_region	c.*115	NULL	tier3	77	0	0.000	109	32	0.227
922185	5	82817833	82817833	C	T	SNP	*VCAN*	ENST00000265077	1	silent	c.3708	p.I1236	tier1	739	3	0.004	1063	55	0.049
922185	5	126753323	126753323	C	T	SNP	*MEGF10*	ENST00000274473	1	splice_region	c.1131-7	e9-7	tier3	47	0	0.000	55	24	0.304
922185	5	137298188	137298188	T	C	SNP	*FAM13B*	ENST00000033079	-1	intronic	c.1180-30	e9-30	tier3	49	1	0.020	78	25	0.240
922185	7	39990405	39990406	-	CCGC	INS	*CDK13*	ENST00000181839	1	frame_shift_ins	c.165_166	p.L57fs	tier1	27	0	0.000	19	7	0.269
922185	7	55241540	55241540	G	T	SNP	*EGFR*	ENST00000275493	1	intronic	c.2062-74	e18-74	tier3	187	1	0.005	211	13	0.058
922185	9	111954473	111954473	A	T	SNP	*EPB41L4B*	ENST00000374566	-1	intronic	c.2301+85	e22+85	tier3	83	0	0.000	86	25	0.225
922185	10	126678193	126678193	A	G	SNP	*CTBP2*	ENST00000309035	-1	missense	c.2852	p.I951T	tier1	70	0	0.000	81	15	0.156
922185	11	57970725	57970725	A	C	SNP	*OR1S2*	ENST00000302592	-1	missense	c.929	p.M310R	tier1	105	3	0.028	142	45	0.241
922185	11	117340626	117340626	C	T	SNP	*DSCAML1*	ENST00000321322	-1	silent	c.3204	p.K1068	tier1	134	1	0.007	122	41	0.252
922185	11	134605431	134605431	G	A	SNP	*ENSG00000251226*	ENST00000513405	1	5_prime_flanking_region	c.-59	NULL	tier2	449	14	0.030	333	121	0.266
922185	12	10146243	10146243	A	C	SNP	*CLEC1B*	ENST00000298527	-1	intronic	c.546-357	e6-357	tier3	45	0	0.000	57	16	0.219
922185	12	50026453	50026453	G	T	SNP	*PRPF40B*	ENST00000548436	1	3_prime_untranslated_region	c.*50026453	NULL	tier3	710	1	0.001	594	169	0.221
922185	14	21968662	21968662	A	G	SNP	*METTL3*	ENST00000298717	-1	missense	c.1279	p.F427L	tier1	60	1	0.016	80	26	0.245
922185	14	93704243	93704243	T	C	SNP	*BTBD7*	ENST00000334746	-1	3_prime_untranslated_region	c.*4376	NULL	tier3	50	0	0.000	67	22	0.247
922185	15	34519872	34519872	A	C	SNP	*EMC4*	ENST00000561246	1	3_prime_untranslated_region	c.*34519872	NULL	tier3	41	0	0.000	45	11	0.196
922185	15	49926994	49926994	A	-	DEL	*DTWD1*	ENST00000251250	1	splice_region_del	c.667+3	e3+3	tier3	77	0	0.000	145	16	0.099
922185	15	89386622	89386622	C	T	SNP	*ACAN*	ENST00000439576	1	missense	c.794	p.T265I	tier1	86	4	0.044	71	27	0.276
922185	17	15457016	15457016	C	A	SNP	*TVP23C*	ENST00000225576	-1	missense	c.223	p.D75Y	tier1	108	1	0.009	170	46	0.213
922185	17	48668000	48668000	G	A	SNP	*CACNA1G*	ENST00000359106	1	intronic	c.2453+17	e10+17	tier3	461	0	0.000	578	45	0.072
922185	18	19781636	19781636	A	T	SNP	*GATA6*	ENST00000269216	1	3_prime_untranslated_region	c.*850	NULL	tier2	144	0	0.000	260	70	0.212
922185	18	21140392	21140392	G	A	SNP	*NPC1*	ENST00000269228	-1	silent	c.684	p.D228	tier1	31	0	0.000	54	14	0.206
922185	22	38686807	38686808	-	T	INS	*CSNK1E*	ENST00000359867	-1	3_prime_untranslated_region	c.*2486	NULL	tier2	78	0	0.000	134	16	0.107
933226	1	45798446	45798446	C	T	SNP	*MUTYH*	ENST00000450313	-1	missense	c.565	p.G189R	tier1	53	0	0.000	68	34	0.333
933226	2	179532466	179532466	T	-	DEL	*TTN*	ENST00000342992	-1	intronic	c.31483+2479	e151+2479	tier2	15	0	0.000	76	43	0.361
933226	2	228512849	228512849	G	A	SNP	*ENSG00000250599*	ENST00000509872	-1	5_prime_untranslated_region	c.-228512849	NULL	tier3	64	0	0.000	119	53	0.308
933226	2	241976165	241976165	G	A	SNP	*SNED1*	ENST00000310397	1	intronic	c.806-42	e5-42	tier2	14	0	0.000	7	8	0.533
933226	2	242755726	242755726	G	T	SNP	*NEU4*	ENST00000325935	1	silent	c.84	p.R28	tier1	36	0	0.000	36	30	0.455
933226	3	11303055	11303055	C	T	SNP	*HRH1*	ENST00000397056	1	3_prime_untranslated_region	c.*868	NULL	tier4	40	0	0.000	62	50	0.446
933226	3	142546497	142546497	G	A	SNP	*ENSG00000240950*	ENST00000489462	-1	5_prime_untranslated_region	c.-142546497	NULL	tier3	44	0	0.000	63	32	0.337
933226	3	195512549	195512549	A	G	SNP	*MUC4*	ENST00000463781	-1	missense	c.5902	p.S1968P	tier1	209	0	0.000	335	72	0.176
933226	4	665776	665776	G	T	SNP	*PCGF3*	ENST00000362003	1	5_prime_flanking_region	c.-61694	NULL	tier3	76	0	0.000	70	41	0.369
933226	4	7741871	7741871	C	T	SNP	*SORCS2*	ENST00000507866	1	intronic	c.3416-56	e27-56	tier3	20	0	0.000	19	19	0.500
933226	4	55161723	55161723	G	A	SNP	*PDGFRA*	ENST00000257290	1	3_prime_untranslated_region	c.*284	NULL	tier3	42	0	0.000	125	70	0.359
933226	4	187628190	187628190	T	A	SNP	*FAT1*	ENST00000441802	-1	missense	c.2792	p.N931I	tier1	37	0	0.000	55	37	0.402
933226	4	189068340	189068342	TGG	-	DEL	*TRIML1*	ENST00000332517	1	in_frame_del	c.1221_1223	p.G408in_frame_del	tier1	65	0	0.000	99	52	0.344
933226	5	1283509	1283509	A	C	SNP	*TERT*	ENST00000310581	-1	intronic	c.1574-770	e3-770	tier3	904	15	0.016	1313	83	0.059
933226	5	13793657	13793657	A	G	SNP	*DNAH5*	ENST00000265104	-1	silent	c.8191	p.L2731	tier1	390	0	0.000	514	271	0.344
933226	5	31511227	31511227	C	T	SNP	*DROSHA*	ENST00000512076	-1	missense	c.631	p.G211R	tier1	65	0	0.000	101	48	0.322
933226	5	34182770	34182770	C	T	SNP	*LOC100653061*	ENST00000514048	-1	intronic	c.NULL	NULL	tier3	1352	1	0.001	2412	159	0.062
933226	5	118309302	118309319	GCCTCCTTGCTCGCGGCA	-	DEL	*DTWD2*	ENST00000510708	-1	intronic	c.218+14670_218+14653	e1+14670	tier2	64	2	0.030	43	16	0.271
933226	6	29911836	29911836	C	T	SNP	*HLA-A*	ENST00000376806	1	intronic	c.620-63	e4-63	tier2	208	1	0.005	312	19	0.057
933226	6	29911844	29911844	T	A	SNP	*HLA-A*	ENST00000376806	1	intronic	c.620-55	e4-55	tier2	230	1	0.004	341	20	0.055
933226	6	169623535	169623535	C	T	SNP	*THBS2*	ENST00000366787	-1	missense	c.2809	p.D937N	tier1	36	0	0.000	80	44	0.355
933226	7	72455428	72455428	C	G	SNP	*STAG3L3*	ENST00000436857	-1	intronic	c.NULL	NULL	tier3	16	0	0.000	18	29	0.617
933226	7	94157586	94157586	T	-	DEL	*CASD1*	ENST00000297273	1	intronic	c.459+24	e5+24	tier4	18	0	0.000	151	69	0.314
933226	7	157652472	157652472	A	C	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1857+38893	e12+38893	tier3	433	7	0.016	742	49	0.062
933226	7	157897557	157897557	T	C	SNP	*PTPRN2*	ENST00000404321	-1	intronic	c.1712+5964	e10+5964	tier4	167	1	0.006	370	28	0.070
933226	8	91963467	91963467	T	-	DEL	*NECAB1*	ENST00000417640	1	intronic	c.1030+35	e12+35	tier3	17	1	0.056	59	52	0.469
933226	8	139277974	139277974	C	T	SNP	*FAM135B*	ENST00000395297	-1	missense	c.269	p.R90Q	tier1	60	0	0.000	72	47	0.395
933226	8	140767779	140767779	T	G	SNP	*TRAPPC9*	ENST00000389328	-1	intronic	c.3350-23334	e22-23334	tier3	64	0	0.000	131	15	0.102
933226	9	68438512	68438512	C	A	SNP	*ENSG00000215548*	ENST00000376334	-1	intronic	c.NULL	NULL	tier3	164	1	0.006	486	32	0.062
933226	9	68728863	68728863	A	G	SNP	*ENSG00000229789*	ENST00000427066	1	3_prime_untranslated_region	c.*68728863	NULL	tier4	66	1	0.015	399	77	0.162

933226	9	68728891	68728891	C	T	SNP	*ENSG00000229789*	ENST00000427066	1	3_prime_untranslated_region	c.*68728891	NULL	tier3	72	1	0.014	477	62	0.115
933226	9	93976302	93976302	A	G	SNP	*AUH*	ENST00000473695	-1	rna	NULL	NULL	tier1	22	0	0.000	152	92	0.377
933226	10	81609037	81609037	G	A	SNP	*NUTM2E*	ENST00000429984	1	intronic	c.1735-90	e6-90	tier3	69	0	0.000	131	20	0.132
933226	11	62037739	62037739	C	T	SNP	*SCGB2A2*	ENST00000227918	1	silent	c.51	p.Y17	tier1	39	1	0.025	37	28	0.431
933226	11	83497858	83497858	A	T	SNP	*DLG2*	ENST00000376104	-1	intronic	c.1723-23	e16-23	tier3	53	0	0.000	49	33	0.402
933226	12	59307704	59307704	G	A	SNP	*LRIG3*	ENST00000548968	-1	5_prime_untranslated_region	c.-59307704	NULL	tier3	37	0	0.000	175	91	0.342
933226	13	37270408	37270408	A	G	SNP	*SERTM1*	ENST00000315190	1	3_prime_untranslated_region	c.*869	NULL	tier3	13	0	0.000	96	51	0.347
933226	13	108518148	108518148	T	A	SNP	*FAM155A*	ENST00000375915	-1	missense	c.797	p.E266V	tier1	21	0	0.000	40	27	0.403
933226	14	75151331	75151331	A	G	SNP	*AREL1*	ENST00000356357	-1	silent	c.69	p.F23	tier1	26	1	0.037	53	35	0.398
933226	14	103059220	103059220	G	A	SNP	*RCOR1*	ENST00000262241	1	5_prime_untranslated_region	c.-4	NULL	tier2	8	0	0.000	4	7	0.583
933226	15	48056944	48056944	G	A	SNP	*SEMA6D*	ENST00000316364	1	missense	c.1207	p.V403I	tier1	70	0	0.000	97	35	0.265
933226	16	12297268	12297268	A	G	SNP	*SNX29*	ENST00000306030	1	intronic	c.523+3728	e6+3728	tier3	407	7	0.017	740	55	0.069
933226	16	12297294	12297294	T	G	SNP	*SNX29*	ENST00000306030	1	intronic	c.523+3754	e6+3754	tier3	389	4	0.010	709	34	0.046
933226	16	72094682	72094682	A	G	SNP	*HP*	ENST00000355906	1	missense	c.1114	p.T372A	tier1	120	0	0.000	190	25	0.116
933226	17	7578406	7578406	C	T	SNP	*TP53*	ENST00000269305	-1	missense	c.524	p.R175H	tier1	1041	3	0.003	407	1037	0.716
933226	17	18638428	18638428	C	A	SNP	*TRIM16L*	ENST00000395902	1	missense	c.864	p.D288E	tier1	35	0	0.000	61	37	0.378
933226	17	19643645	19643645	G	A	SNP	*ALDH3A1*	ENST00000487650	-1	5_prime_untranslated_region	c.-19643645	NULL	tier3	40	0	0.000	61	30	0.330
933226	18	42531913	42531913	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2608	p.G870S	tier1	532	2	0.004	514	310	0.376
933226	19	1011071	1011071	C	T	SNP	*TMEM259*	ENST00000591128	-1	5_prime_untranslated_region	c.-1011071	NULL	tier2	72	0	0.000	81	31	0.277
933226	19	1754673	1754673	A	T	SNP	*ONECUT3*	ENST00000382349	1	missense	c.1012	p.S338C	tier1	55	0	0.000	42	25	0.373
933226	19	49316512	49316512	C	T	SNP	*HSD17B14*	ENST00000263278	-1	missense	c.733	p.V245M	tier1	51	0	0.000	38	25	0.397
933226	19	51380151	51380151	T	A	SNP	*KLK2*	ENST00000325321	1	missense	c.517	p.C173S	tier1	77	0	0.000	97	59	0.378
933226	20	13269233	13269233	C	T	SNP	*ISM1*	ENST00000262487	1	silent	c.690	p.S230	tier1	68	0	0.000	74	40	0.351
933226	20	60499501	60499501	G	A	SNP	*CDH4*	ENST00000360469	1	missense	c.1738	p.V580I	tier1	54	0	0.000	25	24	0.490
933226	20	62715089	62715089	G	A	SNP	*OPRL1*	ENST00000336866	1	intronic	c.1+3384	e0+3384	tier2	6	0	0.000	1	6	0.857
933226	21	11098586	11098586	G	A	SNP	*BAGE2*	ENST00000470054	-1	intronic	c.NULL	NULL	tier4	38	0	0.000	61	22	0.265
933226	21	34923934	34923934	T	C	SNP	*SON*	ENST00000356577	1	silent	c.2397	p.S799	tier1	175	4	0.022	264	39	0.128
933226	22	16414219	16414219	G	A	SNP	*ENSG00000215268*	ENST00000417863	1	3_prime_untranslated_region	c.*16414219	NULL	tier3	147	0	0.000	221	75	0.253
933226	22	42381976	42381976	G	-	DEL	*03.Sep*	ENST00000460267	1	3_prime_untranslated_region	c.*42381976	NULL	tier3	24	0	0.000	43	24	0.358
933226	X	5821695	5821695	G	A	SNP	*NLGN4X*	ENST00000381093	-1	missense	c.1084	p.P362S	tier1	48	0	0.000	14	72	0.837
933226	X	43626915	43626915	C	G	SNP	*MAOB*	ENST00000378069	-1	intronic	c.1411-50	e15-50	tier4	38	0	0.000	34	78	0.696
933226	X	101624781	101624781	C	T	SNP	*NXF2B*	ENST00000372752	-1	5_prime_untranslated_region	c.-155	NULL	tier3	132	0	0.000	239	147	0.380
933226	X	130423302	130423302	C	A	SNP	*IGSF1*	ENST00000370903	-1	5_prime_untranslated_region	c.-2654	NULL	tier3	21	0	0.000	13	54	0.806
944541	1	50552429	50552429	G	A	SNP	*ELAVL4*	ENST00000448907	1	intronic	c.18+38575	e1+38575	tier3	50	1	0.020	128	61	0.321
944541	2	43453288	43453288	G	A	SNP	*THADA*	ENST00000330266	-1	intronic	c.3189-59383	e20-59383	tier2	60	1	0.016	170	108	0.386
944541	2	97483175	97483175	C	G	SNP	*CNNM3*	ENST00000305510	1	missense	c.1161	p.N387K	tier1	22	0	0.000	29	30	0.509
944541	3	130145131	130145131	G	T	SNP	*COL6A5*	ENST00000265379	1	intronic	c.5199+38	e29+38	tier3	30	0	0.000	62	40	0.392
944541	3	195690360	195690360	G	A	SNP	*SDHAP1*	ENST00000354559	-1	intronic	c.NULL	NULL	tier3	32	0	0.000	167	46	0.214
944541	4	44638032	44638032	C	T	SNP	*YIPF7*	ENST00000332990	-1	missense	c.259	p.A87T	tier1	35	0	0.000	69	38	0.355
944541	5	140482151	140482151	C	T	SNP	*PCDHB3*	ENST00000231130	1	silent	c.1918	p.L640	tier1	223	2	0.009	467	308	0.397
944541	6	33144473	33144473	G	C	SNP	*COL11A2*	ENST00000341947	-1	intronic	c.2115+25	e26+25	tier3	49	0	0.000	113	66	0.369
944541	6	43127615	43127615	A	G	SNP	*PTK7*	ENST00000230419	1	missense	c.2963	p.D988G	tier1	41	0	0.000	79	40	0.336
944541	7	142242469	142242469	G	T	SNP	*TRBV5-3*	ENST00000390362	-1	missense	c.155	p.S52Y	tier1	90	1	0.011	189	24	0.113
944541	8	3253958	3253958	C	T	SNP	*CSMD1*	ENST00000520002	-1	intronic	c.2409-55	e18-55	tier3	142	3	0.021	356	163	0.314
944541	8	21824261	21824261	A	G	SNP	*XPO7*	ENST00000434536	1	intronic	c.19-107	e2-107	tier3	30	0	0.000	132	94	0.416
944541	8	102504720	102504720	C	G	SNP	*LOC101927172*	ENST00000520268	-1	rna	NULL	NULL	tier1	83	0	0.000	169	108	0.390
944541	9	27268422	27268422	G	C	SNP	*LINC00032*	ENST00000425633	-1	rna	NULL	NULL	tier1	13	0	0.000	31	23	0.426
944541	9	139903352	139903353	-	C	INS	*ABCA2*	ENST00000265662	-1	intronic	c.6931-33_6931-32	e47-32	tier3	19	1	0.050	45	32	0.416
944541	11	32414262	32414262	C	G	SNP	*WT1*	ENST00000332351	-1	missense	c.1289	p.R430P	tier1	215	0	0.000	743	71	0.087
944541	11	32417909	32417910	-	GA	INS	*WT1*	ENST00000332351	-1	frame_shift_ins	c.1143_1142	p.A382fs	tier1	330	0	0.000	751	305	0.289
944541	11	32417914	32417915	-	T	INS	*WT1*	ENST00000332351	-1	frame_shift_ins	c.1138_1137	p.R379fs	tier1	322	0	0.000	925	106	0.103
944541	12	6697549	6697549	C	T	SNP	*CHD4*	ENST00000309577	-1	missense	c.3380	p.R1127Q	tier1	358	0	0.000	1112	95	0.079
944541	12	96330312	96330312	A	-	DEL	*CCDC38*	ENST00000344280	-1	intronic	c.1-11	e1-11	tier3	7	0	0.000	21	29	0.580
944541	12	112888189	112888189	G	A	SNP	*PTPN11*	ENST00000351677	1	missense	c.205	p.E69K	tier1	204	3	0.015	535	381	0.416
944541	13	33017732	33017732	C	T	SNP	*N4BP2L2*	ENST00000399396	-1	silent	c.942	p.A314	tier1	17	0	0.000	51	28	0.354
944541	13	50115190	50115190	C	T	SNP	*RCBTB1*	ENST00000258646	-1	intronic	c.1325-48	e10-48	tier3	13	0	0.000	29	31	0.517
944541	15	52427942	52427942	C	A	SNP	*GNB5*	ENST00000261837	-1	silent	c.639	p.A213	tier1	9	0	0.000	15	16	0.516
944541	15	89386618	89386618	T	A	SNP	*ACAN*	ENST00000439576	1	missense	c.790	p.F264I	tier1	33	0	0.000	79	44	0.358
944541	16	11541929	11541929	G	A	SNP	*LOC101929274*	ENST00000344649	-1	missense	c.1222	p.P408S	tier1	61	0	0.000	85	85	0.500
944541	17	40322106	40322106	G	A	SNP	*KCNH4*	ENST00000264661	-1	intronic	c.1390+19	e8+19	tier3	31	0	0.000	79	42	0.342
944541	17	42635299	42635299	G	A	SNP	*FZD2*	ENST00000315323	1	silent	c.243	p.K81	tier1	34	0	0.000	51	27	0.346
944541	18	43684347	43684347	A	C	SNP	*HAUS1*	ENST00000282058	1	5_prime_untranslated_region	c.-31	NULL	tier2	208	0	0.000	533	369	0.409
944541	19	7964800	7964800	C	T	SNP	*LRRC8E*	ENST00000306708	1	missense	c.1393	p.L465F	tier1	30	0	0.000	64	33	0.340
944541	19	10812636	10812636	T	C	SNP	*QTRT1*	ENST00000250237	1	missense	c.254	p.L85P	tier1	45	0	0.000	77	36	0.316
944541	20	56847816	56847816	T	C	SNP	*PPP4R1L*	ENST00000334187	-1	splice_region	c.292+9	e4+9	tier3	8	0	0.000	36	53	0.596
944541	22	20710847	20710847	C	T	SNP	*FAM230A*	ENST00000434783	1	missense	c.2579	p.A860V	tier1	142	0	0.000	497	29	0.055
944541	22	22842205	22842205	G	C	SNP	*ZNF280B*	ENST00000360412	-1	missense	c.1519	p.L507V	tier1	45	0	0.000	126	85	0.403
955252	2	46583272	46583272	A	C	SNP	*EPAS1*	ENST00000463191	1	3_prime_untranslated_region	c.*46583272	NULL	tier3	91	1	0.011	128	25	0.157
955252	2	111881871	111881871	T	-	DEL	*BCL2L11*	ENST00000393256	1	intronic	c.394+155	e1+155	tier4	175	2	0.011	292	22	0.070
955252	3	49721606	49721606	G	A	SNP	*MST1*	ENST00000449682	-1	missense	c.2033	p.P678L	tier1	220	0	0.000	353	20	0.054
955252	3	49721622	49721622	C	T	SNP	*MST1*	ENST00000449682	-1	missense	c.2017	p.G673S	tier1	204	0	0.000	348	21	0.057
955252	3	125535971	125535971	T	C	SNP	*MIR548I1*	ENST00000408810	-1	5_prime_flanking_region	c.-26576	NULL	tier4	28	0	0.000	38	18	0.321
955252	3	125535974	125535974	G	A	SNP	*MIR548I1*	ENST00000408810	-1	5_prime_flanking_region	c.-26579	NULL	tier4	27	0	0.000	36	18	0.333
955252	5	840644	840644	G	C	SNP	*ZDHHC11*	ENST00000283441	-1	missense	c.750	p.H250Q	tier1	128	2	0.015	183	26	0.124

955252	5	140563408	140563408	A	G	SNP	*PCDHB16*	ENST00000361016	1	missense	c.1274	p.D425G	tier1	235	1	0.004	485	24	0.047
955252	7	157652095	157652096	-	CA	INS	*PTPRN2*	ENST00000404321	-1	intronic	c.1857+39269_1857+3926	e12+39269	tier3	133	2	0.015	148	17	0.103
955252	9	139342941	139342941	T	G	SNP	*SEC16A*	ENST00000313084	-1	missense	c.91	p.T31P	tier1	69	0	0.000	133	18	0.115
955252	11	67432799	67432799	G	A	SNP	*ALDH3B2*	ENST00000349015	-1	silent	c.663	p.R221	tier1	240	0	0.000	370	16	0.041
955252	12	30790136	30790137	-	A	INS	*IPO8*	ENST00000256079	-1	intronic	c.2490-16_2490-15	e22-15	tier3	18	0	0.000	49	25	0.338
955252	20	29628205	29628205	T	A	SNP	*FRG1B*	ENST00000278882	1	intronic	c.229-22	e4-22	tier3	469	7	0.015	1948	99	0.048
955252	20	29628229	29628229	G	T	SNP	*FRG1B*	ENST00000479318	1	nonsense	c.115	p.E39*	tier1	534	8	0.015	2248	106	0.045
955252	22	20402385	20402386	GC	-	DEL	*PI4KAP1*	ENST00000416922	-1	rna	NULL	NULL	tier1	17	0	0.000	12	9	0.429
955252	22	34019122	34019122	T	-	DEL	*LARGE*	ENST00000354992	-1	intronic	c.491+3106	e3+3106	tier3	108	1	0.009	284	32	0.101
988638	1	46505876	46505876	G	A	SNP	*PIK3R3*	ENST00000262741	-1	3_prime_untranslated_region	c.*3469	NULL	tier3	182	0	0.000	193	34	0.150
988638	1	161519606	161519606	A	G	SNP	*FCGR3A*	ENST00000367969	-1	missense	c.29	p.F10S	tier1	128	0	0.000	123	26	0.173
988638	1	231956089	231956090	-	T	INS	*DISC1*	ENST00000439617	1	intronic	c.1981+1826_1981+1825	e9+1826	tier3	122	0	0.000	186	20	0.097
988638	1	233091444	233091444	G	A	SNP	*NTPCR*	ENST00000366628	1	missense	c.176	p.R59Q	tier1	124	0	0.000	163	41	0.200
988638	2	102484410	102484410	C	T	SNP	*MAP4K4*	ENST00000498066	1	rna	NULL	NULL	tier1	104	0	0.000	86	10	0.104
988638	2	128387436	128387436	A	G	SNP	*MYO7B*	ENST00000389524	1	intronic	c.4728+35	e33+35	tier3	108	0	0.000	108	15	0.122
988638	2	135957920	135957920	T	C	SNP	*ZRANB3*	ENST00000264159	-1	missense	c.3232	p.K1078E	tier1	94	0	0.000	116	34	0.227
988638	2	175689250	175689250	A	-	DEL	*CHN1*	ENST00000409900	-1	splice_region_del	c.628-4	e8-4	tier3	44	0	0.000	58	11	0.159
988638	2	192257750	192257750	G	C	SNP	*MYO1B*	ENST00000304164	1	intronic	c.2077-49	e19-49	tier3	84	0	0.000	112	15	0.118
988638	2	202467998	202467998	C	A	SNP	*ALS2CR11*	ENST00000286195	-1	missense	c.319	p.V107F	tier1	76	0	0.000	128	39	0.234
988638	3	32997048	32997048	T	A	SNP	*CCR4*	ENST00000330953	1	3_prime_untranslated_region	c.*1051	NULL	tier3	146	3	0.020	242	29	0.107
988638	3	55061774	55061774	C	T	SNP	*CACNA2D3*	ENST00000288197	1	intronic	c.2987+9430	e35+9430	tier2	91	0	0.000	101	21	0.172
988638	6	55990914	55990914	G	T	SNP	*COL21A1*	ENST00000244728	-1	missense	c.1576	p.H526N	tier1	96	0	0.000	154	56	0.265
988638	7	20826548	20826548	G	T	SNP	*SP8*	ENST00000418710	-1	5_prime_flanking_region	c.-131	NULL	tier2	110	0	0.000	91	17	0.157
988638	7	74225436	74225436	T	C	SNP	*GTF2IRD2*	ENST00000405086	-1	missense	c.799	p.M267V	tier1	142	2	0.014	177	118	0.400
988638	8	94937549	94937550	-	T	INS	*PDP1*	ENST00000396200	1	3_prime_untranslated_region	c.*1648	NULL	tier4	27	0	0.000	55	17	0.236
988638	9	44874097	44874097	G	A	SNP	*ENSG00000231454*	ENST00000450729	1	3_prime_untranslated_region	c.*44874097	NULL	tier3	190	1	0.005	224	27	0.108
988638	9	128083745	128083745	G	T	SNP	*GAPVD1*	ENST00000394105	1	nonsense	c.1636	p.G546*	tier1	76	0	0.000	162	34	0.174
988638	10	51829388	51829388	C	T	SNP	*FAM21A*	ENST00000282633	1	missense	c.208	p.R70W	tier1	196	0	0.000	234	46	0.164
988638	11	5842368	5842368	G	C	SNP	*OR52N2*	ENST00000317037	1	missense	c.803	p.G268A	tier1	84	0	0.000	130	26	0.166
988638	11	89531801	89531801	C	A	SNP	*TRIM49*	ENST00000329758	-1	splice_region	c.860-4	e6-4	tier3	57	0	0.000	140	29	0.171
988638	12	40815079	40815079	G	A	SNP	*MUC19*	ENST00000471230	1	rna	NULL	NULL	tier1	115	0	0.000	296	55	0.157
988638	16	89650436	89650436	G	A	SNP	*CPNE7*	ENST00000268720	1	missense	c.658	p.V220M	tier1	96	1	0.010	95	21	0.181
988638	17	44074056	44074056	G	T	SNP	*MAPT*	ENST00000344290	1	intronic	c.1827+26	e10+26	tier3	70	0	0.000	41	18	0.305
988638	17	74732959	74732959	G	T	SNP	*SRSF2*	ENST00000359995	-1	missense	c.284	p.P95H	tier1	392	1	0.003	397	70	0.150
988638	18	42531907	42531907	G	A	SNP	*SETBP1*	ENST00000282030	1	missense	c.2602	p.D868N	tier1	576	0	0.000	629	106	0.144
988638	19	7675544	7675544	G	C	SNP	*CAMSAP3*	ENST00000446248	1	intronic	c.982-42	e9-42	tier3	102	2	0.019	88	20	0.184
988638	19	10561262	10561262	T	-	DEL	*PDE4A*	ENST00000352831	1	intronic	c.621-17	e5-17	tier3	73	0	0.000	86	13	0.131
988638	19	35265460	35265460	C	T	SNP	*ZNF599*	ENST00000329285	-1	5_prime_flanking_region	c.-1714	NULL	tier4	47	0	0.000	53	10	0.159
988638	20	31022441	31022442	-	G	INS	*ASXL1*	ENST00000375687	1	frame_shift_ins	c.1926_1927	p.G645fs	tier1	805	6	0.007	781	132	0.145
988638	20	44815531	44815531	G	A	SNP	*CDH22*	ENST00000372262	-1	silent	c.1479	p.N493	tier1	88	0	0.000	92	18	0.164
988638	X	14338161	14338161	C	T	SNP	-	-	-	-	-	-	tier3	42	0	0.000	48	25	0.343
988638	X	73071846	73071846	A	-	DEL	*XIST*	ENST00000429829	-1	rna	NULL	NULL	tier1	80	1	0.012	97	16	0.142
991140	1	142653596	142653596	C	T	SNP	*ENSG00000266657*	ENST00000580249	1	rna	NULL	NULL	tier1	211	0	0.000	423	50	0.106
991140	1	152279155	152279155	C	-	DEL	*FLG*	ENST00000368799	-1	frame_shift_del	c.8207	p.G2736fs	tier1	374	0	0.000	691	94	0.120
991140	1	181702771	181702771	C	T	SNP	*CACNA1E*	ENST00000367573	1	silent	c.3147	p.S1049	tier1	268	0	0.000	491	126	0.204
991140	1	223938499	223938499	C	T	SNP	*CAPN2*	ENST00000295006	1	intronic	c.814-93	e7-93	tier3	40	0	0.000	92	22	0.193
991140	1	235926068	235926068	C	T	SNP	*LYST*	ENST00000389793	-1	missense	c.6205	p.G2069R	tier1	51	0	0.000	132	64	0.327
991140	2	97833261	97833261	T	A	SNP	*ANKRD36*	ENST00000420699	1	intronic	c.1532-53	e21-53	tier3	186	4	0.021	666	63	0.086
991140	2	166187904	166187904	T	C	SNP	*SCN2A*	ENST00000283256	1	silent	c.2214	p.I738	tier1	217	1	0.005	503	146	0.224
991140	2	189997806	189997806	G	A	SNP	*MIR3129*	ENST00000581095	-1	rna	NULL	NULL	tier1	55	1	0.018	106	37	0.259
991140	3	116163747	116163747	C	T	SNP	*LSAMP*	ENST00000490035	-1	silent	c.132	p.R44	tier1	67	0	0.000	89	43	0.326
991140	3	132201248	132201248	C	T	SNP	*DNAJC13*	ENST00000260818	1	intronic	c.2979+74	e26+74	tier3	62	2	0.031	105	44	0.295
991140	4	16503736	16503737	-	A	INS	*LDB2*	ENST00000509803	-1	5_prime_untranslated_region	c.-16503736	NULL	tier3	66	0	0.000	121	18	0.130
991140	4	36093672	36093672	T	A	SNP	*ARAP2*	ENST00000303965	-1	intronic	c.4286-30	e27-30	tier3	170	1	0.006	474	120	0.202
991140	6	147006987	147006987	C	G	SNP	*ADGB*	ENST00000397944	1	intronic	c.1311+23	e10+23	tier3	39	0	0.000	158	30	0.159
991140	7	34889221	34889221	C	A	SNP	*NPSR1*	ENST00000381539	1	missense	c.1170	p.N390K	tier1	47	0	0.000	49	30	0.380
991140	8	97506480	97506480	G	A	SNP	*SDC2*	ENST00000520233	1	rna	NULL	NULL	tier1	142	0	0.000	367	132	0.265
991140	8	142166004	142166004	G	T	SNP	*DENND3*	ENST00000262585	1	missense	c.891	p.K297N	tier1	131	0	0.000	216	73	0.253
991140	8	142517302	142517302	G	C	SNP	*MROH5*	ENST00000521053	-1	5_prime_untranslated_region	c.-53	NULL	tier3	273	1	0.004	459	155	0.251
991140	9	133254693	133254693	G	A	SNP	*HMCN2*	ENST00000480829	1	5_prime_flanking_region	c.-19336	NULL	tier3	56	0	0.000	109	31	0.220
991140	9	135521201	135521201	C	A	SNP	*DDX31*	ENST00000372159	-1	intronic	c.1695+81	e13+81	tier3	42	0	0.000	61	26	0.299
991140	11	19735518	19735518	G	A	SNP	*NAV2*	ENST00000396087	1	splice_region	c.267+10	e1+10	tier2	35	0	0.000	53	13	0.197
991140	11	30034426	30034426	A	G	SNP	*KCNA4*	ENST00000328224	-1	5_prime_untranslated_region	c.-201	NULL	tier3	123	0	0.000	195	71	0.266
991140	12	15749242	15749242	C	T	SNP	*PTPRO*	ENST00000544706	1	rna	NULL	NULL	tier1	138	0	0.000	149	71	0.323
991140	12	31297989	31297989	C	T	SNP	*LOC100509445*	ENST00000398963	-1	splice_site	c.NULL	NULL	tier1	294	0	0.000	743	27	0.035
991140	12	48378352	48378352	G	A	SNP	*COL2A1*	ENST00000380518	-1	silent	c.1864	p.L622	tier1	38	0	0.000	63	22	0.259
991140	15	45059668	45059668	C	T	SNP	*TRIM69*	ENST00000329464	1	missense	c.1201	p.R401W	tier1	72	0	0.000	126	49	0.280
991140	16	21974018	21974018	G	A	SNP	*UQCRC2*	ENST00000563711	1	3_prime_untranslated_region	c.*21974018	NULL	tier3	75	0	0.000	170	64	0.274
991140	16	70923652	70923652	G	A	SNP	*HYDIN*	ENST00000393567	-1	intronic	c.9657-45	e57-45	tier3	123	0	0.000	186	67	0.265
991140	16	84872357	84872357	G	A	SNP	*CRISPLD2*	ENST00000565561	1	3_prime_untranslated_region	c.*84872357	NULL	tier3	32	0	0.000	53	20	0.274
991140	17	7578190	7578190	T	C	SNP	*TP53*	ENST00000269305	-1	missense	c.659	p.Y220C	tier1	809	1	0.001	2249	59	0.026
991140	17	7578404	7578404	A	C	SNP	*TP53*	ENST00000269305	-1	missense	c.526	p.C176G	tier1	772	4	0.005	1465	487	0.249
991140	17	7579355	7579355	A	T	SNP	*TP53*	ENST00000269305	-1	missense	c.332	p.L111Q	tier1	821	0	0.000	1784	539	0.232
991140	17	34951507	34951507	G	A	SNP	*DHRS11*	ENST00000251312	1	missense	c.254	p.R85H	tier1	52	0	0.000	115	40	0.258

991140	19	44680481	44680481	G	T	SNP	*ZNF226*	ENST00000337433	1	missense	c.1066	p.V356F	tier1	76	2	0.026	153	46	0.231
991140	19	54395724	54395724	A	G	SNP	*PRKCG*	ENST00000540413	1	intronic	c.687-39	e7-39	tier3	102	1	0.010	213	62	0.224
991140	20	57464246	57464246	C	A	SNP	*GNAS*	ENST00000464788	1	rna	NULL	NULL	tier1	20	0	0.000	31	12	0.279
991140	21	41550865	41550865	G	A	SNP	*DSCAM*	ENST00000400454	-1	missense	c.2936	p.A979V	tier1	469	0	0.000	876	283	0.244

All genome coordinates use NCBI Build 37.
UPN, unique patient number.
Chr, chromosome; Var, variant; Ref, reference; VAF, variant allele frequency, listed as a fraction.
The VAF calculation includes non-supporting reads.
Tier, defined in Walter et. al., NEJM. 2012 Mar 22;366(12):1090-8.

Table S4. Validated Somatic Mutations by Ultra-Deep Error-Corrected Sequencing

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
611	1	53547545	53547545	C	T	*PODN*	intronic	c.1806-108	e10-108	tier3	8982	895	887	5	0.006	23761	3272	2325	923	0.284	21120	2119	1473	622	0.297	35709	4411	4405	4	0.000	25601	3509	3504	0	0.000
611	2	25464481	25464481	G	A	*DNMT3A*	nonsense	c.2032	p.Q678*	tier1	2028	226	225	1	0.004	4329	790	747	41	0.052	4130	517	491	24	0.047	3049	490	487	3	0.006	3039	452	451	0	0.000
611	3	31495819	31495819	G	A	*THRAP3P1*	3_prime_untranslated_region	c.*31495819	NULL	tier3	3035	365	365	0	0.000	3102	654	500	152	0.233	1732	188	138	50	0.266	4527	844	842	1	0.000	4125	0	0	0	NA
611	3	64644370	64644370	G	A	*ADAMTS9*	silent	c.777	p.S259	tier1	3123	364	363	0	0.000	3968	649	567	77	0.120	6484	898	790	107	0.119	8990	1366	1364	0	0.000	7793	1287	1285	1	0.000
611	3	130720537	130720537	T	A	*ATP2C1*	3_prime_untranslated_region	c.*343	NULL	tier4	288	17	17	0	0.000	425	69	45	24	0.348	254	17	10	7	0.412	756	94	93	0	0.000	530	78	77	0	0.000
611	4	187540539	187540539	C	T	*FAT1*	missense	c.7201	p.E2401K	tier1	21282	2384	2364	9	0.004	32719	4299	2970	1289	0.303	24310	2850	2007	820	0.290	52691	6679	6675	1	0.000	33041	4166	4160	1	0.000
611	6	33037020	33037020	G	A	*HLA-DPA1*	missense	c.404	p.T135I	tier1	2634	286	282	1	0.004	18565	2550	1805	734	0.289	13574	1591	1098	483	0.306	31106	3993	3991	0	0.000	21027	2758	2753	0	0.000
611	6	43206066	43206066	C	G	*TTBK1*	5_prime_flanking_region	c.-8333	NULL	tier4	5847	541	536	3	0.006	15507	2392	1662	697	0.295	16426	1814	1285	520	0.288	19550	2486	2476	0	0.000	13342	1837	1821	0	0.000
611	7	45753309	45753309	C	T	*ADCY1*	silent	c.3075	p.H1025	tier1	21752	2553	2548	0	0.000	9088	1296	1201	91	0.070	7784	909	870	38	0.042	31696	4296	4293	0	0.000	19415	2938	2929	0	0.000
611	7	100549883	100549883	G	A	*LOC100131514*	missense	c.464	p.S155N	tier1	12274	1185	1181	2	0.002	14429	1813	1189	602	0.336	14811	1654	1141	505	0.307	28000	3067	3062	0	0.000	20095	2213	2207	0	0.000
611	8	17944578	17944578	C	T	*LOC101929066*	rna	NULL	NULL	tier1	2684	191	190	1	0.005	4051	574	409	161	0.282	5753	548	386	158	0.290	6560	884	877	1	0.000	4619	670	665	0	0.000
611	8	72127533	72127533	C	T	*EYA1*	intronic	c.1597+89	e14+89	tier3	1549	105	104	0	0.000	1463	177	121	52	0.301	2375	229	148	75	0.336	4084	459	455	0	0.000	2230	279	275	0	0.000
611	8	116424437	116424437	G	C	*TRPS1*	3_prime_untranslated_region	c.*1814	NULL	tier3	445	34	34	0	0.000	738	133	99	33	0.250	812	69	49	20	0.290	993	143	142	0	0.000	837	0	0	0	NA
611	9	103338826	103338826	C	T	*TMEFF1*	nonsense	c.1087	p.R363*	tier1	9353	999	983	10	0.010	123	2	1	1	0.500	14226	1630	1016	601	0.372	27451	3387	3382	4	0.000	19021	2398	2388	4	0.002
611	9	131502394	131502394	G	A	*ZER1*	silent	c.1858	p.L620	tier1	13177	1286	1276	7	0.005	14496	1927	1487	430	0.224	11271	1139	883	255	0.224	38977	4802	4799	1	0.000	22185	2704	2702	0	0.000
611	11	6648113	6648113	C	T	*DCHS1*	missense	c.6157	p.V2053M	tier1	13448	1544	1529	9	0.006	18292	2787	2385	394	0.142	13078	1624	1304	316	0.195	27951	3995	3992	1	0.000	21789	3272	3265	0	0.000
611	11	25004690	25004690	A	G	*LUZP2*	missense	c.616	p.M206V	tier1	42802	4243	4231	2	0.000	38780	4819	4449	348	0.073	46612	4847	4425	399	0.083	85559	10251	10249	0	0.000	58070	7108	7089	0	0.000
611	11	125298875	125298875	C	T	*PKNOX2*	intronic	c.937-33	e8-33	tier2	23043	2669	2659	4	0.002	21617	2936	2431	492	0.168	27834	3446	2883	532	0.156	55863	7646	7643	0	0.000	36314	5239	5229	0	0.000
611	12	53553483	53553483	T	C	*CSAD*	missense	c.1313	p.N438S	tier1	7170	932	929	3	0.003	20403	3256	2345	879	0.273	19174	2587	1818	745	0.291	26492	3963	3962	0	0.000	18518	2758	2744	0	0.000
611	14	23072764	23072764	T	A	*ABHD4*	3_prime_untranslated_region	c.*23072764	NULL	tier3	15259	1488	1480	8	0.005	21294	3178	2359	777	0.248	11665	1264	956	303	0.241	25949	3426	3424	0	0.000	20752	2877	2866	0	0.000
611	14	104216205	104216205	G	A	*PPP1R13B*	missense	c.895	p.R299C	tier1	5783	516	515	0	0.000	7995	1079	757	317	0.295	7698	833	589	241	0.290	10755	1235	1231	2	0.000	7363	927	925	0	0.000
611	15	66008017	66008017	G	A	*DENND4A*	intronic	c.1808-56	e12-56	tier4	832	102	102	0	0.000	1718	327	236	89	0.274	2125	293	237	56	0.191	2938	509	508	0	0.000	2159	356	356	0	0.000
611	16	3071729	3071729	G	A	*TNFRSF12A*	intronic	c.334+39	e3+39	tier2	15049	1546	1536	6	0.004	26664	3781	2611	1133	0.303	23166	2648	1856	765	0.292	34221	4344	4340	0	0.000	23753	3174	3167	0	0.000
611	17	3661144	3661144	G	A	*ITGAE*	silent	c.876	p.I292	tier1	7346	765	764	0	0.000	13405	2318	1735	574	0.249	6899	821	629	183	0.225	19367	2754	2752	1	0.000	14580	2149	2149	0	0.000
611	17	26087697	26087697	G	T	*NOS2*	missense	c.2962	p.P988T	tier1	40614	4444	4420	16	0.004	49671	6438	4380	1988	0.312	36749	3875	2631	1191	0.312	92973	11598	11592	1	0.000	56334	6900	6884	0	0.000
611	18	42531913	42531913	G	A	*SETBP1*	missense	c.2608	p.G870S	tier1	29437	3285	3261	14	0.004	36346	4819	3395	1393	0.291	33568	3669	2475	1139	0.315	61869	7748	7737	5	0.000	43134	5370	5361	1	0.000
611	19	39787541	39787541	C	T	*IFNL1*	intronic	c.249+19	e2+19	tier3	12877	1445	1436	5	0.003	14639	2041	1449	576	0.284	14489	1615	1077	532	0.331	24841	3192	3190	0	0.000	17614	2334	2329	0	0.000
611	21	33684165	33684165	A	G	*MRAP*	missense	c.377	p.E126G	tier1	21623	2546	2534	10	0.004	24384	3554	2469	1057	0.300	23550	2879	1997	839	0.296	46032	6446	6441	1	0.000	29013	4082	4073	0	0.000
611	22	23922123	23922123	G	A	*IGLL1*	intronic	c.206+49	e1+49	tier2	5101	490	463	24	0.049	12689	1827	1364	433	0.241	14202	1363	917	435	0.322	27798	3368	3350	8	0.002	17682	2407	2385	3	0.001
611	X	9757836	9757836	C	T	*SHROOM2*	intronic	c.165+3086	e1+3086	tier3	3004	273	273	0	0.000	6031	821	665	149	0.183	7411	693	556	135	0.195	21649	2484	2483	0	0.000	14127	1764	1757	0	0.000
130968	1	6101941	6101941	T	A	*KCNAB2*	splice_region	c.119+9	e2+9	tier2	9117	1310	1252	54	0.041	5823	791	466	313	0.402	6722	729	426	297	0.411	7561	1246	1000	237	0.192	11513	1814	1225	575	0.319
130968	1	115258747	115258747	C	T	*NRAS*	missense	c.35	p.G12D	tier1	22176	2785	2772	8	0.003	16437	1825	1544	239	0.134	19940	2099	1435	552	0.278	14718	1972	1785	120	0.063	29726	4004	4000	1	0.000
130968	1	154960473	154960473	C	A	*FLAD1*	rna	NULL	NULL	tier1	26444	3393	3384	5	0.001	20965	2676	2324	340	0.128	18949	2200	1638	550	0.251	14463	2251	2202	48	0.021	36546	5275	5274	0	0.000
130968	1	160144523	160144523	C	T	*ATP1A4*	missense	c.2297	p.T766M	tier1	2849	369	362	7	0.019	9023	1108	644	459	0.416	5251	561	333	226	0.404	6092	774	602	172	0.222	17103	2270	1540	721	0.319
130968	2	76975737	76975737	G	A	*LRRTM4*	3_prime_untranslated_region	c.*84	NULL	tier3	38318	4579	4514	60	0.013	27202	3047	2527	495	0.164	22295	2266	2113	142	0.063	19840	2589	2386	196	0.076	51124	6658	5042	1567	0.237
130968	2	101554339	101554339	C	T	*NPAS2*	intronic	c.558+35	e5+35	tier3	49321	6376	6272	86	0.014	45095	5558	4212	1252	0.229	39405	4472	3959	474	0.107	34517	4962	4481	474	0.096	79904	11014	7434	3431	0.316
130968	3	121100282	121100282	C	T	*STXBP5L*	silent	c.2562	p.F854	tier1	8611	1310	1303	6	0.005	5926	843	735	104	0.124	8520	1114	795	311	0.281	7288	1351	1256	93	0.069	11489	1941	1938	3	0.002
130968	3	140281105	140281105	C	T	*CLSTN2*	nonsense	c.2167	p.R723*	tier1	18107	2411	2404	3	0.001	13321	1665	1350	308	0.186	12228	1331	1241	89	0.067	10131	1645	1482	162	0.099	22880	3250	2225	1010	0.312
130968	3	150877579	150877579	A	G	*MED12L*	intronic	c.838-40	e7-40	tier3	18685	2212	2198	13	0.006	12151	1405	1221	178	0.127	11457	1128	773	343	0.307	11426	1541	1393	141	0.092	26507	3451	3446	3	0.001
130968	4	57389885	57389885	T	G	*ARL9*	missense	c.215	p.I72S	tier1	8449	1098	1055	40	0.037	6808	904	550	350	0.389	11191	1353	785	558	0.415	8153	1289	1052	234	0.182	14210	2181	1517	655	0.302
130968	4	106157023	106157023	C	T	*TET2*	nonsense	c.1924	p.Q642*	tier1	18459	2126	2072	47	0.022	21448	2542	1531	986	0.392	20506	2122	1183	916	0.436	16772	2187	1799	383	0.176	38163	4891	3256	1585	0.327
130968	4	106164913	106164913	C	A	*TET2*	missense	c.3781	p.R1261S	tier1	6002	737	721	16	0.022	7261	824	519	300	0.366	11194	1053	592	449	0.431	8038	1052	879	168	0.160	13392	1731	1196	524	0.305
130968	4	187541079	187541079	C	T	*FAT1*	missense	c.6661	p.G2221R	tier1	14599	2176	2160	15	0.007	11684	1486	1259	225	0.152	10230	1070	731	328	0.310	9121	1420	1292	123	0.087	20004	2988	2984	0	0.000
130968	6	27840011	27840011	T	A	*HIST1H3I*	missense	c.83	p.K28M	tier1	4955	744	743	0	0.000	9103	1120	950	165	0.148	8655	933	862	68	0.073	7667	1153	1040	113	0.098	15432	2235	2232	3	0.001
130968	6	56366476	56366476	C	T	*DST*	missense	c.19489	p.A6497T	tier1	16020	1864	1849	11	0.006	6205	720	641	75	0.105	7924	840	690	147	0.176	7450	942	899	42	0.045	12038	1575	1397	175	0.111
130968	6	123869713	123869713	G	A	*TRDN*	missense	c.277	p.R93C	tier1	4296	903	901	2	0.002	4291	795	704	91	0.114	4150	711	534	175	0.247	3287	731	677	53	0.073	7027	1600	1600	0	0.000
130968	10	126365553	126365553	G	A	*FAM53B*	intronic	c.906+4623	e3+4623	tier3	9441	1171	1160	11	0.009	5714	664	561	102	0.154	6582	699	479	219	0.314	5752	763	698	65	0.085	10966	1444	1443	1	0.000
130968	11	121384952	121384952	A	G	*SORL1*	missense	c.1133	p.E378G	tier1	14954	1997	1967	27	0.014	9054	1266	913	349	0.277	10484	1255	822	419	0.338	9407	1578	1321	255	0.162	18618	2872	2146	712	0.249
130968	12	51752848	51752848	C	T	*GALNT6*	intronic	c.1368+68	e6+68	tier3	22297	2847	2706	127	0.045	17171	2048	1213	807	0.400	18531	1831	1042	755	0.420	15611	2229	1833	385	0.174	31331	4331	2953	1336	0.311
130968	14	99641862	99641862	C	T	*BCL11B*	silent	c.1311	p.K437	tier1	13222	1697	1676	19	0.011	8577	1104	900	200	0.182	9510	1055	983	68	0.065	8743	1306	1229	77	0.059	15836	2284	1761	514	0.226
130968	15	100272161	100272161	G	T	*LYSMD4*	missense	c.44	p.A15D	tier1	5120	1117	1093	21	0.019	4272	717	503	212	0.297	3973	634	405	226	0.358	4935	1163	993	167	0.144	8252	1856	1373	476	0.257
130968	16	71220653	71220653	G	A	*HYDIN*	intronic	c.135+11	e1+11	tier3	3110	591	589	2	0.003	2607	431	387	43	0.100	3590	576	476	99	0.172	3053	687	666	20	0.029	4943	973	973	0	0.000
130968	17	61790912	61790912	C	T	*STRADA*	intronic	c.227-25	e5-25	tier3	16034	1899	1892	7	0.004	11818	1276	1128	145	0.114	14407	1530	1105	410	0.271	11153	1492	1448	42	0.028	24555	3186	3183	2	0.000
130968	19	10108048	10108048	G	A	*COL5A3*	missense	c.1262	p.P421L	tier1	8756	1136	1132	4	0.004	14354	1597	1349	239	0.151	13525	1345	957	380	0.284	10315	1371	1248	118	0.086	24474	3188	3184	3	0.000
130968	20	31022288	31022288	C	G	*ASXL1*	nonsense	c.1773	p.Y591*	tier1	32968	5334	5098	219	0.041	24920	4058	2379	1635	0.407	23199	4124	2252	1846	0.450	22452	3922	3203	709	0.181	46067	7919	5307	2560	0.325
130968	21	18821227	18821227	C	T	*C21orf37*	3_prime_untranslated_region	c.*1	NULL	tier3	20272	2336	2271	64	0.027	16624	1834	1225	598	0.328	20640	2139	1302	816	0.385	14293	1786	1520	263	0.148	33118	4259	3195	1038	0.245
130968	21	36206702	36206702	C	T	*RUNX1*	5_prime_untranslated_region	c.-36206702	NULL	tier2	42079	5223	5184	34	0.007	30632	3634	3088	526	0.146	25673	2711	1831	849	0.317	20439	2764	2524	230	0.084	52143	6729	6715	11	0.002
130968	21	36252865	36252865	C	T	*RUNX1*	missense	c.497	p.R166Q	tier1	21753	2745	2708	34	0.012	13284	1636	1526	104	0.064	15615	1649	1594	52	0.032	13223	1974	1958	14	0.007	25664	3597	3588	7	0.002
130968	21	39673268	39673268	C	T	*KCNJ15*	3_prime_untranslated_region	c.*957	NULL	tier3	6888	1028	998	30	0.029	4683	590	348	240	0.408	6821	635	347	282	0.448	6256	1051	853	192	0.184	8479	1306	861	435	0.336
130968	X	37028271	37028271	G	A	*FAM47C*	silent	c.1788	p.P596	tier1	1206	200	200	0	0.000	571	97	76	21	0.216	585	47	23	23	0.500	882	165	140	25	0.152	1324	228	228	0	0.000
130968	X	107512279	107512279	C	T	*COL4A6*	rna	NULL	NULL	tier1	3999	430	422	7	0.016	4341	600	411	186	0.312	5729	663	257	403	0.611	4435	724	607	116	0.160	7689	1151	1150	1	0.000
145094	1	16073346	16073346	C	T	*TMEM82*	intronic	c.758-16	e5-16	tier3	46837	6152	5876	268	0.044	18012	2445	1233	1208	0.495	14407	2114	1338	773	0.366	145506	6324	6306	14	0.002	83639	8067	7958	106	0.013
145094	1	186084343	186084343	G	A	*HMCN1*	intronic	c.11405-47	e75-47	tier3	34328	5239	5210	27	0.005	14329	2027	1138	875	0.435	16049	2511	2007	500	0.199	174964	12202	12178	15	0.001	59386	7438	7413	15	0.002
145094	1	200880497	200880497	C	T	*C1orf106*	intronic	c.1215-84	e9-84	tier2	21731	2822	2797	24	0.009	9373	1274	656	616	0.484	14563	1927	1514	409	0.213	203231	8232	8219	11	0.001	64412	5518	5464	52	0.009
145094	1	206945563	206945563	C	G	*IL10*	intronic	c.165+53	e1+53	tier3	15323	2347	2334	13	0.006	8188	1130	599	528	0.469	7136	1035	795	235	0.228	48458	3463	3459	2	0.000	20373	2654	2634	18	0.007
145094	2	116520209	116520209	C	T	*DPP10*	intronic	c.1125+23	e12+23	tier3	16613	2422	2419	2	0.001	5966	872	538	331	0.381	10245	1509	1326	179	0.119	31630	2740	2736	3	0.001	47005	5158	5132	24	0.005
145094	2	122004343	122004343	C	G	*TFCP2L1*	intronic	c.657+51	e6+51	tier3	29545	5453	5427	23	0.004	12314	2252	1203	1035	0.462	15775	2702	2160	530	0.197	267115	15785	15748	14	0.001	96397	11216	11093	108	0.010
145094	2	233651863	233651863	G	A	*GIGYF2*	missense	c.602	p.R201K	tier1	30314	4153	4141	12	0.003	10384	1316	912	404	0.307	10326	1477	1250	226	0.153	109718	8821	8808	8	0.001	60154	7275	7218	53	0.007
145094	4	48563681	48563681	G	C	*FRYL*	intronic	c.3697-28	e30-28	tier3	26012	3447	3434	12	0.003	9859	1131	698	429	0.381	18734	2416	2043	362	0.151	252892	20635	20619	10	0.000	105341	12956	12930	18	0.001
145094	4	54880073	54880073	T	C	*CHIC2*	splice_region	c.388-10	e5-10	tier3	1729	365	361	4	0.011	1180	237	109	128	0.540	1024	246	186	60	0.244	2762	652	651	0	0.000	1427	349	345	4	0.011
145094	7	2962258	2962258	G	A	*CARD11*	splice_region	c.2269+10	e16+10	tier3	43827	5748	5706	40	0.007	23464	3128	1673	1430	0.461	43065	5688	4438	1231	0.217	460555	21257	21246	8	0.000	226502	20415	20396	13	0.001
145094	7	128520034	128520034	G	A	*KCP*	5_prime_untranslated_region	c.-128520034	NULL	tier2	3558	864	858	6	0.007	706	140	73	66	0.475	356	79	61	18	0.228	1356	319	318	1	0.000	767	170	167	2	0.000
145094	8	30702831	30702831	C	G	*TEX15*	missense	c.3703	p.V1235L	tier1	25571	3391	3389	2	0.001	6535	849	731	118	0.139	14336	1894	1819	74	0.039	226211	11600	11595	1	0.000	77495	7792	7777	13	0.002
145094	8	134239796	134239796	A	G	*WISP1*	missense	c.947	p.K316R	tier1	31377	5014	5000	14	0.003	10181	1877	1185	684	0.366	20221	3475	2933	530	0.153	284827	16927	16907	11	0.001	94916	11093	11020	69	0.006
145094	9	35079180	35079180	T	G	*FANCG*	missense	c.143	p.E48A	tier1	21756	2447	2429	18	0.007	7631	907	444	463	0.510	12457	1500	1139	360	0.240	259709	9913	9894	13	0.001	88235	7269	7186	80	0.011
145094	10	18829133	18829133	G	C	*CACNB2*	3_prime_untranslated_region	c.*480	NULL	tier3	11114	1552	1547	5	0.003	4726	598	310	287	0.481	6156	806	629	177	0.220	87756	4745	4739	6	0.001	29461	3191	3151	37	0.012
145094	10	75526485	75526485	A	G	*SEC24C*	intronic	c.1800-33	e12-33	tier3	14372	1950	1938	11	0.006	4820	632	335	296	0.469	7441	1042	810	231	0.222	95229	6059	6043	5	0.001	31214	3654	3599	48	0.013
145094	12	120638934	120638934	C	G	*RPLP0*	5_prime_untranslated_region	c.-348	NULL	tier2	30465	4525	4502	21	0.005	13664	2034	1055	972	0.480	23771	3537	2756	772	0.219	117258	9621	9599	17	0.002	94884	10881	10741	124	0.011
145094	15	45266191	45266191	A	G	*C15orf43*	intronic	c.523+38	e6+38	tier2	8413	1131	1122	8	0.007	3534	435	235	199	0.459	4265	582	450	132	0.227	11375	930	928	2	0.000	16995	2043	2012	31	0.015
145094	17	7577120	7577120	C	T	*TP53*	missense	c.818	p.R273H	tier1	50566	6425	6205	214	0.033	5799	715	95	619	0.867	20549	2635	1874	754	0.287	814080	33992	33957	22	0.001	248587	22341	22206	116	0.005
145094	17	29552143	29552143	C	A	*NF1*	missense	c.1876	p.L626I	tier1	5965	814	808	5	0.006	1203	147	24	122	0.836	877	113	88	25	0.221	2779	0	0	0	NA	5374	665	664	1	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
145094	21	44324363	44324363	G	A	*NDUFV3*	missense	c.1241	p.G414E	tier1	64410	7969	7908	54	0.007	24417	3048	1615	1419	0.468	40570	5090	3905	1167	0.230	694415	26990	26965	18	0.001	218769	18522	18445	61	0.003
145094	X	18845595	18845595	A	T	*PPEF1*	missense	c.1952	p.N651I	tier1	23300	3453	3410	41	0.012	12714	1690	93	1596	0.945	22525	3192	1768	1418	0.445	403663	20214	20160	36	0.002	140265	14019	13687	306	0.022
147444	1	34164429	34164429	G	T	*CSMD2*	missense	c.3849	p.S1283R	tier1	10290	1129	1128	0	0.000	16483	2413	1916	485	0.202	6187	946	590	354	0.375	15888	2354	2354	0	0.000	21486	0	0	0	NA
147444	1	38262323	38262323	C	A	*MANEAL*	intronic	c.661-93	e3-93	tier3	2165	275	275	0	0.000	7229	1513	1130	379	0.251	462	97	63	34	0.351	4264	891	890	0	0.000	3351	714	714	0	0.000
147444	1	89480937	89480937	G	A	*GBP3*	intronic	c.318+33	e2+33	tier3	7300	649	647	2	0.003	11614	1649	1280	359	0.219	9529	1155	783	363	0.317	13756	1811	1803	0	0.000	16354	1990	1986	0	0.000
147444	1	163306613	163306613	C	T	*NUF2*	missense	c.410	p.T137M	tier1	3443	301	301	0	0.000	4347	572	427	145	0.254	5278	633	411	221	0.350	5388	705	701	2	0.000	6979	866	864	1	0.000
147444	1	201016781	201016781	C	T	*CACNA1S*	intronic	c.4442-27	e37-27	tier3	16351	1886	1885	0	0.000	25629	3574	2693	870	0.244	14418	1908	1146	754	0.397	25369	3725	3717	1	0.000	36926	5116	5106	2	0.000
147444	1	226061960	226061960	G	A	*TMEM63A*	intronic	c.266+28	e2+28	tier3	16399	2317	2312	5	0.002	29734	3693	2795	881	0.240	15664	2217	1412	799	0.361	30394	4252	4244	3	0.001	41701	5988	5975	2	0.000
147444	2	42119915	42119915	C	A	*LOC388942*	rna	NULL	NULL	tier1	15872	1949	1949	0	0.000	33223	4789	3666	1062	0.225	13828	1925	1192	728	0.379	29304	4375	4363	1	0.000	43219	6097	6090	1	0.000
147444	2	42936013	42936013	G	T	*MTA3*	splice_site	c.1303-1	e14-1	tier1	5984	0	0	0	0.000	1321	196	141	54	0.277	2977	393	226	166	0.423	7442	921	920	0	0.000	2843	354	353	0	0.000
147444	2	128262356	128262356	T	C	*IWS1*	missense	c.1123	p.M375V	tier1	1566	0	0	0	0.000	5088	1002	775	218	0.220	1101	192	125	63	0.335	3646	695	694	0	0.000	2270	377	377	0	0.000
147444	2	216972458	216972458	C	G	*XRCC5*	intronic	c.1+37	e0+37	tier2	13512	1330	1329	0	0.000	22640	3716	2783	915	0.247	7246	1084	652	424	0.394	18493	2929	2923	1	0.000	24099	3335	3330	0	0.000
147444	3	158306755	158306755	A	T	*MLF1*	intronic	c.96-3468	e2-3468	tier4	10373	943	942	0	0.000	14220	2013	1495	498	0.250	6438	865	527	337	0.390	15470	2192	2188	0	0.000	16084	2054	2052	0	0.000
147444	4	100761543	100761543	C	A	*DAPP1*	missense	c.322	p.H108N	tier1	16889	1615	1614	0	0.000	16531	2137	1767	362	0.170	15332	1944	1456	479	0.248	23704	3119	3117	0	0.000	39234	5007	5006	0	0.000
147444	4	149358015	149358015	C	T	*NR3C2*	splice_site	c.1-1	e1-1	tier1	8884	737	737	0	0.000	18409	2745	2187	536	0.197	7838	1045	720	318	0.306	17182	2480	2478	0	0.000	17484	2372	2370	0	0.000
147444	5	1331845	1331845	C	T	*CLPTM1L*	5_prime_untranslated_region	c.-1331845	NULL	tier3	7188	709	709	0	0.000	18907	2183	1651	528	0.242	8869	1189	735	452	0.381	18715	2550	2548	0	0.000	27835	3489	3488	1	0.000
147444	5	38464253	38464253	C	T	*EGFLAM*	3_prime_untranslated_region	c.*165	NULL	tier3	25273	2674	2673	1	0.000	37488	4629	3523	1081	0.235	21658	2897	1888	994	0.345	39935	5325	5322	0	0.000	65825	8669	8666	1	0.000
147444	5	39331903	39331903	C	T	*C9*	missense	c.490	p.G164R	tier1	3614	396	392	3	0.008	7230	846	578	266	0.315	5114	681	419	257	0.380	7180	929	928	0	0.000	10463	1327	1323	2	0.000
147444	6	39841127	39841127	G	A	*DAAM2*	missense	c.1158	p.M386I	tier1	22892	2709	2708	1	0.000	36571	4423	3222	1184	0.269	23555	3154	1965	1172	0.374	27379	3620	3616	1	0.000	55044	7235	7228	2	0.000
147444	6	72086766	72086766	A	G	*LINC00472*	intronic	c.NULL	NULL	tier3	5832	722	719	1	0.001	8420	1484	1127	352	0.238	5386	913	569	341	0.375	8670	1526	1524	1	0.000	12365	2034	2032	1	0.000
147444	6	167571516	167571516	G	A	*GPR31*	5_prime_untranslated_region	c.-197	NULL	tier3	8744	1006	1006	0	0.000	14622	2606	1969	630	0.242	3344	584	391	192	0.329	16196	2761	2759	0	0.000	14664	2330	2329	0	0.000
147444	7	57522854	57522854	A	T	*ZNF716*	missense	c.242	p.E81V	tier1	2895	288	287	1	0.003	3974	838	584	249	0.299	1176	177	70	107	0.605	4731	890	888	0	0.000	4150	625	624	0	0.000
147444	7	100190385	100190385	C	T	*FBXO24*	intronic	c.673-21	e5-21	tier3	4295	457	457	0	0.000	7017	1252	863	378	0.305	1137	187	56	130	0.699	6729	0	0	0	NA	10618	1514	1510	3	0.000
147444	9	43628454	43628454	G	A	*SPATA31A6*	intronic	c.309-76	e4-76	tier3	3697	578	578	0	0.000	8414	1541	1206	330	0.215	2425	526	356	170	0.323	6629	1354	1352	0	0.000	8862	1746	1746	0	0.000
147444	10	24762962	24762962	C	T	*KIAA1217*	missense	c.1652	p.A551V	tier1	24207	2668	2665	1	0.000	34026	4225	3132	1062	0.253	14479	1937	1231	705	0.364	37714	4858	4845	1	0.000	45456	5957	5948	2	0.000
147444	10	46148449	46148449	A	T	*ZFAND4*	nonsense	c.243	p.Y81*	tier1	15979	0	0	0	0.000	15247	2183	1575	601	0.276	20851	2692	1644	1028	0.385	24361	3340	3337	0	0.000	32088	4172	4172	0	0.000
147444	11	3687330	3687330	C	T	*CHRNA10*	3_prime_untranslated_region	c.*7	NULL	tier3	11245	1190	1189	0	0.000	10857	1639	1316	319	0.195	4935	619	394	225	0.363	13933	1998	1996	0	0.000	19592	2631	2631	0	0.000
147444	11	64821688	64821688	C	A	*NAALADL1*	intronic	c.992+34	e6+34	tier3	4423	555	554	0	0.000	12071	2706	2112	581	0.216	782	165	95	70	0.424	8350	1819	1817	0	0.000	4226	885	884	0	0.000
147444	12	57579580	57579580	C	T	*LRP1*	missense	c.6730	p.R2244W	tier1	6181	696	696	0	0.000	26763	3903	2873	1013	0.261	6627	914	554	360	0.394	17975	2775	2772	0	0.000	33845	4700	4693	4	0.000
147444	12	57627594	57627594	G	T	*SHMT2*	missense	c.1186	p.A396S	tier1	13274	1571	1571	0	0.000	22545	3253	2353	886	0.274	7162	1122	636	483	0.432	18905	3067	3061	2	0.000	25936	3859	3858	1	0.000
147444	12	113444369	113444369	G	A	*OAS2*	silent	c.1620	p.K540	tier1	15418	1653	1651	1	0.001	21520	2598	2053	539	0.208	17323	2268	1479	773	0.343	31905	4057	4054	1	0.000	39100	4943	4940	2	0.000
147444	14	50612016	50612016	C	G	*SOS2*	missense	c.2539	p.V847L	tier1	10465	965	965	0	0.000	18080	2343	1784	553	0.237	18691	2434	1589	838	0.345	21243	2773	2770	2	0.000	31737	3941	3935	0	0.000
147444	16	4384836	4384836	C	T	*GLIS2*	missense	c.380	p.P127L	tier1	7854	786	786	0	0.000	15154	2076	1685	388	0.187	3524	497	356	141	0.284	13459	1988	1988	0	0.000	29256	3913	3913	0	0.000
147444	16	68721437	68721437	G	A	*CDH3*	silent	c.1593	p.T531	tier1	15403	1868	1863	2	0.001	34448	4447	3531	907	0.204	13791	1934	1200	720	0.375	35130	4812	4805	1	0.000	62205	8515	8499	1	0.000
147444	17	6902088	6902088	T	A	*ALOX12*	missense	c.474	p.D158E	tier1	14246	1722	1719	1	0.001	23871	3684	2667	996	0.272	8290	1350	845	499	0.371	21448	3702	3696	1	0.000	24367	3965	3961	0	0.000
147444	17	7578212	7578212	G	A	*TP53*	nonsense	c.637	p.R213*	tier1	22258	2460	2455	4	0.002	30580	3693	1741	1930	0.526	19813	2508	550	1946	0.780	37541	4758	4755	2	0.000	61329	7953	7945	1	0.000
147444	17	42981590	42981590	C	T	*FAM187A*	silent	c.393	p.D131	tier1	47868	5772	5768	2	0.000	55298	7527	5501	1980	0.265	37199	4994	3021	1943	0.391	62573	8697	8692	1	0.000	97167	13188	13178	3	0.000
147444	17	67079228	67079228	T	C	*ABCA6*	intronic	c.4476-74	e35-74	tier3	8915	676	674	0	0.000	19158	3211	2397	789	0.248	7217	949	618	327	0.346	15634	2403	2396	0	0.000	17567	2311	2294	0	0.000
147444	19	15511862	15511862	A	G	*AKAP8L*	splice_region	c.817-8	e6-8	tier3	7462	1023	1021	0	0.000	14061	2968	2183	754	0.257	4029	817	518	297	0.364	13847	2715	2706	0	0.000	9776	2093	2093	0	0.000
147444	X	49857254	49857254	C	T	*CLCN5*	3_prime_untranslated_region	c.*378	NULL	tier3	1676	225	223	0	0.000	2153	481	360	118	0.247	1424	302	192	109	0.362	3530	763	761	0	0.000	2350	441	440	0	0.000
147457	1	1275514	1275514	G	A	*DVL1*	silent	c.813	p.N271	tier1	71838	7953	7887	60	0.008	50023	3998	3104	882	0.221	NA	NA	NA	NA	NA	563315	2136	2114	15	0.007	NA	NA	NA	NA	NA
147457	1	6021933	6021933	C	T	*NPHP4*	silent	c.594	p.A198	tier1	82192	9236	9137	90	0.010	74813	5482	3969	1493	0.273	NA	NA	NA	NA	NA	663553	2621	2617	4	0.000	NA	NA	NA	NA	NA
147457	1	6532561	6532561	C	T	*PLEKHG5*	intronic	c.1317+26	e11+26	tier2	61797	6723	6687	33	0.005	73116	4965	3989	954	0.193	NA	NA	NA	NA	NA	680691	2889	2877	7	0.002	NA	NA	NA	NA	NA
147457	1	9790439	9790439	C	T	*CLSTN1*	5_prime_untranslated_region	c.-9790439	NULL	tier2	26926	3208	3189	17	0.005	35139	2892	2028	852	0.296	NA	NA	NA	NA	NA	99329	539	532	3	0.006	NA	NA	NA	NA	NA
147457	1	12908093	12908093	C	T	*HNRNPCL1*	missense	c.50	p.R17H	tier1	9864	2381	2368	12	0.005	16084	3228	2899	321	0.100	NA	NA	NA	NA	NA	18011	228	228	0	0.000	NA	NA	NA	NA	NA
147457	1	15701093	15701093	G	A	*FHAD1*	missense	c.526	p.A176T	tier1	10299	1917	1907	8	0.004	13715	1704	1423	275	0.162	NA	NA	NA	NA	NA	59604	320	310	10	0.031	NA	NA	NA	NA	NA
147457	1	22852716	22852716	G	A	*ZBTB40*	missense	c.3547	p.V1183M	tier1	29783	3717	3680	32	0.009	43150	3737	2697	1031	0.277	NA	NA	NA	NA	NA	260521	1028	1024	2	0.000	NA	NA	NA	NA	NA
147457	1	24410953	24410953	C	T	*MYOM3*	5_prime_untranslated_region	c.-24410953	NULL	tier3	5017	626	623	3	0.005	12370	1208	873	331	0.275	NA	NA	NA	NA	NA	28532	138	138	0	0.000	NA	NA	NA	NA	NA
147457	1	27220835	27220835	G	A	*GPATCH3*	missense	c.943	p.R315W	tier1	32106	3849	3812	32	0.008	37292	3057	2139	903	0.297	NA	NA	NA	NA	NA	158407	692	692	0	0.000	NA	NA	NA	NA	NA
147457	1	27708286	27708286	C	T	*CD164L2*	silent	c.357	p.P119	tier1	35777	4612	4574	35	0.008	45162	4310	3078	1215	0.283	NA	NA	NA	NA	NA	217441	1006	1002	2	0.000	NA	NA	NA	NA	NA
147457	1	29365837	29365837	G	A	*EPB41*	missense	c.1535	p.R512Q	tier1	14177	1779	1772	7	0.004	9657	1013	799	212	0.210	NA	NA	NA	NA	NA	57921	312	305	7	0.022	NA	NA	NA	NA	NA
147457	1	29609283	29609283	C	T	*PTPRU*	missense	c.1964	p.A655V	tier1	12730	1935	1912	21	0.011	15638	2322	1630	685	0.296	NA	NA	NA	NA	NA	27637	198	198	0	0.000	NA	NA	NA	NA	NA
147457	1	43897426	43897426	C	T	*SZT2*	nonsense	c.4957	p.R1653*	tier1	21536	2851	2828	22	0.008	34721	2606	2024	577	0.222	NA	NA	NA	NA	NA	169689	779	771	4	0.000	NA	NA	NA	NA	NA
147457	1	46206734	46206734	C	T	*IPP*	missense	c.563	p.R188Q	tier1	55584	6791	6730	50	0.007	55801	4833	3639	1168	0.243	NA	NA	NA	NA	NA	427469	1745	1727	8	0.000	NA	NA	NA	NA	NA
147457	1	52826134	52826134	C	T	*CC2D1B*	missense	c.565	p.E189K	tier1	49228	5448	5388	56	0.010	57021	4206	2900	1285	0.307	NA	NA	NA	NA	NA	570889	2107	2087	13	0.006	NA	NA	NA	NA	NA
147457	1	54670978	54670978	G	A	*MRPL37*	missense	c.541	p.V181M	tier1	12313	1787	1762	19	0.011	19411	2293	1586	693	0.304	NA	NA	NA	NA	NA	47840	259	257	1	0.000	NA	NA	NA	NA	NA
147457	1	74905278	74905278	C	T	*FPGT-TNNI3K*	silent	c.2286	p.G762	tier1	42020	5018	4963	50	0.010	41060	3368	2359	1000	0.298	NA	NA	NA	NA	NA	141869	701	694	7	0.010	NA	NA	NA	NA	NA
147457	1	116609238	116609238	C	T	*SLC22A15*	missense	c.1463	p.P488L	tier1	2974	699	694	5	0.007	4704	1085	745	337	0.311	NA	NA	NA	NA	NA	9884	117	117	0	0.000	NA	NA	NA	NA	NA
147457	1	151507600	151507600	G	A	*CGN*	missense	c.2987	p.R996Q	tier1	8922	808	800	8	0.010	18411	1792	1291	492	0.276	NA	NA	NA	NA	NA	56683	225	224	0	0.000	NA	NA	NA	NA	NA
147457	1	155019719	155019719	C	T	*DCST1*	missense	c.1543	p.R515W	tier1	48530	6387	6306	75	0.012	44954	4562	3223	1320	0.291	NA	NA	NA	NA	NA	320274	1300	1290	5	0.004	NA	NA	NA	NA	NA
147457	1	156713349	156713349	G	A	*HDGF*	5_prime_untranslated_region	c.-156713349	NULL	tier3	41864	4661	4628	30	0.006	40129	2865	2181	679	0.237	NA	NA	NA	NA	NA	379633	1507	1495	5	0.003	NA	NA	NA	NA	NA
147457	1	160604556	160604556	G	A	*SLAMF1*	missense	c.547	p.H183Y	tier1	31255	3700	3662	33	0.009	32539	2290	1652	636	0.278	NA	NA	NA	NA	NA	193973	817	817	0	0.000	NA	NA	NA	NA	NA
147457	1	162492585	162492585	C	T	*UHMK1*	3_prime_untranslated_region	c.*245	NULL	tier3	8801	1314	1296	12	0.009	17055	2466	1694	761	0.310	NA	NA	NA	NA	NA	32134	267	266	0	0.000	NA	NA	NA	NA	NA
147457	1	165182958	165182958	G	A	*LMX1A*	missense	c.589	p.R197C	tier1	55702	5828	5763	61	0.010	50926	3244	2242	985	0.305	NA	NA	NA	NA	NA	450199	1680	1658	15	0.009	NA	NA	NA	NA	NA
147457	1	171308645	171308645	C	T	*TOP1P1*	3_prime_untranslated_region	c.*171308645	NULL	tier3	69234	7907	7816	86	0.011	64746	5246	4048	1184	0.226	NA	NA	NA	NA	NA	593218	2505	2479	19	0.008	NA	NA	NA	NA	NA
147457	1	172410952	172410952	G	A	*PIGC*	missense	c.811	p.R271C	tier1	57537	6495	6446	41	0.006	55001	3951	2905	1034	0.263	NA	NA	NA	NA	NA	415952	1687	1666	10	0.000	NA	NA	NA	NA	NA
147457	1	201168470	201168470	C	T	*IGFN1*	missense	c.376	p.R126W	tier1	10047	1755	1724	23	0.013	25404	3112	2167	933	0.301	NA	NA	NA	NA	NA	157050	651	647	0	0.000	NA	NA	NA	NA	NA
147457	1	201184183	201184183	G	A	*IGFN1*	missense	c.8896	p.V2966M	tier1	42787	5253	5210	33	0.006	61698	5059	4015	1029	0.204	NA	NA	NA	NA	NA	451315	1882	1879	1	0.000	NA	NA	NA	NA	NA
147457	1	215298011	215298011	G	A	*KCNK2*	silent	c.393	p.P131	tier1	38898	4675	4639	29	0.006	37233	3212	2489	715	0.223	NA	NA	NA	NA	NA	318300	1232	1224	4	0.000	NA	NA	NA	NA	NA
147457	1	220340567	220340567	G	A	*RAB3GAP2*	intronic	c.3087+68	e26+68	tier3	30284	4011	3977	33	0.008	29862	3184	2414	765	0.241	NA	NA	NA	NA	NA	152044	655	647	3	0.005	NA	NA	NA	NA	NA
147457	1	228033658	228033658	G	A	*PRSS38*	missense	c.730	p.D244N	tier1	3900	655	646	9	0.014	6886	1042	761	279	0.268	NA	NA	NA	NA	NA	30197	154	153	0	0.000	NA	NA	NA	NA	NA
147457	1	236898908	236898908	G	A	*ACTN2*	intronic	c.698-27	e8-27	tier3	5790	1387	1371	15	0.011	8936	1816	1317	487	0.270	NA	NA	NA	NA	NA	11011	134	134	0	0.000	NA	NA	NA	NA	NA
147457	1	244230451	244230451	C	T	*ENSG00000237759*	5_prime_flanking_region	c.-40216	NULL	tier3	8546	1091	1080	11	0.010	15039	1339	944	394	0.294	NA	NA	NA	NA	NA	19888	129	124	5	0.039	NA	NA	NA	NA	NA
147457	2	1652185	1652185	C	T	*PXDN*	missense	c.3367	p.G1123R	tier1	37419	4363	4309	51	0.012	45147	3657	2572	1067	0.293	NA	NA	NA	NA	NA	212069	889	864	15	0.000	NA	NA	NA	NA	NA
147457	2	3469478	3469478	C	T	*TRAPPC12*	missense	c.35	p.T12M	tier1	71192	8355	8289	59	0.007	40437	3760	3099	654	0.174	NA	NA	NA	NA	NA	495804	1841	1827	11	0.006	NA	NA	NA	NA	NA
147457	2	10059126	10059126	G	A	*TAF1B*	intronic	c.1272-44	e13-44	tier2	6517	1030	1017	12	0.012	12414	1756	1229	519	0.297	NA	NA	NA	NA	NA	18225	162	162	0	0.000	NA	NA	NA	NA	NA
147457	2	18112379	18112379	G	A	*KCNS3*	missense	c.104	p.R35Q	tier1	6471	852	850	2	0.002	22486	2453	1929	520	0.212	NA	NA	NA	NA	NA	104213	456	456	0	0.000	NA	NA	NA	NA	NA
147457	2	20845070	20845070	G	A	*HS1BP3*	intronic	c.198+30	e2+30	tier2	9896	2323	2305	18	0.008	12505	1753	1298	454	0.259	NA	NA	NA	NA	NA	29305	341	337	4	0.012	NA	NA	NA	NA	NA
147457	2	24255779	24255779	G	A	*C2orf44*	missense	c.1856	p.A619V	tier1	18282	2455	2424	22	0.009	21091	3271	2299	956	0.294	NA	NA	NA	NA	NA	112416	587	586	0	0.000	NA	NA	NA	NA	NA
147457	2	25457176	25457176	G	A	*DNMT3A*	missense	c.2711	p.P904L	tier1	24026	2799	2758	36	0.013	24172	2059	1394	653	0.319	NA	NA	NA	NA	NA	181910	676	650	18	0.027	NA	NA	NA	NA	NA
147457	2	25466800	25466800	G	A	*DNMT3A*	missense	c.1903	p.R635W	tier1	37880	4963	4922	35	0.007	49822	4628	3431	1183	0.256	NA	NA	NA	NA	NA	230984	1120	1107	12	0.011	NA	NA	NA	NA	NA
147457	2	25469932	25469932	G	A	*DNMT3A*	silent	c.1110	p.Y370	tier1	74731	8071	7967	93	0.012	65493	4574	3183	1378	0.302	NA	NA	NA	NA	NA	539224	2259	2243	12	0.005	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	2	26177162	26177162	G	A	*KIF3C*	silent	c.1863	p.N621	tier1	27245	3864	3823	35	0.009	34757	3636	2585	1031	0.285	NA	NA	NA	NA	NA	55934	352	344	7	0.020	NA	NA	NA	NA	NA
147457	2	26644243	26644243	G	A	*CCDC164*	missense	c.331	p.E111K	tier1	52526	6231	6157	71	0.011	49967	4340	3163	1169	0.270	NA	NA	NA	NA	NA	419492	1765	1757	8	0.005	NA	NA	NA	NA	NA
147457	2	26800492	26800492	G	A	*C2orf70*	missense	c.457	p.V153I	tier1	17275	2496	2483	12	0.005	31085	3339	2489	836	0.251	NA	NA	NA	NA	NA	37946	275	274	0	0.000	NA	NA	NA	NA	NA
147457	2	27261955	27261955	C	T	*TMEM214*	missense	c.1448	p.T483M	tier1	25164	3393	3357	31	0.009	28439	2917	2030	875	0.301	NA	NA	NA	NA	NA	196050	815	813	2	0.000	NA	NA	NA	NA	NA
147457	2	27310227	27310227	C	T	*KHK*	splice_region	c.92+8	e1+8	tier2	12150	1593	1573	17	0.011	19205	2114	1308	798	0.379	NA	NA	NA	NA	NA	98513	389	384	5	0.013	NA	NA	NA	NA	NA
147457	2	27592008	27592008	G	A	*EIF2B4*	missense	c.283	p.R95W	tier1	48723	5745	5696	44	0.008	31799	2663	1991	660	0.249	NA	NA	NA	NA	NA	340406	1359	1357	1	0.000	NA	NA	NA	NA	NA
147457	2	27801023	27801023	G	A	*C2orf16*	silent	c.1584	p.T528	tier1	49704	5839	5767	68	0.012	62611	4740	3400	1317	0.279	NA	NA	NA	NA	NA	398132	1510	1504	4	0.003	NA	NA	NA	NA	NA
147457	2	56403145	56403145	C	T	*LOC100129434*	5_prime_untranslated_region	c.-56403145	NULL	tier2	30072	3662	3615	35	0.010	39079	3050	2166	878	0.288	NA	NA	NA	NA	NA	123501	631	627	2	0.000	NA	NA	NA	NA	NA
147457	2	58459235	58459235	G	A	*FANCL*	missense	c.109	p.H37Y	tier1	13637	1776	1763	13	0.007	17012	1659	1163	491	0.297	NA	NA	NA	NA	NA	57782	276	273	3	0.000	NA	NA	NA	NA	NA
147457	2	61331050	61331050	G	A	*KIAA1841*	silent	c.1428	p.P476	tier1	18861	2518	2491	24	0.010	26024	2812	1988	814	0.291	NA	NA	NA	NA	NA	58194	266	265	1	0.000	NA	NA	NA	NA	NA
147457	2	70504464	70504464	C	T	*PCYOX1*	silent	c.1458	p.N486	tier1	20184	2781	2738	41	0.015	42952	4283	2982	1283	0.301	NA	NA	NA	NA	NA	229202	948	945	2	0.000	NA	NA	NA	NA	NA
147457	2	73829499	73829499	C	T	*ALMS1*	splice_region	c.12295+4	e20+4	tier2	36808	4521	4479	37	0.008	33371	3007	2047	950	0.317	NA	NA	NA	NA	NA	184306	816	802	8	0.010	NA	NA	NA	NA	NA
147457	2	74173887	74173887	G	A	*DGUOK*	missense	c.297	p.M99I	tier1	20765	3307	3272	34	0.010	28136	3815	2704	1098	0.289	NA	NA	NA	NA	NA	91628	539	518	18	0.034	NA	NA	NA	NA	NA
147457	2	74867224	74867224	C	T	*C2orf65*	missense	c.179	p.R60H	tier1	55784	6862	6761	84	0.012	52644	5052	3606	1419	0.282	NA	NA	NA	NA	NA	475210	2051	2017	28	0.014	NA	NA	NA	NA	NA
147457	2	75158001	75158001	C	T	*ENSG00000204792*	rna	NULL	NULL	tier1	34294	4184	4139	43	0.010	47513	4285	3048	1224	0.287	NA	NA	NA	NA	NA	190008	830	821	7	0.008	NA	NA	NA	NA	NA
147457	2	91800800	91800800	G	A	*ENSG00000233991*	3_prime_untranslated_region	c.*91800800	NULL	tier2	133344	17358	17292	41	0.002	147828	13612	12816	745	0.055	NA	NA	NA	NA	NA	424083	2440	2412	8	0.003	NA	NA	NA	NA	NA
147457	2	131704217	131704217	C	T	*ARHGEF4*	missense	c.3004	p.R1002C	tier1	18730	2500	2478	22	0.009	24811	2622	1910	699	0.268	NA	NA	NA	NA	NA	74943	362	350	7	0.020	NA	NA	NA	NA	NA
147457	2	141459402	141459402	G	A	*LRP1B*	silent	c.6315	p.N2105	tier1	59363	6861	6824	30	0.004	54726	4706	3676	1009	0.215	NA	NA	NA	NA	NA	582577	2229	2229	0	0.000	NA	NA	NA	NA	NA
147457	2	160983105	160983105	G	A	*ITGB6*	silent	c.1668	p.G556	tier1	8514	1059	1053	6	0.006	8706	948	719	228	0.241	NA	NA	NA	NA	NA	69591	277	277	0	0.000	NA	NA	NA	NA	NA
147457	2	170134318	170134318	C	T	*LRP2*	missense	c.1709	p.R570H	tier1	22666	2925	2893	31	0.011	20311	2603	1812	786	0.303	NA	NA	NA	NA	NA	241150	975	970	5	0.000	NA	NA	NA	NA	NA
147457	2	179613743	179613743	C	T	*TTN*	missense	c.13384	p.E4462K	tier1	2413	310	307	3	0.010	6760	742	540	202	0.272	NA	NA	NA	NA	NA	13490	65	65	0	0.000	NA	NA	NA	NA	NA
147457	2	198274685	198274685	C	T	*SF3B1*	missense	c.713	p.R238H	tier1	15354	1483	1470	11	0.007	20271	1773	1310	458	0.259	NA	NA	NA	NA	NA	73244	222	222	0	0.000	NA	NA	NA	NA	NA
147457	2	201619547	201619547	C	T	*AOX2P*	3_prime_untranslated_region	c.*201619547	NULL	tier3	36167	4367	4329	33	0.008	36897	3282	2461	803	0.246	NA	NA	NA	NA	NA	392259	1448	1432	12	0.008	NA	NA	NA	NA	NA
147457	2	203948117	203948117	G	A	*NBEAL1*	missense	c.860	p.R287H	tier1	12825	2428	2401	26	0.011	19494	2420	1709	709	0.293	NA	NA	NA	NA	NA	65429	799	799	0	0.000	NA	NA	NA	NA	NA
147457	2	213886807	213886807	G	A	*IKZF2*	missense	c.622	p.R208C	tier1	12114	1633	1621	12	0.007	21353	2293	1778	513	0.224	NA	NA	NA	NA	NA	84581	416	414	1	0.000	NA	NA	NA	NA	NA
147457	2	215798769	215798769	C	T	*ABCA12*	intronic	c.7680+33	e52+33	tier3	17922	2244	2233	10	0.004	12457	1227	1003	221	0.181	NA	NA	NA	NA	NA	123380	531	528	1	0.000	NA	NA	NA	NA	NA
147457	2	218938006	218938006	C	T	*RUFY4*	missense	c.427	p.R143C	tier1	44597	5378	5337	35	0.007	49790	4124	2927	1187	0.289	NA	NA	NA	NA	NA	315806	1307	1293	7	0.005	NA	NA	NA	NA	NA
147457	2	219538351	219538351	G	A	*STK36*	missense	c.88	p.V30M	tier1	26783	3613	3585	27	0.007	29394	3507	2485	1009	0.289	NA	NA	NA	NA	NA	193441	843	830	12	0.014	NA	NA	NA	NA	NA
147457	2	219544699	219544699	C	T	*STK36*	silent	c.1032	p.L344	tier1	13816	2376	2359	17	0.007	21860	2554	1869	680	0.267	NA	NA	NA	NA	NA	43770	343	343	0	0.000	NA	NA	NA	NA	NA
147457	2	220312930	220312930	C	T	*SPEG*	silent	c.1050	p.T350	tier1	51172	6462	6396	54	0.008	39196	3226	2368	846	0.263	NA	NA	NA	NA	NA	265917	1402	1396	2	0.000	NA	NA	NA	NA	NA
147457	2	226447163	226447163	G	A	*NYAP2*	missense	c.1030	p.V344M	tier1	7589	1459	1362	16	0.012	9152	1699	1258	390	0.237	NA	NA	NA	NA	NA	57406	316	311	0	0.000	NA	NA	NA	NA	NA
147457	2	226447731	226447731	G	A	*NYAP2*	missense	c.1598	p.R533H	tier1	26535	3480	3444	35	0.010	27168	2294	1629	659	0.288	NA	NA	NA	NA	NA	68068	384	383	0	0.000	NA	NA	NA	NA	NA
147457	2	227872842	227872842	C	T	*COL4A4*	silent	c.4701	p.A1567	tier1	43657	4699	4678	17	0.004	31418	2319	1979	338	0.146	NA	NA	NA	NA	NA	221277	930	920	5	0.005	NA	NA	NA	NA	NA
147457	2	227915822	227915822	G	A	*COL4A4*	silent	c.3021	p.Y1007	tier1	8324	1031	1022	9	0.009	12382	1111	782	327	0.295	NA	NA	NA	NA	NA	16473	103	103	0	0.000	NA	NA	NA	NA	NA
147457	2	238245159	238245159	C	T	*COL6A3*	missense	c.8584	p.V2862I	tier1	4878	1195	1178	16	0.013	6734	1357	968	385	0.285	NA	NA	NA	NA	NA	14056	127	122	4	0.032	NA	NA	NA	NA	NA
147457	2	238461018	238461018	C	T	*MLPH*	nonsense	c.1714	p.R572*	tier1	17479	2156	2135	19	0.009	19667	1753	1365	384	0.220	NA	NA	NA	NA	NA	63549	352	352	0	0.000	NA	NA	NA	NA	NA
147457	2	241517127	241517127	C	T	*RNPEPL1*	missense	c.1303	p.R435C	tier1	53678	6279	6228	45	0.007	44715	3667	2675	980	0.268	NA	NA	NA	NA	NA	297421	1153	1141	8	0.007	NA	NA	NA	NA	NA
147457	3	9768381	9768381	C	T	*CPNE9*	missense	c.572	p.S191L	tier1	10305	1355	1341	12	0.009	11500	1246	879	367	0.295	NA	NA	NA	NA	NA	69500	326	324	2	0.000	NA	NA	NA	NA	NA
147457	3	11468460	11468460	C	T	*ATG7*	intronic	c.2079+60	e17+60	tier3	2640	574	564	9	0.016	8229	1675	1158	512	0.307	NA	NA	NA	NA	NA	5342	69	69	0	0.000	NA	NA	NA	NA	NA
147457	3	14552987	14552987	G	A	*GRIP2*	5_prime_untranslated_region	c.-14552987	NULL	tier3	2635	638	632	5	0.008	4623	983	678	303	0.309	NA	NA	NA	NA	NA	3152	44	37	7	0.159	NA	NA	NA	NA	NA
147457	3	14862667	14862667	C	T	*FGD5*	missense	c.2089	p.R697W	tier1	55830	6689	6614	71	0.011	48724	4014	2853	1146	0.287	NA	NA	NA	NA	NA	610856	2242	2218	18	0.008	NA	NA	NA	NA	NA
147457	3	16269593	16269593	C	T	*GALNTL2*	3_prime_untranslated_region	c.*586	NULL	tier3	33101	4452	4418	27	0.006	32854	3175	2492	678	0.214	NA	NA	NA	NA	NA	316446	1244	1244	0	0.000	NA	NA	NA	NA	NA
147457	3	24231711	24231711	C	T	*THRB*	missense	c.137	p.R46H	tier1	35652	4117	4055	49	0.012	39849	2943	2134	797	0.272	NA	NA	NA	NA	NA	188872	814	805	8	0.010	NA	NA	NA	NA	NA
147457	3	32811381	32811381	G	A	*CNOT10*	silent	c.2187	p.A729	tier1	22238	3380	3360	20	0.006	32939	3942	2887	1045	0.266	NA	NA	NA	NA	NA	169875	780	771	9	0.012	NA	NA	NA	NA	NA
147457	3	46450139	46450139	C	T	*CCRL2*	missense	c.605	p.P202L	tier1	46260	5488	5423	61	0.011	49499	4126	2870	1235	0.301	NA	NA	NA	NA	NA	309794	1158	1148	8	0.007	NA	NA	NA	NA	NA
147457	3	48266702	48266702	C	T	*CAMP*	intronic	c.391-81	e4-81	tier2	9428	1571	1555	14	0.009	13795	1892	1361	524	0.278	NA	NA	NA	NA	NA	32489	231	230	0	0.000	NA	NA	NA	NA	NA
147457	3	48694445	48694445	G	A	*CELSR3*	missense	c.4085	p.A1362V	tier1	42529	5343	5285	50	0.009	31874	3095	2153	918	0.299	NA	NA	NA	NA	NA	50590	316	316	0	0.000	NA	NA	NA	NA	NA
147457	3	52559275	52559275	G	A	*NT5DC2*	missense	c.1156	p.R386C	tier1	20100	3093	3066	21	0.007	27328	2781	1987	782	0.282	NA	NA	NA	NA	NA	137165	668	663	3	0.000	NA	NA	NA	NA	NA
147457	3	68781240	68781240	C	T	*FAM19A4*	3_prime_untranslated_region	c.*1053	NULL	tier3	5284	1198	1180	18	0.015	7990	1846	1321	518	0.282	NA	NA	NA	NA	NA	7026	93	93	0	0.000	NA	NA	NA	NA	NA
147457	3	69987598	69987598	C	T	*MITF*	3_prime_untranslated_region	c.*69987598	NULL	tier3	18109	2554	2521	32	0.013	24475	3159	2195	954	0.303	NA	NA	NA	NA	NA	80086	425	419	4	0.009	NA	NA	NA	NA	NA
147457	3	70014355	70014355	C	T	*MITF*	missense	c.1537	p.R513W	tier1	23250	2682	2666	16	0.006	30361	2809	2283	518	0.185	NA	NA	NA	NA	NA	117705	480	474	6	0.013	NA	NA	NA	NA	NA
147457	3	101050880	101050880	C	T	*SENP7*	missense	c.2647	p.V883I	tier1	19986	2519	2487	29	0.012	23847	2393	1904	485	0.203	NA	NA	NA	NA	NA	146257	679	678	1	0.000	NA	NA	NA	NA	NA
147457	3	101308992	101308992	G	A	*PCNP*	3_prime_untranslated_region	c.*101308992	NULL	tier3	10991	1521	1498	23	0.015	12730	1784	1157	625	0.351	NA	NA	NA	NA	NA	56430	331	328	2	0.000	NA	NA	NA	NA	NA
147457	3	122329604	122329604	G	A	*PARP15*	intronic	c.543+27	e3+27	tier3	15389	2262	2233	27	0.012	20689	2499	1814	681	0.273	NA	NA	NA	NA	NA	54904	317	317	0	0.000	NA	NA	NA	NA	NA
147457	3	123044224	123044224	C	T	*ADCY5*	missense	c.2033	p.R678H	tier1	47365	6168	6125	38	0.006	57488	5394	4120	1252	0.233	NA	NA	NA	NA	NA	255929	1216	1204	8	0.000	NA	NA	NA	NA	NA
147457	3	123210530	123210530	G	A	*PTPLB*	3_prime_untranslated_region	c.*3205	NULL	tier2	5202	1116	1109	6	0.005	5893	1120	916	203	0.181	NA	NA	NA	NA	NA	11082	106	106	0	0.000	NA	NA	NA	NA	NA
147457	3	133193895	133193895	C	A	*BFSP2*	3_prime_untranslated_region	c.*79	NULL	tier3	32770	4972	4933	38	0.008	38358	4462	3427	1021	0.230	NA	NA	NA	NA	NA	228864	977	971	6	0.006	NA	NA	NA	NA	NA
147457	3	138341122	138341122	C	T	*FAIM*	silent	c.306	p.D102	tier1	11352	1499	1492	7	0.005	20583	2508	1777	722	0.289	NA	NA	NA	NA	NA	104017	500	490	9	0.018	NA	NA	NA	NA	NA
147457	3	156431808	156431808	C	T	*METTL15P1*	5_prime_untranslated_region	c.-156431808	NULL	tier3	9300	1155	1142	11	0.010	14452	1382	984	390	0.284	NA	NA	NA	NA	NA	18272	114	112	2	0.000	NA	NA	NA	NA	NA
147457	3	184289092	184289092	C	T	*EPHB3*	intronic	c.119-14	e2-14	tier3	41686	4580	4514	48	0.011	31884	2129	1433	690	0.325	NA	NA	NA	NA	NA	368882	1473	1438	14	0.010	NA	NA	NA	NA	NA
147457	3	186336256	186336256	G	A	*AHSG*	intronic	c.772-69	e6-69	tier3	19634	2632	2597	31	0.012	30886	3502	2404	1082	0.310	NA	NA	NA	NA	NA	127468	593	591	1	0.000	NA	NA	NA	NA	NA
147457	3	194081495	194081495	G	A	*LRRC15*	missense	c.296	p.T99M	tier1	73754	8720	8623	87	0.010	62659	4872	3453	1399	0.288	NA	NA	NA	NA	NA	416842	1671	1667	4	0.002	NA	NA	NA	NA	NA
147457	3	196387275	196387275	C	T	*LRRC33*	missense	c.761	p.T254M	tier1	3772	691	689	2	0.003	5593	822	599	223	0.271	NA	NA	NA	NA	NA	15638	78	73	5	0.064	NA	NA	NA	NA	NA
147457	3	196751232	196751232	G	A	*MFI2*	silent	c.429	p.P143	tier1	18421	2732	2725	7	0.003	15904	1848	1395	451	0.244	NA	NA	NA	NA	NA	69505	430	430	0	0.000	NA	NA	NA	NA	NA
147457	4	1332229	1332229	G	A	*MAEA*	missense	c.919	p.G307S	tier1	62770	8548	8443	79	0.009	65605	6090	4466	1591	0.263	NA	NA	NA	NA	NA	347430	1536	1524	6	0.004	NA	NA	NA	NA	NA
147457	4	9828063	9828063	G	A	*SLC2A9*	silent	c.1581	p.I527	tier1	52485	6497	6467	28	0.004	45468	4637	3867	763	0.165	NA	NA	NA	NA	NA	313716	1400	1383	9	0.006	NA	NA	NA	NA	NA
147457	4	15691400	15691400	G	A	*FAM200B*	3_prime_untranslated_region	c.*15691400	NULL	tier4	10478	1339	1327	11	0.008	15820	1489	1081	403	0.272	NA	NA	NA	NA	NA	50640	217	214	3	0.014	NA	NA	NA	NA	NA
147457	4	17868743	17868743	C	T	*LCORL*	intronic	c.776+18948	e6+18948	tier3	8094	1474	1456	18	0.012	12310	2163	1515	644	0.298	NA	NA	NA	NA	NA	30898	197	197	0	0.000	NA	NA	NA	NA	NA
147457	4	42509034	42509034	G	A	*ATP8A1*	silent	c.2085	p.I695	tier1	29195	3171	3160	10	0.003	22589	1357	1177	179	0.132	NA	NA	NA	NA	NA	158376	744	735	7	0.000	NA	NA	NA	NA	NA
147457	4	44177057	44177057	C	T	*KCTD8*	missense	c.1172	p.R391H	tier1	14531	2428	2410	16	0.007	19599	2531	1848	675	0.268	NA	NA	NA	NA	NA	51380	375	375	0	0.000	NA	NA	NA	NA	NA
147457	4	57384937	57384937	G	A	*ARL9*	missense	c.302	p.R101Q	tier1	19786	2530	2503	22	0.009	31894	2986	2108	869	0.292	NA	NA	NA	NA	NA	146056	633	619	14	0.022	NA	NA	NA	NA	NA
147457	4	69048233	69048233	C	T	*FTLP10*	3_prime_untranslated_region	c.*69048233	NULL	tier3	19584	2906	2874	28	0.010	21402	2187	1521	659	0.302	NA	NA	NA	NA	NA	76868	463	451	6	0.000	NA	NA	NA	NA	NA
147457	4	85758110	85758110	C	T	*WDFY3*	missense	c.548	p.R183Q	tier1	27765	3184	3156	27	0.008	31231	2557	1916	639	0.250	NA	NA	NA	NA	NA	250186	880	879	1	0.000	NA	NA	NA	NA	NA
147457	4	88293939	88293939	G	A	*HSD17B11*	missense	c.479	p.T160M	tier1	7789	987	983	2	0.002	4847	638	532	102	0.161	NA	NA	NA	NA	NA	92324	350	349	0	0.000	NA	NA	NA	NA	NA
147457	4	119461591	119461591	G	A	*CEP170P1*	intronic	c.NULL	NULL	tier3	42152	5491	5449	40	0.007	47794	4165	3151	1003	0.241	NA	NA	NA	NA	NA	306887	1945	1935	7	0.004	NA	NA	NA	NA	NA
147457	4	122846298	122846298	G	A	*TRPC3*	nonsense	c.1051	p.R351*	tier1	56755	6779	6733	42	0.006	57864	5187	3982	1192	0.230	NA	NA	NA	NA	NA	350208	1455	1439	7	0.005	NA	NA	NA	NA	NA
147457	4	162421108	162421108	C	T	*FSTL5*	intronic	c.1458+60	e11+60	tier3	21814	3051	3037	13	0.004	17604	2730	2113	610	0.224	NA	NA	NA	NA	NA	149467	586	582	2	0.000	NA	NA	NA	NA	NA
147457	4	166009582	166009582	C	T	*TMEM192*	intronic	c.574+38	e4+38	tier3	59431	7221	7150	66	0.009	70494	5521	3885	1620	0.294	NA	NA	NA	NA	NA	469978	1901	1891	9	0.005	NA	NA	NA	NA	NA
147457	4	187630302	187630302	C	T	*FAT1*	missense	c.680	p.R227H	tier1	64479	6897	6837	56	0.008	55371	3809	2988	809	0.213	NA	NA	NA	NA	NA	496818	1911	1903	8	0.004	NA	NA	NA	NA	NA
147457	4	189026057	189026057	C	T	*TRIML2*	silent	c.69	p.S23	tier1	8762	2133	2115	18	0.008	13473	2196	1680	505	0.231	NA	NA	NA	NA	NA	22387	533	533	0	0.000	NA	NA	NA	NA	NA
147457	5	770160	770160	C	T	*ZDHHC11*	intronic	c.1239+25854	e12+25854	tier3	48032	5900	5860	33	0.006	57439	4792	4015	760	0.159	NA	NA	NA	NA	NA	146974	573	565	8	0.014	NA	NA	NA	NA	NA
147457	5	1293693	1293693	C	T	*TERT*	silent	c.1308	p.A436	tier1	37263	4470	4446	21	0.005	28882	2304	1858	438	0.191	NA	NA	NA	NA	NA	155464	625	624	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	5	1338034	1338034	G	A	*CLPTM1L*	silent	c.663	p.R221	tier1	87830	9964	9853	77	0.008	70248	5076	3463	1585	0.314	NA	NA	NA	NA	NA	638897	2695	2660	23	0.009	NA	NA	NA	NA	NA
147457	5	1483662	1483662	G	A	*LPCAT1*	intronic	c.668-61	e6-61	tier3	14481	2628	2599	26	0.010	24837	3664	2555	1093	0.300	NA	NA	NA	NA	NA	24241	220	210	9	0.041	NA	NA	NA	NA	NA
147457	5	6602599	6602599	C	T	*NSUN2*	missense	c.1972	p.V658M	tier1	23099	3676	3627	44	0.012	34628	4399	3049	1337	0.305	NA	NA	NA	NA	NA	44723	352	352	0	0.000	NA	NA	NA	NA	NA
147457	5	13762777	13762777	C	T	*DNAH5*	intronic	c.10281+54	e60+54	tier3	8630	2100	2088	11	0.005	13119	2377	1745	623	0.263	NA	NA	NA	NA	NA	24603	236	236	0	0.000	NA	NA	NA	NA	NA
147457	5	31995780	31995780	C	T	*PDZD2*	silent	c.1077	p.H359	tier1	28942	3461	3416	37	0.011	63181	4432	3112	1307	0.296	NA	NA	NA	NA	NA	191301	881	872	5	0.000	NA	NA	NA	NA	NA
147457	5	34190535	34190535	C	T	*ENSG00000215156*	3_prime_untranslated_region	c.*34190535	NULL	tier3	65126	8005	7980	11	0.001	88107	7460	7089	361	0.048	NA	NA	NA	NA	NA	92824	652	645	0	0.000	NA	NA	NA	NA	NA
147457	5	35910093	35910093	C	T	*CAPSL*	missense	c.400	p.E134K	tier1	35003	4451	4416	32	0.007	29265	3263	2422	839	0.257	NA	NA	NA	NA	NA	232307	923	917	5	0.005	NA	NA	NA	NA	NA
147457	5	41149449	41149449	G	A	*C6*	silent	c.2517	p.D839	tier1	4240	1041	1032	9	0.009	6757	1406	973	432	0.307	NA	NA	NA	NA	NA	7136	88	88	0	0.000	NA	NA	NA	NA	NA
147457	5	129521471	129521471	G	A	*CHSY3*	missense	c.2636	p.R879Q	tier1	20992	3037	3009	28	0.009	29467	3080	2128	946	0.308	NA	NA	NA	NA	NA	74738	397	396	0	0.000	NA	NA	NA	NA	NA
147457	5	140308059	140308059	C	T	*PCDHAC1*	missense	c.1582	p.R528W	tier1	6970	635	624	10	0.016	15984	2042	1421	617	0.303	NA	NA	NA	NA	NA	25924	136	136	0	0.000	NA	NA	NA	NA	NA
147457	5	140751057	140751057	G	A	*PCDHGB3*	missense	c.1096	p.V366I	tier1	8638	2079	2062	15	0.007	14673	2882	2012	864	0.300	NA	NA	NA	NA	NA	11893	154	154	0	0.000	NA	NA	NA	NA	NA
147457	5	145610359	145610359	C	T	*RBM27*	silent	c.729	p.I243	tier1	64532	7397	7324	63	0.009	54129	4069	3128	921	0.227	NA	NA	NA	NA	NA	293020	1215	1207	4	0.000	NA	NA	NA	NA	NA
147457	5	146236055	146236055	C	T	*PPP2R2B*	splice_region	c.37+7	e1+7	tier3	14142	1911	1880	26	0.014	12947	1595	1138	456	0.286	NA	NA	NA	NA	NA	84759	354	350	1	0.000	NA	NA	NA	NA	NA
147457	5	147929769	147929769	G	A	*HTR4*	missense	c.83	p.T28M	tier1	26378	4464	4435	27	0.006	28473	3328	2600	719	0.217	NA	NA	NA	NA	NA	93684	524	520	4	0.008	NA	NA	NA	NA	NA
147457	5	149584221	149584221	C	T	*SLC6A7*	intronic	c.1432+27	e11+27	tier3	48554	5469	5434	33	0.006	27050	2421	1948	470	0.194	NA	NA	NA	NA	NA	244160	1102	1102	0	0.000	NA	NA	NA	NA	NA
147457	5	153434852	153434852	C	T	*MFAP3*	3_prime_untranslated_region	c.*1579	NULL	tier3	7924	1862	1841	16	0.009	14135	2844	2136	699	0.247	NA	NA	NA	NA	NA	15556	242	242	0	0.000	NA	NA	NA	NA	NA
147457	5	159665575	159665575	G	A	*FABP6*	intronic	c.481-38	e6-38	tier3	3160	438	433	4	0.009	5099	602	433	169	0.281	NA	NA	NA	NA	NA	11801	57	57	0	0.000	NA	NA	NA	NA	NA
147457	5	173534383	173534383	C	T	*HMP19*	missense	c.391	p.R131C	tier1	41742	5492	5454	28	0.005	45667	4730	3448	1268	0.269	NA	NA	NA	NA	NA	292563	1662	1656	5	0.000	NA	NA	NA	NA	NA
147457	5	176308809	176308809	G	A	*HK3*	silent	c.2277	p.I759	tier1	37127	4454	4404	44	0.010	29955	2621	1856	753	0.289	NA	NA	NA	NA	NA	224006	899	890	4	0.004	NA	NA	NA	NA	NA
147457	6	3127540	3127540	C	T	*BPHL*	silent	c.276	p.V92	tier1	13044	1802	1772	26	0.014	19683	2361	1583	770	0.327	NA	NA	NA	NA	NA	58578	400	397	0	0.000	NA	NA	NA	NA	NA
147457	6	25727357	25727357	G	A	*HIST1H2BA*	missense	c.221	p.R74H	tier1	14792	1833	1813	17	0.009	19814	1607	1139	466	0.290	NA	NA	NA	NA	NA	56511	318	318	0	0.000	NA	NA	NA	NA	NA
147457	6	27217008	27217008	C	T	*PRSS16*	missense	c.467	p.A156V	tier1	23019	2712	2696	15	0.006	23150	2008	1579	421	0.211	NA	NA	NA	NA	NA	153372	626	626	0	0.000	NA	NA	NA	NA	NA
147457	6	31913016	31913016	G	A	*C2*	missense	c.2141	p.R714H	tier1	19525	2823	2787	34	0.012	29159	3121	2181	932	0.299	NA	NA	NA	NA	NA	100033	489	480	5	0.000	NA	NA	NA	NA	NA
147457	6	33554497	33554497	C	T	*GGNBP1*	missense	c.148	p.R50C	tier1	29872	3713	3672	35	0.009	37994	3349	2304	1027	0.308	NA	NA	NA	NA	NA	122612	513	512	0	0.000	NA	NA	NA	NA	NA
147457	6	33990389	33990389	C	T	*GRM4*	3_prime_untranslated_region	c.*209	NULL	tier3	27642	3366	3335	26	0.008	19411	1722	1180	539	0.314	NA	NA	NA	NA	NA	205524	762	751	5	0.000	NA	NA	NA	NA	NA
147457	6	42985429	42985429	C	T	*KLHDC3*	missense	c.41	p.T14M	tier1	43747	5968	5909	54	0.009	51510	5286	3654	1608	0.306	NA	NA	NA	NA	NA	163688	764	761	3	0.004	NA	NA	NA	NA	NA
147457	6	52522264	52522264	C	T	*TMEM14A*	5_prime_flanking_region	c.-19637	NULL	tier3	15182	1890	1872	12	0.006	30946	2509	2109	392	0.157	NA	NA	NA	NA	NA	94944	690	677	7	0.010	NA	NA	NA	NA	NA
147457	6	55270421	55270421	G	A	*GFRAL*	3_prime_flanking_region	c.*3770	NULL	tier3	27260	3329	3300	26	0.008	27849	2266	1698	565	0.250	NA	NA	NA	NA	NA	135270	550	550	0	0.000	NA	NA	NA	NA	NA
147457	6	105726111	105726111	C	T	*PREP*	missense	c.2041	p.G681R	tier1	22255	2815	2780	33	0.012	34450	3182	2236	933	0.294	NA	NA	NA	NA	NA	50811	292	292	0	0.000	NA	NA	NA	NA	NA
147457	6	108985689	108985689	G	A	*FOXO3*	silent	c.1653	p.S551	tier1	18776	2205	2194	11	0.005	19185	1635	1344	289	0.177	NA	NA	NA	NA	NA	53710	394	394	0	0.000	NA	NA	NA	NA	NA
147457	6	136709445	136709445	C	T	*MAP7*	intronic	c.592+86	e5+86	tier3	15212	2356	2341	7	0.003	16160	2179	1732	435	0.201	NA	NA	NA	NA	NA	111582	514	509	2	0.000	NA	NA	NA	NA	NA
147457	6	136944051	136944051	G	A	*MAP3K5*	silent	c.2085	p.Y695	tier1	9715	1825	1813	10	0.005	14977	2452	1768	677	0.277	NA	NA	NA	NA	NA	23103	210	210	0	0.000	NA	NA	NA	NA	NA
147457	6	151672062	151672062	G	A	*AKAP12*	missense	c.2536	p.V846M	tier1	9376	1208	1197	9	0.007	16711	1668	1268	394	0.237	NA	NA	NA	NA	NA	32831	197	197	0	0.000	NA	NA	NA	NA	NA
147457	6	157527582	157527582	C	T	*ARID1B*	silent	c.5427	p.D1809	tier1	6651	981	966	13	0.013	10590	1189	855	333	0.280	NA	NA	NA	NA	NA	30684	153	153	0	0.000	NA	NA	NA	NA	NA
147457	6	157529705	157529705	G	A	*ARID1B*	3_prime_untranslated_region	c.*680	NULL	tier3	44344	5882	5858	19	0.003	29280	3098	2477	614	0.199	NA	NA	NA	NA	NA	293392	1040	1040	0	0.000	NA	NA	NA	NA	NA
147457	6	160481709	160481709	G	A	*IGF2R*	silent	c.3222	p.A1074	tier1	57923	7512	7427	82	0.011	53917	5179	3685	1478	0.286	NA	NA	NA	NA	NA	333617	1392	1388	4	0.003	NA	NA	NA	NA	NA
147457	6	170594817	170594817	C	T	*DLL1*	intronic	c.732-30	e6-30	tier3	13104	2257	2240	12	0.005	19957	2054	1525	525	0.256	NA	NA	NA	NA	NA	187112	808	793	15	0.019	NA	NA	NA	NA	NA
147457	7	2474107	2474107	C	T	*CHST12*	3_prime_untranslated_region	c.*588	NULL	tier4	16773	1731	1722	8	0.005	18335	1241	1004	235	0.190	NA	NA	NA	NA	NA	212637	852	844	6	0.000	NA	NA	NA	NA	NA
147457	7	20762660	20762660	G	A	*ABCB5*	missense	c.1108	p.V370I	tier1	16040	2039	2023	13	0.006	10803	1314	1048	264	0.201	NA	NA	NA	NA	NA	242932	926	921	5	0.005	NA	NA	NA	NA	NA
147457	7	42005169	42005169	C	T	*GLI3*	missense	c.3502	p.G1168R	tier1	24615	3256	3218	31	0.010	24901	2445	1728	709	0.291	NA	NA	NA	NA	NA	91000	389	382	5	0.013	NA	NA	NA	NA	NA
147457	7	48139220	48139220	C	T	*UPP1*	intronic	c.45-47	e2-47	tier3	33132	4254	4208	44	0.010	30690	3073	2101	960	0.314	NA	NA	NA	NA	NA	277967	1093	1093	0	0.000	NA	NA	NA	NA	NA
147457	7	75609676	75609676	C	T	*POR*	missense	c.386	p.P129L	tier1	32700	4069	4019	43	0.011	38807	3512	2480	1020	0.291	NA	NA	NA	NA	NA	371747	1412	1388	21	0.015	NA	NA	NA	NA	NA
147457	7	76610187	76610187	G	A	*ENSG00000186704*	3_prime_untranslated_region	c.*76610187	NULL	tier3	32416	4589	4555	32	0.007	29461	3193	2404	780	0.245	NA	NA	NA	NA	NA	191448	858	852	5	0.006	NA	NA	NA	NA	NA
147457	7	94293941	94293941	G	A	*PEG10*	3_prime_untranslated_region	c.*95	NULL	tier3	35381	5299	5231	53	0.010	53096	6296	4460	1790	0.286	NA	NA	NA	NA	NA	105272	594	594	0	0.000	NA	NA	NA	NA	NA
147457	7	97872988	97872988	C	T	*TECPR1*	intronic	c.532-84	e4-84	tier3	67798	7496	7419	69	0.009	55014	4186	2929	1245	0.298	NA	NA	NA	NA	NA	539200	2268	2249	9	0.004	NA	NA	NA	NA	NA
147457	7	97920701	97920701	G	A	*BRI3*	3_prime_untranslated_region	c.*146	NULL	tier3	1717	410	408	2	0.005	2514	569	381	188	0.330	NA	NA	NA	NA	NA	2959	41	41	0	0.000	NA	NA	NA	NA	NA
147457	7	98258817	98258817	G	A	*NPTX2*	3_prime_untranslated_region	c.*876	NULL	tier3	13175	1619	1602	15	0.009	18386	2152	1507	632	0.295	NA	NA	NA	NA	NA	38468	407	397	4	0.000	NA	NA	NA	NA	NA
147457	7	100730606	100730606	G	A	*TRIM56*	missense	c.13	p.G5R	tier1	30984	4262	4235	27	0.006	31974	3034	2287	731	0.242	NA	NA	NA	NA	NA	133271	725	717	8	0.011	NA	NA	NA	NA	NA
147457	7	133894966	133894966	C	T	*LRGUK*	intronic	c.1843+8638	e15+8638	tier3	32529	3784	3772	12	0.003	21152	1643	1390	251	0.153	NA	NA	NA	NA	NA	177378	679	677	0	0.000	NA	NA	NA	NA	NA
147457	7	134632353	134632353	C	T	*CALD1*	missense	c.940	p.R314C	tier1	19940	2391	2363	25	0.010	22935	2063	1467	591	0.287	NA	NA	NA	NA	NA	94318	394	382	6	0.000	NA	NA	NA	NA	NA
147457	7	138522637	138522637	C	T	*TMEM213*	nonsense	c.178	p.R60*	tier1	32952	5232	5192	29	0.006	43908	4478	3377	1086	0.243	NA	NA	NA	NA	NA	127233	724	720	4	0.006	NA	NA	NA	NA	NA
147457	7	139801866	139801866	C	T	*JHDM1D*	missense	c.1523	p.R508Q	tier1	13831	1714	1697	16	0.009	26611	2517	1745	766	0.305	NA	NA	NA	NA	NA	67081	317	317	0	0.000	NA	NA	NA	NA	NA
147457	7	143010124	143010124	C	T	*HINT1P1*	5_prime_untranslated_region	c.-143010124	NULL	tier3	30428	4027	3989	36	0.009	37087	3657	2645	999	0.274	NA	NA	NA	NA	NA	254380	1056	1036	17	0.016	NA	NA	NA	NA	NA
147457	7	150939682	150939682	C	T	*SMARCD3*	missense	c.464	p.R155Q	tier1	39205	5080	5050	30	0.006	43654	4064	3183	873	0.215	NA	NA	NA	NA	NA	185019	970	966	4	0.004	NA	NA	NA	NA	NA
147457	8	8185940	8185940	G	A	*SGK223*	silent	c.2352	p.S784	tier1	16891	2042	2023	18	0.009	20306	1792	1216	570	0.319	NA	NA	NA	NA	NA	89879	374	369	5	0.013	NA	NA	NA	NA	NA
147457	8	8235576	8235576	G	A	*SGK223*	nonsense	c.343	p.R115*	tier1	9076	1331	1318	13	0.010	9603	1230	895	334	0.272	NA	NA	NA	NA	NA	32132	128	128	0	0.000	NA	NA	NA	NA	NA
147457	8	10464473	10464473	C	T	*RP1L1*	missense	c.7135	p.G2379R	tier1	34199	4334	4289	36	0.008	34908	3306	2361	940	0.285	NA	NA	NA	NA	NA	200667	902	893	6	0.007	NA	NA	NA	NA	NA
147457	8	11223131	11223131	G	A	*TDH*	3_prime_untranslated_region	c.*11223131	NULL	tier3	15570	2181	2160	18	0.008	34234	3283	2291	985	0.301	NA	NA	NA	NA	NA	87225	483	474	3	0.000	NA	NA	NA	NA	NA
147457	8	12232826	12232826	G	A	*ENSG00000254423*	5_prime_untranslated_region	c.-12232826	NULL	tier3	16712	3022	3001	20	0.007	28449	3154	2628	519	0.165	NA	NA	NA	NA	NA	28060	226	226	0	0.000	NA	NA	NA	NA	NA
147457	8	21927047	21927047	G	A	*EPB49*	intronic	c.211+18	e3+18	tier3	10466	1213	1191	14	0.012	9653	741	524	216	0.292	NA	NA	NA	NA	NA	83826	351	348	0	0.000	NA	NA	NA	NA	NA
147457	8	27094400	27094400	C	T	*STMN4*	missense	c.614	p.R205Q	tier1	24614	3177	3147	30	0.009	34984	3345	2503	830	0.249	NA	NA	NA	NA	NA	197409	942	934	6	0.006	NA	NA	NA	NA	NA
147457	8	32505766	32505766	G	A	*NRG1*	missense	c.530	p.R177H	tier1	59429	5765	5690	71	0.012	48992	3129	2179	945	0.303	NA	NA	NA	NA	NA	432849	1712	1686	15	0.009	NA	NA	NA	NA	NA
147457	8	38109809	38109809	A	C	*DDHD2*	splice_region	c.1617+4	e12+4	tier3	3928	948	932	14	0.015	6270	1305	864	439	0.337	NA	NA	NA	NA	NA	11244	114	114	0	0.000	NA	NA	NA	NA	NA
147457	8	41791093	41791093	C	T	*KAT6A*	missense	c.4645	p.G1549S	tier1	10163	1827	1816	10	0.005	12820	1499	1145	352	0.235	NA	NA	NA	NA	NA	27826	223	222	0	0.000	NA	NA	NA	NA	NA
147457	8	48955608	48955608	G	A	*UBE2V2*	missense	c.32	p.R11H	tier1	42503	5112	5085	23	0.005	30055	2639	2132	507	0.192	NA	NA	NA	NA	NA	513322	1825	1820	4	0.002	NA	NA	NA	NA	NA
147457	8	61192308	61192308	G	A	*CA8*	nonsense	c.232	p.R78*	tier1	43305	5775	5739	29	0.005	47637	4689	3687	985	0.211	NA	NA	NA	NA	NA	187268	934	933	0	0.000	NA	NA	NA	NA	NA
147457	8	88249205	88249205	C	T	*CNBD1*	silent	c.636	p.N212	tier1	39445	5035	4981	44	0.009	38888	3833	2679	1141	0.299	NA	NA	NA	NA	NA	196094	900	894	5	0.006	NA	NA	NA	NA	NA
147457	8	125592809	125592809	G	A	*MTSS1*	splice_region	c.461-6	e7-6	tier3	20640	2572	2529	32	0.012	43475	3925	2760	1152	0.294	NA	NA	NA	NA	NA	242304	1012	999	9	0.009	NA	NA	NA	NA	NA
147457	8	143618381	143618381	C	T	*BAI1*	missense	c.3604	p.R1202W	tier1	40160	5607	5535	67	0.012	46198	4515	3226	1272	0.283	NA	NA	NA	NA	NA	207772	1012	993	16	0.016	NA	NA	NA	NA	NA
147457	8	144620573	144620573	G	A	*ZC3H3*	missense	c.964	p.R322W	tier1	35154	4567	4517	41	0.009	26033	2607	1906	691	0.266	NA	NA	NA	NA	NA	149455	654	644	8	0.012	NA	NA	NA	NA	NA
147457	8	144946163	144946163	C	T	*EPPK1*	missense	c.1259	p.R420H	tier1	23160	2663	2635	24	0.009	16207	1193	828	361	0.304	NA	NA	NA	NA	NA	133745	508	508	0	0.000	NA	NA	NA	NA	NA
147457	9	368135	368135	G	A	*DOCK8*	silent	c.1797	p.P599	tier1	655	145	144	1	0.007	1479	363	249	114	0.314	NA	NA	NA	NA	NA	731	21	9	12	0.571	NA	NA	NA	NA	NA
147457	9	34551979	34551979	G	A	*CNTFR*	3_prime_untranslated_region	c.*90	NULL	tier2	10394	1349	1331	18	0.013	11606	1061	739	321	0.303	NA	NA	NA	NA	NA	48202	224	224	0	0.000	NA	NA	NA	NA	NA
147457	9	35664015	35664015	G	A	*C9orf100*	missense	c.463	p.R155W	tier1	25255	3326	3299	25	0.008	33788	3036	2360	669	0.221	NA	NA	NA	NA	NA	273229	1191	1188	3	0.003	NA	NA	NA	NA	NA
147457	9	39176062	39176062	C	T	*CNTNAP3*	missense	c.955	p.G319R	tier1	35257	4541	4526	10	0.002	33972	3659	3484	169	0.046	NA	NA	NA	NA	NA	144901	601	601	0	0.000	NA	NA	NA	NA	NA
147457	9	43709787	43709787	C	T	*CNTNAP3B*	intronic	c.196+27	e2+27	tier3	32487	3606	3567	33	0.009	23409	1648	1149	491	0.299	NA	NA	NA	NA	NA	343694	1186	1179	5	0.004	NA	NA	NA	NA	NA
147457	9	78973784	78973784	C	T	*PCSK5*	silent	c.5529	p.D1843	tier1	18697	2759	2725	30	0.011	20061	2696	1949	741	0.275	NA	NA	NA	NA	NA	55262	318	302	15	0.047	NA	NA	NA	NA	NA
147457	9	82333659	82333659	G	A	*TLE4*	missense	c.1459	p.A487T	tier1	50729	5329	5282	42	0.008	53993	3739	2655	1074	0.288	NA	NA	NA	NA	NA	243197	924	921	2	0.000	NA	NA	NA	NA	NA
147457	9	95872991	95872991	C	T	*C9orf89*	missense	c.292	p.R98C	tier1	73234	8287	8190	84	0.010	67103	5009	3493	1494	0.300	NA	NA	NA	NA	NA	637909	2556	2526	15	0.006	NA	NA	NA	NA	NA
147457	9	97847849	97847849	G	A	*C9orf3*	intronic	c.2460-1115	e16-1115	tier3	50605	5799	5762	34	0.006	49383	3469	2613	849	0.245	NA	NA	NA	NA	NA	412774	1598	1579	13	0.008	NA	NA	NA	NA	NA
147457	9	99711889	99711889	C	T	*HIATL2*	missense	c.343	p.G115S	tier1	960	237	234	2	0.008	3171	597	406	186	0.314	NA	NA	NA	NA	NA	2649	25	25	0	0.000	NA	NA	NA	NA	NA
147457	9	103339628	103339628	G	A	*TMEFF1*	3_prime_untranslated_region	c.*746	NULL	tier2	8950	1486	1466	19	0.013	7800	1248	966	280	0.225	NA	NA	NA	NA	NA	34160	264	263	1	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	9	116050499	116050499	C	T	*PRPF4*	missense	c.980	p.A327V	tier1	41232	4913	4862	42	0.009	28328	2358	1785	569	0.242	NA	NA	NA	NA	NA	289464	1202	1198	2	0.000	NA	NA	NA	NA	NA
147457	9	117087344	117087344	C	T	*ORM1*	missense	c.452	p.T151M	tier1	43442	5148	5102	40	0.008	45158	3364	2337	1019	0.304	NA	NA	NA	NA	NA	321610	1637	1632	4	0.002	NA	NA	NA	NA	NA
147457	9	117143546	117143546	C	T	*AKNA*	missense	c.68	p.R23H	tier1	25536	3062	3042	20	0.007	21248	1684	1201	479	0.285	NA	NA	NA	NA	NA	100152	464	462	2	0.000	NA	NA	NA	NA	NA
147457	9	123370046	123370046	C	T	*MEGF9*	missense	c.1441	p.D481N	tier1	48167	6040	5974	60	0.010	56049	4463	3161	1287	0.289	NA	NA	NA	NA	NA	458612	2039	2009	26	0.013	NA	NA	NA	NA	NA
147457	9	131394806	131394806	G	A	*SPTAN1*	intronic	c.7013+43	e52+43	tier3	21776	3028	2987	36	0.012	25400	2621	1827	783	0.300	NA	NA	NA	NA	NA	109225	451	449	2	0.000	NA	NA	NA	NA	NA
147457	9	131893899	131893899	G	A	*PPP2R4*	silent	c.546	p.T182	tier1	36364	4427	4364	57	0.013	43101	3550	2453	1079	0.305	NA	NA	NA	NA	NA	181531	921	914	6	0.007	NA	NA	NA	NA	NA
147457	9	139616703	139616703	C	T	*FAM69B*	missense	c.433	p.R145W	tier1	46754	5817	5759	54	0.009	56331	4669	3392	1261	0.271	NA	NA	NA	NA	NA	276498	1161	1146	10	0.009	NA	NA	NA	NA	NA
147457	10	21827795	21827795	C	T	*MLLT10*	missense	c.194	p.P65L	tier1	7289	1124	1110	14	0.012	9731	1542	1083	459	0.298	NA	NA	NA	NA	NA	42645	199	199	0	0.000	NA	NA	NA	NA	NA
147457	10	25890983	25890983	G	A	*GPR158*	3_prime_untranslated_region	c.*2780	NULL	tier2	13525	1967	1954	9	0.005	19086	2231	1525	704	0.316	NA	NA	NA	NA	NA	49958	313	313	0	0.000	NA	NA	NA	NA	NA
147457	10	27048066	27048066	G	A	*ABI1*	nonsense	c.1006	p.R336*	tier1	30980	4260	4208	51	0.012	39115	3912	2803	1098	0.281	NA	NA	NA	NA	NA	144662	759	758	0	0.000	NA	NA	NA	NA	NA
147457	10	28023604	28023604	G	A	*MKX*	missense	c.619	p.R207W	tier1	25388	3737	3698	39	0.010	23584	2608	1889	709	0.273	NA	NA	NA	NA	NA	230541	986	976	9	0.009	NA	NA	NA	NA	NA
147457	10	29813480	29813480	C	T	*SVIL*	missense	c.2507	p.R836Q	tier1	28768	3511	3456	50	0.014	38761	3325	2225	1090	0.329	NA	NA	NA	NA	NA	142275	604	604	0	0.000	NA	NA	NA	NA	NA
147457	10	30654823	30654823	C	T	*ENSG00000241621*	5_prime_untranslated_region	c.-30654823	NULL	tier3	64504	7125	7065	53	0.007	51786	3709	2698	1002	0.271	NA	NA	NA	NA	NA	700337	2714	2703	6	0.000	NA	NA	NA	NA	NA
147457	10	34671634	34671634	C	T	*PARD3*	silent	c.1233	p.P411	tier1	11500	2162	2143	17	0.008	10021	1482	1071	407	0.275	NA	NA	NA	NA	NA	22089	180	177	3	0.017	NA	NA	NA	NA	NA
147457	10	46210567	46210567	G	A	*ENSG00000237840*	intronic	c.NULL	NULL	tier3	11019	1471	1449	19	0.013	17159	1585	1144	436	0.276	NA	NA	NA	NA	NA	128881	549	544	4	0.000	NA	NA	NA	NA	NA
147457	10	47747160	47747160	G	A	*ENSG00000244599*	3_prime_untranslated_region	c.*47747160	NULL	tier3	3978	970	963	6	0.006	8468	1471	1038	427	0.291	NA	NA	NA	NA	NA	5260	56	56	0	0.000	NA	NA	NA	NA	NA
147457	10	64967543	64967543	C	T	*JMJD1C*	missense	c.3886	p.G1296R	tier1	14831	2382	2356	23	0.010	22850	3087	2166	912	0.296	NA	NA	NA	NA	NA	42188	322	320	1	0.000	NA	NA	NA	NA	NA
147457	10	86004953	86004953	C	T	*RGR*	intronic	c.79+28	e1+28	tier3	45596	5198	5142	51	0.010	44955	3371	2361	1004	0.298	NA	NA	NA	NA	NA	185736	888	878	4	0.000	NA	NA	NA	NA	NA
147457	10	87379729	87379729	G	A	*GRID1*	missense	c.2255	p.T752M	tier1	19872	2337	2307	30	0.013	29761	2116	1519	590	0.280	NA	NA	NA	NA	NA	51666	289	282	6	0.021	NA	NA	NA	NA	NA
147457	10	100022513	100022513	G	A	*LOXL4*	silent	c.264	p.Y88	tier1	37675	4141	4091	43	0.010	49311	3360	2608	744	0.222	NA	NA	NA	NA	NA	366339	1433	1433	0	0.000	NA	NA	NA	NA	NA
147457	10	103870964	103870964	G	A	*LDB1*	intronic	c.173+49	e3+49	tier3	1757	446	438	6	0.014	3090	494	338	155	0.314	NA	NA	NA	NA	NA	3584	48	48	0	0.000	NA	NA	NA	NA	NA
147457	10	104245343	104245343	C	T	*ACTR1A*	intronic	c.440+23	e5+23	tier3	51377	6085	6025	53	0.009	52683	4547	3342	1183	0.261	NA	NA	NA	NA	NA	326326	1340	1329	11	0.008	NA	NA	NA	NA	NA
147457	10	104628872	104628872	C	T	*C10orf32*	intronic	c.321-690	e6-690	tier4	17829	2892	2865	24	0.008	20664	2389	1688	694	0.291	NA	NA	NA	NA	NA	84668	455	454	0	0.000	NA	NA	NA	NA	NA
147457	10	106160477	106160477	C	T	*CCDC147*	missense	c.1855	p.R619W	tier1	22373	3031	2997	30	0.010	33327	3504	2500	995	0.285	NA	NA	NA	NA	NA	98505	490	490	0	0.000	NA	NA	NA	NA	NA
147457	10	116008560	116008560	C	T	*VWA2*	intronic	c.52+36	e1+36	tier3	6753	1120	1109	10	0.009	12508	1762	1266	490	0.279	NA	NA	NA	NA	NA	17474	125	125	0	0.000	NA	NA	NA	NA	NA
147457	10	118969094	118969094	G	A	*KCNK18*	missense	c.439	p.V147I	tier1	2666	631	627	4	0.006	5543	1106	792	311	0.282	NA	NA	NA	NA	NA	3206	54	54	0	0.000	NA	NA	NA	NA	NA
147457	10	123976222	123976222	G	A	*TACC2*	silent	c.7425	p.A2475	tier1	78841	7991	7897	87	0.011	63935	3972	2763	1196	0.302	NA	NA	NA	NA	NA	624264	2450	2405	36	0.015	NA	NA	NA	NA	NA
147457	10	124402685	124402685	G	A	*DMBT1*	missense	c.7400	p.R2467H	tier1	34281	4393	4356	34	0.008	44382	4010	2919	1079	0.270	NA	NA	NA	NA	NA	204867	908	907	1	0.000	NA	NA	NA	NA	NA
147457	10	135011989	135011989	C	T	*KNDC1*	silent	c.2055	p.N685	tier1	27057	3060	3036	24	0.008	28776	2078	1584	492	0.237	NA	NA	NA	NA	NA	156800	712	704	6	0.008	NA	NA	NA	NA	NA
147457	11	1316941	1316941	C	T	*TOLLIP*	silent	c.117	p.A39	tier1	50306	6544	6491	49	0.007	39252	3768	2776	983	0.262	NA	NA	NA	NA	NA	220882	846	841	2	0.000	NA	NA	NA	NA	NA
147457	11	6048700	6048700	C	T	*OR56A1*	missense	c.235	p.V79M	tier1	29802	3684	3637	43	0.012	34623	2788	1947	830	0.299	NA	NA	NA	NA	NA	232288	963	949	14	0.015	NA	NA	NA	NA	NA
147457	11	6232207	6232207	G	A	*C11orf42*	missense	c.937	p.D313N	tier1	22205	3081	3046	31	0.010	33765	3860	2727	1117	0.291	NA	NA	NA	NA	NA	153786	771	770	1	0.000	NA	NA	NA	NA	NA
147457	11	10500213	10500213	C	T	*AMPD3*	missense	c.362	p.T121M	tier1	24495	3140	3106	33	0.011	28673	2613	1799	805	0.309	NA	NA	NA	NA	NA	68968	442	438	4	0.000	NA	NA	NA	NA	NA
147457	11	16823374	16823374	G	A	*PLEKHA7*	splice_region	c.2158-10	e16-10	tier3	54269	6564	6457	75	0.011	83499	6625	4752	1842	0.279	NA	NA	NA	NA	NA	518776	2490	2478	8	0.003	NA	NA	NA	NA	NA
147457	11	17659970	17659970	C	T	*OTOG*	intronic	c.7832-28	e47-28	tier3	24964	3796	3751	42	0.011	39494	4142	2869	1259	0.305	NA	NA	NA	NA	NA	85212	505	505	0	0.000	NA	NA	NA	NA	NA
147457	11	17801160	17801160	C	T	*KCNC1*	silent	c.1662	p.Y554	tier1	45883	5356	5290	61	0.011	28596	2556	1800	747	0.293	NA	NA	NA	NA	NA	249496	1005	1000	2	0.000	NA	NA	NA	NA	NA
147457	11	26558879	26558879	G	A	*ANO3*	intronic	c.977-74	e10-74	tier3	33579	4551	4518	17	0.004	29990	3412	2685	720	0.211	NA	NA	NA	NA	NA	223079	929	923	3	0.003	NA	NA	NA	NA	NA
147457	11	43515299	43515299	C	T	*TTC17*	intronic	c.3295-24	e24-24	tier3	22743	2981	2971	10	0.003	28946	3063	2500	553	0.181	NA	NA	NA	NA	NA	120416	552	552	0	0.000	NA	NA	NA	NA	NA
147457	11	44253924	44253924	C	T	*EXT2*	missense	c.1783	p.R595W	tier1	44040	5372	5308	58	0.011	54963	4503	3151	1331	0.297	NA	NA	NA	NA	NA	390855	1719	1698	8	0.005	NA	NA	NA	NA	NA
147457	11	45877647	45877647	C	T	*CRY2*	3_prime_untranslated_region	c.*45877647	NULL	tier3	2908	695	686	8	0.012	6194	1177	859	314	0.268	NA	NA	NA	NA	NA	2411	40	38	2	0.000	NA	NA	NA	NA	NA
147457	11	46741344	46741344	C	T	*F2*	nonsense	c.172	p.R58*	tier1	24463	2659	2626	32	0.012	44744	3040	2120	908	0.300	NA	NA	NA	NA	NA	147165	757	755	0	0.000	NA	NA	NA	NA	NA
147457	11	46819420	46819420	G	A	*CKAP5*	missense	c.1273	p.R425C	tier1	38477	4793	4753	35	0.007	43588	3993	2789	1191	0.299	NA	NA	NA	NA	NA	191071	880	873	6	0.007	NA	NA	NA	NA	NA
147457	11	49897778	49897778	C	A	*OR4R3P*	5_prime_flanking_region	c.-46823	NULL	tier3	7829	1364	1347	16	0.012	10234	1502	990	507	0.339	NA	NA	NA	NA	NA	21543	149	145	4	0.027	NA	NA	NA	NA	NA
147457	11	55761663	55761663	C	T	*OR5F1*	missense	c.439	p.G147R	tier1	4689	1103	1087	15	0.014	10384	1868	1304	555	0.299	NA	NA	NA	NA	NA	5586	83	83	0	0.000	NA	NA	NA	NA	NA
147457	11	55839272	55839272	G	A	*OR5J1P*	3_prime_untranslated_region	c.*55839272	NULL	tier3	7064	985	972	12	0.012	14064	1842	1313	521	0.284	NA	NA	NA	NA	NA	16809	122	122	0	0.000	NA	NA	NA	NA	NA
147457	11	59623312	59623312	G	A	*TCN1*	intronic	c.937+30	e6+30	tier3	31010	3938	3897	39	0.010	31051	2887	2167	711	0.247	NA	NA	NA	NA	NA	263243	1369	1366	2	0.000	NA	NA	NA	NA	NA
147457	11	61295431	61295431	C	T	*SYT7*	missense	c.578	p.R193Q	tier1	20629	2560	2531	28	0.011	41913	3302	2307	986	0.299	NA	NA	NA	NA	NA	206810	788	788	0	0.000	NA	NA	NA	NA	NA
147457	11	62571274	62571274	G	A	*NXF1*	nonsense	c.205	p.R69*	tier1	12205	1955	1937	17	0.009	20016	2754	1964	783	0.285	NA	NA	NA	NA	NA	50430	359	352	6	0.017	NA	NA	NA	NA	NA
147457	11	62751103	62751103	G	A	*SLC22A6*	missense	c.511	p.R171C	tier1	35765	4324	4302	21	0.005	30939	2598	1968	623	0.240	NA	NA	NA	NA	NA	187640	784	778	6	0.000	NA	NA	NA	NA	NA
147457	11	64882321	64882321	C	T	*TM7SF2*	3_prime_untranslated_region	c.*64882321	NULL	tier3	37392	4735	4677	51	0.011	41465	4014	2793	1201	0.301	NA	NA	NA	NA	NA	194442	896	893	0	0.000	NA	NA	NA	NA	NA
147457	11	64882420	64882420	C	T	*TM7SF2*	missense	c.242	p.T81M	tier1	71433	7866	7775	83	0.011	81337	5944	4262	1650	0.279	NA	NA	NA	NA	NA	756378	2996	2979	11	0.004	NA	NA	NA	NA	NA
147457	11	65305479	65305479	C	T	*SCYL1*	missense	c.2036	p.P679L	tier1	31467	4167	4119	41	0.010	36821	3609	2540	1057	0.294	NA	NA	NA	NA	NA	127899	602	601	0	0.000	NA	NA	NA	NA	NA
147457	11	65427692	65427692	C	T	*RELA*	5_prime_untranslated_region	c.-65427692	NULL	tier3	16617	3034	3012	21	0.007	33221	3518	2554	950	0.271	NA	NA	NA	NA	NA	56749	537	537	0	0.000	NA	NA	NA	NA	NA
147457	11	66633819	66633819	C	T	*PC*	missense	c.1024	p.V342I	tier1	17028	3719	3666	21	0.006	19398	3204	2326	855	0.269	NA	NA	NA	NA	NA	24102	278	277	0	0.000	NA	NA	NA	NA	NA
147457	11	67795455	67795455	C	T	*ALDH3B1*	3_prime_untranslated_region	c.*67795455	NULL	tier3	46150	5667	5586	69	0.012	45159	3746	2610	1122	0.301	NA	NA	NA	NA	NA	570208	2211	2178	24	0.011	NA	NA	NA	NA	NA
147457	11	68701368	68701368	G	A	*IGHMBP2*	silent	c.1524	p.S508	tier1	31447	4705	4653	47	0.010	42965	4356	3106	1222	0.282	NA	NA	NA	NA	NA	120570	1634	1600	27	0.017	NA	NA	NA	NA	NA
147457	11	68822767	68822767	G	A	*TPCN2*	missense	c.376	p.E126K	tier1	3042	482	478	2	0.004	1945	227	184	43	0.189	NA	NA	NA	NA	NA	9975	32	32	0	0.000	NA	NA	NA	NA	NA
147457	11	72540399	72540399	C	T	*ATG16L2*	missense	c.1156	p.R386C	tier1	42868	5406	5338	60	0.011	42519	4087	2841	1234	0.303	NA	NA	NA	NA	NA	299907	1332	1320	8	0.006	NA	NA	NA	NA	NA
147457	11	74559446	74559446	G	A	*XRRA1*	missense	c.1418	p.T473M	tier1	31336	4003	3952	43	0.011	37844	3626	2527	1089	0.301	NA	NA	NA	NA	NA	163290	846	406	416	0.000	NA	NA	NA	NA	NA
147457	11	78565287	78565287	G	A	*ODZ4*	missense	c.1543	p.R515C	tier1	23261	3021	2979	38	0.013	24012	2041	1382	649	0.320	NA	NA	NA	NA	NA	285225	1018	1005	12	0.012	NA	NA	NA	NA	NA
147457	11	99827584	99827584	G	A	*CNTN5*	silent	c.720	p.A240	tier1	4754	866	859	7	0.008	7009	951	667	280	0.296	NA	NA	NA	NA	NA	9806	94	94	0	0.000	NA	NA	NA	NA	NA
147457	11	104872776	104872776	G	A	*CASP5*	silent	c.735	p.D245	tier1	28717	4741	4703	34	0.007	34195	4483	3171	1290	0.289	NA	NA	NA	NA	NA	106751	633	628	3	0.005	NA	NA	NA	NA	NA
147457	11	106558472	106558472	G	A	*GUCY1A2*	nonsense	c.2095	p.R699*	tier1	16447	2225	2201	23	0.010	22246	2714	1893	815	0.301	NA	NA	NA	NA	NA	67389	308	306	2	0.000	NA	NA	NA	NA	NA
147457	11	111167571	111167571	C	T	*C11orf92*	5_prime_untranslated_region	c.-368	NULL	tier3	9098	1615	1594	10	0.006	16949	1942	1500	438	0.226	NA	NA	NA	NA	NA	27444	227	227	0	0.000	NA	NA	NA	NA	NA
147457	11	122722537	122722537	G	A	*CRTAM*	silent	c.330	p.V110	tier1	30959	3370	3339	29	0.009	33301	2476	1724	744	0.301	NA	NA	NA	NA	NA	250276	1105	1096	6	0.005	NA	NA	NA	NA	NA
147457	11	122828004	122828004	G	A	*C11orf63*	intronic	c.2011-67	e7-67	tier3	19269	2090	2087	2	0.001	13715	896	817	77	0.086	NA	NA	NA	NA	NA	183987	730	728	2	0.000	NA	NA	NA	NA	NA
147457	12	3390547	3390547	C	T	*TSPAN9*	intronic	c.564+52	e5+52	tier2	13852	1575	1551	23	0.015	20464	1559	1060	495	0.318	NA	NA	NA	NA	NA	220702	777	771	3	0.004	NA	NA	NA	NA	NA
147457	12	5154521	5154521	G	A	*KCNA5*	missense	c.1208	p.R403H	tier1	4066	674	673	1	0.001	19346	1974	1344	622	0.316	NA	NA	NA	NA	NA	39521	227	214	10	0.045	NA	NA	NA	NA	NA
147457	12	7125761	7125761	G	T	*LPCAT3*	5_prime_untranslated_region	c.-33	NULL	tier2	42458	5520	5472	42	0.008	33645	3608	2694	896	0.250	NA	NA	NA	NA	NA	340930	1278	1265	11	0.009	NA	NA	NA	NA	NA
147457	12	7922788	7922788	C	T	*NANOGNB*	silent	c.312	p.P104	tier1	21324	2522	2491	28	0.011	15648	1506	1065	435	0.290	NA	NA	NA	NA	NA	177906	635	623	12	0.019	NA	NA	NA	NA	NA
147457	12	10659128	10659128	G	A	*ENSG00000180574*	silent	c.627	p.A209	tier1	37065	4703	4658	41	0.009	38124	3668	2732	929	0.254	NA	NA	NA	NA	NA	231021	1097	1090	6	0.005	NA	NA	NA	NA	NA
147457	12	16713647	16713647	G	A	*LMO3*	intronic	c.261-175	e3-175	tier2	20802	2555	2526	26	0.010	20055	1998	1501	497	0.249	NA	NA	NA	NA	NA	165188	660	647	8	0.000	NA	NA	NA	NA	NA
147457	12	40820395	40820395	C	T	*MUC19*	nonsense	c.1060	p.R354*	tier1	6751	1223	1206	14	0.011	9260	1515	1049	459	0.304	NA	NA	NA	NA	NA	38254	236	236	0	0.000	NA	NA	NA	NA	NA
147457	12	41337805	41337805	C	T	*CNTN1*	nonsense	c.1516	p.R506*	tier1	7468	1083	1073	9	0.008	8943	1301	942	355	0.274	NA	NA	NA	NA	NA	23729	129	124	5	0.039	NA	NA	NA	NA	NA
147457	12	47630017	47630017	C	T	*FAM113B*	missense	c.1171	p.R391W	tier1	22498	2544	2520	19	0.007	18788	1436	1051	384	0.268	NA	NA	NA	NA	NA	121263	518	518	0	0.000	NA	NA	NA	NA	NA
147457	12	48723716	48723716	C	T	*H1FNT*	silent	c.642	p.D214	tier1	14789	1986	1967	17	0.009	16793	1859	1293	563	0.303	NA	NA	NA	NA	NA	160641	690	680	8	0.012	NA	NA	NA	NA	NA
147457	12	49719830	49719830	C	T	*TROAP*	intronic	c.634-29	e5-29	tier3	23705	3172	3144	25	0.008	20498	2124	1620	492	0.233	NA	NA	NA	NA	NA	113958	549	545	4	0.007	NA	NA	NA	NA	NA
147457	12	56607793	56607793	G	A	*RNF41*	silent	c.39	p.D13	tier1	21402	3032	3001	24	0.008	27419	3139	2259	865	0.277	NA	NA	NA	NA	NA	69384	380	377	1	0.000	NA	NA	NA	NA	NA
147457	12	65230315	65230315	G	A	*TBC1D30*	missense	c.1129	p.V377I	tier1	23178	2919	2900	18	0.006	19370	2071	1588	480	0.232	NA	NA	NA	NA	NA	176139	699	693	5	0.007	NA	NA	NA	NA	NA
147457	12	111345179	111345179	G	A	*CCDC63*	missense	c.1591	p.D531N	tier1	38407	5411	5364	39	0.007	49738	4516	3434	1066	0.237	NA	NA	NA	NA	NA	144049	911	906	2	0.000	NA	NA	NA	NA	NA
147457	12	117653072	117653072	C	T	*NOS1*	3_prime_untranslated_region	c.*42	NULL	tier3	23912	3618	3580	35	0.010	29228	3092	2206	877	0.284	NA	NA	NA	NA	NA	76264	557	553	1	0.000	NA	NA	NA	NA	NA
147457	12	119583293	119583293	G	A	*SRRM4*	silent	c.879	p.S293	tier1	18568	2917	2885	25	0.009	21716	2990	2087	891	0.299	NA	NA	NA	NA	NA	38266	358	354	4	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	12	123201344	123201344	G	A	*HCAR3*	5_prime_untranslated_region	c.-60	NULL	tier3	602	115	115	0	0.000	991	231	168	63	0.273	NA	NA	NA	NA	NA	1932	27	27	0	0.000	NA	NA	NA	NA	NA
147457	12	124175149	124175149	G	A	*TCTN2*	missense	c.961	p.V321I	tier1	20603	2953	2938	13	0.004	21561	2690	2187	493	0.184	NA	NA	NA	NA	NA	116220	518	512	5	0.010	NA	NA	NA	NA	NA
147457	12	124422048	124422048	C	T	*CCDC92*	missense	c.553	p.V185M	tier1	37792	4600	4553	44	0.010	37393	3037	2219	811	0.268	NA	NA	NA	NA	NA	236682	1101	1092	7	0.006	NA	NA	NA	NA	NA
147457	12	131498748	131498748	G	A	*GPR133*	missense	c.1336	p.A446T	tier1	28429	3454	3433	21	0.006	33326	3258	2562	688	0.212	NA	NA	NA	NA	NA	204438	786	773	8	0.010	NA	NA	NA	NA	NA
147457	13	21562125	21562125	C	T	*LATS2*	silent	c.1794	p.S598	tier1	42168	6122	6054	62	0.010	55136	5267	3828	1417	0.270	NA	NA	NA	NA	NA	236772	1173	1172	0	0.000	NA	NA	NA	NA	NA
147457	13	23928871	23928871	G	A	*SACS*	missense	c.1880	p.T627M	tier1	28547	3238	3203	35	0.011	55441	3717	2559	1150	0.310	NA	NA	NA	NA	NA	356541	1497	1494	2	0.000	NA	NA	NA	NA	NA
147457	13	24410420	24410420	G	A	*MIPEP*	nonsense	c.1612	p.R538*	tier1	17591	2092	2070	16	0.008	13194	1411	1088	319	0.227	NA	NA	NA	NA	NA	128482	562	553	7	0.013	NA	NA	NA	NA	NA
147457	13	39450219	39450219	G	A	*FREM2*	missense	c.8342	p.R2781H	tier1	56370	6018	5976	38	0.006	53571	3379	2385	982	0.292	NA	NA	NA	NA	NA	341187	1499	1473	20	0.013	NA	NA	NA	NA	NA
147457	13	45857726	45857726	C	T	*GTF2F2*	3_prime_untranslated_region	c.*30	NULL	tier3	10482	1435	1417	16	0.011	18585	2325	1580	738	0.318	NA	NA	NA	NA	NA	37285	287	287	0	0.000	NA	NA	NA	NA	NA
147457	13	95118904	95118904	G	A	*DCT*	missense	c.604	p.R202C	tier1	24558	3082	3055	26	0.008	19234	1790	1347	438	0.245	NA	NA	NA	NA	NA	267773	950	933	11	0.012	NA	NA	NA	NA	NA
147457	13	111329450	111329450	G	A	*CARS2*	missense	c.656	p.A219V	tier1	23587	3509	3489	19	0.005	39503	3377	2638	733	0.217	NA	NA	NA	NA	NA	271081	1204	1199	2	0.000	NA	NA	NA	NA	NA
147457	13	113838700	113838700	G	A	*PCID2*	silent	c.807	p.Y269	tier1	18347	2497	2466	28	0.011	22041	2449	1688	751	0.308	NA	NA	NA	NA	NA	88239	440	431	7	0.016	NA	NA	NA	NA	NA
147457	14	21552150	21552150	C	T	*ARHGEF40*	missense	c.3730	p.R1244W	tier1	53336	6562	6516	44	0.007	33253	2855	2223	624	0.219	NA	NA	NA	NA	NA	537389	2063	2040	11	0.005	NA	NA	NA	NA	NA
147457	14	21861926	21861926	C	T	*CHD8*	missense	c.6028	p.E2010K	tier1	51044	5879	5834	42	0.007	52833	3891	3029	852	0.220	NA	NA	NA	NA	NA	369809	1535	1515	12	0.008	NA	NA	NA	NA	NA
147457	14	38261600	38261600	G	A	*TTC6*	missense	c.3689	p.R1230Q	tier1	13147	1634	1613	20	0.012	11439	1085	757	324	0.300	NA	NA	NA	NA	NA	86742	327	323	4	0.012	NA	NA	NA	NA	NA
147457	14	45664649	45664649	G	A	*FANCM*	intronic	c.5341-726	e21-726	tier3	6493	1025	1013	5	0.005	7469	1293	955	334	0.259	NA	NA	NA	NA	NA	41637	242	235	5	0.021	NA	NA	NA	NA	NA
147457	14	52471285	52471285	C	T	*C14orf166*	3_prime_untranslated_region	c.*51	NULL	tier3	31774	3449	3414	33	0.010	41248	2746	1943	794	0.290	NA	NA	NA	NA	NA	191435	811	808	0	0.000	NA	NA	NA	NA	NA
147457	14	57713531	57713531	C	T	*EXOC5*	missense	c.168	p.M56I	tier1	12407	1685	1663	19	0.011	16095	1998	1443	551	0.276	NA	NA	NA	NA	NA	60344	299	299	0	0.000	NA	NA	NA	NA	NA
147457	14	68047847	68047847	G	A	*PLEKHH1*	intronic	c.3284+92	e22+92	tier3	55976	6306	6230	71	0.011	61545	4371	3135	1225	0.281	NA	NA	NA	NA	NA	433248	1975	1959	15	0.008	NA	NA	NA	NA	NA
147457	14	76259462	76259462	G	A	*TTLL5*	intronic	c.3171+19	e26+19	tier3	42262	4989	4948	37	0.007	41206	3264	2439	814	0.250	NA	NA	NA	NA	NA	321279	1389	1380	6	0.004	NA	NA	NA	NA	NA
147457	14	91211188	91211188	C	T	*TTC7B*	missense	c.524	p.C175Y	tier1	4775	584	574	8	0.014	7167	818	581	234	0.287	NA	NA	NA	NA	NA	12924	76	72	4	0.000	NA	NA	NA	NA	NA
147457	14	91700696	91700696	G	A	*GPR68*	silent	c.729	p.T243	tier1	16166	2906	2875	27	0.009	27269	3480	2500	969	0.279	NA	NA	NA	NA	NA	31381	206	206	0	0.000	NA	NA	NA	NA	NA
147457	14	93706769	93706769	G	A	*BTBD7*	3_prime_untranslated_region	c.*1850	NULL	tier2	20889	3634	3629	4	0.001	30925	4724	4371	344	0.073	NA	NA	NA	NA	NA	77610	543	543	0	0.000	NA	NA	NA	NA	NA
147457	14	102801015	102801015	G	A	*ZNF839*	intronic	c.1509+32	e4+32	tier3	3908	447	441	6	0.013	5131	700	484	211	0.304	NA	NA	NA	NA	NA	31345	165	164	0	0.000	NA	NA	NA	NA	NA
147457	14	105419206	105419206	G	A	*AHNAK2*	missense	c.2582	p.P861L	tier1	95151	10551	10435	84	0.008	67942	4996	3922	1058	0.212	NA	NA	NA	NA	NA	649421	2498	2456	30	0.012	NA	NA	NA	NA	NA
147457	15	23313159	23313159	G	A	*HERC2P2*	5_prime_untranslated_region	c.-23313159	NULL	tier2	10419	1202	1188	12	0.010	9851	1031	739	291	0.283	NA	NA	NA	NA	NA	59430	252	251	0	0.000	NA	NA	NA	NA	NA
147457	15	25349836	25349836	C	T	*SNORD116-28*	rna	NULL	NULL	tier1	14452	2046	2022	23	0.011	26056	2703	1904	791	0.294	NA	NA	NA	NA	NA	90007	468	457	9	0.019	NA	NA	NA	NA	NA
147457	15	28517461	28517461	C	T	*HERC2*	missense	c.983	p.R328H	tier1	34159	3813	3791	18	0.005	49992	3031	2665	360	0.119	NA	NA	NA	NA	NA	117607	580	570	6	0.010	NA	NA	NA	NA	NA
147457	15	33936693	33936693	C	T	*RYR3*	silent	c.3738	p.N1246	tier1	16350	2252	2241	11	0.005	25093	2819	1995	810	0.289	NA	NA	NA	NA	NA	52243	342	342	0	0.000	NA	NA	NA	NA	NA
147457	15	40099429	40099429	C	T	*GPR176*	missense	c.203	p.R68H	tier1	5650	698	697	1	0.001	2937	311	260	51	0.164	NA	NA	NA	NA	NA	36078	141	140	1	0.000	NA	NA	NA	NA	NA
147457	15	40532849	40532849	C	T	*ENSG00000259288*	missense	c.131	p.T44M	tier1	12911	1449	1446	3	0.002	15680	1124	1064	60	0.053	NA	NA	NA	NA	NA	142267	730	729	1	0.000	NA	NA	NA	NA	NA
147457	15	40583762	40583762	C	T	*PLCB2*	3_prime_untranslated_region	c.*205	NULL	tier2	31095	4688	4604	81	0.017	41254	4079	2789	1268	0.313	NA	NA	NA	NA	NA	238420	1788	1780	6	0.000	NA	NA	NA	NA	NA
147457	15	44673070	44673070	G	A	*CASC4*	missense	c.968	p.R323H	tier1	38594	4678	4650	28	0.006	25298	2118	1740	374	0.177	NA	NA	NA	NA	NA	371329	1453	1448	4	0.003	NA	NA	NA	NA	NA
147457	15	52622645	52622645	C	T	*MYO5A*	missense	c.4460	p.R1487Q	tier1	46289	5046	5014	32	0.006	33849	2611	1936	671	0.257	NA	NA	NA	NA	NA	352307	1397	1384	13	0.009	NA	NA	NA	NA	NA
147457	15	63964722	63964722	G	A	*HERC1*	missense	c.8018	p.P2673L	tier1	25385	3203	3190	12	0.004	44121	3995	2987	996	0.250	NA	NA	NA	NA	NA	224348	1001	1001	0	0.000	NA	NA	NA	NA	NA
147457	15	66181422	66181422	C	T	*RAB11A*	3_prime_untranslated_region	c.*1244	NULL	tier3	20600	3162	3142	16	0.005	17204	2414	1938	474	0.197	NA	NA	NA	NA	NA	239065	910	910	0	0.000	NA	NA	NA	NA	NA
147457	15	68603671	68603671	C	T	*ITGA11*	missense	c.3044	p.S1015N	tier1	97022	10671	10572	94	0.009	79883	6397	4538	1824	0.287	NA	NA	NA	NA	NA	724888	2836	2818	14	0.005	NA	NA	NA	NA	NA
147457	15	68608000	68608000	G	A	*ITGA11*	silent	c.2781	p.L927	tier1	44141	5400	5349	49	0.009	43549	4111	3026	1070	0.261	NA	NA	NA	NA	NA	250100	988	986	2	0.000	NA	NA	NA	NA	NA
147457	15	72454738	72454738	G	A	*GRAMD2*	intronic	c.957-20	e11-20	tier3	17000	2348	2330	13	0.006	23369	2623	1979	639	0.244	NA	NA	NA	NA	NA	59372	356	352	4	0.011	NA	NA	NA	NA	NA
147457	15	73889591	73889591	G	A	*NPTN*	missense	c.211	p.R71W	tier1	65268	7059	6984	69	0.010	57945	3732	2638	1085	0.291	NA	NA	NA	NA	NA	401646	1836	1811	9	0.000	NA	NA	NA	NA	NA
147457	15	79069906	79069906	G	A	*ADAMTS7*	silent	c.1347	p.D449	tier1	4170	584	577	6	0.010	8365	983	750	231	0.235	NA	NA	NA	NA	NA	46497	192	190	0	0.000	NA	NA	NA	NA	NA
147457	15	79339147	79339147	G	A	*RASGRF1*	silent	c.819	p.A273	tier1	64610	7523	7463	48	0.006	49141	3654	2827	819	0.225	NA	NA	NA	NA	NA	549482	2171	2161	5	0.002	NA	NA	NA	NA	NA
147457	15	85805937	85805937	C	T	*ENSG00000218052*	5_prime_untranslated_region	c.-85805937	NULL	tier3	10307	1159	1144	15	0.013	12017	822	584	236	0.288	NA	NA	NA	NA	NA	48073	278	278	0	0.000	NA	NA	NA	NA	NA
147457	15	90192982	90192982	G	A	*KIF7*	silent	c.519	p.R173	tier1	15896	2121	2100	20	0.009	23585	2562	1820	736	0.288	NA	NA	NA	NA	NA	75538	358	358	0	0.000	NA	NA	NA	NA	NA
147457	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	34631	4343	4297	46	0.011	32714	2474	1680	788	0.319	NA	NA	NA	NA	NA	129473	553	546	5	0.009	NA	NA	NA	NA	NA
147457	15	91577490	91577490	G	A	*ENSG00000214432*	intronic	c.NULL	NULL	tier3	49011	5748	5685	59	0.010	57583	4846	3442	1382	0.286	NA	NA	NA	NA	NA	444544	1788	1762	20	0.011	NA	NA	NA	NA	NA
147457	15	99671249	99671249	C	T	*SYNM*	missense	c.2681	p.A894V	tier1	41682	5534	5483	41	0.007	56979	5023	3950	1049	0.210	NA	NA	NA	NA	NA	222949	1166	1150	12	0.010	NA	NA	NA	NA	NA
147457	16	593258	593258	C	T	*SOLH*	intronic	c.1-3559	e1-3559	tier3	10915	1473	1465	5	0.003	15190	1347	931	407	0.304	NA	NA	NA	NA	NA	53874	238	238	0	0.000	NA	NA	NA	NA	NA
147457	16	1255229	1255229	C	T	*CACNA1H*	missense	c.2567	p.P856L	tier1	25972	2773	2724	35	0.013	29833	1988	1432	553	0.279	NA	NA	NA	NA	NA	269664	901	876	23	0.026	NA	NA	NA	NA	NA
147457	16	1397840	1397840	C	T	*BAIAP3*	intronic	c.3130+18	e31+18	tier2	23752	3513	3471	27	0.008	20326	3045	2174	851	0.281	NA	NA	NA	NA	NA	186939	885	875	2	0.000	NA	NA	NA	NA	NA
147457	16	4431260	4431260	C	T	*VASN*	missense	c.382	p.R128C	tier1	53795	7126	7043	72	0.010	58122	4977	3537	1417	0.286	NA	NA	NA	NA	NA	153828	746	746	0	0.000	NA	NA	NA	NA	NA
147457	16	28914739	28914739	C	T	*ATP2A1*	missense	c.46	p.R16C	tier1	38145	4299	4249	45	0.010	27030	2017	1410	604	0.300	NA	NA	NA	NA	NA	206602	772	761	7	0.009	NA	NA	NA	NA	NA
147457	16	31519174	31519174	G	A	*C16orf58*	missense	c.326	p.S109F	tier1	26150	3155	3136	17	0.005	36230	3126	2530	590	0.189	NA	NA	NA	NA	NA	148804	659	658	0	0.000	NA	NA	NA	NA	NA
147457	16	33740957	33740957	C	T	*ENSG00000260781*	5_prime_flanking_region	c.-1323	NULL	tier3	2225	277	273	4	0.014	4102	356	277	78	0.220	NA	NA	NA	NA	NA	4117	26	26	0	0.000	NA	NA	NA	NA	NA
147457	16	46638006	46638006	G	A	*SHCBP1*	missense	c.973	p.R325C	tier1	10217	1335	1316	17	0.013	18885	1779	1226	551	0.310	NA	NA	NA	NA	NA	69735	332	332	0	0.000	NA	NA	NA	NA	NA
147457	16	56397961	56397961	G	A	*AMFR*	silent	c.1656	p.G552	tier1	11631	2072	2050	20	0.010	24048	2964	2047	904	0.306	NA	NA	NA	NA	NA	38537	282	282	0	0.000	NA	NA	NA	NA	NA
147457	16	58550812	58550812	G	A	*SETD6*	missense	c.772	p.A258T	tier1	54011	6253	6199	50	0.008	46849	3981	2837	1132	0.285	NA	NA	NA	NA	NA	362799	1647	1645	1	0.000	NA	NA	NA	NA	NA
147457	16	67573993	67573993	G	A	*FAM65A*	missense	c.512	p.R171H	tier1	57615	6633	6587	43	0.006	54887	4429	3333	1073	0.244	NA	NA	NA	NA	NA	335674	1418	1415	1	0.000	NA	NA	NA	NA	NA
147457	16	83378566	83378566	C	T	*CDH13*	missense	c.736	p.R246W	tier1	35275	4039	4012	23	0.006	27287	2015	1583	428	0.213	NA	NA	NA	NA	NA	310275	1048	1033	10	0.010	NA	NA	NA	NA	NA
147457	16	83994327	83994327	G	A	*OSGIN1*	missense	c.358	p.V120M	tier1	35457	3934	3915	19	0.005	32438	2601	2029	567	0.218	NA	NA	NA	NA	NA	280770	1044	1040	2	0.000	NA	NA	NA	NA	NA
147457	16	84529437	84529437	G	A	*KIAA1609*	missense	c.236	p.A79V	tier1	2844	285	283	2	0.007	6876	403	276	127	0.315	NA	NA	NA	NA	NA	34679	114	113	0	0.000	NA	NA	NA	NA	NA
147457	16	88747899	88747899	G	A	*SNAI3*	silent	c.300	p.A100	tier1	41848	5108	5068	36	0.007	47816	3822	2853	957	0.251	NA	NA	NA	NA	NA	280148	1143	1140	2	0.000	NA	NA	NA	NA	NA
147457	17	6377943	6377943	G	A	*PITPNM3*	intronic	c.1086-19	e10-19	tier2	14496	1534	1515	19	0.012	17258	957	640	312	0.328	NA	NA	NA	NA	NA	84099	381	377	3	0.000	NA	NA	NA	NA	NA
147457	17	7492394	7492394	G	A	*MPDU1*	3_prime_untranslated_region	c.*586	NULL	tier2	40517	5050	4986	57	0.011	38378	3587	2446	1122	0.314	NA	NA	NA	NA	NA	536201	2003	1999	0	0.000	NA	NA	NA	NA	NA
147457	17	7506344	7506344	C	T	*FXR2*	intronic	c.450-24	e6-24	tier2	6787	766	758	8	0.010	10241	772	537	234	0.304	NA	NA	NA	NA	NA	83056	297	293	4	0.013	NA	NA	NA	NA	NA
147457	17	8216386	8216386	C	T	*ARHGEF15*	missense	c.748	p.R250C	tier1	10133	1371	1351	17	0.012	12592	1578	1075	497	0.316	NA	NA	NA	NA	NA	40783	241	238	3	0.012	NA	NA	NA	NA	NA
147457	17	9632002	9632002	G	A	*USP43*	missense	c.3067	p.V1023I	tier1	10054	1396	1380	14	0.010	12981	1436	1074	362	0.252	NA	NA	NA	NA	NA	78350	345	344	0	0.000	NA	NA	NA	NA	NA
147457	17	16330812	16330812	C	T	*TRPV2*	missense	c.1301	p.T434M	tier1	18763	2421	2381	39	0.016	38844	3316	2351	951	0.288	NA	NA	NA	NA	NA	165269	694	682	3	0.004	NA	NA	NA	NA	NA
147457	17	16344404	16344404	G	A	*C17orf76-AS1*	3_prime_untranslated_region	c.*16344404	NULL	tier2	9465	1628	1614	11	0.007	11464	1877	1464	412	0.220	NA	NA	NA	NA	NA	89828	391	391	0	0.000	NA	NA	NA	NA	NA
147457	17	16981370	16981370	C	T	*MPRIP*	missense	c.247	p.R83C	tier1	48842	6394	6338	53	0.008	56670	5320	3850	1453	0.274	NA	NA	NA	NA	NA	347826	1596	1592	4	0.003	NA	NA	NA	NA	NA
147457	17	18996977	18996977	T	G	*LOC100132472*	missense	c.315	p.S105R	tier1	22368	2812	2769	37	0.013	20815	1919	1351	566	0.295	NA	NA	NA	NA	NA	115265	502	493	4	0.008	NA	NA	NA	NA	NA
147457	17	19315938	19315938	G	A	*RNF112*	missense	c.79	p.D27N	tier1	69994	8308	8238	58	0.007	70503	5607	4098	1487	0.266	NA	NA	NA	NA	NA	406063	1793	1778	9	0.000	NA	NA	NA	NA	NA
147457	17	26574933	26574933	G	A	*ENSG00000197825*	5_prime_flanking_region	c.-44102	NULL	tier2	21132	2943	2921	20	0.007	17786	2060	1603	454	0.221	NA	NA	NA	NA	NA	135822	616	610	6	0.010	NA	NA	NA	NA	NA
147457	17	26817411	26817411	C	T	*SLC13A2*	silent	c.318	p.L106	tier1	61861	6941	6905	32	0.005	51929	3582	2993	576	0.161	NA	NA	NA	NA	NA	341380	1528	1528	0	0.000	NA	NA	NA	NA	NA
147457	17	27013676	27013676	G	A	*SUPT6H*	missense	c.2569	p.A857T	tier1	15041	2937	2909	28	0.010	26055	4316	3228	1069	0.249	NA	NA	NA	NA	NA	29870	311	303	7	0.023	NA	NA	NA	NA	NA
147457	17	28395764	28395764	C	T	*EFCAB5*	intronic	c.2737+9045	e14+9045	tier2	51589	6332	6301	27	0.004	40834	3455	2936	510	0.148	NA	NA	NA	NA	NA	286683	1366	1337	22	0.016	NA	NA	NA	NA	NA
147457	17	29533403	29533403	C	T	*NF1*	intronic	c.1392+14	e12+14	tier2	25569	3274	3240	31	0.009	24772	2724	1889	827	0.304	NA	NA	NA	NA	NA	292251	1127	1112	12	0.011	NA	NA	NA	NA	NA
147457	17	33328217	33328217	G	A	*LIG3*	intronic	c.2332-59	e16-59	tier4	4769	614	604	10	0.016	7508	650	452	198	0.305	NA	NA	NA	NA	NA	22998	95	95	0	0.000	NA	NA	NA	NA	NA
147457	17	34312816	34312816	G	A	*CCL14*	missense	c.95	p.P32L	tier1	20585	3325	3290	31	0.009	29196	3865	2711	1140	0.296	NA	NA	NA	NA	NA	131631	1098	1080	17	0.015	NA	NA	NA	NA	NA
147457	17	36622583	36622583	G	A	*ARHGAP23*	missense	c.659	p.R220Q	tier1	7064	1097	1084	11	0.010	8509	1248	897	345	0.278	NA	NA	NA	NA	NA	19365	100	100	0	0.000	NA	NA	NA	NA	NA
147457	17	36689701	36689701	G	A	*SRCIN1*	intronic	c.3418-35	e19-35	tier2	12871	1516	1505	10	0.007	8938	773	584	184	0.240	NA	NA	NA	NA	NA	44186	216	216	0	0.000	NA	NA	NA	NA	NA
147457	17	37075080	37075080	C	T	*LASP1*	3_prime_untranslated_region	c.*49	NULL	tier2	27500	3223	3188	28	0.009	26803	1951	1347	601	0.309	NA	NA	NA	NA	NA	184853	741	736	4	0.005	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	17	38146349	38146349	C	T	*PSMD3*	nonsense	c.880	p.R294*	tier1	15821	1944	1926	16	0.008	19025	1675	1172	494	0.297	NA	NA	NA	NA	NA	60870	367	365	0	0.000	NA	NA	NA	NA	NA
147457	17	39740595	39740595	C	T	*KRT14*	missense	c.679	p.E227K	tier1	12535	1278	1268	8	0.006	31582	1908	1363	538	0.283	NA	NA	NA	NA	NA	436058	1697	1666	12	0.007	NA	NA	NA	NA	NA
147457	17	40063711	40063711	C	T	*ACLY*	missense	c.893	p.R298Q	tier1	23162	2794	2766	26	0.009	26911	2118	1442	672	0.318	NA	NA	NA	NA	NA	124013	539	539	0	0.000	NA	NA	NA	NA	NA
147457	17	41026210	41026210	C	T	*ENSG00000260105*	3_prime_untranslated_region	c.*41026210	NULL	tier2	1422	359	356	3	0.008	4299	654	457	196	0.300	NA	NA	NA	NA	NA	5356	61	61	0	0.000	NA	NA	NA	NA	NA
147457	17	44144025	44144025	G	A	*KANSL1*	nonsense	c.1726	p.R576*	tier1	35110	3766	3729	37	0.010	42552	2795	1981	808	0.290	NA	NA	NA	NA	NA	375355	1418	1413	2	0.000	NA	NA	NA	NA	NA
147457	17	48434597	48434597	G	A	*XYLT2*	missense	c.1925	p.R642Q	tier1	19353	2525	2506	17	0.007	46569	3984	3073	905	0.228	NA	NA	NA	NA	NA	178105	817	809	7	0.000	NA	NA	NA	NA	NA
147457	17	52993020	52993020	C	T	*TOM1L1*	intronic	c.604-87	e7-87	tier2	21550	2773	2745	26	0.009	20172	1948	1404	536	0.276	NA	NA	NA	NA	NA	137545	687	682	1	0.000	NA	NA	NA	NA	NA
147457	17	56606542	56606542	C	T	*43347*	5_prime_untranslated_region	c.-7	NULL	tier2	17969	2205	2189	14	0.006	18362	1795	1240	549	0.307	NA	NA	NA	NA	NA	171324	724	724	0	0.000	NA	NA	NA	NA	NA
147457	17	59668192	59668192	G	A	*NACA2*	missense	c.350	p.S117L	tier1	14123	1670	1661	8	0.005	14304	1283	1006	274	0.214	NA	NA	NA	NA	NA	96326	548	544	3	0.005	NA	NA	NA	NA	NA
147457	17	60754754	60754754	G	A	*MRC2*	silent	c.1959	p.T653	tier1	30319	3746	3700	42	0.011	27678	2592	1859	723	0.280	NA	NA	NA	NA	NA	381542	1304	1285	10	0.000	NA	NA	NA	NA	NA
147457	17	61611215	61611215	C	T	*KCNH6*	intronic	c.676-32	e5-32	tier2	18072	3168	3132	36	0.011	30425	3932	2680	1240	0.316	NA	NA	NA	NA	NA	17372	175	175	0	0.000	NA	NA	NA	NA	NA
147457	17	64873540	64873540	C	T	*CACNG5*	silent	c.90	p.T30	tier1	37343	4442	4400	39	0.009	41951	3026	2150	867	0.287	NA	NA	NA	NA	NA	138308	761	745	16	0.021	NA	NA	NA	NA	NA
147457	17	74900341	74900341	G	A	*MGAT5B*	missense	c.560	p.R187H	tier1	40682	5669	5644	21	0.004	33268	3693	2977	709	0.192	NA	NA	NA	NA	NA	320545	1296	1296	0	0.000	NA	NA	NA	NA	NA
147457	17	76167847	76167847	C	T	*SYNGR2*	missense	c.505	p.R169C	tier1	32825	3983	3945	35	0.009	34027	2940	2163	769	0.262	NA	NA	NA	NA	NA	216621	937	919	16	0.017	NA	NA	NA	NA	NA
147457	17	76803689	76803689	C	T	*USP36*	silent	c.1437	p.P479	tier1	10289	1675	1653	20	0.012	14710	1628	1139	489	0.300	NA	NA	NA	NA	NA	34702	197	197	0	0.000	NA	NA	NA	NA	NA
147457	17	77081692	77081692	C	T	*ENGASE*	splice_region	c.1701-10	e13-10	tier3	35488	4166	4123	38	0.009	30387	2481	1844	631	0.255	NA	NA	NA	NA	NA	195147	883	881	0	0.000	NA	NA	NA	NA	NA
147457	17	77083117	77083117	G	A	*ENGASE*	3_prime_untranslated_region	c.*686	NULL	tier3	37228	4808	4758	47	0.010	38239	3488	2378	1096	0.315	NA	NA	NA	NA	NA	185511	842	824	17	0.020	NA	NA	NA	NA	NA
147457	17	78247071	78247071	G	A	*RNF213*	silent	c.129	p.S43	tier1	19809	2110	2092	17	0.008	15825	1260	971	284	0.226	NA	NA	NA	NA	NA	95659	421	417	3	0.000	NA	NA	NA	NA	NA
147457	18	5397381	5397381	G	A	*EPB41L3*	silent	c.2517	p.P839	tier1	30093	3685	3664	21	0.006	27923	2749	2147	597	0.218	NA	NA	NA	NA	NA	321328	1314	1313	1	0.000	NA	NA	NA	NA	NA
147457	18	6837314	6837314	C	T	*ARHGAP28*	silent	c.444	p.A148	tier1	29197	3267	3249	17	0.005	20827	1396	1152	241	0.173	NA	NA	NA	NA	NA	169370	663	658	5	0.008	NA	NA	NA	NA	NA
147457	18	13072806	13072806	C	T	*CEP192*	nonsense	c.5401	p.R1801*	tier1	44687	5534	5494	37	0.007	36812	3414	2561	841	0.247	NA	NA	NA	NA	NA	264181	1119	1119	0	0.000	NA	NA	NA	NA	NA
147457	18	19024347	19024347	C	T	*GREB1L*	missense	c.1370	p.T457M	tier1	12675	1867	1849	18	0.010	20959	2736	2049	680	0.249	NA	NA	NA	NA	NA	104212	442	437	5	0.011	NA	NA	NA	NA	NA
147457	18	19780629	19780629	C	T	*GATA6*	missense	c.1631	p.P544L	tier1	18601	2243	2220	23	0.010	17809	1436	1015	417	0.291	NA	NA	NA	NA	NA	92247	478	478	0	0.000	NA	NA	NA	NA	NA
147457	18	24126926	24126926	G	A	*KCTD1*	silent	c.1575	p.D525	tier1	23659	3227	3201	24	0.007	16203	1472	1164	302	0.206	NA	NA	NA	NA	NA	200356	716	709	5	0.000	NA	NA	NA	NA	NA
147457	18	34340699	34340699	C	T	*FHOD3*	silent	c.4029	p.D1343	tier1	26245	2927	2899	27	0.009	23979	2017	1324	687	0.342	NA	NA	NA	NA	NA	202310	811	800	10	0.012	NA	NA	NA	NA	NA
147457	18	47527556	47527556	C	T	*MYO5B*	intronic	c.612+69	e5+69	tier2	40300	4764	4690	65	0.014	50113	4494	3058	1412	0.316	NA	NA	NA	NA	NA	291438	1179	1153	14	0.012	NA	NA	NA	NA	NA
147457	19	648900	648900	C	T	*RNF126*	missense	c.652	p.V218I	tier1	31606	3928	3893	31	0.008	28990	2506	1763	738	0.295	NA	NA	NA	NA	NA	158706	694	680	10	0.014	NA	NA	NA	NA	NA
147457	19	806592	806592	C	T	*PTBP1*	intronic	c.1119+36	e10+36	tier2	21508	2823	2798	21	0.007	21674	2125	1472	651	0.307	NA	NA	NA	NA	NA	62240	341	341	0	0.000	NA	NA	NA	NA	NA
147457	19	1046266	1046266	G	A	*ABCA7*	missense	c.1483	p.D495N	tier1	33339	3688	3643	38	0.010	25302	1769	1199	568	0.321	NA	NA	NA	NA	NA	167520	673	666	7	0.010	NA	NA	NA	NA	NA
147457	19	3976654	3976654	G	A	*EEF2*	silent	c.2475	p.F825	tier1	33995	4940	4882	52	0.011	41540	4404	3006	1377	0.314	NA	NA	NA	NA	NA	110150	630	626	4	0.006	NA	NA	NA	NA	NA
147457	19	4511513	4511513	G	A	*PLIN4*	missense	c.2417	p.T806M	tier1	10301	1067	1066	1	0.001	25303	1776	1715	60	0.034	NA	NA	NA	NA	NA	530049	1684	1678	4	0.000	NA	NA	NA	NA	NA
147457	19	4930798	4930798	C	T	*UHRF1*	missense	c.518	p.T173M	tier1	31456	3133	3095	35	0.011	50025	3203	2266	931	0.291	NA	NA	NA	NA	NA	390756	1523	1517	3	0.000	NA	NA	NA	NA	NA
147457	19	7267653	7267653	C	T	*INSR*	missense	c.355	p.A119T	tier1	49792	5721	5642	76	0.013	40105	3725	2635	1083	0.291	NA	NA	NA	NA	NA	276016	1029	1020	9	0.009	NA	NA	NA	NA	NA
147457	19	7620282	7620282	G	A	*PNPLA6*	intronic	c.2966+29	e24+29	tier2	3735	398	386	12	0.030	7418	967	510	457	0.473	NA	NA	NA	NA	NA	15629	104	102	2	0.000	NA	NA	NA	NA	NA
147457	19	8027941	8027941	C	T	*ELAVL1*	3_prime_untranslated_region	c.*426	NULL	tier3	20071	2492	2462	27	0.011	33174	2997	2189	799	0.267	NA	NA	NA	NA	NA	103429	541	541	0	0.000	NA	NA	NA	NA	NA
147457	19	8617070	8617070	C	T	*MYO1F*	intronic	c.505-22	e7-22	tier3	31249	3658	3627	27	0.007	30018	2426	1757	664	0.274	NA	NA	NA	NA	NA	154879	643	643	0	0.000	NA	NA	NA	NA	NA
147457	19	10099957	10099957	G	A	*COL5A3*	intronic	c.2091+41	e26+41	tier3	46912	5246	5179	55	0.011	43655	3244	2235	998	0.309	NA	NA	NA	NA	NA	404777	1537	1505	24	0.016	NA	NA	NA	NA	NA
147457	19	10753529	10753529	C	T	*SLC44A2*	intronic	c.2014+402	e21+402	tier2	1478	0	0	0	0.000	2361	546	426	118	0.217	NA	NA	NA	NA	NA	3322	38	38	0	0.000	NA	NA	NA	NA	NA
147457	19	13007031	13007031	G	A	*GCDH*	silent	c.648	p.S216	tier1	25391	3467	3428	37	0.011	33742	3280	2316	954	0.292	NA	NA	NA	NA	NA	99223	589	589	0	0.000	NA	NA	NA	NA	NA
147457	19	13409955	13409955	C	T	*CACNA1A*	missense	c.2504	p.R835H	tier1	17691	2597	2572	23	0.009	13595	2138	1463	663	0.312	NA	NA	NA	NA	NA	121489	537	531	6	0.011	NA	NA	NA	NA	NA
147457	19	13441256	13441256	C	T	*CACNA1A*	intronic	c.1256-106	e10-106	tier4	24093	3529	3484	38	0.011	24482	2864	2015	839	0.294	NA	NA	NA	NA	NA	221077	947	935	10	0.011	NA	NA	NA	NA	NA
147457	19	13930271	13930271	G	A	*ZSWIM4*	silent	c.1674	p.P558	tier1	19297	2684	2651	29	0.011	37058	3047	2169	867	0.286	NA	NA	NA	NA	NA	301075	1371	1347	11	0.008	NA	NA	NA	NA	NA
147457	19	14071785	14071785	G	A	*DCAF15*	missense	c.1781	p.R594Q	tier1	33171	4154	4107	45	0.011	41724	3696	2574	1106	0.301	NA	NA	NA	NA	NA	141060	624	614	6	0.010	NA	NA	NA	NA	NA
147457	19	14211653	14211653	C	T	*PRKACA*	missense	c.404	p.R135Q	tier1	29851	3622	3575	42	0.012	43803	3642	2501	1124	0.310	NA	NA	NA	NA	NA	188788	846	845	1	0.000	NA	NA	NA	NA	NA
147457	19	16855367	16855367	G	A	*NWD1*	missense	c.334	p.E112K	tier1	31655	4102	4060	40	0.010	34431	3198	2221	967	0.303	NA	NA	NA	NA	NA	236443	1071	1054	9	0.008	NA	NA	NA	NA	NA
147457	19	20308488	20308488	G	A	*ZNF486*	silent	c.969	p.T323	tier1	11149	1697	1676	18	0.011	21435	2674	1860	802	0.301	NA	NA	NA	NA	NA	40392	313	311	1	0.000	NA	NA	NA	NA	NA
147457	19	33487078	33487078	C	T	*RHPN2*	missense	c.1274	p.R425Q	tier1	28865	3149	3099	43	0.014	25187	1608	1132	470	0.293	NA	NA	NA	NA	NA	285259	1105	1094	8	0.007	NA	NA	NA	NA	NA
147457	19	34925778	34925778	C	T	*UBA2*	nonsense	c.364	p.R122*	tier1	9937	1288	1283	5	0.004	5985	636	565	71	0.112	NA	NA	NA	NA	NA	88090	401	401	0	0.000	NA	NA	NA	NA	NA
147457	19	42091848	42091848	G	A	*CEACAM21*	missense	c.850	p.G284S	tier1	22670	3092	3057	29	0.009	28088	3181	2270	890	0.282	NA	NA	NA	NA	NA	108638	539	539	0	0.000	NA	NA	NA	NA	NA
147457	19	42525580	42525580	G	A	*GRIK5*	missense	c.1744	p.R582C	tier1	45844	6023	5974	42	0.007	53983	4685	3271	1384	0.297	NA	NA	NA	NA	NA	204640	992	988	3	0.003	NA	NA	NA	NA	NA
147457	19	47910756	47910756	C	T	*MEIS3*	missense	c.926	p.R309Q	tier1	38375	4964	4914	46	0.009	56601	4857	3509	1325	0.274	NA	NA	NA	NA	NA	365534	1515	1482	17	0.011	NA	NA	NA	NA	NA
147457	19	48956016	48956016	G	A	*GRWD1*	missense	c.1075	p.V359I	tier1	47697	6258	6209	38	0.006	46128	4592	3328	1249	0.273	NA	NA	NA	NA	NA	190533	881	878	2	0.000	NA	NA	NA	NA	NA
147457	19	49113254	49113254	C	T	*FAM83E*	missense	c.637	p.V213M	tier1	31931	3652	3605	37	0.010	30214	2492	1764	722	0.290	NA	NA	NA	NA	NA	143706	669	667	0	0.000	NA	NA	NA	NA	NA
147457	19	50563467	50563467	C	T	*FLJ26850*	intronic	c.NULL	NULL	tier3	24350	4177	4135	37	0.009	27432	3378	2412	958	0.284	NA	NA	NA	NA	NA	56592	402	401	0	0.000	NA	NA	NA	NA	NA
147457	19	51128500	51128500	G	A	*SYT3*	silent	c.1626	p.A542	tier1	34376	3874	3833	39	0.010	36529	2794	1943	842	0.302	NA	NA	NA	NA	NA	123588	550	550	0	0.000	NA	NA	NA	NA	NA
147457	19	54204449	54204449	C	T	*MIR521-2*	5_prime_flanking_region	c.-15399	NULL	tier3	6109	1097	1086	11	0.010	10888	1336	923	412	0.309	NA	NA	NA	NA	NA	45518	250	250	0	0.000	NA	NA	NA	NA	NA
147457	19	54760964	54760964	C	T	*LILRB5*	5_prime_untranslated_region	c.-54760964	NULL	tier3	13985	2500	2475	21	0.008	16799	2097	1481	606	0.290	NA	NA	NA	NA	NA	28550	263	263	0	0.000	NA	NA	NA	NA	NA
147457	19	55710221	55710221	G	A	*PTPRH*	missense	c.1480	p.R494C	tier1	55569	7223	7157	60	0.008	56269	4624	3308	1303	0.283	NA	NA	NA	NA	NA	180258	984	979	5	0.005	NA	NA	NA	NA	NA
147457	19	55870015	55870015	G	A	*FAM71E2*	missense	c.2221	p.R741C	tier1	46892	3896	3857	37	0.010	41885	1914	1349	562	0.294	NA	NA	NA	NA	NA	241982	905	905	0	0.000	NA	NA	NA	NA	NA
147457	19	55943894	55943894	G	A	*SHISA7*	3_prime_untranslated_region	c.*629	NULL	tier3	55479	5548	5487	58	0.010	46841	2833	2033	793	0.281	NA	NA	NA	NA	NA	329295	1223	1212	10	0.008	NA	NA	NA	NA	NA
147457	19	57133465	57133465	C	T	*ZNF71*	silent	c.810	p.Y270	tier1	37894	3954	3909	41	0.010	26685	1779	1238	538	0.303	NA	NA	NA	NA	NA	380734	1401	1387	13	0.009	NA	NA	NA	NA	NA
147457	19	59061551	59061551	G	A	*TRIM28*	missense	c.2231	p.R744H	tier1	29923	4221	4168	49	0.012	44947	4829	3283	1520	0.316	NA	NA	NA	NA	NA	170711	801	791	7	0.009	NA	NA	NA	NA	NA
147457	20	4707604	4707604	G	A	*PRND*	3_prime_untranslated_region	c.*1876	NULL	tier3	99502	10575	10435	127	0.012	94309	6338	4377	1928	0.306	NA	NA	NA	NA	NA	682778	2945	2934	7	0.002	NA	NA	NA	NA	NA
147457	20	18805846	18805846	C	T	*C20orf78*	intronic	c.116+64	e2+64	tier3	11524	1915	1897	15	0.008	25499	3172	2238	923	0.292	NA	NA	NA	NA	NA	238464	932	925	2	0.000	NA	NA	NA	NA	NA
147457	20	20152504	20152504	G	A	*C20orf26*	3_prime_untranslated_region	c.*52	NULL	tier3	28018	3337	3311	25	0.007	18403	1614	1255	357	0.221	NA	NA	NA	NA	NA	191718	745	745	0	0.000	NA	NA	NA	NA	NA
147457	20	31023408	31023408	C	T	*ASXL1*	nonsense	c.2893	p.R965*	tier1	46952	6005	5979	22	0.004	50052	4112	3309	794	0.194	NA	NA	NA	NA	NA	220663	908	906	2	0.000	NA	NA	NA	NA	NA
147457	20	35060416	35060416	G	A	*DLGAP4*	missense	c.296	p.R99Q	tier1	25180	3465	3435	27	0.008	30690	3252	2357	881	0.272	NA	NA	NA	NA	NA	91991	506	499	7	0.000	NA	NA	NA	NA	NA
147457	20	37630380	37630380	G	A	*DHX35*	missense	c.650	p.R217Q	tier1	12530	1598	1596	2	0.001	10071	976	843	133	0.136	NA	NA	NA	NA	NA	43329	231	231	0	0.000	NA	NA	NA	NA	NA
147457	20	40122259	40122259	C	T	*CHD6*	missense	c.341	p.R114H	tier1	42262	4869	4846	19	0.004	43536	3324	2647	672	0.202	NA	NA	NA	NA	NA	496012	1735	1723	9	0.005	NA	NA	NA	NA	NA
147457	20	44050134	44050134	C	T	*PIGT*	missense	c.1145	p.P382L	tier1	50386	6020	5954	63	0.010	49995	4089	2962	1107	0.272	NA	NA	NA	NA	NA	483848	2015	2003	4	0.000	NA	NA	NA	NA	NA
147457	20	49620923	49620923	C	T	*KCNG1*	missense	c.1195	p.E399K	tier1	24511	3058	3029	27	0.009	37836	3655	2534	1109	0.304	NA	NA	NA	NA	NA	51773	336	330	5	0.000	NA	NA	NA	NA	NA
147457	20	53208320	53208320	C	T	*DOK5*	missense	c.575	p.T192M	tier1	36327	4115	4063	50	0.012	32354	2483	1757	718	0.290	NA	NA	NA	NA	NA	517274	1934	1930	3	0.000	NA	NA	NA	NA	NA
147457	20	60704165	60704165	G	A	*LSM14B*	intronic	c.661-1175	e5-1175	tier3	34209	4730	4699	30	0.006	43797	3934	3209	717	0.183	NA	NA	NA	NA	NA	251155	1136	1135	0	0.000	NA	NA	NA	NA	NA
147457	20	60910153	60910153	G	A	*LAMA5*	silent	c.2406	p.H802	tier1	27661	3104	3072	26	0.008	28452	1831	1275	553	0.303	NA	NA	NA	NA	NA	86588	462	462	0	0.000	NA	NA	NA	NA	NA
147457	20	62037970	62037970	G	A	*KCNQ2*	3_prime_untranslated_region	c.*27	NULL	tier2	11304	1461	1451	8	0.005	3785	450	361	89	0.198	NA	NA	NA	NA	NA	7102	56	56	0	0.000	NA	NA	NA	NA	NA
147457	20	62055538	62055538	C	T	*KCNQ2*	silent	c.1209	p.P403	tier1	31063	4043	4010	28	0.007	45513	4490	3095	1377	0.308	NA	NA	NA	NA	NA	179034	837	832	3	0.000	NA	NA	NA	NA	NA
147457	21	31744090	31744090	G	A	*KRTAP13-2*	missense	c.442	p.R148C	tier1	19008	2815	2777	35	0.012	23084	2527	1794	726	0.288	NA	NA	NA	NA	NA	137690	650	650	0	0.000	NA	NA	NA	NA	NA
147457	21	33318470	33318470	G	A	*HUNK*	missense	c.733	p.D245N	tier1	13346	1744	1721	22	0.013	23712	2407	1686	717	0.298	NA	NA	NA	NA	NA	58155	305	305	0	0.000	NA	NA	NA	NA	NA
147457	21	33696887	33696887	C	T	*URB1*	missense	c.5147	p.R1716Q	tier1	13587	1655	1624	28	0.017	31627	2628	1822	800	0.305	NA	NA	NA	NA	NA	110605	524	508	13	0.025	NA	NA	NA	NA	NA
147457	21	34945659	34945659	G	A	*SON*	missense	c.6931	p.V2311I	tier1	6691	894	880	13	0.015	10734	1260	886	370	0.295	NA	NA	NA	NA	NA	53418	235	235	0	0.000	NA	NA	NA	NA	NA
147457	21	36206893	36206893	G	A	*RUNX1*	missense	c.619	p.R207W	tier1	17232	2850	2819	28	0.010	28426	3483	2428	1042	0.300	NA	NA	NA	NA	NA	78666	434	426	6	0.014	NA	NA	NA	NA	NA
147457	21	43547924	43547924	G	A	*UMODL1*	missense	c.4057	p.G1353R	tier1	25722	3535	3496	36	0.010	34789	3746	2608	1125	0.301	NA	NA	NA	NA	NA	63343	360	357	3	0.008	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
147457	21	43984766	43984766	G	A	*SLC37A1*	intronic	c.1136-52	e13-52	tier3	78694	8566	8479	72	0.008	64098	4715	3720	981	0.209	NA	NA	NA	NA	NA	707573	2923	2911	4	0.000	NA	NA	NA	NA	NA
147457	21	46363698	46363698	G	A	*FAM207A*	missense	c.229	p.V77I	tier1	16968	2090	2071	16	0.008	20962	1807	1262	540	0.300	NA	NA	NA	NA	NA	41648	241	236	4	0.017	NA	NA	NA	NA	NA
147457	22	21349265	21349265	G	A	*LZTR1*	missense	c.1892	p.R631Q	tier1	13742	1710	1691	16	0.009	18524	1659	1164	493	0.298	NA	NA	NA	NA	NA	42995	251	251	0	0.000	NA	NA	NA	NA	NA
147457	22	23077532	23077532	C	T	*IGLV2-18*	silent	c.309	p.D103	tier1	37981	5120	5091	28	0.005	38538	3976	2949	1016	0.256	NA	NA	NA	NA	NA	246785	1093	1087	6	0.005	NA	NA	NA	NA	NA
147457	22	25598652	25598652	C	T	*CRYBB3*	silent	c.87	p.Y29	tier1	26233	3344	3300	39	0.012	35699	3034	2170	851	0.282	NA	NA	NA	NA	NA	253231	1082	1067	7	0.007	NA	NA	NA	NA	NA
147457	22	37319436	37319436	C	T	*CSF2RB*	intronic	c.200+27	e2+27	tier3	29488	3041	3023	14	0.005	25804	1542	1248	290	0.189	NA	NA	NA	NA	NA	130760	569	569	0	0.000	NA	NA	NA	NA	NA
147457	22	37892522	37892522	C	T	*CARD10*	missense	c.1993	p.E665K	tier1	7072	1147	1135	10	0.009	12107	1715	1279	433	0.253	NA	NA	NA	NA	NA	18615	146	146	0	0.000	NA	NA	NA	NA	NA
147457	22	38062929	38062929	G	A	*PDXP*	3_prime_untranslated_region	c.*1051	NULL	tier2	32675	3739	3698	34	0.009	27225	1997	1519	474	0.238	NA	NA	NA	NA	NA	275521	1042	1040	0	0.000	NA	NA	NA	NA	NA
147457	X	2406917	2406917	C	T	*ZBED1*	missense	c.1844	p.R615H	tier1	43312	6503	6426	69	0.011	44160	4762	3374	1379	0.290	NA	NA	NA	NA	NA	120964	708	707	0	0.000	NA	NA	NA	NA	NA
147457	X	20070889	20070889	C	T	*MAP7D2*	intronic	c.595+107	e5+107	tier3	53914	6343	6289	47	0.007	45177	3601	2758	838	0.233	NA	NA	NA	NA	NA	188162	742	730	9	0.012	NA	NA	NA	NA	NA
147457	X	29973688	29973688	G	A	*IL1RAPL1*	silent	c.1842	p.T614	tier1	45477	5734	5671	58	0.010	49124	4546	3206	1318	0.291	NA	NA	NA	NA	NA	120988	512	498	12	0.024	NA	NA	NA	NA	NA
147457	X	29974566	29974566	G	A	*IL1RAPL1*	3_prime_untranslated_region	c.*629	NULL	tier3	11625	1711	1697	12	0.007	15316	2088	1494	586	0.282	NA	NA	NA	NA	NA	34432	365	363	1	0.000	NA	NA	NA	NA	NA
147457	X	41530801	41530801	C	T	*CASK*	intronic	c.430-18	e6-18	tier4	6687	1019	1003	16	0.016	9343	1184	822	360	0.305	NA	NA	NA	NA	NA	21317	139	139	0	0.000	NA	NA	NA	NA	NA
147457	X	49032048	49032048	G	A	*PRICKLE3*	nonsense	c.1822	p.R608*	tier1	30094	3327	3286	39	0.012	24630	1705	1302	401	0.235	NA	NA	NA	NA	NA	144633	581	570	6	0.010	NA	NA	NA	NA	NA
147457	X	69595890	69595890	C	T	*KIF4A*	intronic	c.1924-60	e17-60	tier3	20196	2557	2542	13	0.005	16532	1619	1383	234	0.145	NA	NA	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836264	70836264	C	T	*CXCR3*	missense	c.1199	p.R400Q	tier1	41171	5462	5428	31	0.006	42969	4051	2958	1079	0.267	NA	NA	NA	NA	NA	78679	373	351	22	0.059	NA	NA	NA	NA	NA
147457	X	71427464	71427464	C	A	*ERCC6L*	missense	c.1153	p.V385L	tier1	12556	1953	1940	13	0.007	15638	2553	1965	584	0.229	NA	NA	NA	NA	NA	52191	273	270	3	0.011	NA	NA	NA	NA	NA
147457	X	79281277	79281277	G	A	*TBX22*	splice_site	c.633+1	e4+1	tier1	29891	3894	3872	21	0.005	48498	4549	3408	1128	0.249	NA	NA	NA	NA	NA	203552	841	841	0	0.000	NA	NA	NA	NA	NA
147457	X	84525966	84525966	C	T	*ZNF711*	missense	c.1442	p.P481L	tier1	52528	6434	6365	62	0.010	60448	5486	4068	1386	0.254	NA	NA	NA	NA	NA	210960	859	842	17	0.020	NA	NA	NA	NA	NA
147457	X	103316458	103316458	C	T	*H2BFWT*	5_prime_flanking_region	c.-48226	NULL	tier3	61088	7275	7196	68	0.009	52134	4352	3233	1101	0.254	NA	NA	NA	NA	NA	375428	1507	1481	18	0.012	NA	NA	NA	NA	NA
147457	X	105144665	105144665	C	T	*NRK*	missense	c.766	p.P256S	tier1	7692	1223	1215	6	0.005	16562	2319	1838	466	0.202	NA	NA	NA	NA	NA	27407	128	128	0	0.000	NA	NA	NA	NA	NA
147457	X	120181966	120181966	G	A	*GLUD2*	missense	c.428	p.R143H	tier1	19731	3613	3563	42	0.012	29697	3525	2480	1024	0.292	NA	NA	NA	NA	NA	42373	740	738	0	0.000	NA	NA	NA	NA	NA
147457	X	123215311	123215311	C	T	*STAG2*	nonsense	c.2857	p.R953*	tier1	38027	4879	4852	21	0.004	33850	3454	2661	781	0.227	NA	NA	NA	NA	NA	171103	691	687	3	0.004	NA	NA	NA	NA	NA
147457	X	128929233	128929233	G	A	*ENSG00000240143*	intronic	c.NULL	NULL	tier3	20269	3119	3079	37	0.012	26671	3093	2179	902	0.293	NA	NA	NA	NA	NA	87583	382	378	4	0.010	NA	NA	NA	NA	NA
147457	X	129190113	129190113	C	T	*BCORL1*	3_prime_untranslated_region	c.*2	NULL	tier3	40006	4594	4545	37	0.008	31277	2243	1814	421	0.188	NA	NA	NA	NA	NA	132083	501	499	0	0.000	NA	NA	NA	NA	NA
147457	X	129318354	129318354	C	T	*RAB33A*	silent	c.354	p.D118	tier1	33357	4217	4176	40	0.009	47449	3781	2746	1021	0.271	NA	NA	NA	NA	NA	55018	250	250	0	0.000	NA	NA	NA	NA	NA
147457	X	129658059	129658059	G	A	*ENSG00000229702*	5_prime_untranslated_region	c.-129658059	NULL	tier2	8763	1510	1498	7	0.005	13164	1850	1397	445	0.242	NA	NA	NA	NA	NA	35695	149	147	2	0.000	NA	NA	NA	NA	NA
147457	X	138678815	138678815	G	A	*MCF2*	nonsense	c.2605	p.R869*	tier1	8524	1103	1091	11	0.010	13628	1460	1002	455	0.312	NA	NA	NA	NA	NA	21660	117	117	0	0.000	NA	NA	NA	NA	NA
147457	X	153660704	153660704	C	T	*ATP6AP1*	silent	c.456	p.L152	tier1	38293	4612	4576	35	0.008	33550	2766	2138	625	0.226	NA	NA	NA	NA	NA	146124	512	509	2	0.000	NA	NA	NA	NA	NA
147457	X	153696165	153696165	G	A	*PLXNA3*	missense	c.3641	p.R1214Q	tier1	67610	7812	7711	89	0.011	72459	5126	3485	1625	0.318	NA	NA	NA	NA	NA	268586	1007	976	15	0.015	NA	NA	NA	NA	NA
169510	1	115258745	115258745	C	G	*NRAS*	missense	c.37	p.G13R	tier1	22977	2771	2677	86	0.031	18987	2368	1379	967	0.412	4019	24	24	0	0.000	15410	508	507	1	0.000	NA	NA	NA	NA	NA
169510	2	39053173	39053173	C	T	*DHX57*	missense	c.2830	p.G944R	tier1	8622	1010	939	68	0.068	7536	923	502	414	0.452	1116	7	3	4	NA	7696	322	322	0	0.000	NA	NA	NA	NA	NA
169510	2	73316541	73316541	G	A	*RAB11FIP5*	rna	NULL	NULL	tier1	21839	2804	2637	155	0.056	14239	1684	888	775	0.466	1793	12	8	4	0.333	13260	417	417	0	0.000	NA	NA	NA	NA	NA
169510	3	184922434	184922434	C	G	*EHHADH*	missense	c.680	p.C227S	tier1	40109	5263	5092	156	0.030	25056	3318	2023	1238	0.380	13593	41	41	0	0.000	26178	718	717	1	0.000	NA	NA	NA	NA	NA
169510	4	96044976	96044976	C	G	*BMPR1B*	missense	c.455	p.P152R	tier1	3573	342	334	6	0.018	3154	340	232	104	0.310	1108	0	0	0	NA	5083	298	298	0	0.000	NA	NA	NA	NA	NA
169510	5	141236840	141236840	C	T	*PCDH1*	missense	c.3296	p.G1099E	tier1	20878	2560	2394	153	0.060	22627	2768	1582	1152	0.421	7304	32	31	1	0.000	15208	502	502	0	0.000	NA	NA	NA	NA	NA
169510	6	111688892	111688892	A	T	*REV3L*	silent	c.6099	p.S2033	tier1	5120	1038	995	42	0.041	8622	1826	1125	689	0.380	1758	24	24	0	0.000	7924	416	416	0	0.000	NA	NA	NA	NA	NA
169510	7	77585348	77585348	G	A	*PHTF2*	3_prime_untranslated_region	c.*1153	NULL	tier3	22699	2680	2473	194	0.073	16692	2069	1110	947	0.460	5368	26	19	7	0.269	17433	584	584	0	0.000	NA	NA	NA	NA	NA
169510	7	89581765	89581765	C	T	*STEAP2-AS1*	intronic	c.NULL	NULL	tier4	26994	3151	2956	187	0.059	20913	2523	1408	1094	0.437	9713	48	36	12	0.250	19113	667	667	0	0.000	NA	NA	NA	NA	NA
169510	8	17206503	17206503	G	A	*MTMR7*	missense	c.556	p.R186W	tier1	9263	1229	1165	61	0.050	8780	1318	822	484	0.371	1683	19	18	1	0.000	7442	403	402	0	0.000	NA	NA	NA	NA	NA
169510	9	99691238	99691238	G	C	*NUTM2G*	5_prime_untranslated_region	c.-69	NULL	tier3	6199	764	752	11	0.014	7177	920	732	183	0.200	2133	6	6	0	NA	5458	145	145	0	0.000	NA	NA	NA	NA	NA
169510	10	102703909	102703909	T	G	*FAM178A*	intronic	c.2757+24	e12+24	tier3	10772	1355	1304	50	0.037	6340	825	468	354	0.431	3923	16	16	0	0.000	7654	186	186	0	0.000	NA	NA	NA	NA	NA
169510	11	6191332	6191332	C	T	*OR52B2*	silent	c.225	p.L75	tier1	36738	5172	4823	325	0.063	31061	4946	2710	2198	0.448	11326	48	30	18	0.375	25971	869	869	0	0.000	NA	NA	NA	NA	NA
169510	12	149069	149069	G	A	*FAM138D*	rna	NULL	NULL	tier1	3334	672	633	38	0.057	1014	212	126	84	0.400	524	0	0	0	NA	1436	74	73	1	0.000	NA	NA	NA	NA	NA
169510	12	22625197	22625197	A	T	*C2CD5*	intronic	c.2169+23	e17+23	tier3	702	60	59	1	0.017	464	33	31	2	0.061	11	0	0	0	NA	705	41	41	0	0.000	NA	NA	NA	NA	NA
169510	12	58215300	58215300	C	T	*CTDSP2*	3_prime_untranslated_region	c.*2085	NULL	tier3	20678	2548	2341	199	0.078	21232	2694	1565	1113	0.416	4087	19	12	7	0.368	23866	745	745	0	0.000	NA	NA	NA	NA	NA
169510	12	110783211	110783211	T	A	*ATP2A2*	intronic	c.2741+24	e18+24	tier3	30738	3880	3609	254	0.066	20690	2664	1497	1149	0.434	4869	17	9	8	0.471	21388	533	533	0	0.000	NA	NA	NA	NA	NA
169510	14	21216226	21216226	C	G	*EDDM3A*	3_prime_untranslated_region	c.*43	NULL	tier3	24904	2955	2882	68	0.023	15428	1821	1252	559	0.309	3189	24	24	0	0.000	15942	589	589	0	0.000	NA	NA	NA	NA	NA
169510	15	85383164	85383164	C	T	*ALPK3*	silent	c.1260	p.P420	tier1	9319	1247	1151	94	0.076	7614	1031	622	405	0.394	1242	0	0	0	NA	8640	303	302	1	0.000	NA	NA	NA	NA	NA
169510	16	57250830	57250830	A	T	*RSPRY1*	missense	c.784	p.T262S	tier1	6753	707	652	54	0.076	9511	1057	595	460	0.436	2795	15	8	7	0.467	7252	312	312	0	0.000	NA	NA	NA	NA	NA
169510	16	89597025	89597025	C	T	*SPG7*	intronic	c.862-66	e7-66	tier3	17923	2260	2139	113	0.050	21956	3075	1803	1244	0.408	6535	27	22	5	0.185	20010	537	536	0	0.000	NA	NA	NA	NA	NA
169510	17	7414546	7414546	G	C	*POLR2A*	missense	c.3826	p.V1276L	tier1	49275	6489	6282	195	0.030	26607	3705	2307	1371	0.373	8486	47	47	0	0.000	25217	723	722	1	0.000	NA	NA	NA	NA	NA
169510	17	7832533	7832533	C	T	*KCNAB3*	missense	c.221	p.R74Q	tier1	5517	676	624	52	0.077	6684	859	608	244	0.286	4590	27	24	3	0.111	10428	407	407	0	0.000	NA	NA	NA	NA	NA
169510	17	10352234	10352234	G	A	*MYH4*	nonsense	c.4312	p.R1438*	tier1	31499	4467	4256	188	0.042	22795	3244	1971	1239	0.386	8326	40	40	0	0.000	24915	877	874	1	0.000	NA	NA	NA	NA	NA
169510	17	49835349	49835349	C	T	*CA10*	intronic	c.298-10171	e4-10171	tier3	6614	734	688	43	0.059	12685	1538	905	625	0.409	2768	15	10	5	0.333	12423	420	419	1	0.000	NA	NA	NA	NA	NA
169510	17	73997619	73997619	A	G	*CDK3*	missense	c.113	p.D38G	tier1	5053	902	855	45	0.050	8756	1304	739	554	0.428	2165	17	15	2	0.000	6045	339	338	0	0.000	NA	NA	NA	NA	NA
169510	17	74733199	74733199	G	T	*SRSF2*	missense	c.44	p.S15Y	tier1	10055	1855	1683	169	0.091	17188	2560	1338	1198	0.472	4437	19	10	9	0.474	12482	409	409	0	0.000	NA	NA	NA	NA	NA
169510	17	74733200	74733200	A	C	*SRSF2*	missense	c.43	p.S15A	tier1	9976	1846	1675	166	0.090	17081	2534	1318	1196	0.476	4442	19	10	9	0.474	12204	405	405	0	0.000	NA	NA	NA	NA	NA
169510	19	15996791	15996791	C	T	*CYP4F2*	missense	c.1058	p.R353H	tier1	14808	1697	1577	116	0.069	12302	1497	848	643	0.431	2687	0	0	0	NA	12500	367	366	1	0.000	NA	NA	NA	NA	NA
169510	19	50753076	50753076	G	A	*MYH14*	missense	c.1652	p.R551Q	tier1	18376	2259	2169	84	0.037	20788	2631	1491	1127	0.430	6624	0	0	0	NA	17522	430	430	0	0.000	NA	NA	NA	NA	NA
169510	20	48600334	48600334	C	T	*SNAI1*	intronic	c.83-27	e2-27	tier2	4603	481	465	16	0.033	9534	1092	889	199	0.183	1370	8	8	0	NA	6898	208	207	0	0.000	NA	NA	NA	NA	NA
169510	20	49575622	49575622	G	T	*MOCS3*	silent	c.243	p.G81	tier1	12313	1467	1391	73	0.050	10253	1288	725	545	0.429	1807	0	0	0	NA	9248	319	318	0	0.000	NA	NA	NA	NA	NA
169510	21	36231782	36231782	C	T	*RUNX1*	missense	c.602	p.R201Q	tier1	14440	2021	1930	90	0.045	13165	1931	1238	679	0.354	1862	17	16	1	0.000	14601	639	637	1	0.000	NA	NA	NA	NA	NA
169510	X	123176411	123176411	A	G	*STAG2*	splice_region	c.386-8	e5-8	tier3	3398	385	366	19	0.049	1923	202	34	168	0.832	837	7	5	2	NA	4625	161	161	0	0.000	NA	NA	NA	NA	NA
185295	1	12032977	12032977	C	T	*PLOD1*	missense	c.2092	p.P698S	tier1	18406	2672	2663	3	0.001	59002	8984	5980	2925	0.328	16913	1147	623	523	0.456	25539	3484	3481	1	0.000	34902	3975	3964	3	0.000
185295	1	167341159	167341159	A	T	*POU2F1*	missense	c.288	p.K96N	tier1	11121	1461	1456	2	0.001	33594	4672	3440	1200	0.259	13943	1409	846	562	0.399	28206	3933	3928	0	0.000	25062	3316	3313	0	0.000
185295	1	176675464	176675464	G	A	*PAPPA2*	intronic	c.3366-31	e9-31	tier3	10415	1316	1307	9	0.007	31819	4196	2709	1455	0.349	16099	1425	814	611	0.429	30601	3989	3983	3	0.000	21721	2442	2435	1	0.000
185295	1	220830533	220830533	C	T	*MARK1*	intronic	c.1989-599	e17-599	tier3	8893	1075	1071	1	0.001	20020	2684	2132	540	0.202	11770	1000	670	325	0.327	24915	3366	3359	4	0.000	15648	1720	1719	0	0.000
185295	1	244218466	244218466	C	A	*ZBTB18*	missense	c.1390	p.R464S	tier1	27361	3571	3554	9	0.003	84979	10979	7615	3261	0.300	29175	1810	1022	783	0.434	56735	6947	6938	3	0.000	60280	5204	5197	2	0.000
185295	4	20529829	20529829	G	A	*SLIT2*	intronic	c.1463-743	e16-743	tier3	4343	1001	998	2	0.002	17887	4295	3141	1127	0.264	3659	517	335	179	0.348	8023	1886	1883	2	0.000	10617	2056	2045	2	0.000
185295	4	69344614	69344614	G	A	*TMPRSS11E*	missense	c.1015	p.A339T	tier1	7027	1142	1140	1	0.001	23651	3712	2727	971	0.263	6552	641	416	221	0.347	13799	1984	1980	3	0.000	13414	1973	1971	2	0.000
185295	4	169195149	169195149	T	C	*DDX60*	missense	c.2390	p.Y797C	tier1	9572	1421	1415	1	0.001	31739	4591	3263	1303	0.285	7983	627	384	241	0.386	18223	2302	2300	0	0.000	17547	1861	1861	0	0.000
185295	6	5144542	5144542	T	C	*LYRM4*	intronic	c.208-34817	e3-34817	tier3	2645	348	343	3	0.009	7719	1019	717	296	0.292	2348	177	93	82	0.469	4195	546	546	0	0.000	5651	0	0	0	NA
185295	6	13365713	13365713	C	T	*GFOD1*	silent	c.435	p.V145	tier1	10359	1334	1331	2	0.002	48606	6158	4251	1865	0.305	13534	824	492	332	0.403	25461	0	0	0	NA	30994	2770	2769	1	0.000
185295	6	157150512	157150512	G	A	*ARID1B*	missense	c.1694	p.R565Q	tier1	14137	1837	1833	2	0.001	42837	5738	4108	1596	0.280	12722	897	532	365	0.407	37104	4693	4680	4	0.000	32836	3302	3298	3	0.000
185295	7	124404234	124404234	C	T	*GPR37*	missense	c.797	p.C266Y	tier1	1974	0	0	0	0.000	19530	2550	1828	696	0.276	4247	371	210	160	0.432	6283	832	829	1	0.000	10395	1141	1141	0	0.000
185295	8	70533457	70533457	G	A	*SULF1*	missense	c.1565	p.R522Q	tier1	3268	664	660	1	0.002	22559	3866	2673	1176	0.306	4258	478	280	196	0.412	13635	1824	1821	2	0.000	16051	2243	2237	2	0.000
185295	8	145737271	145737271	C	G	*RECQL4*	intronic	c.3393+23	e20+23	tier3	15483	2585	2568	11	0.004	37078	5857	4542	1278	0.220	5653	481	338	141	0.294	16788	2415	2413	0	0.000	27471	3251	3242	2	0.000
185295	9	97380079	97380079	C	T	*FBP1*	missense	c.397	p.V133I	tier1	3756	900	900	0	0.000	5637	1424	1111	309	0.218	1740	275	167	108	0.393	3154	769	768	0	0.000	4873	0	0	0	NA
185295	10	88414661	88414661	C	T	*OPN4*	missense	c.121	p.R41W	tier1	25604	3489	3478	6	0.002	96808	12918	9291	3480	0.272	34651	1969	1151	811	0.413	50611	6180	6174	3	0.000	62001	5557	5548	2	0.000
185295	11	17663639	17663639	C	A	*OTOG*	intronic	c.8332-35	e52-35	tier3	32209	4450	4437	10	0.002	99792	13508	9263	4042	0.304	15325	1016	590	423	0.418	54196	6596	6583	4	0.000	64227	6188	6176	6	0.000
185295	12	49719635	49719635	C	T	*TROAP*	missense	c.601	p.R201W	tier1	861	161	160	0	0.000	4136	866	623	238	0.276	338	54	36	18	0.333	280	0	0	0	NA	1203	285	281	3	0.011

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
185295	12	65272304	65272304	C	T	*TBC1D30*	3_prime_untranslated_region	c.*2736	NULL	tier3	30023	4019	4010	4	0.001	99196	12907	9722	3053	0.239	37985	2579	1622	951	0.370	80434	10102	10088	4	0.000	71793	6371	6363	4	0.000
185295	12	124427322	124427322	A	C	*CCDC92*	nonsense	c.192	p.Y64*	tier1	8592	1257	1245	11	0.009	25738	3997	2472	1482	0.375	4710	568	317	251	0.442	7199	1065	1065	0	0.000	12984	1924	1922	0	0.000
185295	13	48547335	48547335	G	A	*SUCLA2*	intronic	c.663+64	e5+64	tier3	1632	210	210	0	0.000	3506	497	366	127	0.258	2675	283	166	117	0.413	3706	530	529	1	0.000	2230	0	0	0	NA
185295	13	52684711	52684711	G	T	*NEK5*	silent	c.315	p.I105	tier1	1982	320	318	2	0.006	19764	2677	1922	745	0.279	6913	564	327	235	0.418	18570	2471	2466	4	0.000	13850	1560	1560	0	0.000
185295	14	96552991	96552991	C	T	*C14orf132*	rna	NULL	NULL	tier1	10922	1708	1703	3	0.002	37248	5111	3487	1592	0.313	7280	638	335	302	0.474	15816	2168	2165	2	0.000	17449	2002	1997	1	0.000
185295	15	85343270	85343270	C	G	*ZNF592*	intronic	c.3273+62	e7+62	tier3	11581	1946	1935	6	0.003	52415	8134	5754	2324	0.288	18696	1449	947	498	0.345	32984	4648	4644	2	0.000	39476	4479	4474	4	0.000
185295	17	10545798	10545798	C	T	*MYH3*	silent	c.1824	p.G608	tier1	24528	3432	3417	2	0.001	67363	9567	7743	1748	0.184	13879	1099	836	260	0.237	45257	5804	5793	2	0.000	46955	4732	4720	3	0.000
185295	17	43008929	43008929	C	T	*KIF18B*	intronic	c.1553+41	e10+41	tier3	34219	4512	4494	10	0.002	110631	14002	9579	4259	0.308	25946	1668	996	669	0.402	67163	8199	8194	1	0.000	79687	6980	6972	2	0.000
185295	21	44524456	44524456	G	A	*U2AF1*	missense	c.101	p.S34F	tier1	7843	1166	1157	8	0.007	15332	2695	1999	687	0.256	7658	909	734	172	0.190	13525	1904	1903	0	0.000	14386	2266	2263	0	0.000
185295	21	47847509	47847509	C	T	*PCNT*	intronic	c.7321-27	e34-27	tier3	27599	3605	3580	25	0.007	79444	10216	6138	3984	0.394	29939	1712	1051	656	0.384	47606	5922	5915	6	0.000	64194	5201	5195	4	0.000
185295	22	39887386	39887386	G	A	*MGAT3*	3_prime_untranslated_region	c.*2432	NULL	tier3	4360	592	592	0	0.000	22192	2926	2019	891	0.306	7993	574	311	262	0.457	11291	1466	1464	0	0.000	11878	1150	1148	0	0.000
185295	X	39921391	39921391	C	T	*BCOR*	splice_site	c.4428+1	e9+1	tier1	8025	986	984	1	0.001	21687	2820	1323	1482	0.528	5162	371	64	306	0.827	35766	4512	4505	2	0.000	19031	1882	1881	1	0.000
187374	1	44467034	44467034	C	G	*SLC6A9*	intronic	c.1419+28	e9+28	tier3	18382	2475	2458	15	0.006	12992	1796	1550	241	0.135	NA	NA	NA	NA	NA	31219	4582	4570	11	0.002	19177	2711	2662	48	0.018
187374	1	47512254	47512254	G	A	*CYP4X1*	missense	c.1189	p.G397R	tier1	23710	2775	2766	9	0.003	29898	3978	2796	1157	0.293	NA	NA	NA	NA	NA	56781	7735	7681	48	0.006	33334	4529	4318	197	0.044
187374	1	176564033	176564033	C	T	*PAPPA2*	silent	c.1293	p.T431	tier1	10718	1674	1666	8	0.005	14829	2077	1331	734	0.355	NA	NA	NA	NA	NA	26831	3972	3936	31	0.008	17316	2573	2388	181	0.070
187374	1	179526224	179526224	G	A	*NPHS2*	silent	c.676	p.L226	tier1	35689	4191	4166	22	0.005	33298	4346	3044	1267	0.294	NA	NA	NA	NA	NA	80138	10706	10634	66	0.006	42424	5718	5487	226	0.040
187374	2	25463295	25463295	T	A	*DNMT3A*	missense	c.2198	p.E733V	tier1	3678	430	429	1	0.002	6584	873	565	303	0.349	NA	NA	NA	NA	NA	12858	2072	2053	15	0.007	8016	1237	1142	91	0.074
187374	2	37458814	37458814	C	A	*CEBPZ*	5_prime_untranslated_region	c.-104	NULL	tier2	19902	2151	2134	14	0.007	19554	2449	1636	805	0.330	NA	NA	NA	NA	NA	36543	4866	4828	38	0.008	20569	2735	2574	150	0.055
187374	2	42280542	42280542	G	A	*PKDCC*	3_prime_untranslated_region	c.*42280542	NULL	tier3	13283	2086	2076	8	0.004	13586	2073	1352	706	0.343	NA	NA	NA	NA	NA	26366	4754	4713	36	0.008	17954	3152	2969	178	0.057
187374	2	196673523	196673523	C	A	*DNAH7*	missense	c.9966	p.W3322C	tier1	18655	2110	2094	9	0.004	19135	2563	1980	570	0.224	NA	NA	NA	NA	NA	43137	6001	5962	29	0.005	22454	3162	3057	97	0.031
187374	2	207570559	207570559	G	A	*DYTN*	missense	c.335	p.A112V	tier1	2160	370	367	2	0.005	1755	327	206	121	0.370	NA	NA	NA	NA	NA	4203	944	935	8	0.008	1952	421	397	24	0.057
187374	3	133667500	133667500	C	T	*SLCO2A1*	missense	c.985	p.V329I	tier1	33511	3691	3666	19	0.005	28340	3526	2315	1167	0.335	NA	NA	NA	NA	NA	57124	7710	7637	62	0.008	35246	4692	4467	216	0.046
187374	6	49676860	49676860	A	G	*CRISP2*	missense	c.50	p.L17S	tier1	12559	1320	1316	4	0.003	13955	1701	1102	579	0.344	NA	NA	NA	NA	NA	26392	3746	3702	40	0.011	15048	2009	1882	120	0.060
187374	7	139083345	139083345	A	T	*LUC7L2*	nonsense	c.355	p.R119*	tier1	8170	870	868	1	0.001	6425	801	482	317	0.397	NA	NA	NA	NA	NA	19092	2513	2489	20	0.008	8096	1026	954	72	0.070
187374	9	101751401	101751401	C	T	*COL15A1*	intronic	c.724-59	e5-59	tier3	23453	3030	3001	23	0.008	20110	2820	1909	889	0.318	NA	NA	NA	NA	NA	36101	5615	5567	44	0.008	25441	3820	3645	169	0.044
187374	9	131708388	131708388	G	A	*DOLK*	nonsense	c.1195	p.R399*	tier1	4590	743	737	6	0.008	4222	670	456	212	0.317	NA	NA	NA	NA	NA	8862	1935	1918	16	0.008	4382	960	902	56	0.058
187374	9	132980111	132980111	G	T	*NCS1*	missense	c.90	p.W30C	tier1	11268	1362	1357	2	0.001	9849	1446	934	499	0.348	NA	NA	NA	NA	NA	18614	3366	3330	32	0.010	11011	1855	1740	112	0.060
187374	10	25465090	25465090	C	T	*GPR158*	silent	c.741	p.G247	tier1	5731	724	718	5	0.007	4535	581	410	167	0.289	NA	NA	NA	NA	NA	10977	1648	1637	8	0.005	5191	767	726	34	0.045
187374	11	36601073	36601073	T	C	*RAG1*	3_prime_untranslated_region	c.*3087	NULL	tier2	557	42	42	0	0.000	834	98	64	34	0.347	NA	NA	NA	NA	NA	1373	197	196	1	0.000	560	73	69	4	0.055
187374	11	70779207	70779207	C	T	*SHANK2*	intronic	c.1072+71	e14+71	tier4	2108	378	377	1	0.003	1520	247	180	64	0.262	NA	NA	NA	NA	NA	3063	703	696	7	0.010	1696	347	331	16	0.046
187374	11	93439939	93439939	C	A	*KIAA1731*	missense	c.5625	p.D1875E	tier1	7573	678	671	3	0.004	8150	846	542	300	0.356	NA	NA	NA	NA	NA	15939	2029	2012	17	0.008	8653	1087	1004	79	0.073
187374	11	93826848	93826848	T	C	*HEPHL1*	intronic	c.2434+42	e13+42	tier2	22662	2638	2623	12	0.005	22411	2829	1821	989	0.352	NA	NA	NA	NA	NA	39413	4962	4927	30	0.006	28176	3611	3387	218	0.060
187374	12	53699798	53699798	T	G	*C12orf10*	missense	c.107	p.V36G	tier1	18490	2188	2182	4	0.002	28643	3793	3053	706	0.188	NA	NA	NA	NA	NA	48631	6846	6813	28	0.004	36841	5083	4947	127	0.025
187374	12	56811467	56811467	G	A	*TIMELESS*	5_prime_untranslated_region	c.-56811467	NULL	tier3	10249	1138	1128	9	0.008	12404	1528	980	539	0.355	NA	NA	NA	NA	NA	24965	3707	3664	32	0.009	17083	2466	2319	141	0.057
187374	13	73334857	73334857	C	T	*DIS3*	intronic	c.2671-68	e20-68	tier3	1723	171	170	0	0.000	1581	185	148	37	0.200	NA	NA	NA	NA	NA	4853	638	635	3	0.005	1022	139	124	15	0.108
187374	17	8011913	8011913	G	A	*ALOXE3*	splice_region	c.1959-6	e13-6	tier3	11967	1293	1285	3	0.002	13830	1735	1153	571	0.331	NA	NA	NA	NA	NA	25442	3630	3597	30	0.008	16762	2301	2170	124	0.054
187374	17	21319856	21319856	G	A	*KCNJ12*	missense	c.1202	p.R401Q	tier1	12847	1358	1354	3	0.002	19786	2421	2212	188	0.078	NA	NA	NA	NA	NA	42822	5929	5902	23	0.004	20108	2715	2658	53	0.020
187374	17	27936061	27936061	C	T	*ANKRD13B*	intronic	c.566-43	e6-43	tier3	32853	3634	3609	18	0.005	27130	3742	2832	882	0.237	NA	NA	NA	NA	NA	63758	9513	9452	47	0.005	35883	5113	4901	207	0.041
187374	17	38926332	38926332	C	T	*KRT26*	missense	c.724	p.V242M	tier1	19052	3564	3532	30	0.008	16174	2855	1932	900	0.318	NA	NA	NA	NA	NA	34709	6275	6222	49	0.008	23370	4151	3925	218	0.053
187374	17	43530828	43530828	C	G	*PLEKHM1*	missense	c.2390	p.C797S	tier1	7623	1021	1016	3	0.003	7082	928	605	319	0.345	NA	NA	NA	NA	NA	13276	2114	2101	13	0.006	7671	1206	1129	77	0.064
187374	19	648180	648180	G	A	*RNF126*	missense	c.884	p.S295L	tier1	11069	1271	1261	7	0.006	11050	1374	878	491	0.359	NA	NA	NA	NA	NA	20181	2731	2699	29	0.011	12396	1643	1535	104	0.063
187374	19	17471347	17471347	C	T	*PLVAP*	missense	c.1312	p.A438T	tier1	6746	715	710	5	0.007	11681	1416	916	494	0.350	NA	NA	NA	NA	NA	21807	3086	3057	27	0.009	14944	2073	1953	115	0.056
187374	20	44037609	44037609	C	T	*DBNDD2*	missense	c.308	p.A103V	tier1	1080	117	116	0	0.000	4223	495	320	168	0.344	NA	NA	NA	NA	NA	9349	1310	1293	14	0.011	5245	704	654	48	0.068
187374	21	35467626	35467626	G	A	*SLC5A3*	silent	c.129	p.G43	tier1	12439	1410	1394	13	0.009	12015	1548	968	568	0.370	NA	NA	NA	NA	NA	26225	3898	3861	32	0.008	15638	2261	2118	141	0.062
187374	21	43412853	43412853	G	C	*ZBTB21*	missense	c.1352	p.A451G	tier1	12965	1793	1786	5	0.003	12807	1788	1187	593	0.333	NA	NA	NA	NA	NA	16957	2820	2789	24	0.009	13853	2114	1987	125	0.059
187374	22	20133674	20133674	C	T	*ZDHHC8*	3_prime_untranslated_region	c.*751	NULL	tier3	9710	936	925	7	0.008	8397	1088	731	336	0.315	NA	NA	NA	NA	NA	19428	2830	2800	22	0.008	11464	1633	1519	107	0.066
187374	X	110489305	110489305	C	T	*CAPN6*	3_prime_untranslated_region	c.*500	NULL	tier3	2511	274	269	5	0.018	1811	243	59	183	0.756	NA	NA	NA	NA	NA	3575	494	481	9	0.018	2070	294	247	46	0.157
189012	2	198266834	198266834	T	C	*SF3B1*	missense	c.2098	p.K700E	tier1	15769	1640	1640	0	0.000	5522	542	503	37	0.069	NA	NA	NA	NA	NA	12890	1211	1209	0	0.000	29093	3798	3789	1	0.000
189012	2	210707164	210707164	C	T	*UNC80*	missense	c.3454	p.R1152C	tier1	5744	467	464	3	0.006	2988	259	189	69	0.267	NA	NA	NA	NA	NA	4259	295	295	0	0.000	6871	821	820	1	0.000
189012	3	172674651	172674651	C	T	*SPATA16*	intronic	c.934-37	e5-37	tier3	5111	493	488	4	0.008	2068	240	202	38	0.158	NA	NA	NA	NA	NA	4995	471	470	0	0.000	4704	666	666	0	0.000
189012	4	39293321	39293321	T	G	*RFC1*	missense	c.3109	p.N1037H	tier1	5911	599	594	4	0.007	3530	377	308	68	0.181	NA	NA	NA	NA	NA	5034	358	357	1	0.000	9404	1327	1315	0	0.000
189012	5	79095309	79095309	G	A	*CMYA5*	missense	c.12080	p.S4027N	tier1	1481	210	210	0	0.000	829	119	107	12	0.101	NA	NA	NA	NA	NA	1065	0	0	0	NA	867	165	165	0	0.000
189012	5	131911487	131911487	G	A	*RAD50*	missense	c.232	p.V78M	tier1	6045	533	530	2	0.004	2399	245	206	39	0.159	NA	NA	NA	NA	NA	4449	342	342	0	0.000	5296	737	737	0	0.000
189012	6	158994487	158994487	G	A	*TMEM181*	missense	c.455	p.R152H	tier1	22262	2532	2515	14	0.006	8929	895	779	113	0.127	NA	NA	NA	NA	NA	10391	1008	1006	0	0.000	34530	4403	4386	7	0.000
189012	11	47753670	47753670	T	C	*FNBP4*	rna	NULL	NULL	tier1	3806	312	309	3	0.010	1388	158	127	28	0.181	NA	NA	NA	NA	NA	2707	193	193	0	0.000	2838	413	411	0	0.000
189012	11	66106152	66106152	C	T	*BRMS1*	5_prime_untranslated_region	c.-66106152	NULL	tier3	10106	983	983	0	0.000	3543	314	297	16	0.051	NA	NA	NA	NA	NA	7971	672	667	0	0.000	17921	2268	2258	5	0.000
189012	14	20853200	20853200	T	C	*TEP1*	silent	c.3051	p.Q1017	tier1	20184	2182	2171	10	0.005	5775	636	541	91	0.144	NA	NA	NA	NA	NA	15678	1467	1466	1	0.000	26125	3551	3542	2	0.000
190938	1	17320299	17320299	A	C	*ATP13A2*	missense	c.1574	p.V525G	tier1	6597	738	729	9	0.012	9179	1289	794	488	0.381	8186	830	588	234	0.285	16349	1733	1723	7	0.004	9453	1361	1361	0	0.000
190938	2	61411861	61411861	A	G	*AHSA2*	missense	c.1	p.M1V	tier1	3783	335	334	1	0.003	3762	515	350	165	0.320	4286	482	347	135	0.280	10685	1426	1419	6	0.004	9160	1067	1066	0	0.000
190938	2	130832517	130832517	T	C	*POTEF*	missense	c.2528	p.Y843C	tier1	846	159	159	0	0.000	180	30	21	9	0.300	926	206	139	66	0.322	552	126	125	1	0.000	944	0	0	0	NA
190938	3	11406161	11406161	G	T	*ATG7*	missense	c.1828	p.D610Y	tier1	3782	675	668	6	0.009	3016	660	428	230	0.350	3928	800	571	228	0.285	7237	1753	1740	10	0.006	8162	1440	1431	0	0.000
190938	4	79394576	79394576	G	T	*FRAS1*	intronic	c.7523-16	e53-16	tier3	7476	1276	1275	0	0.000	6775	1543	1147	395	0.256	8268	1802	1801	0	0.000	24021	5455	5450	4	0.001	20218	3830	3828	0	0.000
190938	4	101386736	101386736	C	T	*EMCN*	intronic	c.260-40	e4-40	tier3	6215	1093	1088	4	0.004	4380	988	775	210	0.213	6597	1466	1213	249	0.170	16813	4049	4028	10	0.002	15013	2831	2826	0	0.000
190938	4	158064963	158064963	C	T	*GLRB*	silent	c.756	p.Y252	tier1	20488	2176	2174	2	0.001	21679	2987	1910	1062	0.357	17816	1816	1650	164	0.090	80400	8401	8385	9	0.001	38763	5035	5022	0	0.000
190938	7	100648826	100648826	G	A	*MUC12*	intronic	c.14956+26	e2+26	tier3	11257	1493	1493	0	0.000	6013	956	560	394	0.413	12288	1524	1522	1	0.000	38573	4353	4348	3	0.000	33514	4720	4716	1	0.000
190938	9	79985394	79985394	C	T	*VPS13A*	missense	c.8807	p.T2936I	tier1	8499	810	809	1	0.001	7880	1034	658	366	0.357	7152	715	649	66	0.092	26827	2946	2942	2	0.000	16147	1956	1938	0	0.000
190938	10	74923711	74923711	A	G	*ECD*	splice_region	c.1-3	e1-3	tier3	6670	709	705	4	0.006	5882	940	580	357	0.381	6346	942	639	303	0.322	18933	2965	2951	13	0.004	16148	2251	2250	0	0.000
190938	11	60230585	60230585	A	T	*MS4A1*	silent	c.270	p.G90	tier1	23144	2612	2607	5	0.002	19072	2714	1764	938	0.347	13116	1793	1652	138	0.077	67224	7023	7010	9	0.001	44296	5783	5776	0	0.000
190938	13	42803590	42803590	G	A	*DGKH*	3_prime_untranslated_region	c.*266	NULL	tier2	16713	1590	1581	9	0.006	13883	1851	1391	449	0.244	12496	1459	1148	308	0.212	78973	8721	8677	30	0.003	41053	4833	4820	0	0.000
190938	15	43572011	43572011	G	C	*TGM7*	missense	c.1490	p.A497G	tier1	24211	2279	2277	1	0.000	17445	2363	1463	882	0.376	20861	2048	2048	0	0.000	32704	4047	4040	1	0.000	45933	5579	5566	0	0.000
190938	17	1028614	1028614	G	A	*ABR*	silent	c.150	p.I50	tier1	19564	2029	2016	10	0.005	12233	1660	708	944	0.571	16403	1757	1221	534	0.304	30854	3447	3415	23	0.007	51326	6254	6248	1	0.000
190938	17	7578190	7578190	T	C	*TP53*	missense	c.659	p.Y220C	tier1	26267	2707	2683	20	0.007	12210	1830	825	1001	0.548	16237	1853	1302	551	0.297	54589	5274	5245	25	0.005	46062	5681	5668	0	0.000
190938	19	50826916	50826916	C	T	*KCNC3*	missense	c.1294	p.V432M	tier1	21553	2186	2186	0	0.000	16444	2251	1483	756	0.338	19233	1923	1918	3	0.002	24832	2757	2752	2	0.000	40547	4879	4864	1	0.000
190938	19	51958846	51958846	G	A	*SIGLEC8*	silent	c.877	p.L293	tier1	21302	2300	2299	1	0.000	15612	2370	1634	719	0.306	16824	1990	1990	0	0.000	27969	3478	3477	0	0.000	42698	5520	5520	0	0.000
190938	20	58381127	58381127	C	G	*PHACTR3*	silent	c.1206	p.L402	tier1	1800	0	0	0	0.000	1524	345	222	120	0.351	1245	0	0	0	NA	2957	0	0	0	NA	3758	729	728	0	0.000
190938	X	124455660	124455660	C	G	*ENSG00000263886*	3_prime_flanking_region	c.*33968	NULL	tier3	12136	1271	1241	18	0.014	9667	1268	351	904	0.720	5644	611	254	344	0.575	31739	3000	2950	26	0.009	22787	2814	2789	1	0.000
199019	1	1747229	1747229	T	C	*GNB1*	missense	c.169	p.K57E	tier1	10791	1322	1304	18	0.014	7034	853	644	200	0.237	NA	NA	NA	NA	NA	7944	1370	1362	4	0.003	8408	172	172	0	0.000
199019	1	100602624	100602624	A	G	*TRMT13*	missense	c.244	p.R82G	tier1	8725	786	764	21	0.027	6678	664	384	278	0.420	NA	NA	NA	NA	NA	11460	1550	1536	13	0.008	12832	277	276	0	0.000
199019	1	104260547	104260547	G	A	*AMYP1*	intronic	c.NULL	NULL	tier3	9674	874	864	10	0.011	6274	643	554	89	0.138	NA	NA	NA	NA	NA	2961	460	456	4	0.009	4764	101	101	0	0.000
199019	1	248402867	248402867	G	T	*OR2M4*	missense	c.637	p.V213F	tier1	7335	778	760	17	0.022	6545	705	506	193	0.276	NA	NA	NA	NA	NA	4623	737	733	3	0.004	8334	179	179	0	0.000
199019	2	95942786	95942786	C	T	*PROM2*	missense	c.749	p.A250V	tier1	16970	1529	1469	57	0.037	9876	970	639	325	0.337	NA	NA	NA	NA	NA	14981	2034	2013	21	0.010	18761	314	314	0	0.000
199019	2	100015184	100015184	G	C	*EIF5B*	3_prime_untranslated_region	c.*100015184	NULL	tier3	11144	1119	1093	23	0.021	6815	791	686	102	0.129	NA	NA	NA	NA	NA	21041	2828	2819	8	0.003	20369	317	315	2	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
199019	2	212288901	212288901	C	T	*ERBB4*	missense	c.2845	p.V949I	tier1	10803	1014	1012	2	0.002	7060	740	589	146	0.199	NA	NA	NA	NA	NA	12503	1694	1692	1	0.000	14646	273	272	0	0.000
199019	2	219267899	219267899	C	T	*CTDSP1*	intronic	c.471+49	e5+49	tier3	14694	1478	1439	38	0.026	13162	1294	887	397	0.309	NA	NA	NA	NA	NA	39467	5308	5263	39	0.007	31541	500	500	0	0.000
199019	4	106156453	106156453	G	T	*TET2*	nonsense	c.1354	p.E452*	tier1	10834	996	955	37	0.037	8474	834	638	186	0.226	NA	NA	NA	NA	NA	16977	2319	2300	15	0.006	17092	286	286	0	0.000
199019	5	7302322	7302322	G	A	*ENSG00000205976*	intronic	c.NULL	NULL	tier3	11932	1270	1246	24	0.019	7810	833	585	242	0.293	NA	NA	NA	NA	NA	18945	2643	2629	8	0.003	18343	245	245	0	0.000
199019	7	57529430	57529430	A	C	*ZNF716*	silent	c.1263	p.S421	tier1	9585	1016	1007	9	0.009	5410	548	447	101	0.184	NA	NA	NA	NA	NA	5713	743	743	0	0.000	18964	228	228	0	0.000
199019	8	38835514	38835514	C	T	*HTRA4*	missense	c.814	p.R272W	tier1	4084	299	285	14	0.047	4666	387	261	123	0.320	NA	NA	NA	NA	NA	4648	605	596	5	0.008	4974	69	68	0	0.000
199019	11	46747390	46747390	C	T	*F2*	intronic	c.560-19	e7-19	tier4	9824	959	944	14	0.015	5954	609	415	189	0.313	NA	NA	NA	NA	NA	11707	1655	1647	3	0.002	13687	191	191	0	0.000
199019	11	65062076	65062076	G	A	*POLA2*	silent	c.1413	p.L471	tier1	16562	1974	1964	9	0.005	9872	1140	924	206	0.182	NA	NA	NA	NA	NA	15439	2237	2226	9	0.000	17132	300	299	1	0.000
199019	11	71949104	71949104	G	A	*INPPL1*	missense	c.3571	p.G1191R	tier1	15200	1686	1686	0	0.000	9280	1082	1033	47	0.044	NA	NA	NA	NA	NA	12253	1852	1850	1	0.000	15189	0	0	0	NA
199019	11	89018012	89018012	G	T	*TYR*	missense	c.1256	p.G419V	tier1	8959	836	831	3	0.004	5386	546	423	122	0.224	NA	NA	NA	NA	NA	11470	1595	1590	4	0.003	11318	215	215	0	0.000
199019	12	124241407	124241407	G	A	*ATP6V0A2*	missense	c.2339	p.R780H	tier1	20664	2603	2550	48	0.018	14513	1805	1201	589	0.329	NA	NA	NA	NA	NA	24533	3871	3847	18	0.005	33089	498	498	0	0.000
199019	14	106357572	106357572	A	G	*IGHD6-19*	silent	c.6	p.Y2	tier1	12705	1521	1508	12	0.008	7058	805	592	207	0.259	NA	NA	NA	NA	NA	8271	1276	1274	0	0.000	11138	240	240	0	0.000
199019	15	50897271	50897271	C	T	*TRPM7*	missense	c.2780	p.S927N	tier1	7473	768	761	6	0.008	4586	531	368	159	0.302	NA	NA	NA	NA	NA	8393	1257	1252	2	0.000	10511	242	242	0	0.000
199019	16	4736332	4736332	G	A	*MGRN1*	3_prime_untranslated_region	c.*32	NULL	tier2	8269	796	776	19	0.024	4986	598	418	175	0.295	NA	NA	NA	NA	NA	7903	1257	1248	9	0.007	11765	242	242	0	0.000
199019	17	7578445	7578445	A	T	*TP53*	missense	c.485	p.I162N	tier1	20913	2310	2229	78	0.034	11259	1203	489	705	0.590	NA	NA	NA	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000
199019	17	61898424	61898424	A	G	*FTSJ3*	silent	c.1938	p.D646	tier1	32049	3302	3159	125	0.038	21842	2214	1447	734	0.337	NA	NA	NA	NA	NA	41729	5776	5724	49	0.008	49762	746	746	0	0.000
199019	17	72589154	72589154	T	C	*C17orf77*	3_prime_untranslated_region	c.*237	NULL	tier3	2098	168	163	4	0.024	1336	130	70	60	0.462	NA	NA	NA	NA	NA	1207	181	178	3	0.017	4356	99	99	0	0.000
199019	17	75209492	75209492	G	A	*SEC14L1*	missense	c.1960	p.D654N	tier1	22753	2266	2264	1	0.000	14123	1349	1198	138	0.103	NA	NA	NA	NA	NA	24385	3201	3193	3	0.000	32465	489	488	0	0.000
199019	X	46513121	46513121	A	T	*SLC9A7*	missense	c.1067	p.F356Y	tier1	5001	733	726	7	0.010	3527	529	379	147	0.279	NA	NA	NA	NA	NA	2380	579	575	3	0.005	3081	129	129	0	0.000
199019	X	132437274	132437274	C	T	*GPC4*	missense	c.1388	p.R463H	tier1	8105	808	797	11	0.014	5560	537	388	148	0.276	NA	NA	NA	NA	NA	6138	825	814	10	0.012	5139	87	87	0	0.000
221833	1	3566445	3566445	A	C	*WRAP73*	intronic	c.69+50	e1+50	tier2	12673	1394	1370	22	0.016	14612	1766	1007	741	0.424	9654	742	714	28	0.038	24767	3365	3358	2	0.000	40647	5815	5810	1	0.000
221833	2	59482372	59482372	G	A	*LOC101927285*	rna	NULL	NULL	tier1	30083	3504	3476	21	0.006	27872	3237	2355	839	0.263	15680	1369	1337	29	0.021	37259	4749	4742	3	0.001	64870	8520	8504	1	0.000
221833	2	74742861	74742861	C	A	*TLX2*	missense	c.502	p.Q168K	tier1	140	0	0	0	0.000	789	66	21	45	0.682	251	11	11	0	0.000	881	98	98	0	0.000	1602	193	192	0	0.000
221833	2	86923062	86923062	T	A	*CHMP3*	intronic	c.1-7614	e1-7614	tier4	20740	2330	2253	74	0.032	26026	2919	1097	1774	0.618	14545	1214	1107	98	0.081	30356	3916	3894	13	0.003	55953	7036	7020	0	0.000
221833	2	198638852	198638852	G	A	*ENSG00000222017*	3_prime_untranslated_region	c.*71	NULL	tier3	8677	1095	1084	8	0.007	9797	1314	989	313	0.240	5521	577	566	10	0.017	12615	1904	1902	1	0.000	18821	3192	3190	0	0.000
221833	3	38766591	38766591	C	A	*SCN10A*	intronic	c.3228+74	e17+74	tier3	8106	1584	1569	13	0.008	7231	1323	757	554	0.423	6156	871	831	39	0.045	12094	2566	2561	4	0.002	22037	5407	5403	1	0.000
221833	3	57616622	57616622	G	A	*DENND6A*	intronic	c.1407+30	e16+30	tier3	989	138	137	1	0.007	2530	330	195	133	0.405	2802	242	231	11	0.045	4159	606	604	0	0.000	6817	1005	1005	0	0.000
221833	3	97806175	97806175	C	T	*OR5AC2*	silent	c.159	p.N53	tier1	36366	4540	4475	61	0.013	42497	5143	2863	2207	0.435	32028	3014	2868	134	0.045	70471	9583	9575	5	0.000	138668	17965	17934	3	0.000
221833	4	115898324	115898324	A	G	*NDST4*	intronic	c.1066+19	e2+19	tier3	9917	1076	1070	6	0.006	11131	1177	766	401	0.344	11510	905	841	62	0.069	21535	2633	2625	1	0.000	36675	4698	4688	0	0.000
221833	5	13901373	13901373	C	T	*DNAH5*	silent	c.2040	p.A680	tier1	25893	3110	3059	51	0.016	23822	2809	1645	1130	0.407	19890	1649	1563	71	0.043	38164	4915	4908	3	0.000	78953	10064	10050	4	0.000
221833	6	33381539	33381539	G	A	*PHF1*	missense	c.614	p.R205Q	tier1	15906	1875	1769	102	0.055	23175	2738	1414	1303	0.480	14525	1154	734	411	0.359	27727	3409	3401	7	0.002	55834	6834	6801	9	0.001
221833	7	36396735	36396735	G	A	*KIAA0895*	missense	c.643	p.P215S	tier1	1273	188	184	3	0.016	1215	172	124	48	0.279	877	82	79	3	0.037	3222	463	462	1	0.000	7875	1523	1522	0	0.000
221833	7	63032656	63032656	G	A	*TNRC18P2*	intronic	c.NULL	NULL	tier2	1219	221	220	1	0.005	1165	236	180	56	0.237	329	33	31	2	0.000	1729	325	324	0	0.000	3386	772	771	0	0.000
221833	7	74482588	74482588	C	T	*WBSCR16*	missense	c.472	p.V158M	tier1	14272	1754	1704	48	0.027	14578	1890	1105	765	0.409	11661	1069	945	122	0.114	23290	3271	3260	5	0.002	46754	6677	6671	3	0.000
221833	9	138642911	138642911	G	A	*KCNT1*	intronic	c.434+24	e4+24	tier3	18945	2191	2124	64	0.029	14896	1690	905	770	0.460	11753	950	856	89	0.094	24238	3019	3013	2	0.000	40980	5202	5184	3	0.000
221833	11	63671439	63671439	C	T	*MARK2*	intronic	c.1515-19	e15-19	tier3	7607	703	675	27	0.038	10371	1140	618	502	0.448	4964	301	190	108	0.362	17753	2029	2020	6	0.003	36251	4540	4528	3	0.000
221833	12	53578786	53578786	C	T	*ZNF740*	missense	c.121	p.R41W	tier1	33692	4397	4340	43	0.010	28859	3649	2253	1353	0.375	21457	2006	1970	30	0.015	48876	6658	6650	4	0.000	103137	13856	13839	3	0.000
221833	14	60395157	60395157	C	T	*LRRC9*	missense	c.220	p.P74S	tier1	22645	2807	2771	35	0.012	19943	2277	1326	923	0.410	14579	1404	1346	52	0.037	35328	4712	4705	4	0.001	58899	8052	8034	2	0.000
221833	15	29488779	29488779	G	A	*FAM189A1*	5_prime_untranslated_region	c.-29488779	NULL	tier3	1675	261	258	3	0.011	2006	330	209	121	0.367	1793	185	182	3	0.016	3814	688	687	1	0.000	6232	1294	1294	0	0.000
221833	16	67650720	67650720	G	A	*CTCF*	missense	c.1025	p.R342H	tier1	11579	1664	1645	19	0.011	11712	1708	1139	558	0.329	10118	1270	1249	21	0.017	21706	3677	3673	3	0.000	40357	7429	7418	2	0.000
221833	16	82033259	82033259	G	A	*SDR42E1*	silent	c.639	p.Y213	tier1	10010	1433	1415	17	0.012	12699	1589	884	695	0.440	9576	909	889	20	0.022	20238	2864	2859	1	0.000	36739	5754	5746	4	0.000
221833	17	80206875	80206875	C	T	*CSNK1D*	missense	c.1073	p.R358Q	tier1	8178	1048	1025	20	0.019	14575	1823	958	845	0.469	9205	801	763	34	0.043	19699	2626	2619	6	0.002	40970	5406	5400	2	0.000
221833	19	54946639	54946639	G	A	*TTYH1*	intronic	c.1126-83	e11-83	tier4	14055	1699	1610	87	0.051	12778	1508	822	678	0.452	10532	903	612	286	0.318	21477	2860	2857	3	0.001	48040	6605	6585	7	0.001
221833	21	46913513	46913513	C	T	*SLC19A1*	3_prime_untranslated_region	c.*2736	NULL	tier3	11648	1345	1340	5	0.004	14559	1764	1116	628	0.360	9630	792	791	1	0.000	22937	2808	2806	1	0.000	47594	6101	6094	1	0.000
221833	X	133547689	133547689	T	C	*PHF6*	splice_site	c.588+2	e5+2	tier1	5499	584	557	23	0.040	4520	505	81	404	0.833	4346	343	326	13	0.038	10932	1348	1346	1	0.000	19624	2612	2607	0	0.000
221833	X	155010932	155010932	A	T	*SPRY3*	3_prime_untranslated_region	c.*6532	NULL	tier3	8191	955	940	14	0.015	9709	1165	652	507	0.437	8045	704	664	40	0.057	14658	1871	1867	2	0.000	33196	4491	4484	1	0.000
222841	3	62142833	62142833	C	A	*PTPRG*	missense	c.775	p.P259T	tier1	5362	915	910	2	0.002	6038	798	706	92	0.115	7659	674	604	70	0.104	4124	732	732	0	0.000	NA	NA	NA	NA	NA
222841	3	195453104	195453104	G	A	*MUC20*	missense	c.1630	p.V544I	tier1	5406	796	795	0	0.000	5437	614	523	88	0.144	4186	333	284	47	0.142	2053	365	365	0	0.000	NA	NA	NA	NA	NA
222841	4	8601068	8601068	G	A	*CPZ*	intronic	c.89-112	e2-112	tier3	33825	4685	4680	0	0.000	33567	3925	3751	157	0.040	60385	3634	3616	12	0.003	17621	2199	2196	2	0.000	NA	NA	NA	NA	NA
222841	5	71496184	71496184	C	G	*MAP1B*	silent	c.7002	p.T2334	tier1	13461	2260	2260	0	0.000	14739	2177	2120	56	0.026	17379	1662	1652	5	0.003	10729	1814	1808	3	0.000	NA	NA	NA	NA	NA
222841	6	101215150	101215150	G	C	*ASCC3*	nonsense	c.1467	p.Y489*	tier1	6742	827	826	1	0.001	7413	736	710	25	0.034	12598	1117	1110	6	0.005	9059	1287	1283	3	0.000	NA	NA	NA	NA	NA
222841	6	117631399	117631399	G	C	*ROS1*	silent	c.6279	p.T2093	tier1	2851	336	335	0	0.000	3685	418	403	15	0.036	2034	329	328	1	0.000	3047	514	513	0	0.000	NA	NA	NA	NA	NA
222841	7	72814623	72814623	C	T	*FZD9*	5_prime_flanking_region	c.-33715	NULL	tier3	4554	570	570	0	0.000	4924	507	492	12	0.024	5424	441	440	0	0.000	3612	528	527	0	0.000	NA	NA	NA	NA	NA
222841	8	22548343	22548343	C	T	*EGR3*	silent	c.807	p.P269	tier1	9709	1282	1281	0	0.000	8115	849	816	32	0.038	24179	1286	1276	8	0.006	5517	614	611	3	0.000	NA	NA	NA	NA	NA
222841	10	42949783	42949783	C	A	*CCNYL2*	5_prime_untranslated_region	c.-42949783	NULL	tier3	14192	1767	1704	62	0.035	13515	1477	1143	326	0.222	25554	1292	1008	281	0.218	15708	1569	1547	20	0.013	NA	NA	NA	NA	NA
222841	10	73497534	73497534	C	G	*C10orf105*	5_prime_untranslated_region	c.-21440	NULL	tier3	3963	638	638	0	0.000	4015	507	486	18	0.036	819	116	115	1	0.000	1571	302	300	0	0.000	NA	NA	NA	NA	NA
222841	11	32444548	32444548	C	G	*WT1*	intronic	c.872+4954	e3+4954	tier3	3987	676	672	0	0.000	4816	634	612	21	0.033	4034	489	485	3	0.006	3005	561	560	0	0.000	NA	NA	NA	NA	NA
222841	12	49170094	49170094	G	A	*ADCY6*	silent	c.1575	p.N525	tier1	10629	1765	1758	2	0.001	12507	1806	1743	59	0.033	17564	1249	1245	2	0.000	9335	1300	1297	1	0.000	NA	NA	NA	NA	NA
222841	12	109604677	109604677	C	G	*ACACB*	missense	c.665	p.S222W	tier1	22803	3046	3045	0	0.000	22271	2326	2196	118	0.051	50013	3113	3090	12	0.004	23005	2800	2786	4	0.000	NA	NA	NA	NA	NA
222841	13	36410159	36410159	A	T	*DCLK1*	intronic	c.1229+11	e7+11	tier3	8867	0	0	0	0.000	9132	1165	1107	54	0.047	9345	1159	1155	3	0.003	7747	1329	1328	0	0.000	NA	NA	NA	NA	NA
222841	17	7577568	7577568	C	T	*TP53*	missense	c.713	p.C238Y	tier1	26650	3406	3325	74	0.022	28104	2962	2110	826	0.281	77815	4050	2972	1059	0.263	29628	3244	3212	26	0.008	NA	NA	NA	NA	NA
222841	17	10350502	10350502	C	A	*MYH4*	missense	c.4997	p.R1666I	tier1	29081	3762	3758	1	0.000	30767	3257	3123	121	0.037	92522	5171	5146	25	0.005	37553	4000	3999	0	0.000	NA	NA	NA	NA	NA
222841	17	10401122	10401122	G	C	*MYH1*	missense	c.4294	p.L1432V	tier1	4259	901	900	0	0.000	4647	723	696	24	0.033	3359	575	574	1	0.000	3066	763	761	0	0.000	NA	NA	NA	NA	NA
222841	19	9176322	9176322	G	C	*OR1M1*	5_prime_flanking_region	c.-27599	NULL	tier3	23584	2989	2988	0	0.000	36026	3640	3523	103	0.028	56431	3220	3195	12	0.004	14112	1674	1669	2	0.000	NA	NA	NA	NA	NA
222841	22	40055124	40055124	G	C	*CACNA1I*	splice_region	c.2348+3	e15+3	tier2	28383	4175	4172	0	0.000	26682	3364	3177	178	0.053	56998	3165	3148	13	0.004	24124	2798	2797	0	0.000	NA	NA	NA	NA	NA
222841	X	152801875	152801875	G	A	*ATP2B3*	missense	c.170	p.S57N	tier1	14382	2036	2035	0	0.000	15193	1735	1666	66	0.038	17669	1094	1092	2	0.000	5584	678	677	0	0.000	NA	NA	NA	NA	NA
229276	1	201172932	201172932	C	T	*IGFN1*	missense	c.814	p.R272C	tier1	13289	1369	1346	22	0.016	8527	647	546	99	0.153	NA	NA	NA	NA	NA	8660	1076	1076	0	0.000	NA	NA	NA	NA	NA
229276	3	38739967	38739967	G	A	*SCN10A*	missense	c.4744	p.R1582C	tier1	15552	1642	1616	24	0.015	11971	863	809	54	0.063	NA	NA	NA	NA	NA	12399	1619	1618	1	0.000	NA	NA	NA	NA	NA
229276	3	53736702	53736702	C	T	*CACNA1D*	missense	c.1255	p.R419W	tier1	3413	378	371	6	0.016	3658	299	261	38	0.127	NA	NA	NA	NA	NA	2415	508	507	1	0.000	NA	NA	NA	NA	NA
229276	3	68684184	68684184	C	T	*ENSG00000244640*	5_prime_flanking_region	c.-677	NULL	tier4	12770	1636	1606	26	0.016	9183	860	745	110	0.129	NA	NA	NA	NA	NA	5385	976	972	1	0.000	NA	NA	NA	NA	NA
229276	4	36214995	36214995	T	C	*ARAP2*	intronic	c.965-54	e3-54	tier3	7118	615	598	15	0.024	6174	395	347	47	0.119	NA	NA	NA	NA	NA	4506	668	667	1	0.000	NA	NA	NA	NA	NA
229276	4	95202758	95202758	T	A	*SMARCAD1*	intronic	c.2732+17	e20+17	tier3	1534	211	207	4	0.019	1232	111	99	12	0.108	NA	NA	NA	NA	NA	800	220	219	1	0.000	NA	NA	NA	NA	NA
229276	5	55237459	55237459	A	C	*IL6ST*	silent	c.2208	p.S736	tier1	11372	1457	1426	30	0.021	9123	829	709	115	0.140	NA	NA	NA	NA	NA	5879	1048	1048	0	0.000	NA	NA	NA	NA	NA
229276	5	60170374	60170374	A	C	*ERCC8*	rna	NULL	NULL	tier1	5240	425	423	2	0.005	3152	172	147	25	0.145	NA	NA	NA	NA	NA	2854	338	338	0	0.000	NA	NA	NA	NA	NA
229276	6	52883236	52883236	C	T	*ICK*	silent	c.555	p.A185	tier1	22669	2496	2455	35	0.014	16103	1257	1105	147	0.117	NA	NA	NA	NA	NA	14633	2014	2007	3	0.000	NA	NA	NA	NA	NA
229276	6	76022886	76022886	G	A	*FILIP1*	missense	c.2662	p.P888S	tier1	6206	714	707	7	0.010	6053	416	350	62	0.150	NA	NA	NA	NA	NA	5455	814	814	0	0.000	NA	NA	NA	NA	NA
229276	6	88125414	88125414	C	T	*C6orf165*	silent	c.294	p.L98	tier1	8056	702	692	9	0.013	5804	362	311	51	0.141	NA	NA	NA	NA	NA	8363	1106	1103	1	0.000	NA	NA	NA	NA	NA
229276	10	15177301	15177301	A	G	*NMT2*	silent	c.363	p.F121	tier1	9164	881	866	14	0.016	7076	435	369	62	0.144	NA	NA	NA	NA	NA	4653	734	733	0	0.000	NA	NA	NA	NA	NA
229276	12	13229047	13229047	A	T	*KIAA1467*	missense	c.1612	p.N538Y	tier1	16523	1797	1766	29	0.016	11695	914	786	126	0.138	NA	NA	NA	NA	NA	9353	1345	1342	1	0.000	NA	NA	NA	NA	NA
229276	12	112657189	112657189	C	T	*HECTD4*	splice_site	c.6558+1	e43+1	tier1	24906	2838	2779	50	0.018	15741	1287	1118	161	0.126	NA	NA	NA	NA	NA	11747	1490	1486	2	0.000	NA	NA	NA	NA	NA
229276	19	36125240	36125240	G	A	*RBM42*	missense	c.1100	p.S367N	tier1	21080	2284	2236	47	0.021	13811	1104	927	169	0.154	NA	NA	NA	NA	NA	8273	1121	1117	2	0.000	NA	NA	NA	NA	NA
229276	X	123179001	123179001	A	G	*STAG2*	intronic	c.463-13	e6-13	tier2	1048	119	115	4	0.034	1479	94	66	28	0.298	NA	NA	NA	NA	NA	516	115	115	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
243777	1	3428641	3428641	T	C	*MEGF6*	missense	c.905	p.N302S	tier1	47798	5255	5247	6	0.001	34014	4096	3761	316	0.078	NA	NA	NA	NA	NA	66578	9124	9116	0	0.000	116508	16030	16007	0	0.000
243777	1	24383863	24383863	C	T	*MYOM3*	silent	c.4314	p.K1438	tier1	19547	2264	2197	63	0.028	10682	1405	1027	370	0.265	NA	NA	NA	NA	NA	23625	3618	3615	1	0.000	50047	7861	7851	0	0.000
243777	1	230921753	230921753	A	G	*CAPN9*	missense	c.1508	p.D503G	tier1	22696	2680	2678	0	0.000	16707	2266	2171	87	0.039	NA	NA	NA	NA	NA	32519	5023	5012	1	0.000	42813	7340	7335	0	0.000
243777	2	103124587	103124587	C	T	*SLC9A4*	silent	c.1248	p.F416	tier1	22627	2438	2425	8	0.003	16664	1902	1700	193	0.102	NA	NA	NA	NA	NA	34960	4647	4642	1	0.000	53972	7229	7218	0	0.000
243777	2	152534686	152534686	C	G	*NEB*	missense	c.3271	p.D1091H	tier1	8375	762	735	23	0.030	6759	698	538	158	0.227	NA	NA	NA	NA	NA	13477	1743	1741	1	0.000	22802	3175	3172	0	0.000
243777	3	58870344	58870344	C	T	*C3orf67*	silent	c.267	p.Q89	tier1	3330	452	436	16	0.035	3569	601	457	144	0.240	NA	NA	NA	NA	NA	6408	1316	1315	0	0.000	8656	1950	1948	2	0.000
243777	4	2932778	2932778	G	A	*MFSD10*	missense	c.1262	p.A421V	tier1	7096	673	669	2	0.003	11229	1548	1227	312	0.203	NA	NA	NA	NA	NA	22441	3640	3636	1	0.000	37714	6377	6374	2	0.000
243777	5	82833952	82833952	C	T	*VCAN*	silent	c.5130	p.D1710	tier1	2852	293	291	1	0.003	4791	783	766	14	0.018	NA	NA	NA	NA	NA	7568	1416	1414	0	0.000	13561	2847	2842	1	0.000
243777	5	140201927	140201927	C	A	*PCDHA5*	missense	c.567	p.N189K	tier1	15891	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	31992	4432	4426	5	0.001	52355	7894	7882	0	0.000
243777	6	7829666	7829666	G	A	*BMP6*	intronic	c.665-15707	e2-15707	tier4	4290	487	477	9	0.019	4377	567	403	162	0.287	NA	NA	NA	NA	NA	8651	1296	1295	0	0.000	8860	1588	1587	0	0.000
243777	6	42985369	42985369	C	A	*KLHDC3*	silent	c.267	p.V89	tier1	9228	1036	1030	2	0.002	16814	2347	2065	267	0.114	NA	NA	NA	NA	NA	29057	4779	4778	0	0.000	50504	8987	8981	0	0.000
243777	6	42985377	42985377	G	A	*KLHDC3*	nonsense	c.275	p.W92*	tier1	9020	1024	1013	3	0.003	16185	2304	2003	274	0.120	NA	NA	NA	NA	NA	28330	4709	4699	0	0.000	49613	8924	8916	1	0.000
243777	6	64290808	64290808	G	A	*PTP4A1*	3_prime_untranslated_region	c.*729	NULL	tier3	4544	490	485	4	0.008	3755	395	334	61	0.154	NA	NA	NA	NA	NA	6555	800	800	0	0.000	14693	1912	1908	0	0.000
243777	7	135263622	135263622	C	T	*NUP205*	missense	c.1001	p.A334V	tier1	11944	1309	1276	29	0.022	15884	1819	1347	461	0.255	NA	NA	NA	NA	NA	27824	3567	3563	3	0.000	56597	7291	7263	2	0.000
243777	8	117859879	117859879	G	A	*RAD21*	nonsense	c.1756	p.R586*	tier1	7435	729	724	2	0.003	9929	1059	943	112	0.106	NA	NA	NA	NA	NA	18835	2368	2364	2	0.000	31132	4057	4057	0	0.000
243777	9	108125237	108125237	G	A	*SLC44A1*	missense	c.1036	p.V346I	tier1	4098	611	598	11	0.018	3651	620	502	116	0.188	NA	NA	NA	NA	NA	6819	1356	1354	0	0.000	11488	2588	2585	0	0.000
243777	10	54076396	54076396	T	C	*DKK1*	silent	c.630	p.C210	tier1	11704	1458	1417	41	0.028	6320	772	543	228	0.296	NA	NA	NA	NA	NA	10253	1441	1433	4	0.003	26513	4029	4012	1	0.000
243777	10	135350563	135350563	G	T	*CYP2E1*	splice_region	c.968-4	e7-4	tier3	15475	1702	1677	22	0.013	11458	1294	1022	268	0.208	NA	NA	NA	NA	NA	21275	2954	2953	0	0.000	34953	5018	5016	1	0.000
243777	11	67552796	67552796	G	T	*ALG1L8P*	3_prime_untranslated_region	c.*67552796	NULL	tier3	7882	748	741	6	0.008	6391	684	520	164	0.240	NA	NA	NA	NA	NA	14249	1756	1756	0	0.000	24092	3075	3075	0	0.000
243777	11	71175151	71175151	C	A	*NADSYN1*	missense	c.370	p.R124S	tier1	20939	2924	2886	28	0.010	34569	4519	3606	873	0.195	NA	NA	NA	NA	NA	62386	9159	9151	2	0.000	104320	14866	14851	4	0.000
243777	11	132081872	132081872	T	A	*NTM*	intronic	c.401-44	e4-44	tier3	12716	1184	1158	25	0.021	10366	1094	855	233	0.214	NA	NA	NA	NA	NA	18915	2518	2515	2	0.000	35985	4874	4867	0	0.000
243777	12	11992117	11992117	G	A	*ETV6*	nonsense	c.207	p.W69*	tier1	33041	3548	3526	13	0.004	25437	2831	2496	318	0.113	NA	NA	NA	NA	NA	48212	6185	6184	0	0.000	91635	11949	11938	0	0.000
243777	16	51175096	51175096	G	A	*SALL1*	missense	c.1037	p.A346V	tier1	15532	1553	1509	42	0.027	16802	1918	1412	492	0.258	NA	NA	NA	NA	NA	29105	3770	3765	3	0.000	49464	6730	6722	3	0.000
243777	17	10451010	10451010	G	A	*MYH2*	intronic	c.204+24	e1+24	tier3	26858	2722	2685	23	0.008	23033	2555	2039	494	0.195	NA	NA	NA	NA	NA	39719	5095	5089	2	0.000	72769	9624	9612	1	0.000
243777	17	78313118	78313118	C	G	*RNF213*	missense	c.4951	p.L1651V	tier1	12490	1398	1365	28	0.020	25412	2949	2179	743	0.254	NA	NA	NA	NA	NA	34291	4477	4474	0	0.000	55311	7290	7285	0	0.000
243777	18	42531917	42531917	T	C	*SETBP1*	missense	c.2612	p.I871T	tier1	29045	3318	3307	10	0.003	28940	3401	3292	96	0.028	NA	NA	NA	NA	NA	48772	6435	6431	0	0.000	78461	10289	10276	0	0.000
243777	18	77896475	77896475	A	T	*ADNP2*	missense	c.3179	p.D1060V	tier1	2959	248	244	4	0.016	3053	287	221	64	0.225	NA	NA	NA	NA	NA	6457	762	761	0	0.000	4593	560	560	0	0.000
243777	19	1525633	1525633	C	T	*PLK5*	5_prime_untranslated_region	c.-1363	NULL	tier2	38807	4443	4372	59	0.013	31055	3789	3055	701	0.187	NA	NA	NA	NA	NA	64060	8600	8586	6	0.000	88350	12391	12363	0	0.000
243777	19	51358189	51358189	T	A	*KLK3*	5_prime_untranslated_region	c.-23	NULL	tier3	6819	572	555	15	0.026	5847	628	449	176	0.282	NA	NA	NA	NA	NA	11601	1447	1446	0	0.000	18744	2464	2460	2	0.000
243777	19	57722941	57722941	A	G	*ZNF264*	missense	c.476	p.D159G	tier1	2742	330	330	0	0.000	3665	574	513	60	0.105	NA	NA	NA	NA	NA	7563	1361	1359	0	0.000	8522	1895	1894	0	0.000
243777	20	3214593	3214593	C	T	*SLC4A11*	silent	c.708	p.R236	tier1	29045	3167	3081	78	0.025	30713	3700	2683	983	0.268	NA	NA	NA	NA	NA	62507	8355	8341	6	0.001	95373	12885	12860	2	0.000
243777	21	44514777	44514777	T	G	*U2AF1*	missense	c.470	p.Q157P	tier1	38655	4203	4150	44	0.010	31107	3449	2647	775	0.226	NA	NA	NA	NA	NA	59638	7201	7198	1	0.000	120187	14390	14365	0	0.000
266995	1	24417462	24417462	C	A	*MYOM3*	missense	c.1260	p.W420C	tier1	43336	5494	5485	4	0.001	33505	3643	3483	155	0.043	20125	2128	2114	12	0.006	11871	1038	1036	0	0.000	NA	NA	NA	NA	NA
266995	1	181706618	181706618	G	A	*CACNA1E*	intronic	c.3423-43	e23-43	tier3	70463	9735	9678	46	0.005	40500	4603	4293	289	0.063	18267	2079	1097	970	0.469	17477	1623	1618	2	0.000	NA	NA	NA	NA	NA
266995	3	39230412	39230412	C	T	*XIRP1*	silent	c.525	p.L175	tier1	4494	539	533	3	0.006	7456	722	673	44	0.061	7423	798	460	334	0.421	2735	192	192	0	0.000	NA	NA	NA	NA	NA
266995	3	100463779	100463779	A	G	*TFG*	splice_region	c.820+4	e6+4	tier3	15955	1822	1810	10	0.005	8975	814	763	43	0.053	7084	748	429	314	0.423	4056	287	285	0	0.000	NA	NA	NA	NA	NA
266995	8	80948699	80948699	C	A	*TPD52*	3_prime_untranslated_region	c.*1652	NULL	tier3	4305	519	518	0	0.000	3996	421	399	22	0.052	4441	521	517	2	0.000	1636	134	133	1	0.000	NA	NA	NA	NA	NA
266995	8	139736829	139736829	G	A	*COL22A1*	intronic	c.2247+29	e24+29	tier3	45418	5778	5746	19	0.003	43903	4921	4564	327	0.067	27203	3006	1718	1254	0.422	16686	1488	1486	0	0.000	NA	NA	NA	NA	NA
266995	10	95720906	95720906	G	A	*PIPSL*	rna	NULL	NULL	tier1	51845	6935	6920	5	0.001	31957	3554	3391	155	0.044	22259	2662	2643	16	0.006	11641	938	937	0	0.000	NA	NA	NA	NA	NA
266995	12	25398262	25398262	C	G	*KRAS*	missense	c.57	p.L19F	tier1	11967	1651	1644	6	0.004	7372	785	721	61	0.078	6171	723	406	312	0.435	2868	242	241	0	0.000	NA	NA	NA	NA	NA
266995	13	101762936	101762936	G	A	*NALCN*	intronic	c.2364+34	e19+34	tier2	3665	451	449	2	0.004	10852	1067	1001	65	0.061	10582	1165	649	509	0.440	3064	245	243	1	0.000	NA	NA	NA	NA	NA
266995	13	101910940	101910940	C	G	*NALCN*	intronic	c.1135-15	e10-15	tier3	5701	1079	1077	1	0.001	17182	2142	2077	59	0.028	13280	1871	1865	6	0.003	4830	426	425	0	0.000	NA	NA	NA	NA	NA
266995	15	101844339	101844339	C	G	*ENSG00000259172*	rna	NULL	NULL	tier1	27996	3565	3549	11	0.003	25641	2746	2529	199	0.073	20858	2369	1271	1081	0.460	11007	869	869	0	0.000	NA	NA	NA	NA	NA
266995	16	81941970	81941970	C	A	*PLCG2*	intronic	c.1558-51	e16-51	tier3	18801	2478	2469	8	0.003	19519	2304	2175	122	0.053	14156	1842	1091	738	0.404	7123	620	620	0	0.000	NA	NA	NA	NA	NA
266995	18	14830201	14830201	C	G	*MIR3156-2*	rna	NULL	NULL	tier1	366	0	0	0	0.000	2430	180	176	4	0.022	2743	275	273	2	0.000	908	65	65	0	0.000	NA	NA	NA	NA	NA
266995	19	9057573	9057573	G	A	*MUC16*	missense	c.29873	p.T9958I	tier1	19724	2700	2690	0	0.000	15161	1699	1608	84	0.050	11552	1544	1520	10	0.007	5837	534	530	0	0.000	NA	NA	NA	NA	NA
270086	6	56473262	56473262	G	A	*DST*	missense	c.6065	p.T2022I	tier1	14808	2146	2131	0	0.000	10934	1260	1243	17	0.013	12988	1654	1651	1	0.000	10847	1493	1487	2	0.000	NA	NA	NA	NA	NA
272848	1	145684679	145684679	G	A	*RNF115*	splice_site	c.667+1	e7+1	tier1	12576	1450	1445	2	0.001	10554	990	615	370	0.376	NA	NA	NA	NA	NA	2493	213	213	0	0.000	4857	428	428	0	0.000
272848	2	65497525	65497525	A	G	*ACTR2*	3_prime_untranslated_region	c.*1657	NULL	tier3	3820	464	462	0	0.000	3523	444	286	156	0.353	NA	NA	NA	NA	NA	438	37	37	0	0.000	1598	156	156	0	0.000
272848	2	90109121	90109121	G	A	*IGKV1D-17*	5_prime_flanking_region	c.-12537	NULL	tier3	22076	2680	2676	2	0.001	22276	2307	1372	906	0.398	NA	NA	NA	NA	NA	5823	640	636	2	0.000	9154	887	886	0	0.000
272848	2	144159094	144159094	A	T	*ARHGAP15*	intronic	c.475-34076	e6-34076	tier2	7896	856	851	1	0.001	7904	748	416	328	0.441	NA	NA	NA	NA	NA	1439	0	0	0	NA	3059	260	260	0	0.000
272848	3	37095520	37095520	A	G	*LRRFIP2*	intronic	c.2056-68	e27-68	tier3	31233	3906	3895	6	0.002	26400	2799	1601	1158	0.420	NA	NA	NA	NA	NA	8095	910	905	0	0.000	12861	1331	1331	0	0.000
272848	4	85654560	85654560	T	A	*WDFY3*	missense	c.7196	p.E2399V	tier1	11424	2175	2169	3	0.001	11438	1762	1027	728	0.415	NA	NA	NA	NA	NA	3009	508	508	0	0.000	4220	708	707	0	0.000
272848	5	76433942	76433942	G	T	*ZBED3-AS1*	intronic	c.NULL	NULL	tier3	5387	654	653	0	0.000	6297	586	422	159	0.274	NA	NA	NA	NA	NA	1120	106	105	0	0.000	4435	381	381	0	0.000
272848	5	140433285	140433285	C	A	*PCDHB1*	missense	c.2230	p.Q744K	tier1	4498	709	708	0	0.000	6612	719	411	302	0.424	NA	NA	NA	NA	NA	659	0	0	0	NA	1559	182	181	0	0.000
272848	8	16026061	16026061	G	A	*MSR1*	missense	c.536	p.S179F	tier1	26274	3529	3522	3	0.001	18771	1984	1292	662	0.339	NA	NA	NA	NA	NA	5080	547	546	0	0.000	10281	1047	1045	2	0.000
272848	8	100523442	100523442	G	C	*VPS13B*	missense	c.4410	p.E1470D	tier1	5044	557	557	0	0.000	4185	377	219	154	0.413	NA	NA	NA	NA	NA	1257	124	124	0	0.000	2048	177	177	0	0.000
272848	9	35480204	35480204	C	T	*ATP8B5P*	rna	NULL	NULL	tier1	13639	1874	1872	0	0.000	11803	1190	681	492	0.419	NA	NA	NA	NA	NA	2660	276	276	0	0.000	5333	594	592	2	0.000
272848	9	115932843	115932843	T	C	*FKBP15*	missense	c.2725	p.N909D	tier1	13038	1717	1715	0	0.000	15641	1624	1229	380	0.236	NA	NA	NA	NA	NA	5451	545	544	0	0.000	7683	749	749	0	0.000
272848	9	136634584	136634584	C	T	*VAV2*	missense	c.2389	p.G797S	tier1	13168	1925	1919	3	0.002	13325	1563	927	613	0.398	NA	NA	NA	NA	NA	3202	332	329	1	0.000	4797	529	528	1	0.000
272848	10	69695996	69695996	T	C	*HERC4*	splice_region	c.2596-4	e21-4	tier4	4276	476	476	0	0.000	4237	386	285	97	0.254	NA	NA	NA	NA	NA	998	0	0	0	NA	2294	219	218	0	0.000
272848	11	9081984	9081984	G	C	*SCUBE2*	missense	c.938	p.T313S	tier1	3243	596	596	0	0.000	6553	937	586	346	0.371	NA	NA	NA	NA	NA	256	0	0	0	NA	996	142	142	0	0.000
272848	11	51411669	51411669	C	T	*OR4A5*	missense	c.727	p.V243I	tier1	8268	905	901	1	0.001	10353	972	777	189	0.196	NA	NA	NA	NA	NA	2326	207	206	1	0.000	4102	353	352	0	0.000
272848	11	85988219	85988219	A	G	*EED*	3_prime_untranslated_region	c.*85988219	NULL	tier3	6048	824	824	0	0.000	5954	674	449	218	0.327	NA	NA	NA	NA	NA	537	48	48	0	0.000	2389	0	0	0	NA
272848	12	58159282	58159282	C	T	*CYP27B1*	missense	c.299	p.R100Q	tier1	11501	1411	1408	2	0.001	10361	1058	636	412	0.393	NA	NA	NA	NA	NA	2869	310	309	0	0.000	4052	379	379	0	0.000
272848	15	41634594	41634594	T	A	*NUSAP1*	nonsense	c.104	p.L35*	tier1	2773	492	491	1	0.002	3726	514	318	193	0.378	NA	NA	NA	NA	NA	328	0	0	0	NA	951	131	131	0	0.000
272848	16	16272771	16272771	C	T	*ABCC6*	missense	c.2299	p.V767I	tier1	16205	2347	2345	1	0.000	16934	1949	1678	256	0.132	NA	NA	NA	NA	NA	5461	549	548	0	0.000	6382	708	708	0	0.000
272848	16	31090611	31090611	C	T	*ZNF646*	missense	c.2966	p.A989V	tier1	33198	4387	4374	5	0.001	35710	3952	2343	1524	0.394	NA	NA	NA	NA	NA	11629	1314	1314	0	0.000	15882	1615	1612	0	0.000
272848	16	53529201	53529201	C	T	*AKTIP*	missense	c.286	p.V96M	tier1	15669	1926	1923	2	0.001	12921	1377	828	539	0.394	NA	NA	NA	NA	NA	3225	339	339	0	0.000	6963	692	691	1	0.000
272848	16	87870085	87870085	C	T	*SLC7A5*	intronic	c.1290+19	e8+19	tier3	16895	2417	2413	4	0.002	16802	1839	1414	403	0.222	NA	NA	NA	NA	NA	7424	861	858	1	0.000	8280	891	888	1	0.000
272848	17	33476023	33476023	C	A	*UNC45B*	missense	c.200	p.S67Y	tier1	27637	3409	3402	2	0.001	24079	2417	1363	1034	0.431	NA	NA	NA	NA	NA	10095	1117	1116	0	0.000	12821	1234	1234	0	0.000
272848	18	42531907	42531907	G	A	*SETBP1*	missense	c.2602	p.D868N	tier1	32873	4181	4178	1	0.000	26396	2839	2315	511	0.181	NA	NA	NA	NA	NA	9543	1057	1054	2	0.000	13198	1396	1396	0	0.000
272848	18	42531913	42531913	G	T	*SETBP1*	missense	c.2608	p.G870C	tier1	32858	4163	4154	4	0.001	26768	2860	2295	544	0.192	NA	NA	NA	NA	NA	9667	1066	1062	1	0.000	13280	1401	1401	0	0.000
272848	19	4310495	4310495	G	A	*FSD1*	missense	c.392	p.R131Q	tier1	42593	5373	5361	7	0.001	37991	3971	2251	1634	0.421	NA	NA	NA	NA	NA	12990	1492	1487	1	0.000	16956	1736	1732	1	0.000
272848	19	19351506	19351506	G	C	*NCAN*	intronic	c.3492+12	e11+12	tier3	14211	1806	1799	2	0.001	11801	1151	696	445	0.390	NA	NA	NA	NA	NA	5836	644	644	0	0.000	6895	683	683	0	0.000
272848	21	46957834	46957834	C	T	*SLC19A1*	missense	c.40	p.V14M	tier1	21360	2581	2570	7	0.003	17689	1634	936	683	0.422	NA	NA	NA	NA	NA	10243	1086	1084	1	0.000	11123	1085	1085	0	0.000
272848	X	12739552	12739552	G	T	*FRMPD4*	3_prime_untranslated_region	c.*900	NULL	tier3	16071	2354	2353	1	0.000	14197	1680	1009	658	0.395	NA	NA	NA	NA	NA	2998	354	353	0	0.000	4152	453	453	0	0.000
272848	X	77224984	77224984	T	C	*PGAM4*	missense	c.152	p.E51G	tier1	17733	2289	2285	2	0.001	15666	1739	1038	689	0.399	NA	NA	NA	NA	NA	4062	484	482	0	0.000	4748	523	522	0	0.000
272848	X	120008710	120008710	T	G	*CT47B1*	intronic	c.775+40	e1+40	tier2	6786	874	871	0	0.000	8825	927	557	362	0.394	NA	NA	NA	NA	NA	1331	121	121	0	0.000	1934	185	185	0	0.000
272848	X	145701712	145701712	G	A	*ENSG00000231686*	5_prime_untranslated_region	c.-145701712	NULL	tier2	8433	1359	1356	2	0.001	8930	1109	652	439	0.402	NA	NA	NA	NA	NA	444	0	0	0	NA	1222	165	165	0	0.000
275454	5	131607200	131607200	C	T	*PDLIM4*	3_prime_untranslated_region	c.*131607200	NULL	tier2	21833	3587	3575	4	0.001	8408	1286	1228	56	0.044	NA	NA	NA	NA	NA	7778	734	730	3	0.004	NA	NA	NA	NA	NA
275454	14	19807134	19807134	G	T	*OR11H13P*	5_prime_untranslated_region	c.-19807134	NULL	tier3	9920	2283	2281	0	0.000	2124	395	387	7	0.018	NA	NA	NA	NA	NA	1373	123	123	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
280837	1	1669668	1669668	G	C	*SLC35E2*	intronic	c.586+92	e3+92	tier2	9681	1209	1190	19	0.016	10714	998	534	462	0.464	11692	1479	826	640	0.437	60277	2293	2262	31	0.014	NA	NA	NA	NA	NA
280837	1	28605680	28605680	G	A	*SESN2*	silent	c.1284	p.V428	tier1	13319	1360	1352	7	0.005	14899	2048	1169	873	0.428	19279	2400	1402	972	0.409	102550	7789	7714	67	0.009	NA	NA	NA	NA	NA
280837	2	25467497	25467497	G	A	*DNMT3A*	nonsense	c.1579	p.Q527*	tier1	70333	10023	9820	176	0.018	51291	6893	3714	3137	0.458	64265	9581	5279	4051	0.434	278961	16532	16337	173	0.010	NA	NA	NA	NA	NA
280837	2	131453866	131453866	T	C	*ENSG00000240253*	intronic	c.NULL	NULL	tier3	6258	584	582	2	0.003	5510	740	410	330	0.446	6138	628	348	278	0.444	27099	2343	2320	22	0.009	NA	NA	NA	NA	NA
280837	2	234184342	234184342	G	A	*ATG16L1*	intronic	c.954+918	e9+918	tier4	31935	4714	4707	7	0.001	24213	3828	3112	707	0.185	31204	4812	4478	317	0.066	124297	8955	8938	11	0.001	NA	NA	NA	NA	NA
280837	3	118913221	118913221	C	T	*UPK1B*	silent	c.624	p.G208	tier1	39622	5047	5017	29	0.006	20108	2658	1488	1162	0.438	26153	3649	2269	1355	0.374	127966	7136	7057	75	0.011	NA	NA	NA	NA	NA
280837	4	1949812	1949812	A	C	*WHSC1*	3_prime_untranslated_region	c.*5684	NULL	tier3	6331	1296	1289	7	0.005	7076	1601	902	696	0.436	7007	1524	850	665	0.439	37456	4426	4379	47	0.011	NA	NA	NA	NA	NA
280837	4	71888174	71888174	G	T	*DCK*	missense	c.298	p.A100S	tier1	5890	646	642	4	0.006	6429	1102	621	480	0.436	5748	744	477	262	0.355	29463	3599	3565	30	0.008	NA	NA	NA	NA	NA
280837	4	76817552	76817552	G	C	*PPEF2*	5_prime_untranslated_region	c.-74	NULL	tier2	42602	5574	5560	13	0.002	28801	4099	2468	1613	0.395	30910	4269	2964	1262	0.299	199372	11731	11635	84	0.007	NA	NA	NA	NA	NA
280837	4	109769882	109769882	C	T	*COL25A1*	intronic	c.1434+33	e26+33	tier3	2621	967	958	9	0.009	2906	724	414	310	0.428	3662	1188	659	529	0.445	18032	2053	2039	14	0.007	NA	NA	NA	NA	NA
280837	5	74712651	74712651	C	A	*COL4A3BP*	intronic	c.1221+50	e8+50	tier3	8707	875	872	2	0.002	6129	801	466	334	0.418	8869	1013	696	311	0.309	76736	6352	6305	46	0.007	NA	NA	NA	NA	NA
280837	6	33136506	33136506	C	T	*COL11A2*	missense	c.3883	p.E1295K	tier1	57055	6946	6901	42	0.006	25285	2410	1348	1055	0.439	34912	4264	2439	1786	0.423	134392	5779	5727	52	0.009	NA	NA	NA	NA	NA
280837	7	150714308	150714308	C	T	*ATG9B*	5_prime_untranslated_region	c.-150714308	NULL	tier2	40833	5544	5536	4	0.001	15091	1936	1318	613	0.317	19717	2684	2446	230	0.086	197641	12873	12844	17	0.001	NA	NA	NA	NA	NA
280837	8	131129068	131129068	C	T	*ASAP1*	intronic	c.2005+58	e21+58	tier3	3325	612	605	6	0.010	4520	1144	642	501	0.438	4563	974	561	411	0.423	21880	2898	2864	33	0.011	NA	NA	NA	NA	NA
280837	9	139903977	139903977	G	A	*ABCA2*	intronic	c.6824+16	e44+16	tier2	966	63	62	1	0.016	6142	788	92	696	0.883	6470	633	77	554	0.878	15744	2436	2339	96	0.039	NA	NA	NA	NA	NA
280837	10	38651191	38651191	G	A	*HSD17B7P2*	3_prime_untranslated_region	c.*38651191	NULL	tier3	18221	2023	2015	8	0.004	16976	2382	1369	1010	0.425	19355	2319	1407	897	0.389	111636	8539	8418	109	0.013	NA	NA	NA	NA	NA
280837	10	68139043	68139043	T	C	*CTNNA3*	silent	c.1599	p.L533	tier1	44029	6712	6687	23	0.003	26718	3792	2344	1435	0.380	33542	5048	3133	1859	0.372	161892	9926	9843	77	0.008	NA	NA	NA	NA	NA
280837	10	119044294	119044294	T	C	*PDZD8*	silent	c.1950	p.Q650	tier1	56391	7083	7072	10	0.001	27321	3780	2478	1294	0.343	28831	3811	2909	870	0.230	248111	15317	15248	68	0.004	NA	NA	NA	NA	NA
280837	11	4107876	4107876	G	T	*STIM1*	intronic	c.1541+103	e11+103	tier3	10940	1341	1332	9	0.007	5943	599	495	100	0.168	7722	1005	881	117	0.117	5489	831	820	11	0.013	NA	NA	NA	NA	NA
280837	11	12225810	12225810	G	C	*MICAL2*	missense	c.278	p.G93A	tier1	59097	7374	7316	55	0.007	25404	2645	1379	1260	0.477	31790	4467	2317	2104	0.476	148293	4929	4866	63	0.013	NA	NA	NA	NA	NA
280837	12	14689595	14689595	A	G	*PLBD1*	missense	c.608	p.L203S	tier1	7917	901	891	9	0.010	7044	832	480	351	0.422	8647	1018	613	397	0.393	54095	2606	2576	29	0.011	NA	NA	NA	NA	NA
280837	17	1563288	1563288	T	A	*PRPF8*	missense	c.4793	p.D1598V	tier1	53750	6375	6329	36	0.006	40103	5019	2849	2148	0.430	52592	6484	3701	2660	0.418	273050	15221	15037	164	0.011	NA	NA	NA	NA	NA
280837	17	27210235	27210235	C	T	*FLOT2*	silent	c.402	p.T134	tier1	16063	2496	2410	81	0.033	21267	3874	2150	1711	0.443	26403	3875	2134	1690	0.442	139781	13386	13242	130	0.010	NA	NA	NA	NA	NA
280837	17	73910078	73910078	C	T	*FBF1*	silent	c.3003	p.Q1001	tier1	40681	4966	4946	19	0.004	21923	2287	1507	775	0.340	28674	3794	2479	1285	0.341	172441	7316	7263	51	0.007	NA	NA	NA	NA	NA
280837	18	5891961	5891961	C	G	*TMEM200C*	missense	c.102	p.R34S	tier1	72630	8874	8814	54	0.006	45356	4824	2653	2147	0.447	48621	5914	3328	2469	0.426	317261	13074	12898	169	0.013	NA	NA	NA	NA	NA
280837	19	9001863	9001863	G	A	*MUC16*	nonsense	c.904	p.R302*	tier1	16873	2093	2081	12	0.006	8565	884	521	361	0.409	12012	1511	890	613	0.408	59170	2293	2275	18	0.008	NA	NA	NA	NA	NA
280837	20	30409206	30409206	C	T	*MYLK2*	intronic	c.474-36	e3-36	tier3	24229	2778	2770	8	0.003	35463	3643	2316	1314	0.362	47807	5947	3804	2069	0.352	333071	13372	13277	80	0.006	NA	NA	NA	NA	NA
280837	X	129147939	129147939	G	A	*BCORL1*	missense	c.1191	p.M397I	tier1	29995	4025	3955	55	0.014	17931	1969	234	1730	0.881	24280	3188	469	2707	0.852	99901	6449	6284	142	0.022	NA	NA	NA	NA	NA
283773	9	20923717	20923717	G	A	*FOCAD*	missense	c.2911	p.V971I	tier1	19746	2206	2203	3	0.001	15008	1546	1249	290	0.188	19650	2393	1998	381	0.160	11988	1046	1043	0	0.000	34366	4442	4433	1	0.000
283773	19	2121672	2121672	C	T	*AP3D1*	intronic	c.1101+61	e12+61	tier3	20522	2418	2411	0	0.000	12541	1319	1096	218	0.166	18871	2400	2149	242	0.101	11961	1035	1035	0	0.000	29951	3921	3913	0	0.000
283773	20	31023112	31023112	T	G	*ASXL1*	nonsense	c.2597	p.L866*	tier1	21481	2590	2585	2	0.001	17274	1785	1528	243	0.137	23913	2958	2620	335	0.113	17173	1473	1470	0	0.000	41409	5450	5440	0	0.000
283773	X	70339865	70339865	T	A	*MED12*	missense	c.398	p.V133D	tier1	23909	2632	2624	5	0.002	24201	2615	2505	96	0.037	29792	3513	3462	49	0.014	9035	687	685	0	0.000	25021	0	0	0	NA
283773	X	106788960	106788960	T	C	*FRMPD3-AS1*	rna	NULL	NULL	tier1	24504	2819	2789	24	0.009	18288	1879	1688	180	0.096	19702	2363	2120	237	0.101	6765	531	530	0	0.000	16237	0	0	0	NA
288033	2	33614218	33614218	G	T	*LTBP1*	intronic	c.4715-33	e32-33	tier3	21884	2522	2455	66	0.026	21049	2058	1174	851	0.420	44295	6019	5863	148	0.025	21500	2622	2614	6	0.002	69944	6949	6933	10	0.001
288033	3	126219009	126219009	C	A	*UROC1*	intronic	c.1146-12	e12-12	tier3	18095	2112	2032	80	0.038	14156	1417	715	684	0.489	26333	3309	3189	119	0.036	14162	1806	1801	3	0.002	40736	3301	3291	7	0.002
288033	4	103611794	103611794	G	A	*MANBA*	missense	c.808	p.P270S	tier1	28387	3193	3089	98	0.031	23133	2126	1114	972	0.466	43865	5721	5524	186	0.033	21269	2607	2598	1	0.000	64328	6011	5983	10	0.002
288033	7	100839218	100839218	C	T	*MOGAT3*	missense	c.832	p.A278T	tier1	23164	2572	2566	4	0.002	17475	1513	1345	162	0.108	33538	4414	4399	8	0.002	16269	2008	2001	3	0.000	52092	4840	4826	5	0.000
288033	9	90503384	90503384	G	C	*SPATA31E1*	missense	c.3982	p.V1328L	tier1	10205	1098	1070	27	0.025	12204	913	489	412	0.457	10089	1441	1390	46	0.032	3448	361	359	0	0.000	10451	1188	1182	2	0.000
288033	9	136918842	136918842	T	C	*BRD3*	5_prime_untranslated_region	c.-243	NULL	tier3	7607	826	805	21	0.025	10888	968	503	452	0.473	13949	1887	1812	73	0.039	6098	809	807	0	0.000	18469	1898	1890	3	0.002
288033	12	133201355	133201355	C	T	*POLE*	silent	c.6789	p.Q2263	tier1	15901	0	0	0	0.000	17481	1459	1383	72	0.049	21613	2859	2787	67	0.023	9948	1187	1185	0	0.000	30486	2829	2822	3	0.000
288033	15	85327071	85327071	C	T	*ZNF592*	missense	c.1165	p.R389W	tier1	18358	2117	2116	1	0.000	15781	1397	1329	65	0.047	15592	2181	2170	4	0.002	6763	785	782	1	0.000	19001	2062	2055	3	0.000
288033	17	10350420	10350420	C	T	*MYH4*	silent	c.5079	p.R1693	tier1	21576	2339	2273	61	0.026	19032	1765	943	799	0.459	32383	4185	4053	128	0.031	16948	2123	2120	1	0.000	60840	4963	4948	6	0.001
288033	19	13941346	13941346	C	G	*ZSWIM4*	missense	c.2452	p.P818A	tier1	8599	1530	1472	48	0.032	8466	1021	538	475	0.469	7868	1703	1650	47	0.028	3417	479	477	0	0.000	10766	1682	1681	0	0.000
288033	20	43723594	43723594	A	T	*KCNS1*	missense	c.1498	p.S500T	tier1	11411	1280	1245	35	0.027	8455	786	408	371	0.476	19061	2579	2487	88	0.034	10813	1355	1351	1	0.000	33805	3187	3182	4	0.001
288033	20	57768618	57768618	G	A	*ZNF831*	silent	c.2544	p.T848	tier1	11308	1254	1215	38	0.030	12566	1159	634	512	0.447	17147	2531	2455	74	0.029	8208	1045	1042	1	0.000	28350	3233	3219	9	0.003
288033	22	41742111	41742111	C	T	*ZC3H7B*	missense	c.1564	p.R522C	tier1	39986	4618	4474	139	0.030	41645	4062	2060	1904	0.480	54798	7115	6877	224	0.032	28026	3514	3508	1	0.000	87132	7486	7455	9	0.000
288033	22	50960184	50960184	G	A	*NCAPH2*	missense	c.1015	p.V339M	tier1	16387	1949	1907	38	0.020	14930	1559	931	609	0.395	16838	2417	2339	75	0.031	6759	0	0	0	NA	24907	2842	2833	4	0.001
293230	1	201947766	201947766	A	G	*RNPEP*	5_prime_flanking_region	c.-4029	NULL	tier3	9482	1174	1152	20	0.017	11720	1397	1142	247	0.178	12159	1602	922	676	0.423	5414	409	400	7	0.017	37045	4989	4981	0	0.000
293230	2	21232014	21232014	G	A	*APOB*	missense	c.7726	p.R2576C	tier1	9351	1212	1208	1	0.001	12256	1530	1425	103	0.067	9514	1253	1238	15	0.012	7202	587	587	0	0.000	21588	2817	2812	1	0.000
293230	2	25457242	25457242	C	T	*DNMT3A*	missense	c.2645	p.R882H	tier1	21044	2480	2375	100	0.040	15763	1754	1354	389	0.223	8307	1134	676	456	0.403	9000	628	613	14	0.022	38996	5188	5187	1	0.000
293230	2	133489315	133489315	G	A	*NCKAP5*	missense	c.5438	p.S1813F	tier1	6377	939	909	30	0.032	8799	1264	974	286	0.227	6299	1145	834	309	0.270	4337	334	326	8	0.024	19744	3454	3450	1	0.000
293230	2	170092614	170092614	G	A	*LRP2*	intronic	c.4692-36	e29-36	tier3	11061	1363	1323	39	0.029	10282	1207	1054	152	0.126	4193	531	455	76	0.143	6228	485	480	5	0.010	20037	2735	2729	0	0.000
293230	5	5462936	5462936	T	C	*KIAA0947*	silent	c.3489	p.T1163	tier1	26129	2831	2742	85	0.030	19170	2096	1697	387	0.186	12834	1764	997	761	0.433	9666	673	656	16	0.024	40534	4971	4968	2	0.000
293230	5	67522723	67522723	G	T	*PIK3R1*	missense	c.220	p.V74L	tier1	25824	2770	2763	2	0.001	15835	1665	1587	72	0.043	15471	2146	2123	20	0.009	7360	422	420	0	0.000	44097	5460	5456	0	0.000
293230	6	125146129	125146129	G	T	*NKAIN2*	3_prime_untranslated_region	c.*1754	NULL	tier3	7619	1198	1169	28	0.023	8321	1112	933	176	0.159	5621	1230	708	519	0.423	3322	232	226	6	0.026	13535	2295	2291	0	0.000
293230	6	159653093	159653093	G	C	*FNDC1*	missense	c.1549	p.G517R	tier1	7632	916	891	24	0.026	8214	934	787	139	0.150	5425	896	520	375	0.419	4385	253	247	5	0.020	24207	3473	3468	0	0.000
293230	9	138641963	138641963	G	A	*KCNT1*	missense	c.274	p.V92I	tier1	27931	3102	3064	36	0.012	23363	2651	2503	139	0.053	21594	3154	2567	582	0.185	13733	952	942	7	0.007	55039	7494	7485	0	0.000
293230	15	34130377	34130377	C	T	*RYR3*	nonsense	c.12196	p.R4066*	tier1	21626	2832	2828	1	0.000	22095	2872	2717	145	0.051	22359	3298	3262	29	0.009	10848	793	791	0	0.000	53873	7441	7422	1	0.000
293230	15	91044236	91044236	G	A	*IQGAP1*	3_prime_untranslated_region	c.*896	NULL	tier3	13014	1391	1391	0	0.000	11352	1229	1154	72	0.059	7931	1127	1116	11	0.010	7128	464	463	0	0.000	22861	2829	2825	0	0.000
293230	16	1116377	1116377	C	T	*ENSG00000261720*	rna	NULL	NULL	tier1	11746	1357	1316	34	0.025	8812	964	776	186	0.193	9564	1265	725	537	0.426	4564	299	288	11	0.037	25728	3203	3191	2	0.000
293230	16	67962332	67962332	G	C	*PSKH1*	3_prime_untranslated_region	c.*787	NULL	tier2	22747	2833	2745	83	0.029	25475	3136	2706	418	0.134	15885	2177	1407	765	0.352	14012	1001	979	20	0.020	60218	8139	8129	4	0.000
298273	1	46159297	46159297	C	T	*TMEM69*	missense	c.464	p.A155V	tier1	4868	1227	1223	2	0.002	4929	778	479	296	0.382	NA	NA	NA	NA	NA	2869	728	723	4	0.000	2502	401	120,258;	22	0.055
298273	1	183498545	183498545	G	T	*SMG7*	silent	c.720	p.V240	tier1	21366	2749	2744	2	0.001	14190	1181	730	435	0.373	NA	NA	NA	NA	NA	31352	3965	3959	4	0.001	21990	1877	879,993;	3	0.002
298273	2	101099723	101099723	G	A	*NMS*	nonsense	c.459	p.W153*	tier1	6569	1256	1254	1	0.001	4970	571	390	176	0.311	NA	NA	NA	NA	NA	5923	1040	1037	0	0.000	4116	554	389,137;	26	0.047
298273	3	46759141	46759141	C	T	*PRSS50*	intronic	c.107-14	e2-14	tier2	18781	3129	3125	1	0.000	21410	2290	1299	931	0.417	NA	NA	NA	NA	NA	18802	2560	2551	5	0.000	16960	1600	724,869;	2	0.000
298273	3	50339933	50339933	C	T	*HYAL1*	missense	c.455	p.R152Q	tier1	26251	3582	3579	1	0.000	21507	2162	1271	865	0.405	NA	NA	NA	NA	NA	40642	4611	4602	3	0.000	28871	1941	1023,914	2	0.000
298273	5	140596188	140596188	G	A	*PCDHB13*	3_prime_untranslated_region	c.*96	NULL	tier3	3626	915	915	0	0.000	4516	560	291	267	0.478	NA	NA	NA	NA	NA	2318	585	582	0	0.000	1455	323	81,204;	38	0.118
298273	6	152461140	152461140	C	T	*SYNE1*	missense	c.25403	p.R8468H	tier1	37325	4968	4956	5	0.001	20696	2257	1328	900	0.404	NA	NA	NA	NA	NA	46640	5229	5221	4	0.000	29151	1846	905,939;	1	0.000
298273	7	131071805	131071805	T	G	*MKLN1*	intronic	c.169-74	e3-74	tier3	4562	0	0	0	0.000	3943	303	157	143	0.477	NA	NA	NA	NA	NA	2609	342	339	0	0.000	1977	255	8,220;	27	0.106
298273	13	49073878	49073878	C	T	*RCBTB2*	silent	c.1278	p.S426	tier1	18591	2390	2388	1	0.000	11807	1116	598	507	0.459	NA	NA	NA	NA	NA	25649	2962	2957	4	0.000	17898	1355	517,582;	253	0.187
298273	14	21841578	21841578	A	G	*SUPT16H*	silent	c.78	p.D26	tier1	3348	822	820	2	0.002	3103	528	278	249	0.472	NA	NA	NA	NA	NA	1960	455	455	0	0.000	1614	267	38,209;	20	0.075
298273	17	1563288	1563288	T	C	*PRPF8*	missense	c.4793	p.D1598G	tier1	33380	4790	4781	2	0.000	27162	2693	1584	1063	0.402	NA	NA	NA	NA	NA	53239	6766	6751	0	0.000	36788	3063	752,130	0	0.000
298273	17	66873661	66873661	G	A	*ABCA8*	missense	c.4198	p.R1400W	tier1	1782	461	459	2	0.004	2133	268	171	96	0.360	NA	NA	NA	NA	NA	1219	280	279	1	0.000	836	0	0,0;	0	NA
298273	19	8436034	8436034	C	T	*ANGPTL4*	silent	c.756	p.H252	tier1	12098	1902	1896	2	0.001	11822	1148	698	438	0.386	NA	NA	NA	NA	NA	20104	2636	2624	8	0.000	15018	1395	152,1145	96	0.069
298273	19	36015866	36015866	C	A	*SBSN*	intronic	c.610-40	e3-40	tier3	6397	1008	1008	0	0.000	9110	954	516	420	0.449	NA	NA	NA	NA	NA	5693	847	843	3	0.004	5247	554	75,406;	69	0.125
298273	20	1106550	1106550	G	A	*PSMF1*	intronic	c.282+257	e2+257	tier3	6544	866	865	0	0.000	10127	779	435	333	0.434	NA	NA	NA	NA	NA	12509	1623	1620	2	0.000	7425	832	432,399;	0	0.000
298273	21	10934043	10934043	G	A	*TPTE*	silent	c.934	p.L312	tier1	5187	775	774	0	0.000	4331	370	299	69	0.188	NA	NA	NA	NA	NA	3476	509	509	0	0.000	1940	260	145,105;	10	0.038
298273	21	43533838	43533838	G	A	*UMODL1*	missense	c.2644	p.V882M	tier1	2427	598	598	0	0.000	3834	453	267	184	0.408	NA	NA	NA	NA	NA	1351	331	330	1	0.000	1476	290	119,148;	23	0.079
307995	1	34052117	34052117	G	A	*CSMD2*	silent	c.7038	p.P2346	tier1	38958	4738	4731	1	0.000	18756	1935	1648	276	0.143	31362	3727	3723	0	0.000	57936	7117	7115	0	0.000	64771	8601	8575	1	0.000
307995	1	159174836	159174836	C	T	*DARC*	intronic	c.21+66	e1+66	tier2	1234	221	220	0	0.000	1023	81	73	8	0.099	490	52	51	0	0.000	1419	0	0	0	NA	2509	460	460	0	0.000
307995	2	27325149	27325149	C	G	*CGREF1*	5_prime_untranslated_region	c.-27325149	NULL	tier2	26207	3095	3093	0	0.000	16920	1728	1497	218	0.127	23963	2507	2497	0	0.000	40912	4597	4592	0	0.000	58421	7431	7416	0	0.000
307995	2	43986084	43986084	A	G	*PLEKHH2*	missense	c.253	p.T85A	tier1	15531	1918	1915	0	0.000	8257	726	583	131	0.183	13384	1530	1530	0	0.000	26028	3151	3145	0	0.000	33898	4501	4495	0	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
307995	2	61510631	61510631	T	C	*USP34*	intronic	c.4833-47	e36-47	tier3	3787	0	0	0	0.000	1349	111	94	17	0.153	2077	0	0	0	NA	4450	429	427	0	0.000	2281	0	0	0	NA
307995	2	138738953	138738953	C	T	*HNMT*	silent	c.358	p.L120	tier1	22240	2688	2684	0	0.000	16074	1610	1361	234	0.147	21010	2141	2133	0	0.000	35264	4055	4048	0	0.000	49152	6483	6477	0	0.000
307995	2	207310122	207310122	T	C	*ADAM23*	silent	c.306	p.S102	tier1	16606	2066	2063	0	0.000	7808	803	660	137	0.172	14513	1574	1573	0	0.000	22705	2581	2575	0	0.000	25337	3372	3366	0	0.000
307995	3	9517257	9517257	G	T	*SETD5*	nonsense	c.3811	p.G1271*	tier1	16932	2046	2042	1	0.000	12666	1192	986	197	0.167	16625	1771	1756	1	0.000	30581	3499	3493	0	0.000	40390	5238	5230	0	0.000
307995	3	30702951	30702951	G	A	*TGFBR2*	intronic	c.530-10179	e5-10179	tier4	21932	3088	3087	1	0.000	12719	1402	1136	255	0.183	19415	2486	2478	0	0.000	35761	4596	4593	1	0.000	44285	6232	6230	1	0.000
307995	3	126180517	126180517	G	A	*ZXDC*	missense	c.1988	p.P663L	tier1	26121	3489	3479	3	0.001	17143	1897	1582	303	0.161	19681	2031	2023	0	0.000	28774	2952	2950	1	0.000	46891	6709	6704	1	0.000
307995	4	107154095	107154095	C	A	*TBCK*	missense	c.1639	p.G547C	tier1	22774	2500	2497	2	0.001	12234	1077	886	186	0.174	17884	1895	1891	0	0.000	36704	3940	3938	0	0.000	38889	4788	4787	1	0.000
307995	5	5235176	5235176	C	T	*ADAMTS16*	missense	c.1900	p.L634F	tier1	41498	5993	5982	1	0.000	24175	2732	2248	461	0.170	28275	3291	3286	0	0.000	52906	6393	6393	0	0.000	64254	9267	9257	0	0.000
307995	5	14364017	14364017	C	A	*TRIO*	silent	c.2568	p.V856	tier1	11759	2486	2485	0	0.000	8545	1420	1183	229	0.162	7732	1311	1309	0	0.000	14980	2672	2669	1	0.000	20910	4722	4719	1	0.000
307995	5	140174742	140174742	C	T	*PCDHA2*	missense	c.193	p.R65W	tier1	10300	1723	1722	1	0.001	5235	595	496	96	0.162	5095	646	645	0	0.000	12490	1585	1583	0	0.000	14042	2508	2506	0	0.000
307995	6	38743672	38743672	G	A	*DNAH8*	missense	c.1256	p.R419K	tier1	12876	1538	1531	0	0.000	7777	745	677	64	0.086	11981	1279	1277	0	0.000	20259	2218	2218	0	0.000	25829	3434	3432	0	0.000
307995	7	29689532	29689532	T	A	*ZNRF2P2*	intronic	c.NULL	NULL	tier2	9555	1238	1236	0	0.000	3907	344	326	14	0.041	8708	1054	1053	0	0.000	15734	1964	1960	0	0.000	22140	2998	2995	0	0.000
307995	9	38414100	38414100	C	T	*IGFBPL1*	silent	c.561	p.T187	tier1	850	0	0	0	0.000	1029	101	84	17	0.168	601	52	52	0	0.000	1054	73	73	0	0.000	2312	0	0	0	NA
307995	9	124737164	124737164	T	C	*TTLL11*	missense	c.1634	p.E545G	tier1	4530	842	841	0	0.000	3253	448	363	82	0.184	2211	0	0	0	NA	4800	565	561	0	0.000	6841	0	0	0	NA
307995	11	67049830	67049830	C	G	*ADRBK1*	missense	c.1046	p.A349G	tier1	17607	2373	2372	1	0.000	9871	930	780	146	0.158	13509	1415	1412	1	0.000	24268	2672	2668	0	0.000	32239	4290	4286	0	0.000
307995	11	90016247	90016247	G	A	*ENSG00000214391*	3_prime_untranslated_region	c.*90016247	NULL	tier2	9251	1416	1410	1	0.001	5881	615	505	109	0.178	8316	1001	997	0	0.000	14878	1962	1962	0	0.000	19995	3123	3120	0	0.000
307995	12	9095076	9095076	C	G	*M6PR*	missense	c.647	p.G216A	tier1	18052	2269	2268	0	0.000	14745	1560	1265	284	0.183	14814	1463	1459	0	0.000	26480	2763	2759	0	0.000	36033	4801	4793	1	0.000
307995	12	50027356	50027356	G	A	*PRPF40B*	intronic	c.580+26	e8+26	tier3	20184	2279	2278	0	0.000	17274	1679	1356	308	0.185	19082	1865	1862	0	0.000	38807	4116	4112	0	0.000	44347	5501	5499	0	0.000
307995	12	52715016	52715016	G	T	*KRT83*	missense	c.104	p.A35D	tier1	17872	2232	2228	2	0.001	11270	1091	906	174	0.161	14742	1522	1520	0	0.000	24864	2656	2656	0	0.000	30211	4075	4072	1	0.000
307995	12	52891238	52891238	T	A	*KRT6C*	5_prime_flanking_region	c.-23717	NULL	tier3	37827	4684	4677	4	0.001	17563	1842	1493	338	0.185	34379	4197	4197	0	0.000	59543	7510	7503	0	0.000	74155	9567	9558	0	0.000
307995	12	109519720	109519720	C	T	*USP30*	intronic	c.781-18	e9-18	tier3	18185	2137	2136	1	0.000	14507	1438	1220	204	0.143	21551	2264	2261	0	0.000	37214	4211	4209	0	0.000	51875	6669	6664	1	0.000
307995	14	94945375	94945375	G	A	*SERPINA9*	intronic	c.NULL	NULL	tier3	14412	2018	2013	0	0.000	8542	927	754	164	0.179	9099	884	881	0	0.000	12602	1228	1222	0	0.000	18950	2683	2678	0	0.000
307995	17	61986092	61986092	G	C	*GH2*	5_prime_flanking_region	c.-26931	NULL	tier3	7436	993	993	0	0.000	5504	643	532	107	0.167	4489	420	418	1	0.000	8630	980	978	0	0.000	11989	1814	1811	1	0.000
307995	18	50683690	50683690	C	T	*DCC*	intronic	c.1262-36	e8-36	tier3	7199	1369	1368	1	0.001	7187	937	779	156	0.167	6715	805	802	1	0.000	10471	1351	1349	1	0.000	15612	2820	2817	1	0.000
307995	20	47247205	47247205	C	T	*PREX1*	intronic	c.4593+61	e36+61	tier3	53682	6200	6199	0	0.000	29856	2963	2421	515	0.175	41606	4321	4313	1	0.000	80057	9181	9177	0	0.000	100875	12640	12635	2	0.000
307995	20	56082765	56082765	C	T	*CTCFL*	silent	c.1326	p.P442	tier1	46865	5735	5729	3	0.001	18320	1737	1393	333	0.193	36410	4191	4180	2	0.000	72397	9117	9111	0	0.000	87757	11408	11399	0	0.000
307995	20	58349240	58349240	G	A	*PHACTR3*	intronic	c.927-58	e7-58	tier3	9829	1423	1419	1	0.001	6694	832	688	143	0.172	7166	850	848	0	0.000	11139	1465	1464	0	0.000	15974	2886	2880	1	0.000
307995	22	20171118	20171118	C	T	*LINC00896*	5_prime_flanking_region	c.-22982	NULL	tier3	41685	5144	5137	2	0.000	27941	2833	2333	468	0.167	35577	3647	3638	0	0.000	64807	7402	7398	0	0.000	82450	10682	10662	1	0.000
307995	X	39911641	39911641	C	T	*BCOR*	nonsense	c.4989	p.W1663*	tier1	2771	0	0	0	0.000	1661	163	120	42	0.259	2252	209	209	0	0.000	3184	355	354	0	0.000	4228	0	0	0	NA
307995	X	53574723	53574723	G	T	*HUWE1*	missense	c.10547	p.A3516D	tier1	4030	855	853	1	0.001	3570	485	322	160	0.332	2956	479	477	0	0.000	6543	1022	1021	0	0.000	8509	1948	1947	1	0.000
307995	X	151336800	151336800	C	T	*GABRA3*	missense	c.1379	p.R460H	tier1	20311	2431	2425	4	0.002	16974	1748	1243	482	0.279	22921	2528	2526	0	0.000	43526	5186	5172	1	0.000	59634	7616	7603	1	0.000
311426	1	15987264	15987264	T	C	*RSC1A1*	silent	c.901	p.L301	tier1	11236	1410	1362	48	0.034	13278	1685	958	720	0.429	NA	NA	NA	NA	NA	17268	2601	2577	12	0.005	10555	751	693	54	0.072
311426	1	23660085	23660085	T	C	*HNRNPR*	missense	c.424	p.T142A	tier1	34856	4681	4522	155	0.033	31282	4074	2318	1713	0.425	NA	NA	NA	NA	NA	40078	5587	5558	18	0.003	35251	2705	2676	23	0.009
311426	1	26795865	26795865	A	G	*DHDDS*	3_prime_untranslated_region	c.*243	NULL	tier3	18900	2359	2222	133	0.056	37140	4742	2588	2089	0.447	NA	NA	NA	NA	NA	56774	7787	7730	37	0.005	42915	3349	2143	1110	0.341
311426	1	211433418	211433418	T	A	*RCOR3*	5_prime_untranslated_region	c.-40	NULL	tier4	1509	91	90	1	0.011	831	51	39	11	0.220	NA	NA	NA	NA	NA	1124	54	54	0	0.000	1144	53	53	0	0.000
311426	3	158380318	158380318	C	T	*GFM1*	intronic	c.1324-99	e11-99	tier3	3823	335	319	16	0.048	4087	478	276	199	0.419	NA	NA	NA	NA	NA	4356	556	555	0	0.000	2385	131	82	48	0.369
311426	5	68849514	68849514	T	G	*OCLN*	rna	NULL	NULL	tier1	5705	692	656	35	0.051	7850	933	483	442	0.478	NA	NA	NA	NA	NA	8984	1232	1220	8	0.007	7575	496	302	193	0.390
311426	5	118824832	118824832	G	A	*HSD17B4*	intronic	c.623-55	e9-55	tier3	3577	328	315	12	0.037	3018	303	207	95	0.315	NA	NA	NA	NA	NA	5915	740	735	4	0.005	3623	199	154	45	0.226
311426	5	156659265	156659265	A	G	*ITK*	intronic	c.714-85	e8-85	tier3	811	88	87	1	0.011	2718	270	146	121	0.453	NA	NA	NA	NA	NA	2963	353	351	1	0.000	2243	113	71	42	0.372
311426	6	96651060	96651060	G	A	*FUT9*	missense	c.29	p.R10H	tier1	962	130	126	4	0.031	621	75	46	29	0.387	NA	NA	NA	NA	NA	1988	253	250	2	0.000	613	46	42	4	0.087
311426	7	100643736	100643736	T	C	*MUC12*	missense	c.9892	p.S3298P	tier1	5417	1193	1187	6	0.005	9120	1900	1753	142	0.075	NA	NA	NA	NA	NA	27308	6506	6489	7	0.001	10639	1279	1257	19	0.015
311426	7	120390342	120390342	C	A	*KCND2*	3_prime_untranslated_region	c.*2430	NULL	tier2	14605	1700	1663	37	0.022	12524	1454	1067	378	0.262	NA	NA	NA	NA	NA	16012	2164	2147	5	0.002	12109	765	760	3	0.004
311426	7	141791778	141791778	G	A	*MGAM*	silent	c.6876	p.R2292	tier1	9691	2042	1954	87	0.043	5994	1175	675	495	0.423	NA	NA	NA	NA	NA	6968	1415	1405	4	0.003	3220	335	229	105	0.314
311426	7	151945554	151945554	G	A	*KMT2C*	silent	c.1965	p.V655	tier1	2051	404	384	20	0.050	1687	347	189	158	0.455	NA	NA	NA	NA	NA	3399	784	777	6	0.008	1394	160	112	48	0.300
311426	8	2857551	2857551	C	T	*CSMD1*	missense	c.8135	p.R2712Q	tier1	16097	2046	1991	54	0.026	10426	1468	971	481	0.331	NA	NA	NA	NA	NA	23571	3789	3770	6	0.002	14243	1095	864	217	0.201
311426	9	35301169	35301169	T	C	*UNC13B*	intronic	c.761+5242	e8+5242	tier3	2887	503	483	19	0.038	2358	407	217	188	0.464	NA	NA	NA	NA	NA	3846	676	670	1	0.000	2386	209	141	68	0.325
311426	9	113086243	113086243	A	G	*TXNDC8*	silent	c.234	p.H78	tier1	14006	2054	1968	85	0.041	12778	1728	1011	712	0.413	NA	NA	NA	NA	NA	20844	3085	3073	7	0.002	14571	1222	775	432	0.358
311426	10	123727090	123727090	A	T	*NSMCE4A*	5_prime_untranslated_region	c.-123727090	NULL	tier3	10703	1305	1257	44	0.034	12857	1523	837	671	0.445	NA	NA	NA	NA	NA	12890	1803	1786	2	0.000	8746	628	624	0	0.000
311426	11	247379	247379	G	A	*PSMD13*	missense	c.505	p.G169R	tier1	15436	2435	2354	81	0.033	13333	2130	1173	939	0.445	NA	NA	NA	NA	NA	20333	3439	3412	13	0.004	14019	1104	1103	0	0.000
311426	11	125616169	125616169	G	A	*PATE1*	5_prime_flanking_region	c.-31	NULL	tier3	45859	6488	6209	264	0.041	30755	4306	2450	1808	0.425	NA	NA	NA	NA	NA	61738	9187	9095	71	0.008	44907	3663	2374	1158	0.328
311426	12	13714497	13714497	C	A	*GRIN2B*	3_prime_untranslated_region	c.*1220	NULL	tier3	8299	1025	1003	20	0.020	7783	931	535	388	0.420	NA	NA	NA	NA	NA	12365	1643	1636	6	0.004	8086	544	494	50	0.092
311426	12	78334060	78334060	C	T	*NAV3*	rna	NULL	NULL	tier1	13034	1724	1650	71	0.041	8383	1068	583	479	0.451	NA	NA	NA	NA	NA	15886	2304	2283	17	0.007	8588	645	404	237	0.370
311426	12	106853134	106853134	A	T	*POLR3B*	missense	c.2558	p.D853V	tier1	410	63	63	0	0.000	452	88	53	34	0.391	NA	NA	NA	NA	NA	720	105	105	0	0.000	288	29	27	2	0.000
311426	13	26114392	26114392	T	C	*ATP8A2*	intronic	c.582-65	e8-65	tier3	12395	1337	1274	62	0.046	7997	939	554	377	0.405	NA	NA	NA	NA	NA	14032	1878	1863	12	0.006	7399	426	271	151	0.358
311426	14	99988655	99988655	G	A	*CCDC85C*	intronic	c.868-78	e3-78	tier3	40	5	5	0	0.000	939	184	105	79	0.429	NA	NA	NA	NA	NA	1656	329	328	0	0.000	854	91	55	35	0.389
311426	15	48065413	48065413	C	T	*SEMA6D*	3_prime_untranslated_region	c.*1431	NULL	tier3	12208	1580	1556	22	0.014	5803	961	619	338	0.353	NA	NA	NA	NA	NA	8724	1497	1493	4	0.003	4594	364	294	65	0.181
311426	15	72037471	72037471	G	A	*THSD4*	missense	c.1933	p.V645M	tier1	4713	620	595	22	0.036	2926	361	189	167	0.469	NA	NA	NA	NA	NA	5834	821	808	1	0.000	8882	663	661	1	0.000
311426	19	16145115	16145115	C	A	*LINC00905*	intronic	c.NULL	NULL	tier3	2171	355	342	12	0.034	1417	210	113	97	0.462	NA	NA	NA	NA	NA	2274	368	366	2	0.000	1351	118	72	46	0.390
311426	19	19767521	19767521	C	T	*ATP13A1*	missense	c.1031	p.R344H	tier1	3002	637	616	21	0.033	2835	544	297	242	0.449	NA	NA	NA	NA	NA	4322	822	818	3	0.004	2252	240	164	76	0.317
311426	21	44524456	44524456	G	A	*U2AF1*	missense	c.101	p.S34F	tier1	11432	1516	1479	37	0.024	9341	1303	953	345	0.266	NA	NA	NA	NA	NA	15677	2334	2327	4	0.002	7939	585	499	77	0.134
329866	1	89615249	89615249	C	T	*GBP7*	missense	c.878	p.G293E	tier1	2893	621	618	2	0.003	2607	385	279	103	0.270	NA	NA	NA	NA	NA	2519	256	254	0	0.000	NA	NA	NA	NA	NA
329866	1	244715862	244715862	A	G	*C1orf101*	missense	c.322	p.T108A	tier1	9861	1653	1651	1	0.001	5686	781	623	154	0.198	NA	NA	NA	NA	NA	6886	446	408	37	0.083	NA	NA	NA	NA	NA
329866	2	238436052	238436052	C	T	*MLPH*	silent	c.913	p.L305	tier1	9376	1529	1527	0	0.000	8026	1092	716	366	0.338	NA	NA	NA	NA	NA	6897	388	332	54	0.140	NA	NA	NA	NA	NA
329866	3	112190167	112190167	C	T	*BTLA*	missense	c.439	p.E147K	tier1	9549	1301	1294	3	0.002	9489	1184	850	324	0.276	NA	NA	NA	NA	NA	10913	459	407	45	0.100	NA	NA	NA	NA	NA
329866	3	127381208	127381208	G	A	*PODXL2*	intronic	c.1206+54	e4+54	tier3	4024	998	994	1	0.001	4105	703	463	239	0.340	NA	NA	NA	NA	NA	2815	279	242	36	0.130	NA	NA	NA	NA	NA
329866	9	35076941	35076941	C	T	*FANCG*	intronic	c.777+27	e6+27	tier3	25625	3508	3503	3	0.001	26267	3014	1984	994	0.334	NA	NA	NA	NA	NA	24996	1104	976	126	0.114	NA	NA	NA	NA	NA
329866	9	36204051	36204051	C	G	*CLTA*	intronic	c.374-14	e4-14	tier3	14161	2205	2197	6	0.003	16635	2113	1314	774	0.371	NA	NA	NA	NA	NA	15411	744	636	105	0.142	NA	NA	NA	NA	NA
329866	11	20178072	20178072	C	T	*DBX1*	silent	c.837	p.K279	tier1	21265	2924	2914	3	0.001	17308	2021	1222	787	0.392	NA	NA	NA	NA	NA	14475	726	615	109	0.151	NA	NA	NA	NA	NA
329866	12	57037304	57037304	T	C	*ATP5B*	missense	c.484	p.S162G	tier1	30409	3982	3973	5	0.001	16674	1981	1433	532	0.271	NA	NA	NA	NA	NA	24573	979	979	0	0.000	NA	NA	NA	NA	NA
329866	16	89776108	89776108	G	A	*VPS9D1*	intronic	c.1388+77	e11+77	tier3	21797	2990	2980	6	0.002	14650	1751	1040	693	0.400	NA	NA	NA	NA	NA	14911	703	555	143	0.205	NA	NA	NA	NA	NA
329866	17	7577581	7577581	A	C	*TP53*	missense	c.700	p.Y234D	tier1	36949	4893	4876	11	0.002	29535	3305	732	2546	0.777	NA	NA	NA	NA	NA	42689	1692	1143	543	0.322	NA	NA	NA	NA	NA
329866	17	40342300	40342300	C	A	*GHDC*	missense	c.1366	p.V456F	tier1	8982	0	0	0	0.000	5605	643	454	184	0.288	NA	NA	NA	NA	NA	6702	297	297	0	0.000	NA	NA	NA	NA	NA
329866	20	62326771	62326771	G	C	*RTEL1*	missense	c.3590	p.G1197A	tier1	37497	4828	4816	1	0.000	15340	1645	1251	382	0.234	NA	NA	NA	NA	NA	27021	1170	1076	93	0.080	NA	NA	NA	NA	NA
329866	21	40823790	40823790	C	T	*SH3BGR*	5_prime_untranslated_region	c.-44	NULL	tier3	17634	2452	2447	0	0.000	12571	1344	836	497	0.373	NA	NA	NA	NA	NA	16557	779	681	94	0.121	NA	NA	NA	NA	NA
340060	1	115258747	115258747	C	T	*NRAS*	missense	c.35	p.G12D	tier1	24300	3213	3195	6	0.002	20870	2635	2525	101	0.038	22093	3097	3092	1	0.000	15936	1340	1336	1	0.000	25822	952	949	1	0.000
340060	5	31267727	31267727	C	A	*CDH6*	missense	c.147	p.N49K	tier1	10704	1307	1304	1	0.001	7847	1011	937	61	0.061	14531	1972	1970	1	0.000	12132	1054	1049	0	0.000	17740	611	609	1	0.000
340060	7	43548582	43548582	G	A	*HECW1*	missense	c.3881	p.G1294D	tier1	32197	4018	4011	1	0.000	23945	2941	2746	182	0.062	34965	4604	4598	2	0.000	35679	2823	2820	1	0.000	45482	1417	1417	0	0.000
340060	10	112356156	112356156	G	T	*SMC3*	missense	c.1964	p.G655V	tier1	6482	760	760	0	0.000	3800	437	378	55	0.127	1237	0	0	0	NA	8261	776	774	0	0.000	7242	427	425	0	0.000
340060	12	43827516	43827516	C	A	*ADAMTS20*	intronic	c.2720+532	e19+532	tier4	2909	439	435	3	0.007	2451	311	302	7	0.023	2804	531	518	10	0.019	4499	620	609	6	0.010	4679	311	300	7	0.023
340060	13	28592642	28592642	C	A	*FLT3*	missense	c.2503	p.D835Y	tier1	9196	1681	1680	0	0.000	11071	1615	1522	88	0.055	8252	1637	1637	0	0.000	7006	1080	1076	0	0.000	15200	876	875	1	0.000
340060	14	58038541	58038541	A	C	*SLC35F4*	intronic	c.1041+71	e5+71	tier3	9543	1102	1099	3	0.003	5713	643	551	92	0.143	7081	970	970	0	0.000	7817	823	818	0	0.000	9852	508	507	0	0.000
340060	17	61995194	61995194	C	G	*GH1*	missense	c.382	p.V128L	tier1	5666	1007	1003	4	0.004	7839	1307	1133	167	0.128	5228	976	975	1	0.000	2580	334	332	0	0.000	7600	400	399	1	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
346313	1	115258744	115258744	C	T	*NRAS*	missense	c.38	p.G13D	tier1	15135	2345	2345	0	0.000	22148	2769	1917	817	0.299	9508	75	44	31	0.413	12656	1666	1659	1	0.000	NA	NA	NA	NA	NA
346313	1	185815276	185815276	G	A	*HMCN1*	intronic	c.339+48	e2+48	tier3	6596	904	899	5	0.006	9266	1023	626	388	0.383	6413	50	30	20	0.400	5756	719	712	1	0.000	NA	NA	NA	NA	NA
346313	1	237494338	237494338	G	A	*RYR2*	intronic	c.270+52	e4+52	tier3	6976	0	0	0	0.000	10457	1484	1109	367	0.249	4945	59	39	20	0.339	9559	1403	1398	3	0.000	NA	NA	NA	NA	NA
346313	2	79914651	79914651	C	T	*CTNNA2*	intronic	c.204+35867	e2+35867	tier3	8130	1132	1127	4	0.004	7887	997	599	392	0.396	9373	58	31	27	0.466	10541	1507	1504	1	0.000	NA	NA	NA	NA	NA
346313	2	95976762	95976762	G	A	*KCNIP3*	3_prime_untranslated_region	c.*95976762	NULL	tier3	14797	1887	1879	8	0.004	12604	1599	937	647	0.408	8658	46	21	24	0.533	13523	1768	1765	0	0.000	NA	NA	NA	NA	NA
346313	2	97493997	97493997	C	T	*CNNM3*	3_prime_untranslated_region	c.*97493997	NULL	tier3	17734	2331	2323	7	0.003	16375	1841	1134	695	0.380	16681	97	58	39	0.402	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA
346313	2	103148926	103148926	G	A	*SLC9A4*	missense	c.2176	p.G726S	tier1	15907	2288	2279	9	0.004	18575	2517	1566	930	0.373	9661	60	38	22	0.367	17004	2467	2463	1	0.000	NA	NA	NA	NA	NA
346313	2	198267359	198267359	C	A	*SF3B1*	missense	c.1998	p.K666N	tier1	1971	484	484	0	0.000	3428	660	449	211	0.320	1140	27	20	7	0.259	1344	284	283	0	0.000	NA	NA	NA	NA	NA
346313	3	124180873	124180873	A	G	*KALRN*	intronic	c.3915+70	e24+70	tier3	6616	1154	1153	0	0.000	8408	1184	818	352	0.301	3526	41	29	12	0.293	4038	543	541	0	0.000	NA	NA	NA	NA	NA
346313	3	157363624	157363624	A	T	*C3orf55*	nonsense	c.151	p.K51*	tier1	12912	2008	2005	3	0.001	12504	1663	998	656	0.397	11554	80	52	28	0.350	17018	2350	2344	1	0.000	NA	NA	NA	NA	NA
346313	3	185362401	185362401	C	T	*IGF2BP2*	3_prime_untranslated_region	c.*918	NULL	tier3	3106	473	470	2	0.004	3119	384	193	188	0.493	2875	20	11	9	0.450	4110	620	615	0	0.000	NA	NA	NA	NA	NA
346313	4	47888007	47888007	T	C	*NFXL1*	missense	c.1553	p.Y518C	tier1	7936	1262	1261	1	0.001	10623	1323	793	524	0.398	9853	74	41	33	0.446	12932	1797	1792	1	0.000	NA	NA	NA	NA	NA
346313	5	180659955	180659955	C	T	*TRIM41*	3_prime_untranslated_region	c.*180659955	NULL	tier3	6908	1005	1001	3	0.003	8436	948	681	263	0.279	2747	24	19	5	0.208	6031	819	818	0	0.000	NA	NA	NA	NA	NA
346313	7	141794384	141794384	G	A	*MGAM*	intronic	c.4619-36	e38-36	tier3	3954	754	745	9	0.012	9432	1324	227	1086	0.827	8804	44	12	32	0.727	19245	2505	2495	2	0.000	NA	NA	NA	NA	NA
346313	8	39111964	39111964	C	T	*ADAM32*	missense	c.1934	p.S645L	tier1	2218	306	305	1	0.003	2951	311	201	108	0.350	1323	11	6	5	0.455	2929	348	345	1	0.000	NA	NA	NA	NA	NA
346313	8	56362027	56362027	G	A	*XKR4*	intronic	c.1007-73813	e3-73813	tier2	10991	1801	1799	2	0.001	19862	2655	1622	1018	0.386	6570	45	32	13	0.289	10399	1572	1571	1	0.000	NA	NA	NA	NA	NA
346313	9	2058252	2058252	A	T	*SMARCA2*	intronic	c.1348-39	e7-39	tier3	6687	1167	1166	1	0.001	12790	1563	924	626	0.404	3677	28	20	8	0.286	7690	1002	997	1	0.000	NA	NA	NA	NA	NA
346313	9	116770653	116770653	C	T	*ZNF618*	missense	c.670	p.R224W	tier1	23849	3026	3015	11	0.004	27911	3054	1840	1188	0.392	21495	115	70	45	0.391	29547	3875	3864	3	0.000	NA	NA	NA	NA	NA
346313	9	139848263	139848263	G	C	*LCN12*	rna	NULL	NULL	tier1	4511	1130	1128	2	0.002	5237	1046	627	416	0.399	1844	25	20	5	0.200	1463	327	325	0	0.000	NA	NA	NA	NA	NA
346313	10	43612131	43612131	C	T	*RET*	silent	c.2236	p.L746	tier1	11710	1924	1921	3	0.002	12939	1785	1093	678	0.383	7954	54	30	24	0.444	8090	1127	1127	0	0.000	NA	NA	NA	NA	NA
346313	10	71631922	71631922	C	T	*COL13A1*	splice_region	c.365-10	e3-10	tier3	6454	0	0	0	0.000	5986	868	573	287	0.334	4679	34	23	11	0.324	2959	550	547	0	0.000	NA	NA	NA	NA	NA
346313	11	32413565	32413565	C	T	*WT1*	missense	c.1385	p.R462Q	tier1	1659	0	0	0	0.000	1890	218	131	86	0.396	1176	13	7	6	0.462	729	82	80	0	0.000	NA	NA	NA	NA	NA
346313	11	66330311	66330311	C	T	*ACTN3*	silent	c.2562	p.N854	tier1	25840	3654	3646	4	0.001	26088	3426	2080	1320	0.388	15836	115	75	40	0.348	22332	3070	3063	3	0.000	NA	NA	NA	NA	NA
346313	11	74880778	74880778	C	T	*SLCO2B1*	silent	c.750	p.R250	tier1	12979	2156	2152	4	0.002	17961	2483	1507	942	0.385	6260	44	25	19	0.432	9284	1391	1384	0	0.000	NA	NA	NA	NA	NA
346313	12	22606832	22606832	G	C	*C2CD5*	missense	c.2869	p.Q957E	tier1	10580	1420	1415	4	0.003	11566	1283	914	362	0.284	6766	56	43	13	0.232	17261	2289	2288	0	0.000	NA	NA	NA	NA	NA
346313	12	112926910	112926910	G	C	*PTPN11*	missense	c.1530	p.Q510H	tier1	18281	2384	2384	0	0.000	17722	2050	1967	67	0.033	8551	50	50	0	0.000	15428	2108	2098	2	0.000	NA	NA	NA	NA	NA
346313	12	133384599	133384599	C	T	*GOLGA3*	silent	c.1056	p.A352	tier1	20252	2717	2714	3	0.001	18422	2142	1324	795	0.375	8874	61	39	22	0.361	14650	1946	1944	0	0.000	NA	NA	NA	NA	NA
346313	13	95363388	95363388	G	A	*SOX21*	3_prime_untranslated_region	c.*85	NULL	tier2	10957	1679	1673	3	0.002	9798	1204	751	447	0.373	8922	64	35	29	0.453	11181	1486	1484	1	0.000	NA	NA	NA	NA	NA
346313	13	99030086	99030086	C	T	*FARP1*	missense	c.410	p.A137V	tier1	10284	1799	1794	5	0.003	13249	1897	1169	718	0.381	5654	44	28	16	0.364	13410	1963	1958	2	0.000	NA	NA	NA	NA	NA
346313	14	38274022	38274022	A	T	*TTC6*	splice_region	c.357+3	e3+3	tier3	11618	1556	1555	0	0.000	14057	1605	1126	467	0.293	10576	81	56	25	0.309	15067	1903	1899	0	0.000	NA	NA	NA	NA	NA
346313	14	70442537	70442537	G	A	*SMOC1*	splice_region	c.478+6	e4+6	tier2	9708	1305	1303	1	0.001	11480	1164	833	324	0.280	10514	77	51	26	0.338	11093	1380	1375	2	0.000	NA	NA	NA	NA	NA
346313	14	101429460	101429460	A	T	*SNORD114-7*	rna	NULL	NULL	tier1	1456	395	394	1	0.003	858	143	82	61	0.427	453	9	4	5	NA	714	139	138	0	0.000	NA	NA	NA	NA	NA
346313	16	790001	790001	G	A	*NARFL*	5_prime_untranslated_region	c.-3603	NULL	tier3	23157	3246	3238	3	0.001	15854	1949	1462	460	0.239	4948	30	28	2	0.000	16881	2183	2175	2	0.000	NA	NA	NA	NA	NA
346313	19	35991219	35991219	T	C	*DMKN*	5_prime_untranslated_region	c.-35991219	NULL	tier3	7531	1700	1694	3	0.002	7260	1150	677	463	0.406	2283	31	22	9	0.290	1591	251	248	0	0.000	NA	NA	NA	NA	NA
346313	19	38782452	38782452	C	T	*SPINT2*	3_prime_untranslated_region	c.*38782452	NULL	tier3	11953	1849	1845	4	0.002	16199	2163	1360	788	0.367	8989	44	31	13	0.295	12445	1704	1698	2	0.000	NA	NA	NA	NA	NA
346313	21	11039295	11039295	C	G	*BAGE2*	rna	NULL	NULL	tier1	25556	3425	3422	2	0.001	33801	3958	3719	229	0.058	23736	167	156	11	0.066	28976	3884	3859	12	0.000	NA	NA	NA	NA	NA
346313	21	45744779	45744779	T	G	*PFKL*	missense	c.1997	p.I666S	tier1	9459	1727	1723	2	0.001	9416	1315	840	461	0.354	3521	34	16	18	0.529	5170	757	755	0	0.000	NA	NA	NA	NA	NA
346313	Y	28654460	28654460	C	T	*TPTE2P4*	intronic	c.NULL	NULL	tier3	1887	498	497	1	0.002	2212	422	116	303	0.723	665	14	6	8	0.571	1225	265	265	0	0.000	NA	NA	NA	NA	NA
350719	17	7577568	7577568	C	T	*TP53*	missense	c.713	p.C238Y	tier1	44403	5315	5308	0	0.000	50723	5999	5697	280	0.047	23554	2370	2297	66	0.028	190924	16738	16711	0	0.000	98222	12643	12634	0	0.000
350719	19	46214702	46214702	A	T	*FBXO46*	3_prime_untranslated_region	c.*240	NULL	tier2	6764	618	597	0	0.000	4462	362	342	5	0.014	2338	167	150	2	0.000	13024	1285	1211	2	0.000	8621	859	778	4	0.005
353053	1	20981993	20981993	A	G	*DDOST*	missense	c.542	p.L181P	tier1	20889	3114	3113	1	0.000	9118	1303	1186	114	0.088	304	8	7	1	NA	47199	4130	4118	0	0.000	41884	6596	6584	0	0.000
353053	1	196887311	196887311	T	C	*CFHR4*	intronic	c.1538-29	e10-29	tier2	1054	0	0	0	0.000	389	38	34	3	0.081	16	1	1	0	NA	1425	180	179	0	0.000	1751	0	0	0	NA
353053	1	205801794	205801794	G	A	*PM20D1*	missense	c.1217	p.A406V	tier1	5170	702	701	0	0.000	2574	367	341	26	0.071	60	0	0	0	NA	4799	0	0	0	NA	5476	1015	1012	0	0.000
353053	1	222833276	222833276	A	G	*MIA3*	missense	c.4903	p.M1635V	tier1	3091	418	417	0	0.000	3561	503	449	53	0.106	64	2	2	0	NA	4010	0	0	0	NA	9708	1496	1495	0	0.000
353053	5	14713807	14713807	G	A	*ANKH*	intronic	c.1142-31	e10-31	tier3	11343	1607	1606	0	0.000	3480	511	466	45	0.088	135	5	4	1	NA	15365	1265	1262	1	0.000	13305	2262	2261	0	0.000
353053	7	139094357	139094357	C	T	*LUC7L2*	nonsense	c.934	p.R312*	tier1	20391	2503	2500	2	0.001	10008	1047	971	70	0.067	327	12	10	2	0.000	59758	5729	5701	9	0.000	49373	6425	6413	2	0.000
353053	9	135073547	135073547	C	T	*NTNG2*	silent	c.408	p.D136	tier1	37406	5047	5041	4	0.001	10253	1247	1126	117	0.094	399	12	11	1	0.000	56769	5003	4995	6	0.000	58850	8218	8200	4	0.000
353053	12	102291646	102291646	C	T	*DRAM1*	missense	c.137	p.T46M	tier1	106	0	0	0	0.000	636	101	87	12	0.121	9	0	0	0	NA	114	0	0	0	NA	529	91	90	1	0.000
353053	13	113538580	113538580	C	A	*ATP11A*	3_prime_untranslated_region	c.*2202	NULL	tier2	17904	2159	2159	0	0.000	6557	770	710	57	0.074	146	1	1	0	NA	20399	2386	2382	0	0.000	19304	2683	2678	1	0.000
353053	15	23689650	23689650	G	A	*GOLGA6L2*	splice_region	c.214-3	e3-3	tier3	25990	3372	3371	0	0.000	8107	941	843	93	0.099	357	9	8	1	NA	30746	2321	2316	4	0.000	17477	2529	2521	0	0.000
353053	15	45392025	45392025	G	A	*DUOX2*	nonsense	c.3250	p.R1084*	tier1	27547	3592	3589	1	0.000	9397	1151	1034	110	0.096	407	10	9	1	NA	41162	3470	3452	8	0.000	53022	7123	7119	1	0.000
353053	17	16723414	16723414	C	T	*ENSG00000226145*	splice_site	c.NULL	NULL	tier1	37570	4748	4742	0	0.000	14169	1610	1496	108	0.067	404	14	13	1	0.000	24882	2254	2252	1	0.000	44577	5869	5865	0	0.000
353053	21	36164611	36164611	C	A	*RUNX1*	nonsense	c.1264	p.E422*	tier1	17986	2248	2247	0	0.000	4662	502	446	54	0.108	216	6	5	1	NA	6714	716	711	1	0.000	792	0	0	0	NA
353053	X	133547986	133547986	A	G	*PHF6*	missense	c.722	p.Y241C	tier1	11134	0	0	0	0.000	4942	624	560	62	0.100	173	5	4	1	NA	35377	2941	2936	0	0.000	11959	1516	1514	0	0.000
368402	1	154215669	154215669	G	A	*UBAP2L*	3_prime_untranslated_region	c.*154215669	NULL	tier3	22538	2922	2904	15	0.005	172843	17667	14759	2789	0.159	33333	4068	2799	1235	0.306	137257	6863	6860	2	0.000	181037	7644	7544	100	0.013
368402	2	11702607	11702607	A	G	*GREB1*	missense	c.176	p.N59S	tier1	23035	3016	2975	35	0.012	178452	16987	13731	3091	0.184	36391	4548	3093	1397	0.311	204053	10954	10948	3	0.000	209517	8779	8658	117	0.013
368402	2	20460043	20460043	C	A	*PUM2*	intronic	c.2355+55	e14+55	tier2	13700	1660	1644	14	0.008	75800	7451	6013	1399	0.189	15473	2121	1528	582	0.276	65589	2918	2917	0	0.000	94638	4313	4226	84	0.019
368402	2	179596201	179596201	T	A	*TTN*	silent	c.13560	p.L4520	tier1	91055	12446	12351	84	0.007	201024	22793	19302	3291	0.146	40568	5628	4133	1437	0.258	218106	12035	12033	2	0.000	226430	11126	10972	150	0.013
368402	3	38418449	38418449	T	C	*XYLB*	silent	c.1161	p.I387	tier1	35325	4643	4632	9	0.002	118976	11822	10450	1334	0.113	22494	2980	2432	534	0.180	232662	15001	14998	2	0.000	144379	7082	7004	76	0.011
368402	4	22421553	22421553	C	T	*GPR125*	intronic	c.1809+956	e12+956	tier3	21458	3607	3565	37	0.010	65263	9794	7827	1917	0.197	12041	1726	1192	525	0.306	52926	4382	4376	2	0.000	73463	6070	5952	112	0.018
368402	4	140432050	140432050	T	C	*SETD7*	3_prime_untranslated_region	c.*767	NULL	tier3	244	0	0	0	0.000	5974	1532	1232	298	0.195	1028	184	114	70	0.380	4255	0	0	0	NA	8833	1441	1418	22	0.015
368402	4	166915437	166915437	A	T	*TLL1*	intronic	c.362-96	e4-96	tier3	1318	306	304	2	0.007	4485	1083	860	220	0.204	720	113	85	28	0.248	1846	0	0	0	NA	2056	380	372	7	0.018
368402	5	115319116	115319116	G	A	*AQPEP*	missense	c.828	p.M276I	tier1	25257	3482	3477	4	0.001	76205	7228	6897	309	0.043	13019	1581	1509	67	0.043	351441	17352	17346	0	0.000	112995	5851	5822	23	0.004
368402	5	156924056	156924056	C	T	*ADAM19*	missense	c.152	p.S51N	tier1	55700	7165	7111	49	0.007	268975	21177	16999	4003	0.191	54692	7053	4840	2138	0.306	440165	17475	17471	2	0.000	338822	11444	11220	218	0.019
368402	9	78973756	78973756	G	A	*PCSK5*	missense	c.5501	p.R1834Q	tier1	54108	6970	6927	41	0.006	196616	15958	13311	2552	0.161	39131	4930	3736	1164	0.238	635086	25383	25356	16	0.000	229662	8388	8248	134	0.016
368402	9	79319663	79319663	G	A	*PRUNE2*	intronic	c.6436+14	e1+14	tier2	9166	2342	2321	19	0.008	32637	7458	5916	1502	0.202	7953	1794	1167	615	0.345	25240	2789	2786	2	0.000	49140	3994	3914	78	0.020
368402	9	79319664	79319664	G	T	*PRUNE2*	intronic	c.6436+13	e1+13	tier2	9144	2342	2323	18	0.008	32635	7456	5915	1501	0.202	7942	1793	1165	614	0.345	25151	2790	2787	2	0.000	49038	3994	3915	78	0.020
368402	10	115963109	115963109	C	A	*TDRD1*	intronic	c.802-38	e7-38	tier3	16909	2272	2252	18	0.008	76279	9331	7433	1838	0.198	16253	1810	1240	561	0.311	120363	9163	9158	1	0.000	85428	5472	5364	103	0.019
368402	12	124826497	124826497	T	C	*NCOR2*	missense	c.5081	p.N1694S	tier1	54114	5513	5477	33	0.006	214559	17566	13895	3486	0.201	55673	7250	4842	2319	0.324	166312	8359	8355	3	0.000	330870	11682	11470	200	0.017
368402	16	34290568	34290568	C	G	*CCNYL3*	3_prime_untranslated_region	c.*34290568	NULL	tier3	26955	3592	3552	38	0.011	101548	12296	9685	2512	0.206	19725	2567	1750	807	0.316	140278	8547	8539	2	0.000	116520	6498	6377	117	0.018
368402	17	74732959	74732959	G	C	*SRSF2*	missense	c.284	p.P95R	tier1	13689	2019	1999	19	0.009	96315	9993	7907	1980	0.200	22152	2879	1846	1002	0.352	71655	6091	6088	1	0.000	149026	7377	7238	132	0.018
368402	21	36231802	36231802	T	A	*RUNX1*	missense	c.582	p.K194N	tier1	32248	4548	4509	35	0.008	207735	17947	14278	3535	0.198	43219	5829	3809	1969	0.341	235866	13073	13068	4	0.000	244599	10266	10076	186	0.018
368402	21	36259137	36259137	T	C	*RUNX1*	splice_region	c.351+3	e3+3	tier3	55476	7040	7008	28	0.004	194581	16743	14070	2526	0.152	36538	4980	3507	1418	0.288	291596	16104	16099	0	0.000	257715	10022	9875	141	0.014
368402	X	18911675	18911675	C	G	*PHKA2*	missense	c.3636	p.M1212I	tier1	18048	2436	2413	21	0.009	145665	12947	10372	2485	0.193	32433	4116	2727	1359	0.333	57930	2545	2545	0	0.000	69717	2597	2504	92	0.035
377158	1	16621238	16621238	C	A	*FBXO42*	rna	NULL	NULL	tier1	3313	491	490	1	0.002	6971	1093	769	320	0.294	7507	1064	713	347	0.327	7513	633	632	0	0.000	NA	NA	NA	NA	NA
377158	1	20471088	20471088	C	T	*PLA2G2F*	silent	c.330	p.H110	tier1	49914	6718	6687	28	0.004	31088	4306	2703	1577	0.368	35294	4662	2688	1914	0.416	26593	2153	2144	0	0.000	NA	NA	NA	NA	NA
377158	1	78191328	78191328	A	C	*USP33*	missense	c.1348	p.L450V	tier1	60202	7708	7685	17	0.002	33474	4360	2806	1527	0.352	38027	4549	2813	1681	0.374	38621	2151	2147	0	0.000	NA	NA	NA	NA	NA
377158	1	226413278	226413278	C	A	*MIXL1*	missense	c.464	p.P155Q	tier1	4747	546	529	17	0.031	2925	469	284	182	0.391	5425	625	328	295	0.474	4500	587	582	0	0.000	NA	NA	NA	NA	NA
377158	3	1415578	1415578	C	T	*CNTN6*	intronic	c.1946-30	e15-30	tier3	9603	1081	1078	3	0.003	5906	780	493	282	0.364	8216	881	530	344	0.394	9280	1034	1033	0	0.000	NA	NA	NA	NA	NA
377158	4	123260564	123260564	G	A	*KIAA1109*	splice_site	c.12352+1	e70+1	tier1	7878	791	786	4	0.005	4318	513	292	220	0.430	4113	406	244	161	0.398	6571	731	730	0	0.000	NA	NA	NA	NA	NA
377158	4	156135650	156135650	C	T	*NPY2R*	missense	c.559	p.R187W	tier1	52237	7634	7603	28	0.004	17897	2700	1604	1078	0.402	24694	3449	1953	1462	0.428	18952	1738	1736	1	0.000	NA	NA	NA	NA	NA
377158	5	140532032	140532032	G	C	*PCDHB6*	missense	c.2194	p.G732R	tier1	21923	3564	3554	8	0.002	17090	2433	1463	967	0.398	19539	2881	1663	1196	0.418	21707	1411	1407	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
377158	7	44268486	44268486	C	T	*CAMK2B*	silent	c.1377	p.R459	tier1	31191	3768	3745	19	0.005	19872	2875	1857	996	0.349	22934	2598	1604	971	0.377	24679	2025	2016	0	0.000	NA	NA	NA	NA	NA
377158	8	1616604	1616604	C	T	*DLGAP2*	missense	c.1730	p.T577M	tier1	15778	2105	2028	76	0.036	9926	1438	870	567	0.395	12449	1643	894	744	0.454	10886	1208	1207	0	0.000	NA	NA	NA	NA	NA
377158	8	93029456	93029456	G	A	*RUNX1T1*	missense	c.257	p.T86M	tier1	27247	3518	3500	16	0.005	13337	1840	1085	749	0.408	16786	2071	1165	889	0.433	15475	1318	1317	0	0.000	NA	NA	NA	NA	NA
377158	10	125521468	125521468	C	A	*CPXM2*	missense	c.1697	p.R566L	tier1	33234	4104	4081	17	0.004	16084	2218	1289	921	0.417	19750	2413	1228	1167	0.487	17617	1314	1313	1	0.000	NA	NA	NA	NA	NA
377158	11	132177495	132177495	A	G	*NTM*	intronic	c.527-88	e5-88	tier3	28441	4036	4028	6	0.001	11035	1798	1189	599	0.335	12341	1711	1086	615	0.362	15135	1756	1754	0	0.000	NA	NA	NA	NA	NA
377158	12	53439709	53439709	C	T	*LOC283335*	intronic	c.NULL	NULL	tier3	7825	1595	1585	8	0.005	6157	1216	747	462	0.382	5787	1148	636	510	0.445	6550	1008	1004	0	0.000	NA	NA	NA	NA	NA
377158	14	20216351	20216351	C	T	*OR4Q3*	silent	c.765	p.C255	tier1	62824	8606	8581	21	0.002	35001	5096	3330	1744	0.344	42145	5873	3768	2041	0.351	37687	2135	2134	0	0.000	NA	NA	NA	NA	NA
377158	14	38296537	38296537	G	A	*TTC6*	missense	c.1457	p.G486E	tier1	11863	1418	1416	2	0.001	5038	661	514	146	0.221	7275	826	635	190	0.230	9058	682	678	0	0.000	NA	NA	NA	NA	NA
377158	14	94750258	94750258	A	T	*SERPINA10*	3_prime_untranslated_region	c.*44	NULL	tier3	8996	1348	1344	4	0.003	4692	846	620	225	0.266	5827	917	616	298	0.326	7137	775	770	0	0.000	NA	NA	NA	NA	NA
377158	16	67242195	67242195	C	T	*LRRC29*	intronic	c.285+20	e2+20	tier3	8952	1373	1365	7	0.005	16228	2461	1502	941	0.385	17279	2332	1324	987	0.427	13870	1272	1270	0	0.000	NA	NA	NA	NA	NA
377158	17	37901877	37901877	C	A	*GRB7*	intronic	c.1278+86	e11+86	tier3	16607	2191	2180	8	0.004	9627	1320	807	509	0.387	10492	1311	763	534	0.412	8051	460	460	0	0.000	NA	NA	NA	NA	NA
377158	17	48653205	48653205	G	A	*CACNA1G*	missense	c.1442	p.S481N	tier1	9770	1740	1735	5	0.003	11808	1725	1037	683	0.397	12564	1917	1026	876	0.461	9331	842	842	0	0.000	NA	NA	NA	NA	NA
377158	19	12221114	12221114	T	C	*ENSG00000188474*	splice_region	c.1-6	e1-6	tier3	7396	1332	1325	5	0.004	9178	1894	1189	699	0.370	9366	1822	1117	694	0.383	8348	1197	1195	0	0.000	NA	NA	NA	NA	NA
377158	19	16008165	16008165	G	A	*CYP4F2*	intronic	c.198+59	e1+59	tier3	3096	291	279	12	0.041	2033	290	229	57	0.199	2418	217	192	24	0.111	3932	493	490	1	0.000	NA	NA	NA	NA	NA
377158	19	33792822	33792822	C	A	*CEBPA*	nonsense	c.499	p.E167*	tier1	13866	1815	1811	4	0.002	7305	1070	998	71	0.066	8461	1146	1041	103	0.090	9772	666	665	0	0.000	NA	NA	NA	NA	NA
377158	20	33573852	33573852	T	C	*MYH7B*	intronic	c.932-51	e12-51	tier3	21988	3958	3933	22	0.006	21653	3676	2260	1395	0.382	25678	3746	2188	1507	0.408	19145	1491	1489	0	0.000	NA	NA	NA	NA	NA
377158	21	36231773	36231773	C	T	*RUNX1*	missense	c.611	p.R204Q	tier1	40567	5888	5865	20	0.003	21930	3339	2312	1004	0.303	24949	3385	2261	1093	0.326	25246	2469	2464	0	0.000	NA	NA	NA	NA	NA
377158	21	39672197	39672197	T	C	*KCNJ15*	silent	c.1014	p.D338	tier1	11992	1306	1297	6	0.005	8572	1316	797	513	0.392	9617	1048	623	419	0.402	11157	882	881	0	0.000	NA	NA	NA	NA	NA
377158	21	44514777	44514777	T	G	*U2AF1*	missense	c.470	p.Q157P	tier1	82039	9989	9944	40	0.004	49155	6122	3547	2538	0.417	55897	6555	3561	2916	0.450	43879	2129	2126	0	0.000	NA	NA	NA	NA	NA
377158	21	44838927	44838927	G	A	*SIK1*	missense	c.1436	p.T479I	tier1	26814	3642	3635	6	0.002	19946	3338	1988	1334	0.402	22098	3416	1998	1389	0.410	21113	1921	1919	1	0.000	NA	NA	NA	NA	NA
377158	22	40425476	40425476	G	A	*FAM83F*	intronic	c.1454-44	e5-44	tier3	34812	4648	4507	131	0.028	26490	3367	1999	1351	0.403	30682	4106	2159	1897	0.468	26129	1479	1476	0	0.000	NA	NA	NA	NA	NA
377158	X	54948751	54948751	G	A	*TRO*	5_prime_untranslated_region	c.-347	NULL	tier3	37994	5332	5310	13	0.002	19061	2629	1655	954	0.366	21036	2797	1648	1114	0.403	9334	684	681	0	0.000	NA	NA	NA	NA	NA
377158	X	62974526	62974526	G	A	*ARHGEF9*	rna	NULL	NULL	tier1	43937	6008	5985	20	0.003	21090	2911	1755	1143	0.394	25009	3235	1844	1370	0.426	10902	688	688	0	0.000	NA	NA	NA	NA	NA
377158	X	152826317	152826317	C	A	*ATP2B3*	missense	c.3023	p.T1008N	tier1	92654	12135	12117	9	0.001	46732	5759	4027	1702	0.297	50740	6400	4392	1959	0.308	23593	942	942	0	0.000	NA	NA	NA	NA	NA
378511	1	38185727	38185727	C	T	*EPHA10*	missense	c.2416	p.G806S	tier1	21546	2925	2920	1	0.000	18962	1928	1164	758	0.394	NA	NA	NA	NA	NA	30926	3276	3272	0	0.000	23367	3297	3288	3	0.000
378511	1	103471831	103471831	T	A	*COL11A1*	missense	c.1760	p.K587I	tier1	1429	0	0	0	0.000	1611	288	222	66	0.229	NA	NA	NA	NA	NA	2658	183	183	0	0.000	1680	217	216	0	0.000
378511	1	159505705	159505705	G	C	*OR10J5*	missense	c.93	p.F31L	tier1	3661	659	658	0	0.000	13904	1999	1476	511	0.257	NA	NA	NA	NA	NA	15527	1741	1739	0	0.000	15301	2267	2260	1	0.000
378511	1	215990362	215990362	T	C	*USH2A*	missense	c.9547	p.I3183V	tier1	14189	1685	1684	1	0.001	16726	1755	889	862	0.492	NA	NA	NA	NA	NA	25758	2729	2728	0	0.000	22257	2928	2913	1	0.000
378511	1	218458652	218458652	C	T	*RRP15*	5_prime_untranslated_region	c.-7	NULL	tier2	12418	1616	1615	0	0.000	13735	1749	1315	420	0.242	NA	NA	NA	NA	NA	16938	1787	1783	1	0.000	16115	2104	2103	1	0.000
378511	2	10797867	10797867	C	T	*NOL10*	splice_site	c.906+1	e11+1	tier1	806	0	0	0	0.000	1567	294	199	94	0.321	NA	NA	NA	NA	NA	960	117	116	1	0.000	837	0	0	0	NA
378511	2	89246763	89246763	C	A	*IGKV7-3*	5_prime_flanking_region	c.-31869	NULL	tier3	850	178	177	0	0.000	1668	263	165	98	0.373	NA	NA	NA	NA	NA	1504	199	199	0	0.000	1151	237	237	0	0.000
378511	2	127805801	127805801	G	A	*BIN1*	5_prime_untranslated_region	c.-127805801	NULL	tier3	10081	1171	1169	0	0.000	6982	753	456	295	0.393	NA	NA	NA	NA	NA	14152	1420	1420	0	0.000	11943	1540	1538	1	0.000
378511	2	191366422	191366422	T	A	*MFSD6*	3_prime_untranslated_region	c.*1478	NULL	tier3	11321	1652	1650	1	0.001	10329	1372	935	430	0.315	NA	NA	NA	NA	NA	17494	1967	1967	0	0.000	19206	2853	2838	0	0.000
378511	4	70826715	70826715	G	T	*CSN2*	5_prime_untranslated_region	c.-2	NULL	tier3	7585	1007	1004	0	0.000	4801	516	339	176	0.342	NA	NA	NA	NA	NA	9615	1042	1042	0	0.000	7253	931	926	3	0.000
378511	4	85562062	85562062	C	T	*CDS1*	silent	c.951	p.F317	tier1	4008	542	540	1	0.002	5099	804	499	303	0.378	NA	NA	NA	NA	NA	5142	466	464	0	0.000	3867	692	690	0	0.000
378511	4	150509056	150509056	A	G	*ENSG00000234828*	intronic	c.NULL	NULL	tier3	3066	298	297	0	0.000	4860	639	402	235	0.369	NA	NA	NA	NA	NA	4027	307	307	0	0.000	3565	480	480	0	0.000
378511	5	134059300	134059300	T	C	*SEC24A*	missense	c.3107	p.I1036T	tier1	9326	1069	1069	0	0.000	8121	842	525	316	0.376	NA	NA	NA	NA	NA	11239	918	917	0	0.000	12232	1497	1490	0	0.000
378511	5	140033542	140033542	A	G	*IK*	missense	c.424	p.K142E	tier1	2392	514	514	0	0.000	1999	343	281	61	0.178	NA	NA	NA	NA	NA	3084	0	0	0	NA	2519	514	513	0	0.000
378511	5	140719581	140719581	A	C	*PCDHGA2*	missense	c.1043	p.Y348S	tier1	27244	3452	3442	3	0.001	21120	2020	1333	675	0.336	NA	NA	NA	NA	NA	42166	4557	4557	0	0.000	37637	4930	4904	0	0.000
378511	5	145616829	145616829	T	C	*RBM27*	intronic	c.1145-32	e8-32	tier3	5226	831	831	0	0.000	5415	758	508	246	0.326	NA	NA	NA	NA	NA	7509	923	923	0	0.000	4567	800	799	0	0.000
378511	6	23855602	23855602	A	G	*SPTLC1P2*	3_prime_flanking_region	c.*1324	NULL	tier3	9216	1200	1199	0	0.000	5384	477	286	191	0.400	NA	NA	NA	NA	NA	12055	1406	1404	0	0.000	11387	1491	1491	0	0.000
378511	6	122777603	122777603	T	C	*SERINC1*	intronic	c.371+23	e3+23	tier3	9944	0	0	0	0.000	6140	753	536	215	0.286	NA	NA	NA	NA	NA	12719	1140	1139	0	0.000	15044	1865	1857	0	0.000
378511	8	22477862	22477862	T	C	*CCAR2*	3_prime_untranslated_region	c.*667	NULL	tier3	22845	2955	2950	0	0.000	16629	1659	1057	596	0.361	NA	NA	NA	NA	NA	35585	3905	3903	0	0.000	30985	4046	4026	0	0.000
378511	8	33451288	33451288	G	A	*DUSP26*	intronic	c.222-23	e2-23	tier3	11299	1799	1797	0	0.000	10575	1155	734	416	0.362	NA	NA	NA	NA	NA	15548	1857	1856	0	0.000	12404	2059	2051	2	0.000
378511	9	23692597	23692597	T	A	*ELAVL2*	silent	c.1038	p.V346	tier1	41450	5259	5253	0	0.000	28831	2689	1683	1000	0.373	NA	NA	NA	NA	NA	62099	6923	6920	0	0.000	53149	6846	6821	2	0.000
378511	9	77415313	77415313	G	T	*TRPM6*	missense	c.2095	p.L699I	tier1	25225	3314	3304	3	0.001	20881	1921	1242	672	0.351	NA	NA	NA	NA	NA	45394	5143	5140	1	0.000	38445	5024	5006	4	0.000
378511	9	116811952	116811952	G	C	*ZNF618*	missense	c.2370	p.E790D	tier1	10750	1585	1582	0	0.000	15810	1790	1082	701	0.393	NA	NA	NA	NA	NA	21311	2481	2481	0	0.000	24771	3235	3230	2	0.000
378511	10	43691546	43691546	G	A	*RASGEF1A*	3_prime_untranslated_region	c.*146	NULL	tier3	8005	867	866	1	0.001	6321	879	641	237	0.270	NA	NA	NA	NA	NA	9605	734	734	0	0.000	10938	1340	1339	1	0.000
378511	11	18955245	18955245	C	A	*ENSG00000255244*	5_prime_flanking_region	c.-1287	NULL	tier3	11963	2262	2262	0	0.000	25811	3317	2684	621	0.188	NA	NA	NA	NA	NA	15564	1896	1895	0	0.000	17059	2685	2680	2	0.000
378511	11	20805389	20805389	T	G	*NELL1*	intronic	c.335+13	e3+13	tier3	18659	2209	2205	2	0.001	16645	1900	1192	697	0.369	NA	NA	NA	NA	NA	21714	1908	1907	0	0.000	19207	2479	2465	0	0.000
378511	11	34186853	34186853	G	A	*ABTB2*	silent	c.1806	p.G602	tier1	11352	1607	1606	0	0.000	14379	1669	1049	615	0.370	NA	NA	NA	NA	NA	18008	2026	2026	0	0.000	14713	2274	2267	2	0.000
378511	11	66152452	66152452	G	T	*NPAS4*	5_prime_flanking_region	c.-36199	NULL	tier4	3614	397	396	0	0.000	4356	563	342	220	0.391	NA	NA	NA	NA	NA	4807	425	424	0	0.000	4358	568	566	2	0.000
378511	11	71939384	71939384	G	A	*INPPL1*	splice_region	c.247-8	e3-8	tier3	7102	838	837	0	0.000	10426	1095	686	404	0.371	NA	NA	NA	NA	NA	12713	1225	1225	0	0.000	12312	1768	1762	2	0.000
378511	11	72492296	72492296	C	T	*STARD10*	5_prime_untranslated_region	c.-70	NULL	tier2	11425	1300	1300	0	0.000	13158	1322	807	513	0.389	NA	NA	NA	NA	NA	16699	1518	1516	0	0.000	17930	2292	2286	2	0.000
378511	11	119025065	119025065	T	C	*ABCG4*	missense	c.452	p.M151T	tier1	26379	3719	3713	2	0.001	33204	3292	2062	1218	0.371	NA	NA	NA	NA	NA	57468	6703	6698	0	0.000	53081	7188	7166	1	0.000
378511	11	129739492	129739492	G	A	*NFRKB*	missense	c.3503	p.A1168V	tier1	23455	2897	2894	0	0.000	22107	2381	1500	873	0.368	NA	NA	NA	NA	NA	29596	2831	2829	0	0.000	22854	3047	3038	3	0.000
378511	12	52182517	52182517	T	A	*SCN8A*	silent	c.4266	p.A1422	tier1	18391	2850	2846	1	0.000	19645	2260	1442	807	0.359	NA	NA	NA	NA	NA	22575	2622	2620	0	0.000	20041	3068	3055	1	0.000
378511	12	133768616	133768616	T	C	*ZNF268*	intronic	c.457+27	e4+27	tier3	12439	1762	1757	0	0.000	11169	1448	949	495	0.343	NA	NA	NA	NA	NA	16136	1718	1718	0	0.000	11066	1648	1645	0	0.000
378511	13	95361880	95361880	T	C	*LINC00391*	5_prime_flanking_region	c.-6764	NULL	tier2	5072	623	623	0	0.000	4848	644	408	235	0.365	NA	NA	NA	NA	NA	5775	0	0	0	NA	6079	872	869	0	0.000
378511	15	25928387	25928387	G	A	*ATP10A*	intronic	c.3492+46	e17+46	tier3	17057	2322	2320	2	0.001	14622	2011	1350	656	0.327	NA	NA	NA	NA	NA	22840	2559	2558	0	0.000	20765	2890	2886	0	0.000
378511	15	44090170	44090170	G	A	*SERINC4*	silent	c.60	p.S20	tier1	22865	3051	3042	3	0.001	18136	2079	1303	770	0.371	NA	NA	NA	NA	NA	29818	3256	3255	0	0.000	24954	3391	3385	4	0.000
378511	17	7910348	7910348	T	C	*GUCY2D*	intronic	c.1379-30	e4-30	tier3	16840	2027	2025	1	0.000	13855	1426	898	520	0.367	NA	NA	NA	NA	NA	20885	2087	2083	0	0.000	17413	2324	2309	3	0.001
378511	17	39551774	39551774	A	G	*KRT31*	silent	c.690	p.S230	tier1	4508	601	600	0	0.000	14365	1506	880	595	0.403	NA	NA	NA	NA	NA	10303	979	966	0	0.000	10251	1558	1506	0	0.000
378511	17	59557555	59557555	C	G	*TBX4*	missense	c.896	p.A299G	tier1	19726	2618	2610	1	0.000	14993	1712	1145	562	0.329	NA	NA	NA	NA	NA	35299	3819	3818	0	0.000	32897	4306	4300	1	0.000
378511	18	60999185	60999185	T	C	*KDSR*	intronic	c.880-51	e10-51	tier3	7000	970	968	1	0.001	9778	1195	744	447	0.375	NA	NA	NA	NA	NA	15744	1607	1605	0	0.000	14460	2007	1997	0	0.000
378511	18	61570598	61570598	G	T	*SERPINB2*	3_prime_untranslated_region	c.*59	NULL	tier3	1052	143	143	0	0.000	2201	494	357	136	0.276	NA	NA	NA	NA	NA	1785	179	179	0	0.000	1171	200	199	0	0.000
378511	19	51648220	51648220	G	A	*SIGLEC7*	splice_region	c.760+4	e3+4	tier3	4624	939	938	0	0.000	12218	1403	914	488	0.348	NA	NA	NA	NA	NA	14817	1709	1707	1	0.000	12605	1962	1953	5	0.000
378511	20	11906923	11906923	T	G	*BTBD3*	3_prime_untranslated_region	c.*2609	NULL	tier2	583	0	0	0	0.000	1729	305	201	104	0.341	NA	NA	NA	NA	NA	1576	149	149	0	0.000	649	0	0	0	NA
378511	21	44514777	44514777	T	C	*U2AF1*	missense	c.470	p.Q157R	tier1	40027	4691	4690	0	0.000	27190	2295	2090	199	0.087	NA	NA	NA	NA	NA	55037	5535	5533	0	0.000	43056	5395	5383	2	0.000
378511	22	24401850	24401850	C	T	*GSTTP2*	rna	NULL	NULL	tier1	9067	1208	1206	1	0.001	6039	757	508	247	0.327	NA	NA	NA	NA	NA	11907	0	0	0	NA	10616	1416	1416	0	0.000
378511	22	32162607	32162607	G	T	*DEPDC5*	missense	c.316	p.D106Y	tier1	3791	463	462	0	0.000	4823	601	437	161	0.269	NA	NA	NA	NA	NA	10795	1033	1031	0	0.000	8998	1267	1254	1	0.000
378511	X	26179440	26179440	C	T	*MAGEB6P1*	3_prime_untranslated_region	c.*26179440	NULL	tier3	14023	1817	1815	1	0.001	12825	1102	304	795	0.723	NA	NA	NA	NA	NA	40914	4563	4555	3	0.000	35006	4658	4649	3	0.000
395344	1	25611201	25611201	G	A	*RHD*	missense	c.286	p.G96S	tier1	21881	3685	3572	109	0.030	14824	2154	1251	893	0.417	NA	NA	NA	NA	NA	13292	1880	1863	16	0.009	9750	1576	1552	12	0.008
395344	1	53972518	53972518	C	A	*GLIS1*	intronic	c.1706-69	e8-69	tier3	32616	5322	5268	47	0.009	17580	2412	1417	973	0.407	NA	NA	NA	NA	NA	27562	2039	2021	17	0.008	16324	1876	1866	9	0.005
395344	2	47748558	47748558	C	A	*KCNK12*	missense	c.781	p.D261Y	tier1	22483	3271	3154	112	0.034	11837	1665	951	702	0.425	NA	NA	NA	NA	NA	10881	1263	1241	21	0.017	8178	1193	1179	12	0.010
395344	2	131520055	131520055	C	T	*AMER3*	missense	c.410	p.P137L	tier1	19622	3061	3003	53	0.017	18756	2146	1341	783	0.369	NA	NA	NA	NA	NA	25479	2374	2353	17	0.007	14431	1845	1827	12	0.007
395344	2	141130704	141130704	T	A	*LRP1B*	missense	c.10641	p.R3547S	tier1	10863	1300	1284	15	0.012	7427	768	413	353	0.461	NA	NA	NA	NA	NA	9410	1026	1008	16	0.016	7409	928	921	6	0.006
395344	2	167759975	167759975	G	A	*XIRP2*	5_prime_untranslated_region	c.-18	NULL	tier2	7235	793	784	8	0.010	3868	427	256	170	0.399	NA	NA	NA	NA	NA	6646	736	730	6	0.008	4464	569	559	8	0.014
395344	4	134073863	134073863	C	T	*PCDH10*	silent	c.2568	p.I856	tier1	36802	5054	5005	42	0.008	19165	2622	1658	939	0.362	NA	NA	NA	NA	NA	21112	2319	2300	18	0.008	16966	2367	2344	16	0.007
395344	5	140431040	140431040	G	A	*PCDHB1*	5_prime_untranslated_region	c.-16	NULL	tier3	13096	2560	2546	13	0.005	7271	940	881	59	0.063	NA	NA	NA	NA	NA	8423	1340	1330	5	0.004	8070	1346	1341	2	0.000
395344	5	162932633	162932633	C	T	*MAT2B*	5_prime_untranslated_region	c.-60	NULL	tier2	2613	541	541	0	0.000	1119	132	124	8	0.061	NA	NA	NA	NA	NA	2200	462	459	2	0.000	1626	337	335	2	0.000
395344	7	1484979	1484979	G	C	*MICALL2*	missense	c.727	p.P243A	tier1	35095	5051	4972	68	0.013	23102	2677	1555	1095	0.413	NA	NA	NA	NA	NA	28092	2706	2677	24	0.009	18280	2300	2271	16	0.007

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
395344	8	124383531	124383531	C	T	*ATAD2*	missense	c.584	p.R195H	tier1	14629	1830	1818	11	0.006	14848	1841	1287	550	0.299	NA	NA	NA	NA	NA	20090	1662	1632	24	0.014	11134	1240	1225	10	0.008
395344	11	3041385	3041385	C	T	*CARS*	intronic	c.1266+65	e11+65	tier3	7112	1194	1183	11	0.009	9548	1111	665	436	0.396	NA	NA	NA	NA	NA	10051	908	902	5	0.006	6338	725	720	4	0.006
395344	11	103043939	103043939	C	A	*DYNC2H1*	missense	c.5463	p.D1821E	tier1	30737	3704	3676	23	0.006	27370	3236	1869	1333	0.416	NA	NA	NA	NA	NA	50846	4421	4370	50	0.011	25479	3026	3002	19	0.006
395344	12	42866304	42866304	C	T	*PRICKLE1*	missense	c.15	p.M5I	tier1	42612	5402	5337	61	0.011	27001	3358	2428	902	0.271	NA	NA	NA	NA	NA	55646	4485	4462	17	0.004	29418	3245	3236	9	0.003
395344	13	95095724	95095724	G	A	*DCT*	silent	c.1446	p.D482	tier1	37506	5536	5386	143	0.026	20964	3033	1890	1115	0.371	NA	NA	NA	NA	NA	27709	2945	2915	22	0.007	17198	2402	2383	14	0.006
395344	16	32914951	32914951	C	A	*IGHV3OR16-15*	3_prime_untranslated_region	c.*32914951	NULL	tier3	16195	1983	1979	0	0.000	11281	1319	967	343	0.262	NA	NA	NA	NA	NA	25985	2350	2340	6	0.003	12523	1498	1488	1	0.000
395344	19	36216047	36216047	T	C	*KMT2B*	intronic	c.3528+59	e10+59	tier3	27609	3427	3388	36	0.011	18206	1968	1122	817	0.421	NA	NA	NA	NA	NA	21799	2020	2002	15	0.007	14284	1689	1669	16	0.009
395344	21	36252865	36252865	C	T	*RUNX1*	missense	c.497	p.R166Q	tier1	26896	3450	3425	23	0.007	17808	2122	1297	806	0.383	NA	NA	NA	NA	NA	19449	2241	2214	23	0.010	14055	1978	1949	20	0.010
395344	21	44524456	44524456	G	A	*U2AF1*	missense	c.101	p.S34F	tier1	12143	1825	1800	25	0.014	7376	961	651	308	0.321	NA	NA	NA	NA	NA	17805	2119	2109	10	0.005	9216	1398	1390	7	0.005
395344	22	19452777	19452777	T	A	*UFD1L*	missense	c.443	p.N148I	tier1	50171	6290	6212	63	0.010	39442	5176	3069	2030	0.398	NA	NA	NA	NA	NA	58929	4568	4513	39	0.009	31360	3453	3388	29	0.008
429745	1	1078202	1078202	G	A	*LOC254099*	rna	NULL	NULL	tier1	5931	911	907	4	0.004	4908	690	421	263	0.385	2088	234	151	81	0.349	7726	722	622	93	0.130	13784	2100	1849	240	0.115
429745	1	78189035	78189035	T	C	*USP33*	missense	c.1463	p.Q488R	tier1	2431	445	441	4	0.009	2906	416	253	163	0.392	795	123	92	31	0.252	2851	277	248	29	0.105	5122	835	734	99	0.119
429745	1	103400670	103400670	C	T	*COL11A1*	splice_site	c.3475-1	e45-1	tier1	154	0	0	0	0.000	334	49	43	6	0.122	79	6	4	2	NA	345	0	0	0	NA	643	106	106	0	0.000
429745	1	193018974	193018974	G	T	*UCHL5*	missense	c.148	p.H50N	tier1	635	102	102	0	0.000	697	103	52	51	0.495	265	24	17	7	0.292	758	55	48	7	0.127	1191	186	161	25	0.134
429745	1	197021696	197021696	T	A	*F13B*	intronic	c.1555+68	e9+68	tier3	2218	180	180	0	0.000	1632	136	76	60	0.441	1399	89	68	20	0.227	3010	151	137	13	0.087	4203	326	291	35	0.107
429745	1	240071866	240071866	C	T	*CHRM3*	missense	c.1115	p.P372L	tier1	18828	3031	3005	21	0.007	12958	1506	905	580	0.391	11480	1361	966	389	0.287	30654	3547	3130	382	0.109	48285	6995	6216	749	0.108
429745	2	234231616	234231616	G	A	*SAG*	missense	c.400	p.V134M	tier1	366	64	63	1	0.016	775	112	74	38	0.339	253	32	18	14	0.438	914	71	68	3	0.042	1357	190	171	19	0.100
429745	3	38010850	38010850	G	T	*CTDSPL*	intronic	c.426+1477	e5+1477	tier3	18584	2730	2701	28	0.010	14632	1646	959	660	0.408	8380	807	522	282	0.351	23175	2227	1951	249	0.113	38870	5267	4584	644	0.123
429745	3	197807179	197807179	C	T	*ANKRD18DP*	splice_region	c.NULL	NULL	tier2	5395	618	617	0	0.000	2321	200	143	54	0.274	2081	182	158	24	0.132	6352	550	520	27	0.049	12351	1431	1356	73	0.051
429745	5	126667153	126667153	G	A	*MEGF10*	intronic	c.116+37	e1+37	tier3	1043	100	99	1	0.010	1329	126	61	63	0.508	475	37	26	11	0.297	1280	82	67	15	0.183	2260	222	189	33	0.149
429745	5	134705108	134705108	G	C	*H2AFY*	silent	c.465	p.A155	tier1	5079	644	639	5	0.008	5428	589	360	226	0.386	2986	271	160	110	0.407	8240	703	598	99	0.142	12226	1587	1360	223	0.141
429745	5	139222426	139222426	G	A	*PSD2*	3_prime_untranslated_region	c.*367	NULL	tier3	4475	724	717	5	0.007	3764	458	266	187	0.413	1861	187	122	64	0.344	5627	555	487	67	0.121	9745	1340	1177	155	0.116
429745	5	176008570	176008570	C	T	*CDHR2*	missense	c.2045	p.T682I	tier1	33969	4456	4449	6	0.001	20616	2221	1786	411	0.187	19249	2116	1955	152	0.072	48165	5253	5006	221	0.042	74751	9832	9357	447	0.046
429745	5	176709402	176709402	A	G	*NSD1*	intronic	c.5893-64	e18-64	tier3	91	0	0	0	0.000	262	39	25	13	0.342	44	4	3	1	NA	257	18	15	3	0.167	648	94	89	5	0.053
429745	6	27278373	27278373	T	C	*POM121L2*	missense	c.1577	p.D526G	tier1	13531	2189	2166	20	0.009	10136	1360	783	565	0.419	5544	677	493	176	0.263	15079	1771	1562	191	0.109	28268	4382	3844	516	0.118
429745	7	53854870	53854870	C	T	*ENSG00000232418*	3_prime_untranslated_region	c.*53854870	NULL	tier2	28223	3696	3663	32	0.009	16551	1547	869	669	0.435	21358	2326	1589	720	0.312	32748	3504	3109	367	0.106	53630	6754	5954	768	0.114
429745	10	11376350	11376350	T	G	*CELF2*	3_prime_untranslated_region	c.*5334	NULL	tier3	7924	1006	997	8	0.008	9395	951	590	350	0.372	4952	443	266	174	0.395	11674	1004	875	124	0.124	22812	2631	2291	331	0.126
429745	10	35300792	35300792	T	C	*CUL2*	missense	c.2147	p.N716S	tier1	12515	1709	1701	8	0.005	7221	875	506	360	0.416	7582	881	612	266	0.303	15443	1835	1662	164	0.090	22763	3133	2791	325	0.104
429745	11	62302518	62302518	C	T	*AHNAK*	nonsense	c.299	p.W100*	tier1	40270	5304	5267	33	0.006	32662	3139	1825	1256	0.408	27065	2795	1838	928	0.336	63305	6506	5702	719	0.112	103605	12896	11222	1538	0.121
429745	11	67020214	67020214	G	A	*KDM2A*	missense	c.2818	p.A940T	tier1	4708	612	604	6	0.010	4879	579	347	223	0.391	2010	203	123	78	0.388	5587	502	445	54	0.108	10662	1403	1212	181	0.130
429745	11	67565182	67565182	C	T	*FAM86C2P*	5_prime_untranslated_region	c.-67565182	NULL	tier3	5336	901	891	10	0.011	4344	544	333	209	0.386	3552	451	355	95	0.211	11610	1395	1295	97	0.070	20829	3034	2825	201	0.066
429745	12	102074329	102074329	G	A	*MYBPC1*	intronic	c.3433+22	e29+22	tier3	8975	1137	1127	10	0.009	5589	529	322	204	0.388	6302	560	413	145	0.260	10666	939	834	102	0.109	17843	2176	1926	245	0.113
429745	12	109569189	109569189	G	T	*ACACB*	5_prime_untranslated_region	c.-8097	NULL	tier3	30163	4131	4094	36	0.009	17652	1755	1153	585	0.337	20162	2093	1634	444	0.214	41852	4379	4009	331	0.076	65401	8618	7781	798	0.093
429745	14	31405745	31405745	C	A	*STRN3*	missense	c.802	p.G268C	tier1	5682	743	736	7	0.009	3901	377	200	176	0.468	3361	300	192	107	0.358	6926	594	518	72	0.122	11384	1425	1212	211	0.148
429745	14	64921502	64921502	A	G	*MTHFD1*	missense	c.2627	p.E876G	tier1	10842	1847	1839	3	0.002	8856	1246	952	284	0.230	4353	531	469	62	0.117	11915	1322	1244	75	0.057	21260	3302	3094	199	0.060
429745	14	81950742	81950742	C	A	*SEL1L*	splice_site	c.1874-1	e19-1	tier1	5768	750	746	4	0.005	5934	562	400	161	0.287	5403	507	344	160	0.317	11050	976	900	73	0.075	17560	2058	1878	172	0.084
429745	17	26817851	26817851	C	T	*SLC13A2*	silent	c.648	p.N216	tier1	35629	4792	4734	51	0.011	29023	2846	1632	1175	0.419	26022	2702	1811	863	0.323	62777	6918	5985	825	0.121	96371	12380	10778	1502	0.122
429745	17	45913390	45913390	T	A	*LRRC46*	splice_region	c.383-9	e6-9	tier3	23684	3885	3845	36	0.009	15678	3109	1923	1168	0.378	11367	2212	1501	702	0.319	25059	4294	3821	448	0.105	49365	9397	8401	960	0.103
429745	17	65871717	65871717	T	G	*BPTF*	missense	c.1910	p.L637R	tier1	3509	546	538	8	0.015	2406	251	141	105	0.427	1873	185	117	68	0.368	4984	495	440	53	0.108	6940	948	828	120	0.127
429745	17	74018124	74018124	C	A	*EVPL*	intronic	c.646-15	e7-15	tier2	9941	1398	1389	8	0.006	6621	705	417	284	0.405	4673	500	321	179	0.358	13595	1329	1145	167	0.127	22685	2952	2588	353	0.120
429745	18	40849590	40849590	A	T	*SYT4*	3_prime_untranslated_region	c.*716	NULL	tier3	7324	1098	1091	5	0.005	4754	571	415	155	0.272	4847	525	427	95	0.182	10257	1036	985	51	0.049	17125	2353	2252	101	0.043
429745	19	11019894	11019894	C	T	*CARM1*	intronic	c.558+11	e4+11	tier3	15814	2634	2608	24	0.009	10454	1428	743	678	0.477	5749	738	429	305	0.416	15483	1972	1671	293	0.149	33302	5339	4549	746	0.141
429745	19	48643310	48643310	G	C	*LIG1*	silent	c.1005	p.L335	tier1	24641	3313	3288	24	0.007	11486	1069	696	367	0.345	13968	1434	996	429	0.301	35611	3743	3396	328	0.088	50989	6502	5859	612	0.095
429745	20	23860305	23860305	C	T	*CST5*	nonsense	c.9	p.W3*	tier1	32468	4210	4198	10	0.002	21028	2134	1323	781	0.371	16849	1885	1277	596	0.318	37344	4224	3725	462	0.110	69981	8921	7814	1049	0.118
429745	X	39931644	39931644	A	T	*BCOR*	nonsense	c.2955	p.Y985*	tier1	21735	3596	3579	17	0.005	17040	2020	1192	797	0.401	17842	1941	1212	702	0.367	20944	2366	1954	392	0.167	37479	5446	4363	1062	0.196
430998	1	24421386	24421386	C	T	*MYOM3*	silent	c.888	p.S296	tier1	11116	1269	1267	1	0.001	13689	1397	1266	128	0.092	14896	1110	1091	15	0.014	22697	1993	1988	1	0.000	19652	2910	2904	3	0.000
430998	1	32162944	32162944	T	C	*COL16A1*	intronic	c.658-43	e6-43	tier4	22900	2716	2626	87	0.032	17132	1826	1126	678	0.376	21580	1794	930	834	0.473	40374	3720	3704	10	0.003	31782	4544	4504	38	0.008
430998	2	42553171	42553171	T	G	*EML4*	intronic	c.2243-123	e21-123	tier3	3175	248	241	6	0.024	6208	557	330	224	0.404	7042	431	192	234	0.549	10863	1210	1202	2	0.000	8873	1125	1105	17	0.015
430998	2	196851848	196851848	T	C	*DNAH7*	missense	c.1696	p.I566V	tier1	10547	1001	968	33	0.033	9650	949	566	375	0.399	12984	809	391	406	0.509	19009	1655	1646	7	0.004	16222	2153	2121	26	0.012
430998	2	198266834	198266834	T	C	*SF3B1*	missense	c.2098	p.K700E	tier1	19316	2274	2213	60	0.026	11842	1190	741	439	0.372	37768	3386	1691	1614	0.488	40841	2440	2419	16	0.007	38413	4776	4722	48	0.010
430998	3	46486788	46486788	C	T	*LTF*	silent	c.1497	p.T499	tier1	18118	1956	1822	126	0.065	17915	1876	1095	754	0.408	18282	1319	662	628	0.487	34590	2782	2762	11	0.004	31487	4351	4291	56	0.013
430998	3	184557400	184557400	G	T	*VPS8*	3_prime_untranslated_region	c.*851	NULL	tier3	4300	492	490	2	0.004	2893	285	229	56	0.196	4440	375	307	68	0.181	7531	749	745	4	0.005	7421	1065	1060	4	0.004
430998	4	20574880	20574880	A	G	*SLIT2*	missense	c.3124	p.K1042E	tier1	5875	864	860	3	0.003	6993	819	765	53	0.065	3761	326	322	2	0.000	12290	1948	1940	1	0.000	7677	1718	1715	3	0.002
430998	5	93217240	93217240	C	T	*FAM172A*	missense	c.722	p.R241H	tier1	1654	191	187	4	0.021	1562	180	165	15	0.083	968	86	85	1	0.000	2802	654	650	2	0.000	1702	365	365	0	0.000
430998	6	123786098	123786098	G	A	*TRDN*	missense	c.884	p.P295L	tier1	1758	134	133	1	0.007	2384	228	166	62	0.272	1993	115	90	25	0.217	5007	576	573	1	0.000	4498	571	569	2	0.000
430998	9	6534811	6534811	G	A	*GLDC*	intronic	c.2839-23	e24-23	tier3	9910	1214	1185	26	0.021	9592	1106	700	400	0.364	5323	379	194	182	0.484	14679	1884	1878	5	0.003	11248	1894	1878	14	0.007
430998	10	105831879	105831879	C	T	*COL17A1*	intronic	c.416-42	e7-42	tier3	21959	2749	2669	74	0.027	18807	2162	1309	828	0.387	27238	2310	1193	1067	0.472	36772	3063	3052	11	0.004	33736	4834	4789	42	0.009
430998	11	89606363	89606363	C	G	*TRIM64B*	intronic	c.758+73	e4+73	tier3	2118	286	282	4	0.014	1490	175	141	34	0.194	703	60	44	16	0.267	2652	599	591	1	0.000	1495	305	299	5	0.016
430998	12	3662052	3662052	C	T	*PRMT8*	3_prime_untranslated_region	c.*3662052	NULL	tier3	7634	951	923	28	0.029	9635	1150	708	431	0.378	6091	510	263	244	0.481	21278	1679	1668	10	0.006	15536	2282	2257	24	0.011
430998	14	106391086	106391086	C	T	*KIAA0125*	rna	NULL	NULL	tier1	1155	170	163	7	0.041	1067	172	87	83	0.488	208	21	9	12	0.571	1033	217	213	1	0.000	752	176	172	4	0.023
430998	16	1251965	1251965	C	T	*CACNA1H*	silent	c.1515	p.R505	tier1	15507	1949	1907	40	0.021	16330	1875	1099	758	0.408	20293	1776	886	854	0.491	35778	2036	2023	10	0.005	26438	3589	3538	42	0.012
430998	16	70044642	70044642	G	A	*PDXDC2P*	intronic	c.NULL	NULL	tier3	17295	2840	2830	6	0.002	15267	2276	2161	110	0.048	20148	2686	1469	1195	0.449	34019	3008	2987	11	0.004	32022	5103	5067	29	0.006
430998	17	10403963	10403963	G	A	*MYH1*	missense	c.3845	p.A1282V	tier1	26475	3073	3052	16	0.005	22729	2462	2236	216	0.088	37706	3195	3118	66	0.021	55207	3029	3024	3	0.000	47823	5794	5789	4	0.000
430998	17	48267657	48267657	G	A	*COL1A1*	intronic	c.2451+31	e35+31	tier3	1263	159	154	5	0.031	1257	150	104	46	0.307	598	45	19	26	0.578	1750	210	208	2	0.000	1664	258	256	2	0.000
430998	17	66146458	66146458	A	G	*LRRC37A16P*	5_prime_untranslated_region	c.-66146458	NULL	tier3	11403	1344	1306	38	0.028	9093	865	536	321	0.375	16414	1342	694	635	0.478	27863	2120	2111	7	0.003	28465	3898	3858	38	0.010
430998	19	1806137	1806137	C	T	*ATP8B3*	missense	c.709	p.V237M	tier1	25951	3117	3037	75	0.024	22161	2433	1532	875	0.364	34374	3221	1630	1526	0.484	48484	2551	2537	11	0.004	45586	5286	5231	44	0.008
430998	19	12767474	12767474	C	T	*MAN2B1*	nonsense	c.165	p.W55*	tier1	13858	1937	1934	2	0.001	11485	1461	1419	41	0.028	4596	432	312	120	0.278	21918	2260	2244	7	0.003	16443	3001	2996	4	0.001
430998	19	22941441	22941441	G	T	*ZNF99*	missense	c.997	p.P333T	tier1	2700	296	293	3	0.010	2934	327	203	123	0.377	853	52	25	27	0.519	7293	730	725	2	0.000	5161	796	785	6	0.008
430998	19	54722897	54722897	C	T	*LILRB3*	intronic	c.1477+101	e9+101	tier3	16983	1755	1738	17	0.010	16389	1611	1451	154	0.096	25454	1878	1138	698	0.380	46642	3715	3703	7	0.002	36025	4792	4768	21	0.004
430998	22	47075722	47075722	T	C	*GRAMD4*	3_prime_flanking_region	c.*2574	NULL	tier2	8772	963	930	30	0.031	8488	876	538	334	0.383	14289	1227	676	537	0.443	21962	1526	1513	9	0.006	18027	2391	2369	22	0.009
430998	X	54319632	54319632	C	T	*WNK3*	missense	c.1822	p.V608I	tier1	7958	896	854	40	0.045	6148	655	174	479	0.734	9891	785	27	756	0.966	32259	2151	2143	5	0.002	26429	3408	3365	40	0.012
430998	X	134992384	134992384	T	C	*SAGE1*	intronic	c.1864+55	e14+55	tier3	5719	713	679	33	0.046	4972	647	141	503	0.781	5488	437	18	419	0.959	16634	2074	2058	10	0.005	13150	2216	2196	15	0.007
435866	2	230127480	230127480	C	T	*PID1*	silent	c.42	p.S14	tier1	33344	2308	2263	45	0.019	19259	1492	992	496	0.333	26648	1237	1213	24	0.019	178030	4013	4013	0	0.000	250535	4962	4954	7	0.001
435866	3	45718805	45718805	C	T	*LIMD1*	3_prime_untranslated_region	c.*254	NULL	tier3	13712	1999	1964	33	0.017	5446	1050	595	453	0.432	13258	1083	1062	21	0.019	51068	2622	2622	0	0.000	61156	3286	3276	7	0.002
435866	3	185978207	185978207	T	C	*DGKG*	intronic	c.1424+21	e15+21	tier3	27788	2351	2306	44	0.019	20155	1416	793	621	0.439	19208	1081	1059	22	0.020	179711	4520	4517	3	0.001	155545	3520	3515	5	0.001
435866	4	66356333	66356333	G	A	*EPHA5*	silent	c.1164	p.D388	tier1	20461	1575	1556	18	0.011	14463	1460	877	580	0.398	22003	1163	1137	23	0.020	133068	3318	3313	3	0.000	132737	3485	3477	8	0.002
435866	5	138658293	138658293	A	T	*MATR3*	missense	c.1785	p.R595S	tier1	4139	872	866	6	0.007	2342	564	323	239	0.425	7243	798	785	13	0.016	31853	2014	2013	0	0.000	28669	1984	1978	6	0.003
435866	5	142254704	142254704	C	T	*ARHGAP26*	missense	c.280	p.L94F	tier1	26906	2001	1988	12	0.006	18017	1520	1118	400	0.264	29890	1460	1437	23	0.016	253846	5909	5909	0	0.000	215952	4611	4608	3	0.001
435866	5	172745042	172745042	G	A	*STC2*	silent	c.717	p.H239	tier1	29475	2262	2206	55	0.024	23219	2120	1303	815	0.385	37490	1888	1835	51	0.027	182962	4733	4729	1	0.000	221653	5680	5655	18	0.003
435866	7	89551249	89551249	G	T	*STEAP2-AS1*	intronic	c.NULL	NULL	tier3	19112	2104	2091	12	0.006	15320	1783	1013	763	0.430	18324	1273	1255	16	0.013	142505	4414	4408	2	0.000	141243	4348	4338	8	0.002
435866	7	123269290	123269290	T	C	*ASB15*	silent	c.1242	p.N414	tier1	24143	1981	1937	41	0.021	17542	1434	844	589	0.411	27429	1238	1203	35	0.028	217400	4872	4871	1	0.000	147649	3234	3227	7	0.002
435866	7	149481922	149481922	C	T	*SSPO*	3_prime_untranslated_region	c.*149481922	NULL	tier3	32965	2094	2062	29	0.014	20550	1380	790	582	0.424	26583	1084	1060	23	0.021	200089	3918	3913	0	0.000	193793	3670	3655	12	0.003

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
435866	7	151882645	151882645	C	A	*MLL3*	missense	c.5080	p.V1694L	tier1	18341	3179	3137	41	0.013	8337	1660	1049	606	0.366	19306	2029	1995	34	0.017	105404	6095	6092	0	0.000	100372	6151	6136	11	0.002
435866	8	68024182	68024182	G	A	*CSPP1*	intronic	c.1226-25	e12-25	tier3	28617	2605	2573	32	0.012	14377	1643	1008	631	0.385	24083	1401	1369	31	0.022	163255	4606	4606	0	0.000	128108	3781	3773	8	0.002
435866	8	139727925	139727925	C	A	*COL22A1*	missense	c.2517	p.K839N	tier1	14770	1481	1456	25	0.017	6594	812	465	344	0.425	13358	871	843	28	0.032	74830	2249	2249	0	0.000	47347	2114	2110	4	0.002
435866	10	81921715	81921715	G	T	*ANXA11*	silent	c.1156	p.R386	tier1	28956	2256	2244	12	0.005	27498	2104	1088	1007	0.481	32356	1496	1486	10	0.007	230558	5119	5117	1	0.000	262348	5468	5448	18	0.003
435866	10	120810716	120810716	A	G	*EIF3A*	missense	c.2314	p.Y772H	tier1	15834	2265	2253	10	0.004	8732	1502	893	604	0.403	16716	1341	1328	13	0.010	89665	3829	3829	0	0.000	82069	3736	3729	6	0.002
435866	15	28420657	28420657	C	T	*HERC2*	splice_site	c.9831+1	e63+1	tier1	9040	828	812	16	0.019	5494	551	305	245	0.445	8678	438	423	15	0.034	32185	1144	1144	0	0.000	52632	1429	1425	4	0.003
435866	16	3341019	3341019	C	T	*ZNF263*	3_prime_untranslated_region	c.*461	NULL	tier2	41409	2681	2649	32	0.012	27111	1794	1274	516	0.288	37079	1501	1476	25	0.017	310483	6336	6332	4	0.000	258758	5137	5126	10	0.002
435866	16	87870242	87870242	C	T	*SLC7A5*	silent	c.1152	p.T384	tier1	51148	3783	3763	17	0.004	34652	3116	1778	1330	0.428	44181	1996	1972	22	0.011	277199	6340	6339	1	0.000	345963	7896	7869	24	0.003
435866	17	40049260	40049260	A	G	*ACLY*	intronic	c.1763+26	e15+26	tier2	19218	1932	1908	23	0.012	12423	1333	925	404	0.304	19972	1270	1245	23	0.018	129367	3722	3722	0	0.000	150179	3843	3842	1	0.000
435866	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	17829	1296	1268	26	0.020	18244	1580	873	702	0.446	23322	1205	1184	21	0.017	114677	3195	3193	2	0.000	168820	4035	4026	9	0.002
435866	18	61226995	61226995	C	G	*SERPINB12*	intronic	c.384+44	e3+44	tier2	18158	2791	2763	27	0.010	8346	1647	998	647	0.393	17288	1453	1426	27	0.019	76142	3486	3485	1	0.000	88700	4323	4312	9	0.002
435866	20	14830634	14830634	A	G	*MACROD2*	3_prime_untranslated_region	c.*14830634	NULL	tier3	4060	789	786	3	0.004	1600	356	194	160	0.452	3377	364	362	2	0.000	16068	924	922	0	0.000	12242	801	799	2	0.000
435866	22	38884063	38884063	T	C	*DDX17*	missense	c.1505	p.Y502C	tier1	47445	4127	4050	74	0.018	31334	2786	1724	1053	0.379	48316	2487	2423	64	0.026	330616	8032	8031	0	0.000	314458	7601	7588	13	0.002
435866	X	79971691	79971691	C	G	*BRWD3*	missense	c.2290	p.E764Q	tier1	15971	1677	1649	28	0.017	7953	825	474	347	0.423	11898	765	748	17	0.022	48921	1557	1556	1	0.000	33426	1092	1087	4	0.004
435866	X	105450024	105450024	C	T	*MUM1L1*	missense	c.599	p.S200L	tier1	20377	2063	2022	41	0.020	9473	1402	770	625	0.448	16794	1075	1037	38	0.035	57612	1879	1879	0	0.000	47350	1819	1809	10	0.005
437422	1	22186507	22186507	G	T	*HSPG2*	intronic	c.5015-12	e41-12	tier3	6210	757	751	6	0.008	18971	2526	1695	806	0.322	7469	1114	676	435	0.392	20271	2076	2075	0	0.000	NA	NA	NA	NA	NA
437422	1	27736195	27736195	T	C	*WASF2*	missense	c.1330	p.I444V	tier1	39553	5203	5176	24	0.005	45505	5661	4508	1091	0.195	22789	3091	2535	547	0.177	38378	4209	4208	0	0.000	NA	NA	NA	NA	NA
437422	1	167802237	167802237	C	A	*ADCY10*	missense	c.3581	p.S1194I	tier1	48246	6354	6310	38	0.006	54754	6518	4536	1892	0.294	36721	4905	3194	1683	0.345	53584	5840	5839	0	0.000	NA	NA	NA	NA	NA
437422	1	190067860	190067860	C	T	*BRINP3*	missense	c.1589	p.R530H	tier1	5912	779	772	7	0.009	10489	1421	937	476	0.337	3869	611	378	232	0.380	6350	563	563	0	0.000	NA	NA	NA	NA	NA
437422	1	208061976	208061976	C	T	*CD34*	intronic	c.972+51	e7+51	tier3	18308	2319	2298	17	0.007	27880	3295	2198	1014	0.316	13762	1929	1131	744	0.397	14095	1205	1205	0	0.000	NA	NA	NA	NA	NA
437422	2	75105821	75105821	G	A	*HK2*	silent	c.1038	p.K346	tier1	44629	5762	5722	36	0.006	50097	6406	4761	1563	0.247	24618	3335	2544	777	0.234	48945	5265	5265	0	0.000	NA	NA	NA	NA	NA
437422	3	167006710	167006710	C	G	*ZBBX*	missense	c.1941	p.L647F	tier1	9013	1149	1145	3	0.003	17092	2055	1482	553	0.272	6258	844	515	327	0.388	10012	996	996	0	0.000	NA	NA	NA	NA	NA
437422	4	166416855	166416855	C	T	*CPE*	intronic	c.1332+26	e8+26	tier3	6557	608	599	6	0.010	8555	928	684	240	0.260	2666	365	298	65	0.179	5769	485	484	0	0.000	NA	NA	NA	NA	NA
437422	5	133898014	133898014	G	A	*PHF15*	missense	c.809	p.G270E	tier1	50979	6709	6650	53	0.008	73568	8933	6541	2249	0.256	35058	4418	2614	1778	0.405	66875	7560	7556	0	0.000	NA	NA	NA	NA	NA
437422	7	6193554	6193554	C	T	*USP42*	missense	c.2369	p.A790V	tier1	3404	344	341	3	0.009	11954	1499	952	538	0.361	2454	303	149	154	0.508	13019	1462	1462	0	0.000	NA	NA	NA	NA	NA
437422	7	77885784	77885784	C	T	*MAGI2*	missense	c.1523	p.R508H	tier1	30588	3946	3942	2	0.001	34134	4080	3868	189	0.047	17554	2389	2364	19	0.008	30241	3233	3231	1	0.000	NA	NA	NA	NA	NA
437422	7	120428042	120428042	C	T	*TSPAN12*	3_prime_untranslated_region	c.*604	NULL	tier2	1472	133	132	1	0.008	1502	165	97	66	0.405	1501	200	78	122	0.610	1946	142	142	0	0.000	NA	NA	NA	NA	NA
437422	8	113299258	113299258	T	C	*CSMD3*	intronic	c.9331+35	e58+35	tier3	17383	1991	1982	7	0.004	18396	2131	1693	419	0.198	9338	1227	981	237	0.195	14994	1457	1457	0	0.000	NA	NA	NA	NA	NA
437422	11	46686904	46686904	T	G	*ATG13*	intronic	c.901-29	e11-29	tier3	14943	2657	2636	20	0.008	23533	3805	2787	978	0.260	6979	1265	771	489	0.388	13833	1866	1863	0	0.000	NA	NA	NA	NA	NA
437422	11	130067769	130067769	G	A	*ST14*	missense	c.1388	p.R463Q	tier1	42157	5856	5813	38	0.006	65488	8559	5739	2666	0.317	23607	3278	2152	1116	0.341	54687	6245	6239	1	0.000	NA	NA	NA	NA	NA
437422	12	122091150	122091150	T	G	*MORN3*	missense	c.479	p.Y160S	tier1	16248	1872	1852	17	0.009	24384	2836	2111	692	0.247	8373	1173	890	279	0.239	22977	2190	2189	0	0.000	NA	NA	NA	NA	NA
437422	16	10721483	10721483	C	T	*TEKT5*	missense	c.1415	p.R472H	tier1	55554	7362	7296	62	0.008	70491	8711	5995	2588	0.302	39020	4875	3188	1662	0.343	73592	8724	8714	3	0.000	NA	NA	NA	NA	NA
437422	17	7576851	7576851	A	C	*TP53*	splice_site	c.993+2	e8+2	tier1	44688	5679	5636	42	0.007	52860	6575	4754	1704	0.264	31257	4164	2524	1613	0.390	47704	5128	5127	0	0.000	NA	NA	NA	NA	NA
437422	17	7578431	7578431	G	A	*TP53*	nonsense	c.499	p.Q167*	tier1	52545	6923	6900	20	0.003	78898	9845	7659	2086	0.214	28499	3380	2758	613	0.182	80392	9700	9697	2	0.000	NA	NA	NA	NA	NA
437422	18	33269094	33269094	G	A	*GALNT1*	intronic	c.861-43	e6-43	tier3	1816	212	211	1	0.005	5990	694	523	170	0.245	4179	598	342	254	0.426	5678	534	533	0	0.000	NA	NA	NA	NA	NA
437422	20	33068598	33068598	G	A	*ITCH*	intronic	c.2075+61	e18+61	tier3	2547	316	316	0	0.000	3956	544	507	35	0.065	3017	475	364	111	0.234	3652	344	343	1	0.000	NA	NA	NA	NA	NA
437422	X	76812922	76812922	C	T	*ATRX*	silent	c.6699	p.K2233	tier1	12647	1740	1722	17	0.010	15796	2144	1747	387	0.181	13178	2060	1651	401	0.195	6504	714	713	0	0.000	NA	NA	NA	NA	NA
439820	1	2077399	2077399	C	G	*PRKCZ*	intronic	c.553-67	e7-67	tier3	3972	868	867	1	0.001	3608	717	672	43	0.060	NA	NA	NA	NA	NA	3046	275	275	0	0.000	NA	NA	NA	NA	NA
439820	1	22927251	22927251	G	C	*EPHA8*	missense	c.2486	p.W829S	tier1	11075	1786	1786	0	0.000	13409	2249	2098	147	0.065	NA	NA	NA	NA	NA	8471	698	698	0	0.000	NA	NA	NA	NA	NA
439820	1	35250948	35250948	C	T	*GJB3*	silent	c.585	p.S195	tier1	50530	7090	7090	0	0.000	39647	4714	3793	856	0.184	NA	NA	NA	NA	NA	39431	3154	3146	7	0.002	NA	NA	NA	NA	NA
439820	1	97981408	97981408	G	A	*DPYD*	silent	c.1614	p.A538	tier1	2406	311	309	2	0.006	15584	1996	1139	843	0.425	NA	NA	NA	NA	NA	16890	1170	679	477	0.413	NA	NA	NA	NA	NA
439820	1	115258745	115258745	C	G	*NRAS*	missense	c.37	p.G13R	tier1	32763	4218	4213	2	0.000	34895	4425	3843	554	0.126	NA	NA	NA	NA	NA	29109	1940	1938	1	0.000	NA	NA	NA	NA	NA
439820	1	115258747	115258747	C	G	*NRAS*	missense	c.35	p.G12A	tier1	32909	4233	4230	0	0.000	35447	4462	4273	168	0.038	NA	NA	NA	NA	NA	29087	1944	1943	1	0.000	NA	NA	NA	NA	NA
439820	1	145417057	145417057	C	G	*HFE2*	3_prime_untranslated_region	c.*121	NULL	tier3	25656	3558	3546	10	0.003	22793	3207	1711	1464	0.461	NA	NA	NA	NA	NA	16884	1190	174	1003	0.852	NA	NA	NA	NA	NA
439820	1	160090882	160090882	C	T	*ATP1A2*	3_prime_untranslated_region	c.*160090882	NULL	tier3	57745	7362	7346	12	0.002	100462	12788	10734	1902	0.151	NA	NA	NA	NA	NA	77993	6156	5995	131	0.021	NA	NA	NA	NA	NA
439820	1	186089086	186089086	G	C	*HMCN1*	intronic	c.12095-57	e80-57	tier3	11180	1459	1458	0	0.000	10910	1324	1231	89	0.067	NA	NA	NA	NA	NA	11113	663	661	2	0.000	NA	NA	NA	NA	NA
439820	2	38295746	38295746	C	T	*CYP1B1*	3_prime_untranslated_region	c.*2119	NULL	tier3	7272	829	828	1	0.001	4082	485	356	126	0.261	NA	NA	NA	NA	NA	4226	255	227	28	0.110	NA	NA	NA	NA	NA
439820	2	89292205	89292205	C	T	*IGKV1-8*	missense	c.68	p.R23Q	tier1	4142	877	876	0	0.000	4763	928	884	44	0.047	NA	NA	NA	NA	NA	2339	219	219	0	0.000	NA	NA	NA	NA	NA
439820	2	91927043	91927043	T	C	*ENSG00000223703*	3_prime_untranslated_region	c.*91927043	NULL	tier3	1245	212	211	1	0.005	1142	201	121	80	0.398	NA	NA	NA	NA	NA	525	30	19	11	0.367	NA	NA	NA	NA	NA
439820	2	98349520	98349520	G	A	*ZAP70*	intronic	c.702+36	e3+36	tier3	17487	2465	2462	3	0.001	17065	2268	1347	898	0.400	NA	NA	NA	NA	NA	8678	621	598	20	0.032	NA	NA	NA	NA	NA
439820	2	119739805	119739805	C	G	*MARCO*	silent	c.975	p.G325	tier1	35566	4557	4536	14	0.003	45478	5531	2994	2474	0.452	NA	NA	NA	NA	NA	34236	2527	1369	1097	0.445	NA	NA	NA	NA	NA
439820	2	179459370	179459370	A	C	*TTN*	missense	c.50147	p.V16716G	tier1	12442	3154	3139	13	0.004	9463	2137	1182	948	0.445	NA	NA	NA	NA	NA	7671	2401	1375	1024	0.427	NA	NA	NA	NA	NA
439820	3	10401760	10401760	C	T	*ATP2B2*	silent	c.1707	p.T569	tier1	46208	6064	6059	2	0.000	63937	8283	7827	410	0.050	NA	NA	NA	NA	NA	39914	2773	2767	1	0.000	NA	NA	NA	NA	NA
439820	3	12227025	12227025	C	T	*SYN2*	rna	NULL	NULL	tier1	36719	4721	4703	16	0.003	41360	5424	3306	2051	0.383	NA	NA	NA	NA	NA	22749	1666	1013	626	0.382	NA	NA	NA	NA	NA
439820	3	53224001	53224001	C	G	*PRKCD*	missense	c.1856	p.P619R	tier1	26428	3696	3695	0	0.000	28096	4186	3920	255	0.061	NA	NA	NA	NA	NA	20642	1454	1454	0	0.000	NA	NA	NA	NA	NA
439820	3	164783108	164783108	G	A	*SI*	missense	c.748	p.R250C	tier1	2807	0	0	0	0.000	3054	337	304	31	0.093	NA	NA	NA	NA	NA	1663	62	62	0	0.000	NA	NA	NA	NA	NA
439820	3	194146027	194146027	A	G	*ATP13A3*	intronic	c.3313+44	e28+44	tier3	4469	551	540	11	0.020	4306	507	277	228	0.451	NA	NA	NA	NA	NA	3986	270	154	115	0.428	NA	NA	NA	NA	NA
439820	4	23796009	23796009	G	A	*PPARGC1A*	3_prime_untranslated_region	c.*1436	NULL	tier3	14147	1755	1751	1	0.001	9384	1416	848	559	0.397	NA	NA	NA	NA	NA	8111	474	306	165	0.350	NA	NA	NA	NA	NA
439820	4	159634313	159634313	C	G	*PPID*	silent	c.852	p.L284	tier1	44929	5786	5782	1	0.000	36517	4809	4263	513	0.107	NA	NA	NA	NA	NA	21449	1433	1430	2	0.000	NA	NA	NA	NA	NA
439820	5	40998245	40998245	C	T	*MROH2B*	missense	c.4667	p.R1556H	tier1	11359	1402	1392	9	0.006	20245	2602	1467	1118	0.433	NA	NA	NA	NA	NA	10570	708	409	293	0.417	NA	NA	NA	NA	NA
439820	5	81583110	81583110	G	C	*ATP6AP1L*	intronic	c.1+6280	e0+6280	tier3	24405	3134	3125	1	0.000	20771	2795	2648	131	0.047	NA	NA	NA	NA	NA	17856	1203	1202	0	0.000	NA	NA	NA	NA	NA
439820	6	131941851	131941851	C	A	*MED23*	nonsense	c.514	p.E172*	tier1	3293	350	349	1	0.003	6119	700	517	178	0.256	NA	NA	NA	NA	NA	2142	134	98	36	0.269	NA	NA	NA	NA	NA
439820	6	146244843	146244843	G	C	*SHPRH*	missense	c.3508	p.R1170G	tier1	16324	2081	2068	11	0.005	21558	2762	1528	1214	0.443	NA	NA	NA	NA	NA	23081	1690	946	722	0.433	NA	NA	NA	NA	NA
439820	6	168466523	168466523	G	C	*FRMD1*	5_prime_untranslated_region	c.-168466523	NULL	tier3	13716	1625	1624	1	0.001	15626	1829	1611	210	0.115	NA	NA	NA	NA	NA	9202	546	545	0	0.000	NA	NA	NA	NA	NA
439820	7	14217686	14217686	C	T	*DGKB*	missense	c.2216	p.R739Q	tier1	25545	3115	3110	3	0.001	40582	5021	3154	1803	0.364	NA	NA	NA	NA	NA	28786	1907	1873	30	0.016	NA	NA	NA	NA	NA
439820	7	92888838	92888838	G	A	*CCDC132*	3_prime_untranslated_region	c.*92888838	NULL	tier3	5802	654	654	0	0.000	3544	511	388	122	0.239	NA	NA	NA	NA	NA	2934	172	135	35	0.206	NA	NA	NA	NA	NA
439820	8	2909983	2909983	C	T	*CSMD1*	splice_site	c.7663+1	e51+1	tier1	15839	2000	1993	7	0.004	22753	2797	1615	1157	0.417	NA	NA	NA	NA	NA	18362	1292	718	555	0.436	NA	NA	NA	NA	NA
439820	8	102555673	102555673	C	A	*GRHL2*	3_prime_untranslated_region	c.*102555673	NULL	tier3	23475	2943	2934	7	0.002	20567	2598	1518	1057	0.410	NA	NA	NA	NA	NA	20956	1405	1373	28	0.020	NA	NA	NA	NA	NA
439820	8	133192501	133192501	C	T	*KCNQ3*	missense	c.680	p.R227Q	tier1	7691	1575	1574	1	0.001	11411	2025	1913	105	0.052	NA	NA	NA	NA	NA	7183	554	554	0	0.000	NA	NA	NA	NA	NA
439820	9	39178241	39178241	C	A	*CNTNAP3*	nonsense	c.655	p.G219*	tier1	266	0	0	0	0.000	1109	219	153	65	0.298	NA	NA	NA	NA	NA	792	60	60	0	0.000	NA	NA	NA	NA	NA
439820	10	5925962	5925962	G	A	*ANKRD16*	silent	c.657	p.D219	tier1	1166	231	230	1	0.004	969	164	142	22	0.134	NA	NA	NA	NA	NA	613	62	56	6	0.097	NA	NA	NA	NA	NA
439820	10	46210670	46210670	G	C	*FAM21FP*	5_prime_untranslated_region	c.-46210670	NULL	tier2	4302	450	449	0	0.000	5772	781	723	50	0.065	NA	NA	NA	NA	NA	3039	173	172	0	0.000	NA	NA	NA	NA	NA
439820	10	71627506	71627506	C	T	*COL13A1*	intronic	c.365-4426	e3-4426	tier2	37097	4641	4620	19	0.004	33798	4243	2205	1986	0.474	NA	NA	NA	NA	NA	35173	2618	1391	1170	0.457	NA	NA	NA	NA	NA
439820	10	114925313	114925313	G	C	*TCF7L2*	splice_site	c.1443-1	e15-1	tier1	31559	4093	4042	1	0.000	40616	5098	4371	662	0.132	NA	NA	NA	NA	NA	27970	1888	1857	0	0.000	NA	NA	NA	NA	NA
439820	11	2906566	2906566	C	A	*CDKN1C*	nonsense	c.154	p.E52*	tier1	35882	4381	4374	6	0.001	32141	4156	2416	1688	0.411	NA	NA	NA	NA	NA	30949	2155	2084	67	0.031	NA	NA	NA	NA	NA
439820	11	57471814	57471814	G	A	*MED19*	missense	c.626	p.P209L	tier1	8944	1163	1159	4	0.003	7611	1017	674	333	0.331	NA	NA	NA	NA	NA	5190	343	272	67	0.198	NA	NA	NA	NA	NA
439820	11	62364143	62364143	T	C	*MTA2*	missense	c.848	p.Y283C	tier1	55994	7124	7087	31	0.004	70044	8764	4563	4049	0.470	NA	NA	NA	NA	NA	50305	3771	1952	1699	0.465	NA	NA	NA	NA	NA
439820	11	124413410	124413410	C	G	*OR8B12*	silent	c.141	p.L47	tier1	2439	364	364	0	0.000	21560	3207	3011	180	0.056	NA	NA	NA	NA	NA	21308	1821	1821	0	0.000	NA	NA	NA	NA	NA
439820	11	124789263	124789263	C	G	*HEPN1*	5_prime_untranslated_region	c.-384	NULL	tier3	12718	2614	2613	1	0.000	12763	2459	2113	333	0.136	NA	NA	NA	NA	NA	10467	979	974	3	0.003	NA	NA	NA	NA	NA
439820	12	6965657	6965657	A	G	*USP5*	intronic	c.584+43	e5+43	tier3	18190	2311	2298	11	0.005	17358	2126	1257	845	0.402	NA	NA	NA	NA	NA	16660	993	602	378	0.386	NA	NA	NA	NA	NA
439820	12	47186868	47186868	G	A	*SLC38A4*	5_prime_untranslated_region	c.-14	NULL	tier3	20713	2425	2421	2	0.001	20190	2425	1556	840	0.351	NA	NA	NA	NA	NA	18708	1159	823	315	0.277	NA	NA	NA	NA	NA
439820	12	51844830	51844830	G	C	*SLC4A8*	intronic	c.277+24	e3+24	tier3	8506	1261	1261	0	0.000	7804	1218	1155	58	0.048	NA	NA	NA	NA	NA	6103	427	426	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
439820	12	112888165	112888165	G	C	*PTPN11*	missense	c.181	p.D61H	tier1	17019	2381	2381	0	0.000	27691	3692	3552	127	0.035	NA	NA	NA	NA	NA	8182	600	599	1	0.000	NA	NA	NA	NA	NA
439820	14	24518609	24518609	A	G	*DHRS4L1*	intronic	c.NULL	NULL	tier3	11208	1382	1346	35	0.025	8552	1062	569	488	0.462	NA	NA	NA	NA	NA	8219	520	285	229	0.446	NA	NA	NA	NA	NA
439820	14	24524337	24524337	G	T	*LRRC16B*	missense	c.523	p.V175F	tier1	42204	5515	5451	59	0.011	64239	8489	5435	2861	0.345	NA	NA	NA	NA	NA	27810	2145	1365	730	0.348	NA	NA	NA	NA	NA
439820	14	100792064	100792064	A	G	*SLC25A47*	intronic	c.29-61	e2-61	tier3	33480	4481	4466	13	0.003	48595	6186	3338	2733	0.450	NA	NA	NA	NA	NA	33562	2482	1356	1052	0.437	NA	NA	NA	NA	NA
439820	15	91438809	91438809	G	C	*FES*	3_prime_untranslated_region	c.*21	NULL	tier3	65267	8280	8038	226	0.027	71347	8751	4374	4236	0.492	NA	NA	NA	NA	NA	71441	5563	2723	2601	0.489	NA	NA	NA	NA	NA
439820	16	2098338	2098338	A	G	*TSC2*	intronic	c.1-250	e1-250	tier2	18307	2518	2446	70	0.028	21592	2809	1461	1303	0.471	NA	NA	NA	NA	NA	22564	1514	841	630	0.428	NA	NA	NA	NA	NA
439820	16	7761443	7761443	G	A	*RBFOX1*	3_prime_untranslated_region	c.*1800	NULL	tier3	2496	298	298	0	0.000	2507	381	315	64	0.169	NA	NA	NA	NA	NA	1075	65	61	4	0.062	NA	NA	NA	NA	NA
439820	16	24582766	24582766	G	A	*RBBP6*	missense	c.4379	p.R1460H	tier1	17959	2428	2420	7	0.003	17409	2195	1405	773	0.355	NA	NA	NA	NA	NA	12458	864	832	31	0.036	NA	NA	NA	NA	NA
439820	16	29576812	29576812	T	C	*ENSG00000205534*	5_prime_untranslated_region	c.-29576812	NULL	tier3	1391	306	304	1	0.003	467	90	70	20	0.222	NA	NA	NA	NA	NA	872	87	69	18	0.207	NA	NA	NA	NA	NA
439820	16	50835415	50835415	A	G	*CYLD*	3_prime_untranslated_region	c.*4996	NULL	tier3	4653	771	766	5	0.006	4221	757	475	281	0.372	NA	NA	NA	NA	NA	1830	149	51	98	0.658	NA	NA	NA	NA	NA
439820	16	50835731	50835731	C	G	*CYLD*	3_prime_untranslated_region	c.*5312	NULL	tier3	8889	1109	1102	7	0.006	7198	877	494	379	0.434	NA	NA	NA	NA	NA	4248	288	275	13	0.045	NA	NA	NA	NA	NA
439820	17	7577538	7577538	C	T	*TP53*	missense	c.743	p.R248Q	tier1	52868	6841	6796	41	0.006	48827	6763	3251	3434	0.514	NA	NA	NA	NA	NA	54609	5015	583	4355	0.882	NA	NA	NA	NA	NA
439820	17	15942836	15942836	G	C	*NCOR1*	missense	c.6866	p.P2289R	tier1	10804	1457	1450	7	0.005	27645	3562	1980	1546	0.438	NA	NA	NA	NA	NA	15923	1078	1056	22	0.020	NA	NA	NA	NA	NA
439820	18	7034550	7034550	A	G	*LAMA1*	missense	c.1979	p.M660T	tier1	23162	3026	3013	12	0.004	25313	3185	1683	1473	0.467	NA	NA	NA	NA	NA	16596	1119	611	492	0.446	NA	NA	NA	NA	NA
439820	18	14752893	14752893	A	T	*ANKRD30B*	missense	c.392	p.D131V	tier1	20437	2533	2516	15	0.006	23599	2708	1563	1114	0.416	NA	NA	NA	NA	NA	14513	973	552	408	0.425	NA	NA	NA	NA	NA
439820	18	29046556	29046556	G	C	*DSG3*	missense	c.1475	p.C492S	tier1	10536	1356	1354	1	0.001	10670	1545	1355	181	0.118	NA	NA	NA	NA	NA	7036	455	455	0	0.000	NA	NA	NA	NA	NA
439820	18	34205430	34205430	G	A	*FHOD3*	intronic	c.958-44	e10-44	tier3	41360	5457	5440	14	0.003	72467	9398	5602	3588	0.390	NA	NA	NA	NA	NA	37662	2681	2623	54	0.020	NA	NA	NA	NA	NA
439820	18	42531907	42531907	G	A	*SETBP1*	missense	c.2602	p.D868N	tier1	51353	6527	6524	2	0.000	57353	7166	5804	1291	0.182	NA	NA	NA	NA	NA	43185	3202	3197	2	0.000	NA	NA	NA	NA	NA
439820	19	1529504	1529504	G	T	*PLK5*	intronic	c.490+15	e5+15	tier3	31908	4066	4053	8	0.002	61117	8129	6082	1914	0.239	NA	NA	NA	NA	NA	48578	3616	2823	674	0.193	NA	NA	NA	NA	NA
439820	19	9007457	9007457	C	G	*MUC16*	intronic	c.39481+30	e43+30	tier3	10321	1911	1909	0	0.000	17429	2955	2833	114	0.039	NA	NA	NA	NA	NA	11975	901	897	2	0.000	NA	NA	NA	NA	NA
439820	20	61291782	61291782	G	C	*SLCO4A1*	missense	c.906	p.E302D	tier1	28170	0	0	0	0.000	35961	4117	3851	241	0.059	NA	NA	NA	NA	NA	34128	2211	2203	4	0.002	NA	NA	NA	NA	NA
439820	21	44514777	44514777	T	G	*U2AF1*	missense	c.470	p.Q157P	tier1	82663	9996	9964	29	0.003	72468	8904	4774	3977	0.454	NA	NA	NA	NA	NA	71838	5386	2886	2289	0.442	NA	NA	NA	NA	NA
439820	X	31462671	31462671	G	A	*DMD*	missense	c.9011	p.T3004I	tier1	1252	252	250	2	0.008	1950	343	35	308	0.898	NA	NA	NA	NA	NA	1066	82	11	71	0.866	NA	NA	NA	NA	NA
439820	X	110439784	110439784	G	C	*PAK3*	silent	c.1431	p.P477	tier1	15220	1855	1852	1	0.001	18680	2359	2083	270	0.115	NA	NA	NA	NA	NA	10952	717	715	1	0.000	NA	NA	NA	NA	NA
439820	X	128781951	128781951	C	G	*APLN*	intronic	c.128-57	e2-57	tier3	15355	1915	1910	1	0.001	27274	3302	2875	403	0.123	NA	NA	NA	NA	NA	19751	1355	1354	1	0.000	NA	NA	NA	NA	NA
476807	1	26671642	26671642	C	A	*AIM1L*	intronic	c.169+204	e2+204	tier3	26825	3130	3079	47	0.015	18889	2234	1466	735	0.334	10329	930	926	0	0.000	19161	1789	1786	0	0.000	NA	NA	NA	NA	NA
476807	1	176525591	176525591	T	C	*PAPPA2*	silent	c.133	p.L45	tier1	27459	4743	4734	6	0.001	33177	5047	4199	797	0.160	23438	2273	2272	1	0.000	38444	5788	5765	0	0.000	NA	NA	NA	NA	NA
476807	2	177065811	177065811	C	T	*ENSG00000218175*	5_prime_untranslated_region	c.-177065811	NULL	tier2	12225	2393	2352	36	0.015	13526	2481	1643	821	0.333	8020	1176	1175	1	0.000	22146	3628	3620	0	0.000	NA	NA	NA	NA	NA
476807	2	231906196	231906196	G	T	*C2orf72*	intronic	c.748+72	e2+72	tier3	43393	6048	5956	89	0.015	39518	5641	3617	1951	0.350	25848	2421	2167	251	0.104	41531	5734	5722	0	0.000	NA	NA	NA	NA	NA
476807	3	41290971	41290971	C	T	*ULK4*	splice_region	c.3764+9	e35+9	tier3	12559	1618	1563	53	0.033	15126	2777	1729	1016	0.370	6906	1192	712	476	0.401	14701	2140	2130	0	0.000	NA	NA	NA	NA	NA
476807	4	15937803	15937803	G	A	*FGFBP1*	silent	c.453	p.V151	tier1	20767	2413	2405	7	0.003	25432	4080	3441	598	0.148	22016	2491	2489	1	0.000	30540	4620	4601	0	0.000	NA	NA	NA	NA	NA
476807	4	66388703	66388703	G	A	*EPHA5*	intronic	c.911-27442	e4-27442	tier3	24146	2659	2619	38	0.014	18130	2190	1474	707	0.324	13564	1493	1492	1	0.000	22748	2567	2565	0	0.000	NA	NA	NA	NA	NA
476807	4	126389815	126389815	C	G	*FAT4*	missense	c.12048	p.D4016E	tier1	25267	2770	2721	45	0.016	16861	2011	1288	713	0.356	20450	2061	2056	3	0.001	23099	2502	2498	0	0.000	NA	NA	NA	NA	NA
476807	4	183601392	183601392	T	C	*TENM3*	splice_region	c.1538-9	e8-9	tier3	33948	3900	3791	104	0.027	33966	4245	2462	1729	0.413	27668	2943	1787	1154	0.392	36682	4303	4291	0	0.000	2	0	0	0	NA
476807	5	137589102	137589102	G	A	*GFRA3*	intronic	c.1025-38	e7-38	tier3	20660	2558	2533	22	0.009	36371	5100	3330	1706	0.339	27372	2641	2634	3	0.000	37247	4754	4744	0	0.000	NA	NA	NA	NA	NA
476807	6	32007827	32007827	C	A	*CYP21A2*	missense	c.784	p.L262I	tier1	56872	7169	7050	100	0.014	57645	7513	4682	2714	0.367	27770	2414	2147	266	0.110	64531	8202	8185	0	0.000	NA	NA	NA	NA	NA
476807	7	77764563	77764563	C	T	*MAGI2*	intronic	c.2846-40	e17-40	tier3	16597	1964	1933	28	0.014	14620	2108	1336	747	0.359	10572	1613	1608	3	0.002	16791	1925	1916	0	0.000	NA	NA	NA	NA	NA
476807	7	92764778	92764778	A	C	*SAMD9L*	missense	c.507	p.D169E	tier1	9773	1101	1076	25	0.023	7547	965	588	376	0.390	8657	983	842	141	0.143	14316	1606	1602	0	0.000	NA	NA	NA	NA	NA
476807	7	100684392	100684392	C	T	*MUC17*	missense	c.9695	p.T3232M	tier1	21942	2929	2923	6	0.002	14823	2175	1808	363	0.167	8148	689	688	0	0.000	18481	2480	2473	1	0.000	NA	NA	NA	NA	NA
476807	8	74529737	74529737	T	C	*STAU2*	intronic	c.411-51	e4-51	tier3	8990	796	782	14	0.018	9486	1337	891	439	0.330	9873	1563	1430	132	0.085	14308	1665	1663	0	0.000	NA	NA	NA	NA	NA
476807	11	35016453	35016453	C	T	*PDHX*	splice_region	c.1248-8	e11-8	tier3	19559	2434	2364	62	0.026	22984	2969	1918	1035	0.350	21029	1969	1221	747	0.380	30761	3801	3798	0	0.000	NA	NA	NA	NA	NA
476807	11	93417105	93417105	C	T	*KIAA1731*	intronic	c.950-25	e8-25	tier3	23420	2145	2124	20	0.009	24692	2818	2486	319	0.114	32148	3885	3880	4	0.000	40371	4047	4041	0	0.000	NA	NA	NA	NA	NA
476807	12	53670353	53670353	G	A	*ESPL1*	intronic	c.1701-51	e7-51	tier3	4800	612	587	24	0.039	14189	1855	1085	756	0.411	5260	622	354	266	0.429	11486	1448	1448	0	0.000	NA	NA	NA	NA	NA
476807	12	114377861	114377861	G	T	*RBM19*	silent	c.1842	p.G614	tier1	12704	1730	1704	25	0.014	21714	3041	1822	1201	0.397	11847	1246	1116	130	0.104	18819	2343	2341	0	0.000	NA	NA	NA	NA	NA
476807	15	21071137	21071137	G	A	*POTEB2*	intronic	c.410+64	e1+64	tier3	7095	889	888	1	0.001	12431	2402	2262	133	0.056	3462	753	752	0	0.000	8141	885	882	0	0.000	NA	NA	NA	NA	NA
476807	15	38228468	38228468	A	G	*TMCO5A*	intronic	c.1-47	e1-47	tier3	7537	797	774	22	0.028	8280	1130	664	452	0.405	5345	623	408	212	0.342	7754	985	975	0	0.000	NA	NA	NA	NA	NA
476807	15	87097682	87097682	C	T	*AGBL1*	missense	c.2770	p.R924W	tier1	32486	3625	3616	5	0.001	22597	2704	2224	468	0.174	21328	2137	2135	1	0.000	27823	3139	3135	0	0.000	NA	NA	NA	NA	NA
476807	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	41534	4957	4873	79	0.016	31568	3824	2384	1399	0.370	16720	1578	1574	4	0.003	35221	3980	3966	2	0.000	NA	NA	NA	NA	NA
476807	17	9066111	9066111	T	C	*NTN1*	intronic	c.1019-19	e2-19	tier3	11743	1163	1137	21	0.018	6599	857	540	311	0.365	5330	616	611	3	0.005	11294	1183	1172	0	0.000	NA	NA	NA	NA	NA
476807	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	12077	1313	1290	23	0.018	16671	2214	1370	824	0.376	7622	855	759	96	0.112	19023	2309	2305	0	0.000	2	0	0	0	NA
476807	19	8654876	8654876	C	T	*ADAMTS10*	splice_site	c.1798-1	e14-1	tier1	23483	2892	2855	36	0.012	29023	3810	2539	1223	0.325	14836	1567	1564	2	0.000	27846	3420	3400	0	0.000	NA	NA	NA	NA	NA
476807	19	36321785	36321785	C	T	*NPHS1*	silent	c.3555	p.P1185	tier1	26668	2992	2966	25	0.008	23833	2886	1888	964	0.338	21965	2192	2184	4	0.000	32129	3716	3703	1	0.000	NA	NA	NA	NA	NA
476807	19	56303709	56303709	G	A	*NLRP11*	missense	c.2471	p.T824M	tier1	51492	7220	7176	38	0.005	38173	5820	5105	681	0.118	25560	2899	2895	1	0.000	43588	6245	6233	1	0.000	NA	NA	NA	NA	NA
476807	20	31531576	31531576	C	T	*EFCAB8*	5_prime_flanking_region	c.-16075	NULL	tier3	50713	6498	6418	76	0.012	40553	5279	3458	1759	0.337	33422	2918	2551	361	0.124	59421	7392	7373	1	0.000	NA	NA	NA	NA	NA
476807	20	48914916	48914916	G	T	*LOC284751*	rna	NULL	NULL	tier1	13761	1657	1635	19	0.011	20479	3267	2063	1179	0.364	14738	2398	2127	267	0.112	21055	2571	2568	0	0.000	NA	NA	NA	NA	NA
480109	2	55177887	55177887	C	T	*EML6*	missense	c.4184	p.A1395V	tier1	18431	2312	2299	11	0.005	17869	2205	1633	558	0.255	24312	3132	3127	2	0.000	21360	2493	2482	10	0.004	NA	NA	NA	NA	NA
480109	2	172951837	172951837	G	T	*DLX1*	3_prime_untranslated_region	c.*172951837	NULL	tier2	31735	4249	4218	27	0.006	35042	4146	2881	1208	0.295	26269	3538	3533	0	0.000	36974	4685	4661	20	0.004	NA	NA	NA	NA	NA
480109	4	106588612	106588612	T	C	*ARHGEF38*	missense	c.1900	p.Y634H	tier1	13062	1677	1664	10	0.006	16091	1998	1391	584	0.296	10947	1495	1494	0	0.000	15472	1844	1840	1	0.000	NA	NA	NA	NA	NA
480109	4	153784943	153784943	A	C	*ARFIP1*	intronic	c.202+77	e2+77	tier3	13012	1592	1588	2	0.001	9353	1040	815	222	0.214	18071	2428	2427	0	0.000	13355	1521	1519	2	0.000	NA	NA	NA	NA	NA
480109	5	38489182	38489182	G	T	*LIFR*	nonsense	c.2333	p.S778*	tier1	10376	1104	1099	3	0.003	11632	1291	1059	224	0.175	18387	2436	2428	3	0.000	19514	2351	2349	1	0.000	NA	NA	NA	NA	NA
480109	5	118834979	118834979	A	G	*HSD17B4*	intronic	c.973-33	e13-33	tier3	8934	1161	1155	2	0.002	6048	679	419	255	0.378	11079	1471	1469	0	0.000	11292	1203	1200	3	0.002	NA	NA	NA	NA	NA
480109	9	5073770	5073770	G	T	*JAK2*	missense	c.1849	p.V617F	tier1	20495	2432	2404	21	0.009	12016	1157	884	261	0.228	23086	3061	3054	4	0.000	18472	2059	2042	13	0.006	NA	NA	NA	NA	NA
480109	9	125282293	125282293	C	T	*OR1J4*	silent	c.874	p.L292	tier1	17992	2581	2553	23	0.009	16720	2058	1420	625	0.306	28299	3655	3649	4	0.000	21802	2787	2776	8	0.003	NA	NA	NA	NA	NA
480109	11	24927450	24927450	G	C	*LUZP2*	intronic	c.397-87	e6-87	tier3	2206	247	243	4	0.016	1953	225	159	66	0.293	2248	296	296	0	0.000	3439	354	353	0	0.000	NA	NA	NA	NA	NA
480109	11	65655168	65655168	C	T	*FIBP*	missense	c.314	p.R105Q	tier1	22536	3812	3792	19	0.005	23182	3440	2875	543	0.159	14543	2500	2497	1	0.000	27653	4326	4324	0	0.000	NA	NA	NA	NA	NA
480109	11	112071453	112071453	A	G	*BCO2*	missense	c.983	p.Q328R	tier1	4537	671	667	4	0.006	7366	895	633	258	0.290	8497	1329	1329	0	0.000	9817	1260	1252	5	0.004	NA	NA	NA	NA	NA
480109	12	6701122	6701122	T	C	*CHD4*	missense	c.3050	p.K1017R	tier1	16854	2578	2563	13	0.005	18008	2478	2065	396	0.161	21270	3185	3184	0	0.000	27477	4079	4072	1	0.000	NA	NA	NA	NA	NA
480109	12	40689290	40689290	G	C	*LRRK2*	missense	c.2940	p.E980D	tier1	2238	354	351	3	0.008	2658	450	319	128	0.286	923	182	181	0	0.000	2935	384	382	2	0.000	NA	NA	NA	NA	NA
480109	12	122983394	122983394	C	T	*ZCCHC8*	silent	c.222	p.L74	tier1	5441	0	0	0	0.000	7933	763	714	48	0.063	9425	1259	1258	1	0.000	8187	962	961	1	0.000	NA	NA	NA	NA	NA
480109	14	21862072	21862072	C	T	*CHD8*	missense	c.5882	p.R1961H	tier1	13050	1660	1648	11	0.007	9585	1195	976	212	0.178	13655	1768	1764	4	0.000	14557	1900	1898	1	0.000	NA	NA	NA	NA	NA
480109	16	32956973	32956973	G	T	*ENSG00000260921*	5_prime_flanking_region	c.-49885	NULL	tier3	117	0	0	0	0.000	13850	1538	1357	172	0.112	3919	502	502	0	0.000	10611	1433	1406	7	0.005	NA	NA	NA	NA	NA
480109	16	57935363	57935363	G	C	*CNGB1*	intronic	c.2893-24	e28-24	tier3	20080	2893	2866	23	0.008	32411	4167	2920	1196	0.291	15124	2237	2233	0	0.000	32525	4146	4125	9	0.002	NA	NA	NA	NA	NA
480109	17	7577114	7577114	C	T	*TP53*	missense	c.824	p.C275Y	tier1	6627	891	884	7	0.008	29772	3252	2228	969	0.303	35335	4402	4398	1	0.000	34666	4224	4205	17	0.004	NA	NA	NA	NA	NA
480109	17	16829225	16829225	A	C	*TBC1D27*	rna	NULL	NULL	tier1	14533	1835	1808	17	0.009	22259	2907	2020	849	0.296	13146	1726	1722	0	0.000	25426	3426	3402	12	0.004	NA	NA	NA	NA	NA
480109	20	43744353	43744353	G	C	*KCNS1*	5_prime_flanking_region	c.-16476	NULL	tier3	17097	2199	2181	12	0.005	12265	1480	1060	409	0.278	9289	1256	1248	3	0.000	11812	1343	1339	1	0.000	NA	NA	NA	NA	NA
480109	22	42046726	42046726	G	C	*XRCC6*	splice_site	c.961-1	e7-1	tier1	10317	1251	1246	5	0.004	38381	4790	3277	1432	0.304	24900	3636	3632	1	0.000	42340	5610	5577	29	0.005	NA	NA	NA	NA	NA
480109	X	8538673	8538673	G	T	*KAL1*	missense	c.929	p.T310N	tier1	32424	4644	4595	41	0.009	27279	3428	2490	904	0.266	14560	1941	1940	1	0.000	20081	2698	2671	24	0.009	NA	NA	NA	NA	NA
480109	X	153042601	153042601	A	G	*PLXNB3*	intronic	c.4997-62	e29-62	tier3	23388	2911	2884	16	0.006	26101	3067	2187	850	0.280	8532	1125	1124	0	0.000	16081	1873	1854	12	0.006	NA	NA	NA	NA	NA
481668	1	16262371	16262371	C	T	*SPEN*	silent	c.9636	p.A3212	tier1	4149	487	485	2	0.004	12052	1306	966	335	0.257	13158	1417	1100	310	0.220	39058	4930	4921	0	0.000	28331	3571	3569	2	0.000
481668	1	17256868	17256868	G	A	*CROCC*	intronic	c.683+26	e6+26	tier3	7366	646	641	5	0.008	6371	544	464	78	0.144	7390	608	545	60	0.099	15916	1607	1605	0	0.000	12555	1313	1311	1	0.000
481668	1	46724275	46724275	A	G	*RAD54L*	intronic	c.211-83	e4-83	tier3	3787	358	355	3	0.008	4250	487	350	131	0.272	4774	457	353	103	0.226	6873	691	686	0	0.000	7793	992	991	0	0.000
481668	1	46724283	46724283	A	C	*RAD54L*	intronic	c.211-75	e4-75	tier3	3773	350	345	3	0.009	4263	477	341	133	0.281	4682	450	347	102	0.227	6779	674	671	0	0.000	7629	969	969	0	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
481668	1	46724289	46724289	A	G	*RAD54L*	intronic	c.211-69	e4-69	tier3	3728	352	348	3	0.009	4127	467	333	129	0.279	4663	442	341	100	0.227	6618	663	660	0	0.000	7398	958	953	0	0.000
481668	1	46724300	46724300	A	C	*RAD54L*	intronic	c.211-58	e4-58	tier3	3721	348	345	3	0.009	3860	409	290	114	0.282	4346	408	317	91	0.223	6286	634	629	0	0.000	6955	874	871	0	0.000
481668	1	152382172	152382172	G	T	*CRNN*	silent	c.1386	p.T462	tier1	3656	699	673	26	0.037	4598	845	495	347	0.412	3837	682	429	251	0.369	7407	1549	1542	0	0.000	6010	1393	1393	0	0.000
481668	1	182827980	182827980	A	G	*DHX9*	missense	c.1013	p.N338S	tier1	13613	1470	1424	38	0.026	11084	1197	635	554	0.466	12071	1209	753	441	0.369	24757	3098	3090	0	0.000	21291	2749	2744	0	0.000
481668	1	247094587	247094587	T	C	*AHCTF1*	5_prime_untranslated_region	c.-59	NULL	tier2	8842	960	946	10	0.010	9923	1202	946	250	0.209	11692	1277	1010	252	0.200	11538	1532	1526	0	0.000	16834	2591	2576	0	0.000
481668	2	1457512	1457512	C	G	*TPO*	missense	c.529	p.L177V	tier1	5765	702	697	4	0.006	6019	713	552	157	0.221	6186	692	562	128	0.186	9818	1206	1204	0	0.000	12114	2003	2003	0	0.000
481668	2	98853198	98853198	A	G	*VWA3B*	rna	NULL	NULL	tier1	5984	1092	1074	16	0.015	6090	1039	745	290	0.280	5740	941	734	207	0.220	9855	1695	1694	0	0.000	10850	0	0	0	NA
481668	4	95223388	95223388	A	G	*HPGDS*	missense	c.344	p.M115T	tier1	12213	1137	1122	15	0.013	11031	1005	745	252	0.253	12423	1090	887	199	0.183	26792	2858	2851	0	0.000	22357	2518	2516	0	0.000
481668	5	40959580	40959580	T	C	*C7*	missense	c.1519	p.S507P	tier1	7747	819	809	10	0.012	7204	885	667	210	0.239	8286	866	706	159	0.184	18259	2312	2310	0	0.000	16683	2352	2349	0	0.000
481668	6	31760727	31760727	G	C	*VARS*	5_prime_untranslated_region	c.-31760727	NULL	tier3	24956	2944	2901	35	0.012	20786	2318	1680	611	0.267	23466	2570	1914	629	0.247	43507	5492	5491	0	0.000	48077	6563	6556	0	0.000
481668	6	135513482	135513482	A	G	*MYB*	missense	c.548	p.N183S	tier1	35587	3818	3791	18	0.005	26391	2634	2017	591	0.227	34159	3561	2856	685	0.193	76034	9071	9057	0	0.000	57160	7122	7118	0	0.000
481668	7	34118627	34118627	C	T	*BMPER*	missense	c.1237	p.R413C	tier1	14570	1549	1549	0	0.000	11823	1351	1303	44	0.033	12466	1281	1227	48	0.038	21312	2525	2522	0	0.000	28573	3860	3857	2	0.000
481668	7	81593304	81593304	T	G	*CACNA2D1*	intronic	c.2816+68	e34+68	tier3	1705	109	109	0	0.000	2205	196	141	53	0.273	2172	170	128	42	0.247	3870	330	329	0	0.000	3117	0	0	0	NA
481668	7	100635373	100635373	C	A	*MUC12*	missense	c.1529	p.A510D	tier1	2463	396	392	4	0.010	4026	708	608	96	0.136	3048	458	401	56	0.123	3012	478	478	0	0.000	3124	688	688	0	0.000
481668	7	148506166	148506166	T	A	*EZH2*	missense	c.2192	p.Y731F	tier1	8451	912	903	6	0.007	8077	890	667	213	0.242	9517	923	727	191	0.208	18595	2258	2248	0	0.000	18191	2380	2378	0	0.000
481668	9	117138957	117138957	C	T	*AKNA*	missense	c.1130	p.R377H	tier1	22983	2341	2339	0	0.000	28470	2718	2683	31	0.011	33291	3187	3146	36	0.011	61527	6990	6987	1	0.000	51395	6372	6365	1	0.000
481668	10	128933807	128933807	T	C	*FAM196A*	3_prime_untranslated_region	c.*2294	NULL	tier3	21752	2267	2260	4	0.002	14782	1446	1037	402	0.279	17718	1730	1335	374	0.219	41494	4873	4871	0	0.000	35598	4377	4365	0	0.000
481668	10	133761131	133761131	G	T	*PPP2R2D*	missense	c.825	p.M275I	tier1	10710	988	970	17	0.017	10104	1020	715	289	0.288	11101	961	745	202	0.213	16775	1728	1717	0	0.000	18919	2252	2246	0	0.000
481668	11	71903432	71903432	A	G	*FOLR1*	intronic	c.168+47	e1+47	tier3	14145	1616	1592	21	0.013	11382	1245	938	302	0.244	13164	1428	1148	272	0.192	31410	3880	3875	0	0.000	26207	3615	3609	0	0.000
481668	12	21608977	21608977	G	T	*PYROXD1*	missense	c.698	p.S233I	tier1	5224	530	528	2	0.004	4079	411	310	101	0.246	4963	511	393	114	0.225	11108	1256	1255	0	0.000	7277	0	0	0	NA
481668	12	113599210	113599210	C	A	*DDX54*	rna	NULL	NULL	tier1	20029	2240	2213	24	0.011	13203	1300	974	316	0.245	15970	1689	1421	260	0.155	43807	5340	5338	0	0.000	33543	4263	4263	0	0.000
481668	13	33223009	33223009	C	T	*PDS5B*	nonsense	c.100	p.R34*	tier1	16363	1781	1779	2	0.001	12157	1188	927	251	0.213	14519	1510	1322	180	0.120	34218	4018	4016	0	0.000	25116	3035	3032	0	0.000
481668	15	56704519	56704519	G	A	*TEX9*	missense	c.848	p.R283K	tier1	2211	293	280	9	0.031	1985	289	210	76	0.266	2392	295	233	58	0.199	3371	475	474	0	0.000	3742	651	640	0	0.000
481668	16	30456662	30456662	C	T	*SEPHS2*	silent	c.216	p.G72	tier1	12494	1355	1353	2	0.001	13959	1454	1178	269	0.186	16910	1703	1432	263	0.155	43178	5513	5510	0	0.000	38962	5225	5222	0	0.000
481668	17	1559855	1559855	T	C	*PRPF8*	missense	c.5624	p.H1875R	tier1	15946	1834	1797	34	0.019	16758	1956	1420	510	0.264	19459	2136	1660	450	0.213	31923	4209	4197	0	0.000	34447	4901	4898	0	0.000
481668	17	37425012	37425012	A	G	*FBXL20*	intronic	c.933+68	e12+68	tier3	10846	1172	1165	7	0.006	10269	1198	982	211	0.177	10353	1111	989	120	0.108	28442	3479	3474	0	0.000	15377	2154	2153	0	0.000
481668	17	37879957	37879957	C	T	*ERBB2*	intronic	c.2208+44	e18+44	tier3	5212	521	520	0	0.000	6237	677	512	159	0.237	6555	617	498	115	0.188	13991	1512	1504	0	0.000	14415	1838	1837	1	0.000
481668	19	9067438	9067438	C	T	*MUC16*	missense	c.20008	p.V6670I	tier1	19427	2262	2245	15	0.007	19226	2052	1714	324	0.159	21888	2334	1986	340	0.146	30956	3817	3813	0	0.000	34532	4457	4456	0	0.000
481668	19	15219913	15219913	C	G	*SYDE1*	silent	c.135	p.P45	tier1	4176	377	368	8	0.021	5572	568	342	223	0.395	5464	497	328	166	0.336	7978	724	721	1	0.000	9781	1307	1306	0	0.000
485523	4	39474726	39474726	G	A	*LIAS*	missense	c.961	p.E321K	tier1	3132	0	0	0	0.000	2170	258	246	12	0.047	1363	116	115	1	0.000	1319	141	141	0	0.000	3714	578	576	2	0.000
485523	4	55976980	55976980	G	A	*KDR*	intronic	c.977-45	e8-45	tier3	10736	1448	1448	0	0.000	6523	861	808	48	0.056	5751	648	645	2	0.000	4205	454	454	0	0.000	13940	2116	2116	0	0.000
485523	5	176939370	176939370	C	T	*DDX41*	missense	c.1574	p.R525H	tier1	15143	1773	1771	2	0.001	9232	1070	965	101	0.095	6583	566	558	3	0.000	5809	622	621	0	0.000	17630	2449	2439	5	0.000
485523	6	73904728	73904728	A	T	*KCNQ5*	missense	c.2420	p.N807I	tier1	4057	669	668	0	0.000	3091	499	451	46	0.093	517	55	54	0	0.000	536	52	52	0	0.000	2353	568	567	0	0.000
485523	14	24517447	24517447	G	A	*DHRS4L1*	rna	NULL	NULL	tier1	16574	1653	1652	0	0.000	12727	1385	1281	99	0.072	8756	776	773	2	0.000	7359	814	813	0	0.000	23426	3123	3117	2	0.000
485523	15	75706652	75706652	C	T	*SIN3A*	missense	c.367	p.V123M	tier1	18578	2034	2033	1	0.000	10359	956	884	67	0.070	7976	659	657	1	0.000	8994	935	935	0	0.000	26905	3326	3320	3	0.000
485523	18	47462642	47462642	G	A	*MYO5B*	silent	c.1983	p.N661	tier1	30820	4342	4339	1	0.000	19168	2449	2251	189	0.077	12579	1392	1378	11	0.008	11197	1485	1481	2	0.000	35643	5349	5344	3	0.000
485523	19	7805616	7805616	G	C	*CD209*	3_prime_untranslated_region	c.*2309	NULL	tier3	23867	2928	2928	0	0.000	11672	1256	1228	27	0.022	12178	1241	1238	1	0.000	10998	1328	1323	2	0.000	38242	4856	4848	2	0.000
489196	1	1871145	1871145	G	A	*C1orf222*	missense	c.614	p.P205L	tier1	34401	4744	4713	29	0.006	23253	3172	1667	1474	0.469	NA	NA	NA	NA	NA	59604	8730	8705	19	0.002	42642	6498	6493	0	0.000
489196	1	116386058	116386058	C	T	*NHLH2*	5_prime_untranslated_region	c.-5065	NULL	tier4	1716	121	120	1	0.008	2196	233	177	56	0.240	NA	NA	NA	NA	NA	3850	412	412	0	0.000	3393	323	323	0	0.000
489196	1	248651829	248651829	A	T	*OR2G6*	5_prime_flanking_region	c.-33119	NULL	tier3	23017	2650	2639	8	0.003	25844	3025	2454	544	0.181	NA	NA	NA	NA	NA	59089	7667	7655	4	0.001	47650	6078	6072	0	0.000
489196	2	172930961	172930961	A	G	*METAP1D*	intronic	c.498-31	e5-31	tier3	9381	873	870	3	0.003	9646	1055	736	302	0.291	NA	NA	NA	NA	NA	13737	1730	1723	4	0.002	13755	1627	1626	0	0.000
489196	2	178483636	178483636	C	T	*TTC30A*	5_prime_untranslated_region	c.-207	NULL	tier2	15422	1790	1784	5	0.003	10553	1153	784	361	0.315	NA	NA	NA	NA	NA	29428	3780	3773	4	0.001	21122	2634	2634	0	0.000
489196	2	196863801	196863801	G	T	*DNAH7*	3_prime_untranslated_region	c.*13	NULL	tier4	16104	1886	1876	9	0.005	15440	1761	1263	479	0.275	NA	NA	NA	NA	NA	32944	4230	4223	5	0.001	25011	3219	3218	0	0.000
489196	2	219501054	219501054	C	T	*PLCD4*	silent	c.2121	p.D707	tier1	1407	147	146	1	0.007	2236	327	229	97	0.298	NA	NA	NA	NA	NA	1617	155	154	0	0.000	1478	0	0	0	NA
489196	2	233407276	233407276	C	T	*CHRNG*	intronic	c.604+46	e6+46	tier3	29710	3482	3467	13	0.004	21876	2582	1612	948	0.370	NA	NA	NA	NA	NA	50293	6631	6619	10	0.002	46026	5672	5672	0	0.000
489196	3	77607305	77607305	G	A	*ROBO2*	splice_region	c.1437+5	e9+5	tier3	13480	1285	1283	2	0.002	12045	1201	960	233	0.195	NA	NA	NA	NA	NA	25611	3089	3081	2	0.000	18314	2013	2011	0	0.000
489196	3	113327118	113327118	G	T	*SIDT1*	intronic	c.1602+54	e16+54	tier3	14757	1786	1770	13	0.007	13582	1807	1280	509	0.285	NA	NA	NA	NA	NA	24564	3403	3394	6	0.002	17913	2459	2457	0	0.000
489196	5	32135733	32135733	A	G	*GOLPH3*	silent	c.417	p.H139	tier1	15550	1674	1673	1	0.001	13131	1371	1181	179	0.132	NA	NA	NA	NA	NA	29394	3632	3625	3	0.001	23013	0	0	0	NA
489196	5	122713937	122713937	G	A	*CEP120*	intronic	c.2196+93	e15+93	tier4	9522	1044	1041	3	0.003	8152	904	760	138	0.154	NA	NA	NA	NA	NA	16068	2045	2042	1	0.000	13527	1679	1679	0	0.000
489196	5	140768657	140768657	A	T	*PCDHGB4*	missense	c.1206	p.L402F	tier1	11454	1504	1498	6	0.004	12047	1785	1284	481	0.273	NA	NA	NA	NA	NA	13963	2015	2014	1	0.000	14706	2342	2341	0	0.000
489196	6	2623069	2623069	C	T	*C6orf195*	3_prime_untranslated_region	c.*604	NULL	tier3	16317	1977	1973	2	0.001	16077	2115	1504	588	0.281	NA	NA	NA	NA	NA	20612	2866	2859	2	0.000	20449	3052	3046	1	0.000
489196	6	36685089	36685089	G	A	*RAB44*	missense	c.215	p.R72K	tier1	31676	3387	3360	27	0.008	22514	2442	1776	635	0.263	NA	NA	NA	NA	NA	47718	6097	6090	3	0.000	41443	0	0	0	NA
489196	6	112671088	112671088	G	T	*RFPL4B*	missense	c.178	p.A60S	tier1	18208	2164	2156	6	0.003	13938	1458	1045	400	0.277	NA	NA	NA	NA	NA	35899	4582	4573	6	0.001	26180	3229	3226	0	0.000
489196	6	143094282	143094282	C	T	*HIVEP2*	missense	c.1594	p.E532K	tier1	16348	1932	1924	5	0.003	13050	1684	1276	400	0.239	NA	NA	NA	NA	NA	30102	4074	4069	4	0.001	20944	2786	2786	0	0.000
489196	7	23625386	23625386	G	A	*ENSG00000232553*	5_prime_untranslated_region	c.-23625386	NULL	tier2	34247	4479	4438	37	0.008	19904	2485	1472	997	0.404	NA	NA	NA	NA	NA	60502	8007	7987	14	0.002	56155	7421	7419	1	0.000
489196	8	1857452	1857452	T	A	*ARHGEF10*	splice_region	c.2043-9	e18-9	tier3	16253	2034	2024	9	0.004	11770	1517	1089	420	0.278	NA	NA	NA	NA	NA	23971	3374	3361	9	0.003	22728	3132	3128	0	0.000
489196	8	87519260	87519260	T	C	*RMDN1*	missense	c.211	p.I71V	tier1	6605	664	663	1	0.002	7693	853	603	245	0.289	NA	NA	NA	NA	NA	12404	1430	1427	2	0.000	10255	1222	1221	0	0.000
489196	8	126011647	126011647	T	C	*SQLE*	missense	c.2	p.M1T	tier1	12462	1228	1223	4	0.003	10679	1094	750	336	0.309	NA	NA	NA	NA	NA	16966	1950	1939	4	0.002	16574	1894	1892	0	0.000
489196	9	127300323	127300323	G	C	*NR6A1*	intronic	c.824+48	e6+48	tier3	12251	1458	1444	13	0.009	12931	1836	1269	544	0.300	NA	NA	NA	NA	NA	20280	2790	2783	6	0.002	15711	2357	2356	0	0.000
489196	10	23326305	23326305	G	A	*ARMC3*	missense	c.2516	p.G839E	tier1	13801	1380	1376	4	0.003	8999	1119	883	228	0.205	NA	NA	NA	NA	NA	9272	1111	1109	1	0.000	15911	1917	1914	0	0.000
489196	10	79797037	79797037	A	G	*RPS24*	missense	c.365	p.K122R	tier1	4466	421	420	1	0.002	5508	644	464	177	0.276	NA	NA	NA	NA	NA	7542	930	930	0	0.000	6893	818	818	0	0.000
489196	11	20676288	20676288	G	A	*SLC6A5*	silent	c.2268	p.P756	tier1	15922	2332	2323	8	0.003	18264	2527	1808	698	0.279	NA	NA	NA	NA	NA	41288	6155	6138	13	0.002	29983	4507	4504	0	0.000
489196	11	46400551	46400551	T	A	*DGKZ*	missense	c.2993	p.L998Q	tier1	8970	1109	1098	11	0.010	7588	913	618	288	0.318	NA	NA	NA	NA	NA	14666	1886	1877	7	0.004	13033	1762	1760	0	0.000
489196	11	48454279	48454279	G	A	*OR4C10P*	5_prime_untranslated_region	c.-48454279	NULL	tier3	36722	5012	5001	10	0.002	25074	3308	2501	773	0.236	NA	NA	NA	NA	NA	52647	7373	7353	11	0.001	43620	6044	6041	0	0.000
489196	11	56000330	56000330	C	T	*OR5T2*	missense	c.332	p.C111Y	tier1	6615	668	665	3	0.004	9239	1155	819	328	0.286	NA	NA	NA	NA	NA	11981	1358	1352	3	0.002	12077	1495	1494	0	0.000
489196	12	9007449	9007449	T	C	*A2ML1*	intronic	c.2764+22	e22+22	tier3	21531	2774	2764	8	0.003	13572	1595	1126	452	0.286	NA	NA	NA	NA	NA	30163	4090	4069	4	0.001	27580	3612	3608	0	0.000
489196	12	52946663	52946663	C	T	*KRT71*	missense	c.199	p.G67R	tier1	21853	2434	2429	3	0.001	14597	1586	1240	337	0.214	NA	NA	NA	NA	NA	19872	2473	2467	5	0.002	29039	3513	3511	0	0.000
489196	12	54686621	54686621	C	T	*NFE2*	missense	c.659	p.G220E	tier1	15878	2270	2257	13	0.006	12798	1831	1231	582	0.321	NA	NA	NA	NA	NA	26664	3727	3718	5	0.001	19820	3118	3118	0	0.000
489196	12	56110725	56110725	A	G	*BLOC1S1*	missense	c.154	p.R52G	tier1	12197	1494	1489	4	0.003	11709	1557	1095	451	0.292	NA	NA	NA	NA	NA	15075	2053	2049	0	0.000	16476	2398	2393	0	0.000
489196	13	28009534	28009534	T	C	*GTF3A*	intronic	c.567-36	e6-36	tier3	22439	2529	2518	11	0.004	17324	2012	1417	577	0.289	NA	NA	NA	NA	NA	36702	4698	4694	3	0.001	32667	4215	4215	0	0.000
489196	14	59670661	59670661	G	T	*DAAM1*	intronic	c.1+15175	e0+15175	tier3	23767	2606	2600	6	0.002	19050	2079	1490	568	0.276	NA	NA	NA	NA	NA	45298	5673	5658	8	0.001	32789	4005	4003	0	0.000
489196	14	106945697	106945697	G	A	*LINC00221*	intronic	c.NULL	NULL	tier3	11546	1404	1397	6	0.004	12909	1773	1290	468	0.266	NA	NA	NA	NA	NA	14659	2019	2006	4	0.000	12436	1766	1763	1	0.000
489196	15	20457242	20457242	C	T	*ENSG00000258628*	5_prime_untranslated_region	c.-20457242	NULL	tier3	44850	5066	5052	9	0.002	36153	3990	3681	286	0.072	NA	NA	NA	NA	NA	45044	5688	5678	2	0.000	50746	6198	6196	1	0.000
489196	15	66191080	66191080	T	A	*MEGF11*	missense	c.2960	p.N987I	tier1	14795	1630	1625	4	0.002	15927	2110	1503	579	0.278	NA	NA	NA	NA	NA	16202	2079	2078	1	0.000	20266	2785	2782	0	0.000
489196	16	57712000	57712000	G	T	*GPR97*	intronic	c.346-82	e4-82	tier3	16178	2139	2132	5	0.002	14150	1865	1389	466	0.251	NA	NA	NA	NA	NA	22832	3029	3023	5	0.000	22817	3167	3163	1	0.000
489196	16	66956068	66956068	G	A	*RRAD*	missense	c.838	p.R280C	tier1	28961	3695	3657	34	0.009	27811	3682	2502	1131	0.311	NA	NA	NA	NA	NA	42261	5984	5961	16	0.003	42644	6074	6067	1	0.000
489196	17	976071	976071	C	T	*ABR*	intronic	c.754-77	e8-77	tier3	13299	1460	1458	2	0.001	8419	837	573	258	0.310	NA	NA	NA	NA	NA	25080	3131	3127	2	0.000	16133	1876	1875	0	0.000
489196	17	43185926	43185926	G	A	*NMT1*	3_prime_untranslated_region	c.*2919	NULL	tier3	12740	1599	1594	3	0.002	14633	1896	1474	401	0.214	NA	NA	NA	NA	NA	37204	5148	5137	3	0.001	25490	3570	3568	0	0.000
489196	18	28971008	28971008	C	T	*DSG4*	intronic	c.685-33	e7-33	tier3	4489	308	307	0	0.000	6617	661	496	162	0.246	NA	NA	NA	NA	NA	10376	1072	1068	2	0.000	9407	918	916	0	0.000
489196	19	40589158	40589158	C	T	*ZNF780A*	intronic	c.10-14	e2-14	tier3	35700	4243	4226	14	0.003	27601	3206	2295	866	0.274	NA	NA	NA	NA	NA	55468	7222	7193	16	0.002	47919	6175	6168	0	0.000
489196	19	43920107	43920107	C	T	*TEX101*	silent	c.90	p.L30	tier1	17241	2035	2031	3	0.001	16270	1970	1360	590	0.303	NA	NA	NA	NA	NA	24794	3421	3409	2	0.000	23937	3201	3197	0	0.000
489196	20	9496180	9496180	G	T	*LAMP5*	missense	c.145	p.V49L	tier1	20857	3634	3614	18	0.005	20979	3230	2297	905	0.283	NA	NA	NA	NA	NA	32664	5249	5236	9	0.002	24558	4273	4271	0	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
489196	21	45820168	45820168	C	T	*TRPM2*	silent	c.2235	p.G745	tier1	34108	4082	4056	22	0.005	34778	4093	2798	1222	0.304	NA	NA	NA	NA	NA	75462	10316	10286	12	0.001	54985	7242	7236	0	0.000
489196	22	46677825	46677825	G	A	*TTC38*	intronic	c.561+210	e6+210	tier3	34260	4122	4102	16	0.004	26194	2932	2248	660	0.227	NA	NA	NA	NA	NA	73321	9718	9703	6	0.001	46987	5789	5785	0	0.000
489196	X	73041567	73041567	C	T	*XIST*	rna	NULL	NULL	tier1	11895	1242	1230	10	0.008	9624	973	706	265	0.273	NA	NA	NA	NA	NA	13631	1661	1654	6	0.004	8642	995	994	1	0.000
489196	X	153049418	153049418	C	G	*SRPK3*	intronic	c.908-11	e10-11	tier3	5196	437	435	2	0.005	4626	478	332	143	0.301	NA	NA	NA	NA	NA	3137	347	345	2	0.000	3545	393	393	0	0.000
489196	X	153799950	153799950	G	A	*G6PD*	5_prime_flanking_region	c.-25580	NULL	tier3	11537	1214	1213	0	0.000	9553	1134	1084	35	0.031	NA	NA	NA	NA	NA	10962	1440	1424	0	0.000	11745	1444	1439	0	0.000
489513	1	173684860	173684860	A	G	*KLHL20*	intronic	c.1-282	e1-282	tier2	7687	1062	1032	29	0.027	3661	447	219	227	0.509	NA	NA	NA	NA	NA	3526	670	666	4	0.006	NA	NA	NA	NA	NA
489513	1	240351440	240351440	T	C	*FMN2*	intronic	c.1931-67	e4-67	tier3	1690	178	176	2	0.011	942	82	36	46	0.561	NA	NA	NA	NA	NA	2941	393	384	9	0.023	NA	NA	NA	NA	NA
489513	3	42735190	42735190	C	T	*HHATL*	nonsense	c.1167	p.W389*	tier1	42803	6640	6483	147	0.022	15733	2200	1175	1001	0.460	NA	NA	NA	NA	NA	39384	5362	5286	68	0.013	NA	NA	NA	NA	NA
489513	3	46792243	46792243	C	T	*PRSS50*	intronic	c.1-2102	e1-2102	tier2	2747	488	473	15	0.031	1107	163	100	62	0.383	NA	NA	NA	NA	NA	1506	306	303	3	0.010	NA	NA	NA	NA	NA
489513	3	53844274	53844274	C	T	*CACNA1D*	silent	c.6201	p.F2067	tier1	41736	5111	4999	105	0.021	17998	1858	1010	823	0.449	NA	NA	NA	NA	NA	42641	5681	5590	72	0.013	NA	NA	NA	NA	NA
489513	4	152498539	152498539	G	A	*FAM160A1*	intronic	c.106-63	e2-63	tier3	18260	2039	1984	52	0.026	7899	824	443	374	0.458	NA	NA	NA	NA	NA	10697	1601	1578	19	0.012	NA	NA	NA	NA	NA
489513	5	20304957	20304957	G	T	*ENSG00000214132*	5_prime_untranslated_region	c.-20304957	NULL	tier3	3140	609	601	8	0.013	2086	339	191	146	0.433	NA	NA	NA	NA	NA	3159	738	730	7	0.009	NA	NA	NA	NA	NA
489513	5	137680472	137680472	T	C	*FAM53C*	intronic	c.137-42	e3-42	tier4	5474	558	547	10	0.018	2653	220	124	95	0.434	NA	NA	NA	NA	NA	2757	365	362	3	0.008	NA	NA	NA	NA	NA
489513	6	41011404	41011404	G	T	*TSPO2*	silent	c.282	p.L94	tier1	11098	2070	2003	64	0.031	6397	997	553	441	0.444	NA	NA	NA	NA	NA	8035	1795	1781	13	0.007	NA	NA	NA	NA	NA
489513	7	131844359	131844359	G	C	*PLXNA4*	missense	c.4533	p.N1511K	tier1	24100	2980	2902	76	0.026	11137	1173	659	502	0.432	NA	NA	NA	NA	NA	24642	3512	3457	47	0.013	NA	NA	NA	NA	NA
489513	8	56367730	56367730	C	T	*XKR4*	intronic	c.1007-68110	e3-68110	tier2	14043	1674	1627	47	0.028	5091	474	268	205	0.433	NA	NA	NA	NA	NA	17876	2343	2320	17	0.007	NA	NA	NA	NA	NA
489513	9	16215272	16215272	C	T	*C9orf92*	missense	c.196	p.G66R	tier1	41132	5051	4945	100	0.020	12803	1316	754	549	0.421	NA	NA	NA	NA	NA	27768	3830	3790	32	0.008	NA	NA	NA	NA	NA
489513	9	32974446	32974446	C	T	*APTX*	splice_region	c.916+10	e7+10	tier3	5780	577	569	8	0.014	4635	423	234	187	0.444	NA	NA	NA	NA	NA	12127	1671	1649	17	0.010	NA	NA	NA	NA	NA
489513	9	101798470	101798470	G	C	*COL15A1*	missense	c.2308	p.G770R	tier1	13774	1387	1357	27	0.020	5729	537	284	248	0.466	NA	NA	NA	NA	NA	5617	778	762	14	0.018	NA	NA	NA	NA	NA
489513	9	136402651	136402651	G	A	*ADAMTSL2*	missense	c.542	p.R181Q	tier1	54189	7103	6931	157	0.022	18674	2142	1309	805	0.381	NA	NA	NA	NA	NA	44383	6365	6318	41	0.006	NA	NA	NA	NA	NA
489513	10	48373412	48373412	G	A	*ZNF488*	3_prime_untranslated_region	c.*1857	NULL	tier3	3512	641	618	22	0.034	1407	214	118	96	0.449	NA	NA	NA	NA	NA	1268	264	262	2	0.000	NA	NA	NA	NA	NA
489513	10	87615842	87615842	G	A	*GRID1*	missense	c.1057	p.R353W	tier1	23954	3097	3094	2	0.001	10954	1260	1204	49	0.039	NA	NA	NA	NA	NA	20858	3054	3041	2	0.000	NA	NA	NA	NA	NA
489513	12	130883190	130883190	C	A	*RIMBP2*	3_prime_untranslated_region	c.*490	NULL	tier3	4458	545	535	10	0.018	6367	710	404	297	0.424	NA	NA	NA	NA	NA	9049	1279	1263	14	0.011	NA	NA	NA	NA	NA
489513	15	97634474	97634474	A	G	*ENSG00000215948*	3_prime_flanking_region	c.*18	NULL	tier4	18333	2225	2172	51	0.023	6681	641	372	265	0.416	NA	NA	NA	NA	NA	17743	2529	2500	24	0.010	NA	NA	NA	NA	NA
489513	17	78180746	78180746	C	T	*SGSH*	rna	NULL	NULL	tier1	56063	7291	7156	123	0.017	16485	1730	951	754	0.442	NA	NA	NA	NA	NA	57883	7469	7371	85	0.011	NA	NA	NA	NA	NA
489513	18	72113811	72113811	C	G	*FAM69C*	intronic	c.876+30	e2+30	tier3	22786	3096	3027	65	0.021	9806	1085	602	469	0.438	NA	NA	NA	NA	NA	20954	3102	3053	42	0.014	NA	NA	NA	NA	NA
489513	19	40834389	40834389	C	T	*C19orf47*	missense	c.481	p.D161N	tier1	58706	7545	7359	172	0.023	20482	2078	1112	930	0.455	NA	NA	NA	NA	NA	51235	6581	6471	96	0.015	NA	NA	NA	NA	NA
489513	19	59081697	59081697	G	A	*MZF1*	5_prime_untranslated_region	c.-59081697	NULL	tier3	8951	1997	1910	83	0.042	3245	570	47	522	0.917	NA	NA	NA	NA	NA	2154	532	520	11	0.021	NA	NA	NA	NA	NA
489513	20	18772588	18772588	G	A	*LINC00652*	rna	NULL	NULL	tier1	23487	3150	3069	76	0.024	13692	1603	864	721	0.455	NA	NA	NA	NA	NA	27964	4395	4325	60	0.014	NA	NA	NA	NA	NA
489513	21	31964779	31964779	C	T	*KRTAP6-3*	5_prime_untranslated_region	c.-7	NULL	tier3	20233	2641	2574	67	0.025	15439	1508	837	653	0.438	NA	NA	NA	NA	NA	40721	5091	5022	60	0.012	NA	NA	NA	NA	NA
489513	21	44524456	44524456	G	T	*U2AF1*	missense	c.101	p.S34Y	tier1	12826	1791	1765	24	0.013	4167	535	318	215	0.403	NA	NA	NA	NA	NA	15729	2277	2264	13	0.006	NA	NA	NA	NA	NA
489513	X	118215369	118215369	G	A	*KIAA1210*	missense	c.5053	p.P1685S	tier1	4732	565	538	26	0.046	2442	275	17	256	0.938	NA	NA	NA	NA	NA	4732	673	657	16	0.024	NA	NA	NA	NA	NA
491309	17	7577580	7577580	T	C	*TP53*	missense	c.701	p.Y234C	tier1	24823	3109	3103	2	0.001	48885	5769	5602	138	0.024	65674	8304	7619	641	0.078	109990	14706	14602	80	0.005	NA	NA	NA	NA	NA
491309	19	16629981	16629981	C	T	*CHERP*	missense	c.2740	p.E914K	tier1	9280	1125	1121	4	0.004	16539	2098	1986	105	0.050	18651	2178	2121	54	0.025	23755	2963	2952	7	0.002	NA	NA	NA	NA	NA
496321	1	986249	986249	C	T	*AGRN*	intronic	c.5253+32	e30+32	tier2	6395	552	517	35	0.063	8718	816	416	392	0.485	6467	722	719	2	0.000	14977	1510	1509	0	0.000	15007	0	0	0	NA
496321	1	47276735	47276735	G	A	*CYP4B1*	intronic	c.323-77	e3-77	tier3	4197	345	326	18	0.052	11848	1385	733	633	0.463	11871	1413	1410	0	0.000	17351	1849	1843	0	0.000	20371	2710	2710	0	0.000
496321	1	114397144	114397144	C	A	*PTPN22*	missense	c.699	p.R233S	tier1	1335	153	143	9	0.059	4786	823	423	394	0.482	2914	0	0	0	NA	5853	756	753	0	0.000	8644	1743	1743	0	0.000
496321	2	241513196	241513196	C	T	*RNPEPL1*	missense	c.133	p.R45C	tier1	9848	1017	958	54	0.053	21160	2388	1545	821	0.347	19773	2461	2368	83	0.034	50301	6190	6186	1	0.000	49385	6370	6348	4	0.001
496321	3	38141928	38141928	G	A	*DLEC1*	intronic	c.2864+12	e19+12	tier3	16399	1549	1455	91	0.059	29864	3096	1961	1090	0.357	36047	4383	4356	17	0.004	61010	7160	7144	3	0.000	67095	8374	8360	1	0.000
496321	3	125643455	125643455	C	T	*FAM86JP*	intronic	c.NULL	NULL	tier3	11340	1170	1111	54	0.046	20544	2564	1450	1089	0.429	18090	2336	2335	0	0.000	35729	4398	4392	0	0.000	45730	5960	5949	0	0.000
496321	3	172835422	172835422	A	T	*SPATA16*	missense	c.100	p.L34I	tier1	3805	301	282	18	0.060	7638	965	550	408	0.426	10093	1341	1335	5	0.004	12209	1384	1379	0	0.000	16432	0	0	0	NA
496321	3	193125021	193125021	G	A	*ATP13A4*	intronic	c.3378+81	e29+81	tier3	20047	2140	1989	135	0.064	42463	5137	2864	2195	0.434	32762	4464	4462	1	0.000	69275	9003	8980	0	0.000	86732	11474	11464	0	0.000
496321	4	106190881	106190881	A	T	*TET2*	missense	c.4159	p.N1387Y	tier1	6589	714	674	40	0.056	22773	2856	1517	1315	0.464	9002	1476	1467	4	0.003	41099	5339	5334	1	0.000	39618	5441	5438	0	0.000
496321	4	106193892	106193892	C	T	*TET2*	nonsense	c.4354	p.R1452*	tier1	8009	1490	1391	96	0.065	18629	3142	1761	1344	0.433	18588	3185	3181	2	0.000	28645	4770	4759	1	0.000	33807	6290	6286	1	0.000
496321	6	152746604	152746604	C	T	*SYNE1*	splice_site	c.5291-1	e40-1	tier1	10011	998	947	42	0.042	11679	1339	883	447	0.336	19450	2661	2659	0	0.000	28713	3535	3531	0	0.000	25810	3507	3505	0	0.000
496321	6	159660601	159660601	G	A	*FNDC1*	missense	c.3919	p.G1307R	tier1	12638	1267	1162	95	0.076	18506	2158	1111	1019	0.478	18926	2329	2325	1	0.000	35793	4425	4423	0	0.000	34839	4464	4463	0	0.000
496321	6	160199944	160199944	G	A	*ACAT2*	rna	NULL	NULL	tier1	1180	89	85	4	0.045	1396	181	129	52	0.287	2436	0	0	0	NA	1883	191	191	0	0.000	3944	0	0	0	NA
496321	7	1132922	1132922	G	A	*GPER1*	3_prime_untranslated_region	c.*430	NULL	tier2	26962	3041	2802	209	0.069	49332	6440	3339	2973	0.471	37598	5443	5442	0	0.000	82140	10896	10884	0	0.000	89729	12405	12396	0	0.000
496321	7	100652450	100652450	T	C	*MUC12*	splice_region	c.15251+10	e5+10	tier2	6692	694	654	37	0.054	14888	2075	1110	952	0.462	13200	1783	1781	2	0.000	25236	3204	3196	0	0.000	27673	4292	4286	0	0.000
496321	7	150835438	150835438	G	A	*AGAP3*	intronic	c.1666+38	e12+38	tier2	8273	821	801	19	0.023	13351	1469	1019	440	0.302	15577	1937	1936	0	0.000	30244	3649	3645	0	0.000	33013	4077	4075	0	0.000
496321	12	48375943	48375943	C	T	*COL2A1*	missense	c.2302	p.G768S	tier1	2436	235	222	12	0.051	7219	972	572	398	0.410	4586	738	737	1	0.000	10067	1264	1261	0	0.000	13155	2153	2153	0	0.000
496321	13	61141522	61141522	C	T	*TDRD3*	intronic	c.2119-137	e13-137	tier3	3734	286	269	17	0.059	6789	742	420	315	0.429	8868	1028	1026	0	0.000	8492	677	676	0	0.000	10373	1049	1049	0	0.000
496321	14	75248223	75248223	C	T	*YLPM1*	nonsense	c.1477	p.Q493*	tier1	5548	579	535	37	0.065	8884	1045	548	486	0.470	10227	1306	1304	2	0.000	13961	1639	1634	0	0.000	15883	2133	2126	2	0.000
496321	15	42434172	42434172	C	T	*PLA2G4F*	3_prime_untranslated_region	c.*10	NULL	tier3	11869	1094	1027	63	0.058	24016	2873	1571	1262	0.445	17709	2157	1995	157	0.073	34899	3800	3798	1	0.000	44450	5530	5528	0	0.000
496321	15	75219024	75219024	A	G	*COX5A*	intronic	c.339+83	e3+83	tier3	7596	572	526	45	0.079	8994	886	474	406	0.461	11659	1264	1256	7	0.006	16952	1598	1597	0	0.000	16932	1935	1935	0	0.000
496321	16	29820921	29820921	C	T	*MAZ*	missense	c.1340	p.P447L	tier1	8524	731	690	36	0.050	17066	1943	1063	860	0.447	15758	1868	1865	3	0.000	31555	3489	3486	0	0.000	33330	4218	4211	1	0.000
496321	19	33792431	33792431	C	G	*CEBPA*	missense	c.890	p.R297P	tier1	12913	1305	1243	57	0.044	26570	3027	1699	1292	0.432	18095	2231	2229	0	0.000	48300	6051	6046	0	0.000	48152	6015	6010	1	0.000
496321	19	36727961	36727961	T	C	*ZNF146*	missense	c.619	p.S207P	tier1	5190	536	498	36	0.067	19533	2447	1254	1170	0.483	15199	2013	2011	0	0.000	36290	4771	4761	0	0.000	36029	4830	4826	0	0.000
496321	19	55697038	55697038	G	A	*PTPRH*	splice_region	c.2902-8	e18-8	tier3	3132	303	273	29	0.096	14024	1991	1125	853	0.431	10162	1403	1402	0	0.000	19527	2180	2177	0	0.000	29463	4243	4241	0	0.000
499258	1	40033490	40033490	T	C	*PABPC4*	missense	c.905	p.D302G	tier1	14249	1861	1848	11	0.006	10422	1428	1096	328	0.230	NA	NA	NA	NA	NA	11880	739	440	299	0.405	NA	NA	NA	NA	NA
499258	1	155028802	155028802	C	G	*ADAM15*	3_prime_untranslated_region	c.*155028802	NULL	tier3	52141	8255	8228	22	0.003	27904	3735	3317	410	0.110	NA	NA	NA	NA	NA	34195	1568	1338	226	0.145	NA	NA	NA	NA	NA
499258	1	182850554	182850554	A	G	*DHX9*	missense	c.2780	p.D927G	tier1	22237	3739	3713	25	0.007	19489	3076	2468	603	0.196	NA	NA	NA	NA	NA	16861	970	551	418	0.431	NA	NA	NA	NA	NA
499258	1	240969528	240969528	G	A	*RGS7*	missense	c.1181	p.P394L	tier1	26119	3297	3295	2	0.001	11599	1422	1384	36	0.025	NA	NA	NA	NA	NA	10250	387	370	17	0.044	NA	NA	NA	NA	NA
499258	2	43905981	43905981	A	G	*PLEKHH2*	intronic	c.124-21	e2-21	tier2	9516	1067	1064	3	0.003	10879	1205	996	208	0.173	NA	NA	NA	NA	NA	6877	438	270	168	0.384	NA	NA	NA	NA	NA
499258	2	88825827	88825827	C	T	*C2orf51*	intronic	c.28-96	e2-96	tier4	28199	3928	3904	23	0.006	9015	831	682	148	0.178	NA	NA	NA	NA	NA	19779	700	412	287	0.411	NA	NA	NA	NA	NA
499258	2	197645323	197645323	A	G	*GTF3C3*	missense	c.1178	p.M393T	tier1	31560	4788	4755	32	0.007	22064	3233	2618	610	0.189	NA	NA	NA	NA	NA	18826	1075	639	432	0.403	NA	NA	NA	NA	NA
499258	4	100266176	100266176	G	A	*ADH1C*	missense	c.410	p.P137L	tier1	25106	3546	3532	12	0.003	15843	2060	1707	351	0.171	NA	NA	NA	NA	NA	19636	850	592	254	0.300	NA	NA	NA	NA	NA
499258	7	135376425	135376425	G	A	*C7orf73*	3_prime_untranslated_region	c.*135376425	NULL	tier3	44581	5918	5902	14	0.002	31252	3800	3054	733	0.194	NA	NA	NA	NA	NA	14714	738	284	453	0.615	NA	NA	NA	NA	NA
499258	9	87322805	87322805	C	T	*NTRK2*	missense	c.406	p.R136C	tier1	41582	5491	5467	21	0.004	37323	4348	3812	530	0.122	NA	NA	NA	NA	NA	41953	2084	1311	767	0.369	NA	NA	NA	NA	NA
499258	10	22680773	22680773	T	C	*SPAG6*	missense	c.1349	p.V450A	tier1	53278	6677	6651	24	0.004	29807	2968	2590	372	0.126	NA	NA	NA	NA	NA	47090	1722	1317	403	0.234	NA	NA	NA	NA	NA
499258	10	49291796	49291796	C	T	*ENSG00000249871*	intronic	c.NULL	NULL	tier3	7264	933	925	8	0.009	7050	1012	830	182	0.180	NA	NA	NA	NA	NA	6803	426	257	168	0.395	NA	NA	NA	NA	NA
499258	12	100904941	100904941	A	T	*NR1H4*	intronic	c.475+20	e2+20	tier3	240	57	56	1	0.018	4046	1017	811	205	0.202	NA	NA	NA	NA	NA	2713	301	161	140	0.465	NA	NA	NA	NA	NA
499258	15	25224990	25224990	T	C	*SNURF*	intronic	c.216-104	e4-104	tier2	21487	2871	2854	17	0.006	15894	2045	1629	414	0.203	NA	NA	NA	NA	NA	26094	1192	749	440	0.370	NA	NA	NA	NA	NA
499258	16	72821316	72821316	A	G	*ZFHX3*	missense	c.10859	p.V3620A	tier1	24490	3281	3275	5	0.002	5277	838	789	48	0.057	NA	NA	NA	NA	NA	17596	707	599	108	0.153	NA	NA	NA	NA	NA
499258	17	38450574	38450574	G	T	*CDC6*	intronic	c.944-42	e6-42	tier2	22192	3062	3037	24	0.008	24049	3510	2866	639	0.182	NA	NA	NA	NA	NA	21038	1254	706	546	0.436	NA	NA	NA	NA	NA
499258	17	42152474	42152474	G	A	*G6PC3*	intronic	c.535+19	e4+19	tier2	73415	10278	10202	67	0.007	45174	5217	4161	1049	0.201	NA	NA	NA	NA	NA	62979	2502	1490	1006	0.403	NA	NA	NA	NA	NA
499258	19	56423693	56423693	G	A	*NLRP13*	missense	c.1490	p.T497M	tier1	23855	3361	3347	13	0.004	10328	1222	1081	139	0.114	NA	NA	NA	NA	NA	15804	761	564	196	0.258	NA	NA	NA	NA	NA
499258	21	36252865	36252865	C	G	*RUNX1*	missense	c.497	p.R166P	tier1	41798	5905	5868	28	0.005	38376	4769	4088	670	0.141	NA	NA	NA	NA	NA	30513	1372	827	541	0.395	NA	NA	NA	NA	NA
499258	22	21804391	21804391	A	G	*HIC2*	3_prime_untranslated_region	c.*3359	NULL	tier3	30138	3960	3928	30	0.008	17198	2226	1787	436	0.196	NA	NA	NA	NA	NA	30599	1624	917	703	0.434	NA	NA	NA	NA	NA
499258	X	24813697	24813697	T	C	*POLA1*	intronic	c.2965-14318	e27-14318	tier3	25781	3252	3203	45	0.014	18704	2084	1238	842	0.405	NA	NA	NA	NA	NA	21277	836	131	701	0.843	NA	NA	NA	NA	NA
502635	1	28208733	28208733	C	T	*THEMIS2*	missense	c.898	p.R300W	tier1	26299	2909	2899	4	0.001	23825	2572	2295	264	0.103	25627	2594	2505	84	0.032	11651	824	698	121	0.148	NA	NA	NA	NA	NA
502635	3	111775924	111775924	C	T	*TMPRSS7*	missense	c.878	p.T293I	tier1	12769	1466	1459	5	0.003	14474	1608	1514	91	0.057	20213	2190	2135	50	0.023	7190	564	492	67	0.120	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
502635	4	119644046	119644046	T	C	*SEC24D*	rna	NULL	NULL	tier1	1320	161	160	0	0.000	1910	212	202	9	0.043	3521	406	402	4	0.010	746	68	59	9	0.132	NA	NA	NA	NA	NA
502635	4	129192341	129192341	A	G	*PGRMC2*	3_prime_untranslated_region	c.*130	NULL	tier3	6482	696	694	1	0.001	7016	734	664	69	0.094	11664	1107	1088	18	0.016	3708	265	226	38	0.144	NA	NA	NA	NA	NA
502635	11	89515227	89515227	G	T	*TRIM64DP*	3_prime_untranslated_region	c.*89515227	NULL	tier3	2097	0	0	0	0.000	3679	346	327	18	0.052	6779	607	593	14	0.023	1074	64	55	9	0.141	NA	NA	NA	NA	NA
502635	12	119583250	119583250	G	A	*SRRM4*	missense	c.836	p.R279Q	tier1	29334	3284	3278	2	0.001	19115	2254	2051	190	0.085	24188	2596	2546	43	0.017	10772	836	713	116	0.140	NA	NA	NA	NA	NA
502635	13	101881935	101881935	C	T	*NALCN*	missense	c.1435	p.V479I	tier1	4923	554	554	0	0.000	6221	718	666	50	0.070	9292	966	953	13	0.013	2741	225	201	23	0.103	NA	NA	NA	NA	NA
502635	15	31086780	31086780	G	T	*GOLGA8UP*	3_prime_untranslated_region	c.*31086780	NULL	tier3	10486	1232	1230	1	0.001	13369	1508	1435	71	0.047	10850	1174	1154	19	0.016	7523	517	489	24	0.047	NA	NA	NA	NA	NA
502635	15	43995984	43995984	C	G	*STRC*	intronic	c.1+14335	e0+14335	tier3	767	138	137	0	0.000	662	102	99	3	0.029	846	107	104	3	0.028	515	56	48	8	0.143	NA	NA	NA	NA	NA
502635	17	7577538	7577538	C	T	*TP53*	missense	c.743	p.R248Q	tier1	38153	4433	4425	6	0.001	32945	3829	3532	283	0.074	28494	3174	3108	63	0.020	15180	1077	928	139	0.130	NA	NA	NA	NA	NA
502635	17	7578551	7578551	A	T	*TP53*	missense	c.379	p.S127T	tier1	13818	1658	1655	1	0.001	16613	1916	1722	184	0.097	12532	1356	1324	30	0.022	8583	676	560	110	0.164	NA	NA	NA	NA	NA
502635	19	852255	852255	G	T	*ELANE*	5_prime_untranslated_region	c.-74	NULL	tier2	4171	489	487	2	0.004	3406	404	371	32	0.079	3728	337	330	5	0.015	1862	171	148	21	0.124	NA	NA	NA	NA	NA
565435	1	114641862	114641862	G	A	*SYT6*	silent	c.1218	p.L406	tier1	13332	1460	1436	21	0.014	12358	1356	1011	336	0.249	13950	2053	1500	545	0.267	30410	4732	4706	23	0.005	21075	2074	2071	0	0.000
565435	2	86267544	86267544	G	A	*POLR1A*	silent	c.3711	p.G1237	tier1	15427	1412	1395	16	0.011	16396	1788	1293	479	0.270	13673	1612	1140	468	0.291	34567	3791	3764	23	0.006	20206	1117	1113	2	0.000
565435	2	97849131	97849131	A	G	*ANKRD36*	intronic	c.1838-65	e27-65	tier3	528	46	45	1	0.022	1085	113	85	28	0.248	765	93	70	22	0.239	1638	370	368	2	0.000	3649	0	0	0	NA
565435	2	130750444	130750444	C	T	*ENSG00000250207*	5_prime_untranslated_region	c.-130750444	NULL	tier2	351	26	25	0	0.000	636	61	48	12	0.200	355	41	24	17	0.415	563	120	119	1	0.000	1926	339	338	0	0.000
565435	2	219267322	219267322	C	A	*CTDSP1*	intronic	c.378+194	e4+194	tier3	8388	714	711	2	0.003	7748	826	714	105	0.128	4654	597	463	132	0.222	19292	2606	2603	3	0.001	14893	1211	1210	0	0.000
565435	3	44776777	44776777	T	C	*ZNF501*	3_prime_untranslated_region	c.*48	NULL	tier3	7090	579	573	5	0.009	7945	811	649	160	0.198	11616	1406	1190	216	0.154	31913	4940	4926	14	0.003	17342	2067	2063	0	0.000
565435	3	133465239	133465239	A	G	*TF*	5_prime_untranslated_region	c.-46	NULL	tier2	3473	238	235	3	0.013	3364	269	192	76	0.284	1841	165	123	42	0.255	8407	1147	1140	7	0.006	5576	0	0	0	NA
565435	3	155314188	155314188	T	C	*PLCH1*	intronic	c.44-21	e2-21	tier3	9276	793	785	7	0.009	8745	953	753	191	0.202	14495	1629	1288	339	0.208	27101	3325	3311	11	0.003	15555	1226	1221	0	0.000
565435	3	185300560	185300560	G	C	*SENP2*	missense	c.26	p.C9S	tier1	9745	864	851	12	0.014	14733	1605	1208	385	0.242	13183	1730	1266	452	0.263	32185	4173	4144	23	0.006	24573	1659	1655	0	0.000
565435	4	73615881	73615881	G	A	-	-	-	-	tier3	26937	2477	2430	43	0.017	26692	2859	2242	589	0.208	26582	3244	2450	771	0.239	76644	8771	8732	32	0.004	36637	2514	2513	0	0.000
565435	5	13900350	13900350	G	A	*DNAH5*	nonsense	c.2224	p.R742*	tier1	5591	438	434	4	0.009	4799	460	353	96	0.214	7223	868	628	234	0.271	13127	2282	2253	22	0.010	11748	1543	1541	0	0.000
565435	5	43295963	43295963	G	A	*HMGCS1*	missense	c.796	p.P266S	tier1	4562	289	279	7	0.024	4865	382	280	99	0.261	8802	864	619	240	0.279	15512	2493	2475	12	0.005	11081	1346	1344	0	0.000
565435	6	31974832	31974832	G	A	*CYP21A1P*	3_prime_untranslated_region	c.*31974832	NULL	tier3	19729	1949	1903	31	0.016	30673	3473	2601	848	0.246	21705	2676	2013	650	0.244	65202	6589	6567	18	0.003	30819	1590	1588	0	0.000
565435	6	54208081	54208081	C	T	*TINAG*	missense	c.682	p.P228S	tier1	12078	986	968	17	0.017	10417	1004	729	273	0.272	13417	1445	1043	387	0.271	32114	4012	3989	22	0.005	14691	1140	1138	0	0.000
565435	6	80774316	80774316	T	G	*ENSG00000218418*	5_prime_untranslated_region	c.-80774316	NULL	tier3	634	69	69	0	0.000	1258	155	116	37	0.242	732	108	73	35	0.324	2184	503	501	2	0.000	3436	475	475	0	0.000
565435	7	5434025	5434025	A	T	*TNRC18*	intronic	c.343+46	e2+46	tier3	28683	2819	2744	69	0.025	38038	4331	3092	1173	0.275	21117	2581	1840	726	0.283	81084	8697	8607	72	0.008	39889	2285	2281	0	0.000
565435	7	122255199	122255199	A	C	*CADPS2*	intronic	c.1223+36	e6+36	tier3	16095	1339	1324	14	0.010	13338	1225	870	348	0.286	20287	2269	1663	594	0.263	37737	4585	4559	22	0.005	20122	1472	1469	0	0.000
565435	7	150894251	150894251	C	T	*IQCA1P1*	intronic	c.NULL	NULL	tier3	18487	2029	2007	19	0.009	17305	2041	1617	413	0.203	13181	1698	1319	378	0.223	46816	4639	4622	13	0.003	25609	1611	1611	0	0.000
565435	8	144399939	144399939	G	A	*TOP1MT*	silent	c.1284	p.Y428	tier1	24944	2355	2315	28	0.012	28184	3061	2293	740	0.244	23661	2765	1988	765	0.278	64552	7314	7266	40	0.005	26804	1782	1779	0	0.000
565435	9	32631391	32631391	C	T	*TAF1L*	missense	c.4187	p.R1396H	tier1	7746	844	824	14	0.017	6167	767	558	207	0.271	8987	1462	1057	394	0.272	17753	3052	3028	16	0.005	13268	1185	1181	1	0.000
565435	9	74299332	74299332	T	C	*TMEM2*	5_prime_untranslated_region	c.-74299332	NULL	tier3	8801	690	684	5	0.007	7996	721	597	121	0.169	8110	889	699	189	0.213	27911	3462	3448	13	0.004	13679	1229	1229	0	0.000
565435	9	84608191	84608191	T	C	*SPATA31D1*	missense	c.2806	p.S936P	tier1	13459	1305	1287	17	0.013	13293	1507	1079	414	0.277	12511	1524	1118	399	0.263	30199	3568	3552	11	0.003	17830	1385	1385	0	0.000
565435	10	95849013	95849013	G	A	*PLCE1*	silent	c.162	p.Q54	tier1	40409	3967	3916	47	0.012	41148	4573	3346	1164	0.258	32204	3872	2697	1136	0.296	113707	11487	11398	72	0.006	43245	2411	2411	0	0.000
565435	11	56738588	56738588	G	A	*OR5AK3P*	3_prime_untranslated_region	c.*56738588	NULL	tier3	974	104	104	0	0.000	2719	366	332	32	0.088	2050	355	347	8	0.023	5834	1395	1389	4	0.003	6721	0	0	0	NA
565435	14	21853909	21853909	C	T	*CHD8*	missense	c.7609	p.E2537K	tier1	3194	392	384	7	0.018	5685	728	564	162	0.223	4068	697	527	167	0.241	12904	2928	2912	13	0.004	10531	1431	1431	0	0.000
565435	14	56120281	56120281	C	G	*KTN1*	missense	c.2768	p.S923C	tier1	3547	215	214	1	0.005	2375	219	193	26	0.119	4545	492	422	70	0.142	6401	1029	1023	4	0.004	3293	0	0	0	NA
565435	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	20548	1867	1830	29	0.016	21572	2270	1589	652	0.291	16737	1964	1388	566	0.290	53292	5895	5855	37	0.006	29666	1639	1638	0	0.000
565435	16	69738490	69738490	C	T	*ENSG00000260772*	rna	NULL	NULL	tier1	6698	420	408	6	0.014	7831	632	470	160	0.254	11905	1052	767	276	0.265	20725	2711	2689	17	0.006	12974	1225	1219	0	0.000
565435	17	10402323	10402323	C	T	*MYH1*	missense	c.3952	p.E1318K	tier1	12078	989	983	0	0.000	14276	1460	1361	96	0.066	20545	2326	2317	8	0.003	33779	4053	4049	2	0.000	17892	1284	1279	1	0.000
565435	17	56620367	56620367	G	T	*C17orf47*	missense	c.1181	p.P394Q	tier1	20216	2203	2140	53	0.024	25963	3020	2083	903	0.302	23592	3081	2092	962	0.315	77374	8800	8727	67	0.008	33866	2351	2351	0	0.000
565435	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	11855	1012	989	14	0.014	10001	939	683	246	0.265	7174	876	651	221	0.253	30938	3877	3847	25	0.006	24590	1643	1642	0	0.000
565435	19	11342899	11342899	G	A	*DOCK6*	missense	c.697	p.R233W	tier1	2408	362	361	1	0.003	5267	722	535	185	0.257	4843	1038	722	305	0.297	10801	2335	2322	12	0.005	10083	980	979	0	0.000
565435	X	39916576	39916576	T	C	*BCOR*	splice_site	c.4429-2	e10-2	tier1	15562	1547	1546	0	0.000	14079	1649	1514	130	0.079	9435	1179	1173	4	0.003	59646	6348	6340	0	0.000	36082	1813	1810	0	0.000
565435	X	123197716	123197716	C	T	*STAG2*	nonsense	c.1840	p.R614*	tier1	4395	395	395	0	0.000	4557	467	388	76	0.164	5434	613	560	53	0.086	25098	3338	3331	3	0.000	14042	1433	1431	0	0.000
565435	X	123220440	123220440	C	T	*STAG2*	nonsense	c.3097	p.R1033*	tier1	4467	228	226	2	0.009	3655	247	182	65	0.263	4360	395	219	176	0.446	19416	1838	1833	0	0.000	15905	1441	1435	0	0.000
596762	1	77987426	77987426	C	T	*AK5*	intronic	c.1312-86	e12-86	tier3	27091	3086	3083	0	0.000	8467	1119	765	345	0.311	NA	NA	NA	NA	NA	35713	4796	4782	5	0.000	23851	2764	2760	1	0.000
596762	1	177906320	177906320	A	T	*SEC16B*	intronic	c.2503+29	e18+29	tier3	34786	4139	4133	0	0.000	12980	1855	1257	580	0.316	NA	NA	NA	NA	NA	33606	5007	4983	0	0.000	31326	3749	3731	0	0.000
596762	4	2160973	2160973	G	A	*POLN*	intronic	c.1555-35	e12-35	tier3	1967	184	183	0	0.000	1039	156	91	65	0.417	NA	NA	NA	NA	NA	1765	231	229	2	0.000	2021	354	353	0	0.000
596762	4	17528425	17528425	C	A	*CLRN2*	intronic	c.434-15	e3-15	tier3	31911	3404	3395	1	0.000	14994	2135	1372	752	0.354	NA	NA	NA	NA	NA	49753	6929	6916	4	0.001	34700	4464	4459	0	0.000
596762	7	151841948	151841948	G	A	*KMT2C*	missense	c.6862	p.H2288Y	tier1	21782	2464	2464	0	0.000	7770	1161	979	180	0.155	NA	NA	NA	NA	NA	43284	5833	5826	3	0.000	27200	3563	3554	7	0.000
596762	8	87242499	87242499	C	T	*SLC7A13*	missense	c.8	p.R3K	tier1	37256	3579	3578	0	0.000	7209	796	652	144	0.181	NA	NA	NA	NA	NA	62592	7899	7890	4	0.001	34026	4121	4116	0	0.000
596762	11	62496026	62496026	C	T	*TTC9C*	missense	c.191	p.S64F	tier1	29020	3236	3232	0	0.000	9288	1416	953	453	0.322	NA	NA	NA	NA	NA	36512	5212	5207	2	0.000	26266	3823	3821	0	0.000
596762	11	92531510	92531510	C	T	*FAT3*	silent	c.5331	p.S1777	tier1	17934	1631	1631	0	0.000	6135	830	484	341	0.413	NA	NA	NA	NA	NA	21296	2997	2996	1	0.000	18597	2427	2427	0	0.000
596762	12	57850452	57850452	G	C	*INHBE*	missense	c.874	p.A292P	tier1	5749	858	858	0	0.000	3995	839	558	279	0.333	NA	NA	NA	NA	NA	5611	1257	1255	1	0.000	5944	1450	1448	1	0.000
596762	12	113379563	113379563	G	T	*OAS3*	missense	c.366	p.E122D	tier1	64755	7292	7289	1	0.000	24155	3103	2231	855	0.277	NA	NA	NA	NA	NA	82609	10612	10596	11	0.001	57220	6135	6126	3	0.000
596762	13	86369756	86369756	C	T	*SLITRK6*	missense	c.888	p.M296I	tier1	13905	1472	1472	0	0.000	3862	501	367	133	0.266	NA	NA	NA	NA	NA	13342	1945	1940	1	0.000	13258	1728	1726	2	0.000
596762	14	62547892	62547892	G	A	*SYT16*	missense	c.1334	p.R445Q	tier1	10145	947	947	0	0.000	5317	891	842	48	0.054	NA	NA	NA	NA	NA	7687	1193	1189	3	0.000	9174	1514	1510	2	0.000
596762	17	4109540	4109540	A	G	*ANKFY1*	intronic	c.1024+76	e7+76	tier3	24843	2276	2276	0	0.000	6143	727	513	210	0.290	NA	NA	NA	NA	NA	36005	4800	4791	2	0.000	24567	3077	3075	0	0.000
596762	17	38438120	38438120	G	C	*WIPF2*	3_prime_untranslated_region	c.*3643	NULL	tier3	29590	3055	3050	1	0.000	10364	1464	975	485	0.332	NA	NA	NA	NA	NA	29005	4069	4059	5	0.000	23208	3176	3168	4	0.000
596762	17	56357291	56357291	C	A	*MPO*	silent	c.333	p.T111	tier1	28590	2947	2946	1	0.000	9501	1266	891	368	0.292	NA	NA	NA	NA	NA	41881	5646	5628	10	0.002	32577	4141	4135	2	0.000
596762	18	7774085	7774085	T	A	*PTPRM*	intronic	c.74-62	e2-62	tier3	33648	4126	4125	0	0.000	13280	2046	1472	569	0.279	NA	NA	NA	NA	NA	37828	5921	5911	2	0.000	31339	4402	4399	0	0.000
596762	20	45355585	45355585	G	A	*SLC2A10*	silent	c.1371	p.A457	tier1	30205	3263	3260	2	0.001	9450	1245	922	315	0.255	NA	NA	NA	NA	NA	42538	5606	5588	5	0.000	28182	3360	3355	1	0.000
596762	20	60895795	60895795	C	G	*LAMA5*	missense	c.6648	p.Q2216H	tier1	80061	9114	9108	1	0.000	18989	2480	1755	713	0.289	NA	NA	NA	NA	NA	88191	11366	11345	5	0.000	52450	5798	5796	1	0.000
597501	2	21228297	21228297	C	T	*APOB*	missense	c.11443	p.V3815M	tier1	33469	4862	4819	21	0.004	11631	1311	1200	103	0.079	NA	NA	NA	NA	NA	46804	3914	3885	9	0.002	NA	NA	NA	NA	NA
597501	2	61006923	61006923	G	A	*PAPOLG*	intronic	c.833+13	e9+13	tier3	975	61	59	2	0.033	829	71	53	18	0.254	NA	NA	NA	NA	NA	935	144	144	0	0.000	NA	NA	NA	NA	NA
597501	2	121744080	121744080	G	A	*GLI2*	missense	c.2183	p.R728Q	tier1	32358	4269	4135	132	0.031	21072	2394	1223	1148	0.484	NA	NA	NA	NA	NA	48093	3673	3619	45	0.012	NA	NA	NA	NA	NA
597501	3	38913145	38913145	C	A	*SCN11A*	missense	c.3550	p.V1184F	tier1	15780	1751	1704	46	0.026	11413	1108	547	543	0.498	NA	NA	NA	NA	NA	25083	2982	2924	38	0.013	NA	NA	NA	NA	NA
597501	3	138724564	138724564	C	T	*PRR23A*	missense	c.547	p.A183T	tier1	10301	1130	1128	2	0.002	8130	764	675	86	0.113	NA	NA	NA	NA	NA	14992	1404	1396	5	0.004	NA	NA	NA	NA	NA
597501	4	89022286	89022286	C	T	*ABCG2*	intronic	c.1367+96	e10+96	tier3	463	50	49	1	0.020	481	48	24	24	0.500	NA	NA	NA	NA	NA	493	117	115	2	0.000	NA	NA	NA	NA	NA
597501	4	106157074	106157074	C	T	*TET2*	nonsense	c.1975	p.Q659*	tier1	16720	2050	1974	75	0.037	13514	1347	690	647	0.484	NA	NA	NA	NA	NA	42895	3321	3280	39	0.012	NA	NA	NA	NA	NA
597501	4	106183003	106183003	C	T	*TET2*	nonsense	c.4042	p.Q1348*	tier1	8650	932	920	12	0.013	5464	522	316	200	0.388	NA	NA	NA	NA	NA	17466	2175	2153	13	0.006	NA	NA	NA	NA	NA
597501	4	109773495	109773495	C	T	*COL25A1*	intronic	c.1345-59	e25-59	tier3	16786	1978	1947	31	0.016	4999	468	299	167	0.358	NA	NA	NA	NA	NA	34424	3763	3732	27	0.007	NA	NA	NA	NA	NA
597501	4	115544516	115544516	T	C	*UGT8*	silent	c.480	p.T160	tier1	14139	1785	1750	34	0.019	8415	951	526	419	0.443	NA	NA	NA	NA	NA	27329	2638	2604	29	0.011	NA	NA	NA	NA	NA
597501	6	29069942	29069942	G	A	*OR2B3*	5_prime_flanking_region	c.-14917	NULL	tier3	1921	262	257	4	0.015	1044	140	75	64	0.460	NA	NA	NA	NA	NA	4700	743	741	2	0.000	NA	NA	NA	NA	NA
597501	6	42330640	42330640	C	T	*TRERF1*	intronic	c.1+95	e0+95	tier3	1456	308	299	9	0.029	1473	217	108	106	0.495	NA	NA	NA	NA	NA	2251	405	399	5	0.012	NA	NA	NA	NA	NA
597501	6	136429913	136429913	C	T	*PDE7B*	missense	c.127	p.R43C	tier1	1606	259	251	8	0.031	1581	208	130	78	0.375	NA	NA	NA	NA	NA	1094	240	240	0	0.000	NA	NA	NA	NA	NA
597501	6	139237014	139237014	C	T	*REPS1*	silent	c.1701	p.R567	tier1	8755	1048	1018	29	0.028	5002	486	235	247	0.512	NA	NA	NA	NA	NA	8206	1002	985	15	0.015	NA	NA	NA	NA	NA
597501	6	163990584	163990584	A	G	*QKI*	3_prime_untranslated_region	c.*4842	NULL	tier3	9937	1215	1184	31	0.026	5058	490	266	220	0.453	NA	NA	NA	NA	NA	17282	1570	1543	23	0.015	NA	NA	NA	NA	NA
597501	7	131122618	131122618	T	G	*MKLN1*	silent	c.1035	p.R345	tier1	14887	1846	1775	63	0.034	8483	911	479	424	0.470	NA	NA	NA	NA	NA	12545	1638	1621	14	0.009	NA	NA	NA	NA	NA
597501	8	3045393	3045393	G	A	*CSMD1*	missense	c.5621	p.S1874L	tier1	1103	124	123	1	0.008	698	71	46	25	0.352	NA	NA	NA	NA	NA	2364	309	302	4	0.013	NA	NA	NA	NA	NA
597501	9	116079186	116079186	C	T	*WDR31*	missense	c.947	p.C316Y	tier1	28524	3859	3744	110	0.029	18042	1954	979	937	0.489	NA	NA	NA	NA	NA	39051	3181	3125	42	0.013	NA	NA	NA	NA	NA
597501	10	49447649	49447649	G	A	*FRMPD2*	missense	c.787	p.R263C	tier1	7974	1027	978	46	0.045	7566	766	385	374	0.493	NA	NA	NA	NA	NA	28717	2189	2167	20	0.009	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
597501	10	135015401	135015401	C	T	*KNDC1*	missense	c.3392	p.P1131L	tier1	1958	243	234	9	0.037	4299	445	258	186	0.419	NA	NA	NA	NA	NA	5562	473	466	3	0.000	NA	NA	NA	NA	NA
597501	11	31531364	31531364	C	T	*ELP4*	silent	c.33	p.A11	tier1	27473	3999	3971	24	0.006	19624	2414	2007	382	0.160	NA	NA	NA	NA	NA	20172	1795	1782	9	0.005	NA	NA	NA	NA	NA
597501	12	117715866	117715866	C	A	*NOS1*	missense	c.1562	p.R521L	tier1	3155	537	516	20	0.037	3394	508	259	248	0.489	NA	NA	NA	NA	NA	4660	918	907	7	0.008	NA	NA	NA	NA	NA
597501	13	25060389	25060389	G	A	*PARP4*	silent	c.1269	p.T423	tier1	1065	174	170	4	0.023	1410	234	124	110	0.470	NA	NA	NA	NA	NA	1212	278	277	0	0.000	NA	NA	NA	NA	NA
597501	14	25100251	25100251	G	A	*GZMB*	3_prime_untranslated_region	c.*26	NULL	tier3	22328	2840	2769	70	0.025	15565	1542	810	722	0.471	NA	NA	NA	NA	NA	30947	2864	2816	32	0.011	NA	NA	NA	NA	NA
597501	14	86089071	86089071	C	G	*FLRT2*	missense	c.1213	p.L405V	tier1	11507	1841	1788	53	0.029	8447	1090	621	460	0.426	NA	NA	NA	NA	NA	26350	2636	2613	19	0.007	NA	NA	NA	NA	NA
597501	15	34651895	34651895	C	T	*LPCAT4*	missense	c.1294	p.G432S	tier1	20898	2652	2572	73	0.028	17216	1747	1007	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA
597501	15	91574882	91574882	T	A	*LOC101926911*	intronic	c.NULL	NULL	tier3	134	20	19	1	0.050	187	24	19	5	0.208	NA	NA	NA	NA	NA	122	31	31	0	0.000	NA	NA	NA	NA	NA
597501	16	2522630	2522630	G	A	*NTN3*	missense	c.928	p.A310T	tier1	10326	1406	1373	33	0.023	6192	761	444	315	0.415	NA	NA	NA	NA	NA	3675	500	492	5	0.010	NA	NA	NA	NA	NA
597501	17	11532944	11532944	C	T	*DNAH9*	intronic	c.1518+43	e7+43	tier3	33290	4249	4236	12	0.003	19803	2073	1984	76	0.037	NA	NA	NA	NA	NA	28820	2610	2604	2	0.000	NA	NA	NA	NA	NA
597501	17	28900664	28900664	C	T	*LOC101927093*	rna	NULL	NULL	tier1	3062	551	534	17	0.031	3737	478	243	231	0.487	NA	NA	NA	NA	NA	4772	684	675	6	0.009	NA	NA	NA	NA	NA
597501	17	29422352	29422352	T	G	*NF1*	missense	c.25	p.W9G	tier1	1964	236	235	1	0.004	3233	309	266	40	0.131	NA	NA	NA	NA	NA	1351	108	108	0	0.000	NA	NA	NA	NA	NA
597501	17	30219342	30219342	C	G	*UTP6*	missense	c.361	p.A121P	tier1	11134	1686	1655	29	0.017	6298	726	402	319	0.442	NA	NA	NA	NA	NA	20253	2333	2313	16	0.007	NA	NA	NA	NA	NA
597501	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	10293	1262	1212	49	0.039	8221	943	489	448	0.478	NA	NA	NA	NA	NA	14711	1525	1507	17	0.011	NA	NA	NA	NA	NA
597501	18	29523048	29523048	C	T	*ENSG00000263823*	rna	NULL	NULL	tier1	9944	1283	1238	44	0.034	8373	963	495	459	0.481	NA	NA	NA	NA	NA	10009	890	878	11	0.012	NA	NA	NA	NA	NA
597501	19	17440815	17440815	G	A	*ANO8*	missense	c.1282	p.R428W	tier1	18125	2340	2297	39	0.017	16282	1820	1289	504	0.281	NA	NA	NA	NA	NA	33601	3412	3379	21	0.006	NA	NA	NA	NA	NA
597501	19	47884624	47884624	G	A	*DHX34*	3_prime_untranslated_region	c.*47884624	NULL	tier3	41418	5490	5361	121	0.022	18930	2084	1128	933	0.453	NA	NA	NA	NA	NA	80784	5946	5873	58	0.010	NA	NA	NA	NA	NA
597501	19	54080590	54080590	T	C	*ZNF331*	missense	c.776	p.I259T	tier1	15559	1995	1949	45	0.023	10394	1170	652	505	0.436	NA	NA	NA	NA	NA	28227	3026	2971	41	0.014	NA	NA	NA	NA	NA
597501	20	48098486	48098486	G	A	*KCNB1*	silent	c.532	p.L178	tier1	16072	2068	1992	74	0.036	9762	1145	590	542	0.479	NA	NA	NA	NA	NA	27257	2577	2544	32	0.012	NA	NA	NA	NA	NA
597501	X	10084387	10084387	T	C	*WWC3*	intronic	c.975-71	e9-71	tier3	32016	4112	4011	99	0.024	16975	1721	885	814	0.479	NA	NA	NA	NA	NA	63246	5639	5578	56	0.010	NA	NA	NA	NA	NA
597501	X	70357542	70357542	C	T	*MED12*	intronic	c.5836-34	e41-34	tier3	18298	2446	2377	67	0.027	8295	924	465	456	0.495	NA	NA	NA	NA	NA	33528	2365	2337	25	0.011	NA	NA	NA	NA	NA
621996	1	4772000	4772000	C	A	*AJAP1*	missense	c.70	p.H24N	tier1	21542	2074	2032	36	0.017	34011	3568	2250	1270	0.361	28983	2915	1603	1275	0.443	33573	4104	4095	6	0.000	50278	6422	6415	1	0.000
621996	1	91404719	91404719	T	C	*ZNF644*	missense	c.2192	p.N731S	tier1	11123	990	976	14	0.014	14226	1396	851	528	0.383	15909	1537	861	657	0.433	20461	2305	2297	5	0.000	37025	5065	5060	4	0.000
621996	1	154841865	154841865	G	A	*KCNN3*	silent	c.576	p.S192	tier1	7417	724	716	8	0.011	12115	1249	834	398	0.323	12983	1394	808	569	0.413	11537	1270	1269	0	0.000	18414	2897	2896	0	0.000
621996	1	176769238	176769238	C	T	*PAPPA2*	silent	c.5172	p.P1724	tier1	9531	990	970	20	0.020	10865	1175	783	388	0.331	12110	1297	726	564	0.437	11017	1305	1305	0	0.000	22967	3292	3289	1	0.000
621996	2	98354060	98354060	C	T	*ZAP70*	missense	c.1414	p.R472W	tier1	12198	1552	1550	0	0.000	25854	2879	2392	465	0.163	26318	3171	2781	362	0.115	24275	2923	2916	1	0.000	49497	7446	7430	3	0.000
621996	2	166223736	166223736	G	A	*SCN2A*	missense	c.3530	p.R1177Q	tier1	98	9	9	0	0.000	127	19	12	7	0.368	213	28	13	15	0.536	179	0	0	0	NA	488	84	84	0	0.000
621996	2	179604342	179604342	C	T	*TTN*	missense	c.13105	p.V4369M	tier1	6466	601	596	4	0.007	6700	691	437	250	0.364	8076	787	449	334	0.427	8898	1067	1065	1	0.000	12585	1891	1891	0	0.000
621996	2	197709191	197709191	T	C	*PGAP1*	intronic	c.2337+57	e24+57	tier3	1048	86	83	3	0.035	1292	107	56	51	0.477	1690	128	72	56	0.438	1301	127	126	1	0.000	3502	443	442	0	0.000
621996	3	38291377	38291377	G	A	*OXSR1*	intronic	c.1323-80	e15-80	tier3	3291	323	321	2	0.006	3035	327	226	100	0.307	3164	352	210	142	0.403	3956	441	441	0	0.000	6631	1199	1191	1	0.000
621996	3	50312255	50312255	C	G	*SEMA3B*	3_prime_untranslated_region	c.*50312255	NULL	tier2	17760	2173	2145	25	0.012	27636	3136	2023	1079	0.348	27358	3188	1796	1328	0.425	28112	3621	3615	3	0.000	44541	7415	7398	3	0.000
621996	3	125879686	125879686	G	A	*ALDH1L1*	splice_region	c.127+10	e1+10	tier3	57489	6208	6190	4	0.001	50722	5652	4444	1109	0.200	45533	4909	3578	1253	0.259	63552	8069	8058	0	0.000	91484	11615	11579	0	0.000
621996	4	125592366	125592366	T	G	*ANKRD50*	missense	c.2066	p.H689P	tier1	17618	2018	1975	39	0.019	32256	3727	2433	1239	0.337	41529	4967	2768	2091	0.430	35605	4752	4739	4	0.000	54131	8759	8755	2	0.000
621996	5	133483867	133483867	T	G	*TCF7*	3_prime_untranslated_region	c.*1873	NULL	tier3	4571	424	418	6	0.014	5018	472	336	135	0.287	5461	504	317	184	0.367	5853	575	575	0	0.000	14536	0	0	0	NA
621996	5	154255096	154255096	C	A	*CNOT8*	3_prime_untranslated_region	c.*97	NULL	tier3	15241	1862	1844	17	0.009	18256	2288	1498	768	0.339	17860	2200	1256	920	0.423	25501	3479	3477	1	0.000	49890	7806	7796	2	0.000
621996	5	176012012	176012012	C	A	*CDHR2*	missense	c.2730	p.N910K	tier1	11919	1473	1453	18	0.012	26552	3257	2079	1126	0.351	28440	3573	2056	1461	0.415	27572	3651	3642	3	0.000	39145	6190	6181	6	0.000
621996	5	176016191	176016191	C	T	*CDHR2*	splice_region	c.3008+8	e21+8	tier3	13734	1236	1211	21	0.017	18072	1669	1077	574	0.348	15960	1563	792	750	0.486	16979	1823	1823	0	0.000	32438	4762	4761	0	0.000
621996	6	36569780	36569780	A	G	*SRSF3*	3_prime_untranslated_region	c.*14	NULL	tier3	3402	249	249	0	0.000	5215	445	277	166	0.375	6475	432	227	205	0.475	6405	648	644	0	0.000	15180	1897	1889	0	0.000
621996	7	48964818	48964818	G	A	*ENSG00000218305*	3_prime_untranslated_region	c.*48964818	NULL	tier2	307	35	35	0	0.000	801	120	80	40	0.333	1222	170	85	82	0.491	515	0	0	0	NA	1491	271	271	0	0.000
621996	7	100846447	100846447	C	T	*DGAT2L7P*	5_prime_untranslated_region	c.-100846447	NULL	tier2	12196	1184	1162	19	0.016	26119	2851	1695	1121	0.398	22109	2473	1271	1172	0.480	22387	2667	2665	1	0.000	22002	3457	3453	1	0.000
621996	7	112724366	112724366	C	T	*GPR85*	silent	c.411	p.T137	tier1	26053	2652	2646	2	0.001	44971	4816	3182	1547	0.327	43527	4544	2535	1921	0.431	52235	6647	6642	2	0.000	70217	9661	9650	3	0.000
621996	8	3224668	3224668	C	T	*CSMD1*	missense	c.3004	p.G1002R	tier1	21813	2357	2316	38	0.016	28657	3173	2014	1125	0.358	27281	2926	1600	1294	0.447	31061	3915	3910	3	0.000	47330	5730	5726	3	0.000
621996	11	6243580	6243580	G	A	*FAM160A2*	intronic	c.1191+92	e5+92	tier3	13842	1264	1246	17	0.013	15206	1516	983	518	0.345	13064	1350	760	583	0.434	18558	2158	2156	2	0.000	31429	4018	4016	0	0.000
621996	11	24750764	24750764	C	T	*LUZP2*	nonsense	c.112	p.R38*	tier1	12705	1242	1219	21	0.017	16093	1689	1015	658	0.393	15697	1692	862	815	0.486	18100	2207	2193	7	0.000	31110	4739	4733	3	0.000
621996	11	46404356	46404356	G	A	*MDK*	missense	c.464	p.R155H	tier1	10043	729	686	9	0.013	10234	912	562	309	0.355	9719	805	353	385	0.522	11638	1064	1046	1	0.000	19492	2712	2630	3	0.000
621996	11	116718092	116718092	C	T	*SIK3*	intronic	c.3808+100	e22+100	tier3	34837	3496	3462	29	0.008	42663	4473	3325	1055	0.241	37490	3757	2581	1116	0.302	50428	6033	6026	1	0.000	61883	8278	8268	3	0.000
621996	12	113405327	113405327	C	T	*OAS3*	missense	c.2794	p.R932W	tier1	15738	1420	1396	20	0.014	18368	1863	1178	666	0.361	15757	1498	800	683	0.461	19151	2225	2220	1	0.000	33830	4626	4616	4	0.000
621996	12	123419982	123419982	G	A	*ABCB9*	splice_region	c.1744-4	e9-4	tier3	17817	1918	1879	37	0.019	31732	3857	2473	1311	0.346	27279	3367	1897	1425	0.429	31011	4057	4053	2	0.000	55775	9335	9320	5	0.000
621996	14	24887568	24887568	C	G	*NYNRIN*	3_prime_untranslated_region	c.*916	NULL	tier3	34097	3727	3671	49	0.013	40933	4632	3005	1547	0.340	38035	4280	2413	1804	0.428	46936	6050	6042	2	0.000	66782	8779	8754	3	0.000
621996	14	63269293	63269293	A	G	*KCNH5*	missense	c.1576	p.S526P	tier1	13097	1606	1575	30	0.019	18567	2400	1506	868	0.366	20735	3034	1676	1320	0.441	23669	3606	3599	4	0.000	43251	8439	8421	4	0.000
621996	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	18315	1711	1705	6	0.004	29064	2954	1924	981	0.338	28090	2567	1398	1116	0.444	29739	3538	3533	2	0.000	35982	4659	4655	1	0.000
621996	17	45249355	45249355	A	G	*CDC27*	missense	c.179	p.L60P	tier1	2301	0	0	0	0.000	2490	226	155	70	0.311	2535	241	137	103	0.429	3300	320	318	0	0.000	7960	1095	1093	0	0.000
621996	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	8158	813	796	14	0.017	13708	1373	879	478	0.352	14171	1396	731	651	0.471	15535	1881	1877	2	0.000	23979	3328	3327	0	0.000
621996	18	55024279	55024279	A	C	*ST8SIA3*	silent	c.438	p.S146	tier1	10937	931	906	21	0.023	7595	687	433	243	0.359	13129	1222	691	518	0.428	10280	961	953	0	0.000	25053	3200	3195	2	0.000
621996	19	52726744	52726744	G	A	*PPP2R1A*	intronic	c.1661+1250	e13+1250	tier4	1112	175	172	3	0.017	1702	301	196	105	0.349	2035	343	188	153	0.449	1538	276	275	1	0.000	1457	0	0	0	NA
621996	22	20172250	20172250	G	A	*LINC00896*	5_prime_flanking_region	c.-21850	NULL	tier3	24563	2394	2385	5	0.002	29247	3084	2027	1007	0.332	29608	2912	1661	1209	0.421	31957	3763	3759	1	0.000	53288	6707	6702	0	0.000
621996	X	151092940	151092940	G	A	*MAGEA4*	silent	c.804	p.A268	tier1	1338	128	128	0	0.000	999	123	87	35	0.287	1128	105	82	23	0.219	883	113	113	0	0.000	1201	0	0	0	NA
621996	Y	14077927	14077927	C	T	*MXRA5P1*	3_prime_untranslated_region	c.*14077927	NULL	tier2	9982	888	885	2	0.002	13088	1355	444	895	0.668	11212	1013	131	876	0.870	14423	1545	1543	0	0.000	26472	3464	3461	0	0.000
624702	1	143914212	143914212	T	A	*SRGAP2P2*	3_prime_untranslated_region	c.*143914212	NULL	tier3	29133	3671	3642	27	0.007	53563	5829	3896	1860	0.323	NA	NA	NA	NA	NA	235358	10481	10478	0	0.000	226966	3966	3966	0	0.000
624702	1	156043138	156043138	A	C	*LMNA*	5_prime_flanking_region	c.-41572	NULL	tier3	42481	6328	6274	46	0.007	53152	7631	4742	2812	0.372	NA	NA	NA	NA	NA	182080	12935	12921	1	0.000	260990	6669	6668	0	0.000
624702	1	158057760	158057760	G	A	*KIRREL*	intronic	c.768-36	e7-36	tier2	6467	1598	1586	12	0.008	6724	1657	1035	618	0.374	NA	NA	NA	NA	NA	17353	2089	2087	0	0.000	36653	1301	1301	0	0.000
624702	1	214204427	214204427	C	T	*PROX1*	intronic	c.2029-4565	e4-4565	tier3	2105	425	415	10	0.024	6652	1179	515	618	0.545	NA	NA	NA	NA	NA	23032	2433	2433	0	0.000	19993	736	733	2	0.000
624702	2	133403009	133403009	C	T	*GPR39*	missense	c.1192	p.R398C	tier1	16648	2848	2845	2	0.001	35979	5375	3532	1799	0.337	NA	NA	NA	NA	NA	96968	6796	6789	2	0.000	167362	3680	3679	1	0.000
624702	2	179454700	179454700	C	T	*TTN*	silent	c.35133	p.E11711	tier1	37711	5095	5034	60	0.012	50959	6583	4086	2451	0.375	NA	NA	NA	NA	NA	213491	12548	12542	1	0.000	265658	4927	4927	0	0.000
624702	2	187627370	187627370	G	T	*FAM171B*	silent	c.2301	p.G767	tier1	57912	7057	7052	3	0.000	74148	8718	5615	3047	0.352	NA	NA	NA	NA	NA	358514	17484	17479	0	0.000	307069	6479	6477	2	0.000
624702	2	238287631	238287631	C	T	*COL6A3*	silent	c.2145	p.S715	tier1	51337	5876	5873	2	0.000	76856	7633	6121	1481	0.195	NA	NA	NA	NA	NA	301122	11592	11587	1	0.000	385996	6149	6148	1	0.000
624702	5	80368977	80368977	T	C	*RASGRF2*	intronic	c.634-41	e5-41	tier3	13360	2192	2173	17	0.008	22062	3430	2153	1267	0.370	NA	NA	NA	NA	NA	36499	5369	5367	0	0.000	83194	3472	3471	0	0.000
624702	5	102503818	102503818	G	A	*PPIP5K2*	missense	c.2105	p.R702H	tier1	7323	1006	1000	6	0.006	8936	1186	781	402	0.340	NA	NA	NA	NA	NA	21308	1686	1681	2	0.000	38208	1445	1444	1	0.000
624702	6	35936771	35936771	C	T	*SLC26A8*	5_prime_untranslated_region	c.-35936771	NULL	tier3	43716	5348	5305	42	0.008	51318	5735	3462	2236	0.392	NA	NA	NA	NA	NA	158820	6688	6683	0	0.000	247648	4534	4532	1	0.000
624702	6	109830321	109830321	G	A	*AKD1*	intronic	c.4481+61	e32+61	tier3	7771	1935	1935	0	0.000	9572	2288	1465	805	0.355	NA	NA	NA	NA	NA	40198	6099	6096	2	0.000	54528	2974	2972	1	0.000
624702	7	6031678	6031678	A	G	*PMS2*	missense	c.914	p.L305P	tier1	18667	2356	2352	3	0.001	14838	1597	1364	229	0.144	NA	NA	NA	NA	NA	81307	4562	4562	0	0.000	124236	2427	2426	0	0.000
624702	8	7698557	7698557	G	A	*DEFB104A*	silent	c.60	p.V20	tier1	22814	2859	2848	10	0.003	19801	2408	1968	436	0.181	NA	NA	NA	NA	NA	32648	1718	1715	1	0.000	136418	2408	2408	0	0.000
624702	9	27610004	27610004	G	C	*CTAGE12P*	5_prime_untranslated_region	c.-27610004	NULL	tier3	7754	1056	1048	5	0.005	11205	1466	922	538	0.368	NA	NA	NA	NA	NA	44869	3590	3587	0	0.000	67090	1567	1566	1	0.000
624702	12	104254945	104254945	T	A	*GNN*	5_prime_untranslated_region	c.-104254945	NULL	tier3	9150	2249	2244	4	0.002	16299	2771	2002	756	0.274	NA	NA	NA	NA	NA	62107	7476	7472	0	0.000	130067	4675	4675	0	0.000
624702	14	50789470	50789470	G	T	*ATP5S*	missense	c.394	p.A132S	tier1	15086	1667	1653	13	0.008	28175	3485	2134	1337	0.385	NA	NA	NA	NA	NA	106008	5335	5335	0	0.000	111656	2157	2155	0	0.000
624702	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	13296	1936	1910	24	0.012	27657	3594	2185	1385	0.388	NA	NA	NA	NA	NA	126281	7489	7484	1	0.000	139204	3903	3900	2	0.000
624702	19	6678085	6678085	A	G	*C3*	intronic	c.4851-51	e41-51	tier3	2347	570	565	5	0.009	2510	566	346	216	0.384	NA	NA	NA	NA	NA	11835	2377	2370	0	0.000	11470	981	979	0	0.000
624702	20	18744043	18744043	A	G	*DTD1*	3_prime_untranslated_region	c.*19147	NULL	tier3	40039	5354	5317	36	0.007	44095	5976	4153	1767	0.298	NA	NA	NA	NA	NA	170990	10958	10953	0	0.000	223156	5500	5500	0	0.000
624702	20	44505588	44505588	C	T	*ZSWIM3*	nonsense	c.391	p.Q131*	tier1	17544	1708	1694	13	0.008	22288	2521	1515	995	0.396	NA	NA	NA	NA	NA	87167	4929	4922	1	0.000	103963	1590	1589	1	0.000
624702	22	38341047	38341047	A	G	*C22orf23*	splice_site	c.481+2	e4+2	tier1	43243	5537	5530	1	0.000	75838	8733	5573	3071	0.355	NA	NA	NA	NA	NA	285092	13752	13745	0	0.000	299491	5593	5591	0	0.000
624702	X	123176411	123176411	A	G	*STAG2*	splice_region	c.386-8	e5-8	tier3	15587	1986	1986	0	0.000	6998	858	422	434	0.507	NA	NA	NA	NA	NA	45134	2687	2687	0	0.000	57170	1225	1225	0	0.000
625338	20	31022824	31022824	C	G	*ASXL1*	nonsense	c.2309	p.S770*	tier1	3625	0	0	0	0.000	7944	773	756	14	0.018	7526	737	734	3	0.004	22378	2969	2963	0	0.000	37268	4055	4053	0	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
625338	21	36231782	36231782	C	T	*RUNX1*	missense	c.602	p.R201Q	tier1	27269	3823	3818	2	0.001	15956	2090	2041	42	0.020	13997	1319	1310	7	0.005	34911	5289	5285	3	0.000	93815	10945	10941	0	0.000
625338	21	36252865	36252865	C	T	*RUNX1*	missense	c.497	p.R166Q	tier1	27077	3350	3349	1	0.000	11292	1186	1152	30	0.025	12298	1138	1128	10	0.009	37453	5311	5307	0	0.000	42670	4903	4900	1	0.000
627844	2	10224073	10224073	G	A	*ENSG00000233502*	splice_site	c.165+1	e1+1	tier1	22088	2486	2466	18	0.007	26382	3471	2707	750	0.217	33344	4412	4396	16	0.004	56061	7553	7544	5	0.000	51131	6045	6040	0	0.000
627844	3	31674390	31674390	A	T	*STT3B*	intronic	c.2188-37	e15-37	tier3	5173	513	509	3	0.006	7302	1335	928	397	0.300	11962	1724	1720	4	0.002	15477	2362	2358	0	0.000	16990	2293	2291	0	0.000
627844	3	122432409	122432409	A	G	*PARP14*	missense	c.3758	p.N1253S	tier1	9170	972	957	15	0.015	16600	2288	1487	787	0.346	15323	1939	1929	10	0.005	23362	3068	3066	0	0.000	25468	3056	3054	0	0.000
627844	4	20530641	20530641	G	A	*SLIT2*	missense	c.1532	p.R511H	tier1	8277	901	899	2	0.002	12327	1644	1505	137	0.083	11470	1579	1579	0	0.000	21940	3005	3002	1	0.000	19508	2342	2337	2	0.000
627844	6	69795034	69795034	C	T	*BAI3*	intronic	c.2480+9104	e15+9104	tier3	6593	621	611	8	0.013	25424	3258	2092	1142	0.353	17212	1969	1953	14	0.007	22372	2603	2600	0	0.000	22841	2344	2339	0	0.000
627844	6	135515531	135515531	G	A	*MYB*	missense	c.881	p.R294Q	tier1	4308	415	412	3	0.007	15388	1791	1462	321	0.180	18041	2118	2100	16	0.008	30939	3838	3835	2	0.000	20305	1946	1941	1	0.000
627844	6	146719968	146719968	C	T	*GRM1*	missense	c.1793	p.A598V	tier1	5415	502	499	3	0.006	14772	1879	1298	566	0.304	12703	1475	1463	8	0.005	23733	2877	2876	0	0.000	23184	2557	2552	0	0.000
627844	7	27236580	27236580	G	A	*HOXA13*	3_prime_untranslated_region	c.*1237	NULL	tier3	2953	190	189	1	0.005	2439	250	184	62	0.252	5482	560	557	0	0.000	7055	721	720	0	0.000	7531	554	553	0	0.000
627844	7	80303472	80303472	G	A	*CD36*	3_prime_untranslated_region	c.*9	NULL	tier2	4025	247	245	1	0.004	5162	620	430	183	0.299	7630	735	726	8	0.011	10410	1042	1041	0	0.000	11879	1070	1068	0	0.000
627844	8	82373788	82373788	G	A	*FABP9*	5_prime_untranslated_region	c.-30	NULL	tier3	22416	2311	2288	19	0.008	39215	4843	3315	1483	0.309	42733	5081	5062	15	0.003	71337	8935	8928	3	0.000	55364	5922	5917	1	0.000
627844	8	105503259	105503259	C	T	*LRP12*	missense	c.2165	p.R722H	tier1	11375	1292	1280	10	0.008	16557	2232	1585	624	0.282	17302	2239	2233	5	0.002	30729	4178	4175	1	0.000	23471	2850	2848	1	0.000
627844	11	73980724	73980724	A	G	*P4HA3*	silent	c.1440	p.Y480	tier1	25154	2444	2418	25	0.010	39632	4778	3157	1575	0.333	28032	3297	3273	19	0.006	59221	7211	7205	0	0.000	57035	5848	5845	0	0.000
627844	12	8186333	8186333	G	T	*FOXJ2*	5_prime_untranslated_region	c.-6096	NULL	tier2	829	127	126	1	0.008	5559	1185	1094	89	0.075	5694	0	0	0	NA	7809	1517	1515	0	0.000	9569	1672	1672	0	0.000
627844	12	64841839	64841839	A	G	*XPOT*	intronic	c.2863-46	e24-46	tier3	6777	610	606	3	0.005	20947	2609	2349	240	0.093	17522	1979	1977	0	0.000	39917	4834	4832	0	0.000	32445	3249	3242	0	0.000
627844	12	112185009	112185009	C	T	*ACAD10*	3_prime_untranslated_region	c.*112185009	NULL	tier3	5275	471	470	1	0.002	8750	1314	1085	220	0.169	9514	1207	1201	4	0.003	14527	1924	1922	0	0.000	18831	2384	2379	0	0.000
627844	12	112884192	112884192	C	T	*PTPN11*	missense	c.127	p.L43F	tier1	25136	2456	2452	4	0.002	39423	5037	4467	535	0.107	43769	5135	5133	0	0.000	65353	8100	8096	0	0.000	61427	6649	6646	0	0.000
627844	14	86088433	86088433	T	A	*FLRT2*	missense	c.575	p.I192N	tier1	25520	2429	2421	7	0.003	38670	4755	3908	796	0.169	29989	3437	3428	9	0.003	67453	8379	8369	0	0.000	53919	5524	5523	0	0.000
627844	15	75798204	75798204	G	C	*PTPN9*	silent	c.780	p.P260	tier1	15640	1769	1760	9	0.005	20641	2706	2528	169	0.063	18404	2319	2317	0	0.000	36426	4783	4780	0	0.000	31203	3567	3565	0	0.000
627844	16	47675018	47675018	G	A	*PHKB*	intronic	c.1514+17	e15+17	tier3	7847	741	737	4	0.005	9527	1226	973	247	0.202	14238	1601	1598	1	0.000	19727	2361	2360	0	0.000	17331	1744	1740	0	0.000
627844	16	89836214	89836214	G	C	*FANCA*	3_prime_untranslated_region	c.*27	NULL	tier3	15798	1453	1431	21	0.014	23007	3037	2001	1011	0.336	26819	3434	3406	26	0.008	41923	5467	5465	0	0.000	37877	4168	4167	0	0.000
627844	17	9282009	9282009	C	G	*STX8*	intronic	c.542-39	e7-39	tier3	7514	853	845	8	0.009	9564	1517	1010	497	0.330	11850	1693	1682	8	0.005	18722	2862	2859	0	0.000	16798	2181	2177	1	0.000
627844	17	11622752	11622752	G	A	*DNAH9*	missense	c.5654	p.R1885H	tier1	9774	1127	1115	11	0.010	16539	2497	1641	840	0.339	8450	1159	1154	4	0.003	22633	3261	3259	1	0.000	25002	3404	3400	1	0.000
627844	18	61323095	61323095	G	A	*SERPINB3*	silent	c.969	p.L323	tier1	13174	1288	1266	22	0.017	24056	3005	2017	953	0.321	13982	1689	1677	11	0.007	34058	4209	4204	2	0.000	32700	3484	3481	3	0.000
627844	19	20045145	20045145	G	A	*ZNF93*	missense	c.1381	p.A461T	tier1	5354	481	480	0	0.000	5729	724	588	135	0.187	11047	1333	1327	6	0.005	15713	1998	1998	0	0.000	12317	1297	1295	1	0.000
627844	X	13337504	13337504	C	T	*ATXN3L*	missense	c.550	p.E184K	tier1	8492	885	873	12	0.014	8287	1095	501	588	0.540	12108	1497	1482	15	0.010	20652	2716	2710	2	0.000	17110	1885	1883	1	0.000
627844	X	119387527	119387527	A	G	*ZBTB33*	missense	c.257	p.Y86C	tier1	4911	365	358	7	0.019	9814	1168	371	794	0.682	10059	1056	1037	19	0.018	17729	1941	1939	0	0.000	17129	1615	1613	0	0.000
635308	1	65307066	65307066	C	G	*JAK1*	intronic	c.2555-44	e18-44	tier3	7983	863	861	0	0.000	4637	574	515	57	0.100	2413	0	0	0	NA	1833	351	351	0	0.000	21	0	0	0	NA
635308	1	84394863	84394863	T	A	*TTLL7*	silent	c.1098	p.V366	tier1	15865	1769	1760	6	0.003	13655	1503	1341	153	0.102	12523	1522	1520	0	0.000	48958	5596	5582	1	0.000	48044	5917	5914	0	0.000
635308	1	86591118	86591118	C	T	*COL24A1*	missense	c.901	p.V301M	tier1	346	60	60	0	0.000	504	81	68	13	0.160	1111	191	183	7	0.037	348	88	86	2	0.000	277	0	0	0	NA
635308	1	222802593	222802593	C	T	*MIA3*	missense	c.778	p.L260F	tier1	1972	340	337	3	0.009	4488	873	730	137	0.158	4624	840	838	1	0.000	2106	476	471	3	0.006	436	39	39	0	0.000
635308	3	112328837	112328837	C	T	*CCDC80*	missense	c.2413	p.A805T	tier1	13554	2190	2177	12	0.005	20404	2878	2524	343	0.120	16904	2791	2780	10	0.004	50090	6621	6605	7	0.000	56541	8126	8118	1	0.000
635308	3	131217024	131217024	C	G	*MRPL3*	missense	c.467	p.R156P	tier1	9976	1161	1149	11	0.009	5937	698	603	94	0.135	6987	938	934	1	0.000	8235	1150	1148	1	0.000	28191	3227	3221	5	0.000
635308	4	68930609	68930609	G	A	*TMPRSS11F*	missense	c.809	p.P270L	tier1	3624	490	488	0	0.000	2799	485	426	59	0.122	3729	596	594	2	0.000	1678	412	411	0	0.000	1455	237	237	0	0.000
635308	4	183723682	183723682	C	G	*TENM3*	3_prime_untranslated_region	c.*2178	NULL	tier2	19803	2442	2428	10	0.004	13248	1527	1341	179	0.118	12864	1639	1635	0	0.000	29664	3325	3302	5	0.000	51288	5935	5923	0	0.000
635308	4	187088020	187088020	G	C	*FAM149A*	intronic	c.2038-102	e12-102	tier3	1410	126	125	1	0.008	775	70	62	8	0.114	1840	225	223	2	0.000	2170	308	304	2	0.000	5078	655	654	1	0.000
635308	5	60253633	60253633	A	G	*NDUFAF2*	intronic	c.127+12424	e1+12424	tier3	12806	1357	1350	4	0.003	8247	872	761	110	0.126	10272	1219	1206	12	0.010	24842	3241	3220	16	0.005	29296	3671	3669	2	0.000
635308	5	73178364	73178364	C	A	*ARHGEF28*	missense	c.2882	p.A961D	tier1	17468	1980	1977	2	0.001	8861	921	889	32	0.035	8304	994	992	2	0.000	51966	5993	5955	33	0.006	27762	0	0	0	NA
635308	5	137464931	137464931	C	T	*NME5*	intronic	c.335+21	e2+21	tier3	13667	1665	1659	1	0.001	12622	1353	1256	93	0.069	15231	1894	1884	0	0.000	68415	8481	8453	7	0.000	50257	6893	6879	0	0.000
635308	5	171706385	171706385	A	C	*UBTD2*	intronic	c.70+4215	e1+4215	tier4	1818	277	277	0	0.000	1512	245	198	47	0.192	2053	362	359	1	0.000	835	204	204	0	0.000	358	0	0	0	NA
635308	6	41575854	41575854	G	A	*MDFI*	5_prime_flanking_region	c.-30634	NULL	tier3	12771	1373	1366	5	0.004	7411	755	657	98	0.130	8709	1084	1084	0	0.000	20974	2422	2416	1	0.000	34026	4238	4236	1	0.000
635308	6	161565095	161565095	C	T	*AGPAT4*	3_prime_untranslated_region	c.*66	NULL	tier3	9416	1016	1010	4	0.004	12411	1349	1132	211	0.157	10813	1228	1220	5	0.004	39467	4533	4508	7	0.000	29358	4012	4008	2	0.000
635308	7	70252341	70252341	G	A	*AUTS2*	missense	c.2455	p.A819T	tier1	20519	2271	2252	16	0.007	14670	2073	1677	384	0.186	13121	1772	1760	12	0.007	28515	3530	3518	5	0.001	9882	1274	1273	1	0.000
635308	7	123152386	123152386	A	G	*IQUB*	silent	c.9	p.N3	tier1	2434	292	289	3	0.010	2293	354	313	41	0.116	3318	470	470	0	0.000	5143	803	802	0	0.000	6144	0	0	0	NA
635308	9	124441020	124441020	C	T	*DAB2IP*	missense	c.188	p.P63L	tier1	18408	1881	1875	3	0.002	20164	2250	2000	238	0.106	15237	1830	1829	0	0.000	41878	5251	5226	5	0.000	25728	3398	3395	0	0.000
635308	9	124751442	124751442	G	A	*TTLL11*	missense	c.1571	p.P524L	tier1	36279	4243	4214	25	0.006	28928	3270	2677	569	0.175	17547	2012	2004	4	0.002	85526	9675	9650	10	0.001	43767	5732	5726	3	0.001
635308	11	47364238	47364238	C	T	*MYBPC3*	silent	c.1515	p.K505	tier1	19486	2466	2456	7	0.003	32201	4024	3410	583	0.146	22180	2866	2864	0	0.000	43679	4834	4823	2	0.000	70508	8864	8861	1	0.000
635308	11	50379335	50379335	G	A	*ENSG00000214883*	3_prime_untranslated_region	c.*50379335	NULL	tier2	5682	654	649	5	0.008	7117	836	693	135	0.163	9092	1188	1178	5	0.004	11814	1617	1610	2	0.000	26134	3323	3318	1	0.000
635308	11	56019747	56019747	A	T	*OR5T3*	silent	c.72	p.S24	tier1	14035	1563	1541	19	0.012	9307	965	808	153	0.159	8134	945	938	7	0.007	30729	3717	3680	27	0.007	39094	4595	4586	1	0.000
635308	11	62327453	62327453	T	A	*MIR3654*	intronic	c.1578+88	e9+88	tier3	8850	1036	1030	6	0.006	8795	1161	979	179	0.155	14106	0	0	0	NA	10019	1260	1253	0	0.000	33480	5292	5288	0	0.000
635308	11	132306614	132306614	G	A	*OPCML*	silent	c.724	p.L242	tier1	55818	7302	7265	32	0.004	38652	4896	4244	631	0.129	23980	2993	2991	0	0.000	70492	6833	6821	2	0.000	77097	9459	9451	1	0.000
635308	12	7363619	7363619	T	A	*PEX5*	3_prime_untranslated_region	c.*800	NULL	tier3	6048	1029	1021	6	0.006	5216	981	850	113	0.117	6507	1472	1472	0	0.000	3542	725	711	0	0.000	14550	3254	3251	0	0.000
635308	12	32854280	32854280	A	G	*DNM1L*	intronic	c.103-69	e2-69	tier3	3879	428	427	1	0.002	4363	458	403	53	0.116	5558	748	747	1	0.000	4607	744	743	0	0.000	13475	0	0	0	NA
635308	12	52966303	52966303	C	T	*KRT74*	missense	c.620	p.G207E	tier1	1131	138	137	1	0.007	1020	183	177	6	0.033	448	0	0	0	NA	173	37	37	0	0.000	2	0	0	0	NA
635308	13	29600575	29600575	G	T	*MTUS2*	missense	c.1770	p.L590F	tier1	11395	1407	1400	5	0.004	22675	2822	2403	406	0.145	13791	1672	1662	9	0.005	63945	6129	6070	50	0.008	39732	4950	4947	3	0.000
635308	14	33292181	33292181	G	A	*AKAP6*	missense	c.5162	p.R1721H	tier1	38757	5455	5427	22	0.004	28411	3986	3569	408	0.103	21061	3226	3219	3	0.000	93656	9300	9271	7	0.000	70292	10020	10011	2	0.000
635308	14	63453786	63453786	T	A	*KCNH5*	splice_region	c.549+4	e5+4	tier2	6662	613	612	1	0.002	4645	486	419	64	0.133	7881	938	935	1	0.000	8522	1173	1168	1	0.000	27088	3309	3309	0	0.000
635308	16	848710	848710	G	A	*GNG13*	3_prime_untranslated_region	c.*9	NULL	tier3	15990	2154	2142	10	0.005	17496	2246	1879	358	0.160	12287	1681	1670	11	0.007	42963	5074	5069	3	0.001	33912	4674	4673	1	0.000
635308	16	85145834	85145834	C	T	*FAM92B*	intronic	c.20+105	e1+105	tier3	7259	516	496	20	0.039	9918	951	440	503	0.533	2748	180	180	0	0.000	23761	2916	2900	5	0.002	2621	166	165	0	0.000
635308	17	79898724	79898724	G	A	*MYADML2*	silent	c.894	p.S298	tier1	28317	3555	3524	28	0.008	21062	2572	2210	351	0.137	15133	1957	1957	0	0.000	47056	5323	5315	3	0.001	55041	6590	6582	0	0.000
635308	19	9088712	9088712	C	G	*MUC16*	missense	c.3103	p.V1035L	tier1	55855	7019	6962	47	0.007	49935	6339	5198	1079	0.172	41728	5409	5368	39	0.007	93785	10319	10197	81	0.008	155441	18062	18046	3	0.000
635308	19	49464172	49464172	G	A	*BAX*	splice_site	c.474+1	e5+1	tier1	7876	773	769	2	0.003	8697	888	744	137	0.156	4858	459	456	2	0.000	15570	1911	1892	13	0.007	7086	924	924	0	0.000
635308	21	47918578	47918578	G	C	*DIP2A*	missense	c.487	p.V163L	tier1	23241	2981	2962	13	0.004	19453	2687	2283	388	0.145	15776	2294	2266	27	0.012	57790	6185	6126	32	0.005	19900	2536	2532	0	0.000
635308	X	57620926	57620926	A	T	*ZXDB*	3_prime_untranslated_region	c.*33	NULL	tier3	11377	1405	1399	5	0.004	8235	966	860	105	0.109	5992	0	0	0	NA	37777	4254	4251	1	0.000	16287	2104	2103	0	0.000
635308	X	153283630	153283630	G	A	*IRAK1*	intronic	c.795-59	e7-59	tier3	22605	2952	2934	10	0.003	19260	2605	2314	283	0.109	15906	2111	2106	5	0.002	42495	4452	4414	27	0.006	15807	2177	2176	1	0.000
639691	1	45296629	45296629	C	T	*PTCH2*	missense	c.704	p.R235Q	tier1	9587	943	913	28	0.030	4502	463	389	73	0.158	11440	1062	874	176	0.168	17378	2634	1389	1224	0.468	NA	NA	NA	NA	NA
639691	1	118644343	118644343	G	A	*SPAG17*	intronic	c.634+20	e5+20	tier3	26036	3191	3179	11	0.003	7376	779	632	146	0.188	22289	2595	2196	384	0.149	29234	4079	2230	1822	0.450	NA	NA	NA	NA	NA
639691	1	160105026	160105026	G	A	*ATP1A2*	missense	c.2056	p.V686I	tier1	37881	4494	4475	12	0.003	12584	1263	903	345	0.276	40381	4707	3783	881	0.189	45100	6559	6394	152	0.023	NA	NA	NA	NA	NA
639691	1	205389686	205389686	T	C	*LEMD1*	rna	NULL	NULL	tier1	2243	249	249	0	0.000	4097	382	321	58	0.153	13648	1314	1147	166	0.126	12308	1709	1068	631	0.371	NA	NA	NA	NA	NA
639691	2	9558907	9558907	T	G	*ITGB1BP1*	intronic	c.1-46	e1-46	tier4	4891	415	414	0	0.000	1477	147	127	17	0.118	6456	495	456	34	0.069	9149	1181	1159	13	0.011	NA	NA	NA	NA	NA
639691	2	9558909	9558909	T	A	*ITGB1BP1*	intronic	c.1-48	e1-48	tier4	5344	0	0	0	0.000	1619	154	133	18	0.119	7283	523	482	35	0.068	9930	1247	1229	11	0.009	NA	NA	NA	NA	NA
639691	2	89160377	89160377	G	C	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	15627	1797	1796	1	0.001	2777	252	222	29	0.116	11649	1301	1223	69	0.053	17874	2545	2522	22	0.009	NA	NA	NA	NA	NA
639691	2	89160663	89160663	T	C	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	2862	0	0	0	0.000	954	169	152	17	0.101	4044	569	554	15	0.026	7168	1711	1703	7	0.004	NA	NA	NA	NA	NA
639691	2	89160789	89160789	C	T	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	2817	0	0	0	0.000	816	128	126	2	0.016	3375	435	434	1	0.000	7268	1564	1560	1	0.000	NA	NA	NA	NA	NA
639691	2	89160801	89160801	C	T	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	2764	357	356	0	0.000	803	123	121	2	0.016	3366	427	424	1	0.000	7109	1506	1498	1	0.000	NA	NA	NA	NA	NA
639691	2	89160806	89160806	A	G	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	2602	329	328	0	0.000	715	114	112	2	0.018	3102	363	362	1	0.000	6569	1380	1366	1	0.000	NA	NA	NA	NA	NA
639691	2	89160841	89160841	A	G	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	7456	754	753	0	0.000	1208	117	114	2	0.017	5075	497	497	0	0.000	10150	1549	1543	0	0.000	NA	NA	NA	NA	NA
639691	2	89160860	89160860	G	C	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	8615	741	740	0	0.000	1324	114	112	2	0.018	5711	495	490	1	0.000	11407	1534	1533	1	0.000	NA	NA	NA	NA	NA
639691	2	89160962	89160962	A	G	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	8554	845	845	0	0.000	1063	112	103	9	0.080	5829	570	559	11	0.019	11221	1718	1696	12	0.007	NA	NA	NA	NA	NA
639691	2	89160986	89160986	C	T	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	8354	825	825	0	0.000	1023	105	96	9	0.086	5429	526	513	12	0.023	10605	1555	1521	12	0.008	NA	NA	NA	NA	NA
639691	2	89160999	89160999	T	A	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	8457	825	825	0	0.000	1015	98	93	5	0.051	5531	527	524	3	0.006	10756	1561	1549	8	0.005	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
639691	2	89161003	89161003	C	G	*ENSG00000231486*	intronic	c.NULL	NULL	tier3	8446	830	830	0	0.000	1049	105	100	5	0.048	5509	528	522	3	0.006	11048	1600	1588	8	0.005	NA	NA	NA	NA	NA
639691	2	89185292	89185292	T	C	*IGKV4-1*	intronic	c.50-64	e2-64	tier3	8501	799	798	0	0.000	2038	245	211	34	0.139	8231	787	704	80	0.102	12597	2121	2090	20	0.009	NA	NA	NA	NA	NA
639691	2	89246918	89246918	G	A	*IGKV1-5*	silent	c.252	p.F84	tier1	2318	284	284	0	0.000	1207	194	190	4	0.021	3708	464	460	4	0.009	5344	1224	1220	4	0.003	NA	NA	NA	NA	NA
639691	2	89246947	89246947	T	G	*IGKV1-5*	missense	c.223	p.S75R	tier1	2294	284	284	0	0.000	1194	193	190	3	0.016	3680	457	452	4	0.009	5349	1215	1211	4	0.003	NA	NA	NA	NA	NA
639691	2	89246969	89246969	C	G	*IGKV1-5*	missense	c.201	p.K67N	tier1	2338	290	290	0	0.000	1207	197	193	4	0.020	3690	450	446	4	0.009	5462	1236	1232	4	0.003	NA	NA	NA	NA	NA
639691	2	89246970	89246970	T	C	*IGKV1-5*	missense	c.200	p.K67R	tier1	2316	283	283	0	0.000	1191	194	189	4	0.021	3698	463	459	4	0.009	5377	1209	1205	3	0.002	NA	NA	NA	NA	NA
639691	2	89247181	89247181	T	G	*IGKV1-5*	intronic	c.55+59	e1+59	tier3	6057	494	492	1	0.002	1359	163	125	38	0.233	4642	326	265	60	0.185	1645	206	199	5	0.025	NA	NA	NA	NA	NA
639691	2	89247195	89247195	T	C	*IGKV1-5*	intronic	c.55+45	e1+45	tier3	5051	467	466	1	0.002	1363	161	122	38	0.238	4210	304	251	50	0.166	2805	214	209	5	0.023	NA	NA	NA	NA	NA
639691	2	89247280	89247280	G	T	*IGKV1-5*	silent	c.15	p.V5	tier1	4549	674	673	1	0.001	1513	279	194	85	0.305	3748	482	376	100	0.210	4527	1031	1009	21	0.020	NA	NA	NA	NA	NA
639691	2	202436665	202436665	T	G	*ALS2CR11*	missense	c.832	p.T278P	tier1	32477	3714	3705	8	0.002	11831	1222	874	330	0.274	37336	4115	3335	746	0.183	50275	7051	6874	139	0.020	NA	NA	NA	NA	NA
639691	3	38592896	38592896	G	A	*SCN5A*	missense	c.4967	p.A1656V	tier1	33890	3887	3884	2	0.001	8817	826	689	135	0.164	26746	2936	2472	453	0.155	30002	3942	2142	1781	0.454	NA	NA	NA	NA	NA
639691	3	193007798	193007798	G	C	*ATP13A5*	missense	c.2899	p.Q967E	tier1	6327	514	511	3	0.006	2429	282	258	22	0.079	8015	657	609	41	0.063	8252	1270	1251	8	0.006	NA	NA	NA	NA	NA
639691	4	100273911	100273911	G	T	*ADH1C*	5_prime_untranslated_region	c.-79	NULL	tier3	6054	655	650	1	0.002	1925	187	150	37	0.198	6784	805	724	74	0.093	6972	1015	1005	8	0.008	NA	NA	NA	NA	NA
639691	4	189013998	189013998	T	C	*TRIML2*	3_prime_untranslated_region	c.*4297	NULL	tier4	21908	3323	3315	7	0.002	8212	1467	1077	386	0.264	28026	4842	3885	926	0.192	34567	6431	6267	148	0.023	NA	NA	NA	NA	NA
639691	5	38968092	38968092	G	A	*RICTOR*	missense	c.1013	p.P338L	tier1	3780	382	382	0	0.000	4111	433	380	53	0.122	9735	1018	918	98	0.096	11334	1773	1309	461	0.260	NA	NA	NA	NA	NA
639691	6	15501389	15501389	C	T	*JARID2*	missense	c.2197	p.R733C	tier1	22037	2217	2204	10	0.005	6584	650	515	131	0.203	18952	1713	1468	232	0.136	28697	3919	3864	44	0.011	NA	NA	NA	NA	NA
639691	6	76343330	76343330	T	C	*SENP6*	missense	c.241	p.S81P	tier1	17217	1940	1936	3	0.002	4979	449	371	78	0.174	17536	2009	1704	295	0.148	18203	2527	1381	1125	0.449	NA	NA	NA	NA	NA
639691	6	119285878	119285878	A	C	*FAM184A*	missense	c.3092	p.V1031G	tier1	12696	1711	1706	5	0.003	4883	643	430	211	0.329	15829	2182	1756	420	0.193	19208	2880	2799	69	0.024	NA	NA	NA	NA	NA
639691	7	43484053	43484053	C	A	*HECW1*	missense	c.1282	p.Q428K	tier1	10580	1259	1256	3	0.002	4591	606	447	156	0.259	11798	1306	1015	274	0.213	17024	2995	2914	71	0.024	NA	NA	NA	NA	NA
639691	8	26628125	26628125	G	A	*ADRA1A*	silent	c.942	p.L314	tier1	17986	1926	1923	1	0.001	4704	519	415	103	0.199	14964	1610	1385	209	0.131	19764	3136	3080	50	0.016	NA	NA	NA	NA	NA
639691	8	40012484	40012484	A	C	*C8orf4*	3_prime_untranslated_region	c.*1112	NULL	tier2	8452	738	734	4	0.005	3364	306	233	72	0.236	8709	710	563	142	0.201	7132	901	882	19	0.021	NA	NA	NA	NA	NA
639691	8	145745801	145745801	A	C	*LRRC14*	missense	c.509	p.D170A	tier1	11508	1199	1198	0	0.000	9150	1010	694	303	0.304	22730	2195	1756	418	0.192	34910	5021	4844	126	0.025	NA	NA	NA	NA	NA
639691	9	13217161	13217161	C	T	*MPDZ*	intronic	c.1201+18	e8+18	tier3	886	64	63	1	0.016	1466	138	102	35	0.255	3896	246	190	55	0.224	3612	459	445	10	0.022	NA	NA	NA	NA	NA
639691	10	124458903	124458903	C	A	*C10orf120*	missense	c.202	p.D68Y	tier1	5489	713	712	1	0.001	2839	306	232	73	0.239	9234	875	707	162	0.186	12332	1871	1824	37	0.020	NA	NA	NA	NA	NA
639691	11	6235593	6235593	T	C	*FAM160A2*	intronic	c.2599+48	e10+48	tier3	9267	1190	1187	3	0.003	6103	689	561	125	0.182	21131	2560	2215	335	0.131	22491	3358	1809	1522	0.457	NA	NA	NA	NA	NA
639691	11	64794980	64794980	C	T	*SNX15*	5_prime_untranslated_region	c.-30	NULL	tier2	2830	244	243	1	0.004	1687	163	131	32	0.196	4498	431	353	75	0.175	6750	943	512	427	0.455	NA	NA	NA	NA	NA
639691	12	70349145	70349145	C	G	*MYRFL*	missense	c.473	p.S158C	tier1	9660	807	805	2	0.002	3563	294	217	76	0.259	11360	926	733	184	0.201	9256	1098	1063	34	0.031	NA	NA	NA	NA	NA
639691	12	93477504	93477504	C	A	*ENSG00000257322*	intronic	c.NULL	NULL	tier4	5468	462	461	1	0.002	2282	274	227	45	0.165	7489	642	551	85	0.134	9608	1541	910	617	0.404	NA	NA	NA	NA	NA
639691	13	31002525	31002525	G	A	*UBE2L5P*	3_prime_untranslated_region	c.*31002525	NULL	tier2	201	0	0	0	0.000	208	38	29	9	0.237	574	34	28	6	0.176	809	132	86	46	0.348	NA	NA	NA	NA	NA
639691	14	20264803	20264803	G	A	*OR4N1P*	3_prime_untranslated_region	c.*20264803	NULL	tier3	9350	883	877	5	0.006	2503	276	215	61	0.221	8833	796	689	104	0.131	10978	1506	1474	28	0.019	NA	NA	NA	NA	NA
639691	14	77844469	77844469	C	A	*SAMD15*	silent	c.708	p.T236	tier1	5020	647	645	1	0.002	5474	651	530	118	0.182	16249	1728	1451	262	0.153	19603	3242	1742	1479	0.459	NA	NA	NA	NA	NA
639691	14	106329350	106329350	C	G	*ENSG00000244620*	5_prime_flanking_region	c.-26592	NULL	tier2	25170	2749	2742	7	0.003	6776	587	415	170	0.291	21423	2265	1790	455	0.203	27279	3490	3384	103	0.030	NA	NA	NA	NA	NA
639691	14	106329945	106329945	C	T	*ENSG00000244620*	5_prime_flanking_region	c.-25997	NULL	tier3	7418	582	580	1	0.002	1641	167	92	75	0.449	4990	365	278	84	0.232	9883	1275	1230	34	0.027	NA	NA	NA	NA	NA
639691	14	106329978	106329978	C	G	*ENSG00000244620*	5_prime_flanking_region	c.-25964	NULL	tier3	7435	580	579	1	0.002	1712	167	89	78	0.467	4999	363	276	84	0.233	10057	1265	1230	32	0.025	NA	NA	NA	NA	NA
639691	14	106330001	106330001	G	C	*ENSG00000244620*	5_prime_flanking_region	c.-25941	NULL	tier3	7354	584	582	1	0.002	1678	168	90	78	0.464	4936	366	277	87	0.239	9901	1278	1242	33	0.026	NA	NA	NA	NA	NA
639691	14	107034793	107034793	C	A	*IGHV5-51*	missense	c.287	p.S96I	tier1	20369	2500	2496	3	0.001	4747	459	344	113	0.247	16760	2029	1658	366	0.181	18674	2550	2499	49	0.019	NA	NA	NA	NA	NA
639691	14	107034840	107034840	G	A	*IGHV5-51*	silent	c.240	p.S80	tier1	44721	5401	5393	4	0.001	10189	1082	848	231	0.214	30919	3661	3124	523	0.143	38415	5402	5320	75	0.014	NA	NA	NA	NA	NA
639691	14	107034897	107034897	C	T	*IGHV5-51*	silent	c.183	p.G61	tier1	12567	1310	1309	1	0.001	5508	511	396	111	0.219	15706	1401	1180	214	0.154	27204	3409	3354	49	0.014	NA	NA	NA	NA	NA
639691	14	107034930	107034930	G	A	*IGHV5-51*	silent	c.150	p.S50	tier1	13024	1348	1345	1	0.001	5854	537	423	108	0.203	16027	1440	1217	214	0.150	29280	3673	3602	55	0.015	NA	NA	NA	NA	NA
639691	14	107034940	107034940	C	A	*IGHV5-51*	missense	c.140	p.S47I	tier1	20341	1997	1995	1	0.001	8098	712	601	106	0.150	23709	2127	1899	210	0.100	39925	4824	4763	51	0.011	NA	NA	NA	NA	NA
639691	14	107034956	107034956	T	C	*IGHV5-51*	missense	c.124	p.K42E	tier1	20589	2020	2019	1	0.000	8094	737	618	112	0.153	24378	2180	1956	206	0.095	40665	5160	5069	54	0.011	NA	NA	NA	NA	NA
639691	14	107035010	107035010	C	T	*IGHV5-51*	missense	c.70	p.V24M	tier1	18339	1613	1610	2	0.001	4749	379	337	40	0.106	16126	1389	1296	89	0.064	22545	2633	2615	11	0.004	NA	NA	NA	NA	NA
639691	14	107035027	107035027	C	G	*IGHV5-51*	missense	c.53	p.C18S	tier1	11075	1132	1132	0	0.000	4696	466	372	93	0.200	13181	1419	1248	169	0.119	22156	3013	2968	43	0.014	NA	NA	NA	NA	NA
639691	14	107035049	107035049	A	G	*IGHV5-51*	intronic	c.47-16	e2-16	tier3	11058	1128	1128	0	0.000	4697	465	369	93	0.201	13127	1413	1240	169	0.120	22149	3010	2945	43	0.014	NA	NA	NA	NA	NA
639691	14	107035075	107035075	A	G	*IGHV5-51*	intronic	c.46+42	e1+42	tier3	13566	1697	1695	0	0.000	5335	562	452	108	0.193	15110	1793	1586	203	0.113	25501	3820	3737	54	0.014	NA	NA	NA	NA	NA
639691	14	107035146	107035146	A	G	*IGHV5-51*	missense	c.17	p.I6T	tier1	6068	605	605	0	0.000	1361	136	115	21	0.154	4990	434	393	40	0.092	7932	1080	1064	12	0.011	NA	NA	NA	NA	NA
639691	14	107178814	107178814	C	G	*IGHV1-69*	5_prime_flanking_region	c.-8447	NULL	tier3	2393	186	184	1	0.005	1860	116	105	11	0.095	3348	244	232	12	0.049	4940	379	375	2	0.000	NA	NA	NA	NA	NA
639691	14	107178822	107178822	T	C	*IGHV2-70*	missense	c.355	p.I119V	tier1	2509	191	190	1	0.005	1845	110	103	7	0.064	3422	254	245	9	0.035	4945	376	373	2	0.000	NA	NA	NA	NA	NA
639691	14	107178861	107178861	T	C	*IGHV2-70*	missense	c.316	p.M106V	tier1	1519	65	65	0	0.000	1202	69	30	38	0.559	3044	111	43	67	0.609	3240	146	124	22	0.151	NA	NA	NA	NA	NA
639691	14	107178871	107178871	T	C	*IGHV2-70*	silent	c.306	p.T102	tier1	1646	132	131	0	0.000	1280	101	86	15	0.149	3169	199	175	23	0.116	3726	490	479	9	0.018	NA	NA	NA	NA	NA
639691	14	107178884	107178884	T	A	*IGHV2-70*	missense	c.293	p.Q98L	tier1	1880	163	163	0	0.000	1244	98	60	38	0.388	3460	218	149	69	0.317	4112	530	505	25	0.047	NA	NA	NA	NA	NA
639691	14	107178935	107178935	C	A	*IGHV2-70*	missense	c.242	p.S81I	tier1	4902	775	775	0	0.000	1549	239	185	51	0.216	4600	583	520	63	0.108	4478	745	734	10	0.013	NA	NA	NA	NA	NA
639691	14	107179009	107179009	G	A	*IGHV2-70*	silent	c.168	p.S56	tier1	9184	767	767	0	0.000	2564	210	166	41	0.198	7668	527	450	74	0.141	5835	368	357	10	0.027	NA	NA	NA	NA	NA
639691	14	107179158	107179158	C	T	*IGHV2-70*	intronic	c.47-28	e2-28	tier3	2083	220	220	0	0.000	2707	299	241	56	0.189	6675	600	523	76	0.127	12979	1944	1899	25	0.013	NA	NA	NA	NA	NA
639691	16	1261371	1261371	G	A	*CACNA1H*	3_prime_untranslated_region	c.*1261371	NULL	tier3	32059	3320	3306	11	0.003	12697	1340	1172	155	0.117	40583	4082	3771	278	0.069	54595	8138	8092	32	0.004	NA	NA	NA	NA	NA
639691	16	56652567	56652567	C	T	*MT1L*	rna	NULL	NULL	tier1	7174	748	748	0	0.000	2064	289	222	64	0.224	7499	753	643	106	0.142	7055	1230	1212	12	0.010	NA	NA	NA	NA	NA
639691	16	67580350	67580350	C	T	*FAM65A*	missense	c.3704	p.A1235V	tier1	6055	806	805	1	0.001	4209	520	463	56	0.108	11966	1395	1290	99	0.071	14087	2291	2278	6	0.003	NA	NA	NA	NA	NA
639691	17	7579349	7579349	A	C	*TP53*	missense	c.338	p.F113C	tier1	27067	2813	2807	5	0.002	10704	1062	799	257	0.243	31629	3467	2816	617	0.180	23380	3466	640	2811	0.815	NA	NA	NA	NA	NA
639691	17	56277172	56277172	G	A	*EPX*	intronic	c.1537+17	e9+17	tier3	39819	4703	4688	13	0.003	20003	1966	1425	521	0.268	60785	6996	5585	1314	0.190	74877	9804	9563	221	0.023	NA	NA	NA	NA	NA
639691	17	61972742	61972742	T	G	*CSH1*	missense	c.547	p.K183Q	tier1	152	11	11	0	0.000	34	5	4	1	0.200	136	15	11	4	0.267	170	35	33	2	0.000	NA	NA	NA	NA	NA
639691	18	14810028	14810028	A	G	*ANKRD30B*	intronic	c.2313+1450	e25+1450	tier3	167	0	0	0	0.000	170	29	27	2	0.069	363	27	27	0	0.000	229	45	45	0	0.000	NA	NA	NA	NA	NA
639691	18	20979505	20979505	T	C	*TMEM241*	intronic	c.279+25	e4+25	tier3	5665	1020	1016	4	0.004	2093	385	305	79	0.206	7424	1306	1121	181	0.139	8843	2088	2055	28	0.013	NA	NA	NA	NA	NA
639691	22	23223246	23223246	A	T	*IGLV3-1*	intronic	c.47-31	e2-31	tier3	41459	4929	4910	14	0.003	10474	1083	750	324	0.302	33409	3723	2932	757	0.205	39796	5312	5134	141	0.027	NA	NA	NA	NA	NA
639691	22	23223346	23223346	T	C	*IGLV3-1*	missense	c.116	p.I39T	tier1	861	102	101	1	0.010	369	48	27	20	0.426	1119	105	73	32	0.305	2175	367	352	11	0.030	NA	NA	NA	NA	NA
639691	22	23223372	23223372	G	A	*IGLV3-1*	missense	c.142	p.D48N	tier1	824	94	93	1	0.011	286	41	22	19	0.463	1142	104	73	31	0.298	1621	256	250	5	0.020	NA	NA	NA	NA	NA
639691	22	23223397	23223397	A	C	*IGLV3-1*	missense	c.167	p.Q56P	tier1	1339	98	97	1	0.010	449	36	21	15	0.417	1499	106	77	29	0.274	2540	266	258	8	0.030	NA	NA	NA	NA	NA
639691	22	23223436	23223436	A	G	*IGLV3-1*	missense	c.206	p.D69G	tier1	1034	112	111	0	0.000	313	47	23	24	0.511	1136	96	64	32	0.333	1845	337	325	11	0.033	NA	NA	NA	NA	NA
639691	22	23223446	23223446	G	C	*IGLV3-1*	silent	c.216	p.R72	tier1	1413	95	94	1	0.011	348	41	21	20	0.488	1346	63	40	23	0.365	2075	271	260	10	0.037	NA	NA	NA	NA	NA
639691	22	23223480	23223480	A	C	*IGLV3-1*	missense	c.250	p.N84H	tier1	16809	1797	1791	6	0.003	5703	709	527	174	0.248	18554	2146	1818	310	0.146	23462	3774	3677	79	0.021	NA	NA	NA	NA	NA
639691	X	69455923	69455923	C	T	*AWAT1*	silent	c.189	p.G63	tier1	9770	1047	1046	1	0.001	3343	408	334	74	0.181	10220	950	797	147	0.156	12441	2044	1053	972	0.480	NA	NA	NA	NA	NA
639691	X	101972409	101972409	T	C	*GPRASP2*	3_prime_untranslated_region	c.*95	NULL	tier3	4766	503	502	1	0.002	1534	197	153	44	0.223	4889	498	424	67	0.136	3576	646	632	14	0.022	NA	NA	NA	NA	NA
639691	X	153134255	153134255	C	G	*L1CAM*	intronic	c.1385+41	e11+41	tier3	16648	2322	2318	1	0.000	6132	791	636	154	0.195	18774	2699	2317	364	0.136	25817	4277	2263	1988	0.468	NA	NA	NA	NA	NA
678913	3	78700929	78700929	C	A	*ROBO1*	missense	c.2765	p.R922L	tier1	5738	590	581	8	0.014	14277	1652	968	662	0.406	NA	NA	NA	NA	NA	37240	4442	4419	14	0.003	37102	4771	4749	8	0.002
678913	3	78700930	78700930	G	T	*ROBO1*	missense	c.2764	p.R922S	tier1	5714	585	576	8	0.014	14298	1644	963	666	0.409	NA	NA	NA	NA	NA	37212	4438	4410	18	0.004	37268	4774	4762	9	0.002
678913	5	150407642	150407642	T	G	*GPX3*	missense	c.632	p.I211S	tier1	28544	3564	3501	54	0.015	20939	2934	1711	1185	0.409	NA	NA	NA	NA	NA	26570	3612	3593	10	0.003	44855	6406	6395	7	0.001
678913	6	33261595	33261595	G	A	*RGL2*	silent	c.1485	p.L495	tier1	9058	948	929	19	0.020	12744	1521	815	695	0.460	NA	NA	NA	NA	NA	12079	1547	1541	6	0.004	30565	3941	3937	1	0.000
678913	7	116166678	116166678	G	T	*CAV1*	missense	c.130	p.A44S	tier1	29112	3564	3485	48	0.014	25016	3232	1921	1270	0.398	NA	NA	NA	NA	NA	43492	4716	4695	17	0.004	54903	6742	6722	17	0.003
678913	7	141321598	141321598	C	A	*AGK*	silent	c.585	p.I195	tier1	1180	131	129	2	0.015	1287	217	134	82	0.380	NA	NA	NA	NA	NA	1156	0	0	0	NA	1541	299	298	0	0.000
678913	7	151945083	151945083	C	T	*KMT2C*	missense	c.2436	p.M812I	tier1	50079	5745	5737	3	0.001	45387	5263	5059	159	0.030	NA	NA	NA	NA	NA	124842	14373	14348	13	0.000	115099	14377	14351	8	0.000
678913	12	2912387	2912387	C	T	*FKBP4*	missense	c.1343	p.T448M	tier1	4149	560	550	8	0.014	4578	753	446	303	0.405	NA	NA	NA	NA	NA	7241	1517	1511	3	0.000	6201	1375	1370	2	0.000
678913	12	39761659	39761659	T	C	*KIF21A*	intronic	c.600+26	e4+26	tier3	4425	383	379	4	0.010	4058	542	315	224	0.416	NA	NA	NA	NA	NA	9813	1667	1666	1	0.000	7168	1113	1112	1	0.000
678913	15	50784950	50784950	C	T	*USP8*	missense	c.2287	p.R763W	tier1	24370	2861	2628	220	0.077	20451	2354	2139	210	0.089	NA	NA	NA	NA	NA	38679	4510	4053	448	0.100	60757	7569	6915	635	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
678913	16	5040788	5040788	C	T	*SEC14L5*	silent	c.366	p.D122	tier1	16442	1859	1829	29	0.016	19631	2677	1469	1174	0.444	NA	NA	NA	NA	NA	34069	5025	5010	11	0.002	45945	7001	6985	10	0.001
678913	20	30618789	30618789	C	T	*LOC101929636*	rna	NULL	NULL	tier1	17783	2184	2152	29	0.013	13197	1712	1032	664	0.392	NA	NA	NA	NA	NA	32513	3978	3968	6	0.002	36871	5220	5211	5	0.000
678913	21	27542825	27542825	G	C	*APP*	intronic	c.57+57	e1+57	tier2	13118	1435	1410	24	0.017	9791	1054	590	454	0.435	NA	NA	NA	NA	NA	7400	923	918	3	0.003	21146	2738	2731	4	0.001
715413	1	201781078	201781078	A	C	*NAV1*	missense	c.5000	p.N1667T	tier1	4255	598	597	0	0.000	7661	1306	1248	54	0.041	NA	NA	NA	NA	NA	24275	3980	3971	0	0.000	12702	701	698	0	0.000
715413	6	75851871	75851871	C	A	*COL12A1*	missense	c.4834	p.V1612L	tier1	6174	808	805	2	0.002	6843	883	834	47	0.053	NA	NA	NA	NA	NA	22345	3156	3154	0	0.000	13555	735	734	1	0.000
715413	20	29612347	29612347	C	A	*FRG1B*	rna	NULL	NULL	tier1	30952	3895	3542	339	0.087	29846	3923	3599	317	0.081	NA	NA	NA	NA	NA	106519	11051	11043	6	0.000	17614	523	491	31	0.000
717045	1	47548156	47548156	G	A	*CYP4Z1*	intronic	c.492+23	e4+23	tier3	6888	1164	1151	10	0.009	2447	334	198	135	0.405	NA	NA	NA	NA	NA	3749	37	37	0	0.000	2526	475	472	2	0.000
717045	1	200878061	200878061	G	A	*C1orf106*	missense	c.1033	p.E345K	tier1	9569	1547	1527	15	0.010	4371	450	302	144	0.323	NA	NA	NA	NA	NA	13009	77	75	1	0.000	5912	879	872	5	0.006
717045	2	32666548	32666548	T	G	*BIRC6*	intronic	c.3944+18	e17+18	tier3	2230	340	333	7	0.021	922	124	80	44	0.355	NA	NA	NA	NA	NA	1367	14	14	0	0.000	1245	199	198	1	0.000
717045	2	179481333	179481333	A	T	*TTN*	nonsense	c.40481	p.L13494*	tier1	30653	4147	4095	46	0.011	8277	788	490	292	0.373	NA	NA	NA	NA	NA	29213	144	143	0	0.000	17902	2359	2342	9	0.004
717045	2	198266834	198266834	T	C	*SF3B1*	missense	c.2098	p.K700E	tier1	25635	3423	3343	71	0.021	5493	515	309	199	0.392	NA	NA	NA	NA	NA	35694	201	201	0	0.000	15687	1931	1919	11	0.006
717045	2	217280235	217280235	T	C	*SMARCAL1*	missense	c.808	p.Y270H	tier1	3481	490	479	11	0.022	2272	190	150	40	0.211	NA	NA	NA	NA	NA	6845	0	0	0	NA	7963	1112	1108	2	0.000
717045	3	71355167	71355167	T	C	*FOXP1*	intronic	c.1-6136	e1-6136	tier2	9490	1403	1390	3	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	11332	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	A	*ANAPC4*	intronic	c.1320+69	e17+69	tier3	3267	547	539	7	0.013	1934	290	174	114	0.396	NA	NA	NA	NA	NA	3579	0	0	0	NA	1149	230	228	2	0.000
717045	4	105393360	105393360	C	T	*CXXC4*	rna	NULL	NULL	tier1	1241	95	95	0	0.000	675	49	31	18	0.367	NA	NA	NA	NA	NA	1811	49	49	0	0.000	923	116	116	0	0.000
717045	6	129475728	129475728	G	A	*LAMA2*	missense	c.1106	p.R369H	tier1	19868	2525	2480	42	0.017	4971	418	277	139	0.334	NA	NA	NA	NA	NA	20889	117	115	1	0.000	11026	1492	1486	4	0.003
717045	7	73973313	73973313	G	A	*GTF2IRD1*	missense	c.2275	p.G759S	tier1	3212	534	524	9	0.017	2398	309	216	90	0.294	NA	NA	NA	NA	NA	2015	15	15	0	0.000	1155	199	197	1	0.000
717045	7	151878771	151878771	T	C	*KMT2C*	silent	c.6174	p.G2058	tier1	14778	2969	2922	46	0.015	4446	667	416	249	0.374	NA	NA	NA	NA	NA	15495	133	133	0	0.000	3741	821	817	4	0.005
717045	8	9639151	9639151	A	G	*TNKS*	3_prime_untranslated_region	c.*4905	NULL	tier3	1352	195	193	2	0.010	1136	134	79	54	0.406	NA	NA	NA	NA	NA	1294	0	0	0	NA	878	130	129	1	0.000
717045	10	61666207	61666207	G	A	*CCDC6*	5_prime_untranslated_region	c.-25	NULL	tier2	12004	1530	1512	18	0.012	3647	342	220	119	0.351	NA	NA	NA	NA	NA	10798	73	73	0	0.000	6044	846	843	3	0.004
717045	10	71620368	71620368	C	T	*COL13A1*	intronic	c.365-11564	e3-11564	tier3	21700	2851	2794	54	0.019	6809	636	400	234	0.369	NA	NA	NA	NA	NA	29706	154	154	0	0.000	10151	1246	1240	5	0.004
717045	12	49724201	49724201	G	A	*TROAP*	missense	c.1573	p.A525T	tier1	11571	1517	1495	17	0.011	3004	289	205	83	0.288	NA	NA	NA	NA	NA	10363	0	0	0	NA	6945	886	879	4	0.005
717045	14	88945999	88945999	G	A	*PTPN21*	silent	c.1776	p.P592	tier1	9582	1363	1342	16	0.012	3009	377	241	126	0.343	NA	NA	NA	NA	NA	6962	79	79	0	0.000	2622	451	449	2	0.000
717045	15	101432730	101432730	G	C	*ALDH1A3*	missense	c.361	p.D121H	tier1	18641	2775	2740	30	0.011	4893	555	413	134	0.245	NA	NA	NA	NA	NA	19272	102	102	0	0.000	7718	1098	1096	2	0.000
717045	16	66432084	66432084	G	T	*CDH5*	intronic	c.1485+75	e8+75	tier3	18545	2425	2406	17	0.007	4073	376	275	98	0.263	NA	NA	NA	NA	NA	23912	112	112	0	0.000	10567	1319	1315	4	0.003
717045	17	40731892	40731892	C	T	*FAM134C*	3_prime_untranslated_region	c.*1939	NULL	tier3	5159	1170	1152	18	0.015	2301	331	199	131	0.397	NA	NA	NA	NA	NA	2789	36	36	0	0.000	1440	356	352	3	0.008
717045	19	1046259	1046259	C	G	*ABCA7*	silent	c.1476	p.P492	tier1	18745	2445	2423	20	0.008	4267	409	264	142	0.350	NA	NA	NA	NA	NA	21192	99	99	0	0.000	8651	1076	1075	1	0.000
717045	20	39992390	39992390	C	T	*EMILIN3*	silent	c.402	p.T134	tier1	17366	3269	3215	47	0.014	3282	810	510	300	0.370	NA	NA	NA	NA	NA	13665	0	0	0	NA	3847	744	741	1	0.000
732217	1	1896486	1896486	G	A	*C1orf222*	silent	c.171	p.D57	tier1	9674	1101	1083	18	0.016	26093	3330	1866	1416	0.431	28888	3230	1802	1367	0.431	23324	2863	2855	3	0.001	NA	NA	NA	NA	NA
732217	1	19549161	19549161	C	T	*EMC1*	missense	c.95	p.R32K	tier1	8174	922	907	13	0.014	14888	1744	908	819	0.474	16817	1911	958	936	0.494	12097	1311	1308	2	0.000	NA	NA	NA	NA	NA
732217	1	20518895	20518895	C	T	*UBXN10*	3_prime_untranslated_region	c.*998	NULL	tier3	1142	137	135	2	0.015	5710	700	392	307	0.439	6232	785	412	368	0.472	5373	633	633	0	0.000	NA	NA	NA	NA	NA
732217	1	46079781	46079781	A	G	*NASP*	missense	c.1526	p.N509S	tier1	4624	421	415	6	0.014	7233	644	316	323	0.505	7093	528	242	280	0.536	7638	680	678	1	0.000	NA	NA	NA	NA	NA
732217	2	112588927	112588927	C	G	*ANAPC1*	missense	c.2561	p.G854A	tier1	604	50	46	3	0.061	984	146	87	56	0.392	1153	102	54	48	0.471	635	78	78	0	0.000	NA	NA	NA	NA	NA
732217	2	236949476	236949476	G	A	*AGAP1*	missense	c.1882	p.E628K	tier1	18761	2182	2164	13	0.006	18854	2432	1563	840	0.350	18896	2091	1336	718	0.350	15653	1820	1819	0	0.000	NA	NA	NA	NA	NA
732217	4	106164914	106164914	G	A	*TET2*	missense	c.3782	p.R1261H	tier1	5578	518	493	24	0.046	5690	711	73	626	0.896	6924	565	34	527	0.939	8545	826	822	2	0.000	NA	NA	NA	NA	NA
732217	4	125593542	125593542	A	G	*ANKRD50*	missense	c.890	p.I297T	tier1	961	92	85	7	0.076	1571	253	14	239	0.945	1647	162	7	152	0.956	1174	173	172	1	0.000	NA	NA	NA	NA	NA
732217	7	31378474	31378474	G	A	*NEUROD6*	nonsense	c.409	p.R137*	tier1	17479	1858	1823	26	0.014	16925	1858	1044	790	0.431	20004	1904	1028	844	0.451	16912	1771	1770	0	0.000	NA	NA	NA	NA	NA
732217	7	48545892	48545892	G	A	*ABCA13*	intronic	c.13292-40	e49-40	tier3	20390	2472	2418	49	0.020	24827	2963	1537	1397	0.476	30348	3483	1771	1659	0.484	21564	2461	2455	4	0.002	NA	NA	NA	NA	NA
732217	7	73475359	73475359	T	C	*ELN*	intronic	c.1952-72	e27-72	tier4	2791	391	387	4	0.010	9501	1208	639	559	0.467	8732	914	478	430	0.474	7089	876	876	0	0.000	NA	NA	NA	NA	NA
732217	8	145255402	145255402	G	A	*MROH1*	missense	c.1099	p.V367M	tier1	31133	3651	3548	78	0.022	38897	4451	2452	1929	0.440	42647	4754	2424	2226	0.479	30995	3454	3448	3	0.000	NA	NA	NA	NA	NA
732217	9	33386977	33386977	G	T	*AQP7*	silent	c.258	p.G86	tier1	974	0	0	0	0.000	4772	542	432	105	0.196	3682	334	247	87	0.260	2455	280	279	0	0.000	NA	NA	NA	NA	NA
732217	9	130897518	130897518	A	C	*PTGES2*	5_prime_flanking_region	c.-7522	NULL	tier4	11667	1349	1328	16	0.012	10428	1227	863	356	0.292	15567	1701	1253	429	0.255	7806	932	929	0	0.000	NA	NA	NA	NA	NA
732217	10	102296470	102296470	T	C	*HIF1AN*	intronic	c.428+52	e2+52	tier2	16081	1767	1726	40	0.023	17104	1836	917	896	0.494	20815	2087	1086	963	0.470	16980	1775	1771	4	0.002	NA	NA	NA	NA	NA
732217	10	119003712	119003712	C	T	*SLC18A2*	missense	c.352	p.P118S	tier1	9364	1253	1210	40	0.032	11148	1576	878	683	0.438	12653	1422	759	654	0.463	9906	1371	1363	3	0.002	NA	NA	NA	NA	NA
732217	11	14279305	14279305	G	T	*SPON1*	rna	NULL	NULL	tier1	5524	547	530	13	0.024	9562	1118	773	341	0.306	11420	1073	760	303	0.285	9263	998	998	0	0.000	NA	NA	NA	NA	NA
732217	11	59244984	59244984	T	C	*OR4D10*	missense	c.82	p.F28L	tier1	5445	711	697	12	0.017	13117	1932	1213	702	0.367	16242	2232	1369	850	0.383	13793	1890	1887	1	0.000	NA	NA	NA	NA	NA
732217	12	57484814	57484814	G	T	*NAB2*	intronic	c.84-94	e2-94	tier2	23130	2706	2640	54	0.020	30482	3770	1992	1716	0.463	36696	4018	2032	1906	0.484	27671	3201	3191	6	0.002	NA	NA	NA	NA	NA
732217	12	95926996	95926996	C	T	*USP44*	missense	c.1037	p.C346Y	tier1	4562	604	595	5	0.008	7599	1125	606	507	0.456	7955	920	466	449	0.491	6959	1020	1018	1	0.000	NA	NA	NA	NA	NA
732217	12	118199039	118199039	G	A	*KSR2*	missense	c.763	p.R255W	tier1	4756	470	460	10	0.021	21835	2662	1412	1217	0.463	22983	2556	1332	1196	0.473	17788	2014	2013	1	0.000	NA	NA	NA	NA	NA
732217	14	35264956	35264956	G	T	*BAZ1A*	missense	c.1144	p.R382S	tier1	381	36	36	0	0.000	1544	230	147	83	0.361	1089	112	76	36	0.321	1468	223	223	0	0.000	NA	NA	NA	NA	NA
732217	15	79059795	79059795	G	A	*ADAMTS7*	missense	c.2785	p.R929W	tier1	3148	290	287	3	0.010	5294	711	481	226	0.320	5612	564	365	194	0.347	5807	653	652	1	0.000	NA	NA	NA	NA	NA
732217	17	72363579	72363579	T	A	*GPR142*	5_prime_untranslated_region	c.-66	NULL	tier3	4665	624	614	10	0.016	12057	1828	1017	792	0.438	14109	1729	950	744	0.439	8298	1015	1011	2	0.000	NA	NA	NA	NA	NA
732217	17	72948180	72948180	C	T	*HID1*	intronic	c.2145-22	e18-22	tier3	25364	2824	2745	64	0.023	47592	5272	2834	2324	0.451	51267	5480	2706	2654	0.495	44664	4841	4833	7	0.001	NA	NA	NA	NA	NA
732217	17	74732959	74732959	G	A	*SRSF2*	missense	c.284	p.P95L	tier1	6394	472	466	4	0.009	10267	1298	845	444	0.344	9758	926	601	314	0.343	11479	1300	1297	3	0.002	NA	NA	NA	NA	NA
732217	19	41557967	41557967	C	T	*CYP2G2P*	5_prime_untranslated_region	c.-41557967	NULL	tier3	2420	236	228	6	0.026	2373	286	145	139	0.489	3528	286	143	141	0.496	1919	189	188	1	0.000	NA	NA	NA	NA	NA
732217	X	106482271	106482271	T	C	*PIH1D3*	intronic	c.515+34	e5+34	tier3	3599	319	312	7	0.022	3345	311	17	293	0.945	3898	289	13	275	0.955	3977	339	339	0	0.000	NA	NA	NA	NA	NA
754150	1	10683092	10683092	T	C	*PEX14*	missense	c.401	p.L134P	tier1	2567	446	446	0	0.000	2740	420	383	36	0.086	1133	216	213	3	0.014	765	115	115	0	0.000	72	0	0	0	NA
754150	2	149793838	149793838	G	A	*KIF5C*	missense	c.332	p.R111Q	tier1	20999	2400	2387	11	0.005	29830	3960	3177	753	0.192	26336	2758	2707	38	0.014	47454	5661	5638	7	0.001	35547	4075	3283	749	0.186
754150	2	219221645	219221645	C	G	*C2orf62*	intronic	c.25+13	e1+13	tier3	15518	2013	2013	0	0.000	18800	2481	2278	195	0.079	15009	1516	1502	4	0.003	21858	2248	2246	2	0.000	14578	1224	1223	1	0.000
754150	2	239973727	239973727	T	A	*HDAC4*	3_prime_untranslated_region	c.*1066	NULL	tier3	31278	3777	3662	113	0.030	18377	2398	1338	1042	0.438	21375	2033	1279	751	0.370	37942	4481	4438	37	0.008	46123	6081	4884	1155	0.191
754150	3	52012429	52012429	T	A	*ABHD14A*	3_prime_untranslated_region	c.*52012429	NULL	tier3	7402	790	784	5	0.006	14810	1897	1565	315	0.168	8222	824	807	17	0.021	41065	4766	4760	1	0.000	24484	2989	2443	526	0.177
754150	3	69915190	69915190	G	A	*MITF*	intronic	c.105-13095	e2-13095	tier3	18286	2580	2560	18	0.007	23839	3322	2653	654	0.198	19223	1919	1894	23	0.012	59409	7323	7301	9	0.001	24639	2895	2313	570	0.198
754150	3	182933850	182933850	G	C	*MCF2L2*	missense	c.2403	p.F801L	tier1	17009	2566	2566	0	0.000	18004	2790	2579	199	0.072	13225	1814	1805	4	0.002	10203	1349	1347	0	0.000	14812	1751	1751	0	0.000
754150	4	20852133	20852133	G	T	*KCNIP4*	5_prime_untranslated_region	c.-20852133	NULL	tier3	2241	286	276	10	0.035	2541	275	172	103	0.375	1725	239	153	85	0.357	4605	473	468	3	0.006	811	34	30	4	0.118
754150	4	25677760	25677760	G	A	*SLC34A2*	missense	c.1462	p.A488T	tier1	29623	3929	3919	4	0.001	31033	4192	3744	431	0.103	17245	1746	1734	8	0.005	55103	6737	6726	3	0.000	39427	4966	4964	1	0.000
754150	5	26906108	26906108	C	G	*CDH9*	silent	c.771	p.T257	tier1	17106	1963	1961	1	0.001	22663	3035	2738	287	0.095	23188	2348	2335	6	0.003	10963	1208	1205	1	0.000	20116	2454	2453	0	0.000
754150	5	55168187	55168187	C	T	*IL31RA*	missense	c.362	p.T121M	tier1	2629	448	437	11	0.025	1902	343	223	120	0.350	1986	485	327	156	0.323	711	120	120	0	0.000	714	89	73	16	0.180
754150	5	115177743	115177743	G	C	*AP3S1*	missense	c.9	p.K3N	tier1	5211	885	866	19	0.021	9375	1528	908	610	0.402	5752	964	630	333	0.346	5349	884	878	6	0.007	95	2	1	1	NA
754150	5	139941115	139941115	T	C	*APBB3*	intronic	c.762+57	e7+57	tier2	14430	1940	1870	68	0.035	10731	1711	1011	689	0.405	6384	727	519	208	0.286	14851	1805	1794	10	0.006	9913	1120	934	184	0.165
754150	5	178413301	178413301	C	T	*GRM6*	missense	c.1954	p.A652T	tier1	26019	3051	3005	41	0.013	22290	2922	1637	1258	0.435	9505	913	587	324	0.356	46958	5322	5308	5	0.001	19956	2139	1625	501	0.236
754150	6	52400654	52400654	A	C	*TRAM2*	splice_region	c.121-10	e2-10	tier2	14697	1559	1500	58	0.037	9390	1063	555	502	0.475	8040	858	516	340	0.397	28801	3079	3058	17	0.006	16572	1937	1598	330	0.171
754150	7	31127292	31127292	T	C	*ADCYAP1R1*	missense	c.85	p.C29R	tier1	7408	1174	1172	1	0.001	4950	912	821	90	0.099	2303	402	399	1	0.000	3916	507	506	0	0.000	1896	0	0	0	NA
754150	7	42005086	42005086	G	T	*GLI3*	missense	c.3585	p.N1195K	tier1	19646	2424	2356	65	0.027	14818	1946	1103	827	0.429	9642	1031	647	384	0.372	21574	2455	2439	13	0.005	20285	2455	1927	515	0.211
754150	11	34192643	34192643	C	T	*ABTB2*	intronic	c.1398-25	e5-25	tier3	11770	2046	2042	3	0.001	15896	2738	2409	323	0.118	10791	1463	1451	10	0.007	18249	2546	2539	4	0.000	16195	1953	1951	0	0.000
754150	11	48346968	48346968	C	T	*OR4C3*	missense	c.476	p.T159I	tier1	39528	4667	4613	52	0.011	28613	3472	3045	405	0.117	15394	1502	1387	112	0.075	34704	3947	3937	8	0.002	21918	2235	2103	123	0.055
754150	12	19653148	19653148	A	T	*AEBP2*	missense	c.1292	p.H431L	tier1	2436	207	206	1	0.005	2552	247	182	64	0.260	5187	703	525	177	0.252	2071	198	197	1	0.000	2682	293	257	36	0.123
754150	13	101712169	101712169	C	T	*NALCN*	splice_site	c.4905+1	e41+1	tier1	3120	509	499	10	0.020	2422	414	287	127	0.307	1816	414	298	116	0.280	1830	218	216	2	0.000	100	13	11	2	0.000
754150	14	91467486	91467486	C	T	*RPS6KA5*	missense	c.121	p.A41T	tier1	5292	540	532	8	0.015	6709	817	477	333	0.411	12458	1517	975	537	0.355	4600	510	509	1	0.000	13014	1607	1267	334	0.209
754150	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	24812	2921	2820	98	0.034	17605	2245	1055	1178	0.528	9868	969	512	456	0.471	45138	5264	5223	31	0.006	22704	2588	2015	547	0.214
754150	17	74732959	74732959	G	C	*SRSF2*	missense	c.284	p.P95R	tier1	9661	1103	1071	31	0.028	12055	1712	921	780	0.459	4914	608	383	224	0.369	8732	1060	1051	8	0.000	474	12	12	0	0.000
754150	19	6906516	6906516	C	T	*EMR1*	missense	c.1022	p.A341V	tier1	9834	1112	1096	16	0.014	15087	1959	1420	530	0.272	17828	1694	1449	243	0.144	24638	2834	2821	10	0.004	27921	3273	2865	391	0.120
754150	19	15654862	15654862	G	A	*CYP4F22*	intronic	c.1006+14	e7+14	tier3	28635	3791	3708	75	0.020	25389	3880	2121	1717	0.447	17751	1657	1066	588	0.356	42389	5413	5402	4	0.000	23926	2990	2374	597	0.201

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
754150	20	3127469	3127469	C	G	*FASTKD5*	missense	c.2248	p.E750Q	tier1	8547	944	912	31	0.033	17344	2205	1194	998	0.455	10908	1081	645	436	0.403	30850	3383	3354	27	0.008	16604	1874	1515	355	0.190
754150	20	29652147	29652147	A	G	*MLLT10P1*	5_prime_flanking_region	c.-14087	NULL	tier4	41376	7127	6538	527	0.075	18439	2659	2479	170	0.064	20947	4228	3918	305	0.000	33089	4590	3963	585	0.129	2644	209	191	18	0.000
754150	20	55967777	55967777	G	C	*RBM38*	missense	c.305	p.R102P	tier1	15263	2080	2043	32	0.015	30050	3990	2450	1496	0.379	12918	1305	897	403	0.310	30621	3631	3624	3	0.001	25388	2858	2188	647	0.228
754150	22	50903351	50903351	C	T	*SBF1*	splice_region	c.1333-5	e13-5	tier2	14749	2452	2404	45	0.018	13321	2725	1614	1079	0.401	4423	658	459	195	0.298	12482	1977	1961	15	0.008	6304	771	643	123	0.161
754150	X	73064091	73064091	A	G	*XIST*	rna	NULL	NULL	tier1	8126	1021	960	61	0.060	9415	1375	133	1241	0.903	11277	1103	323	777	0.706	61253	7703	7657	44	0.006	21689	2666	2065	586	0.221
754150	X	123505288	123505288	T	C	*SH2D1A*	rna	NULL	NULL	tier1	2972	378	356	22	0.058	2096	333	32	300	0.904	2654	494	138	355	0.720	4714	610	604	4	0.007	8943	1195	956	233	0.196
769516	1	116947126	116947126	C	G	*ATP1A1*	3_prime_untranslated_region	c.*60	NULL	tier3	4379	903	898	5	0.006	21673	3270	2398	847	0.261	NA	NA	NA	NA	NA	9447	1255	1247	5	0.004	3764	301	147,147;	7	0.023
769516	1	170927719	170927719	G	T	*MROH9*	intronic	c.152+38	e3+38	tier3	6124	916	916	0	0.000	15862	2328	2038	287	0.123	NA	NA	NA	NA	NA	11442	1559	1555	2	0.000	10996	1518	1499,8;	8	0.005
769516	1	200943970	200943970	G	A	*KIF21B*	silent	c.4686	p.S1562	tier1	30045	4414	4382	24	0.005	58382	8718	6087	2524	0.293	NA	NA	NA	NA	NA	27640	4100	4055	42	0.010	20505	2778	32,1934	208	0.075
769516	3	186288815	186288815	A	G	*DNAJB11*	intronic	c.68+61	e1+61	tier2	9068	1299	86	9	0.095	18749	2517	340	34	0.091	NA	NA	NA	NA	NA	6400	879	197	3	0.000	1573	168	36,29;	0	0.000
769516	4	74361009	74361009	C	T	*AFM*	3_prime_untranslated_region	c.*74361009	NULL	tier3	20688	2713	2695	5	0.002	31126	3996	3348	623	0.157	NA	NA	NA	NA	NA	24465	3130	3113	16	0.005	21395	2757	325,139	38	0.014
769516	4	187541903	187541903	C	T	*FAT1*	missense	c.5837	p.S1946N	tier1	18839	2348	2344	4	0.002	31206	3969	2813	1128	0.286	NA	NA	NA	NA	NA	18065	2235	2228	5	0.002	12830	1496	0,1451;	40	0.027
769516	5	15936967	15936967	C	T	*FBXL7*	missense	c.1148	p.A383V	tier1	45492	5016	5001	14	0.003	111272	13453	9607	3678	0.277	NA	NA	NA	NA	NA	60333	7882	7841	34	0.004	40486	5549	429,201	101	0.018
769516	5	73168759	73168759	T	A	*ARHGEF28*	intronic	c.2567-65	e21-65	tier3	3926	763	760	2	0.003	12210	1939	1383	544	0.282	NA	NA	NA	NA	NA	6441	913	911	2	0.000	3970	344	72,262;	10	0.029
769516	9	100137897	100137897	C	G	*CCDC180*	3_prime_untranslated_region	c.*100137897	NULL	tier3	26103	4043	4026	7	0.002	69060	10464	7499	2842	0.275	NA	NA	NA	NA	NA	41497	6046	6009	30	0.005	18833	2454	079,133	42	0.017
769516	9	127549340	127549340	C	T	*OLFML2A*	silent	c.177	p.D59	tier1	11993	1888	1881	6	0.003	26202	3916	2880	1008	0.259	NA	NA	NA	NA	NA	14504	2032	2027	4	0.002	8607	1160	481,645;	32	0.028
769516	13	32783001	32783001	C	T	*FRY*	nonsense	c.4030	p.R1344*	tier1	29902	3840	3832	7	0.002	71199	9365	6966	2291	0.247	NA	NA	NA	NA	NA	31719	4091	4081	8	0.002	18021	2029	67,1618	41	0.020
769516	14	59113492	59113492	C	T	*DACT1*	silent	c.2151	p.Y717	tier1	27387	3265	3250	12	0.004	60077	7305	5202	2043	0.282	NA	NA	NA	NA	NA	36538	4619	4600	16	0.003	12268	1544	1420,86;	37	0.024
769516	16	81208267	81208267	A	C	*PKD1L2*	missense	c.604	p.C202G	tier1	626	121	119	2	0.017	5527	830	583	243	0.294	NA	NA	NA	NA	NA	1417	199	198	1	0.000	2	0	0,0;	0	NA
769516	17	71361450	71361450	T	C	*SDK2*	missense	c.5252	p.N1751S	tier1	13306	2032	2026	5	0.002	25360	3981	2888	1069	0.270	NA	NA	NA	NA	NA	13517	2099	2089	7	0.003	6345	767	760,0;	7	0.009
769516	17	74732959	74732959	G	C	*SRSF2*	missense	c.284	p.P95R	tier1	13419	2024	2016	5	0.002	31580	3381	2412	946	0.282	NA	NA	NA	NA	NA	17820	2431	2420	10	0.004	326	0	0,0;	0	NA
769516	18	14361468	14361468	G	A	*ENSG00000265437*	5_prime_untranslated_region	c.-14361468	NULL	tier3	21053	3364	3348	9	0.003	25555	4492	3223	1233	0.277	NA	NA	NA	NA	NA	9823	2009	2001	5	0.002	2823	282	49,225;	8	0.028
769516	22	19130308	19130308	G	A	*DGCR14*	missense	c.235	p.R79W	tier1	17674	2331	2318	12	0.005	49652	6802	4723	2011	0.299	NA	NA	NA	NA	NA	15778	2169	2139	24	0.011	5436	687	218,408;	61	0.089
783437	6	102516350	102516350	C	T	*GRIK2*	silent	c.2691	p.N897	tier1	23399	3242	3235	1	0.000	13388	1363	1337	22	0.016	30048	3106	3065	34	0.011	29579	3249	3237	1	0.000	NA	NA	NA	NA	NA
783437	8	143369132	143369132	G	C	*TSNARE1*	intronic	c.1291-3286	e10-3286	tier3	17065	2199	2194	3	0.001	7403	755	735	20	0.026	5800	682	671	11	0.016	5172	631	631	0	0.000	NA	NA	NA	NA	NA
796518	1	55611693	55611693	C	T	*USP24*	silent	c.1860	p.E620	tier1	2735	306	305	0	0.000	2750	289	208	78	0.273	4172	363	266	95	0.263	4630	544	544	0	0.000	4025	379	378	0	0.000
796518	2	98846643	98846643	G	A	*VWA3B*	missense	c.2281	p.V761I	tier1	3446	0	0	0	0.000	3850	409	336	72	0.176	3596	288	228	59	0.206	6741	798	796	0	0.000	6897	637	636	0	0.000
796518	2	171379066	171379066	T	C	*MYO3B*	intronic	c.3602+3016	e30+3016	tier3	11063	0	0	0	0.000	12509	1466	1031	421	0.290	14926	1522	1051	463	0.306	20224	2722	2718	1	0.000	20329	2141	2138	2	0.000
796518	2	179346878	179346878	G	A	*PLEKHA3*	intronic	c.40+1242	e1+1242	tier3	3836	642	642	0	0.000	3467	500	389	107	0.216	4079	512	423	88	0.172	6296	1174	1173	0	0.000	4252	659	659	0	0.000
796518	2	198266834	198266834	T	C	*SF3B1*	missense	c.2098	p.K700E	tier1	18394	2435	2433	0	0.000	20454	2571	2410	148	0.058	19730	2099	1959	136	0.065	30517	4012	4009	0	0.000	35369	4442	4432	0	0.000
796518	2	198267483	198267483	C	A	*SF3B1*	missense	c.1874	p.R625L	tier1	3722	520	520	0	0.000	3949	538	521	16	0.030	4192	362	359	2	0.000	7985	1218	1217	1	0.000	5274	635	635	0	0.000
796518	4	151682922	151682922	T	C	*LRBA*	intronic	c.5645+13	e34+13	tier4	674	0	0	0	0.000	1457	161	151	10	0.062	889	67	55	12	0.179	1728	185	185	0	0.000	1419	130	130	0	0.000
796518	4	155254236	155254236	C	T	*DCHS2*	missense	c.1627	p.G543S	tier1	11394	1883	1880	3	0.002	13827	2246	1646	579	0.260	10147	1138	827	296	0.264	20024	3577	3572	4	0.001	21124	3282	3280	0	0.000
796518	5	140202971	140202971	C	T	*PCDHA5*	silent	c.1611	p.R537	tier1	1653	0	0	0	0.000	655	122	53	69	0.566	601	70	35	35	0.500	1960	305	304	0	0.000	2503	394	394	0	0.000
796518	6	170591580	170591580	G	A	*DLL1*	3_prime_untranslated_region	c.*382	NULL	tier3	2950	0	0	0	0.000	2716	321	230	88	0.277	3426	296	202	92	0.313	4031	509	505	1	0.000	3178	312	311	1	0.000
796518	7	28319235	28319235	C	G	*ENSG00000174495*	5_prime_untranslated_region	c.-28319235	NULL	tier3	3407	0	0	0	0.000	4523	623	517	103	0.166	4202	413	361	52	0.126	9641	1240	1240	0	0.000	8509	982	982	0	0.000
796518	12	48179692	48179692	G	T	*ENSG00000268069*	3_prime_untranslated_region	c.*353	NULL	tier3	10808	1767	1767	0	0.000	10771	1519	1092	413	0.274	8069	849	606	236	0.280	13552	2333	2327	1	0.000	20204	2897	2888	5	0.002
796518	13	101733940	101733940	G	A	*NALCN*	nonsense	c.3823	p.R1275*	tier1	11729	1438	1437	1	0.001	15703	1787	1700	81	0.045	15221	1448	1376	67	0.046	23670	3041	3037	0	0.000	19157	2186	2180	1	0.000
796518	15	32929534	32929534	C	A	*ARHGAP11A*	missense	c.2560	p.Q854K	tier1	10923	1293	1293	0	0.000	13570	1477	1061	408	0.278	10655	979	715	258	0.265	25768	3325	3320	3	0.000	23055	2417	2412	3	0.000
796518	16	56919177	56919177	A	G	*SLC12A3*	missense	c.1826	p.E609G	tier1	4986	679	678	0	0.000	6581	799	556	232	0.294	2924	272	182	89	0.328	3994	538	535	0	0.000	10163	1111	1108	1	0.000
796518	17	986858	986858	G	A	*ABR*	missense	c.541	p.L181F	tier1	31085	4098	4095	1	0.000	39897	4979	3450	1460	0.297	20203	2102	1453	628	0.302	58897	8026	8015	8	0.001	70838	8775	8767	2	0.000
796518	17	51900882	51900882	G	A	*KIF2B*	missense	c.488	p.R163H	tier1	4720	0	0	0	0.000	2910	380	257	122	0.322	1254	145	105	40	0.276	9285	1297	1295	2	0.000	6827	900	898	2	0.000
796518	18	47383269	47383269	A	G	*MYO5B*	splice_region	c.3945-9	e30-9	tier3	29377	4078	4075	0	0.000	33035	4218	2987	1185	0.284	28341	3065	2198	820	0.272	48547	6832	6827	3	0.000	52944	6594	6582	4	0.001
796518	20	31877714	31877714	T	C	*BPIFB1*	missense	c.281	p.I94T	tier1	31471	4071	4064	3	0.001	35854	4617	3256	1288	0.283	24965	2625	1856	739	0.285	52471	7228	7203	5	0.001	64901	7846	7820	4	0.001
818831	1	75107026	75107026	G	A	*C1orf173*	missense	c.433	p.P145S	tier1	12106	1526	1507	18	0.012	15729	2080	1735	338	0.163	7766	632	632	0	0.000	7660	1014	1013	0	0.000	NA	NA	NA	NA	NA
818831	1	181706695	181706695	C	T	*CACNA1E*	missense	c.3457	p.R1153C	tier1	4108	793	790	3	0.004	7336	1587	1554	30	0.019	2480	275	275	0	0.000	3915	829	828	0	0.000	NA	NA	NA	NA	NA
818831	2	92031582	92031582	G	A	*ABCD1P5*	3_prime_untranslated_region	c.*92031582	NULL	tier3	952	158	157	1	0.006	595	103	93	10	0.097	886	95	94	1	0.000	570	99	98	0	0.000	NA	NA	NA	NA	NA
818831	2	101666881	101666881	G	A	*TBC1D8*	missense	c.854	p.P285L	tier1	16644	2107	2104	1	0.000	33039	4573	4159	391	0.086	30284	2536	2519	8	0.003	19580	2776	2772	0	0.000	NA	NA	NA	NA	NA
818831	5	112926812	112926812	C	A	*YTHDC2*	missense	c.3900	p.N1300K	tier1	2270	362	360	1	0.003	3976	774	706	68	0.088	1384	140	139	1	0.000	1523	299	299	0	0.000	NA	NA	NA	NA	NA
818831	14	102445717	102445717	C	A	*DYNC1H1*	silent	c.406	p.R136	tier1	26005	3360	3313	45	0.013	28558	3721	3118	587	0.158	13778	1105	1092	9	0.008	16772	2215	2211	0	0.000	NA	NA	NA	NA	NA
818831	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	17629	2229	2187	37	0.017	26269	3426	2889	516	0.152	17063	1424	1416	5	0.004	17273	2269	2265	3	0.001	NA	NA	NA	NA	NA
818831	20	33577635	33577635	G	A	*MYH7B*	silent	c.1806	p.A602	tier1	13455	1819	1783	36	0.020	20741	2808	2376	420	0.150	8881	723	720	3	0.004	12330	1629	1626	0	0.000	NA	NA	NA	NA	NA
819544	1	1747229	1747229	T	C	*GNB1*	missense	c.169	p.K57E	tier1	12174	2045	2042	0	0.000	10938	1379	1343	35	0.025	11441	1994	1940	52	0.026	19144	2954	2951	0	0.000	35448	5278	5269	0	0.000
819544	2	141143461	141143461	C	T	*LRP1B*	splice_site	c.10531+1	e67+1	tier1	7556	1171	1171	0	0.000	10020	1250	1222	27	0.022	8986	1530	1472	53	0.035	18744	2879	2877	0	0.000	21318	3291	3290	0	0.000
819544	5	176940748	176940748	C	G	*DDX41*	missense	c.1036	p.A346P	tier1	27810	3765	3750	5	0.001	22065	2392	2274	107	0.045	16971	2279	2107	163	0.072	35571	4526	4517	2	0.000	50003	6503	6496	1	0.000
819544	12	50037698	50037698	G	T	*PRPF40B*	nonsense	c.2497	p.E833*	tier1	6433	875	872	0	0.000	10622	1113	1082	25	0.023	9376	1234	1171	59	0.048	18504	2316	2314	0	0.000	27552	3604	3602	0	0.000
829970	1	151238730	151238730	G	T	*PSMD4*	3_prime_untranslated_region	c.*151238730	NULL	tier3	12436	3171	3165	4	0.001	86795	7694	4309	3328	0.436	16273	3876	2232	1620	0.421	84141	11684	11670	2	0.000	90233	11894	11884	3	0.000
829970	2	1665807	1665807	T	C	*PXDN*	intronic	c.1680+37	e13+37	tier2	51988	6492	6484	5	0.001	152340	4935	2606	2299	0.469	28584	3721	2110	1578	0.428	151160	7193	7186	0	0.000	227572	8626	8626	0	0.000
829970	2	21238083	21238083	G	A	*APOB*	silent	c.3558	p.T1186	tier1	53606	8193	8051	2	0.000	138062	8472	5006	3191	0.389	29395	4212	2718	1415	0.342	172851	13654	13148	6	0.000	197191	14495	13945	3	0.000
829970	2	95944840	95944840	G	T	*PROM2*	nonsense	c.1222	p.E408*	tier1	29916	3809	3807	2	0.001	102720	3554	1943	1595	0.451	19118	2437	1356	1075	0.442	131254	6058	6057	0	0.000	144110	5756	5756	0	0.000
829970	2	105442572	105442572	C	G	*LOC100506421*	intronic	c.NULL	NULL	tier3	56432	8226	8217	5	0.001	170389	9392	5620	3667	0.395	31233	4182	2436	1702	0.411	172568	13881	13873	0	0.000	209225	14443	14441	0	0.000
829970	3	38151817	38151817	G	C	*DLEC1*	intronic	c.3443+45	e23+45	tier3	64655	8105	8101	2	0.000	191330	6688	4236	2404	0.362	30643	3816	2817	980	0.258	249637	12414	12405	0	0.000	307421	12886	12881	3	0.000
829970	3	56766462	56766462	A	G	*ARHGEF3*	splice_region	c.1138-10	e11-10	tier3	20381	3578	3577	1	0.000	110778	7799	4994	2744	0.355	20803	3007	1976	1006	0.337	130905	12970	12961	1	0.000	139579	11965	11961	1	0.000
829970	3	101477008	101477008	A	T	*CEP97*	missense	c.1558	p.N520Y	tier1	1693	0	0	0	0.000	11006	2068	1097	964	0.468	1826	346	194	152	0.439	7262	0	0	0	NA	8473	2010	2010	0	0.000
829970	3	182910694	182910694	G	C	*MCF2L2*	5_prime_untranslated_region	c.-182910694	NULL	tier3	25043	3632	3629	2	0.001	83799	4155	2463	1671	0.404	13966	2087	1272	807	0.388	104136	6753	6750	1	0.000	112672	7491	7491	0	0.000
829970	4	5857824	5857824	A	T	*CRMP1*	intronic	c.820+46	e4+46	tier3	51044	6663	6653	6	0.001	187930	7219	3924	3246	0.453	22438	2724	1583	1124	0.415	188022	11095	11090	1	0.000	178177	10569	10567	0	0.000
829970	4	15839802	15839802	T	A	*CD38*	intronic	c.659+14	e5+14	tier3	18942	2530	2530	0	0.000	39555	1985	1713	267	0.135	8587	1145	901	236	0.208	67017	4690	4687	0	0.000	76383	4555	4555	0	0.000
829970	4	70255405	70255405	C	A	*ENSG00000215110*	3_prime_untranslated_region	c.*70255405	NULL	tier3	2666	684	684	0	0.000	9415	1623	839	777	0.481	2173	426	292	132	0.311	7638	1826	1826	0	0.000	10439	2260	2259	0	0.000
829970	5	7303612	7303612	G	A	*LOC442132*	intronic	c.NULL	NULL	tier3	14348	1898	1897	1	0.001	48620	2902	1580	1307	0.453	7714	838	508	325	0.390	45484	4038	4036	1	0.000	45895	3699	3697	1	0.000
829970	5	149439406	149439406	C	T	*CSF1R*	silent	c.1989	p.T663	tier1	57139	7342	7332	5	0.001	82332	3806	457	3337	0.880	19716	2679	678	1994	0.746	190219	11449	11430	5	0.000	246940	11646	11641	2	0.000
829970	6	66803321	66803321	C	T	*NUFIP1P*	3_prime_flanking_region	c.*3	NULL	tier3	12783	1933	1930	3	0.002	55548	3714	3143	552	0.149	8119	1096	893	201	0.184	47111	4943	4940	1	0.000	37893	3756	3753	2	0.000
829970	8	73125568	73125568	C	T	*ENSG00000250979*	5_prime_untranslated_region	c.-73125568	NULL	tier2	21661	3045	3042	0	0.000	78753	5390	3347	2017	0.376	25259	3397	2310	1068	0.316	41422	4483	4481	0	0.000	87421	6112	6106	2	0.000
829970	10	82279156	82279156	A	G	*TSPAN14*	3_prime_untranslated_region	c.*1424	NULL	tier3	12472	3172	3170	0	0.000	42206	4754	2491	2232	0.473	8512	1891	1002	880	0.468	38145	6721	6713	0	0.000	47831	8085	8082	0	0.000
829970	10	127477858	127477858	G	T	*UROS*	5_prime_untranslated_region	c.-127477858	NULL	tier3	136399	16747	16730	12	0.001	542812	16667	9566	6839	0.417	83090	10516	6335	4041	0.389	694030	29518	29498	6	0.000	704824	26452	26443	4	0.000
829970	11	49897871	49897871	C	T	*ENSG00000255190*	3_prime_untranslated_region	c.*49897871	NULL	tier3	7443	1003	1001	1	0.001	15015	1174	579	594	0.506	5864	673	341	329	0.491	10037	1108	1107	0	0.000	29417	2897	2892	1	0.000
829970	12	5603366	5603366	C	A	*NTF3*	missense	c.25	p.Q9K	tier1	82767	11594	11572	10	0.001	214130	12259	7344	4788	0.395	43952	5794	3657	2059	0.360	234301	20187	20170	1	0.000	248725	18809	18803	2	0.000
829970	12	18760087	18760087	T	G	*PIK3C2G*	intronic	c.4088-2382	e30-2382	tier2	28366	4482	4478	0	0.000	96593	5328	5001	319	0.060	20101	3091	2960	122	0.040	99568	8630	8624	0	0.000	103297	7835	7834	0	0.000
829970	12	27919782	27919782	C	A	*MANSC4*	intronic	c.230-50	e2-50	tier2	32162	4309	4307	1	0.000	76569	4188	3220	955	0.229	14405	1941	1628	312	0.161	108171	8302	8296	0	0.000	124286	7734	7734	0	0.000
829970	13	99446895	99446895	C	T	*DOCK9*	missense	c.1993	p.V665I	tier1	58982	9940	9933	4	0.000	163885	10115	5160	4857	0.485	34216	5722	3198	2466	0.435	160016	14678	14665	7	0.000	172345	14861	14850	5	0.000
829970	14	60577741	60577741	A	G	*C14orf135*	3_prime_untranslated_region	c.*2692	NULL	tier4	13866	2410	2404	3	0.001	55331	5401	2843	2522	0.470	9648	1461	848	607	0.417	47490	6896	6889	1	0.000	48271	6433	6431	0	0.000
829970	14	90650882	90650882	A	C	*KCNK13*	missense	c.762	p.Q254H	tier1	22108	2853	2850	2	0.001	61776	2823	2475	342	0.121	15620	1953	1602	343	0.176	64072	4024	4023	0	0.000	94271	6209	6206	0	0.000
829970	15	24926165	24926165	A	T	*C15orf2*	3_prime_untranslated_region	c.*1680	NULL	tier4	29826	4404	4402	2	0.000	160478	6984	3670	3239	0.469	22506	3261	1757	1489	0.459	165642	10258	10251	0	0.000	139479	7910	7905	0	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
829970	15	58007312	58007312	A	T	*POLR2M*	3_prime_untranslated_region	c.*435	NULL	tier3	17889	2733	2733	0	0.000	24527	2393	2007	376	0.158	10531	1419	1268	148	0.105	23746	2949	2946	0	0.000	37343	4007	4001	0	0.000
829970	16	72829450	72829450	A	G	*ZFHX3*	silent	c.7131	p.P2377	tier1	65842	8099	8093	4	0.000	220053	6568	3723	2801	0.429	39904	5153	2947	2181	0.425	274693	12266	12261	1	0.000	303829	12310	12307	0	0.000
829970	17	7577094	7577094	G	A	*TP53*	missense	c.844	p.R282W	tier1	42359	5489	5479	7	0.001	99618	3652	409	3224	0.887	19432	2511	601	1904	0.760	208625	11018	11002	4	0.000	243764	11574	11565	2	0.000
829970	19	17763404	17763404	A	T	*UNC13A*	intronic	c.1703+36	e13+36	tier3	24156	3848	3844	3	0.001	143446	6046	3217	2799	0.465	24442	3752	2115	1607	0.432	144133	9806	9796	2	0.000	158867	10029	10021	1	0.000
829970	19	18378165	18378165	T	G	*KIAA1683*	missense	c.185	p.K62T	tier1	60614	7436	7432	1	0.000	351109	10301	9767	504	0.049	47292	6159	5891	256	0.042	449565	17831	17829	0	0.000	430796	16176	16171	0	0.000
829970	19	39214520	39214520	G	C	*ACTN4*	intronic	c.1552-57	e14-57	tier3	18493	3153	3143	5	0.002	47830	3698	2035	1649	0.448	9229	1181	750	424	0.361	33152	4838	4813	2	0.000	63944	5988	5983	0	0.000
829970	19	53793213	53793213	A	T	*BIRC8*	missense	c.415	p.S139T	tier1	8821	1628	1624	2	0.001	45234	5091	2678	2380	0.471	6860	947	557	387	0.410	35152	5449	5446	0	0.000	35809	5161	5159	0	0.000
829970	20	30785389	30785389	G	C	*PLAGL2*	silent	c.357	p.T119	tier1	9332	1375	1375	0	0.000	29576	1963	1330	621	0.318	5178	699	508	190	0.272	41021	3266	3262	1	0.000	45205	3275	3273	0	0.000
829970	21	31655211	31655211	C	G	*KRTAP24-1*	missense	c.40	p.V14L	tier1	33433	4364	4356	4	0.001	119572	6297	3361	2884	0.462	25184	3378	2022	1344	0.399	147714	9761	9751	2	0.000	149189	9355	9351	2	0.000
829970	21	42694456	42694456	G	A	*FAM3B*	intronic	c.20-394	e2-394	tier4	14752	2300	2298	2	0.001	61745	4709	2938	1752	0.374	10902	1470	907	558	0.381	64284	7089	7086	1	0.000	67722	6909	6908	1	0.000
829970	21	45877697	45877697	G	A	*LRRC3*	3_prime_untranslated_region	c.*396	NULL	tier3	63833	8705	8704	1	0.000	232119	9581	5287	4170	0.441	45194	6079	3512	2501	0.416	305112	15863	15856	0	0.000	368306	16212	16208	1	0.000
829970	22	33255649	33255649	T	C	*TIMP3*	3_prime_untranslated_region	c.*285	NULL	tier3	8345	1083	1082	1	0.001	15331	923	561	360	0.391	6165	701	429	270	0.386	12831	0	0	0	NA	21898	1865	1865	0	0.000
839903	1	82436028	82436028	C	T	*LPHN2*	missense	c.2752	p.H918Y	tier1	16021	1977	1975	2	0.001	10125	1338	1077	254	0.191	14759	1912	1860	48	0.025	29834	2968	2967	0	0.000	35199	4572	4572	0	0.000
839903	1	115258747	115258747	C	T	*NRAS*	missense	c.35	p.G12D	tier1	13256	1591	1589	1	0.001	21386	2683	2358	310	0.116	19040	2396	2363	24	0.010	40180	4913	4910	1	0.000	56196	7343	7334	0	0.000
839903	1	177927426	177927426	C	T	*SEC16B*	missense	c.136	p.A46T	tier1	18951	2560	2556	3	0.001	24301	3416	1797	1587	0.469	24429	3372	3108	253	0.075	44549	5407	5404	0	0.000	44986	5858	5855	0	0.000
839903	1	222705451	222705451	C	A	*HHIPL2*	missense	c.1580	p.R527L	tier1	3662	401	400	0	0.000	3425	403	347	55	0.137	5921	715	702	13	0.018	10791	1308	1298	0	0.000	16444	2203	2203	0	0.000
839903	1	223568401	223568401	G	A	*C1orf65*	silent	c.1584	p.K528	tier1	14942	1917	1912	4	0.002	23633	3360	1928	1405	0.422	22610	3139	2936	197	0.063	42509	5373	5367	1	0.000	44194	5949	5946	0	0.000
839903	2	26677567	26677567	G	T	*DRC1*	missense	c.1972	p.D658Y	tier1	13984	1671	1664	3	0.002	18947	2523	1712	800	0.318	23621	3115	2989	124	0.040	43144	4466	4464	0	0.000	55025	7187	7186	0	0.000
839903	2	44203321	44203321	G	A	*LRPPRC*	missense	c.698	p.A233V	tier1	7918	841	840	0	0.000	17347	2207	1995	208	0.094	19424	2497	2470	25	0.010	35835	3621	3620	0	0.000	67422	8974	8969	0	0.000
839903	2	187367384	187367384	G	A	*ZC3H15*	intronic	c.534+70	e5+70	tier3	11850	1262	1259	1	0.001	8032	932	834	93	0.100	11241	1347	1343	2	0.000	17248	2132	2132	0	0.000	39208	5088	5087	0	0.000
839903	3	16217151	16217151	G	T	*GALNT15*	missense	c.493	p.A165S	tier1	12286	1808	1798	5	0.003	16378	2137	1187	929	0.439	20824	3448	3248	190	0.055	31150	3693	3690	0	0.000	34060	5234	5226	0	0.000
839903	3	57447266	57447266	G	A	*DNAH12*	nonsense	c.2617	p.Q873*	tier1	3954	451	449	0	0.000	1921	222	123	97	0.441	4228	548	508	35	0.064	3886	0	0	0	NA	20142	2610	2608	0	0.000
839903	3	78680237	78680237	A	G	*ROBO1*	intronic	c.3626+74	e24+74	tier3	27223	3276	3274	0	0.000	19918	2479	2184	284	0.115	22538	2981	2942	36	0.012	41854	4224	4219	0	0.000	85366	10709	10701	0	0.000
839903	3	130317212	130317212	G	C	*COL6A6*	missense	c.4537	p.A1513P	tier1	321	45	45	0	0.000	1549	237	134	100	0.427	538	59	54	5	0.085	2842	697	697	0	0.000	2	0	0	0	NA
839903	4	145050305	145050305	T	A	*GYPA*	intronic	c.38-8564	e2-8564	tier3	533	0	0	0	0.000	617	90	63	27	0.300	255	25	25	0	0.000	1781	411	411	0	0.000	NA	NA	NA	NA	NA
839903	5	101726657	101726657	G	A	*SLCO6A1*	intronic	c.1879+28	e11+28	tier3	1176	0	0	0	0.000	4934	496	286	207	0.420	4057	366	351	13	0.036	10569	1566	1560	0	0.000	7285	800	798	0	0.000
839903	5	131326603	131326603	A	G	*ACSL6*	missense	c.328	p.Y110H	tier1	6567	821	814	0	0.000	16117	2125	1190	912	0.434	22355	2975	2799	170	0.057	38415	4468	4456	0	0.000	32138	4528	4519	0	0.000
839903	5	140203552	140203552	G	T	*PCDHA5*	missense	c.2192	p.C731F	tier1	8679	1086	1080	1	0.001	9480	1388	940	442	0.320	11864	1541	1484	55	0.036	21627	2771	2768	1	0.000	29412	3784	3782	0	0.000
839903	6	30229312	30229312	G	T	*HCG17*	intronic	c.NULL	NULL	tier3	831	125	125	0	0.000	1417	249	155	90	0.367	565	72	66	6	0.083	2257	521	521	0	0.000	3	0	0	0	NA
839903	7	151082221	151082221	G	A	*WDR86*	missense	c.815	p.T272M	tier1	5581	1014	1012	2	0.002	10832	2225	1875	340	0.154	7063	1288	1249	38	0.030	18522	3784	3781	0	0.000	3403	0	0	0	NA
839903	8	1649371	1649371	G	A	*DLGAP2*	missense	c.2735	p.R912H	tier1	14210	1645	1641	4	0.002	21248	2891	1546	1322	0.461	20485	2632	2432	193	0.074	38133	5051	5047	1	0.000	23433	3051	3048	1	0.000
839903	8	65496059	65496059	C	T	*BHLHE22*	3_prime_untranslated_region	c.*1566	NULL	tier2	7201	772	770	0	0.000	7932	936	819	110	0.118	8762	1004	993	8	0.008	16563	2506	2500	2	0.000	30797	3990	3983	0	0.000
839903	9	32624147	32624147	T	A	*ENSG00000223440*	5_prime_flanking_region	c.-9305	NULL	tier4	10999	1258	1253	0	0.000	6781	900	747	150	0.167	12571	1608	1601	7	0.004	23472	2945	2944	0	0.000	47045	6174	6173	0	0.000
839903	10	5494360	5494360	G	A	*NET1*	missense	c.403	p.A135T	tier1	6161	947	943	2	0.002	7354	1317	705	602	0.461	4947	775	728	46	0.059	15103	3139	3127	1	0.000	10558	1565	1565	0	0.000
839903	10	90582658	90582658	G	A	*ANKRD22*	rna	NULL	NULL	tier1	2327	198	198	0	0.000	13685	1464	847	604	0.416	15452	1732	1628	100	0.058	32174	4065	4064	0	0.000	56788	7642	7630	0	0.000
839903	10	112356174	112356174	G	C	*SMC3*	missense	c.1982	p.R661P	tier1	2238	0	0	0	0.000	1960	187	173	14	0.075	3461	385	383	1	0.000	4746	498	497	0	0.000	16697	2195	2194	0	0.000
839903	10	131634749	131634749	C	T	*EBF3*	3_prime_untranslated_region	c.*1444	NULL	tier3	298	24	24	0	0.000	460	36	25	11	0.306	139	0	0	0	NA	666	114	114	0	0.000	2	0	0	0	NA
839903	11	1083328	1083328	C	A	*MUC2*	splice_region	c.2219+9	e16+9	tier2	6632	826	822	1	0.001	6001	792	492	287	0.368	6163	808	771	34	0.042	12008	1621	1617	0	0.000	12507	1690	1690	0	0.000
839903	11	46334349	46334349	C	T	*CREB3L1*	intronic	c.963-53	e8-53	tier3	10799	1282	1280	2	0.002	16663	2226	1345	862	0.391	19110	2500	2371	125	0.050	35000	3903	3901	0	0.000	36345	4718	4716	0	0.000
839903	11	55322753	55322753	C	T	*OR4C15*	missense	c.971	p.A324V	tier1	11073	1238	1237	0	0.000	12460	1655	1495	156	0.094	12179	1467	1434	32	0.022	25077	3536	3533	0	0.000	54254	7205	7198	1	0.000
839903	11	107219570	107219570	T	G	*CWF19L2*	5_prime_untranslated_region	c.-107219570	NULL	tier3	1223	139	139	0	0.000	2335	325	186	132	0.415	1223	121	115	6	0.050	3500	593	592	0	0.000	7581	0	0	0	NA
839903	12	43945607	43945607	G	T	*ADAMTS20*	intronic	c.91+27	e1+27	tier2	17826	2013	2009	3	0.001	25514	3486	1988	1455	0.423	21667	2780	2623	152	0.055	47487	6269	6262	2	0.000	37539	4621	4620	0	0.000
839903	12	49725038	49725038	C	T	*TROAP*	missense	c.2140	p.R714C	tier1	6430	866	863	3	0.003	13393	1935	1148	769	0.401	19398	2622	2484	134	0.051	31953	3657	3654	1	0.000	41013	5357	5356	0	0.000
839903	13	36401953	36401953	T	G	*DCLK1*	intronic	c.1288-62	e9-62	tier3	751	0	0	0	0.000	1093	117	62	55	0.470	866	92	86	6	0.065	4909	0	0	0	NA	17971	2345	2339	0	0.000
839903	14	76211445	76211445	G	A	*TTLL5*	missense	c.1289	p.R430H	tier1	4121	375	375	0	0.000	6838	790	765	24	0.030	5685	659	658	1	0.000	12188	1512	1509	0	0.000	26461	3502	3497	4	0.000
839903	14	106135124	106135124	C	T	*IGHGP*	5_prime_untranslated_region	c.-106135124	NULL	tier3	8889	1059	1059	0	0.000	12333	1565	1361	199	0.128	13943	1828	1764	62	0.034	24025	2032	2030	1	0.000	23846	0	0	0	NA
839903	15	57999148	57999148	C	T	*POLR2M*	silent	c.108	p.R36	tier1	3085	397	396	0	0.000	7090	959	838	116	0.122	10598	1332	1314	13	0.010	16848	2267	2262	2	0.000	18720	2272	2271	0	0.000
839903	16	29851667	29851667	C	T	*MVP*	missense	c.1078	p.R360C	tier1	4971	583	583	0	0.000	14488	2016	1084	914	0.457	10796	1354	1272	78	0.058	26067	3017	3008	2	0.000	15099	2009	2007	0	0.000
839903	16	30722141	30722141	G	T	*SRCAP*	nonsense	c.1201	p.E401*	tier1	12239	1488	1485	2	0.001	16843	2400	1663	722	0.303	21021	2928	2801	120	0.041	39412	4993	4990	0	0.000	36464	4913	4909	0	0.000
839903	16	87160454	87160454	A	G	*C16orf95*	intronic	c.NULL	NULL	tier3	12158	1405	1401	1	0.001	14687	1794	1581	201	0.113	18000	2256	2239	15	0.007	29916	3197	3193	0	0.000	44014	5789	5788	0	0.000
839903	17	7010496	7010496	G	T	*ASGR2*	intronic	c.512-26	e6-26	tier3	12157	1394	1390	2	0.001	34577	4608	2623	1929	0.424	31167	3931	3680	235	0.060	66328	7528	7528	0	0.000	79359	10372	10362	0	0.000
839903	17	39041424	39041424	C	T	*KRT20*	missense	c.14	p.R5H	tier1	19666	2443	2429	9	0.004	19385	2676	1577	1075	0.405	22134	2976	2793	179	0.060	41608	5280	5272	2	0.000	48791	6386	6382	1	0.000
839903	18	21452994	21452994	C	T	*LAMA3*	5_prime_untranslated_region	c.-15	NULL	tier3	9722	1491	1489	2	0.001	14169	2412	1348	1051	0.438	12511	1974	1838	134	0.068	27087	4614	4610	2	0.000	15862	2057	2056	1	0.000
839903	19	13136234	13136234	G	T	*NFIX*	nonsense	c.403	p.E135*	tier1	8119	1096	1095	1	0.001	11128	1799	1427	364	0.203	10777	1564	1543	21	0.013	24312	3724	3722	0	0.000	18315	2335	2333	0	0.000
839903	19	42219296	42219296	G	A	*CEACAM5*	3_prime_untranslated_region	c.*42219296	NULL	tier3	5237	748	746	1	0.001	6917	1030	612	418	0.406	7037	983	928	54	0.055	13075	1654	1653	0	0.000	11531	0	0	0	NA
839903	20	16349047	16349047	C	G	*KIF16B*	intronic	c.3499-576	e23-576	tier3	3220	504	501	2	0.004	9020	1330	785	540	0.408	6834	916	849	66	0.072	15742	2668	2665	0	0.000	5845	0	0	0	NA
839903	X	48926088	48926088	C	T	*CCDC120*	missense	c.1985	p.A662V	tier1	11764	1315	1311	2	0.002	24504	3063	1650	1379	0.455	21113	2695	2515	169	0.063	43443	5186	5181	0	0.000	29471	3775	3773	1	0.000
839903	X	77222318	77222318	C	T	*ATP7A*	intronic	c.1-4800	e1-4800	tier4	3356	384	383	1	0.003	5066	627	349	276	0.442	4496	559	524	35	0.063	9506	1168	1168	0	0.000	20835	2785	2774	1	0.000
839903	X	153631127	153631127	G	A	*DNASE1L1*	missense	c.830	p.A277V	tier1	9408	0	0	0	0.000	21032	2659	2589	64	0.024	21933	2919	2909	5	0.002	38624	3475	3474	1	0.000	50451	6644	6644	0	0.000
848524	1	150432709	150432709	T	C	*RPRD2*	silent	c.1327	p.L443	tier1	15924	2860	2814	46	0.016	6005	1091	900	190	0.174	NA	NA	NA	NA	NA	32761	5742	5739	0	0.000	62769	7946	7935	0	0.000
848524	1	168161365	168161365	C	T	*TIPRL*	intronic	c.516+627	e4+627	tier3	14733	1924	1888	35	0.018	2781	303	231	72	0.238	NA	NA	NA	NA	NA	28753	3746	3746	0	0.000	53098	6112	6104	4	0.000
848524	1	243419492	243419492	A	G	*SDCCAG8*	missense	c.17	p.E6G	tier1	10815	1489	1451	38	0.026	4186	519	278	238	0.461	NA	NA	NA	NA	NA	21959	3000	2995	1	0.000	24499	3150	3147	0	0.000
848524	2	237103618	237103618	C	T	*ASB18*	missense	c.1298	p.R433H	tier1	12353	1698	1649	48	0.028	4035	417	215	200	0.482	NA	NA	NA	NA	NA	24644	3181	3172	3	0.000	36840	4253	4249	0	0.000
848524	3	50138116	50138116	G	A	*RBM5*	3_prime_untranslated_region	c.*609	NULL	tier3	787	73	72	1	0.014	723	68	44	24	0.353	NA	NA	NA	NA	NA	4434	436	434	0	0.000	33	0	0	0	NA
848524	3	57611690	57611690	A	G	*DENND6A*	3_prime_untranslated_region	c.*2251	NULL	tier2	2296	286	281	5	0.017	1174	119	68	51	0.429	NA	NA	NA	NA	NA	7753	0	0	0	NA	4008	444	443	0	0.000
848524	4	1803182	1803182	C	A	*FGFR3*	silent	c.534	p.A178	tier1	17944	2303	2244	56	0.024	7914	846	507	337	0.399	NA	NA	NA	NA	NA	50425	6406	6402	2	0.000	41016	5300	5296	1	0.000
848524	4	8234226	8234226	G	A	*SH3TC1*	3_prime_untranslated_region	c.*8234226	NULL	tier2	20447	3008	3000	8	0.003	3202	519	419	99	0.191	NA	NA	NA	NA	NA	27640	4595	4593	0	0.000	49035	5920	5919	0	0.000
848524	4	54324769	54324769	T	C	*FIP1L1*	3_prime_untranslated_region	c.*54324769	NULL	tier3	14812	1857	1817	39	0.021	2805	273	154	119	0.436	NA	NA	NA	NA	NA	18415	2345	2341	0	0.000	76356	8221	8220	0	0.000
848524	4	67142574	67142574	T	A	*MIR1269A*	rna	NULL	NULL	tier1	20128	2740	2656	82	0.030	5930	682	405	271	0.401	NA	NA	NA	NA	NA	32285	4381	4378	2	0.000	36193	4023	4023	0	0.000
848524	4	165187407	165187407	T	C	*43160*	intronic	c.1+116932	e0+116932	tier4	9555	1249	1234	15	0.012	2790	278	209	69	0.248	NA	NA	NA	NA	NA	16614	2088	2087	0	0.000	50348	5500	5497	0	0.000
848524	5	80064748	80064748	C	G	*MSH3*	missense	c.2179	p.R727G	tier1	7927	935	931	4	0.004	1659	139	129	10	0.072	NA	NA	NA	NA	NA	12177	1439	1436	0	0.000	49492	5681	5678	1	0.000
848524	5	140221091	140221091	G	T	*PCDHA8*	missense	c.185	p.R62L	tier1	13256	2228	2173	52	0.023	4823	674	373	296	0.442	NA	NA	NA	NA	NA	24693	3713	3710	2	0.000	24425	3080	3078	1	0.000
848524	5	176016454	176016454	C	A	*CDHR2*	3_prime_untranslated_region	c.*176016454	NULL	tier3	18031	2850	2773	76	0.027	10503	1379	753	618	0.451	NA	NA	NA	NA	NA	61345	8827	8818	4	0.000	52369	6186	6183	0	0.000
848524	6	88757740	88757740	C	T	*SPACA1*	silent	c.117	p.A39	tier1	5426	806	789	17	0.021	1588	185	104	80	0.435	NA	NA	NA	NA	NA	11512	1606	1606	0	0.000	1435	0	0	0	NA
848524	7	53103572	53103572	C	T	*POM121L12*	missense	c.208	p.R70C	tier1	9131	1261	1217	43	0.034	3096	418	186	231	0.554	NA	NA	NA	NA	NA	21822	3395	3392	0	0.000	10159	1263	1260	1	0.000
848524	8	51449330	51449330	G	A	*SNTG1*	silent	c.642	p.S214	tier1	6847	1100	1085	15	0.014	2540	392	231	160	0.409	NA	NA	NA	NA	NA	14995	2626	2623	0	0.000	24408	2609	2600	0	0.000
848524	8	92982935	92982935	G	A	*RUNX1T1*	missense	c.1523	p.A508V	tier1	3148	605	589	16	0.026	1622	281	157	122	0.437	NA	NA	NA	NA	NA	6673	1263	1263	0	0.000	2721	642	641	0	0.000
848524	8	144800290	144800290	C	G	*MAPK15*	3_prime_untranslated_region	c.*144800290	NULL	tier3	27039	3560	3469	86	0.024	7763	810	438	370	0.458	NA	NA	NA	NA	NA	46370	6005	6004	0	0.000	84621	9965	9961	0	0.000
848524	9	98242628	98242628	T	C	*PTCH1*	intronic	c.945+44	e6+44	tier3	10053	1153	1143	9	0.008	4419	438	399	35	0.081	NA	NA	NA	NA	NA	29179	3637	3631	0	0.000	71511	8729	8716	0	0.000
848524	11	69631012	69631012	C	A	*FGF3*	intronic	c.324+76	e2+76	tier3	23138	3526	3433	92	0.026	9346	1194	678	506	0.427	NA	NA	NA	NA	NA	50774	7264	7260	2	0.000	63906	7448	7445	1	0.000
848524	11	78601098	78601098	G	A	*TENM4*	intronic	c.849-33	e5-33	tier3	18152	2661	2587	73	0.027	4764	546	317	225	0.415	NA	NA	NA	NA	NA	29562	4245	4241	2	0.000	35147	0	0	0	NA
848524	12	3432534	3432534	G	T	*ENSG00000236908*	rna	NULL	NULL	tier1	20271	2884	2799	84	0.029	8093	1042	580	458	0.441	NA	NA	NA	NA	NA	55691	7727	7724	2	0.000	41558	5021	5020	1	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
848524	17	40666295	40666295	C	T	*MIR5010*	rna	NULL	NULL	tier1	15202	2089	2024	64	0.031	8197	876	487	387	0.443	NA	NA	NA	NA	NA	53662	7044	7038	0	0.000	96862	11601	11587	0	0.000
848524	17	48594960	48594960	C	T	*MYCBPAP*	missense	c.422	p.P141L	tier1	1871	388	386	2	0.005	1201	248	165	81	0.329	NA	NA	NA	NA	NA	3750	730	730	0	0.000	9	0	0	0	NA
848524	18	42531907	42531907	G	A	*SETBP1*	missense	c.2602	p.D868N	tier1	33806	4405	4361	43	0.010	10538	1209	878	327	0.271	NA	NA	NA	NA	NA	60890	8051	8045	2	0.000	90832	9836	9825	2	0.000
848524	19	1043430	1043430	C	G	*ABCA7*	silent	c.888	p.L296	tier1	12979	1709	1680	27	0.016	3119	331	174	157	0.474	NA	NA	NA	NA	NA	17315	2188	2187	0	0.000	12310	0	0	0	NA
848524	19	37064363	37064363	A	T	*LOC101927599*	rna	NULL	NULL	tier1	4280	554	538	16	0.029	2810	339	194	143	0.424	NA	NA	NA	NA	NA	13995	1821	1819	0	0.000	39	0	0	0	NA
855934	1	228403429	228403429	G	A	*OBSCN*	missense	c.1994	p.R665Q	tier1	22300	2989	2893	94	0.031	24643	2799	1434	1323	0.480	19684	2930	1552	1365	0.468	57126	5792	5784	2	0.000	82543	5668	5646	0	0.000
855934	2	81421390	81421390	G	A	*ENSG00000234429*	3_prime_flanking_region	c.*71	NULL	tier2	9501	1286	1266	20	0.016	8989	1121	583	530	0.476	5443	997	502	494	0.496	15179	2898	2896	1	0.000	21579	2130	2112	0	0.000
855934	2	166611398	166611398	G	T	*GALNT3*	intronic	c.1524+44	e7+44	tier3	3312	365	363	0	0.000	1413	122	100	22	0.180	2969	386	314	70	0.182	3645	0	0	0	NA	5340	544	539	0	0.000
855934	2	172231602	172231602	C	T	*ENSG00000224553*	5_prime_untranslated_region	c.-172231602	NULL	tier3	7597	1034	1034	0	0.000	8960	1103	626	472	0.430	6232	947	517	430	0.454	20792	2574	2573	0	0.000	20542	1608	1589	0	0.000
855934	4	106157845	106157845	C	T	*TET2*	nonsense	c.2746	p.Q916*	tier1	5968	737	736	1	0.001	8791	959	682	274	0.287	4649	614	415	197	0.322	11492	1839	1839	0	0.000	11340	1010	1009	0	0.000
855934	5	140783754	140783754	G	A	*PCDHGA9*	missense	c.1235	p.R412Q	tier1	23881	2830	2801	23	0.008	17004	1485	873	598	0.407	22431	3092	1773	1307	0.424	41261	4457	4452	1	0.000	54408	4705	4655	0	0.000
855934	6	30530949	30530949	C	T	*PRR3*	rna	NULL	NULL	tier1	2715	383	378	2	0.005	5694	610	318	289	0.476	2764	446	246	200	0.448	10805	1511	1507	0	0.000	10715	964	960	0	0.000
855934	6	31637272	31637272	C	T	*CSNK2B*	nonsense	c.544	p.Q182*	tier1	28782	3963	3955	3	0.001	32051	3923	2086	1757	0.457	33542	4653	2378	2245	0.486	56317	6721	6709	0	0.000	96178	6943	6885	0	0.000
855934	7	6439714	6439714	T	C	*RAC1*	3_prime_untranslated_region	c.*6439714	NULL	tier3	21570	2662	2660	2	0.001	16783	1701	1139	544	0.323	15399	2032	1576	448	0.221	50068	4599	4595	0	0.000	66552	4153	4147	0	0.000
855934	7	101758501	101758501	C	T	*CUX1*	nonsense	c.655	p.R219*	tier1	11794	1325	1323	2	0.002	8454	716	383	329	0.462	13207	1757	908	845	0.482	18061	2086	2085	1	0.000	30000	2631	2612	0	0.000
855934	8	139668092	139668092	C	T	*COL22A1*	intronic	c.3333+48	e44+48	tier3	4597	599	594	4	0.007	5273	552	299	250	0.455	2443	334	170	162	0.488	7959	1219	1217	1	0.000	11226	1202	1183	0	0.000
855934	8	145773426	145773426	C	T	*ARHGAP39*	silent	c.1044	p.S348	tier1	10243	1257	1247	8	0.006	16542	1656	772	866	0.529	12829	1766	917	844	0.479	35100	3956	3953	0	0.000	52895	4242	4215	0	0.000
855934	10	3183033	3183033	A	G	*PITRM1*	intronic	c.2649-29	e24-29	tier3	18710	2268	2266	0	0.000	13126	1173	741	422	0.363	20424	2819	1718	1094	0.389	35437	3868	3866	0	0.000	40465	3273	3270	0	0.000
855934	10	43651051	43651051	A	G	*CSGALNACT2*	missense	c.454	p.T152A	tier1	12655	1579	1574	5	0.003	8911	947	547	395	0.419	19417	2578	1530	1043	0.405	22682	2376	2372	0	0.000	29049	2253	2246	0	0.000
855934	10	71695049	71695049	G	A	*COL13A1*	intronic	c.1696-57	e30-57	tier3	2449	463	460	2	0.004	5289	873	489	377	0.435	1146	293	164	129	0.440	6555	1646	1643	0	0.000	5556	851	815	0	0.000
855934	10	104120904	104120904	G	A	*GBF1*	rna	NULL	NULL	tier1	17610	2163	2106	2	0.001	17647	1664	887	731	0.452	13624	1935	1031	888	0.463	32774	3721	3689	0	0.000	47533	3347	3160	0	0.000
855934	10	115528652	115528652	G	A	*PLEKHS1*	splice_region	c.417+3	e5+3	tier2	10392	1388	1377	11	0.008	10020	1043	590	440	0.427	8026	1167	671	493	0.424	21668	2847	2844	0	0.000	20478	1772	1763	0	0.000
855934	12	54796846	54796846	G	A	*ITGA5*	5_prime_untranslated_region	c.-54796846	NULL	tier3	13237	1766	1753	10	0.006	21520	2436	1280	1134	0.470	25246	3351	1777	1563	0.468	49193	4781	4777	1	0.000	87747	5500	5474	0	0.000
855934	12	70064230	70064230	T	G	*BEST3*	missense	c.590	p.D197A	tier1	5724	810	802	8	0.010	7819	895	479	412	0.462	5483	792	430	360	0.456	16909	2383	2379	0	0.000	28269	2139	2113	0	0.000
855934	16	84888372	84888372	C	T	*CRISPLD2*	missense	c.646	p.R216W	tier1	23506	3083	3052	28	0.009	28205	3122	1659	1411	0.460	31179	4347	2386	1941	0.449	64346	7136	7129	1	0.000	129438	10114	10073	0	0.000
855934	18	30253100	30253100	C	T	*KLHL14*	3_prime_untranslated_region	c.*1520	NULL	tier2	2685	230	226	3	0.013	2275	152	82	70	0.461	2913	320	170	149	0.467	3991	582	580	0	0.000	3466	448	426	0	0.000
855934	19	43679576	43679576	C	T	*PSG5*	missense	c.755	p.R252H	tier1	1478	249	246	2	0.008	4143	697	389	303	0.438	669	168	83	84	0.503	5239	1286	1282	1	0.000	2985	492	482	0	0.000
855934	19	57772501	57772501	C	G	*ZNF460*	5_prime_flanking_region	c.-19674	NULL	tier3	13320	1487	1414	69	0.047	15188	1320	683	620	0.476	10949	1540	727	799	0.524	28212	3401	3399	0	0.000	22066	2146	2127	0	0.000
855934	20	49199177	49199177	A	C	*PTPN1*	intronic	c.1285-52	e10-52	tier3	7893	1359	1320	35	0.026	7056	978	491	479	0.494	4892	963	513	448	0.466	14097	2432	2430	0	0.000	15762	1949	1944	0	0.000
855934	21	44514777	44514777	T	G	*U2AF1*	missense	c.470	p.Q157P	tier1	43629	4878	4825	47	0.010	37753	3682	1883	1742	0.481	40446	5307	2738	2535	0.481	92104	7022	7020	0	0.000	136549	7411	7406	0	0.000
855934	X	76888698	76888698	G	A	*ATRX*	missense	c.5131	p.P1711S	tier1	4150	513	512	0	0.000	4019	394	36	357	0.908	3741	542	29	513	0.946	8281	882	882	0	0.000	23645	1720	1700	0	0.000
856550	1	26317279	26317279	G	A	*PAFAH2*	missense	c.29	p.P10L	tier1	16035	281	280	0	0.000	14052	1791	1006	772	0.434	NA	NA	NA	NA	NA	18225	2226	2205	20	0.009	26779	3401	3394	4	0.001
856550	1	32127089	32127089	C	A	*COL16A1*	intronic	c.3727-30	e60-30	tier3	39309	589	585	1	0.002	27117	3296	2237	1026	0.314	NA	NA	NA	NA	NA	47593	6147	6098	39	0.006	69107	9132	9112	11	0.001
856550	1	115258747	115258747	C	T	*NRAS*	missense	c.35	p.G12D	tier1	19330	438	438	0	0.000	23250	2588	1574	983	0.384	NA	NA	NA	NA	NA	30695	3931	3910	15	0.004	37678	5089	5074	4	0.001
856550	1	204960404	204960404	G	A	*NFASC*	intronic	c.3092+2466	e23+2466	tier2	28176	466	466	0	0.000	29900	3837	2181	1631	0.428	NA	NA	NA	NA	NA	40119	5343	5280	50	0.009	51007	7119	7095	9	0.001
856550	1	206941873	206941873	A	G	*IL10*	3_prime_untranslated_region	c.*108	NULL	tier3	10642	211	210	0	0.000	5142	572	335	234	0.411	NA	NA	NA	NA	NA	10066	1234	1228	5	0.004	13124	1804	1799	2	0.000
856550	2	202514343	202514343	C	T	*MPP4*	missense	c.1540	p.V514I	tier1	27057	531	531	0	0.000	26057	3420	1943	1438	0.425	NA	NA	NA	NA	NA	27407	3812	3763	44	0.012	42712	5718	5702	9	0.002
856550	3	57232440	57232440	A	T	*HESX1*	missense	c.438	p.N146K	tier1	4022	0	0	0	0.000	3237	298	187	106	0.362	NA	NA	NA	NA	NA	4745	520	515	4	0.008	8517	1142	1140	0	0.000
856550	3	178546013	178546013	C	T	*KCNMB2*	missense	c.275	p.T92M	tier1	35800	497	494	2	0.004	39344	4727	3116	1548	0.332	NA	NA	NA	NA	NA	55388	7371	7304	60	0.008	71546	9435	9415	8	0.000
856550	5	24487247	24487247	C	A	*CDH10*	3_prime_untranslated_region	c.*525	NULL	tier4	4434	147	146	1	0.007	1283	85	55	29	0.345	NA	NA	NA	NA	NA	1814	144	144	0	0.000	3160	319	316	1	0.000
856550	5	112403792	112403792	C	A	*MCC*	missense	c.1444	p.V482L	tier1	1244	77	77	0	0.000	640	74	41	32	0.438	NA	NA	NA	NA	NA	394	68	68	0	0.000	496	83	82	0	0.000
856550	5	153190809	153190809	G	A	*GRIA1*	3_prime_untranslated_region	c.*24	NULL	tier3	1617	70	69	0	0.000	1193	133	78	55	0.414	NA	NA	NA	NA	NA	1093	197	196	1	0.000	1803	319	317	1	0.000
856550	6	66044805	66044805	C	T	*EYS*	3_prime_untranslated_region	c.*49	NULL	tier2	12924	267	267	0	0.000	5258	559	481	77	0.138	NA	NA	NA	NA	NA	15724	1962	1956	3	0.002	20651	2754	2747	4	0.000
856550	6	131179391	131179391	G	C	*EPB41L2*	5_prime_untranslated_region	c.-131179391	NULL	tier3	17553	265	264	1	0.004	26292	3321	2064	1238	0.375	NA	NA	NA	NA	NA	26967	3425	3410	13	0.004	42276	5340	5330	6	0.000
856550	7	131853016	131853016	A	G	*PLXNA4*	intronic	c.4286+47	e21+47	tier3	19038	277	277	0	0.000	20272	2530	1509	1007	0.400	NA	NA	NA	NA	NA	30147	3910	3874	33	0.008	45543	6132	6121	6	0.001
856550	7	148507436	148507436	T	C	*EZH2*	missense	c.2018	p.N673S	tier1	44237	759	759	0	0.000	21302	2599	1698	881	0.342	NA	NA	NA	NA	NA	42445	5536	5508	20	0.004	64878	8719	8702	6	0.001
856550	9	99233221	99233221	T	C	*HABP4*	intronic	c.744-72	e5-72	tier3	3440	198	196	0	0.000	1004	92	65	27	0.293	NA	NA	NA	NA	NA	1829	192	192	0	0.000	2961	444	441	1	0.000
856550	9	99233241	99233241	G	C	*HABP4*	intronic	c.744-52	e5-52	tier3	4869	0	0	0	0.000	1679	178	134	44	0.247	NA	NA	NA	NA	NA	2983	473	473	0	0.000	4805	956	954	1	0.000
856550	10	89118109	89118109	T	C	*NUTM2D*	silent	c.87	p.L29	tier1	16607	278	278	0	0.000	13296	1374	1057	304	0.223	NA	NA	NA	NA	NA	19825	2297	2286	11	0.005	25471	3331	3318	2	0.000
856550	11	5537218	5537218	C	T	*UBQLNL*	missense	c.454	p.V152M	tier1	25257	440	439	0	0.000	14891	2046	1478	559	0.274	NA	NA	NA	NA	NA	22199	3048	3033	13	0.004	32585	4634	4626	3	0.000
856550	11	72294529	72294529	G	T	*PDE2A*	missense	c.1681	p.Q561K	tier1	24974	505	505	0	0.000	17415	2313	1525	773	0.336	NA	NA	NA	NA	NA	33970	4718	4689	27	0.006	40078	5693	5681	4	0.001
856550	11	83770488	83770488	C	T	*DLG2*	silent	c.789	p.V263	tier1	8249	0	0	0	0.000	6595	660	385	272	0.414	NA	NA	NA	NA	NA	6910	812	804	7	0.009	8572	1189	1182	5	0.004
856550	11	117282559	117282559	G	A	*CEP164*	silent	c.4212	p.A1404	tier1	29513	597	596	0	0.000	30592	4095	2547	1501	0.371	NA	NA	NA	NA	NA	35054	5094	5073	12	0.002	43918	7203	7183	4	0.000
856550	12	46205132	46205132	T	G	*ARID2*	intronic	c.285-69	e4-69	tier3	1249	86	86	0	0.000	270	22	15	7	0.318	NA	NA	NA	NA	NA	369	71	71	0	0.000	463	60	59	0	0.000
856550	12	48376914	48376914	G	A	*COL2A1*	missense	c.2056	p.P686S	tier1	18647	338	338	0	0.000	17409	2094	1163	920	0.442	NA	NA	NA	NA	NA	20075	2690	2661	23	0.009	26600	3954	3945	4	0.001
856550	12	54734318	54734318	C	T	*COPZ1*	silent	c.30	p.F10	tier1	8728	194	194	0	0.000	9574	1150	643	499	0.437	NA	NA	NA	NA	NA	9845	1315	1306	7	0.005	13876	2006	1998	5	0.002
856550	12	125453425	125453425	C	T	*DHX37*	silent	c.1281	p.P427	tier1	27309	611	611	0	0.000	27687	3580	2001	1525	0.433	NA	NA	NA	NA	NA	27115	3651	3596	53	0.015	41979	5988	5970	8	0.000
856550	15	65496649	65496649	A	G	*CILP*	silent	c.876	p.T292	tier1	17835	305	305	0	0.000	20488	2479	1349	1098	0.449	NA	NA	NA	NA	NA	23446	2966	2928	26	0.009	29497	3956	3920	3	0.001
856550	16	13297355	13297355	C	G	*SHISA9*	missense	c.919	p.Q307E	tier1	34415	457	457	0	0.000	47556	5823	3290	2452	0.427	NA	NA	NA	NA	NA	69365	8764	8683	65	0.007	93396	11385	11338	19	0.002
856550	17	1028517	1028517	C	A	*ABR*	splice_site	c.246+1	e2+1	tier1	12596	304	304	0	0.000	11852	1421	774	637	0.451	NA	NA	NA	NA	NA	15851	2159	2146	13	0.006	20065	3137	3131	5	0.002
856550	17	11757380	11757380	G	A	*DNAH9*	missense	c.9568	p.A3190T	tier1	32662	603	600	2	0.003	39575	5099	5005	89	0.017	NA	NA	NA	NA	NA	47123	6716	6700	10	0.000	68857	9853	9835	10	0.000
856550	17	48356336	48356336	G	A	*TMEM92*	silent	c.345	p.A115	tier1	23718	0	0	0	0.000	28459	3427	2055	1314	0.390	NA	NA	NA	NA	NA	36645	4453	4402	35	0.008	47543	6337	6320	6	0.000
856550	17	59479337	59479337	C	G	*TBX2*	intronic	c.441+25	e2+25	tier2	10778	132	132	0	0.000	18489	2276	1360	903	0.399	NA	NA	NA	NA	NA	21898	2798	2767	27	0.010	30452	3916	3904	5	0.001
856550	17	74387223	74387223	G	C	*UBE2O*	missense	c.3680	p.S1227W	tier1	34296	623	621	1	0.002	38442	4406	2446	1865	0.433	NA	NA	NA	NA	NA	48713	6094	6035	39	0.006	62358	8651	8621	10	0.001
856550	20	45052040	45052040	C	T	*ELMO2*	intronic	c.1+9493	e0+9493	tier4	29133	504	504	0	0.000	22188	2833	1663	1152	0.409	NA	NA	NA	NA	NA	35226	4720	4685	31	0.007	52083	6885	6870	6	0.000
856550	20	57484420	57484420	C	T	*GNAS*	missense	c.604	p.R202C	tier1	16924	333	333	0	0.000	13647	1493	829	650	0.439	NA	NA	NA	NA	NA	20655	2529	2209	304	0.121	25685	3493	3477	5	0.001
856550	21	36252998	36252998	C	G	*RUNX1*	missense	c.364	p.G122R	tier1	29047	462	461	0	0.000	7001	878	400	474	0.542	NA	NA	NA	NA	NA	32413	4129	4119	10	0.002	50645	6353	6346	3	0.000
856550	22	16414079	16414079	G	A	*ENSG00000215268*	3_prime_untranslated_region	c.*16414079	NULL	tier3	12238	474	472	2	0.004	7527	1003	747	250	0.251	NA	NA	NA	NA	NA	9342	1711	1688	21	0.012	9754	2030	2012	17	0.008
856550	22	18628675	18628675	C	T	*TUBA8*	missense	c.745	p.R249C	tier1	5890	199	199	0	0.000	7136	733	411	317	0.435	NA	NA	NA	NA	NA	8905	1134	1124	10	0.009	11880	1722	1716	4	0.002
856550	22	45277142	45277142	G	A	*PHF21B*	3_prime_untranslated_region	c.*1824	NULL	tier2	2325	132	131	1	0.008	1632	140	96	43	0.309	NA	NA	NA	NA	NA	1355	200	199	0	0.000	1456	188	187	1	0.000
856550	X	41782248	41782248	G	C	*CASK*	rna	NULL	NULL	tier1	15191	237	237	0	0.000	31995	3763	2099	1617	0.435	NA	NA	NA	NA	NA	27092	3403	3334	63	0.019	31960	4346	4334	9	0.002
856550	X	86063662	86063662	A	G	*DACH2*	intronic	c.1241-4197	e8-4197	tier3	2018	0	0	0	0.000	1573	109	71	27	0.276	NA	NA	NA	NA	NA	1269	129	126	2	0.000	1787	185	184	1	0.000
856550	X	133527979	133527979	G	T	*PHF6*	nonsense	c.415	p.E139*	tier1	5157	0	0	0	0.000	4863	527	353	173	0.329	NA	NA	NA	NA	NA	6074	937	932	5	0.005	6805	1129	1126	2	0.000
875301	1	148887714	148887714	C	T	*ENSG00000231448*	3_prime_untranslated_region	c.*148887714	NULL	tier2	30370	3432	3419	0	0.000	51839	6182	6050	113	0.018	30827	3182	3174	2	0.000	131028	16631	16612	0	0.000	2	0	0	0	NA
875301	2	64807082	64807082	T	G	*AFTPH*	3_prime_untranslated_region	c.*64807082	NULL	tier3	10354	1080	1079	0	0.000	14182	1591	1467	117	0.074	13232	1535	1531	1	0.000	36868	4864	4863	0	0.000	4	0	0	0	NA
875301	2	198264776	198264776	T	G	*SF3B1*	splice_region	c.3013+3	e20+3	tier3	650	0	0	0	0.000	1640	180	176	4	0.022	2285	322	322	0	0.000	6196	685	685	0	0.000	NA	NA	NA	NA	NA
875301	3	50334761	50334761	G	C	*NAT6*	missense	c.200	p.P67R	tier1	3967	495	493	0	0.000	16911	2114	1993	112	0.053	11596	1558	1557	1	0.000	52721	7819	7812	1	0.000	1	0	0	0	NA
875301	4	183723267	183723267	G	A	*TENM3*	3_prime_untranslated_region	c.*1763	NULL	tier2	16957	1669	1665	1	0.001	19578	2151	2097	44	0.021	15833	1925	1906	15	0.008	59057	7505	7499	0	0.000	6	0	0	0	NA
875301	7	50450292	50450292	A	G	*IKZF1*	missense	c.476	p.N159S	tier1	25159	2558	2554	0	0.000	42802	4584	4338	222	0.049	29537	3348	3338	6	0.002	109535	14041	14021	0	0.000	6	0	0	0	NA
875301	11	121475955	121475955	C	T	*SORL1*	splice_region	c.4778+7	e34+7	tier3	4164	0	0	0	0.000	6993	834	779	52	0.063	5053	0	0	0	NA	17169	2364	2363	0	0.000	NA	NA	NA	NA	NA
876752	1	153190890	153190890	G	A	*PRR9*	silent	c.270	p.Q90	tier1	11491	1427	1405	21	0.015	14125	1638	1003	616	0.380	20071	3166	1771	1373	0.437	29907	3993	3987	4	0.001	NA	NA	NA	NA	NA
876752	1	207881643	207881643	A	G	*CR1L*	intronic	c.1414+35	e10+35	tier4	12296	1303	1289	10	0.008	10127	1019	850	164	0.162	19966	2614	2135	472	0.181	40343	4855	4845	4	0.001	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
876752	1	207881649	207881649	C	T	*CR1L*	intronic	c.1414+41	e10+41	tier4	12376	1303	1293	10	0.008	10290	1023	859	163	0.159	20065	2617	2138	472	0.181	40890	4862	4856	4	0.001	NA	NA	NA	NA	NA
876752	1	237947039	237947039	C	T	*RYR2*	silent	c.12045	p.N4015	tier1	14136	1517	1492	23	0.015	10916	1151	707	435	0.381	21593	2863	1626	1220	0.429	38543	4556	4554	1	0.000	NA	NA	NA	NA	NA
876752	2	233899445	233899445	G	A	*NEU2*	missense	c.821	p.G274E	tier1	9112	875	857	17	0.019	12898	1291	718	556	0.436	21521	2810	1451	1320	0.476	28854	3233	3230	3	0.001	NA	NA	NA	NA	NA
876752	3	38621021	38621021	C	T	*SCN5A*	intronic	c.3229-35	e17-35	tier3	12076	1090	1072	17	0.016	20091	1904	1203	673	0.359	40819	4978	2975	1960	0.397	67806	7261	7255	1	0.000	NA	NA	NA	NA	NA
876752	4	82026868	82026868	C	T	*PRKG2*	intronic	c.2063+99	e15+99	tier3	3984	382	377	5	0.013	3323	283	190	90	0.321	7152	889	499	386	0.436	11741	1292	1288	1	0.000	NA	NA	NA	NA	NA
876752	11	71373771	71373771	G	A	*ENPP7P8*	5_prime_flanking_region	c.-49015	NULL	tier3	2648	257	254	3	0.012	2703	246	142	103	0.420	3880	466	281	182	0.393	6877	829	829	0	0.000	NA	NA	NA	NA	NA
876752	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	15949	1632	1623	7	0.004	19357	1889	1838	47	0.025	32590	4102	3874	210	0.051	58015	6552	6545	5	0.001	NA	NA	NA	NA	NA
876752	17	6703354	6703354	C	G	*TEKT1*	missense	c.1249	p.V417L	tier1	20602	2173	2143	29	0.013	22234	2373	1464	880	0.375	43341	5841	3302	2473	0.428	77372	9235	9226	2	0.000	NA	NA	NA	NA	NA
876752	18	47380016	47380016	G	A	*MYO5B*	silent	c.4024	p.L1342	tier1	18885	2141	2113	26	0.012	27633	3101	1940	1123	0.367	44704	6356	3691	2602	0.413	84493	10512	10501	7	0.001	NA	NA	NA	NA	NA
876752	19	7944301	7944301	G	A	*FLJ22184*	5_prime_flanking_region	c.-5727	NULL	tier3	10051	991	974	16	0.016	13345	1233	656	569	0.464	23116	2961	1442	1494	0.509	33369	3719	3716	1	0.000	NA	NA	NA	NA	NA
876752	22	21153574	21153574	G	A	*PI4KA*	splice_region	c.1821-10	e16-10	tier3	20389	2190	2152	36	0.016	35600	3730	2237	1429	0.390	55400	7319	4134	3109	0.429	95222	11027	11022	4	0.000	NA	NA	NA	NA	NA
882325	1	112525116	112525116	T	G	*KCND3*	missense	c.233	p.D78A	tier1	15808	1730	1720	10	0.006	13690	1496	1073	408	0.275	10699	1537	1451	83	0.054	22914	3036	3030	1	0.000	NA	NA	NA	NA	NA
882325	1	228464970	228464970	G	T	*OBSCN*	missense	c.6710	p.C2237F	tier1	28759	3856	3821	25	0.007	34249	4299	2788	1435	0.340	23115	3128	3095	29	0.009	60989	8328	8321	6	0.001	NA	NA	NA	NA	NA
882325	1	228464971	228464971	T	A	*OBSCN*	nonsense	c.6711	p.C2237*	tier1	28078	3859	3830	26	0.007	33335	4255	2712	1465	0.351	22736	3116	3082	27	0.009	59209	8291	8280	0	0.000	NA	NA	NA	NA	NA
882325	2	25457242	25457242	C	T	*DNMT3A*	missense	c.2645	p.R882H	tier1	14740	1599	1564	30	0.019	15434	1582	1058	510	0.325	10194	1368	1039	326	0.239	43274	5239	5220	10	0.002	NA	NA	NA	NA	NA
882325	2	209113112	209113112	C	A	*IDH1*	0	c.395	p.R132L	tier1	14745	1776	1760	7	0.004	13079	1345	881	451	0.339	6426	918	918	0	0.000	32412	4049	4039	4	0.000	NA	NA	NA	NA	NA
882325	2	211421474	211421474	C	T	*CPS1*	missense	c.35	p.T12I	tier1	5578	453	444	8	0.018	5055	420	278	141	0.337	3282	445	417	24	0.054	11043	1140	1133	4	0.000	NA	NA	NA	NA	NA
882325	2	238253632	238253632	T	C	*COL6A3*	intronic	c.7163-37	e34-37	tier3	7767	770	767	2	0.003	9814	852	508	332	0.395	5982	824	762	60	0.073	11970	1487	1484	0	0.000	NA	NA	NA	NA	NA
882325	4	170913470	170913470	G	A	*MFAP3L*	splice_region	c.299-10	e2-10	tier3	12788	2049	2037	9	0.004	28959	3383	2143	1198	0.359	21112	3168	3119	45	0.014	51199	7071	7062	8	0.000	NA	NA	NA	NA	NA
882325	5	150923971	150923971	A	G	*FAT2*	silent	c.6717	p.H2239	tier1	27691	3126	3092	27	0.009	23836	2473	1519	910	0.375	19691	2653	2649	0	0.000	37293	4773	4766	0	0.000	NA	NA	NA	NA	NA
882325	8	54871008	54871008	T	C	*RGS20*	missense	c.1157	p.I386T	tier1	733	63	63	0	0.000	2216	177	113	63	0.358	1124	126	125	0	0.000	3504	279	279	0	0.000	NA	NA	NA	NA	NA
882325	9	139910760	139910760	C	T	*ABCA2*	missense	c.1136	p.R379Q	tier1	18561	2153	2125	23	0.011	33358	3630	2244	1330	0.372	23310	3091	2947	138	0.045	73115	9243	9222	8	0.000	NA	NA	NA	NA	NA
882325	11	56237381	56237381	A	G	*OR5M3*	missense	c.593	p.I198T	tier1	15520	1706	1693	11	0.006	12600	1299	818	470	0.365	13631	1794	1783	10	0.006	34812	4280	4278	0	0.000	NA	NA	NA	NA	NA
882325	11	64973991	64973991	C	G	*CAPN1*	missense	c.1411	p.R471G	tier1	11183	1922	1900	19	0.010	19232	2256	1386	846	0.379	9760	1801	1716	81	0.045	35681	5415	5401	10	0.000	NA	NA	NA	NA	NA
882325	11	89405200	89405200	C	A	*FOLH1B*	intronic	c.NULL	NULL	tier3	628	70	69	0	0.000	3671	315	261	52	0.166	3550	473	473	0	0.000	11020	1296	1294	0	0.000	NA	NA	NA	NA	NA
882325	12	21051353	21051353	C	A	*SLCO1B3*	intronic	c.1683-17	e12-17	tier2	5598	552	549	1	0.002	4182	404	268	135	0.335	5034	660	658	1	0.000	7046	829	828	1	0.000	NA	NA	NA	NA	NA
882325	12	111655648	111655648	G	A	*CUX2*	intronic	c.175-46	e3-46	tier3	17172	2192	2189	1	0.000	14704	1479	1078	391	0.266	11151	1778	1769	3	0.000	37860	5161	5152	3	0.000	NA	NA	NA	NA	NA
882325	15	33833126	33833126	G	T	*RYR3*	intronic	c.646+35	e7+35	tier3	10029	1150	1144	3	0.003	17877	2029	1565	446	0.222	17532	2516	2513	2	0.000	42068	5482	5468	3	0.000	NA	NA	NA	NA	NA
882325	17	74732959	74732959	G	A	*SRSF2*	missense	c.284	p.P95L	tier1	4807	550	548	2	0.004	12515	1282	949	327	0.256	5526	932	931	1	0.000	27616	3520	3520	0	0.000	NA	NA	NA	NA	NA
882325	18	55996142	55996142	G	A	*NEDD4L*	intronic	c.681-85	e10-85	tier3	27109	3159	3142	12	0.004	21948	2458	1635	785	0.324	22237	3121	3115	1	0.000	51693	6787	6775	0	0.000	NA	NA	NA	NA	NA
882325	19	2435136	2435136	G	A	*LMNB2*	missense	c.718	p.R240C	tier1	4710	463	457	6	0.013	10972	1161	671	474	0.414	5908	819	763	51	0.063	14607	1951	1945	1	0.000	NA	NA	NA	NA	NA
882325	X	50350816	50350816	C	G	*SHROOM4*	missense	c.3326	p.W1109S	tier1	63	10	9	1	0.100	600	86	21	65	0.756	301	74	27	47	0.635	623	108	107	1	0.000	NA	NA	NA	NA	NA
882325	X	53441798	53441798	A	G	*SMC1A*	missense	c.320	p.I107T	tier1	14554	1637	1636	1	0.001	16035	1652	1478	166	0.101	14576	2151	2149	0	0.000	41344	5491	5490	0	0.000	NA	NA	NA	NA	NA
882325	X	77911875	77911875	T	C	*ZCCHC5*	3_prime_untranslated_region	c.*615	NULL	tier2	8704	1085	1068	16	0.015	6620	749	213	535	0.715	7899	1036	1033	2	0.000	16660	2142	2141	0	0.000	NA	NA	NA	NA	NA
907471	1	237947546	237947546	C	T	*RYR2*	silent	c.12552	p.N4184	tier1	6362	834	832	0	0.000	12673	1284	1225	48	0.038	NA	NA	NA	NA	NA	21648	2744	2739	2	0.000	10792	1506	1505	0	0.000
907471	2	25457243	25457243	G	A	*DNMT3A*	missense	c.2644	p.R882C	tier1	14362	1706	1703	2	0.001	17463	1619	1574	43	0.027	NA	NA	NA	NA	NA	49099	5501	5498	2	0.000	41014	4616	4606	2	0.000
907471	5	82817864	82817864	G	A	*VCAN*	missense	c.3739	p.D1247N	tier1	14387	0	0	0	0.000	14541	1655	1631	23	0.014	NA	NA	NA	NA	NA	42167	3817	3813	3	0.000	42092	4109	4094	4	0.000
907471	5	112227415	112227415	G	A	*ZRSR1*	missense	c.79	p.A27T	tier1	8295	1057	1052	1	0.001	12405	1385	1357	28	0.020	NA	NA	NA	NA	NA	29706	3036	3026	9	0.000	21793	2470	2461	2	0.000
907471	5	142301123	142301123	G	T	*ARHGAP26*	rna	NULL	NULL	tier1	27548	3424	3419	0	0.000	20910	2010	1958	49	0.024	NA	NA	NA	NA	NA	74052	7542	7524	17	0.000	73643	7648	7597	13	0.000
907471	5	142301124	142301124	G	T	*ARHGAP26*	rna	NULL	NULL	tier1	27606	3418	3417	0	0.000	20792	1993	1942	47	0.024	NA	NA	NA	NA	NA	74170	7542	7533	6	0.000	73804	7653	7628	5	0.000
907471	12	32948971	32948971	C	T	*PKP2*	intronic	c.2489+72	e12+72	tier3	43308	7605	7585	11	0.001	38542	6065	5900	138	0.023	NA	NA	NA	NA	NA	83460	7704	4175	3484	0.000	70887	6778	3656	3079	0.000
907471	16	89805075	89805075	G	A	*FANCA*	silent	c.4302	p.A1434	tier1	9192	1143	1141	0	0.000	12241	1299	1278	17	0.013	NA	NA	NA	NA	NA	17364	2469	2461	2	0.000	12810	1926	1918	2	0.000
913698	1	91973859	91973859	A	G	*CDC7*	silent	c.240	p.Q80	tier1	23337	2946	2870	71	0.024	18422	2064	1375	671	0.328	14953	1424	970	444	0.314	27016	3474	3403	69	0.020	75242	8839	8835	1	0.000
913698	1	118426264	118426264	G	A	*GDAP2*	intronic	c.1108-15	e10-15	tier3	150	29	27	2	0.069	610	109	74	35	0.321	443	66	39	27	0.409	678	173	170	3	0.017	69	0	0	0	NA
913698	1	142826527	142826527	G	A	*ANKRD20A14P*	3_prime_untranslated_region	c.*142826527	NULL	tier3	95	20	19	1	0.050	986	210	94	116	0.552	490	70	23	47	0.671	681	175	170	5	0.029	4	0	0	0	NA
913698	1	182791320	182791320	G	A	*NPL*	missense	c.724	p.A242T	tier1	12451	1599	1580	14	0.009	11272	1233	1026	195	0.160	7594	762	584	174	0.230	15313	1962	1929	23	0.012	23434	2883	2883	0	0.000
913698	2	196636498	196636498	G	A	*DNAH7*	silent	c.11319	p.Y3773	tier1	2661	572	572	0	0.000	4491	862	734	128	0.148	1797	271	220	51	0.188	2146	496	492	1	0.000	79	0	0	0	NA
913698	2	227924194	227924194	C	T	*COL4A4*	silent	c.2310	p.P770	tier1	16222	2169	2099	64	0.030	13768	1656	1143	503	0.306	9193	906	610	292	0.324	15440	1902	1867	33	0.017	19236	2339	2335	3	0.000
913698	3	112300106	112300106	C	T	*SLC35A5*	missense	c.1142	p.P381L	tier1	6448	885	854	29	0.033	10045	1481	1018	456	0.309	5777	656	458	187	0.290	9018	1581	1555	26	0.016	350	16	16	0	0.000
913698	4	1656787	1656787	C	T	*FAM53A*	missense	c.800	p.G267E	tier1	9935	1354	1318	35	0.026	11923	1349	984	355	0.265	9197	906	655	246	0.273	18554	2476	2427	46	0.019	23974	3101	3100	0	0.000
913698	5	43277155	43277155	G	A	*NIM1*	splice_region	c.293-4	e2-4	tier3	13654	1689	1613	40	0.024	16177	1764	1290	449	0.258	12551	1181	794	351	0.307	24866	3415	3339	59	0.017	44029	5450	5394	1	0.000
913698	7	100468311	100468311	C	T	*TRIP6*	missense	c.266	p.A89V	tier1	8502	1522	1515	3	0.002	23805	3576	2972	584	0.164	16202	2171	1822	343	0.158	23806	3505	3488	12	0.003	23890	3318	3315	1	0.000
913698	9	119461034	119461034	C	T	*TRIM32*	missense	c.1013	p.A338V	tier1	13943	2028	1980	44	0.022	16341	2036	1449	569	0.282	12960	1437	1003	429	0.300	21413	2739	2686	51	0.019	39860	5106	5105	1	0.000
913698	9	124530916	124530916	C	G	*DAB2IP*	splice_region	c.1899+4	e10+4	tier3	2567	334	321	13	0.039	14457	1652	1148	492	0.300	9798	979	672	300	0.309	19662	2415	2366	45	0.019	25238	3206	3204	1	0.000
913698	11	5536564	5536564	G	A	*UBQLNL*	missense	c.1108	p.H370Y	tier1	18921	2714	2657	45	0.017	29330	4040	2972	1029	0.257	20192	2392	1690	680	0.287	33780	4711	4639	67	0.014	67474	9228	9214	1	0.000
913698	11	120744937	120744937	G	A	*GRIK4*	splice_region	c.1059+10	e8+10	tier3	27170	3556	3469	82	0.023	19900	2315	1624	671	0.292	16277	1752	1169	568	0.327	33343	4247	4164	77	0.018	60858	7953	7938	2	0.000
913698	12	91363823	91363823	G	A	*EPYC*	nonsense	c.796	p.Q266*	tier1	23958	3165	3161	0	0.000	15237	1915	1671	235	0.123	12576	1407	1232	171	0.122	21633	2782	2774	6	0.002	51957	6086	6081	0	0.000
913698	15	90631934	90631934	C	T	*IDH2*	missense	c.419	p.R140Q	tier1	19494	2514	2500	10	0.004	25435	2971	2370	589	0.199	17733	1809	1386	412	0.229	32784	4053	4021	27	0.007	56179	7096	7090	4	0.001
913698	16	88808530	88808530	G	A	*ENSG00000260617*	rna	NULL	NULL	tier1	21796	4162	4140	13	0.003	24988	4390	4247	135	0.031	17579	2989	2853	132	0.044	27546	4430	4428	1	0.000	17634	3481	3481	0	0.000
913698	17	39122986	39122986	G	A	*KRT39*	silent	c.123	p.V41	tier1	28240	3700	3590	99	0.027	23051	2635	1871	744	0.285	17974	1872	1294	566	0.304	32884	4110	4038	61	0.015	82017	9613	9604	2	0.000
913698	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	5322	732	714	17	0.023	15029	2026	1397	611	0.304	10487	1072	699	361	0.341	18928	2510	2462	46	0.018	765	0	0	0	NA
913698	20	40701696	40701696	C	T	*PTPRT*	3_prime_untranslated_region	c.*7823	NULL	tier2	21976	2943	2871	69	0.023	11962	1329	934	392	0.296	11465	1149	759	378	0.332	20042	2768	2710	51	0.018	57979	7084	7081	3	0.000
913698	20	60773672	60773672	G	A	*MTG2*	intronic	c.469-18	e4-18	tier3	14513	2006	1949	54	0.027	17837	2291	1590	689	0.302	12523	1428	968	449	0.317	25074	3101	3044	54	0.017	36105	4442	4441	1	0.000
913698	21	36252877	36252877	C	T	*RUNX1*	missense	c.485	p.R162K	tier1	24881	3629	3453	168	0.046	17147	2402	1021	1363	0.572	11843	1342	506	823	0.619	23144	3369	3277	90	0.027	39149	5210	5206	3	0.001
913698	X	52679352	52679352	T	G	*SSX7*	intronic	c.330+51	e4+51	tier3	455	72	70	2	0.028	2385	463	318	144	0.312	1078	137	94	43	0.314	942	227	217	9	0.040	24	0	0	0	NA
913698	X	140967238	140967238	G	A	*MAGEC3*	intronic	c.515+21	e3+21	tier3	4134	569	550	18	0.032	2878	402	256	143	0.358	2174	212	144	68	0.321	1123	191	187	4	0.021	41	0	0	0	NA
918051	1	94586694	94586694	A	G	*ABCA4*	5_prime_flanking_region	c.-93	NULL	tier3	6009	761	759	2	0.003	6890	774	456	314	0.408	3900	455	307	147	0.324	10048	950	950	0	0.000	NA	NA	NA	NA	NA
918051	1	94586695	94586695	C	G	*ABCA4*	5_prime_flanking_region	c.-94	NULL	tier3	6011	765	763	2	0.003	7093	797	471	324	0.408	3912	453	305	147	0.325	10191	968	967	1	0.000	NA	NA	NA	NA	NA
918051	7	105668989	105668989	C	T	*CDHR3*	3_prime_untranslated_region	c.*105668989	NULL	tier3	24843	3393	3392	1	0.000	17216	2061	1174	858	0.422	17435	2033	1326	691	0.343	26508	2801	2795	0	0.000	NA	NA	NA	NA	NA
918051	9	2907139	2907139	G	A	*CARM1P1*	5_prime_untranslated_region	c.-2907139	NULL	tier3	13417	2222	2220	2	0.001	9574	1302	748	543	0.421	11919	1581	1050	517	0.330	12519	1388	1387	0	0.000	NA	NA	NA	NA	NA
918051	9	88452656	88452656	C	T	*ENSG00000165121*	intronic	c.NULL	NULL	tier3	917	158	158	0	0.000	2140	268	199	69	0.257	2847	315	269	45	0.143	3230	372	370	1	0.000	NA	NA	NA	NA	NA
918051	10	19616672	19616672	T	A	*C10orf112*	intronic	c.1575+70	e8+70	tier3	10137	1760	1756	0	0.000	14265	1867	1061	778	0.423	13799	1711	1213	487	0.286	19961	2240	2238	0	0.000	NA	NA	NA	NA	NA
918051	10	55581617	55581617	A	T	*PCDH15*	rna	NULL	NULL	tier1	2006	339	339	0	0.000	3696	462	285	176	0.382	5249	546	375	168	0.309	4759	508	508	0	0.000	NA	NA	NA	NA	NA
918051	10	73492123	73492123	C	T	*CDH23*	silent	c.4110	p.D1370	tier1	46155	6931	6834	91	0.013	37811	5378	3076	2198	0.417	34154	4552	3045	1441	0.321	60650	7590	7586	2	0.000	NA	NA	NA	NA	NA
918051	10	85968514	85968514	G	A	*CDHR1*	silent	c.1197	p.L399	tier1	3592	360	359	1	0.003	5603	630	386	242	0.385	6253	736	546	186	0.254	8974	990	989	0	0.000	NA	NA	NA	NA	NA
918051	10	115985820	115985820	G	A	*TDRD1*	nonsense	c.3020	p.W1007*	tier1	11527	1518	1500	4	0.003	11499	1379	775	589	0.432	12086	1375	890	471	0.346	17460	1825	1822	0	0.000	NA	NA	NA	NA	NA
918051	11	63342376	63342376	T	C	*PLA2G16*	rna	NULL	NULL	tier1	5193	692	690	2	0.003	6380	707	411	288	0.412	4981	499	317	178	0.360	7134	617	616	0	0.000	NA	NA	NA	NA	NA
918051	11	92533422	92533422	T	C	*FAT3*	missense	c.7243	p.C2415R	tier1	19570	2669	2669	0	0.000	15976	1779	1065	691	0.394	13367	1357	946	401	0.298	17848	1735	1734	0	0.000	NA	NA	NA	NA	NA
918051	12	116446681	116446681	T	C	*MED13L*	missense	c.1537	p.I513V	tier1	24172	3119	3112	6	0.002	14780	1574	906	655	0.420	13662	1454	960	483	0.335	26328	2681	2680	0	0.000	NA	NA	NA	NA	NA
918051	14	57070634	57070634	A	G	*TMEM260*	missense	c.446	p.N149S	tier1	12957	1656	1656	0	0.000	10044	1038	585	447	0.433	13449	1344	904	434	0.324	12301	1134	1131	0	0.000	NA	NA	NA	NA	NA
918051	15	62359822	62359822	C	A	*C2CD4A*	missense	c.10	p.L4M	tier1	37148	4926	4917	5	0.001	25707	2913	1848	1015	0.355	14357	1575	1202	370	0.235	38024	3688	3685	0	0.000	NA	NA	NA	NA	NA
918051	16	780298	780298	G	A	*NARFL*	rna	NULL	NULL	tier1	16553	2511	2494	13	0.005	13918	1814	1205	595	0.331	9139	1107	851	252	0.228	21625	2202	2201	0	0.000	NA	NA	NA	NA	NA

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
918051	19	39869235	39869235	G	A	*SAMD4B*	splice_region	c.1530+6	e7+6	tier3	6187	876	875	0	0.000	4900	620	409	205	0.334	2161	309	231	77	0.250	3344	456	455	0	0.000	NA	NA	NA	NA	NA
918051	20	1920551	1920551	T	C	*LOC727993*	5_prime_flanking_region	c.-7341	NULL	tier2	5027	531	531	0	0.000	3216	295	177	117	0.398	2798	245	173	71	0.291	5984	471	470	0	0.000	NA	NA	NA	NA	NA
918051	20	34022502	34022502	G	A	*GDF5*	silent	c.711	p.A237	tier1	1807	321	321	0	0.000	1676	223	172	51	0.229	996	131	107	23	0.177	1868	227	226	0	0.000	NA	NA	NA	NA	NA
918051	20	44979120	44979120	G	C	*SLC35C2*	silent	c.1098	p.P366	tier1	15851	2109	2102	3	0.001	16967	1857	1053	780	0.426	19518	2020	1321	676	0.339	22750	2141	2140	0	0.000	NA	NA	NA	NA	NA
922185	2	20100829	20100829	T	A	*TTC32*	silent	c.54	p.S18	tier1	11579	1137	1128	9	0.008	9937	1117	898	213	0.192	19306	2189	1918	261	0.120	28612	3370	3364	0	0.000	55171	6624	6615	0	0.000
922185	2	179638759	179638759	A	G	*TTN*	missense	c.7136	p.V2379A	tier1	6889	676	663	9	0.013	8345	942	877	61	0.065	11713	1237	1150	82	0.067	17793	1942	1932	0	0.000	21615	2958	2956	0	0.000
922185	4	71463976	71463976	C	T	*AMBN*	intronic	c.136-97	e4-97	tier3	2122	199	194	5	0.025	2936	400	339	57	0.144	3839	399	355	44	0.110	6701	928	928	0	0.000	4196	0	0	0	NA
922185	4	100544120	100544120	T	A	*MTTP*	3_prime_untranslated_region	c.*115	NULL	tier3	14402	1241	1225	14	0.011	12855	1228	1031	192	0.157	20965	2042	1803	226	0.111	31808	3270	3269	0	0.000	56375	7374	7357	0	0.000
922185	5	82817833	82817833	C	T	*VCAN*	silent	c.3708	p.I1236	tier1	1830	234	231	3	0.013	3563	662	641	21	0.032	3284	587	562	23	0.039	6046	1038	1038	0	0.000	832	0	0	0	NA
922185	5	126753323	126753323	C	T	*MEGF10*	splice_region	c.1131-7	e9-7	tier3	16710	1905	1877	24	0.013	21308	2854	2236	593	0.210	35477	4834	3994	801	0.167	46324	6261	6257	0	0.000	52952	7682	7674	0	0.000
922185	5	137298188	137298188	T	C	*FAM13B*	intronic	c.1180-30	e9-30	tier3	18640	1982	1954	25	0.013	20216	2558	1974	564	0.222	32330	4085	3430	622	0.154	48280	6335	6330	0	0.000	60373	7832	7832	0	0.000
922185	7	55241540	55241540	G	T	*EGFR*	intronic	c.2062-74	e18-74	tier3	14771	1690	1668	13	0.008	17884	2294	2183	109	0.048	26533	3419	3199	204	0.060	40671	5321	5314	1	0.000	39964	4525	4507	0	0.000
922185	9	111954473	111954473	A	T	*EPB41L4B*	intronic	c.2301+85	e22+85	tier3	1765	168	165	3	0.018	4244	648	491	157	0.242	3941	521	396	124	0.238	6496	927	926	0	0.000	45	0	0	0	NA
922185	10	126678193	126678193	A	G	*CTBP2*	missense	c.2852	p.I951T	tier1	1417	158	157	1	0.006	2593	399	310	88	0.221	2973	423	341	82	0.194	3829	571	571	0	0.000	189	0	0	0	NA
922185	11	57970725	57970725	A	C	*OR1S2*	missense	c.929	p.M310R	tier1	8713	826	819	6	0.007	11552	1357	1091	264	0.195	18503	2051	1714	334	0.163	26136	3122	3120	0	0.000	38939	5766	5763	0	0.000
922185	11	117340626	117340626	C	T	*DSCAML1*	silent	c.3204	p.K1068	tier1	37155	4197	4166	18	0.004	46284	5756	4595	1093	0.192	76183	9897	8462	1339	0.137	118577	15253	15249	0	0.000	125825	14400	14392	2	0.000
922185	12	50026453	50026453	G	T	*PRPF40B*	3_prime_untranslated_region	c.*50026453	NULL	tier3	6993	654	645	7	0.011	9349	1135	851	271	0.242	15098	1631	1344	275	0.170	18410	2035	2032	0	0.000	8904	1201	1200	0	0.000
922185	14	21968662	21968662	A	G	*METTL3*	missense	c.1279	p.F427L	tier1	13707	1347	1329	15	0.011	13491	1612	1209	384	0.241	20059	2359	1828	513	0.219	28170	3281	3278	0	0.000	33906	4179	4169	0	0.000
922185	14	93704243	93704243	T	C	*BTBD7*	3_prime_untranslated_region	c.*4376	NULL	tier3	7080	722	718	4	0.006	7552	818	612	202	0.248	11852	1332	1115	211	0.159	16197	1803	1800	0	0.000	25317	3263	3261	0	0.000
922185	15	34519872	34519872	A	C	*EMC4*	3_prime_untranslated_region	c.*34519872	NULL	tier3	11316	1104	1095	8	0.007	15074	1648	1295	346	0.211	26812	3167	2590	565	0.179	36802	4180	4179	0	0.000	40071	5114	5103	0	0.000
922185	15	89386622	89386622	C	T	*ACAN*	missense	c.794	p.T265I	tier1	16654	1641	1620	19	0.012	19660	2404	1912	472	0.198	25186	2823	2371	423	0.151	40121	4902	4900	0	0.000	24487	2915	2914	0	0.000
922185	17	15457016	15457016	C	A	*TVP23C*	missense	c.223	p.D75Y	tier1	2110	109	108	1	0.009	2842	282	210	72	0.255	4169	290	243	41	0.144	6808	646	645	0	0.000	52	0	0	0	NA
922185	17	48668000	48668000	G	A	*CACNA1G*	intronic	c.2453+17	e10+17	tier3	14549	1571	1565	3	0.002	14559	1861	1800	51	0.028	25997	3267	3138	123	0.038	35281	4438	4436	1	0.000	41143	5542	5526	0	0.000
922185	18	19781636	19781636	A	T	*GATA6*	3_prime_untranslated_region	c.*850	NULL	tier2	2117	193	193	0	0.000	3671	420	336	84	0.200	5949	643	551	92	0.143	8277	1001	1000	0	0.000	16122	2031	2029	0	0.000
922185	18	21140392	21140392	G	A	*NPC1*	silent	c.684	p.D228	tier1	9686	1881	1866	15	0.008	12398	2384	2222	158	0.066	16282	3122	2822	292	0.094	26447	5240	5238	1	0.000	38363	6161	6157	0	0.000
933226	1	45798446	45798446	C	T	*MUTYH*	missense	c.565	p.G189R	tier1	20382	2781	2778	1	0.000	NA	NA	NA	NA	NA	21975	583	419	164	0.281	7614	768	768	0	0.000	32898	4250	4249	1	0.000
933226	2	228512849	228512849	G	A	*ENSG00000250599*	5_prime_untranslated_region	c.-228512849	NULL	tier3	21594	3322	3316	3	0.001	NA	NA	NA	NA	NA	16075	434	302	131	0.303	5776	653	651	1	0.000	24762	3460	3451	6	0.002
933226	2	241976165	241976165	G	A	*SNED1*	intronic	c.806-42	e5-42	tier2	15789	2591	2590	1	0.000	NA	NA	NA	NA	NA	7177	202	110	92	0.455	3663	434	432	1	0.000	14457	1932	1928	1	0.000
933226	2	242755726	242755726	G	T	*NEU4*	silent	c.84	p.R28	tier1	17300	2427	2423	3	0.001	NA	NA	NA	NA	NA	11078	306	222	84	0.275	4801	445	443	2	0.000	22155	2880	2872	5	0.002
933226	3	11303055	11303055	C	T	*HRH1*	3_prime_untranslated_region	c.*868	NULL	tier4	12616	2006	2003	2	0.001	NA	NA	NA	NA	NA	6500	194	124	69	0.358	3807	432	432	0	0.000	19516	2753	2747	4	0.001
933226	3	142546497	142546497	G	A	*ENSG00000240950*	5_prime_untranslated_region	c.-142546497	NULL	tier3	6013	923	922	1	0.001	NA	NA	NA	NA	NA	1665	57	32	25	0.439	1235	141	140	1	0.000	5351	832	829	1	0.000
933226	4	665776	665776	G	T	*PCGF3*	5_prime_flanking_region	c.-61694	NULL	tier3	15308	2598	2594	1	0.000	NA	NA	NA	NA	NA	8845	300	184	116	0.387	3924	0	0	0	NA	14810	2200	2199	1	0.000
933226	4	7741871	7741871	C	T	*SORCS2*	intronic	c.3416-56	e27-56	tier3	23134	2962	2960	1	0.000	NA	NA	NA	NA	NA	18441	425	252	172	0.406	7996	939	935	3	0.003	28710	3476	3469	5	0.001
933226	4	55161723	55161723	G	A	*PDGFRA*	3_prime_untranslated_region	c.*284	NULL	tier3	7931	1253	1253	0	0.000	NA	NA	NA	NA	NA	2852	103	82	21	0.204	1529	169	168	1	0.000	8389	1228	1225	1	0.000
933226	4	187628190	187628190	T	A	*FAT1*	missense	c.2792	p.N931I	tier1	35293	5096	5094	1	0.000	NA	NA	NA	NA	NA	13777	370	228	142	0.384	7642	870	863	5	0.006	40486	5401	5382	10	0.002
933226	5	13793657	13793657	A	G	*DNAH5*	silent	c.8191	p.L2731	tier1	6089	900	899	0	0.000	NA	NA	NA	NA	NA	4220	115	103	11	0.096	3712	406	406	0	0.000	19064	2505	2503	1	0.000
933226	5	31511227	31511227	C	T	*DROSHA*	missense	c.631	p.G211R	tier1	26906	3593	3592	1	0.000	NA	NA	NA	NA	NA	31433	804	496	304	0.380	10601	1174	1174	0	0.000	48864	6008	5998	4	0.001
933226	5	34182770	34182770	C	T	*LOC100653061*	intronic	c.NULL	NULL	tier3	22040	4128	4128	0	0.000	NA	NA	NA	NA	NA	2417	148	140	8	0.054	7262	957	956	0	0.000	17464	2869	2867	0	0.000
933226	6	169623535	169623535	C	T	*THBS2*	missense	c.2809	p.D937N	tier1	3863	670	669	1	0.001	NA	NA	NA	NA	NA	3321	101	62	39	0.386	1456	182	181	0	0.000	6197	830	829	1	0.000
933226	8	139277974	139277974	C	T	*FAM135B*	missense	c.269	p.R90Q	tier1	4393	1097	1096	1	0.001	NA	NA	NA	NA	NA	847	66	33	33	0.500	851	146	144	2	0.000	2888	686	682	2	0.000
933226	9	93976302	93976302	A	G	*AUH*	rna	NULL	NULL	tier1	2982	472	471	1	0.002	NA	NA	NA	NA	NA	719	55	28	26	0.481	570	58	57	1	0.000	2565	425	424	1	0.000
933226	11	62037739	62037739	C	T	*SCGB2A2*	silent	c.51	p.Y17	tier1	4524	595	592	2	0.003	NA	NA	NA	NA	NA	1244	47	31	16	0.340	997	112	110	1	0.000	3866	539	537	2	0.000
933226	11	83497858	83497858	A	T	*DLG2*	intronic	c.1723-23	e16-23	tier3	4458	0	0	0	0.000	NA	NA	NA	NA	NA	4292	115	64	50	0.439	1433	133	133	0	0.000	4991	704	702	1	0.000
933226	12	59307704	59307704	G	A	*LRIG3*	5_prime_untranslated_region	c.-59307704	NULL	tier3	778	164	163	0	0.000	NA	NA	NA	NA	NA	41	9	6	3	NA	100	15	14	0	0.000	280	0	0	0	NA
933226	13	37270408	37270408	A	G	*SERTM1*	3_prime_untranslated_region	c.*869	NULL	tier3	4790	801	799	2	0.002	NA	NA	NA	NA	NA	8751	290	160	128	0.444	1157	117	117	0	0.000	7411	1098	1095	2	0.000
933226	13	108518148	108518148	T	A	*FAM155A*	missense	c.797	p.E266V	tier1	43614	5851	5847	2	0.000	NA	NA	NA	NA	NA	18938	435	347	87	0.200	9814	1237	1230	6	0.005	46076	5845	5836	4	0.001
933226	14	75151331	75151331	A	G	*AREL1*	silent	c.69	p.F23	tier1	24086	3329	3325	4	0.001	NA	NA	NA	NA	NA	11152	325	234	91	0.280	6096	640	637	3	0.005	28840	3867	3860	5	0.001
933226	15	48056944	48056944	G	A	*SEMA6D*	missense	c.1207	p.V403I	tier1	6863	1114	1112	0	0.000	NA	NA	NA	NA	NA	2220	87	55	30	0.353	1584	226	226	0	0.000	5708	904	902	1	0.000
933226	17	7578406	7578406	C	T	*TP53*	missense	c.524	p.R175H	tier1	56741	7368	7340	24	0.003	NA	NA	NA	NA	NA	48589	1207	164	1039	0.864	20838	2443	2419	20	0.008	79816	9614	9578	22	0.002
933226	17	18638428	18638428	C	A	*TRIM16L*	missense	c.864	p.D288E	tier1	1826	0	0	0	0.000	NA	NA	NA	NA	NA	41	3	1	2	NA	194	0	0	0	NA	783	196	194	1	0.000
933226	17	19643645	19643645	G	A	*ALDH3A1*	5_prime_untranslated_region	c.-19643645	NULL	tier3	12571	2224	2222	1	0.000	NA	NA	NA	NA	NA	2180	87	44	43	0.494	2436	328	327	0	0.000	9156	1452	1446	3	0.002
933226	18	42531913	42531913	G	A	*SETBP1*	missense	c.2608	p.G870S	tier1	34058	4565	4560	3	0.001	NA	NA	NA	NA	NA	18319	448	271	176	0.394	11003	1329	1327	2	0.000	48519	5838	5830	2	0.000
933226	19	1011071	1011071	C	T	*TMEM259*	5_prime_untranslated_region	c.-1011071	NULL	tier2	15710	2612	2610	1	0.000	NA	NA	NA	NA	NA	9408	314	250	64	0.204	6229	794	792	1	0.000	24950	3486	3478	2	0.000
933226	19	1754673	1754673	A	T	*ONECUT3*	missense	c.1012	p.S338C	tier1	22665	2976	2971	2	0.001	NA	NA	NA	NA	NA	15949	421	273	148	0.352	6665	770	767	3	0.004	26330	3306	3300	3	0.001
933226	19	49316512	49316512	C	T	*HSD17B14*	missense	c.733	p.V245M	tier1	26666	3716	3711	3	0.001	NA	NA	NA	NA	NA	18791	570	310	259	0.455	7520	873	866	4	0.005	32386	4154	4143	7	0.002
933226	19	51380151	51380151	T	A	*KLK2*	missense	c.517	p.C173S	tier1	17206	2291	2288	1	0.000	NA	NA	NA	NA	NA	9640	263	145	117	0.447	5258	535	531	4	0.007	17174	2278	2270	3	0.001
933226	20	13269233	13269233	C	T	*ISM1*	silent	c.690	p.S230	tier1	21789	2996	2993	1	0.000	NA	NA	NA	NA	NA	7466	206	138	68	0.330	5767	676	675	0	0.000	23149	2943	2939	1	0.000
933226	20	60499501	60499501	G	A	*CDH4*	missense	c.1738	p.V580I	tier1	27874	4122	4117	0	0.000	NA	NA	NA	NA	NA	26004	652	454	194	0.299	11660	1404	1402	2	0.000	48071	5901	5888	6	0.001
933226	21	11098586	11098586	G	A	*BAGE2*	intronic	c.NULL	NULL	tier4	22217	2827	2825	2	0.001	NA	NA	NA	NA	NA	8828	203	143	60	0.296	6657	802	799	3	0.004	25402	3097	3088	4	0.001
933226	22	16414219	16414219	G	A	*ENSG00000215268*	3_prime_untranslated_region	c.*16414219	NULL	tier3	10766	2458	2454	1	0.000	NA	NA	NA	NA	NA	3105	193	148	45	0.233	1790	307	307	0	0.000	4891	1055	1052	2	0.000
933226	X	5821695	5821695	G	A	*NLGN4X*	missense	c.1084	p.P362S	tier1	12786	1813	1809	2	0.001	NA	NA	NA	NA	NA	4393	123	31	92	0.748	3271	376	373	3	0.008	13570	1738	1736	1	0.000
933226	X	43626915	43626915	C	G	*MAOB*	intronic	c.1411-50	e15-50	tier4	1577	258	257	1	0.004	NA	NA	NA	NA	NA	438	21	3	18	0.857	517	79	79	0	0.000	1327	278	274	3	0.011
933226	X	130423302	130423302	C	A	*IGSF1*	5_prime_untranslated_region	c.-2654	NULL	tier3	5671	668	668	0	0.000	NA	NA	NA	NA	NA	2543	84	14	70	0.833	1577	152	152	0	0.000	5845	760	759	1	0.000
944541	1	50552429	50552429	G	A	*ELAVL4*	intronic	c.18+38575	e1+38575	tier3	12700	1455	1439	8	0.006	11656	1133	671	448	0.400	NA	NA	NA	NA	NA	34166	3448	3443	1	0.000	17095	1450	1445	2	0.000
944541	2	43453288	43453288	G	A	*THADA*	intronic	c.3189-59383	e20-59383	tier2	7263	824	824	0	0.000	4311	402	301	101	0.251	NA	NA	NA	NA	NA	12903	1060	1058	0	0.000	6317	480	480	0	0.000
944541	2	97483175	97483175	C	G	*CNNM3*	missense	c.1161	p.N387K	tier1	40050	5456	5408	31	0.006	48430	5771	3431	2234	0.394	NA	NA	NA	NA	NA	121867	14816	14795	3	0.000	46282	2902	2894	7	0.000
944541	4	44638032	44638032	C	T	*YIPF7*	missense	c.259	p.A87T	tier1	14120	1809	1799	7	0.004	17896	1975	1264	690	0.353	NA	NA	NA	NA	NA	54147	6078	6072	1	0.000	28579	1847	1843	3	0.000
944541	6	33144473	33144473	G	C	*COL11A2*	intronic	c.2115+25	e26+25	tier3	6828	942	926	12	0.013	11753	1471	963	500	0.342	NA	NA	NA	NA	NA	28432	3558	3555	0	0.000	10425	933	932	0	0.000
944541	6	43127615	43127615	A	G	*PTK7*	missense	c.2963	p.D988G	tier1	6141	867	858	9	0.010	12596	1469	847	607	0.417	NA	NA	NA	NA	NA	25039	2937	2935	0	0.000	11308	799	799	0	0.000
944541	8	3253958	3253958	C	T	*CSMD1*	intronic	c.2409-55	e18-55	tier3	22006	2748	2735	11	0.004	18382	2014	1339	656	0.329	NA	NA	NA	NA	NA	50771	5654	5642	1	0.000	26778	1743	1741	1	0.000
944541	8	21824261	21824261	A	G	*XPO7*	intronic	c.19-107	e2-107	tier3	2384	389	386	2	0.005	3826	594	374	218	0.368	NA	NA	NA	NA	NA	6522	809	806	1	0.000	1874	0	0	0	NA
944541	8	102504720	102504720	C	G	*LOC101927172*	rna	NULL	NULL	tier1	30943	3852	3825	26	0.007	28557	2867	1799	1024	0.363	NA	NA	NA	NA	NA	85167	9156	9145	0	0.000	42477	2974	2970	4	0.000
944541	11	32414262	32414262	C	G	*WT1*	missense	c.1289	p.R430P	tier1	6367	917	914	0	0.000	13660	1549	1517	32	0.021	NA	NA	NA	NA	NA	31846	3551	3546	1	0.000	14041	947	947	0	0.000
944541	12	6697549	6697549	C	T	*CHD4*	missense	c.3380	p.R1127Q	tier1	16812	1927	1925	0	0.000	12314	1227	1157	64	0.052	NA	NA	NA	NA	NA	30532	2900	2899	0	0.000	9487	843	840	1	0.000
944541	12	112888189	112888189	G	A	*PTPN11*	missense	c.205	p.E69K	tier1	3222	696	689	7	0.010	4511	782	481	299	0.383	NA	NA	NA	NA	NA	8678	1544	1544	0	0.000	3766	599	598	1	0.000
944541	13	33017732	33017732	C	T	*N4BP2L2*	silent	c.942	p.A314	tier1	9582	1093	1086	5	0.005	6984	717	480	236	0.330	NA	NA	NA	NA	NA	16206	1462	1460	0	0.000	4658	515	514	0	0.000
944541	13	50115190	50115190	C	T	*RCBTB1*	intronic	c.1325-48	e10-48	tier3	13814	1637	1629	5	0.003	6151	551	408	140	0.255	NA	NA	NA	NA	NA	24510	2349	2346	0	0.000	9195	991	990	0	0.000
944541	15	52427942	52427942	C	A	*GNB5*	silent	c.639	p.A213	tier1	16777	2315	2297	16	0.007	14835	1860	1116	721	0.392	NA	NA	NA	NA	NA	30392	3445	3438	0	0.000	12847	0	0	0	NA
944541	15	89386618	89386618	T	A	*ACAN*	missense	c.790	p.F264I	tier1	22794	3107	3079	25	0.008	18427	2228	1390	810	0.368	NA	NA	NA	NA	NA	44611	4955	4953	0	0.000	21847	1726	1723	0	0.000
944541	16	11541929	11541929	G	A	*LOC101929274*	missense	c.1222	p.P408S	tier1	22413	2630	2604	19	0.007	30696	3051	1772	1217	0.407	NA	NA	NA	NA	NA	96110	10738	10727	0	0.000	47466	3288	3281	5	0.000
944541	17	40322106	40322106	G	A	*KCNH4*	intronic	c.1390+19	e8+19	tier3	39863	6068	5994	58	0.010	41505	5460	3098	2269	0.423	NA	NA	NA	NA	NA	110861	15410	15393	1	0.000	44539	3323	3316	3	0.000
944541	17	42635299	42635299	G	A	*FZD2*	silent	c.243	p.K81	tier1	13810	1697	1682	15	0.009	12184	1411	872	525	0.376	NA	NA	NA	NA	NA	34225	3917	3914	0	0.000	13940	857	856	1	0.000

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count*	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Unique Count*	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Unique Count*	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Unique Count*	D100 Ref Count	D100 Var Count	D100 VAF
944541	18	43684347	43684347	A	C	*HAUS1*	5_prime_untranslated_region	c.-31	NULL	tier2	11027	1328	1312	12	0.009	13788	1600	957	628	0.396	NA	NA	NA	NA	NA	33591	3482	3479	0	0.000	14203	1323	1322	0	0.000
944541	19	7964800	7964800	C	T	*LRRC8E*	missense	c.1393	p.L465F	tier1	5974	938	931	5	0.005	7353	986	639	337	0.345	NA	NA	NA	NA	NA	20434	2639	2637	0	0.000	8027	502	502	0	0.000
944541	19	10812636	10812636	T	C	*QTRT1*	missense	c.254	p.L85P	tier1	23240	2829	2816	11	0.004	20901	2251	1505	713	0.321	NA	NA	NA	NA	NA	58019	6392	6388	0	0.000	30292	2159	2159	0	0.000
944541	22	22842205	22842205	G	C	*ZNF280B*	missense	c.1519	p.L507V	tier1	8650	1098	1086	9	0.008	8992	942	602	333	0.356	NA	NA	NA	NA	NA	23496	2451	2441	1	0.000	11831	980	978	0	0.000
955252	5	140563408	140563408	A	G	*PCDHB16*	missense	c.1274	p.D425G	tier1	19016	1999	1995	1	0.001	30781	3400	3308	86	0.025	20176	2048	1993	49	0.024	53519	6240	6236	0	0.000	69767	8440	8439	0	0.000
988638	1	46505876	46505876	G	A	*PIK3R3*	3_prime_untranslated_region	c.*3469	NULL	tier3	33975	4464	4459	3	0.001	16212	1664	1440	219	0.132	19080	2465	1453	1004	0.409	47391	6016	6009	5	0.001	74351	6783	6772	7	0.001
988638	1	161519606	161519606	A	G	*FCGR3A*	missense	c.29	p.F10S	tier1	9443	1261	1248	13	0.010	4771	514	392	118	0.231	11339	1462	834	624	0.428	13636	1782	1780	2	0.000	13208	1274	1273	0	0.000
988638	1	233091444	233091444	G	A	*NTPCR*	missense	c.176	p.R59Q	tier1	217	0	0	0	0.000	301	26	24	2	0.077	194	29	17	12	0.414	1262	114	114	0	0.000	NA	NA	NA	NA	NA
988638	2	102484410	102484410	C	T	*MAP4K4*	rna	NULL	NULL	tier1	23756	3338	3337	1	0.000	12674	1483	1297	181	0.122	19108	2545	1527	1011	0.398	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002
988638	2	128387436	128387436	A	G	*MYO7B*	intronic	c.4728+35	e33+35	tier3	45360	6579	6575	2	0.000	29056	3277	2815	439	0.135	49505	6799	4037	2721	0.403	81115	11019	11011	4	0.000	89255	8408	8388	11	0.001
988638	2	135957920	135957920	T	C	*ZRANB3*	missense	c.3232	p.K1078E	tier1	9963	1257	1240	15	0.012	6748	744	590	150	0.203	7880	1143	676	467	0.409	21453	2846	2841	3	0.001	22076	2352	2344	2	0.000
988638	2	192257750	192257750	G	C	*MYO1B*	intronic	c.2077-49	e19-49	tier3	10356	1367	1363	0	0.000	4502	481	456	25	0.052	4538	710	505	204	0.288	15276	2111	2110	0	0.000	26840	2439	2437	1	0.000
988638	2	202467998	202467998	C	A	*ALS2CR11*	missense	c.319	p.V107F	tier1	26814	3488	3453	34	0.010	17074	1750	1346	395	0.227	21636	2900	1679	1206	0.418	53474	6809	6800	3	0.000	90453	8383	8370	9	0.001
988638	3	55061774	55061774	C	T	*CACNA2D3*	intronic	c.2987+9430	e35+9430	tier2	8406	1406	1405	1	0.001	11215	1343	1154	181	0.136	17279	2872	1659	1198	0.419	36744	5437	5430	3	0.000	19032	1837	1833	4	0.002
988638	7	20826548	20826548	G	T	*SP8*	5_prime_flanking_region	c.-131	NULL	tier2	1843	367	367	0	0.000	2386	310	272	34	0.111	3879	656	376	278	0.425	8289	1154	1150	1	0.000	4661	685	684	0	0.000
988638	9	44874097	44874097	G	A	*ENSG00000231454*	3_prime_untranslated_region	c.*44874097	NULL	tier3	1723	0	0	0	0.000	2207	237	194	43	0.181	2353	305	179	124	0.409	5943	772	772	0	0.000	4939	0	0	0	NA
988638	9	128083745	128083745	G	T	*GAPVD1*	nonsense	c.1636	p.G546*	tier1	22704	3267	3230	31	0.010	21985	2513	2059	438	0.175	25659	3664	2598	1059	0.290	63694	8641	8633	3	0.000	73099	7490	7478	4	0.000
988638	10	51829388	51829388	C	T	*FAM21A*	missense	c.208	p.R70W	tier1	8444	1026	1023	1	0.001	4290	461	381	79	0.172	2797	435	256	179	0.411	14768	1895	1894	1	0.000	4954	665	663	1	0.000
988638	11	5842368	5842368	G	C	*OR52N2*	missense	c.803	p.G268A	tier1	5574	1335	1332	1	0.001	4387	763	660	99	0.130	4901	1257	722	535	0.426	12603	2795	2793	0	0.000	1033	158	158	0	0.000
988638	12	40815079	40815079	G	A	*MUC19*	rna	NULL	NULL	tier1	811	117	117	0	0.000	595	73	66	7	0.096	575	106	91	15	0.142	1687	252	252	0	0.000	NA	NA	NA	NA	NA
988638	16	89650436	89650436	G	A	*CPNE7*	missense	c.658	p.V220M	tier1	21007	3057	3049	4	0.001	10223	1196	1027	159	0.134	16016	2561	1463	1091	0.427	26149	3780	3771	4	0.001	10693	1371	1368	1	0.000
988638	17	44074056	44074056	G	T	*MAPT*	intronic	c.1827+26	e10+26	tier3	13914	1839	1819	17	0.009	10418	1118	888	202	0.185	15722	2272	1334	904	0.404	28154	3628	3620	5	0.001	5472	696	695	1	0.000
988638	17	74732959	74732959	G	T	*SRSF2*	missense	c.284	p.P95H	tier1	10311	1436	1435	1	0.001	10008	1210	1024	178	0.148	20068	3093	1795	1272	0.415	28552	3910	3907	2	0.000	482	0	0	0	NA
988638	18	42531907	42531907	G	A	*SETBP1*	missense	c.2602	p.D868N	tier1	26792	3478	3477	0	0.000	26771	3040	2581	444	0.147	47339	6331	3697	2593	0.412	78462	10064	10049	5	0.000	77196	6858	6837	13	0.002
988638	19	7675544	7675544	G	C	*CAMSAP3*	intronic	c.982-42	e9-42	tier3	13605	1826	1799	26	0.014	8017	873	656	207	0.240	12692	1912	1082	815	0.430	22406	2906	2896	1	0.000	6492	676	675	1	0.000
988638	19	35265460	35265460	C	T	*ZNF599*	5_prime_flanking_region	c.-1714	NULL	tier4	2054	377	371	5	0.013	1485	241	196	45	0.187	2262	548	311	236	0.431	4699	938	937	1	0.000	1645	193	193	0	0.000
988638	20	44815531	44815531	G	A	*CDH22*	silent	c.1479	p.N493	tier1	24890	3995	3945	48	0.012	32926	3919	3029	837	0.217	69113	9955	5755	4119	0.417	101385	14575	14551	12	0.001	101380	10080	10049	20	0.002
988638	X	14338161	14338161	C	T	-	-	-	-	tier3	18629	2604	2598	5	0.002	9550	1070	765	300	0.282	12520	1786	338	1443	0.810	29780	4105	4095	7	0.002	39185	3787	3779	7	0.002
991140	1	181702771	181702771	C	T	*CACNA1E*	silent	c.3147	p.S1049	tier1	25606	3230	3224	5	0.002	31176	3713	2869	815	0.221	21422	2645	2291	343	0.130	43362	5206	5175	29	0.006	43964	4789	4781	0	0.000
991140	1	223938499	223938499	C	T	*CAPN2*	intronic	c.814-93	e7-93	tier3	23839	2789	2777	10	0.004	17359	1943	1509	419	0.217	22663	2695	2320	361	0.135	38645	4335	4307	23	0.005	81316	0	0	0	NA
991140	1	235926068	235926068	C	T	*LYST*	missense	c.6205	p.G2069R	tier1	2734	284	284	0	0.000	5008	510	387	117	0.232	2316	237	200	35	0.149	7062	713	707	4	0.006	17007	2081	2080	0	0.000
991140	2	166187904	166187904	T	C	*SCN2A*	silent	c.2214	p.I738	tier1	12601	1364	1358	5	0.004	7677	842	651	188	0.224	8846	974	888	83	0.085	16189	1647	1632	11	0.007	43391	4861	4856	0	0.000
991140	3	116163747	116163747	C	T	*LSAMP*	silent	c.132	p.R44	tier1	11740	1553	1550	3	0.002	32947	4167	3195	939	0.227	37323	4927	4262	642	0.131	61809	6830	6787	40	0.006	50384	5382	5378	0	0.000
991140	3	132201248	132201248	C	T	*DNAJC13*	intronic	c.2979+74	e26+74	tier3	11745	1555	1549	5	0.003	4943	693	497	192	0.279	10516	1420	1282	135	0.095	16281	2010	1994	14	0.007	29503	3318	3317	0	0.000
991140	4	36093672	36093672	T	A	*ARAP2*	intronic	c.4286-30	e27-30	tier3	1214	44	44	0	0.000	682	54	36	18	0.333	554	22	18	4	0.182	911	30	30	0	0.000	1	0	0	0	NA
991140	6	147006987	147006987	C	G	*ADGB*	intronic	c.1311+23	e10+23	tier3	18270	1860	1855	4	0.002	16919	1810	1396	395	0.221	10919	1093	925	161	0.148	21293	2093	2078	11	0.005	54505	6536	6527	1	0.000
991140	7	34889221	34889221	C	A	*NPSR1*	missense	c.1170	p.N390K	tier1	10102	1262	1260	2	0.002	8432	1049	724	320	0.307	8431	1065	875	182	0.172	15523	1841	1827	12	0.007	26942	3080	3080	0	0.000
991140	8	97506480	97506480	G	A	*SDC2*	rna	NULL	NULL	tier1	16062	1868	1861	6	0.003	34522	4065	3086	940	0.233	25172	2885	2437	404	0.142	42390	4597	4561	28	0.006	54088	6253	6252	0	0.000
991140	8	142166004	142166004	G	T	*DENND3*	missense	c.891	p.K297N	tier1	14765	1623	1621	1	0.001	15150	1627	1342	280	0.173	9478	991	853	135	0.137	20985	2052	2042	7	0.003	39177	4993	4990	0	0.000
991140	8	142517302	142517302	G	C	*MROH5*	5_prime_untranslated_region	c.-53	NULL	tier3	2088	248	248	0	0.000	7761	956	804	149	0.156	7812	968	856	106	0.110	10128	1167	1165	2	0.000	8736	943	942	1	0.000
991140	9	133254693	133254693	G	A	*HMCN2*	5_prime_flanking_region	c.-19336	NULL	tier3	6954	1375	1368	5	0.004	4495	592	452	138	0.234	4291	730	642	87	0.119	7533	1122	1111	10	0.009	701	119	119	0	0.000
991140	9	135521201	135521201	C	A	*DDX31*	intronic	c.1695+81	e13+81	tier3	41758	5520	5495	18	0.003	41178	5091	3869	1174	0.233	34834	4676	3922	730	0.157	59268	7463	7397	62	0.008	73022	8078	8071	0	0.000
991140	11	19735518	19735518	G	A	*NAV2*	splice_region	c.267+10	e1+10	tier2	10905	1514	1509	4	0.003	10235	1264	1085	173	0.138	11995	1506	1396	105	0.070	14664	1634	1630	3	0.002	7152	0	0	0	NA
991140	11	30034426	30034426	A	G	*KCNA4*	5_prime_untranslated_region	c.-201	NULL	tier3	12279	1719	1714	4	0.002	22305	2641	2079	547	0.208	20784	2782	2446	327	0.118	35004	4307	4282	22	0.005	43999	0	0	0	NA
991140	12	15749242	15749242	C	T	*PTPRO*	rna	NULL	NULL	tier1	15344	1748	1746	2	0.001	1651	155	105	49	0.318	10476	1279	1065	211	0.165	22177	2646	2631	15	0.006	60003	6351	6350	0	0.000
991140	12	48378352	48378352	G	A	*COL2A1*	silent	c.1864	p.L622	tier1	18268	2364	2361	3	0.001	28723	3723	2739	948	0.257	27966	3521	2987	509	0.146	33904	3962	3934	23	0.006	32681	0	0	0	NA
991140	15	45059668	45059668	C	T	*TRIM69*	missense	c.1201	p.R401W	tier1	5814	723	721	1	0.001	9320	1110	832	275	0.248	10539	1349	1135	211	0.157	14493	1799	1784	13	0.007	11278	0	0	0	NA
991140	16	21974018	21974018	G	A	*UQCRC2*	3_prime_untranslated_region	c.*21974018	NULL	tier3	5087	721	719	2	0.003	4622	439	334	101	0.232	4555	430	351	75	0.176	7001	620	614	2	0.000	2251	228	227	0	0.000
991140	16	70923652	70923652	G	A	*HYDIN*	intronic	c.9657-45	e57-45	tier3	1308	155	155	0	0.000	11217	1337	1019	309	0.233	10078	1082	906	171	0.159	10097	961	953	8	0.008	1343	0	0	0	NA
991140	16	84872357	84872357	G	A	*CRISPLD2*	3_prime_untranslated_region	c.*84872357	NULL	tier3	14095	1530	1525	4	0.003	29900	3390	2527	822	0.245	15679	1600	1375	214	0.135	25758	2518	2501	13	0.005	8183	804	803	0	0.000
991140	17	7578190	7578190	T	C	*TP53*	missense	c.659	p.Y220C	tier1	14135	1640	1639	0	0.000	25477	3072	2969	99	0.032	28948	3609	3589	19	0.005	46759	5765	5753	11	0.002	64839	6851	6846	0	0.000
991140	17	7578404	7578404	A	C	*TP53*	missense	c.526	p.C176G	tier1	33254	4107	4101	6	0.001	65407	8363	6243	2007	0.243	58296	7550	6351	1146	0.153	88165	11085	11034	48	0.004	93382	10094	10090	0	0.000
991140	17	7579355	7579355	A	T	*TP53*	missense	c.332	p.L111Q	tier1	22168	2540	2538	2	0.001	29800	3411	2585	782	0.232	36610	4319	3636	664	0.154	52402	6025	5982	42	0.007	81300	9491	9488	0	0.000
991140	17	34951507	34951507	G	A	*DHRS11*	missense	c.254	p.R85H	tier1	23390	2757	2747	7	0.003	31720	3889	3051	801	0.208	31252	3891	3340	535	0.138	41556	4931	4888	39	0.008	70925	7774	7763	2	0.000
991140	19	44680481	44680481	G	T	*ZNF226*	missense	c.1066	p.V356F	tier1	23810	2799	2788	10	0.004	15379	1774	1317	433	0.247	16414	2019	1791	223	0.111	44078	5365	5336	24	0.004	67550	7413	7413	0	0.000
991140	19	54395724	54395724	A	G	*PRKCG*	intronic	c.687-39	e7-39	tier3	5402	652	652	0	0.000	6715	895	704	183	0.206	10975	1323	1089	224	0.171	13562	1541	1528	9	0.006	2811	0	0	0	NA
991140	20	57464246	57464246	C	A	*GNAS*	rna	NULL	NULL	tier1	9704	1078	1074	4	0.004	86	9	7	2	0.222	9414	1144	987	149	0.131	12353	1428	1416	12	0.008	22382	2396	2391	0	0.000
991140	21	41550865	41550865	G	A	*DSCAM*	missense	c.2936	p.A979V	tier1	24636	3077	3069	6	0.002	26225	3195	2820	360	0.113	24104	2945	2813	127	0.043	41778	5075	5063	12	0.002	69695	7552	7545	1	0.000

UPN, unique patient number; NA, not available.
Chr, chromosome; Var, variant; Ref, reference; VAF, variant allele frequency, listed as a fraction; Pre, pre-transplant; D30, day 30 post-alloHCT; D100, day 100 post-alloHCT.
*,unique call includes "N' bases where the sequencer does not make a call. The ref and var count only include ACTG base calls.
The read count listed as 0 if mutation was not detected with adequate coverage.
Tier, defined in Walter et. al., NEJM. 2012 Mar 22;366(12):1090-8.
All genome coordinates use NCBI Build 37.

Table S5. International Prognostic Scoring System-Revised Classification System

Score	Cytogenetics	Blast %	Hemoglobin	Platelets	Absolute Neutrophil Count
0	Very Good	≤2	≥10	≥100	≥0.8
0.5				50-<100	<0.8
1.0	Good	>2-<5	8-<10	<50	
1.5			<8		
2.0	Intermediate	5-10			
3.0	Poor	>10			
4.0	Very Poor				

Prognostic Subgroups	Cytogenetic abnormalities
Very Good	-Y, del(11q)
Good	Normal, del(5q), del(12p), del(20q), double including del(5q)
Intermediate	del(7q), +8, +19, i(17q), any other single or double independent clones
Poor	-7, inv(3)/t(3q)/del(3q), double including -7/del(7q), complex: 3 abnormalities
Very Poor	Complex:>3 abnormalities

International Prognostic Scoring System-Revised Score	Risk Category	Median Overall Survival (years)	Median time to 25% leukemia evolution (years)
≤1.5	Very Low	8.8	Not reached
>1.5-3.0	Low	5.3	10.8
>3-4.5	Intermediate	3.0	3.2
>4.5-6	High	1.6	1.4
>6	Very High	0.8	0.73

From: Greenberg PL, Tuechler H, Schanz J, Sanz G, Garcia-Manero G, Sole F, et al. Revised international prognostic scoring system for myelodysplastic syndromes. Blood. 2012;120(12):2454-65.20(12):2

Table S6. 40 Gene Panel List

Gene symbol	Category	Target(s)
BRAF	Activated signaling	V600E
FLT3	Activated signaling	TKD and ITD
JAK2	Activated signaling	V617, exon 12
KIT	Activated signaling	exons 2, 8-13, 17
KRAS	Activated signaling	G12, G13, Q61
MPL	Activated signaling	exon 10
NF1	Activated signaling	whole gene
NRAS	Activated signaling	G12, G13, Q61
PTPN11	Activated signaling	exons 3, 13, 14
ASXL1	Chromatin modifiers	whole gene
EZH2	Chromatin modifiers	whole gene
SUZ12	Chromatin modifiers	whole gene
CSF3R	Chromatin modifiers	whole gene
RAD21	Cohesin	whole gene
SMC1A	Cohesin	whole gene
SMC3	Cohesin	whole gene
STAG2	Cohesin	whole gene
DNMT3A	DNA methylation	whole gene
IDH1	DNA methylation	R132
IDH2	DNA methylation	R140, R172
TET2	DNA methylation	whole gene
CALR	Other genes	exon 9
CBL	Other genes	exons 8, 9
NPM1	Other genes	exon 11
PIGA	Other genes	whole gene
PPM1D	Other genes	exon 6
CUX1	Other genes	whole gene
SF3B1	Spliceosome	whole gene
SRSF2	Spliceosome	exon 1
U2AF1	Spliceosome	exons 2, 6
ZRSR2	Spliceosome	whole gene
BCOR	Transcriptional regulator	whole gene
BCORL1	Transcriptional regulator	whole gene
CEBPA	Transcriptional regulator	whole gene
ETV6	Transcriptional regulator	whole gene
GATA2	Transcriptional regulator	whole gene
RUNX1	Transcriptional regulator	whole gene
PHF6	Tumor suppressors	whole gene
TP53	Tumor suppressors	whole gene
WT1	Tumor suppressors	whole gene