

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

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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Supplement to: Duncavage EJ, Jacoby MA, Chang GS, *et al.* Mutation clearance after transplant for myelodysplastic syndrome.

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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 $\geq 5\%$ 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 bwa³ 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) samtools⁴ 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 1.0.4⁵ (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) VarScan⁶ 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) Strelka⁷ 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) GATK⁹ somatic-indel version 5336, 2) pindel¹⁰ 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) VarScan⁶ version 2.3.6 (params: --nobaq --version r982) filtered by varscan-high-confidence-indel v1 and 4) Strelka⁷ 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 (initial 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 $\geq 1\%$ and had a VAF of $\leq 10\%$ in the normal skin sample and had $\geq 10\times$ 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 $\geq 0.5\%$. 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 $\geq 0.5\%$ 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 $\geq 0.5\%$ 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 $\geq 0.5\%$ (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 $\geq 0.5\%$ (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 $\geq 0.5\%$ (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 $\geq 0.1\%$ (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 $\geq 1\%$ (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 $\geq 2.5\%$ (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 $\geq 0.5\%$ (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

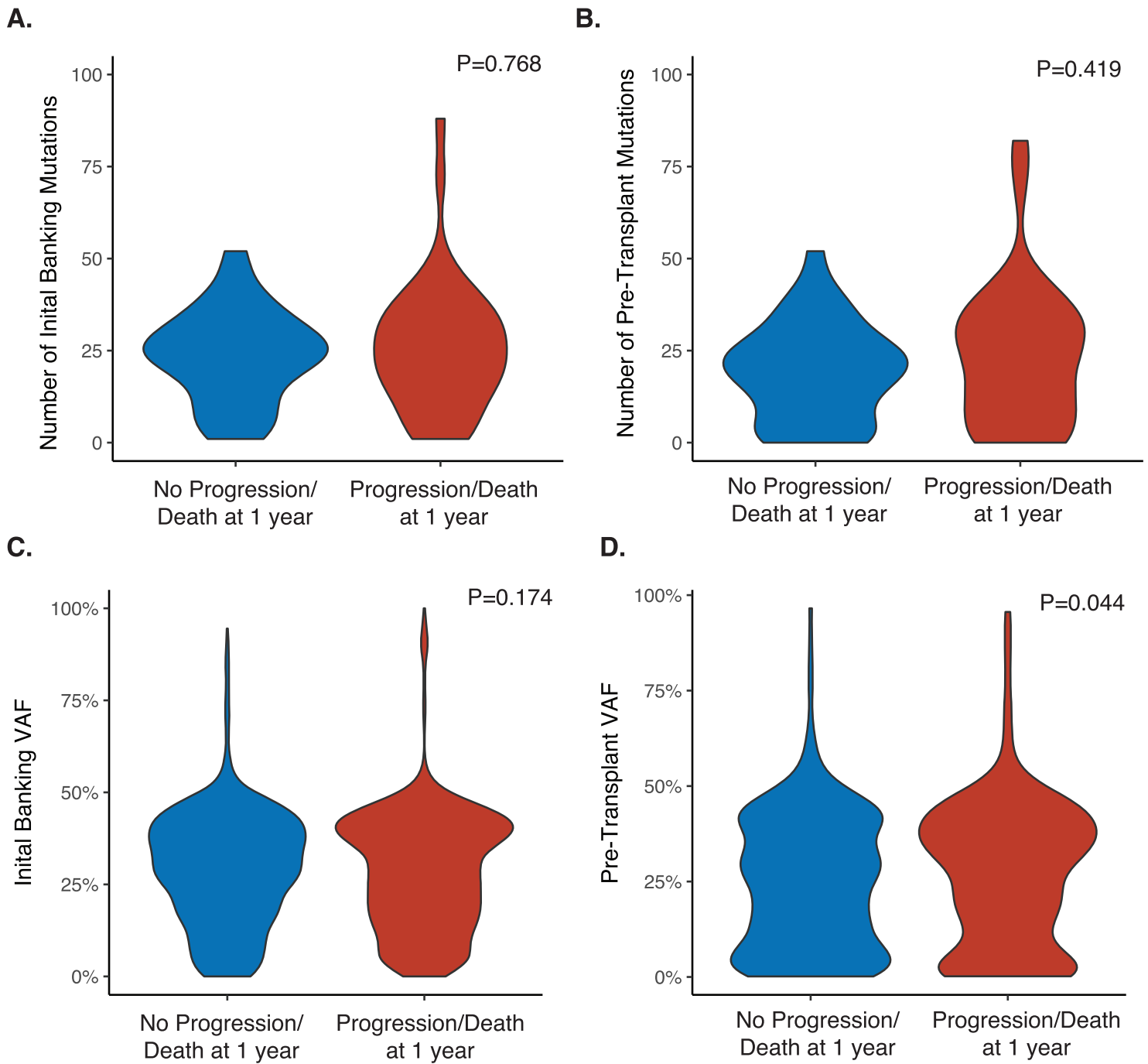
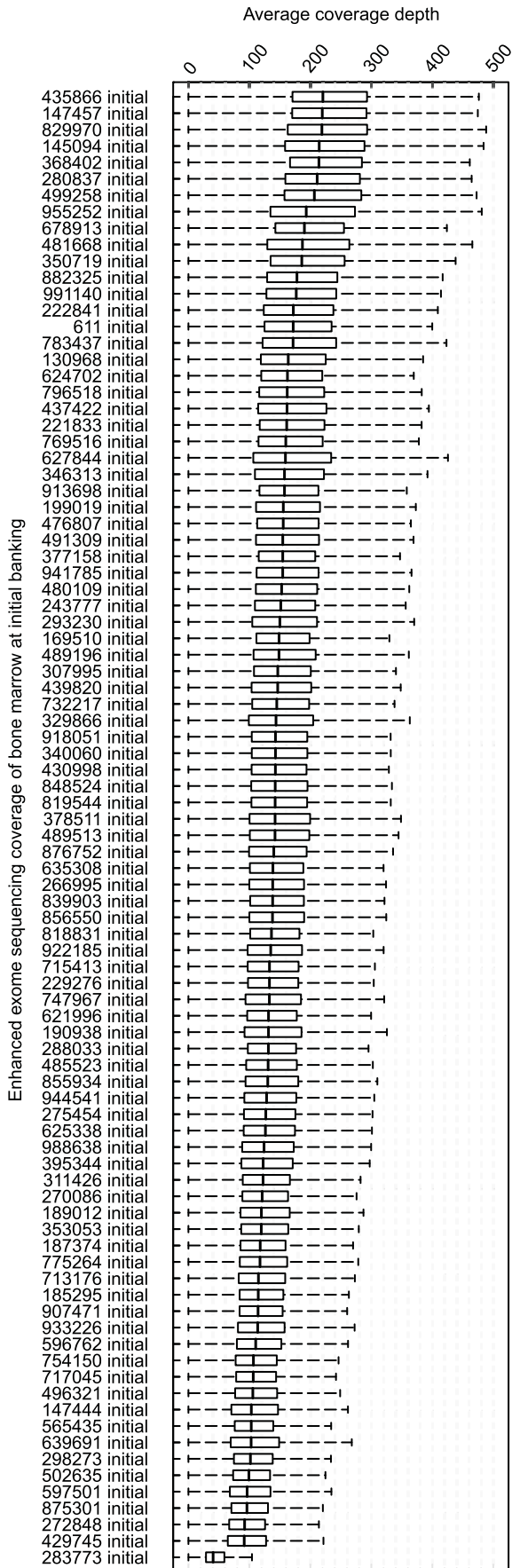


Figure S2. Sequencing Metrics

A.



B.

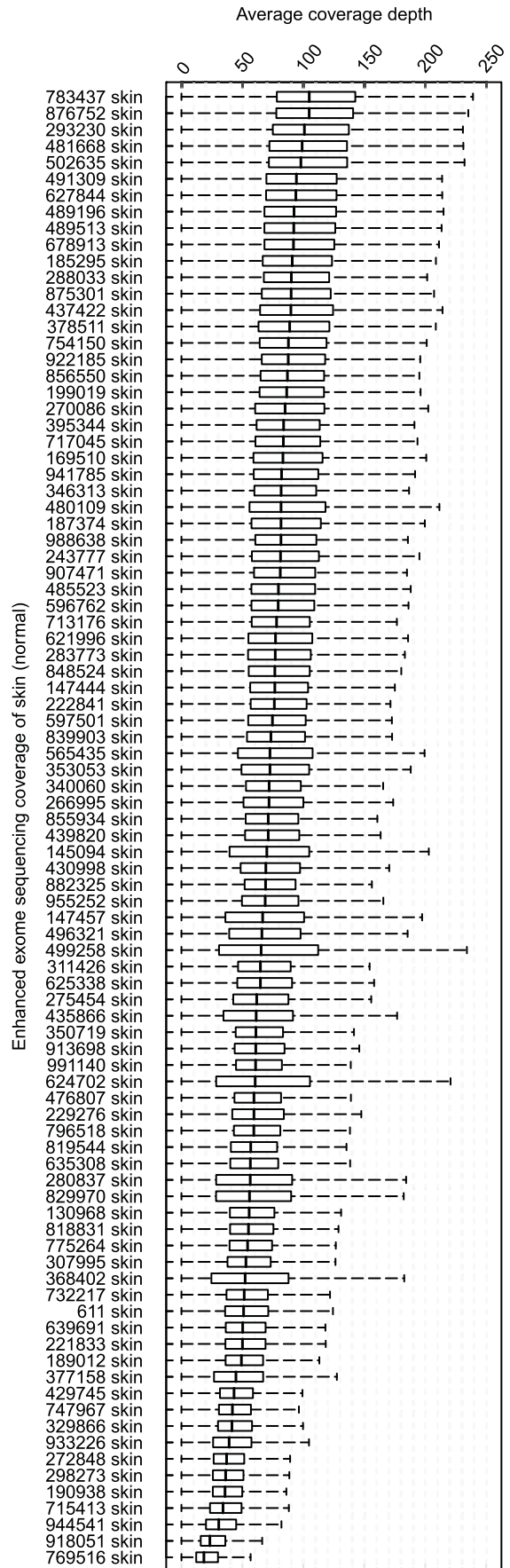
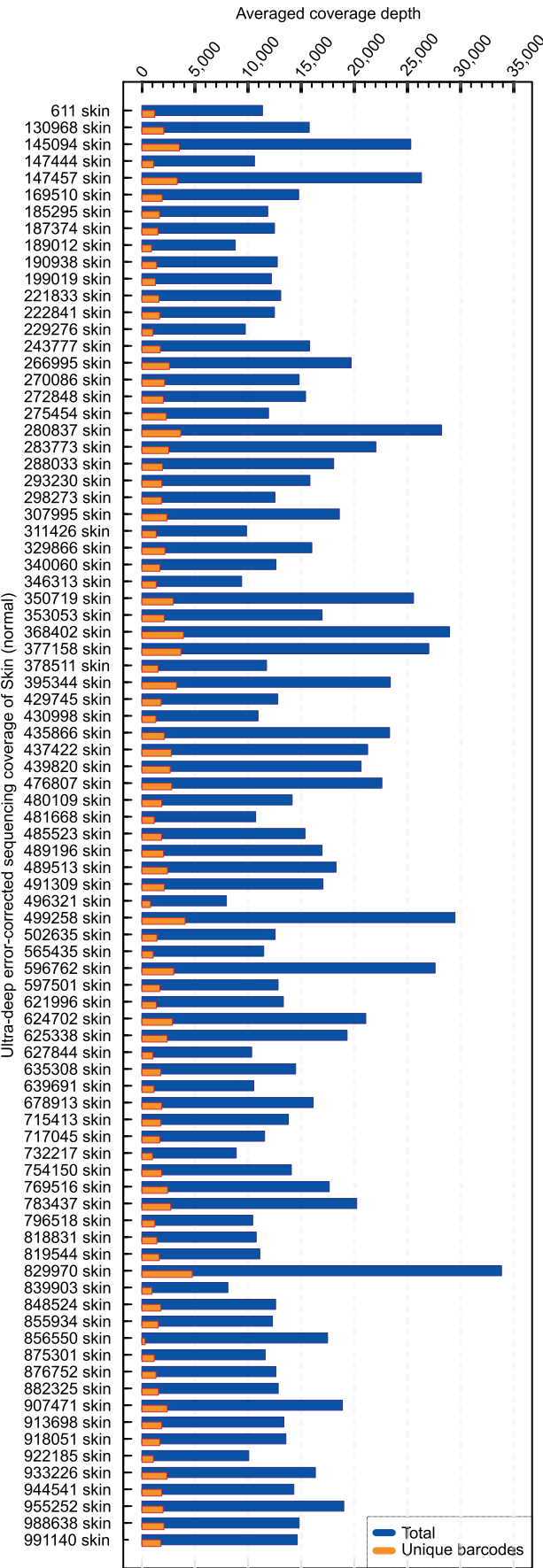


Figure S2. Sequencing Metrics

C.



D.

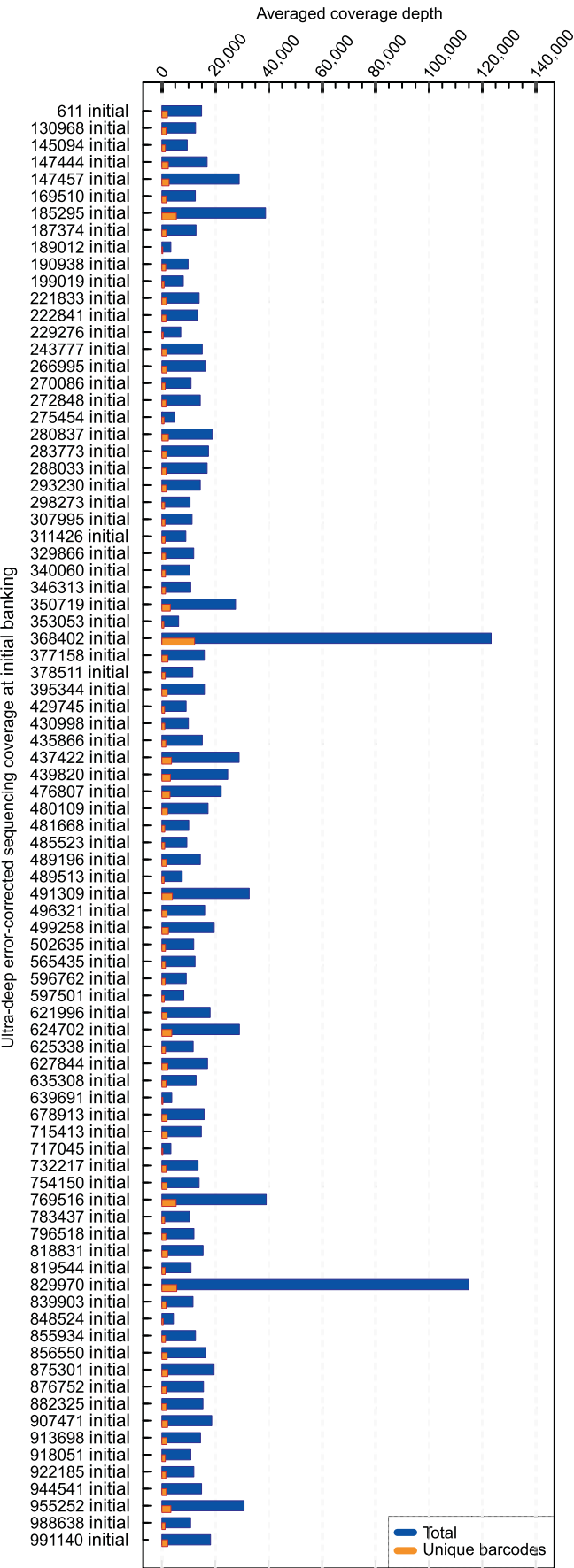
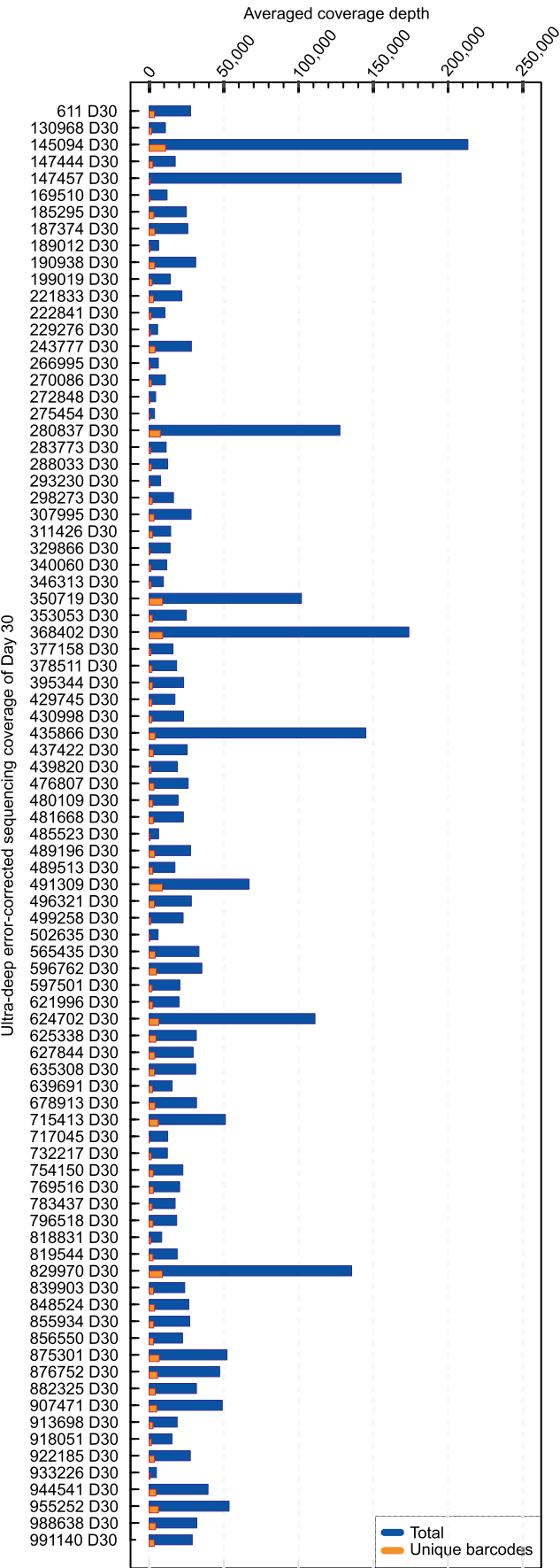


Figure S2. Sequencing Metrics

E.



F.

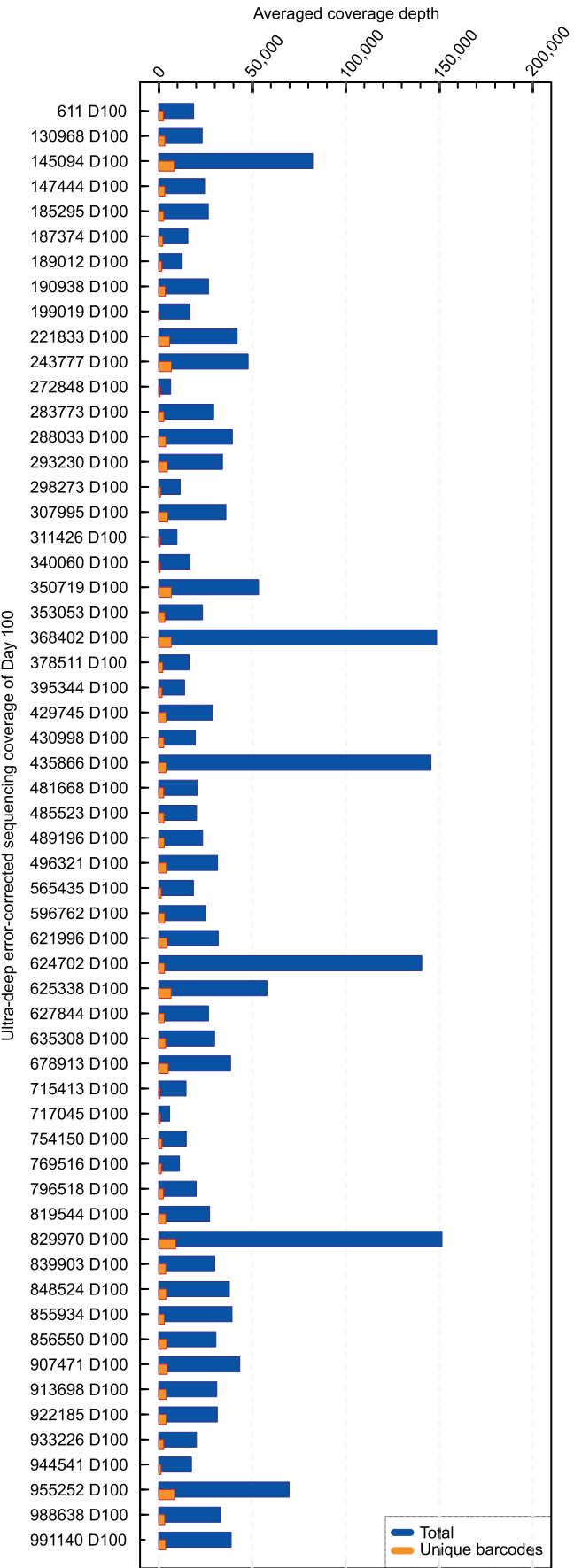


Figure S2. Sequencing Metrics

G.

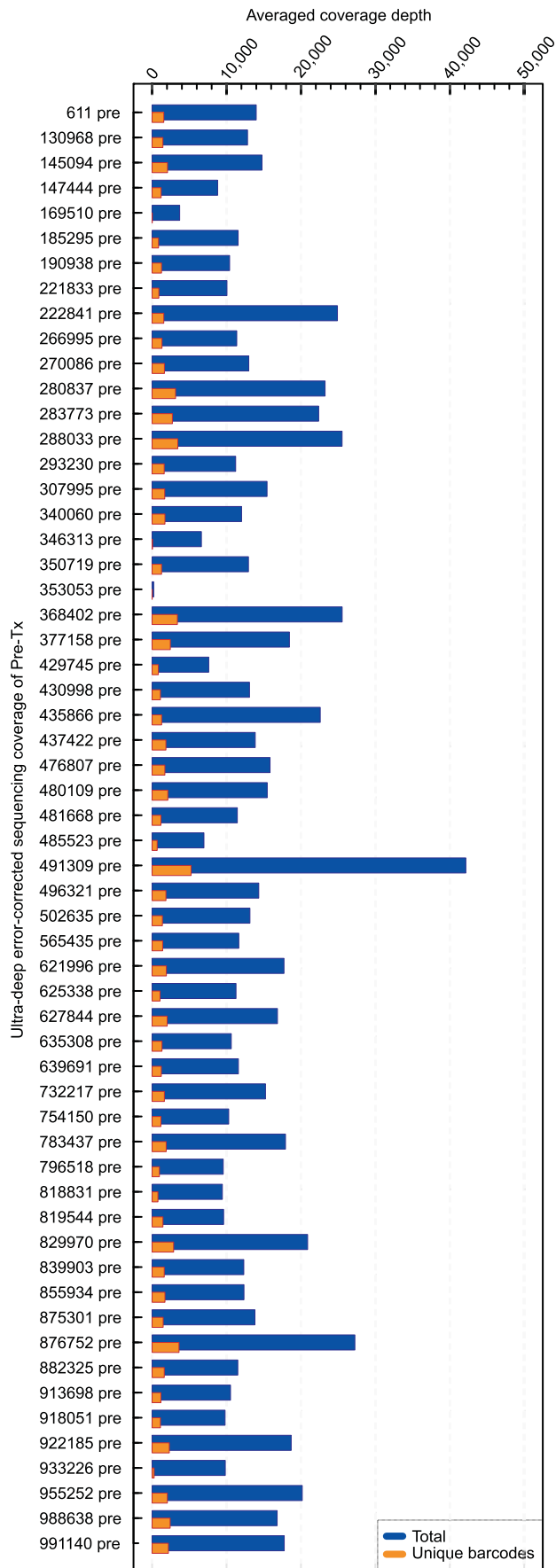
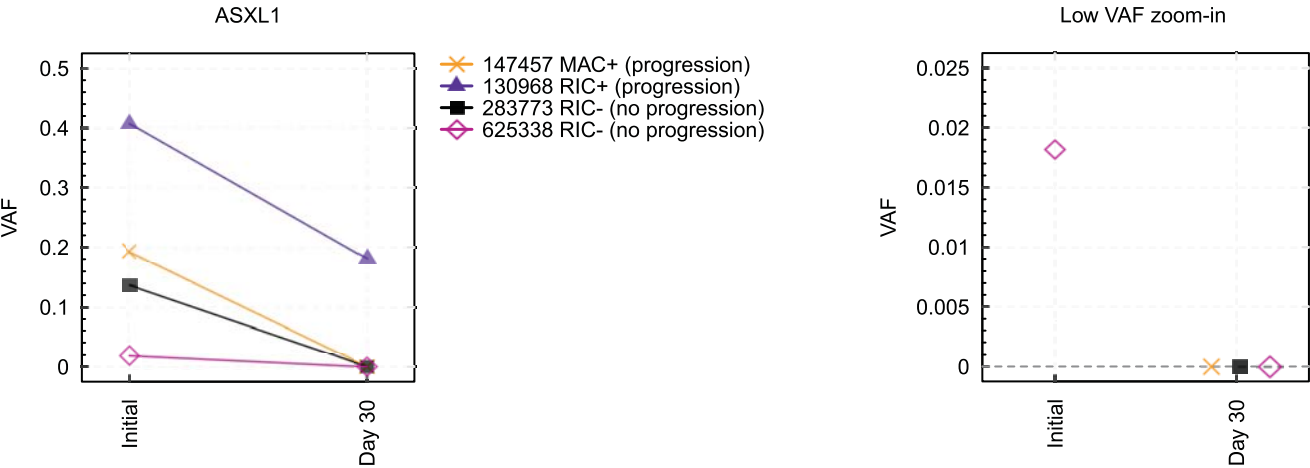
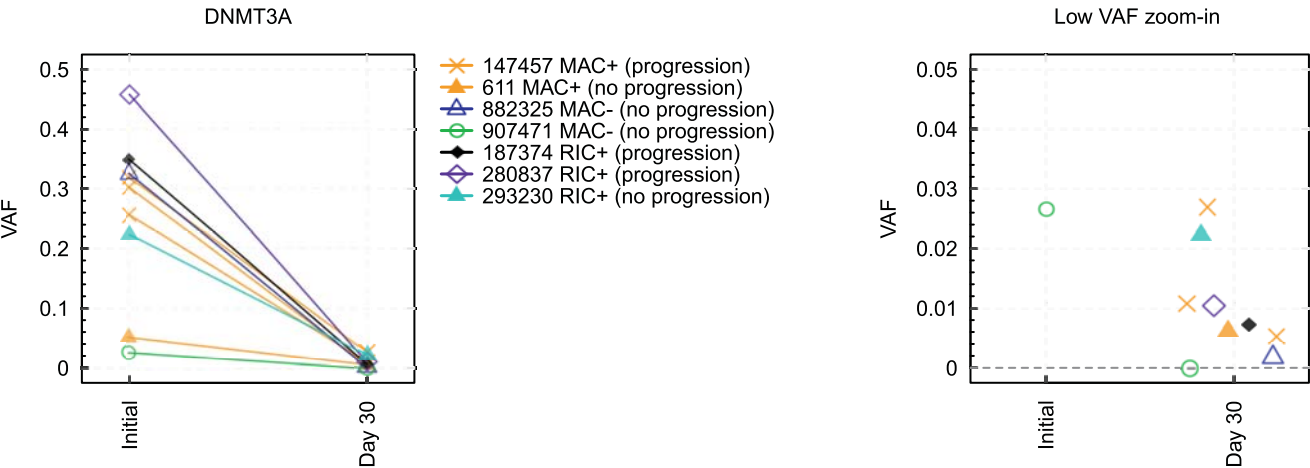


Figure S3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant

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B.



C.

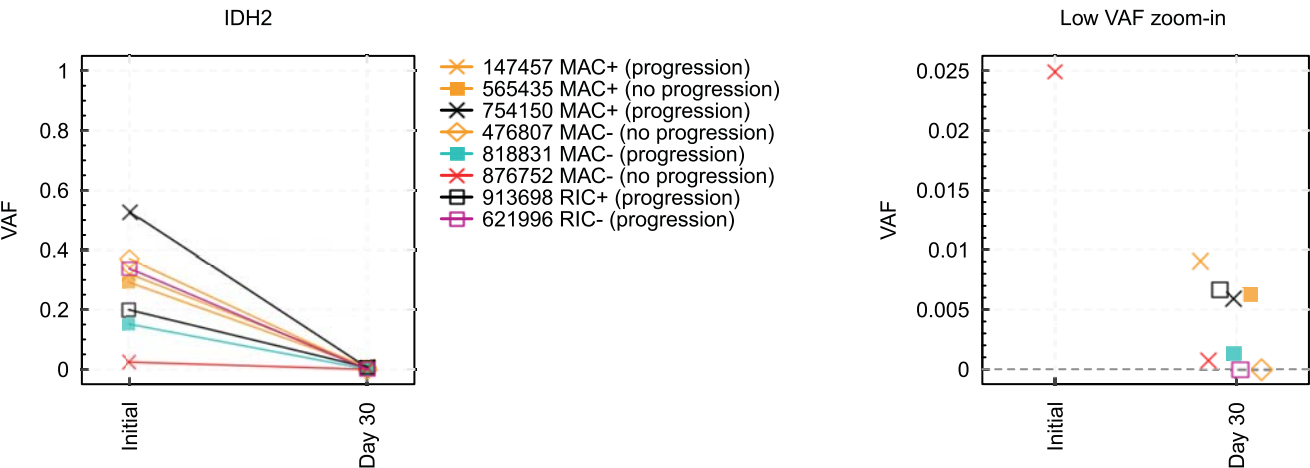
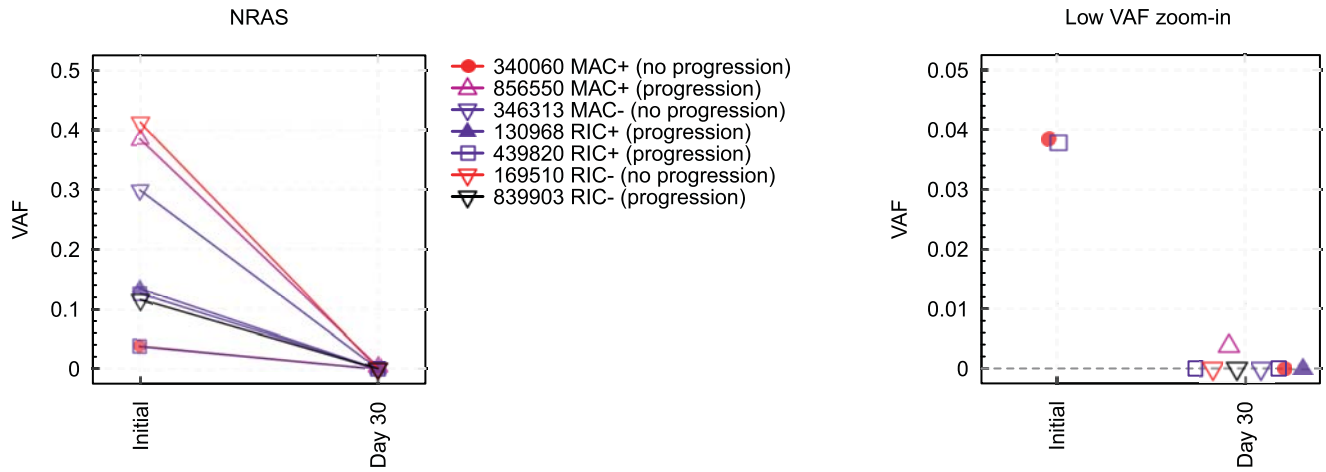
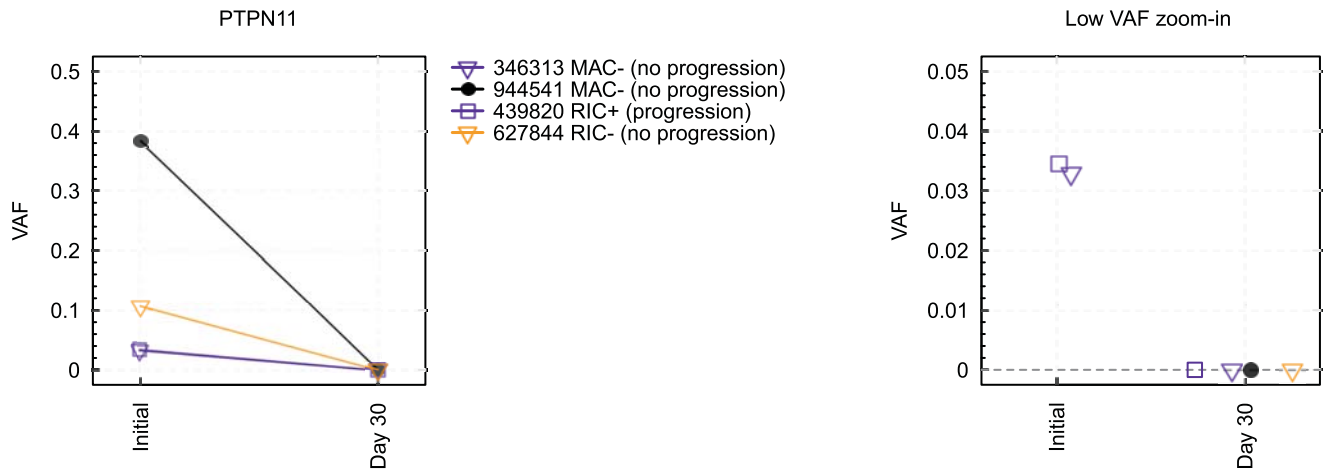


Figure S3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant

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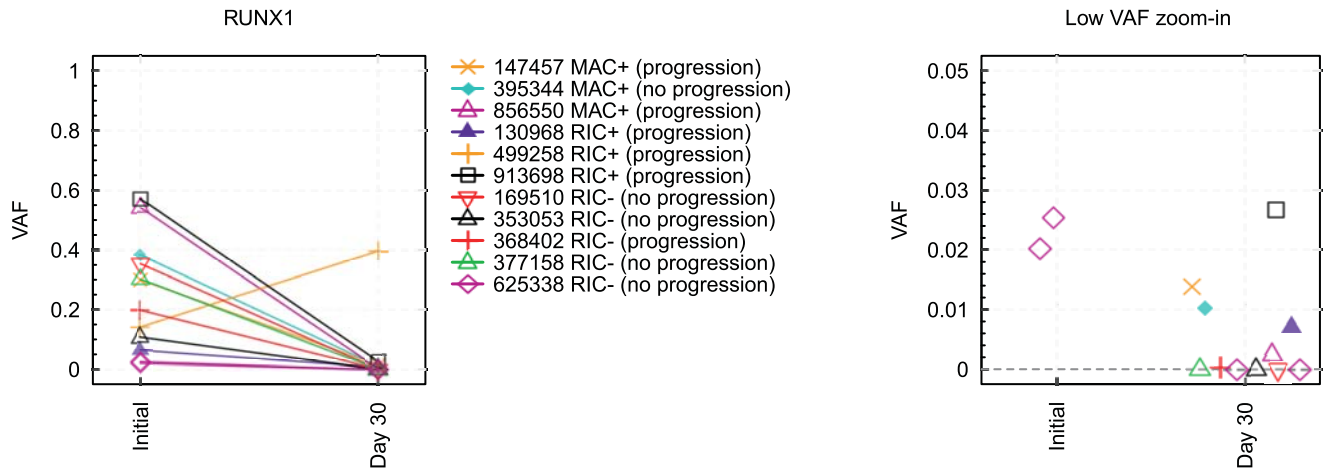
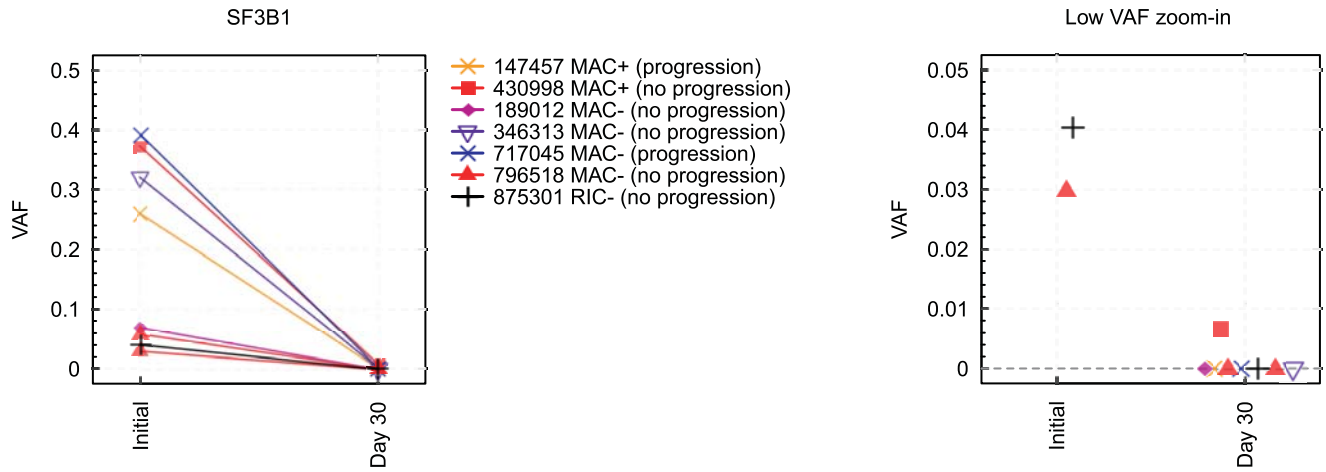
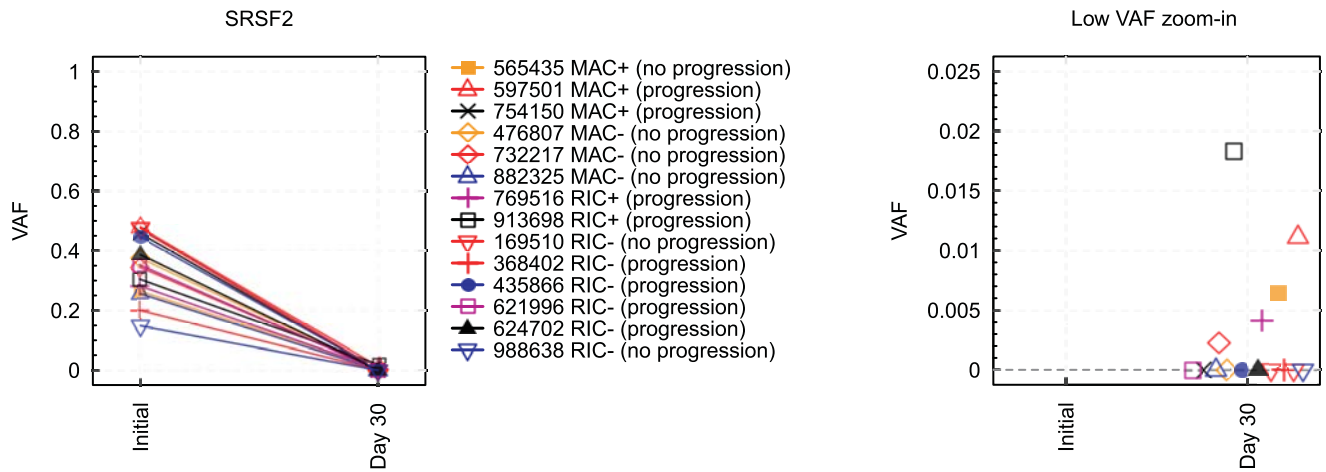


Figure S3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant

G.



H.



I.

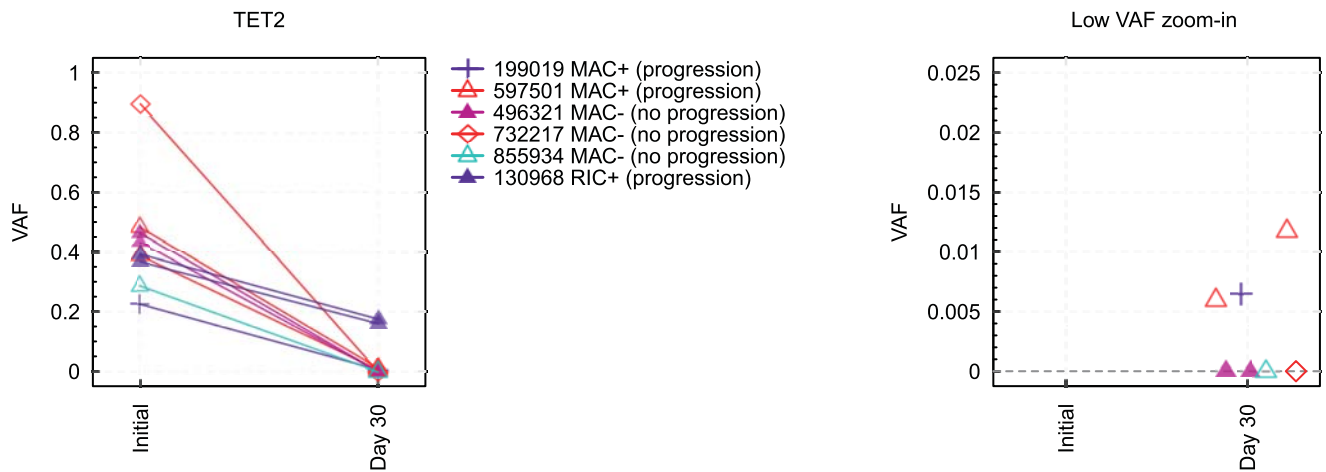
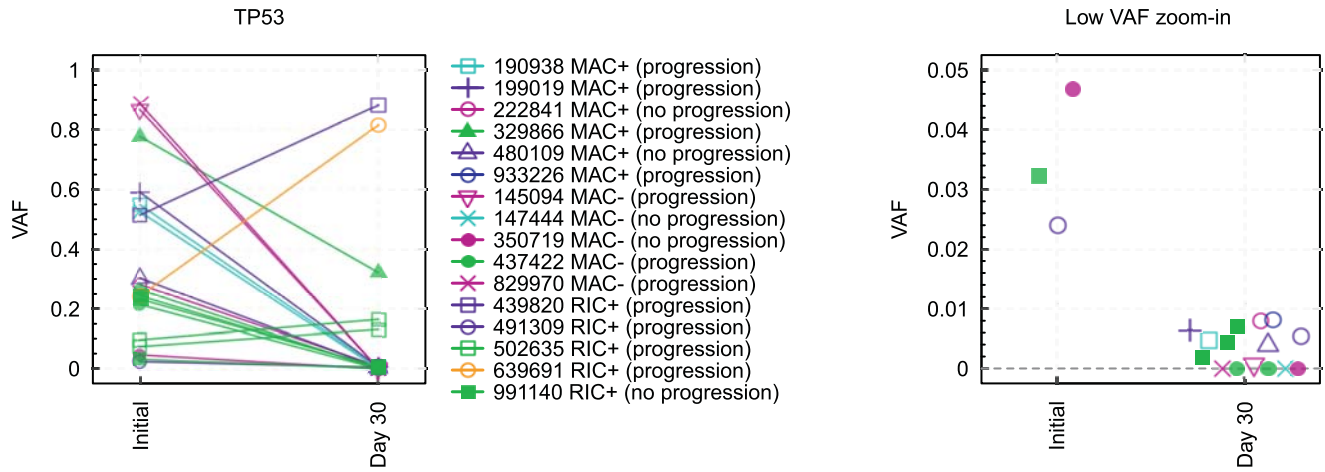


Figure S3. Mutation Clearance of Selected Genes at Day 30 Post-Allogeneic Hematopoietic Cell Transplant

J.



K.

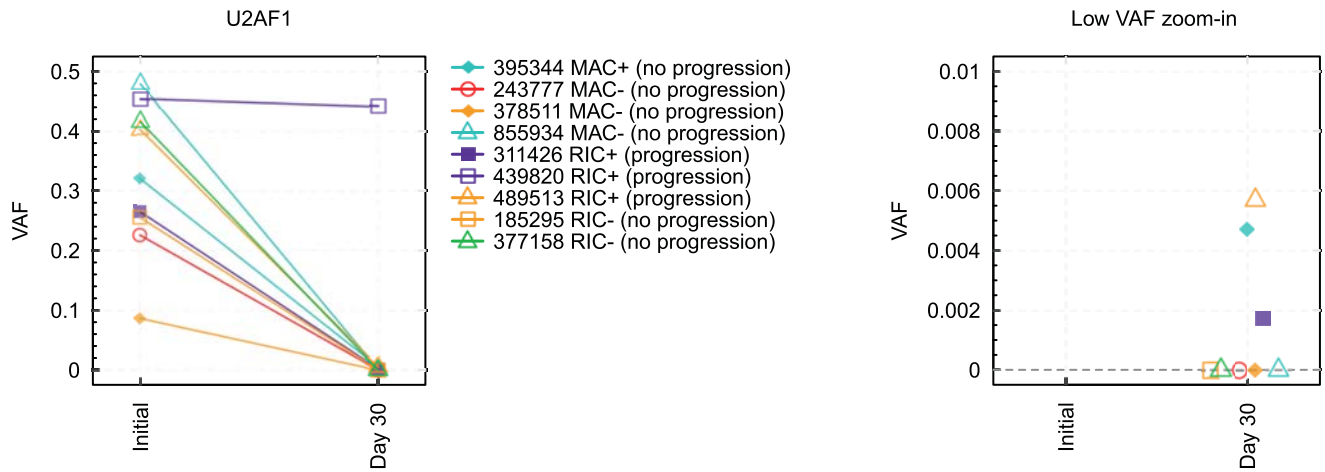


Figure S4. Association of Mutation Clearance at Day 30 post-alloHCT with Outcomes

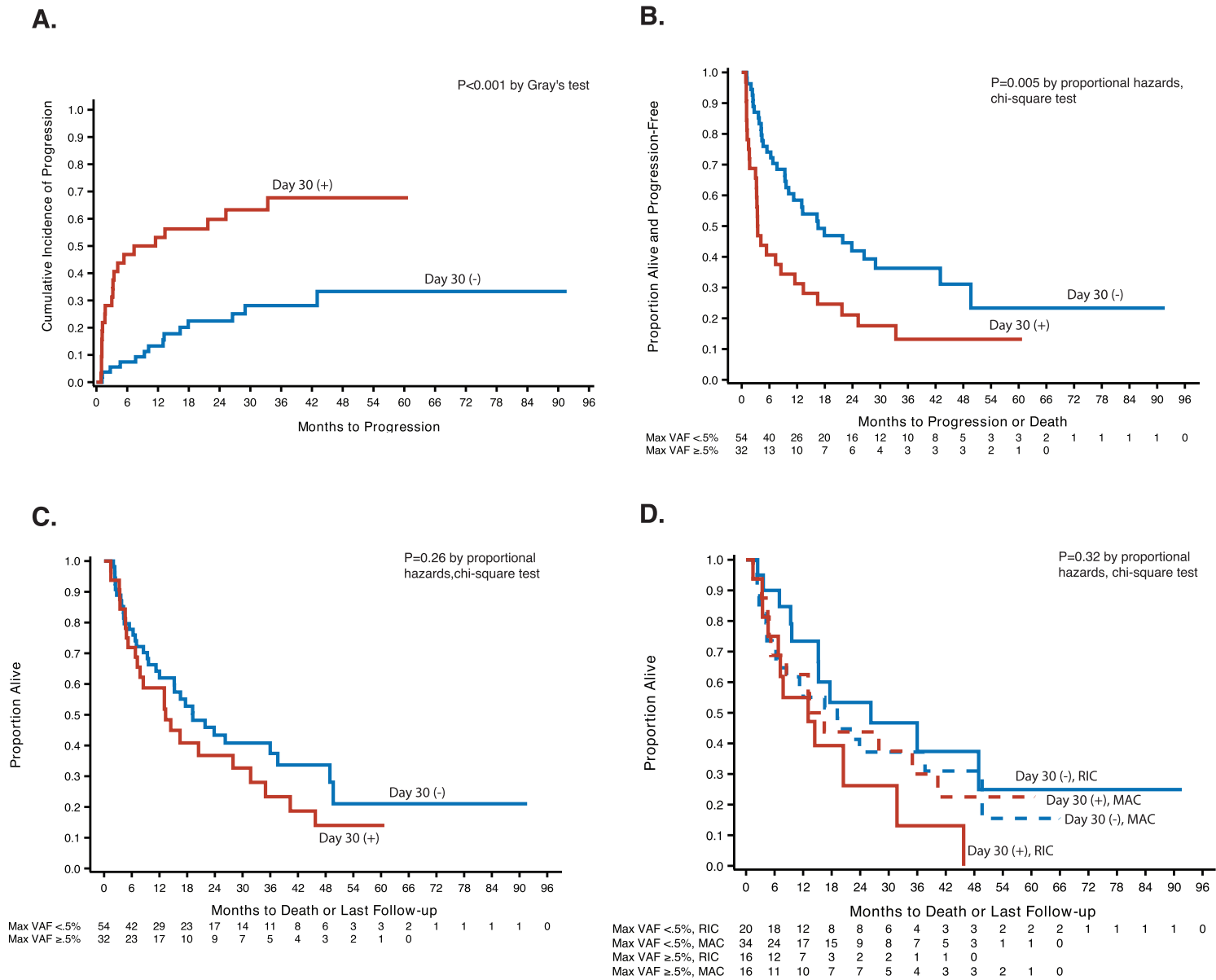


Figure S5. Association of Mutation Clearance at Day 100 post-alloHCT with Outcomes

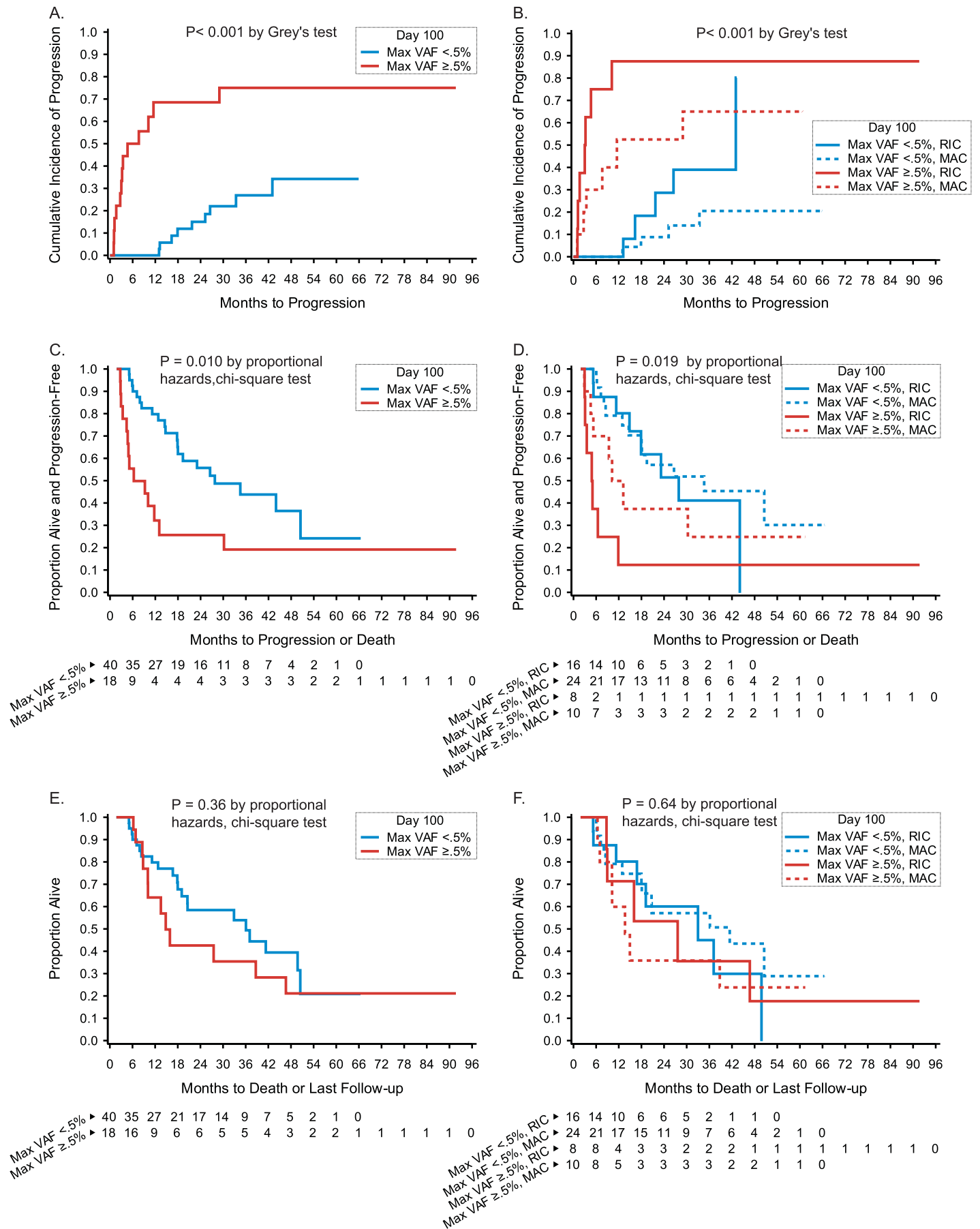


Figure S6. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 0.1%

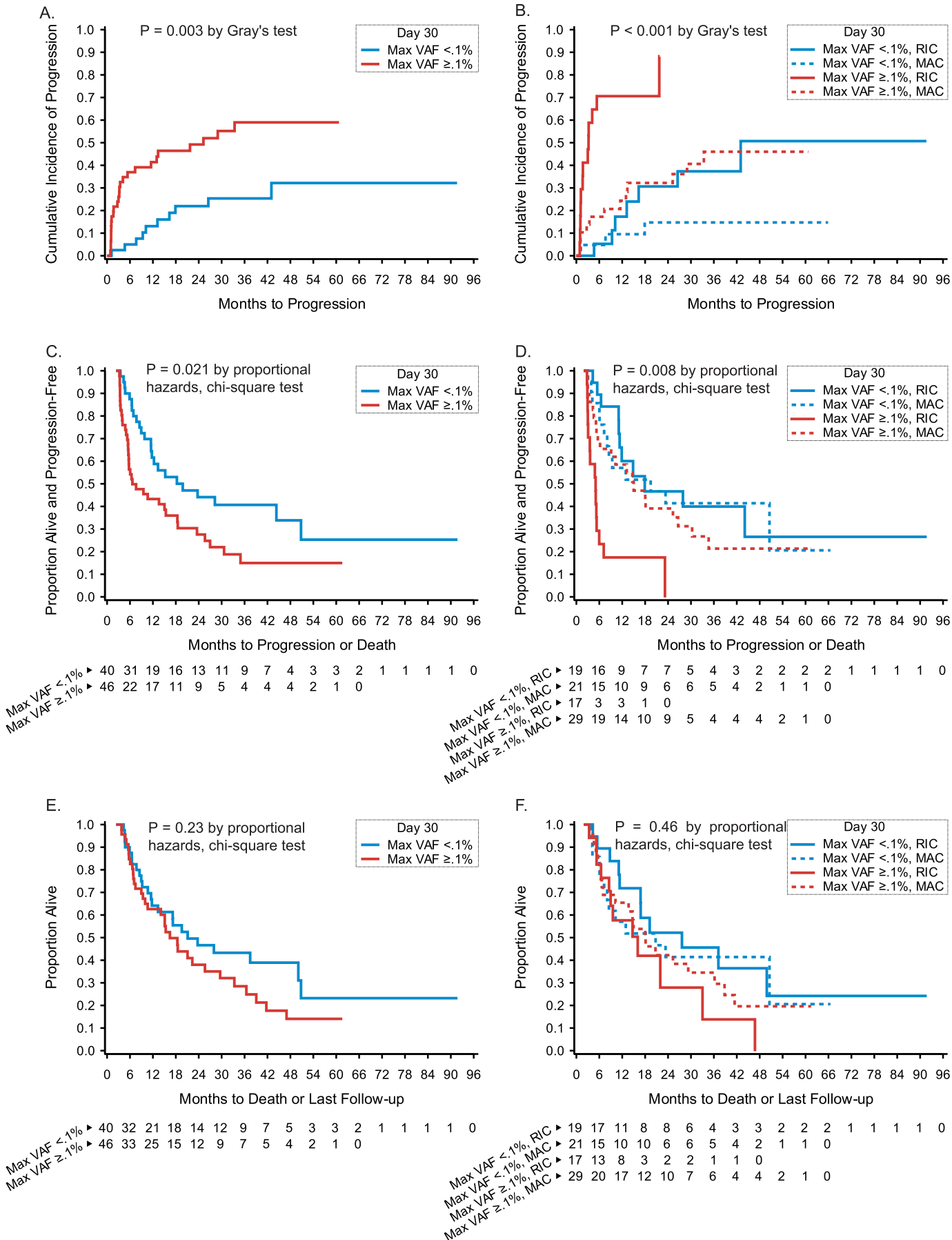


Figure S7. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 1%

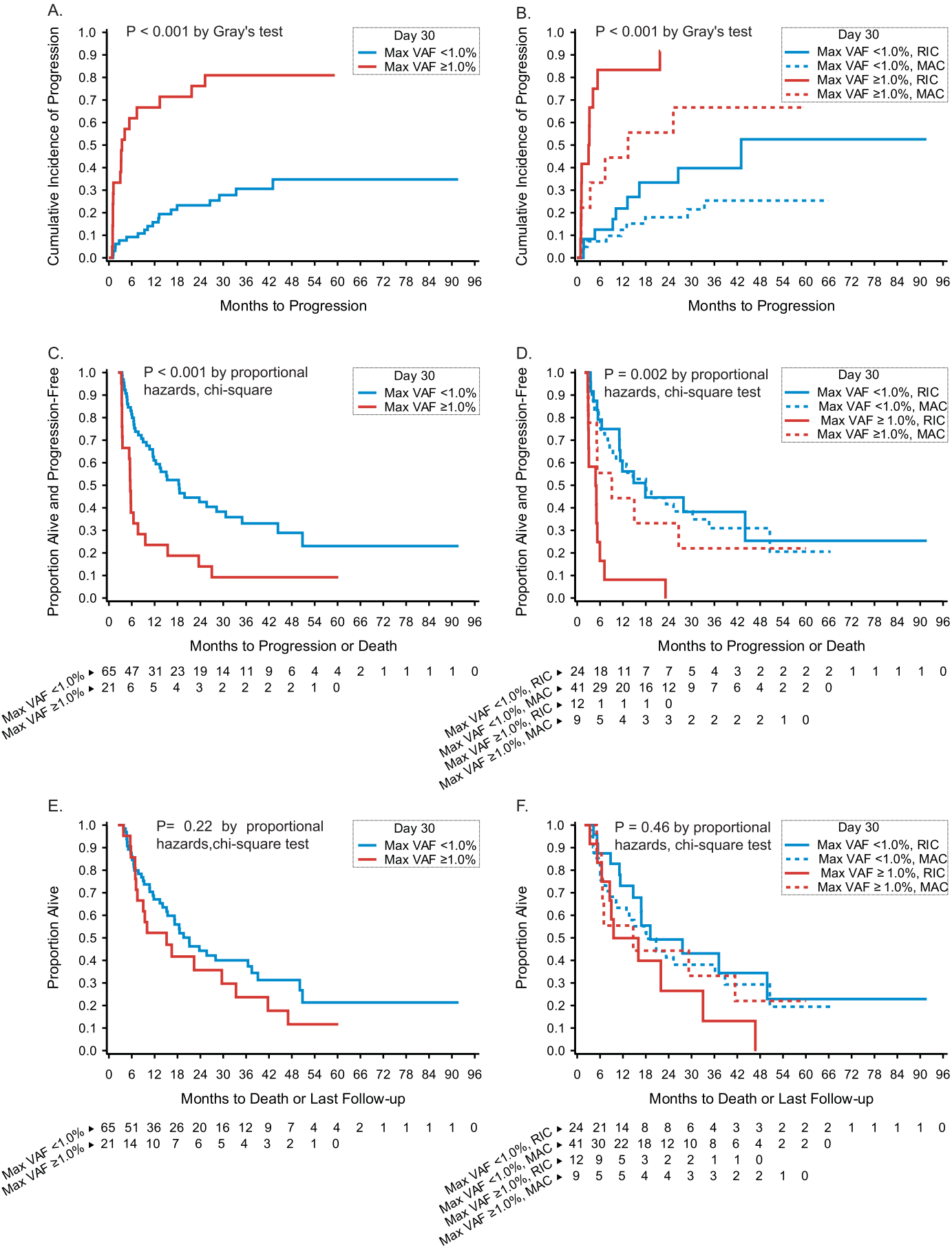


Figure S8. Association of Mutation Clearance with Outcomes Using a Variant Allele Frequency Threshold of 2.5%5%

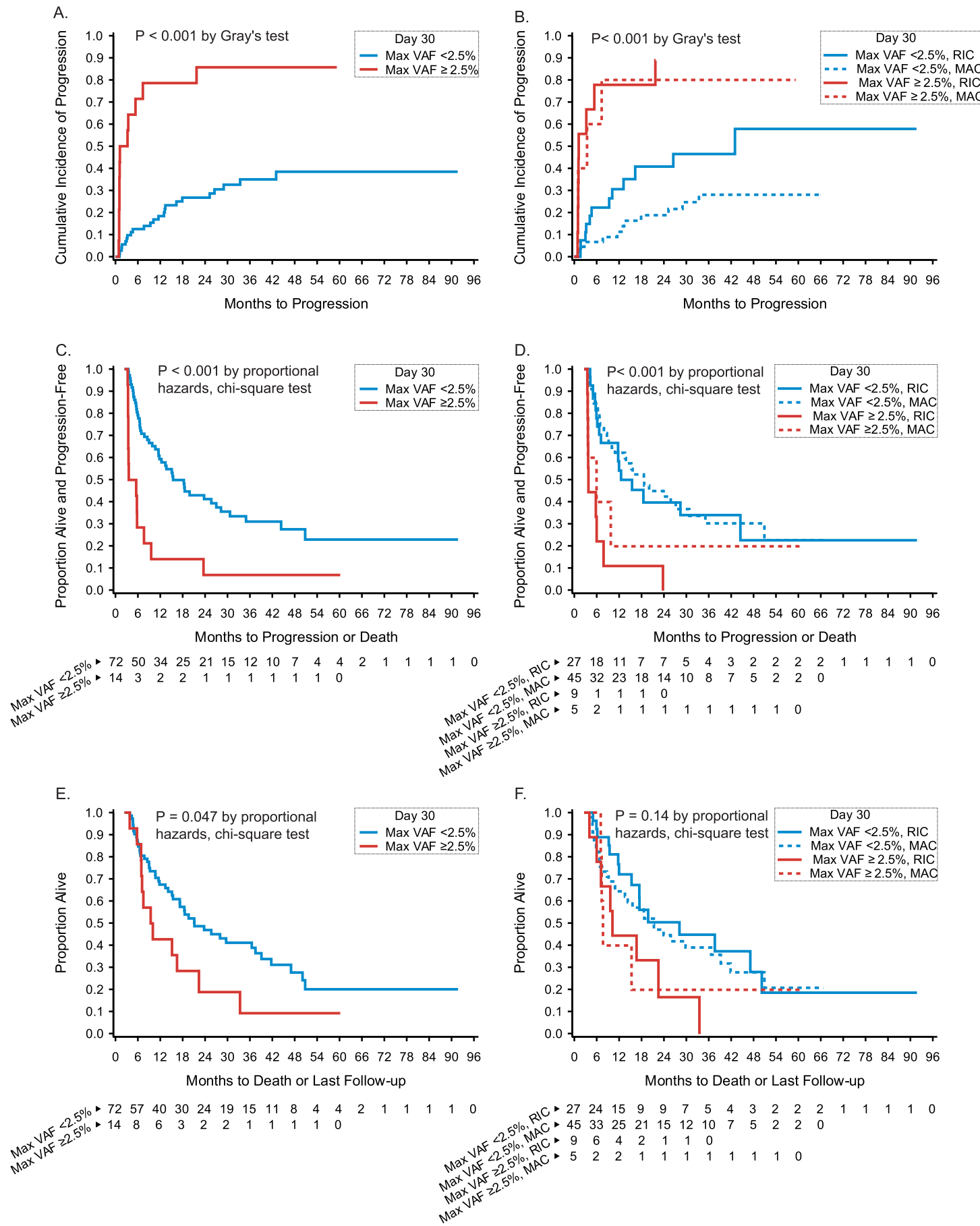


Figure S9. Association of Mutation Clearance with Outcomes Using Any Detectable Variant Allele Frequency

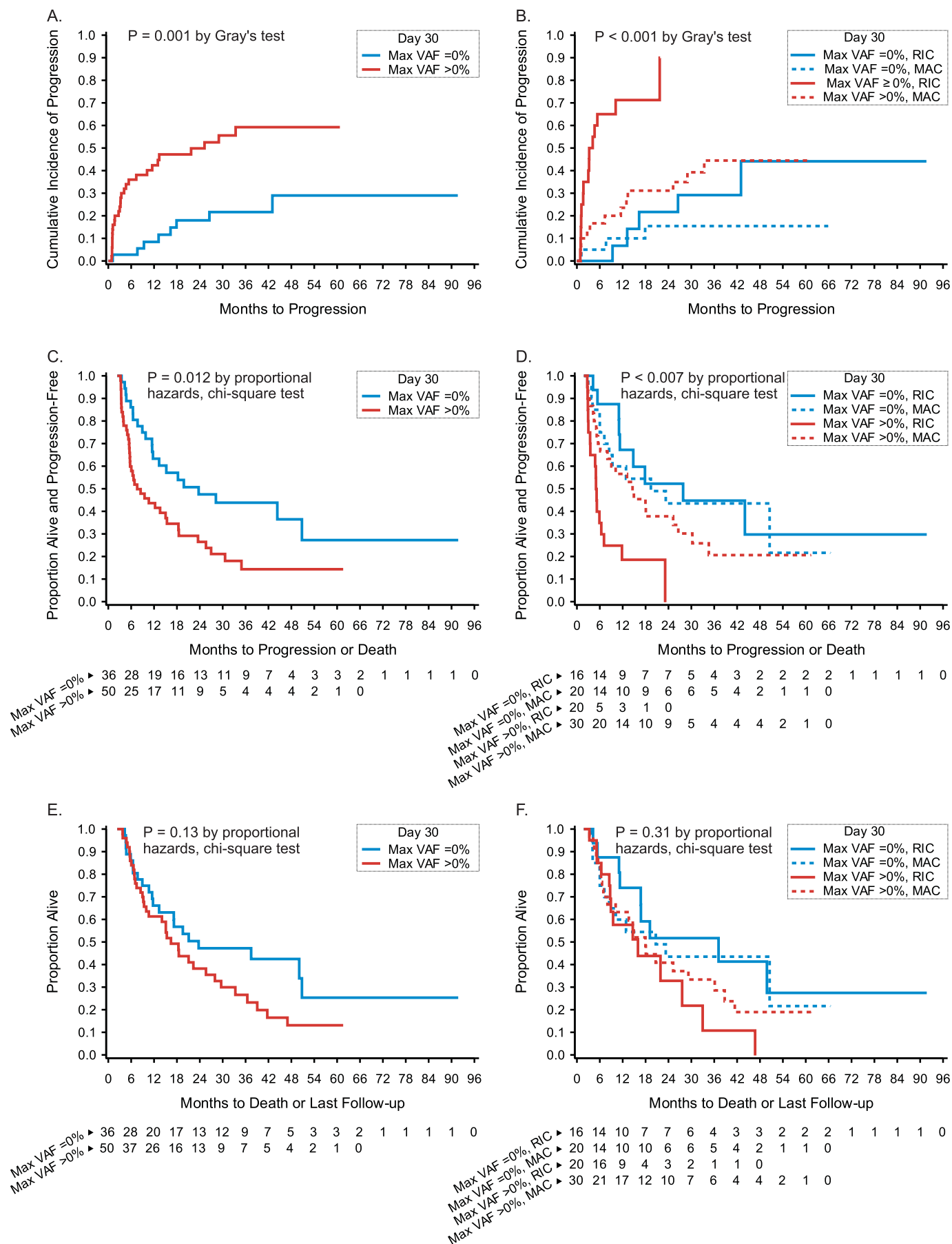
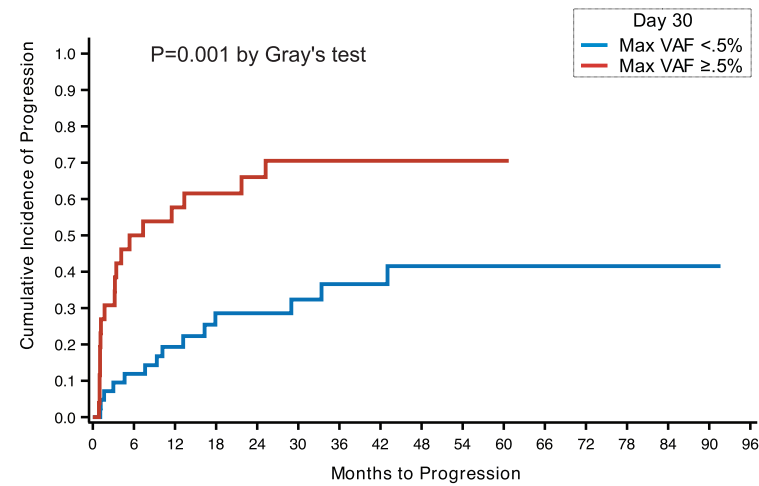
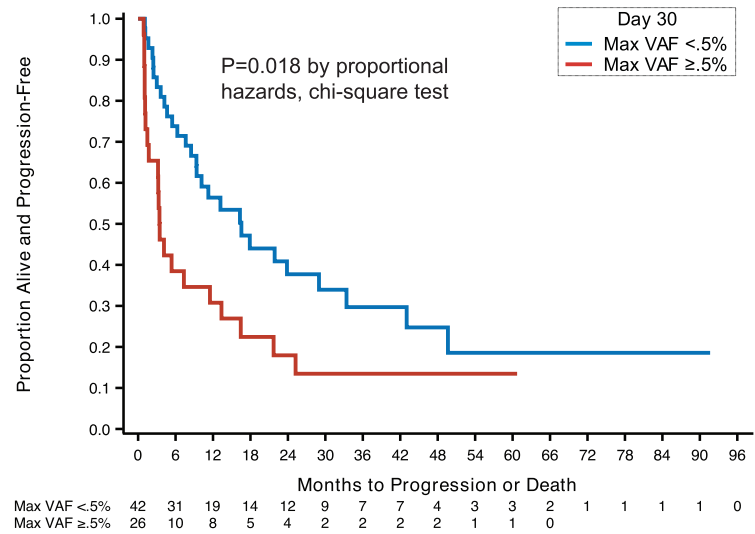


Figure S10. Association of Overall Survival with Mutation Clearance Determined by a 40 Gene-Panel

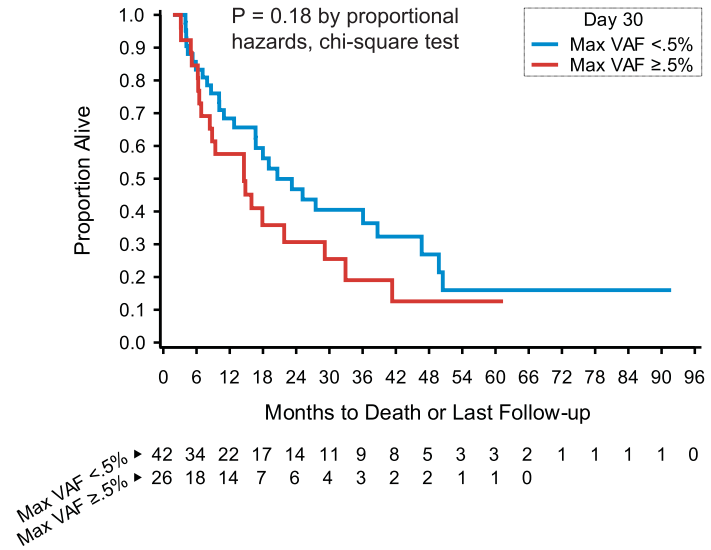
A.



B.



C.



D.

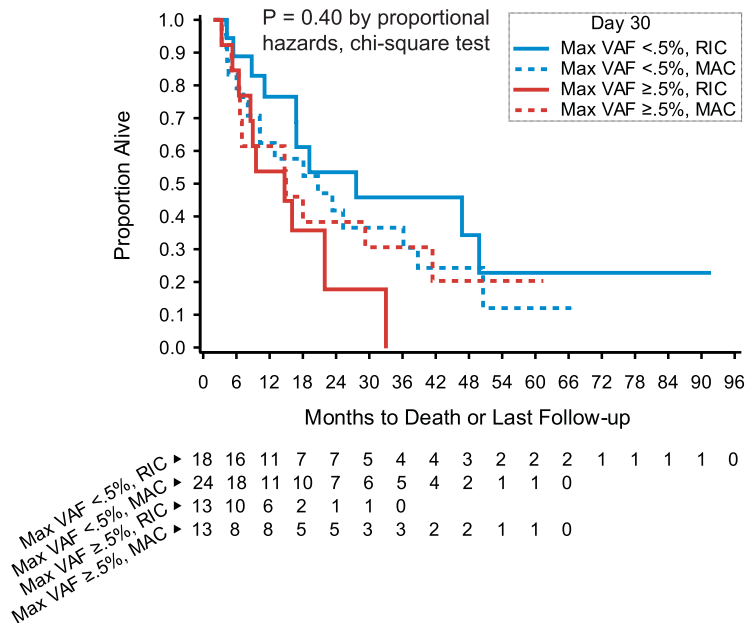


Table S1. Recurrently Mutated Genes in AML and MDS

ENSG ID	Gene symbol	Chr	Start	End	Strand
ENSG00000078369	<i>GNB1</i>	1	1716729	1822495	-
ENSG00000120952	<i>PRAMEF2</i>	1	12916941	12921764	+
ENSG00000065526	<i>SPEN</i>	1	16174359	16266955	+
ENSG00000058453	<i>CROCC</i>	1	17222232	17299474	+
ENSG00000142661	<i>MYOM3</i>	1	24382525	24438665	-
ENSG00000162521	<i>RBBP4</i>	1	33116749	33151812	+
ENSG00000188910	<i>GJB3</i>	1	35246790	35251970	+
ENSG00000054118	<i>THRAP3</i>	1	36690017	36770958	+
ENSG00000183317	<i>EPHA10</i>	1	38179561	38230824	-
ENSG00000162434	<i>JAK1</i>	1	65298906	65432187	-
ENSG00000162654	<i>GBP4</i>	1	89646831	89664633	-
ENSG00000203914	<i>HSP90B3P</i>	1	92100568	92109633	+
ENSG00000213281	<i>NRAS</i>	1	115247078	115259515	-
ENSG00000143373	<i>ZNF687</i>	1	151254094	151264381	+
ENSG00000143631	<i>FLG</i>	1	152274651	152297679	-
ENSG00000160691	<i>SHC1</i>	1	154934774	154946959	-
ENSG00000196189	<i>SEMA4A</i>	1	156117157	156147543	+
ENSG00000162733	<i>DDR2</i>	1	162601163	162750255	+
ENSG00000034971	<i>MYOC</i>	1	171604557	171621811	-
ENSG00000198216	<i>CACNA1E</i>	1	181382295	181770716	+
ENSG00000143341	<i>HMCN1</i>	1	185703683	186160085	+
ENSG00000162670	<i>BRINP3</i>	1	190066792	190446759	-
ENSG00000134369	<i>NAV1</i>	1	201592411	201796097	+
ENSG00000084674	<i>APOB</i>	2	21224301	21266945	-
ENSG00000119772	<i>DNMT3A</i>	2	25455496	25565459	-
ENSG00000091106	<i>NLR4</i>	2	32449518	32490923	-
ENSG00000115808	<i>STRN</i>	2	37070783	37193615	-
ENSG00000068878	<i>PSME4</i>	2	54091204	54197977	-
ENSG00000135636	<i>DYSF</i>	2	71680753	71913898	+
ENSG00000168702	<i>LRP1B</i>	2	140988992	142889270	-
ENSG00000144285	<i>SCN1A</i>	2	166845670	166930149	-
ENSG00000115524	<i>SF3B1</i>	2	198256698	198299815	-
ENSG00000138413	<i>IDH1</i>	2	209100951	209130798	-
ENSG00000078018	<i>MAP2</i>	2	210288771	210598842	+
ENSG00000054356	<i>PTPRN</i>	2	220154345	220174370	-
ENSG00000072195	<i>SPEG</i>	2	220299568	220363009	+
ENSG00000204120	<i>GIGYF2</i>	2	233562009	233725287	+
ENSG00000085978	<i>ATG16L1</i>	2	234118697	234204320	+
ENSG00000168334	<i>XIRP1</i>	3	39224701	39234087	-
ENSG00000008300	<i>CELSR3</i>	3	48673896	48700348	-
ENSG00000164061	<i>BSN</i>	3	49591922	49708982	+
ENSG00000157445	<i>CACNA2D3</i>	3	54156574	55108584	+
ENSG00000163618	<i>CADPS</i>	3	62384021	62861064	-
ENSG00000114861	<i>FOXP1</i>	3	71003844	71633140	-
ENSG00000175161	<i>CADM2</i>	3	85008132	86117951	+
ENSG00000145103	<i>ILDR1</i>	3	121706170	121741051	-
ENSG00000173175	<i>ADCY5</i>	3	123001143	123168605	-
ENSG00000114626	<i>ABTB1</i>	3	127391778	127399763	+
ENSG00000179348	<i>GATA2</i>	3	128198265	128212030	-
ENSG00000118007	<i>STAG1</i>	3	136055077	136471220	-
ENSG00000090402	<i>SI</i>	3	164696686	164796283	-

ENSG00000136527	<i>TRA2B</i>	3	185632356	185655924	-
ENSG00000038219	<i>BOD1L1</i>	4	13570362	13629347	-
ENSG00000047365	<i>ARAP2</i>	4	36067620	36246131	-
ENSG00000075539	<i>FRYL</i>	4	48499378	48782339	-
ENSG00000072201	<i>LNK1</i>	4	54325468	54567572	-
ENSG00000134853	<i>PDGFRA</i>	4	55095264	55164414	+
ENSG00000157404	<i>KIT</i>	4	55524085	55606881	+
ENSG00000128052	<i>KDR</i>	4	55944426	55991762	-
ENSG00000118777	<i>ABCG2</i>	4	89011416	89152474	-
ENSG00000168769	<i>TET2</i>	4	106067032	106200973	+
ENSG00000145362	<i>ANK2</i>	4	113739239	114304896	+
ENSG00000198589	<i>LRBA</i>	4	151185594	151936879	-
ENSG00000197410	<i>DCHS2</i>	4	155155527	155412930	-
ENSG00000039139	<i>DNAH5</i>	5	13690437	13944652	-
ENSG00000131711	<i>MAP1B</i>	5	71403061	71505397	+
ENSG00000164309	<i>CMYA5</i>	5	78985659	79096063	+
ENSG00000038427	<i>VCAN</i>	5	82767284	82878122	+
ENSG00000164176	<i>EDIL3</i>	5	83236373	83680611	-
ENSG00000120733	<i>KDM3B</i>	5	137688285	137772717	+
ENSG00000081842	<i>PCDHA6</i>	5	140206816	140391929	+
ENSG00000239389	<i>PCDHA13</i>	5	140261793	140391929	+
ENSG00000171815	<i>PCDHB1</i>	5	140430961	140433547	+
ENSG00000146001	<i>PCDHB18</i>	5	140613936	140617101	+
ENSG00000182578	<i>CSF1R</i>	5	149432854	149492935	-
ENSG00000019582	<i>CD74</i>	5	149781200	149792332	-
ENSG00000132911	<i>NMUR2</i>	5	151771093	151784840	-
ENSG00000118322	<i>ATP10B</i>	5	159990127	160279219	-
ENSG00000134516	<i>DOCK2</i>	5	169064251	169510386	+
ENSG00000181163	<i>NPM1</i>	5	170814708	170838141	+
ENSG00000113739	<i>STC2</i>	5	172741716	172756506	-
ENSG00000183258	<i>DDX41</i>	5	176938578	176944470	-
ENSG00000112739	<i>PRPF4B</i>	6	4021501	4065217	+
ENSG00000095951	<i>HIVEP1</i>	6	12008995	12165232	+
ENSG00000112137	<i>PHACTR1</i>	6	12717833	13288075	+
ENSG00000137411	<i>VAR2S</i>	6	30881982	30894233	+
ENSG00000197283	<i>SYNGAP1</i>	6	33387847	33421466	+
ENSG00000096433	<i>ITPR3</i>	6	33588522	33664351	+
ENSG00000112624	<i>GLTSCR1L</i>	6	42714696	42836296	+
ENSG00000146216	<i>TTBK1</i>	6	43211222	43255997	+
ENSG00000170927	<i>PKHD1</i>	6	51480098	51952423	-
ENSG00000151914	<i>DST</i>	6	56322785	56819413	-
ENSG00000079841	<i>RIMS1</i>	6	72596406	73112508	+
ENSG00000111799	<i>COL12A1</i>	6	75794042	75915767	-
ENSG00000146247	<i>PHIP</i>	6	79644136	79788011	-
ENSG00000164418	<i>GRIK2</i>	6	101846664	102517958	+
ENSG00000112333	<i>NR2E1</i>	6	108487215	108510013	+
ENSG00000213079	<i>SCAF8</i>	6	155054459	155230002	+
ENSG00000164619	<i>BMPER</i>	7	33944523	34195484	+
ENSG00000002746	<i>HECW1</i>	7	43152198	43602938	+
ENSG00000146648	<i>EGFR</i>	7	55086714	55324313	+
ENSG00000187391	<i>MAGI2</i>	7	77646374	79082890	-
ENSG00000075213	<i>SEMA3A</i>	7	83587659	84122040	-
ENSG00000198822	<i>GRM3</i>	7	86273224	86494200	+
ENSG00000066923	<i>STAG3</i>	7	99775186	99819111	+
ENSG00000154415	<i>PPP1R3A</i>	7	113516832	113715975	-

ENSG00000105976	<i>MET</i>	7	116312444	116438440	+
ENSG00000179603	<i>GRM8</i>	7	126078652	126893348	-
ENSG00000128594	<i>LRRC4</i>	7	127667124	127672160	-
ENSG00000128578	<i>STRIP2</i>	7	129073731	129128240	+
ENSG00000269955	<i>LUC7L2</i>	7	139026106	139107345	+
ENSG00000157764	<i>BRAF</i>	7	140419127	140624564	-
ENSG00000197448	<i>GSTK1</i>	7	142941186	142967947	+
ENSG00000055130	<i>CUL1</i>	7	148395006	148498202	+
ENSG00000106462	<i>EZH2</i>	7	148504475	148581414	-
ENSG00000055118	<i>KCNH2</i>	7	150642049	150675403	-
ENSG00000055609	<i>KMT2C</i>	7	151832007	152133628	-
ENSG00000183117	<i>CSMD1</i>	8	2792875	4852328	-
ENSG00000164741	<i>DLC1</i>	8	12940870	13372396	-
ENSG00000215262	<i>KCNU1</i>	8	36641842	36793643	+
ENSG00000248522	<i>SBF1P1</i>	8	56362069	56367699	-
ENSG00000121005	<i>CRISPLD1</i>	8	75896843	75946793	+
ENSG00000079102	<i>RUNX1T1</i>	8	92971152	93107443	-
ENSG00000205038	<i>PKHD1L1</i>	8	110374706	110543500	+
ENSG00000164796	<i>CSMD3</i>	8	113235157	114449328	-
ENSG00000164754	<i>RAD21</i>	8	117858173	117887105	-
ENSG00000136997	<i>MYC</i>	8	128747680	128753674	+
ENSG00000226807	<i>MROH5</i>	8	142443929	142517330	-
ENSG00000227184	<i>EPPK1</i>	8	144935822	144947434	-
ENSG00000096968	<i>JAK2</i>	9	4985033	5128183	+
ENSG00000122735	<i>DNAI1</i>	9	34457412	34520982	+
ENSG00000083067	<i>TRPM3</i>	9	73149949	74061820	-
ENSG00000165119	<i>HNRNP</i>	9	86582998	86595569	-
ENSG00000185920	<i>PTCH1</i>	9	98205262	98279339	-
ENSG00000197816	<i>CCDC180</i>	9	100000779	100139569	+
ENSG00000041982	<i>TNC</i>	9	117782805	117880486	-
ENSG00000106804	<i>C5</i>	9	123714613	123837452	-
ENSG00000107147	<i>KCNT1</i>	9	138594031	138684992	+
ENSG00000148408	<i>CACNA1B</i>	9	140772241	141019076	+
ENSG00000095787	<i>WAC</i>	10	28821422	28911862	+
ENSG00000204176	<i>SYT15</i>	10	46955444	46971400	-
ENSG00000138336	<i>TET1</i>	10	70320117	70454239	+
ENSG00000107731	<i>UNC5B</i>	10	72972298	73062621	+
ENSG00000148602	<i>LRIT1</i>	10	85991276	86001217	-
ENSG00000182771	<i>GRID1</i>	10	87359312	88126250	-
ENSG00000171862	<i>PTEN</i>	10	89622870	89731687	+
ENSG00000138193	<i>PLCE1</i>	10	95753746	96088149	+
ENSG00000166024	<i>R3HCC1L</i>	10	99894381	100004654	+
ENSG00000107593	<i>PKD2L1</i>	10	102047903	102090243	-
ENSG00000229256	<i>ST13P13</i>	10	104975466	104976557	+
ENSG00000108055	<i>SMC3</i>	10	112327449	112364394	+
ENSG00000165813	<i>C10orf118</i>	10	115880621	115934364	-
ENSG00000117983	<i>MUC5B</i>	11	1142474	1288726	+
ENSG00000110328	<i>GALNT18</i>	11	11292421	11643561	-
ENSG00000129173	<i>E2F8</i>	11	19245614	19263389	-
ENSG00000182255	<i>KCNA4</i>	11	30031765	30038488	-
ENSG00000184937	<i>WT1</i>	11	32409321	32457176	-
ENSG00000149480	<i>MTA2</i>	11	62360675	62369303	-
ENSG00000168066	<i>SF1</i>	11	64532078	64546258	-
ENSG00000175591	<i>P2RY2</i>	11	72929344	72947397	+
ENSG00000074266	<i>EED</i>	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	<i>CNTNAP4</i>	16	76311176	76593135	+
ENSG00000166473	<i>PKD1L2</i>	16	81134484	81253975	-
ENSG00000158545	<i>ZC3H18</i>	16	88636789	88698374	+
ENSG00000187741	<i>FANCA</i>	16	89803957	89883065	-
ENSG00000187624	<i>C17orf97</i>	17	260118	264367	+
ENSG00000174231	<i>PRPF8</i>	17	1553923	1588176	-
ENSG00000141510	<i>TP53</i>	17	7565257	7590863	-
ENSG00000264424	<i>MYH4</i>	17	10346607	10372876	-
ENSG00000007174	<i>DNAH9</i>	17	11501748	11873485	+
ENSG00000141027	<i>NCOR1</i>	17	15932471	16121499	-
ENSG00000196712	<i>NF1</i>	17	29421945	29705949	+
ENSG00000178691	<i>SUZ12</i>	17	30264044	30328064	+
ENSG00000171345	<i>KRT19</i>	17	39679869	39684641	-
ENSG00000073670	<i>ADAM11</i>	17	42836568	42859214	+
ENSG00000120071	<i>KANSL1</i>	17	44107282	44270166	-
ENSG00000006283	<i>CACNA1G</i>	17	48638429	48704835	+
ENSG00000141200	<i>KIF2B</i>	17	51900239	51902573	+
ENSG00000180891	<i>CUEDC1</i>	17	55940337	56032684	-
ENSG00000265206	<i>MIR142</i>	17	56408593	56408679	-
ENSG00000109066	<i>TMEM104</i>	17	72772622	72835922	+
ENSG00000161547	<i>SRSF2</i>	17	74730197	74733413	-
ENSG00000173821	<i>RNF213</i>	17	78234665	78370085	+
ENSG00000152217	<i>SETBP1</i>	18	42260138	42648475	+
ENSG00000167306	<i>MYO5B</i>	18	47349101	47721384	-
ENSG00000197561	<i>ELANE</i>	19	851014	856242	+
ENSG00000181143	<i>MUC16</i>	19	8959520	9092018	-
ENSG00000080573	<i>COL5A3</i>	19	10070237	10121147	-
ENSG00000105397	<i>TYK2</i>	19	10461204	10491248	-
ENSG00000179218	<i>CALR</i>	19	13049414	13055304	+
ENSG00000105639	<i>JAK3</i>	19	17935591	17958870	-
ENSG00000130518	<i>KIAA1683</i>	19	18367906	18385319	-
ENSG00000105701	<i>FKBP8</i>	19	18642568	18654383	-
ENSG00000245848	<i>CEBPA</i>	19	33790840	33793470	-
ENSG00000126249	<i>PDCD2L</i>	19	34895303	34917073	+
ENSG00000196218	<i>RYR1</i>	19	38924340	39078204	+
ENSG00000090920	<i>FCGBP</i>	19	40353963	40440533	-
ENSG00000105429	<i>MEGF8</i>	19	42829761	42882921	+
ENSG00000063244	<i>U2AF2</i>	19	56165512	56186081	+
ENSG00000171456	<i>ASXL1</i>	20	30946153	31027122	+
ENSG00000088305	<i>DNMT3B</i>	20	31350191	31397162	+
ENSG00000196090	<i>PTPRT</i>	20	40701392	41818610	-
ENSG00000087460	<i>GNAS</i>	20	57414773	57486247	+
ENSG00000075043	<i>KCNQ2</i>	20	62037542	62103993	-
ENSG00000159216	<i>RUNX1</i>	21	36160098	37357047	-
ENSG00000171587	<i>DSCAM</i>	21	41382926	42219065	-
ENSG00000160201	<i>U2AF1</i>	21	44513066	44527697	-
ENSG00000099954	<i>CECR2</i>	22	17840837	18033845	+
ENSG00000100038	<i>TOP3B</i>	22	21075651	22337213	-
ENSG00000099995	<i>SF3A1</i>	22	30727977	30752936	-
ENSG00000146950	<i>SHROOM2</i>	X	9754496	9917483	+
ENSG00000169249	<i>ZRSR2</i>	X	15808595	15841383	+
ENSG00000102098	<i>SCML2</i>	X	18257433	18372847	-
ENSG00000185448	<i>FAM47A</i>	X	34147873	34150428	-
ENSG00000183337	<i>BCOR</i>	X	39909068	40036582	-
ENSG00000124486	<i>USP9X</i>	X	40944888	41095832	+

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

All genome coordinates use NCBI Build 37.

Chr, chromosome.

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 Count	Normal VAF	Tumor Count	Tumor VAF		
611	1	53547545	53547545	G	T	SNP	POZN	ENST0000021553	-1	intronic	c.1896-108	e110-108	tier3	19	0	0.000	52	21	0.288
611	1	63153953	63153953	G	T	SNP	DOCK7	ENST00000261157	-1	5_prime_untranslated_region	c.18	leu3	14	0	0.000	25	19	0.432	
611	2	25604481	25604481	G	A	SNP	DNMT3A	ENST00000264709	-1	nonsense	c.2032	p.Q67R*	tier1	292	4	0.014	1146	70	0.057
611	3	31495819	31495819	G	A	SNP	THRAP3P1	ENST00000417753	-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	3_prime_untranslated_region	c.777	p.S259	tier1	79	2	0.025	140	68	0.327
611	3	130720537	130720537	T	A	SNP	ATP2C1	ENST000004428331	-1	missense	c.343	NULL	tier4	42	0	0.000	159	91	0.364
611	4	187540539	187540539	G	T	SNP	FAT1	ENST00000441802	-1	missense	c.7201	p.E240K	tier1	33	1	0.029	94	36	0.277
611	6	33037020	33037020	C	G	SNP	HLA-DPA1	ENST00000259170	-1	5_prime_flanking_region	c.404	p.T130I	tier1	57	0	0.000	138	77	0.358
611	6	43206066	43206066	C	G	SNP	TTBK1	ENST00000259750	-1	missense	c.4333	NULL	tier4	58	0	0.000	177	49	0.217
611	7	45753309	45753309	C	T	SNP	ADCY1	ENST00000297323	1	silent	c.3075	p.H102S	tier1	91	2	0.021	92	56	0.378
611	7	100549883	100549883	G	C	SNP	LOC10131514	ENST00000379458	1	missense	c.464	p.S155N	tier1	19	0	0.000	51	28	0.350
611	8	17944578	17944578	G	T	SNP	LOC101929066	ENST00000499554	1	missense	NULL	NULL	tier1	85	0	0.000	182	79	0.303
611	8	72127533	72127533	G	T	SNP	EYAI	ENST00000340726	-1	intronic	c.1597-89	e14-89	tier3	74	2	0.026	192	62	0.244
611	8	16424437	16424437	G	C	SNP	TRPS1	ENST00000395715	-1	intronic	c.1814	NULL	tier3	64	1	0.015	97	35	0.263
611	8	12272633	12272633	G	T	SNP	TRAPPC9	ENST00000389328	-1	intronic	c.3350-24487	e22-24487	tier3	64	1	0.015	95	43	0.312
611	9	10338826	10338826	C	T	SNP	TMEFF1	ENST00000374879	1	nonsense	c.1087	p.R363*	tier1	51	0	0.000	76	22	0.225
611	9	131502394	131502394	G	C	SNP	ZER1	ENST00000291900	-1	silent	c.1858	p.L620	tier1	31	0	0.000	76	22	0.225
611	11	6648113	6648113	G	T	SNP	DCHS1	ENST00000336930	-1	missense	c.6157	p.M206V	tier1	58	0	0.000	93	32	0.254
611	11	25004690	25004690	A	G	SNP	LUZP2	ENST00000298282	1	intronic	c.837-33	e8-33	tier2	44	1	0.022	91	46	0.338
611	12	53553483	53553483	T	A	SNP	PKNOX2	ENST00000268282	1	missense	c.1313	NULL	tier1	23	0	0.000	90	33	0.266
611	14	23072764	23072764	T	C	SNP	ABHD4	ENST00000267085	-1	missense	c.2775	p.N438S	tier1	23	0	0.011	160	61	0.276
611	14	04216205	04216205	G	A	SNP	PPR138	ENST00000205566	-1	missense	c.23072764	NULL	tier3	86	1	0.011	160	61	0.276
611	15	63615709	63615709	A	-	DEL	CA12	ENST00000205566	-1	missense	c.2775	p.R399C	tier1	57	0	0.000	203	67	0.248
611	15	66080017	66080017	G	A	SNP	DEIN4A	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	0.289
611	17	3651144	3651144	G	T	SNP	ITGAE	ENST00000263087	-1	silent	c.876	p.I292	tier1	56	0	0.000	142	43	0.232
611	17	5077452	5077452	G	T	SNP	USP6	ENST00000250066	-1	3_prime_untranslated_region	c.1179	NULL	tier3	76	0	0.000	360	131	0.267
611	17	2607697	2607697	G	-	INS	NOS2	ENST0000031735	-1	missense	c.2962	p.P988T	tier1	160	2	0.012	318	166	0.342
611	17	2953477	2953477	G	-	INS	NFI	ENST00000358273	-1	frame_shift_ins	c.2026..2027	p.I679fs	tier1	207	0	0.000	653	174	0.210
611	18	42531913	42531913	G	C	SNP	SEBTP1	ENST00000282030	1	missense	c.2608	p.G670S	tier1	160	4	0.009	798	358	0.310
611	19	39787541	39787541	G	A	SNP	INPL1	ENST00000336225	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.337	p.E126G	tier1	30	0	0.000	78	29	0.271
611	22	21480989	21480989	G	A	SNP	POW1Z1L7	ENST00000329449	-1	missense	c.377	p.P133A	tier1	49	0	0.000	111	40	0.261
611	22	23822123	23822123	G	A	SNP	POW1Z1L7	ENST00000330077	-1	intronic	c.165-3066	e1+3066	tier2	46	2	0.040	125	75	0.373
611	X	9757256	9757256	G	A	SNP	SHROOM2	ENST00000300913	-1	splice_region	c.119+9	e2+9	tier2	117	9	0.071	176	130	0.425
130968	1	6101841	6101841	T	A	SNP	KDM62	ENST00000764247	-1	missense	c.33	p.S12D	tier1	290	0	0.000	686	113	0.146
130968	1	11362673	11362673	C	A	SNP	KDM62	ENST00000955535	-1	missense	c.33	p.S12D	tier1	290	0	0.000	686	113	0.146
130968	1	11362673	11362673	C	A	SNP	KDM62	ENST00000955535	-1	missense	c.33	p.S12D	tier1	290	0	0.000	686	113	0.146
130968	1	16944523	16944523	G	T	SNP	ATP14A	ENST0000068088	-1	nonsense	c.2297	p.T768M	tier1	59	0	0.000	75	4	0.350
130968	2	76975723	76975723	G	A	SNP	LRRT44	ENST00000409911	-1	missense	c.784	NULL	tier3	61	0	0.000	110	32	0.222
130968	2	101554339	101554339	G	T	SNP	NPA52	ENST00000452504	1	intronic	c.559+35	e5+35	tier3	42	0	0.000	113	27	0.193
130968	3	12100282	12100282	C	T	SNP	STXB95L	ENST00000273666	1	silent	c.2562	p.R723*	tier1	89	2	0.022	233	38	0.193
130968	3	140281105	140281105	A	G	SNP	CLSTG2	ENST00000459420	1	nonsense	c.2167	p.R554	tier1	55	0	0.000	159	38	0.193
130968	3	15975759	15975759	A	T	SNP	ATP1B3	ENST00000285371	1	missense	c.58	p.L20V	tier1	4	0	0.000	5	18	0.783
130968	4	57898985	57898985	T	A	SNP	MED12L	ENST00000474524	1	missense	c.838-40	e7-40	tier3	48	0	0.000	132	21	0.137
130968	4	106157023	106157023	C	G	SNP	ARL9	ENST00000360096	1	missense	c.215	p.I72S	tier1	97	2	0.020	153	99	0.391
130968	4	106164913	106164913	C	A	SNP	TET2	ENST00000380013	1	missense	c.1924	p.O642*	tier1	413	7	0.017	712	422	0.372
130968	4	18754079	18754079	C	T	SNP	FAT1	ENST00000441802	-1	missense	c.3781	p.R126I*	tier1	214	16	0.070	378	265	0.412
130968	6	27840011	27840011	T	C	SNP	HST1H3I	ENST00000328488	-1	missense	c.6661	p.G221R	tier1	55	0	0.000	99	28	0.221
130968	6	56366476	56366476	C	T	SNP	DST	ENST00000370754	-1	missense	c.83	p.K28M	tier1	65	0	0.000	135	25	0.156
130968	6	123868713	123868713	G	T	SNP	TRDN	ENST00000398178	-1	missense	c.19489	p.A6497T	tier1	260	11	0.041	578	402	0.410
130968	7	30692952	30692952	CC	-	DEL	CHRR2	ENST00000348438	-1	missense	c.277	p.R93C	tier1	41	0	0.000	106	19	0.152
130968	7	30692957	30692957	CC	-	DEL	CHRR2	ENST00000348438	-1	missense	c.124	NULL	tier3	26	0	0.000	37	13	0.260
130968	7	45140023	45140023	A	-	DEL	TBRG4	ENST00000348438	-1	3_prime_untranslated_region	c.119	NULL	tier3	28	0	0.000	38	13	0.255
130968	7	135282052	135282052	A	-	DEL	NUP205	ENST00000258770	-1	splice_site_del	c.1795-6..1795-1	e10-1	tier1	49	0	0.000	73	19	0.207
130968	10	126365553	126365553	G	A	SNP	FAM53B	ENST00000462316	-1	3_prime_untranslated_region	c.135282052	NULL	tier3	49	0	0.000	141	25	0.151
130968	11	121384952	121384952	A	G	SNP	SORL1	ENST00000337318	-1	intronic	c.906+4623	e3+4623	tier3	95	0	0.000	214	21	0.089
130968	12	51752848	51752848	C	T	SNP	GALNT6	ENST00000260197	-1	missense	c.1133	p.E378G	tier1	58	3	0.049	115	60	0.343
130968	14	99641862	99641862	C	T	SNP	BCL11B	ENST00000356317	-1	silent	c.1368+68	e5+68	tier3	40	3	0.070	71	55	0.437
130968	15	100272161	100272161	G	T	SNP	LYSMO4	ENST00000337195	-1	intronic	c.1311	p.K437	tier1	41	1	0.024	71	24	0.253
130968	16	71220653	71220653	G	A	SNP	HYDM	ENST00000332728	-1	missense	c.44	p.A15D	tier1	83	5	0.057	125	102	0.449
130968	17	7788427	7788427	C	T	SNP	LSMO1	ENST00000332728	-1	intronic	c.135+11	e1+11	tier3	357	2	0.006	879	138	0.135
130968	17	7788427	7788427	C	T	SNP	LSMO1	ENST00000332728	-1	intronic	c.135+11	e1+11	tier3	357	2	0.006	879	138	0.135
130968	17	7788427	7788427	C	T	SNP	LSMO1	ENST00000332728	-1	intronic	c.135+11	e1+11	tier3	357	2	0.006	879	138	0.135
130968	17	61790912	61790912	-	T	INS	UBE2Z	ENST00000370555	-1	3_prime_untranslated_region	c.1875	NULL	tier2	28	1	0.035	61	27	0.307
130968	19	10108048	10108048	G	A	SNP	STRADA	ENST00000336174	-1	intronic	c.227+25	e5+25	tier3	58	0	0.000	179	29	0.138
130968	19	33793102	33793103	C	A	SNP	COL5A3	ENST00000336174	-1	missense	c.1262	p.P421L	tier1	152	0	0.000	448	72	0.138
130968	20	31022288	31022288	C	A	SNP	CEBPA	ENST00000498907	-1	frame_shift_ins	c.219..218	p.N74fs	tier1	468	0	0.000	1259	273	0.178
130968	21	18621227	18621227	C	T	SNP	C21orf37	ENST00000375887	-1	nonsense	c.1773	p.Y991*</							

147444	16	4384536	4384536	C	T	SNP	GLI/S2	ENST00000262366	1	missense	c.360	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	G	A	SNP	FAM197A	ENST00000331733	-1	silent	c.393	p.D131	tier1	39	0	0.000	49	13	0.210
147444	17	67079228	67079228	T	A	SNP	ABCA6	ENST00000284425	-1	intronic	c.47676.74	ex-8	tier3	110	0	0.000	93	31	0.250
147444	19	15511962	15511962	C	G	SNP	AKAP9L	ENST00000394110	-1	splice_region	c.817-8	ex-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
147444	X	609179	609179	G	A	SNP	DVL1	ENST00000415461	-1	3_prime_untranslated_region	c.809179	NULL	tier2	69	0	0.000	523	203	0.279
147451	1	1275514	1275514	G	A	SNP	C10orf22	ENST00000376886	-1	silent	c.813	p.N271	tier1	38	1	0.025	174	77	0.307
147451	1	1601586	1601586	G	C	SNP	PITPRU	ENST00000349364	-1	silent	c.1068	p.P356	tier1	35	0	0.000	212	86	0.285
147451	1	6621933	6621933	G	C	SNP	PITRG5	ENST00000376196	-1	silent	c.394	p.A196	tier1	29	0	0.000	143	57	0.285
147451	1	6525261	6525261	C	T	SNP	PRKCG	ENST00000357145	-1	intronic	c.19126	ex-126	tier2	29	0	0.000	140	39	0.262
147451	1	3290939	3290939	C	T	SNP	SLC22A15	ENST00000374254	-1	5_prime_untranslated_region	c.9190439	ex-126	tier2	27	0	0.000	270	118	0.262
147451	1	3290939	3290939	C	T	SNP	HNRNPCL1	ENST00000371866	-1	missense	c.9190439	p.R17H	tier1	490	1	0.002	1500	165	0.089
147451	1	15701093	15701093	G	A	SNP	FUAD1	ENST00000401324	-1	missense	c.526	p.A176T	tier1	29	0	0.000	139	55	0.284
147451	1	21695871	21695871	C	A	SNP	ECE1	ENST00000374833	-1	intronic	c.280-13	ex-13	tier3	16	0	0.000	215	97	0.311
147451	1	22852716	22852716	G	A	SNP	ZBTB40	ENST00000375647	-1	missense	c.9547	p.V183M	tier1	20	0	0.000	195	75	0.278
147451	1	22902834	22902834	G	A	SNP	EPHA8	ENST00000316244	1	missense	c.384	p.R95Q	tier1	83	0	0.000	211	64	0.230
147451	1	24395364	24395364	G	A	SNP	MYOM3	ENST00000330666	-1	missense	c.4059-50	NULL	tier3	109	0	0.000	485	204	0.296
147451	1	24410953	24410953	G	A	SNP	MYOM3	ENST00000475306	-1	5_prime_untranslated_region	c.24410953	NULL	tier3	227	3	0.013	635	306	0.325
147451	1	24711443	24711443	C	T	SNP	RHL3	ENST00000350501	-1	intronic	c.1454-22	ex-22	tier3	21	0	0.000	94	42	0.309
147451	1	2673790	2673790	G	A	SNP	DHODS	ENST00000360009	1	intronic	c.441-260	ex-260	tier4	191	5	0.025	142	49	0.257
147451	1	2720835	2720835	G	A	SNP	GPATCH3	ENST00000361720	-1	missense	c.943	p.R315W	tier1	60	0	0.000	180	90	0.333
147451	1	27708286	27708286	G	T	SNP	CD164L2	ENST00000374030	-1	silent	c.357	p.P119	tier1	49	0	0.000	164	85	0.341
147451	1	29365837	29365837	G	C	SNP	EPBA1	ENST00000343067	1	missense	c.1535	p.R512Q	tier1	91	0	0.000	271	103	0.275
147451	1	29609283	29609283	C	T	SNP	PITPRU	ENST00000345512	1	missense	c.1964	p.A655V	tier1	26	1	0.037	143	75	0.343
147451	1	31186218	31186218	G	A	SNP	MATN1	ENST00000337765	-1	missense	c.211	NULL	tier3	92	1	0.011	219	81	0.270
147451	1	32090677	32090677	G	A	SNP	HCTR1	ENST00000337061	-1	missense	c.1045	p.A349T	tier1	23	0	0.000	113	54	0.321
147451	1	37316001	37316001	C	T	SNP	GRK3	ENST00000337091	-1	missense	c.194-73	p.G413R	tier1	33	2	0.000	188	71	0.274
147451	1	43818426	43818426	C	T	SNP	FAM163A	ENST00000335282	-1	intronic	c.1237	ex-73	tier3	34	0	0.056	115	56	0.328
147451	1	43897426	43897426	C	T	SNP	SZT2	ENST000000562955	-1	nonsense	c.4957	p.R1653*	tier1	24	0	0.000	107	47	0.305
147451	1	46206734	46206734	C	T	SNP	IPP	ENST00000396478	-1	nonsense	c.563	p.R188Q	tier1	101	0	0.000	175	68	0.280
147451	1	52826134	52826134	C	T	SNP	CC2D1B	ENST00000371586	-1	missense	c.565	p.E189K	tier1	20	0	0.000	242	128	0.344
147451	1	54670978	54670978	G	A	SNP	MRPL37	ENST00000360840	-1	missense	c.541	p.V181M	tier1	41	0	0.000	107	48	0.310
147451	1	57085113	57085113	C	T	SNP	ENSG00000442812	-1	5_prime_untranslated_region	c.57085113	NULL	tier3	233	2	0.009	451	206	0.313	
147451	1	74955278	74955278	C	T	SNP	FFG7-TNNI3K	ENST00000370891	-1	silent	c.2286	p.G762	tier1	109	0	0.000	169	76	0.309
147451	1	78031830	78031830	G	A	SNP	ZZZ3	ENST00000370801	-1	missense	c.2503	p.R835W	tier1	147	1	0.007	282	133	0.321
147451	1	10127523	10127523	G	T	SNP	GSTM2	ENST00000241337	1	3_prime_untranslated_region	c.765	NULL	tier3	16	0	0.000	149	64	0.301
147451	1	11660238	11660238	C	T	SNP	SLC22A15	ENST00000365003	-1	missense	c.1463	p.P488L	tier1	132	0	0.000	222	95	0.300
147451	1	148914970	148914970	G	T	SNP	OTUD7B	ENST00000369135	-1	3_prime_untranslated_region	c.786	NULL	tier3	36	0	0.000	100	49	0.329
147451	1	15507600	15507600	G	A	SNP	CGN	ENST00000271636	-1	missense	c.2987	p.R96Q	tier1	52	0	0.000	133	67	0.333
147451	1	15509719	15509719	G	T	SNP	DCST1	ENST00000295542	-1	missense	c.1543	p.R515W	tier1	78	1	0.013	288	125	0.303
147451	1	155894452	155894452	G	T	SNP	MEF2D	ENST00000245564	-1	3_prime_untranslated_region	c.388	NULL	tier3	48	1	0.020	203	91	0.309
147451	1	156437379	156437379	G	A	SNP	HOGF	ENST00000464356	-1	5_prime_untranslated_region	c.156437379	NULL	tier3	58	2	0.033	382	175	0.314
147451	1	156713349	156713349	G	A	SNP	SLAMF1	ENST00000477306	-1	5_prime_untranslated_region	c.156713349	NULL	tier3	24	1	0.040	135	75	0.356
147451	1	162492585	162492585	G	T	SNP	UHMK1	ENST00000302035	-1	missense	c.547	p.H183Y	tier1	53	1	0.019	230	124	0.348
147451	1	165182958	165182958	G	A	SNP	LUXA1	ENST0000048294	-1	3_prime_untranslated_region	c.245	NULL	tier3	47	0	0.000	106	47	0.307
147451	1	171308645	171308645	G	T	SNP	TOPBP1	ENST00000294816	-1	missense	c.589	NULL	tier1	120	0	0.000	220	83	0.273
147451	1	172410952	172410952	G	A	SNP	PGIC	ENST00000404238	-1	5_prime_flanking_region	c.811	p.R197C	tier3	127	5	0.038	261	121	0.316
147451	1	175014844	175014844	G	A	SNP	HMCN1	ENST00000256324	-1	missense	c.31711	p.R271C	tier1	122	0	0.000	184	77	0.294
147451	1	186010193	186010193	G	A	SNP	TMN	ENST00000271588	-1	missense	c.6229	NULL	tier2	85	0	0.000	101	54	0.346
147451	1	200183198	200183198	G	T	SNP	FAM658BP	ENST00000426019	-1	3_prime_untranslated_region	c.200183198	p.D2077N	tier1	111	3	0.026	374	166	0.307
147451	1	20168470	20168470	C	T	SNP	IGFHR1	ENST00000335211	1	missense	c.376	NULL	tier2	34	1	0.029	242	88	0.267
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.6896	p.Y302I	tier1	40	1	0.024	144	75	0.343
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.904	p.Y302I	tier1	16	0	0.000	134	56	0.293
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0.243
147451	1	20168470	20168470	C	T	SNP	ELF3	ENST00000335211	1	missense	c.1503	p.P501	tier1	92	0	0.000	224	72	0

147457	3	194081495	194081495	G	A	SNP	LRRc15	ENST00000438944	-1	missense	c.296	tier1	22	0	0.000	99	39	0.281
147457	3	195503143	195503143	G	A	SNP	MUC4	ENST000004463781	-1	missense	c.9308	tier1	226	2	0.009	1333	87	0.061
147457	3	196387275	196387275	G	T	SNP	LRRc33	ENST00000328557	-1	missense	c.761	tier1	17	0	0.000	147	74	0.335
147457	3	196751232	196751232	G	A	SNP	MF12	ENST00000296350	-1	silent	c.429	tier1	24	0	0.000	175	81	0.316
147457	4	1332229	1332229	G	A	SNP	MAEA	ENST00000303400	-1	missense	c.919	tier1	33	0	0.000	274	120	0.305
147457	4	2941321	2941321	G	A	SNP	NOP14	ENST00000418614	-1	missense	c.2251	tier1	18	0	0.000	116	57	0.330
147457	4	4317442	4317442	G	T	SNP	ZBTB49	ENST00000337872	-1	nonsense	c.1456	tier1	73	0	0.000	124	67	0.349
147457	4	8304175	8304175	G	A	SNP	LRRc3	ENST00000303758	-1	intronic	c.1032-15	tier3	30	0	0.000	93	44	0.319
147457	4	9620663	9620663	G	A	SNP	SLC22A9	ENST00000264784	-1	silent	c.1581	tier3	91	1	0.011	131	54	0.292
147457	4	15891400	15891400	G	A	SNP	FLM206B	ENST000003054137	-1	3_prime untranslated_region	c.15891400	tier4	99	2	0.020	172	73	0.298
147457	4	17886743	17886743	G	T	SNP	LRRc15	ENST00000326877	-1	intronic	c.1787-18948	tier4	44	0	0.000	103	44	0.299
147457	4	42359034	42359034	G	T	SNP	LRRc1	ENST00000331686	-1	silent	c.2085	tier4	135	0	0.000	193	66	0.255
147457	4	44172057	44172057	G	T	SNP	ACTD8	ENST00000330029	-1	missense	c.1172	tier4	197	3	0.015	247	91	0.268
147457	4	47632032	47632032	G	T	SNP	TEC	ENST00000351501	-1	missense	c.109	tier4	113	3	0.026	238	85	0.292
147457	4	57532163	57532163	G	T	SNP	ALDO	ENST00000331686	-1	missense	c.109	tier4	113	3	0.026	238	85	0.292
147457	4	6743923	6743923	G	T	SNP	FTL10	ENST00000303647	-1	missense	c.109	tier4	113	3	0.026	238	85	0.292
147457	4	71099788	71099788	G	T	SNP	FDCSP	ENST00000317987	-1	3_prime untranslated_region	c.189045233	tier4	149	0	0.000	281	115	0.290
147457	4	75768110	75768110	G	T	SNP	WDFY3	ENST00000337888	-1	missense	c.153	tier4	190	1	0.005	161	55	0.255
147457	4	8293939	8293939	G	T	SNP	HS217B11	ENST00000358290	-1	missense	c.548	tier4	136	3	0.022	255	124	0.326
147457	4	119461691	119461691	G	A	SNP	TRPC3	ENST00000412784	-1	intronic	c.479	tier4	195	2	0.010	302	120	0.267
147457	4	122846298	122846298	G	A	SNP	FTSL5	ENST00000379645	-1	nonsense	c.1051	tier4	171	0	0.000	103	64	0.383
147457	4	162421108	162421108	G	T	SNP	TMEM192	ENST00000306480	-1	intronic	c.1459-60	tier4	161	0	0.000	184	84	0.313
147457	4	16600582	16600582	C	T	SNP	FAT1	ENST00000260147	-1	missense	c.574-38	tier4	111	2	0.018	184	85	0.316
147457	4	18763032	18763032	C	T	SNP	TRMAL2	ENST00000260147	-1	missense	c.680	tier4	34	0	0.000	104	59	0.362
147457	5	770160	770160	C	T	SNP	TERF	ENST00000242784	-1	intronic	c.69	tier4	112	0	0.000	127	61	0.323
147457	5	123693	123693	C	T	SNP	CLPTMIL	ENST00000310581	-1	silent	c.1308	tier4	126	0	0.000	750	334	0.307
147457	5	1336034	1336034	G	A	SNP	LFCAT1	ENST000002028315	-1	intronic	c.663	tier4	31	0	0.000	118	45	0.276
147457	5	1463662	1463662	G	A	SNP	KIA00947	ENST00000296564	-1	silent	c.3924	tier4	48	0	0.000	233	74	0.240
147457	5	6602599	6602599	G	T	SNP	DNAH5	ENST00000264670	-1	missense	c.10281+54	tier4	31	0	0.000	80	31	0.279
147457	5	13762777	13762777	C	T	SNP	DNAH5	ENST00000265104	-1	intronic	c.192-10	tier4	76	1	0.013	294	135	0.315
147457	5	31931209	31931209	C	T	SNP	POZD2	ENST00000282493	-1	splice_region	c.1077	tier4	223	0	0.000	660	228	0.041
147457	5	31995780	31995780	C	T	SNP	POZD2	ENST00000282493	-1	splice_region	c.1077	tier4	223	0	0.000	660	228	0.041
147457	5	34190535	34190535	C	T	SNP	CAPSL	ENST00000332686	-1	3_prime untranslated_region	c.34190535	tier4	77	3	0.038	236	104	0.304
147457	5	35910093	35910093	C	T	SNP	C6	ENST00000397366	-1	missense	c.400	tier4	636	6	0.009	4301	196	0.043
147457	5	41149449	41149449	C	T	SNP	CRSP8P	ENST00000263413	-1	silent	c.2517	tier4	106	2	0.019	138	74	0.239
147457	5	79646877	79646877	C	T	SNP	CHST3	ENST00000514260	-1	missense	c.79646877	tier4	107	1	0.009	498	173	0.257
147457	5	129521471	129521471	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	140221632	140221632	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	14030059	14030059	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	140720521	140720521	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	14075057	14075057	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	14075057	14075057	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	145610359	145610359	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	146230055	146230055	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	14792769	14792769	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	148594221	148594221	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	15344652	15344652	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	15966575	15966575	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	17353383	17353383	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	17591565	17591565	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	17630809	17630809	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	5	176359183	176359183	G	A	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	3127540	3127540	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	25727357	25727357	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	27271008	27271008	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	31550086	31550086	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	31531016	31531016	G	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4	28	0	0.000	92	47	0.338
147457	6	33534497	33534497	C	T	SNP	PCDH48	ENST00000305031	-1	missense	c.2636	tier4						

147457	7	2474107	2474107	C	T	SNP	CHST12	ENST00000258711	1	3_prime_untranslated_region	c:588	NULL	56	1	0.018	90	34	0.270	
147457	7	6005211	6005211	C	T	SNP	RSBH09	ENST00000337579	-1	intronic	c:330+57	e2-57	tier3	15	0	0.000	59	32	0.352
147457	7	2072860	2072860	G	A	SNP	ABC85	ENST00000258738	-1	missense	c:1108	p.V270I	tier1	103	0	0.000	110	51	0.317
147457	7	2196048	2196048	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	ENST00000359525	-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	0.005	156	49	0.238
147457	7	51454298	51454298	G	A	SNP	POR	ENST00000444643	1	5_prime_untranslated_region	c:51454298	NULL	tier3	67	1	0.015	812	282	0.257
147457	7	75095676	75095676	G	A	SNP	HEPACAM2	ENST00000425797	1	missense	c:386	p.P128L	tier1	20	0	0.000	110	40	0.265
147457	7	76010187	76010187	G	A	SNP	PEG10	ENST00000394468	1	intronic	c:76010187	NULL	tier3	58	0	0.000	346	137	0.283
147457	7	94233941	94233941	G	A	SNP	TECOT1	ENST00000482106	1	3_prime_untranslated_region	c:79+391	e1+391	tier3	59	0	0.000	69	34	0.330
147457	7	97622583	97622583	G	T	SNP	ARG3	ENST00000375795	1	intronic	c:95	NULL	tier3	44	2	0.044	131	49	0.271
147457	7	98248701	98248701	G	A	SNP	TRAF3	ENST00000297230	1	3_prime_untranslated_region	c:532+84	e4-84	tier3	20	0	0.000	172	60	0.259
147457	7	98736968	98736968	G	A	SNP	TRAF6	ENST00000372340	1	3_prime_untranslated_region	c:146	NULL	tier3	39	0	0.000	49	38	0.277
147457	7	100720608	100720608	G	A	SNP	TRAF6	ENST00000309545	1	missense	c:1376	p.G55R	tier3	189	0	0.000	219	79	0.257
147457	7	10562648	10562648	G	A	SNP	CDH3	ENST00000468477	1	missense	c:236	p.T73M	tier1	25	0	0.000	176	70	0.282
147457	7	12359438	12359438	G	A	SNP	SPAL1	ENST00000340011	1	missense	c:314	p.T30M	tier1	105	1	0.009	216	93	0.282
147457	7	13894966	13894966	G	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier1	98	0	0.000	103	43	0.295
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928	1	intronic	c:1843+9638	p.R305H	tier3	12	0	0.000	126	77	0.379
147457	7	13894966	13894966	C	T	SNP	LRG1K	ENST00000258928											

147457	15	83331848	83331848	G	A	T	SNP	BMC1	ENSG00000218052	ENST00000345382	-1	missense	5_prime untranslated_region	c.2155	58	1	0.017	128	54	0.297
147457	15	85005937	85005937	G	T	SNP	SNP	KIF7	ENST00000361209	ENST00000361209	-1	5_prime untranslated_region	silent	c.519	18	0	0.032	269	131	0.328
147457	15	90192982	90192982	C	A	SNP	SNP	IDH2	ENST00000394412	ENST00000394412	-1	missense	silent	c.419	30	1	0.006	62	43	0.410
147457	15	90631934	90631934	G	T	SNP	SNP	PGPEPIL	ENST00000330662	ENST00000330662	-1	intronic	intronic	c.NULL	173	1	0.006	705	334	0.321
147457	15	91577480	91577480	G	T	SNP	SNP	SYNM	ENST00000357804	ENST00000357804	-1	intronic	intronic	c.145-39	84	0	0.000	322	152	0.321
147457	15	99512919	99512919	C	T	SNP	SNP	ADAMTS17	ENST00000336292	ENST00000336292	-1	missense	missense	c.2681	27	0	0.000	181	82	0.311
147457	15	100821502	100821502	C	T	SNP	SNP	COL1A1	ENST00000268070	ENST00000268070	-1	intronic	intronic	c.721	38	0	0.000	184	66	0.264
147457	15	102362626	102362626	G	A	SNP	SNP	SLN	ENST00000361463	ENST00000361463	-1	intronic	intronic	c.NULL	78	0	0.000	272	122	0.309
147457	16	933258	933258	-	CCCTG	SNP	SNP	COL1A1	ENST00000219811	ENST00000219811	-1	intronic	intronic	c.153589	57	0	0.000	317	152	0.324
147457	16	7217198	7217198	-	T	SNP	SNP	COL1A1	ENST00000446427	ENST00000446427	-1	intronic	intronic	c.1+28495_28496	31	0	0.000	84	53	0.282
147457	16	1255228	1255228	C	T	SNP	SNP	CACNA1H	ENST00000346261	ENST00000346261	-1	missense	missense	c.2367	19	0	0.000	170	78	0.312
147457	16	1397640	1397640	C	T	SNP	SNP	CACNA1H	ENST00000324385	ENST00000324385	-1	intronic	intronic	c.3103+18	47	0	0.000	161	88	0.352
147457	16	2136860	2136860	G	A	SNP	SNP	COL1A1	ENST00000359196	ENST00000359196	-1	intronic	intronic	c.327	23	0	0.000	168	83	0.352
147457	16	2136860	2136860	G	A	SNP	SNP	COL1A1	ENST00000359196	ENST00000359196	-1	intronic	intronic	c.327	28	1	0.000	178	143	0.313
147457	16	1101032	1101032	G	T	SNP	SNP	COL1A1	ENST00000347835	ENST00000347835	-1	missense	missense	c.382	27	0	0.000	182	74	0.278
147457	16	1101032	1101032	G	T	SNP	SNP	COL1A1	ENST00000347835	ENST00000347835	-1	missense	missense	c.382	27	0	0.000	182	74	0.278
147457	16	1121344	1121344	G	A	SNP	SNP	COL1A1	ENST00000404239	ENST00000404239	-1	3_prime untranslated_region	3_prime untranslated_region	c.11121344	148	2	0.013	213	97	0.312
147457	16	15457738	15457738	G	A	SNP	SNP	LOC642778	ENST00000360151	ENST00000360151	-1	missense	missense	c.833	321	0	0.000	1487	151	0.083
147457	16	31519174	31519174	G	T	SNP	SNP	ATP2A1	ENST00000364112	ENST00000364112	-1	missense	missense	c.48	122	3	0.024	234	107	0.313
147457	16	33740957	33740957	G	T	SNP	SNP	C16orf69	ENST00000327237	ENST00000327237	-1	missense	missense	c.326	28	0	0.000	220	80	0.286
147457	16	46638006	46638006	G	T	SNP	SNP	SHCBP1	ENST00000367025	ENST00000367025	-1	missense	missense	c.1323	333	2	0.006	1132	225	0.166
147457	16	46390961	46390961	G	A	SNP	SNP	AMFR	ENST00000360649	ENST00000360649	-1	missense	missense	c.1656	35	0	0.000	88	44	0.333
147457	16	5752349	5752349	G	A	SNP	SNP	CCDC135	ENST00000360716	ENST00000360716	-1	missense	missense	c.1168	22	0	0.008	267	112	0.286
147457	16	5850812	5850812	G	A	SNP	SNP	SETD6	ENST00000219315	ENST00000219315	-1	missense	missense	c.772	59	0	0.000	161	54	0.251
147457	16	67469912	67469912	G	A	SNP	SNP	HSO1B2	ENST00000236152	ENST00000236152	-1	silent	silent	c.531	29	0	0.000	138	60	0.303
147457	16	67573993	67573993	G	A	SNP	SNP	FAM65A	ENST0000042602	ENST0000042602	-1	missense	missense	c.512	94	2	0.021	491	217	0.307
147457	16	83378666	83378666	G	T	SNP	SNP	CDH13	ENST00000366620	ENST00000366620	-1	intronic	intronic	c.736	43	0	0.000	141	65	0.316
147457	16	83520057	83520057	G	A	SNP	SNP	CDH13	ENST00000366620	ENST00000366620	-1	intronic	intronic	c.782-25	77	1	0.013	198	51	0.204
147457	16	83994327	83994327	G	A	SNP	SNP	OSGNI1	ENST00000361711	ENST00000361711	-1	missense	missense	c.358	29	0	0.000	220	79	0.264
147457	16	84529437	84529437	G	A	SNP	SNP	NAI1609	ENST00000334629	ENST00000334629	-1	missense	missense	c.236	25	0	0.000	106	46	0.301
147457	16	87478989	87478989	G	A	SNP	SNP	NAI1609	ENST00000334629	ENST00000334629	-1	missense	missense	c.236	25	0	0.000	106	46	0.301
147457	16	89178494	89178494	G	T	SNP	SNP	ACSF3	ENST00000332281	ENST00000332281	-1	silent	silent	c.300	66	0	0.000	440	176	0.285
147457	16	3526660	3526660	G	T	SNP	SNP	SHPK	ENST00000317447	ENST00000317447	-1	splice_region	splice_region	c.823-6	79	1	0.013	241	30	0.111
147457	16	6377943	6377943	G	A	SNP	SNP	PITPM3	ENST0000022519	ENST0000022519	-1	missense	missense	c.620	21	0	0.000	159	78	0.329
147457	16	7492394	7492394	G	A	SNP	SNP	PITPM3	ENST0000022519	ENST0000022519	-1	missense	missense	c.1086-19	15	0	0.000	251	122	0.327
147457	16	7506344	7506344	C	T	SNP	SNP	FXR2	ENST00000250113	ENST00000250113	-1	3_prime untranslated_region	3_prime untranslated_region	c.586	16	0	0.000	135	75	0.357
147457	16	8216386	8216386	G	T	SNP	SNP	ARHGEF15	ENST00000361926	ENST00000361926	-1	intronic	intronic	c.450-24	26	0	0.000	306	120	0.281
147457	16	9632002	9632002	G	A	SNP	SNP	MYH8	ENST00000285199	ENST00000285199	-1	missense	missense	c.748	91	0	0.000	107	58	0.352
147457	16	10322056	10322056	G	A	SNP	SNP	MYH8	ENST00000252173	ENST00000252173	-1	missense	missense	c.417	21	0	0.000	172	62	0.265
147457	16	10404747	10404747	G	T	SNP	SNP	TRPV2	ENST00000226207	ENST00000226207	-1	intronic	intronic	c.3418	120	0	0.000	378	164	0.303
147457	16	16330812	16330812	C	T	SNP	SNP	DNAH9	ENST00000338560	ENST00000338560	-1	missense	missense	c.5710-35	150	0	0.000	520	235	0.310
147457	16	16344404	16344404	C	T	SNP	SNP	TRPV2	ENST00000460249	ENST00000460249	-1	missense	missense	c.1301	32	0	0.000	186	85	0.314
147457	16	1681370	1681370	C	T	SNP	SNP	MPRIIP	ENST00000395811	ENST00000395811	-1	missense	missense	c.247	38	0	0.000	206	81	0.281
147457	16	1681370	1681370	C	T	SNP	SNP	MPRIIP	ENST00000465046	ENST00000465046	-1	missense	missense	c.18148237	21	0	0.000	186	83	0.307
147457	16	18969877	18969877	T	G	SNP	SNP	LOC100132472	ENST00000442828	ENST00000442828	-1	missense	missense	c.315	49	1	0.020	537	220	0.291
147457	16	19315938	19315938	G	A	SNP	SNP	RNF112	ENST00000355177	ENST00000355177	-1	missense	missense	c.44102	14	0	0.000	110	69	0.386
147457	16	26574933	26574933	G	T	SNP	SNP	SLC13A2	ENST00000444914	ENST00000444914	-1	silent	silent	c.318	23	0	0.000	172	79	0.312
147457	16	26574933	26574933	G	T	SNP	SNP	SLC13A2	ENST00000444914	ENST00000444914	-1	silent	silent	c.318	23	0	0.000	172	79	0.312
147457	16	27013676	27013676	G	A	SNP	SNP	EFCAB5	ENST00000314616	ENST00000314616	-1	missense	missense	c.2569	50	0	0.000	171	59	0.257
147457	16	28395764	28395764	G	T	SNP	SNP	MYH11	ENST00000394835	ENST00000394835	-1	intronic	intronic	c.2737+9045	47	1	0.021	171	59	0.257
147457	16	3120043	3120043	C	T	SNP	SNP	MYH11	ENST00000358273	ENST00000358273	-1	intronic	intronic	c.1392+14	51	0	0.000	212	90	0.298
147457	16	3120043	3120043	C	T	SNP	SNP	MYH11	ENST00000358273	ENST00000358273	-1	intronic	intronic	c.1392+14	51	0	0.000	212	90	0.298
147457	16	3326217	3326217	G	A	SNP	SNP	SPACA3	ENST00000269553	ENST00000269553	-1	intronic	intronic	e1+1053	81	1	0.012	301	103	0.254
147457	16	3412816	3412816	G	A	SNP	SNP	CCL14	ENST00000375526	ENST00000375526	-1	missense	missense	c.2332-59	23	0	0.000	78	30	0.278
147457	16	36222583	36222583	G	A	SNP	SNP	ARHGAP23	ENST00000435911	ENST00000435911	-1	missense	missense	c.95	87	2	0.023	164	67	0.267
147457	16	36222583	36222583	G	A	SNP	SNP	ARHGAP23	ENST00000435911	ENST00000435911	-1	missense	missense	c.95	87	2	0.023	164	67	0.267
147457	16	37075060	37075060	G	A	SNP	SNP	LAPSF1	ENST00000264659	ENST00000264659	-1	intronic	intronic	c.3418-35	36	0	0.000	344	161	0.316
147457	16	38146549	38146549	C	T	SNP	SNP	KIF17	ENST00000315006	ENST00000315006	-1	missense	missense	c.49	20	0	0.000	217	141	0.394
147457	16	38146549	38146549	C	T	SNP	SNP	KIF17	ENST00000315006	ENST00000315006	-1	missense	missense	c.49	20	0	0.000	217	141	0.394
147457	16	39649693	39649693	G	A	SNP	SNP	LEPREL4	ENST00000465039	ENST00000465039	-1	intronic	intronic	c.880	53	0	0.000	150	58	0.279
147457	16	4083711	4083711	C	T	SNP	SNP	ACLY	ENST00000401700	ENST00000401700	-1	missense	missense	c.139	116	3	0.020	224	88	0.277
147457	16	4108210	4108210	C	T	SNP	SNP	KANS1	ENST00000372017	ENST00000372017	-1	missense	missense	c.93	28	0	0.000	163	69	0.269
147457	16	41444025	41444025	C	T	SNP	SNP	KANS1	ENST00000372017	ENST00000372017	-1	missense	missense	c.93	28	0	0.000	163	69	0.269
147457	16	4634597	4634597	G	T	SNP	SNP													

147457	17	76167847	76167847	C	T	SNP	SYNGR2	ENST00000225777	1	missense	c.505	tier1	18	0	0.000	148	53	0.264
147457	SNP	USP36	ENST00000312010	-1	silent	c.1437	p.R169C	tier1	18	0	0.000	54	31	0.385				
147457	SNP	ENGASE	ENST00000300682	-1	splice_region	c.1701-10	e13-10	tier1	14	0	0.000	101	41	0.289				
147457	SNP	ENGASE	ENST00000300682	-1	3_prime_untranslated_region		NULL	tier3	24	1	0.040	175	90	0.340				
147457	SNP	RNF213	ENST00000306828	-1	silent	c.786	p.S43	tier1	281	6	0.021	830	332	0.285				
147457	SNP	ARHGAP28	ENST00000341928	-1	silent	c.2517	p.P339	tier1	27	0	0.000	95	42	0.302				
147457	SNP	GVAL	ENST00000340091	-1	silent	c.444	p.A148	tier1	89	0	0.000	243	88	0.265				
147457	SNP	CEP192	ENST00000334049	-1	missense	c.934	p.A312T	tier1	67	1	0.015	168	62	0.268				
147457	SNP	GREY1L	ENST00000305447	1	nonense	c.9401	p.R801*	tier1	166	2	0.012	197	98	0.332				
147457	SNP	GATF6	ENST00000342526	1	missense	c.1370	p.L457M	tier1	129	0	0.000	231	78	0.252				
147457	SNP	KCTD1	ENST00000269216	1	missense	c.1631	p.P344L	tier1	54	1	0.016	178	98	0.355				
147457	SNP	DG53	ENST00000417602	-1	silent	c.1575	p.D325	tier1	20	0	0.000	97	43	0.307				
147457	SNP	PROX1A	ENST00000327189	-1	missense	c.1612	p.V353	tier1	53	3	0.034	124	46	0.278				
147457	SNP	PROX1A	ENST00000357384	-1	intronic	c.7835-133	p.V4133	tier2	7	0	0.000	138	58	0.265				
147457	SNP	PROX1A	ENST00000357384	-1	intronic	c.7835-133	p.V4133	tier2	7	0	0.000	138	58	0.265				
147457	SNP	MYO5B	ENST00000369395	-1	silent	c.1483	p.S469	tier1	75	0	0.000	498	212	0.268				
147457	SNP	MYO5B	ENST00000369395	-1	intronic	c.0.1689	p.V2181	tier2	94	2	0.021	333	185	0.347				
147457	SNP	RNF126	ENST00000340092	-1	intronic	c.1119-36	e10-36	tier2	56	0	0.000	187	100	0.367				
147457	SNP	PBP1	ENST00000356948	-1	intronic	c.1483	p.D493M	tier1	53	0	0.000	472	164	0.264				
147457	SNP	ABC7	ENST00000326904	-1	missense	c.2475	p.F925	tier1	37	0	0.000	342	124	0.284				
147457	SNP	EEF2	ENST00000309311	-1	intronic	c.2475	e5-13	tier3	25	0	0.000	132	59	0.319				
147457	SNP	PLIN4	ENST00000301284	-1	intronic	c.490-113	p.T606M	tier1	54	0	0.000	368	48	0.115				
147457	SNP	UHRF1	ENST000003098240	-1	missense	c.518	p.T173M	tier1	29	0	0.000	169	62	0.268				
147457	SNP	INSR	ENST00000302850	-1	missense	c.355	p.A119T	tier1	24	0	0.000	90	35	0.280				
147457	SNP	ELAVL1	ENST00000414982	-1	3_prime_untranslated_region	c.2966-29	e24-29	tier2	12	0	0.000	68	43	0.387				
147457	SNP	FBN3	ENST00000407827	-1	missense	c.426	NULL	tier2	75	3	0.039	147	66	0.310				
147457	SNP	FBN3	ENST00000270509	-1	intronic	c.7893	p.T2628M	tier1	39	0	0.000	283	123	0.303				
147457	SNP	MYO1F	ENST00000270509	-1	intronic	c.2954-56	e19-56	tier3	39	1	0.025	367	147	0.285				
147457	SNP	COL5A3	ENST00000338257	-1	intronic	c.505-22	e7-22	tier3	32	0	0.000	111	39	0.258				
147457	SNP	SLC4A2	ENST00000264828	-1	intronic	c.2091-41	e26-41	tier3	109	2	0.018	460	190	0.292				
147457	SNP	GCDH	ENST00000335757	1	intronic	c.648	p.S216	tier2	47	1	0.021	190	67	0.260				
147457	SNP	CACNA1A	ENST00000222214	1	silent	c.2504	p.R335H	tier1	66	1	0.015	305	119	0.280				
147457	SNP	CACNA1A	ENST00000418012	-1	intronic	c.1256-106	e10-106	tier4	41	0	0.043	413	140	0.253				
147457	SNP	ZSWIM4	ENST00000254323	1	missense	c.1674	p.P558	tier1	89	4	0.000	75	29	0.279				
147457	SNP	DKAF15	ENST00000254337	1	silent	c.404	p.R394Q	tier1	22	0	0.000	270	111	0.291				
147457	SNP	PRKACA	ENST00000308677	-1	missense	c.1781	p.R135Q	tier1	26	0	0.000	136	58	0.299				
147457	SNP	PRKACA	ENST00000308677	-1	intronic	c.47-34	e2-34	tier3	105	1	0.009	172	91	0.346				
147457	SNP	CYP4F3	ENST00000221307	1	missense	c.563	p.R188H	tier1	97	0	0.000	344	143	0.293				
147457	SNP	NUD1	ENST00000379808	1	missense	c.334	p.E112K	tier1	39	0	0.000	180	96	0.348				
147457	SNP	FOH01	ENST00000252771	1	silent	c.2079	p.A693	tier1	32	1	0.030	124	50	0.287				
147457	SNP	RNF486	ENST00000335117	1	silent	c.969	p.T323	tier1	133	2	0.015	219	96	0.304				
147457	SNP	RNF681	ENST00000402377	-1	silent	c.798	p.S266	tier1	107	1	0.009	209	56	0.211				
147457	SNP	RHPN2	ENST00000254260	-1	missense	c.1274	p.R425Q	tier1	27	0	0.000	153	66	0.301				
147457	SNP	UBA2	ENST00000246548	1	nonense	c.364	p.R122*	tier1	89	0	0.000	195	69	0.260				
147457	SNP	RYR1	ENST00000359596	1	missense	c.2645	p.A828V	tier1	131	0	0.000	670	240	0.263				
147457	SNP	FCGBP	ENST00000221347	-1	silent	c.6645	p.N2215	tier1	170	1	0.006	770	207	0.212				
147457	SNP	CEACAM21	ENST00000401445	-1	missense	c.850	p.G284S	tier1	49	0	0.000	169	75	0.305				
147457	SNP	GRK6	ENST00000301218	-1	missense	c.1744	p.R92C	tier1	72	0	0.000	332	120	0.266				
147457	SNP	ZFP112	ENST00000303997	-1	silent	c.1398	p.A466	tier1	112	1	0.009	247	109	0.306				
147457	SNP	MEIS3	ENST00000359524	-1	missense	c.926	p.R309Q	tier1	23	0	0.000	228	84	0.289				
147457	SNP	GRWD1	ENST00000252337	1	missense	c.1075	p.V359I	tier1	34	0	0.000	248	94	0.275				
147457	SNP	FAM83E	ENST0000026266	-1	missense	c.637	p.V273M	tier1	30	1	0.032	168	72	0.300				
147457	SNP	CGB	ENST00000357383	-1	3_prime_untranslated_region	c.14	NULL	tier2	34	0	0.000	185	95	0.339				
147457	SNP	FLJ26550	ENST00000527209	1	intronic	c.NULL	NULL	tier2	60	0	0.000	95	38	0.286				
147457	SNP	SYT13	ENST00000338916	-1	silent	c.1626	p.A542	tier1	36	0	0.000	240	137	0.363				
147457	SNP	ZNF911	ENST00000319783	-1	missense	c.1922	p.R641H	tier1	73	2	0.011	383	153	0.280				
147457	SNP	MF321-2	ENST00000384616	-1	5_prime_flanking_region	c.15399	NULL	tier3	114	5	0.042	310	111	0.264				
147457	SNP	LCR65	ENST00000463460	-1	5_prime_untranslated_region	c.34760694	NULL	tier3	32	0	0.000	191	63	0.303				
147457	SNP	FAH1E2	ENST00000376380	-1	missense	c.140	p.R241C	tier1	29	0	0.000	207	95	0.315				
147457	SNP	SH3BP1	ENST00000375325	-1	missense	c.2251	p.R241C	tier1	41	0	0.000	118	44	0.272				
147457	SNP	ZNF71	ENST00000228070	-1	3_prime_untranslated_region	c.810	p.Y270	tier3	32	0	0.000	311	142	0.313				
147457	SNP	TRIM28	ENST00000326024	1	missense	c.2231	p.R244H	tier1	17	0	0.000	120	54	0.310				
147457	SNP	VPS16	ENST00000380445	1	silent	c.1041	p.A347	tier1	49	0	0.000	176	64	0.266				
147457	SNP	PAS49P1	ENST00000329152	1	missense	c.358	p.G120R	tier1	21	0	0.000	111	53	0.321				
147457	SNP	PRND	ENST00000305817	1	3_prime_untranslated_region	c.164	NULL	tier3	31	0	0.000	114	58	0.337				
147457	SNP	PRND	ENST00000305817	1	3_prime_intronic	c.116-64	e2-64	tier3	63	3	0.048	132	62	0.318				
147457	SNP	C20orf78	ENST00000278706	1	3_prime_untranslated_region	c.52	NULL	tier3	50	1	0.020	180	79	0.305				
147457	SNP	C20orf26	ENST00000377306	1	nonense	c.2893	p.R96S*	tier3	26	0	0.000	111	42	0.273				
147457	SNP	AXL1	ENST00000358966	1	missense	c.2116	p.D706N	tier1	160	1	0.006	738	319	0.302				
147457	SNP	DNMT3B	ENST00000328111	1	missense	c.296	p.R99Q	tier1	321	4	0.012	718	315	0.304				
147457	SNP	DLGAP4	ENST00000339266	1	missense	c.650	p.R217Q	tier1	19	0	0.000	226	95	0.296				
147457	SNP	DHX35	ENST00000252011	1	missense			tier1	77	0	0.000	154	78	0.335				

147457	20	40118424	40118424	G	A	T	SNP	CHD6	ENST00000440697	-1	missense	c.762	p.T261M	tier1	45	0	0.000	187	80	0.300
147457	20	40122259	40122259	C	T	SNP	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	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	SNP	KCNK1	ENST00000371571	-1	missense	c.1195	p.E399K	tier1	30	0	0.000	189	72	0.275
147457	20	53208320	53208320	C	T	SNP	SNP	DKO5	ENST00000262593	-1	missense	c.575	p.T192M	tier1	154	2	0.013	245	133	0.352
147457	20	60704165	60704165	G	A	SNP	SNP	LSMT4B	ENST00000253001	-1	intronic	c.681-1175	e5-11872	tier3	41	0	0.000	141	76	0.347
147457	20	60910153	60910153	G	A	SNP	SNP	LAMA5	ENST00000252999	-1	silent	c.2406	p.H802	tier3	25	0	0.000	303	132	0.303
147457	20	62037970	62037970	G	C	SNP	SNP	KCNK2	ENST00000354587	-1	3_prime_untranslated_region	c.27	NULL	tier2	35	0	0.000	177	99	0.250
147457	20	62055538	62055538	G	C	SNP	SNP	KRTAP13-2	ENST00000354587	-1	silent	c.1209	p.P403	tier2	62	2	0.024	387	162	0.295
147457	21	33116470	33116470	G	A	SNP	SNP	HUNK	ENST00000399889	-1	missense	c.442	p.R146C	tier1	54	1	0.019	156	78	0.333
147457	21	33596867	33596867	G	A	SNP	SNP	HUNK	ENST00000270112	-1	missense	c.733	p.D245N	tier1	52	0	0.000	136	58	0.297
147457	21	34546639	34546639	G	A	SNP	SNP	SOX1	ENST00000335771	-1	missense	c.8147	p.R176Q	tier1	160	1	0.010	249	111	0.308
147457	21	36259853	36259853	G	A	SNP	SNP	SOX1	ENST00000335771	-1	missense	c.8931	p.V2311I	tier1	104	2	0.012	270	97	0.243
147457	21	36259853	36259853	G	A	SNP	SNP	ROCK1	ENST00000335771	-1	missense	c.8931	p.V2311I	tier1	104	2	0.012	270	97	0.243
147457	21	37440960	37440960	G	A	SNP	SNP	ROCK1	ENST00000335771	-1	missense	c.8931	p.V2311I	tier1	104	2	0.012	270	97	0.243
147457	21	4364766	4364766	G	A	SNP	SNP	SLC37A1	ENST00000362133	-1	missense	c.15857	p.P458R	tier1	113	1	0.007	755	326	0.316
147457	21	4364766	4364766	G	A	SNP	SNP	SLC37A1	ENST00000362133	-1	missense	c.15857	p.P458R	tier1	113	1	0.007	755	326	0.316
147457	21	46363698	46363698	G	A	SNP	SNP	FA2H7A	ENST00000291834	-1	intronic	c.1220	e1352	tier3	16	0	0.000	189	75	0.309
147457	21	47766132	47766132	G	A	SNP	SNP	PCNT	ENST00000291834	-1	splice_region	c.1220	e1352	tier3	16	0	0.000	189	75	0.309
147457	21	47766132	47766132	G	A	SNP	SNP	PCNT	ENST00000291834	-1	splice_region	c.1220	e1352	tier3	16	0	0.000	189	75	0.309
147457	22	21022153	21022153	G	A	SNP	SNP	FAM109A5P	ENST00000359568	-1	5_prime_untranslated_region	c.270+10	e4-10	tier3	43	1	0.023	149	59	0.282
147457	22	21022153	21022153	G	A	SNP	SNP	FAM109A5P	ENST00000359568	-1	5_prime_untranslated_region	c.270+10	e4-10	tier3	43	1	0.023	149	59	0.282
147457	22	2149265	2149265	G	A	SNP	SNP	LTFR1	ENST00000215739	-1	missense	c.21022153	NULL	tier2	34	0	0.000	424	172	0.289
147457	22	23077532	23077532	G	A	SNP	SNP	IGLV2-18	ENST00000390310	-1	silent	c.309	p.R631Q	tier1	37	0	0.000	264	118	0.308
147457	22	24440098	24440098	G	A	SNP	SNP	IGLV2-18	ENST00000390310	-1	silent	c.309	p.R631Q	tier1	37	0	0.000	264	118	0.308
147457	22	25598652	25598652	G	A	SNP	SNP	CRYBB3	ENST00000414583	-1	3_prime_untranslated_region	c.24649098	D.D103	tier3	88	0	0.000	551	256	0.317
147457	22	37319436	37319436	C	T	SNP	SNP	CRYBB3	ENST00000262825	-1	silent	c.87	NULL	tier3	149	0	0.000	172	54	0.239
147457	22	37892522	37892522	C	T	SNP	SNP	CARD10	ENST00000262825	-1	intronic	c.200+27	e2+27	tier3	17	0	0.000	134	89	0.399
147457	22	38062929	38062929	G	A	SNP	SNP	PDXP	ENST00000251973	-1	missense	c.1993	p.E656K	tier2	97	3	0.030	148	61	0.292
147457	22	39558204	39558204	G	A	SNP	SNP	APOBEC3A	ENST00000251973	-1	missense	c.1051	NULL	tier2	97	3	0.030	148	61	0.292
147457	22	46125385	46125385	G	A	SNP	SNP	ATXN10	ENST00000252934	-1	missense	c.571	p.R191W	tier1	34	0	0.000	178	80	0.309
147457	22	50728653	50728653	C	T	SNP	SNP	PLXNB2	ENST00000252934	-1	missense	c.609	p.R270Q	tier1	67	2	0.029	152	62	0.290
147457	22	50900128	50900128	C	T	SNP	SNP	SBF1	ENST00000337034	-1	missense	c.361	p.A121T	tier1	22	0	0.000	186	83	0.309
147457	22	50962222	50962222	C	T	SNP	SNP	SCD2	ENST00000337034	-1	missense	c.2693	p.R898H	tier1	50	0	0.000	291	131	0.309
147457	22	5182575	5182575	C	T	SNP	SNP	ACR	ENST00000252785	-1	missense	c.619	p.V207M	tier1	48	2	0.040	206	80	0.280
147457	22	5182575	5182575	C	T	SNP	SNP	ACR	ENST00000252785	-1	missense	c.652	p.R218C	tier1	59	2	0.033	273	109	0.285
147457	22	2406917	2406917	G	A	SNP	SNP	ZBED1	ENST00000381218	-1	missense	c.1844	p.R615H	tier1	41	0	0.000	282	118	0.293
147457	22	13765025	13765025	C	T	SNP	SNP	OFD1	ENST00000381218	-1	missense	c.781	p.V281I	tier1	293	4	0.014	415	190	0.312
147457	22	29070889	29070889	G	A	SNP	SNP	MAPT2D	ENST00000379843	-1	intronic	c.595+107	e5+107	tier3	67	0	0.000	144	58	0.283
147457	22	29873688	29873688	G	A	SNP	SNP	IL1RAPL1	ENST00000379843	-1	missense	c.929	p.T614	tier1	98	2	0.020	185	80	0.302
147457	22	34961466	34961466	G	A	SNP	SNP	FAM7B	ENST00000379843	-1	missense	c.215	NULL	tier3	154	1	0.007	371	139	0.272
147457	22	41530801	41530801	G	A	SNP	SNP	CASK	ENST00000379843	-1	missense	c.629	p.R72H	tier1	183	4	0.021	504	240	0.323
147457	22	49032048	49032048	G	A	SNP	SNP	PRICKLE3	ENST00000379843	-1	missense	c.430+18	e6+18	tier4	231	4	0.017	520	212	0.289
147457	22	51639618	51639618	C	T	SNP	SNP	MAGED1	ENST00000376317	-1	nonsense	c.1822	p.R608*	tier1	47	2	0.041	326	129	0.283
147457	22	70823895	70823895	C	T	SNP	SNP	KIF4A	ENST00000375695	-1	silent	c.1035	p.G345	tier1	35	0	0.000	340	138	0.288
147457	22	70823895	70823895	C	T	SNP	SNP	KIF4A	ENST00000375695	-1	silent	c.1035	p.G345	tier1	35	0	0.000	340	138	0.288
147457	22	71427464	71427464	C	T	SNP	SNP	ERCC6L	ENST00000374003	-1	missense	c.768	p.D256	tier1	121	1	0.008	363	118	0.244
147457	22	71427464	71427464	C	T	SNP	SNP	ERCC6L	ENST00000374003	-1	missense	c.768	p.D256	tier1	121	1	0.008	363	118	0.244
147457	22	84259966	84259966	G	A	SNP	SNP	TBX22	ENST00000334463	-1	missense	c.1153	p.V865L	tier1	85	1	0.012	218	87	0.284
147457	22	84259966	84259966	G	A	SNP	SNP	TBX22	ENST00000334463	-1	missense	c.1153	p.V865L	tier1	85	1	0.012	218	87	0.284
147457	22	84259966	84259966	G	A	SNP	SNP	TBX22	ENST00000334463	-1	missense	c.1153	p.V865L	tier1	85	1	0.012	218	87	0.284
147457	22	103316458	103316458	C	T	SNP	SNP	ZNF711	ENST00000395402	-1	missense	c.1442	p.P481L	tier1	119	1	0.008	236	105	0.308
147457	22	10514665	10514665	C	T	SNP	SNP	H2BFWT	ENST00000219326	-1	missense	c.428	NULL	tier3	288	4	0.014	491	187	0.275
147457	22	10514665	10514665	C	T	SNP	SNP	H2BFWT	ENST00000219326	-1	missense	c.428	NULL	tier3	288	4	0.014	491	187	0.275
147457	22	10514665	10514665	C	T	SNP	SNP	H2BFWT	ENST00000219326	-1	missense	c.428	NULL	tier3	288	4	0.014	491	187	0.275
147457	22	120181966	120181966	G	A	SNP	SNP	GLUD2	ENST00000328078	-1	missense	c.2657	p.R434H	tier1	168	2	0.012	398	194	0.327
147457	22	12321331	12321331	G	T	SNP	SNP	STAG2	ENST00000328078	-1	nonsense	c.2657	p.R434H	tier1	168	2	0.012	398	194	0.327
147457	22	12321331	12321331	G	T	SNP	SNP	STAG2	ENST00000328078	-1	nonsense	c.2657	p.R434H	tier1	168	2	0.012	398	194	0.327
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297
147457	22	129190113	129190113	C	T	SNP	SNP	BOORL1	ENST00000303743	-1	3_prime_untranslated_region	c.2	NULL	tier3	85	0	0.000	142	57	0.297

169510	8	9634628	9634628	A	G	SNP	TMKS	ENST00000310430	1	3_prime_untranslated_region	c.382	NULL	tier3	90	6	0.062	73	60	0.451
169510	8	17206503	17206503	G	T	SNP	MTMR7	ENST00000180173	-1	missense	c.556	p.R196W	tier1	112	5	0.043	111	74	0.400
169510	9	8485187	8485187	T	A	SNP	PTFRD	ENST00000356435	-1	intronic	c.3153+40	e18+40	tier3	67	2	0.029	57	51	0.468
169510	9	99091238	99091238	G	C	SNP	NUTM2G	ENST00000356449	-1	5_prime_untranslated_region	c.49	NULL	tier3	90	0	0.000	185	41	0.181
169510	9	139845309	139845309	G	C	SNP	LCN12	ENST00000371633	-1	missense	c.341	p.A114G	tier1	82	5	0.056	139	91	0.396
169510	10	42832502	42832502	-	TATCG	INS	LOC441666	ENST00000609841	-1	missense	NULL	NULL	tier1	264	1	0.004	263	14	0.051
169510	10	42832522	42832522	C	G	SNP	LOC441666	ENST00000609841	-1	missense	c.2737+24	e12+24	tier1	258	2	0.008	261	15	0.053
169510	10	102703909	102703909	T	G	SNP	FAM178A	ENST00000370269	1	intronic	c.2782	p.E28K	tier3	57	1	0.017	44	35	0.443
169510	11	1065942	1065942	G	T	SNP	MUC2	ENST00000441003	1	intronic	c.2782	p.E28K	tier3	45	4	0.082	41	36	0.468
169510	11	6191332	6191332	G	T	SNP	OR32B2	ENST00000350810	-1	silent	c.225	NULL	tier1	91	9	0.071	97	69	0.416
169510	12	149069	149069	G	T	SNP	OR32B2	ENST00000350810	-1	missense	c.225	NULL	tier1	91	9	0.071	97	69	0.416
169510	12	22625197	22625197	G	T	SNP	CCDC5	ENST00000333597	-1	missense	c.2169+23	e17+23	tier1	187	9	0.046	312	172	0.355
169510	12	36215300	36215300	C	T	SNP	CCDC5	ENST00000333597	-1	3_prime_untranslated_region	c.2085	e17+23	tier3	211	9	0.041	182	123	0.402
169510	12	91652919	91652919	C	T	SNP	CDSP2	ENST00000350873	-1	intronic	c.2085	NULL	tier3	271	1	0.038	36	27	0.403
169510	12	91652919	91652919	C	T	SNP	CDSP2	ENST00000350873	-1	intronic	c.2085	NULL	tier3	271	1	0.038	36	27	0.403
169510	12	91652919	91652919	C	T	SNP	CDSP2	ENST00000350873	-1	intronic	c.2085	NULL	tier3	271	1	0.038	36	27	0.403
169510	12	91652919	91652919	C	T	SNP	CDSP2	ENST00000350873	-1	intronic	c.2085	NULL	tier3	271	1	0.038	36	27	0.403
169510	14	21216226	21216226	T	G	SNP	ATP2A2	ENST00000459396	-1	intronic	c.2717+60	e30+60	tier3	54	2	0.038	64	36	0.404
169510	14	21216226	21216226	T	G	SNP	ATP2A2	ENST00000459396	-1	intronic	c.2717+60	e30+60	tier3	54	2	0.038	64	36	0.404
169510	15	65393164	65393164	C	G	SNP	ATP2A2	ENST00000459396	-1	intronic	c.2717+60	e30+60	tier3	54	2	0.038	64	36	0.404
169510	15	65393164	65393164	C	G	SNP	ATP2A2	ENST00000459396	-1	intronic	c.2717+60	e30+60	tier3	54	2	0.038	64	36	0.404
169510	15	65393164	65393164	C	G	SNP	ATP2A2	ENST00000459396	-1	intronic	c.2717+60	e30+60	tier3	54	2	0.038	64	36	0.404
169510	16	32070812	32070812	C	T	SNP	ALPK3	ENST00000258888	1	3_prime_untranslated_region	c.143	p.R420	tier3	389	36	0.000	89	39	0.305
169510	16	32070812	32070812	C	T	SNP	ALPK3	ENST00000258888	1	3_prime_untranslated_region	c.143	p.R420	tier3	389	36	0.000	89	39	0.305
169510	16	67509300	67509300	A	T	SNP	IGH/OIGR16.3	ENST00000568138	1	3_prime_untranslated_region	c.1260	NULL	tier2	213	1	0.005	355	18	0.048
169510	16	67509300	67509300	A	T	SNP	IGH/OIGR16.3	ENST00000568138	1	3_prime_untranslated_region	c.1260	NULL	tier2	213	1	0.005	355	18	0.048
169510	16	89597025	89597025	A	T	SNP	RSRPY1	ENST00000268704	1	missense	c.784	p.T262S	tier1	134	5	0.038	110	105	0.486
169510	16	89597025	89597025	A	T	SNP	RSRPY1	ENST00000268704	1	missense	c.784	p.T262S	tier1	134	5	0.038	110	105	0.486
169510	17	7414546	7414546	G	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	T	SNP	SPG7	ENST00000268704	1	intronic	c.862+66	e7+66	tier3	42	1	0.023	52	38	0.422
169510	17	7832533	7832533	G	T	SNP	KOLR2A	ENST00000325644	1	missense	c.3826	p.V1278L	tier1	59	3	0.048	60	58	0.492
169510	17	10352234	10352234	G	T	SNP	KOLR2A	ENST00000325644	1	missense	c.3826	p.V1278L	tier1	59	3	0.048	60	58	0.492
169510	17	49835349	49835349	G	T	SNP	KOLR2A	ENST00000325644	1	missense	c.3826	p.V1278L	tier1	59	3	0.048	60	58	0.492
169510	17	73976119	73976119	G	T	SNP	MYH4	ENST00000393790	-1	missense	c.4312	p.R1438*	tier1	67	29	0.042	704	508	0.419
169510	17	73976119	73976119	G	T	SNP	MYH4	ENST00000393790	-1	missense	c.4312	p.R1438*	tier1	67	29	0.042	704	508	0.419
169510	17	73976119	73976119	G	T	SNP	MYH4	ENST00000393790	-1	missense	c.4312	p.R1438*	tier1	67	29	0.042	704	508	0.419
169510	17	73976119	73976119	G	T	SNP	MYH4	ENST00000393790	-1	missense	c.4312	p.R1438*	tier1	67	29	0.042	704	508	0.419
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c.113	e4-10171	tier3	96	2	0.020	106	70	0.388
169510	17	74733199	74733199	A	G	SNP	CDK3	ENST00000340813	-1	intronic	c								

190938	13	60230655	60230655	A	T	SNP	MS441	ENST000000345732	1	silent	c.270	p.G90	27	0	0.000	62	26	0.296	
190938	13	42803590	42803590	G	-	SNP	DGKH	ENST000000373243	-1	3_prime_untranslated_region	c.266	NULL	tier2	28	0	0.000	68	51	0.429
190938	14	54416601	54416602	-	AT	INS	BMP4	ENST000000245451	-1	3_prime_untranslated_region	c.1490	NULL	tier4	66	1	0.015	276	44	0.138
190938	15	43572011	43572011	G	A	SNP	TGM7	ENST000000452443	-1	missense	c.1500	p.A497G	tier1	89	0	0.000	136	82	0.374
190938	17	1028614	1028614	G	A	SNP	ABR	ENST000000302538	-1	silent	c.150	p.I60	tier1	84	0	0.000	49	54	0.519
190938	17	7578190	7578190	T	C	SNP	TP53	ENST000000269305	-1	missense	c.659	p.Y220C	tier1	797	7	0.009	495	636	0.561
190938	19	50526916	50526916	C	T	SNP	KCNK3	ENST00000047616	-1	missense	c.1294	p.V432M	tier1	18	0	0.000	21	13	0.382
190938	19	51958646	51958646	G	C	SNP	SGLEC8	ENST000000321424	-1	silent	c.877	p.L263	tier1	33	0	0.000	60	35	0.368
190938	20	95381127	95381127	C	G	SNP	PHACTR3	ENST000000371015	-1	silent	c.1206	p.L263	tier1	76	0	0.000	106	59	0.358
190938	X	12445660	12445660	A	G	SNP	ENSG000000263866	ENST000000360355	-1	3_prime_flanking_region	c.33988	NULL	tier3	39	0	0.000	30	70	0.700
190919	1	168624	168624	C	-	DEL	NADK	ENST000000344463	-1	intronic	c.576-75	65-75	tier3	123	1	0.008	162	22	0.106
190919	1	1747228	1747228	T	C	SNP	GMP1	ENST000000375609	-1	missense	c.169	p.K67E	tier1	636	12	0.019	623	296	0.321
190919	1	10602624	10602624	A	T	SNP	TRMT13	ENST000000370141	-1	missense	c.169	p.K62G	tier1	604	1	0.010	176	126	0.415
190919	1	12630566	12630566	G	A	SNP	TRMT13	ENST000000375609	-1	intronic	c.169	p.K62G	tier1	604	1	0.010	176	126	0.415
190919	1	2436367	2436367	G	T	SNP	OR2A4	ENST000000369680	-1	missense	c.169	p.Y13E	tier1	81	2	0.024	132	63	0.219
190919	2	6542786	6542786	T	SNP	SNP	PROX2	ENST000000375609	-1	missense	c.373	p.Y13E	tier1	71	2	0.038	145	97	0.262
190919	2	10015184	10015184	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3	0.030	111	38	0.252
190919	2	21228801	21228801	G	C	SNP	EFEB9	ENST000000370233	-1	missense	c.10015184	p.A326V	tier1	96	3				

222841	2	9185956	9185956	A	-	C	SNP	ENSG00000203572	ENST00000438174	-1	intronic	c.NULL	c.701+15_701+14	NULL	tie3	421	4	0.009	1163	50	0.041
222841	3	17418001	17418002	-	INS	DEL	INS	TBC1D5	ENST00000253952	-1	intronic	c.989	c.701+15_701+14	e8+15	tie3	78	0	0.000	207	22	0.096
222841	3	49571621	49571621	-	DEL	DEL	DEL	DAG1	ENST00000308775	-1	3_prime untranslated_region	c.775	c.989	p.P259T	tie3	40	0	0.000	63	14	0.182
222841	3	62142833	62142833	C	SNP	SNP	SNP	PTPRG	ENST00000447489	1	missense	c.1630	c.775	p.P259T	tie1	85	1	0.012	206	26	0.112
222841	3	195453104	195453104	G	SNP	SNP	SNP	MUC20	ENST00000447234	1	missense	c.89-112	c.1630	p.V544I	tie1	152	0	0.000	234	20	0.079
222841	4	8601068	8601068	G	SNP	SNP	SNP	CPZ	ENST00000360986	-1	splice_site	c.315-1	c.89-112	e2-112	tie3	137	0	0.000	280	25	0.082
222841	4	76894321	76894321	G	SNP	SNP	SNP	CNOT6L	ENST00000264903	-1	silent	c.467	c.315-1	e4-1	tie1	180	0	0.000	341	53	0.134
222841	5	11486164	11486164	C	SNP	SNP	SNP	MAP1B	ENST00000296755	-1	nonense	c.6279	c.467	p.T2334	tie1	371	1	0.003	767	51	0.062
222841	6	10121510	10121510	G	SNP	SNP	SNP	ASCC3	ENST00000385008	-1	silent	c.33715	c.6279	p.Y488*	tie1	198	1	0.005	489	28	0.054
222841	7	17631399	17631399	G	SNP	SNP	SNP	ROST	ENST00000344575	-1	5_prime flanking_region	c.17	c.33715	p.T2093	tie1	145	0	0.000	267	16	0.057
222841	7	12614623	12614623	C	SNP	SNP	SNP	FZD9	ENST00000320670	-1	missense	c.607	c.17	NULL	tie3	210	0	0.005	345	25	0.068
222841	8	19894560	19894560	C	SNP	SNP	SNP	ITF310	ENST00000337216	-1	silent	c.358+28614	c.607	p.S8C	tie1	113	0	0.000	246	21	0.079
222841	8	22546343	22546343	C	SNP	SNP	SNP	EGRC	ENST00000337216	-1	silent	c.358+28614	c.358+28614	e2-23614	tie1	276	0	0.000	952	23	0.045
222841	9	12246845	12246845	A	SNP	SNP	SNP	CHST3	ENST00000359338	-1	intronic	c.24373	c.358+28614	e2-23614	tie3	82	1	0.011	159	22	0.122
222841	9	6249763	6249763	A	SNP	SNP	SNP	CHST3	ENST00000359338	-1	intronic	c.24373	c.24373	e2-23614	tie3	82	1	0.011	159	22	0.122
222841	10	73497534	73497534	G	SNP	SNP	SNP	CHST3	ENST00000359338	-1	5_prime untranslated_region	c.31440	c.24373	e2-23614	tie3	284	1	0.000	505	38	0.049
222841	10	3244646	3244646	G	SNP	SNP	SNP	MT1	ENST00000332351	-1	intronic	c.872+4954	c.31440	e3+954	tie1	220	0	0.000	491	33	0.083
222841	11	49170094	49170094	G	SNP	SNP	SNP	ADCV6	ENST00000307885	-1	silent	c.1575	c.872+4954	e3+954	tie1	412	2	0.005	742	31	0.043
222841	12	109604677	109604677	C	SNP	SNP	SNP	ACACB	ENST00000338432	-1	missense	c.665	c.1575	p.S522W	tie1	109	0	0.000	193	17	0.081
222841	13	36410159	36410159	C	SNP	SNP	SNP	DCI41	ENST00000360631	-1	intronic	c.1229+11	c.665	e7+11	tie3	246	0	0.000	666	50	0.070
222841	16	81412314	81412314	G	SNP	SNP	SNP	GAN	ENST00000366107	-1	3_prime untranslated_region	c.1113	c.1229+11	NULL	tie3	107	0	0.000	297	21	0.066
222841	17	7577668	7577668	C	SNP	SNP	SNP	TP53	ENST00000265305	-1	missense	c.713	c.1113	p.C238Y	tie1	803	19	0.023	873	482	0.355
222841	17	10350502	10350502	C	SNP	SNP	SNP	MYH4	ENST00000255381	-1	missense	c.4294	c.713	p.R1668I	tie1	417	2	0.005	928	47	0.048
222841	17	10401122	10401122	G	SNP	SNP	SNP	MYH4	ENST00000255381	-1	missense	c.4294	c.4294	p.L1432V	tie1	323	0	0.000	620	26	0.040
222841	19	9176322	9176322	G	SNP	SNP	SNP	OR11W1	ENST00000425666	1	missense	c.2548+3	c.4294	NULL	tie3	198	0	0.000	428	21	0.047
222841	22	40055124	40055124	G	SNP	SNP	SNP	CACNA1I	ENST00000335930	-1	splice_region	c.539	c.2548+3	e15+3	tie3	263	0	0.000	169	15	0.082
222841	X	137714472	137714472	G	SNP	SNP	SNP	FGF13	ENST00000263519	-1	missense	c.170	c.539	p.S57N	tie3	94	0	0.000	883	39	0.042
222841	X	152801875	152801875	G	SNP	INS	SNP	WASH7P	ENST00000438504	-1	splice_site_ins	c.NULL	c.170	NULL	tie1	7	0	0.000	2	12	0.857
222841	1	15903	15904	-	C	SNP	SNP	MS1L	ENST00000445405	-1	missense	c.457+69	c.NULL	NULL	tie1	141	3	0.021	378	42	0.100
222841	1	17084269	17084269	G	SNP	DEL	DEL	PTGS2	ENST00000335211	-1	intronic	c.814	c.457+69	e4+69	tie3	33	0	0.000	73	18	0.198
222841	1	186647324	186647324	C	SNP	DEL	DEL	PTGS2	ENST00000335211	-1	missense	c.814	c.814	p.R272C	tie1	71	0	0.000	116	26	0.183
222841	1	201172932	201172932	C	SNP	DEL	DEL	IGF1I	ENST00000258400	-1	frame_shift_ins	c.613_612	c.814	p.L2046	tie1	61	0	0.000	125	19	0.132
222841	2	231974064	231974065	G	INS	SNP	SNP	HTBZ	ENST00000449082	-1	missense	c.4744	c.613_612	p.R1982C	tie1	74	0	0.000	195	30	0.133
222841	3	38739967	38739967	G	SNP	SNP	SNP	SCN10A	ENST00000288139	-1	missense	c.1255	c.4744	p.R419W	tie1	76	2	0.026	165	33	0.167
222841	3	68684184	68684184	C	SNP	SNP	SNP	CACNA1D	ENST00000461635	-1	5_prime flanking_region	c.677	c.1255	NULL	tie4	65	0	0.000	109	26	0.193
222841	4	15055756	15055756	C	SNP	SNP	SNP	CPEB2	ENST00000538197	-1	silent	c.965-54	c.677	p.E792	tie1	102	1	0.010	229	46	0.167
222841	4	36214995	36214995	T	SNP	SNP	SNP	ARAP2	ENST00000303965	-1	intronic	c.865-54	c.965-54	e19-62	tie3	43	0	0.000	78	14	0.152
222841	4	39628393	39628393	-	INS	SNP	SNP	POSSA	ENST00000303538	-1	splice_site	c.429+2	c.865-54	e19-62	tie3	43	0	0.000	78	14	0.152
222841	4	95202758	95202758	T	SNP	SNP	SNP	IL6ST	ENST00000335905	-1	intronic	c.2732+17	c.429+2	e3+2	tie3	195	1	0.005	312	20	0.059
222841	5	55237459	55237459	C	SNP	SNP	SNP	SMARCA1	ENST00000338909	-1	silent	c.2208	c.2732+17	e20+17	tie3	64	0	0.000	85	12	0.124
222841	5	60770374	60770374	A	SNP	SNP	SNP	MRCS1B8	ENST00000446279	-1	missense	c.602	c.2208	p.S736	tie1	77	1	0.013	162	26	0.138
222841	6	30933399	30933399	C	SNP	SNP	SNP	ICK	ENST00000350062	-1	missense	c.555	c.602	p.P201Q	tie1	60	0	0.000	200	33	0.142
222841	6	52883236	52883236	G	SNP	SNP	SNP	FLIP1	ENST00000350062	-1	missense	c.2662	c.555	p.A185	tie1	99	0	0.000	196	33	0.144
222841	6	76022866	76022866	G	SNP	SNP	SNP	C6orf165	ENST00000369562	-1	missense	c.294	c.2662	p.P888S	tie1	88	0	0.000	183	32	0.149
222841	6	8125414	8125414	C	SNP	SNP	SNP	MAN1B1	ENST00000358349	1	3_prime untranslated_region	c.13997605	c.294	p.L98	tie1	169	0	0.000	273	45	0.142
222841	9	13997605	13997605	A	SNP	SNP	SNP	MAN1B1	ENST00000358349	1	3_prime untranslated_region	c.13997644	c.13997605	NULL	tie3	81	1	0.012	173	42	0.194
222841	9	13997644	13997644	A	SNP	SNP	SNP	MAN1B1	ENST00000358349	1	3_prime untranslated_region	c.13997644	c.13997644	NULL	tie3	75	3	0.039	141	50	0.254
222841	10	15777301	15777301	A	SNP	SNP	SNP	NTM2	ENST00000378165	-1	silent	c.363	c.13997644	p.F121	tie3	30	0	0.000	38	14	0.269
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018	618	110	0.151
222841	12	12064418	12064418	-	INS	SNP	SNP	ETV6	ENST00000396373	-1	frame_shift_ins	c.385_386	c.363	p.S131fs	tie1	379	7	0.018			

243777	6	42985377	42985377	G	A	SNP	KLHDC3	ENST00000328974	1	nonsense	c.275	p.W92*	tier1	63	0	0.000	137	21	0.133
243777	6	64290608	64290608	C	SNP	P1P4A1		ENST00000370651	1	3_prime_untranslated_region	c.729	NULL	tier3	100	0	0.000	158	39	0.197
243777	7	13256262	13256262	G	T	NUP205		ENST00000285968	1	missense	c.1001	p.A334V	tier3	151	5	0.032	216	55	0.202
243777	8	10152892	10152892	A	-	ANKRD46		ENST00000290552	-1	intronic	c.637-25	e4-25	tier3	38	0	0.000	48	10	0.172
243777	8	11795879	11795879	G	A	RAD21		ENST00000302338	-1	nonsense	c.7356	p.R586*	tier1	810	5	0.006	1188	130	0.099
243777	9	10812537	10812537	G	T	SLC44A1		ENST00000374720	1	missense	c.1036	p.V346I	tier1	123	0	0.000	203	50	0.198
243777	10	54076396	54076396	C	SNP	DKR1		ENST00000373970	1	silent	c.630	p.C210	tier1	71	1	0.014	75	33	0.306
243777	10	13535063	13535063	G	T	CYP2E1		ENST00000252445	1	splice_region	c.988-4	e7-4	tier3	51	0	0.000	85	19	0.183
243777	11	67532796	67532796	G	T	ATG16L1		ENST00000353887	1	3_prime_untranslated_region	c.57/552796	NULL	tier3	97	0	0.000	146	46	0.240
243777	11	7175151	7175151	T	-	NADSLRN1		ENST00000319023	1	missense	c.370	p.R742S	tier1	40	0	0.000	39	17	0.304
243777	11	10816267	10816267	T	-	ATM		ENST00000278616	1	intronic	c.6347+19	e42+19	tier3	59	0	0.000	69	13	0.159
243777	11	11982117	11982117	C	SNP	TYM		ENST00000359799	1	intronic	c.401-44	e4-44	tier3	65	2	0.023	91	23	0.216
243777	12	12270600	12270600	T	A	SVX2		ENST00000396373	1	nonsense	c.270	p.V169*	tier1	696	3	0.003	876	122	0.122
243777	16	17175098	17175098	T	C	SLC11A1		ENST00000360630	-1	intronic	c.232333470	e6-470	tier3	265	3	0.011	150	36	0.265
243777	16	17175098	17175098	G	T	SLC11A1		ENST00000360630	-1	missense	c.10337	p.D146V	tier1	131	0	0.011	93	36	0.368
243777	17	10451010	10451010	G	T	MYH9		ENST00000403437	-1	intronic	c.21-56	e21-56	tier3	168	2	0.012	223	46	0.171
243777	17	10451010	10451010	T	INS	MYH9		ENST00000403437	-1	intronic	c.2889-57/2889-56	e1-24	tier3	168	2	0.012	223	46	0.171
243777	17	62399169	62399169	-	T	PRK31P57		ENST00000245031	-1	5_prime_flanking_region	c.204-24	e1-24	tier3	168	2	0.013	268	63	0.190
243777	17	78313118	78313118	G	T	RNF213		ENST00000461109	-1	missense	c.3109	NULL	tier3	85	0	0.000	103	37	0.284
243777	18	42531917	42531917	C	G	SEB2P1		ENST00000282930	1	missense	c.4951	p.L1851V	tier1	565	18	0.031	806	234	0.225
243777	18	7796475	7796475	C	SNP	ADNP2		ENST00000282930	1	missense	c.2612	p.D1860V	tier1	545	3	0.006	951	30	0.031
243777	19	1525633	1525633	C	T	PLK5		ENST00000334770	1	missense	c.3179	NULL	tier2	92	0	0.039	159	77	0.326
243777	19	5158189	5158189	C	T	KLK5		ENST00000334770	1	missense	c.1363	NULL	tier2	92	0	0.039	159	77	0.326
243777	20	3214593	3214593	T	A	ZNF264		ENST00000326003	1	5_prime_untranslated_region	c.1363	NULL	tier3	81	1	0.012	100	43	0.301
243777	20	3214593	3214593	C	G	SLC411		ENST00000326003	1	5_prime_untranslated_region	c.23	p.D159G	tier3	81	0	0.012	100	43	0.301
243777	20	31022762	31022762	C	T	ASXL1		ENST00000380059	-1	missense	c.475	p.R236	tier1	89	0	0.015	95	34	0.264
243777	20	31022762	31022762	C	-	ASXL1		ENST00000375887	-1	frame_shift_del	c.708	p.V751fs	tier1	89	0	0.015	95	34	0.264
243777	21	9755905	9755905	G	T	U2AF1		ENST00000291552	-1	missense	c.2247	NULL	tier3	314	0	0.000	72	33	0.314
243777	21	44514177	44514177	T	G	MYO3		ENST00000330666	-1	missense	c.470	p.Q157P	tier3	314	0	0.000	72	33	0.314
243777	21	24417462	24417462	C	A	CACNA1E		ENST00000330666	-1	missense	c.1260	p.W420C	tier1	329	1	0.003	901	40	0.043
266995	1	181706618	181706618	G	A	RI1		ENST00000367573	1	intronic	c.3423-43	e23-43	tier3	354	0	0.003	511	43	0.077
266995	2	15267722	15267722	T	-	LSM3		ENST00000243326	1	intronic	c.105-52	e2-52	tier2	20	0	0.000	12	7	0.368
266995	3	39230412	39230412	C	T	XIRP1		ENST00000306024	1	intronic	c.229-19/229-18	e4-18	tier2	88	0	0.000	114	13	0.102
266995	3	10463779	10463779	A	G	TFG		ENST00000340369	-1	splice_region	c.525	p.L175	tier1	530	2	0.004	988	64	0.061
266995	3	137981440	137981440	A	-	ARMC8		ENST00000340369	-1	splice_region	c.820-4	e6-4	tier3	107	1	0.009	185	21	0.102
266995	6	132067939	132067939	A	G	ENPP3		ENST00000469044	1	intronic	c.1135-1141	e13-1141	tier4	58	0	0.000	60	9	0.130
266995	6	129028658	129028658	T	-	AHCYL2		ENST00000491079	1	missense	c.2371	p.E824G	tier1	140	0	0.000	200	16	0.074
266995	7	80048699	80048699	C	A	TPD52		ENST00000518937	-1	3_prime_untranslated_region	c.129028858	NULL	tier3	86	1	0.012	104	14	0.119
266995	8	139736829	139736829	G	A	COL22A1		ENST00000530345	-1	intronic	c.1652	NULL	tier3	112	0	0.000	106	9	0.078
266995	8	95720906	95720906	G	A	PPSL		ENST00000480546	-1	missense	c.2247-29	e24-29	tier3	65	0	0.000	91	17	0.157
266995	12	25386262	25386262	G	G	KRAS		ENST00000256078	-1	missense	c.57	NULL	tier1	161	0	0.000	270	18	0.063
266995	12	54389181	54389181	G	G	HOXC11		ENST00000546378	-1	missense	p.L19F	p.L19F	tier1	184	0	0.000	750	46	0.058
266995	13	101762936	101762936	G	A	MUC8		ENST00000595994	-1	silent	c.183	p.G300A	tier1	184	0	0.000	339	18	0.050
266995	13	101762936	101762936	G	A	MUC8		ENST00000595994	-1	silent	c.183	p.L61	tier1	130	0	0.000	129	12	0.085
266995	13	101910940	101910940	C	G	NALCN		ENST00000251127	-1	intronic	c.2364-34	e19-34	tier2	390	2	0.005	454	47	0.094
266995	15	101844339	101844339	C	G	NALCN		ENST00000251127	-1	intronic	c.1135-15	e10-15	tier3	234	0	0.000	381	34	0.081
266995	16	81941970	81941970	C	A	PLCG2		ENST00000359376	1	intronic	NULL	e15-51	tier1	114	0	0.000	179	17	0.087
266995	18	14330201	14330201	C	G	MIR3156-2		ENST00000381101	1	missense	c.1558-51	e15-51	tier3	113	0	0.000	199	15	0.070
266995	18	14330201	14330201	C	G	MIR3156-2		ENST00000381101	1	missense	c.1558-51	e15-51	tier3	113	0	0.000	199	15	0.070
266995	19	9057573	9057573	G	A	MUC16		ENST00000397910	1	missense	c.29873	p.T9958I	tier1	243	0	0.000	247	12	0.046
266995	19	9057573	9057573	G	A	MUC16		ENST00000397910	1	missense	c.29873	p.T9958I	tier1	243	0	0.000	247	12	0.046
266995	19	10781978	10781978	G	A	COL4A5		ENST00000328300	1	intronic	c.322-11	e6-11	tier1	734	0	0.000	1536	68	0.042
266995	19	96473262	96473262	G	A	DST		ENST00000370754	-1	missense	c.6065	p.T2022I	tier3	220	0	0.000	320	28	0.080
266995	6	114563154	114563154	C	A	MDIC		ENST00000393486	1	missense	c.66	p.G22	tier1	777	0	0.000	1084	44	0.039
266995	7	3596348	3596348	C	T	HRC11		ENST00000354323	1	in_frame_del	c.64_66	NULL	tier1	6	0	0.000	1	8	0.889
266995	14	2387683	2387683	A	-	C16orf19		ENST00000319074	-1	3_prime_untranslated_region	c.593	p.L25n_frame_del	tier1	74	0	0.000	89	11	0.110
266995	19	633529	633530	-	G	CTG		ENST00000586649	-1	5_prime_untranslated_region	c.17	NULL	tier4	86	0	0.000	124	13	0.095
266995	19	4817310	4817310	A	G	TICAM1		ENST00000248244	-1	silent	c.1080	p.P360	tier1	186	2	0.011	256	24	0.085
266995	21	14469103	14469103	G	A	ZNF35P		ENST00000427301	-1	5_prime_untranslated_region	c.14469103	NULL	tier3	347	0	0.000	347	15	0.041
266995	21	145684679	145684679	G	A	RNF115		ENST00000369291	1	splice_site	c.687+1	e7+1	tier1	48	2	0.039	118	60	0.337
266995	2	65497525	65497525	A	G	ACTR2		ENST00000260641	1	3_prime_untranslated_region	c.1657	NULL	tier3	46	0	0.000	62	43	0.410
266995	2	90109121	90109121	G	A	IGKV1D-17		ENST00000483379	1	5_prime_flanking_region	c.12537	NULL	tier3	49	0	0.000	81	46	0.362
266995	2	144159094	144159094	A	T	ARHGAP15		ENST00000295095	-1	intronic	c.475-34076	e6-34076	tier2	29	0	0.000	78	36	0.316
266995	3	37095520	37095520	A	G	LRRFP2		ENST00000336686	-1	intronic	c.2056-48	e27-48	tier3	19	0	0.000	26	28	0.519
266995	3	39453515	39453515	A	G	RP5A		ENST00000301821	1	silent	c.756	p.V252	tier2	29	0	0.000	118	17	0.126
266995	3	41722946	41722946	G	-	ULK4		ENST00000301821	1	silent	c.2978-53	e28-53	tier3	62	0	0.000	57	32	0.360
266995	3	3891295	3891295	G	T	OR7E63P		ENST00000305943	-1	intronic	c.3891295	NULL	tier3	43	0	0.000	67	35	0.343
266995	4	85654560	85654560	T	T	WDFY3		ENST00000295888	-1	missense	c.7196	p.E239V	tier1	48	0	0.000	47	49	0.510
266995	4	140619263	140619263	C	A	MGST2		ENST00000265498	1	missense	c.229-2842	e3-2842	tier3	50	0	0.000	105	16	0.132
266995	5	76433942	76433942	G	T	ZBED3-AS1		ENST00000305433	1	intronic	c.NULL	NULL	tier3						

280837	12	50344754	50344754	G	A	SNP	AQF2	ENST00000198280	1	silent	c.141	p.A47	tier1	30	0	0.000	143	120	0.456
280837	17	1563288	1563288	T	A	SNP	PRF8	ENST00000304992	-1	missense	c.4793	p.D1598V	tier1	87	1	0.011	479	400	0.454
280837	17	27210235	27210235	T	A	SNP	FLO2	ENST00000394906	-1	silent	c.402	p.T134	tier1	19	1	0.050	125	112	0.473
280837	17	73910078	73910078	C	T	SNP	FBF1	ENST00000388570	-1	silent	c.3003	p.Q1001	tier1	9	0	0.000	150	123	0.447
280837	18	5891961	5891961	G	T	SNP	TMEM200C	ENST00000383490	-1	missense	c.102	p.R34S	tier1	23	0	0.000	84	96	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	18535578	18535578	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	LM2	ENST00000221973	-1	silent	c.225	p.A7S	tier1	28	0	0.000	91	58	0.389
280837	20	30495206	30495206	C	T	SNP	MYL2C	ENST00000375985	-1	intronic	c.474-36	p.A7S	tier1	18	0	0.000	80	96	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
280837	X	33767435	33767435	G	A	SNP	AK2	ENST00000303744	-1	splice_site	c.695-1	p.M397I	tier1	108	0	0.000	83	9	0.098
280837	1	69236209	69236209	G	T	SNP	KP02	ENST00000370521	-1	intronic	c.622+57	p.G522T	tier3	53	0	0.000	22	6	0.214
280837	1	20116702	20116702	G	C	SNP	IP01	ENST00000353211	1	silent	c.6691	NULL	tier3	273	0	0.000	120	7	0.055
280837	1	20163204	20163204	G	A	SNP	HEC2	ENST0000035589	-1	3_prime_untranslated_region	c.364	NULL	tier3	31	0	0.000	77	0	0.250
280837	2	10343234	10343234	A	INS	SNP	SLC11A	ENST00000482879	-1	5_prime_untranslated_region	c.532-31	p.A5-31	tier1	153	0	0.000	50	7	0.230
280837	2	8468265	8468265	A	DEL	SNP	SLC11A	ENST00000482879	-1	5_prime_untranslated_region	c.532-31	p.A5-31	tier1	153	0	0.000	50	7	0.230
280837	2	18298497	18298498	A	INS	SNP	ITGA4	ENST00000370533	-1	intronic	c.284-46	p.G27-46	tier3	7	0	0.000	3	7	0.700
280837	2	22082366	22082366	A	DEL	SNP	ABC36	ENST00000265316	-1	intronic	c.697-26	p.G27-46	tier3	51	1	0.019	33	10	0.233
280837	5	13203198	13203198	T	DEL	SNP	KF3A	ENST00000378735	-1	3_prime_untranslated_region	c.*988	NULL	tier3	48	0	0.000	35	9	0.205
280837	6	10040004	10040004	G	A	SNP	ANKRD1	ENST00000297183	-1	missense	c.4572	p.F1524L	tier1	115	0	0.000	27	4	0.129
280837	7	86547738	86547738	A	G	SNP	MC92	ENST00000450689	-1	missense	c.20	p.S7Y	tier1	108	0	0.000	22	4	0.154
280837	7	10152282	10152282	T	DEL	SNP	ZNFR90	ENST00000450689	-1	intronic	c.1593-20	p.T2-20	tier3	85	0	0.000	17	4	0.191
280837	8	10522892	10522892	G	-	SNP	FOCAD	ENST00000502552	-1	intronic	c.1984-56	p.A4-56	tier3	50	0	0.000	15	5	0.250
280837	9	20923717	20923717	G	A	SNP	NRP1	ENST00000338382	-1	missense	c.637-25	p.V971I	tier3	41	0	0.000	14	5	0.263
280837	10	33619598	33619598	G	T	SNP	DMBT1	ENST00000265371	-1	intronic	c.291-38	p.G27-25	tier2	139	0	0.000	24	6	0.200
280837	11	559313	559313	C	C	SNP	GTF2H3	ENST00000338354	-1	intronic	c.3310+25	p.G27-25	tier3	184	1	0.005	140	15	0.097
280837	12	124144573	124144573	C	DEL	SNP	SPAL1	ENST00000527620	1	5_prime_flanking_region	c.821-20	NULL	tier1	66	0	0.000	15	4	0.211
280837	14	72171435	72171435	T	-	SNP	TMEM87A	ENST0000055818	1	splice_region	c.821-20	p.E12-20	tier3	83	1	0.012	34	8	0.191
280837	15	42503954	42503954	A	-	SNP	C16orf71	ENST00000389834	-1	splice_region_del	c.3647-3	p.E20-7	tier3	105	0	0.000	25	4	0.138
280837	16	4796867	4796867	G	A	SNP	AP3D1	ENST00000299320	-1	silent	c.1927-7	p.E407	tier1	115	0	0.000	22	6	0.214
280837	20	31023112	31023112	T	G	SNP	AXL1	ENST00000355272	-1	intronic	c.1101+61	p.E12+61	tier3	53	0	0.000	40	5	0.111
280837	20	31451686	31451686	G	A	SNP	EACA8B	ENST00000375687	-1	nonsense	c.2597	p.L866*	tier1	1114	3	0.003	346	99	0.222
280837	21	33919729	33919729	G	A	SNP	RNASP490	ENST00000405522	1	intronic	c.42+46	p.L146	tier3	69	0	0.000	39	6	0.133
280837	22	22114660	22114661	INS	DEL	SNP	MAPK1	ENST00000517141	1	5_prime_flanking_region	c.6106	NULL	tier3	54	0	0.000	34	7	0.171
280837	22	29593980	29593980	G	-	SNP	THOC5	ENST00000215832	-1	3_prime_untranslated_region	c.*8833	NULL	tier3	39	0	0.000	21	6	0.222
280837	22	50439189	50439189	G	DEL	SNP	IL1REL	ENST00000397871	-1	frame_shift_del	c.354+38	p.Q72fs	tier3	48	0	0.000	19	5	0.208
280837	X	70339865	70339865	T	A	SNP	MED12	ENST00000333646	-1	missense	c.398	p.V133D	tier1	755	3	0.004	301	15	0.364
280837	X	76709731	76709731	C	T	SNP	FRMPD3-A51	ENST00000439435	1	silent	c.84	p.S328	tier1	145	0	0.000	52	5	0.088
280837	X	10678960	10678960	G	C	SNP	NBPF13P	ENST00000415252	1	intronic	c.NULL	NULL	tier1	149	0	0.000	30	4	0.111
280837	1	146491965	146491965	G	C	SNP	NBPF13P	ENST00000444680	-1	intronic	c.NULL	NULL	tier3	123	2	0.016	240	27	0.101
280837	2	33614218	33614218	G	T	SNP	LTBP1	ENST00000444680	-1	intronic	c.NULL	NULL	tier3	75	1	0.013	81	14	0.143
280837	2	122369100	122369100	G	T	SNP	CLASP1	ENST00000354476	-1	intronic	c.4715-33	p.E1-3344	tier3	91	2	0.022	81	91	0.529
280837	3	183903211	183903211	G	A	SNP	NCKAP1	ENST00000263710	-1	5_prime_untranslated_region	c.15344	NULL	tier4	93	1	0.011	135	18	0.118
280837	4	103617794	103617794	G	A	SNP	UROCT1	ENST00000360962	-1	intronic	c.384	p.E12-12	tier2	8	0	0.000	0	7	1.000
280837	7	100839218	100839218	G	A	SNP	MANBA	ENST00000226578	-1	missense	c.808	p.P270S	tier3	106	3	0.028	79	63	0.444
280837	9	45202089	45202089	G	T	SNP	MOGAT3	ENST00000279423	-1	missense	c.44489	p.A278T	tier1	102	3	0.029	78	74	0.484
280837	9	95033364	95033364	G	T	SNP	BRD3	ENST00000417850	-1	5_prime_flanking_region	c.4489	NULL	tier3	34	0	0.000	31	11	0.262
280837	9	13691842	13691842	T	C	SNP	MRPL23	ENST00000433041	-1	missense	c.3982	p.V1328L	tier1	42	1	0.023	19	27	0.587
280837	11	1997318	1997318	T	C	SNP	SLC6A15	ENST0000035066	-1	intronic	c.497+3330	NULL	tier3	74	1	0.013	65	33	0.337
280837	12	64474024	64474024	A	-	DEL	POLE	ENST0000026682	-1	5_prime_untranslated_region	c.1324+42	p.E1-42	tier4	89	2	0.022	62	13	0.173
280837	12	85265921	85265921	A	-	DEL	POLE	ENST00000320574	-1	silent	c.22	NULL	tier4	40	0	0.000	37	8	0.178
280837	14	106330469	106330469	C	T	SNP	IGHA4	ENST000004461719	-1	missense	c.6789	p.Q2263	tier1	147	0	0.000	167	16	0.079
280837	15	65327071	65327071	T	C	SNP	ZNFX2	ENST00000295927	-1	missense	c.1165	p.Y1C	tier1	353	0	0.000	472	16	0.037
280837	17	19137420	19137420	G	T	SNP	ABD114	ENST00000355381	-1	silent	c.807	p.R169S	tier1	79	0	0.000	87	13	0.330
280837	17	19137420	19137420	G	T	SNP	ABD114	ENST00000355381	-1	missense	c.250+52	p.R169S	tier1	79	0	0.000	87	13	0.330
280837	19	1941144	1941144	G	G	INS	ZSWIM4	ENST00000254233	-1	missense	c.4532	p.R18A	tier3	92	0	0.000	33	0	0.163
280837	19	33793253	33793253	C	INS	SNP	CEBPA	ENST00000496007	-1	frame_shift_ins	c.69-68	p.H21A	tier1	28	0	0.000	23	27	0.540
280837	20	43723594	43723594	G	T	SNP	KCNJ51	ENST00000368117	-1	missense	c.1498	p.S500T	tier1	46	0	0.001	857	164	0.161
280837	20	57768618	57768618	A	T	SNP	ZNF391	ENST00000371030	-1	missense	c.2544	p.T848	tier1	39	2	0.049	50	46	0.479
280837	21	42438904	42438904	A	DEL	SNP	TM6PSS2	ENST00000395855	-1	intronic	c.1579+14	p.E14-14	tier3	58	0	0.000	71	10	0.124
280837	22	41742111	41742111	C	-	SNP	ZC3H7B	ENST00000351589	-1	missense	c.1564	p.R522C	tier1	55	2	0.035	44	47	0.517
280837	X	5096184	5096184	G	A	SNP	NCKAP2	ENST00000299821	-1	missense	c.1015	p.V339M	tier1	76	3	0.038	66	82	0.554
280837	X	107512391	107512391	G	-	DEL	COL4A6	ENST00000461897	-1	splice_region_del	c.NULL	NULL	tier3	107	0	0.000	106	11	0.094
280837	1	201847766	201847766	A	G	SNP	RNPEP	ENST00000295540	-1	5_prime_flanking_region	c.4029	NULL	tier3	156	5	0.031	149	43	0.223
280837	2	21323014	21323014	G	A	SNP	APOB	ENST00000233242	-1	missense	c.7796	p.R2576C	tier1	827	3	0.004	1221	99	0.075
280837	2	25457242	25457242	G	T	SNP	DNMT3A	ENST00000264709	-1	missense	c.2645	p.R82H	tier1	420	19	0.043	385	138	0.284
280837	2	133489315	133489315	G	A	SNP	NCKAP5	ENST00000317721	-1	missense	c.5438	p.S181Sf	tier1	105	1	0.009	115	46	0.264
280837	2	170092614	170092614	G	A	SNP	LRP2	ENST00000263816	-1	intronic	c.4692-36	p.E25-36	tier3	58	1	0.017	72	18	0.200

[illegible]

307995	12	9095076	9095076	C	G	SNP	MEPR	ENST000000000412	-1	missense	c.647	ber1	57	0	0.000	129	20	0.135
307995	12	50027356	50027356	G	A	SNP	PRFF408	ENST000000486825	-1	intronic	c.584+26	ber3	496	0	0.000	1312	317	0.194
307995	12	52715016	52715016	G	A	SNP	KRT63	ENST0000000293670	-1	missense	c.304	ber1	102	0	0.000	219	73	0.249
307995	12	52691238	52691238	G	A	SNP	KRT6C	ENST0000000252520	-1	5_prime_fanking_region	p.A350	ber3	185	0	0.000	390	106	0.213
307995	12	10951920	10951920	T	C	SNP	UGF30	ENST0000000257548	-1	intronic	c.23717	ber3	44	0	0.000	420	22	0.155
307995	14	19376051	19376051	G	C	SNP	SRH17H2	ENST000000050708	-1	missense	c.761-18	ber3	1326	0	0.000	3626	167	0.044
307995	14	94945375	94945375	G	A	SNP	ORP17M9	ENST0000000538349	-1	intronic	c.488	ber3	133	0	0.000	266	94	0.170
307995	15	45725117	45725117	G	A	INS	C16orf46	ENST0000000344300	-1	intronic	c.184-29,164-28	ber3	13	0	0.000	261	54	0.070
307995	15	48315688	48315688	T	C	SNP	CELM47	ENST0000000219197	-1	5_prime_untranslanted_region	e4-28	ber3	13	0	0.014	114	20	0.149
307995	17	61963692	61963692	G	A	SNP	GR2	ENST0000000259157	-1	5_prime_fanking_region	c.-372	ber3	13	0	0.000	34	23	0.404
307995	19	94953690	94953690	CCC	C	SNP	ORC	ENST0000000352600	-1	intronic	NULL	ber3	135	0	0.000	233	57	0.196
307995	20	57177225	57177225	C	T	SNP	PREL1	ENST0000000376164	-1	intronic	c.1262-36	ber3	94	0	0.000	153	29	0.265
307995	20	56927405	56927405	C	T	SNP	CTEL	ENST0000000392651	-1	silent	c.459361	ber3	42	0	0.000	147	28	0.169
307995	20	8349450	8349450	CCC	C	SNP	PHACTF3	ENST0000000370135	-1	intronic	p.P42	ber1	81	0	0.000	159	37	0.228
307995	21	36525904	36525904	G	A	SNP	RUVN1	ENST0000000370135	-1	intrae_shift_ins	c.927-58	ber3	83	0	0.000	159	37	0.228
307995	22	20171118	20171118	CC	C	SNP	UNC00686	ENST0000000402378	-1	5_prime_fanking_region	c.385,367	ber3	83	0	0.000	104	374	0.158
307995	X	53574723	53574723	G	A	SNP	BOCR	ENST0000000378444	-1	missense	c.2982	ber3	27	0	0.000	104	374	0.158
307995	X	3991164	3991164	T	C	SNP	HUW1	ENST0000000378444	-1	missense	c.689	ber3	27	0	0.000	104	374	0.158
307995	X	15134800	15134800	C	T	SNP	GABR3	ENST0000000370314	-1	missense	p.W1663*	ber1	189	0	0.000	371	135	0.268
307995	X	15987264	15987264	C	T	SNP	RSC1A1	ENST0000000370314	-1	missense	p.A360H	ber1	41	0	0.000	158	62	0.282
307995	X	23660085	23660085	C	T	SNP	HNRNP	ENST0000000345034	-1	missense	p.R409H	ber1	75	0	0.000	54	41	0.432
307995	X	26795865	26795865	C	T	SNP	FOXQ3	ENST000000034793	-1	missense	c.10547	ber1	31	0	0.000	158	62	0.282
307995	X	47900400	47900400	G	A	SNP	HDHD3	ENST0000000360039	-1	missense	c.1379	ber1	75	0	0.000	54	41	0.432
307995	X	21433418	21433418	T	A	SNP	ROD2	ENST0000000367005	-1	missense	c.901	ber1	31	0				

346313	11	7480778	7480778	C	T	SNP	SLC22B1	ENST00000288575	1	silent	c.750	p.R250	tier1	50	0	0.000	39	35	0.473
346313	12	8073897	8073897	G	A	SNP	SLC23A3	ENST00000448295	-1	5_prime_untranslated_region	c.-8073897	NULL	tier3	135	1	0.007	213	18	0.078
346313	12	2206832	2206832	G	A	SNP	C22D5	ENST00000339557	-1	missense	c.2669	p.O857E	tier3	84	0	0.000	99	59	0.373
346313	12	11292910	11292910	G	C	SNP	PITPN1	ENST00000351677	-1	missense	c.1530	p.Q510H	tier1	758	0	0.000	1191	33	0.027
346313	12	133394599	133394599	G	C	SNP	GOLGA3	ENST00000204726	-1	silent	c.1056	p.A352	tier1	102	0	0.000	85	90	0.388
346313	13	95363388	95363388	G	A	SNP	SOX21	ENST00000376945	-1	3_prime_untranslated_region	c.810	NULL	tier2	52	0	0.000	53	34	0.391
346313	13	96030086	96030086	C	T	SNP	FARP1	ENST00000376986	-1	missense	c.470	p.A137V	tier1	64	0	0.000	69	36	0.343
346313	14	38274022	38274022	A	T	SNP	ITIC6	ENST00000478811	1	splice_region	c.373+3	e4+6	tier3	167	1	0.006	191	110	0.365
346313	14	7042537	7042537	G	A	SNP	SMOC1	ENST00000361956	1	splice_region	c.378+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	92397237	92397236	-	GT	INS	SNORD14-7	ENST00000316445	-1	rna	c.159_160	p.G539L	tier1	25	0	0.000	34	14	0.292
346313	16	795001	795001	G	A	SNP	NAPFL	ENST00000316445	-1	5_prime_untranslated_region	c.159_160	NULL	tier1	30	0	0.000	67	41	0.380
346313	17	45684777	45684777	T	C	SNP	NPEP3	ENST00000405966	-1	intronic	c.3603	NULL	tier3	27	0	0.000	47	34	0.420
346313	18	35992717	35992717	T	C	SNP	NPEP3	ENST00000405966	-1	intronic	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	19	35992717	35992717	T	C	SNP	NPEP3	ENST00000405966	-1	5_prime_untranslated_region	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	19	35992717	35992717	T	C	SNP	NPEP3	ENST00000405966	-1	5_prime_untranslated_region	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	20	36332452	36332452	A	T	SNP	NPEP3	ENST00000405966	-1	5_prime_untranslated_region	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	20	36332452	36332452	A	T	SNP	NPEP3	ENST00000405966	-1	5_prime_untranslated_region	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	20	36332452	36332452	A	T	SNP	NPEP3	ENST00000405966	-1	5_prime_untranslated_region	c.1085+97	e9+67	tier3	86	0	0.000	104	61	0.370
346313	21	11039295	11039295	C	G	SNP	BAGE2	ENST00000470954	-1	missense	c.141	p.P181T	tier1	95	0	0.000	537	41	0.071
346313	21	11039295	11039295	C	G	SNP	BAGE2	ENST00000470954	-1	missense	c.141	p.P181T	tier1	95	0	0.000	537	41	0.071
346313	21	45744779	45744779	T	C	SNP	PKFL	ENST00000403390	-1	missense	c.1097	NULL	tier208	1	0	0.000	5435	378	0.065
346313	21	19037666	19037666	A	T	SNP	GP64	ENST00000479496	-1	missense	c.1097	p.I665S	tier1	85	1	0.000	61	31	0.333
346313	X	123164976	123164977	A	T	INS	STAC2	ENST00000479496	-1	5_prime_untranslated_region	c.19037686	e3+1	tier4	46	0	0.000	76	15	0.163
346313	X	123164976	123164977	A	T	INS	STAC2	ENST00000479496	-1	5_prime_untranslated_region	c.19037686	e3+1	tier4	46	0	0.000	76	15	0.163
346313	Y	2865460	2865460	C	T	SNP	TPTC9P4	ENST00000259599	-1	splice_site_intron	c.288+1_288+1	c3+1	tier1	293	0	0.000	142	477	0.771
350719	17	757768	757768	C	T	SNP	TP53	ENST00000269305	-1	intronic	c.713	NULL	tier3	84	0	0.000	1426	85	0.056
350719	18	15272098	15272098	C	T	SNP	BNP3P3	ENST00000677336	-1	5_prime_flanking_region	c.24102	p.C238Y	tier3	72	2	0.027	367	71	0.162
350719	19	46214702	46214702	C	A	SNP	FBXO46	ENST00000317683	-1	3_prime_untranslated_region	c.24102	NULL	tier3	87	1	0.011	214	28	0.114
353053	1	20881411	20881412	-	A	INS	FAM43B	ENST0000032947	-1	3_prime_untranslated_region	c.955	NULL	tier3	45	0	0.000	87	18	0.171
353053	1	20881993	20881993	-	A	INS	DOOST	ENST00000375048	-1	missense	c.542	p.L181P	tier3	45	0	0.000	75	16	0.176
353053	1	196887311	196887311	G	C	SNP	CHFR4	ENST00000367146	-1	intronic	c.1538+29	e10+29	tier2	68	0	0.000	83	11	0.117
353053	1	205801794	205801794	G	A	SNP	PM2D1	ENST00000367136	-1	missense	c.1217	p.A406V	tier1	165	0	0.000	256	29	0.102
353053	5	14713807	14713807	G	A	SNP	ANKK	ENST00000344441	-1	missense	c.4903	p.M1635V	tier3	62	0	0.000	98	19	0.162
353053	5	139094357	139094357	G	A	SNP	MA3	ENST00000284268	-1	intronic	c.1142+31	e10+31	tier3	56	0	0.000	97	20	0.171
353053	9	135073547	135073547	C	T	SNP	NTNG2	ENST00000541515	-1	nonsense	c.934	p.R1312*	tier1	449	0	0.000	741	63	0.078
353053	11	75141266	75141266	C	T	SNP	KHLH35	ENST00000360670	1	silent	c.408	p.D136	tier1	88	0	0.000	111	11	0.090
353053	12	102291646	102291646	C	T	SNP	DLH1	ENST00000339798	-1	missense	c.137	p.G137S	tier1	6	0	0.000	5	12	0.706
353053	12	102291646	102291646	C	T	SNP	PARBP	ENST00000258534	-1	missense	c.137	p.T46M	tier1	85	0	0.000	145	15	0.094
353053	12	102576308	102576308	T	-	DEL	IPPO5	ENST00000358383	1	intronic	c.1185+19	e8+19	tier3	63	1	0.018	112	23	0.170
353053	13	98634738	98634738	T	-	DEL	ATP11A	ENST00000261574	-1	intronic	c.145+19	e3+19	tier3	53	1	0.016	95	18	0.159
353053	13	113536580	113536580	G	A	SNP	GOLGA6L2	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	DUX2	ENST00000388039	-1	splice_region	c.214+3	e3+3	tier3	149	0	0.000	277	32	0.104
353053	15	45392025	45392025	G	A	SNP	ENSO00000226145	ENST00000388039	-1	nonsense	c.3290	p.R1084*	tier1	65	0	0.000	102	16	0.136
353053	17	16723414	16723414	C	T	SNP	RUNX1	ENST00000417510	-1	splice_site	c.1264	NULL	tier1	190	0	0.000	221	20	0.083
353053	21	36164611	36164611	T	C	SNP	TCEAL4	ENST00000300305	-1	nonsense	c.1264	NULL	tier1	706	1	0.001	833	106	0.113
353053	X	102840637	102840637	C	T	SNP	PHF6	ENST00000394292	-1	missense	c.268	p.W90G	tier1	76	2	0.026	88	19	0.176
353053	X	133547986	133547986	G	A	SNP	UBAP2L	ENST00000394292	-1	missense	c.722	p.Y241C	tier3	392	0	0.000	601	84	0.123
388402	1	154215669	154215669	G	A	SNP	ESRRG	ENST00000446173	-1	missense	c.154215669	e5+13846	tier3	79	1	0.013	228	59	0.206
388402	2	11702607	11702607	A	G	SNP	GREB1	ENST00000408911	-1	intronic	c.602+13846	e5+13846	tier2	118	0	0.000	281	62	0.181
388402	2	20460043	20460043	C	T	SNP	TTN	ENST00000234142	-1	missense	c.176	p.N59S	tier1	27	0	0.000	206	62	0.231
388402	2	179596201	179596201	T	C	SNP	PUM2	ENST00000361078	-1	intronic	c.2355+55	e14+55	tier2	51	1	0.019	86	20	0.189
388402	3	38418449	38418449	T	A	SNP	XYLB	ENST00000342992	-1	silent	c.13560	p.L4520	tier1	79	0	0.000	213	36	0.145
388402	3	2241553	2241553	C	T	SNP	SETD7	ENST00000207870	-1	intronic	c.1161	p.I887	tier3	97	2	0.018	189	47	0.198
388402	4	140432050	140432050	T	C	SNP	GRIT25	ENST00000334304	-1	3_prime_untranslated_region	c.1809+956	e12+956	tier3	126	0	0.000	191	41	0.177
388402	5	37239010	37239010	A	T	SNP	TLL1	ENST00000274031	-1	intronic	c.767	NULL	tier3	126	0	0.000	191	41	0.177
388402	5	115319116	115319116	G	A	SNP	ADRP	ENST00000240061	-1	frame_shift_del	c.362+96	e4+96	tier3	168	0	0.000	184	48	0.206
388402	7	44105132	44105132	G	T	SNP	PCAM2	ENST00000425232	-1	missense	c.887	p.S246S	tier1	124	1	0.008	351	62	0.189
388402	7	7873756	7873756	G	A	SNP	PCAM2	ENST00000517374	-1	missense	c.152	p.S51N	tier1	22	0	0.000	169	57	0.252
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PCAM2	ENST00000425232	-1	missense	c.4	NULL	tier3	8	0	0.000	67	60	0.544
388402	9	7873756	7873756	G	A	SNP	PC												

481688	1	247094597	247094597	T	C	G	-	C	SNP	SNP	AHCTF1	ENST000000366508	-1	5_prime_untranslated_region	c-59	NULL	tier2	34	0	0.000	37	9	0.196
481688	2	1457512	1457512	C	G	-	DEL	SNP	DEL	TPO	ENST000000239066	1	1	missense	c.529	p.L177V	tier1	111	0	0.000	119	36	0.232
481688	2	61009939	61009939	T	C	-	SNP	SNP	SNP	PAPOLG	ENST000000238714	1	1	intronic	c.1112-34	e12-34	tier3	68	0	0.000	131	17	0.115
481688	2	98653198	98653198	A	G	-	INS	SNP	SNP	VWA3B	ENST000000485216	1	1	rna	NULL	NULL	tier1	69	2	0.028	81	31	0.277
481688	4	15070967	15070968	-	A	-	INS	SNP	SNP	CFEB2	ENST000000538197	-1	3_prime_untranslated_region	missense	c.2963	NULL	tier2	104	2	0.019	179	57	0.242
481688	4	95223388	95223388	A	G	-	SNP	SNP	SNP	HPGD5	ENST000000295256	-1	missense	c.344	p.M101T	tier1	94	1	0.011	146	46	0.240	
481688	5	40959580	40959580	T	A	-	SNP	SNP	SNP	CT	ENST000000313164	-1	missense	c.1519	c.1519	tier1	92	4	0.042	130	47	0.266	
481688	5	4182663	4182663	A	T	-	DEL	SNP	SNP	OCRT1	ENST00000196371	-1	intronic	c.75-11	e2-11	tier4	93	0	0.000	135	19	0.123	
481688	6	325150	325150	A	-	C	-	SNP	SNP	DUSP22	ENST00000419235	-1	5_prime_untranslated_region	missense	c.139-9964	e4-9964	tier3	459	16	0.034	630	64	0.117
481688	6	31760727	31760727	G	A	-	SNP	SNP	SNP	VRB	ENST00000495010	-1	missense	c.31760727	NULL	tier3	96	2	0.020	117	46	0.281	
481688	6	135513462	135513462	G	A	-	SNP	SNP	SNP	BMFER	ENST000000341911	-1	missense	c.546	p.N183S	tier1	122	0	0.000	131	47	0.264	
481688	7	81933304	81933304	T	C	-	SNP	SNP	SNP	ENKZF1	ENST000000257161	-1	missense	c.1237	p.R413C	tier1	736	0	0.000	1026	53	0.049	
481688	7	10655973	10655973	T	G	-	SNP	SNP	SNP	UCR2	ENST000000356233	-1	intronic	c.1626	e34-66	tier3	91	0	0.000	46	26	0.361	
481688	7	14655973	14655973	T	G	-	SNP	SNP	SNP	UCR2	ENST000000356233	-1	missense	c.1626	p.Y101D	tier1	263	1	0.004	819	65	0.165	
481688	7	11713965	11713965	T	A	-	SNP	SNP	SNP	AKNA	ENST00000037586	-1	missense	c.4202	e10-44	tier1	400	0	0.000	486	22	0.185	
481688	9	11713965	11713965	T	A	-	SNP	SNP	SNP	AKNA	ENST00000037586	-1	missense	c.4202	p.R377H	tier1	350	0	0.000	726	46	0.332	
481688	10	28933807	28933807	T	C	-	SNP	SNP	SNP	FAM16A	ENST0000004522781	-1	3_prime_untranslated_region	missense	c.2234	NULL	tier3	147	0	0.000	214	75	0.259
481688	10	133761131	133761131	G	A	-	SNP	SNP	SNP	PRP22D	ENST00000455566	1	missense	c.825	p.M275I	tier1	148	1	0.007	213	57	0.211	
481688	11	71903432	71903432	G	A	-	SNP	SNP	SNP	FOLR1	ENST00000031293	1	intronic	c.169-47	e1-47	tier3	63	0	0.000	70	26	0.271	
481688	12	21608977	21608977	G	A	-	SNP	SNP	SNP	PYRXD1	ENST00000240651	-1	missense	c.698	p.S233I	tier1	91	2	0.022	141	54	0.277	
481688	12	57929244	57929245	AC	-	-	DEL	SNP	SNP	DCX2	ENST000000551142	-1	5_prime_untranslated_region	missense	c.57929244	NULL	tier3	91	0	0.000	137	17	0.110
481688	13	11359210	11359210	C	A	-	SNP	SNP	SNP	DCX2	ENST000000315596	-1	nonense	NULL	p.R34*	tier1	109	0	0.000	122	26	0.176	
481688	13	33223009	33223009	C	A	-	SNP	SNP	SNP	POSSB	ENST00000031125	-1	splice_region_3ps	c.100	p.R34*	tier1	77	1	0.013	130	64	0.327	
481688	15	5095475	5095476	-	A	-	INS	SNP	SNP	TEX9	ENST000000346246	-1	missense	c.848	e26-3	tier3	69	0	0.000	144	16	0.100	
481688	15	56704519	56704519	G	A	-	DEL	SNP	SNP	MAK43	ENST000000352903	-1	3_prime_untranslated_region	missense	c.1759	p.R283K	tier1	167	0	0.000	216	98	0.312
481688	16	30456662	30456662	AC	-	-	DEL	SNP	SNP	SEPH2	ENST000000542752	-1	missense	c.216	NULL	tier4	53	0	0.000	67	11	0.141	
481688	17	37425012	37425012	C	T	C	SNP	SNP	SNP	PRPF8	ENST000000304992	-1	silent	c.5624	p.H1875R	tier1	821	6	0.009	997	410	0.290	
481688	17	37425012	37425012	C	T	C	SNP	SNP	SNP	PRPF8	ENST000000304992	-1	intronic	c.933-68	e12-68	tier3	63	2	0.031	86	46	0.349	
481688	19	9067438	9067438	C	C	-	SNP	SNP	SNP	FBLX20	ENST000000265671	-1	intronic	c.2208-44	e18-44	tier3	41	0	0.000	31	22	0.400	
481688	19	15219913	15219913	C	C	-	SNP	SNP	SNP	MUC16	ENST000000397910	-1	missense	c.2008	p.V670I	tier1	906	9	0.010	1848	610	0.247	
481688	19	2528203	2528203	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000342784	-1	silent	c.135	p.P45	tier1	38	1	0.026	30	28	0.483	
481688	20	2528203	2528203	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000342784	-1	intronic	c.555-22	e5-22	tier3	100	2	0.020	167	26	0.135	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019	165	28	0.144	
481688	20	2528206	2528206	C	T	-	DEL	SNP	SNP	YDFE1	ENST000000358864	1	intronic	c.555-22	e5-22	tier3	103	2	0.019</				

489196	8	87519260	87519260	T	C	SNP	RMDW1	ENST000000408452	-1	missense	c.211	p.V1V	tier1	169	0	0.000	275	99	0.264
489196	8	126011647	126011647	T	C	SNP	NR6A1	ENST000000265996	-1	missense	c.2	p.M1T	tier3	79	0	0.000	80	28	0.259
489196	9	127300323	127300323	T	C	SNP	NR6A1	ENST000000487099	-1	intronic	c.824+48	e6+48	tier3	59	2	0.033	38	23	0.377
489196	10	23326305	23326305	G	A	SNP	AFMC3	ENST000000298032	-1	missense	c.2516	p.G539E	tier1	139	0	0.000	98	49	0.333
489196	10	79797037	79797037	G	A	SNP	RP524	ENST000000406932	1	missense	c.365	p.K122R	tier1	68	0	0.000	73	27	0.270
489196	11	20676288	20676288	G	A	SNP	SLC6A5	ENST000000525748	1	silent	c.2288	p.P756	tier1	128	0	0.000	118	47	0.285
489196	11	4600551	4600551	T	A	SNP	DKK2	ENST000000454345	-1	missense	c.2993	p.L398Q	tier1	19	0	0.000	24	18	0.429
489196	11	48454279	48454279	G	A	SNP	ORC4L0P	ENST000000434991	-1	5_prime_untranslated_region	c.4845+279	NULL	tier3	238	0	0.000	205	87	0.298
489196	11	96000330	96000330	C	T	SNP	OR572	ENST000000313264	-1	missense	c.332	p.C111Y	tier3	33	0	0.000	72	29	0.287
489196	12	907449	907449	C	T	SNP	ZKX1L	ENST000000295998	-1	intronic	c.2764+22	e22+22	tier3	176	0	0.000	162	56	0.257
489196	12	52946663	52946663	C	T	SNP	ATRT1	ENST000000267119	-1	missense	c.199	p.G67R	tier3	225	1	0.004	202	82	0.289
489196	12	9468621	9468621	C	T	SNP	MEZ	ENST000000312156	-1	missense	c.659	p.G320E	tier1	76	0	0.000	87	28	0.250
489196	12	9510725	9510725	A	G	SNP	BLCC1S1	ENST000000496225	-1	missense	c.154	p.R22G	tier1	116	0	0.000	107	42	0.282
489196	12	7661235	7661235	A	G	SNP	NR1L1	ENST000000451324	-1	5_prime_untranslated_region	c.7661+235	NULL	tier3	16	0	0.000	35	19	0.540
489196	13	62909094	62909094	T	A	SNP	TCF7L1	ENST000000451324	-1	intronic	c.52+36	NULL	tier3	3	0	0.000	10	2	0.390
489196	13	5293939	5293939	C	G	SNP	LOC10193678	ENST000000451298	-1	missense	c.52+36	NULL	tier3	305	3	0.010	435	26	0.166
489196	14	96870661	96870661	G	A	SNP	DNAH1	ENST000000351081	-1	intronic	c.1+1575	e6+1575	tier3	68	0	0.000	121	37	0.234
489196	14	16944697	16944697	G	A	SNP	LOC10193678	ENST000000351081	-1	intronic	c.1+1575	e6+1575	tier3	68	0	0.000	121	37	0.234
489196	15	20457242	20457242	C	T	SNP	LOC10193678	ENST000000351081	-1	intronic	c.1+1575	e6+1575	tier3	68	0	0.000	121	37	0.234
489196	15	66191080	66191080	T	A	SNP	ENSG00000238628	ENST000000351081	-1	5_prime_untranslated_region	c.20457+242	NULL	tier3	615	3	0.005	691	51	0.069
489196	16	66191080	66191080	T	A	SNP	MEGF11	ENST000000409699	-1	missense	c.2960	p.N887I	tier3	615	3	0.005	691	51	0.069
489196	16	66956068	66956068	G	A	SNP	RRAD	ENST000000334933	-1	intronic	c.346+82	e4+82	tier3	189	3	0.016	139	55	0.284
489196	17	976071	976071	G	A	SNP	ABR	ENST000000299759	-1	missense	c.838	p.R280C	tier1	66	1	0.015	60	28	0.318
489196	17	43185926	43185926	G	A	SNP	MTT1	ENST000000302538	-1	intronic	c.754+77	e5+77	tier3	81	0	0.000	71	27	0.273
489196	17	62892220	62892220	G	A	SNP	LRRRC37A3	ENST000000319651	-1	intronic	c.754+77	e5+77	tier3	81	0	0.000	71	27	0.273
489196	18	28971008	28971008	G	C	SNP	DSG4	ENST000000359147	-1	missense	c.2919	p.P386A	tier3	146	0	0.000	131	53	0.288
489196	19	40589158	40589158	C	T	SNP	ZNF780A	ENST000000359147	-1	intronic	c.156	e7+33	tier3	374	0	0.000	512	109	0.175
489196	19	43920107	43920107	C	T	SNP	TEX101	ENST000000253435	-1	intronic	c.885+33	e7+33	tier3	208	1	0.005	178	87	0.327
489196	20	9496180	9496180	G	T	SNP	LAMP5	ENST000000246070	1	silent	c.10+14	p.L30	tier3	77	0	0.000	40	22	0.355
489196	20	29623299	29623299	G	T	SNP	TRPM2	ENST000000278882	-1	missense	c.145	p.V49L	tier3	90	1	0.011	98	86	0.467
489196	20	31073554	31073555	-	G	SNP	XIST	ENST000000300482	-1	3_prime_untranslated_region	c.66+45	e1+45	tier3	691	9	0.013	1509	65	0.041
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000021961	-1	intronic	c.19	p.G45	tier3	76	0	0.000	74	36	0.327
489196	22	46677825	46677825	G	C	SNP	LAMP5	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	46677825	46677825	G	C	SNP	FRG1B	ENST000000246070	1	intronic	c.10+14	e5+210	tier3	50	0	0.000	40	19	0.322
489196	22	466																	

[illegible]

933226	9	68728891	68728891	C	T	G	SNP	ENSG00000202789	ENST00000427066	3_prime_untranslated_region	c.68728891	NULL	NULL	72	1	0.014	477	62	0.115
933226	10	93976302	93976302	A	G	SNP	SNP	933226	10	93976302	93976302	933226	10	93976302	93976302	933226	10	93976302	93976302
933226	11	62037379	62037379	A	G	SNP	SNP	933226	11	62037379	62037379	933226	11	62037379	62037379	933226	11	62037379	62037379
933226	12	83497858	83497858	C	T	SNP	SNP	933226	12	83497858	83497858	933226	12	83497858	83497858	933226	12	83497858	83497858
933226	13	95307704	95307704	G	A	SNP	SNP	933226	13	95307704	95307704	933226	13	95307704	95307704	933226	13	95307704	95307704
933226	14	10851548	10851548	T	A	SNP	SNP	933226	14	10851548	10851548	933226	14	10851548	10851548	933226	14	10851548	10851548
933226	15	75151331	75151331	G	A	SNP	SNP	933226	15	75151331	75151331	933226	15	75151331	75151331	933226	15	75151331	75151331
933226	16	10359220	10359220	G	A	SNP	SNP	933226	16	10359220	10359220	933226	16	10359220	10359220	933226	16	10359220	10359220
933226	17	40569944	40569944	G	A	SNP	SNP	933226	17	40569944	40569944	933226	17	40569944	40569944	933226	17	40569944	40569944
933226	18	12237263	12237263	T	A	SNP	SNP	933226	18	12237263	12237263	933226	18	12237263	12237263	933226	18	12237263	12237263
933226	19	75764662	75764662	A	G	SNP	SNP	933226	19	75764662	75764662	933226	19	75764662	75764662	933226	19	75764662	75764662
933226	20	16834028	16834028	G	A	SNP	SNP	933226	20	16834028	16834028	933226	20	16834028	16834028	933226	20	16834028	16834028
933226	21	19643645	19643645	G	A	SNP	SNP	933226	21	19643645	19643645	933226	21	19643645	19643645	933226	21	19643645	19643645
933226	22	4231913	4231913	G	A	SNP	SNP	933226	22	4231913	4231913	933226	22	4231913	4231913	933226	22	4231913	4231913
933226	23	1011071	1011071	C	T	SNP	SNP	933226	23	1011071	1011071	933226	23	1011071	1011071	933226	23	1011071	1011071
933226	24	1754673	1754673	C	T	SNP	SNP	933226	24	1754673	1754673	933226	24	1754673	1754673	933226	24	1754673	1754673
933226	25	49316512	49316512	T	C	SNP	SNP	933226	25	49316512	49316512	933226	25	49316512	49316512	933226	25	49316512	49316512
933226	26	13269233	13269233	C	T	SNP	SNP	933226	26	13269233	13269233	933226	26	13269233	13269233	933226	26	13269233	13269233
933226	27	80499501	80499501	G	A	SNP	SNP	933226	27	80499501	80499501	933226	27	80499501	80499501	933226	27	80499501	80499501
933226	28	82715089	82715089	G	A	SNP	SNP	933226	28	82715089	82715089	933226	28	82715089	82715089	933226	28	82715089	82715089
933226	29	11098586	11098586	G	A	SNP	SNP	933226	29	11098586	11098586	933226	29	11098586	11098586	933226	29	11098586	11098586
933226	30	34523934	34523934	T	C	SNP	SNP	933226	30	34523934	34523934	933226	30	34523934	34523934	933226	30	34523934	34523934
933226	31	16414219	16414219	G	A	SNP	SNP	933226	31	16414219	16414219	933226	31	16414219	16414219	933226	31	16414219	16414219
933226	32	42381976	42381976	G	A	SNP	SNP	933226	32	42381976	42381976	933226	32	42381976	42381976	933226	32	42381976	42381976
933226	33	5821895	5821895	G	A	SNP	SNP	933226	33	5821895	5821895	933226	33	5821895	5821895	933226	33	5821895	5821895
933226	34	43626915	43626915	G	A	SNP	SNP	933226	34	43626915	43626915	933226	34	43626915	43626915	933226	34	43626915	43626915
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933226	36	30423302	30423302	C	T	SNP	SNP	933226	36	30423302	30423302	933226	36	30423302	30423302	933226	36	30423302	30423302
933226	37	90552429	90552429	G	A	SNP	SNP	933226	37	90552429	90552429	933226	37	90552429	90552429	933226	37	90552429	90552429
933226	38	43453288	43453288	G	A	SNP	SNP	933226	38	43453288	43453288	933226	38	43453288	43453288	933226	38	43453288	43453288
933226	39	97483175	97483175	C	G	SNP	SNP	933226	39	97483175	97483175	933226	39	97483175	97483175	933226	39	97483175	97483175
933226	40	130145131	130145131	G	A	SNP	SNP	933226	40	130145131	130145131	933226	40	130145131	130145131	933226	40	130145131	130145131
933226	41	95890360	95890360	G	A	SNP	SNP	933226	41	95890360	95890360	933226	41	95890360	95890360	933226	41	95890360	95890360
933226	42	44638032	44638032	C	T	SNP	SNP	933226	42	44638032	44638032	933226	42	44638032	44638032	933226	42	44638032	44638032
933226	43	14048251	14048251	G	A	SNP	SNP	933226	43	14048251	14048251	933226	43	14048251	14048251	933226	43	14048251	14048251
933226	44	33144473	33144473	G	A	SNP	SNP	933226	44	33144473	33144473	933226	44	33144473	33144473	933226	44	33144473	33144473
933226	45	4327615	4327615	G	A	SNP	SNP	933226	45	4327615	4327615	933226	45	4327615	4327615	933226	45	4327615	4327615
933226	46	14224269	14224269	G	A	SNP	SNP	933226	46	14224269	14224269	933226	46	14224269	14224269	933226	46	14224269	14224269
933226	47	21924261	21924261	A	C	SNP	SNP	933226	47	21924261	21924261	933226	47	21924261	21924261	933226	47	21924261	21924261
933226	48	102504720	102504720	C	G	SNP	SNP	933226	48	102504720	102504720	933226	48	102504720	102504720	933226	48	102504720	102504720
933226	49	27268422	27268422	G	A	SNP	SNP	933226	49	27268422	27268422	933226	49	27268422	27268422	933226	49	27268422	27268422
933226	50	32414262	32414262	C	G	SNP	SNP	933226	50	32414262	32414262	933226	50	32414262	32414262	933226	50	32414262	32414262
933226	51	32417915	32417915	-	-	GA	GA	933226	51	32417915	32417915	933226	51	32417915	32417915	933226	51	32417915	32417915
933226	52	6697549	6697549	-	-	T	T	933226	52	6697549	6697549	933226	52	6697549	6697549	933226	52	6697549	6697549
933226	53	96530312	96530312	A	-	DEL	DEL	933226	53	96530312	96530312	933226	53	96530312	96530312	933226	53	96530312	96530312
933226	54	112885189	112885189	G	A	SNP	SNP	933226	54	112885189	112885189	933226	54	112885189	112885189	933226	54	112885189	112885189
933226	55	33017732	33017732	C	T	SNP	SNP	933226	55	33017732	33017732	933226	55	33017732	33017732	933226	55	33017732	33017732
933226	56	50115190	50115190	C	T	SNP	SNP	933226	56	50115190	50115190	933226	56	50115190	50115190	933226	56	50115190	50115190
933226	57	52427942	52427942	C	T	SNP	SNP	933226	57	52427942	52427942	933226	57	52427942	52427942	933226	57	52427942	52427942
933226	58	69386616	69386616	T	A	SNP	SNP	933226	58	69386616	69386616	933226	58	69386616	69386616	933226	58	69386616	69386616
933226	59	11341929	11341929	G	A	SNP	SNP	933226	59	11341929	11341929	933226	59	11341929	11341929	933226	59	11341929	11341929
933226	60	42635306	42635306	G	A	SNP	SNP	933226	60	42635306	42635306	933226	60	42635306	42635306	933226	60	42635306	42635306
933226	61	43634347	43634347	A	C	SNP	SNP	933226	61	43634347	43634347	933226	61	43634347	43634347	933226	61	43634347	43634347
933226	62	7864900	7864900	A	C	SNP	SNP	933226	62	7864900	7864900	933226	62	7864900	7864900	933226	62	7864900	7864900
933226	63	10812636	10812636	T	C	SNP	SNP	933226	63	10812636	10812636	933226	63	10812636	10812636	933226	63	10812636	10812636
933226	64	66847816	66847816	T	C	SNP	SNP	933226	64	66847816	66847816	933226	64	66847816	66847816	933226	64	66847816	66847816
933226	65	20710847	20710847	G	A	SNP	SNP	933226	65	20710847	20710847	933226	65	20710847	20710847	933226	65	20710847	20710847
933226	66	22842205	22842205	G	A	SNP	SNP	933226	66	22842205	22842205	933226	66	22842205	22842205	933226	66	22842205	22842205
933226	67	46839272	46839272	T	A	SNP	SNP	933226	67	46839272	46839272	933226	67	46839272	46839272	933226	67	46839272	46839272
933226	68	11881871	11881871	A	-	DEL	DEL	933226	68	11881871	11881871	933226	68	11881871	11881871	933226	68	11881871	11881871
933226	69	49721606	49721606	G	A	SNP	SNP	933226	69	49721606	49721606	933226	69</						

991140	19	44680481	44680481	G	T	SNP	ZNF226	ENST0000037433	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	ENST0000046788	1	rna	NULL	NULL	tier1	20	0	0.000	31	12	0.279
991140	21	41550865	41550865	G	A	SNP	DSCAM	ENST0000040454	-1	missense	c.2936	p.A979V	tier1	469	0	0.000	876	283	0.244

All genome coordinates use NCBI Build 37.
 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 22:368(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 Change	Tier	Total Normal	Normal Ref	Normal Var	Initial Total	Initial Ref	Initial Var	Pre Total	Pre Ref	Pre Var	D30 Total	D30 Ref	D30 Var	D30 Count	D30 VAF	D100 Total	D100 Ref	D100 Var	D100 Count	D100 VAF				
130611	1	53527545	53547545	C	T	PDYN	intronic	c.1806-108	G10-L08	ter3	8892	8895	8897	5	0.006	27671	3272	2335	923	0.288	21120	2119	1473	622	0.037	35709	4411	4405	4	0.000			
130611	1	53547545	53547545	G	A	PDYN	noncoding			ter3	8892	8895	8897	5	0.006	27671	3272	2335	923	0.288	21120	2119	1473	622	0.037	35709	4411	4405	4	0.000			
130611	1	53547545	53547545	A	G	PDYN	noncoding			ter3	8892	8895	8897	5	0.006	27671	3272	2335	923	0.288	21120	2119	1473	622	0.037	35709	4411	4405	4	0.000			
611	3	64643370	64644370	G	A	ADAMTS19	3_prime	c.3149-819	3_prime	ter1	3035	3035	3035	0	0.000	3968	649	567	7	0.120	6438	698	79	107	0.010	8990	1366	1364	0	0.000			
611	3	64643370	64644370	G	A	ADAMTS19	3_prime	c.3149-819	3_prime	ter1	3035	3035	3035	0	0.000	3968	649	567	7	0.120	6438	698	79	107	0.010	8990	1366	1364	0	0.000			
611	3	130720537	130720537	T	A	FAT2	3_prime	c.743	3_prime	ter1	2188	2188	2188	0	0.004	32719	4279	2970	1289	0.303	24310	2850	2007	820	0.042	756	93	0.000	530	78	77	0	0.000
611	3	130720537	130720537	T	A	FAT2	3_prime	c.743	3_prime	ter1	2188	2188	2188	0	0.004	32719	4279	2970	1289	0.303	24310	2850	2007	820	0.042	756	93	0.000	530	78	77	0	0.000
611	4	187540539	187540539	C	T	ATP1A1	missense	c.7201	p.E2401K	ter1	2384	2384	2384	0	0.004	18565	2550	1805	784	0.288	13574	1591	1098	483	0.036	3106	3993	3991	0	0.000			
611	4	187540539	187540539	C	T	ATP1A1	missense	c.7201	p.E2401K	ter1	2384	2384	2384	0	0.004	18565	2550	1805	784	0.288	13574	1591	1098	483	0.036	3106	3993	3991	0	0.000			
611	4	187540539	187540539	C	T	ATP1A1	missense	c.7201	p.E2401K	ter1	2384	2384	2384	0	0.004	18565	2550	1805	784	0.288	13574	1591	1098	483	0.036	3106	3993	3991	0	0.000			
611	7	43280486	43280486	G	A	ITIK1	missense	c.4833	p.L135I	ter1	3584	3584	3584	0	0.006	3507	1862	1682	1814	0.295	14076	1814	1285	520	0.088	19550	2486	2476	0	0.000			
611	7	43280486	43280486	G	A	ITIK1	missense	c.4833	p.L135I	ter1	3584	3584	3584	0	0.006	3507	1862	1682	1814	0.295	14076	1814	1285	520	0.088	19550	2486	2476	0	0.000			
611	7	10054983	10054983	C	T	LOC101931514	missense	c.664	p.S155N	ter1	12274	12274	12274	0	0.002	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	7	10054983	10054983	C	T	LOC101931514	missense	c.664	p.S155N	ter1	12274	12274	12274	0	0.002	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662	0	0.000			
611	8	17945478	17945478	C	T	LOC101929066	missense			ter1	12674	12674	12674	0	0.005	14429	1813	1389	602	0.336	1811	1654	1141	505	0.307	28000	3697	3662					

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Normal			Initial			Pre			D30			D100																
										Normal	Total	Ref	Normal	Total	Ref	Initial	Total	Ref	Pre	Total	Ref	Pre	Total	Ref	D100	Total	Ref	D100	Total	Ref								
145994	X	18845593	18845595	G	A	PRF1	missense	c.1352	p.N631S	10300	3459	2410	41	0.0002	127114	1690	93	1.596	946	25257	3192	1798	1418	0.445	4588683	2354	2354	0	0.0002	140255	14015	13687	306	0.022	0	NA	0	0.000
147444	X	34164429	34164429	G	A	CMO2	missense	c.3849	p.S1238R	10300	1129	1128	0	0.000	16483	2413	1916	485	0.205	6817	940	500	354	0.375	4508683	2354	2354	0	0.000	140255	14015	13687	306	0.022	0	NA	0	0.000
147444	X	38262323	38262323	G	A	MANEAL	intronic	c.61-93	trp3	2105	275	275	0	0.000	7229	1513	1130	379	0.251	462	97	63	34	0.351	4264	811	890	0	0.000	1654	1591	714	0	0.000	0	0.000	0	0.000
147444	X	89480937	89480937	G	A	GP3	intronic	c.138-43	e+33	trp3	649	647	2	0.003	11614	1649	1280	359	0.219	492	97	1155	783	363	0.317	13756	1811	1803	0	0.000	1654	1591	714	0	0.000	0	0.000	
147444	X	163306613	163306613	C	T	MU2	missense	c.410	p.T1377M	10300	301	301	0	0.000	4347	427	427	145	0.254	5278	333	411	22	0.000	6979	865	864	1	0.000	1654	1591	714	0	0.000	0	0.000		
147444	X	226061860	226061860	C	T	TM6A63A	intronic	c.266-28	e+28	trp3	1639	2317	2312	5	0.002	29734	3693	2795	881	0.246	1566	2217	1412	799	0.361	3084	425	424	3	0.001	41701	588	5975	2	0.000	0	0.000	
147444	X	42119915	42119915	G	A	LOC-388942	splice_site	NULL	NULL	15872	1949	1949	0	0.000	3323	198	141	54	0.277	3977	1925	1192	738	0.379	29304	4375	4363	1	0.000	43219	6097	6090	1	0.000	0	0.000		
147444	X	42936013	42936013	G	T	MTA3	missense	c.1303-1	e+1-1	trp3	5884	0	0	0.000	1321	196	141	54	0.277	3977	1925	1192	738	0.379	29304	4375	4363	1	0.000	43219	6097	6090	1	0.000	0	0.000		
147444	X	128262356	128262356	C	G	W51	intronic	c.1123	p.M375V	10300	1129	1128	0	0.000	5088	1002	775	218	0.220	1141	1082	125	63	0.335	3646	695	694	0	0.000	2270	377	377	0	0.000	0	0.000		
147444	X	216972458	216972458	C	G	ARC5	intronic	c.1+37	e+37	trp3	1332	1330	1329	0	0.000	2246	3716	2785	915	0.247	7246	1084	625	424	0.394	18493	2929	2923	1	0.000	24099	3335	3330	0	0.000	0	0.000	
147444	X	109751543	109751543	C	T	DMF1	intronic	c.168	p.L108R	10300	168	165	3	0.000	1653	1317	1167	362	0.210	1533	1644	1456	79	0.238	27304	3110	3110	0	0.000	39234	5007	5002	0	0.000	0	0.000		
147444	X	109751543	109751543	C	T	DMF1	splice_site	NULL	NULL	1688	1651	1651	0	0.000	1653	1317	1167	362	0.210																			

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[illegible]

47457 9 103339628 103339628 G

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Ref Count	Normal Var Count	Normal VAF	Initial Total Count	Initial Ref Count	Initial Var Count	Initial VAF	Pre Total Count	Pre Ref Count	Pre Var Count	Pre VAF	D30 Total Count	D30 Ref Count	D30 Var Count	D30 VAF	D100 Total Count	D100 Ref Count	D100 Var Count	D100 VAF			
147457	12	132021344	132021344	G	A	HC63	5_prime_untranslated_region	c-60	NUL	ter1	2603	2953	2938	13	0.000	911	231	168	0.3	NA	NA	NA	NA	NA	1932	518	512	5	0.000	NA	NA	NA	
147457	12	124175149	124175149	G	T	TCN2	missense	c-91	p.R231I	ter1	6003	2953	2938	13	0.000	911	2690	2187	693	0.273	NA	NA	NA	NA	NA	1932	518	512	5	0.000	NA	NA	NA
147457	12	124175149	124175149	G	T	TCN2	missense	c-91	p.R231I	ter1	6003	2953	2938	13	0.000	911	2690	2187	693	0.273	NA	NA	NA	NA	NA	1932	518	512	5	0.000	NA	NA	NA
147457	12	124202048	124202048	G	T	CD333	missense	c-533	p.A588G	ter1	3719	3725	3425	44	0.010	3936	3937	3719	0.111	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	124202048	124202048	G	T	CD333	missense	c-533	p.A588G	ter1	3719	3725	3425	44	0.010	3936	3937	3719	0.111	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	21502125	21502125	G	A	LA73	silent	c-1794	p.S598R	ter1	42168	6122	6094	62	0.010	53136	5267	3828	0.147	0.270	NA	NA	NA	21872	1173	1172	0	0.000	NA	NA	NA	NA	
147457	12	23328871	23328871	G	A	SACS	missense	c.1880	p.T627M	ter1	28547	3238	3203	35	0.011	55441	3717	2559	0.150	0.310	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	23328871	23328871	G	A	MIP6P	missense	c.1880	p.T627M	ter1	28547	3238	3203	35	0.011	55441	3717	2559	0.150	0.310	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	24410420	24410420	G	A	PRM2	missense	c.1612	p.R2783H	ter1	17991	2092	2070	16	0.006	53571	3379	2385	0.982	0.292	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	39450219	39450219	G	A	PRM2	missense	c.1612	p.R2783H	ter1	17991	2092	2070	16	0.006	53571	3379	2385	0.982	0.292	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	45807726	45807726	G	T	PT22	3_prime_untranslated_region	c-8342	NUL	ter1	10482	1435	1417	16	0.011	18555	2385	738	0.318	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	45807726	45807726	G	T	PT22	3_prime_untranslated_region	c-8342	NUL	ter1	10482	1435	1417	16	0.011	18555	2385	738	0.318	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	113328460	113328460	G	A	GAS2	missense	c-656	p.A215V	ter1	23587	3596	3489	19	0.005	39953	3377	2638	0.733	0.217	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	113328460	113328460	G	A	GAS2	missense	c-656	p.A215V	ter1	23587	3596	3489	19	0.005	39953	3377	2638	0.733	0.217	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	113328460	113328460	G	A	PCO2	silent	c-807	p.T659R	ter1	18347	2497	2466	28	0.011	22041	1469	1688	0.751	0.308	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	113328460	113328460	G	A	PCO2	silent	c-807	p.T659R	ter1	18347	2497	2466	28	0.011	22041	1469	1688	0.751	0.308	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	152152150	152152150	C	T	AHG6F40	missense	c.3730	p.R1244M	ter1	53336	6562	6516	44	0.007	33253	2855	2223	0.624	0.219	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	152152150	152152150	C	T	AHG6F40	missense	c.3730	p.R1244M	ter1	53336	6562	6516	44	0.007	33253	2855	2223	0.624	0.219	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	152152150	152152150	C	T	CHD8	missense	c.6028	p.E2010K	ter1	51044	5879	5834	42	0.007	52833	3891	3029	0.821	0.220	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	152152150	152152150	C	T	CHD8	missense	c.6028	p.E2010K	ter1	51044	5879	5834	42	0.007	52833	3891	3029	0.821	0.220	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	18201600	18201600	G	A	TTG6	missense	c.3869	p.R1230Q	ter1	13147	1634	1613	20	0.012	11439	1085	757	0.324	0.300	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	18201600	18201600	G	A	TTG6	missense	c.3869	p.R1230Q	ter1	13147	1634	1613	20	0.012	11439	1085	757	0.324	0.300	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	45848448	45848448	G	A	FANCA	missense	c.3341726	p.L42176I	ter1	6493	1025	1013	13	0.005	44678	1295	1053	0.334	0.289	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	45848448	45848448	G	A	FANCA	missense	c.3341726	p.L42176I	ter1	6493	1025	1013	13	0.005	44678	1295	1053	0.334	0.289	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333	3_prime_untranslated_region	c-1309-32	p.A321V	ter1	3908	447	441	6	0.013	5313	700	484	0.211	0.304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
147457	12	107713531	107713531	C	T	CD333																											

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count	Normal Ref Var	Initial Normal Count	Initial Unique Count	Initial Ref Var	Initial Total Count	Initial Unique Count	Pre Initial Total Count	Pre Initial Unique Count	Pre Ref Var	D30 Total Count	D30 Unique Count	D30 Ref Var	D30 Var	D30 Total Count	D30 Unique Count	D100 Total Count	D100 Unique Count	D100 Var	D100 Total Count	D100 Unique Count	D100 Var
147457	21	43847466	43847466	G	A	SLC27L1	c.1136-52	intronic	e13-52	ter3	78694	8566	8479	72	0.008	64098	4715	3720	981	0.209	NA	NA	NA	707573	2923	2911	4	0.000	NA	NA	NA	NA	NA
147457	21	46343688	46343688	G	A	FAM707A	c.229	missense	p.V771	ter3	18668	2091	16	0.008	29642	1827	1262	540	0.300	NA	NA	NA	NA	41468	241	236	4	0.017	NA	NA	NA	NA	NA
147457	21	13162635	13162635	G	T	L7R1H	c.802	missense	p.R802Q	ter1	33742	1710	91	0.009	4854	1639	144	493	0.286	NA	NA	NA	NA	42995	251	251	0	0.000	NA	NA	NA	NA	NA
147457	22	25193653	25193653	C	T	CEP350	c.107	missense	p.R107G	ter3	3500	3500	3500	35	0.009	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500	3500
147457	22	25598652	25598652	C	T	CPYH8	c.87	silent	p.Y29	ter1	26233	3444	3300	39	0.012	36699	3044	2710	851	0.282	NA	NA	NA	25321	1082	1067	7	0.007	NA	NA	NA	NA	NA
147457	22	37319436	37319436	C	T	CSF2RB	c.200-27	intronic	c.200-27	ter3	29488	3041	3023	14	0.005	29488	1542	1248	290	0.283	NA	NA	NA	130760	569	569	0	0.000	NA	NA	NA	NA	NA
147457	22	37319436	37319436	C	T	CSF2RB	c.1665K	missense	p.L665K	ter1	7072	1147	1135	10	0.009	12107	1278	1719	433	0.253	NA	NA	NA	18615	146	146	0	0.000	NA	NA	NA	NA	NA
147457	22	37892522	37892522	C	T	CD10	c.1993	missense	c.1993	ter3	32675	3739	3698	34	0.009	27225	1997	1519	474	0.238	NA	NA	NA	27521	1042	1040	0	0.000	NA	NA	NA	NA	NA
147457	22	38062929	38062929	C	A	PDPX	c.1051	missense	p.L1051L	ter3	4312	6003	6426	69	0.011	44160	4762	3774	1379	0.290	NA	NA	NA	120694	708	707	0	0.000	NA	NA	NA	NA	NA
147457	X	2406917	2406917	C	T	ZEB2	c.1854	missense	p.R1854H	ter1	4312	6003	6426	69	0.011	44160	4762	3774	1379	0.290	NA	NA	NA	120694	708	707	0	0.000	NA	NA	NA	NA	NA
147457	X	2406917	2406917	C	T	ZEB2	c.1854	missense	p.R1854H	ter1	4312	6003	6426	69	0.011	44160	4762	3774	1379	0.290	NA	NA	NA	120694	708	707	0	0.000	NA	NA	NA	NA	NA
147457	X	29976888	29976888	C	T	IL1RAPL1	c.1842	missense	p.E1842	ter1	45477	5734	5671	58	0.010	49174	4546	3206	1338	0.282	NA	NA	NA	120688	512	498	12	0.024	NA	NA	NA	NA	NA
147457	X	29976888	29976888	C	T	IL1RAPL1	c.1842	missense	p.E1842	ter1	45477	5734	5671	58	0.010	49174	4546	3206	1338	0.282	NA	NA	NA	120688	512	498	12	0.024	NA	NA	NA	NA	NA
147457	X	29976888	29976888	C	T	IL1RAPL1	c.1842	missense	p.E1842	ter1	45477	5734	5671	58	0.010	49174	4546	3206	1338	0.282	NA	NA	NA	120688	512	498	12	0.024	NA	NA	NA	NA	NA
147457	X	41530801	41530801	C	T	CASK	c.430-18	intronic	c.430-18	ter3	6687	1019	1036	16	0.016	9343	1184	822	360	0.303	NA	NA	NA	21137	139	139	0	0.000	NA	NA	NA	NA	NA
147457	X	49032048	49032048	C	T	PHCKE3	c.1822	missense	p.R1822	ter1	30094	3327	3286	39	0.012	24630	1705	1302	401	0.235	NA	NA	NA	144663	581	570	6	0.010	NA	NA	NA	NA	NA
147457	X	69525880	69525880	C	T	KIF4	c.1324-60	intronic	c.1324-60	ter1	20196	2557	2542	13	0.005	16532	1619	1383	234	0.145	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345	3	0.000	NA	NA	NA	NA	NA
147457	X	70836404	70836404	C	T	KIF4	c.1109	missense	p.R1109Q	ter1	19731	3813	3563	42	0.012	29697	3525	2480	1024	0.252	NA	NA	NA	94147	348	345							

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Position	Coding Change	Amino Acid	Tier	Normal Total	Normal Unique	Normal Ref	Normal Count	Normal Var	Initial VAF	Initial Total	Initial Unique	Initial Ref	Initial Count	Initial Var	Pre VAF	Pre Total	Pre Unique	Pre Ref	Pre Count	D30 Unique	D30 Ref	D30 Count	D30 Var	D30 Total	D100 Unique	D100 Ref	D100 Count	D100 Var	D100 Total	D100 Unique	D100 Ref	D100 Count	D100 Var
185295	12	63272304	63272324	C	T	CTC93D	3_prime_untranslated_region	c.7232	NUL	Ter	30023	4019	4210	4	0.001	99196	3997	9722	3083	0.239	37985	2579	1622	951	0.372	80434	10052	10088	4	0.000	71793	6371	6383	4	0.000	71793	6371	6383	4	0.000	
185295	12	124472322	124472322	A	C	SLC42L2	nonsense	c.12736	p.Y64*	Ter	8592	1219	1245	11	0.009	25296	1297	2472	1483	0.239	37985	2579	1622	951	0.372	80434	10052	10088	4	0.000	71793	6371	6383	4	0.000						
185295	12	145817435	145817435	G	A	SLC42L2	nonsense	c.6834-64	c.6834-64	Ter	1832	210	210	1	0.000	3506	97	186	127	0.258	2675	335	106	17	0.413	1616	330	329	1	0.000	2230	150	150	0	NA						
185295	12	145817435	145817435	G	T	SLC42L2	nonsense	c.6834-64	c.6834-64	Ter	1832	210	210	1	0.000	3506	97	186	127	0.258	2675	335	106	17	0.413	1616	330	329	1	0.000	2230	150	150	0	NA						
185295	14	9652991	9652991	G	T	CLAF132	intron	NUL	NUL	Ter	10922	1708	1703	3	0.002	3238	511	3487	1592	0.313	7280	638	335	0.02	0.374	15816	2168	2165	2	0.000	17469	2002	1997	1	0.000						
185295	2	2NF592		C	T	2NF592	intron	c.373-62	c.7-62	Ter	13181	1946	1935	6	0.003	52415	8134	2324	0.288	18696	1449	947	498	0.345	32384	4648	4644	2	0.000	39476	4479	4474	4	0.000							
185295	17	85343202	85343207	C	T	MYH3	intron	c.1824	p.G608	Ter	24528	3432	3417	10	0.001	67363	9567	1748	0.184	13879	1099	836	260	0.237	45257	5804	5793	2	0.000	46955	4732	4720	3	0.000							
185295	17	85343202	85343207	C	T	MYH3	intron	c.1824	p.G608	Ter	24528	3432	3417	10	0.001	67363	9567	1748	0.184	13879	1099	836	260	0.237	45257	5804	5793	2	0.000	46955	4732	4720	3	0.000							
185295	21	44524466	44524466	G	A	KIF68	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	21	44524466	44524466	G	A	KIF68	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	22	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	22	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969	734	172	0.190	13252	1904	1903	0	0.000	14386	2266	2263	0	0.000							
185295	3	39921396	39921396	C	T	MYH3	intron	c.101	p.S44*	Ter	34219	4512	4494	10	0.007	15332	1999	887	0.209	7658	969																				

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Normal	Normal Ref	Normal Var	Initial	Initial Ref	Initial Var	Pre	Pre Ref	Pre Var	D30	D30 Ref	D30 Var	D100	D100 Ref	D100 Var									
199019	4	21322899	21302789	C	T	CTF1	intronic	c.471-49	p.A49V	16494	1478	1439	38	0.026	13162	1234	887	37	0.037	8474	5398	5263	39	0.007	17902	286	286	0	0.000	0	0.000		
199019	4	10615643	10615643	G	T	TF12	nonsense	c.135-48	p.E452*	10834	1976	955	37	0.037	8474	1384	887	37	0.037	8474	5398	5263	39	0.007	17902	286	286	0	0.000	0	0.000		
199019	5	7303232	7303232	G	A	ENG5000002025976	intronic	c.NULL	NULL	11932	1270	1246	24	0.019	7810	833	585	242	0.293	NA	NA	18945	2643	2629	8	0.003	18843	245	245	0	0.000	0	0.000
199019	7	5752940	5752940	C	A	2NF176	intronic	c.1263	p.S421	19585	1016	1007	9	0.009	5410	548	447	0.184	NA	NA	5713	743	0	0.000	18843	228	228	0	0.000	0	0.000		
199019	8	34885514	34885514	C	T	HTP44	missense	c.814	p.R272W	14084	299	285	14	0.047	4666	367	261	123	0.320	NA	NA	4648	605	596	5	0.008	4974	68	68	0	0.000	0	0.000
199019	11	65062076	65062076	C	T	HTP44	intronic	c.1411	p.G471	14084	299	285	14	0.047	4666	367	261	123	0.320	NA	NA	4648	605	596	5	0.008	4974	68	68	0	0.000	0	0.000
199019	11	71949104	71949104	C	T	WNP11	missense	c.3571	p.G191R	15200	1686	1686	0	0.005	9827	1140	924	206	0.183	NA	NA	15439	2237	2226	9	0.000	17132	300	298	1	0.000	0	0.000
199019	11	89018012	89018012	G	T	TYR	missense	c.1256	p.A619V	14911	8959	836	31	0.004	5386	546	423	122	0.224	NA	NA	12253	1852	1850	1	0.000	15189	0	0	0	0	0	0.000
199019	12	12421407	12421407	G	A	ATP90A042	missense	c.C2339	p.R780R	12705	2603	2530	48	0.018	14513	1805	1201	589	0.393	NA	NA	11470	1595	1590	4	0.003	11318	215	215	0	0.000	0	0.000
199019	14	10635752	10635752	A	C	IGH06-19	silent	c.6	p.Y2	12705	1521	1508	12	0.008	7058	805	592	507	0.259	NA	NA	24533	3871	3847	18	0.005	33089	498	498	0	0.000	0	0.000
199019	16	4736331	4736331	G	T	ALKBH1	missense	c.723	p.S72N	14911	8959	836	31	0.004	5386	546	423	122	0.224	NA	NA	7903	1257	1248	9	0.007	11165	242	242	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3879	25	0.006	36911	427	426	0	0.000	0	0.000
199019	17	7578445	7578445	A	T	TFP3	3_prime_untranslated_region	c.485	p.I62N	14911	20913	2229	79	0.024	488	598	418	175	0.29	NA	NA	30370	3906	3									

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Position	Coding	Amino Change	Tier	Normal Total Count	Normal Unique Ref	Normal Var	Normal Count	Initial VAF	Initial Total Count	Initial Unique Ref	Initial Var	Initial Count	Pre VAF	Pre Total Count	Pre Unique Ref	Pre Var	Pre Count	D30 VAF	D30 Total Count	D30 Unique Ref	D30 Var	D30 Count	D30 VAF	D100 Total Count	D100 Unique Ref	D100 Var	D100 Count	D100 VAF	
243777	1	3428641	3428641	T	C	MEG6	missense	c.905	p.L302S	ter1 4798	5255	5247	6	0.001	34014	4096	3761	316	0.075	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	1	3438363	2438363	T	C	MEG6	silent	c.4314	p.A3438	ter1 3947	2626	2197	63	0.028	16062	1055	1027	370	0.285	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	1	3438363	2438363	A	G	CANX	missense	c.1508	p.D507V	ter1 2266	177	169	8	0.000	6707	2666	177	169	8	0.000	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	2	13254686	13254686	C	G	MEI	missense	c.371	p.D109H	ter1 8375	763	735	28	0.000	6759	698	538	158	0.227	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	3	58870344	58870344	G	T	C5orf67	silent	c.267	p.A421V	ter1 3330	452	436	16	0.035	3569	601	457	144	0.240	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	4	7932778	7932778	G	A	M5FD10	missense	c.1262	p.A212V	ter1 7096	673	669	2	0.003	11229	1548	1227	312	0.203	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	5	8283952	8283952	C	A	VCAN	missense	c.5130	p.D1710	ter1 2852	393	291	1	0.003	4791	783	766	14	0.018	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	5	14001927	14001927	C	A	PCD4AS	missense	c.967	p.A188K	ter1 13891	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
243777	6	4298369	4298369	G	A	PCD4AS	missense	c.267	p.A267V	ter1 4298	1566	1546	16	0.010	14937	1745	1372	364	0.2																		

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Position	Coding	Amino Acid Change	Tier	Normal Total Count	Normal Unique Count	Normal Ref Var	Initial Total Count	Initial Unique Count	Initial Ref Var	Initial Total Unique Count	Pre Var	Pre Total Count	D30 Unique Count	D30 Ref Var	D30 Total Count	D30 Unique Count	D30 Ref Var	D100 Total Count	D100 Unique Count	D100 Ref Var	D100 Total Unique Count	D100 VAF						
346313	1	115238744	115238744	C	T	NRAS	missense	c.339-48	C339	p.L338L	ter1	15135	2345	2345	0	0.006	2268	2769	1917	817	0.299	9508	75	44	31	0.043	12656	1666	1659	1	0.000	NA	NA	NA	NA	NA
346313	1	185015276	185015276	G	A	HR23A	intronic	c.339-48	C339	p.L338L	ter1	6596	904	899	5	0.000	9246	1033	626	388	0.833	6413	712	1	0.000	NA	NA	NA	NA	NA	NA	NA	NA	NA		
346313	1	227494338	227494338	G	A	HR23A	intronic	c.339-48	C339	p.L338L	ter1	6976	904	899	5	0.000	9246	1033	626	388	0.833	6413	712	1	0.000	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
346313	2	99376162	99376162	G	A	KOMP3	3_prime_untranslated_region	c.99376162	99376162	NULL	ter1	1312	1127	1127	8	0.004	12604	1599	937	647	0.408	8658	46	21	0.4	0.333	13523	1768	1765	0	0.000	NA	NA	NA	NA	NA
346313	2	97493997	97493997	G	T	CNNM3	3_prime_untranslated_region	c.97493997	97493997	NULL	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	2	103148926	103148926	G	A	CFTR	missense	c.103148926	103148926	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	2	19827359	19827359	C	A	CFTR	missense	c.19827359	19827359	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	3	124108073	124108073	A	G	KALN1	intronic	c.124108073	124108073	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	3	185362401	185362401	A	T	CFTR	missense	c.185362401	185362401	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	4	47888007	47888007	T	C	NRX1	missense	c.47888007	47888007	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	4	18065955	18065955	C	A	NRX1	missense	c.18065955	18065955	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	7	141794384	141794384	G	T	MGAT1	intronic	c.141794384	141794384	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	8	39111964	39111964	C	A	ADAM32	missense	c.39111964	39111964	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	8	95030086	95030086	G	A	ADAM32	missense	c.95030086	95030086	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	8	116770653	116770653	G	T	ADAM32	missense	c.116770653	116770653	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	9	139848263	139848263	G	C	ADAM32	missense	c.139848263	139848263	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	10	43612131	43612131	C	T	RET	splice_region	c.43612131	43612131	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	11	32413505	32413505	C	T	WNT1	missense	c.32413505	32413505	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	11	74880278	74880278	C	T	SLC28B1	missense	c.74880278	74880278	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	12	22668832	22668832	G	C	CR2D5	missense	c.22668832	22668832	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	12	112926910	112926910	G	C	PTPBL1	missense	c.112926910	112926910	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	13	133384598	133384598	G	A	SOX21	3_prime_untranslated_region	c.133384598	133384598	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	13	95030086	95030086	G	A	ADAM32	missense	c.95030086	95030086	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	14	7042537	7042537	G	A	SMOCT	splice_region	c.7042537	7042537	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	14	101429460	101429460	A	T	SVNOR114-7	missense	c.101429460	101429460	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	16	790001	790001	G	A	MAF1	missense	c.790001	790001	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	35912119	35912119	T	C	DMN	missense	c.35912119	35912119	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	38724252	38724252	C	T	SPN12	missense	c.38724252	38724252	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	21	45742779	45742779	C	G	PRK1	missense	c.45742779	45742779	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	21	26854460	26854460	C	T	PTP2P4	missense	c.26854460	26854460	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	17	757568	757568	C	T	PRK2	missense	c.757568	757568	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	4642702	4642702	A	T	PRK2	missense	c.4642702	4642702	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	20981993	20981993	A	G	DOO57	missense	c.20981993	20981993	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	15687311	15687311	T	C	CHM4	missense	c.15687311	15687311	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	222832376	222832376	A	G	PRK2	missense	c.222832376	222832376	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	14713807	14713807	G	A	ANKH	missense	c.14713807	14713807	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	13909457	13909457	C	T	MYO2	missense	c.13909457	13909457	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	135073547	135073547	C	T	MYO2	missense	c.135073547	135073547	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462	17673	2370	2365	4	0.000	NA	NA	NA	NA	NA	
346313	19	10291646	10291646	C	T	DMN1	missense	c.10291646	10291646	p.G560S	ter1	1734	2233	2233	7	0.003	16751	1134	695	0.380	16681	97	58	39	0.462											

UPN	Chr	Start	Reference	Variant	Gene Symbol	Mutation Type	Coding Ref	Amino Acid	Normal	Normal Ref	Normal Var	Initial Unique	Initial Ref	Initial Var	Pre	Pre Ref	Pre Var	D30 Var	D30 Ref	D30 Var	D100 Var	D100 Ref	D100 Var	D1000 Var	D1000 Ref	D1000 Var
371758	8	1616604	4329486	C	GNAQ2	missense	c.1372	ser	37150	3760	3745	10356	159572	10356	159572	10356	159572	10356	159572	10356	159572	10356	159572	10356	159572	
371758	8	1616604	4616604	C	GNAQ2	missense	c.1730	p.T578M	ter1	15778	2038	76	0.036	9637	1438	807	567	0.036	9637	1438	807	0.000	NA	NA	NA	
371758	8	93029456	93029456	C	RUNX1T1	missense	c.257	p.R568L	ter1	27247	3518	3500	16	0.036	13337	1438	1095	749	0.036	13337	1438	1095	0.000	NA	NA	
371758	10	12521468	12521468	C	CPW2	missense	c.1697	p.E568L	ter1	13234	4034	4081	7	0.004	16084	2218	1289	599	0.004	16084	2218	1289	0.000	NA	NA	
371758	10	13177495	13177495	C	NTM	missense	c.57-58	del	ter1	28441	4036	4028	6	0.001	11035	1798	1189	599	0.001	11035	1798	1189	0.000	NA	NA	
371758	12	53439709	53439709	C	LOC28335	intronic	c.785	NULL	ter3	7824	1955	1585	8	0.005	6157	1217	747	462	0.005	6157	1217	747	0.000	NA	NA	
371758	14	20243551	20243551	C	CHUS	silent	c.1155	p.C235S	ter1	82824	8698	8581	21	0.002	55001	5096	1340	1744	0.002	55001	5096	1340	0.000	NA	NA	
371758	14	20243551	20243551	C	CHUS	silent	c.1155	p.C235S	ter1	82824	8698	8581	21	0.002	55001	5096	1340	1744	0.002	55001	5096	1340	0.000	NA	NA	
371758	14	9470258	9470258	C	SEPRNA10	3_prime_untranslated_region	c.44	del	NULL	ter3	8956	1348	1344	4	0.003	4622	941	225	0.003	4622	941	225	0.000	NA	NA	
371758	16	6742195	6742195	C	LRCR29	intronic	c.285-20	del	ter3	8956	1348	1344	4	0.003	4622	941	225	0.003	4622	941	225	0.000	NA	NA		
371758	17	37901877	37901877	C	GNR7	intronic	c.1278-86	del	p.D138E	ter1	11992	336	1365	7	0.005	16228	2461	1502	941	0.005	16228	2461	1502	0.000	NA	
371758	17	48653205	48653205	G	CACM1G	missense	c.1748-86	p.L481N	ter3	16607	2151	2180	8	0.004	9627	1320	807	509	0.004	9627	1320	807	0.000	NA	NA	
371758	19	12221114	12221114	C	ENG	splice_region	c.16	del	p.E16G	ter1	7396	1332	1325	5	0.004	9178	1894	1189	599	0.004	9178	1894	1189	0.000	NA	
371758	19	16008365	16008365	G	CPW2	intronic	c.1845-59	p.E159G	ter3	396	291	279	12	0.004	2033	229	77	0.004	2033	229	77	0.000	NA	NA		
371758	19	16008365	16008365	G	CPW2	intronic	c.1845-59	p.E159G	ter3	396	291	279	12	0.004	2033	229	77	0.004	2033	229	77	0.000	NA	NA		
371758	20	33573882	33573882	C	MYH9	intronic	c.932-51	del	ter1	21988	3988	3933	22	0.006	21653	369	2260	1395	0.006	21653	369	2260	0.000	NA	NA	
371758	21	3623173	3623173	C	RUNX1	missense	c.611	p.R204Q	ter1	40567	5888	5865	20	0.003	21653	369	2260	1395	0.003	21653	369	2260	0.000	NA	NA	
371758	21	3623173	3623173	C	RUNX1	missense	c.611	p.R204Q	ter1	40567	5888	5865	20	0.003	21653	369	2260	1395	0.003	21653	369	2260	0.000	NA	NA	
371758	21	36572197	36572197	T	GNR7	silent	c.1014	p.D138E	ter1	11992	336	1297	6	0.005	972	1316	797	513	0.005	972	1316	797	0.000	NA	NA	
371758	21	44514777	44514777	T	GNR7	missense	c.470	p.Q157R	ter1	82039	9989	9944	4	0.004	49155	6122	337	1587	0.004	49155	6122	337	0.000	NA	NA	
371758	21	44889977	44889977	G	SVI	missense	c.1436	p.A1436G	ter1	26814	3642	3635	6	0.002	19946	3388	1988	1334	0.002	19946	3388	1988	0.000	NA	NA	
371758	24	40425476	40425476	G	ABRBP	intronic	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	40425476	40425476	G	ABRBP	intronic	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131	0.028	26400	3968	1999	1331	0.028	26400	3968	1999	0.000	NA	NA	
371758	24	62945636	62945636	G	ABRBP	5_prime_untranslated_region	c.1404-44	del	ter3	38432	4648	4507	131													

[illegible]

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Position	Coding	Amino Change	Tier	Normal Total	Normal Unique	Normal Ref	Normal Count	Initial VAF	Initial Total	Initial Unique	Initial Ref	Initial Count	Pre VAF	Pre Total	Pre Unique	Pre Ref	Pre Count	D30 VAF	D30 Total	D30 Unique	D30 Ref	D30 Count	D30 VAF	D30 Total	D30 Unique	D30 Ref	D30 Count	D100 VAF	D100 Total	D100 Unique	D100 Ref	D100 Count	D100 VAF	
435866	7	15188245	15188245	C	A	MLL3	missense	c.5080		p.L694L	ter1	18341	2675	3137	41	0.013	8337	1660	1049	606	0.386	19306	2029	1369	34	0.017	165240	6095	6092	0	0.000	100372	6151	6136	11	0.002						
435866	8	68024182	68024182	G	A	CSP1	intronic	c.1326-25	e13-25		ter3	18417	3169	2573	32	0.012	14377	1640	631	0.382	14308	1401	1369	31	0.012	163555	4666	4666	0	0.000	128108	3781	3773	8	0.002							
435866	8	139773725	139773725	G	A	MLL3	missense	c.2517		p.R397H	ter1	14776	1811	1566	25	0.017	6584	812	465	0.544	6442	1358	871	843	28	0.032	92380	1114	1114	0	0.000	47347	3811	3803	4	0.002						
435866	10	120810716	120810716	G	A	EFRA2	missense	c.2314		p.R777H	ter1	15804	2265	2253	43	0.017	1502	893	604	0.604	16716	1341	1328	13	0.010	89665	3829	3829	0	0.000	82609	3786	3779	6	0.002							
435866	15	28420657	28420657	C	T	MLL3	splice_site	c.9831+1	e93+1		ter1	9540	828	812	16	0.019	5040	551	305	0.445	8678	438	423	15	0.034	32185	1144	1144	0	0.000	52632	1429	1425	4	0.003							
435866	16	17820242	17820242	C	T	ZNF263	3_prime_untranslated_region	c.461			NULL	ter1	4109	828	2649	37	0.012	27411	1794	1274	0.516	2288	1078	1051	1476	25	0.011	310483	6336	6332	4	0.000	285758	5137	5126	10	0.002					
435866	16	40929280	40929280	A	G	ACLY	intronic	c.1152		p.T384	ter1	5148	3783	3763	17	0.004	34652	3136	175	0.340	19972	1270	1245	22	0.018	125897	3722	3722	0	0.000	150179	3843	3842	1	0.000							
435866	16	40929280	40929280	A	G	ACLY	intronic	c.1152-26	e15-26		ter1	5148	3783	3763	17	0.004	34652	3136	175	0.340	19972	1270	1245	22	0.018	125897	3722	3722	0	0.000	150179	3843	3842	1	0.000							
435866	16	40929280	40929280	A	G	ACLY	intronic	c.1152-26	e15-26		ter1	5148	3783	3763	17	0.004	34652	3136	175	0.340	19972	1270	1245	22	0.018	125897	3722	3722	0	0.000	150179	3843	3842	1	0.000							
435866	18	61226951	61226951	G	G	SPRBD1	intronic	c.384-44			ter4	18158	729	7263	27	0.001	8346	1667	988	0.447	9395	1288	1453	1466	27	0.019	16427	3485	3485	1	0.000	88700	4323	4312	9	0.002						
435866	20	14830634	14830634	A	G	MACOD2	3_prime_untranslated_region	c.14830634			ter4	18158	729	7263	27	0.001	8346	1667	988	0.447	9395	1288	1453	1466	27	0.019	16427	3485	3485	1	0.000	88700	4323	4312	9	0.002						
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	22	38884063	38884063	T	C	DDX17	missense	c.1250		p.Y502C	ter1	47445	4127	4050	74	0.018	31334	2786	1724	0.373	48316	2487	2423	64	0.026	330616	8032	8032	1	0.000	314458	7601	7588	13	0.002							
435866	2																																									

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Change	Normal			Normal			Initial			Pre			D30			D100			D100		
										Total	Unique	Ref	Total	Unique	Ref	Total	Unique	Ref	Total	Unique	Ref	Total	Unique	Ref						
481668	1	46724300	46724300	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724312	46724312	G	T	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724322	46724322	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724367	46724367	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724380	46724380	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724390	46724390	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724400	46724400	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724410	46724410	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724420	46724420	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724430	46724430	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724440	46724440	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724450	46724450	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724460	46724460	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724470	46724470	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724480	46724480	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724490	46724490	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724500	46724500	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724510	46724510	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724520	46724520	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724530	46724530	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724540	46724540	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724550	46724550	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724560	46724560	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724570	46724570	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724580	46724580	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724590	46724590	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724600	46724600	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724610	46724610	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724620	46724620	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724630	46724630	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724640	46724640	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724650	46724650	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724660	46724660	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724670	46724670	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724680	46724680	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724690	46724690	A	C	CHW	intronic	c.211-58	e4-58	ter1	3721	348	345	3	0.009	3860	409	290	114	0.282	4643	442	317	90	0.000	7398	958	953	0	0.000
481668	1	46724700	46724700	A	C	CHW	intronic																							

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Ref Var	Normal Unique Count	Initial Normal Count	Initial Ref Var	Initial Unique Count	Pre Initial Count	Pre Ref Var	Pre Unique Count	D20 Total Count	D20 Ref Var	D20 Unique Count	D30 Total Count	D30 Ref Var	D30 Unique Count	D100 Total Count	D100 Ref Var	D100 Unique Count	D100 Var	D100 Count	D100 VAF		
502835	4	119640406	119640446	T	C	SEC24D	na	c.1330	NUL	ter1	632	161	160	0	0.000	1916	212	202	9	0.043	3521	406	402	4	0.010	746	68	59	9	0.132	NA	NA	NA
502835	4	129192341	129192341	G	C	RGMC2	3_prime_untranslated_region	c.1330	NUL	ter1	632	161	160	0	0.000	1916	212	202	9	0.043	3521	406	402	4	0.010	746	68	59	9	0.132	NA	NA	NA
502835	4	169513227	169513227	G	T	TRM64DOP	3_prime_untranslated_region	c.89531227	NUL	ter3	348	696	694	0	0.000	17016	746	664	69	0.094	11664	1007	1088	18	0.016	3708	265	236	38	0.144	NA	NA	NA
502835	12	108181935	108181935	G	A	TRM64DOP	3_prime_untranslated_region	c.1330	NUL	ter3	348	696	694	0	0.000	17016	746	664	69	0.094	11664	1007	1088	18	0.016	3708	265	236	38	0.144	NA	NA	NA
502835	12	108181935	108181935	G	A	MALCN	missense	c.1435	p.A47H	ter1	4923	354	554	0	0.000	6221	718	666	50	0.070	992	966	953	13	0.013	2741	225	201	23	0.103	NA	NA	NA
502835	15	108678780	108678780	G	T	GOLGA8IP	3_prime_untranslated_region	c.131086780	NUL	ter3	10486	1232	1230	1	0.001	1362	108	935	71	0.047	10850	1174	1154	9	0.016	7523	517	489	24	0.047	NA	NA	NA
502835	15	43995984	43995984	C	G	STIC	intronic	c.10143435	p.434335	ter3	767	138	137	0	0.000	662	102	93	3	0.029	846	107	104	3	0.028	515	56	48	8	0.143	NA	NA	NA
502835	17	757538	757538	C	T	TP53	missense	c.743	p.R248Q	ter1	38153	4433	4425	6	0.001	32945	3829	3532	283	0.074	28494	3174	3108	63	0.020	15380	1077	928	139	0.130	NA	NA	NA
502835	17	7578551	7578551	C	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13818	1658	1655	1	0.001	16913	1916	1722	104	0.097	12532	1356	1324	30	0.022	8883	676	560	110	0.184	NA	NA	NA
502835	17	7578551	7578551	G	T	TP53	missense	c.379	p.S327T	ter1	13																						

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Position	Coding	Amino Acid Change	Tier	Normal Total Count	Normal Ref Count	Normal Var Count	Initial VAF	Initial Total Count	Initial Unique Count	Initial Ref Count	Initial Var Count	Pre Pre	Pre Total Count	Pre Unique Count	Pre Ref Count	Pre Var Count	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D30 Total Count	D30 Unique Count	D30 Ref Count	D30 Var Count	D100 Total Count	D100 Unique Count	D100 Ref Count	D100 Var Count	D100 Total Count	D100 Unique Count	D100 Ref Count	D100 Var Count					
597501	10	135015401	135015401	C	T	ENCL1	missense	c.3392	c.3392	p.L1311	ter1	1978	2371	24	0.006	1929	445	258	186	0.419	NA	NA	NA	NA	NA	20172	473	466	3	0.003	NA	5562	3	0.005	NA	NA	NA	NA	NA	NA	NA				
597501	11	31513364	31513364	C	T	ENCL1	silent	c.3393	c.3393	p.A1311	ter1	1978	2371	999	394	0.037	1424	2414	2007	382	1578	1795	1782	9	0.008	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			
597501	11	31513366	31513366	C	A	ENCL1	missense	c.3394	c.3394	p.G311	ter1	1978	2371	16	0.003	1388	539	488	1480	NA	NA	NA	NA	NA	918	107	0	0.008	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		
597501	12	25100251	25100251	G	A	GNM1	missense	c.76	c.76	p.G26	3_prime_untranslated_region	2840	2769	70	0.025	15565	1542	810	722	0.471	NA	NA	NA	NA	NA	30947	2816	32	0.011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		
597501	13	86089071	86089071	C	G	FLP4T2	missense	c.1213	c.1213	p.G4325	ter1	11307	1841	1788	53	0.029	8747	1090	621	460	0.426	NA	NA	NA	NA	NA	26550	2636	2613	9	0.007	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		
597501	15	34605185	34605185	C	T	LOC101926911	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		
597501	15	91574882	91574882	T	A	LOC101926911	intronic	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		
597501	16	2527630	2527630	G	A	MTN3	missense	c.928	c.928	p.A3107	ter1	10326	1406	1373	33	0.032	612	781	444	313	0.415	NA	NA	NA	NA	NA	3675	500	492	5	0.010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	16	2527630	2527630	G	A	MTN3	missense	c.928	c.928	p.A3107	ter1	10326	1406	1373	33	0.032	612	781	444	313	0.415	NA	NA	NA	NA	NA	3675	500	492	5	0.010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	17	28806664	28806664	C	T	LOC101927083	missense	c.1414	c.1414	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	17	28806664	28806664	C	T	LOC101927083	missense	c.1414	c.1414	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	17	29422352	29422352	T	G	NFI	missense	c.25	c.25	p.A96	ter1	1964	256	235	17	0.004	3327	478	243	0.483	NA	NA	NA	NA	NA	4772	684	675	6	0.009	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	17	30219342	30219342	C	G	UTP6	missense	c.361	c.361	p.A121P	ter1	11134	1686	1655	29	0.017	6298	726	402	319	0.442	NA	NA	NA	NA	NA	20523	2333	2313	16	0.007	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
597501	17	74732959	74732959	G	T	SKR57	missense	c.824	c.824	p.A95H	ter1	10393	1262	1212	49	0.039	821	963	459	0.481	NA	NA	NA	NA	NA	14711	1525	1507	17	0.011	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	20898	2652	1782	73	0.028	17216	1747	707	0.412	NA	NA	NA	NA	NA	47201	3973	3940	24	0.006	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
597501	18	39523048	39523048	G	A	ANKK8	missense	c.1294	c.1294	p.A40529	ter1	2089																																	

[illegible]

UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Acid Change	Tier	Normal Total Count	Normal Ref Count	Normal Var Count	Initial VAF	Initial Total Count	Initial Ref Count	Initial Var Count	Pre VAF	Pre Total Count	Pre Ref Count	Pre Var Count	D30 VAF	D30 Total Count	D30 Ref Count	D30 Var Count	D30 VAF	D30 Total Count	D30 Ref Count	D30 Var Count	D100 VAF	D100 Total Count	D100 Ref Count	D100 Var Count	
678913	16	3004788	5040788	C	T	SEC24L5	missense	c-366	p.D112	ter1_17682	1859	1829	29	0.016	19631	2677	1469	1174	0.442	NA	NA	NA	NA	NA	33459	5025	5010	11	0.002	45945	7001	6885	10	0.001
LOC101929636				C	T		silent	NULL		ter2_13197	1664	2152	29	0.013	13197	1032	664	0.392	NA	NA	NA	NA	NA	32613	5220	5211	55	0.000	36871	5220	5215	10	0.000	
718813	21	75142625	75142625	C	T	LOC101929636	intronic	c-37457		ter2_13197	1054	900	24	0.013	13197	1054	900	0.435	NA	NA	NA	NA	NA	32613	5220	5211	55	0.000	36871	5220	5215	10	0.000	
718813	21	75142625	75142625	C	T	LOC101929636	missense	c-37457		ter2_13197	1054	900	24	0.013	13197	1054	900	0.435	NA	NA	NA	NA	NA	32613	5220	5211	55	0.000	36871	5220	5215	10	0.000	
715413	6	74851871	74851871	A	C	ACV1	missense	c-4834	p.V612L	ter1_6174	808	805	2	0.002	6843	883	884	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	intronic	NULL		ter1_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	4748156	G	A	CPY21	intronic	c-49223		ter3_6888	1164	1151	10	0.009	2447	339	138	0.135	0.405	NA	NA	NA	NA	NA	3749	37	37	0	0.000	2526	475	472	1	0.000
717045	1	20087601	20087601	G	A	LOC106	intronic	c-1033	p.E345K	ter1_9569	1547	1527	15	0.010	4371	450	302	0.44	0.323	NA	NA	NA	NA	NA	13009	77	75	1	0.000	5912	879	872	5	0.006
717045	2	3266548	3266548	T	G	BRG1	missense	c-38444-18	p.T1718	ter3_2230	340	333	7	0.021	922	124	80	0.44	0.355	NA	NA	NA	NA	NA	1367	14	14	0	0.000	1245	199	198	1	0.000
717045	2	3266548	3266548	T	G	BRG1	missense	c-38444-18	p.T1718	ter3_2230	340	333	7	0.021	922	124	80	0.44	0.355	NA	NA	NA	NA	NA	1367	14	14	0	0.000	1245	199	198	1	0.000
717045	2	18826834	18826834	A	T	SBF1	missense	c-208	p.A700E	ter1_4145	309	305	4	0.012	2472	515	309	169	0.323	NA	NA	NA	NA	NA	3564	201	201	0	0.000	15867	1831	1819	1	0.006
717045	2	21728035	21728035	T	C	SMARCA1	missense	c-208	p.A700E	ter1_4145	309	305	4	0.012	2472	515	309	169	0.323	NA	NA	NA	NA	NA	3564	201	201	0	0.000	15867	1831	1819	1	0.006
717045	2	21728035	21728035	T	C	SMARCA1	missense	c-208	p.A700E	ter1_4145	309	305	4	0.012	2472	515	309	169	0.323	NA	NA	NA	NA	NA	3564	201	201	0	0.000	15867	1831	1819	1	0.006
717045	3	9639151	9639151	A	G	TW5	3_prime_untranslated_region	c-4905		ter3_14378	2969	2922	46	0.015	4446	667	416	249	0.374	NA	NA	NA	NA	NA	1594	133	133	0	0.000	7963	1112	1108	2	0.000
717045	3	9639151	9639151	A	G	TW5	3_prime_untranslated_region	c-4905		ter3_14378	2969	2922	46	0.015	4446	667	416	249	0.374	NA	NA	NA	NA	NA	1594	133	133	0	0.000	7963	1112	1108	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045	4	25407313	25407313	G	C	AMAPC1	intronic	c-1320-69	p.E1636	ter2_9490	1403	1390	7	0.002	2813	374	275	98	0.263	NA	NA	NA	NA	NA	1132	58	58	0	0.000	6491	872	869	2	0.000
717045																																		

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UPN	Chr	Start	Stop	Reference	Variant	Gene Symbol	Mutation Type	Coding Position	Amino Change	Tier	Normal Total	Normal Unique	Normal Ref	Normal Count	Normal Var	Initial Total	Initial Unique	Initial Ref	Initial Count	Initial Var	Pre Total	Pre Unique	Pre Ref	Pre Count	Pre Var	D30 Total	D30 Unique	D30 Ref	D30 Count	D30 Var	D100 Total	D100 Unique	D100 Ref	D100 Count	D100 Var	
944541	18	13684347	73848347	A	C	HAUS1	5_prime_untranslated_region	c-331	NULL	ter1	11027	1328	1312	12	0.009	13788	1600	957	628	0.396	NA	NA	NA	NA	NA	NA	3334	3482	3479	0	0.000	14203	1323	1322	0	0.000
944541	19	7954800	7954800	T	C	LRRC5	missense	c-139	p.L465F	ter1	5974	5974	5974	3	0.005	7353	986	937	637	0.345	NA	NA	NA	NA	NA	NA	2039	2639	2637	0	0.000	8027	502	502	0	0.000
944541	19	13812636	13812636	T	C	CDY1	missense	c-254	p.L83V	ter1	2340	2829	2816	11	0.004	26001	2231	305	713	0.321	NA	NA	NA	NA	NA	NA	3392	3388	3387	0	0.000	30292	2159	2159	0	0.000
944541	22	14056180	14056180	G	T	ZNF703	missense	c-174	p.D42S	ter1	19016	1999	1995	1	0.001	30781	3400	3308	86	0.025	20176	2048	1993	49	0.024	5319	6240	6236	0	0.000	69167	8440	8439	0	0.000	
955252	5	140563408	140563408	A	G	PCDH8	missense	c-1274	p.D42S	ter1	19016	1999	1995	1	0.001	30781	3400	3308	86	0.025	20176	2048	1993	49	0.024	5319	6240	6236	0	0.000	69167	8440	8439	0	0.000	
988638	1	161519606	161519606	G	A	PKNOX3	3_prime_untranslated_region	c-3469	NULL	ter3	33975	4464	4459	3	0.001	16242	1640	245	1453	0.009	47391	6601	6009	5	0.001	74351	6783	6772	7	0.001	74351	6783	6772	7	0.001	
988638	1	161519606	161519606	A	G	PKNOX3	missense	c-29	p.T105	ter1	9443	1261	1248	13	0.001	16242	1640	245	1453	0.009	47391	6601	6009	5	0.001	74351	6783	6772	7	0.001	74351	6783	6772	7	0.001	
988638	2	10284410	10284410	C	A	MTOR	missense	c-176	p.Q59Q	ter1	217	0	0	0	0.000	301	26	24	2	0.077	194	29	17	10	0.044	1262	114	114	0	0.000	NA	NA	NA	NA	NA	
988638	2	10284410	10284410	C	A	MTOR	missense	c-176	p.Q59Q	ter1	217	0	0	0	0.000	301	26	24	2	0.077	194	29	17	10	0.044	1262	114	114	0	0.000	NA	NA	NA	NA	NA	
988638	2	10284410	10284410	C	A	MTOR	missense	c-176	p.Q59Q	ter1	217	0	0	0	0.000	301	26	24	2	0.077	194	29	17	10	0.044	1262	114	114	0	0.000	NA	NA	NA	NA	NA	
988638	2	10284410	10284410	C	A	MTOR	missense	c-176	p.Q59Q	ter1	217	0	0	0	0.000	301	26	24	2	0.077	194	29	17	10	0.044	1262	114	114	0	0.000	NA	NA	NA	NA	NA	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR3	missense	c-332	p.L107S	ter1	3337	3337	3337	1	0.000	12674	1483	1297	181	0.022	19108	2545	1527	101	0.038	36793	5089	5084	4	0.001	27712	2853	2848	5	0.002	
988638	2	13595920	13595920	T	G	WDR																														

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