**Table S2 SNV and indel**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Class | Samples | Genes | Chromosome | Position | Ref | Alt | Variant\_class | SIFT | HGVSp | AF | gnomAD\_AF | CGC | ACMG |
| Somatic | FAM-100T | NFKB2 | 10 | 104157142 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000410256.1:p.Arg160His |  | 5.69E-05 | T |  |
| Somatic | 09-679-T | ALDH2 | 12 | 112229903 | CCT | C | Frame\_Shift\_Del |  | ENSP00000403349.3:p.Leu232GlnfsTer54 |  |  | T |  |
| Somatic | 11-1060-T | COL2A1 | 12 | 48367337 | C | T | Splice\_Site |  |  |  |  | T |  |
| Somatic | 09-679-T | KMT2D | 12 | 49434076 | C | CGGTTT | Frame\_Shift\_Ins |  | ENSP00000301067.7:p.Gly2493LysfsTer52 |  |  | T |  |
| Somatic | 09-679-T | HOXC13 | 12 | 54333210 | T | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000243056.3:p.Phe174Leu |  |  | T |  |
| Somatic | 09-679-T | CHD4 | 12 | 6707479 | G | T | Missense\_Mutation | Tolerated (0.08) | ENSP00000440392.1:p.Pro529Gln |  |  | T |  |
| Somatic | 09-679-T | CHD4 | 12 | 6707480 | G | T | Missense\_Mutation | Tolerated (0.08) | ENSP00000440392.1:p.Pro529Thr |  |  | T |  |
| Somatic | FAM-100T | FOXA1 | 14 | 38061432 | G | GAGAT | Frame\_Shift\_Ins |  | ENSP00000440178.1:p.Ala153AspfsTer42 |  |  | T |  |
| Somatic | 11-849-T | HIF1A | 14 | 62193438 | G | C | Missense\_Mutation | Tolerated (0.12) | ENSP00000451696.1:p.Gly99Arg |  |  | T |  |
| Somatic | 09-679-T | RAD51B | 14 | 68331717 | TAGA | T | Splice\_Site |  |  |  |  | T |  |
| Somatic | 11-1060-T | TRIP11 | 14 | 92470536 | T | C | Missense\_Mutation | Tolerated (0.06) | ENSP00000267622.4:p.Lys1262Glu |  | 4.07E-06 | T |  |
| Somatic | TAR-06B | B2M | 15 | 45007899 | G | GATCGA | Frame\_Shift\_Ins |  | ENSP00000453350.1:p.Asp118IlefsTer32 |  |  | T |  |
| Somatic | 09-679-T | CREBBP | 16 | 3778870 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000371502.3:p.Arg2022Gly |  |  | T |  |
| Somatic | 09-679-T | CREBBP | 16 | 3778872 | GGTGGCTGCACGCTGGGC | G | Frame\_Shift\_Del |  | ENSP00000371502.3:p.Met2015IlefsTer282 |  |  | T |  |
| Somatic | 09-679-T | CREBBP | 16 | 3778891 | TCCGGG | T | Frame\_Shift\_Del |  | ENSP00000371502.3:p.Pro2013HisfsTer288 |  |  | T |  |
| Somatic | 11-849-T | RARA | 17 | 38498974 | AGTG | A | In\_Frame\_Del |  | ENSP00000377643.3:p.Val7del |  |  | T |  |
| Somatic | 36599042-T | STAT3 | 17 | 40476815 | G | T | Missense\_Mutation | Deleterious (0.04) | ENSP00000467985.1:p.Ala505Asp |  |  | T |  |
| Somatic | 11-849-T | PER1 | 17 | 8047101 | G | T | Missense\_Mutation | Tolerated (0.59) | ENSP00000462064.1:p.Ala829Glu |  |  | T |  |
| Somatic | 09-679-T | DNM2 | 19 | 10916615 | TGA | T | Frame\_Shift\_Del |  | ENSP00000468734.1:p.Asn507GlnfsTer49 |  |  | T |  |
| Somatic | 09-679-T | STK11 | 19 | 1220466 | G | A | Missense\_Mutation | Tolerated (0.18) | ENSP00000324856.6:p.Gly187Ser |  | 2.99E-05 | T |  |
| Somatic | 09-679-T | STK11 | 19 | 1220467 | G | A | Missense\_Mutation | Tolerated (1.0) | ENSP00000324856.6:p.Gly187Asp |  |  | T |  |
| Somatic | 36599042-T | JAK3 | 19 | 17943714 | G | GA | Frame\_Shift\_Ins |  | ENSP00000436421.1:p.Thr792IlefsTer9 |  |  | T |  |
| Somatic | 09-679-T | BCL3 | 19 | 45261664 | C | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000164227.5:p.Ser351Arg |  |  | T |  |
| Somatic | 11-1060-T | POLD1 | 19 | 50905898 | G | GTGCTCTTCCGAT | In\_Frame\_Ins |  | ENSP00000473052.1:p.Val290\_Leu291insCysSerSerAsp |  |  | T |  |
| Somatic | 09-679-T | NOTCH2 | 1 | 120612011 | G | T | Missense\_Mutation | Tolerated\_low\_confidence (0.08) | ENSP00000256646.2:p.Leu4Met |  |  | T |  |
| Somatic | TAR-06B | FH | 1 | 241675422 | CATTTA | C | Frame\_Shift\_Del |  | ENSP00000355518.3:p.Leu132Ter |  |  | T |  |
| Somatic | 09-679-T | MAFB | 20 | 39316626 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000380167.1:p.Arg289Cys |  | 4.06E-06 | T |  |
| Somatic | FAM-100T | NF2 | 22 | 30057328 | G | GGT | Frame\_Shift\_Ins |  |  |  |  | T |  |
| Somatic | FAM-100T | ALK | 2 | 29448407 | A | AG | Frame\_Shift\_Ins |  | ENSP00000373700.3:p.Leu1031ProfsTer47 |  |  | T |  |
| Somatic | 36599042-T | FBLN2 | 3 | 13612347 | C | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000445705.1:p.Asp190Glu |  |  | T |  |
| Somatic | 11-1060-T | SETD2 | 3 | 47125824 | C | A | Nonsense\_Mutation |  | ENSP00000386759.3:p.Glu1816Ter |  |  | T |  |
| Somatic | 11-1060-T | PBRM1 | 3 | 52598082 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000386529.1:p.Glu1262Lys |  |  | T |  |
| Somatic | 11-849-T | CSF1R | 5 | 149452958 | C | T | Missense\_Mutation | Tolerated (0.78) | ENSP00000286301.3:p.Gly330Ser |  |  | T |  |
| Somatic | 09-323-T | FLT4 | 5 | 180053011 | TC | T | Frame\_Shift\_Del |  | ENSP00000426057.1:p.Lys427ArgfsTer66 |  |  | T |  |
| Somatic | FAM-100T | HLA-A | 6 | 29910723 | C | CAGAGATCTCCAAGACCAACGCACAGATTGACCTAGAGAGCCTGCGGATCGCGCTCCGCTACT | Frame\_Shift\_Ins |  | ENSP00000379873.1:p.Arg89GlufsTer24 |  |  | T |  |
| Somatic | 09-679-T | ELN | 7 | 73462848 | C | A | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000403162.1:p.Ala244Glu |  |  | T |  |
| Somatic | 09-679-T | ANK1 | 8 | 41551522 | G | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000380149.1:p.His1142Gln |  |  | T |  |
| Somatic | 09-679-T | NOTCH1 | 9 | 139405165 | G | GGGC | In\_Frame\_Ins |  | ENSP00000277541.6:p.Cys893\_His894insAla |  |  | T |  |
| Somatic | 09-679-T | NOTCH1 | 9 | 139405168 | A | AACT | In\_Frame\_Ins |  | ENSP00000277541.6:p.Arg892\_Cys893insSer |  |  | T |  |
| Somatic | 09-679-T | NOTCH1 | 9 | 139417424 | C | A | Missense\_Mutation | Tolerated (0.17) | ENSP00000277541.6:p.Arg207Leu |  |  | T |  |
| Somatic | TAR-06B | FLNA | X | 153580815 | TCTGCAGGGTGGGGATGGGCTAGTGAGCAGCAGCCCTGGGCTCCACCCCTCCTCTTGGGGCTGCTTGAGCCCCAGGACCCCTCCCCAGGCTTCCCACAGCCCCTAC | T | Splice\_Site |  |  |  |  | T |  |
| Somatic | 36599042-T | RBM10 | X | 47044722 | C | A | Missense\_Mutation | Tolerated (0.29) | ENSP00000366829.3:p.His708Asn |  |  | T |  |
| Somatic | 09-323-T | AMER1 | X | 63411276 | G | A | Nonsense\_Mutation |  | ENSP00000384722.1:p.Arg631Ter |  |  | T |  |
| Germline.pathgenic | 11-849-T | ALDH1A3 | 15 | 101440938 | G | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000343294.6:p.Asp241Asn |  | 2.04E-05 | F | Likely pathogenic |
| Germline.pathgenic | 36599042-T | ALDH2 | 12 | 112241766 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000403349.3:p.Glu457Lys | 0.0357 | 0.01811 | T | Likely pathogenic |
| Germline.pathgenic | 36599042-T | APOE | 19 | 45412079 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000252486.3:p.Arg176Cys | 0.0751 | 0.06122 | F | Likely pathogenic |
| Germline.pathgenic | TAR-06B | BCR | 22 | 23653975 | T | TCCGG | Frame\_Shift\_Ins |  | ENSP00000352535.3:p.Val1050ArgfsTer17 |  | 1.23E-05 | T | Likely pathogenic |
| Germline.pathgenic | 09-679-T | CCNL1 | 3 | 156864362 | G | A | Nonsense\_Mutation |  | ENSP00000420277.1:p.Arg423Ter |  | 9.68E-06 | F | Likely pathogenic |
| Germline.pathgenic | FAM-100T | COL4A2 | 13 | 111143586 | A | AGG | Frame\_Shift\_Ins |  | ENSP00000353654.5:p.Phe1120AspfsTer17 |  |  | F | Likely pathogenic |
| Germline.pathgenic | 11-1060-T | EYS | 6 | 66204599 | C | T | Nonsense\_Mutation |  | ENSP00000424243.1:p.Trp235Ter |  |  | F | Likely pathogenic |
| Germline.pathgenic | 11-1060-T | ITGB3 | 17 | 45360816 | C | T | Nonsense\_Mutation |  | ENSP00000461626.1:p.Arg88Ter |  |  | F | Likely pathogenic |
| Germline.pathgenic | 09-679-T | NMNAT1 | 1 | 10042628 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000366410.1:p.Arg237Cys |  | 5.28E-05 | F | Likely pathogenic |
| Germline.pathgenic | 11-849-T | PLCZ1 | 12 | 18865906 | C | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000443349.1:p.Gly58Val |  |  | F | Likely pathogenic |
| Germline.pathgenic | 09-679-T | C7 | 5 | 40936439 | G | T | Splice\_Site |  |  | 0.0002 | 0.0001017 | F | Pathogenic |
| Germline.pathgenic | TAR-06B | FH | 1 | 241667341 | C | T | Splice\_Site |  |  |  |  | T | Pathogenic |
| Germline.pathgenic | 09-323-T | MAK | 6 | 10813894 | G | GC | Frame\_Shift\_Ins |  | ENSP00000442250.1:p.Ala114GlyfsTer5 |  | 1.22E-05 | F | Pathogenic |
| Germline.pathgenic | 09-679-T | NBEA | 13 | 35619082 | A | C | Splice\_Site |  |  |  |  | T | Pathogenic |
| Germline.pathgenic | TAR-06B | NDUFS1 | 2 | 207017232 | G | A | Nonsense\_Mutation |  | ENSP00000392709.2:p.Arg36Ter |  | 2.84E-05 | F | Pathogenic |
| Germline.pathgenic | 11-1060-T | TTC37 | 5 | 94886284 | C | A | Splice\_Site |  |  |  |  | F | Pathogenic |
| Germline | 36599042-T | ABL2 | 1 | 179077415 | G | C | Missense\_Mutation | Deleterious\_low\_confidence (0.02) | ENSP00000423578.1:p.Pro981Arg | 0.0052 | 0.003026 | T | Uncertain significance |
| Germline | FAM-100T | ACSL6 | 5 | 131307317 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000445154.1:p.Arg338Trp |  | 3.29E-05 | T | Uncertain significance |
| Germline | FAM-100T | AFF1 | 4 | 87968162 | G | A | Missense\_Mutation | Tolerated (0.9) | ENSP00000378578.4:p.Gly159Ser | 0.0008 | 0.0001585 | T | Uncertain significance |
| Germline | 09-323-T | AFF3 | 2 | 100199339 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000386834.1:p.Asn930Ser | 0.0062 | 0.001921 | T | Likely benign |
| Germline | 36599042-T | AFF3 | 2 | 100210022 | A | T | Missense\_Mutation | Tolerated (0.45) | ENSP00000386834.1:p.Ser726Thr |  |  | T | Uncertain significance |
| Germline | 11-849-T | ALK | 2 | 29445432 | T | C | Missense\_Mutation | Tolerated (0.36) | ENSP00000373700.3:p.Gln1134Arg |  |  | T | Uncertain significance |
| Germline | 11-1060-T | ALK | 2 | 29474044 | T | G | Missense\_Mutation | Deleterious (0.02) | ENSP00000373700.3:p.Ser711Arg |  |  | T | Uncertain significance |
| Germline | 36599042-T | ANK1 | 8 | 41550356 | A | G | Missense\_Mutation | Deleterious (0.0) | ENSP00000380149.1:p.Val1223Ala | 0.0024 | 0.001139 | T | Benign |
| Germline | TAR-06B | ANK1 | 8 | 41550356 | A | G | Missense\_Mutation | Deleterious (0.0) | ENSP00000380149.1:p.Val1223Ala | 0.0024 | 0.001139 | T | Benign |
| Germline | FAM-100T | ANK1 | 8 | 41561570 | C | T | Missense\_Mutation | Deleterious (0.02) | ENSP00000380149.1:p.Glu762Lys |  | 1.22E-05 | T | Uncertain significance |
| Germline | 09-323-T | ARHGAP5 | 14 | 32561778 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000452222.1:p.Arg635Trp | 0.0038 | 0.0007695 | T | Uncertain significance |
| Germline | TAR-06B | ARHGAP5 | 14 | 32561778 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000452222.1:p.Arg635Trp | 0.0038 | 0.0007695 | T | Uncertain significance |
| Germline | 11-1060-T | ARHGEF10 | 8 | 1824881 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000427909.1:p.Arg276His | 0.0026 | 0.001275 | T | Uncertain significance |
| Germline | TAR-06B | ARHGEF10 | 8 | 1871213 | C | A | Missense\_Mutation | Tolerated (0.59) | ENSP00000427909.1:p.Gln705Lys |  | 2.03E-05 | T | Uncertain significance |
| Germline | 11-849-T | ARHGEF10L | 1 | 17982574 | C | G | Missense\_Mutation | Deleterious (0.04) | ENSP00000399401.1:p.Ile855Met | 0.0002 | 1.96E-05 | T | Uncertain significance |
| Germline | FAM-100T | ARID1A | 1 | 27089638 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.47) | ENSP00000387636.2:p.Asn865Ser |  | 3.66E-05 | T | Uncertain significance |
| Germline | FAM-100T | ARID1A | 1 | 27107098 | G | A | Missense\_Mutation | Tolerated (0.25) | ENSP00000442437.1:p.Ala565Thr |  | 5.29E-05 | T | Uncertain significance |
| Germline | 11-1060-T | ARID1B | 6 | 157099402 | C | CCAG | In\_Frame\_Ins |  | ENSP00000356116.1:p.Gln131dup |  |  | T | Uncertain significance |
| Germline | 11-1060-T | ARNT | 1 | 150785811 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.11) | ENSP00000423851.1:p.Pro692Leu | 0.0006 | 0.001096 | T | Uncertain significance |
| Germline | TAR-06B | ASXL1 | 20 | 31023474 | G | A | Missense\_Mutation | Deleterious (0.03) | ENSP00000364839.4:p.Gly987Arg | 0.0002 | 4.06E-05 | T | Likely benign |
| Germline | 11-1060-T | ATIC | 2 | 216191608 | A | G | Missense\_Mutation | Tolerated (0.93) | ENSP00000440523.1:p.Lys140Glu | 0.001 | 0.0006498 | T | Uncertain significance |
| Germline | 11-849-T | BCL6 | 3 | 187447438 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000413122.2:p.Asn252Ser |  | 5.69E-05 | T | Uncertain significance |
| Germline | TAR-06B | BCOR | X | 39933661 | GGCT | G | In\_Frame\_Del |  | ENSP00000380512.3:p.Gln312del |  | 0.0002285 | T | Uncertain significance |
| Germline | TAR-06B | BCORL1 | X | 129149380 | A | G | Missense\_Mutation |  | ENSP00000437775.1:p.Ser878Gly | 0.0037 | 0.002 | T | Likely benign |
| Germline | 09-679-T | BIRC6 | 2 | 32770913 | G | A | Missense\_Mutation |  | ENSP00000393596.2:p.Val4266Met | 0.0004 | 0.0002642 | T | Uncertain significance |
| Germline | 36599042-T | BLM | 15 | 91298125 | G | A | Missense\_Mutation | Tolerated (0.29) | ENSP00000454158.1:p.Met348Ile | 0.0002 | 0.000228 | T | Likely benign |
| Germline | 09-323-T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | 09-679-T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | 11-1060-T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | 11-849-T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | 36599042-T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | FAM-100T | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | TAR-06B | BMPR1A | 10 | 88635779 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000361107.1:p.Pro2Thr |  |  | T | Benign |
| Germline | 11-849-T | BRCA1 | 17 | 41219631 | T | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000467329.1:p.Lys181Gln |  | 2.84E-05 | T | Likely benign |
| Germline | 36599042-T | BRCA2 | 13 | 32910842 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000439902.1:p.Met784Val | 0.0036 | 0.0002278 | T | Likely benign |
| Germline | 36599042-T | BRCA2 | 13 | 32930651 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000439902.1:p.Gly2508Ser |  | 0.0001544 | T | Likely benign |
| Germline | 11-1060-T | CALR | 19 | 13054615 | A | C | Missense\_Mutation | Tolerated (0.31) | ENSP00000320866.4:p.Glu381Ala | 0.0038 | 0.004829 | T | Likely benign |
| Germline | 36599042-T | CASP3 | 4 | 185550609 | C | A | Missense\_Mutation | Deleterious (0.03) | ENSP00000428929.1:p.Gln217His |  | 4.88E-05 | T | Uncertain significance |
| Germline | 36599042-T | CBLB | 3 | 105421090 | G | T | Missense\_Mutation | Tolerated\_low\_confidence (0.32) | ENSP00000384938.1:p.Gln603Lys |  | 7.72E-05 | T | Uncertain significance |
| Germline | 11-1060-T | CBLB | 3 | 105438902 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000384938.1:p.Asn466Asp | 0.0088 | 0.003843 | T | Uncertain significance |
| Germline | 11-1060-T | CDH1 | 16 | 68856080 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000414946.2:p.Leu569Val | 0.0012 | 0.0003858 | T | Benign |
| Germline | 11-1060-T | CHD4 | 12 | 6711144 | A | C | Missense\_Mutation | Tolerated\_low\_confidence (0.22) | ENSP00000440392.1:p.Asp137Glu | 0.0074 | 0.005047 | T | Likely benign |
| Germline | 09-679-T | CHD4 | 12 | 6707488 | G | A | Missense\_Mutation | Tolerated (0.12) | ENSP00000440392.1:p.Thr526Met | 0.0002 | 1.22E-05 | T | Uncertain significance |
| Germline | 36599042-T | CHEK2 | 22 | 29091846 | G | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000442458.1:p.His150Tyr | 0.0002 | 0.0004545 | T | Uncertain significance |
| Germline | 09-679-T | CIC | 19 | 42797228 | C | T | Missense\_Mutation | Deleterious\_low\_confidence (0.01) | ENSP00000458663.2:p.Ser1197Phe |  | 8.53E-06 | T | Uncertain significance |
| Germline | 09-323-T | CIC | 19 | 42799006 | A | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000458663.2:p.Tyr1497Phe |  |  | T | Uncertain significance |
| Germline | 09-323-T | CLTCL1 | 22 | 19178928 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000441158.1:p.Cys1404Tyr |  |  | T | Uncertain significance |
| Germline | 09-323-T | CLTCL1 | 22 | 19188995 | G | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000441158.1:p.Arg1204Gly |  | 0.0001497 | T | Uncertain significance |
| Germline | 11-1060-T | CLTCL1 | 22 | 19209603 | C | T | Missense\_Mutation | Tolerated (0.06) | ENSP00000441158.1:p.Arg811Gln | 0.004 | 0.004217 | T | Uncertain significance |
| Germline | 36599042-T | CLTCL1 | 22 | 19209603 | C | T | Missense\_Mutation | Tolerated (0.06) | ENSP00000441158.1:p.Arg811Gln | 0.004 | 0.004217 | T | Uncertain significance |
| Germline | 36599042-T | CNOT3 | 19 | 54649769 | A | C | Missense\_Mutation | Tolerated (0.45) | ENSP00000383954.1:p.Asn276Thr | 0.001 | 0.0003259 | T | Uncertain significance |
| Germline | 36599042-T | CNTNAP2 | 7 | 146818173 | G | A | Missense\_Mutation | Tolerated (0.19) | ENSP00000354778.3:p.Arg286Gln |  | 4.88E-05 | T | Uncertain significance |
| Germline | 09-323-T | CNTNAP2 | 7 | 147092838 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000354778.3:p.Asn546Asp | 0.0004 | 8.55E-05 | T | Uncertain significance |
| Germline | 36599042-T | COL3A1 | 2 | 189870953 | C | A | Missense\_Mutation | Tolerated (0.24) | ENSP00000304408.3:p.Leu1021Ile | 0.001 | 0.0004022 | T | Benign |
| Germline | 11-849-T | COL3A1 | 2 | 189872804 | G | C | Missense\_Mutation |  | ENSP00000315243.5:p.Ser851Thr | 0.0004 | 1.63E-05 | T | Uncertain significance |
| Germline | 09-679-T | CREB3L2 | 7 | 137593176 | A | C | Missense\_Mutation | Tolerated (0.08) | ENSP00000403550.1:p.Val197Gly |  |  | T | Uncertain significance |
| Germline | 11-849-T | CRLF2 | X | 1314990 | G | A | Missense\_Mutation | Tolerated (0.63) | ENSP00000370979.3:p.Pro224Leu |  |  | T | Uncertain significance |
| Germline | FAM-100T | CSMD3 | 8 | 113349885 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000412263.2:p.Gly2139Asp | 0.0028 | 0.001134 | T | Uncertain significance |
| Germline | 09-679-T | CSMD3 | 8 | 113694827 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000412263.2:p.Ile737Val |  |  | T | Uncertain significance |
| Germline | FAM-100T | CTNND1 | 11 | 57581818 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000435789.1:p.Asn832Asp | 0.0014 | 0.0003874 | T | Uncertain significance |
| Germline | 11-849-T | CUX1 | 7 | 101848448 | C | T | Missense\_Mutation | Tolerated (0.06) | ENSP00000451558.1:p.Ser885Leu | 0.0026 | 0.0008124 | T | Uncertain significance |
| Germline | TAR-06B | DAXX | 6 | 33287796 | G | C | Missense\_Mutation | Tolerated (0.28) | ENSP00000396876.2:p.Ala411Gly | 0.0086 | 0.008881 | T | Likely benign |
| Germline | FAM-100T | DCC | 18 | 50866195 | T | G | Missense\_Mutation | Tolerated (0.06) | ENSP00000464582.1:p.Ile414Met | 0.003 | 0.000878 | T | Benign |
| Germline | 09-679-T | DCC | 18 | 50929215 | G | A | Missense\_Mutation | Tolerated (1.0) | ENSP00000464582.1:p.Val598Ile | 0.0004 | 9.75E-05 | T | Uncertain significance |
| Germline | 36599042-T | DDB2 | 11 | 47260392 | C | T | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000367866.3:p.Arg362Trp |  |  | T | Uncertain significance |
| Germline | FAM-100T | DDX6 | 11 | 118656777 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.29) | ENSP00000442266.1:p.Met62Val | 0.0086 | 0.003008 | T | Likely benign |
| Germline | TAR-06B | DICER1 | 14 | 95579431 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000444719.1:p.Val680Ile | 0.0002 | 5.28E-05 | T | Likely benign |
| Germline | 11-849-T | DICER1 | 14 | 95582104 | G | T | Missense\_Mutation | Tolerated (0.18) | ENSP00000444719.1:p.Pro603Thr |  | 4.06E-06 | T | Uncertain significance |
| Germline | FAM-100T | ELN | 7 | 73455561 | C | T | Missense\_Mutation | Deleterious\_low\_confidence (0.01) | ENSP00000403162.1:p.Ala61Val | 0.0044 | 0.001563 | T | Benign |
| Germline | 11-1060-T | EP300 | 22 | 41527626 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000263253.7:p.Met506Thr |  |  | T | Uncertain significance |
| Germline | TAR-06B | ERBB3 | 12 | 56495023 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000449129.1:p.Arg368His | 0.0038 | 0.0007231 | T | Uncertain significance |
| Germline | 09-323-T | ERC1 | 12 | 1137117 | G | C | Missense\_Mutation | Tolerated (0.23) | ENSP00000468263.1:p.Gln16His | 0.0044 | 0.001459 | T | Uncertain significance |
| Germline | 36599042-T | EZR | 6 | 159210399 | T | C | Missense\_Mutation | Tolerated (0.15) | ENSP00000376016.4:p.Asn6Ser | 0.004 | 0.001608 | T | Benign |
| Germline | 11-1060-T | FANCA | 16 | 89818581 | G | A | Missense\_Mutation | Tolerated (0.24) | ENSP00000456829.1:p.Arg1011Cys |  | 0.0001178 | T | Likely benign |
| Germline | 36599042-T | FANCC | 9 | 97887391 | C | T | Missense\_Mutation | Tolerated (0.17) | ENSP00000364454.1:p.Ala325Thr | 0.0014 | 0.0007309 | T | Benign |
| Germline | 36599042-T | FANCD2 | 3 | 10106532 | C | T | Missense\_Mutation | Tolerated (0.31) | ENSP00000398754.1:p.Pro714Leu |  |  | T | Benign |
| Germline | TAR-06B | FANCD2 | 3 | 10106532 | C | T | Missense\_Mutation | Tolerated (0.31) | ENSP00000398754.1:p.Pro714Leu |  |  | T | Benign |
| Germline | TAR-06B | FAT3 | 11 | 92531148 | G | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000432586.1:p.Val1507Leu | 0.0012 | 0.0001994 | T | Uncertain significance |
| Germline | 11-1060-T | FAT3 | 11 | 92568041 | A | G | Missense\_Mutation | Tolerated (0.19) | ENSP00000432586.1:p.Ile3143Val |  | 0.0002206 | T | Uncertain significance |
| Germline | 09-679-T | FAT3 | 11 | 92623876 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000436399.1:p.Pro759Leu |  | 4.08E-05 | T | Uncertain significance |
| Germline | FAM-100T | FAT4 | 4 | 126398497 | G | A | Missense\_Mutation | Tolerated (0.36) | ENSP00000335169.5:p.Asp2424Asn | 0.0094 | 0.00302 | T | Benign |
| Germline | 11-1060-T | FCRL4 | 1 | 157559068 | C | T | Missense\_Mutation | Tolerated (0.42) | ENSP00000271532.1:p.Arg78Gln | 0.0096 | 0.008708 | T | Likely benign |
| Germline | FAM-100T | FCRL4 | 1 | 157559068 | C | T | Missense\_Mutation | Tolerated (0.42) | ENSP00000271532.1:p.Arg78Gln | 0.0096 | 0.008708 | T | Likely benign |
| Germline | FAM-100T | FH | 1 | 241671953 | T | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000355518.3:p.Lys230Glu |  |  | T | Uncertain significance |
| Germline | 11-1060-T | FIP1L1 | 4 | 54257655 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.29) | ENSP00000425456.1:p.Asn217Ser | 0.0008 | 0.0005283 | T | Uncertain significance |
| Germline | TAR-06B | FLNA | X | 153593613 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000416926.1:p.Val528Met | 0.0085 | 0.003 | T | Benign |
| Germline | 11-1060-T | FOXO1 | 13 | 41134096 | G | A | Missense\_Mutation | Tolerated (0.48) | ENSP00000368880.4:p.Ala511Val | 0.0036 | 0.001414 | T | Benign |
| Germline | 09-679-T | GOLGA5 | 14 | 93276667 | T | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000348252.2:p.Leu354Pro | 0.001 | 0.0003819 | T | Uncertain significance |
| Germline | FAM-100T | GPC5 | 13 | 92101156 | G | A | Missense\_Mutation | Tolerated (0.57) | ENSP00000366267.3:p.Arg102Gln |  | 4.08E-05 | T | Uncertain significance |
| Germline | 36599042-T | GRM3 | 7 | 86468250 | G | T | Missense\_Mutation | Tolerated (0.41) | ENSP00000444064.1:p.Val66Leu |  |  | T | Uncertain significance |
| Germline | 11-1060-T | HLA-A | 6 | 29910371 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000379873.1:p.Ser14Leu |  |  | T | Benign |
| Germline | 11-849-T | HLA-A | 6 | 29910371 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000379873.1:p.Ser14Leu |  |  | T | Benign |
| Germline | 36599042-T | HLA-A | 6 | 29910371 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000379873.1:p.Ser14Leu |  |  | T | Benign |
| Germline | FAM-100T | HLA-A | 6 | 29910371 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000379873.1:p.Ser14Leu |  |  | T | Benign |
| Germline | TAR-06B | HLA-A | 6 | 29910371 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000379873.1:p.Ser14Leu |  |  | T | Benign |
| Germline | 11-1060-T | HLA-A | 6 | 29911261 | C | G | Missense\_Mutation | Tolerated\_low\_confidence (0.56) | ENSP00000379873.1:p.Thr187Arg |  |  | T | Benign |
| Germline | FAM-100T | HLA-A | 6 | 29911261 | C | G | Missense\_Mutation | Tolerated\_low\_confidence (0.56) | ENSP00000379873.1:p.Thr187Arg |  |  | T | Benign |
| Germline | 09-679-T | HLA-A | 6 | 29912030 | G | C | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000379873.1:p.Asp251His |  |  | T | Benign |
| Germline | 09-679-T | HLA-A | 6 | 29912042 | G | A | Missense\_Mutation | Deleterious\_low\_confidence (0.01) | ENSP00000379873.1:p.Val255Met |  |  | T | Benign |
| Germline | TAR-06B | HLA-A | 6 | 29912297 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.12) | ENSP00000379873.1:p.Ile306Val |  |  | T | Benign |
| Germline | 11-1060-T | HLA-A | 6 | 29912315 | A | C | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000379873.1:p.Ile312Leu |  |  | T | Benign |
| Germline | 11-849-T | HLA-A | 6 | 29912315 | A | C | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000379873.1:p.Ile312Leu |  |  | T | Benign |
| Germline | FAM-100T | HLA-A | 6 | 29912315 | A | C | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000379873.1:p.Ile312Leu |  |  | T | Benign |
| Germline | TAR-06B | HLA-A | 6 | 29912315 | A | C | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000379873.1:p.Ile312Leu |  |  | T | Benign |
| Germline | 09-323-T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | 09-679-T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | 11-1060-T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | 11-849-T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | 36599042-T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | FAM-100T | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | TAR-06B | HLA-A | 6 | 29912856 | A | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000379873.1:p.Thr345Ser |  |  | T | Benign |
| Germline | 11-1060-T | HLA-A | 6 | 29912373 | T | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000379873.1:p.Met331Arg |  | 0.002743 | T | Likely benign |
| Germline | 11-849-T | HLA-A | 6 | 29912373 | T | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000379873.1:p.Met331Arg |  | 0.002743 | T | Likely benign |
| Germline | 36599042-T | HLA-A | 6 | 29912373 | T | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000379873.1:p.Met331Arg |  | 0.002743 | T | Likely benign |
| Germline | FAM-100T | HLA-A | 6 | 29912373 | T | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000379873.1:p.Met331Arg |  | 0.002743 | T | Likely benign |
| Germline | TAR-06B | HLA-A | 6 | 29912373 | T | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000379873.1:p.Met331Arg |  | 0.002743 | T | Likely benign |
| Germline | 11-849-T | HOXC11 | 12 | 54367410 | G | A | Missense\_Mutation | Tolerated (0.31) | ENSP00000446680.1:p.Ala129Thr | 0.0004 | 0.0001277 | T | Uncertain significance |
| Germline | 09-323-T | IKBKB | 8 | 42186655 | G | A | Missense\_Mutation | Tolerated (0.42) | ENSP00000430868.1:p.Ala708Thr | 0.001 | 0.0004259 | T | Benign |
| Germline | TAR-06B | IKBKB | 8 | 42175185 | G | T | Missense\_Mutation | Tolerated (0.53) | ENSP00000430868.1:p.Gly377Val |  | 1.22E-05 | T | Uncertain significance |
| Germline | 09-679-T | IKBKB | 8 | 42188946 | G | GT | Frame\_Shift\_Ins |  | ENSP00000428892.1:p.Ter110LeufsTer101 |  |  | T | Uncertain significance |
| Germline | 36599042-T | IL7R | 5 | 35867500 | G | A | Missense\_Mutation | Tolerated (0.12) | ENSP00000425309.1:p.Ser105Asn | 0.0006 | 0.000407 | T | Uncertain significance |
| Germline | 09-679-T | KAT6A | 8 | 41794796 | ATCT | A | In\_Frame\_Del |  | ENSP00000385888.1:p.Glu1109del | 0.007 | 0.006709 | T | Uncertain significance |
| Germline | TAR-06B | KAT6A | 8 | 41794796 | ATCT | A | In\_Frame\_Del |  | ENSP00000385888.1:p.Glu1109del | 0.007 | 0.006709 | T | Uncertain significance |
| Germline | 36599042-T | KDM5A | 12 | 438072 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000382688.2:p.Ala633Thr | 0.003 | 0.001024 | T | Uncertain significance |
| Germline | TAR-06B | KEAP1 | 19 | 10610685 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.46) | ENSP00000377245.1:p.Gly9Arg | 0.0008 | 0.0003211 | T | Uncertain significance |
| Germline | 36599042-T | KIAA1549 | 7 | 138603714 | C | G | Missense\_Mutation | Tolerated (0.24) | ENSP00000406661.1:p.Ala220Pro | 0.0098 | 0.00956 | T | Likely benign |
| Germline | 09-679-T | KIAA1549 | 7 | 138604055 | G | A | Missense\_Mutation | Tolerated (0.67) | ENSP00000406661.1:p.Pro106Leu |  | 7.72E-05 | T | Uncertain significance |
| Germline | FAM-100T | KIT | 4 | 55594068 | G | A | Missense\_Mutation | Tolerated (0.09) | ENSP00000288135.5:p.Met618Ile | 0.0002 | 1.63E-05 | T | Uncertain significance |
| Germline | 09-323-T | KMT2A | 11 | 118375998 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000436786.1:p.Gly3131Ser | 0.0048 | 0.002378 | T | Benign |
| Germline | FAM-100T | KMT2A | 11 | 118375998 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000436786.1:p.Gly3131Ser | 0.0048 | 0.002378 | T | Benign |
| Germline | 36599042-T | KMT2C | 7 | 151935910 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly845Glu |  |  | T | Benign |
| Germline | 09-323-T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | 09-679-T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | 11-1060-T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | 11-849-T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | 36599042-T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | FAM-100T | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | TAR-06B | KMT2C | 7 | 151945007 | C | T | Missense\_Mutation |  | ENSP00000347325.2:p.Gly838Ser |  |  | T | Benign |
| Germline | 09-323-T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | 09-679-T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | 11-1060-T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | 11-849-T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | 36599042-T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | FAM-100T | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | TAR-06B | KMT2C | 7 | 151945204 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ser772Leu |  |  | T | Benign |
| Germline | 36599042-T | KMT2C | 7 | 151970931 | G | A | Missense\_Mutation |  | ENSP00000347325.2:p.Leu291Phe |  |  | T | Benign |
| Germline | 09-323-T | KMT2C | 7 | 151945334 | T | C | Missense\_Mutation |  | ENSP00000347325.2:p.Asn729Asp |  |  | T | Likely benign |
| Germline | 11-1060-T | KMT2C | 7 | 151945334 | T | C | Missense\_Mutation |  | ENSP00000347325.2:p.Asn729Asp |  |  | T | Likely benign |
| Germline | 11-849-T | KMT2C | 7 | 151945334 | T | C | Missense\_Mutation |  | ENSP00000347325.2:p.Asn729Asp |  |  | T | Likely benign |
| Germline | 36599042-T | KMT2C | 7 | 151846114 | A | G | Missense\_Mutation |  | ENSP00000347325.2:p.Ser4357Pro | 0.0004 | 0.0002854 | T | Uncertain significance |
| Germline | TAR-06B | KMT2C | 7 | 151882672 | C | A | Missense\_Mutation |  | ENSP00000347325.2:p.Ala1685Ser |  | 0.006733 | T | Uncertain significance |
| Germline | 36599042-T | KMT2C | 7 | 151945225 | T | C | Missense\_Mutation |  | ENSP00000347325.2:p.Glu765Gly |  | 0.003204 | T | Uncertain significance |
| Germline | 36599042-T | KMT2C | 7 | 151945256 | G | A | Nonsense\_Mutation |  | ENSP00000347325.2:p.Gln755Ter |  | 0.002165 | T | Uncertain significance |
| Germline | FAM-100T | KMT2D | 12 | 49420078 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000301067.7:p.Arg5224His | 0.002 | 0.0009586 | T | Likely benign |
| Germline | 09-323-T | KMT2D | 12 | 49431094 | T | C | Missense\_Mutation | Tolerated (0.24) | ENSP00000301067.7:p.Met3349Val | 0.006 | 0.00272 | T | Likely benign |
| Germline | 09-679-T | KMT2D | 12 | 49431094 | T | C | Missense\_Mutation | Tolerated (0.24) | ENSP00000301067.7:p.Met3349Val | 0.006 | 0.00272 | T | Likely benign |
| Germline | 11-849-T | KMT2D | 12 | 49431094 | T | C | Missense\_Mutation | Tolerated (0.24) | ENSP00000301067.7:p.Met3349Val | 0.006 | 0.00272 | T | Likely benign |
| Germline | TAR-06B | KMT2D | 12 | 49431094 | T | C | Missense\_Mutation | Tolerated (0.24) | ENSP00000301067.7:p.Met3349Val | 0.006 | 0.00272 | T | Likely benign |
| Germline | 11-849-T | KTN1 | 14 | 56085911 | G | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000391964.2:p.Val282Met |  | 1.23E-05 | T | Uncertain significance |
| Germline | 36599042-T | LIFR | 5 | 38493874 | T | C | Missense\_Mutation | Tolerated (0.08) | ENSP00000398368.2:p.Ile633Met | 0.0092 | 0.008858 | T | Likely benign |
| Germline | 09-679-T | LRP1B | 2 | 140995783 | C | T | Missense\_Mutation | Deleterious (0.04) | ENSP00000374135.3:p.Val4500Ile |  |  | T | Uncertain significance |
| Germline | FAM-100T | LRP1B | 2 | 141092084 | T | G | Missense\_Mutation | Tolerated (0.64) | ENSP00000374135.3:p.Glu4054Ala | 0.0022 | 0.003604 | T | Uncertain significance |
| Germline | 09-679-T | LYL1 | 19 | 13211685 | C | T | Missense\_Mutation | Tolerated (0.12) | ENSP00000264824.3:p.Ala101Thr |  | 3.46E-05 | T | Uncertain significance |
| Germline | 36599042-T | MALT1 | 18 | 56390435 | C | T | Missense\_Mutation | Tolerated (0.06) | ENSP00000319279.4:p.Arg392Cys |  | 5.69E-05 | T | Uncertain significance |
| Germline | 11-1060-T | MAP3K1 | 5 | 56152558 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.09) | ENSP00000382423.3:p.Arg205Lys |  | 4.88E-05 | T | Uncertain significance |
| Germline | FAM-100T | MAPK1 | 22 | 22221700 | G | A | Missense\_Mutation | Tolerated (0.15) | ENSP00000440842.1:p.Pro11Ser |  |  | T | Uncertain significance |
| Germline | 09-679-T | MKL1 | 22 | 40814545 | C | T | Missense\_Mutation | Tolerated (0.12) | ENSP00000385835.1:p.Glu633Lys | 0.0014 | 0.0005491 | T | Uncertain significance |
| Germline | 11-1060-T | MKL1 | 22 | 40825445 | C | T | Missense\_Mutation |  | ENSP00000385076.1:p.Gly156Ser |  |  | T | Uncertain significance |
| Germline | 09-323-T | MLLT6 | 17 | 36868139 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.3) | ENSP00000367377.5:p.Ala198Thr | 0.0054 | 0.003284 | T | Likely benign |
| Germline | 11-1060-T | MN1 | 22 | 28194933 | T | TTGC | In\_Frame\_Ins |  | ENSP00000304956.4:p.Gln550dup |  |  | T | Benign |
| Germline | 11-1060-T | MSH2 | 2 | 47656972 | C | T | Missense\_Mutation | Deleterious (0.01) | ENSP00000442697.1:p.Leu324Phe | 0.0028 | 0.001531 | T | Likely benign |
| Germline | FAM-100T | MUC16 | 19 | 9057936 | G | A | Missense\_Mutation |  | ENSP00000381008.2:p.Thr9837Ile | 0.0014 | 0.001447 | T | Likely benign |
| Germline | 36599042-T | MUC16 | 19 | 9085315 | G | A | Missense\_Mutation |  | ENSP00000381008.2:p.Pro2167Leu | 0.002 | 0.0009077 | T | Likely benign |
| Germline | 11-1060-T | MUC16 | 19 | 8987281 | G | A | Missense\_Mutation |  | ENSP00000381008.2:p.Arg13936Cys | 0.001 | 0.0005484 | T | Uncertain significance |
| Germline | 09-323-T | MUC16 | 19 | 9046501 | A | C | Missense\_Mutation |  | ENSP00000381008.2:p.His11710Gln |  |  | T | Uncertain significance |
| Germline | 36599042-T | MUC16 | 19 | 9056878 | GAGA | G | In\_Frame\_Del |  | ENSP00000381008.2:p.Ser10189del | 0.0014 | 0.000688 | T | Uncertain significance |
| Germline | 11-1060-T | MUC16 | 19 | 9075292 | T | A | Missense\_Mutation |  | ENSP00000381008.2:p.Thr4052Ser | 0.0002 | 0.0004107 | T | Uncertain significance |
| Germline | TAR-06B | MUC16 | 19 | 9076822 | T | C | Missense\_Mutation |  | ENSP00000381008.2:p.Ile3542Val |  |  | T | Uncertain significance |
| Germline | FAM-100T | MUC16 | 19 | 9083557 | G | A | Missense\_Mutation |  | ENSP00000381008.2:p.Ala2753Val |  | 2.85E-05 | T | Uncertain significance |
| Germline | 11-849-T | MUC4 | 3 | 195511331 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.28) | ENSP00000420243.1:p.Ser2374Pro |  |  | T | Benign |
| Germline | TAR-06B | MUC4 | 3 | 195511331 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.28) | ENSP00000420243.1:p.Ser2374Pro |  |  | T | Benign |
| Germline | 11-849-T | MUC4 | 3 | 195512245 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.61) | ENSP00000420243.1:p.Asn2069Ser |  |  | T | Benign |
| Germline | 36599042-T | MUC4 | 3 | 195512245 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.61) | ENSP00000420243.1:p.Asn2069Ser |  |  | T | Benign |
| Germline | TAR-06B | MUC4 | 3 | 195512245 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.61) | ENSP00000420243.1:p.Asn2069Ser |  |  | T | Benign |
| Germline | 09-323-T | MUC4 | 3 | 195508021 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.3) | ENSP00000420243.1:p.Ser3477Asn |  | 0.00477 | T | Likely benign |
| Germline | 09-323-T | MUC4 | 3 | 195508022 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.35) | ENSP00000420243.1:p.Ser3477Gly |  | 0.003684 | T | Likely benign |
| Germline | TAR-06B | MUC4 | 3 | 195510793 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.46) | ENSP00000420243.1:p.Ala2553Val | 0.0056 | 0.0005974 | T | Likely benign |
| Germline | TAR-06B | MUC4 | 3 | 195512699 | C | G | Missense\_Mutation | Deleterious\_low\_confidence (0.03) | ENSP00000420243.1:p.Ala1918Pro |  |  | T | Uncertain significance |
| Germline | 36599042-T | MUC4 | 3 | 195516022 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000420243.1:p.Ala810Val | 0.0012 | 0.0003008 | T | Uncertain significance |
| Germline | TAR-06B | MUC4 | 3 | 195517013 | A | G | Missense\_Mutation | Tolerated\_low\_confidence (0.14) | ENSP00000420243.1:p.Phe480Leu | 0.0008 | 0.0003208 | T | Uncertain significance |
| Germline | 11-1060-T | MYC | 8 | 128748848 | T | G | Missense\_Mutation | Tolerated\_low\_confidence (0.06) | ENSP00000430235.1:p.Phe3Leu |  | 2.04E-05 | T | Uncertain significance |
| Germline | 36599042-T | MYCL | 1 | 40366925 | G | C | Missense\_Mutation | Tolerated (0.2) | ENSP00000389358.1:p.Pro61Arg |  | 4.47E-06 | T | Uncertain significance |
| Germline | 09-323-T | MYH11 | 16 | 15818199 | T | C | Missense\_Mutation | Tolerated (0.49) | ENSP00000458731.1:p.Lys1395Arg |  |  | T | Uncertain significance |
| Germline | 36599042-T | N4BP2 | 4 | 40122958 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000261435.6:p.Thr1076Met | 0.0004 | 0.000509 | T | Uncertain significance |
| Germline | 11-849-T | NACA | 12 | 57114067 | T | C | Missense\_Mutation | Tolerated\_low\_confidence (0.11) | ENSP00000448035.1:p.Lys416Arg | 0.0046 | 0.001302 | T | Likely benign |
| Germline | 09-679-T | NACA | 12 | 57109669 | G | C | Missense\_Mutation | Deleterious\_low\_confidence (0.01) | ENSP00000448035.1:p.Thr729Arg | 0.0006 | 0.0002552 | T | Uncertain significance |
| Germline | 36599042-T | NACA | 12 | 57110738 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000403817.1:p.Pro1526Ser |  |  | T | Uncertain significance |
| Germline | FAM-100T | NBN | 8 | 90965508 | G | T | Missense\_Mutation | Tolerated (0.74) | ENSP00000386924.1:p.Phe521Leu | 0.0006 | 0.0003625 | T | Likely benign |
| Germline | TAR-06B | NBN | 8 | 90965508 | G | T | Missense\_Mutation | Tolerated (0.74) | ENSP00000386924.1:p.Phe521Leu | 0.0006 | 0.0003625 | T | Likely benign |
| Germline | 11-849-T | NBN | 8 | 90965660 | T | C | Missense\_Mutation | Tolerated (0.19) | ENSP00000386924.1:p.Met471Val |  | 8.13E-06 | T | Likely benign |
| Germline | 09-323-T | NCOR2 | 12 | 124838655 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000400281.2:p.Arg1216His | 0.0006 | 0.0003666 | T | Uncertain significance |
| Germline | 09-679-T | NCOR2 | 12 | 124838655 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000400281.2:p.Arg1216His | 0.0006 | 0.0003666 | T | Uncertain significance |
| Germline | 09-679-T | NCOR2 | 12 | 124907067 | C | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000400281.2:p.Ala454Ser |  | 4.48E-05 | T | Uncertain significance |
| Germline | FAM-100T | NCOR2 | 12 | 124968240 | T | C | Missense\_Mutation | Deleterious (0.02) | ENSP00000400281.2:p.Ser105Gly | 0.003 | 0.0009355 | T | Uncertain significance |
| Germline | 09-323-T | NDRG1 | 8 | 134296551 | A | C | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000429007.1:p.Ser2Ala |  | 2.03E-05 | T | Uncertain significance |
| Germline | 09-323-T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | 09-679-T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | 11-1060-T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | 11-849-T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | 36599042-T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | FAM-100T | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | TAR-06B | NOTCH2 | 1 | 120539331 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.93) | ENSP00000473427.1:p.Gly225Arg |  |  | T | Benign |
| Germline | 11-849-T | NTHL1 | 16 | 2097751 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (1.0) | ENSP00000219066.1:p.Arg33Lys | 0.0012 | 0.0004978 | T | Likely benign |
| Germline | 09-679-T | NUMA1 | 11 | 71728822 | G | C | Missense\_Mutation | Deleterious (0.05) | ENSP00000377298.3:p.Leu344Val | 0.0024 | 0.001989 | T | Likely benign |
| Germline | TAR-06B | NUMA1 | 11 | 71734188 | G | C | Missense\_Mutation | Tolerated (0.12) | ENSP00000377298.3:p.Arg72Gly | 0.0004 | 0.0005656 | T | Uncertain significance |
| Germline | 09-679-T | NUTM1 | 15 | 34648635 | C | T | Missense\_Mutation | Tolerated (0.3) | ENSP00000444896.1:p.Thr809Met | 0.0054 | 0.003309 | T | Likely benign |
| Germline | TAR-06B | NUTM2B | 10 | 81466022 | G | A | Missense\_Mutation | Tolerated (0.69) | ENSP00000391631.1:p.Val203Ile |  | 0.005444 | T | Likely benign |
| Germline | TAR-06B | NUTM2B | 10 | 81472107 | T | C | Missense\_Mutation | Tolerated (0.63) | ENSP00000394623.1:p.Tyr835His |  |  | T | Uncertain significance |
| Germline | 11-849-T | PABPC1 | 8 | 101719033 | GCTAAAAAATAAGAACATTTTGTATTTTTATCTTGCTCTTTCAAATTGGTGATCAATTTTTAAAGGAAGGATTAAGACTCAC | G | Splice\_Site |  |  |  |  | T | Benign |
| Germline | 11-1060-T | PABPC1 | 8 | 101719121 | G | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000429395.1:p.Arg449Cys |  |  | T | Benign |
| Germline | 11-849-T | PABPC1 | 8 | 101719121 | G | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000429395.1:p.Arg449Cys |  |  | T | Benign |
| Germline | FAM-100T | PABPC1 | 8 | 101719121 | G | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000429395.1:p.Arg449Cys |  |  | T | Benign |
| Germline | TAR-06B | PABPC1 | 8 | 101719121 | G | A | Missense\_Mutation | Tolerated (0.07) | ENSP00000429395.1:p.Arg449Cys |  |  | T | Benign |
| Germline | 11-1060-T | PABPC1 | 8 | 101730064 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000429395.1:p.Thr115Met |  |  | T | Benign |
| Germline | 11-849-T | PABPC1 | 8 | 101730064 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000429395.1:p.Thr115Met |  |  | T | Benign |
| Germline | 36599042-T | PABPC1 | 8 | 101730064 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000429395.1:p.Thr115Met |  |  | T | Benign |
| Germline | 11-1060-T | PABPC1 | 8 | 101730073 | T | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000429395.1:p.His112Arg |  |  | T | Benign |
| Germline | 11-849-T | PABPC1 | 8 | 101730073 | T | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000429395.1:p.His112Arg |  |  | T | Benign |
| Germline | 36599042-T | PABPC1 | 8 | 101730073 | T | C | Missense\_Mutation | Deleterious (0.0) | ENSP00000429395.1:p.His112Arg |  |  | T | Benign |
| Germline | TAR-06B | PABPC1 | 8 | 101719225 | G | GGATGAGGT | Frame\_Shift\_Ins |  | ENSP00000429395.1:p.Pro414HisfsTer24 |  | 0.00256 | T | Uncertain significance |
| Germline | TAR-06B | PABPC1 | 8 | 101721709 | T | A | Missense\_Mutation | Tolerated (0.13) | ENSP00000429395.1:p.Tyr376Phe |  | 0.0003198 | T | Uncertain significance |
| Germline | 11-1060-T | PABPC1 | 8 | 101730110 | A | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000429395.1:p.Cys100Gly |  |  | T | Uncertain significance |
| Germline | 11-1060-T | PABPC1 | 8 | 101730117 | C | T | Splice\_Site |  |  |  | 0 | T | Uncertain significance |
| Germline | FAM-100T | PCM1 | 8 | 17815267 | C | G | Missense\_Mutation | Deleterious (0.0) | ENSP00000430521.1:p.Leu676Val |  | 2.05E-05 | T | Uncertain significance |
| Germline | 09-323-T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144865850 | G | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Asp1995Glu |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144866643 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Arg1952Cys |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144868170 | C | T | Missense\_Mutation | Tolerated (0.25) | ENSP00000435654.1:p.Ala1842Thr |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144874815 | T | C | Missense\_Mutation | Tolerated (0.64) | ENSP00000435654.1:p.His1734Arg |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144877176 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Arg1640Gln |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144879090 | T | C | Missense\_Mutation | Tolerated (0.3) | ENSP00000435654.1:p.Lys1590Glu |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144879090 | T | C | Missense\_Mutation | Tolerated (0.3) | ENSP00000435654.1:p.Lys1590Glu |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144879090 | T | C | Missense\_Mutation | Tolerated (0.3) | ENSP00000435654.1:p.Lys1590Glu |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144879339 | C | T | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Val1507Ile |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144879339 | C | T | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Val1507Ile |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144879339 | C | T | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Val1507Ile |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144879375 | T | C | Missense\_Mutation | Tolerated (0.11) | ENSP00000435654.1:p.Lys1495Glu |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144880832 | T | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Lys1402Glu |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144880832 | T | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Lys1402Glu |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144880832 | T | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Lys1402Glu |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144880832 | T | C | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Lys1402Glu |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144882823 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000435654.1:p.Ala1203Thr |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144886197 | A | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000435654.1:p.Phe1150Ile |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144912233 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000435654.1:p.Arg818His |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144915561 | G | A | Nonsense\_Mutation |  | ENSP00000435654.1:p.Arg759Ter |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144916748 | C | G | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Ser673Thr |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144917841 | T | C | Missense\_Mutation | Tolerated (0.33) | ENSP00000435654.1:p.His619Arg |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144918957 | T | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000435654.1:p.Glu547Val |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144922583 | G | A | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Ser412Leu |  |  | T | Benign |
| Germline | 09-323-T | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | 09-679-T | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | 11-1060-T | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | 11-849-T | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144952220 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000435654.1:p.Ala304Thr |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 145015877 | G | T | Missense\_Mutation | Deleterious (0.02) | ENSP00000435654.1:p.Leu142Ile |  |  | T | Benign |
| Germline | FAM-100T | PDE4DIP | 1 | 145015877 | G | T | Missense\_Mutation | Deleterious (0.02) | ENSP00000435654.1:p.Leu142Ile |  |  | T | Benign |
| Germline | 36599042-T | PDE4DIP | 1 | 145075775 | G | A | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000435654.1:p.Pro30Ser |  |  | T | Benign |
| Germline | TAR-06B | PDE4DIP | 1 | 144854608 | T | G | Missense\_Mutation | Tolerated (0.14) | ENSP00000435654.1:p.Lys2373Gln |  | 0.002978 | T | Uncertain significance |
| Germline | FAM-100T | PDGFRB | 5 | 149500865 | C | A | Missense\_Mutation | Tolerated (0.76) | ENSP00000261799.4:p.Ala789Ser | 0.0002 | 0.0001584 | T | Uncertain significance |
| Germline | 09-323-T | PLCG1 | 20 | 39766463 | C | T | Missense\_Mutation | Tolerated (0.09) | ENSP00000362369.2:p.Thr61Met |  | 5.08E-05 | T | Uncertain significance |
| Germline | 09-679-T | PMS1 | 2 | 190671154 | C | T | Missense\_Mutation | Tolerated (0.07) | ENSP00000363959.4:p.His142Tyr | 0.0004 | 9.06E-05 | T | Likely benign |
| Germline | TAR-06B | PMS2 | 7 | 6031688 | C | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000392843.2:p.Val196Phe |  | 8.13E-06 | T | Uncertain significance |
| Germline | 09-679-T | PPM1D | 17 | 58678037 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.08) | ENSP00000306682.2:p.Pro88Ser | 0.0044 | 0.001387 | T | Likely benign |
| Germline | FAM-100T | PPM1D | 17 | 58678037 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.08) | ENSP00000306682.2:p.Pro88Ser | 0.0044 | 0.001387 | T | Likely benign |
| Germline | 09-679-T | PRDM16 | 1 | 3102694 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.41) | ENSP00000421400.1:p.Gly15Ser |  | 2.89E-05 | T | Uncertain significance |
| Germline | FAM-100T | PRDM16 | 1 | 3328487 | G | A | Missense\_Mutation | Tolerated (0.09) | ENSP00000421400.1:p.Glu577Lys |  | 0.0001466 | T | Uncertain significance |
| Germline | 09-679-T | PRDM2 | 1 | 14108437 | G | A | Missense\_Mutation | Tolerated (0.13) | ENSP00000411103.1:p.Val1182Met | 0.0008 | 0.000467 | T | Uncertain significance |
| Germline | TAR-06B | PTCH1 | 9 | 98209721 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.74) | ENSP00000389744.1:p.Glu1207Lys |  | 1.35E-05 | T | Uncertain significance |
| Germline | 11-849-T | RABEP1 | 17 | 5241375 | C | G | Missense\_Mutation | Deleterious (0.04) | ENSP00000437701.2:p.Ala197Gly |  | 6.10E-05 | T | Uncertain significance |
| Germline | 11-849-T | RANBP2 | 2 | 109371654 | G | A | Missense\_Mutation | Tolerated (0.31) | ENSP00000283195.6:p.Arg802Gln | 0.0012 | 0.0006629 | T | Benign |
| Germline | 36599042-T | RBM15 | 1 | 110882052 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.05) | ENSP00000473638.1:p.Val9Met | 0.0038 | 0.001537 | T | Likely benign |
| Germline | 09-679-T | RECQL4 | 8 | 145738410 | TGGTGCA | T | In\_Frame\_Del |  | ENSP00000475456.1:p.Cys857\_Thr858del | 0.0038 | 0.007391 | T | Likely benign |
| Germline | TAR-06B | RECQL4 | 8 | 145740779 | G | A | Missense\_Mutation | Tolerated (0.41) | ENSP00000475456.1:p.Pro441Ser | 0.0006 | 0.0001549 | T | Uncertain significance |
| Germline | 09-679-T | RGPD3 | 2 | 107049593 | T | C | Missense\_Mutation | Tolerated (0.13) | ENSP00000386588.3:p.Lys785Arg |  | 0.009599 | T | Likely benign |
| Germline | 11-1060-T | RGPD3 | 2 | 107049593 | T | C | Missense\_Mutation | Tolerated (0.13) | ENSP00000386588.3:p.Lys785Arg |  | 0.009599 | T | Likely benign |
| Germline | 11-849-T | RGPD3 | 2 | 107049593 | T | C | Missense\_Mutation | Tolerated (0.13) | ENSP00000386588.3:p.Lys785Arg |  | 0.009599 | T | Likely benign |
| Germline | 36599042-T | RGPD3 | 2 | 107049593 | T | C | Missense\_Mutation | Tolerated (0.13) | ENSP00000386588.3:p.Lys785Arg |  | 0.009599 | T | Likely benign |
| Germline | TAR-06B | RGPD3 | 2 | 107049593 | T | C | Missense\_Mutation | Tolerated (0.13) | ENSP00000386588.3:p.Lys785Arg |  | 0.009599 | T | Likely benign |
| Germline | 11-1060-T | RGPD3 | 2 | 107039712 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000386588.3:p.Gly1571Arg |  | 0.0008936 | T | Uncertain significance |
| Germline | 36599042-T | RGPD3 | 2 | 107039712 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000386588.3:p.Gly1571Arg |  | 0.0008936 | T | Uncertain significance |
| Germline | 09-323-T | RGPD3 | 2 | 107040572 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000386588.3:p.His1284Arg |  |  | T | Uncertain significance |
| Germline | 11-849-T | RGPD3 | 2 | 107040572 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000386588.3:p.His1284Arg |  |  | T | Uncertain significance |
| Germline | 09-323-T | RGPD3 | 2 | 107040897 | G | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000386588.3:p.Leu1176Phe |  |  | T | Uncertain significance |
| Germline | 36599042-T | RGPD3 | 2 | 107041032 | T | C | Missense\_Mutation | Tolerated (0.96) | ENSP00000386588.3:p.Met1131Val |  | 1.66E-05 | T | Uncertain significance |
| Germline | 11-1060-T | RGPD3 | 2 | 107051646 | T | G | Missense\_Mutation | Deleterious (0.0) | ENSP00000386588.3:p.Asn591His |  | 0.001061 | T | Uncertain significance |
| Germline | 11-1060-T | RGPD3 | 2 | 107073489 | C | T | Missense\_Mutation | Tolerated (1.0) | ENSP00000386588.3:p.Glu115Lys |  |  | T | Uncertain significance |
| Germline | 11-849-T | RNF213 | 17 | 78252695 | G | A | Missense\_Mutation |  | ENSP00000425956.2:p.Ala132Thr | 0.0004 | 0.000517 | T | Likely benign |
| Germline | 11-849-T | RNF43 | 17 | 56436044 | C | T | Missense\_Mutation | Tolerated (0.41) | ENSP00000463069.1:p.Ala365Thr | 0.0044 | 0.003494 | T | Likely benign |
| Germline | TAR-06B | ROS1 | 6 | 117662652 | C | G | Missense\_Mutation | Tolerated (0.27) | ENSP00000357494.3:p.Glu1605Gln | 0.0002 | 0.0001504 | T | Uncertain significance |
| Germline | 09-679-T | RUNX1T1 | 8 | 93107611 | G | A | Missense\_Mutation | Deleterious\_low\_confidence (0.02) | ENSP00000402257.2:p.Arg29Trp | 0.0008 | 0.0002269 | T | Uncertain significance |
| Germline | 11-849-T | SALL4 | 20 | 50408673 | C | T | Missense\_Mutation | Tolerated (0.67) | ENSP00000379319.3:p.Gly117Arg | 0.0052 | 0.001722 | T | Benign |
| Germline | 09-679-T | SETD2 | 3 | 47165548 | G | A | Missense\_Mutation | Deleterious\_low\_confidence (0.0) | ENSP00000386759.3:p.Pro193Leu | 0.0044 | 0.0008936 | T | Uncertain significance |
| Germline | TAR-06B | SGK1 | 6 | 134583262 | T | A | Missense\_Mutation | Tolerated\_low\_confidence (0.33) | ENSP00000435724.1:p.Met32Leu |  | 0.0005295 | T | Likely benign |
| Germline | 11-849-T | SMO | 7 | 128850877 | A | T | Missense\_Mutation | Tolerated (0.1) | ENSP00000249373.3:p.Lys575Met |  | 8.13E-05 | T | Uncertain significance |
| Germline | 11-1060-T | SND1 | 7 | 127569336 | A | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000346762.3:p.Lys541Asn |  |  | T | Uncertain significance |
| Germline | TAR-06B | SPEN | 1 | 16261677 | C | T | Missense\_Mutation | Deleterious (0.03) | ENSP00000364912.3:p.Thr2981Met |  | 1.22E-05 | T | Uncertain significance |
| Germline | 36599042-T | SS18L1 | 20 | 60733910 | C | T | Missense\_Mutation | Tolerated\_low\_confidence (0.47) | ENSP00000359885.4:p.Pro23Ser | 0.008 | 0.003289 | T | Likely benign |
| Germline | FAM-100T | STK11 | 19 | 1221319 | C | T | Missense\_Mutation | Tolerated (0.43) | ENSP00000324856.6:p.Pro281Leu | 0.0008 | 0.0001382 | T | Likely benign |
| Germline | 09-679-T | TAF15 | 17 | 34149736 | C | T | Missense\_Mutation | Deleterious\_low\_confidence (0.01) | ENSP00000467528.1:p.Ser37Leu | 0.0004 | 8.12E-06 | T | Uncertain significance |
| Germline | FAM-100T | TCF3 | 19 | 1612374 | T | C | Missense\_Mutation | Tolerated (0.6) | ENSP00000468487.1:p.Met549Val |  | 8.14E-06 | T | Uncertain significance |
| Germline | 36599042-T | TET1 | 10 | 70333555 | C | T | Missense\_Mutation | Tolerated (0.62) | ENSP00000362748.4:p.Ser487Leu | 0.0076 | 0.004098 | T | Likely benign |
| Germline | FAM-100T | TET2 | 4 | 106156616 | G | A | Missense\_Mutation | Tolerated (0.39) | ENSP00000442867.1:p.Arg506Lys |  | 2.45E-05 | T | Uncertain significance |
| Germline | TAR-06B | TET2 | 4 | 106158030 | G | A | Missense\_Mutation | Tolerated (0.18) | ENSP00000442867.1:p.Met977Ile |  |  | T | Uncertain significance |
| Germline | TAR-06B | TET2 | 4 | 106158215 | C | T | Missense\_Mutation | Deleterious (0.02) | ENSP00000442867.1:p.Ser1039Leu | 0.0066 | 0.001451 | T | Uncertain significance |
| Germline | 09-323-T | TFEB | 6 | 41658481 | C | T | Missense\_Mutation | Tolerated (0.14) | ENSP00000384203.4:p.Val130Met | 0.007 | 0.002629 | T | Uncertain significance |
| Germline | 11-849-T | TFRC | 3 | 195800925 | T | C | Missense\_Mutation | Tolerated (0.31) | ENSP00000390133.1:p.Thr23Ala | 0.0008 | 0.0007635 | T | Uncertain significance |
| Germline | 11-849-T | TMEM127 | 2 | 96920586 | C | T | Missense\_Mutation | Tolerated (0.15) | ENSP00000411810.1:p.Ala48Thr |  | 0.0001422 | T | Uncertain significance |
| Germline | 11-849-T | TPR | 1 | 186320550 | A | G | Missense\_Mutation | Deleterious (0.0) | ENSP00000356448.3:p.Ile841Thr |  | 2.05E-05 | T | Uncertain significance |
| Germline | 09-323-T | TPR | 1 | 186344126 | G | A | Missense\_Mutation | Deleterious (0.01) | ENSP00000356448.3:p.Thr12Met | 0.0034 | 0.00115 | T | Uncertain significance |
| Germline | FAM-100T | TRRAP | 7 | 98574585 | G | C | Missense\_Mutation | Tolerated (0.32) | ENSP00000403708.3:p.Glu2732Asp | 0.0006 | 0.0005563 | T | Likely benign |
| Germline | 11-1060-T | TRRAP | 7 | 98602764 | C | T | Missense\_Mutation | Deleterious (0.0) | ENSP00000403708.3:p.Arg3491Trp |  | 4.08E-06 | T | Uncertain significance |
| Germline | 11-849-T | USP44 | 12 | 95914908 | G | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000442629.2:p.Pro602Ser | 0.0056 | 0.002603 | T | Uncertain significance |
| Germline | 36599042-T | USP44 | 12 | 95914908 | G | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000442629.2:p.Pro602Ser | 0.0056 | 0.002603 | T | Uncertain significance |
| Germline | 11-849-T | USP44 | 12 | 95927804 | C | T | Missense\_Mutation | Deleterious (0.02) | ENSP00000448670.1:p.Val77Ile | 0.0002 | 0.0002437 | T | Uncertain significance |
| Germline | 09-679-T | USP6 | 17 | 5041471 | C | A | Missense\_Mutation | Tolerated\_low\_confidence (0.09) | ENSP00000460380.1:p.Phe327Leu | 0.008 | 0.002457 | T | Likely benign |
| Germline | 09-323-T | USP6 | 17 | 5071261 | G | A | Missense\_Mutation | Tolerated\_low\_confidence (0.1) | ENSP00000460380.1:p.Arg1024Gln | 0.0044 | 0.001404 | T | Uncertain significance |
| Germline | 09-323-T | USP8 | 15 | 50790833 | T | A | Missense\_Mutation | Tolerated (0.37) | ENSP00000405537.1:p.Ser1027Thr |  | 2.85E-05 | T | Uncertain significance |
| Germline | 09-679-T | USP8 | 15 | 50790833 | T | A | Missense\_Mutation | Tolerated (0.37) | ENSP00000405537.1:p.Ser1027Thr |  | 2.85E-05 | T | Uncertain significance |
| Germline | FAM-100T | VTI1A | 10 | 114286892 | T | C | Missense\_Mutation | Tolerated (0.07) | ENSP00000395017.1:p.Leu104Pro | 0.0018 | 0.0005259 | T | Uncertain significance |
| Germline | 09-679-T | WAS | X | 48547748 | C | T | Missense\_Mutation | Tolerated (0.11) | ENSP00000365891.4:p.Pro460Ser | 0.0058 | 0.003386 | T | Benign |
| Germline | 11-1060-T | WAS | X | 48547748 | C | T | Missense\_Mutation | Tolerated (0.11) | ENSP00000365891.4:p.Pro460Ser | 0.0058 | 0.003386 | T | Benign |
| Germline | FAM-100T | WNK2 | 9 | 96055097 | G | A | Missense\_Mutation |  | ENSP00000411181.2:p.Val1396Met | 0.0002 | 0.0003165 | T | Likely benign |
| Germline | 36599042-T | XPC | 3 | 14220017 | T | G | Missense\_Mutation | Tolerated\_low\_confidence (0.06) | ENSP00000404002.2:p.Ser18Arg |  |  | T | Likely benign |
| Germline | 11-1060-T | ZEB1 | 10 | 31784716 | G | A | Missense\_Mutation | Tolerated (0.57) | ENSP00000444891.2:p.Gly23Arg | 0.0022 | 0.0009362 | T | Uncertain significance |
| Germline | TAR-06B | ZFHX3 | 16 | 72830889 | C | A | Missense\_Mutation | Deleterious (0.02) | ENSP00000438926.3:p.Gly984Trp |  | 2.84E-05 | T | Likely benign |
| Germline | TAR-06B | ZFHX3 | 16 | 72832153 | C | T | Missense\_Mutation | Tolerated (0.26) | ENSP00000438926.3:p.Met562Ile | 0.0008 | 0.0006784 | T | Likely benign |
| Germline | 09-323-T | ZFHX3 | 16 | 72984669 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000438926.3:p.Ser58Leu | 0.006 | 0.005554 | T | Likely benign |
| Germline | 09-679-T | ZFHX3 | 16 | 72984669 | G | A | Missense\_Mutation | Deleterious (0.0) | ENSP00000438926.3:p.Ser58Leu | 0.006 | 0.005554 | T | Likely benign |
| Germline | 09-323-T | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | 09-679-T | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | 11-1060-T | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | 36599042-T | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | FAM-100T | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | TAR-06B | ZNF479 | 7 | 57188016 | A | G | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Met369Thr |  |  | T | Benign |
| Germline | 09-323-T | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | 09-679-T | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | 11-1060-T | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | 36599042-T | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | FAM-100T | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | TAR-06B | ZNF479 | 7 | 57188718 | T | C | Missense\_Mutation | Tolerated (1.0) | ENSP00000333776.4:p.Tyr135Cys |  |  | T | Benign |
| Germline | 11-849-T | ZNF479 | 7 | 57193730 | T | C | Missense\_Mutation | Tolerated (0.07) | ENSP00000333776.4:p.His86Arg |  |  | T | Likely benign |
| Germline | FAM-100T | ZNF479 | 7 | 57193730 | T | C | Missense\_Mutation | Tolerated (0.07) | ENSP00000333776.4:p.His86Arg |  |  | T | Likely benign |