SF3B1-mutated chronic lymphocytic leukemia shows evidence of NOTCH1 pathway activation including CD20 downregulation

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Supplementary Information for

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Supplementary Information:

Supplementary Methods

Next Generation Sequencing

For targeted sequencing, specific PCR primers were designed and modified according to Illumina (San Diego, CA). Multiplex PCR products were a high fidelity Taq polymerase (Phusion High-Fidelity DNA Polymerase, ThermoFisher Scientific, Waltham, MA) and subsequently tagged with specific index according to modified procedures for NexteraXT (Illumina). Purified libraries were pooled, and paired-end sequenced in a MiSeq instrument (Illumina). For NexteraXT-based sequencing, PCR amplicons were generated using a high fidelity Taq polymerase (Phusion High-Fidelity DNA Polymerase, ThermoFisher Scientific), fragmented and subjected to NGS on a MiSeq sequencer (Illumina). Data were analyzed with MiSeq Reporter (Illumina) or aligned using HISAT2[1] against human genome assembly hg19, analyzed with custom pipelines and visualized with IGV software[2]. Results were expressed as Variant Allele Frequency (VAF). Variants with a "Strand Bias" or "LowGQ" flag were discarded.

Targeted splicing variant analysis

Target genes *DVL2*, *GCC2* and *MAP3K7* were selected among the highest-scoring alternatively-spliced transcripts identified by Wang et al.[3]. For determination of alternative splicing variant abundance by NGS, single amplicons spanning the alternative splice site were sequenced by ultradeep NGS and the coverage across the spliced and not spliced regions was computed using the SAMtools *depth* command. A "percent spliced-in" (PSI) metric was defined as the ratio between the abundance of the alternative spliced isoform and the abundance of the total transcript. Alternative splicing of *DVL2* (*altDVL2*) by RT-qPCR was evaluated using the reported[3] hydrolysis assay and normalized against total *DVL2*.

Quantitative Real-Time PCR

RNA for Quantitative Real-Time PCR (RT-qPCR) was extracted with TRIZOL Reagent (ThermoFisher Scientific) or the RNeasy MicroKit (Qiagen, Hilden, Germany) with DNaseI digestion; reverse transcription was carried out using oligodT primers and ImpromII reverse transcriptase with RNaseIn RNase inhibitors (all from Promega, Madison, WI). Transcript expression of genes of interest was assessed on a CFX96 Real-Time PCR system (Bio-Rad, Hercules, CA) using FastStart Universal PCR Master Mix (Roche, Basel, Switzerland) using hydrolysis probe-based assays (total *DVL2* Hs.PT.58.40551087, *DTX1* Hs.PT.58.26105230, *HES1* Hs.PT.58.4181121, *HEY1* Hs.PT.58.4299267, *MS4A1* Hs.PT.56a.24784282 IDT Integrated DNA Technologies, Leuven, Belgium; *CD300A* Hs00381974_m1, *IL1R2* Hs00174759_m1, *HES4* Hs00368353_g1 ThermoFisher Scientific) and normalized against total beta-2-microglobulin (forward primer, CCTGAATCTTTGGAGTACGCT; reverse primer, GGCATTCCTGAAGCTGACA; probe, CTAAGGCCACGGAGCGAGACATC, IDT). Abundance of the alternatively spliced *DVL2* was evaluated using the reported assay[3] and normalized against total *DVL2*.

Gene expression profiling (GEP) and data mining tools

CLL cases for GEP experiments were selected among those with a CD5+ purity >90%, unmutated IGHV status and absence of trisomy 12. Total RNA for GEP was extracted using the TRIZOL Reagent (Thermo Fisher Scientific) and validated for integrity using the 2200 Tapestation system (Agilent Technologies, Santa Clara, CA). RNA samples were labeled with the Low Input Quick Amp Gene Expression Labeling Kits, hybridized on oligonucleotide microarray slides (SurePrint G3 Human GE v2 8x60K Microarray 8x60K, Agilent design ID 039494, https://earray.chem.agilent.com/earray/) and acquired with a microarray scanner (all reagents and instruments from Agilent Technologies) as previously described[4]. The hybridization signal values for the multiple probes were generated with the use of Agilent Feature Extraction Software 10.7.3 (Agilent Technologies, Santa Clara, CA). Microarray data are available at GEO (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE137024.

Bioinformatic analyses were performed using GeneSpringGX 11.5 software (Agilent Technologies). Differentially expressed genes were selected by moderated t-test with Bonferroni-Holm correction for multiple testing for a p value <0.05 and a fold change >1.5. For clustering purposes, only known genes were employed, excluding unannotated probes, generic ORFs, antisense RNAs, long intergenic RNAs and uncharacterized loci. Unsupervised hierarchical clustering was performed using Cluster3 (http://bonsai.hgc.jp/~mdehoon /software/cluster/),[5] applying complete-linkage method with Euclidean distance.

Gene Set Enrichment Analysis (GSEA, http://www.broad.mit.edu/gsea/index.jsp) was performed with GSEA-3 and 1000 phenotype permutations on all detected probes. In presence of multiple probes per gene, the one with the greatest difference in fold change between phenotypes was included. NOTCH1-related gene sets were either collected from the Molecular Signature Database v6.2 (http://software.broadinstitute.org/gsea/ msigdb) or manually loaded from published signatures.[6] Gene sets were assessed as significantly enriched in one of the phenotypes if the nominal p value was less than 0.05 and, for multiple hypothesis correction, a FDR-q value less than 0.1.

Western blot (WB)

Total proteins were extracted in RIPA lysis buffer (Santa Cruz Biotechnology, Heidelberg, Germany), quantified through Bradford assay (Bio-Rad) and ran in 4-20% SDS-PAGE precast gels (Bio-Rad) prior to transfer to nitrocellulose membranes (Trans-Blot Turbo pack, Bio-Rad). Immunoblotting was performed with anti-NICD (cleaved NOTCH1 Val1744 D3B8, Cell Signaling Technology, Leiden, The Netherlands), anti-DVL2 (30D2, Cell Signaling Technology) and anti-β-actin (AC15, Sigma-Aldrich, Milan, Italy) as loading control. Detection was performed with HRP -conjugated antibodies (Bethil Labs, Montgomery, TX) and ClarityECL (Bio-Rad) on a ChemiDoc Touch Imaging System (Bio-Rad). Image analysis and quantification was performed with ImageLab software (Bio-Rad).

Cell Sorting

CD19+/CD5+ CLL cells from selected *SF3B1*-mutated cases were sorted according to CD20 expression using a PE-conjugated anti-CD20 antibody (clone L27, BD Biosciences, Milan, Italy) utilizing a FACSAriaIII cell sorter (BD Biosciences). High and low gates were set on the distribution tails to include about 15% and no more than 20% of the entire population.

Mantle Cell Lymphoma samples and Cell lines

Mantle Cell Lymphoma samples (CD19+/CD5+/CD23-/BCL1$^{t(11;14)}$) used for CD20 expression comparison derive from diagnostic routine. CLL-like MEC1 cells were obtained by DSMZ and maintained in RPMI1640 medium (Sigma-Aldrich) supplemented with 10% heat-inactivated fetal bovine serum (FBS Superior; Merck). The Notch CSL reporter HEK293 cell line was obtained by BPS Bioscience (San Diego, CA) and maintained according to manufacturer's protocol.

DVL2 expression vectors generation

DVL2 and altDVL2 expression vectors were generated as previously reported[4] by PCR amplification of *DVL2* from a CLL sample bearing the *SF3B1* K700E mutation and subsequent cloning in a pCR3.1-NT/GFP backbone (ThermoFisher Scientific).

Transfection of RBPJ (CSL) reporter- HEK293 cell line and luciferase assay

RBPJ (CSL) reporter- HEK293 cells were seeded at 30% confluecy; the day after were transfected using calcium phosphate and 8µg of DVL2 vector. After 48 hours, luciferase was detected using the ONE-Glo Luciferase Assay System (Promega) on a Infinite 1000Pro (TECAN, Männedorf, CH). For western blot analyses, 25µL were taken and subjected to SDS-PAGE as previously reported. For control of NOTCH1

inhibition, cells were treated with 10μM DAPT (D5942, Sigma-Aldrich). Experimental transfections were performed three times in triplicate, while controls were performed three times in duplicate.

Transfection with small interfering RNA (siRNA)

CLL-like MEC1 cells were transfected with siRNA for *DVL2* (TriFECTa DsiRNA kit hs.Ri.DVL2.13, IDT) using Amaxa Nucleofector, L kit and program C-005(Lonza, Basel, Switzerland). Cells were resuspended in 0.5mL of pre-warmed RPMI+20%FBS, let stand for 15 minutes and seeded in the appropriate volume.

Complement-dependent cytotoxicity (CDC) assay

For CDC assay, 2x105 primary CLL cells were incubated with rituximab (5μg/ml) in a final volume of 150 μl for 10 min at room temperature prior to the addition of pooled normal human serum (25%) and a further incubation at 37° C for 1 hour.

Statistical analyses

For clinical evaluation, TTFT was defined as the time between diagnosis and initiation of first therapy. Patients who did not receive any treatment were censored at their last confirmed treatment-free follow-up date. Probability of treatment was estimated by the Kaplan–Meier method, and patients alive and untreated were censored at the last follow-up. The log-rank test was used to compare probabilities between subgroups.

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Supplementary Figure Legends.

Supplementary Figure 1. Analysis of Time-to-First-treatment.
(A) Upper panel: Kaplan-Meyer survival analysis for Time-to-First-Treatment in 180 CLL cases with unmutated (UM) IGHV status and mutations of *SF3B1* (n= 24), *NOTCH1* (n=46) or none of them (WT, n=110; p=0.0244, Log-rank test); Lower panel: Kaplan-Meyer survival analysis for Time-to-First-Treatment in 195 CLL cases with mutated (M) IGHV status and mutations of *SF3B1* (n= 10), *NOTCH1* (n=5) or none of them (WT, n=180; p=0.0285, Log-rank test). (B) Kaplan-Meyer survival analysis for Time-to-First-Treatment in 382 CLL cases, as from Figure 1C, dissecting the contribution of cases with concomitant mutations of *SF3B1* and *NOTCH1* (n=3; p<0.0001, Log-rank test).

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(A) Box-and-whiskers plots showing CD20 expression in Mantle Cell Lymphoma cells (MCL, n=13), normal B cells (n=26) or CLL (n=537), further dissected for the presence (n=121) or absence (n=416) trisomy 12. (B) Pie plot showing frequency of *SF3B1* and *NOTCH1* mutations in 537 CLL cases with respect of trisomy 12. Percentages are relative to the number of cases within the trisomy 12/non-trisomy 12 categories. (C) Gating strategy for analysis of the CD20dim population. P1 denotes a linear gate from peak value comprising the whole CD20-bright population (black area); dashed line indicates subtraction of P1 from residual population, mirrored from the right side of the histogram; grey area indicates the differential area between the left and the right sides corresponding to the CD20dim population. (D) Prototypical CD20 expression of two CLL cases with a homogeneous (left panel) or heterogeneous (right panel) CD20 expression. The histogram within the P1 gate is indicated in black, the CD20dim fraction is indicated in grey. The corresponding CD19/CD20 dot-plot is reported below. (E) Stability of CD20dim fraction in consecutive samples of 10 untreated CLL cases; upper panel: absolute CD20dim fraction values; lower panel: absolute difference of CD20dim fraction at each timepoint from initial sample, black line represents the mean value at each timepoint, error bars represent standard deviation. (F) Expression of CD20 MFI and CD20dim fraction as determined by flow cytometry in *SF3B1*-mut (SF3B1, n=42), *NOTCH1*-mut (NOTCH1, n=41), *SF3B1/NOTCH1*-mut (SF3B1+NOTCH1, n=6) or unmutated (WT, n=327) CLL cases. (G) Expression of CD20 MFI and CD20dim fraction as determined by flow cytometry or RT-qPCR in *SF3B1*-mut (SF3B1, n=6), *NOTCH1*-mut (NOTCH1, n=36) or unmutated (WT, n=79) CLL cases with trisomy 12.
MFI, mean fluorescence intensity. Data are shown by Tukey's box and whisker plots. Outliers indicate data outside the 1.5 interquartile range. * p≤0.05, ** p≤0.01, *** p≤0.001, n.s. not significant, as determined by two-sided Mann-Whitney rank-test.

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Supplementary Figure 7: Correlation between NOTCH1 signaling, *DVL2* expression and CD20 downregulation. (A) Activity of the NOTCH1 pathway in a HEK293-CSL reporter cell line with constitutively active signaling, transfected with either a wild-type *DVL2* or *altDVL2*. Controls include transfection with no DNA (Mock), treatment with the gamma-secretase inhibitor DAPT, no transfection (Pos ctrl) and no luciferase reagent (No Luc). Mock vs. *DVL2*, p=0.0244; Mock vs. *altDVL2*, p=0.96; *DVL2* vs. *altDVL2*, p= 0.0040. RLU: Relative Luciferase Units. Transfections were performed three times in triplicate, while controls were performed three times in duplicate. Data are shown by Tukey's box and whisker plots. Outliers indicate data outside the 1.5 interquartile range. Right panel: western blot analyses for transfection of DVL2/altDVL2 in transfected cells. (B) Density plots (log10 density) of *DTX1* expression versus CD20dim fraction for WT (n=155), *SF3B1*-mut (n=35) and *NOTCH1*-mut (n=32) cases. Quadrant gates were set at the modal value of each param eter for WT cases; population frequency of each quadrant is reported. (C) Transcript expression of *MS4A1* determined by RT-qPCR (left panel) and *SF3B1* variant allele frequency determined by NGS in the CD20-High and CD20-Low subpopulations of sorted samples (n=9). Data are shown as dot-and-line diagrams. (D) Correlation between CD20 expression and percentage of relative lysis by complement-dependent cytotoxicity in *SF3B1*-mut, *NOTCH1*-mut and WT CLL cases. The Spearman's rank correlation coefficient (rho) and p-value are reported.
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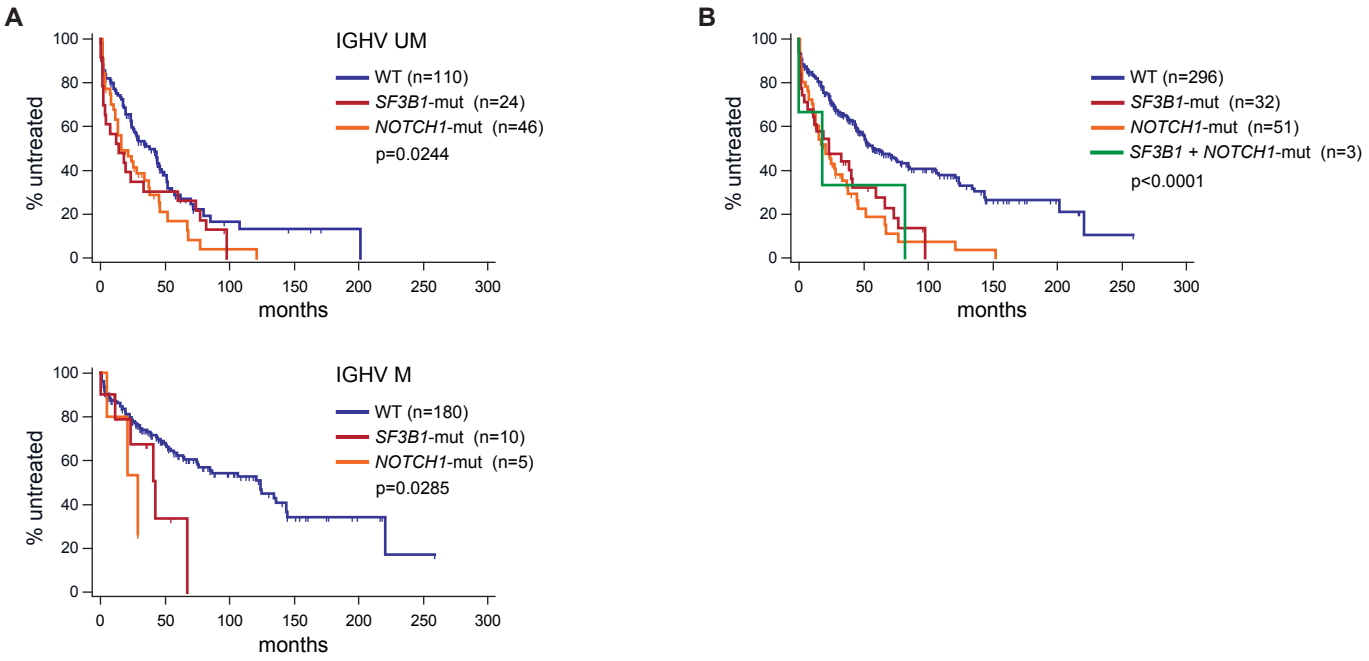
Supplementary Figure 1



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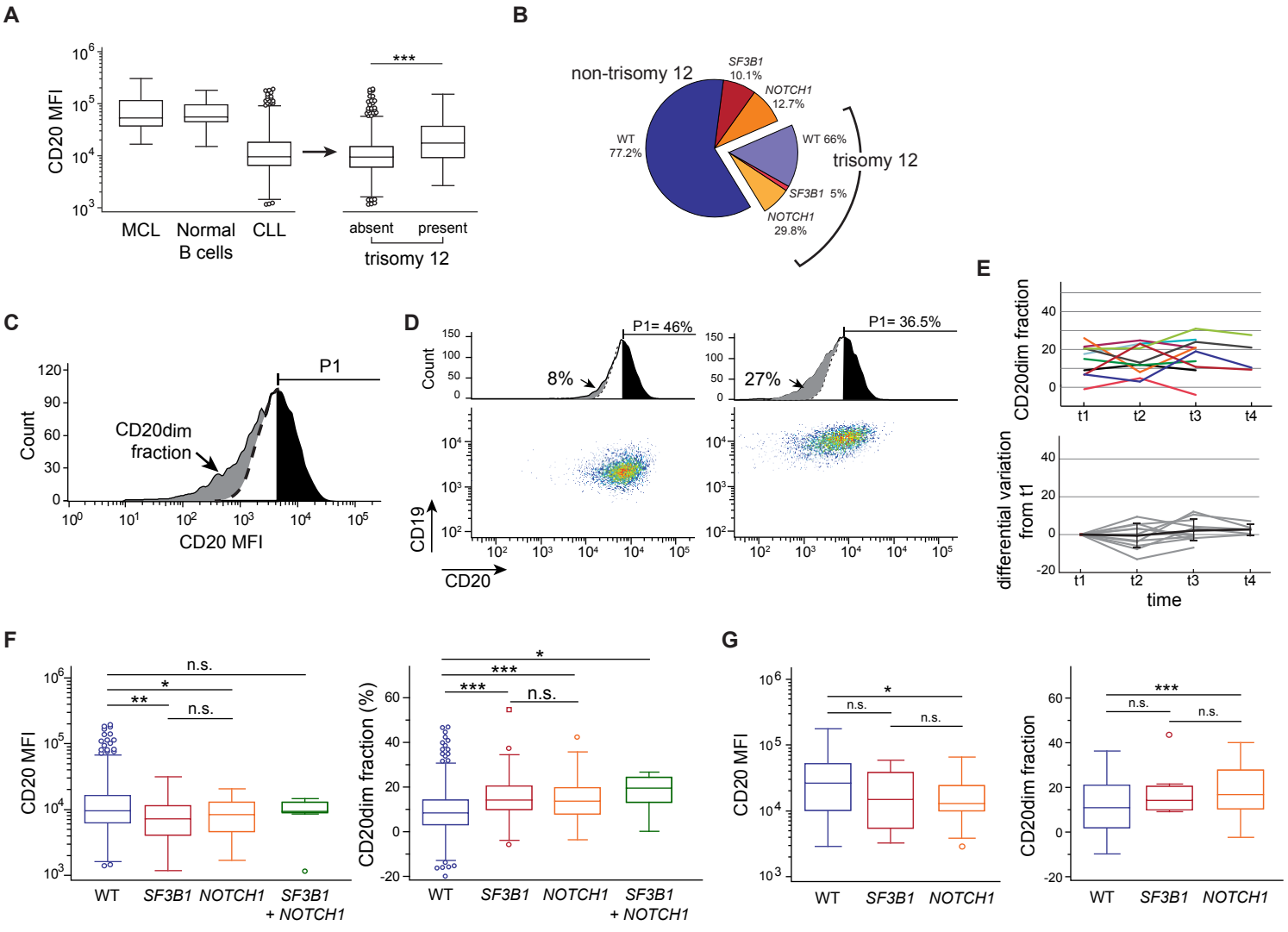
Supplementary Figure 2



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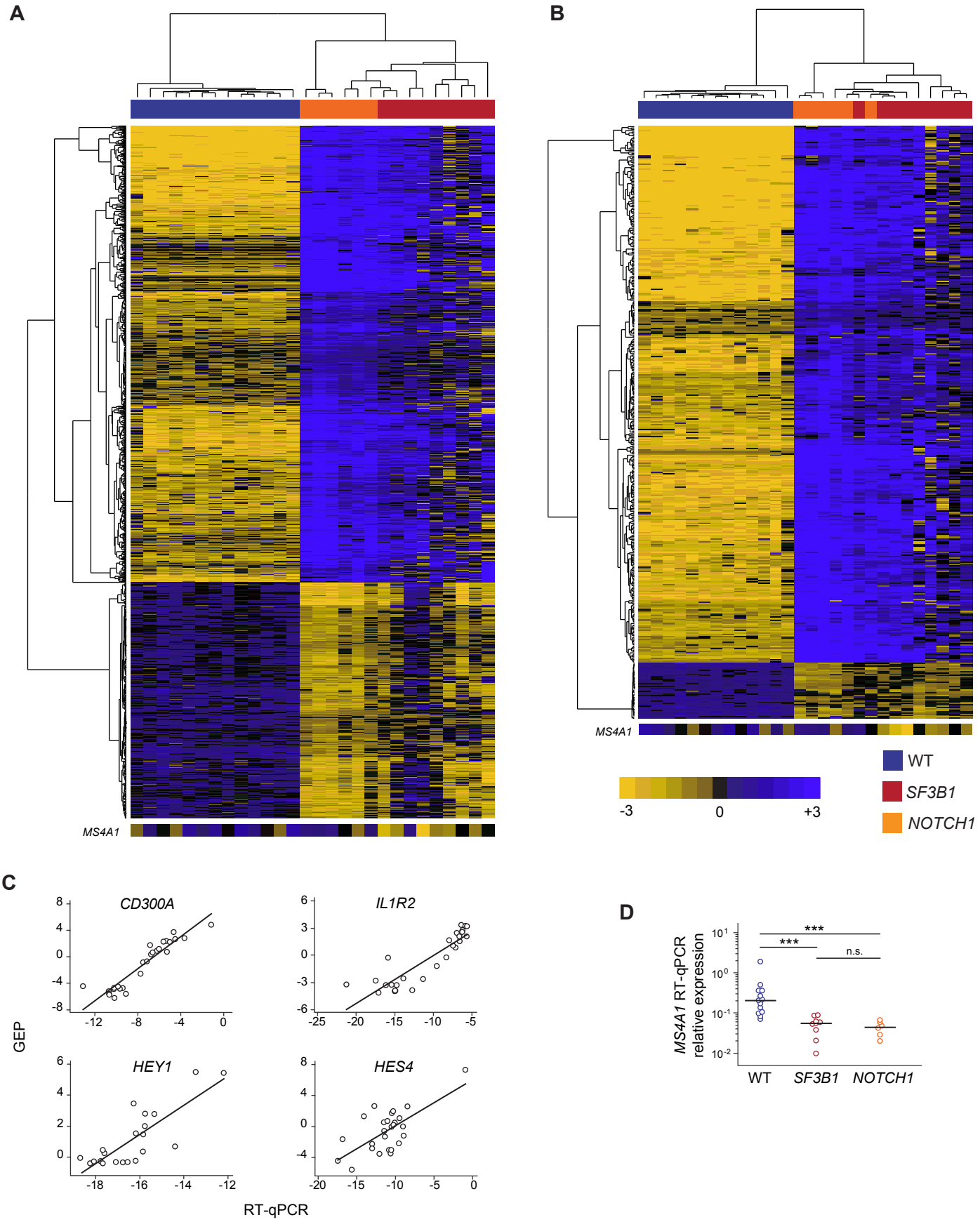

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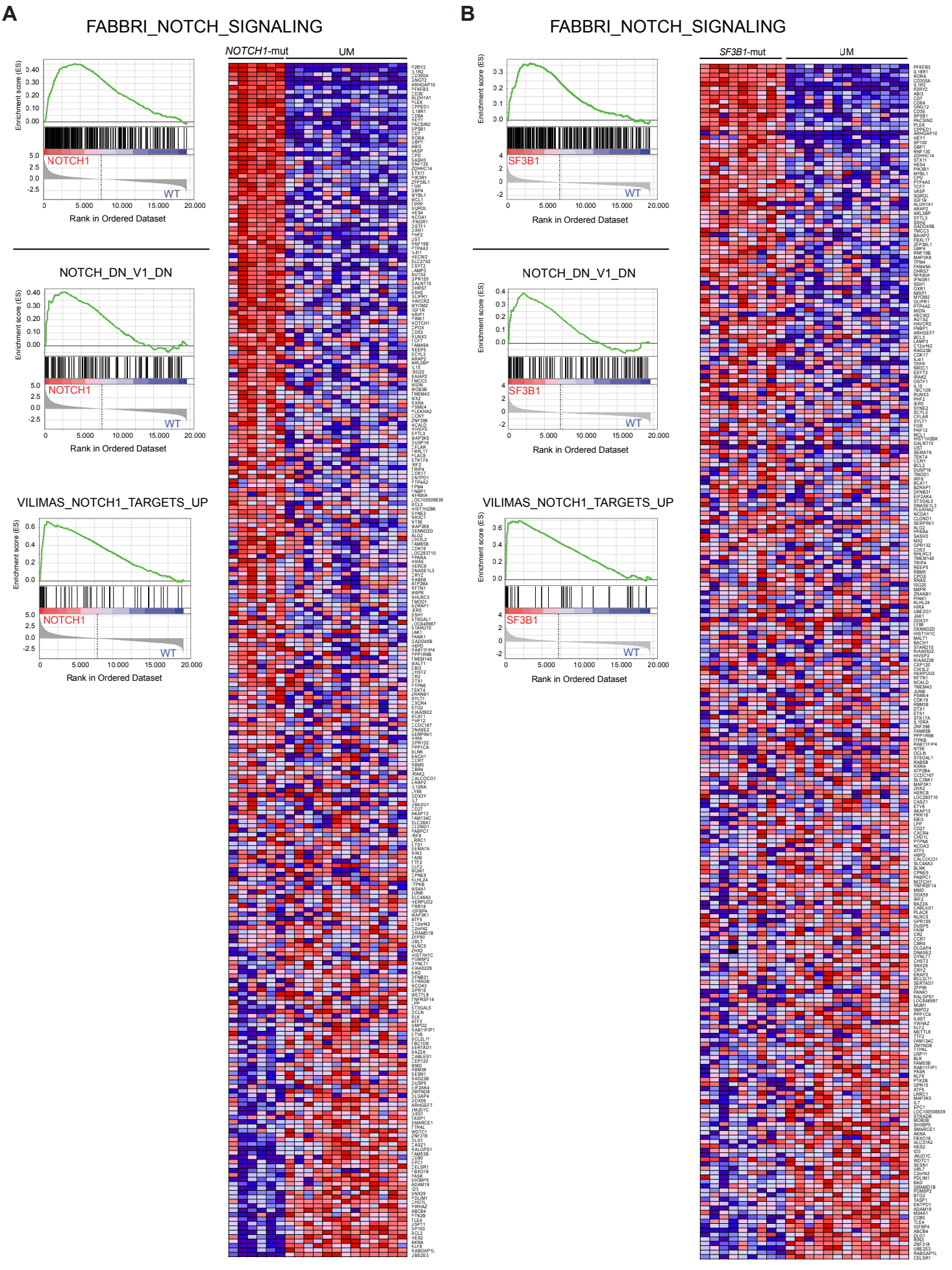

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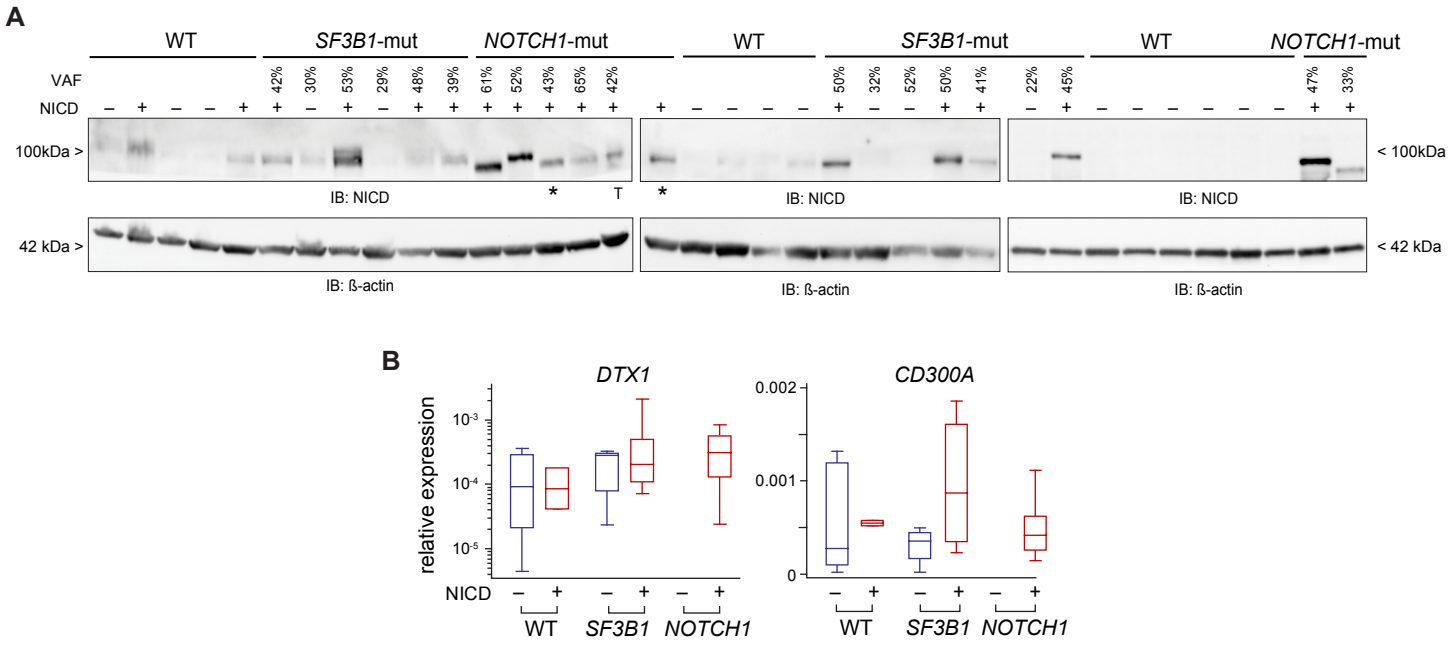

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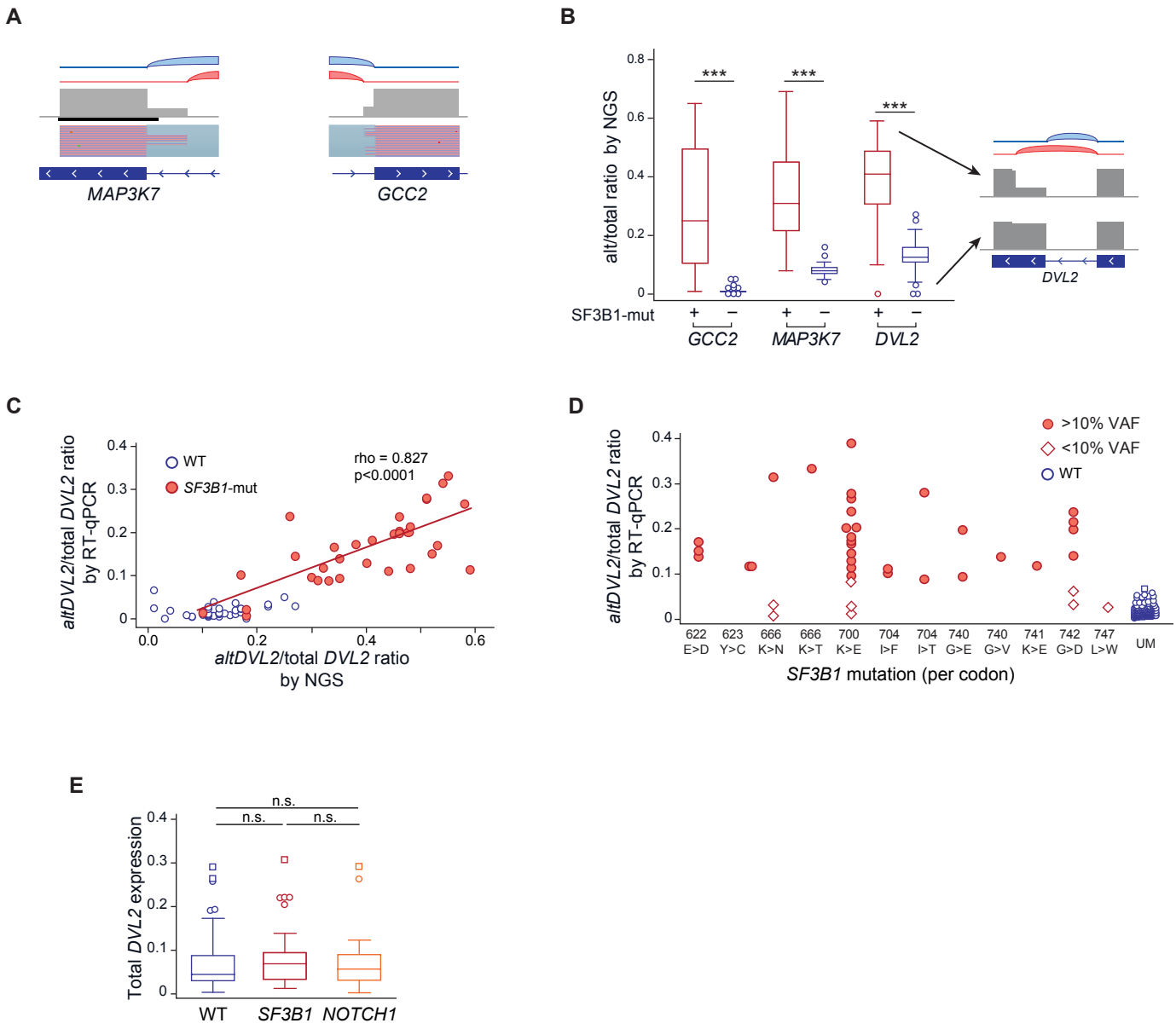
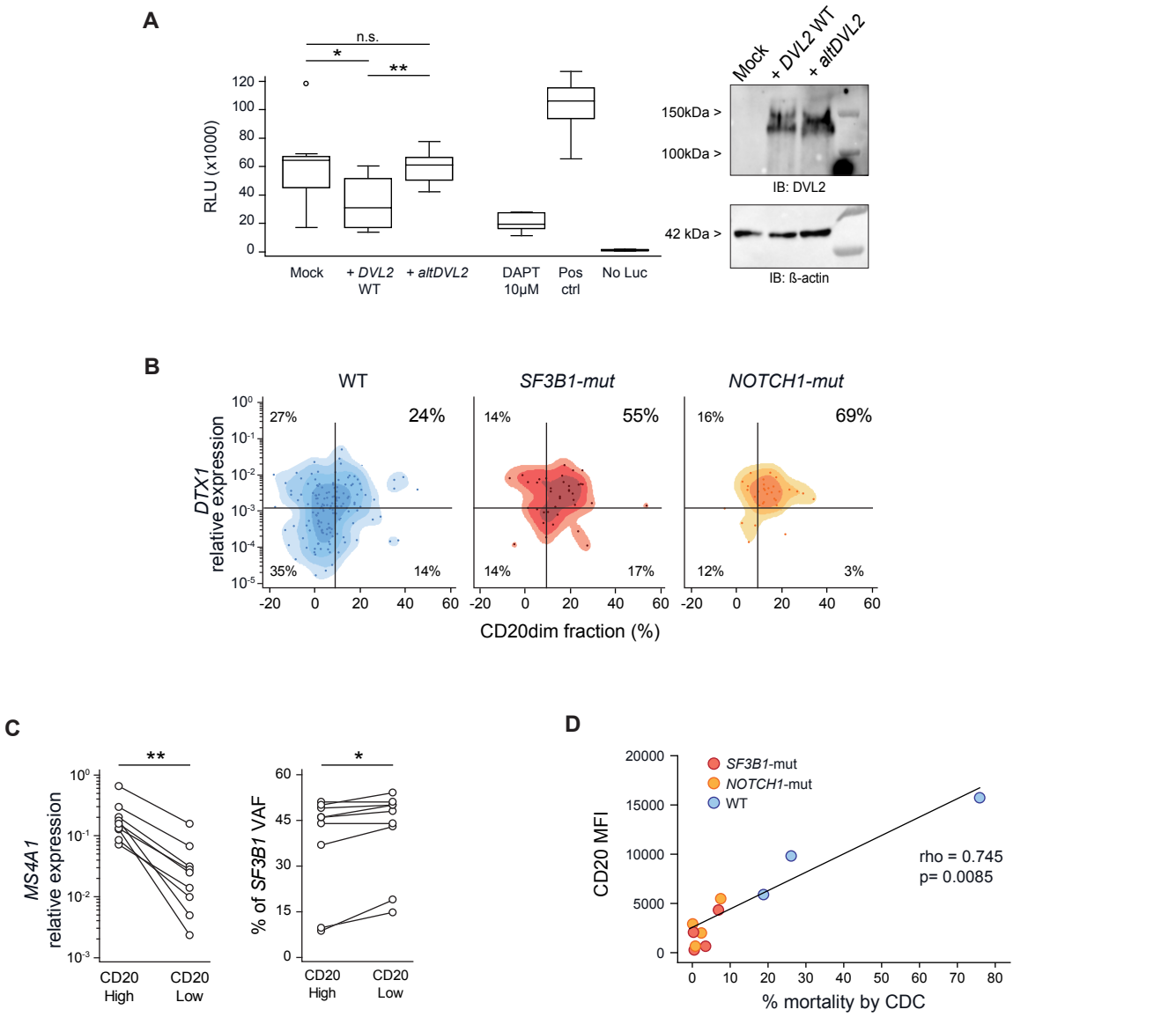


Supplementary Figure 6: SF3B1 mutations induce alternative splicing. (A) Depiction of alternative splicing events triggered by *SF3B1* mutations on *GCC2 and MAP3K7* as from IGV software. Gapped alignments are presented in light blue. Blue and red arches represent canonical and alternative splicing events, respectively. (B) Fraction of alternatively spliced isoforms in *SF3B1*-mut (n=34) or WT (n=39) cases. (C) Correlation of *altDVL2* fraction determined either by NGS or RT-qPCR. The Spearman's rank correlation coefficient (rho) and p-value are reported for *SF3B1*-mut (n=34) cases. WT cases (n=39) are reported for comparison. (D) *altDVL2* expression in relation with *SF3B1* mutations according to the mutated amino-acidic residue and burden (n=35). WT cases (n=155) are reported for comparison. Horizontal line represents the median. See also Figure 2D. (E) Expression of total *DVL2* transcript expression in *SF3B1*-mut (SF3B1, n=35), *NOTCH1*-mut (NOTCH1, n=32) or unmutated (WT, n=155) CLL cases. Data are shown by Tukey's box and whisker plots. Outliers indicate data outside the 1.5 interquartile range. * p≤0.05, ** p≤0.01, *** p≤0.001, n.s. not significant, as determined by two-sided Mann-Whitney rank-test.

Supplementary Figure 7



Supplementary Figure 7: Correlation between NOTCH1 signaling, DVL2 expression and CD20 downregulation. (A) Activity of the NOTCH1 pathway in a HEK293-CSL reporter cell line with constitutively active signaling, transfected with either a wild-type *DVL2* or *altDVL2*. Controls include transfection with no DNA (Mock), treatment with the gamma-secretase inhibitor DAPT, no transfection (Pos ctrl) and no luciferase reagent (No Luc). Mock vs. *DVL2*, p=0.0244; Mock vs. *altDVL2*, p=0.96; *DVL2* vs. *altDVL2*, p= 0.0040. RLU: Relative Luciferase Units. Transfections were performed three times in triplicate, while controls were performed three times in duplicate. Data are shown by Tukey's box and whisker plots. Outliers indicate data outside the 1.5 interquartile range. Right panel: western blot analyses for transfection of *DVL2/altDVL2* in transfected cells. (B) Density plots (log10 density) of *DTX1* expression versus CD20dim fraction for WT (n=155), *SF3B1*-mut (n=35) and *NOTCH1*-mut (n=32) cases. Quadrant gates were set at the modal value of each parameter for WT cases; population frequency of each quadrant is reported. (C) Transcript expression of *MS4A1* determined by RT-qPCR (left panel) and *SF3B1* variant allele frequency determined by NGS in the CD20-High and CD20-Low subpopulations of sorted samples (n=9). Data are shown as dot-and-line diagrams. (D) Correlation between CD20 expression and percentage of relative lysis by complement-dependent cytotoxicity in *SF3B1*-mut, *NOTCH1*-mut and WT CLL cases. The Spearman's rank correlation coefficient (rho) and p-value are reported. * p≤0.05, ** p≤0.01, *** p≤0.001, n.s. not significant, as determined by two-sided Mann-Whitney rank-test.

Suplementary Table 1. Biological characterization of the CLL cohort (537 cases).

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
2469	del11q	absent	UM	wt	wt	mut	76203	2,4
2473	del17p	present	UM	wt	p.P2514Rfs*4 17%; p.L2457V 2.7%	wt	6619	19,2
2476	tris12	present	M	wt	wt	wt	84636	1
2480	del11q	absent	UM	wt	wt	wt	5243	27
2483	del17p	absent	UM	wt	wt	wt	10456	28,2
2495	del11q	present	UM	wt	p.P2514Rfs*4 3.3%	n.a.	16262	7,4
2496	del17p	absent	M	wt	wt	mut	1397	12,6
2499	del13q	absent	M	wt	wt	wt	14526	11,2
2521	del11q	absent	n.a.	p.G742D 17%	p.P2514Rfs*4 30%	wt	9828	29,4
2526	del13q	absent	M	wt	wt	wt	6530	8,6
2528	tris12	present	M	wt	wt	wt	113087	3,2
2530	tris12	present	n.a.	wt	p.P2514Rfs*4 37.5%	wt	10013	16
2548	del13q	absent	M	wt	wt	wt	5284	13,6
2561	del13q	absent	M	wt	wt	wt	14899	14,2
2581	tris12	present	UM	wt	wt	wt	2820	33
2586	del11q	absent	UM	wt	p.Q2444* 17%	wt	4240	50,4
2598	normal	absent	M	wt	p.P2514Rfs*4 35%	wt	7576	34,4
2601	tris12	present	M	wt	p.P2514Rfs*4 11.8%	wt	27337	12,8
2604	del13q	absent	UM	p.K700E 22%	wt	wt	2606	31,4
2607	tris12	present	M	wt	wt	wt	25350	8,4
2612	del17p	absent	UM	wt	wt	wt	7421	14
2621	del13q	absent	UM	wt	wt	wt	7695	4,4
2622	del17p	absent	UM	wt	p.P2514Rfs*4 1.59%	mut	1738	41,6
2623	tris12	present	UM	wt	wt	wt	32150	10,4
2630	tris12	present	UM	p.K666R 7%	wt	wt	4796	9,8
2631	normal	absent	UM	wt	wt	wt	6094	17,2
2635	tris12	present	UM	wt	wt	mut	7961	20,8
2649	tris12	present	UM	wt	p.P2514Rfs*4 18.5%	n.a.	11168	36
2655	del11q	absent	UM	wt	wt	wt	7687	12,6
2660	del13q	absent	M	wt	wt	wt	6779	9,6
2663	del11q	absent	UM	wt	wt	wt	3590	45,6
2674	tris12	present	M	wt	wt	wt	4957	11,8
2682	normal	absent	UM	p.K700E 21%	p.P2514Rfs*4 20.9%	wt	1182	58,8
2685	del11q	absent	UM	wt	wt	wt	4994	35
2688	del13q	absent	M	wt	wt	wt	15304	15
2690	tris12	present	M	wt	wt	wt	102820	9,4
2692	tris12	present	UM	wt	wt	wt	13203	21
2703	del17p	absent	UM	wt	wt	mut	6574	21,6
2707	tris12	present	UM	wt	p.P2514Rfs*4 61%	wt	31230	7
2710	del11q	absent	UM	wt	wt	wt	7030	44,8
2714	del17p	absent	M	wt	wt	mut	53604	5,4
2715	del13q	absent	n.a.	wt	wt	wt	6432	12,6
2717	del13q	absent	UM	wt	wt	wt	4279	26,4
2719	del13q	absent	UM	wt	wt	wt	12289	13,2
2723	del13q	absent	M	wt	wt	wt	4949	13,6
2730	del11q	absent	UM	wt	wt	n.a.	9421	16,8
2731	tris12	present	M	wt	wt	mut	13518	13
2735	tris12	present	UM	wt	wt	wt	3110	36
2738	tris12	present	UM	wt	wt	wt	6401	22
2741	tris12	present	UM	wt	wt	wt	3125	24
2749	normal	absent	M	wt	wt	wt	9620	9,8
2750	normal	absent	M	wt	wt	wt	4694	30
2757	del13q	absent	M	wt	wt	wt	13437	13,4
2759	normal	absent	n.a.	wt	wt	wt	11252	12
2763	del17p	absent	M	wt	wt	mut	54336	7,8
2764	normal	absent	UM	wt	p.P2514Rfs*4 6%	wt	4177	33,4
2766	normal	absent	M	wt	wt	wt	6637	5,6
2768	del13q	absent	UM	wt	p.P2514Rfs*4 15%	n.a.	19128	25,6
2769	tris12	present	M	wt	wt	wt	73263	0,2
2770	del13q	absent	UM	wt	wt	wt	8403	20,4
2774	tris12	present	M	wt	wt	wt	17437	9,4
2778	del13q	absent	UM	p.K741N 35%	p.P2514Rfs*4 23%	wt	9971	12,2
2782	tris12	present	UM	wt	wt	wt	21315	27
2786	normal	absent	M	wt	wt	wt	4530	22,2
2787	tris12	present	UM	wt	wt	wt	8040	24
2795	del17p	present	UM	wt	wt	mut	29372	14,2
2798	del13q	absent	UM	wt	wt	wt	22855	25,4
2799	del11q	absent	M	wt	wt	mut	27842	6
2803	tris12	present	M	wt	wt	wt	76416	1,4
2823	del11q	absent	UM	wt	p.P2514Rfs*4 48%	wt	4708	34,6
2825	del17p	present	UM	wt	p.P2514Rfs*4 68%	mut	49530	28
2832	del13q	absent	M	p.K700E 6%	wt	wt	2749	25
2833	normal	absent	M	wt	wt	wt	3808	36,2
2836	del13q	absent	UM	wt	wt	wt	13427	9
2837	del11q	absent	UM	wt	p.P2514Rfs*4 42%; p.Q2444* 2%	wt	9679	24,2
2839	del13q	absent	M	wt	wt	wt	7264	10,4
2840	tris12	present	M	wt	wt	wt	6049	21,6
2841	normal	absent	M	wt	wt	wt	13788	13,6
2842	del13q	absent	M	wt	wt	wt	15781	16,8
2843	del17p	absent	M	wt	wt	mut	43564	10,2
2845	normal	absent	UM	wt	p.P2514Rfs*4 15%	wt	7602	25

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
2846	del13q	absent	UM	wt	wt	wt	6120	9,2
2848	del11q	absent	UM	wt	p.P2514Rfs*4 43%	wt	4471	19,8
2849	tris12	present	UM	wt	c.*7668+371A>G 52%	wt	3887	28
2850	del13q	absent	M	wt	wt	wt	2698	8,6
2851	tris12	present	UM	wt	wt	wt	33202	10,8
2854	del13q	absent	UM	wt	wt	wt	8389	14,4
2859	normal	absent	M	wt	wt	wt	32455	15
2862	tris12	present	UM	wt	wt	wt	11938	4,2
2863	normal	absent	UM	wt	wt	mut	3520	38,8
2866	del13q	absent	M	wt	wt	mut	10020	31
2867	normal	absent	M	wt	wt	wt	43074	9,2
2868	normal	absent	UM	p.K700E 18%	c.*7668+371A>G 25%; p.P2514Rfs*4 1%	wt	13350	9
2869	del13q	absent	M	wt	wt	mut	3877	44,6
2872	del13q	absent	M	wt	p.P2514Rfs*4 3% p.F2296fs*56 2%	wt	2625	38,8
2874	del13q	absent	UM	wt	p.P2514Rfs*4 54%	mut	4605	22
2876	del13q	absent	M	wt	wt	wt	35267	0,6
2877	del13q	absent	UM	wt	p.S2274Pfs*79 50%	mut	17125	21,8
2878	tris12	present	UM	wt	wt	wt	11674	17,6
2879	del13q	absent	M	wt	wt	wt	8222	11,6
2880	del17p	present	UM	wt	p.P2514Rfs*4 81%	mut	36080	21,8
2881	del13q	absent	M	wt	wt	wt	7512	8
2883	del17p	absent	UM	p.E622D 30%	wt	mut	9424	30,2
2884	normal	absent	UM	wt	c.*7668+378A>G 16%; p.Q2503* 2%; p.Q2501* 22%; p.Y2490* 11%	wt	9325	18,8
2887	del13q	absent	M	wt	wt	wt	34485	5,4
2888	del13q	absent	M	wt	wt	wt	2620	15,2
2889	del13q	absent	M	wt	wt	wt	39914	-5,6
2890	normal	absent	M	wt	wt	wt	6418	14,2
2891	del13q	absent	M	wt	wt	wt	21087	19,4
2892	del13q	absent	M	wt	wt	wt	7999	4
2893	normal	absent	UM	p.G742D 41%	wt	wt	8263	31
2895	del13q	absent	M	wt	wt	wt	8198	29,4
2896	normal	absent	UM	wt	wt	wt	6138	26,6
2898	del13q	absent	M	wt	wt	wt	10856	5,2
2899	del13q	absent	M	wt	wt	wt	14242	9,6
2900	del17p	absent	UM	wt	wt	mut	45539	9,8
2901	normal	absent	M	wt	wt	wt	7920	13,6
2902	del13q	absent	M	wt	wt	wt	36261	-4,8
2905	tris12	present	UM	wt	c.*7668+371A>G 45.9%	wt	13843	11,8
2906	del11q	absent	M	wt	wt	wt	13146	32
2907	del17p	absent	M	wt	wt	mut	65039	3,8
2908	del13q	absent	UM	wt	wt	mut	3737	26,4
2909	del11q	absent	UM	wt	wt	wt	8731	13,8
2912	del17p	absent	UM	wt	c.*7668+378A>G 33.3%	mut	8438	13,2
2913	del13q	absent	UM	wt	wt	wt	3372	37,4
2914	del13q	absent	M	wt	wt	wt	51540	9,8
2915	del13q	absent	M	wt	wt	wt	8365	14
2917	tris12	present	UM	wt	wt	wt	7886	4,6
2921	del13q	absent	UM	wt	c.*7668+371A>G 47.4%	wt	7314	34,2
2923	del13q	absent	UM	wt	wt	wt	6293	16,6
2925	normal	absent	M	wt	wt	wt	2619	-14
2926	del17p	absent	M	wt	wt	mut	54015	2,2
2928	normal	absent	M	wt	wt	wt	178310	3,2
2929	del13q	absent	M	wt	wt	wt	66826	5,8
2933	del11q	absent	UM	p.K700E 40%	wt	n.a.	1219	71,2
2934	del13q	absent	M	wt	wt	wt	8025	23,2
2935	normal	absent	M	wt	wt	wt	9782	5,2
2936	normal	absent	M	wt	wt	wt	4880	27,6
2937	normal	absent	M	wt	wt	wt	4420	10
2938	tris12	present	n.a.	wt	wt	wt	43153	-4,8
2941	del13q	absent	UM	wt	wt	wt	3115	23,4
2942	del11q	absent	UM	wt	wt	wt	5019	25,2
2943	normal	absent	M	wt	wt	wt	79864	8,4
2944	del13q	absent	M	wt	wt	wt	5630	3
2945	del13q	absent	M	wt	wt	wt	5255	14
2948	normal	absent	UM	wt	c.*7668+378A>G 9%	n.a.	7366	10,6
2950	del17p	absent	UM	wt	wt	mut	28641	-2,2
2956	normal	absent	M	wt	wt	wt	1837	31
2957	tris12	present	M	wt	wt	wt	28679	12
2959	del11q	absent	UM	wt	wt	wt	9912	-6,2
2960	del13q	absent	M	wt	wt	wt	3939	27,2
2964	del13q	absent	UM	p.G740E 44%	wt	wt	9078	11
2966	tris12	present	UM	wt	p.P2514Rfs*4 24%	wt	12268	25
2971	del17p	absent	UM	wt	wt	mut	36347	17,4
2972	del13q	absent	M	wt	wt	wt	6158	4
2973	del13q	absent	UM	wt	wt	wt	6592	13,2
2974	normal	absent	M	wt	wt	mut	5148	16,4
2975	del17p	absent	UM	p.K666N 53%	wt	mut	10524	1
2976	normal	absent	M	wt	wt	wt	9756	4,2
2977	tris12	present	UM	wt	wt	wt	6571	22,8
2979	normal	absent	M	wt	wt	wt	108669	15,6
2982	tris12	present	UM	wt	wt	wt	7133	8,4

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
2983	del13q	absent	M	p.G742D 34%	wt	mut	1144	62,8
2984	del13q	absent	UM	wt	wt	mut	5124	23,6
2985	tris12	present	UM	wt	p.P2514Rfs*4 18.9%	wt	10735	18,2
2986	tris12	present	UM	wt	p.P2514Rfs*4 48%	mut	19725	15,8
2987	del13q	absent	UM	wt	wt	wt	4787	34
2989	del17p	absent	M	wt	wt	wt	42545	1
2994	tris12	present	M	wt	wt	wt	39813	-3,4
2995	normal	absent	UM	wt	wt	wt	5853	19,2
2996	tris12	present	M	p.I704T 10.4%	wt	wt	34410	12,6
2997	tris12	present	M	wt	wt	wt	98101	-4
3001	tris12	present	UM	wt	p.Q2444* 36%	wt	11025	11,6
3002	normal	absent	M	wt	wt	wt	2396	10,2
3003	del13q	absent	M	wt	wt	wt	9991	21,8
3004	del13q	absent	M	wt	wt	wt	12499	53,2
3007	tris12	present	M	wt	wt	wt	32394	13
3009	del13q	absent	UM	wt	wt	wt	7423	16,8
3011	tris12	present	UM	wt	wt	mut	16756	7,8
3012	tris12	present	M	wt	wt	wt	29959	2,6
3013	del17p	absent	M	wt	wt	mut	34423	4,4
3015	del17p	absent	UM	wt	wt	mut	16545	12,4
3016	normal	absent	UM	wt	wt	wt	6649	-2,4
3019	tris12	present	M	wt	p.Q2501* 22%; p.P2514Rfs*4 0.9%	wt	23162	15,6
3020	normal	absent	UM	wt	wt	wt	63697	5,6
3021	del11q	absent	UM	wt	wt	wt	9164	26,4
3026	tris12	present	M	wt	wt	wt	27775	15
3027	tris12	present	M	wt	wt	wt	93672	3
3028	normal	absent	UM	wt	wt	wt	183025	2,6
3029	del13q	absent	M	wt	wt	wt	51176	-4,2
3030	normal	absent	UM	wt	wt	wt	8274	15
3033	del17p	absent	UM	wt	wt	mut	10145	1,4
3034	del13q	absent	M	wt	wt	wt	12252	9,4
3035	tris12	present	UM	wt	wt	wt	9427	-7,8
3038	normal	absent	M	wt	wt	wt	3706	23
3040	del11q	present	UM	wt	wt	wt	4063	29,8
3043	del17p	absent	UM	wt	wt	wt	22232	23,4
3044	del17p	absent	UM	wt	wt	mut	2048	54,6
3045	del13q	absent	UM	wt	wt	wt	6248	19,6
3049	tris12	present	M	wt	wt	wt	52716	2
3050	del11q	absent	UM	p.G742D 46%	wt	wt	10855	46,2
3051	del13q	absent	UM	wt	wt	wt	5158	17,8
3053	del13q	absent	UM	wt	p.P2514Rfs*4 13%	mut	17841	12,6
3055	del13q	absent	UM	wt	p.P2514Rfs*4 5%; p.Q2404* 2%	wt	4128	18,2
3059	del17p	absent	M	wt	wt	mut	11960	17,2
3060	del17p	absent	UM	p.G742D 45%	wt	mut	1971	39,8
3061	normal	absent	UM	wt	p.P2514Rfs*4 37%	wt	7197	15,8
3062	normal	absent	UM	wt	wt	wt	44954	-23,2
3065	del11q	absent	UM	wt	p.Q2409* 58%	wt	6104	22
3066	tris12	present	M	p.E768K 34%	wt	wt	26463	16,4
3072	del13q	absent	UM	wt	wt	wt	10648	17
3081	normal	absent	M	wt	wt	wt	8792	26,6
3082	normal	absent	M	wt	wt	wt	8372	12
3083	normal	absent	UM	wt	wt	wt	64332	22,2
3086	del17p	absent	M	wt	wt	mut	36362	-6,2
3088	del17p	absent	UM	wt	wt	mut	13341	21,8
3090	normal	absent	UM	wt	c.*7668+371A>G 38.7%; p.P2514Rfs*4 3.5%	wt	12396	19,6
3092	tris12	present	UM	wt	p.Q2440* 48%	wt	7297	39,6
3094	del13q	absent	M	wt	wt	wt	9368	21,8
3096	del13q	absent	UM	wt	wt	wt	3994	41,8
3097	del13q	absent	UM	wt	wt	wt	9536	16,6
3099	del17p	absent	M	wt	wt	mut	113557	1,4
3100	del11q	absent	M	wt	p.P2514Rfs*4 43%	wt	6303	29
3101	del13q	absent	M	wt	p.P2514Rfs*4 6%	wt	11223	26,8
3102	del11q	absent	M	p.K700E 42%	wt	wt	27553	25,2
3103	tris12	present	M	wt	wt	wt	91161	5,2
3104	del13q	absent	M	wt	wt	n.a.	6736	15,6
3106	del13q	absent	M	wt	wt	wt	53586	20
3107	del11q	absent	UM	wt	wt	wt	4264	25,4
3108	del11q	absent	UM	wt	wt	wt	21291	23,4
3109	tris12	present	M	wt	wt	wt	153103	0,6
3110	tris12	present	UM	wt	p.P2514Rfs*4 51%	mut	2646	36
3114	normal	absent	UM	p.K700E 41%	p.P2514Rfs*4 3%	n.a.	9840	35,8
3118	normal	absent	UM	wt	p.P2514Rfs*4 84%	wt	11504	15,6
3119	normal	absent	M	wt	wt	wt	45932	20,6
3120	del11q	absent	UM	wt	wt	mut	6582	14,4
3124	normal	absent	M	wt	wt	wt	13672	26,8
3125	normal	absent	UM	wt	p.V2278Gfs*75 21%; c.*7668+371A>G 4%; p.P2514Rfs*4 0.47%	wt	4292	20,2
3126	del13q	absent	M	wt	wt	wt	6732	9
3127	normal	absent	UM	p.I704T 11%	wt	wt	4839	1,6
3132	tris12	present	M	wt	p.P2514Rfs*4 33%	wt	15891	8
3133	normal	absent	M	wt	wt	wt	5346	29,8
3134	del13q	absent	M	wt	wt	wt	8547	18,6
3136	normal	absent	M	wt	wt	wt	9995	-10,4

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
3137	del17p	absent	M	wt	wt	mut	80419	-12,6
3138	del13q	absent	M	wt	wt	wt	9981	17,2
3140	del11q	absent	UM	wt	wt	wt	5821	30,6
3142	tris12	present	UM	wt	wt	mut	13529	21
3143	tris12	present	n.a.	wt	p.S2274Pfs*79 12%; p.P2514Rfs*4 29.5%	wt	10378	26,2
3144	tris12	present	UM	wt	wt	wt	19867	6,6
3146	del13q	absent	M	wt	wt	wt	6895	31
3147	del17p	present	M	wt	wt	wt	8746	15,2
3148	normal	absent	M	wt	wt	wt	138107	6,2
3155	del17p	absent	M	wt	wt	mut	2566	29,4
3156	tris12	present	UM	wt	p.L2482* 25.2%; p.P2514Rfs*4 1.8%	wt	15753	18
3157	normal	absent	M	wt	wt	wt	4310	14,8
3159	del13q	absent	M	wt	wt	wt	7378	-2,2
3160	del13q	absent	M	wt	wt	wt	7149	15,4
3161	del13q	absent	M	wt	wt	wt	6175	18,2
3164	tris12	present	UM	wt	p.P2465Afs*13 51%	wt	33004	19
3165	del11q	absent	M	wt	wt	wt	35776	5
3166	normal	absent	M	wt	wt	wt	5270	10
3167	normal	absent	M	p.K700E 9%	wt	wt	11548	15,6
3168	tris12	present	M	wt	wt	wt	47828	16,8
3169	normal	absent	M	wt	wt	wt	6777	35,8
3170	del11q	absent	UM	wt	wt	wt	6009	35,6
3171	del13q	absent	M	wt	wt	wt	7574	22,6
3172	del13q	absent	M	p.Y623C 50%	wt	mut	5880	43,4
3175	tris12	present	M	wt	wt	wt	47103	2
3176	del13q	absent	M	wt	wt	wt	10014	13,8
3177	del11q	absent	UM	wt	p.P2514Rfs*4 46%	wt	13341	29,4
3178	del13q	absent	M	wt	wt	wt	36822	-3,4
3179	del13q	absent	M	wt	wt	wt	43479	-6,8
3180	normal	absent	M	wt	wt	wt	75008	-7
3182	del13q	absent	M	wt	wt	wt	15251	14,4
3184	del17p	absent	UM	wt	wt	mut	58079	-1,2
3185	tris12	present	UM	wt	wt	mut	4327	19,2
3186	del11q	absent	UM	wt	wt	wt	57210	12,6
3189	normal	absent	M	wt	wt	wt	94075	20,2
3190	del13q	absent	M	wt	wt	wt	21073	30
3191	del13q	absent	M	wt	wt	wt	16663	15,4
3192	del11q	absent	UM	wt	c.*7668+378A>G 51%	wt	12949	16
3193	normal	absent	M	wt	p.P2514Rfs*4 5.1%	wt	13449	7,2
3195	del11q	absent	M	wt	wt	wt	7662	12
3196	del11q	absent	M	wt	wt	wt	7293	-7,6
3202	del11q	absent	UM	wt	wt	wt	12511	17,8
3203	normal	absent	M	wt	wt	wt	4761	22,4
3205	del13q	absent	n.a.	wt	wt	wt	17715	9,6
3206	tris12	present	UM	wt	wt	wt	17978	21
3211	del13q	absent	UM	wt	wt	wt	19140	14,4
3212	del17p	absent	M	wt	wt	mut	8652	18,4
3213	tris12	present	UM	wt	p.P2514Rfs*4 37.7%	wt	16932	6
3214	del11q	absent	UM	p.K700E 5%	wt	wt	1406	14,4
3215	del13q	absent	UM	p.delQ699 41%	p.P2514Rfs*4 53%	wt	14358	33
3220	del17p	absent	M	wt	wt	mut	15215	29,4
3221	del13q	absent	M	wt	wt	wt	36365	15,6
3222	del17p	absent	M	wt	wt	mut	9271	11,2
3223	del13q	absent	UM	wt	wt	wt	7435	25,2
3225	del17p	absent	M	wt	wt	wt	23590	12,8
3226	del13q	absent	M	wt	wt	mut	9915	11,2
3228	normal	absent	M	wt	wt	wt	10044	15,8
3230	normal	absent	M	wt	wt	wt	7867	12,8
3234	tris12	present	M	wt	wt	wt	41445	3,56
3236	del11q	present	UM	wt	p.P2514Rfs*4 42%	wt	21319	4,4
3237	del17p	absent	UM	p.I704T 46%	wt	mut	6933	58,8
3239	del11q	absent	M	wt	wt	wt	7684	29,6
3240	del13q	absent	M	wt	wt	wt	5289	8,8
3241	del11q	absent	UM	wt	wt	wt	5028	34,8
3244	del13q	absent	M	wt	wt	wt	6043	7,6
3245	normal	absent	UM	wt	p.S2432Rfs*4 45%	wt	6774	9,8
3246	tris12	present	n.a.	wt	wt	wt	25438	21,4
3249	normal	absent	UM	wt	wt	mut	3945	29
3250	del17p	absent	M	wt	wt	mut	51333	12
3251	del13q	absent	M	wt	wt	wt	9270	17,6
3252	del13q	absent	UM	p.I704F 18%	wt	wt	22427	41,2
3253	normal	absent	UM	wt	wt	wt	19442	6,6
3254	del13q	absent	M	wt	wt	wt	8323	10,8
3255	normal	absent	M	wt	wt	wt	10560	20,4
3257	del17p	absent	M	wt	wt	mut	12849	14,4
3258	del13q	absent	M	wt	wt	wt	17172	10,2
3259	del17p	absent	M	wt	wt	mut	66120	1,4
3260	del13q	absent	M	wt	wt	wt	7795	23,2
3261	del13q	absent	UM	wt	wt	wt	8030	13,4
3264	del13q	absent	M	wt	wt	wt	14941	12,6
3266	tris12	present	UM	wt	wt	wt	31291	32,8
3267	del11q	absent	UM	p.G742D 29%	wt	wt	9567	14,4
3268	del17p	absent	UM	wt	wt	mut	6273	27,4
3269	tris12	present	M	wt	wt	wt	47057	2,8

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
3270	del13q	absent	UM	wt	wt	wt	9461	12,8
3271	tris12	present	UM	wt	p.P2514Rfs*4 45%	wt	12255	13,2
3276	del11q	absent	UM	p.K700E 18%	wt	mut	2346	36,8
3278	normal	absent	UM	wt	p.P2514Rfs*4 22%; p.Q2519* 7%	wt	11428	23,4
3280	del11q	absent	UM	wt	p.P2514Rfs*4 23%	wt	2316	33,6
3281	normal	absent	M	wt	wt	wt	191301	5,4
3282	normal	absent	n.a.	wt	p.P2514Rfs*4 50%	wt	1653	28,2
3284	normal	absent	M	wt	wt	wt	7499	7,4
3286	del13q	absent	UM	wt	wt	wt	13877	11,4
3287	tris12	present	n.a.	wt	p.P2514Rfs*4 23%; p.Q2487* 9%; p.Q2459* 8%	wt	9695	31,6
3289	normal	absent	n.a.	wt	wt	wt	12598	18,8
3290	normal	absent	M	wt	wt	wt	16477	9,2
3293	del11q	present	UM	wt	p.S2492* 23%	wt	9571	35,4
3294	normal	absent	UM	wt	p.P2514Rfs*4 4%; p.S2471Rfs*6 9%	wt	15503	10,4
3296	del17p	absent	UM	wt	wt	mut	4875	51,2
3297	normal	absent	UM	wt	p.P2514Rfs*4 7.9%	wt	4362	29
3299	del17p	absent	M	wt	wt	mut	58621	3
3300	del13q	absent	UM	wt	wt	mut	4432	35,4
3301	normal	absent	UM	p.R625C 10%; p.G740E 6%; p.G742D 13%	wt	mut	3525	36,8
3302	tris12	present	UM	wt	wt	wt	6833	15,8
3303	tris12	present	UM	wt	wt	wt	31358	29
3304	normal	absent	M	wt	wt	wt	11012	10,4
3308	del13q	absent	M	wt	wt	wt	10761	9,6
3309	normal	absent	n.a.	wt	wt	wt	165113	-7,8
3320	normal	absent	M	wt	wt	wt	10621	11,2
3322	normal	absent	M	p.K700E 46%	wt	wt	4787	13,2
3324	tris12	present	M	wt	wt	wt	12353	19,6
3325	del13q	absent	M	wt	wt	wt	23375	12,6
3329	normal	absent	M	wt	wt	wt	5319	12,8
3330	del17p	present	UM	wt	wt	mut	4063	29,6
3333	normal	absent	UM	wt	wt	wt	16171	11,4
3336	normal	absent	n.a.	wt	wt	mut	19655	37
3337	del13q	absent	M	wt	wt	wt	3212	15,2
3338	tris12	present	UM	wt	wt	wt	11085	-5,6
3339	del13q	absent	UM	p.E622D 39.2%	wt	wt	11165	12
3340	del13q	absent	M	wt	wt	wt	10099	9,6
3349	del13q	absent	M	wt	wt	wt	11305	10,4
3352	normal	absent	M	wt	wt	wt	137364	11,4
3353	del11q	absent	M	wt	wt	wt	9147	23,8
3355	tris12	present	M	wt	wt	wt	32676	-5
3356	normal	absent	UM	wt	wt	wt	5052	37
3357	del13q	absent	UM	wt	p.Q2501* 48%	wt	13661	1,8
3362	normal	absent	M	wt	wt	wt	10791	14,4
3363	normal	absent	UM	wt	wt	wt	47956	40,4
3365	tris12	present	n.a.	wt	wt	wt	80283	-3,6
3366	tris12	present	UM	wt	p.P2514Rfs*4 65%	wt	14135	8,4
3368	normal	absent	M	wt	wt	wt	41776	2,6
3369	normal	absent	UM	wt	wt	wt	54740	4,6
3371	del13q	absent	M	wt	wt	wt	8323	14
3372	normal	absent	UM	wt	p.P2514Rfs*4 12%	wt	9901	18,2
3373	tris12	present	UM	wt	p.P2514Rfs*4 16.6%	wt	8773	13,6
3374	normal	absent	n.a.	wt	wt	mut	1445	-7,4
3375	tris12	present	n.a.	wt	wt	wt	19646	9,8
3380	tris12	present	M	wt	p.P2514Rfs*4 19%; p.L2482* 4%	wt	47388	4
3381	del17p	absent	UM	wt	p.P2514Rfs*4 47.3%	mut	15085	27,2
3383	tris12	present	M	wt	wt	wt	127962	-1,4
3384	del13q	absent	M	wt	wt	wt	11186	44
3385	normal	absent	M	wt	wt	wt	42965	6
3386	del11q	absent	UM	wt	wt	wt	2470	50,4
3387	del13q	absent	UM	wt	wt	wt	7244	36
3388	normal	absent	UM	p.I704F 28%	wt	wt	4870	31,8
3390	del11q	absent	UM	wt	wt	wt	9958	20,4
3391	normal	absent	M	p.K700E 36%	wt	wt	6657	10,8
3393	del13q	absent	UM	p.G740E 46%	wt	mut	1753	35,2
3396	del11q	absent	UM	wt	wt	wt	9149	18,8
3398	normal	absent	UM	wt	p.Q2391* 42%	wt	10514	30,8
3399	del17p	absent	M	wt	wt	mut	53018	10,2
3400	del11q	absent	UM	wt	c.*7668+378A>G 12%	wt	9927	23,4
3401	del13q	absent	DISC	wt	wt	wt	12064	11,8
3402	del13q	absent	UM	wt	p.L2482* 33%	wt	10563	33,4
3405	tris12	present	UM	wt	c.*7668+378A>G 36%	wt	5686	28,6
3406	del17p	absent	UM	wt	p.P2514Rfs*4 48%	mut	15128	8,8
3407	del13q	absent	UM	wt	wt	wt	8577	24,6
3409	del17p	absent	M	wt	wt	mut	7065	19,2
3410	del11q	absent	UM	wt	wt	wt	12609	39,4
3411	normal	absent	M	wt	wt	wt	9422	8,2
3413	tris12	present	M	wt	p.Q2403fs*19 25%	wt	58794	8,4
3414	tris12	present	M	wt	wt	wt	92236	-2,2
3415	normal	absent	M	wt	wt	wt	10087	36,2
3417	tris12	present	UM	wt	wt	wt	12961	11,6

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
3423	del13q	absent	M	wt	wt	wt	4209	43,6
3424	normal	absent	n.a.	wt	wt	wt	6928	15
3425	normal	absent	UM	wt	wt	mut	13039	21,4
3426	tris12	present	UM	wt	wt	wt	30250	10,8
3428	n.a.	absent	M	wt	p.Q2503* 8%	wt	9264	13,2
3430	normal	absent	UM	wt	wt	mut	4550	21,8
3431	del13q	absent	M	wt	wt	wt	15428	2,6
3432	del13q	absent	n.a.	wt	wt	wt	11261	15
3433	tris12	present	M	wt	wt	wt	13376	16,2
3435	normal	absent	UM	p.K741E 34%	wt	wt	15079	20
3436	del17p	absent	UM	wt	wt	mut	6640	43,8
3437	tris12	present	n.a.	p.Y765del 26%	wt	wt	53227	10,4
3438	del13q	absent	M	wt	wt	wt	22640	8,8
3439	del13q	absent	M	wt	wt	wt	8779	25
3440	tris12	present	M	wt	wt	wt	44450	4,4
3442	normal	absent	M	wt	wt	wt	11329	9,4
3443	del13q	absent	M	wt	wt	wt	10431	16,6
3444	normal	absent	UM	wt	wt	wt	4214	19,2
3447	normal	absent	UM	wt	p.P2514Rfs*4 42%	wt	3486	32,2
3449	tris12	present	M	wt	wt	wt	55293	5,4
3450	normal	absent	M	wt	wt	wt	8641	9,6
3452	del13q	absent	M	wt	wt	wt	15241	14,8
3453	del13q	absent	UM	wt	wt	wt	6561	11
3454	tris12	present	M	wt	wt	wt	5627	27
3455	normal	absent	M	wt	wt	wt	9988	23,2
3458	del13q	absent	UM	wt	wt	wt	10130	57,6
3460	normal	absent	M	wt	wt	wt	5603	18,8
3461	del13q	absent	UM	wt	wt	wt	15498	41,6
3462	tris12	present	UM	wt	wt	wt	3419	36
3465	del13q	absent	M	wt	wt	wt	9538	12
3467	del13q	absent	M	wt	wt	wt	11223	24
3468	del17p	absent	M	wt	wt	mut	11846	19,8
3469	normal	absent	M	wt	wt	wt	16280	10,6
3473	del13q	absent	UM	wt	wt	wt	16283	13,2
3475	tris12	present	n.a.	wt	wt	wt	17849	-7,2
3477	normal	absent	UM	p.E622D 32%	wt	wt	9251	9,2
3478	normal	absent	M	wt	wt	wt	71946	16,4
3479	normal	absent	UM	wt	wt	mut	7471	26,4
3480	del11q	absent	UM	wt	wt	wt	9144	20,4
3489	del13q	absent	M	wt	wt	wt	12546	15,8
3490	del13q	absent	M	wt	wt	wt	7249	17,6
3491	tris12	present	M	wt	wt	wt	47591	1
3492	normal	absent	M	wt	wt	wt	7389	12
3494	tris12	present	UM	wt	p.P2514Rfs*4 49.5%; p.R2104H 2%	wt	12031	-2,4
3499	normal	absent	M	wt	wt	wt	37639	6,6
3501	del13q	absent	M	wt	wt	mut	16624	5,4
3503	del13q	absent	M	wt	wt	wt	10190	26,8
3505	del13q	absent	M	wt	wt	wt	9844	11
3510	del13q	absent	M	wt	wt	wt	6177	26,2
3512	del13q	absent	M	wt	wt	wt	6753	27,4
3513	del13q	absent	M	wt	wt	wt	13778	14,6
3514	del17p	absent	UM	p.K666N 33%	wt	mut	16616	21,8
3515	tris12	present	UM	wt	wt	wt	8823	33,8
3518	del13q	absent	UM	wt	wt	wt	5220	17
3525	normal	absent	M	wt	wt	wt	5736	35,6
3526	normal	absent	M	wt	wt	wt	5199	27,6
3527	normal	absent	M	wt	wt	wt	48900	21,6
3528	del17p	absent	M	wt	wt	mut	8561	18,6
3529	normal	absent	M	wt	wt	wt	113648	1
3531	normal	absent	M	wt	wt	wt	5257	24,8
3532	normal	absent	M	wt	wt	wt	4417	21,6
3533	normal	absent	M	wt	wt	wt	5140	18,4
3536	tris12	present	M	wt	wt	wt	66702	1,4
3537	del13q	absent	M	wt	wt	wt	24774	11,8
3538	normal	absent	M	wt	wt	wt	101582	10,4
3539	normal	absent	M	wt	wt	wt	8034	4,4
3541	del13q	absent	n.a.	wt	wt	wt	14740	39,2
3543	tris12	present	UM	wt	wt	wt	22322	27,2
3544	tris12	present	UM	wt	p.P2514Rfs*4 37.8%	wt	19970	17,8
3550	tris12	present	M	wt	wt	wt	14278	11,2
3551	del13q	absent	M	wt	wt	wt	7497	16
3552	tris12	present	M	wt	wt	wt	43002	-9,8
3555	normal	absent	M	wt	wt	n.a.	11511	11,6
3558	tris12	present	UM	wt	p.P2514Rfs*4 47%	wt	3643	27,2
3559	normal	absent	UM	p.K666T 48%	wt	mut	7836	20,2
3560	normal	absent	UM	wt	p.P2514Rfs*4 8%	wt	5293	22,8
3561	del13q	absent	M	p.K700E 39%	wt	wt	4846	28,4
3564	normal	absent	UM	wt	wt	wt	81317	14
3565	del13q	absent	M	wt	wt	wt	1603	56,8
3566	normal	absent	UM	p.K700E 45%	wt	mut	6043	25,4
3569	normal	absent	M	wt	wt	wt	8004	15,6
3570	del13q	absent	UM	wt	wt	wt	10067	13,8
3571	del13q	absent	n.a.	wt	wt	wt	7925	11,2
3572	del13q	absent	UM	wt	wt	wt	5481	18,6
3574	del11q	absent	UM	wt	wt	wt	8333	15,6

ID	FISH[A]	Trisomy 12	IGHV[B]	*SF3B1* status[C]	*NOTCH1* status[C]	*TP53* status[C]	CD20 MFI	CD20dim fraction (%)
3575	normal	absent	UM	wt	wt	wt	12195	34,2
3576	tris12	present	UM	p.G740E 38%	wt	wt	7370	42,8
3584	tris12	present	M	wt	wt	wt	34757	5,6
3585	del13q	absent	M	wt	p.P2235Gfs*12 38%	wt	15547	8,2
3586	normal	absent	M	wt	wt	wt	18592	4,2
3589	del13q	absent	M	wt	wt	wt	10174	8,4
3590	del11q	absent	UM	wt	wt	wt	16561	12,6
3593	tris12	present	UM	wt	p.P2514Rfs*4 37.4%	wt	5031	30
3594	normal	absent	M	p.K700E 42%	wt	wt	12915	20,2
3597	del11q	absent	UM	wt	wt	wt	10509	23,2
3598	del17p	absent	UM	wt	wt	n.a.	5460	31,6
3599	tris12	present	UM	wt	p.Q2503Gfs*3 33%; p.V2504L 39%	wt	11337	14,8
3603	del13q	absent	M	wt	wt	wt	9844	12
3606	normal	absent	M	wt	wt	wt	5890	9,2
3610	normal	absent	M	wt	wt	wt	39747	32,8
3613	normal	absent	M	wt	wt	mut	5298	23,2
3614	del13q	absent	M	wt	wt	wt	12301	7,6
3617	del13q	absent	M	wt	wt	wt	4891	9,2
3620	del13q	absent	M	p.G740V 44%	wt	wt	17401	7,4
3621	del13q	absent	UM	wt	p.R2431Gfs*4 23%; p.P2514Rfs*4 3.6%	wt	9507	15,4
3622	del13q	absent	M	wt	wt	wt	3701	32,8
3624	del11q	absent	UM	wt	wt	wt	11965	29,8
3625	tris12	present	M	wt	wt	wt	123166	28,6
3626	normal	absent	M	wt	wt	wt	9170	4,6
3627	tris12	present	UM	wt	wt	mut	15166	17,4
3628	normal	absent	UM	p.K700E 34%	wt	wt	6957	16
3632	normal	absent	UM	wt	p.P2514Rfs*4 34%; p.Q2395K 3%	wt	4808	25
3647	del13q	absent	UM	p.K700E 41.5%; p.G742D 12%	wt	wt	4025	40,8
3652	del13q	absent	M	wt	wt	wt	7764	13,2
3655	normal	absent	M	wt	wt	wt	4570	21,2
3657	del13q	absent	DISC	wt	wt	wt	1944	-2,8
3658	normal	absent	M	wt	wt	wt	9496	21
3663	normal	absent	M	wt	wt	mut	20812	18,6
3664	del13q	absent	UM	wt	wt	wt	13276	11,2
3667	tris12	present	M	wt	wt	wt	49583	-4,8
3674	del13q	absent	M	wt	wt	wt	11143	23,8
3675	tris12	present	UM	p.P780R 50%	wt	wt	3164	21,2
3678	del13q	absent	M	wt	wt	wt	11063	25,4
3684	normal	absent	M	wt	wt	wt	2606	21,6
3699	del11q	absent	UM	wt	wt	wt	11944	21,6
3700	del11q	absent	UM	wt	wt	wt	7616	10,2
3701	del11q	absent	UM	wt	wt	mut	6373	51
3702	del13q	absent	UM	p.G740E 37%	wt	mut	6629	16,6
3704	del17p	absent	M	wt	wt	mut	11640	15,2

A: FISH status was determined according to Dal Bo et al., Leukemia 2016.

B: IGHV status was established according to the conventional cut-off, as reported in Dal Bo et al., Leukemia 2016.

C: as determined by Next Generation Sequencing.

ID: identification number; FISH: norm, normal karyotype; n.a., not available; IGHV status: UM, IGHV unmutated, M, IGHV mutated, DISC, Discordant.

Supplementary Table 2. Association between SF3B1 mutations and biological prognosticators for CLL.

		SF3B1 [n (%)]		Chi-squared
		unmutated	mutated	
del11q	absent	432 (80.4)	41 (7.6)	p=0.5507
	present	57 (10.6)	7 (1.3)	
del13q	absent	251 (46.7)	29 (5.4)	p=0.2295
	present	238 (44.3)	19 (3.5)	
tris12	absent	374 (69.6)	42 (7.8)	p=0.0815
	present	115 (21.4)	6 (1.1)	
del17p	absent	437 (81.4)	43 (8)	p=0.9628
	present	52 (9.7)	5 (0.9)	
IGHV	M	260 (50.7)	12 (2.3)	p=0.0006
	UM	207 (40.4)	34 (6.6)	
NOTCH1	unmutated	406 (75.6)	42 (7.8)	p=0.4268
	mutated	83 (15.5)	6 (1.1)	
TP53	unmutated	405 (76.9)	33 (6.3)	p=0.0313
	mutated	76 (14.4)	13 (2.5)	

Supplementary Table 3. Differentially expressed probes between SF3B1-mut and WT CLL cases.

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
A_19_P00317504	Homo sapiens cDNA FLJ42830 fis, clone BRCAN2017905. [AK124820]	miscellaneous	1.25E-02	4.17E-07	down	-2.14	Not used
A_21_P0005204	not provided	unannotated probe	3.42E-02	1.14E-06	down	-2.31	Not used
A_21_P0006753	AGENCOURT_8058623 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6213075 5', mRNA sequence [BU146091]	miscellaneous	3.04E-02	1.02E-06	down	-2.88	Not used
A_21_P0008460	numb homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:8060] [ENST00000557577]	miscellaneous	3.70E-02	1.24E-06	up	6.38	Not used
A_21_P0008678	not provided	unannotated probe	1.39E-02	4.64E-07	down	-1.92	Not used
A_21_P0011295	hect domain and RLD 2 pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:4871] [ENST00000429926]	pseudogene	1.80E-02	5.99E-07	down	-3.03	Not used
A_21_P0013340	CCZ1 vacuolar protein trafficking and biogenesis associated homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:21691] [ENST00000478672]	miscellaneous	5.57E-03	1.85E-07	down	-2.05	Not used
A_21_P0014281	BX096603 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998H151782, mRNA sequence [BX096603]	miscellaneous	1.03E-02	3.41E-07	up	3.72	Not used
A_21_P0014386	not provided	unannotated probe	2.50E-02	8.34E-07	down	-3.29	Not used
A_21_P0014540	not provided	unannotated probe	2.43E-02	8.11E-07	down	-3.51	Not used
A_21_P0014591	Q25I99_MACFA (Q25I99) Brain cDNA, clone: QflA-19334, partial (47%) [THC2602892]	miscellaneous	2.08E-02	6.92E-07	down	-2.50	Not used
A_24_P126741	glutaredoxin (thioltransferase) pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:34049] [ENST00000470810]	pseudogene	1.23E-06	4.05E-11	up	16.09	Not used
A_24_P357468	T cell receptor alpha variable 8-2 [Source:HGNC Symbol;Acc:HGNC:12147] [ENST00000390434]	miscellaneous	4.61E-03	1.53E-07	up	3.90	Not used
A_33_P3232688	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:HGNC:2435] [ENST00000381524]	miscellaneous	3.28E-04	1.08E-08	up	8.20	Not used
A_33_P3243230	HSINTLK8M interleukin 8 (Homo sapiens) (exp=-1; wgp=0; cg=0), partial (97%) [THC2544321]	miscellaneous	3.72E-08	1.22E-12	up	225.52	Not used
A_33_P3269019	Homo sapiens cDNA FLJ13275 fis, clone OVARC1001032. [AK023337]	miscellaneous	4.86E-03	1.61E-07	down	-3.14	Not used
A_33_P3321372	contactin associated protein-like 3B [Source:HGNC Symbol;Acc:HGNC:32035] [ENST00000276974]	miscellaneous	3.30E-06	1.09E-10	up	33.00	Not used
A_33_P3331791	not provided	unannotated probe	2.36E-02	7.88E-07	down	-2.26	Not used
A_33_P3338292	not provided	unannotated probe	1.63E-02	5.43E-07	down	-3.06	Not used
A_33_P3347503	not provided	unannotated probe	2.86E-02	9.56E-07	up	11.63	Not used
A_33_P3352980	not provided	unannotated probe	6.83E-03	2.27E-07	down	-2.39	Not used
A_33_P3397127	Homo sapiens mRNA for T cell receptor beta variable 6, partial cds, clone: un 226. [AB306238]	miscellaneous	1.06E-03	3.52E-08	up	3.47	Not used
A_33_P3421907	nitric oxide synthase 2 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:7875] [ENST00000580780]	pseudogene	4.52E-02	1.51E-06	down	-2.73	Not used
AAK1	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA [NM_014911]	gene	1.74E-07	5.71E-12	up	9.53	1
AAK1	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA [NM_014911]	gene	9.82E-03	3.27E-07	up	4.37	Not used
AAK1	Homo sapiens cDNA clone IMAGE:5226225. [BC090950]	miscellaneous	4.07E-02	1.36E-06	up	2.32	Not used
ABI3	Homo sapiens ABI family, member 3 (ABI3), transcript variant 1, mRNA [NM_016428]	gene	6.03E-04	1.99E-08	up	3.01	2
ACPP	Homo sapiens acid phosphatase, prostate (ACPP), transcript variant 1, mRNA [NM_001099]	gene	2.11E-03	6.98E-08	up	8.37	3
ACSL1	Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), transcript variant 1, mRNA [NM_001995]	gene	1.82E-02	6.06E-07	up	3.40	4
ACSL6	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), transcript variant 2, mRNA [NM_001009185]	gene	1.29E-02	4.28E-07	up	4.30	5
ACTL8	Homo sapiens actin-like 8 (ACTL8), mRNA [NM_030812]	gene	3.68E-03	1.22E-07	down	-2.29	6
ACTN1	Homo sapiens actinin, alpha 1 (ACTN1), transcript variant 2, mRNA [NM_001102]	gene	9.36E-07	3.08E-11	up	24.29	7
ACVR1C	Homo sapiens activin A receptor, type IC (ACVR1C), transcript variant 1, mRNA [NM_145259]	gene	1.90E-03	6.31E-08	up	4.39	8
ADAMTS10	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 10 (ADAMTS10), transcript variant 1, mRNA [NM_030957]	gene	1.14E-03	3.78E-08	up	7.19	9
ADM	Homo sapiens adrenomedullin (ADM), mRNA [NM_001124]	gene	1.10E-02	3.66E-07	up	43.98	10
AGPAT9	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9), transcript variant 1, mRNA [NM_032717]	gene	7.72E-03	2.56E-07	up	10.08	11
AIF1	Homo sapiens allograft inflammatory factor 1 (AIF1), transcript variant 2, mRNA [NM_004847]	gene	5.70E-05	1.88E-09	up	10.63	12
AKR1C3	Homo sapiens aldo-keto reductase family 1, member C3 (AKR1C3), transcript variant 1, mRNA [NM_003739]	gene	1.51E-05	4.99E-10	up	12.46	13
AMPD2	Homo sapiens adenosine monophosphate deaminase 2 (AMPD2), transcript variant 1, mRNA [NM_004037]	gene	4.72E-03	1.57E-07	up	3.16	14
ANPEP	Homo sapiens alanyl (membrane) aminopeptidase (ANPEP), mRNA [NM_001150]	gene	4.43E-03	1.47E-07	up	5.62	15
ANXA1	Homo sapiens annexin A1 (ANXA1), mRNA [NM_000700]	gene	4.17E-05	1.38E-09	up	52.11	16
ANXA3	Homo sapiens annexin A3 (ANXA3), mRNA [NM_005139]	gene	9.63E-08	3.16E-12	up	70.79	17
AOAH	Homo sapiens acyloxyacyl hydrolase (neutrophil) (AOAH), transcript variant 1, mRNA [NM_001637]	gene	9.30E-03	3.09E-07	up	9.53	18
APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2 [Source:HGNC Symbol;Acc:HGNC:579] [ENST00000382938]	gene	8.79E-03	2.92E-07	up	7.57	19
APOBEC3A	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A (APOBEC3A), transcript variant 1, mRNA [NM_145699]	gene	8.93E-12	2.93E-16	up	238.50	20
APOBEC3B	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B (APOBEC3B), transcript variant 1, mRNA [NM_004900]	gene	3.01E-05	9.94E-10	up	15.88	21
APOBR	Homo sapiens apolipoprotein B receptor (APOBR), mRNA [NM_018690]	gene	1.45E-05	4.78E-10	up	28.85	22
AQP9	Homo sapiens aquaporin 9 (AQP9), mRNA [NM_020980]	gene	1.99E-14	6.52E-19	up	722.10	23
ARAP3	Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 (ARAP3), mRNA [NM_022481]	gene	4.39E-09	1.44E-13	up	61.91	24
ARG1	Homo sapiens arginase 1 (ARG1), transcript variant 1, mRNA [NM_001244438]	gene	1.52E-05	5.00E-10	up	48.07	25
ARG1	Homo sapiens arginase 1 (ARG1), transcript variant 1, mRNA [NM_001244438]	gene	1.25E-05	4.11E-10	up	38.38	Not used
ARHGAP26	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), transcript variant 1, mRNA [NM_015071]	gene	5.31E-03	1.77E-07	up	8.22	26
ARPC2	Homo sapiens actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA [NM_152862]	gene	3.27E-03	1.09E-07	up	1.73	27
ARRB2	Homo sapiens arrestin, beta 2 (ARRB2), transcript variant 1, mRNA [NM_004313]	gene	5.30E-03	1.76E-07	up	2.78	28
ASAH1	Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA [NM_177924]	gene	3.77E-02	1.26E-06	up	2.12	29
ASGR1	Homo sapiens asialoglycoprotein receptor 1 (ASGR1), transcript variant 1, mRNA [NM_001671]	gene	2.10E-02	7.00E-07	up	8.16	30
ASPH	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 4, mRNA [NM_032467]	gene	1.17E-06	3.85E-11	up	48.12	31
ASPH	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 1, mRNA [NM_004318]	gene	1.81E-02	6.02E-07	up	3.76	Not used
ASRGL1	Homo sapiens asparaginase like 1 (ASRGL1), transcript variant 1, mRNA [NM_001083926]	gene	2.24E-04	7.42E-09	down	-2.67	32
ATF7	Homo sapiens activating transcription factor 7 (ATF7), transcript variant 4, mRNA [NM_001206682]	gene	4.22E-02	1.41E-06	up	2.00	33
ATP9A	Homo sapiens ATPase, class II, type 9A (ATP9A), mRNA [NM_006045]	gene	7.41E-04	2.45E-08	up	8.51	34
B3GNT5	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5), mRNA [NM_032047]	gene	1.30E-10	4.28E-15	up	73.62	35
BAIAP2L2	Homo sapiens BAI1-associated protein 2-like 2 (BAIAP2L2), mRNA [NM_025045]	gene	4.30E-02	1.44E-06	down	-2.82	36
BASP1	Homo sapiens brain abundant, membrane attached signal protein 1 (BASP1), transcript variant 1, mRNA [NM_006317]	gene	2.52E-03	8.36E-08	up	6.17	37
BCL11B	Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 1, mRNA [NM_138576]	gene	3.73E-05	1.23E-09	up	20.73	38
BCL2A1	Homo sapiens BCL2-related protein A1 (BCL2A1), transcript variant 1, mRNA [NM_004049]	gene	2.43E-05	8.01E-10	up	26.03	39
BID	Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA [NM_197966]	gene	2.46E-04	8.12E-09	up	8.81	40
BID	Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA [NM_197966]	gene	2.85E-04	9.42E-09	up	8.16	Not used
BPI	Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA [NM_001725]	gene	2.71E-04	8.96E-09	up	40.03	41
BRI3	Homo sapiens brain protein I3 (BRI3), transcript variant 1, mRNA [NM_015379]	gene	4.07E-02	1.36E-06	up	3.18	42
BST1	Homo sapiens bone marrow stromal cell antigen 1 (BST1), mRNA [NM_004334]	gene	4.27E-05	1.41E-09	up	12.76	43
BTNL8	Homo sapiens butyrophilin-like 8 (BTNL8), transcript variant 2, mRNA [NM_001040462]	gene	4.43E-03	1.47E-07	up	17.88	44
C10orf105	Homo sapiens chromosome 10 open reading frame 105 (C10orf105), transcript variant 1, mRNA [NM_001164375]	generic ORF	2.90E-02	9.69E-07	up	6.90	Not used
C10orf54	Homo sapiens chromosome 10 open reading frame 54 (C10orf54), mRNA [NM_022153]	generic ORF	2.36E-06	7.77E-11	up	8.14	Not used
C12orf75	Homo sapiens chromosome 12 open reading frame 75 (C12orf75), mRNA [NM_001145199]	generic ORF	2.47E-02	8.25E-07	up	9.05	Not used
C19orf38	Homo sapiens chromosome 19 open reading frame 38 (C19orf38), mRNA [NM_001136482]	generic ORF	2.38E-05	7.86E-10	up	3.50	Not used
C1orf21	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA [NM_030806]	generic ORF	2.88E-05	9.50E-10	up	15.21	Not used
C4orf50	chromosome 4 open reading frame 50 [Source:HGNC Symbol;Acc:HGNC:33766] [ENST00000531445]	generic ORF	8.67E-03	2.88E-07	up	3.93	Not used
C5AR1	Homo sapiens complement component 5a receptor 1 (C5AR1), mRNA [NM_001736]	gene	6.09E-08	2.00E-12	up	116.92	45
C5AR2	Homo sapiens complement component 5a receptor 2 (C5AR2), transcript variant 1, mRNA [NM_001271749]	gene	4.45E-02	1.49E-06	up	2.66	46
C8orf60	Homo sapiens cDNA FLJ12193 fis, clone MAMMA1000856. [AK022255]	miscellaneous	2.04E-03	6.76E-08	up	22.83	Not used
CA4	Homo sapiens carbonic anhydrase IV (CA4), mRNA [NM_000717]	gene	9.78E-05	3.23E-09	up	9.27	47
CACNA1I	Homo sapiens calcium channel, voltage-dependent, T type, alpha 1I subunit (CACNA1I), transcript variant 1, mRNA [NM_021096]	gene	1.38E-03	4.56E-08	up	6.19	48
CADM1	Homo sapiens cell adhesion molecule 1 (CADM1), transcript variant 3, mRNA [NM_001301043]	gene	2.86E-04	9.45E-09	up	6.78	49
CAMP	Homo sapiens cathelicidin antimicrobial peptide (CAMP), mRNA [NM_004345]	gene	8.99E-05	2.97E-09	up	128.82	50
CATSPER1	Homo sapiens cation channel, sperm associated 1 (CATSPER1), mRNA [NM_053054]	gene	1.60E-03	5.29E-08	up	6.32	51
CCDC129	coiled-coil domain containing 129 [Source:HGNC Symbol;Acc:HGNC:27363] [ENST00000409717]	gene	1.12E-02	3.72E-07	down	-2.11	52
CCDC147-AS1	Homo sapiens CCDC147 antisense RNA 1 (head to head) (CCDC147-AS1), long non-coding RNA [NR_108036]	ncRNA	2.25E-02	7.52E-07	up	15.22	Not used
CCDC149	Homo sapiens coiled-coil domain containing 149 (CCDC149), transcript variant 1, mRNA [NM_173463]	gene	1.58E-03	5.22E-08	up	6.10	53
CCDC149	Homo sapiens coiled-coil domain containing 149 (CCDC149), transcript variant 1, mRNA [NM_173463]	gene	3.10E-03	1.03E-07	up	5.09	Not used
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	8.68E-03	2.89E-07	up	20.07	54
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	3.02E-03	1.00E-07	up	8.85	Not used
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	1.97E-02	6.57E-07	up	5.62	Not used
CCL5	Homo sapiens chemokine (C-C motif) ligand 5 (CCL5), transcript variant 1, mRNA [NM_002985]	gene	4.15E-04	1.37E-08	up	14.99	55
CCNJL	Homo sapiens cyclin J-like (CCNJL), mRNA [NM_024565]	gene	1.80E-03	5.95E-08	up	11.94	56
CCNL2	Homo sapiens cyclin L2 (CCNL2), transcript variant 1, mRNA [NM_030937]	gene	1.63E-02	5.42E-07	down	-1.93	57
CCR1	Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA [NM_001295]	gene	5.28E-12	1.73E-16	up	161.86	58
CCR3	Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA [NM_001837]	gene	1.76E-02	5.87E-07	up	8.67	59
CCR5	Homo sapiens chemokine (C-C motif) receptor 5 (gene/pseudogene) (CCR5), transcript variant A, mRNA [NM_000579]	gene	2.78E-03	9.23E-08	up	2.70	60
CD14	Homo sapiens CD14 molecule (CD14), transcript variant 3, mRNA [NM_001174104]	gene	2.35E-08	7.73E-13	up	37.46	61
CD163	Homo sapiens CD163 molecule (CD163), transcript variant 1, mRNA [NM_004244]	gene	3.43E-02	1.15E-06	up	22.03	62
CD2	Homo sapiens CD2 molecule (CD2), mRNA [NM_001767]	gene	4.01E-05	1.32E-09	up	15.35	63
CD226	CD226 molecule [Source:HGNC Symbol;Acc:HGNC:16961] [ENST00000280200]	gene	1.58E-06	5.22E-11	up	3.61	64
CD244	Homo sapiens CD244 molecule, natural killer cell receptor 2B4 (CD244), transcript variant 1, mRNA [NM_016382]	gene	4.60E-05	1.52E-09	up	4.30	65
CD247	Homo sapiens CD247 molecule (CD247), transcript variant 1, mRNA [NM_198053]	gene	6.35E-05	2.10E-09	up	31.83	66
CD28	Homo sapiens CD28 molecule (CD28), transcript variant 1, mRNA [NM_006139]	gene	3.95E-10	1.30E-14	up	39.29	67
CD300A	Homo sapiens CD300a molecule (CD300A), transcript variant 1, mRNA [NM_007261]	gene	8.93E-05	2.95E-09	up	56.23	68
CD300LF	Homo sapiens CD300 molecule-like family member f (CD300LF), transcript variant 1, mRNA [NM_139018]	gene	8.29E-12	2.72E-16	up	33.47	69
CD302	Homo sapiens CD302 molecule (CD302), transcript variant 1, mRNA [NM_014880]	gene	1.01E-02	3.35E-07	up	6.54	70
CD302	Homo sapiens CD302 molecule (CD302), transcript variant 1, mRNA [NM_014880]	gene	7.17E-03	2.38E-07	up	6.06	Not used
CD33	Homo sapiens CD33 molecule (CD33), transcript variant 1, mRNA [NM_001772]	gene	3.41E-03	1.13E-07	up	14.37	71
CD36	Homo sapiens CD36 molecule (thrombospondin receptor) (CD36), transcript variant 2, mRNA [NM_001001547]	gene	5.82E-04	1.93E-08	up	19.94	72
CD3D	Homo sapiens CD3d molecule, delta (CD3-TCR complex) (CD3D), transcript variant 1, mRNA [NM_000732]	gene	3.01E-07	9.90E-12	up	15.55	73
CD3E	Homo sapiens CD3e molecule, epsilon (CD3-TCR complex) (CD3E), mRNA [NM_000733]	gene	2.42E-02	8.06E-07	up	4.38	74
CD3G	Homo sapiens CD3g molecule, gamma (CD3-TCR complex) (CD3G), mRNA [NM_000073]	gene	3.46E-05	1.14E-09	up	42.16	75
CD7	Homo sapiens CD7 molecule (CD7), mRNA [NM_006137]	gene	1.46E-03	4.82E-08	up	4.77	76

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
CD8A	Homo sapiens CD8a molecule (CD8A), transcript variant 1, mRNA [NM_001768]	gene	4.80E-03	1.59E-07	up	17.86	77
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]	gene	1.16E-02	3.87E-07	up	22.55	78
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 4, mRNA [NM_172102]	gene	9.35E-05	3.09E-09	up	9.51	Not used
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]	gene	1.77E-02	5.91E-07	up	7.02	Not used
CD93	Homo sapiens CD93 molecule (CD93), mRNA [NM_012072]	gene	3.89E-06	1.28E-10	up	24.05	79
CDA	Homo sapiens cytidine deaminase (CDA), mRNA [NM_001785]	gene	3.97E-06	1.31E-10	up	15.81	80
CDK5RAP3	Homo sapiens CDK5 regulatory subunit associated protein 3 (CDK5RAP3), transcript variant 5, mRNA [NM_001278198]	gene	2.70E-02	9.01E-07	down	-2.04	81
CEACAM8	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA [NM_001816]	gene	5.86E-06	1.93E-10	up	84.75	82
CEBPA	Homo sapiens CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA), transcript variant 1, mRNA [NM_004364]	gene	1.04E-03	3.44E-08	up	16.25	83
CEBPB	Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), transcript variant 1, mRNA [NM_005194]	gene	2.21E-04	7.31E-09	up	10.75	84
CEBPE	Homo sapiens CCAAT/enhancer binding protein (C/EBP), epsilon (CEBPE), mRNA [NM_001805]	gene	2.36E-02	7.88E-07	up	8.20	85
CECR2	PREDICTED: Homo sapiens cat eye syndrome chromosome region, candidate 2 (CECR2), transcript variant X3, mRNA [XM_006724079]	gene	2.23E-02	7.43E-07	down	-1.90	86
CECR7	Homo sapiens cat eye syndrome chromosome region, candidate 7 (non-protein coding) (CECR7), long non-coding RNA [NR_015352]	gene	2.30E-02	7.69E-07	down	-1.88	87
CES1	Homo sapiens carboxylesterase 1 (CES1), transcript variant 1, mRNA [NM_001025195]	gene	1.41E-04	4.66E-09	up	33.28	88
CFD	Homo sapiens complement factor D (adipsin) (CFD), mRNA [NM_001928]	gene	6.01E-04	1.99E-08	up	45.97	89
CFP	Homo sapiens complement factor properdin (CFP), transcript variant 1, mRNA [NM_002621]	gene	2.22E-03	7.37E-08	up	11.07	90
CHI3L1	Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA [NM_001276]	gene	3.19E-05	1.05E-09	up	67.08	91
CHN2	Homo sapiens chimerin 2 (CHN2), transcript variant 4, mRNA [NM_001293070]	gene	8.56E-04	2.83E-08	up	7.68	92
CIC	capicua transcriptional repressor [Source:HGNC Symbol;Acc:HGNC:14214] [ENST00000572681]	gene	7.06E-03	2.35E-07	down	-1.88	93
CLC	Homo sapiens Charcot-Leyden crystal galectin (CLC), mRNA [NM_001828]	gene	8.84E-09	2.90E-13	up	71.75	94
CLEC11A	Homo sapiens C-type lectin domain family 11, member A (CLEC11A), mRNA [NM_002975]	gene	1.24E-02	4.13E-07	up	6.69	95
CLEC4A	Homo sapiens C-type lectin domain family 4, member A (CLEC4A), transcript variant 1, mRNA [NM_016184]	gene	2.98E-02	9.95E-07	up	3.66	96
CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA [NM_080387]	gene	5.79E-08	1.90E-12	up	36.35	97
CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA [NM_080387]	gene	1.52E-06	4.99E-11	up	28.80	Not used
CLEC7A	Homo sapiens C-type lectin domain family 7, member A (CLEC7A), transcript variant 6, mRNA [NM_197954]	gene	5.51E-11	1.81E-15	up	61.46	98
CMTM2	Homo sapiens CKLF-like MARVEL transmembrane domain containing 2 (CMTM2), transcript variant 1, mRNA [NM_144673]	gene	4.63E-04	1.53E-08	up	38.46	99
CREB5	Homo sapiens cAMP responsive element binding protein 5 (CREB5), transcript variant 1, mRNA [NM_182898]	gene	1.20E-04	3.95E-09	up	22.22	100
CRISPLD2	Homo sapiens cysteine-rich secretory protein LCCL domain containing 2 (CRISPLD2), mRNA [NM_031476]	gene	2.15E-05	7.09E-10	up	3.26	101
CRTAM	Homo sapiens cytotoxic and regulatory T cell molecule (CRTAM), mRNA [NM_019604]	gene	1.94E-02	6.48E-07	up	8.29	102
CSF2RA	Homo sapiens colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) (CSF2RA), transcript variant 6, mRNA [NM_172249]	gene	1.53E-05	5.05E-10	up	11.86	103
CSF3R	Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 3, mRNA [NM_156039]	gene	4.23E-10	1.39E-14	up	88.29	104
CSGALNACT1	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 1 (CSGALNACT1), transcript variant 2, mRNA [NM_018371]	gene	1.11E-04	3.66E-09	up	14.42	105
CSGALNACT1	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 1 (CSGALNACT1), transcript variant 1, mRNA [NM_001130518]	gene	1.13E-02	3.76E-07	up	9.39	Not used
CST7	Homo sapiens cystatin F (leukocystatin) (CST7), mRNA [NM_003650]	gene	2.56E-06	8.42E-11	up	27.24	106
CSTA	Homo sapiens cystatin A (stefin A) (CSTA), mRNA [NM_005213]	gene	1.50E-08	4.93E-13	up	64.31	107
CTSG	Homo sapiens cathepsin G (CTSG), mRNA [NM_001911]	gene	1.42E-02	4.72E-07	up	30.68	108
CX3CR1	Homo sapiens chemokine (C-X3-C motif) receptor 1 (CX3CR1), transcript variant 4, mRNA [NM_001337]	gene	4.80E-02	1.60E-06	up	16.15	109
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), transcript variant 1, mRNA [NM_001511]	gene	2.28E-06	7.49E-11	up	151.17	110
CXCL8	Homo sapiens chemokine (C-X-C motif) ligand 8 (CXCL8), mRNA [NM_000584]	gene	1.13E-07	3.73E-12	up	395.16	111
CXCR1	Homo sapiens chemokine (C-X-C motif) receptor 1 (CXCR1), mRNA [NM_000634]	gene	2.19E-05	7.22E-10	up	22.32	112
CXCR2	Homo sapiens chemokine (C-X-C motif) receptor 2 (CXCR2), transcript variant 1, mRNA [NM_001557]	gene	8.97E-08	2.95E-12	up	85.88	113
CXorf57	Homo sapiens chromosome X open reading frame 57 (CXorf57), transcript variant 1, mRNA [NM_018015]	gene	3.72E-03	1.24E-07	up	5.62	114
CYP1B1	Homo sapiens cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA [NM_000104]	gene	5.43E-06	1.79E-10	up	14.51	115
CYP27A1	Homo sapiens cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), mRNA [NM_000784]	gene	2.34E-06	7.72E-11	up	53.24	116
CYP4F3	Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 3 (CYP4F3), transcript variant 1, mRNA [NM_000896]	gene	2.05E-03	6.78E-08	up	25.53	117
CYTH1	cytohesin 1 [Source:HGNC Symbol;Acc:HGNC:9501] [ENST00000586299]	gene	3.65E-04	1.21E-08	down	-1.98	118
CYTH3	Homo sapiens cytohesin 3 (CYTH3), mRNA [NM_004227]	gene	1.03E-03	3.40E-08	up	4.19	119
DACH1	Homo sapiens dachshund family transcription factor 1 (DACH1), transcript variant 1, mRNA [NM_080759]	gene	1.18E-05	3.90E-10	up	6.72	120
DEFA3	Homo sapiens defensin, alpha 3, neutrophil-specific (DEFA3), mRNA [NM_005217]	gene	6.07E-06	2.00E-10	up	1252.22	121
DEFA4	Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA [NM_001925]	gene	1.20E-06	3.96E-11	up	191.87	122
DENND3	DENN/MADD domain containing 3 [Source:HGNC Symbol;Acc:HGNC:29134] [ENST00000520482]	gene	1.88E-04	6.22E-09	up	31.25	123
DENND3	Homo sapiens DENN/MADD domain containing 3 (DENND3), mRNA [NM_014957]	gene	1.01E-05	3.31E-10	up	12.08	Not used
DGAT2	Homo sapiens diacylglycerol O-acyltransferase 2 (DGAT2), transcript variant 1, mRNA [NM_032564]	gene	3.51E-03	1.16E-07	up	8.08	124
DHRS3	Homo sapiens dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA [NM_004753]	gene	6.03E-04	2.00E-08	up	16.56	125
DLG5	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA [NM_004747]	gene	3.19E-02	1.07E-06	up	4.16	126
DNMT1	Homo sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1), transcript variant 1, mRNA [NM_001130823]	gene	1.50E-02	4.99E-07	up	2.12	127
DOCK5	Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA [NM_024940]	gene	2.23E-06	7.33E-11	up	9.02	128
DOCK5	Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA [NM_024940]	gene	5.52E-06	1.82E-10	up	7.53	Not used
EIF4E3	Homo sapiens eukaryotic translation initiation factor 4E family member 3 (EIF4E3), transcript variant 2, mRNA [NM_173359]	gene	1.09E-04	3.60E-09	up	11.79	129
EMR2	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 2 (EMR2), transcript variant 1, mRNA [NM_013447]	gene	1.98E-10	6.51E-15	up	50.75	130
EMR3	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 3 (EMR3), transcript variant 1, mRNA [NM_032571]	gene	6.95E-06	2.29E-10	up	26.45	131
EOMES	Homo sapiens eomesodermin (EOMES), transcript variant 2, mRNA [NM_005442]	gene	3.05E-03	1.01E-07	up	11.79	132
EPAS1	Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA [NM_001430]	gene	1.58E-07	5.19E-12	up	16.04	133
ETS2	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene homolog 2 (ETS2), transcript variant 1, mRNA [NM_005239]	gene	2.23E-10	7.31E-15	up	25.44	134
F2R	Homo sapiens coagulation factor II (thrombin) receptor, mRNA (cDNA clone IMAGE:4849569), with apparent retained intron. [BC016059]	miscellaneous	2.38E-03	7.88E-08	up	16.32	135
F2R	Homo sapiens coagulation factor II (thrombin) receptor (F2R), mRNA [NM_001992]	gene	1.81E-04	5.97E-09	up	7.57	Not used
FAM101B	Homo sapiens family with sequence similarity 101, member B (FAM101B), mRNA [NM_182705]	gene	5.05E-08	1.66E-12	up	91.55	136
FAM105A	Homo sapiens family with sequence similarity 105, member A (FAM105A), mRNA [NM_019018]	gene	1.41E-02	4.68E-07	up	12.11	137
FAM129A	Homo sapiens family with sequence similarity 129, member A (FAM129A), mRNA [NM_052966]	gene	1.40E-06	4.61E-11	up	77.21	138
FAM13A	Homo sapiens family with sequence similarity 13, member A (FAM13A), transcript variant 1, mRNA [NM_014883]	gene	1.46E-04	4.82E-09	up	7.30	139
FAM169A	Homo sapiens family with sequence similarity 169, member A (FAM169A), transcript variant 1, mRNA [NM_015566]	gene	1.28E-03	4.25E-08	up	13.65	140
FAM169A	Homo sapiens family with sequence similarity 169, member A (FAM169A), transcript variant 1, mRNA [NM_015566]	gene	2.87E-02	9.57E-07	up	6.22	Not used
FAM212A	Homo sapiens family with sequence similarity 212, member A (FAM212A), mRNA [NM_203370]	gene	1.64E-02	5.46E-07	down	-1.67	141
FAM49B	Homo sapiens family with sequence similarity 49, member B (FAM49B), transcript variant 2, mRNA [NM_016623]	gene	1.37E-04	4.53E-09	up	2.76	142
FAR2	Homo sapiens fatty acyl CoA reductase 2 (FAR2), transcript variant 2, mRNA [NM_018099]	gene	1.20E-02	4.01E-07	up	4.49	143
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	3.09E-02	1.03E-06	up	4.07	144
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	1.90E-02	6.34E-07	up	3.70	Not used
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	4.89E-02	1.63E-06	up	3.50	Not used
FCAR	Homo sapiens Fc fragment of IgA, receptor for (FCAR), transcript variant 3, mRNA [NM_133271]	gene	6.63E-08	2.18E-12	up	106.78	145
FCAR	Homo sapiens Fc fragment of IgA, receptor for (FCAR), transcript variant 1, mRNA [NM_002000]	gene	1.52E-06	5.00E-11	up	32.62	Not used
FCER1G	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G), mRNA [NM_004106]	gene	2.75E-05	9.08E-10	up	11.80	146
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 1, mRNA [NM_001017986]	gene	8.33E-05	2.75E-09	up	41.87	147
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 3, mRNA [NM_001244910]	gene	6.89E-05	2.27E-09	up	16.39	Not used
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 3, mRNA [NM_001244910]	gene	5.56E-04	1.84E-08	up	14.10	Not used
FCGR2C	Homo sapiens Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene) (FCGR2C), transcript variant 1, mRNA [NM_201563]	gene	3.26E-03	1.08E-07	up	11.48	148
FCGR3A	Homo sapiens Fc fragment of IgG, low affinity IIIa, receptor (CD16a) (FCGR3A), transcript variant 1, mRNA [NM_000569]	gene	2.46E-07	8.08E-12	up	201.74	149
FCN1	Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA [NM_002003]	gene	1.54E-06	5.08E-11	up	84.34	150
FCN1	Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA [NM_002003]	gene	1.28E-06	4.20E-11	up	43.63	Not used
FEZ1	Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA [NM_005103]	gene	1.72E-02	5.73E-07	up	2.74	151
FFAR2	Homo sapiens free fatty acid receptor 2 (FFAR2), mRNA [NM_005306]	gene	4.68E-04	1.55E-08	up	15.90	152
FGD4	Homo sapiens FYVE, RhoGEF and PH domain containing 4 (FGD4), mRNA [NM_139241]	gene	4.08E-06	1.34E-10	up	19.70	153
FGD4	Homo sapiens FYVE, RhoGEF and PH domain containing 4 (FGD4), mRNA [NM_139241]	gene	7.12E-06	2.35E-10	up	9.98	Not used
FGD4	FYVE, RhoGEF and PH domain containing 4 [Source:HGNC Symbol;Acc:HGNC:19125] [ENST00000472289]	gene	4.29E-05	1.41E-09	up	9.08	Not used
FGFBP2	Homo sapiens fibroblast growth factor binding protein 2 (FGFBP2), mRNA [NM_031950]	gene	2.07E-04	6.84E-09	up	21.69	154
FLJ36777	uncharacterized LOC730971 [Source:EntrezGene;Acc:730971] [ENST00000501888]	uncharacterized locus	2.69E-02	8.99E-07	down	-1.78	Not used
FNDC3B	Homo sapiens fibronectin type III domain containing 3B (FNDC3B), transcript variant 1, mRNA [NM_022763]	gene	1.32E-02	4.39E-07	up	7.25	155
FNDC3B	Homo sapiens fibronectin type III domain containing 3B (FNDC3B), transcript variant 1, mRNA [NM_022763]	gene	7.83E-04	2.59E-08	up	4.77	Not used
FNIP2	Homo sapiens folliculin interacting protein 2 (FNIP2), mRNA [NM_020840]	gene	3.25E-02	1.09E-06	up	14.77	156
FOLR3	Homo sapiens folate receptor 3 (gamma) (FOLR3), mRNA [NM_000804]	gene	6.96E-10	2.28E-14	up	19.76	157
FOSL2	Homo sapiens FOS-like antigen 2 (FOSL2), mRNA [NM_005253]	gene	6.63E-04	2.19E-08	up	31.32	158
FPR1	Homo sapiens formyl peptide receptor 1 (FPR1), transcript variant 2, mRNA [NM_002029]	gene	3.52E-12	1.16E-16	up	377.81	159
FPR2	Homo sapiens formyl peptide receptor 2 (FPR2), transcript variant 1, mRNA [NM_001462]	gene	8.09E-10	2.65E-14	up	43.69	160
FTH1	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA [NM_002032]	gene	4.04E-03	1.34E-07	up	1.78	161
FYB	Homo sapiens FYN binding protein (FYB), transcript variant 1, mRNA [NM_001465]	gene	5.05E-08	1.66E-12	up	98.07	162
G0S2	Homo sapiens G0/G1 switch 2 (G0S2), mRNA [NM_015714]	gene	4.97E-10	1.63E-14	up	857.35	163
GALC	Homo sapiens galactosylceramidase (GALC), transcript variant 1, mRNA [NM_000153]	gene	1.27E-02	4.24E-07	up	2.30	164
GATA3	Homo sapiens GATA binding protein 3 (GATA3), transcript variant 1, mRNA [NM_001002295]	gene	3.55E-02	1.19E-06	up	13.34	165
GCLM	Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA [NM_002061]	gene	7.21E-03	2.40E-07	down	-2.44	166
GIMAP1	Homo sapiens GTPase, IMAP family member 1 (GIMAP1), mRNA [NM_130759]	gene	3.09E-04	1.02E-08	up	4.85	167
GIMAP4	Homo sapiens GTPase, IMAP family member 4 (GIMAP4), mRNA [NM_018326]	gene	3.93E-09	1.29E-13	up	63.49	168
GIMAP5	Homo sapiens GTPase, IMAP family member 5 (GIMAP5), mRNA [NM_018384]	gene	1.41E-03	4.66E-08	up	13.18	169
GIMAP6	Homo sapiens GTPase, IMAP family member 6 (GIMAP6), transcript variant 1, mRNA [NM_024711]	gene	4.52E-02	1.51E-06	up	9.39	170
GIMAP7	Homo sapiens GTPase, IMAP family member 7 (GIMAP7), mRNA [NM_153236]	gene	1.37E-04	4.52E-09	up	36.97	171
GJD4	Homo sapiens gap junction protein, delta 4, 40.1kDa (GJD4), mRNA [NM_153368]	gene	2.34E-02	7.79E-07	down	-1.78	172
GLIPR2	Homo sapiens GLI pathogenesis-related 2 (GLIPR2), transcript variant 3, mRNA [NM_001287011]	gene	2.42E-02	8.08E-07	up	5.06	173
GLRX	Homo sapiens glutaredoxin (thioltransferase) (GLRX), transcript variant 1, mRNA [NM_002064]	gene	2.70E-06	8.88E-11	up	16.00	174
GLT1D1	Homo sapiens glycosyltransferase 1 domain containing 1 (GLT1D1), mRNA [NM_144669]	gene	1.60E-14	5.25E-19	up	184.39	175
GNAQ	Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA [NM_002072]	gene	1.08E-06	3.54E-11	up	11.77	176

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
GNGT2	Homo sapiens guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2 (GNGT2), transcript variant 1, mRNA [NM_031498]	gene	1.24E-02	4.14E-07	up	5.95	177
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	9.75E-03	3.24E-07	up	2.36	178
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	3.53E-02	1.18E-06	up	2.16	Not used
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	4.08E-02	1.36E-06	up	2.15	Not used
GPR56	Homo sapiens G protein-coupled receptor 56 (GPR56), transcript variant 3, mRNA [NM_201525]	gene	1.84E-02	6.14E-07	up	25.82	179
GPR84	Homo sapiens G protein-coupled receptor 84 (GPR84), mRNA [NM_020370]	gene	1.21E-02	4.02E-07	up	17.56	180
GRB10	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 4, mRNA [NM_001001555]	gene	2.55E-08	8.37E-13	up	16.75	181
GZMA	Homo sapiens granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA), mRNA [NM_006144]	gene	1.23E-02	4.11E-07	up	34.41	182
GZMB	Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA [NM_004131]	gene	1.20E-02	3.99E-07	up	16.90	183
GZMH	Homo sapiens granzyme H (cathepsin G-like 2, protein h-CCPX) (GZMH), transcript variant 1, mRNA [NM_033423]	gene	1.31E-02	4.35E-07	up	26.48	184
GZMK	Homo sapiens granzyme K (granzyme 3; tryptase II) (GZMK), mRNA [NM_002104]	gene	4.85E-02	1.62E-06	up	20.57	185
HCAR3	Homo sapiens hydroxycarboxylic acid receptor 3 (HCAR3), mRNA [NM_006018]	gene	9.94E-09	3.26E-13	up	521.29	186
HCK	Homo sapiens HCK proto-oncogene, Src family tyrosine kinase (HCK), transcript variant 1, mRNA [NM_002110]	gene	1.35E-04	4.45E-09	up	12.86	187
HDC	Homo sapiens histidine decarboxylase (HDC), mRNA [NM_002112]	gene	5.92E-03	1.97E-07	up	9.62	188
HIVEP3	Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), transcript variant 3, non-coding RNA [NR_038260]	gene	3.42E-03	1.14E-07	up	3.99	189
HNMT	Homo sapiens histamine N-methyltransferase (HNMT), transcript variant 2, mRNA [NM_001024074]	gene	5.18E-04	1.71E-08	up	8.28	190
HP	Homo sapiens haptoglobin (HP), transcript variant 1, mRNA [NM_005143]	gene	1.76E-03	5.84E-08	up	17.72	191
HPSE	Homo sapiens heparanase (HPSE), transcript variant 1, mRNA [NM_006665]	gene	1.49E-02	4.95E-07	up	12.75	192
HS3ST3B1	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), transcript variant 1, mRNA [NM_006041]	gene	1.86E-08	6.10E-13	up	7.25	193
ICAM1	Homo sapiens intercellular adhesion molecule 1 (ICAM1), mRNA [NM_000201]	gene	3.50E-04	1.16E-08	up	17.99	194
ID2	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA [NM_002166]	gene	1.70E-06	5.60E-11	up	25.85	195
ID2	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA [NM_002166]	gene	1.19E-03	3.96E-08	up	21.02	Not used
IER3	Homo sapiens immediate early response 3 (IER3), mRNA [NM_003897]	gene	4.57E-03	1.52E-07	up	20.40	196
IER3	Homo sapiens immediate early response 3 (IER3), mRNA [NM_003897]	gene	8.68E-04	2.87E-08	up	20.23	Not used
IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA [NM_006332]	gene	1.27E-02	4.22E-07	up	10.77	197
IFIT1	Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 1, mRNA [NM_001548]	gene	2.19E-02	7.30E-07	up	12.40	198
IFITM2	Homo sapiens interferon induced transmembrane protein 2 (IFITM2), mRNA [NM_006435]	gene	3.33E-02	1.11E-06	up	5.37	199
IFITM3	Homo sapiens interferon induced transmembrane protein 3 (IFITM3), transcript variant 1, mRNA [NM_021034]	gene	3.26E-02	1.09E-06	up	4.73	200
IFNG	Homo sapiens interferon, gamma (IFNG), mRNA [NM_000619]	gene	2.19E-07	7.21E-12	up	15.36	201
IGFBP7	Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), transcript variant 1, mRNA [NM_001553]	gene	1.17E-03	3.86E-08	up	13.19	202
IGSF6	Homo sapiens immunoglobulin superfamily, member 6 (IGSF6), mRNA [NM_005849]	gene	2.17E-02	7.23E-07	up	9.99	203
IL13RA1	Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA [NM_001560]	gene	3.22E-02	1.07E-06	up	8.23	204
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	3.59E-05	1.19E-09	up	12.00	205
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	1.22E-02	4.07E-07	up	7.72	Not used
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	1.04E-03	3.44E-08	up	4.58	Not used
IL18RAP	Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA [NM_003853]	gene	5.41E-05	1.79E-09	up	48.93	206
IL18RAP	Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA [NM_003853]	gene	7.33E-05	2.42E-09	up	6.27	Not used
IL1B	Homo sapiens interleukin 1, beta (IL1B), mRNA [NM_000576]	gene	4.45E-04	1.47E-08	up	49.88	207
IL1R2	Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA [NM_004633]	gene	1.24E-04	4.10E-09	up	21.32	208
IL1RN	Homo sapiens interleukin 1 receptor antagonist (IL1RN), transcript variant 4, mRNA [NM_173843]	gene	3.60E-09	1.18E-13	up	409.54	209
IL1RN	Homo sapiens interleukin 1 receptor antagonist (IL1RN), transcript variant 4, mRNA [NM_173843]	gene	4.56E-02	1.52E-06	up	4.07	Not used
IL32	Homo sapiens interleukin 32 (IL32), transcript variant 1, mRNA [NM_001012631]	gene	2.02E-03	6.71E-08	up	15.08	210
IL32	Homo sapiens interleukin 32 (IL32), transcript variant 4, mRNA [NM_001012633]	gene	9.37E-03	3.12E-07	up	3.49	Not used
IL7R	Homo sapiens interleukin 7 receptor (IL7R), transcript variant 1, mRNA [NM_002185]	gene	5.89E-05	1.94E-09	up	47.60	211
IRAK3	Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), transcript variant 1, mRNA [NM_007199]	gene	1.34E-06	4.42E-11	up	55.05	212
IRG1	Homo sapiens immunoresponsive 1 homolog (mouse) (IRG1), mRNA [NM_001258406]	gene	1.08E-04	3.55E-09	down	-2.66	213
ITGA6	Homo sapiens integrin, alpha 6 (ITGA6), transcript variant 2, mRNA [NM_000210]	gene	1.68E-03	5.58E-08	up	7.06	214
ITGB2	Homo sapiens integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) (ITGB2), transcript variant 1, mRNA [NM_000211]	gene	6.72E-03	2.23E-07	up	7.78	215
ITK	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA [NM_005546]	gene	9.26E-07	3.05E-11	up	29.03	216
KCNJ15	Homo sapiens potassium channel, inwardly rectifying subfamily J, member 15 (KCNJ15), transcript variant 1, mRNA [NM_170736]	gene	1.27E-02	4.22E-07	up	10.44	217
KCTD12	Homo sapiens potassium channel tetramerization domain containing 12 (KCTD12), mRNA [NM_138444]	gene	2.76E-03	9.15E-08	up	21.20	218
KIAA0513	Homo sapiens KIAA0513 (KIAA0513), transcript variant 2, mRNA [NM_014732]	gene	5.86E-04	1.94E-08	up	6.01	219
KIAA1324	Homo sapiens KIAA1324 (KIAA1324), transcript variant 1, mRNA [NM_020775]	gene	2.76E-02	9.19E-07	up	7.32	220
KIR2DS2	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 (KIR2DS2), transcript variant 1, mRNA [NM_012312]	gene	8.08E-04	2.68E-08	up	13.30	221
KIR3DL2	Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 (KIR3DL2), transcript variant 1, mRNA [NM_006737]	gene	1.22E-02	4.05E-07	up	5.24	222
KLF17	Homo sapiens Kruppel-like factor 17 (KLF17), mRNA [NM_173484]	gene	3.77E-02	1.26E-06	down	-1.79	223
KLRB1	Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), mRNA [NM_002258]	gene	4.45E-04	1.47E-08	up	26.01	224
KLRC1	Homo sapiens killer cell lectin-like receptor subfamily C, member 1 (KLRC1), transcript variant 1, mRNA [NM_002259]	gene	1.28E-03	4.23E-08	up	11.26	225
KLRD1	Homo sapiens killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA [NM_002262]	gene	9.34E-03	3.11E-07	up	16.82	226
KLRD1	Homo sapiens killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA [NM_002262]	gene	9.45E-08	3.10E-12	up	16.60	Not used
KLRK1	Homo sapiens killer cell lectin-like receptor subfamily K, member 1 (KLRK1), mRNA [NM_007360]	gene	5.00E-04	1.65E-08	up	7.73	227
KRBA2	Homo sapiens KRAB-A domain containing 2 (KRBA2), mRNA [NM_213597]	gene	2.53E-03	8.40E-08	down	-2.05	228
KREMEN1	Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 3, mRNA [NM_001039570]	gene	5.00E-05	1.65E-09	up	18.18	229
KRT23	Homo sapiens keratin 23, type I (KRT23), transcript variant 1, mRNA [NM_015515]	gene	2.76E-03	9.14E-08	up	30.43	230
KRT8P41	Homo sapiens keratin 8 pseudogene 41 (KRT8P41), non-coding RNA [NR_027713]	gene	2.93E-03	9.73E-08	down	-2.00	231
KRTAP3-1	Homo sapiens keratin associated protein 3-1 (KRTAP3-1), mRNA [NM_031958]	gene	2.11E-02	7.05E-07	down	-2.42	232
LACTB	Homo sapiens lactamase, beta (LACTB), transcript variant 2, mRNA [NM_171846]	gene	3.33E-02	1.11E-06	up	2.79	233
LCN2	Homo sapiens lipocalin 2 (LCN2), mRNA [NM_005564]	gene	7.14E-07	2.35E-11	up	99.27	234
LDLR	Homo sapiens low density lipoprotein receptor (LDLR), transcript variant 1, mRNA [NM_000527]	gene	2.50E-07	8.22E-12	up	23.96	235
LGALS12	Homo sapiens lectin, galactoside-binding, soluble, 12 (LGALS12), transcript variant 2, mRNA [NM_033101]	gene	5.28E-03	1.75E-07	up	3.11	236
LGALS3	Homo sapiens lectin, galactoside-binding, soluble, 3 (LGALS3), transcript variant 1, mRNA [NM_002306]	gene	1.17E-04	3.87E-09	up	24.55	237
LILRA2	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), transcript variant 2, mRNA [NM_006866]	gene	4.04E-02	1.35E-06	up	7.03	238
LILRA5	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5 (LILRA5), transcript variant 3, mRNA [NM_181879]	gene	1.82E-06	6.01E-11	up	18.69	239
LILRA6	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 (LILRA6), transcript variant 2, non-coding RNA [NR_104098]	gene	2.76E-11	9.06E-16	up	123.49	240
LILRB3	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), transcript variant 2, mRNA [NM_006864]	gene	3.91E-05	1.29E-09	up	52.25	241
LIMK2	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA [NM_016733]	gene	5.71E-07	1.88E-11	up	8.14	242
LIMK2	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 1, mRNA [NM_001031801]	gene	1.24E-04	4.10E-09	up	4.44	Not used
LIN7A	Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA [NM_004664]	gene	2.72E-11	8.92E-16	up	60.80	243
LINC00243	Homo sapiens cDNA FLJ40693 fis, clone THYMU2025042. [AK098012]	miscellaneous	9.78E-04	3.24E-08	down	-2.69	Not used
LINC00472	Homo sapiens long intergenic non-protein coding RNA 472 (LINC00472), transcript variant 4, long non-coding RNA [NR_121614]	lincRNA	3.56E-03	1.18E-07	down	-2.47	Not used
LINC00892	Homo sapiens long intergenic non-protein coding RNA 892 (LINC00892), transcript variant 1, long non-coding RNA [NR_038461]	ncRNA	6.19E-04	2.05E-08	up	6.06	Not used
LINC00937	Homo sapiens long intergenic non-protein coding RNA 937 (LINC00937), long non-coding RNA [NR_024420]	ncRNA	6.42E-04	2.12E-08	up	20.67	Not used
LINC00937	Homo sapiens long intergenic non-protein coding RNA 937 (LINC00937), long non-coding RNA [NR_024420]	ncRNA	2.75E-05	9.05E-10	up	19.86	Not used
LINC01272	Homo sapiens long intergenic non-protein coding RNA 1272 (LINC01272), mRNA [NM_001278655]	long intergenic RNA	3.21E-02	1.07E-06	up	5.78	Not used
LINC01550	Homo sapiens long intergenic non-protein coding RNA 1550 (LINC01550), long non-coding RNA [NR_015430]	ncRNA	1.34E-04	4.41E-09	up	5.27	Not used
LMO2	Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), transcript variant 1, mRNA [NM_005574]	gene	1.44E-02	4.80E-07	up	16.74	244
lnc-ALPL-1	LNCipedia lincRNA (lnc-ALPL-1), lincRNA [lnc-ALPL-1:1]	lincRNA	5.54E-04	1.83E-08	up	9.12	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:6]	lincRNA	1.40E-04	4.61E-09	up	55.85	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:1]	lincRNA	2.43E-04	8.05E-09	up	53.89	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:14]	lincRNA	3.51E-02	1.17E-06	up	12.48	Not used
lnc-ATP6V1D-1	LNCipedia lincRNA (lnc-ATP6V1D-1), lincRNA [lnc-ATP6V1D-1:1]	lincRNA	3.03E-03	1.01E-07	down	-3.02	Not used
lnc-CHL1-1	LNCipedia lincRNA (lnc-CHL1-1), lincRNA [lnc-CHL1-1:1]	lincRNA	8.37E-04	2.77E-08	down	-2.47	Not used
lnc-GPCPD1-1	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (11%) [THC2678782]	miscellaneous	4.12E-02	1.38E-06	down	-2.60	Not used
lnc-HRCT1-3	LNCipedia lincRNA (lnc-HRCT1-3), lincRNA [lnc-HRCT1-3:3]	lincRNA	3.68E-02	1.23E-06	down	-3.80	Not used
lnc-IGSF3-1	CD014608 Human CD34+ ESTs from primary hematopoietic stem-progenitor cells Homo sapiens cDNA 3', mRNA sequence [GD150158]	miscellaneous	1.12E-04	3.70E-09	up	6.13	Not used
lnc-IL16-2	LNCipedia lincRNA (lnc-IL16-2), lincRNA [lnc-IL16-2:1]	lincRNA	2.10E-02	6.99E-07	down	-2.83	Not used
lnc-IL4R-1	LNCipedia lincRNA (lnc-IL4R-1), lincRNA [lnc-IL4R-1:1]	lincRNA	6.76E-04	2.24E-08	down	-2.09	Not used
lnc-KY-1	LNCipedia lincRNA (lnc-KY-1), lincRNA [lnc-KY-1:1]	lincRNA	4.80E-03	1.59E-07	up	5.07	Not used
lnc-PDE6B-1	LNCipedia lincRNA (lnc-PDE6B-1), lincRNA [lnc-PDE6B-1:9]	lincRNA	4.00E-02	1.34E-06	down	-2.30	Not used
lnc-PPP1R26-2	LNCipedia lincRNA (lnc-PPP1R26-2), lincRNA [lnc-PPP1R26-2:1]	lincRNA	3.61E-02	1.20E-06	down	-1.75	Not used
lnc-RAB28-4	LNCipedia lincRNA (lnc-RAB28-4), lincRNA [lnc-RAB28-4:1]	lincRNA	2.40E-02	8.02E-07	down	-1.76	Not used
lnc-SHCBP1L-1	Homo sapiens cDNA FLJ10580 fis, clone NT2RP2003533. [AK001442]	miscellaneous	4.51E-02	1.51E-06	down	-1.93	Not used
lnc-TM4SF4-2	Homo sapiens cDNA, FLJ99482. [AK309441]	miscellaneous	1.97E-02	6.56E-07	up	3.32	Not used
lnc-VPS18-1	LNCipedia lincRNA (lnc-VPS18-1), lincRNA [lnc-VPS18-1:2]	lincRNA	3.43E-02	1.15E-06	down	-1.93	Not used
lnc-WDR7-2	AGENCOURT_14276563 NIH_MGC_180 Homo sapiens cDNA clone IMAGE:30386298 5', mRNA sequence [CD359767]	miscellaneous	1.48E-04	4.90E-09	down	-2.54	Not used
lnc-ZKSCAN1-1	LNCipedia lincRNA (lnc-ZKSCAN1-1), lincRNA [lnc-ZKSCAN1-1:2]	lincRNA	1.52E-03	5.03E-08	down	-2.86	Not used
lnc-ZNF74-1	LNCipedia lincRNA (lnc-ZNF74-1), lincRNA [lnc-ZNF74-1:6]	lincRNA	2.49E-02	8.30E-07	down	-1.81	Not used
LOC100134868	Homo sapiens uncharacterized LOC100134868 (LOC100134868), long non-coding RNA [NR_004846]	ncRNA	1.04E-03	3.45E-08	down	-2.93	Not used
LOC101060038	PREDICTED: Homo sapiens uncharacterized LOC101060038 (LOC101060038), ncRNA [XR_424318]	ncRNA	4.59E-02	1.53E-06	up	5.90	Not used
LOC101927156	not provided	unannotated probe	3.66E-07	1.20E-11	up	20.82	Not used
LOC101927156	not provided	unannotated probe	9.88E-04	3.27E-08	up	4.14	Not used
LOC101928173	PREDICTED: Homo sapiens uncharacterized LOC101928173 (LOC101928173), transcript variant X2, ncRNA [XR_245039]	ncRNA	1.10E-04	3.64E-09	up	10.93	Not used
LOC101928303	not provided	unannotated probe	3.43E-02	1.15E-06	down	-2.82	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
LOC101929450	Homo sapiens uncharacterized LOC101929450 (LOC101929450), transcript variant 2, long non-coding RNA [NR_125815]	ncRNA	9.33E-03	3.10E-07	down	-1.85	Not used
LOC101929531	PREDICTED: Homo sapiens uncharacterized LOC101929531 (LOC101929531), ncRNA [XR_241262]	ncRNA	3.20E-08	1.05E-12	up	16.51	Not used
LOC101929634	PREDICTED: Homo sapiens uncharacterized LOC101929634 (LOC101929634), misc_RNA [XR_245823]	uncharacterized locus	7.66E-03	2.55E-07	down	-1.78	Not used
LOC102724491	PREDICTED: Homo sapiens uncharacterized LOC102724491 (LOC102724491), ncRNA [XR_433775]	ncRNA	8.10E-03	2.69E-07	down	-1.93	Not used
LOC254896	Homo sapiens uncharacterized LOC254896 (LOC254896), long non-coding RNA [NR_046173]	ncRNA	1.86E-03	6.16E-08	up	11.50	Not used
LOC442132	Homo sapiens golgin A6 family-like 1 pseudogene (LOC442132), non-coding RNA [NR_033906]	pseudogene	2.31E-02	7.69E-07	down	-1.90	Not used
LOC729609	Homo sapiens uncharacterized LOC729609 (LOC729609), long non-coding RNA [NR_024440]	ncRNA	4.73E-04	1.57E-08	down	-1.88	Not used
LPAR6	Homo sapiens lysophosphatidic acid receptor 6 (LPAR6), transcript variant 1, mRNA [NM_005767]	gene	1.32E-02	4.40E-07	up	13.76	245
LPCAT2	Homo sapiens lysophosphatidylcholine acyltransferase 2 (LPCAT2), mRNA [NM_017839]	gene	3.89E-03	1.29E-07	up	6.57	246
LRG1	Homo sapiens leucine-rich alpha-2-glycoprotein 1 (LRG1), mRNA [NM_052972]	gene	3.58E-05	1.18E-09	up	18.55	247
LRRC25	Homo sapiens leucine rich repeat containing 25 (LRRC25), mRNA [NM_145256]	gene	1.79E-06	5.89E-11	up	20.87	248
LRRC55	Homo sapiens leucine rich repeat containing 55 (LRRC55), mRNA [NM_001005210]	gene	1.85E-02	6.18E-07	up	10.67	249
LST1	Homo sapiens leukocyte specific transcript 1 (LST1), transcript variant 1, mRNA [NM_007161]	gene	3.55E-06	1.17E-10	up	16.17	250
LTF	Homo sapiens lactotransferrin (LTF), transcript variant 1, mRNA [NM_002343]	gene	6.00E-08	1.97E-12	up	260.07	251
LUCAT1	Homo sapiens lung cancer associated transcript 1 (non-protein coding) (LUCAT1), transcript variant 1, long non-coding RNA [NR_103548]	gene	1.98E-02	6.59E-07	up	16.46	252
LYAR	Homo sapiens Ly1 antibody reactive (LYAR), transcript variant 1, mRNA [NM_017816]	gene	2.77E-03	9.20E-08	up	3.55	253
MAF	Homo sapiens v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog (MAF), transcript variant 2, mRNA [NM_001031804]	gene	1.39E-05	4.59E-10	up	7.81	254
MAFB	Homo sapiens v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B (MAFB), mRNA [NM_005461]	gene	6.69E-06	2.20E-10	up	230.52	255
MAL	Homo sapiens mal, T-cell differentiation protein (MAL), transcript variant a, mRNA [NM_002371]	gene	6.46E-07	2.13E-11	up	45.43	256
MARC1	Homo sapiens mitochondrial amidoxime reducing component 1 (MARC1), mRNA [NM_022746]	gene	8.59E-05	2.84E-09	up	7.92	257
MARCO	Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA [NM_006770]	gene	3.44E-02	1.15E-06	up	11.97	258
MATK	Homo sapiens megakaryocyte-associated tyrosine kinase (MATK), transcript variant 1, mRNA [NM_139355]	gene	2.01E-02	6.70E-07	up	6.40	259
MBOAT7	Homo sapiens membrane bound O-acyltransferase domain containing 7 (MBOAT7), transcript variant 4, mRNA [NM_001146082]	gene	7.15E-06	2.36E-10	up	9.56	260
MCEMP1	Homo sapiens mast cell-expressed membrane protein 1 (MCEMP1), mRNA [NM_174918]	gene	1.79E-07	5.89E-12	up	33.65	261
MGAM	Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA [NM_004668]	gene	1.22E-03	4.04E-08	up	13.56	262
MGAT4A	Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A (MGAT4A), transcript variant 1, mRNA [NM_012214]	gene	6.91E-04	2.29E-08	up	21.96	263
MGST1	Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 3, mRNA [NM_145791]	gene	8.01E-03	2.66E-07	up	13.12	264
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	gene	2.47E-03	8.20E-08	up	14.64	265
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	4.77E-03	1.59E-07	up	12.31	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	8.31E-03	2.76E-07	up	10.64	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	1.82E-03	6.02E-08	up	5.36	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	4.93E-02	1.65E-06	up	3.95	Not used
MICALCL	Homo sapiens MICAL C-terminal like (MICALCL), mRNA [NM_032867]	gene	8.77E-05	2.90E-09	up	6.78	266
MINOS1-NBL1	Homo sapiens MINOS1-NBL1 readthrough (MINOS1-NBL1), transcript variant 1, mRNA [NM_001204088]	gene	6.32E-03	2.10E-07	up	4.34	267
MLC1	Homo sapiens megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1), transcript variant 1, mRNA [NM_015166]	gene	2.04E-02	6.79E-07	up	7.71	268
MME	Homo sapiens membrane metallo-endopeptidase (MME), transcript variant 2b, mRNA [NM_007289]	gene	2.60E-03	8.62E-08	up	18.12	269
MME	Homo sapiens membrane metallo-endopeptidase (MME), transcript variant 2b, mRNA [NM_007289]	gene	1.83E-04	6.03E-09	up	11.98	Not used
MMP25	Homo sapiens matrix metallopeptidase 25 (MMP25), mRNA [NM_022468]	gene	4.95E-07	1.63E-11	up	45.40	270
MMP9	Homo sapiens matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA [NM_004994]	gene	1.36E-06	4.47E-11	up	36.02	271
MPO	Homo sapiens myeloperoxidase (MPO), mRNA [NM_000250]	gene	2.08E-02	6.94E-07	up	21.97	272
MPP1	Homo sapiens membrane protein, palmitoylated 1, 55kDa (MPP1), transcript variant 1, mRNA [NM_002436]	gene	1.28E-03	4.22E-08	up	11.45	273
MPP1	Homo sapiens membrane protein, palmitoylated 1, 55kDa (MPP1), transcript variant 3, mRNA [NM_001166461]	gene	2.02E-04	6.67E-09	up	10.97	Not used
MT2A	Homo sapiens metallothionein 2A (MT2A), mRNA [NM_005953]	gene	8.13E-03	2.70E-07	up	9.04	274
MXD1	Homo sapiens MAX dimerization protein 1 (MXD1), transcript variant 1, mRNA [NM_002357]	gene	2.66E-03	8.81E-08	up	4.52	275
MXD1	Homo sapiens MAX dimerization protein 1 (MXD1), transcript variant 1, mRNA [NM_002357]	gene	3.98E-02	1.33E-06	up	4.25	Not used
NACC2	Homo sapiens NACC family member 2, BEN and BTB (POZ) domain containing (NACC2), mRNA [NM_144653]	gene	8.69E-06	2.86E-10	up	24.29	276
NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA [NM_005746]	gene	2.01E-02	6.70E-07	up	7.66	277
NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA [NM_005746]	gene	8.54E-03	2.84E-07	up	5.44	Not used
NANOS2	Homo sapiens nanos homolog 2 (Drosophila) (NANOS2), mRNA [NM_001029861]	gene	3.90E-02	1.30E-06	down	-3.27	278
NBAT1	Homo sapiens neuroblastoma associated transcript 1 (NBAT1), long non-coding RNA [NR_034143]	gene	4.93E-03	1.64E-07	down	-2.42	279
NEFL	Homo sapiens neurofilament, light polypeptide (NEFL), mRNA [NM_006158]	gene	2.18E-02	7.28E-07	up	4.02	280
NELL2	Homo sapiens NEL-like 2 (chicken) (NELL2), transcript variant 2, mRNA [NM_006159]	gene	7.59E-07	2.50E-11	up	19.82	281
NFAM1	Homo sapiens NFAT activating protein with ITAM motif 1 (NFAM1), mRNA [NM_145912]	gene	1.56E-10	5.13E-15	up	98.89	282
NFE2	Homo sapiens nuclear factor, erythroid 2 (NFE2), transcript variant 1, mRNA [NM_006163]	gene	5.45E-06	1.79E-10	up	42.95	283
NFIL3	Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), transcript variant 3, mRNA [NM_005384]	gene	3.68E-08	1.21E-12	up	18.53	284
NINJ1	Homo sapiens ninjurin 1 (NINJ1), mRNA [NM_004148]	gene	1.27E-02	4.21E-07	up	18.11	285
NKG7	Homo sapiens natural killer cell granule protein 7 (NKG7), mRNA [NM_005601]	gene	3.72E-03	1.24E-07	up	23.84	286
NLRP12	Homo sapiens NLR family, pyrin domain containing 12 (NLRP12), transcript variant 3, mRNA [NM_001277126]	gene	1.59E-03	5.28E-08	up	14.40	287
NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 3, mRNA [NM_001079821]	gene	3.42E-05	1.13E-09	up	29.07	288
NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 6, mRNA [NM_001243133]	gene	8.06E-07	2.65E-11	up	21.58	Not used
NME8	Homo sapiens NME/NM23 family member 8 (NME8), mRNA [NM_016616]	gene	6.38E-04	2.11E-08	up	16.02	289
NPC2	Homo sapiens Niemann-Pick disease, type C2 (NPC2), mRNA [NM_006432]	gene	5.72E-03	1.90E-07	up	1.90	290
NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 2, mRNA [NM_001200050]	gene	5.87E-03	1.95E-07	up	7.81	291
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) [Source:HGNC Symbol;Acc:HGNC:16781] [ENST00000463899]	gene	1.79E-03	5.94E-08	down	-2.00	Not used
NR6A1	Homo sapiens nuclear receptor subfamily 6, group A, member 1 (NR6A1), transcript variant 1, mRNA [NM_033334]	gene	9.01E-03	3.00E-07	up	11.61	292
NUAK1	Homo sapiens NUAK family, SNF1-like kinase, 1 (NUAK1), mRNA [NM_014840]	gene	4.05E-02	1.35E-06	up	5.24	293
NUCB2	Homo sapiens nucleobindin 2 (NUCB2), mRNA [NM_005013]	gene	6.58E-03	2.18E-07	up	5.36	294
OASL	Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 1, mRNA [NM_003733]	gene	1.39E-02	4.64E-07	up	9.81	295
OGFR	Homo sapiens opioid growth factor receptor (OGFR), mRNA [NM_007346]	gene	7.34E-03	2.44E-07	down	-1.79	296
OLFM2	olfactomedin 2 [Source:HGNC Symbol;Acc:HGNC:17189] [ENST00000264833]	gene	4.73E-02	1.58E-06	down	-2.31	297
OLIG1	Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA [NM_138983]	gene	7.25E-07	2.38E-11	up	33.26	298
ONECUT2	Homo sapiens one cut homeobox 2 (ONECUT2), mRNA [NM_004852]	gene	1.84E-02	6.12E-07	down	-2.94	299
OR1L6	Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), mRNA [NM_001004453]	gene	3.37E-03	1.12E-07	down	-1.72	300
ORM2	Homo sapiens orosomucoid 2 (ORM2), mRNA [NM_000608]	gene	4.30E-02	1.44E-06	up	6.40	301
OSBPL1A	Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant 2, mRNA [NM_080597]	gene	1.66E-03	5.49E-08	up	4.62	302
OSM	Homo sapiens oncostatin M (OSM), mRNA [NM_020530]	gene	1.88E-04	6.22E-09	up	14.44	303
P2RY13	Homo sapiens purinergic receptor P2Y, G-protein coupled, 13 (P2RY13), mRNA [NM_176894]	gene	4.29E-07	1.41E-11	up	18.19	304
P2RY2	Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 1, mRNA [NM_176072]	gene	6.95E-05	2.29E-09	up	23.39	305
PADI2	Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA [NM_007365]	gene	1.66E-03	5.51E-08	up	11.81	306
PAG1	Homo sapiens phosphoprotein membrane anchor with glycosphingolipid microdomains 1 (PAG1), mRNA [NM_018440]	gene	1.61E-07	5.29E-12	up	25.43	307
PAG1	Homo sapiens phosphoprotein membrane anchor with glycosphingolipid microdomains 1 (PAG1), mRNA [NM_018440]	gene	9.13E-05	3.01E-09	up	13.73	Not used
PAM	Homo sapiens peptidylglycine alpha-amidating monooxygenase (PAM), transcript variant 1, mRNA [NM_000919]	gene	1.97E-07	6.48E-12	up	4.87	308
PCED1B-AS1	Homo sapiens PCED1B antisense RNA 1 (PCED1B-AS1), long non-coding RNA [NR_026544]	ncRNA	5.91E-03	1.96E-07	down	-2.67	Not used
PCNXL4	Homo sapiens cDNA FLJ38170 fis, clone FCBBF1000024. [AK095489]	gene	1.64E-03	5.42E-08	down	-2.14	309
PCSK5	Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), transcript variant 2, mRNA [NM_006200]	gene	3.93E-08	1.29E-12	up	14.62	310
PDE4D	Homo sapiens phosphodiesterase 4D, cAMP-specific (PDE4D), transcript variant 3, mRNA [NM_001165899]	gene	5.68E-06	1.87E-10	up	11.91	311
PFKFB3	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), transcript variant 1, mRNA [NM_004566]	gene	6.91E-08	2.27E-12	up	12.25	312
PFKFB3	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), transcript variant 1, mRNA [NM_004566]	gene	4.04E-02	1.35E-06	up	7.35	Not used
PFKFB4	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4), mRNA [NM_004567]	gene	3.19E-03	1.06E-07	up	5.22	313
PGLYRP1	Homo sapiens peptidoglycan recognition protein 1 (PGLYRP1), mRNA [NM_005091]	gene	2.91E-06	9.58E-11	up	73.68	314
PI3	Homo sapiens peptidase inhibitor 3, skin-derived (PI3), mRNA [NM_002638]	gene	5.00E-03	1.66E-07	up	16.29	315
PI4KA	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha (PI4KA), mRNA [NM_058004]	gene	3.50E-02	1.17E-06	down	-1.72	316
PLAUR	Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 3, mRNA [NM_001005377]	gene	1.33E-06	4.36E-11	up	68.44	317
PLEKHG3	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (PLEKHG3), mRNA [NM_015549]	gene	2.04E-07	6.72E-12	up	46.38	318
PLEKHG3	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (PLEKHG3), mRNA [NM_015549]	gene	2.92E-09	9.60E-14	up	26.51	Not used
PLSCR1	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA [NM_021105]	gene	5.39E-03	1.79E-07	up	5.59	319
PLXDC2	Homo sapiens plexin domain containing 2 (PLXDC2), transcript variant 1, mRNA [NM_032812]	gene	3.11E-04	1.03E-08	up	14.78	320
PRKCH	Homo sapiens protein kinase C, eta (PRKCH), mRNA [NM_006255]	gene	2.42E-06	7.97E-11	up	26.16	321
PRKCQ	Homo sapiens protein kinase C, theta (PRKCQ), transcript variant 1, mRNA [NM_006257]	gene	1.81E-03	5.99E-08	up	8.61	322
PRKCQ-AS1	Homo sapiens PRKCQ antisense RNA 1 (PRKCQ-AS1), transcript variant 1, long non-coding RNA [NR_036502]	ncRNA	4.83E-08	1.59E-12	up	39.44	Not used
PRKCQ-AS1	PRKCQ antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44689] [ENST00000561822]	RNA antisense	1.02E-02	3.41E-07	up	4.29	Not used
PROK2	Homo sapiens prokineticin 2 (PROK2), transcript variant 2, mRNA [NM_021935]	gene	1.15E-06	3.79E-11	up	209.32	323
PRR5L	Homo sapiens proline rich 5 like (PRR5L), transcript variant 2, mRNA [NM_024841]	gene	6.72E-03	2.23E-07	up	3.19	324
PRSS23	Homo sapiens protease, serine, 23 (PRSS23), transcript variant 1, mRNA [NM_007173]	gene	7.76E-04	2.57E-08	up	11.18	325
PTAFR	Homo sapiens platelet-activating factor receptor (PTAFR), transcript variant 3, mRNA [NM_000952]	gene	6.05E-06	1.99E-10	up	26.43	326
PTGER2	Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA [NM_000956]	gene	8.09E-08	2.66E-12	up	31.76	327
PTGIR	Homo sapiens prostaglandin I2 (prostacyclin) receptor (IP) (PTGIR), mRNA [NM_000960]	gene	7.47E-03	2.48E-07	up	5.56	328
PTGS2	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA [NM_000963]	gene	1.79E-02	5.95E-07	up	14.91	329
PTPN5	Homo sapiens protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched) (PTPN5), transcript variant 1, mRNA [NM_006906]	gene	9.09E-03	3.02E-07	down	-2.98	330
PVRL2	Homo sapiens poliovirus receptor-related 2 (herpesvirus entry mediator B) (PVRL2), transcript variant delta, mRNA [NM_001042724]	gene	4.41E-02	1.48E-06	up	16.11	331
PYGL	Homo sapiens phosphorylase, glycogen, liver (PYGL), transcript variant 1, mRNA [NM_002863]	gene	4.35E-08	1.43E-12	up	124.43	332
QPCT	Homo sapiens glutaminyl-peptide cyclotransferase (QPCT), mRNA [NM_012413]	gene	9.26E-06	3.05E-10	up	57.44	333
QPCT	Homo sapiens glutaminyl-peptide cyclotransferase (QPCT), mRNA [NM_012413]	gene	2.61E-06	8.59E-11	up	29.92	Not used
RAB33A	Homo sapiens RAB33A, member RAS oncogene family (RAB33A), mRNA [NM_004794]	gene	1.28E-04	4.23E-09	up	3.30	334
RAB44	Homo sapiens RAB44, member RAS oncogene family (RAB44), mRNA [NM_001257357]	gene	3.53E-02	1.18E-06	up	11.37	335

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
RASGRP4	Homo sapiens RAS guanyl releasing protein 4 (RASGRP4), transcript variant a, mRNA [NM_170604]	gene	2.58E-02	8.61E-07	up	3.94	336
RBP7	Homo sapiens retinol binding protein 7, cellular (RBP7), mRNA [NM_052960]	gene	1.86E-09	6.12E-14	up	40.16	337
RETN	Homo sapiens resistin (RETN), transcript variant 1, mRNA [NM_020415]	gene	7.90E-06	2.60E-10	up	27.09	338
RETN	Homo sapiens resistin (RETN), transcript variant 1, mRNA [NM_020415]	gene	1.22E-05	4.01E-10	up	22.15	Not used
RFFL	Homo sapiens ring finger and FYVE-like domain containing E3 ubiquitin protein ligase (RFFL), transcript variant 2, mRNA [NM_001017368]	gene	4.48E-02	1.50E-06	up	2.08	339
RFX8	Homo sapiens RFX family member 8, lacking RFX DNA binding domain (RFX8), mRNA [NM_001145664]	gene	1.47E-02	4.89E-07	down	-1.93	340
RGL4	Homo sapiens ral guanine nucleotide dissociation stimulator-like 4 (RGL4), mRNA [NM_153615]	gene	7.64E-07	2.51E-11	up	97.75	341
RGS18	Homo sapiens regulator of G-protein signaling 18 (RGS18), mRNA [NM_130782]	gene	2.43E-02	8.09E-07	up	16.99	342
RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA [NM_002934]	gene	1.77E-04	5.86E-09	up	26.72	343
RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA [NM_002934]	gene	4.47E-04	1.48E-08	up	21.23	Not used
RNF166	Homo sapiens ring finger protein 166 (RNF166), transcript variant 1, mRNA [NM_178841]	gene	7.97E-03	2.65E-07	up	2.57	344
RORA	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 2, mRNA [NM_134260]	gene	1.11E-04	3.67E-09	up	12.89	345
RRAGD	Homo sapiens Ras-related GTP binding D (RRAGD), mRNA [NM_021244]	gene	5.15E-05	1.70E-09	up	20.72	346
RUNX2	Homo sapiens runt-related transcription factor 2 (RUNX2), transcript variant 1, mRNA [NM_001024630]	gene	2.87E-06	9.44E-11	up	9.03	347
S100A11	Homo sapiens S100 calcium binding protein A11 (S100A11), mRNA [NM_005620]	gene	6.97E-03	2.32E-07	up	12.95	348
S100A11	Homo sapiens S100 calcium binding protein A11 (S100A11), mRNA [NM_005620]	gene	4.12E-03	1.37E-07	up	11.35	Not used
S100A12	Homo sapiens S100 calcium binding protein A12 (S100A12), mRNA [NM_005621]	gene	4.14E-12	1.36E-16	up	936.58	349
S100A12	Homo sapiens S100 calcium binding protein A12 (S100A12), mRNA [NM_005621]	gene	1.61E-11	5.28E-16	up	600.81	Not used
S100A8	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA [NM_002964]	gene	2.86E-07	9.41E-12	up	1117.30	350
S100A9	Homo sapiens S100 calcium binding protein A9 (S100A9), mRNA [NM_002965]	gene	4.91E-08	1.61E-12	up	767.23	351
S100P	Homo sapiens S100 calcium binding protein P (S100P), mRNA [NM_005980]	gene	8.86E-07	2.91E-11	up	100.69	352
S1PR5	Homo sapiens sphingosine-1-phosphate receptor 5 (S1PR5), transcript variant 1, mRNA [NM_030760]	gene	4.72E-03	1.57E-07	up	12.64	353
SAMD3	Homo sapiens sterile alpha motif domain containing 3 (SAMD3), transcript variant 1, mRNA [NM_001017373]	gene	2.14E-05	7.04E-10	up	14.96	354
SAMD3	Homo sapiens sterile alpha motif domain containing 3 (SAMD3), transcript variant 3, mRNA [NM_001258275]	gene	3.16E-03	1.05E-07	up	8.19	Not used
SAP30	Homo sapiens Sin3A-associated protein, 30kDa (SAP30), mRNA [NM_003864]	gene	5.78E-05	1.91E-09	up	7.29	355
SEC14L4	Homo sapiens SEC14-like 4 (S. cerevisiae) (SEC14L4), transcript variant 1, mRNA [NM_174977]	gene	4.95E-03	1.65E-07	down	-2.23	356
SECTM1	Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA [NM_003004]	gene	1.45E-06	4.76E-11	up	56.35	357
SEMA4C	Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C (SEMA4C), mRNA [NM_017789]	gene	3.49E-07	1.15E-11	up	7.67	358
SERPINA1	Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 2, mRNA [NM_001002236]	gene	8.75E-10	2.87E-14	up	75.13	359
SERPINB10	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), mRNA [NM_005024]	gene	2.04E-02	6.80E-07	up	4.00	360
SFTA1P	Homo sapiens surfactant associated 1, pseudogene (SFTA1P), non-coding RNA [NR_027082]	pseudogene	3.18E-02	1.06E-06	down	-1.73	361
SGK1	Homo sapiens serum/glucocorticoid regulated kinase 1 (SGK1), transcript variant 1, mRNA [NM_005627]	gene	1.03E-02	3.43E-07	up	13.18	362
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 1, mRNA [NM_002351]	gene	1.76E-06	5.81E-11	up	15.73	363
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 1, mRNA [NM_002351]	gene	2.26E-04	7.48E-09	up	9.42	Not used
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 2, mRNA [NM_001114937]	gene	3.69E-05	1.22E-09	up	8.00	Not used
SH2D1B	Homo sapiens SH2 domain containing 1B (SH2D1B), mRNA [NM_053282]	gene	9.97E-05	3.29E-09	up	13.26	364
SH2D2A	Homo sapiens SH2 domain containing 2A (SH2D2A), transcript variant 2, mRNA [NM_003975]	gene	1.68E-02	5.61E-07	up	2.66	365
SIPA1L2	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA [NM_020808]	gene	3.72E-05	1.23E-09	up	24.53	366
SIRPA	Homo sapiens signal-regulatory protein alpha (SIRPA), transcript variant 1, mRNA [NM_001040022]	gene	2.35E-04	7.78E-09	up	19.33	367
SIRPB1	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), transcript variant 3, mRNA [NM_001135844]	gene	8.08E-03	2.69E-07	up	5.19	368
SIRPB1	PREDICTED: Homo sapiens signal-regulatory protein beta 1 (SIRPB1), mRNA [XM_006710250]	miscellaneous	1.66E-03	5.50E-08	down	-2.23	Not used
SIRPD	Homo sapiens signal-regulatory protein delta (SIRPD), mRNA [NM_178460]	gene	2.32E-03	7.68E-08	up	4.95	369
SIRPG	Homo sapiens signal-regulatory protein gamma (SIRPG), transcript variant 1, mRNA [NM_018556]	gene	6.52E-08	2.14E-12	up	21.47	370
SLC11A1	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 (SLC11A1), mRNA [NM_000578]	gene	2.15E-04	7.09E-09	up	16.13	371
SLC11A1	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 (SLC11A1), mRNA [NM_000578]	gene	4.86E-02	1.63E-06	up	6.05	Not used
SLC19A1	Homo sapiens solute carrier family 19 (folate transporter), member 1 (SLC19A1), transcript variant 1, mRNA [NM_194255]	gene	3.63E-02	1.21E-06	up	3.98	372
SLC19A3	solute carrier family 19 (thiamine transporter), member 3 [Source:HGNC Symbol;Acc:HGNC:16266] [ENST00000409456]	gene	1.59E-02	5.29E-07	down	-2.98	373
SLC22A4	Homo sapiens solute carrier family 22 (organic cation/zwitterion transporter), member 4 (SLC22A4), mRNA [NM_003059]	gene	2.59E-11	8.51E-16	up	19.41	374
SLC25A37	Homo sapiens solute carrier family 25 (mitochondrial iron transporter), member 37 (SLC25A37), mRNA [NM_016612]	gene	1.55E-04	5.12E-09	up	6.73	375
SLC2A14	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 14 (SLC2A14), transcript variant 1, mRNA [NM_001286233]	gene	9.75E-03	3.24E-07	up	11.59	376
SLC2A3	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3), mRNA [NM_006931]	gene	1.47E-02	4.90E-07	up	11.70	377
SLC31A2	Homo sapiens solute carrier family 31 (copper transporter), member 2 (SLC31A2), mRNA [NM_001860]	gene	2.54E-04	8.41E-09	up	26.84	378
SLC8A1	Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), transcript variant A, mRNA [NM_021097]	gene	3.31E-03	1.10E-07	up	4.55	379
SLCO3A1	Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), transcript variant 1, mRNA [NM_013272]	gene	1.08E-04	3.58E-09	up	9.15	380
SLCO4C1	Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA [NM_180991]	gene	1.23E-02	4.11E-07	up	5.37	381
SLITRK4	Homo sapiens SLIT and NTRK-like family, member 4 (SLITRK4), transcript variant 2, mRNA [NM_173078]	gene	4.57E-02	1.53E-06	up	6.15	382
SLPI	Homo sapiens secretory leukocyte peptidase inhibitor (SLPI), mRNA [NM_003064]	gene	8.29E-06	2.73E-10	up	38.46	383
SMARCD3	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), transcript variant 2, mRNA [NM_003078]	gene	8.99E-05	2.97E-09	up	5.40	384
SMIM3	Homo sapiens small integral membrane protein 3 (SMIM3), mRNA [NM_032947]	gene	5.25E-03	1.74E-07	up	25.62	385
SMPDL3A	Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), transcript variant 1, mRNA [NM_006714]	gene	1.43E-03	4.73E-08	up	9.13	386
SNAR-A3	Homo sapiens small ILF3/NF90-associated RNA A3 (SNAR-A3), small nuclear RNA [NR_024214]	gene	1.64E-02	5.46E-07	down	-1.92	387
SOCS3	Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA [NM_003955]	gene	2.99E-06	9.85E-11	up	42.91	388
SOD2	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), transcript variant 2, mRNA [NM_001024465]	gene	5.10E-06	1.68E-10	up	8.98	389
SORL1	Homo sapiens sortilin-related receptor, L(DLR class) A repeats containing (SORL1), mRNA [NM_003105]	gene	3.86E-04	1.28E-08	up	49.50	390
SRGN	Homo sapiens serglycin (SRGN), transcript variant 1, mRNA [NM_002727]	gene	3.57E-03	1.18E-07	up	3.78	391
SRXN1	Homo sapiens sulfiredoxin 1 (SRXN1), mRNA [NM_080725]	gene	3.75E-05	1.24E-09	up	16.00	392
ST3GAL4	Homo sapiens cDNA FLJ11867 fis, clone HEMBA1006976, weakly similar to H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase. [AK021929]	gene	3.20E-03	1.06E-07	up	11.92	393
ST3GAL6	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 6 (ST3GAL6), transcript variant 1, mRNA [NM_006100]	gene	2.57E-02	8.58E-07	up	5.68	394
ST6GALNAC2	Homo sapiens ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 (ST6GALNAC2), mRNA [NM_006456]	gene	7.33E-03	2.44E-07	up	7.84	395
STEAP4	Homo sapiens STEAP family member 4 (STEAP4), transcript variant 2, mRNA [NM_001205315]	gene	3.78E-03	1.25E-07	up	15.11	396
STOM	Homo sapiens stomatin (STOM), transcript variant 2, mRNA [NM_198194]	gene	8.01E-03	2.66E-07	up	7.63	397
SVIL	Homo sapiens supervillin (SVIL), transcript variant 2, mRNA [NM_021738]	gene	2.05E-05	6.77E-10	up	13.25	398
TACSTD2	Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA [NM_002353]	gene	4.56E-02	1.53E-06	up	6.89	399
TARP	Homo sapiens TCR gamma alternate reading frame protein (TARP), transcript variant 1, mRNA [NM_001003799]	gene	1.41E-06	4.63E-11	up	25.40	400
TBC1D28	Homo sapiens TBC1 domain family, member 28 (TBC1D28), mRNA [NM_001039397]	gene	2.77E-03	9.17E-08	down	-2.41	401
TBC1D4	Homo sapiens TBC1 domain family, member 4 (TBC1D4), transcript variant 1, mRNA [NM_014832]	gene	1.86E-04	6.15E-09	up	7.66	402
TC2N	Homo sapiens tandem C2 domains, nuclear (TC2N), transcript variant 1, mRNA [NM_152332]	gene	4.23E-06	1.39E-10	up	12.10	403
TCN1	Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA [NM_001062]	gene	6.32E-06	2.08E-10	up	23.29	404
THBD	Homo sapiens thrombomodulin (THBD), mRNA [NM_000361]	gene	3.51E-08	1.15E-12	up	91.98	405
THEMIS	Homo sapiens thymocyte selection associated (THEMIS), transcript variant 1, mRNA [NM_001164685]	gene	4.47E-05	1.47E-09	up	9.06	406
TIAM1	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA [NM_003253]	gene	5.88E-06	1.94E-10	up	20.93	407
TLR4	Homo sapiens toll-like receptor 4 (TLR4), transcript variant 1, mRNA [NM_138554]	gene	2.16E-02	7.21E-07	up	15.54	408
TLR4	Homo sapiens toll-like receptor 4 (TLR4), transcript variant 1, mRNA [NM_138554]	gene	1.53E-02	5.10E-07	up	12.36	Not used
TLR8	Homo sapiens toll-like receptor 8 (TLR8), transcript variant 1, mRNA [NM_016610]	gene	4.29E-08	1.41E-12	up	19.13	409
TMEM173	Homo sapiens transmembrane protein 173 (TMEM173), transcript variant 1, mRNA [NM_198282]	gene	5.61E-06	1.85E-10	up	5.64	410
TMEM175	Homo sapiens transmembrane protein 175 (TMEM175), transcript variant 6, mRNA [NM_001297427]	gene	3.09E-02	1.03E-06	down	-2.32	411
TMEM40	Homo sapiens transmembrane protein 40 (TMEM40), transcript variant 1, mRNA [NM_001284406]	gene	9.56E-03	3.18E-07	down	-2.11	412
TMEM45B	Homo sapiens transmembrane protein 45B (TMEM45B), mRNA [NM_138788]	gene	9.65E-03	3.21E-07	up	6.60	413
TNFAIP2	Homo sapiens tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA [NM_006291]	gene	8.62E-08	2.83E-12	up	170.14	414
TNFAIP6	Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA [NM_007115]	gene	5.67E-03	1.89E-07	up	38.13	415
TNFRSF10C	Homo sapiens tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain (TNFRSF10C), mRNA [NM_003841]	gene	5.44E-11	1.78E-15	up	256.57	416
TNFRSF1A	Homo sapiens tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), mRNA [NM_001065]	gene	3.15E-03	1.05E-07	up	4.91	417
TNFRSF25	Homo sapiens tumor necrosis factor receptor superfamily, member 25 (TNFRSF25), transcript variant 1, mRNA [NM_148965]	gene	6.60E-07	2.17E-11	up	29.76	418
TNFRSF25	Homo sapiens tumor necrosis factor receptor superfamily, member 25 (TNFRSF25), transcript variant 12, mRNA [NM_001039664]	gene	1.57E-03	5.20E-08	up	3.95	Not used
TNFSF13B	Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), transcript variant 1, mRNA [NM_006573]	gene	1.98E-02	6.60E-07	up	4.22	419
TNFSF14	Homo sapiens tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14), transcript variant 1, mRNA [NM_003807]	gene	3.14E-03	1.04E-07	up	14.17	420
TNIK	Homo sapiens TRAF2 and NCK interacting kinase (TNIK), transcript variant 1, mRNA [NM_015028]	gene	3.08E-02	1.03E-06	up	4.84	421
TRAPPC3L	trafficking protein particle complex 3-like [Source:HGNC Symbol;Acc:HGNC:21090] [ENST00000356128]	gene	9.04E-03	3.01E-07	down	-2.08	422
TRAT1	Homo sapiens T cell receptor associated transmembrane adaptor 1 (TRAT1), mRNA [NM_016388]	gene	2.25E-06	7.40E-11	up	33.54	423
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 1, mRNA [NM_018643]	gene	2.90E-08	9.53E-13	up	197.86	424
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 2, mRNA [NM_001242589]	gene	4.89E-04	1.62E-08	up	64.90	Not used
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 1, mRNA [NM_018643]	gene	2.06E-03	6.84E-08	up	13.26	Not used
TRERF1	Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 1, mRNA [NM_001297573]	gene	4.98E-03	1.65E-07	up	5.54	425
TSHZ3	Homo sapiens teashirt zinc finger homeobox 3 (TSHZ3), mRNA [NM_020856]	gene	5.54E-03	1.84E-07	up	3.98	426
TSPAN14	Homo sapiens tetraspanin 14 (TSPAN14), transcript variant 1, mRNA [NM_030927]	gene	8.08E-03	2.69E-07	up	4.11	427
TSPAN16	Homo sapiens tetraspanin 16 (TSPAN16), transcript variant 1, mRNA [NM_012466]	gene	4.92E-02	1.65E-06	up	8.00	428
TTTY14	Homo sapiens testis-specific transcript, Y-linked 14 (non-protein coding) (TTTY14), transcript variant 5, long non-coding RNA [NR_001543]	gene	4.69E-04	1.55E-08	down	-2.36	429
TYROBP	Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP), transcript variant 1, mRNA [NM_003332]	gene	2.47E-04	8.16E-09	up	16.07	430
UBASH3A	Homo sapiens ubiquitin associated and SH3 domain containing A (UBASH3A), transcript variant 1, mRNA [NM_018961]	gene	3.87E-03	1.28E-07	up	6.17	431
UPP1	Homo sapiens uridine phosphorylase 1 (UPP1), transcript variant 4, mRNA [NM_001287428]	gene	3.84E-06	1.27E-10	up	11.99	432
VCAN	Homo sapiens versican (VCAN), transcript variant 1, mRNA [NM_004385]	gene	6.09E-05	2.01E-09	up	13.41	433
VDR	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), transcript variant 2, mRNA [NM_001017535]	gene	1.03E-02	3.44E-07	up	9.80	434
VNN1	Homo sapiens vanin 1 (VNN1), mRNA [NM_004666]	gene	1.40E-12	4.58E-17	up	16.78	435
VSTM1	Homo sapiens V-set and transmembrane domain containing 1 (VSTM1), transcript variant 1, mRNA [NM_198481]	gene	5.86E-07	1.93E-11	up	51.57	436
WDFY3	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:HGNC:20751] [ENST00000426414]	gene	1.71E-09	5.61E-14	up	27.79	437

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
WDFY3	Homo sapiens WD repeat and FYVE domain containing 3 (WDFY3), mRNA [NM_014991]	gene	6.47E-04	2.14E-08	up	10.33	Not used
WDR6	Homo sapiens WD repeat domain 6 (WDR6), mRNA [NM_018031]	gene	9.37E-05	3.09E-09	down	-2.13	438
XCL1	Homo sapiens chemokine (C motif) ligand 1 (XCL1), mRNA [NM_002995]	gene	3.65E-02	1.22E-06	up	8.27	439
XLOC_l2_005415	BROAD Institute lincRNA (XLOC_l2_005415), lincRNA [TCONS_l2_00010039]	lincRNA	1.13E-02	3.76E-07	down	-1.85	Not used
YY2	Homo sapiens YY2 transcription factor (YY2), mRNA [NM_206923]	gene	2.98E-03	9.87E-08	down	-1.87	440
ZBTB32	Homo sapiens zinc finger and BTB domain containing 32 (ZBTB32), mRNA [NM_014383]	gene	1.87E-02	6.22E-07	down	-1.98	441
ZMIZ1	Homo sapiens zinc finger, MIZ-type containing 1 (ZMIZ1), mRNA [NM_020338]	gene	3.78E-03	1.25E-07	up	11.98	442
ZNF700	Homo sapiens zinc finger protein 700 (ZNF700), transcript variant 1, mRNA [NM_144566]	gene	4.49E-02	1.50E-06	down	-2.78	443

Supplementary Table 4. Differentially expressed probes between *NOTCH1* -mut and WT CLL cases.

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
A_19_P00315810	not provided	unannotated probe	7.48E-07	2.15E-02	down	-2.28	Not used
A_19_P00318390	not provided	unannotated probe	6.04E-07	1.74E-02	down	-4.21	Not used
A_19_P00318679	PREDICTED: Homo sapiens uncharacterized LOC102723493 (LOC102723493), transcript variant X1, ncRNA [XR_424607]	ncRNA	1.65E-06	4.68E-02	down	-4.08	Not used
A_19_P00318904	not provided	unannotated probe	4.23E-11	1.27E-06	up	10.91	Not used
A_19_P00319413	not provided	unannotated probe	1.51E-06	4.29E-02	up	11.50	Not used
A_19_P00320108	not provided	unannotated probe	2.13E-08	6.29E-04	down	-2.84	Not used
A_19_P00320780	not provided	unannotated probe	1.18E-06	3.37E-02	down	-2.23	Not used
A_19_P00321461	not provided	unannotated probe	8.38E-07	2.40E-02	down	-2.46	Not used
A_19_P00322569	Homo sapiens precursor microRNA mir-34a, complete sequence. [EF609116]	miscellaneous	2.07E-07	6.02E-03	down	-2.49	Not used
A_19_P00804120	not provided	unannotated probe	3.73E-07	1.08E-02	down	-3.43	Not used
A_19_P00809068	Homo sapiens cDNA FLJ42830 fis, clone BRCAN2017905. [AK124820]	miscellaneous	1.08E-08	3.19E-04	down	-3.87	Not used
A_19_P00810205	CCNB2 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:50850] [ENST00000399411]	pseudogene	1.60E-06	4.54E-02	up	2.39	Not used
A_21_P0001917	not provided	unannotated probe	2.06E-08	6.09E-04	down	-2.35	Not used
A_21_P0001948	not provided	unannotated probe	1.41E-06	4.02E-02	down	-2.90	Not used
A_21_P0001971	not provided	unannotated probe	6.96E-07	2.00E-02	down	-2.26	Not used
A_21_P0003332	not provided	unannotated probe	4.54E-07	1.31E-02	down	-2.32	Not used
A_21_P0003411	not provided	unannotated probe	7.93E-08	2.32E-03	down	-3.64	Not used
A_21_P0004809	not provided	unannotated probe	1.85E-08	5.46E-04	down	-3.84	Not used
A_21_P0005323	RST29330 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG209803]	miscellaneous	7.61E-08	2.23E-03	down	-2.77	Not used
A_21_P0005760	not provided	unannotated probe	7.72E-07	2.22E-02	down	-2.35	Not used
A_21_P0005878	not provided	unannotated probe	9.24E-07	2.65E-02	down	-4.21	Not used
A_21_P0006073	not provided	unannotated probe	3.63E-07	1.05E-02	down	-3.01	Not used
A_21_P0006435	Homo sapiens cDNA clone IMAGE:2329410 3' similar to contains Alu repetitive element;mRNA sequence [AI932388]	miscellaneous	4.94E-07	1.42E-02	down	-3.61	Not used
A_21_P0008460	numb homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:8060] [ENST00000557577]	miscellaneous	3.48E-09	1.04E-04	up	22.09	Not used
A_21_P0008692	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 362430. [AL109706]	miscellaneous	1.14E-09	3.40E-05	up	7.67	Not used
A_21_P0008913	not provided	unannotated probe	1.08E-06	3.07E-02	down	-2.74	Not used
A_21_P0008949	not provided	unannotated probe	1.22E-07	3.58E-03	up	9.76	Not used
A_21_P0009251	not provided	unannotated probe	2.86E-09	8.51E-05	down	-4.00	Not used
A_21_P0009956	not provided	unannotated probe	1.59E-08	4.71E-04	down	-3.98	Not used
A_21_P0010382	not provided	unannotated probe	1.47E-08	4.35E-04	down	-4.61	Not used
A_21_P0010812	supervillin pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:44959] [ENST00000422642]	pseudogene	1.04E-10	3.14E-06	up	9.63	Not used
A_21_P0010899	not provided	unannotated probe	6.95E-07	2.00E-02	down	-4.15	Not used
A_21_P0011052	ribosomal protein L7 pseudogene 38 [Source:HGNC Symbol;Acc:HGNC:36731] [ENST00000488396]	pseudogene	3.15E-07	9.14E-03	down	-3.93	Not used
A_21_P0011259	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:45250] [ENST00000509515]	pseudogene	2.96E-07	8.60E-03	up	12.47	Not used
A_21_P0011332	chondroitin sulfate proteoglycan 4 pseudogene 13 [Source:HGNC Symbol;Acc:HGNC:49195] [ENST00000567704]	pseudogene	8.44E-07	2.42E-02	down	-2.48	Not used
A_21_P0011573	not provided	unannotated probe	2.19E-08	6.46E-04	down	-4.02	Not used
A_21_P0011712	not provided	unannotated probe	7.56E-07	2.17E-02	down	-2.08	Not used
A_21_P0012018	CD8b molecule [Source:HGNC Symbol;Acc:HGNC:1707] [ENST00000431506]	miscellaneous	1.74E-08	5.14E-04	up	15.09	Not used
A_21_P0012105	crystallin, gamma E, pseudogene [Source:HGNC Symbol;Acc:HGNC:2412] [ENST00000440809]	pseudogene	1.12E-07	3.26E-03	down	-2.63	Not used
A_21_P0012520	ribosomal protein SA pseudogene 31 [Source:HGNC Symbol;Acc:HGNC:35558] [ENST00000416648]	pseudogene	1.24E-08	3.66E-04	down	-5.56	Not used
A_21_P0012528	family with sequence similarity 157, member C [Source:HGNC Symbol;Acc:HGNC:34081] [ENST00000570230]	miscellaneous	1.23E-06	3.50E-02	up	3.04	Not used
A_21_P0012555	RST25461 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG206026]	miscellaneous	6.86E-07	1.97E-02	down	-3.04	Not used
A_21_P0012887	Homo sapiens programmed cell death 6 pseudogene, mRNA (cDNA clone IMAGE:2901119), with apparent retained intron. [BC020552]	miscellaneous	2.04E-08	6.03E-04	down	-2.64	Not used
A_21_P0013000	MT-ND4 pseudogene 12 [Source:HGNC Symbol;Acc:HGNC:42199] [ENST00000498999]	pseudogene	5.85E-07	1.68E-02	down	-2.18	Not used
A_21_P0013065	not provided	unannotated probe	1.37E-07	4.01E-03	down	-7.31	Not used
A_21_P0013136	not provided	unannotated probe	1.15E-09	3.43E-05	down	-5.47	Not used
A_21_P0013201	trinucleotide repeat containing 18 pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:34015] [ENST00000441896]	pseudogene	1.85E-08	5.48E-04	down	-2.06	Not used
A_21_P0013254	not provided	unannotated probe	7.42E-08	2.18E-03	down	-2.36	Not used
A_21_P0013307	DB088317 TESTI4 Homo sapiens cDNA clone TESTI4036494 5', mRNA sequence [DB088317]	miscellaneous	6.50E-07	1.87E-02	down	-2.77	Not used
A_21_P0013340	CCZ1 vacuolar protein trafficking and biogenesis associated homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:21691] [ENST00000478672]	miscellaneous	2.00E-08	5.91E-04	down	-2.16	Not used
A_21_P0013704	not provided	unannotated probe	5.44E-07	1.57E-02	down	-2.63	Not used
A_21_P0013807	not provided	unannotated probe	1.28E-07	3.73E-03	down	-3.34	Not used
A_21_P0013934	af85e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1048828 3', mRNA sequence [AA778499]	miscellaneous	2.45E-08	7.24E-04	down	-2.34	Not used
A_21_P0013961	Homo sapiens cDNA FLJ46332 fis, clone TESTI4045470. [AK128835]	miscellaneous	4.75E-11	1.43E-06	down	-25.22	Not used
A_21_P0013999	not provided	unannotated probe	7.25E-09	2.15E-04	up	9.00	Not used
A_21_P0014131	not provided	unannotated probe	1.76E-06	4.99E-02	up	3.42	Not used
A_21_P0014192	not provided	unannotated probe	2.05E-07	5.95E-03	down	-2.28	Not used
A_21_P0014266	PREDICTED: Homo sapiens uncharacterized LOC100507417 (LOC100507417), misc_RNA [XR_132956]	uncharacterized locus	1.53E-15	4.65E-11	up	12.71	Not used
A_21_P0014281	BX096603 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998H151782, mRNA sequence [BX096603]	miscellaneous	3.06E-08	9.03E-04	up	7.86	Not used
A_21_P0014391	not provided	unannotated probe	3.97E-07	1.15E-02	down	-2.36	Not used
A_21_P0014468	not provided	unannotated probe	1.05E-06	3.01E-02	down	-4.18	Not used
A_21_P0014504	long intergenic non-protein coding RNA 402 [Source:HGNC Symbol;Acc:HGNC:42732] [ENST00000419499]	long intergenic RNA	4.81E-13	1.46E-08	up	14.11	Not used
A_21_P0014745	Homo sapiens mRNA; cDNA DKFZp781J0350 (from clone DKFZp781J0350). [CR933683]	miscellaneous	9.17E-07	2.62E-02	down	-3.73	Not used
A_21_P0014771	not provided	unannotated probe	8.79E-08	2.58E-03	up	12.39	Not used
A_21_P0014780	not provided	unannotated probe	9.40E-08	2.75E-03	down	-2.92	Not used
A_21_P0014876	not provided	unannotated probe	1.35E-07	3.94E-03	down	-3.45	Not used
A_21_P0014925	not provided	unannotated probe	4.68E-07	1.35E-02	down	-2.34	Not used
A_23_P319557	long intergenic non-protein coding RNA 334 [Source:HGNC Symbol;Acc:HGNC:16425] [ENST00000328344]	long intergenic RNA	7.57E-07	2.17E-02	down	-3.35	Not used
A_23_P333129	double homeobox 4 like 11 [Source:HGNC Symbol;Acc:HGNC:38687] [ENST00000611504]	miscellaneous	2.85E-08	8.40E-04	down	-3.09	Not used
A_23_P46673	protein tyrosine phosphatase type IVA, member 1 pseudogene 7 [Source:HGNC Symbol;Acc:HGNC:41934] [ENST00000423476]	pseudogene	1.27E-06	3.62E-02	down	-8.23	Not used
A_23_P68807	Homo sapiens hypothetical protein FLJ23185, mRNA (cDNA clone IMAGE:4994346), with apparent retained intron. [BC021857]	miscellaneous	1.05E-06	2.99E-02	up	10.86	Not used
A_24_P126741	glutaredoxin (thioltransferase) pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:34049] [ENST00000470810]	pseudogene	7.87E-14	2.39E-09	up	61.02	Not used
A_24_P128727	olfactory receptor, family 7, subfamily E, member 62 pseudogene [Source:HGNC Symbol;Acc:HGNC:8438] [ENST00000456741]	pseudogene	2.28E-07	6.62E-03	down	-3.48	Not used
A_24_P135628	PREDICTED: Homo sapiens uncharacterized LOC100996760 (LOC100996760), transcript variant X1, mRNA [XM_005276385]	uncharacterized locus	2.39E-09	7.13E-05	down	-4.23	Not used
A_24_P153324	ribosomal protein L7 pseudogene 44 [Source:HGNC Symbol;Acc:HGNC:36143] [ENST00000424827]	pseudogene	1.46E-07	4.27E-03	down	-9.71	Not used
A_24_P15502	interferon induced transmembrane protein 8 pseudogene [Source:HGNC Symbol;Acc:HGNC:32202] [ENST00000522529]	pseudogene	4.97E-10	1.49E-05	up	14.01	Not used
A_24_P15640	Homo sapiens chromosome 19 open reading frame 31, mRNA (cDNA clone MGC:168625 IMAGE:9021002), complete cds. [BC137009]	miscellaneous	2.19E-08	6.47E-04	down	-5.96	Not used
A_24_P212819	Homo sapiens cDNA FLJ25155 fis, clone CBR07976. [AK057884]	miscellaneous	1.87E-10	5.61E-06	down	-6.26	Not used
A_24_P213763	Homo sapiens cDNA clone IMAGE:4341068, **** WARNING: chimeric clone ****. [BC013798]	miscellaneous	1.39E-07	4.07E-03	up	13.09	Not used
A_24_P24002	not provided	unannotated probe	1.12E-07	3.28E-03	down	-2.96	Not used
A_24_P254833	T cell receptor beta variable 7-9 [Source:HGNC Symbol;Acc:HGNC:12243] [ENST00000612787]	miscellaneous	4.21E-07	1.21E-02	up	5.09	Not used
A_24_P306964	ribosomal protein S11 pseudogene 7 [Source:HGNC Symbol;Acc:HGNC:36724] [ENST00000442125]	pseudogene	1.73E-06	4.92E-02	down	-3.94	Not used
A_24_P323635	ribosomal protein L10a pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:29803] [ENST00000462503]	pseudogene	9.94E-07	2.84E-02	down	-4.55	Not used
A_24_P333106	not provided	unannotated probe	8.32E-07	2.38E-02	down	-2.76	Not used
A_24_P340976	Q2L9X0_CERAE (Q2L9X0) Laminin receptor 1, partial (81%) [THC2530888]	miscellaneous	2.14E-07	6.21E-03	down	-1.85	Not used
A_24_P341677	GB	unannotated probe	2.71E-07	7.86E-03	down	-2.08	Not used
A_24_P348083	Homo sapiens chromosome 18 open reading frame 23, mRNA (cDNA clone MGC:120885 IMAGE:7939695), complete cds. [BC093850]	miscellaneous	4.31E-09	1.28E-04	down	-6.65	Not used
A_24_P350307	ribosomal protein L18 pseudogene 11 [Source:HGNC Symbol;Acc:HGNC:35742] [ENST00000494933]	pseudogene	1.98E-07	5.77E-03	down	-2.21	Not used
A_24_P357468	T cell receptor alpha variable 8-2 [Source:HGNC Symbol;Acc:HGNC:12147] [ENST00000390434]	miscellaneous	4.76E-09	1.41E-04	up	6.51	Not used
A_24_P366457	not provided	unannotated probe	1.36E-06	3.87E-02	down	-2.82	Not used
A_24_P41149	not provided	unannotated probe	1.54E-06	4.37E-02	down	-5.44	Not used
A_24_P418189	ribosomal protein S4X pseudogene 13 [Source:HGNC Symbol;Acc:HGNC:36522] [ENST00000483219]	pseudogene	3.97E-07	1.15E-02	down	-4.06	Not used
A_24_P58308	ribosomal protein S15a pseudogene 11 [Source:HGNC Symbol;Acc:HGNC:36707] [ENST00000594193]	pseudogene	1.49E-06	4.23E-02	down	-1.51	Not used
A_24_P58894	NOP56 ribonucleoprotein pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:49800] [ENST00000447491]	pseudogene	7.04E-07	2.02E-02	down	-4.44	Not used
A_24_P631848	not provided	unannotated probe	4.67E-07	1.35E-02	down	-5.32	Not used
A_24_P723735	zinc finger protein 720 pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:34505] [ENST00000562403]	pseudogene	5.28E-07	1.52E-02	down	-6.27	Not used
A_24_P743672	GB	unannotated probe	1.25E-07	3.64E-03	down	-3.20	Not used
A_24_P7934	not provided	unannotated probe	1.30E-06	3.69E-02	up	1.62	Not used
A_24_P84781	Homo sapiens cDNA FLJ11871 fis, clone HEMBA1007052. [AK021933]	miscellaneous	2.62E-08	7.74E-04	down	-2.74	Not used
A_24_P93452	ribosomal protein L5 pseudogene 30 [Source:HGNC Symbol;Acc:HGNC:35837] [ENST00000465511]	pseudogene	8.23E-07	2.36E-02	down	-7.62	Not used
A_32_P200237	ens	unannotated probe	1.61E-06	4.57E-02	down	-2.25	Not used
A_32_P874898	T cell receptor beta variable 5-1 [Source:HGNC Symbol;Acc:HGNC:12218] [ENST00000390381]	miscellaneous	2.21E-10	6.65E-06	up	9.25	Not used
A_32_P93036	Synthetic construct Homo sapiens gateway clone IMAGE:100023427 3' read APOE mRNA. [CU678501]	miscellaneous	7.01E-07	2.01E-02	down	-2.37	Not used
A_33_P3211965	UI-E-EJ0-ahi-b-22-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone UI-E-EJ0-ahi-b-22-0-UI 3', mRNA sequence [BM674043]	miscellaneous	6.62E-07	1.90E-02	down	-2.20	Not used
A_33_P3213134	not provided	unannotated probe	1.45E-06	4.14E-02	down	-2.95	Not used
A_33_P3214042	not provided	unannotated probe	2.05E-07	5.97E-03	down	-2.53	Not used
A_33_P3218564	not provided	unannotated probe	1.38E-11	4.17E-07	down	-4.92	Not used
A_33_P3219682	yx87g09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268768 5', mRNA sequence [N35358]	miscellaneous	5.02E-08	1.48E-03	down	-2.22	Not used
A_33_P3220015	T cell receptor gamma variable 10 (non-functional) [Source:HGNC Symbol;Acc:HGNC:12285] [ENST00000390341]	miscellaneous	2.56E-09	7.64E-05	up	12.55	Not used
A_33_P3221134	not provided	unannotated probe	4.32E-09	1.28E-04	up	10.99	Not used
A_33_P3221828	Homo sapiens cDNA FLJ31666 fis, clone NT2RI2004783. [AK056228]	miscellaneous	1.59E-07	4.64E-03	down	-2.38	Not used
A_33_P3224882	T cell receptor gamma variable 9 [Source:HGNC Symbol;Acc:HGNC:12295] [ENST00000444775]	miscellaneous	2.57E-09	7.67E-05	up	8.24	Not used
A_33_P3224971	not provided	unannotated probe	5.89E-07	1.70E-02	down	-3.48	Not used
A_33_P3230037	Homo sapiens FKSG58 (FKSG58) mRNA, complete cds. [AF336885]	miscellaneous	1.30E-08	3.84E-04	down	-3.07	Not used
A_33_P3230073	ribosomal protein L4 pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:36836] [ENST00000447259]	pseudogene	3.02E-07	8.75E-03	down	-4.65	Not used
A_33_P3232688	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) [Source:HGNC Symbol;Acc:HGNC:2435] [ENST00000381524]	miscellaneous	2.08E-13	6.31E-09	up	24.12	Not used
A_33_P3233030	not provided	unannotated probe	3.30E-07	9.57E-03	down	-3.87	Not used
A_33_P3233404	T cell receptor beta variable 28 [Source:HGNC Symbol;Acc:HGNC:12209] [ENST00000390400]	miscellaneous	4.46E-07	1.29E-02	up	17.24	Not used
A_33_P3234410	HUMRPL18A ribosomal protein L18 (Homo sapiens) (exp=-1; wgp=0; cg=0), partial (71%) [THC2587207]	miscellaneous	1.00E-06	2.87E-02	down	-3.00	Not used
A_33_P3237344	not provided	unannotated probe	3.21E-07	9.30E-03	down	-4.34	Not used
A_33_P3237704	not provided	unannotated probe	2.60E-08	7.67E-04	down	-2.46	Not used
A_33_P3240340	not provided	unannotated probe	1.43E-06	4.06E-02	down	-2.25	Not used
A_33_P3241596	not provided	unannotated probe	3.06E-07	8.86E-03	down	-2.84	Not used
A_33_P3241771	PREDICTED: Homo sapiens uncharacterized LOC440313 (LOC440313), misc_RNA [XR_109230]	uncharacterized locus	2.87E-07	8.34E-03	down	-2.31	Not used
A_33_P3242231	ribosomal protein L7a pseudogene 26 [Source:HGNC Symbol;Acc:HGNC:36815] [ENST00000488538]	pseudogene	7.93E-08	2.33E-03	down	-5.49	Not used
A_33_P3242355	Homo sapiens cDNA clone IMAGE:5200632, partial cds. [BC027847]	miscellaneous	1.75E-07	5.10E-03	down	-2.38	Not used
A_33_P3243230	HSINTLK8M interleukin 8 (Homo sapiens) (exp=-1; wgp=0; cg=0), partial (97%) [THC2544321]	miscellaneous	2.95E-13	8.94E-09	up	378.38	Not used
A_33_P3245160	olfactory receptor, family 1, subfamily P, member 1 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:8222] [ENST00000571766]	pseudogene	3.91E-07	1.13E-02	down	-2.91	Not used
A_33_P3245623	not provided	unannotated probe	8.06E-07	2.31E-02	down	-3.95	Not used
A_33_P3246010	Homo sapiens cDNA FLJ35175 fis, clone PLACE6013400. [AK092494]	miscellaneous	2.28E-07	6.62E-03	down	-2.77	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
A_33_P3246995	not provided	unannotated probe	1.64E-06	4.67E-02	down	-2.79	Not used
A_33_P3247210	not provided	unannotated probe	1.38E-07	4.03E-03	down	-1.96	Not used
A_33_P3256031	T cell receptor beta variable 4-1 [Source:HGNC Symbol;Acc:HGNC:12215] [ENST00000390357]	miscellaneous	9.64E-08	2.82E-03	up	6.81	Not used
A_33_P3260021	not provided	unannotated probe	3.92E-07	1.13E-02	down	-2.57	Not used
A_33_P3261433	not provided	unannotated probe	2.01E-07	5.84E-03	down	-2.64	Not used
A_33_P3264416	T cell receptor beta variable 18 [Source:HGNC Symbol;Acc:HGNC:12193] [ENST00000611520]	miscellaneous	3.61E-07	1.04E-02	up	4.93	Not used
A_33_P3265467	growth differentiation factor 5 opposite strand [Source:HGNC Symbol;Acc:HGNC:33435] [ENST00000374375]	miscellaneous	1.22E-08	3.61E-04	down	-2.33	Not used
A_33_P3266091	not provided	unannotated probe	1.42E-08	4.20E-04	down	-3.26	Not used
A_33_P3266614	not provided	unannotated probe	5.96E-09	1.77E-04	down	-8.77	Not used
A_33_P3266848	olfactory receptor, family 5, subfamily BS, member 1 pseudogene [Source:HGNC Symbol;Acc:HGNC:19627] [ENST00000328207]	pseudogene	5.71E-07	1.64E-02	down	-2.78	Not used
A_33_P3268167	not provided	unannotated probe	2.66E-07	7.71E-03	down	-3.17	Not used
A_33_P3271126	not provided	unannotated probe	6.54E-11	1.97E-06	down	-7.65	Not used
A_33_P3273399	UI-E-EJ0-aho-h-10-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone UI-E-EJ0-aho-h-10-0-UI 3', mRNA sequence [BU739610]	miscellaneous	5.46E-07	1.57E-02	down	-3.43	Not used
A_33_P3274009	SLIT-ROBO Rho GTPase activating protein 2 [Source:HGNC Symbol;Acc:HGNC:19751] [ENST00000624686]	miscellaneous	1.24E-10	3.72E-06	down	-4.76	Not used
A_33_P3276520	Homo sapiens cDNA FLJ41710 fis, clone HLUNG2011041. [AK123704]	miscellaneous	1.40E-06	3.98E-02	down	-3.56	Not used
A_33_P3277805	not provided	unannotated probe	7.23E-09	2.15E-04	down	-13.20	Not used
A_33_P3283061	Homo sapiens cDNA FLJ46249 fis, clone TESTI4021377. [AK128128]	miscellaneous	1.25E-06	3.55E-02	down	-2.62	Not used
A_33_P3284854	Homo sapiens cDNA FLJ46084 fis, clone TESTI2006543. [AK127969]	miscellaneous	3.94E-08	1.16E-03	down	-2.87	Not used
A_33_P3285764	not provided	unannotated probe	2.16E-13	6.53E-09	up	37.93	Not used
A_33_P3287636	T cell receptor alpha variable 21 [Source:HGNC Symbol;Acc:HGNC:12118] [ENST00000390449]	miscellaneous	1.56E-07	4.56E-03	down	-2.38	Not used
A_33_P3287716	Homo sapiens cDNA FLJ46168 fis, clone TESTI4003279. [AK128048]	miscellaneous	1.31E-06	3.73E-02	down	-3.31	Not used
A_33_P3289860	Homo sapiens mRNA; cDNA DKFZp686G10213 (from clone DKFZp686G10213). [BX648603]	miscellaneous	3.41E-08	1.01E-03	down	-2.63	Not used
A_33_P3289976	not provided	unannotated probe	3.82E-12	1.15E-07	down	-5.20	Not used
A_33_P3290853	T cell receptor beta variable 11-2 [Source:HGNC Symbol;Acc:HGNC:12181] [ENST00000471935]	miscellaneous	2.04E-11	6.14E-07	up	7.68	Not used
A_33_P3291329	not provided	unannotated probe	9.55E-07	2.73E-02	down	-2.05	Not used
A_33_P3292241	not provided	unannotated probe	1.56E-07	4.54E-03	down	-2.01	Not used
A_33_P3298552	not provided	unannotated probe	4.78E-07	1.38E-02	down	-2.11	Not used
A_33_P3298771	olfactory receptor, family 52, subfamily L, member 2 pseudogene [Source:HGNC Symbol;Acc:HGNC:14788] [ENST00000572217]	pseudogene	1.49E-08	4.41E-04	down	-4.08	Not used
A_33_P3302070	GB	unannotated probe	1.21E-06	3.44E-02	down	-3.45	Not used
A_33_P3303394	not provided	unannotated probe	6.98E-10	2.09E-05	down	-3.59	Not used
A_33_P3303469	not provided	unannotated probe	7.13E-07	2.05E-02	down	-2.51	Not used
A_33_P3309656	not provided	unannotated probe	2.97E-07	8.62E-03	down	-2.74	Not used
A_33_P3312799	Q9UMX8_HUMAN (Q9UMX8) Melanoma antigen, complete [THC2774746]	miscellaneous	7.09E-07	2.04E-02	down	-3.49	Not used
A_33_P3313640	not provided	unannotated probe	7.45E-08	2.19E-03	down	-4.33	Not used
A_33_P3314481	T cell receptor alpha variable 19 [Source:HGNC Symbol;Acc:HGNC:12115] [ENST00000390447]	miscellaneous	8.42E-08	2.47E-03	up	6.32	Not used
A_33_P3316093	not provided	unannotated probe	7.70E-08	2.26E-03	down	-4.34	Not used
A_33_P3316696	not provided	unannotated probe	1.48E-07	4.32E-03	down	-2.89	Not used
A_33_P3317431	ribosomal protein L7 pseudogene 59 [Source:HGNC Symbol;Acc:HGNC:49215] [ENST00000447700]	pseudogene	9.51E-07	2.72E-02	down	-2.16	Not used
A_33_P3317473	not provided	unannotated probe	4.61E-08	1.36E-03	down	-3.20	Not used
A_33_P3318504	Homo sapiens mRNA for putative protein product of Nbla11895, complete cds. [AB072904]	miscellaneous	4.06E-07	1.17E-02	down	-2.44	Not used
A_33_P3319937	not provided	unannotated probe	3.23E-10	9.68E-06	down	-5.76	Not used
A_33_P3321372	contactin associated protein-like 3B [Source:HGNC Symbol;Acc:HGNC:32035] [ENST00000276974]	miscellaneous	6.67E-15	2.03E-10	up	97.88	Not used
A_33_P3321682	not provided	unannotated probe	9.05E-10	2.71E-05	down	-5.88	Not used
A_33_P3323486	Synthetic construct DNA, clone: pF1KE0827	miscellaneous	4.58E-08	1.35E-03	down	-4.15	Not used
A_33_P3325102	BC020650 SEC3L1 protein {Homo sapiens} (exp=-1; wgp=0; cg=0), partial (18%) [THC2739440]	miscellaneous	1.69E-06	4.80E-02	down	-2.27	Not used
A_33_P3326817	not provided	unannotated probe	7.03E-07	2.02E-02	down	-5.27	Not used
A_33_P3328973	Homo sapiens cDNA FLJ26054 fis, clone PRS03205. [AK129565]	miscellaneous	1.82E-07	5.31E-03	down	-2.92	Not used
A_33_P3329104	not provided	unannotated probe	6.82E-07	1.96E-02	down	-4.17	Not used
A_33_P3329737	T cell receptor beta variable 19 [Source:HGNC Symbol;Acc:HGNC:12194] [ENST00000390393]	miscellaneous	2.28E-11	6.86E-07	up	7.21	Not used
A_33_P3331326	not provided	unannotated probe	6.98E-08	2.05E-03	down	-3.09	Not used
A_33_P3331791	not provided	unannotated probe	4.38E-08	1.29E-03	down	-2.80	Not used
A_33_P3333485	not provided	unannotated probe	2.64E-07	7.67E-03	down	-2.73	Not used
A_33_P3335401	not provided	unannotated probe	1.40E-06	3.98E-02	down	-2.70	Not used
A_33_P3336567	not provided	unannotated probe	4.28E-08	1.26E-03	down	-3.18	Not used
A_33_P3337742	not provided	unannotated probe	4.05E-07	1.17E-02	down	-4.12	Not used
A_33_P3338071	not provided	unannotated probe	4.65E-09	1.38E-04	up	14.37	Not used
A_33_P3338292	not provided	unannotated probe	3.10E-09	9.23E-05	down	-4.00	Not used
A_33_P3339197	not provided	unannotated probe	4.61E-08	1.36E-03	down	-3.78	Not used
A_33_P3341568	not provided	unannotated probe	1.14E-06	3.25E-02	down	-2.16	Not used
A_33_P3341722	Synthetic construct Homo sapiens gateway clone IMAGE:100021085 5' read COL23A1 mRNA. [CU692082]	miscellaneous	4.06E-07	1.17E-02	down	-1.93	Not used
A_33_P3347522	not provided	unannotated probe	2.69E-08	7.94E-04	down	-3.22	Not used
A_33_P3349252	Homo sapiens mRNA; cDNA DKFZp547L112 (from clone DKFZp547L112). [AL512723]	miscellaneous	9.01E-09	2.67E-04	down	-5.23	Not used
A_33_P3350452	ribosomal protein L15 pseudogene 20 [Source:HGNC Symbol;Acc:HGNC:36130] [ENST00000482912]	pseudogene	1.70E-07	4.97E-03	down	-4.12	Not used
A_33_P3352407	ferritin, heavy polypeptide 1 pseudogene 20 [Source:HGNC Symbol;Acc:HGNC:37639] [ENST00000434913]	pseudogene	2.31E-09	6.89E-05	up	2.56	Not used
A_33_P3352980	not provided	unannotated probe	2.93E-07	8.49E-03	down	-2.71	Not used
A_33_P3353906	not provided	unannotated probe	1.40E-08	4.16E-04	down	-3.93	Not used
A_33_P3358855	not provided	unannotated probe	4.47E-07	1.29E-02	down	-4.51	Not used
A_33_P3360886	GRP33_ARTSA (P13230) Glycine-rich protein GRP33, partial (8%) [THC2642603]	miscellaneous	1.43E-07	4.17E-03	down	-2.24	Not used
A_33_P3362274	T cell receptor alpha variable 8-7 (non-functional) [Source:HGNC Symbol;Acc:HGNC:12152] [ENST00000390456]	miscellaneous	1.55E-08	4.57E-04	down	-2.71	Not used
A_33_P3365963	not provided	unannotated probe	2.90E-11	8.73E-07	down	-11.85	Not used
A_33_P3371142	not provided	unannotated probe	9.39E-07	2.69E-02	down	-8.62	Not used
A_33_P3371144	not provided	unannotated probe	1.05E-14	3.19E-10	down	-7.97	Not used
A_33_P3372189	Homo sapiens, Similar to LOC223018, clone IMAGE:4732541, mRNA. [BC029410]	miscellaneous	2.96E-07	8.60E-03	up	1.89	Not used
A_33_P3374215	not provided	unannotated probe	1.16E-07	3.38E-03	down	-2.73	Not used
A_33_P3374589	TRNT1_HUMAN (Q96Q11) tRNA-nucleotidyltransferase 1, mitochondrial precursor	miscellaneous	1.41E-06	4.01E-02	down	-2.16	Not used
A_33_P3376273	not provided	unannotated probe	5.13E-07	1.48E-02	up	4.24	Not used
A_33_P3382105	not provided	unannotated probe	6.29E-07	1.81E-02	down	-2.03	Not used
A_33_P3382769	ubiquitin-conjugating enzyme E2Q family member 2 pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:37440] [ENST00000561287]	pseudogene	5.39E-07	1.55E-02	down	-2.45	Not used
A_33_P3383287	Homo sapiens HDCMB45P mRNA, partial cds. [AF068294]	miscellaneous	3.71E-07	1.07E-02	down	-3.15	Not used
A_33_P3383531	not provided	unannotated probe	1.13E-06	3.23E-02	down	-3.65	Not used
A_33_P3385387	ribosomal protein L18 pseudogene 13 [Source:HGNC Symbol;Acc:HGNC:35599] [ENST00000478088]	pseudogene	9.60E-08	2.81E-03	down	-2.75	Not used
A_33_P3385561	Homo sapiens cDNA FLJ27422 fis, clone WMC08087. [AK130932]	miscellaneous	1.62E-07	4.72E-03	down	-2.90	Not used
A_33_P3385662	golgin A8 family, member V, pseudogene [Source:HGNC Symbol;Acc:HGNC:49920] [ENST00000559009]	pseudogene	2.06E-07	6.01E-03	down	-2.39	Not used
A_33_P3385988	tubulin tyrosine ligase-like family, member 8 [Source:HGNC Symbol;Acc:HGNC:34000] [ENST00000266182]	miscellaneous	2.16E-09	6.45E-05	down	-3.84	Not used
A_33_P3389578	not provided	unannotated probe	2.62E-08	7.74E-04	down	-4.41	Not used
A_33_P3393091	DA197111 BRASW1 Homo sapiens cDNA clone BRASW1000106 5', mRNA sequence [DA197111]	miscellaneous	2.92E-07	8.47E-03	down	-2.68	Not used
A_33_P3395237	eukaryotic translation initiation factor 3, subunit K pseudogene 1 [Source:HGNC Symbol;Acc:HGNC:44016] [ENST00000513279]	pseudogene	7.24E-07	2.08E-02	down	-2.78	Not used
A_33_P3395314	not provided	unannotated probe	1.61E-08	4.76E-04	up	23.33	Not used
A_33_P3395636	ribosomal L24 domain containing 1 pseudogene 3 [Source:HGNC Symbol;Acc:HGNC:37883] [ENST00000449255]	pseudogene	8.05E-07	2.31E-02	down	-9.99	Not used
A_33_P3397127	Homo sapiens mRNA for T cell receptor beta variable 6, partial cds, clone: un 226. [AB306238]	miscellaneous	1.92E-09	5.72E-05	up	6.73	Not used
A_33_P3398005	not provided	unannotated probe	9.38E-08	2.75E-03	down	-2.14	Not used
A_33_P3401084	not provided	unannotated probe	1.98E-07	5.78E-03	down	-2.61	Not used
A_33_P3407374	not provided	unannotated probe	1.25E-08	3.69E-04	down	-3.12	Not used
A_33_P3407601	Q39AC8_BURS3 (Q39AC8) Cytochrome B561, partial (9%) [THC2753069]	miscellaneous	2.36E-07	6.85E-03	down	-5.85	Not used
A_33_P3407826	not provided	unannotated probe	2.28E-07	6.64E-03	down	-3.06	Not used
A_33_P3408665	not provided	unannotated probe	9.99E-11	3.00E-06	down	-3.92	Not used
A_33_P3412716	ribosomal protein L17 pseudogene 22 [Source:HGNC Symbol;Acc:HGNC:35761] [ENST00000467688]	pseudogene	2.47E-07	7.16E-03	down	-4.40	Not used
A_33_P3414017	not provided	unannotated probe	3.94E-08	1.16E-03	down	-9.14	Not used
A_33_P3414228	not provided	unannotated probe	8.83E-08	2.59E-03	down	-4.30	Not used
A_33_P3420810	not provided	unannotated probe	4.30E-07	1.24E-02	down	-2.83	Not used
A_33_P3420914	chondroitin sulfate proteoglycan 4 pseudogene 8 [Source:HGNC Symbol;Acc:HGNC:48359] [ENST00000456932]	pseudogene	5.88E-07	1.69E-02	down	-2.38	Not used
A_33_P3421108	PREDICTED: Homo sapiens ADP-ribosylation factor-like 13A (ARL13A), transcript variant X2, mRNA [XM_006724649]	miscellaneous	3.70E-08	1.09E-03	down	-10.10	Not used
A_33_P3422265	Homo sapiens cDNA FLJ43050 fis, clone BRTHA3005046. [AK125040]	miscellaneous	1.86E-08	5.49E-04	down	-2.07	Not used
A_33_P3424153	not provided	unannotated probe	8.15E-07	2.34E-02	down	-3.69	Not used
A_33_P3424867	not provided	unannotated probe	1.04E-06	2.98E-02	down	-3.15	Not used
A_33_P3605969	Homo sapiens cDNA clone IMAGE:3936577, **** WARNING: chimeric clone ****. [BC071847]	miscellaneous	1.58E-08	4.68E-04	down	-2.87	Not used
A_33_P3609431	Homo sapiens cDNA FLJ45949 fis, clone PLACE7007973. [AK127846]	miscellaneous	3.22E-07	9.34E-03	down	-2.61	Not used
A2M-AS1	Homo sapiens A2M antisense RNA 1 (head to head) (A2M-AS1), long non-coding RNA [NR_026971]	ncRNA	6.67E-10	2.00E-05	up	8.02	Not used
AAK1	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA [NM_014911]	gene	1.37E-13	4.14E-09	up	23.56	559
AAK1	AP2 associated kinase 1 [Source:HGNC Symbol;Acc:HGNC:19679] [ENST00000406297]	gene	8.08E-08	2.37E-03	up	11.82	Not used
AAK1	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA [NM_014911]	gene	2.41E-10	7.25E-06	up	8.28	Not used
AAK1	Homo sapiens AP2 associated kinase 1 (AAK1), mRNA [NM_014911]	gene	4.37E-14	1.33E-09	up	6.99	Not used
AAK1	Homo sapiens cDNA clone IMAGE:5226225. [BC090950]	miscellaneous	2.66E-10	7.99E-06	up	4.08	Not used
AATK	Homo sapiens apoptosis-associated tyrosine kinase (AATK), transcript variant 1, mRNA [NM_001080395]	gene	6.26E-07	1.80E-02	up	85.86	75
AATK	apoptosis-associated tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:21] [ENST00000572798]	gene	1.60E-06	4.54E-02	down	-2.83	Not used
ABCA13	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 13 (ABCA13), mRNA [NM_152701]	gene	1.62E-06	4.61E-02	up	6.10	211
ABCC10	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 10 (ABCC10), transcript variant MRP7A, mRNA [NM_033450]	gene	1.28E-09	3.82E-05	down	-2.49	908
ABCC3	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant 1, mRNA [NM_003786]	gene	1.42E-08	4.21E-04	up	11.27	241
ABCC6	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), transcript variant 2, mRNA [NM_001079528]	gene	1.28E-09	3.82E-05	up	6.28	501
ABCC6	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), transcript variant 2, mRNA [NM_001079528]	gene	7.27E-11	2.19E-06	up	3.50	Not used
ABHD2	Homo sapiens abhydrolase domain containing 2 (ABHD2), transcript variant 1, mRNA [NM_007011]	gene	5.14E-08	1.51E-03	up	4.91	458
ABHD5	Homo sapiens abhydrolase domain containing 5 (ABHD5), mRNA [NM_016006]	gene	1.35E-07	3.95E-03	up	8.38	623
ABI3	Homo sapiens ABI family, member 3 (ABI3), transcript variant 1, mRNA [NM_016428]	gene	7.98E-09	2.37E-04	up	6.39	671
ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase) [Source:HGNC Symbol;Acc:HGNC:79] [ENST00000453660]	gene	5.27E-07	1.52E-02	down	-2.34	993
ACAD10	Homo sapiens acyl-CoA dehydrogenase family, member 10 (ACAD10), transcript variant 2, mRNA [NM_025247]	gene	4.32E-09	1.28E-04	down	-2.09	960
ACAP3	Homo sapiens ArfGAP with coiled-coil, ankyrin repeat and PH domains 3 (ACAP3), mRNA [NM_030649]	gene	1.57E-06	4.46E-02	down	-2.08	1123
ACPP	Homo sapiens acid phosphatase, prostate (ACPP), transcript variant 1, mRNA [NM_001099]	gene	2.13E-09	6.37E-05	up	30.30	605
ACSL1	Homo sapiens acyl-CoA synthetase long-chain family member 1 (ACSL1), transcript variant 1, mRNA [NM_001995]	gene	1.17E-09	3.50E-05	up	7.07	339
ACSL6	Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), transcript variant 2, mRNA [NM_001009185]	gene	1.66E-13	5.03E-09	up	9.41	333
ACTA2-AS1	Homo sapiens ACTA2 antisense RNA 1 (ACTA2-AS1), long non-coding RNA [NR_125373]	ncRNA	1.04E-07	3.05E-03	down	-2.81	Not used
ACTL8	Homo sapiens actin-like 8 (ACTL8), mRNA [NM_030812]	gene	1.44E-07	4.20E-03	down	-3.42	1142

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
ACTN1	Homo sapiens actinin, alpha 1 (ACTN1), transcript variant 2, mRNA [NM_001102]	gene	6.61E-13	2.00E-08	up	70.77	78
ACTN4	Homo sapiens actinin, alpha 4 (ACTN4), mRNA [NM_004924]	gene	7.93E-07	2.27E-02	up	2.40	417
ACVR1C	Homo sapiens activin A receptor, type IC (ACVR1C), transcript variant 1, mRNA [NM_145259]	gene	5.57E-14	1.69E-09	up	9.59	366
ADAM33	Homo sapiens ADAM metallopeptidase domain 33 (ADAM33), transcript variant 1, mRNA [NM_025220]	gene	1.62E-07	4.73E-03	down	-2.16	894
ADAM8	Homo sapiens ADAM metallopeptidase domain 8 (ADAM8), transcript variant 1, mRNA [NM_001109]	gene	2.02E-08	5.97E-04	up	7.05	672
ADAMTS10	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 10 (ADAMTS10), transcript variant 1, mRNA [NM_030957]	gene	7.20E-08	2.11E-03	up	9.37	581
ADAMTS7P1	Homo sapiens ADAMTS7 pseudogene 1 (ADAMTS7P1), non-coding RNA [NR_045529]	gene	6.21E-07	1.79E-02	down	-2.66	899
ADAMTSL4	Homo sapiens ADAMTS-like 4 (ADAMTSL4), transcript variant 2, mRNA [NM_025008]	gene	3.14E-08	9.26E-04	up	3.48	388
ADAMTSL5	Homo sapiens ADAMTS-like 5 (ADAMTSL5), mRNA [NM_213604]	gene	1.78E-10	5.35E-06	down	-9.39	841
ADCYAP1R1	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1), transcript variant 3, mRNA [NM_001118]	gene	4.78E-07	1.38E-02	down	-2.22	937
ADRB1	Homo sapiens adrenoceptor beta 1 (ADRB1), mRNA [NM_000684]	gene	4.15E-07	1.20E-02	up	7.85	804
AGAP1	Homo sapiens ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 (AGAP1), transcript variant 1, mRNA [NM_001037131]	gene	8.86E-07	2.54E-02	up	3.19	382
AGBL3	Homo sapiens ATP/GTP binding protein-like 3 (AGBL3), mRNA [NM_178563]	gene	1.23E-06	3.50E-02	down	-2.19	905
AGBL4	Homo sapiens ATP/GTP binding protein-like 4 (AGBL4), mRNA [NM_032785]	gene	2.30E-07	6.67E-03	down	-4.29	1173
AGPAT9	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9), transcript variant 1, mRNA [NM_032717]	gene	2.22E-09	6.63E-05	up	36.52	603
AGTPBP1	Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant 2, mRNA [NM_015239]	gene	1.42E-07	4.14E-03	up	2.82	438
AGTRAP	Homo sapiens angiotensin II receptor-associated protein (AGTRAP), transcript variant 4, mRNA [NM_001040196]	gene	1.92E-07	5.59E-03	up	11.61	652
AIDA	axin interactor, dorsalization associated [Source:HGNC Symbol;Acc:HGNC:25761] [ENST00000474863]	gene	4.92E-07	1.42E-02	down	-3.68	1254
AIF1	Homo sapiens allograft inflammatory factor 1 (AIF1), transcript variant 2, mRNA [NM_004847]	gene	1.53E-12	4.63E-08	up	44.15	95
AKR1C3	Homo sapiens aldo-keto reductase family 1, member C3 (AKR1C3), transcript variant 1, mRNA [NM_003739]	gene	4.80E-10	1.44E-05	up	19.20	543
ALDH1A1	Homo sapiens aldehyde dehydrogenase 1 family, member A1 (ALDH1A1), mRNA [NM_000689]	gene	1.67E-10	5.03E-06	up	25.34	247
ALDH1A3	PREDICTED: Homo sapiens uncharacterized LOC145757 (RP11-66B24.1), transcript variant X1, misc_RNA [XR_109231]	gene	6.94E-09	2.06E-04	down	-3.43	1044
ALDH1L1	Homo sapiens aldehyde dehydrogenase 1 family, member L1 (ALDH1L1), transcript variant 2, mRNA [NM_012190]	gene	1.72E-07	5.02E-03	down	-2.95	1262
ALDH2	Homo sapiens aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), transcript variant 1, mRNA [NM_000690]	gene	9.03E-08	2.64E-03	up	7.22	679
ALOX5AP	Homo sapiens arachidonate 5-lipoxygenase-activating protein (ALOX5AP), transcript variant 1, mRNA [NM_001629]	gene	1.72E-06	4.88E-02	up	5.44	648
ALS2CL	Homo sapiens ALS2 C-terminal like (ALS2CL), transcript variant 1, mRNA [NM_147129]	gene	1.71E-06	4.86E-02	down	-1.99	1131
AMICA1	Homo sapiens adhesion molecule, interacts with CXADR antigen 1 (AMICA1), transcript variant 2, mRNA [NM_153206]	gene	6.85E-07	1.97E-02	up	61.41	516
AMPD2	Homo sapiens adenosine monophosphate deaminase 2 (AMPD2), transcript variant 1, mRNA [NM_004037]	gene	2.45E-09	7.31E-05	up	7.49	343
ANK3	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA [NM_020987]	gene	2.37E-10	7.12E-06	up	17.62	522
ANKFY1	Homo sapiens ankyrin repeat and FYVE domain containing 1 (ANKFY1), transcript variant 3, mRNA [NM_001257999]	gene	5.56E-07	1.60E-02	down	-2.80	885
ANKRD13B	Homo sapiens ankyrin repeat domain 13B (ANKRD13B), mRNA [NM_152345]	gene	1.28E-07	3.75E-03	down	-2.12	909
ANKRD42	Homo sapiens ankyrin repeat domain 42 (ANKRD42), transcript variant 6, mRNA [NM_001300977]	gene	2.18E-07	6.34E-03	down	-1.68	953
ANKRD45	Homo sapiens ankyrin repeat domain 45 (ANKRD45), mRNA [NM_198493]	gene	3.05E-08	8.99E-04	down	-1.95	1095
ANKRD55	Homo sapiens ankyrin repeat domain 55 (ANKRD55), mRNA [NM_024669]	gene	9.09E-07	2.60E-02	up	6.97	230
ANPEP	Homo sapiens alanyl (membrane) aminopeptidase (ANPEP), mRNA [NM_001150]	gene	1.18E-09	3.52E-05	up	11.77	601
ANXA1	Homo sapiens annexin A1 (ANXA1), mRNA [NM_000700]	gene	2.38E-09	7.11E-05	up	97.53	55
ANXA3	Homo sapiens annexin A3 (ANXA3), mRNA [NM_005139]	gene	3.98E-15	1.21E-10	up	167.89	61
AOAH	Homo sapiens acyloxyacyl hydrolase (neutrophil) (AOAH), transcript variant 1, mRNA [NM_001637]	gene	8.19E-10	2.45E-05	up	41.72	556
AP1S2	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), transcript variant 2, mRNA [NM_003916]	gene	3.00E-07	8.69E-03	up	7.03	663
AP1S2	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), transcript variant 2, mRNA [NM_003916]	gene	4.58E-07	1.32E-02	up	3.81	Not used
APBA2	amyloid beta (A4) precursor protein-binding, family A, member 2 [Source:HGNC Symbol;Acc:HGNC:579] [ENST00000382938]	gene	5.72E-09	1.70E-04	up	9.94	363
APOBEC3A	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A (APOBEC3A), transcript variant 1, mRNA [NM_145699]	gene	2.08E-19	6.33E-15	up	900.10	24
APOBEC3B	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B (APOBEC3B), transcript variant 1, mRNA [NM_004900]	gene	2.21E-12	6.68E-08	up	44.24	80
APOBR	Homo sapiens apolipoprotein B receptor (APOBR), mRNA [NM_018690]	gene	2.39E-11	7.20E-07	up	83.44	113
APOL6	Homo sapiens apolipoprotein L, 6 (APOL6), mRNA [NM_030641]	gene	3.33E-07	9.64E-03	up	4.62	381
AQP7P1	Homo sapiens aquaporin 7 pseudogene 1 (AQP7P1), non-coding RNA [NR_002817]	gene	8.76E-07	2.51E-02	down	-3.72	1215
AQP9	Homo sapiens aquaporin 9 (AQP9), mRNA [NM_020980]	gene	1.85E-23	5.65E-19	up	1903.82	5
ARAFP2	Homo sapiens v-raf murine sarcoma 3611 viral oncogene homolog pseudogene, mRNA (cDNA clone IMAGE:5295529). [BC033982]	gene	1.00E-10	3.02E-06	down	-3.45	981
ARAP3	Homo sapiens ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3 (ARAP3), mRNA [NM_022481]	gene	9.25E-17	2.82E-12	up	349.83	43
ARFRP1	ADP-ribosylation factor related protein 1 [Source:HGNC Symbol;Acc:HGNC:662] [ENST00000612772]	gene	6.35E-08	1.87E-03	down	-1.95	1080
ARG1	Homo sapiens arginase 1 (ARG1), transcript variant 1, mRNA [NM_001244438]	gene	1.89E-11	5.69E-07	up	57.05	59
ARG1	Homo sapiens arginase 1 (ARG1), transcript variant 1, mRNA [NM_001244438]	gene	1.47E-11	4.45E-07	up	48.50	Not used
ARHGAP10	Homo sapiens Rho GTPase activating protein 10 (ARHGAP10), mRNA [NM_024605]	gene	2.74E-10	8.22E-06	up	7.97	722
ARHGAP26	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), transcript variant 1, mRNA [NM_015071]	gene	7.37E-10	2.21E-05	up	41.37	552
ARHGAP33	Homo sapiens Rho GTPase activating protein 33 (ARHGAP33), transcript variant 2, mRNA [NM_001172630]	gene	1.30E-09	3.90E-05	down	-7.10	850
ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10 [Source:HGNC Symbol;Acc:HGNC:14103] [ENST00000382795]	gene	2.79E-07	8.10E-03	down	-5.93	1257
ARHGEF28	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 28 (ARHGEF28), transcript variant 2, mRNA [NM_001177693]	gene	4.14E-08	1.22E-03	down	-3.24	1184
ARHGEF40	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 40 (ARHGEF40), transcript variant 1, mRNA [NM_018071]	gene	4.71E-08	1.39E-03	up	26.08	600
ARL5C	Homo sapiens ADP-ribosylation factor-like 5C (ARL5C), mRNA [NM_001143968]	gene	2.70E-07	7.83E-03	down	-2.72	943
ARMCX4	Homo sapiens armadillo repeat containing, X-linked 4 (ARMCX4), transcript variant 1, mRNA [NM_001256155]	gene	1.31E-06	3.72E-02	down	-3.22	1050
ARPC2	Homo sapiens actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA [NM_152862]	gene	4.54E-08	1.33E-03	up	2.18	410
ARPC5	Homo sapiens actin related protein 2/3 complex, subunit 5, 16kDa (ARPC5), transcript variant 2, mRNA [NM_001270439]	gene	3.64E-07	1.05E-02	up	8.17	658
ARRB1	Homo sapiens arrestin, beta 1 (ARRB1), transcript variant 1, mRNA [NM_004041]	gene	1.60E-11	4.81E-07	up	17.28	750
ARRB2	Homo sapiens arrestin, beta 2 (ARRB2), transcript variant 1, mRNA [NM_004313]	gene	2.85E-11	8.59E-07	up	5.11	341
ASAH1	Homo sapiens N-acylsphingosine amidohydrolase (acid ceramidase) 1 (ASAH1), transcript variant 1, mRNA [NM_177924]	gene	4.14E-11	1.25E-06	up	4.36	462
ASAP1	Homo sapiens ArfGAP with SH3 domain, ankyrin repeat and PH domain 1 (ASAP1), transcript variant 2, mRNA [NM_001247996]	gene	6.38E-09	1.90E-04	up	3.63	476
ASAP1-IT1	Homo sapiens ASAP1 intronic transcript 1 (non-protein coding) (ASAP1-IT1), long non-coding RNA [NR_002765]	gene	1.56E-08	4.62E-04	up	5.00	340
ASCL2	Homo sapiens achaete-scute family bHLH transcription factor 2 (ASCL2), mRNA [NM_005170]	gene	2.16E-07	6.28E-03	up	23.80	768
ASGR1	Homo sapiens asialoglycoprotein receptor 1 (ASGR1), transcript variant 1, mRNA [NM_001671]	gene	3.08E-15	9.36E-11	up	43.61	260
ASGR2	Homo sapiens asialoglycoprotein receptor 2 (ASGR2), transcript variant H2', mRNA [NM_080912]	gene	2.79E-13	8.44E-09	up	23.36	288
ASIC2	Homo sapiens acid sensing (proton gated) ion channel 2 (ASIC2), transcript variant MDEG2, mRNA [NM_183377]	gene	9.49E-08	2.78E-03	down	-3.13	1053
ASIC4	Homo sapiens acid sensing (proton gated) ion channel family member 4 (ASIC4), mRNA [NM_182847]	gene	6.36E-07	1.83E-02	down	-4.47	1183
ASPH	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 4, mRNA [NM_032467]	gene	3.18E-11	9.58E-07	up	41.85	37
ASPH	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 1, mRNA [NM_004318]	gene	1.01E-09	3.03E-05	up	7.40	Not used
ASPRV1	Homo sapiens aspartic peptidase, retroviral-like 1 (ASPRV1), mRNA [NM_152792]	gene	1.43E-07	4.19E-03	up	5.30	497
ASRGL1	Homo sapiens asparaginase like 1 (ASRGL1), transcript variant 1, mRNA [NM_001083926]	gene	2.21E-11	6.64E-07	down	-3.21	1146
ATF3	Homo sapiens activating transcription factor 3 (ATF3), transcript variant 4, mRNA [NM_001040619]	gene	6.59E-08	1.93E-03	down	-2.30	938
ATOH8	Homo sapiens mRNA; cDNA DKFZp761E2117 (from clone DKFZp761E2117). [AL831857]	gene	2.50E-07	7.26E-03	down	-5.47	1211
ATP10A	Homo sapiens ATPase, class V, type 10A (ATP10A), mRNA [NM_024490]	gene	1.50E-09	4.48E-05	up	23.70	730
ATP2B3	Homo sapiens ATPase, Ca++ transporting, plasma membrane 3 (ATP2B3), transcript variant 2, mRNA [NM_001001344]	gene	2.73E-07	7.91E-03	down	-2.92	914
ATP6AP1	Homo sapiens ATPase, H+ transporting, lysosomal accessory protein 1 (ATP6AP1), mRNA [NM_001183]	gene	5.51E-07	1.59E-02	up	2.40	429
ATP8B4	Homo sapiens ATPase, class I, type 8B, member 4 (ATP8B4), transcript variant 1, mRNA [NM_024837]	gene	4.78E-12	1.44E-07	up	13.06	220
ATP9A	Homo sapiens ATPase, class II, type 9A (ATP9A), mRNA [NM_006045]	gene	1.07E-09	3.19E-05	up	14.72	557
ATXN2L	Homo sapiens ataxin 2-like (ATXN2L), transcript variant E, mRNA [NM_148416]	gene	9.96E-08	2.92E-03	down	-1.85	954
ATXN7L2	Homo sapiens ataxin 7-like 2 (ATXN7L2), mRNA [NM_153340]	gene	1.63E-07	4.74E-03	down	-2.65	931
AVPI1	Homo sapiens arginine vasopressin-induced 1 (AVPI1), mRNA [NM_021732]	gene	1.74E-06	4.95E-02	down	-2.69	913
B3GAT1	Homo sapiens beta-1,3-glucuronyltransferase 1 (B3GAT1), transcript variant 2, mRNA [NM_054025]	gene	1.04E-09	3.11E-05	up	15.98	521
B3GNT5	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5), mRNA [NM_032047]	gene	8.28E-17	2.52E-12	up	157.73	47
B3GNT7	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 (B3GNT7), mRNA [NM_145236]	gene	8.98E-07	2.57E-02	down	-2.07	919
B3GNT8	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 (B3GNT8), mRNA [NM_198540]	gene	3.62E-10	1.08E-05	up	10.20	641
B4GALNT3	Homo sapiens beta-1,4-N-acetyl-galactosaminyl transferase 3 (B4GALNT3), mRNA [NM_173593]	gene	2.67E-07	7.76E-03	down	-4.26	1037
B4GALT5	Homo sapiens UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5 (B4GALT5), mRNA [NM_004776]	gene	1.01E-08	2.98E-04	up	6.90	322
BACE1	Homo sapiens beta-site APP-cleaving enzyme 1 (BACE1), transcript variant a, mRNA [NM_012104]	gene	1.00E-09	3.00E-05	up	14.44	786
BAIAP2-AS1	Homo sapiens BAIAP2 antisense RNA 1 (head to head) (BAIAP2-AS1), long non-coding RNA [NR_026857]	ncRNA	7.80E-08	2.29E-03	up	8.65	Not used
BARHL1	Homo sapiens BarH-like homeobox 1 (BARHL1), mRNA [NM_020064]	gene	1.50E-06	4.26E-02	down	-3.46	1018
BASP1	Homo sapiens brain abundant, membrane attached signal protein 1 (BASP1), transcript variant 1, mRNA [NM_006317]	gene	4.11E-10	1.23E-05	up	9.96	701
BATF2	Homo sapiens basic leucine zipper transcription factor, ATF-like 2 (BATF2), transcript variant 1, mRNA [NM_138456]	gene	8.20E-09	2.43E-04	up	36.62	268
BCL11B	Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 1, mRNA [NM_138576]	gene	3.76E-12	1.13E-07	up	67.47	185
BCL11B	Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), transcript variant 1, mRNA [NM_138576]	gene	1.28E-11	3.87E-07	up	8.08	Not used
BCL2A1	Homo sapiens BCL2-related protein A1 (BCL2A1), transcript variant 1, mRNA [NM_004049]	gene	3.54E-10	1.06E-05	up	43.10	77
BCL2A1	Homo sapiens BCL2-related protein A1 (BCL2A1), transcript variant 1, mRNA [NM_004049]	gene	1.80E-08	5.33E-04	up	5.96	Not used
BEST1	Homo sapiens bestrophin 1 (BEST1), transcript variant 1, mRNA [NM_004183]	gene	6.03E-10	1.80E-05	up	16.03	251
BEX1	Homo sapiens brain expressed, X-linked 1 (BEX1), mRNA [NM_018476]	gene	4.57E-08	1.34E-03	up	10.55	210
BFSP1	Homo sapiens beaded filament structural protein 1, filensin (BFSP1), transcript variant 1, mRNA [NM_001195]	gene	9.91E-07	2.84E-02	up	6.32	486
BHLHE23	Homo sapiens basic helix-loop-helix family, member e23 (BHLHE23), mRNA [NM_080606]	gene	9.27E-14	2.81E-09	down	-24.97	871
BID	Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA [NM_197966]	gene	3.45E-09	1.03E-04	up	17.22	311
BID	Homo sapiens BH3 interacting domain death agonist (BID), transcript variant 1, mRNA [NM_197966]	gene	2.41E-09	7.19E-05	up	15.61	Not used
BIRC5	Homo sapiens baculoviral IAP repeat containing 5 (BIRC5), transcript variant 3, mRNA [NM_001012271]	gene	5.47E-08	1.61E-03	up	5.86	203
BMP8B	Homo sapiens bone morphogenetic protein 8b (BMP8B), mRNA [NM_001720]	gene	6.71E-07	1.93E-02	down	-3.90	1228
BMX	Homo sapiens BMX non-receptor tyrosine kinase (BMX), transcript variant 2, mRNA [NM_001721]	gene	6.51E-07	1.87E-02	up	14.09	254
BPI	Homo sapiens bactericidal/permeability-increasing protein (BPI), mRNA [NM_001725]	gene	8.19E-13	2.48E-08	up	44.34	144
BRI3	Homo sapiens brain protein I3 (BRI3), transcript variant 1, mRNA [NM_015379]	gene	3.77E-08	1.11E-03	up	4.03	356
BRI3	Homo sapiens brain protein I3 (BRI3), transcript variant 1, mRNA [NM_015379]	gene	2.19E-07	6.38E-03	up	3.30	Not used
BST1	Homo sapiens bone marrow stromal cell antigen 1 (BST1), mRNA [NM_004334]	gene	4.31E-11	1.30E-06	up	39.89	604
BTBD11	Homo sapiens BTB (POZ) domain containing 11 (BTBD11), transcript variant a, mRNA [NM_001018072]	gene	3.47E-13	1.05E-08	up	31.23	187
C10orf105	Homo sapiens chromosome 10 open reading frame 105 (C10orf105), transcript variant 1, mRNA [NM_001164375]	generic ORF	6.45E-14	1.96E-09	up	42.92	Not used
C10orf11	Homo sapiens chromosome 10 open reading frame 11 (C10orf11), mRNA [NM_032024]	generic ORF	5.12E-14	1.55E-09	up	9.54	Not used
C10orf128	Homo sapiens chromosome 10 open reading frame 128 (C10orf128), transcript variant 5, mRNA [NM_001288743]	generic ORF	1.15E-06	3.30E-02	up	9.63	Not used
C10orf54	Homo sapiens chromosome 10 open reading frame 54 (C10orf54), mRNA [NM_022153]	generic ORF	1.06E-13	3.21E-09	up	25.40	Not used
C11orf42	Homo sapiens chromosome 11 open reading frame 42 (C11orf42), mRNA [NM_173525]	generic ORF	5.84E-08	1.71E-03	down	-2.82	Not used
C11orf74	Homo sapiens chromosome 11 open reading frame 74 (C11orf74), transcript variant 4, mRNA [NM_138787]	generic ORF	2.47E-09	7.38E-05	up	8.38	Not used
C11orf95	Homo sapiens chromosome 11 open reading frame 95 (C11orf95), mRNA [NM_001144936]	generic ORF	1.31E-06	3.73E-02	down	-2.63	Not used
C12orf75	Homo sapiens chromosome 12 open reading frame 75 (C12orf75), mRNA [NM_001145199]	generic ORF	9.21E-09	2.73E-04	up	20.72	Not used
C15orf39	Homo sapiens chromosome 15 open reading frame 39 (C15orf39), mRNA [NM_015492]	generic ORF	6.27E-09	1.86E-04	up	14.56	Not used
C15orf59	Homo sapiens chromosome 15 open reading frame 59 (C15orf59), transcript variant 1, mRNA [NM_001039614]	generic ORF	1.27E-06	3.63E-02	down	-2.11	Not used
C15orf62	Homo sapiens chromosome 15 open reading frame 62 (C15orf62), mRNA [NM_001130448]	generic ORF	2.62E-07	7.60E-03	down	-3.27	Not used
C16orf95	chromosome 16 open reading frame 95 [Source:HGNC Symbol;Acc:HGNC:40033] [ENST00000562840]	generic ORF	1.40E-07	4.08E-03	down	-3.42	Not used
C17orf53	Homo sapiens chromosome 17 open reading frame 53 (C17orf53), transcript variant 2, mRNA [NM_001171251]	generic ORF	6.65E-08	1.95E-03	down	-3.47	Not used
C19orf12	Homo sapiens chromosome 19 open reading frame 12 (C19orf12), transcript variant 3, mRNA [NM_001256046]	generic ORF	1.26E-06	3.58E-02	down	-1.90	Not used
C19orf38	Homo sapiens chromosome 19 open reading frame 38 (C19orf38), mRNA [NM_001136482]	generic ORF	1.94E-13	5.87E-09	up	8.58	Not used
C19orf43	Homo sapiens chromosome 19 open reading frame 43 (C19orf43), mRNA [NM_024038]	generic ORF	4.14E-07	1.20E-02	down	-1.84	Not used
C1orf21	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA [NM_030806]	generic ORF	3.16E-10	9.48E-06	up	24.23	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
C1orf21	Homo sapiens chromosome 1 open reading frame 21 (C1orf21), mRNA [NM_030806]	generic ORF	6.11E-14	1.85E-09	up	12.10	Not used
C1orf229	Homo sapiens chromosome 1 open reading frame 229 (C1orf229), mRNA [NM_207401]	generic ORF	1.28E-07	3.75E-03	down	-5.09	Not used
C1QA	Homo sapiens complement component 1, q subcomponent, A chain (C1QA), mRNA [NM_015991]	gene	9.27E-08	2.71E-03	up	5.75	511
C20orf24	Homo sapiens chromosome 20 open reading frame 24 (C20orf24), transcript variant 1, mRNA [NM_018840]	generic ORF	4.03E-09	1.20E-04	up	3.39	Not used
C21orf2	Homo sapiens chromosome 21 open reading frame 2 (C21orf2), transcript variant 3, mRNA [NM_001271441]	generic ORF	5.19E-07	1.50E-02	down	-2.20	Not used
C5AR1	Homo sapiens complement component 5a receptor 1 (C5AR1), mRNA [NM_001736]	gene	3.08E-15	9.35E-11	up	331.20	42
C5AR2	Homo sapiens complement component 5a receptor 2 (C5AR2), transcript variant 1, mRNA [NM_001271749]	gene	5.62E-15	1.71E-10	up	9.18	725
C5orf56	Homo sapiens chromosome 5 open reading frame 56 (C5orf56), long non-coding RNA [NR_045116]	ncRNA	2.07E-07	6.01E-03	up	2.94	Not used
C8orf60	Homo sapiens cDNA FLJ12193 fis, clone MAMMA1000856. [AK022255]	miscellaneous	3.73E-08	1.10E-03	up	64.73	Not used
C9orf139	Homo sapiens chromosome 9 open reading frame 139 (C9orf139), mRNA [NM_207511]	generic ORF	3.54E-11	1.06E-06	up	6.92	Not used
C9orf163	Homo sapiens chromosome 9 open reading frame 163 (C9orf163), mRNA [NM_152571]	generic ORF	1.22E-06	3.48E-02	down	-3.47	Not used
C9orf173	Homo sapiens chromosome 9 open reading frame 173 (C9orf173), transcript variant 1, mRNA [NM_001256699]	generic ORF	2.76E-08	8.13E-04	down	-2.59	Not used
C9orf173-AS1	Homo sapiens C9orf173 antisense RNA 1 (C9orf173-AS1), long non-coding RNA [NR_038389]	ncRNA	1.01E-06	2.88E-02	down	-2.09	Not used
C9orf47	Homo sapiens chromosome 9 open reading frame 47 (C9orf47), transcript variant 1, mRNA [NM_001001938]	generic ORF	1.22E-11	3.69E-07	up	15.12	Not used
C9orf62	Homo sapiens chromosome 9 open reading frame 62 (C9orf62), mRNA [NM_173520]	generic ORF	1.46E-10	4.37E-06	down	-5.39	Not used
CA4	Homo sapiens carbonic anhydrase IV (CA4), mRNA [NM_000717]	gene	1.25E-13	3.79E-09	up	24.37	610
CA6	Synthetic construct Homo sapiens clone IMAGE:100074019 carbonic anhydrase VI (CA6) gene, encodes complete protein. [JF432775]	gene	2.93E-07	8.50E-03	down	-3.77	883
CACNA1I	Homo sapiens calcium channel, voltage-dependent, T type, alpha 1I subunit (CACNA1I), transcript variant 1, mRNA [NM_021096]	gene	2.95E-14	8.95E-10	up	12.51	367
CACNA1S	Homo sapiens calcium channel, voltage-dependent, L type, alpha 1S subunit (CACNA1S), mRNA [NM_000069]	gene	6.67E-07	1.92E-02	down	-2.96	1060
CACNG4	Homo sapiens calcium channel, voltage-dependent, gamma subunit 4 (CACNG4), mRNA [NM_014405]	gene	9.88E-08	2.89E-03	down	-3.43	1026
CACNG6	Homo sapiens calcium channel, voltage-dependent, gamma subunit 6 (CACNG6), transcript variant 1, mRNA [NM_145814]	gene	5.59E-10	1.68E-05	up	13.31	749
CADM1	Homo sapiens cell adhesion molecule 1 (CADM1), transcript variant 3, mRNA [NM_001301043]	gene	5.34E-09	1.59E-04	up	13.48	699
CALY	Homo sapiens calcyon neuron-specific vesicular protein (CALY), mRNA [NM_015722]	gene	1.18E-08	3.50E-04	down	-8.25	843
CAMKK2	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), transcript variant 6, mRNA [NM_172215]	gene	1.06E-07	3.10E-03	up	4.00	346
CAMKV	Homo sapiens CaM kinase-like vesicle-associated (CAMKV), mRNA [NM_024046]	gene	1.48E-06	4.21E-02	down	-3.71	1172
CAMP	Homo sapiens cathelicidin antimicrobial peptide (CAMP), mRNA [NM_004345]	gene	1.81E-09	5.39E-05	up	178.32	10
CAP1	Homo sapiens CAP, adenylate cyclase-associated protein 1 (yeast) (CAP1), transcript variant 1, mRNA [NM_006367]	gene	1.67E-06	4.74E-02	up	2.29	427
CAPZB	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), transcript variant 3, mRNA [NM_001206541]	gene	1.55E-06	4.40E-02	up	2.58	416
CARD11	Homo sapiens caspase recruitment domain family, member 11 (CARD11), mRNA [NM_032415]	gene	7.96E-08	2.33E-03	down	-3.20	1075
CASKIN1	Homo sapiens CASK interacting protein 1 (CASKIN1), mRNA [NM_020764]	gene	8.04E-12	2.43E-07	down	-5.83	854
CASP1	Homo sapiens caspase 1, apoptosis-related cysteine peptidase (CASP1), transcript variant alpha, mRNA [NM_033292]	gene	6.64E-07	1.91E-02	up	7.48	657
CATSPER1	Homo sapiens cation channel, sperm associated 1 (CATSPER1), mRNA [NM_053054]	gene	8.66E-16	2.63E-11	up	21.24	532
CBS	Homo sapiens cystathionine-beta-synthase (CBS), transcript variant 1, mRNA [NM_000071]	gene	2.58E-07	7.50E-03	up	6.56	385
CBX6	chromobox homolog 6 [Source:HGNC Symbol;Acc:HGNC:1556] [ENST00000407418]	gene	1.12E-06	3.19E-02	up	2.35	406
CCDC114	Homo sapiens coiled-coil domain containing 114 (CCDC114), mRNA [NM_144577]	gene	9.30E-08	2.72E-03	down	-3.66	1028
CCDC129	coiled-coil domain containing 129 [Source:HGNC Symbol;Acc:HGNC:27363] [ENST00000409717]	gene	5.23E-08	1.54E-03	down	-2.98	892
CCDC147-AS1	Homo sapiens CCDC147 antisense RNA 1 (head to head) (CCDC147-AS1), long non-coding RNA [NR_108036]	ncRNA	3.90E-12	1.18E-07	up	26.47	Not used
CCDC149	Homo sapiens coiled-coil domain containing 149 (CCDC149), transcript variant 1, mRNA [NM_173463]	gene	1.23E-17	3.75E-13	up	34.54	261
CCDC149	Homo sapiens coiled-coil domain containing 149 (CCDC149), transcript variant 1, mRNA [NM_173463]	gene	1.71E-15	5.19E-11	up	15.69	Not used
CCDC149	Homo sapiens coiled-coil domain containing 149 (CCDC149), transcript variant 1, mRNA [NM_173463]	gene	7.32E-09	2.17E-04	up	7.41	Not used
CCDC166	Homo sapiens coiled-coil domain containing 166 (CCDC166), mRNA [NM_001162914]	gene	9.76E-07	2.79E-02	down	-2.62	928
CCDC172	Homo sapiens coiled-coil domain containing 172 (CCDC172), mRNA [NM_198515]	gene	1.13E-07	3.29E-03	down	-3.09	888
CCDC183-AS1	Homo sapiens CCDC183 antisense RNA 1 (CCDC183-AS1), long non-coding RNA [NR_024580]	ncRNA	1.44E-08	4.26E-04	down	-2.84	Not used
CCDC33	Homo sapiens coiled-coil domain containing 33 (CCDC33), transcript variant 1, mRNA [NM_025055]	gene	1.37E-06	3.89E-02	down	-2.90	1200
CCDC57	coiled-coil domain containing 57 [Source:HGNC Symbol;Acc:HGNC:27564] [ENST00000327026]	gene	7.03E-07	2.02E-02	down	-2.15	939
CCDC65	Homo sapiens coiled-coil domain containing 65 (CCDC65), transcript variant 1, mRNA [NM_033124]	gene	7.08E-10	2.12E-05	up	8.05	218
CCDC88C	Homo sapiens coiled-coil domain containing 88C (CCDC88C), mRNA [NM_001080414]	gene	3.85E-07	1.11E-02	down	-2.94	941
CCL24	Homo sapiens chemokine (C-C motif) ligand 24 (CCL24), mRNA [NM_002991]	gene	1.45E-08	4.30E-04	down	-3.71	978
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	1.42E-07	4.14E-03	up	36.22	93
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	1.69E-09	5.03E-05	up	16.21	Not used
CCL4L2	Homo sapiens chemokine (C-C motif) ligand 4-like 2 (CCL4L2), transcript variant CCL4L2b2, mRNA [NM_001291470]	gene	1.25E-07	3.66E-03	up	3.60	Not used
CCL5	Homo sapiens chemokine (C-C motif) ligand 5 (CCL5), transcript variant 1, mRNA [NM_002985]	gene	5.02E-09	1.49E-04	up	30.13	586
CCM2L	Homo sapiens cerebral cavernous malformation 2-like (CCM2L), mRNA [NM_080625]	gene	5.19E-11	1.56E-06	down	-10.87	872
CCNB2	Homo sapiens cyclin B2 (CCNB2), mRNA [NM_004701]	gene	1.74E-06	4.92E-02	up	3.39	383
CCNJL	Homo sapiens cyclin J-like (CCNJL), mRNA [NM_024565]	gene	6.51E-16	1.98E-11	up	58.29	276
CCNL2	Homo sapiens cyclin L2 (CCNL2), transcript variant 1, mRNA [NM_030937]	gene	2.11E-07	6.14E-03	down	-2.86	946
CCR1	Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA [NM_001295]	gene	5.99E-19	1.82E-14	up	533.56	26
CCR3	Homo sapiens chemokine (C-C motif) receptor 3 (CCR3), transcript variant 1, mRNA [NM_001837]	gene	1.04E-08	3.07E-04	up	48.15	169
CCR5	Homo sapiens chemokine (C-C motif) receptor 5 (gene/pseudogene) (CCR5), transcript variant A, mRNA [NM_000579]	gene	7.57E-07	2.17E-02	up	10.09	506
CD109	Homo sapiens CD109 molecule (CD109), transcript variant 1, mRNA [NM_133493]	gene	1.59E-06	4.53E-02	up	5.70	807
CD14	Homo sapiens CD14 molecule (CD14), transcript variant 3, mRNA [NM_001174104]	gene	1.27E-14	3.85E-10	up	254.00	157
CD160	Homo sapiens CD160 molecule (CD160), transcript variant 1, mRNA [NM_007053]	gene	2.59E-09	7.73E-05	up	13.69	723
CD163	Homo sapiens CD163 molecule (CD163), transcript variant 1, mRNA [NM_004244]	gene	4.81E-12	1.45E-07	up	106.89	150
CD2	Homo sapiens CD2 molecule (CD2), mRNA [NM_001767]	gene	6.30E-11	1.89E-06	up	52.72	567
CD226	CD226 molecule [Source:HGNC Symbol;Acc:HGNC:16961] [ENST00000280200]	gene	2.30E-12	6.94E-08	up	10.03	330
CD244	Homo sapiens CD244 molecule, natural killer cell receptor 2B4 (CD244), transcript variant 1, mRNA [NM_016382]	gene	6.43E-11	1.93E-06	up	10.56	325
CD247	Homo sapiens CD247 molecule (CD247), transcript variant 1, mRNA [NM_198053]	gene	3.62E-09	1.08E-04	up	60.62	573
CD28	Homo sapiens CD28 molecule (CD28), transcript variant 1, mRNA [NM_006139]	gene	2.28E-21	6.94E-17	up	100.97	106
CD300A	Homo sapiens CD300a molecule (CD300A), transcript variant 1, mRNA [NM_007261]	gene	8.14E-11	2.45E-06	up	142.05	40
CD300A	Homo sapiens CD300a molecule (CD300A), transcript variant 1, mRNA [NM_007261]	gene	2.84E-09	8.46E-05	up	7.31	Not used
CD300C	Homo sapiens CD300c molecule (CD300C), mRNA [NM_006678]	gene	6.08E-09	1.81E-04	up	16.79	305
CD300E	Homo sapiens CD300e molecule (CD300E), mRNA [NM_181449]	gene	4.84E-08	1.42E-03	up	3.85	387
CD300LF	Homo sapiens CD300 molecule-like family member f (CD300LF), transcript variant 1, mRNA [NM_139018]	gene	2.28E-17	6.95E-13	up	133.17	108
CD302	Homo sapiens CD302 molecule (CD302), transcript variant 1, mRNA [NM_014880]	gene	8.94E-10	2.68E-05	up	20.64	689
CD302	Homo sapiens CD302 molecule (CD302), transcript variant 1, mRNA [NM_014880]	gene	1.35E-08	4.01E-04	up	18.20	Not used
CD33	Homo sapiens CD33 molecule (CD33), transcript variant 1, mRNA [NM_001772]	gene	1.32E-10	3.96E-06	up	61.19	162
CD36	Homo sapiens CD36 molecule (thrombospondin receptor) (CD36), transcript variant 2, mRNA [NM_001001547]	gene	1.81E-15	5.50E-11	up	194.22	160
CD3D	Homo sapiens CD3d molecule, delta (CD3-TCR complex) (CD3D), transcript variant 1, mRNA [NM_000732]	gene	4.87E-12	1.47E-07	up	43.95	588
CD3E	Homo sapiens CD3e molecule, epsilon (CD3-TCR complex) (CD3E), mRNA [NM_000733]	gene	2.58E-09	7.68E-05	up	8.08	336
CD3G	Homo sapiens CD3g molecule, gamma (CD3-TCR complex) (CD3G), mRNA [NM_000073]	gene	1.20E-09	3.59E-05	up	97.43	139
CD58	Homo sapiens CD58 molecule (CD58), transcript variant 1, mRNA [NM_001779]	gene	9.72E-08	2.85E-03	up	3.87	816
CD58	Homo sapiens CD58 molecule (CD58), transcript variant 1, mRNA [NM_001779]	gene	3.34E-07	9.68E-03	up	3.39	Not used
CD63	Homo sapiens CD63 molecule (CD63), transcript variant 3, mRNA [NM_001257389]	gene	8.59E-08	2.52E-03	up	2.99	451
CD68	Homo sapiens CD68 molecule (CD68), transcript variant 1, mRNA [NM_001251]	gene	3.68E-08	1.08E-03	up	4.73	818
CD7	Homo sapiens CD7 molecule (CD7), mRNA [NM_006137]	gene	6.19E-09	1.84E-04	up	8.47	364
CD72	CD72 molecule [Source:HGNC Symbol;Acc:HGNC:1696] [ENST00000378430]	gene	1.72E-08	5.09E-04	down	-4.27	984
CD8A	Homo sapiens CD8a molecule (CD8A), transcript variant 1, mRNA [NM_001768]	gene	8.08E-09	2.40E-04	up	50.40	128
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]	gene	1.59E-08	4.69E-04	up	104.40	129
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 4, mRNA [NM_172102]	gene	8.40E-10	2.51E-05	up	28.66	Not used
CD8B	Homo sapiens CD8b molecule (CD8B), transcript variant 5, mRNA [NM_004931]	gene	1.81E-09	5.40E-05	up	26.30	Not used
CD93	Homo sapiens CD93 molecule (CD93), mRNA [NM_012072]	gene	7.81E-16	2.37E-11	up	109.28	171
CDA	Homo sapiens cytidine deaminase (CDA), mRNA [NM_001785]	gene	8.45E-16	2.57E-11	up	35.27	81
CDC42EP1	Homo sapiens CDC42 effector protein (Rho GTPase binding) 1 (CDC42EP1), mRNA [NM_152243]	gene	2.80E-07	8.12E-03	up	7.45	783
CDC42EP5	Homo sapiens CDC42 effector protein (Rho GTPase binding) 5 (CDC42EP5), mRNA [NM_145057]	gene	1.63E-09	4.88E-05	down	-5.98	858
CDC6	Homo sapiens cell division cycle 6 (CDC6), mRNA [NM_001254]	gene	7.71E-07	2.21E-02	down	-2.67	1216
CDCA2	Homo sapiens cell division cycle associated 2 (CDCA2), mRNA [NM_152562]	gene	9.61E-07	2.75E-02	up	4.66	489
CDCA7	Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA [NM_031942]	gene	7.94E-08	2.33E-03	up	11.89	713
CDH22	Homo sapiens cadherin 22, type 2 (CDH22), mRNA [NM_021248]	gene	5.95E-08	1.75E-03	down	-4.16	1231
CDH23	Homo sapiens cadherin-related 23 (CDH23), transcript variant 1, mRNA [NM_022124]	gene	2.66E-10	7.99E-06	up	6.21	226
CDK20	Homo sapiens cyclin-dependent kinase 20 (CDK20), transcript variant 3, mRNA [NM_001039803]	gene	4.17E-09	1.24E-04	up	7.40	811
CDK6	Homo sapiens cyclin-dependent kinase 6 (CDK6), transcript variant 1, mRNA [NM_001259]	gene	3.93E-08	1.16E-03	up	24.70	541
CDKN2D	Homo sapiens cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) (CDKN2D), transcript variant 1, mRNA [NM_001800]	gene	2.13E-09	6.37E-05	up	6.25	397
CDRT3	DKFZp686P15240_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686P15240 5', mRNA sequence [BX484257]	gene	1.03E-07	3.00E-03	down	-2.57	906
CDX1	Homo sapiens caudal type homeobox 1 (CDX1), mRNA [NM_001804]	gene	4.80E-07	1.39E-02	down	-3.57	1071
CDX1	Homo sapiens caudal type homeobox 1 (CDX1), mRNA [NM_001804]	gene	6.31E-07	1.81E-02	down	-2.59	Not used
CEACAM3	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3), transcript variant 1, mRNA [NM_001815]	gene	1.03E-08	3.06E-04	up	16.63	633
CEACAM3	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 3 (CEACAM3), transcript variant 2, mRNA [NM_001277163]	gene	1.05E-08	3.11E-04	up	11.97	Not used
CEACAM4	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 4 (CEACAM4), mRNA [NM_001817]	gene	4.97E-09	1.48E-04	up	7.03	638
CEACAM6	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) (CEACAM6), mRNA [NM_002483]	gene	1.57E-08	4.63E-04	up	15.73	198
CEACAM8	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA [NM_001816]	gene	6.19E-13	1.87E-08	up	129.03	145
CEBPA	Homo sapiens CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA), transcript variant 1, mRNA [NM_004364]	gene	2.04E-10	6.14E-06	up	60.46	104
CEBPB	Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), transcript variant 1, mRNA [NM_005194]	gene	1.95E-08	5.76E-04	up	16.66	312
CEBPD	Homo sapiens CCAAT/enhancer binding protein (C/EBP), delta (CEBPD), mRNA [NM_005195]	gene	1.44E-08	4.28E-04	down	-3.66	864
CEBPE	Homo sapiens CCAAT/enhancer binding protein (C/EBP), epsilon (CEBPE), mRNA [NM_001805]	gene	4.51E-09	1.34E-04	up	20.73	306
CECR2	PREDICTED: Homo sapiens cat eye syndrome chromosome region, candidate 2 (CECR2), transcript variant X3, mRNA [XM_006724079]	gene	1.21E-07	3.53E-03	down	-2.46	1090
CECR6	Homo sapiens cat eye syndrome chromosome region, candidate 6 (CECR6), transcript variant 1, mRNA [NM_031890]	gene	1.16E-08	3.45E-04	up	13.75	785
CELSR1	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA [NM_014246]	gene	1.71E-06	4.85E-02	down	-2.20	900
CENPK	Homo sapiens centromere protein K (CENPK), transcript variant 1, mRNA [NM_022145]	gene	2.33E-08	6.88E-04	up	3.84	459
CEP104	centrosomal protein 104kDa [Source:HGNC Symbol;Acc:HGNC:24866] [ENST00000378223]	gene	1.45E-06	4.12E-02	down	-1.85	1092
CES1	Homo sapiens carboxylesterase 1 (CES1), transcript variant 1, mRNA [NM_001025195]	gene	4.32E-09	1.29E-04	up	64.32	125
CFAP46	Homo sapiens cilia and flagella associated protein 46 (CFAP46), mRNA [NM_001200049]	gene	1.04E-07	3.03E-03	down	-3.74	1034
CFAP58	Homo sapiens cilia and flagella associated protein 58 (CFAP58), mRNA [NM_001008723]	gene	7.57E-10	2.26E-05	up	7.14	223
CFD	Homo sapiens complement factor D (adipsin) (CFD), mRNA [NM_001928]	gene	6.29E-09	1.87E-04	up	122.15	149
CFH	Homo sapiens complement factor H (CFH), transcript variant 1, mRNA [NM_000186]	gene	5.21E-07	1.50E-02	up	6.81	386
CFP	Homo sapiens complement factor properdin (CFP), transcript variant 1, mRNA [NM_002621]	gene	5.95E-11	1.79E-06	up	45.16	545
CGB2	Homo sapiens chorionic gonadotropin, beta polypeptide 2 (CGB2), mRNA [NM_033378]	gene	4.36E-09	1.30E-04	down	-8.72	1170
CGREF1	Homo sapiens cell growth regulator with EF-hand domain 1 (CGREF1), transcript variant 5, mRNA [NM_001301324]	gene	6.79E-07	1.95E-02	down	-3.46	1175
CHI3L1	Homo sapiens chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA [NM_001276]	gene	7.00E-18	2.13E-13	up	414.45	14
CHN2	Homo sapiens chimerin 2 (CHN2), transcript variant 4, mRNA [NM_001293070]	gene	8.20E-10	2.45E-05	up	19.89	558
CHN2	Homo sapiens chimerin 2 (CHN2), transcript variant 4, mRNA [NM_001293070]	gene	2.21E-11	6.65E-07	up	16.10	Not used
CHST7	Homo sapiens carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 (CHST7), mRNA [NM_019886]	gene	4.91E-07	1.42E-02	up	7.31	814
CHSY1	Homo sapiens chondroitin sulfate synthase 1 (CHSY1), mRNA [NM_014918]	gene	1.15E-08	3.41E-04	up	5.44	494

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
CIC	capicua transcriptional repressor [Source:HGNC Symbol;Acc:HGNC:14214] [ENST00000572681]	gene	1.69E-07	4.93E-03	down	-2.68	970
CISD3	Homo sapiens CDGSH iron sulfur domain 3 (CISD3), mRNA [NM_001136498]	gene	1.64E-11	4.94E-07	down	-5.15	866
CLC	Homo sapiens Charcot-Leyden crystal galectin (CLC), mRNA [NM_001828]	gene	1.06E-12	3.22E-08	up	321.32	15
CLDN19	Homo sapiens claudin 19 (CLDN19), transcript variant 2, mRNA [NM_001123395]	gene	1.09E-06	3.11E-02	down	-2.37	922
CLDN7	Homo sapiens claudin 7 (CLDN7), transcript variant 1, mRNA [NM_001307]	gene	5.83E-07	1.68E-02	down	-2.21	1087
CLEC11A	Homo sapiens C-type lectin domain family 11, member A (CLEC11A), mRNA [NM_002975]	gene	8.67E-09	2.57E-04	up	13.45	542
CLEC12A	Homo sapiens C-type lectin domain family 12, member A (CLEC12A), transcript variant 1, mRNA [NM_138337]	gene	5.86E-09	1.74E-04	up	25.56	773
CLEC19A	Homo sapiens C-type lectin domain family 19, member A (CLEC19A), mRNA [NM_001256720]	gene	4.02E-07	1.16E-02	down	-2.76	1019
CLEC19A	Homo sapiens C-type lectin domain family 19, member A (CLEC19A), mRNA [NM_001256720]	gene	2.90E-07	8.40E-03	down	-2.73	Not used
CLEC1A	Homo sapiens C-type lectin domain family 1, member A (CLEC1A), transcript variant 4, mRNA [NM_001297750]	gene	8.28E-09	2.46E-04	up	12.55	232
CLEC1B	Homo sapiens C-type lectin domain family 1, member B (CLEC1B), transcript variant 1, mRNA [NM_016509]	gene	2.26E-07	6.58E-03	up	10.30	375
CLEC4A	Homo sapiens C-type lectin domain family 4, member A (CLEC4A), transcript variant 1, mRNA [NM_016184]	gene	3.91E-10	1.17E-05	up	15.35	673
CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA [NM_080387]	gene	1.67E-12	5.04E-08	up	94.47	60
CLEC4D	Homo sapiens C-type lectin domain family 4, member D (CLEC4D), mRNA [NM_080387]	gene	1.30E-12	3.93E-08	up	60.28	Not used
CLEC4E	Homo sapiens C-type lectin domain family 4, member E (CLEC4E), mRNA [NM_014358]	gene	3.92E-09	1.17E-04	up	20.69	249
CLEC7A	Homo sapiens C-type lectin domain family 7, member A (CLEC7A), transcript variant 6, mRNA [NM_197954]	gene	3.11E-18	9.46E-14	up	163.77	46
CLEC7A	Homo sapiens C-type lectin domain family 7, member A (CLEC7A), transcript variant 1, mRNA [NM_197947]	gene	2.19E-08	6.47E-04	up	9.08	Not used
CLHC1	clathrin heavy chain linker domain containing 1 [Source:HGNC Symbol;Acc:HGNC:26453] [ENST00000403506]	gene	9.54E-07	2.73E-02	down	-1.91	955
CLIC3	Homo sapiens chloride intracellular channel 3 (CLIC3), mRNA [NM_004669]	gene	3.23E-07	9.35E-03	up	10.61	735
CMKLR1	Homo sapiens chemokine-like receptor 1 (CMKLR1), transcript variant 1, mRNA [NM_001142343]	gene	6.95E-09	2.06E-04	up	23.14	284
CMPK2	Homo sapiens cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (CMPK2), transcript variant 1, mRNA [NM_207315]	gene	1.16E-08	3.43E-04	up	29.19	269
CMTM2	Homo sapiens CKLF-like MARVEL transmembrane domain containing 2 (CMTM2), transcript variant 1, mRNA [NM_144673]	gene	6.80E-13	2.06E-08	up	222.16	18
CMTM4	Homo sapiens CKLF-like MARVEL transmembrane domain containing 4 (CMTM4), transcript variant 2, mRNA [NM_181521]	gene	2.59E-08	7.64E-04	up	4.37	389
CMTM8	Homo sapiens CKLF-like MARVEL transmembrane domain containing 8 (CMTM8), mRNA [NM_178868]	gene	2.89E-07	8.37E-03	up	11.59	202
CNDP2	Homo sapiens CNDP dipeptidase 2 (metallopeptidase M20 family) (CNDP2), transcript variant 1, mRNA [NM_018235]	gene	1.49E-06	4.23E-02	down	-1.91	1094
CNIH2	Homo sapiens cornichon family AMPA receptor auxiliary protein 2 (CNIH2), transcript variant 1, mRNA [NM_182553]	gene	1.43E-07	4.19E-03	down	-6.57	1244
CNR2	Homo sapiens cannabinoid receptor 2 (macrophage) (CNR2), mRNA [NM_001841]	gene	1.06E-06	3.03E-02	down	-2.66	1137
CNTNAP3	Homo sapiens contactin associated protein-like 3 (CNTNAP3), mRNA [NM_033655]	gene	3.12E-11	9.41E-07	up	19.35	609
CNTNAP3B	Homo sapiens contactin associated protein-like 3B (CNTNAP3B), mRNA [NM_001201380]	gene	7.50E-08	2.20E-03	up	9.50	602
COG7	Homo sapiens component of oligomeric golgi complex 7 (COG7), mRNA [NM_153603]	gene	1.83E-09	5.46E-05	down	-2.57	1084
COL28A1	Homo sapiens partial mRNA for collagen, type XXVIII (COL28 gene), isoform 2. [AJ890452]	gene	2.46E-07	7.13E-03	down	-4.31	884
CORO2A	Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA [NM_003389]	gene	9.97E-07	2.85E-02	up	18.92	592
CORO2A	Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA [NM_003389]	gene	2.18E-07	6.33E-03	up	9.80	Not used
COX6A2	Homo sapiens cytochrome c oxidase subunit VIa polypeptide 2 (COX6A2), mRNA [NM_005205]	gene	6.75E-07	1.94E-02	down	-3.87	1209
CPD	Homo sapiens carboxypeptidase D (CPD), transcript variant 1, mRNA [NM_001304]	gene	2.88E-07	8.37E-03	up	5.92	820
CPNE2	Homo sapiens copine II (CPNE2), mRNA [NM_152727]	gene	1.31E-08	3.87E-04	up	15.24	690
CPPED1	Homo sapiens calcineurin-like phosphoesterase domain containing 1 (CPPED1), transcript variant 1, mRNA [NM_018340]	gene	3.02E-09	9.01E-05	up	27.92	629
CPVL	Homo sapiens carboxypeptidase, vitellogenic-like (CPVL), transcript variant 2, mRNA [NM_019029]	gene	4.50E-12	1.36E-07	up	69.58	290
CR1	Homo sapiens complement component (3b/4b) receptor 1 (Knops blood group) (CR1), transcript variant S, mRNA [NM_000651]	gene	8.45E-07	2.42E-02	up	14.43	711
CRABP2	Homo sapiens cellular retinoic acid binding protein 2 (CRABP2), transcript variant 2, mRNA [NM_001199723]	gene	1.47E-07	4.30E-03	down	-3.12	1007
CREB3L1	Homo sapiens cAMP responsive element binding protein 3-like 1 (CREB3L1), mRNA [NM_052854]	gene	6.45E-07	1.86E-02	down	-2.58	924
CREB5	Homo sapiens cAMP responsive element binding protein 5 (CREB5), transcript variant 1, mRNA [NM_182898]	gene	8.96E-12	2.70E-07	up	81.42	272
CRISPLD2	Homo sapiens cysteine-rich secretory protein LCCL domain containing 2 (CRISPLD2), mRNA [NM_031476]	gene	1.85E-15	5.63E-11	up	12.31	326
CRLF2	Homo sapiens cytokine receptor-like factor 2 (CRLF2), transcript variant 1, mRNA [NM_022148]	gene	2.08E-07	6.05E-03	down	-4.05	1013
CRLF2	Homo sapiens cytokine receptor-like factor 2 (CRLF2), transcript variant 2, mRNA [NM_001012288]	gene	9.62E-07	2.75E-02	down	-3.50	Not used
CRTAM	Homo sapiens cytotoxic and regulatory T cell molecule (CRTAM), mRNA [NM_019604]	gene	2.52E-08	7.44E-04	up	21.08	593
CRTC1	Homo sapiens CREB regulated transcription coactivator 1 (CRTC1), transcript variant 3, mRNA [NM_001098482]	gene	3.98E-09	1.18E-04	down	-3.58	979
CSF1R	Homo sapiens colony stimulating factor 1 receptor (CSF1R), transcript variant 1, mRNA [NM_005211]	gene	2.45E-10	7.35E-06	up	178.01	161
CSF2RA	Homo sapiens colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage) (CSF2RA), transcript variant 6, mRNA [NM_172249]	gene	4.54E-17	1.38E-12	up	32.80	84
CSF3R	Homo sapiens colony stimulating factor 3 receptor (granulocyte) (CSF3R), transcript variant 3, mRNA [NM_156039]	gene	9.88E-20	3.01E-15	up	389.95	44
CSGALNACT1	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 1 (CSGALNACT1), transcript variant 2, mRNA [NM_018371]	gene	3.02E-09	9.00E-05	up	41.90	584
CSGALNACT1	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 1 (CSGALNACT1), transcript variant 1, mRNA [NM_001130518]	gene	1.40E-07	4.08E-03	up	24.19	Not used
CSN1S1	Homo sapiens casein alpha s1 (CSN1S1), transcript variant 1, mRNA [NM_001890]	gene	1.42E-07	4.14E-03	down	-2.15	897
CSPG4	Homo sapiens chondroitin sulfate proteoglycan 4 (CSPG4), mRNA [NM_001897]	gene	1.90E-07	5.54E-03	down	-2.60	963
CST3	Homo sapiens cystatin C (CST3), transcript variant 1, mRNA [NM_000099]	gene	7.10E-08	2.08E-03	up	40.07	163
CST5	Homo sapiens cystatin D (CST5), mRNA [NM_001900]	gene	1.00E-07	2.94E-03	up	20.69	784
CST7	Homo sapiens cystatin F (leukocystatin) (CST7), mRNA [NM_003650]	gene	2.40E-10	7.20E-06	up	37.28	35
CSTA	Homo sapiens cystatin A (stefin A) (CSTA), mRNA [NM_005213]	gene	6.47E-16	1.97E-11	up	181.76	64
CTBP2	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA [NM_022802]	gene	2.61E-09	7.77E-05	up	14.18	645
CTD-3080P12.3	Homo sapiens uncharacterized LOC101928857 (CTD-3080P12.3), long non-coding RNA [NR_109911]	ncRNA	1.17E-07	3.42E-03	down	-2.51	Not used
CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1 [Source:HGNC Symbol;Acc:HGNC:2498] [ENST00000613122]	gene	3.81E-08	1.12E-03	down	-2.65	968
CTSG	Homo sapiens cathepsin G (CTSG), mRNA [NM_001911]	gene	1.64E-09	4.90E-05	up	51.21	153
CTSL	Homo sapiens cathepsin L (CTSL), transcript variant 1, mRNA [NM_001912]	gene	7.88E-07	2.26E-02	up	5.26	355
CTSLP8	Homo sapiens cathepsin L pseudogene 8 (CTSLP8), non-coding RNA [NR_033405]	gene	7.69E-09	2.28E-04	up	8.59	238
CTSW	Homo sapiens cathepsin W (CTSW), mRNA [NM_001335]	gene	2.78E-09	8.30E-05	up	10.62	717
CX3CR1	Homo sapiens chemokine (C-X3-C motif) receptor 1 (CX3CR1), transcript variant 4, mRNA [NM_001337]	gene	1.51E-09	4.52E-05	up	219.93	159
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), transcript variant 1, mRNA [NM_001511]	gene	3.69E-17	1.12E-12	up	339.98	30
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), transcript variant 1, mRNA [NM_001511]	gene	7.38E-10	2.21E-05	up	13.21	Not used
CXCL2	Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA [NM_002089]	gene	1.33E-06	3.79E-02	up	13.73	829
CXCL2	Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA [NM_002089]	gene	1.25E-06	3.55E-02	up	7.75	Not used
CXCL8	Homo sapiens chemokine (C-X-C motif) ligand 8 (CXCL8), mRNA [NM_000584]	gene	3.76E-11	1.13E-06	up	183.15	1
CXCR1	Homo sapiens chemokine (C-X-C motif) receptor 1 (CXCR1), mRNA [NM_000634]	gene	4.97E-13	1.50E-08	up	97.31	90
CXCR2	Homo sapiens chemokine (C-X-C motif) receptor 2 (CXCR2), transcript variant 1, mRNA [NM_001557]	gene	5.19E-14	1.57E-09	up	589.72	16
CXCR2P1	Homo sapiens chemokine (C-X-C motif) receptor 2 pseudogene 1 (CXCR2P1), non-coding RNA [NR_002712]	gene	3.94E-08	1.16E-03	up	21.12	242
CXorf57	Homo sapiens chromosome X open reading frame 57 (CXorf57), transcript variant 1, mRNA [NM_018015]	gene	1.54E-11	4.65E-07	up	14.17	369
CYBB	Homo sapiens cytochrome b-245, beta polypeptide (CYBB), mRNA [NM_000397]	gene	1.83E-07	5.34E-03	up	88.96	74
CYGB	Homo sapiens cytoglobin (CYGB), mRNA [NM_134268]	gene	5.11E-07	1.47E-02	down	-4.98	1223
CYP1B1	Homo sapiens cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA [NM_000104]	gene	5.60E-14	1.70E-09	up	91.15	264
CYP1B1	Homo sapiens cytochrome P450, family 1, subfamily B, polypeptide 1 (CYP1B1), mRNA [NM_000104]	gene	1.13E-11	3.42E-07	up	24.37	Not used
CYP27A1	Homo sapiens cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), mRNA [NM_000784]	gene	9.29E-13	2.81E-08	up	252.09	12
CYP4F2	Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 2 (CYP4F2), mRNA [NM_001082]	gene	2.01E-14	6.10E-10	up	9.86	224
CYP4F3	Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 3 (CYP4F3), transcript variant 1, mRNA [NM_000896]	gene	6.74E-20	2.05E-15	up	96.55	172
CYSTM1	Homo sapiens cysteine-rich transmembrane module containing 1 (CYSTM1), mRNA [NM_032412]	gene	3.56E-07	1.03E-02	up	5.12	815
CYTH1	cytohesin 1 [Source:HGNC Symbol;Acc:HGNC:9501] [ENST00000586299]	gene	1.19E-07	3.47E-03	down	-2.99	971
CYTH3	Homo sapiens cytohesin 3 (CYTH3), mRNA [NM_004227]	gene	6.40E-12	1.93E-07	up	11.04	328
DAB1	Homo sapiens Dab, reelin signal transducer, homolog 1 (Drosophila) (DAB1), mRNA [NM_021080]	gene	5.58E-07	1.61E-02	down	-3.09	1196
DAB2	Homo sapiens Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila) (DAB2), transcript variant 1, mRNA [NM_001343]	gene	8.21E-10	2.46E-05	up	12.03	724
DACH1	Homo sapiens dachshund family transcription factor 1 (DACH1), transcript variant 1, mRNA [NM_080759]	gene	3.24E-14	9.83E-10	up	18.28	654
DAZAP2	Homo sapiens DAZ associated protein 2 (DAZAP2), transcript variant 1, mRNA [NM_014764]	gene	3.91E-07	1.13E-02	up	2.03	420
DEFA3	Homo sapiens defensin, alpha 3, neutrophil-specific (DEFA3), mRNA [NM_005217]	gene	1.47E-09	4.38E-05	up	2241.74	4
DEFA4	Homo sapiens defensin, alpha 4, corticostatin (DEFA4), mRNA [NM_001925]	gene	1.01E-13	3.08E-09	up	358.77	9
DEFB4A	Homo sapiens defensin, beta 4A (DEFB4A), mRNA [NM_004942]	gene	3.34E-07	9.67E-03	down	-3.77	1191
DENND3	DENN/MADD domain containing 3 [Source:HGNC Symbol;Acc:HGNC:29134] [ENST00000520482]	gene	9.09E-09	2.70E-04	up	70.64	114
DENND3	Homo sapiens DENN/MADD domain containing 3 (DENND3), mRNA [NM_014957]	gene	8.56E-12	2.58E-07	up	44.65	Not used
DEPDC5	Homo sapiens DEP domain containing 5 (DEPDC5), transcript variant 4, mRNA [NM_001242896]	gene	1.68E-07	4.91E-03	down	-2.75	1102
DGAT2	Homo sapiens diacylglycerol O-acyltransferase 2 (DGAT2), transcript variant 1, mRNA [NM_032564]	gene	9.37E-10	2.80E-05	up	27.77	308
DGCR2	Homo sapiens DiGeorge syndrome critical region gene 2 (DGCR2), transcript variant 1, mRNA [NM_005137]	gene	1.31E-06	3.74E-02	up	2.43	430
DHRS3	Homo sapiens dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA [NM_004753]	gene	3.52E-07	1.02E-02	up	19.35	579
DIABLO	Homo sapiens diablo, IAP-binding mitochondrial protein (DIABLO), transcript variant 5, mRNA [NM_001278302]	gene	5.72E-10	1.71E-05	down	-4.28	867
DLEC1	Homo sapiens deleted in lung and esophageal cancer 1 (DLEC1), transcript variant DLEC1-N1, mRNA [NM_007335]	gene	1.04E-06	2.98E-02	up	7.20	677
DLG1-AS1	Homo sapiens DLG1 antisense RNA 1 (DLG1-AS1), long non-coding RNA [NR_038289]	ncRNA	1.35E-06	3.84E-02	down	-3.31	Not used
DLG5	Homo sapiens discs, large homolog 5 (Drosophila) (DLG5), mRNA [NM_004747]	gene	7.05E-11	2.12E-06	up	7.40	206
DMWD	Homo sapiens dystrophia myotonica, WD repeat containing (DMWD), mRNA [NM_004943]	gene	7.14E-07	2.05E-02	down	-1.91	1114
DMXL2	Homo sapiens Dmx-like 2 (DMXL2), transcript variant 2, mRNA [NM_015263]	gene	2.19E-16	6.67E-12	up	16.56	250
DNAI2	Homo sapiens dynein, axonemal, intermediate chain 2 (DNAI2), transcript variant 1, mRNA [NM_023036]	gene	4.92E-08	1.45E-03	up	6.18	639
DNAJC4	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 4, mRNA (cDNA clone IMAGE:4309314), complete cds. [BC010145]	gene	8.38E-07	2.40E-02	down	-2.02	1111
DNMT1	Homo sapiens DNA (cytosine-5-)-methyltransferase 1 (DNMT1), transcript variant 1, mRNA [NM_001130823]	gene	3.80E-08	1.12E-03	up	2.71	408
DNTTIP1	Homo sapiens deoxynucleotidyltransferase, terminal, interacting protein 1 (DNTTIP1), mRNA [NM_052951]	gene	1.42E-07	4.13E-03	up	2.76	447
DOCK4	Homo sapiens dedicator of cytokinesis 4 (DOCK4), mRNA [NM_014705]	gene	5.89E-10	1.76E-05	up	15.76	217
DOCK5	Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA [NM_024940]	gene	4.71E-17	1.43E-12	up	42.55	612
DOCK5	Homo sapiens dedicator of cytokinesis 5 (DOCK5), mRNA [NM_024940]	gene	1.47E-13	4.46E-09	up	21.30	Not used
DOK1	Homo sapiens docking protein 1, 62kDa (downstream of tyrosine kinase 1) (DOK1), transcript variant 1, mRNA [NM_001381]	gene	8.41E-07	2.41E-02	up	3.10	481
DPM2	Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit, mRNA (cDNA clone IMAGE:5222515), partial cds. [BC048256]	gene	4.73E-08	1.39E-03	down	-2.28	1135
DPP6	Homo sapiens dipeptidyl-peptidase 6 (DPP6), transcript variant 5, mRNA [NM_001290253]	gene	6.49E-07	1.87E-02	down	-2.78	1047
DRC1	Homo sapiens dynein regulatory complex subunit 1 (DRC1), mRNA [NM_145038]	gene	2.91E-07	8.43E-03	up	8.67	255
DSC2	Homo sapiens desmocollin 2 (DSC2), transcript variant Dsc2a, mRNA [NM_024422]	gene	2.34E-11	7.04E-07	up	11.83	766
DUSP13	Homo sapiens dual specificity phosphatase 13 (DUSP13), transcript variant 1, mRNA [NM_001007271]	gene	1.06E-07	3.10E-03	up	7.58	801
DUSP15	Homo sapiens dual specificity phosphatase 15 (DUSP15), transcript variant 1, mRNA [NM_080611]	gene	3.51E-07	1.02E-02	down	-3.00	901
DYSF	Homo sapiens dysferlin (DYSF), transcript variant 8, mRNA [NM_003494]	gene	6.69E-14	2.03E-09	up	69.08	273
E2F3	Homo sapiens E2F transcription factor 3 (E2F3), transcript variant 1, mRNA [NM_001949]	gene	2.33E-07	6.78E-03	up	5.19	358
EEPD1	Homo sapiens endonuclease/exonuclease/phosphatase family domain containing 1 (EEPD1), mRNA [NM_030636]	gene	1.02E-12	3.08E-08	up	25.98	751
EFNB1	Homo sapiens ephrin-B1 (EFNB1), mRNA [NM_004429]	gene	1.02E-08	3.02E-04	up	4.96	666
EIF4E2	Homo sapiens eukaryotic translation initiation factor 4E family member 2 (EIF4E2), transcript variant 2, mRNA [NM_001282958]	gene	1.20E-06	3.41E-02	down	-2.76	893
EIF4E3	Homo sapiens eukaryotic translation initiation factor 4E family member 3 (EIF4E3), transcript variant 2, mRNA [NM_173359]	gene	5.69E-11	1.71E-06	up	37.89	606
ELANE	Homo sapiens elastase, neutrophil expressed (ELANE), mRNA [NM_001972]	gene	2.33E-09	6.96E-05	up	15.89	199
ELF4	Homo sapiens E74-like factor 4 (ets domain transcription factor) (ELF4), transcript variant 1, mRNA [NM_001421]	gene	1.87E-08	5.53E-04	up	3.17	407
ELFN1	Homo sapiens extracellular leucine-rich repeat and fibronectin type III domain containing 1 (ELFN1), mRNA [NM_001128636]	gene	2.23E-09	6.65E-05	down	-8.94	842
EMILIN1	Homo sapiens elastin microfibril interfacer 1 (EMILIN1), mRNA [NM_007046]	gene	3.50E-11	1.05E-06	down	-7.09	853
EML1	Homo sapiens echinoderm microtubule associated protein like 1 (EML1), transcript variant 1, mRNA [NM_001008707]	gene	2.48E-07	7.19E-03	down	-2.98	1014
EMR2	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 2 (EMR2), transcript variant 1, mRNA [NM_013447]	gene	1.87E-15	5.68E-11	up	253.46	137
EMR3	Homo sapiens egf-like module containing, mucin-like, hormone receptor-like 3 (EMR3), transcript variant 1, mRNA [NM_032571]	gene	2.85E-14	8.65E-10	up	132.11	180
EN2	Homo sapiens engrailed homeobox 2 (EN2), mRNA [NM_001427]	gene	6.76E-11	2.03E-06	down	-8.67	849

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
EOMES	Homo sapiens eomesodermin (EOMES), transcript variant 2, mRNA [NM_005442]	gene	8.54E-12	2.58E-07	up	51.50	195
EPAS1	Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA [NM_001430]	gene	2.24E-14	6.80E-10	up	34.93	536
EPB41L3	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), transcript variant 1, mRNA [NM_012307]	gene	2.16E-12	6.54E-08	up	19.82	805
EPHA4	Homo sapiens EPH receptor A4 (EPHA4), mRNA [NM_004438]	gene	2.82E-07	8.19E-03	up	11.70	696
ERC2-IT1	Homo sapiens ERC2 intronic transcript 1 (non-protein coding) (ERC2-IT1), long non-coding RNA [NR_024615]	gene	1.27E-06	3.62E-02	down	-3.18	1190
ERCC-00041_75	not provided	unannotated probe	1.64E-06	4.65E-02	down	-2.11	Not used
ERCC-00092_138	not provided	unannotated probe	6.10E-09	1.81E-04	down	-3.73	Not used
ERCC-00126_533	not provided	unannotated probe	5.67E-07	1.63E-02	down	-2.22	Not used
ERCC-00137_95	not provided	unannotated probe	2.86E-07	8.30E-03	down	-2.18	Not used
ESR1	Homo sapiens estrogen receptor 1 (ESR1), transcript variant 1, mRNA [NM_000125]	gene	9.78E-07	2.80E-02	down	-2.92	1174
ETS2	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene homolog 2 (ETS2), transcript variant 1, mRNA [NM_005239]	gene	1.59E-17	4.84E-13	up	51.47	115
ETV7	Homo sapiens ets variant 7 (ETV7), transcript variant 1, mRNA [NM_016135]	gene	1.23E-12	3.71E-08	up	28.68	235
EVPLL	Homo sapiens envoplakin-like (EVPLL), mRNA [NM_001145127]	gene	3.91E-08	1.15E-03	down	-6.69	1212
EVX1	Homo sapiens even-skipped homeobox 1 (EVX1), mRNA [NM_001989]	gene	9.14E-07	2.62E-02	down	-4.71	1225
EYS	Homo sapiens eyes shut homolog (Drosophila) (EYS), transcript variant 1, mRNA [NM_001142800]	gene	1.24E-07	3.63E-03	down	-2.60	902
F2R	Homo sapiens coagulation factor II (thrombin) receptor (F2R), mRNA [NM_001992]	gene	2.30E-10	6.90E-06	up	22.01	191
F2R	Homo sapiens coagulation factor II (thrombin) receptor, mRNA (cDNA clone IMAGE:4849569), with apparent retained intron. [BC016059]	miscellaneous	1.74E-06	4.94E-02	up	13.54	Not used
F2RL1	Homo sapiens coagulation factor II (thrombin) receptor-like 1 (F2RL1), mRNA [NM_005242]	gene	5.86E-11	1.76E-06	up	37.39	282
F5	Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5), mRNA [NM_000130]	gene	4.84E-08	1.42E-03	up	14.47	714
FAAH2	Homo sapiens fatty acid amide hydrolase 2 (FAAH2), mRNA [NM_174912]	gene	9.11E-07	2.61E-02	up	10.17	826
FAM101B	Homo sapiens family with sequence similarity 101, member B (FAM101B), mRNA [NM_182705]	gene	2.71E-13	8.21E-09	up	335.58	49
FAM105A	Homo sapiens family with sequence similarity 105, member A (FAM105A), mRNA [NM_019018]	gene	2.87E-08	8.47E-04	up	35.33	103
FAM107A	Homo sapiens family with sequence similarity 107, member A (FAM107A), transcript variant 4, mRNA [NM_001282714]	gene	7.05E-08	2.07E-03	down	-3.66	1197
FAM107A	Homo sapiens family with sequence similarity 107, member A (FAM107A), transcript variant 4, mRNA [NM_001282714]	gene	7.46E-07	2.14E-02	down	-2.21	Not used
FAM129A	Homo sapiens family with sequence similarity 129, member A (FAM129A), mRNA [NM_052966]	gene	1.02E-11	3.07E-07	up	297.91	50
FAM129B	Homo sapiens family with sequence similarity 129, member B (FAM129B), transcript variant 1, mRNA [NM_022833]	gene	3.18E-11	9.59E-07	up	8.56	321
FAM131C	Homo sapiens family with sequence similarity 131, member C (FAM131C), mRNA [NM_182623]	gene	6.47E-07	1.86E-02	down	-3.11	1220
FAM132B	Homo sapiens family with sequence similarity 132, member B (FAM132B), mRNA [NM_001291832]	gene	1.95E-07	5.66E-03	down	-3.04	1249
FAM134B	Homo sapiens family with sequence similarity 134, member B (FAM134B), transcript variant 1, mRNA [NM_001034850]	gene	4.30E-07	1.24E-02	up	23.08	796
FAM13A	Homo sapiens family with sequence similarity 13, member A (FAM13A), transcript variant 1, mRNA [NM_014883]	gene	9.36E-12	2.82E-07	up	21.55	698
FAM157C	Homo sapiens family with sequence similarity 157, member C (FAM157C), long non-coding RNA [NR_126161]	gene	4.13E-11	1.24E-06	up	19.07	279
FAM169A	Homo sapiens family with sequence similarity 169, member A (FAM169A), transcript variant 1, mRNA [NM_015566]	gene	2.79E-09	8.31E-05	up	19.17	583
FAM169A	Homo sapiens family with sequence similarity 169, member A (FAM169A), transcript variant 1, mRNA [NM_015566]	gene	3.65E-12	1.10E-07	up	9.47	Not used
FAM179A	Homo sapiens family with sequence similarity 179, member A (FAM179A), mRNA [NM_199280]	gene	5.17E-09	1.54E-04	up	7.16	319
FAM180A	Homo sapiens family with sequence similarity 180, member A (FAM180A), mRNA [NM_205855]	gene	3.16E-07	9.16E-03	down	-2.03	948
FAM181A	Homo sapiens family with sequence similarity 181, member A (FAM181A), transcript variant 1, mRNA [NM_138344]	gene	7.55E-07	2.17E-02	down	-2.61	1264
FAM181B	Homo sapiens family with sequence similarity 181, member B (FAM181B), mRNA [NM_175885]	gene	4.41E-08	1.30E-03	down	-2.68	886
FAM198B	Homo sapiens family with sequence similarity 198, member B (FAM198B), transcript variant 2, mRNA [NM_016613]	gene	1.44E-14	4.38E-10	up	71.25	293
FAM212A	Homo sapiens family with sequence similarity 212, member A (FAM212A), mRNA [NM_203370]	gene	7.30E-07	2.10E-02	down	-1.98	1091
FAM212B	Homo sapiens family with sequence similarity 212, member B (FAM212B), transcript variant 1, mRNA [NM_019099]	gene	8.84E-08	2.59E-03	up	3.37	491
FAM21C	Homo sapiens family with sequence similarity 21, member C (FAM21C), transcript variant 3, mRNA [NM_001169107]	gene	5.78E-08	1.70E-03	down	-2.73	921
FAM21EP	Homo sapiens family with sequence similarity 21, member E, pseudogene (FAM21EP), non-coding RNA [NR_038275]	gene	1.39E-06	3.96E-02	down	-3.24	935
FAM231A	Homo sapiens family with sequence similarity 231, member A (FAM231A), mRNA [NM_001282321]	gene	6.95E-07	2.00E-02	down	-2.93	1120
FAM231A	Homo sapiens family with sequence similarity 231, member A (FAM231A), mRNA [NM_001282321]	gene	1.86E-07	5.43E-03	down	-1.93	Not used
FAM49B	Homo sapiens family with sequence similarity 49, member B (FAM49B), transcript variant 2, mRNA [NM_016623]	gene	4.99E-14	1.51E-09	up	4.85	342
FAM63A	Homo sapiens family with sequence similarity 63, member A (FAM63A), transcript variant 2, mRNA [NM_001040217]	gene	9.22E-07	2.64E-02	up	5.19	649
FAM66A	Homo sapiens family with sequence similarity 66, member A (FAM66A), long non-coding RNA [NR_026789]	gene	7.59E-07	2.18E-02	down	-2.20	1104
FAM71E2	Homo sapiens family with sequence similarity 71, member E2 (FAM71E2), mRNA [NM_001145402]	gene	1.28E-06	3.65E-02	down	-2.07	907
FAM8A1	Homo sapiens family with sequence similarity 8, member A1 (FAM8A1), mRNA [NM_016255]	gene	4.87E-08	1.43E-03	up	3.19	401
FAR2	Homo sapiens fatty acyl CoA reductase 2 (FAR2), transcript variant 2, mRNA [NM_018099]	gene	4.65E-13	1.41E-08	up	16.15	655
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	6.15E-09	1.83E-04	up	9.13	678
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	2.49E-08	7.36E-04	up	7.66	Not used
FAS	Homo sapiens Fas cell surface death receptor (FAS), transcript variant 1, mRNA [NM_000043]	gene	1.18E-08	3.50E-04	up	6.95	Not used
FASLG	Homo sapiens Fas ligand (TNF superfamily, member 6) (FASLG), transcript variant 1, mRNA [NM_000639]	gene	4.71E-08	1.39E-03	up	13.93	221
FAT3	Homo sapiens FAT atypical cadherin 3 (FAT3), mRNA [NM_001008781]	gene	5.11E-07	1.47E-02	down	-2.61	1021
FBRSL1	Homo sapiens fibrosin-like 1 (FBRSL1), mRNA [NM_001142641]	gene	2.70E-07	7.82E-03	down	-6.57	844
FBXL5	Homo sapiens F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 1, mRNA [NM_012161]	gene	1.52E-07	4.43E-03	up	3.69	413
FBXO17	F-box protein 17 [Source:HGNC Symbol;Acc:HGNC:18754] [ENST00000601394]	gene	1.15E-06	3.29E-02	down	-2.68	964
FCAR	Homo sapiens Fc fragment of IgA, receptor for (FCAR), transcript variant 3, mRNA [NM_133271]	gene	3.62E-15	1.10E-10	up	194.31	28
FCAR	Homo sapiens Fc fragment of IgA, receptor for (FCAR), transcript variant 1, mRNA [NM_002000]	gene	5.95E-15	1.81E-10	up	47.29	Not used
FCER1G	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G), mRNA [NM_004106]	gene	1.94E-13	5.89E-09	up	23.05	82
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 1, mRNA [NM_001017986]	gene	3.04E-13	9.20E-09	up	251.74	158
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 3, mRNA [NM_001244910]	gene	4.79E-12	1.45E-07	up	95.08	Not used
FCGR1B	Homo sapiens Fc fragment of IgG, high affinity Ib, receptor (CD64) (FCGR1B), transcript variant 3, mRNA [NM_001244910]	gene	8.23E-12	2.48E-07	up	90.88	Not used
FCGR2C	Homo sapiens Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene) (FCGR2C), transcript variant 1, mRNA [NM_201563]	gene	9.48E-10	2.84E-05	up	44.17	97
FCGR3A	Homo sapiens Fc fragment of IgG, low affinity IIIa, receptor (CD16a) (FCGR3A), transcript variant 1, mRNA [NM_000569]	gene	8.44E-14	2.56E-09	up	2636.74	21
FCN1	Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA [NM_002003]	gene	8.41E-13	2.54E-08	up	374.05	13
FCN1	Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA [NM_002003]	gene	2.86E-14	8.69E-10	up	191.84	Not used
FCN3	ficolin (collagen/fibrinogen domain containing) 3 [Source:HGNC Symbol;Acc:HGNC:3625] [ENST00000498393]	gene	1.70E-08	5.04E-04	down	-2.94	974
FCRL6	Homo sapiens Fc receptor-like 6 (FCRL6), transcript variant 2, mRNA [NM_001284217]	gene	1.74E-08	5.14E-04	up	21.56	736
FER1L6-AS1	Homo sapiens FER1L6 antisense RNA 1 (FER1L6-AS1), long non-coding RNA [NR_040044]	ncRNA	8.58E-07	2.46E-02	down	-3.95	Not used
FER1L6-AS2	601564882F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925989 5', mRNA sequence [BE729513]	miscellaneous	9.52E-07	2.72E-02	down	-2.49	Not used
FFAR2	Homo sapiens free fatty acid receptor 2 (FFAR2), mRNA [NM_005306]	gene	1.20E-17	3.65E-13	up	56.04	274
FGD4	Homo sapiens FYVE, RhoGEF and PH domain containing 4 (FGD4), mRNA [NM_139241]	gene	9.08E-12	2.74E-07	up	43.77	100
FGD4	Homo sapiens FYVE, RhoGEF and PH domain containing 4 (FGD4), mRNA [NM_139241]	gene	1.43E-12	4.34E-08	up	27.36	Not used
FGD4	FYVE, RhoGEF and PH domain containing 4 [Source:HGNC Symbol;Acc:HGNC:19125] [ENST00000472289]	gene	1.51E-14	4.58E-10	up	16.08	Not used
FGFBP2	Homo sapiens fibroblast growth factor binding protein 2 (FGFBP2), mRNA [NM_031950]	gene	6.84E-10	2.05E-05	up	34.15	563
FGL2	Homo sapiens fibrinogen-like 2 (FGL2), mRNA [NM_006682]	gene	2.46E-08	7.27E-04	up	83.34	270
FIGNL2	Homo sapiens fidgetin-like 2 (FIGNL2), mRNA [NM_001013690]	gene	4.08E-09	1.22E-04	down	-2.51	975
FKBP1A	Homo sapiens FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 1, mRNA [NM_000801]	gene	1.60E-06	4.53E-02	up	2.50	411
FLJ27255	not provided	unannotated probe	2.08E-08	6.13E-04	up	7.98	Not used
FLJ36777	uncharacterized LOC730971 [Source:EntrezGene;Acc:730971] [ENST00000501888]	uncharacterized locus	5.95E-07	1.71E-02	down	-2.21	Not used
FLJ44477	Homo sapiens cDNA FLJ44477 fis, clone UTERU2031703. [AK126441]	miscellaneous	1.12E-06	3.21E-02	down	-1.99	Not used
FLJ46026	PREDICTED: Homo sapiens FLJ46026 protein (FLJ46026), misc_RNA [XR_159298]	miscellaneous	1.10E-07	3.22E-03	down	-3.98	Not used
FLNA	Homo sapiens filamin A, alpha (FLNA), transcript variant 1, mRNA [NM_001456]	gene	3.63E-07	1.05E-02	up	2.95	493
FNDC3B	Homo sapiens fibronectin type III domain containing 3B (FNDC3B), transcript variant 1, mRNA [NM_022763]	gene	2.77E-07	8.04E-03	up	10.07	313
FNDC3B	Homo sapiens fibronectin type III domain containing 3B (FNDC3B), transcript variant 1, mRNA [NM_022763]	gene	4.10E-10	1.23E-05	up	9.48	Not used
FNIP2	Homo sapiens folliculin interacting protein 2 (FNIP2), mRNA [NM_020840]	gene	4.77E-13	1.45E-08	up	32.96	833
FOLR3	Homo sapiens folate receptor 3 (gamma) (FOLR3), mRNA [NM_000804]	gene	2.26E-15	6.88E-11	up	50.34	539
FOSL2	Homo sapiens FOS-like antigen 2 (FOSL2), mRNA [NM_005253]	gene	1.19E-06	3.41E-02	up	21.28	832
FOXB1	Homo sapiens forkhead box B1 (FOXB1), mRNA [NM_012182]	gene	5.73E-09	1.70E-04	down	-6.68	1163
FOXP4	Homo sapiens forkhead box P4 (FOXP4), transcript variant 1, mRNA [NM_001012426]	gene	8.25E-07	2.37E-02	down	-15.35	876
FPR1	Homo sapiens formyl peptide receptor 1 (FPR1), transcript variant 2, mRNA [NM_002029]	gene	2.81E-19	8.56E-15	up	1195.94	25
FPR2	Homo sapiens formyl peptide receptor 2 (FPR2), transcript variant 1, mRNA [NM_001462]	gene	3.29E-16	1.00E-11	up	201.82	67
FRAT1	Homo sapiens frequently rearranged in advanced T-cell lymphomas 1 (FRAT1), mRNA [NM_005479]	gene	1.92E-07	5.59E-03	up	6.56	404
FRAT1	Homo sapiens frequently rearranged in advanced T-cell lymphomas 1 (FRAT1), mRNA [NM_005479]	gene	1.74E-06	4.93E-02	up	4.39	Not used
FRAT2	Homo sapiens frequently rearranged in advanced T-cell lymphomas 2 (FRAT2), mRNA [NM_012083]	gene	1.00E-10	3.02E-06	up	14.22	757
FTH1	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA [NM_002032]	gene	4.66E-08	1.37E-03	up	2.15	448
FTH1	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA [NM_002032]	gene	1.10E-07	3.23E-03	up	2.13	Not used
FTH1	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA [NM_002032]	gene	2.02E-08	5.96E-04	up	2.09	Not used
FUT4	Homo sapiens fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific) (FUT4), mRNA [NM_002033]	gene	7.16E-08	2.10E-03	up	5.44	320
FYB	Homo sapiens FYN binding protein (FYB), transcript variant 1, mRNA [NM_001465]	gene	5.86E-13	1.77E-08	up	463.19	51
G0S2	Homo sapiens G0/G1 switch 2 (G0S2), mRNA [NM_015714]	gene	1.08E-12	3.26E-08	up	1190.15	2
GABRR3	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, rho 3 (gene/pseudogene) (GABRR3), transcript variant 1, mRNA [NM_001105580]	gene	2.26E-07	6.58E-03	down	-3.97	1064
GALC	Homo sapiens galactosylceramidase (GALC), transcript variant 1, mRNA [NM_000153]	gene	1.99E-10	5.96E-06	up	4.85	463
GALR3	Homo sapiens galanin receptor 3 (GALR3), mRNA [NM_003614]	gene	1.23E-12	3.72E-08	down	-7.30	862
GAS7	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant c, mRNA [NM_201433]	gene	8.47E-08	2.48E-03	up	9.75	742
GATA2	Homo sapiens GATA binding protein 2 (GATA2), transcript variant 1, mRNA [NM_001145661]	gene	1.30E-06	3.70E-02	up	5.77	509
GATA3	Homo sapiens GATA binding protein 3 (GATA3), transcript variant 1, mRNA [NM_001002295]	gene	1.91E-07	5.55E-03	up	29.71	517
GBGT1	Homo sapiens globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (GBGT1), transcript variant 3, mRNA [NM_001282632]	gene	8.72E-08	2.56E-03	down	-2.07	1121
GBP1	Homo sapiens guanylate binding protein 1, interferon-inducible (GBP1), mRNA [NM_002053]	gene	3.93E-09	1.17E-04	up	59.51	296
GBP2	Homo sapiens guanylate binding protein 2, interferon-inducible (GBP2), mRNA [NM_004120]	gene	2.03E-07	5.91E-03	up	4.31	455
GBP5	Homo sapiens guanylate binding protein 5 (GBP5), transcript variant 1, mRNA [NM_052942]	gene	3.69E-07	1.07E-02	up	17.76	709
GCA	Homo sapiens grancalcin, EF-hand calcium binding protein (GCA), mRNA [NM_012198]	gene	3.11E-08	9.16E-04	up	9.59	758
GCH1	Homo sapiens GTP cyclohydrolase 1 (GCH1), transcript variant 1, mRNA [NM_000161]	gene	7.07E-07	2.03E-02	up	2.91	441
GCLM	Homo sapiens glutamate-cysteine ligase, modifier subunit (GCLM), mRNA [NM_002061]	gene	4.34E-07	1.25E-02	down	-2.74	1159
GFRA4	Homo sapiens GDNF family receptor alpha 4 (GFRA4), transcript variant 2, mRNA [NM_145762]	gene	1.59E-06	4.51E-02	down	-2.06	1132
GGA1	Homo sapiens golgi-associated, gamma adaptin ear containing, ARF binding protein 1 (GGA1), transcript variant 5, mRNA [NM_001172688]	gene	1.69E-06	4.81E-02	down	-2.23	1076
GGT5	Homo sapiens gamma-glutamyltransferase 5 (GGT5), transcript variant 1, mRNA [NM_001099781]	gene	3.46E-07	1.00E-02	up	4.84	395
GGTA1P	Homo sapiens glycoprotein, alpha-galactosyltransferase 1 pseudogene (GGTA1P), transcript variant 1, non-coding RNA [NR_003191]	gene	8.62E-08	2.53E-03	up	15.32	597
GIMAP1	Homo sapiens GTPase, IMAP family member 1 (GIMAP1), mRNA [NM_130759]	gene	2.73E-10	8.19E-06	up	16.21	675
GIMAP2	Homo sapiens GTPase, IMAP family member 2 (GIMAP2), mRNA [NM_015660]	gene	7.30E-08	2.14E-03	up	5.29	461
GIMAP4	Homo sapiens GTPase, IMAP family member 4 (GIMAP4), mRNA [NM_018326]	gene	1.65E-13	4.99E-09	up	401.49	135
GIMAP5	Homo sapiens GTPase, IMAP family member 5 (GIMAP5), mRNA [NM_018384]	gene	1.00E-12	3.04E-08	up	83.25	186
GIMAP6	Homo sapiens GTPase, IMAP family member 6 (GIMAP6), transcript variant 1, mRNA [NM_024711]	gene	1.45E-12	4.38E-08	up	64.04	188
GIMAP7	Homo sapiens GTPase, IMAP family member 7 (GIMAP7), mRNA [NM_153236]	gene	6.37E-12	1.92E-07	up	174.87	136
GJD3	Homo sapiens gap junction protein, delta 3, 31.9kDa (GJD3), mRNA [NM_152219]	gene	1.60E-07	4.67E-03	down	-2.14	1134
GJD4	Homo sapiens gap junction protein, delta 4, 40.1kDa (GJD4), mRNA [NM_153368]	gene	7.47E-07	2.14E-02	down	-2.00	1098
GK	Homo sapiens glycerol kinase (GK), transcript variant 4, mRNA [NM_001205019]	gene	1.24E-08	3.69E-04	up	7.55	812
GK3P	Homo sapiens glycerol kinase 3 pseudogene (GK3P), non-coding RNA [NR_026575]	gene	1.35E-07	3.94E-03	up	5.87	813
GLI4	GLI family zinc finger 4 [Source:HGNC Symbol;Acc:HGNC:4320] [ENST00000523812]	gene	9.63E-10	2.88E-05	down	-7.17	860
GLIPR2	Homo sapiens GLI pathogenesis-related 2 (GLIPR2), transcript variant 3, mRNA [NM_001287011]	gene	4.47E-11	1.35E-06	up	14.93	769

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
GLIPR2	Homo sapiens GLI pathogenesis-related 2 (GLIPR2), transcript variant 1, mRNA [NM_022343]	gene	4.49E-08	1.32E-03	up	10.20	Not used
GLIS1	Homo sapiens GLIS family zinc finger 1 (GLIS1), mRNA [NM_147193]	gene	1.42E-06	4.04E-02	down	-3.96	1188
GLRX	Homo sapiens glutaredoxin (thioltransferase) (GLRX), transcript variant 1, mRNA [NM_002064]	gene	5.47E-13	1.66E-08	up	65.03	570
GLT1D1	Homo sapiens glycosyltransferase 1 domain containing 1 (GLT1D1), mRNA [NM_144669]	gene	1.86E-21	5.67E-17	up	695.20	27
GLYATL3	Homo sapiens glycine-N-acyltransferase-like 3 (GLYATL3), mRNA [NM_001010904]	gene	2.68E-07	7.77E-03	down	-2.38	1250
GMFG	Homo sapiens glia maturation factor, gamma (GMFG), transcript variant 1, mRNA [NM_004877]	gene	1.06E-07	3.10E-03	up	2.78	418
GNAQ	Homo sapiens guanine nucleotide binding protein (G protein), q polypeptide (GNAQ), mRNA [NM_002072]	gene	1.81E-14	5.49E-10	up	38.64	193
GNB4	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 4 (GNB4), mRNA [NM_021629]	gene	4.31E-07	1.24E-02	up	22.12	528
GNG10	Homo sapiens guanine nucleotide binding protein (G protein), gamma 10 (GNG10), transcript variant 1, mRNA [NM_001017998]	gene	2.67E-10	8.00E-06	up	10.22	726
GNG10	Homo sapiens guanine nucleotide binding protein (G protein), gamma 10 (GNG10), transcript variant 1, mRNA [NM_001017998]	gene	3.12E-07	9.04E-03	up	3.79	Not used
GNGT2	Homo sapiens guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2 (GNGT2), transcript variant 1, mRNA [NM_031498]	gene	8.12E-10	2.43E-05	up	18.67	706
GNLY	granulysin [Source:HGNC Symbol;Acc:HGNC:4414] [ENST00000489214]	gene	1.43E-06	4.07E-02	up	8.00	524
GNRH2	Homo sapiens gonadotropin-releasing hormone 2 (GNRH2), transcript variant 2, mRNA [NM_178332]	gene	1.52E-07	4.44E-03	down	-4.58	1063
GNRH2	gonadotropin-releasing hormone 2 [Source:HGNC Symbol;Acc:HGNC:4420] [ENST00000380347]	gene	9.67E-08	2.83E-03	down	-2.77	Not used
GNS	Homo sapiens glucosamine (N-acetyl)-6-sulfatase (GNS), mRNA [NM_002076]	gene	7.76E-07	2.23E-02	up	4.15	470
GOLGA2P7	Homo sapiens golgin A2 pseudogene 7 (GOLGA2P7), non-coding RNA [NR_027001]	gene	1.98E-08	5.84E-04	down	-3.77	983
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	2.34E-10	7.02E-06	up	4.72	472
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	1.35E-08	4.00E-04	up	3.17	Not used
GOLGA7	Homo sapiens golgin A7 (GOLGA7), transcript variant 2, mRNA [NM_001002296]	gene	1.02E-08	3.02E-04	up	2.98	Not used
GOLGA7B	Homo sapiens golgin A7 family, member B (GOLGA7B), mRNA [NM_001010917]	gene	6.93E-10	2.08E-05	up	7.16	348
GOLM1	Homo sapiens golgi membrane protein 1 (GOLM1), transcript variant 1, mRNA [NM_016548]	gene	8.83E-12	2.66E-07	up	11.86	691
GPA33	Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA [NM_005814]	gene	8.62E-07	2.47E-02	up	12.77	529
GPATCH4	G patch domain containing 4 [Source:HGNC Symbol;Acc:HGNC:25982] [ENST00000527691]	gene	3.81E-07	1.10E-02	down	-2.72	1052
GPR113	Homo sapiens G protein-coupled receptor 113 (GPR113), transcript variant 3, mRNA [NM_153835]	gene	1.07E-06	3.06E-02	down	-3.15	1139
GPR162	Homo sapiens G protein-coupled receptor 162 (GPR162), transcript variant A-2, mRNA [NM_019858]	gene	7.27E-11	2.19E-06	up	30.79	752
GPR176	Homo sapiens G protein-coupled receptor 176 (GPR176), transcript variant 1, mRNA [NM_007223]	gene	5.24E-07	1.51E-02	down	-4.63	1186
GPR25	Homo sapiens G protein-coupled receptor 25 (GPR25), mRNA [NM_005298]	gene	1.20E-07	3.52E-03	down	-2.45	1078
GPR56	Homo sapiens G protein-coupled receptor 56 (GPR56), transcript variant 3, mRNA [NM_201525]	gene	3.22E-07	9.33E-03	up	69.96	130
GPR65	Homo sapiens G protein-coupled receptor 65 (GPR65), mRNA [NM_003608]	gene	8.43E-08	2.47E-03	up	11.82	674
GPR78	Homo sapiens G protein-coupled receptor 78 (GPR78), transcript variant 1, mRNA [NM_080819]	gene	1.67E-06	4.76E-02	down	-3.64	1032
GPR84	Homo sapiens G protein-coupled receptor 84 (GPR84), mRNA [NM_020370]	gene	3.34E-08	9.86E-04	up	12.42	830
GPR97	Homo sapiens G protein-coupled receptor 97 (GPR97), mRNA [NM_170776]	gene	1.64E-10	4.92E-06	up	7.06	640
GPSM1	Homo sapiens G-protein signaling modulator 1 (GPSM1), transcript variant 1, mRNA [NM_001145638]	gene	2.28E-07	6.62E-03	down	-3.12	890
GRB10	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 4, mRNA [NM_001001555]	gene	5.02E-12	1.51E-07	up	25.77	83
GRB10	Homo sapiens growth factor receptor-bound protein 10 (GRB10), transcript variant 4, mRNA [NM_001001555]	gene	1.92E-12	5.81E-08	up	14.40	Not used
GRHL2	Homo sapiens grainyhead-like 2 (Drosophila) (GRHL2), mRNA [NM_024915]	gene	1.45E-08	4.29E-04	down	-3.59	1030
GRIFIN	Homo sapiens galectin-related inter-fiber protein (GRIFIN), mRNA [NM_001291784]	gene	6.13E-07	1.76E-02	down	-2.71	1263
GRK5	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:HGNC:4544] [ENST00000369108]	gene	1.30E-06	3.72E-02	down	-1.83	950
GSN	Homo sapiens gelsolin (GSN), transcript variant 4, mRNA [NM_001127663]	gene	1.13E-08	3.34E-04	up	10.35	743
GSN	Homo sapiens gelsolin (GSN), transcript variant 2, mRNA [NM_198252]	gene	1.35E-11	4.07E-07	up	5.57	Not used
GYG1	Homo sapiens glycogenin 1 (GYG1), transcript variant 1, mRNA [NM_004130]	gene	1.03E-06	2.95E-02	up	3.10	396
GZMA	Homo sapiens granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA), mRNA [NM_006144]	gene	4.74E-08	1.39E-03	up	139.79	126
GZMB	Homo sapiens granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB), mRNA [NM_004131]	gene	6.92E-08	2.03E-03	up	32.58	564
GZMH	Homo sapiens granzyme H (cathepsin G-like 2, protein h-CCPX) (GZMH), transcript variant 1, mRNA [NM_033423]	gene	1.67E-07	4.88E-03	up	58.88	131
GZMK	Homo sapiens granzyme K (granzyme 3; tryptase II) (GZMK), mRNA [NM_002104]	gene	6.62E-09	1.97E-04	up	84.50	127
H3F3A	Homo sapiens H3 histone, family 3A (H3F3A), mRNA [NM_002107]	gene	1.12E-09	3.35E-05	up	4.37	414
H3F3A	Homo sapiens H3 histone, family 3A (H3F3A), mRNA [NM_002107]	gene	2.91E-10	8.72E-06	up	4.26	Not used
H3F3A	Homo sapiens H3 histone, family 3A (H3F3A), mRNA [NM_002107]	gene	9.16E-08	2.68E-03	up	2.63	Not used
H3F3A	Homo sapiens H3 histone, family 3A (H3F3A), mRNA [NM_002107]	gene	1.31E-08	3.88E-04	up	2.54	Not used
HAL	Homo sapiens histidine ammonia-lyase (HAL), transcript variant 1, mRNA [NM_002108]	gene	2.81E-08	8.29E-04	up	9.57	754
HAND1	Homo sapiens heart and neural crest derivatives expressed 1 (HAND1), mRNA [NM_004821]	gene	1.98E-07	5.76E-03	down	-4.85	1179
HAP1	Homo sapiens huntingtin-associated protein 1 (HAP1), transcript variant 2, mRNA [NM_177977]	gene	8.34E-07	2.39E-02	down	-2.87	1056
HAPLN3	Homo sapiens hyaluronan and proteoglycan link protein 3 (HAPLN3), mRNA [NM_178232]	gene	1.84E-07	5.36E-03	up	6.81	791
HBEGF	Homo sapiens heparin-binding EGF-like growth factor (HBEGF), mRNA [NM_001945]	gene	6.77E-11	2.03E-06	up	15.19	594
HCAR3	Homo sapiens hydroxycarboxylic acid receptor 3 (HCAR3), mRNA [NM_006018]	gene	6.47E-16	1.97E-11	up	951.02	3
HCK	Homo sapiens HCK proto-oncogene, Src family tyrosine kinase (HCK), transcript variant 1, mRNA [NM_002110]	gene	1.28E-11	3.86E-07	up	53.63	553
HCN2	Homo sapiens hyperpolarization activated cyclic nucleotide gated potassium channel 2 (HCN2), mRNA [NM_001194]	gene	6.20E-09	1.84E-04	down	-13.77	879
HDAC4	Homo sapiens histone deacetylase 4 (HDAC4), mRNA [NM_006037]	gene	1.62E-09	4.84E-05	up	4.09	464
HDC	Homo sapiens histidine decarboxylase (HDC), mRNA [NM_002112]	gene	4.61E-13	1.40E-08	up	29.19	548
HDGFRP3	Homo sapiens hepatoma-derived growth factor, related protein 3 (HDGFRP3), mRNA [NM_016073]	gene	2.23E-12	6.75E-08	up	9.82	715
HEPH	Homo sapiens hephaestin (HEPH), transcript variant 2, mRNA [NM_014799]	gene	9.19E-07	2.63E-02	down	-2.27	1122
HEY1	Homo sapiens hes-related family bHLH transcription factor with YRPW motif 1 (HEY1), transcript variant 2, mRNA [NM_001040708]	gene	3.29E-09	9.80E-05	up	15.49	234
HHLA2	Homo sapiens HERV-H LTR-associating 2 (HHLA2), transcript variant 4, mRNA [NM_001282558]	gene	1.44E-06	4.09E-02	down	-4.33	1242
HIF3A	hypoxia inducible factor 3, alpha subunit [Source:HGNC Symbol;Acc:HGNC:15825] [ENST00000475432]	gene	1.72E-06	4.88E-02	down	-4.50	1224
HIVEP3	Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), transcript variant 3, non-coding RNA [NR_038260]	gene	6.47E-08	1.90E-03	up	8.19	661
HJURP	Homo sapiens Holliday junction recognition protein (HJURP), transcript variant 1, mRNA [NM_018410]	gene	2.48E-09	7.40E-05	up	8.05	204
HK2	Homo sapiens hexokinase 2 (HK2), mRNA [NM_000189]	gene	1.04E-06	2.98E-02	up	10.67	822
HK3	Homo sapiens hexokinase 3 (white cell) (HK3), mRNA [NM_002115]	gene	2.45E-10	7.36E-06	up	11.54	778
HLA-A	Homo sapiens major histocompatibility complex, class I, A (HLA-A), transcript variant 2 (A*01:01:01:01 allele), mRNA [NM_001242758]	gene	1.74E-06	4.94E-02	down	-3.02	1227
HLX	Homo sapiens H2.0-like homeobox (HLX), mRNA [NM_021958]	gene	4.15E-08	1.22E-03	up	9.70	716
HMG20B	Homo sapiens high mobility group 20B (HMG20B), mRNA [NM_006339]	gene	5.62E-07	1.62E-02	down	-3.01	1237
HMGA2	Homo sapiens high mobility group AT-hook 2 (HMGA2), transcript variant 3, mRNA [NM_001300918]	gene	1.61E-08	4.77E-04	down	-10.78	845
HMX1	Homo sapiens H6 family homeobox 1 (HMX1), mRNA [NM_018942]	gene	4.10E-12	1.24E-07	down	-7.15	852
HMX3	Homo sapiens H6 family homeobox 3 (HMX3), mRNA [NM_001105574]	gene	1.88E-07	5.47E-03	down	-3.51	1143
HNMT	Homo sapiens histamine N-methyltransferase (HNMT), transcript variant 2, mRNA [NM_001024074]	gene	1.71E-16	5.19E-12	up	22.57	533
HNMT	Homo sapiens histamine N-methyltransferase (HNMT), transcript variant 1, mRNA [NM_006895]	gene	1.60E-13	4.86E-09	up	15.58	Not used
HNRNPA1	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRNPA1), transcript variant 1, mRNA [NM_002136]	gene	1.61E-06	4.57E-02	down	-4.22	1260
HOGA1	4-hydroxy-2-oxoglutarate aldolase 1 [Source:HGNC Symbol;Acc:HGNC:25155] [ENST00000465608]	gene	2.45E-08	7.25E-04	down	-3.66	1192
HOPX	Homo sapiens HOP homeobox (HOPX), transcript variant 2, mRNA [NM_139211]	gene	1.57E-08	4.64E-04	up	29.05	565
HOTAIR	Homo sapiens HOX transcript antisense RNA (HOTAIR), transcript variant 3, long non-coding RNA [NR_047518]	gene	4.67E-07	1.35E-02	down	-3.38	1027
HOTAIR	BROAD Institute lincRNA (HOTAIR), lincRNA [TCONS_00079053_HOTAIR]	lincRNA	4.16E-07	1.20E-02	down	-2.51	Not used
HOTAIR	Homo sapiens HOX transcript antisense RNA (HOTAIR), transcript variant 1, long non-coding RNA [NR_047517]	ncRNA	1.50E-06	4.26E-02	down	-2.07	Not used
HOXA10	Homo sapiens homeobox A10 (HOXA10), transcript variant 1, mRNA [NM_018951]	gene	5.51E-07	1.59E-02	down	-5.54	847
HP	Homo sapiens haptoglobin (HP), transcript variant 1, mRNA [NM_005143]	gene	2.10E-08	6.21E-04	up	16.49	200
HPS1	Homo sapiens Hermansky-Pudlak syndrome 1 (HPS1), transcript variant 3, mRNA [NM_182639]	gene	4.47E-07	1.29E-02	down	-2.53	1077
HPSE	Homo sapiens heparanase (HPSE), transcript variant 1, mRNA [NM_006665]	gene	3.51E-09	1.05E-04	up	26.23	258
HR	Homo sapiens hair growth associated (HR), transcript variant 1, mRNA [NM_005144]	gene	9.40E-07	2.69E-02	down	-2.51	917
HR	Homo sapiens hair growth associated (HR), transcript variant 1, mRNA [NM_005144]	gene	1.13E-06	3.24E-02	down	-2.09	Not used
HS3ST3B1	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1 (HS3ST3B1), transcript variant 1, mRNA [NM_006041]	gene	4.10E-11	1.23E-06	up	13.73	368
HSF1	Homo sapiens heat shock transcription factor 1 (HSF1), mRNA [NM_005526]	gene	1.26E-06	3.59E-02	down	-1.51	1110
HSPA1A	Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA [NM_005345]	gene	1.71E-06	4.85E-02	up	12.00	803
HTR3A	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 3A, ionotropic (HTR3A), transcript variant 1, mRNA [NM_213621]	gene	1.68E-06	4.78E-02	down	-4.50	1247
ICAM1	Homo sapiens intercellular adhesion molecule 1 (ICAM1), mRNA [NM_000201]	gene	1.51E-06	4.31E-02	up	16.94	121
ID2	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA [NM_002166]	gene	3.69E-11	1.11E-06	up	62.82	110
ID2	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA [NM_002166]	gene	9.37E-09	2.78E-04	up	45.29	Not used
IER3	Homo sapiens immediate early response 3 (IER3), mRNA [NM_003897]	gene	5.18E-08	1.52E-03	up	25.65	122
IER3	Homo sapiens immediate early response 3 (IER3), mRNA [NM_003897]	gene	8.38E-07	2.40E-02	up	23.59	Not used
IER5L	Homo sapiens immediate early response 5-like (IER5L), mRNA [NM_203434]	gene	7.96E-07	2.28E-02	up	5.57	205
IER5L	Homo sapiens immediate early response 5-like (IER5L), mRNA [NM_203434]	gene	1.49E-08	4.41E-04	down	-2.61	Not used
IFI30	Homo sapiens interferon, gamma-inducible protein 30 (IFI30), mRNA [NM_006332]	gene	1.54E-09	4.61E-05	up	25.27	309
IFIT1	Homo sapiens interferon-induced protein with tetratricopeptide repeats 1 (IFIT1), transcript variant 1, mRNA [NM_001548]	gene	2.74E-09	8.17E-05	up	86.58	165
IFIT2	Homo sapiens interferon-induced protein with tetratricopeptide repeats 2 (IFIT2), mRNA [NM_001547]	gene	1.56E-06	4.45E-02	up	14.76	788
IFIT3	Homo sapiens interferon-induced protein with tetratricopeptide repeats 3 (IFIT3), transcript variant 3, mRNA [NM_001289758]	gene	2.56E-09	7.64E-05	up	96.66	166
IFITM2	Homo sapiens interferon induced transmembrane protein 2 (IFITM2), mRNA [NM_006435]	gene	6.50E-11	1.95E-06	up	17.24	615
IFITM3	Homo sapiens interferon induced transmembrane protein 3 (IFITM3), transcript variant 1, mRNA [NM_021034]	gene	3.01E-10	9.04E-06	up	14.32	616
IFITM4P	Homo sapiens interferon induced transmembrane protein 4 pseudogene (IFITM4P), non-coding RNA [NR_001590]	gene	2.99E-09	8.91E-05	up	11.03	617
IFNA4	Homo sapiens interferon, alpha 4 (IFNA4), mRNA [NM_021068]	gene	3.84E-07	1.11E-02	down	-3.66	1218
IFNG	Homo sapiens interferon, gamma (IFNG), mRNA [NM_000619]	gene	3.74E-09	1.11E-04	up	15.95	590
IFT122	Homo sapiens intraflagellar transport 122 (IFT122), transcript variant 3, mRNA [NM_018262]	gene	1.76E-06	5.00E-02	down	-2.19	1082
IFT22	Homo sapiens intraflagellar transport 22 (IFT22), transcript variant 1, mRNA [NM_022777]	gene	1.55E-06	4.39E-02	down	-2.00	1117
IGF2R	Homo sapiens insulin-like growth factor 2 receptor (IGF2R), mRNA [NM_000876]	gene	2.43E-07	7.07E-03	up	4.23	467
IGFBP7	Homo sapiens insulin-like growth factor binding protein 7 (IGFBP7), transcript variant 1, mRNA [NM_001553]	gene	2.41E-09	7.18E-05	up	33.78	566
IGFL2	Homo sapiens cDNA FLJ43766 fis, clone TESTI2049246. [AK125754]	gene	3.43E-08	1.01E-03	down	-3.74	1185
IGSF6	Homo sapiens immunoglobulin superfamily, member 6 (IGSF6), mRNA [NM_005849]	gene	4.51E-09	1.34E-04	up	25.96	256
IL13RA1	Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA [NM_001560]	gene	3.15E-07	9.14E-03	up	19.13	310
IL16	Homo sapiens interleukin 16 (IL16), transcript variant 3, mRNA [NM_001172128]	gene	2.81E-07	8.16E-03	down	-3.42	969
IL17A	Homo sapiens interleukin 17A (IL17A), mRNA [NM_002190]	gene	3.89E-09	1.16E-04	down	-4.48	1177
IL17RA	Homo sapiens interleukin 17 receptor A (IL17RA), transcript variant 1, mRNA [NM_014339]	gene	1.75E-06	4.97E-02	up	8.39	756
IL17RA	Homo sapiens interleukin 17 receptor A (IL17RA), transcript variant 1, mRNA [NM_014339]	gene	6.46E-10	1.93E-05	up	3.65	Not used
IL17RA	Homo sapiens interleukin 17 receptor A (IL17RA), transcript variant 1, mRNA [NM_014339]	gene	9.03E-09	2.68E-04	up	3.37	Not used
IL17REL	Homo sapiens interleukin 17 receptor E-like (IL17REL), mRNA [NM_001001694]	gene	9.50E-07	2.72E-02	down	-3.52	1193
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	1.44E-09	4.31E-05	up	18.14	316
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	6.98E-07	2.01E-02	up	11.87	Not used
IL18R1	Homo sapiens interleukin 18 receptor 1 (IL18R1), transcript variant 1, mRNA [NM_003855]	gene	2.37E-07	6.88E-03	up	5.35	Not used
IL18RAP	Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA [NM_003853]	gene	5.83E-09	1.73E-04	up	90.58	57
IL18RAP	Homo sapiens interleukin 18 receptor accessory protein (IL18RAP), mRNA [NM_003853]	gene	2.01E-09	6.00E-05	up	10.75	Not used
IL1B	Homo sapiens interleukin 1, beta (IL1B), mRNA [NM_000576]	gene	4.59E-10	1.38E-05	up	93.23	54
IL1R1	Homo sapiens interleukin 1 receptor, type I (IL1R1), transcript variant 1, mRNA [NM_000877]	gene	4.16E-14	1.26E-09	up	12.85	802
IL1R2	Homo sapiens interleukin 1 receptor, type II (IL1R2), transcript variant 1, mRNA [NM_004633]	gene	3.29E-11	9.92E-07	up	61.43	79
IL1RN	Homo sapiens interleukin 1 receptor antagonist (IL1RN), transcript variant 4, mRNA [NM_173843]	gene	8.74E-14	2.65E-09	up	482.51	32
IL1RN	Homo sapiens interleukin 1 receptor antagonist (IL1RN), transcript variant 4, mRNA [NM_173843]	gene	1.56E-06	4.45E-02	up	3.28	Not used
IL32	Homo sapiens interleukin 32 (IL32), transcript variant 1, mRNA [NM_001012631]	gene	1.64E-08	4.86E-04	up	46.01	133

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
IL32	Homo sapiens interleukin 32 (IL32), transcript variant 4, mRNA [NM_001012633]	gene	2.65E-09	7.91E-05	up	10.09	Not used
IL3RA	Homo sapiens interleukin 3 receptor, alpha (low affinity) (IL3RA), transcript variant 1, mRNA [NM_002183]	gene	4.23E-07	1.22E-02	up	6.20	808
IL7R	Homo sapiens interleukin 7 receptor (IL7R), transcript variant 1, mRNA [NM_002185]	gene	8.06E-10	2.41E-05	up	152.49	142
ILDR1	Homo sapiens immunoglobulin-like domain containing receptor 1 (ILDR1), transcript variant 2, mRNA [NM_175924]	gene	1.70E-06	4.83E-02	down	-2.68	1229
IMPA2	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA [NM_014214]	gene	7.71E-08	2.26E-03	up	14.33	741
IMPA2	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2), mRNA [NM_014214]	gene	9.62E-09	2.85E-04	up	12.12	Not used
INHBA	Homo sapiens inhibin, beta A (INHBA), mRNA [NM_002192]	gene	4.82E-08	1.42E-03	up	6.76	213
INHBB	Homo sapiens inhibin, beta B (INHBB), mRNA [NM_002193]	gene	6.80E-07	1.95E-02	up	7.19	643
INHBE	Homo sapiens inhibin, beta E (INHBE), mRNA [NM_031479]	gene	1.46E-06	4.17E-02	down	-2.36	992
INIP	Homo sapiens INTS3 and NABP interacting protein (INIP), mRNA [NM_021218]	gene	4.63E-07	1.34E-02	up	2.07	434
INPP4B	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kDa (INPP4B), transcript variant 1, mRNA [NM_003866]	gene	4.55E-10	1.36E-05	up	29.65	767
IQSEC2	Homo sapiens IQ motif and Sec7 domain 2 (IQSEC2), transcript variant 3, mRNA [NM_001243197]	gene	2.67E-09	7.97E-05	up	14.17	789
IQSEC2	Homo sapiens IQ motif and Sec7 domain 2 (IQSEC2), transcript variant 2, mRNA [NM_015075]	gene	1.38E-08	4.10E-04	down	-2.78	Not used
IQSEC3	Homo sapiens IQ motif and Sec7 domain 3 (IQSEC3), transcript variant 1, mRNA [NM_001170738]	gene	1.59E-07	4.63E-03	down	-3.52	980
IRAK3	Homo sapiens interleukin-1 receptor-associated kinase 3 (IRAK3), transcript variant 1, mRNA [NM_007199]	gene	1.22E-11	3.69E-07	up	80.28	38
IRF2BP2	Homo sapiens interferon regulatory factor 2 binding protein 2 (IRF2BP2), transcript variant 1, mRNA [NM_182972]	gene	9.40E-08	2.75E-03	up	3.21	442
IRG1	Homo sapiens immunoresponsive 1 homolog (mouse) (IRG1), mRNA [NM_001258406]	gene	1.78E-10	5.33E-06	down	-3.50	1151
ITGA6	Homo sapiens integrin, alpha 6 (ITGA6), transcript variant 2, mRNA [NM_000210]	gene	7.06E-10	2.11E-05	up	20.66	731
ITGA6	Homo sapiens integrin, alpha 6 (ITGA6), transcript variant 2, mRNA [NM_000210]	gene	6.77E-11	2.04E-06	up	10.07	Not used
ITGB2	Homo sapiens integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) (ITGB2), transcript variant 1, mRNA [NM_000211]	gene	3.36E-10	1.01E-05	up	26.66	546
ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:HGNC:6155] [ENST00000610622]	gene	2.11E-11	6.36E-07	up	7.70	Not used
ITK	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA [NM_005546]	gene	1.59E-11	4.79E-07	up	66.06	576
ITM2B	Homo sapiens integral membrane protein 2B (ITM2B), mRNA [NM_021999]	gene	3.00E-08	8.84E-04	up	5.92	400
JAKMIP1	Homo sapiens janus kinase and microtubule interacting protein 1 (JAKMIP1), transcript variant 2, mRNA [NM_144720]	gene	4.89E-09	1.46E-04	up	24.45	627
JUND	Homo sapiens jun D proto-oncogene (JUND), transcript variant 1, mRNA [NM_001286968]	gene	7.80E-07	2.24E-02	down	-6.47	1073
KANK3	KN motif and ankyrin repeat domains 3 [Source:HGNC Symbol;Acc:HGNC:24796] [ENST00000610351]	gene	1.36E-06	3.87E-02	down	-2.34	966
KCNA6	Homo sapiens potassium channel, voltage gated shaker related subfamily A, member 6 (KCNA6), mRNA [NM_002235]	gene	2.54E-07	7.37E-03	up	4.69	394
KCNC4	Homo sapiens potassium channel, voltage gated Shaw related subfamily C, member 4 (KCNC4), transcript variant 3, mRNA [NM_001039574]	gene	2.83E-09	8.43E-05	down	-3.02	1199
KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3 [Source:HGNC Symbol;Acc:HGNC:6239] [ENST00000369697]	gene	4.03E-07	1.17E-02	down	-1.87	951
KCNE3	Homo sapiens potassium channel, voltage gated subfamily E regulatory beta subunit 3 (KCNE3), mRNA [NM_005472]	gene	2.49E-13	7.55E-09	up	80.87	294
KCNJ15	Homo sapiens potassium channel, inwardly rectifying subfamily J, member 15 (KCNJ15), transcript variant 1, mRNA [NM_170736]	gene	4.40E-10	1.32E-05	up	52.89	174
KCNJ15	Homo sapiens potassium channel, inwardly rectifying subfamily J, member 15 (KCNJ15), transcript variant 1, mRNA [NM_170736]	gene	3.95E-11	1.19E-06	up	21.22	Not used
KCNJ2	Homo sapiens potassium channel, inwardly rectifying subfamily J, member 2 (KCNJ2), mRNA [NM_000891]	gene	3.86E-07	1.12E-02	up	49.71	527
KCNQ2	Homo sapiens potassium channel, voltage gated KQT-like subfamily Q, member 2 (KCNQ2), transcript variant 5, mRNA [NM_172109]	gene	2.14E-07	6.23E-03	down	-8.37	846
KCNT1	Homo sapiens cDNA FLJ41282 fis, clone BRAMY2037823. [AK123276]	gene	7.55E-09	2.24E-04	down	-3.19	1010
KCP	Homo sapiens kielin/chordin-like protein (KCP), transcript variant 2, mRNA [NM_199349]	gene	1.25E-06	3.56E-02	down	-3.72	1042
KCTD12	Homo sapiens potassium channel tetramerization domain containing 12 (KCTD12), mRNA [NM_138444]	gene	8.28E-12	2.50E-07	up	133.69	167
KCTD12	Homo sapiens potassium channel tetramerization domain containing 12 (KCTD12), mRNA [NM_138444]	gene	1.90E-12	5.73E-08	up	86.36	Not used
KDM8	Homo sapiens lysine (K)-specific demethylase 8 (KDM8), transcript variant 1, mRNA [NM_001145348]	gene	5.89E-07	1.69E-02	down	-2.08	920
KIAA0513	Homo sapiens KIAA0513 (KIAA0513), transcript variant 2, mRNA [NM_014732]	gene	8.49E-14	2.57E-09	up	33.07	613
KIAA1257	Homo sapiens KIAA1257 (KIAA1257), mRNA [NM_020741]	gene	8.06E-13	2.44E-08	up	27.60	634
KIAA1324	Homo sapiens KIAA1324 (KIAA1324), transcript variant 1, mRNA [NM_020775]	gene	3.96E-09	1.18E-04	up	18.76	797
KIAA1324	Homo sapiens KIAA1324 (KIAA1324), transcript variant 1, mRNA [NM_020775]	gene	6.59E-07	1.89E-02	up	7.99	Not used
KIAA1598	Homo sapiens KIAA1598 (KIAA1598), transcript variant 2, mRNA [NM_018330]	gene	1.00E-06	2.86E-02	up	19.26	520
KIAA1671	Homo sapiens KIAA1671 (KIAA1671), mRNA [NM_001145206]	gene	1.51E-06	4.30E-02	down	-3.15	Not used
KIAA1671	Homo sapiens KIAA1671 (KIAA1671), mRNA [NM_001145206]	gene	9.71E-07	2.78E-02	up	16.50	771
KIF16B	Homo sapiens kinesin family member 16B (KIF16B), transcript variant 1, mRNA [NM_001199866]	gene	1.62E-06	4.61E-02	down	-4.60	1070
KIF26B	Homo sapiens kinesin family member 26B (KIF26B), mRNA [NM_018012]	gene	8.04E-08	2.36E-03	down	-2.90	1210
KIR2DS2	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2 (KIR2DS2), transcript variant 1, mRNA [NM_012312]	gene	5.94E-07	1.71E-02	up	13.12	315
KIR3DL2	Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2 (KIR3DL2), transcript variant 1, mRNA [NM_006737]	gene	2.61E-08	7.69E-04	up	5.27	207
KIRREL2	Homo sapiens kin of IRRE like 2 (Drosophila) (KIRREL2), transcript variant 3, mRNA [NM_199180]	gene	7.90E-07	2.27E-02	down	-2.20	994
KLF13	Homo sapiens Kruppel-like factor 13 (KLF13), transcript variant 1, mRNA [NM_015995]	gene	6.77E-07	1.95E-02	up	1.87	423
KLF17	Homo sapiens Kruppel-like factor 17 (KLF17), mRNA [NM_173484]	gene	4.04E-07	1.17E-02	down	-1.94	1096
KLF5	Homo sapiens Kruppel-like factor 5 (intestinal) (KLF5), transcript variant 1, mRNA [NM_001730]	gene	6.42E-10	1.92E-05	up	8.40	212
KLRB1	Homo sapiens killer cell lectin-like receptor subfamily B, member 1 (KLRB1), mRNA [NM_002258]	gene	1.50E-08	4.44E-04	up	47.78	575
KLRC1	Homo sapiens killer cell lectin-like receptor subfamily C, member 1 (KLRC1), transcript variant 1, mRNA [NM_002259]	gene	1.46E-08	4.32E-04	up	25.42	561
KLRC3	Homo sapiens killer cell lectin-like receptor subfamily C, member 3 (KLRC3), transcript variant 2, mRNA [NM_007333]	gene	1.41E-08	4.18E-04	up	11.48	525
KLRC4	Homo sapiens killer cell lectin-like receptor subfamily C, member 4 (KLRC4), mRNA [NM_013431]	gene	9.74E-08	2.85E-03	up	8.85	718
KLRD1	Homo sapiens killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA [NM_002262]	gene	1.87E-10	5.61E-06	up	37.60	Not used
KLRD1	Homo sapiens killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 1, mRNA [NM_002262]	gene	1.77E-07	5.16E-03	up	41.29	190
KLRG1	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA [NM_005810]	gene	2.48E-10	7.43E-06	up	13.03	Not used
KLRG1	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA [NM_005810]	gene	2.50E-07	7.27E-03	up	18.63	687
KLRK1	Homo sapiens killer cell lectin-like receptor subfamily K, member 1 (KLRK1), mRNA [NM_007360]	gene	2.88E-11	8.67E-07	up	31.24	192
KMT2E-AS1	Homo sapiens KMT2E antisense RNA 1 (head to head) (KMT2E-AS1), long non-coding RNA [NR_024586]	ncRNA	1.18E-06	3.37E-02	down	-2.37	Not used
KRBA2	Homo sapiens KRAB-A domain containing 2 (KRBA2), mRNA [NM_213597]	gene	9.41E-07	2.69E-02	down	-2.21	1099
KREMEN1	Homo sapiens kringle containing transmembrane protein 1 (KREMEN1), transcript variant 3, mRNA [NM_001039570]	gene	7.59E-13	2.30E-08	up	63.27	89
KRT17P5	Homo sapiens keratin 17 pseudogene 5 (KRT17P5), non-coding RNA [NR_001443]	gene	9.92E-08	2.90E-03	down	-2.79	999
KRT19	Homo sapiens keratin 19, type I (KRT19), mRNA [NM_002276]	gene	9.43E-07	2.70E-02	down	-3.37	1217
KRT23	Homo sapiens keratin 23, type I (KRT23), transcript variant 1, mRNA [NM_015515]	gene	2.13E-16	6.49E-12	up	20.63	Not used
KRT23	Homo sapiens keratin 23, type I (KRT23), transcript variant 1, mRNA [NM_015515]	gene	1.81E-18	5.52E-14	up	237.26	181
KRT7	Homo sapiens keratin 7, type II (KRT7), mRNA [NM_005556]	gene	5.47E-07	1.58E-02	down	-3.02	1003
KRT81	Homo sapiens keratin 81, type II (KRT81), mRNA [NM_002281]	gene	8.33E-08	2.44E-03	down	-3.36	1000
KRT85	Homo sapiens keratin 85, type II (KRT85), transcript variant 1, mRNA [NM_002283]	gene	1.35E-07	3.93E-03	down	-3.43	1194
KRT8P41	Homo sapiens keratin 8 pseudogene 41 (KRT8P41), non-coding RNA [NR_027713]	gene	1.04E-06	2.98E-02	down	-2.27	1085
KRTAP10-10	Homo sapiens keratin associated protein 10-10 (KRTAP10-10), mRNA [NM_181688]	gene	5.38E-07	1.55E-02	down	-2.28	925
KRTAP19-5	Homo sapiens keratin associated protein 19-5 (KRTAP19-5), mRNA [NM_181611]	gene	5.56E-07	1.60E-02	down	-2.55	918
KRTAP2-4	Homo sapiens keratin associated protein 2-4 (KRTAP2-4), mRNA [NM_033184]	gene	8.20E-10	2.45E-05	down	-6.36	855
KRTAP3-1	Homo sapiens keratin associated protein 3-1 (KRTAP3-1), mRNA [NM_031958]	gene	9.06E-08	2.65E-03	down	-3.21	1039
KRTAP5-11	keratin associated protein 5-11 [Source:HGNC Symbol;Acc:HGNC:23606] [ENST00000617152]	gene	2.72E-07	7.90E-03	down	-2.14	926
KRTAP6-1	Homo sapiens keratin associated protein 6-1 (KRTAP6-1), mRNA [NM_181602]	gene	8.48E-07	2.43E-02	down	-2.14	952
LACTB	Homo sapiens lactamase, beta (LACTB), transcript variant 2, mRNA [NM_171846]	gene	6.55E-07	1.88E-02	up	3.70	347
LAIR2	Homo sapiens leukocyte-associated immunoglobulin-like receptor 2 (LAIR2), transcript variant 1, mRNA [NM_002288]	gene	1.57E-09	4.68E-05	up	26.05	302
LAMB1	laminin, beta 1 [Source:HGNC Symbol;Acc:HGNC:6486] [ENST00000393559]	gene	1.24E-07	3.62E-03	down	-3.12	1195
LAMB3	Homo sapiens laminin, beta 3 (LAMB3), transcript variant 2, mRNA [NM_001017402]	gene	5.02E-08	1.47E-03	up	13.97	831
LAMP2	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant C, mRNA [NM_001122606]	gene	3.44E-10	1.03E-05	up	3.79	Not used
LAMP2	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant B, mRNA [NM_013995]	gene	8.73E-07	2.50E-02	up	4.09	444
LAT2	linker for activation of T cells family, member 2 [Source:HGNC Symbol;Acc:HGNC:12749] [ENST00000398475]	gene	6.48E-08	1.90E-03	down	-2.19	1097
LBR	Homo sapiens lamin B receptor (LBR), transcript variant 1, mRNA [NM_002296]	gene	3.50E-10	1.05E-05	up	5.04	465
LBX1	Homo sapiens ladybird homeobox 1 (LBX1), mRNA [NM_006562]	gene	6.23E-10	1.86E-05	down	-4.33	859
LCE1C	Homo sapiens late cornified envelope 1C (LCE1C), transcript variant 1, mRNA [NM_178351]	gene	6.39E-07	1.84E-02	down	-2.59	1005
LCE3B	Homo sapiens late cornified envelope 3B (LCE3B), mRNA [NM_178433]	gene	4.85E-07	1.40E-02	down	-3.06	1057
LCE6A	Homo sapiens late cornified envelope 6A (LCE6A), mRNA [NM_001128600]	gene	4.30E-10	1.29E-05	down	-5.10	1178
LCN2	Homo sapiens lipocalin 2 (LCN2), mRNA [NM_005564]	gene	9.79E-11	2.94E-06	up	78.66	146
LCP1	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA [NM_002298]	gene	2.89E-08	8.51E-04	up	5.80	474
LDHA	Homo sapiens lactate dehydrogenase A (LDHA), transcript variant 1, mRNA [NM_005566]	gene	1.74E-06	4.94E-02	up	3.26	817
LDLR	Homo sapiens low density lipoprotein receptor (LDLR), transcript variant 1, mRNA [NM_000527]	gene	9.57E-11	2.88E-06	up	25.93	36
LGALS12	Homo sapiens lectin, galactoside-binding, soluble, 12 (LGALS12), transcript variant 2, mRNA [NM_033101]	gene	6.17E-10	1.85E-05	up	5.95	323
LGALS2	Homo sapiens lectin, galactoside-binding, soluble, 2 (LGALS2), mRNA [NM_006498]	gene	3.85E-09	1.15E-04	up	83.25	164
LGALS3	Homo sapiens lectin, galactoside-binding, soluble, 3 (LGALS3), transcript variant 1, mRNA [NM_002306]	gene	1.93E-11	5.82E-07	up	46.99	834
LHX3	Homo sapiens LIM homeobox 3 (LHX3), transcript variant 2, mRNA [NM_014564]	gene	5.95E-11	1.79E-06	down	-18.57	877
LILRA2	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), transcript variant 2, mRNA [NM_006866]	gene	2.15E-09	6.42E-05	up	20.17	683
LILRA3	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 3 (LILRA3), transcript variant 1, mRNA [NM_006865]	gene	2.17E-07	6.31E-03	up	6.15	667
LILRA5	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5 (LILRA5), transcript variant 3, mRNA [NM_181879]	gene	4.55E-15	1.38E-10	up	39.39	537
LILRA6	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 (LILRA6), transcript variant 2, non-coding RNA [NR_104098]	gene	1.04E-17	3.15E-13	up	374.35	45
LILRA6	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 (LILRA6), transcript variant 1, mRNA [NM_024318]	gene	6.06E-07	1.74E-02	up	3.86	Not used
LILRB3	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), transcript variant 2, mRNA [NM_006864]	gene	4.85E-11	1.46E-06	up	218.68	41
LIMK2	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 1, mRNA [NM_001031801]	gene	1.84E-09	5.49E-05	up	7.42	Not used
LIMK2	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2b, mRNA [NM_016733]	gene	7.95E-14	2.41E-09	up	17.37	611
LIN54	Homo sapiens lin-54 DREAM MuvB core complex component (LIN54), transcript variant 1, mRNA [NM_194282]	gene	1.10E-06	3.14E-02	up	3.11	440
LIN7A	Homo sapiens lin-7 homolog A (C. elegans) (LIN7A), mRNA [NM_004664]	gene	1.71E-18	5.21E-14	up	151.14	48
LINC00163	Homo sapiens long intergenic non-protein coding RNA 163 (LINC00163), long non-coding RNA [NR_033840]	ncRNA	4.86E-08	1.43E-03	down	-2.74	Not used
LINC00173	Homo sapiens long intergenic non-protein coding RNA 173 (LINC00173), transcript variant 1, long non-coding RNA [NR_027345]	ncRNA	3.97E-07	1.15E-02	down	-2.57	Not used
LINC00176	Homo sapiens long intergenic non-protein coding RNA 176 (LINC00176), transcript variant 1, long non-coding RNA [NR_027686]	ncRNA	1.97E-07	5.73E-03	down	-3.99	Not used
LINC00189	Homo sapiens long intergenic non-protein coding RNA 189 (LINC00189), long non-coding RNA [NR_027072]	ncRNA	2.50E-07	7.25E-03	up	15.46	Not used
LINC00211	Homo sapiens long intergenic non-protein coding RNA 211 (LINC00211), transcript variant 1, long non-coding RNA [NR_110011]	ncRNA	2.45E-13	7.43E-09	up	33.42	Not used
LINC00211	long intergenic non-protein coding RNA 211 [Source:HGNC Symbol;Acc:HGNC:37459] [ENST00000418746]	long intergenic RNA	7.20E-08	2.11E-03	down	-2.00	Not used
LINC00239	Homo sapiens long intergenic non-protein coding RNA 239 (LINC00239), long non-coding RNA [NR_026774]	ncRNA	3.04E-08	8.96E-04	up	8.57	Not used
LINC00243	Homo sapiens cDNA FLJ40693 fis, clone THYMU2025042. [AK098012]	miscellaneous	8.70E-08	2.55E-03	down	-3.76	Not used
LINC00299	Homo sapiens long intergenic non-protein coding RNA 299 (LINC00299), long non-coding RNA [NR_034135]	ncRNA	5.27E-08	1.55E-03	up	4.52	Not used
LINC00302	CU449054 Homo sapiens ORESTES from keratinocytes Homo sapiens cDNA, mRNA sequence [CU449054]	miscellaneous	4.74E-07	1.37E-02	down	-5.09	Not used
LINC00398	Homo sapiens long intergenic non-protein coding RNA 398 (LINC00398), long non-coding RNA [NR_047012]	ncRNA	1.48E-06	4.22E-02	down	-6.13	Not used
LINC00423	Homo sapiens long intergenic non-protein coding RNA 423 (LINC00423), long non-coding RNA [NR_047020]	ncRNA	1.99E-09	5.94E-05	down	-3.11	Not used
LINC00454	long intergenic non-protein coding RNA 454 [Source:HGNC Symbol;Acc:HGNC:42802] [ENST00000425483]	long intergenic RNA	8.29E-07	2.38E-02	down	-2.00	Not used
LINC00482	Homo sapiens long intergenic non-protein coding RNA 482 (LINC00482), long non-coding RNA [NR_038080]	ncRNA	3.46E-09	1.03E-04	up	3.32	Not used
LINC00577	Homo sapiens long intergenic non-protein coding RNA 577 (LINC00577), long non-coding RNA [NR_046407]	ncRNA	8.98E-11	2.70E-06	down	-5.81	Not used
LINC00588	Homo sapiens long intergenic non-protein coding RNA 588 (LINC00588), long non-coding RNA [NR_026772]	ncRNA	3.44E-08	1.01E-03	down	-3.33	Not used
LINC00630	long intergenic non-protein coding RNA 630 [Source:HGNC Symbol;Acc:HGNC:44263] [ENST00000435966]	long intergenic RNA	1.92E-09	5.72E-05	down	-2.78	Not used
LINC00632	Homo sapiens long intergenic non-protein coding RNA 632 (LINC00632), transcript variant 3, long non-coding RNA [NR_104228]	ncRNA	2.19E-07	6.36E-03	down	-4.46	Not used
LINC00639	Homo sapiens long intergenic non-protein coding RNA 639 (LINC00639), long non-coding RNA [NR_039982]	ncRNA	4.89E-07	1.41E-02	down	-3.07	Not used
LINC00639	Homo sapiens long intergenic non-protein coding RNA 639 (LINC00639), long non-coding RNA [NR_039982]	ncRNA	7.94E-09	2.36E-04	up	7.07	Not used
LINC00658	Homo sapiens long intergenic non-protein coding RNA 658 (LINC00658), transcript variant 1, long non-coding RNA [NR_038239]	ncRNA	8.37E-07	2.40E-02	down	-3.30	Not used
LINC00673	Homo sapiens long intergenic non-protein coding RNA 673 (LINC00673), long non-coding RNA [NR_036488]	ncRNA	5.80E-07	1.67E-02	down	-4.58	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
LINC00707	Homo sapiens long intergenic non-protein coding RNA 707 (LINC00707), long non-coding RNA [NR_038291]	ncRNA	5.94E-07	1.71E-02	down	-3.36	Not used
LINC00861	long intergenic non-protein coding RNA 861 [Source:HGNC Symbol;Acc:HGNC:45133] [ENST00000518964]	long intergenic RNA	1.09E-07	3.19E-03	down	-2.24	Not used
LINC00877	Homo sapiens long intergenic non-protein coding RNA 877 (LINC00877), long non-coding RNA [NR_104116]	ncRNA	1.32E-15	4.00E-11	up	39.59	Not used
LINC00877	long intergenic non-protein coding RNA 877 [Source:HGNC Symbol;Acc:HGNC:27706] [ENST00000469218]	long intergenic RNA	7.27E-08	2.13E-03	down	-2.77	Not used
LINC00892	Homo sapiens long intergenic non-protein coding RNA 892 (LINC00892), transcript variant 1, long non-coding RNA [NR_038461]	ncRNA	1.46E-06	4.15E-02	up	13.43	Not used
LINC00892	Homo sapiens long intergenic non-protein coding RNA 892 (LINC00892), transcript variant 1, long non-coding RNA [NR_038461]	ncRNA	3.15E-10	9.43E-06	up	24.33	Not used
LINC00908	Homo sapiens long intergenic non-protein coding RNA 908 (LINC00908), long non-coding RNA [NR_015417]	ncRNA	2.30E-07	6.70E-03	down	-4.49	Not used
LINC00908	long intergenic non-protein coding RNA 908 [Source:HGNC Symbol;Acc:HGNC:27599] [ENST00000582452]	long intergenic RNA	4.33E-07	1.25E-02	down	-4.20	Not used
LINC00917	long intergenic non-protein coding RNA 917 [Source:HGNC Symbol;Acc:HGNC:48607] [ENST00000600892]	long intergenic RNA	1.76E-07	5.14E-03	down	-3.70	Not used
LINC00937	Homo sapiens long intergenic non-protein coding RNA 937 (LINC00937), long non-coding RNA [NR_024420]	ncRNA	4.67E-11	1.41E-06	up	72.75	Not used
LINC00937	Homo sapiens long intergenic non-protein coding RNA 937 (LINC00937), long non-coding RNA [NR_024420]	ncRNA	1.11E-09	3.31E-05	up	75.76	Not used
LINC00963	long intergenic non-protein coding RNA 963 [Source:HGNC Symbol;Acc:HGNC:48716] [ENST00000419300]	long intergenic RNA	1.38E-08	4.07E-04	up	9.16	Not used
LINC00963	long intergenic non-protein coding RNA 963 [Source:HGNC Symbol;Acc:HGNC:48716] [ENST00000454968]	long intergenic RNA	7.78E-09	2.31E-04	down	-3.26	Not used
LINC01000	capicua transcriptional repressor pseudogene 27 [Source:HGNC Symbol;Acc:HGNC:48835] [ENST00000442987]	pseudogene	1.78E-08	5.27E-04	down	-1.86	Not used
LINC01000	capicua transcriptional repressor pseudogene 27 [Source:HGNC Symbol;Acc:HGNC:48835] [ENST00000442987]	pseudogene	1.30E-07	3.80E-03	down	-1.98	Not used
LINC01001	Homo sapiens long intergenic non-protein coding RNA 1001 (LINC01001), long non-coding RNA [NR_028326]	ncRNA	1.33E-09	3.97E-05	down	-5.71	Not used
LINC01019	Homo sapiens long intergenic non-protein coding RNA 1019 (LINC01019), long non-coding RNA [NR_033898]	ncRNA	5.42E-08	1.59E-03	down	-3.38	Not used
LINC01048	Homo sapiens long intergenic non-protein coding RNA 1048 (LINC01048), long non-coding RNA [NR_125762]	ncRNA	3.87E-07	1.12E-02	down	-5.27	Not used
LINC01122	Homo sapiens long intergenic non-protein coding RNA 1122 (LINC01122), long non-coding RNA [NR_033873]	ncRNA	9.63E-07	2.76E-02	down	-2.97	Not used
LINC01150	Homo sapiens long intergenic non-protein coding RNA 1150 (LINC01150), long non-coding RNA [NR_120534]	ncRNA	3.55E-09	1.06E-04	down	-3.59	Not used
LINC01192	long intergenic non-protein coding RNA 1192 [Source:HGNC Symbol;Acc:HGNC:37197] [ENST00000488173]	long intergenic RNA	4.90E-07	1.41E-02	down	-2.39	Not used
LINC01192	long intergenic non-protein coding RNA 1192 [Source:HGNC Symbol;Acc:HGNC:37197] [ENST00000493473]	long intergenic RNA	8.43E-09	2.50E-04	down	-2.54	Not used
LINC01225	long intergenic non-protein coding RNA 1225 [Source:HGNC Symbol;Acc:HGNC:49677] [ENST00000563550]	long intergenic RNA	1.94E-07	5.64E-03	down	-2.72	Not used
LINC01234	Homo sapiens long intergenic non-protein coding RNA 1234 (LINC01234), transcript variant 1, long non-coding RNA [NR_110026]	ncRNA	5.59E-09	1.66E-04	down	-2.42	Not used
LINC01270	Homo sapiens long intergenic non-protein coding RNA 1270 (LINC01270), long non-coding RNA [NR_034124]	ncRNA	3.82E-08	1.12E-03	up	18.01	Not used
LINC01272	Homo sapiens long intergenic non-protein coding RNA 1272 (LINC01272), mRNA [NM_001278655]	long intergenic RNA	4.72E-13	1.43E-08	up	22.11	Not used
LINC01482	Homo sapiens long intergenic non-protein coding RNA 1482 (LINC01482), long non-coding RNA [NR_110825]	ncRNA	9.07E-07	2.60E-02	down	-2.52	Not used
LINC01503	Homo sapiens long intergenic non-protein coding RNA 1503 (LINC01503), transcript variant 1, long non-coding RNA [NR_120685]	ncRNA	1.34E-10	4.02E-06	up	5.26	Not used
LINC01503	Homo sapiens long intergenic non-protein coding RNA 1503 (LINC01503), transcript variant 1, long non-coding RNA [NR_120685]	ncRNA	1.18E-09	3.52E-05	up	7.24	Not used
LINC01503	Homo sapiens long intergenic non-protein coding RNA 1503 (LINC01503), transcript variant 1, long non-coding RNA [NR_120685]	ncRNA	5.47E-12	1.65E-07	up	10.11	Not used
LINC01506	Homo sapiens long intergenic non-protein coding RNA 1506 (LINC01506), long non-coding RNA [NR_109769]	ncRNA	7.28E-09	2.16E-04	up	16.68	Not used
LINC01512	Homo sapiens long intergenic non-protein coding RNA 1512 (LINC01512), long non-coding RNA [NR_024478]	ncRNA	1.19E-08	3.52E-04	down	-4.61	Not used
LINC01544	Homo sapiens long intergenic non-protein coding RNA 1544 (LINC01544), long non-coding RNA [NR_103449]	ncRNA	3.35E-07	9.69E-03	down	-3.50	Not used
LINC01550	Homo sapiens long intergenic non-protein coding RNA 1550 (LINC01550), long non-coding RNA [NR_015430]	ncRNA	3.64E-10	1.09E-05	up	15.25	Not used
LINC01550	long intergenic non-protein coding RNA 1550 [Source:HGNC Symbol;Acc:HGNC:20111] [ENST00000512901]	long intergenic RNA	1.24E-07	3.63E-03	up	5.70	Not used
LINC01550	long intergenic non-protein coding RNA 1550 [Source:HGNC Symbol;Acc:HGNC:20111] [ENST00000512901]	long intergenic RNA	2.05E-07	5.95E-03	up	7.51	Not used
LINC01550	long intergenic non-protein coding RNA 1550 [Source:HGNC Symbol;Acc:HGNC:20111] [ENST00000554822]	long intergenic RNA	1.10E-08	3.25E-04	up	5.43	Not used
LKAAEAR1	Homo sapiens LKAAEAR motif containing 1 (LKAAEAR1), mRNA [NM_001007125]	gene	8.01E-10	2.40E-05	down	-8.51	856
LMF1	Homo sapiens lipase maturation factor 1 (LMF1), transcript variant 1, mRNA [NM_022773]	gene	9.90E-07	2.83E-02	down	-2.06	1015
LMO2	Homo sapiens LIM domain only 2 (rhombotin-like 1) (LMO2), transcript variant 1, mRNA [NM_005574]	gene	2.13E-09	6.35E-05	up	63.25	535
LMTK3	Homo sapiens lemur tyrosine kinase 3 (LMTK3), mRNA [NM_001080434]	gene	1.65E-06	4.68E-02	up	7.85	530
lnc-AC007405.7.1-2	LNCipedia lincRNA (lnc-AC007405.7.1-2), lincRNA [lnc-AC007405.7.1-2:1]	lincRNA	1.01E-10	3.04E-06	down	-3.04	Not used
lnc-AC068473.1-5	LNCipedia lincRNA (lnc-AC068473.1-5), lincRNA [lnc-AC068473.1-5:3]	lincRNA	2.67E-07	7.75E-03	down	-3.50	Not used
lnc-AC099552.4.1-2	LNCipedia lincRNA (lnc-AC099552.4.1-2), lincRNA [lnc-AC099552.4.1-2:3]	lincRNA	2.60E-08	7.68E-04	down	-3.54	Not used
lnc-ACTR3C-2	LNCipedia lincRNA (lnc-ACTR3C-2), lincRNA [lnc-ACTR3C-2:1]	lincRNA	6.24E-07	1.79E-02	down	-3.21	Not used
lnc-AL669831.1-4	LNCipedia lincRNA (lnc-AL669831.1-4), lincRNA [lnc-AL669831.1-4:1]	lincRNA	1.27E-06	3.61E-02	down	-4.15	Not used
lnc-ALPL-1	LNCipedia lincRNA (lnc-ALPL-1), lincRNA [lnc-ALPL-1:1]	lincRNA	2.80E-08	8.25E-04	up	9.11	Not used
lnc-ANGPTL2-2	LNCipedia lincRNA (lnc-ANGPTL2-2), lincRNA [lnc-ANGPTL2-2:3]	lincRNA	2.76E-09	8.22E-05	down	-3.21	Not used
lnc-AP000679.2.1-1	LNCipedia lincRNA (lnc-AP000679.2.1-1), lincRNA [lnc-AP000679.2.1-1:3]	lincRNA	1.68E-06	4.78E-02	down	-3.45	Not used
lnc-APOL1-1	LNCipedia lincRNA (lnc-APOL1-1), lincRNA [lnc-APOL1-1:1]	lincRNA	1.71E-08	5.05E-04	down	-3.10	Not used
lnc-ARFGEF2-3	LNCipedia lincRNA (lnc-ARFGEF2-3), lincRNA [lnc-ARFGEF2-3:8]	lincRNA	5.88E-07	1.69E-02	down	-2.92	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:10]	lincRNA	2.22E-12	6.71E-08	up	28.97	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:11]	lincRNA	3.22E-07	9.33E-03	up	6.37	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:13]	lincRNA	5.87E-16	1.78E-11	up	29.55	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:14]	lincRNA	4.70E-17	1.43E-12	up	45.15	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:1]	lincRNA	1.55E-15	4.71E-11	up	173.80	Not used
lnc-ARRDC3-1	LNCipedia lincRNA (lnc-ARRDC3-1), lincRNA [lnc-ARRDC3-1:6]	lincRNA	1.55E-16	4.72E-12	up	163.55	Not used
lnc-ASB1-1	LNCipedia lincRNA (lnc-ASB1-1), lincRNA [lnc-ASB1-1:2]	lincRNA	3.06E-09	9.11E-05	down	-4.48	Not used
lnc-ATP6AP2-6	LNCipedia lincRNA (lnc-ATP6AP2-6), lincRNA [lnc-ATP6AP2-6:1]	lincRNA	3.73E-09	1.11E-04	down	-3.35	Not used
lnc-ATP6V1D-1	LNCipedia lincRNA (lnc-ATP6V1D-1), lincRNA [lnc-ATP6V1D-1:1]	lincRNA	5.81E-11	1.75E-06	down	-3.88	Not used
lnc-BAI3-3	RST28357 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG208723]	miscellaneous	4.25E-09	1.26E-04	down	-3.62	Not used
lnc-BCL11B-1	LNCipedia lincRNA (lnc-BCL11B-1), lincRNA [lnc-BCL11B-1:2]	lincRNA	5.33E-10	1.60E-05	up	11.72	Not used
lnc-BTBD10-3	ALU7_HUMAN (P39194) Alu subfamily SQ sequence contamination warning entry, partial (25%) [THC2496717]	miscellaneous	3.94E-09	1.17E-04	down	-5.32	Not used
lnc-C10orf11-1	LNCipedia lincRNA (lnc-C10orf11-1), lincRNA [lnc-C10orf11-1:1]	lincRNA	1.06E-06	3.02E-02	down	-3.77	Not used
lnc-C15orf2-1	LNCipedia lincRNA (lnc-C15orf2-1), lincRNA [lnc-C15orf2-1:1]	lincRNA	1.39E-06	3.96E-02	down	-3.75	Not used
lnc-C16orf42-2	Homo sapiens cDNA FLJ45052 fis, clone BRAWH3022542. [AK126997]	miscellaneous	1.16E-09	3.47E-05	down	-35.70	Not used
lnc-C16orf95-1	LNCipedia lincRNA (lnc-C16orf95-1), lincRNA [lnc-C16orf95-1:7]	lincRNA	1.08E-06	3.08E-02	down	-3.35	Not used
lnc-C3orf38-2	LNCipedia lincRNA (lnc-C3orf38-2), lincRNA [lnc-C3orf38-2:1]	lincRNA	1.74E-06	4.94E-02	down	-3.80	Not used
lnc-C5orf38-1	LNCipedia lincRNA (lnc-C5orf38-1), lincRNA [lnc-C5orf38-1:3]	lincRNA	4.60E-08	1.35E-03	down	-3.04	Not used
lnc-C8orf34-1	LNCipedia lincRNA (lnc-C8orf34-1), lincRNA [lnc-C8orf34-1:1]	lincRNA	4.73E-08	1.39E-03	down	-2.30	Not used
lnc-C9orf50-2	LNCipedia lincRNA (lnc-C9orf50-2), lincRNA [lnc-C9orf50-2:1]	lincRNA	1.27E-07	3.71E-03	down	-3.01	Not used
lnc-C9orf79-1	LNCipedia lincRNA (lnc-C9orf79-1), lincRNA [lnc-C9orf79-1:2]	lincRNA	3.31E-08	9.77E-04	down	-2.16	Not used
lnc-CCDC125-1	Homo sapiens cDNA clone IMAGE:5298846. [BC039391]	miscellaneous	1.61E-06	4.57E-02	down	-3.82	Not used
lnc-CCDC71L-1	LNCipedia lincRNA (lnc-CCDC71L-1), lincRNA [lnc-CCDC71L-1:3]	lincRNA	1.88E-07	5.49E-03	down	-3.01	Not used
lnc-CCDC90A-5	LNCipedia lincRNA (lnc-CCDC90A-5), lincRNA [lnc-CCDC90A-5:1]	lincRNA	2.55E-08	7.54E-04	down	-2.63	Not used
lnc-CCL23-1	LNCipedia lincRNA (lnc-CCL23-1), lincRNA [lnc-CCL23-1:1]	lincRNA	1.73E-06	4.91E-02	down	-3.16	Not used
lnc-CD207-1	LNCipedia lincRNA (lnc-CD207-1), lincRNA [lnc-CD207-1:1]	lincRNA	8.38E-07	2.40E-02	down	-6.25	Not used
lnc-CD300C-1	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (6%) [THC2613887]	miscellaneous	1.89E-07	5.51E-03	up	23.43	Not used
lnc-CDC25A-1	LNCipedia lincRNA (lnc-CDC25A-1), lincRNA [lnc-CDC25A-1:1]	lincRNA	4.60E-07	1.33E-02	down	-2.02	Not used
lnc-CDC42-1	LNCipedia lincRNA (lnc-CDC42-1), lincRNA [lnc-CDC42-1:2]	lincRNA	2.71E-07	7.87E-03	down	-2.64	Not used
lnc-CDH4-1	LNCipedia lincRNA (lnc-CDH4-1), lincRNA [lnc-CDH4-1:1]	lincRNA	1.03E-07	3.00E-03	down	-4.83	Not used
lnc-CHL1-1	LNCipedia lincRNA (lnc-CHL1-1), lincRNA [lnc-CHL1-1:1]	lincRNA	5.15E-08	1.51E-03	down	-2.70	Not used
lnc-CLCNKB-3	LNCipedia lincRNA (lnc-CLCNKB-3), lincRNA [lnc-CLCNKB-3:1]	lincRNA	1.20E-06	3.42E-02	down	-3.35	Not used
lnc-CMTM4-1	LNCipedia lincRNA (lnc-CMTM4-1), lincRNA [lnc-CMTM4-1:1]	lincRNA	1.52E-06	4.31E-02	down	-1.94	Not used
lnc-COX4NB-1	LNCipedia lincRNA (lnc-COX4NB-1), lincRNA [lnc-COX4NB-1:1]	lincRNA	2.30E-07	6.70E-03	down	-3.42	Not used
lnc-CPEB4-1	LNCipedia lincRNA (lnc-CPEB4-1), lincRNA [lnc-CPEB4-1:1]	lincRNA	6.03E-13	1.83E-08	up	18.92	Not used
lnc-CRISP2-1	LNCipedia lincRNA (lnc-CRISP2-1), lincRNA [lnc-CRISP2-1:1]	lincRNA	5.95E-07	1.71E-02	down	-2.98	Not used
lnc-CTSL1-1	PREDICTED: Homo sapiens DAPK1 intronic transcript 1 (non-protein coding) (DAPK1-IT1), misc_RNA [XR_171053]	lincRNA	7.28E-12	2.20E-07	up	23.42	Not used
lnc-CXXC5-1	LNCipedia lincRNA (lnc-CXXC5-1), lincRNA [lnc-CXXC5-1:2]	lincRNA	9.56E-08	2.80E-03	down	-4.21	Not used
lnc-CYS1-2	LNCipedia lincRNA (lnc-CYS1-2), lincRNA [lnc-CYS1-2:2]	lincRNA	3.73E-07	1.08E-02	down	-2.92	Not used
lnc-DCUN1D1-6	LNCipedia lincRNA (lnc-DCUN1D1-6), lincRNA [lnc-DCUN1D1-6:3]	lincRNA	2.73E-07	7.91E-03	down	-5.43	Not used
lnc-DENND5A-1	LNCipedia lincRNA (lnc-DENND5A-1), lincRNA [lnc-DENND5A-1:1]	lincRNA	1.54E-06	4.37E-02	down	-2.20	Not used
lnc-DNAI1-1	Q6UWT2_HUMAN (Q6UWT2) GAAI470, partial (64%) [THC2753675]	lincRNA	6.58E-07	1.89E-02	down	-2.05	Not used
lnc-DTYMK-3	LNCipedia lincRNA (lnc-DTYMK-3), lincRNA [lnc-DTYMK-3:1]	lincRNA	2.12E-07	6.17E-03	down	-2.59	Not used
lnc-EBF3-6	LNCipedia lincRNA (lnc-EBF3-6), lincRNA [lnc-EBF3-6:1]	lincRNA	2.57E-11	7.73E-07	up	10.27	Not used
lnc-EGFL6-2	LNCipedia lincRNA (lnc-EGFL6-2), lincRNA [lnc-EGFL6-2:1]	lincRNA	5.40E-07	1.56E-02	down	-2.22	Not used
lnc-EGLN1-1	LNCipedia lincRNA (lnc-EGLN1-1), lincRNA [lnc-EGLN1-1:4]	lincRNA	2.26E-07	6.57E-03	up	7.93	Not used
lnc-EGLN1-1	LNCipedia lincRNA (lnc-EGLN1-1), lincRNA [lnc-EGLN1-1:6]	lincRNA	2.04E-08	6.02E-04	up	13.39	Not used
lnc-EGLN1-1	LNCipedia lincRNA (lnc-EGLN1-1), lincRNA [lnc-EGLN1-1:6]	lincRNA	6.45E-08	1.89E-03	up	13.56	Not used
lnc-ERGIC2-4	LNCipedia lincRNA (lnc-ERGIC2-4), lincRNA [lnc-ERGIC2-4:1]	lincRNA	2.83E-07	8.21E-03	up	5.15	Not used
lnc-ERI1-3	LNCipedia lincRNA (lnc-ERI1-3), lincRNA [lnc-ERI1-3:1]	lincRNA	4.42E-10	1.32E-05	up	7.36	Not used
lnc-FAF1-1	LNCipedia lincRNA (lnc-FAF1-1), lincRNA [lnc-FAF1-1:1]	lincRNA	8.91E-08	2.61E-03	down	-2.85	Not used
lnc-FAM120B-6	LNCipedia lincRNA (lnc-FAM120B-6), lincRNA [lnc-FAM120B-6:2]	lincRNA	3.13E-07	9.07E-03	down	-3.15	Not used
lnc-FAM160A1-1	PREDICTED: Homo sapiens family with sequence similarity 160, member A1 (FAM160A1), transcript variant X1, mRNA [XM_005263199]	lincRNA	3.81E-08	1.12E-03	up	6.28	Not used
lnc-FAM168A-2	PREDICTED: Homo sapiens uncharacterized LOC100287837 (LOC100287837), mRNA [XM_002343116]	uncharacterized locus	3.20E-07	9.27E-03	down	-4.01	Not used
lnc-FAM182B-1	LNCipedia lincRNA (lnc-FAM182B-1), lincRNA [lnc-FAM182B-1:1]	lincRNA	8.25E-07	2.37E-02	down	-1.90	Not used
lnc-FAM82A1-1	LNCipedia lincRNA (lnc-FAM82A1-1), lincRNA [lnc-FAM82A1-1:1]	lincRNA	5.09E-07	1.47E-02	down	-2.96	Not used
lnc-FBLN2-1	LNCipedia lincRNA (lnc-FBLN2-1), lincRNA [lnc-FBLN2-1:3]	lincRNA	3.01E-08	8.89E-04	down	-3.02	Not used
lnc-FRMD1-3	602494735F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608392 5', mRNA sequence [BG428602]	miscellaneous	5.94E-07	1.71E-02	down	-3.85	Not used
lnc-FTH1-3	LNCipedia lincRNA (lnc-FTH1-3), lincRNA [lnc-FTH1-3:1]	lincRNA	1.23E-07	3.58E-03	down	-3.38	Not used
lnc-GALM-2	LNCipedia lincRNA (lnc-GALM-2), lincRNA [lnc-GALM-2:1]	lincRNA	1.04E-06	2.98E-02	down	-3.53	Not used
lnc-GCA-3	LNCipedia lincRNA (lnc-GCA-3), lincRNA [lnc-GCA-3:1]	lincRNA	1.29E-07	3.75E-03	down	-4.44	Not used
lnc-GDF10-2	LNCipedia lincRNA (lnc-GDF10-2), lincRNA [lnc-GDF10-2:1]	lincRNA	1.04E-06	2.98E-02	down	-2.10	Not used
lnc-GLB1L2-3	LNCipedia lincRNA (lnc-GLB1L2-3), lincRNA [lnc-GLB1L2-3:1]	lincRNA	5.62E-08	1.65E-03	down	-2.38	Not used
lnc-GLI2-3	LNCipedia lincRNA (lnc-GLI2-3), lincRNA [lnc-GLI2-3:2]	lincRNA	1.34E-06	3.81E-02	down	-3.57	Not used
lnc-GPCPD1-1	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (11%) [THC2678782]	miscellaneous	4.29E-08	1.26E-03	down	-4.21	Not used
lnc-GPR125-1	LNCipedia lincRNA (lnc-GPR125-1), lincRNA [lnc-GPR125-1:1]	lincRNA	4.15E-07	1.20E-02	down	-2.38	Not used
lnc-GPR144-1	LNCipedia lincRNA (lnc-GPR144-1), lincRNA [lnc-GPR144-1:1]	lincRNA	8.66E-07	2.48E-02	down	-2.60	Not used
lnc-HDAC2-1	LNCipedia lincRNA (lnc-HDAC2-1), lincRNA [lnc-HDAC2-1:1]	lincRNA	1.71E-06	4.85E-02	up	4.27	Not used
lnc-IGSF3-1	CD014608 Human CD34+ ESTs from primary hematopoietic stem-progenitor cells Homo sapiens cDNA 3', mRNA sequence [GD150158]	miscellaneous	7.12E-08	2.09E-03	up	13.74	Not used
lnc-IL1R2-2	Homo sapiens cDNA FLJ31315 fis, clone LIVER1000303. [AK055877]	miscellaneous	1.52E-09	4.55E-05	up	31.97	Not used
lnc-IL4R-1	LNCipedia lincRNA (lnc-IL4R-1), lincRNA [lnc-IL4R-1:1]	lincRNA	1.73E-09	5.16E-05	down	-2.57	Not used
lnc-IL6-3	LNCipedia lincRNA (lnc-IL6-3), lincRNA [lnc-IL6-3:5]	lincRNA	4.53E-08	1.33E-03	down	-2.79	Not used
lnc-ITGA11-2	LNCipedia lincRNA (lnc-ITGA11-2), lincRNA [lnc-ITGA11-2:3]	lincRNA	1.01E-06	2.90E-02	down	-5.10	Not used
lnc-KATNAL2-4	LNCipedia lincRNA (lnc-KATNAL2-4), lincRNA [lnc-KATNAL2-4:1]	lincRNA	4.19E-07	1.21E-02	down	-2.47	Not used
lnc-KHDRBS3-4	LNCipedia lincRNA (lnc-KHDRBS3-4), lincRNA [lnc-KHDRBS3-4:2]	lincRNA	1.62E-06	4.62E-02	down	-4.56	Not used
lnc-KIAA1328-1	LNCipedia lincRNA (lnc-KIAA1328-1), lincRNA [lnc-KIAA1328-1:1]	lincRNA	2.91E-07	8.45E-03	down	-3.37	Not used
lnc-KLF4-4	LNCipedia lincRNA (lnc-KLF4-4), lincRNA [lnc-KLF4-4:2]	lincRNA	8.86E-09	2.63E-04	down	-4.49	Not used
lnc-KY-1	LNCipedia lincRNA (lnc-KY-1), lincRNA [lnc-KY-1:1]	lincRNA	5.32E-13	1.61E-08	up	21.03	Not used
lnc-LGALSL-1	LNCipedia lincRNA (lnc-LGALSL-1), lincRNA [lnc-LGALSL-1:2]	lincRNA	4.91E-10	1.47E-05	up	15.21	Not used
lnc-LIN28B-1	Q5T552_HUMAN (Q5T552) OTTHUMP00000016913, complete [THC2740889]	lincRNA	3.86E-07	1.11E-02	down	-3.15	Not used
lnc-LRGUK-1	LNCipedia lincRNA (lnc-LRGUK-1), lincRNA [lnc-LRGUK-1:1]	lincRNA	1.06E-06	3.03E-02	down	-7.47	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
lnc-LRRC32-5	LNCipedia lincRNA (lnc-LRRC32-5), lincRNA [lnc-LRRC32-5:1]	lincRNA	4.05E-08	1.19E-03	down	-4.68	Not used
lnc-LYZL1-2	LNCipedia lincRNA (lnc-LYZL1-2), lincRNA [lnc-LYZL1-2:1]	lincRNA	1.14E-07	3.34E-03	down	-2.92	Not used
lnc-MFSD11-2	LNCipedia lincRNA (lnc-MFSD11-2), lincRNA [lnc-MFSD11-2:1]	lincRNA	9.43E-07	2.70E-02	down	-3.57	Not used
lnc-MGAT1-1	Homo sapiens cDNA FLJ30091 fis, clone BNGH41000017. [AK054653]	miscellaneous	1.26E-06	3.59E-02	up	4.31	Not used
lnc-MIB2-1	LNCipedia lincRNA (lnc-MIB2-1), lincRNA [lnc-MIB2-1:5]	lincRNA	1.29E-06	3.67E-02	down	-2.58	Not used
lnc-MOGAT1-1	LNCipedia lincRNA (lnc-MOGAT1-1), lincRNA [lnc-MOGAT1-1:1]	lincRNA	8.10E-07	2.32E-02	down	-3.23	Not used
lnc-NAV1-3	DB229023 TRACH3 Homo sapiens cDNA clone TRACH3022015 5', mRNA sequence [DB229023]	miscellaneous	8.98E-07	2.57E-02	down	-3.54	Not used
lnc-NCF4-2	Homo sapiens cDNA FLJ41638 fis, clone FEBRA2004813. [AK123632]	miscellaneous	5.17E-07	1.49E-02	down	-2.79	Not used
lnc-NDFIP2-12	LNCipedia lincRNA (lnc-NDFIP2-12), lincRNA [lnc-NDFIP2-12:1]	lincRNA	6.82E-09	2.02E-04	down	-4.32	Not used
lnc-NLGN2-1	LNCipedia lincRNA (lnc-NLGN2-1), lincRNA [lnc-NLGN2-1:2]	lincRNA	1.06E-06	3.04E-02	down	-4.01	Not used
lnc-NOL6-2	LNCipedia lincRNA (lnc-NOL6-2), lincRNA [lnc-NOL6-2:1]	lincRNA	4.45E-08	1.31E-03	down	-4.07	Not used
lnc-NPAS2-1	LNCipedia lincRNA (lnc-NPAS2-1), lincRNA [lnc-NPAS2-1:2]	lincRNA	7.96E-07	2.28E-02	down	-3.27	Not used
lnc-NPBWR2-1	LNCipedia lincRNA (lnc-NPBWR2-1), lincRNA [lnc-NPBWR2-1:1]	lincRNA	5.15E-07	1.49E-02	down	-3.39	Not used
lnc-NR1D1-1	LNCipedia lincRNA (lnc-NR1D1-1), lincRNA [lnc-NR1D1-1:1]	lincRNA	7.02E-07	2.02E-02	up	3.20	Not used
lnc-PI3-1	DA674107 NETRP2 Homo sapiens cDNA clone NETRP2004815 5', mRNA sequence [DA674107]	miscellaneous	6.36E-12	1.92E-07	up	27.04	Not used
lnc-PLA2G4A-7	LNCipedia lincRNA (lnc-PLA2G4A-7), lincRNA [lnc-PLA2G4A-7:1]	lincRNA	1.42E-06	4.05E-02	down	-1.92	Not used
lnc-POLR2B-2	LNCipedia lincRNA (lnc-POLR2B-2), lincRNA [lnc-POLR2B-2:2]	lincRNA	1.13E-06	3.22E-02	down	-3.17	Not used
lnc-PPP1R26-2	LNCipedia lincRNA (lnc-PPP1R26-2), lincRNA [lnc-PPP1R26-2:1]	lincRNA	1.66E-06	4.71E-02	down	-1.99	Not used
lnc-PPP1R3D-2	LNCipedia lincRNA (lnc-PPP1R3D-2), lincRNA [lnc-PPP1R3D-2:2]	lincRNA	1.13E-06	3.22E-02	down	-2.95	Not used
lnc-PRC1-1	Homo sapiens cDNA FLJ46625 fis, clone TLUNG2002578. [AK128480]	miscellaneous	9.28E-09	2.75E-04	down	-4.54	Not used
lnc-PREPL-1	LNCipedia lincRNA (lnc-PREPL-1), lincRNA [lnc-PREPL-1:1]	lincRNA	8.93E-08	2.61E-03	down	-4.46	Not used
lnc-RAB28-4	LNCipedia lincRNA (lnc-RAB28-4), lincRNA [lnc-RAB28-4:1]	lincRNA	1.35E-07	3.95E-03	down	-2.20	Not used
lnc-RAD23B-2	LNCipedia lincRNA (lnc-RAD23B-2), lincRNA [lnc-RAD23B-2:1]	lincRNA	1.71E-06	4.85E-02	down	-2.87	Not used
lnc-RBM12B-2	LNCipedia lincRNA (lnc-RBM12B-2), lincRNA [lnc-RBM12B-2:1]	lincRNA	3.56E-08	1.05E-03	down	-2.36	Not used
lnc-RP11-327F22.5.1-3	LNCipedia lincRNA (lnc-RP11-327F22.5.1-3), lincRNA [lnc-RP11-327F22.5.1-3:3]	lincRNA	1.40E-06	4.00E-02	down	-4.87	Not used
lnc-RP11-389E17.1.1-1	Homo sapiens cDNA FLJ37626 fis, clone BRCOC2014748. [AK094945]	miscellaneous	1.33E-07	3.89E-03	down	-2.75	Not used
lnc-RP1-32I10.10.1-1	LNCipedia lincRNA (lnc-RP1-32I10.10.1-1), lincRNA [lnc-RP1-32I10.10.1-1:1]	lincRNA	2.26E-09	6.76E-05	down	-3.27	Not used
lnc-RPL24-2	LNCipedia lincRNA (lnc-RPL24-2), lincRNA [lnc-RPL24-2:4]	lincRNA	1.18E-06	3.36E-02	down	-1.93	Not used
lnc-S1PR2-1	LNCipedia lincRNA (lnc-S1PR2-1), lincRNA [lnc-S1PR2-1:1]	lincRNA	2.70E-07	7.83E-03	down	-1.81	Not used
lnc-SEL1L-7	LNCipedia lincRNA (lnc-SEL1L-7), lincRNA [lnc-SEL1L-7:2]	lincRNA	1.53E-07	4.46E-03	down	-2.87	Not used
lnc-SHCBP1L-1	Homo sapiens cDNA FLJ10580 fis, clone NT2RP2003533. [AK001442]	miscellaneous	1.06E-06	3.02E-02	down	-1.98	Not used
lnc-SLC25A48-2	LNCipedia lincRNA (lnc-SLC25A48-2), lincRNA [lnc-SLC25A48-2:1]	lincRNA	4.58E-07	1.32E-02	down	-3.87	Not used
lnc-SLC25A6-1	ALU2_HUMAN (P39189) Alu subfamily SB sequence contamination warning entry, partial (11%) [THC2723724]	miscellaneous	4.76E-07	1.37E-02	down	-2.06	Not used
lnc-SLC45A4-1	LNCipedia lincRNA (lnc-SLC45A4-1), lincRNA [lnc-SLC45A4-1:1]	lincRNA	4.54E-08	1.34E-03	down	-2.12	Not used
lnc-SSTR4-2	LNCipedia lincRNA (lnc-SSTR4-2), lincRNA [lnc-SSTR4-2:4]	lincRNA	3.63E-07	1.05E-02	down	-2.31	Not used
lnc-STK35-1	LNCipedia lincRNA (lnc-STK35-1), lincRNA [lnc-STK35-1:1]	lincRNA	3.84E-10	1.15E-05	down	-4.86	Not used
lnc-SULF2-1	LNCipedia lincRNA (lnc-SULF2-1), lincRNA [lnc-SULF2-1:1]	lincRNA	7.46E-07	2.14E-02	down	-2.85	Not used
lnc-TBC1D29-1	Homo sapiens cDNA FLJ43993 fis, clone TESTI4020102. [AK125981]	miscellaneous	2.11E-07	6.15E-03	down	-2.19	Not used
lnc-TERF1-2	LNCipedia lincRNA (lnc-TERF1-2), lincRNA [lnc-TERF1-2:1]	lincRNA	5.34E-07	1.54E-02	down	-2.70	Not used
lnc-TEX261-2	DA173998 BRAMY2 Homo sapiens cDNA clone BRAMY2037005 5', mRNA sequence [DA173998]	miscellaneous	3.03E-07	8.77E-03	down	-5.37	Not used
lnc-TIMP1-1	LNCipedia lincRNA (lnc-TIMP1-1), lincRNA [lnc-TIMP1-1:1]	lincRNA	3.46E-08	1.02E-03	down	-4.87	Not used
lnc-TLR5-1	LNCipedia lincRNA (lnc-TLR5-1), lincRNA [lnc-TLR5-1:2]	lincRNA	9.56E-08	2.80E-03	down	-3.75	Not used
lnc-TM2D2-2	LNCipedia lincRNA (lnc-TM2D2-2), lincRNA [lnc-TM2D2-2:1]	lincRNA	3.90E-08	1.15E-03	down	-2.47	Not used
lnc-TM2D3-1	LNCipedia lincRNA (lnc-TM2D3-1), lincRNA [lnc-TM2D3-1:1]	lincRNA	8.11E-07	2.32E-02	down	-2.74	Not used
lnc-TM4SF4-2	Homo sapiens cDNA, FLJ99482. [AK309441]	miscellaneous	1.37E-07	4.01E-03	up	6.57	Not used
lnc-TMEM132C-6	LNCipedia lincRNA (lnc-TMEM132C-6), lincRNA [lnc-TMEM132C-6:4]	lincRNA	8.43E-07	2.42E-02	down	-2.36	Not used
lnc-TMEM88B-4	LNCipedia lincRNA (lnc-TMEM88B-4), lincRNA [lnc-TMEM88B-4:1]	lincRNA	5.06E-07	1.46E-02	down	-2.41	Not used
lnc-TMEM98-1	LNCipedia lincRNA (lnc-TMEM98-1), lincRNA [lnc-TMEM98-1:2]	lincRNA	2.26E-07	6.56E-03	down	-3.94	Not used
lnc-TP53I11-1	LNCipedia lincRNA (lnc-TP53I11-1), lincRNA [lnc-TP53I11-1:1]	lincRNA	6.16E-08	1.81E-03	down	-6.35	Not used
lnc-TP53INP1-1	Homo sapiens hypothetical protein LOC286149, mRNA (cDNA clone IMAGE:40114544). [BC128221]	miscellaneous	8.02E-08	2.35E-03	down	-2.29	Not used
lnc-TPRA1-1	LNCipedia lincRNA (lnc-TPRA1-1), lincRNA [lnc-TPRA1-1:2]	lincRNA	6.52E-10	1.95E-05	down	-3.11	Not used
lnc-TRAPPC12-3	LNCipedia lincRNA (lnc-TRAPPC12-3), lincRNA [lnc-TRAPPC12-3:1]	lincRNA	1.35E-08	3.99E-04	down	-4.98	Not used
lnc-TRMT61B-4	LNCipedia lincRNA (lnc-TRMT61B-4), lincRNA [lnc-TRMT61B-4:1]	lincRNA	3.95E-07	1.14E-02	down	-3.28	Not used
lnc-TSC22D1-1	LNCipedia lincRNA (lnc-TSC22D1-1), lincRNA [lnc-TSC22D1-1:4]	lincRNA	2.52E-10	7.56E-06	down	-24.89	Not used
lnc-TSPYL5-2	LNCipedia lincRNA (lnc-TSPYL5-2), lincRNA [lnc-TSPYL5-2:1]	lincRNA	3.56E-08	1.05E-03	down	-6.52	Not used
lnc-TUBGCP3-6	LNCipedia lincRNA (lnc-TUBGCP3-6), lincRNA [lnc-TUBGCP3-6:2]	lincRNA	5.62E-07	1.62E-02	down	-2.76	Not used
lnc-UTS2R-1	LNCipedia lincRNA (lnc-UTS2R-1), lincRNA [lnc-UTS2R-1:1]	lincRNA	9.79E-08	2.86E-03	down	-4.34	Not used
lnc-UXS1-2	LNCipedia lincRNA (lnc-UXS1-2), lincRNA [lnc-UXS1-2:1]	lincRNA	3.99E-07	1.15E-02	down	-3.90	Not used
lnc-VRK1-5	LNCipedia lincRNA (lnc-VRK1-5), lincRNA [lnc-VRK1-5:8]	lincRNA	4.79E-12	1.45E-07	up	17.14	Not used
lnc-WDR7-2	AGENCOURT_14276563 NIH_MGC_180 Homo sapiens cDNA clone IMAGE:30386298 5', mRNA sequence [CD359767]	miscellaneous	1.69E-09	5.04E-05	down	-2.86	Not used
lnc-WNT7A-1	LNCipedia lincRNA (lnc-WNT7A-1), lincRNA [lnc-WNT7A-1:1]	lincRNA	1.01E-06	2.89E-02	down	-2.60	Not used
lnc-ZADH2-1	LNCipedia lincRNA (lnc-ZADH2-1), lincRNA [lnc-ZADH2-1:3]	lincRNA	2.67E-09	7.96E-05	down	-2.55	Not used
lnc-ZEB2-1	LNCipedia lincRNA (lnc-ZEB2-1), lincRNA [lnc-ZEB2-1:2]	lincRNA	2.01E-15	6.10E-11	up	9.37	Not used
lnc-ZKSCAN1-1	LNCipedia lincRNA (lnc-ZKSCAN1-1), lincRNA [lnc-ZKSCAN1-1:2]	lincRNA	1.55E-06	4.42E-02	down	-3.00	Not used
lnc-ZKSCAN1-1	LNCipedia lincRNA (lnc-ZKSCAN1-1), lincRNA [lnc-ZKSCAN1-1:4]	lincRNA	3.62E-08	1.07E-03	down	-3.17	Not used
lnc-ZKSCAN1-1	LNCipedia lincRNA (lnc-ZKSCAN1-1), lincRNA [lnc-ZKSCAN1-1:5]	lincRNA	4.91E-08	1.44E-03	down	-3.11	Not used
lnc-ZNF30-1	LNCipedia lincRNA (lnc-ZNF30-1), lincRNA [lnc-ZNF30-1:1]	lincRNA	1.32E-06	3.75E-02	down	-5.23	Not used
lnc-ZNF438-3	LNCipedia lincRNA (lnc-ZNF438-3), lincRNA [lnc-ZNF438-3:1]	lincRNA	1.75E-07	5.09E-03	down	-3.83	Not used
lnc-ZNF74-1	LNCipedia lincRNA (lnc-ZNF74-1), lincRNA [lnc-ZNF74-1:6]	lincRNA	5.99E-08	1.76E-03	down	-2.09	Not used
lnc-ZNF793-1	LNCipedia lincRNA (lnc-ZNF793-1), lincRNA [lnc-ZNF793-1:2]	lincRNA	1.01E-08	3.00E-04	down	-4.94	Not used
LOC100128002	PREDICTED: Homo sapiens uncharacterized LOC100128002 (LOC100128002), misc_RNA [XR_159537]	uncharacterized locus	1.41E-09	4.23E-05	down	-3.55	Not used
LOC100128276	Homo sapiens cDNA FLJ43282 fis, clone LIVER2007415. [AK125272]	miscellaneous	1.55E-10	4.65E-06	up	43.87	Not used
LOC100128494	Homo sapiens uncharacterized LOC100128494 (LOC100128494), long non-coding RNA [NR_104178]	ncRNA	2.99E-08	8.83E-04	down	-2.24	Not used
LOC100129215	PREDICTED: Homo sapiens uncharacterized LOC100129215 (LOC100129215), misc_RNA [XR_109334]	uncharacterized locus	7.15E-08	2.10E-03	down	-3.88	Not used
LOC100129322	Homo sapiens cDNA FLJ45776 fis, clone NETRP2004090. [AK127678]	miscellaneous	4.99E-08	1.47E-03	up	21.57	Not used
LOC100129473	PREDICTED: Homo sapiens uncharacterized LOC100129473 (LOC100129473), misc_RNA [XR_247231]	uncharacterized locus	4.89E-07	1.41E-02	down	-3.62	Not used
LOC100129721	Homo sapiens cDNA FLJ44685 fis, clone BRACE3011447. [AK126643]	miscellaneous	2.77E-07	8.05E-03	down	-3.63	Not used
LOC100129846	Homo sapiens cDNA FLJ42869 fis, clone BRHIP2022221. [AK124859]	miscellaneous	9.02E-08	2.64E-03	down	-4.00	Not used
LOC100130238	Homo sapiens uncharacterized LOC100130238 (LOC100130238), long non-coding RNA [NR_024563]	ncRNA	2.58E-07	7.49E-03	down	-4.38	Not used
LOC100130417	Homo sapiens uncharacterized LOC100130417 (LOC100130417), transcript variant 2, long non-coding RNA [NR_122045]	ncRNA	7.40E-08	2.17E-03	down	-4.14	Not used
LOC100130456	Homo sapiens cDNA FLJ37693 fis, clone BRHIP2014954. [AK095012]	miscellaneous	5.07E-09	1.51E-04	down	-2.80	Not used
LOC100130520	PREDICTED: Homo sapiens CD300c molecule-like (LOC100130520), transcript variant X3, mRNA [XM_005275830]	miscellaneous	1.68E-06	4.77E-02	up	5.29	Not used
LOC100130654	Homo sapiens cDNA FLJ37924 fis, clone CTONG2000218. [AK095243]	miscellaneous	2.28E-07	6.62E-03	down	-2.97	Not used
LOC100130987	Homo sapiens uncharacterized LOC100130987 (LOC100130987), long non-coding RNA [NR_024469]	ncRNA	6.86E-07	1.97E-02	down	-4.96	Not used
LOC100131131	Homo sapiens clone DNA180542 AHPA9419 (UNQ9419) mRNA, complete cds. [AY358263]	miscellaneous	2.78E-08	8.22E-04	down	-3.86	Not used
LOC100134040	not provided	unannotated probe	4.89E-07	1.41E-02	down	-3.11	Not used
LOC100134868	Homo sapiens uncharacterized LOC100134868 (LOC100134868), long non-coding RNA [NR_004846]	ncRNA	2.93E-10	8.80E-06	down	-3.86	Not used
LOC100288162	Homo sapiens uncharacterized LOC100288162 (LOC100288162), long non-coding RNA [NR_103772]	ncRNA	1.41E-06	4.00E-02	down	-2.58	Not used
LOC100294145	Homo sapiens uncharacterized LOC100294145 (LOC100294145), transcript variant 2, long non-coding RNA [NR_037178]	ncRNA	5.88E-09	1.75E-04	down	-4.09	Not used
LOC100422737	Homo sapiens uncharacterized LOC100422737 (LOC100422737), long non-coding RNA [NR_033557]	ncRNA	1.35E-06	3.84E-02	down	-3.77	Not used
LOC100422737	Q8VGA8_MOUSE (Q8VGA8) Olfactory receptor MOR174-1, partial (5%) [THC2716877]	gene	3.82E-07	1.10E-02	down	-2.44	Not used
LOC100422737	not provided	unannotated probe	1.06E-06	3.02E-02	down	-3.46	Not used
LOC100505978	Homo sapiens uncharacterized LOC100505978 (LOC100505978), long non-coding RNA [NR_038912]	ncRNA	7.75E-08	2.27E-03	down	-3.56	Not used
LOC100506127	Homo sapiens cDNA FLJ30390 fis, clone BRACE2008308. [AK054952]	miscellaneous	1.34E-06	3.83E-02	down	-2.02	Not used
LOC100506257	Homo sapiens cDNA FLJ61763 complete cds. [AK295076]	miscellaneous	8.21E-07	2.35E-02	down	-2.04	Not used
LOC100506368	Homo sapiens uncharacterized LOC100506368 (LOC100506368), long non-coding RNA [NR_038905]	ncRNA	1.97E-07	5.73E-03	down	-2.24	Not used
LOC100507195	Homo sapiens uncharacterized LOC100507195 (LOC100507195), long non-coding RNA [NR_120458]	ncRNA	5.22E-07	1.50E-02	up	15.81	Not used
LOC100507334	Homo sapiens two pore channel 3 pseudogene (LOC100507334), non-coding RNA [NR_037626]	pseudogene	1.17E-07	3.42E-03	down	-4.60	Not used
LOC100507420	Homo sapiens uncharacterized LOC100507420 (LOC100507420), transcript variant 1, long non-coding RNA [NR_121620]	ncRNA	2.54E-08	7.51E-04	down	-2.14	Not used
LOC100507420	PREDICTED: Homo sapiens uncharacterized LOC101929585 (RP11-150O12.6), transcript variant X2, ncRNA [XR_426300]	ncRNA	1.71E-06	4.87E-02	down	-3.05	Not used
LOC100507548	Homo sapiens cDNA FLJ27342 fis, clone TST02993. [AK130852]	miscellaneous	1.06E-07	3.10E-03	down	-3.33	Not used
LOC100507642	Homo sapiens uncharacterized LOC100507642 (LOC100507642), transcript variant 1, long non-coding RNA [NR_108064]	ncRNA	1.10E-08	3.25E-04	down	-5.84	Not used
LOC100996286	Homo sapiens uncharacterized LOC100996286 (LOC100996286), transcript variant 1, long non-coding RNA [NR_121627]	ncRNA	3.26E-08	9.62E-04	up	22.88	Not used
LOC100996291	Homo sapiens uncharacterized LOC100996291 (LOC100996291), long non-coding RNA [NR_073178]	ncRNA	2.67E-09	7.95E-05	down	-4.19	Not used
LOC101060038	PREDICTED: Homo sapiens uncharacterized LOC101060038 (LOC101060038), ncRNA [XR_424318]	ncRNA	8.83E-09	2.62E-04	up	21.63	Not used
LOC101060524	Homo sapiens D(1B) dopamine receptor-like (LOC101060524), non-coding RNA [NR_111000]	miscellaneous	1.42E-09	4.25E-05	down	-5.70	Not used
LOC101927070	Homo sapiens uncharacterized LOC101927070 (LOC101927070), long non-coding RNA [NR_126337]	ncRNA	7.18E-10	2.15E-05	up	10.64	Not used
LOC101927156	not provided	unannotated probe	1.73E-06	4.90E-02	up	7.57	Not used
LOC101927156	not provided	unannotated probe	4.06E-14	1.23E-09	up	28.61	Not used
LOC101927326	PREDICTED: Homo sapiens uncharacterized LOC101927326 (LOC101927326), ncRNA [XR_244183]	ncRNA	1.52E-08	4.50E-04	down	-2.59	Not used
LOC101927495	Homo sapiens uncharacterized LOC101927495 (LOC101927495), long non-coding RNA [NR_110189]	ncRNA	1.58E-06	4.50E-02	down	-2.97	Not used
LOC101927764	PREDICTED: Homo sapiens uncharacterized LOC101927764 (LOC101927764), transcript variant X4, ncRNA [XR_425464]	ncRNA	3.06E-07	8.86E-03	down	-2.26	Not used
LOC101927851	not provided	unannotated probe	2.31E-12	6.98E-08	up	25.53	Not used
LOC101927993	PREDICTED: Homo sapiens uncharacterized LOC101927993 (LOC101927993), ncRNA [XR_242645]	ncRNA	1.65E-06	4.68E-02	down	-3.02	Not used
LOC101928035	Homo sapiens uncharacterized LOC101928035 (LOC101928035), long non-coding RNA [NR_104657]	ncRNA	5.13E-07	1.48E-02	down	-3.09	Not used
LOC101928047	PREDICTED: Homo sapiens uncharacterized LOC101928047 (LOC101928047), ncRNA [XR_249939]	ncRNA	2.18E-07	6.33E-03	up	5.13	Not used
LOC101928108	PREDICTED: Homo sapiens lymphocyte antigen 6A-2/6E-1-like (LOC101928108), mRNA [XM_006725099]	miscellaneous	2.66E-07	7.73E-03	down	-2.67	Not used
LOC101928143	PREDICTED: Homo sapiens uncharacterized LOC101928143 (LOC101928143), transcript variant X1, ncRNA [XR_245781]	ncRNA	1.54E-13	4.66E-09	up	25.30	Not used
LOC101928152	PREDICTED: Homo sapiens uncharacterized LOC101928152 (LOC101928152), ncRNA [XR_245037]	ncRNA	1.58E-07	4.60E-03	up	12.53	Not used
LOC101928173	PREDICTED: Homo sapiens uncharacterized LOC101928173 (LOC101928173), transcript variant X2, ncRNA [XR_245039]	ncRNA	5.63E-10	1.69E-05	up	24.90	Not used
LOC101928237	PREDICTED: Homo sapiens uncharacterized LOC101928237 (LOC101928237), transcript variant X1, ncRNA [XR_241657]	ncRNA	6.91E-07	1.98E-02	down	-1.95	Not used
LOC101928738	Homo sapiens uncharacterized LOC101928738 (LOC101928738), long non-coding RNA [NR_110851]	ncRNA	3.12E-07	9.04E-03	down	-2.41	Not used
LOC101928973	Homo sapiens uncharacterized LOC101928973 (LOC101928973), long non-coding RNA [NR_125966]	ncRNA	7.67E-07	2.20E-02	down	-2.27	Not used
LOC101928991	PREDICTED: Homo sapiens coiled-coil domain-containing protein 92-like (LOC101928991), mRNA [XM_006710027]	miscellaneous	5.19E-07	1.49E-02	down	-2.03	Not used
LOC101929217	Homo sapiens uncharacterized LOC101929217 (LOC101929217), long non-coding RNA [NR_105004]	ncRNA	2.77E-07	8.05E-03	down	-3.06	Not used
LOC101929309	PREDICTED: Homo sapiens uncharacterized LOC101929309 (LOC101929309), transcript variant X2, ncRNA [XR_242007]	ncRNA	8.82E-07	2.53E-02	down	-2.65	Not used
LOC101929494	PREDICTED: Homo sapiens uncharacterized LOC101929494 (LOC101929494), transcript variant X5, ncRNA [XR_424824]	ncRNA	1.62E-06	4.60E-02	down	-2.65	Not used
LOC101929494	PREDICTED: Homo sapiens uncharacterized LOC101929494 (LOC101929494), transcript variant X6, ncRNA [XR_424825]	ncRNA	1.14E-07	3.34E-03	down	-2.03	Not used
LOC101929531	PREDICTED: Homo sapiens uncharacterized LOC101929531 (LOC101929531), ncRNA [XR_241262]	ncRNA	6.27E-11	1.89E-06	up	50.88	Not used
LOC101929560	PREDICTED: Homo sapiens uncharacterized LOC101929560 (LOC101929560), transcript variant X3, ncRNA [XR_424652]	ncRNA	4.46E-07	1.29E-02	down	-3.99	Not used
LOC101929634	PREDICTED: Homo sapiens uncharacterized LOC101929634 (LOC101929634), misc_RNA [XR_245823]	uncharacterized locus	1.05E-06	3.00E-02	down	-2.33	Not used
LOC101929866	PREDICTED: Homo sapiens uncharacterized LOC101929866 (LOC101929866), ncRNA [XR_253975]	ncRNA	6.54E-13	1.98E-08	up	139.60	Not used

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
LOC101930017	PREDICTED: Homo sapiens transcription initiation factor TFIID subunit 4-like (LOC101930017), mRNA [XM_005276635]	miscellaneous	1.59E-06	4.53E-02	down	-3.39	Not used
LOC101930634	PREDICTED: Homo sapiens uncharacterized LOC101930634 (LOC101930634), ncRNA [XR_248595]	ncRNA	3.95E-08	1.16E-03	down	-4.73	Not used
LOC102723701	Homo sapiens uncharacterized LOC102723701 (LOC102723701), long non-coding RNA [NR_125821]	ncRNA	1.19E-06	3.39E-02	down	-3.28	Not used
LOC102723894	PREDICTED: Homo sapiens uncharacterized LOC102723894 (LOC102723894), ncRNA [XR_424244]	ncRNA	3.60E-11	1.08E-06	up	17.28	Not used
LOC102724545	PREDICTED: Homo sapiens uncharacterized LOC102724545 (LOC102724545), transcript variant X1, ncRNA [XR_425228]	ncRNA	1.88E-07	5.47E-03	up	5.71	Not used
LOC102725127	PREDICTED: Homo sapiens uncharacterized LOC102725127 (LOC102725127), ncRNA [XR_433669]	ncRNA	6.99E-09	2.08E-04	down	-2.69	Not used
LOC113230	Homo sapiens uncharacterized protein LOC113230 (LOC113230), transcript variant 1, mRNA [NM_001291291]	uncharacterized locus	3.35E-08	9.88E-04	down	-3.62	Not used
LOC158435	Homo sapiens uncharacterized LOC158435 (LOC158435), long non-coding RNA [NR_033838]	ncRNA	3.68E-07	1.07E-02	down	-3.77	Not used
LOC254896	Homo sapiens uncharacterized LOC254896 (LOC254896), long non-coding RNA [NR_046173]	ncRNA	9.30E-10	2.78E-05	up	30.42	Not used
LOC283352	Homo sapiens uncharacterized LOC283352 (LOC283352), transcript variant 1, long non-coding RNA [NR_104172]	ncRNA	1.60E-07	4.68E-03	up	3.91	Not used
LOC283731	Homo sapiens uncharacterized LOC283731 (LOC283731), long non-coding RNA [NR_027073]	ncRNA	5.52E-07	1.59E-02	down	-3.01	Not used
LOC284379	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene (LOC284379), non-coding RNA [NR_002938]	pseudogene	8.22E-07	2.36E-02	down	-3.75	Not used
LOC284379	not provided	unannotated probe	7.44E-08	2.18E-03	down	-2.81	Not used
LOC285095	PREDICTED: Homo sapiens uncharacterized LOC285095 (LOC285095), transcript variant X3, misc_RNA [XR_430644]	uncharacterized locus	4.09E-08	1.20E-03	down	-3.04	Not used
LOC285181	Homo sapiens cDNA FLJ36538 fis, clone TRACH2005159. [AK093857]	miscellaneous	4.57E-12	1.38E-07	up	18.08	Not used
LOC338797	Homo sapiens uncharacterized LOC338797 (LOC338797), long non-coding RNA [NR_103736]	ncRNA	7.78E-07	2.23E-02	down	-3.72	Not used
LOC339807	Homo sapiens uncharacterized LOC339807 (LOC339807), long non-coding RNA [NR_034023]	ncRNA	2.73E-07	7.91E-03	down	-2.21	Not used
LOC388242	Homo sapiens coiled-coil domain containing 101 pseudogene (LOC388242), non-coding RNA [NR_002556]	pseudogene	1.10E-07	3.21E-03	up	7.97	Not used
LOC389602	Homo sapiens uncharacterized LOC389602 (LOC389602), mRNA [NM_001291913]	uncharacterized locus	6.23E-07	1.79E-02	down	-1.97	Not used
LOC400558	Homo sapiens uncharacterized LOC400558 (LOC400558), long non-coding RNA [NR_046200]	ncRNA	9.70E-10	2.90E-05	down	-3.92	Not used
LOC401480	PREDICTED: Homo sapiens uncharacterized LOC401480 (LOC401480), misc_RNA [XR_242443]	uncharacterized locus	7.54E-08	2.21E-03	down	-2.00	Not used
LOC401557	Homo sapiens uncharacterized LOC401557 (LOC401557), long non-coding RNA [NR_046107]	ncRNA	6.22E-08	1.82E-03	down	-4.02	Not used
LOC439951	PREDICTED: Homo sapiens uncharacterized LOC439951 (LOC439951), misc_RNA [XR_171055]	uncharacterized locus	1.48E-12	4.48E-08	down	-10.70	Not used
LOC442132	Homo sapiens golgin A6 family-like 1 pseudogene (LOC442132), non-coding RNA [NR_033906]	pseudogene	9.28E-07	2.66E-02	down	-2.07	Not used
LOC643549	Homo sapiens hypothetical protein LOC643549, mRNA (cDNA clone IMAGE:40147028). [BC133006]	miscellaneous	5.50E-08	1.62E-03	down	-2.52	Not used
LOC646513	PREDICTED: Homo sapiens VLGN1945 (LOC646513), misc_RNA [XR_159371]	miscellaneous	1.24E-08	3.66E-04	down	-5.42	Not used
LOC646762	zinc and ring finger 2 pseudogene 2 [Source:HGNC Symbol;Acc:HGNC:42793] [ENST00000442865]	pseudogene	6.13E-08	1.80E-03	down	-2.39	Not used
LOC648044	PREDICTED: Homo sapiens guanine nucleotide binding protein (G protein), gamma 12-like (LOC648044), mRNA [XM_003959952]	miscellaneous	1.37E-06	3.90E-02	down	-2.42	Not used
LOC729040	PREDICTED: Homo sapiens uncharacterized LOC729040 (LOC729040), misc_RNA [XR_241838]	uncharacterized locus	2.51E-08	7.42E-04	up	12.81	Not used
LOC729083	Homo sapiens uncharacterized LOC729083 (LOC729083), long non-coding RNA [NR_122070]	ncRNA	1.44E-06	4.09E-02	up	15.75	Not used
LOC729159	Homo sapiens UPF0607 protein ENSP00000381418-like (LOC729159), mRNA [NM_001282301]	gene	3.91E-07	1.13E-02	down	-3.46	Not used
LOC729159	Homo sapiens UPF0607 protein ENSP00000381418-like (LOC729159), mRNA [NM_001282301]	gene	4.18E-08	1.23E-03	down	-5.90	Not used
LOC729296	Homo sapiens uncharacterized LOC729296 (LOC729296), transcript variant 1, long non-coding RNA [NR_109916]	ncRNA	7.89E-08	2.31E-03	up	6.42	Not used
LOC729609	Homo sapiens uncharacterized LOC729609 (LOC729609), long non-coding RNA [NR_024440]	ncRNA	1.00E-07	2.93E-03	down	-2.04	Not used
LOC729737	Homo sapiens uncharacterized LOC729737 (LOC729737), long non-coding RNA [NR_039983]	ncRNA	6.30E-08	1.85E-03	up	4.95	Not used
LOC729860	Homo sapiens cDNA FLJ41667 fis, clone FEBRA2028366. [AK123661]	miscellaneous	1.65E-08	4.89E-04	up	7.22	Not used
LOC729879	Homo sapiens cDNA FLJ35868 fis, clone TESTI2007972. [AK093187]	miscellaneous	1.55E-06	4.41E-02	down	-2.87	Not used
LOC731424	Homo sapiens uncharacterized LOC731424 (LOC731424), long non-coding RNA [NR_037867]	ncRNA	1.51E-08	4.47E-04	up	13.00	Not used
LOC91450	Homo sapiens uncharacterized LOC91450 (LOC91450), long non-coding RNA [NR_026998]	ncRNA	8.16E-09	2.42E-04	up	10.98	Not used
LOXL3	Homo sapiens lysyl oxidase-like 3 (LOXL3), transcript variant 1, mRNA [NM_032603]	gene	5.00E-08	1.47E-03	up	7.65	327
LPAR6	Homo sapiens lysophosphatidic acid receptor 6 (LPAR6), transcript variant 1, mRNA [NM_005767]	gene	4.62E-14	1.40E-09	up	71.84	189
LPCAT2	Homo sapiens lysophosphatidylcholine acyltransferase 2 (LPCAT2), mRNA [NM_017839]	gene	1.71E-14	5.19E-10	up	30.14	Not used
LPCAT2	Homo sapiens lysophosphatidylcholine acyltransferase 2 (LPCAT2), mRNA [NM_017839]	gene	1.79E-11	5.40E-07	up	47.28	283
LPPR2	Homo sapiens lipid phosphate phosphatase-related protein type 2 (LPPR2), transcript variant 1, mRNA [NM_022737]	gene	3.69E-07	1.07E-02	up	2.60	449
LRFN3	leucine rich repeat and fibronectin type III domain containing 3 [Source:HGNC Symbol;Acc:HGNC:28370] [ENST00000588831]	gene	7.33E-08	2.15E-03	down	-2.74	933
LRG1	Homo sapiens leucine-rich alpha-2-glycoprotein 1 (LRG1), mRNA [NM_052972]	gene	6.29E-11	1.89E-06	up	37.13	99
LRP1	Homo sapiens low density lipoprotein receptor-related protein 1 (LRP1), mRNA [NM_002332]	gene	4.83E-16	1.47E-11	up	11.16	237
LRP3	Homo sapiens low density lipoprotein receptor-related protein 3 (LRP3), mRNA [NM_002333]	gene	5.70E-09	1.69E-04	down	-5.88	848
LRRC25	Homo sapiens leucine rich repeat containing 25 (LRRC25), mRNA [NM_145256]	gene	4.75E-12	1.43E-07	up	47.83	117
LRRC27	Homo sapiens leucine rich repeat containing 27 (LRRC27), transcript variant 2, mRNA [NM_001143757]	gene	6.15E-08	1.81E-03	down	-3.31	973
LRRC4	Homo sapiens leucine rich repeat containing 4 (LRRC4), mRNA [NM_022143]	gene	1.21E-13	3.66E-09	up	40.04	281
LRRC75A	Homo sapiens leucine rich repeat containing 75A (LRRC75A), transcript variant 2, mRNA [NM_207387]	gene	1.04E-07	3.04E-03	up	3.61	466
LRRC8C	Homo sapiens leucine rich repeat containing 8 family, member C (LRRC8C), mRNA [NM_032270]	gene	9.36E-07	2.68E-02	up	3.61	436
LRRN2	Homo sapiens leucine rich repeat neuronal 2 (LRRN2), transcript variant 2, mRNA [NM_201630]	gene	7.87E-09	2.34E-04	down	-1.89	956
LST1	Homo sapiens leukocyte specific transcript 1 (LST1), transcript variant 1, mRNA [NM_007161]	gene	1.52E-12	4.61E-08	up	53.46	96
LTB4R2	Homo sapiens leukotriene B4 receptor 2 (LTB4R2), transcript variant 1, mRNA [NM_019839]	gene	3.09E-07	8.96E-03	down	-2.20	930
LTBP4	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4), transcript variant 1, mRNA [NM_001042544]	gene	2.94E-08	8.69E-04	down	-2.02	Not used
LTBP4	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4), transcript variant 1, mRNA [NM_001042544]	gene	8.36E-08	2.45E-03	down	-2.03	961
LTF	Homo sapiens lactotransferrin (LTF), transcript variant 1, mRNA [NM_002343]	gene	2.09E-11	6.31E-07	up	233.14	11
LUCAT1	Homo sapiens lung cancer associated transcript 1 (non-protein coding) (LUCAT1), transcript variant 1, long non-coding RNA [NR_103548]	gene	3.12E-11	9.39E-07	up	45.73	835
LUCAT1	Homo sapiens lung cancer associated transcript 1 (non-protein coding) (LUCAT1), transcript variant 2, long non-coding RNA [NR_103549]	ncRNA	2.67E-11	8.05E-07	up	27.97	Not used
LUCAT1	lung cancer associated transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:48498] [ENST00000513626]	gene	2.14E-13	6.49E-09	up	39.96	Not used
LYAR	Homo sapiens Ly1 antibody reactive (LYAR), transcript variant 1, mRNA [NM_017816]	gene	2.07E-08	6.12E-04	up	7.53	337
LYNX1	Homo sapiens Ly6/neurotoxin 1 (LYNX1), transcript variant SLURP2, mRNA [NM_177458]	gene	6.45E-09	1.92E-04	down	-16.25	878
MAF	Homo sapiens v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog (MAF), transcript variant 2, mRNA [NM_001031804]	gene	6.94E-14	2.10E-09	up	21.27	370
MAFB	Homo sapiens v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B (MAFB), mRNA [NM_005461]	gene	7.86E-14	2.38E-09	up	31.95	Not used
MAFB	Homo sapiens v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B (MAFB), mRNA [NM_005461]	gene	1.27E-13	3.85E-09	up	996.81	34
MAGEL2	Homo sapiens MAGE-like 2 (MAGEL2), mRNA [NM_019066]	gene	5.64E-07	1.62E-02	down	-7.67	1171
MAL	Homo sapiens mal, T-cell differentiation protein (MAL), transcript variant a, mRNA [NM_002371]	gene	1.43E-11	4.32E-07	up	105.05	140
MALRD1	Homo sapiens MAM and LDL receptor class A domain containing 1 (MALRD1), mRNA [NM_001142308]	gene	6.71E-07	1.93E-02	down	-4.32	1219
MAML3	Homo sapiens mastermind-like 3 (Drosophila) (MAML3), mRNA [NM_018717]	gene	3.67E-09	1.09E-04	up	11.14	644
MANSC1	Homo sapiens MANSC domain containing 1 (MANSC1), mRNA [NM_018050]	gene	7.08E-07	2.03E-02	up	15.87	772
MAP3K3	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), transcript variant 1, mRNA [NM_203351]	gene	5.27E-07	1.52E-02	up	2.29	421
MAP4	Homo sapiens microtubule-associated protein 4 (MAP4), transcript variant 3, mRNA [NM_030885]	gene	4.07E-08	1.20E-03	down	-2.87	1001
MARC1	Homo sapiens mitochondrial amidoxime reducing component 1 (MARC1), mRNA [NM_022746]	gene	3.28E-12	9.91E-08	up	41.42	176
MARCO	Homo sapiens macrophage receptor with collagenous structure (MARCO), mRNA [NM_006770]	gene	3.26E-14	9.90E-10	up	46.59	534
MATK	Homo sapiens megakaryocyte-associated tyrosine kinase (MATK), transcript variant 1, mRNA [NM_139355]	gene	3.58E-08	1.06E-03	up	11.01	582
MATN1-AS1	Homo sapiens MATN1 antisense RNA 1 (MATN1-AS1), long non-coding RNA [NR_034182]	ncRNA	1.85E-07	5.39E-03	down	-2.21	Not used
MBOAT2	Homo sapiens membrane bound O-acyltransferase domain containing 2 (MBOAT2), mRNA [NM_138799]	gene	2.10E-16	6.38E-12	up	25.48	280
MBOAT7	Homo sapiens membrane bound O-acyltransferase domain containing 7 (MBOAT7), transcript variant 4, mRNA [NM_001146082]	gene	3.74E-12	1.13E-07	up	24.27	621
MBOAT7	Homo sapiens membrane bound O-acyltransferase domain containing 7 (MBOAT7), transcript variant 1, mRNA [NM_024298]	gene	9.89E-11	2.97E-06	up	8.25	Not used
MCEMP1	Homo sapiens mast cell-expressed membrane protein 1 (MCEMP1), mRNA [NM_174918]	gene	1.02E-17	3.11E-13	up	49.34	86
MCTP1	Homo sapiens multiple C2 domains, transmembrane 1 (MCTP1), transcript variant L, mRNA [NM_024717]	gene	4.09E-08	1.20E-03	up	9.53	Not used
MCTP1	Homo sapiens multiple C2 domains, transmembrane 1 (MCTP1), transcript variant L, mRNA [NM_024717]	gene	2.24E-17	6.81E-13	up	19.10	252
MDH1B	Homo sapiens malate dehydrogenase 1B, NAD (soluble) (MDH1B), transcript variant 3, non-coding RNA [NR_104261]	gene	6.20E-07	1.78E-02	down	-2.45	940
MEG3	Homo sapiens maternally expressed 3 (non-protein coding) (MEG3), transcript variant 1, long non-coding RNA [NR_002766]	gene	2.59E-08	7.65E-04	down	-2.06	958
MEGF11	Homo sapiens multiple EGF-like-domains 11 (MEGF11), mRNA [NM_032445]	gene	4.31E-08	1.27E-03	down	-2.94	915
MGAM	PREDICTED: Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), transcript variant X1, mRNA [XM_006716168]	gene	5.00E-14	1.52E-09	up	17.40	Not used
MGAM	Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA [NM_004668]	gene	4.19E-14	1.27E-09	up	50.61	178
MGAT4A	Homo sapiens mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A (MGAT4A), transcript variant 1, mRNA [NM_012214]	gene	3.80E-07	1.10E-02	up	31.66	580
MGC45922	Homo sapiens uncharacterized LOC284365 (MGC45922), long non-coding RNA [NR_038359]	gene	5.81E-10	1.74E-05	down	-4.07	982
MGST1	Homo sapiens microsomal glutathione S-transferase 1 (MGST1), transcript variant 3, mRNA [NM_145791]	gene	1.36E-14	4.13E-10	up	61.50	151
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	3.91E-09	1.16E-04	up	7.40	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	3.34E-10	1.00E-05	up	9.83	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	3.83E-08	1.13E-03	up	18.07	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	ncRNA	4.34E-08	1.28E-03	up	21.21	Not used
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 1, long non-coding RNA [NR_003491]	gene	2.56E-08	7.56E-04	up	25.32	585
MIAT	Homo sapiens myocardial infarction associated transcript (non-protein coding) (MIAT), transcript variant 2, long non-coding RNA [NR_033319]	ncRNA	1.73E-06	4.90E-02	up	4.02	Not used
MIATNB	Homo sapiens cDNA: FLJ22849 fis, clone KAIA987. [AK026502]	gene	2.35E-07	6.83E-03	down	-1.88	1138
MICALCL	Homo sapiens MICAL C-terminal like (MICALCL), mRNA [NM_032867]	gene	3.83E-15	1.16E-10	up	22.84	774
MINOS1-NBL1	Homo sapiens MINOS1-NBL1 readthrough (MINOS1-NBL1), transcript variant 1, mRNA [NM_001204088]	gene	6.51E-08	1.91E-03	up	6.35	365
MIOX	Homo sapiens myo-inositol oxygenase (MIOX), mRNA [NM_017584]	gene	9.28E-09	2.75E-04	down	-3.01	934
MIR1247	DIO3 opposite strand/antisense RNA (head to head) [Source:HGNC Symbol;Acc:HGNC:20348] [ENST00000555882]	gene	1.57E-06	4.46E-02	down	-3.28	1268
MIR146A	microRNA 146a [Source:HGNC Symbol;Acc:HGNC:31533] [ENST00000517927]	gene	3.90E-08	1.15E-03	up	7.39	503
MIR181A1HG	Homo sapiens MIR181A1 host gene (non-protein coding) (MIR181A1HG), long non-coding RNA [NR_040073]	gene	5.30E-09	1.58E-04	up	7.20	377
MIR181A1HG	MIR181A1 host gene (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:48659] [ENST00000436880]	gene	2.43E-08	7.19E-04	up	6.01	Not used
MIR4697HG	Homo sapiens MIR4697 host gene (non-protein coding) (MIR4697HG), long non-coding RNA [NR_024344]	ncRNA	6.89E-12	2.08E-07	up	7.98	Not used
MIR4697HG	Homo sapiens MIR4697 host gene (non-protein coding) (MIR4697HG), long non-coding RNA [NR_024344]	ncRNA	4.94E-14	1.50E-09	up	13.98	Not used
MIR4697HG	Homo sapiens MIR4697 host gene (non-protein coding) (MIR4697HG), long non-coding RNA [NR_024344]	gene	3.07E-17	9.36E-13	up	20.13	303
MIR646HG	Homo sapiens cDNA FLJ46426 fis, clone THYMU3013897. [AK128288]	gene	4.61E-08	1.36E-03	down	-2.38	1136
MITF	Homo sapiens microphthalmia-associated transcription factor (MITF), transcript variant 1, mRNA [NM_198159]	gene	1.89E-14	5.74E-10	up	21.09	248
MLC1	Homo sapiens megalencephalic leukoencephalopathy with subcortical cysts 1 (MLC1), transcript variant 1, mRNA [NM_015166]	gene	2.50E-09	7.45E-05	up	24.65	544
MLPH	Homo sapiens melanophilin (MLPH), transcript variant 1, mRNA [NM_024101]	gene	3.45E-08	1.02E-03	down	-3.15	1043
MME	Homo sapiens membrane metallo-endopeptidase (MME), transcript variant 2b, mRNA [NM_007289]	gene	1.78E-10	5.35E-06	up	9.29	Not used
MME	Homo sapiens membrane metallo-endopeptidase (MME), transcript variant 2b, mRNA [NM_007289]	gene	8.14E-15	2.47E-10	up	52.62	Not used
MME	Homo sapiens membrane metallo-endopeptidase (MME), transcript variant 2b, mRNA [NM_007289]	gene	1.08E-17	3.29E-13	up	163.66	182
MMP19	Homo sapiens matrix metallopeptidase 19 (MMP19), transcript variant 1, mRNA [NM_002429]	gene	5.14E-07	1.48E-02	down	-2.52	1009
MMP25	Homo sapiens matrix metallopeptidase 25 (MMP25), mRNA [NM_022468]	gene	1.46E-15	4.45E-11	up	165.01	70
MMP25-AS1	Homo sapiens MMP25 antisense RNA 1 (MMP25-AS1), long non-coding RNA [NR_123723]	ncRNA	4.31E-07	1.24E-02	down	-1.85	Not used
MMP9	Homo sapiens matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase) (MMP9), mRNA [NM_004994]	gene	6.84E-14	2.08E-09	up	60.93	87
MNDA	Homo sapiens myeloid cell nuclear differentiation antigen (MNDA), mRNA [NM_002432]	gene	1.03E-06	2.95E-02	up	76.67	184
MOB1B	Homo sapiens MOB kinase activator 1B (MOB1B), transcript variant 3, mRNA [NM_001244767]	gene	1.23E-09	3.67E-05	down	-4.85	1238
MOCOS	Homo sapiens molybdenum cofactor sulfurase (MOCOS), mRNA [NM_017947]	gene	4.55E-08	1.34E-03	down	-3.59	1066
MON1B	Homo sapiens MON1 secretory trafficking family member B (MON1B), transcript variant 1, mRNA [NM_014940]	gene	1.05E-07	3.08E-03	down	-3.68	986
MOS	Homo sapiens v-mos Moloney murine sarcoma viral oncogene homolog (MOS), mRNA [NM_005372]	gene	3.24E-07	9.38E-03	down	-2.59	944
MPO	Homo sapiens myeloperoxidase (MPO), mRNA [NM_000250]	gene	2.15E-09	6.42E-05	up	48.11	154
MPP1	Homo sapiens membrane protein, palmitoylated 1, 55kDa (MPP1), transcript variant 3, mRNA [NM_001166461]	gene	3.18E-09	9.49E-05	up	18.64	Not used
MPP1	Homo sapiens membrane protein, palmitoylated 1, 55kDa (MPP1), transcript variant 1, mRNA [NM_002436]	gene	1.22E-08	3.63E-04	up	21.57	101
MPZL2	Homo sapiens myelin protein zero-like 2 (MPZL2), transcript variant 1, mRNA [NM_005797]	gene	3.92E-09	1.17E-04	up	9.47	504
MPZL3	Homo sapiens myelin protein zero-like 3 (MPZL3), transcript variant 1, mRNA [NM_198275]	gene	1.30E-07	3.79E-03	up	4.77	Not used
MPZL3	Homo sapiens myelin protein zero-like 3 (MPZL3), transcript variant 1, mRNA [NM_198275]	gene	5.46E-07	1.57E-02	up	9.62	697
MRAS	Homo sapiens muscle RAS oncogene homolog (MRAS), transcript variant 1, mRNA [NM_012219]	gene	2.42E-07	7.03E-03	up	13.09	240

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
MRVI1	Homo sapiens murine retrovirus integration site 1 homolog (MRVI1), transcript variant 2, mRNA [NM_130385]	gene	3.02E-08	8.92E-04	up	42.44	628
MS4A14	Homo sapiens membrane-spanning 4-domains, subfamily A, member 14 (MS4A14), transcript variant 1, mRNA [NM_032597]	gene	1.32E-08	3.92E-04	up	10.45	755
MS4A3	Homo sapiens membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific) (MS4A3), transcript variant 1, mRNA [NM_006138]	gene	7.68E-11	2.31E-06	up	14.48	244
MS4A4A	Homo sapiens membrane-spanning 4-domains, subfamily A, member 4A (MS4A4A), transcript variant 2, mRNA [NM_024021]	gene	7.23E-07	2.08E-02	up	17.52	266
MS4A6A	Homo sapiens membrane-spanning 4-domains, subfamily A, member 6A (MS4A6A), transcript variant 1, mRNA [NM_152852]	gene	4.19E-07	1.21E-02	up	33.42	Not used
MS4A6A	Homo sapiens membrane-spanning 4-domains, subfamily A, member 6A (MS4A6A), transcript variant 2, mRNA [NM_022349]	gene	6.97E-07	2.00E-02	up	58.90	518
MS4A7	Homo sapiens membrane-spanning 4-domains, subfamily A, member 7 (MS4A7), transcript variant 1, mRNA [NM_021201]	gene	1.56E-07	4.55E-03	up	7.66	233
MSL1	Homo sapiens male-specific lethal 1 homolog (Drosophila) (MSL1), mRNA [NM_001012241]	gene	1.13E-06	3.21E-02	up	2.69	425
MSMP	Homo sapiens microseminoprotein, prostate associated (MSMP), mRNA [NM_001044264]	gene	6.70E-07	1.93E-02	down	-2.36	1051
MSRB1	Homo sapiens methionine sulfoxide reductase B1 (MSRB1), mRNA [NM_016332]	gene	1.45E-08	4.29E-04	up	16.63	630
MSX2P1	Homo sapiens msh homeobox 2 pseudogene 1 (MSX2P1), non-coding RNA [NR_002307]	gene	1.17E-09	3.49E-05	up	12.68	732
MT1B	Homo sapiens metallothionein 1B (MT1B), mRNA [NM_005947]	gene	4.01E-08	1.18E-03	up	4.24	487
MT1E	Homo sapiens metallothionein 1E (MT1E), mRNA [NM_175617]	gene	9.07E-07	2.60E-02	up	4.72	Not used
MT1E	Homo sapiens metallothionein 1E (MT1E), mRNA [NM_175617]	gene	4.69E-09	1.39E-04	up	7.11	488
MT1HL1	Homo sapiens metallothionein 1H-like 1 (MT1HL1), mRNA [NM_001276687]	gene	7.84E-07	2.25E-02	up	2.92	412
MT2A	Homo sapiens metallothionein 2A (MT2A), mRNA [NM_005953]	gene	1.81E-08	5.35E-04	up	19.22	547
MTCP1	Homo sapiens mature T-cell proliferation 1 (MTCP1), mRNA [NM_001018025]	gene	3.67E-07	1.06E-02	down	-3.87	1130
MTMR11	Homo sapiens myotubularin related protein 11 (MTMR11), transcript variant 2, mRNA [NM_181873]	gene	4.33E-07	1.25E-02	up	13.63	318
MUC1	Homo sapiens mucin 1, cell surface associated (MUC1), transcript variant 7, mRNA [NM_001044392]	gene	4.72E-07	1.36E-02	down	-3.26	1155
MUC2	Homo sapiens mucin 2, oligomeric mucus/gel-forming (MUC2), mRNA [NM_002457]	gene	2.84E-07	8.24E-03	down	-2.32	889
MUC3A	Homo sapiens mucin 3A, cell surface associated (MUC3A), mRNA [NM_005960]	gene	1.19E-07	3.47E-03	down	-2.03	Not used
MUC3A	Homo sapiens mucin 3A, cell surface associated (MUC3A), mRNA [NM_005960]	gene	1.51E-07	4.40E-03	down	-6.92	1182
MUC8	PREDICTED: Homo sapiens mucin 8 (MUC8), mRNA [XM_005275730]	gene	6.96E-08	2.04E-03	down	-4.71	1248
MXD1	Homo sapiens MAX dimerization protein 1 (MXD1), transcript variant 1, mRNA [NM_002357]	gene	3.38E-08	9.98E-04	up	6.79	Not used
MXD1	Homo sapiens MAX dimerization protein 1 (MXD1), transcript variant 1, mRNA [NM_002357]	gene	4.68E-11	1.41E-06	up	12.59	618
MYBPC3	Homo sapiens myosin binding protein C, cardiac (MYBPC3), mRNA [NM_000256]	gene	2.16E-07	6.29E-03	up	2.91	482
MYBPH	Homo sapiens myosin binding protein H (MYBPH), mRNA [NM_004997]	gene	8.10E-08	2.37E-03	up	12.24	647
MYCL	Homo sapiens v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog (MYCL), transcript variant 1, mRNA [NM_001033081]	gene	2.18E-12	6.59E-08	up	48.63	297
MYH14	Homo sapiens myosin, heavy chain 14, non-muscle (MYH14), transcript variant 1, mRNA [NM_001077186]	gene	2.80E-07	8.11E-03	down	-3.23	891
MYO1F	Homo sapiens myosin IF (MYO1F), mRNA [NM_012335]	gene	1.17E-09	3.48E-05	up	20.27	636
MYOF	Homo sapiens myoferlin (MYOF), transcript variant 1, mRNA [NM_013451]	gene	9.92E-11	2.98E-06	up	40.96	298
NACC2	Homo sapiens NACC family member 2, BEN and BTB (POZ) domain containing (NACC2), mRNA [NM_144653]	gene	1.82E-10	5.47E-06	up	61.69	105
NAMPT	Homo sapiens cDNA FLJ13279 fis, clone OVARC1001055, moderately similar to PRE-B CELL ENHANCING FACTOR PRECURSOR. [AK023341]	miscellaneous	3.29E-07	9.54E-03	up	9.33	Not used
NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA [NM_005746]	gene	7.92E-08	2.32E-03	up	10.16	Not used
NAMPT	Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA [NM_005746]	gene	3.16E-09	9.40E-05	up	20.05	704
NANOS2	Homo sapiens nanos homolog 2 (Drosophila) (NANOS2), mRNA [NM_001029861]	gene	1.02E-07	2.98E-03	down	-3.12	1157
NBAT1	Homo sapiens neuroblastoma associated transcript 1 (NBAT1), long non-coding RNA [NR_034143]	gene	1.32E-07	3.86E-03	down	-3.22	1152
NCAM1	Homo sapiens neural cell adhesion molecule 1 (NCAM1), transcript variant 5, mRNA [NM_001242607]	gene	2.03E-07	5.90E-03	up	11.07	721
NCF2	Homo sapiens neutrophil cytosolic factor 2 (NCF2), transcript variant 1, mRNA [NM_000433]	gene	1.38E-07	4.02E-03	up	18.16	607
NCOA4	Homo sapiens nuclear receptor coactivator 4 (NCOA4), transcript variant 1, mRNA [NM_001145260]	gene	2.35E-10	7.07E-06	up	5.01	468
NCR1	Homo sapiens natural cytotoxicity triggering receptor 1 (NCR1), transcript variant 1, mRNA [NM_004829]	gene	1.53E-10	4.58E-06	up	5.21	225
NCR2	Homo sapiens natural cytotoxicity triggering receptor 2 (NCR2), transcript variant 1, mRNA [NM_004828]	gene	1.44E-06	4.11E-02	down	-2.57	887
NDUFA6-AS1	Homo sapiens NDUFA6 antisense RNA 1 (head to head) (NDUFA6-AS1), long non-coding RNA [NR_034118]	ncRNA	4.47E-07	1.29E-02	down	-1.85	Not used
NEFL	Homo sapiens neurofilament, light polypeptide (NEFL), mRNA [NM_006158]	gene	1.61E-09	4.82E-05	up	9.52	746
NELL2	Homo sapiens NEL-like 2 (chicken) (NELL2), transcript variant 2, mRNA [NM_006159]	gene	1.73E-12	5.24E-08	up	54.30	577
NES	Homo sapiens nestin (NES), mRNA [NM_006617]	gene	5.05E-07	1.46E-02	down	-2.51	1271
NFAM1	Homo sapiens NFAT activating protein with ITAM motif 1 (NFAM1), mRNA [NM_145912]	gene	3.73E-17	1.14E-12	up	608.59	17
NFE2	Homo sapiens nuclear factor, erythroid 2 (NFE2), transcript variant 1, mRNA [NM_006163]	gene	1.20E-11	3.63E-07	up	193.93	138
NFIL3	Homo sapiens nuclear factor, interleukin 3 regulated (NFIL3), transcript variant 3, mRNA [NM_005384]	gene	3.88E-13	1.18E-08	up	29.90	116
NFKBIL1	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1 (NFKBIL1), transcript variant 2, mRNA [NM_001144961]	gene	1.08E-10	3.26E-06	down	-4.42	868
NFYC-AS1	Homo sapiens NFYC antisense RNA 1 (NFYC-AS1), long non-coding RNA [NR_024567]	ncRNA	2.01E-09	6.01E-05	down	-4.09	Not used
NHSL2	NHS-like 2 [Source:HGNC Symbol;Acc:HGNC:33737] [ENST00000373677]	gene	1.30E-06	3.70E-02	up	5.37	469
NID1	Homo sapiens nidogen 1 (NID1), mRNA [NM_002508]	gene	1.05E-09	3.15E-05	up	22.90	299
NID2	Homo sapiens mRNA; cDNA DKFZp686D12108 (from clone DKFZp686D12108). [BX648241]	gene	1.07E-06	3.06E-02	down	-2.76	1058
NINJ1	Homo sapiens ninjurin 1 (NINJ1), mRNA [NM_004148]	gene	1.25E-06	3.57E-02	up	31.15	123
NINJ2	Homo sapiens ninjurin 2 (NINJ2), transcript variant 1, mRNA [NM_016533]	gene	2.78E-08	8.20E-04	up	13.22	745
NKG7	Homo sapiens natural killer cell granule protein 7 (NKG7), mRNA [NM_005601]	gene	7.06E-08	2.07E-03	up	51.56	132
NKX1-2	Homo sapiens NK1 homeobox 2 (NKX1-2), mRNA [NM_001146340]	gene	7.29E-09	2.17E-04	down	-3.40	1004
NKX2-5	Homo sapiens NK2 homeobox 5 (NKX2-5), transcript variant 2, mRNA [NM_001166175]	gene	5.52E-08	1.62E-03	down	-2.97	1002
NLRC3	Homo sapiens mRNA for FLJ00398 protein. [AK090476]	gene	1.01E-11	3.04E-07	down	-4.84	1164
NLRC4	Homo sapiens NLR family, CARD domain containing 4 (NLRC4), transcript variant 1, mRNA [NM_021209]	gene	2.47E-07	7.18E-03	up	25.20	631
NLRP12	Homo sapiens NLR family, pyrin domain containing 12 (NLRP12), transcript variant 3, mRNA [NM_001277126]	gene	9.08E-12	2.74E-07	up	83.20	175
NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 3, mRNA [NM_001079821]	gene	8.79E-09	2.61E-04	up	50.48	124
NLRP3	Homo sapiens NLR family, pyrin domain containing 3 (NLRP3), transcript variant 6, mRNA [NM_001243133]	gene	2.69E-10	8.08E-06	up	39.41	Not used
NME8	Homo sapiens NME/NM23 family member 8 (NME8), mRNA [NM_016616]	gene	7.99E-10	2.39E-05	up	40.64	134
NMUR1	Homo sapiens neuromedin U receptor 1 (NMUR1), mRNA [NM_006056]	gene	1.56E-10	4.69E-06	up	19.21	737
NOBOX	Homo sapiens NOBOX oogenesis homeobox (NOBOX), mRNA [NM_001080413]	gene	1.41E-06	4.01E-02	down	-2.00	1079
NOL3	Homo sapiens nucleolar protein 3 (apoptosis repressor with CARD domain) (NOL3), transcript variant 2, mRNA [NM_003946]	gene	1.54E-06	4.37E-02	up	2.50	484
NOV	Homo sapiens nephroblastoma overexpressed (NOV), mRNA [NM_002514]	gene	2.35E-11	7.08E-07	up	37.16	286
NPB	Homo sapiens neuropeptide B (NPB), mRNA [NM_148896]	gene	1.33E-06	3.80E-02	down	-3.12	1235
NPC1L1	Homo sapiens NPC1-like 1 (NPC1L1), transcript variant 1, mRNA [NM_013389]	gene	3.61E-07	1.05E-02	down	-3.09	936
NPC2	Homo sapiens Niemann-Pick disease, type C2 (NPC2), mRNA [NM_006432]	gene	5.18E-10	1.55E-05	up	2.94	431
NPDC1	Homo sapiens neural proliferation, differentiation and control, 1 (NPDC1), mRNA [NM_015392]	gene	6.21E-09	1.84E-04	up	7.77	335
NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 2, mRNA [NM_001200050]	gene	1.41E-11	4.25E-07	up	7.04	Not used
NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 2, mRNA [NM_001200050]	gene	6.22E-11	1.87E-06	up	32.37	632
NPL	Homo sapiens N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) (NPL), transcript variant 3, mRNA [NM_001200056]	gene	2.35E-09	7.01E-05	up	18.56	Not used
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) [Source:HGNC Symbol;Acc:HGNC:16781] [ENST00000463899]	gene	3.84E-07	1.11E-02	down	-2.03	Not used
NPY6R	Homo sapiens neuropeptide Y receptor Y6 (pseudogene) (NPY6R), non-coding RNA [NR_002713]	gene	1.78E-07	5.19E-03	down	-3.07	1153
NR6A1	Homo sapiens nuclear receptor subfamily 6, group A, member 1 (NR6A1), transcript variant 1, mRNA [NM_033334]	gene	1.04E-10	3.13E-06	up	30.21	Not used
NR6A1	Homo sapiens nuclear receptor subfamily 6, group A, member 1 (NR6A1), transcript variant 1, mRNA [NM_033334]	gene	1.62E-12	4.89E-08	up	45.30	147
NRG1	Homo sapiens neuregulin 1 (NRG1), transcript variant HRG-gamma, mRNA [NM_004495]	gene	1.25E-07	3.66E-03	up	7.49	361
NRIP2	Homo sapiens nuclear receptor interacting protein 2 (NRIP2), mRNA [NM_031474]	gene	2.21E-07	6.43E-03	down	-2.26	1158
NSG1	Homo sapiens neuron specific gene family member 1 (NSG1), transcript variant 3, mRNA [NM_001287763]	gene	6.84E-11	2.06E-06	up	22.19	777
NTNG2	Homo sapiens netrin G2 (NTNG2), mRNA [NM_032536]	gene	6.19E-08	1.82E-03	up	12.37	780
NUCB2	Homo sapiens nucleobindin 2 (NUCB2), mRNA [NM_005013]	gene	1.06E-08	3.15E-04	up	11.02	681
NUDT8	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 8 (NUDT8), transcript variant 2, mRNA [NM_181843]	gene	5.22E-07	1.50E-02	down	-2.22	923
NUMA1	Homo sapiens nuclear mitotic apparatus protein 1 (NUMA1), transcript variant 1, mRNA [NM_006185]	gene	3.08E-07	8.94E-03	down	-2.23	1086
NUP188	Homo sapiens nucleoporin 188kDa (NUP188), mRNA [NM_015354]	gene	4.28E-07	1.24E-02	down	-2.27	1016
OASL	Homo sapiens 2'-5'-oligoadenylate synthetase-like (OASL), transcript variant 1, mRNA [NM_003733]	gene	5.08E-09	1.51E-04	up	19.48	598
OGFR	Homo sapiens opioid growth factor receptor (OGFR), mRNA [NM_007346]	gene	4.49E-08	1.32E-03	down	-2.58	1106
OLFM1	Homo sapiens olfactomedin 1 (OLFM1), transcript variant 2, mRNA [NM_006334]	gene	7.32E-11	2.20E-06	up	6.63	810
OLFM4	Homo sapiens olfactomedin 4 (OLFM4), mRNA [NM_006418]	gene	9.96E-12	3.00E-07	up	77.02	840
OLIG1	Homo sapiens oligodendrocyte transcription factor 1 (OLIG1), mRNA [NM_138983]	gene	1.31E-18	3.99E-14	up	149.58	72
OPLAH	Homo sapiens 5-oxoprolinase (ATP-hydrolysing) (OPLAH), mRNA [NM_017570]	gene	6.23E-08	1.83E-03	up	4.14	349
OPRD1	Homo sapiens opioid receptor, delta 1 (OPRD1), mRNA [NM_000911]	gene	2.72E-07	7.89E-03	down	-2.88	1061
OR10C1	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (gene/pseudogene) (OR10C1), mRNA [NM_013941]	gene	7.51E-07	2.15E-02	down	-4.38	1189
OR10G9	Homo sapiens olfactory receptor, family 10, subfamily G, member 9 (OR10G9), mRNA [NM_001001953]	gene	4.29E-07	1.24E-02	down	-4.19	1038
OR1J4	Homo sapiens olfactory receptor, family 1, subfamily J, member 4 (OR1J4), mRNA [NM_001004452]	gene	2.39E-07	6.96E-03	down	-2.91	1203
OR1L6	Homo sapiens olfactory receptor, family 1, subfamily L, member 6 (OR1L6), mRNA [NM_001004453]	gene	1.72E-11	5.19E-07	down	-3.06	945
OR2A2	Homo sapiens olfactory receptor, family 2, subfamily A, member 2 (OR2A2), mRNA [NM_001005480]	gene	3.65E-08	1.08E-03	down	-4.64	988
OR3A4P	Homo sapiens olfactory receptor, family 3, subfamily A, member 4 pseudogene (OR3A4P), non-coding RNA [NR_024128]	gene	1.67E-07	4.88E-03	down	-2.40	1204
OR4D6	Homo sapiens olfactory receptor, family 4, subfamily D, member 6 (OR4D6), mRNA [NM_001004708]	gene	1.19E-06	3.39E-02	down	-3.32	1233
OR4Q3	Homo sapiens olfactory receptor, family 4, subfamily Q, member 3 (OR4Q3), mRNA [NM_172194]	gene	5.33E-07	1.54E-02	down	-3.12	1048
OR51B5	Homo sapiens olfactory receptor, family 51, subfamily B, member 5 (OR51B5), transcript variant 1, mRNA [NM_001005567]	gene	3.64E-07	1.05E-02	down	-3.24	1251
OR51I2	Homo sapiens olfactory receptor, family 51, subfamily I, member 2 (OR51I2), mRNA [NM_001004754]	gene	4.11E-07	1.19E-02	down	-5.39	1213
OR5C1	Homo sapiens olfactory receptor, family 5, subfamily C, member 1 (OR5C1), mRNA [NM_001001923]	gene	3.40E-07	9.84E-03	down	-4.74	1181
OR6N1	Homo sapiens olfactory receptor, family 6, subfamily N, member 1 (OR6N1), mRNA [NM_001005185]	gene	1.03E-07	3.02E-03	down	-3.54	1035
OR7C2	Homo sapiens olfactory receptor, family 7, subfamily C, member 2 (OR7C2), mRNA [NM_012377]	gene	1.67E-06	4.74E-02	down	-3.42	1206
OSBPL1A	Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), transcript variant 2, mRNA [NM_080597]	gene	6.38E-12	1.93E-07	up	11.78	779
OSBPL8	Homo sapiens oxysterol binding protein-like 8 (OSBPL8), transcript variant 1, mRNA [NM_020841]	gene	4.18E-07	1.21E-02	up	2.25	432
OSCAR	Homo sapiens osteoclast associated, immunoglobulin-like receptor (OSCAR), transcript variant 1, mRNA [NM_206818]	gene	1.48E-08	4.37E-04	down	-3.17	Not used
OSCAR	Homo sapiens osteoclast associated, immunoglobulin-like receptor (OSCAR), transcript variant 1, mRNA [NM_206818]	gene	1.27E-10	3.82E-06	up	6.20	498
OSM	Homo sapiens oncostatin M (OSM), mRNA [NM_020530]	gene	6.21E-08	1.82E-03	up	10.08	838
OTOA	otoancorin [Source:HGNC Symbol;Acc:HGNC:16378] [ENST00000563871]	gene	8.75E-08	2.56E-03	down	-3.20	1266
OTX1	Homo sapiens orthodenticle homeobox 1 (OTX1), transcript variant 1, mRNA [NM_014562]	gene	2.62E-08	7.72E-04	up	8.08	760
OXNAD1	Homo sapiens oxidoreductase NAD-binding domain containing 1 (OXNAD1), mRNA [NM_138381]	gene	3.00E-10	9.00E-06	up	4.29	391
P2RX3	Homo sapiens purinergic receptor P2X, ligand gated ion channel, 3 (P2RX3), mRNA [NM_002559]	gene	9.05E-09	2.68E-04	down	-3.40	1176
P2RY13	Homo sapiens purinergic receptor P2Y, G-protein coupled, 13 (P2RY13), mRNA [NM_176894]	gene	3.42E-17	1.04E-12	up	87.51	91
P2RY2	Homo sapiens purinergic receptor P2Y, G-protein coupled, 2 (P2RY2), transcript variant 1, mRNA [NM_176072]	gene	5.57E-19	1.70E-14	up	75.37	107
PABPN1L	Homo sapiens poly(A) binding protein, nuclear 1-like (cytoplasmic) (PABPN1L), transcript variant 2, mRNA [NM_001294328]	gene	1.20E-06	3.42E-02	down	-3.33	1029
PACSIN2	Homo sapiens protein kinase C and casein kinase substrate in neurons 2 (PACSIN2), transcript variant 2, mRNA [NM_007229]	gene	5.52E-08	1.62E-03	up	3.36	452
PADI2	Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA [NM_007365]	gene	2.99E-15	9.09E-11	up	11.26	Not used
PADI2	Homo sapiens peptidyl arginine deiminase, type II (PADI2), mRNA [NM_007365]	gene	3.57E-14	1.08E-09	up	48.15	275
PADI4	Homo sapiens peptidyl arginine deiminase, type IV (PADI4), mRNA [NM_012387]	gene	2.03E-09	6.07E-05	up	12.32	662
PAG1	Homo sapiens phosphoprotein membrane anchor with glycosphingolipid microdomains 1 (PAG1), mRNA [NM_018440]	gene	2.97E-12	8.97E-08	up	42.74	Not used
PAG1	Homo sapiens phosphoprotein membrane anchor with glycosphingolipid microdomains 1 (PAG1), mRNA [NM_018440]	gene	4.47E-13	1.35E-08	up	85.17	540
PAK1	p21 protein (Cdc42/Rac)-activated kinase 1 [Source:HGNC Symbol;Acc:HGNC:8590] [ENST00000526968]	gene	1.56E-06	4.43E-02	down	-3.08	1031
PAK4	Homo sapiens p21 protein (Cdc42/Rac)-activated kinase 4 (PAK4), transcript variant 1, mRNA [NM_005884]	gene	7.48E-07	2.15E-02	down	-2.26	896
PAM	Homo sapiens peptidylglycine alpha-amidating monooxygenase (PAM), transcript variant 1, mRNA [NM_000919]	gene	1.42E-11	4.29E-07	up	12.21	331
PARD6G-AS1	Homo sapiens PARD6G antisense RNA 1 (PARD6G-AS1), transcript variant 3, long non-coding RNA [NR_028340]	ncRNA	9.45E-09	2.80E-04	down	-3.55	Not used
PARP8	Homo sapiens poly (ADP-ribose) polymerase family, member 8 (PARP8), transcript variant 2, mRNA [NM_024615]	gene	1.35E-07	3.95E-03	up	3.34	445
PAX7	Homo sapiens paired box 7 (PAX7), transcript variant 2, mRNA [NM_013945]	gene	5.31E-07	1.53E-02	down	-3.59	1040

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
PCAT19	Homo sapiens prostate cancer associated transcript 19 (non-protein coding) (PCAT19), long non-coding RNA [NR_040109]	ncRNA	1.11E-07	3.25E-03	down	-3.61	Not used
PCAT19	Homo sapiens prostate cancer associated transcript 19 (non-protein coding) (PCAT19), long non-coding RNA [NR_040109]	gene	4.97E-08	1.46E-03	down	-3.71	1207
PCDHB8	Homo sapiens protocadherin beta 8 (PCDHB8), mRNA [NM_019120]	gene	2.29E-07	6.65E-03	down	-3.55	1243
PCED1B-AS1	Homo sapiens PCED1B antisense RNA 1 (PCED1B-AS1), long non-coding RNA [NR_026544]	ncRNA	3.84E-08	1.13E-03	down	-3.32	Not used
PCNXL4	Homo sapiens cDNA FLJ38170 fis, clone FCBBF1000024. [AK095489]	gene	6.37E-09	1.89E-04	down	-2.56	1147
PCSK1N	Homo sapiens proprotein convertase subtilisin/kexin type 1 inhibitor (PCSK1N), mRNA [NM_013271]	gene	1.05E-11	3.18E-07	down	-15.01	874
PCSK5	Homo sapiens proprotein convertase subtilisin/kexin type 5 (PCSK5), transcript variant 2, mRNA [NM_006200]	gene	1.75E-13	5.31E-09	up	40.30	554
PCTP	Homo sapiens phosphatidylcholine transfer protein (PCTP), transcript variant 1, mRNA [NM_021213]	gene	5.50E-08	1.62E-03	up	11.01	660
PDE3B	Homo sapiens phosphodiesterase 3B, cGMP-inhibited (PDE3B), mRNA [NM_000922]	gene	6.92E-08	2.03E-03	up	40.35	531
PDE4D	Homo sapiens phosphodiesterase 4D, cAMP-specific (PDE4D), transcript variant 3, mRNA [NM_001165899]	gene	5.69E-08	1.67E-03	up	8.63	Not used
PDE4D	Homo sapiens phosphodiesterase 4D, cAMP-specific (PDE4D), transcript variant 3, mRNA [NM_001165899]	gene	1.97E-11	5.92E-07	up	28.04	538
PDE9A	Homo sapiens cDNA FLJ90181 fis, clone MAMMA1000706. [AK074662]	gene	6.90E-09	2.05E-04	down	-2.88	1265
PDGFC	Homo sapiens platelet derived growth factor C (PDGFC), transcript variant 1, mRNA [NM_016205]	gene	9.13E-11	2.74E-06	up	18.31	733
PF4V1	Homo sapiens platelet factor 4 variant 1 (PF4V1), mRNA [NM_002620]	gene	4.36E-07	1.26E-02	up	12.43	243
PFKFB3	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), transcript variant 1, mRNA [NM_004566]	gene	3.04E-10	9.10E-06	up	8.16	317
PFKFB4	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4), mRNA [NM_004567]	gene	2.82E-12	8.52E-08	up	17.46	620
PGC	Homo sapiens progastricsin (pepsinogen C) (PGC), transcript variant 1, mRNA [NM_002630]	gene	1.32E-06	3.76E-02	down	-2.73	1140
PGD	Homo sapiens phosphogluconate dehydrogenase (PGD), mRNA [NM_002631]	gene	3.25E-08	9.58E-04	up	7.03	668
PGLYRP1	Homo sapiens peptidoglycan recognition protein 1 (PGLYRP1), mRNA [NM_005091]	gene	8.68E-16	2.64E-11	up	164.23	62
PGPEP1L	Homo sapiens pyroglutamyl-peptidase I-like (PGPEP1L), transcript variant 2, mRNA [NM_001167902]	gene	7.46E-08	2.19E-03	down	-4.24	1156
PHC2	Homo sapiens polyhomeotic homolog 2 (Drosophila) (PHC2), transcript variant 1, mRNA [NM_198040]	gene	4.59E-09	1.37E-04	up	3.39	478
PHOSPHO1	Homo sapiens phosphatase, orphan 1 (PHOSPHO1), transcript variant 1, mRNA [NM_001143804]	gene	9.16E-09	2.72E-04	up	4.75	499
PI3	Homo sapiens peptidase inhibitor 3, skin-derived (PI3), mRNA [NM_002638]	gene	8.32E-09	2.47E-04	up	67.54	148
PI4KA	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha (PI4KA), mRNA [NM_058004]	gene	2.32E-07	6.75E-03	down	-2.03	1105
PICALM	Homo sapiens phosphatidylinositol binding clathrin assembly protein (PICALM), transcript variant 1, mRNA [NM_007166]	gene	2.58E-08	7.60E-04	up	4.30	446
PID1	Homo sapiens phosphotyrosine interaction domain containing 1 (PID1), transcript variant 1, mRNA [NM_017933]	gene	2.58E-09	7.69E-05	up	18.92	236
PIK3R1	Homo sapiens phosphoinositide-3-kinase, regulatory subunit 1 (alpha) (PIK3R1), transcript variant 1, mRNA [NM_181523]	gene	6.86E-07	1.97E-02	up	3.32	392
PITX1	Homo sapiens paired-like homeodomain 1 (PITX1), mRNA [NM_002653]	gene	2.94E-07	8.51E-03	down	-3.14	1201
PKP4	Homo sapiens plakophilin 4 (PKP4), transcript variant 1, mRNA [NM_003628]	gene	3.96E-07	1.14E-02	up	6.90	229
PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent) [Source:HGNC Symbol;Acc:HGNC:9037] [ENST00000596510]	gene	5.50E-09	1.64E-04	down	-2.84	916
PLA2G7	Homo sapiens phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma) (PLA2G7), transcript variant 1, mRNA [NM_005084]	gene	8.94E-13	2.71E-08	up	35.34	300
PLAUR	Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 3, mRNA [NM_001005377]	gene	1.78E-13	5.40E-09	up	79.40	39
PLB1	Homo sapiens phospholipase B1 (PLB1), transcript variant 1, mRNA [NM_153021]	gene	7.55E-09	2.24E-04	up	8.50	762
PLCB1	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 1, mRNA [NM_015192]	gene	1.04E-06	2.96E-02	up	3.78	Not used
PLCB1	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), transcript variant 2, mRNA [NM_182734]	gene	1.49E-08	4.39E-04	up	6.26	502
PLCH2	Homo sapiens phospholipase C, eta 2 (PLCH2), transcript variant 1, mRNA [NM_014638]	gene	3.99E-07	1.15E-02	down	-2.97	1144
PLEK	Homo sapiens pleckstrin (PLEK), mRNA [NM_002664]	gene	1.41E-07	4.11E-03	up	9.25	314
PLEKHG3	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (PLEKHG3), mRNA [NM_015549]	gene	1.50E-16	4.58E-12	up	118.38	Not used
PLEKHG3	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 3 (PLEKHG3), mRNA [NM_015549]	gene	4.85E-13	1.47E-08	up	213.67	68
PLEKHG5	Homo sapiens pleckstrin homology domain containing, family G (with RhoGef domain) member 5 (PLEKHG5), transcript variant 8, mRNA [NM_001265594]	gene	3.06E-08	9.03E-04	down	-2.72	927
PLEKHO2	Homo sapiens pleckstrin homology domain containing, family O member 2 (PLEKHO2), transcript variant 1, mRNA [NM_025201]	gene	8.65E-08	2.53E-03	up	5.17	344
PLSCR1	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA [NM_021105]	gene	7.42E-09	2.20E-04	up	17.02	685
PLXDC1	Homo sapiens plexin domain containing 1 (PLXDC1), mRNA [NM_020405]	gene	8.66E-09	2.57E-04	up	11.02	372
PLXDC2	Homo sapiens plexin domain containing 2 (PLXDC2), transcript variant 1, mRNA [NM_032812]	gene	2.47E-13	7.48E-09	up	79.28	572
PLXNC1	Homo sapiens plexin C1 (PLXNC1), transcript variant 1, mRNA [NM_005761]	gene	3.17E-09	9.44E-05	up	30.16	102
PMP22	Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 1, mRNA [NM_000304]	gene	8.60E-13	2.60E-08	up	10.31	806
PNPLA2	Homo sapiens patatin-like phospholipase domain containing 2 (PNPLA2), mRNA [NM_020376]	gene	1.05E-07	3.06E-03	down	-2.91	1023
POLR1C	polymerase (RNA) I polypeptide C, 30kDa [Source:HGNC Symbol;Acc:HGNC:20194] [ENST00000512472]	gene	1.81E-07	5.27E-03	down	-2.38	911
POLR2F	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), transcript variant 2, mRNA [NM_001301129]	gene	3.48E-07	1.01E-02	down	-1.65	1112
PPA2	pyrophosphatase (inorganic) 2 [Source:HGNC Symbol;Acc:HGNC:28883] [ENST00000505713]	gene	1.96E-08	5.80E-04	down	-5.82	865
PPDPF	pancreatic progenitor cell differentiation and proliferation factor [Source:HGNC Symbol;Acc:HGNC:16142] [ENST00000370177]	gene	5.05E-09	1.50E-04	down	-5.32	985
PPIAL4G	peptidylprolyl isomerase A (cyclophilin A)-like 4G [Source:HGNC Symbol;Acc:HGNC:33996] [ENST00000419275]	gene	1.14E-07	3.32E-03	down	-3.36	1150
PPM1F	Homo sapiens protein phosphatase, Mg2+/Mn2+ dependent, 1F (PPM1F), mRNA [NM_014634]	gene	2.28E-08	6.73E-04	up	9.24	653
PPP1R12B	Homo sapiens protein phosphatase 1, regulatory subunit 12B (PPP1R12B), transcript variant 1, mRNA [NM_002481]	gene	5.43E-07	1.56E-02	up	2.58	479
PPP1R13B	Homo sapiens protein phosphatase 1, regulatory subunit 13B (PPP1R13B), mRNA [NM_015316]	gene	1.22E-06	3.49E-02	down	-3.19	1129
PPP1R18	Homo sapiens protein phosphatase 1, regulatory subunit 18 (PPP1R18), transcript variant 1, mRNA [NM_133471]	gene	7.03E-07	2.02E-02	up	5.11	Not used
PPP1R18	Homo sapiens protein phosphatase 1, regulatory subunit 18 (PPP1R18), transcript variant 1, mRNA [NM_133471]	gene	3.97E-12	1.20E-07	up	5.98	398
PPP1R3B	Homo sapiens protein phosphatase 1, regulatory subunit 3B (PPP1R3B), transcript variant 1, mRNA [NM_001201329]	gene	5.82E-09	1.73E-04	up	5.99	403
PPP2R2B	Homo sapiens protein phosphatase 2, regulatory subunit B, beta (PPP2R2B), transcript variant 10, mRNA [NM_001271948]	gene	3.27E-10	9.82E-06	up	9.06	719
PPP2R5B	protein phosphatase 2, regulatory subunit B', beta [Source:HGNC Symbol;Acc:HGNC:9310] [ENST00000413292]	gene	3.68E-07	1.06E-02	down	-2.72	1198
PRAM1	Homo sapiens PML-RARA regulated adaptor molecule 1 (PRAM1), mRNA [NM_032152]	gene	2.77E-08	8.18E-04	up	13.25	684
PRDM1	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), transcript variant 1, mRNA [NM_001198]	gene	2.60E-07	7.55E-03	up	27.51	599
PRDM6	Homo sapiens PR domain containing 6 (PRDM6), mRNA [NM_001136239]	gene	9.44E-08	2.76E-03	down	-4.09	1033
PRF1	Homo sapiens perforin 1 (pore forming protein) (PRF1), transcript variant 1, mRNA [NM_005041]	gene	2.38E-10	7.14E-06	up	20.78	523
PRKACA	Homo sapiens protein kinase, cAMP-dependent, catalytic, alpha (PRKACA), transcript variant 1, mRNA [NM_002730]	gene	7.57E-07	2.17E-02	up	2.57	426
PRKCH	Homo sapiens protein kinase C, eta (PRKCH), mRNA [NM_006255]	gene	4.26E-11	1.28E-06	up	62.71	574
PRKCQ	Homo sapiens protein kinase C, theta (PRKCQ), transcript variant 1, mRNA [NM_006257]	gene	3.30E-14	1.00E-09	up	26.03	194
PRKCQ-AS1	Homo sapiens PRKCQ antisense RNA 1 (PRKCQ-AS1), transcript variant 1, long non-coding RNA [NR_036502]	ncRNA	3.91E-12	1.18E-07	up	81.47	Not used
PRKCQ-AS1	PRKCQ antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44689] [ENST00000561822]	RNA antisense	3.64E-07	1.05E-02	up	6.21	Not used
PRKCQ-AS1	PRKCQ antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44689] [ENST00000561822]	RNA antisense	5.44E-07	1.57E-02	up	7.40	Not used
PRLHR	Homo sapiens prolactin releasing hormone receptor (PRLHR), mRNA [NM_004248]	gene	2.22E-07	6.45E-03	down	-2.06	967
PRM1	Homo sapiens protamine 1 (PRM1), mRNA [NM_002761]	gene	3.95E-10	1.18E-05	down	-2.22	996
PROK2	Homo sapiens prokineticin 2 (PROK2), transcript variant 2, mRNA [NM_021935]	gene	2.56E-15	7.79E-11	up	742.48	22
PRR25	Homo sapiens proline rich 25 (PRR25), mRNA [NM_001013638]	gene	4.98E-10	1.49E-05	down	-6.07	851
PRR27	Homo sapiens proline rich 27 (PRR27), mRNA [NM_214711]	gene	8.95E-07	2.56E-02	down	-3.98	1245
PRR33	proline rich 33 [Source:HGNC Symbol;Acc:HGNC:35118] [ENST00000391480]	gene	6.16E-08	1.81E-03	down	-1.82	995
PRR36	Homo sapiens proline rich 36 (PRR36), transcript variant 1, mRNA [NM_001190467]	gene	3.83E-09	1.14E-04	down	-3.57	Not used
PRR36	Homo sapiens proline rich 36 (PRR36), transcript variant 1, mRNA [NM_001190467]	gene	2.82E-09	8.39E-05	down	-16.78	881
PRR5L	Homo sapiens proline rich 5 like (PRR5L), transcript variant 2, mRNA [NM_024841]	gene	2.07E-08	6.11E-04	up	15.44	727
PRRC2B	Homo sapiens proline-rich coiled-coil 2B (PRRC2B), mRNA [NM_013318]	gene	9.78E-07	2.80E-02	down	-2.45	942
PRRT4	Homo sapiens proline-rich transmembrane protein 4 (PRRT4), transcript variant 1, mRNA [NM_001174164]	gene	1.61E-09	4.80E-05	up	6.69	214
PRSS23	Homo sapiens protease, serine, 23 (PRSS23), transcript variant 1, mRNA [NM_007173]	gene	6.08E-15	1.85E-10	up	23.65	278
PSAP	Homo sapiens prosaposin (PSAP), transcript variant 2, mRNA [NM_001042465]	gene	5.01E-07	1.45E-02	up	3.24	415
PSMA6	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), transcript variant 1, mRNA [NM_002791]	gene	1.76E-06	5.00E-02	up	1.83	433
PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 [Source:HGNC Symbol;Acc:HGNC:9555] [ENST00000338548]	gene	9.90E-08	2.90E-03	down	-3.46	1230
PSRC1	Homo sapiens proline/serine-rich coiled-coil 1 (PSRC1), transcript variant 1, mRNA [NM_032636]	gene	3.04E-09	9.07E-05	up	5.18	505
PSTPIP2	Homo sapiens proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2), mRNA [NM_024430]	gene	6.97E-08	2.04E-03	up	11.16	707
PTAFR	Homo sapiens platelet-activating factor receptor (PTAFR), transcript variant 3, mRNA [NM_000952]	gene	1.11E-12	3.35E-08	up	90.96	69
PTEN	Homo sapiens phosphatase and tensin homolog (PTEN), mRNA [NM_000314]	gene	1.86E-07	5.41E-03	up	3.08	419
PTGDR	Homo sapiens prostaglandin D2 receptor (DP) (PTGDR), transcript variant 1, mRNA [NM_000953]	gene	9.14E-07	2.62E-02	up	4.81	384
PTGDR2	Homo sapiens prostaglandin D2 receptor 2 (PTGDR2), mRNA [NM_004778]	gene	7.34E-09	2.18E-04	up	7.26	228
PTGDS	prostaglandin D2 synthase 21kDa (brain) [Source:HGNC Symbol;Acc:HGNC:9592] [ENST00000371623]	gene	6.29E-07	1.81E-02	down	-2.23	1024
PTGER2	Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kDa (PTGER2), mRNA [NM_000956]	gene	1.13E-13	3.44E-09	up	68.58	111
PTGIR	Homo sapiens prostaglandin I2 (prostacyclin) receptor (IP) (PTGIR), mRNA [NM_000960]	gene	3.57E-10	1.07E-05	up	20.46	793
PTGS1	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 1, mRNA [NM_000962]	gene	1.44E-06	4.10E-02	up	9.58	794
PTGS2	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA [NM_000963]	gene	4.69E-11	1.41E-06	up	62.73	170
PTK7	Homo sapiens protein tyrosine kinase 7 (PTK7), transcript variant PTK7-1, mRNA [NM_002821]	gene	4.38E-08	1.29E-03	down	-3.24	1255
PTMS	Homo sapiens parathymosin (PTMS), mRNA [NM_002824]	gene	6.51E-08	1.91E-03	down	-3.75	1232
PTPN5	Homo sapiens protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched) (PTPN5), transcript variant 1, mRNA [NM_006906]	gene	1.64E-07	4.79E-03	down	-3.47	1041
PTPRE	Homo sapiens protein tyrosine phosphatase, receptor type, E (PTPRE), transcript variant 1, mRNA [NM_006504]	gene	2.65E-09	7.89E-05	up	4.26	390
PTX3	Homo sapiens pentraxin 3, long (PTX3), mRNA [NM_002852]	gene	4.26E-07	1.23E-02	up	8.84	307
PXN	Homo sapiens paxillin (PXN), transcript variant 1, mRNA [NM_002859]	gene	3.97E-07	1.15E-02	up	8.19	744
PYGL	Homo sapiens phosphorylase, glycogen, liver (PYGL), transcript variant 1, mRNA [NM_002863]	gene	1.88E-13	5.68E-09	up	396.27	52
QARS	Homo sapiens glutaminyl-tRNA synthetase (QARS), transcript variant 1, mRNA [NM_005051]	gene	1.65E-07	4.81E-03	down	-1.92	1115
QPCT	Homo sapiens glutaminyl-peptide cyclotransferase (QPCT), mRNA [NM_012413]	gene	8.14E-13	2.46E-08	up	105.31	Not used
QPCT	Homo sapiens glutaminyl-peptide cyclotransferase (QPCT), mRNA [NM_012413]	gene	1.41E-11	4.25E-07	up	190.75	20
RAB27A	Homo sapiens RAB27A, member RAS oncogene family (RAB27A), transcript variant 1, mRNA [NM_004580]	gene	2.96E-09	8.82E-05	up	8.21	659
RAB32	Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA [NM_006834]	gene	1.50E-06	4.28E-02	up	26.67	94
RAB33A	Homo sapiens RAB33A, member RAS oncogene family (RAB33A), mRNA [NM_004794]	gene	3.83E-07	1.11E-02	up	4.26	350
RAB3D	Homo sapiens RAB3D, member RAS oncogene family (RAB3D), mRNA [NM_004283]	gene	5.79E-08	1.70E-03	up	9.33	651
RAB44	Homo sapiens RAB44, member RAS oncogene family (RAB44), mRNA [NM_001257357]	gene	2.51E-10	7.52E-06	up	12.45	Not used
RAB44	Homo sapiens RAB44, member RAS oncogene family (RAB44), mRNA [NM_001257357]	gene	7.01E-15	2.13E-10	up	37.62	549
RABGAP1L	RAB GTPase activating protein 1-like [Source:HGNC Symbol;Acc:HGNC:24663] [ENST00000367690]	gene	8.79E-07	2.52E-02	down	-1.85	1093
RAMP1	Homo sapiens receptor (G protein-coupled) activity modifying protein 1 (RAMP1), mRNA [NM_005855]	gene	1.41E-06	4.01E-02	up	4.20	362
RAP1GAP	Homo sapiens RAP1 GTPase activating protein (RAP1GAP), transcript variant 3, mRNA [NM_002885]	gene	7.15E-09	2.12E-04	down	-2.96	998
RAP2B	Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA [NM_002886]	gene	1.02E-07	2.98E-03	up	4.82	495
RARRES3	Homo sapiens retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA [NM_004585]	gene	1.07E-07	3.12E-03	up	8.75	682
RASGRP4	Homo sapiens RAS guanyl releasing protein 4 (RASGRP4), transcript variant a, mRNA [NM_170604]	gene	5.21E-12	1.57E-07	up	13.84	747
RASSF10	Homo sapiens Ras association (RalGDS/AF-6) domain family (N-terminal) member 10 (RASSF10), mRNA [NM_001080521]	gene	4.32E-07	1.25E-02	down	-3.98	1187
RASSF2	Homo sapiens Ras association (RalGDS/AF-6) domain family member 2 (RASSF2), transcript variant 1, mRNA [NM_014737]	gene	2.90E-07	8.40E-03	up	4.79	496
RAX2	Homo sapiens retina and anterior neural fold homeobox 2 (RAX2), mRNA [NM_032753]	gene	1.75E-07	5.11E-03	down	-3.64	1234
RBFOX3	Homo sapiens RNA binding protein, fox-1 homolog (C. elegans) 3 (RBFOX3), mRNA [NM_001082575]	gene	3.78E-07	1.09E-02	down	-3.77	989
RBP7	Homo sapiens retinol binding protein 7, cellular (RBP7), mRNA [NM_052960]	gene	6.97E-15	2.12E-10	up	125.73	71
RCOR1	Homo sapiens REST corepressor 1 (RCOR1), mRNA [NM_015156]	gene	3.70E-07	1.07E-02	up	2.64	443
RDH10	Homo sapiens retinol dehydrogenase 10 (all-trans) (RDH10), mRNA [NM_172037]	gene	3.16E-07	9.14E-03	up	3.22	437
REEP6	Homo sapiens receptor accessory protein 6 (REEP6), mRNA [NM_138393]	gene	1.57E-07	4.57E-03	down	-3.66	1269
REPS2	Homo sapiens RALBP1 associated Eps domain containing 2 (REPS2), transcript variant 1, mRNA [NM_004726]	gene	1.35E-08	3.99E-04	up	17.10	635
REREP3	Homo sapiens arginine-glutamic acid dipeptide (RE) repeats pseudogene 3 (REREP3), non-coding RNA [NR_033735]	gene	2.10E-07	6.10E-03	down	-3.58	1202
RETN	Homo sapiens resistin (RETN), transcript variant 1, mRNA [NM_020415]	gene	1.15E-12	3.49E-08	up	27.50	Not used
RETN	Homo sapiens resistin (RETN), transcript variant 1, mRNA [NM_020415]	gene	1.01E-14	3.07E-10	up	38.35	88
RFFL	Homo sapiens ring finger and FYVE-like domain containing E3 ubiquitin protein ligase (RFFL), transcript variant 2, mRNA [NM_001017368]	gene	3.66E-08	1.08E-03	up	3.09	359
RFX2	Homo sapiens regulatory factor X, 2 (influences HLA class II expression) (RFX2), transcript variant 1, mRNA [NM_000635]	gene	2.47E-08	7.29E-04	up	5.97	492

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
RGL4	Homo sapiens ral guanine nucleotide dissociation stimulator-like 4 (RGL4), mRNA [NM_153615]	gene	5.10E-11	1.54E-06	up	174.53	53
RGS18	Homo sapiens regulator of G-protein signaling 18 (RGS18), mRNA [NM_130782]	gene	1.71E-08	5.07E-04	up	100.03	555
RGS9	Homo sapiens regulator of G-protein signaling 9 (RGS9), transcript variant 1, mRNA [NM_003835]	gene	2.27E-10	6.82E-06	up	11.07	739
RHOA	ras homolog family member A [Source:HGNC Symbol;Acc:HGNC:667] [ENST00000265538]	gene	6.25E-07	1.80E-02	down	-1.96	1125
RHOBTB1	Homo sapiens Rho-related BTB domain containing 1 (RHOBTB1), transcript variant 4, mRNA [NM_001242359]	gene	3.79E-08	1.12E-03	up	8.00	376
RHOG	Homo sapiens ras homolog family member G (RHOG), mRNA [NM_001665]	gene	2.43E-07	7.05E-03	up	3.20	453
RHOU	Homo sapiens ras homolog family member U (RHOU), transcript variant 1, mRNA [NM_021205]	gene	8.97E-14	2.72E-09	up	21.78	790
RIN1	Homo sapiens Ras and Rab interactor 1 (RIN1), mRNA [NM_004292]	gene	5.57E-08	1.64E-03	up	4.58	324
RIN2	Homo sapiens Ras and Rab interactor 2 (RIN2), transcript variant 2, mRNA [NM_018993]	gene	5.84E-09	1.73E-04	up	16.30	795
RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA [NM_002934]	gene	7.32E-11	2.20E-06	up	59.32	Not used
RNASE2	Homo sapiens ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin) (RNASE2), mRNA [NM_002934]	gene	1.30E-11	3.91E-07	up	79.90	155
RNASE3	Homo sapiens ribonuclease, RNase A family, 3 (RNASE3), mRNA [NM_002935]	gene	1.32E-09	3.94E-05	up	39.93	156
RNF126	Homo sapiens ring finger protein 126 (RNF126), mRNA [NM_194460]	gene	2.75E-07	7.99E-03	down	-2.12	910
RNF13	Homo sapiens ring finger protein 13 (RNF13), transcript variant 1, mRNA [NM_007282]	gene	1.00E-07	2.93E-03	up	3.22	Not used
RNF13	Homo sapiens ring finger protein 13 (RNF13), transcript variant 1, mRNA [NM_007282]	gene	1.35E-07	3.93E-03	up	3.26	456
RNF130	Homo sapiens ring finger protein 130 (RNF130), transcript variant 1, mRNA [NM_018434]	gene	9.66E-07	2.76E-02	up	3.76	471
RNF144A	Homo sapiens ring finger protein 144A (RNF144A), mRNA [NM_014746]	gene	9.49E-10	2.84E-05	up	7.04	227
RNF149	Homo sapiens ring finger protein 149 (RNF149), mRNA [NM_173647]	gene	1.34E-06	3.82E-02	up	6.36	507
RNF166	Homo sapiens ring finger protein 166 (RNF166), transcript variant 1, mRNA [NM_178841]	gene	4.33E-09	1.29E-04	up	5.05	393
RNF180	ring finger protein 180 [Source:HGNC Symbol;Acc:HGNC:27752] [ENST00000296615]	gene	1.88E-08	5.54E-04	down	-3.24	1148
RNF207	Homo sapiens ring finger protein 207 (RNF207), mRNA [NM_207396]	gene	8.33E-08	2.44E-03	up	7.17	514
RNF24	Homo sapiens ring finger protein 24 (RNF24), transcript variant 1, mRNA [NM_007219]	gene	2.27E-07	6.59E-03	up	4.48	457
ROPN1L	Homo sapiens rhophilin associated tail protein 1-like (ROPN1L), transcript variant 1, mRNA [NM_031916]	gene	2.59E-08	7.65E-04	up	10.79	781
RORA	Homo sapiens RAR-related orphan receptor A (RORA), transcript variant 2, mRNA [NM_134260]	gene	1.23E-08	3.65E-04	up	17.42	591
RORC	Homo sapiens RAR-related orphan receptor C (RORC), transcript variant 1, mRNA [NM_005060]	gene	7.19E-11	2.16E-06	up	13.00	595
RP2	Homo sapiens retinitis pigmentosa 2 (X-linked recessive) (RP2), mRNA [NM_006915]	gene	1.21E-06	3.46E-02	up	2.37	428
RP9P	Homo sapiens retinitis pigmentosa 9 pseudogene (RP9P), non-coding RNA [NR_003500]	gene	1.52E-09	4.55E-05	down	-4.19	1222
RPL29	Homo sapiens ribosomal protein L29 (RPL29), mRNA [NM_000992]	gene	5.70E-07	1.64E-02	down	-2.70	1054
RPSAP58	Homo sapiens ribosomal protein SA pseudogene 58 (RPSAP58), non-coding RNA [NR_003662]	gene	1.60E-07	4.66E-03	down	-3.06	1221
RRAGD	Homo sapiens Ras-related GTP binding D (RRAGD), mRNA [NM_021244]	gene	1.48E-10	4.43E-06	up	42.38	837
RRH	Homo sapiens retinal pigment epithelium-derived rhodopsin homolog (RRH), mRNA [NM_006583]	gene	1.59E-06	4.51E-02	down	-1.82	1133
RSAD2	Homo sapiens radical S-adenosyl methionine domain containing 2 (RSAD2), mRNA [NM_080657]	gene	4.68E-09	1.39E-04	up	88.61	168
RTBDN	Homo sapiens retbindin (RTBDN), transcript variant 2, mRNA [NM_031429]	gene	6.15E-08	1.81E-03	down	-3.01	965
RTN3	Homo sapiens reticulon 3 (RTN3), transcript variant 1, mRNA [NM_006054]	gene	6.06E-08	1.78E-03	up	7.03	664
RUNX2	Homo sapiens runt-related transcription factor 2 (RUNX2), transcript variant 1, mRNA [NM_001024630]	gene	2.36E-12	7.12E-08	up	25.85	560
RUNX2	Homo sapiens runt-related transcription factor 2 (RUNX2), transcript variant 2, mRNA [NM_001015051]	gene	3.06E-07	8.87E-03	up	4.36	Not used
S100A11	Homo sapiens S100 calcium binding protein A11 (S100A11), mRNA [NM_005620]	gene	1.16E-09	3.48E-05	up	29.51	Not used
S100A11	Homo sapiens S100 calcium binding protein A11 (S100A11), mRNA [NM_005620]	gene	1.03E-08	3.07E-04	up	31.90	608
S100A12	Homo sapiens S100 calcium binding protein A12 (S100A12), mRNA [NM_005621]	gene	2.18E-18	6.64E-14	up	1256.46	Not used
S100A12	Homo sapiens S100 calcium binding protein A12 (S100A12), mRNA [NM_005621]	gene	6.70E-19	2.04E-14	up	1779.21	6
S100A8	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA [NM_002964]	gene	4.17E-11	1.25E-06	up	2377.51	7
S100A9	Homo sapiens S100 calcium binding protein A9 (S100A9), mRNA [NM_002965]	gene	2.41E-12	7.29E-08	up	1378.72	8
S100P	Homo sapiens S100 calcium binding protein P (S100P), mRNA [NM_005980]	gene	2.39E-15	7.28E-11	up	302.08	29
S100Z	Homo sapiens S100 calcium binding protein Z (S100Z), mRNA [NM_130772]	gene	2.99E-14	9.08E-10	up	31.94	289
S1PR3	Homo sapiens sphingosine-1-phosphate receptor 3 (S1PR3), mRNA [NM_005226]	gene	1.25E-14	3.80E-10	up	52.00	295
S1PR5	Homo sapiens sphingosine-1-phosphate receptor 5 (S1PR5), transcript variant 1, mRNA [NM_030760]	gene	2.26E-11	6.81E-07	up	38.75	196
SAMD3	Homo sapiens sterile alpha motif domain containing 3 (SAMD3), transcript variant 1, mRNA [NM_001017373]	gene	6.58E-11	1.98E-06	up	57.71	568
SAMD3	Homo sapiens sterile alpha motif domain containing 3 (SAMD3), transcript variant 3, mRNA [NM_001258275]	gene	3.39E-12	1.03E-07	up	23.82	Not used
SAMHD1	Homo sapiens SAM domain and HD domain 1 (SAMHD1), mRNA [NM_015474]	gene	2.25E-09	6.71E-05	up	16.22	792
SAP30	Homo sapiens Sin3A-associated protein, 30kDa (SAP30), mRNA [NM_003864]	gene	1.69E-11	5.10E-07	up	17.10	700
SASH3	Homo sapiens SAM and SH3 domain containing 3 (SASH3), mRNA [NM_018990]	gene	8.31E-07	2.38E-02	up	1.99	424
SAT1	Homo sapiens spermidine/spermine N1-acetyltransferase 1 (SAT1), transcript variant 1, mRNA [NM_002970]	gene	8.02E-07	2.30E-02	up	3.88	351
SATB1-AS1	Homo sapiens SATB1 antisense RNA 1 (SATB1-AS1), long non-coding RNA [NR_125803]	ncRNA	3.64E-09	1.08E-04	up	8.34	Not used
SATB1-AS1	Homo sapiens SATB1 antisense RNA 1 (SATB1-AS1), long non-coding RNA [NR_125803]	ncRNA	1.44E-08	4.27E-04	up	8.35	Not used
SATB1-AS1	Homo sapiens SATB1 antisense RNA 1 (SATB1-AS1), long non-coding RNA [NR_125803]	ncRNA	2.24E-09	6.68E-05	up	9.75	Not used
SATB1-AS1	Homo sapiens SATB1 antisense RNA 1 (SATB1-AS1), long non-coding RNA [NR_125803]	ncRNA	1.40E-10	4.20E-06	up	31.28	Not used
SCARA3	Homo sapiens scavenger receptor class A, member 3 (SCARA3), transcript variant 1, mRNA [NM_016240]	gene	4.71E-07	1.36E-02	down	-2.46	929
SCARF1	Homo sapiens scavenger receptor class F, member 1 (SCARF1), transcript variant 1, mRNA [NM_003693]	gene	4.78E-11	1.44E-06	up	5.56	642
SCARF2	Homo sapiens scavenger receptor class F, member 2 (SCARF2), transcript variant 1, mRNA [NM_153334]	gene	1.91E-11	5.75E-07	down	-6.33	869
SCGB3A1	Homo sapiens secretoglobin, family 3A, member 1 (SCGB3A1), mRNA [NM_052863]	gene	1.84E-12	5.55E-08	down	-5.12	870
SDCBP	Homo sapiens syndecan binding protein (syntenin) (SDCBP), transcript variant 1, mRNA [NM_005625]	gene	1.86E-07	5.41E-03	up	3.78	454
SDR39U1	Homo sapiens short chain dehydrogenase/reductase family 39U, member 1 (SDR39U1), transcript variant 1, mRNA [NM_020195]	gene	3.20E-07	9.27E-03	down	-1.85	1088
SEC14L4	Homo sapiens SEC14-like 4 (S. cerevisiae) (SEC14L4), transcript variant 1, mRNA [NM_174977]	gene	6.17E-07	1.78E-02	down	-3.29	1161
SECTM1	Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA [NM_003004]	gene	2.35E-11	7.09E-07	up	213.01	19
SELPLG	Homo sapiens selectin P ligand (SELPLG), transcript variant 1, mRNA [NM_001206609]	gene	1.40E-07	4.08E-03	up	6.11	Not used
SELPLG	Homo sapiens selectin P ligand (SELPLG), transcript variant 2, mRNA [NM_003006]	gene	2.45E-08	7.25E-04	up	11.40	693
SEMA4C	Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C (SEMA4C), mRNA [NM_017789]	gene	3.40E-12	1.03E-07	up	16.25	371
SERPINA1	Homo sapiens serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), transcript variant 2, mRNA [NM_001002236]	gene	1.54E-19	4.68E-15	up	264.36	65
SERPINB10	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 10 (SERPINB10), mRNA [NM_005024]	gene	1.05E-06	3.01E-02	up	4.78	208
SERPING1	Homo sapiens serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 (SERPING1), transcript variant 1, mRNA [NM_000062]	gene	8.14E-07	2.33E-02	up	8.12	515
SFTA1P	AGENCOURT_10018270 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6495000 5', mRNA sequence [BU601128]	gene	1.09E-08	3.22E-04	down	-11.66	880
SFTA1P	Homo sapiens surfactant associated 1, pseudogene (SFTA1P), non-coding RNA [NR_027082]	pseudogene	5.35E-09	1.59E-04	down	-2.48	Not used
SFXN5	Homo sapiens sideroflexin 5 (SFXN5), mRNA [NM_144579]	gene	1.48E-06	4.20E-02	down	-2.86	1025
SGK1	Homo sapiens serum/glucocorticoid regulated kinase 1 (SGK1), transcript variant 1, mRNA [NM_005627]	gene	3.71E-09	1.11E-04	up	29.14	550
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 2, mRNA [NM_001114937]	gene	4.29E-10	1.28E-05	up	17.98	Not used
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 1, mRNA [NM_002351]	gene	3.64E-12	1.10E-07	up	22.80	Not used
SH2D1A	Homo sapiens SH2 domain containing 1A (SH2D1A), transcript variant 1, mRNA [NM_002351]	gene	3.85E-14	1.17E-09	up	57.38	197
SH2D1B	Homo sapiens SH2 domain containing 1B (SH2D1B), mRNA [NM_053282]	gene	2.68E-09	7.99E-05	up	33.16	562
SH2D2A	Homo sapiens SH2 domain containing 2A (SH2D2A), transcript variant 5, mRNA [NM_001161444]	gene	3.71E-09	1.10E-04	up	9.71	374
SHANK2	Homo sapiens SH3 and multiple ankyrin repeat domains 2 (SHANK2), transcript variant 1, mRNA [NM_012309]	gene	5.71E-07	1.64E-02	down	-3.80	1256
SHISA7	Homo sapiens shisa family member 7 (SHISA7), mRNA [NM_001145176]	gene	3.69E-07	1.07E-02	down	-3.06	1006
SHQ1	Homo sapiens SHQ1, H/ACA ribonucleoprotein assembly factor (SHQ1), mRNA [NM_018130]	gene	7.17E-07	2.06E-02	down	-2.85	1059
SIGLEC17P	sialic acid binding Ig-like lectin 17, pseudogene [Source:HGNC Symbol;Acc:HGNC:15604] [ENST00000611992]	gene	3.64E-07	1.05E-02	up	19.25	738
SIGLEC7	Homo sapiens sialic acid binding Ig-like lectin 7 (SIGLEC7), transcript variant 1, mRNA [NM_014385]	gene	1.69E-08	5.00E-04	up	7.21	694
SIGLEC9	Homo sapiens sialic acid binding Ig-like lectin 9 (SIGLEC9), transcript variant 2, mRNA [NM_014441]	gene	5.41E-07	1.56E-02	up	7.64	761
SIPA1L2	Homo sapiens signal-induced proliferation-associated 1 like 2 (SIPA1L2), mRNA [NM_020808]	gene	5.64E-14	1.71E-09	up	54.38	173
SIRPA	Homo sapiens signal-regulatory protein alpha (SIRPA), transcript variant 1, mRNA [NM_001040022]	gene	4.78E-10	1.43E-05	up	55.70	120
SIRPB1	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), transcript variant 3, mRNA [NM_001135844]	gene	3.06E-13	9.28E-09	up	12.45	702
SIRPB1	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), transcript variant 1, mRNA [NM_006065]	gene	1.03E-06	2.96E-02	up	3.80	Not used
SIRPB1	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), transcript variant 1, mRNA [NM_006065]	gene	3.53E-07	1.02E-02	up	6.33	Not used
SIRPB2	Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 1, mRNA [NM_001122962]	gene	5.37E-09	1.59E-04	up	12.17	703
SIRPB2	signal-regulatory protein beta 2 [Source:HGNC Symbol;Acc:HGNC:16247] [ENST00000486775]	gene	1.14E-08	3.37E-04	up	10.35	Not used
SIRPD	Homo sapiens signal-regulatory protein delta (SIRPD), mRNA [NM_178460]	gene	1.32E-11	3.97E-07	up	19.83	686
SIRPG	Homo sapiens signal-regulatory protein gamma (SIRPG), transcript variant 3, mRNA [NM_001039508]	gene	2.68E-10	8.03E-06	up	7.75	Not used
SIRPG	Homo sapiens signal-regulatory protein gamma (SIRPG), transcript variant 1, mRNA [NM_018556]	gene	1.01E-12	3.05E-08	up	69.94	109
SLAMF8	Homo sapiens SLAM family member 8 (SLAMF8), mRNA [NM_020125]	gene	1.26E-06	3.60E-02	up	8.16	508
SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10907] [ENST00000469799]	gene	1.23E-11	3.72E-07	up	9.13	Not used
SLC11A1	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 (SLC11A1), mRNA [NM_000578]	gene	3.41E-13	1.03E-08	up	13.36	Not used
SLC11A1	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 (SLC11A1), mRNA [NM_000578]	gene	3.03E-17	9.22E-13	up	36.94	836
SLC17A7	Homo sapiens solute carrier family 17 (vesicular glutamate transporter), member 7 (SLC17A7), mRNA [NM_020309]	gene	9.58E-07	2.74E-02	down	-1.91	957
SLC19A1	Homo sapiens solute carrier family 19 (folate transporter), member 1 (SLC19A1), transcript variant 2, mRNA [NM_001205206]	gene	7.29E-08	2.14E-03	up	3.50	Not used
SLC19A1	Homo sapiens solute carrier family 19 (folate transporter), member 1 (SLC19A1), transcript variant 1, mRNA [NM_194255]	gene	9.26E-11	2.78E-06	up	17.76	705
SLC19A3	solute carrier family 19 (thiamine transporter), member 3 [Source:HGNC Symbol;Acc:HGNC:16266] [ENST00000409456]	gene	7.08E-07	2.03E-02	down	-4.15	1162
SLC22A1	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), transcript variant 2, mRNA [NM_153187]	gene	9.68E-09	2.87E-04	up	3.29	485
SLC22A18AS	Homo sapiens solute carrier family 22 (organic cation transporter), member 18 antisense (SLC22A18AS), transcript variant 1, mRNA [NM_007105]	gene	2.85E-09	8.48E-05	up	7.55	823
SLC22A4	Homo sapiens solute carrier family 22 (organic cation/zwitterion transporter), member 4 (SLC22A4), mRNA [NM_003059]	gene	4.07E-15	1.24E-10	up	54.16	92
SLC24A3	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 3 (SLC24A3), mRNA [NM_020689]	gene	5.11E-08	1.50E-03	up	9.04	378
SLC24A4	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 (SLC24A4), transcript variant 1, mRNA [NM_153646]	gene	1.67E-08	4.94E-04	up	10.07	764
SLC25A19	Homo sapiens solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 (SLC25A19), transcript variant 1, mRNA [NM_001126121]	gene	1.08E-06	3.09E-02	down	-1.81	1118
SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37 [Source:HGNC Symbol;Acc:HGNC:29786] [ENST00000519973]	gene	2.33E-08	6.87E-04	up	7.58	Not used
SLC25A37	Homo sapiens solute carrier family 25 (mitochondrial iron transporter), member 37 (SLC25A37), mRNA [NM_016612]	gene	2.98E-11	8.96E-07	up	14.11	619
SLC25A51	Homo sapiens solute carrier family 25, member 51 (SLC25A51), transcript variant 2, non-coding RNA [NR_024872]	gene	1.14E-06	3.26E-02	down	-2.29	1011
SLC31A1	Homo sapiens solute carrier family 31 (copper transporter), member 1 (SLC31A1), mRNA [NM_001859]	gene	7.15E-09	2.12E-04	up	4.76	809
SLC31A2	Homo sapiens solute carrier family 31 (copper transporter), member 2 (SLC31A2), mRNA [NM_001860]	gene	2.63E-11	7.94E-07	up	130.13	152
SLC40A1	Homo sapiens solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1), mRNA [NM_014585]	gene	8.00E-10	2.39E-05	up	69.92	271
SLC43A2	Homo sapiens solute carrier family 43 (amino acid system L transporter), member 2 (SLC43A2), transcript variant 2, mRNA [NM_152346]	gene	1.33E-08	3.94E-04	up	4.27	360
SLC45A4	Homo sapiens solute carrier family 45, member 4 (SLC45A4), transcript variant 1, mRNA [NM_001286646]	gene	5.27E-09	1.57E-04	up	4.74	352
SLC4A1	Homo sapiens solute carrier family 4 (anion exchanger), member 1 (Diego blood group) (SLC4A1), mRNA [NM_000342]	gene	1.27E-06	3.62E-02	down	-4.53	1065
SLC51A	Homo sapiens solute carrier family 51, alpha subunit (SLC51A), mRNA [NM_152672]	gene	4.88E-10	1.46E-05	up	4.62	209
SLC5A6	Homo sapiens solute carrier family 5 (sodium/multivitamin and iodide cotransporter), member 6 (SLC5A6), transcript variant 1, mRNA [NM_021095]	gene	1.41E-06	4.00E-02	down	-2.04	1126
SLC6A5	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 5 (SLC6A5), mRNA [NM_004211]	gene	3.74E-07	1.08E-02	down	-3.27	1045
SLC6A6	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 6 (SLC6A6), transcript variant 1, mRNA [NM_003043]	gene	1.08E-07	3.15E-03	up	3.22	480
SLC7A4	Homo sapiens solute carrier family 7, member 4 (SLC7A4), mRNA [NM_004173]	gene	2.55E-09	7.59E-05	down	-4.29	1046
SLC8A1	Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), transcript variant A, mRNA [NM_021097]	gene	1.57E-09	4.69E-05	up	16.31	Not used
SLC8A1	Homo sapiens solute carrier family 8 (sodium/calcium exchanger), member 1 (SLC8A1), transcript variant A, mRNA [NM_021097]	gene	8.25E-10	2.47E-05	up	40.77	291
SLC9A3R1	Homo sapiens solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1 (SLC9A3R1), mRNA [NM_004252]	gene	1.06E-07	3.11E-03	up	4.71	475
SLC9A7	Homo sapiens solute carrier family 9, subfamily A (NHE7, cation proton antiporter 7), member 7 (SLC9A7), transcript variant 2, mRNA [NM_032591]	gene	1.74E-06	4.94E-02	down	-2.59	1103
SLCO3A1	Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), transcript variant 1, mRNA [NM_013272]	gene	1.36E-12	4.11E-08	up	8.20	Not used
SLCO3A1	Homo sapiens solute carrier organic anion transporter family, member 3A1 (SLCO3A1), transcript variant 1, mRNA [NM_013272]	gene	1.39E-17	4.22E-13	up	47.39	277
SLCO4C1	Homo sapiens solute carrier organic anion transporter family, member 4C1 (SLCO4C1), mRNA [NM_180991]	gene	4.22E-11	1.27E-06	up	27.74	776
SLITRK4	Homo sapiens SLIT and NTRK-like family, member 4 (SLITRK4), transcript variant 2, mRNA [NM_173078]	gene	1.78E-12	5.39E-08	up	20.82	262
SLITRK5	SLIT and NTRK-like family, member 5 [Source:HGNC Symbol;Acc:HGNC:20295] [ENST00000325089]	gene	8.58E-07	2.46E-02	down	-2.87	1169

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
SLPI	Homo sapiens secretory leukocyte peptidase inhibitor (SLPI), mRNA [NM_003064]	gene	4.95E-13	1.50E-08	up	82.68	63
SMAD1	Homo sapiens SMAD family member 1 (SMAD1), transcript variant 1, mRNA [NM_005900]	gene	7.14E-11	2.15E-06	up	8.57	239
SMARCD3	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), transcript variant 2, mRNA [NM_003078]	gene	1.04E-12	3.15E-08	up	11.88	329
SMCO4	Homo sapiens single-pass membrane protein with coiled-coil domains 4 (SMCO4), mRNA [NM_020179]	gene	7.50E-07	2.15E-02	up	12.27	695
SMG9	Homo sapiens SMG9 nonsense mediated mRNA decay factor (SMG9), mRNA [NM_019108]	gene	9.08E-07	2.60E-02	down	-2.16	1083
SMIM3	Homo sapiens small integral membrane protein 3 (SMIM3), mRNA [NM_032947]	gene	1.48E-07	4.31E-03	up	64.25	112
SMPDL3A	Homo sapiens sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A), transcript variant 1, mRNA [NM_006714]	gene	2.36E-09	7.04E-05	up	18.98	708
SNAR-A3	Homo sapiens small ILF3/NF90-associated RNA A3 (SNAR-A3), small nuclear RNA [NR_024214]	gene	9.68E-08	2.83E-03	down	-2.88	972
SNCA	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), transcript variant 4, mRNA [NM_007308]	gene	1.74E-07	5.08E-03	up	11.60	710
SNHG11	Homo sapiens small nucleolar RNA host gene 11 (non-protein coding) (SNHG11), long non-coding RNA [NR_003239]	gene	5.00E-13	1.51E-08	down	-10.63	873
SNORA70B	UI-H-DT0-aub-m-04-0-UI.s1 NCI_CGAP_DT0 Homo sapiens cDNA clone IMAGE:5867307 3', mRNA sequence [BQ029156]	gene	8.04E-07	2.31E-02	down	-2.66	1017
SNORA71A	AGENCOURT_6611325 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5485440 5', mRNA sequence [BM918074]	gene	1.18E-08	3.48E-04	down	-5.94	1166
SNRPD2P2	Homo sapiens small nuclear ribonucleoprotein D2 pseudogene 2 (SNRPD2P2), non-coding RNA [NR_033826]	gene	6.00E-07	1.73E-02	down	-3.27	1273
SNTB1	Homo sapiens syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1) (SNTB1), mRNA [NM_021021]	gene	9.72E-13	2.94E-08	up	17.89	787
SOCS2	Homo sapiens suppressor of cytokine signaling 2 (SOCS2), transcript variant 1, mRNA [NM_003877]	gene	9.87E-08	2.89E-03	up	9.28	656
SOCS3	Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA [NM_003955]	gene	1.79E-09	5.34E-05	up	38.10	58
SOD2	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), transcript variant 2, mRNA [NM_001024465]	gene	1.66E-14	5.04E-10	up	19.44	622
SORBS2	Homo sapiens sorbin and SH3 domain containing 2 (SORBS2), transcript variant 9, mRNA [NM_001270771]	gene	9.85E-08	2.88E-03	down	-3.69	1036
SORBS3	Homo sapiens sorbin and SH3 domain containing 3 (SORBS3), transcript variant 1, mRNA [NM_005775]	gene	3.60E-07	1.04E-02	down	-3.74	1236
SORL1	Homo sapiens sortilin-related receptor, L(DLR class) A repeats containing (SORL1), mRNA [NM_003105]	gene	1.81E-09	5.39E-05	up	236.88	143
SORT1	Homo sapiens sortilin 1 (SORT1), transcript variant 1, mRNA [NM_002959]	gene	3.11E-07	9.01E-03	up	65.16	519
SP8	Homo sapiens Sp8 transcription factor (SP8), transcript variant 2, mRNA [NM_198956]	gene	3.85E-10	1.15E-05	down	-4.83	1165
SPACA6P	Homo sapiens sperm acrosome associated 6, pseudogene (SPACA6P), long non-coding RNA [NR_024330]	gene	3.48E-08	1.02E-03	up	7.98	379
SPATA6	Homo sapiens spermatogenesis associated 6 (SPATA6), transcript variant 1, mRNA [NM_019073]	gene	7.06E-11	2.12E-06	up	6.22	512
SPEF2	Homo sapiens sperm flagellar 2 (SPEF2), transcript variant 2, mRNA [NM_144722]	gene	1.63E-10	4.89E-06	up	6.96	219
SPI1	Homo sapiens Spi-1 proto-oncogene (SPI1), transcript variant 1, mRNA [NM_001080547]	gene	8.10E-11	2.43E-06	up	5.53	399
SPINK7	Homo sapiens serine peptidase inhibitor, Kazal type 7 (putative) (SPINK7), mRNA [NM_032566]	gene	1.18E-06	3.37E-02	down	-1.91	1127
SPINK8	Homo sapiens serine peptidase inhibitor, Kazal type 8 (putative) (SPINK8), mRNA [NM_001080525]	gene	3.56E-10	1.07E-05	up	12.68	782
SPINT3	Homo sapiens serine peptidase inhibitor, Kunitz type, 3 (SPINT3), mRNA [NM_006652]	gene	9.16E-07	2.62E-02	down	-3.59	1049
SPNS2	Homo sapiens spinster homolog 2 (Drosophila) (SPNS2), mRNA [NM_001124758]	gene	1.84E-07	5.35E-03	up	2.74	409
SPRNP1	Homo sapiens shadow of prion protein homolog (zebrafish) pseudogene 1 (SPRNP1), non-coding RNA [NR_033789]	gene	4.87E-07	1.41E-02	down	-2.47	932
SPRR2E	Homo sapiens small proline-rich protein 2E (SPRR2E), mRNA [NM_001024209]	gene	2.10E-07	6.12E-03	down	-2.16	997
SPSB1	Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA [NM_025106]	gene	1.99E-09	5.95E-05	up	13.80	734
SREBF1	Homo sapiens sterol regulatory element binding transcription factor 1 (SREBF1), transcript variant 1, mRNA [NM_001005291]	gene	1.39E-06	3.95E-02	down	-2.33	1124
SRGN	Homo sapiens serglycin (SRGN), transcript variant 1, mRNA [NM_002727]	gene	1.24E-09	3.69E-05	up	7.40	665
SRMS	Homo sapiens src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites (SRMS), mRNA [NM_080823]	gene	3.17E-11	9.56E-07	up	11.34	646
SRXN1	Homo sapiens sulfiredoxin 1 (SRXN1), mRNA [NM_080725]	gene	1.23E-11	3.72E-07	up	52.06	118
SSPO	SCO-spondin [Source:HGNC Symbol;Acc:HGNC:21998] [ENST00000472850]	gene	4.01E-09	1.19E-04	down	-2.83	898
SSX3	Homo sapiens synovial sarcoma, X breakpoint 3 (SSX3), mRNA [NM_021014]	gene	9.37E-07	2.68E-02	down	-2.23	1108
ST3GAL4	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 4 (ST3GAL4), transcript variant 1, mRNA [NM_006278]	gene	8.25E-12	2.49E-07	up	9.54	720
ST3GAL6	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 6 (ST3GAL6), transcript variant 1, mRNA [NM_006100]	gene	1.51E-14	4.57E-10	up	31.52	253
ST6GALNAC2	Homo sapiens ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2 (ST6GALNAC2), mRNA [NM_006456]	gene	3.18E-13	9.64E-09	up	38.25	177
STAB1	Homo sapiens stabilin 1 (STAB1), mRNA [NM_015136]	gene	6.82E-14	2.07E-09	up	21.14	301
STAT5B	Homo sapiens signal transducer and activator of transcription 5B (STAT5B), mRNA [NM_012448]	gene	1.07E-06	3.07E-02	up	3.87	477
STEAP4	Homo sapiens STEAP family member 4 (STEAP4), transcript variant 2, mRNA [NM_001205315]	gene	1.10E-09	3.29E-05	up	20.56	Not used
STEAP4	Homo sapiens STEAP family member 4 (STEAP4), transcript variant 2, mRNA [NM_001205315]	gene	3.04E-15	9.24E-11	up	65.17	179
STOM	Homo sapiens stomatin (STOM), transcript variant 2, mRNA [NM_198194]	gene	2.26E-07	6.58E-03	up	12.86	625
STX3	Homo sapiens syntaxin 3 (STX3), transcript variant 1, mRNA [NM_004177]	gene	2.30E-08	6.80E-04	up	19.40	624
SUPT20HL1	Homo sapiens suppressor of Ty 20 homolog (S. cerevisiae)-like 1 (SUPT20HL1), mRNA [NM_001136234]	gene	2.68E-07	7.79E-03	down	-4.17	1258
SUV420H2	suppressor of variegation 4-20 homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:28405] [ENST00000402499]	gene	1.48E-06	4.22E-02	down	-2.48	949
SVEP1	Homo sapiens sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 (SVEP1), mRNA [NM_153366]	gene	2.02E-08	5.96E-04	down	-5.06	1180
SVIL	Homo sapiens supervillin (SVIL), transcript variant 2, mRNA [NM_021738]	gene	9.52E-14	2.89E-09	up	41.66	85
SYCP1	Homo sapiens synaptonemal complex protein 1 (SYCP1), transcript variant 1, mRNA [NM_003176]	gene	3.00E-07	8.71E-03	down	-3.13	1067
SYNE1	Homo sapiens spectrin repeat containing, nuclear envelope 1 (SYNE1), transcript variant 2, mRNA [NM_033071]	gene	3.24E-11	9.76E-07	up	16.70	740
SYNJ1	Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 2, mRNA [NM_203446]	gene	1.18E-06	3.36E-02	up	3.25	460
SYNJ2	synaptojanin 2 [Source:HGNC Symbol;Acc:HGNC:11504] [ENST00000449320]	gene	7.44E-07	2.14E-02	down	-4.01	1274
SYNM	Homo sapiens synemin, intermediate filament protein (SYNM), transcript variant A, mRNA [NM_145728]	gene	1.46E-08	4.31E-04	up	11.46	373
SYT2	Homo sapiens synaptotagmin II (SYT2), transcript variant 2, mRNA [NM_001136504]	gene	3.02E-07	8.75E-03	down	-3.58	1261
TAAR8	Homo sapiens trace amine associated receptor 8 (TAAR8), mRNA [NM_053278]	gene	4.18E-07	1.21E-02	down	-4.34	1253
TACSTD2	Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA [NM_002353]	gene	5.08E-11	1.53E-06	up	10.92	215
TALDO1	Homo sapiens transaldolase 1 (TALDO1), mRNA [NM_006755]	gene	1.40E-06	3.98E-02	up	9.00	650
TAPT1-AS1	Homo sapiens TAPT1 antisense RNA 1 (head to head) (TAPT1-AS1), transcript variant 1, long non-coding RNA [NR_027696]	ncRNA	4.42E-08	1.30E-03	down	-2.04	Not used
TARP	Homo sapiens TCR gamma alternate reading frame protein (TARP), transcript variant 1, mRNA [NM_001003799]	gene	5.91E-10	1.77E-05	up	38.87	587
TAS2R9	Homo sapiens taste receptor, type 2, member 9 (TAS2R9), mRNA [NM_023917]	gene	3.80E-07	1.10E-02	down	-4.90	1214
TBC1D2	Homo sapiens TBC1 domain family, member 2 (TBC1D2), transcript variant 1, mRNA [NM_001267571]	gene	1.41E-08	4.17E-04	up	5.63	819
TBC1D4	Homo sapiens TBC1 domain family, member 4 (TBC1D4), transcript variant 1, mRNA [NM_014832]	gene	1.28E-11	3.86E-07	up	19.63	798
TBC1D8	Homo sapiens TBC1 domain family, member 8 (with GRAM domain) (TBC1D8), mRNA [NM_001102426]	gene	3.37E-09	1.00E-04	up	17.40	596
TBL3	transducin (beta)-like 3 [Source:HGNC Symbol;Acc:HGNC:11587] [ENST00000568546]	gene	4.73E-07	1.37E-02	down	-2.16	895
TBX10	Homo sapiens T-box 10 (TBX10), mRNA [NM_005995]	gene	1.37E-06	3.91E-02	down	-2.57	1020
TBX21	Homo sapiens T-box 21 (TBX21), mRNA [NM_013351]	gene	8.50E-07	2.44E-02	up	2.76	422
TBXAS1	Homo sapiens thromboxane A synthase 1 (platelet) (TBXAS1), transcript variant 2, mRNA [NM_030984]	gene	2.45E-08	7.23E-04	up	4.87	500
TC2N	Homo sapiens tandem C2 domains, nuclear (TC2N), transcript variant 1, mRNA [NM_152332]	gene	1.66E-11	5.00E-07	up	31.26	589
TCEANC2	Homo sapiens transcription elongation factor A (SII) N-terminal and central domain containing 2 (TCEANC2), mRNA [NM_153035]	gene	5.35E-07	1.54E-02	down	-1.94	1119
TCF7L2	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), transcript variant 13, mRNA [NM_001198531]	gene	8.75E-07	2.51E-02	up	5.21	Not used
TCF7L2	Homo sapiens transcription factor 7-like 2 (T-cell specific, HMG-box) (TCF7L2), transcript variant 2, mRNA [NM_030756]	gene	8.49E-13	2.57E-08	up	6.47	513
TCN1	Homo sapiens transcobalamin I (vitamin B12 binding protein, R binder family) (TCN1), mRNA [NM_001062]	gene	5.82E-12	1.76E-07	up	29.64	201
TCTE1	Homo sapiens t-complex-associated-testis-expressed 1 (TCTE1), mRNA [NM_182539]	gene	9.33E-08	2.73E-03	down	-5.19	1074
TENM1	Homo sapiens teneurin transmembrane protein 1 (TENM1), transcript variant 1, mRNA [NM_001163278]	gene	1.08E-09	3.22E-05	up	4.58	490
TEX101	Homo sapiens testis expressed 101 (TEX101), transcript variant 1, mRNA [NM_031451]	gene	2.47E-07	7.16E-03	down	-3.09	1208
TFF1	Homo sapiens trefoil factor 1 (TFF1), mRNA [NM_003225]	gene	3.00E-07	8.70E-03	down	-2.83	976
TFF3	Homo sapiens trefoil factor 3 (intestinal) (TFF3), mRNA [NM_003226]	gene	3.39E-08	9.98E-04	up	6.20	216
TGIF1	Homo sapiens TGFB-induced factor homeobox 1 (TGIF1), transcript variant 5, mRNA [NM_173209]	gene	4.33E-07	1.25E-02	down	-3.48	990
TGIF2LY	Homo sapiens TGFB-induced factor homeobox 2-like, Y-linked (TGIF2LY), mRNA [NM_139214]	gene	6.26E-07	1.80E-02	down	-3.52	1270
TGM3	Homo sapiens transglutaminase 3 (TGM3), mRNA [NM_003245]	gene	7.29E-07	2.09E-02	up	5.69	825
THBD	Homo sapiens thrombomodulin (THBD), mRNA [NM_000361]	gene	2.31E-12	6.99E-08	up	125.50	56
THEMIS	Homo sapiens thymocyte selection associated (THEMIS), transcript variant 1, mRNA [NM_001164685]	gene	7.52E-12	2.27E-07	up	50.10	799
TIAM1	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA [NM_003253]	gene	2.27E-12	6.87E-08	up	87.62	569
TIMD4	Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), transcript variant 1, mRNA [NM_138379]	gene	5.91E-07	1.70E-02	up	5.88	Not used
TIMD4	Homo sapiens T-cell immunoglobulin and mucin domain containing 4 (TIMD4), transcript variant 1, mRNA [NM_138379]	gene	5.46E-07	1.57E-02	up	6.08	334
TKT	Homo sapiens transketolase (TKT), transcript variant 1, mRNA [NM_001064]	gene	5.31E-09	1.58E-04	up	6.82	669
TLR2	Homo sapiens toll-like receptor 2 (TLR2), mRNA [NM_003264]	gene	2.54E-07	7.37E-03	up	25.01	626
TLR4	Homo sapiens toll-like receptor 4 (TLR4), transcript variant 1, mRNA [NM_138554]	gene	2.23E-09	6.66E-05	up	49.98	Not used
TLR4	Homo sapiens toll-like receptor 4 (TLR4), transcript variant 1, mRNA [NM_138554]	gene	1.15E-08	3.40E-04	up	119.63	183
TLR8	Homo sapiens toll-like receptor 8 (TLR8), transcript variant 1, mRNA [NM_016610]	gene	1.17E-13	3.55E-09	up	102.35	571
TM6SF1	Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), transcript variant 1, mRNA [NM_023003]	gene	7.65E-11	2.30E-06	up	13.60	759
TMCO4	Homo sapiens transmembrane and coiled-coil domains 4 (TMCO4), mRNA [NM_181719]	gene	1.37E-06	3.92E-02	down	-2.23	1205
TMEM119	Homo sapiens transmembrane protein 119 (TMEM119), mRNA [NM_181724]	gene	2.52E-07	7.31E-03	up	5.70	338
TMEM151B	Homo sapiens transmembrane protein 151B (TMEM151B), mRNA [NM_001137560]	gene	7.78E-08	2.28E-03	down	-4.05	1239
TMEM158	Homo sapiens transmembrane protein 158 (gene/pseudogene) (TMEM158), mRNA [NM_015444]	gene	5.06E-07	1.46E-02	up	7.48	245
TMEM164	Homo sapiens transmembrane protein 164 (TMEM164), transcript variant 2, mRNA [NM_032227]	gene	2.90E-08	8.56E-04	up	5.09	405
TMEM170B	Homo sapiens transmembrane protein 170B (TMEM170B), mRNA [NM_001100829]	gene	1.37E-06	3.90E-02	up	8.36	Not used
TMEM170B	Homo sapiens transmembrane protein 170B (TMEM170B), mRNA [NM_001100829]	gene	2.37E-07	6.89E-03	up	13.09	688
TMEM173	Homo sapiens transmembrane protein 173 (TMEM173), transcript variant 1, mRNA [NM_198282]	gene	1.02E-12	3.08E-08	up	12.43	332
TMEM176B	Homo sapiens transmembrane protein 176B (TMEM176B), transcript variant 1, mRNA [NM_014020]	gene	1.61E-07	4.69E-03	up	19.90	753
TMEM45B	Homo sapiens transmembrane protein 45B (TMEM45B), mRNA [NM_138788]	gene	4.68E-11	1.41E-06	up	34.74	263
TMEM51	Homo sapiens transmembrane protein 51 (TMEM51), transcript variant 1, mRNA [NM_001136216]	gene	1.39E-12	4.20E-08	up	31.93	267
TMEM88B	Homo sapiens transmembrane protein 88B (TMEM88B), mRNA [NM_001146685]	gene	1.78E-07	5.17E-03	down	-2.72	903
TMEM8C	Homo sapiens transmembrane protein 8C (TMEM8C), mRNA [NM_001080483]	gene	1.32E-06	3.75E-02	down	-2.60	1128
TMEM91	Homo sapiens transmembrane protein 91 (TMEM91), transcript variant 5, mRNA [NM_001098824]	gene	9.89E-07	2.83E-02	up	3.66	402
TMPRSS4-AS1	Homo sapiens TMPRSS4 antisense RNA 1 (TMPRSS4-AS1), long non-coding RNA [NR_038318]	ncRNA	1.56E-13	4.73E-09	down	-10.78	Not used
TMSB4X	Homo sapiens thymosin beta 4, X-linked (TMSB4X), mRNA [NM_021109]	gene	3.77E-08	1.11E-03	up	3.60	473
TNFAIP2	Homo sapiens tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA [NM_006291]	gene	3.52E-13	1.07E-08	up	896.56	33
TNFAIP6	Homo sapiens tumor necrosis factor, alpha-induced protein 6 (TNFAIP6), mRNA [NM_007115]	gene	1.27E-12	3.84E-08	up	167.18	76
TNFAIP8L1	Homo sapiens tumor necrosis factor, alpha-induced protein 8-like 1 (TNFAIP8L1), transcript variant 1, mRNA [NM_001167942]	gene	4.47E-09	1.33E-04	down	-2.80	1149
TNFRSF10C	Homo sapiens tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain (TNFRSF10C), mRNA [NM_003841]	gene	5.39E-19	1.64E-14	up	1439.47	23
TNFRSF1A	Homo sapiens tumor necrosis factor receptor superfamily, member 1A (TNFRSF1A), mRNA [NM_001065]	gene	3.60E-08	1.06E-03	up	12.11	676
TNFRSF25	Homo sapiens tumor necrosis factor receptor superfamily, member 25 (TNFRSF25), transcript variant 12, mRNA [NM_001039664]	gene	3.69E-13	1.12E-08	up	7.83	Not used
TNFRSF25	Homo sapiens tumor necrosis factor receptor superfamily, member 25 (TNFRSF25), transcript variant 1, mRNA [NM_148965]	gene	2.38E-11	7.17E-07	up	60.89	141
TNFSF10	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), transcript variant 1, mRNA [NM_003810]	gene	1.30E-06	3.71E-02	up	10.26	Not used
TNFSF10	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10), transcript variant 1, mRNA [NM_003810]	gene	1.55E-07	4.51E-03	up	11.47	763
TNFSF13B	Homo sapiens tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B), transcript variant 1, mRNA [NM_006573]	gene	6.09E-10	1.82E-05	up	12.69	748
TNFSF14	Homo sapiens tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14), transcript variant 1, mRNA [NM_003807]	gene	2.71E-10	8.12E-06	up	28.20	827
TNFSF8	Homo sapiens tumor necrosis factor (ligand) superfamily, member 8 (TNFSF8), transcript variant 1, mRNA [NM_001244]	gene	1.00E-08	2.98E-04	up	5.69	821
TNIK	Homo sapiens TRAF2 and NCK interacting kinase (TNIK), transcript variant 9, non-coding RNA [NR_027767]	gene	1.08E-06	3.10E-02	up	7.70	Not used
TNIK	Homo sapiens TRAF2 and NCK interacting kinase (TNIK), transcript variant 1, mRNA [NM_015028]	gene	5.32E-08	1.56E-03	up	7.97	Not used
TNIK	Homo sapiens TRAF2 and NCK interacting kinase (TNIK), transcript variant 1, mRNA [NM_015028]	gene	1.31E-06	3.73E-02	up	24.42	526
TNRC18	Homo sapiens trinucleotide repeat containing 18 (TNRC18), mRNA [NM_001080495]	gene	8.94E-08	2.62E-03	up	3.51	483
TNS1	Homo sapiens tensin 1 (TNS1), mRNA [NM_022648]	gene	1.39E-06	3.95E-02	up	5.65	824
TONSL	Homo sapiens tonsoku-like, DNA repair protein (TONSL), mRNA [NM_013432]	gene	9.79E-08	2.86E-03	down	-2.57	1008
TOR2A	Homo sapiens torsin family 2, member A (TOR2A), transcript variant 3, mRNA [NM_001134430]	gene	2.88E-10	8.63E-06	down	-4.34	987
TP53TG3	Homo sapiens TP53 target 3 (TP53TG3), transcript variant 1, mRNA [NM_016212]	gene	3.66E-08	1.08E-03	down	-3.23	1145
TPD52L2	Homo sapiens tumor protein D52-like 2 (TPD52L2), transcript variant 1, mRNA [NM_199360]	gene	1.55E-06	4.39E-02	up	2.51	450

Gene Symbol	Description	Feature Type	p-value	Corrected p-value	Regulation in NOTCH1-mut	Fold change (Mut vs WT)	Position in Heatmap
TPP1	Homo sapiens tripeptidyl peptidase I (TPP1), mRNA [NM_000391]	gene	1.56E-07	4.55E-03	down	-3.26	991
TPSG1	Homo sapiens tryptase gamma 1 (TPSG1), mRNA [NM_024467]	gene	3.05E-08	8.98E-04	down	-6.27	861
TRABD2B	Homo sapiens TraB domain containing 2B (TRABD2B), mRNA [NM_001194986]	gene	1.30E-07	3.79E-03	down	-3.54	1062
TRAPPC3L	trafficking protein particle complex 3-like [Source:HGNC Symbol;Acc:HGNC:21090] [ENST00000356128]	gene	1.44E-07	4.20E-03	down	-2.41	1101
TRAT1	Homo sapiens T cell receptor associated transmembrane adaptor 1 (TRAT1), mRNA [NM_016388]	gene	2.57E-13	7.79E-09	up	80.70	578
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 2, mRNA [NM_001242589]	gene	4.63E-12	1.40E-07	up	112.66	Not used
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 1, mRNA [NM_018643]	gene	1.06E-14	3.22E-10	up	30.33	Not used
TREM1	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), transcript variant 1, mRNA [NM_018643]	gene	4.27E-18	1.30E-13	up	410.52	31
TREML4	Homo sapiens triggering receptor expressed on myeloid cells-like 4 (TREML4), mRNA [NM_198153]	gene	4.41E-09	1.31E-04	up	6.70	246
TRERF1	Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 1, mRNA [NM_001297573]	gene	2.18E-11	6.58E-07	up	23.52	770
TRERF1	Homo sapiens transcriptional regulating factor 1 (TRERF1), transcript variant 2, mRNA [NM_033502]	gene	1.38E-06	3.94E-02	up	15.90	Not used
TREX2	Homo sapiens three prime repair exonuclease 2 (TREX2), mRNA [NM_080701]	gene	9.75E-08	2.85E-03	down	-2.15	1107
TRGV7	Homo sapiens T cell receptor gamma variable 7 pseudogene, mRNA (cDNA clone IMAGE:5210958). [BC027954]	gene	9.54E-07	2.73E-02	up	7.71	222
TRIM16	tripartite motif containing 16 [Source:HGNC Symbol;Acc:HGNC:17241] [ENST00000582708]	gene	1.18E-06	3.36E-02	down	-2.71	1055
TRIM33	Homo sapiens tripartite motif containing 33 (TRIM33), transcript variant a, mRNA [NM_015906]	gene	9.42E-09	2.79E-04	up	2.03	435
TRIM46	Homo sapiens tripartite motif containing 46 (TRIM46), transcript variant 8, mRNA [NM_001282379]	gene	1.45E-08	4.29E-04	down	-3.04	904
TRPM6	Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), transcript variant a, mRNA [NM_017662]	gene	7.49E-11	2.25E-06	up	28.14	285
TSEN34	Homo sapiens TSEN34 tRNA splicing endonuclease subunit (TSEN34), transcript variant 3, mRNA [NM_001282332]	gene	9.27E-10	2.77E-05	up	7.52	670
TSHZ3	Homo sapiens teashirt zinc finger homeobox 3 (TSHZ3), mRNA [NM_020856]	gene	1.59E-13	4.82E-09	up	33.69	775
TSPAN14	Homo sapiens tetraspanin 14 (TSPAN14), transcript variant 1, mRNA [NM_030927]	gene	1.19E-06	3.39E-02	up	3.53	Not used
TSPAN14	Homo sapiens tetraspanin 14 (TSPAN14), transcript variant 1, mRNA [NM_030927]	gene	4.88E-10	1.46E-05	up	8.51	Not used
TSPAN14	Homo sapiens tetraspanin 14 (TSPAN14), transcript variant 1, mRNA [NM_030927]	gene	1.08E-07	3.16E-03	up	10.01	680
TSPAN16	Homo sapiens tetraspanin 16 (TSPAN16), transcript variant 1, mRNA [NM_012466]	gene	2.83E-13	8.58E-09	up	40.25	614
TSPAN2	Homo sapiens tetraspanin 2 (TSPAN2), mRNA [NM_005725]	gene	2.76E-07	8.00E-03	up	10.96	231
TSPAN4	Homo sapiens tetraspanin 4 (TSPAN4), transcript variant 1, mRNA [NM_001025237]	gene	7.23E-08	2.12E-03	up	6.43	510
TSPO2	Homo sapiens translocator protein 2 (TSPO2), transcript variant 1, mRNA [NM_001010873]	gene	1.49E-08	4.40E-04	down	-3.61	1252
TTC16	Homo sapiens tetratricopeptide repeat domain 16 (TTC16), mRNA [NM_144965]	gene	4.23E-10	1.27E-05	up	12.07	728
TTTY14	Homo sapiens testis-specific transcript, Y-linked 14 (non-protein coding) (TTTY14), transcript variant 5, long non-coding RNA [NR_001543]	gene	6.44E-09	1.91E-04	down	-2.82	1160
TTYH1	Homo sapiens tweety family member 1 (TTYH1), transcript variant 1, mRNA [NM_020659]	gene	3.80E-07	1.10E-02	down	-3.51	1259
TUSC1	Homo sapiens tumor suppressor candidate 1 (TUSC1), mRNA [NM_001004125]	gene	5.19E-10	1.55E-05	down	-6.25	1241
TUSC8	AGENCOURT_8883169 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6199956 5', mRNA sequence [BQ950045]	gene	1.65E-06	4.69E-02	down	-3.58	1167
TYROBP	Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP), transcript variant 1, mRNA [NM_003332]	gene	4.48E-10	1.34E-05	up	49.40	98
UBASH3A	Homo sapiens ubiquitin associated and SH3 domain containing A (UBASH3A), transcript variant 1, mRNA [NM_018961]	gene	1.02E-13	3.09E-09	up	33.46	800
UBE2E3	ubiquitin-conjugating enzyme E2E 3 [Source:HGNC Symbol;Acc:HGNC:12479] [ENST00000602837]	gene	3.44E-08	1.01E-03	down	-1.60	1113
UCP3	Homo sapiens uncoupling protein 3 (mitochondrial, proton carrier) (UCP3), transcript variant short, mRNA [NM_022803]	gene	2.04E-07	5.92E-03	down	-4.49	1226
UMODL1	uromodulin-like 1 [Source:HGNC Symbol;Acc:HGNC:12560] [ENST00000491559]	gene	3.45E-07	1.00E-02	down	-4.88	1246
UNC13B	Homo sapiens unc-13 homolog B (C. elegans) (UNC13B), mRNA [NM_006377]	gene	9.55E-07	2.73E-02	down	-4.12	1068
UPP1	Homo sapiens uridine phosphorylase 1 (UPP1), transcript variant 3, mRNA [NM_001287426]	gene	2.91E-10	8.72E-06	up	17.85	257
UPP1	Homo sapiens uridine phosphorylase 1 (UPP1), transcript variant 4, mRNA [NM_001287428]	gene	8.43E-11	2.53E-06	up	14.62	Not used
UTS2R	Homo sapiens urotensin 2 receptor (UTS2R), mRNA [NM_018949]	gene	1.49E-10	4.47E-06	down	-7.77	863
VANGL1	Homo sapiens VANGL planar cell polarity protein 1 (VANGL1), transcript variant 1, mRNA [NM_138959]	gene	1.11E-07	3.24E-03	up	11.99	729
VAPA	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), transcript variant 1, mRNA [NM_003574]	gene	1.05E-08	3.12E-04	up	3.16	439
VCAN	Homo sapiens versican (VCAN), transcript variant 1, mRNA [NM_004385]	gene	1.18E-17	3.58E-13	up	62.44	265
VCY	Homo sapiens variable charge, Y-linked (VCY), mRNA [NM_004679]	gene	3.36E-08	9.89E-04	down	-3.41	1267
VDR	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), transcript variant 2, mRNA [NM_001017535]	gene	5.36E-08	1.58E-03	up	18.43	828
VEGFA	Homo sapiens vascular endothelial growth factor A (VEGFA), transcript variant 1, mRNA [NM_001025366]	gene	3.78E-08	1.11E-03	up	12.00	839
VENTX	Homo sapiens VENT homeobox (VENTX), mRNA [NM_014468]	gene	1.41E-10	4.23E-06	up	15.26	304
VHL	Homo sapiens von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase (VHL), transcript variant 1, mRNA [NM_000551]	gene	2.17E-07	6.31E-03	down	-2.35	1012
VNN1	Homo sapiens vanin 1 (VNN1), mRNA [NM_004666]	gene	5.79E-14	1.76E-09	up	76.62	119
VNN2	Homo sapiens vanin 2 (VNN2), transcript variant 1, mRNA [NM_004665]	gene	2.52E-09	7.51E-05	up	16.40	637
VNN3	Homo sapiens vanin 3 (VNN3), transcript variant 5, mRNA [NM_001291703]	gene	2.62E-14	7.97E-10	up	27.61	259
VPS51	Homo sapiens vacuolar protein sorting 51 homolog (S. cerevisiae) (VPS51), transcript variant 1, mRNA [NM_013265]	gene	3.61E-07	1.05E-02	down	-1.71	1116
VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:25608] [ENST00000541903]	gene	2.18E-07	6.33E-03	down	-2.44	912
VSIG4	Homo sapiens V-set and immunoglobulin domain containing 4 (VSIG4), transcript variant 1, mRNA [NM_007268]	gene	1.33E-08	3.94E-04	up	8.60	692
VSTM1	Homo sapiens V-set and transmembrane domain containing 1 (VSTM1), transcript variant 1, mRNA [NM_198481]	gene	1.11E-12	3.35E-08	up	161.82	66
VSX1	Homo sapiens visual system homeobox 1 (VSX1), transcript variant 2, mRNA [NM_199425]	gene	8.60E-10	2.57E-05	down	-6.35	857
WASH1	Homo sapiens WAS protein family homolog 1 (WASH1), mRNA [NM_182905]	gene	6.04E-07	1.74E-02	down	-2.02	1081
WASH5P	Homo sapiens WAS protein family homolog 5 pseudogene (WASH5P), non-coding RNA [NR_033266]	gene	9.74E-07	2.79E-02	down	-2.07	1109
WBP1	Homo sapiens WW domain binding protein 1 (WBP1), mRNA [NM_012477]	gene	2.14E-07	6.23E-03	down	-2.15	962
WDFY3	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:HGNC:20751] [ENST00000426414]	gene	1.14E-18	3.48E-14	up	93.81	73
WDFY3	Homo sapiens WD repeat and FYVE domain containing 3 (WDFY3), mRNA [NM_014991]	gene	3.42E-15	1.04E-10	up	51.66	Not used
WDFY3-AS2	Homo sapiens WDFY3 antisense RNA 2 (WDFY3-AS2), long non-coding RNA [NR_015359]	ncRNA	3.05E-10	9.15E-06	up	8.75	Not used
WDR38	Homo sapiens WD repeat domain 38 (WDR38), transcript variant 2, mRNA [NM_001045476]	gene	3.55E-08	1.05E-03	down	-4.40	1072
WDR6	Homo sapiens WD repeat domain 6 (WDR6), mRNA [NM_018031]	gene	1.70E-07	4.96E-03	down	-1.92	1089
WLS	Homo sapiens wntless Wnt ligand secretion mediator (WLS), transcript variant 2, mRNA [NM_001002292]	gene	1.09E-09	3.25E-05	up	48.56	287
WLS	Homo sapiens wntless Wnt ligand secretion mediator (WLS), transcript variant 1, mRNA [NM_024911]	gene	1.36E-06	3.86E-02	up	13.62	Not used
WNT3A	Homo sapiens wingless-type MMTV integration site family, member 3A (WNT3A), mRNA [NM_033131]	gene	7.37E-07	2.11E-02	down	-2.31	1022
WNT7B	Homo sapiens wingless-type MMTV integration site family, member 7B (WNT7B), mRNA [NM_058238]	gene	4.02E-07	1.16E-02	down	-2.79	1154
WWOX	Homo sapiens WW domain containing oxidoreductase (WWOX), transcript variant 3, non-coding RNA [NR_120435]	gene	1.33E-06	3.79E-02	down	-2.91	1069
XLOC_l2_000123	BROAD Institute lincRNA (XLOC_l2_000123), lincRNA [TCONS_l2_00000181]	lincRNA	7.79E-07	2.23E-02	up	1.72	Not used
XLOC_l2_000900	BROAD Institute lincRNA (XLOC_l2_000900), lincRNA [TCONS_l2_00001221]	lincRNA	3.42E-09	1.02E-04	down	-4.87	Not used
XLOC_l2_001483	BROAD Institute lincRNA (XLOC_l2_001483), lincRNA [TCONS_l2_00002890]	lincRNA	1.65E-06	4.68E-02	down	-2.22	Not used
XLOC_l2_001760	BROAD Institute lincRNA (XLOC_l2_001760), lincRNA [TCONS_l2_00003281]	lincRNA	2.00E-07	5.83E-03	down	-3.06	Not used
XLOC_l2_003758	BROAD Institute lincRNA (XLOC_l2_003758), lincRNA [TCONS_l2_00006892]	lincRNA	8.80E-07	2.52E-02	down	-2.86	Not used
XLOC_l2_004072	BROAD Institute lincRNA (XLOC_l2_004072), lincRNA [TCONS_l2_00007295]	lincRNA	1.02E-06	2.91E-02	down	-2.75	Not used
XLOC_l2_004315	BROAD Institute lincRNA (XLOC_l2_004315), lincRNA [TCONS_l2_00007925]	lincRNA	1.12E-06	3.19E-02	down	-4.43	Not used
XLOC_l2_004594	BROAD Institute lincRNA (XLOC_l2_004594), lincRNA [TCONS_l2_00008470]	lincRNA	9.12E-08	2.67E-03	down	-2.52	Not used
XLOC_l2_004844	BROAD Institute lincRNA (XLOC_l2_004844), lincRNA [TCONS_l2_00008932]	lincRNA	1.61E-08	4.76E-04	down	-4.10	Not used
XLOC_l2_005415	BROAD Institute lincRNA (XLOC_l2_005415), lincRNA [TCONS_l2_00010039]	lincRNA	2.04E-09	6.09E-05	down	-3.04	Not used
XLOC_l2_005490	BROAD Institute lincRNA (XLOC_l2_005490), lincRNA [TCONS_l2_00010170]	lincRNA	2.59E-09	7.73E-05	up	12.86	Not used
XLOC_l2_005933	BROAD Institute lincRNA (XLOC_l2_005933), lincRNA [TCONS_l2_00011027]	lincRNA	3.79E-07	1.10E-02	down	-3.15	Not used
XLOC_l2_006025	BROAD Institute lincRNA (XLOC_l2_006025), lincRNA [TCONS_l2_00011143]	lincRNA	1.21E-06	3.45E-02	down	-4.10	Not used
XLOC_l2_006196	BROAD Institute lincRNA (XLOC_l2_006196), lincRNA [TCONS_l2_00011463]	lincRNA	6.64E-10	1.99E-05	up	28.81	Not used
XLOC_l2_006926	BROAD Institute lincRNA (XLOC_l2_006926), lincRNA [TCONS_l2_00012876]	lincRNA	6.91E-09	2.05E-04	down	-5.39	Not used
XLOC_l2_006958	BROAD Institute lincRNA (XLOC_l2_006958), lincRNA [TCONS_l2_00012917]	lincRNA	5.02E-07	1.45E-02	down	-2.58	Not used
XLOC_l2_007135	BROAD Institute lincRNA (XLOC_l2_007135), lincRNA [TCONS_l2_00013243]	lincRNA	1.61E-06	4.58E-02	down	-3.72	Not used
XLOC_l2_007767	BROAD Institute lincRNA (XLOC_l2_007767), lincRNA [TCONS_l2_00014250]	lincRNA	1.13E-08	3.34E-04	down	-2.62	Not used
XLOC_l2_007967	BROAD Institute lincRNA (XLOC_l2_007967), lincRNA [TCONS_l2_00014514]	lincRNA	1.76E-06	4.98E-02	down	-2.59	Not used
XLOC_l2_008013	BROAD Institute lincRNA (XLOC_l2_008013), lincRNA [TCONS_l2_00014567]	lincRNA	3.59E-09	1.07E-04	up	26.78	Not used
XLOC_l2_009328	BROAD Institute lincRNA (XLOC_l2_009328), lincRNA [TCONS_l2_00017652]	lincRNA	3.12E-08	9.21E-04	down	-2.79	Not used
XLOC_l2_009469	BROAD Institute lincRNA (XLOC_l2_009469), lincRNA [TCONS_l2_00017900]	lincRNA	1.01E-07	2.96E-03	down	-4.71	Not used
XLOC_l2_009639	BROAD Institute lincRNA (XLOC_l2_009639), lincRNA [TCONS_l2_00018461]	lincRNA	6.46E-07	1.86E-02	up	5.15	Not used
XLOC_l2_009773	BROAD Institute lincRNA (XLOC_l2_009773), lincRNA [TCONS_l2_00018665]	lincRNA	4.95E-07	1.43E-02	down	-2.57	Not used
XLOC_l2_009867	BROAD Institute lincRNA (XLOC_l2_009867), lincRNA [TCONS_l2_00018819]	lincRNA	1.18E-07	3.46E-03	down	-2.91	Not used
XLOC_l2_010493	BROAD Institute lincRNA (XLOC_l2_010493), lincRNA [TCONS_l2_00019671]	lincRNA	6.61E-10	1.98E-05	down	-2.43	Not used
XLOC_l2_010751	BROAD Institute lincRNA (XLOC_l2_010751), lincRNA [TCONS_l2_00020645]	lincRNA	2.14E-07	6.23E-03	down	-3.66	Not used
XLOC_l2_010888	BROAD Institute lincRNA (XLOC_l2_010888), lincRNA [TCONS_l2_00021752]	lincRNA	1.43E-07	4.18E-03	down	-3.26	Not used
XLOC_l2_011048	BROAD Institute lincRNA (XLOC_l2_011048), lincRNA [TCONS_l2_00021062]	lincRNA	1.10E-06	3.13E-02	down	-3.43	Not used
XLOC_l2_011426	BROAD Institute lincRNA (XLOC_l2_011426), lincRNA [TCONS_l2_00022102]	lincRNA	7.66E-08	2.25E-03	down	-5.33	Not used
XLOC_l2_015033	BROAD Institute lincRNA (XLOC_l2_015033), lincRNA [TCONS_l2_00029054]	lincRNA	4.03E-11	1.21E-06	up	16.44	Not used
XPO6	Homo sapiens exportin 6 (XPO6), transcript variant 1, mRNA [NM_001270940]	gene	5.02E-07	1.45E-02	up	3.96	353
YJEFN3	Homo sapiens YjeF N-terminal domain containing 3 (YJEFN3), transcript variant 1, mRNA [NM_198537]	gene	1.41E-08	4.17E-04	down	-4.05	1240
YTHDF2	Homo sapiens YTH N(6)-methyladenosine RNA binding protein 2 (YTHDF2), transcript variant 2, mRNA [NM_001173128]	gene	7.21E-07	2.07E-02	down	-2.69	947
ZAK	Homo sapiens sterile alpha motif and leucine zipper containing kinase AZK (ZAK), transcript variant 2, mRNA [NM_133646]	gene	1.42E-06	4.05E-02	up	18.58	712
ZDHHC18	Homo sapiens zinc finger, DHHC-type containing 18 (ZDHHC18), mRNA [NM_032283]	gene	2.11E-07	6.15E-03	up	5.03	345
ZG16B	Homo sapiens zymogen granule protein 16B (ZG16B), mRNA [NM_145252]	gene	7.47E-07	2.14E-02	up	5.38	354
ZMIZ1	Homo sapiens zinc finger, MIZ-type containing 1 (ZMIZ1), mRNA [NM_020338]	gene	8.31E-10	2.49E-05	up	39.92	551
ZNF205	Homo sapiens zinc finger protein 205 (ZNF205), transcript variant 1, mRNA [NM_003456]	gene	1.29E-12	3.89E-08	down	-11.17	875
ZNF329	zinc finger protein 329 [Source:HGNC Symbol;Acc:HGNC:14209] [ENST00000601887]	gene	7.72E-09	2.29E-04	down	-5.27	1168
ZNF438	Homo sapiens zinc finger protein 438 (ZNF438), transcript variant 2, mRNA [NM_182755]	gene	1.23E-06	3.50E-02	up	3.86	Not used
ZNF438	zinc finger protein 438 [Source:HGNC Symbol;Acc:HGNC:21029] [ENST00000609683]	gene	5.50E-08	1.62E-03	up	11.37	380
ZNF467	Homo sapiens zinc finger protein 467 (ZNF467), mRNA [NM_207336]	gene	2.39E-08	7.05E-04	down	-13.51	882
ZNF488	Homo sapiens zinc finger protein 488 (ZNF488), mRNA [NM_153034]	gene	1.27E-06	3.63E-02	down	-2.98	977
ZNF503	Homo sapiens zinc finger protein 503 (ZNF503), transcript variant 1, mRNA [NM_032772]	gene	2.62E-12	7.92E-08	up	38.71	292
ZNF618	Homo sapiens zinc finger protein 618 (ZNF618), mRNA [NM_133374]	gene	1.69E-08	5.01E-04	up	7.87	765
ZNF763	Homo sapiens zinc finger protein 763 (ZNF763), mRNA [NM_001012753]	gene	5.76E-07	1.66E-02	down	-2.04	1100
ZNF890P	Homo sapiens zinc finger protein 890, pseudogene (ZNF890P), non-coding RNA [NR_034163]	gene	4.13E-07	1.19E-02	down	-2.54	1272
ZNF99	Homo sapiens zinc finger protein 99 (ZNF99), mRNA [NM_001080409]	gene	1.30E-06	3.72E-02	down	-2.50	1141
ZSCAN12P1	Homo sapiens zinc finger and SCAN domain containing 12 pseudogene 1 (ZSCAN12P1), non-coding RNA [NR_024063]	gene	3.61E-08	1.06E-03	down	-2.04	959
ZYX	Homo sapiens zyxin (ZYX), transcript variant 1, mRNA [NM_003461]	gene	5.14E-07	1.48E-02	up	5.71	357

Supplementary Table 5. Gene Set Enrichment Analysis of *Notch* -related datasets.

				NOTCH1 **-mut vs. WT**					***SF3B1*** **-mut vs. WT**			
Name	**Description**	**Collection**	**Total size**	**Size**	**NES**	**p-value**	**FDR q-value**	**Colonn**	**Size2**	**NES3**	**p-value4**	**FDR q-value5**
PID_NOTCH_PATHWAY	Notch signaling pathway	C2-CP	61	51	1	0.429	0.384		51	-0.89	0.669	1
KEGG_NOTCH_SIGNALING_PATHWAY	Notch signaling pathway	C2-CP KEGG	49	43	1.17	0.214	0.235		43	0.71	0.916	0.858
REACTOME_ACTIVATED_NOTCH1_TRANSMITS_SIGNAL_TO_THE_NUCLEUS	Genes involved in Activated NOTCH1 Transmits Signal to the Nucleus	C2-CP Reactome	29	20	1.43	0.044	0.074		20	1.06	0.369	0.388
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	Genes involved in NOTCH1 Intracellular Domain Regulates Transcription	C2-CP Reactome	48	40	1.04	0.397	0.38		40	1.17	0.204	0.258
REACTOME_SIGNALING_BY_NOTCH1	Genes involved in Signaling by NOTCH1	C2-CP Reactome	72	58	1.3	0.099	0.145		58	1.29	0.085	0.158
NGUYEN_NOTCH1_TARGETS_DN	Genes down-regulated in primary keratinocytes by expression of constantly active NOTCH1	C2-CPG	88	74	1.69	0.01	0.016		74	1.75	0.002	0.016
NGUYEN_NOTCH1_TARGETS_UP	Genes up-regulated in primary keratinocytes by expression of constantly active NOTCH1	C2-CPG	31	24	1.27	0.156	0.157		24	-0.88	0.689	0.943
VILIMAS_NOTCH1_TARGETS_DN	Genes down-regulated in bone marrow progenitors by constitutively active NOTCH1	C2-CPG	22	18	1.73	<0,001	0.019		18	1.83	0.006	0.016
VILIMAS_NOTCH1_TARGETS_UP	Genes up-regulated in bone marrow progenitors by constitutively active NOTCH1	C2-CPG	54	48	2.04	<0,001	<0,001		48	2.12	<0,001	<0,001
GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	Any process that stops, prevents, or reduces the frequency, rate or extent of the Notch signaling pathway	C5-BP	30	18	1.53	0.046	0.043		18	1.67	0.03	0.023
GO_NOTCH_SIGNALING_PATHWAY	A series of molecular signals initiated by the binding of an extracellular ligand to the receptor Notch on the surface of a target cell, and ending with regulation of a downstream cellular process, e.g. transcription.	C5-BP	116	82	1.03	0.369	0.367		82	0.73	0.912	0.895
GO_POSITIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	Any process that activates or increases the frequency, rate or extent of the Notch signaling pathway	C5-BP	36	24	1.46	0.043	0.066		24	1.64	0.012	0.023
GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	Any process that modulates the frequency, rate or extent of the Notch signaling pathway	C5-BP	69	46	1.59	<0,001	0.028		46	1.72	0.006	0.019
NOTCH_DN_V1_DN	Genes down-regulated in MOLT4 cells (T-ALL) by DAPT [PubChem=16219261], an inhibitor of NOTCH signaling pathway	C6	191	125	1.88	<0,001	0.006		125	1.78	<0,001	0.015
NOTCH_DN_V1_UP	Genes up-regulated in MOLT4 cells (T-ALL) by DAPT [PubChem=16219261], an inhibitor of NOTCH signaling pathway.	C6	195	119	1.68	<0,001	0.015		119	1.47	0.018	0.06
FABBRI_NOTCH_SIGNALING	NOTCH1-dependent CLL signature from Fabbri et al.	Custom	293	270	1.71	<0,001	0.019		270	1.57	0.016	0.038
Hallmark_NOTCH_signaling	Genes up-regulated by activation of Notch signaling	H	34	26	1.65	0.002	0.019		26	1.49	0.037	0.062