Cell, Volume *137*

Supplemental Data

A Genome-wide RNAi Screen Identifies Multiple Synthetic Lethal Interactions with the Ras Oncogene

Ji Luo, Michael J. Emanuele, Danan Li, Chad J. Creighton, Michael R. Schlabach, Thomas F. Westbrook, Kwok-kin Wong, and Stephen J. Elledge

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

shRNA library screen and micoarray hybridization

The pool-based shRNA screen using half-hairpin (HH) barcode deconvolution was carried out as described before (Schlabach et al., 2008). Briefly, DLD-1 Ras mutant (Mut) or wildtype (WT) cells were infected with pools of retroviral shRNA at a representation of ~1,000 and a multiplicity of infection (MOI) of ~1. At day 3 post infection an initial, population-doubling 0 (PD0) sample was taken. The rest of the population were selected with puromycin to remove the minority of uninfected cells and propagated in culture for an additional 17 doublings before the final, PD17 sample was taken. For each passage a minimal representation of 1000 was maintained. Our genomic shRNA library containing 74,905 retroviral shRNAs targeting 32,293 unique human gene transcripts (including 19,542 RefSeqs) were screened as 6 pools of ~13,000 shRNAs per pool in independent triplicates. For each pair of corresponding PD0 and PD17 samples, shRNA HH barcode was PCR-recovered from genomic samples and labeled with Cy5 and Cy3 dyes, respectively. The labeled HH barcode amplicons were competitively hybridized to a microarray containing the corresponding probes. Custom microarrays with HH barcode probe sequences were from Roche Nimblegen. Array hybridization and scanning protocols were based on manufacturer's instructions. The genome-wide mir30 shRNA library was expressed using the retroviral vector MSCV-PM (Schlabach et al., 2008) and is available through Open Biosystems Inc.

Statistical and bioinformatics analysis of shRNA screen

Only informative probes (i.e. those with raw signal 2-fold above negative control probes) were used for analysis. The change in the relative abundance of each shRNA in the library over time is measured using the normalized Cy3/Cy5 ratio of its probe signal (Schlabach et al., 2008). A log2 Cy3/Cy5 ratio of < 0 indicates the shRNA is depleted in the population over time. To identify shRNAs that are synthetically lethal with mutant Ras, the mean log2 Cy3/Cy5 ratios of the Ras Mut triplicates were compared to that of the Ras WT triplicates to derive the log2 ratio difference. A *p*-value of the difference between the two triplicates was calculated using the t-test. A extended list of candidate shRNAs (**Table S1**) were obtained by using a set of cutoff that requires the Ras Mut log2 ratio ≤ –0.7, Ras WT log ratio ≥ –2, the difference in log2 ratios between Ras Mut and Ras WT to be ≤ –0.7, and the *p*-value to be ≤ 0.3. By reducing the *p*-value to ≤ 0.1 a shorter candidate list is obtained (**Table S2**). As the overall validation rate is relatively low (26.7%), we use the statistical analysis mainly as a guide to prioritize candidates for further test and validation. Functional categorization of candidate RSL genes was done using PANTHER (Thomas et al., 2003).

Analysis of human lung tumor profiles

A gene signature of *KRAS* mutant versus *KRAS* wild-type tumors was defined, using a published dataset of 84 lung adenocarcimos from a study by Bhattacharjee *et al*. (Bhattacharjee et al., 2001) for which the *KRAS* mutation status of each tumor was known (genes with $P<0.01$, two-sided *t*-test were selected). This *KRAS* signature was validated by both gene signature similarity scores and by gene set enrichment analysis using two independent cohorts of lung cancer where the KRAS mutation status was known for the tumors (Ding et al., 2008; Beer et al., 2002), (**Figure S8**). This *KRAS* gene signature was then applied to analyze a gene expression profile dataset of 442 human lung adenocarcinomas by Shedden *et al*. (Shedden et al., 2008). Each tumor was scored for manifestation of the Ras pathway by the following. The Shedden tumor profiles were generated among four laboratories, and so within each laboratory subset, expression values for each gene were normalized to standard deviations from the mean. Within each Shedden tumor profile, the average of the genes high (“up”) in the Bhattacharjee *KRAS* signature were compared with the average of the genes low (“down”) in the signature: tumors with higher expression of the “up” genes as compared to the “down” genes ($P<0.01$, t-test) were classified as showing Ras pathway manifestation (“Ras signature+”); tumors with higher expression of the “down” genes ($P<0.01$) were classified as not showing Ras pathway manifestation (“Ras signature–”); tumors that were intermediate between the above two groups were not used in subsequent analyses. Within the Shedden “Ras signature+” tumors (N=143), tumors with expression levels greater than the median for the given candidate RSL gene were compared with the rest of the tumors in the subset, using Kaplan-Meier analysis for time to patient death. In addition, univariate Cox analysis evaluated the expression of the given gene as a continuous variable for correlation with outcome. The same Kaplan-Meier and Cox analyses were also carried out using the Shedden “Ras signature-” tumors (N=116). To correct for multiple hypothesis testing, we carried out simulation tests to estimate the probability of obtaining 3 out of 24 APC/C and COPS9 signalosome associated genes that both had a *p*-value of <0.05 and whose relative expression levels changed in the predicted direction in *KRAS* mutant tumors. Based on these criteria, the expected number of chance significant hits was 0.57 genes (based on 1000 simulations, where both survival *p*-value and direction of change was randomly generated for each of the 24 genes), and the probability of getting 3 or more genes due to multiple testing was $p = 0.02$.

The multi-color competition (MCA) assay

The competition assay used to test candidate genes from the screen was modified from a previous protocol (Torrance et al., 2001; Smogorzewska et al., 2007) and was carried out in 96-well plates in independent triplicates. For this assay, 1,000 each of GFP-labeled Ras

Mut and unlabeled Ras WT cells were seeded in each well. For retroviral shRNA infection, cells were infected at an MOI of 1–5, selected for 3 days with puromycin and propagated for an additional 4–5 days before analyzed by FACS. An shRNA targeting firefly luciferase (shRNA-FF) was used as the negative control. For siRNA transfection, cells were transfected with siGenome siRNAs (Dharmacon) using Lipofectamine RNAiMAX (InVitrogen) and analyzed by FACS 5–6 days post transfection An siRNA targeting luciferase (Luc) was used as the negative control. For drug treatment, cells were treated with drugs for 4-5 days prior to FACS analysis. Untreated wells were used as negative controls. To obtain normalized fitness of Ras Mut cells that can be compared across experiments, the percentage of Ras Mut cells in each sample was normalized to that in the control samples of that experiment. This results in a "normalized mutant fitness" that range from 0% (no Ras mut cells left in population) to 100% (same number of Ras mut cells as control wells). These results have been verified using cell viability assays employing Cell TiterGlo (Promega)

Cell cycle analysis

For cell cycle analysis, cells were ethanol fixed and stained with PI and analyzed using a BD LSR II FACS analyzer (BD Bioscience). Data analysis was carried out with BD FACS Diva and FlowJo softwares. Cell cycle synchronization by double thymidine block was based on a previous protocol (Steegmaier et al., 2007). Briefly, cells were arrested with two rounds of 20-hour thymidine (2.5mM) treatment approximately 12 hours apart and released into mitosis. To trap cells at different stages of mitosis, cells release from double thymidine block were released into the CDK1 inhibitor RO-3306 (10μM) (Vassilev et al., 2006), the PLK1 inhibitor BI-2536 (100nM) (Steegmaier et al., 2007) and the microtubule depolymerizer nocodazle (100ng/ml). For one-step arrest in G2/M or in prometaphase, cells were treated overnight with either RO-3306 (10μM) or the Eg5 kinesin inhibitor monastrol (100μM), respectively. For mitotic entry experiments, cells were synchronized in RO-3306 (10uM) overnight prior to release. For mitotic release experiments, cells were released from overnight synchronization in RO-3306 (10uM) into nocodazole (200ug/ml) for 4 hours and mitotic cells were collected by mitotic shake-off. Cells were then release by washing out the nocodazole. For the analysis of lagging chromosomes and mitotic index by microscopy, cells seeded onto coverslips were arrested in mitosis with 100μM monastrol for 16 hours. Cells were washed and released into fresh media and were fixed at ten minute intervals for two hours in PHEM buffer + 2% formaldehyde + 0.5% triton-X100. Cells were immunostained with DAPI to visualized DNA and antibodies to phospho-histone H3 Ser10 (pH3S10) and to γ-tubulin to identify mitotic cells at different stages. Independent triplicates with >100 cells per replicate were analyzed. For measuing mitotic index by FACS, cells were trypsinzed, fixed with ethanol and stained with PI and pH3S10 antibody.

Cell culture, molecular biology and reagents

Sequence information for additional shRNAs and siRNAs used the validation is in **Table S4**. The DLD-1 and HCT116 isogenic cells were kind gifts from Dr. Bert Vogelstein (Johns Hopkins University School of Medicine) and were maintained in McCoy's 5A media supplemented with 10% FBS and antibiotics. Non-small cell lung cancer cell lines (H23, H358, H647, H1299, H1734, H2030, H2122, H460, H522, H838, H1437, H1650, H1838 and H1975) were maintained in RPMI-1640 media with 10% FBS and antibiotics. For proliferation assays, cells were seeded in either 24-well or 96-well plates and cell number was measured using CellTiterGLO (Promega). For adherent colony assays, 1000 cells were seeded in each well of a 6-well plate and colonies were counted 10 days later by Coomassie staining. For anchorage independent colony assays, 1000 cells were seeded in each well of a 6-well plate in media containing 0.35% low-melting point agarose and colonies were counted 3 weeks later by crystal violet staining. The PCR primers use to amplify HH barcodes from genomic DNA samples are JH353F 5'-tagtgaagccacagatgta-3' and HHR2L 5'-atgtatcaaagagatagcaaggtattcag-3'. BI-2536 was a kind gift from Dr. Nathanael Gray (Harvard Medical School and Dana Faber Cancer Institute). Paclitaxel, nocodazole, MG132 and monastrol were from Sigma-Aldrich. RO-3306 was from EMD Calbiochem. Bortezomib was from LC Laboratories. Rabbit antibody against phospho-PLK1 T210 was from Abcam. Rabbit phosphoH3-S10 antibody was from Covance. Mouse antibodies against PLK1, K-Ras and tubulin were from Santa Cruz Biotechnologies. Rabbit anti-COPS4 antibody was from Bethyl Laboratories. Rabbit anti-APC1 and APC4 antibodies were from Novus. mRNA levels were measured by RT-qPCR using CYBR green (InVitrogen). The following primer pairs were used for RT-qPCR analysis: KNL-1/CASC5, 5'-tacagaaaccccgacagagc-3' and 5'-tcttctggagtaggtggtgtgtt-3'; borealin/CDCA8, 5'-gctgacagcaaagagatcttcc-3' and 5'-gccaataatcgcaggctct-3'; hMis18a/C21ORF45 5'-ggaatcttctctgaaaactaatcca-3' and 5'-ttctgacagatcattctgaccaa-3'.

Mouse xenograft tumor models

DLD-1 cells (5 million cells per site) or HCT116 cells (2 million cells per site) in suspension were mixed with equal volume of matrigel (BD bioscience) and injected subcutaneously into both flanks of 6 week-old female nude mice (Charles River laboratory). Drug treatment began after one week of cell injection. BI-2536 was given by i.v. under a twice per week schedule. The dose of BI-2536 used for DLD-1 xenografts was 50 mg/kg for the first 2 weeks and then increased to 75 mg/kg for the last week. The dose of BI-2536 used for HCT116 xenografts was 50 mg/kg. Measurement of tumor size was performed twice a week, and tumor volume was estimated using the formula: volume = Length x Width^2 x 0.5. The volume of each tumor at serial time points was normalized with the initial tumor volume and comparison of tumor volumes between the drug treatment group and vehicle control group was carried out using 2-way ANOVA with Bonferroni post-tests.

SUPPLEMENTAL FIGURES WITH LEGENDS

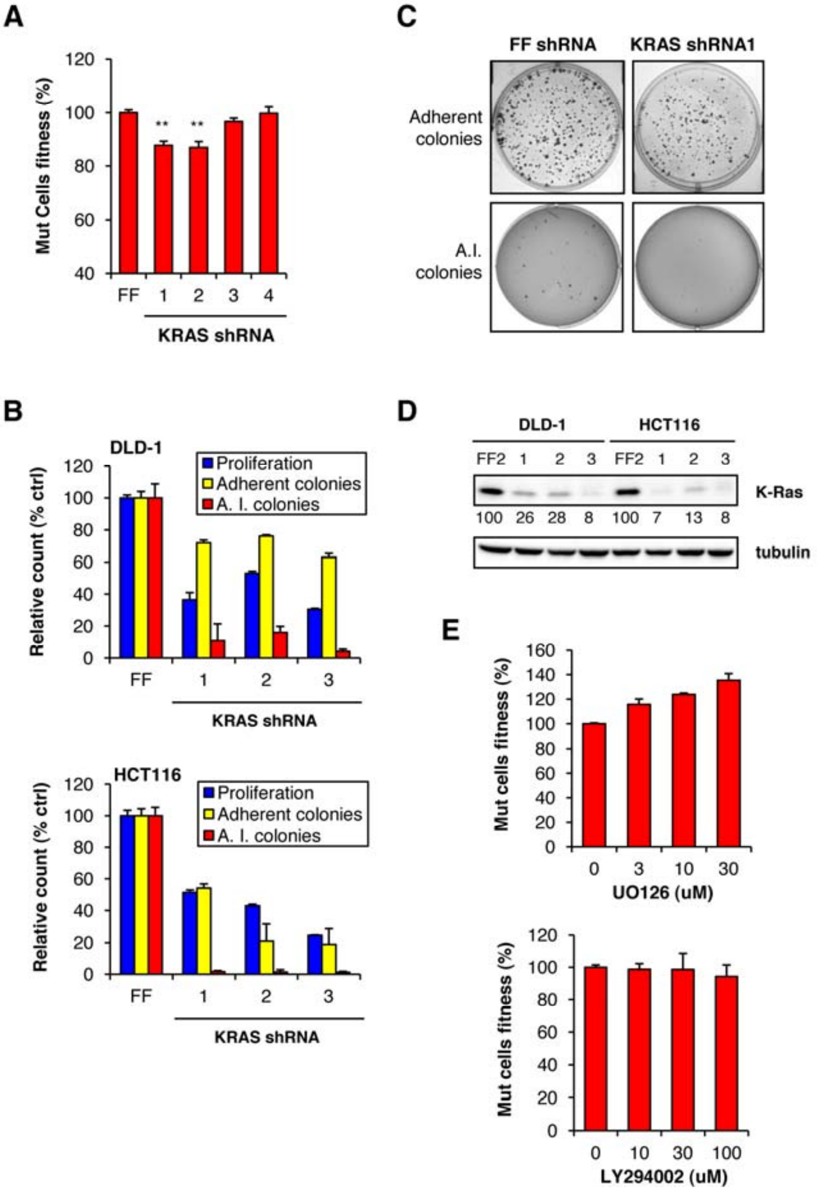

Figure S1. Effect of K-Ras depletion in DLD-1 and HCT116 cells.

A. DLD-1 Ras Mut cell fitness is modestly decreased by K-Ras shRNAs as measured by the competition assay (**$p < 0.01$ compared to respective FF control).

B. Effect of K-Ras shRNAs on cell proliferation, colony formation on adherent surface and colony formation in soft agarose in DLD-1 and HCT116 Ras Mut cells. For the proliferation assay, equal number of cells stably expressing either K-Ras shRNAs or a control firefly luciferase (FF) shRNA were seeded at normal density and cell numbers were estimated 4 days later using CellTiter-GLO assay. For adherent colony formation, cells were seeded at low density on an adherent surface and colonies were counted 10 days later. For anchorage independent colony formation, cells were seeded at low density in soft agarose media and colonies were counted 3 week later ($p< 0.01$ for all shRNAs compares to respective FF control).

C. Representative images of the colony assays in B for K-Ras shRNA1 in DLD-1 cells.

D. K-Ras protein knockdown in cell lines stably expressing K-Ras shRNAs were verified by Western blotting. Numbers under the blot indicate normalized levels of K-Ras proteins after adjusting for loading.

E. Effect of the MEK inhibitor U0126 and the PI3K inhibitor LY294002 on the fitness of DLD-1 Ras Mut cells in the competition assay. The assay was carried out for 5 days in the presence of various drug concentrations as indicated.

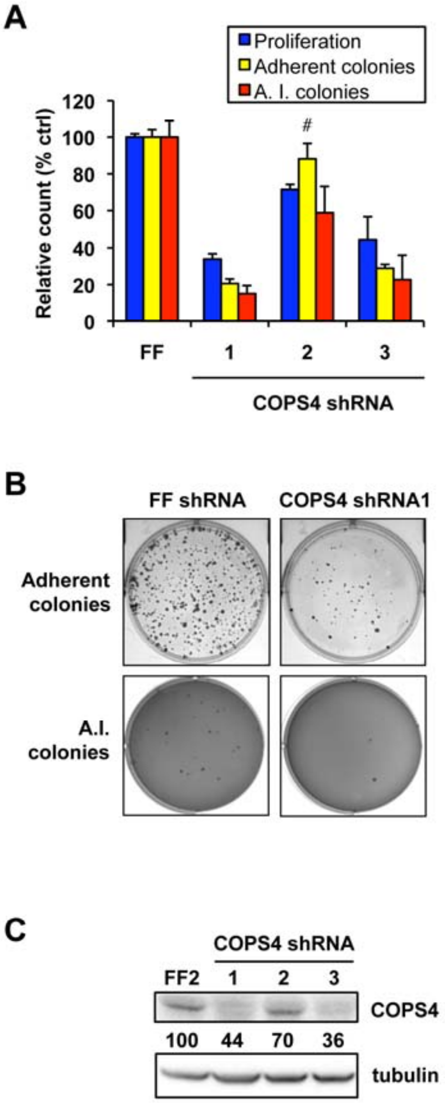

Figure S2. Depletion of COPS4 impairs DLD-1 Ras Mut cell viability.

A. Effect of COPS4 shRNAs on cell proliferation, colony formation on adherent surface and colony formation in soft agarose in DLD-1 Ras Mut cells ($p< 0.05$ for all shRNAs compares to respective FF control, except # not significant).

B. Representative images of the colony assays in B for K-Ras shRNA1 in DLD-1 cells.

C. Knockdown efficiency of COPS4 shRNAs in DLD-1 cells.

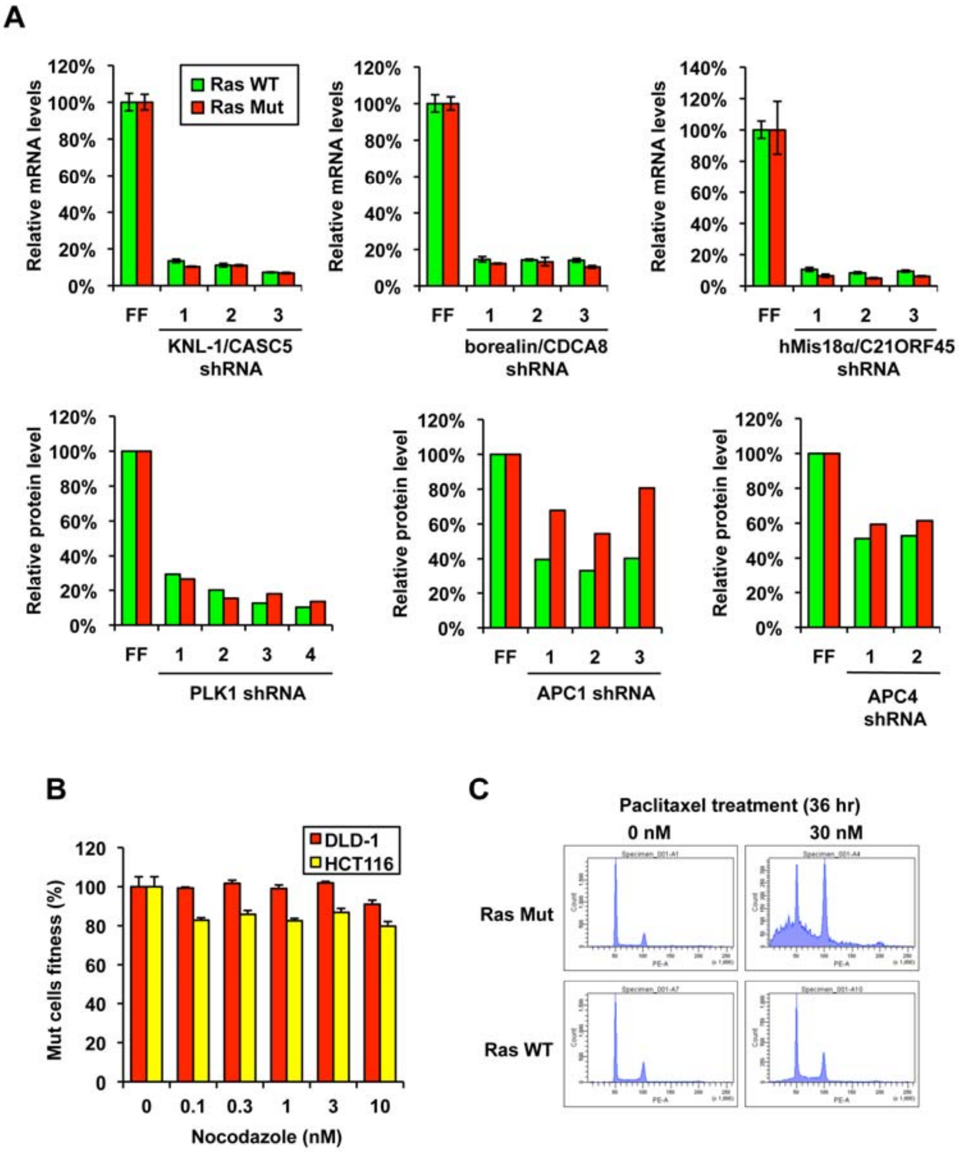

Figure S3. Sensitivity of Ras Mut cells to mitotic gene depletion and to nocodazole and paclitaxel.

A. Validation of depletion of mitotic genes by shRNAs. The mRNA depletion of KNL-1/CACS5, borealin/CDCA8 and hMis18α/C21ORF45 was assessed by RT-qPCR and the protein depletion of PLK1, ANAPC1 and ANAPC4 was assessed by Western Blot.

B. Nocodazole shows no synthetic lethality with mutant Ras. The relative fitness of DLD-1 and HCT116 Ras Mut cells at various concentrations of Nocodazole was measured by the competition assay.

C. DLD-1 Ras Mut cells are hypersensitive to paclitaxel-induced cell cycle arrest.

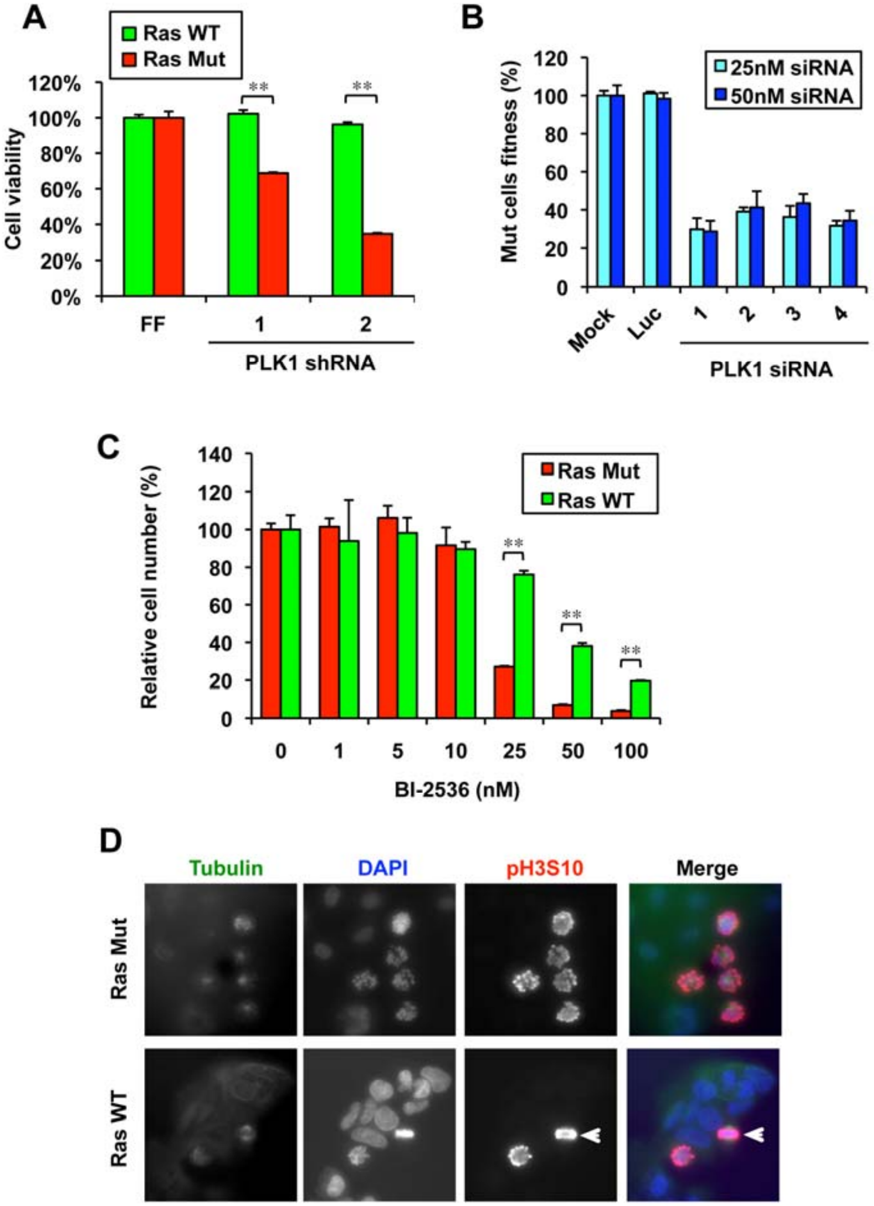
A
Ras WT
Ras Mut
Cell viability
120%
100%
80%
60%
40%
20%
0%
**
**
FF
1
2
PLK1 shRNA
B
Mut cells fitness (%)
120
100
80
60
40
20
0
25nM siRNA
50nM siRNA
Mock
Luc
1
2
3
4
PLK1 siRNA
C
Relative cell number (%)
140
120
100
80
60
40
20
0
Ras Mut
Ras WT
**
**
**
0
1
5
10
25
50
100
BI-2536 (nM)
D
Tubulin
DAPI
pH3S10
Merge
Ras Mut
Ras WT

Figure S4. (A-D)

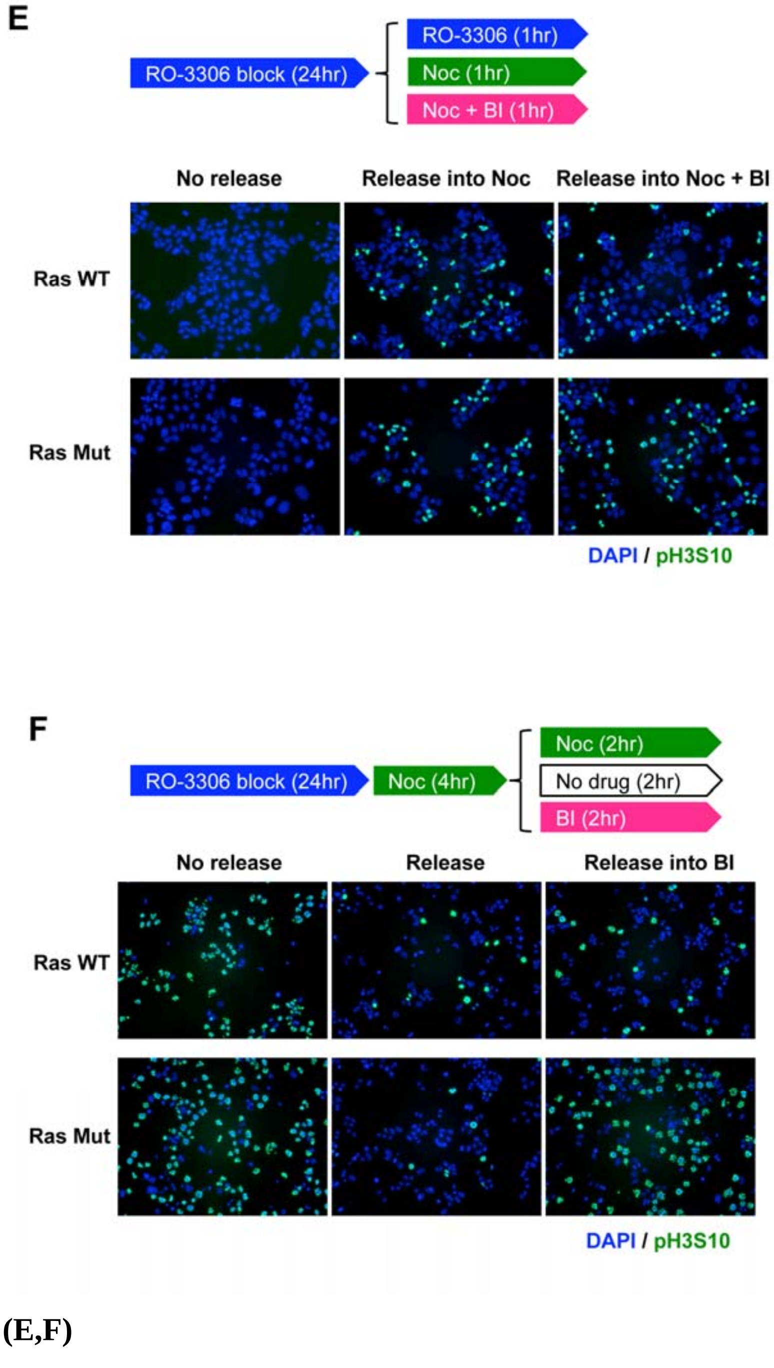
E
RO-3306 block (24hr)
RO-3306 (1hr)
Noc (1hr)
Noc + BI (1hr)
No release
Release into Noc
Release into Noc + BI
Ras WT
Ras Mut
DAPI / pH3S10
F
RO-3306 block (24hr)
Noc (4hr)
Noc (2hr)
No drug (2hr)
BI (2hr)
No release
Release
Release into BI
Ras WT
Ras Mut
DAPI / pH3S10

Figure S4. (E,F)

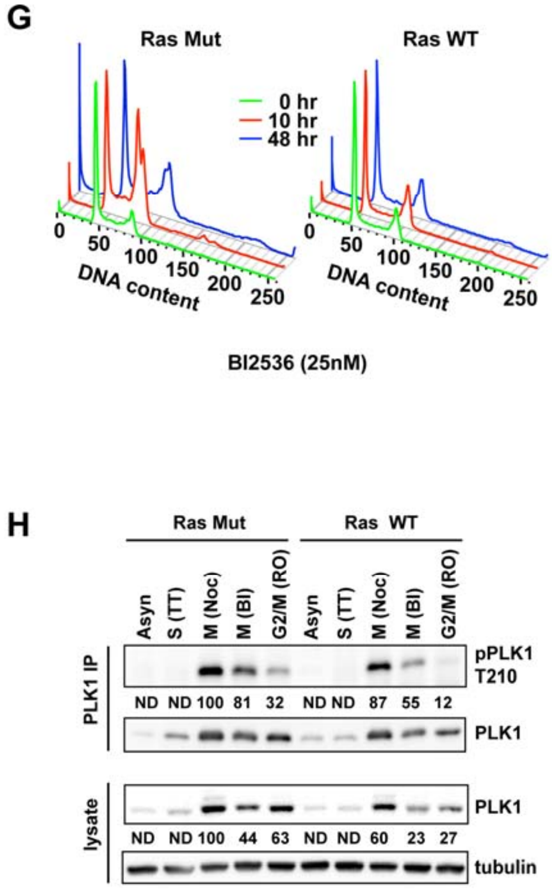

Figure S4.(G,H)

Figure S4. Hypersensitivity of Ras Mut cells to PLK1 inhibition.

A. PLK1 depletion shows enhanced toxicity in DLD-1 Ras Mut cells as measured by CellTiter GLO cell viability assay (** $p<0.01$). Ras Mut and WT cells were infected with PLK1 shRNAs at MOI ~ 1 and cell viability was measured 5 days post infection.

B. PLK1 depletion by siRNA leads to enhanced toxicity in DLD-1 Ras Mut cells. Luc, negative control siRNA targeting firefly luciferase ($p< 0.01$ for all siRNAs compared to respective Luc siRNA control).

C. BI-2536 shows enhanced toxicity in DLD-1 Ras Mut cells as measured by the CellTiter GLO cell viability assay (** $p<0.01$).

D. Representative image of DLD-1 cells treated with 50 nM BI-2536 for 24 hours. Mitotic cells at various stages were identified based on phospho-H3 Ser10 (pH3S10) staining, chromosome morphology (DAPI staining) and mitotic spindle arrangement (tubulin staining). Arrowhead indicates cell with a metaphase plate on bipolar spindle. Whereas a significant number of metaphase Ras WT cells still show fully aligned chromosomes under this condition, few metaphase Ras Mut cells are found to have fully aligned chromosomes.

E. BI-2536 does not differentially affect mitotic entry in DLD-1 Ras Mut and WT cells. Cells synchronization and release scheme is shown on top. Cells synchronized at the G2/M boundary by the CDK1 inhibitor RO-3306 were released into nocodazole (100 ng/ml) together with indicated concentrations of BI-2536 for 1 hour. The mitotic index was measured as the percentage of cells staining positive for phospho-H3 Ser10 (pH3S10).

F. BI-2536 differentially affect mitotic progression in DLD-1 Ras Mut and WT cells. Cells synchronization and release scheme is shown on top. Mitotic cells collected by nocodazole shake-off were released into indicated concentrations of BI-2536 for 2 hours. Mitotic index was measured as the percentage of cells staining positive for phospho-H3 Ser10.

G. Effect of BI-2536 (25 nM) on cell cycle distribution of Ras Mut and Ras WT DLD-1 cells over a 48-hour period.

H. PLK1 protein level and activation (as assessed by T210 phosphorylation) in Ras Mut and WT DLD-1 cells. Numbers below each blot indicates normalized signal intensity after adjusted for loading. Asyn, asynchronous population; S (TT), S phase population arrested by double thymidine block; M (Noc) and M (BI), M phase population collected by releasing from double thymidine block into nocodazole (200 ng/ml) and BI-2536 (100 nM), respectively; G2/M (RO), G2/M population were collected by releasing from double thymidine block into the CDK1 inhibitor RO-3306 (10 uM). Each inhibitor is used at concentrations that cause complete cell cycle arrest as verified by FACS.

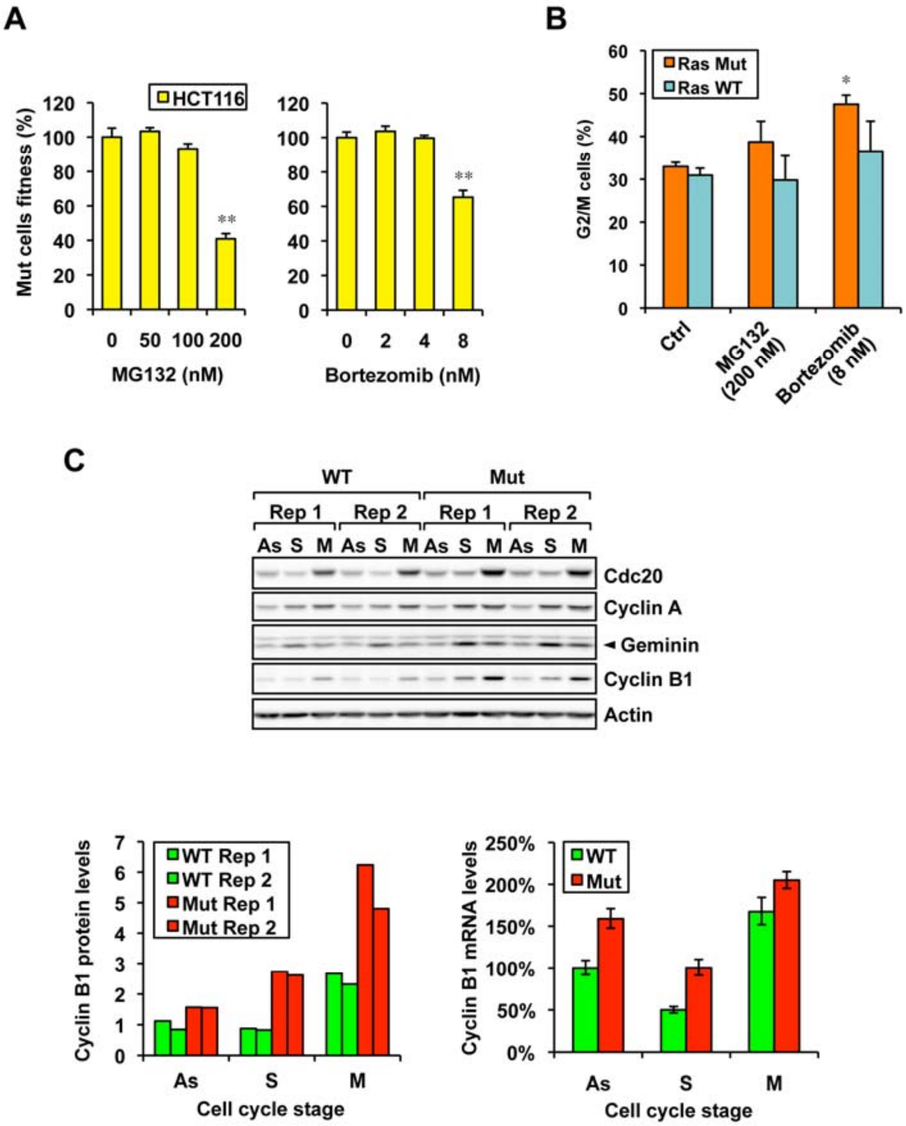

Figure S5. Hypersensitivity of HCT116 Ras Mut cells to proteasome inhibition.

A. The proteasome inhibitors MG132 and bortezomib selectively decreased the fitness of HCT116 Ras Mut cells. The competition assay was carried out in the presence of the drug for 4 days (***p*< 0.01 compared to untreated samples).

B. MG132 and bortezomib preferentially induce the accumulation of Ras Mut HCT116 cells as assessed by FACS using staining (**p*<0.05 compared to untreated samples).

C. DLD-1 Ras Mut cells have elevated cyclin B1 protein and mRNA levels. Ras WT and Mut cells were synchronized by double thymidine block. Asynchronous (As), S-phase cells (S, 2 hrs after release) and mitotic cells (M, 6 hrs after release) were blotted for various cell cycle proteins (2 independent replicates). Cyclin B1 protein and mRNA levels (as measured by RT-qPCR) were quantified.

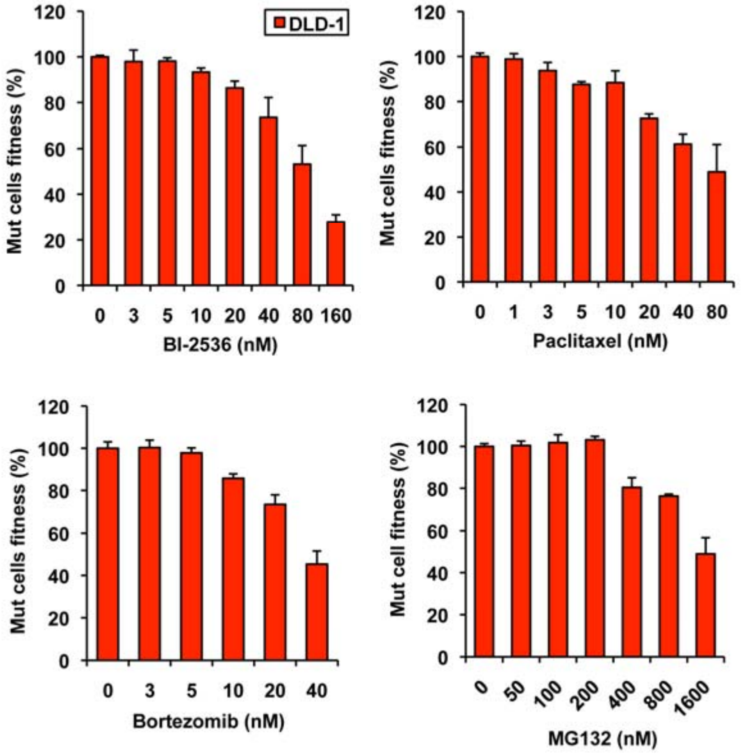

Figure S6. Synthetic lethal effect of mitotic inhibitors when applied as a transient treatment.

The effect of transient treatment with BI-2536, paclitaxel, bortezomib and MG132 on the fitness of DLD-1 Ras Mut cells was measured using the MCA. Cells were treated for a 24-hour period with drugs at the indicated concentrations. Drugs were then washed out and cells were allowed to proliferate for 3 additional days before FACS analysis.

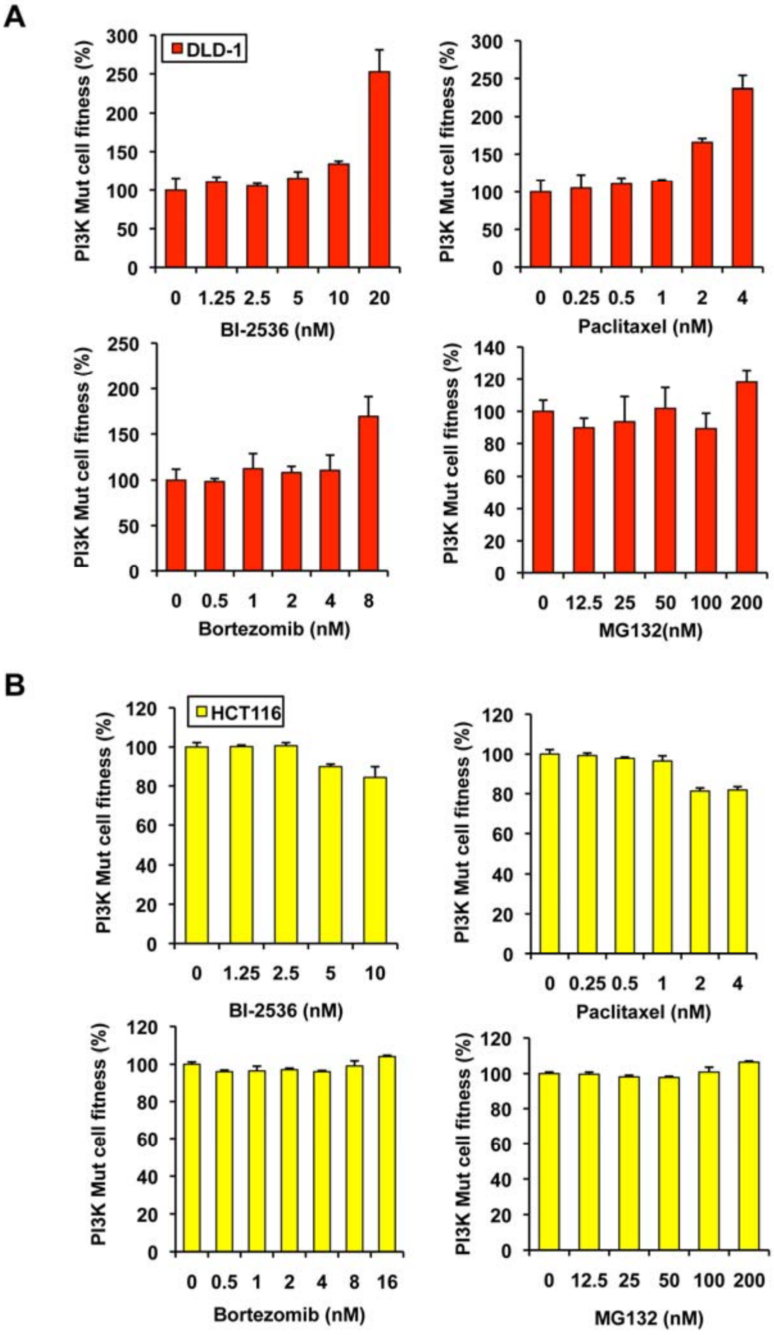

Figure S7. Lack of synthetic lethality of various mitotic inhibitors with the PI3K oncogene.

A. The effect of BI-2536, paclitaxel, bortezomib and MG132 on the fitness of DLD-1 PI3K Mut cells vs. PI3K WT cells as measured by the MCA.

B. The effect of BI-2536, paclitaxel, bortezomib and MG132 on the fitness of HCT116 PI3K Mut cells vs. PI3K WT cells as measured by the MCA.

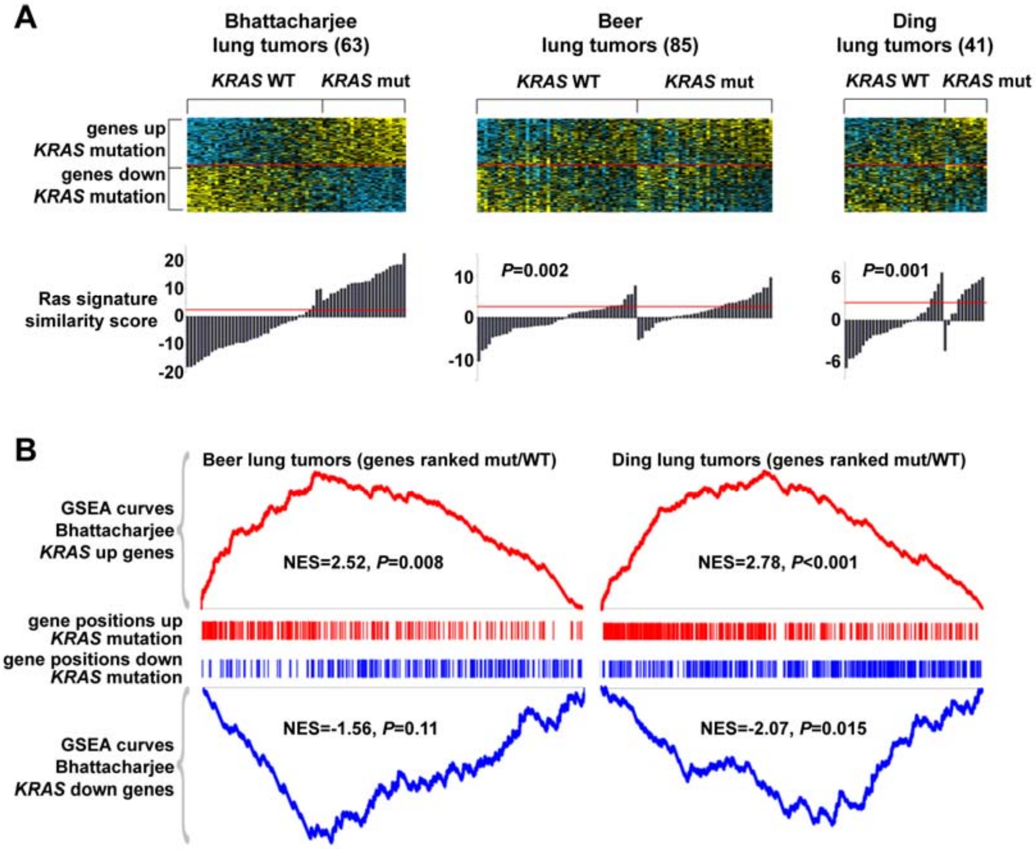

Figure S8. The KRAS signature as defined by the Bhattacharjee dataset is consistently correlated with KRAS mutation status in multiple independent datasets.

A. Activation scores of the KRAS mutation signature for the lung tumors in each of three datasets (Bhattacharjee *et al*., Beer *et al*., Ding *et al*.). Top, heat maps of the KRAS mutation signature show the expression patterns of the tumors, which are ordered (within each tumor group) from low to high similarity to the signature. Bottom, the KRAS similarity scores corresponding to the tumor expression patterns are provided below the heat maps (red line indicate $P<0.01$ significance level of tumor-to-signature correlation by two-sided *t*-test). While the KRAS signature activation scores are not perfectly correlated with KRAS mutation status (e.g. lung tumors without KRAS mutation might still have the KRAS pathway activation via other genes), scores on average are higher for mutant versus WT tumors (as denoted by two-sided t-test *p*-values above the Beer and Ding plots). Importantly, only tumors that either obviously manifested or obviously did not manifest the KRAS signature (with $P<0.01$ significance level) of the Shedden *et al*. dataset were used in the survival analyses shown in Figure 7.

B. The Bhattacharjee KRAS signature is coordinate with the Beer and Ding KRAS mutation-associated expression patterns by gene set enrichment analysis (GSEA). The entire sets of genes represented in the Beer dataset or the Ding dataset were each ranked by higher expression in KRAS mutant over WT (using the t-statistic). The gene positions of the Bhattacharjee signature were plotted along the Beer and Ding ranked lists (Red lines: genes up in Bhattacharjee signature; blue lines: genes down in Bhattacharjee signature). Positive GSEA curves indicate that the gene positions tend to be near the top of the mutant/WT ranked list; negative GSEA curves, near the bottom.

SUPPLEMENTAL REFERENCES

Beer, D. G., Kardia, S. L., Huang, C. C., Giordano, T. J., Levin, A. M., Misek, D. E., Lin, L., Chen, G., Gharib, T. G., Thomas, D. G. et al. (2002). Gene-expression profiles predict survival of patients with lung adenocarcinoma. Nat Med *8*, 816-824.

Bhattacharjee, A., Richards, W. G., Staunton, J., Li, C., Monti, S., Vasa, P., Ladd, C., Beheshti, J., Bueno, R., Gillette, M. et al. (2001). Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses. Proc Natl Acad Sci U S A *98*, 13790-13795.

Ding, L., Getz, G., Wheeler, D. A., Mardis, E. R., McLellan, M. D., Cibulskis, K., Sougnez, C., Greulich, H., Muzny, D. M., Morgan, M. B. et al. (2008). Somatic mutations affect key pathways in lung adenocarcinoma. Nature *455*, 1069-1075.

Schlabach, M. R., Luo, J., Solimini, N. L., Hu, G., Xu, Q., Li, M. Z., Zhao, Z., Smogorzewska, A., Sowa, M. E., Ang, X. L. et al. (2008). Cancer proliferation gene discovery through functional genomics. Science *319*, 620-624.

Shedden, K., Taylor, J. M., Enkemann, S. A., Tsao, M. S., Yeatman, T. J., Gerald, W. L., Eschrich, S., Jurisica, I., Giordano, T. J., Misek, D. E. et al. (2008). Gene expression-based survival prediction in lung adenocarcinoma: a multi-site, blinded validation study. Nat Med *14*, 822-827.

Smogorzewska, A., Matsuoka, S., Vinciguerra, P., McDonald, E. R. r., Hurov, K. E., Luo, J., Ballif, B. A., Gygi, S. P., Hofmann, K., D'Andrea, A. D. et al. (2007). Identification of the FANCI protein, a monoubiquitinated FANCD2 paralog required for DNA repair. Cell *129*, 289-301.

Steegmaier, M., Hoffmann, M., Baum, A., Lenart, P., Petronczki, M., Krssak, M., Gurtler, U., Garin-Chesa, P., Lieb, S., Quant, J. et al. (2007). BI 2536, a potent and selective inhibitor of polo-like kinase 1, inhibits tumor growth in vivo. Curr Biol *17*, 316-322.

Thomas, P. D., Campbell, M. J., Kejariwal, A., Mi, H., Karlak, B., Daverman, R., Diemer, K., Muruganujan, A., and Narechania, A. (2003). PANTHER: a library of protein families and subfamilies indexed by function. Genome Res *13*, 2129-2141.

Torrance, C. J., Agrawal, V., Vogelstein, B., and Kinzler, K. W. (2001). Use of isogenic human cancer cells for high-throughput screening and drug discovery. Nat Biotechnol *19*, 940-945.

Vassilev, L. T., Tovar, C., Chen, S., Knezevic, D., Zhao, X., Sun, H., Heimbrook, D. C., and Chen, L. (2006). Selective small-molecule inhibitor reveals critical mitotic functions of human CDK1. Proc Natl Acad Sci U S A *103*, 10660-10665.

Supplemental Table 1. Candidate RSL shRNAs based on relaxed statistical criteria.

For an shRNA to qualify it must show a Mut log2 ratio <= -0.7, a WT log2 ratio >= -2.0, a Mut vs. WT log2 ratio difference of <= -0.7, and p value <= 0.3.

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_2878	v2HS_220955	TAATGAAGGGAGGATTCATGCA	AK056852	A2M	alpha-2-macroglobulin (A2M), mRNA	-0.70	0.23	0.01	0.60	-0.70	0.17
Hs_12plexchip_5_4881	v2HS_255771	ATAGACTTTCACTATGGCTGGT	NM_000014	A2M	alpha-2-macroglobulin (A2M), mRNA	-1.15	0.46	0.73	0.70	-1.88	0.02
Hs_12plexchip_4_5526	v2HS_17554	TTGTATCTCAACACCGTCTGCA	NM_144670	A2ML1	alpha-2-macroglobulin-like 1 (A2ML1), mRNA	-2.38	0.26	-1.22	1.02	-1.17	0.18
Hs_12plexchip_6_6633	v2HS_200318	TTTAAGAAGCGAAGTGTTGCCA	NM_080282	ABCA10	ATP-binding cassette, sub-family A (ABC1), member 10 (ABCA10), mRNA	-0.84	0.11	0.35	1.02	-1.19	0.18
Hs_12plexchip_3_7348	v2HS_100516	TATATGTCTCGATTTCTCAGGA	NM_178559	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB5), mRNA	-1.18	0.12	0.08	0.15	-1.26	0.00
Hs_12plexchip_6_9652	v2HS_232838	TAGACTTAAACCAAAGGGTCCT	NM_016006	ABHD5	abhydrolase domain containing 5 (ABHD5), mRNA	-1.45	0.56	-0.10	1.33	-1.35	0.21
Hs_12plexchip_5_8224	v2HS_223618	ATATGCATGTTCACCATCTGGC	NM_016428	ABI3	ABI gene family, member 3 (ABI3), mRNA	-0.79	0.15	0.40	1.03	-1.18	0.18
Hs_12plexchip_6_9744	v2HS_232874	ATCTTGTAGAAGATGGTCTCGA	NM_021962	ABR	active BCR-related gene (ABR), transcript variant 1, mRNA	-0.85	0.33	-0.09	0.61	-0.76	0.15
Hs_12plexchip_5_5023	v2HS_81287	TTAGATTATCCCTGAACAGCCT	NM_021804	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA	-1.29	0.36	-0.40	0.14	-0.89	0.04
Hs_12plexchip_3_2132	v2HS_53342	ATAAAGGCACTGTTGATGTGGC	NM_015547	ACOT11	acyl-CoA thioesterase 11 (ACOT11), transcript variant 1, mRNA	-1.46	0.41	-0.66	0.34	-0.79	0.06
Hs_12plexchip_3_5654	v2HS_224084	TTCAACTTCAGCAGGCTGCGGT	NM_016361	ACP6	acid phosphatase 6, lysophosphatidic (ACP6), mRNA	-1.35	1.04	-0.46	0.44	-0.89	0.27
Hs_12plexchip_4_4642	v2HS_238919	TTTATCCAGAGTATCTGCTCCA	NM_022977	ACSL4	acyl-CoA synthetase long-chain family member 4 (ACSL4), transcript variant 2, mRNA	-0.84	0.85	0.32	0.69	-1.16	0.14
Hs_12plexchip_2_1754	v2HS_81153	TTTAGGAAAGCCTGTGGTCCCA	NM_001080454	ACSM4	acyl-CoA synthetase medium-chain family member 4 (ACSM4), mRNA	-1.17	0.59	-0.16	0.45	-1.01	0.08
Hs_12plexchip_2_6269	v2HS_175818	ATACTGAACAACTCTGACAGGC	NM_018477	ACTR10	actin-related protein 10 homolog (S. cerevisiae) (ACTR10), mRNA	-0.77	0.37	0.26	0.41	-1.03	0.03
Hs_12plexchip_5_12652	v2HS_253909	AAGAGAAGGGAGGTGAGTTGGT	NM_005736	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) (ACTR1A), mRNA	-1.34	0.80	-0.61	0.66	-0.74	0.29
Hs_12plexchip_4_1459	v2HS_199170	TTTGTCTTTCATGATATCCGCT	NM_001005386	ACTR2	ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 1, mRNA	-1.48	0.39	-0.72	0.48	-0.76	0.10
Hs_12plexchip_5_6959	v2HS_262231	ATAGTAGACCCTCCAGAAAGCA	NM_001005386	ACTR2	ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 1, mRNA	-1.19	0.23	-0.28	0.35	-0.91	0.03
Hs_12plexchip_5_7113	v2HS_197509	TAAACCTTGAGCGTACAAAGTC	NM_001005386	ACTR2	ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 1, mRNA	-1.31	0.55	-0.19	0.41	-1.12	0.05
Hs_12plexchip_5_11682	v2HS_146619	ATGTCAGGGCTATGTGGTTCCT	AB209449	ACVR2B	ACTIVIN A RECEPTOR, TYPE IIB	-1.94	0.28	-0.74	1.18	-1.20	0.22
Hs_12plexchip_5_5343	v2HS_91340	TAATGATCTGGGAACCTAGCCC	NM_001077401	ACVRL1	activin A receptor type II-like 1 (ACVRL1), transcript variant 2, mRNA	-1.24	0.97	0.52	0.69	-1.76	0.07
Hs0P00011130	v2HS_33582	TTTAACTTCCACAGTCTTGCCT	NM_021723	ADAM22	ADAM metallopeptidase domain 22 (ADAM22), transcript variant 1, mRNA	-1.15	0.16	0.14	0.20	-1.29	0.00
Hs_12plexchip_4_9875	v2HS_199879	TTCAGTTTACACGTTAGGGCTT	NM_014479	ADAMDEC1	ADAM-like, decysin 1 (ADAMDEC1), mRNA	-1.39	0.82	-0.63	0.17	-0.76	0.25
Hs_12plexchip_3_4823	v2HS_123010	TTGGTTTCTTAATATTACGGCA	NM_199355	ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18 (ADAMTS18), mRNA	-1.23	0.30	-0.34	0.49	-0.89	0.07
Hs0P00011915	v2HS_25008	ATAGTGGAGTAGTCGGTGGGCG	NM_213604	ADAMTSL5	ADAMTS-like 5 (ADAMTSL5), mRNA	-1.35	0.20	-0.23	0.36	-1.12	0.02
Hs_12plexchip_4_174	v2HS_94323	ATACAGCTCCTCATTGTCTCGG	NM_001115	ADCY8	adenylate cyclase 8 (brain) (ADCY8), mRNA	-1.60	0.75	-0.25	0.52	-1.35	0.07
Hs_12plexchip_5_10069	v2HS_94354	TTGTACTGAGATAGGCTGAGGA	NM_001122	ADFP	adipose differentiation-related protein (ADFP), mRNA	-0.80	0.61	0.26	0.30	-1.06	0.08
Hs_12plexchip_6_8791	v2HS_285128	TTTAAAGCCACCAAGAATAGCT	NM_000667	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide (ADH1A), mRNA	-0.87	0.06	0.13	0.28	-1.00	0.02
Hs_12plexchip_3_4651	v2HS_111952	TTCACAACCGAATTGGTGTGGG	NM_000675	ADORA2A	adenosine A2a receptor (ADORA2A), mRNA	-1.75	0.15	-1.03	0.21	-0.72	0.01
Hs_12plexchip_6_8644	v2HS_221216	ATTGTAACCCAGGGAGGAGGCG	NM_017825	ADPRHL2	ADP-ribosylhydrolase like 2 (ADPRHL2), mRNA	-0.94	0.59	0.04	0.60	-0.98	0.11
Hs_12plexchip_2_11732	v2HS_45839	TTCTATTATGGGTATAGGTCCT	NM_153207	AEBP2	AE binding protein 2 (AEBP2), mRNA	-1.40	0.65	-0.60	0.10	-0.80	0.16
Hs_12plexchip_2_1689	v2HS_80583	GAAGAATATCCTCTTGCCTGCG	NM_021831	AGBL5	ATP/GTP binding protein-like 5 (AGBL5), transcript variant 1, mRNA	-1.14	0.65	-0.37	0.54	-0.77	0.19
Hs_12plexchip_5_10898	v2HS_130226	AAGTACTTGAAGCTTCGCACGA	NM_006412	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), transcript variant 1, mRNA	-0.76	0.51	0.24	0.59	-0.99	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_6377	v2HS_112014	TTTGTTGAAAGGTTTGAGTGGG	NM_032049	AGTR1	angiotensin II receptor, type 1 (AGTR1), transcript variant 5, mRNA	-1.65	0.43	-0.84	0.37	-0.81	0.07
Hs_12plexchip_3_6625	v2HS_230423	TTTAATTGCGAACTTGAGGGCA	XM_001126456	AHCTF1	PREDICTED:AT hook containing transcription factor 1 (AHCTF1), mRNA	-2.67	0.81	-1.06	0.44	-1.61	0.06
Hs_12plexchip_5_7108	v2HS_112026	TTAGCTCTTAGGGAGGAGAGGT	NM_000687	AHCY	S-adenosylhomocysteine hydrolase (AHCY), mRNA	-0.98	0.55	0.03	0.17	-1.01	0.07
Hs_12plexchip_6_628	v2HS_70477	TAGTCCCATCAGCATTCTTGGG	NM_153326	AKR1A1	aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), transcript variant 2, mRNA	-0.76	1.04	0.14	0.17	-0.89	0.27
Hs_12plexchip_5_10803	v2HS_139166	TTCCTCTATCCAGTCAATTGGG	NM_033087	ALG2	asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase) (ALG2), mRNA	-0.72	1.00	0.83	0.63	-1.55	0.10
Hs_12plexchip_5_2891	v2HS_199745	ATTCATCTTCACAGAGACTGCC	NM_005787	ALG3	asparagine-linked glycosylation 3 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase) (ALG3), mRNA	-1.39	0.75	0.83	2.18	-2.22	0.21
Hs0P00001565	v2HS_63897	ATTACCAACATGAGTTGCTGGC	NM_139178	ALKBH3	alkB, alkylation repair homolog 3 (E. coli) (ALKBH3), mRNA	-1.27	0.16	-0.26	0.22	-1.01	0.00
Hs_12plexchip_3_11335	v2HS_238167	TATTGGTTGCTGCTAGACTCGC	NM_032306	ALKBH7	alkB, alkylation repair homolog 7 (E. coli) (ALKBH7), mRNA	-1.65	0.05	-0.35	0.24	-1.31	0.01
Hs_12plexchip_2_6029	v2HS_175592	TTCAATTCGAGTTATTACTCCA	NM_018436	ALLC	allantoicase (ALLC), transcript variant 1, mRNA	-0.96	0.19	0.08	0.46	-1.04	0.04
Hs_12plexchip_4_2089	v2HS_175593	TTTGGTTGGGAGACAACTTGGT	NM_018436	ALLC	allantoicase (ALLC), transcript variant 1, mRNA	-0.88	0.25	0.00	0.17	-0.88	0.01
Hs_12plexchip_4_10591	v2HS_87865	TATATGAACACAAGAAAGTGCT	NM_015120	ALMS1	Alstrom syndrome 1 (ALMS1), mRNA	-0.95	0.16	0.88	0.16	-1.82	0.00
Hs_12plexchip_4_3916	v2HS_220995	AAGAACTTCCATAGTGGCTGGA	AK130065	ALS2CR16	AMYOTROPHIC LATERAL SCLEROSIS 2 (JUVENILE) CHROMOSOME REGION, CANDIDATE 16	-0.86	0.68	0.56	0.29	-1.43	0.05
Hs_12plexchip_5_2570	v2HS_206751	ATTTGAAGAGATTTGGGACCTG	NM_001144	AMFR	autocrine motility factor receptor (AMFR), mRNA	-0.86	0.43	0.10	0.24	-0.96	0.04
Hs_12plexchip_3_10016	v2HS_132555	ATTGTGAATAATGAAGTATCCT	NM_001635	AMPH	amphiphysin (AMPH), transcript variant 1, mRNA	-0.92	0.16	0.38	0.21	-1.30	0.00
Hs_12plexchip_3_9551	v2HS_238499	AATTTCTAGTCCATGCTAAGCG	NM_022662	ANAPC1	anaphase promoting complex subunit 1 (ANAPC1), mRNA	-0.95	0.29	-0.07	0.95	-0.89	0.24
Hs_12plexchip_4_11284	v2HS_98169	AATAGACATATCCATGGTGCCT	NM_022662	ANAPC1	anaphase promoting complex subunit 1 (ANAPC1), mRNA	-1.74	0.26	0.35	0.66	-2.08	0.02
Hs_12plexchip_6_810	v2HS_98171	TTTATGCAAACAGTTAAATGCT	NM_022662	ANAPC1	anaphase promoting complex subunit 1 (ANAPC1), mRNA	-1.58	0.10	-0.32	0.92	-1.26	0.14
Hs0P00006179	v2HS_98167	TATTAGTAATCGTTTCTGTCCA	NM_022662	ANAPC1	anaphase promoting complex subunit 1 (ANAPC1), mRNA	-1.15	0.43	-0.21	0.61	-0.94	0.10
Hs0P00003370	v2HS_64696	TACTTCTTGCAGTAAGCCTCCA	NM_013366	ANAPC2	ANAPHASE PROMOTING COMPLEX SUBUNIT 2	-1.35	1.42	-0.22	0.04	-1.13	0.30
Hs_12plexchip_5_3713	v2HS_254660	ATACAATGGAATACAGATTGCT	NM_013367	ANAPC4	anaphase promoting complex subunit 4 (ANAPC4), mRNA	-1.32	0.20	0.45	0.63	-1.78	0.03
Hs_12plexchip_6_1012	v2HS_64633	TATACTAAAGACAAAGGCAGCT	NM_013367	ANAPC4	anaphase promoting complex subunit 4 (ANAPC4), mRNA	-0.74	0.36	0.11	0.62	-0.85	0.13
Hs_12plexchip_6_6071	v2HS_245893	ATATTTCTAGGTGAAACAAGCT	NM_153228	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1 (ANKFN1), mRNA	-0.83	0.16	0.28	1.22	-1.11	0.26
Hs0P00003147	v2HS_34481	TTGTAGGATCTCATACGACGTT	XM_001132013	ANKH	PREDICTED:ankylosis, progressive homolog (mouse) (ANKH), mRNA	-1.00	0.50	-0.23	0.68	-0.76	0.20
Hs_12plexchip_2_631	v2HS_117000	TTTCTTTCCTTGGTTAGACGGC	NM_030816	ANKRD13C	ankyrin repeat domain 13C (ANKRD13C), mRNA	-1.39	0.23	-0.58	0.69	-0.81	0.17
Hs_12plexchip_6_5197	v2HS_237714	ATTATTGTCCTTGTCCAGTGCT	NM_032250	ANKRD20A1	ankyrin repeat domain 20 family, member A1 (ANKRD20A1), mRNA	-1.17	0.48	-0.28	1.00	-0.89	0.26
Hs_12plexchip_3_10221	v2HS_96041	TTACATTCACTGATTAACTCCT	NM_014915	ANKRD26	ankyrin repeat domain 26 (ANKRD26), mRNA	-0.76	0.40	0.53	0.38	-1.29	0.02
Hs_12plexchip_5_9857	v2HS_268762	AAGAGTTCACAATTTCAAGGCT	NM_001154	ANXA5	annexin A5 (ANXA5), mRNA	-1.67	0.54	-0.35	0.31	-1.31	0.03
Hs_12plexchip_5_7578	v2HS_267070	TTAGGGTTGTAATTAGACAGGC	NM_001282	AP2B1	adaptor-related protein complex 2, beta 1 subunit (AP2B1), transcript variant 2, mRNA	-0.90	0.72	0.76	0.91	-1.66	0.07
Hs_12plexchip_2_1576	v2HS_86184	TTATGAGTACTGGTTGTTTCGC	NM_007347	AP4E1	adaptor-related protein complex 4, epsilon 1 subunit (AP4E1), mRNA	-1.15	0.25	-0.37	0.53	-0.78	0.11
Hs_12plexchip_3_563	v2HS_48895	CTTTATTGGGATGTTAGTAGGG	NM_001024807	APLP1	amyloid beta (A4) precursor-like protein 1 (APLP1), transcript variant 1, mRNA	-0.82	0.30	-0.11	0.37	-0.71	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_8712	v2HS_236310	TTGATGCGGCTGATGAGTTCCC	NM_001645	APOC1	apolipoprotein C-I (APOC1), mRNA	-1.68	0.30	-0.36	1.08	-1.33	0.16
Hs_12plexchip_5_6098	v2HS_262529	TATAATGATCCTCATATAACCA	NM_001018159	APPBP1	amyloid beta precursor protein binding protein 1 (APPBP1), transcript variant 2, mRNA	-2.57	1.47	0.62	0.08	-3.19	0.06
Hs_12plexchip_4_142	v2HS_239573	TAGTGCAATCATTTCTGCTGGC	NM_001011645	AR	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR), transcript variant 2, mRNA	-1.26	0.61	-0.48	0.28	-0.78	0.14
Hs_12plexchip_3_11199	v2HS_132656	TTAGACTTGAGATCTCGGTGGA	NM_001654	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog (ARAF), mRNA	-1.37	0.79	-0.39	1.05	-0.98	0.27
Hs_12plexchip_4_2811	v2HS_219865	ATTTATTGTGAAAGCTCGTGGG	NM_003491	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae) (ARD1A), mRNA	-1.05	0.54	0.08	0.37	-1.14	0.05
Hs_12plexchip_5_10666	v2HS_268217	TTACGAAGAGACTGAAGCCCTA	NM_001660	ARF4	ADP-ribosylation factor 4 (ARF4), mRNA	-1.13	0.92	-0.37	0.23	-0.76	0.29
Hs_12plexchip_6_5665	v2HS_178481	TATAACCCACTCAGCATTTGGG	NM_033515	ARHGAP18	Rho GTPase activating protein 18 (ARHGAP18), mRNA	-0.89	0.58	0.11	1.07	-1.00	0.25
Hs_12plexchip_2_1027	v2HS_117113	ATATTGTGTTTCCTCTCTCGGT	NM_031305	ARHGAP24	Rho GTPase activating protein 24 (ARHGAP24), transcript variant 2, mRNA	-1.03	0.65	-0.27	0.20	-0.76	0.17
Hs_12plexchip_6_1612	v2HS_201002	ATCTTTGGAGGTAATCTTTCGC	NM_017519	ARID1B	AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 1, mRNA	-1.54	0.28	0.07	1.01	-1.60	0.10
Hs_12plexchip_5_4153	v2HS_257234	TAAGTCTAGAGAAGAAGTCCCT	NM_212481	ARID5A	AT rich interactive domain 5A (MRF1-like) (ARID5A), mRNA	-0.95	0.19	0.49	0.19	-1.44	0.00
Hs_12plexchip_5_4345	v2HS_75283	TTAAGTCTAGAGAAGAAGTCCC	NM_212481	ARID5A	AT rich interactive domain 5A (MRF1-like) (ARID5A), mRNA	-0.81	0.40	0.60	0.03	-1.41	0.02
Hs_12plexchip_3_1507	v2HS_47342	TATTCTTGGAGATTGAGATGCT	NM_001012990	ARL13A	ADP-ribosylation factor-like 13A (ARL13A), mRNA	-1.11	0.19	-0.37	0.20	-0.74	0.01
Hs_12plexchip_4_1272	v2HS_198492	GACCACTTTAAGAAGCACTGCA	NM_001037164	ARL4A	ADP-ribosylation factor-like 4A (ARL4A), transcript variant 3, mRNA	-1.67	0.58	-0.63	0.57	-1.04	0.09
Hs_12plexchip_5_4140	v2HS_87306	ATATACATAGCAAACATGACCG	NM_022374	ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2 (ARL6IP2), mRNA	-0.72	0.02	0.45	0.36	-1.16	0.03
Hs_12plexchip_5_4211	v2HS_84733	ATTTGTAAAGTGATGTTCCTCT	NM_138795	ARL8A	ADP-ribosylation factor-like 8A (ARL8A), mRNA	-1.21	0.62	-0.42	0.51	-0.79	0.17
Hs_12plexchip_2_11040	v2HS_49418	TTAGCCTTGGTCTGTGTCACTG	NM_152583	ARMCX4	ARMADILLO REPEAT CONTAINING, X-LINKED 4	-1.17	0.37	-0.43	0.54	-0.75	0.13
Hs_12plexchip_4_1283	v2HS_5802	TAGCAAAGAGACATTGTATCCT	NM_152862	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA	-1.88	0.10	-0.74	0.41	-1.14	0.03
Hs_12plexchip_4_9167	v2HS_199293	TTTAGACTCAACATACATGGTC	NM_152862	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA	-0.81	0.24	0.25	0.43	-1.06	0.03
Hs_12plexchip_5_2987	v2HS_199425	AATTTCAAAGAAATACTGACCA	NM_152862	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA	-0.99	0.31	-0.13	0.26	-0.86	0.02
Hs_12plexchip_2_12230	v2HS_202600	TTACTTATTCTTATTAAGCGCC	NM_005719	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA	-1.01	0.10	0.20	0.44	-1.22	0.04
Hs_12plexchip_4_1426	v2HS_203286	ATTAAGCGCCAGCTTTAATGCT	NM_005719	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA	-0.70	0.79	1.22	0.95	-1.93	0.06
Hs_12plexchip_2_12494	v2HS_198709	AATCTTCTCGATCTCATCAGCC	NM_005718	ARPC4	actin related protein 2/3 complex, subunit 4, 20kDa (ARPC4), transcript variant 1, mRNA	-1.05	0.30	-0.01	0.86	-1.05	0.16
Hs_12plexchip_5_11722	v2HS_137913	AAGAACTCTTATAATGGAGCCT	NM_030978	ARPC5L	actin related protein 2/3 complex, subunit 5-like (ARPC5L), mRNA	-1.93	0.57	-0.89	1.08	-1.04	0.23
Hs_12plexchip_6_1235	v2HS_89145	CTGCAATACCATTTAATCACGT	NM_001079536	ART5	ADP-ribosyltransferase 5 (ART5), transcript variant 2, mRNA	-0.73	1.73	1.43	1.70	-2.16	0.20
Hs_12plexchip_3_2527	v2HS_57238	ATAGTCCATGGTGTTGGCGCTG	NM_080871	ASB10	ankyrin repeat and SOCS box-containing 10 (ASB10), mRNA	-2.07	0.14	-1.08	0.64	-0.99	0.11
Hs_12plexchip_5_881	v2HS_249261	AATCACTGGTTCTTGGCATGGG	NM_080863	ASB16	ankyrin repeat and SOCS box-containing 16 (ASB16), mRNA	-1.24	0.62	0.37	0.10	-1.61	0.04
Hs_12plexchip_5_3598	v2HS_247779	ATGTAATCTGTGAGTAGTGCGT	NM_080868	ASB17	ankyrin repeat and SOCS box-containing 17 (ASB17), mRNA	-0.85	0.41	1.10	0.24	-1.95	0.00
Hs_12plexchip_5_3523	v2HS_157377	TTTAACTGTAGGATCAGCTCCG	NM_198243	ASB7	ankyrin repeat and SOCS box-containing 7 (ASB7), transcript variant 2, mRNA	-1.03	0.35	0.01	0.82	-1.04	0.15
Hs_12plexchip_4_314	v2HS_201941	TAAGTCTTGGATATAAACTGGC	NM_006828	ASCC3	activating signal cointegrator 1 complex subunit 3 (ASCC3), transcript variant 1, mRNA	-0.82	0.51	0.36	0.46	-1.18	0.04

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_194	v2HS_60298	AATCTCCAATACTTCATCTGCC	NM_014014	ASCC3L1	activating signal cointegrator 1 complex subunit 3-like 1 (ASCC3L1), mRNA	-3.07	0.52	-1.67	1.59	-1.40	0.26
Hs0P00011911	v2HS_15357	TTACTAACTCTGTGTAGCCCGT	NM_004318	ASPH	aspartate beta-hydroxylase (ASPH), transcript variant 1, mRNA	-0.97	0.21	-0.01	0.44	-0.96	0.04
Hs_12plexchip_5_823	v2HS_249750	AAGAGTCATCAAAGAGAAGGCA	NM_020437	ASPHD2	aspartate beta-hydroxylase domain containing 2 (ASPHD2), mRNA	-0.80	0.87	1.55	0.37	-2.34	0.03
Hs_12plexchip_6_6322	v2HS_250829	TTATTGCTACATTCCAGTGCCT	NM_017552	ATAD2B	ATPase family, AAA domain containing 2B (ATAD2B), mRNA	-0.86	0.60	0.38	0.46	-1.24	0.05
Hs_12plexchip_6_10673	v2HS_161507	TTCTTTGAGAACTTGTCCAGCA	NM_033388	ATG16L2	ATG16 autophagy related 16-like 2 (S. cerevisiae) (ATG16L2), mRNA	-1.28	1.17	0.38	1.61	-1.66	0.23
Hs_12plexchip_5_8858	v2HS_118170	TTGAGCAAGAGAACAGATTGCT	NM_052936	ATG4A	ATG4 autophagy related 4 homolog A (S. cerevisiae) (ATG4A), transcript variant 1, mRNA	-1.37	0.80	0.30	1.41	-1.67	0.17
Hs_12plexchip_5_12220	v2HS_249282	TAAGTTTCTGAGATTGTATGCT	NM_004849	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae) (ATG5), mRNA	-1.06	0.74	-0.10	0.30	-0.96	0.14
Hs0P00012021	v2HS_48744	TAGATTTGGGCCATCTGCAGGG	NM_005172	ATOH1	atonal homolog 1 (Drosophila) (ATOH1), mRNA	-1.50	0.72	-0.46	1.23	-1.04	0.29
Hs0P00008576	v2HS_136029	TATAAGTAGTCTGTGGTCTGGC	NM_024490	ATP10A	ATPase, class V, type 10A (ATP10A), mRNA	-0.77	0.20	-0.02	0.22	-0.75	0.01
Hs_12plexchip_2_3491	v2HS_78722	ATATAGATGCTGATGAGGACCC	NM_032279	ATP13A4	ATPase type 13A4 (ATP13A4), mRNA	-0.75	0.40	0.01	0.87	-0.76	0.27
Hs_12plexchip_5_7822	v2HS_112114	TTACCCTCTGATATGATGCCCA	NM_000702	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide (ATP1A2), mRNA	-1.44	1.44	0.12	0.88	-1.56	0.20
Hs_12plexchip_4_8604	v2HS_132777	TTATTACAGTCCACAGTCTGCT	NM_001679	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide (ATP1B3), mRNA	-1.07	0.98	0.43	1.29	-1.50	0.19
Hs_12plexchip_2_6141	v2HS_169195	AATCATGTCATCCTTCTGGGCT	NG_001081	ATP1BL1	ATPASE, NA+/K+ TRANSPORTING, BETA POLYPEPTIDE-LIKE 1	-0.73	0.61	0.02	0.42	-0.75	0.17
Hs_12plexchip_5_11866	v2HS_273055	TTTATCTTGGTTGACAGCTCGT	NM_001681	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2), transcript variant 2, mRNA	-1.46	0.35	-0.25	0.87	-1.21	0.12
Hs_12plexchip_4_1511	v2HS_210068	TATATTTATCCTCTGGCACGGG	NM_006356	ATP5H	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d (ATP5H), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	-2.61	0.13	-1.69	0.47	-0.92	0.07
Hs0P00010661	v2HS_39732	TATAAATCTCCCAGCTGAGCCA	NM_006045	ATP9A	ATPase, class II, type 9A (ATP9A), mRNA	-1.19	0.24	-0.28	0.50	-0.91	0.07
Hs0P00005252	v2HS_115322	TATTGGCAAAGTACTCCATGCA	NM_016301	ATPBD1C	ATP binding domain 1 family, member C (ATPBD1C), mRNA	-1.33	0.57	-0.35	0.66	-0.98	0.13
Hs_12plexchip_5_11693	v2HS_138999	TAAAGGGATCTAGGGCTTCGGC	NM_033027	AXUD1	AXIN1 up-regulated 1 (AXUD1), mRNA	-2.29	0.36	-0.99	0.80	-1.30	0.09
Hs_12plexchip_5_12166	v2HS_243530	TAATAGTTGCGATCACTTTCCG	NM_004776	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5 (B4GALT5), mRNA	-0.74	0.19	0.13	0.14	-0.87	0.00
Hs_12plexchip_5_3392	v2HS_14380	TTAATCATCATCTGGAAATCGT	NM_021813	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2 (BACH2), mRNA	-0.97	0.57	1.25	0.35	-2.22	0.01
Hs_12plexchip_3_9768	v2HS_136710	AAGTAGCAGGTGCTTCTCTGCT	NM_025045	BAIAP2L2	BAI1-associated protein 2-like 2 (BAIAP2L2), mRNA	-1.44	0.37	-0.69	0.68	-0.74	0.19
Hs_12plexchip_5_1696	v2HS_216845	GATGTACTGCACTTTCAGACGC	NM_006317	BASP1	brain abundant, membrane attached signal protein 1 (BASP1), mRNA	-2.57	0.57	-0.79	1.64	-1.78	0.19
Hs_12plexchip_4_4936	v2HS_238907	ATCTTTAAACTGCTGATACCGA	NM_080598	BAT1	HLA-B associated transcript 1 (BAT1), transcript variant 2, mRNA	-3.42	0.30	-1.62	1.17	-1.81	0.11
Hs_12plexchip_5_10118	v2HS_269487	ATTTCCGACTGAAGAGTGAGCC	NM_138578	BCL2L1	BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	-0.97	0.62	-0.05	0.83	-0.91	0.21
Hs_12plexchip_4_11126	v2HS_11736	ATAGACTTGCCCTCAGACAGCG	NM_015367	BCL2L13	BCL2-like 13 (apoptosis facilitator) (BCL2L13), nuclear gene encoding mitochondrial protein, mRNA	-1.44	0.80	-0.51	0.37	-0.93	0.17
Hs_12plexchip_3_5118	v2HS_112157	ATTTAACTCCACAATCCTTGCA	NM_000710	BDKRB1	bradykinin receptor B1 (BDKRB1), mRNA	-0.90	0.43	-0.18	0.46	-0.72	0.12
Hs_12plexchip_5_3956	v2HS_56729	TATAGCAAGCCAAGTCTGGGTG	AK013874	BFAR	BIFUNCTIONAL APOPTOSIS REGULATOR	-0.83	0.91	0.22	0.16	-1.06	0.18
Hs_12plexchip_5_9112	v2HS_233010	ATAGTTTCCCAAAGCCTTTGCT	NM_001195	BFSP1	beaded filament structural protein 1, filensin (BFSP1), mRNA	-1.68	0.39	-0.42	0.28	-1.26	0.01
Hs_12plexchip_6_957	v2HS_15182	TATGCATGTGTTATTAATAGCA	NM_004329	BMPR1A	bone morphogenetic protein receptor, type IA (BMPR1A), mRNA	-1.47	1.64	1.67	2.65	-3.14	0.17

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_6586	v2HS_15167	GAAGAGTAGGATATTCACATGT	NM_004333	BRAF	v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA	-0.84	0.46	-0.12	0.13	-0.72	0.10
Hs_12plexchip_4_5082	v2HS_89236	TTTCCAGTCCACTTTCAGAGGC	NM_000059	BRCA2	breast cancer 2, early onset (BRCA2), mRNA	-0.83	0.56	0.37	0.81	-1.20	0.11
Hs_12plexchip_2_1880	v2HS_73646	CTGTTGCATGAGAGCCTGGGCG	NM_021938	BRUNOL5	bruno-like 5, RNA binding protein (Drosophila) (BRUNOL5), mRNA	-0.87	0.37	-0.16	0.30	-0.71	0.06
Hs_12plexchip_5_11536	v2HS_195805	TATAGAAATCTCAGCAGCGCCA	NM_025238	BTBD1	BTB (POZ) domain containing 1 (BTBD1), transcript variant 1, mRNA	-0.88	0.50	0.38	0.89	-1.26	0.12
Hs0P00004338	v2HS_14497	TAATGACAGAGAAAGCACACCA	AK122818	BTBD11	BTB (POZ) DOMAIN CONTAINING 11	-0.95	0.59	0.13	0.76	-1.08	0.13
Hs_12plexchip_3_2211	v2HS_63299	TAATTGAGGTCCATATCCCGGC	NM_152733	BTBD9	BTB (POZ) domain containing 9 (BTBD9), transcript variant 3, mRNA	-1.23	0.34	-0.53	0.53	-0.70	0.14
Hs_12plexchip_4_9781	v2HS_95148	TTATTGCAGGGACATCTGAGCC	NM_181531	BTN2A2	butyrophilin, subfamily 2, member A2 (BTN2A2), transcript variant 2, mRNA	-1.17	0.38	-0.15	0.96	-1.02	0.20
Hs_12plexchip_6_801	v2HS_36634	TTCCTCTACCATTTAAGGTCCA	NM_004725	BUB3	BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), transcript variant 1, mRNA	-0.96	0.18	0.33	1.06	-1.29	0.17
Hs_12plexchip_3_12487	v2HS_240452	ATTGGGTGCACTTATAGAGCAG	M16601	BVR1	BURKITT LYMPHOMA VARIANT REARRANGING REGION 1	-0.77	0.18	0.17	0.93	-0.94	0.22
Hs_12plexchip_5_4769	v2HS_257526	ATTACTAGATTATTTGGCCGCT	NM_032194	BXDC1	brix domain containing 1 (BXDC1), mRNA	-1.44	0.33	0.43	1.01	-1.87	0.07
Hs_12plexchip_6_2513	v2HS_219526	TTAATCACAAATAGCTTATCCT	NM_018321	BXDC2	brix domain containing 2 (BXDC2), mRNA	-2.56	1.79	-0.72	0.48	-1.84	0.21
Hs_12plexchip_6_3661	v2HS_276935	TTTGTAAATCCGTTTCTTTCTT	NM_018321	BXDC2	brix domain containing 2 (BXDC2), mRNA	-0.72	0.52	0.12	0.36	-0.84	0.09
Hs_12plexchip_6_4225	v2HS_275380	TTGAACAAGGAATTTAGCAGAT	NM_018321	BXDC2	brix domain containing 2 (BXDC2), mRNA	-2.51	0.94	-0.33	1.42	-2.18	0.10
Hs_12plexchip_5_11048	v2HS_235217	TTTACCAAAGTTCAAGATAGGC	NM_025065	BXDC5	brix domain containing 5 (BXDC5), mRNA	-1.09	0.89	0.66	0.41	-1.75	0.06
Hs_12plexchip_3_156	v2HS_39009	TTAACACTTCACTGTAACTCCT	NM_153367	C10orf56	chromosome 10 open reading frame 56 (C10orf56), mRNA	-1.18	0.46	0.19	1.39	-1.36	0.23
Hs_12plexchip_2_7939	v2HS_158351	AATATGCATCCCAAACGTCGGG	BC036365	C10ORF81	CHROMOSOME 10 OPEN READING FRAME 81	-1.04	0.61	-0.09	0.57	-0.95	0.12
Hs_12plexchip_4_3707	v2HS_221262	ATCAAGAACATCTTACTGTCCA	NM_173590	C11ORF36	CHROMOSOME 11 OPEN READING FRAME 36	-1.48	0.75	-0.33	0.46	-1.15	0.10
Hs_12plexchip_4_3792	v2HS_185368	ATAATGATACATGCTCTGCCCT	NM_212555	C11orf38	chromosome 11 open reading frame 38 (C11orf38), mRNA	-0.70	0.46	0.52	0.65	-1.22	0.06
Hs_12plexchip_6_7155	v2HS_228510	AATAGTTTCAGTTGCTCAGCCC	NM_032127	C11orf56	chromosome 11 open reading frame 56 (C11orf56), transcript variant 1, mRNA	-1.75	1.06	0.51	0.61	-2.26	0.04
Hs0P00011939	v2HS_29862	TTGACAAACCAAGGGCTCAGGG	NM_145017	C11orf66	chromosome 11 open reading frame 66 (C11orf66), mRNA	-1.13	0.36	-0.41	0.29	-0.72	0.06
Hs_12plexchip_6_4960	v2HS_285512	TTGTTGTTAGGAGACCTCAGGC	NM_173578	C11orf72	chromosome 11 open reading frame 72 (C11orf72), mRNA	-1.18	0.47	-0.17	0.33	-1.01	0.05
Hs_12plexchip_5_8254	v2HS_264911	TTATACTCTTATTAACATTGCG	NM_001099676	C12orf56	chromosome 12 open reading frame 56 (C12orf56), mRNA	-1.30	0.36	-0.17	0.17	-1.13	0.02
Hs_12plexchip_5_12893	v2HS_59558	ATTAGCATGGATCGTCTGTTCT	NM_014059	C13orf15	chromosome 13 open reading frame 15 (C13orf15), mRNA	-1.48	0.73	0.21	0.69	-1.68	0.04
Hs0P00012174	v2HS_19844	AATAATTCAGACATATCCTCCT	NM_145248	C13orf28	chromosome 13 open reading frame 28 (C13orf28), mRNA	-1.60	0.54	-0.47	0.68	-1.12	0.09
Hs_12plexchip_2_11214	v2HS_45699	TATGCTTAACACAATGCCTGAC	NM_153218	C13orf31	chromosome 13 open reading frame 31 (C13orf31), mRNA	-0.75	0.62	0.65	0.38	-1.39	0.04
Hs_12plexchip_4_4497	v2HS_218412	TTATTTCCTTGATTCGGTTCCT	NM_017970	C14orf102	chromosome 14 open reading frame 102 (C14orf102), transcript variant 1, mRNA	-1.51	0.39	-0.71	0.40	-0.80	0.07
Hs_12plexchip_4_2778	v2HS_176994	ATTCCCAACAGTTCTGGGTCGC	NM_001102367	C14orf159	chromosome 14 open reading frame 159 (C14orf159), transcript variant 2, mRNA	-1.24	0.45	-0.33	0.32	-0.91	0.05
Hs_12plexchip_3_11691	v2HS_221027	ATAATCAAATACAATACAGGGC	NM_017815	C14orf94	chromosome 14 open reading frame 94 (C14orf94), mRNA	-0.88	0.31	-0.05	0.28	-0.83	0.03
Hs_12plexchip_3_3267	v2HS_62948	TTAAATAAGGGCTTTGTGTGCT	L17330	C15ORF31	CHROMOSOME 15 OPEN READING FRAME 31	-1.12	0.43	-0.40	0.37	-0.72	0.09
Hs_12plexchip_6_6781	v2HS_157506	ATAAAGAAGATTGGAGGCCGCA	NM_024731	C16orf44	chromosome 16 open reading frame 44 (C16orf44), mRNA	-0.93	0.12	-0.07	1.02	-0.85	0.28
Hs_12plexchip_2_9753	v2HS_25531	TTCATGGATGGGATTATCAGAA	NM_152308	C16orf75	chromosome 16 open reading frame 75 (C16orf75), mRNA	-1.04	0.31	-0.17	0.46	-0.87	0.06
Hs_12plexchip_6_6855	v2HS_136098	ATGGAGAAAGTCTGGATGTCCT	NM_001100407	C17orf62	chromosome 17 open reading frame 62 (C17orf62), transcript variant 1, mRNA	-0.94	0.28	0.62	1.38	-1.56	0.18
Hs_12plexchip_4_3073	v2HS_221254	TTGGTGTACTTGTAAAGTCGGC	NM_181707	C17orf64	chromosome 17 open reading frame 64 (C17orf64), mRNA	-1.32	1.47	0.15	0.58	-1.47	0.22
Hs_12plexchip_5_11737	v2HS_274367	ATCAGAGGACATATTAATAGGG	NM_025099	C17orf68	chromosome 17 open reading frame 68 (C17orf68), mRNA	-0.91	1.62	0.62	1.02	-1.52	0.25

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_4278	v2HS_255961	TAAAGGTCAAATGAGTTGTGGG	NM_203415	C17orf81	chromosome 17 open reading frame 81 (C17orf81), transcript variant 4, mRNA	-2.38	1.10	-1.06	0.88	-1.32	0.18
Hs_12plexchip_6_5550	v2HS_160761	AATTACTACCACTCAGGGTGCA	NM_173529	C18orf54	chromosome 18 open reading frame 54 (C18orf54), mRNA	-1.01	0.27	-0.12	0.79	-0.88	0.18
Hs_12plexchip_5_12662	v2HS_23231	TTATAAGACAATTTATCAGGCA	NM_134447	C19orf2	chromosome 19 open reading frame 2 (C19orf2), transcript variant 2, mRNA	-3.13	0.71	0.04	1.96	-3.16	0.09
Hs_12plexchip_2_1809	v2HS_87088	TTAAATACTCAGAACGACTCTC	AF218008	C19ORF28	HYPOTHETICAL PROTEIN PP3501	-0.74	0.06	0.14	0.87	-0.88	0.22
Hs_12plexchip_6_10344	v2HS_191151	TTTATTGTGGGAGGTGTCTGGA	NM_001100419	C19orf60	chromosome 19 open reading frame 60 (C19orf60), transcript variant 2, mRNA	-0.91	0.67	-0.15	0.71	-0.76	0.25
Hs_12plexchip_6_2827	v2HS_177170	TTCAGTGATGGTGCTCCATGCT	NM_014388	C1orf107	chromosome 1 open reading frame 107 (C1orf107), mRNA	-2.82	0.64	-1.27	1.23	-1.55	0.15
Hs_12plexchip_4_10615	v2HS_174325	TTTCATCTTCAGGTACCACCGG	NM_017887	C1orf123	chromosome 1 open reading frame 123 (C1orf123), mRNA	-1.01	0.66	0.38	0.96	-1.39	0.12
Hs_12plexchip_5_11563	v2HS_272110	TTGCTCTGATACTCAATGAGCT	NM_030933	C1orf14	chromosome 1 open reading frame 14 (C1orf14), mRNA	-1.27	0.14	0.13	0.76	-1.40	0.08
Hs_12plexchip_5_10776	v2HS_274065	TAATCCCAGGAATGGTTCTCAG	NM_018150	C1orf164	chromosome 1 open reading frame 164 (C1orf164), mRNA	-0.73	0.72	0.01	0.57	-0.74	0.24
Hs_12plexchip_3_416	v2HS_44665	ATTGTAATCCACAGTTGGAGGG	NM_001110533	C1orf177	chromosome 1 open reading frame 177 (C1orf177), transcript variant 2, mRNA	-0.79	0.63	0.19	0.41	-0.98	0.10
Hs0P00006974	v2HS_104041	TTGCTGAGAGATTGGGCCCGGG	NM_199351	C1orf32	chromosome 1 open reading frame 32 (C1orf32), mRNA	-0.85	0.26	0.10	0.60	-0.95	0.10
Hs_12plexchip_3_5773	v2HS_226812	ATAATCTCAAGTATCCCATCCG	NM_001080494	C1orf34	chromosome 1 open reading frame 34 (C1orf34), mRNA	-0.73	0.34	0.04	0.50	-0.76	0.10
Hs_12plexchip_6_8708	v2HS_92022	ATCTAACTCCTGAGGAGGTGGC	AK023774	C1ORF63	CHROMOSOME 1 OPEN READING FRAME 63	-0.81	0.65	0.04	0.29	-0.85	0.14
Hs_12plexchip_2_7945	v2HS_156526	TTTACCAGTGACATCTTGACCC	NM_018252	C1orf75	chromosome 1 open reading frame 75 (C1orf75), mRNA	-0.72	0.28	0.70	0.42	-1.43	0.01
Hs_12plexchip_2_5405	v2HS_183364	TTAGTTACTCTCTTTCCCTCCA	NM_017896	C20orf11	chromosome 20 open reading frame 11 (C20orf11), mRNA	-1.43	0.80	-0.61	0.32	-0.82	0.21
Hs_12plexchip_4_5204	v2HS_17999	TGTAGATTTCATCCAGTCTCTC	NM_024331	C20orf121	chromosome 20 open reading frame 121 (C20orf121), transcript variant 1, mRNA	-2.93	0.22	0.05	0.60	-2.98	0.01
Hs_12plexchip_2_5436	v2HS_183424	ATTGCATTTGGGTGCGGATGGC	NM_080829	C20orf175	chromosome 20 open reading frame 175 (C20orf175), mRNA	-1.34	1.02	-0.32	0.59	-1.02	0.23
Hs_12plexchip_4_91	v2HS_193993	ATTTCTCGATCTACACGATCCA	NR_003678	C20orf191	chromosome 20 open reading frame 191 (C20orf191) on chromosome 20	-0.77	0.73	0.25	0.72	-1.02	0.16
Hs_12plexchip_3_4330	v2HS_39233	AATCCATTCCGATTTCTGAGGA	NM_020356	C20orf32	chromosome 20 open reading frame 32 (C20orf32), mRNA	-0.91	0.55	0.09	0.95	-1.00	0.21
Hs_12plexchip_3_8814	v2HS_96769	TTCAAAGAAGAGGCGCTTGGCT	NM_015511	C20orf4	chromosome 20 open reading frame 4 (C20orf4), mRNA	-1.48	0.98	-0.19	0.38	-1.30	0.14
Hs_12plexchip_4_368	v2HS_96771	TTCAGAGGAAATATGGTTGCCG	NM_015511	C20orf4	chromosome 20 open reading frame 4 (C20orf4), mRNA	-1.46	0.45	-0.73	0.59	-0.73	0.17
Hs_12plexchip_2_12385	v2HS_210503	TAATCACAGCACAATCATTGCA	NM_022099	C20ORF51	CHROMOSOME 20 OPEN READING FRAME 51	-0.97	0.67	0.28	1.19	-1.25	0.21
Hs0P00006727	v2HS_102114	TTATCCACGACATTGCTTAGGT	NM_080574	C20orf70	chromosome 20 open reading frame 70 (C20orf70), mRNA	-0.90	0.44	0.87	0.88	-1.77	0.05
Hs_12plexchip_5_9198	v2HS_267872	ATGAAAGACCAGCTAATCTGGA	XM_032945	C21orf25	chromosome 21 open reading frame 25 (C21orf25), mRNA	-0.88	0.34	0.92	0.70	-1.80	0.03
Hs_12plexchip_3_12552	v2HS_244109	TTGTAATCAAGATTCTTGGGCG	NM_018944	C21orf45	chromosome 21 open reading frame 45 (C21orf45), mRNA	-3.27	0.94	-0.63	0.44	-2.64	0.02
Hs_12plexchip_4_11177	v2HS_52006	ATTTGTAATGCTTTCAAGACAT	NM_018944	C21orf45	chromosome 21 open reading frame 45 (C21orf45), mRNA	-1.04	0.73	-0.01	0.63	-1.03	0.14
Hs_12plexchip_2_11284	v2HS_47645	TAAGGGATGGAGAGACACAGCC	NM_058188	C21ORF67	CHROMOSOME 21 OPEN READING FRAME 67	-1.70	0.20	-0.60	0.63	-1.09	0.08
Hs_12plexchip_6_6841	v2HS_138230	TTTCTCTGAGACGGACTGCGCC	NM_032266	C2orf16	chromosome 2 open reading frame 16 (C2orf16), mRNA	-1.08	1.04	0.18	1.09	-1.27	0.22
Hs_12plexchip_3_392	v2HS_50725	CTGAATAAGGTCAAGATCTGCT	NM_020194	C2orf33	chromosome 2 open reading frame 33 (C2orf33), mRNA	-0.78	0.14	0.82	0.55	-1.59	0.03
Hs_12plexchip_6_7110	v2HS_35694	GATGTAGTACACCTTGGCGGCA	NM_207307	C3orf25	chromosome 3 open reading frame 25 (C3orf25), mRNA	-1.61	0.38	-0.21	0.45	-1.40	0.02
Hs_12plexchip_2_5508	v2HS_178979	TATGTAAATCATTCAGCCTGGT	NM_173657	C3orf33	chromosome 3 open reading frame 33 (C3orf33), mRNA	-0.74	0.30	0.71	0.34	-1.45	0.01
Hs_12plexchip_6_6588	v2HS_258225	TAGCACCATACCACGTGGGCCA	NM_178344	C3ORF35	CHROMOSOME 3 OPEN READING FRAME 35	-1.56	0.79	-0.71	0.48	-0.85	0.20
Hs_12plexchip_5_7316	v2HS_119846	ATTGTGTGACATATCATCTGCA	BC029129	C3ORF55	CHROMOSOME 3 OPEN READING FRAME 55	-2.22	0.27	-1.15	1.11	-1.07	0.23

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_9716	v2HS_210368	TTAGGGATTTATTACAGTTGGG	AB000464	C4ORF10	CHROMOSOME 4 OPEN READING FRAME 10	-0.87	0.22	-0.10	0.44	-0.76	0.08
Hs_12plexchip_6_6858	v2HS_160120	ATTATTCCTAGCAAACACACGG	NM_033211	C5orf30	chromosome 5 open reading frame 30 (C5orf30), mRNA	-0.85	0.52	0.28	0.38	-1.13	0.04
Hs_12plexchip_6_8467	v2HS_284705	TTGGGCCTGTACATAATATGGT	NM_001001343	C5orf40	chromosome 5 open reading frame 40 (C5orf40), mRNA	-1.08	0.05	0.12	0.21	-1.20	0.01
Hs_12plexchip_4_8659	v2HS_89094	TTTGTGAGAGGCTTGAATGGCT	NM_000065	C6	complement component 6 (C6), mRNA	-1.21	0.45	-0.06	0.59	-1.15	0.06
Hs_12plexchip_6_11217	v2HS_260682	TAATATGACAGGTTGGTGACGT	NM_183373	C6orf145	chromosome 6 open reading frame 145 (C6orf145), mRNA	-1.14	0.95	0.66	1.73	-1.80	0.21
Hs_12plexchip_6_4278	v2HS_181637	TTCCAATTTGTCATGATTCCCA	AK092941	C6ORF163	CHROMOSOME 6 OPEN READING FRAME 163	-0.72	0.28	0.66	0.91	-1.38	0.11
Hs_12plexchip_6_1960	v2HS_154208	TTGTAAGTTCTTAGGATATGCC	NM_001040437	C6orf48	chromosome 6 open reading frame 48 (C6orf48), transcript variant 1, mRNA	-1.20	0.13	0.02	0.34	-1.22	0.01
Hs_12plexchip_3_9395	v2HS_136777	ATTAAATCTTCATCTGATGCCT	NM_025059	C6orf97	chromosome 6 open reading frame 97 (C6orf97), mRNA	-0.73	0.35	0.18	0.52	-0.91	0.08
Hs_12plexchip_6_10204	v2HS_111565	TTTGCTTCTCTCATCTTGAGCA	NM_000587	C7	complement component 7 (C7), mRNA	-1.04	0.99	-0.21	0.11	-0.83	0.28
Hs_12plexchip_6_3737	v2HS_174884	ATTGAGACTGAGATATTCACCG	NM_017994	C7orf42	chromosome 7 open reading frame 42 (C7orf42), mRNA	-1.40	0.67	0.10	0.84	-1.50	0.08
Hs_12plexchip_5_9235	v2HS_93686	TTTGCTTTGTCAATCACCAGGA	NM_000562	C8A	complement component 8, alpha polypeptide (C8A), mRNA	-0.75	0.14	-0.03	0.64	-0.72	0.19
Hs_12plexchip_3_11257	v2HS_140412	TTAACATCTTGGTTGGAGCGGC	NM_053279	C8orf13	chromosome 8 open reading frame 13 (C8orf13), mRNA	-0.72	0.85	0.31	0.69	-1.02	0.18
Hs_12plexchip_2_9108	v2HS_21213	TAAATAACCTTCATAATCCCGT	NM_152416	C8orf38	chromosome 8 open reading frame 38 (C8orf38), mRNA	-0.78	0.59	0.22	0.76	-1.00	0.15
Hs_12plexchip_6_1360	v2HS_166148	TACACGTAGGAGACGATCTGGT	NM_001081675	C8ORFK36	hypothetical protein LOC340359 (C8ORFK36), mRNA	-1.90	1.54	0.25	1.90	-2.15	0.21
Hs_12plexchip_6_8721	v2HS_115684	TTTGGAGACAAGTCTGGTGGCG	NM_016390	C9orf114	chromosome 9 open reading frame 114 (C9orf114), mRNA	-1.66	1.00	-0.32	1.34	-1.34	0.24
Hs_12plexchip_5_9018	v2HS_228046	TATTGCATTGGGACGATGAGGG	NM_016481	C9orf156	chromosome 9 open reading frame 156 (C9orf156), mRNA	-2.06	0.58	-1.27	0.52	-0.79	0.16
Hs_12plexchip_5_4096	v2HS_87013	TTTAGCAATGCAGAACTTGGCA	NM_148179	C9orf23	chromosome 9 open reading frame 23 (C9orf23), transcript variant 2, mRNA	-2.09	0.72	0.25	0.22	-2.34	0.02
Hs_12plexchip_3_721	v2HS_46516	ATGTAGTTCAAAGTACGTTCCT	XM_937019	C9orf57	PREDICTED:chromosome 9 open reading frame 57 (C9orf57), mRNA	-1.79	0.61	-0.95	0.92	-0.84	0.27
Hs_12plexchip_6_9509	v2HS_221684	TTCCAATTTCAGTGAGTGTCCG	NM_017985	C9ORF68	CHROMOSOME 9 OPEN READING FRAME 68	-0.91	1.30	0.58	0.60	-1.49	0.17
Hs_12plexchip_6_10789	v2HS_160717	TTTCCAGATTAATCACAAGGCT	NM_173521	C9orf84	chromosome 9 open reading frame 84 (C9orf84), transcript variant 1, mRNA	-1.05	0.60	0.93	1.25	-1.99	0.09
Hs_12plexchip_4_2803	v2HS_186977	TTTGCTCTTATTCCCGTGGGCT	NM_173550	C9orf93	chromosome 9 open reading frame 93 (C9orf93), mRNA	-2.17	0.76	-0.82	0.53	-1.35	0.07
Hs_12plexchip_5_7273	v2HS_263904	TTTCTCTCTACAACTTGATCCT	NM_206925	CA12	carbonic anhydrase XII (CA12), transcript variant 2, mRNA	-1.59	0.07	-0.27	0.15	-1.32	0.00
Hs_12plexchip_5_8963	v2HS_228448	ATACCCTTCAACATATCCAGGT	NM_016289	CAB39	calcium binding protein 39 (CAB39), mRNA	-0.98	0.60	-0.22	0.50	-0.76	0.17
Hs_12plexchip_5_12635	v2HS_248549	TTTAGAAATGGGAGGACCAGCC	NM_006030	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), transcript variant 2, mRNA	-1.16	0.27	0.07	0.30	-1.23	0.01
Hs_12plexchip_5_8200	v2HS_112245	ATAACCTTTCAGAGAGGGTCCC	NM_000725	CACNB3	calcium channel, voltage-dependent, beta 3 subunit (CACNB3), mRNA	-1.17	0.92	0.99	1.53	-2.16	0.12
Hs_12plexchip_4_12251	v2HS_225162	TTAGCACAGTAAATACTGTGCT	NM_001005747	CACNB4	calcium channel, voltage-dependent, beta 4 subunit (CACNB4), transcript variant 1, mRNA	-1.18	0.71	-0.26	0.51	-0.92	0.15
Hs_12plexchip_4_10665	v2HS_158576	TTGAAATAAGGGAGTCTGTGGG	NM_031896	CACNG7	calcium channel, voltage-dependent, gamma subunit 7 (CACNG7), mRNA	-0.97	0.55	-0.16	0.41	-0.81	0.11
Hs_12plexchip_4_10283	v2HS_158567	TTCCTCTTGGACTTGTAGACGC	NM_031895	CACNG8	calcium channel, voltage-dependent, gamma subunit 8 (CACNG8), mRNA	-0.72	0.82	0.14	0.47	-0.86	0.21
Hs_12plexchip_3_9987	v2HS_130329	TTGTCTTGCCACTGTGTTTGCC	NM_033429	CALML4	calmodulin-like 4 (CALML4), transcript variant 1, mRNA	-0.92	0.59	-0.12	0.26	-0.81	0.13
Hs_12plexchip_4_9782	v2HS_15097	TTGTATTCTGAGTCTCCGTGCA	NM_004343	CALR	calreticulin (CALR), mRNA	-2.33	0.73	-0.50	0.86	-1.82	0.05
Hs_12plexchip_6_936	v2HS_112696	TTTATTGATGAGGTCTTTGGCT	NM_172127	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), transcript variant 1, mRNA	-1.34	0.51	-0.64	0.24	-0.70	0.13
Hs0P00002217	v2HS_98761	TACATGATGACTCCAATGGCCC	NM_024046	CAMKV	CAM KINASE-LIKE VESICLE-ASSOCIATED	-2.15	0.68	-1.01	0.80	-1.14	0.13
Hs_12plexchip_5_5676	v2HS_88963	CAAACTTATGAGTTGGACAGCC	NM_173089	CAPN3	calpain 3, (p94) (CAPN3), transcript variant 5, mRNA	-0.95	0.54	0.01	0.40	-0.95	0.08

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_6885	v2HS_62217	TTCTTTGATCCATCTCCAGCCT	NM_004930	CAPZB	capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA	-0.81	0.28	-0.02	0.24	-0.79	0.02
Hs_12plexchip_5_2517	v2HS_212329	CTCCTCAAGCACAGGACAAGGG	NM_014316	CARHSP1	CALCIUM REGULATED HEAT STABLE PROTEIN 1, 24KDA	-1.51	1.70	0.59	1.41	-2.10	0.18
Hs_12plexchip_5_4216	v2HS_256535	ATTTGAATGGGATTTCTATCCT	NM_199141	CARM1	coactivator-associated arginine methyltransferase 1 (CARM1), mRNA	-1.52	0.55	-0.23	0.22	-1.29	0.04
Hs_12plexchip_4_10865	v2HS_38737	ATAGACAAAGGATTTGACAGGC	NM_144508	CASC5	cancer susceptibility candidate 5 (CASC5), transcript variant 2, mRNA	-1.59	0.44	-0.46	0.16	-1.13	0.03
Hs_12plexchip_5_7843	v2HS_112746	ATACAGGATTAGAGAGAGTGGG	NM_001231	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle) (CASQ1), nuclear gene encoding mitochondrial protein, mRNA	-0.82	0.45	0.17	0.38	-0.99	0.05
Hs_12plexchip_5_5327	v2HS_88343	ATAGTGGGATAAATTCTCACCG	NM_053054	CATSPER1	cation channel, sperm associated 1 (CATSPER1), mRNA	-1.93	0.38	-0.32	0.64	-1.61	0.03
Hs_12plexchip_3_3527	v2HS_48406	TTATTGTGAGGGATTGTCTGGA	NM_005188	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence (CBL), mRNA	-1.33	0.39	-0.51	0.30	-0.82	0.05
Hs_12plexchip_4_7111	v2HS_72019	ATAACTCAGGAGTGGGTCATCC	NM_080617	CBLN4	cerebellin 4 precursor (CBLN4), mRNA	-0.81	1.17	1.15	1.94	-1.96	0.22
Hs_12plexchip_5_8103	v2HS_112767	TTCATTATCGGCAGTAACTCGT	NM_001236	CBR3	carbonyl reductase 3 (CBR3), mRNA	-0.79	0.37	0.07	0.40	-0.86	0.05
Hs_12plexchip_5_7130	v2HS_88903	TTTGCCTTTAATCCACTCTGCG	NM_000071	CBS	cystathionine-beta-synthase (CBS), mRNA	-0.87	0.35	0.32	0.39	-1.19	0.02
Hs_12plexchip_5_139	v2HS_245413	TTAGCTCTTCATATATCAACCT	NM_152549	CCDC112	coiled-coil domain containing 112 (CCDC112), transcript variant 2, mRNA	-1.58	0.19	0.09	0.35	-1.67	0.01
Hs_12plexchip_6_2225	v2HS_33560	ATAGTCCAAGAGGAAGTCTCCA	NM_033626	CCDC120	coiled-coil domain containing 120 (CCDC120), mRNA	-1.36	0.43	-0.28	0.41	-1.08	0.03
Hs0P00003928	v2HS_35985	TTTCCTATTTCTTTACTGGCCA	NM_144982	CCDC131	coiled-coil domain containing 131 (CCDC131), mRNA	-0.86	0.23	0.16	0.31	-1.02	0.01
Hs_12plexchip_3_8644	v2HS_98369	TTTGGTAAGGTTATTCCCAGGC	NM_022757	CCDC14	coiled-coil domain containing 14 (CCDC14), mRNA	-1.64	0.64	-0.82	0.27	-0.82	0.14
Hs_12plexchip_6_6684	v2HS_157109	AATGTCACACAGGTGACCAGGG	NM_024661	CCDC51	coiled-coil domain containing 51 (CCDC51), mRNA	-1.32	0.94	-0.55	0.54	-0.77	0.30
Hs_12plexchip_6_180	v2HS_53593	TTAGAATCACAGTCCAACAGTC	AF161533	CCDC82	HYPOTHETICAL PROTEIN FLJ23518	-1.80	0.94	-0.76	0.63	-1.04	0.20
Hs0P00010500	v2HS_178798	TTTCTGGTTGTGTCAGTGGCCG	NM_173618	CCDC95	coiled-coil domain containing 95 (CCDC95), mRNA	-1.79	0.06	-1.00	0.84	-0.79	0.24
Hs_12plexchip_6_4338	v2HS_176445	TTTATGGACTCCCTGGTGGGCA	NM_001105564	CCHCR1	coiled-coil alpha-helical rod protein 1 (CCHCR1), transcript variant 1, mRNA	-0.70	0.32	1.04	0.67	-1.74	0.03
Hs0P00003883	v2HS_197544	TAATGCATTTACTTATTCTCCC	NM_005893	CCIN	CALICIN	-1.41	0.91	0.25	0.62	-1.66	0.07
Hs_12plexchip_4_500	v2HS_112771	TTTGCTTTCCAAGGAGGAACGG	NM_001237	CCNA2	cyclin A2 (CCNA2), mRNA	-1.84	0.56	-0.65	0.58	-1.19	0.06
Hs0P00010228	v2HS_150278	ATTTGTTCCCATATTGCAGGCA	NM_001759	CCND2	CYCLIN D2	-1.04	0.61	-0.13	0.79	-0.92	0.19
Hs_12plexchip_3_10101	v2HS_235350	ATTGTGAGGAATACAGGGAGGA	NM_178445	CCRL1	chemokine (C-C motif) receptor-like 1 (CCRL1), transcript variant 1, mRNA	-1.21	0.30	-0.39	0.17	-0.83	0.02
Hs_12plexchip_4_1037	v2HS_198914	TATTCCATGCTTAAGAATACGT	NM_006431	CCT2	chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA	-2.09	0.48	-0.86	0.26	-1.24	0.03
Hs_12plexchip_5_6818	v2HS_199868	ATTGGTTACCATAAGAGAGGCA	NM_006431	CCT2	chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA	-0.74	0.40	0.13	0.44	-0.87	0.07
Hs_12plexchip_6_9240	v2HS_206188	CATCGGAAGCAAACTAAATGGA	NM_001008883	CCT3	chaperonin containing TCP1, subunit 3 (gamma) (CCT3), transcript variant 2, mRNA	-4.76	0.37	-0.97	3.04	-3.79	0.16
Hs_12plexchip_4_8509	v2HS_150300	ATATACAAGTCCTGCATGTCCC	NM_001762	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), transcript variant 1, mRNA	-0.85	0.98	0.02	0.76	-0.88	0.29
Hs_12plexchip_5_2555	v2HS_252764	ATTTCATAACCTTCTATGACCT	NM_006585	CCT8	chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA	-0.80	0.05	0.56	0.29	-1.36	0.01
Hs_12plexchip_3_5587	v2HS_226879	ATTCTGTCTTGGATCTTAGGCA	NM_001040021	CD14	CD14 molecule (CD14), transcript variant 2, mRNA	-1.37	0.18	-0.63	0.31	-0.74	0.03
Hs_12plexchip_5_2308	v2HS_253311	ATAATAACTAGGTGCCTGACCC	NM_006566	CD226	CD226 molecule (CD226), mRNA	-0.84	0.21	0.55	1.39	-1.38	0.23
Hs_12plexchip_3_1812	v2HS_65350	GTAGAGGTCAAAGTCAATGCGT	NM_006110	CD2BP2	CD2 (cytoplasmic tail) binding protein 2 (CD2BP2), mRNA	-0.76	0.80	0.25	0.80	-1.02	0.19
Hs_12plexchip_3_7175	v2HS_95841	AATAGGGAAGATACAGCAGGCA	NM_014880	CD302	CD302 molecule (CD302), mRNA	-0.95	0.33	-0.14	0.37	-0.81	0.05
Hs_12plexchip_5_12262	v2HS_28520	TAGATTTACCCAGGAAACAGCT	NM_012099	CD3EAP	CD3e molecule, epsilon associated protein (CD3EAP), mRNA	-1.24	0.87	-0.39	0.38	-0.85	0.23
Hs_12plexchip_3_8773	v2HS_229315	AACAAGACACAAGGACTATCCC	AB209380	CD81	CD81 ANTIGEN (TARGET OF ANTIPROLIFERATIVE ANTIBODY 1)	-0.98	0.68	0.49	0.17	-1.47	0.06
Hs_12plexchip_3_9562	v2HS_133577	ATTTGGTGACTTTGATACAGGC	NM_002231	CD82	CD82 molecule (CD82), transcript variant 1, mRNA	-0.70	0.60	0.53	0.50	-1.23	0.05

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_1764	v2HS_212353	TTTGCCTATCACTCTATCTGTC	NM_198196	CD96	CD96 molecule (CD96), transcript variant 1, mRNA	-0.81	0.28	0.51	0.23	-1.32	0.00
Hs_12plexchip_5_3556	v2HS_254661	TATTCTAATCCAATATACAGCA	NM_001078645	CDC16	cell division cycle 16 homolog (S. cerevisiae) (CDC16), transcript variant 2, mRNA	-1.51	0.17	0.03	0.17	-1.54	0.00
Hs_12plexchip_5_6669	v2HS_262434	TAACTAACTCAACAGACTGGGC	NM_021873	CDC25B	cell division cycle 25 homolog B (S. pombe) (CDC25B), transcript variant 1, mRNA	-0.76	0.13	0.00	0.68	-0.77	0.18
Hs_12plexchip_5_3479	v2HS_226246	ATAATGATTCAAAGGGAGACCA	NM_001256	CDC27	cell division cycle 27 homolog (S. cerevisiae) (CDC27), mRNA	-1.11	0.36	0.03	0.29	-1.14	0.01
Hs_12plexchip_4_269	v2HS_24388	TTTGGTTTCACCATAGCGAGGC	NM_031267	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, mRNA	-0.81	0.42	0.24	0.16	-1.05	0.04
Hs_12plexchip_6_847	v2HS_24391	ATAGTTGTGCATCTTTGCTGGC	NM_031267	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller) (CDC2L5), transcript variant 2, mRNA	-0.96	0.41	0.71	1.42	-1.67	0.17
Hs0P00000385	v2HS_24387	ATTTCCAATGAAACTACGTCGT	NM_003718	CDC2L5	CELL DIVISION CYCLE 2-LIKE 5 (CHOLINESTERASE-RELATED CELL DIVISION CONTROLLER)	-0.74	0.16	0.67	0.69	-1.41	0.07
Hs_12plexchip_4_2491	v2HS_174475	AATAAACTGCATTACAACAGCT	NM_017913	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1 (CDC37L1), mRNA	-0.97	0.56	-0.06	0.18	-0.90	0.10
Hs_12plexchip_4_9521	v2HS_172576	TTAATGAGTAATTTGATCTGGG	NM_003504	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA	-1.57	0.36	-0.69	0.09	-0.88	0.05
Hs_12plexchip_5_7026	v2HS_262205	TTCAGCTCAATTACTGAGAGGT	NM_003504	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA	-1.57	0.69	-0.04	1.08	-1.53	0.12
Hs0P00008651	v2HS_112872	TTTAGACACTCTAGCCTCCGGG	NM_001253	CDC5L	CDC5 CELL DIVISION CYCLE 5-LIKE (S. POMBE)	-0.70	0.80	0.32	0.14	-1.02	0.15
Hs_12plexchip_3_9508	v2HS_136197	ATAATTCAGAATCTCAAGTGCG	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-2.05	0.45	-0.14	0.71	-1.91	0.02
Hs_12plexchip_5_10993	v2HS_235686	TTTCCATTACAGACTAGAAGGC	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-2.51	0.80	-0.39	0.75	-2.12	0.03
Hs_12plexchip_5_11993	v2HS_272144	TTAAGTAATGCTAATTTAACCA	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-4.70	1.03	-0.63	0.30	-4.08	0.01
Hs_12plexchip_5_7017	v2HS_99464	TAGTACCTTGCTGCTGTTTGGT	NM_031299	CDCA3	cell division cycle associated 3 (CDCA3), mRNA	-0.75	0.88	0.80	0.61	-1.54	0.08
Hs_12plexchip_4_10431	v2HS_155714	AATTTCCACTAACTAGGGAGGT	NM_018101	CDCA8	cell division cycle associated 8 (CDCA8), mRNA	-2.01	0.82	-0.03	0.27	-1.98	0.04
Hs_12plexchip_5_6926	v2HS_262071	ATAACAAATACCACAGAGAGCC	NM_018101	CDCA8	cell division cycle associated 8 (CDCA8), mRNA	-1.20	0.38	0.13	0.78	-1.33	0.08
Hs_12plexchip_4_8826	v2HS_150461	TTTGTGACTCGGAAGAACTGGC	NM_001795	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA	-1.57	0.99	0.65	1.16	-2.22	0.07
Hs_12plexchip_3_6480	v2HS_112920	TTCTAACGGACCAAACTGTGCC	NM_001261	CDK9	cyclin-dependent kinase 9 (CDK9), mRNA	-0.90	0.81	-0.03	0.51	-0.87	0.20
Hs_12plexchip_3_12615	v2HS_33603	ATTCAAACACCAGGTGAAGCCT	NM_004196	CDKL1	cyclin-dependent kinase-like 1 (CDC2-related kinase) (CDKL1), mRNA	-0.91	0.38	-0.08	0.38	-0.83	0.06
Hs_12plexchip_4_182	v2HS_134767	ATGATCATACAGCCCAAAGCCC	NM_016508	CDKL3	cyclin-dependent kinase-like 3 (CDKL3), mRNA	-1.30	1.14	0.67	0.74	-1.97	0.08
Hs_12plexchip_5_6683	v2HS_134769	ATTTGAACTGAGATTTGCAGCC	NM_016508	CDKL3	cyclin-dependent kinase-like 3 (CDKL3), mRNA	-0.85	0.42	0.23	0.24	-1.08	0.03
Hs_12plexchip_5_12702	v2HS_254033	TTTCTTCATCATCAGACTCCGG	NM_005760	CEBPZ	CCAAT/enhancer binding protein zeta (CEBPZ), mRNA	-0.88	0.41	0.46	1.32	-1.34	0.21
Hs_12plexchip_2_7527	v2HS_154324	AACTTCTGAGCTACTTCCTGGT	NM_177405	CECR1	cat eye syndrome chromosome region, candidate 1 (CECR1), transcript variant 2, mRNA	-0.74	0.40	0.32	0.31	-1.07	0.03
Hs_12plexchip_4_7607	v2HS_150546	TATCACTGAGGTATCTTGGGCC	NM_001813	CENPE	centromere protein E, 312kDa (CENPE), mRNA	-2.78	0.92	-1.83	0.91	-0.95	0.27
Hs0P00009414	v2HS_135881	TTGGCAATACATGCTTTCACGC	NM_024322	CENPO	centromere protein O (CENPO), mRNA	-0.73	0.06	0.17	0.35	-0.90	0.05
Hs_12plexchip_4_7048	v2HS_64314	ATAGGTTGCATCATAGAGGGCA	NM_005507	CFL1	cofilin 1 (non-muscle) (CFL1), mRNA	-1.51	0.51	0.09	1.93	-1.60	0.29
Hs_12plexchip_6_506	v2HS_68418	TTAAAGGGCAGATTCATATGCG	NM_005483	CHAF1A	chromatin assembly factor 1, subunit A (p150) (CHAF1A), mRNA	-1.43	0.22	-0.46	1.07	-0.98	0.25

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_6562	v2HS_68534	TTTGAGGTAGAGCTTGTTGCCT	NM_017780	CHD7	chromodomain helicase DNA binding protein 7 (CHD7), mRNA	-1.13	1.11	0.16	1.01	-1.29	0.21
Hs0P00000804	v2HS_59813	TTGATTCACAATATCCTGGCTT	NM_014043	CHMP2B	chromatin modifying protein 2B (CHMP2B), mRNA	-0.97	1.63	1.21	1.51	-2.18	0.16
Hs_12plexchip_6_10314	v2HS_150582	TTAGATGTGCCATGAGGTACCG	NM_001025201	CHN1	chimerin (chimaerin) 1 (CHN1), transcript variant 2, mRNA	-1.32	0.62	-0.21	0.53	-1.11	0.08
Hs_12plexchip_5_8714	v2HS_226214	TATTTACTTAGGCCTCATCGGC	NM_000750	CHRNB4	cholinergic receptor, nicotinic, beta 4 (CHRNB4), mRNA	-0.76	0.40	1.70	0.41	-2.46	0.00
Hs_12plexchip_6_2469	v2HS_81221	GTAGTAGAAGTCGTAGGTGCGC	NM_022467	CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (CHST8), mRNA	-1.47	0.42	-0.26	1.42	-1.21	0.27
Hs_12plexchip_4_11313	v2HS_63199	AATACAGGTGATGCCATATCCA	NM_175856	CHSY-2	chondroitin synthase-2 (CHSY-2), mRNA	-1.20	0.44	-0.45	0.15	-0.75	0.09
Hs_12plexchip_3_2535	v2HS_67521	TTTGATATTGGATTTGGAGGCA	NM_004882	CIR	CBF1 interacting corepressor (CIR), mRNA	-0.86	0.18	-0.15	0.64	-0.71	0.19
Hs_12plexchip_6_6961	v2HS_219871	ATCATACTCCATAATCTCGCCA	NM_032830	CIRH1A	cirrhosis, autosomal recessive 1A (cirhin) (CIRH1A), mRNA	-2.99	0.63	-1.60	1.61	-1.39	0.27
Hs_12plexchip_3_2222	v2HS_69129	AAGTGCAAAGAGATGACTGCAG	NM_007174	CIT	citron (rho-interacting, serine/threonine kinase 21) (CIT), mRNA	-1.34	0.79	-0.37	1.13	-0.97	0.30
Hs_12plexchip_4_4727	v2HS_201960	ATTTGCTGCAAGTTTATTGGCT	NM_007174	CIT	citron (rho-interacting, serine/threonine kinase 21) (CIT), mRNA	-0.71	0.29	0.08	0.83	-0.79	0.24
Hs_12plexchip_3_8327	v2HS_95214	TTAGTAAACTAAAGCTGCAGGG	NM_001008938	CKAP5	cytoskeleton associated protein 5 (CKAP5), transcript variant 1, mRNA	-3.56	1.02	-1.93	0.73	-1.63	0.09
Hs_12plexchip_6_2053	v2HS_201392	ATTAGAAATATCAAAGACACCG	NM_001015001	CKMT1A	creatine kinase, mitochondrial 1A (CKMT1A), nuclear gene encoding mitochondrial protein, mRNA	-1.04	0.54	-0.14	0.95	-0.89	0.25
Hs_12plexchip_2_2640	v2HS_88703	TTGTGATGGCCATAAATCTGTG	NM_000083	CLCN1	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA	-0.78	0.32	-0.04	0.50	-0.73	0.11
Hs_12plexchip_5_5654	v2HS_256894	TAATTCGAAGCAAATCACAGCT	NM_000083	CLCN1	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA	-1.31	0.45	-0.18	0.22	-1.13	0.03
Hs0P00007094	v2HS_95077	TAACATGTCTATTTAACCTGGA	NM_006984	CLDN10	claudin 10 (CLDN10), transcript variant 2, mRNA	-1.01	0.43	-0.16	0.70	-0.84	0.17
Hs_12plexchip_5_8526	v2HS_113072	ATCTTGTTGGTGTCTGTGTGCA	NM_001288	CLIC1	chloride intracellular channel 1 (CLIC1), mRNA	-2.26	0.55	-0.34	1.31	-1.92	0.11
Hs_12plexchip_5_12863	v2HS_85244	ATTCGTTAGTACATATCCAGGA	NM_013943	CLIC4	chloride intracellular channel 4 (CLIC4), mRNA	-0.70	0.16	0.25	0.72	-0.95	0.15
Hs_12plexchip_5_6542	v2HS_262685	TATACTCCACACATCACAAGGC	NM_003993	CLK2	CDC-like kinase 2 (CLK2), mRNA	-1.07	0.81	0.43	1.14	-1.50	0.14
Hs_12plexchip_6_6739	v2HS_157517	TTAACAGTGTAGGTACGCTCCC	NM_024734	CLMN	calmin (calponin-like, transmembrane) (CLMN), mRNA	-0.93	0.27	-0.03	0.65	-0.90	0.12
Hs_12plexchip_2_2156	v2HS_90670	ATTAGGGACTTCAAACATTGGT	NM_006660	CLPX	ClpX caseinolytic peptidase X homolog (E. coli) (CLPX), mRNA	-0.79	0.89	0.15	0.79	-0.94	0.24
Hs_12plexchip_5_4277	v2HS_259796	TTTCTGTGGGAGCTGGCTAGGC	NM_014718	CLSTN3	calsyntenin 3 (CLSTN3), mRNA	-0.95	0.11	0.53	0.59	-1.49	0.04
Hs0P00010717	v2HS_150632	TTATTGACGTACTTACTTCCCT	NM_001831	CLU	CLUSTERIN	-0.72	0.30	0.45	0.48	-1.17	0.03
Hs_12plexchip_6_4923	v2HS_220463	TTCTTCTTGGTGCCTTTGTCCT	NM_005140	CNGA2	cyclic nucleotide gated channel alpha 2 (CNGA2), mRNA	-1.64	1.03	-0.60	0.73	-1.04	0.24
Hs_12plexchip_3_5087	v2HS_115263	TAAATCAATCAGTAGCTGTGCA	NM_016284	CNOT1	CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 1, mRNA	-2.14	0.59	-0.89	1.47	-1.25	0.28
Hs0P00005661	v2HS_115260	TATCAATGGCATAGGACAGCGT	NM_206999	CNOT1	CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 2, mRNA	-2.09	0.52	0.51	0.34	-2.60	0.00
Hs_12plexchip_6_8614	v2HS_215771	ATGTCTCAAAGGTCTCTGACAT	NM_006586	CNPY3	canopy 3 homolog (zebrafish) (CNPY3), mRNA	-0.98	1.11	0.13	0.42	-1.11	0.22
Hs_12plexchip_3_12772	v2HS_245484	TTTCAATGACAGATGTGCTGCT	NM_175613	CNTN4	contactin 4 (CNTN4), transcript variant 3, mRNA	-1.11	0.89	-0.35	0.32	-0.75	0.28
Hs_12plexchip_6_8734	v2HS_27668	TTAAAGGAGCCCTGTGTGGCCA	NM_003632	CNTNAP1	contactin associated protein 1 (CNTNAP1), mRNA	-1.71	0.77	-0.44	1.05	-1.27	0.17
Hs_12plexchip_5_9154	v2HS_268783	ATATTGTATTTGATGGAATGGT	NM_014900	COBLL1	COBL-like 1 (COBLL1), mRNA	-1.10	0.21	-0.19	0.47	-0.92	0.06
Hs_12plexchip_3_2348	v2HS_71589	TTATTGTCATAGGACATCTCCT	NM_001854	COL11A1	collagen, type XI, alpha 1 (COL11A1), transcript variant A, mRNA	-1.00	0.68	-0.15	0.33	-0.85	0.15
Hs_12plexchip_5_3992	v2HS_261190	TTGAGCATTGCCTTTGATTGCT	NM_000088	COL1A1	collagen, type I, alpha 1 (COL1A1), mRNA	-1.24	1.00	-0.03	1.32	-1.21	0.28
Hs_12plexchip_3_2655	v2HS_69100	AACCAATAGGCAATCCTGGGCC	NM_152890	COL24A1	collagen, type XXIV, alpha 1 (COL24A1), mRNA	-1.41	0.02	-0.37	1.09	-1.04	0.24
Hs_12plexchip_3_4527	v2HS_114742	TTTGAGATGCAAATTATGCCCT	NM_015719	COL5A3	collagen, type V, alpha 3 (COL5A3), mRNA	-0.93	0.39	-0.07	0.45	-0.86	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00004205	v2HS_254700	TTTATTCCCGATTTCATAAGCA	NM_004236	COPS2	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 2 (ARABIDOPSIS)	-1.37	0.10	-0.01	0.06	-1.37	0.00
Hs_12plexchip_4_5654	v2HS_27408	TAAAGAGATGACAAGCATTGCT	NM_003653	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis) (COPS3), mRNA	-0.77	0.64	0.62	1.19	-1.39	0.17
Hs0P00006262	v2MM_21587	TATGATTCCAACATGATATGGC	NM_011991	COPS3	COP9 (CONSTITUTIVE PHOTOMORPHOGENIC) HOMOLOG, SUBUNIT 3 (ARABIDOPSIS THALIANA)	-1.09	0.41	-0.24	0.44	-0.84	0.07
Hs0P00005048	v2HS_229617	TTAGCTTAATACACAGAGACCC	NM_016129	COPS4	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 4 (ARABIDOPSIS)	-3.17	0.96	1.41	0.62	-4.59	0.00
Hs0P00005841	v2HS_258048	ATATTTAGGACACTTCAGAGCA	NM_006837	COPS5	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 5 (ARABIDOPSIS)	-1.56	0.22	-0.29	0.31	-1.27	0.01
Hs_12plexchip_6_1364	v2HS_118859	ATATAAAGCTAGAAGCTGACCA	NM_198189	COPS8	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 2, mRNA	-1.65	1.87	0.12	1.66	-1.77	0.29
Hs_12plexchip_3_8592	v2HS_230806	TTCCATTCTCCATCTTCCTGGG	NM_016057	COPZ1	coatomer protein complex, subunit zeta 1 (COPZ1), mRNA	-0.83	0.32	0.06	0.97	-0.89	0.25
Hs_12plexchip_5_12701	v2HS_197844	TAATCCAAATAATGTCCACCGT	NM_006587	CORIN	corin, serine peptidase (CORIN), mRNA	-0.93	0.28	-0.20	0.36	-0.73	0.06
Hs_12plexchip_4_467	v2HS_159527	TTCTCCTTCTCCTTCAGGGCCT	NM_032609	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung) (COX4I2), nuclear gene encoding mitochondrial protein, mRNA	-2.40	0.26	-0.54	0.49	-1.86	0.01
Hs_12plexchip_6_9703	v2HS_194922	TAAACAATTCATTATTACACCA	NM_001866	COX7B	cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA	-0.84	0.40	-0.05	0.10	-0.79	0.07
Hs_12plexchip_5_12790	v2HS_47731	GTATGAGACCAGTTGTGTGGGC	NM_152930	CPNE1	copine I (CPNE1), transcript variant 7, mRNA	-2.35	1.06	-0.88	0.18	-1.47	0.13
Hs_12plexchip_5_589	v2HS_47732	ATCTTGACACGGATAGTTCCAG	NM_152930	CPNE1	copine I (CPNE1), transcript variant 7, mRNA	-0.90	0.51	-0.12	0.32	-0.78	0.10
Hs_12plexchip_3_2449	v2HS_54192	ATAGTCCACAACTTGGTTTGGG	NM_130808	CPNE4	copine IV (CPNE4), mRNA	-1.33	0.63	-0.15	1.03	-1.18	0.18
Hs_12plexchip_2_12565	v2HS_200540	GTAATCCACAATGAACTTGCGC	NM_020939	CPNE5	copine V (CPNE5), mRNA	-1.51	0.20	-0.65	0.54	-0.86	0.10
Hs_12plexchip_6_4659	v2HS_179686	ATACTTCTTGACATCATGTCCT	NM_017437	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa (CPSF2), mRNA	-1.76	0.43	-0.52	0.97	-1.24	0.14
Hs0P00010064	v2HS_24305	TTGATCTCAGTGGTGCGCACGG	NM_004378	CRABP1	cellular retinoic acid binding protein 1 (CRABP1), mRNA	-2.05	0.87	-0.94	0.26	-1.10	0.15
Hs_12plexchip_2_9846	v2HS_16655	ATGGGTAATAATATTAGTGTCT	NM_003851	CREG1	cellular repressor of E1A-stimulated genes 1 (CREG1), mRNA	-1.39	0.47	-0.14	0.37	-1.25	0.03
Hs_12plexchip_3_9661	v2HS_234794	AATAATTTAAAGGGTAAGTCCG	NM_024324	CRELD2	cysteine-rich with EGF-like domains 2 (CRELD2), mRNA	-0.91	0.33	-0.14	0.26	-0.77	0.03
Hs_12plexchip_5_10727	v2HS_135449	ATACACTTTCCGTGCATGGGCA	NM_016652	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila) (CRNKL1), mRNA	-1.57	0.65	-0.33	0.41	-1.24	0.06
Hs_12plexchip_5_9115	v2HS_97938	TTGATGCATTAGGGTAGATGGG	NM_016190	CRNN	cornulin (CRNN), mRNA	-1.11	0.13	0.23	0.15	-1.34	0.00
Hs_12plexchip_6_3781	v2HS_172863	ATAAGTTAGAGGCGGTTGTCCA	NM_004075	CRY1	cryptochrome 1 (photolyase-like) (CRY1), mRNA	-0.91	0.59	0.05	1.10	-0.96	0.27
Hs_12plexchip_4_7258	v2HS_67009	GTCATATTCAAAGGTCAAGCGG	NM_021117	CRY2	cryptochrome 2 (photolyase-like) (CRY2), mRNA	-1.25	0.22	-0.42	0.92	-0.83	0.26
Hs_12plexchip_4_10537	v2HS_134602	ATAGAGTTTCACCTGGAAGCCT	NM_015974	CRYL1	crystallin, lambda 1 (CRYL1), mRNA	-1.28	1.08	-0.24	0.76	-1.04	0.25
Hs_12plexchip_4_12174	v2HS_150947	AACATAAATGAGGATCTCAGCA	NM_001014444	CRYM	crystallin, mu (CRYM), transcript variant 2, mRNA	-0.80	0.56	0.36	1.30	-1.17	0.26
Hs_12plexchip_2_5379	v2HS_169296	TTAGATAAAGACTTCCAGCCCA	NG_001109	CRYZP1	CRYSTALLIN, ZETA (QUINONE REDUCTASE) PSEUDOGENE 1	-0.80	0.32	-0.04	0.44	-0.75	0.08
Hs_12plexchip_6_4139	v2HS_172878	TTAGGCTTCCTCACTTTCTGGT	NM_198324	CS	citrate synthase (CS), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.03	0.32	0.26	1.02	-1.28	0.15
Hs_12plexchip_4_12319	v2HS_113224	AATGAATGTGCTGTACGGAGGA	NM_001316	CSE1L	CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA	-3.11	0.70	-1.13	1.02	-1.98	0.06
Hs0P00010372	v2HS_191980	TTAATTTCAGTCCATAACTCGT	NM_177436	CSE1L	CSE1 CHROMOSOME SEGREGATION 1-LIKE (YEAST)	-2.14	0.45	-1.40	0.12	-0.74	0.09
Hs_12plexchip_4_12062	v2HS_150957	TTCATTCTGCGAATTTGCTCCT	NM_001890	CSN1S1	casein alpha s1 (CSN1S1), transcript variant 1, mRNA	-0.71	0.35	0.30	0.56	-1.01	0.07
Hs_12plexchip_4_1055	v2HS_671	TATTGGTTCCAGTTTGATTGCT	NM_022048	CSNK1G1	casein kinase 1, gamma 1 (CSNK1G1), mRNA	-1.00	0.75	0.24	0.73	-1.24	0.11
Hs_12plexchip_4_7857	v2HS_150988	ATTAGTCGTAGCTTTCTGTGCT	NM_001895	CSNK2A1	casein kinase 2, alpha 1 polypeptide (CSNK2A1), transcript variant 2, mRNA	-1.60	1.57	-0.03	1.03	-1.56	0.23

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_313	v2HS_203075	TAATCCCTTGAACCAGAAGCCA	NM_001324	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa (CSTF1), transcript variant 2, mRNA	-0.71	0.33	0.05	0.82	-0.77	0.24
Hs_12plexchip_3_8151	v2HS_229799	TTCTCGTAGGAAATAACCTGCT	NM_178561	CTAGE6	CTAGE family, member 6 (CTAGE6), mRNA	-1.76	0.55	-0.71	0.97	-1.05	0.20
Hs_12plexchip_5_6702	v2HS_262377	ATTATTTGAGATGGAACAGGCC	NM_001903	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa (CTNNA1), mRNA	-0.82	0.54	1.07	0.19	-1.89	0.02
Hs_12plexchip_3_11951	v2HS_239988	TTATTTCCAGAGGTTCTGTCCC	NM_003798	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA	-1.29	0.46	-0.12	0.48	-1.17	0.04
Hs_12plexchip_6_1286	v2HS_62138	ATCTGAAAGGAGTTACTATGCT	NM_004937	CTNS	cystinosis, nephropathic (CTNS), transcript variant 2, mRNA	-1.34	0.42	0.46	0.62	-1.80	0.02
Hs_12plexchip_4_4809	v2HS_202045	TTGTTGACATAGTTGACCAGCT	NM_147783	CTSB	cathepsin B (CTSB), transcript variant 5, mRNA	-2.10	0.83	-0.95	1.32	-1.15	0.28
Hs_12plexchip_6_4024	v2HS_178400	ATAAAGTGACATTTCCCTGGGC	NM_033427	CTTNBP2	cortactin binding protein 2 (CTTNBP2), mRNA	-1.16	1.07	1.49	1.42	-2.64	0.07
Hs_12plexchip_3_12285	v2HS_26698	AAGTAACTCAACATCCTTACCA	NM_018704	CTTNBP2NL	CTTNBP2 N-terminal like (CTTNBP2NL), mRNA	-1.80	0.85	-0.67	0.70	-1.13	0.15
Hs_12plexchip_4_8999	v2HS_172448	TTTATTGCTGCCCTGTTTACCC	NM_003478	CUL5	cullin 5 (CUL5), mRNA	-0.98	0.39	0.22	0.31	-1.21	0.01
Hs_12plexchip_6_1487	v2HS_151077	TTTGAGCTGGAGTTGCTGTCCG	NM_181500	CUX1	cut-like homeobox 1 (CUX1), transcript variant 3, mRNA	-2.68	0.94	-1.36	1.08	-1.32	0.19
Hs_12plexchip_4_11416	v2HS_200239	GTATAGACACCGATGGTAAGCT	NM_001100812	CXCL16	chemokine (C-X-C motif) ligand 16 (CXCL16), transcript variant 2, mRNA	-1.60	0.16	-0.47	0.54	-1.13	0.06
Hs_12plexchip_3_2537	v2HS_58298	ATATGGTTTCCCAATCCCTGTC	AK021694	CXORF10	CHROMOSOME X OPEN READING FRAME 10	-1.38	0.26	0.17	0.84	-1.55	0.07
Hs0P00009553	v2HS_144182	TTTCCTGGAGAGTTGCTTGGGC	CR605567	CXORF40A	CHROMOSOME X OPEN READING FRAME 40A	-2.08	0.54	-0.28	0.22	-1.80	0.02
Hs_12plexchip_5_12147	v2HS_137432	ATTTGCAGATCTGGTGTCCCGT	NM_025212	CXXC4	CXXC finger 4 (CXXC4), mRNA	-2.04	0.32	-1.02	0.20	-1.02	0.01
Hs_12plexchip_4_11473	v2HS_136939	TAGACTTGAAGGAGAACTTCCA	NM_025091	CXYORF2	CHROMOSOME X AND Y OPEN READING FRAME 2	-1.17	0.84	0.00	0.82	-1.17	0.16
Hs_12plexchip_5_5008	v2HS_258463	TTTAATAATCTCATCTTTGCCA	NM_014608	CYFIP1	cytoplasmic FMR1 interacting protein 1 (CYFIP1), transcript variant 1, mRNA	-0.76	0.24	0.26	0.85	-1.03	0.16
Hs_12plexchip_4_7839	v2HS_113341	TTATAGAAACCGTGTTGTCCCG	NM_001340	CYLC2	cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA	-0.77	0.31	0.10	0.63	-0.87	0.12
Hs0P00003175	v2HS_81196	ATATACTGTCCTATACTTCCCT	NM_015247	CYLD	CYLINDROMATOSIS (TURBAN TUMOR SYNDROME)	-0.79	0.54	-0.02	0.10	-0.76	0.13
Hs_12plexchip_4_7656	v2HS_93339	TTTATTCTACCCTGCAGGACCC	NM_001026213	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1 (CYP11B1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.49	0.79	0.04	0.62	-1.53	0.06
Hs_12plexchip_2_776	v2HS_112505	TTCTGGATCAGCCTTGCGAGGA	NM_000784	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), nuclear gene encoding mitochondrial protein, mRNA	-0.89	0.42	0.07	0.46	-0.96	0.06
Hs_12plexchip_3_6411	v2HS_227129	TATATTCTACCCAAGGACAGCA	NM_000784	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), nuclear gene encoding mitochondrial protein, mRNA	-0.94	0.34	-0.16	0.27	-0.79	0.04
Hs_12plexchip_4_8214	v2HS_112512	ATAAGAAACCGTAAACCAGGCT	NM_000785	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1 (CYP27B1), nuclear gene encoding mitochondrial protein, mRNA	-0.84	0.35	0.04	0.44	-0.88	0.06
Hs_12plexchip_4_6736	v2HS_54610	ATTTCAGGTCAGACTAGAGGTG	AF372495	CYP2F1P	CYTOCHROME P450, FAMILY 2, SUBFAMILY F, POLYPEPTIDE 1 PSEUDOGENE	-0.84	0.69	0.00	0.30	-0.84	0.16
Hs_12plexchip_4_6165	v2HS_24087	TTTAACTTTATCACTCAGCGCT	NM_004392	DACH1	dachshund homolog 1 (Drosophila) (DACH1), transcript variant 3, mRNA	-1.96	1.65	-0.51	0.48	-1.45	0.26
Hs_12plexchip_6_9470	v2HS_24094	TTAAGGTGGGACATAGGGAGGA	NM_004393	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1), mRNA	-1.16	0.45	-0.11	0.26	-1.05	0.04
Hs_12plexchip_6_9232	v2HS_151103	TATCCCAATGTTATGAGAAGCC	NM_001918	DBT	dihydrolipoamide branched chain transacylase E2 (DBT), nuclear gene encoding mitochondrial protein, mRNA	-0.89	0.78	-0.06	0.73	-0.82	0.25
Hs_12plexchip_4_10498	v2HS_5718	ATAAACTGACATCCGAGCAGCT	NM_080927	DCBLD2	discoidin, CUB and LCCL domain containing 2 (DCBLD2), mRNA	-0.73	0.69	0.20	0.65	-0.93	0.16
Hs_12plexchip_3_5591	v2HS_224241	ATTCGTAGGTAGTATTCGACCA	NM_016356	DCDC2	doublecortin domain containing 2 (DCDC2), mRNA	-1.20	0.27	-0.40	0.56	-0.80	0.11
Hs_12plexchip_5_7128	v2HS_202258	TATTGGGATGTTTCACTCGGCG	NM_001040261	DCLK2	doublecortin-like kinase 2 (DCLK2), transcript variant 2, mRNA	-1.77	0.50	-0.24	0.28	-1.53	0.02
Hs_12plexchip_4_4799	v2HS_201780	TTCCACAAGGTCCTTCTTGGCC	NM_033403	DCLK3	doublecortin-like kinase 3 (DCLK3), mRNA	-1.35	0.67	-0.61	0.56	-0.74	0.22

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_919	v2HS_49607	TATTCTTAGCATTCAAGTTCTC	NM_014881	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A), mRNA	-1.69	1.24	-0.57	0.37	-1.12	0.26
Hs_12plexchip_4_1537	v2HS_215061	ATTGTCACTGAAATAAGAACAC	NM_024348	DCTN3	dynactin 3 (p22) (DCTN3), transcript variant 2, mRNA	-0.81	0.26	0.07	0.22	-0.87	0.01
Hs_12plexchip_5_12832	v2HS_250781	TAAATACAAAGCTTCCTCTGCC	NM_024348	DCTN3	dynactin 3 (p22) (DCTN3), transcript variant 2, mRNA	-0.78	0.56	0.03	0.33	-0.81	0.11
Hs_12plexchip_2_869	v2HS_114977	TTTGTAAGAGTCAGGAGGACCT	NM_016221	DCTN4	dynactin 4 (p62) (DCTN4), mRNA	-1.22	0.16	-0.14	0.37	-1.08	0.02
Hs_12plexchip_4_11616	v2HS_93660	AACACAATGGAACTTGAGTGCT	NM_178152	DCX	doublecortex; lissencephaly, X-linked (doublecortin) (DCX), transcript variant 2, mRNA	-1.37	0.41	-0.41	0.64	-0.96	0.10
Hs_12plexchip_5_8057	v2HS_115266	ATCTGTCAAAGGCCTCCTTGGT	NM_016286	DCXR	dicarbonyl/L-xylulose reductase (DCXR), mRNA	-1.42	0.46	-0.54	0.84	-0.88	0.21
Hs_12plexchip_3_566	v2HS_36557	TTTCTCAATCAAAGGGATGGCA	NM_004728	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 (DDX21), mRNA	-1.91	0.24	-1.12	0.50	-0.78	0.09
Hs_12plexchip_4_4835	v2HS_238813	AATTGAAGGAATGTCCAGACCA	NM_203499	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42), transcript variant 2, mRNA	-0.90	1.05	0.11	0.88	-1.01	0.27
Hs_12plexchip_4_984	v2HS_85487	TTAAAGTCTGAAATGACCTTGT	NM_203499	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42 (DDX42), transcript variant 2, mRNA	-0.88	0.33	-0.09	0.41	-0.79	0.06
Hs_12plexchip_2_9105	v2HS_30469	TAATTGGTGGTAAATCTGCCCA	NM_018665	DDX43	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43 (DDX43), mRNA	-1.42	0.58	-0.31	0.47	-1.11	0.06
Hs_12plexchip_6_900	v2HS_95583	ATAAGCATAACCCTTGTTTCCT	NM_014829	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 (DDX46), mRNA	-1.32	1.16	0.37	0.83	-1.69	0.12
Hs_12plexchip_2_10512	v2HS_25674	AATAACATCCACATTAATACCT	NM_152300	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52 (DDX52), transcript variant 2, mRNA	-0.71	0.26	0.57	0.94	-1.27	0.14
Hs_12plexchip_4_11363	v2HS_35058	TTTCTATCTAGGAAGCTCAGCG	NM_021010	DEFA5	defensin, alpha 5, Paneth cell-specific (DEFA5), mRNA	-0.70	0.54	0.05	0.64	-0.75	0.20
Hs_12plexchip_6_5556	v2HS_229535	ATAATTCCTGGTGTTGAGTCAC	NM_054112	DEFB118	defensin, beta 118 (DEFB118), mRNA	-0.78	0.58	0.44	0.91	-1.22	0.13
Hs_12plexchip_4_8163	v2HS_151156	TTCCATCATCTCCTGCTTGGCC	NM_001927	DES	desmin (DES), mRNA	-1.50	0.33	-0.45	0.85	-1.05	0.15
Hs_12plexchip_5_3806	v2HS_174890	TTGTACAAGTACAGCCCTTGGT	NM_017996	DET1	de-etiolated homolog 1 (Arabidopsis) (DET1), mRNA	-2.12	0.55	-1.32	0.93	-0.80	0.28
Hs_12plexchip_5_9921	v2HS_233215	ATTTACAATATGGTTACCTCGC	NM_001042702	DFNB59	deafness, autosomal recessive 59 (DFNB59), mRNA	-1.09	0.28	-0.22	0.03	-0.87	0.03
Hs0P00006485	v2HS_98186	TTTGGATGACCGTCTGGAGGCC	NM_022719	DGCR14	DiGeorge syndrome critical region gene 14 (DGCR14), mRNA	-2.01	0.56	0.28	1.37	-2.29	0.09
Hs_12plexchip_4_9584	v2HS_36821	TAGCTTCATAAGATCACCAGCT	NM_004717	DGKI	diacylglycerol kinase, iota (DGKI), mRNA	-1.75	0.96	-0.84	0.56	-0.91	0.24
Hs_12plexchip_5_7535	v2HS_227147	ATTCACTAACACGATTTGGCCT	NM_001105571	DHRS7C	dehydrogenase/reductase (SDR family) member 7C (DHRS7C), mRNA	-1.19	0.67	1.13	0.91	-2.31	0.03
Hs_12plexchip_4_12111	v2HS_113419	TAATGTCACCAACTTCAGGGCC	NM_001358	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (DHX15), mRNA	-2.12	0.97	-0.97	1.33	-1.14	0.30
Hs_12plexchip_6_10126	v2HS_96322	ATACTCTCTGGATTCAGCTGCC	NM_138615	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30 (DHX30), transcript variant 1, mRNA	-0.85	0.44	-0.06	0.26	-0.79	0.07
Hs_12plexchip_4_10031	v2HS_60545	TTTATGCAGGTGCTGCTCCCGC	NM_014003	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA	-2.06	1.15	-0.89	0.79	-1.18	0.23
Hs_12plexchip_4_6829	v2HS_60543	TTTGGACTTGCAAATAAGACCA	NM_014003	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA	-2.31	1.04	-0.62	0.08	-1.69	0.11
Hs_12plexchip_6_1175	v2HS_248092	TATTTGTAGGAGGGAGTTGGCA	NM_014003	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA	-1.08	0.73	-0.01	0.20	-1.07	0.12
Hs0P00000365	v2HS_60544	TTGTCTCTGATAATAGTGAGCA	NM_014003	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA	-2.17	0.12	-0.98	0.29	-1.19	0.01
Hs0P00005107	v2HS_113413	AATAGTTAACAAAGTCTCTGGC	NM_001357	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (DHX9), mRNA	-1.55	0.26	-0.74	1.02	-0.81	0.30
Hs_12plexchip_4_517	v2HS_201809	TTTCAGGTCAAGTGAGGCAGGT	NM_177438	DICER1	Dicer1, Dcr-1 homolog (Drosophila) (DICER1), transcript variant 1, mRNA	-1.16	1.30	-0.10	0.68	-1.07	0.30
Hs_12plexchip_4_544	v2HS_201808	TTTAATACCTGCCTGAGCACCG	NM_022105	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 1, mRNA	-2.16	0.95	-0.96	0.20	-1.19	0.16
Hs_12plexchip_4_874	v2HS_202805	TTTAGCTTCCTGCTGATCTGCC	NM_022105	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 1, mRNA	-1.40	0.15	-0.13	0.27	-1.27	0.00
Hs_12plexchip_5_10236	v2HS_101621	TAACCCAAGAATTATATTCGGA	NM_033081	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 4, mRNA	-0.81	0.13	-0.12	0.09	-0.70	0.00

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_6670	v2HS_242872	ATTCTCTTCTGGAAACGGAGGG	NM_033081	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 4, mRNA	-1.10	0.22	0.11	0.83	-1.21	0.12
Hs_12plexchip_6_357	v2HS_63623	AGAAGTGATGCTTTCATGTGCT	NM_022105	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 1, mRNA	-0.87	0.99	0.64	1.41	-1.51	0.21
Hs_12plexchip_6_10094	v2HS_96255	TTTGTTATGAAGATAACTTGCA	NM_014953	DIS3	DIS3 mitotic control homolog (S. cerevisiae) (DIS3), mRNA	-1.45	0.14	-0.57	0.57	-0.89	0.11
Hs_12plexchip_5_2027	v2HS_210791	TTATATTCTCCCAAGAGCCGGT	NM_033425	DIXDC1	DIX domain containing 1 (DIXDC1), transcript variant 2, mRNA	-0.97	0.45	0.95	0.45	-1.92	0.01
Hs_12plexchip_3_5505	v2HS_113450	TTTGATAAGAAATTCTTCAGCG	NM_001363	DKC1	dyskeratosis congenita 1, dyskerin (DKC1), mRNA	-2.95	0.55	-1.38	0.94	-1.56	0.08
Hs_12plexchip_2_3303	v2HS_90800	TAAAGACATAGGCGGCATCCTC	BX537874	DKFZP313P036	HYPOTHETICAL PROTEIN DKFZP313P036	-0.71	0.84	0.51	0.89	-1.22	0.16
Hs_12plexchip_5_5655	v2HS_258802	TTCCCACTGTGCTATGTTTGCA	BX537874	DKFZP313P036	HYPOTHETICAL PROTEIN DKFZP313P036	-1.36	0.80	-0.09	0.54	-1.27	0.09
Hs_12plexchip_6_6453	v2HS_215794	TTCTCAGAACTTAACGTGGGCA	BX647655	DKFZP451A211	DKFZP451A211 PROTEIN	-0.78	0.70	0.07	0.18	-0.86	0.16
Hs_12plexchip_2_4387	v2HS_183817	ATTGGTTAGGACAGTGCTTGGT	AL831931	DKFZP451B082	HYPOTHETICAL GENE SUPPORTED BY AL831931	-1.39	0.64	-0.66	0.80	-0.73	0.29
Hs_12plexchip_5_9420	v2HS_231774	TTCTGGTACCCATTGACTGGGC	NM_001001991	DKFZP586H2123	regeneration associated muscle protease (DKFZP586H2123), transcript variant 2, mRNA	-1.66	0.27	-0.68	0.53	-0.98	0.07
Hs_12plexchip_6_9124	v2HS_242931	TAAAGAGACCTGTATGCACGCA	AL137340	DKFZP761C1711	HYPOTHETICAL PROTEIN DKFZP761C1711	-1.53	0.50	0.56	2.60	-2.09	0.30
Hs_12plexchip_5_4986	v2HS_256423	ATAATCTTTCTAGTCCCTGGCA	BC033120	DLEU2	DELETED IN LYMPHOCYTIC LEUKEMIA, 2	-1.14	0.81	-0.23	0.22	-0.92	0.18
Hs_12plexchip_4_8718	v2HS_113463	TTATCTCCTGGGATGTGCTGGT	NM_001365	DLG4	discs, large homolog 4 (Drosophila) (DLG4), mRNA	-1.16	0.63	-0.03	0.79	-1.12	0.13
Hs_12plexchip_6_8979	v2HS_80186	TTCTCTTCTGGCTTTGTTCGGA	NM_015286	DMN	desmuslin (DMN), transcript variant B, mRNA	-0.90	0.15	0.16	0.25	-1.06	0.01
Hs_12plexchip_2_3346	v2HS_84958	GTCAGACAGCACTTCATATGCC	NM_001039550	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2 (DNAJB2), transcript variant 1, mRNA	-0.71	0.32	0.04	0.47	-0.76	0.09
Hs_12plexchip_3_4119	v2HS_39653	CACAGTCACCGACTTGAGCTGC	NM_153330	DNAJB8	DnaJ (Hsp40) homolog, subfamily B, member 8 (DNAJB8), mRNA	-1.43	0.49	-0.61	0.96	-0.82	0.28
Hs_12plexchip_4_10794	v2HS_156250	TAATTTCAATCTGCGGAAAGCT	NM_018198	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11 (DNAJC11), mRNA	-3.99	0.62	-1.45	1.01	-2.54	0.03
Hs_12plexchip_6_6583	v2HS_218696	ATTCCCAATGAGCCATGCTGGT	NM_173650	DNAJC5G	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma (DNAJC5G), mRNA	-0.71	0.82	0.38	0.58	-1.08	0.14
Hs_12plexchip_3_7955	v2HS_231386	TATAGCAATCGAATGGCTGGGC	NM_014787	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6 (DNAJC6), mRNA	-2.35	0.57	-1.33	1.16	-1.02	0.27
Hs_12plexchip_5_7092	v2HS_257328	TTTGGAGAGGAGGATGGAAGGG	NM_001009934	DNASE1L1	deoxyribonuclease I-like 1 (DNASE1L1), transcript variant 4, mRNA	-0.70	0.09	0.40	0.36	-1.11	0.03
Hs_12plexchip_3_6731	v2HS_96969	AATGGGTATGGAGGAAATGCCT	NM_015569	DNM3	dynamin 3 (DNM3), mRNA	-1.45	0.60	0.48	0.70	-1.93	0.02
Hs_12plexchip_5_12756	v2HS_25257	ATCCACTAAGAGATTATGGCTT	NM_012100	DNPEP	aspartyl aminopeptidase (DNPEP), mRNA	-0.82	0.20	-0.05	0.52	-0.77	0.11
Hs_12plexchip_4_10262	v2HS_118260	TTCTCTGTCCGTAGTGTCTCCA	NM_052951	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1 (DNTTIP1), mRNA	-1.02	1.24	0.92	0.82	-1.94	0.10
Hs_12plexchip_3_12323	v2HS_242218	ATTTCACAACAGACATCTTGCC	AB014594	DOCK10	KIAA0694 GENE PRODUCT	-1.22	1.13	-0.20	0.53	-1.03	0.25
Hs_12plexchip_6_4180	v2HS_176931	TTATCCTTGTAGCTGGGCGGCA	NM_024940	DOCK5	dedicator of cytokinesis 5 (DOCK5), mRNA	-0.74	0.32	0.76	1.09	-1.50	0.13
Hs_12plexchip_5_7472	v2HS_227962	TTAAGTAGCAAGTTGATGAGGG	NM_203316	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase) (DPAGT1), transcript variant 2, mRNA	-1.28	0.15	-0.33	0.58	-0.95	0.10
Hs0P00005098	v2HS_113530	TTGCTATATGGGTCATACCGGT	NM_001383	DPH1	DPH1 homolog (S. cerevisiae) (DPH1), mRNA	-0.83	0.51	0.19	0.24	-1.02	0.05
Hs_12plexchip_5_1838	v2HS_215458	TTTATCCATAAGTAACTTTGCT	NM_199286	DPPA3	developmental pluripotency associated 3 (DPPA3), mRNA	-0.77	0.64	0.52	0.79	-1.29	0.10
Hs_12plexchip_6_2120	v2HS_175264	AAGCCTTAACATTTCAAGGGCT	NM_018370	DRAM	damage-regulated autophagy modulator (DRAM), mRNA	-0.81	0.53	0.21	0.90	-1.02	0.18
Hs_12plexchip_4_6660	v2HS_62024	GTTGGAATCCAAAGTGTAGCCT	NM_024421	DSC1	desmocollin 1 (DSC1), transcript variant Dsc1a, mRNA	-2.08	0.53	-1.09	1.09	-0.99	0.25
Hs_12plexchip_6_8462	v2HS_113567	TTTGGTAGCCACGGATAATCCC	NM_001389	DSCAM	Down syndrome cell adhesion molecule (DSCAM), transcript variant 1, mRNA	-0.90	0.88	0.33	1.22	-1.23	0.24
Hs_12plexchip_5_3353	v2HS_14233	TAATAGATGAGGGAGATGAGGG	NM_015177	DTX4	deltex 4 homolog (Drosophila) (DTX4), mRNA	-0.70	0.67	0.06	0.14	-0.76	0.18

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_2_4285	v2HS_74456	TTTGGTACTGAATTACCGTGCG	NM_015343	DULLARD	dullard homolog (Xenopus laevis) (DULLARD), mRNA	-1.37	0.53	-0.38	0.46	-0.99	0.07
Hs_12plexchip_4_6986	v2HS_72343	ATAACCAATCCCATTCTGCTGC	NM_030640	DUSP16	dual specificity phosphatase 16 (DUSP16), mRNA	-0.73	0.38	0.04	0.16	-0.77	0.05
Hs0P00002692	v2HS_111452	TAGGGCAAGATCTCCACAGGGC	L11329	DUSP2	DUAL SPECIFICITY PHOSPHATASE 2	-0.83	0.59	0.29	0.51	-1.12	0.07
Hs_12plexchip_4_8671	v2HS_111215	TATTCTTCCTTCAGCCACTGCC	XM_001132925	DUSP22	PREDICTED:dual specificity phosphatase 22 (DUSP22), mRNA	-1.64	1.80	0.15	1.06	-1.79	0.23
Hs0P00012140	v2HS_15210	GTGCAATTACCAAGGACAGGCC	U46462	DVL1L1	DISHEVELLED, DSH HOMOLOG 1 (DROSOPHILA)-LIKE 1	-0.88	0.90	-0.13	0.24	-0.75	0.28
Hs_12plexchip_3_11958	v2HS_239658	TATGTTAACGTGTGGGTGTGGG	NM_004423	DVL3	dishevelled, dsh homolog 3 (Drosophila) (DVL3), mRNA	-0.80	0.07	0.21	0.14	-1.01	0.00
Hs_12plexchip_3_2463	v2HS_70419	ATTGGAGAGGACATCCTGATGC	NM_080677	DYNLL2	dynein, light chain, LC8-type 2 (DYNLL2), mRNA	-1.95	0.28	-0.01	0.47	-1.94	0.01
Hs_12plexchip_5_9771	v2HS_269319	TAAATGGAATGAAACTTCCCTT	BC007223	DYNLRB1	DYNEIN LIGHT CHAIN 2A	-0.84	0.55	0.52	0.47	-1.37	0.03
Hs_12plexchip_5_12415	v2HS_250317	ATTCCTGTTAACTTCTCTAGCT	NM_006520	DYNLT3	dynein, light chain, Tctex-type 3 (DYNLT3), mRNA	-2.39	1.12	-0.77	0.36	-1.62	0.12
Hs_12plexchip_5_11636	v2HS_139152	TTTCATCTCATCTAAATGACCC	NM_033083	EAF1	ELL associated factor 1 (EAF1), mRNA	-0.73	0.29	-0.01	0.54	-0.72	0.13
Hs_12plexchip_6_8538	v2HS_113593	ATGGCATTCCTCTTGTTGGGCC	NM_001398	ECH1	enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA	-1.71	1.67	0.33	1.68	-2.04	0.21
Hs_12plexchip_6_9920	v2HS_111410	ATGGGTTATTGCAGAACAGCTT	D86874	ECSA	ABC TRANSPORTER ATP BINDING PROTEIN	-1.45	0.33	-0.61	0.71	-0.84	0.17
Hs_12plexchip_5_5910	v2HS_257261	TTATGATCTCAATGTGACAGGG	NM_021783	EDA2R	ectodysplasin A2 receptor (EDA2R), mRNA	-1.66	0.74	-0.11	0.36	-1.55	0.05
Hs_12plexchip_6_1344	v2HS_116709	TAGGATGTTGGCGGCGTAGGCG	NM_030760	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA	-1.32	3.21	1.33	1.45	-2.66	0.29
Hs_12plexchip_3_4772	v2HS_113620	TTTGTAGACATCCTGGAGAGGC	NM_001402	EEF1A1	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA	-2.31	0.19	-0.58	0.46	-1.73	0.01
Hs_12plexchip_6_3394	v2HS_176517	ATAGATGACAAAGGTGAAGCCA	NM_019065	EFCBP2	EF-hand calcium binding protein 2 (EFCBP2), mRNA	-0.90	0.49	0.03	0.34	-0.93	0.06
Hs_12plexchip_5_12827	v2HS_172951	TTACAAAGGGACTTGTTGTCGA	NM_004093	EFNB2	ephrin-B2 (EFNB2), mRNA	-1.29	0.16	0.28	0.53	-1.58	0.03
Hs_12plexchip_6_6409	v2HS_236932	ATTGACTAGTATGTTGGGCCCA	NM_001040610	EFTUD1	elongation factor Tu GTP binding domain containing 1 (EFTUD1), transcript variant 2, mRNA	-1.07	1.30	0.76	1.89	-1.82	0.25
Hs_12plexchip_4_8011	v2HS_195685	TATCTAGATGGCTCTCTGACCA	AF167462	EIF2AK2	EUKARYOTIC TRANSLATION INITIATION FACTOR 2-ALPHA KINASE 2	-0.74	0.40	1.27	1.05	-2.00	0.07
Hs_12plexchip_5_6160	v2HS_262246	ATGTTGAACACTCGATTCAGCA	NM_003908	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa (EIF2S2), mRNA	-2.28	0.95	-0.87	1.06	-1.42	0.16
Hs_12plexchip_2_10530	v2HS_23913	TTAGCATTTGTTCTTCTGCCCT	NM_003750	EIF3A	eukaryotic translation initiation factor 3, subunit A (EIF3A), mRNA	-1.36	0.50	-0.34	0.77	-1.01	0.14
Hs0P00006261	v2MM_45585	TAAAGGAATTTCTTCCAAACGC	NM_010123	EIF3S10	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 10 (THETA)	-1.16	0.26	0.33	0.38	-1.50	0.01
Hs0P00005681	v2HS_23869	TCTTGTACTCTGTCACTGTCTT	NM_003755	EIF3S4	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 4 DELTA, 44KDA	-1.79	0.95	0.22	0.65	-2.01	0.05
Hs0P00004099	v2HS_188192	ATATTCATGGCCAACATCTGGC	NM_001568	EIF3S6	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 6 48KDA	-1.03	0.17	-0.31	0.10	-0.72	0.01
Hs0P00005621	v2HS_242811	TTAAGAAATCTTGAGGCCAGCG	NM_003752	EIF3S8	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-2.18	0.63	-0.09	0.60	-2.09	0.01
Hs_12plexchip_5_6759	v2HS_255163	TTCTTTACAAAGTTAATGGCCA	NM_014740	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3 (EIF4A3), mRNA	-2.25	0.73	-0.88	0.75	-1.37	0.09
Hs_12plexchip_5_7166	v2HS_255274	ATTCTTTACAAAGTTAATGGCC	NM_014740	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3 (EIF4A3), mRNA	-2.37	0.67	0.30	0.18	-2.66	0.01
Hs_12plexchip_6_8608	v2HS_61908	TTTCAAAGTCCAGGTCTTTGCC	NM_182917	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), transcript variant 1, mRNA	-1.26	1.33	-0.09	0.52	-1.16	0.27
Hs_12plexchip_5_8473	v2HS_263573	AATTTGATTGATCGTCTTTGGT	NM_001042559	EIF4G2	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), transcript variant 2, mRNA	-1.21	1.00	-0.17	0.87	-1.04	0.25
Hs_12plexchip_3_922	v2HS_38546	TTGGTAATTAACATAAAGCGCT	NM_020390	EIF5A2	eukaryotic translation initiation factor 5A2 (EIF5A2), mRNA	-0.89	0.25	0.03	0.45	-0.92	0.05
Hs_12plexchip_5_11077	v2HS_274321	AATCAGCTAGAACTTTGTCCAC	NM_006532	ELL	elongation factor RNA polymerase II (ELL), mRNA	-0.74	0.33	0.95	0.79	-1.69	0.05

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_5897	v2HS_25486	GTACATGATGGCATGAACACCA	NM_152310	ELOVL3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3 (ELOVL3), mRNA	-1.83	0.33	-0.89	0.80	-0.94	0.17
Hs0P00005371	v2HS_119088	ATTCTCTGTGCCACAATTTGCC	NM_001104558	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast) (ELOVL7), transcript variant 2, mRNA	-1.64	0.75	-0.27	1.48	-1.37	0.25
Hs_12plexchip_6_1030	v2HS_197790	TATAGACTTGTGCTTGTCACAG	NM_006331	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae) (EMG1), mRNA	-1.07	1.09	0.01	0.44	-1.07	0.22
Hs_12plexchip_5_10681	v2HS_268779	TAGAGCCCAATCATTGTTTCCA	NM_133455	EMID1	EMI domain containing 1 (EMID1), mRNA	-2.41	0.52	-0.64	0.69	-1.77	0.03
Hs_12plexchip_4_10304	v2HS_96160	ATTATCATAACCATGGTCACCT	NM_014936	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4), mRNA	-1.31	0.75	-0.04	0.24	-1.27	0.09
Hs_12plexchip_4_10482	v2HS_200934	ATAATGCTGCCAAGAGAGACCC	NM_021572	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) (ENPP5), mRNA	-1.77	0.68	-0.38	1.20	-1.39	0.17
Hs_12plexchip_5_21	v2HS_251354	TTTACCTAATATGGTTTGTGCT	NM_021572	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) (ENPP5), mRNA	-1.56	0.56	-0.24	0.50	-1.33	0.04
Hs_12plexchip_6_3588	v2HS_176723	TTAGGATGATATTGAGGCTGGT	NM_018424	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B (EPB41L4B), transcript variant 1, mRNA	-0.96	0.24	0.31	0.38	-1.27	0.01
Hs_12plexchip_5_12564	v2HS_17743	AACCATTCCGAGTAAGAGGCCC	NM_004441	EPHB1	EPH receptor B1 (EPHB1), mRNA	-1.17	1.39	-0.04	0.62	-1.13	0.29
Hs_12plexchip_4_5890	v2HS_17728	TATAAATGTAACCATCTCACCC	NM_004446	EPRS	glutamyl-prolyl-tRNA synthetase (EPRS), mRNA	-2.04	0.31	-0.51	0.55	-1.53	0.02
Hs_12plexchip_2_8908	v2HS_17662	TAAATCAATCAGGCTCACAGCT	NM_004447	EPS8	epidermal growth factor receptor pathway substrate 8 (EPS8), mRNA	-0.70	0.22	0.07	0.36	-0.78	0.04
Hs_12plexchip_2_6285	v2HS_173491	ATCACTGCGCGGACTGACGGGC	NM_017729	EPS8L1	EPS8-like 1 (EPS8L1), transcript variant 2, mRNA	-1.41	1.01	-0.48	0.45	-0.93	0.25
Hs_12plexchip_6_2031	v2HS_241513	TTATTGGAATGGAGAAACAGCA	NM_001006600	ERBB2IP	erbb2 interacting protein (ERBB2IP), transcript variant 7, mRNA	-0.72	0.70	0.29	0.71	-1.01	0.15
Hs_12plexchip_6_10116	v2HS_155116	TTAACTAAGCAGTTTAGGGCCT	NM_017669	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like (ERCC6L), mRNA	-1.30	0.89	-0.01	0.66	-1.30	0.12
Hs0P00008438	v2HS_135051	ATATCCCAGAGACTCCATGGCT	NM_016570	ERGIC2	ERGIC and golgi 2 (ERGIC2), mRNA	-0.81	0.65	-0.06	0.68	-0.76	0.23
Hs_12plexchip_5_12713	v2HS_242534	ATGTGATAGAGGGACTGTTGGG	NM_004450	ERH	enhancer of rudimentary homolog (Drosophila) (ERH), mRNA	-2.18	0.70	0.43	0.15	-2.61	0.02
Hs_12plexchip_5_6453	v2HS_160237	ATGTGTAAAGAATGCAGGTGGG	NM_033266	ERN2	ENDOPLASMIC RETICULUM TO NUCLEUS SIGNALLING 2	-1.28	0.50	-0.07	1.40	-1.21	0.27
Hs_12plexchip_4_12574	v2HS_239524	TTAGCCAGGCGCATGGATTGCT	NM_001040276	ESR2	estrogen receptor 2 (ER beta) (ESR2), transcript variant c, mRNA	-1.35	0.26	-0.47	1.05	-0.87	0.28
Hs_12plexchip_5_6685	v2HS_17544	TTGTAAGCTCAGGTATGGGCTG	NM_004452	ESRRB	estrogen-related receptor beta (ESRRB), mRNA	-1.40	0.66	-0.66	0.25	-0.74	0.19
Hs_12plexchip_5_1655	v2HS_53926	TTATAAACACACAAACACCGGC	NM_147127	EVC2	Ellis van Creveld syndrome 2 (limbin) (EVC2), mRNA	-0.85	0.43	-0.05	0.31	-0.81	0.06
Hs_12plexchip_3_7059	v2HS_97287	TATACTCAGGAACAGCTTACCC	NM_016046	EXOSC1	exosome component 1 (EXOSC1), mRNA	-0.87	0.50	0.02	0.42	-0.89	0.08
Hs_12plexchip_6_4135	v2HS_275659	ATTTAGTTCATATTGATAAGGA	NM_002685	EXOSC10	exosome component 10 (EXOSC10), transcript variant 2, mRNA	-1.26	0.32	0.65	0.50	-1.91	0.01
Hs_12plexchip_5_6463	v2HS_262285	TATATTGACAGTTCACTAGGGC	NM_019037	EXOSC4	exosome component 4 (EXOSC4), mRNA	-2.33	0.50	0.28	0.40	-2.60	0.00
Hs_12plexchip_3_1589	v2HS_61553	TTCATTTATAGTAACTTCAGGC	NM_181503	EXOSC8	exosome component 8 (EXOSC8), mRNA	-1.04	0.43	-0.29	0.51	-0.75	0.13
Hs_12plexchip_2_5132	v2HS_172985	TACTCTAATTCCAGTGCTTGGT	NM_172105	EYA4	eyes absent homolog 4 (Drosophila) (EYA4), transcript variant 4, mRNA	-1.28	0.91	-0.23	0.95	-1.04	0.24
Hs_12plexchip_5_12923	v2HS_46919	ATACATGTGACCATAGAGTGCG	NM_003950	F2RL3	coagulation factor II (thrombin) receptor-like 3 (F2RL3), mRNA	-1.19	0.30	0.28	0.31	-1.47	0.00
Hs_12plexchip_5_11180	v2HS_135793	TTTAGTGCTGATACCAAATCCT	NM_024306	FA2H	fatty acid 2-hydroxylase (FA2H), mRNA	-1.61	1.02	-0.09	0.57	-1.52	0.11
Hs0P00011447	v2HS_172995	TTTCCATCAATTAGCTCCCGCA	NM_004102	FABP3	FATTY ACID BINDING PROTEIN 3, MUSCLE AND HEART (MAMMARY-DERIVED GROWTH INHIBITOR)	-0.97	0.91	0.16	0.86	-1.12	0.20
Hs_12plexchip_4_12309	v2HS_131701	ATGCTCTCTCATAAACTCTCGT	NM_001442	FABP4	fatty acid binding protein 4, adipocyte (FABP4), mRNA	-1.18	0.90	-0.29	0.71	-0.89	0.26
Hs_12plexchip_4_10098	v2HS_28006	TACGATCAGCTCCCTATGGGTT	NM_004265	FADS2	fatty acid desaturase 2 (FADS2), mRNA	-0.83	0.56	-0.12	0.26	-0.71	0.14
Hs_12plexchip_5_535	v2HS_246062	ATACATTCAGCAAGTGTATCCT	NM_138389	FAM114A1	family with sequence similarity 114, member A1 (FAM114A1), mRNA	-0.86	0.35	0.83	1.10	-1.69	0.11

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_10663	v2HS_179101	TTCTCGTGGTTCAGTATAGCCT	NM_173678	FAM139A	family with sequence similarity 139, member A (FAM139A), mRNA	-1.48	0.53	0.90	0.79	-2.37	0.02
Hs_12plexchip_4_11269	v2HS_117684	TTGCCTCATCTTCTTTAGCCTC	NM_032036	FAM14A	family with sequence similarity 14, member A (FAM14A), mRNA	-0.75	0.67	0.15	0.74	-0.90	0.19
Hs0P00007413	v2HS_103507	TTTCAGGAAGAGGTGGGTTCCC	NR_003659	FAM39DP	family with sequence similarity 39, member D pseudogene (FAM39DP) on chromosome 15	-1.24	0.12	-0.32	0.35	-0.92	0.03
Hs_12plexchip_5_9278	v2HS_95877	ATATGCCACTATAGCTTCGGGC	NM_001040020	FAM3C	family with sequence similarity 3, member C (FAM3C), transcript variant 2, mRNA	-1.08	0.61	-0.34	0.38	-0.74	0.16
Hs_12plexchip_6_2716	v2HS_218155	TATGTAGAAGGGATTAGGTCCT	BC047940	FAM41C	FAMILY WITH SEQUENCE SIMILARITY 41, MEMBER C	-1.30	0.60	-0.36	0.33	-0.94	0.09
Hs_12plexchip_5_32	v2HS_207440	TAATAGAAAGGGTGTATATCTT	AK057953	FAM55B	FAMILY WITH SEQUENCE SIMILARITY 55, MEMBER B	-1.48	0.45	-0.56	0.98	-0.91	0.25
Hs_12plexchip_2_5352	v2HS_175299	TTTAGGCAGCACTGTCATTGCA	NM_001040217	FAM63A	family with sequence similarity 63, member A (FAM63A), transcript variant 2, mRNA	-0.86	0.40	0.85	1.17	-1.71	0.11
Hs_12plexchip_5_5432	v2HS_78256	TTAATATCTCATCTGCCCGGCC	NM_138411	FAM71E1	family with sequence similarity 71, member E1 (FAM71E1), mRNA	-1.24	0.41	-0.41	0.26	-0.83	0.05
Hs_12plexchip_6_10430	v2HS_285374	ATATGTGAAAGAATCTTCCCGT	NM_001100910	FAM72B	family with sequence similarity 72, member B (FAM72B), mRNA	-1.40	1.44	0.03	1.15	-1.44	0.25
Hs_12plexchip_2_10236	v2HS_17676	CTTCTTCTGGACTTAGATTGCT	NM_144664	FAM76B	family with sequence similarity 76, member B (FAM76B), mRNA	-0.85	0.05	0.14	0.43	-0.99	0.06
Hs_12plexchip_2_10870	v2HS_17675	TTATTGTGAAATATTGGATCCT	NM_144664	FAM76B	FAMILY WITH SEQUENCE SIMILARITY 76, MEMBER B	-0.97	0.44	0.11	0.33	-1.08	0.03
Hs_12plexchip_2_5284	v2HS_179199	AATATATCTTGCTCAGTTGCCT	AK097501	FAM9B	FAMILY WITH SEQUENCE SIMILARITY 9, MEMBER B	-0.72	0.32	0.04	0.60	-0.75	0.15
Hs_12plexchip_4_4693	v2HS_83637	TTTCTGAGTGGTCATAACTCCT	NM_000135	FANCA	Fanconi anemia, complementation group A (FANCA), transcript variant 1, mRNA	-1.71	0.17	-0.68	0.60	-1.03	0.09
Hs_12plexchip_4_4680	v2HS_238973	TTTCTCTCACTGGAGATTAGCT	NM_000136	FANCC	Fanconi anemia, complementation group C (FANCC), mRNA	-1.05	0.50	-0.16	0.75	-0.90	0.17
Hs_12plexchip_4_4816	v2HS_239038	ATATGCTTCAGTGTCTGGAGCC	NM_000136	FANCC	Fanconi anemia, complementation group C (FANCC), mRNA	-0.84	0.83	1.46	1.47	-2.30	0.09
Hs_12plexchip_4_219	v2HS_139154	ATAAGATGCACCCATACTGGCT	NM_001018115	FANCD2	Fanconi anemia, complementation group D2 (FANCD2), transcript variant 2, mRNA	-1.89	0.56	-0.72	0.84	-1.17	0.13
Hs_12plexchip_5_22	v2HS_215302	TTAAGATCAAACTCTACAAGCT	NM_006567	FARS2	phenylalanyl-tRNA synthetase 2, mitochondrial (FARS2), nuclear gene encoding mitochondrial protein, mRNA	-2.48	0.37	-1.23	0.53	-1.24	0.03
Hs_12plexchip_6_1391	v2HS_96115	TTTCCTCTTAAGAGCAATCGGT	NM_014929	FASTKD2	FAST kinase domains 2 (FASTKD2), mRNA	-0.78	0.62	-0.02	0.88	-0.77	0.29
Hs0P00010700	v2HS_113773	TTCTCTCCATAAACTGATTCCC	NM_001436	FBL	FIBRILLARIN	-2.07	0.04	-0.02	0.69	-2.05	0.03
Hs_12plexchip_4_262	v2HS_202733	ATAGACTGGTCGGTGACGTGGT	NM_032590	FBXL10	F-box and leucine-rich repeat protein 10 (FBXL10), transcript variant 1, mRNA	-0.72	1.29	1.05	1.97	-1.77	0.27
Hs_12plexchip_5_3246	v2HS_51035	TACATTCACAAAGTTCTCTGCG	NM_012308	FBXL11	F-box and leucine-rich repeat protein 11 (FBXL11), mRNA	-1.20	0.34	0.11	0.13	-1.31	0.01
Hs_12plexchip_5_9268	v2HS_229011	TTGTAATAGACACACAGGAGGT	NM_012157	FBXL2	F-box and leucine-rich repeat protein 2 (FBXL2), mRNA	-0.76	0.50	0.39	0.80	-1.15	0.12
Hs_12plexchip_6_3356	v2HS_263207	TTGTGCAAAGGTTCTTAATGCA	NM_032875	FBXL20	F-box and leucine-rich repeat protein 20 (FBXL20), mRNA	-1.24	0.37	0.41	0.26	-1.65	0.00
Hs_12plexchip_5_3333	v2HS_246503	TTCTAGATTCATACAGCACGCA	NM_012304	FBXL7	F-box and leucine-rich repeat protein 7 (FBXL7), mRNA	-1.08	1.21	0.10	0.47	-1.19	0.23
Hs_12plexchip_4_4014	v2HS_202868	TTAGTCTCAAGGACAGACTGCC	NM_024907	FBXO17	F-box protein 17 (FBXO17), transcript variant 2, mRNA	-1.06	0.11	-0.31	0.35	-0.75	0.05
Hs_12plexchip_5_6789	v2HS_262437	TTAAGTTGTGTTCTGAAAGCCT	NM_015176	FBXO28	F-box protein 28 (FBXO28), mRNA	-0.76	0.11	0.18	0.30	-0.93	0.02
Hs_12plexchip_5_7011	v2HS_263195	TTAAATAAACTAAGACGCCGCT	NM_015176	FBXO28	F-box protein 28 (FBXO28), mRNA	-0.72	0.65	0.62	0.86	-1.34	0.10
Hs_12plexchip_5_6011	v2HS_47264	ATTTGACCTCAGAATGACGGTG	NM_174899	FBXO36	F-box protein 36 (FBXO36), mRNA	-2.45	0.25	0.49	1.40	-2.94	0.06
Hs_12plexchip_5_3766	v2HS_237771	ATCACTTAAGAAATTGGGCCCA	NM_016298	FBXO40	F-box protein 40 (FBXO40), mRNA	-0.91	0.58	-0.20	0.06	-0.71	0.17
Hs_12plexchip_5_3909	v2HS_254575	TTCTGACAGCAGTTGTTTACCA	NM_183412	FBXO44	F-box protein 44 (FBXO44), transcript variant 2, mRNA	-0.74	0.48	0.11	0.88	-0.85	0.24
Hs_12plexchip_3_4306	v2HS_49850	TATAGAAACCATCAAGAGACTG	NM_033481	FBXO9	F-box protein 9 (FBXO9), transcript variant 3, mRNA	-0.82	0.55	0.10	0.25	-0.92	0.09
Hs0P00005232	v2HS_239071	TAACACCTTCATACAGTTCCCG	NM_031456	FBXW10	F-BOX AND WD-40 DOMAIN PROTEIN 10	-0.88	1.27	0.63	1.27	-1.51	0.22
Hs_12plexchip_5_7309	v2HS_124071	TTGGTAGTTTCCTTCTGATGGC	NM_012300	FBXW11	F-BOX AND WD-40 DOMAIN PROTEIN 11	-1.13	0.16	-0.40	0.25	-0.73	0.02

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_7702	v2HS_89328	ATATTCTGAGACTTTGCATGGT	NM_001013415	FBXW7	F-box and WD repeat domain containing 7 (FBXW7), transcript variant 3, mRNA	-1.15	0.70	0.34	0.34	-1.49	0.05
Hs_12plexchip_5_7023	v2HS_262108	TAAGACTATGAGAGAGAAAGGG	NM_153348	FBXW8	F-box and WD repeat domain containing 8 (FBXW8), transcript variant 1, mRNA	-0.77	0.30	-0.03	0.13	-0.74	0.03
Hs_12plexchip_2_11868	v2HS_52975	ATTTGCAGACAGGTAGAGTGGC	NM_003890	FCGBP	Fc fragment of IgG binding protein (FCGBP), mRNA	-1.11	0.16	-0.34	0.75	-0.77	0.21
Hs_12plexchip_4_8858	v2HS_93704	TTGTAAGTACTATTTCCTTCCT	NM_000566	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64) (FCGR1A), mRNA	-1.05	0.67	0.50	0.68	-1.55	0.05
Hs_12plexchip_5_4581	v2HS_255856	TTAAATTCCTCATGCACCTGCC	NM_015122	FCHO1	FCH domain only 1 (FCHO1), mRNA	-3.04	0.60	-1.59	1.14	-1.46	0.14
Hs_12plexchip_3_5699	v2HS_118188	ATAAATCGGGTTGCTATCTCCA	NM_052939	FCRL3	Fc receptor-like 3 (FCRL3), mRNA	-1.24	0.44	-0.36	0.29	-0.88	0.05
Hs_12plexchip_3_4414	v2HS_50567	TTTAACTCAGACACTGAGAGCC	NM_001042548	FEZ2	fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), transcript variant 2, mRNA	-1.60	0.55	-0.31	0.79	-1.29	0.09
Hs_12plexchip_4_5288	v2HS_17382	TTTAACCAGGATCCGGTTTCCC	NM_004463	FGD1	FYVE, RhoGEF and PH domain containing 1 (faciogenital dysplasia) (FGD1), mRNA	-1.26	0.37	-0.41	0.26	-0.85	0.04
Hs_12plexchip_6_10249	v2HS_241573	TTGGTGATAGAATTGAAGGGCT	NM_004463	FGD1	FYVE, RhoGEF and PH domain containing 1 (faciogenital dysplasia) (FGD1), mRNA	-1.14	0.29	-0.07	0.79	-1.07	0.13
Hs_12plexchip_5_9928	v2HS_231178	TTCTTCATGGAATACCACCGGG	NM_021870	FGG	fibrinogen gamma chain (FGG), transcript variant gamma-B, mRNA	-0.74	0.24	0.57	0.57	-1.32	0.04
Hs_12plexchip_2_15	v2HS_90389	GTTAGATTTGCCACTTTGCTGT	NM_006682	FGL2	fibrinogen-like 2 (FGL2), mRNA	-0.96	0.86	-0.15	0.59	-0.81	0.26
Hs_12plexchip_2_3987	v2HS_90317	TTTGGGATCAGGTGTAACTCTG	NM_006682	FGL2	fibrinogen-like 2 (FGL2), mRNA	-1.07	0.32	-0.34	0.51	-0.73	0.12
Hs_12plexchip_4_10923	v2HS_155630	TTAATGACAGCCTTCACCAGGT	NM_018086	FIGN	fidgetin (FIGN), mRNA	-0.80	0.06	0.36	0.54	-1.17	0.06
Hs_12plexchip_3_10904	v2HS_137634	ATTTGTAGTAGAGGTTACTGGT	NM_030917	FIP1L1	FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA	-0.95	0.42	-0.19	0.89	-0.76	0.28
Hs_12plexchip_3_9109	v2HS_137633	TTTCACAGTAAGCTTTCCAGGT	NM_030917	FIP1L1	FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA	-1.11	0.25	-0.13	0.47	-0.98	0.05
Hs_12plexchip_5_7201	v2HS_123403	ATTTAAGATGGTGAAGGTGCCA	XR_015906	FLJ10120	PREDICTED:hypothetical protein FLJ10120 (FLJ10120), misc RNA	-0.74	0.06	0.04	0.32	-0.78	0.05
Hs_12plexchip_6_9356	v2HS_155310	TTGTAAGATCTGTCACAGACCC	NM_018029	FLJ10213	hypothetical protein FLJ10213 (FLJ10213), mRNA	-1.14	1.39	2.22	1.06	-3.36	0.03
Hs_12plexchip_6_6434	v2HS_194024	ATCTGTGATTAGATGACATCCT	AK022609	FLJ12547	HYPOTHETICAL PROTEIN FLJ12547	-0.97	1.55	0.42	0.43	-1.38	0.26
Hs_12plexchip_6_1964	v2HS_155243	TAATTGACTAACACGCCTCCGA	NM_017694	FLJ20160	FLJ20160 protein (FLJ20160), mRNA	-1.32	0.05	-0.34	0.53	-0.99	0.08
Hs0P00003265	v2HS_43260	TTCATGTTTGGGTGAAGGGCTC	NM_152675	FLJ23754	HYPOTHETICAL PROTEIN FLJ23754	-0.90	0.37	-0.11	0.36	-0.79	0.06
Hs_12plexchip_3_12842	v2HS_36158	GTTGTCATCCATAATATCAGCT	NM_144967	FLJ30058	hypothetical protein FLJ30058 (FLJ30058), mRNA	-1.87	0.35	-1.05	0.76	-0.82	0.19
Hs_12plexchip_3_12157	v2HS_242505	AATAAGAATGGTTTGGTTTGGT	NM_153008	FLJ30277	HYPOTHETICAL PROTEIN FLJ30277	-1.60	0.53	-0.78	0.53	-0.82	0.13
Hs_12plexchip_5_7504	v2HS_267294	AATCCCAAATTGGTAAGTCCCT	AK055400	FLJ30838	HYPOTHETICAL GENE SUPPORTED BY AL832565	-2.68	1.44	-0.88	0.10	-1.80	0.16
Hs_12plexchip_2_10398	v2HS_18875	TAATACAATCACCAAGGGAGCC	NM_152497	FLJ32206	HYPOTHETICAL PROTEIN FLJ32206	-0.83	0.47	0.74	0.68	-1.58	0.04
Hs_12plexchip_6_11477	v2HS_271938	TAATGCTGTAATTGCGGAGGCC	NM_001001702	FLJ33360	FLJ33360 protein (FLJ33360), mRNA	-0.95	0.27	0.25	1.19	-1.20	0.22
Hs0P00012742	v2HS_103190	TTATTGCCTTTACTTCTGTGGG	AK092066	FLJ34747	HYPOTHETICAL GENE SUPPORTED BY AK092066	-1.43	0.08	0.23	0.50	-1.66	0.03
Hs_12plexchip_3_5089	v2HS_121263	ATATTCACACAGTGACATGGCG	AK093463	FLJ36144	HYPOTHETICAL PROTEIN FLJ36144	-0.92	0.42	-0.21	0.26	-0.71	0.08
Hs_12plexchip_3_2898	v2HS_57174	TTATATTCTGGGCCTAGGACCT	AK095662	FLJ38343	HYPOTHETICAL PROTEIN FLJ38343	-0.79	0.04	-0.09	0.62	-0.70	0.19
Hs_12plexchip_3_7526	v2HS_101040	TTTATTGCTCTTATATTCAGCC	NM_198441	FLJ40296	FLJ40296 protein (FLJ40296), mRNA	-0.71	0.30	0.25	0.56	-0.96	0.08
Hs_12plexchip_6_9231	v2HS_284622	TATACCAGTTGCTGCAAATCCT	NM_001001705	FLJ41649	FLJ41649 PROTEIN	-0.90	0.72	0.69	0.74	-1.59	0.06
Hs_12plexchip_4_2413	v2HS_184873	TAAATAGATGACCAAATCAGGT	AK124171	FLJ42177	FLJ42177 PROTEIN	-0.95	1.22	1.63	1.47	-2.57	0.08
Hs_12plexchip_3_5599	v2HS_129545	ATTTGCCTTGAGGACATTTGCC	AK124699	FLJ42709	HYPOTHETICAL GENE SUPPORTED BY AK124699	-1.20	0.58	0.60	0.41	-1.80	0.01
Hs_12plexchip_6_12023	v2HS_166261	TAGTAGGTAAACAGGAAGGCCT	NM_207414	FLJ43860	FLJ43860 protein (FLJ43860), mRNA	-1.34	0.62	0.05	1.22	-1.39	0.18
Hs_12plexchip_6_5687	v2HS_286019	TTTCCCAAGCAGGAAGGTCCGT	NM_207458	FLJ46026	FLJ46026 PROTEIN	-1.79	0.36	1.24	2.11	-3.03	0.13
Hs_12plexchip_3_11113	v2HS_142496	AAGACCGTAGAAGTCATAGCCC	NM_001004330	FLJ46688	FLJ46688 protein (FLJ46688), mRNA	-1.40	0.35	-0.52	0.67	-0.88	0.13
Hs_12plexchip_3_4576	v2HS_121611	TTAACCATTTAGGTGATGGGCA	AK075161	FLJ90680	FLJ90680 PROTEIN	-1.67	0.33	-0.59	0.65	-1.08	0.08
Hs_12plexchip_5_12296	v2HS_247736	TATTTGAGCCATTCTGTGACCC	NM_013231	FLRT2	fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA	-1.39	0.17	-0.18	0.40	-1.21	0.02
Hs_12plexchip_4_10954	v2HS_173816	TTTGCATTTGGTGATAGGTGCA	NM_017791	FLVCR2	feline leukemia virus subgroup C cellular receptor family, member 2 (FLVCR2), mRNA	-1.50	0.25	-0.68	0.84	-0.82	0.23
Hs0P00009898	v2HS_138374	ATTGGTGTGGGTTGACCTGGCC	NM_032296	FLYWCH1	FLYWCH-type zinc finger 1 (FLYWCH1), transcript variant 1, mRNA	-2.97	0.45	-1.88	0.73	-1.09	0.11
Hs_12plexchip_5_7418	v2HS_122733	TTCTAAGCTATATCCATCGGCT	NM_001103184	FMN1	formin 1 (FMN1), mRNA	-1.01	0.48	-0.26	0.29	-0.75	0.10
Hs_12plexchip_6_7169	v2HS_246651	AAGAGAGCGGCAATAAATGGGC	NM_152578	FMR1NB	fragile X mental retardation 1 neighbor (FMR1NB), mRNA	-0.91	0.33	0.11	0.63	-1.03	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_10339	v2HS_86208	TAAGAGGAGTTCATAATGGGCC	NM_021784	FOXA2	forkhead box A2 (FOXA2), transcript variant 1, mRNA	-0.88	0.63	-0.03	0.89	-0.85	0.25
Hs_12plexchip_5_3203	v2HS_204193	AACAATTCGGAGTTTATACCTG	XM_941378	FOXR1	PREDICTED:forkhead box R1 (FOXR1), mRNA	-1.40	0.44	-0.31	0.23	-1.08	0.03
Hs_12plexchip_5_6695	v2HS_262100	ATAGGAGGCAGCAGTAAATGCA	NM_004958	FRAP1	FK506 binding protein 12-rapamycin associated protein 1 (FRAP1), mRNA	-0.84	0.34	0.59	0.81	-1.42	0.08
Hs_12plexchip_3_857	v2HS_36153	CTAATGATGGATACTTTGGCCT	NM_144966	FREM1	FRAS1 related extracellular matrix 1 (FREM1), mRNA	-1.00	0.32	0.07	0.20	-1.07	0.01
Hs_12plexchip_3_8782	v2HS_95990	ATTGATAACCTGGCTAATCCCA	NM_014907	FRMPD1	FERM and PDZ domain containing 1 (FRMPD1), mRNA	-1.10	0.15	0.01	0.54	-1.11	0.06
Hs_12plexchip_6_8856	v2HS_83407	TTAGGGTTGGACATGATATCCC	NM_001097641	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group) (FUT3), transcript variant 4, mRNA	-1.32	0.71	0.16	1.56	-1.47	0.24
Hs_12plexchip_2_7469	v2HS_158516	ATGCAGGATAAATAACAAGGCC	NM_031866	FZD8	frizzled homolog 8 (Drosophila) (FZD8), mRNA	-0.73	0.62	0.36	0.58	-1.09	0.09
Hs_12plexchip_4_9676	v2HS_5829	ATACTGTCTCACAAATTCCCGC	NM_198395	G3BP1	GTPase activating protein (SH3 domain) binding protein 1 (G3BP1), transcript variant 2, mRNA	-1.27	1.15	-0.36	0.18	-0.91	0.30
Hs_12plexchip_4_6875	v2HS_66086	ATCTTGGTTCCAACTGTCTGAT	NM_001081686	G6PC2	glucose-6-phosphatase, catalytic, 2 (G6PC2), transcript variant 2, mRNA	-0.72	0.42	0.43	0.14	-1.15	0.03
Hs_12plexchip_5_7602	v2HS_265494	ATATGTAATGGTGTTCGGTCCA	NM_005254	GABPB2	GA binding protein transcription factor, beta subunit 2 (GABPB2), transcript variant beta-1, mRNA	-2.92	0.87	-1.44	0.52	-1.48	0.08
Hs_12plexchip_5_11157	v2HS_238118	TTTGAGGAGTAGGATTATTGCT	NM_000811	GABRA6	gamma-aminobutyric acid (GABA) A receptor, alpha 6 (GABRA6), mRNA	-0.80	0.65	0.52	1.10	-1.32	0.16
Hs_12plexchip_5_5905	v2HS_259511	ATTGGGATTCCTCTTCTTAGCT	NM_001037525	GALC	galactosylceramidase (GALC), transcript variant 2, mRNA	-1.24	0.29	-0.41	0.49	-0.83	0.08
Hs_12plexchip_3_10279	v2HS_136380	TAATGATATCGATCACAGGGCA	NM_024572	GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14) (GALNT14), mRNA	-1.00	0.65	0.21	0.81	-1.21	0.12
Hs_12plexchip_6_6522	v2HS_99826	ATCGATTGCAAGGGAATCTGGT	NM_054110	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (GALNTL2), mRNA	-0.97	0.37	0.15	1.14	-1.12	0.22
Hs_12plexchip_6_6980	v2HS_159872	TTATTCTCTCCATTCTGCTCCA	NM_033106	GALP	galanin-like peptide (GALP), mRNA	-0.88	0.56	0.03	0.74	-0.91	0.17
Hs_12plexchip_5_12561	v2HS_42851	TAAAGTTACAATGCAGTCTTGC	NM_005257	GATA6	GATA binding protein 6 (GATA6), mRNA	-1.40	0.09	-0.12	0.07	-1.28	0.00
Hs_12plexchip_5_12941	v2HS_42849	TTCTTAACAAATAGAGAAAGGC	NM_005257	GATA6	GATA binding protein 6 (GATA6), mRNA	-0.73	0.23	1.12	0.07	-1.85	0.00
Hs_12plexchip_6_2560	v2HS_155064	AATGCTGTGGATTTGCTGAGCC	NM_017660	GATAD2A	GATA zinc finger domain containing 2A (GATAD2A), mRNA	-1.57	0.58	0.68	0.07	-2.24	0.02
Hs_12plexchip_3_8483	v2HS_98134	TAGTAAACTCATATACCCTGGC	NM_021996	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (GBGT1), mRNA	-1.93	0.51	-1.15	0.60	-0.78	0.16
Hs_12plexchip_5_7564	v2HS_265805	ATGGAGAATTACTTTCACAGGA	NM_000583	GC	group-specific component (vitamin D binding protein) (GC), mRNA	-0.89	0.10	-0.13	0.60	-0.76	0.15
Hs0P00003410	v2HS_36125	TTTGGGAAGGAAGGGCAAGGCT	NM_004752	GCM2	glial cells missing homolog 2 (Drosophila) (GCM2), mRNA	-1.61	0.36	-0.44	0.58	-1.17	0.05
Hs_12plexchip_5_12786	v2HS_249954	TTCTCATCCAGGAAGAGGACCC	NM_004962	GDF10	growth differentiation factor 10 (GDF10), mRNA	-2.00	0.44	-0.78	0.67	-1.22	0.07
Hs_12plexchip_6_5273	v2HS_232129	AATAAGCTCTCTTTCCTCTGCG	NM_182828	GDF7	growth differentiation factor 7 (GDF7), mRNA	-0.81	0.13	0.08	0.79	-0.89	0.19
Hs_12plexchip_5_5249	v2HS_83571	TTGTGACATAGGATTATTTGGA	NM_182833	GDPD4	glycerophosphodiester phosphodiesterase domain containing 4 (GDPD4), mRNA	-0.70	0.44	0.12	0.12	-0.82	0.08
Hs_12plexchip_3_7977	v2HS_96642	TTTCTGAAGGAGCTCTTGGGCC	NM_015465	GEMIN5	gem (nuclear organelle) associated protein 5 (GEMIN5), mRNA	-0.94	0.95	0.20	0.76	-1.14	0.18
Hs_12plexchip_2_12706	v2HS_50314	ATCAGATGAAAGGTGGTGATGG	NM_005110	GFPT2	glutamine-fructose-6-phosphate transaminase 2 (GFPT2), mRNA	-0.83	0.33	-0.12	0.44	-0.70	0.10
Hs_12plexchip_3_4845	v2HS_114535	AATGACAATCTCTCTATTTCCC	NM_015660	GIMAP2	GTPase, IMAP family member 2 (GIMAP2), mRNA	-0.82	0.48	0.28	0.63	-1.10	0.08
Hs_12plexchip_2_8870	v2HS_25936	TTCAGTAAAGGTGTTTCCGTCT	NG_000861	GKP3	GLYCEROL KINASE PSEUDOGENE 3	-1.15	0.50	-0.37	0.22	-0.78	0.10
Hs_12plexchip_5_9944	v2HS_232389	ATATCATAGAGGGAGGAAGCCA	NM_000404	GLB1	galactosidase, beta 1 (GLB1), transcript variant 1, mRNA	-0.78	0.37	-0.06	0.32	-0.72	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_12552	v2HS_212899	TTTCAGTGATCTGTTGTGGCAG	NM_000168	GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA	-1.31	0.52	0.68	0.38	-1.99	0.01
Hs_12plexchip_5_8454	v2HS_225069	ATGGTCCAAGGTATAATTTGCA	NM_031302	GLT8D2	glycosyltransferase 8 domain containing 2 (GLT8D2), mRNA	-1.20	0.34	-0.34	0.82	-0.86	0.20
Hs_12plexchip_6_9018	v2HS_227178	ATTGCTGACTATGATAGAGGCA	NM_002066	GML	GPI anchored molecule like protein (GML), mRNA	-0.85	0.21	0.85	1.88	-1.70	0.26
Hs_12plexchip_3_1559	v2HS_65339	TTATTCCATACAGCCCTGGCCC	NM_013334	GMPPB	GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 1, mRNA	-1.30	0.61	-0.28	0.18	-1.02	0.09
Hs_12plexchip_5_5631	v2HS_256081	TTGGAAACTAGCATTCTTTCCA	NM_021955	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1 (GNGT1), mRNA	-2.43	0.76	-1.24	0.89	-1.20	0.15
Hs_12plexchip_6_1270	v2HS_220370	ATACTGTTGCTCTTAGGGCGGT	NM_019067	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like (GNL3L), mRNA	-1.13	0.27	0.01	0.70	-1.14	0.09
Hs_12plexchip_5_12176	v2HS_68690	TTAGATATTGAGAGTTTGTGCC	NM_005471	GNPDA1	glucosamine-6-phosphate deaminase 1 (GNPDA1), mRNA	-0.76	0.31	0.10	0.23	-0.86	0.02
Hs_12plexchip_3_4986	v2HS_114193	TTTGGTTCTTGGATCTTCTGCC	NM_002076	GNS	glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) (GNS), mRNA	-2.34	0.70	-1.23	0.30	-1.11	0.10
Hs_12plexchip_4_5831	v2HS_16968	TTTCAACTTGAGATTGTCTGCT	NM_004487	GOLGB1	golgin B1, golgi integral membrane protein (GOLGB1), mRNA	-0.85	0.18	0.49	0.84	-1.35	0.10
Hs_12plexchip_5_10795	v2HS_138347	TTAACCTTCTCTACTTCCTGCA	NM_032292	GON4L	gon-4-like (C. elegans) (GON4L), transcript variant 2, mRNA	-1.40	0.07	-0.25	0.24	-1.15	0.01
Hs_12plexchip_4_6417	v2HS_67737	CTGCAATATGTCTCTATGCCGC	NM_001007025	GOSR1	golgi SNAP receptor complex member 1 (GOSR1), transcript variant 2, mRNA	-1.47	0.98	-0.55	0.85	-0.92	0.29
Hs_12plexchip_5_8789	v2HS_114221	TTTGCAGACCATAGTGAAGGCT	NM_002080	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA	-0.78	0.17	-0.05	0.43	-0.73	0.09
Hs_12plexchip_2_2826	v2HS_82773	GAAGCCTTTGGTCAGGTGCTCC	NM_000174	GP9	glycoprotein IX (platelet) (GP9), mRNA	-1.45	0.93	-0.71	0.03	-0.74	0.30
Hs_12plexchip_4_10256	v2HS_155287	TTTAGGTGTGAAATCCACAGGT	NM_018025	GPATCH1	G patch domain containing 1 (GPATCH1), mRNA	-2.86	0.79	-1.68	0.86	-1.18	0.15
Hs_12plexchip_4_11387	v2HS_155370	TATACTTCGAGAATGGTCTCCT	NM_018040	GPATCH2	G patch domain containing 2 (GPATCH2), mRNA	-2.08	0.88	-0.84	0.74	-1.24	0.14
Hs_12plexchip_5_233	v2HS_42299	TATTGGGTAGACAAATAGGCCT	NM_005276	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble) (GPD1), mRNA	-2.27	0.18	-1.45	0.21	-0.82	0.01
Hs_12plexchip_6_10697	v2HS_222249	TTTCTTTGGCACTTTCATTCCC	NM_032777	GPR124	G protein-coupled receptor 124 (GPR124), mRNA	-0.84	0.45	-0.11	0.08	-0.73	0.10
Hs_12plexchip_6_6027	v2HS_258769	TACACTTGGGTGACTCAGGGAT	AK026883	GPR157	G PROTEIN-COUPLED RECEPTOR 157	-1.43	0.25	-0.65	0.27	-0.77	0.02
Hs_12plexchip_4_1142	v2HS_196666	CAAACATGGCCAGGTAGAGGGC	NM_007264	GPR182	G protein-coupled receptor 182 (GPR182), mRNA	-0.89	0.93	0.18	0.99	-1.07	0.25
Hs_12plexchip_6_3687	v2HS_169334	TTAGCACCCATAGATAGAGGCC	NG_001132	GPR33	G PROTEIN-COUPLED RECEPTOR 33	-0.92	0.50	0.05	1.00	-0.97	0.23
Hs_12plexchip_6_2843	v2HS_169533	AACCACATGCAAAGAAAGGGCC	NG_001217	GPR53P	G PROTEIN-COUPLED RECEPTOR 53, PSEUDOGENE	-1.09	0.68	-0.30	0.67	-0.80	0.22
Hs_12plexchip_6_374	v2HS_55806	CTGCTTCATCACATGGGCAGGT	NM_005682	GPR56	G protein-coupled receptor 56 (GPR56), transcript variant 1, mRNA	-2.85	1.14	0.24	1.68	-3.08	0.07
Hs_12plexchip_6_6363	v2HS_158747	TTGAAGAAGCAGACAAACTGCT	NM_031936	GPR61	G protein-coupled receptor 61 (GPR61), mRNA	-1.36	0.91	-0.04	1.03	-1.32	0.17
Hs_12plexchip_4_10370	v2HS_159238	TAAAGCATTGATTGACTGAGCC	NM_032554	GPR81	G protein-coupled receptor 81 (GPR81), mRNA	-1.89	0.88	0.33	0.44	-2.23	0.03
Hs_12plexchip_3_5887	v2HS_228172	AACCACACTCAGCGTATCGGGC	NM_001039848	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), transcript variant 3, mRNA	-2.56	0.17	-1.31	1.20	-1.25	0.21
Hs_12plexchip_4_7095	v2HS_68798	TATAGTCATGGAGTCCAGCCTT	NM_004810	GRAP2	GRB2-related adaptor protein 2 (GRAP2), mRNA	-2.01	0.69	-0.72	0.46	-1.28	0.06
Hs_12plexchip_2_3020	v2HS_86391	AAGTTATATGACCCATATCCCA	NM_198182	GRHL1	grainyhead-like 1 (Drosophila) (GRHL1), transcript variant 2, mRNA	-1.02	0.48	-0.16	0.17	-0.86	0.08
Hs_12plexchip_2_5247	v2HS_176825	TATTTCTCAGATATCGCTTCCA	NM_024915	GRHL2	grainyhead-like 2 (Drosophila) (GRHL2), mRNA	-1.10	0.43	-0.33	0.17	-0.77	0.07
Hs_12plexchip_6_2743	v2HS_179819	ATATAGTCACCAATGTTCAGCA	XM_940982	GRIP2	PREDICTED:glutamate receptor interacting protein 2, transcript variant 2 (GRIP2), mRNA	-1.24	0.53	-0.51	0.73	-0.73	0.24

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_4378	v2HS_179821	TATTTCCACCATCAAGGGTCCC	XM_940982	GRIP2	PREDICTED:glutamate receptor interacting protein 2, transcript variant 2 (GRIP2), mRNA	-1.34	0.72	-0.14	0.25	-1.19	0.09
Hs_12plexchip_6_10297	v2HS_274056	ATAACCAAGTAGCTCTTTCCCA	NM_000845	GRM8	glutamate receptor, metabotropic 8 (GRM8), mRNA	-0.79	0.37	0.10	1.01	-0.90	0.26
Hs_12plexchip_6_2297	v2HS_157433	TAAACAAACAGTCCCAGATCCG	NM_024719	GRTP1	growth hormone regulated TBC protein 1 (GRTP1), mRNA	-0.96	1.40	1.03	0.83	-1.99	0.12
Hs_12plexchip_5_7179	v2HS_158871	AATACATAGAGGAGGAGTGCCA	NM_031965	GSG2	germ cell associated 2 (haspin) (GSG2), mRNA	-0.96	0.59	-0.06	0.89	-0.90	0.23
Hs_12plexchip_5_8971	v2HS_265999	TTATTAATTAGCACAATTAGGT	NM_002094	GSPT1	G1 to S phase transition 1 (GSPT1), mRNA	-1.06	0.27	0.15	0.40	-1.20	0.02
Hs_12plexchip_4_7996	v2HS_130925	ATATCAATTAGGGCTCTCTCCT	NM_000847	GSTA3	glutathione S-transferase A3 (GSTA3), mRNA	-0.97	0.80	-0.06	0.24	-0.91	0.18
Hs_12plexchip_5_12270	v2HS_77622	TAAGTGTTTCCTATCTACTGGC	NM_172196	GTF2A1L	general transcription factor IIA, 1-like (GTF2A1L), transcript variant 2, mRNA	-1.22	0.83	1.28	2.44	-2.50	0.21
Hs_12plexchip_4_9146	v2HS_16839	ATCTGTTGAGACTGTATGAGCT	NM_004492	GTF2A2	general transcription factor IIA, 2, 12kDa (GTF2A2), mRNA	-0.86	0.47	-0.07	0.80	-0.79	0.23
Hs0P00009792	v2HS_132058	TTTGTCATTGCTGAAAGTTCGC	NM_001514	GTF2B	general transcription factor IIB (GTF2B), mRNA	-1.40	0.96	-0.28	0.78	-1.12	0.19
Hs_12plexchip_6_3222	v2HS_176636	ATTTCATCCACCTGGAACTCCG	NM_019096	GTPBP2	GTP binding protein 2 (GTPBP2), mRNA	-0.85	0.71	0.46	0.22	-1.32	0.07
Hs0P00005158	v2HS_203524	TAATACTTCACAAGTCTCTCCA	NM_020771	HACE1	HECT DOMAIN AND ANKYRIN REPEAT CONTAINING, E3 UBIQUITIN PROTEIN LIGASE 1	-0.87	0.88	0.35	1.26	-1.22	0.25
Hs_12plexchip_6_8772	v2HS_132998	TTACAGTTCTGGCAAATTTCCC	NM_002108	HAL	histidine ammonia-lyase (HAL), mRNA	-0.77	0.57	0.23	0.24	-1.01	0.08
Hs_12plexchip_5_4151	v2HS_260265	AATATTAAAGATGAGGATTCGG	NM_006620	HBS1L	HBS1-like (S. cerevisiae) (HBS1L), mRNA	-2.37	0.29	-1.23	0.41	-1.13	0.02
Hs_12plexchip_6_8600	v2HS_213783	GTAGAAGCTCATGTTCTCTGCA	NM_005844	HCG9	HLA complex group 9 (HCG9), mRNA	-2.30	1.64	-0.65	0.75	-1.65	0.22
Hs_12plexchip_5_7036	v2HS_133007	TTTGAGAATGTATTGCCTCCGA	NM_002110	HCK	hemopoietic cell kinase (HCK), mRNA	-1.01	0.27	0.05	0.54	-1.06	0.06
Hs_12plexchip_5_7143	v2HS_202598	AAGTAGGATCCATCGGTGAGGC	NM_020897	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel 3 (HCN3), mRNA	-1.47	0.87	-0.54	0.27	-0.93	0.20
Hs_12plexchip_6_9173	v2HS_202999	TAATGATCTCCTCGCGAAGCGG	NM_020897	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel 3 (HCN3), mRNA	-0.86	0.41	-0.16	0.69	-0.71	0.22
Hs_12plexchip_5_10270	v2HS_262107	ATTTGGCAGAAACATGGTAGCC	NM_016596	HDAC7A	histone deacetylase 7A (HDAC7A), transcript variant 2, mRNA	-2.18	0.99	-0.90	1.08	-1.28	0.21
Hs_12plexchip_4_4747	v2HS_238946	ATCATCCTTTGCATCTTGTGCT	NM_178423	HDAC9	histone deacetylase 9 (HDAC9), transcript variant 4, mRNA	-1.78	0.63	-0.88	1.08	-0.90	0.29
Hs_12plexchip_4_10195	v2HS_155545	TATTAAATGACACTGCTTTGGG	NM_018072	HEATR1	HEAT repeat containing 1 (HEATR1), mRNA	-3.41	1.69	-1.04	0.05	-2.38	0.14
Hs_12plexchip_5_10673	v2HS_269202	TATTCTTGTCTCGTGGTATGGC	NM_018072	HEATR1	HEAT repeat containing 1 (HEATR1), mRNA	-3.04	0.13	-0.73	2.78	-2.30	0.29
Hs_12plexchip_5_2373	v2HS_250230	TATGTTTACAGACTACTGTCCT	NM_014320	HEBP2	heme binding protein 2 (HEBP2), mRNA	-1.09	0.55	0.09	0.79	-1.18	0.11
Hs_12plexchip_3_7743	v2HS_97861	TTATCCACAGCAATGACTCGGC	NM_016173	HEMK1	HemK methyltransferase family member 1 (HEMK1), mRNA	-1.19	0.10	-0.32	0.15	-0.87	0.00
Hs_12plexchip_3_3016	v2HS_53633	TTCCGTAAAGACGTAGAGTGCG	NM_020707	HHATL	hedgehog acyltransferase-like (HHATL), mRNA	-0.71	0.69	0.28	0.90	-0.99	0.21
Hs_12plexchip_5_2196	v2HS_198444	AATGATCAGGAAAGTTTCAGGA	NM_014362	HIBCH	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), transcript variant 1, mRNA	-0.79	0.25	0.01	0.10	-0.80	0.02
Hs_12plexchip_5_3240	v2HS_211804	TTACACAAAGGGTCACTTCCTC	NM_138820	HIGD2A	HIG1 domain family, member 2A (HIGD2A), mRNA	-1.70	0.64	-0.22	0.45	-1.48	0.04
Hs_12plexchip_6_976	v2HS_37618	TTACACAGACGTTTAATTAGCT	NM_005339	HIP2	huntingtin interacting protein 2 (HIP2), mRNA	-0.81	0.40	0.17	0.82	-0.99	0.16
Hs_12plexchip_4_11067	v2HS_100054	TACTTGCTTTGGGCTTTATGGT	NM_170745	HIST1H2AA	histone cluster 1, H2aa (HIST1H2AA), mRNA	-0.98	0.62	0.25	0.85	-1.23	0.12
Hs_12plexchip_6_1261	v2HS_33915	TTGTATACTTGGTGACAGCCTT	NM_003518	HIST1H2BG	histone cluster 1, H2bg (HIST1H2BG), mRNA	-1.61	0.98	0.37	1.67	-1.98	0.17
Hs_12plexchip_3_9250	v2HS_133056	AATCTTCTGGAGAGTCTGTGCC	NM_002120	HLA-DOB	major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA	-0.92	0.12	0.20	0.83	-1.12	0.14
Hs_12plexchip_4_707	v2HS_202837	ATTTCTCTTTCTTCTCCAGCCC	NM_178580	HM13	histocompatibility (minor) 13 (HM13), transcript variant 2, mRNA	-1.17	0.74	0.35	1.07	-1.52	0.12
Hs_12plexchip_5_11055	v2HS_136359	TTATCTACTAAGTCACACAGCT	NM_024567	HMBOX1	homeobox containing 1 (HMBOX1), mRNA	-0.89	1.14	0.38	0.50	-1.27	0.18
Hs_12plexchip_6_8484	v2HS_195302	TTTAGGGAGTTAAGTCTCTGCT	NG_001141	HMG17P1	HIGH-MOBILITY GROUP (NONHISTONE CHROMOSOMAL) PROTEIN 17 PSEUDOGENE 1	-1.27	0.88	0.03	1.20	-1.30	0.21
Hs_12plexchip_6_1839	v2HS_195911	ATCTAGAAATGGAACCACTGCT	NM_005517	HMGN2	high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA	-1.74	0.60	0.12	0.47	-1.87	0.02
Hs_12plexchip_4_2251	v2HS_218617	TTTCACATTTATGTAGTGCCGT	NM_004133	HNF4G	hepatocyte nuclear factor 4, gamma (HNF4G), mRNA	-0.95	0.10	-0.18	0.71	-0.78	0.20
Hs_12plexchip_6_78	v2HS_117147	ATGGGATAAGATTTCTAAACCC	NM_004500	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRNPC), transcript variant 2, mRNA	-2.01	0.72	-0.86	0.21	-1.14	0.10

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_9368	v2HS_196353	ATTTATTCCAAATCCTATGCCT	NM_005968	HNRPM	heterogeneous nuclear ribonucleoprotein M (HNRPM), transcript variant 1, mRNA	-2.91	0.46	-1.73	0.25	-1.18	0.03
Hs_12plexchip_4_9135	v2HS_27873	TTTCCTTTGAGGGTAGCCAGTT	NM_004272	HOMER1	homer homolog 1 (Drosophila) (HOMER1), mRNA	-0.90	0.26	0.13	0.55	-1.02	0.06
Hs_12plexchip_4_8899	v2HS_133162	ATATTTACAAGCTTTGGGCCCT	NM_002147	HOXB5	homeobox B5 (HOXB5), mRNA	-1.13	0.96	1.29	0.62	-2.42	0.03
Hs_12plexchip_4_9806	v2HS_196528	TTTAGTTCGAGGATTGTTCGGC	NM_014212	HOXC11	homeobox C11 (HOXC11), mRNA	-2.35	1.04	-1.20	0.47	-1.15	0.18
Hs0P00007673	v2HS_136048	TTCTTCTGTTTCATCCTGCGGT	NM_024501	HOXD1	homeobox D1 (HOXD1), mRNA	-1.18	0.40	0.24	0.46	-1.42	0.02
Hs_12plexchip_5_3171	v2HS_215498	AACCTTCATCATCCATTGTGCT	NM_007216	HPS5	Hermansky-Pudlak syndrome 5 (HPS5), transcript variant 2, mRNA	-0.73	0.60	0.27	0.34	-1.00	0.08
Hs0P00011266	v2HS_92889	TTGTCTGCAATGGAAGGGACGG	NM_000412	HRG	histidine-rich glycoprotein (HRG), mRNA	-0.79	0.52	1.09	0.96	-1.88	0.06
Hs_12plexchip_6_10290	v2HS_198166	TATAGTGATGCCGTTGTCAGTG	NM_005836	HRSP12	heat-responsive protein 12 (HRSP12), mRNA	-0.93	0.24	-0.10	0.56	-0.83	0.11
Hs0P00000216	v2HS_59634	ATTTCCCTAGGCACTCTCACTG	AK091074	HS3ST5	HEPARAN SULFATE (GLUCOSAMINE) 3-O-SULFOTRANSFERASE 5	-0.74	0.09	0.17	0.28	-0.90	0.02
Hs_12plexchip_6_5240	v2HS_230354	TTAGAAGGTACAGTCCTCTGCT	NM_172002	HSCB	HscB iron-sulfur cluster co-chaperone homolog (E. coli) (HSCB), mRNA	-2.78	1.40	-0.92	1.51	-1.87	0.19
Hs_12plexchip_2_4291	v2HS_82370	TTTGATAATGTGACTGTGTGGC	NM_000198	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2), mRNA	-1.22	0.30	0.13	0.50	-1.35	0.02
Hs_12plexchip_6_6626	v2HS_137326	TAGAAGTCCCTCATGATCTGGT	NM_025193	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 (HSD3B7), mRNA	-1.86	0.41	-0.58	0.29	-1.28	0.01
Hs_12plexchip_3_11020	v2HS_138414	TTTAGATGCAAGGTAGGTGCCT	NM_032303	HSDL2	hydroxysteroid dehydrogenase like 2 (HSDL2), mRNA	-1.31	0.81	0.08	0.46	-1.39	0.08
Hs_12plexchip_3_7417	v2HS_97802	TTGATTGATCACTCTACAAGCC	NM_016153	HSFX1	heat shock transcription factor family, X linked 1 (HSFX1), mRNA	-0.70	0.27	0.09	0.48	-0.79	0.09
Hs0P00012615	v2HS_97805	ATTGACCAGCACATATTCTGCC	NM_016153	HSFX1	heat shock transcription factor family, X linked 1 (HSFX1), mRNA	-1.25	1.04	-0.23	0.50	-1.02	0.23
Hs_12plexchip_4_521	v2HS_115310	ATTAAATCCAGCAGCTCTAGCT	NM_016299	HSPA14	heat shock 70kDa protein 14 (HSPA14), transcript variant 1, mRNA	-1.67	0.87	0.14	0.79	-1.81	0.06
Hs_12plexchip_2_6111	v2HS_173169	ATTGTTTGGGTTGGTGACAGCC	NM_004134	HSPA9	heat shock 70kDa protein 9 (mortalin) (HSPA9), nuclear gene encoding mitochondrial protein, mRNA	-2.33	0.41	-0.64	0.41	-1.69	0.01
Hs_12plexchip_3_12424	v2HS_15950	TCTGCAATTGACTTTGTCCGAG	NM_145168	HSPC105	NAD(P) dependent steroid dehydrogenase-like (HSPC105), mRNA	-0.98	0.60	0.10	0.79	-1.09	0.14
Hs_12plexchip_5_7702	v2HS_264750	TAATTCTTCTCATCACGGGCCA	NM_016391	HSPC111	hypothetical protein HSPC111 (HSPC111), mRNA	-3.06	1.12	-1.94	0.73	-1.12	0.23
Hs_12plexchip_2_12383	v2HS_199019	TATTCTGGGTATAATGGCTCGG	NM_014181	HSPC159	galectin-related protein (HSPC159), mRNA	-0.79	0.46	0.02	0.30	-0.81	0.07
Hs_12plexchip_4_1198	v2HS_198948	ATAGAGGTGGTTTAAATCAGCC	NM_014181	HSPC159	galectin-related protein (HSPC159), mRNA	-1.56	0.59	-0.68	0.37	-0.88	0.11
Hs_12plexchip_3_11065	v2HS_193423	TTTAAGTTCAGCAATTACAGCA	NM_199440	HSPD1	heat shock 60kDa protein 1 (chaperonin) (HSPD1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.42	0.27	-0.02	0.51	-1.40	0.02
Hs_12plexchip_2_8738	v2HS_22070	ATAATCAATCGCGTTTGGACCT	X53943	HSSUCCDH	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT	-0.76	0.22	0.04	0.13	-0.80	0.01
Hs_12plexchip_3_5015	v2HS_110972	ATAGCCAACAGTAGCATGTGGC	NM_031407	HUWE1	HECT, UBA and WWE domain containing 1 (HUWE1), mRNA	-1.48	0.39	-0.37	0.31	-1.11	0.02
Hs_12plexchip_5_6173	v2HS_262858	TTTAGGATCAGATTTATCTGCT	NM_031407	HUWE1	HECT, UBA and WWE domain containing 1 (HUWE1), mRNA	-1.29	0.70	0.24	0.61	-1.53	0.05
Hs_12plexchip_5_11771	v2HS_133238	TTAATCAGATATAATCTGAGGG	NM_013417	IARS	isoleucyl-tRNA synthetase (IARS), transcript variant long, mRNA	-2.72	0.34	-0.75	0.24	-1.96	0.00
Hs_12plexchip_6_9815	v2HS_155481	ATAGTCTCAAATGTTGTTTCCA	NM_018060	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial (IARS2), mRNA	-2.36	0.67	-0.66	1.13	-1.69	0.10
Hs_12plexchip_5_3710	v2HS_96821	TTAAACACTCAGAAACAAACCA	NM_015525	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase (IBTK), mRNA	-1.03	0.38	0.19	0.17	-1.23	0.02
Hs_12plexchip_3_7629	v2HS_232253	TATTGTGTCAATTTCACTGGCT	NM_016513	ICK	intestinal cell (MAK-like) kinase (ICK), transcript variant 2, mRNA	-0.92	0.48	0.21	0.39	-1.14	0.04
Hs_12plexchip_3_8593	v2HS_96065	ATATTGTGTCAATTTCACTGGC	NM_016513	ICK	intestinal cell (MAK-like) kinase (ICK), transcript variant 2, mRNA	-0.86	0.44	-0.14	0.30	-0.72	0.09
Hs_12plexchip_4_5070	v2HS_96066	TATTGGGTACACACTGTGGCCA	NM_016513	ICK	intestinal cell (MAK-like) kinase (ICK), transcript variant 2, mRNA	-1.23	0.68	-0.30	0.67	-0.93	0.17

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_12688	v2HS_244502	ATCTTAGTTGGGACTATTTGCA	NM_012405	ICMT	isoprenylcysteine carboxyl methyltransferase (ICMT), mRNA	-0.93	0.18	-0.14	0.41	-0.79	0.06
Hs0P00010589	v2HS_28548	GTTAAGTCAGACTCTCCGTGGT	NM_012092	ICOS	inducible T-cell co-stimulator (ICOS), mRNA	-1.73	0.21	-0.89	0.42	-0.84	0.06
Hs_12plexchip_6_9268	v2HS_22567	TAAGAGACTGATACTGGATCCT	M96843	ID2B	INHIBITOR OF DNA BINDING 2B, DOMINANT NEGATIVE HELIX-LOOP-HELIX PROTEIN	-1.12	0.87	0.16	1.50	-1.28	0.29
Hs_12plexchip_5_8334	v2HS_264362	ATCGAGATACTTGTGGGTGGCG	NM_022873	IFI6	interferon, alpha-inducible protein 6 (IFI6), transcript variant 3, mRNA	-1.21	1.21	0.01	0.31	-1.22	0.22
Hs_12plexchip_3_8920	v2HS_132251	TTTACGTAAGCATTCCAGGGCT	NM_001547	IFIT2	interferon-induced protein with tetratricopeptide repeats 2 (IFIT2), mRNA	-0.99	0.23	0.24	0.30	-1.22	0.01
Hs_12plexchip_4_10272	v2HS_194395	TATAGAGTTTGTCTAGAAGCCT	NM_021002	IFNA6	interferon, alpha 6 (IFNA6), mRNA	-1.15	0.82	-0.42	0.45	-0.73	0.26
Hs_12plexchip_6_6547	v2HS_161087	ATATTCATGGAGAATAGCAGGA	NM_020800	IFT80	intraflagellar transport 80 homolog (Chlamydomonas) (IFT80), mRNA	-0.78	1.78	2.15	1.02	-2.93	0.08
Hs_12plexchip_4_7426	v2HS_63065	CTGTGGGTATAAGCATAACTCC	X93614	IGHD3-16	IMMUNOGLOBULIN HEAVY DIVERSITY 3-16	-0.97	0.72	0.24	1.12	-1.21	0.20
Hs_12plexchip_3_2183	v2HS_54618	TAGTTACAACCGCAAATGTCAC	M12025	IGLV@	IMMUNOGLOBULIN LAMBDA VARIABLE GROUP	-0.70	0.27	0.08	0.37	-0.79	0.05
Hs_12plexchip_4_6153	v2HS_27524	ATAATTATGCTCTCAAACAGCC	NM_003640	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA	-1.30	0.95	0.49	0.89	-1.79	0.08
Hs_12plexchip_5_6182	v2HS_255250	TTCATGAAGGTATCTAAGCGCA	NM_001556	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta (IKBKB), mRNA	-0.96	0.77	0.15	0.46	-1.10	0.11
Hs_12plexchip_5_8872	v2HS_263816	ATAAAGAAACAATATTCCCGCC	NM_001079526	IKZF2	IKAROS family zinc finger 2 (Helios) (IKZF2), transcript variant 2, mRNA	-0.98	0.34	-0.26	0.19	-0.71	0.05
Hs0P00006032	v2HS_132313	TTTGCAGATGGGTGCCAGAGGT	NM_001558	IL10RA	INTERLEUKIN 10 RECEPTOR, ALPHA	-0.75	0.61	0.25	0.30	-1.01	0.09
Hs_12plexchip_5_7783	v2HS_266151	TTCTTCAGTTGCTTAGAGGGCC	AK095107	IL1RAP	INTERLEUKIN 1 RECEPTOR ACCESSORY PROTEIN	-1.22	0.48	-0.02	0.41	-1.20	0.03
Hs_12plexchip_6_8558	v2HS_16605	GAAAGGAAGGCCATAATCTTCC	NM_003854	IL1RL2	interleukin 1 receptor-like 2 (IL1RL2), mRNA	-0.96	1.00	0.61	0.53	-1.57	0.09
Hs_12plexchip_5_7608	v2HS_227105	TATTGTTATCAACTTTGGAGCA	NM_181309	IL22RA2	interleukin 22 receptor, alpha 2 (IL22RA2), transcript variant 2, mRNA	-0.70	0.28	0.37	0.15	-1.07	0.01
Hs_12plexchip_5_4294	v2HS_257379	TTTAACAATCCAAAGACAGGCC	NM_006850	IL24	interleukin 24 (IL24), transcript variant 1, mRNA	-0.73	0.52	0.31	0.85	-1.04	0.16
Hs_12plexchip_6_1664	v2HS_175429	ATACAGTGGCTCAATTTCTGCC	NM_018402	IL26	interleukin 26 (IL26), mRNA	-0.77	0.38	0.74	0.05	-1.51	0.02
Hs_12plexchip_3_11093	v2HS_131086	TTGTAGAAGCATGTGAACTGGG	NM_000878	IL2RB	interleukin 2 receptor, beta (IL2RB), mRNA	-1.17	0.59	-0.29	0.93	-0.89	0.25
Hs_12plexchip_6_10224	v2HS_77306	TATGTCTATAATCCACTGATTG	NM_000206	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA	-0.72	0.52	0.25	0.28	-0.97	0.06
Hs_12plexchip_5_10372	v2HS_93693	TTATTGAGATGAATGCATTGGT	NM_000564	IL5RA	interleukin 5 receptor, alpha (IL5RA), transcript variant 1, mRNA	-1.18	0.23	-0.33	0.19	-0.85	0.01
Hs0P00010325	v2HS_226020	TTGCTATTTGTATATTCTCCCG	NM_000584	IL8	INTERLEUKIN 8	-1.13	1.00	-0.32	0.53	-0.82	0.30
Hs_12plexchip_3_12824	v2HS_48793	ATTTCACAACATTTCAACAGCA	NM_004515	ILF2	interleukin enhancer binding factor 2, 45kDa (ILF2), mRNA	-2.64	0.60	-1.62	0.80	-1.02	0.16
Hs_12plexchip_5_7150	v2HS_246159	AATACGGTTGAGATTCTGGCCC	NM_001014795	ILK	integrin-linked kinase (ILK), transcript variant 3, mRNA	-1.50	1.77	0.78	1.53	-2.28	0.17
Hs_12plexchip_3_2704	v2HS_63421	TACTACTAGAGGAACAAACTGG	NM_198218	ING1	inhibitor of growth family, member 1 (ING1), transcript variant 2, mRNA	-0.70	0.23	0.01	0.74	-0.71	0.23
Hs_12plexchip_3_10131	v2HS_139496	AATAGTGGCGACAGTATACGGC	NM_015693	INTU	inturned planar cell polarity effector homolog (Drosophila) (INTU), mRNA	-1.08	0.31	-0.38	0.51	-0.70	0.13
Hs0P00002117	v2HS_65842	TAAGCTGTACGGGTCCTCTTAT	AF049893	IPF1	INSULIN PROMOTER FACTOR 1, HOMEODOMAIN TRANSCRIPTION FACTOR	-2.46	0.57	-1.12	0.61	-1.35	0.05
Hs_12plexchip_2_6922	v2HS_155619	TTTCACTAGGGCTGTCACTGCC	NM_018085	IPO9	importin 9 (IPO9), mRNA	-0.87	0.39	-0.09	0.63	-0.78	0.16
Hs_12plexchip_5_11292	v2HS_139323	TTACCCTATAAGGTCCAATGGA	U12897	IPW	IMPRINTED IN PRADER-WILLI SYNDROME	-0.77	0.55	-0.04	0.14	-0.72	0.14
Hs0P00001242	v2HS_1945	ATTCCTATTAATATACCGATTC	NM_007199	IRAK3	INTERLEUKIN-1 RECEPTOR-ASSOCIATED KINASE 3	-0.77	0.72	-0.03	0.22	-0.74	0.21
Hs_12plexchip_4_7333	v2HS_72166	TTGAAGAAGAACACGGGCAGGG	NM_004136	IREB2	iron-responsive element binding protein 2 (IREB2), mRNA	-1.97	0.43	-0.50	0.63	-1.47	0.03
Hs_12plexchip_3_11195	v2HS_233988	TTATATAGCTCCATGGTGGCCT	NM_030980	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2 (ISG20L2), mRNA	-1.48	0.22	-0.67	0.38	-0.80	0.05
Hs_12plexchip_3_4753	v2HS_116860	ATTTGATTTAGGTCTGTCAGCT	NM_030790	ITFG1	integrin alpha FG-GAP repeat containing 1 (ITFG1), mRNA	-1.31	0.29	-0.50	0.53	-0.81	0.10
Hs_12plexchip_4_9088	v2HS_133433	TAAGATTCTGCAATCTGCTCCT	NM_002205	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), mRNA	-1.97	1.44	-0.57	0.93	-1.40	0.24

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00000643	v2HS_67751	ATTACCAAGGACACTCTATCTG	NM_004867	ITM2A	integral membrane protein 2A (ITM2A), mRNA	-1.05	0.62	0.00	0.16	-1.05	0.09
Hs_12plexchip_6_12091	v2HS_162162	AATTCCTGAGACCTCTTAACCA	NM_203395	IYD	iodotyrosine deiodinase (IYD), mRNA	-0.72	0.24	0.22	0.82	-0.94	0.18
Hs_12plexchip_4_993	v2HS_133559	TTTCACCAAATCATACTGTCCC	NM_002227	JAK1	Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA	-1.98	0.31	-0.56	0.50	-1.42	0.02
Hs_12plexchip_5_3991	v2HS_91498	ATAATGCTCCACACACTGTCGG	NM_006618	JARID1B	jumonji, AT rich interactive domain 1B (JARID1B), mRNA	-1.53	1.04	-0.10	0.58	-1.43	0.12
Hs_12plexchip_3_11418	v2HS_135205	TTTGCATATGATCTCGAAACCA	NM_016604	JMJD1B	jumonji domain containing 1B (JMJD1B), mRNA	-1.70	0.36	-0.66	0.61	-1.04	0.08
Hs_12plexchip_5_2459	v2HS_250225	TTTAACAGAGACTTTGTTGCCC	NM_007064	KALRN	kalirin, RhoGEF kinase (KALRN), transcript variant 3, mRNA	-1.06	0.32	-0.31	0.49	-0.74	0.10
Hs_12plexchip_5_933	v2HS_247394	TTATAATTTCTGGAATTGGCCA	NM_005548	KARS	lysyl-tRNA synthetase (KARS), mRNA	-1.44	0.27	-0.40	0.41	-1.04	0.03
Hs_12plexchip_5_3444	v2HS_241931	TTATGTTTAGTCCAACTAAGGA	NM_152433	KBTBD3	kelch repeat and BTB (POZ) domain containing 3 (KBTBD3), transcript variant 1, mRNA	-0.71	0.66	0.23	0.13	-0.94	0.13
Hs_12plexchip_3_456	v2HS_52418	ATATTCATAAATACACACAGCA	NM_020122	KCMF1	potassium channel modulatory factor 1 (KCMF1), mRNA	-1.09	0.38	0.07	0.76	-1.16	0.10
Hs_12plexchip_5_6348	v2HS_261861	TATTAAGAGAGTCTGTGCTGCC	NM_005549	KCNA10	potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10), mRNA	-1.01	0.41	-0.05	0.06	-0.96	0.05
Hs_12plexchip_3_10869	v2HS_133596	TAACCAAGACCGAGACGATGGC	NM_002234	KCNA5	potassium voltage-gated channel, shaker-related subfamily, member 5 (KCNA5), mRNA	-2.06	0.92	-0.74	1.25	-1.32	0.22
Hs_12plexchip_5_3965	v2HS_203246	ATGTAATACGGCGTGATTGCCA	NM_172344	KCNG3	potassium voltage-gated channel, subfamily G, member 3 (KCNG3), transcript variant 2, mRNA	-1.92	1.09	-0.81	0.48	-1.11	0.21
Hs_12plexchip_6_6202	v2HS_224052	TAAAGGCCCTTGATGGACGGCG	NM_172347	KCNG4	potassium voltage-gated channel, subfamily G, member 4 (KCNG4), transcript variant 1, mRNA	-2.08	0.70	-1.03	0.59	-1.05	0.12
Hs_12plexchip_5_6399	v2HS_18665	ATAGCGTCAGAGGTAACCACGC	NM_012285	KCNH4	potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA	-0.90	0.25	0.74	0.45	-1.64	0.01
Hs_12plexchip_4_207	v2HS_160244	AATATTCTTCAAGACGTTGCCT	NM_173162	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 2, mRNA	-1.00	0.39	0.40	0.55	-1.40	0.03
Hs_12plexchip_4_4613	v2HS_160241	ATATCGATCCAGTTTCCTGGCC	NM_173162	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 2, mRNA	-1.12	0.83	0.51	0.26	-1.63	0.07
Hs_12plexchip_3_9507	v2HS_133627	TATTCGTTGAAGTTTCATGGGC	NM_002239	KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3 (KCNJ3), mRNA	-0.84	0.27	0.24	0.21	-1.07	0.01
Hs_12plexchip_4_7194	v2HS_65811	ATCTCTTCTCACAATGCCTGTT	NM_001014797	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), transcript variant 1, mRNA	-0.91	0.47	0.25	1.32	-1.16	0.26
Hs_12plexchip_3_3404	v2HS_34562	TTTCTCAAAGTGTTTCTGGCGG	NM_019842	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5), mRNA	-0.99	0.58	-0.25	0.39	-0.74	0.15
Hs_12plexchip_4_135	v2HS_218648	ATGTACCTCCACAAGAGCAGGT	NM_173605	KCNRG	potassium channel regulator (KCNRG), transcript variant 1, mRNA	-0.98	0.43	1.58	0.47	-2.56	0.00
Hs_12plexchip_6_12263	v2HS_104098	TAAGTTTCTGAGACTCAGTCCT	NM_198503	KCNT2	potassium channel, subfamily T, member 2 (KCNT2), mRNA	-1.43	0.98	-0.23	1.34	-1.20	0.28
Hs_12plexchip_6_742	v2HS_198117	GATAATATACACATGAAGGCCA	NM_014379	KCNV1	potassium channel, subfamily V, member 1 (KCNV1), mRNA	-0.98	0.14	-0.15	0.61	-0.83	0.14
Hs_12plexchip_5_3542	v2HS_14575	ATTCCATGTAAGAGTAAAGGCA	NM_138444	KCTD12	potassium channel tetramerisation domain containing 12 (KCTD12), mRNA	-2.25	0.34	-0.49	0.58	-1.76	0.02
Hs_12plexchip_3_10328	v2HS_97671	TTTGTCTTTGTCTCCATGTGGC	NM_016121	KCTD3	potassium channel tetramerisation domain containing 3 (KCTD3), mRNA	-1.20	0.83	-0.32	0.39	-0.88	0.20
Hs_12plexchip_5_9238	v2HS_98989	TTAAGGTGTAGTGACATAGGCT	NM_024089	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1 (KDELC1), mRNA	-1.04	0.47	0.25	0.19	-1.29	0.03
Hs_12plexchip_4_9985	v2HS_198147	TTTGCACTTGTAATTGGCTTCC	NM_006558	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA	-1.15	0.65	-0.40	0.63	-0.75	0.23
Hs_12plexchip_5_1686	v2HS_216731	ATTGAGTTTAATATTCACTGCG	NM_015050	KIAA0082	KIAA0082 (KIAA0082), mRNA	-0.90	0.05	0.61	0.44	-1.51	0.03
Hs_12plexchip_5_4566	v2HS_73018	AGAACTAGACACTTAATTTGGT	NM_001029989	KIAA0101	KIAA0101 (KIAA0101), transcript variant 2, mRNA	-1.30	0.27	0.01	0.05	-1.31	0.01
Hs_12plexchip_6_9040	v2HS_285028	ATTTGGTGTTACAAGGGCACGT	NM_014792	KIAA0125	KIAA0125	-0.97	0.74	-0.04	0.12	-0.94	0.16

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_10174	v2HS_95371	TATTGTATAGATGGAGGCTGCG	XM_941746	KIAA0258	PREDICTED:KIAA0258, transcript variant 3 (KIAA0258), mRNA	-2.37	0.85	0.07	0.15	-2.45	0.03
Hs_12plexchip_5_9831	v2HS_230811	TAAATGCCAAAGAGACTATCCC	D87447	KIAA0258	KIAA0258	-1.14	0.30	-0.09	0.22	-1.05	0.01
Hs_12plexchip_6_10424	v2HS_225405	TTATTTCTAGGTCCCTGCGGCT	NM_014686	KIAA0355	KIAA0355 (KIAA0355), mRNA	-0.97	0.30	0.93	1.61	-1.90	0.17
Hs_12plexchip_4_9094	v2HS_74142	TTTGCAATGCAGACTCTGTTGC	NM_014702	KIAA0408	KIAA0408 (KIAA0408), mRNA	-0.87	0.64	0.07	0.84	-0.93	0.21
Hs_12plexchip_3_5502	v2HS_120193	TTTCTCCATGATTTCTACCCGT	NM_015091	KIAA0423	KIAA0423 (KIAA0423), mRNA	-0.77	0.38	0.01	0.74	-0.78	0.20
Hs_12plexchip_5_975	v2HS_248634	AAGTGTATGTTCCAATGACCGG	NM_207306	KIAA0495	KIAA0495 (KIAA0495), mRNA	-1.47	0.63	-0.47	0.67	-1.01	0.13
Hs_12plexchip_5_4402	v2HS_259524	ATCTTCAACTATAGAATGTCCT	AB007978	KIAA0509	KIAA0509 PROTEIN	-1.67	0.98	1.27	1.81	-2.94	0.09
Hs_12plexchip_5_5051	v2HS_256709	ATGGTTAAGGTCAAAGTTTGGC	AB007978	KIAA0509	KIAA0509 PROTEIN	-0.73	0.95	0.15	0.38	-0.88	0.25
Hs_12plexchip_4_422	v2HS_202565	TAGATACAAGAAAGAGGTGGCC	AI278633	KIAA0676	KIAA0676 PROTEIN	-1.68	0.66	-0.90	0.31	-0.78	0.17
Hs0P00011684	v2HS_53708	TTCCAAAGGCACAATAACACCA	NM_020701	KIAA1160	KIAA1160 PROTEIN	-1.92	0.53	-0.89	0.31	-1.04	0.06
Hs_12plexchip_3_3039	v2HS_62688	TAATGCCAATAGTTAGTGAGTC	NM_015443	KIAA1267	KIAA1267 (KIAA1267), mRNA	-0.89	0.32	0.18	0.56	-1.06	0.06
Hs_12plexchip_4_3337	v2HS_222689	ATCATTATTGGGAGAACATGGA	NM_018330	KIAA1598	KIAA1598 (KIAA1598), mRNA	-1.09	0.06	-0.26	0.33	-0.83	0.05
Hs_12plexchip_5_2841	v2HS_209056	ATTTAACACGGCACCAATGCTG	NM_020961	KIAA1627	KIAA1627 protein (KIAA1627), mRNA	-0.75	0.63	0.12	0.74	-0.87	0.20
Hs_12plexchip_5_6933	v2HS_231987	TTACTGATCCAGATGTTGTCCA	NM_030636	KIAA1706	KIAA1706 protein (KIAA1706), mRNA	-1.01	0.36	0.39	1.64	-1.40	0.27
Hs_12plexchip_3_3109	v2HS_60041	TTTCTGAATGAGCTCCTGTCCC	AB058746	KIAA1843	KIAA1843 PROTEIN	-1.43	1.12	-0.35	0.51	-1.08	0.24
Hs_12plexchip_2_5631	v2HS_184080	AACGGTTTCGGTGCAGGGAGCC	BC036932	KIAA1856	KIAA1856 PROTEIN	-1.69	0.53	-0.60	0.62	-1.09	0.08
Hs0P00003088	v2HS_40650	ATTGTCAAAGCCTTCCTGGCGC	AB058778	KIAA1875	KIAA1875 PROTEIN	-1.38	0.14	-0.55	0.73	-0.84	0.18
Hs_12plexchip_5_1023	v2HS_247406	TTGTTCTCTAGGTAGAGCCGGC	NM_199205	KIAA1967	KIAA1967 (KIAA1967), transcript variant 2, mRNA	-1.39	0.31	-0.42	0.13	-0.97	0.02
Hs_12plexchip_3_1275	v2HS_48561	TTATGTACTTCTAGCATGGCCT	NM_004523	KIF11	kinesin family member 11 (KIF11), mRNA	-1.69	0.90	-0.27	0.82	-1.41	0.12
Hs_12plexchip_3_7235	v2HS_95809	TATGTCTCTGACTTTACCTGCA	NM_014875	KIF14	kinesin family member 14 (KIF14), mRNA	-1.27	0.47	-0.43	0.50	-0.84	0.10
Hs_12plexchip_4_9195	v2HS_78033	ATTCTTGCTTATTCAGTGGGCG	NM_006845	KIF2C	kinesin family member 2C (KIF2C), mRNA	-1.22	0.33	-0.02	0.30	-1.21	0.01
Hs_12plexchip_6_752	v2HS_202062	ATTTATTTGAGCTTTCTCACGA	NM_012310	KIF4A	kinesin family member 4A (KIF4A), mRNA	-0.86	0.06	0.13	0.43	-0.99	0.05
Hs_12plexchip_5_6756	v2HS_262283	TTAATGTAGTCCTTGACATGCT	NM_004522	KIF5C	kinesin family member 5C (KIF5C), mRNA	-1.12	0.94	0.14	0.31	-1.26	0.14
Hs_12plexchip_4_697	v2HS_76969	TATGTCATACATTTCAGCAGGT	NM_000222	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), transcript variant 1, mRNA	-0.87	0.42	-0.14	0.44	-0.73	0.10
Hs_12plexchip_6_476	v2HS_69732	TAATACAGGGTGACCATCGCGG	NM_175737	KLB	klotho beta (KLB), mRNA	-2.55	1.12	-0.55	1.80	-2.00	0.19
Hs_12plexchip_6_1429	v2HS_235477	ATGTGTTAGATAATGGGAGGCA	NM_016531	KLF3	Kruppel-like factor 3 (basic) (KLF3), mRNA	-0.88	0.71	0.14	0.38	-1.01	0.12
Hs_12plexchip_4_12291	v2HS_80810	AATGTTCAGCAGTTCTCTCGGG	NM_022480	KLHL25	kelch-like 25 (Drosophila) (KLHL25), mRNA	-1.20	0.69	-0.01	0.36	-1.19	0.08
Hs_12plexchip_5_2310	v2HS_252721	TATGACTAAATTGTTGGTGGCC	NM_020803	KLHL8	kelch-like 8 (Drosophila) (KLHL8), mRNA	-0.77	2.01	1.50	1.20	-2.27	0.18
Hs_12plexchip_2_12443	v2HS_216034	ATTAAGGGAGATCTAGTGCTTA	NM_144507	KLK8	kallikrein-related peptidase 8 (KLK8), transcript variant 4, mRNA	-0.86	0.35	-0.14	0.61	-0.72	0.17
Hs_12plexchip_3_10158	v2HS_238589	ATTTCCATTTGGATTATACGCT	NM_007334	KLRD1	killer cell lectin-like receptor subfamily D, member 1 (KLRD1), transcript variant 2, mRNA	-1.19	0.94	-0.05	1.26	-1.14	0.28
Hs_12plexchip_2_4006	v2HS_85137	TTTGAGATTGGGATGCAGCCTG	NM_001025231	KPRP	keratinocyte proline-rich protein (KPRP), mRNA	-1.52	0.42	-0.36	0.77	-1.16	0.10
Hs_12plexchip_4_11729	v2HS_169384	TTTCCTACTAGGACCATAGGCA	NM_033360	KRAS	V-HA-RAS HARVEY RAT SARCOMA VIRAL ONCOGENE HOMOLOG	-2.04	0.53	-0.86	0.70	-1.18	0.09
Hs_12plexchip_5_1316	v2HS_65213	TGAATGACTCAAAGTAGGGCTC	NM_006121	KRT1	keratin 1 (epidermolytic hyperkeratosis) (KRT1), mRNA	-1.42	0.88	-0.22	0.43	-1.20	0.13
Hs_12plexchip_4_11915	v2HS_133836	ATGGTCCTGAAATGAGACTGGT	NM_002278	KRT32	keratin 32 (KRT32), mRNA	-2.35	1.31	-0.30	0.44	-2.05	0.10
Hs_12plexchip_6_631	v2HS_64836	TTTGCATTTCAGGCAATGACCC	NM_080747	KRT72	keratin 72 (KRT72), mRNA	-0.87	1.10	0.42	0.92	-1.29	0.20
Hs_12plexchip_3_1569	v2HS_63207	ATACATGGTGAGACAAGCTCTG	NM_175858	KRTAP11-1	keratin associated protein 11-1 (KRTAP11-1), mRNA	-1.33	0.05	-0.55	0.65	-0.78	0.17
Hs_12plexchip_4_9050	v2HS_22431	TTTGCATTTGACTGACATGGCA	NG_000940	KRTHBP2	KERATIN, HAIR, BASIC PSEUDOGENE 2	-1.84	0.29	-0.67	0.80	-1.17	0.12
Hs_12plexchip_4_6009	v2HS_22392	TTACTCACAGATATTCACAGCA	NG_000943	KRTHBP3	KERATIN, HAIR, BASIC PSEUDOGENE 3	-1.10	0.18	-0.39	0.34	-0.71	0.05
Hs_12plexchip_4_9156	v2HS_84597	TTATACAGCCACTCAGAGGTCC	NM_006762	LAPTM5	lysosomal associated multispanning membrane protein 5 (LAPTM5), mRNA	-1.23	0.98	0.05	0.43	-1.28	0.14
Hs_12plexchip_6_6205	v2HS_233109	ATGATACCAGCAGTTCTCGGGC	NM_031206	LAS1L	LAS1-like (S. cerevisiae) (LAS1L), mRNA	-2.35	0.67	-1.14	1.20	-1.22	0.22
Hs0P00007022	v2HS_99204	TTTCCCTTTAACGCACTTTCCG	NM_031206	LAS1L	LAS1-like (S. cerevisiae) (LAS1L), mRNA	-1.87	0.47	-1.01	0.33	-0.86	0.07
Hs_12plexchip_5_4850	v2HS_74382	TTAGGAGTACACTTGGGAGGGC	NM_178438	LCE5A	late cornified envelope 5A (LCE5A), mRNA	-1.19	0.90	0.44	0.69	-1.62	0.07
Hs_12plexchip_4_1983	v2HS_221457	TTGAGAAATAAGCTCCCATGCT	NG_001155	LDHBP	LACTATE DEHYDROGENASE B PSEUDOGENE	-1.44	0.24	-0.51	0.60	-0.94	0.10
Hs_12plexchip_3_9093	v2HS_138318	ATTGCTCATCACATACTTACCT	NM_032287	LDOC1L	leucine zipper, down-regulated in cancer 1-like (LDOC1L), mRNA	-1.49	0.80	-0.55	0.41	-0.94	0.17
Hs_12plexchip_5_9042	v2HS_118360	AATTTAAAGCGTACATCTGCCT	NM_052971	LEAP2	liver expressed antimicrobial peptide 2 (LEAP2), mRNA	-0.90	0.34	0.37	0.79	-1.27	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_10487	v2HS_237144	TATATTAGCCCATGGCCCTGCC	NM_002302	LECT2	leukocyte cell-derived chemotaxin 2 (LECT2), mRNA	-1.12	0.14	-0.42	0.35	-0.71	0.06
Hs0P00007707	v2HS_135851	TTCTCTTGCCTCTCTTTCTCCT	NM_024316	LENG1	leukocyte receptor cluster (LRC) member 1 (LENG1), mRNA	-1.92	0.70	-0.96	0.85	-0.95	0.21
Hs_12plexchip_4_509	v2HS_202898	ATTCTTATGCACCTGGACTCGC	NM_013975	LIG3	ligase III, DNA, ATP-dependent (LIG3), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA	-1.11	0.49	-0.21	0.40	-0.89	0.07
Hs_12plexchip_6_9628	v2HS_245111	TTGATACACCTCTCGAATAGCT	NM_004664	LIN7A	lin-7 homolog A (C. elegans) (LIN7A), mRNA	-2.32	1.95	-0.53	0.27	-1.79	0.25
Hs_12plexchip_2_5212	v2HS_175213	TATTCGGGATATATAGATTGGA	NM_018362	LIN7C	lin-7 homolog C (C. elegans) (LIN7C), mRNA	-0.71	0.74	0.55	0.48	-1.26	0.08
Hs_12plexchip_5_1080	v2HS_247651	TAAACAGAAGAGATTTGCTCCA	NM_006033	LIPG	lipase, endothelial (LIPG), mRNA	-0.71	0.25	0.34	0.21	-1.06	0.01
Hs_12plexchip_6_5849	v2HS_81001	TTATTGAGTGACATGGAGAGGT	NM_021819	LMAN1L	lectin, mannose-binding, 1 like (LMAN1L), mRNA	-1.84	0.04	-1.06	0.81	-0.79	0.24
Hs_12plexchip_2_10956	v2HS_30926	TAAAGTTATGAAACCCTCAGCT	NM_001001395	LMO3	LIM domain only 3 (rhombotin-like 2) (LMO3), transcript variant 2, mRNA	-0.91	0.25	-0.19	0.46	-0.71	0.10
Hs_12plexchip_5_575	v2HS_51161	TTATGTGATGGAATTATACCCG	NR_003590	LOC100101117	testis-specific transcript, Y-linked 2-like (LOC100101117) on chromosome Y	-1.78	1.13	0.59	1.44	-2.37	0.09
Hs0P00012482	v2HS_51166	ATATAGACAGAGATGGCATGCT	NR_003590	LOC100101117	testis-specific transcript, Y-linked 2-like (LOC100101117) on chromosome Y	-0.80	0.35	0.04	0.32	-0.83	0.04
Hs_12plexchip_4_10838	v2HS_217710	TTTCTGTTTCATCTGCTCTGGG	NM_001101321	LOC120126	hypothetical protein (LOC120126), mRNA	-2.28	0.57	-1.28	0.79	-0.99	0.16
Hs_12plexchip_5_2301	v2HS_209586	TTAGCATATTCTGCAGCTACTT	XR_016217	LOC120318	PREDICTED:similar to 40S ribosomal protein S6 (LOC120318), mRNA	-1.15	0.37	0.25	0.28	-1.40	0.01
Hs_12plexchip_5_3126	v2HS_214370	CTTTCTTACAACACACTGGTGG	XR_016217	LOC120318	PREDICTED:similar to 40S ribosomal protein S6 (LOC120318), mRNA	-1.02	1.64	0.78	1.34	-1.80	0.22
Hs_12plexchip_6_6390	v2HS_159427	AATTGTGATCAAAGCTGTACCA	XR_016411	LOC121456	PREDICTED:similar to solute carrier family 9, member 7 (LOC121456), mRNA	-1.35	1.00	-0.02	0.41	-1.32	0.14
Hs_12plexchip_5_4991	v2HS_259415	TTGTATTTGCAATTAGCTGCCT	XR_016263	LOC121906	PREDICTED:similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) (LOC121906), mRNA	-1.29	0.45	0.01	0.46	-1.30	0.02
Hs_12plexchip_6_5637	v2HS_191039	TTGCCATGGATAAGTAATTGGT	XR_017783	LOC121981	PREDICTED:similar to peptidyl-Pro cis trans isomerase (LOC121981), misc RNA	-0.74	0.39	0.00	0.43	-0.74	0.09
Hs_12plexchip_5_8984	v2HS_263490	TTCATCTGTAGGGTGTAACGGG	XM_928661	LOC125242	PREDICTED:similar to Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-18) (K18) (LOC125242), mRNA	-0.96	0.38	-0.07	0.30	-0.89	0.04
Hs_12plexchip_6_6734	v2HS_161686	TTATCAAGGGTCTATATTTCCA	BC015457	LOC127841	HYPOTHETICAL PROTEIN LOC127841	-1.06	0.82	-0.29	0.58	-0.77	0.26
Hs0P00001573	v2HS_59672	TTCTTTAATAGGAACATCTGGT	XM_060943	LOC128322	PREDICTED:similar to Nuclear transport factor 2 (NTF-2) (LOC128322), mRNA	-1.41	0.11	-0.71	0.40	-0.70	0.08
Hs_12plexchip_3_11184	v2HS_237854	ATTCAGTGGCCGGAGCAGTGGG	XR_019305	LOC129841	PREDICTED:similar to laminin receptor 1 (ribosomal protein SA) (LOC129841), mRNA	-1.26	0.45	-0.39	0.57	-0.87	0.11
Hs_12plexchip_6_7185	v2HS_191934	ATTGTAATTAGGAGCCAGTCGA	XM_941747	LOC130773	PREDICTED:similar to 60S ribosomal protein L23a (LOC130773), mRNA	-1.81	0.29	-0.68	0.40	-1.13	0.02
Hs_12plexchip_5_202	v2HS_41539	ATCTGTCATCACCTTAACACTC	NR_003550	LOC132430	similar to poly(A) binding protein, cytoplasmic 4 (inducible form) (LOC132430) on chromosome 4	-1.30	0.48	-0.26	0.92	-1.04	0.18
Hs_12plexchip_4_6853	v2HS_54846	TTCTCCACTAAGATGGTTTGGG	AK023718	LOC145474	HYPOTHETICAL PROTEIN LOC145474	-1.03	0.19	-0.21	0.91	-0.82	0.25
Hs_12plexchip_5_3793	v2HS_226918	ATGCAGCATGACAAATCCAGGC	XM_936571	LOC146517	PREDICTED:hypothetical protein LOC146517 (LOC146517), mRNA	-0.73	0.37	0.24	1.23	-0.97	0.30
Hs_12plexchip_6_3784	v2HS_181312	ATAGATGGTTTCTGAGCATCGA	AK125037	LOC147791	HYPOTHETICAL PROTEIN LOC147791	-1.28	0.80	-0.46	0.51	-0.83	0.22
Hs_12plexchip_4_3309	v2HS_181356	TTGAACTCAAATAAAGCAGGGC	BX647231	LOC148145	HYPOTHETICAL PROTEIN LOC148145	-1.29	0.16	-0.18	0.53	-1.10	0.06
Hs_12plexchip_5_9366	v2HS_101498	TTTAAGGCATGGTTTCAGAGGA	AK055155	LOC149157	HYPOTHETICAL PROTEIN LOC149157	-1.12	0.78	-0.42	0.11	-0.71	0.25
Hs_12plexchip_4_5768	v2HS_26291	GAACATAGTGACAGTCAGTGCA	BC040263	LOC150297	HYPOTHETICAL PROTEIN LOC150297	-1.63	0.49	-0.15	0.60	-1.48	0.03
Hs_12plexchip_5_1522	v2HS_68105	TTAGGAGACGAGTTTGTGGGTC	BC064972	LOC158435	HYPOTHETICAL PROTEIN BC008050	-0.79	0.32	0.50	0.06	-1.29	0.02
Hs_12plexchip_5_9047	v2HS_120186	ATTCCTGCTATAGATCGGTCCT	NM_001014830	LOC196913	hypothetical protein LOC196913 (LOC196913), mRNA	-1.34	0.61	0.38	0.91	-1.72	0.06
Hs_12plexchip_6_3034	v2HS_277821	ATGCATCACTATCGTCAAGGGC	AK023628	LOC199725	HYPOTHETICAL PROTEIN LOC199725	-1.12	0.79	0.15	0.93	-1.27	0.15
Hs_12plexchip_5_8944	v2HS_120340	ATAATGGTCTACCTAGTTTGCT	NM_001008393	LOC201725	hypothetical protein LOC201725 (LOC201725), mRNA	-0.91	0.58	0.45	1.32	-1.36	0.21
Hs_12plexchip_3_11259	v2HS_141037	TAAGACTGCTCATGTGTCAGGC	AK055023	LOC219690	HYPOTHETICAL PROTEIN LOC219690	-1.46	1.20	-0.40	0.07	-1.06	0.27

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_10147	v2HS_141322	TACGCAAACGACATAAATGCCC	XM_001130636	LOC221091	PREDICTED:similar to hypothetical protein (LOC221091), mRNA	-1.60	0.41	-0.75	0.76	-0.85	0.18
Hs_12plexchip_5_11871	v2HS_141208	ATGCCATCTAGGAATATTCCGA	BC033371	LOC221946	HYPOTHETICAL PROTEIN LOC221946	-2.10	0.22	-1.07	0.85	-1.03	0.16
Hs_12plexchip_5_4716	v2HS_258133	CTGATCTCTGATAATATGGCGT	XM_172860	LOC255649	PREDICTED:similar to oocyte secreted protein 1 (LOC255649), mRNA	-1.71	0.82	0.67	2.21	-2.38	0.20
Hs_12plexchip_4_1689	v2HS_213536	ATTCTGATGAATTGGCTGGGCT	BC039539	LOC255654	HYPOTHETICAL PROTEIN LOC255654	-1.25	0.75	0.89	0.17	-2.14	0.03
Hs_12plexchip_2_4978	v2HS_168749	TATCTAGATGCCTCTGCCTGCT	NR_001286	LOC260339	processed pseudogene mtTFA 3 (LOC260339) on chromosome 6	-1.29	0.49	-0.34	1.08	-0.95	0.26
Hs_12plexchip_5_3914	v2HS_254656	TTCTAGCAAGAGAAGCCATCTT	XM_208043	LOC283116	PREDICTED:similar to Tripartite motif protein 49 (RING finger protein 18) (Testis-specific ring-finger protein) (LOC283116), mRNA	-0.75	0.67	0.81	1.07	-1.56	0.11
Hs_12plexchip_5_778	v2HS_245259	TTATGGCACATTTCGTTCAGCT	XM_208043	LOC283116	PREDICTED:similar to Tripartite motif protein 49 (RING finger protein 18) (Testis-specific ring-finger protein) (LOC283116), mRNA	-3.63	0.44	0.06	3.54	-3.69	0.21
Hs_12plexchip_4_2518	v2HS_182453	TTTCTCTTTCAGATTGGTTCCT	XM_378312	LOC283143	PREDICTED:hypothetical protein LOC283143 (LOC283143), mRNA	-0.85	0.61	0.65	0.20	-1.50	0.04
Hs_12plexchip_6_11076	v2HS_182508	TTTCTCTTTCTCTTCACATCCA	AK091446	LOC283194	HYPOTHETICAL PROTEIN LOC283194	-1.27	0.22	-0.25	0.24	-1.02	0.01
Hs_12plexchip_3_8982	v2HS_131660	TACAAATAGCACAGGAGGACCC	XM_497352	LOC283412	PREDICTED:similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP) (LOC283412), mRNA	-1.66	0.17	-0.28	0.77	-1.39	0.08
Hs_12plexchip_5_9355	v2HS_100281	AACGAAAGTCCATGAATGTCCA	NM_178514	LOC283487	HYPOTHETICAL PROTEIN LOC283487	-2.17	0.79	-1.26	0.42	-0.91	0.18
Hs0P00007920	v2HS_142836	TTACCCTGTCATTCTGTCTCCC	AK092322	LOC283575	HYPOTHETICAL PROTEIN LOC283575	-1.80	0.69	-0.55	0.65	-1.25	0.08
Hs_12plexchip_6_11763	v2HS_163979	ATGCTGTAATAGTTGCTGAGCT	AK097486	LOC283738	HYPOTHETICAL PROTEIN LOC283738	-1.20	0.53	0.59	0.40	-1.79	0.01
Hs0P00008258	v2HS_142129	ATGATCCTCTCCATGCAGACCA	XR_017053	LOC284226	PREDICTED:similar to kinesin family member 1C (LOC284226), mRNA	-2.37	0.50	-1.32	0.47	-1.05	0.06
Hs_12plexchip_5_10591	v2HS_103411	ATAAGTTGTGGGTTCATCTGGG	AK097672	LOC284344	HYPOTHETICAL PROTEIN LOC284344	-1.53	0.49	-0.10	0.44	-1.43	0.02
Hs_12plexchip_5_9148	v2HS_103423	ATCAGCTCTCCAGAGAACAGGC	NR_002938	LOC284379	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene (LOC284379) on chromosome 19	-1.13	0.23	0.00	0.22	-1.14	0.00
Hs_12plexchip_6_2724	v2HS_182880	TTTAATCGCGAGACAATACGGG	AK094324	LOC284408	HYPOTHETICAL PROTEIN LOC284408	-1.27	0.83	0.25	0.44	-1.52	0.07
Hs_12plexchip_6_3557	v2HS_223527	TTATGCAATCCTTCGTGTACCT	BC036876	LOC284898	HYPOTHETICAL PROTEIN LOC284898	-0.79	0.66	0.24	0.79	-1.03	0.16
Hs_12plexchip_2_9250	v2HS_21776	TTAAGGCAACAAATAGTGTCGT	XM_373030	LOC285556	PREDICTED:hypothetical protein LOC285556 (LOC285556), mRNA	-1.08	0.60	0.21	0.60	-1.30	0.06
Hs_12plexchip_6_12232	v2HS_194538	ATTTGAGACAATGTCATGCCCT	AK091672	LOC286161	HYPOTHETICAL PROTEIN LOC286161	-1.08	0.47	-0.35	0.81	-0.73	0.26
Hs_12plexchip_6_11682	v2HS_190151	AAGAGATTGAGCAATCAAAGCG	XR_018534	LOC286348	PREDICTED:hypothetical LOC286348 (LOC286348), mRNA	-4.20	1.18	-0.93	2.40	-3.27	0.13
Hs_12plexchip_5_3258	v2HS_254721	TTCAGGTCTATATTCAATGGCT	XR_017027	LOC286495	PREDICTED:similar to Tetratricopeptide repeat protein 3 (TPR repeat protein 3) (TPR repeat protein D) (LOC286495), mRNA	-0.96	0.55	0.18	0.69	-1.14	0.09
Hs_12plexchip_2_336	v2HS_102466	CTGCAGTGGTAGGTTCTCTGGG	XM_497238	LOC338586	PREDICTED:similar to hydroxysteroid dehydrogenase like 2 (LOC338586), mRNA	-1.77	0.51	-1.00	0.82	-0.76	0.26
Hs_12plexchip_4_5868	v2HS_25313	AATGGGAAGGAGGAAACAGCGT	BC043002	LOC339298	HYPOTHETICAL PROTEIN LOC339298	-1.23	0.50	-0.40	0.34	-0.83	0.08
Hs_12plexchip_4_1442	v2HS_213268	ATGGTGAATGATCTTAGCGGTG	XM_291007	LOC339766	PREDICTED:hypothetical protein LOC339766 (LOC339766), mRNA	-1.10	0.51	-0.02	0.10	-1.08	0.06
Hs0P00004455	v2HS_240580	TAGGCTTTGATGCTCATGCGGC	XM_290345	LOC339799	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA	-2.45	0.86	-1.30	0.19	-1.15	0.14
Hs_12plexchip_6_3131	v2HS_222390	TATTACTCTCATATCCTCAGCA	BC042977	LOC340094	HYPOTHETICAL PROTEIN LOC340094	-0.71	0.22	0.03	0.82	-0.74	0.26
Hs_12plexchip_2_5841	v2HS_185922	TTAGAACAGGTCACCAGTTCCA	BC042751	LOC340239	HYPOTHETICAL PROTEIN LOC340239	-0.91	0.16	0.04	0.77	-0.95	0.16
Hs_12plexchip_4_3340	v2HS_219782	TTAGTATGAGCCTGGTGTCCCT	AK074459	LOC340335	HYPOTHETICAL PROTEIN LOC340335	-1.16	0.53	0.41	1.13	-1.57	0.12
Hs_12plexchip_3_5583	v2HS_227339	TACTCTCTTGGTATCAGGCCCA	XR_017303	LOC341056	PREDICTED:similar to Ubiquitin-like 1-activating enzyme E1A (SUMO-1-activating enzyme subunit 1) (LOC341056), mRNA	-1.38	0.65	-0.44	0.69	-0.94	0.16
Hs_12plexchip_2_3848	v2HS_73359	ATTGCAAATGGAAGCACGTGGT	XR_017487	LOC341689	PREDICTED:similar to Cutaneous T-cell lymphoma-associated antigen 5 (cTAGE-5 protein) (cTAGE family member 5) (Meningioma-expressed antigen 6/11) (MEA6/MEA11) (LOC341689), mRNA	-1.11	0.43	-0.38	0.41	-0.72	0.10
Hs_12plexchip_5_8133	v2HS_263836	ATAGCAGTACTCAGCCTACGTT	XM_936951	LOC342293	PREDICTED:similar to ATP-binding cassette transporter sub-family A member 15 (LOC342293), mRNA	-0.70	0.64	0.21	0.74	-0.91	0.18

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_11223	v2HS_194223	TTCTTGATAAATTTGAGGGCCT	XM_294581	LOC347292	PREDICTED:similar to ribosomal protein L36 (LOC347292), mRNA	-1.84	1.47	-0.55	0.64	-1.29	0.27
Hs_12plexchip_6_11679	v2HS_162290	TTTGGCAAGTCTTTGCATGGCC	NM_001010895	LOC375748	RAD26L hypothetical protein (LOC375748), mRNA	-1.89	1.48	-0.45	0.35	-1.43	0.23
Hs0P00007277	v2HS_103048	TTTGCAGGGCACCTACTCAGGA	BC040665	LOC387790	HYPOTHETICAL LOC387790	-0.85	0.41	-0.13	0.36	-0.72	0.09
Hs_12plexchip_5_11429	v2HS_271522	ATGCTGCTTAAGAGCCTATGCA	XM_370697	LOC387867	PREDICTED:similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma laminin-binding protein) (NEM/1CHD4) (Multidrug resistance-associated protein MGr1-Ag) (LOC387867), mRNA	-2.64	0.59	-1.73	0.24	-0.91	0.10
Hs_12plexchip_6_6813	v2HS_285588	TTACCACAACAATATGTACCCA	NM_207376	LOC387882	HYPOTHETICAL PROTEIN	-1.58	0.56	0.38	0.73	-1.97	0.02
Hs0P00004001	v2HS_41456	TTTCTTGGGCTCCTTAGAAGCT	XR_018003	LOC388242	PREDICTED:LOC112869 pseudogene (LOC388242), misc RNA	-0.86	0.59	0.50	0.31	-1.36	0.04
Hs_12plexchip_3_10622	v2HS_145157	ATCAAGGTTATCTGTCTCAGCC	XM_371825	LOC389396	PREDICTED:similar to BXMAS2-10 protein (LOC389396), mRNA	-1.99	0.82	-0.93	0.66	-1.06	0.16
Hs_12plexchip_3_11361	v2HS_237760	TAAGTGGTAATGCTTCATACCA	NM_001089587	LOC389435	hCG21078 (LOC389435), mRNA	-1.44	0.08	-0.34	0.25	-1.10	0.01
Hs_12plexchip_4_6577	v2HS_53836	TTTCCTGAGGATGCTGTGGGCC	XM_372343	LOC390031	PREDICTED:similar to Ssu72 RNA polymerase II CTD phosphatase homolog (LOC390031), mRNA	-0.77	1.00	0.59	0.94	-1.35	0.16
Hs_12plexchip_5_1502	v2HS_66351	TTTGACAATGTCACTCTGTGGT	XR_019377	LOC391081	PREDICTED:similar to 3 beta-hydroxysteroid dehydrogenase/delta 5--_4-isomerase type I (3Beta-HSD I) (Trophoblast antigen FDO161G) (LOC391081), mRNA	-1.78	0.35	-0.38	0.95	-1.40	0.11
Hs_12plexchip_6_7316	v2HS_244097	TTCTGGTAAGTGGAGGTGCCAA	XR_017118	LOC391106	PREDICTED:similar to Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM) (LOC391106), mRNA	-1.12	0.72	-0.35	0.35	-0.77	0.20
Hs_12plexchip_5_10900	v2HS_274679	TACATTAAGCAGAGTAATTCCA	XR_018908	LOC391135	PREDICTED:similar to ribosomal protein L4 (LOC391135), mRNA	-3.85	0.94	-1.92	1.60	-1.93	0.16
Hs0P00001342	v2HS_70326	TTGCTTCAAGTGTTTGATGGCT	XR_017648	LOC391592	PREDICTED:similar to basic leucine zipper and W2 domains 1 (LOC391592), mRNA	-0.98	0.25	0.39	0.09	-1.37	0.01
Hs_12plexchip_4_6431	v2HS_64664	ATCAGCAAACACAGGTGCAGTG	XR_019056	LOC391640	PREDICTED:similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) (HDP) (LOC391640), mRNA	-1.04	1.40	0.51	1.72	-1.55	0.30
Hs_12plexchip_6_10802	v2HS_52910	GTAATCTTCCTGAATGGTGCCT	XM_373042	LOC391722	PREDICTED:similar to myosin regulatory light chain-like (LOC391722), mRNA	-1.54	1.32	-0.23	0.88	-1.31	0.24
Hs_12plexchip_4_8574	v2HS_21735	ATACGATGTACAGCAAAGCGAC	XR_016978	LOC391777	PREDICTED:similar to 40S ribosomal protein S4, X isoform (LOC391777), mRNA	-2.95	0.75	-1.48	1.11	-1.47	0.14
Hs0P00000848	v2HS_61787	TTTCCTTCTCAGACCGTTTCTC	XR_016640	LOC391798	PREDICTED:similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1) (LOC391798), mRNA	-0.92	0.55	-0.06	0.30	-0.86	0.10
Hs_12plexchip_3_12388	v2HS_23953	AACTTCTTGCAGTTGTTGCGGC	XR_019520	LOC392424	PREDICTED:similar to ribosomal protein S5 (LOC392424), mRNA	-2.30	0.10	-1.38	0.10	-0.92	0.00
Hs_12plexchip_6_12330	v2HS_124337	TTGTATCTATGTTTGAAGTGCC	XR_016360	LOC392452	PREDICTED:hypothetical LOC392452 (LOC392452), mRNA	-0.82	0.43	0.01	0.25	-0.83	0.06
Hs_12plexchip_2_4525	v2HS_182180	TTATCTGGTGAGAATCTATGGT	AK097673	LOC399706	HYPOTHETICAL LOC399706	-1.04	0.57	-0.17	0.32	-0.86	0.10
Hs_12plexchip_6_1327	v2HS_95865	ATTGGAAAGTACTTTAGCTCGA	XR_019557	LOC400061	PREDICTED:similar to CDK105 protein (LOC400061), mRNA	-3.56	0.95	-0.92	2.71	-2.64	0.23
Hs_12plexchip_6_1934	v2HS_95868	TTCATTGCAGACATGTATGGCT	XR_019557	LOC400061	PREDICTED:similar to CDK105 protein (LOC400061), mRNA	-1.79	0.95	-0.92	0.70	-0.87	0.27
Hs_12plexchip_6_11984	v2HS_192962	TTTATCTGGCAATTCCAAGGCT	XR_018253	LOC401197	PREDICTED:similar to ribosomal protein L7-like 1 (LOC401197), mRNA	-2.15	0.28	-0.45	0.16	-1.71	0.00
Hs0P00004694	v2HS_121075	TTATCACATCAAGGTGCGCGCC	XR_017915	LOC401242	PREDICTED:hypothetical gene supported by AK055503 (LOC401242), misc RNA	-1.40	0.69	-0.46	1.07	-0.94	0.28

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_582	v2HS_63127	TTTACACAGGATATGGGCTGTT	XR_017359	LOC401825	PREDICTED:similar to MKI67 FHA domain-interacting nucleolar phosphoprotein (Nucleolar protein interacting with the FHA domain of pKI-67) (hNIFK) (Nucleolar phosphoprotein Nopp34) (LOC401825), mRNA	-2.14	0.32	-0.83	1.62	-1.32	0.29
Hs_12plexchip_6_11164	v2HS_122980	TACTTCTCACAGTCCACCTGGA	XR_019598	LOC401864	PREDICTED:similar to Chloride intracellular channel protein 1 (Nuclear chloride ion channel 27) (NCC27) (Chloride channel ABP) (Regulatory nuclear chloride ion channel protein) (hRNCC) (LOC401864), mRNA	-0.97	0.69	0.16	1.35	-1.13	0.29
Hs_12plexchip_3_11638	v2HS_222868	TTGGCATAAGACTTAATGACCT	XR_019345	LOC402142	PREDICTED:similar to proteasome (prosome, macropain) 26S subunit, ATPase 2 (LOC402142), mRNA	-1.63	1.30	-0.53	0.46	-1.11	0.28
Hs_12plexchip_3_1643	v2HS_66260	TTCTGCAAGGTTCTTGACCTCT	XR_017047	LOC402229	PREDICTED:similar to splicing factor 4 (LOC402229), mRNA	-0.87	0.29	0.74	1.29	-1.61	0.16
Hs_12plexchip_6_390	v2HS_72079	TAAGGAAATATTCTGATGCCCA	NM_001089591	LOC440567	hCG25371 (LOC440567), mRNA	-1.22	1.53	0.43	1.87	-1.65	0.30
Hs_12plexchip_6_8626	v2HS_93802	TAGGACATGTCCAGCAGCTGGT	XM_496442	LOC440733	PREDICTED:similar to 40S ribosomal protein S15 (RIG protein) (LOC440733), mRNA	-1.91	1.37	-0.61	0.15	-1.30	0.24
Hs_12plexchip_2_4388	v2HS_185686	TAGCAGATCACCTCGAAGCGGC	XM_498961	LOC441005	PREDICTED:hypothetical LOC441005 (LOC441005), mRNA	-1.21	1.30	-0.11	0.46	-1.10	0.28
Hs_12plexchip_6_12168	v2HS_165316	ATCAACTTTCGTGGAATCTGGG	XM_496697	LOC441018	PREDICTED:similar to UDP-glucuronosyltransferase 2B7 precursor (UDPGT) (3,4-catechol estrogen specific) (UDPGTh-2) (LOC441018), mRNA	-1.23	0.34	0.26	0.22	-1.49	0.01
Hs_12plexchip_2_9741	v2HS_17568	TACACTTCCAACTTGAACTGGT	XR_016245	LOC441066	PREDICTED:hypothetical LOC441066 (LOC441066), mRNA	-1.22	0.89	-0.20	0.77	-1.02	0.21
Hs_12plexchip_2_10710	v2HS_20689	TTTAATACCAGGCCATTGCCCT	BC039003	LOC441086	HYPOTHETICAL GENE SUPPORTED BY BC039003	-1.17	0.19	-0.18	0.84	-1.00	0.17
Hs0P00007564	v2HS_105466	ATCTGGAGGTGGAATGATGGCC	XM_499019	LOC441119	PREDICTED:hypothetical LOC441119 (LOC441119), mRNA	-1.31	0.45	-0.39	0.31	-0.92	0.05
Hs0P00011576	v2HS_188312	TTAATAACTGTGAGAACATGGG	NR_003536	LOC441246	hCG1983332 (LOC441246) on chromosome 7	-1.95	0.10	-0.75	0.66	-1.20	0.08
Hs_12plexchip_6_11150	v2HS_192295	TTCAGAAATGTCCCTGATTGCT	XM_496991	LOC441377	PREDICTED:similar to 40S ribosomal protein S26 (LOC441377), mRNA	-0.81	0.56	0.35	1.02	-1.17	0.18
Hs_12plexchip_5_422	v2HS_35267	ATTGTAGTGCTCTTCCTGGCCC	XR_016738	LOC442114	PREDICTED:similar to keratin 19 (LOC442114), mRNA	-2.78	0.90	-1.43	1.31	-1.34	0.22
Hs_12plexchip_3_11451	v2HS_131616	TATATGCATACCCTTGATGGCC	XR_016559	LOC442232	PREDICTED:similar to 60S ribosomal protein L17 (L23) (LOC442232), mRNA	-1.13	1.12	-0.17	0.53	-0.96	0.28
Hs_12plexchip_5_1110	v2HS_57651	TAAGGTGAATACAAAGATTGGA	XR_016559	LOC442232	PREDICTED:similar to 60S ribosomal protein L17 (L23) (LOC442232), mRNA	-0.76	0.21	0.00	0.15	-0.76	0.01
Hs_12plexchip_5_10471	v2HS_267422	TTTGTACTAGCTTCATGTTGGT	XR_016496	LOC442240	PREDICTED:similar to zinc finger protein 259 (LOC442240), mRNA	-1.32	0.13	0.10	1.09	-1.42	0.15
Hs_12plexchip_3_12450	v2HS_242842	ATAGTAGTACACGGAGATGCGG	NR_003598	LOC442308	similar to tubulin, beta 5 (LOC442308) on chromosome 7	-0.79	0.33	0.00	0.80	-0.79	0.22
Hs_12plexchip_4_2527	v2HS_182104	TTTGATAAAGTGTCTGTGTCCT	XR_018022	LOC442332	PREDICTED:hypothetical LOC442332 (LOC442332), mRNA	-2.42	0.48	-1.44	0.70	-0.98	0.13
Hs_12plexchip_6_9650	v2HS_263491	TATTGCCTGAGAGATGATGGCC	NM_016490	LOC51252	hypothetical protein LOC51252 (LOC51252), mRNA	-0.78	1.01	0.09	0.25	-0.87	0.27
Hs_12plexchip_2_7890	v2HS_166302	TTAGGGAACCATATGGGAGCCC	XR_016138	LOC642319	PREDICTED:similar to transgelin 2 (LOC642319), mRNA	-0.94	0.56	0.05	0.61	-0.99	0.11
Hs_12plexchip_6_6839	v2HS_219398	TAATGCTACCATGGTGTTGGCT	XR_016431	LOC642397	PREDICTED:similar to WAS protein homology region 2 domain containing 1 (LOC642397), mRNA	-0.70	0.30	0.12	0.42	-0.82	0.06
Hs_12plexchip_4_130	v2HS_182227	TTATTAGTGGGAGTTCTGAGTC	XM_942991	LOC642934	PREDICTED:hypothetical LOC642934 (LOC642934), mRNA	-0.72	0.16	0.03	0.33	-0.75	0.04
Hs_12plexchip_6_7221	v2HS_251202	ATAGAATCCTCCTCAAGAGGGC	XR_016235	LOC642979	PREDICTED:similar to sorting nexin associated golgi protein 1 (LOC642979), mRNA	-0.87	0.88	0.19	0.44	-1.06	0.16
Hs_12plexchip_4_6761	v2HS_61543	TAGCAAGTAGATGGACAGGCCT	XR_016378	LOC643579	PREDICTED:hypothetical LOC643579 (LOC643579), mRNA	-0.80	1.06	0.41	0.84	-1.21	0.20

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_10604	v2HS_12094	ATATCCCACACTACTTTCTGGT	XM_938941	LOC643790	PREDICTED:similar to Nonhistone chromosomal protein HMG-14 (High-mobility group nucleosome-binding domain-containing protein 1) (LOC643790), mRNA	-1.98	0.75	-0.68	1.13	-1.30	0.18
Hs_12plexchip_5_11559	v2HS_144280	TAGTTGCTACAAGGACCATGGT	XM_927548	LOC644402	PREDICTED:hypothetical LOC644402 (LOC644402), mRNA	-1.05	0.19	0.44	0.28	-1.49	0.00
Hs_12plexchip_6_4787	v2HS_180581	ATTCTGTAAGTCTTTGCTACCA	XR_018194	LOC644415	PREDICTED:similar to prohibitin (LOC644415), mRNA	-1.47	1.46	0.16	0.27	-1.63	0.19
Hs_12plexchip_4_5837	v2HS_25353	CTTCACCTTGGCTTTATCTCCT	XM_927624	LOC644498	PREDICTED:similar to Nonhistone chromosomal protein HMG-17 (High-mobility group nucleosome-binding domain-containing protein 2) (LOC644498), mRNA	-2.66	0.34	-1.77	0.76	-0.89	0.17
Hs_12plexchip_3_6812	v2HS_229870	CTCATATGCAACATTTAGGGCC	XR_019446	LOC644616	PREDICTED:similar to interleukin enhancer binding factor 2 (LOC644616), mRNA	-0.82	0.79	1.90	1.41	-2.71	0.06
Hs_12plexchip_2_10359	v2HS_32694	ATTAATAAGTGCTGTCAGACCA	XM_927812	LOC644717	PREDICTED:similar to sarcoma antigen 1 (LOC644717), mRNA	-1.41	0.45	-0.34	0.13	-1.07	0.05
Hs_12plexchip_6_6067	v2HS_190051	ATGCATACAGTGAGCCGCAGCC	XM_928136	LOC645100	PREDICTED:similar to CG11699-PA (LOC645100), mRNA	-1.28	0.57	0.54	1.07	-1.82	0.08
Hs_12plexchip_5_11696	v2HS_134507	TATATCCACACTGGAAAGTGCA	XR_017268	LOC645175	PREDICTED:similar to Protein C2orf4 (C21orf19-like protein) (LOC645175), mRNA	-0.94	0.20	-0.18	0.20	-0.76	0.01
Hs_12plexchip_6_2617	v2HS_180920	TTGAGGTACCTGAGCAGGTGCT	XR_016939	LOC645382	PREDICTED:similar to PRAME family member 10 (LOC645382), mRNA	-1.09	1.14	0.24	0.21	-1.33	0.18
Hs_12plexchip_3_5357	v2HS_119370	TTGATCATCTCCAGGAGCCGCC	XR_016930	LOC645412	PREDICTED:similar to 40S ribosomal protein S16 (LOC645412), mRNA	-2.69	0.55	-1.24	0.49	-1.45	0.03
Hs_12plexchip_4_3476	v2HS_180644	TTTAATCCTCGAAAGAGTTCCT	XR_016872	LOC645430	PREDICTED:hypothetical LOC645430 (LOC645430), mRNA	-1.19	0.16	-0.33	0.61	-0.86	0.13
Hs_12plexchip_6_12616	v2HS_163195	TTGTGTATGTGGACGATGTCCA	XR_017007	LOC645614	PREDICTED:similar to sorting nexin associated golgi protein 1 (LOC645614), mRNA	-1.33	0.31	-0.52	0.57	-0.81	0.12
Hs_12plexchip_6_7300	v2HS_188155	ATCTCCTCATATCTCTTCTGGC	XR_017484	LOC645715	PREDICTED:similar to eukaryotic translation elongation factor 1 alpha 2 (LOC645715), mRNA	-0.89	0.53	0.19	0.71	-1.08	0.11
Hs_12plexchip_3_2510	v2HS_69667	GTAGTGGAGGAGATTACTTTGC	XR_016928	LOC645773	PREDICTED:similar to tubulin, alpha 1 (LOC645773), mRNA	-0.80	0.33	0.05	0.26	-0.85	0.03
Hs_12plexchip_3_2564	v2HS_69670	CATCAGCTTGAACTTGTGGTCC	XR_016928	LOC645773	PREDICTED:similar to tubulin, alpha 1 (LOC645773), mRNA	-1.58	0.65	-0.68	0.34	-0.90	0.12
Hs_12plexchip_6_12808	v2HS_193874	ATCTTGGACAAGTTTAGCTCCA	XR_016831	LOC645808	PREDICTED:similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60) (LOC645808), mRNA	-2.30	0.91	-0.22	1.24	-2.08	0.08
Hs_12plexchip_5_11513	v2HS_274830	TAGGGTGGACAATACTGAGGCC	XR_019608	LOC646048	PREDICTED:similar to cytoplasmic beta-actin (LOC646048), mRNA	-0.92	0.96	-0.13	0.31	-0.79	0.29
Hs_12plexchip_6_2510	v2HS_161718	TTTCGGGAGCTGCTTCAGTGCC	NM_001101401	LOC646643	similar to protein kinase Bsk146 (LOC646643), mRNA	-0.88	0.66	0.14	0.40	-1.03	0.09
Hs0P00011059	v2HS_192822	AACTCAGCTCCTTACAAGGGCT	XM_929703	LOC646753	PREDICTED:similar to 40S ribosomal protein S26 (LOC646753), mRNA	-1.28	0.03	-0.50	0.25	-0.78	0.03
Hs_12plexchip_6_2822	v2HS_184074	TTTCTTCACTCCTCTGTACGCC	XM_935722	LOC646762	PREDICTED:hypothetical protein LOC646762 (LOC646762), mRNA	-1.56	0.62	-0.12	0.31	-1.44	0.04
Hs_12plexchip_3_11479	v2HS_233964	AATTTCTTGGACATGGTTTCCT	XR_017618	LOC647039	PREDICTED:similar to Death domain-containing protein CRADD (Caspase and RIP adapter with death domain) (RIP-associated protein with a death domain) (LOC647039), mRNA	-1.08	0.46	0.41	0.48	-1.49	0.02
Hs_12plexchip_3_7313	v2HS_94974	TATCAATATCTTCTTCATGGCT	XR_017416	LOC647073	PREDICTED:similar to Signal recognition particle 72 kDa protein (SRP72) (LOC647073), mRNA	-0.96	0.66	-0.24	0.37	-0.73	0.19
Hs_12plexchip_4_2826	v2HS_181661	ATAGGAGAACCCTTTCCTAGCC	XM_001129735	LOC647123	PREDICTED:similar to Rieske iron-sulfur protein (LOC647123), mRNA	-2.14	0.42	-0.99	1.06	-1.14	0.19

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00012092	v2HS_189672	TTTCCACGCGATTTGGCTGGCG	XM_934407	LOC647131	PREDICTED:hypothetical LOC647131 (LOC647131), mRNA	-0.73	0.57	0.52	0.47	-1.26	0.04
Hs_12plexchip_2_6794	v2HS_165807	ATCGACTGTAGGGAGATGGGCC	XM_930163	LOC647145	PREDICTED:similar to Splicing factor, arginine/serine-rich, 46kD (LOC647145), mRNA	-0.71	0.45	0.40	0.58	-1.11	0.06
Hs_12plexchip_5_10137	v2HS_107164	AATTAACAGGTTCAGATCGGCA	XM_930163	LOC647145	PREDICTED:similar to Splicing factor, arginine/serine-rich, 46kD (LOC647145), mRNA	-0.92	0.26	0.36	0.32	-1.28	0.01
Hs_12plexchip_3_8689	v2HS_101886	AATTCTACCCAATCTCTAGCCA	XR_018477	LOC648987	PREDICTED:hypothetical LOC648987 (LOC648987), mRNA	-1.52	0.32	0.11	0.27	-1.64	0.00
Hs_12plexchip_3_5574	v2HS_224813	GTAGAGCTGTAATGAGTTTGGC	XR_018674	LOC649925	PREDICTED:hypothetical LOC649925 (LOC649925), mRNA	-0.77	0.26	0.87	0.68	-1.64	0.04
Hs_12plexchip_5_9695	v2HS_268515	AATTATTGTGGAACTGTGAGTG	XM_939249	LOC650167	PREDICTED:similar to zinc finger protein 617 (LOC650167), mRNA	-0.76	0.08	0.31	0.19	-1.07	0.00
Hs_12plexchip_5_7718	v2HS_121873	TTCATGGTGGACATTCTAAGGT	XM_940582	LOC651430	PREDICTED:hypothetical LOC651430 (LOC651430), mRNA	-1.44	0.34	-0.44	0.34	-1.00	0.02
Hs_12plexchip_2_425	v2HS_93650	ATAACAATGCTCTTTGGTGCCC	XM_942001	LOC652522	PREDICTED:similar to Werner syndrome protein (LOC652522), mRNA	-0.79	0.73	-0.03	0.37	-0.75	0.21
Hs_12plexchip_3_12580	v2HS_242292	TTAATCTTGAACCTTGGAGGCT	XR_019381	LOC652549	PREDICTED:similar to SNW domain-containing protein 1 (Nuclear protein SkiP) (Ski-interacting protein) (Nuclear receptor coactivator NCoA-62) (LOC652549), mRNA	-1.51	0.44	-0.11	0.35	-1.39	0.01
Hs_12plexchip_4_1504	v2HS_205865	TTATTGAAGAAACCAATCCTGG	XM_942509	LOC652826	PREDICTED:similar to 26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7) (LOC652826), mRNA	-1.94	0.18	-0.93	0.52	-1.01	0.06
Hs0P00000274	v2HS_67557	TTCTGGATTCATGTCAGGCCCG	AK096379	LOC653466	HYPOTHETICAL PROTEIN LOC401589	-1.30	0.61	-0.22	0.79	-1.09	0.14
Hs_12plexchip_6_5621	v2HS_69578	TTGAGTTCAGTCATTGCTGCCT	NM_001097610	LOC653486	similar to secretoglobin, family 1C, member 1 (LOC653486), mRNA	-0.90	0.33	0.18	0.69	-1.08	0.09
Hs_12plexchip_4_7297	v2HS_61213	GTTCTCTGAGATTGAGTGAGGG	NR_003528	LOC653501	zinc finger protein 658 pseudogene (LOC653501) on chromosome 9	-0.79	0.56	0.36	1.09	-1.15	0.20
Hs_12plexchip_5_5042	v2HS_258204	TTTACAGCATTTCCAATCGGCC	XM_927769	LOC653506	PREDICTED:similar to meteorin, glial cell differentiation regulator-like (LOC653506), mRNA	-0.92	0.30	-0.08	0.46	-0.84	0.07
Hs_12plexchip_5_11384	v2HS_142082	AATATGATGCTCATGATGCCCA	XM_001126126	LOC727910	PREDICTED:hypothetical protein LOC727910 (LOC727910), mRNA	-1.85	0.80	-0.61	1.07	-1.24	0.19
Hs0P00000340	v2HS_66915	TTCTGATCTCAGTTGAGCACTC	XM_001126453	LOC727915	PREDICTED:hypothetical protein LOC727915 (LOC727915), mRNA	-0.85	0.24	-0.07	0.76	-0.78	0.21
Hs_12plexchip_6_12462	v2HS_191564	AATTTCACAAAGCGAGTGAGGT	XR_015346	LOC728128	PREDICTED:similar to 60S ribosomal protein L7a (LOC728128), mRNA	-4.04	0.59	-1.40	2.49	-2.65	0.20
Hs0P00008004	v2HS_144610	TTCCTCAGAAACTTCGATTCGC	XM_001126653	LOC728135	PREDICTED:similar to Protein C21orf63 precursor (SUE21) (LOC728135), mRNA	-1.15	0.33	-0.40	0.36	-0.75	0.06
Hs_12plexchip_5_5284	v2HS_72858	ATCTTTCCACATGTCCTCTGTC	XM_001131465	LOC728434	PREDICTED:hypothetical protein LOC728434 (LOC728434), mRNA	-1.59	0.36	-0.65	0.91	-0.95	0.20
Hs_12plexchip_2_8266	v2HS_153489	ATAATCCAGGAGTATATAACCA	XR_015916	LOC729466	PREDICTED:hypothetical protein LOC729466 (LOC729466), mRNA	-1.27	1.17	-0.28	0.67	-0.99	0.29
Hs_12plexchip_5_1807	v2HS_253397	AACGACATAGAAGTTGTCTCCT	XM_001130823	LOC729623	PREDICTED:similar to cAMP-dependent protein kinase type I-beta regulatory subunit (LOC729623), mRNA	-1.06	0.79	0.30	1.13	-1.36	0.17
Hs_12plexchip_6_8207	v2HS_218098	TTGTGGTCTCAGAGCCTGCGGT	XM_001131329	LOC729792	PREDICTED:hypothetical protein LOC729792 (LOC729792), mRNA	-1.48	0.27	-0.44	1.07	-1.04	0.23
Hs_12plexchip_5_634	v2HS_41661	TAAGGACTCCGAAGAAACTGGT	XM_001131663	LOC729890	PREDICTED:hypothetical protein LOC729890 (LOC729890), mRNA	-1.64	0.48	0.06	0.65	-1.70	0.03
Hs0P00007175	v2HS_108059	TAGATTTGAGGTTAGATGGGCT	XM_001131998	LOC729995	PREDICTED:hypothetical protein LOC729995 (LOC729995), mRNA	-1.20	0.60	-0.40	0.68	-0.80	0.20
Hs_12plexchip_5_5556	v2HS_117690	TTTATTGCAGGTTCCAACCGGG	XM_001132025	LOC730000	PREDICTED:similar to testis-specific serine kinase 6 (LOC730000), mRNA	-1.35	0.42	-0.24	0.57	-1.10	0.06
Hs0P00002514	v2HS_61516	TTTGCTCCTGCCGCTGAGGCTT	XM_001132293	LOC730072	PREDICTED:hypothetical protein LOC730072 (LOC730072), mRNA	-1.44	0.31	-0.71	0.32	-0.73	0.05

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_5734	v2HS_191108	TATTAAACAATCCTTCCGTGGA	NR_003370	LOC730092	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene (LOC730092) on chromosome 16	-0.99	0.70	0.12	1.24	-1.11	0.27
Hs_12plexchip_2_1732	v2HS_81993	ATTGTTTAGCACGCAGACTGCC	XM_001133022	LOC730222	PREDICTED:similar to Tubulin alpha-2 chain (Alpha-tubulin 2) (LOC730222), mRNA	-1.17	0.68	-0.34	0.23	-0.83	0.16
Hs_12plexchip_5_3665	v2HS_254576	ATAATGAGTAACTTCAGAAGGC	XM_001124597	LOC730411	PREDICTED:similar to zinc finger and BTB domain containing 8 (LOC730411), mRNA	-1.10	0.24	1.08	0.08	-2.18	0.00
Hs_12plexchip_6_5649	v2HS_100710	TTGCATAATAATTCAGGAGCCT	XM_001128811	LOC731210	PREDICTED:similar to Protein MICAL-3 (LOC731210), mRNA	-1.21	0.11	0.16	1.02	-1.37	0.14
Hs_12plexchip_4_5390	v2HS_22009	ATGTATAGTCACATGAATGCCT	AK023635	LOC90246	HYPOTHETICAL PROTEIN LOC90246	-0.93	0.26	0.52	0.61	-1.44	0.04
Hs_12plexchip_4_3293	v2HS_179882	ATTAGGGTGTAGAATTGATGGT	AL080202	LOC92249	HYPOTHETICAL PROTEIN LOC92249	-0.76	0.21	0.61	0.35	-1.38	0.01
Hs_12plexchip_5_3279	v2HS_14425	TAACTACATAAACAGCAGAGGT	NM_024778	LONRF3	LON peptidase N-terminal domain and ring finger 3 (LONRF3), transcript variant 2, mRNA	-0.76	0.54	0.03	0.69	-0.80	0.19
Hs_12plexchip_6_8694	v2HS_238170	TTGCCTGTGCACTGGATCTCGT	NM_002318	LOXL2	lysyl oxidase-like 2 (LOXL2), mRNA	-1.49	0.23	-0.75	0.29	-0.74	0.03
Hs_12plexchip_5_9470	v2HS_267470	TAGTTGTTCCAGACGTACAGCT	NM_001008701	LPHN1	latrophilin 1 (LPHN1), transcript variant 1, mRNA	-0.88	0.63	0.11	0.75	-0.99	0.16
Hs_12plexchip_6_12384	v2HS_142522	TTATTTGAGGAGCTCATGAGCT	NM_201550	LRRC10	LEUCINE RICH REPEAT CONTAINING 10	-1.80	1.01	-0.15	0.49	-1.65	0.09
Hs_12plexchip_5_1241	v2HS_247143	TTATACAAAGAGTTGGTCCCGA	NM_005512	LRRC32	leucine rich repeat containing 32 (LRRC32), mRNA	-1.54	0.08	0.47	0.94	-2.01	0.06
Hs_12plexchip_4_10281	v2HS_18850	TGATACTTTCAATTTCAGTGGG	NM_144620	LRRC39	leucine rich repeat containing 39 (LRRC39), mRNA	-0.77	0.38	0.09	0.50	-0.86	0.08
Hs_12plexchip_4_1632	v2HS_214960	ATAACAAAGCTCATCCTAGCCA	NM_020873	LRRN1	leucine rich repeat neuronal 1 (LRRN1), mRNA	-1.61	0.95	-0.18	1.17	-1.43	0.18
Hs0P00007114	v2HS_96960	ATTCTTCTTAAAGTGGGAGGGC	NM_015564	LRRTM2	leucine rich repeat transmembrane neuronal 2 (LRRTM2), mRNA	-1.42	0.71	-0.38	0.18	-1.05	0.12
Hs_12plexchip_6_8446	v2HS_214377	CATAAATTCGCTCATCTAGGCT	NM_014463	LSM3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM3), mRNA	-0.89	0.70	-0.15	0.49	-0.74	0.22
Hs_12plexchip_3_420	v2HS_50487	TTTCCTTATCACTCTTCATCAC	NM_012322	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM5), mRNA	-1.92	0.85	-0.01	0.35	-1.92	0.04
Hs_12plexchip_4_8205	v2HS_134081	TTCATACAGCTTCTGCACGGCC	NM_001001438	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase) (LSS), transcript variant 2, mRNA	-1.23	0.77	-0.44	0.49	-0.79	0.22
Hs_12plexchip_3_7032	v2HS_229857	TTAGACGTATAAAGCCTTGGCT	NM_000428	LTBP2	latent transforming growth factor beta binding protein 2 (LTBP2), mRNA	-1.28	0.37	-0.26	1.04	-1.01	0.23
Hs_12plexchip_3_11090	v2HS_134105	ATCAGTTCCAGCAGAATGAGGC	NM_002344	LTK	leukocyte tyrosine kinase (LTK), transcript variant 1, mRNA	-0.97	0.48	-0.04	0.27	-0.93	0.06
Hs_12plexchip_6_6188	v2HS_158471	AATGGGAGCTAGGGAGAGACGA	NM_025261	LY6G6C	lymphocyte antigen 6 complex, locus G6C (LY6G6C), mRNA	-1.44	0.26	-0.62	0.41	-0.82	0.05
Hs_12plexchip_5_4694	v2HS_258799	TAATTGAAATTGGGTATTGCAT	NM_015364	LY96	lymphocyte antigen 96 (LY96), mRNA	-0.79	0.62	0.01	0.08	-0.80	0.15
Hs_12plexchip_6_1730	v2HS_202025	TTAATCCTCCGTACAGTCACGT	NM_001003787	LYK5	protein kinase LYK5 (LYK5), transcript variant 1, mRNA	-1.02	0.48	0.08	0.87	-1.10	0.15
Hs_12plexchip_5_4662	v2HS_260496	TTTCTATTTCTGATGGCGTGCT	NM_000081	LYST	lysosomal trafficking regulator (LYST), mRNA	-1.34	0.63	-0.51	0.38	-0.83	0.14
Hs_12plexchip_6_11442	v2HS_229912	TTAGTTCCATTTCTTTGTTCCT	NM_080676	MACROD2	MACRO domain containing 2 (MACROD2), transcript variant 1, mRNA	-0.82	0.12	0.07	0.90	-0.89	0.23
Hs_12plexchip_4_11539	v2HS_234422	ATATTTGAGATAACTACAACCA	NM_002358	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA	-3.18	0.42	-1.48	0.45	-1.69	0.01
Hs_12plexchip_2_4749	v2HS_177234	TTTCAATTCGTATTGTGGCCCA	NM_032717	MAG1	lung cancer metastasis-associated protein (MAG1), mRNA	-0.75	0.21	0.11	0.24	-0.86	0.01
Hs_12plexchip_4_11140	v2HS_201106	AAGAAATAGGAGTGGTTGTCGG	NM_138702	MAGEC3	melanoma antigen family C, 3 (MAGEC3), transcript variant 1, mRNA	-1.94	0.40	-1.02	0.88	-0.93	0.20
Hs_12plexchip_6_6416	v2HS_227605	ATCACCAAGAGGAGACTCAGCC	NM_001098800	MAGED4	melanoma antigen family D, 4 (MAGED4), mRNA	-1.53	0.30	-0.79	0.41	-0.73	0.07
Hs0P00002357	v2HS_59106	TTATTCTCTTCAGTTCCTCCAT	NM_002370	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila) (MAGOH), mRNA	-2.52	0.45	-1.45	0.18	-1.07	0.04
Hs_12plexchip_5_6928	v2HS_170531	ATTAGCTTTCTGGCCATGACCA	NM_002755	MAP2K1	mitogen-activated protein kinase kinase 1 (MAP2K1), mRNA	-0.96	0.51	0.42	0.50	-1.38	0.03
Hs_12plexchip_3_7278	v2HS_98043	TTCTAGGCTGACAATTAGTCCT	NM_021970	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA	-1.03	0.42	-0.08	0.12	-0.95	0.05
Hs_12plexchip_4_4739	v2HS_201713	ATCCCTGAAGAGTAACTGCGGC	NM_002757	MAP2K5	mitogen-activated protein kinase kinase 5 (MAP2K5), transcript variant B, mRNA	-1.11	0.82	-0.32	0.27	-0.79	0.23

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_3581	v2HS_100863	TTTCATGGAGATACGAAAGGCC	NM_005921	MAP3K1	mitogen-activated protein kinase kinase kinase 1 (MAP3K1), mRNA	-1.23	1.32	0.08	0.15	-1.31	0.23
Hs_12plexchip_2_92	v2HS_151563	TATCTCTCCCTCAATGTCTGGA	NM_030885	MAP4	microtubule-associated protein 4 (MAP4), transcript variant 3, mRNA	-1.28	0.57	-0.15	0.97	-1.12	0.18
Hs0P00000072	v2HS_71361	TGAAGTACTGATGTTCAGCGGG	NM_139033	MAPK7	MITOGEN-ACTIVATED PROTEIN KINASE 7	-0.78	0.23	0.63	0.71	-1.40	0.06
Hs_12plexchip_3_11702	v2HS_217930	TTCTTCTAGGGATTTCTGTGGT	NM_139049	MAPK8	mitogen-activated protein kinase 8 (MAPK8), transcript variant JNK1-a2, mRNA	-1.23	0.10	-0.25	0.45	-0.98	0.06
Hs0P00011475	v2HS_27291	TTTACTAATCAGAAAGGTCGGT	NM_003668	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5 (MAPKAPK5), transcript variant 1, mRNA	-1.48	0.46	-0.50	0.64	-0.98	0.11
Hs_12plexchip_3_11703	v2HS_173986	ATAATGGTTCATATGACTGCCA	NM_017824	MARCH5	membrane-associated ring finger (C3HC4) 5 (MARCH5), mRNA	-1.39	0.85	-0.13	0.75	-1.26	0.13
Hs_12plexchip_6_2004	v2HS_99593	AATTCAAACATTTCTGCTGGCT	NM_052858	MARVELD3	MARVEL domain containing 3 (MARVELD3), transcript variant 2, mRNA	-0.84	0.38	0.46	0.84	-1.29	0.10
Hs_12plexchip_5_6111	v2HS_177829	TTTGTGCTACAGACTAAATCCA	NM_032844	MASTL	microtubule associated serine/threonine kinase-like (MASTL), mRNA	-2.97	0.75	-0.17	2.18	-2.80	0.15
Hs_12plexchip_4_12292	v2HS_151587	TATAACCTTCAAAGCACTGGCA	NM_030583	MATN2	matrilin 2 (MATN2), transcript variant 2, mRNA	-1.50	0.68	-0.40	0.27	-1.10	0.09
Hs_12plexchip_5_1859	v2HS_253434	TTTAACCCTCGTGTGGCAGGCT	NR_002724	MBL1P1	mannose-binding lectin (protein A) 1, pseudogene 1 (MBL1P1) on chromosome 10	-0.97	0.37	-0.09	0.60	-0.87	0.11
Hs_12plexchip_2_3066	v2HS_84920	CAGAGTGATGACATGCTTGGCC	NM_006739	MCM5	minichromosome maintenance complex component 5 (MCM5), mRNA	-1.03	0.91	-0.06	0.68	-0.97	0.22
Hs_12plexchip_5_12577	v2HS_252067	ATTGATTTATTCAGTAACCGGA	NM_005915	MCM6	minichromosome maintenance complex component 6 (MCM6), mRNA	-1.87	0.72	-0.94	0.22	-0.92	0.15
Hs_12plexchip_3_2395	v2HS_69010	ATGAACTACCAGATGCAGGTTG	NM_024596	MCPH1	microcephalin 1 (MCPH1), mRNA	-1.43	0.56	-0.42	0.16	-1.01	0.08
Hs_12plexchip_4_1313	v2HS_211486	GCAATTTGAGCTTTAGCTCGGT	NM_005917	MDH1	malate dehydrogenase 1, NAD (soluble) (MDH1), mRNA	-1.38	0.62	0.28	1.45	-1.66	0.17
Hs_12plexchip_6_9531	v2HS_251349	TTAACCGGATTGGCAATGACGC	NM_005918	MDH2	malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA	-1.08	0.98	0.04	1.16	-1.12	0.27
Hs_12plexchip_6_2145	v2HS_100737	ATAAGGTGCTAGGTGATGGCGG	NM_015335	MED13L	mediator complex subunit 13-like (MED13L), mRNA	-1.90	0.88	-0.48	1.59	-1.42	0.27
Hs_12plexchip_3_2125	v2HS_68244	TTTAAATGGGTGCTACACTGGT	NM_004830	MED23	mediator complex subunit 23 (MED23), transcript variant 1, mRNA	-0.98	0.39	-0.13	0.50	-0.86	0.08
Hs_12plexchip_2_3191	v2HS_74476	AATTCACTGGCGGTAAAGTCCT	NM_022566	MESDC1	mesoderm development candidate 1 (MESDC1), mRNA	-1.26	0.44	-0.42	0.36	-0.84	0.06
Hs_12plexchip_6_903	v2HS_197525	ATTCCAAATCTCTTCACTTGCC	NM_006838	METAP2	methionyl aminopeptidase 2 (METAP2), mRNA	-2.36	0.32	-0.37	0.75	-1.98	0.03
Hs_12plexchip_4_6122	v2HS_20520	AACACATTTATGGCCCACAGTG	BC019880	MGC21881	HYPOTHETICAL PROTEIN LOC286286	-0.71	0.41	0.26	0.71	-0.97	0.13
Hs_12plexchip_3_4352	v2HS_36090	ATATCATAGGAGTTGTATCGCT	NM_144973	MGC24039	hypothetical protein MGC24039 (MGC24039), mRNA	-0.99	0.59	-0.20	0.56	-0.79	0.17
Hs_12plexchip_6_4740	v2HS_179347	ATTTAGTGTAATAGCCATTCCT	NM_173802	MGC50559	hypothetical protein MGC50559 (MGC50559), mRNA	-1.24	0.24	-0.46	0.80	-0.77	0.23
Hs_12plexchip_6_8840	v2HS_212220	TAGTAATCTCCCTGAACGCTGC	NM_006533	MIA	melanoma inhibitory activity (MIA), mRNA	-1.18	0.51	-0.40	0.87	-0.79	0.26
Hs_12plexchip_4_11095	v2HS_98414	AATGTTCTCCAGATCAATGCCT	NM_022765	MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1 (MICAL1), mRNA	-1.51	0.93	-0.75	0.04	-0.76	0.29
Hs_12plexchip_5_3248	v2HS_49368	TTCCTGTCATTGATTATATGCT	NM_001098624	MID1	midline 1 (Opitz/BBB syndrome) (MID1), transcript variant 4, mRNA	-2.07	0.41	-0.74	0.51	-1.33	0.03
Hs_12plexchip_2_7674	v2HS_151786	TTTCCCTTAGGAGTTCTCAGCT	NM_002417	MKI67	antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA	-0.73	0.29	0.20	0.58	-0.94	0.09
Hs_12plexchip_6_726	v2HS_151785	TTTCCTTAGGAGTTTGTAGCCG	NM_002417	MKI67	antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA	-0.98	0.13	0.64	0.59	-1.62	0.04
Hs_12plexchip_4_10628	v2HS_100809	AATGAAATTCATGGTCTCTGCA	NM_182493	MLCK	MLCK protein (MLCK), mRNA	-1.62	0.20	-0.68	0.54	-0.94	0.08
Hs_12plexchip_5_1542	v2HS_249839	ATAGCAAAGGGATCCATCAGGA	NM_005439	MLF2	myeloid leukemia factor 2 (MLF2), mRNA	-1.44	0.51	-0.02	0.30	-1.42	0.02
Hs0P00005246	v2HS_120224	TTGTAACAGAGAAGCGTGCCCA	AL833362	MLKL	MIXED LINEAGE KINASE DOMAIN-LIKE	-1.10	1.54	1.14	0.81	-2.24	0.11
Hs_12plexchip_2_12570	v2HS_198375	TATTGGTTTGCGAATAAGACCT	NM_005933	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) (MLL), mRNA	-1.30	0.53	-0.24	0.44	-1.06	0.06
Hs_12plexchip_6_736	v2HS_196843	TTTCTTCTTGATCTTATCTCCA	NM_005933	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) (MLL), mRNA	-0.74	0.67	0.61	0.54	-1.35	0.06
Hs_12plexchip_6_1814	v2HS_117180	ATACTGTAGAACATGACATCCT	NM_031415	MLZE	melanoma-derived leucine zipper, extra-nuclear factor (MLZE), mRNA	-1.52	1.05	1.12	1.25	-2.64	0.05

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_4136	v2HS_178440	TAGATCATGCACTCTGACTGCT	NM_033467	MMEL1	membrane metallo-endopeptidase-like 1 (MMEL1), mRNA	-1.39	0.39	-0.31	0.93	-1.09	0.17
Hs_12plexchip_4_8554	v2HS_151858	TAAATTAACCCTTTCCGGTCCA	NM_002430	MN1	meningioma (disrupted in balanced translocation) 1 (MN1), mRNA	-1.31	0.86	-0.07	1.03	-1.24	0.19
Hs_12plexchip_4_7836	v2HS_151873	TTAACATTCATTGGTCCTTCCT	NM_002432	MNDA	myeloid cell nuclear differentiation antigen (MNDA), mRNA	-1.04	0.47	0.04	0.63	-1.08	0.08
Hs_12plexchip_5_1540	v2HS_54255	TTTCGGAAGAACGGAAGAAGCA	NM_130807	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast) (MOBKL2A), mRNA	-1.55	0.13	-0.32	0.52	-1.23	0.05
Hs_12plexchip_5_11551	v2HS_272336	TTGTATTCCTGGTTCTTATGGC	NM_032332	MORG1	mitogen-activated protein kinase organizer 1 (MORG1), transcript variant 2, mRNA	-1.52	0.40	-0.18	0.49	-1.33	0.02
Hs_12plexchip_5_7127	v2HS_36817	AACTTAACTGTCCTCCAGTGCG	NM_005372	MOS	v-mos Moloney murine sarcoma viral oncogene homolog (MOS), mRNA	-1.01	0.55	-0.06	0.82	-0.95	0.18
Hs_12plexchip_5_12339	v2HS_242606	ATTCATCACAAGCAGGTTTCCC	NM_003829	MPDZ	multiple PDZ domain protein (MPDZ), mRNA	-0.99	1.05	-0.11	0.06	-0.88	0.28
Hs0P00010208	v2HS_16945	TTCTTCCATCATGCTCAACGGC	NM_003829	MPDZ	multiple PDZ domain protein (MPDZ), mRNA	-2.39	0.93	-0.95	0.49	-1.44	0.10
Hs_12plexchip_6_7023	v2HS_59513	TTTACGTACTACATCATCCCAA	NM_005791	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (MPHOSPH10), mRNA	-2.12	0.98	-1.02	0.73	-1.10	0.20
Hs_12plexchip_5_2567	v2HS_204825	ATTAATAACTATAGAGACACCA	NM_005792	MPHOSPH6	M-phase phosphoprotein 6 (MPHOSPH6), mRNA	-4.05	0.27	-1.21	0.89	-2.84	0.02
Hs_12plexchip_6_10381	v2HS_36836	AATGTTCGGGAGAAACACTTCA	NM_005373	MPL	myeloproliferative leukemia virus oncogene (MPL), mRNA	-1.53	0.82	-0.29	0.76	-1.24	0.13
Hs_12plexchip_2_2373	v2HS_76384	TTGTAGGAACGGTACGTGGGCA	NM_000250	MPO	myeloperoxidase (MPO), nuclear gene encoding mitochondrial protein, mRNA	-1.52	0.82	-0.70	0.62	-0.82	0.24
Hs_12plexchip_6_5149	v2HS_66661	TTTCTCGGGAAACAGATCTGGG	NM_021134	MRPL23	mitochondrial ribosomal protein L23 (MRPL23), nuclear gene encoding mitochondrial protein, mRNA	-0.83	0.25	0.31	0.70	-1.14	0.09
Hs_12plexchip_5_12676	v2HS_253656	TATTCTCCACACTTTCAGTCCA	NM_007208	MRPL3	mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding mitochondrial protein, mRNA	-3.03	1.07	-1.22	1.30	-1.81	0.14
Hs_12plexchip_6_9149	v2HS_237290	GTGATTGCTCTCTTTAGAGGCG	NM_145213	MRPL30	mitochondrial ribosomal protein L30 (MRPL30), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA	-2.60	0.11	-0.29	0.30	-2.31	0.00
Hs_12plexchip_6_9486	v2HS_154405	TTTATTAAAGAGATCATTCCGC	NM_080794	MRPL39	mitochondrial ribosomal protein L39 (MRPL39), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.70	0.64	-0.53	1.10	-1.18	0.20
Hs0P00002853	v2HS_62393	CTAGAATTTGAATTGCTGAGCC	BG327319	MRPL49	MITOCHONDRIAL RIBOSOMAL PROTEIN L49	-1.40	0.45	0.28	0.37	-1.68	0.01
Hs_12plexchip_3_2049	v2HS_61946	AATTGCAGAATCGTGAGATGGT	AY135343	MRPS36P4	MITOCHONDRIAL RIBOSOMAL PROTEIN S36 PSEUDOGENE 4	-1.87	0.65	-0.62	0.45	-1.25	0.06
Hs_12plexchip_2_7140	v2HS_155898	AATGGTAGAAATTGGAAGTGGC	NM_018133	MSL2L1	male-specific lethal 2-like 1 (Drosophila) (MSL2L1), mRNA	-0.91	0.81	0.15	0.43	-1.06	0.14
Hs_12plexchip_6_8569	v2HS_59450	ATGCTTTAGGACGTCCAGCTGC	NM_013404	MSLN	mesothelin (MSLN), transcript variant 2, mRNA	-0.90	0.25	0.04	0.14	-0.94	0.01
Hs_12plexchip_4_9734	v2HS_20397	TTAAGAGAAGCAATGACTCGCT	NM_012228	MSRB2	methionine sulfoxide reductase B2 (MSRB2), mRNA	-0.75	0.83	0.14	0.37	-0.89	0.19
Hs_12plexchip_5_6885	v2HS_36306	TTTGCAACCAACTCTAATCTCG	NM_004739	MTA2	metastasis associated 1 family, member 2 (MTA2), mRNA	-1.29	0.38	-0.42	0.10	-0.87	0.05
Hs_12plexchip_6_9835	v2HS_191887	TATTTCTCTGGTTTGGAAAGGT	AK022122	MTBP	MDM2, TRANSFORMED 3T3 CELL DOUBLE MINUTE 2, P53 BINDING PROTEIN (MOUSE) BINDING PROTEIN, 104KDA	-1.68	0.14	-0.66	0.74	-1.03	0.13
Hs_12plexchip_5_5479	v2HS_257732	AATTTCCCTGATATGATCTGGT	NM_000254	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase (MTR), mRNA	-0.84	0.70	0.34	0.25	-1.18	0.09
Hs_12plexchip_4_1019	v2HS_196467	TTAACAAATTGGACTATTGGAC	NM_001006635	MTX2	metaxin 2 (MTX2), transcript variant 2, mRNA	-2.45	0.72	-0.35	0.30	-2.09	0.02
Hs_12plexchip_6_12695	v2HS_163117	ATATGTTAATGGAGTACTTCCT	NM_001040105	MUC17	mucin 17, cell surface associated (MUC17), mRNA	-0.81	0.47	0.15	0.40	-0.96	0.06
Hs_12plexchip_5_4771	v2HS_257856	ATAGAAATTCATTCCAATTCCC	NM_000255	MUT	methylmalonyl Coenzyme A mutase (MUT), nuclear gene encoding mitochondrial protein, mRNA	-0.76	0.35	0.25	0.28	-1.01	0.02
Hs_12plexchip_3_769	v2HS_50240	ATGAGGGTTGATTTCAGGCCCA	NM_005115	MVP	major vault protein (MVP), transcript variant 2, mRNA	-1.22	0.17	-0.22	0.58	-1.00	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_9369	v2HS_152028	TAATTCACAAAGCCTGGCAGCT	NM_002462	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA	-1.85	0.25	-1.14	0.68	-0.71	0.21
Hs_12plexchip_6_9438	v2HS_263085	TTGTTGTTAGCACCAGGAGCCG	NM_002466	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), mRNA	-1.67	0.51	-0.89	0.77	-0.78	0.23
Hs_12plexchip_5_4462	v2HS_255399	ATGTGGGACACCTTTATGCGGC	NM_000256	MYBPC3	myosin binding protein C, cardiac (MYBPC3), mRNA	-1.75	1.03	-0.29	0.29	-1.46	0.12
Hs_12plexchip_4_5398	v2HS_16475	AATGGTTGTCAAAGAGTTTGGT	NM_014981	MYH15	myosin, heavy chain 15 (MYH15), mRNA	-0.82	0.52	0.19	0.74	-1.01	0.13
Hs_12plexchip_5_3585	v2HS_71122	TAAGCTATCCTATTAATTGGGC	NM_013262	MYLIP	myosin regulatory light chain interacting protein (MYLIP), mRNA	-2.03	1.07	0.98	1.43	-3.01	0.05
Hs_12plexchip_3_3191	v2HS_70160	TAATACCATCACGGTTCTGGTC	NM_013292	MYLPF	fast skeletal myosin light chain 2 (MYLPF), mRNA	-0.98	0.18	0.04	0.54	-1.02	0.07
Hs_12plexchip_3_1572	v2HS_61202	TAAAGTACTCAATGGGTGTCCA	NM_004998	MYO1E	myosin IE (MYO1E), mRNA	-2.05	0.32	-1.25	0.13	-0.79	0.04
Hs_12plexchip_5_520	v2HS_50269	TATTGGAATGGGATCAGCACGG	NM_012330	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4 (MYST4), mRNA	-0.96	0.42	-0.17	0.34	-0.79	0.07
Hs_12plexchip_4_5674	v2HS_16444	TTAAATTGTCAAAGTACATCGT	AF006822	MYT2	MYELIN TRANSCRIPTION FACTOR 2	-0.89	0.26	-0.18	0.35	-0.72	0.05
Hs_12plexchip_6_6546	v2HS_139425	GTGGAGTAAAGAATGGCAAGGC	X74613	NA	NA	-2.17	1.06	-0.50	1.16	-1.68	0.14
Hs_12plexchip_2_2845	v2HS_83390	ATTTCAACCGACTGATTTGCGG	NM_023018	NADK	NAD kinase (NADK), mRNA	-1.27	0.43	-0.08	0.39	-1.20	0.02
Hs_12plexchip_4_6500	v2HS_66759	GTAGAATATCACGCAGGCAGGG	NM_153006	NAGS	N-acetylglutamate synthase (NAGS), mRNA	-1.70	0.44	-0.64	0.22	-1.05	0.03
Hs_12plexchip_2_11833	v2HS_43386	TTATCACAGATGATTTCAGCCT	NM_152667	NANP	N-acetylneuraminic acid phosphatase (NANP), mRNA	-1.13	0.19	-0.38	0.46	-0.75	0.09
Hs_12plexchip_6_11820	v2HS_121992	TTATACTCATAGTCCTCAACCT	XR_017910	NAP1L6	PREDICTED:nucleosome assembly protein 1-like 6 (NAP1L6), misc RNA	-1.63	0.07	-0.11	0.55	-1.51	0.04
Hs_12plexchip_5_11516	v2HS_272934	TTTATTCATTGCTTTATAAGCC	NM_057175	NARG1	NMDA receptor regulated 1 (NARG1), mRNA	-1.63	0.19	0.32	0.02	-1.95	0.00
Hs0P00007747	v2HS_136909	TTTCATTCAAATTCTCTACCGC	NM_057175	NARG1	NMDA receptor regulated 1 (NARG1), mRNA	-2.05	0.33	-1.28	0.30	-0.77	0.04
Hs_12plexchip_2_11058	v2HS_48258	TTTAATGGTAATCTTCTTTGCT	NM_004539	NARS	asparaginyl-tRNA synthetase (NARS), mRNA	-1.36	0.47	-0.54	0.66	-0.82	0.16
Hs_12plexchip_2_4327	v2HS_90025	TTGTAATATACTGCTCTCTCCT	NM_000015	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase) (NAT2), mRNA	-1.30	0.57	-0.33	0.65	-0.97	0.12
Hs_12plexchip_6_8842	v2HS_46816	TAAGAGTATGAGGGTTCGAGGC	NM_003960	NAT8	N-acetyltransferase 8 (NAT8), mRNA	-0.71	0.59	0.34	0.49	-1.04	0.08
Hs_12plexchip_5_9142	v2HS_267506	TTTAAATTAGAGGCTCCCTGGA	NM_014903	NAV3	neuron navigator 3 (NAV3), mRNA	-1.65	0.67	-0.36	0.61	-1.29	0.07
Hs_12plexchip_6_9437	v2HS_250396	AATAGGTAGCGATTCTGACCTT	NR_003108	NBR2	neighbor of BRCA1 gene 2 (NBR2) on chromosome 17	-1.20	0.50	-0.01	0.40	-1.19	0.04
Hs0P00004781	v2HS_111710	ATTCCACACCACTGAGATCCGC	NM_000615	NCAM1	neural cell adhesion molecule 1 (NCAM1), transcript variant 1, mRNA	-1.83	0.54	-1.01	0.78	-0.82	0.21
Hs_12plexchip_6_1620	v2HS_95758	ATTGCTTCCCACAATTTCTGGC	NM_014865	NCAPD2	non-SMC condensin I complex, subunit D2 (NCAPD2), mRNA	-1.08	0.56	1.18	0.64	-2.27	0.01
Hs_12plexchip_2_3320	v2HS_87782	AATTAGAATCAATTGTTGACCT	NM_022346	NCAPG	non-SMC condensin I complex, subunit G (NCAPG), mRNA	-1.08	0.46	-0.17	0.44	-0.91	0.07
Hs_12plexchip_3_2325	v2HS_58556	TTTGTCGATAAGATAGGATGGT	NM_013436	NCKAP1	NCK-associated protein 1 (NCKAP1), transcript variant 1, mRNA	-1.95	0.36	-0.29	1.21	-1.67	0.13
Hs0P00005864	v2HS_115886	TTTGGTAATAGGCCACCAAGGC	NM_184231	NCKIPSD	NCK interacting protein with SH3 domain (NCKIPSD), transcript variant 2, mRNA	-0.82	0.16	0.09	0.32	-0.91	0.02
Hs_12plexchip_6_8471	v2HS_36645	TTTCCTAGTCATACCAATTCTG	NM_005381	NCL	nucleolin (NCL), mRNA	-2.38	0.99	-0.74	0.66	-1.64	0.08
Hs0P00001416	v2HS_59235	TTATCAGGTGATGGTGGCACGG	NM_014071	NCOA6	nuclear receptor coactivator 6 (NCOA6), mRNA	-0.73	0.20	0.15	0.74	-0.88	0.17
Hs_12plexchip_4_8307	v2HS_152160	TTTAAAGTTGACTCACGGTGGG	NM_002487	NDN	necdin homolog (mouse) (NDN), mRNA	-0.99	0.67	0.14	0.17	-1.13	0.09
Hs_12plexchip_3_668	v2HS_35485	AATAATGAGAATGTATTTGCCT	NM_004784	NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3 (NDST3), mRNA	-0.77	0.42	0.38	0.11	-1.15	0.03
Hs_12plexchip_2_9274	v2HS_22185	TTGTCTTTACTTGTAAGGTGTT	NM_018838	NDUFA12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 (NDUFA12), mRNA	-0.85	0.80	0.08	0.29	-0.93	0.17
Hs_12plexchip_4_6295	v2HS_20571	CTAAATGTTGACGGTCTTGGCC	NM_005002	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), mRNA	-1.56	0.82	0.09	0.73	-1.65	0.06
Hs_12plexchip_4_7809	v2HS_152197	TACATGGACTATAAATACTGCA	NM_002495	NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase) (NDUFS4), mRNA	-1.60	0.10	-0.79	0.28	-0.80	0.03
Hs_12plexchip_4_2918	v2HS_169409	AATTTCTTCAATATCCTTAGCT	NM_021074	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa (NDUFV2), mRNA	-1.04	0.73	-0.09	0.19	-0.95	0.14
Hs_12plexchip_6_1813	v2HS_96761	ATAGACTATCACTTGGAAAGCA	NM_015509	NECAP1	NECAP endocytosis associated 1 (NECAP1), mRNA	-0.78	0.62	0.06	0.66	-0.83	0.19

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_3280	v2HS_80461	AATGATCCTCATTACAGAGGCC	NM_015277	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like (NEDD4L), mRNA	-2.12	0.43	-0.92	0.89	-1.20	0.13
Hs0P00001564	v2HS_64585	ATATGATGCCTCATTATGAGCG	NM_006156	NEDD8	neural precursor cell expressed, developmentally down-regulated 8 (NEDD8), mRNA	-0.73	0.86	1.04	0.21	-1.77	0.06
Hs_12plexchip_4_6314	v2HS_64532	ATCAGATAGGAGCTGGTCTGTA	NM_006158	NEFL	neurofilament, light polypeptide 68kDa (NEFL), mRNA	-2.22	0.96	-1.29	0.50	-0.93	0.24
Hs_12plexchip_3_12082	v2HS_240615	AATTTCTTTCCATGGACCTGGG	NM_145043	NEIL2	nei like 2 (E. coli) (NEIL2), mRNA	-0.80	0.98	0.17	0.64	-0.96	0.24
Hs_12plexchip_5_6456	v2HS_262163	TTTATTCTTTCCAACCTTTCCT	NM_012224	NEK1	NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA	-1.33	0.55	-0.14	0.24	-1.19	0.05
Hs_12plexchip_6_843	v2HS_202951	TTTAGCTTCATTATCTTCTGCT	NM_012224	NEK1	NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA	-0.88	1.00	1.27	1.07	-2.15	0.06
Hs_12plexchip_5_12256	v2HS_207578	TTAATAGGTAGGAGACCTCCAG	NM_005863	NET1	neuroepithelial cell transforming gene 1 (NET1), transcript variant 2, mRNA	-0.72	0.44	0.36	0.39	-1.09	0.03
Hs_12plexchip_5_10282	v2HS_230876	ATTGATAGTCAGTCATGGTGGT	NM_000434	NEU1	sialidase 1 (lysosomal sialidase) (NEU1), mRNA	-0.88	0.98	-0.04	0.66	-0.84	0.29
Hs_12plexchip_4_8799	v2HS_76032	TTTCATCTTCAACTTCACTGCA	NM_000267	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), transcript variant 2, mRNA	-0.84	0.22	0.37	0.50	-1.21	0.04
Hs_12plexchip_5_5040	v2HS_76027	ATTACGTTTGAAACTGCCAGCG	NM_000267	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), transcript variant 2, mRNA	-0.89	0.34	1.48	0.32	-2.37	0.00
Hs_12plexchip_5_5442	v2HS_260806	TTAAGTAATGCGATATTGAGCA	NM_000267	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), transcript variant 2, mRNA	-1.23	0.12	2.30	0.39	-3.53	0.00
Hs_12plexchip_5_7033	v2HS_259783	TTATAAACCACCATATGCTCCC	NM_181833	NF2	neurofibromin 2 (bilateral acoustic neuroma) (NF2), transcript variant 9, mRNA	-0.84	0.10	0.19	0.43	-1.02	0.05
Hs_12plexchip_6_2489	v2HS_200375	TAATGGTATTGTGCTTGCTGCT	NM_181832	NF2	neurofibromin 2 (bilateral acoustic neuroma) (NF2), transcript variant 8, mRNA	-1.12	1.72	0.73	0.88	-1.85	0.20
Hs0P00002730	v2HS_50017	CTATCTTCTCATAGCTGGTGGT	NM_012340	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), transcript variant 1, mRNA	-2.04	0.30	-0.80	1.07	-1.24	0.17
Hs_12plexchip_4_11015	v2HS_136998	TTATGTTACATAGTAGAATCCA	AK022471	NGLY1	N-GLYCANASE 1	-1.29	0.83	-0.10	0.17	-1.19	0.12
Hs_12plexchip_3_10040	v2HS_136186	TAAATCTGATGGTTCTTCAGCC	NM_024528	NKAP	NFKB activating protein (NKAP), mRNA	-1.69	0.38	-0.84	0.53	-0.85	0.10
Hs_12plexchip_3_2186	v2HS_60796	TTTGTTACAGATGTGATGTGCC	NM_021209	NLRC4	NLR family, CARD domain containing 4 (NLRC4), mRNA	-0.76	0.65	0.40	0.81	-1.16	0.13
Hs_12plexchip_5_459	v2HS_41115	TTTCTTCATCCATTTGAATGCC	NM_004688	NMI	N-myc (and STAT) interactor (NMI), mRNA	-0.75	0.08	0.48	0.41	-1.23	0.03
Hs_12plexchip_3_8465	v2HS_98549	TTAGCGATCCATTCATTCACCA	NM_022787	NMNAT1	nicotinamide nucleotide adenylyltransferase 1 (NMNAT1), mRNA	-1.38	0.24	-0.32	0.46	-1.06	0.04
Hs_12plexchip_2_11578	v2HS_49926	ATTAACAGTGTCATTAGCTCCA	NM_182977	NNT	nicotinamide nucleotide transhydrogenase (NNT), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-0.91	0.25	-0.20	0.45	-0.71	0.09
Hs_12plexchip_6_7107	v2HS_158377	TAACTTTAAATCGATCATCGGT	NM_024894	NOL10	nucleolar protein 10 (NOL10), mRNA	-2.44	3.15	0.94	3.10	-3.38	0.26
Hs_12plexchip_6_5511	v2HS_161165	TAATAAGCTCAGGTATAAACCT	NM_003703	NOL14	nucleolar protein 14 (NOL14), mRNA	-1.33	0.47	-0.39	0.62	-0.94	0.11
Hs0P00010705	v2HS_47052	TTCACTTCCAGCGGTACTGGGC	NM_003946	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain) (NOL3), mRNA	-1.44	0.40	0.18	0.54	-1.62	0.02
Hs_12plexchip_2_10055	v2HS_23380	TTGAATTAAGAATAGATAGCCT	NM_003787	NOL4	nucleolar protein 4 (NOL4), mRNA	-0.78	0.13	0.57	0.30	-1.35	0.01
Hs_12plexchip_4_10140	v2HS_197422	TTAAACTTAACTTTGGCACGGG	NM_006392	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat) (NOL5A), mRNA	-2.24	1.76	0.35	1.14	-2.59	0.11
Hs_12plexchip_5_3215	v2HS_253869	ATTAAACTTAACTTTGGCACGG	NM_006392	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat) (NOL5A), mRNA	-2.61	0.66	-0.98	0.15	-1.63	0.04
Hs_12plexchip_6_5083	v2HS_116373	AACTGCAAGACACTTCTCAGGA	NM_139235	NOL6	nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant gamma, mRNA	-3.00	0.62	-0.23	1.93	-2.77	0.12
Hs_12plexchip_3_11626	v2HS_174662	TTTCAGATTCATTTATTGAGGG	NM_017948	NOL8	nucleolar protein 8 (NOL8), mRNA	-1.09	0.42	0.38	0.10	-1.47	0.02
Hs_12plexchip_4_6028	v2HS_30849	TTTCTTCAGCGTATAGACTCGA	NM_018648	NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA	-1.04	0.27	0.24	0.81	-1.27	0.10
Hs_12plexchip_3_12100	v2HS_25502	ATACTTAAGAGCTTTGCATCCT	NG_000886	NPM1P13	NUCLEOPHOSMIN 1 (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) PSEUDOGENE 13	-1.10	0.21	-0.40	0.14	-0.70	0.01

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_5492	v2HS_25500	ATCTTCTATGGGTTTGTGGCAC	NG_000886	NPM1P13	NUCLEOPHOSMIN 1 (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) PSEUDOGENE 13	-1.76	0.41	-0.69	0.37	-1.07	0.03
Hs_12plexchip_2_6256	v2HS_169580	AATGTGATCATCTTTGTCGGCC	NG_001233	NPM1P17	NUCLEOPHOSMIN 1 (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) PSEUDOGENE 17	-1.13	0.67	0.23	1.23	-1.36	0.19
Hs_12plexchip_4_2788	v2HS_179585	TAAAGTGATCACTTCGTCGGCC	X54171	NPM1P2	NUCLEOPHOSMIN 1 (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) PSEUDOGENE 2	-1.89	0.31	-0.75	1.31	-1.14	0.27
Hs_12plexchip_2_9842	v2HS_23482	TTAGTTCTGGAGTTGTTAGCGT	NM_001033047	NPNT	nephronectin (NPNT), mRNA	-0.98	0.28	-0.26	0.46	-0.72	0.09
Hs0P00001619	v2HS_131236	ATACACAATGCGCCCGTTGGCC	NM_000907	NPR2	NATRIURETIC PEPTIDE RECEPTOR B/GUANYLATE CYCLASE B (ATRIONATRIURETIC PEPTIDE RECEPTOR B)	-2.36	0.42	-1.03	0.98	-1.33	0.13
Hs_12plexchip_6_9954	v2HS_131222	ATGCAATTTCAGGAGCAAAGCT	NM_000904	NQO2	NAD(P)H dehydrogenase, quinone 2 (NQO2), mRNA	-1.40	0.95	0.34	0.58	-1.74	0.07
Hs_12plexchip_4_1897	v2HS_12592	TTATCCCAAGGGATGAGAGCCG	NM_007121	NR1H2	nuclear receptor subfamily 1, group H, member 2 (NR1H2), mRNA	-1.31	0.82	-0.34	0.84	-0.97	0.22
Hs_12plexchip_4_12610	v2HS_239394	TTTGTAGTTCCAGACACTGCCA	NM_022002	NR1I2	nuclear receptor subfamily 1, group I, member 2 (NR1I2), transcript variant 2, mRNA	-2.26	1.28	-1.21	0.51	-1.05	0.29
Hs_12plexchip_4_12431	v2HS_239566	ATTTAGCAAACTCGGTTATCCT	NM_004959	NR5A1	nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA	-1.00	0.85	-0.25	0.53	-0.76	0.27
Hs_12plexchip_5_7176	v2HS_61886	ACTTAGTAGGCGAGTGTCCGGG	NM_004959	NR5A1	nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA	-1.10	0.61	0.71	0.15	-1.81	0.03
Hs_12plexchip_4_8910	v2HS_152364	TTACTATTCCACAGTTCAGCCC	NM_001101662	NRD1	nardilysin (N-arginine dibasic convertase) (NRD1), transcript variant 2, mRNA	-0.72	0.52	0.90	0.33	-1.62	0.02
Hs_12plexchip_3_12053	v2HS_31428	GTAGTATACCTGTTTGAGGCCC	NM_007243	NRM	nurim (nuclear envelope membrane protein) (NRM), mRNA	-0.94	0.65	0.00	0.46	-0.94	0.12
Hs_12plexchip_5_12770	v2HS_246996	ATACATTCATACATATCTTCCT	NM_004801	NRXN1	neurexin 1 (NRXN1), transcript variant alpha, mRNA	-0.75	1.24	1.49	0.29	-2.24	0.08
Hs_12plexchip_6_4951	v2HS_157200	TAAAGTGGTAAAGTGGAGGCCC	NM_024677	NSUN7	NOL1/NOP2/Sun domain family, member 7 (NSUN7), mRNA	-1.93	0.78	-0.40	1.27	-1.53	0.16
Hs_12plexchip_4_9973	v2HS_23979	TTAAAGGGTGACATCTTCTGGC	NM_001005744	NUMB	numb homolog (Drosophila) (NUMB), transcript variant 2, mRNA	-0.73	0.27	0.02	0.87	-0.76	0.27
Hs_12plexchip_5_9201	v2HS_268280	AATATGATCGAGACTATAGCGA	NM_015231	NUP160	nucleoporin 160kDa (NUP160), mRNA	-3.50	1.54	-1.23	0.95	-2.27	0.11
Hs_12plexchip_5_11467	v2HS_139799	TATTCCAATGACTGCCAGAGGG	NM_015135	NUP205	nucleoporin 205kDa (NUP205), mRNA	-2.67	1.05	-0.52	0.26	-2.15	0.06
Hs_12plexchip_2_10682	v2HS_18093	ATTTCATAGGAACTAGCAAGCC	NM_005085	NUP214	nucleoporin 214kDa (NUP214), mRNA	-1.49	1.05	-0.12	0.24	-1.37	0.15
Hs_12plexchip_3_12543	v2HS_18094	ATAGGTTAGAGGTATTTGAGGT	NM_005085	NUP214	nucleoporin 214kDa (NUP214), mRNA	-3.00	1.47	-1.81	0.16	-1.20	0.29
Hs0P00011283	v2HS_18091	ATTTGGTGTGAGATTCTATGGT	NM_005085	NUP214	nucleoporin 214kDa (NUP214), mRNA	-2.08	0.60	-1.27	0.26	-0.81	0.13
Hs_12plexchip_6_1324	v2HS_157038	ATTTACAGTAAGAATCTCAGGA	NM_198887	NUP43	nucleoporin 43kDa (NUP43), transcript variant 1, mRNA	-0.84	0.59	0.38	0.64	-1.22	0.07
Hs_12plexchip_5_4195	v2HS_259822	TATAGATATAAATTTGCCGCGC	NM_014669	NUP93	NUCLEOPORIN 93KDA	-3.13	1.47	-1.23	0.21	-1.90	0.15
Hs_12plexchip_5_4320	v2HS_79283	TTCTTGAGTAAAGTCAAGGGCG	NM_014669	NUP93	NUCLEOPORIN 93KDA	-1.91	0.67	-0.22	0.67	-1.69	0.04
Hs_12plexchip_6_776	v2HS_152410	AATAGTTCTCTCAGCTTCTGCT	NM_206840	NVL	nuclear VCP-like (NVL), transcript variant 2, mRNA	-1.50	0.72	0.23	1.64	-1.73	0.20
Hs_12plexchip_5_12479	v2HS_197439	ATCATTTACAATACATAGCCCT	NM_006362	NXF1	nuclear RNA export factor 1 (NXF1), transcript variant 1, mRNA	-3.73	1.47	-1.06	1.22	-2.68	0.07
Hs_12plexchip_5_12758	v2HS_197810	TTTCTTTGAGGGAAATTAACGC	NM_006362	NXF1	nuclear RNA export factor 1 (NXF1), transcript variant 1, mRNA	-1.64	0.36	-0.33	0.46	-1.30	0.02
Hs0P00004247	v2HS_233222	TTCCAGTATCTCATTGACGGCC	NM_016118	NYREN18	NEDD8 ULTIMATE BUSTER-1	-0.96	0.34	-0.08	0.79	-0.88	0.19
Hs_12plexchip_5_9496	v2HS_100250	TTAGGGTCTAAACGTTCAAGGA	NM_178507	OAF	OAF homolog (Drosophila) (OAF), mRNA	-1.68	1.10	-0.22	0.20	-1.46	0.14
Hs_12plexchip_4_8550	v2HS_152429	ATTAAATGATCCATAGACGCCA	NM_002539	ODC1	ornithine decarboxylase 1 (ODC1), mRNA	-2.58	1.46	-0.42	1.42	-2.16	0.14
Hs_12plexchip_3_3067	v2HS_62571	TTGTAGAACCAGTTCTTGTCCC	NM_175881	ODF3L1	outer dense fiber of sperm tails 3-like 1 (ODF3L1), mRNA	-1.44	1.02	-0.23	0.65	-1.21	0.17
Hs_12plexchip_4_6899	v2HS_62574	ATGCTGTAAGTAGGGCTGCGGT	NM_175881	ODF3L1	outer dense fiber of sperm tails 3-like 1 (ODF3L1), mRNA	-2.24	1.09	-1.09	0.79	-1.15	0.22
Hs_12plexchip_4_5845	v2HS_22853	TTCTATCGTCATCTTCTCTGCT	NM_153003	OFCC1	orofacial cleft 1 candidate 1 (OFCC1), mRNA	-0.85	0.16	-0.09	0.14	-0.75	0.00
Hs_12plexchip_6_8498	v2HS_91268	ATTAGTATTCATAACAACTGCT	NM_007280	OIP5	Opa interacting protein 5 (OIP5), mRNA	-1.46	0.59	-0.10	0.74	-1.36	0.07
Hs_12plexchip_4_9119	v2HS_197303	TTGAGATTGGATATGACCATCA	NM_005806	OLIG2	oligodendrocyte lineage transcription factor 2 (OLIG2), mRNA	-1.01	0.40	-0.30	0.21	-0.72	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_1849	v2HS_252101	AAGAGGGAAACTTGCATCTCGG	NM_001005280	OR10A7	olfactory receptor, family 10, subfamily A, member 7 (OR10A7), mRNA	-1.76	0.50	-0.95	0.58	-0.81	0.14
Hs_12plexchip_5_7540	v2HS_265914	ATTATCAGCTGAATGCAGACTT	NM_001005491	OR10AG1	olfactory receptor, family 10, subfamily AG, member 1 (OR10AG1), mRNA	-0.97	0.65	0.09	0.31	-1.06	0.09
Hs_12plexchip_5_8245	v2HS_263857	CTATTAGGTGAGATGAGCAGGT	NM_001005491	OR10AG1	olfactory receptor, family 10, subfamily AG, member 1 (OR10AG1), mRNA	-0.97	0.58	0.02	0.07	-0.99	0.10
Hs_12plexchip_3_4630	v2HS_120544	TAAGAACACCCGGTATTCTGGG	NM_001004297	OR13A1	olfactory receptor, family 13, subfamily A, member 1 (OR13A1), mRNA	-1.28	0.11	-0.40	0.91	-0.88	0.24
Hs_12plexchip_6_9462	v2HS_245063	ATAATCCAGCAACCAGCAGGGC	NM_012360	OR1F1	olfactory receptor, family 1, subfamily F, member 1 (OR1F1), mRNA	-0.86	1.17	0.21	0.63	-1.07	0.26
Hs_12plexchip_5_717	v2HS_246187	AAGAGAGAAATAAATTTGCCCT	NM_001004492	OR2B11	olfactory receptor, family 2, subfamily B, member 11 (OR2B11), mRNA	-0.77	0.05	0.37	0.31	-1.14	0.02
Hs_12plexchip_5_12900	v2HS_198794	TTTGCAGAGTTAATCCTCAGCA	NM_007160	OR2H2	olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA	-2.22	0.77	-0.92	0.70	-1.30	0.10
Hs_12plexchip_6_6274	v2HS_241031	TTAGAAACCATGTCTGCCAGGA	NM_001001964	OR2T11	olfactory receptor, family 2, subfamily T, member 11 (OR2T11), mRNA	-0.77	1.53	1.00	1.02	-1.77	0.18
Hs_12plexchip_6_12088	v2HS_272380	ATAAGTACAGGATACTGCAGGG	NM_001004699	OR2Z1	olfactory receptor, family 2, subfamily Z, member 1 (OR2Z1), mRNA	-0.84	0.18	0.46	0.98	-1.30	0.15
Hs_12plexchip_3_6064	v2HS_120864	TAAAGAATGCACACAGGATCCC	NM_001004701	OR4C16	olfactory receptor, family 4, subfamily C, member 16 (OR4C16), mRNA	-0.75	0.55	0.67	0.90	-1.42	0.09
Hs_12plexchip_5_8955	v2HS_264386	ATTGGGTTCTTAAGTGCCTGGC	NM_001004701	OR4C16	olfactory receptor, family 4, subfamily C, member 16 (OR4C16), mRNA	-2.16	0.47	-1.04	0.32	-1.12	0.03
Hs_12plexchip_4_6976	v2HS_68313	TTTCGAAGAGAAACCAGGATGA	NM_001001912	OR4E2	olfactory receptor, family 4, subfamily E, member 2 (OR4E2), mRNA	-0.87	0.15	0.40	0.66	-1.27	0.07
Hs_12plexchip_5_11676	v2HS_273833	TTCGTTAGGGTCATAATTTCCA	NM_001004063	OR4K1	olfactory receptor, family 4, subfamily K, member 1 (OR4K1), mRNA	-1.37	0.23	-0.30	0.16	-1.07	0.00
Hs_12plexchip_5_1583	v2HS_67552	ATACATGGGCACATGAAGGTTA	NM_001004052	OR52B2	olfactory receptor, family 52, subfamily B, member 2 (OR52B2), mRNA	-0.79	0.54	-0.01	0.25	-0.78	0.11
Hs_12plexchip_6_11958	v2HS_226927	ATTGGCGATAGATTTGGGAGCC	NM_001001966	OR5AT1	olfactory receptor, family 5, subfamily AT, member 1 (OR5AT1), mRNA	-1.42	0.79	-0.04	1.20	-1.38	0.18
Hs_12plexchip_5_9051	v2HS_120781	TATTAGGCTGACAGAGAATCCA	NM_001004743	OR5M9	olfactory receptor, family 5, subfamily M, member 9 (OR5M9), mRNA	-0.70	0.28	0.42	1.08	-1.12	0.21
Hs_12plexchip_5_10581	v2HS_154440	AATAAGGAGACAACTGAGAGGT	NM_001005190	OR7A10	olfactory receptor, family 7, subfamily A, member 10 (OR7A10), mRNA	-1.01	0.14	-0.30	0.53	-0.71	0.14
Hs_12plexchip_4_1458	v2HS_204974	GAAATGTGGCATAGATGGGCCA	NM_001001658	OR9A2	olfactory receptor, family 9, subfamily A, member 2 (OR9A2), mRNA	-0.88	0.69	1.10	1.00	-1.98	0.05
Hs_12plexchip_4_9157	v2HS_152494	AACAGTCACATTTCTGTCAGCC	NM_181747	ORC5L	origin recognition complex, subunit 5-like (yeast) (ORC5L), transcript variant 2, mRNA	-3.64	0.46	-0.77	2.84	-2.87	0.22
Hs_12plexchip_5_10876	v2HS_274419	TTAGACTATTTCCCGAGCTGCT	NM_024586	OSBPL9	oxysterol binding protein-like 9 (OSBPL9), transcript variant 6, mRNA	-1.01	0.10	0.06	0.51	-1.07	0.06
Hs0P00002400	v2HS_68955	TTAAGCTCATCAATCTTGGGTT	NM_194248	OTOF	otoferlin (OTOF), transcript variant 1, mRNA	-0.72	0.41	0.31	0.28	-1.03	0.03
Hs0P00010880	v2HS_20220	GTAATACTCAATATGGTCTCCT	NM_005015	OXA1L	oxidase (cytochrome c) assembly 1-like (OXA1L), mRNA	-2.15	0.83	-0.78	0.86	-1.37	0.12
Hs0P00006557	v2HS_92987	TTTGATTCTAATTCCATAACCT	NM_000430	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA	-2.29	0.63	-1.13	0.16	-1.16	0.08
Hs_12plexchip_3_11738	v2HS_218448	TAAGTAAGGAGATGAATGTGCG	NM_017734	PALMD	palmdelphin (PALMD), mRNA	-0.98	0.43	0.27	0.33	-1.25	0.02
Hs_12plexchip_5_8998	v2HS_98327	TTAGTTGTGCCATAGACCAGGT	NM_022750	PARP12	poly (ADP-ribose) polymerase family, member 12 (PARP12), mRNA	-1.10	0.43	-0.07	0.38	-1.03	0.04
Hs_12plexchip_4_10171	v2HS_12702	TTGTATAAGTAGGTGGAGACCC	NM_032052	PATZ1	POZ (BTB) and AT hook containing zinc finger 1 (PATZ1), transcript variant 3, mRNA	-0.76	0.71	0.15	0.47	-0.90	0.15
Hs_12plexchip_5_12791	v2HS_13712	ATACTGCAGAAGTTGCTGGGCC	NM_032052	PATZ1	POZ (BTB) and AT hook containing zinc finger 1 (PATZ1), transcript variant 3, mRNA	-1.77	0.91	-0.46	1.16	-1.31	0.20
Hs_12plexchip_4_7731	v2HS_22921	CAATGGCTAATCAATGTCCGGC	NG_000916	PCBP2P1	POLY(RC) BINDING PROTEIN 2, PSEUDOGENE 1	-1.48	0.54	-0.67	0.58	-0.81	0.15
Hs_12plexchip_2_4271	v2HS_78386	TTTACAAATGCAGTTTATCCCT	NM_007144	PCGF2	polycomb group ring finger 2 (PCGF2), mRNA	-0.73	0.69	0.23	0.79	-0.96	0.19
Hs_12plexchip_5_11295	v2HS_138812	ATCTAACTTCAGTTCAAGAGGT	NM_032373	PCGF5	polycomb group ring finger 5 (PCGF5), mRNA	-0.91	1.14	0.20	0.38	-1.10	0.23
Hs_12plexchip_2_5176	v2HS_175340	TATTGGACTATCACGGTCTGGC	NM_018386	PCID2	PCI domain containing 2 (PCID2), mRNA	-2.38	0.91	-1.25	0.42	-1.13	0.15
Hs_12plexchip_2_7761	v2HS_152725	ATTACAGAGGTGATGCAATGGG	NM_002594	PCSK2	proprotein convertase subtilisin/kexin type 2 (PCSK2), mRNA	-0.99	0.38	0.23	0.68	-1.23	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_7037	v2HS_92131	AATGCAGTTCAGGTACTGACCC	NM_014976	PDCD11	programmed cell death 11 (PDCD11), mRNA	-1.80	1.04	-0.31	0.71	-1.48	0.12
Hs_12plexchip_3_3652	v2HS_37058	ATAAGGTAATTCTCTACTGCTT	NM_004708	PDCD5	programmed cell death 5 (PDCD5), mRNA	-0.77	0.35	0.18	0.43	-0.95	0.04
Hs_12plexchip_4_7810	v2HS_131308	TTTAGCCTTTACATGGTTAGCT	NM_000921	PDE3A	phosphodiesterase 3A, cGMP-inhibited (PDE3A), mRNA	-1.16	1.45	0.83	0.46	-1.99	0.13
Hs_12plexchip_6_3677	v2HS_183211	ATGCAATAACGGAAGAAATGCT	AB042555	PDE4DIP	PHOSPHODIESTERASE 4D INTERACTING PROTEIN (MYOMEGALIN)	-1.13	1.17	0.38	0.82	-1.51	0.15
Hs_12plexchip_5_11185	v2HS_271860	ATAAATTCACAAATGGGCCGCA	NM_000925	PDHB	pyruvate dehydrogenase (lipoamide) beta (PDHB), mRNA	-1.58	0.10	-0.79	0.72	-0.79	0.20
Hs_12plexchip_3_3413	v2HS_38683	TTTGATTAGACAATCCTCCCTG	NM_020381	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2 (PDSS2), mRNA	-0.74	0.38	0.01	0.50	-0.75	0.11
Hs_12plexchip_4_8763	v2HS_77249	GTTGAATAGGAACTCCTTCTCC	NM_000209	PDX1	pancreatic and duodenal homeobox 1 (PDX1), mRNA	-1.00	0.53	-0.10	0.61	-0.90	0.13
Hs_12plexchip_6_2901	v2HS_179289	TTTATTGACTGACTTGCTAGCT	NM_173791	PDZD8	PDZ domain containing 8 (PDZD8), mRNA	-0.77	0.87	0.09	0.49	-0.86	0.23
Hs_12plexchip_4_12002	v2HS_169829	TTTGACCTTTCTGTTCTGAGCC	NM_002614	PDZK1	PDZ domain containing 1 (PDZK1), mRNA	-1.40	0.81	0.03	1.36	-1.42	0.21
Hs_12plexchip_4_31	v2HS_169828	ATATTATCACTCAAACCTTGCT	NM_002614	PDZK1	PDZ domain containing 1 (PDZK1), mRNA	-0.81	0.20	0.08	0.18	-0.89	0.01
Hs_12plexchip_4_3593	v2HS_169874	TTCTGTTCACTGAGATTCAGCT	NM_002622	PFDN1	prefoldin subunit 1 (PFDN1), mRNA	-1.46	0.15	-0.25	0.79	-1.20	0.11
Hs_12plexchip_5_9908	v2HS_100037	TATGAGGATCTGATGCAGTCCA	NM_170725	PGBD2	piggyBac transposable element derived 2 (PGBD2), transcript variant 1, mRNA	-2.10	0.70	-1.29	0.59	-0.81	0.20
Hs_12plexchip_4_7213	v2HS_65544	ATAACCTCCTCCATGATGGCCC	NM_016134	PGCP	plasma glutamate carboxypeptidase (PGCP), mRNA	-2.03	1.52	-0.05	1.16	-1.98	0.15
Hs0P00005147	v2HS_117230	ATTAGCTTTCCAGACGTGGGCA	NM_017712	PGPEP1	pyroglutamyl-peptidase I (PGPEP1), mRNA	-0.85	0.20	0.10	0.22	-0.95	0.01
Hs_12plexchip_6_4360	v2HS_176972	TATAGTAGGAGACTGACTTGGT	NM_024947	PHC3	polyhomeotic homolog 3 (Drosophila) (PHC3), mRNA	-0.82	0.29	0.13	0.61	-0.95	0.10
Hs_12plexchip_5_5650	v2HS_261411	ATATAGTCCGCATTTCCAGGCC	NM_015288	PHF15	PHD finger protein 15 (PHF15), mRNA	-0.90	0.37	-0.11	0.96	-0.79	0.29
Hs_12plexchip_4_9518	v2HS_73006	ATAGAGCACTGAATACAAGCCC	NM_014735	PHF16	PHD finger protein 16 (PHF16), transcript variant 1, mRNA	-2.47	0.86	-0.96	1.49	-1.51	0.22
Hs0P00003901	v2HS_115816	ATAACAGGTGTATTTCTCGGGC	NM_016436	PHF20	PHD FINGER PROTEIN 20	-0.89	0.71	0.51	0.17	-1.40	0.07
Hs0P00005894	v2HS_262439	TAACAGGTGTATTTCTCGGGCA	NM_016436	PHF20	PHD FINGER PROTEIN 20	-0.98	0.48	0.19	0.25	-1.17	0.03
Hs_12plexchip_3_2997	v2HS_70208	GTCTGGAATCAGAGTCTTTGGC	NM_138415	PHF21B	PHD finger protein 21B (PHF21B), mRNA	-0.92	0.87	0.52	0.78	-1.44	0.10
Hs_12plexchip_6_3812	v2HS_276861	AATAATATGAGACTAGTGGGCT	NM_032758	PHF5A	PHD finger protein 5A (PHF5A), mRNA	-3.13	0.62	-1.11	2.12	-2.02	0.24
Hs_12plexchip_5_3785	v2HS_75540	TTCTTCTATACTATTGTGAGGA	NM_016483	PHF7	PHD finger protein 7 (PHF7), transcript variant 1, mRNA	-1.02	0.75	1.05	1.23	-2.07	0.08
Hs_12plexchip_4_2383	v2HS_169417	TTTATGTGAAAGTTAAAGCCCA	NG_001173	PHKBP2	PHOSPHORYLASE KINASE, BETA PSEUDOGENE 2	-1.10	0.84	1.53	0.68	-2.63	0.01
Hs_12plexchip_5_2198	v2HS_209334	ATTTCCAACACAGACATATCCA	NM_006608	PHTF1	putative homeodomain transcription factor 1 (PHTF1), mRNA	-1.61	0.50	-0.41	0.86	-1.19	0.12
Hs_12plexchip_5_6227	v2HS_221355	TTTATTGGAAAGTGGATGAGAG	NM_002638	PI3	peptidase inhibitor 3, skin-derived (SKALP) (PI3), mRNA	-0.84	0.07	0.15	0.12	-0.98	0.00
Hs_12plexchip_6_1766	v2HS_97840	TAAAGCTCTAGAATGATCCGGA	NM_016166	PIAS1	protein inhibitor of activated STAT, 1 (PIAS1), mRNA	-1.41	1.97	0.67	1.54	-2.08	0.23
Hs_12plexchip_4_2502	v2HS_174061	ATTGAGAATGCATGAGGAAGCC	NM_017837	PIGV	phosphatidylinositol glycan anchor biosynthesis, class V (PIGV), mRNA	-1.51	0.69	-0.71	0.11	-0.80	0.18
Hs0P00000883	v2HS_77585	ATACTGGACTTTAATGACTGGT	NM_006875	PIM2	PIM-2 ONCOGENE	-1.05	0.75	0.08	0.63	-1.12	0.12
Hs_12plexchip_4_9658	v2HS_58415	ATAAATACTGTGTGACGGTGGC	NM_006221	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA	-1.13	0.51	1.00	1.00	-2.13	0.05
Hs_12plexchip_5_6616	v2HS_234804	ATTCAGTTCAAGGCACATACGT	NM_032409	PINK1	PTEN induced putative kinase 1 (PINK1), nuclear gene encoding mitochondrial protein, mRNA	-1.13	0.43	-0.01	0.67	-1.11	0.08
Hs0P00011923	v2HS_19861	TTAAACTTGAAATGGCTCGGCA	NM_005028	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha (PIP4K2A), mRNA	-1.04	0.65	0.23	0.19	-1.26	0.07
Hs_12plexchip_5_9845	v2HS_229814	ATAAACATACGGAGGAGTCGGC	NM_153427	PITX2	paired-like homeodomain 2 (PITX2), transcript variant 1, mRNA	-0.91	0.60	0.49	0.41	-1.40	0.03
Hs_12plexchip_2_9910	v2HS_20770	TAACAGACTAACAAGCATGGGC	NM_152431	PIWIL4	piwi-like 4 (Drosophila) (PIWIL4), mRNA	-0.75	0.64	0.74	0.27	-1.49	0.04
Hs_12plexchip_6_11224	v2HS_224114	ATAAGAGGTGAAGGTATTCGGA	XM_001133467	PKD1L3	PREDICTED:polycystic kidney disease 1-like 3 (PKD1L3), mRNA	-1.23	0.49	-0.32	0.40	-0.91	0.07
Hs_12plexchip_4_10173	v2HS_97624	TATGTGTCATTGATGATGGCCA	NM_016112	PKD2L1	polycystic kidney disease 2-like 1 (PKD2L1), mRNA	-1.62	0.34	-0.62	1.08	-1.00	0.25
Hs_12plexchip_5_4399	v2HS_259559	TTACTGGGTGAACACTTGAGCC	NM_181839	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 7, mRNA	-2.60	0.63	-1.47	0.96	-1.13	0.18

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_10351	v2HS_92232	ATTCACCAAATTCCCATGGGCC	NM_000300	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), mRNA	-1.42	0.32	0.38	0.17	-1.79	0.00
Hs_12plexchip_4_5655	v2HS_28160	ATATACTTCAAGACACTCGCCA	NM_001031689	PLAA	phospholipase A2-activating protein (PLAA), transcript variant 1, mRNA	-1.48	1.19	-0.15	1.13	-1.34	0.23
Hs0P00010471	v2HS_170081	TTCAAGCTCCAGGATTGGGCCC	NM_002659	PLAUR	plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, mRNA	-0.74	0.53	0.29	0.30	-1.03	0.06
Hs_12plexchip_3_12018	v2HS_22403	ATAGTGGACCAGATCATTGCAG	NM_153021	PLB1	phospholipase B1 (PLB1), mRNA	-0.77	1.01	0.31	0.69	-1.08	0.21
Hs_12plexchip_5_3221	v2HS_201045	TAGTATGAAGCCACGTGGACGC	NM_138790	PLD4	phospholipase D family, member 4 (PLD4), mRNA	-1.45	0.11	0.17	1.00	-1.62	0.11
Hs0P00002268	v2HS_60835	ATGAACTCCCATTTAATTCCTT	NM_021200	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1 (PLEKHB1), mRNA	-0.98	0.57	0.44	0.29	-1.42	0.03
Hs_12plexchip_5_4091	v2HS_78311	TTTAGTGCACATATTAACTGGT	NM_006832	PLEKHC1	pleckstrin homology domain containing, family C (with FERM domain) member 1 (PLEKHC1), mRNA	-0.90	0.26	0.13	0.45	-1.03	0.04
Hs_12plexchip_5_6733	v2HS_255275	ATCAGAACAAATCTCCTTGGGC	NM_022835	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2 (PLEKHG2), mRNA	-2.85	2.06	-0.10	0.38	-2.75	0.14
Hs_12plexchip_4_4980	v2HS_203563	TTATTCTTGCTGTAGAGCGCGT	NM_015432	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4 (PLEKHG4), mRNA	-1.15	0.80	-0.38	0.34	-0.77	0.23
Hs0P00000426	v2HS_19708	TGTAATTAGGAGTCCCACACAG	NM_005030	PLK1	POLO-LIKE KINASE 1 (DROSOPHILA)	-1.75	0.22	-0.35	0.10	-1.41	0.00
Hs0P00011638	v2HS_19709	TATTCTGTACAATTCATATGGT	NM_005030	PLK1	polo-like kinase 1 (Drosophila) (PLK1), mRNA	-1.19	1.25	-0.19	0.10	-1.00	0.30
Hs_12plexchip_4_9426	v2HS_91307	TTTGTCAAATCTGTCATCTCGT	NM_006622	PLK2	polo-like kinase 2 (Drosophila) (PLK2), mRNA	-1.07	0.59	-0.36	0.54	-0.71	0.20
Hs_12plexchip_4_7863	v2HS_93532	AAGAAACACAATCCAGTGGCCA	NM_199478	PLP1	proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated) (PLP1), transcript variant 2, mRNA	-1.46	0.71	-0.70	0.51	-0.76	0.21
Hs_12plexchip_5_3199	v2HS_198817	ATAAACTTGTCATAGATTCGCT	NM_007221	PMF1	POLYAMINE-MODULATED FACTOR 1	-1.84	0.50	-1.01	0.34	-0.84	0.08
Hs_12plexchip_6_6873	v2HS_160694	TATTTCTCACACCTGCTCGCGT	NM_173516	PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1 (PNLDC1), mRNA	-1.95	0.83	-0.32	1.41	-1.63	0.18
Hs_12plexchip_5_9437	v2HS_267706	AACATACAGATCTAGCTGCCCT	NM_004650	PNPLA4	patatin-like phospholipase domain containing 4 (PNPLA4), mRNA	-1.23	0.21	0.08	0.37	-1.31	0.01
Hs_12plexchip_5_6895	v2HS_261985	ATGAATGCCCACATAGGGCCGG	NM_015352	POFUT1	protein O-fucosyltransferase 1 (POFUT1), transcript variant 1, mRNA	-0.81	0.72	-0.07	0.55	-0.74	0.23
Hs_12plexchip_6_1230	v2HS_154166	TAATGATGAACTCTAAATTGGG	NM_016937	POLA1	polymerase (DNA directed), alpha 1 (POLA1), mRNA	-2.90	0.61	-0.06	0.35	-2.84	0.00
Hs_12plexchip_6_2203	v2HS_154165	ATATCTAATCCTTTGAGCTCCT	NM_016937	POLA1	polymerase (DNA directed), alpha 1 (POLA1), mRNA	-2.88	1.03	-1.44	1.34	-1.45	0.22
Hs_12plexchip_2_6022	v2HS_170204	TTGATTCTGAAGTGAAGCTGGG	NM_002690	POLB	polymerase (DNA directed), beta (POLB), mRNA	-0.84	0.46	-0.03	0.25	-0.81	0.07
Hs_12plexchip_4_4716	v2HS_202193	TTTCCAGATAAAGCTGGTCCGC	NM_006591	POLD3	polymerase (DNA-directed), delta 3, accessory subunit (POLD3), mRNA	-1.21	0.97	-0.37	0.47	-0.84	0.28
Hs_12plexchip_4_5532	v2HS_138460	ATTCACAGTCATCTTGGTGCCT	NM_178136	POLDIP3	polymerase (DNA-directed), delta interacting protein 3 (POLDIP3), transcript variant 2, mRNA	-1.50	0.53	-0.52	1.12	-0.98	0.27
Hs_12plexchip_2_4638	v2HS_181050	GAAGCAGGTAGGGAGAAGAGGT	AF128541	POLE	POLYMERASE (DNA DIRECTED), EPSILON	-0.94	0.48	-0.24	0.14	-0.70	0.12
Hs_12plexchip_2_4787	v2HS_170220	TTTGTTGATTTCCAGAGCACGG	NM_002693	POLG	polymerase (DNA directed), gamma (POLG), mRNA	-0.92	0.21	0.13	0.12	-1.05	0.00
Hs_12plexchip_4_3123	v2HS_170221	TTAAACTGCATTAGTAAGCGCT	NM_002693	POLG	polymerase (DNA directed), gamma (POLG), mRNA	-1.13	0.18	0.64	1.64	-1.77	0.20
Hs_12plexchip_6_754	v2HS_98038	TAAATGTATCTTGGTGACTCCA	NM_016218	POLK	polymerase (DNA directed) kappa (POLK), mRNA	-0.80	0.35	0.48	0.70	-1.27	0.07
Hs_12plexchip_4_486	v2HS_70473	AATGAGACACTGCACATCAGGG	NM_013284	POLM	polymerase (DNA directed), mu (POLM), mRNA	-1.98	0.77	-0.04	0.28	-1.94	0.04
Hs_12plexchip_5_1259	v2HS_67630	TATAATGATCTCGAACCCGGGC	NM_004875	POLR1C	polymerase (RNA) I polypeptide C, 30kDa (POLR1C), transcript variant 2, mRNA	-2.02	0.43	0.56	2.32	-2.58	0.19
Hs0P00000733	v2HS_58143	TTTACATCTAAGATTAGATCCA	NM_006232	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H (POLR2H), mRNA	-2.34	0.15	-1.21	0.27	-1.13	0.01
Hs_12plexchip_5_6194	v2HS_262739	TTGTGATTTAATGATGTTTCCC	NM_006234	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa (POLR2J), mRNA	-1.84	0.44	-0.85	0.21	-0.99	0.04

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_27	v2HS_155605	TTTATATACAAGGCAACGCCCA	NM_018082	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B (POLR3B), mRNA	-2.67	0.28	-0.95	0.96	-1.72	0.08
Hs_12plexchip_4_475	v2HS_201722	AATACATTTGAGTTAAAGAGTG	NM_006466	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa (POLR3F), mRNA	-2.61	0.59	0.64	0.29	-3.25	0.00
Hs_12plexchip_5_10139	v2HS_229159	TAATTCACTCTATTTCAGTGGA	NM_001018161	PON2	paraoxonase 2 (PON2), transcript variant 2, mRNA	-2.19	0.72	-0.67	0.66	-1.52	0.06
Hs_12plexchip_6_4178	v2HS_170242	TTTCTTTCGGTGTCTGTGTGCT	NM_002698	POU2F2	POU class 2 homeobox 2 (POU2F2), mRNA	-2.16	0.50	-0.89	1.51	-1.27	0.28
Hs0P00000858	v2HS_58128	TTTGAGGTCCAGTTTCTCGGCG	NM_006237	POU4F1	POU class 4 homeobox 1 (POU4F1), mRNA	-1.00	0.80	-0.12	0.74	-0.88	0.23
Hs_12plexchip_4_12043	v2HS_170252	TTTAAGGTCCAGTTTCTCAGCG	NM_002700	POU4F3	POU class 4 homeobox 3 (POU4F3), mRNA	-1.40	0.41	-0.01	1.41	-1.38	0.23
Hs_12plexchip_6_1104	v2HS_27774	TTCTCTTTCCAAGACAGCACGA	NM_177423	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), transcript variant 1, mRNA	-0.75	0.46	0.66	1.05	-1.41	0.13
Hs_12plexchip_5_10062	v2HS_97355	AAGCTTCATGACTTGCAAAGCC	NM_016059	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1 (PPIL1), mRNA	-0.88	0.67	0.21	0.38	-1.09	0.09
Hs_12plexchip_6_2534	v2HS_170282	TTAATGACTTCCTTAGTCACCT	NM_002705	PPL	periplakin (PPL), mRNA	-2.03	1.03	-0.55	1.15	-1.47	0.17
Hs_12plexchip_5_10616	v2HS_95988	ATATCATGAGTCTTTCTGAGCT	NM_014906	PPM1E	protein phosphatase 1E (PP2C domain containing) (PPM1E), mRNA	-1.09	0.41	-0.39	0.63	-0.70	0.19
Hs_12plexchip_6_3930	v2HS_202496	ATCAGCAAGGAAGGTGTGGGCT	NM_138558	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8 (PPP1R8), transcript variant 2, mRNA	-1.27	1.02	-0.19	0.53	-1.08	0.20
Hs0P00002401	v2HS_170331	ATGTTTCCTAACTTTGTCTCCT	NM_002713	PPP1R8	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 8	-1.45	0.70	0.02	0.59	-1.47	0.05
Hs0P00002406	v2HS_202452	TTTAAACCTCAGCTTAACTGCA	NM_014110	PPP1R8	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 8	-0.78	0.71	0.42	0.22	-1.20	0.09
Hs_12plexchip_4_12156	v2HS_170348	ATTGGAGATGATATTCAAACGA	NM_002716	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform (PPP2R1B), transcript variant 1, mRNA	-0.90	1.83	1.44	0.90	-2.35	0.14
Hs_12plexchip_2_2573	v2HS_74523	ATGTTTAACAAATTCAATTCCC	NM_015342	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1 (PPWD1), mRNA	-0.78	0.76	1.14	0.30	-1.92	0.03
Hs_12plexchip_6_3210	v2HS_173692	AATGAGGTAGGTGGTAGGAGGG	NM_001040125	PQLC2	PQ loop repeat containing 2 (PQLC2), transcript variant 1, mRNA	-0.79	0.15	0.24	0.80	-1.02	0.15
Hs_12plexchip_5_12716	v2HS_44323	ATTGACTGACGGAGAACAAGCT	NM_012406	PRDM4	PR domain containing 4 (PRDM4), mRNA	-1.97	1.05	-0.48	1.14	-1.49	0.17
Hs_12plexchip_6_422	v2HS_63833	TTAGCTTAAGCCTGTCTGCTGA	NM_013397	PRICKLE4	prickle homolog 4 (Drosophila) (PRICKLE4), mRNA	-1.53	1.14	-0.39	1.04	-1.14	0.27
Hs_12plexchip_4_7603	v2HS_170430	TTAGAAAGTGATGTTAAAGCCT	NM_002736	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA	-1.13	0.55	0.06	1.01	-1.19	0.17
Hs_12plexchip_4_1961	v2HS_222846	TTATTGTATTGAGGTCACAGGT	NM_001001329	PRKCSH	protein kinase C substrate 80K-H (PRKCSH), transcript variant 2, mRNA	-0.75	0.26	0.33	0.27	-1.09	0.01
Hs_12plexchip_5_11186	v2HS_131456	TATTGTTCTCAGGAGTCCCGGG	NM_000949	PRLR	prolactin receptor (PRLR), mRNA	-0.99	1.11	-0.06	0.55	-0.93	0.28
Hs_12plexchip_3_11179	v2HS_235964	TAAGGAAACACCCTAATTGCCT	NM_032414	PROK1	prokineticin 1 (PROK1), mRNA	-0.95	0.28	-0.23	0.42	-0.71	0.08
Hs_12plexchip_5_12847	v2HS_71819	TTGTTCTATAGGAAGGACTCGT	NM_006017	PROM1	prominin 1 (PROM1), mRNA	-1.26	0.24	-0.11	0.49	-1.15	0.04
Hs_12plexchip_4_9414	v2HS_87229	ATAAACATGATTAGAGACAGGG	NM_014502	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae) (PRPF19), mRNA	-0.94	0.56	0.89	0.19	-1.83	0.02
Hs_12plexchip_4_9165	v2HS_12663	ATCTTGGTTACCACTATCACCA	NM_007244	PRR4	proline rich 4 (lacrimal) (PRR4), transcript variant 2, mRNA	-0.72	0.90	0.53	0.16	-1.24	0.14
Hs0P00004090	v2HS_45919	AATTCAAGTCATACCCTGGCCA	NM_020200	PRTFDC1	phosphoribosyl transferase domain containing 1 (PRTFDC1), mRNA	-2.24	0.69	-0.96	1.30	-1.28	0.23
Hs_12plexchip_6_3798	v2HS_170634	ATGTCGTTCAGTTTGTTCTCCG	NM_002777	PRTN3	PROTEINASE 3 (SERINE PROTEINASE, NEUTROPHIL, WEGENER GRANULOMATOSIS AUTOANTIGEN)	-0.78	0.39	-0.03	0.24	-0.75	0.06
Hs_12plexchip_5_6793	v2HS_89936	TAATAATGTAAGGCACAAACCA	NM_000021	PSEN1	presenilin 1 (Alzheimer disease 3) (PSEN1), mRNA	-2.71	0.49	-0.31	0.86	-2.39	0.02
Hs_12plexchip_6_755	v2HS_159974	TTTCTCTTGCTCCACATATGCC	NM_033126	PSKH2	protein serine kinase H2 (PSKH2), mRNA	-1.34	0.83	0.09	0.77	-1.42	0.10
Hs_12plexchip_3_11631	v2HS_170669	AATAGTTAGCAGATGGACAGGT	NM_002786	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1 (PSMA1), transcript variant 2, mRNA	-1.28	0.73	-0.10	0.89	-1.18	0.15
Hs_12plexchip_4_8883	v2HS_170688	TTATTTCCAATGCATGTGGCCT	NM_001102667	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), transcript variant 2, mRNA	-1.28	0.38	-0.50	0.47	-0.78	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_4428	v2HS_170685	AATACCTTTGAGCAATGAGCCT	NM_001102667	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4 (PSMA4), transcript variant 2, mRNA	-1.16	1.04	0.09	0.96	-1.24	0.20
Hs_12plexchip_4_2478	v2HS_221829	TTCTCTTCTCCACAGCTAGGCA	NM_002790	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA	-1.84	0.37	-0.33	0.55	-1.51	0.02
Hs_12plexchip_4_7706	v2HS_170690	ATTCTCTTCTCCACAGCTAGGC	NM_002790	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA	-1.92	0.21	-0.74	0.61	-1.17	0.07
Hs_12plexchip_6_3705	v2HS_275540	TTGTATTTCCAGTTAGCTGCCT	NM_002791	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA	-2.77	0.90	-1.38	1.32	-1.39	0.21
Hs_12plexchip_6_890	v2HS_170707	AATAAATGGAATGGAAAGGCCT	NM_002792	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA	-0.73	0.55	0.01	0.83	-0.73	0.28
Hs_12plexchip_4_2902	v2HS_170731	TTGAAACCGGTTGTAAGAACGG	NM_002796	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA	-0.71	0.48	0.78	0.23	-1.49	0.02
Hs_12plexchip_4_3837	v2HS_170736	TATAAATAGGATGGAGGATGGG	NM_002797	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5 (PSMB5), mRNA	-2.15	0.49	0.66	0.27	-2.81	0.00
Hs_12plexchip_4_4471	v2HS_170733	ATTTCGAAGCTCATAGATTCGA	NM_002797	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5 (PSMB5), mRNA	-1.33	0.33	-0.20	0.92	-1.13	0.16
Hs_12plexchip_2_6001	v2HS_170743	ATTGCATACTAGAATCCCAGGA	NM_002798	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6 (PSMB6), mRNA	-1.58	0.78	0.30	0.65	-1.88	0.03
Hs_12plexchip_4_8031	v2HS_170784	TAATGGGTCTACCTTGTTGGGC	NM_002805	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5 (PSMC5), mRNA	-3.40	1.60	-1.61	0.33	-1.79	0.19
Hs_12plexchip_4_8198	v2HS_170848	AATTAATCGAAGTTTGATAGGA	NM_002816	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA	-2.60	0.22	-0.78	0.32	-1.82	0.00
Hs_12plexchip_3_6679	v2HS_95516	ATAGAATACAATATCCAATCGG	NM_014814	PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 (PSMD6), mRNA	-4.35	0.13	-1.97	0.73	-2.38	0.03
Hs_12plexchip_5_4340	v2HS_78720	TTTCATCTACCTGTTCTCAGGC	NM_006814	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31) (PSMF1), transcript variant 1, mRNA	-1.10	0.84	-0.34	0.31	-0.75	0.25
Hs_12plexchip_4_3920	v2HS_170902	TTTGTTCTTAGGAAGCTTGGCC	NM_002827	PTPN1	protein tyrosine phosphatase, non-receptor type 1 (PTPN1), mRNA	-1.34	0.30	-0.25	0.24	-1.08	0.01
Hs_12plexchip_6_9690	v2HS_252883	ATTTCCAGTAGAATCATCTGGG	NM_007062	PWP1	PWP1 homolog (S. cerevisiae) (PWP1), mRNA	-0.80	0.27	0.59	0.17	-1.39	0.00
Hs_12plexchip_6_10419	v2HS_19130	AATAGTCAGACGCATATGTGAC	NM_005051	QARS	glutaminyl-tRNA synthetase (QARS), mRNA	-2.33	0.50	1.14	1.42	-3.47	0.04
Hs_12plexchip_5_9311	v2HS_231422	ATACTGTGTCTGTTACTGCGGC	NM_014925	R3HDM2	R3H domain containing 2 (R3HDM2), mRNA	-1.12	0.99	-0.11	0.70	-1.02	0.23
Hs0P00001171	v2HS_58078	ATAGACCATCAAATTAAACCTG	NM_020673	RAB22A	RAB22A, member RAS oncogene family (RAB22A), mRNA	-1.01	0.27	-0.16	0.98	-0.85	0.27
Hs_12plexchip_6_2596	v2HS_99448	TTAAATTATCCAGGTAGGACCA	NM_031296	RAB33B	RAB33B, member RAS oncogene family (RAB33B), mRNA	-0.73	0.59	-0.02	0.31	-0.71	0.16
Hs_12plexchip_5_4862	v2HS_81488	TTATACAAGGATAAGTCAGCCT	NM_175624	RAB3IP	RAB3A interacting protein (rabin3) (RAB3IP), transcript variant beta 1, mRNA	-1.16	0.59	-0.32	0.50	-0.85	0.13
Hs0P00009092	v2HS_144193	ATTCCAGTTCGATTTCAACCGT	NM_001032726	RAB41	RAB41, member RAS oncogene family (RAB41), mRNA	-1.14	0.75	-0.39	0.44	-0.76	0.22
Hs_12plexchip_6_4010	v2HS_276051	ATAGGCCCAGAAGCTAAGGCCA	NM_002868	RAB5B	RAB5B, member RAS oncogene family (RAB5B), mRNA	-1.10	0.23	-0.11	0.34	-0.99	0.02
Hs_12plexchip_5_12710	v2HS_243193	ATTCCGGATCACAAATTGAGGG	NM_003929	RAB7L1	RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA	-0.83	0.23	-0.02	0.55	-0.80	0.11
Hs_12plexchip_6_1618	v2HS_115619	ATCAGAACCTTGTCTCTTACCC	NM_016370	RAB9B	RAB9B, member RAS oncogene family (RAB9B), mRNA	-2.64	0.57	-1.05	0.51	-1.59	0.02
Hs_12plexchip_3_8825	v2HS_228604	ATTCTCCAGGAAATGCATTGGT	NM_198829	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1) (RAC1), transcript variant Rac1c, mRNA	-0.80	0.58	0.31	0.11	-1.11	0.08
Hs_12plexchip_6_3778	v2HS_254742	TTTGACCTGCTACTGGAAAGGC	NM_002874	RAD23B	RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA	-1.18	1.22	0.76	2.40	-1.94	0.30
Hs_12plexchip_3_10454	v2HS_143342	TAAGTCCATTGGAAACTGAGGG	NM_001099218	RAD51AP2	RAD51-associated protein 2 (RAD51AP2), mRNA	-1.24	1.02	-0.27	0.38	-0.97	0.24
Hs_12plexchip_2_3053	v2HS_88184	ATATGTGACAATGTTGTTGCCT	NM_015106	RAD54L2	RAD54-like 2 (S. cerevisiae) (RAD54L2), mRNA	-0.94	0.53	0.09	0.62	-1.03	0.10
Hs_12plexchip_2_10317	v2HS_20443	AATGGATATAGGAGCATGTGTA	NM_152442	RAD9B	RAD9 homolog B (S. cerevisiae) (RAD9B), mRNA	-0.89	0.29	-0.15	0.28	-0.74	0.03
Hs_12plexchip_5_3410	v2HS_13044	AAGAGTAGATACATTGTACCCA	NM_000448	RAG1	recombination activating gene 1 (RAG1), mRNA	-0.78	0.88	0.84	0.93	-1.62	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_2_449	v2HS_93554	TTTAAGGGTAGGACTCTTTGGG	NM_000536	RAG2	recombination activating gene 2 (RAG2), mRNA	-1.16	0.21	-0.37	0.31	-0.79	0.03
Hs_12plexchip_4_623	v2HS_66320	ATTAGGGAGGTACCTACAGCGG	NM_001100428	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1 (RAP1GDS1), transcript variant 4, mRNA	-1.18	0.33	-0.19	0.34	-0.99	0.02
Hs_12plexchip_5_579	v2HS_38146	ATTTCGTTGTGGTCAATGAGGG	NM_005312	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1 (RAPGEF1), transcript variant 1, mRNA	-2.14	1.28	-0.42	0.44	-1.72	0.13
Hs_12plexchip_4_1028	v2HS_199986	TTTCACCATAACAATCTCTCCT	NM_014247	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2 (RAPGEF2), mRNA	-1.47	1.16	-0.28	0.91	-1.18	0.24
Hs_12plexchip_6_4142	v2HS_276400	TTTCTCAAAGTTGACGTGTCCA	NM_175062	RASGEF1C	RasGEF domain family, member 1C (RASGEF1C), mRNA	-1.01	0.33	-0.23	0.77	-0.79	0.21
Hs_12plexchip_2_6456	v2HS_179646	ATAATGTAAGGAGTTCTTTCGT	NM_006909	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2 (RASGRF2), mRNA	-1.12	0.32	-0.27	0.40	-0.85	0.05
Hs_12plexchip_2_3771	v2HS_76793	TTTGACTTTGGGAGACAGAGCC	NM_206827	RASL11A	RAS-like, family 11, member A (RASL11A), mRNA	-1.17	0.50	-0.19	0.43	-0.98	0.06
Hs0P00005044	v2HS_94795	ATATTCTTCTTTCGTCTGCGCA	NM_006910	RBBP6	RETINOBLASTOMA BINDING PROTEIN 6	-1.76	0.21	-0.75	0.92	-1.01	0.19
Hs_12plexchip_5_1445	v2HS_247544	TTGTAAATTGTTTGCCATTGCT	NM_184234	RBM39	RNA binding motif protein 39 (RBM39), transcript variant 1, mRNA	-1.64	0.36	0.07	1.45	-1.71	0.17
Hs_12plexchip_6_10160	v2HS_195463	TATCCTGTTCGCCTGTCGAGGT	NM_005105	RBM8A	RNA binding motif protein 8A (RBM8A), mRNA	-4.40	0.15	-0.52	3.15	-3.88	0.17
Hs_12plexchip_5_3595	v2HS_255132	ATGAAACTGAACAGTGGATCGT	NM_015436	RCHY1	ring finger and CHY zinc finger domain containing 1 (RCHY1), transcript variant 1, mRNA	-1.35	1.05	1.41	1.37	-2.76	0.05
Hs_12plexchip_4_6187	v2HS_32989	ATTTAGGGTTCCAAAGACTGGG	NM_002909	REG1A	regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein) (REG1A), mRNA	-0.83	0.43	0.10	0.50	-0.93	0.07
Hs_12plexchip_4_5435	v2HS_19386	TATAAACATTATCAATTGCCCA	NM_173054	RELN	reelin (RELN), transcript variant 2, mRNA	-1.31	0.47	1.81	1.94	-3.13	0.10
Hs_12plexchip_6_7075	v2HS_286133	TTAGATTTCTTGGTTGGGACCC	NM_032579	RETNLB	resistin like beta (RETNLB), mRNA	-1.07	0.65	0.35	1.01	-1.42	0.12
Hs_12plexchip_4_11944	v2HS_32856	GTAGAATTGCAGCACAAGATCA	NM_181558	RFC3	replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 2, mRNA	-1.07	0.74	0.01	0.57	-1.08	0.12
Hs_12plexchip_5_5089	v2HS_261707	ATTAGATACAGACACAATGCCA	NM_181578	RFC5	replication factor C (activator 1) 5, 36.5kDa (RFC5), transcript variant 2, mRNA	-0.91	0.06	0.11	0.36	-1.03	0.04
Hs_12plexchip_5_3694	v2HS_254848	CAAACTCATTGAGTCCTATGGT	NM_006605	RFPL2	ret finger protein-like 2 (RFPL2), transcript variant 1, mRNA	-2.59	0.38	-1.72	0.62	-0.88	0.12
Hs_12plexchip_4_7588	v2HS_191440	AATTGGGTGATGAGTTTCCGGT	NM_032491	RFX4	regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 1, mRNA	-2.14	0.69	-0.64	0.41	-1.50	0.04
Hs_12plexchip_5_8462	v2HS_114554	AATACATATGGTCCTAACTCCT	NM_015668	RGS22	regulator of G-protein signaling 22 (RGS22), mRNA	-1.19	1.03	-0.27	0.48	-0.92	0.26
Hs_12plexchip_5_12799	v2HS_240324	TAGAATGAAGAGACTATAAGCC	NM_003617	RGS5	regulator of G-protein signaling 5 (RGS5), mRNA	-1.50	1.73	0.62	0.67	-2.12	0.16
Hs_12plexchip_4_2121	v2HS_219058	TAGTAAATAAACACTGCCAGCT	NM_017821	RHBDL2	rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), mRNA	-1.84	1.15	1.80	1.29	-3.64	0.02
Hs_12plexchip_5_3401	v2HS_95941	TTAGATTTCGAGAAGTGTACCA	NM_014899	RHOBTB3	Rho-related BTB domain containing 3 (RHOBTB3), mRNA	-0.73	1.18	0.54	0.66	-1.28	0.20
Hs_12plexchip_5_10250	v2HS_96371	TTTCTCCATGAATATGTCGCCT	NM_014989	RIMS1	regulating synaptic membrane exocytosis 1 (RIMS1), mRNA	-1.32	0.67	0.04	0.54	-1.37	0.05
Hs0P00000957	v2HS_117526	TATGGTTCTCATTCTATTTGCC	NM_031480	RIOK1	RIO KINASE 1 (YEAST)	-1.38	0.20	-0.55	0.17	-0.82	0.01
Hs_12plexchip_6_1994	v2HS_226463	TTTGCTAAAGGGATAGCTTGGC	NM_199462	RIPK5	receptor interacting protein kinase 5 (RIPK5), transcript variant 2, mRNA	-1.17	0.58	-0.23	0.99	-0.93	0.25
Hs_12plexchip_6_8571	v2HS_223596	ATATAGTGAAATTCCAAAGCCA	NM_199462	RIPK5	receptor interacting protein kinase 5 (RIPK5), transcript variant 2, mRNA	-0.86	0.11	0.14	0.67	-1.00	0.12
Hs_12plexchip_4_9499	v2HS_43940	TATCTGCATCAAATACTGAGCT	NM_012421	RLF	rearranged L-myc fusion (RLF), mRNA	-1.25	0.77	0.03	0.71	-1.28	0.10
Hs_12plexchip_4_1882	v2HS_214378	CTTGATGCTGAATTTACAGCGG	X04255	RN7SLP5	RNA, 7SL, CYTOPLASMIC, PSEUDOGENE 5	-0.98	0.40	-0.01	0.49	-0.97	0.06
Hs_12plexchip_5_3903	v2HS_14672	ATACAATTCAATGCACACAGCA	NM_194463	RNF128	ring finger protein 128 (RNF128), transcript variant 1, mRNA	-0.87	0.66	-0.07	0.56	-0.80	0.19
Hs_12plexchip_5_3691	v2HS_175587	TTTACTGATGGCTTTCTTGGCT	NM_018434	RNF130	ring finger protein 130 (RNF130), mRNA	-1.07	0.33	-0.33	0.37	-0.74	0.06
Hs_12plexchip_4_10413	v2HS_100984	AAGAATGTTGACGTGTTGCCCG	NM_178841	RNF166	ring finger protein 166 (RNF166), mRNA	-1.45	0.74	0.13	1.41	-1.59	0.18
Hs0P00006251	v2MM_94009	TTTGTTCTCCTCAAGCTCTGCA	NM_019592	RNF20	HYPOTHETICAL PROTEIN FLJ20382	-0.88	0.03	-0.14	0.92	-0.74	0.30
Hs_12plexchip_5_10273	v2HS_95293	TTGTTCTTGAACTGTAGTACCT	NM_014771	RNF40	ring finger protein 40 (RNF40), mRNA	-0.74	0.46	-0.01	0.27	-0.72	0.09
Hs0P00005031	v2HS_95298	TATTCATCACAATTAACAGCCT	NM_014771	RNF40	RING FINGER PROTEIN 40	-1.09	0.54	0.21	0.64	-1.31	0.06
Hs_12plexchip_5_3561	v2HS_51805	TTTCACAAGGAGACCTAAAGGG	AK020527	RNF41	RING FINGER PROTEIN 41	-0.84	0.50	0.55	0.29	-1.39	0.02

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_41	v2HS_221358	ATAGTTTAAGGGATATCTTGCT	AK096543	RP11-506K6.3	HYPOTHETICAL LOC389362	-1.19	0.26	-0.17	0.73	-1.02	0.12
Hs_12plexchip_2_10249	v2HS_32164	TTTAAGAAGAGAAACTCCTGAG	NM_002946	RPA2	replication protein A2, 32kDa (RPA2), mRNA	-2.15	1.08	-0.24	0.96	-1.92	0.08
Hs_12plexchip_4_8497	v2HS_92393	ATTATTTCCGGTAACAACAGCA	NM_001034853	RPGR	retinitis pigmentosa GTPase regulator (RPGR), transcript variant C, mRNA	-0.72	0.28	0.56	0.21	-1.28	0.00
Hs_12plexchip_2_10303	v2HS_15050	GTAACTAGGTACTATGTGTGCT	NM_144563	RPIA	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase) (RPIA), mRNA	-1.20	0.85	-0.37	0.79	-0.83	0.28
Hs_12plexchip_3_9604	v2HS_131580	TTCTTATAGACGTTCCGGACGG	NM_000977	RPL13	ribosomal protein L13 (RPL13), transcript variant 1, mRNA	-2.08	0.96	-1.12	0.92	-0.95	0.28
Hs_12plexchip_4_7518	v2HS_149891	TTCTTGACTTCTTTGATATCCT	NG_001000	RPL24P1	RIBOSOMAL PROTEIN L24 PSEUDOGENE 1	-3.47	0.44	-1.69	2.12	-1.78	0.28
Hs_12plexchip_3_10290	v2HS_236675	TTGTCTGATCATCTTCAGAGTC	NM_000989	RPL30	ribosomal protein L30 (RPL30), mRNA	-3.57	0.28	-1.68	0.86	-1.89	0.05
Hs0P00008958	v2HS_131668	TTGTAGGAAAGCCTACGTCGGT	NM_033625	RPL34	ribosomal protein L34 (RPL34), transcript variant 2, mRNA	-1.25	1.58	0.88	1.72	-2.13	0.19
Hs_12plexchip_4_9155	v2HS_198101	TTAATAACTGTGAGAACACGGG	NM_007209	RPL35	ribosomal protein L35 (RPL35), mRNA	-2.25	0.19	-1.06	0.38	-1.19	0.02
Hs_12plexchip_4_11541	v2HS_189837	ATTAACCCATTTATTACAGGCC	NG_000988	RPL37AP1	RIBOSOMAL PROTEIN L37A PSEUDOGENE 1	-1.72	0.15	-0.78	0.14	-0.94	0.00
Hs0P00011901	v2HS_195073	TTTCAGCTTGATATGGTAACAT	NM_001000	RPL39	ribosomal protein L39 (RPL39), mRNA	-0.93	0.63	-0.19	0.70	-0.75	0.24
Hs_12plexchip_2_10719	v2HS_21538	TTACAACAACAAATATGATGAG	NG_000974	RPL7AL3	RIBOSOMAL PROTEIN L7A-LIKE 3	-0.74	0.43	0.40	0.70	-1.14	0.09
Hs_12plexchip_4_1574	v2HS_209659	TTACACACCAGAACTAACAGCA	NM_183005	RPP38	ribonuclease P/MRP 38kDa subunit (RPP38), transcript variant 1, mRNA	-1.11	0.69	-0.02	0.78	-1.09	0.14
Hs_12plexchip_5_9679	v2HS_269619	ATTTGAAATACTCTTCAATGAC	NM_001016	RPS12	ribosomal protein S12 (RPS12), mRNA	-0.93	0.18	0.38	0.10	-1.31	0.00
Hs_12plexchip_6_8991	v2HS_56919	ATGTGTAGGGCGGTGATACCCA	NM_001025071	RPS14	ribosomal protein S14 (RPS14), transcript variant 1, mRNA	-0.95	0.43	-0.23	0.53	-0.72	0.14
Hs_12plexchip_3_7841	v2HS_232330	AATTCGCTTCATCAGATGCGTG	NM_001021	RPS17	ribosomal protein S17 (RPS17), mRNA	-1.98	0.96	-1.13	0.68	-0.85	0.29
Hs_12plexchip_6_8655	v2HS_267525	ATCTCTTTGTCCCTGAGGTGTC	NM_001022	RPS19	ribosomal protein S19 (RPS19), mRNA	-1.15	1.09	0.17	0.68	-1.32	0.16
Hs_12plexchip_3_6982	v2HS_93855	TTGATAAGTCCTTTACTAAGGA	NM_001028	RPS25	ribosomal protein S25 (RPS25), mRNA	-0.84	0.79	0.22	1.17	-1.05	0.27
Hs_12plexchip_5_1217	v2HS_69321	ATAAGCCAAACCAGTGTCATCT	NM_005444	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1), mRNA	-1.95	0.39	-0.07	0.57	-1.88	0.01
Hs_12plexchip_5_6742	v2HS_242012	ATTGGCTATGGGTACCCAAGGG	NM_001003699	RREB1	ras responsive element binding protein 1 (RREB1), transcript variant 1, mRNA	-0.95	0.35	-0.11	0.14	-0.84	0.04
Hs_12plexchip_3_7921	v2HS_93881	TAATTGTAAGAGAAATCTCGGT	NM_001033	RRM1	ribonucleotide reductase M1 polypeptide (RRM1), mRNA	-2.17	0.14	-1.26	0.39	-0.91	0.04
Hs_12plexchip_6_987	v2HS_93885	TAAATAGTTTCAAAGATCTGCT	NM_001033	RRM1	ribonucleotide reductase M1 polypeptide (RRM1), mRNA	-2.65	1.21	-0.51	2.43	-2.14	0.27
Hs_12plexchip_5_6170	v2HS_267976	ATTGGAAAGATGACAAACCGGC	NM_015713	RRM2B	ribonucleotide reductase M2 B (TP53 inducible) (RRM2B), mRNA	-1.27	0.35	-0.31	0.93	-0.96	0.21
Hs_12plexchip_5_12841	v2HS_37141	AAGGAGGATAAGAGTGTCAGGA	NM_004704	RRP9	RRP9, small subunit (SSU) processome component, homolog (yeast) (RRP9), mRNA	-2.38	0.32	-0.45	1.07	-1.93	0.08
Hs_12plexchip_2_1533	v2HS_87171	TTAAATCCTCAAATAAGTTCTT	NM_015169	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (RRS1), mRNA	-2.19	1.36	-0.93	0.55	-1.26	0.25
Hs_12plexchip_4_10907	v2HS_87174	TAAGTTCTTAATCTCCAAAGTC	NM_015169	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (RRS1), mRNA	-2.08	0.37	-0.33	0.14	-1.75	0.01
Hs_12plexchip_4_11123	v2HS_175228	TTTAAGCCTTATATGCCAGGCT	NM_018364	RSBN1	round spermatid basic protein 1 (RSBN1), mRNA	-1.52	0.56	0.13	0.34	-1.65	0.02
Hs_12plexchip_5_2823	v2HS_212690	TTTGCTGATGATCTCTTGGGCC	NM_014433	RTDR1	rhabdoid tumor deletion region gene 1 (RTDR1), mRNA	-1.74	0.60	-0.74	0.77	-1.00	0.16
Hs_12plexchip_5_6636	v2HS_262563	AACACAATCTGGATAATGTCCG	NM_032957	RTEL1	regulator of telomere elongation helicase 1 (RTEL1), transcript variant 2, mRNA	-1.08	0.40	-0.21	0.37	-0.86	0.05
Hs0P00000698	v2HS_56938	TTCGGCTTTGGCTTTGGATCCG	NM_206900	RTN2	reticulon 2 (RTN2), transcript variant 2, mRNA	-1.84	0.83	-0.18	0.83	-1.66	0.07
Hs_12plexchip_3_8348	v2HS_100563	AACAGGTAGAGGATGGTGAGGC	NM_178570	RTN4RL2	reticulon 4 receptor-like 2 (RTN4RL2), mRNA	-2.44	0.63	-1.51	0.59	-0.93	0.13
Hs_12plexchip_4_12701	v2HS_30012	ATCAGGAATTGGATCAGTAGGC	M15971	RVNP2	RETROVIRAL SEQUENCES NP2	-1.38	0.74	-0.63	0.41	-0.75	0.22
Hs_12plexchip_4_12621	v2HS_239475	TTGGACACCAACTCTGTAAGGA	X66225	RXRG	RETINOID X RECEPTOR GAMMA	-2.10	0.50	-0.85	1.10	-1.25	0.18
Hs_12plexchip_4_869	v2HS_94832	ATGTGTTTAACCAGAGATCCGG	NM_006917	RXRG	retinoid X receptor, gamma (RXRG), transcript variant 1, mRNA	-0.70	0.66	0.17	0.70	-0.87	0.19
Hs_12plexchip_5_7107	v2HS_93897	ATAATTCAGGACGCTCTCTGCT	NM_001035	RYR2	ryanodine receptor 2 (cardiac) (RYR2), mRNA	-0.85	1.10	0.91	0.68	-1.76	0.09
Hs0P00004961	v2HS_64402	TTTAACTATGACATCCCTGGAG	NM_005500	SAE1	SUMO-1 ACTIVATING ENZYME SUBUNIT 1	-1.68	0.14	-0.44	0.22	-1.25	0.00
Hs_12plexchip_6_181	v2HS_55515	TTGAATGAACTGTCACTCCGGA	NM_052837	SCAMP3	secretory carrier membrane protein 3 (SCAMP3), transcript variant 2, mRNA	-2.11	0.65	-1.08	1.08	-1.04	0.24
Hs0P00011554	v2HS_26960	TTCCCTGTGGAGGCGCAGAGGC	NM_145349	SCARF1	scavenger receptor class F, member 1 (SCARF1), transcript variant 2, mRNA	-1.67	0.46	-0.95	0.45	-0.72	0.12

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_10669	v2HS_97596	ATATTCAATGTAGTTGCCTCCT	NM_182835	SCFD1	sec1 family domain containing 1 (SCFD1), transcript variant 2, mRNA	-2.14	0.89	-0.96	0.86	-1.19	0.17
Hs_12plexchip_5_497	v2HS_50441	ATATATATGAGAAGGATCAGCA	NM_152540	SCFD2	sec1 family domain containing 2 (SCFD2), mRNA	-1.08	0.21	0.42	1.10	-1.50	0.14
Hs_12plexchip_5_7041	v2HS_261909	TTAAGACATCTTTGTCTGGGCT	NM_000334	SCN4A	sodium channel, voltage-gated, type IV, alpha subunit (SCN4A), mRNA	-0.85	1.27	0.59	0.56	-1.44	0.18
Hs_12plexchip_5_6806	v2HS_251693	TATACTCTTCCCAATCAAAGCC	NM_014191	SCN8A	sodium channel, voltage gated, type VIII, alpha subunit (SCN8A), mRNA	-0.78	0.14	0.14	0.27	-0.92	0.01
Hs_12plexchip_5_4162	v2HS_259547	TTCCTCCAGTTGATTAATAGCT	NM_006642	SDCCAG8	serologically defined colon cancer antigen 8 (SDCCAG8), mRNA	-1.21	0.40	0.09	0.74	-1.30	0.07
Hs_12plexchip_5_7265	v2HS_265275	TTGTTGATCTTCTTTACTTCCC	NM_183352	SEC13	SEC13 homolog (S. cerevisiae) (SEC13), mRNA	-3.50	0.06	-1.20	0.39	-2.30	0.01
Hs_12plexchip_3_3370	v2HS_41405	ATTCCACTTGGTGTGATGAGCC	NM_174975	SEC14L3	SEC14-like 3 (S. cerevisiae) (SEC14L3), mRNA	-1.55	0.51	-0.26	0.11	-1.29	0.04
Hs_12plexchip_5_9171	v2HS_99249	TTATGATTATCGAACTGAGCCA	NM_001013437	SEH1L	SEH1-like (S. cerevisiae) (SEH1L), transcript variant 1, mRNA	-0.92	0.18	1.22	0.62	-2.14	0.02
Hs_12plexchip_6_5747	v2HS_99250	TTATATTCCAACTCACTCGCCA	NM_001013437	SEH1L	SEH1-like (S. cerevisiae) (SEH1L), transcript variant 1, mRNA	-2.69	0.30	-1.83	0.81	-0.86	0.20
Hs_12plexchip_4_4512	v2HS_175639	TTTCCTTCTTGCATGCTGTCCC	NM_203472	SELS	selenoprotein S (SELS), transcript variant 1, mRNA	-2.03	0.90	-0.99	0.49	-1.04	0.18
Hs_12plexchip_6_10273	v2HS_28047	GTCATCAAATACACATAGAGCT	NM_004263	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F (SEMA4F), mRNA	-1.39	0.52	-0.28	1.08	-1.11	0.21
Hs_12plexchip_6_1170	v2HS_27976	ATTTAGAGTGGAACAATGGCGT	NM_003612	SEMA7A	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group) (SEMA7A), mRNA	-0.77	0.87	0.08	0.57	-0.85	0.24
Hs_12plexchip_5_3489	v2HS_254654	TTTGAGGTAACAATAGTGGCCC	NM_152699	SENP5	SUMO1/sentrin specific peptidase 5 (SENP5), mRNA	-1.74	0.73	-0.80	0.31	-0.95	0.14
Hs_12plexchip_5_10377	v2HS_99499	ATGAGGGTGGATTTCCCTAGGC	NM_052838	SEPT1	septin 1 (SEPT1), mRNA	-0.83	0.40	0.84	1.37	-1.67	0.16
Hs_12plexchip_5_10753	v2HS_145332	AAGTAAAGACACACGTGGACGC	NM_207366	SEPT14	septin 14 (SEPT14), mRNA	-2.03	1.22	-0.31	0.77	-1.73	0.12
Hs0P00003291	v2HS_47661	TTATTTCCTCTGAGTCTCTGGG	NM_080415	SEPT4	septin 4 (SEPT4), transcript variant 2, mRNA	-1.08	0.20	-0.11	0.33	-0.97	0.02
Hs_12plexchip_4_10911	v2HS_200669	ATTCAGTTGTTCTTCCATTCCT	NM_020755	SERINC1	serine incorporator 1 (SERINC1), mRNA	-1.48	1.21	-0.31	0.71	-1.17	0.24
Hs_12plexchip_2_11081	v2HS_43826	GGAAATCAACACTTTCAATCGT	NM_080474	SERPINB12	serpin peptidase inhibitor, clade B (ovalbumin), member 12 (SERPINB12), mRNA	-1.14	0.38	-0.39	0.76	-0.75	0.23
Hs_12plexchip_6_3896	v2HS_169968	AATTGAGTTGTTGATCTGACCT	NM_002639	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5 (SERPINB5), mRNA	-1.48	0.60	-0.13	0.59	-1.35	0.05
Hs0P00004057	v2HS_198275	ATATCTTGTACTTGGGTGTCCT	NM_005877	SF3A1	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA	-1.78	0.50	-0.80	0.41	-0.98	0.06
Hs_12plexchip_3_7330	v2HS_97294	TATATCATACATTTCTTCAGCT	NM_016047	SF3B14	splicing factor 3B, 14 kDa subunit (SF3B14), mRNA	-2.92	0.67	-1.96	0.85	-0.96	0.20
Hs_12plexchip_4_10244	v2HS_97296	ATATGTATCAAAGTTTCAAGCA	NM_016047	SF3B14	splicing factor 3B, 14 kDa subunit (SF3B14), mRNA	-3.56	1.84	-1.76	0.87	-1.80	0.23
Hs_12plexchip_5_12865	v2HS_240572	ATAGGGCTTGAGATTTGTTGGT	NM_005066	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA	-0.99	0.83	-0.12	0.84	-0.87	0.27
Hs_12plexchip_4_365	v2HS_202018	TTATCTACACCAATACATTGGA	NM_001078166	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), transcript variant 2, mRNA	-1.13	0.38	-0.24	0.20	-0.89	0.04
Hs_12plexchip_4_9652	v2HS_23708	ATCAGATCTTCTTGTAGGAGGC	NM_003769	SFRS9	splicing factor, arginine/serine-rich 9 (SFRS9), mRNA	-0.87	1.25	1.18	1.24	-2.05	0.11
Hs_12plexchip_5_8825	v2HS_225440	TTGGTGTTTAACCTAATGGGCT	NM_178858	SFXN2	sideroflexin 2 (SFXN2), mRNA	-0.90	0.21	0.53	0.24	-1.43	0.00
Hs_12plexchip_4_495	v2HS_202269	ATAAGACTCAATGTCCAGTCCT	NM_024776	SGK269	NKF3 kinase family member (SGK269), mRNA	-1.72	0.12	-0.54	0.74	-1.18	0.11
Hs_12plexchip_4_7273	v2HS_53458	ATATACAAAGGAACATGGTGGT	NM_147156	SGMS1	sphingomyelin synthase 1 (SGMS1), mRNA	-0.74	0.47	0.02	0.39	-0.76	0.10
Hs_12plexchip_6_8658	v2HS_68216	TACCAATAGCAGGTGAAGGGCG	NM_005490	SH2D3A	SH2 domain containing 3A (SH2D3A), mRNA	-1.30	0.52	0.02	0.85	-1.32	0.10
Hs_12plexchip_3_8888	v2HS_230983	ATAATCATAGAGAACCCTGGCC	NM_016009	SH3GLB1	SH3-domain GRB2-like endophilin B1 (SH3GLB1), mRNA	-1.51	0.28	-0.58	0.76	-0.92	0.16
Hs_12plexchip_5_11115	v2HS_141439	TTCATCAATTGGTATCAGGCGT	NM_001017995	SH3PXD2B	SH3 and PX domains 2B (SH3PXD2B), mRNA	-1.38	0.13	0.75	0.19	-2.13	0.00
Hs_12plexchip_3_11364	v2HS_136410	ATAGGAAGAGACATCCCTTGGG	NM_024577	SH3TC2	SH3 domain and tetratricopeptide repeats 2 (SH3TC2), mRNA	-1.26	0.24	-0.45	0.09	-0.81	0.02

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_12275	v2HS_32047	TACATTCATCACAGTTGCTGGG	NM_001010846	SHE	Src homology 2 domain containing E (SHE), mRNA	-1.93	0.46	-0.97	0.79	-0.96	0.16
Hs0P00010492	v2HS_33286	ATTATCCTCCCAGACATGTGCA	NM_006304	SHFM1	split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA	-1.61	0.21	-0.46	0.48	-1.15	0.04
Hs_12plexchip_5_3317	v2HS_195697	TTTCTCATCCAGCATTCGGCCC	NM_138392	SHKBP1	SH3KBP1 binding protein 1 (SHKBP1), mRNA	-2.85	0.90	-1.05	1.04	-1.80	0.09
Hs_12plexchip_3_1044	v2HS_41530	ATTTCTCTGGCATTCTTCTCGG	NM_080792	SIRPA	signal-regulatory protein alpha (SIRPA), transcript variant 3, mRNA	-0.91	0.55	0.62	0.33	-1.53	0.02
Hs_12plexchip_4_4718	v2HS_202737	ATACAATTGACTTGCTGCTGCA	NM_170679	SKP1	S-phase kinase-associated protein 1 (SKP1), transcript variant 2, mRNA	-2.85	0.46	-1.38	1.33	-1.47	0.19
Hs_12plexchip_3_6246	v2HS_111725	TTAGAGATGCTTACCGTATGCC	NM_000617	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2), mRNA	-1.76	0.47	-0.61	0.60	-1.15	0.06
Hs_12plexchip_3_11403	v2HS_238406	TTAAGCATAGAGGACACTTGGC	NM_016582	SLC15A3	solute carrier family 15, member 3 (SLC15A3), mRNA	-1.35	0.33	-0.38	0.29	-0.98	0.02
Hs_12plexchip_6_1259	v2HS_243817	TTTCTGAAAGGAGATGGGAGCT	NM_020309	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (SLC17A7), mRNA	-0.90	0.37	0.06	0.57	-0.97	0.08
Hs_12plexchip_3_7924	v2HS_231081	TTGGGAATGAAATCTGTCACCG	NM_021977	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3 (SLC22A3), mRNA	-0.83	0.32	0.26	0.15	-1.09	0.01
Hs_12plexchip_5_2605	v2HS_253085	TAGATGACAAACACTATGGCCA	NM_005984	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1), mRNA	-1.65	0.09	-0.65	0.28	-0.99	0.02
Hs_12plexchip_4_962	v2HS_201867	TTAACATCAAATGGACAGGGCC	NM_031947	SLC25A2	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 2 (SLC25A2), nuclear gene encoding mitochondrial protein, mRNA	-0.97	0.47	0.01	0.37	-0.98	0.05
Hs_12plexchip_5_6278	v2HS_160463	TAGAATTATAACCATCTTGCCT	NM_173471	SLC25A26	solute carrier family 25, member 26 (SLC25A26), mRNA	-0.93	0.12	0.09	0.79	-1.02	0.15
Hs_12plexchip_3_8816	v2HS_99234	ATAGGTCATGAAGTGAATGGCT	NM_031212	SLC25A28	solute carrier family 25, member 28 (SLC25A28), mRNA	-1.28	0.72	-0.36	0.23	-0.92	0.15
Hs_12plexchip_5_8328	v2HS_266973	TAAATATCCGTGTCTGGCACCT	NM_001040454	SLC26A6	solute carrier family 26, member 6 (SLC26A6), transcript variant 4, mRNA	-1.40	0.80	-0.26	0.39	-1.14	0.12
Hs_12plexchip_3_8966	v2HS_92464	ATTGAGTATGAGATTGTGGGCA	NM_000340	SLC2A2	solute carrier family 2 (facilitated glucose transporter), member 2 (SLC2A2), mRNA	-2.49	0.45	-1.54	0.57	-0.95	0.09
Hs_12plexchip_6_3900	v2HS_172347	ATGGTAAGTGAGCGTAAGGGCC	NM_003459	SLC30A3	solute carrier family 30 (zinc transporter), member 3 (SLC30A3), mRNA	-1.01	0.93	0.29	0.28	-1.30	0.13
Hs_12plexchip_6_2538	v2HS_234764	ATAGTTGGCACAAGGATGACCA	NM_018018	SLC38A4	solute carrier family 38, member 4 (SLC38A4), mRNA	-0.71	1.84	0.88	0.84	-1.59	0.27
Hs_12plexchip_2_5062	v2HS_177602	AATGTAGAGAAATGCCTCAGGC	NM_032803	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (SLC7A3), transcript variant 1, mRNA	-1.24	0.92	-0.18	0.29	-1.06	0.17
Hs_12plexchip_6_3523	v2HS_172487	TTGAGGGATGAGATTCGTACCA	NM_003486	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA	-2.17	0.74	-1.12	0.54	-1.05	0.13
Hs_12plexchip_3_11150	v2HS_238776	TTCAGGATGAGCACTTTGAGCT	NM_032539	SLITRK2	SLIT and NTRK-like family, member 2 (SLITRK2), mRNA	-1.58	0.39	0.16	0.78	-1.74	0.04
Hs_12plexchip_2_12060	v2HS_216620	TTGGAGAATTAGCCTGTTCCAC	NM_006425	SLU7	SLU7 splicing factor homolog (S. cerevisiae) (SLU7), mRNA	-1.22	0.64	-0.31	0.25	-0.91	0.12
Hs_12plexchip_5_2833	v2HS_250915	ATCTCATTTATAATACACTCCT	NM_006425	SLU7	SLU7 splicing factor homolog (S. cerevisiae) (SLU7), mRNA	-1.15	0.41	-0.21	0.53	-0.94	0.08
Hs_12plexchip_4_610	v2HS_68088	TTTCAACTTAATACTAAGTGCA	NM_001002800	SMC4	structural maintenance of chromosomes 4 (SMC4), transcript variant 2, mRNA	-1.54	0.38	-0.74	0.07	-0.81	0.06
Hs_12plexchip_4_7961	v2HS_92490	ATTAGCTACTTCACAGATTGGG	NM_000344	SMN1	survival of motor neuron 1, telomeric (SMN1), transcript variant d, mRNA	-1.38	1.10	-0.42	0.22	-0.97	0.26
Hs_12plexchip_5_3234	v2HS_98265	AATTTCTATGTCGTTGTGACCT	NM_022739	SMURF2	SMAD specific E3 ubiquitin protein ligase 2 (SMURF2), mRNA	-1.01	1.06	0.26	1.45	-1.27	0.29
Hs_12plexchip_4_9947	v2HS_16985	TAAATGATAAAGAAGAACAGCA	NM_130798	SNAP23	synaptosomal-associated protein, 23kDa (SNAP23), transcript variant 2, mRNA	-1.12	0.08	0.24	0.43	-1.36	0.03
Hs_12plexchip_6_8448	v2HS_153275	TTCCTTGTTGAAATGCAGCCGT	NM_003093	SNRPC	small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA	-2.23	1.47	0.02	2.47	-2.26	0.26

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_1666	v2HS_228001	TAGAAACAATGCAAGCTGGGCA	NM_022808	SNRPN	small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 5, mRNA	-1.79	0.89	0.25	0.45	-2.05	0.04
Hs_12plexchip_6_10461	v2HS_84743	TTTGAGAGGGATGATCTTCCTG	NM_006750	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2) (SNTB2), mRNA	-1.15	0.40	-0.34	0.15	-0.81	0.06
Hs_12plexchip_5_12441	v2HS_252521	TAGAATCGGAAATCAGTCTGGC	NM_001042588	SNUPN	snurportin 1 (SNUPN), transcript variant 3, mRNA	-2.21	1.65	-0.43	1.18	-1.78	0.21
Hs_12plexchip_4_9555	v2HS_19895	TTTACTGGGCCTATAAATACTC	NM_012245	SNW1	SNW domain containing 1 (SNW1), mRNA	-1.38	0.33	0.46	0.22	-1.84	0.00
Hs_12plexchip_6_1153	v2HS_247594	TAAGGCAAACTTGTGAATTGCT	NM_013322	SNX10	sorting nexin 10 (SNX10), mRNA	-1.15	0.47	-0.15	0.87	-1.00	0.18
Hs_12plexchip_4_12266	v2HS_153307	TTTCTTCAAACCATGCATCCGA	NM_003100	SNX2	sorting nexin 2 (SNX2), mRNA	-1.22	0.18	-0.02	0.52	-1.20	0.05
Hs_12plexchip_4_9656	v2HS_53158	GTATAGCATGATATTCTTGTCT	NM_003877	SOCS2	suppressor of cytokine signaling 2 (SOCS2), mRNA	-0.83	0.71	0.38	0.95	-1.21	0.16
Hs_12plexchip_6_10325	v2HS_153362	ATAGGTTGGCCTACAATTTGCA	NM_003112	SP4	Sp4 transcription factor (SP4), mRNA	-1.52	1.52	0.13	0.44	-1.65	0.20
Hs_12plexchip_4_157	v2HS_96222	TTTAGTTCTCGGATAGGACCCA	NM_199436	SPAST	spastin (SPAST), transcript variant 2, mRNA	-1.87	0.20	0.32	1.06	-2.20	0.07
Hs_12plexchip_5_3220	v2HS_210161	TAAATGCCTGATATATGCCCGA	NM_138796	SPATA17	spermatogenesis associated 17 (SPATA17), mRNA	-1.82	0.50	-0.23	0.67	-1.59	0.03
Hs_12plexchip_5_10248	v2HS_101426	TTTGAAATGGATCTGACCACGG	AK075287	SPBC24	SPINDLE POLE BODY COMPONENT 24 HOMOLOG (S. CEREVISIAE)	-4.22	1.52	-1.85	1.56	-2.36	0.13
Hs_12plexchip_5_967	v2HS_65137	TTATTGTGTAACTTGACAGCCC	NM_001033554	SPECC1	sperm antigen with calponin homology and coiled-coil domains 1 (SPECC1), transcript variant NSP5alpha3alpha, mRNA	-0.94	0.21	-0.22	0.81	-0.72	0.26
Hs_12plexchip_4_653	v2HS_200998	TAATGGTTCAAGGAAGCTGCCA	NM_021972	SPHK1	sphingosine kinase 1 (SPHK1), transcript variant 1, mRNA	-1.00	0.48	-0.17	0.30	-0.83	0.07
Hs_12plexchip_3_2439	v2HS_66993	TACTGAGAGCAGTTTGGCGTTC	NM_021114	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor) (SPINK2), mRNA	-0.87	0.81	0.92	2.24	-1.80	0.30
Hs_12plexchip_3_3362	v2HS_51341	TTCTCATAGAAGGTGCAGTTCC	NM_001077238	SPPL2B	signal peptide peptidase-like 2B (SPPL2B), transcript variant 3, mRNA	-1.10	0.36	-0.27	0.72	-0.82	0.18
Hs_12plexchip_4_9926	v2HS_197602	ATAGTCAATCACGTTCTGGGCC	NM_005842	SPRY2	sprouty homolog 2 (Drosophila) (SPRY2), mRNA	-1.29	1.18	-0.32	0.38	-0.97	0.29
Hs_12plexchip_3_10829	v2HS_234466	TAAGGAAACTCTCCCGGAGGGC	NM_016642	SPTBN5	spectrin, beta, non-erythrocytic 5 (SPTBN5), mRNA	-1.04	0.42	0.14	0.37	-1.17	0.02
Hs_12plexchip_5_1865	v2HS_213472	TTTGCTTTCAACTTTGGGAGGT	NM_194285	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae) (SPTY2D1), mRNA	-1.05	0.46	0.03	0.31	-1.08	0.03
Hs_12plexchip_3_2641	v2HS_65728	TATCGGTAGGAGATCTTCTCGT	NM_021199	SQRDL	sulfide quinone reductase-like (yeast) (SQRDL), mRNA	-0.72	0.63	0.00	0.13	-0.72	0.18
Hs_12plexchip_3_447	v2HS_47985	TTGTTCTTACAAATGGAGGGCA	NM_003900	SQSTM1	sequestosome 1 (SQSTM1), mRNA	-1.25	0.60	-0.54	0.66	-0.71	0.24
Hs_12plexchip_6_9192	v2HS_269798	ATATTGATAACAGGTACAGGCT	NM_001047	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA	-0.77	0.66	0.53	0.56	-1.30	0.06
Hs_12plexchip_3_10491	v2HS_136503	ATATCTTCAGATACTTTCTGCT	NM_024592	SRD5A3	steroid 5 alpha-reductase 3 (SRD5A3), mRNA	-1.38	0.19	-0.49	0.51	-0.89	0.08
Hs_12plexchip_3_3437	v2HS_47125	TTCACCAAGGACTCTATAGCTC	NM_004599	SREBF2	sterol regulatory element binding transcription factor 2 (SREBF2), mRNA	-1.02	0.30	-0.09	0.62	-0.92	0.11
Hs_12plexchip_3_3045	v2HS_58606	ATGTTGGCTGACTTGATGACCT	NM_080823	SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites (SRMS), mRNA	-1.63	0.94	-0.87	0.27	-0.76	0.29
Hs_12plexchip_2_7909	v2HS_153496	TTTAGCATAGCATTCAATACCT	NM_003136	SRP54	signal recognition particle 54kDa (SRP54), mRNA	-0.77	0.63	0.08	0.51	-0.85	0.15
Hs_12plexchip_4_519	v2HS_197188	ATCAATGAGCTGGACAATGGTC	NM_014370	SRPK3	SFRS protein kinase 3 (SRPK3), mRNA	-0.89	0.43	-0.14	0.75	-0.75	0.22
Hs_12plexchip_2_3607	v2HS_73263	ATGACAAACCAGGCTCTTGCAT	NM_021947	SRR	serine racemase (SRR), mRNA	-1.99	0.85	-0.79	0.83	-1.20	0.15
Hs_12plexchip_5_840	v2HS_65291	ATTGAACTGGAGAAACTGAGGC	NM_080725	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae) (SRXN1), mRNA	-0.84	0.65	0.39	0.50	-1.23	0.06
Hs_12plexchip_5_12632	v2HS_214513	TTTGATACACAAATTCCATGCC	NM_007107	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma) (SSR3), mRNA	-1.12	0.25	-0.23	0.53	-0.88	0.09
Hs_12plexchip_4_835	v2HS_137870	AATCATGTCCATAGTTTCAGCC	NM_030965	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5 (ST6GALNAC5), mRNA	-0.85	0.66	0.43	0.34	-1.28	0.06
Hs_12plexchip_4_10510	v2HS_175479	ATAGTAAGTAAGAGGCTCTCGT	NM_021908	ST7	suppression of tumorigenicity 7 (ST7), transcript variant b, mRNA	-0.78	0.24	0.23	0.69	-1.01	0.11
Hs_12plexchip_3_3929	v2HS_40842	ATCTGGAAAGGCACTGAGGTTC	NM_015879	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 (ST8SIA3), mRNA	-0.98	0.48	0.00	0.18	-0.98	0.06

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_9855	v2HS_92520	TTTCCGATCTTCTGCAGGACCT	NM_000349	STAR	steroidogenic acute regulatory protein (STAR), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA	-0.70	0.28	0.04	0.05	-0.73	0.04
Hs_12plexchip_2_5453	v2HS_182540	ATTTATTACGGTTATCTTCGCT	NM_006645	STARD10	StAR-related lipid transfer (START) domain containing 10 (STARD10), mRNA	-0.76	0.57	0.30	0.82	-1.06	0.15
Hs0P00001673	v2HS_63989	TTCATATTTCCTTCGTAGCGCT	NM_139171	STARD6	StAR-related lipid transfer (START) domain containing 6 (STARD6), mRNA	-0.70	0.29	0.09	0.50	-0.78	0.09
Hs_12plexchip_4_1657	v2HS_51744	TTTAATCTCCATATTCTTGGCT	NM_020151	STARD7	StAR-related lipid transfer (START) domain containing 7 (STARD7), mRNA	-2.05	0.34	-0.67	1.17	-1.38	0.17
Hs_12plexchip_5_12291	v2HS_86641	CATCTTCTTGAGTAACAGCTGT	NM_007315	STAT1	signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant alpha, mRNA	-0.83	0.11	0.09	0.35	-0.93	0.03
Hs_12plexchip_5_6109	v2HS_257485	TTTGGATACAGATACTTCAGGG	NM_007315	STAT1	signal transducer and activator of transcription 1, 91kDa (STAT1), transcript variant alpha, mRNA	-0.86	0.78	1.14	0.67	-2.00	0.03
Hs_12plexchip_5_2673	v2HS_207632	TTAAGAGTCCAATTAGAAACAC	NM_014393	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila) (STAU2), mRNA	-1.10	0.06	-0.17	0.08	-0.93	0.00
Hs_12plexchip_4_10862	v2HS_200978	TGAATGATCCACCTTGTCTCAT	NM_030906	STK33	serine/threonine kinase 33 (STK33), mRNA	-0.79	0.88	0.38	0.84	-1.17	0.17
Hs_12plexchip_3_12227	v2HS_242448	TTATTTGGAAGCTTCTTGTGGT	NM_145286	STOML3	stomatin (EPB72)-like 3 (STOML3), mRNA	-0.77	0.67	-0.07	0.67	-0.70	0.27
Hs_12plexchip_5_11897	v2HS_133518	TTAGCATAAGAGGGATCCAGCA	NM_152713	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) (STT3A), mRNA	-1.10	0.11	0.00	0.17	-1.10	0.00
Hs_12plexchip_5_9442	v2HS_94011	TTCTGGAGCCTCTTGGTCAGGC	NM_001054	SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2 (SULT1A2), transcript variant 1, mRNA	-0.80	0.19	0.19	1.10	-0.99	0.26
Hs_12plexchip_5_2336	v2HS_207077	TTTAGGAAGAAGATCAGTCGGT	NM_014465	SULT1B1	sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA	-0.85	0.12	-0.13	0.26	-0.71	0.03
Hs_12plexchip_6_8736	v2HS_217410	ATCATTCATAAACCTCCGGCAG	NM_014351	SULT4A1	sulfotransferase family 4A, member 1 (SULT4A1), mRNA	-0.81	0.31	0.85	0.44	-1.66	0.01
Hs_12plexchip_5_2353	v2HS_209161	TTAGGGTTTCGAAATATCACCA	NM_001032377	SULT6B1	sulfotransferase family, cytosolic, 6B, member 1 (SULT6B1), mRNA	-1.13	0.93	-0.04	0.90	-1.09	0.22
Hs_12plexchip_5_7120	v2HS_262274	TTAAGTACACATATACTAAGCT	NM_024670	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila) (SUV39H2), mRNA	-1.95	0.14	0.14	0.36	-2.08	0.00
Hs_12plexchip_3_8127	v2HS_97193	TATTGATAACAGGAGCAGGCGC	NM_016028	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila) (SUV420H1), transcript variant 2, mRNA	-1.44	0.67	-0.48	0.29	-0.96	0.12
Hs_12plexchip_5_4015	v2HS_74301	TAAGATTAAAGTCATGCATGCT	NM_015355	SUZ12	suppressor of zeste 12 homolog (Drosophila) (SUZ12), mRNA	-0.84	0.80	1.06	1.19	-1.91	0.09
Hs_12plexchip_3_11332	v2HS_237459	TTTAAGCATGGGTTTGACTGGC	NM_153366	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 (SVEP1), mRNA	-1.52	0.48	-0.69	0.84	-0.83	0.23
Hs_12plexchip_2_4682	v2HS_183183	ATGGGACAGCAAGGGAAGAGGG	NM_001040709	SYPL2	synaptophysin-like 2 (SYPL2), mRNA	-1.00	0.21	0.05	0.23	-1.05	0.00
Hs_12plexchip_5_715	v2HS_244554	ATACAGTCTAAACCGAACTGCA	NM_153262	SYT14	synaptotagmin XIV (SYT14), mRNA	-2.85	1.34	-0.85	0.89	-2.01	0.11
Hs_12plexchip_6_6223	v2HS_274283	ATGTATCCCGATGCCAAATGGA	NM_206930	SYTL2	synaptotagmin-like 2 (SYTL2), transcript variant f, mRNA	-1.04	0.18	0.16	0.73	-1.20	0.10
Hs_12plexchip_3_3711	v2HS_42673	ATAAATCTTGAGACAGCGTCCA	NM_004606	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa (TAF1), transcript variant 1, mRNA	-0.72	0.43	0.13	0.75	-0.85	0.18
Hs_12plexchip_6_353	v2HS_56338	AACCCTTTACAAATCCTGCTAA	NM_005644	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa (TAF12), mRNA	-0.76	0.32	0.44	1.00	-1.20	0.17
Hs_12plexchip_4_8915	v2HS_172494	AACAGTCATCAGTATGGTCGGT	NM_003487	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa (TAF15), transcript variant 2, mRNA	-2.29	0.93	-1.12	1.20	-1.17	0.26
Hs_12plexchip_4_9828	v2HS_94996	TATCCCAAAGAAGCACTCTGCC	NM_006951	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa (TAF5), mRNA	-2.33	0.55	-1.37	0.51	-0.96	0.09
Hs_12plexchip_4_9448	v2HS_56318	ATAGAAGTAAAGCTCCCGGCCC	NM_139315	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa (TAF6), transcript variant 2, mRNA	-0.79	0.21	0.02	0.58	-0.81	0.12
Hs_12plexchip_5_6208	v2HS_261946	ATATTTGTGAAGTGACACTCGT	NM_020791	TAOK1	TAO kinase 1 (TAOK1), mRNA	-0.76	0.21	0.05	0.42	-0.81	0.06

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_6455	v2HS_202996	TTTAGACTTCAAACTCTTAGGC	NM_020791	TAOK1	TAO kinase 1 (TAOK1), mRNA	-1.03	0.72	0.74	1.39	-1.77	0.15
Hs_12plexchip_6_10176	v2HS_93598	TTATAGCGACAGACTTCATGCT	NM_018833	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) (TAP2), transcript variant 2, mRNA	-0.72	0.99	0.82	1.09	-1.55	0.14
Hs_12plexchip_5_1955	v2HS_206836	ATAGATTAGCACTTACCAGGCC	AY114096	TAS2R62P	TASTE RECEPTOR, TYPE 2, MEMBER 62 PSEUDOGENE	-1.57	0.19	-0.52	0.16	-1.04	0.00
Hs_12plexchip_5_3709	v2HS_255072	TTTAAGGTGGAATTGCTCAGCT	NM_015173	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1), mRNA	-0.90	0.58	0.21	1.01	-1.11	0.19
Hs_12plexchip_6_9376	v2HS_211591	TAAACCTGTGAGAACCTGCTGG	NM_005993	TBCD	tubulin folding cofactor D (TBCD), mRNA	-2.24	0.50	0.50	0.60	-2.74	0.00
Hs_12plexchip_6_6539	v2HS_286944	ATTTGTCCCAAAGCTCCTTGGT	NM_020417	TBX20	T-box 20 (TBX20), transcript variant 2, mRNA	-1.06	0.82	0.15	1.28	-1.21	0.25
Hs_12plexchip_6_8852	v2HS_153809	TTAAGTACTCGGATGCATTGCT	NM_003198	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A) (TCEB3), mRNA	-2.18	0.27	-0.42	1.24	-1.76	0.13
Hs_12plexchip_2_2587	v2HS_85843	TTGCTGAATAACCTTAACTCCA	NM_006706	TCERG1	transcription elongation regulator 1 (TCERG1), transcript variant 1, mRNA	-1.50	0.12	-0.60	1.00	-0.90	0.26
Hs_12plexchip_2_8818	v2HS_32488	TTTGATAATCCTTGGAGTTCCT	NM_001008536	TCHHL1	trichohyalin-like 1 (TCHHL1), mRNA	-1.48	0.91	-0.75	0.17	-0.73	0.30
Hs_12plexchip_5_7121	v2HS_262360	TAGTTCCAACCCATGGTGGGCA	NM_001008656	TCOF1	Treacher Collins-Franceschetti syndrome 1 (TCOF1), transcript variant 1, mRNA	-3.18	0.81	-1.01	1.16	-2.17	0.06
Hs_12plexchip_5_7990	v2HS_120432	ATTCCACTCGAAATTCATGCCG	NM_182539	TCTE1	t-complex-associated-testis-expressed 1 (TCTE1), mRNA	-1.27	0.63	-0.43	0.17	-0.84	0.14
Hs0P00004203	v2HS_42514	TTGTGAATTGACTCTCTCAGTC	NM_174910	TCTE3	t-complex-associated-testis-expressed 3 (TCTE3), mRNA	-0.73	0.14	0.22	0.49	-0.95	0.07
Hs_12plexchip_4_2910	v2HS_174999	TTTGTTTCAGAGAGATCGTGCT	NM_001008744	TDP1	tyrosyl-DNA phosphodiesterase 1 (TDP1), transcript variant 2, mRNA	-1.77	0.80	-0.51	1.57	-1.26	0.30
Hs_12plexchip_6_3289	v2HS_175002	ATATGGCACAGGAAAGGTGGCC	NM_001008744	TDP1	tyrosyl-DNA phosphodiesterase 1 (TDP1), transcript variant 2, mRNA	-1.27	0.68	-0.44	0.21	-0.83	0.16
Hs_12plexchip_5_4712	v2HS_72674	TATAGCCCTAGTTATAGCAGGT	NM_021961	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor) (TEAD1), mRNA	-0.88	1.25	0.47	0.99	-1.35	0.22
Hs_12plexchip_2_9032	v2HS_32310	TTCAACTTGGACTGGATTTCCC	NM_003598	TEAD2	TEA domain family member 2 (TEAD2), mRNA	-1.01	0.14	0.09	0.46	-1.09	0.05
Hs_12plexchip_4_8769	v2HS_153885	TAAAGAGGAGACACATCGAGCC	NM_003216	TEF	thyrotrophic embryonic factor (TEF), mRNA	-1.27	1.01	-0.26	0.89	-1.01	0.27
Hs_12plexchip_5_4898	v2HS_87448	GTAATTGGTCTAATAATTCCCT	NM_022366	TFB2M	transcription factor B2, mitochondrial (TFB2M), mRNA	-2.38	0.87	-1.27	1.28	-1.11	0.29
Hs_12plexchip_2_1857	v2HS_86331	TAAGTCCATCCAAGAGGGCCTG	NM_014553	TFCP2L1	transcription factor CP2-like 1 (TFCP2L1), mRNA	-0.80	0.18	0.11	0.20	-0.91	0.00
Hs_12plexchip_5_4816	v2HS_256721	TAAACTGATTAGGGTCTTTGCC	NM_021809	TGIF2	TGFB-induced factor homeobox 2 (TGIF2), mRNA	-1.85	1.01	0.39	0.68	-2.24	0.04
Hs_12plexchip_3_1335	v2HS_51937	AATTATGCTGATACTCAACTGT	NM_020147	THAP10	THAP domain containing 10 (THAP10), mRNA	-0.76	0.15	0.05	0.51	-0.82	0.10
Hs_12plexchip_4_160	v2HS_49799	ATAGCAAGAGAAATAATAGCTA	NM_005131	THOC1	THO complex 1 (THOC1), mRNA	-1.35	0.54	-0.11	0.45	-1.24	0.04
Hs0P00008263	v2HS_136850	TAATGTCTCATGCCTGTCTGGA	NM_025075	THOC7	THO complex 7 homolog (Drosophila) (THOC7), mRNA	-0.84	0.36	-0.04	0.58	-0.80	0.13
Hs_12plexchip_4_12280	v2HS_239298	ATCTAGAACCAAGTCCATGGCC	NM_003250	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian) (THRA), transcript variant 2, mRNA	-1.82	0.51	-1.02	0.72	-0.80	0.20
Hs_12plexchip_6_8515	v2HS_154053	TATTTCCTTGTCACCTCCTGGG	NM_003251	THRSP	thyroid hormone responsive (SPOT14 homolog, rat) (THRSP), mRNA	-0.77	0.12	0.12	0.80	-0.89	0.19
Hs_12plexchip_5_945	v2HS_248909	TTGAACTGTAAGGTGTGTGGCG	NM_013337	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22), mRNA	-1.33	0.17	0.04	0.75	-1.37	0.08
Hs_12plexchip_6_9575	v2HS_243560	AACAAGTCTCAGGATTGGTCCG	NM_004614	TK2	thymidine kinase 2, mitochondrial (TK2), mRNA	-1.33	0.54	-0.22	0.28	-1.11	0.05
Hs_12plexchip_2_9996	v2HS_20095	TTACTGAATAATCTTGCTGTCT	NM_152453	TMCO5	transmembrane and coiled-coil domains 5 (TMCO5), mRNA	-0.70	0.34	0.34	0.26	-1.04	0.02
Hs_12plexchip_5_4550	v2HS_261717	ATAGACTTTCTCAACATTTGCT	NM_006827	TMED10	transmembrane emp24-like trafficking protein 10 (yeast) (TMED10), mRNA	-1.32	0.51	0.74	0.61	-2.06	0.01
Hs_12plexchip_3_8402	v2HS_233295	TAGTAATAGCCCTCCAAAGGCA	AK095650	TMED8	TRANSMEMBRANE EMP24 PROTEIN TRANSPORT DOMAIN CONTAINING 8	-0.84	0.32	0.18	0.48	-1.02	0.04
Hs_12plexchip_2_300	v2HS_100302	TAACAGGATTCCAGGTCCAGTT	NM_178518	TMEM102	transmembrane protein 102 (TMEM102), mRNA	-1.18	1.60	0.14	0.78	-1.31	0.29

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_7645	v2HS_226022	TTTATTCTTCACATCATGTGCC	NM_024092	TMEM109	transmembrane protein 109 (TMEM109), mRNA	-0.93	0.24	-0.08	0.66	-0.85	0.14
Hs0P00009636	v2HS_138173	ATAGTCTGTAATGATATATGCT	NM_032256	TMEM117	transmembrane protein 117 (TMEM117), mRNA	-0.97	0.66	1.68	0.40	-2.65	0.01
Hs_12plexchip_5_11148	v2HS_138271	TAAGATGTTCCCTTTGTGTGGT	NM_032273	TMEM126A	transmembrane protein 126A (TMEM126A), mRNA	-2.07	1.20	-0.66	0.52	-1.41	0.17
Hs_12plexchip_2_656	v2HS_116379	AATACATGGAAATTGTTGTGCT	NM_022918	TMEM135	transmembrane protein 135 (TMEM135), mRNA	-1.66	0.27	-0.79	0.51	-0.87	0.08
Hs_12plexchip_6_6601	v2HS_39455	TTTGCCCTAAAGGAAGTGAGGG	NM_001031738	TMEM150	transmembrane protein 150 (TMEM150), transcript variant 1, mRNA	-0.74	0.45	0.08	0.81	-0.82	0.22
Hs_12plexchip_4_2516	v2HS_181968	TTGGAATTTCAGAGTGAGAGCA	NM_198276	TMEM17	transmembrane protein 17 (TMEM17), mRNA	-0.90	0.49	-0.16	0.73	-0.74	0.23
Hs_12plexchip_5_9298	v2HS_99077	TAGGGTAAATGTTTGATTCGGA	NM_001105199	TMEM177	transmembrane protein 177 (TMEM177), transcript variant 3, mRNA	-1.43	0.61	0.21	0.62	-1.64	0.03
Hs_12plexchip_5_11856	v2HS_245873	TATCTTATCAGGCAGCCGGGCT	NM_001097620	TMEM184A	transmembrane protein 184A (TMEM184A), mRNA	-0.82	0.15	0.05	0.70	-0.87	0.16
Hs_12plexchip_6_2084	v2HS_156668	ATGTATACCCAAAGTTTAACCC	NM_018279	TMEM19	transmembrane protein 19 (TMEM19), mRNA	-1.22	0.19	0.49	1.19	-1.71	0.13
Hs_12plexchip_6_5231	v2HS_158438	AATGAGACAATAATAATCAGGT	NM_025246	TMEM22	transmembrane protein 22 (TMEM22), transcript variant 1, mRNA	-1.61	0.41	-0.64	0.41	-0.97	0.04
Hs_12plexchip_3_2291	v2HS_72413	TTTAACAAGCATGTTCTCCCTC	NM_001017970	TMEM30B	transmembrane protein 30B (TMEM30B), mRNA	-1.28	0.13	-0.18	0.80	-1.10	0.14
Hs_12plexchip_6_9408	v2HS_155633	ATAAATGAGTGCATGAGTTGCT	NM_018087	TMEM48	transmembrane protein 48 (TMEM48), mRNA	-2.78	0.17	-0.48	0.57	-2.30	0.01
Hs_12plexchip_6_6716	v2HS_137756	TTAGGGTTGCACCAAAGAAGGT	NM_030938	TMEM49	transmembrane protein 49 (TMEM49), mRNA	-1.32	0.18	-0.30	0.27	-1.02	0.01
Hs_12plexchip_6_11346	v2HS_222241	TTCCTCCGTAGGGTATGCAGGT	NM_182532	TMEM61	transmembrane protein 61 (TMEM61), mRNA	-0.90	1.32	0.38	0.70	-1.28	0.23
Hs_12plexchip_4_4033	v2HS_179359	TAGTAGGTGGTCATGATCACCA	NM_173804	TMEM86B	transmembrane protein 86B (TMEM86B), mRNA	-0.99	0.44	-0.29	0.67	-0.71	0.21
Hs_12plexchip_5_76	v2HS_117739	TTCTTGCTGGAGATGCATTCCC	NM_001077263	TMPRSS13	transmembrane protease, serine 13 (TMPRSS13), mRNA	-1.01	0.97	0.43	1.19	-1.44	0.18
Hs_12plexchip_6_5694	v2HS_59743	AGGAAATACCAGAGTAGCACCC	NM_153609	TMPRSS6	transmembrane protease, serine 6 (TMPRSS6), mRNA	-1.70	0.74	-0.34	1.35	-1.36	0.22
Hs_12plexchip_5_6576	v2HS_262250	ATTGCCCTGAATATGAGATGGT	NM_015028	TNIK	TRAF2 and NCK interacting kinase (TNIK), mRNA	-1.23	2.26	0.67	1.23	-1.90	0.29
Hs_12plexchip_3_9886	v2HS_134621	TAAATGAAGTAGAGACAGCCCA	NM_015978	TNNI3K	TNNI3 interacting kinase (TNNI3K), mRNA	-0.97	0.25	-0.25	0.58	-0.72	0.15
Hs_12plexchip_6_10415	v2HS_84672	TTAGGTCTTTGTTCTGACGCTT	NM_001042781	TNNT3	troponin T type 3 (skeletal, fast) (TNNT3), transcript variant 3, mRNA	-1.15	0.34	-0.44	0.44	-0.71	0.10
Hs0P00003586	v2HS_50868	TTGACCTATGGCACTGACTGGA	NM_018996	TNRC6C	HYPOTHETICAL PROTEIN FLJ20015	-0.89	0.88	0.22	0.45	-1.11	0.15
Hs_12plexchip_4_10657	v2HS_158900	TTTATTGCTCCTGTACGAACCC	NM_032470	TNXB	tenascin XB (TNXB), transcript variant XB-S, mRNA	-0.81	0.25	-0.08	0.63	-0.73	0.17
Hs_12plexchip_5_9109	v2HS_270206	ATACCCAGAACACATTAAGCCT	NM_014765	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast) (TOMM20), mRNA	-1.21	0.35	0.13	0.30	-1.35	0.01
Hs0P00002247	v2HS_65386	ATTTATACCGAGGAGATGGGAA	NM_006114	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast) (TOMM40), mRNA	-0.93	0.72	-0.11	0.52	-0.83	0.19
Hs_12plexchip_3_7485	v2HS_94079	ATACATGTCCACATAACTACGA	NM_001067	TOP2A	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA	-0.73	0.25	0.64	0.41	-1.37	0.01
Hs_12plexchip_5_12911	v2HS_67513	ATGGATTAGCACATAGTCTCCA	NM_147184	TP53I3	tumor protein p53 inducible protein 3 (TP53I3), transcript variant 2, mRNA	-1.58	1.51	0.44	1.80	-2.02	0.21
Hs_12plexchip_2_9531	v2HS_33878	TTTGAGATACTCTCTGCAAGCA	NM_004179	TPH1	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase) (TPH1), mRNA	-1.39	1.04	-0.50	0.18	-0.89	0.28
Hs_12plexchip_4_7624	v2HS_171497	ATAGTTCACAAAGTAGTGGGCA	NM_003291	TPP2	tripeptidyl peptidase II (TPP2), mRNA	-1.78	0.67	-0.10	0.84	-1.68	0.06
Hs_12plexchip_3_11699	v2HS_175495	TATTTCTTGCATGGAGATACGC	NM_033502	TRERF1	transcriptional regulating factor 1 (TRERF1), mRNA	-0.91	0.13	-0.18	0.17	-0.73	0.01
Hs_12plexchip_6_9503	v2HS_153528	AAGTATCAGCCACGGATTGGCT	NM_003141	TRIM21	tripartite motif-containing 21 (TRIM21), mRNA	-1.04	0.51	-0.15	0.94	-0.88	0.24
Hs0P00004139	v2HS_250531	TTGGGTTGTCCTTTCGTTTGCC	NM_033278	TRIM3	TRIPARTITE MOTIF-CONTAINING 3	-2.28	0.46	0.43	0.11	-2.72	0.01
Hs_12plexchip_5_3544	v2HS_26742	ATTAGTTACGAAGGTTAACGCT	NM_018700	TRIM36	tripartite motif-containing 36 (TRIM36), transcript variant 1, mRNA	-1.80	0.16	-0.23	0.69	-1.57	0.05
Hs_12plexchip_4_7689	v2HS_195606	TTCCTTCAACTCTAGCTCAGCA	NM_172016	TRIM39	tripartite motif-containing 39 (TRIM39), transcript variant 2, mRNA	-1.72	0.86	-0.41	0.69	-1.30	0.11
Hs_12plexchip_6_2045	v2HS_154686	AATTCAGAACACATGGAATGGG	NM_017583	TRIM44	tripartite motif-containing 44 (TRIM44), mRNA	-3.92	0.38	-1.00	1.42	-2.92	0.06

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_9574	v2HS_195867	ATGTCTGGAGGGCTTCAGTGGC	NM_025058	TRIM46	tripartite motif-containing 46 (TRIM46), mRNA	-0.75	0.42	0.16	0.51	-0.91	0.08
Hs_12plexchip_5_3851	v2HS_12220	TAAGTACTTCCTGGGCATAGCC	NM_025058	TRIM46	tripartite motif-containing 46 (TRIM46), mRNA	-0.86	0.38	0.30	0.27	-1.16	0.02
Hs_12plexchip_4_10547	v2HS_177429	ATTAGTTATACCACTGTCACCG	NM_032765	TRIM52	tripartite motif-containing 52 (TRIM52), mRNA	-1.20	0.77	-0.05	0.90	-1.15	0.17
Hs0P00012741	v2HS_97055	TTAACTATAAATAAGCCAAGGT	NM_182916	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1 (TRNT1), mRNA	-0.77	0.72	1.15	0.35	-1.93	0.03
Hs_12plexchip_6_8684	v2HS_218375	TTCTTGCTTGTCATTGTTGCCG	NM_003307	TRPM2	transient receptor potential cation channel, subfamily M, member 2 (TRPM2), mRNA	-1.98	0.74	0.17	2.21	-2.15	0.23
Hs_12plexchip_3_8698	v2HS_230250	ATCCCGTGTCATACAATATCCA	NM_000549	TSHB	thyroid stimulating hormone, beta (TSHB), mRNA	-1.37	0.52	-0.63	0.52	-0.75	0.15
Hs0P00003738	v2HS_50110	TTTGGTCAGTACTGAGTGTGGG	NM_012339	TSPAN15	tetraspanin 15 (TSPAN15), mRNA	-2.49	0.52	-0.32	0.47	-2.18	0.01
Hs_12plexchip_5_5706	v2HS_73609	TTGCAACCTGTCCTAGAGTGCC	NR_002781	TSPYL3	TSPY-like 3 (pseudogene) (TSPYL3) on chromosome 20	-2.79	1.52	-0.88	1.35	-1.91	0.18
Hs_12plexchip_6_1465	v2HS_178469	TTACACCCACTGGAAATAACCC	NM_033512	TSPYL5	TSPY-like 5 (TSPYL5), mRNA	-1.42	0.10	-0.71	0.42	-0.71	0.09
Hs_12plexchip_4_900	v2HS_117659	TTTATGGATCTTGCCCAGAGCT	NM_032028	TSSK1B	testis-specific serine kinase 1B (TSSK1B), mRNA	-1.51	0.43	-0.48	0.13	-1.03	0.04
Hs_12plexchip_6_718	v2HS_202692	TAACAGCTATAAATCCATTGCT	NM_173500	TTBK2	tau tubulin kinase 2 (TTBK2), mRNA	-1.83	1.12	0.03	1.74	-1.86	0.21
Hs_12plexchip_6_5974	v2HS_157607	TTTAATAAGAGCTCAGCCAGGT	NM_024753	TTC21B	tetratricopeptide repeat domain 21B (TTC21B), mRNA	-1.58	0.90	0.06	0.81	-1.64	0.08
Hs_12plexchip_4_7003	v2HS_54477	TTTGAAATAGAGGACATGGGCT	NM_001010854	TTC7B	tetratricopeptide repeat domain 7B (TTC7B), mRNA	-0.87	0.50	0.21	0.34	-1.09	0.04
Hs_12plexchip_6_2285	v2HS_225026	TTATTTGGTGTTGGATCCAGGA	NM_001025930	TTLL3	tubulin tyrosine ligase-like family, member 3 (TTLL3), transcript variant 1, mRNA	-0.98	0.30	-0.21	0.47	-0.77	0.09
Hs_12plexchip_2_6905	v2HS_158729	TTTGGGACATAGAGTGTGAGCA	NR_001537	TTTY13	testis-specific transcript, Y-linked 13 (TTTY13) on chromosome Y	-0.80	0.74	0.08	0.80	-0.88	0.23
Hs_12plexchip_2_8296	v2HS_159397	TTATTCTCCAGTGTACATCCCA	NR_001527	TTTY6	testis-specific transcript, Y-linked 6 (TTTY6) on chromosome Y	-0.78	0.66	0.04	0.31	-0.83	0.15
Hs_12plexchip_4_10917	v2HS_157889	TTAGGTCTACATTCAAGGGCCC	NM_024803	TUBAL3	tubulin, alpha-like 3 (TUBAL3), mRNA	-3.57	0.58	-1.53	1.41	-2.04	0.11
Hs_12plexchip_5_8400	v2HS_116774	TTGCTAGATCGAATGCTGTCCA	NM_030773	TUBB1	tubulin, beta 1 (TUBB1), mRNA	-1.47	0.72	0.08	1.06	-1.55	0.11
Hs_12plexchip_4_1805	v2HS_5722	TTTAGCAAGTCCATTAAGTGCC	NM_006322	TUBGCP3	tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA	-0.92	0.74	0.06	1.18	-0.98	0.30
Hs_12plexchip_4_9302	v2HS_199028	TTATTGAGAACATCCAACAGGT	NM_006322	TUBGCP3	tubulin, gamma complex associated protein 3 (TUBGCP3), mRNA	-1.60	0.67	-0.84	0.49	-0.77	0.19
Hs_12plexchip_5_12240	v2HS_200049	ATAGGATAAAGGATTGAGCCAG	NM_014444	TUBGCP4	tubulin, gamma complex associated protein 4 (TUBGCP4), mRNA	-1.22	0.13	0.04	0.09	-1.26	0.00
Hs_12plexchip_3_4474	v2HS_118095	TAATGAAATATTTGTACAGGGC	NM_001102610	TUBGCP5	tubulin, gamma complex associated protein 5 (TUBGCP5), transcript variant 2, mRNA	-1.47	0.33	-0.50	0.55	-0.97	0.07
Hs_12plexchip_5_9682	v2HS_231097	ATGAATGCATTTAGACACCGGA	NM_000474	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) (TWIST1), mRNA	-1.25	0.21	0.08	0.21	-1.33	0.00
Hs_12plexchip_4_9998	v2HS_85892	TTATCAATTCCATCTCAGAGGT	NM_006701	TXNL4A	thioredoxin-like 4A (TXNL4A), mRNA	-1.77	1.08	-0.76	0.86	-1.01	0.28
Hs_12plexchip_2_3705	v2HS_84679	TTACGGTAAATGTTCAAGAGGG	NM_001025204	U2AF1	U2 small nuclear RNA auxiliary factor 1 (U2AF1), transcript variant c, mRNA	-1.70	0.84	-0.55	0.51	-1.15	0.13
Hs0P00003414	v2HS_68112	TTATCTCATGACTGGTTATGCA	NM_005499	UBA2	SUMO-1 ACTIVATING ENZYME SUBUNIT 2	-1.62	0.28	-0.90	0.79	-0.72	0.25
Hs0P00005613	v2HS_255026	TTATCTAAAGCATTCATAACCA	NM_005499	UBA2	SUMO-1 ACTIVATING ENZYME SUBUNIT 2	-2.90	1.21	-1.71	0.24	-1.19	0.23
Hs_12plexchip_4_11785	v2HS_171713	TTTGACCTTCTTCTTGGGACGC	NM_003333	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), transcript variant 2, mRNA	-2.06	1.10	-0.05	1.98	-2.01	0.22
Hs_12plexchip_5_8132	v2HS_111298	AACTGAGAGAACATCAGCTGCC	NM_177967	UBAC2	UBA domain containing 2 (UBAC2), mRNA	-1.07	0.61	-0.08	0.32	-1.00	0.09
Hs_12plexchip_5_10756	v2HS_268066	ATTGCTCCAAGAACTGGGAGCC	NM_014847	UBAP2L	ubiquitin associated protein 2-like (UBAP2L), mRNA	-1.17	0.40	-0.38	0.46	-0.79	0.09
Hs0P00006216	v2HS_188439	ATTCTCAATGGTGTCACTCGGC	NM_021009	UBC	UBIQUITIN C	-1.66	0.25	-0.54	1.16	-1.11	0.24
Hs_12plexchip_6_773	v2HS_171717	TTTAAAGCTAATCTTCTTAGGT	NM_153280	UBE1	ubiquitin-activating enzyme E1 (UBE1), transcript variant 2, mRNA	-1.04	0.36	0.37	0.65	-1.42	0.04
Hs0P00004936	v2HS_171718	TAAGGCTACCAGTTCTGCTGCA	NM_003334	UBE1	UBIQUITIN-ACTIVATING ENZYME E1 (A1S9T AND BN75 TEMPERATURE SENSITIVITY COMPLEMENTING)	-1.05	1.80	0.48	0.78	-1.53	0.28

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_3302	v2HS_255120	TTATATATTAGGACAATCAGGT	NM_018227	UBE1L2	ubiquitin-activating enzyme E1-like 2 (UBE1L2), mRNA	-0.79	0.31	0.47	0.85	-1.26	0.11
Hs_12plexchip_5_3289	v2HS_171745	TTGAGTGTTCAAATTCAGGGCA	NM_003338	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) (UBE2D1), mRNA	-0.89	0.63	-0.11	0.35	-0.78	0.15
Hs_12plexchip_5_3620	v2HS_255135	TACTGCAATAATCAGAAGGGCT	NM_003338	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) (UBE2D1), mRNA	-1.16	0.85	0.64	0.36	-1.79	0.05
Hs_12plexchip_3_11143	v2HS_134649	TACGTTTAAGAGTCTCTCTCCC	NM_015983	UBE2D4	ubiquitin-conjugating enzyme E2D 4 (putative) (UBE2D4), mRNA	-2.22	0.81	-1.33	0.55	-0.89	0.20
Hs0P00005111	v2HS_171753	TACAATGATAGATTCTTGTCCG	NM_003341	UBE2E1	UBIQUITIN-CONJUGATING ENZYME E2E 1 (UBC4/5 HOMOLOG, YEAST)	-0.82	0.54	0.56	0.36	-1.38	0.03
Hs_12plexchip_4_2276	v2HS_171781	TATAAACACAAAGGAAGTGGCG	NM_194261	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) (UBE2I), transcript variant 4, mRNA	-2.56	0.64	-1.32	0.79	-1.25	0.10
Hs_12plexchip_5_3552	v2HS_254973	ATTTAGAAGTTCCTGTATTCCT	NM_194261	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) (UBE2I), transcript variant 4, mRNA	-0.80	0.52	-0.01	0.45	-0.79	0.12
Hs_12plexchip_6_3261	v2HS_171776	TTGGCAGTAAATCGTGTAGGCC	NM_194261	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) (UBE2I), transcript variant 4, mRNA	-1.99	1.01	0.16	2.51	-2.16	0.27
Hs_12plexchip_5_3549	v2HS_46734	ATTCATTTCCCATCGCTGAGTG	NM_003969	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (UBE2M), mRNA	-1.45	0.65	-0.06	0.65	-1.38	0.06
Hs_12plexchip_5_6130	v2HS_263284	TTTATGTCCTTCTGGATCCGCA	NM_003969	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (UBE2M), mRNA	-1.02	1.34	0.53	1.18	-1.56	0.21
Hs_12plexchip_5_6272	v2HS_263146	TTAAGTTCTTGATGGACAAGGG	NM_022066	UBE2O	ubiquitin-conjugating enzyme E2O (UBE2O), mRNA	-0.81	0.18	1.00	0.22	-1.81	0.00
Hs_12plexchip_5_7050	v2HS_202876	TTGAGCCTGCAGTTTGTAAGCG	NM_022066	UBE2O	ubiquitin-conjugating enzyme E2O (UBE2O), mRNA	-1.21	0.32	-0.34	0.14	-0.87	0.03
Hs_12plexchip_4_239	v2HS_173914	TTGATGCAGTATTCCGCCAGGG	NM_017811	UBE2R2	ubiquitin-conjugating enzyme E2R 2 (UBE2R2), mRNA	-1.19	1.11	0.21	0.46	-1.40	0.15
Hs_12plexchip_5_3354	v2HS_254989	ATATGCGCCTTGAAGTAGCCGC	NM_017811	UBE2R2	ubiquitin-conjugating enzyme E2R 2 (UBE2R2), mRNA	-1.76	0.51	-0.33	0.36	-1.43	0.02
Hs_12plexchip_5_3886	v2HS_19154	GGTAGTAATCACTAAATGAGGT	NM_152489	UBE2U	ubiquitin-conjugating enzyme E2U (putative) (UBE2U), mRNA	-1.16	0.25	-0.43	0.59	-0.73	0.15
Hs_12plexchip_4_10216	v2HS_82195	ATACTCAAGCAGACTTTCCCAT	NM_023079	UBE2Z	ubiquitin-conjugating enzyme E2Z (UBE2Z), mRNA	-0.86	0.39	0.63	0.81	-1.49	0.07
Hs_12plexchip_5_6199	v2HS_262978	TTAGGATGGGATCCATCTTCCC	NM_130466	UBE3B	ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA	-1.05	0.30	0.38	0.28	-1.44	0.00
Hs_12plexchip_6_10210	v2HS_195955	AATGAACTGCTGGTTGGGTCCA	NM_013444	UBQLN2	ubiquilin 2 (UBQLN2), mRNA	-1.50	2.36	1.64	1.37	-3.14	0.13
Hs_12plexchip_5_12253	v2HS_199008	ATATAGTCTCTCATGATCTCCT	NM_014233	UBTF	upstream binding transcription factor, RNA polymerase I (UBTF), transcript variant 1, mRNA	-2.02	0.08	-0.80	0.70	-1.22	0.09
Hs_12plexchip_6_2286	v2HS_212292	TTTGGAACTAACCTTCTGAGCT	NM_181713	UBXD4	UBX domain containing 4 (UBXD4), mRNA	-0.82	0.27	1.40	1.00	-2.21	0.05
Hs0P00008050	v2HS_134653	ATTGCCAAACGTGCACTGAGCC	NM_015984	UCHL5	ubiquitin carboxyl-terminal hydrolase L5 (UCHL5), mRNA	-1.74	0.16	-0.85	0.58	-0.89	0.11
Hs_12plexchip_5_1406	v2HS_64096	TAAACATACTTCAAACACAGCA	NM_001003684	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD) (UCRC), transcript variant 2, mRNA	-1.67	0.20	-0.56	0.46	-1.11	0.04
Hs_12plexchip_6_12649	v2HS_141734	TAGTGGTAGTAGAGGTAGTGGC	NM_001015072	UFSP1	inactive Ufm1-specific protease 1 (UFSP1), mRNA	-0.77	0.15	0.02	0.90	-0.79	0.27
Hs_12plexchip_4_820	v2HS_171830	ATACTTTGCAACTTCATATCCT	NM_003358	UGCG	UDP-glucose ceramide glucosyltransferase (UGCG), mRNA	-0.78	0.44	-0.04	0.05	-0.74	0.10
Hs_12plexchip_2_9330	v2HS_21480	ATATAGAAGGGTATTAACTGCC	NM_152404	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1 (UGT3A1), mRNA	-0.72	0.21	0.03	0.69	-0.76	0.19
Hs0P00000352	v2HS_203109	TATCATCCACATGGAACAACCC	NM_175866	UHMK1	U2AF HOMOLOGY MOTIF (UHM) KINASE 1	-0.84	0.56	-0.13	0.29	-0.71	0.15
Hs_12plexchip_4_7431	v2HS_149461	TTTCACCACCTTATAAATGCCA	NM_152896	UHRF2	ubiquitin-like, containing PHD and RING finger domains, 2 (UHRF2), mRNA	-1.63	0.57	-0.71	0.49	-0.92	0.10
Hs_12plexchip_6_6730	v2HS_137460	TATGTTAGGTATAACTGCTGGT	NM_025217	ULBP2	UL16 binding protein 2 (ULBP2), mRNA	-0.89	0.66	0.17	0.65	-1.07	0.12
Hs_12plexchip_6_505	v2HS_63858	TTTATAGGCCCTTAAAGCTGCT	XM_941380	UNC13C	PREDICTED:unc-13 homolog C (C. elegans), transcript variant 4 (UNC13C), mRNA	-0.71	0.15	0.07	0.90	-0.78	0.27
Hs_12plexchip_6_3640	v2HS_174805	TAGTCTCCACATTTGAACAGCT	NM_001039675	UNC45A	unc-45 homolog A (C. elegans) (UNC45A), transcript variant 3, mRNA	-1.21	0.20	-0.29	0.99	-0.92	0.24

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_3471	v2HS_14546	ATATTCACATTGCTAAGATGCA	NM_023076	UNKL	unkempt homolog (Drosophila)-like (UNKL), transcript variant 1, mRNA	-0.79	0.55	1.38	0.40	-2.17	0.01
Hs_12plexchip_5_11657	v2HS_140620	ATAGCTCTGAACAACACATGGG	NM_198464	UNQ9391	tryptophan/serine protease (UNQ9391), mRNA	-0.72	0.17	0.50	0.51	-1.21	0.04
Hs_12plexchip_2_9718	v2HS_32895	ATATGTTCTGGTACTGGTAGGC	NM_002911	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast) (UPF1), mRNA	-1.47	0.25	-0.48	0.51	-0.98	0.06
Hs_12plexchip_5_3509	v2HS_63901	TTCAGCTTTCATTTGGAAGGCA	NM_013396	USP25	ubiquitin specific peptidase 25 (USP25), mRNA	-1.78	2.09	0.16	1.01	-1.94	0.25
Hs_12plexchip_5_3292	v2HS_159709	TTTAGGGTTGTGTTGACTAGGT	NM_032663	USP30	ubiquitin specific peptidase 30 (USP30), mRNA	-1.24	0.79	0.18	0.55	-1.42	0.07
Hs_12plexchip_6_1523	v2HS_159253	TTTCAGAAGGCTTGTGTGAGGC	NM_032557	USP38	ubiquitin specific peptidase 38 (USP38), mRNA	-0.89	3.03	1.77	1.14	-2.66	0.27
Hs_12plexchip_6_1044	v2HS_13479	TTAGATATGGAGGCAACTTGGT	NM_006590	USP39	ubiquitin specific peptidase 39 (USP39), mRNA	-1.40	0.31	-0.30	0.74	-1.10	0.11
Hs0P00003468	v2HS_196240	AATTCATACCATTTGCCTGTCC	NM_006590	USP39	UBIQUITIN SPECIFIC PEPTIDASE 39	-1.15	0.57	-0.29	0.85	-0.86	0.23
Hs0P00003809	v2HS_62694	TTGCTTCTTTATATGACCTGCC	XM_300919	USP49	Homo sapiens ubiquitin specific protease 49	-0.87	0.41	0.50	1.21	-1.36	0.18
Hs_12plexchip_5_281	v2HS_243816	AATATTGGTTTGGGTAGGTCCC	NM_004505	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene) (USP6), mRNA	-1.54	0.83	0.02	0.40	-1.56	0.06
Hs_12plexchip_5_3434	v2HS_41519	ATAATCATTGAACTTGATTGCA	NM_001039591	USP9X	ubiquitin specific peptidase 9, X-linked (USP9X), transcript variant 4, mRNA	-0.84	0.87	0.29	0.54	-1.13	0.14
Hs_12plexchip_5_12261	v2HS_245827	TTAAGAGGTGGCATATTCAGGT	NM_004654	USP9Y	UBIQUITIN SPECIFIC PEPTIDASE 9, Y-LINKED (FAT FACETS-LIKE, DROSOPHILA)	-1.03	0.62	0.09	0.36	-1.12	0.07
Hs_12plexchip_5_2412	v2HS_253404	TTATTAAGTGATTTAGAGCCCA	NM_005800	USPL1	ubiquitin specific peptidase like 1 (USPL1), mRNA	-0.82	0.40	1.14	0.67	-1.96	0.02
Hs_12plexchip_2_2126	v2HS_90838	TTTGGCAAATCCGCTAGTTCTT	NM_006649	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast) (UTP14A), mRNA	-1.22	0.57	-0.34	0.25	-0.88	0.10
Hs_12plexchip_3_4502	v2HS_118064	TTTAATAAAGGTTCGATATGCA	NM_032175	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae) (UTP15), mRNA	-1.62	0.42	-0.67	0.63	-0.96	0.10
Hs_12plexchip_3_4961	v2HS_118066	TTAAGAACATGACTGATTTCCT	NM_032175	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae) (UTP15), mRNA	-1.60	0.65	-0.61	1.20	-0.99	0.30
Hs_12plexchip_3_2869	v2HS_71746	GGTACATAACATCCAGACAGCT	NM_182645	VGLL2	vestigial like 2 (Drosophila) (VGLL2), transcript variant 1, mRNA	-1.51	0.40	-0.72	0.72	-0.80	0.19
Hs_12plexchip_5_6251	v2HS_263273	TTTGAGCACAGGAATTGTGCCC	NM_198156	VHL	von Hippel-Lindau tumor suppressor (VHL), transcript variant 2, mRNA	-1.05	0.62	-0.25	0.77	-0.80	0.24
Hs_12plexchip_2_11994	v2HS_41380	CTAGAGGATAATATTAACCCGG	NM_004666	VNN1	vanin 1 (VNN1), mRNA	-1.28	0.08	-0.24	0.32	-1.03	0.03
Hs_12plexchip_5_5571	v2HS_255610	TTTACCAATACTGGATATTCGG	NM_014703	VPRBP	Vpr (HIV-1) binding protein (VPRBP), mRNA	-2.99	0.73	-0.58	0.32	-2.41	0.02
Hs0P00009437	v2HS_139560	TAATTTATCAATTTGGCCAGCC	NM_018080	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae) (VPS13C), transcript variant 1B, mRNA	-0.73	0.55	0.02	0.62	-0.75	0.19
Hs_12plexchip_5_9020	v2HS_223892	TTAACATCATCCATCCAGAGGC	NM_022916	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae) (VPS33A), mRNA	-1.23	0.07	-0.44	0.29	-0.79	0.04
Hs_12plexchip_6_5803	v2HS_156712	ATTTCCTTCGCTCTGGTACGCA	NM_018289	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae) (VPS53), mRNA	-1.47	0.62	0.30	1.78	-1.77	0.22
Hs_12plexchip_6_6773	v2HS_156711	TAATCTTGGCAAGTTCTGCCCT	NM_018289	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae) (VPS53), mRNA	-1.46	0.59	0.94	2.66	-2.40	0.26
Hs_12plexchip_2_10445	v2HS_20965	TTTGGTATCCAGCCTCTAGTCT	NM_145206	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast) (VTI1A), transcript variant 2, mRNA	-1.18	0.38	-0.39	0.33	-0.79	0.06
Hs_12plexchip_5_11762	v2HS_135340	TTTCTTGTGGAGAGTAACTGGT	NM_100486	WAC	WW domain containing adaptor with coiled-coil (WAC), transcript variant 3, mRNA	-1.32	0.25	-0.33	0.23	-0.99	0.01
Hs0P00008259	v2HS_135345	AATTATTCACATCTTCACACCA	NM_100486	WAC	WW domain containing adaptor with coiled-coil (WAC), transcript variant 3, mRNA	-0.92	0.17	0.18	0.49	-1.10	0.05
Hs_12plexchip_3_5507	v2HS_123467	TTTCTCAATCTGATCCGTCGGT	NR_003558	WBP11P1	WW domain binding protein 11 pseudogene 1 (WBP11P1) on chromosome 18	-2.53	0.43	-1.16	0.45	-1.38	0.02
Hs_12plexchip_5_8982	v2HS_123465	TTTCAGGACTATGTACCATGCC	NR_003558	WBP11P1	WW domain binding protein 11 pseudogene 1 (WBP11P1) on chromosome 18	-1.01	0.64	-0.13	0.69	-0.88	0.18
Hs_12plexchip_5_5273	v2HS_84276	TATAAGTTCAACATCAGAGCCC	NM_006784	WDR3	WD repeat domain 3 (WDR3), mRNA	-2.84	0.58	-1.50	0.24	-1.34	0.04
Hs_12plexchip_4_6384	v2HS_56762	TTTACATTCCACAACTGCAGGC	NM_139281	WDR36	WD repeat domain 36 (WDR36), mRNA	-2.84	1.42	0.21	0.95	-3.04	0.04
Hs_12plexchip_4_9846	v2HS_60148	ATTCACACAAATGTAATGCCCT	NM_014023	WDR37	WD repeat domain 37 (WDR37), mRNA	-1.94	0.57	-0.80	0.66	-1.14	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_11078	v2HS_274001	ATTAATTAACTCTGCTACCCGT	XM_293354	WDR42C	PREDICTED:WD repeat domain 42C (WDR42C), mRNA	-0.84	0.18	-0.04	0.23	-0.79	0.01
Hs_12plexchip_3_7805	v2HS_229697	TTATACATCAGGATTGTTAGGA	NM_015420	WDSOF1	WD repeats and SOF1 domain containing (WDSOF1), mRNA	-1.46	0.65	-0.15	0.57	-1.32	0.06
Hs_12plexchip_5_1388	v2HS_57489	ATATTCCAAGTCTCAGGACCCT	NM_080869	WFDC12	WAP four-disulfide core domain 12 (WFDC12), mRNA	-1.04	0.78	0.31	0.72	-1.36	0.09
Hs_12plexchip_5_10529	v2HS_100106	TTTGCAGGTTAGATATTGGGCC	NM_172005	WFDC13	WAP four-disulfide core domain 13 (WFDC13), mRNA	-4.35	0.73	-1.80	1.14	-2.55	0.04
Hs0P00007741	v2HS_138653	TTCTAGCTGCTCTTTGCTGGGC	NM_032345	WIBG	within bgcn homolog (Drosophila) (WIBG), mRNA	-1.01	0.70	0.01	0.41	-1.02	0.11
Hs_12plexchip_2_4822	v2HS_179677	TATAGTGAGCAATGTGTCCCGT	NM_001002838	WNK3	WNK lysine deficient protein kinase 3 (WNK3), transcript variant 2, mRNA	-0.87	0.90	0.11	0.94	-0.98	0.26
Hs_12plexchip_2_4502	v2HS_172039	TTCTCACACCATGTGCAATGCC	NM_003395	WNT9A	wingless-type MMTV integration site family, member 9A (WNT9A), mRNA	-0.81	0.50	0.28	0.69	-1.08	0.10
Hs_12plexchip_2_4319	v2HS_81482	TTCAGCTTTCAGGATCTCAGGG	NM_015238	WWC1	WW and C2 domain containing 1 (WWC1), mRNA	-1.07	0.59	0.09	0.59	-1.16	0.07
Hs_12plexchip_2_2750	v2HS_88697	TTCGATGAGGCTGATATCTGCA	NM_024949	WWC2	WW and C2 domain containing 2 (WWC2), mRNA	-0.74	0.29	0.02	0.67	-0.76	0.18
Hs_12plexchip_6_2109	v2HS_59066	TTCTTCTCTCTCCTGACCAGGT	NM_133179	XAGE3	X antigen family, member 3 (XAGE3), transcript variant 1, mRNA	-0.75	0.24	0.24	0.34	-0.99	0.02
Hs_12plexchip_6_2859	v2HS_179133	TTGCTTTAGAATATCCTGTCCT	NM_173683	XKR6	XK, Kell blood group complex subunit-related family, member 6 (XKR6), transcript variant 2, mRNA	-0.86	1.20	0.26	0.80	-1.12	0.26
Hs_12plexchip_4_4183	v2HS_219836	TTTGTAGTCCATAGTATTTCGT	NM_003400	XPO1	exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA	-1.01	0.47	-0.22	0.32	-0.79	0.08
Hs_12plexchip_6_4455	v2HS_219111	TTTATGTTTCTCTTCATCAGCC	NM_003400	XPO1	exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA	-2.39	1.31	-1.07	0.99	-1.33	0.24
Hs0P00010609	v2HS_172053	TTTGACAGAGACTTTCGCTGGT	NM_003400	XPO1	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-1.62	0.69	-0.34	0.29	-1.28	0.07
Hs_12plexchip_5_12640	v2HS_56413	TAAAGAAAGAAGTGCTTGCCCT	NM_006297	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1), mRNA	-0.94	0.18	0.87	0.49	-1.81	0.02
Hs_12plexchip_6_9636	v2HS_134639	AATCCGTAACCATTCCGGACGT	NM_015982	YBX2	Y box binding protein 2 (YBX2), mRNA	-1.50	2.02	1.64	2.50	-3.14	0.17
Hs_12plexchip_4_11979	v2HS_69602	GTAGTGTTTCACATTGTCACCC	NM_005433	YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1), mRNA	-1.64	0.70	-0.77	0.72	-0.87	0.21
Hs_12plexchip_4_5079	v2HS_203477	TTTGGTAACCATCCGCTTTGCT	NM_014263	YME1L1	YME1-like 1 (S. cerevisiae) (YME1L1), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA	-1.43	1.50	0.12	1.70	-1.55	0.30
Hs_12plexchip_2_10673	v2HS_15608	AATTTGGAACAATGTGAATGAC	NM_001099270	ZBTB34	zinc finger and BTB domain containing 34 (ZBTB34), mRNA	-0.82	0.20	-0.06	0.50	-0.77	0.10
Hs_12plexchip_5_3524	v2HS_95592	TTAAGGGTGGAACTGTAGTGCC	NM_014830	ZBTB39	zinc finger and BTB domain containing 39 (ZBTB39), mRNA	-2.52	0.35	-1.48	0.70	-1.04	0.11
Hs_12plexchip_5_3512	v2HS_95794	TACTTCTATGCTATGGGCTGCT	NM_014872	ZBTB5	zinc finger and BTB domain containing 5 (ZBTB5), mRNA	-1.82	0.67	-0.26	0.14	-1.56	0.05
Hs_12plexchip_3_7011	v2HS_233704	ATGCTAAGTACTTTCACTTCCC	NM_178547	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand (ZBTB8OS), mRNA	-0.80	0.62	0.29	0.70	-1.09	0.12
Hs_12plexchip_3_7825	v2HS_100450	TTCATTATAGACCTGCATTGCT	NM_178547	ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand (ZBTB8OS), mRNA	-0.73	0.02	0.04	0.06	-0.77	0.00
Hs_12plexchip_2_6697	v2HS_177528	TATGACCTTGGCCTGATTGCGG	NM_032786	ZC3H10	zinc finger CCCH-type containing 10 (ZC3H10), mRNA	-1.55	0.22	0.06	0.59	-1.61	0.03
Hs_12plexchip_4_1308	v2HS_205155	TTTCTTCTTACTTTGCTGGGCT	NM_015070	ZC3H13	zinc finger CCCH-type containing 13 (ZC3H13), mRNA	-1.90	0.51	-0.81	0.58	-1.09	0.07
Hs_12plexchip_6_6092	v2HS_175791	AACAGGAACAGCATCAATGGCT	NM_018471	ZC3H15	zinc finger CCCH-type containing 15 (ZC3H15), mRNA	-1.04	0.90	0.99	0.22	-2.03	0.05
Hs0P00010747	v2HS_19370	TTTCATAGTCATAATAAGGGTC	NM_144604	ZC3H18	zinc finger CCCH-type containing 18 (ZC3H18), mRNA	-2.32	0.58	-0.62	0.23	-1.71	0.02
Hs0P00011471	v2HS_19371	TATAGATATATTTCTGATCCGG	NM_144604	ZC3H18	zinc finger CCCH-type containing 18 (ZC3H18), mRNA	-2.59	0.79	-0.46	0.09	-2.14	0.04
Hs_12plexchip_4_10479	v2HS_70944	TGACAGTATCCTTTAGCATCTA	NM_080660	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like (ZC3HAV1L), mRNA	-1.84	0.72	-0.34	0.69	-1.50	0.06
Hs_12plexchip_3_11428	v2HS_140667	TAGGATCCTTACAGTCTTTGGC	NM_203303	ZCCHC13	zinc finger, CCHC domain containing 13 (ZCCHC13), mRNA	-0.94	0.52	0.16	0.76	-1.11	0.12

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00008945	v2HS_138554	ATTTGTGCTCCCTTAAGCAGCA	NM_198044	ZDHHC16	zinc finger, DHHC-type containing 16 (ZDHHC16), transcript variant 3, mRNA	-0.82	0.33	0.59	0.87	-1.42	0.09
Hs_12plexchip_4_11356	v2HS_99114	ATGTACAGTAAGGGAGGATCGT	NM_030613	ZFP2	zinc finger protein 2 homolog (mouse) (ZFP2), mRNA	-1.01	0.37	-0.31	0.62	-0.70	0.18
Hs_12plexchip_6_3384	v2HS_172099	TATGGTAAGTAAGAGATGAGCT	NM_003408	ZFP37	zinc finger protein 37 homolog (mouse) (ZFP37), mRNA	-0.72	0.37	-0.02	0.12	-0.70	0.07
Hs_12plexchip_4_12302	v2HS_219992	ATTTCATTGTCATCCATTTGCT	NM_003410	ZFX	zinc finger protein, X-linked (ZFX), mRNA	-0.75	0.80	0.28	0.73	-1.03	0.17
Hs_12plexchip_5_4843	v2HS_257672	TTAGAGCATCCTTATATATGGT	NM_001105251	ZFYVE16	zinc finger, FYVE domain containing 16 (ZFYVE16), transcript variant 2, mRNA	-0.86	0.79	0.94	0.29	-1.80	0.04
Hs_12plexchip_6_5942	v2HS_203541	TTTCCCTCCAGGAAGAACGGGC	NM_181485	ZGPAT	zinc finger, CCCH-type with G patch domain (ZGPAT), transcript variant 3, mRNA	-1.09	0.41	0.07	0.77	-1.16	0.10
Hs_12plexchip_5_4248	v2HS_260005	TATGGTCCTGAATAGGTCTGGA	NM_001011657	ZMAT1	zinc finger, matrin type 1 (ZMAT1), transcript variant 1, mRNA	-1.16	0.16	0.27	0.21	-1.43	0.00
Hs_12plexchip_5_3151	v2HS_5924	TTATACATCCAGAACACGTGCA	NM_001039650	ZMYM5	zinc finger, MYM-type 5 (ZMYM5), transcript variant 1, mRNA	-1.49	1.76	0.57	0.32	-2.06	0.18
Hs_12plexchip_4_7916	v2HS_172208	AATGTCTTTCAAGAATGGCCCA	NM_003433	ZNF132	zinc finger protein 132 (ZNF132), mRNA	-0.91	0.76	-0.19	0.11	-0.72	0.24
Hs_12plexchip_5_12877	v2HS_249122	TTCCTGGAGTCGAGTAAGAGCC	NM_006299	ZNF193	zinc finger protein 193 (ZNF193), mRNA	-1.06	0.82	-0.17	0.60	-0.89	0.21
Hs_12plexchip_6_280	v2HS_72407	CTTTAGAGTCATTTCCATGGCC	NM_001017396	ZNF2	zinc finger protein 2 (ZNF2), transcript variant 2, mRNA	-1.36	1.01	0.31	1.51	-1.67	0.20
Hs_12plexchip_6_3551	v2HS_172336	ATTTCTTGTGACATATATGGCA	NM_003457	ZNF207	zinc finger protein 207 (ZNF207), transcript variant 1, mRNA	-1.69	0.32	-0.24	1.30	-1.45	0.19
Hs_12plexchip_4_10162	v2HS_194812	TTATAACCTTCTTTGTTCACCT	NM_203282	ZNF254	zinc finger protein 254 (ZNF254), mRNA	-0.75	0.47	0.57	1.19	-1.32	0.18
Hs_12plexchip_2_1211	v2HS_78271	ATATTGTGATGTTTAATGAGGT	NM_001012756	ZNF260	zinc finger protein 260 (ZNF260), mRNA	-1.22	0.22	-0.14	0.52	-1.08	0.05
Hs_12plexchip_5_9625	v2HS_269844	CACTGATCACATCTATAGGGCT	NM_006973	ZNF32	zinc finger protein 32 (ZNF32), transcript variant 1, mRNA	-1.03	0.63	-0.09	0.70	-0.95	0.16
Hs_12plexchip_3_8078	v2HS_95012	TTATTGATGAATACAACTTCCC	NM_006954	ZNF33A	zinc finger protein 33A (ZNF33A), transcript variant 1, mRNA	-0.99	0.21	-0.24	0.19	-0.74	0.01
Hs_12plexchip_3_3548	v2HS_44697	TTTGTAAGTCCCATTATCTCCC	NM_152604	ZNF383	zinc finger protein 383 (ZNF383), mRNA	-0.93	0.24	-0.23	0.32	-0.71	0.04
Hs_12plexchip_5_10078	v2HS_269427	ATAAGTACCCAGTTCTCCAGCA	NM_133460	ZNF418	zinc finger protein 418 (ZNF418), mRNA	-2.73	0.15	-1.42	1.45	-1.32	0.25
Hs0P00002755	v2HS_50817	ATAAGTACTTCCATACTGACAT	NM_145312	ZNF485	zinc finger protein 485 (ZNF485), mRNA	-1.05	0.39	-0.22	0.27	-0.82	0.05
Hs_12plexchip_5_10988	v2HS_138954	ATTTATGTAGTACTTCCTGGCT	NM_032434	ZNF512	zinc finger protein 512 (ZNF512), mRNA	-0.90	0.19	0.23	0.60	-1.13	0.07
Hs_12plexchip_3_7494	v2HS_101447	TAACAAGAGAAGAATGGGCGCT	NR_003127	ZNF542	zinc finger protein 542 (ZNF542) on chromosome 19	-0.86	0.77	0.33	0.81	-1.19	0.14
Hs_12plexchip_5_756	v2HS_45336	ATTAATCACCAATAAAGTACCC	NM_153231	ZNF550	ZINC FINGER PROTEIN 550	-0.98	0.56	0.24	0.68	-1.22	0.08
Hs_12plexchip_2_5625	v2HS_177071	ATGTGAATTAATTTGCACAGGT	NM_024967	ZNF556	zinc finger protein 556 (ZNF556), mRNA	-0.79	0.48	-0.01	0.26	-0.78	0.09
Hs_12plexchip_6_1603	v2HS_17118	TTATCTCTTCCTTGAAACACGC	NM_144694	ZNF570	zinc finger protein 570 (ZNF570), mRNA	-0.86	0.66	0.25	1.32	-1.12	0.28
Hs_12plexchip_6_7051	v2HS_44731	TTGAACTCCCGCTGGCAGCGCA	NM_152600	ZNF579	zinc finger protein 579 (ZNF579), mRNA	-1.34	1.10	-0.17	1.14	-1.17	0.27
Hs_12plexchip_6_6835	v2HS_160859	TTTCCAGTGCTGATAGAGGCCT	NM_173548	ZNF584	zinc finger protein 584 (ZNF584), mRNA	-1.16	0.54	0.42	0.55	-1.58	0.02
Hs_12plexchip_5_4624	v2HS_256407	ATATTGACCCGGGATTAGCGGG	NM_020747	ZNF608	zinc finger protein 608 (ZNF608), mRNA	-1.33	0.13	-0.55	0.52	-0.78	0.12
Hs_12plexchip_6_7902	v2HS_190494	TTGGAATGAAACTTGCAGGCCC	NM_020394	ZNF695	zinc finger protein 695 (ZNF695), mRNA	-1.28	0.19	-0.52	0.44	-0.76	0.08
Hs_12plexchip_6_9382	v2HS_156561	TTTCTCTTGTGTGTACTTCCCG	NM_018260	ZNF701	zinc finger protein 701 (ZNF701), mRNA	-0.70	1.20	0.47	1.25	-1.18	0.30
Hs_12plexchip_6_2598	v2HS_172179	TTAATGAGACAGTGGTTCTGGC	NM_003426	ZNF74	zinc finger protein 74 (ZNF74), transcript variant 1, mRNA	-0.70	0.87	0.66	0.67	-1.36	0.10
Hs_12plexchip_2_4774	v2HS_172188	TTAATTGACTGTGGTGTCAGGA	NM_003427	ZNF76	zinc finger protein 76 (expressed in testis) (ZNF76), mRNA	-0.71	0.98	0.25	0.15	-0.95	0.23
Hs_12plexchip_2_6568	v2HS_179114	TTGGGCTTCTGGCTGAAGCGGC	NM_173680	ZNF775	zinc finger protein 775 (ZNF775), mRNA	-1.63	0.53	-0.70	0.64	-0.93	0.13
Hs_12plexchip_5_7160	v2HS_114647	ATTGTCAAGGAAATTAACAGCC	NM_015694	ZNF777	zinc finger protein 777 (ZNF777), mRNA	-0.72	0.14	0.20	0.61	-0.93	0.11
Hs_12plexchip_5_12603	v2HS_245331	AATAATCCATCTTAAGACTCCT	NM_004773	ZNHIT3	zinc finger, HIT type 3 (ZNHIT3), mRNA	-0.75	0.56	0.05	0.44	-0.80	0.13
Hs_12plexchip_5_3497	v2HS_14719	TTTGAAACCACTATGGCGAGCC	BG475343	ZNRF1	HYPOTHETICAL PROTEIN DKFZP434E229	-2.54	0.86	-1.66	0.45	-0.88	0.21
Hs_12plexchip_5_3477	v2HS_14391	TTAAATCCTCCAAACATGTGCG	NM_147128	ZNRF2	zinc and ring finger 2 (ZNRF2), mRNA	-0.74	0.16	-0.04	0.15	-0.70	0.01
Hs_12plexchip_4_8079	v2HS_14651	ATTTCACTTGGGACCATGACCT	NM_032173	ZNRF3	zinc and ring finger 3 (ZNRF3), mRNA	-1.84	0.94	-0.92	0.25	-0.92	0.23
Hs_12plexchip_3_8540	v2HS_96860	ATATGGAAGCCCAATATCAGCC	NM_015534	ZZZ3	zinc finger, ZZ-type containing 3 (ZZZ3), mRNA	-1.05	0.66	-0.28	0.76	-0.77	0.26

Supplemental Table 2. Candidate RSL shRNAs based on stringent statistical criteria.

The qualifying criteria for shRNAs are the same as listed in Table 1 legent except with a p value <= 0.1.

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_4881	v2HS_255771	ATAGACTTTCACTATGGCTGGT	NM_000014	A2M	alpha-2-macroglobulin (A2M), mRNA	-1.15	0.46	0.73	0.70	-1.88	0.02
Hs_12plexchip_3_7348	v2HS_100516	TATATGTCTCGATTTCTCAGGA	NM_178559	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5 (ABCB5), mRNA	-1.18	0.12	0.08	0.15	-1.26	0.00
Hs_12plexchip_2_1754	v2HS_81153	TTTAGGAAAGCCTGTGGTCCCA	NM_001080454	ACSM4	acyl-CoA synthetase medium-chain family member 4 (ACSM4), mRNA	-1.17	0.59	-0.16	0.45	-1.01	0.08
Hs_12plexchip_5_7113	v2HS_197509	TAAACCTTGAGCGTACAAAGTC	NM_001005386	ACTR2	ARP2 actin-related protein 2 homolog (yeast) (ACTR2), transcript variant 1, mRNA	-1.31	0.55	-0.19	0.41	-1.12	0.05
Hs_12plexchip_5_5343	v2HS_91340	TAATGATCTGGGAACCTAGCCC	NM_001077401	ACVRL1	activin A receptor type II-like 1 (ACVRL1), transcript variant 2, mRNA	-1.24	0.97	0.52	0.69	-1.76	0.07
Hs0P00011130	v2HS_33582	TTTAACTTCCACAGTCTTGCCT	NM_021723	ADAM22	ADAM metallopeptidase domain 22 (ADAM22), transcript variant 1, mRNA	-1.15	0.16	0.14	0.20	-1.29	0.00
Hs0P00011915	v2HS_25008	ATAGTGGAGTAGTCGGTGGGCG	NM_213604	ADAMTSL5	ADAMTS-like 5 (ADAMTSL5), mRNA	-1.35	0.20	-0.23	0.36	-1.12	0.02
Hs_12plexchip_4_174	v2HS_94323	ATACAGCTCCTCATTGTCTCGG	NM_001115	ADCY8	adenylate cyclase 8 (brain) (ADCY8), mRNA	-1.60	0.75	-0.25	0.52	-1.35	0.07
Hs0P00001565	v2HS_63897	ATTACCAACATGAGTTGCTGGC	NM_139178	ALKBH3	alkB, alkylation repair homolog 3 (E. coli) (ALKBH3), mRNA	-1.27	0.16	-0.26	0.22	-1.01	0.00
Hs_12plexchip_3_11335	v2HS_238167	TATTGGTTGCTGCTAGACTCGC	NM_032306	ALKBH7	alkB, alkylation repair homolog 7 (E. coli) (ALKBH7), mRNA	-1.65	0.05	-0.35	0.24	-1.31	0.01
Hs_12plexchip_4_11284	v2HS_98169	AATAGACATATCCATGGTGCCT	NM_022662	ANAPC1	anaphase promoting complex subunit 1 (ANAPC1), mRNA	-1.74	0.26	0.35	0.66	-2.08	0.02
Hs_12plexchip_5_3713	v2HS_254660	ATACAATGGAATACAGATTGCT	NM_013367	ANAPC4	anaphase promoting complex subunit 4 (ANAPC4), mRNA	-1.32	0.20	0.45	0.63	-1.78	0.03
Hs_12plexchip_5_9857	v2HS_268762	AAGAGTTCACAATTTCAAGGCT	NM_001154	ANXA5	annexin A5 (ANXA5), mRNA	-1.67	0.54	-0.35	0.31	-1.31	0.03
Hs_12plexchip_5_6098	v2HS_262529	TATAATGATCCTCATATAACCA	NM_001018159	APPBP1	amyloid beta precursor protein binding protein 1 (APPBP1), transcript variant 2, mRNA	-2.57	1.47	0.62	0.08	-3.19	0.06
Hs_12plexchip_4_2811	v2HS_219865	ATTTATTGTGAAAGCTCGTGGG	NM_003491	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae) (ARD1A), mRNA	-1.05	0.54	0.08	0.37	-1.14	0.05
Hs_12plexchip_6_1612	v2HS_201002	ATCTTTGGAGGTAATCTTTCGC	NM_017519	ARID1B	AT rich interactive domain 1B (SWI1-like) (ARID1B), transcript variant 1, mRNA	-1.54	0.28	0.07	1.01	-1.60	0.10
Hs_12plexchip_4_1272	v2HS_198492	GACCACTTTAAGAAGCACTGCA	NM_001037164	ARL4A	ADP-ribosylation factor-like 4A (ARL4A), transcript variant 3, mRNA	-1.67	0.58	-0.63	0.57	-1.04	0.09
Hs_12plexchip_4_1283	v2HS_5802	TAGCAAAGAGACATTGTATCCT	NM_152862	ARPC2	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA	-1.88	0.10	-0.74	0.41	-1.14	0.03
Hs_12plexchip_2_12230	v2HS_202600	TTACTTATTCTTATTAAGCGCC	NM_005719	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA	-1.01	0.10	0.20	0.44	-1.22	0.04
Hs_12plexchip_5_881	v2HS_249261	AATCACTGGTTCTTGGCATGGG	NM_080863	ASB16	ankyrin repeat and SOCS box-containing 16 (ASB16), mRNA	-1.24	0.62	0.37	0.10	-1.61	0.04
Hs_12plexchip_5_11693	v2HS_138999	TAAAGGGATCTAGGGCTTCGGC	NM_033027	AXUD1	AXIN1 up-regulated 1 (AXUD1), mRNA	-2.29	0.36	-0.99	0.80	-1.30	0.09
Hs_12plexchip_5_9112	v2HS_233010	ATAGTTTCCCAAAGCCTTTGCT	NM_001195	BFSP1	beaded filament structural protein 1, filensin (BFSP1), mRNA	-1.68	0.39	-0.42	0.28	-1.26	0.01
Hs_12plexchip_5_4769	v2HS_257526	ATTACTAGATTATTTGGCCGCT	NM_032194	BXDC1	brix domain containing 1 (BXDC1), mRNA	-1.44	0.33	0.43	1.01	-1.87	0.07
Hs_12plexchip_6_4225	v2HS_275380	TTGAACAAGGAATTTAGCAGAT	NM_018321	BXDC2	brix domain containing 2 (BXDC2), mRNA	-2.51	0.94	-0.33	1.42	-2.18	0.10
Hs_12plexchip_5_11048	v2HS_235217	TTTACCAAAGTTCAAGATAGGC	NM_025065	BXDC5	brix domain containing 5 (BXDC5), mRNA	-1.09	0.89	0.66	0.41	-1.75	0.06
Hs_12plexchip_4_3707	v2HS_221262	ATCAAGAACATCTTACTGTCCA	NM_173590	C11ORF36	CHROMOSOME 11 OPEN READING FRAME 36	-1.48	0.75	-0.33	0.46	-1.15	0.10
Hs_12plexchip_6_7155	v2HS_228510	AATAGTTTCAGTTGCTCAGCCC	NM_032127	C11orf56	chromosome 11 open reading frame 56 (C11orf56), transcript variant 1, mRNA	-1.75	1.06	0.51	0.61	-2.26	0.04
Hs_12plexchip_6_4960	v2HS_285512	TTGTTGTTAGGAGACCTCAGGC	NM_173578	C11orf72	chromosome 11 open reading frame 72 (C11orf72), mRNA	-1.18	0.47	-0.17	0.33	-1.01	0.05
Hs_12plexchip_5_8254	v2HS_264911	TTATACTCTTATTAACATTGCG	NM_001099676	C12orf56	chromosome 12 open reading frame 56 (C12orf56), mRNA	-1.30	0.36	-0.17	0.17	-1.13	0.02
Hs_12plexchip_5_12893	v2HS_59558	ATTAGCATGGATCGTCTGTTCT	NM_014059	C13orf15	chromosome 13 open reading frame 15 (C13orf15), mRNA	-1.48	0.73	0.21	0.69	-1.68	0.04
Hs0P00012174	v2HS_19844	AATAATTCAGACATATCCTCCT	NM_145248	C13orf28	chromosome 13 open reading frame 28 (C13orf28), mRNA	-1.60	0.54	-0.47	0.68	-1.12	0.09
Hs_12plexchip_5_12662	v2HS_23231	TTATAAGACAATTTATCAGGCA	NM_134447	C19orf2	chromosome 19 open reading frame 2 (C19orf2), transcript variant 2, mRNA	-3.13	0.71	0.04	1.96	-3.16	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_11563	v2HS_272110	TTGCTCTGATACTCAATGAGCT	NM_030933	C1orf14	chromosome 1 open reading frame 14 (C1orf14), mRNA	-1.27	0.14	0.13	0.76	-1.40	0.08
Hs_12plexchip_4_5204	v2HS_17999	TGTAGATTTCATCCAGTCTCTC	NM_024331	C20orf121	chromosome 20 open reading frame 121 (C20orf121), transcript variant 1, mRNA	-2.93	0.22	0.05	0.60	-2.98	0.01
Hs_12plexchip_3_12552	v2HS_244109	TTGTAATCAAGATTCTTGGGCG	NM_018944	C21orf45	chromosome 21 open reading frame 45 (C21orf45), mRNA	-3.27	0.94	-0.63	0.44	-2.64	0.02
Hs_12plexchip_2_11284	v2HS_47645	TAAGGGATGGAGAGACACAGCC	NM_058188	C21ORF67	CHROMOSOME 21 OPEN READING FRAME 67	-1.70	0.20	-0.60	0.63	-1.09	0.08
Hs_12plexchip_6_7110	v2HS_35694	GATGTAGTACACCTTGGCGGCA	NM_207307	C3orf25	chromosome 3 open reading frame 25 (C3orf25), mRNA	-1.61	0.38	-0.21	0.45	-1.40	0.02
Hs_12plexchip_6_8467	v2HS_284705	TTGGGCCTGTACATAATATGGT	NM_001001343	C5orf40	chromosome 5 open reading frame 40 (C5orf40), mRNA	-1.08	0.05	0.12	0.21	-1.20	0.01
Hs_12plexchip_4_8659	v2HS_89094	TTTGTGAGAGGCTTGAATGGCT	NM_000065	C6	complement component 6 (C6), mRNA	-1.21	0.45	-0.06	0.59	-1.15	0.06
Hs_12plexchip_6_1960	v2HS_154208	TTGTAAGTTCTTAGGATATGCC	NM_001040437	C6orf48	chromosome 6 open reading frame 48 (C6orf48), transcript variant 1, mRNA	-1.20	0.13	0.02	0.34	-1.22	0.01
Hs_12plexchip_6_3737	v2HS_174884	ATTGAGACTGAGATATTCACCG	NM_017994	C7orf42	chromosome 7 open reading frame 42 (C7orf42), mRNA	-1.40	0.67	0.10	0.84	-1.50	0.08
Hs_12plexchip_5_4096	v2HS_87013	TTTAGCAATGCAGAACTTGGCA	NM_148179	C9orf23	chromosome 9 open reading frame 23 (C9orf23), transcript variant 2, mRNA	-2.09	0.72	0.25	0.22	-2.34	0.02
Hs_12plexchip_6_10789	v2HS_160717	TTTCCAGATTAATCACAAGGCT	NM_173521	C9orf84	chromosome 9 open reading frame 84 (C9orf84), transcript variant 1, mRNA	-1.05	0.60	0.93	1.25	-1.99	0.09
Hs_12plexchip_4_2803	v2HS_186977	TTTGCTCTTATTCCCGTGGGCT	NM_173550	C9orf93	chromosome 9 open reading frame 93 (C9orf93), mRNA	-2.17	0.76	-0.82	0.53	-1.35	0.07
Hs_12plexchip_5_7273	v2HS_263904	TTTCTCTCTACAACTTGATCCT	NM_206925	CA12	carbonic anhydrase XII (CA12), transcript variant 2, mRNA	-1.59	0.07	-0.27	0.15	-1.32	0.00
Hs_12plexchip_5_12635	v2HS_248549	TTTAGAAATGGGAGGACCAGCC	NM_006030	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2 (CACNA2D2), transcript variant 2, mRNA	-1.16	0.27	0.07	0.30	-1.23	0.01
Hs_12plexchip_4_9782	v2HS_15097	TTGTATTCTGAGTCTCCGTGCA	NM_004343	CALR	calreticulin (CALR), mRNA	-2.33	0.73	-0.50	0.86	-1.82	0.05
Hs_12plexchip_5_4216	v2HS_256535	ATTTGAATGGGATTTCTATCCT	NM_199141	CARM1	coactivator-associated arginine methyltransferase 1 (CARM1), mRNA	-1.52	0.55	-0.23	0.22	-1.29	0.04
Hs_12plexchip_4_10865	v2HS_38737	ATAGACAAAGGATTTGACAGGC	NM_144508	CASC5	cancer susceptibility candidate 5 (CASC5), transcript variant 2, mRNA	-1.59	0.44	-0.46	0.16	-1.13	0.03
Hs_12plexchip_5_5327	v2HS_88343	ATAGTGGGATAAATTCTCACCG	NM_053054	CATSPER1	cation channel, sperm associated 1 (CATSPER1), mRNA	-1.93	0.38	-0.32	0.64	-1.61	0.03
Hs_12plexchip_5_139	v2HS_245413	TTAGCTCTTCATATATCAACCT	NM_152549	CCDC112	coiled-coil domain containing 112 (CCDC112), transcript variant 2, mRNA	-1.58	0.19	0.09	0.35	-1.67	0.01
Hs_12plexchip_6_2225	v2HS_33560	ATAGTCCAAGAGGAAGTCTCCA	NM_033626	CCDC120	coiled-coil domain containing 120 (CCDC120), mRNA	-1.36	0.43	-0.28	0.41	-1.08	0.03
Hs0P00003883	v2HS_197544	TAATGCATTTACTTATTCTCCC	NM_005893	CCIN	CALICIN	-1.41	0.91	0.25	0.62	-1.66	0.07
Hs_12plexchip_4_500	v2HS_112771	TTTGCTTTCCAAGGAGGAACGG	NM_001237	CCNA2	cyclin A2 (CCNA2), mRNA	-1.84	0.56	-0.65	0.58	-1.19	0.06
Hs_12plexchip_4_1037	v2HS_198914	TATTCCATGCTTAAGAATACGT	NM_006431	CCT2	chaperonin containing TCP1, subunit 2 (beta) (CCT2), mRNA	-2.09	0.48	-0.86	0.26	-1.24	0.03
Hs_12plexchip_5_3556	v2HS_254661	TATTCTAATCCAATATACAGCA	NM_001078645	CDC16	cell division cycle 16 homolog (S. cerevisiae) (CDC16), transcript variant 2, mRNA	-1.51	0.17	0.03	0.17	-1.54	0.00
Hs_12plexchip_5_3479	v2HS_226246	ATAATGATTCAAAGGGAGACCA	NM_001256	CDC27	cell division cycle 27 homolog (S. cerevisiae) (CDC27), mRNA	-1.11	0.36	0.03	0.29	-1.14	0.01
Hs_12plexchip_5_11993	v2HS_272144	TTAAGTAATGCTAATTTAACCA	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-4.70	1.03	-0.63	0.30	-4.08	0.01
Hs_12plexchip_4_10431	v2HS_155714	AATTTCCACTAACTAGGGAGGT	NM_018101	CDCA8	cell division cycle associated 8 (CDCA8), mRNA	-2.01	0.82	-0.03	0.27	-1.98	0.04
Hs_12plexchip_4_8826	v2HS_150461	TTTGTGACTCGGAAGAACTGGC	NM_001795	CDH5	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA	-1.57	0.99	0.65	1.16	-2.22	0.07
Hs_12plexchip_4_182	v2HS_134767	ATGATCATACAGCCCAAAGCCC	NM_016508	CDKL3	cyclin-dependent kinase-like 3 (CDKL3), mRNA	-1.30	1.14	0.67	0.74	-1.97	0.08
Hs_12plexchip_6_10314	v2HS_150582	TTAGATGTGCCATGAGGTACCG	NM_001025201	CHN1	chimerin (chimaerin) 1 (CHN1), transcript variant 2, mRNA	-1.32	0.62	-0.21	0.53	-1.11	0.08
Hs_12plexchip_5_5654	v2HS_256894	TAATTCGAAGCAAATCACAGCT	NM_000083	CLCN1	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA	-1.31	0.45	-0.18	0.22	-1.13	0.03

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00005661	v2HS_115260	TATCAATGGCATAGGACAGCGT	NM_206999	CNOT1	CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 2, mRNA	-2.09	0.52	0.51	0.34	-2.60	0.00
Hs0P00004205	v2HS_254700	TTTATTCCCGATTTCATAAGCA	NM_004236	COPS2	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 2 (ARABIDOPSIS)	-1.37	0.10	-0.01	0.06	-1.37	0.00
Hs0P00005048	v2HS_229617	TTAGCTTAATACACAGAGACCC	NM_016129	COPS4	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 4 (ARABIDOPSIS)	-3.17	0.96	1.41	0.62	-4.59	0.00
Hs0P00005841	v2HS_258048	ATATTTAGGACACTTCAGAGCA	NM_006837	COPS5	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 5 (ARABIDOPSIS)	-1.56	0.22	-0.29	0.31	-1.27	0.01
Hs0P00006089	v2HS_118859	ATATAAAGCTAGAAGCTGACCA	NM_198189	COPS8	COP9 CONSTITUTIVE PHOTOMORPHOGENIC HOMOLOG SUBUNIT 8 (ARABIDOPSIS)	-1.15	0.70	0.53	0.23	-1.68	0.04
Hs_12plexchip_4_467	v2HS_159527	TTCTCCTTCTCCTTCAGGGCCT	NM_032609	COX4I2	cytochrome c oxidase subunit IV isoform 2 (lung) (COX4I2), nuclear gene encoding mitochondrial protein, mRNA	-2.40	0.26	-0.54	0.49	-1.86	0.01
Hs_12plexchip_2_9846	v2HS_16655	ATGGGTAATAATATTAGTGTCT	NM_003851	CREG1	cellular repressor of E1A-stimulated genes 1 (CREG1), mRNA	-1.39	0.47	-0.14	0.37	-1.25	0.03
Hs_12plexchip_5_10727	v2HS_135449	ATACACTTTCCGTGCATGGGCA	NM_016652	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila) (CRNKL1), mRNA	-1.57	0.65	-0.33	0.41	-1.24	0.06
Hs_12plexchip_5_9115	v2HS_97938	TTGATGCATTAGGGTAGATGGG	NM_016190	CRNN	cornulin (CRNN), mRNA	-1.11	0.13	0.23	0.15	-1.34	0.00
Hs_12plexchip_3_11951	v2HS_239988	TTATTTCCAGAGGTTCTGTCCC	NM_003798	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA	-1.29	0.46	-0.12	0.48	-1.17	0.04
Hs_12plexchip_6_1286	v2HS_62138	ATCTGAAAGGAGTTACTATGCT	NM_004937	CTNS	cystinosis, nephropathic (CTNS), transcript variant 2, mRNA	-1.34	0.42	0.46	0.62	-1.80	0.02
Hs_12plexchip_6_4024	v2HS_178400	ATAAAGTGACATTTCCCTGGGC	NM_033427	CTTNBP2	cortactin binding protein 2 (CTTNBP2), mRNA	-1.16	1.07	1.49	1.42	-2.64	0.07
Hs_12plexchip_4_11416	v2HS_200239	GTATAGACACCGATGGTAAGCT	NM_001100812	CXCL16	chemokine (C-X-C motif) ligand 16 (CXCL16), transcript variant 2, mRNA	-1.60	0.16	-0.47	0.54	-1.13	0.06
Hs_12plexchip_3_2537	v2HS_58298	ATATGGTTTCCCAATCCCTGTC	AK021694	CXORF10	CHROMOSOME X OPEN READING FRAME 10	-1.38	0.26	0.17	0.84	-1.55	0.07
Hs0P00009553	v2HS_144182	TTTCCTGGAGAGTTGCTTGGGC	CR605567	CXORF40A	CHROMOSOME X OPEN READING FRAME 40A	-2.08	0.54	-0.28	0.22	-1.80	0.02
Hs_12plexchip_4_7656	v2HS_93339	TTTATTCTACCCTGCAGGACCC	NM_001026213	CYP11B1	cytochrome P450, family 11, subfamily B, polypeptide 1 (CYP11B1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.49	0.79	0.04	0.62	-1.53	0.06
Hs_12plexchip_6_9470	v2HS_24094	TTAAGGTGGGACATAGGGAGGA	NM_004393	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1), mRNA	-1.16	0.45	-0.11	0.26	-1.05	0.04
Hs_12plexchip_5_7128	v2HS_202258	TATTGGGATGTTTCACTCGGCG	NM_001040261	DCLK2	doublecortin-like kinase 2 (DCLK2), transcript variant 2, mRNA	-1.77	0.50	-0.24	0.28	-1.53	0.02
Hs_12plexchip_2_869	v2HS_114977	TTTGTAAGAGTCAGGAGGACCT	NM_016221	DCTN4	dynactin 4 (p62) (DCTN4), mRNA	-1.22	0.16	-0.14	0.37	-1.08	0.02
Hs_12plexchip_2_9105	v2HS_30469	TAATTGGTGGTAAATCTGCCCA	NM_018665	DDX43	DEAD (Asp-Glu-Ala-Asp) box polypeptide 43 (DDX43), mRNA	-1.42	0.58	-0.31	0.47	-1.11	0.06
Hs0P00006485	v2HS_98186	TTTGGATGACCGTCTGGAGGCC	NM_022719	DGCR14	DiGeorge syndrome critical region gene 14 (DGCR14), mRNA	-2.01	0.56	0.28	1.37	-2.29	0.09
Hs_12plexchip_5_7535	v2HS_227147	ATTCACTAACACGATTTGGCCT	NM_001105571	DHRS7C	dehydrogenase/reductase (SDR family) member 7C (DHRS7C), mRNA	-1.19	0.67	1.13	0.91	-2.31	0.03
Hs0P00000365	v2HS_60544	TTGTCTCTGATAATAGTGAGCA	NM_014003	DHX38	DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA	-2.17	0.12	-0.98	0.29	-1.19	0.01
Hs_12plexchip_4_874	v2HS_202805	TTTAGCTTCCTGCTGATCTGCC	NM_022105	DIDO1	death inducer-obliterator 1 (DIDO1), transcript variant 1, mRNA	-1.40	0.15	-0.13	0.27	-1.27	0.00
Hs_12plexchip_5_5655	v2HS_258802	TTCCCACTGTGCTATGTTTGCA	BX537874	DKFZP313P036	HYPOTHETICAL PROTEIN DKFZP313P036	-1.36	0.80	-0.09	0.54	-1.27	0.09
Hs_12plexchip_3_6731	v2HS_96969	AATGGGTATGGAGGAAATGCCT	NM_015569	DNM3	dynamin 3 (DNM3), mRNA	-1.45	0.60	0.48	0.70	-1.93	0.02
Hs_12plexchip_4_10262	v2HS_118260	TTCTCTGTCCGTAGTGTCTCCA	NM_052951	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1 (DNTTIP1), mRNA	-1.02	1.24	0.92	0.82	-1.94	0.10
Hs_12plexchip_3_2463	v2HS_70419	ATTGGAGAGGACATCCTGATGC	NM_080677	DYNLL2	dynein, light chain, LC8-type 2 (DYNLL2), mRNA	-1.95	0.28	-0.01	0.47	-1.94	0.01
Hs_12plexchip_5_5910	v2HS_257261	TTATGATCTCAATGTGACAGGG	NM_021783	EDA2R	ectodysplasin A2 receptor (EDA2R), mRNA	-1.66	0.74	-0.11	0.36	-1.55	0.05
Hs_12plexchip_3_4772	v2HS_113620	TTTGTAGACATCCTGGAGAGGC	NM_001402	EEF1A1	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA	-2.31	0.19	-0.58	0.46	-1.73	0.01
Hs_12plexchip_5_12827	v2HS_172951	TTACAAAGGGACTTGTTGTCGA	NM_004093	EFNB2	ephrin-B2 (EFNB2), mRNA	-1.29	0.16	0.28	0.53	-1.58	0.03
Hs0P00006261	v2MM_45585	TAAAGGAATTTCTTCCAAACGC	NM_010123	EIF3S10	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 10 (THETA)	-1.16	0.26	0.33	0.38	-1.50	0.01

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs0P00005681	v2HS_23869	TCTTGTACTCTGTCACTGTCTT	NM_003755	EIF3S4	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 4 DELTA, 44KDA	-1.79	0.95	0.22	0.65	-2.01	0.05
Hs0P00005621	v2HS_242811	TTAAGAAATCTTGAGGCCAGCG	NM_003752	EIF3S8	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 8, 110KDA	-2.18	0.63	-0.09	0.60	-2.09	0.01
Hs_12plexchip_5_7166	v2HS_255274	ATTCTTTACAAAGTTAATGGCC	NM_014740	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3 (EIF4A3), mRNA	-2.37	0.67	0.30	0.18	-2.66	0.01
Hs_12plexchip_5_10681	v2HS_268779	TAGAGCCCAATCATTGTTTCCA	NM_133455	EMID1	EMI domain containing 1 (EMID1), mRNA	-2.41	0.52	-0.64	0.69	-1.77	0.03
Hs_12plexchip_4_10304	v2HS_96160	ATTATCATAACCATGGTCACCT	NM_014936	ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4), mRNA	-1.31	0.75	-0.04	0.24	-1.27	0.09
Hs_12plexchip_5_21	v2HS_251354	TTTACCTAATATGGTTTGTGCT	NM_021572	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function) (ENPP5), mRNA	-1.56	0.56	-0.24	0.50	-1.33	0.04
Hs_12plexchip_4_5890	v2HS_17728	TATAAATGTAACCATCTCACCC	NM_004446	EPRS	glutamyl-prolyl-tRNA synthetase (EPRS), mRNA	-2.04	0.31	-0.51	0.55	-1.53	0.02
Hs_12plexchip_5_12713	v2HS_242534	ATGTGATAGAGGGACTGTTGGG	NM_004450	ERH	enhancer of rudimentary homolog (Drosophila) (ERH), mRNA	-2.18	0.70	0.43	0.15	-2.61	0.02
Hs_12plexchip_6_4135	v2HS_275659	ATTTAGTTCATATTGATAAGGA	NM_002685	EXOSC10	exosome component 10 (EXOSC10), transcript variant 2, mRNA	-1.26	0.32	0.65	0.50	-1.91	0.01
Hs_12plexchip_5_6463	v2HS_262285	TATATTGACAGTTCACTAGGGC	NM_019037	EXOSC4	exosome component 4 (EXOSC4), mRNA	-2.33	0.50	0.28	0.40	-2.60	0.00
Hs_12plexchip_5_12923	v2HS_46919	ATACATGTGACCATAGAGTGCG	NM_003950	F2RL3	coagulation factor II (thrombin) receptor-like 3 (F2RL3), mRNA	-1.19	0.30	0.28	0.31	-1.47	0.00
Hs_12plexchip_6_10663	v2HS_179101	TTCTCGTGGTTCAGTATAGCCT	NM_173678	FAM139A	family with sequence similarity 139, member A (FAM139A), mRNA	-1.48	0.53	0.90	0.79	-2.37	0.02
Hs_12plexchip_4_4693	v2HS_83637	TTTCTGAGTGGTCATAACTCCT	NM_000135	FANCA	Fanconi anemia, complementation group A (FANCA), transcript variant 1, mRNA	-1.71	0.17	-0.68	0.60	-1.03	0.09
Hs0P00010700	v2HS_113773	TTCTCTCCATAAACTGATTCCC	NM_001436	FBL	FIBRILLARIN	-2.07	0.04	-0.02	0.69	-2.05	0.03
Hs_12plexchip_5_3246	v2HS_51035	TACATTCACAAAGTTCTCTGCG	NM_012308	FBXL11	F-box and leucine-rich repeat protein 11 (FBXL11), mRNA	-1.20	0.34	0.11	0.13	-1.31	0.01
Hs_12plexchip_6_3356	v2HS_263207	TTGTGCAAAGGTTCTTAATGCA	NM_032875	FBXL20	F-box and leucine-rich repeat protein 20 (FBXL20), mRNA	-1.24	0.37	0.41	0.26	-1.65	0.00
Hs_12plexchip_5_6011	v2HS_47264	ATTTGACCTCAGAATGACGGTG	NM_174899	FBXO36	F-box protein 36 (FBXO36), mRNA	-2.45	0.25	0.49	1.40	-2.94	0.06
Hs_12plexchip_4_7702	v2HS_89328	ATATTCTGAGACTTTGCATGGT	NM_001013415	FBXW7	F-box and WD repeat domain containing 7 (FBXW7), transcript variant 3, mRNA	-1.15	0.70	0.34	0.34	-1.49	0.05
Hs_12plexchip_4_8858	v2HS_93704	TTGTAAGTACTATTTCCTTCCT	NM_000566	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64) (FCGR1A), mRNA	-1.05	0.67	0.50	0.68	-1.55	0.05
Hs_12plexchip_3_4414	v2HS_50567	TTTAACTCAGACACTGAGAGCC	NM_001042548	FEZ2	fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), transcript variant 2, mRNA	-1.60	0.55	-0.31	0.79	-1.29	0.09
Hs_12plexchip_6_9356	v2HS_155310	TTGTAAGATCTGTCACAGACCC	NM_018029	FLJ10213	hypothetical protein FLJ10213 (FLJ10213), mRNA	-1.14	1.39	2.22	1.06	-3.36	0.03
Hs0P00012742	v2HS_103190	TTATTGCCTTTACTTCTGTGGG	AK092066	FLJ34747	HYPOTHETICAL GENE SUPPORTED BY AK092066	-1.43	0.08	0.23	0.50	-1.66	0.03
Hs_12plexchip_3_5599	v2HS_129545	ATTTGCCTTGAGGACATTTGCC	AK124699	FLJ42709	HYPOTHETICAL GENE SUPPORTED BY AK124699	-1.20	0.58	0.60	0.41	-1.80	0.01
Hs_12plexchip_3_4576	v2HS_121611	TTAACCATTTAGGTGATGGGCA	AK075161	FLJ90680	FLJ90680 PROTEIN	-1.67	0.33	-0.59	0.65	-1.08	0.08
Hs_12plexchip_5_12296	v2HS_247736	TATTTGAGCCATTCTGTGACCC	NM_013231	FLRT2	fibronectin leucine rich transmembrane protein 2 (FLRT2), mRNA	-1.39	0.17	-0.18	0.40	-1.21	0.02
Hs_12plexchip_5_3203	v2HS_204193	AACAATTCGGAGTTTATACCTG	XM_941378	FOXR1	PREDICTED:forkhead box R1 (FOXR1), mRNA	-1.40	0.44	-0.31	0.23	-1.08	0.03
Hs_12plexchip_3_857	v2HS_36153	CTAATGATGGATACTTTGGCCT	NM_144966	FREM1	FRAS1 related extracellular matrix 1 (FREM1), mRNA	-1.00	0.32	0.07	0.20	-1.07	0.01
Hs_12plexchip_3_8782	v2HS_95990	ATTGATAACCTGGCTAATCCCA	NM_014907	FRMPD1	FERM and PDZ domain containing 1 (FRMPD1), mRNA	-1.10	0.15	0.01	0.54	-1.11	0.06
Hs_12plexchip_5_12561	v2HS_42851	TAAAGTTACAATGCAGTCTTGC	NM_005257	GATA6	GATA binding protein 6 (GATA6), mRNA	-1.40	0.09	-0.12	0.07	-1.28	0.00
Hs_12plexchip_6_2560	v2HS_155064	AATGCTGTGGATTTGCTGAGCC	NM_017660	GATAD2A	GATA zinc finger domain containing 2A (GATAD2A), mRNA	-1.57	0.58	0.68	0.07	-2.24	0.02
Hs0P00003410	v2HS_36125	TTTGGGAAGGAAGGGCAAGGCT	NM_004752	GCM2	glial cells missing homolog 2 (Drosophila) (GCM2), mRNA	-1.61	0.36	-0.44	0.58	-1.17	0.05
Hs_12plexchip_5_12786	v2HS_249954	TTCTCATCCAGGAAGAGGACCC	NM_004962	GDF10	growth differentiation factor 10 (GDF10), mRNA	-2.00	0.44	-0.78	0.67	-1.22	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_12552	v2HS_212899	TTTCAGTGATCTGTTGTGGCAG	NM_000168	GLI3	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome) (GLI3), mRNA	-1.31	0.52	0.68	0.38	-1.99	0.01
Hs_12plexchip_3_1559	v2HS_65339	TTATTCCATACAGCCCTGGCCC	NM_013334	GMPPB	GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 1, mRNA	-1.30	0.61	-0.28	0.18	-1.02	0.09
Hs_12plexchip_6_1270	v2HS_220370	ATACTGTTGCTCTTAGGGCGGT	NM_019067	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like (GNL3L), mRNA	-1.13	0.27	0.01	0.70	-1.14	0.09
Hs_12plexchip_5_10795	v2HS_138347	TTAACCTTCTCTACTTCCTGCA	NM_032292	GON4L	gon-4-like (C. elegans) (GON4L), transcript variant 2, mRNA	-1.40	0.07	-0.25	0.24	-1.15	0.01
Hs_12plexchip_6_374	v2HS_55806	CTGCTTCATCACATGGGCAGGT	NM_005682	GPR56	G protein-coupled receptor 56 (GPR56), transcript variant 1, mRNA	-2.85	1.14	0.24	1.68	-3.08	0.07
Hs_12plexchip_4_10370	v2HS_159238	TAAAGCATTGATTGACTGAGCC	NM_032554	GPR81	G protein-coupled receptor 81 (GPR81), mRNA	-1.89	0.88	0.33	0.44	-2.23	0.03
Hs_12plexchip_4_7095	v2HS_68798	TATAGTCATGGAGTCCAGCCTT	NM_004810	GRAP2	GRB2-related adaptor protein 2 (GRAP2), mRNA	-2.01	0.69	-0.72	0.46	-1.28	0.06
Hs_12plexchip_6_4378	v2HS_179821	TATTTCCACCATCAAGGGTCCC	XM_940982	GRIP2	PREDICTED:glutamate receptor interacting protein 2, transcript variant 2 (GRIP2), mRNA	-1.34	0.72	-0.14	0.25	-1.19	0.09
Hs_12plexchip_5_8971	v2HS_265999	TTATTAATTAGCACAATTAGGT	NM_002094	GSPT1	G1 to S phase transition 1 (GSPT1), mRNA	-1.06	0.27	0.15	0.40	-1.20	0.02
Hs_12plexchip_5_7036	v2HS_133007	TTTGAGAATGTATTGCCTCCGA	NM_002110	HCK	hemopoietic cell kinase (HCK), mRNA	-1.01	0.27	0.05	0.54	-1.06	0.06
Hs_12plexchip_5_3240	v2HS_211804	TTACACAAAGGGTCACTTCCTC	NM_138820	HIGD2A	HIG1 domain family, member 2A (HIGD2A), mRNA	-1.70	0.64	-0.22	0.45	-1.48	0.04
Hs_12plexchip_6_1839	v2HS_195911	ATCTAGAAATGGAACCACTGCT	NM_005517	HMGN2	high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA	-1.74	0.60	0.12	0.47	-1.87	0.02
Hs_12plexchip_6_78	v2HS_117147	ATGGGATAAGATTTCTAAACCC	NM_004500	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRNPC), transcript variant 2, mRNA	-2.01	0.72	-0.86	0.21	-1.14	0.10
Hs_12plexchip_4_8899	v2HS_133162	ATATTTACAAGCTTTGGGCCCT	NM_002147	HOXB5	homeobox B5 (HOXB5), mRNA	-1.13	0.96	1.29	0.62	-2.42	0.03
Hs0P00007673	v2HS_136048	TTCTTCTGTTTCATCCTGCGGT	NM_024501	HOXD1	homeobox D1 (HOXD1), mRNA	-1.18	0.40	0.24	0.46	-1.42	0.02
Hs_12plexchip_2_4291	v2HS_82370	TTTGATAATGTGACTGTGTGGC	NM_000198	HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2), mRNA	-1.22	0.30	0.13	0.50	-1.35	0.02
Hs_12plexchip_6_6626	v2HS_137326	TAGAAGTCCCTCATGATCTGGT	NM_025193	HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 (HSD3B7), mRNA	-1.86	0.41	-0.58	0.29	-1.28	0.01
Hs_12plexchip_3_11020	v2HS_138414	TTTAGATGCAAGGTAGGTGCCT	NM_032303	HSDL2	hydroxysteroid dehydrogenase like 2 (HSDL2), mRNA	-1.31	0.81	0.08	0.46	-1.39	0.08
Hs_12plexchip_4_521	v2HS_115310	ATTAAATCCAGCAGCTCTAGCT	NM_016299	HSPA14	heat shock 70kDa protein 14 (HSPA14), transcript variant 1, mRNA	-1.67	0.87	0.14	0.79	-1.81	0.06
Hs_12plexchip_2_6111	v2HS_173169	ATTGTTTGGGTTGGTGACAGCC	NM_004134	HSPA9	heat shock 70kDa protein 9 (mortalin) (HSPA9), nuclear gene encoding mitochondrial protein, mRNA	-2.33	0.41	-0.64	0.41	-1.69	0.01
Hs_12plexchip_3_11065	v2HS_193423	TTTAAGTTCAGCAATTACAGCA	NM_199440	HSPD1	heat shock 60kDa protein 1 (chaperonin) (HSPD1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA	-1.42	0.27	-0.02	0.51	-1.40	0.02
Hs_12plexchip_5_6173	v2HS_262858	TTTAGGATCAGATTTATCTGCT	NM_031407	HUWE1	HECT, UBA and WWE domain containing 1 (HUWE1), mRNA	-1.29	0.70	0.24	0.61	-1.53	0.05
Hs_12plexchip_5_11771	v2HS_133238	TTAATCAGATATAATCTGAGGG	NM_013417	IARS	isoleucyl-tRNA synthetase (IARS), transcript variant long, mRNA	-2.72	0.34	-0.75	0.24	-1.96	0.00
Hs_12plexchip_6_9815	v2HS_155481	ATAGTCTCAAATGTTGTTTCCA	NM_018060	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial (IARS2), mRNA	-2.36	0.67	-0.66	1.13	-1.69	0.10
Hs_12plexchip_5_3710	v2HS_96821	TTAAACACTCAGAAACAAACCA	NM_015525	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase (IBTK), mRNA	-1.03	0.38	0.19	0.17	-1.23	0.02
Hs_12plexchip_4_6153	v2HS_27524	ATAATTATGCTCTCAAACAGCC	NM_003640	IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein (IKBKAP), mRNA	-1.30	0.95	0.49	0.89	-1.79	0.08
Hs_12plexchip_5_7783	v2HS_266151	TTCTTCAGTTGCTTAGAGGGCC	AK095107	IL1RAP	INTERLEUKIN 1 RECEPTOR ACCESSORY PROTEIN	-1.22	0.48	-0.02	0.41	-1.20	0.03
Hs_12plexchip_4_7333	v2HS_72166	TTGAAGAAGAACACGGGCAGGG	NM_004136	IREB2	iron-responsive element binding protein 2 (IREB2), mRNA	-1.97	0.43	-0.50	0.63	-1.47	0.03
Hs0P00000643	v2HS_67751	ATTACCAAGGACACTCTATCTG	NM_004867	ITM2A	integral membrane protein 2A (ITM2A), mRNA	-1.05	0.62	0.00	0.16	-1.05	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_4_993	v2HS_133559	TTTCACCAAATCATACTGTCCC	NM_002227	JAK1	Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA	-1.98	0.31	-0.56	0.50	-1.42	0.02
Hs_12plexchip_3_11418	v2HS_135205	TTTGCATATGATCTCGAAACCA	NM_016604	JMJD1B	jumonji domain containing 1B (JMJD1B), mRNA	-1.70	0.36	-0.66	0.61	-1.04	0.08
Hs_12plexchip_5_933	v2HS_247394	TTATAATTTCTGGAATTGGCCA	NM_005548	KARS	lysyl-tRNA synthetase (KARS), mRNA	-1.44	0.27	-0.40	0.41	-1.04	0.03
Hs_12plexchip_3_456	v2HS_52418	ATATTCATAAATACACACAGCA	NM_020122	KCMF1	potassium channel modulatory factor 1 (KCMF1), mRNA	-1.09	0.38	0.07	0.76	-1.16	0.10
Hs_12plexchip_4_4613	v2HS_160241	ATATCGATCCAGTTTCCTGGCC	NM_173162	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 2, mRNA	-1.12	0.83	0.51	0.26	-1.63	0.07
Hs_12plexchip_5_3542	v2HS_14575	ATTCCATGTAAGAGTAAAGGCA	NM_138444	KCTD12	potassium channel tetramerisation domain containing 12 (KCTD12), mRNA	-2.25	0.34	-0.49	0.58	-1.76	0.02
Hs_12plexchip_5_9238	v2HS_98989	TTAAGGTGTAGTGACATAGGCT	NM_024089	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1 (KDELC1), mRNA	-1.04	0.47	0.25	0.19	-1.29	0.03
Hs_12plexchip_5_4566	v2HS_73018	AGAACTAGACACTTAATTTGGT	NM_001029989	KIAA0101	KIAA0101 (KIAA0101), transcript variant 2, mRNA	-1.30	0.27	0.01	0.05	-1.31	0.01
Hs_12plexchip_5_9831	v2HS_230811	TAAATGCCAAAGAGACTATCCC	D87447	KIAA0258	KIAA0258	-1.14	0.30	-0.09	0.22	-1.05	0.01
Hs_12plexchip_5_4402	v2HS_259524	ATCTTCAACTATAGAATGTCCT	AB007978	KIAA0509	KIAA0509 PROTEIN	-1.67	0.98	1.27	1.81	-2.94	0.09
Hs0P00011684	v2HS_53708	TTCCAAAGGCACAATAACACCA	NM_020701	KIAA1160	KIAA1160 PROTEIN	-1.92	0.53	-0.89	0.31	-1.04	0.06
Hs_12plexchip_2_5631	v2HS_184080	AACGGTTTCGGTGCAGGGAGCC	BC036932	KIAA1856	KIAA1856 PROTEIN	-1.69	0.53	-0.60	0.62	-1.09	0.08
Hs_12plexchip_4_9195	v2HS_78033	ATTCTTGCTTATTCAGTGGGCG	NM_006845	KIF2C	kinesin family member 2C (KIF2C), mRNA	-1.22	0.33	-0.02	0.30	-1.21	0.01
Hs_12plexchip_4_12291	v2HS_80810	AATGTTCAGCAGTTCTCTCGGG	NM_022480	KLHL25	kelch-like 25 (Drosophila) (KLHL25), mRNA	-1.20	0.69	-0.01	0.36	-1.19	0.08
Hs_12plexchip_2_4006	v2HS_85137	TTTGAGATTGGGATGCAGCCTG	NM_001025231	KPRP	keratinocyte proline-rich protein (KPRP), mRNA	-1.52	0.42	-0.36	0.77	-1.16	0.10
Hs_12plexchip_4_11729	v2HS_169384	TTTCCTACTAGGACCATAGGCA	NM_033360	KRAS	V-HA-RAS HARVEY RAT SARCOMA VIRAL ONCOGENE HOMOLOG	-2.04	0.53	-0.86	0.70	-1.18	0.09
Hs_12plexchip_4_11915	v2HS_133836	ATGGTCCTGAAATGAGACTGGT	NM_002278	KRT32	keratin 32 (KRT32), mRNA	-2.35	1.31	-0.30	0.44	-2.05	0.10
Hs_12plexchip_5_4850	v2HS_74382	TTAGGAGTACACTTGGGAGGGC	NM_178438	LCE5A	late cornified envelope 5A (LCE5A), mRNA	-1.19	0.90	0.44	0.69	-1.62	0.07
Hs_12plexchip_5_575	v2HS_51161	TTATGTGATGGAATTATACCCG	NR_003590	LOC100101117	testis-specific transcript, Y-linked 2-like (LOC100101117) on chromosome Y	-1.78	1.13	0.59	1.44	-2.37	0.09
Hs_12plexchip_5_2301	v2HS_209586	TTAGCATATTCTGCAGCTACTT	XR_016217	LOC120318	PREDICTED:similar to 40S ribosomal protein S6 (LOC120318), mRNA	-1.15	0.37	0.25	0.28	-1.40	0.01
Hs_12plexchip_5_4991	v2HS_259415	TTGTATTTGCAATTAGCTGCCT	XR_016263	LOC121906	PREDICTED:similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) (LOC121906), mRNA	-1.29	0.45	0.01	0.46	-1.30	0.02
Hs_12plexchip_6_7185	v2HS_191934	ATTGTAATTAGGAGCCAGTCGA	XM_941747	LOC130773	PREDICTED:similar to 60S ribosomal protein L23a (LOC130773), mRNA	-1.81	0.29	-0.68	0.40	-1.13	0.02
Hs_12plexchip_4_3309	v2HS_181356	TTGAACTCAAATAAAGCAGGGC	BX647231	LOC148145	HYPOTHETICAL PROTEIN LOC148145	-1.29	0.16	-0.18	0.53	-1.10	0.06
Hs_12plexchip_4_5768	v2HS_26291	GAACATAGTGACAGTCAGTGCA	BC040263	LOC150297	HYPOTHETICAL PROTEIN LOC150297	-1.63	0.49	-0.15	0.60	-1.48	0.03
Hs_12plexchip_5_9047	v2HS_120186	ATTCCTGCTATAGATCGGTCCT	NM_001014830	LOC196913	hypothetical protein LOC196913 (LOC196913), mRNA	-1.34	0.61	0.38	0.91	-1.72	0.06
Hs_12plexchip_4_1689	v2HS_213536	ATTCTGATGAATTGGCTGGGCT	BC039539	LOC255654	HYPOTHETICAL PROTEIN LOC255654	-1.25	0.75	0.89	0.17	-2.14	0.03
Hs_12plexchip_6_11076	v2HS_182508	TTTCTCTTTCTCTTCACATCCA	AK091446	LOC283194	HYPOTHETICAL PROTEIN LOC283194	-1.27	0.22	-0.25	0.24	-1.02	0.01
Hs_12plexchip_3_8982	v2HS_131660	TACAAATAGCACAGGAGGACCC	XM_497352	LOC283412	PREDICTED:similar to 60S ribosomal protein L29 (Cell surface heparin-binding protein HIP) (LOC283412), mRNA	-1.66	0.17	-0.28	0.77	-1.39	0.08
Hs0P00007920	v2HS_142836	TTACCCTGTCATTCTGTCTCCC	AK092322	LOC283575	HYPOTHETICAL PROTEIN LOC283575	-1.80	0.69	-0.55	0.65	-1.25	0.08
Hs_12plexchip_6_11763	v2HS_163979	ATGCTGTAATAGTTGCTGAGCT	AK097486	LOC283738	HYPOTHETICAL PROTEIN LOC283738	-1.20	0.53	0.59	0.40	-1.79	0.01
Hs_12plexchip_5_10591	v2HS_103411	ATAAGTTGTGGGTTCATCTGGG	AK097672	LOC284344	HYPOTHETICAL PROTEIN LOC284344	-1.53	0.49	-0.10	0.44	-1.43	0.02
Hs_12plexchip_5_9148	v2HS_103423	ATCAGCTCTCCAGAGAACAGGC	NR_002938	LOC284379	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene (LOC284379) on chromosome 19	-1.13	0.23	0.00	0.22	-1.14	0.00
Hs_12plexchip_6_2724	v2HS_182880	TTTAATCGCGAGACAATACGGG	AK094324	LOC284408	HYPOTHETICAL PROTEIN LOC284408	-1.27	0.83	0.25	0.44	-1.52	0.07
Hs_12plexchip_2_9250	v2HS_21776	TTAAGGCAACAAATAGTGTCGT	XM_373030	LOC285556	PREDICTED:hypothetical protein LOC285556 (LOC285556), mRNA	-1.08	0.60	0.21	0.60	-1.30	0.06
Hs_12plexchip_4_1442	v2HS_213268	ATGGTGAATGATCTTAGCGGTG	XM_291007	LOC339766	PREDICTED:hypothetical protein LOC339766 (LOC339766), mRNA	-1.10	0.51	-0.02	0.10	-1.08	0.06
Hs_12plexchip_6_6813	v2HS_285588	TTACCACAACAATATGTACCCA	NM_207376	LOC387882	HYPOTHETICAL PROTEIN	-1.58	0.56	0.38	0.73	-1.97	0.02

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_11361	v2HS_237760	TAAGTGGTAATGCTTCATACCA	NM_001089587	LOC389435	hCG21078 (LOC389435), mRNA	-1.44	0.08	-0.34	0.25	-1.10	0.01
Hs_12plexchip_6_11984	v2HS_192962	TTTATCTGGCAATTCCAAGGCT	XR_018253	LOC401197	PREDICTED:similar to ribosomal protein L7-like 1 (LOC401197), mRNA	-2.15	0.28	-0.45	0.16	-1.71	0.00
Hs_12plexchip_6_12168	v2HS_165316	ATCAACTTTCGTGGAATCTGGG	XM_496697	LOC441018	PREDICTED:similar to UDP-glucuronosyltransferase 2B7 precursor (UDPGT) (3,4-catechol estrogen specific) (UDPGTh-2) (LOC441018), mRNA	-1.23	0.34	0.26	0.22	-1.49	0.01
Hs0P00011576	v2HS_188312	TTAATAACTGTGAGAACATGGG	NR_003536	LOC441246	hCG1983332 (LOC441246) on chromosome 7	-1.95	0.10	-0.75	0.66	-1.20	0.08
Hs_12plexchip_5_11559	v2HS_144280	TAGTTGCTACAAGGACCATGGT	XM_927548	LOC644402	PREDICTED:hypothetical LOC644402 (LOC644402), mRNA	-1.05	0.19	0.44	0.28	-1.49	0.00
Hs_12plexchip_2_10359	v2HS_32694	ATTAATAAGTGCTGTCAGACCA	XM_927812	LOC644717	PREDICTED:similar to sarcoma antigen 1 (LOC644717), mRNA	-1.41	0.45	-0.34	0.13	-1.07	0.05
Hs_12plexchip_6_6067	v2HS_190051	ATGCATACAGTGAGCCGCAGCC	XM_928136	LOC645100	PREDICTED:similar to CG11699-PA (LOC645100), mRNA	-1.28	0.57	0.54	1.07	-1.82	0.08
Hs_12plexchip_6_12808	v2HS_193874	ATCTTGGACAAGTTTAGCTCCA	XR_016831	LOC645808	PREDICTED:similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60) (LOC645808), mRNA	-2.30	0.91	-0.22	1.24	-2.08	0.08
Hs_12plexchip_6_2822	v2HS_184074	TTTCTTCACTCCTCTGTACGCC	XM_935722	LOC646762	PREDICTED:hypothetical protein LOC646762 (LOC646762), mRNA	-1.56	0.62	-0.12	0.31	-1.44	0.04
Hs_12plexchip_3_11479	v2HS_233964	AATTTCTTGGACATGGTTTCCT	XR_017618	LOC647039	PREDICTED:similar to Death domain-containing protein CRADD (Caspase and RIP adapter with death domain) (RIP-associated protein with a death domain) (LOC647039), mRNA	-1.08	0.46	0.41	0.48	-1.49	0.02
Hs_12plexchip_3_8689	v2HS_101886	AATTCTACCCAATCTCTAGCCA	XR_018477	LOC648987	PREDICTED:hypothetical LOC648987 (LOC648987), mRNA	-1.52	0.32	0.11	0.27	-1.64	0.00
Hs_12plexchip_5_7718	v2HS_121873	TTCATGGTGGACATTCTAAGGT	XM_940582	LOC651430	PREDICTED:hypothetical LOC651430 (LOC651430), mRNA	-1.44	0.34	-0.44	0.34	-1.00	0.02
Hs_12plexchip_3_12580	v2HS_242292	TTAATCTTGAACCTTGGAGGCT	XR_019381	LOC652549	PREDICTED:similar to SNW domain-containing protein 1 (Nuclear protein SkiP) (Ski-interacting protein) (Nuclear receptor coactivator NCoA-62) (LOC652549), mRNA	-1.51	0.44	-0.11	0.35	-1.39	0.01
Hs_12plexchip_4_1504	v2HS_205865	TTATTGAAGAAACCAATCCTGG	XM_942509	LOC652826	PREDICTED:similar to 26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7) (LOC652826), mRNA	-1.94	0.18	-0.93	0.52	-1.01	0.06
Hs_12plexchip_5_634	v2HS_41661	TAAGGACTCCGAAGAAACTGGT	XM_001131663	LOC729890	PREDICTED:hypothetical protein LOC729890 (LOC729890), mRNA	-1.64	0.48	0.06	0.65	-1.70	0.03
Hs_12plexchip_5_5556	v2HS_117690	TTTATTGCAGGTTCCAACCGGG	XM_001132025	LOC730000	PREDICTED:similar to testis-specific serine kinase 6 (LOC730000), mRNA	-1.35	0.42	-0.24	0.57	-1.10	0.06
Hs_12plexchip_5_3665	v2HS_254576	ATAATGAGTAACTTCAGAAGGC	XM_001124597	LOC730411	PREDICTED:similar to zinc finger and BTB domain containing 8 (LOC730411), mRNA	-1.10	0.24	1.08	0.08	-2.18	0.00
Hs_12plexchip_6_12384	v2HS_142522	TTATTTGAGGAGCTCATGAGCT	NM_201550	LRRC10	LEUCINE RICH REPEAT CONTAINING 10	-1.80	1.01	-0.15	0.49	-1.65	0.09
Hs_12plexchip_5_1241	v2HS_247143	TTATACAAAGAGTTGGTCCCGA	NM_005512	LRRC32	leucine rich repeat containing 32 (LRRC32), mRNA	-1.54	0.08	0.47	0.94	-2.01	0.06
Hs_12plexchip_3_420	v2HS_50487	TTTCCTTATCACTCTTCATCAC	NM_012322	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM5), mRNA	-1.92	0.85	-0.01	0.35	-1.92	0.04
Hs_12plexchip_4_12292	v2HS_151587	TATAACCTTCAAAGCACTGGCA	NM_030583	MATN2	matrilin 2 (MATN2), transcript variant 2, mRNA	-1.50	0.68	-0.40	0.27	-1.10	0.09
Hs_12plexchip_3_2395	v2HS_69010	ATGAACTACCAGATGCAGGTTG	NM_024596	MCPH1	microcephalin 1 (MCPH1), mRNA	-1.43	0.56	-0.42	0.16	-1.01	0.08
Hs_12plexchip_6_903	v2HS_197525	ATTCCAAATCTCTTCACTTGCC	NM_006838	METAP2	methionyl aminopeptidase 2 (METAP2), mRNA	-2.36	0.32	-0.37	0.75	-1.98	0.03
Hs_12plexchip_5_3248	v2HS_49368	TTCCTGTCATTGATTATATGCT	NM_001098624	MID1	midline 1 (Opitz/BBB syndrome) (MID1), transcript variant 4, mRNA	-2.07	0.41	-0.74	0.51	-1.33	0.03
Hs_12plexchip_5_1542	v2HS_249839	ATAGCAAAGGGATCCATCAGGA	NM_005439	MLF2	myeloid leukemia factor 2 (MLF2), mRNA	-1.44	0.51	-0.02	0.30	-1.42	0.02
Hs_12plexchip_2_12570	v2HS_198375	TATTGGTTTGCGAATAAGACCT	NM_005933	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) (MLL), mRNA	-1.30	0.53	-0.24	0.44	-1.06	0.06

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_6_1814	v2HS_117180	ATACTGTAGAACATGACATCCT	NM_031415	MLZE	melanoma-derived leucine zipper, extra-nuclear factor (MLZE), mRNA	-1.52	1.05	1.12	1.25	-2.64	0.05
Hs_12plexchip_4_7836	v2HS_151873	TTAACATTCATTGGTCCTTCCT	NM_002432	MNDA	myeloid cell nuclear differentiation antigen (MNDA), mRNA	-1.04	0.47	0.04	0.63	-1.08	0.08
Hs_12plexchip_5_1540	v2HS_54255	TTTCGGAAGAACGGAAGAAGCA	NM_130807	MOBKL2A	MOB1, Mps One Binder kinase activator-like 2A (yeast) (MOBKL2A), mRNA	-1.55	0.13	-0.32	0.52	-1.23	0.05
Hs_12plexchip_5_11551	v2HS_272336	TTGTATTCCTGGTTCTTATGGC	NM_032332	MORG1	mitogen-activated protein kinase organizer 1 (MORG1), transcript variant 2, mRNA	-1.52	0.40	-0.18	0.49	-1.33	0.02
Hs0P00010208	v2HS_16945	TTCTTCCATCATGCTCAACGGC	NM_003829	MPDZ	multiple PDZ domain protein (MPDZ), mRNA	-2.39	0.93	-0.95	0.49	-1.44	0.10
Hs_12plexchip_6_9149	v2HS_237290	GTGATTGCTCTCTTTAGAGGCG	NM_145213	MRPL30	mitochondrial ribosomal protein L30 (MRPL30), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA	-2.60	0.11	-0.29	0.30	-2.31	0.00
Hs0P00002853	v2HS_62393	CTAGAATTTGAATTGCTGAGCC	BG327319	MRPL49	MITOCHONDRIAL RIBOSOMAL PROTEIN L49	-1.40	0.45	0.28	0.37	-1.68	0.01
Hs_12plexchip_3_2049	v2HS_61946	AATTGCAGAATCGTGAGATGGT	AY135343	MRPS36P4	MITOCHONDRIAL RIBOSOMAL PROTEIN S36 PSEUDOGENE 4	-1.87	0.65	-0.62	0.45	-1.25	0.06
Hs_12plexchip_4_1019	v2HS_196467	TTAACAAATTGGACTATTGGAC	NM_001006635	MTX2	metaxin 2 (MTX2), transcript variant 2, mRNA	-2.45	0.72	-0.35	0.30	-2.09	0.02
Hs_12plexchip_3_769	v2HS_50240	ATGAGGGTTGATTTCAGGCCCA	NM_005115	MVP	major vault protein (MVP), transcript variant 2, mRNA	-1.22	0.17	-0.22	0.58	-1.00	0.09
Hs_12plexchip_5_3585	v2HS_71122	TAAGCTATCCTATTAATTGGGC	NM_013262	MYLIP	myosin regulatory light chain interacting protein (MYLIP), mRNA	-2.03	1.07	0.98	1.43	-3.01	0.05
Hs_12plexchip_2_2845	v2HS_83390	ATTTCAACCGACTGATTTGCGG	NM_023018	NADK	NAD kinase (NADK), mRNA	-1.27	0.43	-0.08	0.39	-1.20	0.02
Hs_12plexchip_4_6500	v2HS_66759	GTAGAATATCACGCAGGCAGGG	NM_153006	NAGS	N-acetylglutamate synthase (NAGS), mRNA	-1.70	0.44	-0.64	0.22	-1.05	0.03
Hs_12plexchip_6_11820	v2HS_121992	TTATACTCATAGTCCTCAACCT	XR_017910	NAP1L6	PREDICTED:nucleosome assembly protein 1-like 6 (NAP1L6), misc RNA	-1.63	0.07	-0.11	0.55	-1.51	0.04
Hs_12plexchip_5_11516	v2HS_272934	TTTATTCATTGCTTTATAAGCC	NM_057175	NARG1	NMDA receptor regulated 1 (NARG1), mRNA	-1.63	0.19	0.32	0.02	-1.95	0.00
Hs_12plexchip_5_9142	v2HS_267506	TTTAAATTAGAGGCTCCCTGGA	NM_014903	NAV3	neuron navigator 3 (NAV3), mRNA	-1.65	0.67	-0.36	0.61	-1.29	0.07
Hs_12plexchip_6_9437	v2HS_250396	AATAGGTAGCGATTCTGACCTT	NR_003108	NBR2	neighbor of BRCA1 gene 2 (NBR2) on chromosome 17	-1.20	0.50	-0.01	0.40	-1.19	0.04
Hs_12plexchip_6_1620	v2HS_95758	ATTGCTTCCCACAATTTCTGGC	NM_014865	NCAPD2	non-SMC condensin I complex, subunit D2 (NCAPD2), mRNA	-1.08	0.56	1.18	0.64	-2.27	0.01
Hs_12plexchip_6_8471	v2HS_36645	TTTCCTAGTCATACCAATTCTG	NM_005381	NCL	nucleolin (NCL), mRNA	-2.38	0.99	-0.74	0.66	-1.64	0.08
Hs_12plexchip_4_6295	v2HS_20571	CTAAATGTTGACGGTCTTGGCC	NM_005002	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa (NDUFA9), mRNA	-1.56	0.82	0.09	0.73	-1.65	0.06
Hs_12plexchip_5_6456	v2HS_262163	TTTATTCTTTCCAACCTTTCCT	NM_012224	NEK1	NIMA (never in mitosis gene a)-related kinase 1 (NEK1), mRNA	-1.33	0.55	-0.14	0.24	-1.19	0.05
Hs_12plexchip_5_5442	v2HS_260806	TTAAGTAATGCGATATTGAGCA	NM_000267	NF1	neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), transcript variant 2, mRNA	-1.23	0.12	2.30	0.39	-3.53	0.00
Hs_12plexchip_3_8465	v2HS_98549	TTAGCGATCCATTCATTCACCA	NM_022787	NMNAT1	nicotinamide nucleotide adenylyltransferase 1 (NMNAT1), mRNA	-1.38	0.24	-0.32	0.46	-1.06	0.04
Hs0P00010705	v2HS_47052	TTCACTTCCAGCGGTACTGGGC	NM_003946	NOL3	nucleolar protein 3 (apoptosis repressor with CARD domain) (NOL3), mRNA	-1.44	0.40	0.18	0.54	-1.62	0.02
Hs_12plexchip_5_3215	v2HS_253869	ATTAAACTTAACTTTGGCACGG	NM_006392	NOL5A	nucleolar protein 5A (56kDa with KKE/D repeat) (NOL5A), mRNA	-2.61	0.66	-0.98	0.15	-1.63	0.04
Hs_12plexchip_3_11626	v2HS_174662	TTTCAGATTCATTTATTGAGGG	NM_017948	NOL8	nucleolar protein 8 (NOL8), mRNA	-1.09	0.42	0.38	0.10	-1.47	0.02
Hs_12plexchip_4_6028	v2HS_30849	TTTCTTCAGCGTATAGACTCGA	NM_018648	NOLA3	nucleolar protein family A, member 3 (H/ACA small nucleolar RNPs) (NOLA3), mRNA	-1.04	0.27	0.24	0.81	-1.27	0.10
Hs_12plexchip_4_5492	v2HS_25500	ATCTTCTATGGGTTTGTGGCAC	NG_000886	NPM1P13	NUCLEOPHOSMIN 1 (NUCLEOLAR PHOSPHOPROTEIN B23, NUMATRIN) PSEUDOGENE 13	-1.76	0.41	-0.69	0.37	-1.07	0.03
Hs_12plexchip_6_9954	v2HS_131222	ATGCAATTTCAGGAGCAAAGCT	NM_000904	NQO2	NAD(P)H dehydrogenase, quinone 2 (NQO2), mRNA	-1.40	0.95	0.34	0.58	-1.74	0.07
Hs_12plexchip_5_7176	v2HS_61886	ACTTAGTAGGCGAGTGTCCGGG	NM_004959	NR5A1	nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA	-1.10	0.61	0.71	0.15	-1.81	0.03
Hs_12plexchip_5_11467	v2HS_139799	TATTCCAATGACTGCCAGAGGG	NM_015135	NUP205	nucleoporin 205kDa (NUP205), mRNA	-2.67	1.05	-0.52	0.26	-2.15	0.06
Hs_12plexchip_5_4320	v2HS_79283	TTCTTGAGTAAAGTCAAGGGCG	NM_014669	NUP93	NUCLEOPORIN 93KDA	-1.91	0.67	-0.22	0.67	-1.69	0.04
Hs_12plexchip_5_12758	v2HS_197810	TTTCTTTGAGGGAAATTAACGC	NM_006362	NXF1	nuclear RNA export factor 1 (NXF1), transcript variant 1, mRNA	-1.64	0.36	-0.33	0.46	-1.30	0.02
Hs_12plexchip_6_8498	v2HS_91268	ATTAGTATTCATAACAACTGCT	NM_007280	OIP5	Opa interacting protein 5 (OIP5), mRNA	-1.46	0.59	-0.10	0.74	-1.36	0.07

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_12900	v2HS_198794	TTTGCAGAGTTAATCCTCAGCA	NM_007160	OR2H2	olfactory receptor, family 2, subfamily H, member 2 (OR2H2), mRNA	-2.22	0.77	-0.92	0.70	-1.30	0.10
Hs_12plexchip_5_11676	v2HS_273833	TTCGTTAGGGTCATAATTTCCA	NM_001004063	OR4K1	olfactory receptor, family 4, subfamily K, member 1 (OR4K1), mRNA	-1.37	0.23	-0.30	0.16	-1.07	0.00
Hs_12plexchip_5_10876	v2HS_274419	TTAGACTATTTCCCGAGCTGCT	NM_024586	OSBPL9	oxysterol binding protein-like 9 (OSBPL9), transcript variant 6, mRNA	-1.01	0.10	0.06	0.51	-1.07	0.06
Hs_12plexchip_5_8998	v2HS_98327	TTAGTTGTGCCATAGACCAGGT	NM_022750	PARP12	poly (ADP-ribose) polymerase family, member 12 (PARP12), mRNA	-1.10	0.43	-0.07	0.38	-1.03	0.04
Hs_12plexchip_5_3785	v2HS_75540	TTCTTCTATACTATTGTGAGGA	NM_016483	PHF7	PHD finger protein 7 (PHF7), transcript variant 1, mRNA	-1.02	0.75	1.05	1.23	-2.07	0.08
Hs_12plexchip_4_2383	v2HS_169417	TTTATGTGAAAGTTAAAGCCCA	NG_001173	PHKBP2	PHOSPHORYLASE KINASE, BETA PSEUDOGENE 2	-1.10	0.84	1.53	0.68	-2.63	0.01
Hs_12plexchip_4_9658	v2HS_58415	ATAAATACTGTGTGACGGTGGC	NM_006221	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA	-1.13	0.51	1.00	1.00	-2.13	0.05
Hs_12plexchip_5_6616	v2HS_234804	ATTCAGTTCAAGGCACATACGT	NM_032409	PINK1	PTEN induced putative kinase 1 (PINK1), nuclear gene encoding mitochondrial protein, mRNA	-1.13	0.43	-0.01	0.67	-1.11	0.08
Hs0P00011923	v2HS_19861	TTAAACTTGAAATGGCTCGGCA	NM_005028	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha (PIP4K2A), mRNA	-1.04	0.65	0.23	0.19	-1.26	0.07
Hs_12plexchip_5_10351	v2HS_92232	ATTCACCAAATTCCCATGGGCC	NM_000300	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), mRNA	-1.42	0.32	0.38	0.17	-1.79	0.00
Hs0P00000426	v2HS_19708	TGTAATTAGGAGTCCCACACAG	NM_005030	PLK1	POLO-LIKE KINASE 1 (DROSOPHILA)	-1.75	0.22	-0.35	0.10	-1.41	0.00
Hs_12plexchip_5_9437	v2HS_267706	AACATACAGATCTAGCTGCCCT	NM_004650	PNPLA4	patatin-like phospholipase domain containing 4 (PNPLA4), mRNA	-1.23	0.21	0.08	0.37	-1.31	0.01
Hs_12plexchip_6_1230	v2HS_154166	TAATGATGAACTCTAAATTGGG	NM_016937	POLA1	polymerase (DNA directed), alpha 1 (POLA1), mRNA	-2.90	0.61	-0.06	0.35	-2.84	0.00
Hs_12plexchip_4_486	v2HS_70473	AATGAGACACTGCACATCAGGG	NM_013284	POLM	polymerase (DNA directed), mu (POLM), mRNA	-1.98	0.77	-0.04	0.28	-1.94	0.04
Hs_12plexchip_6_27	v2HS_155605	TTTATATACAAGGCAACGCCCA	NM_018082	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B (POLR3B), mRNA	-2.67	0.28	-0.95	0.96	-1.72	0.08
Hs_12plexchip_4_475	v2HS_201722	AATACATTTGAGTTAAAGAGTG	NM_006466	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa (POLR3F), mRNA	-2.61	0.59	0.64	0.29	-3.25	0.00
Hs_12plexchip_5_10139	v2HS_229159	TAATTCACTCTATTTCAGTGGA	NM_001018161	PON2	paraoxonase 2 (PON2), transcript variant 2, mRNA	-2.19	0.72	-0.67	0.66	-1.52	0.06
Hs0P00002401	v2HS_170331	ATGTTTCCTAACTTTGTCTCCT	NM_002713	PPP1R8	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 8	-1.45	0.70	0.02	0.59	-1.47	0.05
Hs_12plexchip_5_12847	v2HS_71819	TTGTTCTATAGGAAGGACTCGT	NM_006017	PROM1	prominin 1 (PROM1), mRNA	-1.26	0.24	-0.11	0.49	-1.15	0.04
Hs_12plexchip_5_6793	v2HS_89936	TAATAATGTAAGGCACAAACCA	NM_000021	PSEN1	presenilin 1 (Alzheimer disease 3) (PSEN1), mRNA	-2.71	0.49	-0.31	0.86	-2.39	0.02
Hs_12plexchip_6_755	v2HS_159974	TTTCTCTTGCTCCACATATGCC	NM_033126	PSKH2	protein serine kinase H2 (PSKH2), mRNA	-1.34	0.83	0.09	0.77	-1.42	0.10
Hs_12plexchip_4_2478	v2HS_221829	TTCTCTTCTCCACAGCTAGGCA	NM_002790	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA	-1.84	0.37	-0.33	0.55	-1.51	0.02
Hs_12plexchip_4_3837	v2HS_170736	TATAAATAGGATGGAGGATGGG	NM_002797	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5 (PSMB5), mRNA	-2.15	0.49	0.66	0.27	-2.81	0.00
Hs_12plexchip_2_6001	v2HS_170743	ATTGCATACTAGAATCCCAGGA	NM_002798	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6 (PSMB6), mRNA	-1.58	0.78	0.30	0.65	-1.88	0.03
Hs_12plexchip_4_8198	v2HS_170848	AATTAATCGAAGTTTGATAGGA	NM_002816	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA	-2.60	0.22	-0.78	0.32	-1.82	0.00
Hs_12plexchip_4_3920	v2HS_170902	TTTGTTCTTAGGAAGCTTGGCC	NM_002827	PTPN1	protein tyrosine phosphatase, non-receptor type 1 (PTPN1), mRNA	-1.34	0.30	-0.25	0.24	-1.08	0.01
Hs_12plexchip_6_10419	v2HS_19130	AATAGTCAGACGCATATGTGAC	NM_005051	QARS	glutaminyl-tRNA synthetase (QARS), mRNA	-2.33	0.50	1.14	1.42	-3.47	0.04
Hs_12plexchip_5_3595	v2HS_255132	ATGAAACTGAACAGTGGATCGT	NM_015436	RCHY1	ring finger and CHY zinc finger domain containing 1 (RCHY1), transcript variant 1, mRNA	-1.35	1.05	1.41	1.37	-2.76	0.05
Hs_12plexchip_4_5435	v2HS_19386	TATAAACATTATCAATTGCCCA	NM_173054	RELN	reelin (RELN), transcript variant 2, mRNA	-1.31	0.47	1.81	1.94	-3.13	0.10
Hs_12plexchip_4_7588	v2HS_191440	AATTGGGTGATGAGTTTCCGGT	NM_032491	RFX4	regulatory factor X, 4 (influences HLA class II expression) (RFX4), transcript variant 1, mRNA	-2.14	0.69	-0.64	0.41	-1.50	0.04
Hs_12plexchip_4_2121	v2HS_219058	TAGTAAATAAACACTGCCAGCT	NM_017821	RHBDL2	rhomboid, veinlet-like 2 (Drosophila) (RHBDL2), mRNA	-1.84	1.15	1.80	1.29	-3.64	0.02

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_10250	v2HS_96371	TTTCTCCATGAATATGTCGCCT	NM_014989	RIMS1	regulating synaptic membrane exocytosis 1 (RIMS1), mRNA	-1.32	0.67	0.04	0.54	-1.37	0.05
Hs_12plexchip_4_9499	v2HS_43940	TATCTGCATCAAATACTGAGCT	NM_012421	RLF	rearranged L-myc fusion (RLF), mRNA	-1.25	0.77	0.03	0.71	-1.28	0.10
Hs0P00005031	v2HS_95298	TATTCATCACAATTAACAGCCT	NM_014771	RNF40	RING FINGER PROTEIN 40	-1.09	0.54	0.21	0.64	-1.31	0.06
Hs_12plexchip_2_10249	v2HS_32164	TTTAAGAAGAGAAACTCCTGAG	NM_002946	RPA2	replication protein A2, 32kDa (RPA2), mRNA	-2.15	1.08	-0.24	0.96	-1.92	0.08
Hs_12plexchip_5_1217	v2HS_69321	ATAAGCCAAACCAGTGTCATCT	NM_005444	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1), mRNA	-1.95	0.39	-0.07	0.57	-1.88	0.01
Hs_12plexchip_5_12841	v2HS_37141	AAGGAGGATAAGAGTGTCAGGA	NM_004704	RRP9	RRP9, small subunit (SSU) processome component, homolog (yeast) (RRP9), mRNA	-2.38	0.32	-0.45	1.07	-1.93	0.08
Hs_12plexchip_4_10907	v2HS_87174	TAAGTTCTTAATCTCCAAAGTC	NM_015169	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (RRS1), mRNA	-2.08	0.37	-0.33	0.14	-1.75	0.01
Hs_12plexchip_4_11123	v2HS_175228	TTTAAGCCTTATATGCCAGGCT	NM_018364	RSBN1	round spermatid basic protein 1 (RSBN1), mRNA	-1.52	0.56	0.13	0.34	-1.65	0.02
Hs0P00000698	v2HS_56938	TTCGGCTTTGGCTTTGGATCCG	NM_206900	RTN2	reticulon 2 (RTN2), transcript variant 2, mRNA	-1.84	0.83	-0.18	0.83	-1.66	0.07
Hs0P00004961	v2HS_64402	TTTAACTATGACATCCCTGGAG	NM_005500	SAE1	SUMO-1 ACTIVATING ENZYME SUBUNIT 1	-1.68	0.14	-0.44	0.22	-1.25	0.00
Hs_12plexchip_5_4162	v2HS_259547	TTCCTCCAGTTGATTAATAGCT	NM_006642	SDCCAG8	serologically defined colon cancer antigen 8 (SDCCAG8), mRNA	-1.21	0.40	0.09	0.74	-1.30	0.07
Hs_12plexchip_3_3370	v2HS_41405	ATTCCACTTGGTGTGATGAGCC	NM_174975	SEC14L3	SEC14-like 3 (S. cerevisiae) (SEC14L3), mRNA	-1.55	0.51	-0.26	0.11	-1.29	0.04
Hs_12plexchip_6_3896	v2HS_169968	AATTGAGTTGTTGATCTGACCT	NM_002639	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5 (SERPINB5), mRNA	-1.48	0.60	-0.13	0.59	-1.35	0.05
Hs_12plexchip_6_8658	v2HS_68216	TACCAATAGCAGGTGAAGGGCG	NM_005490	SH2D3A	SH2 domain containing 3A (SH2D3A), mRNA	-1.30	0.52	0.02	0.85	-1.32	0.10
Hs_12plexchip_5_11115	v2HS_141439	TTCATCAATTGGTATCAGGCGT	NM_001017995	SH3PXD2B	SH3 and PX domains 2B (SH3PXD2B), mRNA	-1.38	0.13	0.75	0.19	-2.13	0.00
Hs0P00010492	v2HS_33286	ATTATCCTCCCAGACATGTGCA	NM_006304	SHFM1	split hand/foot malformation (ectrodactyly) type 1 (SHFM1), mRNA	-1.61	0.21	-0.46	0.48	-1.15	0.04
Hs_12plexchip_3_6246	v2HS_111725	TTAGAGATGCTTACCGTATGCC	NM_000617	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2), mRNA	-1.76	0.47	-0.61	0.60	-1.15	0.06
Hs_12plexchip_3_11150	v2HS_238776	TTCAGGATGAGCACTTTGAGCT	NM_032539	SLITRK2	SLIT and NTRK-like family, member 2 (SLITRK2), mRNA	-1.58	0.39	0.16	0.78	-1.74	0.04
Hs_12plexchip_4_9947	v2HS_16985	TAAATGATAAAGAAGAACAGCA	NM_130798	SNAP23	synaptosomal-associated protein, 23kDa (SNAP23), transcript variant 2, mRNA	-1.12	0.08	0.24	0.43	-1.36	0.03
Hs_12plexchip_6_1666	v2HS_228001	TAGAAACAATGCAAGCTGGGCA	NM_022808	SNRPN	small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 5, mRNA	-1.79	0.89	0.25	0.45	-2.05	0.04
Hs_12plexchip_4_9555	v2HS_19895	TTTACTGGGCCTATAAATACTC	NM_012245	SNW1	SNW domain containing 1 (SNW1), mRNA	-1.38	0.33	0.46	0.22	-1.84	0.00
Hs_12plexchip_4_12266	v2HS_153307	TTTCTTCAAACCATGCATCCGA	NM_003100	SNX2	sorting nexin 2 (SNX2), mRNA	-1.22	0.18	-0.02	0.52	-1.20	0.05
Hs_12plexchip_4_157	v2HS_96222	TTTAGTTCTCGGATAGGACCCA	NM_199436	SPAST	spastin (SPAST), transcript variant 2, mRNA	-1.87	0.20	0.32	1.06	-2.20	0.07
Hs_12plexchip_5_3220	v2HS_210161	TAAATGCCTGATATATGCCCGA	NM_138796	SPATA17	spermatogenesis associated 17 (SPATA17), mRNA	-1.82	0.50	-0.23	0.67	-1.59	0.03
Hs_12plexchip_3_10829	v2HS_234466	TAAGGAAACTCTCCCGGAGGGC	NM_016642	SPTBN5	spectrin, beta, non-erythrocytic 5 (SPTBN5), mRNA	-1.04	0.42	0.14	0.37	-1.17	0.02
Hs_12plexchip_5_1865	v2HS_213472	TTTGCTTTCAACTTTGGGAGGT	NM_194285	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae) (SPTY2D1), mRNA	-1.05	0.46	0.03	0.31	-1.08	0.03
Hs_12plexchip_5_11897	v2HS_133518	TTAGCATAAGAGGGATCCAGCA	NM_152713	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae) (STT3A), mRNA	-1.10	0.11	0.00	0.17	-1.10	0.00
Hs_12plexchip_5_7120	v2HS_262274	TTAAGTACACATATACTAAGCT	NM_024670	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila) (SUV39H2), mRNA	-1.95	0.14	0.14	0.36	-2.08	0.00
Hs_12plexchip_2_4682	v2HS_183183	ATGGGACAGCAAGGGAAGAGGG	NM_001040709	SYPL2	synaptophysin-like 2 (SYPL2), mRNA	-1.00	0.21	0.05	0.23	-1.05	0.00
Hs_12plexchip_6_6223	v2HS_274283	ATGTATCCCGATGCCAAATGGA	NM_206930	SYTL2	synaptotagmin-like 2 (SYTL2), transcript variant f, mRNA	-1.04	0.18	0.16	0.73	-1.20	0.10
Hs_12plexchip_5_1955	v2HS_206836	ATAGATTAGCACTTACCAGGCC	AY114096	TAS2R62P	TASTE RECEPTOR, TYPE 2, MEMBER 62 PSEUDOGENE	-1.57	0.19	-0.52	0.16	-1.04	0.00
Hs_12plexchip_6_9376	v2HS_211591	TAAACCTGTGAGAACCTGCTGG	NM_005993	TBCD	tubulin folding cofactor D (TBCD), mRNA	-2.24	0.50	0.50	0.60	-2.74	0.00
Hs_12plexchip_2_9032	v2HS_32310	TTCAACTTGGACTGGATTTCCC	NM_003598	TEAD2	TEA domain family member 2 (TEAD2), mRNA	-1.01	0.14	0.09	0.46	-1.09	0.05
Hs_12plexchip_5_4816	v2HS_256721	TAAACTGATTAGGGTCTTTGCC	NM_021809	TGIF2	TGFB-induced factor homeobox 2 (TGIF2), mRNA	-1.85	1.01	0.39	0.68	-2.24	0.04
Hs_12plexchip_4_160	v2HS_49799	ATAGCAAGAGAAATAATAGCTA	NM_005131	THOC1	THO complex 1 (THOC1), mRNA	-1.35	0.54	-0.11	0.45	-1.24	0.04

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_5_945	v2HS_248909	TTGAACTGTAAGGTGTGTGGCG	NM_013337	TIMM22	translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22), mRNA	-1.33	0.17	0.04	0.75	-1.37	0.08
Hs_12plexchip_6_9575	v2HS_243560	AACAAGTCTCAGGATTGGTCCG	NM_004614	TK2	thymidine kinase 2, mitochondrial (TK2), mRNA	-1.33	0.54	-0.22	0.28	-1.11	0.05
Hs_12plexchip_5_4550	v2HS_261717	ATAGACTTTCTCAACATTTGCT	NM_006827	TMED10	transmembrane emp24-like trafficking protein 10 (yeast) (TMED10), mRNA	-1.32	0.51	0.74	0.61	-2.06	0.01
Hs_12plexchip_5_9298	v2HS_99077	TAGGGTAAATGTTTGATTCGGA	NM_001105199	TMEM177	transmembrane protein 177 (TMEM177), transcript variant 3, mRNA	-1.43	0.61	0.21	0.62	-1.64	0.03
Hs_12plexchip_6_9408	v2HS_155633	ATAAATGAGTGCATGAGTTGCT	NM_018087	TMEM48	transmembrane protein 48 (TMEM48), mRNA	-2.78	0.17	-0.48	0.57	-2.30	0.01
Hs_12plexchip_6_6716	v2HS_137756	TTAGGGTTGCACCAAAGAAGGT	NM_030938	TMEM49	transmembrane protein 49 (TMEM49), mRNA	-1.32	0.18	-0.30	0.27	-1.02	0.01
Hs_12plexchip_5_9109	v2HS_270206	ATACCCAGAACACATTAAGCCT	NM_014765	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast) (TOMM20), mRNA	-1.21	0.35	0.13	0.30	-1.35	0.01
Hs_12plexchip_4_7624	v2HS_171497	ATAGTTCACAAAGTAGTGGGCA	NM_003291	TPP2	tripeptidyl peptidase II (TPP2), mRNA	-1.78	0.67	-0.10	0.84	-1.68	0.06
Hs0P00004139	v2HS_250531	TTGGGTTGTCCTTTCGTTTGCC	NM_033278	TRIM3	TRIPARTITE MOTIF-CONTAINING 3	-2.28	0.46	0.43	0.11	-2.72	0.01
Hs_12plexchip_5_3544	v2HS_26742	ATTAGTTACGAAGGTTAACGCT	NM_018700	TRIM36	tripartite motif-containing 36 (TRIM36), transcript variant 1, mRNA	-1.80	0.16	-0.23	0.69	-1.57	0.05
Hs0P00003959	v2HS_195606	TTCCTTCAACTCTAGCTCAGCA	NM_021253	TRIM39	TRIPARTITE MOTIF-CONTAINING 39	-1.42	0.38	-0.21	0.41	-1.21	0.02
Hs_12plexchip_6_2045	v2HS_154686	AATTCAGAACACATGGAATGGG	NM_017583	TRIM44	tripartite motif-containing 44 (TRIM44), mRNA	-3.92	0.38	-1.00	1.42	-2.92	0.06
Hs0P00003738	v2HS_50110	TTTGGTCAGTACTGAGTGTGGG	NM_012339	TSPAN15	tetraspanin 15 (TSPAN15), mRNA	-2.49	0.52	-0.32	0.47	-2.18	0.01
Hs_12plexchip_4_900	v2HS_117659	TTTATGGATCTTGCCCAGAGCT	NM_032028	TSSK1B	testis-specific serine kinase 1B (TSSK1B), mRNA	-1.51	0.43	-0.48	0.13	-1.03	0.04
Hs_12plexchip_6_5974	v2HS_157607	TTTAATAAGAGCTCAGCCAGGT	NM_024753	TTC21B	tetratricopeptide repeat domain 21B (TTC21B), mRNA	-1.58	0.90	0.06	0.81	-1.64	0.08
Hs_12plexchip_5_12240	v2HS_200049	ATAGGATAAAGGATTGAGCCAG	NM_014444	TUBGCP4	tubulin, gamma complex associated protein 4 (TUBGCP4), mRNA	-1.22	0.13	0.04	0.09	-1.26	0.00
Hs_12plexchip_5_9682	v2HS_231097	ATGAATGCATTTAGACACCGGA	NM_000474	TWIST1	twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) (TWIST1), mRNA	-1.25	0.21	0.08	0.21	-1.33	0.00
Hs_12plexchip_5_8132	v2HS_111298	AACTGAGAGAACATCAGCTGCC	NM_177967	UBAC2	UBA domain containing 2 (UBAC2), mRNA	-1.07	0.61	-0.08	0.32	-1.00	0.09
Hs_12plexchip_6_773	v2HS_171717	TTTAAAGCTAATCTTCTTAGGT	NM_153280	UBE1	ubiquitin-activating enzyme E1 (UBE1), transcript variant 2, mRNA	-1.04	0.36	0.37	0.65	-1.42	0.04
Hs_12plexchip_5_3620	v2HS_255135	TACTGCAATAATCAGAAGGGCT	NM_003338	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) (UBE2D1), mRNA	-1.16	0.85	0.64	0.36	-1.79	0.05
Hs0P00006197	v2HS_171781	TATAAACACAAAGGAAGTGGCG	NM_194261	UBE2I	UBIQUITIN-CONJUGATING ENZYME E2I (UBC9 HOMOLOG, YEAST)	-1.85	0.11	-0.67	0.08	-1.18	0.00
Hs_12plexchip_5_3549	v2HS_46734	ATTCATTTCCCATCGCTGAGTG	NM_003969	UBE2M	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (UBE2M), mRNA	-1.45	0.65	-0.06	0.65	-1.38	0.06
Hs_12plexchip_5_3354	v2HS_254989	ATATGCGCCTTGAAGTAGCCGC	NM_017811	UBE2R2	ubiquitin-conjugating enzyme E2R 2 (UBE2R2), mRNA	-1.76	0.51	-0.33	0.36	-1.43	0.02
Hs_12plexchip_5_6199	v2HS_262978	TTAGGATGGGATCCATCTTCCC	NM_130466	UBE3B	ubiquitin protein ligase E3B (UBE3B), transcript variant 1, mRNA	-1.05	0.30	0.38	0.28	-1.44	0.00
Hs_12plexchip_5_12253	v2HS_199008	ATATAGTCTCTCATGATCTCCT	NM_014233	UBTF	upstream binding transcription factor, RNA polymerase I (UBTF), transcript variant 1, mRNA	-2.02	0.08	-0.80	0.70	-1.22	0.09
Hs_12plexchip_5_1406	v2HS_64096	TAAACATACTTCAAACACAGCA	NM_001003684	UCRC	ubiquinol-cytochrome c reductase complex (7.2 kD) (UCRC), transcript variant 2, mRNA	-1.67	0.20	-0.56	0.46	-1.11	0.04
Hs0P00005210	v2HS_149461	TTTCACCACCTTATAAATGCCA	AB071698	UHRF2	UBIQUITIN-LIKE, CONTAINING PHD AND RING FINGER DOMAINS, 2	-1.95	0.16	-0.20	0.38	-1.75	0.01
Hs_12plexchip_5_3292	v2HS_159709	TTTAGGGTTGTGTTGACTAGGT	NM_032663	USP30	ubiquitin specific peptidase 30 (USP30), mRNA	-1.24	0.79	0.18	0.55	-1.42	0.07
Hs_12plexchip_5_281	v2HS_243816	AATATTGGTTTGGGTAGGTCCC	NM_004505	USP6	ubiquitin specific peptidase 6 (Tre-2 oncogene) (USP6), mRNA	-1.54	0.83	0.02	0.40	-1.56	0.06
Hs_12plexchip_5_12261	v2HS_245827	TTAAGAGGTGGCATATTCAGGT	NM_004654	USP9Y	UBIQUITIN SPECIFIC PEPTIDASE 9, Y-LINKED (FAT FACETS-LIKE, DROSOPHILA)	-1.03	0.62	0.09	0.36	-1.12	0.07
Hs_12plexchip_2_11994	v2HS_41380	CTAGAGGATAATATTAACCCGG	NM_004666	VNN1	vanin 1 (VNN1), mRNA	-1.28	0.08	-0.24	0.32	-1.03	0.03
Hs_12plexchip_5_5571	v2HS_255610	TTTACCAATACTGGATATTCGG	NM_014703	VPRBP	Vpr (HIV-1) binding protein (VPRBP), mRNA	-2.99	0.73	-0.58	0.32	-2.41	0.02
Hs_12plexchip_4_6384	v2HS_56762	TTTACATTCCACAACTGCAGGC	NM_139281	WDR36	WD repeat domain 36 (WDR36), mRNA	-2.84	1.42	0.21	0.95	-3.04	0.04
Hs_12plexchip_4_9846	v2HS_60148	ATTCACACAAATGTAATGCCCT	NM_014023	WDR37	WD repeat domain 37 (WDR37), mRNA	-1.94	0.57	-0.80	0.66	-1.14	0.09

Probe ID	v2HS	Sequence	Accession	Symbol	Gene Name	Mut log2 mean	Mut log2 SD	WT log2 Mean	WT log2 SD	log2 difference	P-value
Hs_12plexchip_3_7805	v2HS_229697	TTATACATCAGGATTGTTAGGA	NM_015420	WDSOF1	WD repeats and SOF1 domain containing (WDSOF1), mRNA	-1.46	0.65	-0.15	0.57	-1.32	0.06
Hs_12plexchip_5_1388	v2HS_57489	ATATTCCAAGTCTCAGGACCCT	NM_080869	WFDC12	WAP four-disulfide core domain 12 (WFDC12), mRNA	-1.04	0.78	0.31	0.72	-1.36	0.09
Hs_12plexchip_2_4319	v2HS_81482	TTCAGCTTTCAGGATCTCAGGG	NM_015238	WWC1	WW and C2 domain containing 1 (WWC1), mRNA	-1.07	0.59	0.09	0.59	-1.16	0.07
Hs0P00010609	v2HS_172053	TTTGACAGAGACTTTCGCTGGT	NM_003400	XPO1	EXPORTIN 1 (CRM1 HOMOLOG, YEAST)	-1.62	0.69	-0.34	0.29	-1.28	0.07
Hs_12plexchip_5_3512	v2HS_95794	TACTTCTATGCTATGGGCTGCT	NM_014872	ZBTB5	zinc finger and BTB domain containing 5 (ZBTB5), mRNA	-1.82	0.67	-0.26	0.14	-1.56	0.05
Hs_12plexchip_2_6697	v2HS_177528	TATGACCTTGGCCTGATTGCGG	NM_032786	ZC3H10	zinc finger CCCH-type containing 10 (ZC3H10), mRNA	-1.55	0.22	0.06	0.59	-1.61	0.03
Hs_12plexchip_4_1308	v2HS_205155	TTTCTTCTTACTTTGCTGGGCT	NM_015070	ZC3H13	zinc finger CCCH-type containing 13 (ZC3H13), mRNA	-1.90	0.51	-0.81	0.58	-1.09	0.07
Hs_12plexchip_6_6092	v2HS_175791	AACAGGAACAGCATCAATGGCT	NM_018471	ZC3H15	zinc finger CCCH-type containing 15 (ZC3H15), mRNA	-1.04	0.90	0.99	0.22	-2.03	0.05
Hs0P00011471	v2HS_19371	TATAGATATATTTCTGATCCGG	NM_144604	ZC3H18	zinc finger CCCH-type containing 18 (ZC3H18), mRNA	-2.59	0.79	-0.46	0.09	-2.14	0.04
Hs_12plexchip_4_10479	v2HS_70944	TGACAGTATCCTTTAGCATCTA	NM_080660	ZC3HAV1L	zinc finger CCCH-type, antiviral 1-like (ZC3HAV1L), mRNA	-1.84	0.72	-0.34	0.69	-1.50	0.06
Hs_12plexchip_6_5942	v2HS_203541	TTTCCCTCCAGGAAGAACGGGC	NM_181485	ZGPAT	zinc finger, CCCH-type with G patch domain (ZGPAT), transcript variant 3, mRNA	-1.09	0.41	0.07	0.77	-1.16	0.10
Hs_12plexchip_5_4248	v2HS_260005	TATGGTCCTGAATAGGTCTGGA	NM_001011657	ZMAT1	zinc finger, matrin type 1 (ZMAT1), transcript variant 1, mRNA	-1.16	0.16	0.27	0.21	-1.43	0.00
Hs_12plexchip_2_1211	v2HS_78271	ATATTGTGATGTTTAATGAGGT	NM_001012756	ZNF260	zinc finger protein 260 (ZNF260), mRNA	-1.22	0.22	-0.14	0.52	-1.08	0.05
Hs_12plexchip_6_6835	v2HS_160859	TTTCCAGTGCTGATAGAGGCCT	NM_173548	ZNF584	zinc finger protein 584 (ZNF584), mRNA	-1.16	0.54	0.42	0.55	-1.58	0.02
Hs0P00010224	v2HS_112771	TTTGCTTTCCAAGGAGGAACGG	NM_001237	CCNA2	CYCLIN A2	-1.53	0.28	0.21	0.15	-1.73	0.00
Hs0P00005647	v2HS_254661	TATTCTAATCCAATATACAGCA	NM_003903	CDC16	CDC16 CELL DIVISION CYCLE 16 HOMOLOG (S. CEREVISIAE)	-1.17	0.17	0.24	0.14	-1.41	0.00
Hs_12plexchip_5_10993	v2HS_235686	TTTCCATTACAGACTAGAAGGC	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-2.51	0.80	-0.39	0.75	-2.12	0.03
Hs_12plexchip_3_9508	v2HS_136197	ATAATTCAGAATCTCAAGTGCG	NM_024529	CDC73	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae) (CDC73), mRNA	-2.05	0.45	-0.14	0.71	-1.91	0.02
Hs_12plexchip_5_6926	v2HS_262071	ATAACAAATACCACAGAGAGCC	NM_018101	CDCA8	cell division cycle associated 8 (CDCA8), mRNA	-1.20	0.38	0.13	0.78	-1.33	0.08
Hs0P00004945	v2HS_201808	TTTAATACCTGCCTGAGCACCG	NM_022105	DIDO1	DEATH INDUCER-OBLITERATOR 1	-1.43	0.50	-0.37	0.54	-1.06	0.07
Hs_12plexchip_5_6759	v2HS_255163	TTCTTTACAAAGTTAATGGCCA	NM_014740	EIF4A3	eukaryotic translation initiation factor 4A, isoform 3 (EIF4A3), mRNA	-2.25	0.73	-0.88	0.75	-1.37	0.09
Hs_12plexchip_3_5015	v2HS_110972	ATAGCCAACAGTAGCATGTGGC	NM_031407	HUWE1	HECT, UBA and WWE domain containing 1 (HUWE1), mRNA	-1.48	0.39	-0.37	0.31	-1.11	0.02
Hs0P00000186	v2HS_133559	TTTCACCAAATCATACTGTCCC	NM_002227	JAK1	JANUS KINASE 1 (A PROTEIN TYROSINE KINASE)	-1.42	0.68	0.02	0.64	-1.44	0.06
Hs_12plexchip_4_207	v2HS_160244	AATATTCTTCAAGACGTTGCCT	NM_173162	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7 (KCNH7), transcript variant 2, mRNA	-1.00	0.39	0.40	0.55	-1.40	0.03
Hs_12plexchip_4_10174	v2HS_95371	TATTGTATAGATGGAGGCTGCG	XM_941746	KIAA0258	PREDICTED:KIAA0258, transcript variant 3 (KIAA0258), mRNA	-2.37	0.85	0.07	0.15	-2.45	0.03
Hs_12plexchip_4_7706	v2HS_170690	ATTCTCTTCTCCACAGCTAGGC	NM_002790	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5 (PSMA5), mRNA	-1.92	0.21	-0.74	0.61	-1.17	0.07
Hs0P00010747	v2HS_19370	TTTCATAGTCATAATAAGGGTC	NM_144604	ZC3H18	zinc finger CCCH-type containing 18 (ZC3H18), mRNA	-2.32	0.58	-0.62	0.23	-1.71	0.02

Supplemental Table 3. Validated shRNAs

Qualifying shRNAs are those that reduce the normalized fitness of DLD-1 Ras Mut cells to below 90% of control FF shRNA in the competition assay. N/A, not analyzed.

				DLD-1 Mut cells fitness (% FF)		**HCT116 Mut cells fitness (% FF)**	
Symbol	**Accession**	**v2SH**	**Sequence**	**Mean**	**SD**	**Mean**	**SD**
ANAPC1	NM_022662	v2HS_98169	AATAGACATATCCATGGTGCCT	82.2	3.2	48.3	3.7
ANAPC1	NM_022662	v2HS_98171	TTTATGCAAACAGTTAAATGCT	55.1	1.9	81.0	6.9
ANAPC1	NM_022662	v2HS_98167	TATTAGTAATCGTTTCTGTCCA	75.5	1.7	104.9	10.7
ANAPC4	NM_013367	v2HS_254660	ATACAATGGAATACAGATTGCT	92.1	5.8	51.4	1.7
ANAPC4	NM_013367	v2HS_64633	TATACTAAAGACAAAGGCAGCT	84.8	4.4	59.2	4.8
BXDC1	NM_032194	v2HS_257526	ATTACTAGATTATTTGGCCGCT	84.6	4.6	89.3	3.0
BXDC2	NM_018321	v2HS_275380	TTGAACAAGGAATTTAGCAGAT	79.4	7.9	64.7	2.7
BXDC5	NM_025065	v2HS_235217	TTTACCAAAGTTCAAGATAGGC	71.4	3.9	67.1	3.2
C19orf2	NM_134447	v2HS_23231	TTATAAGACAATTTATCAGGCA	78.2	2.9	67.1	4.5
C20orf121	NM_024331	v2HS_17999	TGTAGATTTCATCCAGTCTCTC	85.2	2.9	83.1	2.0
C21orf45	NM_018944	v2HS_244109	TTGTAATCAAGATTCTTGGGCG	80.9	1.3	68.5	4.8
CASC5	NM_144508	v2HS_38737	ATAGACAAAGGATTTGACAGGC	68.2	2.6	62.7	6.4
CCNA2	NM_001237	v2HS_112771	TTTGCTTTCCAAGGAGGAACGG	61.1	1.3	N/A	N/A
CCT2	NM_006431	v2HS_198914	TATTCCATGCTTAAGAATACGT	82.1	5.8	90.7	2.2
CDC16	NM_003903	v2HS_254661	TATTCTAATCCAATATACAGCA	51.9	6.8	N/A	N/A
CDC27	NM_001256	v2HS_112887	ATTTGGATCAACTTGGATAGCT	89.8	18.3	N/A	N/A
CDCA8	NM_018101	v2HS_262071	ATAACAAATACCACAGAGAGCC	83.3	2.8	56.8	1.7
COPS3	NM_011991	v2MM_21587	TATGATTCCAACATGATATGGC	81.5	1.4	N/A	N/A
COPS4	NM_016129	v2HS_229617	TTAGCTTAATACACAGAGACCC	83.0	2.6	N/A	N/A
COPS8	NM_198189	v2HS_118859	ATATAAAGCTAGAAGCTGACCA	86.7	5.0	N/A	N/A
CSE1L	NM_001316	v2HS_113224	AATGAATGTGCTGTACGGAGGA	66.2	3.0	46.2	3.7
CXORF40A	CR605567	v2HS_144182	TTTCCTGGAGAGTTGCTTGGGC	76.1	6.0	95.4	4.1
DATF1	NM_022105	v2HS_202805	TTTAGCTTCCTGCTGATCTGCC	72.7	10.9	N/A	N/A
DCTN4	NM_016221	v2HS_114977	TTTGTAAGAGTCAGGAGGACCT	81.5	1.8	92.4	1.6
DHX8	D50487	v2HS_130548	TATAAATGTCACCAATGGTGGG	39.0	6.4	22.0	1.4
EIF3S4	NM_003755	v2HS_23869	TCTTGTACTCTGTCACTGTCTT	53.4	9.6	N/A	N/A
EIF3S8	NM_003752	v2HS_242811	TTAAGAAATCTTGAGGCCAGCG	65.7	4.8	N/A	N/A
ERH	NM_004450	v2HS_242534	ATGTGATAGAGGGACTGTTGGG	61.0	2.5	45.4	1.8
FBL	NM_001436	v2HS_113773	TTCTCTCCATAAACTGATTCCC	81.2	4.6	35.7	6.2
FIP1L1	NM_030917	v2HS_137633	TTTCACAGTAAGCTTTCCAGGT	86.7	1.9	59.1	1.1
FLJ34747	AK092066	v2HS_103190	TTATTGCCTTTACTTCTGTGGG	53.2	7.6	53.7	4.9
FREM1	NM_144966	v2HS_36153	CTAATGATGGATACTTTGGCCT	83.8	11.7	96.9	2.1
GDF10	NM_004962	v2HS_249954	TTCTCATCCAGGAAGAGGACCC	87.9	7.9	103.7	1.8
GSPT1	NM_002094	v2HS_265999	TTATTAATTAGCACAATTAGGT	85.5	3.5	79.9	3.0
HNRNPC	NM_004500	v2HS_117147	ATGGGATAAGATTTCTAAACCC	42.1	6.8	66.0	6.1
IL10RA	NM_001558	v2HS_132313	TTTGCAGATGGGTGCCAGAGGT	49.6	4.3	91.8	22.0
IL1RAP	AK095107	v2HS_266151	TTCTTCAGTTGCTTAGAGGGCC	54.6	12.7	94.3	5.0
IREB2	NM_004136	v2HS_72166	TTGAAGAAGAACACGGGCAGGG	78.7	4.7	93.2	2.3
JAK1	NM_002227	v2HS_133559	TTTCACCAAATCATACTGTCCC	79.8	20.1	57.0	24.8
KCNH7	NM_173162	v2HS_160241	ATATCGATCCAGTTTCCTGGCC	70.3	6.2	96.6	2.4
KIAA0258	XM_941746	v2HS_95371	TATTGTATAGATGGAGGCTGCG	24.6	5.9	49.5	1.9
KIF2C	NM_006845	v2HS_78033	ATTCTTGCTTATTCAGTGGGCG	89.0	6.4	99.3	1.9
LOC149654	XM_086625	v2HS_101621	TAACCCAAGAATTATATTCGGA	74.0	4.4	N/A	N/A
LOC283194	AK091446	v2HS_182508	TTTCTCTTTCTCTTCACATCCA	74.1	9.0	56.3	2.6
LOC285556	XM_373030	v2HS_21776	TTAAGGCAACAAATAGTGTCGT	84.6	4.9	87.5	3.1
LOC730000	XM_001132025	v2HS_117690	TTTATTGCAGGTTCCAACCGGG	89.0	4.5	91.2	2.3
MAPK7	NM_139033	v2HS_71361	TGAAGTACTGATGTTCAGCGGG	71.6	5.9	N/A	N/A
METAP2	NM_006838	v2HS_197525	ATTCCAAATCTCTTCACTTGCC	83.0	12.7	94.2	6.9
MTX2	NM_001006635	v2HS_196467	TTAACAAATTGGACTATTGGAC	74.4	1.4	78.6	5.5
NEDD8	NM_006156	v2HS_64585	ATATGATGCCTCATTATGAGCG	62.7	4.1	60.9	5.8
NF1	NM_000267	v2HS_260806	TTAAGTAATGCGATATTGAGCA	83.4	2.0	92.5	6.7
NOL5A	NM_006392	v2HS_253869	ATTAAACTTAACTTTGGCACGG	76.2	4.6	89.7	3.7
NUP93	NM_014669	v2HS_79283	TTCTTGAGTAAAGTCAAGGGCG	57.6	7.6	66.5	7.8
NUP93	NM_014669	v2HS_259822	TATAGATATAAATTTGCCGCGC	28.3	29.2	72.2	15.5
NXF1	NM_006362	v2HS_197810	TTTCTTTGAGGGAAATTAACGC	74.4	0.4	33.1	4.1
PLK1	NM_005030	v2HS_19708	TGTAATTAGGAGTCCCACACAG	7.5	3.4	N/A	N/A
PPP1R8	NM_002713	v2HS_170331	ATGTTTCCTAACTTTGTCTCCT	86.8	1.2	N/A	N/A
PSEN1	NM_000021	v2HS_89936	TAATAATGTAAGGCACAAACCA	19.9	8.3	39.1	3.4
PSMA5	NM_002790	v2HS_221829	TTCTCTTCTCCACAGCTAGGCA	69.5	7.9	80.6	4.5
PSMB5	NM_002797	v2HS_170736	TATAAATAGGATGGAGGATGGG	46.3	2.5	57.9	8.4
PSMB6	NM_002798	v2HS_277575	AACACATCTCCTTAAAGAGGCT	62.6	2.8	84.7	14.9
QARS	NM_005051	v2HS_19130	AATAGTCAGACGCATATGTGAC	78.2	1.8	85.9	2.3
RIMS1	NM_014989	v2HS_96371	TTTCTCCATGAATATGTCGCCT	81.9	2.5	88.5	4.7
RIOK1	NM_031480	v2HS_117526	TATGGTTCTCATTCTATTTGCC	39.5	18.6	71.6	12.6
SAE1	NM_005500	v2HS_64402	TTTAACTATGACATCCCTGGAG	58.6	3.8	84.6	14.4
SHFM1	NM_006304	v2HS_33286	ATTATCCTCCCAGACATGTGCA	64.9	1.8	64.3	4.1
SMC4	NM_001002800	v2HS_68088	TTTCAACTTAATACTAAGTGCA	81.7	2.1	59.8	8.1
SUV39H2	NM_024670	v2HS_262274	TTAAGTACACATATACTAAGCT	52.7	5.0	54.8	6.8
THOC1	NM_005131	v2HS_49799	ATAGCAAGAGAAATAATAGCTA	66.1	4.1	33.8	5.5
TMED10	NM_006827	v2HS_261717	ATAGACTTTCTCAACATTTGCT	70.7	12.1	89.9	3.5
TRIM44	NM_017583	v2HS_154686	AATTCAGAACACATGGAATGGG	83.4	4.1	107.3	0.7
UBA2	NM_005499	v2HS_255026	TTATCTAAAGCATTCATAACCA	43.4	1.1	45.0	5.1
UBE1	NM_153280	v2HS_171717	TTTAAAGCTAATCTTCTTAGGT	84.7	5.3	45.1	13.4
UBE2I	NM_194261	v2HS_171776	TTGGCAGTAAATCGTGTAGGCC	25.3	7.6	64.2	1.0
UBE2I	NM_194261	v2HS_171781	TATAAACACAAAGGAAGTGGCG	50.9	3.6	132.1	21.0
UCRC	NM_001003684	v2HS_64096	TAAACATACTTCAAACACAGCA	76.9	2.8	92.2	4.8
UHRF2	NM_152896	v2HS_149461	TTTCACCACCTTATAAATGCCA	57.6	12.1	N/A	N/A
USP39	NM_006590	v2HS_196240	AATTCATACCATTTGCCTGTCC	58.4	1.0	47.7	8.2
WDSOF1	NM_015420	v2HS_229697	TTATACATCAGGATTGTTAGGA	82.1	6.3	96.4	2.4
XPO1	NM_003400	v2HS_172053	TTTGACAGAGACTTTCGCTGGT	78.6	11.8	N/A	N/A
ZC3H18	NM_144604	v2HS_19371	TATAGATATATTTCTGATCCGG	80.7	2.1	59.6	9.4
ZC3H18	NM_144604	v2HS_19370	TTTCATAGTCATAATAAGGGTC	89.4	0.5	64.0	3.0
ZC3HAV1L	NM_080660	v2HS_70944	TGACAGTATCCTTTAGCATCTA	76.2	4.6	84.8	5.2

Supplemental Table 4. Additional sequence infromation of shRNAs and siRNAs used in validation expeirments

Gene symbol	Accession	shRNA/ siRNA	ID #	Catalog #	Sequence
Firefly luciferase (FF)	N/A	shRNA	FF	N/A	CCCGCCTGAAGTCTCTGATTAA
ANAPC1	NM_022662	shRNA	1	v2HS_237650	ACGCTTAGCATGGACTAGAAAT
ANAPC1	NM_022662	shRNA	3	v2HS_98171	TTTATGCAAACAGTTAAATGCT
ANAPC1	NM_022662	shRNA	2	v2HS_98167	TATTAGTAATCGTTTCTGTCCA
ANAPC4	NM_013367	shRNA	1	v2HS_64632	AACTCTCTTGATGAATCAGTTA
ANAPC4	NM_013367	shRNA	2	v2HS_64629	ACCGCTTTAGCTCCAGAGATAG
THOC1	NM_005131	shRNA	1	v2HS_49801	CTGACTCTGCAAGTTAAGACCT
THOC1	NM_005131	shRNA	2	v2HS_243240	TATTTCTTCAGAAGGAGGCGGT
THOC1	NM_005131	shRNA	3	v2HS_245224	TATTATCAGGGCAAAGATTCCA
THOC1	NM_005131	shRNA	4	v2HS_49802	TTTGATTTCCAAGTAGCAACAT
DHX8	D50487	shRNA	1	v2HS_130548	TATAAATGTCACCAATGGTGGG
DHX8	D50487	shRNA	2	v2HS_203261	TTTCTGTTTCACGAATCCTGGG
DHX8	D50487	shRNA	3	v2HS_202419	TTTGGAAAGGACATTGGCAGCA
USP39	NM_006590	shRNA	1	v2HS_196240	AATTCATACCATTTGCCTGTCC
USP39	NM_006590	shRNA	2	v2HS_13479	TTAGATATGGAGGCAACTTGGT
USP39	NM_006590	shRNA	3	v2HS_197637	TTTAGTGAAGATCCTCATGGAC
UBE2I	NM_194261	shRNA	1	v2HS_171781	TATAAACACAAAGGAAGTGGCG
UBE2I	NM_194261	shRNA	2	v2HS_171776	TTGGCAGTAAATCGTGTAGGCC
COPS3	NM_011991	shRNA	1	v2MM_38091	TTACAGATATCCATCATATCCA
COPS3	NM_011991	shRNA	2	v2MM_21587	TATGATTCCAACATGATATGGC
COPS4	NM_016129	shRNA	1	v2HS_229617	TTAGCTTAATACACAGAGACCC
COPS4	NM_016129	shRNA	2	v2HS_97713	AATGAAATGACTCTAGGCTGGA
COPS4	NM_016129	shRNA	3	v2HS_230530	ATCCATTCATACGTCCTTCGGT
COPS4	NM_016129	shRNA	4	v2HS_233448	TTTAGCCACAGATATTTCACCT
COPS4	NM_016129	shRNA	5	v2HS_97714	TTTATGTAAGCCTCTGCCTGGA
C21orf45	NM_018944	shRNA	1	v2HS_244109	TTGTAATCAAGATTCTTGGGCG
C21orf45	NM_018944	shRNA	2	v2HS_52005	TAATGCTTTCAAGACATCTTCC
C21orf45	NM_018944	shRNA	3	v2HS_52006	ATTTGTAATGCTTTCAAGACAT
CASC5	NM_144508	shRNA	1	v2HS_38737	ATAGACAAAGGATTTGACAGGC
CASC5	NM_144508	shRNA	2	v2HS_38738	ATATATTGAGAAGGACTTAGGT
CASC5	NM_144508	shRNA	3	v2HS_38668	AATTAGCTAGAAATGATGTGGT
CDCA8	NM_018101	shRNA	1	v2HS_262071	ATAACAAATACCACAGAGAGCC
CDCA8	NM_018101	shRNA	2	v2HS_155714	AATTTCCACTAACTAGGGAGGT
CDCA8	NM_018101	shRNA	3	v2HS_155711	ATTCCCTTAGAGGAACATGGCT
SMC4	NM_001002800	shRNA	1	v2HS_68088	TTTCAACTTAATACTAAGTGCA
SMC4	NM_001002800	shRNA	2	v2HS_68092	TTTACCGATTTGCTGAAACCCA
PLK1	NM_005030	shRNA	1	v2HS_19708	TGTAATTAGGAGTCCCACACAG
PLK1	NM_005030	shRNA	2	v2HS_19711	TATAGCCAGAAGTAAAGAACTC
PLK1	NM_005030	shRNA	3	v2HS_19709	TATTCTGTACAATTCATATGGT
PLK1	NM_005030	shRNA	4	v2HS_241437	TTGCGGAAATATTTAAGGAGGG
PSMB5	NM_002797	shRNA	1	v2HS_170736	TATAAATAGGATGGAGGATGGG
PSMA5	NM_002790	shRNA	1	v2HS_221829	TTCTCTTCTCCACAGCTAGGCA
PSMB6	NM_002798	shRNA	1	V2HS_277575	AACACATCTCCTTAAAGAGGCT
KRAS	NM_033360	shRNA	1	v2HS_178283	AAGAATCATCATCAGGAAGCCC
KRAS	NM_033360	shRNA	2	v2HS_203252	TAGTAGCATGTAAATATAGCCC
KRAS	NM_033360	shRNA	3	v2HS_169384	TTTCCTACTAGGACCATAGGCA
KRAS	NM_033360	shRNA	4	v2HS_275818	TTAGTGATTAGGTCAAATCCCT
LUC (luciferase)	N/A	siRNA	LUC	N/A	CGUACGCGGAAUACUUCGA
PLK1	NM_005030	siRNA	1	Dhmarcon #D-0032960-05	CAACCAAAGUCGAAUAUGAUU
PLK1	NM_005030	siRNA	2	Dhmarcon #D-0032960-06	CAAGAAGAAUGAAUACAGUUU
PLK1	NM_005030	siRNA	3	Dhmarcon #D-0032960-07	GAAGAUGUCCAUGGAAAUAUU
PLK1	NM_005030	siRNA	4	Dhmarcon #D-0032960-08	CAACACGCCUCAUCCUCUAUU
ANAPC1	NM_022662	siRNA	siGneome	Dhmarcon #D-013843	Mix of 4 siRNA sequences
ANAPC4	NM_013367	siRNA	siGneome	Dhmarcon #D-013642	Mix of 4 siRNA sequences
CDC16	NM_003903	siRNA	siGneome	Dhmarcon #D-003223	Mix of 4 siRNA sequences
CDC27	NM_001256	siRNA	siGneome	Dhmarcon #D-001256	Mix of 4 siRNA sequences