SUPPLEMENTARY APPENDIX

Disrupting the leukemia niche in the central nervous system attenuates leukemia chemoresistance

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Supplemental Materials

Supplemental Methods

Leukemia co-culture: Leukemia cells were plated onto ~60-70% confluent primary meningeal cells, typically at a 3:1 ratio of leukemia to meningeal cells, and grown in a mixture of RPMI and meningeal cell media with FBS 10%. Non-adherent leukemia cells were removed by aspirating the media after overnight co-culture. Fresh media was then added and the cells were co-cultured for 24-48 hours in the presence or absence of drugs. Drugs, including cytarabine, methotrexate, and Me6TREN, were obtained from Sigma-Aldrich. Drug doses were based on the literature[1–5] and drug titrations that identified concentrations of cytarabine and methotrexate that caused significant apoptosis to leukemia cells in suspension. After the specified co-culture period, media containing non-adherent leukemia cells was collected. Next, leukemia cells were removed from adhesion to meningeal cells with 0.05% Trypsin and manual pipetting. Leukemia cells were combined and assessed for apoptosis and cell cycle by flow cytometry as described. During flow cytometry, leukemia cells were distinguished from any contaminating meningeal cells by staining with leukemia-specific fluorescent antibodies (CD19, CD3, CD45; eBioscience) or the leukemia cells were fluorescently labeled with CellTrace dye (ThermoFisher) immediately prior to co-culture. For some experiments, the leukemia cells were isolated from meningeal cells after co-culture using immunomagnetic separation with either CD19 or CD3 antibodies (StemCell Technologies or Miltenyi Biotec).

Apoptosis and cell cycle analyses: To assess apoptosis, leukemia cells were treated as described, stained with annexin-V antibody (eBioscience) and a fixable viability dye (ThermoFisher) or 7-AAD, and analyzed by flow cytometry using a BD FACSCanto. TMRE (Abcam) and Caspase 3/7 assays (ThermoFisher) were performed according to the manufacturer's instructions. The Human Apoptosis Antibody Array (Abcam; 43 targets) was performed with protein lysates from leukemia cells grown in suspension or isolated from co-culture using immunomagnetic separation. Cell cycle and proliferation were assessed using a Click-iT Plus EdU flow cytometry kit (ThermoFisher). To differentiate G0 from G1 phases of the cell cycle, leukemia cells were stained with both Hoechst 33342 (Sigma-Aldrich) and pyronin Y (Sigma-Aldrich) and analyzed by flow cytometry[6]. To assess long-term quiescence *in vivo*, immediately prior to transplantation leukemia cells were labeled with the membrane dye DiR (1,1'-Dioctadecyl-3, 3, 3', 3'-Tetramethylindotricarbocyanine Iodide; ThermoFisher) for microscopy or DiD (1,1′-dioctadecyl-3, 3, 3′, 3′-tetramethylindodicarbocyanine, 4-

chlorobenzenesulfonate salt; ThermoFisher) for flow cytometry[5,7–10]. Ki-67 levels were measured with a fluorescent antibody (eBioscience) and flow cytometry.

Immunohistochemistry: NSG and C57BL/6 mice were transplanted as described with human and mouse leukemia cells, respectively. At signs of systemic leukemia, mice were euthanized and cardiac perfused with PBS followed by paraformaldehyde 4%. The brains and meninges were removed, embedded in paraffin, processed, and stained with either human CD19 or mouse CD45.1 antibody.

Microscopy: Leukemia cells stably expressing GFP were labeled with the fluorescent membrane dye dIR (ThermoFisher) immediately prior to xenotransplantation[7,8]. At signs of systemic leukemia, mice were euthanized and cardiac perfused with PBS followed by paraformaldehyde 4% (pH 7.4). Skin, subcutaneous tissue, nasal bones and the mandible were then removed. The cranium was decalcified using a Pelco BioWave Pro Processor[11] and then the skull, brain and intact meninges were sectioned with a vibratome at ~600 μm per section. Sections were re-processed in a Pelco BioWave Pro Processor to improve depth of imaging and reduce light scatter. Meningeal sections were imaged using a Nikon A1R FLIM Confocal Microscope using the 488 nM and 640 nM laser for GFP and DiR detection, respectively. Images were analyzed using ImageJ software.

Glucose Uptake: The effect of co-culture on leukemia glucose uptake was measured using the Glucose Uptake Assay Kit (Abcam) according to the manufacturer's instructions. In brief, leukemia cells were cultured in regular media in suspension or adherent to meningeal cells. After 48 hours, the media was switched to RPMI supplemented with FBS 0.5% and a fluorescent glucose analog. After one hour, leukemia adhesion was disrupted by trypsinization and manual pipetting. The leukemia cells were then washed, suspended in Analysis Buffer, and analyzed by flow cytometry to determine median fluorescent intensity (MFI).

Gene expression profiling: Primary meningeal cells were treated in duplicate with Me6TREN 100 μM or mock-treated. After 48 hours, meningeal RNA was extracted using a RNeasy RNA Isolation Kit (Qiagen). RNA-seq was performed at the University of Minnesota Genomic Center with a HiSeq 2500 sequencer (50-bp paired-end reads). Differentially regulated genes were determined using *edgeR* (Absolute Fold Change>2 and FDR<0.05) and then used with

Ingenuity Pathway Analsyis (IPA; Quiagen) to identify meningeal pathways altered by Me6TREN.

Mouse Hematopoiesis: Baseline complete blood counts were obtained on C57 BL/6 mice using a Hemavet Blood Analyzer (Drew Scientific). Mice were then treated with cytarabine (50 mg/kg x 5 day), cytarabine (50 mg/kg x 5 day)/Me6TREN (10 mg/kg x 5 days), or untreated. Complete blood counts were then measured at days 5, 10, and 20.

Conditioned Media: Primary meningeal cells were cultured until ~60-70% confluent and then fresh media was added. After an additional 48-72 hours, media was collected, centrifuged at 2000 rpm for 10 minutes to remove any cellular debris, and then filtered through as 0.45 μm filter (Millipore).

Cytokine measurement: Conditioned media was collected from leukemia cells, primary meningeal cells, or co-cultures after 48 hours. Media was centrifuged at 2000 rpm for 10 minutes to remove any cellular debris and then filtered through as 0.45 μm filter (Millipore). The conditioned media was then provided to the Cytokine Reference Laboratory (University of Minnesota) for measurement of SDF-1α, CCL19, and CCL21 levels. SDF-1α was measured by Quantikine ELISA (R&D Systems) while CCL21 and CCL19 were measured by Magnetic Luminex Assay (R&D Systems).

BH3 Profiling: BH3 profiling was performed as described[12,13]. Leukemia cells labeled with CellTrace dye were grown in suspension or co-culture with primary meningeal cells for 24-48 hours and then suspended in membrane extraction buffer containing digitonin 100 μg/mL (Sigma-Aldrich). The leukemia cells were then incubated with the BIM peptide 50 μM (GenScript) for 90 minutes. After incubation, leukemia cells were fixed with paraformaldehyde 4%, permeabilized, stained for cytochrome c (eBioscience), and analyzed by flow cytometry.

Adhesion assay: 1-2 x 10^5 leukemia cells labeled with CellTrace violet (Invitrogen) were added to ~80% confluent meningeal cells. Me6TREN (100 μM, Alfa Aesar), Anti-CD99 antibody (5 μg/ml, Millipore), anti-hVCAM-1 antibody (5 μg/ml, R&D), MMP-9 inhibitor I (1 μM, Calbiochem), Isotype control antibody (5 μg/ml, Mouse IgG2a kappa Isotype Control, clone EBM2a, eBioscience), AMD3100 (100 μM, Millipore, CXCR4 antagonist), Batimastat (500 nM, BioVision, MMP inhibitor), A205804 (1 μM , Tocis Bioscience, E-selectin and ICAM-1 inhibitor), KF38789 (200 μM, Tocris Bioscience, P-selectin inhibitor), or RGD peptide (20 μM, Sigma, integrin inhibitor) were added to co-culture at the same time as leukemia cells. There were at least 4 replicates for each condition. After 24-48 hours, the media, including non-adherent leukemia cells, was gently removed and viable leukemia cells quantitated by both manual counting with a hemocytometer and flow cytometry with Count Bright Absolute counting beads (ThermoFisher).

Supplemental Figure Legends

Supplemental Figure 1. Leukemia cells localize to the meninges within the CNS. (A) Schematic illustrating the xenotransplantation model. (B-C) NSG or C57BL/6 mice were transplanted with human NALM-6 ($2x10^6$ cells; N=5 mice) or murine BCR/ABL p190 (3000 cells; N=5 mice) leukemia cells, respectively. After 3 weeks (NALM-6 mice) or 10 days (BCR/ABL p190 mice), the mice were euthanized and cardiac perfused with PBS followed by fixative. IHC for human CD19 (B) or mouse CD45.1 (C) was then used to identify leukemia cells within the CNS. Leukemia cells stain brown. Original magnification x20 for panels B-C.

Supplemental Figure 2. Chemotherapy does not significantly affect the viability of primary human meningeal cells. Primary human meningeal cells at ~80% confluence were treated with either cytarabine (Ara-C) 500 nM, methotrexate (MTX) 500 nM, or mock treated for 48 hours and then viability assessed with annexin-V staining and flow cytometry. *ns*, not significant.

Supplemental Figure 3: Meningeal cells tilt the apoptotic balance of leukemia cells toward survival. (A-B) NALM-6 and Jurkat leukemia cells cultured in suspension or adherent to meningeal cells were treated with methotrexate 500 nM for 48 hours and caspase-7 activity (A) and TMRE staining (B) assessed by flow cytometry. For both graphs, data are the mean +/- SEM from three independent experiments and *P*: ****, <0.0001 by ANOVA.

Supplemental Figure 4. Co-culture with meningeal cells decreases glucose uptake by leukemia cells. NALM-6 and Jurkat leukemia cells were cultured in suspension or adherent to meningeal cells for 48 hours prior to treatment with a fluorescent glucose analog. Uptake of the analog was then determined by measuring the median fluorescent intensity (MFI) by flow cytometry. *P*: **, <0.01, ***, <0.001 by t-test.

Supplemental Figure 5: Systemic cytarabine reduces the leukemia burden in the CNS. Mice transplanted with NALM-6 leukemia cells ($2x10^6$ cells; N=5 per group) were treated with cytarabine (50 mg/kg intraperitoneal) x 5 days or PBS. 48 hours after completing therapy mice were euthanized, cardiac perfused, meninges isolated and dissociated, stained with human CD19 antibody, and leukemia cells quantitated by flow cytometry. *P*: ***, <0.001 by t-test.

Supplemental Figure 6: Identification of compounds that disrupt the adhesion of leukemia and meningeal cells. (A) NALM-6 leukemia cells were added to primary meningeal cells in the presence of A205804 1 μM (E-selectin and ICAM-1 inhibitor), AMD3100 100 μM (CXCR4 antagonist), KF38789 200 μM (P-selectin inhibitor), Me6TREN 100 μM, or RGD 20 μM (integrin inhibitor). After 24 hours, the media, and any non-adherent leukemia cells were removed, and leukemia cells quantified with counts beads and flow cytometry. *P*: ****, <0.0001 by ANOVA. (B-C) NALM-6 (B) and Jurkat (C) leukemia cells were added to primary meningeal cells in the presence of increasing concentrations of Me6TREN. After 24 hours, the non-adherent leukemia cells were removed and leukemia cells quantified with counts beads and flow cytometry. (D) NALM-6 leukemia cells and primary meningeal cells were treated with Me6TREN 100 μM or mock treated for 48 hours and then viability assessed with annexin-V staining and flow cytometry. Viability relative to the mock treated cells is plotted.

Supplemental Figure 7: Different drug treatment regimens tested *in vivo.* Schematics illustrating the different *in vivo* dosing regimens used for NALM-6, Jurkat, and primary B-ALL PDX leukemia cells. Treatment start dates and duration of cytarabine treatment varied between the xenografts because of differences in the rate of CNS engraftment and baseline cytarabine sensitivity. In all experiments, the dose of cytarabine was 50 mg/kg IP daily and Me6TREN 10 mg/kg sc daily.

Supplemental Figure 8: Me6TREN extends the survival of PDX mice treated with cytarabine. NSG mice were transplanted with primary B-ALL leukemia cells (PRoXe Sample CBAB-62871-V1; $2x10^6$ cells; N=4 per group). From days 11-15 mice were mock treated, treated with cytarabine (50 mg/kg intraperitoneal), or cytarabine + Me6TREN (10 mg/kg subcutaneous). Kaplan-Meier survival curves are shown for the different mouse cohorts. Logrank (Mantel-Cox) test was used to calculate *P* values comparing the survival curves. Cytarabine versus the combination of cytarabine and Me6TREN, *P: *,* < 0.05.

Supplemental Figure 9: Effect of Me6TREN and chemotherapy on hematopoiesis. C57 BL/6 mice were untreated (black), treated with cytarabine (50 mg/kg x 5 days; red) or cytarabine/Me6TREN (10 mg/kg x 5 days; blue) and then blood counts were measured on specified days. White blood cell (A) and platelet (B) counts are shown for individual mice.

Supplemental Figure 10: Effect of Me6TREN on leukemia burden in multiple organs and tissues. Mice transplanted were transplanted with primary B-ALL (PRoXe Sample CBAB-62871-V1; $2x10^6$ cells; N=5 per group) and at day 11 treated with Me6TREN (10 mg/kg subcutaneous) x 5 days or mock treated. 72 hours after completing therapy mice were euthanized and multiple tissues harvested (brain parenchyma, liver, kidney, bone marrow, spleen), tissue disrupted, filtered, and leukemia burden assessed by CD19 staining and flow cytometry. *P*: *ns*, not significant, **, <0.01 by *t*-test.

Supplemental Figure 11: Me6TREN disrupts leukemia-meningeal adhesion by multiple mechanisms. (A) Meningeal pathways altered by Me6TREN treatment were identified using RNA-seq data of Me6TREN or mock treated meningeal cells and Ingenuity Pathway Analysis. (B) Comparison on CD99 and VCAM-1 expression in Me6TREN or mock treated meningeal cells. (C-D) NALM-6 and Jurkat leukemia cells were added to human primary meningeal cells with Me6TREN 100 μM, anti-CD99 antibody 5 μg/ml, anti-hVCAM-1 antibody 5 μg/ml, IgG isotype control 5 μg/ml, Me6TREN 100 μM + MMP-9 inhibitor I 1 μM, or Me6TREN 100 μM + Batimastat 500 nM. After 24 hours, the media was collected from each well and non-adherent leukemia cells quantified using count beads and flow cytometry. *P*: **, <0.01, ***, <0.001, ****, <0.0001 by ANOVA.

Supplemental Figure 12: Effect of Me6TREN on CNS leukemia infiltration pathways. (A) NALM-6 and Jurkat leukemia cells were either treated with Me6TREN 100 μM or untreated for 48 hours and then CXCR4 and CCR7 expression measured with fluorescent antibodies and flow cytometry. Median Fluorescent Intensity (MFI) is shown. *P*: *ns*, not significant, *, <0.05 by *t*-test.

Supplemental Table Legend

Supplemental Table 1*.* Multiple human leukemia cell lines cultured either in suspension or adherent to primary human meningeal cells were treated with cytarabine or methotrexate for 48 hours and then apoptosis was measured using annexin-V staining and flow cytometry. In the table, + signifies that $P < 0.05$ when comparing leukemia chemosensitivity in suspension versus in co-culture.

Supplemental Table 2. Meningeal genes regulated by Me6TREN (Absolute Fold Change>2 and FDR<0.05).

Supplemental Table 3. The levels of ligands for CXCR4 (SDF-1α) and CCR7 (CCL19 and CCL21) were measured in media conditioned for 48 hours by leukemia cells, primary meningeal cells, or both in either the presence or absence of Me6TREN 100 μM. LLOQ=lower limit of quantitation.

Supplemental References

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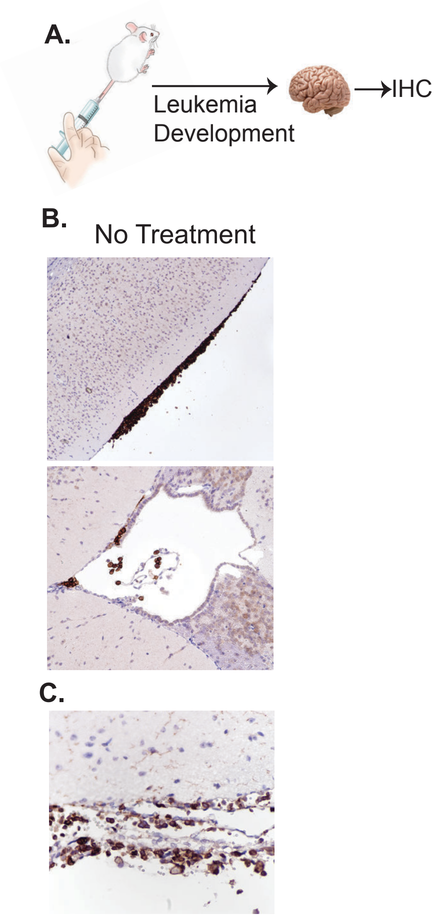
Supplemental Figure 1



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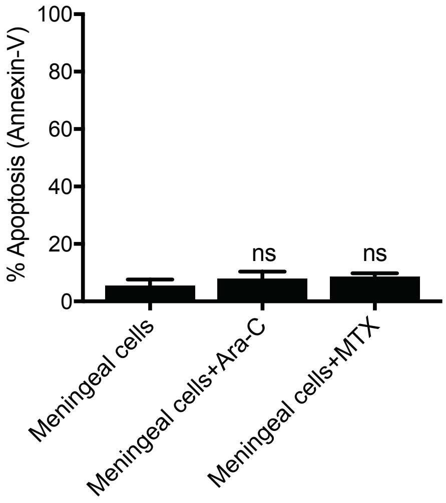

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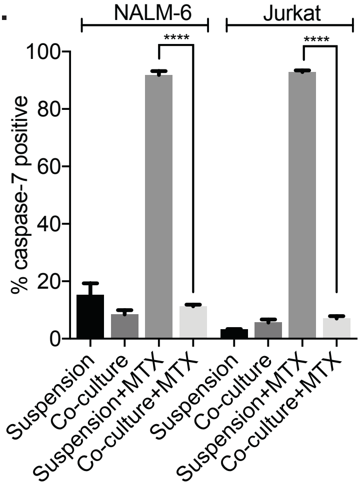
A.



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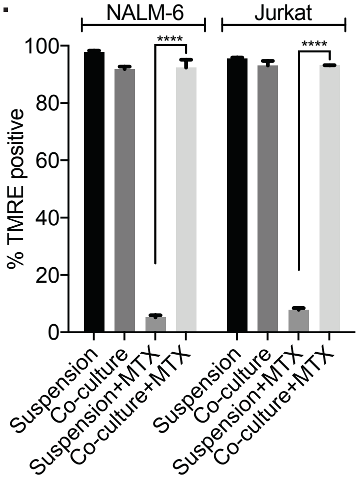

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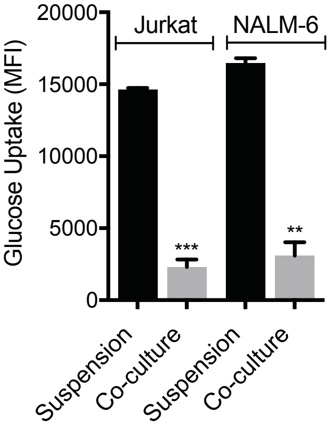

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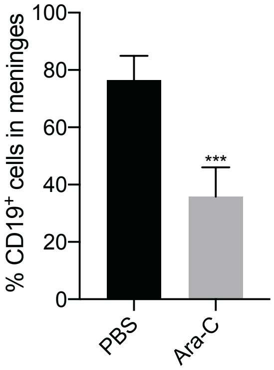

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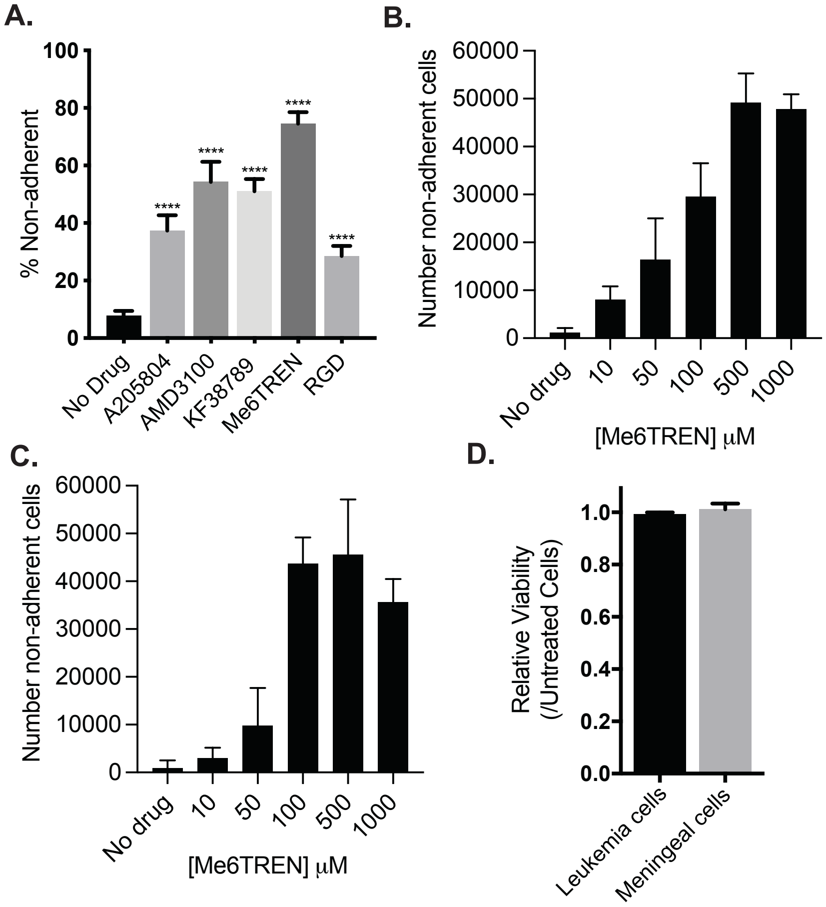

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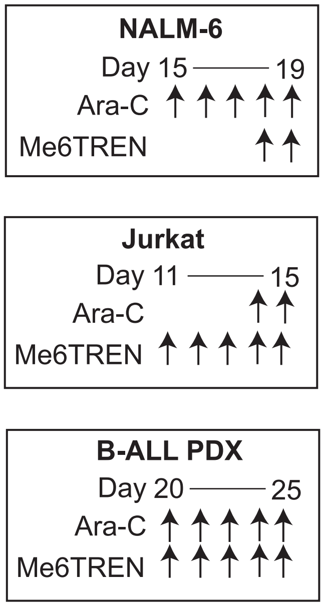

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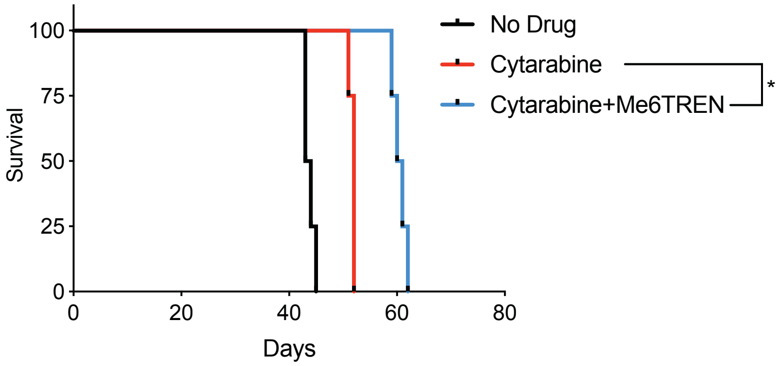

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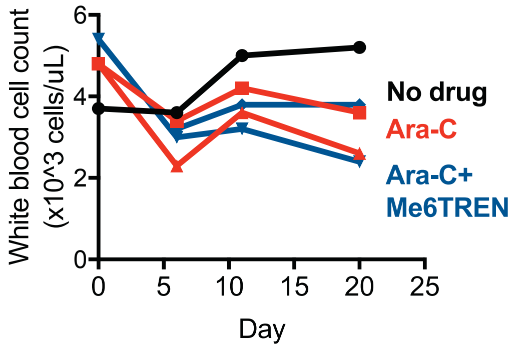

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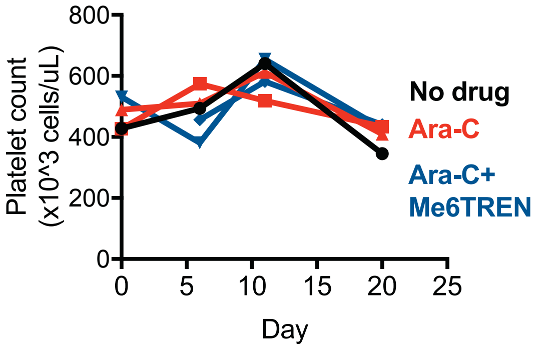

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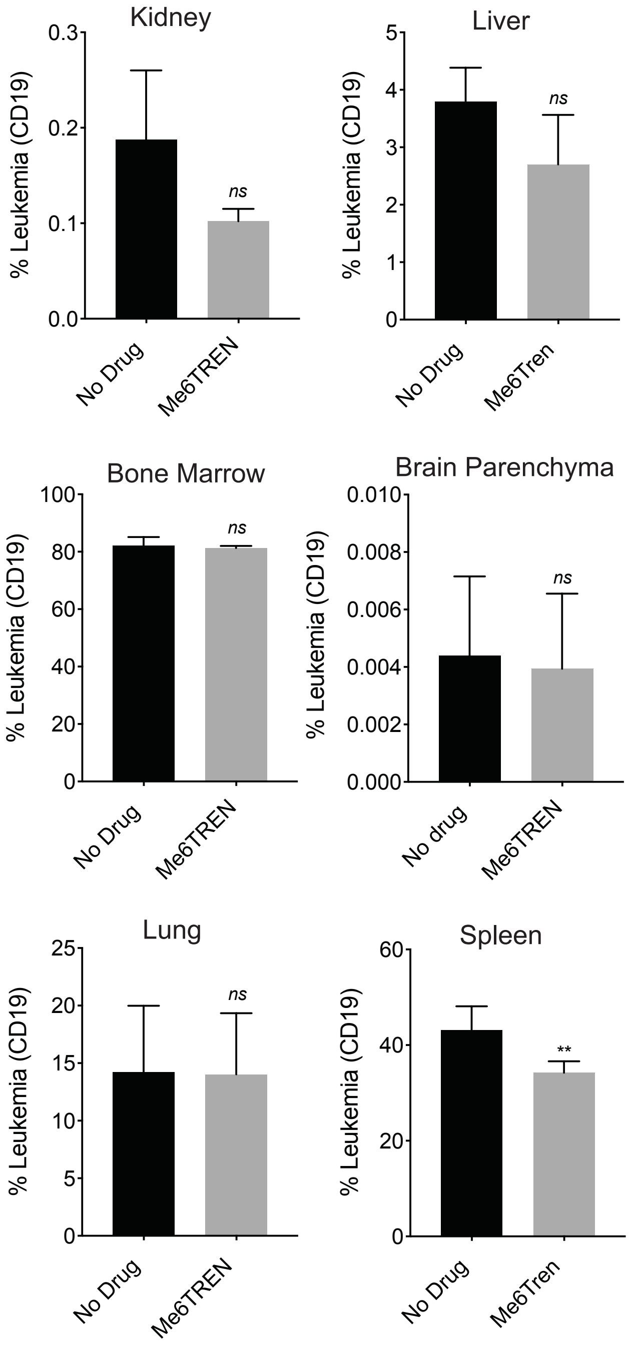
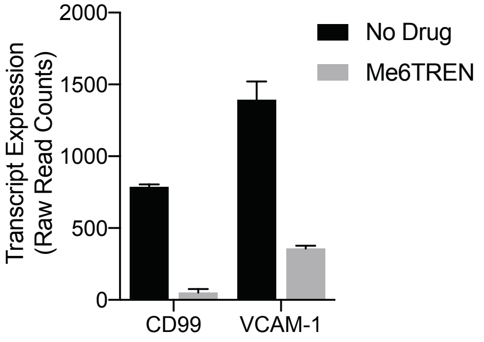


Supplemental Figure 11

A.

Molecular & Cellular Function	P-value	#Genes
Cellular Movement	1.97E-04-3.98E-16	176
Lipid Metabolism	1.94E-04-2.54E-14	110
Small Molecule Biochemistry	1.94E-04-2.54E-14	121
Cell-cell Signaling & Interaction	1.84E-04-1.53E-09	138
Cellular Growth & Proliferation	1.87E-04-4.79E-09	189

B.



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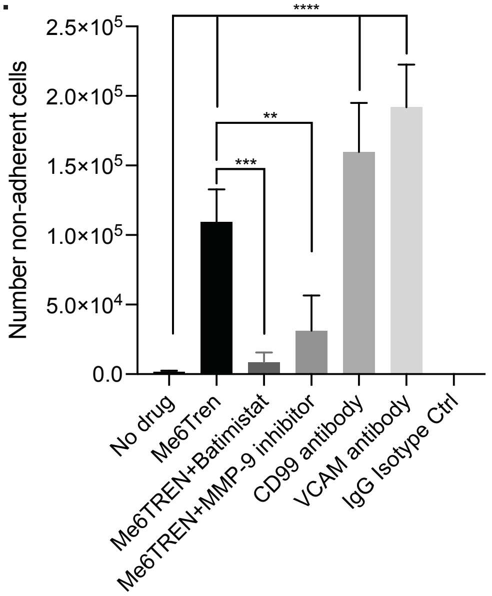

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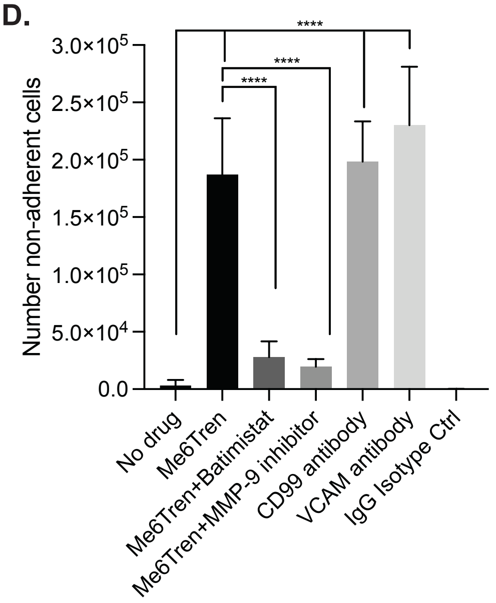
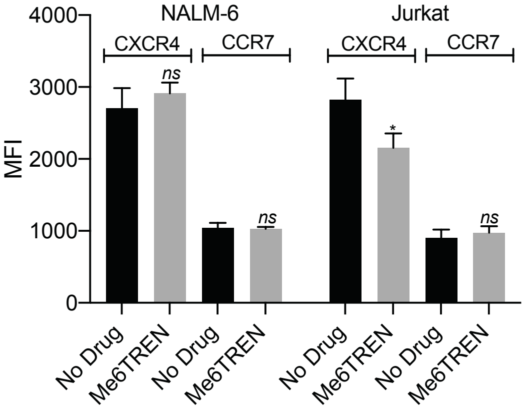


Supplemental Figure 12



Supplemental Table 1

	Cytarabine	Methotrexate
NALM-6	+	+
Jurkat	+	+
REH	-	+
SEM	+	+
CEM	+	+
MOLT-13	+	+

Supplemental Table 2

Feature ID	Experiment - Range (original values)	Experiment - IQR (original values)	Experiment - Difference (original values)	Experiment - Fold Change (original values)	EDGE test: group 1 (no drug) vs group 2 (Me6TREN), tagwise dispersions - P-value	EDGE test: group 1 (no drug) vs group 2 (Me6TREN), tagwise dispersions - Fold change	EDGE test: group 1 vs group 2, tagwise dispersions - Weighted difference	EDGE test: group 1 vs group 2, tagwise dispersions - Bonferroni	EDGE test: group 1 (no drug) vs group 2 (Me6TREN), tagwise dispersions - FDR p-value correction	group 1 - G1_Meningeal.alone.nodrug.S65 - Expression values	group 1 - G1_Meningeal.alone.nodrug2.S66 - Expression values	group 1 - Means	cd	group 2 - G2_Meningeal.alone.w.Me62 - Expression values	group 2 - Means
ABCA1	2608	1689	-2535	-12.418919	0	-11.203792	-9.485E-05	0	0	2810	2704	2757	202	242	222
ABCA10	52	43	-46	-3.3	8.653E-06	-2.5264895	-1.509E-06	0.2291649	0.0001021	67	65	66	25	22	23.5
ABCA3	115	52	-60	-2.9047619	5.357E-05	-2.6162516	-2.133E-06	1	0.0005259	103	80	91.5	17	46	31.5
ABCA4	26	11	18	6.1428571	0.0003439	-4.3994153	-5.127E-07	1	0.0027764	23	12	17.5	3	4	3.5
ABCA6	1220	828	-1173.5	-6.1356674	7.85E-103	-5.5301699	-4.338E-05	2.079E-98	1.12E-100	1435	1369	1402	242	215	228.5
ABCA7	96	72	-66	-3	0.0003315	-2.7067006	-2.363E-06	1	0.0026919	97	101	99	27	39	33
ABCA8	607	350	-445	-2.5921288	9.079E-16	-2.3341358	-1.563E-05	2.405E-11	4.697E-14	765	684	724.5	308	251	279.5
ABCA9	224	207	-215.5	-6.6710526	1.25E-18	-6.0034288	-7.989E-06	3.312E-14	7.98E-17	251	256	253.5	44	32	38
ABCG1	516	346	382	64.666667	9.957E-30	-25.029286	-6.133E-06	2.637E-25	9.59E-28	172	166	169	2	10	6
ABI3BP	731	250	430.5	2.820296	1.117E-09	-2.1168228	-1.106E-05	2.96E-05	2.7E-08	570	540	555	226	247	236.5
ACACA	119	55	93	9.0869565	0.0019217	-2.8149919	-8.831E-07	1	0.0124626	28	44	36	16	7	11.5
ACBD4	102	54	-91.5	-3.0333333	4.058E-09	-2.7351581	-3.278E-06	0.0001075	8.979E-08	129	144	136.5	48	42	45
ACE	121	73	-104.5	-3.1111111	4.494E-11	-2.8082079	-3.753E-06	1.19E-06	1.318E-09	144	164	154	43	56	49.5
ACKR4	13	9	-11	-12	0.0003245	-9.9151114	-4.119E-07	1	0.0026421	11	13	12	2	0	1
ACOT1	64	50	-57.5	-4.4848485	8.738E-11	-4.0237936	-2.102E-06	2.314E-06	2.467E-09	80	68	74	16	17	16.5
ACOT11	66	19	41.5	3.0243902	8.198E-08	3.0413116	1.59E-06	0.0021712	1.457E-06	18	23	20.5	54	59	56.5
ACOT12	16	4	-12.5	-13.5	5.056E-05	-11.169545	-4.695E-07	1	0.0004998	10	17	13.5	1	1	1
ACOX2	52	31	-38.5	-2.4528302	0.001537	-2.0602956	-1.268E-06	1	0.010269	58	72	65	21	36	28.5
ACPP	16	11	-15	-16	2.483E-06	-13.179742	-5.625E-07	0.065764	3.254E-05	16	16	16	2	0	1
ACSBG1	27	13	13.5	3.7	0.007004	-2.9331938	-4.127E-07	1	0.0380044	20	13	16.5	3	7	5
ACSL3	5063	2819	-4128.5	-2.8016583	0	-2.528995	-0.0001466	0	0	6478	6362	6420	2181	2402	2291.5
ACSM5	5	5	-4.5	#DIV/0!	0.0080121	-40.581854	-1.702E-07	1	0.0426364	4	5	4.5	0	0	0
ACTBL2	72	18	50	2.9230769	2.863E-07	2.6781025	1.655E-06	0.0075824	4.59E-06	26	26	26	60	66	63
ACTC1	74	36	49.5	15.142857	8.456E-08	7.5615439	8.947E-07	0.0022397	1.498E-06	5	2	3.5	30	19	24.5
ACTG2	1373	399	844	2.3881579	3.266E-31	2.3048227	2.996E-05	8.65E-27	3.289E-29	632	584	608	1346	1180	1263
ACVRL1	680	126	451.5	3.0616438	2.927E-21	-2.3083421	-1.2E-05	7.752E-17	2.13E-19	571	550	560.5	216	222	219
ADAM19	8397	2630	5248.5	2.5611243	2.39E-64	2.2514542	0.0001589	6.33E-60	3.197E-62	3488	3236	3362	6611	7044	6827.5
ADAM28	13	7	-10	-21	0.0006764	-15.945953	-3.77E-07	1	0.0050434	8	13	10.5	0	1	0.5
ADAM8	709	667	-700.5	-7.4562212	1.65E-126	-6.7245401	-2.603E-05	4.36E-122	2.42E-124	802	816	809	110	107	108.5
ADAMTS13	32	24	-26.5	-3.5238095	0.0029358	-2.2146026	-7.685E-07	1	0.0181165	39	35	37	18	12	15
ADAMTS14	36	22	-24	-2.3333333	0.0066776	-2.0404135	-8.097E-07	1	0.0365257	48	36	42	14	23	18.5
ADAMTS16	35	19	-23	-2.483871	0.0038769	-2.1653098	-7.863E-07	1	0.0228838	34	43	38.5	20	12	16
ADAMTS18	9	4	7.5	#DIV/0!	7.607E-05	73.973745	3.138E-07	1	0.0007211	0	0	0	6	9	7.5
ADAMTS5	330	207	236.5	8.7540984	0.0007238	-2.2790912	-1.64E-06	1	0.0053554	92	63	77.5	34	27	30.5
ADGRB2	77	45	-66.5	-2.4	4.404E-06	-2.1645628	-2.321E-06	0.1166372	5.504E-05	109	119	114	48	47	47.5
ADGRB3	66	28	54.5	6.7368421	1.06E-07	4.3476558	1.212E-06	0.0028072	1.846E-06	16	3	9.5	37	38	37.5
ADGRG2	11	8	8.5	2.5454545	0.0081265	2.7827391	3.781E-07	1	0.0431757	5	6	5.5	12	16	14
ADHFE1	31	26	-28	-5.6666667	0.0005387	-2.6548377	-8.038E-07	1	0.0041232	32	36	34	11	12	11.5
ADM2	36	22	-28	-3.0740741	8.673E-05	-2.7557453	-9.997E-07	1	0.0008117	48	35	41.5	12	15	13.5
ADRA1B	160	35	119.5	3.3431373	8.312E-14	3.1551003	4.161E-06	2.201E-09	3.388E-12	51	51	51	129	162	145.5
ADRA1D	205	77	175.5	5.2804878	3.394E-29	5.8394223	7.509E-06	8.988E-25	3.222E-27	45	37	41	191	242	216.5
ADRB2	121	76	79.5	2.8488372	3.65E-10	3.1633879	3.515E-06	9.668E-06	9.488E-09	52	34	43	143	102	122.5
AFAP1L2	120	90	-109.5	-44.8	5.868E-37	-38.935507	-4.133E-06	1.554E-32	6.343E-35	102	122	112	2	3	2.5
AIM1	732	345	545	4.1594203	1.714E-19	-2.5734897	-1.137E-05	4.539E-15	1.146E-17	512	473	492.5	173	172	172.5
AIM2	11	3	-8	-9	0.0027489	-7.4473186	-2.975E-07	1	0.0171063	11	7	9	0	2	1
AK7	13	10	-9	#DIV/0!	0.0008747	-80.728413	-3.429E-07	1	0.0063039	5	13	9	0	0	0
AKR1C2	107	39	-65	-3.4528302	5.371E-05	-3.0773678	-2.319E-06	1	0.0005271	124	59	91.5	36	17	26.5
AKR1C3	45	28	-35	-4.0434783	1.366E-05	-3.6249467	-1.273E-06	0.3616729	0.0001546	51	42	46.5	6	17	11.5
AKT3	72	63	-41	-12.714286	0.0003258	-11.388074	-1.559E-06	1	0.0026499	19	70	44.5	0	7	3.5
ALDH6A1	565	201	364.5	2.836272	2.964E-16	-2.0938691	-9.098E-06	7.851E-12	1.619E-14	470	452	461	209	188	198.5
ALDOC	588	328	394.5	3.5700326	2.291E-10	-2.3275929	-8.544E-06	6.068E-06	6.173E-09	405	388	396.5	168	139	153.5
ALOX15B	10	6	-7.5	-6	0.009007	-5.1260042	-2.771E-07	1	0.0471437	9	9	9	3	0	1.5
AMIGO2	616	267	361.5	1.982337	4.569E-23	2.2003568	1.667E-05	1.21E-18	3.58E-21	398	338	368	768	691	729.5
AMPD3	847	793	-820	-2.3279352	0	-2.0999309	-2.845E-05	0	0	1450	1425	1437.5	632	603	617.5
ANGPTL1	46	14	-30	-3.7272727	0.0005553	-3.325769	-1.08E-06	1	0.0042357	54	28	41	8	14	11
ANKRD1	6254	3886	5535	3.651497	4.008E-26	4.0483522	0.0002404	1.061E-21	3.503E-24	2099	2076	2087.5	7957	7288	7622.5
ANKRD18A	6	5	-5	#DIV/0!	0.0037042	-45.012227	-1.893E-07	1	0.0220365	4	6	5	0	0	0
ANKRD6	16	10	-10.5	-4	0.0036791	-3.5357848	-3.825E-07	1	0.021897	13	15	14	4	3	3.5
ANXA9	36	26	-30	-2.2244898	0.001133	-2.0047787	-1.035E-06	1	0.007911	52	57	54.5	21	28	24.5
AP1M2	8	6	6	7	0.0082793	7.0545873	2.554E-07	1	0.0438118	0	2	1	8	6	7
APCDD1L	955	270	617	2.7936047	1.86E-38	2.6396084	2.131E-05	4.926E-34	2.052E-36	353	335	344	776	863	819.5
APCDD1L-AS	48	28	36	2.1428571	6.553E-06	2.3740097	1.638E-06	0.1735679	7.944E-05	39	24	31.5	63	72	67.5
APOC1	35	27	-30	-3	0.0007205	-2.3766545	-9.863E-07	1	0.0053365	48	42	45	20	14	17
APOD	95	48	-74.5	-3.6140351	1.003E-08	-3.2419236	-2.686E-06	0.0002657	2.101E-07	121	85	103	31	26	28.5
APOL1	602	102	426	3.4695652	4.008E-17	-2.2918108	-9.339E-06	1.062E-12	2.349E-15	417	459	438	184	161	172.5
APOL3	609	159	429.5	3.497093	1.877E-18	-2.2774173	-9.204E-06	4.971E-14	1.192E-16	423	445	434	169	175	172
APOL6	1217	315	798	3.6778523	4.869E-14	-2.172596	-1.462E-05	1.289E-09	2.06E-12	755	680	717.5	250	346	298
AREG	538	200	347.5	3.2347267	5.378E-12	-2.3152502	-8.561E-06	1.424E-07	1.773E-10	438	361	399.5	132	179	155.5
ARHGAP28	44	39	-42	-2.75	3.713E-06	-2.4742533	-1.488E-06	0.0983337	4.707E-05	67	65	66	25	23	24
ARHGAP6	223	80	-177.5	-4.55	1.87E-26	-4.0979239	-6.501E-06	4.952E-22	1.656E-24	228	227	227.5	56	44	50
ARHGAP9	64	59	51.5	#DIV/0!	0.0007553	-53.564996	-2.26E-07	1	0.0055594	8	4	6	0	0	0
ARMC4	36	19	-23	-2.3142857	0.0064776	-2.0740042	-7.923E-07	1	0.0355858	49	32	40.5	22	13	17.5
ASAH2B	59	22	-32.5	-2.4772727	0.0044258	2.2019158	1.251E-06	1	0.0256155	32	23	27.5	71	38	54.5
ASGR1	18	13	-16.5	-4	0.0002652	-3.56001	-6.004E-07	1	0.0022032	23	21	22	5	6	5.5
ASIC1	108	62	-88.5	-2.3828125	1.153E-06	-2.1443838	-3.071E-06	0.0305384	1.626E-05	170	135	152.5	62	66	64

ASS1	147	60	-95	-2.6101695	2.306E-09	-2.3533248	-3.349E-06	6.107E-05	5.338E-08	151	157	154	61	57	59
ATAD3C	69	22	37.5	76	0.0010107	19.948049	4.406E-07	1	0.007167	0	1	0.5	8	14	11
ATOH8	2061	890	1516.5	5.1604938	7.633E-30	2.4483595	1.991E-05	2.022E-25	7.405E-28	414	315	364.5	764	844	804
AUNIP	329	95	189	2.3846154	2.645E-08	2.0891087	5.607E-06	0.0007006	5.148E-07	158	115	136.5	290	223	256.5
BBC3	95	72	-83.5	-2.6372549	5.675E-08	-2.3760797	-2.943E-06	0.001503	1.044E-06	141	128	134.5	46	56	51
BCL3	1145	409	-795	-2.426009	0	-2.1863137	-2.771E-05	0	0	1409	1296	1352.5	590	525	557.5
BDH1	41	20	-23.5	-8.8333333	0.0024424	-7.609386	-8.626E-07	1	0.0154052	41	12	26.5	6	0	3
BDKRB1	278	75	181.5	3.147929	4.668E-12	-2.4926268	-5.29E-06	1.236E-07	1.551E-10	252	216	234	92	77	84.5
BDKRB2	2030	1369	-1881	-6.7347561	0	-6.0703734	-6.963E-05	0	0	2339	2079	2209	309	347	328
BDP1	26	22	-24	-4.4285714	0.00054	-3.9575196	-8.791E-07	1	0.0041309	30	32	31	6	8	7
BEX2	7	4	-5.5	#DIV/0!	0.0027614	-49.471127	-2.084E-07	1	0.0171723	4	7	5.5	0	0	0
BISPR	30	22	25	51	2.617E-05	-18.858937	-4.507E-07	0.6929829	0.0002786	14	11	12.5	1	0	0.5
BLK	308	195	221	2.7065637	2.502E-07	2.1434452	5.595E-06	0.0066253	4.035E-06	136	123	129.5	235	266	250.5
BMF	152	81	112	7.2222222	0.0004679	-2.226064	-9.299E-07	1	0.0036478	37	52	44.5	23	13	18
BMP4	98	58	-86.5	-20.222222	4.815E-27	-17.899671	-3.256E-06	1.275E-22	4.294E-25	81	101	91	3	6	4.5
BMP5	10	3	-6.5	#DIV/0!	0.0011646	-58.495088	-2.472E-07	1	0.0080958	3	10	6.5	0	0	0
BMP6	13	10	9.5	4.8	0.0053632	5.1117819	4.072E-07	1	0.0303447	1	4	2.5	10	14	12
BRCAT54	5	4	4.5	#DIV/0!	0.0054159	44.795134	1.883E-07	1	0.0306232	0	0	0	4	5	4.5
BST2	412	351	341.5	69.3	0.0002245	-3.7303108	-5.833E-07	1	0.0019009	23	19	21	5	5	5
BTBD8	30	18	18	2.8947368	0.0056705	-2.3545404	-5.447E-07	1	0.0318395	30	20	25	10	9	9.5
C10orf10	451	171	309	5.262069	3.133E-08	-2.6596031	-5.049E-06	0.0008298	6.004E-07	261	169	215	81	64	72.5
C10orf55	148	76	-109	-2.3974359	1.001E-06	-2.1561465	-3.779E-06	0.0265178	1.426E-05	218	156	187	71	85	78
C11orf96	326	89	227	7.9846154	5.983E-57	-6.6273094	-7.679E-06	1.584E-52	7.767E-55	255	224	239.5	27	38	32.5
C11orf98	49	20	27	2.125	0.0053234	2.102231	1E-06	1	0.0301605	32	16	24	38	53	45.5
C16orf74	305	185	227.5	1.8096085	3.359E-11	2.000492	1.065E-05	8.897E-07	1.003E-09	249	313	281	497	520	508.5
C16orf86	31	21	-21.5	-2.8695652	0.0005336	-2.5712567	-7.63E-07	1	0.0040928	39	27	33	9	14	11.5
C1orf115	176	35	134	4.4358974	2.889E-09	-2.6329892	-2.672E-06	7.651E-05	6.556E-08	118	110	114	34	44	39
C1QL1	28	16	-20.5	-5.5555556	3.814E-05	-4.9414443	-7.594E-07	1	0.0003904	18	32	25	4	5	4.5
C1QTNF2	23	10	11.5	3.875	0.0032619	3.7939221	4.351E-07	1	0.0198098	2	6	4	16	12	14
C1R	5280	1200	4112	5.1451613	0	-3.3276592	-9.669E-05	0	0	3808	3515	3661.5	994	990	992
C1RL	677	462	-633	-3.0063391	7.506E-35	-2.7151746	-2.266E-05	1.988E-30	8.016E-33	907	990	948.5	313	318	315.5
C1S	3905	776	2828	3.6882129	0	-2.3325766	-5.87E-05	0	0	2868	2577	2722.5	1053	1051	1052
C22orf15	17	11	11	5.4	0.0096195	-4.172829	-3.464E-07	1	0.0497895	16	8	12	5	0	2.5
C3	3350	698	2484.5	11.709052	6.098E-47	-5.3607625	-4.237E-05	1.615E-42	7.547E-45	1359	1397	1378	227	237	232
C3orf52	279	65	184.5	2.5439331	1.439E-16	2.3829453	6.247E-06	3.812E-12	8.145E-15	122	117	119.5	257	257	257
C4orf22	18	5	11.5	5.6	0.0011357	5.3428206	4.29E-07	1	0.0079278	2	3	2.5	13	12	12.5
C5AR2	24	6	17	9.5	0.0022394	4.7822129	3.015E-07	1	0.0142542	4	0	2	10	8	9
C5orf46	11	6	7.5	16	0.0002535	14.641085	3.161E-07	1	0.0021169	1	0	0.5	8	8	8
C6orf99	19	8	13.5	3.25	0.000483	3.5617611	5.907E-07	1	0.0037417	8	4	6	23	16	19.5
C7	43	28	-35.5	-8.1	2.248E-05	-7.2162896	-1.325E-06	0.5952745	0.0002427	36	45	40.5	2	8	5
C9orf84	18	7	-12.5	-4.5714286	0.0061362	-3.1667974	-4.176E-07	1	0.0340063	12	20	16	5	4	4.5
CA11	48	23	37	8.4	0.006417	-3.3532955	-5.03E-07	1	0.0352969	29	9	19	6	4	5
CA9	12	5	8.5	#DIV/0!	0.0002544	-62.635285	-2.651E-07	1	0.0021224	5	9	7	0	0	0
CACNA1B	14	8	-8	#DIV/0!	0.000661	-70.451862	-2.987E-07	1	0.0049567	14	2	8	0	0	0
CACNA2D3	95	43	-75.5	-2.9113924	1.181E-06	-2.620864	-2.691E-06	0.0312693	1.661E-05	112	118	115	50	29	39.5
CADM1	91	50	-71	-7.4545455	3.583E-05	-3.1166598	-2.097E-06	0.9488588	0.0003691	101	63	82	34	13	23.5
CAMK1D	519	418	409	8.1130435	1.464E-07	-2.463737	-3.531E-06	0.003878	2.475E-06	148	166	157	59	56	57.5
CASP1	681	345	-583	-3.2773438	2.043E-46	-2.955592	-2.097E-05	5.41E-42	2.505E-44	859	819	839	253	259	256
CASP10	147	70	104.5	6.225	0.0011653	-2.4929784	-1.257E-06	1	0.0080984	59	52	55.5	21	19	20
CCDC102B	218	139	-188.5	-3.4966887	2.366E-17	-3.1460995	-6.796E-06	6.267E-13	1.408E-15	287	241	264	82	69	75.5
CCDC103	39	31	-34.5	-2.4081633	0.0002612	-2.1695809	-1.204E-06	1	0.0021769	57	61	59	22	27	24.5
CCDC144CP	6	5	5.5	12	0.0034471	11.010063	2.323E-07	1	0.0207541	0	1	0.5	6	6	6
CCDC146	75	41	-47	-2.6785714	0.0014972	-2.4115189	-1.655E-06	1	0.0100438	88	62	75	13	43	28
CCDC17	19	12	-15	-5.2857143	0.0002003	-4.6575748	-5.515E-07	1	0.0017133	21	16	18.5	2	5	3.5
CCDC69	665	460	506.5	9.8859649	2.144E-06	-2.4654984	-3.506E-06	0.0567947	2.847E-05	182	131	156.5	62	52	57
CCL2	4469	3367	-4122	-8.6688372	7.24E-132	-7.8142004	-0.0001533	1.92E-127	1.08E-129	4969	4350	4659.5	500	575	537.5
CCL7	45	23	-34	-23.666667	2.638E-10	-19.978041	-1.273E-06	6.987E-06	7.015E-09	45	26	35.5	0	3	1.5
CCNE2	718	254	463	2.5255354	2.134E-13	2.0655431	1.222E-05	5.653E-09	8.24E-12	314	293	303.5	617	513	565
CCR1	42	31	26.5	#DIV/0!	0.0003377	-62.403382	-2.641E-07	1	0.0027357	8	6	7	0	0	0
CD24	1771	1635	1403.5	1404.5	0.0015831	-7.4397724	-2.974E-07	1	0.0105321	13	5	9	2	0	1
CD274	560	231	330.5	1.9924925	1.167E-21	2.1801986	1.487E-05	3.09E-17	8.654E-20	314	352	333	628	684	656
CD38	341	229	244	7.1	3.341E-07	-2.4755253	-2.477E-06	0.0088477	5.263E-06	118	102	110	37	43	40
CD74	13996	12906	11205	701.3125	4.962E-09	-3.5319815	-1.707E-06	0.0001314	1.085E-07	71	55	63	14	18	16
CD79B	1653	1342	1268.5	#DIV/0!	0.0025504	44.785012	1.883E-07	1	0.0160257	0	0	0	2	7	4.5
CD82	1910	430	1359	3.6568915	0	-2.9825171	-4.244E-05	0	0	1726	1655	1690.5	469	554	511.5
CD99	1319	758	-753	-23.147059	9.972E-14	-14.218105	-2.764E-05	2.641E-09	4.002E-12	799	775	787	32	68	50
CDCP1	4855	3573	-4777	-3.3625124	2.309E-14	-3.0344377	-0.0001722	6.116E-10	1.016E-12	6849	6749	6799	1994	2050	2022
CDH1	9	5	-7	#DIV/0!	0.0043666	7.0873969	2.557E-07	1	0.0253394	2	0	1	9	5	7
CDH6	293	167	176.5	2.2047782	6.092E-12	2.40397	7.78E-06	1.613E-07	1.997E-10	143	150	146.5	264	373	318.5
CDH8	81	64	53	3.7179487	8.888E-07	4.0944826	2.303E-06	0.0235394	1.281E-05	13	26	19.5	92	53	72.5
CDK18	119	68	81	28	0.0093704	-4.4432095	-4.469E-07	1	0.0487237	6	24	15	2	4	3
CDKL2	23	5	-13.5	-4.8571429	0.0029768	-4.3130916	-5.003E-07	1	0.0183007	9	25	17	5	2	3.5
CELF6	31	15	19.5	#DIV/0!	8.757E-05	-80.177473	-3.405E-07	1	0.0008192	8	10	9	0	0	0
CELSR3	118	55	84	3.7540984	6.478E-06	-2.7416129	-2.226E-06	0.1715577	7.862E-05	85	100	92.5	16	45	30.5
CERS1	8	6	-6.5	-14	0.005442	-10.635349	-2.432E-07	1	0.0307513	8	6	7	1	0	0.5
CETP	47	13	26.5	8.5714286	0.0004258	-4.7860088	-5.712E-07	1	0.0033563	19	19	19	4	3	3.5
CFI	374	122	246	3.4477612	4.754E-14	-2.9551533	-8.228E-06	1.259E-09	2.015E-12	352	307	329.5	86	115	100.5
CGB5	7	4	6.5	#DIV/0!	0.0002947	59.41639	2.512E-07	1	0.0024209	0	0	0	6	6	6
CGB7	31	29	30	9.5714286	2.035E-07	10.300534	1.271E-06	0.00539	3.352E-06	3	4	3.5	34	33	33.5
CGB8	20	13	17	12.333333	3.706E-07	12.765673	7.175E-07	0.009816	5.788E-06	1	2	1.5	16	21	18.5
CGNL1	25	8	-19.5	-10.75	6.402E-07	-9.2944532	-7.298E-07	0.016955	9.43E-06	18	25	21.5	0	4	2
CH25H	27	10	-19.5	#DIV/0!	4.469E-08	-171.35647	-7.326E-07	0.0011836	8.318E-07	27	12	19.5	0	0	0
CHL1	603	321	441	15	9.442E-08	2.4753113	1.761E-06	0.0025007	1.657E-06	32	31	31.5	66	75	70.5
CHRNA1	81	62	-71.5	-5.0857143	3.473E-12	-4.5687435	-2.628E-06	9.198E-08	1.173E-10	93	85	89	12	23	17.5
CHST15	582	317	385.5	3.0450928	1.681E-17	-2.5854209	-1.252E-05	4.451E-13	1.012E-15	574	508	541	193	184	188.5
CHST3	1532	459	947.5	2.4388762	1.5E-20	2.0584034	2.638E-05	3.972E-16	1.051E-18	604	713	658.5	1202	1249	1225.5
CHST6	24	11	-15.5	-4.875	0.0008265	-4.2879764	-5.648E-07	1	0.0060068	28	11	19.5	4	4	4

CIDEA	33	24	-28.5	-29.5	2.598E-08	-8.59642	-9.871E-07	0.0006881	5.067E-07	33	26	29.5	4	2	3
CIITA	979	968	759	#DIV/0!	0.0094929	-36.081023	-1.509E-07	1	0.0492178	6	2	4	0	0	0
CLCA2	8	4	-6	#DIV/0!	0.0015867	-53.914555	-2.276E-07	1	0.0105484	4	8	6	0	0	0
CLCN6	650	512	-574.5	-2.4080882	0	-2.1699564	-1.999E-05	0	0	1044	921	982.5	407	409	408
CLDN1	740	400	-566	-2.8557377	7.744E-30	-2.577055	-2.014E-05	2.051E-25	7.486E-28	884	858	871	282	328	305
CLDN16	11	7	-8.5	-5.25	0.0063687	-4.5611009	-3.132E-07	1	0.0350824	10	11	10.5	0	4	2
CLDN5	34	12	-23	-4.2857143	0.0001374	-3.8365326	-8.444E-07	1	0.0012216	22	38	30	10	4	7
CLIC3	248	47	173	4.0350877	6.828E-14	2.8830729	4.066E-06	1.808E-09	2.817E-12	52	62	57	159	138	148.5
CLMN	273	199	-253.5	-5.6090909	4.746E-45	-5.0483678	-9.34E-06	1.257E-40	5.688E-43	327	290	308.5	56	54	55
CLRN3	10	6	-7	#DIV/0!	0.0024555	-62.949996	-2.664E-07	1	0.0154698	4	10	7	0	0	0
CLU	660	435	-517	-2.4301521	1.104E-23	-2.1913938	-1.803E-05	2.925E-19	8.937E-22	927	830	878.5	332	391	361.5
CNIH3	95	66	-80.5	-3.4029851	1.602E-05	-2.2044005	-2.351E-06	0.424302	0.000179	127	101	114	50	43	46.5
CNN1	1382	680	918.5	2.1059603	1.874E-49	2.3379238	4.191E-05	4.963E-45	2.352E-47	916	745	830.5	1746	1752	1749
CNR1	97	64	-80.5	-4.6590909	1.007E-09	-4.202916	-2.96E-06	2.667E-05	2.458E-08	94	111	102.5	14	30	22
COL11A1	1791	1078	-1137.5	-2.3696568	7.555E-12	-2.1427522	-3.974E-05	2.001E-07	2.449E-10	1812	2124	1968	830	831	830.5
COL12A1	49709	13875	33696	3.7162146	0	-2.2515779	-0.0006494	0	0	31562	30299	30930.5	11079	13732	12405.5
COL24A1	36	32	-32.5	-2.6666667	0.0001228	-2.3983285	-1.148E-06	1	0.0011043	53	51	52	19	20	19.5
COL3A1	47853	12916	32702.5	3.5217844	0	-2.7529608	-0.0009517	0	0	39185	39892	39538.5	12702	13234	12968
COL4A6	749	373	-508	-2.420979	8.864E-15	-2.1887817	-1.778E-05	2.348E-10	4.17E-13	831	900	865.5	311	404	357.5
COL5A3	184	89	-158.5	-11.931034	1.546E-31	-10.722919	-5.947E-06	4.095E-27	1.587E-29	150	196	173	17	12	14.5
COL7A1	1544	1421	-1482.5	-5.084022	0	-4.5888047	-5.453E-05	0	0	1870	1821	1845.5	326	400	363
COLEC12	2017	1413	-1964.5	-8.1566485	0	-7.3667738	-7.313E-05	0	0	2231	2247	2239	230	319	274.5
COMP	14	10	8.5	#DIV/0!	0.0006831	83.869415	3.564E-07	1	0.0050866	0	0	0	10	7	8.5
CORO1A	2939	2451	2262.5	42.513761	5.025E-05	2.077331	2.227E-06	1	0.0004977	47	62	54.5	94	111	102.5
CPA3	107	91	-99	-4.1935484	1.572E-09	-2.6020007	-3.025E-06	4.163E-05	3.737E-08	133	127	130	46	44	45
CPT1C	288	197	-237.5	-2.2369792	3.343E-10	-2.0192569	-8.193E-06	8.853E-06	8.74E-09	433	426	429.5	172	212	192
CPXM1	1143	967	888	39.608696	0.0002265	-2.3213124	-1.279E-06	1	0.0019167	69	50	59.5	27	19	23
CRHBP	38	23	-30	-5.2857143	8.832E-05	-4.7278778	-1.109E-06	1	0.0008257	31	43	37	8	6	7
CRIP1	19	14	13.5	2.5882353	0.0012225	2.8470672	6E-07	1	0.0084208	11	6	8.5	19	25	22
CRIPAK	114	89	-101.5	-2.3716216	1.259E-06	-2.1391276	-3.536E-06	0.0333555	1.76E-05	169	182	175.5	80	68	74
CRLF1	338	104	242.5	8.0289855	4.546E-18	5.1130173	5.397E-06	1.204E-13	2.82E-16	23	46	34.5	175	145	160
CSDC2	49	45	-46.5	-32	1.444E-11	-27.112603	-1.752E-06	3.823E-07	4.509E-10	47	49	48	1	2	1.5
CSF3	1575	843	-1395.5	-10.525597	1.45E-122	-9.4861128	-5.201E-05	3.84E-118	2.12E-120	1686	1398	1542	111	182	146.5
CST1	27	4	-21	-2.5	0.003298	-2.2489374	-7.378E-07	1	0.0199835	31	39	35	16	12	14
CST4	8	5	6	#DIV/0!	0.0037116	-40.498279	-1.699E-07	1	0.0220698	5	4	4.5	0	0	0
CTSK	1233	756	-1003.5	-2.4213881	0	-2.1804099	-3.488E-05	0	0	1902	1517	1709.5	669	743	706
CTSS	516	269	350.5	5.8344828	6.185E-12	-2.5935013	-4.842E-06	1.638E-07	2.025E-10	240	178	209	65	80	72.5
CXCL1	3467	623	2517.5	6.1907216	0	-4.6393041	-7.389E-05	0	0	2647	2345	2496	454	516	485
CXCL16	44	22	37	10.25	3.42E-05	-4.7573248	-6.452E-07	0.9058739	0.0003537	20	23	21.5	2	6	4
CXCL2	288	87	196.5	2.7863636	1.555E-17	-2.4797419	-6.822E-06	4.117E-13	9.4E-16	304	301	302.5	112	108	110
CXCL3	325	76	221.5	2.9954955	5.536E-14	-2.4636945	-6.804E-06	1.466E-09	2.32E-12	303	303	303	96	126	111
CXCL5	3911	1226	2714.5	4.4667944	0	-3.1720526	-7.12E-05	0	0	2780	2724	2752	752	814	783
CXCL6	901	200	610	12.090909	1.787E-40	-7.512279	-1.504E-05	4.732E-36	2.022E-38	462	456	459	64	46	55
CYGB	695	528	-629	-3.0063796	1.012E-27	-2.7100845	-2.245E-05	2.681E-23	9.213E-26	995	890	942.5	300	327	313.5
CYP1B1	2473	1216	-1860	-3.136703	0	-2.8357539	-6.691E-05	0	0	2544	2917	2730.5	856	885	870.5
CYP1B1-AS1	15	12	-13	-7.5	0.0001457	-6.4882719	-4.829E-07	1	0.0012845	15	15	15	1	3	2
CYP26B1	1114	814	-933.5	-2.3607872	0	-2.1305697	-3.25E-05	0	0	1576	1663	1619.5	732	640	686
CYP4X1	49	34	-41	-11.25	2.581E-10	-7.9579664	-1.487E-06	6.836E-06	6.894E-09	52	38	45	6	4	5
CYP51A1	1480	1234	-1381	-2.4865447	0	-2.2420556	-4.832E-05	0	0	2402	2218	2310	922	936	929
CYSLTR2	16	11	-13.5	#DIV/0!	4.081E-07	-119.86829	-5.112E-07	0.0108081	6.324E-06	11	16	13.5	0	0	0
DACT1	122	49	75.5	1.9934211	1.166E-07	2.0498914	3.015E-06	0.0030886	2.011E-06	84	68	76	143	138	140.5
DBP	54	30	43	9.6	0.0025253	-3.2047071	-4.709E-07	1	0.0158901	17	19	18	4	6	5
DEC1	15	10	11.5	12.5	6.468E-06	12.526294	4.853E-07	0.1713001	7.858E-05	0	2	1	11	14	12.5
DENND2A	241	227	-230	-5.9462366	1.184E-41	-5.3585395	-8.503E-06	3.135E-37	1.363E-39	273	280	276.5	44	49	46.5
DHCR24	4323	3867	-4046.5	-2.8190605	0	-2.5460283	-0.0001439	0	0	6219	6323	6271	2097	2352	2224.5
DHCR7	2016	1794	-1942.5	-3.3502722	0	-3.0231243	-7E-05	0	0	2811	2727	2769	795	858	826.5
DHRS12	102	72	-71	-2.245614	1.636E-05	-2.0235807	-2.446E-06	0.4333574	0.0001823	136	120	128	50	64	57
DHRS13	143	96	115	4.1081081	4.994E-05	-2.0969071	-1.703E-06	1	0.0004948	82	90	86	31	43	37
DHX58	127	70	-109	-2.297619	7.793E-08	-2.0725157	-3.778E-06	0.0020639	1.396E-06	187	199	193	89	79	84
DIRAS1	18	16	13	#DIV/0!	0.0093057	39.944773	1.675E-07	1	0.0484269	0	0	0	4	4	4
DIRC3	63	43	-48	-2.5238095	0.000135	-2.2721005	-1.681E-06	1	0.0012025	87	72	79.5	24	39	31.5
DLL3	64	37	39.5	2.7954545	0.0043567	2.1056791	9.25E-07	1	0.0252887	19	25	22	37	47	42
DLL4	336	169	-288.5	-3.0981818	3.001E-15	-2.7880286	-1.03E-05	7.948E-11	1.466E-13	473	379	426	137	138	137.5
DLX2	14	4	9	7	0.0007294	7.2530225	3.821E-07	1	0.0053885	0	3	1.5	7	14	10.5
DNAH5	744	335	-529	-2.9849906	1.077E-21	-2.6883997	-1.884E-05	2.853E-17	8.013E-20	871	720	795.5	254	279	266.5
DNAJA3	70	55	-37	-19.5	0.0004682	10.379444	1.467E-06	1	0.0036493	2	6	4	6	72	39
DNAJC12	116	27	77.5	6.9615385	2.186E-08	-4.0835139	-1.692E-06	0.000579	4.321E-07	46	72	59	14	12	13
DPPA4	15	5	-12	-9	0.0001178	-7.6765338	-4.477E-07	1	0.001068	12	15	13.5	0	3	1.5
DRD2	34	18	-26	-27	1.382E-08	-22.300556	-9.827E-07	0.0003659	2.841E-07	20	34	27	0	2	1
DSP	466	217	265	2.2412178	1.276E-12	2.4588324	1.177E-05	3.379E-08	4.493E-11	215	212	213.5	452	496	474
DTWD2	51	28	42	2.5	0.0001661	-2.1436856	-1.345E-06	1	0.0014466	57	76	66.5	25	31	28
DTX4	42	23	-30	-2.5	0.0008548	-2.2458762	-1.048E-06	1	0.0061859	58	42	50	16	24	20
DUSP1	11973	2998	7465.5	2.308245	2.216E-61	2.0100379	0.0002174	5.87E-57	2.906E-59	6124	5289	5706.5	10364	10303	10333.5
DUSP2	177	116	129	9.6	0.0065391	2.2784939	7.294E-07	1	0.0358788	16	14	15	22	40	31
EAF2	76	46	53.5	3.7435897	0.0041346	2.1997292	8.919E-07	1	0.024243	13	26	19.5	31	47	39
EDN1	405	228	330	3.192691	2.14E-52	3.5349908	1.443E-05	5.667E-48	2.725E-50	145	156	150.5	475	486	480.5
EDNRB	20	3	-14	#DIV/0!	4.14E-07	-123.31934	-5.26E-07	0.0109639	6.408E-06	20	8	14	0	0	0
EEF1A2	108	38	78.5	3.6610169	0.000157	2.4288327	1.594E-06	1	0.001378	37	22	29.5	78	51	64.5
EFCC1	10	5	-6	#DIV/0!	0.0047303	-54.286622	-2.292E-07	1	0.0271705	2	10	6	0	0	0
EFHD1	38	29	28	2.75	0.000771	3.0331175	1.239E-06	1	0.0056638	15	17	16	48	40	44
EFNB3	40	22	-31	-5.7692308	2.652E-07	-5.1284757	-1.141E-06	0.0070232	4.267E-06	45	30	37.5	5	8	6.5
EFR3B	35	15	22	3.2	0.0067501	2.420244	5.429E-07	1	0.0368589	9	11	10	20	24	22
EHF	39	8	23	24	7.959E-05	-10.707229	-4.484E-07	1	0.0007504	15	11	13	2	0	1
ELN	389	175	301.5	87.142857	5.298E-49	35.474357	4.702E-06	1.403E-44	6.619E-47	6	1	3.5	108	123	115.5
ENPP2	209	75	147	2.9864865	5.941E-08	-2.0405054	-3.228E-06	0.0015736	1.087E-06	172	163	167.5	71	77	74
ENTPD3-AS1	14	11	10.5	2.5	0.0087138	2.7379673	4.679E-07	1	0.0457999	5	9	7	18	17	17.5
EPHA7	12	2	-6	#DIV/0!	0.0065352	-52.863274	-2.23E-07	1	0.0358653	12	0	6	0	0	0

EREG	1378	686	-968.5	-3.3337349	0	-3.0033276	-3.482E-05	0	0	1470	1297	1383.5	422	408	415
ERMP1	1157	293	766	3.3247344	1.637E-21	-2.1433488	-1.577E-05	4.337E-17	1.211E-19	773	791	782	293	366	329.5
ERVMER34-	26	11	19.5	20.5	0.0039866	-7.0175992	-2.779E-07	1	0.0234736	13	4	8.5	2	0	1
ESAM	431	267	337	49.142857	7.743E-12	8.1196314	1.916E-06	2.051E-07	2.507E-10	5	9	7	63	41	52
ESM1	1648	651	1128.5	2.7008289	2.081E-44	2.9931426	4.994E-05	5.511E-40	2.46E-42	688	639	663.5	1687	1897	1792
ESR2	49	41	-47	-16.666667	2.077E-15	-14.567151	-1.763E-06	5.501E-11	1.036E-13	51	49	50	4	2	3
ETV1	729	345	-538	-2.2779097	0	-2.0549808	-1.86E-05	0	0	966	952	959	425	417	421
F10	40	16	30	3.1428571	0.0001316	-2.6977837	-1.003E-06	1	0.0011742	36	48	42	17	11	14
FABP3	71	58	-61.5	-4.075	2.082E-07	-3.6560571	-2.238E-06	0.0055141	3.416E-06	85	78	81.5	26	14	20
FADS1	6320	5039	-6015	-5.1640706	0	-4.6581623	-0.0002212	0	0	7704	7215	7459.5	1384	1505	1444.5
FADS2	12496	11659	-12376	-9.0572917	0	-8.1771534	-0.0004614	0	0	13949	13875	13912	1453	1619	1536
FAIM2	12	4	-8	#DIV/0!	0.0026055	-12.051242	-2.791E-07	1	0.0163177	12	4	8	1	0	0.5
FAM129A	1052	417	-680	-2.3863405	0	-2.1554023	-2.372E-05	0	0	1143	1198	1170.5	465	516	490.5
FAM132A	33	15	19	3.2352941	0.0011161	2.9183468	6.231E-07	1	0.0078262	11	6	8.5	30	15	22.5
FAM160A1	14	8	-12	-13	4.324E-05	-10.726575	-4.489E-07	1	0.0004369	14	12	13	0	2	1
FAM163A	10	2	-6	#DIV/0!	0.0042982	-53.157194	-2.243E-07	1	0.0250413	10	2	6	0	0	0
FAM180A	26	18	14	2.037037	0.0053383	2.2477148	6.422E-07	1	0.0302236	12	15	13.5	33	22	27.5
FAM196A	20	10	-12	-3.1818182	0.0067283	-2.8373793	-4.31E-07	1	0.0367497	17	18	17.5	5	6	5.5
FAM196B	873	442	507	1.845	5.395E-22	2.0473378	2.37E-05	1.429E-17	4.083E-20	668	532	600	1020	1194	1107
FAM19A2	6	2	-4.5	#DIV/0!	0.0043415	-40.623064	-1.704E-07	1	0.0252379	3	6	4.5	0	0	0
FAM213A	337	212	261	5.7454545	2.95E-10	-3.1555123	-4.972E-06	7.814E-06	7.791E-09	217	169	193	52	58	55
FAM46C	87	47	-66.5	-2.9850746	7.426E-09	-2.6852546	-2.371E-06	0.0001967	1.586E-07	110	90	100	31	36	33.5
FAM63A	270	147	-186.5	-2.3417266	4.182E-10	-2.1146306	-6.488E-06	1.107E-05	1.074E-08	318	333	325.5	125	153	139
FAM65C	477	390	-433.5	-7.7209302	9.677E-46	-6.9412741	-1.609E-05	2.563E-41	1.176E-43	524	472	498	82	47	64.5
FAM66B	13	8	-10.5	-8	0.0008094	-6.8098855	-3.898E-07	1	0.0059041	14	10	12	1	2	1.5
FAM72C	30	11	24.5	4.7692308	0.0084718	2.6973514	4.242E-07	1	0.0446695	6	7	6.5	15	17	16
FAM83G	1144	305	747.5	2.497996	9.338E-37	2.2563924	2.368E-05	2.473E-32	1.005E-34	509	489	499	985	1047	1016
FAM84A	82	65	-73	-3.1470588	2.799E-09	-2.8369513	-2.621E-06	7.413E-05	6.385E-08	104	110	107	28	40	34
FAM84B	156	107	-135.5	-5.3709677	5.017E-21	-4.8247123	-4.98E-06	1.329E-16	3.582E-19	186	147	166.5	30	32	31
FASN	11433	10249	-10841	-3.3952718	0	-3.0647143	-0.000391	0	0	15662	15072	15367	4229	4823	4526
FAXDC2	97	69	-75.5	-2.9868421	6.28E-07	-2.7002363	-2.712E-06	0.016632	9.276E-06	93	134	113.5	37	39	38
FBXO32	366	185	-305	-3.961165	1.827E-22	-3.5666072	-1.107E-05	4.839E-18	1.398E-20	454	362	408	88	118	103
FCRLA	80	58	58.5	9.3571429	0.0035231	2.7374914	4.676E-07	1	0.0211156	4	10	7	16	19	17.5
FDFT1	4758	3395	-4280	-2.7244158	0	-2.45448	-0.0001512	0	0	7211	6313	6762	2511	2453	2482
FENDRR	1983	471	1306.5	2.591352	0	-2.0854179	-3.731E-05	0	0	1954	1842	1898	789	853	821
FER1L5	44	22	-33	-3.3571429	5.643E-05	-2.8089652	-1.143E-06	1	0.0005509	56	38	47	12	18	15
FER1L6	37	31	-34	-12.333333	7.622E-10	-10.806192	-1.272E-06	2.019E-05	1.895E-08	37	37	37	0	6	3
FGF5	1989	1258	1378	1.8096357	7.809E-46	2.0083829	6.473E-05	2.068E-41	9.532E-44	1854	1550	1702	2984	3176	3080
FGF7	586	331	434	5.15311	1.576E-08	-2.1077835	-4.855E-06	0.0004173	3.195E-07	252	237	244.5	116	93	104.5
FGFR3	157	104	122.5	5.8039216	9.907E-08	2.9880139	1.927E-06	0.0026238	1.732E-06	20	31	25.5	79	59	69
FGFR4	166	148	-159	-12.357143	1.682E-44	-11.086053	-5.953E-06	4.454E-40	1.997E-42	169	177	173	11	17	14
FIBIN	1262	996	-1248.5	-5.1272727	3.79E-127	-4.6248396	-4.594E-05	1E-122	5.61E-125	1552	1550	1551	315	290	302.5
FIRRE	33	19	29	5.8333333	0.0078254	2.6466433	3.802E-07	1	0.0417942	6	6	6	12	17	14.5
FLNC	26964	6329	17526	2.4573424	1.596E-39	2.2041576	0.000547	4.226E-35	1.783E-37	12219	11833	12026	22868	24981	23924.5
FLRT3	90	65	-75	-3.2727273	1.761E-08	-2.7839702	-2.621E-06	0.0004665	3.542E-07	98	118	108	33	37	35
FLVCR2	100	79	-94.5	-3.3333333	1.16E-11	-3.0017571	-3.403E-06	3.071E-07	3.678E-10	139	131	135	39	42	40.5
FMO3	9	4	-6.5	#DIV/0!	0.0009572	-57.83903	-2.444E-07	1	0.0068239	9	4	6.5	0	0	0
FMOD	50	13	33	5.7142857	0.000174	-3.5727649	-7.662E-07	1	0.0015085	24	32	28	12	2	7
FNDC5	42	23	-31	-5.4285714	4.765E-06	-4.853751	-1.147E-06	0.1261958	5.925E-05	30	46	38	10	4	7
FOS	274	227	-250.5	-3.7081081	3.431E-07	2.7470131	9.139E-06	0.0090864	5.396E-06	194	85	139.5	354	332	343
FOSB	142	68	108.5	8.2333333	2.096E-18	9.0905814	4.616E-06	5.55E-14	1.328E-16	16	14	15	156	91	123.5
FOXP3	10	6	-7.5	#DIV/0!	0.0002346	-67.117319	-2.843E-07	1	0.0019777	5	10	7.5	0	0	0
FPR1	11	7	-10	-3.5	0.0065065	-3.1020227	-3.611E-07	1	0.0357224	15	13	14	4	4	4
FRAS1	42	27	-27	-2.255814	0.0064523	-2.0274708	-9.3E-07	1	0.0354691	51	46	48.5	25	18	21.5
FRMD3	66	45	58	9.9230769	1.037E-19	10.849373	2.457E-06	2.747E-15	6.972E-18	10	3	6.5	69	60	64.5
FRMD4B	253	189	198	8.6153846	0.0002825	-2.0280398	-1.123E-06	1	0.0023345	56	61	58.5	20	32	26
FRY	1282	397	849.5	2.5102222	0	-2.1273871	-2.656E-05	0	0	1397	1259	1328	583	542	562.5
FSIP1	37	11	22.5	2.0714286	0.0028297	2.0000399	7.98E-07	1	0.0175186	19	23	21	42	34	38
FST	2160	1312	-1985.5	-2.4056637	0	-2.168768	-6.912E-05	0	0	3559	3237	3398	1399	1426	1412.5
FSTL3	5955	1361	3883	2.4307296	1.671E-83	2.0980201	0.0001125	4.425E-79	2.329E-81	2875	2553	2714	5036	5230	5133
FSTL4	31	25	24.5	#DIV/0!	0.0004998	54.538487	2.302E-07	1	0.0038568	0	0	0	5	6	5.5
FTCD	5	4	-4.5	#DIV/0!	0.0042555	-40.494548	-1.698E-07	1	0.0248252	5	4	4.5	0	0	0
GAB1	1087	805	800	7.2015504	5.017E-08	-2.0986166	-5.94E-06	0.0013288	9.299E-07	317	284	300.5	132	126	129
GABRA2	35	27	-30.5	-4.5882353	4.499E-05	-4.1061162	-1.119E-06	1	0.0004515	36	42	39	10	7	8.5
GALNT15	659	163	496	5.9849246	2.902E-31	-4.5285857	-1.472E-05	7.687E-27	2.934E-29	510	490	500	103	96	99.5
GAS1	356	174	257	5.6306306	1.985E-06	-2.150777	-2.679E-06	0.0525597	2.66E-05	138	127	132.5	55	56	55.5
GAS7	1043	852	836.5	65.346154	5.969E-08	-3.8958478	-1.59E-06	0.0015808	1.091E-06	56	57	56.5	18	8	13
GATA2	907	129	656	3.0030534	8.317E-31	2.5832901	1.958E-05	2.203E-26	8.219E-29	346	309	327.5	747	779	763
GATS	220	117	-139.5	-2.3676471	2.689E-06	-2.1404557	-4.867E-06	0.0712137	3.503E-05	235	248	241.5	77	127	102
GBP2	329	114	-274	-6.48	2.977E-67	-5.8415443	-1.015E-05	7.885E-63	4.043E-65	318	330	324	44	56	50
GBP4	1493	1378	1202.5	105.56522	4.879E-06	-3.4970689	-1.215E-06	0.1292308	6.056E-05	49	41	45	21	2	11.5
GCSAM	405	345	282	17.114286	0.0033102	2.3252542	8.842E-07	1	0.0200389	13	22	17.5	29	45	37
GDF15	980	778	-964.5	-4.4569892	9.011E-71	-4.0210932	-3.53E-05	2.387E-66	1.237E-68	1252	1235	1243.5	272	286	279
GDF5	241	166	-212.5	-4.5714286	1.052E-25	-4.1121506	-7.77E-06	2.787E-21	9.05E-24	293	251	272	67	52	59.5
GDF6	82	41	44	2.1578947	2.213E-05	2.3327796	1.915E-06	0.5860188	0.0002394	45	31	38	72	88	80
GEM	189	128	-176	-2.8723404	1.65E-15	-2.5920338	-6.27E-06	4.369E-11	8.291E-14	265	275	270	86	102	94
GFAP	29	9	-19	-7.3333333	0.0008418	-6.4522949	-7.104E-07	1	0.0061016	15	29	22	6	0	3
GFPT2	4542	3596	-4209	-2.6467136	0	-2.3887324	-0.0001485	0	0	6927	6603	6765	2385	2727	2556
GGNBP2	54	3	-28	-29	0.0092264	5.2190295	9.771E-07	1	0.0480837	5	7	6	4	54	29
GINS2	1000	237	639	1.94387	6.324E-23	2.0228207	2.612E-05	1.675E-18	4.926E-21	740	614	677	1255	1212	1233.5
GK	1466	756	-1100.5	-2.3108993	0	-2.0836129	-3.809E-05	0	0	2026	1854	1940	827	852	839.5
GLDC	85	47	62	11.333333	0.0001192	-3.6369967	-6.735E-07	1	0.0010769	27	22	24.5	4	8	6
GLIDR	61	36	-45.5	-2.3	0.0001154	-2.0721815	-1.577E-06	1	0.0010489	77	84	80.5	41	29	35
GLT8D2	248	175	-218	-2.963964	2.122E-09	-2.6679419	-7.765E-06	5.619E-05	4.946E-08	347	311	329	123	99	111
GNG2	2367	747	1538	2.5303483	0	-2.2287807	-5.167E-05	0	0	2558	2406	2482	908	1102	1005
GOLT1A	6	4	-5	#DIV/0!	0.0029263	-44.842323	-1.885E-07	1	0.0180659	6	4	5	0	0	0
GPNMB	290	207	-277.5	-3.3417722	6.305E-23	-3.0156022	-1.001E-05	1.67E-18	4.926E-21	393	399	396	109	128	118.5

GPR137C	113	37	81	3.7	0.0002491	2.08348	1.233E-06	1	0.0020865	27	33	30	66	47	56.5
GPR160	86	61	59.5	#DIV/0!	0.0030459	49.537553	2.087E-07	1	0.0186739	0	0	0	1	9	5
GPR17	29	20	-24	-2.8461538	0.0001523	2.7214042	9.832E-07	1	0.001338	14	16	15	41	33	37
GPR19	35	13	21.5	3.6875	0.0048235	2.74906	5.351E-07	1	0.0276277	10	6	8	17	23	20
GPR4	80	10	52	2.3506494	1.702E-05	2.0701339	1.56E-06	0.4506809	0.000189	40	37	38.5	70	74	72
GPR68	58	55	-57	-2.9655172	2.124E-07	-2.6704192	-2.035E-06	0.0056262	3.479E-06	85	87	86	29	29	29
GPR87	23	12	14.5	3.4166667	0.0011141	3.2895125	5.28E-07	1	0.0078142	8	4	6	22	14	18
GPT	8	6	-6.5	-14	0.0019424	-10.652982	-2.435E-07	1	0.012575	7	7	7	0	1	0.5
GREM1	1154	180	836.5	4.1506591	4.893E-62	3.850469	2.854E-05	1.296E-57	6.448E-60	305	226	265.5	866	976	921
GREM2	49	10	43	7.6153846	4.995E-13	8.3067192	1.828E-06	1.323E-08	1.83E-11	4	9	6.5	53	46	49.5
GRIK2	216	58	137.5	3.1653543	6.307E-11	2.5155028	3.637E-06	1.67E-06	1.808E-09	73	54	63.5	154	134	144
GRK5	858	691	-784.5	-2.2344611	0	-2.0169119	-2.706E-05	0	0	1407	1433	1420	625	646	635.5
GSTM5	180	107	-118.5	-2.3166667	3.062E-06	-2.0825561	-4.089E-06	0.081087	3.942E-05	230	187	208.5	107	73	90
GTF2IP1	1372	1055	882	5.3771712	0.0001254	-3.1832042	-1.841E-05	1	0.0011263	1082	357	719.5	181	222	201.5
HBD	58	19	-40.5	-4.6818182	2.564E-05	3.1642729	1.481E-06	0.6789433	0.0002735	18	18	18	67	36	51.5
HDAC5	729	396	489	3.3623188	1.132E-10	2.1746039	9.204E-06	2.998E-06	3.146E-09	192	222	207	446	367	406.5
HES2	36	22	24	2.92	0.0012785	3.2238152	1.056E-06	1	0.0087427	16	9	12.5	31	42	36.5
HES7	21	7	11.5	12.5	0.0047235	-7.469256	-2.989E-07	1	0.0271471	7	11	9	2	0	1
HGF	1975	1255	-1928.5	-6.364395	0	-5.7446575	-7.144E-05	0	0	2246	2330	2288	364	355	359.5
HGFAC	6	5	-5	-11	0.0089109	-8.4062285	-1.87E-07	1	0.046715	5	6	5.5	1	0	0.5
HLA-F	12	7	10.5	22	0.00715	-9.886444	-2.243E-07	1	0.0386861	8	5	6.5	1	0	0.5
HMCN1	70	32	39.5	3.0789474	0.0004811	-2.3848084	-1.109E-06	1	0.0037289	56	45	50.5	24	14	19
HMGCR	1817	796	-1175.5	-2.2270355	0	-2.0081532	-4.044E-05	0	0	2228	2039	2133.5	934	982	958
HMGCS1	1839	1494	-1749	-3.722179	0	-3.3627503	-6.35E-05	0	0	2390	2393	2391.5	554	731	642.5
HNRNPA1P3	9	7	8	#DIV/0!	0.000579	59.453369	2.514E-07	1	0.0043965	0	0	0	7	5	6
HOGA1	16	12	-13.5	-6.4	0.0017411	-5.5803677	-4.997E-07	1	0.0114427	16	16	16	4	1	2.5
HPCAL1	1562	1175	-1414.5	-2.7292176	0	-2.4591065	-4.999E-05	0	0	2371	2094	2232.5	827	809	818
HRASLS5	14	6	-11	#DIV/0!	0.0049056	-4.7554853	-3.306E-07	1	0.0280227	14	8	11	2	2	2
HRAT17	15	5	9.5	10.5	0.0014657	10.561185	4.007E-07	1	0.0098578	2	0	1	6	15	10.5
HSD17B2	57	29	-40	-4.0769231	2.157E-06	-3.66434	-1.46E-06	0.057133	2.861E-05	52	54	53	7	19	13
HSD17B7P2	55	49	-52	-5.7272727	3.695E-08	-5.1253518	-1.919E-06	0.0009786	6.98E-07	64	62	63	13	9	11
HSH2D	34	31	33	6.5	0.0057596	3.0060995	4.628E-07	1	0.0322256	7	5	6	8	25	16.5
HSPB3	6	2	4	#DIV/0!	0.0070002	39.944356	1.675E-07	1	0.037992	0	0	0	4	4	4
HSPB7	206	81	173.5	4.2429907	4.194E-18	4.710254	7.497E-06	1.111E-13	2.614E-16	63	44	53.5	250	204	227
HTR1F	212	50	121.5	2.4210526	2.215E-10	2.3294134	4.292E-06	5.867E-06	5.98E-09	99	72	85.5	180	179	179.5
HYAL1	10	4	-7	#DIV/0!	0.0002846	-62.724873	-2.654E-07	1	0.0023505	4	10	7	0	0	0
ICA1	14	12	-12	-3.6666667	0.0089551	-2.9358343	-4.137E-07	1	0.0469097	17	16	16.5	6	4	5
ICAM1	15716	3553	10400	3.503611	0	-2.2813618	-0.0002229	0	0	10707	10307	10507	4212	4096	4154
ICAM4	56	27	35	3.0588235	0.0023416	-2.3077985	-9.35E-07	1	0.0148294	40	47	43.5	10	24	17
ID1	8634	2336	6500	4.7746806	1.089E-14	3.0381729	0.0001325	2.884E-10	4.99E-13	1826	1618	1722	4763	4667	4715
ID2	2024	594	1521.5	9.2021563	6.94E-109	6.0830602	3.56E-05	1.84E-104	9.99E-107	203	168	185.5	1122	911	1016.5
ID3	10518	1864	7678.5	4.8556365	3.251E-41	4.14552	0.0002365	8.611E-37	3.712E-39	2097	1886	1991.5	7440	7445	7442.5
ID4	91	32	65	4.8235294	2.568E-09	3.632331	1.703E-06	6.802E-05	5.895E-08	14	20	17	60	52	56
IDH1	3246	2258	-2875	-2.5013055	0	-2.253394	-0.0001005	0	0	5152	4428	4790	1906	1924	1915
IDI1	1427	1234	-1360.5	-2.6411339	0	-2.3817608	-4.797E-05	0	0	2250	2129	2189.5	835	823	829
IDI2-AS1	44	18	-29.5	-3.36	0.0010667	-2.5951325	-9.738E-07	1	0.0075138	53	31	42	9	20	14.5
IDO1	16	8	9.5	7.3333333	0.0017762	-5.9756711	-3.339E-07	1	0.0116412	10	11	10.5	2	1	1.5
IER3	78	28	-45.5	-2.3787879	8.582E-05	-2.144198	-1.584E-06	1	0.0008037	82	75	78.5	22	44	33
IFI27L2	162	2	-82	#DIV/0!	1.262E-09	-704.07681	-3.023E-06	3.343E-05	3.039E-08	162	2	82	0	0	0
IFIH1	278	115	171.5	3.005848	3.119E-08	-2.146622	-4.113E-06	0.0008261	5.982E-07	194	213	203.5	98	73	85.5
IFIT1	657	451	-579.5	-6.9742268	1.462E-89	-6.2803011	-2.145E-05	3.873E-85	2.049E-87	739	614	676.5	82	112	97
IFITM1	465	306	-414.5	-3.1873351	3.967E-17	-2.871838	-1.487E-05	1.051E-12	2.33E-15	626	582	604	201	178	189.5
IFITM10	64	11	45.5	4.9565217	6.218E-05	2.872279	8.216E-07	1	0.0006004	10	13	11.5	31	29	30
IGDCC4	65	53	-59	-3.8095238	1.286E-09	-3.4261496	-2.144E-06	3.406E-05	3.093E-08	77	83	80	24	18	21
IGF2	854	307	557.5	3.4505495	4.445E-13	2.087335	9.334E-06	1.177E-08	1.639E-11	253	202	227.5	469	386	427.5
IL12RB1	51	26	28.5	4	0.0048434	-2.7324465	-6.978E-07	1	0.0277239	28	30	29	14	5	9.5
IL16	376	297	296.5	20.766667	7.885E-08	-3.7672544	-1.751E-06	0.0020884	1.408E-06	64	62	63	19	11	15
IL17B	7	5	4.5	#DIV/0!	0.0062626	44.912466	1.888E-07	1	0.0346058	0	0	0	7	2	4.5
IL18R1	247	85	189.5	4.0079365	7.758E-10	-2.9172245	-5.069E-06	2.055E-05	1.926E-08	203	205	204	71	55	63
IL1B	15916	11278	-14885	-3.755716	0	-3.3866488	-0.0005397	0	0	21178	19395	20286.5	5262	5541	5401.5
IL1RAPL2	45	27	-36	-2.6744186	4.449E-05	-2.4053143	-1.271E-06	1	0.0004473	61	54	57.5	19	24	21.5
IL21R	290	195	205.5	14.258065	0.0006312	-2.7315606	-1.13E-06	1	0.0047547	43	51	47	12	19	15.5
IL24	66	25	36.5	4.173913	0.0001353	3.0221293	8.854E-07	1	0.0012046	15	8	11.5	32	31	31.5
IL2RB	77	24	56.5	5.1851852	0.0040728	-2.1991964	-6.828E-07	1	0.0239333	30	36	33	12	15	13.5
IL31RA	534	311	-444	-2.5913978	7.599E-19	-2.3341648	-1.558E-05	2.013E-14	4.921E-17	795	651	723	261	297	279
IL33	622	474	-577	-4.9656357	1.156E-24	-4.4705046	-2.118E-05	3.061E-20	9.656E-23	744	701	722.5	169	122	145.5
IL6	1060	169	688	3.4140351	7.617E-20	-2.4317211	-1.708E-05	2.017E-15	5.16E-18	786	750	768	259	311	285
IL7	13	7	-10	-4.3333333	0.0029609	-3.8181389	-3.656E-07	1	0.0182195	13	13	13	0	6	3
INMT	63	29	-48	-10.6	1.048E-10	-9.351986	-1.784E-06	2.775E-06	2.93E-09	67	39	53	4	6	5
INSIG1	4265	3976	-4212.5	-10.509029	1.17E-154	-9.4916919	-0.0001574	3.11E-150	1.75E-152	4656	4655	4655.5	391	495	443
INSL3	8	7	-5	#DIV/0!	0.0072987	-44.55701	-1.873E-07	1	0.0393937	8	2	5	0	0	0
INTS3	158	63	-79	-27.333333	0.0013628	8.2268717	1.266E-06	1	0.0092463	3	6	4.5	66	2	34
ISG20	277	214	214.5	54.625	8E-13	-11.957688	-1.882E-06	2.119E-08	2.875E-11	69	40	54.5	4	4	4
ITGA11	757	480	-707	-3.0582242	4.342E-26	-2.7564692	-2.528E-05	1.15E-21	3.783E-24	1091	1010	1050.5	353	334	343.5
ITGB1BP2	24	19	16	2.0666667	0.0043971	2.2777608	7.303E-07	1	0.0254774	13	17	15	29	33	31
ITGB4	28	26	-22	-3.4444444	0.0023122	-3.0896579	-7.964E-07	1	0.014675	28	34	31	9	9	9
ITGB8	92	56	-75	-17.666667	1.818E-12	-15.582505	-2.805E-06	4.815E-08	6.302E-11	93	66	79.5	1	8	4.5
ITPK1	18	16	-17	#DIV/0!	8.635E-08	-150.23522	-6.418E-07	0.0022869	1.525E-06	18	16	17	0	0	0
ITPKA	63	46	-46	-2.3939394	0.0005519	-2.154926	-1.599E-06	1	0.0042135	88	70	79	25	41	33
IZUMO4	26	18	-21.5	-4.3076923	0.0052209	-2.5051255	-6.372E-07	1	0.0296599	31	25	28	13	7	10
JAKMIP2	38	11	33.5	17.75	4.721E-07	-9.278493	-7.286E-07	0.0125025	7.21E-06	21	22	21.5	1	3	2
KCCAT198	17	10	-15	-11	0.0089643	-2.9400016	-4.145E-07	1	0.0469487	15	18	16.5	5	5	5
KCCAT211	100	21	66.5	2.9	4.074E-05	-2.0325122	-1.517E-06	1	0.0004137	84	74	79	32	38	35
KCNA7	36	27	31.5	8.875	2.106E-08	9.5470281	1.335E-06	0.0005577	4.172E-07	0	8	4	36	35	35.5
KCNAB2	865	682	651.5	39.323529	0.0022828	-2.2714673	-9.105E-07	1	0.0145055	47	39	43	17	17	17
KCNF1	10	6	-6	#DIV/0!	0.0012615	-53.33436	-2.251E-07	1	0.0086492	10	2	6	0	0	0
KCNG2	26	12	-23.5	-8.8333333	7.836E-08	-7.7329329	-8.748E-07	0.0020752	1.402E-06	28	25	26.5	4	2	3

KCNIP2	24	17	-19.5	-3.1666667	0.0052722	-2.2241115	-5.944E-07	1	0.0299067	31	26	28.5	9	14	11.5
KCNJ2	660	356	548	7.7654321	3.213E-21	-3.8528951	-9.685E-06	8.51E-17	2.331E-19	393	301	347	76	86	81
KCNJ2-AS1	46	29	-37.5	-2.7045455	7.966E-05	-2.3767501	-1.303E-06	1	0.0007509	66	53	59.5	21	24	22.5
KCNMB4	69	60	-61	-3.5957447	1.906E-08	-3.2368878	-2.209E-06	0.0005047	3.806E-07	86	83	84.5	17	30	23.5
KCNQ5	381	237	302.5	10.029851	8.435E-06	2.5362523	1.955E-06	0.2233978	9.973E-05	27	40	33.5	74	80	77
KDR	331	87	210	2.7213115	5.725E-09	-2.1346477	-5.794E-06	0.0001516	1.24E-07	268	308	288	100	144	122
KIAA0895	30	16	-17.5	-4.5	0.0015282	-3.9657564	-6.347E-07	1	0.0102158	32	13	22.5	8	2	5
KIAA1875	18	11	-12.5	-4.125	0.0027733	-3.6449401	-4.543E-07	1	0.0172379	20	13	16.5	4	4	4
KIRREL3	40	17	28	3.9473684	7.379E-07	4.3233997	1.209E-06	0.0195424	1.08E-05	7	12	9.5	28	47	37.5
KISS1	769	480	681	3.3402062	3.236E-62	3.7092137	2.972E-05	8.571E-58	4.285E-60	338	244	291	931	1013	972
KITLG	1963	528	1179	2.0545617	1.693E-51	2.0368904	4.377E-05	4.483E-47	2.145E-49	1169	1067	1118	2092	2014	2053
KLB	16	12	10.5	5.2	0.0033402	5.1154213	4.066E-07	1	0.0201885	2	3	2.5	6	18	12
KLF15	32	20	23.5	7.7142857	4.471E-05	-5.4326009	-6.687E-07	1	0.0004492	15	28	21.5	4	3	3.5
KLF2	763	244	513	2.3153846	8.167E-31	2.429147	2.106E-05	2.163E-26	8.101E-29	398	382	390	878	831	854.5
KLHL7-AS1	27	13	15	3	0.0012293	3.3045839	6.618E-07	1	0.0084656	9	6	7.5	33	12	22.5
KLRC2	25	18	-21.5	-22.5	1.517E-08	-18.53662	-8.093E-07	0.0004017	3.088E-07	20	25	22.5	0	2	1
KLRC3	10	6	-8	-9	0.0041434	-7.4538887	-2.978E-07	1	0.0242678	10	8	9	0	2	1
KRT18	11650	6626	7658	1.9052544	1.222E-43	2.1135114	0.0003557	3.238E-39	1.439E-41	8753	8166	8459.5	16582	15653	16117.5
KRT7	16334	2383	11814.5	5.2582447	1.075E-53	4.6924425	0.0003868	2.847E-49	1.382E-51	2877	2672	2774.5	11935	11541	11738
KRT81	472	203	353.5	9.7283951	1.178E-24	4.1536871	4.836E-06	3.121E-20	9.815E-23	43	38	40.5	158	146	152
KRT86	106	76	78.5	9.2631579	1.191E-05	3.4705841	8.965E-07	0.3154559	0.0001361	11	8	9.5	24	36	30
KYNU	2506	438	1801	3.9646091	0	-2.4173424	-3.608E-05	0	0	1640	1617	1628.5	651	564	607.5
LAMA2	647	230	394.5	3.4202454	2.734E-09	-2.1865429	-8.099E-06	7.241E-05	6.247E-08	401	389	395	152	174	163
LAMA5	3152	2576	-2903	-2.8269352	0	-2.551491	-0.0001032	0	0	4614	4370	4492	1462	1716	1589
LBH	431	329	311.5	6.1065574	2.005E-07	2.5123223	3.484E-06	0.0053093	3.308E-06	71	51	61	152	124	138
LCMT1-AS2	8	3	5.5	12	0.003917	11.020105	2.32E-07	1	0.0230998	1	0	0.5	4	8	6
LCNL1	20	15	-17.5	#DIV/0!	7.055E-08	-155.00346	-6.623E-07	0.0018684	1.275E-06	15	20	17.5	0	0	0
LDLR	7258	6534	-7219.5	-5.3530298	0	-4.8312241	-0.0002661	0	0	8847	8909	8878	1666	1651	1658.5
LDLRAD2	26	17	-23	-6.1111111	0.0085735	2.1766679	6.251E-07	1	0.0451431	20	8	14	30	25	27.5
LGALS9	54	27	35	4.1818182	0.003891	-2.2877234	-5.986E-07	1	0.0229516	24	32	28	11	11	11
LHCGR	43	12	-34.5	-5.3125	1.615E-07	-4.740397	-1.268E-06	0.0042785	2.713E-06	48	37	42.5	5	11	8
LHPP	160	50	106.5	2.9906542	8.763E-08	-2.6096734	-3.619E-06	0.0023208	1.545E-06	173	138	155.5	70	37	53.5
LIMS2	376	163	219	2.4313725	2.693E-12	2.6494623	9.564E-06	7.132E-08	9.227E-11	134	172	153	397	336	366.5
LINC00327	45	16	-28.5	-2.6285714	0.0009089	-2.3548836	-9.983E-07	1	0.0065128	59	33	46	16	19	17.5
LINC00547	66	43	42.5	2.328125	4.081E-05	2.5755645	1.914E-06	1	0.0004143	29	35	32	90	59	74.5
LINC00607	52	37	45.5	2.4677419	1.17E-07	2.7323702	2.034E-06	0.0030987	2.016E-06	35	27	31	79	74	76.5
LINC00842	32	20	25	2.25	5.323E-05	2.4830652	1.127E-06	1	0.0005234	18	22	20	40	50	45
LINC00908	17	10	-13.5	-28	0.0001011	-21.070816	-5.062E-07	1	0.0009317	17	11	14	0	1	0.5
LINC00926	32	23	-27.5	-4.9285714	0.0037759	-2.3795856	-7.57E-07	1	0.0224026	38	31	34.5	14	12	13
LINC01355	61	46	-50.5	-3.1956522	3.954E-06	-2.8799228	-1.815E-06	0.1047162	4.977E-05	74	73	73.5	13	33	23
LINC01372	8	6	-7	-15	0.0059432	-11.3849	-2.622E-07	1	0.0330819	8	7	7.5	1	0	0.5
LINC01431	6	5	-5	-11	0.0092251	-8.3931605	-1.866E-07	1	0.0480837	6	5	5.5	1	0	0.5
LINC01583	30	14	-21	-2.826087	0.000867	2.5555055	8.301E-07	1	0.0062605	12	16	14	26	39	32.5
LIPG	153	97	-124	-32	9.698E-22	-16.220153	-4.522E-06	2.568E-17	7.235E-20	155	101	128	4	10	7
LLPH-AS1	10	5	6	7	0.0094942	7.090325	2.554E-07	1	0.0492178	2	0	1	7	7	7
LMNTD1	25	12	-18.5	-3.0555556	0.0007137	2.7491882	7.347E-07	1	0.0052963	10	12	11	22	33	27.5
LMO7	5200	2331	3162.5	1.8734981	3.209E-69	2.0771745	0.0001473	8.498E-65	4.381E-67	3684	3557	3620.5	6914	6652	6783
LOC1001280	16	12	-14.5	-3.6363636	0.0012645	-3.2402522	-5.253E-07	1	0.0086641	20	20	20	4	7	5.5
LOC1001292	7	4	-5.5	#DIV/0!	0.0016039	-49.427156	-2.083E-07	1	0.0106461	4	7	5.5	0	0	0
LOC1001295	8	8	-8	-5	0.0080369	-4.3395681	-2.94E-07	1	0.0427597	10	10	10	2	2	2
LOC1001304	83	27	68	28.2	1.214E-28	29.110814	2.774E-06	3.216E-24	1.137E-26	3	2	2.5	71	66	68.5
LOC1001308	266	212	-227	-3.4808743	3.496E-21	-3.1407333	-8.211E-06	9.259E-17	2.523E-19	306	331	318.5	94	89	91.5
LOC1001328	11	6	6.5	5.3333333	0.0072905	5.5756751	2.779E-07	1	0.0393577	3	0	1.5	5	11	8
LOC1002681	70	60	64.5	2.3578947	1.528E-09	2.6100075	2.896E-06	4.047E-05	3.643E-08	47	48	47.5	116	108	112
LOC1005057	15	6	-8	-17	0.0057186	-12.705063	-2.957E-07	1	0.032034	15	2	8.5	1	0	0.5
LOC1005061	79	37	-63.5	-22.166667	2.35E-17	-19.305991	-2.377E-06	6.224E-13	1.402E-15	81	52	66.5	2	4	3
LOC1005061	35	18	-24.5	-2.6333333	0.0089475	-2.3613296	-8.635E-07	1	0.0468885	38	41	39.5	24	6	15
LOC1005074	15	9	11.5	2.7692308	0.0017047	3.0375856	5.085E-07	1	0.0112168	8	5	6.5	19	17	18
LOC1019271	40	12	26	2.5757576	0.0030784	-2.0147578	-7.054E-07	1	0.0188336	41	33	37	17	16	16.5
LOC1019272	111	19	73.5	2.96	3.565E-06	2.2604726	1.79E-06	0.094417	4.537E-05	41	34	37.5	86	67	76.5
LOC1019274	35	21	-21.5	-3.047619	0.0010919	-2.7357168	-7.71E-07	1	0.007675	28	36	32	13	8	10.5
LOC1019277	9	6	5	#DIV/0!	0.0041483	49.637952	2.092E-07	1	0.0242906	0	0	0	4	6	5
LOC1019283	45	16	25	2.3157895	0.0007957	2.2406982	8.951E-07	1	0.0058183	21	17	19	40	37	38.5
LOC1024670	13	7	10.5	4	0.0019306	4.325766	4.537E-07	1	0.0125076	4	3	3.5	12	16	14
LOC284950	12	4	7	#DIV/0!	0.0004472	68.904265	2.92E-07	1	0.0035063	0	0	0	2	12	7
LOC401052	21	14	-17.5	-4.8888889	0.0011694	-4.3460352	-6.438E-07	1	0.0081112	21	23	22	2	7	4.5
LOC440028	53	32	-42.5	-3.1794872	0.0001335	-2.8518956	-1.523E-06	1	0.0011893	64	60	62	28	11	19.5
LOC440600	17	8	9.5	7.3333333	0.0001736	7.6282874	4.038E-07	1	0.0015066	2	1	1.5	10	12	11
LOC541472	26	13	15.5	1.9117647	0.0054206	2.1082982	7.177E-07	1	0.0306435	13	21	17	34	31	32.5
LOC613037	28	3	13.5	28	0.0003545	25.333351	5.625E-07	1	0.002854	1	0	0.5	0	28	14
LOC653160	61	37	40	3	6.099E-05	-2.5679039	-1.321E-06	1	0.0005913	48	66	57	24	16	20
LOC90246	59	17	45	4.9130435	0.0044021	-2.1464252	-5.569E-07	1	0.025501	29	26	27.5	11	12	11.5
LOX	25335	8753	16836	3.2091589	5.412E-37	2.1123932	0.0003202	1.433E-32	5.898E-35	7761	7481	7621	14622	14421	14521.5
LOXL4	923	760	-877	-2.517301	0	-2.2704198	-3.075E-05	0	0	1494	1416	1455	571	585	578
LPAR3	31	15	-25	-3.0833333	0.0001117	-2.7628689	-8.936E-07	1	0.0010207	41	33	37	14	10	12
LPIN1	2123	1711	-2030	-3.6397919	1.243E-14	-3.2830466	-7.351E-05	3.293E-10	5.649E-13	2875	2723	2799	752	786	769
LRIG1	817	385	-581.5	-3.3734694	9.294E-26	-3.0482394	-2.102E-05	2.462E-21	8.044E-24	772	881	826.5	245	245	245
LRRC4	37	26	33.5	5.1875	4.508E-07	5.6870642	1.437E-06	0.0119397	6.914E-06	8	8	8	45	38	41.5
LRRC43	33	9	-18.5	-2.7619048	0.0092374	-2.4604879	-6.494E-07	1	0.0481317	39	19	29	15	6	10.5
LRRN3	957	393	548.5	2.0765456	6.632E-22	2.2912534	2.49E-05	1.756E-17	4.976E-20	468	551	509.5	1084	1026	1055
LRRN4CL	57	34	-46.5	-16.5	2.772E-13	-14.408297	-1.74E-06	7.343E-09	1.058E-11	57	42	49.5	0	6	3
LRRTM2	32	24	-22.5	-4.2142857	5.489E-05	-3.7491872	-8.182E-07	1	0.0005375	36	23	29.5	10	4	7
LSM14A	406	285	345.5	10.597222	0.0017832	5.1459616	5.665E-06	1	0.0116841	34	38	36	295	38	166.5
LSS	508	384	-446	-2.5300172	2.215E-11	-2.2870688	-1.57E-05	5.866E-07	6.79E-10	719	756	737.5	248	335	291.5
LURAP1L	389	266	-306.5	-2.6887052	1.23E-14	-2.4278492	-1.085E-05	3.258E-10	5.599E-13	487	489	488	158	205	181.5
LVRN	53	45	-38	-2.2881356	0.0003734	-2.064712	-1.32E-06	1	0.0029883	59	76	67.5	29	30	29.5
LY75	12	7	10.5	#DIV/0!	4.239E-05	-80.152178	-3.404E-07	1	0.0004293	8	10	9	0	0	0

LYPD1	310	74	240	2.6053512	4.973E-14	2.6501892	9.317E-06	1.317E-09	2.101E-12	160	139	149.5	387	327	357
LYPLAL1-AS1	34	12	29	3.32	0.0016803	-2.3697248	-7.228E-07	1	0.0110923	34	32	33	13	12	12.5
MACROD2	30	21	26	27	0.0034425	-7.0268071	-2.781E-07	1	0.0207325	13	4	8.5	0	2	1
MALL	107	59	77	4.08	2.295E-06	3.6573868	2.52E-06	0.0607901	3.021E-05	26	24	25	109	56	82.5
MAN1C1	35	18	-25.5	-3.125	0.000476	-2.8112114	-9.171E-07	1	0.0036971	33	42	37.5	9	15	12
MAP2K6	58	37	39.5	5.9375	0.0077412	-2.7753658	-6.028E-07	1	0.0414364	36	14	25	10	6	8
MAP6D1	269	101	159	2.426009	6.185E-16	2.6320544	6.867E-06	1.638E-11	3.257E-14	131	92	111.5	248	281	264.5
MAPK10	88	59	-70	-2.75	3.634E-08	-2.4779671	-2.481E-06	0.0009625	6.885E-07	112	108	110	35	45	40
MARCH10	55	14	34	3.8333333	0.0033737	2.2948194	5.931E-07	1	0.0203492	9	15	12	26	24	25
MARCH9	101	68	81	4.3061224	0.0007193	-2.0985853	-1.131E-06	1	0.0053316	51	63	57	21	28	24.5
MASP1	33	15	20.5	9.2	0.0029396	-4.7183347	-4.059E-07	1	0.0181271	12	15	13.5	5	0	2.5
MCC	666	296	-493.5	-2.8622642	1.354E-24	-2.58167	-1.756E-05	3.586E-20	1.124E-22	766	751	758.5	269	261	265
MCOLN2	6	6	-5	#DIV/0!	0.0041387	-45.018853	-1.893E-07	1	0.0242506	4	6	5	0	0	0
MCTP1	111	101	-93	-3.3544304	1.468E-06	-3.0152014	-3.343E-06	0.0388673	2.025E-05	144	121	132.5	42	37	39.5
MEDAG	550	528	-546	-3.9673913	4.138E-93	-3.5793085	-1.988E-05	1.096E-88	5.829E-91	726	734	730	184	184	184
METTL7A	489	144	335	7.146789	1.404E-24	-3.9972048	-6.848E-06	3.719E-20	1.162E-22	236	247	241.5	44	65	54.5
MFAP5	17	11	11.5	3.3	0.0031716	3.6189558	5.033E-07	1	0.0193506	9	1	5	18	15	16.5
MID1IP1	907	684	-811.5	-2.2193839	0	-2.0013958	-2.791E-05	0	0	1521	1433	1477	671	660	665.5
MID1IP1-AS	53	29	-39	-3.6	0.0003306	-2.3091918	-1.157E-06	1	0.0026855	61	47	54	22	20	21
MIR22HG	11	2	6.5	#DIV/0!	0.0025787	64.585715	2.734E-07	1	0.016181	0	0	0	11	2	6.5
MIR3189	5	4	-4.5	#DIV/0!	0.0054476	-40.567749	-1.702E-07	1	0.0307764	4	5	4.5	0	0	0
MIR4500HG	22	15	-18	-5	0.000119	-4.426295	-6.608E-07	1	0.001076	24	21	22.5	7	2	4.5
MIR99AHG	37	19	-26	-2.6774194	0.0032389	-2.2016757	-8.608E-07	1	0.0196886	32	51	41.5	19	15	17
MMAB	630	555	-576	-2.92	1.071E-20	-2.6361243	-2.055E-05	2.838E-16	7.588E-19	868	884	876	287	313	300
MMD	3259	502	2193.5	2.7512974	0	-2.0402723	-5.456E-05	0	0	2765	2896	2830.5	1266	1239	1252.5
MME	7843	1726	5285.5	3.1936086	0	-2.3023584	-0.0001313	0	0	6357	5940	6148.5	2252	2567	2409.5
MMP3	28	14	16.5	4.6666667	0.00159	-3.8290046	-5.461E-07	1	0.0105676	23	16	19.5	8	1	4.5
MPZ	72	35	-60.5	-3.6304348	2.422E-09	-3.2639476	-2.191E-06	6.416E-05	5.584E-08	84	83	83.5	27	19	23
MRGPRF-AS	8	7	-7.5	-16	0.0034581	-12.151196	-2.813E-07	1	0.0208109	8	8	8	0	1	0.5
MSMO1	1827	1406	-1615	-3.2524407	0	-2.9286519	-5.796E-05	0	0	2467	2197	2332	791	643	717
MTMR9LP	88	66	-72	-3.2857143	3.235E-05	-2.0053927	-1.962E-06	0.8566671	0.0003366	106	101	103.5	47	46	46.5
MTRNR2L2	12	5	-9	-19	0.0008931	-14.426247	-3.389E-07	1	0.0064156	7	12	9.5	1	0	0.5
MTUS1	407	306	-380.5	-7.3416667	1.055E-62	-6.6155045	-1.412E-05	2.794E-58	1.404E-60	457	424	440.5	50	70	60
MURC	127	62	86.5	2.9010989	6.19E-09	3.2262359	3.824E-06	0.0001639	1.334E-07	56	35	45.5	162	102	132
MVK	610	442	-532.5	-2.8393782	6.298E-22	-2.5566181	-1.888E-05	1.668E-17	4.739E-20	888	756	822	301	278	289.5
MX2	43	14	33	34	1.147E-08	-16.877561	-7.332E-07	0.0003038	2.379E-07	18	23	20.5	2	0	1
MXRA5	176	141	160.5	7.9782609	0.0006726	-2.0569258	-1.023E-06	1	0.0050183	46	59	52.5	26	20	23
MYCBP	18	5	14	2.5555556	0.0037816	2.5658882	5.393E-07	1	0.0224212	8	10	9	22	20	21
MYLIP	238	95	-215.5	-5.8426966	1.078E-41	-5.2640498	-7.96E-06	2.856E-37	1.247E-39	261	259	260	39	50	44.5
MYLK	9922	3166	6982.5	3.5008954	0	-3.1382295	-0.00025	0	0	10017	9414	9715.5	2776	2808	2792
MYO15B	40	30	-34	-3.1935484	0.0003702	-2.8655471	-1.221E-06	1	0.0029682	49	50	49.5	21	10	15.5
MYO7B	241	177	179.5	10.702703	2.244E-05	3.0102525	1.416E-06	0.5942736	0.0002425	15	22	18.5	57	44	50.5
MYOZ2	37	10	21	4.2307692	0.0004887	3.3644505	5.915E-07	1	0.003779	4	9	6.5	20	20	20
N4BP2L1	61	44	46.5	24.25	0.0053142	-4.3442934	-2.942E-07	1	0.0301256	9	11	10	0	4	2
NBEA	98	51	-74.5	-2.9350649	5.929E-08	-2.6351336	-2.643E-06	0.0015703	1.087E-06	136	90	113	39	38	38.5
NCKAP5	476	244	-341	-2.4004107	2.636E-11	-2.1690531	-1.192E-05	6.982E-07	8.016E-10	559	610	584.5	227	260	243.5
NDE1	31	6	15	11	0.0011488	11.574995	6.399E-07	1	0.0080003	3	0	1.5	31	2	16.5
NFATC4	724	525	-608.5	-2.4053118	0	-2.1755478	-2.129E-05	0	0	986	1097	1041.5	373	493	433
NGF	71	52	60	1.9677419	2.419E-07	2.1776674	2.766E-06	0.0064057	3.915E-06	57	67	62	128	116	122
NIPAL4	42	28	33	7.6	1.15E-10	8.2570498	1.403E-06	3.045E-06	3.189E-09	4	6	5	40	36	38
NLGN1	106	54	53.5	1.9145299	1.002E-05	2.1231505	2.481E-06	0.2653646	0.0001162	69	48	58.5	101	123	112
NOG	51	9	32.5	2.5116279	7.868E-05	2.606348	1.306E-06	1	0.000743	31	12	21.5	52	49	50.5
NOL4	9	7	7	#DIV/0!	0.0076254	44.656745	1.877E-07	1	0.0409072	0	0	0	1	8	4.5
NOMO1	795	212	628	4.6195965	6.93E-06	-2.8930894	-1.379E-05	0.1835287	8.363E-05	559	556	557.5	209	138	173.5
NOV	18	14	-17.5	#DIV/0!	4.436E-08	-154.78034	-6.613E-07	0.001175	8.281E-07	17	18	17.5	0	0	0
NOVA1	34	27	-27	-4.6	0.0002989	-3.08336	-8.812E-07	1	0.0024496	41	28	34.5	10	10	10
NOXA1	17	14	-15.5	-11.333333	0.0029998	-3.3550455	-4.541E-07	1	0.0184211	16	18	17	6	3	4.5
NPAS1	239	86	149	3.2238806	3.833E-13	3.5517513	6.502E-06	1.015E-08	1.426E-11	45	89	67	221	211	216
NPPA	9	5	-7.5	-4.75	0.0095079	-4.1203687	-2.747E-07	1	0.0492698	11	8	9.5	2	2	2
NPPA-AS1	28	13	-20.5	-11.25	0.0027772	-3.0764214	-5.744E-07	1	0.0172543	29	16	22.5	8	5	6.5
NPPB	292	247	239	2.225641	1.54E-13	2.4638539	1.08E-05	4.08E-09	6.044E-12	190	200	195	421	447	434
NPTX2	103	67	-85	-4.0357143	8.62E-10	-3.637461	-3.106E-06	2.283E-05	2.122E-08	100	126	113	33	23	28
NR1H3	227	181	-221	-2.2521246	2.477E-11	-2.0314177	-7.626E-06	6.56E-07	7.549E-10	402	393	397.5	175	178	176.5
NR4A1	327	103	227.5	2.5423729	4.576E-19	2.5996994	8.915E-06	1.212E-14	3.007E-17	155	140	147.5	334	358	346
NRG4	19	11	-14.5	-3.9	0.0089495	-2.4941361	-4.442E-07	1	0.0468895	18	21	19.5	6	8	7
NTAN1	398	278	-318.5	-3.3505535	0.0003795	-2.2070462	-9.381E-06	1	0.0030347	462	446	454	187	184	185.5
NTF4	19	12	-15	-7	0.0004132	4.2250628	5.628E-07	1	0.0032745	3	6	4.5	19	16	17.5
NTN5	12	2	-7	#DIV/0!	0.0025787	-63.25709	-2.677E-07	1	0.016181	2	12	7	0	0	0
NTRK3	18	10	-15	#DIV/0!	6.062E-07	-133.0722	-5.68E-07	0.0160542	8.979E-06	12	18	15	0	0	0
OAS1	44	33	35.5	5.7333333	0.0012634	-3.3162489	-7.366E-07	1	0.0086598	41	15	28	5	10	7.5
OAS2	514	401	362	15.196078	3.475E-05	-2.8860181	-2.017E-06	0.9204762	0.0003589	78	85	81.5	14	37	25.5
OBSL1	325	263	-294	-2.2618026	2.756E-14	-2.0426574	-1.017E-05	7.299E-10	1.2E-12	511	543	527	218	248	233
OLFM2	18	10	11	2.375	0.0077859	2.6118584	4.936E-07	1	0.041625	9	7	8	19	19	19
OLFML2A	65	40	-54.5	-4.0277778	3.494E-09	-3.6192042	-1.984E-06	9.253E-05	7.815E-08	77	68	72.5	12	24	18
OLFML2B	77	13	-56.5	-3.3541667	1.102E-06	-3.0093788	-2.026E-06	0.0291753	1.56E-05	97	64	80.5	20	28	24
OLFML3	188	150	-185	-5.8051948	4.039E-18	-5.2297168	-6.834E-06	1.07E-13	2.523E-16	223	224	223.5	36	41	38.5
OLMALINC	70	52	-57.5	-4.2857143	4.242E-08	-3.8613451	-2.106E-06	0.0011235	7.94E-07	69	81	75	11	24	17.5
OPCML	12	5	9.5	4.1666667	0.0016274	4.4923945	4.104E-07	1	0.0107836	4	2	3	14	11	12.5
OPLAH	133	103	-107	-2.8448276	1.607E-08	-2.5578427	-3.789E-06	0.0004257	3.252E-07	189	141	165	56	60	58
ORAI3	365	304	-359.5	-3.3420195	8.581E-27	-3.0152724	-1.296E-05	2.273E-22	7.626E-25	508	518	513	153	154	153.5
OXTR	1423	992	931	1.8231653	1.081E-17	2.0197705	4.361E-05	2.862E-13	6.595E-16	1101	1161	1131	2153	1971	2062
P2RX6	9	3	-7	#DIV/0!	0.0002904	-62.647591	-2.651E-07	1	0.0023927	5	9	7	0	0	0
P2RX7	19	12	15.5	#DIV/0!	0.0009236	-53.546515	-2.26E-07	1	0.0066039	8	4	6	0	0	0
PADI1	49	38	-39	-3.516129	3.698E-08	3.6405989	1.659E-06	0.0009795	6.982E-07	14	19	16.5	57	52	54.5
PAK3	20	11	-14	-3.3333333	0.002942	-2.975753	-5.053E-07	1	0.0181376	17	23	20	9	3	6
PANK4	42	2	-22	#DIV/0!	0.0004789	-17.774064	-7.727E-07	1	0.0037158	42	2	22	0	2	1
PAPPA	13604	3045	9308	5.1918487	0	-2.8110095	-0.0001683	0	0	7113	6723	6918	2117	2324	2220.5

PAQR8	341	116	249.5	4.2193548	1.406E-09	-2.1039991	-3.587E-06	3.724E-05	3.355E-08	193	169	181	77	78	77.5
PARD3B	114	98	-109	-2.3212121	1.978E-05	-2.0924737	-3.78E-06	0.5239047	0.0002164	193	190	191.5	86	79	82.5
PARD6B	18	12	-12.5	-3.0833333	0.0072024	-2.7483016	-4.47E-07	1	0.0389375	20	17	18.5	8	4	6
PARK2	6	6	-6	#DIV/0!	0.0009223	-53.70387	-2.266E-07	1	0.0065999	6	6	6	0	0	0
PBX1	1865	474	1280	2.6070308	0	-2.1671907	-3.893E-05	0	0	1972	1856	1914	790	803	796.5
PCBP3	141	97	-114	-2.373494	6.458E-10	-2.1387783	-3.963E-06	1.71E-05	1.624E-08	205	189	197	85	81	83
PCDH18	3259	1652	-3105.5	-6.5504915	0	-5.9079783	-0.000115	0	0	3794	3536	3665	535	584	559.5
PCDHGA10	108	59	-96	-2.699115	3.751E-09	-2.4349534	-3.4E-06	9.935E-05	8.334E-08	148	157	152.5	52	61	56.5
PCDHGA9	65	28	44	2.7254902	0.0002792	-2.1963814	-1.282E-06	1	0.002309	48	76	62	25	26	25.5
PCDHGB6	73	44	-44	-3.0952381	3.199E-05	-2.7836166	-1.575E-06	0.8471808	0.0003331	69	61	65	17	25	21
PCDHGB7	301	88	190	2.4179104	1.657E-07	-2.0122787	-5.688E-06	0.0043896	2.776E-06	294	304	299	147	121	134
PCDHGC5	28	16	-19.5	-4.25	0.0006276	-3.7681241	-7.073E-07	1	0.0047344	34	17	25.5	6	6	6
PCGF2	77	2	-39	#DIV/0!	1.462E-07	-351.67227	-1.508E-06	0.0038714	2.472E-06	1	77	39	0	0	0
PCOLCE2	108	86	96.5	9.7727273	3.269E-05	3.1017043	8.816E-07	0.8658945	0.0003397	13	9	11	23	39	31
PCSK9	165	156	-159.5	-32.9	5.411E-45	-22.494671	-5.942E-06	1.433E-40	6.456E-43	167	162	164.5	6	7	6.5
PDE2A	69	49	-59.5	-2.75	8.523E-07	-2.4798234	-2.111E-06	0.0225734	1.232E-05	91	96	93.5	27	41	34
PDE9A	29	15	-24	-25	3.961E-10	-20.519764	-9.009E-07	1.049E-05	1.023E-08	29	21	25	0	2	1
PDGFD	169	140	-154.5	-2.9192547	1.503E-08	-2.6316033	-5.511E-06	0.0003982	3.065E-07	230	240	235	90	71	80.5
PDGFRA	6942	2841	5108	6.4110169	0	-2.8054704	-7.139E-05	0	0	3026	2849	2937.5	978	910	944
PDGFRL	149	87	-107.5	-2.6165414	1.193E-07	-2.354038	-3.776E-06	0.0031589	2.051E-06	194	154	174	66	67	66.5
PDK4	155	152	-153.5	-17.157895	1.61E-45	-15.328144	-5.76E-06	4.264E-41	1.938E-43	164	162	163	9	10	9.5
PDLIM3	411	332	-371.5	-3.336478	1.027E-25	-3.0097811	-1.338E-05	2.719E-21	8.858E-24	549	512	530.5	138	180	159
PDZD2	121	85	-110	-5.8888889	5.282E-18	-5.2888847	-4.058E-06	1.399E-13	3.261E-16	142	123	132.5	21	24	22.5
PDZRN3	54	25	-41.5	-6.1875	2.066E-08	-5.5043008	-1.53E-06	0.0005472	4.096E-07	58	41	49.5	12	4	8
PEG10	1254	883	-1122	-2.3955224	0	-2.1583898	-3.901E-05	0	0	2035	1817	1926	827	781	804
PF4	10	6	5.5	#DIV/0!	0.0087982	39.880225	1.672E-07	1	0.0462158	0	0	0	2	6	4
PFKFB4	202	154	-188.5	-4.9684211	2.72E-26	-4.4802757	-6.932E-06	7.204E-22	2.393E-24	231	241	236	39	56	47.5
PGPEP1	611	524	-561.5	-2.4718218	0	-2.2084486	-1.948E-05	0	0	984	902	943	376	394	385
PIANP	23	14	-18.5	-3.0555556	0.0011978	-2.7374153	-6.617E-07	1	0.0082724	29	26	27.5	6	12	9
PIEZO2	211	154	-187.5	-4	2.479E-08	-3.5962146	-6.824E-06	0.0006565	4.849E-07	249	251	250	85	40	62.5
PIK3IP1	302	42	211.5	4.6153846	1.182E-18	-3.1675613	-5.316E-06	3.131E-14	7.564E-17	205	206	205.5	50	67	58.5
PIP5KL1	37	16	-25	-3.2727273	0.0003502	-2.9477501	-9.044E-07	1	0.002825	28	44	36	7	15	11
PITPNM3	110	68	69.5	1.9084967	2.915E-06	2.1175937	3.23E-06	0.0772145	3.77E-05	85	68	76.5	153	139	146
PKN2-AS1	9	6	6.5	#DIV/0!	0.0068131	39.944313	1.675E-07	1	0.0371518	0	0	0	4	4	4
PKNOX2	24	9	-16.5	-4	0.0019446	-3.5732242	-6.04E-07	1	0.0125836	16	28	22	7	4	5.5
PLA2G3	44	39	-41.5	#DIV/0!	3.768E-18	-365.27672	-1.567E-06	9.981E-14	2.36E-16	44	39	41.5	0	0	0
PLA2G4C	30	17	-20.5	-2.3225806	0.0043503	-2.0856328	-7.093E-07	1	0.0252673	40	32	36	16	15	15.5
PLAU	34115	24053	-32300	-2.9390665	1.883E-13	-2.6515658	-0.0011516	4.987E-09	7.323E-12	50272	47643	48957.5	16157	17158	16657.5
PLCB4	233	179	215	2.4982578	2.209E-21	2.7672331	9.589E-06	5.851E-17	1.625E-19	142	145	143.5	360	357	358.5
PLCE1-AS1	152	79	-99	-2.1314286	1.882E-06	2.3422992	4.484E-06	0.0498391	2.532E-05	100	77	88.5	217	156	186.5
PLCXD1	20	4	10.5	#DIV/0!	0.0002741	102.50893	4.365E-07	1	0.0022725	0	0	0	1	20	10.5
PLD1	572	265	-371.5	-2.5132383	1.339E-11	-2.2664255	-1.302E-05	3.545E-07	4.211E-10	630	604	617	247	244	245.5
PLEK	21	7	15.5	#DIV/0!	0.0006115	-53.758199	-2.269E-07	1	0.0046184	5	7	6	0	0	0
PLEK2	794	236	487.5	2.1818182	2.863E-26	2.2000226	1.869E-05	7.582E-22	2.511E-24	437	388	412.5	783	854	818.5
PLEKHA7	713	171	456.5	2.66	2.247E-26	2.4796606	1.536E-05	5.952E-22	1.984E-24	296	254	275	645	584	614.5
PLEKHH1	14	6	-11	-6.5	0.0008726	-5.6143818	-4.065E-07	1	0.0062922	15	11	13	3	1	2
PLXNA2	5217	1233	3448.5	2.8017241	1.497E-45	2.6997788	0.0001228	3.966E-41	1.811E-43	2045	1783	1914	4361	4958	4659.5
PNMAL1	81	42	-61.5	-2.3369565	7.872E-05	-2.1012648	-2.129E-06	1	0.000743	113	102	107.5	60	32	46
PNPLA3	400	351	-382.5	-3.7717391	2.176E-25	-2.7941647	-1.263E-05	5.763E-21	1.859E-23	531	510	520.5	163	173	168
PODXL	704	401	591.5	9.1586207	6.474E-31	4.783688	1.037E-05	1.715E-26	6.471E-29	79	66	72.5	310	316	313
POM121L9P	205	153	-183	-3.6521739	3.253E-10	-2.3348412	-5.451E-06	8.615E-06	8.522E-09	239	265	252	86	109	97.5
POU2F2	699	516	-668.5	-4.0044944	1.101E-93	-3.6154747	-2.437E-05	2.917E-89	1.56E-91	879	903	891	204	241	222.5
PPARA	560	161	362	2.8756477	4.559E-14	-2.0793031	-8.722E-06	1.207E-09	1.944E-12	440	449	444.5	174	212	193
PPFIA2	25	13	-19.5	-8.8	8.72E-06	-7.6448608	-7.239E-07	0.2309449	0.0001027	27	17	22	2	3	2.5
PPM1E	79	62	71.5	18.875	0.0035941	-3.5466853	-4.371E-07	1	0.0214681	16	16	16	2	6	4
PPP1R14A	141	109	115.5	2.5931034	4.741E-11	2.8747789	5.142E-06	1.256E-06	1.386E-09	74	71	72.5	212	164	188
PPP1R9A	15	10	-12	-5.8	0.0007057	-5.0746793	-4.435E-07	1	0.0052414	14	15	14.5	0	5	2.5
PPP2R2C	312	162	223.5	8.5762712	1.356E-15	5.0788861	4.559E-06	3.592E-11	6.868E-14	32	27	29.5	132	139	135.5
PRCD	15	13	-14.5	-4.2222222	0.0010676	-3.7472569	-5.293E-07	1	0.0075182	19	19	19	4	5	4.5
PRG4	13	5	-9	#DIV/0!	0.0001421	-80.570798	-3.422E-07	1	0.0012565	5	13	9	0	0	0
PRKG2	87	61	-72	-3.2857143	1.337E-09	-2.9538822	-2.585E-06	3.541E-05	3.205E-08	116	91	103.5	29	34	31.5
PRLR	61	24	38.5	2	6.96E-05	2.0882955	1.584E-06	1	0.0006671	48	29	38.5	69	76	72.5
PRPF31	10	5	6.5	14	0.0031374	12.878432	2.749E-07	1	0.0191593	1	0	0.5	10	4	7
PRPF8	120	32	56	10.333333	0.0001584	11.148733	2.344E-06	1	0.0013865	6	6	6	2	122	62
PRRT2	47	38	-42	-4.36	2.897E-08	-3.9136267	-1.537E-06	0.0007673	5.601E-07	51	58	54.5	12	13	12.5
PRRX2	1307	418	921.5	3.1862396	4.069E-28	2.0966206	1.746E-05	1.078E-23	3.768E-26	432	411	421.5	757	838	797.5
PRUNE2	396	207	252.5	4.5815603	9.086E-06	-2.1999502	-3.541E-06	0.2406476	0.0001066	162	181	171.5	51	90	70.5
PSD	32	17	-22	-3.4444444	0.0005117	-3.0748008	-7.903E-07	1	0.0039407	39	23	31	7	11	9
PSG6	43	18	27	3.4545455	1.219E-06	3.7062236	1.135E-06	0.0322984	1.709E-05	13	9	11	42	32	37
PSMB3	1040	840	513	22.375	5.436E-06	-15.972873	-1.513E-05	0.1439756	6.697E-05	860	16	438	28	20	24
PTCH1	394	199	289	5.2814815	1.259E-08	-2.076191	-3.047E-06	0.0003335	2.599E-07	157	154	155.5	73	62	67.5
PTGDR2	37	24	-33.5	#DIV/0!	6.676E-15	-295.7051	-1.267E-06	1.768E-10	3.186E-13	30	37	33.5	0	0	0
PTGDS	58	26	-40.5	-4	2.616E-06	-3.5770535	-1.467E-06	0.0692949	3.419E-05	67	41	54	12	15	13.5
PTGS1	2841	406	1961.5	3.1390403	0	-2.0753659	-4.128E-05	0	0	2110	2106	2108	863	971	917
PTPRE	1081	422	727	3.7642586	5.236E-25	-2.4636182	-1.613E-05	1.387E-20	4.431E-23	703	733	718	273	253	263
PTPRR	29	20	26	6.7777778	8.627E-09	7.3584383	1.108E-06	0.0002285	1.822E-07	5	4	4.5	33	28	30.5
PTX3	12808	4367	8509.5	3.8603361	0	-3.4643483	-0.0003069	0	0	11687	11156	11421.5	2841	3109	2975
QPRT	1056	906	-943.5	-3.592033	0	-3.2390418	-3.414E-05	0	0	1340	1275	1307.5	369	359	364
RAB26	38	18	-27	-10	0.0043569	-2.6790701	-7.097E-07	1	0.0252887	39	21	30	8	12	10
RAB27B	950	722	-906.5	-2.8239437	0	-2.5474594	-3.223E-05	0	0	1392	1415	1403.5	529	465	497
RAB37	9	5	-7	-15	0.0041766	-11.420142	-2.629E-07	1	0.0244244	6	9	7.5	0	1	0.5
RAB9B	28	15	-20.5	-3.05	0.002085	-2.4926538	-6.94E-07	1	0.0133609	25	36	30.5	12	10	11
RADIL	24	18	-15	-2.5789474	0.0073995	-2.3086084	-5.258E-07	1	0.0398809	30	19	24.5	7	12	9.5
RAMP1	29	19	-21.5	-2.72	0.0033625	-2.4397577	-7.596E-07	1	0.0203029	37	31	34	12	13	12.5
RANBP3L	50	37	-48	-20.2	7.639E-17	-17.555214	-1.803E-06	2.023E-12	4.408E-15	50	51	50.5	1	4	2.5
RAPGEF5	286	261	232.5	16.5	0.007992	-2.0351425	-6.547E-07	1	0.0425433	38	30	34	16	14	15
RARRES1	4013	2953	-3766.5	-2.8545052	0	-2.5739841	-0.0001338	0	0	6021	5574	5797.5	2008	2054	2031

RASGRP3	37	21	25.5	2.4166667	0.0002783	2.6746934	1.145E-06	1	0.0023036	20	16	18	53	34	43.5
RASIP1	28	15	-19.5	-2.6956522	0.0041522	-2.4182525	-6.891E-07	1	0.024293	32	30	31	12	11	11.5
RASL11A	564	91	402.5	2.6035857	8.721E-18	2.2184055	1.155E-05	2.31E-13	5.346E-16	263	239	251	525	479	502
RASL12	72	51	-61.5	#DIV/0!	3.413E-21	-543.0729	-2.331E-06	9.039E-17	2.47E-19	51	72	61.5	0	0	0
RBM12B-AS	31	20	16	2.28	0.0036617	2.3827079	6.59E-07	1	0.0218179	12	13	12.5	31	23	27
RCSD1	5564	4931	4454.5	891.9	0.0034627	-2.8534604	-3.957E-07	1	0.0208337	13	19	16	0	10	5
REC8	365	275	-331	-2.4391304	9.288E-16	-2.2026666	-1.159E-05	2.46E-11	4.795E-14	532	590	561	235	225	230
REN	33	21	21	1.8571429	0.0010473	2.0517157	9.792E-07	1	0.007395	20	29	24.5	50	41	45.5
RENBP	48	29	40	7.1538462	0.002246	-3.4648106	-6.823E-07	1	0.0142785	39	12	25.5	9	4	6.5
REPS2	21	10	11	5.4	0.0060303	-4.0256736	-3.293E-07	1	0.0335109	13	10	11.5	0	5	2.5
RFTN2	19	17	-18	-3.1176471	0.0012138	-2.7903888	-6.449E-07	1	0.0083652	27	26	26.5	9	8	8.5
RGCC	1063	804	-933.5	-3.3484277	0	-3.0143162	-3.356E-05	0	0	1424	1238	1331	434	361	397.5
RGS17	232	182	-210.5	-3.5987654	7.343E-23	-3.241525	-7.61E-06	1.945E-18	5.703E-21	310	273	291.5	78	84	81
RGS18	49	40	-44.5	-5.2380952	7.616E-09	-4.6953587	-1.64E-06	0.0002017	1.622E-07	53	57	55	8	13	10.5
RHBDL3	12	4	7	#DIV/0!	0.0005565	69.42095	2.942E-07	1	0.0042426	0	0	0	12	2	7
RHPN1	127	107	94	32.333333	0.0008296	-4.8400587	-4.988E-07	1	0.0060232	14	19	16.5	3	3	3
RILP	17	0	-8.5	#DIV/0!	0.0011297	-77.050478	-3.27E-07	1	0.007894	0	17	8.5	0	0	0
RLTPR	357	257	268.5	16.342857	1.453E-17	6.6504795	3.754E-06	3.848E-13	8.825E-16	21	14	17.5	95	116	105.5
RND2	48	19	-36.5	-3.7037037	1.896E-05	-3.3321707	-1.329E-06	0.5020396	0.0002083	41	59	50	16	11	13.5
RNF157	227	99	-149.5	-2.4375	1.027E-08	-2.1996104	-5.222E-06	0.0002721	2.146E-07	263	244	253.5	82	126	104
RNF212B	18	9	11.5	4.8333333	0.0091238	-3.6635925	-3.46E-07	1	0.0476331	14	11	12.5	3	3	3
RNF213	4857	1214	3061	2.7436628	0	-2.0407995	-7.646E-05	0	0	4364	3589	3976.5	1626	1885	1755.5
RNFT2	47	31	32	9	0.0025788	-3.5546145	-4.385E-07	1	0.016181	12	20	16	2	6	4
RNH1	140	84	92	14.142857	0.0032089	-6.1957777	-1.553E-06	1	0.0195517	96	4	50	12	2	7
ROBO2	27	14	18.5	3.1764706	0.0045261	-2.7422557	-6.261E-07	1	0.0261392	28	24	26	2	15	8.5
ROR2	42	30	-35.5	-2.6904762	0.0001099	-2.4243284	-1.258E-06	1	0.0010058	51	62	56.5	20	22	21
RPS6KA2	1013	615	-824.5	-2.7285115	0	-2.4626804	-2.921E-05	0	0	1305	1298	1301.5	455	499	477
RSPO1	7	4	-5.5	#DIV/0!	0.0014904	-49.201788	-2.073E-07	1	0.0100062	7	4	5.5	0	0	0
RUNX1T1	34	9	-21.5	-5.3	0.0004871	-4.6678507	-7.841E-07	1	0.0037688	38	15	26.5	6	4	5
S100A3	64	46	-47.5	-2.5833333	0.0011221	-2.3269737	-1.671E-06	1	0.0078516	81	74	77.5	25	35	30
S1PR1	1128	229	745.5	2.2221311	4.834E-37	2.2391995	2.854E-05	1.28E-32	5.29E-35	643	577	610	1235	1228	1231.5
SAA2	139	30	105	6.1219512	9.245E-10	-3.7218269	-2.346E-06	2.449E-05	2.265E-08	97	73	85	16	25	20.5
SALL2	337	81	218.5	2.9508929	1.664E-09	-2.1101312	-5.215E-06	4.408E-05	3.95E-08	277	248	262.5	129	95	112
SAMD11	849	337	702.5	24.032787	4.651E-67	9.3358969	9.649E-06	1.232E-62	6.285E-65	25	36	30.5	255	261	258
SAP30L-AS1	121	56	64	1.8205128	4.524E-05	2.010278	2.992E-06	1	0.0004531	61	95	78	151	133	142
SCARNA27	18	10	-14	-3.1538462	0.0035285	2.6518435	5.376E-07	1	0.021143	8	9	8.5	23	18	20.5
SCARNA6	6	6	-5	#DIV/0!	0.0039512	-44.827898	-1.885E-07	1	0.0232863	6	4	5	0	0	0
SCD	37355	34261	-36535.5	-16.860864	0	-15.214145	-0.0013706	0	0	39576	38102	38839	2221	2386	2303.5
SCG2	505	408	-488.5	-7.737931	2.394E-80	-6.9814848	-1.817E-05	6.341E-76	3.32E-78	560	562	561	57	88	72.5
SCUBE3	1582	954	1499	9.5902579	5.838E-37	10.619065	6.346E-05	1.546E-32	6.337E-35	171	178	174.5	1635	1712	1673.5
SEC24B-AS1	31	9	-20.5	-6.8571429	0.0057623	-2.8471757	-5.879E-07	1	0.0322256	33	15	24	7	8	7.5
SEMA3B	67	56	-59.5	-4.1315789	1.237E-08	-3.7133803	-2.169E-06	0.0003275	2.557E-07	82	75	78.5	15	23	19
SEMA3D	48	22	27	2.7419355	0.0055684	-2.0905237	-7.129E-07	1	0.0313518	31	41	36	19	12	15.5
SEPT4	33	11	28	5.6666667	0.0001792	-3.6467814	-6.756E-07	1	0.0015506	22	27	24.5	2	10	6
SERPINA3	64	35	-46.5	-4.1	2.594E-06	-3.6626179	-1.684E-06	0.0687135	3.392E-05	78	45	61.5	16	14	15
SERPINA9	55	19	35.5	36.5	0.0015757	9.5480248	3.585E-07	1	0.0104856	2	0	1	3	16	9.5
SERPINB7	350	245	300.5	2.6465753	3.257E-27	2.9373363	1.334E-05	8.626E-23	2.954E-25	210	155	182.5	466	500	483
SERPINB9P1	67	27	-52.5	-6.5263158	2.698E-11	-5.8302323	-1.94E-06	7.145E-07	8.184E-10	71	53	62	4	15	9.5
SERPINF1	717	413	-572	-3.0875912	9.071E-34	-2.7812449	-2.044E-05	2.403E-29	9.496E-32	923	769	846	261	287	274
SETBP1	22	6	-16	-2.7777778	0.0041665	-2.4941651	-5.691E-07	1	0.0243708	22	28	25	6	12	9
SGPP2	19	16	13	4.7142857	0.0007219	5.0796455	5.573E-07	1	0.0053434	3	4	3.5	11	22	16.5
SH3GL1P2	8	2	-5	#DIV/0!	0.0034958	-45.184576	-1.9E-07	1	0.0209853	2	8	5	0	0	0
SH3PXD2B	1784	945	-1230	-2.2576687	0	-2.0335301	-4.233E-05	0	0	2398	2018	2208	977	979	978
SH3RF2	69	52	43.5	2.2794118	0.0005646	2.3774169	1.77E-06	1	0.0042969	41	27	34	54	92	73
SHC4	123	70	-102.5	-3.1354167	2.183E-12	-2.8209123	-3.669E-06	5.781E-08	7.537E-11	162	139	150.5	54	42	48
SHF	47	30	35	15	0.0053286	-4.0326272	-3.304E-07	1	0.0301813	10	13	11.5	2	3	2.5
SHISA3	117	50	84	4.36	1.67E-13	-3.7619748	-2.903E-06	4.424E-09	6.525E-12	102	107	104.5	24	26	25
SIPA1L2	68	39	40	3.5	0.0035727	-2.267274	-8.546E-07	1	0.0213583	50	31	40.5	17	15	16
SIX3	50	28	-38	-4.8	0.0006104	-2.6223267	-1.127E-06	1	0.0046125	42	54	48	14	19	16.5
SKIL	1630	470	1093.5	2.7384738	1.748E-34	2.0271166	2.439E-05	4.631E-30	1.838E-32	662	596	629	1174	1125	1149.5
SLA	201	99	154	6.5	9.436E-05	-2.0758751	-1.266E-06	1	0.0008769	60	69	64.5	28	28	28
SLAIN1	327	274	250.5	56.666667	0.0003397	-4.0415917	-5.859E-07	1	0.0027479	21	20	20.5	3	6	4.5
SLC14A1	89	85	-88	-3.0952381	4.873E-11	-2.7883552	-3.153E-06	1.291E-06	1.42E-09	130	130	130	43	41	42
SLC15A3	336	71	214.5	3.2941176	2.5E-10	-2.1658638	-4.566E-06	6.621E-06	6.694E-09	230	219	224.5	80	107	93.5
SLC16A6	799	366	-671	-6.0451128	3.02E-119	-5.4581013	-2.484E-05	8E-115	4.39E-117	771	837	804	125	141	133
SLC18B1	298	142	196.5	3.1593407	2.57E-06	-2.1279463	-4.309E-06	0.0680749	3.363E-05	239	192	215.5	111	71	91
SLC1A2	39	31	-31	-2.7714286	0.000501	-2.4870046	-1.097E-06	1	0.0038649	52	45	48.5	22	13	17.5
SLC22A1	6	4	-5	-11	0.0075303	-8.4007576	-1.867E-07	1	0.0404837	6	5	5.5	0	1	0.5
SLC22A15	32	11	-22	-3.3157895	0.0001441	-2.9692857	-7.914E-07	1	0.0012724	34	29	31.5	7	12	9.5
SLC22A18	26	18	-21.5	-4.9090909	1.718E-05	-4.3703128	-7.909E-07	0.454912	0.0001904	24	30	27	7	4	5.5
SLC22A23	343	264	-302.5	-3.176259	1.261E-15	-2.859388	-1.084E-05	3.339E-11	6.422E-14	470	413	441.5	151	127	139
SLC22A3	10	7	9.5	5.75	0.0008122	6.0861418	4.061E-07	1	0.0059213	2	2	2	12	11	11.5
SLC22A4	281	150	-193.5	-2.3298969	1.242E-11	-2.1015399	-6.711E-06	3.289E-07	3.915E-10	354	324	339	126	165	145.5
SLC25A45	46	34	-33	-3.8695652	5.24E-06	-3.4601067	-1.196E-06	0.1387759	6.479E-05	51	38	44.5	15	8	11.5
SLC26A4-AS	15	10	-12.5	-13.5	4.277E-05	-11.156666	-4.687E-07	1	0.0004325	12	15	13.5	0	2	1
SLC29A2	125	62	-88.5	-3.95	1.608E-11	-3.5495519	-3.215E-06	4.258E-07	4.991E-10	128	109	118.5	33	27	30
SLC2A12	93	42	-45	-3.195122	0.0007271	-2.872162	-1.62E-06	1	0.0053743	58	73	65.5	31	10	20.5
SLC40A1	221	159	-202	-4.9607843	8.385E-28	-4.4654826	-7.413E-06	2.221E-23	7.658E-26	269	237	253	48	54	51
SLC51B	33	21	-27	#DIV/0!	9.668E-11	-239.05478	-1.024E-06	2.56E-06	2.715E-09	21	33	27	0	0	0
SLC5A10	195	35	133	2.6625	8.862E-14	2.5347038	4.643E-06	2.347E-09	3.589E-12	83	77	80	189	177	183
SLC6A15	993	691	-957	-6.104	1.427E-66	-5.5071302	-3.539E-05	3.78E-62	1.919E-64	1162	1127	1144.5	169	206	187.5
SLC6A9	86	50	-72.5	-3.1014493	4.896E-09	-2.7981484	-2.604E-06	0.0001297	1.072E-07	97	117	107	31	38	34.5
SLC7A5	10100	2959	6056	2.2490461	2.57E-54	2.1857617	0.0002175	6.807E-50	3.321E-52	4642	5055	4848.5	9549	9600	9574.5
SLC7A7	68	30	47	2.3823529	1.636E-05	-2.120154	-1.599E-06	0.4332749	0.0001823	81	79	80	29	39	34
SLC9A9	605	548	471	14.457143	0.0002089	-2.1191649	-1.645E-06	1	0.0017786	92	73	82.5	37	33	35
SLC9B1	14	8	-9	-7	0.0027195	-5.9510485	-3.325E-07	1	0.0169471	14	7	10.5	3	0	1.5
SLITRK5	1086	759	-1023	-4.3268293	1.68E-113	-3.9041469	-3.738E-05	4.45E-109	2.43E-111	1364	1297	1330.5	278	337	307.5

SLITRK6	12	5	-9	#DIV/0!	2.054E-05	-79.8455	-3.391E-07	0.5441168	0.000224	12	6	9	0	0	0
SMAD6	653	137	493.5	5.2727273	1.117E-48	4.0288398	1.321E-05	2.96E-44	1.389E-46	129	102	115.5	430	409	419.5
SMAD7	945	167	688.5	5.6053512	3.547E-96	3.7537437	1.556E-05	9.395E-92	5.051E-94	152	147	149.5	505	508	506.5
SMAD9	808	288	541	8.8978102	3.3E-27	4.6514357	9.445E-06	8.741E-23	2.983E-25	81	56	68.5	255	320	287.5
SMIM10L2B	34	8	19	3.7142857	0.009658	-2.4284784	-4.249E-07	1	0.0499495	18	20	19	8	6	7
SNAP25	229	165	-206	-4.4621849	1.253E-16	-4.0141411	-7.524E-06	3.32E-12	7.124E-15	285	246	265.5	63	56	59.5
SNED1	145	120	-132	-3.3362832	1.056E-14	-3.0090013	-4.762E-06	2.797E-10	4.873E-13	179	198	188.5	59	54	56.5
SNORA27	27	10	18.5	1.8604651	0.0054923	2.0559267	8.631E-07	1	0.0309759	19	24	21.5	46	34	40
SNORD27	79	60	-69.5	-2.1393443	3.324E-08	2.1889599	2.969E-06	0.0008803	6.338E-07	66	66	66	124	137	130.5
SNORD30	38	33	34.5	1.8313253	7.491E-05	2.0280241	1.615E-06	1	0.0007114	44	39	41.5	75	77	76
SNORD74	25	19	16	2.0322581	0.0028562	2.2435055	7.339E-07	1	0.0176742	14	17	15.5	36	27	31.5
SOBP	168	68	113.5	6.9736842	3.454E-10	-4.2894393	-2.63E-06	9.147E-06	9.003E-09	110	72	91	17	21	19
SOCS1	141	75	-128.5	-4.1728395	7.986E-17	-3.7543027	-4.685E-06	2.115E-12	4.588E-15	174	164	169	48	33	40.5
SOCS2	4215	3494	3180	8.8908189	7.04E-14	2.2847229	1.952E-05	1.864E-09	2.895E-12	449	357	403	834	824	829
SOD2	7184	2429	4898.5	3.6870543	4.441E-16	-3.2538352	-0.000172	1.176E-11	2.367E-14	6899	6260	6579.5	1789	1857	1823
SOD3	66	43	-55.5	-2.5205479	1.865E-06	-2.2711812	-1.947E-06	0.0493867	2.513E-05	95	89	92	29	44	36.5
SORL1	1518	1191	1175	196.83333	0.0055954	-2.7487541	-4.472E-07	1	0.0314705	19	18	18.5	10	2	6
SOX2	26	14	-21	-8	0.0005329	-3.2894776	-6.328E-07	1	0.0040883	28	20	24	6	7	6.5
SPATA18	227	198	-204.5	-2.2431611	8.683E-11	-2.0258927	-7.071E-06	2.3E-06	2.454E-09	347	391	369	165	164	164.5
SPATC1L	36	2	18.5	#DIV/0!	1.064E-05	179.62464	7.681E-07	0.2818789	0.0001226	0	0	0	1	36	18.5
SPIRE2	92	42	-60.5	-2.9516129	5.534E-05	-2.222451	-1.898E-06	1	0.0005413	108	75	91.5	33	41	37
SPOCK2	146	102	-124.5	-4.2763158	7.342E-13	-3.8531639	-4.557E-06	1.944E-08	2.649E-11	150	175	162.5	47	29	38
SPRY1	465	220	312.5	5.6296296	7.385E-16	-3.416125	-6.841E-06	1.956E-11	3.85E-14	263	249	256	71	64	67.5
SPTLC3	163	112	115	4.8983051	0.0003547	-2.274126	-1.578E-06	1	0.0028549	79	70	74.5	24	35	29.5
SPX	20	13	-16	-5	0.0001634	-4.4166092	-5.869E-07	1	0.0014258	23	17	20	4	4	4
SQLE	1534	1251	-1421	-2.4918635	0	-2.2465185	-4.972E-05	0	0	2482	2265	2373.5	948	957	952.5
SREBF1	2994	1880	-2788.5	-3.3452481	0	-3.0167019	-0.0001004	0	0	4144	3811	3977.5	1150	1228	1189
SREBF2	4504	2968	-4276	-4.0840245	0	-3.6818367	-0.0001557	0	0	5849	5476	5662.5	1428	1345	1386.5
ST8SIA4	281	170	207	30.571429	0.0023522	-3.0655689	-6.145E-07	1	0.0148824	22	26	24	8	6	7
ST8SIA6	16	12	-11	-12	0.0008814	-9.9250903	-4.121E-07	1	0.0063383	11	13	12	1	1	1
STAB1	33	29	-32.5	-4.0952381	0.0001202	-2.5757201	-9.964E-07	1	0.001085	43	43	43	15	15	15
STAG3L5P	13	10	9	4	0.0035646	4.3080511	3.895E-07	1	0.0213258	2	4	3	15	9	12
STAR	199	153	-171	-5.275	1.38E-16	-4.7361536	-6.284E-06	3.654E-12	7.825E-15	225	197	211	54	26	40
STAT5A	368	101	234	3.2718447	1.184E-11	-2.2425617	-5.365E-06	3.136E-07	3.746E-10	275	238	256.5	109	97	103
STBD1	36	10	23.5	2.46875	0.0083014	2.0008059	6.093E-07	1	0.0439112	15	17	16	27	31	29
STC1	6773	5293	-6159.5	-2.2731501	0	-2.0526695	-0.0002131	0	0	11158	10837	10997.5	4385	5291	4838
STK19	43	21	-21.5	-22.5	0.0004259	-18.093842	-7.909E-07	1	0.0033563	43	2	22.5	2	0	1
STRA6	64	53	-52.5	-2.5441176	0.0001147	-2.2894671	-1.841E-06	1	0.0010425	93	80	86.5	32	36	34
STXBP6	301	151	214.5	3.4375	1.971E-21	3.8158707	9.353E-06	5.22E-17	1.454E-19	102	74	88	315	290	302.5
SULT1C4	17	9	-13	-7.5	0.0002701	-6.4888492	-4.838E-07	1	0.0022411	13	17	15	4	0	2
SUN3	17	8	12	7	0.0001106	7.4116846	5.114E-07	1	0.0010117	3	1	2	18	10	14
SV2A	704	98	514	3.7413333	4.295E-28	-2.7107294	-1.344E-05	1.137E-23	3.963E-26	544	582	563	184	191	187.5
SVEP1	815	348	-507.5	-2.5194611	6.538E-15	-2.276404	-1.784E-05	1.731E-10	3.125E-13	826	857	841.5	296	372	334
SYNE2	825	292	514.5	3.296875	3.522E-08	-2.043706	-9.777E-06	0.0009327	6.686E-07	596	421	508.5	176	272	224
SYNPO2L	112	48	99.5	8.6538462	4.504E-30	9.518895	4.222E-06	1.193E-25	4.418E-28	11	15	13	123	102	112.5
SYT15	166	59	107	8.6428571	2.134E-10	4.5966276	1.92E-06	5.653E-06	5.768E-09	11	17	14	57	60	58.5
SYTL2	671	537	-636	-3.3909774	5.252E-29	-3.058879	-2.293E-05	1.391E-24	4.968E-27	924	880	902	253	279	266
SYTL3	486	180	330.5	2.0836066	3.716E-20	2.2610587	1.453E-05	9.841E-16	2.57E-18	313	297	305	577	668	622.5
TAGLN	37944	16527	25298	2.1374489	1.598E-46	2.372248	0.0011516	4.232E-42	1.969E-44	23563	20919	22241	48209	46869	47539
TAGLN3	27	13	19	3.375	7.601E-05	3.7037143	8.291E-07	1	0.0007208	7	9	8	32	22	27
TARID	20	13	-16.5	-4.3	0.0038268	-2.7430898	-5.185E-07	1	0.0226337	23	20	21.5	8	6	7
TAS1R1	8	2	-5	#DIV/0!	0.0083705	-45.315333	-1.906E-07	1	0.0441971	2	8	5	0	0	0
TBC1D17	482	410	-472	-2.6445993	1.037E-28	-2.3859756	-1.666E-05	2.748E-24	9.743E-27	764	754	759	282	292	287
TBC1D3P1-D	67	6	-32.5	-17.25	0.0026714	6.9217865	1.251E-06	1	0.0166791	7	4	5.5	67	2	34.5
TCAF2P1	10	9	7	#DIV/0!	0.0037431	-53.174385	-2.244E-07	1	0.0222227	10	2	6	0	0	0
TCN2	256	101	172	4.0714286	5.575E-14	-3.1273615	-4.998E-06	1.476E-09	2.332E-12	176	212	194	57	55	56
TCP11L2	82	47	-70	-2.9178082	1.514E-08	-2.632247	-2.501E-06	0.0004011	3.085E-07	97	116	106.5	34	39	36.5
TCTEX1D4	29	18	-22.5	-3.0454545	0.0069939	-2.0787487	-6.597E-07	1	0.0379653	30	37	33.5	16	13	14.5
TEX21P	15	10	12.5	5.1666667	0.00013	5.5574426	5.355E-07	1	0.0011613	4	2	3	14	17	15.5
TGFB3	51	32	-35	-2.7073171	0.0002453	-2.4449339	-1.245E-06	1	0.0020601	47	64	55.5	13	28	20.5
TGM1	34	9	22.5	1.9574468	0.0038716	2.1591212	1.035E-06	1	0.0228578	22	25	23.5	36	56	46
TGM4	8	8	-5	#DIV/0!	0.0091645	-44.529946	-1.872E-07	1	0.0478173	8	2	5	0	0	0
THBS2	12650	4898	-8534.5	-2.7494107	0	-2.4839169	-0.0003029	0	0	13356	13470	13413	4438	5319	4878.5
THEMIS2	120	62	-107.5	-2.25	9.386E-07	-2.0312161	-3.716E-06	0.0248581	1.347E-05	187	200	193.5	80	92	86
TIMM8A	402	206	274.5	1.8145401	4.902E-16	2.0097291	1.287E-05	1.298E-11	2.591E-14	322	352	337	634	589	611.5
TLE2	39	9	26	14	0.0003066	-5.6201949	-4.07E-07	1	0.002507	14	12	13	4	0	2
TM4SF18	53	33	38	3.1714286	1.826E-07	3.4911479	1.661E-06	0.0048365	3.038E-06	12	23	17.5	55	56	55.5
TM7SF2	80	53	-62	-3.3396226	3.541E-08	-3.0042012	-2.233E-06	0.0009379	6.719E-07	89	88	88.5	30	23	26.5
TMCC3	1374	1002	1041.5	9.9399142	1.47E-06	-2.162777	-5.681E-06	0.0389297	2.028E-05	279	280	279.5	127	106	116.5
TMEFF2	1229	448	-901.5	-2.2374743	0	-2.0186707	-3.109E-05	0	0	1624	1636	1630	757	700	728.5
TMEM100	714	271	540.5	4.6153846	7.205E-14	-2.2393743	-7.764E-06	1.908E-09	2.954E-12	390	353	371.5	151	148	149.5
TMEM119	94	52	-74	-75	2.088E-17	-61.772016	-2.807E-06	5.53E-13	1.254E-15	56	94	75	2	0	1
TMEM132B	209	139	-178	-3.2967742	2.593E-15	-2.9791817	-6.428E-06	6.867E-11	1.277E-13	231	280	255.5	71	84	77.5
TMEM135	651	526	-572.5	-2.967354	1.107E-23	-2.6719964	-2.039E-05	2.931E-19	8.937E-22	922	805	863.5	311	271	291
TMEM154	542	407	-476.5	-4.8273092	8.697E-35	-4.3434897	-1.744E-05	2.303E-30	9.25E-33	666	536	601	124	125	124.5
TMEM155	847	348	624.5	6.5511111	3.48E-23	3.0780913	8.844E-06	9.216E-19	2.743E-21	109	116	112.5	347	278	312.5
TMEM158	3838	3126	-3482	-4.5458248	0	-4.0978744	-0.0001273	0	0	4758	4170	4464	920	1044	982
TMEM229B	29	15	23.5	24.5	4.194E-05	-11.123643	-4.672E-07	1	0.0004252	16	11	13.5	0	2	1
TMEM26	14	9	-12.5	#DIV/0!	4.441E-07	-110.91844	-4.727E-07	0.011762	6.83E-06	11	14	12.5	0	0	0
TMEM35	313	207	-264	-4.1616766	5.385E-15	-3.7397594	-9.6E-06	1.426E-10	2.593E-13	384	311	347.5	96	71	83.5
TMEM50B	96	9	49	8	0.0005307	8.7349165	2.064E-06	1	0.004075	10	4	7	12	100	56
TMEM71	53	36	-38	-2.3103448	0.0012845	-2.0781324	-1.313E-06	1	0.0087728	75	59	67	25	33	29
TMEM92-AS	16	11	-12.5	-7.25	0.0001851	-6.264041	-4.634E-07	1	0.001596	16	13	14.5	2	2	2
TMOD1	15	9	12	5.8	0.0092471	-4.0170671	-3.287E-07	1	0.048163	15	8	11.5	2	3	2.5
TNC	5277	838	3489	3.6869465	0	-2.1777527	-6.393E-05	0	0	3260	3002	3131	1057	1540	1298.5
TNFAIP6	93	56	-79.5	-3.4461538	7.314E-10	-3.1060602	-2.871E-06	1.937E-05	1.824E-08	114	110	112	21	44	32.5
TNFRSF18	8	5	-7	#DIV/0!	0.0002539	-62.560987	-2.647E-07	1	0.0021194	6	8	7	0	0	0

TNFRSF19	2085	1288	-2059.5	-5.1648129	0	-4.6591933	-7.579E-05	0	0	2570	2538	2554	504	485	494.5
TNFSF11	194	87	-177.5	-5.0340909	2.23E-24	-4.5287036	-6.519E-06	5.905E-20	1.84E-22	231	212	221.5	51	37	44
TNFSF15	74	59	-62.5	-7.5789474	3.056E-07	-6.7928985	-2.327E-06	0.0080951	4.868E-06	67	77	72	8	11	9.5
TNFSF9	31	9	19.5	20.5	0.0006039	-8.6964217	-3.552E-07	1	0.0045684	9	12	10.5	0	2	1
TOX	55	9	33.5	3.3103448	0.0016664	2.3198858	7.289E-07	1	0.0110143	13	16	14.5	30	31	30.5
TP53I11	879	518	689.5	4.162844	4.279E-16	-2.3580519	-1.239E-05	1.133E-11	2.303E-14	598	542	570	197	239	218
TP53INP1	1217	340	730	3.6691042	8.013E-10	-2.0311886	-1.183E-05	2.122E-05	1.987E-08	625	608	616.5	309	238	273.5
TPD52L1	62	52	-41.5	-2.0641026	6.206E-05	2.2350012	1.867E-06	1	0.0005997	48	32	40	94	67	80.5
TPM1	16551	6633	9725	1.8804889	3.314E-74	2.0676491	0.0004454	8.778E-70	4.572E-72	11301	10789	11045	20833	20360	20596.5
TPPP	27	12	22.5	3.1428571	6.931E-06	3.4618718	9.859E-07	0.1835763	8.363E-05	13	8	10.5	35	31	33
TRANK1	782	234	535.5	5.2	3.428E-27	-3.2258829	-1.189E-05	9.078E-23	3.088E-25	507	407	457	127	128	127.5
TREM1	12	4	8	9	0.0038193	-7.052931	-2.796E-07	1	0.0225944	7	10	8.5	2	0	1
TRIM47	152	81	-113	-2.8833333	4.184E-07	-2.5876489	-4.001E-06	0.0110825	6.462E-06	199	147	173	73	47	60
TRIML2	38	35	30.5	7.7777778	1.082E-06	8.430799	1.294E-06	0.0286561	1.535E-05	5	4	4.5	30	40	35
TRO	275	228	-258	-2.4175824	2.622E-15	-2.182256	-9.015E-06	6.944E-11	1.288E-13	425	455	440	184	180	182
TRPA1	9468	2453	6694.5	3.8487234	0	-2.346808	-0.0001326	0	0	6169	6060	6114.5	2444	2256	2350
TRPM8	15	13	-13	-7.5	0.000194	-6.4854374	-4.829E-07	1	0.0016646	15	15	15	2	2	2
TSLP	40	18	-29	-4.0526316	4.274E-05	-3.6419658	-1.06E-06	1	0.0004324	34	43	38.5	3	16	9.5
TSNARE1	97	43	-70	-3.295082	0.0001422	-2.1486319	-2.025E-06	1	0.001257	120	81	100.5	43	41	42
TSPAN13	850	326	473.5	1.9432271	1.154E-14	2.0342192	1.956E-05	3.057E-10	5.271E-13	579	425	502	1002	834	918
TSTD1	169	104	119	5.4074074	0.0002988	-2.2339985	-1.401E-06	1	0.0024496	66	68	67	30	24	27
TVP23A	15	7	10	2.5384615	0.005944	2.7765525	4.448E-07	1	0.0330819	3	10	6.5	17	16	16.5
TYRP1	56	27	49.5	25.75	2.559E-07	11.631558	8.464E-07	0.0067769	4.122E-06	4	0	2	24	20	22
UBQLNL	8	6	6	#DIV/0!	0.002309	-44.981072	-1.891E-07	1	0.0146584	4	6	5	0	0	0
UBR7	54	9	-27	#DIV/0!	2.128E-06	-232.82904	-9.969E-07	0.0563585	2.828E-05	54	0	27	0	0	0
UCN2	68	62	-65	-7.8421053	1.021E-14	-7.0155616	-2.418E-06	2.703E-10	4.721E-13	73	76	74.5	8	11	9.5
VAT1L	79	48	-63.5	-3.1896552	4.733E-07	-2.8708921	-2.277E-06	0.0125358	7.221E-06	100	85	92.5	21	37	29
VCAM1	2157	414	1483	5.1482517	1.328E-52	-3.5106222	-3.76E-05	3.516E-48	1.699E-50	1484	1303	1393.5	372	343	357.5
VIPR1	26	8	-18.5	-5.1111111	0.0001141	-4.5164158	-6.784E-07	1	0.0010388	27	19	23	8	1	4.5
VNN2	35	22	27.5	#DIV/0!	3.481E-07	-123.3364	-5.261E-07	0.0092196	5.462E-06	20	8	14	0	0	0
VNN3	12	8	-10	#DIV/0!	0.0001165	-89.140395	-3.79E-07	1	0.0010574	8	12	10	0	0	0
VPS13C	2172	527	1372	3.1075269	0	-2.0005996	-2.724E-05	0	0	1456	1427	1441.5	538	764	651
VWA5A	4301	1246	3114	9.698324	2.21E-156	-6.1801449	-7.76E-05	5.86E-152	3.33E-154	2528	2375	2451.5	309	407	358
WBP2	1795	1338	-1574	-2.3204698	0	-2.0946865	-5.465E-05	0	0	2707	2825	2766	1222	1162	1192
WDR17	26	12	20	11	0.0027954	-4.758895	-3.311E-07	1	0.0173468	13	9	11	4	0	2
WDR86	30	16	-21.5	-7.1428571	0.0005364	-6.2747234	-7.945E-07	1	0.0041105	30	20	25	2	5	3.5
WISP1	5001	1050	3705.5	6.2190141	0	-4.0263552	-9E-05	0	0	3360	2986	3173	729	691	710
WNT7B	100	81	-90.5	-3.1547619	2.012E-09	-2.8419514	-3.249E-06	5.328E-05	4.711E-08	129	136	132.5	48	36	42
XAF1	299	196	-247.5	-2.8065693	9.953E-15	-2.5250272	-8.759E-06	2.636E-10	4.617E-13	423	346	384.5	150	124	137
XKR6	70	26	41.5	3.4411765	0.0007277	-2.5168329	-1.087E-06	1	0.0053777	40	55	47.5	20	14	17
YPEL1	77	56	66.5	5.2903226	0.0011454	-2.2312836	-8.042E-07	1	0.0079812	42	35	38.5	14	17	15.5
YWHAE	1795	1448	882	7.6315789	9.111E-08	-5.5205203	-2.519E-05	0.0024131	1.602E-06	1578	88	833	130	136	133
ZC2HC1C	25	12	-20	-2.9047619	0.0009818	-2.6012738	-7.108E-07	1	0.0069731	35	26	30.5	10	11	10.5
ZFHX4-AS1	208	114	169	3.1528662	5.336E-17	3.4942273	7.41E-06	1.413E-12	3.093E-15	77	80	78.5	285	210	247.5
ZFP14	87	43	-51.5	-2.3733333	1.738E-05	-2.1397646	-1.795E-06	0.4604393	0.0001927	84	94	89	39	36	37.5
ZFP42	20	8	13	#DIV/0!	0.0002535	64.269256	2.721E-07	1	0.0021169	0	0	0	6	7	6.5
ZFPM2-AS1	79	68	-79	-3.9259259	2.167E-07	-2.330026	-2.288E-06	0.0057401	3.541E-06	106	106	106	38	44	41
ZMIZ1-AS1	108	91	-102	-11.2	4.277E-25	-10.014306	-3.815E-06	1.133E-20	3.642E-23	109	115	112	13	7	10
ZNF185	857	250	557	2.8292282	8.287E-23	2.3120211	1.51E-05	2.195E-18	6.418E-21	310	299	304.5	659	611	635
ZNF197-AS1	8	6	5.5	#DIV/0!	0.0017533	54.434486	2.298E-07	1	0.0115024	0	0	0	3	8	5.5
ZNF423	74	51	53.5	10.727273	0.0011699	-3.6632467	-6.23E-07	1	0.0081112	18	27	22.5	0	11	5.5
ZNF442	66	27	46	4.68	2.572E-07	4.0185006	1.434E-06	0.006811	4.14E-06	18	7	12.5	44	47	45.5
ZNF454	31	17	-21	-2.4482759	0.0022211	-2.2005335	-7.343E-07	1	0.0141543	34	37	35.5	17	12	14.5
ZNF460	40	13	26.5	2.325	0.0005953	2.2963148	9.826E-07	1	0.0045127	26	14	20	35	48	41.5
ZNF474	43	14	32.5	4.4210526	0.0004972	2.9555595	7.096E-07	1	0.0038403	11	8	9.5	28	23	25.5
ZNF521	87	60	-72.5	-3.1969697	3.959E-06	-2.8871734	-2.615E-06	0.1048448	4.981E-05	92	119	105.5	32	34	33
ZNF530	180	74	102	1.8259109	3.895E-08	2.0197356	4.771E-06	0.0010315	7.336E-07	108	139	123.5	236	215	225.5
ZNF583	134	103	93.5	1.8348214	5.913E-07	2.0322954	4.378E-06	0.0156619	8.799E-06	103	121	112	237	174	205.5
ZNF670	345	238	262	3.1044177	6.661E-07	2.0126315	4.764E-06	0.0176407	9.795E-06	130	119	124.5	231	221	226
ZNF704	113	89	79	#DIV/0!	0.0028135	44.862261	1.886E-07	1	0.0174385	0	0	0	8	1	4.5
ZNF850	119	81	69.5	2.0859375	0.0022049	2.0396246	2.524E-06	1	0.0140645	57	71	64	78	159	118.5
ZP1	32	27	-27.5	-3.2	7.579E-05	-2.8744514	-9.888E-07	1	0.000719	38	42	40	11	14	12.5
ZPLD1	30	19	17.5	5.375	0.0007714	5.8532088	7.509E-07	1	0.0056641	6	2	4	25	18	21.5
ZSWIM5	119	51	-102.5	-3.6282051	8.323E-14	-3.2622973	-3.704E-06	2.204E-09	3.388E-12	156	127	141.5	41	37	39
ZXDA	68	55	-60	-2.6216216	3.59E-07	-2.3606824	-2.113E-06	0.0095074	5.616E-06	102	92	97	34	40	37

Supplemental Table 3

			No Drug			Me-6TREN	
Sample		**SDF-1a**	**CCL21**	**CCL19**	**SDF-1a**	**CCL21**	**CCL19**
Jurkat	Average	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 1	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 2	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
NALM-6	Average	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 1	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 2	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
Meningeal Cells	Average	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 1	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 2	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
Jurkat-Meningeal Co-Cx	Average	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 1	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 2	< LLOQ	7.38	< LLOQ	< LLOQ	< LLOQ	< LLOQ
NALM6-Meningeal Co-Cx	Average	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 1	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
	Replicate 2	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ	< LLOQ
Control Meningeal Media	Average	< LLOQ	< LLOQ	< LLOQ			
	Replicate 1	< LLOQ	< LLOQ	< LLOQ			
	Replicate 2	< LLOQ	< LLOQ	< LLOQ			
Control RPMI Media	Average	< LLOQ	< LLOQ	< LLOQ			
	Replicate 1	< LLOQ	< LLOQ	< LLOQ			
	Replicate 2	< LLOQ	< LLOQ	< LLOQ			
	LLOQ	**19.5 pg/mL**	**7.38 pg/mL**	**1.0 pg/mL**			