Supplementary Material

Expression of Hypoxia-Inducible Factor 1α (HIF-1α) and Genes of Related Pathways in Altered Gravity

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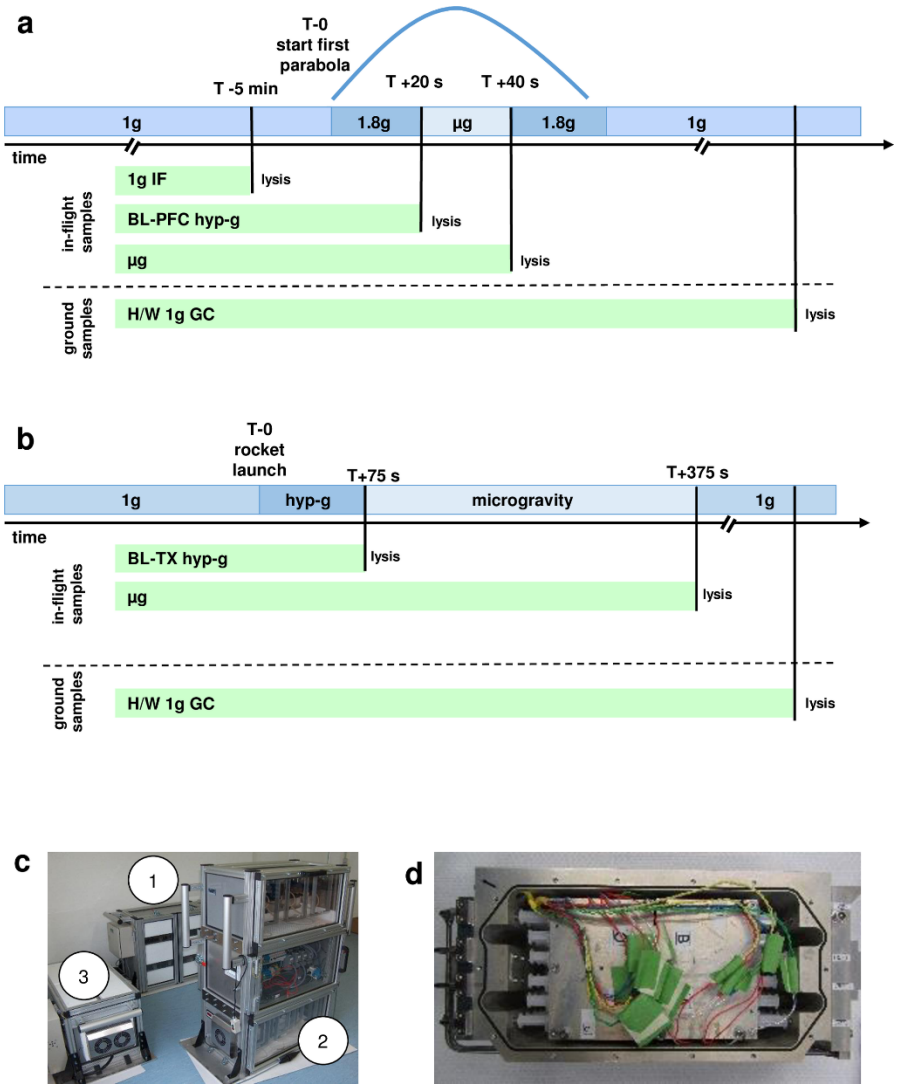
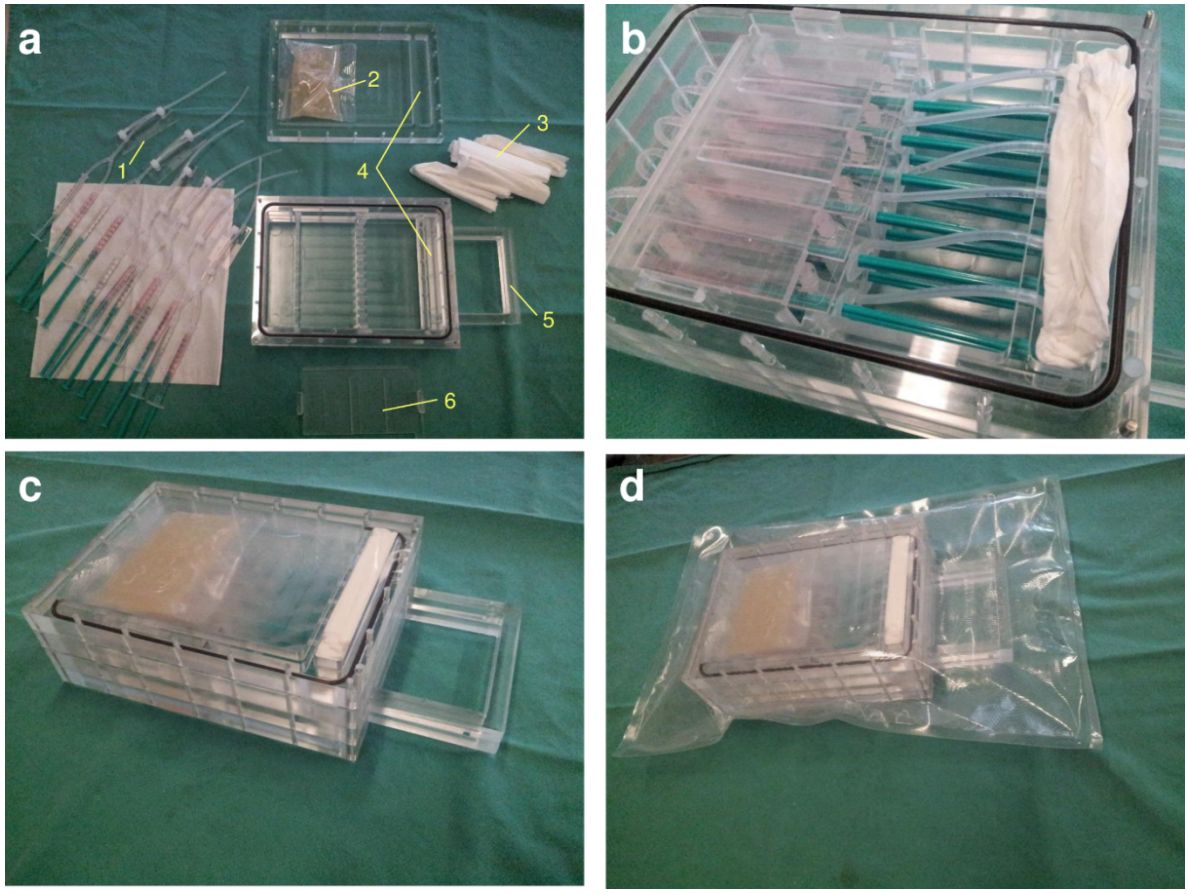


Supplementary Figure S1. Experiment design of the parabolic flight (19th and 23rd DLR PFC) and suborbital ballistic rocket (TEXUS-49 and TEXUS-51) experiments. **(a)** During the parabolic flight campaigns, U937 or Jurkat T cells were analyzed before and during the first parabola. 1g in-flight control (1g IF) samples were lysed 5 min before the first parabola, 1.8g hypergravity samples at the end of the first 1.8g phase, and microgravity samples at the end of the first microgravity phase. After the flight, 1g ground controls were performed in the experiment hardware inside the aircraft. **(b)** During the suborbital ballistic rocket missions, U937 and Jurkat T cells were lysed at time point T+75 s to monitor the hypergravity and vibration effects of the rocket launch. Microgravity samples and 1g in-flight reference centrifuge control samples (for the TEXUS-51 mission) were lysed after 415s post-launch. Additionally, hardware 1g ground controls were lysed post-flight approximately 15min after the rocket launch. **(c)** In-flight experiment system for parabolic flights on board the Airbus A300 / A310 ZERO-G. **(c1)** Experiment hardware structure which consists of an incubator rack to store the cell containers at 37°C before the experiment (1), an experiment rack, in which all technical aggregates are accommodated for the execution of the experiment and where the living cells are processed during

altered gravity (2), and a cooling rack to store all cell containers at 4°C after the injection of the lysis solution until landing (3). **(d)** In-flight experiment system for the suborbital ballistic rocket flight of the TEXUS-49 and TEXUS-51 payload. TEXUS consists of a VSB-30 engine (not shown) and of the payload structure. Sets of three sterile syringes were filled with cell suspension, medium, and lysis buffer connected by a T-piece with small plugs at the outlet ports to prevent premature contact of the fluids. The syringe systems are accommodated in tempered and vacuum-resistant containers at the static or centrifuge (TEXUS-51) position.



Supplementary Figure S2. Cell container designed and used for adherent cells used in the First Swiss Parabolic Flight campaign. (a) Container before packaging. IBIDI-slides containing the cells (1) were incubated for two days to ensure firm adherence of the cells. The inlet of the slides is connected to two syringes one containing cell culture medium (red) and the other fixing solution (colorless). Six sets of these syringe / IBIDI-slide assemblies can be mounted to the container equipped with two release handles (5) that operate six syringes of the same kind simultaneously. The handles have a locking mechanism that ensured that only one handle can be operated at the same time and that only the handle that operates the syringes containing the cell culture medium can be operated first. The outlet of the IBIDI-slides is connected with a tube that directs the waste fluids into a waste compartment (4) that is filled with soaking material (3). Attached to the cover of the container is a gel pad warmed to 37°C (2). (b) All six syringe / IBIDI-slide assemblies fitted into the container, secured in place with a slide holder (6 in (a)) and the outlet tubing guided to the waste compartment filled with the soaking material. (c) Container closed and sealed into a watertight plastic bag (d) as required for security reasons.

Supplementary Table S1. List of HIF-related genes. A list of 176 genes relevant for HIF1 signaling was compiled comprising the 100 genes from KEGG database entry hsa04066, "HIF1 signaling pathway - Homo sapiens (human)" (https://www.genome.jp/dbget-bin/www_bget?pathway+hsa04066) and 76 genes which are known from the literature to also interact with HIF1 signaling. These genes are represented by 375 probe sets on the applied NimbleGen arrays based on the hg18 annotation, used for analysis of the human U937 cells. 175 of the 176 genes (one gene was not present on the array) are represented by 184 transcript clusters on the Affymetrix GeneChip® Human Transcriptome Array (Thermo Fisher Scientific, Waltham, MA, USA) used for analysis of the human Jurkat T cells.

Gene Symbol	Entrez Gene ID	Number of transcript clusters	Transcript Cluster IDs	Number of probe sets	Probe set IDs
ADM	133	1	TC11000182.hg.1	1	NM_001124
ADORA2A	135	1	TC22001457.hg.1	2	BC013780, NM_000675
ADRA1B	147	1	TC05000889.hg.1	1	NM_000679
AKT1	207	1	TC14001560.hg.1	3	BC084538, BX647722, NM_001014431
AKT2	208	1	TC19001532.hg.1	1	NM_001626
ALDOA	226	1	TC16000338.hg.1	3	CR592372, NM_000034, NM_184041
ALDOC	230	1	TC17001301.hg.1	2	BC106925, NM_005165
ANGPT1	284	1	TC08001521.hg.1	2	BC029406, NM_001146
ANGPT2	285	1	TC08000902.hg.1	3	AF187858, AF218015, NM_001147
ARG1	383	1	TC06000983.hg.1	2	BC020653, NM_000045
ARNT	405	1	TC01003212.hg.1	3	AB209877, BC060838, NM_001668
BCL2	596	1	TC18000554.hg.1	3	BC027258, NM_000633, NM_000657
CXCR5	643	1	TC11001073.hg.1	1	NM_001716
CA9	768	1	TC09000191.hg.1	1	NM_001216
CAMK2A	815	1	TC05001934.hg.1	3	AF145710, AF145711, NM_015981
CAMK2B	816	1	TC07001338.hg.1	6	NM_001220, NM_172078, NM_172080, NM_172081, NM_172082, NM_172084
CAMK2D	817	1	TC04001486.hg.1	4	AB209288, NM_001221, NM_172115, NM_172127
CAMK2G	818	1	TC10001420.hg.1	1	NM_001222
CAMP	820	1	TC03000276.hg.1	2	BC055089, NM_004345
CD36	948	1	TC07000509.hg.1	3	BC008406, NM_000072, NM_001001548
CDKN1A	1026	1	TC06000532.hg.1	2	NM_000389, NM_078467
CDKN1B	1027	1	TC12000178.hg.1	1	NM_004064
CCR1	1230	1	TC03001355.hg.1	2	BC051306, NM_001295
CCR5	1234	1	TC03000256.hg.1	2	BC038398, NM_000579
CCR7	1236	1	TC17001466.hg.1	1	NM_001838
CREBBP	1387	1	TC16000823.hg.1	2	NM_004380, U85962
MAPK14	1432	1	TC06000523.hg.1	3	BC000092, NM_001315, NM_139013
CTLA4	1493	1	TC02001201.hg.1	5	BC069566, BC074842, BC074893, NM_001037631, NM_005214
CTSD	1509	1	TC11003472.hg.1	1	NM_001909
CYBB	1536	1	TC0X000171.hg.1	2	BC032720, NM_000397
DEFB1	1672	1	TC08000906.hg.1	2	BC033298, NM_005218

S1PR1	1901	1	TC01000909.hg.1	1	NM_001400
EDN1	1906	1	TC06000087.hg.1	2	CR605456, NM_001955
EGF	1950	1	TC04000568.hg.1	2	BC093731, NM_001963
EGFR	1956	1	TC07000328.hg.1	6	BC094761, K03193, NM_005228, NM_201282, NM_201283, NM_201284
EIF4E	1977	1	TC04001403.hg.1	3	BC012611, BC035166, NM_001968
EIF4EBP1	1978	1	TC08000281.hg.1	2	BC058073, NM_004095
ENG	2022	1	TC09001609.hg.1	2	BC014271, NM_000118
ENO1	2023	1	TC01002175.hg.1	3	BC050642, BC073991, NM_001428
ENO2	2026	1	TC12000099.hg.1	1	NM_001975
ENO3	2027	1	TC17000058.hg.1	3	BC017249, NM_001976, NM_053013
EP300	2033	1	TC22000332.hg.1	1	NM_001429
EPAS1	2034	1	TC02000281.hg.1	1	NM_001430
EPO	2056	1	TC07000632.hg.1	2	BC093628, NM_000799
ERBB2	2064	1	TC17000480.hg.1	3	AF177761, AK131568, NM_001005862
FLT1	2321	1	TC13000517.hg.1	2	BC039007, NM_002019
FN1	2335	1	TC02002747.hg.1	5	AB191261, BX538018, CR749317, NM_002026, NM_054034
MTOR	2475	1	TC01002197.hg.1	1	NM_004958
GAPDH	2597	1	TC12000084.hg.1	3	BC001601, BC009081, NM_002046
GPI	2821	1	TC19000442.hg.1	2	BC004982, NM_000175
MKNK2	2872	1	TC19001019.hg.1	3	AF237775, NM_017572, NM_199054
CXCL2	2920	1	TC04001286.hg.1	2	BC015753, NM_002089
HDAC2	3066	1	TC06002035.hg.1	1	NM_001527
HIF1A	3091	1	TC14002197.hg.1	2	NM_001530, NM_181054
HK1	3098	1	TC10000419.hg.1	1	NM_000188
HK2	3099	1	TC02000466.hg.1	2	BC021116, NM_000189
HK3	3101	1	TC05002100.hg.1	1	NM_002115
HMOX1	3162	1	TC22000259.hg.1	2	BC001491, NM_002133
ICAM1	3383	1	TC19000174.hg.1	1	NM_000201
IFNG	3458	1	TC12001696.hg.1	1	NM_000619
IFNGR1	3459	1	TC06002152.hg.1	1	NM_000416
IFNGR2	3460	1	TC21000129.hg.1	1	NM_005534
IGF1	3479	1	TC12001890.hg.1	4	M11568, M29644, M37484, NM_000618
IGF1R	3480	2	TC15000949.hg.1, TC15000951.hg.1	1	NM_000875
IGF2 (aka GRDF; IGF-II; PP9974; C11orf43)	3481	0	-	2	BC053318, NM_000612
IGFBP1	3484	1	TC07000294.hg.1	2	NM_000596, NM_001013029
IGFBP2	3485	1	TC02001281.hg.1	1	NM_000597
IGFBP3	3486	1	TC07001355.hg.1	2	BC000013, NM_000598
IL1B	3553	1	TC02002219.hg.1	1	NM_000576
IL6	3569	1	TC07000137.hg.1	1	NM_000600

IL6R	3570	1	TC01001276.hg.1	2	BC089410, NM_000565
CXCL8	3576	1	TC04000408.hg.1	1	NM_000584
IL12A	3592	1	TC03000870.hg.1	2	BC104982, NM_000882
TNFRSF9	3604	1	TC01002163.hg.1	1	NM_001561
INS	3630	1	TC11001274.hg.1	2	BC005255, NM_000207
INSR	3643	1	TC19001111.hg.1	2	NM_000208, X02160
ITGAM	3684	1	TC16000374.hg.1	3	BC096346, J03925, NM_000632
ITGB2	3689	1	TC21000538.hg.1	2	AK097864, NM_000211
KDR	3791	1	TC04001208.hg.1	1	NM_002253
KRT14	3861	1	TC17001513.hg.1	1	NM_000526
KRT18	3875	1	TC12000424.hg.1	4	BC000180, BC004253, NM_000224, NM_199187
KRT19	3880	1	TC17002906.hg.1	2	BC007628, NM_002276
LAG3	3902	1	TC12000091.hg.1	2	BC052589, NM_002286
LDHA	3939	1	TC11000240.hg.1	1	NM_005566
LEP	3952	1	TC07000768.hg.1	3	BC069323, D49487, NM_000230
LRP1	4035	1	TC12000521.hg.1	3	BC045107, BC052593, NM_002332
LTBR	4055	1	TC12000078.hg.1	1	NM_002342
MMP2	4313	1	TC16000454.hg.1	2	BC002576, NM_004530
MMP9	4318	1	TC20000363.hg.1	1	NM_004994
MMP14	4323	1	TC14000133.hg.1	2	BC064803, NM_004995
NFKB1	4790	1	TC04000526.hg.1	3	BC051765, M58603, NM_003998
NOS2	4843	1	TC17002894.hg.1	1	NM_000625
NOS3	4846	1	TC07001009.hg.1	2	BC069465, NM_000603
NPPA	4878	1	TC01002204.hg.1	2	BC005893, NM_006172
SERPINE1	5054	1	TC07000643.hg.1	2	BC010860, NM_000602
PDGFB	5155	1	TC22000802.hg.1	4	BC029822, BC077725, NM_002608, X83705
PDHA1	5160	1	TC0X000092.hg.1	2	CR614489, NM_000284
PDHA2	5161	1	TC04000504.hg.1	1	NM_005390
PDHB	5162	1	TC03001499.hg.1	1	NM_000925
PDK1	5163	1	TC02001031.hg.1	3	BC039158, DQ234350, NM_002610
PFKFB3	5209	1	TC10000053.hg.1	3	AF056320, AK131307, NM_004566
PFKL	5211	1	TC21000222.hg.1	2	BX537446, NM_001002021
PGK1	5230	1	TC0X000425.hg.1	3	BC023234, BC103752, NM_000291
ABCB1	5243	1	TC07001579.hg.1	2	AF016535, NM_000927
PIK3CA	5290	1	TC03000951.hg.1	1	NM_006218
PIK3CB	5291	1	TC03001824.hg.1	2	CR749357, NM_006219
PIK3CD	5293	1	TC01000118.hg.1	2	NM_005026, U57843
PIK3R1	5295	1	TC05000291.hg.1	3	BC030815, BC094795, NM_181504
PIK3R2	5296	1	TC19002628.hg.1	1	NM_005027
PKM	5315	1	TC15002776.hg.1	1	NM_002654
PLAUR	5329	1	TC19001593.hg.1	3	NM_001005376, NM_001005377, NM_002659

PLCG1	5335	1	TC20000303.hg.1	1	NM_002660
PLCG2	5336	2	TC16000642.hg.1, TC16000643.hg.1	2	BC007565, NM_002661
PRKCA	5578	1	TC17000783.hg.1	2	BC109273, NM_002737
PRKCB	5579	1	TC16000260.hg.1	3	BC036472, NM_002738, NM_212535
PRKCG	5582	1	TC19000866.hg.1	2	BC047876, NM_002739
MAPK1	5594	1	TC22000547.hg.1	4	BC099905, NM_002745, NM_138957, Z11695
MAPK3	5595	1	TC16001021.hg.1	3	AY033607, NM_001040056, NM_002746
MAP2K1	5604	1	TC15000613.hg.1	1	NM_002755
MAP2K2	5605	1	TC19001058.hg.1	1	NM_030662
RELA	5970	1	TC11001939.hg.1	4	BC011603, BC014095, BC110830, NM_021975
RORC	6097	1	TC01006373.hg.1	3	BC031554, BC110571, NM_001001523
RPS6	6194	1	TC09000938.hg.1	1	NM_001010
RPS6KB1	6198	1	TC17000729.hg.1	3	BC036033, BC053365, NM_003161
RPS6KB2	6199	1	TC11000691.hg.1	3	BC000094, BC006106, NM_001007071
CCL2	6347	1	TC17000383.hg.1	1	NM_002982
CXCL6	6372	1	TC04000409.hg.1	1	NM_002993
SELL	6402	1	TC01003500.hg.1	3	AJ246000, BC020758, NM_000655
SLC2A1	6513	1	TC01002578.hg.1	1	NM_006516
SLC2A3	6515	1	TC12001170.hg.1	2	BC039196, NM_006931
SLC11A1	6556	1	TC02001300.hg.1	3	BC041787, NM_000578, NM_001032220
STAT3	6774	1	TC17001531.hg.1	4	BC000627, BC014482, NM_003150, NM_213662
STAT4	6775	1	TC02002625.hg.1	1	NM_003151
ELOC	6921	1	TC08001332.hg.1	4	BC093065, BC100028, BC100283, NM_005648
ELOB	6923	1	TC16000791.hg.1	4	BC013306, BC065000, NM_007108, NM_207013
TCF7	6932	1	TC05000657.hg.1	3	BC048769, NM_003202, NM_201633
TEK	7010	1	TC09000121.hg.1	1	NM_000459
TF	7018	1	TC03000723.hg.1	2	AK126941, NM_001063
TFF3	7033	1	TC21000484.hg.1	2	BC017859, NM_003226
TFRC	7037	1	TC03002155.hg.1	2	BC001188, NM_003234
TGFA	7039	1	TC02001963.hg.1	4	AF149096, AF149098, BC005308, NM_003236
TGFB1	7040	1	TC19001553.hg.1	2	BC000125, NM_000660
TGFB3	7043	1	TC14001326.hg.1	2	BC018503, NM_003239
THBS1	7057	1	TC15000270.hg.1	1	NM_003246
TIMP1	7076	1	TC0X000238.hg.1	2	BC000866, NM_003254
TLR4	7099	1	TC09000601.hg.1	3	NM_003266, NM_138554, NM_138557
TNF	7124	8	TC06000371.hg.1, TC6_apd_hap1000036.hg.1, TC6_cox_hap2000067.hg.1, TC6_dbb_hap3000058.hg.1, TC6_mann_hap4000059.hg.1,	1	NM_000594

			TC6_mcf_hap5000053.hg.1, TC6_qbl_hap6000058.hg.1, TC6_ssto_hap7000054.hg.1		
TP	7167	1	TC12000096.hg.1	4	BC007086, BC017917, BC070129, NM_000365
TNFRSF4	7293	1	TC01002086.hg.1	1	NM_003327
VEGFA	7422	1	TC06000608.hg.1	5	AF323587, AY263145, M27281, NM_001025366, S85192
VHL	7428	1	TC03000055.hg.1	3	BC058831, L15409, NM_000551
VIM	7431	1	TC10000126.hg.1	4	AK093924, BC030573, BC066956, NM_003380
CXCR4	7852	1	TC02002378.hg.1	1	NM_001008540
EOMES	8320	1	TC03001257.hg.1	1	NM_005442
CUL2	8453	1	TC10001173.hg.1	1	NM_003591
PIK3R3	8503	1	TC01002616.hg.1	2	AF028785, NM_003629
MKNK1	8569	1	TC01006353.hg.1	4	AB000409, AK096423, NM_003684, NM_198973
TNFRSF18	8784	1	TC01002085.hg.1	2	NM_004195, NM_148901
NRP1	8829	1	TC10001166.hg.1	5	AF268691, AF280547, NM_001024628, NM_001024629, NM_003873
EIF4E2	9470	1	TC02001404.hg.1	1	NM_004846
RBX1	9978	1	TC22000327.hg.1 (Entrez ID 63929)	1	NM_014248
AKT3	10000	1	TC01004040.hg.1	2	NM_005465, NM_181690
TBX21	30009	1	TC17000613.hg.1	1	NM_013351
AK3	50808	1	TC09000884.hg.1	2	BC013771, NM_016282
FOXP3	50943	1	TC0X001031.hg.1	1	NM_014009
ANGPT4	51378	1	TC20000546.hg.1	3	BC111976, BC111978, NM_015985
EGLN1	54583	1	TC01003968.hg.1	2	BC005369, NM_022051
HIF1AN	55662	1	TC10000724.hg.1	3	AK025680, BC007719, NM_017902
HAMP	57817	1	TC19000464.hg.1	1	NM_021175
HKDC1	80201	1	TC10000418.hg.1	3	AK026414, BC110504, NM_025130
PROK1	84432	1	TC01000966.hg.1	1	NM_032414
RETNLB	84666	1	TC03001633.hg.1	2	BC069318, NM_032579
EGLN2	112398	1	TC19002634.hg.1	2	NM_017555, NM_053046
EGLN3	112399	1	TC14001022.hg.1	2	AK123350, NM_022073
EIF4E1B	253314	1	TC05001004.hg.1	3	XM_171094, XM_927854, XM_932348
ENO4	387712	1	TC10000848.hg.1	1	XM_370577

Supplementary Table S2. Expression fold changes of 175 of the 176 HIF-related genes (one gene was not present on the microarray).The 175 genes are represented by 184 transcript cluster IDs analyzed in human Jurkat T cells exposed to different gravitational conditions during parabolic flight (23rd DLR PFC). The analysis was made with the Affymetrix GeneChip® Human Transcriptome Array (Thermo Fisher Scientific, Waltham, MA, USA).

				1g IF vs H/W 1g GC		BL-PFC hyp-g vs H/W		BL-PFC hyp-g vs 1g IF		µg vs H/W 1g GC		µg vs 1g IF		µg vs BL-PFC hyp-g	
Gene Symbol	**Entrez ID**	**Transcript Cluster ID**	**Description**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**
ADM	133	TC11000182.hg.1	adrenomedullin	1.2	0.0002	1.17	0.0011	-1.03	0.2901	1.12	0.0003	-1.07	0.0300	-1.04	0.3310
ADORA2A	135	TC22001457.hg.1	adenosine A2a receptor	1.1	0.0049	1.02	0.2254	-1.07	0.0028	1.03	0.1775	-1.07	0.0236	1.01	0.6247
ADRA1B	147	TC05000889.hg.1	adrenoceptor alpha 1B; adrenergic, alpha-1B-, receptor	1.17	0.0021	1.12	0.0000	-1.05	0.2537	1.12	0.0006	-1.05	0.3225	1	0.9371
AKT1	207	TC14001560.hg.1	v-akt murine thymoma viral oncogene homolog 1	1.01	0.4663	1.03	0.3247	1.02	0.8387	1.05	0.0372	1.03	0.4179	1.01	0.5618
AKT2	208	TC19001532.hg.1	v-akt murine thymoma viral oncogene homolog 2	-1.07	0.0043	-1.08	0.0028	-1.02	0.2969	-1.07	0.0035	-1.01	0.7081	1.01	0.4725
ALDOA	226	TC16000338.hg.1	aldolase A, fructose-bisphosphate	-1.03	0.6823	-1	0.1359	1.02	0.0951	1.01	0.4750	1.03	0.3075	1.01	0.3608
ALDOC	230	TC17001301.hg.1	aldolase C, fructose-bisphosphate	1.07	0.2721	1.06	0.1082	-1	0.9758	1.01	0.8740	-1.06	0.1994	-1.06	0.0464
ANGPT1	284	TC08001521.hg.1	angiopoietin 1	1.01	0.3598	1.02	0.5641	1.01	0.8532	1.01	0.1305	1.01	0.9456	-1	0.7788
ANGPT2	285	TC08000902.hg.1	angiopoietin 2	-1.01	0.7178	-1.01	0.5720	1	0.8365	-1.01	0.7029	1	0.9681	1	0.8840
ARG1	383	TC06000983.hg.1	arginase 1; arginase, liver	1.06	0.0129	1	0.7601	-1.05	0.0352	1.01	0.5436	-1.04	0.0555	1.01	0.7812
ARNT	405	TC01003212.hg.1	aryl hydrocarbon receptor nuclear translocator	1.12	0.0035	1.15	0.0007	1.03	0.2120	1.16	0.0004	1.03	0.1182	1.01	0.7522
BCL2	596	TC18000554.hg.1	B-cell CLL/lymphoma 2	-1.02	0.1129	1.06	0.1522	1.08	0.0259	1.04	0.6140	1.06	0.0603	-1.02	0.2571
CXCR5	643	TC11001073.hg.1	chemokine (C-X-C motif) receptor 5	1.01	0.3770	1.02	0.4904	1	0.8263	1.02	0.1909	1.01	0.7806	1	0.5901
CA9	768	TC09000191.hg.1	carbonic anhydrase IX	1.09	0.0287	1.07	0.1624	-1.02	0.1416	1.06	0.0857	-1.03	0.1925	-1.01	0.6410
CAMK2A	815	TC05001934.hg.1	calcium/calmodulin-dependent protein kinase II alpha	1.1	0.0041	1.06	0.0294	-1.04	0.1218	1.07	0.0352	-1.03	0.3586	1.01	0.6634
CAMK2B	816	TC07001338.hg.1	calcium/calmodulin-dependent protein kinase II beta	1.12	0.0008	1.06	0.0320	-1.05	0.0081	1.06	0.0335	-1.06	0.0274	-1.01	0.7907
CAMK2D	817	TC04001486.hg.1	calcium/calmodulin-dependent protein kinase II delta	1.04	0.4922	1.11	0.0014	1.07	0.0018	1.11	0.0019	1.07	0.0027	1	0.8087
CAMK2G	818	TC10001420.hg.1	calcium/calmodulin-dependent protein kinase II gamma	1.21	0.0000	1.25	0.0000	1.04	0.2606	1.32	0.0000	1.09	0.0111	1.05	0.1702

CAMP	820	TC03000276.hg.1	cathelicidin antimicrobial peptide	1.16	0.1007	1.09	0.3065	-1.07	0.2872	1.14	0.0852	-1.02	0.9141	1.05	0.2370
CD36	948	TC07000509.hg.1	CD36 molecule (thrombospondin receptor)	1.03	0.3345	1.01	0.4982	-1.02	0.5298	-1.01	0.5907	-1.04	0.0649	-1.02	0.0168
CDKN1A	1026	TC06000532.hg.1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.23	0.0005	1.13	0.0080	-1.09	0.1116	1.12	0.0113	-1.1	0.0873	-1.01	0.8698
CDKN1B	1027	TC12000178.hg.1	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1.31	0.0002	1.38	0.0001	1.05	0.1619	1.32	0.0001	1.01	0.6501	-1.05	0.2833
CCR1	1230	TC03001355.hg.1	chemokine (C-C motif) receptor 1	1.08	0.4411	1.01	0.8819	-1.06	0.6054	1.03	0.4602	-1.05	0.9668	1.02	0.6036
CCR5	1234	TC03000256.hg.1	chemokine (C-C motif) receptor 5 (gene/pseudogene); chemokine (C-C motif) receptor 5	1.03	0.4591	-1.03	0.8664	-1.05	0.5887	1	0.9656	-1.02	0.5438	1.03	0.8649
CCR7	1236	TC17001466.hg.1	chemokine (C-C motif) receptor 7	1.38	0.0006	1.38	0.0032	-1	0.4596	1.41	0.0007	1.02	0.9003	1.02	0.5166
CREBBP	1387	TC16000823.hg.1	CREB binding protein	-1.11	0.1203	1.06	0.9619	1.19	0.1057	-1	0.9670	1.11	0.0749	-1.07	0.9902
MAPK14	1432	TC06000523.hg.1	mitogen-activated protein kinase 14	-1.01	0.5032	1.08	0.0036	1.1	0.0033	1.04	0.0167	1.06	0.0127	-1.04	0.1836
CTLA4	1493	TC02001201.hg.1	cytotoxic T-lymphocyte-associated protein 4	1.11	0.0121	1.01	0.2702	-1.1	0.1182	1.02	0.1587	-1.09	0.0432	1	0.8190
CTSD	1509	TC11003472.hg.1	cathepsin D	1.05	0.3127	1.09	0.0135	1.03	0.3450	1.05	0.0252	-1	0.5980	-1.03	0.5142
CYBB	1536	TC0X000171.hg.1	cytochrome b-245, beta polypeptide	1.05	0.1040	-1.01	0.5846	-1.06	0.1996	-1.07	0.5204	-1.13	0.0823	-1.06	0.3244
DEFB1	1672	TC08000906.hg.1	defensin, beta 1	1.17	0.0688	-1	0.5819	-1.18	0.0053	1.11	0.1351	-1.06	0.5592	1.11	0.0103
S1PR1	1901	TC01000909.hg.1	sphingosine-1-phosphate receptor 1	-1.2	0.0010	-1.24	0.0006	-1.04	0.5051	-1.21	0.0010	-1.01	0.7430	1.03	0.7403
EDN1	1906	TC06000087.hg.1	endothelin 1	1.05	0.1739	-1	0.8277	-1.05	0.3263	1.01	0.5196	-1.04	0.3609	1.01	0.7974
EGF	1950	TC04000568.hg.1	epidermal growth factor; epidermal growth factor (beta-urogastrone)	1.09	0.0046	1.04	0.0153	-1.05	0.2145	1.04	0.0049	-1.05	0.0532	-1	0.3980
EGFR	1956	TC07000328.hg.1	epidermal growth factor receptor; epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	1.06	0.0038	1.03	0.0941	-1.03	0.1489	1.05	0.0214	-1.01	0.3686	1.02	0.5089
EIF4E	1977	TC04001403.hg.1	eukaryotic translation initiation factor 4E	-1.16	0.0001	-1.09	0.0011	1.07	0.0502	-1.16	0.0000	1	0.8036	-1.07	0.0204

EIF4EBP1	1978	TC08000281.hg.1	eukaryotic translation initiation factor 4E binding protein 1	1.03	0.3728	1	0.6361	-1.03	0.1614	1.01	0.6902	-1.03	0.1632	1	0.9059
ENG	2022	TC09001609.hg.1	endoglin	1.06	0.0972	1.04	0.3511	-1.02	0.3191	1.04	0.1063	-1.01	0.8719	1	0.3684
ENO1	2023	TC01002175.hg.1	enolase 1, (alpha)	-1.06	0.0896	-1.04	0.1933	1.03	0.3663	-1.11	0.0070	-1.04	0.3018	-1.07	0.0208
ENO2	2026	TC12000099.hg.1	enolase 2 (gamma, neuronal)	1.04	0.0642	1	0.8574	-1.04	0.1947	1.04	0.8659	1.01	0.2346	1.04	0.9923
ENO3	2027	TC17000058.hg.1	enolase 3 (beta, muscle)	-1.02	0.3498	-1.05	0.1518	-1.03	0.3711	-1.01	0.3228	1.01	0.8981	1.04	0.4337
EP300; MIR1281	2033	TC22000332.hg.1	E1A binding protein p300; microRNA 1281	-1.1	0.1506	1.04	0.7909	1.15	0.1051	1.05	0.4435	1.16	0.0477	1.01	0.6150
EPAS1	2034	TC02000281.hg.1	endothelial PAS domain protein 1	1.39	0.0009	1.25	0.0032	-1.11	0.3535	1.39	0.0000	1	0.8181	1.12	0.1672
EPO	2056	TC07000632.hg.1	erythropoietin	1.1	0.0078	1.04	0.0928	-1.06	0.3066	1.08	0.0115	-1.01	0.8315	1.04	0.3997
ERBB2; MIR4728	2064	TC17000480.hg.1	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2; microRNA 4728; v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	1.06	0.0111	1.01	0.1791	-1.04	0.1231	1.02	0.0313	-1.03	0.1071	1.01	0.7278
FLT1	2321	TC13000517.hg.1	fms-related tyrosine kinase 1; fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	1.03	0.1129	1.12	0.0008	1.08	0.0024	1.14	0.0068	1.1	0.0246	1.02	0.9834
FN1	2335	TC02002747.hg.1	fibronectin 1	1.04	0.0997	1.03	0.0661	-1.01	0.7894	1.03	0.1362	-1.01	0.7737	1	0.9437
MTOR	2475	TC01002197.hg.1	mechanistic target of rapamycin (serine/threonine kinase)	-1.2	0.0000	-1.18	0.0000	1.01	0.9830	-1.18	0.0000	1.02	0.3989	1	0.5158
GAPDH	2597	TC12000084.hg.1	glyceraldehyde-3-phosphate dehydrogenase	1.03	0.2594	1.01	0.3041	-1.02	0.6786	-1.01	0.5646	-1.04	0.0798	-1.02	0.0482
GPI	2821	TC19000442.hg.1	glucose-6-phosphate isomerase	-1.12	0.0044	-1.04	0.2414	1.08	0.0260	-1.08	0.0048	1.04	0.2837	-1.03	0.0472
MKNK2	2872	TC19001019.hg.1	MAP kinase interacting serine/threonine kinase 2	1.07	0.2851	1.12	0.2053	1.05	0.6501	1.17	0.0152	1.09	0.0973	1.04	0.4576
CXCL2	2920	TC04001286.hg.1	chemokine (C-X-C motif) ligand 2	1.14	0.0015	1.02	0.1332	-1.12	0.0254	1.06	0.3146	-1.08	0.0512	1.03	0.9136
HDAC2	3066	TC06002035.hg.1	histone deacetylase 2	-1.09	0.0009	-1.05	0.0543	1.04	0.0702	-1.1	0.0047	-1	0.4139	-1.05	0.2617
HIF1A	3091	TC14002197.hg.1	hypoxia inducible factor 1, alpha subunit (basic helix-	1.12	0.0011	1.25	0.0000	1.11	0.0016	1.21	0.0000	1.07	0.0063	-1.04	0.2370

			loop-helix transcription factor)												
HK1	3098	TC10000419.hg.1	hexokinase 1	1.14	0.0019	1.14	0.0023	1	0.8576	1.13	0.0027	-1	0.7820	-1.01	0.6665
HK2	3099	TC02000466.hg.1	hexokinase 2	-1.24	0.0011	-1.16	0.0075	1.07	0.0446	-1.23	0.0008	1.01	0.6689	-1.05	0.0348
HK3	3101	TC05002100.hg.1	hexokinase 3 (white cell)	1.14	0.0010	1.07	0.1561	-1.07	0.0439	1.03	0.2688	-1.1	0.0015	-1.03	0.4974
HMOX1	3162	TC22000259.hg.1	heme oxygenase (decycling) 1	1.12	0.0033	1.03	0.1454	-1.09	0.0175	1.03	0.1676	-1.09	0.0475	-1	0.8646
ICAM1	3383	TC19000174.hg.1	intercellular adhesion molecule 1	1.09	0.0229	1.04	0.2392	-1.04	0.1743	1.05	0.6169	-1.03	0.1221	1.01	0.6565
IFNG	3458	TC12001696.hg.1	interferon, gamma	1.06	0.2721	-1.01	0.7131	-1.08	0.2213	-1.01	0.7969	-1.07	0.2831	1.01	0.9944
IFNGR1	3459	TC06002152.hg.1	interferon gamma receptor 1	1.09	0.0365	1.13	0.0145	1.04	0.5012	1.13	0.0052	1.04	0.2236	-1	0.6146
IFNGR2	3460	TC21000129.hg.1	interferon gamma receptor 2 (interferon gamma transducer 1)	-1.14	0.0050	-1.06	0.0558	1.07	0.1089	-1.08	0.0071	1.06	0.5372	-1.01	0.2233
IGF1	3479	TC12001890.hg.1	insulin-like growth factor 1 (somatomedin C)	1.07	0.0077	1.04	0.0558	-1.02	0.3323	1.05	0.0013	-1.02	0.2491	1	0.8863
IGF1R	3480	TC15000949.hg.1	insulin-like growth factor 1 receptor	1.15	0.0032	1.18	0.0007	1.03	0.3974	1.19	0.0003	1.03	0.0984	1.01	0.3233
IGF1R	3480	TC15000951.hg.1	insulin-like growth factor 1 receptor	1.4	0.0052	1.27	0.0013	-1.11	0.4209	1.33	0.0016	-1.05	0.6223	1.05	0.6340
IGFBP1	3484	TC07000294.hg.1	insulin-like growth factor binding protein 1	1.06	0.0602	-1.01	0.4156	-1.07	0.0115	1.02	0.4541	-1.04	0.3511	1.03	0.1548
IGFBP2	3485	TC02001281.hg.1	insulin-like growth factor binding protein 2, 36kDa	1.06	0.4016	1.05	0.2353	-1.01	0.9097	1.08	0.0035	1.02	0.2438	1.03	0.1914
IGFBP3	3486	TC07001355.hg.1	insulin-like growth factor binding protein 3	1.09	0.0106	1.05	0.2310	-1.04	0.2409	1.05	0.0137	-1.04	0.3189	1	0.5720
IL1B	3553	TC02002219.hg.1	interleukin 1, beta	1.1	0.0002	1.05	0.0920	-1.05	0.0964	1.06	0.0022	-1.04	0.0115	1.01	0.6589
IL6	3569	TC07000137.hg.1	interleukin 6; interleukin 6 (interferon, beta 2)	-1	0.2700	1.02	0.3954	1.02	0.7366	1.08	0.0074	1.08	0.3754	1.05	0.1585
IL6R	3570	TC01001276.hg.1	interleukin 6 receptor	1.09	0.0007	1.02	0.2065	-1.07	0.0457	1.03	0.0912	-1.06	0.0145	1.01	0.9914
CXCL8; IL8	3576	TC04000408.hg.1	chemokine (C-X-C motif) ligand 8; interleukin 8	1.07	0.2568	1.01	0.5232	-1.06	0.9258	-1.02	0.7988	-1.09	0.1834	-1.03	0.4352
IL12A	3592	TC03000870.hg.1	interleukin 12A; interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	1.08	0.0262	1.03	0.2637	-1.05	0.0927	1.03	0.2416	-1.05	0.1680	-1	0.8668
TNFRSF9	3604	TC01002163.hg.1	tumor necrosis factor receptor superfamily, member 9	1.05	0.1626	1.04	0.2233	-1.01	0.8221	1	0.7379	-1.05	0.1663	-1.04	0.2420

INS; IGF2; INS-IGF2; AC132217.4	3630	TC11001274.hg.1	insulin; insulin-like growth factor 2 (somatomedin A); INS-IGF2 readthrough; novel transcript, 3'_overlapping_ncRNA IGF2	1.09	0.0184	1.05	0.1426	-1.04	0.2095	1.05	0.1157	-1.04	0.2980	-1	0.8581
INSR	3643	TC19001111.hg.1	insulin receptor	1.16	0.0016	1.23	0.0000	1.06	0.2563	1.22	0.0000	1.05	0.1759	-1.01	0.7062
ITGAM	3684	TC16000374.hg.1	integrin, alpha M (complement component 3 receptor 3 subunit)	1.1	0.0081	1.05	0.1856	-1.05	0.0473	1.04	0.2960	-1.06	0.0317	-1.01	0.7481
ITGB2	3689	TC21000538.hg.1	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-1.01	0.7248	-1.01	0.2640	-1	0.5403	-1.03	0.1089	-1.02	0.3187	-1.02	0.6612
KDR	3791	TC04001208.hg.1	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.08	0.0060	1.02	0.2407	-1.06	0.0589	1.05	0.0338	-1.03	0.1183	1.03	0.3723
KRT14	3861	TC17001513.hg.1	keratin 14	1.07	0.0279	1.01	0.5850	-1.06	0.1903	1.02	0.3483	-1.05	0.1364	1.01	0.8990
KRT18	3875	TC12000424.hg.1	keratin 18	1.06	0.0080	-1	0.3660	-1.06	0.0315	1.06	0.0104	-1.01	0.6824	1.06	0.0464
KRT19	3880	TC17002906.hg.1	keratin 19	1.07	0.0367	1.05	0.5071	-1.03	0.0526	1.04	0.5279	-1.03	0.2263	-1.01	0.9016
LAG3	3902	TC12000091.hg.1	lymphocyte-activation gene 3	1.1	0.1856	1.02	0.8450	-1.08	0.0120	1.04	0.8764	-1.06	0.1550	1.01	0.6493
LDHA	3939	TC11000240.hg.1	lactate dehydrogenase A	-1.11	0.0369	-1.08	0.0632	1.02	0.5939	-1.11	0.0064	-1.01	0.0996	-1.03	0.0359
LEP	3952	TC07000768.hg.1	leptin	1.09	0.0766	1.02	0.6256	-1.07	0.0181	1.09	0.0490	-1	0.4357	1.07	0.0253
LRP1	4035	TC12000521.hg.1	low density lipoprotein receptor-related protein 1	1.12	0.0058	1.05	0.1830	-1.06	0.1141	1.07	0.0345	-1.04	0.1843	1.02	0.6014
LTBR	4055	TC12000078.hg.1	lymphotoxin beta receptor (TNFR superfamily, member 3)	1.11	0.0133	1.06	0.0942	-1.04	0.0772	1.07	0.0240	-1.03	0.3662	1.01	0.2074
MMP2	4313	TC16000454.hg.1	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	1.1	0.0048	1.02	0.1417	-1.08	0.0866	1.05	0.0414	-1.05	0.3592	1.02	0.4423
MMP9	4318	TC20000363.hg.1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	1.15	0.0031	1.07	0.0231	-1.07	0.1740	1.09	0.0074	-1.05	0.1724	1.02	0.8470
MMP14	4323	TC14000133.hg.1	matrix metallopeptidase 14 (membrane-inserted)	1.22	0.0029	1.25	0.0035	1.03	0.8593	1.36	0.0004	1.11	0.0725	1.08	0.1333
NFKB1	4790	TC04000526.hg.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	-1.03	0.0496	-1	0.9974	1.03	0.1628	-1.04	0.2007	-1.01	0.9529	-1.04	0.2887

NOS2	4843	TC17002894.hg.1	nitric oxide synthase 2, inducible	1.1	0.0057	1.06	0.0100	-1.03	0.2059	1.05	0.0073	-1.04	0.1989	-1.01	0.9835
NOS3; ATG9B	4846	TC07001009.hg.1	nitric oxide synthase 3 (endothelial cell); ATG9 autophagy related 9 homolog B (S. cerevisiae)	1	0.6362	-1.03	0.0272	-1.03	0.0751	-1.04	0.0329	-1.04	0.1164	-1.01	0.4720
NPPA	4878	TC01002204.hg.1	natriuretic peptide A; natriuretic peptide precursor A	1.06	0.1827	-1.02	0.6859	-1.08	0.3027	1.01	0.5639	-1.04	0.1992	1.03	0.9075
SERPINE1	5054	TC07000643.hg.1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	1.17	0.0040	1.13	0.0242	-1.04	0.1251	1.14	0.0073	-1.03	0.4521	1.01	0.3308
PDGFB	5155	TC22000802.hg.1	platelet-derived growth factor beta polypeptide; platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	1.09	0.0040	1.04	0.0715	-1.05	0.0704	1.04	0.1126	-1.05	0.1947	-1	0.8404
PDHA1	5160	TC0X000092.hg.1	pyruvate dehydrogenase (lipoamide) alpha 1	-1.23	0.0025	-1.21	0.0007	1.02	0.6613	-1.25	0.0002	-1.02	0.4954	-1.04	0.0470
PDHA2	5161	TC04000504.hg.1	pyruvate dehydrogenase (lipoamide) alpha 2	1.03	0.0781	-1.01	0.4545	-1.04	0.3579	-1	0.2900	-1.03	0.2898	1.01	0.9110
PDHB	5162	TC03001499.hg.1	pyruvate dehydrogenase (lipoamide) beta	-1.15	0.0757	-1.11	0.1940	1.03	0.4763	-1.18	0.0066	-1.02	0.3977	-1.06	0.0744
PDK1	5163	TC02001031.hg.1	pyruvate dehydrogenase kinase, isozyme 1	1.06	0.0029	1.07	0.0014	1.01	0.3570	1.07	0.0007	1.01	0.4445	-1	0.6384
PFKFB3	5209	TC10000053.hg.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	1.07	0.0522	1.07	0.0401	-1	0.6722	1.08	0.0075	1.01	0.4115	1.01	0.7941
PFKL	5211	TC21000222.hg.1	phosphofructokinase, liver	-1.07	0.0509	-1.13	0.0002	-1.06	0.0061	-1.12	0.0006	-1.05	0.0247	1.01	0.4674
PGK1; LOC100652805; LOC100653302	5230	TC0X000425.hg.1	phosphoglycerate kinase 1; uncharacterized LOC100652805; uncharacterized LOC100653302	-1.1	0.0377	-1.06	0.3276	1.04	0.0990	-1.12	0.0222	-1.02	0.9552	-1.06	0.0438
ABCB1	5243	TC07001579.hg.1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.06	0.0281	1.04	0.3061	-1.02	0.3168	1.01	0.5181	-1.04	0.0278	-1.02	0.4819
PIK3CA	5290	TC03000951.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha;	1.08	0.0144	1.18	0.0000	1.09	0.0007	1.2	0.0002	1.11	0.0085	1.02	0.9973

			phosphoinositide-3-kinase, catalytic, alpha polypeptide												
PIK3CB	5291	TC03001824.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta; phosphoinositide-3-kinase, catalytic, beta polypeptide	-1.12	0.0014	-1.03	0.0504	1.09	0.0124	-1.02	0.1180	1.11	0.0397	1.02	0.9331
PIK3CD	5293	TC01000118.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta; phosphoinositide-3-kinase, catalytic, delta polypeptide	1.06	0.0037	1.03	0.0935	-1.03	0.2896	1.04	0.0306	-1.01	0.1673	1.02	0.9668
PIK3R1	5295	TC05000291.hg.1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	-1.16	0.0003	1.05	0.1319	1.21	0.0003	1.01	0.8662	1.17	0.0131	-1.03	0.3982
PIK3R2	5296	TC19002628.hg.1	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	1.1	0.0528	1.07	0.1774	-1.02	0.4858	1.12	0.0020	1.02	0.4725	1.04	0.1096
PKM	5315	TC15002776.hg.1	pyruvate kinase, muscle	1.05	0.0269	1.08	0.0070	1.04	0.3197	1.07	0.0002	1.02	0.2409	-1.02	0.8313
PLAUR	5329	TC19001593.hg.1	plasminogen activator, urokinase receptor	1.1	0.0016	1.16	0.0016	1.05	0.3185	1.12	0.0008	1.01	0.8915	-1.04	0.2478
PLCG1	5335	TC20000303.hg.1	phospholipase C, gamma 1	1.07	0.0246	1.14	0.0010	1.06	0.1005	1.15	0.0001	1.07	0.0128	1.01	0.4432
PLCG2	5336	TC16000642.hg.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	1.07	0.2072	1.05	0.1756	-1.02	0.9361	1.04	0.0477	-1.03	0.9141	-1	0.9978
PLCG2	5336	TC16000643.hg.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.15	0.0047	-1.2	0.0001	-1.05	0.1367	-1.19	0.0005	-1.04	0.2429	1.01	0.9192
PRKCA	5578	TC17000783.hg.1	protein kinase C, alpha	-1.15	0.0035	-1.1	0.0268	1.05	0.2808	-1.05	0.0970	1.1	0.0180	1.05	0.1872
PRKCB	5579	TC16000260.hg.1	protein kinase C, beta	1.11	0.0001	1.06	0.0090	-1.05	0.0643	1.1	0.0008	-1.01	0.4773	1.04	0.2536
PRKCG	5582	TC19000866.hg.1	protein kinase C, gamma	1.19	0.0007	1.13	0.0403	-1.05	0.0651	1.13	0.0043	-1.05	0.1109	-1	0.4667
MAPK1	5594	TC22000547.hg.1	mitogen-activated protein kinase 1	-1.03	0.8452	1.03	0.1608	1.05	0.1010	1	0.9763	1.03	0.7915	-1.03	0.0537
MAPK3	5595	TC16001021.hg.1	mitogen-activated protein kinase 3	1.08	0.0258	1.05	0.2006	-1.03	0.3105	1.08	0.0170	-1.01	0.8641	1.03	0.3112
MAP2K1	5604	TC15000613.hg.1	mitogen-activated protein kinase kinase 1	1.23	0.0000	1.3	0.0000	1.06	0.0454	1.29	0.0000	1.05	0.0395	-1.01	0.8193
MAP2K2	5605	TC19001058.hg.1	mitogen-activated protein kinase kinase 2	1.07	0.0747	1.08	0.1089	1.01	0.9078	1.11	0.0061	1.04	0.3812	1.03	0.3464
RELA	5970	TC11001939.hg.1	v-rel avian reticuloendotheliosis viral oncogene homolog A; v-rel reticuloendotheliosis viral	-1.07	0.0494	-1.07	0.0590	1	0.8477	-1.07	0.0333	1.01	0.8109	1	0.6803

			oncogene homolog A (avian)												
RORC	6097	TC01006373.hg.1	RAR-related orphan receptor C	1.11	0.0004	1.11	0.0000	1.01	0.4874	1.13	0.0000	1.02	0.2115	1.01	0.5797
RPS6	6194	TC09000938.hg.1	ribosomal protein S6	1.05	0.1394	1.13	0.0264	1.08	0.1996	1.05	0.2094	-1	0.3904	-1.08	0.0526
RPS6KB1	6198	TC17000729.hg.1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.2	0.0000	-1.15	0.0000	1.04	0.0892	-1.18	0.0000	1.02	0.4990	-1.02	0.1274
RPS6KB2	6199	TC11000691.hg.1	ribosomal protein S6 kinase, 70kDa, polypeptide 2	1.07	0.1789	1.03	0.7790	-1.04	0.3016	1.06	0.2883	-1.01	0.8856	1.03	0.4279
CCL2	6347	TC17000383.hg.1	chemokine (C-C motif) ligand 2	1.01	0.6685	1.08	0.0734	1.07	0.1662	1.04	0.6008	1.03	0.8954	-1.04	0.2712
CXCL6	6372	TC04000409.hg.1	chemokine (C-X-C motif) ligand 6; chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	1.09	0.0071	1.04	0.1880	-1.06	0.0464	1.05	0.0748	-1.04	0.1511	1.02	0.4960
SELL	6402	TC01003500.hg.1	selectin L	-1.44	0.0001	-1.62	0.0000	-1.13	0.0528	-1.72	0.0000	-1.2	0.0114	-1.07	0.3195
SLC2A1	6513	TC01002578.hg.1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.16	0.0011	-1.11	0.0100	1.05	0.0231	-1.17	0.0009	-1.01	0.5102	-1.06	0.0126
SLC2A3	6515	TC12001170.hg.1	solute carrier family 2 (facilitated glucose transporter), member 3	1.24	0.0012	1.38	0.0000	1.11	0.0216	1.34	0.0000	1.08	0.1944	-1.03	0.1175
SLC11A1	6556	TC02001300.hg.1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.08	0.0014	1.04	0.0301	-1.04	0.0340	1.05	0.0583	-1.03	0.0791	1	0.8528
STAT3	6774	TC17001531.hg.1	signal transducer and activator of transcription 3 (acute-phase response factor)	1.25	0.0000	1.33	0.0000	1.06	0.0488	1.31	0.0000	1.05	0.0510	-1.01	0.5966
STAT4	6775	TC02002625.hg.1	signal transducer and activator of transcription 4	1.18	0.0000	1.15	0.0008	-1.03	0.3524	1.19	0.0002	1.01	0.5882	1.04	0.2525
TCEB1	6921	TC08001332.hg.1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.01	0.9366	1.04	0.0981	1.04	0.0332	-1.01	0.8946	-1.01	0.9297	-1.05	0.0558
TCEB2	6923	TC16000791.hg.1	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.11	0.0081	1.08	0.0116	-1.04	0.6138	1.07	0.0457	-1.04	0.7267	-1	0.9741

TCF7	6932	TC05000657.hg.1	transcription factor 7 (T-cell specific, HMG-box)	1.19	0.0428	1.3	0.0740	1.09	0.9707	1.27	0.0023	1.07	0.1713	-1.02	0.2620
TEK	7010	TC09000121.hg.1	TEK tyrosine kinase, endothelial	1.05	0.0110	-1	0.3337	-1.05	0.2763	1.01	0.5918	-1.05	0.0798	1.01	0.6379
TF; TFP1	7018	TC03000723.hg.1	transferrin; transferrin pseudogene 1	1.11	0.0035	1.03	0.1072	-1.08	0.0597	1.03	0.1755	-1.08	0.0276	1.01	0.7031
TFF3	7033	TC21000484.hg.1	trefoil factor 3 (intestinal)	1.04	0.1176	1.01	0.5098	-1.03	0.6036	-1.04	0.5879	-1.08	0.1253	-1.05	0.3648
TFRC	7037	TC03002155.hg.1	transferrin receptor; transferrin receptor (p90, CD71)	-1.15	0.0578	-1.07	0.1338	1.08	0.3651	-1.17	0.0129	-1.02	0.7328	-1.09	0.1279
TGFA	7039	TC02001963.hg.1	transforming growth factor, alpha	1.09	0.0005	1.05	0.0331	-1.04	0.0535	1.07	0.0044	-1.02	0.1597	1.02	0.4619
TGFB1	7040	TC19001553.hg.1	transforming growth factor, beta 1	1.23	0.0360	1.39	0.0172	1.13	0.7692	1.36	0.0001	1.1	0.2233	-1.03	0.3741
TGFB3	7043	TC14001326.hg.1	transforming growth factor, beta 3	1.04	0.1534	1	0.7887	-1.04	0.2633	1.01	0.9130	-1.04	0.2043	1	0.8804
THBS1	7057	TC15000270.hg.1	thrombospondin 1	1.07	0.0164	1.04	0.3193	-1.03	0.1516	1.03	0.0891	-1.03	0.1258	-1.01	0.6711
TIMP1	7076	TC0X000238.hg.1	TIMP metallopeptidase inhibitor 1	1.19	0.0009	1.14	0.0048	-1.04	0.1679	1.11	0.0241	-1.07	0.0412	-1.02	0.3417
TLR4	7099	TC09000601.hg.1	toll-like receptor 4	1.1	0.0024	1.01	0.9914	-1.09	0.0128	1.01	0.9840	-1.09	0.0127	-1	0.9807
TNF	7124	TC06000371.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TNF	7124	TC6_apd_hap 1000036.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.11	0.1761	1.11	0.1906	1	0.7617	1.18	0.0733	1.06	0.8036	1.06	0.4959
TNF	7124	TC6_cox_hap 2000067.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TNF	7124	TC6_dbb_hap 3000058.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TNF	7124	TC6_mann_hap 4000059.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TNF	7124	TC6_mcf_hap 5000053.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TNF	7124	TC6_qbl_hap 6000058.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579

TNF	7124	TC6_ssto_hap 7000054.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.14	0.0634	1.12	0.1120	-1.01	0.5901	1.15	0.0421	1.01	0.7316	1.02	0.7579
TPI1	7167	TC12000096.hg.1	triosephosphate isomerase 1	-1.12	0.0057	-1.06	0.0630	1.05	0.1838	-1.1	0.0044	1.02	0.6600	-1.03	0.2358
TNFRSF4	7293	TC01002086.hg.1	tumor necrosis factor receptor superfamily, member 4	1.11	0.0026	1.05	0.1001	-1.06	0.0539	1.03	0.1431	-1.08	0.1731	-1.02	0.8417
VEGFA	7422	TC06000608.hg.1	vascular endothelial growth factor A	-1.08	0.0014	-1.11	0.0008	-1.03	0.3687	-1.11	0.0004	-1.02	0.2852	1	0.9026
VHL	7428	TC03000055.hg.1	von Hippel-Lindau tumor suppressor, E3 ubiquitin protein ligase; von Hippel-Lindau tumor suppressor	1.01	0.1718	1.07	0.0006	1.06	0.0109	1.04	0.0052	1.03	0.0709	-1.02	0.4321
VIM	7431	TC10000126.hg.1	vimentin	1.16	0.0009	1.19	0.0017	1.03	0.7901	1.21	0.0000	1.04	0.5095	1.02	0.7929
CXCR4	7852	TC02002378.hg.1	chemokine (C-X-C motif) receptor 4	-1.47	0.0000	-1.5	0.0000	-1.02	0.6746	-1.49	0.0000	-1.01	0.6819	1.01	0.9757
EOMES	8320	TC03001257.hg.1	eomesodermin; eomesodermin homolog (Xenopus laevis)	-1.06	0.0160	-1.12	0.0016	-1.06	0.3446	-1.11	0.0056	-1.05	0.4051	1.01	0.9311
CUL2	8453	TC10001173.hg.1	cullin 2	-1.21	0.0001	-1.05	0.0766	1.15	0.0006	-1.09	0.0312	1.11	0.0178	-1.04	0.3220
PIK3R3; RP11-322N21.2	8503	TC01002616.hg.1	phosphoinositide-3-kinase, regulatory subunit 3 (gamma); novel transcript	-1.08	0.0013	1.05	0.0176	1.13	0.0001	-1.01	0.4865	1.07	0.0031	-1.05	0.1705
MKNK1	8569	TC01006353.hg.1	MAP kinase interacting serine/threonine kinase 1	1.14	0.0001	1.09	0.0436	-1.04	0.2896	1.18	0.0011	1.04	0.6019	1.08	0.2173
TNFRSF18	8784	TC01002085.hg.1	tumor necrosis factor receptor superfamily, member 18	1.12	0.0651	1.1	0.3785	-1.02	0.2438	1.07	0.4362	-1.04	0.2179	-1.03	0.9184
NRP1	8829	TC10001166.hg.1	neuropilin 1	1.15	0.0000	1.13	0.0001	-1.01	0.8616	1.15	0.0000	-1	0.7753	1.01	0.9693
EIF4E2	9470	TC02001404.hg.1	eukaryotic translation initiation factor 4E family member 2	-1.15	0.0014	-1.14	0.0019	1.01	0.5509	-1.14	0.0008	1	0.7654	-1	0.3142
AKT3	10000	TC01004040.hg.1	v-akt murine thymoma viral oncogene homolog 3; v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	1.02	0.6228	1.05	0.1930	1.03	0.6188	1.09	0.0036	1.07	0.1564	1.03	0.2417
TBX21	30009	TC17000613.hg.1	T-box 21	1.12	0.0018	1.05	0.0116	-1.07	0.1492	1.09	0.0082	-1.03	0.2405	1.03	0.7596
AK3	50808	TC09000884.hg.1	adenylate kinase 3	-1.07	0.0574	-1.06	0.0258	1	0.9841	-1.04	0.0692	1.02	0.6241	1.02	0.5516
FOXP3	50943	TC0X001031.hg.1	forkhead box P3	1.09	0.0262	1.06	0.0397	-1.03	0.4270	1.05	0.0670	-1.03	0.5815	-1	0.8851
ANGPT4	51378	TC20000546.hg.1	angiopoietin 4	1.1	0.0240	1.06	0.1083	-1.04	0.1252	1.05	0.1434	-1.05	0.2681	-1.01	0.9846

EGLN1	54583	TC01003968.hg.1	egl-9 family hypoxia-inducible factor 1; egl nine homolog 1 (C. elegans)	-1.24	0.0003	-1.1	0.0053	1.13	0.0083	-1.09	0.0222	1.14	0.1000	1.01	0.4745
HIF1AN	55662	TC10000724.hg.1	hypoxia inducible factor 1, alpha subunit inhibitor	-1.03	0.2697	1.01	0.3951	1.05	0.0685	-1	0.9558	1.03	0.2101	-1.02	0.1830
HAMP	57817	TC19000464.hg.1	hepcidin antimicrobial peptide	1.17	0.0006	1.04	0.4512	-1.13	0.0024	1.06	0.1961	-1.11	0.0240	1.02	0.5047
XPNPEP3; RBX1	63929	TC22000327.hg.1	X-prolyl aminopeptidase (aminopeptidase P) 3, putative; ring-box 1, E3 ubiquitin protein ligase; ring-box 1	-1.07	0.0273	-1.03	0.3686	1.04	0.0769	-1.08	0.0219	-1	0.4719	-1.04	0.0814
HKDC1	80201	TC10000418.hg.1	hexokinase domain containing 1	1.04	0.3694	-1.01	0.6689	-1.05	0.7304	-1.01	0.4528	-1.05	0.0548	1	0.2675
PROK1	84432	TC01000966.hg.1	prokineticin 1	1.08	0.1628	1.08	0.1714	1	0.9413	1.08	0.1089	1	0.6233	-1	0.5755
RETNLB	84666	TC03001633.hg.1	resistin like beta	1.1	0.0291	1.05	0.0648	-1.04	0.3855	1.07	0.0442	-1.03	0.5277	1.01	0.7358
EGLN2	112398	TC19002634.hg.1	egl-9 family hypoxia-inducible factor 2	1	0.9012	-1.02	0.7454	-1.02	0.6541	-1.01	0.9535	-1.01	0.8172	1.01	0.7497
EGLN3	112399	TC14001022.hg.1	egl-9 family hypoxia-inducible factor 3; egl nine homolog 3 (C. elegans)	1.08	0.0023	1.06	0.1415	-1.02	0.5786	1.08	0.0073	1.01	0.5343	1.02	0.3651
EIF4E1B	253314	TC05001004.hg.1	eukaryotic translation initiation factor 4E family member 1B	1.1	0.0049	1.05	0.0626	-1.04	0.0476	1.08	0.0402	-1.02	0.2044	1.02	0.5248
ENO4	387712	TC10000848.hg.1	enolase family member 4	1.08	0.0014	1.04	0.2461	-1.04	0.0633	1.04	0.0627	-1.04	0.0638	1	0.6384

Supplementary Table S3. Expression fold changes of 175 of the 176 HIF-related genes (one gene was not present on the microarray).The 175 genes are represented by 184 transcript cluster IDs analyzed in human Jurkat T cells exposed to different gravitational conditions during a suborbital ballistic rocket flight (TEXUS-51). The analysis was made with the Affymetrix GeneChip® Human Transcriptome Array (Thermo Fisher Scientific, Waltham, MA, USA).

				H/W 1g GC vs CC		BL-TX hyp-g vs H/W 1g GC		1g IF vs BL-TX hyp-g		BL-TX hyp-g vs 1gIF		µg vs 1g IF		1g IF vs H/W 1g GC		µg vs.BL-TX hyp-g		ug vs H/W 1g GC	
Gene Symbol	**Entrez ID**	**Transcript Cluster ID**	**Description**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**
ADM	133	TC11000182.hg.1	adrenomedullin	1.44	0.0000	-1.12	0.0274	1.18	0.0006	-1.18	0.0006	-1.24	0.0003	1.05	0.2867	-1.05	0.6792	-1.18	0.0140
ADORA2A	135	TC22001457.hg.1	adenosine A2a receptor	1.28	0.0000	-1.17	0.0003	1.12	0.0010	-1.12	0.0010	-1.1	0.0076	-1.04	0.3776	1.02	0.5504	-1.14	0.0023
ADRA1B	147	TC05000889.hg.1	adrenoceptor alpha 1B; adrenergic, alpha-1B-, receptor	1.44	0.0000	-1.1	0.0509	1.12	0.0121	-1.12	0.0121	-1.2	0.0007	1.02	0.8496	-1.08	0.1503	-1.18	0.0051
AKT1	207	TC14001560.hg.1	v-akt murine thymoma viral oncogene homolog 1	1.19	0.0000	1.08	0.0624	1.09	0.0141	-1.09	0.0141	-1.07	0.0083	1.18	0.0000	1.03	0.2167	1.11	0.0000
AKT2	208	TC19001532.hg.1	v-akt murine thymoma viral oncogene homolog 2	1.11	0.0001	-1.09	0.0008	1.07	0.0017	-1.07	0.0017	-1.04	0.0135	-1.02	0.9553	1.02	0.1226	-1.06	0.0058
ALDOA	226	TC16000338.hg.1	aldolase A, fructose-bisphosphate	1.11	0.0001	-1.02	0.1710	1.06	0.0067	-1.06	0.0067	-1.06	0.0445	1.04	0.0314	1	0.1606	-1.02	0.8587
ALDOC	230	TC17001301.hg.1	aldolase C, fructose-bisphosphate	-1.78	0.0000	-1.05	0.1519	1.05	0.0906	-1.05	0.0906	1.04	0.9896	-1	0.6856	1.09	0.0558	1.04	0.5625
ANGPT1	284	TC08001521.hg.1	angiopoietin 1	1.14	0.0001	-1.04	0.0972	1.01	0.0738	-1.01	0.0738	-1.01	0.0199	-1.03	0.8689	-1	0.8876	-1.04	0.0320
ANGPT2	285	TC08000902.hg.1	angiopoietin 2	1.19	0.0000	-1.07	0.0038	1.08	0.0037	-1.08	0.0037	-1.06	0.0091	1.01	0.5519	1.02	0.6719	-1.06	0.0225
ARG1	383	TC06000983.hg.1	arginase 1; arginase, liver	1.21	0.0001	-1.07	0.0854	1.05	0.0203	-1.05	0.0203	-1.05	0.0047	-1.03	0.8130	1	0.7983	-1.07	0.0361
ARNT	405	TC01003212.hg.1	aryl hydrocarbon receptor nuclear translocator	-1.33	0.0000	1.1	0.0271	-1.05	0.1282	1.05	0.1282	1.05	0.0184	1.05	0.1302	-1	0.6735	1.1	0.0036
BCL2	596	TC18000554.hg.1	B-cell CLL/lymphoma 2	-1.66	0.0000	1.33	0.0012	-1.14	0.0018	1.14	0.0018	1.11	0.0201	1.17	0.0301	-1.03	0.6849	1.29	0.0030
CXCR5	643	TC11001073.hg.1	chemokine (C-X-C motif) receptor 5	1.37	0.0011	-1.17	0.1156	1.14	0.0116	-1.14	0.0116	-1.2	0.0073	-1.03	0.9068	-1.05	0.5834	-1.23	0.0605
CA9	768	TC09000191.hg.1	carbonic anhydrase IX	1.29	0.0002	-1.17	0.0121	1.21	0.0004	-1.21	0.0004	-1.25	0.0001	1.03	0.6504	-1.03	0.4887	-1.21	0.0037
CAMK2A	815	TC05001934.hg.1	calcium/calmodulin-dependent protein kinase II alpha	1.29	0.0000	-1.12	0.0054	1.09	0.0002	-1.09	0.0002	-1.09	0.0025	-1.04	0.6777	-1.01	0.6866	-1.13	0.0089
CAMK2B	816	TC07001338.hg.1	calcium/calmodulin-dependent protein kinase II beta	1.34	0.0000	-1.13	0.0048	1.12	0.0000	-1.12	0.0000	-1.13	0.0001	-1	0.9979	-1	0.8750	-1.13	0.0040
CAMK2D	817	TC04001486.hg.1	calcium/calmodulin-dependent protein kinase II delta	-1.23	0.0000	1.06	0.0024	-1.04	0.0723	1.04	0.0723	1.03	0.2759	1.02	0.3168	-1.01	0.2969	1.05	0.0200

CAMK2G	818	TC10001420.hg.1	calcium/calmodulin-dependent protein kinase II gamma	1.11	0.0005	-1.04	0.0608	-1.02	0.2873	1.02	0.2873	1.01	0.4377	-1.06	0.0079	-1.01	0.6402	-1.05	0.0157
CAMP	820	TC03000276.hg.1	cathelicidin antimicrobial peptide	1.25	0.0001	-1.13	0.0117	1.14	0.0020	-1.14	0.0020	-1.14	0.0079	1	0.6077	-1	0.8511	-1.13	0.0389
CD36	948	TC07000509.hg.1	CD36 molecule (thrombospondin receptor)	1.12	0.0000	-1.04	0.0742	1.04	0.0664	-1.04	0.0664	-1.05	0.0441	1.01	0.8330	-1	0.5733	-1.04	0.0556
CDKN1A	1026	TC06000532.hg.1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.31	0.0001	-1.12	0.0515	1.14	0.0003	-1.14	0.0003	-1.13	0.0002	1.02	0.4898	1.01	0.7629	-1.11	0.0298
CDKN1B	1027	TC12000178.hg.1	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-1.05	0.0071	1.06	0.0119	-1.06	0.0334	1.06	0.0334	1.05	0.0906	-1.01	0.9637	-1.01	0.7870	1.04	0.0856
CCR1	1230	TC03001355.hg.1	chemokine (C-C motif) receptor 1	1.08	0.0154	-1.01	0.8140	1.07	0.4070	-1.07	0.4070	-1.08	0.3369	1.06	0.3489	-1.01	0.8635	-1.02	0.9466
CCR5	1234	TC03000256.hg.1	chemokine (C-C motif) receptor 5 (gene/pseudogene); chemokine (C-C motif) receptor 5	1.22	0.0001	-1.09	0.0220	1.11	0.0232	-1.11	0.0232	-1.09	0.0915	1.02	0.8741	1.02	0.5482	-1.07	0.0886
CCR7	1236	TC17001466.hg.1	chemokine (C-C motif) receptor 7	1.14	0.0116	-1.02	0.8843	1.07	0.1872	-1.07	0.1872	-1.22	0.0012	1.05	0.1809	-1.15	0.0197	-1.17	0.0044
CREBBP	1387	TC16000823.hg.1	CREB binding protein	-1.43	0.0000	1.44	0.0000	-1.17	0.0010	1.17	0.0010	1.18	0.0008	1.23	0.0001	1.01	0.9219	1.45	0.0000
MAPK14	1432	TC06000523.hg.1	mitogen-activated protein kinase 14	-1.81	0.0000	1.14	0.0029	-1.15	0.0044	1.15	0.0044	1.12	0.0171	-1.01	0.4962	-1.03	0.6196	1.11	0.0093
CTLA4	1493	TC02001201.hg.1	cytotoxic T-lymphocyte-associated protein 4	1.26	0.0000	-1.1	0.0199	1.11	0.0064	-1.11	0.0064	-1.11	0.0072	1.01	0.6480	-1	0.6788	-1.1	0.0258
CTSD	1509	TC11003472.hg.1	cathepsin D	1.27	0.0000	-1.11	0.0011	1.1	0.0158	-1.1	0.0158	-1.17	0.0452	-1.01	0.9363	-1.07	0.8782	-1.19	0.0338
CYBB	1536	TC0X000171.hg.1	cytochrome b-245, beta polypeptide	1.15	0.0006	-1.04	0.5299	1.04	0.0444	-1.04	0.0444	-1.04	0.0054	1	0.3502	1	0.6708	-1.04	0.3013
DEFB1	1672	TC08000906.hg.1	defensin, beta 1	1.34	0.0001	-1.05	0.1599	1.1	0.0236	-1.1	0.0236	-1.14	0.0098	1.04	0.2247	-1.04	0.9912	-1.1	0.1020
S1PR1	1901	TC01000909.hg.1	sphingosine-1-phosphate receptor 1	1.03	0.2497	1.06	0.0096	-1.12	0.0001	1.12	0.0001	1.09	0.0007	-1.06	0.0580	-1.03	0.2001	1.03	0.0933
EDN1	1906	TC06000087.hg.1	endothelin 1	1.16	0.0008	-1.01	0.3083	1.13	0.0023	-1.13	0.0023	-1.11	0.0035	1.12	0.0689	1.01	0.6917	1.01	0.4461
EGF	1950	TC04000568.hg.1	epidermal growth factor; epidermal growth factor (beta-urogastrone)	1.21	0.0000	-1.05	0.0521	1.05	0.0062	-1.05	0.0062	-1.06	0.0015	1.01	0.4393	-1.01	0.9587	-1.05	0.0217
EGFR	1956	TC07000328.hg.1	epidermal growth factor receptor; epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	1.28	0.0000	-1.1	0.0104	1.11	0.0016	-1.11	0.0016	-1.12	0.0014	1.02	0.8719	-1.01	0.8103	-1.1	0.0070
EIF4E	1977	TC04001403.hg.1	eukaryotic translation initiation factor 4E	-1.49	0.0000	1.22	0.0019	-1.19	0.0018	1.19	0.0018	1.13	0.0547	1.02	0.5959	-1.05	0.3596	1.16	0.0418

EIF4EBP1	1978	TC08000281.hg.1	eukaryotic translation initiation factor 4E binding protein 1	1.42	0.0000	-1.07	0.1420	1.18	0.0001	-1.18	0.0001	-1.17	0.0000	1.1	0.0117	1.01	0.9521	-1.07	0.1118
ENG	2022	TC09001609.hg.1	endoglin	1.3	0.0001	-1.13	0.0242	1.16	0.0001	-1.16	0.0001	-1.21	0.0000	1.02	0.5388	-1.04	0.1320	-1.18	0.0032
ENO1	2023	TC01002175.hg.1	enolase 1, (alpha)	-1.22	0.0000	1.07	0.1896	-1.05	0.6694	1.05	0.6694	1.06	0.0211	1.03	0.3432	1.01	0.0858	1.08	0.0002
ENO2	2026	TC12000099.hg.1	enolase 2 (gamma, neuronal)	-1.09	0.0019	-1.05	0.0738	1.02	0.0966	-1.02	0.0966	1.01	0.5888	-1.03	0.9731	1.03	0.0794	-1.02	0.4443
ENO3	2027	TC17000058.hg.1	enolase 3 (beta, muscle)	1.15	0.0000	-1.12	0.0000	1.1	0.0009	-1.1	0.0009	-1.07	0.0038	-1.02	0.3847	1.03	0.3039	-1.09	0.0002
EP300; MIR1281	2033	TC22000332.hg.1	E1A binding protein p300; microRNA 1281	-1.63	0.0000	1.56	0.0001	-1.34	0.0002	1.34	0.0002	1.42	0.0011	1.17	0.0545	1.06	0.9983	1.65	0.0004
EPAS1	2034	TC02000281.hg.1	endothelial PAS domain protein 1	1.28	0.0000	-1.11	0.0008	1.1	0.0000	-1.1	0.0000	-1.11	0.0000	-1.01	0.4173	-1.01	0.9149	-1.12	0.0004
EPO	2056	TC07000632.hg.1	erythropoietin	1.42	0.0000	-1.12	0.0655	1.11	0.0092	-1.11	0.0092	-1.22	0.0065	-1.01	0.9958	-1.11	0.3481	-1.24	0.0271
ERBB2; MIR4728	2064	TC17000480.hg.1	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2; microRNA 4728; v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	1.28	0.0000	-1.15	0.0016	1.17	0.0002	-1.17	0.0002	-1.17	0.0006	1.01	0.8404	1	0.8773	-1.15	0.0038
FLT1	2321	TC13000517.hg.1	fms-related tyrosine kinase 1; fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	-1.67	0.0000	1.32	0.0000	-1.2	0.0003	1.2	0.0003	1.13	0.0289	1.11	0.0023	-1.06	0.3894	1.25	0.0005
FN1	2335	TC02002747.hg.1	fibronectin 1	1.22	0.0000	-1.07	0.0128	1.08	0.0005	-1.08	0.0005	-1.09	0.0013	1.01	0.9530	-1	0.9925	-1.08	0.0135
MTOR	2475	TC01002197.hg.1	mechanistic target of rapamycin (serine/threonine kinase)	-1.22	0.0001	1.06	0.2996	-1.08	0.0448	1.08	0.0448	1.1	0.0046	-1.02	0.6494	1.03	0.2711	1.09	0.0617
GAPDH	2597	TC12000084.hg.1	glyceraldehyde-3-phosphate dehydrogenase	1.02	0.2816	-1.02	0.0892	-1.03	0.7456	1.03	0.7456	1.04	0.1354	-1.05	0.1880	1.01	0.0639	-1.01	0.8717
GPI	2821	TC19000442.hg.1	glucose-6-phosphate isomerase	-1.13	0.0016	-1.03	0.1377	1.03	0.0873	-1.03	0.0873	-1.01	0.4773	1	0.4425	1.02	0.1465	-1.01	0.9241
MKNK2	2872	TC19001019.hg.1	MAP kinase interacting serine/threonine kinase 2	1.2	0.0000	1.01	0.8171	1.09	0.0110	-1.09	0.0110	-1.08	0.0026	1.1	0.0009	1.01	0.8116	1.02	0.4849
CXCL2	2920	TC04001286.hg.1	chemokine (C-X-C motif) ligand 2	1.27	0.0001	-1.12	0.0153	1.1	0.0012	-1.1	0.0012	-1.13	0.0002	-1.02	0.9801	-1.03	0.2381	-1.16	0.0033
HDAC2	3066	TC06002035.hg.1	histone deacetylase 2	-2.04	0.0000	1.41	0.0003	-1.26	0.0092	1.26	0.0092	1.11	0.0973	1.12	0.1679	-1.14	0.5062	1.23	0.0125
HIF1A	3091	TC14002197.hg.1	hypoxia inducible factor 1, alpha subunit (basic helix-	-2.38	0.0000	1.66	0.0007	-1.55	0.0009	1.55	0.0009	1.3	0.0362	1.07	0.2663	-1.19	0.3220	1.4	0.0124

			loop-helix transcription factor)															
HK1	3098	TC10000419.hg.1	hexokinase 1	-1.26	0.0000	1.08	0.1621	-1.01	0.3033	1.01	0.3033	1.03	0.3802	1.07	0.0006	1.02	0.1318	1.1	0.0002
HK2	3099	TC02000466.hg.1	hexokinase 2	1.09	0.0048	-1.06	0.0728	-1.18	0.0001	1.18	0.0001	1.28	0.0001	-1.25	0.0000	1.09	0.4785	1.03	0.3288
HK3	3101	TC05002100.hg.1	hexokinase 3 (white cell)	1.42	0.0000	-1.2	0.0017	1.18	0.0001	-1.18	0.0001	-1.14	0.0002	-1.02	0.6490	1.03	0.7576	-1.16	0.0029
HMOX1	3162	TC22000259.hg.1	heme oxygenase (decycling) 1	1.23	0.0001	-1.12	0.0089	1.18	0.0001	-1.18	0.0001	-1.24	0.0000	1.06	0.5567	-1.05	0.0857	-1.17	0.0009
ICAM1	3383	TC19000174.hg.1	intercellular adhesion molecule 1	1.43	0.0000	-1.14	0.0075	1.14	0.0010	-1.14	0.0010	-1.18	0.0015	1	0.6940	-1.03	0.9306	-1.17	0.0103
IFNG	3458	TC12001696.hg.1	interferon, gamma	1.14	0.0001	1.01	0.4260	1.04	0.4784	-1.04	0.4784	-1.07	0.3323	1.05	0.2564	-1.03	0.6723	-1.02	0.9166
IFNGR1	3459	TC06002152.hg.1	interferon gamma receptor 1	-1.61	0.0000	1.36	0.0000	-1.15	0.0232	1.15	0.0232	1.07	0.1987	1.18	0.0003	-1.07	0.5233	1.26	0.0015
IFNGR2	3460	TC21000129.hg.1	interferon gamma receptor 2 (interferon gamma transducer 1)	-1.07	0.0044	1.01	0.7075	1.02	0.1189	-1.02	0.1189	-1.01	0.7557	1.03	0.1733	1.01	0.2502	1.02	0.3598
IGF1	3479	TC12001890.hg.1	insulin-like growth factor 1 (somatomedin C)	1.18	0.0000	-1.05	0.0590	1.08	0.0214	-1.08	0.0214	-1.04	0.0777	1.02	0.3720	1.03	0.1506	-1.02	0.3308
IGF1R	3480	TC15000949.hg.1	insulin-like growth factor 1 receptor	-1.05	0.0039	1.08	0.0237	-1.05	0.3860	1.05	0.3860	1.07	0.0078	1.03	0.0605	1.02	0.1299	1.1	0.0001
IGF1R	3480	TC15000951.hg.1	insulin-like growth factor 1 receptor	-1.03	0.1524	-1.08	0.1386	1.14	0.0150	-1.14	0.0150	-1.1	0.1067	1.05	0.1625	1.03	0.3011	-1.04	0.7725
IGFBP1	3484	TC07000294.hg.1	insulin-like growth factor binding protein 1	1.33	0.0000	-1.22	0.0006	1.16	0.0028	-1.16	0.0028	-1.04	0.1031	-1.05	0.4007	1.11	0.1286	-1.09	0.0270
IGFBP2	3485	TC02001281.hg.1	insulin-like growth factor binding protein 2, 36kDa	1.08	0.0012	1	0.8647	1.11	0.0013	-1.11	0.0013	-1.11	0.0000	1.12	0.0000	1	0.9946	1	0.7720
IGFBP3	3486	TC07001355.hg.1	insulin-like growth factor binding protein 3	1.34	0.0000	-1.13	0.0113	1.15	0.0000	-1.15	0.0000	-1.19	0.0000	1.01	0.7689	-1.04	0.3040	-1.18	0.0030
IL1B	3553	TC02002219.hg.1	interleukin 1, beta	1.26	0.0000	-1.1	0.0043	1.07	0.0013	-1.07	0.0013	-1.06	0.0017	-1.02	0.4661	1.01	0.6974	-1.08	0.0038
IL6	3569	TC07000137.hg.1	interleukin 6; interleukin 6 (interferon, beta 2)	1.19	0.0000	-1.04	0.0202	1.08	0.0010	-1.08	0.0010	-1.1	0.0002	1.04	0.0585	-1.02	0.4600	-1.06	0.0076
IL6R	3570	TC01001276.hg.1	interleukin 6 receptor	1.39	0.0000	-1.13	0.0192	1.18	0.0000	-1.18	0.0000	-1.23	0.0001	1.05	0.4765	-1.04	0.6779	-1.17	0.0147
CXCL8; IL8	3576	TC04000408.hg.1	chemokine (C-X-C motif) ligand 8; interleukin 8	1.17	0.0001	-1.05	0.4581	1.05	0.3924	-1.05	0.3924	-1.11	0.0044	1	0.9693	-1.06	0.1255	-1.11	0.0092
IL12A	3592	TC03000870.hg.1	interleukin 12A; interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	1.26	0.0000	-1.05	0.1455	1.12	0.0027	-1.12	0.0027	-1.15	0.0010	1.07	0.0436	-1.02	0.8589	-1.07	0.0973
TNFRSF9	3604	TC01002163.hg.1	tumor necrosis factor receptor superfamily, member 9	1.2	0.0001	-1.11	0.0060	1.14	0.0001	-1.14	0.0001	-1.12	0.0007	1.03	0.4978	1.02	0.3804	-1.09	0.0208

INS; IGF2; INS-IGF2; AC132217.4	3630	TC11001274.hg.1	insulin; insulin-like growth factor 2 (somatomedin A); INS-IGF2 readthrough; novel transcript, 3'_overlapping_ncRNA IGF2	1.35	0.0000	-1.14	0.0050	1.16	0.0000	-1.16	0.0000	-1.15	0.0004	1.01	0.7546	1	0.7645	-1.14	0.0079
INSR	3643	TC19001111.hg.1	insulin receptor	1.24	0.0000	-1.09	0.0036	-1.04	0.1528	1.04	0.1528	1.05	0.0382	-1.14	0.0001	1	0.4553	-1.09	0.0145
ITGAM	3684	TC16000374.hg.1	integrin, alpha M (complement component 3 receptor 3 subunit)	1.28	0.0000	-1.11	0.0043	1.13	0.0001	-1.13	0.0001	-1.15	0.0005	1.02	0.6855	-1.02	0.9317	-1.13	0.0066
ITGB2	3689	TC21000538.hg.1	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	1.27	0.0000	-1.13	0.0000	1.09	0.0002	-1.09	0.0002	-1.06	0.0130	-1.04	0.0122	1.03	0.3117	-1.1	0.0002
KDR	3791	TC04001208.hg.1	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.24	0.0000	-1.09	0.0091	1.08	0.0000	-1.08	0.0000	-1.07	0.0001	-1.01	0.8950	1.01	0.5854	-1.08	0.0138
KRT14	3861	TC17001513.hg.1	keratin 14	1.23	0.0007	-1.09	0.1528	1.11	0.0048	-1.11	0.0048	-1.13	0.0001	1.02	0.7106	-1.02	0.0501	-1.11	0.0119
KRT18	3875	TC12000424.hg.1	keratin 18	1.19	0.0011	-1.13	0.0122	1.14	0.0086	-1.14	0.0086	-1.11	0.0189	1.01	0.5785	1.03	0.4416	-1.1	0.0176
KRT19	3880	TC17002906.hg.1	keratin 19	1.34	0.0000	-1.12	0.0124	1.11	0.0002	-1.11	0.0002	-1.11	0.0029	-1	0.9142	-1	0.8112	-1.12	0.0194
LAG3	3902	TC12000091.hg.1	lymphocyte-activation gene 3	1.24	0.0009	-1.11	0.0529	1.14	0.0013	-1.14	0.0013	-1.16	0.0012	1.03	0.6702	-1.01	0.7919	-1.12	0.0337
LDHA	3939	TC11000240.hg.1	lactate dehydrogenase A	-2.29	0.0000	1.4	0.0017	-1.23	0.0116	1.23	0.0116	1.16	0.1248	1.14	0.2404	-1.06	0.4053	1.32	0.0222
LEP	3952	TC07000768.hg.1	leptin	1.23	0.0000	-1.05	0.0335	1.16	0.0004	-1.16	0.0004	-1.22	0.0006	1.11	0.0944	-1.04	0.5312	-1.09	0.0386
LRP1	4035	TC12000521.hg.1	low density lipoprotein receptor-related protein 1	1.33	0.0000	-1.14	0.0008	1.15	0.0014	-1.15	0.0014	-1.14	0.0067	1.01	0.3000	1	0.5558	-1.14	0.0024
LTBR	4055	TC12000078.hg.1	lymphotoxin beta receptor (TNFR superfamily, member 3)	1.46	0.0000	-1.14	0.0095	1.22	0.0000	-1.22	0.0000	-1.28	0.0000	1.07	0.1139	-1.05	0.4630	-1.2	0.0031
MMP2	4313	TC16000454.hg.1	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	1.35	0.0000	-1.13	0.0133	1.17	0.0003	-1.17	0.0003	-1.17	0.0009	1.03	0.4497	-1	0.8804	-1.14	0.0219
MMP9	4318	TC20000363.hg.1	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	1.56	0.0000	-1.24	0.0022	1.19	0.0024	-1.19	0.0024	-1.17	0.0004	-1.04	0.3218	1.02	0.8780	-1.21	0.0004
MMP14	4323	TC14000133.hg.1	matrix metallopeptidase 14 (membrane-inserted)	1.3	0.0000	-1.12	0.0017	1.13	0.0011	-1.13	0.0011	-1.1	0.0089	1.01	0.4538	1.03	0.3576	-1.08	0.0061
NFKB1	4790	TC04000526.hg.1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	-1.42	0.0000	1.22	0.0001	-1.18	0.0014	1.18	0.0014	1.24	0.0033	1.03	0.0829	1.05	0.6939	1.28	0.0006

NOS2	4843	TC17002894.hg.1	nitric oxide synthase 2, inducible	1.27	0.0000	-1.11	0.0009	1.15	0.0000	-1.15	0.0000	-1.17	0.0000	1.03	0.2850	-1.02	0.6319	-1.13	0.0011
NOS3; ATG9B	4846	TC07001009.hg.1	nitric oxide synthase 3 (endothelial cell); ATG9 autophagy related 9 homolog B (S. cerevisiae)	1.29	0.0000	-1.12	0.0034	1.19	0.0001	-1.19	0.0001	-1.17	0.0001	1.06	0.1204	1.01	0.8313	-1.1	0.0074
NPPA	4878	TC01002204.hg.1	natriuretic peptide A; natriuretic peptide precursor A	1.41	0.0000	-1.16	0.0050	1.13	0.0349	-1.13	0.0349	-1.15	0.0208	-1.03	0.7555	-1.02	0.7101	-1.18	0.0074
SERPINE1	5054	TC07000643.hg.1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	1.26	0.0000	-1.09	0.0105	1.11	0.0007	-1.11	0.0007	-1.11	0.0023	1.02	0.6033	1	0.5559	-1.09	0.0248
PDGFB	5155	TC22000802.hg.1	platelet-derived growth factor beta polypeptide; platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	1.44	0.0000	-1.15	0.0152	1.16	0.0005	-1.16	0.0005	-1.17	0.0005	1.01	0.7158	-1.01	0.7321	-1.16	0.0099
PDHA1	5160	TC0X000092.hg.1	pyruvate dehydrogenase (lipoamide) alpha 1	-1.33	0.0000	1.11	0.0087	-1.2	0.0002	1.2	0.0002	1.28	0.0008	-1.08	0.3955	1.06	0.6887	1.19	0.0152
PDHA2	5161	TC04000504.hg.1	pyruvate dehydrogenase (lipoamide) alpha 2	1.31	0.0000	-1.14	0.0289	1.13	0.0466	-1.13	0.0466	-1.07	0.4385	-1.01	0.9717	1.06	0.2236	-1.07	0.4100
PDHB	5162	TC03001499.hg.1	pyruvate dehydrogenase (lipoamide) beta	-1.34	0.0000	1.02	0.2627	-1.21	0.0000	1.21	0.0000	1.21	0.0002	-1.19	0.0015	-1	0.8984	1.02	0.4173
PDK1	5163	TC02001031.hg.1	pyruvate dehydrogenase kinase, isozyme 1	-2.3	0.0000	1.17	0.0010	-1.09	0.0284	1.09	0.0284	1.06	0.2242	1.07	0.1210	-1.03	0.4599	1.14	0.0189
PFKFB3	5209	TC10000053.hg.1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	1.04	0.0418	-1.07	0.0043	1.03	0.0613	-1.03	0.0613	-1.05	0.0118	-1.04	0.2920	-1.02	0.4917	-1.09	0.0009
PFKL	5211	TC21000222.hg.1	phosphofructokinase, liver	1.08	0.0011	-1.07	0.0072	1.12	0.0002	-1.12	0.0002	-1.08	0.0051	1.05	0.0464	1.03	0.2326	-1.03	0.1565
PGK1; LOC100652805; LOC100653302	5230	TC0X000425.hg.1	phosphoglycerate kinase 1; uncharacterized LOC100652805; uncharacterized LOC100653302	-1.42	0.0000	1.13	0.0442	-1.12	0.0418	1.12	0.0418	1.12	0.0152	1.01	0.9018	-1	0.6581	1.13	0.0187
ABCB1	5243	TC07001579.hg.1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.16	0.0000	-1.05	0.0196	1.08	0.0005	-1.08	0.0005	-1.08	0.0007	1.03	0.0762	1	0.9580	-1.05	0.0400
PIK3CA	5290	TC03000951.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha; phosphoinositide-3-kinase, catalytic, alpha polypeptide	-3.15	0.0000	1.63	0.0013	-1.38	0.0057	1.38	0.0057	1.29	0.0606	1.18	0.1645	-1.07	0.4944	1.53	0.0127
PIK3CB	5291	TC03001824.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit beta;	-2.54	0.0000	1.36	0.0000	-1.22	0.0045	1.22	0.0045	1.22	0.0206	1.11	0.0102	-1	0.9172	1.36	0.0004

			phosphoinositide-3-kinase, catalytic, beta polypeptide															
PIK3CD	5293	TC01000118.hg.1	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit delta; phosphoinositide-3-kinase, catalytic, delta polypeptide	1.23	0.0000	-1.11	0.0004	1.11	0.0011	-1.11	0.0011	-1.09	0.0036	-1	0.7489	1.02	0.3083	-1.09	0.0013
PIK3R1	5295	TC05000291.hg.1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	-2.16	0.0000	1.21	0.0316	-1.37	0.0003	1.37	0.0003	1.26	0.0042	-1.13	0.1598	-1.09	0.3888	1.11	0.1557
PIK3R2	5296	TC19002628.hg.1	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	1.4	0.0000	-1.04	0.1658	1.13	0.0000	-1.13	0.0000	-1.09	0.0009	1.08	0.0008	1.04	0.3689	-1.01	0.7028
PKM	5315	TC15002776.hg.1	pyruvate kinase, muscle	-1.05	0.0266	1.03	0.8982	-1.02	0.6682	1.02	0.6682	1.03	0.5352	1	0.7094	1	0.2349	1.03	0.1247
PLAUR	5329	TC19001593.hg.1	plasminogen activator, urokinase receptor	1.14	0.0001	-1.15	0.0009	1.17	0.0004	-1.17	0.0004	-1.1	0.0005	1.02	0.8695	1.06	0.1846	-1.08	0.0009
PLCG1	5335	TC20000303.hg.1	phospholipase C, gamma 1	1.07	0.0254	-1.04	0.1283	-1.01	0.3752	1.01	0.3752	1.03	0.1672	-1.05	0.3505	1.02	0.0366	-1.02	0.8886
PLCG2	5336	TC16000642.hg.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	1.15	0.2507	-1.2	0.0248	1.15	0.0451	-1.15	0.0451	-1.07	0.2073	-1.05	0.8229	1.07	0.4281	-1.12	0.1514
PLCG2	5336	TC16000643.hg.1	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.16	0.0001	-1.05	0.2256	-1	0.8491	1	0.8491	1.05	0.0007	-1.05	0.1393	1.05	0.0023	1	0.1912
PRKCA	5578	TC17000783.hg.1	protein kinase C, alpha	-1.65	0.0000	1.41	0.0001	-1.24	0.0017	1.24	0.0017	1.27	0.0035	1.14	0.0111	1.02	0.9409	1.45	0.0002
PRKCB	5579	TC16000260.hg.1	protein kinase C, beta	-1.25	0.0000	1.12	0.0097	-1.19	0.0005	1.19	0.0005	1.29	0.0018	-1.07	0.6120	1.09	0.8331	1.22	0.0157
PRKCG	5582	TC19000866.hg.1	protein kinase C, gamma	1.4	0.0000	-1.15	0.0207	1.16	0.0005	-1.16	0.0005	-1.2	0.0002	1.01	0.6794	-1.03	0.3801	-1.19	0.0065
MAPK1	5594	TC22000547.hg.1	mitogen-activated protein kinase 1	-1.46	0.0000	1.37	0.0001	-1.22	0.0001	1.22	0.0001	1.23	0.0007	1.12	0.0697	1.01	0.9334	1.38	0.0002
MAPK3	5595	TC16001021.hg.1	mitogen-activated protein kinase 3	1.14	0.0000	-1.1	0.0006	1.09	0.0006	-1.09	0.0006	-1.06	0.0150	-1.01	0.7176	1.03	0.1334	-1.07	0.0102
MAP2K1	5604	TC15000613.hg.1	mitogen-activated protein kinase kinase 1	1.09	0.0329	1.07	0.0198	-1.07	0.0004	1.07	0.0004	1.06	0.0191	-1	0.9236	-1.01	0.7388	1.06	0.0804
MAP2K2	5605	TC19001058.hg.1	mitogen-activated protein kinase kinase 2	1.33	0.0000	-1.05	0.1598	1.12	0.0048	-1.12	0.0048	-1.08	0.0141	1.07	0.0144	1.04	0.3195	-1.01	0.6387
RELA	5970	TC11001939.hg.1	v-rel avian reticuloendotheliosis viral oncogene homolog A; v-rel reticuloendotheliosis viral oncogene homolog A (avian)	1.28	0.0000	-1.1	0.0023	1.07	0.0146	-1.07	0.0146	-1.1	0.0182	-1.02	0.7875	-1.02	0.8876	-1.12	0.0159
RORC	6097	TC01006373.hg.1	RAR-related orphan receptor C	1.07	0.0263	-1.11	0.0123	1.13	0.0002	-1.13	0.0002	-1.12	0.0155	1.02	0.5397	1.01	0.5280	-1.1	0.0992
RPS6	6194	TC09000938.hg.1	ribosomal protein S6	-1.52	0.0000	1.32	0.0003	-1.21	0.0057	1.21	0.0057	1.31	0.0022	1.09	0.0253	1.08	0.5444	1.43	0.0001

RPS6KB1	6198	TC17000729.hg.1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.95	0.0000	1.26	0.0012	-1.3	0.0005	1.3	0.0005	1.23	0.0076	-1.03	0.9085	-1.05	0.5062	1.2	0.0139
RPS6KB2	6199	TC11000691.hg.1	ribosomal protein S6 kinase, 70kDa, polypeptide 2	1.28	0.0000	-1.05	0.0790	1.14	0.0009	-1.14	0.0009	-1.09	0.0237	1.09	0.0031	1.05	0.0676	1	0.7795
CCL2	6347	TC17000383.hg.1	chemokine (C-C motif) ligand 2	1.2	0.0094	1.04	0.2735	1.07	0.2604	-1.07	0.2604	-1.21	0.0019	1.11	0.0397	-1.13	0.0277	-1.09	0.2591
CXCL6	6372	TC04000409.hg.1	chemokine (C-X-C motif) ligand 6; chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	1.27	0.0000	-1.08	0.0296	1.13	0.0016	-1.13	0.0016	-1.2	0.0030	1.04	0.2960	-1.07	0.6925	-1.16	0.0408
SELL	6402	TC01003500.hg.1	selectin L	-2.58	0.0000	1.76	0.0003	-1.15	0.1692	1.15	0.1692	1.12	0.2468	1.54	0.0003	-1.03	0.6940	1.72	0.0001
SLC2A1	6513	TC01002578.hg.1	solute carrier family 2 (facilitated glucose transporter), member 1	1.15	0.0000	-1.03	0.0283	1.09	0.0028	-1.09	0.0028	-1.05	0.0448	1.06	0.1585	1.04	0.0663	1	0.5335
SLC2A3	6515	TC12001170.hg.1	solute carrier family 2 (facilitated glucose transporter), member 3	-1.28	0.0000	1.08	0.0563	-1.04	0.1307	1.04	0.1307	1.05	0.0058	1.04	0.3307	1.01	0.2222	1.09	0.0045
SLC11A1	6556	TC02001300.hg.1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.23	0.0000	-1.11	0.0005	1.1	0.0000	-1.1	0.0000	-1.14	0.0000	-1.01	0.6679	-1.03	0.4942	-1.15	0.0003
STAT3	6774	TC17001531.hg.1	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.38	0.0000	1.26	0.0008	-1.08	0.3405	1.08	0.3405	1.08	0.0899	1.16	0.0004	-1.01	0.4956	1.25	0.0002
STAT4	6775	TC02002625.hg.1	signal transducer and activator of transcription 4	1.11	0.0000	-1.04	0.0021	1.05	0.0076	-1.05	0.0076	-1.04	0.0074	1	0.9470	1	0.5876	-1.04	0.0024
TCEB1	6921	TC08001332.hg.1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.31	0.0000	1.08	0.0061	-1.09	0.0010	1.09	0.0010	1.05	0.0682	-1.01	0.9001	-1.04	0.2810	1.04	0.1361
TCEB2	6923	TC16000791.hg.1	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.56	0.0000	1	0.2559	1.09	0.0020	-1.09	0.0020	-1.04	0.0784	1.1	0.0164	1.05	0.0275	1.06	0.2558
TCF7	6932	TC05000657.hg.1	transcription factor 7 (T-cell specific, HMG-box)	-1.09	0.0132	1	0.3095	-1.01	0.8134	1.01	0.8134	-1.02	0.2694	-1.01	0.4197	-1.03	0.3867	-1.03	0.0479
TEK	7010	TC09000121.hg.1	TEK tyrosine kinase, endothelial	1.2	0.0000	-1.05	0.0095	1.06	0.0036	-1.06	0.0036	-1.06	0.0714	1.01	0.9712	-1.01	0.4436	-1.06	0.1079
TF; TFP1	7018	TC03000723.hg.1	transferrin; transferrin pseudogene 1	1.25	0.0000	-1.11	0.0088	1.11	0.0003	-1.11	0.0003	-1.11	0.0027	1.01	0.8895	1	0.4917	-1.11	0.0241
TFF3	7033	TC21000484.hg.1	trefoil factor 3 (intestinal)	1.37	0.0000	-1.12	0.0640	1.19	0.0004	-1.19	0.0004	-1.18	0.0005	1.06	0.0212	1.01	0.9521	-1.11	0.0901

TFRC	7037	TC03002155.hg.1	transferrin receptor; transferrin receptor (p90, CD71)	-2.56	0.0000	1.63	0.0002	-1.45	0.0006	1.45	0.0006	1.3	0.0380	1.12	0.1888	-1.11	0.3455	1.46	0.0086
TGFA	7039	TC02001963.hg.1	transforming growth factor, alpha	1.26	0.0000	-1.12	0.0116	1.15	0.0000	-1.15	0.0000	-1.13	0.0016	1.03	0.3849	1.02	0.4868	-1.1	0.0590
TGFB1	7040	TC19001553.hg.1	transforming growth factor, beta 1	1.21	0.0002	-1.08	0.0489	1.09	0.0342	-1.09	0.0342	-1.05	0.1641	1.01	0.6491	1.04	0.3471	-1.04	0.2857
TGFB3	7043	TC14001326.hg.1	transforming growth factor, beta 3	1.21	0.0002	-1.08	0.0349	1.06	0.0131	-1.06	0.0131	-1.05	0.0255	-1.02	0.7473	1.01	0.6684	-1.07	0.0706
THBS1	7057	TC15000270.hg.1	thrombospondin 1	1.26	0.0000	-1.09	0.0066	1.09	0.0008	-1.09	0.0008	-1.15	0.0013	1	0.8717	-1.05	0.8298	-1.15	0.0061
TIMP1	7076	TC0X000238.hg.1	TIMP metallopeptidase inhibitor 1	1.37	0.0000	-1.14	0.0117	1.2	0.0007	-1.2	0.0007	-1.21	0.0001	1.05	0.2107	-1.01	0.6459	-1.16	0.0036
TLR4	7099	TC09000601.hg.1	toll-like receptor 4	1.24	0.0000	-1.07	0.0559	1.14	0.0009	-1.14	0.0009	-1.12	0.0010	1.06	0.1658	1.01	0.9640	-1.05	0.0631
TNF	7124	TC06000371.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_apd_hap1000036.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.76	0.0000	-1.35	0.0026	1.31	0.0000	-1.31	0.0000	-1.32	0.0001	-1.03	0.6111	-1.01	0.8450	-1.36	0.0044
TNF	7124	TC6_cox_hap2000067.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_dbb_hap3000058.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_mann_hap4000059.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_mcf_hap5000053.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_qbl_hap6000058.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TNF	7124	TC6_ssto_hap7000054.hg.1	tumor necrosis factor; tumor necrosis factor (TNF superfamily, member 2)	1.73	0.0000	-1.35	0.0018	1.27	0.0001	-1.27	0.0001	-1.25	0.0000	-1.06	0.7019	1.02	0.5330	-1.33	0.0009
TPI1	7167	TC12000096.hg.1	triosephosphate isomerase 1	1.2	0.0000	1.03	0.3676	1.04	0.0662	-1.04	0.0662	1.01	0.5112	1.07	0.0014	1.05	0.0151	1.08	0.0000
TNFRSF4	7293	TC01002086.hg.1	tumor necrosis factor receptor superfamily, member 4	1.36	0.0000	-1.15	0.0029	1.18	0.0000	-1.18	0.0000	-1.16	0.0003	1.03	0.5189	1.02	0.7561	-1.13	0.0094
VEGFA	7422	TC06000608.hg.1	vascular endothelial growth factor A	1.03	0.0884	-1.05	0.1235	1.13	0.0000	-1.13	0.0000	-1.11	0.0009	1.08	0.0236	1.02	0.6759	-1.03	0.3078
VHL	7428	TC03000055.hg.1	von Hippel-Lindau tumor suppressor, E3 ubiquitin	-1.22	0.0000	1.12	0.0001	-1.06	0.0165	1.06	0.0165	1.05	0.1168	1.05	0.1921	-1.01	0.5285	1.1	0.0088

			protein ligase; von Hippel-Lindau tumor suppressor																
VIM	7431	TC10000126.hg.1	vimentin	-1.51	0.0000	1.14	0.0047	-1.09	0.0468	1.09	0.0468	1.05	0.1922	1.05	0.3702	-1.04	0.2792	1.1	0.0262
CXCR4	7852	TC02002378.hg.1	chemokine (C-X-C motif) receptor 4	-1.22	0.0001	1.18	0.0003	-1.11	0.0019	1.11	0.0019	1.12	0.0011	1.06	0.0828	1	0.6486	1.18	0.0001
EOMES	8320	TC03001257.hg.1	eomesodermin; eomesodermin homolog (Xenopus laevis)	1.09	0.0012	-1.02	0.2570	1.09	0.0008	-1.09	0.0008	-1.08	0.0000	1.07	0.0133	1.01	0.7663	-1.01	0.2230
CUL2	8453	TC10001173.hg.1	cullin 2	-2.14	0.0000	1.26	0.0075	-1.27	0.0011	1.27	0.0011	1.26	0.0165	-1.01	0.8643	-1.01	0.7330	1.25	0.0382
PIK3R3; RP11-322N21.2	8503	TC01002616.hg.1	phosphoinositide-3-kinase, regulatory subunit 3 (gamma); novel transcript	-2.14	0.0000	1.3	0.0000	-1.16	0.0177	1.16	0.0177	1.13	0.0718	1.12	0.0978	-1.03	0.6731	1.26	0.0018
MKNK1	8569	TC01006353.hg.1	MAP kinase interacting serine/threonine kinase 1	-1.01	0.7755	1.02	0.3534	1.03	0.0170	-1.03	0.0170	-1.01	0.7298	1.06	0.0047	1.02	0.0555	1.04	0.0149
TNFRSF18	8784	TC01002085.hg.1	tumor necrosis factor receptor superfamily, member 18	1.28	0.0016	-1.16	0.0209	1.15	0.0000	-1.15	0.0000	-1.15	0.0003	-1.01	0.8419	-1.01	0.7849	-1.16	0.0147
NRP1	8829	TC10001166.hg.1	neuropilin 1	1.27	0.0000	-1.07	0.0401	1.11	0.0011	-1.11	0.0011	-1.11	0.0005	1.03	0.5675	1	0.8226	-1.07	0.0211
EIF4E2	9470	TC02001404.hg.1	eukaryotic translation initiation factor 4E family member 2	1	0.6744	1.11	0.0009	1.02	0.1767	-1.02	0.1767	1.01	0.7412	1.14	0.0000	1.04	0.1067	1.15	0.0000
AKT3	10000	TC01004040.hg.1	v-akt murine thymoma viral oncogene homolog 3; v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-1.4	0.0000	1.06	0.0012	1	0.9269	-1	0.9269	1	0.9697	1.07	0.0079	1	0.9731	1.07	0.0226
TBX21	30009	TC17000613.hg.1	T-box 21	1.5	0.0000	-1.15	0.0339	1.16	0.0002	-1.16	0.0002	-1.17	0.0002	1.01	0.4620	-1.01	0.6881	-1.16	0.0354
AK3	50808	TC09000884.hg.1	adenylate kinase 3	-1.12	0.0003	-1.01	0.1391	-1.05	0.1641	1.05	0.1641	1.06	0.3283	-1.06	0.5604	1	0.6987	-1	0.2137
FOXP3	50943	TC0X001031.hg.1	forkhead box P3	1.34	0.0000	-1.14	0.0044	1.19	0.0000	-1.19	0.0000	-1.2	0.0002	1.04	0.3106	-1.01	0.7378	-1.15	0.0176
ANGPT4	51378	TC20000546.hg.1	angiopoietin 4	1.21	0.0037	-1.08	0.2102	1.17	0.0003	-1.17	0.0003	-1.2	0.0000	1.08	0.0746	-1.03	0.4849	-1.11	0.0764
EGLN1	54583	TC01003968.hg.1	egl-9 family hypoxia-inducible factor 1; egl nine homolog 1 (C. elegans)	-1.76	0.0000	1.27	0.0001	-1.26	0.0009	1.26	0.0009	1.26	0.0043	1.01	0.9069	-1	0.8381	1.26	0.0027
HIF1AN	55662	TC10000724.hg.1	hypoxia inducible factor 1, alpha subunit inhibitor	-1.18	0.0007	1.09	0.1383	-1.07	0.1442	1.07	0.1442	1.16	0.0001	1.01	0.7623	1.08	0.0154	1.17	0.0004
HAMP	57817	TC19000464.hg.1	hepcidin antimicrobial peptide	1.31	0.0002	-1.06	0.1684	1.09	0.0500	-1.09	0.0500	-1.2	0.0005	1.03	0.6614	-1.1	0.0369	-1.17	0.0038
XPNPEP3; RBX1	63929	TC22000327.hg.1	X-prolyl aminopeptidase (aminopeptidase P) 3, putative; ring-box 1, E3	-1.28	0.0000	1.11	0.0126	-1.1	0.0081	1.1	0.0081	1.1	0.0285	1	0.6536	1	0.9469	1.11	0.0303

			ubiquitin protein ligase; ring-box 1																
HKDC1	80201	TC10000418.hg.1	hexokinase domain containing 1	1.27	0.0000	-1.11	0.0024	1.11	0.0002	-1.11	0.0002	-1.1	0.0006	-1	0.8566	1	0.9474	-1.1	0.0038
PROK1	84432	TC01000966.hg.1	prokineticin 1	1.18	0.0003	-1.07	0.1067	1.1	0.0154	-1.1	0.0154	-1.16	0.0001	1.03	0.6481	-1.05	0.0082	-1.13	0.0015
RETNLB	84666	TC03001633.hg.1	resistin like beta	1.16	0.0000	-1.03	0.2053	1.08	0.0216	-1.08	0.0216	-1.08	0.0083	1.05	0.1511	1	0.8914	-1.03	0.1254
EGLN2	112398	TC19002634.hg.1	egl-9 family hypoxia-inducible factor 2	1.1	0.0002	-1.02	0.1183	1.08	0.0121	-1.08	0.0121	-1.05	0.1822	1.06	0.4550	1.02	0.2401	1	0.6268
EGLN3	112399	TC14001022.hg.1	egl-9 family hypoxia-inducible factor 3; egl nine homolog 3 (C. elegans)	1.09	0.0242	-1.05	0.2165	1.04	0.0348	-1.04	0.0348	-1.03	0.2862	-1	0.5082	1.01	0.2583	-1.04	0.7854
EIF4E1B	253314	TC05001004.hg.1	eukaryotic translation initiation factor 4E family member 1B	1.39	0.0000	-1.19	0.0058	1.26	0.0007	-1.26	0.0007	-1.22	0.0008	1.06	0.9984	1.04	0.8332	-1.15	0.0056
ENO4	387712	TC10000848.hg.1	enolase family member 4	1.21	0.0001	-1.11	0.0556	1.13	0.0038	-1.13	0.0038	-1.13	0.0204	1.02	0.7158	1	0.7988	-1.1	0.1128

Supplementary Table S4. Expression fold changes of 176 HIF-related genes represented by 375 probe set IDs analyzed in human U937 cells exposed to different gravitational conditions during parabolic flight (19th DLR PFC). The analysis was made with the NimbleGen expression microarray based on the hg18 annotation.

				1g IF vs HW 1g GC		BL-PFC hyp-g vs 1g IF		µg vs BL-PFC hyp-g		µg vs 1g IF		BL-PFC hyp-g vs HW 1g GC		µg vs HW 1g GC	
Gene Symbol	**Entrez Gene ID**	**Probe set ID**	**Description**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**
ADM	133	NM_001124	adrenomedullin	1.01	0.9409	1.23	0.3740	-1.12	0.6665	1.09	0.7036	1.24	0.3316	1.11	0.6692
ADORA2A	135	BC013780	adenosine A2a receptor	-1.21	0.3323	-1.20	0.3624	1.20	0.5133	1.00	0.9915	-1.45	0.1532	-1.21	0.4587
ADORA2A	135	NM_000675	adenosine A2a receptor	1.00	0.9801	1.14	0.2984	-1.03	0.8496	1.11	0.4027	1.14	0.4110	1.11	0.4987
ADRA1B	147	NM_000679	adrenergic, alpha-1B-, receptor	1.13	0.5589	1.73	0.0579	-1.70	0.0626	1.01	0.9420	1.96	0.0510	1.15	0.5132
AKT1	207	BC084538	v-akt murine thymoma viral oncogene homolog 1	-1.01	0.9151	-1.25	0.1093	1.17	0.3563	-1.06	0.5676	-1.26	0.2555	-1.08	0.6396
AKT1	207	BX647722	v-akt murine thymoma viral oncogene homolog 1	1.34	0.0177	-1.27	0.0851	1.55	0.0043	1.22	0.0853	1.06	0.5971	1.64	0.0007
AKT1	207	NM_001014431	v-akt murine thymoma viral oncogene homolog 1	1.10	0.2272	-1.27	0.0155	1.20	0.0585	-1.06	0.1661	-1.15	0.3048	1.04	0.6174
AKT2	208	NM_001626	v-akt murine thymoma viral oncogene homolog 2	-1.04	0.8233	-1.81	0.0637	1.27	0.5192	-1.43	0.0686	-1.89	0.1060	-1.49	0.1082
ALDOA	226	CR592372	aldolase A, fructose-bisphosphate	-1.05	0.4004	1.03	0.6182	-1.01	0.8904	1.02	0.6601	-1.02	0.8011	-1.03	0.6504
ALDOA	226	NM_000034	aldolase A, fructose-bisphosphate	-1.06	0.1865	1.04	0.3970	-1.00	0.9408	1.03	0.5574	-1.02	0.6233	-1.02	0.6774
ALDOA	226	NM_184041	aldolase A, fructose-bisphosphate	-1.02	0.7502	-1.01	0.8483	1.01	0.8701	1.00	0.9915	-1.03	0.6717	-1.02	0.8065
ALDOC	230	BC106925	aldolase C, fructose-bisphosphate	1.95	0.0002	-1.27	0.1561	1.13	0.5368	-1.12	0.3756	1.54	0.0980	1.75	0.0107
ALDOC	230	NM_005165	aldolase C, fructose-bisphosphate	1.39	0.0304	-1.14	0.4131	1.03	0.8539	-1.11	0.4140	1.22	0.3167	1.25	0.1277
ANGPT1	284	BC029406	angiopoietin 1	-1.09	0.3194	1.04	0.0516	-1.02	0.4889	1.02	0.3691	-1.04	0.6669	-1.07	0.4650
ANGPT1	284	NM_001146	angiopoietin 1	-1.04	0.2616	1.03	0.2645	-1.02	0.5536	1.01	0.7303	-1.01	0.7873	-1.03	0.4492
ANGPT2	285	AF187858	angiopoietin 2	-1.01	0.8564	1.24	0.0270	-1.16	0.1058	1.07	0.2674	1.22	0.0711	1.06	0.4407
ANGPT2	285	AF218015	angiopoietin 2	-1.01	0.6916	1.13	0.0222	-1.06	0.2378	1.06	0.0767	1.12	0.0482	1.05	0.1361
ANGPT2	285	NM_001147	angiopoietin 2	-1.02	0.5353	1.13	0.0254	-1.14	0.0274	-1.01	0.8845	1.11	0.0603	-1.03	0.4943
ARG1	383	BC020653	arginase, liver	-1.27	0.1391	1.00	0.9832	-1.01	0.9127	-1.00	0.9667	-1.27	0.1615	-1.28	0.0974
ARG1	383	NM_000045	arginase, liver	-1.13	0.0401	1.09	0.0252	-1.12	0.0107	-1.03	0.4637	-1.04	0.5046	-1.17	0.0204

ARNT	405	AB209877	aryl hydrocarbon receptor nuclear translocator	1.11	0.2563	-1.42	0.0217	1.23	0.2072	-1.15	0.1341	-1.28	0.1597	-1.04	0.7269
ARNT	405	BC060838	aryl hydrocarbon receptor nuclear translocator	-1.39	0.1168	-1.27	0.2909	1.13	0.6821	-1.12	0.5956	-1.76	0.0501	-1.56	0.0896
ARNT	405	NM_001668	aryl hydrocarbon receptor nuclear translocator	1.05	0.7394	-1.43	0.0769	1.08	0.7037	-1.33	0.1425	-1.36	0.0601	-1.26	0.1941
BCL2	596	BC027258	B-cell CLL/lymphoma 2	-1.48	0.1130	-1.69	0.0877	1.20	0.2581	-1.40	0.1689	-2.50	0.0028	-2.08	0.0028
BCL2	596	NM_000633	B-cell CLL/lymphoma 2	-2.31	0.0156	-2.23	0.0906	1.22	0.4035	-1.83	0.1132	-5.16	0.0014	-4.23	0.0005
BCL2	596	NM_000657	B-cell CLL/lymphoma 2	1.17	0.3200	1.33	0.0578	-1.17	0.2635	1.13	0.4215	1.56	0.0045	1.33	0.0907
BLR1	643	NM_001716	Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)	1.52	0.1012	1.70	0.0579	-1.35	0.2550	1.26	0.2735	2.60	0.0194	1.92	0.0318
CA9	768	NM_001216	carbonic anhydrase IX	1.08	0.5647	1.85	0.0214	-1.53	0.0975	1.21	0.2113	2.00	0.0360	1.31	0.1705
CAMK2A	815	AF145710	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	1.30	0.2728	1.30	0.2290	-1.01	0.9468	1.28	0.2432	1.70	0.0605	1.67	0.0628
CAMK2A	815	AF145711	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	1.33	0.2031	1.44	0.1267	-1.17	0.5103	1.23	0.3265	1.91	0.0437	1.63	0.0778
CAMK2A	815	NM_015981	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	-1.02	0.7554	1.20	0.0142	-1.16	0.0158	1.03	0.6808	1.17	0.0336	1.00	0.9626
CAMK2B	816	NM_001220	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1.12	0.6263	1.93	0.0262	-1.37	0.2790	1.41	0.1680	2.17	0.0483	1.58	0.1750
CAMK2B	816	NM_172078	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1.16	0.5120	1.90	0.0117	-1.44	0.1009	1.32	0.1535	2.19	0.0121	1.53	0.0721

CAMK2B	816	NM_172080	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1.10	0.7217	2.12	0.0308	-1.71	0.0942	1.24	0.3941	2.34	0.0414	1.37	0.2842
CAMK2B	816	NM_172081	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1.04	0.8516	1.99	0.0051	-1.53	0.0393	1.30	0.1536	2.07	0.0102	1.36	0.1455
CAMK2B	816	NM_172082	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	-1.07	0.6950	1.99	0.0028	-1.39	0.1168	1.43	0.0654	1.86	0.0166	1.34	0.1915
CAMK2B	816	NM_172084	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1.18	0.4627	1.81	0.0560	-1.31	0.3583	1.38	0.1381	2.14	0.0648	1.64	0.1017
CAMK2D	817	NM_172115	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.07	0.7436	-2.09	0.0075	1.38	0.2177	-1.52	0.0341	-2.23	0.0197	-1.62	0.0500
CAMK2D	817	AB209288	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.17	0.1613	-1.06	0.4230	-1.06	0.0963	-1.12	0.0838	-1.24	0.0795	-1.31	0.0165
CAMK2D	817	NM_001221	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.49	0.1749	-2.04	0.0736	1.23	0.3845	-1.65	0.1226	-3.05	0.0043	-2.47	0.0046
CAMK2D	817	NM_172127	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.36	0.3856	-2.55	0.0797	1.35	0.1934	-1.88	0.1143	-3.46	0.0084	-2.56	0.0082
CAMK2G	818	NM_001222	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-1.05	0.4747	-1.32	0.0009	1.17	0.0047	-1.13	0.0097	-1.39	0.0026	-1.19	0.0094
CAMP	820	BC055089	cathelicidin antimicrobial peptide	-1.38	0.1018	1.25	0.0675	-1.32	0.0137	-1.06	0.5241	-1.10	0.6200	-1.46	0.0539
CAMP	820	NM_004345	cathelicidin antimicrobial peptide	1.21	0.5203	1.11	0.6768	1.28	0.2995	1.42	0.1627	1.34	0.2541	1.71	0.0642

CD36	948	BC008406	CD36 molecule (thrombospondin receptor)	-1.10	0.3529	-1.23	0.1058	1.16	0.3055	-1.06	0.5856	-1.36	0.0549	-1.17	0.2201
CD36	948	NM_000072	CD36 molecule (thrombospondin receptor)	-1.17	0.2902	-1.54	0.0430	1.30	0.2779	-1.18	0.3266	-1.80	0.0168	-1.38	0.0890
CD36	948	NM_001001548	CD36 molecule (thrombospondin receptor)	1.08	0.2608	-1.35	0.0089	1.22	0.1559	-1.10	0.2734	-1.24	0.0910	-1.02	0.8693
CDKN1A	1026	NM_000389	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.08	0.6638	1.44	0.0838	-1.21	0.4215	1.19	0.3315	1.55	0.1162	1.29	0.2996
CDKN1A	1026	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.04	0.8425	1.48	0.0538	-1.23	0.3787	1.20	0.3583	1.54	0.1127	1.25	0.4004
CDKN1B	1027	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-1.83	0.0712	-3.53	0.0522	1.33	0.4473	-2.66	0.0466	-6.46	0.0008	-4.86	0.0002
CCR1	1230	BC051306	chemokine (C-C motif) receptor 1	-2.56	0.0098	1.13	0.6029	-1.07	0.8160	1.06	0.8058	-2.26	0.0438	-2.42	0.0169
CCR1	1230	NM_001295	chemokine (C-C motif) receptor 1	-1.85	0.0034	1.10	0.5467	-1.07	0.7477	1.03	0.8567	-1.68	0.0357	-1.80	0.0114
CCR5	1234	BC038398	chemokine (C-C motif) receptor 5	1.47	0.2190	1.90	0.1060	-1.56	0.2516	1.22	0.4895	2.80	0.0630	1.80	0.1358
CCR5	1234	NM_000579	chemokine (C-C motif) receptor 5	1.58	0.1852	2.26	0.0648	-1.71	0.1916	1.32	0.3439	3.56	0.0477	2.09	0.0929
CCR7	1236	NM_001838	chemokine (C-C motif) receptor 7	1.32	0.3311	1.88	0.0374	-1.72	0.0510	1.10	0.6205	2.48	0.0263	1.45	0.1354
CREBBP	1387	NM_004380	CREB binding protein (Rubinstein-Taybi syndrome)	-2.36	0.0282	-1.78	0.1712	1.03	0.8914	-1.73	0.1308	-4.21	0.0082	-4.09	0.0026
CREBBP	1387	U85962	CREB binding protein (Rubinstein-Taybi syndrome)	-1.40	0.2561	-1.41	0.4022	-1.00	0.9959	-1.41	0.3159	-1.97	0.0674	-1.97	0.0290
MAPK14	1432	BC000092	mitogen-activated protein kinase 14	-1.07	0.3785	-1.43	0.0008	1.20	0.1658	-1.20	0.0320	-1.53	0.0040	-1.28	0.0324
MAPK14	1432	NM_001315	mitogen-activated protein kinase 14	-1.16	0.1219	-1.11	0.3444	1.04	0.7182	-1.07	0.5068	-1.29	0.0324	-1.24	0.0383
MAPK14	1432	NM_139013	mitogen-activated protein kinase 14	-1.12	0.2742	-1.68	0.0042	1.42	0.0644	-1.18	0.1029	-1.88	0.0055	-1.32	0.0358

CTLA4	1493	BC069566	cytotoxic T-lymphocyte-associated protein 4	-1.04	0.6862	1.35	0.0167	-1.18	0.0397	1.14	0.1240	1.29	0.0199	1.09	0.1034
CTLA4	1493	BC074842	cytotoxic T-lymphocyte-associated protein 4	1.08	0.7404	1.53	0.1268	-1.20	0.4551	1.27	0.2081	1.65	0.1405	1.37	0.1737
CTLA4	1493	BC074893	cytotoxic T-lymphocyte-associated protein 4	1.05	0.5381	1.57	0.0088	-1.39	0.0622	1.13	0.2932	1.64	0.0151	1.18	0.2161
CTLA4	1493	NM_001037631	cytotoxic T-lymphocyte-associated protein 4	1.30	0.3718	1.59	0.1322	-1.35	0.2564	1.17	0.3565	2.07	0.0890	1.53	0.0978
CTLA4	1493	NM_005214	cytotoxic T-lymphocyte-associated protein 4	1.32	0.2652	1.35	0.2779	-1.38	0.2407	-1.02	0.9326	1.78	0.0930	1.29	0.2643
CTSD	1509	NM_001909	cathepsin D (lysosomal aspartyl peptidase)	1.06	0.3334	-1.07	0.2629	1.08	0.1915	1.01	0.8594	-1.01	0.8724	1.06	0.2454
CYBB	1536	BC032720	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	-1.00	0.9815	-1.82	0.0044	1.37	0.1290	-1.33	0.0337	-1.82	0.0166	-1.34	0.0755
CYBB	1536	NM_000397	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	1.01	0.9481	-1.81	0.0039	1.36	0.1587	-1.33	0.0569	-1.79	0.0115	-1.32	0.1024
DEFB1	1672	BC033298	defensin, beta 1	-1.10	0.6707	-1.18	0.3807	1.05	0.7184	-1.12	0.5358	-1.30	0.1961	-1.23	0.2966
DEFB1	1672	NM_005218	defensin, beta 1	1.04	0.8350	1.93	0.0048	-1.64	0.0273	1.18	0.2694	2.00	0.0181	1.22	0.3376
EDG1	1901	NM_001400	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	1.45	0.2599	1.52	0.1829	-1.19	0.5994	1.28	0.3522	2.20	0.0969	1.85	0.1274
EDN1	1906	CR605456	endothelin 1	1.05	0.3114	1.13	0.0900	-1.08	0.3286	1.05	0.3705	1.19	0.0584	1.10	0.1399
EDN1	1906	NM_001955	endothelin 1	-1.07	0.3919	1.02	0.7668	-1.02	0.7959	1.00	0.9943	-1.04	0.5383	-1.07	0.4448
EGF	1950	BC093731	epidermal growth factor (beta-urogastrone)	1.14	0.2912	1.05	0.6618	1.02	0.8801	1.08	0.5626	1.20	0.1625	1.22	0.1662
EGF	1950	NM_001963	epidermal growth factor (beta-urogastrone)	1.05	0.5322	1.01	0.8358	-1.03	0.4217	-1.01	0.8277	1.06	0.0504	1.03	0.3869
EGFR	1956	BC094761	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.11	0.5427	1.45	0.0598	-1.13	0.5544	1.29	0.1746	1.61	0.0469	1.43	0.1116

EGFR	1956	K03193	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.06	0.1343	1.14	0.0286	-1.08	0.2774	1.06	0.2824	1.21	0.0174	1.11	0.0941
EGFR	1956	NM_005228	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	-1.13	0.3647	1.11	0.3581	-1.09	0.3190	1.01	0.8892	-1.02	0.8922	-1.11	0.3509
EGFR	1956	NM_201282	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	-1.08	0.3561	1.34	0.0037	-1.12	0.3312	1.20	0.0958	1.25	0.0292	1.12	0.3419
EGFR	1956	NM_201283	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.44	0.2674	1.73	0.0295	-1.53	0.0799	1.13	0.5780	2.49	0.0178	1.62	0.1510
EGFR	1956	NM_201284	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.11	0.5697	-1.02	0.8874	1.02	0.8701	1.01	0.9590	1.09	0.6609	1.12	0.5846
EIF4E	1977	BC012611	eukaryotic translation initiation factor 4E	-1.00	0.9849	1.03	0.8557	-1.09	0.6823	-1.05	0.7668	1.03	0.8738	-1.05	0.7638
EIF4E	1977	BC035166	eukaryotic translation initiation factor 4E	1.34	0.3613	1.05	0.8771	-1.18	0.4154	-1.12	0.6704	1.41	0.0911	1.19	0.3120
EIF4E	1977	NM_001968	eukaryotic translation initiation factor 4E	1.07	0.5726	-1.01	0.9600	-1.10	0.5876	-1.10	0.4417	1.06	0.7162	-1.03	0.8495
EIF4EBP1	1978	BC058073	eukaryotic translation initiation factor 4E binding protein 1	-1.02	0.6951	-1.04	0.3557	1.05	0.1967	1.01	0.8635	-1.06	0.2557	-1.01	0.7451
EIF4EBP1	1978	NM_004095	eukaryotic translation initiation factor 4E binding protein 1	1.02	0.7394	-1.03	0.4968	1.02	0.6644	-1.01	0.7546	-1.01	0.8939	1.01	0.8935
ENG	2022	BC014271	endoglin (Osler-Rendu-Weber syndrome 1)	-1.03	0.7002	-1.31	0.0139	1.16	0.2131	-1.13	0.0384	-1.35	0.0528	-1.16	0.1187

ENG	2022	NM_000118	endoglin (Osler-Rendu-Weber syndrome 1)	-1.05	0.5565	-1.26	0.0297	1.17	0.1850	-1.08	0.2513	-1.33	0.0627	-1.14	0.2146
ENO1	2023	BC050642	enolase 1, (alpha)	-1.00	0.9537	-1.10	0.2549	1.10	0.1951	1.01	0.8844	-1.10	0.3184	1.00	0.9529
ENO1	2023	BC073991	enolase 1, (alpha)	1.02	0.7657	-1.07	0.3733	1.06	0.4620	-1.01	0.8114	-1.05	0.5396	1.00	0.9361
ENO1	2023	NM_001428	enolase 1, (alpha)	-1.01	0.9078	-1.08	0.3456	1.04	0.5580	-1.03	0.5262	-1.09	0.3853	-1.04	0.5169
ENO2	2026	NM_001975	enolase 2 (gamma, neuronal)	1.13	0.3610	-1.08	0.4857	1.06	0.6507	-1.02	0.8707	1.05	0.6609	1.11	0.4809
ENO3	2027	BC017249	enolase 3 (beta, muscle)	-1.22	0.1968	-1.21	0.2379	1.05	0.7618	-1.15	0.3770	-1.48	0.0177	-1.41	0.0396
ENO3	2027	NM_001976	enolase 3 (beta, muscle)	-1.20	0.2708	-1.28	0.1563	1.03	0.8546	-1.24	0.2516	-1.54	0.0120	-1.49	0.0373
ENO3	2027	NM_053013	enolase 3 (beta, muscle)	-1.22	0.2250	-1.24	0.1781	1.02	0.8835	-1.22	0.2520	-1.52	0.0209	-1.48	0.0349
EP300	2033	NM_001429	E1A binding protein p300	-1.14	0.0992	-1.04	0.7700	1.02	0.9111	-1.02	0.8336	-1.19	0.2764	-1.17	0.1953
EPAS1	2034	NM_001430	endothelial PAS domain protein 1	-1.18	0.3113	1.11	0.4721	-1.01	0.9563	1.10	0.6165	-1.06	0.7439	-1.08	0.7383
EPO	2056	BC093628	erythropoietin	1.16	0.6579	1.24	0.3969	-1.09	0.7264	1.14	0.5348	1.44	0.3272	1.32	0.3731
EPO	2056	NM_000799	erythropoietin	1.02	0.8937	1.67	0.0030	-1.33	0.0748	1.25	0.1308	1.71	0.0133	1.28	0.1944
ERBB2	2064	AF177761	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	1.31	0.3908	1.82	0.0315	-1.39	0.1632	1.31	0.2200	2.38	0.0212	1.72	0.0692
ERBB2	2064	AK131568	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	1.07	0.7316	1.36	0.1967	1.05	0.8223	1.43	0.0630	1.46	0.1720	1.53	0.0532
ERBB2	2064	NM_001005862	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	-1.27	0.0396	1.18	0.2721	-1.20	0.2502	-1.02	0.8699	-1.07	0.6339	-1.29	0.0429
FLT1	2321	BC039007	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeabilit	1.05	0.6351	1.14	0.3071	-1.31	0.0835	-1.14	0.1990	1.20	0.2578	-1.09	0.5120
FLT1	2321	NM_002019	fms-related tyrosine kinase 1 (vascular	1.15	0.4813	2.21	0.0251	-1.69	0.1040	1.30	0.2317	2.53	0.0336	1.49	0.1337

			endothelial growth factor/vascular permeabilit												
FN1	2335	AB191261	fibronectin 1	-1.16	0.1226	-1.06	0.1542	1.04	0.4682	-1.02	0.6288	-1.23	0.0819	-1.18	0.0978
FN1	2335	BX538018	fibronectin 1	-1.08	0.4138	-1.10	0.2151	-1.01	0.8930	-1.11	0.1724	-1.19	0.0677	-1.20	0.0478
FN1	2335	CR749317	fibronectin 1	-1.14	0.0687	-1.04	0.4158	-1.00	0.9760	-1.04	0.4125	-1.19	0.0307	-1.19	0.0213
FN1	2335	NM_002026	fibronectin 1	-1.16	0.2740	-1.20	0.1243	1.07	0.4425	-1.13	0.2736	-1.39	0.0202	-1.30	0.0367
FN1	2335	NM_054034	fibronectin 1	1.02	0.8394	-1.26	0.0821	1.02	0.7382	-1.23	0.0501	-1.23	0.0555	-1.20	0.0199
FRAP1	2475	NM_004958	FK506 binding protein 12-rapamycin associated protein 1	-1.37	0.0005	-1.26	0.0691	1.09	0.4506	-1.16	0.0987	-1.74	0.0001	-1.59	0.0000
GAPDH	2597	BC001601	glyceraldehyde-3-phosphate dehydrogenase	1.04	0.4602	-1.13	0.1002	1.09	0.2572	-1.03	0.5363	-1.08	0.3696	1.01	0.8728
GAPDH	2597	BC009081	glyceraldehyde-3-phosphate dehydrogenase	1.01	0.8921	-1.07	0.4897	1.10	0.3183	1.03	0.6795	-1.06	0.6160	1.04	0.6181
GAPDH	2597	NM_002046	glyceraldehyde-3-phosphate dehydrogenase	1.00	0.9962	-1.10	0.1673	1.04	0.4709	-1.05	0.1961	-1.10	0.3360	-1.05	0.4367
GPI	2821	BC004982	glucose phosphate isomerase	-1.00	0.9270	-1.13	0.0641	1.08	0.2458	-1.04	0.2232	-1.13	0.1220	-1.05	0.3118
GPI	2821	NM_000175	glucose phosphate isomerase	1.00	0.9316	-1.08	0.3015	1.05	0.5181	-1.02	0.5507	-1.07	0.4662	-1.02	0.7502
MKNK2	2872	AF237775	MAP kinase interacting serine/threonine kinase 2	-1.07	0.6112	-1.21	0.3929	1.10	0.7181	-1.11	0.5080	-1.30	0.3047	-1.19	0.3196
MKNK2	2872	NM_017572	MAP kinase interacting serine/threonine kinase 2	-1.01	0.9320	-1.19	0.4504	1.06	0.8385	-1.13	0.4794	-1.20	0.4920	-1.14	0.5056
MKNK2	2872	NM_199054	MAP kinase interacting serine/threonine kinase 2	1.21	0.2247	1.11	0.4760	1.04	0.8260	1.15	0.3371	1.35	0.1343	1.40	0.0926
CXCL2	2920	BC015753	chemokine (C-X-C motif) ligand 2	-1.42	0.0062	1.22	0.2159	1.00	0.9858	1.22	0.0168	-1.17	0.3601	-1.17	0.1260
CXCL2	2920	NM_002089	chemokine (C-X-C motif) ligand 2	-1.61	0.1039	1.04	0.5563	1.15	0.4935	1.19	0.3159	-1.55	0.1909	-1.35	0.3232
HDAC2	3066	NM_001527	histone deacetylase 2	-1.04	0.4793	-1.13	0.0678	1.00	0.9841	-1.13	0.1101	-1.17	0.0712	-1.17	0.0916

HIF1A	3091	NM_001530	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor	-1.30	0.1998	-1.46	0.1736	1.11	0.7265	-1.31	0.2362	-1.89	0.0312	-1.70	0.0289
HIF1A	3091	NM_181054	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor	-1.29	0.1543	-1.65	0.0577	1.25	0.4870	-1.32	0.2216	-2.13	0.0100	-1.70	0.0304
HK1	3098	NM_000188	hexokinase 1	1.01	0.9066	-1.29	0.0685	1.17	0.2506	-1.10	0.1720	-1.27	0.2137	-1.08	0.4831
HK2	3099	BC021116	hexokinase 2	1.10	0.5024	-1.34	0.1323	1.09	0.6791	-1.23	0.1325	-1.22	0.3986	-1.12	0.4991
HK2	3099	NM_000189	hexokinase 2	-1.01	0.9574	1.08	0.7163	-1.17	0.5231	-1.09	0.6516	1.07	0.7385	-1.10	0.6247
HK3	3101	NM_002115	hexokinase 3 (white cell)	-1.66	0.0932	-1.30	0.3320	1.46	0.1870	1.12	0.5774	-2.15	0.0615	-1.48	0.1829
HMOX1	3162	BC001491	heme oxygenase (decycling) 1	1.62	0.2382	1.88	0.1080	-1.25	0.5986	1.51	0.3582	3.04	0.0309	2.44	0.1387
HMOX1	3162	NM_002133	heme oxygenase (decycling) 1	1.72	0.1989	1.63	0.2241	-1.17	0.7234	1.39	0.4458	2.80	0.0567	2.39	0.1471
ICAM1	3383	NM_000201	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	-1.01	0.9167	1.02	0.8572	-1.02	0.8683	-1.00	0.9936	1.01	0.9223	-1.01	0.9214
IFNG	3458	NM_000619	interferon, gamma	-1.02	0.3928	1.10	0.0168	-1.06	0.3785	1.05	0.3783	1.08	0.0752	1.02	0.6952
IFNGR1	3459	NM_000416	interferon gamma receptor 1	-1.10	0.3157	-1.29	0.0799	1.11	0.5250	-1.16	0.2472	-1.42	0.0157	-1.27	0.0595
IFNGR2	3460	NM_005534	interferon gamma receptor 2 (interferon gamma transducer 1)	1.07	0.1222	-1.45	0.0001	1.21	0.0383	-1.20	0.0011	-1.35	0.0033	-1.12	0.0637
IGF1	3479	M11568	insulin-like growth factor 1 (somatomedin C)	1.25	0.4999	1.56	0.1435	-1.51	0.0909	1.03	0.8790	1.94	0.0659	1.29	0.2402
IGF1	3479	M29644	insulin-like growth factor 1 (somatomedin C)	1.51	0.2119	1.54	0.1651	-1.21	0.4995	1.27	0.3537	2.33	0.0421	1.92	0.0517
IGF1	3479	M37484	insulin-like growth factor 1 (somatomedin C)	1.34	0.1834	1.35	0.1641	-1.21	0.3474	1.11	0.5906	1.81	0.0171	1.49	0.0728
IGF1	3479	NM_000618	insulin-like growth factor 1 (somatomedin C)	1.08	0.2169	1.07	0.4663	-1.07	0.4265	-1.00	0.9949	1.15	0.1531	1.08	0.1115
IGF1R	3480	NM_000875	insulin-like growth factor 1 receptor	-1.03	0.8367	-1.32	0.0737	1.06	0.6965	-1.25	0.0186	-1.36	0.1722	-1.29	0.1081

IGF2	3481	BC053318	insulin-like growth factor 2 (somatomedin A)	-1.02	0.8596	1.57	0.0030	-1.27	0.1310	1.23	0.1761	1.54	0.0041	1.21	0.2289
IGF2	3481	NM_000612	insulin-like growth factor 2 (somatomedin A)	-1.01	0.9064	1.34	0.0150	-1.34	0.0109	1.00	0.9823	1.33	0.0165	-1.01	0.9093
IGFBP1	3484	NM_000596	insulin-like growth factor binding protein 1	-1.04	0.4088	1.07	0.1980	1.10	0.5202	1.17	0.2317	1.02	0.7294	1.13	0.4405
IGFBP1	3484	NM_001013029	insulin-like growth factor binding protein 1	-1.05	0.4091	1.32	0.0039	-1.18	0.0543	1.12	0.0808	1.26	0.0187	1.07	0.2956
IGFBP2	3485	NM_000597	insulin-like growth factor binding protein 2, 36kDa	1.11	0.1761	-1.24	0.0256	1.09	0.3720	-1.14	0.0435	-1.12	0.3392	-1.03	0.7447
IGFBP3	3486	BC000013	insulin-like growth factor binding protein 3	1.28	0.1258	1.88	0.0423	-1.65	0.0800	1.14	0.3686	2.41	0.0296	1.46	0.0192
IGFBP3	3486	NM_000598	insulin-like growth factor binding protein 3	1.08	0.5559	1.91	0.0235	-1.54	0.1012	1.24	0.1307	2.07	0.0385	1.35	0.1044
IL1B	3553	NM_000576	interleukin 1, beta	-1.47	0.0340	1.71	0.0025	-1.65	0.0156	1.04	0.8106	1.17	0.4234	-1.41	0.1058
IL6	3569	NM_000600	interleukin 6 (interferon, beta 2)	1.20	0.1997	1.11	0.4291	-1.14	0.1285	-1.03	0.7629	1.33	0.0310	1.16	0.0926
IL6R	3570	BC089410	interleukin 6 receptor	-1.04	0.7238	-1.22	0.1467	1.07	0.6209	-1.13	0.0707	-1.27	0.2497	-1.18	0.2225
IL6R	3570	NM_000565	interleukin 6 receptor	-1.16	0.4073	-1.17	0.4418	1.03	0.9092	-1.14	0.3791	-1.36	0.2833	-1.32	0.2040
IL8	3576	NM_000584	interleukin 8	-1.31	0.6278	1.09	0.8906	1.02	0.9741	1.11	0.8617	-1.21	0.7450	-1.18	0.7699
IL12A	3592	BC104982	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte matura	-1.86	0.0295	-1.15	0.0283	1.13	0.0082	-1.02	0.6808	-2.14	0.0342	-1.89	0.0258
IL12A	3592	NM_000882	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte matura	-1.07	0.5346	-1.14	0.1306	1.03	0.3199	-1.10	0.1510	-1.22	0.0667	-1.18	0.0536
TNFRSF9	3604	NM_001561	tumor necrosis factor receptor superfamily, member 9	-1.28	0.2675	1.04	0.8227	-1.05	0.7749	-1.01	0.9744	-1.23	0.3704	-1.29	0.2295
INS	3630	BC005255	insulin	-1.02	0.9071	-1.26	0.1074	1.03	0.7980	-1.22	0.1427	-1.28	0.0600	-1.24	0.1058
INS	3630	NM_000207	insulin	-1.05	0.5453	-1.10	0.3398	1.03	0.8561	-1.07	0.5732	-1.16	0.2330	-1.12	0.4092
INSR	3643	NM_000208	insulin receptor	1.09	0.5218	-1.33	0.0661	1.08	0.6259	-1.22	0.0405	-1.22	0.3734	-1.12	0.4531
INSR	3643	X02160	insulin receptor	1.04	0.8001	1.01	0.9287	-1.02	0.9176	-1.00	0.9714	1.05	0.7985	1.03	0.8525
ITGAM	3684	BC096346	integrin, alpha M (complement	-1.25	0.1456	-1.06	0.6643	-1.07	0.6501	-1.13	0.2067	-1.32	0.1788	-1.41	0.0496

			component 3 receptor 3 subunit)												
ITGAM	3684	J03925	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.59	0.0734	1.04	0.8388	-1.16	0.3964	-1.12	0.5156	-1.54	0.1297	-1.79	0.0353
ITGAM	3684	NM_000632	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.45	0.0646	1.06	0.6914	-1.15	0.4029	-1.08	0.6075	-1.37	0.1455	-1.57	0.0398
ITGB2	3689	AK097864	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	1.41	0.0886	1.04	0.8540	1.09	0.5800	1.12	0.4324	1.46	0.0560	1.58	0.0034
ITGB2	3689	NM_000211	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-1.16	0.0988	-1.02	0.8606	1.01	0.9248	-1.01	0.9324	-1.18	0.1957	-1.17	0.1335
KDR	3791	NM_002253	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.01	0.8927	1.22	0.0352	-1.14	0.1401	1.07	0.3204	1.23	0.0356	1.08	0.2551
KRT14	3861	NM_000526	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	1.13	0.7442	3.03	0.0235	-1.88	0.1203	1.61	0.1294	3.41	0.0442	1.82	0.1454
KRT18	3875	BC000180	keratin 18	1.31	0.5193	2.62	0.0237	-1.47	0.2670	1.78	0.0990	3.43	0.0290	2.33	0.0696
KRT18	3875	BC004253	keratin 18	1.33	0.5309	2.70	0.0162	-1.46	0.2560	1.85	0.0937	3.60	0.0183	2.47	0.0612
KRT18	3875	NM_000224	keratin 18	1.20	0.6709	2.67	0.0137	-1.41	0.2806	1.90	0.0631	3.20	0.0241	2.27	0.0684
KRT18	3875	NM_199187	keratin 18	1.32	0.5517	2.49	0.0176	-1.47	0.2138	1.69	0.1136	3.28	0.0209	2.23	0.0739
KRT19	3880	BC007628	keratin 19	1.05	0.8101	2.35	0.0042	-1.59	0.0766	1.47	0.0753	2.46	0.0129	1.55	0.1119
KRT19	3880	NM_002276	keratin 19	1.22	0.2805	1.61	0.0871	-1.32	0.2714	1.22	0.2279	1.97	0.0601	1.49	0.0546
LAG3	3902	BC052589	lymphocyte-activation gene 3	1.05	0.7834	2.84	0.0015	-2.10	0.0092	1.35	0.0879	2.97	0.0051	1.42	0.1103
LAG3	3902	NM_002286	lymphocyte-activation gene 3	1.18	0.6541	2.11	0.0919	-1.51	0.3031	1.40	0.2970	2.49	0.1041	1.65	0.2191
LDHA	3939	NM_005566	lactate dehydrogenase A	-1.02	0.7968	1.17	0.1071	-1.07	0.4783	1.09	0.2442	1.14	0.2606	1.07	0.4852
LEP	3952	BC069323	leptin (obesity homolog, mouse)	1.62	0.0952	1.32	0.2848	-1.17	0.5704	1.12	0.6722	2.13	0.0212	1.81	0.0925
LEP	3952	D49487	leptin (obesity homolog, mouse)	1.43	0.1845	1.20	0.3952	-1.25	0.1872	-1.04	0.8195	1.72	0.0538	1.38	0.1067

LEP	3952	NM_000230	leptin (obesity homolog, mouse)	1.37	0.1789	1.11	0.5912	-1.01	0.9507	1.10	0.6399	1.52	0.0399	1.50	0.0742
LRP1	4035	BC045107	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.23	0.2679	1.46	0.0506	-1.33	0.0957	1.10	0.5264	1.79	0.0133	1.35	0.0709
LRP1	4035	BC052593	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.04	0.7628	1.74	0.0016	-1.37	0.0233	1.27	0.0615	1.81	0.0025	1.32	0.0393
LRP1	4035	NM_002332	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.25	0.4377	1.62	0.0773	-1.25	0.4084	1.30	0.3325	2.02	0.0318	1.62	0.1362
LTBR	4055	NM_002342	lymphotoxin beta receptor (TNFR superfamily, member 3)	-1.08	0.3008	-1.01	0.9004	1.07	0.5726	1.06	0.5372	-1.09	0.4129	-1.02	0.8598
MMP2	4313	BC002576	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	1.13	0.1169	-1.27	0.0176	1.09	0.4097	-1.16	0.0086	-1.12	0.4178	-1.03	0.7783
MMP2	4313	NM_004530	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	1.10	0.2164	-1.17	0.1301	1.01	0.9527	-1.16	0.0252	-1.07	0.6152	-1.06	0.4886
MMP9	4318	NM_004994	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	-2.09	0.0704	1.30	0.1666	-1.23	0.4146	1.05	0.8391	-1.61	0.2396	-1.98	0.1029
MMP14	4323	BC064803	matrix metallopeptidase 14 (membrane-inserted)	1.34	0.0681	-1.23	0.1127	1.20	0.3280	-1.02	0.8999	1.09	0.5666	1.31	0.2074
MMP14	4323	NM_004995	matrix metallopeptidase 14 (membrane-inserted)	1.08	0.7391	-1.06	0.7962	1.14	0.4647	1.08	0.6909	1.02	0.9088	1.17	0.4362

NFKB1	4790	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.05	0.3676	-1.08	0.3803	-1.06	0.5810	-1.14	0.0188	-1.14	0.2274	-1.20	0.0068
NFKB1	4790	BC051765	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.04	0.5444	-1.07	0.3971	-1.03	0.7772	-1.10	0.0865	-1.11	0.2975	-1.14	0.0662
NFKB1	4790	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.08	0.1449	-1.02	0.7934	-1.07	0.5229	-1.09	0.1275	-1.10	0.3457	-1.18	0.0308
NOS2A	4843	NM_000625	nitric oxide synthase 2A (inducible, hepatocytes)	1.09	0.2998	1.57	0.0136	-1.29	0.1385	1.21	0.0530	1.71	0.0216	1.32	0.0419
NOS3	4846	BC069465	nitric oxide synthase 3 (endothelial cell)	-1.80	0.0258	1.15	0.4134	-1.14	0.4898	1.01	0.9337	-1.56	0.1076	-1.77	0.0316
NOS3	4846	NM_000603	nitric oxide synthase 3 (endothelial cell)	-1.76	0.0138	1.37	0.1463	-1.36	0.1585	1.00	0.9845	-1.29	0.2945	-1.75	0.0156
NPPA	4878	BC005893	natriuretic peptide precursor A	-1.14	0.4085	1.49	0.0108	-1.29	0.0651	1.15	0.2211	1.31	0.1247	1.02	0.9104
NPPA	4878	NM_006172	natriuretic peptide precursor A	-1.13	0.4634	1.36	0.0591	-1.20	0.2455	1.13	0.3494	1.21	0.3241	1.01	0.9731
SERPINE1	5054	BC010860	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), m	1.24	0.5610	1.73	0.2666	-1.48	0.4268	1.17	0.7015	2.14	0.1973	1.44	0.4141
SERPINE1	5054	NM_000602	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), m	1.11	0.6285	1.95	0.0335	-1.36	0.3206	1.44	0.1827	2.16	0.0419	1.59	0.1536
PDGFB	5155	BC029822	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	1.11	0.6341	1.06	0.8083	-1.01	0.9636	1.05	0.8335	1.18	0.5063	1.16	0.5224
PDGFB	5155	BC077725	platelet-derived growth factor beta polypeptide (simian	1.26	0.4449	1.78	0.0344	-1.31	0.2749	1.36	0.2015	2.24	0.0263	1.71	0.0924

			sarcoma viral (v-sis) oncogene												
PDGFB	5155	NM_002608	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	-1.01	0.9342	1.27	0.1393	1.04	0.8263	1.33	0.1338	1.25	0.2179	1.31	0.2096
PDGFB	5155	X83705	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	-1.12	0.4831	1.31	0.0760	-1.15	0.3281	1.14	0.3410	1.17	0.3626	1.02	0.9169
PDHA1	5160	CR614489	pyruvate dehydrogenase (lipoamide) alpha 1	-1.04	0.1698	-1.10	0.0229	1.04	0.2885	-1.05	0.0171	-1.14	0.0200	-1.10	0.0115
PDHA1	5160	NM_000284	pyruvate dehydrogenase (lipoamide) alpha 1	-1.13	0.0021	-1.09	0.1604	-1.01	0.9155	-1.10	0.0147	-1.24	0.0118	-1.25	0.0003
PDHA2	5161	NM_005390	pyruvate dehydrogenase (lipoamide) alpha 2	1.30	0.2600	1.36	0.2876	-1.15	0.5971	1.18	0.3115	1.77	0.1535	1.53	0.0679
PDHB	5162	NM_000925	pyruvate dehydrogenase (lipoamide) beta	-1.30	0.0045	-1.07	0.6919	-1.02	0.9079	-1.09	0.4256	-1.39	0.0490	-1.41	0.0015
PDK1	5163	BC039158	pyruvate dehydrogenase kinase, isozyme 1	1.18	0.0169	1.10	0.1436	-1.04	0.5403	1.06	0.2746	1.30	0.0140	1.25	0.0081
PDK1	5163	DQ234350	pyruvate dehydrogenase kinase, isozyme 1	1.20	0.0001	-1.13	0.0061	1.16	0.0177	1.02	0.6090	1.06	0.1529	1.23	0.0016
PDK1	5163	NM_002610	pyruvate dehydrogenase kinase, isozyme 1	1.17	0.0115	1.05	0.2752	-1.01	0.8538	1.04	0.3332	1.23	0.0044	1.22	0.0030
PFKFB3	5209	AF056320	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.03	0.7359	1.12	0.1721	-1.13	0.1810	-1.01	0.9411	1.09	0.0511	-1.03	0.6957
PFKFB3	5209	AK131307	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.01	0.8819	1.09	0.2787	-1.10	0.2390	-1.02	0.8695	1.08	0.0657	-1.03	0.7445
PFKFB3	5209	NM_004566	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.11	0.3814	-1.02	0.8519	-1.11	0.5644	-1.14	0.4574	-1.13	0.1907	-1.26	0.1726

PFKL	5211	NM_001002021	phosphofructokinase, liver	-1.17	0.2103	-1.45	0.0209	1.19	0.2768	-1.23	0.0197	-1.70	0.0202	-1.43	0.0139
PFKL	5211	BX537446	phosphofructokinase, liver	-1.13	0.2922	-1.27	0.0986	1.15	0.3973	-1.11	0.1995	-1.44	0.0887	-1.25	0.1075
PGK1	5230	BC023234	phosphoglycerate kinase 1	-1.09	0.2597	-1.03	0.6972	-1.00	0.9725	-1.03	0.6277	-1.11	0.2756	-1.12	0.2009
PGK1	5230	BC103752	phosphoglycerate kinase 1	-1.01	0.9430	-1.06	0.3568	1.06	0.4575	-1.01	0.9204	-1.07	0.4757	-1.01	0.8888
PGK1	5230	NM_000291	phosphoglycerate kinase 1	-1.01	0.8469	1.04	0.6356	-1.05	0.5840	-1.01	0.9218	1.02	0.7869	-1.02	0.7801
ABCB1	5243	AF016535	ATP-binding cassette, sub-family B (MDR/TAP), member 1	-1.03	0.8293	1.43	0.0671	-1.21	0.2876	1.18	0.1936	1.39	0.1387	1.14	0.3428
ABCB1	5243	NM_000927	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.14	0.2093	1.47	0.1314	-1.39	0.2177	1.06	0.6930	1.68	0.1071	1.21	0.2759
PIK3CA	5290	NM_006218	phosphoinositide-3-kinase, catalytic, alpha polypeptide	-1.13	0.5602	-1.95	0.0401	1.29	0.4552	-1.52	0.0839	-2.20	0.0187	-1.71	0.0294
PIK3CB	5291	NM_006219	phosphoinositide-3-kinase, catalytic, beta polypeptide	-1.32	0.0711	-1.77	0.0337	1.14	0.5993	-1.55	0.0304	-2.34	0.0011	-2.05	0.0002
PIK3CB	5291	CR749357	phosphoinositide-3-kinase, catalytic, beta polypeptide	-1.26	0.3051	-1.33	0.2100	-1.05	0.7482	-1.39	0.0894	-1.67	0.0508	-1.75	0.0143
PIK3CD	5293	U57843	phosphoinositide-3-kinase, catalytic, delta polypeptide	-1.18	0.1240	-1.20	0.0561	1.02	0.8076	-1.18	0.0214	-1.42	0.0220	-1.39	0.0070
PIK3CD	5293	NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide	-1.23	0.0190	-1.11	0.3709	-1.03	0.8302	-1.15	0.1724	-1.37	0.0282	-1.41	0.0055
PIK3R1	5295	BC030815	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	1.04	0.7875	-1.37	0.0832	1.08	0.7251	-1.27	0.0321	-1.32	0.2924	-1.22	0.2671
PIK3R1	5295	BC094795	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-1.19	0.5348	-2.43	0.0247	1.30	0.4025	-1.86	0.0270	-2.88	0.0223	-2.22	0.0172
PIK3R1	5295	NM_181504	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-1.03	0.7601	-1.29	0.0955	-1.02	0.8974	-1.33	0.0144	-1.34	0.1479	-1.37	0.0411

PIK3R2	5296	NM_005027	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	1.04	0.7462	-1.17	0.2886	1.08	0.6384	-1.08	0.4875	-1.13	0.5222	-1.04	0.7807
PKM2	5315	NM_002654	pyruvate kinase, muscle	-1.11	0.2198	-1.01	0.8437	1.07	0.3655	1.05	0.3084	-1.12	0.2881	-1.05	0.5508
PLAUR	5329	NM_001005376	plasminogen activator, urokinase receptor	1.32	0.0246	1.08	0.5642	-1.10	0.5761	-1.01	0.9172	1.43	0.0199	1.30	0.1120
PLAUR	5329	NM_001005377	plasminogen activator, urokinase receptor	1.27	0.0708	1.10	0.5345	-1.05	0.7819	1.04	0.7891	1.39	0.0457	1.32	0.1263
PLAUR	5329	NM_002659	plasminogen activator, urokinase receptor	1.33	0.0197	1.11	0.4107	-1.10	0.5448	1.01	0.9386	1.48	0.0104	1.34	0.0754
PLCG1	5335	NM_002660	phospholipase C, gamma 1	1.07	0.7177	-1.34	0.1136	1.22	0.3036	-1.10	0.5369	-1.25	0.3475	-1.03	0.8920
PLCG2	5336	BC007565	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.35	0.0012	-1.15	0.1064	1.07	0.4657	-1.08	0.2908	-1.55	0.0007	-1.45	0.0004
PLCG2	5336	NM_002661	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.38	0.0003	-1.21	0.0428	1.10	0.2882	-1.10	0.1664	-1.67	0.0002	-1.51	0.0000
PRKCA	5578	BC109273	protein kinase C, alpha	-1.06	0.2834	1.37	0.0636	-1.32	0.1118	1.04	0.6029	1.28	0.1889	-1.03	0.7641
PRKCA	5578	NM_002737	protein kinase C, alpha	1.04	0.6970	1.30	0.0672	-1.27	0.1145	1.02	0.8016	1.35	0.0895	1.06	0.6010
PRKCB1	5579	NM_212535	protein kinase C, beta 1	-1.27	0.1790	-1.10	0.4862	-1.17	0.2398	-1.29	0.0167	-1.40	0.1377	-1.63	0.0131
PRKCB1	5579	BC036472	protein kinase C, beta 1	-1.25	0.0176	-1.09	0.4101	-1.06	0.6182	-1.15	0.0961	-1.36	0.0191	-1.44	0.0014
PRKCB1	5579	NM_002738	protein kinase C, beta 1	-1.13	0.4720	-1.44	0.1200	1.14	0.4164	-1.26	0.2198	-1.63	0.0037	-1.43	0.0097
PRKCG	5582	BC047876	protein kinase C, gamma	1.24	0.3085	2.85	0.0023	-1.80	0.0354	1.58	0.0372	3.55	0.0047	1.97	0.0237
PRKCG	5582	NM_002739	protein kinase C, gamma	1.29	0.3230	2.61	0.0113	-1.71	0.0882	1.52	0.0523	3.37	0.0181	1.97	0.0361
MAPK1	5594	NM_138957	mitogen-activated protein kinase 1	-1.29	0.1468	-1.96	0.0213	1.33	0.2324	-1.48	0.0420	-2.54	0.0018	-1.91	0.0008
MAPK1	5594	Z11695	mitogen-activated protein kinase 1	1.01	0.8892	-1.51	0.0136	1.21	0.2249	-1.25	0.0339	-1.49	0.0299	-1.23	0.0609
MAPK1	5594	BC099905	mitogen-activated protein kinase 1	-1.11	0.3164	1.04	0.7443	-1.04	0.7803	1.00	0.9892	-1.07	0.6277	-1.11	0.3969
MAPK1	5594	NM_002745	mitogen-activated protein kinase 1	-1.18	0.5167	-1.36	0.2472	-1.11	0.5086	-1.52	0.1136	-1.60	0.0441	-1.79	0.0167

MAPK3	5595	NM_002746	mitogen-activated protein kinase 3	1.22	0.0470	-1.30	0.0378	1.08	0.5471	-1.21	0.0221	-1.06	0.6788	1.01	0.9022
MAPK3	5595	AY033607	mitogen-activated protein kinase 3	1.24	0.3419	-1.50	0.1438	1.27	0.2736	-1.18	0.3465	-1.21	0.5064	1.05	0.7644
MAPK3	5595	NM_001040056	mitogen-activated protein kinase 3	1.14	0.1930	-1.04	0.6958	-1.01	0.9635	-1.05	0.6717	1.09	0.5807	1.08	0.6207
MAP2K1	5604	NM_002755	mitogen-activated protein kinase kinase 1	1.07	0.4820	-1.18	0.1248	1.12	0.3382	-1.06	0.5563	-1.10	0.3942	1.01	0.9117
MAP2K2	5605	NM_030662	mitogen-activated protein kinase kinase 2	-1.04	0.6285	-1.15	0.1033	1.05	0.6084	-1.10	0.1944	-1.20	0.1326	-1.14	0.1795
RELA	5970	BC011603	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.23	0.2221	-1.34	0.2404	1.19	0.5996	-1.13	0.5025	-1.65	0.1167	-1.39	0.1654
RELA	5970	BC014095	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.14	0.2904	-1.01	0.9761	1.05	0.8354	1.04	0.7886	-1.15	0.5190	-1.10	0.6299
RELA	5970	BC110830	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.19	0.2177	1.12	0.6486	-1.06	0.8461	1.06	0.7625	-1.06	0.8095	-1.13	0.5547
RELA	5970	NM_021975	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.20	0.2255	-1.37	0.1749	1.21	0.5245	-1.13	0.4920	-1.64	0.0956	-1.35	0.1747
RORC	6097	BC031554	RAR-related orphan receptor C	1.10	0.4074	1.35	0.0366	-1.23	0.1716	1.10	0.4291	1.48	0.0250	1.20	0.1896
RORC	6097	BC110571	RAR-related orphan receptor C	1.19	0.2082	-1.02	0.9056	-1.19	0.1634	-1.21	0.1846	1.17	0.1075	-1.01	0.8923
RORC	6097	NM_001001523	RAR-related orphan receptor C	-1.05	0.6217	1.66	0.0215	-1.43	0.0882	1.16	0.1996	1.58	0.0651	1.10	0.4526
RPS6	6194	NM_001010	ribosomal protein S6	1.10	0.4975	1.04	0.6804	-1.05	0.4940	-1.01	0.8708	1.14	0.3867	1.08	0.4978
RPS6KB1	6198	BC053365	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.04	0.6098	-1.33	0.0132	1.13	0.3161	-1.18	0.0474	-1.38	0.0200	-1.22	0.0442

RPS6KB1	6198	BC036033	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.14	0.2782	-1.27	0.1491	1.08	0.7264	-1.18	0.2898	-1.45	0.0485	-1.34	0.0878
RPS6KB1	6198	NM_003161	ribosomal protein S6 kinase, 70kDa, polypeptide 1	1.07	0.4739	-1.18	0.1045	1.06	0.4982	-1.11	0.1884	-1.10	0.4474	-1.03	0.7457
RPS6KB2	6199	BC000094	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.03	0.7897	-1.40	0.0303	1.25	0.2340	-1.12	0.2991	-1.44	0.0844	-1.15	0.3472
RPS6KB2	6199	BC006106	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.02	0.8793	-1.41	0.0316	1.29	0.1553	-1.10	0.3956	-1.44	0.0888	-1.12	0.4530
RPS6KB2	6199	NM_001007071	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.04	0.6708	-1.31	0.0356	1.20	0.2652	-1.09	0.4028	-1.36	0.0880	-1.14	0.3680
CCL2	6347	NM_002982	chemokine (C-C motif) ligand 2	1.03	0.9288	-1.04	0.8530	-1.04	0.8177	-1.08	0.5854	-1.01	0.9757	-1.05	0.8635
CXCL6	6372	NM_002993	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	-1.19	0.1518	-1.03	0.4858	1.02	0.7451	-1.01	0.7947	-1.22	0.1650	-1.20	0.1409
SELL	6402	BC020758	selectin L (lymphocyte adhesion molecule 1)	-1.40	0.0408	-1.42	0.0376	-1.06	0.6168	-1.51	0.0097	-1.99	0.0015	-2.10	0.0002
SELL	6402	NM_000655	selectin L (lymphocyte adhesion molecule 1)	-1.41	0.0424	-1.25	0.1981	-1.18	0.3446	-1.48	0.0051	-1.77	0.0190	-2.08	0.0007
SELL	6402	AJ246000	selectin L (lymphocyte adhesion molecule 1)	-1.40	0.1010	-1.53	0.0708	1.07	0.6534	-1.43	0.0708	-2.15	0.0040	-2.00	0.0018
SLC2A1	6513	NM_006516	solute carrier family 2 (facilitated glucose transporter), member 1	-1.25	0.4182	1.06	0.8667	1.06	0.8764	1.12	0.7007	-1.18	0.6359	-1.12	0.7185
SLC2A3	6515	BC039196	solute carrier family 2 (facilitated glucose transporter), member 3	1.52	0.0925	1.16	0.5984	-1.16	0.6221	-1.00	0.9878	1.75	0.0988	1.51	0.1622
SLC2A3	6515	NM_006931	solute carrier family 2 (facilitated glucose transporter), member 3	1.51	0.0382	1.20	0.3444	-1.15	0.4989	1.04	0.8142	1.81	0.0151	1.57	0.0471
SLC11A1	6556	BC041787	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.17	0.3635	1.45	0.0261	-1.21	0.2053	1.19	0.1381	1.69	0.0297	1.39	0.0715

SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-1.02	0.9322	1.47	0.0550	-1.12	0.5454	1.31	0.1981	1.44	0.0614	1.29	0.2440
SLC11A1	6556	NM_001032220	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	1.08	0.6329	1.68	0.0181	-1.43	0.1090	1.17	0.4166	1.81	0.0184	1.26	0.2834
STAT3	6774	BC000627	signal transducer and activator of transcription 3 (acute-phase response factor)	1.05	0.5343	-1.23	0.0222	1.08	0.3917	-1.14	0.0144	-1.17	0.1898	-1.09	0.2838
STAT3	6774	BC014482	signal transducer and activator of transcription 3 (acute-phase response factor)	1.04	0.6164	-1.23	0.0410	1.07	0.4954	-1.15	0.0048	-1.18	0.2510	-1.10	0.2725
STAT3	6774	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.23	0.0619	-1.10	0.5460	1.04	0.8836	-1.06	0.7333	-1.36	0.0751	-1.31	0.1538
STAT3	6774	NM_213662	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.17	0.1186	-1.08	0.6467	1.03	0.9016	-1.05	0.7717	-1.26	0.1638	-1.23	0.2210
STAT4	6775	NM_003151	signal transducer and activator of transcription 4	1.25	0.2699	1.31	0.1903	-1.14	0.5169	1.14	0.4755	1.63	0.0422	1.43	0.1074
TCEB1	6921	BC093065	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	1.17	0.2684	1.23	0.1793	-1.25	0.1818	-1.01	0.9415	1.44	0.0801	1.16	0.3297
TCEB1	6921	BC100028	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	1.18	0.2361	1.22	0.2191	-1.23	0.2193	-1.01	0.9274	1.44	0.0991	1.17	0.3062
TCEB1	6921	BC100283	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	1.19	0.2944	1.20	0.2226	-1.19	0.2421	1.00	0.9733	1.43	0.1050	1.19	0.2964

TCEB1	6921	NM_005648	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	1.13	0.3874	1.22	0.2225	-1.24	0.2002	-1.02	0.8867	1.38	0.1359	1.11	0.4657
TCEB2	6923	BC013306	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.29	0.0072	1.02	0.7270	1.05	0.5546	1.08	0.3929	1.32	0.0013	1.39	0.0080
TCEB2	6923	BC065000	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.18	0.0071	1.06	0.0577	1.07	0.3479	1.14	0.0493	1.26	0.0026	1.34	0.0042
TCEB2	6923	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.26	0.0202	1.01	0.9040	1.05	0.5424	1.07	0.3976	1.27	0.0396	1.34	0.0074
TCEB2	6923	NM_207013	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.24	0.0053	1.04	0.4812	1.02	0.7156	1.07	0.3054	1.29	0.0012	1.32	0.0015
TCF7	6932	BC048769	transcription factor 7 (T-cell specific, HMG-box)	-1.60	0.0425	-1.03	0.7835	-1.15	0.2247	-1.18	0.1969	-1.65	0.0582	-1.89	0.0153
TCF7	6932	NM_003202	transcription factor 7 (T-cell specific, HMG-box)	-1.78	0.0402	-1.01	0.9373	-1.08	0.4520	-1.09	0.3726	-1.80	0.0731	-1.94	0.0242
TCF7	6932	NM_201633	transcription factor 7 (T-cell specific, HMG-box)	-1.38	0.0280	1.13	0.3383	-1.08	0.5257	1.05	0.6426	-1.23	0.1865	-1.32	0.0425
TEK	7010	NM_000459	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal	-1.00	0.8218	1.03	0.1282	-1.02	0.3696	1.01	0.4431	1.03	0.2337	1.01	0.6240
TF	7018	AK126941	transferrin	-1.09	0.3212	1.34	0.0344	-1.31	0.0917	1.03	0.7943	1.23	0.1675	-1.06	0.6411
TF	7018	NM_001063	transferrin	-1.29	0.0081	1.31	0.0014	-1.13	0.1872	1.16	0.0961	1.02	0.8413	-1.11	0.3051
TFF3	7033	BC017859	trefoil factor 3 (intestinal)	1.10	0.5641	1.63	0.0197	-1.58	0.0178	1.03	0.8037	1.79	0.0226	1.13	0.3606
TFF3	7033	NM_003226	trefoil factor 3 (intestinal)	1.38	0.3933	1.94	0.0762	-1.57	0.1942	1.24	0.4414	2.68	0.0574	1.71	0.1676
TFRC	7037	BC001188	transferrin receptor (p90, CD71)	-1.01	0.9167	-1.07	0.6556	1.09	0.5953	1.02	0.8389	-1.08	0.6754	1.01	0.9447

TFRC	7037	NM_003234	transferrin receptor (p90, CD71)	-1.01	0.9313	-1.01	0.9667	1.06	0.6978	1.05	0.6039	-1.02	0.9267	1.04	0.7472
TGFA	7039	AF149096	transforming growth factor, alpha	-1.11	0.1982	1.13	0.2575	1.03	0.8562	1.16	0.2114	1.02	0.8515	1.05	0.7082
TGFA	7039	AF149098	transforming growth factor, alpha	1.07	0.6478	-1.05	0.7819	1.06	0.6693	1.01	0.9272	1.03	0.8011	1.09	0.5086
TGFA	7039	BC005308	transforming growth factor, alpha	1.44	0.1466	1.04	0.8798	-1.04	0.8943	1.01	0.9779	1.50	0.1615	1.45	0.1164
TGFA	7039	NM_003236	transforming growth factor, alpha	-1.48	0.0539	-1.19	0.0387	1.16	0.1755	-1.03	0.7820	-1.76	0.0299	-1.52	0.0504
TGFB1	7040	BC000125	transforming growth factor, beta 1 (Camurati-Engelmann disease)	1.15	0.0681	-1.11	0.1247	1.01	0.8995	-1.10	0.0984	1.03	0.7474	1.04	0.6164
TGFB1	7040	NM_000660	transforming growth factor, beta 1 (Camurati-Engelmann disease)	1.14	0.1458	-1.06	0.4397	-1.00	0.9907	-1.06	0.3477	1.08	0.5522	1.08	0.4853
TGFB3	7043	BC018503	transforming growth factor, beta 3	-1.05	0.7632	-1.30	0.1560	1.19	0.3473	-1.10	0.5393	-1.36	0.1019	-1.15	0.3688
TGFB3	7043	NM_003239	transforming growth factor, beta 3	-1.10	0.4583	-1.13	0.3748	1.06	0.6436	-1.07	0.5302	-1.25	0.1657	-1.18	0.1763
THBS1	7057	NM_003246	thrombospondin 1	1.18	0.4354	1.26	0.3504	-1.16	0.5580	1.08	0.7334	1.49	0.1502	1.28	0.3277
TIMP1	7076	BC000866	TIMP metallopeptidase inhibitor 1	1.04	0.3643	-1.05	0.5139	-1.01	0.9288	-1.06	0.3740	-1.01	0.9436	-1.01	0.8417
TIMP1	7076	NM_003254	TIMP metallopeptidase inhibitor 1	-1.12	0.2806	1.12	0.3531	-1.12	0.4304	1.00	0.9933	1.01	0.9640	-1.12	0.3909
TLR4	7099	NM_003266	toll-like receptor 4	-1.40	0.1133	-1.37	0.2438	1.08	0.8374	-1.27	0.3022	-1.92	0.0627	-1.78	0.0508
TLR4	7099	NM_138554	toll-like receptor 4	-1.53	0.0438	-1.01	0.9676	1.04	0.8800	1.03	0.8756	-1.54	0.1078	-1.48	0.1289
TLR4	7099	NM_138557	toll-like receptor 4	-1.47	0.1281	-1.65	0.1311	1.19	0.6689	-1.39	0.1986	-2.42	0.0335	-2.04	0.0275
TNF	7124	NM_000594	tumor necrosis factor (TNF superfamily, member 2)	-1.39	0.0927	2.02	0.0041	-1.35	0.1571	1.50	0.0238	1.45	0.1431	1.08	0.7213
TPI1	7167	BC007086	triosephosphate isomerase 1	1.13	0.0881	-1.08	0.3668	1.12	0.1285	1.04	0.4611	1.05	0.5907	1.18	0.0133
TPI1	7167	BC017917	triosephosphate isomerase 1	1.07	0.1658	-1.04	0.2786	1.02	0.6390	-1.03	0.3475	1.03	0.6784	1.04	0.3615
TPI1	7167	BC070129	triosephosphate isomerase 1	1.14	0.0059	-1.06	0.3390	1.11	0.0856	1.05	0.2818	1.08	0.2091	1.19	0.0005

TPI1	7167	NM_000365	triosephosphate isomerase 1	1.12	0.1749	-1.08	0.3470	1.10	0.1741	1.02	0.5720	1.04	0.7381	1.15	0.0742
TNFRSF4	7293	NM_003327	tumor necrosis factor receptor superfamily, member 4	-1.04	0.7167	1.33	0.1033	-1.31	0.1163	1.02	0.8971	1.28	0.1477	-1.03	0.8206
VEGF	7422	AF323587	vascular endothelial growth factor	-1.28	0.1189	-1.31	0.1007	1.25	0.1182	-1.05	0.6658	-1.68	0.0164	-1.35	0.0494
VEGF	7422	AY263145	vascular endothelial growth factor	-1.19	0.2406	-1.16	0.3582	-1.04	0.8296	-1.20	0.2157	-1.38	0.0696	-1.42	0.0293
VEGF	7422	M27281	vascular endothelial growth factor	-1.19	0.1407	-1.32	0.0646	1.10	0.4265	-1.20	0.0908	-1.57	0.0058	-1.43	0.0023
VEGF	7422	NM_001025366	vascular endothelial growth factor	-1.30	0.0228	-1.18	0.2998	1.10	0.5388	-1.07	0.5904	-1.53	0.0068	-1.39	0.0066
VEGF	7422	S85192	vascular endothelial growth factor	-1.61	0.0261	-1.27	0.2821	1.06	0.7973	-1.20	0.3327	-2.06	0.0118	-1.94	0.0058
VHL	7428	BC058831	von Hippel-Lindau tumor suppressor	1.25	0.1730	-2.20	0.0006	1.38	0.1817	-1.60	0.0008	-1.76	0.0854	-1.27	0.2543
VHL	7428	L15409	von Hippel-Lindau tumor suppressor	1.20	0.3220	-2.01	0.0026	1.36	0.1780	-1.48	0.0091	-1.68	0.0958	-1.24	0.3076
VHL	7428	NM_000551	von Hippel-Lindau tumor suppressor	1.22	0.2405	-2.14	0.0012	1.42	0.1661	-1.50	0.0059	-1.75	0.0879	-1.23	0.3378
VIM	7431	AK093924	vimentin	1.32	0.3528	-2.16	0.0217	1.83	0.0241	-1.18	0.4457	-1.64	0.1919	1.12	0.6776
VIM	7431	BC030573	vimentin	-1.16	0.3067	-1.01	0.9256	1.00	0.9880	-1.01	0.9344	-1.18	0.4016	-1.18	0.3497
VIM	7431	BC066956	vimentin	-1.14	0.2726	-1.03	0.8114	1.06	0.6770	1.03	0.7520	-1.18	0.3478	-1.11	0.4815
VIM	7431	NM_003380	vimentin	-1.17	0.2335	1.01	0.9167	1.03	0.8531	1.05	0.6928	-1.16	0.4342	-1.12	0.4342
CXCR4	7852	NM_001008540	chemokine (C-X-C motif) receptor 4	-1.04	0.5741	-1.16	0.0405	1.01	0.8359	-1.14	0.0069	-1.20	0.0688	-1.19	0.0238
EOMES	8320	NM_005442	eomesodermin homolog (Xenopus laevis)	1.07	0.5955	1.44	0.0387	-1.17	0.3554	1.23	0.1300	1.54	0.0455	1.31	0.1002
CUL2	8453	NM_003591	cullin 2	-1.19	0.2100	-1.01	0.9608	-1.12	0.6717	-1.13	0.5494	-1.20	0.3554	-1.35	0.1635
PIK3R3	8503	AF028785	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	-1.05	0.7872	-2.32	0.0020	1.61	0.1406	-1.44	0.0757	-2.44	0.0104	-1.51	0.1073
PIK3R3	8503	NM_003629	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	-1.40	0.1120	-1.48	0.0836	1.14	0.5446	-1.29	0.2284	-2.07	0.0084	-1.81	0.0160
MKNK1	8569	AB000409	MAP kinase interacting serine/threonine kinase 1	-1.29	0.0812	-1.28	0.0858	1.20	0.3692	-1.07	0.6374	-1.65	0.0240	-1.37	0.0928

MKNK1	8569	AK096423	MAP kinase interacting serine/threonine kinase 1	-1.29	0.0575	-1.12	0.3533	1.06	0.7378	-1.06	0.6537	-1.44	0.0428	-1.36	0.0668
MKNK1	8569	NM_003684	MAP kinase interacting serine/threonine kinase 1	-1.31	0.0158	-1.19	0.0538	1.17	0.2481	-1.01	0.9021	-1.56	0.0084	-1.33	0.0465
MKNK1	8569	NM_198973	MAP kinase interacting serine/threonine kinase 1	-1.27	0.1621	-1.26	0.1603	1.19	0.4556	-1.06	0.7150	-1.59	0.0676	-1.34	0.1765
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	1.05	0.6897	1.25	0.1875	-1.05	0.7936	1.19	0.1857	1.31	0.1779	1.25	0.1540
TNFRSF18	8784	NM_148901	tumor necrosis factor receptor superfamily, member 18	1.07	0.6372	1.27	0.1815	-1.11	0.5241	1.15	0.3761	1.37	0.0699	1.23	0.1450
NRP1	8829	AF268691	neuropilin 1	1.26	0.0635	1.02	0.8353	-1.01	0.9321	1.01	0.8390	1.28	0.1010	1.27	0.0343
NRP1	8829	AF280547	neuropilin 1	1.15	0.2729	1.00	0.9764	-1.01	0.9710	-1.00	0.9925	1.16	0.2252	1.15	0.3234
NRP1	8829	NM_001024628	neuropilin 1	1.15	0.1049	-1.23	0.0499	1.15	0.2722	-1.06	0.5070	-1.07	0.6040	1.08	0.4958
NRP1	8829	NM_001024629	neuropilin 1	1.11	0.2355	-1.04	0.5877	-1.05	0.6028	-1.10	0.2590	1.06	0.5658	1.01	0.9556
NRP1	8829	NM_003873	neuropilin 1	-1.38	0.1748	-1.20	0.3816	-1.01	0.9716	-1.22	0.3607	-1.66	0.0883	-1.68	0.0642
EIF4E2	9470	NM_004846	eukaryotic translation initiation factor 4E member 2	-1.14	0.2337	-1.03	0.8561	-1.10	0.5135	-1.13	0.2998	-1.17	0.2700	-1.29	0.0350
RBX1	9978	NM_014248	ring-box 1	1.00	0.9823	1.02	0.8656	-1.03	0.7854	-1.01	0.9505	1.03	0.7622	-1.01	0.9595
AKT3	10000	NM_005465	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-1.35	0.3184	-2.44	0.0532	1.30	0.3727	-1.88	0.0781	-3.29	0.0043	-2.53	0.0043
AKT3	10000	NM_181690	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-1.34	0.3842	-3.41	0.0502	1.54	0.2416	-2.22	0.0745	-4.58	0.0024	-2.98	0.0025
TBX21	30009	NM_013351	T-box 21	1.20	0.4451	1.73	0.0406	-1.19	0.4679	1.46	0.0715	2.07	0.0365	1.75	0.0411
AK3	50808	BC013771	adenylate kinase 3	-1.12	0.5736	-1.23	0.3281	1.11	0.6827	-1.11	0.5416	-1.38	0.2560	-1.24	0.3416
AK3	50808	NM_016282	adenylate kinase 3	-1.58	0.1324	-1.15	0.5905	-1.12	0.6036	-1.29	0.2884	-1.82	0.0882	-2.04	0.0281
FOXP3	50943	NM_014009	forkhead box P3	1.26	0.2764	1.19	0.4358	-1.19	0.4381	-1.00	0.9851	1.49	0.1319	1.25	0.3028
ANGPT4	51378	BC111976	angiopoietin 4	-1.46	0.0231	1.15	0.1447	-1.17	0.0990	-1.02	0.7804	-1.27	0.1862	-1.48	0.0185
ANGPT4	51378	BC111978	angiopoietin 4	-1.68	0.0196	1.74	0.0144	-1.71	0.0238	1.02	0.8567	1.03	0.8910	-1.65	0.0320
ANGPT4	51378	NM_015985	angiopoietin 4	-1.29	0.0997	1.78	0.0053	-1.41	0.0653	1.26	0.1369	1.38	0.1099	-1.03	0.8694

EGLN1	54583	BC005369	egl nine homolog 1 (C. elegans)	-1.16	0.2072	-1.15	0.3232	-1.01	0.9740	-1.16	0.4034	-1.33	0.0534	-1.34	0.1163
EGLN1	54583	NM_022051	egl nine homolog 1 (C. elegans)	-1.40	0.2053	-1.55	0.2403	1.30	0.5797	-1.19	0.6176	-2.17	0.0473	-1.66	0.1442
HIF1AN	55662	AK025680	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.11	0.4216	-1.41	0.0401	1.10	0.6574	-1.28	0.1075	-1.56	0.0403	-1.41	0.0699
HIF1AN	55662	BC007719	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.31	0.1362	-1.44	0.0515	1.17	0.5028	-1.24	0.1690	-1.89	0.0268	-1.62	0.0358
HIF1AN	55662	NM_017902	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.09	0.1042	-1.11	0.1189	1.02	0.8137	-1.09	0.1679	-1.21	0.0398	-1.18	0.0389
HAMP	57817	NM_021175	hepcidin antimicrobial peptide	1.29	0.3593	1.91	0.0159	-1.30	0.2782	1.48	0.1003	2.46	0.0126	1.90	0.0434
HKDC1	80201	AK026414	hexokinase domain containing 1	-1.02	0.8197	1.37	0.0670	-1.29	0.1403	1.06	0.5519	1.34	0.1332	1.04	0.7325
HKDC1	80201	BC110504	hexokinase domain containing 1	-1.07	0.5432	1.53	0.0055	-1.40	0.0285	1.09	0.4846	1.43	0.0242	1.02	0.8876
HKDC1	80201	NM_025130	hexokinase domain containing 1	-1.01	0.9644	1.42	0.0226	-1.24	0.0951	1.15	0.3057	1.41	0.0318	1.14	0.3453
PROK1	84432	NM_032414	prokineticin 1	1.26	0.4256	1.21	0.4218	1.06	0.8340	1.28	0.3445	1.52	0.1639	1.61	0.1574
RETNLB	84666	BC069318	resistin like beta	1.19	0.4838	2.13	0.0111	-1.57	0.0907	1.36	0.1409	2.54	0.0191	1.61	0.1016
RETNLB	84666	NM_032579	resistin like beta	1.28	0.3437	1.37	0.1248	-1.03	0.8886	1.33	0.2405	1.75	0.0449	1.69	0.1018
EGLN2	112398	NM_017555	egl nine homolog 2 (C. elegans)	-1.20	0.1551	-1.28	0.0974	1.22	0.2817	-1.04	0.7143	-1.53	0.0414	-1.25	0.1645
EGLN2	112398	NM_053046	egl nine homolog 2 (C. elegans)	-1.11	0.2026	-1.25	0.0387	1.22	0.1651	-1.02	0.8101	-1.39	0.0397	-1.13	0.2909
EGLN3	112399	AK123350	egl nine homolog 3 (C. elegans)	1.13	0.1824	1.17	0.2131	-1.06	0.6841	1.10	0.3225	1.32	0.0949	1.25	0.0957
EGLN3	112399	NM_022073	egl nine homolog 3 (C. elegans)	1.17	0.1895	-1.02	0.8464	-1.01	0.9059	-1.03	0.7605	1.14	0.0988	1.13	0.1497
FLJ36951	253314	XM_171094	similar to eukaryotic translation initiation factor 4e 1a	1.21	0.5588	2.17	0.0247	-1.68	0.1317	1.29	0.3574	2.62	0.0448	1.56	0.2823
FLJ36951	253314	XM_927854	similar to eukaryotic translation initiation factor 4e 1a	1.33	0.2629	1.10	0.6328	-1.03	0.8633	1.07	0.7267	1.47	0.0311	1.43	0.0797
FLJ36951	253314	XM_932348	similar to eukaryotic translation initiation factor 4e 1a	1.56	0.1545	1.74	0.0465	-1.34	0.2911	1.30	0.3225	2.72	0.0139	2.03	0.0642

DKFZp781N1041	387712	XM_370577	similar to RIKEN cDNA 6430537H07 gene	1.25	0.2657	-1.31	0.1892	1.21	0.3742	-1.08	0.6946	-1.05	0.7669	1.15	0.4935

Supplementary Table S5. Expression fold changes of 176 HIF-related genes represented by 375 probe set IDs analyzed in human U937 cells exposed to different gravitational conditions during a suborbital ballistic rocket flight (TEXUS-49). The analysis was made with the NimbleGen expression microarray based on the hg18 annotation.

				μg vs BL-TX hyp-g		BL-TX hyp-g vs HW 1g GC		μg vs HW 1g GC	
Gene Symbol	**Entrez Gene ID**	**Probe set ID**	**Description**	**Fold Change**	**p-value**	**Fold Change**	**p-value**	**Fold Change**	**p-value**
ADM	133	NM_001124	adrenomedullin	1.43	0.1949	1.07	0.6203	1.53	0.1034
ADORA2A	135	BC013780	adenosine A2a receptor	-1.41	0.3167	-1.44	0.3685	-2.03	0.1069
ADORA2A	135	NM_000675	adenosine A2a receptor	1.05	0.8061	-1.33	0.1953	-1.26	0.2288
ADRA1B	147	NM_000679	adrenergic, alpha-1B-, receptor	1.84	0.0885	-1.88	0.1500	-1.02	0.9419
AKT1	207	BC084538	v-akt murine thymoma viral oncogene homolog 1	-1.19	0.1811	1.23	0.1489	1.03	0.7966
AKT1	207	BX647722	v-akt murine thymoma viral oncogene homolog 1	1.70	0.1578	-1.31	0.2707	1.29	0.3372
AKT1	207	NM_001014431	v-akt murine thymoma viral oncogene homolog 1	-1.11	0.3300	1.10	0.4325	-1.01	0.9040
AKT2	208	NM_001626	v-akt murine thymoma viral oncogene homolog 2	-1.35	0.3026	-1.20	0.4833	-1.62	0.0895
ALDOA	226	CR592372	aldolase A, fructose-bisphosphate	1.06	0.1023	-1.07	0.0559	-1.01	0.8368
ALDOA	226	NM_000034	aldolase A, fructose-bisphosphate	-1.02	0.4955	-1.04	0.2344	-1.06	0.0502
ALDOA	226	NM_184041	aldolase A, fructose-bisphosphate	1.02	0.5277	-1.00	0.9843	1.01	0.5904
ALDOC	230	BC106925	aldolase C, fructose-bisphosphate	-1.30	0.3143	-1.13	0.5555	-1.47	0.0980
ALDOC	230	NM_005165	aldolase C, fructose-bisphosphate	-1.32	0.2574	1.21	0.4058	-1.09	0.7259
ANGPT1	284	BC029406	angiopoietin 1	-1.44	0.0345	-1.02	0.9488	-1.46	0.1090
ANGPT1	284	NM_001146	angiopoietin 1	1.00	0.9727	1.05	0.2889	1.05	0.4474
ANGPT2	285	AF187858	angiopoietin 2	1.39	0.0130	-1.52	0.2336	-1.09	0.7298
ANGPT2	285	AF218015	angiopoietin 2	1.10	0.5773	-1.03	0.8690	1.07	0.6512
ANGPT2	285	NM_001147	angiopoietin 2	1.00	0.9852	1.01	0.9302	1.01	0.9344
ARG1	383	BC020653	arginase, liver	1.07	0.5715	-1.13	0.2970	-1.05	0.5997
ARG1	383	NM_000045	arginase, liver	1.08	0.6857	-1.17	0.4386	-1.09	0.6395
ARNT	405	AB209877	aryl hydrocarbon receptor nuclear translocator	-1.53	0.1571	1.11	0.6624	-1.37	0.3298
ARNT	405	BC060838	aryl hydrocarbon receptor nuclear translocator	-1.75	0.1459	1.88	0.0451	1.07	0.8814
ARNT	405	NM_001668	aryl hydrocarbon receptor nuclear translocator	-1.81	0.0891	1.63	0.0658	-1.11	0.8025
BCL2	596	BC027258	B-cell CLL/lymphoma 2	-1.64	0.1676	1.63	0.1292	-1.01	0.9879
BCL2	596	NM_000633	B-cell CLL/lymphoma 2	-1.90	0.1412	3.88	0.0057	2.04	0.2525
BCL2	596	NM_000657	B-cell CLL/lymphoma 2	1.75	0.1024	-1.45	0.0792	1.21	0.4610

BLR1	643	NM_001716	Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)	3.86	0.0825	-2.71	0.1564	1.42	0.4852
CA9	768	NM_001216	carbonic anhydrase IX	3.12	0.1189	-2.27	0.1005	1.37	0.5098
CAMK2A	815	AF145710	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	1.75	0.2483	-1.45	0.3989	1.20	0.6126
CAMK2A	815	AF145711	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	2.36	0.0895	-1.90	0.1880	1.24	0.5847
CAMK2A	815	NM_015981	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	1.82	0.0827	-2.37	0.0529	-1.30	0.4063
CAMK2B	816	NM_001220	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	6.23	0.1142	-1.81	0.3716	3.45	0.1387
CAMK2B	816	NM_172078	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	4.25	0.1675	-1.56	0.5172	2.74	0.2051
CAMK2B	816	NM_172080	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	6.13	0.1390	-2.37	0.2964	2.59	0.2429
CAMK2B	816	NM_172081	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	8.43	0.0959	-3.14	0.2312	2.69	0.2026
CAMK2B	816	NM_172082	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	7.21	0.1533	-2.07	0.3023	3.48	0.1950
CAMK2B	816	NM_172084	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	3.70	0.1397	-2.06	0.0981	1.80	0.3246
CAMK2D	817	NM_172115	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.57	0.2100	1.66	0.1105	1.06	0.8807
CAMK2D	817	AB209288	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.10	0.0291	1.07	0.4607	-1.03	0.7303
CAMK2D	817	NM_001221	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.90	0.1017	2.50	0.0139	1.31	0.5389
CAMK2D	817	NM_172127	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-1.78	0.1799	4.60	0.0046	2.58	0.1478
CAMK2G	818	NM_001222	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma	-1.28	0.0565	-1.05	0.6140	-1.34	0.0100
CAMP	820	BC055089	cathelicidin antimicrobial peptide	1.64	0.0892	-1.27	0.1654	1.29	0.3013
CAMP	820	NM_004345	cathelicidin antimicrobial peptide	1.80	0.1168	-2.03	0.0614	-1.13	0.6650
CD36	948	BC008406	CD36 molecule (thrombospondin receptor)	-1.37	0.0507	1.58	0.0082	1.15	0.2964
CD36	948	NM_000072	CD36 molecule (thrombospondin receptor)	-2.11	0.0199	2.33	0.0003	1.11	0.7990
CD36	948	NM_001001548	CD36 molecule (thrombospondin receptor)	-1.67	0.0758	1.96	0.0312	1.17	0.3875
CDKN1A	1026	NM_000389	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-1.01	0.8519	1.01	0.9309	-1.01	0.9496
CDKN1A	1026	NM_078467	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.02	0.6913	-1.05	0.6080	-1.03	0.6923
CDKN1B	1027	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	-2.35	0.0083	2.23	0.0006	-1.05	0.8952

CCR1	1230	BC051306	chemokine (C-C motif) receptor 1	-1.78	0.0392	2.35	0.0001	1.32	0.4458
CCR1	1230	NM_001295	chemokine (C-C motif) receptor 1	-1.41	0.0818	1.55	0.0384	1.10	0.6812
CCR5	1234	BC038398	chemokine (C-C motif) receptor 5	1.40	0.2362	-1.39	0.2173	1.01	0.9697
CCR5	1234	NM_000579	chemokine (C-C motif) receptor 5	1.35	0.3647	-1.06	0.7782	1.28	0.3827
CCR7	1236	NM_001838	chemokine (C-C motif) receptor 7	1.73	0.2080	-1.26	0.5868	1.38	0.4080
CREBBP	1387	NM_004380	CREB binding protein (Rubinstein-Taybi syndrome)	-1.91	0.1097	4.69	0.0038	2.46	0.1153
CREBBP	1387	U85962	CREB binding protein (Rubinstein-Taybi syndrome)	-1.49	0.2553	1.53	0.2221	1.03	0.9388
MAPK14	1432	BC000092	mitogen-activated protein kinase 14	-1.40	0.0671	1.40	0.0056	-1.00	0.9858
MAPK14	1432	NM_001315	mitogen-activated protein kinase 14	-1.67	0.0318	1.57	0.0022	-1.06	0.8102
MAPK14	1432	NM_139013	mitogen-activated protein kinase 14	-1.50	0.0596	1.41	0.0284	-1.07	0.7564
CTLA4	1493	BC069566	cytotoxic T-lymphocyte-associated protein 4	1.03	0.8638	-1.34	0.0692	-1.30	0.0514
CTLA4	1493	BC074842	cytotoxic T-lymphocyte-associated protein 4	1.29	0.3802	-1.05	0.8126	1.23	0.3701
CTLA4	1493	BC074893	cytotoxic T-lymphocyte-associated protein 4	1.03	0.9259	1.10	0.6445	1.13	0.6395
CTLA4	1493	NM_001037631	cytotoxic T-lymphocyte-associated protein 4	2.44	0.2634	-3.13	0.2735	-1.29	0.7089
CTLA4	1493	NM_005214	cytotoxic T-lymphocyte-associated protein 4	3.32	0.2038	-3.51	0.1914	-1.06	0.9304
CTSD	1509	NM_001909	cathepsin D (lysosomal aspartyl peptidase)	1.02	0.7466	-1.10	0.1252	-1.08	0.0488
CYBB	1536	BC032720	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	-1.97	0.0596	1.82	0.0086	-1.08	0.8501
CYBB	1536	NM_000397	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	-1.96	0.0771	1.79	0.0101	-1.09	0.8414
DEFB1	1672	BC033298	defensin, beta 1	-1.40	0.1198	-1.40	0.0660	-1.96	0.0026
DEFB1	1672	NM_005218	defensin, beta 1	2.30	0.1222	-2.86	0.2303	-1.24	0.6903
EDG1	1901	NM_001400	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	1.72	0.3280	-1.61	0.4006	1.07	0.8794
EDN1	1906	CR605456	endothelin 1	1.05	0.4277	-1.01	0.9131	1.04	0.5859
EDN1	1906	NM_001955	endothelin 1	-1.05	0.6028	-1.46	0.1153	-1.53	0.0426
EGF	1950	BC093731	epidermal growth factor (beta-urogastrone)	1.25	0.1117	-1.28	0.1467	-1.03	0.8541
EGF	1950	NM_001963	epidermal growth factor (beta-urogastrone)	1.06	0.7720	1.00	0.9864	1.07	0.7461
EGFR	1956	BC094761	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	3.37	0.1872	-2.62	0.0903	1.28	0.6634
EGFR	1956	K03193	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.74	0.1685	-1.73	0.2068	1.00	0.9906
EGFR	1956	NM_005228	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.07	0.6787	-1.29	0.1514	-1.21	0.2223
EGFR	1956	NM_201282	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.15	0.5976	-1.69	0.0231	-1.46	0.1041

EGFR	1956	NM_201283	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	4.04	0.0789	-3.11	0.2448	1.30	0.6442
EGFR	1956	NM_201284	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene hom	1.51	0.1358	-1.23	0.2669	1.23	0.3806
EIF4E	1977	BC012611	eukaryotic translation initiation factor 4E	-2.11	0.0161	2.00	0.0001	-1.06	0.8745
EIF4E	1977	BC035166	eukaryotic translation initiation factor 4E	1.24	0.4388	-1.07	0.7718	1.17	0.5615
EIF4E	1977	NM_001968	eukaryotic translation initiation factor 4E	-2.07	0.0137	2.15	0.0001	1.04	0.9198
EIF4EBP1	1978	BC058073	eukaryotic translation initiation factor 4E binding protein 1	1.03	0.3281	-1.03	0.5313	1.00	0.9654
EIF4EBP1	1978	NM_004095	eukaryotic translation initiation factor 4E binding protein 1	1.04	0.2187	-1.05	0.1690	-1.01	0.7900
ENG	2022	BC014271	endoglin (Osler-Rendu-Weber syndrome 1)	-1.10	0.3934	-1.14	0.3146	-1.25	0.0560
ENG	2022	NM_000118	endoglin (Osler-Rendu-Weber syndrome 1)	-1.09	0.5051	-1.09	0.5411	-1.18	0.1883
ENO1	2023	BC050642	enolase 1, (alpha)	-1.01	0.7349	1.03	0.3931	1.02	0.5191
ENO1	2023	BC073991	enolase 1, (alpha)	-1.01	0.6366	1.01	0.5181	-1.01	0.8360
ENO1	2023	NM_001428	enolase 1, (alpha)	-1.02	0.6153	1.00	0.9342	-1.02	0.6520
ENO2	2026	NM_001975	enolase 2 (gamma, neuronal)	-1.15	0.4581	1.04	0.8147	-1.10	0.5669
ENO3	2027	BC017249	enolase 3 (beta, muscle)	-1.05	0.7402	-1.05	0.8014	-1.10	0.5619
ENO3	2027	NM_001976	enolase 3 (beta, muscle)	-1.08	0.6540	-1.01	0.9636	-1.09	0.6859
ENO3	2027	NM_053013	enolase 3 (beta, muscle)	-1.04	0.8178	-1.07	0.7124	-1.11	0.5472
EP300	2033	NM_001429	E1A binding protein p300	-1.51	0.0782	1.51	0.0543	-1.00	0.9936
EPAS1	2034	NM_001430	endothelial PAS domain protein 1	-1.60	0.0683	2.05	0.0079	1.28	0.4576
EPO	2056	BC093628	erythropoietin	3.60	0.0896	-1.93	0.2031	1.87	0.2320
EPO	2056	NM_000799	erythropoietin	2.49	0.0260	-1.83	0.0230	1.36	0.2797
ERBB2	2064	AF177761	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	3.01	0.0985	-1.78	0.2898	1.69	0.2770
ERBB2	2064	AK131568	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	2.25	0.0642	-1.61	0.1225	1.40	0.3099
ERBB2	2064	NM_001005862	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived	1.36	0.2392	1.16	0.3930	1.58	0.0937
FLT1	2321	BC039007	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeabilit	-1.94	0.0767	3.30	0.0052	1.70	0.2047
FLT1	2321	NM_002019	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeabilit	1.06	0.4494	-1.05	0.5351	1.01	0.9073
FN1	2335	AB191261	fibronectin 1	1.01	0.9723	-1.41	0.3318	-1.40	0.2898

FN1	2335	BX538018	fibronectin 1	-1.09	0.6871	-1.31	0.2164	-1.42	0.1056
FN1	2335	CR749317	fibronectin 1	1.08	0.5974	-1.03	0.7967	1.04	0.7416
FN1	2335	NM_002026	fibronectin 1	-1.18	0.3942	-1.04	0.8979	-1.22	0.4103
FN1	2335	NM_054034	fibronectin 1	-1.06	0.6108	-1.21	0.3515	-1.28	0.2044
FRAP1	2475	NM_004958	FK506 binding protein 12-rapamycin associated protein 1	-1.33	0.0519	1.36	0.0179	1.03	0.8719
GAPDH	2597	BC001601	glyceraldehyde-3-phosphate dehydrogenase	1.03	0.4748	1.05	0.1872	1.08	0.0694
GAPDH	2597	BC009081	glyceraldehyde-3-phosphate dehydrogenase	1.05	0.3451	1.05	0.4575	1.10	0.1206
GAPDH	2597	NM_002046	glyceraldehyde-3-phosphate dehydrogenase	-1.00	0.9516	1.08	0.0954	1.08	0.0738
GPI	2821	BC004982	glucose phosphate isomerase	-1.02	0.6728	-1.00	0.9626	-1.02	0.6383
GPI	2821	NM_000175	glucose phosphate isomerase	-1.06	0.4306	-1.01	0.9507	-1.07	0.3862
MKNK2	2872	AF237775	MAP kinase interacting serine/threonine kinase 2	-1.07	0.7128	1.03	0.8862	-1.04	0.7920
MKNK2	2872	NM_017572	MAP kinase interacting serine/threonine kinase 2	-1.10	0.6397	1.00	0.9871	-1.09	0.6199
MKNK2	2872	NM_199054	MAP kinase interacting serine/threonine kinase 2	-1.02	0.8505	1.17	0.1181	1.15	0.1581
CXCL2	2920	BC015753	chemokine (C-X-C motif) ligand 2	1.51	0.0897	-1.08	0.4705	1.40	0.1115
CXCL2	2920	NM_002089	chemokine (C-X-C motif) ligand 2	-1.22	0.4470	1.27	0.3324	1.05	0.8474
HDAC2	3066	NM_001527	histone deacetylase 2	-1.35	0.0472	1.54	0.0013	1.14	0.4208
HIF1A	3091	NM_001530	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor	-1.99	0.0630	2.28	0.0044	1.14	0.7872
HIF1A	3091	NM_181054	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor	-2.02	0.0642	2.49	0.0013	1.23	0.6765
HK1	3098	NM_000188	hexokinase 1	-1.46	0.1643	-1.10	0.5756	-1.61	0.0494
HK2	3099	BC021116	hexokinase 2	-1.58	0.1550	1.31	0.2793	-1.21	0.5156
HK2	3099	NM_000189	hexokinase 2	-1.86	0.0399	2.19	0.0001	1.18	0.6742
HK3	3101	NM_002115	hexokinase 3 (white cell)	-1.30	0.3826	-1.12	0.7366	-1.46	0.2607
HMOX1	3162	BC001491	heme oxygenase (decycling) 1	-1.36	0.1515	-1.01	0.9726	-1.37	0.2655
HMOX1	3162	NM_002133	heme oxygenase (decycling) 1	-1.36	0.2212	-1.12	0.6770	-1.51	0.1727
ICAM1	3383	NM_000201	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	1.00	0.9534	-1.00	0.9879	1.00	0.9855
IFNG	3458	NM_000619	interferon, gamma	-1.19	0.3501	1.06	0.7843	-1.12	0.3547
IFNGR1	3459	NM_000416	interferon gamma receptor 1	-2.10	0.0155	2.26	0.0000	1.08	0.8488
IFNGR2	3460	NM_005534	interferon gamma receptor 2 (interferon gamma transducer 1)	-1.29	0.0687	1.39	0.0084	1.08	0.6172
IGF1	3479	M11568	insulin-like growth factor 1 (somatomedin C)	2.74	0.2295	-2.18	0.2316	1.25	0.6772
IGF1	3479	M29644	insulin-like growth factor 1 (somatomedin C)	1.75	0.0825	-1.82	0.1015	-1.04	0.9040
IGF1	3479	M37484	insulin-like growth factor 1 (somatomedin C)	2.56	0.1323	-1.52	0.4416	1.69	0.2905
IGF1	3479	NM_000618	insulin-like growth factor 1 (somatomedin C)	-1.23	0.0539	1.00	0.9671	-1.22	0.0283
IGF1R	3480	NM_000875	insulin-like growth factor 1 receptor	-1.33	0.3047	1.17	0.5196	-1.14	0.5914

IGF2	3481	BC053318	insulin-like growth factor 2 (somatomedin A)	2.10	0.2741	-1.06	0.8777	1.99	0.2508
IGF2	3481	NM_000612	insulin-like growth factor 2 (somatomedin A)	3.59	0.1887	-1.57	0.2147	2.28	0.2551
IGFBP1	3484	NM_000596	insulin-like growth factor binding protein 1	1.06	0.6414	-1.46	0.4366	-1.38	0.4207
IGFBP1	3484	NM_001013029	insulin-like growth factor binding protein 1	1.30	0.1376	-1.34	0.2030	-1.03	0.8642
IGFBP2	3485	NM_000597	insulin-like growth factor binding protein 2, 36kDa	-1.27	0.1459	1.15	0.2040	-1.11	0.4315
IGFBP3	3486	BC000013	insulin-like growth factor binding protein 3	1.28	0.3060	-1.08	0.6052	1.19	0.4271
IGFBP3	3486	NM_000598	insulin-like growth factor binding protein 3	1.39	0.2040	-1.31	0.0475	1.06	0.7601
IL1B	3553	NM_000576	interleukin 1, beta	-1.43	0.0457	1.28	0.0754	-1.12	0.5714
IL6	3569	NM_000600	interleukin 6 (interferon, beta 2)	1.84	0.2540	-1.70	0.1250	1.08	0.8511
IL6R	3570	BC089410	interleukin 6 receptor	-1.26	0.2663	1.22	0.2861	-1.03	0.8402
IL6R	3570	NM_000565	interleukin 6 receptor	-1.57	0.1549	1.42	0.1157	-1.11	0.7363
IL8	3576	NM_000584	interleukin 8	-1.98	0.0402	2.17	0.0005	1.10	0.8284
IL12A	3592	BC104982	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte matura	-1.35	0.3592	1.73	0.0602	1.29	0.4594
IL12A	3592	NM_000882	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte matura	-1.15	0.3370	1.06	0.6569	-1.09	0.5773
TNFRSF9	3604	NM_001561	tumor necrosis factor receptor superfamily, member 9	-1.00	0.9909	-1.50	0.0860	-1.50	0.0650
INS	3630	BC005255	insulin	1.13	0.7000	-1.29	0.4240	-1.14	0.6867
INS	3630	NM_000207	insulin	6.45	0.1320	-2.05	0.0489	3.15	0.1742
INSR	3643	NM_000208	insulin receptor	-1.54	0.2439	1.14	0.6413	-1.34	0.3929
INSR	3643	X02160	insulin receptor	-1.60	0.0725	1.64	0.0110	1.02	0.9402
ITGAM	3684	BC096346	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.14	0.3263	-1.02	0.8850	-1.17	0.2321
ITGAM	3684	J03925	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.41	0.0913	1.99	0.0021	1.41	0.1932
ITGAM	3684	NM_000632	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.18	0.3668	1.02	0.9082	-1.15	0.4582
ITGB2	3689	AK097864	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	2.12	0.0238	-2.08	0.0067	1.02	0.9239
ITGB2	3689	NM_000211	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	-1.10	0.3811	1.12	0.1930	1.02	0.8217
KDR	3791	NM_002253	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.31	0.2868	-1.41	0.3319	-1.07	0.8169
KRT14	3861	NM_000526	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	4.01	0.1353	-1.87	0.2014	2.14	0.2456
KRT18	3875	BC000180	keratin 18	3.52	0.1505	-3.93	0.2534	-1.12	0.8655
KRT18	3875	BC004253	keratin 18	3.51	0.1144	-3.41	0.2878	1.03	0.9612
KRT18	3875	NM_000224	keratin 18	3.50	0.1258	-3.99	0.2709	-1.14	0.8457

KRT18	3875	NM_199187	keratin 18	3.66	0.1072	-3.18	0.2828	1.15	0.8162
KRT19	3880	BC007628	keratin 19	2.55	0.0656	-2.05	0.2812	1.24	0.6323
KRT19	3880	NM_002276	keratin 19	3.17	0.0561	-2.32	0.1424	1.37	0.4596
LAG3	3902	BC052589	lymphocyte-activation gene 3	3.38	0.1585	-1.84	0.3812	1.84	0.3450
LAG3	3902	NM_002286	lymphocyte-activation gene 3	4.91	0.1080	-2.33	0.2711	2.11	0.2608
LDHA	3939	NM_005566	lactate dehydrogenase A	-1.45	0.0101	1.37	0.0300	-1.06	0.6665
LEP	3952	BC069323	leptin (obesity homolog, mouse)	1.86	0.2130	-1.48	0.3945	1.26	0.5825
LEP	3952	D49487	leptin (obesity homolog, mouse)	1.82	0.1530	-1.87	0.3031	-1.03	0.9498
LEP	3952	NM_000230	leptin (obesity homolog, mouse)	1.41	0.0980	-1.74	0.1090	-1.24	0.3996
LRP1	4035	BC045107	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.46	0.1368	-2.04	0.0019	-1.40	0.0932
LRP1	4035	BC052593	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.38	0.1195	-1.96	0.0839	1.22	0.6050
LRP1	4035	NM_002332	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.74	0.0746	-2.09	0.0395	1.31	0.4658
LTBR	4055	NM_002342	lymphotoxin beta receptor (TNFR superfamily, member 3)	-1.03	0.7233	-1.08	0.3121	-1.12	0.1434
MMP2	4313	BC002576	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	-1.32	0.2175	1.10	0.6141	-1.20	0.4554
MMP2	4313	NM_004530	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	-1.39	0.1049	1.23	0.2229	-1.13	0.5998
MMP9	4318	NM_004994	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	1.23	0.3265	-1.07	0.7400	1.15	0.4512
MMP14	4323	BC064803	matrix metallopeptidase 14 (membrane-inserted)	2.00	0.0780	-1.64	0.0268	1.22	0.4626
MMP14	4323	NM_004995	matrix metallopeptidase 14 (membrane-inserted)	2.03	0.0699	-1.73	0.0104	1.17	0.5545
NFKB1	4790	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.56	0.0391	1.46	0.0020	-1.07	0.7691
NFKB1	4790	BC051765	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.62	0.0471	1.47	0.0043	-1.10	0.6976
NFKB1	4790	M58603	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-1.61	0.0557	1.49	0.0016	-1.08	0.7673
NOS2A	4843	NM_000625	nitric oxide synthase 2A (inducible, hepatocytes)	2.27	0.1319	-1.34	0.1569	1.69	0.2238
NOS3	4846	BC069465	nitric oxide synthase 3 (endothelial cell)	1.19	0.3465	-1.15	0.4137	1.04	0.8344
NOS3	4846	NM_000603	nitric oxide synthase 3 (endothelial cell)	1.18	0.2947	-1.23	0.2274	-1.05	0.7718
NPPA	4878	BC005893	natriuretic peptide precursor A	1.86	0.0897	-1.88	0.0853	-1.01	0.9729
NPPA	4878	NM_006172	natriuretic peptide precursor A	1.81	0.1393	-1.61	0.2726	1.12	0.7538
SERPINE1	5054	BC010860	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), m	-1.49	0.1378	1.21	0.4634	-1.22	0.4975

SERPINE1	5054	NM_000602	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), m	-1.40	0.0591	1.50	0.0011	1.07	0.6995
PDGFB	5155	BC029822	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	1.52	0.1189	-1.36	0.3134	1.12	0.6663
PDGFB	5155	BC077725	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	2.46	0.0607	-1.39	0.3890	1.77	0.1613
PDGFB	5155	NM_002608	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	1.90	0.1122	-1.28	0.2705	1.48	0.2415
PDGFB	5155	X83705	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene	1.56	0.2063	-1.19	0.2542	1.31	0.3661
PDHA1	5160	CR614489	pyruvate dehydrogenase (lipoamide) alpha 1	-1.19	0.0952	1.19	0.0305	1.00	0.9937
PDHA1	5160	NM_000284	pyruvate dehydrogenase (lipoamide) alpha 1	-1.19	0.0646	1.16	0.0444	-1.02	0.8173
PDHA2	5161	NM_005390	pyruvate dehydrogenase (lipoamide) alpha 2	3.86	0.1873	-4.72	0.1455	-1.22	0.7517
PDHB	5162	NM_000925	pyruvate dehydrogenase (lipoamide) beta	-1.58	0.0493	1.04	0.6541	-1.52	0.0660
PDK1	5163	BC039158	pyruvate dehydrogenase kinase, isozyme 1	-1.56	0.0159	1.48	0.0008	-1.05	0.7545
PDK1	5163	DQ234350	pyruvate dehydrogenase kinase, isozyme 1	-1.29	0.0220	1.37	0.0002	1.06	0.6045
PDK1	5163	NM_002610	pyruvate dehydrogenase kinase, isozyme 1	-1.56	0.0184	1.62	0.0004	1.04	0.8349
PFKFB3	5209	AF056320	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.15	0.1187	1.35	0.0004	1.18	0.0837
PFKFB3	5209	AK131307	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.21	0.0726	1.38	0.0012	1.14	0.2844
PFKFB3	5209	NM_004566	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.42	0.1680	1.57	0.0315	1.10	0.7134
PFKL	5211	NM_001002021	phosphofructokinase, liver	-1.02	0.8517	-1.07	0.4940	-1.09	0.2835
PFKL	5211	BX537446	phosphofructokinase, liver	1.04	0.7122	-1.10	0.3140	-1.06	0.3226
PGK1	5230	BC023234	phosphoglycerate kinase 1	-1.14	0.0638	1.17	0.0006	1.03	0.6513
PGK1	5230	BC103752	phosphoglycerate kinase 1	-1.12	0.0762	1.14	0.0128	1.01	0.8636
PGK1	5230	NM_000291	phosphoglycerate kinase 1	-1.10	0.0645	1.16	0.0120	1.06	0.3270
ABCB1	5243	AF016535	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.45	0.2028	-1.69	0.0083	-1.17	0.4901
ABCB1	5243	NM_000927	ATP-binding cassette, sub-family B (MDR/TAP), member 1	-1.09	0.4238	-1.57	0.0222	-1.71	0.0021
PIK3CA	5290	NM_006218	phosphoinositide-3-kinase, catalytic, alpha polypeptide	-1.90	0.1379	2.72	0.0105	1.43	0.5275
PIK3CB	5291	NM_006219	phosphoinositide-3-kinase, catalytic, beta polypeptide	-1.93	0.0783	1.91	0.0168	-1.01	0.9858
PIK3CB	5291	CR749357	phosphoinositide-3-kinase, catalytic, beta polypeptide	-1.97	0.0256	2.77	0.0027	1.41	0.2559

PIK3CD	5293	U57843	phosphoinositide-3-kinase, catalytic, delta polypeptide	1.01	0.9384	-1.19	0.1568	-1.18	0.0636
PIK3CD	5293	NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide	-1.20	0.0800	-1.00	0.9756	-1.20	0.1241
PIK3R1	5295	BC030815	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-1.81	0.1445	1.12	0.6583	-1.61	0.2160
PIK3R1	5295	BC094795	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-1.73	0.2124	2.00	0.0887	1.15	0.7963
PIK3R1	5295	NM_181504	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-1.75	0.1192	1.44	0.1550	-1.22	0.6005
PIK3R2	5296	NM_005027	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	-1.11	0.5099	1.29	0.1162	1.16	0.4206
PKM2	5315	NM_002654	pyruvate kinase, muscle	-1.02	0.5475	-1.00	0.9841	-1.03	0.5202
PLAUR	5329	NM_001005376	plasminogen activator, urokinase receptor	-1.20	0.0530	1.06	0.3086	-1.13	0.1909
PLAUR	5329	NM_001005377	plasminogen activator, urokinase receptor	-1.25	0.1610	1.01	0.8963	-1.23	0.1332
PLAUR	5329	NM_002659	plasminogen activator, urokinase receptor	-1.16	0.0727	1.00	0.9993	-1.16	0.0432
PLCG1	5335	NM_002660	phospholipase C, gamma 1	-1.44	0.0949	-1.08	0.7319	-1.56	0.1012
PLCG2	5336	BC007565	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.16	0.1367	1.22	0.0138	1.05	0.6870
PLCG2	5336	NM_002661	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.15	0.2443	1.13	0.1779	-1.02	0.8704
PRKCA	5578	BC109273	protein kinase C, alpha	1.61	0.1224	-1.67	0.1692	-1.04	0.8963
PRKCA	5578	NM_002737	protein kinase C, alpha	1.85	0.0946	-2.15	0.1615	-1.16	0.6932
PRKCB1	5579	NM_212535	protein kinase C, beta 1	-1.77	0.0166	1.57	0.0021	-1.13	0.5976
PRKCB1	5579	BC036472	protein kinase C, beta 1	-1.48	0.0457	1.30	0.0024	-1.14	0.4714
PRKCB1	5579	NM_002738	protein kinase C, beta 1	-2.01	0.0263	2.40	0.0075	1.19	0.5247
PRKCG	5582	BC047876	protein kinase C, gamma	3.72	0.1731	-1.64	0.5505	2.27	0.2723
PRKCG	5582	NM_002739	protein kinase C, gamma	4.69	0.0718	-2.14	0.2930	2.19	0.1819
MAPK1	5594	NM_138957	mitogen-activated protein kinase 1	-1.72	0.0659	1.52	0.0501	-1.13	0.7170
MAPK1	5594	Z11695	mitogen-activated protein kinase 1	-1.86	0.0423	1.90	0.0043	1.02	0.9502
MAPK1	5594	BC099905	mitogen-activated protein kinase 1	-2.07	0.0141	2.87	0.0000	1.38	0.4239
MAPK1	5594	NM_002745	mitogen-activated protein kinase 1	-1.74	0.0409	3.65	0.0000	2.10	0.0628
MAPK3	5595	NM_002746	mitogen-activated protein kinase 3	1.09	0.1978	-1.08	0.2932	1.00	0.9388
MAPK3	5595	AY033607	mitogen-activated protein kinase 3	-1.14	0.5712	-1.12	0.6197	-1.28	0.2751
MAPK3	5595	NM_001040056	mitogen-activated protein kinase 3	1.02	0.8119	-1.04	0.5941	-1.02	0.8220
MAP2K1	5604	NM_002755	mitogen-activated protein kinase kinase 1	-1.48	0.0695	1.68	0.0064	1.14	0.6025
MAP2K2	5605	NM_030662	mitogen-activated protein kinase kinase 2	1.05	0.3736	-1.06	0.2654	-1.01	0.8482
RELA	5970	BC011603	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.23	0.3378	-1.18	0.3729	-1.46	0.0662
RELA	5970	BC014095	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.15	0.4102	-1.17	0.3473	-1.34	0.0831

RELA	5970	BC110830	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.24	0.2445	-1.08	0.7330	-1.33	0.2306
RELA	5970	NM_021975	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light po	-1.20	0.4070	-1.17	0.4016	-1.40	0.0892
RORC	6097	BC031554	RAR-related orphan receptor C	1.13	0.3642	-1.11	0.5271	1.02	0.8476
RORC	6097	BC110571	RAR-related orphan receptor C	1.02	0.9228	-1.29	0.3105	-1.27	0.2847
RORC	6097	NM_001001523	RAR-related orphan receptor C	1.06	0.7904	1.13	0.5695	1.20	0.4785
RPS6	6194	NM_001010	ribosomal protein S6	1.12	0.5066	1.18	0.4840	1.32	0.1430
RPS6KB1	6198	BC053365	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.64	0.1190	1.53	0.0512	-1.07	0.8416
RPS6KB1	6198	BC036033	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.96	0.0633	1.83	0.0073	-1.07	0.8602
RPS6KB1	6198	NM_003161	ribosomal protein S6 kinase, 70kDa, polypeptide 1	-1.37	0.0077	1.79	0.0000	1.30	0.0454
RPS6KB2	6199	BC000094	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.09	0.5157	-1.01	0.9501	-1.10	0.4160
RPS6KB2	6199	BC006106	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.06	0.6860	1.01	0.9711	-1.05	0.6819
RPS6KB2	6199	NM_001007071	ribosomal protein S6 kinase, 70kDa, polypeptide 2	-1.06	0.6380	-1.03	0.8221	-1.09	0.4382
CCL2	6347	NM_002982	chemokine (C-C motif) ligand 2	-1.44	0.0579	1.48	0.0365	1.03	0.8868
CXCL6	6372	NM_002993	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	-1.01	0.9159	1.03	0.8703	1.02	0.9094
SELL	6402	BC020758	selectin L (lymphocyte adhesion molecule 1)	-1.80	0.0908	2.43	0.0064	1.35	0.4707
SELL	6402	NM_000655	selectin L (lymphocyte adhesion molecule 1)	-1.61	0.0532	1.89	0.0012	1.18	0.5814
SELL	6402	AJ246000	selectin L (lymphocyte adhesion molecule 1)	-1.77	0.1066	2.04	0.0327	1.15	0.7248
SLC2A1	6513	NM_006516	solute carrier family 2 (facilitated glucose transporter), member 1	-1.34	0.2891	-1.17	0.5071	-1.57	0.1082
SLC2A3	6515	BC039196	solute carrier family 2 (facilitated glucose transporter), member 3	-1.51	0.0630	1.50	0.0099	-1.01	0.9694
SLC2A3	6515	NM_006931	solute carrier family 2 (facilitated glucose transporter), member 3	-1.40	0.0365	1.50	0.0007	1.07	0.7093
SLC11A1	6556	BC041787	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	2.47	0.1280	-1.23	0.6553	2.02	0.1458
SLC11A1	6556	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	2.22	0.1128	-1.42	0.1969	1.56	0.2633
SLC11A1	6556	NM_001032220	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	2.05	0.1352	-1.09	0.6820	1.88	0.1294
STAT3	6774	BC000627	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.09	0.0755	1.31	0.0004	1.20	0.0056
STAT3	6774	BC014482	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.07	0.1427	1.30	0.0008	1.21	0.0012

STAT3	6774	NM_003150	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.67	0.1091	1.62	0.0404	-1.03	0.9368
STAT3	6774	NM_213662	signal transducer and activator of transcription 3 (acute-phase response factor)	-1.67	0.1005	1.67	0.0366	1.00	0.9999
STAT4	6775	NM_003151	signal transducer and activator of transcription 4	1.23	0.0235	-1.64	0.1542	-1.33	0.2557
TCEB1	6921	BC093065	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.38	0.2365	1.29	0.4157	-1.07	0.6993
TCEB1	6921	BC100028	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.40	0.2048	1.28	0.4324	-1.09	0.6256
TCEB1	6921	BC100283	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.32	0.3778	1.28	0.5054	-1.03	0.8769
TCEB1	6921	NM_005648	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	-1.34	0.2935	1.19	0.6107	-1.13	0.5461
TCEB2	6923	BC013306	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.19	0.1920	-1.05	0.6149	1.13	0.2826
TCEB2	6923	BC065000	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	1.04	0.6348	-1.08	0.1161	-1.04	0.5314
TCEB2	6923	NM_007108	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	-1.07	0.5593	-1.02	0.7810	-1.09	0.4363
TCEB2	6923	NM_207013	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	-1.03	0.7214	-1.05	0.3642	-1.07	0.3240
TCF7	6932	BC048769	transcription factor 7 (T-cell specific, HMG-box)	-1.26	0.1897	1.17	0.4467	-1.07	0.6812
TCF7	6932	NM_003202	transcription factor 7 (T-cell specific, HMG-box)	-1.02	0.8709	1.11	0.4446	1.09	0.5039
TCF7	6932	NM_201633	transcription factor 7 (T-cell specific, HMG-box)	1.67	0.1336	-1.43	0.3279	1.17	0.6438
TEK	7010	NM_000459	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal	-1.08	0.1633	-1.23	0.1832	-1.33	0.0396
TF	7018	AK126941	transferrin	1.17	0.2817	-1.40	0.1470	-1.20	0.3531
TF	7018	NM_001063	transferrin	2.59	0.1642	-1.57	0.4255	1.65	0.3330
TFF3	7033	BC017859	trefoil factor 3 (intestinal)	4.00	0.1445	-1.25	0.4870	3.21	0.1383
TFF3	7033	NM_003226	trefoil factor 3 (intestinal)	5.03	0.1387	-1.97	0.1643	2.55	0.2121
TFRC	7037	BC001188	transferrin receptor (p90, CD71)	-1.98	0.0548	2.27	0.0007	1.14	0.7746
TFRC	7037	NM_003234	transferrin receptor (p90, CD71)	-2.07	0.0428	2.29	0.0005	1.11	0.8240
TGFA	7039	AF149096	transforming growth factor, alpha	-1.13	0.3324	1.07	0.6057	-1.06	0.5710
TGFA	7039	AF149098	transforming growth factor, alpha	-1.12	0.4613	1.19	0.3705	1.07	0.6880
TGFA	7039	BC005308	transforming growth factor, alpha	-1.04	0.7025	1.57	0.0027	1.50	0.0041
TGFA	7039	NM_003236	transforming growth factor, alpha	-1.43	0.1833	3.14	0.0029	2.20	0.0157

TGFB1	7040	BC000125	transforming growth factor, beta 1 (Camurati-Engelmann disease)	1.02	0.7315	-1.06	0.3919	-1.05	0.4635
TGFB1	7040	NM_000660	transforming growth factor, beta 1 (Camurati-Engelmann disease)	-1.01	0.8357	1.02	0.7733	1.00	0.9462
TGFB3	7043	BC018503	transforming growth factor, beta 3	-1.10	0.4774	1.45	0.0204	1.32	0.0708
TGFB3	7043	NM_003239	transforming growth factor, beta 3	-1.50	0.0223	1.50	0.0021	-1.00	0.9888
THBS1	7057	NM_003246	thrombospondin 1	1.04	0.8452	1.31	0.0410	1.35	0.1233
TIMP1	7076	BC000866	TIMP metallopeptidase inhibitor 1	-1.01	0.9314	1.14	0.1804	1.13	0.1788
TIMP1	7076	NM_003254	TIMP metallopeptidase inhibitor 1	-1.05	0.4277	1.18	0.0911	1.12	0.1886
TLR4	7099	NM_003266	toll-like receptor 4	-1.98	0.0839	1.97	0.0233	-1.01	0.9910
TLR4	7099	NM_138554	toll-like receptor 4	-1.60	0.1461	1.87	0.0194	1.17	0.6716
TLR4	7099	NM_138557	toll-like receptor 4	-1.89	0.1620	1.89	0.0754	1.00	0.9944
TNF	7124	NM_000594	tumor necrosis factor (TNF superfamily, member 2)	1.17	0.0986	-1.43	0.0630	-1.22	0.1462
TPI1	7167	BC007086	triosephosphate isomerase 1	1.01	0.8098	1.01	0.7052	1.02	0.5877
TPI1	7167	BC017917	triosephosphate isomerase 1	1.02	0.5229	1.01	0.5823	1.03	0.3180
TPI1	7167	BC070129	triosephosphate isomerase 1	-1.01	0.8885	1.10	0.2055	1.09	0.0830
TPI1	7167	NM_000365	triosephosphate isomerase 1	1.00	0.9027	1.02	0.6912	1.02	0.6306
TNFRSF4	7293	NM_003327	tumor necrosis factor receptor superfamily, member 4	3.37	0.2294	-1.23	0.2254	2.73	0.2297
VEGF	7422	AF323587	vascular endothelial growth factor	1.14	0.2088	-1.18	0.5878	-1.03	0.8854
VEGF	7422	AY263145	vascular endothelial growth factor	-1.30	0.2222	1.33	0.1066	1.02	0.8941
VEGF	7422	M27281	vascular endothelial growth factor	-1.20	0.1624	1.31	0.0397	1.09	0.4574
VEGF	7422	NM_001025366	vascular endothelial growth factor	-1.18	0.2346	1.45	0.0050	1.22	0.1805
VEGF	7422	S85192	vascular endothelial growth factor	-1.47	0.1457	1.51	0.0689	1.02	0.9316
VHL	7428	BC058831	von Hippel-Lindau tumor suppressor	-1.61	0.0856	1.57	0.0335	-1.03	0.9198
VHL	7428	L15409	von Hippel-Lindau tumor suppressor	-1.70	0.1762	1.92	0.0550	1.13	0.7751
VHL	7428	NM_000551	von Hippel-Lindau tumor suppressor	-1.60	0.0936	1.45	0.0802	-1.10	0.7249
VIM	7431	AK093924	vimentin	-1.12	0.5931	-1.34	0.4869	-1.50	0.2765
VIM	7431	BC030573	vimentin	-1.32	0.1236	1.22	0.0912	-1.09	0.6041
VIM	7431	BC066956	vimentin	-1.34	0.0971	1.16	0.1901	-1.15	0.3297
VIM	7431	NM_003380	vimentin	-1.43	0.0966	1.33	0.0605	-1.08	0.7138
CXCR4	7852	NM_001008540	chemokine (C-X-C motif) receptor 4	-1.19	0.0350	1.40	0.0005	1.17	0.1040
EOMES	8320	NM_005442	eomesodermin homolog (Xenopus laevis)	2.17	0.0817	-1.95	0.2977	1.11	0.8075
CUL2	8453	NM_003591	cullin 2	-1.88	0.0770	1.62	0.0371	-1.16	0.7219
PIK3R3	8503	AF028785	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	-1.90	0.1696	2.25	0.0419	1.19	0.7480
PIK3R3	8503	NM_003629	phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	-1.85	0.1051	2.59	0.0055	1.40	0.4885
MKNK1	8569	AB000409	MAP kinase interacting serine/threonine kinase 1	-1.36	0.2366	1.23	0.3638	-1.10	0.7126

MKNK1	8569	AK096423	MAP kinase interacting serine/threonine kinase 1	-1.26	0.2628	1.14	0.4884	-1.10	0.6424
MKNK1	8569	NM_003684	MAP kinase interacting serine/threonine kinase 1	-1.23	0.2770	1.16	0.3972	-1.06	0.7557
MKNK1	8569	NM_198973	MAP kinase interacting serine/threonine kinase 1	-1.37	0.2128	1.21	0.3865	-1.14	0.6020
TNFRSF18	8784	NM_004195	tumor necrosis factor receptor superfamily, member 18	2.94	0.1252	-1.74	0.0208	1.69	0.2878
TNFRSF18	8784	NM_148901	tumor necrosis factor receptor superfamily, member 18	3.91	0.2270	-1.52	0.0226	2.57	0.2692
NRP1	8829	AF268691	neuropilin 1	-1.29	0.1054	1.09	0.2621	-1.18	0.2841
NRP1	8829	AF280547	neuropilin 1	1.20	0.2619	-1.73	0.0534	-1.45	0.1005
NRP1	8829	NM_001024628	neuropilin 1	-1.31	0.1622	1.21	0.1515	-1.08	0.6859
NRP1	8829	NM_001024629	neuropilin 1	-1.23	0.2473	1.15	0.2721	-1.07	0.6715
NRP1	8829	NM_003873	neuropilin 1	-1.74	0.0802	1.92	0.0111	1.10	0.7752
EIF4E2	9470	NM_004846	eukaryotic translation initiation factor 4E member 2	-1.05	0.7364	1.41	0.0729	1.34	0.0091
RBX1	9978	NM_014248	ring-box 1	-1.70	0.0290	1.21	0.2500	-1.40	0.0817
AKT3	10000	NM_005465	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-1.93	0.1343	2.57	0.0271	1.33	0.5833
AKT3	10000	NM_181690	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-2.04	0.1318	2.28	0.0572	1.12	0.8431
TBX21	30009	NM_013351	T-box 21	2.74	0.0924	-1.92	0.1645	1.43	0.4050
AK3	50808	BC013771	adenylate kinase 3	-1.79	0.1222	1.81	0.0362	1.01	0.9817
AK3	50808	NM_016282	adenylate kinase 3	-1.91	0.0528	3.01	0.0003	1.58	0.3176
FOXP3	50943	NM_014009	forkhead box P3	2.45	0.0717	-1.87	0.0423	1.31	0.4424
ANGPT4	51378	BC111976	angiopoietin 4	1.27	0.0948	-1.28	0.1763	-1.01	0.9536
ANGPT4	51378	BC111978	angiopoietin 4	1.00	0.9880	-1.24	0.3289	-1.24	0.1983
ANGPT4	51378	NM_015985	angiopoietin 4	1.43	0.0512	-1.39	0.0839	1.03	0.8539
EGLN1	54583	BC005369	egl nine homolog 1 (C. elegans)	-1.45	0.0941	1.50	0.0380	1.04	0.8704
EGLN1	54583	NM_022051	egl nine homolog 1 (C. elegans)	-1.66	0.1747	1.57	0.1582	-1.06	0.8868
HIF1AN	55662	AK025680	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.56	0.1871	-1.00	0.9944	-1.56	0.1677
HIF1AN	55662	BC007719	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.47	0.1531	-1.00	0.9970	-1.47	0.1783
HIF1AN	55662	NM_017902	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.22	0.2476	-1.07	0.6816	-1.30	0.1725
HAMP	57817	NM_021175	hepcidin antimicrobial peptide	3.25	0.0767	-1.95	0.1779	1.67	0.2668
HKDC1	80201	AK026414	hexokinase domain containing 1	1.47	0.1634	-1.57	0.0534	-1.07	0.7807
HKDC1	80201	BC110504	hexokinase domain containing 1	1.75	0.0378	-1.62	0.1691	1.09	0.7592
HKDC1	80201	NM_025130	hexokinase domain containing 1	1.87	0.1029	-1.90	0.1135	-1.02	0.9533
PROK1	84432	NM_032414	prokineticin 1	2.25	0.1851	-1.80	0.1839	1.25	0.6059

RETNLB	84666	BC069318	resistin like beta	1.87	0.2629	-2.27	0.2871	-1.21	0.7219
RETNLB	84666	NM_032579	resistin like beta	1.72	0.2424	-2.01	0.3197	-1.17	0.7577
EGLN2	112398	NM_017555	egl nine homolog 2 (C. elegans)	-1.12	0.3876	1.07	0.6528	-1.04	0.7830
EGLN2	112398	NM_053046	egl nine homolog 2 (C. elegans)	-1.02	0.7879	1.00	0.9624	-1.02	0.7897
EGLN3	112399	AK123350	egl nine homolog 3 (C. elegans)	1.31	0.2688	-1.40	0.0278	-1.07	0.7287
EGLN3	112399	NM_022073	egl nine homolog 3 (C. elegans)	-1.12	0.2563	-1.16	0.4483	-1.30	0.1341
FLJ36951	253314	XM_171094	similar to eukaryotic translation initiation factor 4e 1a	1.52	0.4884	1.05	0.9408	1.59	0.3160
FLJ36951	253314	XM_927854	similar to eukaryotic translation initiation factor 4e 1a	1.72	0.0537	-1.52	0.1337	1.13	0.6048
FLJ36951	253314	XM_932348	similar to eukaryotic translation initiation factor 4e 1a	3.02	0.1274	-1.82	0.3622	1.66	0.3142
DKFZp781 N1041	387712	XM_370577	similar to RIKEN cDNA 6430537H07 gene	-1.04	0.8982	-1.21	0.5278	-1.26	0.2926