

**Probiotic bacteria change *E. coli*-induced gene expression in cultured colonocytes: implications in intestinal pathophysiology (supplementary tables)**

Pinaki Panigrahi, Gheorghe T Braileanu, Hegang Chen, O Colin Stine

**Supplementary table 1. List of genes influenced by *E. coli*; 145 up-regulated (A), and 166 down-regulated (B)**

<b>A</b>	<b>Genes up-regulated in descending order</b>	<b>E.c. (+)</b>	<b>L.p.</b>	<b>Mix</b>
1	136080:R35478:136080:Hs.5011:RNA binding motif protein 9:RBM9:22:22q13.1:3:149813	3.35	0.29	1.61
2	3106662:BQ028065:3106662:Hs.75722:ribophorin II:RPN2:20:20q12-q13.1:3:213255	3.32	0.40	-0.31
3	28351:R13349:28351:Hs.286131:CGI-101 protein:F-LAN-1:17::2:28351	3.25	0.88	0.36
4	110384:T84327:110384:Hs.278994:Rhesus blood group, CcEe antigens:RHCE:1:1p36.11:0:110384	3.23	0.35	-0.74
5	44744:H06841:44744:Hs.8768:hypothetical protein FLJ10849:FLJ10849:4:4q13.3:0:44744	3.15	1.52	-0.88
6	5210034:BI767927:5210034:Hs.82609:hydroxymethylbilane synthase:HMBS:11:11q23.3:3:200651	3.12	0.53	-0.65
7	214877:H74123:214877:Hs.48297:zinc finger protein 363:ZNF363:4:4q21.1:0:214877	3.02	0.29	0.46
8	213989:H72399:213989:Hs.60082:PRO2086 protein:PRO2086:3:3q22.2:2:213989	2.99	0.58	0.45
9	206766:R98267:206766:Hs.26410:Homo sapiens cDNA FLJ38890 fis, clone NESOP1000108::4::0:206766	2.97	0.61	-0.33
10	207556:H60213:207556:Hs.12126:Hepatocellular antigen 112:HCA112:7:7q35:0:207556	2.97	1.90	-0.32
11	221318:H91988:221318:Hs.83758:CDC28 protein kinase regulatory subunit 2:CKS2:9:9q22:0:221318	2.96	1.76	-0.47
12	207215:BM793706:207215:Hs.77961:major histocompatibility complex, class I, C:HLA-C:6:6p21.3:3:207215	2.92	1.79	-0.83
13	4499521:BG287101:4499521:Hs.195614:splicing factor 3b, subunit 3, 130kDa:SF3B3:16:16q22.3:3:38855	2.91	0.67	-0.61
14	110257:T71497:110257:Hs.78854:ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 2 polypeptide:ATP1B2:17:17p13.1:0:110257	2.90	1.42	-0.76
15	183194:H45000:183194:Hs.74122:caspase 4, apoptosis-related cysteine protease:CASP4:11:11q22.2-q22.3:0:183194	2.87	1.38	-0.54
16	51863:H23109:51863:Hs.75297:fibroblast growth factor 1 (acidic):FGF1:5:5q31:0:51863	2.84	0.64	-0.49

17	4869966:BG766736:4869966:Hs.7744:NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa:NDUFV1:11:11q13:3:140576	2.81	0.62	-0.36
18	183201:H45010:183201:Hs.173274:integrin cytoplasmic domain-associated protein 1:ICAP-1A:2:2p25.2:0:183201	2.80	0.16	-0.75
19	5194735:BI756203:5194735:Hs.296847:spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive):SPG7:16:16q24.3:3:32105	2.75	1.40	-0.91
20	196882:R83448:196882:Hs.22580:alkylglycerone phosphate synthase:AGPS:2:2q31:0:196882	2.74	0.02	-0.79
21	5846385:BQ006820:5846385:Hs.7733:tetratricopeptide repeat domain 1:TTC1:5:5q32-q33.2:3:193882	2.71	1.91	-0.59
22	128945:R10282:128945:Hs.408495:tripartite motif-containing 10:TRIM10:6:6p21.3:0:128945	2.70	1.46	-0.75
23	135050:R33892:135050:Hs.22554:homeo box B5:HOXB5:17:17q21-q22:0:135050	2.65	0.49	-0.92
24	46266:H09427:46266:Hs.377783:adenylate cyclase activating polypeptide 1 (pituitary) receptor type I:ADCYAP1R1:7:7p14:0:46266	2.64	0.74	-0.55
25	142927:R71120:142927:Hs.103000:KIAA0831 protein:KIAA0831:14:14q22.1:0:142927	2.62	0.81	-0.47
26	151630:H03272:151630:Hs.283728:PEST-containing nuclear protein:PCNP:3:3q13.11:2:151630	2.62	0.45	0.09
27	123690:R02753:123690:Hs.33010:KIAA0633 protein:COBL:7:7p14.3:0:123690	2.61	-0.75	0.56
28	110274:T71494:110274:Hs.34497:SMC6 protein:SMC6:2:2p24.1:0:110274	2.59	1.36	-0.94
29	145057:R77327:145057:Hs.120911:neurexophilin 4:NXP4:::0:145057	2.59	1.49	-1.58
30	213683:H71721:213683:Hs.128387:Homo sapiens cDNA FLJ38426 fis, clone FEBRA2012507:::0:213683	2.59	0.83	-0.65
31	50348:H17686:50348:Hs.155545:37 kDa leucine-rich repeat (LRR) protein:P37NB:7:7q11.22:0:50348	2.58	1.14	-0.47
32	113314:T83895:113314:Hs.375017:ANKHZN protein:ANKHZN:17:17p13:0:113314	2.56	0.91	-0.30
33	310908:W25455:310908:Hs.394:adrenomedullin:ADM:11:11p15.4:0:310908	2.56	-0.22	1.09
34	142227:R69742:142227:Hs.5881:ELL gene (11-19 lysine-rich leukemia gene):ELL:19:19p13.1:0:142227	2.55	0.99	-0.78
35	205931:H57643:205931:Hs.250822:serine/threonine kinase 6:STK6:20:20q13.2-q13.3:0:205931	2.52	1.10	-0.54
36	486668:AA043477:486668:Hs.343586:zinc finger protein 36, C3H type, homolog (mouse):ZFP36:19:19q13.1:0:486668	2.52	-0.08	0.13
37	214116:H72503:214116:Hs.32922:hypothetical protein	2.51	1.69	-0.41

	FLJ20036:FLJ20036:4:4q35.1:0:214116			
38	4999673:BI092679:4999673:Hs.352114:PP1201 protein:PP1201:2:2p24.3-p24.1:3:214835	2.50	-0.20	0.50
39	271744:N42596:271744:Hs.115263:epiregulin:REG:4:4q13.3:1:271744	2.49	0.62	-0.28
40	172076:H18892:172076:Hs.375616:solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7:SLC17A7:19:19q13.0:172076	2.48	0.23	0.34
41	24600:T80484:24600:Hs.10031:tumor up-regulated CARD-containing antagonist of caspase nine:TUCAN:19:19q13.33:0:24600	2.48	0.83	-0.60
42	188359:H44711:188359:Hs.54960:uncharacterized hematopoietic stem/progenitor cells protein MDS033:MDS033:19:19q13.13:0:188359	2.48	0.73	-0.61
43	138701:R63553:138701:Hs.9728:ALEX1 protein:ALEX1:X:Xq21.33-q22.2:0:138701	2.48	1.25	-0.51
44	214568:H73223:214568:Hs.288971:myeloid/lymphoid or mixed-lineage leukemia3:MLL3:7:7q34-q36:1:214568	2.45	1.17	-0.70
45	175090:H39162:175090:Hs.240534:1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha):AGPAT1:6:6p21.3:0:175090	2.45	0.86	0.62
46	159376:H15003:159376:Hs.351796:glycosylated 38 kDa sperm protein C-7/8 precursor:MGC24663:15::2:159376	2.44	0.36	-0.92
47	162247:H25970:162247:Hs.127273:LIM and senescent cell antigen-like domains 2:LIMS2:2:2q14.2:0:162247	2.42	0.77	0.20
48	44863:H06958:44863:Hs.74624:protein tyrosine phosphatase, receptor type, N polypeptide 2:PTPRN2:7:7q36:0:44863	2.42	1.37	0.52
49	23875:T77120:23875:Hs.3132:steroidogenic acute regulatory protein:STAR:8:8p11.2:2:23875	2.42	1.83	0.90
50	132828:R27172:132828:Hs.22380:Down syndrome critical region gene 1-like 2:DSCR1L2:1:1p35.3-p33:0:132828	2.42	1.67	1.09
51	4747126:BG675590:4747126:Hs.250618:UL16 binding protein 2:ULBP2:6:6q25.3:36353	2.42	0.77	-0.64
52	4157162:BF346819:4157162:Hs.7357:CLIP-170-related protein:CLIPR-59:19:19q13.13:3:188392	2.41	1.73	-0.32
53	173315:H21153:173315:Hs.153227:cyclin G associated kinase:GAK:4:4p16:0:173315	2.40	1.64	-0.41
54	141297:R64413:141297:Hs.343877:hypothetical protein FLJ20039:FLJ20039:11:11q13.2:0:141297	2.39	0.93	-0.86
55	202740:H53893:202740:Hs.31034:peroxisomal biogenesis factor 11A:PEX11A:15:15q25.2:0:202740	2.39	0.67	-0.10
56	211054:H65795:211054:Hs.301005:histone H2A.F/Z variant:H2AV:7:7p13:0:211054	2.38	1.02	-0.38

57	489541:AA099265:489541:Hs.29640:reversion-inducing-cysteine-rich protein with kazal motifs:RECK:9:9p13-p12:3:133298	2.38	0.82	-0.50
58	46931:H10029:46931:Hs.90034:hypothetical protein FLJ21916:FLJ21916:14:14q32.13:0:46931	2.37	0.25	-0.18
59	4335316:BF976490:4335316:Hs.26054:SH2 domain containing 3C:SH2D3C:9:9q34.13:3:40060	2.36	0.17	-0.35
60	125781:R07729:125781:Hs.171802:Homo sapiens, clone IMAGE-3956746, mRNA, partial cds::2::0:125781	2.35	1.13	1.59
61	220695:H95520:220695:Hs.152292:SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1:SMARCA1:X:Xq25:0:220695	2.35	-0.03	-0.28
62	193436:H47269:193436:Hs.184167:splicing factor, arginine/serine-rich 7, 35kDa:SFRS7:2:2p22-p21:0:193436	2.34	-0.54	0.43
63	211879:H68441:211879:Hs.13528:hypothetical protein FLJ14054:FLJ14054:5:5p13.2:1:211879	2.33	0.48	0.03
64	140452:R65820:140452:Hs.170088:SLC2A4 regulator:SLC2A4RG:20:20q13.33:0:140452	2.33	0.39	-0.47
65	160793:H24707:160793:Hs.154294:discs, large (Drosophila) homolog 1:DLG1:3:3q29:0:160793	2.32	1.84	0.15
66	38754:R49716:38754:Hs.247423:adducin 2 (beta):ADD2:2:2p14-p13:0:38754	2.30	0.11	-0.07
67	41811:R54138:41811:Hs.86122:likely ortholog of mouse gene rich cluster, A gene:GRCA:12:12p13:0:41811	2.30	0.75	-0.37
68	5175619:BI819401:5175619:Hs.183:Duffy blood group:FY:1:1q21-q22:3:159421	2.29	-0.41	-0.76
69	206717:H59530:206717:Hs.20295:CHK1 checkpoint homolog (S. pombe):CHEK1:11:11q24-q24:0:206717	2.29	0.58	0.11
70	180436:R85013:180436:Hs.59457:hypothetical protein FLJ22127:FLJ22127:22:22q11.2:0:180436	2.29	0.61	0.23
71	135177:R32923:135177:Hs.24563:NTF2-like export factor 1:NXT1:20:20p12-p11.2:0:135177	2.28	0.87	-1.24
72	111656:T84581:111656:Hs.8349:apobec-1 complementation factor:ACF:10:10q21.1:2:111656	2.28	0.21	-0.04
73	197512:H52061:197512:Hs.30211:hypothetical protein FLJ22313:FLJ22313:7:7p15.3:0:197512	2.28	-0.19	-0.93
74	136983:R35752:136983:Hs.2465:G protein-coupled receptor 105:GPR105:3:3q21-q25:0:136983	2.27	1.09	-0.57
75	44915:H08053:44915:Hs.344069:KIAA1910 protein:KIAA1910:13:13q31.1:0:44915	2.27	0.04	-0.64
76	41676:R52906:41676:Hs.82772:collagen, type XI, alpha 1:COL11A1:1:1p21:1:41676	2.26	0.75	0.40
77	219635:H84532:219635:Hs.75069:serine	2.25	0.26	-1.07

	hydroxymethyltransferase 2 (mitochondrial):SHMT2:12:12q12-q14:0:219635			
78	41757:R52804:41757:Hs.25956:cystine-knot containing secreted protein:DKFZp564D206:7:7p21.3:0:41757	2.25	0.78	-0.96
79	52925:H29166:52925:Hs.5345:arginyl aminopeptidase (aminopeptidase B)-like 1:RNPEPL1:2:2q37.3:0:52925	2.24	0.81	-0.12
80	200978:R99791:200978:Hs.389836:iron-responsive element binding protein 2:IREB2:15:15q24.1:0:200978	2.24	-0.53	-0.11
81	188272:H45773:188272:Hs.332053:serum amyloid A2:SAA2:11:11p15.1-p14:0:188272	2.23	1.89	-0.13
82	182473:R86053:182473:Hs.73090:nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100):NFKB2:10:10q24:0:182473	2.23	0.93	-0.99
83	201127:R98517:201127:Hs.7644:H1 histone family, member 2:H1F2:6:6p21.3:0:201127	2.22	0.50	-1.37
84	110744:T90560:110744:Hs.180903:hypothetical protein 384D8_6:384D8-2:22:22q13.33:0:110744	2.22	0.44	-0.55
85	40022:R54062:40022:Hs.268281:Crn, crooked neck-like 1 (Drosophila):CRNKL1:20:20p11.2:2:40022	2.22	-0.31	-0.82
86	109456:T81523:109456:Hs.79219:RalGDS-like gene:RGL:1:1q24.3:0:109456	2.21	0.33	-0.60
87	156312:R72685:156312:Hs.74573:likely ortholog of mouse phospholipase D3:PLD3:19:19q13.2:0:156312	2.21	-0.07	-0.66
88	172878:H20358:172878:Hs.31549:KIAA1501 protein:KIAA1501:16:16p11.1:1:172878	2.21	0.28	-0.64
89	214388:H71637:214388:Hs.743:Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide:FCER1G:1:1q23:0:214388	2.21	0.98	-0.47
90	206765:R98272:206765:Hs.35804:hect domain and RLD 3:HERC3:4:4q21:0:206765	2.20	0.21	-0.41
91	194718:R89879:194718:Hs.121528:hypothetical protein BC011916:LOC112817:10:10q24.32:0:194718	2.20	0.47	0.02
92	125802:BM840842:125802:Hs.32916:nascent-polypeptide-associated complex alpha polypeptide:NACA:12:12q23-q24.1:3:125802	2.20	0.02	-0.27
93	41972:R61009:41972:Hs.2522:adenylate cyclase 8 (brain):ADCY8:8:8q24:0:41972	2.19	0.82	-0.22
94	177800:H46056:177800:Hs.263671:radixin:RDX:11:11q23:0:177800	2.19	0.34	-0.97
95	5555941:BM806591:5555941:Hs.380048:Homo sapiens pp7052 mRNA, complete cds:::3:111185	2.18	1.02	0.21
96	143800:R77664:143800:Hs.75874:pregnancy-associated plasma protein A:PAPPA:9:9q33.1:0:143800	2.18	0.99	-0.13
97	120579:T95210:120579:Hs.5320:esophageal	2.18	0.63	-0.20

	protein:MGC16824:16:16p13.13:0:120579			
98	195346:R88887:195346:Hs.367690:FLJ00005 protein:FLJ00005:15:15:0:195346	2.17	0.91	0.55
99	5760018:BM923884:5760018:Hs.226795:glutathione S- transferase pi:GSTP1:11:11q13:3:266375	2.16	1.39	-0.34
100	154218:R52052:154218:Hs.53447:hypothetical protein BC012357:LOC89953:6:6p21.1:0:154218	2.16	1.24	0.34
101	50416:H17201:50416:Hs.21814:interleukin 20 receptor, alpha:IL20RA:6:6q22.33-q23.1:0:50416	2.15	0.73	-0.10
102	21798:T66128:21798:Hs.9728:ALEX1 protein:ALEX1:X:Xq21.33- q22.2:0:21798	2.15	-0.74	-0.24
103	201111:R98509:201111:Hs.35947:methyl-CpG binding domain protein 4:MBD4:3:3q21-q22:1:201111	2.15	1.06	-0.05
104	219593:H80810:219593:Hs.7149:formin homology 2 domain containing 2:FHOD2:2:2q23.3:0:219593	2.14	1.37	-0.43
105	210623:H64252:210623:Hs.14791:acyl-Coenzyme A dehydrogenase family, member 8:ACAD8:11:11q25:0:210623	2.14	1.26	-0.38
106	138555:R63281:138555:Hs.268744:KIAA1796 protein:KIAA1796:10:10q11:0:138555	2.14	1.48	-0.89
107	130334:R21204:130334:Hs.82098:Homo sapiens, Similar to hypothetical gene LOC122525, clone IMAGE-4421196, mRNA, partial cds::14::0:130334	2.14	1.45	-0.65
108	183721:H44469:183721:Hs.95870:PTD015 protein:PTD015:11:11q13.4:1:183721	2.13	1.02	-0.07
109	29649:R15222:29649:Hs.13775:homeodomain only protein:LAGY:4:4q11-q12:0:29649	2.13	1.10	-0.40
110	200714:R98113:200714:Hs.23759:CD209 antigen- like:CD209L:19:19p13:0:200714	2.12	1.35	-0.50
111	34615:R24566:34615:Hs.166351:partner of PIX 1:POPX1:17:17q24.2:1:34615	2.12	0.06	-0.31
112	159406:H15019:159406:Hs.75354:GCN1 general control of amino-acid synthesis 1-like 1 (yeast):GCN1L1:12:12q24.2:0:159406	2.12	1.33	-0.58
113	49912:H15240:49912:Hs.352358:hypothetical protein FLJ90005:FLJ90005:1:1p34.3:0:49912	2.11	1.01	-0.85
114	27020:R18784:27020:Hs.200016:nudix (nucleoside diphosphate linked moiety X)-type motif 11:NUDT11:X:Xp11.23:1:27020	2.11	0.21	0.03
115	136508:R34567:136508:Hs.264981:2'-5'-oligoadenylate synthetase 2, 69/71kDa:OAS2:12:12q24.2:0:136508	2.11	1.62	-0.59
116	137531:R39428:137531:Hs.89627:protein tyrosine phosphatase, receptor type, G:PTPRG:3:3p21-p14:0:137531	2.10	0.62	-0.64
117	25771:R12509:25771:Hs.347340:H-2K binding factor- 2:LOC51580:9:9:1:25771	2.09	0.71	-0.46

118	33723:R19556:33723:Hs.108681:NAG14 protein:NAG14:7:7q31:0:33723	2.09	0.67	-0.96
119	186331:H28872:186331:Hs.80758:aspartyl-tRNA synthetase:DARS:2:2q14.3:0:186331	2.09	0.45	-0.31
120	5803632:BQ069305:5803632:Hs.96200:neighbor of A-kinase anchoring protein 95:NAKAP95:19:19p13.13:3:172893	2.09	1.75	0.24
121	141606:R69183:141606:Hs.182591:RAS guanyl releasing protein 1 (calcium and DAG-regulated):RASGRP1:15:15q15:2:141606	2.08	-0.16	-0.16
122	29305:R14519:29305:Hs.97393:Alstrom syndrome 1:ALMS1:2:2p13:0:29305	2.07	1.54	0.36
123	51338:H20864:51338:Hs.182215:ADP-ribosylation factor-like 3:ARL3:10:10q23.3:0:51338	2.07	-0.17	1.02
124	155057:R70211:155057:Hs.79630:CD79A antigen (immunoglobulin-associated alpha):CD79A:19:19q13.2:0:155057	2.06	0.05	0.18
125	203203:H54669:203203:Hs.352601:hypothetical protein MGC30052:MGC30052:4:4q21.1:0:203203	2.06	0.64	0.20
126	415635:W78724:415635:Hs.15441:Crm, cramped-like (Drosophila):CRAMP1L:16:16p13.3:0:415635	2.06	-0.08	1.12
127	151129:H03806:151129:Hs.24640:sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A:SEMA7A:15:15q22.3-q23:0:151129	2.05	1.56	-0.46
128	219614:H83817:219614:Hs.275675:katanin p80 (WD40-containing) subunit B 1:KATNB1:16:16q13:0:219614	2.04	-0.48	-0.94
129	23904:T77428:23904:Hs.408991:homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2:HELO1:6:6p21.1-p12.1:0:23904	2.04	0.23	0.56
130	34947:R19764:34947:Hs.7542:KIAA1802 protein:KIAA1802:18:18:0:34947	2.04	1.53	-0.19
131	111160:T84160:111160:Hs.15467:hypothetical protein FLJ20725:FLJ20725:14:14q22.1:2:111160	2.03	1.51	-0.29
132	34593:R19699:34593:Hs.380621:EBP50-PDZ interactor of 64 kD:EPI64:22:22q12.1-qter:0:34593	2.03	-0.09	-0.56
133	109277:T80906:109277:Hs.14794:zinc finger protein 28 homolog (mouse):ZFP28:19::0:109277	2.03	0.88	-1.10
134	31339:R20832:31339:Hs.7967:ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal - human (fragments) [H.sapiens]::1::0:31339	2.02	-0.72	0.34
135	41486:R59266:41486:Hs.22998:neurexin 1:NRXN1:2:2p21:0:41486	2.01	0.42	-0.06
136	45984:H08589:45984:Hs.396167:adenylyl cyclase-associated protein 2:CAP2:6:6p22.2:0:45984	2.01	-0.19	-0.57
137	3299462:BE856570:3299462:Hs.133517:Homo sapiens FKSG35 (FKSG35) mRNA, complete cds:::3:184354	2.01	0.86	0.76

138	207601:H60244:207601:Hs.198891:PRP4 pre-mRNA processing factor 4 homolog B (yeast):PRPF4B:6:6p24.2:0:207601	2.01	0.25	-1.01
139	109357:T81068:109357:Hs.392825:Homo sapiens PP1416 mRNA, complete cds::21::1:109357	2.01	1.30	-0.72
140	220125:H82615:220125:Hs.74592:special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's):SATB1:3:3p23:0:220125	2.01	0.47	-0.44
141	47504:H12194:47504:Hs.26312:glioma amplified on chromosome 1 protein (leucine-rich):GAC1:1:1q32.1:0:47504	2.01	0.42	-0.11
142	52732:H29419:52732:Hs.167464:glutamate receptor, ionotropic, N-methyl D-aspartate 2A:GRIN2A:16:16p13.2:0:52732	2.01	0.00	0.18
143	162236:H26072:162236:Hs.77436:pleckstrin:PLEK:2:2p13.3:0:162236	2.00	0.15	-1.25
144	200882:R98881:200882:Hs.109655:sex comb on midleg-like 1 (Drosophila):SCML1:X:Xp22.2-p22.1:0:200882	2.00	1.56	-0.83
145	110335:T82046:110335:Hs.101821:hypothetical protein FLJ13639:FLJ13639:13:13q14.13:0:110335	2.00	1.01	-0.59
<b>B</b>	<b>Genes down-regulated in descending order</b>	E.c. (-)	L.p.	Mix
1	37842:R60610:37842:Hs.7041:MGC4170 protein:MGC4170:12:12q23.1:0:37842	-2.00	-0.70	0.05
2	120176:T95687:120176:Hs.7940:RAP1, GTP-GDP dissociation stimulator 1:RAP1GDS1:4:4q23-q25:2:120176	-2.01	-0.49	0.68
3	50044:H17697:50044:Hs.388479:component of oligomeric golgi complex 7:COG7:16:16p11.2:0:50044	-2.02	-0.55	1.13
4	133088:R26339:133088:Hs.19121:adaptor-related protein complex 2, alpha 2 subunit:AP2A2:11:11:2:133088	-2.02	-1.20	1.32
5	182905:H45128:182905:Hs.389752:Homo sapiens clone 6B.1 immunoglobulin heavy chain variable region DP-54 mRNA, partial cds:::0:182905	-2.02	-0.60	-0.29
6	110999:T83053:110999:Hs.198166:activating transcription factor 2:ATF2:2:2q32:0:110999	-2.03	-0.59	-0.02
7	135967:R33553:135967:Hs.178292:protein O-fucosyltransferase 1:POFUT1:20::0:135967	-2.03	-0.68	1.15
8	42553:R61223:42553:Hs.377830:Homo sapiens cDNA FLJ36675 fis, clone UTERU2004520::6::0:42553	-2.04	0.96	-0.68
9	182264:H30141:182264:Hs.73800:selectin P (granule membrane protein 140kDa, antigen CD62):SELP:1:1q22-q25:0:182264	-2.04	-0.01	-0.19
10	154742:R55379:154742:Hs.26401:tumor necrosis factor (ligand) superfamily, member 12:TNFSF12:17:17p13:0:154742	-2.04	-1.71	0.36
11	3612949:BE388699:3612949:Hs.4188:hypothetical protein MGC10812:MGC10812:19:19p13.11:3:111342	-2.04	-1.07	1.23
12	44110:H05327:44110:Hs.21050:g20 protein:LOC51161:3:3p21.3:0:44110	-2.06	-1.15	0.09

13	131137:R23999:131137:Hs.211573:heparan sulfate proteoglycan 2 (perlecan):HSPG2:1:1p36.1-p35:0:131137	-2.06	-0.60	0.92
14	183103:H42963:183103:Hs.129883:KIAA0420 gene product:KIAA0420:16:16p13.13:0:183103	-2.06	-0.24	-0.35
15	188331:H44693:188331:Hs.220745:hypothetical protein FLJ25604:FLJ25604:1:1q24.1-q24.2:0:188331	-2.06	-0.58	0.59
16	274619:R84565:274619:Hs.99872:fetal Alzheimer antigen:FALZ:17:17q24:0:274619	-2.06	0.67	0.10
17	212340:H69430:212340:Hs.170414:paired basic amino acid cleaving system 4:PACE4:15:15q26:0:212340	-2.06	-1.20	0.80
18	183593:H44192:183593:Hs.26285:nischarin:NISCH:3:3p21.1:0:183593	-2.06	-0.51	0.09
19	179445:H51378:179445:Hs.20950:phospholysine phosphohistidine inorganic pyrophosphate phosphatase:LHPP:10:10q26.13:0:179445	-2.07	-1.40	0.39
20	134269:R31174:134269:Hs.153880:polymerase (RNA) mitochondrial (DNA directed):POLRMT:19:19p13.3:0:134269	-2.07	-0.41	0.31
21	136480:R33249:136480:Hs.321231:UDP-Gal-betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3:B4GALT3:1:1q21-q23:0:136480	-2.07	0.43	0.32
22	138844:R62721:138844:Hs.333513:small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating):SCYE1:4:4q24:0:138844	-2.08	0.28	1.18
23	3887550:BE877114:3887550:Hs.182982:golgin-67:GOLGIN-67:15:15q11.2:3:41395	-2.08	-0.09	1.21
24	195224:R91352:195224:Hs.197114:serine/arginine repetitive matrix 2:SRRM2:16:16p13.3:0:195224	-2.08	-1.56	0.38
25	49573:H15181:49573:Hs.57475:sex comb on midleg homolog 1:SCMH1:1:1p34:0:49573	-2.09	1.32	0.33
26	179041:H50029:179041:Hs.75875:ubiquitin-conjugating enzyme E2 variant 1:UBE2V1:20:20q13.2:0:179041	-2.09	-0.67	0.88
27	37420:R35261:37420:Hs.24947:dermatan-4-sulfotransferase-1:D4ST-1:15:0:37420	-2.09	-0.67	0.26
28	143829:R77688:143829:Hs.351629:HSPC003 protein:HSPC003:1:1q21.2:0:143829	-2.09	0.16	0.68
29	24943:T80567:24943:Hs.26450:KIAA0725 protein:KIAA0725:8:8p11.21:0:24943	-2.11	-0.46	0.40
30	220197:H82654:220197:Hs.184085:crystallin, alpha A:CRYAA:21:21q22.3:0:220197	-2.12	-0.40	0.16
31	127244:R08293:127244:Hs.2375:egf-like module containing, mucin-like, hormone receptor-like sequence 1:EMR1:19:19p13.3:0:127244	-2.12	-0.39	0.26
32	163487:H14191:163487:Hs.288891:MMS19-like (MET18	-2.12	-0.05	0.52

	homolog, <i>S. cerevisiae</i> ):MMS19L:10:10q24-q25:0:163487			
33	51095:H18550:51095:Hs.173724:creatine kinase, brain:CKB:14:14q32:0:51095	-2.13	0.38	0.71
34	138695:R63498:138695:Hs.274256:hypothetical protein FLJ23563:FLJ23563:5:5q12.1:0:138695	-2.13	-0.05	1.27
35	147839:R81839:147839:Hs.29877:TXK tyrosine kinase:TXK:4:4p12:0:147839	-2.13	-0.24	0.23
36	152067:H04619:152067:Hs.346509:hypothetical protein FLJ33282:FLJ33282:2:2q33.2:0:152067	-2.14	-1.28	1.61
37	276508:N48445:276508:Hs.56294:RAB33A, member RAS oncogene family:RAB33A:X:Xq26.1:0:276508	-2.14	-0.74	1.18
38	135619:R31507:135619:Hs.295944:tissue factor pathway inhibitor 2:TFPI2:7:7q22:0:135619	-2.14	-0.16	0.99
39	134560:R27740:134560:Hs.409030:lipopolysaccharide specific response-68 protein:LSR68:14:14q24.1:0:134560	-2.14	-0.53	0.20
40	154907:R54918:154907:Hs.404434:hypothetical protein FLJ13912:FLJ13912:16:16q21:0:154907	-2.16	-0.50	0.93
41	4402305:R35722:4402305:Hs.75283:sorting nexin 1:SNX1:15:15q22.1:3:38232	-2.18	-0.98	0.86
42	34958:R20384:34958:Hs.8054:leucine carboxyl methyltransferase:LCMT:16:16p12.3-16p12.1:0:34958	-2.18	-1.13	-0.14
43	166406:R88458:166406:Hs.183800:Ran GTPase activating protein 1:RANGAP1:22:22q13:0:166406	-2.18	-0.56	0.15
44	222616:H84246:222616:Hs.7934:secretory carrier membrane protein 5:SCAMP5:15:15q22.33:1:222616	-2.18	-0.93	0.53
45	32952:R19492:32952:Hs.55276:potassium voltage-gated channel, Shal-related subfamily, member 1:KCND1:X:Xp11.23:3:32553	-2.20	-1.15	0.93
46	183945:H30300:183945:Hs.48375:small nuclear ribonucleoprotein polypeptide N:SNRPN:15:15q12:0:183945	-2.20	-0.30	0.26
47	25730:R12040:25730:Hs.106260:sorting nexin 10:SNX10:7:7p21.1:0:25730	-2.20	0.46	0.35
48	151542:H03760:151542:Hs.30096:zinc finger protein 354B:ZNF354B::0:151542	-2.20	-0.90	0.53
49	207963:H60496:207963:Hs.167584:solute carrier family 2 (facilitated glucose transporter), member 2:SLC2A2:3:3q26.1-q26.2:0:207963	-2.21	-0.93	-0.32
50	109540:T81553:109540:Hs.75305:aryl hydrocarbon receptor interacting protein:AIP:11:11q13.3:0:109540	-2.21	-0.56	0.66
51	4777275:BG742997:4777275:Hs.170098:KIAA0372 gene product:KIAA0372:5:5q21.1-q21.2:3:192703	-2.21	-0.70	0.72
52	232714:H73130:232714:Hs.79241:B-cell CLL/lymphoma 2:BCL2:18:18q21.3:0:232714	-2.21	-1.27	0.73

53	37338:R35160:37338:Hs.76473:insulin-like growth factor 2 receptor:IGF2R:6:6q26:0:37338	-2.23	-0.16	0.62
54	133090:R26340:133090:Hs.23889:SAM domain and HD domain 1:SAMHD1:20:20pter-q12:0:133090	-2.23	-0.79	0.26
55	203560:H55982:203560:Hs.75655:procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	-2.25	-1.33	0.65
56	44164:H06541:44164:Hs.173034:amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen):AMPH:7:7p14-p13:0:44164	-2.25	0.74	1.00
57	175199:H40206:175199:Hs.334802:hypothetical protein FLJ10101:FLJ10101:9:9q34.3:0:175199	-2.25	-0.30	0.87
58	22487:T74004:22487:Hs.356084:G protein-coupled receptor 27:GPR27:3:3p21-p14:1:22487	-2.25	-0.62	-0.34
59	21815:T65624:21815:Hs.180383:dual specificity phosphatase 6:DUSP6:12:12q22-q23:0:21815	-2.26	-0.14	0.70
60	161495:H26124:161495:Hs.54457:CD81 antigen (target of antiproliferative antibody 1):CD81:11:11p15.5:0:161495	-2.26	-0.99	-0.24
61	501553:AA135707:501553:Hs.75279:laminin, alpha 2 (merosin, congenital muscular dystrophy):LAMA2:6:6q22-q23:0:501553	-2.27	-1.03	0.98
62	26049:R12051:26049:Hs.264915:Homo sapiens, clone MGC-20197 IMAGE-4543414, mRNA, complete cds::3::0:26049	-2.27	-0.42	0.22
63	129593:R16652:129593:Hs.279881:mannosidase, alpha, class 1B, member 1:MAN1B1:9:9q34:0:129593	-2.27	-0.08	0.06
64	26922:R13936:26922:Hs.79064:deoxyhypusine synthase:DHPS:19:19p13.11-p13.12:0:26922	-2.28	-1.17	0.57
65	23443:T75313:23443:Hs.12365:synaptotagmin XIII:SYT13:11:11p12-p11:0:23443	-2.30	-0.95	0.64
66	5824296:BQ018983:5824296:Hs.326249:ribosomal protein L22:RPL22:1:1p36.3-p36.2:3:171634	-2.32	-1.43	0.04
67	144233:R77028:144233:Hs.1116:lymphotoxin beta receptor (TNFR superfamily, member 3):LTBR:12:12p13:0:144233	-2.32	-1.02	-0.03
68	25837:R12044:25837:Hs.15711:kinesin family member 13B:KIF13B:8:8p21.1:0:25837	-2.34	0.78	0.28
69	130781:R22108:130781:Hs.101414:hypothetical protein AF447587:LOC146562:16:16p13.13:0:130781	-2.34	0.33	-0.23
70	109692:T81697:109692:Hs.154680:DKFZP434M154 protein:DKFZP434M154:19:19q13.32:0:109692	-2.35	-0.17	0.87
71	46187:H09181:46187:Hs.285714:copine V:CPNE5:6:6p21.1:1:46187	-2.36	-0.11	0.32
72	23456:T75394:23456:Hs.283627:eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa:EIF2B3:1:1p34.1:0:23456	-2.37	-0.33	0.15
73	204673:H57208:204673:Hs.334409:metallothionein	-2.37	-0.59	-0.29

	1G:MT1G:16:16q13:0:204673			
74	146669:R80273:146669:Hs.375599:immunoglobulin lambda joining 3:IGLJ3:22:22q11.1-q11.2:0:146669	-2.38	-1.47	0.17
75	146850:R80719:146850:Hs.381081:proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2):PSMB9:6:6p21.3:0:146850	-2.38	0.58	-0.55
76	153088:R50087:153088:Hs.193914:GREB1 protein:GREB1:2:2p25.1:0:153088	-2.38	-0.90	0.80
77	4710621:BG566154:4710621:Hs.252259:ribosomal protein S3:RPS3:11:11q13.3-q13.5:3:198940	-2.38	-0.18	-0.57
78	199680:R96672:199680:Hs.218619:cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., -metabolizing), polypeptide 6:CYP2D6:22:22q13.1:0:199680	-2.38	-0.26	0.46
79	173343:H21167:173343:Hs.23978:scaffold attachment factor B:SAFB:19:19p13.3-p13.2:0:173343	-2.39	-1.60	0.19
80	47936:H12016:47936:Hs.380084:hypothetical protein FLJ21839:FLJ21839:2:2p23.3:0:47936	-2.40	-0.06	-0.55
81	50586:H17730:50586:Hs.127270:KIAA1545 protein:KIAA1545:12:12q24.33:0:50586	-2.41	-0.70	-0.41
82	4560877:BG323833:4560877:Hs.119122:ribosomal protein L13a:RPL13A:19:19q13.3:3:113996	-2.41	-1.38	0.60
83	149516:H00267:149516:Hs.83097:hypothetical protein FLJ22955:FLJ22955:17::0:149516	-2.43	0.37	-0.11
84	376648:AA045146:376648:Hs.91251:hypothetical protein FLJ11198:FLJ11198:3:3q28.3:171854	-2.44	-0.75	-0.08
85	158998:R76008:158998:Hs.239018:RAB11B, member RAS oncogene family:RAB11B:19:19p13.3:0:158998	-2.44	-1.62	1.23
86	211234:H67999:211234:Hs.172323:cytochrome P450, subfamily IIIA, polypeptide 7:CYP3A7:7:7q21-q22.1:0:211234	-2.44	1.21	0.53
87	153650:R48713:153650:Hs.131728:KIAA1140 protein:KIAA1140:2:2p16.3:0:153650	-2.45	-0.27	1.11
88	184087:H30717:184087:Hs.30687:GRB2-associated binding protein 2:GAB2:11:11q13.4:0:184087	-2.45	-1.75	0.53
89	167245:R90768:167245:Hs.8004:huntingtin-associated protein interacting protein (duo):HAPIP:3:3q21.3:0:167245	-2.46	-0.74	1.39
90	153190:R50700:153190:Hs.248267:mercaptopyruvate sulfurtransferase:MPST:22:22q13.1:0:153190	-2.46	-0.88	0.13
91	204550:H58642:204550:Hs.17546:hypothetical protein FLJ23499:FLJ23499:11:11q13-q22:0:204550	-2.48	-1.01	0.23
92	4471444:BG250890:4471444:Hs.277728:SEC14-like 2 (S. cerevisiae):SEC14L2:22:22q12.2:3:38215	-2.49	-1.05	0.59
93	141293:R64412:141293:Hs.381590:Homo sapiens, clone IMAGE-4431121, mRNA, partial cds::10::0:141293	-2.50	-0.22	1.07

94	39167:R54351:39167:Hs.12773:acyl-Coenzyme A oxidase 3, pristanoyl:ACOX3:4:4p15.3:0:39167	-2.51	0.28	-0.16
95	132026:R24904:132026:Hs.6748:hypothetical protein PP1665:PP1665:11:11q13.3:2:132026	-2.51	0.03	0.78
96	124670:R02511:124670:Hs.9994:lipase, hepatic:LIPC:15:15q21-q23:0:124670	-2.52	-0.67	0.00
97	233786:H66389:233786:Hs.38069:complement component 8, beta polypeptide:C8B:1:1p32:0:233786	-2.52	-0.98	0.96
98	5809010:BQ056602:5809010:Hs.150580:putative translation initiation factor:SUI1:17:17:3:115010	-2.52	-0.63	0.82
99	153613:R48696:153613:Hs.103147:hypothetical protein FLJ21347:FLJ21347:17:17q24.1:0:153613	-2.53	-1.59	1.33
100	5762776:BQ066997:5762776:Hs.343586:zinc finger protein 36, C3H type, homolog (mouse):ZFP36:19:19q13.1:3:116852	-2.54	-1.06	0.98
101	125797:R07694:125797:Hs.20017:chromosome 22 open reading frame 4:C22orf4:22:22q13.3:0:125797	-2.54	-0.01	-0.24
102	5934101:BQ052715:5934101:Hs.198281:pyruvate kinase, muscle:PKM2:15:15q22:3:179182	-2.55	-0.34	0.59
103	115436:T87534:115436:Hs.351874:major histocompatibility complex, class II, DO alpha:HLA-DOA:6:6p21.3:0:115436	-2.55	-0.65	0.80
104	31250:R21465:31250:Hs.101174:microtubule-associated protein tau:MAPT:17:17q21.1:0:31250	-2.56	-0.20	-0.03
105	187164:R83142:187164:Hs.85155:zinc finger protein 36, C3H type-like 1:ZFP36L1:14:14q22-q24:2:187164	-2.57	-0.31	0.47
106	180697:R85183:180697:Hs.286128:chromosome 20 open reading frame 98:C20orf98:20:20p13:0:180697	-2.58	-0.25	0.71
107	190898:H38361:190898:Hs.302441:vacuolar protein sorting 16 (yeast):VPS16:20:20p13-p12:0:190898	-2.58	-0.64	0.38
108	186965:H43394:186965:Hs.170098:KIAA0372 gene product:KIAA0372:5:5q21.1-q21.2:0:186965	-2.60	-1.34	0.67
109	124447:R01824:124447:Hs.375161:myofibrillogenesis regulator 1:MR-1:2:2:0:124447	-2.60	-0.56	0.22
110	188404:H44733:188404:Hs.90408:neogenin homolog 1 (chicken):NEO1:15:15q22.3-q23:0:188404	-2.61	-1.16	-0.22
111	145150:R77592:145150:Hs.279704:chromatin accessibility complex 1:CHRAC1:8:8q24.3:0:145150	-2.61	-1.41	0.62
112	186858:R83247:186858:Hs.79222:galactosidase, beta 1:GLB1:3:3p21.33:0:186858	-2.61	0.12	0.08
113	135543:R31364:135543:Hs.128676:Homo sapiens, clone MGC-23971 IMAGE-4714217, mRNA, complete cds::12::0:135543	-2.62	-0.06	0.41
114	198257:R94457:198257:Hs.5398:TRK-fused gene:TFG:3:3q11-q12:0:198257	-2.62	-0.17	0.06
115	167191:R90895:167191:Hs.5307:synaptopodin:KIAA1029:5:5q33	-2.62	-0.92	0.31

	.1:1:167191			
116	34930:R19920:34930:Hs.6343:KIAA1464 protein:KIAA1464:16:16q22.2:0:34930	-2.63	-0.74	0.73
117	4476547:BG255790:4476547:Hs.347969:cytochrome c oxidase subunit IV isoform 1:COX4I1:16:16q22-qter:3:173210	-2.66	1.20	-0.38
118	120813:T95538:120813:Hs.396018:mitogen-activated protein kinase 3:MAP4K3:2:2p22.3:1:120813	-2.67	-0.93	-0.96
119	5824004:BQ018724:5824004:Hs.409123:ret finger protein 2:RFP2:13:13q14:3:126766	-2.68	-0.14	1.13
120	42708:R67199:42708:Hs.21479:ubiquitin 1:UBN1:16:16p13.3:2:42708	-2.69	-0.78	-0.09
121	4769467:BG622939:4769467:Hs.282847:pregnancy specific beta-1-glycoprotein 1:PSG1:19:19q13.2:3:139582	-2.70	-0.93	-0.45
122	204629:H57025:204629:Hs.279928:annexin A9:ANXA9:1:1q21:0:204629	-2.71	-1.33	0.13
123	131476:R23374:131476:Hs.100895:hypothetical protein FLJ10462:FLJ10462:12:12p12.2-p12.1:0:131476	-2.72	-0.80	-0.55
124	179371:H50436:179371:Hs.293970:aldehyde dehydrogenase 6 family, member A1:ALDH6A1:14:14q24.2:0:179371	-2.73	-1.28	-0.05
125	125313:R05896:125313:Hs.16179:hypothetical protein FLJ23467:FLJ23467:1:1q21.2:0:125313	-2.74	-0.46	0.10
126	176889:H45241:176889:Hs.409245:ribosomal protein L41:RPL41:12:12q13:1:176889	-2.78	-0.62	0.88
127	145033:R77311:145033:Hs.396010:Homo sapiens cDNA PSEC0254 fis, clone NT2RP3003474, moderately similar to ELASTIN PRECURSOR::7::1:145033	-2.79	-0.26	0.15
128	149667:H00498:149667:Hs.28219:protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha:PPP2R3A:3:3q22.3:0:149667	-2.79	-1.08	-0.30
129	166315:R88526:166315:Hs.212318:scotin:SCOTIN:3:3p21.31:0:166315	-2.80	-1.02	0.17
130	109344:T81051:109344:Hs.132160:Homo sapiens cDNA FLJ39737 fis, clone SMINT2016396:::0:109344	-2.83	-0.82	0.23
131	39152:R54234:39152:Hs.12827:Homo sapiens, clone IMAGE-5260726, mRNA, partial cds::5::0:39152	-2.85	-0.90	0.23
132	122721:T98990:122721:Hs.7285:KIAA0759 protein:KIAA0759:14:14q24.3:0:122721	-2.86	-1.43	1.55
133	43065:R61149:43065:Hs.200286:hypothetical protein DKFZp547I048:DKFZp547I048:1:1p31.1:0:43065	-2.86	-0.86	1.59
134	42175:R60407:42175:Hs.26770:fatty acid binding protein 7, brain:FABP7:6:6q22-q23:0:42175	-2.89	-1.39	1.02
135	186682:R83818:186682:Hs.350470:trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed	-2.91	-0.82	0.49

	in):TFF1:21:21q22.3:0:186682			
136	116272:T89583:116272:Hs.102669:KIAA1892 protein:KIAA1892:9:9p11.2:3:114064	-2.94	0.34	-0.29
137	4778815:BG740839:4778815:Hs.351161:Homo sapiens, clone IMAGE-3908496, mRNA, partial cds:::3:40458	-2.96	-0.76	0.90
138	4867267:BG822880:4867267:Hs.298262:ribosomal protein S19:RPS19:19:19q13.2:3:139515	-2.98	-1.60	0.99
139	124326:R02211:124326:Hs.6664:Homo sapiens cDNA FLJ37640 fis, clone BRHIP1000174:::0:124326	-3.00	-0.69	-0.92
140	159355:H14999:159355:Hs.79307:Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6:ARHGEF6:X:Xq26:0:159355	-3.01	-0.22	0.60
141	153750:R48060:153750:Hs.92700:DKFZP564O243 protein:DKFZP564O243:3:3p21.1:0:153750	-3.08	-1.21	0.63
142	166034:R87386:166034:Hs.179770:protein tyrosine phosphatase, receptor type, H:PTPRH:19:19q13.4:0:166034	-3.10	-0.93	-0.05
143	42868:R61165:42868:Hs.47166:HT021:HT021:3:3p14.3:0:42868	-3.12	-1.38	0.50
144	133254:R26941:133254:Hs.349344:hypothetical protein BC001573:LOC134147:5:5p15.32:0:133254	-3.14	0.01	0.35
145	37631:R60599:37631:Hs.23044:similar to RIKEN cDNA 2610036L13:MGC16386:11:11q13.1:0:37631	-3.14	-0.64	0.77
146	38849:R51281:38849:Hs.40137:anaphase-promoting complex 1; meiotic checkpoint regulator:MCPR:2:2q12.1:0:38849	-3.15	-0.70	-0.04
147	219888:H85192:219888:Hs.218842:glutamate rich WD repeat protein GRWD:GRWD:19:19q13.33:2:219888	-3.17	-1.94	0.20
148	165774:R86861:165774:Hs.6755:RaP2 interacting protein 8:RPIP8:17:17q21.31:0:165774	-3.18	0.63	0.43
149	158130:H26559:158130:Hs.75822:TGFB1-induced anti-apoptotic factor 1:TIAF1:17:17q11.1-q11.2:0:158130	-3.19	-0.04	-0.27
150	129365:R16448:129365:Hs.18349:mitochondrial ribosomal protein L15:MRPL15:8:8q11.2-q13:0:129365	-3.20	-0.63	0.87
151	22278:T73985:22278:Hs.134406:hypothetical protein FLJ20511:FLJ20511:16:16q23.1:2:22278	-3.21	0.73	0.01
152	122393:T99307:122393:Hs.103315:zinc finger protein 384:ZNF384:12::0:122393	-3.24	-0.33	0.60
153	166550:R88469:166550:Hs.34074:dipeptidylpeptidase VI:DPP6:7:7q36.1-q36.2:0:166550	-3.25	-1.01	0.44
154	5239635:BI522464:5239635:Hs.301547:ribosomal protein S7:RPS7:2:2p25.3:129870	-3.28	-0.26	0.23
155	114969:T86264:114969:Hs.286:ribosomal protein L4:RPL4:15:15q22:10:115641	-3.29	0.84	-0.34
156	5530061:BM454879:5530061:Hs.172182:poly(A) binding protein, cytoplasmic 1:PABPC1:8:8q22.2-q23:3:27347	-3.33	-0.08	0.71
157	46841:H10126:46841:Hs.288146:KIAA0169	-3.35	-0.43	0.42

	protein:KIAA0169:9:9q34.13:0:46841			
158	37992:R61444:37992:Hs.16063:hypothetical protein FLJ21877:FLJ21877:2:2p22.1:0:37992	-3.40	-1.42	0.35
159	510054:AA053064:510054:Hs.15396:Homo sapiens, clone IMAGE-3948909, mRNA, partial cds::11::3:116450	-3.42	-1.49	0.80
160	126839:R07291:126839:Hs.13645:likely ortholog of the mouse thymocyte protein Thy28:THY28:11:11q25:0:126839	-3.42	-0.51	0.01
161	3952101:R14772:3952101:Hs.6839:hypothetical protein FLJ12154:FLJ12154:14:14q11.1:3:30076	-3.46	-1.13	1.43
162	5829576:BQ021774:5829576:Hs.195851:actin, alpha 2, smooth muscle, aorta:ACTA2:10:10q23.3:3:161468	-3.48	-0.43	0.74
163	182425:H42103:182425:Hs.293650:regucalcin gene promotor region related protein:RGPR:1:1q24.1:0:182425	-3.55	-1.16	0.13
164	130243:R22632:130243:Hs.16740:hypothetical protein FLJ11036:FLJ11036:3:3p25.1:2:130243	-3.75	0.79	-0.76
165	122420:T99317:122420:Hs.5250:Homo sapiens, similar to Molybdenum cofactor synthesis protein cinnamon, clone IMAGE- 3858121, mRNA, partial cds::1::0:122420	-3.98	-1.40	0.21
166	122756:T99046:122756:Hs.74376:olfactomedin 1:OLFM1:9:9q34.3:3:121389	-4.35	-0.90	0.35

**Supplementary Table 2. List of genes influenced by *Lactobacillus plantarum*;**

**38 up-regulated (A), and 26 down-regulated (B)**

<b>A</b>	<b>Genes up-regulated in descending order</b>	<b>E.c.</b>	<b>L.p. (+)</b>	<b>Mix</b>
1	211054:H65795:211054:Hs.301005:histone H2A.F/Z variant:H2AV:7:7p13:0:211054	1.23	3.70	- 0.65
2	136080:R35478:136080:Hs.5011:RNA binding motif protein 9:RBM9:22:22q13.1:3:149813	-1.31	2.92	0.41
3	125802:BM840842:125802:Hs.32916:nascent-polypeptide-associated complex alpha polypeptide:NACA:12:12q23-q24.1:3:125802	0.67	2.92	- 0.59
4	489649:AA099459:489649:Hs.772:glycogen synthase 1 (muscle):GYS1:19:19q13.3:0:489649	0.20	2.88	- 0.52
5	172010:H18766:172010:Hs.158184:KIAA1966 protein:KIAA1966:4:4q13.1:0:172010	1.22	2.79	- 0.64
6	5264345:BI550180:5264345:Hs.182278:calmodulin 2 (phosphorylase kinase, delta):CALM2:2:2p21:3:66368	1.56	2.67	- 1.14
7	120355:T97240:120355:Hs.111782:myosin 5C:MYO5C:15:15q21:3:114951	1.01	2.52	0.13
8	5475845:BM560994:5475845:Hs.273415:aldolase A, fructose-bisphosphate:ALDOA:16:16q22-q24:3:148239	1.67	2.51	- 0.51
9	206766:R98267:206766:Hs.26410:Homo sapiens cDNA FLJ38890 fis, clone NESOP1000108::4::0:206766	-0.84	2.49	0.16
10	5636122:BM857788:5636122:Hs.287994:nuclear receptor co-repressor 2:NCOR2:12:12q24:10:180447	0.43	2.36	- 0.15
11	5467595:BM556894:5467595:Hs.20677:raptor:raptor:17:17q25.3:3:32759	0.50	2.35	- 0.25
12	197498:H51983:197498:Hs.352054:pregnancy specific beta-1-glycoprotein 9:PSG9:19:19q13.2:0:197498	1.78	2.33	- 0.84
13	34947:R19764:34947:Hs.7542:KIAA1802 protein:KIAA1802:18:18:0:34947	0.24	2.26	- 0.62
14	135291:R31058:135291:Hs.33818:RecQ protein-like 5:RECQL5:17:17q25.2-q25.3:0:135291	0.99	2.24	- 0.12
15	5809216:BQ056781:5809216:Hs.100002:dynein light chain 2A:DNLC2A:20:20q11.21:3:301946	0.33	2.24	- 0.82
16	320507:W31774:320507:Hs.173724:creatine	1.66	2.24	-

	kinase, brain:CKB:14:14q32:0:320507			1.59
17	5578122:BM468475:5578122:Hs.302499:karyopherin alpha 4 (importin alpha 3):KPNA4:11:11q22:3:43536	0.66	2.24	- 1.24
18	136472:R34213:136472:Hs.149436:kinesin family member 5B:KIF5B:10:10pter-q22.1:0:136472	1.57	2.23	- 1.59
19	486652:AA044231:486652:Hs.62654:kringle containing transmembrane protein:KREMEN:22:22q12.1:0:486652	-0.45	2.20	- 0.19
20	5707999:BM993314:5707999:Mm.22695:collapsing response mediator protein 1:Crmp1:5:5 21.0 cM:10:116797	0.34	2.18	0.19
21	123690:R02753:123690:Hs.33010:KIAA0633 protein:COBL:7:7p14.3:0:123690	-0.69	2.17	- 0.37
22	4042897:BF105982:4042897:Hs.75736:apolipoprotein D:APOD:3:3q26.2-qter:3:503910	0.28	2.17	- 0.24
23	5755043:BQ067508:5755043:Hs.169476:glyceraldehyde-3-phosphate dehydrogenase:GAPD:12:12p13:3:503601	-0.24	2.16	- 0.69
24	248848:H80740:248848:Hs.75160:phosphofruktokinase, muscle:PFKM:12:12q13.3:0:248848	0.40	2.14	- 0.62
25	248427:N78172:248427:Hs.333555:echinoderm microtubule associated protein like 4:EML4:2:2p22-p21:0:248427	0.07	2.08	- 0.90
26	322612:W39304:322612:Hs.391576:testis expressed sequence 27:TEX27:6:6pter-p22.3:0:322612	0.67	2.08	- 1.69
27	210360:H65544:210360:Hs.20369:hypothetical protein FLJ36991:FLJ36991:19:19q13.13:0:210360	1.36	2.07	- 0.39
28	1857635:AI284184:1857635:Hs.301496:ATP-binding cassette, sub-family A (ABC1), member 9:ABCA9:17:17q24:3:376845	0.66	2.06	- 1.35
29	136326:R34021:136326:Hs.251064:high-mobility group nucleosome binding domain 1:HMGN1:21:21q22.2:0:136326	1.43	2.05	- 0.94
30	134732:R28329:134732:Hs.288544:hypothetical protein MGC16063:MGC16063:17:17q21.31:0:134732	1.25	2.04	- 0.77
31	143843:R75983:143843:Hs.84700:serologically defined colon cancer antigen 28:SDCCAG28:11:11q13:0:143843	1.61	2.04	- 0.82
32	5444580:BM009874:5444580:Hs.350077:ribosom	1.26	2.04	-

	al protein L21:RPL21:10:10q26.13:3:307798			1.65
33	136522:R34468:136522:Hs.278671:KIAA0336 gene product:KIAA0336:2:2q12.2:0:136522	0.42	2.03	- 1.10
34	5927927:BQ071508:5927927:Hs.334895:ribosomal protein L10a:RPL10A:6:6p21.3-p21.2:3:343823	1.13	2.01	- 1.02
35	279086:N51791:279086:Hs.232409:hypothetical protein FLJ20296:FLJ20296:2:2p11.2:0:279086	-0.34	2.01	0.16
36	258999:N42245:258999:Hs.119571:collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV)	-0.35	2.00	1.14
37	149550:H00332:149550:Hs.181349:hypothetical protein 628:LOC56270:17:17q25.3:0:149550	1.19	2.00	- 0.33
38	5751639:BQ067255:5751639:Hs.275243:S100 calcium binding protein A6 (calcyclin):S100A6:1:1q21.3:310393	0.58	2.00	- 0.37
<b>B</b>	<b>Genes down-regulated in descending order</b>	E.c.	L.p. (-)	Mix
1	22487:T74004:22487:Hs.356084:G protein-coupled receptor 27:GPR27:3:3p21-p14:1:22487	-0.13	-2.03	- 0.06
2	4343462:BF796187:4343462:Hs.177534:dual specificity phosphatase 10:DUSP10:1:1q41.3:258760	-0.09	-2.03	1.52
3	132142:R23610:132142:Hs.209125:LOC223082:LOC223082:7:7p15.3:0:132142	-1.47	-2.05	- 0.32
4	415658:W78998:415658:Hs.62954:ferritin, heavy polypeptide 1:FTH1:11:11q13:0:415658	-0.62	-2.05	0.40
5	51004:H18570:51004:Hs.380:solute carrier family 1 (glial high affinity glutamate transporter), member 2	-0.36	-2.07	0.29
6	110352:T82054:110352:Hs.814:major histocompatibility complex, class II, DP beta 1:HLA-DPB1:6:6p21.3:0:110352	-1.56	-2.07	- 0.03
7	241788:H91815:241788:Hs.7645:fibrinogen, B beta polypeptide:FGB:4:4q28:0:241788	-0.88	-2.08	- 1.45
8	244912:N72344:244912:Hs.1478:serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1	-0.17	-2.08	0.31
9	3952101:R14772:3952101:Hs.6839:hypothetical protein FLJ12154:FLJ12154:14:14q11.1:3:30076	0.89	-2.10	0.40
10	429684:AA011701:429684:Hs.155470:zinc finger protein 3 (A8-51):ZNF3:7:7q22.1:0:429684	-0.03	-2.14	0.78
11	428413:AA004287:428413:Hs.59260:NTT5 protein:NTT5:19:19q13.1-q13.4:1:428413	0.50	-2.14	0.43
12	26884:R13798:26884:Hs.176977:oligodendrocyte	-1.24	-2.14	-

	lineage transcription factor 2:OLIG2:21:21q22.11:2:26884			0.02
13	289846:N77116:289846:Hs.143434:contactin 1:CNTN1:12:12q11-q12:0:289846	0.35	-2.18	- 0.29
14	266488:N28915:266488:Hs.330046:ceramide kinase:CERK:22:22q13.31:0:266488	0.24	-2.19	- 0.08
15	428035:AA002016:428035:Hs.65993:CDC14 cell division cycle 14 homolog A (S. cerevisiae):CDC14A:1:1p21:0:428035	0.72	-2.21	0.63
16	141677:R69649:141677:Hs.352054:pregnancy specific beta-1-glycoprotein 9:PSG9:19:19q13.2:0:141677	-0.89	-2.23	- 0.27
17	173299:H20935:173299:Hs.271277:likely ortholog of chicken repulsive guidance molecule:RGM:15:15q26.1:0:173299	-1.01	-2.24	0.30
18	510054:AA053064:510054:Hs.15396:Homo sapiens, clone IMAGE-3948909, mRNA, partial cds::11::3:116450	0.69	-2.25	- 0.09
19	4859208:BG762226:4859208:Hs.93164:proprotein convertase subtilisin/kexin type 2:PCSK2:20:20p11.2:3:382701	0.17	-2.35	0.76
20	126839:R07291:126839:Hs.13645:likely ortholog of the mouse thymocyte protein Thy28:THY28:11:11q25:0:126839	0.57	-2.40	- 0.51
21	116272:T89583:116272:Hs.102669:KIAA1892 protein:KIAA1892:9:9p11.2:3:114064	0.11	-2.40	0.81
22	109344:T81051:109344:Hs.132160:Homo sapiens cDNA FLJ39737 fis, clone SMINT2016396::::0:109344	-0.10	-2.50	- 0.74
23	196806:R92843:196806:Hs.107924:Homo sapiens mRNA for OK/KNS-CL.4, complete cds::9::0:196806	-1.15	-2.61	0.73
24	309260:W40184:309260:Hs.179866:solute carrier family 25 (mitochondrial carrier, Aralar), member 12:SLC25A12:2:2q24:0:309260	-0.39	-2.79	1.43
25	187580:R83651:187580:Hs.222399:CEGP1 protein:CEGP1:11:11p15.3:0:187580	-1.24	-2.87	- 0.30
26	122420:T99317:122420:Hs.5250:Homo sapiens, similar to Molybdenum cofactor synthesis protein cinnamon, clone IMAGE-3858121	0.00	-3.64	- 1.02

**Supplementary table 3. List of genes influenced by Mix; 23 up-regulated (A) and 59 down-regulated (B)**

<b>A</b>	<b>Genes up-regulated in descending order</b>	<b>E.c.</b>	<b>L.p.</b>	<b>Mix (+)</b>
1	298203:W01422:298203:Hs.173034:amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen):AMPH:7:7p14-p13:0:298203	0.17	-0.55	3.04
2	32055:R17244:32055:Hs.172700:neuralized-like (Drosophila):NEURL:10:10q25.1:1:32055	0.29	-1.25	2.91
3	323874:W46270:323874:Hs.106534:hypothetical protein FLJ22625:FLJ22625:5:5q31.2:0:323874	0.52	0.39	2.91
4	327574:W35163:327574:Hs.23467:neuron navigator 2:NAV2:11:11p15.1:0:327574	-0.41	0.78	2.83
5	5113334:BI256660:5113334:Hs.169793:ribosomal protein L32:RPL32:3:3p25-p24:3:281891	-0.54	-1.36	2.80
6	486573:AA043380:486573:Hs.123070:homeo box D10:HOXD10:2:2q31.1:0:486573	1.32	-0.64	2.50
7	248288:N78092:248288:Hs.30127:PHD finger protein 7:PHF7:3:3p21.31:0:248288	-0.36	-1.31	2.44
8	5583401:BM457144:5583401:Hs.196352:neutrophil cytosolic factor 4, 40kDa:NCF4:22:22q13.1:3:485178	-0.63	-0.97	2.39
9	306037:W20061:306037:Hs.388203:T-cell activation WD repeat protein:TA-WDRP:5:5q21.3:0:306037	0.17	0.43	2.37
10	418025:W90717:418025:Hs.177386:solute carrier family 24 (sodium/potassium/calcium exchanger), member 4:SLC24A4:14:14q32.12-q32.13:1:418025	-1.18	-1.96	2.35
11	1587322:AA977146:1587322:Hs.80988:collagen, type VI, alpha 3:COL6A3:2:2q37.3:136035	0.20	0.03	2.33
12	248488:N72652:248488:Hs.84522:hypothetical protein FLJ31842:FLJ31842:1:1p21.3:0:248488	0.46	0.50	2.27
13	383127:AA074291:383127:Hs.79389:NEL-like 2 (chicken):NELL2:12:12q13.11-q13.12:0:383127	0.60	-0.30	2.25
14	278004:N94709:278004:Hs.101949:hypothetical protein FLJ30685:FLJ30685:11:11q22.3:1:278004	0.14	0.10	2.23
15	298251:W03694:298251:Hs.166852:KIAA1683 protein:KIAA1683:19:19p13.1:0:298251	-0.13	0.39	2.22
16	50282:H17600:50282:Hs.103042:microtubule-associated protein 1B:MAP1B:5:5q13.2:50282	-0.63	-0.83	2.13
17	416840:W87308:416840:Hs.15282:Homo sapiens cDNA FLJ39225 fis, clone OCBBF2007224, highly similar to Homo sapiens candidate tumor suppressor protein DICE1 mRNA	-1.05	0.13	2.12
18	290759:W01300:290759:Hs.87149:integrin, beta 3	-0.36	-0.56	2.11

	(platelet glycoprotein IIIa, antigen CD61):ITGB3:17:17q21.32:0:290759			
19	298412:W04870:298412:Hs.74569:KIAA0842 protein:KIAA0842:1:1p36.13:0:298412	0.33	0.10	2.10
20	182282:H41937:182282:Hs.24135:transmembrane protein vezatin:VEZATIN:12:12q21.33:0:182282	-0.90	-0.47	2.06
21	306146:W20101:306146:Hs.54627:methionyl-tRNA formyltransferase, mitochondrial:MtFMT:15:15q22.2:0:306146	-0.31	0.37	2.04
22	279214:N48838:279214:Hs.249223:ganglioside-induced differentiation-associated protein 1:GDAP1:8:8q13.2:0:279214	-0.28	-0.24	2.02
23	1721285:A1151284:1721285:Hs.156351:hypothetical protein FLJ23471:FLJ23471:7:7p22.3:3:502520	-1.44	-0.27	2.01
<b>B</b>	<b>Genes down-regulated in descending order</b>	E.c.	L.p.	Mix (-)
1	278777:W01758:278777:Hs.5085:dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit:DPM1:20:20q13.13:0:278777	-0.26	1.11	-2.00
2	321259:W55913:321259:Hs.184014:ribosomal protein L31:RPL31:2:2q11.2:1:321259	0.80	1.92	-2.01
3	267697:N34161:267697:Hs.82643:protein tyrosine kinase 9:PTK9:12:12p11.22:0:267697	0.12	1.44	-2.01
4	5540049:BM464024:5540049:Hs.169248:cytochrome c:HCS:7:7p21.2:3:470899	-0.98	0.00	-2.02
5	5928074:BO071631:5928074:Hs.75355:ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast):UBE2N:12:12q21.33:3:488512	-0.27	1.22	-2.02
6	415290:W92121:415290:Hs.295112:Williams Beuren syndrome chromosome region 20C:WBSR20C:7:7q11.23:0:415290	-0.70	0.82	-2.03
7	282440:N54628:282440:Hs.75290:ADP-ribosylation factor 4:ARF4:3:3p21.2-p21.1:0:282440	0.32	0.53	-2.03
8	322866:W45086:322866:Hs.55879:multidrug resistance-associated protein 7:SIMRP7:6:6p12.3:0:322866	1.14	0.28	-2.05
9	346386:W79220:346386:Hs.174070:ubiquitin carrier protein:E2-EPF:19:19q13.43:0:346386	0.15	0.88	-2.05
10	291985:W02106:291985:Hs.29981:solute carrier family 26 (sulfate transporter), member 2:SLC26A2:5:5q31-q34:0:291985	0.15	0.99	-2.06
11	418103:W90498:418103:Hs.83715:Sjogren syndrome antigen B (autoantigen La):SSB:2:2q31.1:0:418103	-0.48	0.35	-2.08
12	182411:H42095:182411:Hs.326035:early growth response 1:EGR1:5:5q31.1:0:182411	-0.42	0.86	-2.08

13	4545721:BG248268:4545721:Hs.77039:ribosomal protein S3A:RPS3A:4:4q31.2-q31.3:3:298773	0.84	0.28	-2.08
14	503752:AA130076:503752:Hs.306098:aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-0.48	1.71	-2.09
15	110503:T82817:110503:Hs.283565:FOS-like antigen 1:FOSL1:11:11q13:0:110503	-0.64	0.38	-2.09
16	272619:N44142:272619:Hs.11899:3-hydroxy-3-methylglutaryl-Coenzyme A reductase:HMGCR:5:5q13.3-q14:0:272619	-0.32	0.09	-2.10
17	269107:N36667:269107:Hs.343911:etoposide-induced mRNA:PIG8:11:11q24:0:269107	0.21	0.71	-2.11
18	5787428:BQ049548:5787428:Hs.103180:DC2 protein:DC2:4:4q24:3:270524	0.25	0.88	-2.12
19	140447:R66021:140447:Hs.378493:Homo sapiens cDNA FLJ36123 fis, clone TESTI2022874, weakly similar to ZINC FINGER PROTEIN 135::8::0:140447	0.24	1.42	-2.14
20	245844:N77334:245844:Hs.52763:anaphase-promoting complex subunit 7:APC7:12:12q13.12:0:245844	0.20	0.20	-2.15
21	446686:AA203633:446686:Hs.183858:transcriptional intermediary factor 1:TIF1:7:7q32-q34:0:446686	-1.50	0.73	-2.15
22	243600:N49822:243600:Hs.89552:glutathione S-transferase A1:GSTA1:6:6p12.1:0:243600	-0.29	-0.30	-2.15
23	5754316:BM922198:5754316:Hs.251653:tubulin, beta, 2:TUBB2:::3:301465	0.01	1.73	-2.15
24	485828:AA040366:485828:Hs.173288:likely ortholog of mouse TPR-containing, SH2-binding phosphoprotein:TSBP:11:11p15.3:0:485828	-0.37	0.29	-2.16
25	247674:BQ045383:247674:Hs.169476:glyceraldehyde-3-phosphate dehydrogenase:GAPD:12:12p13.3:247674	0.97	1.95	-2.16
26	366763:AA029330:366763:Hs.12461:LCHN protein:LCHN:7:7q32.3:0:366763	0.38	0.06	-2.16
27	269771:N40071:269771:Hs.3886:karyopherin alpha 3 (importin alpha 4):KPNA3:13:13q14.3:0:269771	-0.46	0.62	-2.18
28	248446:N72642:248446:Hs.27258:Siah-interacting protein:SIP:1:1q24-q25:0:248446	-0.77	-0.14	-2.18
29	261835:N23581:261835:Hs.110796:SAR1 protein:SAR1:10:10q22.3:0:261835	-0.55	0.68	-2.18
30	5823226:R32051:5823226:Hs.204354:ras homolog gene family, member B:ARHB:2:2pter-p12:3:134390	0.65	1.14	-2.19
31	2270793:AI690073:2270793:Hs.378632:glutamate-cysteine ligase, catalytic subunit:GCLC:6:6p12:3:288667	-0.66	0.40	-2.21
32	322177:W37945:322177:Hs.3530:FUS interacting protein	0.08	0.16	-2.21

	(serine-arginine rich) 1:FUSIP1:1:1p36.11:0:322177			
33	5931494:BQ066818:5931494:Hs.177592:ribosomal protein, large, P1:RPLP1:15:15q22:3:239082	1.13	1.74	-2.21
34	5475349:BM913272:5475349:Hs.90107:adhesion regulating molecule 1:ADRM1:20:20q13.33:3:488619	-0.29	0.65	-2.25
35	341055:W58163:341055:Hs.78888:diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein):DBI:2:2q12-q21:0:341055	-0.27	0.51	-2.25
36	270772:N42428:270772:Hs.180450:ribosomal protein S24:RPS24:10:10q22-q23:0:270772	0.41	1.80	-2.25
37	272575:N43981:272575:Hs.429:ATP synthase, H+ transporting, mitochondrial FO complex, subunit c (subunit 9) isoform 3:ATP5G3:2:2q31.1:0:272575	0.65	0.91	-2.26
38	5406583:BI862422:5406583:Hs.119192:H2A histone family, member Z:H2AFZ:4:4q24:3:375854	0.09	1.33	-2.26
39	50615:H17836:50615:Hs.80288:heat shock 70kDa protein 1-like:HSPA1L:6:6p21.3:0:50615	0.23	0.46	-2.26
40	5226345:BI839018:5226345:Hs.296585:nucleolar protein 5A (56kDa with KKE/D repeat):NOL5A:20:20p13:3:114158	-0.27	0.17	-2.27
41	489783:AA098888:489783:Hs.77324:eukaryotic translation termination factor 1:ETF1:5:5q31.1:0:489783	-0.61	0.75	-2.27
42	22658:T74240:22658:Hs.8997:heat shock 70kDa protein 1A:HSPA1A:6:6p21.3:1:22658	0.84	1.09	-2.28
43	269776:N36269:269776:Hs.5308:ubiquitin A-52 residue ribosomal protein fusion product 1:UBA52:19:19p13.1-p12:0:269776	0.61	0.77	-2.29
44	5421424:BM006748:5421424:Hs.254105:enolase 1, (alpha):ENO1:1:1p36.3-p36.2:3:341125	0.54	0.75	-2.34
45	274227:H49804:274227:Hs.75431:fibrinogen, gamma polypeptide:FGG:4:4q28:0:274227	-0.57	0.41	-2.36
46	5481755:BM915559:5481755:Hs.76244:spermidine synthase:SRM:1:1p36-p22:3:114896	1.69	1.08	-2.39
47	491155:BQ028619:491155:Hs.111611:ribosomal protein L27:RPL27:17:17q21.1-q21.2:3:491155	0.92	1.67	-2.43
48	4723376:BG565707:4723376:Hs.75431:fibrinogen, gamma polypeptide:FGG:4:4q28:3:301385	-0.42	0.12	-2.45
49	5494320:BM450631:5494320:Hs.289088:heat shock 90kDa protein 1, alpha:HSPCA:14:14q32.33:3:36189	-0.34	0.42	-2.46
50	282039:N53607:282039:Hs.172673:S-adenosylhomocysteine hydrolase:AHCY:20:20cen-q13.1:0:282039	0.95	0.33	-2.48
51	5208247:BI771912:5208247:Hs.169793:ribosomal protein L32:RPL32:3:3p25-p24:3:69342	1.21	1.86	-2.57

52	5549800:BM552637:5549800:Hs.76053:DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kDa):DDX5:17:17q21:3:306186	-0.65	0.92	-2.71
53	5834627:AA033871:5834627:Hs.77502:methionine adenosyltransferase II, alpha:MAT2A:2:2p11.2:3:471121	0.11	0.49	-2.74
54	4585524:BG425162:4585524:Hs.5174:ribosomal protein S17:RPS17:15:15q:3:470534	0.73	1.31	-2.75
55	323428:W45582:323428:Hs.621:lectin, galactoside-binding, soluble, 3 (galectin 3):LGALS3:14:14q21-q22:0:323428	0.38	1.05	-2.75
56	302623:W37168:302623:Hs.73965:hypothetical protein ET:ET:17:17q25:0:302623	-1.50	0.34	-2.87
57	322088:W37644:322088:Hs.73965:hypothetical protein ET:ET:17:17q25:0:322088	-1.28	0.30	-2.88
58	328927:W40235:328927:Hs.36927:heat shock 105kD:HSP105B:13:13q12.3:0:328927	-1.92	0.61	-2.93
59	208059:H62639:208059:Hs.180414:heat shock 70kDa protein 8:HSPA8:11:11q24.1:0:208059	-0.21	0.81	-2.97