Supplementary Table 1: Differentially expressed genes in late stage type 1 diabetes compared to HC 1.5 fold change lower bound 90% CI

probe set	gene	Accession	EntrezGene	Description	HC_109nMSC_(HG-U133_Plus_2).CEL	HC_110nMSC_(HG-U133_Plus_2).CEL	HC_RO1_(HG-U133_Plus_2).CEL	baseline mean	baseline mean's SE	LS_T1D_A02_(HG-U133_Plus_2).CEL	LS_T1D_A03_(HG-U133_Plus_2).CEL	LS_T1D_A05_(HG-U133_Plus_2).CEL	experiment mean	experiment mean's SE	fold change	lower bound of FC	upper bound of FC	filtered
1552610_a_at	JAK1: Janus kinase 1 (a protein tyrosine kinase)	NM_002227	3716	gb:NM_002227.1 /DB_XREF=gi:4504802 /GEN=JAK1 /TID=Hs2.50651.1 /CNT=135 /FEA=FLmRNA /TIER=FL /STK=2 /LL=3716 /UG=Hs.50651 /DEF=Homo sapiens Janus kinase 1 (a protein tyrosine kinase) (JAK1), mRNA. /PROD=janus kinase 1 /FL=gb:M64174.1 gb:NM_002227.1	32,87	19,49	25,26	25,87	3,87	77,26	60,81	53,6	63,89	7	2,47	1,84	3,42	*
1552658_a_at	NAV3: neuron navigator 3	NM_014903	89795	gb:NM_014903.2 /DB_XREF=gi:27734089 /GEN=NAV3 /TID=Hs2.174188.1 /CNT=31 /FEA=FLmRNA /TIER=FL /STK=2 /LL=89795 /UG=Hs.174188 /DEF=Homo sapiens neuron navigator 3 (NAV3), mRNA. /PROD=neuron navigator 3 /FL=gb:NM_014903.2	30,35	13,38	3,92	15,88	7,73	38,69	57,31	42,09	46,03	5,72	2,9	1,53	14,6	*
1553055_a_at	SLFN5: schlafen family member 5	NM_144975	162394	gb:NM_144975.1 /DB_XREF=gi:21450660 /TID=Hs2.352216.1 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=2 /LL=162394 /UG_GENE=MGC19764 /UG=Hs.352216 /UG_TITLE=hypothetical protein MGC19764 /DEF=Homo sapiens hypothetical protein MGC19764 (MGC19764), mRNA. /FL=gb:NM_144975.1 gb:BC021238.1	11,58	13,42	3,53	9,51	3,04	31,14	26,82	21,7	26,55	2,73	2,79	1,76	5,95	*
1553112_s_at	CDK8: cyclin-dependent kinase 8	NM_001260	1024	gb:NM_001260.1 /DB_XREF=gi:4502744 /GEN=CDK8 /TID=Hs2.397734.1 /CNT=32 /FEA=FLmRNA /TIER=FL /STK=1 /LL=1024 /UG=Hs.397734 /DEF=Homo sapiens cyclin-dependent kinase 8 (CDK8), mRNA. /PROD=cyclin-dependent kinase 8 /FL=gb:NM_001260.1	23,7	13,79	8,48	15,32	4,46	32,56	45,83	37,4	38,59	3,88	2,52	1,63	4,9	*
1553117_a_at	STK38: serine/threonine kinase 38	NM_007271	11329	gb:NM_007271.1 /DB_XREF=gi:6005813 /GEN=STK38 /TID=Hs2.8724.1 /CNT=37 /FEA=FLmRNA /TIER=FL /STK=1 /LL=11329 /UG=Hs.8724 /DEF=Homo sapiens serinethreonine kinase 38 (STK38), mRNA. /PROD=serinethreonine kinase 38 /FL=gb:NM_007271.1	41,02	28,46	15,34	28,27	7,41	96,16	83,25	59,12	79,51	10,85	2,81	1,81	5,1	*
1553685_s_at	SP1: Sp1 transcription factor	NM_138473	6667	gb:NM_138473.1 /DB_XREF=gi:19924004 /TID=Hs2.348374.1 /CNT=35 /FEA=FLmRNA /TIER=FL /STK=0 /LL=144467 /UG_GENE=LOC144467 /UG=Hs.348374 /UG_TITLE=hypothetical protein BC012008 /DEF=Homo sapiens hypothetical protein BC012008 (LOC144467), mRNA. /FL=gb:NM_138473.1 gb:BC012008.1	7,57	5,98	4,14	5,9	0,99	12,32	15,63	10,56	12,84	1,49	2,18	1,58	3,14	*
1554027_a_at	SLC4A4: solute carrier family 4, sodium bicarbonate cotransporter, member 4	BC030977	8671	gb:BC030977.1 /DB_XREF=gi:21411309 /TID=Hs2.5462.2 /CNT=13 /FEA=FLmRNA /TIER=FL /STK=6 /LL=8671 /UG_GENE=SLC4A4 /UG=Hs.5462 /DEF=Homo sapiens, Similar to solute carrier family 4, sodium bicarbonate cotransporter, member 4, clone MGC:32627 IMAGE:4610968, mRNA, complete cds. /PROD=Similar to solute carrier family 4, sodiumbicarbonate cotransporter, member 4 /FL=gb:BC030977.1	8,27	6,43	4,61	6,44	1,06	19,28	16,25	20,83	18,79	1,35	2,92	2,23	4,07	*
1554726_at	ZNF655: zinc finger protein 655	AY099353	79027	gb:AY099353.1 /DB_XREF=gi:22552707 /GEN=VIK /TID=Hs2.115659.3 /CNT=4 /FEA=FLmRNA /TIER=FL /STK=1 /LL=79027 /UG=Hs.115659 /DEF=Homo sapiens vav-1 interacting Kruppel-like protein (VIK) mRNA, complete cds. /PROD=vav-1 interacting Kruppel-like protein /FL=gb:AY099353.1	7,5	3,88	3,53	4,97	1,27	12,57	10,44	9,93	10,98	0,81	2,21	1,52	3,85	*
1554885_a_at	PRIM2A: primase, polypeptide 2A, 58kDa	BC017833	5558	gb:BC017833.1 /DB_XREF=gi:17389608 /TID=Hs2.74519.2 /CNT=3 /FEA=FLmRNA /TIER=FL /STK=1 /LL=5558 /UG_GENE=PRIM2A /UG=Hs.74519 /DEF=Homo sapiens, Similar to primase, polypeptide 2A (58kD), clone MGC:22486 IMAGE:4307922, mRNA, complete cds. /PROD=Similar to primase, polypeptide 2A (58kD) /FL=gb:BC017833.1	14,03	10,8	6,41	10,41	2,21	23,19	27,2	22,73	24,37	1,42	2,34	1,71	3,63	*
1554930_a_at	FUT8: fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	AB049740	2530	gb:AB049740.2 /DB_XREF=gi:18265337 /TID=Hs2.118722.3 /CNT=3 /FEA=FLmRNA /TIER=FL /STK=1 /LL=2530 /UG_GENE=FUT8 /UG=Hs.118722 /DEF=Homo sapiens mRNA for alpha 1,6-fucosyltransferase, complete cds. /PROD=alpha 1,6-fucosyltransferase /FL=gb:AB049740.2	25,15	10,83	14,41	16,79	4,3	38,58	47,52	47,49	44,53	2,98	2,65	1,83	4,62	*
1554997_a_at	PTGS2: prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	AY151286	5743	gb:AY151286.1 /DB_XREF=gi:24430027 /TID=Hs2.196384.2 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=1 /LL=5743 /UG_GENE=PTGS2 /UG=Hs.196384 /DEF=Homo sapiens cyclooxygenase 2b mRNA, complete cds; alternatively spliced. /PROD=cyclooxygenase 2b /FL=gb:AY151286.1	3,56	3,07	3,53	3,38	0,16	39,15	9,26	19,87	22,76	8,75	6,73	2,47	11,06	*
1555097_a_at	PTGFR: prostaglandin F receptor (FP)	BC035694	5737	gb:BC035694.1 /DB_XREF=gi:23272756 /TID=Hs2.89418.2 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=1 /LL=5737 /UG_GENE=PTGFR /UG=Hs.89418 /DEF=Homo sapiens, prostaglandin F receptor (FP), clone MGC:46203 IMAGE:5760478, mRNA, complete cds. /PROD=prostaglandin F receptor (FP) /FL=gb:BC035694.1	4,18	3,56	4,14	3,96	0,2	29,33	13,83	16,92	20,03	4,74	5,05	3,07	7,11	*
1555154_a_at	QKI: quaking homolog, KH domain RNA binding (mouse)	AF142421	9444	gb:AF142421.1 /DB_XREF=gi:7542354 /GEN=QUAKING /TID=Hs2.15020.4 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=1 /LL=9444 /UG=Hs.15020 /DEF=Homo sapiens QUAKING isoform 5 (QUAKING) mRNA, complete cds. /PROD=QUAKING isoform 5 /FL=gb:AF142421.1 gb:AF142420.1	33,26	22,48	18,29	24,68	4,46	64,52	70,25	52,17	62,31	5,33	2,53	1,87	3,67	*
1555202_a_at	P15RS: hypothetical protein FLJ10656	BC010136	55197	gb:BC010136.1 /DB_XREF=gi:14603355 /TID=Hs2.300906.2 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=1 /LL=55197 /UG_GENE=P15RS /UG=Hs.300906 /DEF=Homo sapiens, clone MGC:19513 IMAGE:4109857, mRNA, complete cds. /PROD=Unknown (protein for MGC:19513) /FL=gb:BC010136.1	6,17	4,96	4,55	5,23	0,49	8,35	10,91	10,98	10,08	0,86	1,93	1,57	2,38	*
1555240_s_at	GNG12: guanine nucleotide binding protein (G protein), gamma 12	AF493879	55970	gb:AF493879.1 /DB_XREF=gi:20147650 /GEN=GNG12 /TID=Hs2.8107.2 /CNT=2 /FEA=FLmRNA /TIER=FL /STK=1 /LL=55970 /UG=Hs.8107 /DEF=Homo sapiens guanine nucleotide binding protein gamma 12 (GNG12) mRNA, complete cds. /PROD=guanine nucleotide binding protein gamma 12 /FL=gb:AF493879.1	74	47,72	6,54	42,75	19,63	177,6	220,3	108,81	168,9	32,48	3,95	1,99	16,41	*
1555247_a_at	RAPGEF6: Rap guanine nucleotide exchange factor (GEF) 6	AF394782	51735	gb:AF394782.1 /DB_XREF=gi:15077825 /TID=Hs2.174795.3 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=51735 /UG_GENE=RA-GEF-2 /UG=Hs.174795 /DEF=Homo sapiens rap guanine nucleotide exchange factor mRNA, complete cds. /PROD=rap guanine nucleotide exchange factor /FL=gb:AF394782.1	6,29	4,3	3,45	4,68	0,84	8,16	9,85	10,83	9,61	0,78	2,06	1,53	2,97	*
1555326_a_at	ADAM9: ADAM metallopeptidase domain 9 (meltrin gamma)	AF495383	8754	gb:AF495383.1 /DB_XREF=gi:21359695 /GEN=ADAM9 /TID=Hs2.2442.2 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=8754 /UG=Hs.2442 /DEF=Homo sapiens disintegrinmetalloproteinase domain 9 short protein precursor (ADAM9) mRNA, complete cds; alternatively spliced. /PROD=disintegrinmetalloproteinase domain 9 shortprotein precursor /FL=gb:AF495383.1	32,33	19,67	16,03	22,68	4,94	59,71	48,18	45,1	51	4,45	2,25	1,59	3,57	*
1555334_s_at	SLC30A5: solute carrier family 30 (zinc transporter), member 5	AF439324	64924	gb:AF439324.1 /DB_XREF=gi:19071290 /GEN=ZTL1 /TID=Hs2Affx.1.207 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /NOTE=sequence(s) not in UniGene /DEF=Homo sapiens zinc transporter ZTL1 (ZTL1) mRNA, complete cds. /PROD=zinc transporter ZTL1 /FL=gb:AF439324.1	39,97	19,87	8,13	22,66	9,3	72	81,97	63,69	72,55	5,28	3,2	1,88	9,88	*
1555388_s_at	SNX25: sorting nexin 25	BC029868	83891	gb:BC029868.1 /DB_XREF=gi:20987397 /TID=Hs2.306881.2 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=83891 /UG_GENE=MSTP043 /UG=Hs.306881 /DEF=Homo sapiens, Similar to MSTP043 protein, clone MGC:34107 IMAGE:5171892, mRNA, complete cds. /PROD=Similar to MSTP043 protein /FL=gb:BC029868.1	31,92	27,27	12,66	23,95	5,8	74,78	76,09	48,86	66,58	8,87	2,78	1,83	4,78	*
1555411_a_at	CCNL1: cyclin L1	AF367476	57018	gb:AF367476.1 /DB_XREF=gi:20385176 /TID=Hs2.4859.3 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=57018 /UG_GENE=LOC57018 /UG=Hs.4859 /DEF=Homo sapiens cyclin L beta mRNA, complete cds; alternatively spliced. /PROD=cyclin L beta /FL=gb:AF367476.1	28,85	15,44	7,56	17,29	6,22	49,26	42,08	48,57	46,64	2,29	2,7	1,68	6,62	*
1555460_a_at	SLC39A6: solute carrier family 39 (zinc transporter), member 6	BC039498	25800	gb:BC039498.1 /DB_XREF=gi:24659963 /TID=Hs2.79136.2 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=25800 /UG_GENE=LIV-1 /UG=Hs.79136 /DEF=Homo sapiens, Similar to LIV-1 protein, estrogen regulated, clone MGC:50406 IMAGE:5552785, mRNA, complete cds. /PROD=Similar to LIV-1 protein, estrogen regulated /FL=gb:BC039498.1	20,4	14,71	8,17	14,42	3,53	40,64	38,67	28,28	35,87	3,83	2,49	1,68	4,26	*
1555561_a_at	UGCGL2: UDP-glucose ceramide glucosyltransferase-like 2	BC032302	55757	gb:BC032302.1 /DB_XREF=gi:21619565 /TID=Hs2.22983.2 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=55757 /UG_GENE=UGCGL2 /UG=Hs.22983 /DEF=Homo sapiens, similar to UDP-glucose ceramide glucosyltransferase-like 2, clone MGC:40268 IMAGE:5169731, mRNA, complete cds. /PROD=similar to UDP-glucose ceramideglucosyltransferase-like 2 /FL=gb:BC032302.1	10,68	7,9	3,84	7,47	1,98	20,67	16,6	18,24	18,5	1,18	2,48	1,69	4,43	*
1555609_a_at	ZMAT3: zinc finger, matrin type 3	AF355465	64393	gb:AF355465.1 /DB_XREF=gi:15077640 /TID=Hs2.252406.3 /CNT=1 /FEA=FLmRNA /TIER=FL /STK=1 /LL=64393 /UG_GENE=WIG1 /UG=Hs.252406 /DEF=Homo sapiens WIG-1PAG608 protein mRNA, complete cds. /PROD=WIG-1PAG608 protein /FL=gb:AF355465.1	10,16	10,52	7,06	9,25	1,1	26,72	29,34	13,01	23,03	5,06	2,49	1,54	3,64	*
1555830_s_at	FAM62B: family with sequence similarity 62 (C2 domain containing) member B	BC001224	57488	gb:BC001224.1 /DB_XREF=gi:12654762 /TID=Hs2Affx.1.469 /CNT=1 /FEA=FLmRNA /TIER=ConsEnd /STK=0 /NOTE=sequence(s) not in UniGene /DEF=Homo sapiens, clone MGC:982 IMAGE:3354306, mRNA, complete cds. /PROD=Unknown (protein for MGC:982) /FL=gb:BC001224.1	17,28	10,35	4,54	10,72	3,68	35,61	38,35	22,72	32,23	4,82	3,01	1,76	7,07	*
1557181_s_at	LOC399947: similar to expressed sequence AI593442	AA633992	399947	gb:AA633992 /DB_XREF=gi:2557206 /DB_XREF=ac33g02.s1 /CLONE=IMAGE:858290 /TID=Hs2.172982.1 /CNT=12 /FEA=mRNA /TIER=ConsEnd /STK=1 /UG=Hs.172982 /UG_TITLE=Homo sapiens cDNA FLJ33767 fis, clone BRHIP1000108.	7,93	10,24	4,04	7,4	1,81	13,67	18,04	24,28	18,66	3,08	2,52	1,59	4,43	*
1558636_s_at	ADAMTS5: ADAM metallopeptidase with thrombospondin type 1 motif, 5 (aggrecanase-2)	BI254089	11096	gb:BI254089 /DB_XREF=gi:14806159 /DB_XREF=602978195F1 /CLONE=IMAGE:5123159 /TID=Hs2.407354.1 /CNT=8 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.407354 /UG_TITLE=Homo sapiens full length insert cDNA clone ZD50E03	2,8	3,86	2,73	3,13	0,36	13,52	7,08	8,14	9,58	1,99	3,06	1,95	4,41	*
1558882_at	LOC401233: similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription	BI868572	401233	gb:BI868572 /DB_XREF=gi:16042245 /DB_XREF=603392679F1 /CLONE=IMAGE:5402706 /TID=Hs2.435991.1 /CNT=6 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.435991 /UG_TITLE=Homo sapiens, clone IMAGE:5289038, mRNA	2,43	2,92	2,21	2,52	0,21	20,99	9,13	9,36	13,16	3,92	5,22	2,64	8	*
1559249_at	ATXN1: Ataxin 1	BC010948	6310	gb:BC010948.1 /DB_XREF=gi:15301440 /TID=Hs2.396468.1 /CNT=6 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.396468 /UG_TITLE=Homo sapiens, clone IMAGE:4282854, mRNA /DEF=Homo sapiens, clone IMAGE:4282854, mRNA.	9,16	8,04	4,03	7,08	1,56	20,17	11,64	23,11	18,31	3,44	2,59	1,6	4,35	*
1559952_x_at	FAM66C /// FAM66E /// LOC647351: family with sequence similarity 66, member C /// family with sequence similarity 66, member E /// hypothetical protein LOC647351	AI140607	440078 /// 441342 /// 647351	gb:AI140607 /DB_XREF=gi:3648064 /DB_XREF=qe05f05.x1 /CLONE=IMAGE:1738113 /TID=Hs2.429718.1 /CNT=4 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.429718 /UG_TITLE=Homo sapiens beta-defensin 109 (DEFB109) pseudogene mRNA, partial sequence	18,36	19,21	19,58	19,05	0,36	11,58	10,98	7,87	10,14	1,15	-1,88	-1,58	-2,31	*
1559965_at	LOC646345: hypothetical protein LOC646345	BC037827	646345	gb:BC037827.1 /DB_XREF=gi:23138647 /TID=Hs2.205434.1 /CNT=7 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.205434 /UG_TITLE=Homo sapiens, clone IMAGE:4811567, mRNA /DEF=Homo sapiens, clone IMAGE:4811567, mRNA.	8,28	9,09	3,72	7,03	1,67	28,62	21,63	24,89	25,05	2,02	3,56	2,48	5,93	*

1562062_at	NBPF1 /// NBPF3 /// NBPF11 /// NBPF20 /// NBPF9 /// NBPF10 /// NBPF8: neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 9 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 8	BM041211	200030 /// 400818 /// 440670 /// 440673 /// 55672 /// 641559 /// 84224	gb:BM041211 /DB_XREF=gi:16770478 /DB_XREF=603614396F1 /CLONE=IMAGE:5420423 /TID=Hs2.351620.1 /CNT=3 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.351620 /UG_TITLE=Homo sapiens cDNA FLJ40685 fis, clone THYMU2023943.	58,6	63,21	90,7	70,84	10,02	33,15	38,47	35,52	35,71	1,54	-1,98	-1,51	-2,48	*
1564053_a_at	YTHDF3: YTH domain family, member 3	AK093081	253943	gb:AK093081.1 /DB_XREF=gi:21751833 /TID=Hs2.5518.4 /CNT=1 /FEA=mRNA /TIER=ConsEnd /STK=0 /LL=253943 /UG_GENE=FLJ31657 /UG=Hs.5518 /UG_TITLE=hypothetical protein FLJ31657 /DEF=Homo sapiens cDNA FLJ35762 fis, clone TESTI2004793, moderately similar to Homo sapiens NY-REN-2 antigen mRNA.	28,53	16,27	5,25	16,68	6,72	61,81	55,14	58,89	58,62	1,93	3,51	2,11	10,43	*
1566887_x_at	Multiple myeloma susceptibility mRNA sequence	AY094612		gb:AY094612.1 /DB_XREF=gi:21217409 /TID=Hs2.374678.1 /CNT=1 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.374678 /UG_TITLE=Homo sapiens multiple myeloma susceptibility mRNA sequence /DEF=Homo sapiens multiple myeloma susceptibility mRNA sequence.	129,16	225,03	262,85	205,68	39,79	78,28	90,05	103,55	90,63	7,3	-2,27	-1,52	-3,1	*
1569253_at	INTS4: integrator complex subunit 4	BC018672	92105	gb:BC018672.1 /DB_XREF=gi:17391479 /TID=Hs2.367149.1 /CNT=6 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.367149 /UG_TITLE=Homo sapiens, clone IMAGE:4280013, mRNA /DEF=Homo sapiens, clone IMAGE:4280013, mRNA.	6,22	3,79	2,52	4,17	1,09	9,04	13,35	9,77	10,72	1,33	2,57	1,68	4,61	*
200737_at	PGK1: phosphoglycerate kinase 1	NM_000291	5230	gb:NM_000291.1 /DB_XREF=gi:4505762 /GEN=PGK1 /FEA=FLmRNA /CNT=450 /TID=Hs.78771.0 /TIER=FL+Stack /STK=249 /UG=Hs.78771 /LL=5230 /DEF=Homo sapiens phosphoglycerate kinase 1 (PGK1), mRNA. /PROD=phosphoglycerate kinase 1 /FL=gb:NM_000291.1	685,27	636,3	298,96	540,18	121,44	1443,32	1254,24	1088,39	1261,98	102,53	2,34	1,65	3,76	*
200806_s_at	HSPD1: heat shock 60kDa protein 1 (chaperonin)	BE256479	3329	gb:BE256479 /DB_XREF=gi:9126938 /DB_XREF=601111293F1 /CLONE=IMAGE:3352031 /FEA=FLmRNA /CNT=475 /TID=Hs.79037.0 /TIER=Stack /STK=15 /UG=Hs.79037 /LL=3329 /UG_GENE=HSPD1 /UG_TITLE=heat shock 60kD protein 1 (chaperonin) /FL=gb:NM_002156.1 gb:M34664.1 gb:M22382.1 gb:BC002676.1 gb:BC003030.1	405,09	226,48	7,89	213,15	114,86	666,54	751,12	611,47	676,38	40,61	3,17	1,66	27,93	*
201041_s_at	DUSP1: dual specificity phosphatase 1	NM_004417	1843	gb:NM_004417.2 /DB_XREF=gi:7108342 /GEN=DUSP1 /FEA=FLmRNA /CNT=409 /TID=Hs.171695.0 /TIER=FL+Stack /STK=99 /UG=Hs.171695 /LL=1843 /DEF=Homo sapiens dual specificity phosphatase 1 (DUSP1), mRNA. /PROD=dual specificity phosphatase 1 /FL=gb:NM_004417.2	319,21	572,26	251,02	380,83	97,72	1233,59	1147,31	706	1028,96	163,39	2,7	1,7	4,88	*
201120_s_at	PGRMC1: progesterone receptor membrane component 1	AL547946	10857	gb:AL547946 /DB_XREF=gi:12882489 /DB_XREF=AL547946 /CLONE=CS0DI035YB22 (5 prime) /FEA=FLmRNA /CNT=357 /TID=Hs.90061.0 /TIER=Stack /STK=11 /UG=Hs.90061 /LL=10857 /UG_GENE=HPR6.6 /UG_TITLE=progesterone binding protein /FL=gb:NM_006667.2	160,52	103,9	68,28	110,9	26,86	290,46	248,29	225,71	254,82	18,97	2,3	1,6	3,86	*
201474_s_at	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	NM_002204	3675	gb:NM_002204.1 /DB_XREF=gi:4504746 /GEN=ITGA3 /FEA=FLmRNA /CNT=350 /TID=Hs.265829.1 /TIER=FL+Stack /STK=65 /UG=Hs.265829 /LL=3675 /DEF=Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant a, mRNA. /PROD=integrin alpha 3 isoform a precursor /FL=gb:NM_002204.1 gb:M59911.1	75,16	75,51	94,19	81,62	6,29	27,48	37,69	47,18	37,45	5,69	-2,18	-1,68	-2,97	*
201739_at	SGK: serum/glucocorticoid regulated kinase	NM_005627	6446	gb:NM_005627.1 /DB_XREF=gi:5032090 /GEN=SGK /FEA=FLmRNA /CNT=255 /TID=Hs.296323.0 /TIER=FL+Stack /STK=137 /UG=Hs.296323 /LL=6446 /DEF=Homo sapiens serumglucocorticoid regulated kinase (SGK), mRNA. /PROD=serumglucocorticoid regulated kinase /FL=gb:BC001263.1 gb:NM_005627.1 gb:AF153609.1	579,99	608,07	321,89	503,32	91,07	1076,37	1209,14	1135,44	1140,31	38,4	2,27	1,73	3,24	*
201792_at	AEBP1: AE binding protein 1	NM_001129	165	gb:NM_001129.2 /DB_XREF=gi:4755145 /GEN=AEBP1 /FEA=FLmRNA /CNT=208 /TID=Hs.118397.0 /TIER=FL+Stack /STK=78 /UG=Hs.118397 /LL=165 /DEF=Homo sapiens AE-binding protein 1 (AEBP1), mRNA. /PROD=adipocyte enhancer binding protein 1 precursor /FL=gb:AF053944.1 gb:NM_001129.2 gb:D86479.1	208,91	251,11	240	233,34	12,63	128,92	104,94	125,75	119,87	7,52	-1,95	-1,7	-2,24	*
201848_s_at	BNIP3: BCL2/adenovirus E1B 19kDa interacting protein 3	U15174	664	gb:U15174.1 /DB_XREF=gi:558845 /GEN=BNIP3 /FEA=FLmRNA /CNT=227 /TID=Hs.79428.0 /TIER=FL /STK=0 /UG=Hs.79428 /LL=664 /DEF=Homo sapiens BCL2adenovirus E1B 19kD-interacting protein 3 (BNIP3) mRNA, complete cds. /PROD=BCL2adenovirus E1B 19kD-interacting protein 3 /FL=gb:AF002697.1 gb:NM_004052.2 gb:U15174.1	219,71	224,11	174,1	205,97	15,99	751,77	689,34	508,18	649,76	73,05	3,15	2,49	3,92	*
201858_s_at	PRG1: proteoglycan 1, secretory granule	J03223	5552	gb:J03223.1 /DB_XREF=gi:190419 /GEN=PRG1 /FEA=FLmRNA /CNT=337 /TID=Hs.1908.0 /TIER=FL /STK=0 /UG=Hs.1908 /LL=5552 /UG_TITLE=proteoglycan 1, secretory granule /DEF=Human secretory granule proteoglycan peptide core mRNA, complete cds. /FL=gb:J03223.1 gb:NM_002727.1	816,32	963,04	12,66	597,34	295,39	1794,16	1851,52	1614,42	1753,37	71,42	2,94	1,61	15,74	*
201893_x_at	DCN: decorin	AF138300	1634	gb:AF138300.1 /DB_XREF=gi:5532410 /FEA=FLmRNA /CNT=238 /TID=Hs.76152.0 /TIER=FL+Stack /STK=11 /UG=Hs.76152 /LL=1634 /UG_GENE=DCN /DEF=Homo sapiens decorin variant A mRNA, complete cds. /PROD=decorin variant A /FL=gb:NM_001920.1 gb:AF138300.1 gb:AF138304.1 gb:M14219.1	167,16	606,3	285,7	353,05	131,17	2523,16	1002,88	954,55	1493,53	515,01	4,23	1,63	11,87	*
201896_s_at	PSRC1: proline/serine-rich coiled-coil 1	BC001425	84722	gb:BC001425.1 /DB_XREF=gi:12655140 /FEA=FLmRNA /CNT=233 /TID=Hs.77550.0 /TIER=FL /STK=1 /UG=Hs.77550 /LL=1163 /UG_GENE=CKS1 /DEF=Homo sapiens, Similar to differential display and activated by p53, clone MGC:1780, mRNA, complete cds. /PROD=Similar to differential display and activated byp53 /FL=gb:BC001425.1 gb:NM_001826.1 gb:AF274941.1 gb:AF279897.1	179,04	184,34	224,36	195,92	14,31	71,8	83,25	116,41	90,48	13,38	-2,17	-1,68	-2,92	*
202129_s_at	RIOK3: RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	AW006290	8780	gb:AW006290 /DB_XREF=gi:5855068 /DB_XREF=wq69f11.x1 /CLONE=IMAGE:2476557 /FEA=FLmRNA /CNT=160 /TID=Hs.209061.0 /TIER=Stack /STK=15 /UG=Hs.209061 /LL=8780 /UG_GENE=SUDD /UG_TITLE=sudD (suppressor of bimD6, Aspergillus nidulans) homolog /FL=gb:NM_003831.1 gb:AF013591.1	43,44	31,28	9,93	28,22	9,79	83,49	84,37	65,47	77,78	6,16	2,76	1,71	6,46	*
202202_s_at	LAMA4: laminin, alpha 4	NM_002290	3910	gb:NM_002290.2 /DB_XREF=gi:9845494 /GEN=LAMA4 /FEA=FLmRNA /CNT=195 /TID=Hs.78672.0 /TIER=FL /STK=3 /UG=Hs.78672 /LL=3910 /DEF=Homo sapiens laminin, alpha 4 (LAMA4), mRNA. /PROD=laminin, alpha 4 precursor /FL=gb:NM_002290.2	82,98	80,63	33,64	65,75	16,07	189,38	150,84	244,7	194,97	27,24	2,97	1,93	5,14	*
202213_s_at	CUL4B: cullin 4B	AI650819	8450	gb:AI650819 /DB_XREF=gi:4734798 /DB_XREF=wa95a10.x1 /CLONE=IMAGE:2303898 /FEA=FLmRNA /CNT=168 /TID=Hs.155976.0 /TIER=Stack /STK=10 /UG=Hs.155976 /LL=8450 /UG_GENE=CUL4B /UG_TITLE=cullin 4B /FL=gb:AB014595.1 gb:NM_003588.1	86,8	73,85	8,03	56,23	24,39	180,01	153,01	152,35	161,79	9,11	2,88	1,66	10,06	*
202241_at	TRIB1: tribbles homolog 1 (Drosophila)	NM_025195	10221	gb:NM_025195.1 /DB_XREF=gi:13399327 /GEN=C8FW /FEA=FLmRNA /CNT=184 /TID=Hs.7837.0 /TIER=FL+Stack /STK=96 /UG=Hs.7837 /LL=10221 /DEF=Homo sapiens phosphoprotein regulated by mitogenic pathways (C8FW), mRNA. /PROD=G-protein-coupled receptor induced protein /FL=gb:AF205437.1 gb:NM_025195.1	140,83	91,33	236,32	156,16	42,55	366,6	435,65	574,3	458,85	61,07	2,94	1,88	5,48	*
202291_s_at	MGP: matrix Gla protein	NM_000900	4256	gb:NM_000900.1 /DB_XREF=gi:4505178 /GEN=MGP /FEA=FLmRNA /CNT=227 /TID=Hs.279009.0 /TIER=FL+Stack /STK=84 /UG=Hs.279009 /LL=4256 /DEF=Homo sapiens matrix Gla protein (MGP), mRNA. /PROD=matrix Gla protein /FL=gb:NM_000900.1 gb:M58549.1	5,53	52,28	10,24	22,68	14,86	177,24	112,99	50,14	113,46	36,69	5	1,74	100000000	*
202393_s_at	KLF10: Kruppel-like factor 10	NM_005655	7071	gb:NM_005655.1 /DB_XREF=gi:5032176 /GEN=TIEG /FEA=FLmRNA /CNT=128 /TID=Hs.82173.0 /TIER=FL+Stack /STK=35 /UG=Hs.82173 /LL=7071 /DEF=Homo sapiens TGFB inducible early growth response (TIEG), mRNA. /PROD=TGFB inducible early growth response /FL=gb:U21847.1 gb:NM_005655.1	549,43	651,34	613,34	604,7	29,73	2271,2	1905,78	2448,07	2208,35	159,67	3,65	3,15	4,2	*
202554_s_at	GSTM3: glutathione S-transferase M3 (brain)	AL527430	2947	gb:AL527430 /DB_XREF=gi:12790923 /DB_XREF=AL527430 /CLONE=CS0DC021YF13 (5 prime) /FEA=FLmRNA /CNT=157 /TID=Hs.2006.0 /TIER=Stack /STK=54 /UG=Hs.2006 /LL=2947 /UG_GENE=GSTM3 /UG_TITLE=glutathione S-transferase M3 (brain) /FL=gb:NM_000849.1 gb:BC000088.1 gb:J05459.1	895,02	905,05	663,9	821,32	78,76	523,5	190	313,63	342,38	97,34	-2,4	-1,57	-4,57	*
202619_s_at	PLOD2: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	AI754404	5352	gb:AI754404 /DB_XREF=gi:5132668 /DB_XREF=cr24g06.x1 /CLONE=HBMSC_cr24g06 /FEA=FLmRNA /CNT=167 /TID=Hs.41270.0 /TIER=Stack /STK=20 /UG=Hs.41270 /LL=5352 /UG_GENE=PLOD2 /UG_TITLE=procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 /FL=gb:NM_000935.1 gb:U84573.1	814,3	616,02	11,43	480,58	241,46	1410,07	1579,41	1299,99	1429,82	81,26	2,98	1,61	17,16	*
202730_s_at	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)	NM_014456	27250	gb:NM_014456.1 /DB_XREF=gi:7657448 /GEN=PDCD4 /FEA=FLmRNA /CNT=138 /TID=Hs.296251.0 /TIER=FL /STK=0 /UG=Hs.296251 /LL=27250 /DEF=Homo sapiens programmed cell death 4 (PDCD4), mRNA. /PROD=programmed cell death 4 /FL=gb:NM_014456.1 gb:U96628.1	47,58	34,09	15,06	32,24	9,43	93,12	87,93	57,63	79,56	11,07	2,47	1,54	4,89	*
202934_at	HK2: hexokinase 2	AI761561	3099	gb:AI761561 /DB_XREF=gi:5177228 /DB_XREF=wi61h11.x1 /CLONE=IMAGE:2394789 /FEA=FLmRNA /CNT=127 /TID=Hs.198427.0 /TIER=Stack /STK=53 /UG=Hs.198427 /LL=3099 /UG_GENE=HK2 /UG_TITLE=hexokinase 2 /FL=gb:NM_000189.1 gb:AF148513.1	139,39	160,98	90,6	130,32	20,82	247,53	302,51	279,83	276,62	15,95	2,12	1,65	2,91	*
202948_at	IL1R1: interleukin 1 receptor, type I	NM_000877	3554	gb:NM_000877.1 /DB_XREF=gi:4504658 /GEN=IL1R1 /FEA=FLmRNA /CNT=156 /TID=Hs.82112.0 /TIER=FL+Stack /STK=49 /UG=Hs.82112 /LL=3554 /DEF=Homo sapiens interleukin 1 receptor, type I (IL1R1), mRNA. /PROD=interleukin 1 receptor, type I /FL=gb:NM_000877.1 gb:M27492.1	136,73	138,32	35,68	103,58	33,95	326,27	174,21	325,99	275,49	50,64	2,66	1,51	5,99	*
203015_s_at	SSX2IP: synovial sarcoma, X breakpoint 2 interacting protein	AW136988	117178	gb:AW136988 /DB_XREF=gi:6141121 /DB_XREF=UI-H-BI1-acu-b-04-0-UI.s1 /CLONE=IMAGE:2715582 /FEA=FLmRNA /CNT=165 /TID=Hs.22587.0 /TIER=Stack /STK=10 /UG=Hs.22587 /LL=22892 /UG_GENE=KIAA0923 /UG_TITLE=KIAA0923 protein /FL=gb:AB023140.1 gb:NM_014021.1	8,55	6,77	5,69	7	0,84	11,52	13,77	16,67	13,99	1,49	2	1,54	2,62	*
203131_at	PDGFRA: platelet-derived growth factor receptor, alpha polypeptide	NM_006206	5156	gb:NM_006206.1 /DB_XREF=gi:5453869 /GEN=PDGFRA /FEA=FLmRNA /CNT=148 /TID=Hs.74615.0 /TIER=FL+Stack /STK=62 /UG=Hs.74615 /LL=5156 /DEF=Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /PROD=platelet-derived growth factor receptor, alphapolypeptide /FL=gb:NM_006206.1 gb:M21574.1	219,29	299,5	208,35	242,38	28,73	865,86	488,65	929,41	761,31	137,56	3,14	2,12	4,41	*
203147_s_at	TRIM14: tripartite motif-containing 14	BE962483	9830	gb:BE962483 /DB_XREF=gi:11765431 /DB_XREF=601655782R1 /CLONE=IMAGE:3846116 /FEA=FLmRNA /CNT=97 /TID=Hs.179703.0 /TIER=Stack /STK=12 /UG=Hs.179703 /LL=9830 /UG_GENE=KIAA0129 /UG_TITLE=KIAA0129 gene product /FL=gb:D50919.1 gb:NM_014788.1	28,53	28,01	34,42	30,32	2,06	16,65	13,3	13,33	14,43	1,11	-2,1	-1,78	-2,5	*
203293_s_at	LMAN1: lectin, mannose-binding, 1	NM_005570	3998	gb:NM_005570.2 /DB_XREF=gi:10862689 /GEN=LMAN1 /FEA=FLmRNA /CNT=89 /TID=Hs.287912.0 /TIER=FL /STK=0 /UG=Hs.287912 /LL=3998 /DEF=Homo sapiens lectin, mannose-binding, 1 (LMAN1), mRNA. /PROD=lectin, mannose-binding, 1 precursor /FL=gb:NM_005570.2 gb:U09716.1	10,37	9,71	7,98	9,36	0,71	20,18	21,39	15,43	19	1,82	2,03	1,65	2,48	*
203423_at	RBP1: retinol binding protein 1, cellular	NM_002899	5947	gb:NM_002899.2 /DB_XREF=gi:8400726 /GEN=RBP1 /FEA=FLmRNA /CNT=125 /TID=Hs.101850.0 /TIER=FL+Stack /STK=72 /UG=Hs.101850 /LL=5947 /DEF=Homo sapiens retinol-binding protein 1, cellular (RBP1), mRNA. /PROD=retinol-binding protein 1, cellular /FL=gb:NM_002899.2 gb:M11433.1	183,72	131,03	90,39	135,05	27,02	54,52	30,7	70,49	51,9	11,56	-2,6	-1,57	-4,44	*

203502_at	BPGM: 2,3-bisphosphoglycerate mutase /// 2,3-bisphosphoglycerate mutase	NM_001724	669	gb:NM_001724.1 /DB_XREF=gi:4502444 /GEN=BPGM /FEA=FLmRNA /CNT=150 /TID=Hs.198365.0 /TIER=FL+Stack /STK=67 /UG=Hs.198365 /LL=669 /DEF=Homo sapiens 2,3-bisphosphoglycerate mutase (BPGM), mRNA. /PROD=2,3-bisphosphoglycerate mutase /FL=gb:NM_001724.1	174,63	163,86	63,59	134,03	35,35	289,96	376,8	312,71	326,49	26	2,44	1,65	4,35	*
203821_at	HBEGF: heparin-binding EGF-like growth factor	NM_001945	1839	gb:NM_001945.1 /DB_XREF=gi:4503412 /GEN=DTR /FEA=FLmRNA /CNT=86 /TID=Hs.799.0 /TIER=FL+Stack /STK=34 /UG=Hs.799 /LL=1839 /DEF=Homo sapiens diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor) (DTR), mRNA. /PROD=diphtheria toxin receptor (heparin-bindingepidermal growth factor-like growth factor) /FL=gb:NM_001945.1 gb:M60278.1	137,76	136,76	121,61	132,04	5,22	287,66	267,17	360,13	304,98	28,2	2,31	1,94	2,7	*
203852_s_at	SMN1 /// SMN2: survival of motor neuron 1, telomeric /// survival of motor neuron 2, centromeric	NM_000344	6606 /// 6607	gb:NM_000344.2 /DB_XREF=gi:13259515 /GEN=SMN1 /FEA=FLmRNA /CNT=85 /TID=Hs.288986.0 /TIER=FL /STK=6 /UG=Hs.288986 /LL=6606 /DEF=Homo sapiens survival of motor neuron 1, telomeric (SMN1), transcript variant d, mRNA. /PROD=survival of motor neuron 1, telomeric isoform d /FL=gb:U18423.1 gb:NM_000344.2	87,3	82,15	10,34	59,93	24,84	143,51	181,68	149,42	158,2	11,86	2,64	1,54	8,32	*
204011_at	SPRY2: sprouty homolog 2 (Drosophila)	NM_005842	10253	gb:NM_005842.1 /DB_XREF=gi:5032114 /GEN=SPRY2 /FEA=FLmRNA /CNT=79 /TID=Hs.18676.0 /TIER=FL+Stack /STK=31 /UG=Hs.18676 /LL=10253 /DEF=Homo sapiens sprouty (Drosophila) homolog 2 (SPRY2), mRNA. /PROD=sprouty (Drosophila) homolog 2 /FL=gb:AF039843.1 gb:NM_005842.1	140,62	149,88	98,1	129,53	15,94	315,72	278,93	248,43	281,03	19,45	2,17	1,74	2,79	*
204014_at	DUSP4: dual specificity phosphatase 4	NM_001394	1846	gb:NM_001394.2 /DB_XREF=gi:12707552 /GEN=DUSP4 /FEA=FLmRNA /CNT=105 /TID=Hs.2359.0 /TIER=FL /STK=4 /UG=Hs.2359 /LL=1846 /DEF=Homo sapiens dual specificity phosphatase 4 (DUSP4), mRNA. /PROD=dual specificity phosphatase 4 /FL=gb:NM_001394.2 gb:BC002671.1 gb:U48807.1 gb:U21108.1	21,41	30,87	13,55	21,95	5,01	96,21	56,58	70,02	74,27	11,64	3,38	2,19	5,69	*
204036_at	EDG2: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	AW269335	1902	gb:AW269335 /DB_XREF=gi:6656365 /DB_XREF=xs47d05.x1 /CLONE=IMAGE:2772777 /FEA=FLmRNA /CNT=88 /TID=Hs.75794.0 /TIER=Stack /STK=11 /UG=Hs.75794 /LL=1902 /UG_GENE=EDG2 /UG_TITLE=endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 /FL=gb:U78192.1 gb:U80811.1 gb:NM_001401.1	154,01	164,99	34,63	117,88	41,74	392,03	271,32	321,36	328,24	35,01	2,78	1,69	6,74	*
204154_at	CDO1: cysteine dioxygenase, type I	NM_001801	1036	gb:NM_001801.1 /DB_XREF=gi:4502754 /GEN=CDO1 /FEA=FLmRNA /CNT=84 /TID=Hs.3229.0 /TIER=FL+Stack /STK=46 /UG=Hs.3229 /LL=1036 /DEF=Homo sapiens cysteine dioxygenase, type I (CDO1), mRNA. /PROD=cysteine dioxygenase, type I /FL=gb:NM_001801.1 gb:D85777.1	47,77	53,9	16	39,22	11,75	125,95	75,29	114,65	105,29	15,35	2,68	1,65	5,44	*
204347_at	LOC645619: similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase)	AI653169	645619	gb:AI653169 /DB_XREF=gi:4737148 /DB_XREF=wb43g08.x1 /CLONE=IMAGE:2308478 /FEA=FLmRNA /CNT=133 /TID=Hs.274691.0 /TIER=Stack /STK=27 /UG=Hs.274691 /LL=205 /UG_GENE=AK3 /UG_TITLE=adenylate kinase 3 /FL=gb:NM_013410.1	19,03	29,37	10,87	19,76	5,35	70,69	88,61	64,76	74,69	7,17	3,78	2,51	6,92	*
204348_s_at	AK3L1: adenylate kinase 3-like 1	NM_013410	205	gb:NM_013410.1 /DB_XREF=gi:8051578 /GEN=AK3 /FEA=FLmRNA /CNT=133 /TID=Hs.274691.0 /TIER=FL+Stack /STK=17 /UG=Hs.274691 /LL=205 /DEF=Homo sapiens adenylate kinase 3 (AK3), nuclear gene encoding mitochondrial protein, mRNA. /PROD=adenylate kinase 3 /FL=gb:NM_013410.1	86,99	184,34	39,42	103,58	42,65	337,29	387,24	280,28	334,94	30,9	3,23	1,87	10,07	*
204439_at	IFI44L: interferon-induced protein 44-like	NM_006820	10964	gb:NM_006820.1 /DB_XREF=gi:5803026 /GEN=GS3686 /FEA=FLmRNA /CNT=58 /TID=Hs.75470.0 /TIER=FL+Stack /STK=19 /UG=Hs.75470 /LL=10964 /DEF=Homo sapiens hypothetical protein, expressed in osteoblast (GS3686), mRNA. /PROD=hypothetical protein, expressed in osteoblast /FL=gb:NM_006820.1 gb:AB000115.1	31,62	10,52	4,24	15,46	8,28	85,51	29,36	60,93	58,6	16,25	3,79	1,57	32,23	*
204470_at	CXCL1: chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511	2919	gb:NM_001511.1 /DB_XREF=gi:4504152 /GEN=GRO1 /FEA=FLmRNA /CNT=58 /TID=Hs.789.0 /TIER=FL+Stack /STK=30 /UG=Hs.789 /LL=2919 /DEF=Homo sapiens GRO1 oncogene (melanoma growth stimulating activity, alpha) (GRO1), mRNA. /PROD=GRO1 oncogene (melanoma growth stimulatingactivity, alpha) /FL=gb:NM_001511.1	23,86	22,23	20,85	22,31	0,87	89,18	37,33	149,5	92	32,41	4,12	1,73	6,55	*
204720_s_at	DNAJC6: DnaJ (Hsp40) homolog, subfamily C, member 6	AV729634	9829	gb:AV729634 /DB_XREF=gi:10839055 /DB_XREF=AV729634 /CLONE=HTEAFB10 /FEA=FLmRNA /CNT=79 /TID=Hs.44896.0 /TIER=Stack /STK=21 /UG=Hs.44896 /LL=9829 /UG_GENE=DNAJC6 /UG_TITLE=DnaJ (Hsp40) homolog, subfamily B, member 6 /FL=gb:AB007942.1 gb:NM_014787.1	35,24	24,45	5,18	21,62	8,79	120,56	76,02	69,1	88,56	16,13	4,1	2,19	12,63	*
204790_at	SMAD7: SMAD, mothers against DPP homolog 7 (Drosophila)	NM_005904	4092	gb:NM_005904.1 /DB_XREF=gi:5174516 /GEN=MADH7 /FEA=FLmRNA /CNT=47 /TID=Hs.100602.0 /TIER=FL+Stack /STK=12 /UG=Hs.100602 /LL=4092 /DEF=Homo sapiens MAD (mothers against decapentaplegic, Drosophila) homolog 7 (MADH7), mRNA. /PROD=MAD (mothers against decapentaplegic,Drosophila) homolog 7 /FL=gb:AF015261.1 gb:AF010193.1 gb:NM_005904.1	203,96	260,27	94,21	186,15	48,76	685,41	461,86	660,81	602,69	70,77	3,24	2,13	5,82	*
204826_at	CCNF: cyclin F	NM_001761	899	gb:NM_001761.1 /DB_XREF=gi:4502620 /GEN=CCNF /FEA=FLmRNA /CNT=44 /TID=Hs.1973.0 /TIER=FL+Stack /STK=8 /UG=Hs.1973 /LL=899 /DEF=Homo sapiens cyclin F (CCNF), mRNA. /PROD=cyclin F /FL=gb:NM_001761.1 gb:U17105.1	145,75	150,75	209,86	168,79	20,59	67,05	74,71	100,03	80,6	9,96	-2,09	-1,57	-2,8	*
204948_s_at	FST: follistatin	NM_013409	10468	gb:NM_013409.1 /DB_XREF=gi:7242221 /GEN=FST /FEA=FLmRNA /CNT=60 /TID=Hs.9914.1 /TIER=FL+Stack /STK=21 /UG=Hs.9914 /LL=10468 /DEF=Homo sapiens follistatin (FST), transcript variant FST344, mRNA. /PROD=follistatin isoform FST344 precursor /FL=gb:NM_013409.1 gb:BC004107.1	155,29	391,33	208,83	251,82	71,45	910,14	807,39	530,24	749,26	113,45	2,98	1,84	5,77	*
204969_s_at	RDX: radixin	NM_002906	5962	gb:NM_002906.1 /DB_XREF=gi:4506466 /GEN=RDX /FEA=FLmRNA /CNT=46 /TID=Hs.250613.0 /TIER=FL /STK=0 /UG=Hs.250613 /LL=5962 /DEF=Homo sapiens radixin (RDX), mRNA. /PROD=radixin /FL=gb:L02320.1 gb:NM_002906.1	17,12	10,98	4,71	10,94	3,58	24,54	38,38	22,7	28,54	4,95	2,61	1,51	5,84	*
205207_at	IL6: interleukin 6 (interferon, beta 2)	NM_000600	3569	gb:NM_000600.1 /DB_XREF=gi:10834983 /GEN=IL6 /FEA=FLmRNA /CNT=56 /TID=Hs.93913.0 /TIER=FL+Stack /STK=16 /UG=Hs.93913 /LL=3569 /DEF=Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA. /PROD=interleukin 6 (interferon, beta 2) /FL=gb:M29150.1 gb:M54894.1 gb:M18403.1 gb:M14584.1 gb:NM_000600.1	101,33	275,2	28,44	134,99	73,19	788,51	459,54	402,1	550,05	120,38	4,07	1,86	37,97	*
205219_s_at	GALK2 /// RBBP8: galactokinase 2 /// retinoblastoma binding protein 8	NM_002044	2585 /// 5932	gb:NM_002044.1 /DB_XREF=gi:4503896 /GEN=GALK2 /FEA=FLmRNA /CNT=33 /TID=Hs.129228.0 /TIER=FL /STK=0 /UG=Hs.129228 /LL=2585 /DEF=Homo sapiens galactokinase 2 (GALK2), mRNA. /PROD=galactokinase 2 /FL=gb:BC005141.1 gb:NM_002044.1 gb:M84443.1	33,91	23,51	20,59	26,01	4,04	62,94	47,73	47,28	52,65	5,15	2,02	1,52	2,81	*
205249_at	EGR2: early growth response 2 (Krox-20 homolog, Drosophila)	NM_000399	1959	gb:NM_000399.2 /DB_XREF=gi:9845523 /GEN=EGR2 /FEA=FLmRNA /CNT=44 /TID=Hs.1395.0 /TIER=FL+Stack /STK=21 /UG=Hs.1395 /LL=1959 /DEF=Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA. /PROD=early growth response 2 protein /FL=gb:NM_000399.2 gb:AF139463.1 gb:J04076.1	77,4	88,39	178,56	114,78	32,05	237,55	287,23	366,58	297,12	37,57	2,59	1,66	4,9	*
205266_at	LIF: leukemia inhibitory factor (cholinergic differentiation factor)	NM_002309	3976	gb:NM_002309.2 /DB_XREF=gi:6006018 /GEN=LIF /FEA=FLmRNA /CNT=44 /TID=Hs.2250.0 /TIER=FL+Stack /STK=14 /UG=Hs.2250 /LL=3976 /DEF=Homo sapiens leukemia inhibitory factor (cholinergic differentiation factor) (LIF), mRNA. /PROD=leukemia inhibitory factor (cholinergicdifferentiation factor) /FL=gb:NM_002309.2	60,61	97,05	130,86	96,17	20,29	614,76	256,24	401,09	424,03	104,13	4,41	2,44	7,59	*
205289_at	BMP2: bone morphogenetic protein 2	AA583044	650	gb:AA583044 /DB_XREF=gi:2360404 /DB_XREF=nn80f11.s1 /CLONE=IMAGE:1090221 /FEA=FLmRNA /CNT=59 /TID=Hs.73853.0 /TIER=Stack /STK=8 /UG=Hs.73853 /LL=650 /UG_GENE=BMP2 /UG_TITLE=bone morphogenetic protein 2 /FL=gb:NM_001200.1	12,11	17,39	5,43	11,65	3,46	105,44	46,17	45,67	65,76	19,84	5,65	2,57	12,26	*
205321_at	EIF2S3: eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	NM_001415	1968	gb:NM_001415.1 /DB_XREF=gi:4503506 /GEN=EIF2S3 /FEA=FLmRNA /CNT=39 /TID=Hs.211539.0 /TIER=FL /STK=0 /UG=Hs.211539 /LL=1968 /DEF=Homo sapiens eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD) (EIF2S3), mRNA. /PROD=eukaryotic translation initiation factor 2,subunit 3 (gamma, 52kD) /FL=gb:L19161.1 gb:NM_001415.1	136,97	90,88	9,24	79,03	37,34	284,2	235,03	167,69	228,97	33,77	2,9	1,52	13,12	*
205479_s_at	PLAU: plasminogen activator, urokinase	NM_002658	5328	gb:NM_002658.1 /DB_XREF=gi:4505862 /GEN=PLAU /FEA=FLmRNA /CNT=41 /TID=Hs.77274.0 /TIER=FL /STK=1 /UG=Hs.77274 /LL=5328 /DEF=Homo sapiens plasminogen activator, urokinase (PLAU), mRNA. /PROD=plasminogen activator, urokinase /FL=gb:NM_002658.1 gb:M15476.1	548,23	818,02	276,1	547,45	156,44	1376,66	1160,28	1147,72	1228,22	74,31	2,24	1,5	4,26	*
205514_at	ZNF415: zinc finger protein 415	NM_018355	55786	gb:NM_018355.1 /DB_XREF=gi:8922928 /GEN=FLJ11191 /FEA=FLmRNA /CNT=35 /TID=Hs.21838.0 /TIER=FL+Stack /STK=12 /UG=Hs.21838 /LL=55786 /DEF=Homo sapiens hypothetical protein FLJ11191 (FLJ11191), mRNA. /PROD=hypothetical protein FLJ11191 /FL=gb:NM_018355.1	7,35	7,24	4,14	6,24	1,05	14,74	16,65	10,91	14,1	1,69	2,26	1,63	3,27	*
205543_at	HSPA4L: heat shock 70kDa protein 4-like	NM_014278	22824	gb:NM_014278.1 /DB_XREF=gi:7656893 /GEN=APG-1 /FEA=FLmRNA /CNT=36 /TID=Hs.71992.0 /TIER=FL /STK=6 /UG=Hs.71992 /LL=22824 /DEF=Homo sapiens heat shock protein (hsp110 family) (APG-1), mRNA. /PROD=heat shock protein (hsp110 family) /FL=gb:NM_014278.1 gb:AB023421.1	9,41	10,74	8,15	9,43	0,75	20,01	18,44	16,97	18,47	0,88	1,96	1,69	2,29	*
205891_at	ADORA2B: adenosine A2b receptor	NM_000676	136	gb:NM_000676.1 /DB_XREF=gi:4501950 /GEN=ADORA2B /FEA=FLmRNA /CNT=32 /TID=Hs.45743.0 /TIER=FL+Stack /STK=9 /UG=Hs.45743 /LL=136 /DEF=Homo sapiens adenosine A2b receptor (ADORA2B), mRNA. /PROD=adenosine A2b receptor /FL=gb:M97759.1 gb:NM_000676.1	37,6	39,58	27,62	34,93	3,7	68,1	59,61	87,78	71,83	8,34	2,06	1,58	2,66	*
205991_s_at	PRRX1: paired related homeobox 1	NM_006902	5396	gb:NM_006902.2 /DB_XREF=gi:12707578 /GEN=PMX1 /FEA=FLmRNA /CNT=27 /TID=Hs.155606.0 /TIER=FL /STK=0 /UG=Hs.155606 /LL=5396 /DEF=Homo sapiens paired mesoderm homeo box 1 (PMX1), transcript variant pmx-1a, mRNA. /PROD=paired mesoderm homeobox 1, isoform pmx-1a /FL=gb:NM_006902.2	87,95	63,81	7,33	53,03	23,89	188,72	155,98	162,72	169,14	9,98	3,19	1,81	12,33	*
205996_s_at	AK2: adenylate kinase 2	NM_013411	204	gb:NM_013411.1 /DB_XREF=gi:7524345 /GEN=AK2 /FEA=FLmRNA /CNT=25 /TID=Hs.171811.0 /TIER=FL /STK=0 /UG=Hs.171811 /LL=204 /DEF=Homo sapiens adenylate kinase 2 (AK2), nuclear gene encoding mitochondrial protein, transcript variant AK2B, mRNA. /PROD=adenylate kinase 2 isoform b /FL=gb:NM_013411.1 gb:U54645.1	41,94	35,5	35,22	37,55	2,19	66,92	72,86	63,34	67,71	2,78	1,8	1,61	2,03	*
206336_at	CXCL6: chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993	6372	gb:NM_002993.1 /DB_XREF=gi:4506850 /GEN=SCYB6 /FEA=FLmRNA /CNT=16 /TID=Hs.164021.0 /TIER=FL /STK=3 /UG=Hs.164021 /LL=6372 /DEF=Homo sapiens small inducible cytokine subfamily B (Cys-X-Cys), member 6 (granulocyte chemotactic protein 2) (SCYB6), mRNA. /PROD=small inducible cytokine subfamily B(Cys-X-Cys), member 6 (granulocyte chemotactic protein 2) /FL=gb:U81234.1 gb:NM_002993.1	22,15	15,7	2,66	13,5	5,73	193,64	26,82	91,25	103,9	48,57	7,69	1,66	28,37	*
206383_s_at	G3BP2: Ras-GTPase activating protein SH3 domain-binding protein 2	NM_012297	9908	gb:NM_012297.1 /DB_XREF=gi:7110662 /GEN=KIAA0660 /FEA=FLmRNA /CNT=20 /TID=Hs.6727.0 /TIER=FL /STK=0 /UG=Hs.6727 /LL=9908 /DEF=Homo sapiens Ras-GTPase activating protein SH3 domain-binding protein 2 (KIAA0660), mRNA. /PROD=Ras-GTPase activating protein SH3 domain-bindingprotein 2 /FL=gb:AF053535.1 gb:AF051311.1 gb:NM_012297.1	18,27	14,86	6,5	13,21	3,5	30,22	32,03	30,39	30,88	0,58	2,34	1,63	4,14	*
206631_at	PTGER2: prostaglandin E receptor 2 (subtype EP2), 53kDa	NM_000956	5732	gb:NM_000956.1 /DB_XREF=gi:4506254 /GEN=PTGER2 /FEA=FLmRNA /CNT=17 /TID=Hs.2090.0 /TIER=FL /STK=2 /UG=Hs.2090 /LL=5732 /DEF=Homo sapiens prostaglandin E receptor 2 (subtype EP2), 53kD (PTGER2), mRNA. /PROD=prostaglandin E receptor 2 (subtype EP2), 53kD /FL=gb:U19487.1 gb:NM_000956.1	8,68	21,75	24,8	18,41	4,94	47,53	79,51	88,01	71,68	12,32	3,89	2,37	7,3	*
206675_s_at	SKIL: SKI-like	NM_005414	6498	gb:NM_005414.1 /DB_XREF=gi:4885598 /GEN=SKIL /FEA=FLmRNA /CNT=11 /TID=Hs.38783.0 /TIER=FL /STK=0 /UG=Hs.38783 /LL=6498 /DEF=Homo sapiens SKI-like (SKIL), mRNA. /PROD=SKI-like /FL=gb:NM_005414.1	11,45	5,92	3,83	7,07	2,27	16,07	21,65	18,43	18,72	1,62	2,65	1,68	5,67	*

206765_at	KCNJ2: potassium inwardly-rectifying channel, subfamily J, member 2	AF153820	3759	gb:AF153820.1 /DB_XREF=gi:8132296 /GEN=KCNJ2 /FEA=FLmRNA /CNT=16 /TID=Hs.1547.0 /TIER=FL /STK=2 /UG=Hs.1547 /LL=3759 /DEF=Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) mRNA, complete cds. /PROD=inwardly-rectifying potassium channel Kir2.1 /FL=gb:U22413.1 gb:AF011904.1 gb:AF153820.1 gb:NM_000891.1 gb:U24055.1 gb:AF021139.1 gb:U16861.1 gb:U12507.1	6,31	12,3	7,31	8,64	1,85	29,35	18,1	19,81	22,42	3,5	2,6	1,7	4,23	*
206796_at	WISP1: WNT1 inducible signaling pathway protein 1	NM_003882	8840	gb:NM_003882.1 /DB_XREF=gi:4507920 /GEN=WISP1 /FEA=FLmRNA /CNT=8 /TID=Hs.194680.0 /TIER=FL /STK=0 /UG=Hs.194680 /LL=8840 /DEF=Homo sapiens WNT1 inducible signaling pathway protein 1 (WISP1), mRNA. /PROD=WNT1 inducible signaling pathway protein 1 /FL=gb:NM_003882.1 gb:AF100779.1	66,08	90,74	24,49	60,44	19,33	183,08	210,88	166,83	186,93	12,86	3,09	1,99	6,56	*
207147_at	DLX2: distal-less homeobox 2	NM_004405	1746	gb:NM_004405.2 /DB_XREF=gi:6996003 /GEN=DLX2 /FEA=FLmRNA /CNT=7 /TID=Hs.419.0 /TIER=FL /STK=1 /UG=Hs.419 /LL=1746 /DEF=Homo sapiens distal-less homeo box 2 (DLX2), mRNA. /PROD=distal-less homeo box 2 /FL=gb:NM_004405.2	17,98	11,01	14,55	14,52	2,01	218,48	87,66	152,98	153,04	37,76	10,54	6,05	16,19	*
207316_at	HAS1: hyaluronan synthase 1	NM_001523	3036	gb:NM_001523.1 /DB_XREF=gi:4504338 /GEN=HAS1 /FEA=FLmRNA /CNT=8 /TID=Hs.57697.0 /TIER=FL /STK=2 /UG=Hs.57697 /LL=3036 /DEF=Homo sapiens hyaluronan synthase 1 (HAS1), mRNA. /PROD=hyaluronan synthase 1 /FL=gb:U59269.1 gb:NM_001523.1 gb:D84424.1	159,01	504,79	164,5	276,1	114,36	1058,6	578,25	909,34	848,73	141,94	3,07	1,66	9,81	*
207495_at	RAB28: RAB28, member RAS oncogene family	NM_004249	9364	gb:NM_004249.1 /DB_XREF=gi:4758993 /GEN=RAB28 /FEA=FLmRNA /CNT=5 /TID=Hs.296371.0 /TIER=FL /STK=0 /UG=Hs.296371 /LL=9364 /DEF=Homo sapiens RAB28, member RAS oncogene family (RAB28), mRNA. /PROD=RAB28, member RAS oncogene family /FL=gb:NM_004249.1	7,98	9,61	4,73	7,44	1,43	14,51	15,96	14,43	14,97	0,5	2,01	1,52	2,95	*
207574_s_at	GADD45B: growth arrest and DNA-damage-inducible, beta	NM_015675	4616	gb:NM_015675.1 /DB_XREF=gi:9945331 /GEN=GADD45B /FEA=FLmRNA /CNT=3 /TID=Hs.110571.0 /TIER=FL /STK=0 /UG=Hs.110571 /LL=4616 /DEF=Homo sapiens growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA. /PROD=DKFZP566B133 protein /FL=gb:NM_015675.1 gb:AF090950.1	318,6	436,47	775,31	510,13	136,89	1841,11	1475,01	2003,54	1773,22	156,3	3,48	2,33	6,3	*
207686_s_at	CASP8: caspase 8, apoptosis-related cysteine peptidase	NM_001228	841	gb:NM_001228.1 /DB_XREF=gi:4502582 /GEN=CASP8 /FEA=FLmRNA /CNT=3 /TID=Hs.19949.0 /TIER=FL /STK=0 /UG=Hs.19949 /LL=841 /DEF=Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA. /PROD=caspase 8, apoptosis-related cysteine protease /FL=gb:U60520.1 gb:NM_001228.1	18,13	10,52	9,83	12,83	2,66	27,27	33,44	22,9	27,87	3,06	2,17	1,52	3,39	*
207821_s_at	PTK2: PTK2 protein tyrosine kinase 2	NM_005607	5747	gb:NM_005607.1 /DB_XREF=gi:5032000 /GEN=PTK2 /FEA=FLmRNA /CNT=3 /TID=Hs.740.0 /TIER=FL /STK=0 /UG=Hs.740 /LL=5747 /DEF=Homo sapiens PTK2 protein tyrosine kinase 2 (PTK2), mRNA. /PROD=PTK2 protein tyrosine kinase 2 /FL=gb:NM_005607.1 gb:L05186.1	18,1	19,74	15,41	17,75	1,26	31,85	43,49	30,28	35,21	4,17	1,98	1,56	2,47	*
208047_s_at	NAB1: NGFI-A binding protein 1 (EGR1 binding protein 1)	NM_005966	4664	gb:NM_005966.1 /DB_XREF=gi:5174604 /GEN=NAB1 /FEA=FLmRNA /CNT=2 /TID=Hs.107474.0 /TIER=FL /STK=0 /UG=Hs.107474 /LL=4664 /DEF=Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA. /PROD=NGFI-A binding protein 1 (ERG1 binding protein1) /FL=gb:U47007.1 gb:NM_005966.1	9,41	5,99	3,59	6,33	1,69	14,49	15,93	13,13	14,51	0,81	2,29	1,57	4,11	*
208394_x_at	ESM1: endothelial cell-specific molecule 1	NM_007036	11082	gb:NM_007036.2 /DB_XREF=gi:13259505 /GEN=ESM1 /FEA=FLmRNA /CNT=2 /TID=Hs.41716.0 /TIER=FL /STK=0 /UG=Hs.41716 /LL=11082 /DEF=Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA. /PROD=endothelial cell-specific molecule 1 precursor /FL=gb:NM_007036.2	17,14	19,84	5,95	14,31	4,25	24,53	77,75	90,18	64,15	20,13	4,48	1,98	9,8	*
208510_s_at	PPARG: peroxisome proliferative activated receptor, gamma	NM_015869	5468	gb:NM_015869.1 /DB_XREF=gi:7705548 /GEN=PPARG /FEA=FLmRNA /CNT=4 /TID=Hs.100724.1 /TIER=FL /STK=0 /UG=Hs.100724 /LL=5468 /DEF=Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), mRNA. /PROD=peroxisome proliferative activated receptorgamma, isoform 2 /FL=gb:NM_015869.1 gb:U63415.1 gb:D83233.1 gb:U79012.1	16,83	19,86	22,38	19,69	1,6	47,97	31,74	47,01	42,24	5,26	2,15	1,65	2,72	*
208894_at	HLA-DRA: major histocompatibility complex, class II, DR alpha /// major histocompatibility complex, class II, DR alpha	M60334	3122	gb:M60334.1 /DB_XREF=gi:188255 /GEN=HLA-DRA /FEA=FLmRNA /CNT=470 /TID=Hs.76807.0 /TIER=FL /STK=0 /UG=Hs.76807 /LL=3122 /DEF=Human MHC class II HLA-DR-alpha mRNA, complete cds. /PROD=cell surface glycoprotein /FL=gb:M60334.1 gb:NM_019111.1	9,25	12,08	25,55	15,62	5,03	35,77	47,79	41,27	41,61	3,47	2,66	1,69	5,71	*
208937_s_at	ID1: inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	D13889	3397	gb:D13889.1 /DB_XREF=gi:464181 /GEN=Id-1H /FEA=FLmRNA /CNT=355 /TID=Hs.75424.1 /TIER=FL /STK=0 /UG=Hs.75424 /LL=3397 /DEF=Human mRNA for Id-1H, complete cds. /PROD=Id-1H /FL=gb:NM_002165.1 gb:BC000613.1 gb:D13889.1	227	250,32	515,28	330,87	92,45	1213,21	849,11	898,37	986,9	114,05	2,98	1,93	5,63	*
209086_x_at	MCAM: melanoma cell adhesion molecule	BE964361	4162	gb:BE964361 /DB_XREF=gi:11767830 /DB_XREF=601658062R1 /CLONE=IMAGE:3876255 /FEA=FLmRNA /CNT=242 /TID=Hs.211579.2 /TIER=Stack /STK=14 /UG=Hs.211579 /LL=4162 /UG_GENE=MCAM /UG_TITLE=melanoma adhesion molecule /FL=gb:AF089868.1 gb:NM_006500.1	230,58	160,89	153,05	181,51	24,64	86,98	93,36	70,01	83,45	6,97	-2,18	-1,64	-2,79	*
209098_s_at	JAG1: jagged 1 (Alagille syndrome)	U61276	182	gb:U61276.1 /DB_XREF=gi:1438936 /GEN=HJ1 /FEA=FLmRNA /CNT=199 /TID=Hs.91143.0 /TIER=FL /STK=0 /UG=Hs.91143 /LL=182 /DEF=Human transmembrane protein Jagged 1 (HJ1) mRNA, complete cds. /PROD=transmembrane protein Jagged 1 /FL=gb:AF003837.1 gb:U61276.1 gb:NM_000214.1 gb:U73936.1 gb:AF028593.1	6,92	7,75	7,23	7,3	0,24	12,21	22,35	15,21	16,59	3,01	2,27	1,59	2,97	*
209189_at	FOS: v-fos FBJ murine osteosarcoma viral oncogene homolog	BC004490	2353	gb:BC004490.1 /DB_XREF=gi:13325363 /FEA=FLmRNA /CNT=139 /TID=Hs.25647.0 /TIER=FL /STK=0 /UG=Hs.25647 /LL=2353 /UG_GENE=FOS /DEF=Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074, mRNA, complete cds. /PROD=v-fos FBJ murine osteosarcoma viral oncogenehomolog /FL=gb:NM_005252.2 gb:BC004490.1	9,46	10,95	10,38	10,27	0,44	105,02	49,95	67,11	74,03	16,27	7,21	4,58	9,91	*
209204_at	LMO4: LIM domain only 4	AI824831	8543	gb:AI824831 /DB_XREF=gi:5445502 /DB_XREF=wb02d08.x1 /CLONE=IMAGE:2304495 /FEA=FLmRNA /CNT=175 /TID=Hs.3844.0 /TIER=Stack /STK=13 /UG=Hs.3844 /LL=8543 /UG_GENE=LMO4 /UG_TITLE=LIM domain only 4 /FL=gb:NM_006769.2 gb:U24576.1 gb:BC003600.1	194,17	190,76	210,13	198,35	5,97	90,93	99,64	107,87	99,48	4,89	-1,99	-1,82	-2,2	*
209355_s_at	PPAP2B: phosphatidic acid phosphatase type 2B	AB000889	8613	gb:AB000889.1 /DB_XREF=gi:2467299 /FEA=FLmRNA /CNT=126 /TID=Hs.331371.1 /TIER=FL+Stack /STK=8 /UG=Hs.331371 /LL=8613 /UG_GENE=PPAP2B /DEF=Homo sapiens mRNA for phosphatidic acid phosphatase 2b, complete cds. /PROD=phosphatidic acid phosphatase 2b /FL=gb:AF017786.1 gb:AB000889.1 gb:U79294.1	102,08	123,88	91,36	105,77	9,57	421,95	181,92	323,74	309,2	69,67	2,92	1,81	4,17	*
209424_s_at	AMACR: alpha-methylacyl-CoA racemase	AI796120	23600	gb:AI796120 /DB_XREF=gi:5361583 /DB_XREF=wh42f03.x1 /CLONE=IMAGE:2383421 /FEA=FLmRNA /CNT=163 /TID=Hs.128749.0 /TIER=Stack /STK=9 /UG=Hs.128749 /LL=23600 /UG_GENE=AMACR /UG_TITLE=alpha-methylacyl-CoA racemase /FL=gb:NM_014324.1 gb:AF047020.1 gb:AF158378.1	29,59	26,72	11,37	22,56	5,65	70,08	69,07	39,66	59,6	9,98	2,64	1,65	4,72	*
209676_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	J03225	7035	gb:J03225.1 /DB_XREF=gi:180545 /GEN=TFPI /FEA=FLmRNA /CNT=91 /TID=Hs.170279.0 /TIER=FL /STK=1 /UG=Hs.170279 /LL=7035 /UG_TITLE=tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) /DEF=Human lipoprotein-associated coagulation inhibitor mRNA, complete cds. /FL=gb:NM_006287.2 gb:J03225.1	5,99	6,46	4,76	5,74	0,51	24,57	27,91	13,84	22,11	4,24	3,85	2,58	5,29	*
209681_at	SLC19A2: solute carrier family 19 (thiamine transporter), member 2	AF153330	10560	gb:AF153330.1 /DB_XREF=gi:5453325 /GEN=TC1 /FEA=FLmRNA /CNT=77 /TID=Hs.30246.0 /TIER=FL+Stack /STK=26 /UG=Hs.30246 /LL=10560 /DEF=Homo sapiens thiamine carrier 1 (TC1) mRNA, complete cds. /PROD=thiamine carrier 1 /FL=gb:AF135488.1 gb:AF153330.1 gb:AF160812.1	65,04	46,49	2,87	38,13	18,43	103,52	117,12	99,48	106,71	5,33	2,8	1,55	13,64	*
209706_at	NKX3-1: NK3 transcription factor related, locus 1 (Drosophila)	AF247704	4824	gb:AF247704.1 /DB_XREF=gi:9963969 /FEA=FLmRNA /CNT=97 /TID=Hs.55999.0 /TIER=FL+Stack /STK=30 /UG=Hs.55999 /LL=4824 /UG_GENE=NKX3A /DEF=Homo sapiens homeobox protein NKX3.1 mRNA, complete cds. /PROD=homeobox protein NKX3.1 /FL=gb:AF249672.1 gb:AF249670.1 gb:NM_006167.1 gb:U91540.1 gb:AF247704.1 gb:U80669.1	35,17	46,48	19,17	33,61	7,92	75,16	118,03	100,19	97,79	12,43	2,91	1,94	4,91	*
209728_at	HLA-DRB4: major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 4	BC005312	3126	gb:BC005312.1 /DB_XREF=gi:13529055 /FEA=FLmRNA /CNT=84 /TID=Hs.318720.0 /TIER=FL+Stack /STK=31 /UG=Hs.318720 /DEF=Homo sapiens, clone MGC:12387, mRNA, complete cds. /PROD=Unknown (protein for MGC:12387) /FL=gb:M16942.1 gb:BC005312.1	16,66	17,67	23,67	19,34	2,19	60,69	94,67	59,17	71,51	11,59	3,7	2,6	5,06	*
209763_at	CHRDL1: chordin-like 1	AL049176	91851	gb:AL049176 /DB_XREF=gi:4808226 /FEA=FLmRNA /CNT=84 /TID=Hs.82223.0 /TIER=Stack /STK=46 /UG=Hs.82223 /LL=57803 /UG_GENE=LOC57803 /UG_TITLE=chordin-like /DEF=Human DNA sequence from clone 141H5 on chromosome Xq22.1-23. Contains parts of a novel Chordin LIKE protein with von Willebrand factor type C domains. Contains ESTs, STSs and GSSs /FL=gb:BC002909.1	18,34	33,07	22,14	24,52	4,42	75,75	43,21	102,69	73,89	17,19	3,01	1,75	4,86	*
209960_at	HGF: hepatocyte growth factor (hepapoietin A; scatter factor)	X16323	3082	gb:X16323.1 /DB_XREF=gi:32081 /FEA=FLmRNA /CNT=42 /TID=Hs.809.0 /TIER=Stack /STK=8 /UG=Hs.809 /LL=3082 /UG_GENE=HGF /UG_TITLE=hepatocyte growth factor (hepapoietin A; scatter factor) /DEF=Human mRNA for hepatocyte growth factor (HGF). /FL=gb:M73240.1 gb:M73239.1 gb:M60718.1 gb:M29145.1	4,2	9,86	3,83	5,96	1,95	25,53	21,94	41,33	29,6	5,96	4,96	2,75	11,22	*
209984_at	JMJD2C: jumonji domain containing 2C	AB037901	23081	gb:AB037901.1 /DB_XREF=gi:10567163 /GEN=GASC-1 /FEA=FLmRNA /CNT=24 /TID=Hs.149918.0 /TIER=FL+Stack /STK=10 /UG=Hs.149918 /LL=23081 /UG_TITLE=gene amplified in squamous cell carcinoma 1; KIAA0780 protein /DEF=Homo sapiens GASC-1 mRNA, complete cds. /FL=gb:AB037901.1	48,95	43,38	15,92	36,08	10,21	90,13	79,7	76,42	82,08	4,13	2,27	1,54	4,27	*
210148_at	gb:AF305239.1 /DB_XREF=gi:10998781 /GEN=FIST3 /FEA=FLmRNA /CNT=16 /TID=Hs.30148.1 /TIER=FL /STK=0 /UG=Hs.30148 /LL=10114 /DEF=Homo sapiens Fas-interacting serinethreonine kinase 3 (FIST3) mRNA, complete cds. /PROD=Fas-interacting serinethreonine kinase 3 /FL=gb:AF305239.1	AF305239		gb:AF305239.1 /DB_XREF=gi:10998781 /GEN=FIST3 /FEA=FLmRNA /CNT=16 /TID=Hs.30148.1 /TIER=FL /STK=0 /UG=Hs.30148 /LL=10114 /DEF=Homo sapiens Fas-interacting serinethreonine kinase 3 (FIST3) mRNA, complete cds. /PROD=Fas-interacting serinethreonine kinase 3 /FL=gb:AF305239.1	7,56	3,79	3,52	4,95	1,3	15,14	17,33	25,72	19,4	3,22	3,92	2,42	7,22	*
210284_s_at	MAP3K7IP2: mitogen-activated protein kinase kinase kinase 7 interacting protein 2	AF241230	23118	gb:AF241230.1 /DB_XREF=gi:7677465 /FEA=FLmRNA /CNT=12 /TID=Hs.109727.0 /TIER=FL /STK=0 /UG=Hs.109727 /LL=23118 /UG_GENE=KIAA0733 /DEF=Homo sapiens TAK1-binding protein 2 mRNA, complete cds. /PROD=TAK1-binding protein 2 /FL=gb:AF241230.1	62,73	34,38	21,68	39,6	12,13	107,59	116,53	86,83	103,65	8,8	2,62	1,69	5,33	*
212805_at	KIAA0367: KIAA0367	AB002365	23273	gb:AB002365.1 /DB_XREF=gi:2224674 /GEN=kIAA0367 /FEA=mRNA /CNT=114 /TID=Hs.23311.0 /TIER=Stack /STK=49 /UG=Hs.23311 /LL=23273 /UG_TITLE=KIAA0367 protein /DEF=Human mRNA for KIAA0367 gene, partial cds.	21,76	35,7	25,98	27,82	4,13	101,3	56,26	54,62	70,73	15,29	2,54	1,56	3,85	*
212865_s_at	COL14A1: collagen, type XIV, alpha 1 (undulin)	BF449063	7373	gb:BF449063 /DB_XREF=gi:11515232 /DB_XREF=7o64f12.x1 /CLONE=IMAGE:3579023 /FEA=mRNA /CNT=105 /TID=Hs.36131.0 /TIER=Stack /STK=40 /UG=Hs.36131 /LL=7373 /UG_GENE=COL14A1 /UG_TITLE=collagen, type XIV, alpha 1 (undulin)	8,3	21,74	4,69	11,58	5,19	32,1	31,72	30,27	31,36	0,56	2,71	1,56	10,31	*
213222_at	PLCB1: phospholipase C, beta 1 (phosphoinositide-specific)	AL049593	23236	gb:AL049593 /DB_XREF=gi:10443476 /FEA=FLmRNA /CNT=57 /TID=Hs.41143.0 /TIER=Stack /STK=14 /UG=Hs.41143 /LL=23236 /UG_GENE=KIAA0581 /UG_TITLE=phosphoinositide-specific phospholipase C-beta 1 /DEF=Human DNA sequence from clone RP4-654A7 on chromosome 20. Contains the gene for phospholipase C-beta-1 (KIAA0581, 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1) (PLCB1, PLC-I), ESTs and GSSs /FL=gb:NM_015192.1	20,01	26,02	6,13	17,39	5,89	60,31	42,52	42,99	48,61	5,85	2,8	1,7	6,41	*

213429_at	CDNA FLJ26539 fis, clone KDN09310	AW025579		gb:AW025579 /DB_XREF=gi:5879109 /DB_XREF=wu75b04.x1 /CLONE=IMAGE:2525839 /FEA=mRNA /CNT=40 /TID=Hs.100261.0 /TIER=Stack /STK=14 /UG=Hs.100261 /UG_TITLE=Homo sapiens mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222)	214,78	203,49	25,34	147,87	61,35	552,52	342,07	488,17	460,92	62,26	3,12	1,74	9,93	*
213547_at	CAND2: cullin-associated and neddylation-dissociated 2 (putative)	AB014567	23066	gb:AB014567.1 /DB_XREF=gi:3327147 /GEN=KIAA0667 /FEA=mRNA /CNT=39 /TID=Hs.154740.0 /TIER=Stack /STK=21 /UG=Hs.154740 /LL=23066 /DEF=Homo sapiens mRNA for KIAA0667 protein, partial cds. /PROD=KIAA0667 protein	101,89	154,01	140,97	132,29	15,66	49,48	42,6	45,46	45,85	2	-2,89	-2,3	-3,5	*
213791_at	PENK: proenkephalin	NM_006211	5179	gb:NM_006211.1 /DB_XREF=gi:5453875 /GEN=PENK /FEA=FLmRNA /CNT=41 /TID=Hs.93557.0 /TIER=FL+Stack /STK=25 /UG=Hs.93557 /LL=5179 /DEF=Homo sapiens proenkephalin (PENK), mRNA. /PROD=proenkephalin /FL=gb:NM_006211.1	61,67	180,4	240,44	160,84	52,53	1564,38	555,23	647,71	922,44	322,08	5,74	2,23	13,89	*
213805_at	ABHD5: abhydrolase domain containing 5	AI692428	51099	gb:AI692428 /DB_XREF=gi:4969768 /DB_XREF=wd69c12.x1 /CLONE=IMAGE:2336854 /FEA=EST /CNT=26 /TID=Hs.184019.1 /TIER=Stack /STK=8 /UG=Hs.184019 /UG_TITLE=Homo sapiens clone 23551 mRNA sequence	23,39	12,59	2,37	12,78	6,07	33,46	37,73	41,59	37,59	2,35	2,94	1,63	13,45	*
213905_x_at	BGN /// TSHZ1: biglycan /// teashirt family zinc finger 1	AA845258	10194 /// 633	gb:AA845258 /DB_XREF=gi:2931709 /DB_XREF=ak84a11.s1 /CLONE=IMAGE:1414556 /FEA=EST /CNT=21 /TID=Hs.821.1 /TIER=Stack /STK=11 /UG=Hs.821 /LL=633 /UG_GENE=BGN /UG_TITLE=biglycan	1585,2	1618,88	1425,19	1543,09	59,75	682,53	613,65	721,99	672,72	31,66	-2,29	-2,08	-2,54	*
214446_at	ELL2: elongation factor, RNA polymerase II, 2	NM_012081	22936	gb:NM_012081.1 /DB_XREF=gi:6912353 /GEN=ELL2 /FEA=FLmRNA /CNT=24 /TID=Hs.173334.2 /TIER=FL /STK=5 /UG=Hs.173334 /LL=22936 /DEF=Homo sapiens ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA. /PROD=ELL-RELATED RNA POLYMERASE II, ELONGATIONFACTOR /FL=gb:NM_012081.1	34,55	25,39	9,96	23,3	7,17	98,05	93,96	59,15	83,72	12,34	3,59	2,18	7,48	*
214581_x_at	TNFRSF21: tumor necrosis factor receptor superfamily, member 21	BE568134	27242	gb:BE568134 /DB_XREF=gi:9811854 /DB_XREF=601341661F1 /CLONE=IMAGE:3683823 /FEA=FLmRNA /CNT=70 /TID=Hs.159651.0 /TIER=ConsEnd /STK=0 /UG=Hs.159651 /LL=27242 /UG_GENE=DR6 /UG_TITLE=death receptor 6 /FL=gb:NM_014452.1 gb:AF068868.1	20,37	10,88	5,22	12,16	4,42	30,28	37,46	38,22	35,32	2,53	2,91	1,78	7,26	*
214587_at	COL8A1: collagen, type VIII, alpha 1	BE877796	1295	gb:BE877796 /DB_XREF=gi:10326572 /DB_XREF=601486365F1 /CLONE=IMAGE:3888665 /FEA=FLmRNA /CNT=35 /TID=Hs.114599.0 /TIER=ConsEnd /STK=0 /UG=Hs.114599 /LL=1295 /UG_GENE=COL8A1 /UG_TITLE=collagen, type VIII, alpha 1 /FL=gb:NM_001850.1	19,85	9,99	3,19	11,01	4,83	68,74	38,37	47,95	51,69	8,96	4,69	2,47	17,16	*
214696_at	MGC14376: hypothetical protein MGC14376	AF070569	84981	gb:AF070569.1 /DB_XREF=gi:3387938 /FEA=mRNA /CNT=39 /TID=Hs.29206.0 /TIER=ConsEnd /STK=0 /UG=Hs.29206 /UG_TITLE=Homo sapiens clone 24659 mRNA sequence /DEF=Homo sapiens clone 24659 mRNA sequence.	400,05	514,56	95,63	336,75	125,01	887,73	879,38	897,75	888,29	5,31	2,64	1,64	6,77	*
214761_at	ZNF423: zinc finger protein 423	AW149417	23090	gb:AW149417 /DB_XREF=gi:6197313 /DB_XREF=xf36h07.x1 /CLONE=IMAGE:2620189 /FEA=mRNA /CNT=19 /TID=Hs.137168.0 /TIER=ConsEnd /STK=2 /UG=Hs.137168 /LL=23090 /UG_GENE=KIAA0760 /UG_TITLE=OLF-1EBF associated zinc finger gene	46,29	52,37	23,97	40,88	8,63	168,85	70,36	120,57	119,93	28,43	2,93	1,65	5,02	*
214954_at	SUSD5: sushi domain containing 5	BF977837	26032	gb:BF977837 /DB_XREF=gi:12345052 /DB_XREF=602148677F1 /CLONE=IMAGE:4307442 /FEA=mRNA /CNT=8 /TID=Hs.196647.0 /TIER=ConsEnd /STK=0 /UG=Hs.196647 /LL=26032 /UG_GENE=KIAA0527 /UG_TITLE=KIAA0527 protein	10,13	10,21	3,39	7,91	2,26	35,64	24,69	21,82	27,38	4,21	3,46	2,13	6,75	*
215116_s_at	DNM1: dynamin 1	AF035321	1759	gb:AF035321.1 /DB_XREF=gi:2661086 /FEA=mRNA /CNT=8 /TID=Hs.166161.2 /TIER=ConsEnd /STK=0 /UG=Hs.166161 /LL=1759 /UG_GENE=DNM1 /UG_TITLE=dynamin 1 /DEF=Homo sapiens clone 23944 mRNA sequence.	92,03	78,16	253,5	141,23	56,28	32,7	27,52	31,46	30,56	1,56	-4,62	-1,59	-7,72	*
215617_at	CDNA FLJ11754 fis, clone HEMBA1005588	AU145711		gb:AU145711 /DB_XREF=gi:11007232 /DB_XREF=AU145711 /CLONE=HEMBA1005588 /FEA=mRNA /CNT=4 /TID=Hs.301006.0 /TIER=ConsEnd /STK=1 /UG=Hs.301006 /UG_TITLE=Homo sapiens cDNA FLJ11754 fis, clone HEMBA1005588	15,36	7,75	8,15	10,42	2,47	44,05	25,81	34,18	34,68	5,27	3,33	2,15	5,71	*
216521_s_at	BRCC3: BRCA1/BRCA2-containing complex, subunit 3	S72931	79184	gb:S72931 /DB_XREF=gi:639612 /FEA=DNA /CNT=1 /TID=Hs.301927.3 /TIER=ConsEnd /STK=0 /UG=Hs.301927 /LL=79184 /UG_GENE=C6.1A /UG_TITLE=c6.1A /DEF=Homo sapiens T-cell receptor alpha chain-c6.1A fusion protein (c6.1A-TCRC) gene, partial cds	9,92	6,72	5,22	7,28	1,39	16,31	17,2	12,88	15,46	1,32	2,12	1,55	3,15	*
218013_x_at	DCTN4: dynactin 4 (p62)	NM_016221	51164	gb:NM_016221.1 /DB_XREF=gi:7705892 /GEN=LOC51164 /FEA=FLmRNA /CNT=189 /TID=Hs.180952.0 /TIER=FL /STK=1 /UG=Hs.180952 /LL=51164 /DEF=Homo sapiens dynactin p62 subunit (LOC51164), mRNA. /PROD=dynactin p62 subunit /FL=gb:NM_016221.1 gb:AF195120.1	73,62	55,99	9,34	46,32	19,18	165,99	141,12	104,38	137,16	17,89	2,96	1,66	9,38	*
218036_x_at	NMD3: NMD3 homolog (S. cerevisiae)	NM_015938	51068	gb:NM_015938.1 /DB_XREF=gi:7705711 /GEN=LOC51068 /FEA=FLmRNA /CNT=155 /TID=Hs.181022.0 /TIER=FL /STK=1 /UG=Hs.181022 /LL=51068 /DEF=Homo sapiens CGI-07 protein (LOC51068), mRNA. /PROD=CGI-07 protein /FL=gb:NM_015938.1 gb:AF132941.1	43,2	16,63	4,73	21,52	11,37	65,22	72,48	50,17	62,63	6,57	2,91	1,51	22,3	*
218613_at	LOC653754: similar to pleckstrin and Sec7 domain containing 3	NM_018422	653754	gb:NM_018422.1 /DB_XREF=gi:8922171 /GEN=DKFZp761K1423 /FEA=FLmRNA /CNT=85 /TID=Hs.236438.0 /TIER=FL+Stack /STK=48 /UG=Hs.236438 /LL=55358 /DEF=Homo sapiens hypothetical protein DKFZp761K1423 (DKFZp761K1423), mRNA. /PROD=hypothetical protein DKFZp761K1423 /FL=gb:NM_018422.1	80,05	48,39	9,83	46,09	20,3	122,54	121,23	139,68	127,82	5,94	2,77	1,6	10,08	*
218647_s_at	YRDC: yrdC domain containing (E. coli)	NM_024640	79693	gb:NM_024640.1 /DB_XREF=gi:13375875 /GEN=FLJ23476 /FEA=FLmRNA /CNT=75 /TID=Hs.46736.0 /TIER=FL /STK=0 /UG=Hs.46736 /LL=79693 /DEF=Homo sapiens hypothetical protein FLJ23476 (FLJ23476), mRNA. /PROD=hypothetical protein FLJ23476 /FL=gb:NM_024640.1	190,65	220,93	177,21	196,26	12,93	348,29	346,93	311,16	335,46	12,16	1,71	1,52	1,94	*
219054_at	C5orf23: chromosome 5 open reading frame 23	NM_024563	79614	gb:NM_024563.1 /DB_XREF=gi:13375730 /GEN=FLJ14054 /FEA=FLmRNA /CNT=55 /TID=Hs.13528.0 /TIER=FL+Stack /STK=19 /UG=Hs.13528 /LL=79614 /DEF=Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA. /PROD=hypothetical protein FLJ14054 /FL=gb:NM_024563.1	58,85	49,4	17,36	41,87	12,55	238,04	113,73	201,7	184,49	36,9	4,41	2,5	9,14	*
219298_at	ECHDC3: enoyl Coenzyme A hydratase domain containing 3	NM_024693	79746	gb:NM_024693.1 /DB_XREF=gi:13375972 /GEN=FLJ20909 /FEA=FLmRNA /CNT=41 /TID=Hs.98855.0 /TIER=FL+Stack /STK=12 /UG=Hs.98855 /LL=79746 /DEF=Homo sapiens hypothetical protein FLJ20909 (FLJ20909), mRNA. /PROD=hypothetical protein FLJ20909 /FL=gb:NM_024693.1	98,3	132,33	165,47	132,03	19,39	73,52	60,08	63,42	65,67	4,04	-2,01	-1,5	-2,56	*
219326_s_at	B3GNT2: UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	NM_006577	10678	gb:NM_006577.2 /DB_XREF=gi:9845237 /GEN=BETA3GNT /FEA=FLmRNA /CNT=43 /TID=Hs.48730.0 /TIER=FL /STK=0 /UG=Hs.48730 /LL=10678 /DEF=Homo sapiens beta-1,3-N-acetylglucosaminyltransferase (BETA3GNT), mRNA. /PROD=beta-1,3-N-acetylglucosaminyltransferase /FL=gb:NM_006577.2 gb:AF288208.1 gb:AF092051.2	18,53	9,5	4,14	10,72	4,2	30,48	39,1	27,94	32,51	3,38	3,03	1,78	8,58	*
219789_at	NPR3: natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	AI628360	4883	gb:AI628360 /DB_XREF=gi:4665160 /DB_XREF=ty75e10.x1 /CLONE=IMAGE:2284938 /FEA=FLmRNA /CNT=36 /TID=Hs.123655.0 /TIER=Stack /STK=10 /UG=Hs.123655 /LL=4883 /UG_GENE=NPR3 /UG_TITLE=natriuretic peptide receptor Cguanylate cyclase C (atrionatriuretic peptide receptor C) /FL=gb:M59305.1 gb:NM_000908.1 gb:AF025998.1	32,86	26,55	9,95	23,12	6,83	129,98	68,19	104,23	100,8	17,92	4,36	2,57	8,85	*
219872_at	C4orf18: chromosome 4 open reading frame 18	NM_016613	51313	gb:NM_016613.1 /DB_XREF=gi:7706151 /GEN=LOC51313 /FEA=FLmRNA /CNT=21 /TID=Hs.323583.0 /TIER=FL /STK=2 /UG=Hs.323583 /LL=51313 /DEF=Homo sapiens AD021 protein (LOC51313), mRNA. /PROD=AD021 protein /FL=gb:NM_016613.1 gb:AF223468.1	16,24	10,99	5,31	10,85	3,16	22,33	30,66	32,19	28,39	3,06	2,62	1,69	5,1	*
219888_at	SPAG4: sperm associated antigen 4	NM_003116	6676	gb:NM_003116.1 /DB_XREF=gi:11037054 /GEN=SPAG4 /FEA=FLmRNA /CNT=17 /TID=Hs.123159.0 /TIER=FL+Stack /STK=11 /UG=Hs.123159 /LL=6676 /DEF=Homo sapiens sperm associated antigen 4 (SPAG4), mRNA. /PROD=sperm associated antigen 4 /FL=gb:AF262992.1 gb:NM_003116.1	20,36	31,06	39,3	30,24	5,48	85,55	58,82	57,44	67,27	9,15	2,22	1,55	3,34	*
219956_at	GALNT6: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	NM_007210	11226	gb:NM_007210.2 /DB_XREF=gi:13124893 /GEN=GALNT6 /FEA=FLmRNA /CNT=14 /TID=Hs.151678.0 /TIER=FL /STK=0 /UG=Hs.151678 /LL=11226 /DEF=Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) (GALNT6), mRNA. /PROD=polypeptide N-acetylgalactosaminyltransferase 6 /FL=gb:NM_007210.2	80,37	37,06	45,21	54,21	13,29	13,94	24,88	19,41	19,41	3,16	-2,79	-1,59	-4,43	*
220123_at	SLC35F5: solute carrier family 35, member F5	NM_025181	80255	gb:NM_025181.1 /DB_XREF=gi:13376773 /GEN=FLJ22004 /FEA=FLmRNA /CNT=9 /TID=Hs.108812.0 /TIER=FL /STK=0 /UG=Hs.108812 /LL=80255 /DEF=Homo sapiens hypothetical protein FLJ22004 (FLJ22004), mRNA. /PROD=hypothetical protein FLJ22004 /FL=gb:NM_025181.1	10,83	6,68	3,85	7,12	2,02	16,95	17,74	15,93	16,87	0,52	2,37	1,61	4,46	*
220386_s_at	EML4: echinoderm microtubule associated protein like 4	NM_019063	27436	gb:NM_019063.1 /DB_XREF=gi:9506630 /GEN=C2ORF2 /FEA=FLmRNA /CNT=6 /TID=Hs.13472.0 /TIER=FL /STK=3 /UG=Hs.13472 /LL=27436 /DEF=Homo sapiens chromosome 2 open reading frame 2 (C2ORF2), mRNA. /PROD=hypothetical protein /FL=gb:NM_019063.1	34,77	24,49	15,65	24,97	5,52	71,58	56,03	61,37	62,99	4,56	2,52	1,8	4,01	*
220436_at	CNTNAP3B: contactin associated protein-like 3B	NM_024879	389734	gb:NM_024879.1 /DB_XREF=gi:13376319 /GEN=FLJ14195 /FEA=FLmRNA /CNT=7 /TID=Hs.212839.0 /TIER=FL /STK=3 /UG=Hs.212839 /LL=79937 /DEF=Homo sapiens hypothetical protein FLJ14195 (FLJ14195), mRNA. /PROD=hypothetical protein FLJ14195 /FL=gb:NM_024879.1	6,84	6,91	5,49	6,41	0,46	19,41	16,83	12,93	16,39	1,89	2,56	2,02	3,17	*
220477_s_at	C20orf30: chromosome 20 open reading frame 30	NM_014145	29058	gb:NM_014145.1 /DB_XREF=gi:7661833 /GEN=HSPC274 /FEA=FLmRNA /CNT=7 /TID=Hs.323476.0 /TIER=FL /STK=0 /UG=Hs.323476 /LL=29058 /DEF=Homo sapiens HSPC274 protein (HSPC274), mRNA. /PROD=HSPC274 protein /FL=gb:NM_014145.1 gb:AF161392.1	215,7	172,94	28,07	138,9	56,77	417,1	504	289,2	403,43	62,38	2,9	1,6	9	*
220765_s_at	LIMS2: LIM and senescent cell antigen-like domains 2	NM_017980	55679	gb:NM_017980.1 /DB_XREF=gi:8922203 /GEN=FLJ10044 /FEA=FLmRNA /CNT=3 /TID=Hs.127273.0 /TIER=FL /STK=0 /UG=Hs.127273 /LL=55679 /DEF=Homo sapiens hypothetical protein FLJ10044 (FLJ10044), mRNA. /PROD=hypothetical protein FLJ10044 /FL=gb:NM_017980.1	84,83	117,38	112,35	104,86	10,12	61,02	54,17	47,37	54,19	3,94	-1,94	-1,57	-2,35	*
220796_x_at	SLC35E1: solute carrier family 35, member E1	NM_024881	79939	gb:NM_024881.1 /DB_XREF=gi:13376323 /GEN=FLJ14251 /FEA=FLmRNA /CNT=3 /TID=Hs.214178.0 /TIER=FL /STK=0 /UG=Hs.214178 /LL=79939 /DEF=Homo sapiens hypothetical protein FLJ14251 (FLJ14251), mRNA. /PROD=hypothetical protein FLJ14251 /FL=gb:NM_024881.1	249,8	312,26	338,21	300,09	26,24	171,35	173,92	163,13	169,47	3,25	-1,77	-1,51	-2,03	*
220955_x_at	RAB23: RAB23, member RAS oncogene family	NM_016277	51715	gb:NM_016277.1 /DB_XREF=gi:7706472 /GEN=RAB23 /FEA=FLmRNA /CNT=3 /TID=Hs.94769.0 /TIER=FL /STK=0 /UG=Hs.94769 /LL=51715 /DEF=Homo sapiens RAB23, member RAS oncogene family (RAB23), mRNA. /PROD=RAB23 protein /FL=gb:NM_016277.1 gb:AB034244.1	42,9	16,79	3,39	21,03	11,6	75,7	61,1	56,4	64,4	5,81	3,06	1,57	33,16	*
221016_s_at	TCF7L1: transcription factor 7-like 1 (T-cell specific, HMG-box) /// transcription factor 7-like 1 (T-cell specific, HMG-box)	NM_031283	83439	gb:NM_031283.1 /DB_XREF=gi:13786122 /GEN=TCF-3 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900240.146 /TIER=FL /STK=0 /DEF=Homo sapiens HMG-box transcription factor TCF-3 (TCF-3), mRNA. /PROD=HMG-box transcription factor TCF-3 /FL=gb:NM_031283.1	81,02	70,24	32,67	61,31	14,66	20,87	20,88	27,07	22,94	2,07	-2,67	-1,6	-3,87	*
221111_at	IL26: interleukin 26	NM_018402	55801	gb:NM_018402.1 /DB_XREF=gi:8923755 /GEN=HSA251549 /FEA=FLmRNA /CNT=3 /TID=Hs.272350.0 /TIER=FL /STK=0 /UG=Hs.272350 /LL=55801 /DEF=Homo sapiens AK155 protein (AK155 gene) (HSA251549), mRNA. /PROD=AK155 protein (AK155 gene) /FL=gb:NM_018402.1	2,63	3,39	2,63	2,88	0,25	9,22	6,45	5,35	7	1,15	2,43	1,73	3,24	*

221268_s_at	SGPP1: sphingosine-1-phosphate phosphatase 1 /// sphingosine-1-phosphate phosphatase 1	NM_030791	81537	gb:NM_030791.1 /DB_XREF=gi:13540568 /GEN=LOC81537 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900063.54 /TIER=FL /STK=0 /DEF=Homo sapiens sphingosine-1-phosphatase (LOC81537), mRNA. /PROD=sphingosine-1-phosphatase /FL=gb:NM_030791.1	74,39	46,42	5,74	42,19	19,93	147,51	162,69	145,92	152,04	5,35	3,6	2,02	16,17	*
221423_s_at	YIPF5: Yip1 domain family, member 5 /// Yip1 domain family, member 5	NM_030799	81555	gb:NM_030799.1 /DB_XREF=gi:13540583 /GEN=AF140225 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900070.1077 /TIER=FL /STK=0 /DEF=Homo sapiens hypothetical protein AF140225 (AF140225), mRNA. /PROD=hypothetical protein AF140225 /FL=gb:NM_030799.1	166,37	143,16	14,99	108,17	47,07	298,38	363,26	233,85	298,5	37,36	2,76	1,53	9,79	*
221428_s_at	TBL1XR1: transducin (beta)-like 1X-linked receptor 1 /// transducin (beta)-like 1X-linked receptor 1	NM_030921	79718	gb:NM_030921.1 /DB_XREF=gi:13569880 /GEN=DC42 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900115.1082 /TIER=FL /STK=0 /DEF=Homo sapiens hypothetical protein DC42 (DC42), mRNA. /PROD=hypothetical protein DC42 /FL=gb:NM_030921.1	33,6	16,2	2,45	17,42	9,01	92,82	65,73	60,71	73,08	9,97	4,2	2,14	28,29	*
221673_s_at	CSNK1G1: casein kinase 1, gamma 1	AB042563	53944	gb:AB042563.1 /DB_XREF=gi:11177009 /GEN=CSNK1G1L /FEA=FLmRNA /CNT=1 /TID=Hs.157777.1 /TIER=FL /STK=0 /UG=Hs.157777 /LL=53944 /DEF=Homo sapiens CSNK1G1L mRNA for casein kinase 1 gamma 1L, complete cds. /PROD=casein kinase 1 gamma 1L /FL=gb:AB042563.1	14,76	11,97	12,9	13,21	0,82	22,38	23,87	21,11	22,45	0,8	1,7	1,52	1,92	*
221814_at	GPR124: G protein-coupled receptor 124	BF511315	25960	gb:BF511315 /DB_XREF=gi:11594613 /DB_XREF=UI-H-BI4-aoj-h-02-0-UI.s1 /CLONE=IMAGE:3085275 /FEA=mRNA /CNT=130 /TID=Hs.17270.0 /TIER=Stack /STK=9 /UG=Hs.17270 /LL=25960 /UG_GENE=DKFZP434C211 /UG_TITLE=DKFZP434C211 protein	137,88	135,81	139,28	137,66	1,01	76,35	69,01	79,88	75,08	3,2	-1,83	-1,71	-1,97	*
222162_s_at	ADAMTS1: ADAM metallopeptidase with thrombospondin type 1 motif, 1	AK023795	9510	gb:AK023795.1 /DB_XREF=gi:10435838 /FEA=mRNA /CNT=4 /TID=Hs.8230.1 /TIER=ConsEnd /STK=0 /UG=Hs.8230 /LL=9510 /UG_GENE=ADAMTS1 /UG_TITLE=a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 /DEF=Homo sapiens cDNA FLJ13733 fis, clone PLACE3000147, highly similar to Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA.	235,16	280,15	35,2	183,5	75,28	595,22	718,02	674,3	662,52	35,93	3,61	2,13	11,12	*
222890_at	CCDC113: coiled-coil domain containing 113	BG054922	29070	gb:BG054922 /DB_XREF=gi:12512131 /DB_XREF=nac92c01.x1 /CLONE=IMAGE:3441769 /FEA=FLmRNA /CNT=36 /TID=Hs.11614.0 /TIER=Stack /STK=12 /UG=Hs.11614 /LL=29070 /UG_GENE=HSPC065 /UG_TITLE=HSPC065 protein /FL=gb:NM_014157.1 gb:AF161550.1	9,35	8,78	3,56	7,23	1,84	27,34	21,6	15,05	21,33	3,55	2,95	1,84	5,32	*
223611_s_at	LNX1: ligand of numb-protein X 1	AI738919	84708	gb:AI738919 /DB_XREF=gi:5100900 /DB_XREF=wi12a04.x1 /CLONE=IMAGE:2389998 /FEA=FLmRNA /CNT=27 /TID=Hs.66295.1 /TIER=Stack /STK=12 /UG=Hs.66295 /LL=81608 /UG_GENE=DKFZP586K0717 /UG_TITLE=hypothetical protein DKFZp586K0717 /FL=gb:AF237782.1	11,5	17,25	7,53	12,09	2,82	36,27	32,02	27,72	32	2,47	2,65	1,86	4,35	*
223627_at	RKHD3: ring finger and KH domain containing 3	AL136778	84206	gb:AL136778.1 /DB_XREF=gi:12053068 /GEN=DKFZp434J0617 /FEA=FLmRNA /CNT=27 /TID=Hs.104744.0 /TIER=FL /STK=0 /UG=Hs.104744 /DEF=Homo sapiens mRNA; cDNA DKFZp434J0617 (from clone DKFZp434J0617); complete cds. /PROD=hypothetical protein /FL=gb:AL136778.1	27,12	27,35	4,62	19,7	7,54	125,71	70,98	64,7	87,13	19,37	4,42	2,27	12,4	*
223735_at	ARL6: ADP-ribosylation factor-like 6	AL136815	84100	gb:AL136815.1 /DB_XREF=gi:12053140 /GEN=DKFZp434L1123 /FEA=FLmRNA /CNT=13 /TID=Hs.182133.0 /TIER=FL /STK=0 /UG=Hs.182133 /DEF=Homo sapiens mRNA; cDNA DKFZp434L1123 (from clone DKFZp434L1123); complete cds. /PROD=hypothetical protein /FL=gb:AL136815.1	6,93	6,02	2,18	5,04	1,45	14,47	13,09	9,43	12,33	1,51	2,44	1,56	4,75	*
223925_s_at	MTPN: Myotrophin	AF130088	136319	gb:AF130088.1 /DB_XREF=gi:11493480 /FEA=FLmRNA /CNT=4 /TID=Hs.21321.0 /TIER=FL /STK=0 /UG=Hs.21321 /DEF=Homo sapiens clone FLB9213 PRO2474 mRNA, complete cds. /PROD=PRO2474 /FL=gb:AF130088.1	26,95	13,8	7,43	16,06	5,75	46,4	47,74	44,55	46,23	0,93	2,88	1,81	7	*
224397_s_at	TMTC1 /// LOC653626: transmembrane and tetratricopeptide repeat containing 1 /// transmembrane and tetratricopeptide repeat containing 1 /// similar to ARG99 protein /// similar to ARG99 protein	AF319520	653626 /// 83857	gb:AF319520.1 /DB_XREF=gi:13604166 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900593.486 /TIER=FL /STK=0 /DEF=Homo sapiens ARG99 mRNA, complete cds. /PROD=ARG99 /FL=gb:AF319520.1	18,41	16,55	10,99	15,32	2,23	72,81	61,67	55,49	63,32	5,07	4,13	3,2	5,57	*
225016_at	APCDD1: adenomatosis polyposis coli down-regulated 1	N48299	147495	gb:N48299 /DB_XREF=gi:1189465 /DB_XREF=yy77f10.s1 /CLONE=IMAGE:279595 /FEA=EST /CNT=126 /TID=Hs.20665.0 /TIER=Stack /STK=61 /UG=Hs.20665 /UG_TITLE=ESTs, Moderately similar to NFY-C (H.sapiens)	54,2	28,09	35,46	39,25	7,77	13,58	8,53	16,78	12,96	2,4	-3,03	-1,89	-4,79	*
225420_at	GPAM: glycerol-3-phosphate acyltransferase, mitochondrial	AV699379	57678	gb:AV699379 /DB_XREF=gi:10301350 /DB_XREF=AV699379 /CLONE=GKCFVD06 /FEA=mRNA /CNT=120 /TID=Hs.42586.0 /TIER=Stack /STK=13 /UG=Hs.42586 /LL=57678 /UG_GENE=KIAA1560 /UG_TITLE=KIAA1560 protein	69,53	47,4	4,57	40,5	19,07	178,05	153,65	106,67	146,12	20,95	3,61	1,9	16,12	*
225429_at	gb:BF437011 /DB_XREF=gi:11449329 /DB_XREF=7p61e06.x1 /CLONE=IMAGE:3650387 /FEA=EST /CNT=101 /TID=Hs.7256.1 /TIER=Stack /STK=29 /UG=Hs.7256 /LL=23592 /UG_GENE=MAN1 /UG_TITLE=integral inner nuclear membrane protein	BF437011		gb:BF437011 /DB_XREF=gi:11449329 /DB_XREF=7p61e06.x1 /CLONE=IMAGE:3650387 /FEA=EST /CNT=101 /TID=Hs.7256.1 /TIER=Stack /STK=29 /UG=Hs.7256 /LL=23592 /UG_GENE=MAN1 /UG_TITLE=integral inner nuclear membrane protein	24,74	19,06	5,55	16,45	5,69	41,41	48,02	46,23	45,22	1,97	2,75	1,74	6,39	*
225496_s_at	SYTL2: synaptotagmin-like 2	N21426	54843	gb:N21426 /DB_XREF=gi:1126596 /DB_XREF=yx58d01.s1 /CLONE=IMAGE:265921 /FEA=mRNA /CNT=96 /TID=Hs.92254.1 /TIER=Stack /STK=20 /UG=Hs.92254 /LL=54843 /UG_GENE=FLJ20163 /UG_TITLE=hypothetical protein FLJ20163	17,34	22,09	10,87	16,77	3,25	90,35	29,78	53,25	57,79	17,63	3,45	1,64	6,03	*
225602_at	C9orf19: chromosome 9 open reading frame 19	H92988	152007	gb:H92988 /DB_XREF=gi:1099316 /DB_XREF=yv07d05.s1 /CLONE=IMAGE:242025 /FEA=EST /CNT=142 /TID=Hs.75544.1 /TIER=Stack /STK=93 /UG=Hs.75544 /LL=7533 /UG_GENE=YWHAH /UG_TITLE=tyrosine 3-monooxygenasetryptophan 5-monooxygenase activation protein, eta polypeptide	172,07	191,14	182,5	181,9	5,51	80,71	88,8	107,78	92,43	8,02	-1,97	-1,71	-2,31	*
226034_at	Homo sapiens, clone IMAGE:3881549, mRNA	BE222344		gb:BE222344 /DB_XREF=gi:8909662 /DB_XREF=hu10g08.x1 /CLONE=IMAGE:3166238 /FEA=EST /CNT=70 /TID=Hs.166975.4 /TIER=Stack /STK=24 /UG=Hs.166975 /LL=6430 /UG_GENE=SFRS5 /UG_TITLE=splicing factor, arginineserine-rich 5	14,31	16,91	5	12,07	3,62	35,05	28,49	33,57	32,37	1,99	2,68	1,77	5,31	*
226650_at	ZFAND2A: zinc finger, AN1-type domain 2A	AI984061	90637	gb:AI984061 /DB_XREF=gi:5811280 /DB_XREF=wz56a07.x1 /CLONE=IMAGE:2562036 /FEA=EST /CNT=37 /TID=Hs.116567.0 /TIER=Stack /STK=25 /UG=Hs.116567 /UG_TITLE=ESTs, Weakly similar to predicted using Genefinder (C.elegans)	123,13	237,03	71,54	143,9	48,89	404,96	411,12	285,93	367,34	40,74	2,55	1,56	5,86	*
227300_at	TMEM119: transmembrane protein 119	AL521682	338773	gb:AL521682 /DB_XREF=gi:12785175 /DB_XREF=AL521682 /CLONE=CS0DB003YH17 (3 prime) /FEA=EST /CNT=42 /TID=Hs.93135.0 /TIER=Stack /STK=37 /UG=Hs.93135 /UG_TITLE=ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY (H.sapiens)	562,71	597,18	1729,11	963	383,19	194,14	155,27	298,37	215,93	42,72	-4,46	-1,5	-8,48	*
227655_at	CDNA FLJ38512 fis, clone HCHON2000503	AI631964		gb:AI631964 /DB_XREF=gi:4683294 /DB_XREF=wa38c03.x1 /CLONE=IMAGE:2300356 /FEA=EST /CNT=33 /TID=Hs.34447.0 /TIER=Stack /STK=30 /UG=Hs.34447 /UG_TITLE=ESTs	235,5	243,38	239,81	239,56	2,28	126,42	121,98	121,78	123,39	1,51	-1,94	-1,89	-1,99	*
227819_at	LGR6: leucine-rich repeat-containing G protein-coupled receptor 6	AA524536	59352	gb:AA524536 /DB_XREF=gi:2265464 /DB_XREF=ng45g03.s1 /CLONE=IMAGE:937780 /FEA=mRNA /CNT=32 /TID=Hs.59483.0 /TIER=Stack /STK=17 /UG=Hs.59483 /UG_TITLE=Homo sapiens VTS20631 mRNA, g-protein coupled receptor family, partial cds	25,84	24,47	29,22	26,51	1,41	12,9	15,55	15,33	14,59	0,85	-1,82	-1,6	-2,07	*
228303_at	Transcribed locus, strongly similar to NP_009141.1 polypeptide N-acetylgalactosaminyltransferase 6; GalNAc transferase 6; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 6; protein-UDP acetylgalactosaminyltransferase 6 [Homo sapiens]	AW014155		gb:AW014155 /DB_XREF=gi:5862912 /DB_XREF=UI-H-BI0-aaj-c-11-0-UI.s1 /CLONE=IMAGE:2709501 /FEA=EST /CNT=18 /TID=Hs.20726.0 /TIER=Stack /STK=15 /UG=Hs.20726 /UG_TITLE=ESTs	87,52	52,57	59,96	66,68	10,64	18,76	35,92	24,79	26,49	5,03	-2,52	-1,68	-3,9	*
228802_at	RBPMS2: RNA binding protein with multiple splicing 2	BE348466	348093	gb:BE348466 /DB_XREF=gi:9260319 /DB_XREF=ht69c12.x1 /CLONE=IMAGE:3151990 /FEA=EST /CNT=19 /TID=Hs.78293.0 /TIER=Stack /STK=14 /UG=Hs.78293 /UG_TITLE=ESTs	128,27	144,85	91,26	121,46	15,84	67,85	36,98	63,5	56,11	9,65	-2,16	-1,53	-3,18	*
228885_at	MAMDC2: MAM domain containing 2	AI862120	256691	gb:AI862120 /DB_XREF=gi:5526227 /DB_XREF=tw37a12.x1 /CLONE=IMAGE:2261854 /FEA=EST /CNT=18 /TID=Hs.131987.0 /TIER=Stack /STK=8 /UG=Hs.131987 /UG_TITLE=ESTs	31,08	20,1	5,84	19,01	7,31	56,59	146,63	55,73	86,32	30,16	4,54	1,72	13,42	*
229074_at	Transcribed locus	AI692267		gb:AI692267 /DB_XREF=gi:4969607 /DB_XREF=wc83d03.x1 /CLONE=IMAGE:2325221 /FEA=EST /CNT=13 /TID=Hs.150073.0 /TIER=Stack /STK=9 /UG=Hs.150073 /UG_TITLE=ESTs, Moderately similar to alternatively spliced product using exon 13A (H.sapiens)	215,66	362,29	289,13	289,02	42,33	106,08	166,36	141,28	137,91	17,48	-2,1	-1,5	-2,88	*
229308_at	Transcribed locus	AW273796		gb:AW273796 /DB_XREF=gi:6660826 /DB_XREF=xv24a05.x1 /CLONE=IMAGE:2814032 /FEA=EST /CNT=20 /TID=Hs.42500.1 /TIER=Stack /STK=16 /UG=Hs.42500 /LL=26225 /UG_GENE=ARL5 /UG_TITLE=ADP-ribosylation factor-like 5	8,92	11,8	3,32	8,01	2,49	30,04	29,06	24,78	27,96	1,62	3,49	2,28	7,17	*
229500_at	gb:AI609256 /DB_XREF=gi:4618423 /DB_XREF=tw83e12.x1 /CLONE=IMAGE:2266318 /FEA=EST /CNT=13 /TID=Hs.270956.1 /TIER=Stack /STK=9 /UG=Hs.270956 /LL=10463 /UG_GENE=C4ORF1 /UG_TITLE=chromosome 4 open reading frame 1	AI609256		gb:AI609256 /DB_XREF=gi:4618423 /DB_XREF=tw83e12.x1 /CLONE=IMAGE:2266318 /FEA=EST /CNT=13 /TID=Hs.270956.1 /TIER=Stack /STK=9 /UG=Hs.270956 /LL=10463 /UG_GENE=C4ORF1 /UG_TITLE=chromosome 4 open reading frame 1	14,71	13,36	2,94	10,34	3,72	32,47	30,54	30,59	31,2	0,64	3,02	1,89	7,4	*
229802_at	CDNA FLJ14388 fis, clone HEMBA1002716	AA147884		gb:AA147884 /DB_XREF=gi:1717300 /DB_XREF=zl50b04.s1 /CLONE=IMAGE:505327 /FEA=EST /CNT=13 /TID=Hs.9812.0 /TIER=Stack /STK=8 /UG=Hs.9812 /UG_TITLE=ESTs	130,84	180,89	6,38	106,04	51,88	580,55	454,82	397,69	477,69	54,01	4,5	2,4	23,17	*
230542_at	ZNF597: zinc finger protein 597	AI825587	146434	gb:AI825587 /DB_XREF=gi:5446258 /DB_XREF=wb74b10.x1 /CLONE=IMAGE:2311387 /FEA=EST /CNT=13 /TID=Hs.88630.0 /TIER=Stack /STK=8 /UG=Hs.88630 /UG_TITLE=ESTs, Weakly similar to T14748 hypothetical protein DKFZp434G1621.1 (H.sapiens)	8,2	6,27	3,79	6,09	1,28	14,97	12,26	16,57	14,6	1,26	2,4	1,72	3,73	*
230710_at	CDNA FLJ41489 fis, clone BRTHA2004582	W05495		gb:W05495 /DB_XREF=gi:1278246 /DB_XREF=za81b10.r1 /CLONE=IMAGE:298939 /FEA=EST /CNT=8 /TID=Hs.218710.0 /TIER=Stack /STK=8 /UG=Hs.218710 /UG_TITLE=ESTs	20,46	32,82	30,61	27,96	3,8	86,08	63,82	56,58	68,83	8,87	2,46	1,8	3,38	*
231055_at	Transcribed locus	BF432941		gb:BF432941 /DB_XREF=gi:11445104 /DB_XREF=7n28g07.x1 /CLONE=IMAGE:3566028 /FEA=EST /CNT=13 /TID=Hs.263462.0 /TIER=Stack /STK=10 /UG=Hs.263462 /UG_TITLE=ESTs	11,7	8,74	7,87	9,44	1,16	16,32	17,31	23,19	18,94	2,15	2,01	1,52	2,66	*
231292_at	EID3: E1A-like inhibitor of differentiation 3	AI964053	493861	gb:AI964053 /DB_XREF=gi:5756766 /DB_XREF=wt88d10.x1 /CLONE=IMAGE:2514547 /FEA=EST /CNT=8 /TID=Hs.170337.0 /TIER=Stack /STK=8 /UG=Hs.170337 /UG_TITLE=ESTs	6,56	7,25	6,94	6,91	0,2	12,62	12,54	18,82	14,66	2,08	2,12	1,62	2,63	*
233512_at	Clone 23571 and 23784 mRNA sequence	AF035291		gb:AF035291.1 /DB_XREF=gi:2661045 /FEA=mRNA /CNT=3 /TID=Hs.113744.0 /TIER=ConsEnd /STK=2 /UG=Hs.113744 /UG_TITLE=Homo sapiens clone 23571 and 23784 mRNA sequence /DEF=Homo sapiens clone 23571 and 23784 mRNA sequence.	10,07	8,59	9,94	9,53	0,47	35,77	43,02	28,68	35,82	4,14	3,76	3	4,56	*
233775_x_at	CDNA FLJ13242 fis, clone OVARC1000578	AK023304		gb:AK023304.1 /DB_XREF=gi:10435181 /FEA=mRNA /CNT=2 /TID=Hs.296731.0 /TIER=ConsEnd /STK=0 /UG=Hs.296731 /UG_TITLE=Homo sapiens cDNA FLJ13242 fis, clone OVARC1000578 /DEF=Homo sapiens cDNA FLJ13242 fis, clone OVARC1000578.	143,18	142,3	170,52	152	9,26	81,99	92,74	93,52	89,42	3,72	-1,7	-1,5	-1,91	*
234975_at	CDNA FLJ38048 fis, clone CTONG2014264 /// CDNA FLJ39067 fis, clone NT2RP7014910	BE544748		gb:BE544748 /DB_XREF=gi:9773393 /DB_XREF=601075513F1 /CLONE=IMAGE:3461475 /FEA=EST /CNT=35 /TID=Hs.10592.0 /TIER=ConsEnd /STK=0 /UG=Hs.10592 /UG_TITLE=ESTs	6,47	4,91	3,85	5,08	0,76	12,62	11,85	10,36	11,61	0,67	2,29	1,8	3,07	*

235182_at	C20orf82: chromosome 20 open reading frame 82	AI816793	140862	gb:AI816793 /DB_XREF=gi:5435872 /DB_XREF=wj34b11.x1 /CLONE=IMAGE:2404701 /FEA=EST /CNT=13 /TID=Hs.135100.0 /TIER=ConsEnd /STK=4 /UG=Hs.135100 /UG_TITLE=ESTs	7,53	7,23	7,32	7,36	0,09	48,48	18,57	25,34	30,79	9,05	4,19	2,16	6,21	*
235276_at	gb:AA781795 /DB_XREF=gi:2841126 /DB_XREF=ai51d05.s1 /CLONE=1360521 /FEA=EST /CNT=14 /TID=Hs.122587.0 /TIER=ConsEnd /STK=1 /UG=Hs.122587 /UG_TITLE=ESTs	AA781795		gb:AA781795 /DB_XREF=gi:2841126 /DB_XREF=ai51d05.s1 /CLONE=1360521 /FEA=EST /CNT=14 /TID=Hs.122587.0 /TIER=ConsEnd /STK=1 /UG=Hs.122587 /UG_TITLE=ESTs	13,91	17,31	8,86	13,36	2,45	64,15	20,21	54,52	46,29	13,33	3,47	1,74	5,88	*
235606_at	LOC344595: hypothetical LOC344595	AA417117	344595	gb:AA417117 /DB_XREF=gi:2077402 /DB_XREF=zu07f03.r1 /CLONE=IMAGE:731165 /FEA=EST /CNT=9 /TID=Hs.122643.0 /TIER=ConsEnd /STK=0 /UG=Hs.122643 /UG_TITLE=ESTs	14,95	15,99	5,24	12,06	3,42	33,66	29,45	22,87	28,66	3,14	2,38	1,54	4,54	*
235683_at	SESN3: sestrin 3	BF685808	143686	gb:BF685808 /DB_XREF=gi:11971216 /DB_XREF=602140491F1 /CLONE=IMAGE:4301567 /FEA=EST /CNT=13 /TID=Hs.132927.0 /TIER=ConsEnd /STK=0 /UG=Hs.132927 /UG_TITLE=ESTs, Moderately similar to p53 regulated PA26-T2 nuclear protein (H.sapiens)	15,6	21,15	23,68	20,14	2,39	70,69	52,22	29,34	50,75	11,96	2,52	1,5	3,74	*
235821_at	CDNA FLJ14388 fis, clone HEMBA1002716	AI917494		gb:AI917494 /DB_XREF=gi:5637349 /DB_XREF=ts84f07.x1 /CLONE=IMAGE:2237989 /FEA=EST /CNT=9 /TID=Hs.131329.0 /TIER=ConsEnd /STK=7 /UG=Hs.131329 /UG_TITLE=ESTs	89,95	116,16	25,18	77,1	27,04	288,06	284,5	248,9	273,82	12,5	3,55	2,24	8,41	*
235882_at	CDNA clone IMAGE:5303499	BF115777		gb:BF115777 /DB_XREF=gi:10985253 /DB_XREF=7n64f11.x1 /CLONE=IMAGE:3569444 /FEA=EST /CNT=12 /TID=Hs.148185.0 /TIER=ConsEnd /STK=3 /UG=Hs.148185 /UG_TITLE=ESTs	15,19	13,9	12,24	13,78	0,86	22,76	29,38	25,05	25,73	1,94	1,87	1,58	2,19	*
236480_at	CDNA FLJ41489 fis, clone BRTHA2004582	AA543084		gb:AA543084 /DB_XREF=gi:2291564 /DB_XREF=nf96g04.s1 /CLONE=IMAGE:927798 /FEA=EST /CNT=6 /TID=Hs.154077.0 /TIER=ConsEnd /STK=6 /UG=Hs.154077 /UG_TITLE=ESTs	7,19	9,97	7,85	8,34	0,84	22,35	19,54	20,1	20,66	0,86	2,48	2,09	3,01	*
236835_at	LOC645431: hypothetical protein LOC645431	AI654093	645431	gb:AI654093 /DB_XREF=gi:4738072 /DB_XREF=ty61f08.x1 /CLONE=IMAGE:2283591 /FEA=EST /CNT=5 /TID=Hs.43397.0 /TIER=ConsEnd /STK=5 /UG=Hs.43397 /UG_TITLE=ESTs	9,69	10,22	4,99	8,3	1,66	19,61	17,11	18,7	18,47	0,73	2,23	1,66	3,33	*
238332_at	ANKRD29: ankyrin repeat domain 29	AI307802	147463	gb:AI307802 /DB_XREF=gi:4002406 /DB_XREF=tb28c10.x1 /CLONE=IMAGE:2055666 /FEA=EST /CNT=23 /TID=Hs.135560.0 /TIER=ConsEnd /STK=4 /UG=Hs.135560 /UG_TITLE=ESTs, Weakly similar to T43458 hypothetical protein DKFZp434F0621.1 (H.sapiens)	16,09	53,76	14,23	28,03	12,88	123,15	109,98	92,94	108,69	8,75	3,88	2,16	15,94	*
238455_at	CDNA FLJ45742 fis, clone KIDNE2016327	AA329676		gb:AA329676 /DB_XREF=gi:1981918 /DB_XREF=EST33315 /FEA=EST /CNT=12 /TID=Hs.72639.0 /TIER=ConsEnd /STK=0 /UG=Hs.72639 /UG_TITLE=ESTs	21,83	11,63	3,49	12,31	5,31	47,28	30,61	32,03	36,64	5,34	2,98	1,62	10,34	*
238465_at	MGC33648: hypothetical protein MGC33648	AI265933	133383	gb:AI265933 /DB_XREF=gi:3884091 /DB_XREF=qq90e10.x1 /CLONE=IMAGE:1938666 /FEA=EST /CNT=12 /TID=Hs.85950.0 /TIER=ConsEnd /STK=1 /UG=Hs.85950 /UG_TITLE=ESTs	58,93	17,16	6,81	27,63	15,93	80,38	91,84	76,08	82,77	4,7	3	1,52	58,01	*
238623_at	CDNA FLJ37310 fis, clone BRAMY2016706	AI633559		gb:AI633559 /DB_XREF=gi:4684889 /DB_XREF=th68f02.x1 /CLONE=IMAGE:2123835 /FEA=EST /CNT=9 /TID=Hs.310359.0 /TIER=ConsEnd /STK=0 /UG=Hs.310359 /UG_TITLE=ESTs	158,96	189,59	31,99	126,85	48,25	521,65	428,86	563,51	504,67	39,79	3,98	2,39	10,68	*
241773_at	gb:AI679812 /DB_XREF=gi:4889994 /DB_XREF=tu66a10.x1 /CLONE=IMAGE:2255994 /FEA=EST /CNT=3 /TID=Hs.43057.0 /TIER=ConsEnd /STK=3 /UG=Hs.43057 /UG_TITLE=ESTs	AI679812		gb:AI679812 /DB_XREF=gi:4889994 /DB_XREF=tu66a10.x1 /CLONE=IMAGE:2255994 /FEA=EST /CNT=3 /TID=Hs.43057.0 /TIER=ConsEnd /STK=3 /UG=Hs.43057 /UG_TITLE=ESTs	7,01	8,79	7,98	7,92	0,51	34,35	23,79	38,7	32,28	4,43	4,07	3,1	5,14	*
242149_at	CAMP-binding guanine nucleotide exchange factor IV (cAMP-GEFIV) mRNA, clone W15, partial sequence	R02709		gb:R02709 /DB_XREF=gi:752445 /DB_XREF=ye80g05.r1 /CLONE=IMAGE:124088 /FEA=EST /CNT=9 /TID=Hs.289083.0 /TIER=ConsEnd /STK=0 /UG=Hs.289083 /UG_TITLE=ESTs	15,34	9,11	3,8	9,42	3,34	21,25	29,33	23,18	24,59	2,43	2,61	1,59	6,32	*
242245_at	SYDE2: Synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	N90719	84144	gb:N90719 /DB_XREF=gi:1444046 /DB_XREF=za90a12.s1 /CLONE=IMAGE:299806 /FEA=EST /CNT=3 /TID=Hs.94445.0 /TIER=ConsEnd /STK=3 /UG=Hs.94445 /UG_TITLE=ESTs	8,71	4,93	2,65	5,43	1,77	15,11	11,1	14,43	13,55	1,24	2,5	1,57	5,43	*
243813_at	CDNA FLJ31059 fis, clone HSYRA2000832	AA418028		gb:AA418028 /DB_XREF=gi:2079857 /DB_XREF=zv97f02.s1 /CLONE=IMAGE:767739 /FEA=EST /CNT=3 /TID=Hs.98284.0 /TIER=ConsEnd /STK=3 /UG=Hs.98284 /UG_TITLE=ESTs	32,09	21,27	10,21	21,19	6,32	115,61	99,67	62,45	92,58	15,75	4,37	2,6	8,9	*
244025_at	gb:BF590917 /DB_XREF=gi:11683241 /DB_XREF=7h46a08.x1 /CLONE=IMAGE:3318998 /FEA=EST /CNT=6 /TID=Hs.224432.0 /TIER=ConsEnd /STK=3 /UG=Hs.224432 /UG_TITLE=ESTs	BF590917		gb:BF590917 /DB_XREF=gi:11683241 /DB_XREF=7h46a08.x1 /CLONE=IMAGE:3318998 /FEA=EST /CNT=6 /TID=Hs.224432.0 /TIER=ConsEnd /STK=3 /UG=Hs.224432 /UG_TITLE=ESTs	25,11	24,22	34,83	28,05	3,4	73,93	47,16	57,25	59,44	7,8	2,12	1,57	2,85	*

Supplementary Table 2: Differentially expressed genes in early type 1 diabetes compared to HC 1.5 fold change lower bound 90% CI

probe set	gene	Accession	EntrezGene	Description	HC_109nMSC_(HG-U133_Plus_2).CEL	HC_110nMSC_(HG-U133_Plus_2).CEL	HC_RO1_(HG-U133_Plus_2).CEL	baseline mean	baseline mean's SE	ES_T1D_A15_(HG-U133_Plus_2).CEL	ES_T1D_A17_(HG-U133_Plus_2).CEL	ES_T1D_A20_(HG-U133_Plus_2).CEL	experiment mean	experiment mean's SE	fold change	lower bound of FC	upper bound of FC	filtered
1558882_at	LOC401233: similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription	BI868572	401233	gb:BI868572 /DB_XREF=gi:16042245 /DB_XREF=603392679F1 /CLONE=IMAGE:5402706 /TID=Hs2.435991.1 /CNT=6 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.435991 /UG_TITLE=Homo sapiens, clone IMAGE:5289038, mRNA	2,43	2,92	2,21	2,52	0,21	6,48	8,34	4,29	6,37	1,17	2,53	1,73	3,42	*
201348_at	GPX3: glutathione peroxidase 3 (plasma)	NM_002084	2878	gb:NM_002084.2 /DB_XREF=gi:6006000 /GEN=GPX3 /FEA=FLmRNA /CNT=468 /TID=Hs.172153.0 /TIER=FL+Stack /STK=256 /UG=Hs.172153 /LL=2878 /DEF=Homo sapiens glutathione peroxidase 3 (plasma) (GPX3), mRNA. /PROD=plasma glutathione peroxidase 3 precursor /FL=gb:NM_002084.2 gb:D00632.1 gb:AF217787.1	31,03	21,62	59,08	37,25	11,25	13,08	11,4	12,16	12,21	0,49	-3,05	-1,53	-4,59	*
201909_at	RPS4Y1: ribosomal protein S4, Y-linked 1	NM_001008	6192	gb:NM_001008.1 /DB_XREF=gi:4506726 /GEN=RPS4Y /FEA=FLmRNA /CNT=295 /TID=Hs.180911.0 /TIER=FL+Stack /STK=39 /UG=Hs.180911 /LL=6192 /DEF=Homo sapiens ribosomal protein S4, Y-linked (RPS4Y), mRNA. /PROD=ribosomal protein S4, Y-linked /FL=gb:AF116711.1 gb:M58459.1 gb:NM_001008.1	35,42	19,63	2160,98	738,67	711,17	3378,03	4411,63	3697,38	3829,01	305,55	5,18	1,98	100000000	*
203131_at	PDGFRA: platelet-derived growth factor receptor, alpha polypeptide	NM_006206	5156	gb:NM_006206.1 /DB_XREF=gi:5453869 /GEN=PDGFRA /FEA=FLmRNA /CNT=148 /TID=Hs.74615.0 /TIER=FL+Stack /STK=62 /UG=Hs.74615 /LL=5156 /DEF=Homo sapiens platelet-derived growth factor receptor, alpha polypeptide (PDGFRA), mRNA. /PROD=platelet-derived growth factor receptor, alphapolypeptide /FL=gb:NM_006206.1 gb:M21574.1	219,29	299,5	208,35	242,38	28,73	861,2	1286,74	401,82	849,92	255,52	3,51	1,74	5,55	*
204014_at	DUSP4: dual specificity phosphatase 4	NM_001394	1846	gb:NM_001394.2 /DB_XREF=gi:12707552 /GEN=DUSP4 /FEA=FLmRNA /CNT=105 /TID=Hs.2359.0 /TIER=FL /STK=4 /UG=Hs.2359 /LL=1846 /DEF=Homo sapiens dual specificity phosphatase 4 (DUSP4), mRNA. /PROD=dual specificity phosphatase 4 /FL=gb:NM_001394.2 gb:BC002671.1 gb:U48807.1 gb:U21108.1	21,41	30,87	13,55	21,95	5,01	90,78	34,2	127	83,99	27	3,83	1,7	7,2	*
204409_s_at	EIF1AY: eukaryotic translation initiation factor 1A, Y-linked	BC005248	9086	gb:BC005248.1 /DB_XREF=gi:13528902 /FEA=FLmRNA /CNT=113 /TID=Hs.155103.0 /TIER=FL+Stack /STK=59 /UG=Hs.155103 /LL=9086 /UG_GENE=EIF1AY /DEF=Homo sapiens, clone MGC:12282, mRNA, complete cds. /PROD=Unknown (protein for MGC:12282) /FL=gb:AF000987.1 gb:NM_004681.1 gb:BC005248.1	3,59	3,55	4,78	3,97	0,4	172,62	118,14	236,4	175,72	34,17	44,22	29,25	61,73	*
205000_at	DDX3Y: DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	NM_004660	8653	gb:NM_004660.2 /DB_XREF=gi:13514808 /GEN=DBY /FEA=FLmRNA /CNT=47 /TID=Hs.99120.0 /TIER=FL+Stack /STK=11 /UG=Hs.99120 /LL=8653 /DEF=Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide, Y chromosome (DBY), mRNA. /PROD=DEADH (Asp-Glu-Ala-AspHis) box polypeptide, Ychromosome /FL=gb:NM_004660.2 gb:AF000985.1 gb:AF000984.1	3,51	2,46	4,82	3,59	0,68	99,7	103,92	106,79	103,47	2,06	28,79	21,88	41,95	*
205743_at	STAC: SH3 and cysteine rich domain	NM_003149	6769	gb:NM_003149.1 /DB_XREF=gi:4507246 /GEN=STAC /FEA=FLmRNA /CNT=30 /TID=Hs.56045.0 /TIER=FL+Stack /STK=12 /UG=Hs.56045 /LL=6769 /DEF=Homo sapiens src homology three (SH3) and cysteine rich domain (STAC), mRNA. /PROD=src homology three (SH3) and cysteine richdomain /FL=gb:NM_003149.1 gb:D86640.1	25,15	34,92	53,68	37,92	8,37	94,2	95,76	63,58	84,51	10,47	2,23	1,52	3,62	*
205830_at	CLGN: calmegin	NM_004362	1047	gb:NM_004362.1 /DB_XREF=gi:4758003 /GEN=CLGN /FEA=FLmRNA /CNT=33 /TID=Hs.86368.0 /TIER=FL /STK=4 /UG=Hs.86368 /LL=1047 /DEF=Homo sapiens calmegin (CLGN), mRNA. /PROD=calmegin /FL=gb:NM_004362.1 gb:D86322.1	3,05	7,94	2,16	4,38	1,8	21,07	16,63	27,1	21,6	3,03	4,93	2,75	15,31	*
206777_s_at	CRYBB2: crystallin, beta B2	NM_000496	1415	gb:NM_000496.1 /DB_XREF=gi:4503062 /GEN=CRYBB2 /FEA=FLmRNA /CNT=77 /TID=Hs.169286.0 /TIER=FL /STK=4 /UG=Hs.169286 /LL=1415 /DEF=Homo sapiens crystallin, beta B2 (CRYBB2), mRNA. /PROD=crystallin, beta B2 /FL=gb:L10035.1 gb:NM_000496.1	210,04	31,57	272,46	171,35	72,18	29,8	31,61	40,32	33,91	3,25	-5,05	-1,54	-8,82	*
207703_at	NLGN4Y: neuroligin 4, Y-linked	NM_014893	22829	gb:NM_014893.1 /DB_XREF=gi:7662399 /GEN=KIAA0951 /FEA=FLmRNA /CNT=3 /TID=Hs.227327.0 /TIER=FL /STK=0 /UG=Hs.227327 /LL=22829 /DEF=Homo sapiens KIAA0951 protein (KIAA0951), mRNA. /PROD=KIAA0951 protein /FL=gb:AB023168.1 gb:NM_014893.1	4,47	3,71	3,31	3,83	0,34	10,65	19,43	15,93	15,34	2,55	4	2,83	5,35	*
209086_x_at	MCAM: melanoma cell adhesion molecule	BE964361	4162	gb:BE964361 /DB_XREF=gi:11767830 /DB_XREF=601658062R1 /CLONE=IMAGE:3876255 /FEA=FLmRNA /CNT=242 /TID=Hs.211579.2 /TIER=Stack /STK=14 /UG=Hs.211579 /LL=4162 /UG_GENE=MCAM /UG_TITLE=melanoma adhesion molecule /FL=gb:AF089868.1 gb:NM_006500.1	230,58	160,89	153,05	181,51	24,64	101,77	84,56	83,28	89,87	5,96	-2,02	-1,54	-2,55	*
209189_at	FOS: v-fos FBJ murine osteosarcoma viral oncogene homolog	BC004490	2353	gb:BC004490.1 /DB_XREF=gi:13325363 /FEA=FLmRNA /CNT=139 /TID=Hs.25647.0 /TIER=FL /STK=0 /UG=Hs.25647 /LL=2353 /UG_GENE=FOS /DEF=Homo sapiens, v-fos FBJ murine osteosarcoma viral oncogene homolog, clone MGC:11074, mRNA, complete cds. /PROD=v-fos FBJ murine osteosarcoma viral oncogenehomolog /FL=gb:NM_005252.2 gb:BC004490.1	9,46	10,95	10,38	10,27	0,44	36,96	21,79	29,94	29,56	4,38	2,88	2,16	3,63	*
209291_at	ID4: inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094	3400	gb:AW157094 /DB_XREF=gi:6228495 /DB_XREF=au91g11.x1 /CLONE=IMAGE:2783684 /FEA=FLmRNA /CNT=175 /TID=Hs.34853.0 /TIER=Stack /STK=26 /UG=Hs.34853 /LL=3400 /UG_GENE=ID4 /UG_TITLE=inhibitor of DNA binding 4, dominant negative helix-loop-helix protein /FL=gb:NM_001546.1 gb:U16153.1 gb:U28368.1	54	86,79	63,27	68,02	9,76	319,92	399,87	122,13	280,64	82,55	4,13	2,07	6,67	*
214983_at	TTTY15: testis-specific transcript, Y-linked 15	AL080135	64595	gb:AL080135.1 /DB_XREF=gi:5262576 /FEA=mRNA /CNT=12 /TID=Hs.45068.0 /TIER=ConsEnd /STK=6 /UG=Hs.45068 /LL=64595 /UG_GENE=DKFZP434I143 /UG_TITLE=hypothetical protein DKFZp434I143 /DEF=Homo sapiens mRNA; cDNA DKFZp434I143 (from clone DKFZp434I143).	6,97	6,28	8,38	7,21	0,62	14,98	20,86	12,25	16,03	2,54	2,22	1,6	2,94	*
226490_at	NHSL1: NHS-like 1	AA503387	57224	gb:AA503387 /DB_XREF=gi:2238354 /DB_XREF=ne45c10.s1 /CLONE=IMAGE:900306 /FEA=mRNA /CNT=48 /TID=Hs.170162.1 /TIER=Stack /STK=16 /UG=Hs.170162 /LL=57224 /UG_GENE=KIAA1357 /UG_TITLE=KIAA1357 protein	42,24	38,24	19,81	33,43	6,91	69,48	86,8	63,22	73,17	7,05	2,19	1,56	3,39	*
227196_at	RHPN2: rhophilin, Rho GTPase binding protein 2	BG054987	85415	gb:BG054987 /DB_XREF=gi:12512261 /DB_XREF=nac93e04.x1 /CLONE=IMAGE:3441894 /FEA=mRNA /CNT=37 /TID=Hs.184598.0 /TIER=Stack /STK=16 /UG=Hs.184598 /UG_TITLE=Homo sapiens cDNA: FLJ23241 fis, clone COL01375	6,18	7,24	5,52	6,31	0,5	10,65	11,68	15,79	12,71	1,57	2,01	1,56	2,54	*
227705_at	TCEAL7: transcription elongation factor A (SII)-like 7	BF591534	56849	gb:BF591534 /DB_XREF=gi:11683858 /DB_XREF=nac13g12.x1 /CLONE=IMAGE:3277270 /FEA=mRNA /CNT=42 /TID=Hs.21861.0 /TIER=Stack /STK=13 /UG=Hs.21861 /LL=56849 /UG_GENE=LOC56849 /UG_TITLE=hypothetical protein MPMGp800C04260Q003	39,16	73,24	21,6	44,67	15,16	117,69	114,16	102,35	111,4	4,64	2,49	1,59	5,66	*
228492_at	USP9Y: ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	AV681765	8287	gb:AV681765 /DB_XREF=gi:10283628 /DB_XREF=AV681765 /CLONE=GKBAKH05 /FEA=EST /CNT=21 /TID=Hs.1870.1 /TIER=Stack /STK=15 /UG=Hs.1870 /LL=5053 /UG_GENE=PAH /UG_TITLE=phenylalanine hydroxylase	3,56	3,75	3,6	3,64	0,06	12,67	25,62	17,12	18,47	3,8	5,08	3,36	6,8	*
230744_at	Transcribed locus	N22766		gb:N22766 /DB_XREF=gi:1136916 /DB_XREF=yx65f08.s1 /CLONE=IMAGE:266631 /FEA=EST /CNT=17 /TID=Hs.42419.0 /TIER=Stack /STK=16 /UG=Hs.42419 /UG_TITLE=ESTs	19,97	20,25	20,79	20,34	0,24	34,15	74,25	74,44	60,95	13,4	3	1,91	4,08	*
230760_at	ZFY: Zinc finger protein, Y-linked	BF592062	7544	gb:BF592062 /DB_XREF=gi:11684386 /DB_XREF=7n98h06.x1 /CLONE=IMAGE:3572962 /FEA=EST /CNT=11 /TID=Hs.233890.0 /TIER=Stack /STK=10 /UG=Hs.233890 /UG_TITLE=ESTs	2,78	2,68	2,68	2,72	0,03	16,02	13,88	19,72	16,54	1,71	6,09	5,05	7,13	*
232618_at	CYorf15A: chromosome Y open reading frame 15A	AF332224	246126	gb:AF332224.1 /DB_XREF=gi:13161080 /FEA=mRNA /CNT=9 /TID=Hs.171857.0 /TIER=ConsEnd /STK=5 /UG=Hs.171857 /DEF=Homo sapiens testis protein mRNA, partial cds. /PROD=testis protein	3,3	2,58	3,84	3,24	0,36	19,76	15,82	30,43	22	4,37	6,79	4,43	9,64	*
233512_at	Clone 23571 and 23784 mRNA sequence	AF035291		gb:AF035291.1 /DB_XREF=gi:2661045 /FEA=mRNA /CNT=3 /TID=Hs.113744.0 /TIER=ConsEnd /STK=2 /UG=Hs.113744 /UG_TITLE=Homo sapiens clone 23571 and 23784 mRNA sequence /DEF=Homo sapiens clone 23571 and 23784 mRNA sequence.	10,07	8,59	9,94	9,53	0,47	22,23	14,23	21,88	19,44	2,61	2,04	1,57	2,53	*
236088_at	NTNG1: netrin G1	AV723308	22854	gb:AV723308 /DB_XREF=gi:10826596 /DB_XREF=AV723308 /CLONE=HTBBFC07 /FEA=EST /CNT=11 /TID=Hs.171136.0 /TIER=ConsEnd /STK=2 /UG=Hs.171136 /UG_TITLE=ESTs	6,98	9,63	8,31	8,31	0,77	20,86	33	27,02	26,96	3,5	3,24	2,46	4,19	*
238178_at	gb:BF110268 /DB_XREF=gi:10939958 /DB_XREF=7n51g03.x1 /CLONE=IMAGE:3568301 /FEA=EST /CNT=6 /TID=Hs.264433.0 /TIER=ConsEnd /STK=6 /UG=Hs.264433 /UG_TITLE=ESTs	BF110268		gb:BF110268 /DB_XREF=gi:10939958 /DB_XREF=7n51g03.x1 /CLONE=IMAGE:3568301 /FEA=EST /CNT=6 /TID=Hs.264433.0 /TIER=ConsEnd /STK=6 /UG=Hs.264433 /UG_TITLE=ESTs	3,61	2,68	3,16	3,15	0,27	11,1	12,93	6,16	10,06	2,02	3,2	2,1	4,42	*

238332_at	ANKRD29: ankyrin repeat domain 29	AI307802	147463	gb:AI307802 /DB_XREF=gi:4002406 /DB_XREF=tb28c10.x1 /CLONE=IMAGE:2055666 /FEA=EST /CNT=23 /TID=Hs.135560.0 /TIER=ConsEnd /STK=4 /UG=Hs.135560 /UG_TITLE=ESTs, Weakly similar to T43458 hypothetical protein DKFZp434F0621.1 (H.sapiens)	16,09	53,76	14,23	28,03	12,88	101,38	131,74	47,8	93,64	24,54	3,34	1,51	14,09	*
238623_at	CDNA FLJ37310 fis, clone BRAMY2016706	AI633559		gb:AI633559 /DB_XREF=gi:4684889 /DB_XREF=th68f02.x1 /CLONE=IMAGE:2123835 /FEA=EST /CNT=9 /TID=Hs.310359.0 /TIER=ConsEnd /STK=0 /UG=Hs.310359 /UG_TITLE=ESTs	158,96	189,59	31,99	126,85	48,25	725,56	547,24	302,72	525,18	122,56	4,14	2,08	11,52	*
239208_s_at	gb:AW945538 /DB_XREF=gi:8123293 /DB_XREF=RC0-EN0024-120500-031-a06 /FEA=EST /CNT=7 /TID=Hs.194589.0 /TIER=ConsEnd /STK=0 /UG=Hs.194589 /UG_TITLE=ESTs	AW945538		gb:AW945538 /DB_XREF=gi:8123293 /DB_XREF=RC0-EN0024-120500-031-a06 /FEA=EST /CNT=7 /TID=Hs.194589.0 /TIER=ConsEnd /STK=0 /UG=Hs.194589 /UG_TITLE=ESTs	89,66	77,88	91,81	86,45	4,33	27,42	44,35	6,95	26,24	10,81	-3,29	-1,95	-10,24	*
244740_at	MGC9913: Hypothetical protein MGC9913	BE855713	386759	gb:BE855713 /DB_XREF=gi:10368199 /DB_XREF=7g08d09.x1 /CLONE=IMAGE:3305873 /FEA=EST /CNT=6 /TID=Hs.23133.1 /TIER=ConsEnd /STK=2 /UG=Hs.23133 /UG_TITLE=ESTs, Weakly similar to A33569 alcohol sulfotransferase (R.norvegicus)	186,18	218,76	230,09	211,67	13,16	74,28	100,91	79,17	84,78	8,18	-2,5	-2,08	-3,04	*
244741_s_at	gb:BE855713 /DB_XREF=gi:10368199 /DB_XREF=7g08d09.x1 /CLONE=IMAGE:3305873 /FEA=EST /CNT=6 /TID=Hs.23133.1 /TIER=ConsEnd /STK=2 /UG=Hs.23133 /UG_TITLE=ESTs, Weakly similar to A33569 alcohol sulfotransferase (R.norvegicus)	BE855713		gb:BE855713 /DB_XREF=gi:10368199 /DB_XREF=7g08d09.x1 /CLONE=IMAGE:3305873 /FEA=EST /CNT=6 /TID=Hs.23133.1 /TIER=ConsEnd /STK=2 /UG=Hs.23133 /UG_TITLE=ESTs, Weakly similar to A33569 alcohol sulfotransferase (R.norvegicus)	181,36	182,23	164,49	176,02	5,77	72,78	85,11	66,38	74,75	5,5	-2,35	-2,07	-2,71	*

Supplementary Table 3. Gene ontology analysis comparing MSCs from healthy and late stage T1D donors

GO term and p-val	Gene name	Acc. No.	Healthy (mean, n=3)	Late T1D (mean, n=3)	Fold difference
Growth factor activity	BMP2	AA583044	11.65	65.76	5.65
p-val:0.000536	CXCL1	NM_001511	22.31	92.00	4.12
	ESM1	NM_007036	14.31	64.15	4.48
	HBEGF	NM_001945	132.04	304.98	2.31
	HGF	X16323	5.96	29.60	4.96
	IL6	NM_000600	134.99	550.05	4.07
	JAG1	U61276	7.30	16.59	2.27
	LIF	NM_002309	96.17	424.03	4.41
Multicellular organismal development	AEBP1	NM_001129	233.34	119.87	-1.95
p-val:0.000373	BGN	AA845258	1543.09	672.72	-2.29
	BMP2	AA583044	11.65	65.76	5.65
	CHRDL1	AL049176	24.52	73.89	3.01
	COL8A1	BE877796	11.01	51.69	4.69
	CXCL1	NM_001511	22.31	92.00	4.12
	DCN	AF138300	353.05	1493.53	4.23
	DLX2	NM_004405	14.52	153.04	10.54
	EGR2	NM_000399	114.78	297.12	2.59
	FST	NM_013409	251.82	749.26	2.98
	FUT8	AB049740	16.79	44.53	2.65
	GADD45B	NM_015675	510.13	1773.22	3.48
	GSTM3	AL527430	821.32	342.38	-2.4
	HBEGF	NM_001945	132.04	304.98	2.31
	ID1	D13889	330.87	986.90	2.98
	JAG1	U61276	7.30	16.59	2.27
	KLF10	NM_005655	604.70	2208.35	3.65
	LAMA4	NM_002290	65.75	194.97	2.97

	LIF	NM_002309	96.17	424.03	4.41
	LMO4	AI824831	198.35	99.48	-1.99
	MBNL1	AL562860	6.39	15.52	2.43
	MGP	NM_000900	22.68	113.46	5
	MTPN	AF130088	16.06	46.23	2.88
	NKX3-1	AF247704	33.61	97.79	2.91
	NPR3	AI628360	23.12	100.80	4.36
	PRRX1	NM_006902	53.03	169.14	3.19
	PTP4A1	BF576710	89.69	254.69	2.84
	QKI	AF142421	24.68	62.31	2.53
	SFRP1	NM_003012	14.70	48.37	3.29
	SKIL	NM_005414	7.07	18.72	2.65
	SPRY2	NM_005842	129.53	281.03	2.17
	TRIM14	BE962483	30.32	14.43	-2.1
Multicellular organismal process p-val:0.000484	ADORA2B	NM_000676	34.93	71.83	2.06
	AEBP1	NM_001129	233.34	119.87	-1.95
	BGN	AA845258	1543.09	672.72	-2.29
	BMP2	AA583044	11.65	65.76	5.65
	BPGM	NM_001724	134.03	326.49	2.44
	CHRDL1	AL049176	24.52	73.89	3.01
	COL8A1	BE877796	11.01	51.69	4.69
	CXCL1	NM_001511	22.31	92	4.12
	DCN	AF138300	353.05	1493.53	4.23
	DLX2	NM_004405	14.52	153.04	10.54
	DNM1	AF035321	141.23	30.56	-4.62
	EGR2	NM_000399	114.78	297.12	2.59
	FST	NM_013409	251.82	749.26	2.98
	FUT8	AB049740	16.79	44.53	2.65
	GADD45B	NM_015675	510.13	1773.22	3.48
	GSTM3	AL527430	821.32	342.38	-2.4
	HBEGF	NM_001945	132.04	304.98	2.31
	HGF	X16323	5.96	29.6	4.96

	ID1	D13889	330.87	986.9	2.98
	IL6	NM_000600	134.99	550.05	4.07
	JAG1	U61276	7.3	16.59	2.27
	KLF10	NM_005655	604.7	2208.35	3.65
	LAMA4	NM_002290	65.75	194.97	2.97
	LIF	NM_002309	96.17	424.03	4.41
	LMAN1	NM_005570	9.36	19	2.03
	LMO4	AI824831	198.35	99.48	-1.99
	MBNL1	AL562860	6.39	15.52	2.43
	MGP	NM_000900	22.68	113.46	5
	MTPN	AF130088	16.06	46.23	2.88
	NKX3-1	AF247704	33.61	97.79	2.91
	NPR3	AI628360	23.12	100.8	4.36
	PDE7B	AI638433	56.96	173.43	3.04
	PLAU	NM_002658	547.45	1228.22	2.24
	PRRX1	NM_006902	53.03	169.14	3.19
	PTGS2	AY151286	3.38	22.76	6.73
	PTGFR	BC035694	3.96	20.03	5.05
	PTP4A1	BF576710	89.69	254.69	2.84
	QKI	AF142421	24.68	62.31	2.53
	SCUBE3	AI733234	39.67	142.95	3.6
	SFRP1	NM_003012	14.7	48.37	3.29
	SKIL	NM_005414	7.07	18.72	2.65
	SLC19A2	AF153330	38.13	106.71	2.8
	SPRY2	NM_005842	129.53	281.03	2.17
	TFPI	J03225	5.74	22.11	3.85
	TRIM14	BE962483	30.32	14.43	-2.1
Response to external stimulus p-val:0.000694	CDO1	NM_001801	39.22	105.29	2.68
	CXCL1	NM_001511	22.31	92	4.12
	CXCL6	NM_002993	13.5	103.9	7.69
	EGR2	NM_000399	114.78	297.12	2.59
	FOS	BC004490	10.27	74.03	7.21

	HGF	X16323	5.96	29.6	4.96
	IL1R1	NM_000877	103.58	275.49	2.66
	IL6	NM_000600	134.99	550.05	4.07
	LMAN1	NM_005570	9.36	19	2.03
	PLAU	NM_002658	547.45	1228.22	2.24
	PPARG	NM_015869	19.69	42.24	2.15
	PTGS2	AY151286	3.38	22.76	6.73
	SCUBE3	AI733234	39.67	142.95	3.6
	TFPI	J03225	5.74	22.11	3.85
Response to stress	PTGS2	AY151286	3.38	22.76	6.73
p-val:0.000198	POLH	AW665155	15.66	34.81	2.22
	HSPD1	BE256479	213.15	676.38	3.17
	DUSP1	NM_004417	380.83	1028.96	2.7
	SGK	NM_005627	503.32	1140.31	2.27
	BNIP3	U15174	205.97	649.76	3.15
	IL1R1	NM_000877	103.58	275.49	2.66
	LMAN1	NM_005570	9.36	19	2.03
	CDO1	NM_001801	39.22	105.29	2.68
	CXCL1	NM_001511	22.31	92	4.12
	SMAD7	NM_005904	186.15	602.69	3.24
	IL6	NM_000600	134.99	550.05	4.07
	GALK2	NM_002044	26.01	52.65	2.02
	PLAU	NM_002658	547.45	1228.22	2.24
	HSPA4L	NM_014278	9.43	18.47	1.96
	CXCL6	NM_002993	13.5	103.9	7.69
	GADD45B	NM_015675	510.13	1773.22	3.48
	FOS	BC004490	10.27	74.03	7.21
	TFPI	J03225	5.74	22.11	3.85
	HGF	X16323	5.96	29.6	4.96
	SCUBE3	AI733234	39.67	142.95	3.6
Response to wounding	PTGS2	AY151286	3.38	22.76	6.73
p-val:0.000419	IL1R1	NM_000877	103.58	275.49	2.66
	LMAN1	NM_005570	9.36	19	2.03

	CDO1	NM_001801	39.22	105.29	2.68
	CXCL1	NM_001511	22.31	92	4.12
	IL6	NM_000600	134.99	550.05	4.07
	PLAU	NM_002658	547.45	1228.22	2.24
	CXCL6	NM_002993	13.5	103.9	7.69
	FOS	BC004490	10.27	74.03	7.21
	TFPI	J03225	5.74	22.11	3.85
	HGF	X16323	5.96	29.6	4.96
	SCUBE3	AI733234	39.67	142.95	3.6
Protein domain Adenylate kinase	LOC645619	AI653169	19.76	74.69	3.78
p-val:0.000763	AK3L1	NM_013410	103.58	334.94	3.23
	AK2	NM_013411	37.55	67.71	1.8
Pathway TGFb signaling	JAK1	NM_002227	25.87	63.89	2.47
p-val:0.000023	SMAD7	NM_005904	186.15	602.69	3.24
	FST	NM_013409	251.82	749.26	2.98
	LIF	NM_002309	96.17	424.03	4.41
	SKIL	NM_005414	7.07	18.72	2.65
	FOS	BC004490	10.27	74.03	7.21
	ZNF423	AW149417	40.88	119.93	2.93
Chromosome '20p12' genes	BMP2	AA583044	11.65	65.76	5.65
p-val:0.000037	JAG1	U61276	7.3	16.59	2.27
	PLCB1	AL049593	17.39	48.61	2.8
	C20orf30	NM_014145	138.9	403.43	2.9
	C20orf82	AI816793	7.36	30.79	4.19

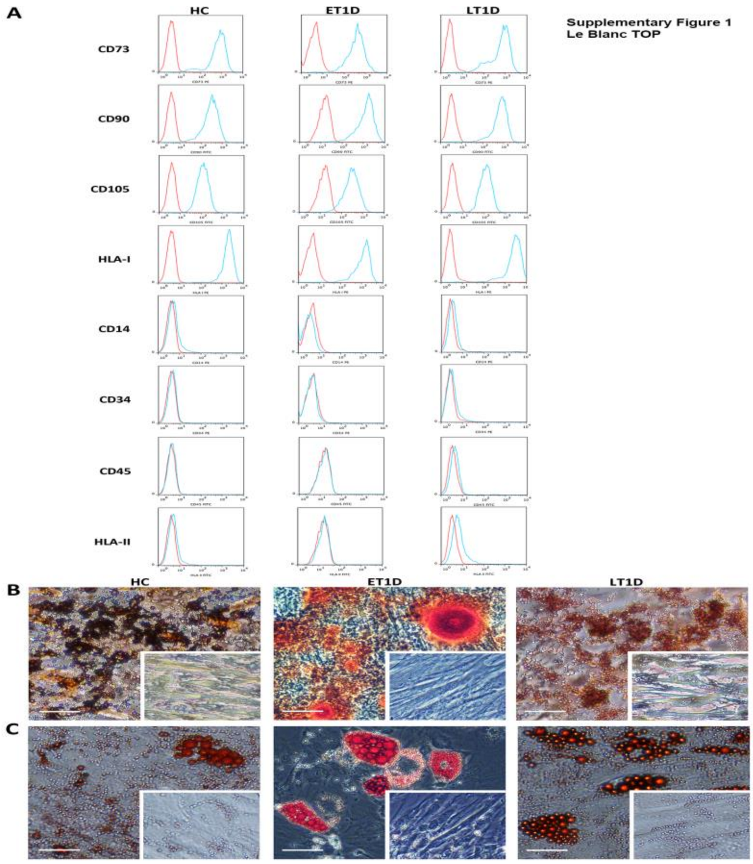
Gene ontology (GO)-term analysis for 1.5-fold differentially expressed genes comparing MSCs from healthy and late stage T1D donors. The data was compared by dCHIP using lower bound of 90% CI.

SUPPLEMENTAL DATA

Supplementary Table 1: Differentially expressed genes in LT1D compared to HC 1.5 fold change lower bound 90% CI

Supplementary Table 2: Differentially expressed genes in ET1D compared to HC 1.5 fold change lower bound 90% CI

Supplementary Table 3: Gene ontology analysis comparing MSCs from healthy and late stage T1D donors



Supplementary Figure 1: Characterization of MSCs according to ISCT guidelines.

Isolated bone marrow cells from T1D donors and HCs were characterized as MSCs according to current standards. **(A)** Flow cytometry analyses confirmed expression of MSC-marker profile (positive for CD73, CD90, CD105 and HLA-I and negative for CD14, CD34, CD45 and HLA-II). Differentiation assays confirmed **(B)** osteogenic capacity as demonstrated by Alizarin red staining, and **(C)** adipogenic capacity as demonstrated by Oil red O staining. Scale bars=20 µm; small inserts represents non-induced control cultures.