Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
1	1552509_a_at	146894	CD300LG	CD300 molecule-like family member g	0.30	1.57E-02	-0.11	4.72E-01	-0.41	8.49E-03	-0.18	7.02E-02	-0.03	7.59E-01	0.15	2.03E-01	-0.02
1	1554574_a_at	1727	CYB5R3	cytochrome b5 reductase 3	0.11	4.33E-01	0.02	9.05E-01	-0.09	6.05E-01	0.00	9.68E-01	0.02	8.76E-01	0.01	9.16E-01	0.32
1	1555725_a_at	8490	RGS5	regulator of G-protein signaling 5	0.55	1.82E-03	0.37	7.99E-02	-0.18	3.92E-01	-0.13	3.30E-01	0.00	9.78E-01	0.13	4.20E-01	-0.07
1	1561180_at		---	---	0.43	3.81E-12	0.02	7.34E-01	-0.41	4.71E-08	0.02	6.03E-01	0.04	3.80E-01	0.02	7.31E-01	-0.02
1	200602_at	351	APP	amyloid beta (A4) precursor protein	0.50	1.56E-05	0.13	3.54E-01	-0.38	7.70E-03	0.02	7.97E-01	-0.01	9.41E-01	-0.03	7.76E-01	0.48
1	200603_at	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	0.32	2.42E-06	0.03	7.44E-01	-0.29	3.80E-04	-0.01	7.86E-01	0.03	5.12E-01	0.05	4.14E-01	-0.01
1	200693_at	10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	0.32	7.35E-06	0.08	3.02E-01	-0.23	6.83E-03	-0.11	3.41E-02	-0.04	5.02E-01	0.08	2.25E-01	-0.20
1	200758_s_at	4779	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	0.19	4.17E-02	0.31	7.47E-03	0.11	3.40E-01	0.06	4.37E-01	0.14	8.08E-02	0.08	3.65E-01	-0.07
1	200762_at	1808	DPYSL2	dihydropyrimidinase-like 2	0.35	9.23E-05	0.15	1.65E-01	-0.20	6.03E-02	0.01	8.68E-01	0.02	7.49E-01	0.01	8.85E-01	0.06
1	200785_s_at		LOC100134190 /// LRP1	similar to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) /// low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	0.32	1.64E-04	0.07	5.01E-01	-0.25	1.48E-02	0.03	6.79E-01	-0.01	9.01E-01	-0.03	6.43E-01	0.20
1	200974_at	59	ACTA2	actin, alpha 2, smooth muscle, aorta	0.55	7.02E-03	-0.16	5.02E-01	-0.71	4.94E-03	-0.09	5.54E-01	-0.17	3.16E-01	-0.07	6.94E-01	-0.19
1	201147_s_at	7078	TIMP3	TIMP metallopeptidase inhibitor 3	0.43	5.92E-06	0.23	3.53E-02	-0.20	8.49E-02	-0.03	6.68E-01	-0.02	7.67E-01	0.01	9.20E-01	0.01
1	201162_at	3490	IGFBP7	insulin-like growth factor binding protein 7	0.34	1.28E-02	-0.05	7.43E-01	-0.39	2.01E-02	-0.09	3.80E-01	0.03	7.98E-01	0.12	3.29E-01	0.22
1	201163_s_at	3490	IGFBP7	insulin-like growth factor binding protein 7	0.34	1.48E-02	-0.16	3.34E-01	-0.50	4.01E-03	-0.05	6.25E-01	0.06	6.03E-01	0.11	3.79E-01	0.18
1	201304_at	4698	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	0.18	3.54E-03	-0.16	2.52E-02	-0.35	9.93E-06	0.01	8.56E-01	-0.01	8.08E-01	-0.02	7.10E-01	-0.02
1	201481_s_at	5834	PYGB	phosphorylase, glycogen; brain	0.14	3.07E-02	-0.21	8.93E-03	-0.35	2.85E-05	0.03	4.94E-01	-0.05	3.70E-01	-0.08	1.67E-01	0.02
1	201560_at	25932	CLIC4	chloride intracellular channel 4	0.35	1.86E-03	0.01	9.15E-01	-0.33	1.54E-02	0.13	1.28E-01	0.06	4.88E-01	-0.07	4.96E-01	0.06
1	201589_at	8243	SMC1A	structural maintenance of chromosomes 1A	0.32	3.52E-05	0.09	3.18E-01	-0.23	1.46E-02	-0.10	8.81E-02	-0.02	6.94E-01	0.08	2.69E-01	-0.08
1	201616_s_at	800	CALD1	caldesmon 1	0.61	4.19E-07	0.11	4.44E-01	-0.50	5.63E-04	-0.06	5.35E-01	-0.08	4.05E-01	-0.02	8.28E-01	0.14
1	202104_s_at	6687	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	0.25	4.59E-04	-0.06	4.75E-01	-0.32	4.63E-04	0.08	1.40E-01	0.00	9.49E-01	-0.09	1.89E-01	0.02
1	202274_at	72	ACTG2	actin, gamma 2, smooth muscle, enteric	0.40	2.57E-02	-0.75	5.29E-04	-1.16	5.41E-07	-0.03	8.33E-01	0.01	9.51E-01	0.04	8.14E-01	0.01
1	202743_at	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	0.25	1.38E-02	-0.36	3.45E-03	-0.62	2.70E-06	0.02	7.67E-01	0.01	9.13E-01	-0.01	8.77E-01	-0.19
1	202917_s_at	6279	S100A8	S100 calcium binding protein A8	0.05	8.28E-01	-0.18	5.40E-01	-0.24	4.43E-01	-0.43	2.82E-02	-0.18	3.71E-01	0.25	2.80E-01	-0.05
1	202948_at	3554	IL1R1	interleukin 1 receptor, type I	0.51	3.02E-08	0.19	6.93E-02	-0.32	3.77E-03	-0.04	5.30E-01	0.07	2.96E-01	0.12	1.42E-01	0.04
1	203044_at	22856	CHSY1	chondroitin sulfate synthase 1	0.31	2.17E-04	0.08	4.07E-01	-0.23	2.57E-02	-0.01	9.16E-01	0.02	7.60E-01	0.03	7.16E-01	-0.19
1	203666_at	6387	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	0.34	1.62E-05	-0.08	3.62E-01	-0.42	1.49E-05	-0.05	4.38E-01	0.10	9.40E-02	0.15	3.16E-02	-0.08
1	203895_at	5332	PLCB4	phospholipase C, beta 4	0.47	5.51E-07	0.08	4.55E-01	-0.39	6.27E-04	0.05	4.45E-01	0.04	6.36E-01	-0.02	8.20E-01	0.03
1	203896_s_at	5332	PLCB4	phospholipase C, beta 4	0.34	1.30E-06	-0.02	8.25E-01	-0.36	3.32E-05	0.02	7.50E-01	0.06	3.05E-01	0.04	5.17E-01	-0.04
1	204363_at	2152	F3	coagulation factor III (thromboplastin, tissue factor)	0.30	2.83E-04	0.15	1.30E-01	-0.15	1.29E-01	-0.03	6.81E-01	0.00	9.61E-01	0.02	7.60E-01	-0.06
1	204368_at	6578	SLCO2A1	solute carrier organic anion transporter family, member 2A1	0.25	1.45E-09	-0.12	1.28E-02	-0.37	2.33E-12	-0.05	9.58E-02	0.00	9.51E-01	0.05	1.72E-01	-0.01
1	204422_s_at	2247	FGF2	fibroblast growth factor 2 (basic)	0.58	1.73E-13	0.16	6.81E-02	-0.42	4.82E-06	0.01	9.05E-01	-0.01	9.29E-01	-0.01	8.56E-01	-0.05
1	204567_s_at	9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	0.37	4.49E-03	-0.01	9.50E-01	-0.38	1.83E-02	-0.16	1.10E-01	0.00	9.69E-01	0.16	1.63E-01	-0.15
1	204938_s_at	5350	PLN	phospholamban	0.23	1.38E-01	-0.17	3.67E-01	-0.39	3.96E-02	-0.15	2.17E-01	-0.14	2.76E-01	0.01	9.39E-01	-0.03
1	204948_s_at	10468	FST	follistatin	0.23	1.03E-02	0.33	2.94E-03	0.09	4.13E-01	0.00	9.91E-01	-0.07	3.59E-01	-0.07	4.18E-01	0.02
1	205003_at	9732	DOCK4	dedicator of cytokinesis 4	0.31	6.09E-03	0.08	5.46E-01	-0.23	9.92E-02	0.12	1.89E-01	-0.11	2.46E-01	-0.22	3.18E-02	-0.03
1	205525_at	800	CALD1	caldesmon 1	0.32	2.42E-09	0.04	5.54E-01	-0.28	1.14E-05	0.03	3.74E-01	-0.04	3.55E-01	-0.07	1.14E-01	-0.02
1	205700_at	8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	0.02	8.21E-01	-0.37	1.73E-04	-0.38	1.46E-04	0.01	8.81E-01	0.01	8.95E-01	0.00	9.93E-01	-0.02
1	205854_at	7289	TULP3	tubby like protein 3	0.33	9.68E-08	0.12	8.87E-02	-0.21	4.83E-03	0.11	1.69E-02	-0.02	6.71E-01	-0.13	1.60E-02	0.05
1	207016_s_at	8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	0.32	4.51E-04	0.06	5.84E-01	-0.26	1.95E-02	0.04	5.28E-01	0.04	6.28E-01	-0.01	9.18E-01	-0.06
1	207431_s_at	8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	0.33	6.06E-04	0.01	9.56E-01	-0.33	6.29E-03	-0.12	1.09E-01	-0.02	7.53E-01	0.09	2.77E-01	0.02
1	207738_s_at	10787	NCKAP1	NCK-associated protein 1	0.34	5.18E-05	-0.02	8.07E-01	-0.36	4.38E-04	0.06	3.13E-01	0.03	6.17E-01	-0.03	6.80E-01	0.08
1	208655_at		---	---	0.31	5.81E-06	0.07	3.85E-01	-0.24	3.72E-03	0.15	3.24E-03	0.11	4.26E-02	-0.04	4.74E-01	0.02
1	208683_at	824	CAPN2	calpain 2, (m/II) large subunit	0.31	9.60E-06	0.07	4.08E-01	-0.24	4.39E-03	0.11	3.32E-02	0.01	7.93E-01	-0.10	1.13E-01	-0.15
1	208694_at	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	0.37	2.32E-10	0.07	2.71E-01	-0.30	1.97E-05	0.11	8.92E-03	-0.02	7.34E-01	-0.13	1.15E-02	-0.03
1	209047_at	358	AQP1	aquaporin 1 (Colton blood group)	0.51	1.40E-04	0.10	5.17E-01	-0.41	1.27E-02	0.04	7.07E-01	0.06	5.55E-01	0.02	8.35E-01	0.04
1	209070_s_at	8490	RGS5	regulator of G-protein signaling 5	0.38	1.97E-02	0.10	6.09E-01	-0.28	1.62E-01	-0.10	4.33E-01	0.05	7.00E-01	0.15	3.12E-01	0.19
1	209120_at	7026	NR2F2	nuclear receptor subfamily 2, group F, member 2	0.44	2.55E-04	0.07	6.05E-01	-0.37	1.28E-02	-0.18	5.76E-02	-0.03	7.83E-01	0.15	1.69E-01	-0.03
1	209169_at	2824	GPM6B	glycoprotein M6B	0.30	2.21E-07	-0.06	3.67E-01	-0.37	5.02E-07	0.04	4.07E-01	-0.03	5.31E-01	-0.06	2.06E-01	0.01
1	209295_at	8795	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	0.31	1.46E-05	0.15	6.76E-02	-0.16	6.84E-02	0.01	8.57E-01	0.03	5.74E-01	0.02	7.26E-01	0.08
1	209297_at	6453	ITSN1	intersectin 1 (SH3 domain protein)	0.28	2.59E-04	-0.02	8.63E-01	-0.30	1.77E-03	0.01	8.79E-01	-0.01	9.17E-01	-0.02	8.24E-01	0.00
1	209386_at	4071	TM4SF1	transmembrane 4 L six family member 1	0.47	1.42E-04	0.22	1.38E-01	-0.26	8.93E-02	0.00	9.74E-01	0.10	2.92E-01	0.10	3.60E-01	0.00
1	209387_s_at	4071	TM4SF1	transmembrane 4 L six family member 1	0.71	2.21E-09	0.24	7.18E-02	-0.47	9.34E-04	-0.08	3.54E-01	0.11	2.43E-01	0.19	6.75E-02	-0.03
1	209684_at	54453	RIN2	Ras and Rab interactor 2	0.36	1.43E-03	0.18	1.66E-01	-0.18	2.03E-01	0.04	6.38E-01	0.06	5.40E-01	0.01	8.83E-01	0.14
1	210275_s_at	7763	ZFAND5	zinc finger, AN1-type domain 5	0.32	5.02E-04	0.36	9.29E-04	0.04	6.97E-01	0.10	1.34E-01	0.07	3.60E-01	-0.04	6.46E-01	-0.02
1	211559_s_at	901	CCNG2	cyclin G2	0.32	6.50E-04	0.22	4.59E-02	-0.10	3.88E-01	-0.11	1.34E-01	0.08	2.68E-01	0.19	2.43E-02	0.11
1	211748_x_at	5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	0.20	2.95E-01	-0.30	1.95E-01	-0.50	3.72E-02	0.22	1.38E-01	-0.06	6.80E-01	-0.29	1.03E-01	0.67
1	211922_s_at	847	CAT	catalase	0.07	6.06E-01	0.32	4.23E-02	0.25	1.21E-01	-0.05	6.04E-01	-0.08	4.26E-01	-0.03	7.87E-01	0.01
1	211959_at	3488	IGFBP5	insulin-like growth factor binding protein 5	0.55	3.41E-07	0.34	6.15E-03	-0.21	1.08E-01	0.09	2.82E-01	0.15	7.12E-02	0.07	4.81E-01	-0.01
1	211964_at	1284	COL4A2	collagen, type IV, alpha 2	0.28	1.40E-02	-0.09	5.28E-01	-0.37	9.84E-03	0.08	3.83E-01	0.12	2.12E-01	0.04	7.08E-01	0.05
1	211980_at	1282	COL4A1	collagen, type IV, alpha 1	0.34	8.39E-04	-0.04	7.64E-01	-0.37	2.81E-03	0.02	7.93E-01	0.10	2.25E-01	0.08	3.87E-01	-0.02
1	211981_at	1282	COL4A1	collagen, type IV, alpha 1	0.37	6.72E-03	0.27	9.32E-02	-0.10	5.59E-01	-0.07	4.93E-01	0.05	6.58E-01	0.12	3.27E-01	-0.08
1	212143_s_at	3486	IGFBP3	insulin-like growth factor binding protein 3	0.54	2.09E-08	0.16	1.53E-01	-0.38	9.20E-04	0.03	6.44E-01	-0.07	3.81E-01	-0.10	2.40E-01	-0.08
1	212160_at	11260	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	0.35	1.93E-06	0.17	5.33E-02	-0.19	3.64E-02	0.01	8.40E-01	0.07	2.22E-01	0.06	3.56E-01	-0.09
1	212192_at	115207	KCTD12	potassium channel tetramerisation domain containing 12	0.38	6.26E-04	0.06	6.52E-01	-0.32	1.85E-02	-0.03	7.12E-01	0.04	6.45E-01	0.07	4.68E-01	0.13
1	212224_at	216	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0.83	8.63E-06	0.32	1.41E-01	-0.51	2.38E-02	-0.07	6.30E-01	-0.09	5.54E-01	-0.02	9.04E-01	0.13
1	212230_at	8613	PPAP2B	phosphatidic acid phosphatase type 2B	0.35	3.31E-04	0.06	6.29E-01	-0.29	1.37E-02	-0.01	9.28E-01	0.03	7.36E-01	0.03	7.05E-01	-0.14
1	212344_at	23213	SULF1	sulfatase 1	0.26	1.12E-05	-0.12	8.93E-02	-0.37	3.71E-07	-0.01	8.31E-01	-0.03	5.09E-01	-0.02	6.82E-01	0.02
1	212538_at	23348	DOCK9	dedicator of cytokinesis 9	0.50	4.90E-05	0.15	2.85E-01	-0.35	2.09E-02	0.06	5.50E-01	0.01	9.09E-01	-0.04	6.84E-01	-0.14
1	212560_at	6653	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	0.18	1.88E-01	-0.53	1.52E-03	-0.71	4.85E-05	0.00	9.67E-01	-0.07	5.42E-01	-0.07	5.61E-01	0.20
1	212950_at	221395	GPR116	G protein-coupled receptor 116	0.46	4.98E-05	-0.01	9.51E-01	-0.47	7.88E-04	-0.01	9.38E-01	0.01	9.48E-01	0.01	9.01E-01	-0.05
1	212951_at	221395	GPR116	G protein-coupled receptor 116	0.51	5.95E-08	0.10	3.36E-01	-0.41	3.42E-04	0.04	6.08E-01	-0.04	6.00E-01	-0.07	3.66E-01	-0.03
1	213222_at	23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	0.40	1.04E-05	0.35	9.77E-04	-0.05	6.66E-01	-0.06	3.63E-01	0.07	3.06E-01	0.14	9.21E-02	0.05
1	213404_s_at	6009	RHEB	Ras homolog enriched in brain	0.26	7.89E-06	-0.06	3.85E-01	-0.32	9.98E-06	-0.03	5.05E-01	-0.02	6.24E-01	0.01	8.97E-01	-0.10
1	213415_at	1193	CLIC2	chloride intracellular channel 2	0.31	4.70E-05	0.22	1.52E-02	-0.09	3.14E-01	-0.05	3.76E-01	0.04	5.01E-01	0.09	1.76E-01	0.11
1	214853_s_at	6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	0.33	4.23E-07	0.05	5.13E-01	-0.28	3.88E-04	0.06	2.20E-01	0.04	3.95E-01	-0.02	7.76E-01	-0.02

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					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
1	215785_s_at	26999	CYFIP2	cytoplasmic FMR1 interacting protein 2	-0.12	3.13E-01	-0.50	7.82E-04	-0.38	1.39E-02	0.01	8.94E-01	0.01	9.51E-01	-0.01	9.53E-01	-0.23
1	217757_at	2	A2M	alpha-2-macroglobulin	0.50	2.49E-05	0.17	2.19E-01	-0.33	2.20E-02	0.06	4.71E-01	0.10	2.69E-01	0.04	7.06E-01	0.00
1	217894_at	51133	KCTD3	potassium channel tetramerisation domain containing 3	0.46	6.07E-10	0.08	3.39E-01	-0.38	2.01E-05	-0.07	2.24E-01	0.03	5.56E-01	0.10	1.19E-01	-0.01
1	217966_s_at	116496	FAM129A	family with sequence similarity 129, member A	0.11	3.66E-01	0.14	3.49E-01	0.03	8.62E-01	0.25	1.29E-02	0.21	3.85E-02	-0.03	7.85E-01	-0.12
1	217967_s_at	116496	FAM129A	family with sequence similarity 129, member A	0.45	5.21E-04	0.22	1.49E-01	-0.23	1.47E-01	0.10	3.14E-01	0.20	5.30E-02	0.10	3.78E-01	-0.15
1	218236_s_at	23683	PRKD3	protein kinase D3	0.32	7.85E-06	0.14	9.05E-02	-0.18	3.86E-02	-0.09	9.99E-02	-0.05	3.60E-01	0.04	5.58E-01	0.01
1	218764_at	5583	PRKCH	protein kinase C, eta	0.16	1.54E-01	-0.09	4.77E-01	-0.25	6.72E-02	-0.04	6.73E-01	0.11	2.09E-01	0.15	1.39E-01	-0.34
1	219825_at	56603	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	0.81	2.15E-14	-0.03	7.93E-01	-0.84	5.39E-11	-0.07	3.47E-01	-0.03	7.21E-01	0.04	6.30E-01	-0.04
1	220170_at	9457	FHL5	four and a half LIM domains 5	0.44	7.59E-06	0.00	9.91E-01	-0.44	2.53E-04	-0.04	5.94E-01	-0.01	8.97E-01	0.03	7.35E-01	-0.03
1	221087_s_at	80833	APOL3	apolipoprotein L, 3	0.16	6.29E-02	0.09	3.77E-01	-0.07	5.13E-01	0.03	6.40E-01	0.04	6.12E-01	0.00	9.56E-01	-0.20
1	222453_at	79901	CYBRD1	cytochrome b reductase 1	0.31	9.35E-03	0.36	1.27E-02	0.05	7.58E-01	0.02	8.23E-01	0.02	8.12E-01	0.00	9.83E-01	0.20
1	222484_s_at	9547	CXCL14	chemokine (C-X-C motif) ligand 14	0.34	4.08E-03	0.11	4.37E-01	-0.23	1.12E-01	0.19	3.46E-02	0.18	6.39E-02	-0.02	8.85E-01	-0.05
1	223077_at	29766	TMOD3	tropomodulin 3 (ubiquitous)	0.49	1.30E-10	0.20	1.78E-02	-0.29	1.43E-03	-0.11	5.28E-02	0.02	6.98E-01	0.13	4.62E-02	-0.07
1	223449_at	57556	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	0.37	1.58E-08	0.14	5.98E-02	-0.23	3.33E-03	0.00	9.44E-01	0.03	5.75E-01	0.03	5.75E-01	-0.04
1	224817_at	9644	SH3PXD2A	SH3 and PX domains 2A	0.36	3.18E-10	0.19	3.61E-03	-0.17	1.11E-02	0.06	1.65E-01	0.04	4.07E-01	-0.02	6.59E-01	-0.07
1	224894_at	10413	YAP1	Yes-associated protein 1, 65kDa	0.42	5.31E-06	0.13	2.34E-01	-0.29	8.89E-03	-0.10	1.60E-01	0.06	4.33E-01	0.15	5.85E-02	-0.07
1	225079_at	2013	EMP2	epithelial membrane protein 2	0.51	3.56E-09	0.12	2.29E-01	-0.39	1.52E-04	-0.12	5.62E-02	-0.02	7.69E-01	0.10	1.71E-01	-0.04
1	225720_at	171024	SYNPO2	synaptopodin 2	0.21	9.63E-02	-0.14	3.66E-01	-0.35	2.77E-02	-0.12	2.41E-01	-0.04	7.06E-01	0.08	5.08E-01	-0.08
1	225721_at	171024	SYNPO2	synaptopodin 2	0.19	1.29E-01	-0.14	3.65E-01	-0.33	3.67E-02	-0.16	1.08E-01	-0.07	4.73E-01	0.08	4.64E-01	0.13
1	226022_at	23328	SASH1	SAM and SH3 domain containing 1	0.49	4.61E-04	0.22	1.87E-01	-0.28	1.10E-01	0.02	8.45E-01	0.09	4.41E-01	0.07	6.01E-01	0.31
1	226302_at	5205	ATP8B1	ATPase, class I, type 8B, member 1	0.48	6.59E-07	-0.01	9.61E-01	-0.49	3.99E-05	-0.02	7.69E-01	0.04	5.70E-01	0.06	4.48E-01	-0.02
1	226420_at	2122	EVI1	ecotropic viral integration site 1	0.40	9.01E-06	0.22	3.77E-02	-0.18	9.47E-02	-0.04	5.60E-01	0.03	6.81E-01	0.07	3.88E-01	0.01
1	226685_at	6645	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	0.35	1.14E-04	0.07	5.32E-01	-0.28	1.06E-02	-0.13	5.24E-02	-0.12	9.64E-02	0.01	8.67E-01	-0.10
1	227095_at		---	---	0.28	3.76E-03	-0.02	8.30E-01	-0.30	1.08E-02	-0.03	7.31E-01	-0.04	5.93E-01	-0.02	8.52E-01	0.15
1	227758_at	85004	RERG	RAS-like, estrogen-regulated, growth inhibitor	0.31	8.16E-05	0.04	6.72E-01	-0.27	4.90E-03	0.03	6.05E-01	-0.01	9.30E-01	-0.04	6.03E-01	0.01
1	227870_at	57722	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	0.31	8.65E-03	0.35	1.31E-02	0.04	7.82E-01	0.09	3.11E-01	-0.03	7.23E-01	-0.13	2.39E-01	-0.07
1	228202_at	5350	PLN	Phospholamban, mRNA (cDNA clone MGC:12311 IMAGE:3934199)	0.42	1.64E-02	-0.16	4.46E-01	-0.57	7.87E-03	-0.13	3.16E-01	-0.08	5.59E-01	0.05	7.39E-01	-0.03
1	228434_at	153579	BTNL9	butyrophilin-like 9	0.32	1.03E-02	-0.05	7.55E-01	-0.37	1.78E-02	-0.01	9.35E-01	-0.03	7.63E-01	-0.02	8.41E-01	-0.11
1	230250_at	5787	PTPRB	protein tyrosine phosphatase, receptor type, B	0.30	7.68E-03	-0.04	7.91E-01	-0.34	1.61E-02	0.00	9.72E-01	-0.08	3.87E-01	-0.08	4.21E-01	-0.05
1	233734_s_at	114879	OSBPL5	oxysterol binding protein-like 5	0.22	1.02E-05	-0.15	8.31E-03	-0.37	3.62E-09	0.00	9.27E-01	0.01	7.78E-01	0.01	8.62E-01	0.09
1	238066_at	116362	RBP7	retinol binding protein 7, cellular	0.39	7.72E-03	-0.18	2.91E-01	-0.57	1.67E-03	-0.01	9.21E-01	0.14	2.42E-01	0.15	2.58E-01	0.25
1	37512_at	8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	0.03	6.65E-01	-0.34	5.72E-04	-0.37	2.57E-04	0.00	9.39E-01	0.01	8.93E-01	0.01	8.53E-01	-0.04
1	41644_at	23328	SASH1	SAM and SH3 domain containing 1	0.38	2.76E-05	0.28	7.42E-03	-0.09	3.87E-01	0.07	3.02E-01	0.05	4.93E-01	-0.02	7.89E-01	0.10
2	1552584_at	3594	IL12RB1	interleukin 12 receptor, beta 1	-0.11	1.39E-01	0.09	3.00E-01	0.20	2.91E-02	0.03	6.16E-01	-0.03	6.30E-01	-0.06	3.92E-01	-0.23
2	1554240_a_at	3683	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	-0.15	5.15E-02	0.06	5.19E-01	0.22	2.89E-02	-0.03	5.98E-01	-0.05	4.85E-01	-0.01	8.61E-01	-0.28
2	200675_at	975	CD81	CD81 molecule	0.22	1.43E-02	0.03	8.07E-01	-0.20	8.02E-02	0.10	1.40E-01	0.06	4.48E-01	-0.05	5.61E-01	-0.27
2	201301_s_at	307	ANXA4	annexin A4	0.20	5.24E-02	0.32	9.53E-03	0.12	3.41E-01	-0.07	3.51E-01	0.14	9.04E-02	0.21	2.16E-02	-0.17
2	201761_at	10797	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	0.33	5.12E-03	0.30	3.40E-02	-0.03	8.21E-01	0.03	7.38E-01	0.15	1.13E-01	0.12	2.56E-01	-0.18
2	201963_at	2180	ACSL1	acyl-CoA synthetase long-chain family member 1	0.18	1.49E-01	0.06	6.67E-01	-0.11	4.53E-01	-0.10	2.83E-01	-0.15	1.26E-01	-0.05	6.48E-01	-0.27
2	202073_at	10133	OPTN	optineurin	0.06	5.41E-01	0.14	2.70E-01	0.07	5.68E-01	0.09	2.84E-01	-0.01	9.00E-01	-0.10	3.06E-01	-0.26
2	202074_s_at	10133	OPTN	optineurin	-0.20	3.52E-02	0.00	9.69E-01	0.21	8.19E-02	0.06	4.03E-01	0.02	8.13E-01	-0.04	6.17E-01	-0.42
2	202345_s_at		FABP5 /// FABP5L2 /// FABP5L7	fatty acid binding protein 5 (psoriasis-associated) /// fatty acid binding protein 5-like 2 /// fatty acid binding protein 5-like 7	0.16	1.79E-01	-0.11	4.12E-01	-0.27	6.18E-02	-0.16	7.41E-02	0.01	9.09E-01	0.17	1.04E-01	-0.33
2	202422_s_at	2182	ACSL4	acyl-CoA synthetase long-chain family member 4	0.25	6.27E-03	-0.12	2.66E-01	-0.37	1.16E-03	-0.08	2.56E-01	0.13	9.16E-02	0.21	1.39E-02	-0.11
2	202430_s_at	5359	PLSCR1	phospholipid scramblase 1	0.00	9.92E-01	0.13	4.02E-01	0.13	4.15E-01	-0.22	3.02E-02	0.05	6.62E-01	0.27	2.56E-02	-0.28
2	202688_at	8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	0.30	1.83E-02	0.43	4.44E-03	0.13	3.90E-01	-0.21	3.05E-02	0.19	6.10E-02	0.40	5.14E-04	-0.38
2	202705_at	9133	CCNB2	cyclin B2	0.07	4.01E-01	0.01	9.33E-01	-0.06	5.51E-01	0.03	6.00E-01	0.00	9.43E-01	-0.03	7.02E-01	-0.08
2	202761_s_at	23224	SYNE2	spectrin repeat containing, nuclear envelope 2	0.01	9.33E-01	0.11	4.31E-01	0.10	4.89E-01	-0.05	5.93E-01	-0.06	5.31E-01	-0.01	9.16E-01	-0.41
2	202763_at	836	CASP3	caspase 3, apoptosis-related cysteine peptidase	0.07	2.31E-01	0.03	7.23E-01	-0.05	5.31E-01	-0.04	4.06E-01	0.08	1.16E-01	0.11	3.52E-02	-0.26
2	202912_at	133	ADM	adrenomedullin	-0.14	3.41E-01	0.17	3.52E-01	0.31	9.68E-02	0.00	9.81E-01	0.07	5.81E-01	0.06	6.36E-01	-0.44
2	203213_at	983	CDC2	cell division cycle 2, G1 to S and G2 to M	0.14	1.34E-01	0.12	2.79E-01	-0.02	8.68E-01	0.01	8.91E-01	0.01	8.46E-01	0.00	9.55E-01	-0.12
2	204170_s_at	1164	CKS2	CDC28 protein kinase regulatory subunit 2	0.01	9.57E-01	0.14	2.39E-01	0.14	2.74E-01	-0.06	4.54E-01	0.02	7.93E-01	0.08	3.83E-01	-0.27
2	204562_at	3662	IRF4	interferon regulatory factor 4	-0.02	8.00E-01	0.00	9.85E-01	0.02	8.24E-01	0.01	8.33E-01	-0.01	9.01E-01	-0.02	7.71E-01	-0.36
2	204613_at	5336	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	0.16	4.17E-02	0.00	9.80E-01	-0.15	1.05E-01	-0.02	6.99E-01	0.01	8.81E-01	0.03	6.43E-01	-0.27
2	204781_s_at	355	FAS	Fas (TNF receptor superfamily, member 6)	-0.03	7.06E-01	0.04	6.88E-01	0.08	4.90E-01	0.05	5.01E-01	0.11	1.22E-01	0.07	4.16E-01	-0.33
2	204858_s_at	1890	TYMP	thymidine phosphorylase	-0.17	2.11E-01	-0.05	7.77E-01	0.13	4.62E-01	0.02	8.40E-01	-0.03	8.09E-01	-0.05	6.98E-01	-0.37
2	205099_s_at	1230	CCR1	chemokine (C-C motif) receptor 1	-0.06	6.21E-01	0.07	6.37E-01	0.13	3.94E-01	0.08	3.79E-01	-0.01	9.24E-01	-0.09	4.05E-01	-0.09
2	205241_at	9997	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	-0.27	2.72E-02	-0.03	8.62E-01	0.24	1.05E-01	0.04	6.93E-01	0.01	9.37E-01	-0.03	7.91E-01	-0.42
2	205568_at	366	AQP9	aquaporin 9	0.11	4.25E-01	-0.07	6.95E-01	-0.18	3.08E-01	-0.01	8.91E-01	-0.01	9.58E-01	0.01	9.45E-01	-0.35
2	205590_at	10125	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	-0.33	1.38E-03	0.11	3.44E-01	0.44	5.24E-04	-0.06	4.45E-01	0.06	4.66E-01	0.12	1.93E-01	-0.18
2	205768_s_at	11001	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	-0.05	3.85E-01	-0.02	7.81E-01	0.03	6.65E-01	0.02	6.89E-01	0.00	9.74E-01	-0.02	7.11E-01	-0.18
2	205769_at	11001	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	0.04	5.14E-01	0.02	7.89E-01	-0.02	7.89E-01	0.04	4.10E-01	0.02	6.18E-01	-0.01	7.98E-01	-0.26
2	205801_s_at	25780	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	0.07	3.98E-01	0.12	1.99E-01	0.06	5.75E-01	0.02	7.66E-01	0.01	9.31E-01	-0.01	8.61E-01	-0.33
2	205831_at	914	CD2	CD2 molecule	-0.28	9.92E-04	0.05	6.40E-01	0.33	1.90E-03	-0.09	1.68E-01	-0.03	7.02E-01	0.06	4.04E-01	-0.21
2	205842_s_at	3717	JAK2	Janus kinase 2 (a protein tyrosine kinase)	-0.08	3.81E-01	0.06	5.52E-01	0.14	2.01E-01	-0.10	1.51E-01	-0.08	2.61E-01	0.02	8.26E-01	-0.28
2	205988_at	8832	CD84	CD84 molecule	-0.01	8.75E-01	0.06	4.55E-01	0.07	3.97E-01	0.05	3.13E-01	-0.02	6.58E-01	-0.07	2.10E-01	-0.19
2	205992_s_at	3600	IL15	interleukin 15	0.06	5.71E-01	0.09	4.57E-01	0.03	7.94E-01	-0.13	9.48E-02	0.11	1.97E-01	0.24	1.05E-02	-0.14
2	206515_at	4051	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	0.06	6.18E-01	-0.05	7.36E-01	-0.11	4.68E-01	-0.01	8.74E-01	-0.02	8.28E-01	-0.01	9.53E-01	-0.32
2	206991_s_at		CCR5 /// LOC727797	chemokine (C-C motif) receptor 5 /// C-C chemokine receptor type 5-like	-0.25	2.85E-02	-0.01	9.66E-01	0.24	8.37E-02	-0.06	4.90E-01	0.02	8.44E-01	0.08	4.45E-01	-0.51
2	207008_at	3579	IL8RB	interleukin 8 receptor, beta	0.13	4.95E-01	-0.11	6.12E-01	-0.24	2.99E-01	-0.05	7.13E-01	-0.06	7.11E-01	0.00	9.86E-01	-0.51
2	207181_s_at	840	CASP7	caspase 7, apoptosis-related cysteine peptidase	0.27	4.67E-04	0.20	2.92E-02	-0.07	4.48E-01	-0.14	1.71E-02	0.15	1.61E-02	0.29	4.01E-05	-0.20
2	207275_s_at	2180	ACSL1	acyl-CoA synthetase long-chain family member 1	0.10	5.57E-01	0.19	3.64E-01	0.09	6.87E-01	-0.16	2.26E-01	-0.15	3.03E-01	0.02	9.11E-01	-0.35
2	207536_s_at	3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	-0.02	7.12E-01	0.03	6.66E-01	0.04	4.76E-01	0.01	7.44E-01	-0.01	7.26E-01	-0.03	5.54E-01	-0.23
2	207614_s_at	8454	CUL1	cullin 1	0.03	5.96E-01	0.07	2.76E-01	0.04	5.32E-01	-0.07	8.68E-02	-0.01	8.94E-01	0.07	1.80E-01	-0.29
2	207681_at	2833	CXCR3	chemokine (C-X-C motif) receptor 3	-0.08	2.27E-01	-0.01	9.27E-01	0.08	3.76E-01	-0.02	7.43E-01	-0.01	8.63E-01	0.01	9.01E-01	-0.30

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
2	207907_at	8740	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	0.10	1.02E-01	0.05	4.80E-01	-0.05	5.21E-01	-0.01	8.76E-01	0.03	5.59E-01	0.04	5.12E-01	-0.25
2	208002_s_at	11332	ACOT7	acyl-CoA thioesterase 7	0.04	5.10E-01	0.02	8.09E-01	-0.02	7.66E-01	0.00	9.70E-01	-0.02	6.90E-01	-0.02	6.97E-01	-0.20
2	209091_s_at	51100	SH3GLB1	SH3-domain GRB2-like endophilin B1	0.12	1.47E-01	0.14	1.50E-01	0.02	8.24E-01	-0.08	1.98E-01	-0.01	8.31E-01	0.07	3.64E-01	-0.17
2	209197_at	23208	SYT11	synaptotagmin XI	0.08	2.52E-01	-0.01	8.86E-01	-0.09	2.88E-01	-0.01	8.26E-01	0.01	8.74E-01	0.02	7.42E-01	-0.25
2	209369_at	306	ANXA3	annexin A3	0.23	2.68E-01	-0.41	1.04E-01	-0.65	1.45E-02	-0.05	7.68E-01	-0.13	4.46E-01	-0.08	6.66E-01	-0.17
2	209593_s_at	27348	TOR1B	torsin family 1, member B (torsin B)	0.01	8.91E-01	0.02	8.19E-01	0.01	9.12E-01	-0.08	1.35E-01	-0.01	8.12E-01	0.07	2.89E-01	-0.29
2	209770_at	11119	BTN3A1	butyrophilin, subfamily 3, member A1	-0.03	7.75E-01	0.15	1.67E-01	0.18	1.19E-01	-0.11	1.15E-01	0.04	5.71E-01	0.16	6.55E-02	-0.34
2	210354_at	3458	IFNG	interferon, gamma	-0.16	7.76E-02	0.05	6.60E-01	0.21	6.51E-02	-0.04	5.91E-01	0.00	9.48E-01	0.03	6.90E-01	-0.50
2	212048_s_at	8565	YARS	tyrosyl-tRNA synthetase	0.00	9.43E-01	0.11	1.05E-01	0.12	1.05E-01	0.13	5.80E-03	0.06	1.94E-01	-0.06	2.27E-01	-0.20
2	212203_x_at	10410	IFITM3	interferon induced transmembrane protein 3 (1-8U)	-0.11	3.23E-01	0.18	1.75E-01	0.30	3.62E-02	-0.32	3.45E-04	0.12	1.96E-01	0.44	3.28E-05	-0.32
2	212657_s_at	3557	IL1RN	interleukin 1 receptor antagonist	0.25	6.63E-02	0.17	2.90E-01	-0.08	6.41E-01	0.04	6.84E-01	-0.02	8.40E-01	-0.06	5.98E-01	-0.13
2	212845_at	23034	SAMD4A	sterile alpha motif domain containing 4A	0.20	5.13E-02	0.17	1.63E-01	-0.03	8.17E-01	0.11	1.62E-01	-0.02	8.33E-01	-0.13	1.68E-01	-0.25
2	213787_s_at	10682	EBP	emopamil binding protein (sterol isomerase)	-0.08	3.06E-01	-0.01	9.36E-01	0.07	4.55E-01	-0.04	5.05E-01	-0.03	6.02E-01	0.01	9.19E-01	-0.18
2	216565_x_at		---	---	-0.14	1.54E-01	0.16	1.74E-01	0.30	1.45E-02	-0.20	9.33E-03	0.08	3.20E-01	0.28	2.06E-03	-0.26
2	217677_at	59339	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	0.08	1.58E-01	0.00	9.48E-01	-0.08	2.82E-01	-0.03	4.90E-01	-0.02	6.36E-01	0.01	8.69E-01	-0.33
2	217738_at	10135	NAMPT	nicotinamide phosphoribosyltransferase	0.24	9.00E-02	0.22	2.03E-01	-0.03	8.87E-01	0.06	5.84E-01	0.13	2.62E-01	0.07	5.89E-01	-0.28
2	218085_at	51510	CHMP5	chromatin modifying protein 5	0.08	3.16E-01	0.05	5.73E-01	-0.03	7.90E-01	-0.03	6.01E-01	0.01	8.88E-01	0.04	5.68E-01	-0.30
2	218254_s_at	51128	SAR1B	SAR1 homolog B (S. cerevisiae)	-0.06	4.54E-01	-0.08	4.37E-01	-0.02	8.84E-01	-0.01	9.32E-01	0.01	9.03E-01	0.01	8.56E-01	-0.17
2	218397_at	55120	FANCL	Fanconi anemia, complementation group L	0.22	9.20E-03	0.06	5.34E-01	-0.16	1.29E-01	-0.06	3.59E-01	-0.03	6.90E-01	0.03	6.71E-01	-0.31
2	219073_s_at	114884	OSBPL10	oxysterol binding protein-like 10	0.28	1.42E-02	0.07	6.31E-01	-0.22	1.27E-01	-0.09	3.23E-01	0.00	9.96E-01	0.09	4.02E-01	-0.29
2	219356_s_at	51510	CHMP5	chromatin modifying protein 5	0.13	5.87E-02	0.08	3.70E-01	-0.06	5.05E-01	-0.07	1.78E-01	0.04	5.36E-01	0.11	8.96E-02	-0.30
2	222154_s_at	26010	LOC26010	viral DNA polymerase-transactivated protein 6	0.12	3.24E-01	0.00	9.76E-01	-0.11	4.44E-01	0.08	3.79E-01	0.18	6.97E-02	0.10	3.78E-01	-0.46
2	223502_s_at	10673	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	-0.21	1.07E-01	0.17	2.60E-01	0.38	1.76E-02	-0.19	5.13E-02	-0.09	3.76E-01	0.10	3.82E-01	-0.13
2	225663_at	91452	ACBD5	acyl-Coenzyme A binding domain containing 5	0.06	3.01E-01	0.05	5.40E-01	-0.02	8.07E-01	0.00	9.37E-01	0.04	4.17E-01	0.05	4.27E-01	-0.23
2	230464_at	53637	S1PR5	sphingosine-1-phosphate receptor 5	-0.11	3.69E-01	-0.02	8.77E-01	0.09	5.65E-01	-0.01	9.16E-01	0.01	8.88E-01	0.02	8.29E-01	-0.23
2	231769_at	26270	FBXO6	F-box protein 6	-0.14	1.68E-01	-0.08	5.12E-01	0.06	6.30E-01	-0.11	1.60E-01	-0.05	5.25E-01	0.06	5.28E-01	-0.38
2	232629_at	60675	PROK2	prokineticin 2	-0.01	9.36E-01	0.04	8.46E-01	0.05	8.01E-01	-0.01	9.40E-01	-0.03	8.35E-01	-0.02	9.02E-01	-0.48
2	238327_at	440836	ODF3B	outer dense fiber of sperm tails 3B	-0.28	1.04E-02	0.13	2.92E-01	0.41	2.21E-03	0.03	7.20E-01	-0.07	4.39E-01	-0.10	3.19E-01	-0.10
2	238600_at	152789	JAKMIP1	janus kinase and microtubule interacting protein 1	-0.23	9.68E-03	0.04	6.91E-01	0.27	1.36E-02	-0.08	2.54E-01	0.01	9.04E-01	0.09	2.80E-01	-0.29
2	241869_at	80830	APOL6	apolipoprotein L, 6	0.40	2.06E-03	0.05	7.32E-01	-0.35	2.96E-02	-0.02	8.11E-01	0.02	8.17E-01	0.05	6.82E-01	-0.42
2	241916_at		---	---	-0.01	8.31E-01	0.29	6.80E-04	0.30	5.74E-04	-0.03	6.43E-01	0.00	9.95E-01	0.02	6.97E-01	-0.08
2	242234_at	54739	XAF1	XIAP associated factor 1	-0.24	3.05E-02	0.14	3.12E-01	0.38	6.91E-03	-0.03	7.16E-01	-0.09	3.35E-01	-0.06	5.80E-01	-0.28
2	244261_at	163702	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	0.02	8.29E-01	-0.02	8.32E-01	-0.04	7.05E-01	0.12	8.36E-02	0.02	8.25E-01	-0.11	2.01E-01	-0.38
2	AFFX-HUMISGF3A/M97935_5_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.13	1.16E-01	-0.01	9.05E-01	0.12	2.48E-01	-0.14	2.53E-02	0.00	9.61E-01	0.15	5.10E-02	-0.11
3	200657_at	292	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	0.14	5.27E-02	-0.17	4.92E-02	-0.31	6.36E-04	-0.07	2.01E-01	0.01	8.92E-01	0.08	2.26E-01	0.04
3	200862_at	1718	DHCR24	24-dehydrocholesterol reductase	-0.10	5.11E-01	-0.13	4.50E-01	-0.04	8.43E-01	0.18	1.22E-01	-0.13	2.74E-01	-0.31	2.24E-02	-0.26
3	201128_s_at	47	ACLY	ATP citrate lyase	0.12	4.30E-01	-0.64	8.08E-04	-0.77	1.26E-04	-0.01	9.08E-01	-0.09	4.88E-01	-0.07	6.02E-01	-0.14
3	201489_at	10105	PPIF	peptidylprolyl isomerase F	-0.14	2.22E-01	-0.33	1.96E-02	-0.19	2.01E-01	0.00	9.79E-01	-0.06	5.21E-01	-0.06	5.51E-01	0.07
3	202022_at	230	ALDOC	aldolase C, fructose-bisphosphate	-0.46	3.31E-04	-0.31	3.92E-02	0.15	3.41E-01	0.07	4.98E-01	-0.02	8.71E-01	-0.08	4.70E-01	-0.02
3	202068_s_at	3949	LDLR	low density lipoprotein receptor	-0.03	8.32E-01	0.00	9.79E-01	0.03	8.84E-01	0.03	7.93E-01	0.03	7.80E-01	0.00	9.79E-01	-0.39
3	202884_s_at	5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	0.25	6.47E-02	-0.19	2.50E-01	-0.44	9.84E-03	0.00	9.99E-01	-0.01	9.05E-01	-0.01	9.14E-01	-0.06
3	203945_at	384	ARG2	arginase, type II	0.21	1.10E-02	-0.11	2.57E-01	-0.32	1.82E-03	0.06	3.57E-01	-0.05	4.19E-01	-0.11	1.33E-01	-0.02
3	204348_s_at		AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	0.08	4.28E-01	-0.32	4.85E-03	-0.40	8.65E-04	0.05	4.57E-01	0.00	9.98E-01	-0.05	5.28E-01	0.08
3	204663_at	10873	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	0.29	1.59E-06	-0.16	1.97E-02	-0.45	2.94E-09	0.03	4.47E-01	0.00	9.45E-01	-0.04	4.78E-01	-0.01
3	205108_s_at	338	APOB	apolipoprotein B (including Ag(x) antigen)	0.00	9.70E-01	-0.75	2.41E-09	-0.75	6.52E-09	-0.01	8.58E-01	0.00	9.94E-01	0.01	8.74E-01	-0.02
3	205334_at	6271	S100A1	S100 calcium binding protein A1	-0.16	2.50E-01	-0.64	1.78E-04	-0.48	6.23E-03	0.21	4.88E-02	-0.01	9.36E-01	-0.22	8.00E-02	0.00
3	206012_at	7044	LEFTY2	left-right determination factor 2	0.00	9.75E-01	-0.32	6.56E-08	-0.32	1.95E-07	0.03	3.46E-01	-0.04	3.62E-01	-0.07	1.07E-01	0.03
3	206210_s_at	1071	CETP	cholesteryl ester transfer protein, plasma	0.27	8.32E-03	-0.24	4.84E-02	-0.50	7.35E-05	-0.05	5.27E-01	-0.04	6.53E-01	0.01	8.91E-01	0.06
3	207096_at	6291	SAA4	serum amyloid A4, constitutive	-0.18	1.87E-01	-0.79	3.52E-06	-0.61	4.73E-04	-0.02	8.64E-01	0.02	8.25E-01	0.04	7.31E-01	0.00
3	208607_s_at		SAA1 /// SAA2	serum amyloid A1 /// serum amyloid A2	-0.99	1.78E-03	-1.62	2.23E-05	-0.64	1.00E-01	-0.14	5.51E-01	0.11	6.73E-01	0.25	3.76E-01	0.04
3	209146_at	6307	SC4MOL	sterol-C4-methyl oxidase-like	-0.08	4.81E-01	-0.18	1.56E-01	-0.11	4.23E-01	-0.01	8.93E-01	0.08	3.85E-01	0.09	3.72E-01	-0.33
3	209496_at	5919	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	-0.44	3.03E-04	-0.49	7.29E-04	-0.05	7.31E-01	-0.02	8.64E-01	-0.03	7.64E-01	-0.01	9.02E-01	0.03
3	209605_at	7263	TST	thiosulfate sulfurtransferase (rhodanese)	-0.32	5.91E-03	-0.15	2.85E-01	0.17	2.26E-01	-0.06	5.18E-01	-0.14	1.40E-01	-0.08	4.40E-01	0.22
3	210337_s_at	47	ACLY	ATP citrate lyase	0.02	9.09E-01	-0.38	3.95E-02	-0.40	3.78E-02	-0.05	6.51E-01	-0.05	7.18E-01	0.01	9.50E-01	-0.15
3	210512_s_at	7422	VEGFA	vascular endothelial growth factor A	0.23	6.75E-02	-0.15	3.20E-01	-0.37	1.55E-02	0.00	9.93E-01	-0.02	8.67E-01	-0.02	8.75E-01	0.12
3	210949_s_at		EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	0.11	3.04E-01	-0.31	1.81E-02	-0.42	2.05E-03	0.02	8.53E-01	-0.12	1.87E-01	-0.13	1.81E-01	0.05
3	211423_s_at	6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	-0.08	4.01E-01	-0.40	2.48E-04	-0.33	3.80E-03	0.02	8.03E-01	0.03	6.85E-01	0.01	8.81E-01	-0.08
3	211708_s_at	6319	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	-0.01	9.72E-01	-0.86	9.02E-03	-0.85	1.27E-02	-0.04	8.64E-01	-0.02	9.32E-01	0.02	9.45E-01	0.00
3	212274_at	23175	LPIN1	lipin 1	0.04	7.50E-01	-0.29	3.60E-02	-0.32	2.30E-02	0.07	4.56E-01	-0.03	7.34E-01	-0.10	3.48E-01	-0.15
3	218434_s_at	65985	AACS	acetoacetyl-CoA synthetase	-0.06	7.30E-01	-0.44	3.67E-02	-0.38	8.15E-02	0.07	5.90E-01	0.02	8.99E-01	-0.06	7.29E-01	-0.05
3	218856_at	27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.20	1.29E-01	-0.12	4.34E-01	-0.32	4.85E-02	0.10	3.40E-01	0.03	7.72E-01	-0.06	5.79E-01	0.17
3	222011_s_at	6950	TCP1	t-complex 1	0.24	1.79E-03	-0.12	1.67E-01	-0.36	1.42E-04	-0.07	2.13E-01	-0.01	9.05E-01	0.07	3.40E-01	-0.13
3	222351_at	5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	0.07	6.62E-01	-0.49	1.57E-02	-0.56	7.53E-03	0.03	8.10E-01	0.05	7.18E-01	0.02	9.05E-01	0.01
3	223839_s_at		SCD /// SCDOS	stearoyl-CoA desaturase (delta-9-desaturase) /// stearoyl-CoA desaturase opposite strand	0.80	3.49E-04	-0.33	2.07E-01	-1.13	5.02E-05	-0.05	7.49E-01	0.00	1.00E+00	0.05	7.85E-01	-0.17
3	224650_at	114569	MAL2	mal, T-cell differentiation protein 2	-0.08	5.22E-01	-0.36	1.95E-02	-0.28	8.08E-02	-0.02	8.79E-01	0.00	9.78E-01	0.01	9.16E-01	0.00
3	224812_at	11112	HIBADH	3-hydroxyisobutyrate dehydrogenase	-0.05	4.61E-01	-0.32	4.36E-05	-0.28	6.94E-04	-0.02	6.18E-01	-0.02	6.79E-01	0.00	9.57E-01	0.10
3	228309_at		---	---	0.37	3.52E-05	0.00	9.73E-01	-0.37	6.77E-04	0.10	1.53E-01	0.01	9.14E-01	-0.09	2.63E-01	-0.04
3	234312_s_at	55902	ACSS2	acyl-CoA synthetase short-chain family member 2	-0.06	5.87E-01	-0.41	1.96E-03	-0.35	1.02E-02	0.00	9.96E-01	-0.11	2.19E-01	-0.11	2.69E-01	0.12
4	1553575_at	4541	ND6	NADH dehydrogenase, subunit 6 (complex I)	0.37	5.02E-02	0.08	7.34E-01	-0.29	2.08E-01	0.37	1.29E-02	-0.14	3.56E-01	-0.51	3.45E-03	0.30
4	1566342_at	6648	SOD2	CDNA clone IMAGE:5301545	0.57	1.25E-03	0.03	8.72E-01	-0.54	1.37E-02	0.35	1.03E-02	-0.01	9.36E-01	-0.36	2.39E-02	-0.05
4	208844_at	7419	VDAC3	voltage-dependent anion channel 3	0.22	1.11E-01	0.11	5.17E-01	-0.11	5.06E-01	0.18	9.31E-02	-0.12	2.71E-01	-0.30	1.64E-02	-0.05
4	213655_at		---	---	-0.09	5.03E-01	0.13	4.12E-01	0.23	1.84E-01	0.32	2.58E-03	-0.02	8.90E-01	-0.34	7.01E-03	0.06
4	213736_at	1329	COX5B	Cytochrome c oxidase subunit Vb, mRNA (cDNA clone MGC:10622 IMAGE:3952882)	0.10	3.23E-01	-0.16	2.01E-01	-0.26	4.32E-02	0.34	2.52E-05	-0.03	6.82E-01	-0.38	7.61E-05	0.00
4	216246_at		---	---	0.17	7.99E-02	-0.01	9.47E-01	-0.17	1.39E-01	0.35	3.27E-06	-0.02	8.35E-01	-0.37	3.05E-05	0.04
4	217383_at	5230	PGK1	MRNA encoding phosphoglycerate kinase	0.39	3.88E-02	0.10	6.64E-01	-0.29	2.09E-01	0.38	9.30E-03	0.16	3.06E-01	-0.22	1.88E-01	-0.12
4	222027_at	64710	NUCKS1	CDNA clone IMAGE:4513453	0.24	1.20E-01	0.21	2.66E-01	-0.04	8.55E-01	0.36	3.28E-03	-0.15	2.48E-01	-0.51	4.58E-04	0.10

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
4	228435_at		---	---	-0.25	2.01E-02	0.02	8.65E-01	0.27	4.13E-02	0.52	2.42E-09	-0.25	4.75E-03	-0.77	3.40E-13	-0.06
4	228634_s_at	8531	CSDA	DNA-binding protein A (dbpA) gene, 3' end	0.15	2.42E-01	0.17	2.63E-01	0.02	8.91E-01	0.45	1.34E-05	-0.06	5.97E-01	-0.50	2.99E-05	-0.02
4	MTCYB_at				0.48	2.17E-02	-0.05	8.43E-01	-0.53	4.10E-02	0.62	1.44E-04	-0.09	5.99E-01	-0.71	2.16E-04	0.12
4	MTND6_at				0.43	3.88E-02	0.09	7.26E-01	-0.35	1.81E-01	0.32	4.68E-02	-0.13	4.41E-01	-0.45	1.77E-02	0.28
4	MTTA_at				1.43	2.46E-03	-0.47	3.97E-01	-1.90	1.19E-03	0.05	8.87E-01	-0.32	4.05E-01	-0.37	3.86E-01	-0.36
4	MTTA_x_at				1.38	2.44E-03	-0.45	4.00E-01	-1.83	1.21E-03	0.04	9.19E-01	-0.37	3.19E-01	-0.40	3.28E-01	-0.37
4	MTTE_at				0.16	5.17E-01	-0.06	8.23E-01	-0.22	4.60E-01	0.34	6.88E-02	-0.18	3.52E-01	-0.53	1.78E-02	0.28
4	MTTN_x_at				0.94	1.36E-04	0.03	9.23E-01	-0.91	2.59E-03	0.36	5.64E-02	-0.23	2.33E-01	-0.59	7.51E-03	0.24
4	MTTP_s_at				0.96	1.54E-03	-0.37	3.00E-01	-1.33	4.23E-04	0.54	2.03E-02	-0.40	1.03E-01	-0.94	6.86E-04	0.53
4	MTTQ_at				1.05	2.20E-04	-0.11	7.40E-01	-1.16	9.46E-04	0.29	1.77E-01	-0.30	1.91E-01	-0.59	2.12E-02	0.85
4	MTTS1_x_at				0.50	1.40E-02	0.37	1.25E-01	-0.13	6.05E-01	0.29	6.24E-02	-0.07	6.79E-01	-0.36	5.07E-02	-0.07
4	MTTT_x_at				0.22	4.63E-01	-0.39	2.73E-01	-0.61	1.00E-01	-0.05	8.32E-01	-0.39	1.03E-01	-0.35	2.01E-01	0.09
4	MTTW_x_at				0.16	5.25E-01	-0.16	5.99E-01	-0.32	3.09E-01	0.23	2.46E-01	-0.16	4.29E-01	-0.39	9.08E-02	0.38
5	1555229_a_at	716	C1S	complement component 1, s subcomponent	0.13	3.39E-01	0.48	3.56E-03	0.35	3.91E-02	-0.16	1.21E-01	-0.03	7.94E-01	0.14	2.76E-01	-0.01
5	1555814_a_at	387	RHOA	ras homolog gene family, member A	0.15	3.15E-01	0.54	3.13E-03	0.39	3.89E-02	-0.23	4.79E-02	0.04	7.68E-01	0.27	5.16E-02	0.04
5	1557910_at	3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	-0.12	5.52E-01	0.22	3.71E-01	0.34	1.81E-01	-0.17	2.95E-01	0.01	9.32E-01	0.18	3.34E-01	0.39
5	200604_s_at	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	0.05	7.75E-01	0.21	3.09E-01	0.16	4.52E-01	-0.17	1.88E-01	-0.06	6.67E-01	0.11	4.61E-01	0.52
5	200641_s_at	7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0.21	1.86E-01	0.48	1.43E-02	0.26	1.89E-01	-0.16	2.07E-01	-0.06	6.32E-01	0.10	5.17E-01	0.26
5	200866_s_at	5660	PSAP	prosaposin	0.30	2.08E-02	0.35	2.31E-02	0.05	7.42E-01	0.07	4.50E-01	0.02	8.31E-01	-0.05	6.51E-01	-0.02
5	201539_s_at	2273	FHL1	four and a half LIM domains 1	0.02	9.34E-01	0.51	3.29E-02	0.49	4.63E-02	-0.14	3.64E-01	-0.03	8.60E-01	0.11	5.38E-01	0.21
5	208750_s_at	375	ARF1	ADP-ribosylation factor 1	0.19	1.50E-01	0.32	4.57E-02	0.13	4.39E-01	-0.06	5.96E-01	0.03	7.94E-01	0.08	4.94E-01	0.01
5	210317_s_at	7531	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	0.24	1.81E-01	0.22	3.18E-01	-0.03	9.07E-01	-0.17	2.25E-01	0.01	9.45E-01	0.18	2.74E-01	0.53
5	210338_s_at	3312	HSPA8	heat shock 70kDa protein 8	-0.09	5.16E-01	0.31	6.07E-02	0.40	2.02E-02	-0.13	2.17E-01	-0.02	8.73E-01	0.11	3.63E-01	-0.17
5	213872_at		---	---	-0.29	2.68E-01	0.44	1.63E-01	0.73	2.60E-02	-0.05	8.15E-01	-0.02	9.19E-01	0.03	9.14E-01	1.05
5	214040_s_at	2934	GSN	gelsolin (amyloidosis, Finnish type)	-0.32	4.74E-02	0.47	1.56E-02	0.79	1.10E-04	-0.06	6.34E-01	0.02	8.86E-01	0.08	5.94E-01	0.10
5	214359_s_at	3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	0.09	4.61E-01	0.33	1.93E-02	0.25	9.41E-02	-0.05	5.86E-01	0.02	8.72E-01	0.07	5.43E-01	0.11
5	217294_s_at	2023	ENO1	enolase 1, (alpha)	0.04	7.89E-01	0.43	3.51E-02	0.38	6.85E-02	0.04	7.56E-01	0.04	7.64E-01	0.00	9.96E-01	-0.10
5	220477_s_at	29058	C20orf30	chromosome 20 open reading frame 30	0.06	6.32E-01	0.31	2.61E-02	0.26	7.70E-02	-0.22	1.72E-02	0.06	5.64E-01	0.27	1.12E-02	0.16
5	AFFX-HSAC07/X00351_5_at	60	ACTB	actin, beta	0.17	3.70E-01	0.63	4.76E-03	0.46	4.33E-02	-0.11	4.60E-01	0.03	8.16E-01	0.14	4.03E-01	-0.05
5	AFFX-HSAC07/X00351_M_at	60	ACTB	actin, beta	0.24	5.43E-02	0.31	3.87E-02	0.07	6.55E-01	-0.13	1.73E-01	-0.02	8.75E-01	0.12	3.08E-01	-0.03
5	AFFX-HUMGAPDH/M33197_5_at	2597	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	-0.22	5.08E-02	0.09	4.84E-01	0.32	2.49E-02	0.07	3.97E-01	0.07	4.42E-01	0.00	9.74E-01	-0.12
6	1555058_a_at	9926	LPGAT1	lysophosphatidylglycerol acyltransferase 1	-0.66	1.06E-06	-0.43	6.72E-03	0.23	1.50E-01	0.08	4.52E-01	-0.03	7.58E-01	-0.11	3.60E-01	-0.15
6	1555938_x_at	7431	VIM	vimentin	-0.02	8.54E-01	0.30	5.14E-02	0.33	4.28E-02	-0.04	6.65E-01	0.02	8.67E-01	0.06	6.04E-01	-0.03
6	1557100_s_at	25831	HECTD1	HECT domain containing 1	0.06	4.88E-01	0.01	9.30E-01	-0.05	6.35E-01	0.09	1.48E-01	-0.26	2.19E-04	-0.35	7.82E-06	-0.01
6	1557994_at	7273	TTN	titin	-0.05	7.67E-01	-0.12	5.10E-01	-0.08	6.91E-01	0.41	1.02E-03	-0.12	3.50E-01	-0.53	3.10E-04	0.03
6	1558924_s_at	6249	CLIP1	CAP-GLY domain containing linker protein 1	-0.45	2.56E-03	0.04	8.37E-01	0.49	8.35E-03	0.15	2.03E-01	-0.03	7.73E-01	-0.18	1.80E-01	-0.26
6	200702_s_at	57062	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-0.47	2.02E-04	0.07	6.48E-01	0.54	5.86E-04	0.05	6.35E-01	0.05	6.02E-01	0.01	9.51E-01	-0.01
6	201009_s_at	10628	TXNIP	thioredoxin interacting protein	-0.09	6.01E-01	0.36	7.71E-02	0.45	3.40E-02	0.14	2.74E-01	-0.15	2.73E-01	-0.30	5.68E-02	0.10
6	201030_x_at	3945	LDHB	lactate dehydrogenase B	-0.05	7.59E-01	0.20	2.98E-01	0.25	2.12E-01	-0.10	4.25E-01	-0.33	1.33E-02	-0.23	1.21E-01	0.08
6	201069_at	4313	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	0.51	1.36E-05	0.44	1.40E-03	-0.07	6.28E-01	0.00	9.90E-01	0.06	5.19E-01	0.06	5.57E-01	0.05
6	201198_s_at	5707	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-0.15	2.47E-02	0.20	1.18E-02	0.35	3.16E-05	0.09	7.02E-02	0.02	7.64E-01	-0.08	2.01E-01	0.09
6	201465_s_at	3725	JUN	jun oncogene	-0.55	1.77E-07	0.06	6.34E-01	0.61	2.72E-06	0.15	6.66E-02	-0.11	1.81E-01	-0.26	6.21E-03	0.09
6	201466_s_at	3725	JUN	jun oncogene	-0.06	6.65E-01	0.34	3.97E-02	0.40	2.00E-02	0.04	7.26E-01	-0.06	5.93E-01	-0.10	4.38E-01	-0.06
6	201508_at	3487	IGFBP4	insulin-like growth factor binding protein 4	0.35	5.64E-05	0.26	1.21E-02	-0.09	3.75E-01	-0.01	8.50E-01	0.05	4.62E-01	0.06	4.13E-01	0.01
6	201917_s_at	55186	SLC25A36	solute carrier family 25, member 36	-0.34	6.28E-03	-0.04	7.72E-01	0.30	5.25E-02	0.10	2.76E-01	-0.17	8.33E-02	-0.28	1.38E-02	-0.10
6	201968_s_at	5236	PGM1	phosphoglucomutase 1	-0.29	1.19E-03	0.09	3.92E-01	0.37	6.27E-04	0.07	3.18E-01	0.08	2.62E-01	0.01	8.78E-01	0.01
6	201996_s_at	23013	SPEN	spen homolog, transcriptional regulator (Drosophila)	-0.39	3.15E-03	0.13	3.95E-01	0.52	1.46E-03	0.09	3.90E-01	-0.05	6.38E-01	-0.14	2.49E-01	0.13
6	202118_s_at	8895	CPNE3	copine III	-0.11	5.24E-01	0.51	1.16E-02	0.62	3.37E-03	0.13	3.03E-01	-0.10	4.59E-01	-0.23	1.25E-01	0.08
6	202554_s_at	2947	GSTM3	glutathione S-transferase mu 3 (brain)	0.13	4.35E-01	0.09	6.52E-01	-0.04	8.46E-01	0.02	8.67E-01	-0.01	9.27E-01	-0.03	8.22E-01	0.15
6	202587_s_at	203	AK1	adenylate kinase 1	-0.33	3.89E-03	0.01	9.15E-01	0.35	1.47E-02	0.08	3.49E-01	0.23	1.55E-02	0.14	1.66E-01	-0.07
6	202780_at	5019	OXCT1	3-oxoacid CoA transferase 1	0.11	4.29E-01	0.07	7.03E-01	-0.05	7.88E-01	0.12	2.91E-01	-0.21	8.08E-02	-0.32	1.44E-02	-0.15
6	202785_at	4701	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	-0.31	4.56E-04	-0.05	6.11E-01	0.25	1.78E-02	-0.06	3.71E-01	0.01	8.51E-01	0.07	3.53E-01	0.07
6	202934_at	3099	HK2	hexokinase 2	0.17	3.68E-01	-0.04	8.44E-01	-0.21	3.60E-01	0.10	4.89E-01	-0.49	1.24E-03	-0.59	5.40E-04	-0.16
6	202942_at	2109	ETFB	electron-transfer-flavoprotein, beta polypeptide	-0.33	1.07E-04	-0.14	1.64E-01	0.19	6.53E-02	-0.07	3.04E-01	-0.06	4.08E-01	0.01	8.92E-01	0.06
6	202947_s_at	2995	GYPC	glycophorin C (Gerbich blood group)	-0.35	3.03E-03	0.17	2.14E-01	0.52	3.82E-04	-0.08	3.95E-01	-0.02	8.20E-01	0.06	6.02E-01	-0.07
6	203542_s_at	687	KLF9	Kruppel-like factor 9	-0.36	1.60E-03	0.08	5.52E-01	0.44	1.87E-03	0.12	1.83E-01	-0.06	4.89E-01	-0.18	8.07E-02	0.17
6	203548_s_at	4023	LPL	lipoprotein lipase	0.00	9.95E-01	0.29	1.62E-01	0.29	1.76E-01	0.04	7.48E-01	-0.46	1.16E-03	-0.50	1.49E-03	0.26
6	203549_s_at	4023	LPL	lipoprotein lipase	0.04	8.26E-01	0.18	3.65E-01	0.14	4.86E-01	-0.01	9.54E-01	-0.41	2.24E-03	-0.40	7.03E-03	0.25
6	203683_s_at	7423	VEGFB	vascular endothelial growth factor B	-0.20	1.50E-02	0.11	2.73E-01	0.31	2.74E-03	0.03	6.05E-01	0.02	7.86E-01	-0.01	8.44E-01	0.00
6	203722_at	8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	-0.39	1.29E-04	-0.06	6.36E-01	0.33	7.49E-03	-0.06	4.69E-01	-0.08	3.41E-01	-0.02	8.14E-01	-0.05
6	203781_at	9553	MRPL33	mitochondrial ribosomal protein L33	-0.17	5.04E-02	-0.11	2.59E-01	0.05	6.20E-01	-0.08	2.50E-01	-0.02	7.22E-01	0.05	5.07E-01	0.30
6	203851_at	3489	IGFBP6	insulin-like growth factor binding protein 6	-0.06	6.68E-01	0.37	4.06E-02	0.43	2.06E-02	-0.07	5.32E-01	-0.11	3.75E-01	-0.04	7.93E-01	0.03
6	203936_s_at	4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	0.67	1.20E-05	0.72	7.28E-05	0.05	7.77E-01	0.02	8.80E-01	0.00	9.94E-01	-0.02	9.03E-01	-0.15
6	203946_s_at	384	ARG2	arginase, type II	0.13	4.49E-01	0.03	8.91E-01	-0.10	6.33E-01	-0.33	1.68E-02	0.09	5.46E-01	0.42	1.02E-02	0.07
6	204174_at	241	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	-0.30	8.18E-03	0.06	6.25E-01	0.36	9.32E-03	-0.05	5.47E-01	0.02	8.28E-01	0.07	4.79E-01	-0.18
6	204278_s_at	9166	EBAG9	estrogen receptor binding site associated, antigen, 9	-0.19	4.99E-04	0.15	2.08E-02	0.33	8.93E-07	-0.02	6.35E-01	-0.04	2.97E-01	-0.03	5.96E-01	0.04
6	204388_s_at	4128	MAOA	monoamine oxidase A	0.07	7.95E-01	0.03	9.39E-01	-0.05	8.92E-01	-0.59	7.76E-03	-0.52	2.32E-02	0.06	8.07E-01	-0.06
6	204389_at	4128	MAOA	monoamine oxidase A	-0.10	5.55E-01	0.10	6.11E-01	0.21	3.34E-01	-0.43	1.47E-03	-0.28	4.28E-02	0.14	3.54E-01	0.00
6	204416_x_at	341	APOC1	apolipoprotein C-I	0.34	4.85E-02	0.00	9.82E-01	-0.34	1.06E-01	0.04	7.46E-01	0.05	7.38E-01	0.00	9.81E-01	0.05
6	204881_s_at	7357	UGCG	UDP-glucose ceramide glucosyltransferase	0.08	3.38E-01	0.29	5.30E-03	0.21	5.27E-02	0.10	1.41E-01	-0.03	6.21E-01	-0.13	9.08E-02	0.23
6	204997_at	2819	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.29	6.88E-03	0.36	5.44E-03	0.65	2.11E-06	0.02	7.95E-01	0.10	2.51E-01	0.08	4.20E-01	0.06
6	205132_at	70	ACTC1	actin, alpha, cardiac muscle 1	-0.16	4.15E-01	-0.23	3.05E-01	-0.08	7.40E-01	0.04	7.91E-01	0.41	8.78E-03	0.37	3.32E-02	-0.03

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
6	205145_s_at		LOC649851 /// MYL5	similar to Superfast myosin regulatory light chain 2 (MyLC-2) (MYLC2) (Myosin regulatory light chain 5) /// myosin, light chain 5, regulatory	-0.03	8.72E-01	-0.01	9.57E-01	0.02	9.39E-01	0.36	7.61E-03	0.24	9.08E-02	-0.12	4.37E-01	0.03
6	205200_at	7123	CLEC3B	C-type lectin domain family 3, member B	-0.15	2.41E-01	0.37	1.74E-02	0.52	1.34E-03	0.00	9.71E-01	-0.06	5.46E-01	-0.07	5.68E-01	0.17
6	205404_at	3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	0.32	4.79E-02	0.85	2.27E-05	0.52	1.01E-02	-0.17	1.80E-01	-0.04	7.58E-01	0.13	3.86E-01	-0.05
6	205890_s_at		GABBR1 /// UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D	-0.03	6.75E-01	0.26	2.74E-03	0.30	1.30E-03	-0.32	4.42E-08	0.11	6.75E-02	0.43	7.98E-10	0.00
6	205898_at	1524	CX3CR1	chemokine (C-X3-C motif) receptor 1	-0.42	1.61E-04	-0.05	6.73E-01	0.36	7.49E-03	-0.13	1.21E-01	0.11	2.17E-01	0.24	1.59E-02	-0.16
6	206029_at	27063	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	-0.21	3.78E-01	0.06	8.21E-01	0.27	3.53E-01	-0.39	3.37E-02	0.25	1.85E-01	0.64	3.01E-03	-0.05
6	206262_at	126	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.06	4.97E-01	0.35	5.74E-04	0.29	5.09E-03	-0.07	2.97E-01	0.02	7.68E-01	0.09	2.50E-01	0.01
6	206306_at	6263	RYR3	ryanodine receptor 3	0.16	2.34E-01	0.05	7.37E-01	-0.11	5.23E-01	-0.33	1.53E-03	-0.26	1.78E-02	0.07	5.47E-01	-0.02
6	206372_at	4618	MYF6	myogenic factor 6 (herculin)	-0.33	7.58E-03	-0.05	7.41E-01	0.28	6.46E-02	0.00	9.85E-01	0.23	2.14E-02	0.23	3.77E-02	-0.01
6	206407_s_at	6357	CCL13	chemokine (C-C motif) ligand 13	0.11	3.41E-01	0.49	4.65E-04	0.38	8.21E-03	0.02	7.86E-01	0.06	5.51E-01	0.03	7.62E-01	0.04
6	206453_s_at	57447	NDRG2	NDRG family member 2	-0.18	1.46E-02	0.15	9.15E-02	0.33	3.85E-04	0.16	5.78E-03	0.04	5.60E-01	-0.12	6.47E-02	0.11
6	206717_at	4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	-0.14	3.18E-01	-0.06	7.45E-01	0.09	6.23E-01	-0.26	2.02E-02	0.16	1.83E-01	0.42	1.69E-03	-0.05
6	207057_at	9194	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-0.51	5.35E-03	-0.25	2.54E-01	0.26	2.43E-01	0.11	4.38E-01	-0.27	7.19E-02	-0.38	2.38E-02	-0.01
6	207191_s_at	3671	ISLR	immunoglobulin superfamily containing leucine-rich repeat	0.20	6.98E-03	0.34	1.63E-04	0.14	1.30E-01	0.00	9.91E-01	0.07	2.61E-01	0.07	3.19E-01	-0.04
6	207709_at	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	0.04	7.18E-01	-0.10	4.56E-01	-0.14	3.13E-01	0.20	1.97E-02	-0.15	1.06E-01	-0.35	6.91E-04	0.04
6	207876_s_at	2318	FLNC	filamin C, gamma (actin binding protein 280)	-0.14	1.77E-01	-0.04	7.08E-01	0.09	4.65E-01	0.28	3.83E-04	-0.08	3.59E-01	-0.36	1.36E-04	-0.02
6	208610_s_at	23524	SRRM2	serine/arginine repetitive matrix 2	-0.50	8.47E-03	0.08	7.20E-01	0.58	1.36E-02	0.13	3.82E-01	-0.15	3.29E-01	-0.28	1.07E-01	0.38
6	208624_s_at	1981	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	-0.24	9.65E-03	-0.13	2.55E-01	0.12	3.13E-01	0.13	7.96E-02	0.00	9.71E-01	-0.12	1.44E-01	-0.33
6	208629_s_at	3030	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	-0.45	1.21E-05	0.13	2.76E-01	0.59	5.66E-06	-0.02	8.17E-01	-0.11	1.93E-01	-0.09	3.32E-01	0.19
6	208711_s_at	595	CCND1	cyclin D1	-0.56	2.35E-06	-0.07	5.92E-01	0.48	7.58E-04	-0.01	9.30E-01	-0.01	9.07E-01	0.00	9.77E-01	0.03
6	208747_s_at	716	C1S	complement component 1, s subcomponent	0.27	1.14E-02	0.51	9.10E-05	0.24	7.21E-02	-0.10	2.31E-01	0.09	3.21E-01	0.18	5.74E-02	0.04
6	208900_s_at	7150	TOP1	topoisomerase (DNA) I	-0.37	7.17E-05	-0.10	3.59E-01	0.27	1.75E-02	0.17	1.61E-02	-0.06	3.92E-01	-0.23	5.12E-03	0.07
6	208998_at	7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	0.19	1.18E-01	0.31	3.41E-02	0.12	4.29E-01	0.08	3.83E-01	0.27	7.06E-03	0.19	9.14E-02	0.05
6	209122_at	123	ADFP	adipose differentiation-related protein	0.10	2.83E-01	0.36	2.12E-03	0.26	3.36E-02	-0.06	4.16E-01	-0.09	2.31E-01	-0.03	7.03E-01	-0.02
6	209160_at	8644	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	-0.02	9.04E-01	0.08	7.10E-01	0.10	6.48E-01	0.06	6.47E-01	0.02	8.82E-01	-0.04	7.97E-01	0.22
6	209183_s_at	11067	C10orf10	chromosome 10 open reading frame 10	0.04	7.65E-01	0.59	2.90E-04	0.55	1.07E-03	-0.05	6.27E-01	0.18	1.04E-01	0.23	6.21E-02	-0.10
6	209257_s_at	9126	SMC3	structural maintenance of chromosomes 3	-0.16	1.84E-01	0.04	7.60E-01	0.20	1.73E-01	0.08	3.93E-01	0.01	8.82E-01	-0.06	5.51E-01	-0.38
6	209283_at	1410	CRYAB	crystallin, alpha B	-0.12	1.93E-01	0.23	4.74E-02	0.35	3.31E-03	-0.09	2.44E-01	-0.01	9.38E-01	0.08	3.56E-01	-0.07
6	209335_at	1634	DCN	decorin	0.16	1.46E-01	0.34	1.12E-02	0.18	1.96E-01	-0.02	8.43E-01	-0.04	6.71E-01	-0.02	8.32E-01	0.04
6	209355_s_at	8613	PPAP2B	phosphatidic acid phosphatase type 2B	-0.33	6.72E-04	0.26	2.27E-02	0.59	1.41E-06	0.01	8.87E-01	0.04	6.34E-01	0.03	7.60E-01	0.01
6	209555_s_at	948	CD36	CD36 molecule (thrombospondin receptor)	-0.41	8.16E-02	-0.30	2.93E-01	0.11	6.93E-01	-0.40	2.93E-02	-0.58	2.93E-03	-0.18	4.07E-01	-0.22
6	209612_s_at	125	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	0.01	8.97E-01	0.38	3.85E-03	0.37	7.15E-03	-0.11	2.08E-01	0.13	1.41E-01	0.24	1.76E-02	-0.03
6	209669_s_at	26135	SERBP1	SERPINE1 mRNA binding protein 1	-0.32	5.69E-05	-0.04	6.75E-01	0.28	3.87E-03	0.11	6.31E-02	-0.08	1.92E-01	-0.20	6.35E-03	-0.10
6	209924_at	6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0.43	2.62E-02	0.24	2.93E-01	-0.19	4.29E-01	0.04	7.95E-01	0.06	7.14E-01	0.02	9.15E-01	0.03
6	210069_at		CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	-0.11	3.58E-01	0.04	7.82E-01	0.14	3.14E-01	0.17	5.37E-02	-0.20	3.88E-02	-0.37	5.68E-04	-0.03
6	210070_s_at		CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	-0.04	7.05E-01	0.05	7.04E-01	0.08	5.02E-01	0.20	1.15E-02	-0.18	3.40E-02	-0.38	6.91E-05	0.02
6	210072_at	6363	CCL19	chemokine (C-C motif) ligand 19	-0.32	3.07E-03	-0.02	8.70E-01	0.30	2.48E-02	-0.01	8.85E-01	-0.01	9.34E-01	0.00	9.61E-01	0.00
6	210284_s_at	23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-0.07	4.51E-01	0.23	4.46E-02	0.31	1.14E-02	-0.03	7.36E-01	-0.01	9.28E-01	0.02	8.37E-01	-0.08
6	211149_at		LOC100130224 /// UTY	hypothetical protein LOC100130224 /// ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	-0.05	7.35E-01	0.30	7.09E-02	0.34	4.44E-02	0.07	4.88E-01	0.14	2.04E-01	0.07	5.84E-01	-0.01
6	211169_s_at	5506	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A	-0.08	4.72E-01	-0.06	6.45E-01	0.02	8.92E-01	0.52	9.98E-09	-0.08	3.95E-01	-0.59	1.98E-08	0.01
6	211560_s_at	212	ALAS2	aminolevulinate, delta-, synthase 2	-0.27	3.12E-02	0.03	8.17E-01	0.30	4.98E-02	-0.04	7.01E-01	0.01	9.38E-01	0.04	6.92E-01	-0.08
6	211969_at	3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	-0.09	2.37E-01	0.23	1.07E-02	0.32	7.27E-04	-0.03	5.79E-01	-0.03	6.75E-01	0.01	9.22E-01	0.03
6	212240_s_at	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	-0.13	3.57E-01	0.33	4.74E-02	0.46	8.34E-03	-0.10	3.35E-01	-0.11	3.33E-01	-0.01	9.64E-01	0.07
6	212922_s_at	56950	SMYD2	SET and MYND domain containing 2	-0.08	2.64E-01	-0.06	4.84E-01	0.02	8.19E-01	-0.19	9.66E-04	0.14	2.52E-02	0.33	2.53E-06	-0.04
6	213564_x_at	3945	LDHB	lactate dehydrogenase B	-0.02	9.10E-01	0.13	5.28E-01	0.15	4.85E-01	-0.10	4.50E-01	-0.36	1.13E-02	-0.26	1.01E-01	0.05
6	213880_at	8549	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	0.17	2.00E-01	0.01	9.29E-01	-0.16	3.43E-01	0.17	9.86E-02	-0.30	7.00E-03	-0.47	1.66E-04	0.01
6	214211_at	2495	FTH1	ferritin, heavy polypeptide 1	0.27	3.68E-02	0.35	2.44E-02	0.08	6.22E-01	0.28	5.01E-03	-0.04	6.67E-01	-0.33	5.61E-03	0.14
6	214305_s_at	23451	SF3B1	splicing factor 3b, subunit 1, 155kDa	-0.69	2.36E-09	0.09	5.07E-01	0.78	4.49E-08	0.21	1.22E-02	0.01	8.94E-01	-0.20	4.31E-02	0.14
6	214474_at	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	0.00	9.71E-01	-0.06	5.66E-01	-0.06	5.61E-01	0.32	8.25E-07	0.00	9.61E-01	-0.32	2.67E-05	0.03
6	214788_x_at	23109	DDN	dendrin	-0.08	6.28E-01	-0.10	5.97E-01	-0.02	9.05E-01	0.27	3.51E-02	0.37	5.03E-03	0.11	4.63E-01	0.00
6	215368_at	4703	NEB	nebulin	-0.19	7.55E-02	0.01	9.40E-01	0.20	1.32E-01	0.28	7.44E-04	-0.14	1.17E-01	-0.42	2.57E-05	-0.04
6	215795_at	57644	MYH7B	myosin, heavy chain 7B, cardiac muscle, beta	-0.11	1.61E-01	-0.03	7.28E-01	0.08	4.25E-01	0.15	1.88E-02	-0.15	2.23E-02	-0.30	7.02E-05	-0.04
6	216438_s_at		TMSB4X /// TMSL3	thymosin beta 4, X-linked /// thymosin-like 3	0.08	2.45E-01	0.05	6.05E-01	-0.04	6.60E-01	-0.22	1.53E-04	0.13	3.49E-02	0.35	5.93E-07	-0.04
6	217626_at	1645	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	-0.34	3.83E-04	-0.07	5.53E-01	0.28	1.98E-02	0.04	6.26E-01	0.00	9.63E-01	-0.03	7.09E-01	0.01
6	217717_s_at	7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	-0.12	1.29E-01	0.23	1.78E-02	0.35	5.29E-04	0.09	1.75E-01	-0.10	1.12E-01	-0.19	1.05E-02	-0.12
6	217973_at	51181	DCXR	dicarbonyl/L-xylulose reductase	-0.35	3.24E-03	0.13	3.48E-01	0.48	1.12E-03	-0.13	1.53E-01	-0.08	3.90E-01	0.05	6.53E-01	-0.04
6	218934_s_at	27129	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	-0.44	3.04E-04	-0.34	2.10E-02	0.11	4.67E-01	0.04	6.35E-01	-0.02	8.78E-01	-0.06	5.88E-01	0.03
6	218959_at	3226	HOXC10	homeobox C10	-0.42	5.26E-02	0.11	6.68E-01	0.53	4.84E-02	-0.51	2.44E-03	0.13	4.53E-01	0.65	1.21E-03	-0.04
6	221051_s_at	27231	ITGB1BP3	integrin beta 1 binding protein 3	-0.34	1.83E-01	0.00	9.99E-01	0.33	2.83E-01	-0.11	5.59E-01	0.43	3.60E-02	0.55	1.80E-02	-0.02
6	221058_s_at	51192	CKLF	chemokine-like factor	-0.10	2.49E-01	-0.03	7.85E-01	0.07	5.05E-01	0.01	9.22E-01	0.06	3.73E-01	0.06	4.75E-01	0.22
6	221295_at	1149	CIDEA	cell death-inducing DFFA-like effector a	-0.74	2.45E-05	0.07	7.18E-01	0.81	1.68E-04	0.03	8.27E-01	0.01	9.43E-01	-0.02	9.03E-01	-0.02
6	222407_s_at	64397	ZFP106	zinc finger protein 106 homolog (mouse)	-0.37	8.34E-04	-0.17	1.94E-01	0.20	1.39E-01	0.07	3.80E-01	-0.03	7.37E-01	-0.11	2.95E-01	-0.05
6	222538_s_at	26060	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	-0.18	5.09E-02	0.18	1.22E-01	0.36	2.39E-03	0.17	2.04E-02	0.06	4.17E-01	-0.11	2.08E-01	-0.09
6	222586_s_at	114885	OSBPL11	oxysterol binding protein-like 11	-0.10	3.04E-01	0.26	2.99E-02	0.36	3.73E-03	-0.04	6.10E-01	-0.10	2.23E-01	-0.06	5.11E-01	0.00
6	222725_s_at	54873	PALMD	palmdelphin	-0.14	1.63E-01	0.16	1.89E-01	0.30	1.74E-02	0.15	6.91E-02	0.06	4.89E-01	-0.09	3.50E-01	0.03
6	223210_at	91612	CHURC1	churchill domain containing 1	-0.28	7.62E-02	0.23	2.19E-01	0.51	9.40E-03	0.00	9.78E-01	0.11	4.01E-01	0.11	4.38E-01	0.16

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
6	223465_at	10087	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-0.22	1.21E-02	0.19	6.70E-02	0.40	1.88E-04	0.15	2.89E-02	0.00	9.82E-01	-0.15	5.96E-02	-0.04
6	223649_s_at	51629	SLC25A39	solute carrier family 25, member 39	-0.16	9.70E-02	0.14	2.08E-01	0.30	1.12E-02	0.01	8.56E-01	0.04	5.87E-01	0.03	7.40E-01	0.03
6	224330_s_at	51264	MRPL27	mitochondrial ribosomal protein L27	-0.27	3.81E-04	0.03	7.23E-01	0.30	1.32E-03	-0.12	3.99E-02	-0.09	1.22E-01	0.03	7.10E-01	-0.01
6	224797_at	57561	ARRDC3	arrestin domain containing 3	0.14	2.41E-01	0.32	3.24E-02	0.17	2.59E-01	0.07	4.67E-01	-0.24	1.63E-02	-0.31	5.85E-03	0.02
6	225207_at	5166	PDK4	pyruvate dehydrogenase kinase, isozyme 4	0.31	3.13E-01	0.22	5.59E-01	-0.10	8.02E-01	-0.06	7.97E-01	-0.08	7.65E-01	-0.01	9.61E-01	0.35
6	225294_s_at	58485	TRAPPC1	trafficking protein particle complex 1	0.01	9.30E-01	0.02	8.68E-01	0.01	9.28E-01	-0.06	4.10E-01	0.07	3.55E-01	0.13	1.27E-01	0.34
6	226096_at	252995	FNDC5	fibronectin type III domain containing 5	0.01	9.39E-01	0.01	9.35E-01	0.00	9.87E-01	0.34	5.41E-04	-0.02	8.28E-01	-0.36	1.65E-03	0.00
6	226616_s_at	4731	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	-0.43	8.78E-04	-0.42	6.07E-03	0.01	9.58E-01	-0.08	3.94E-01	-0.02	8.67E-01	0.07	5.65E-01	0.21
6	226875_at	139818	DOCK11	dedicator of cytokinesis 11	0.00	9.98E-01	0.34	7.32E-05	0.34	1.29E-04	0.02	6.80E-01	-0.03	6.10E-01	-0.05	4.20E-01	-0.14
6	228057_at	115265	DDIT4L	DNA-damage-inducible transcript 4-like	-0.18	1.86E-01	0.16	3.30E-01	0.34	4.56E-02	-0.07	5.40E-01	0.21	6.95E-02	0.27	3.25E-02	-0.07
6	228766_at	948	CD36	CD36 molecule (thrombospondin receptor)	-0.08	6.98E-01	-0.24	3.42E-01	-0.16	5.45E-01	-0.21	2.03E-01	-0.45	1.13E-02	-0.23	2.30E-01	-0.01
6	228885_at	256691	MAMDC2	MAM domain containing 2	0.41	5.07E-03	0.23	1.87E-01	-0.18	3.12E-01	-0.01	9.45E-01	0.02	8.65E-01	0.03	8.33E-01	-0.02
6	229119_s_at	125150	ZSWIM7	zinc finger, SWIM-type containing 7	-0.16	2.24E-01	0.24	1.28E-01	0.40	1.49E-02	-0.17	9.96E-02	0.09	4.08E-01	0.25	3.29E-02	0.12
6	231042_s_at		---	---	-0.13	2.37E-01	0.31	1.85E-02	0.44	1.40E-03	0.18	3.64E-02	-0.04	6.23E-01	-0.22	2.66E-02	-0.20
6	231078_at		---	---	-0.16	1.74E-01	0.19	1.78E-01	0.35	1.73E-02	-0.04	6.27E-01	0.00	9.79E-01	0.05	6.62E-01	0.03
6	231274_s_at		---	---	-0.33	3.27E-03	0.14	3.02E-01	0.47	8.35E-04	-0.09	2.72E-01	-0.03	7.65E-01	0.07	5.04E-01	-0.12
6	232311_at	567	B2M	Beta 2- mu =beta 2-microglobulin [human, SK-MEL-33 cells, mRNA Mutant, 433 nt]	-0.31	2.62E-05	0.00	9.74E-01	0.31	6.92E-04	-0.01	8.50E-01	0.00	9.91E-01	0.01	8.64E-01	-0.09
6	235128_at	11346	SYNPO	synaptopodin	-0.34	2.78E-04	-0.08	4.74E-01	0.26	2.23E-02	0.24	8.78E-04	0.07	3.75E-01	-0.17	3.81E-02	-0.05
6	238909_at	6281	S100A10	Calpactin I light chain, 5'UTR region	-0.14	9.67E-02	0.42	5.93E-05	0.56	3.40E-07	0.00	9.89E-01	0.01	9.35E-01	0.01	9.33E-01	0.02
6	242903_at	3459	IFNGR1	interferon gamma receptor 1	-0.25	1.36E-04	0.13	8.26E-02	0.39	3.10E-06	0.06	2.67E-01	-0.05	3.27E-01	-0.11	6.94E-02	0.17
6	32128_at	6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	0.51	9.13E-03	0.27	2.48E-01	-0.24	3.14E-01	0.05	7.58E-01	0.05	7.48E-01	0.00	9.80E-01	0.04
6	34471_at	4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	-0.15	2.83E-01	0.00	9.77E-01	0.15	3.71E-01	-0.22	3.88E-02	0.14	1.98E-01	0.36	3.89E-03	-0.04
6	AFFX-HUMRGE/M10098_3_at		---	---	-0.71	9.91E-05	-0.07	7.50E-01	0.64	4.09E-03	0.14	3.02E-01	-0.08	5.71E-01	-0.23	1.67E-01	0.28
6	AFFX-HUMRGE/M10098_5_at		---	---	-1.31	4.89E-06	-0.15	6.61E-01	1.17	8.72E-04	0.75	6.21E-04	-0.26	2.55E-01	-1.01	9.91E-05	0.36
6	AFFX-HUMRGE/M10098_M_at		---	---	-1.14	3.80E-08	-0.19	4.13E-01	0.95	1.57E-04	0.42	6.86E-03	-0.25	1.25E-01	-0.67	2.85E-04	0.04
6	MTCO1_at				0.18	2.95E-01	0.04	8.41E-01	-0.14	5.15E-01	-0.02	9.03E-01	-0.04	7.58E-01	-0.03	8.64E-01	0.32
7	201251_at	5315	PKM2	pyruvate kinase, muscle	0.14	3.95E-01	-0.14	4.81E-01	-0.28	1.73E-01	0.18	1.49E-01	0.14	2.79E-01	-0.04	7.93E-01	0.33
7	201540_at	2273	FHL1	four and a half LIM domains 1	0.07	6.70E-01	0.01	9.60E-01	-0.06	7.67E-01	0.07	6.10E-01	-0.01	9.52E-01	-0.07	6.26E-01	0.58
7	201938_at	8099	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	0.31	1.59E-03	-0.04	7.54E-01	-0.34	4.34E-03	0.07	3.46E-01	0.06	4.10E-01	-0.01	9.48E-01	0.31
7	203817_at	2983	GUCY1B3	guanylate cyclase 1, soluble, beta 3	0.42	9.12E-03	0.05	8.03E-01	-0.37	6.08E-02	0.04	7.76E-01	-0.06	6.25E-01	-0.10	4.97E-01	0.26
7	206390_x_at	5196	PF4	platelet factor 4	-0.17	5.58E-01	-0.19	5.84E-01	-0.02	9.55E-01	0.01	9.52E-01	0.01	9.75E-01	-0.01	9.81E-01	0.55
7	207550_at	4352	MPL	myeloproliferative leukemia virus oncogene	0.09	5.99E-01	0.02	9.09E-01	-0.07	7.54E-01	0.06	6.90E-01	0.05	7.50E-01	-0.01	9.56E-01	0.45
7	207815_at	5197	PF4V1	platelet factor 4 variant 1	0.08	7.67E-01	-0.13	6.84E-01	-0.20	5.28E-01	0.04	8.37E-01	0.01	9.57E-01	-0.03	8.99E-01	0.28
7	210986_s_at	7168	TPM1	tropomyosin 1 (alpha)	0.24	2.26E-01	-0.21	3.83E-01	-0.45	7.01E-02	0.03	8.34E-01	-0.09	5.78E-01	-0.12	5.00E-01	0.41
7	212148_at	5087	PBX1	pre-B-cell leukemia homeobox 1	0.41	1.15E-04	-0.12	3.42E-01	-0.53	6.38E-05	-0.08	3.20E-01	-0.05	5.90E-01	0.03	7.14E-01	0.18
7	212667_at	6678	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	0.38	1.23E-02	0.04	8.02E-01	-0.33	7.37E-02	0.18	1.12E-01	0.19	1.24E-01	0.00	9.82E-01	0.22
7	212687_at	3987	LIMS1	LIM and senescent cell antigen-like domains 1	0.28	2.86E-03	-0.02	8.54E-01	-0.30	9.60E-03	0.09	1.91E-01	-0.02	7.70E-01	-0.12	1.70E-01	0.15
7	214146_s_at	5473	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	0.02	9.54E-01	-0.40	2.23E-01	-0.41	2.22E-01	0.00	9.97E-01	-0.02	9.11E-01	-0.03	9.18E-01	0.44
7	215813_s_at	5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0.08	6.43E-01	-0.05	8.02E-01	-0.13	5.38E-01	0.05	6.81E-01	0.01	9.28E-01	-0.04	7.88E-01	0.47
7	217963_s_at	27018	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	-0.08	6.37E-01	-0.03	8.80E-01	0.05	8.15E-01	0.05	7.13E-01	-0.14	3.45E-01	-0.19	2.47E-01	0.37
7	218711_s_at	8436	SDPR	serum deprivation response (phosphatidylserine binding protein)	-0.05	8.08E-01	0.31	2.31E-01	0.36	1.77E-01	-0.02	9.26E-01	0.00	9.98E-01	0.02	9.38E-01	0.54
7	222717_at	8436	SDPR	serum deprivation response (phosphatidylserine binding protein)	0.07	8.09E-01	0.05	8.84E-01	-0.02	9.56E-01	-0.02	9.44E-01	0.04	8.78E-01	0.05	8.43E-01	0.55
7	229830_at		---	---	0.13	2.11E-01	0.01	9.64E-01	-0.12	3.34E-01	0.23	4.83E-03	-0.08	3.64E-01	-0.30	1.42E-03	0.20
7	230942_at	116173	CMTM5	CKLF-like MARVEL transmembrane domain containing 5	0.09	6.44E-01	-0.07	7.67E-01	-0.16	5.10E-01	0.09	5.28E-01	-0.03	8.41E-01	-0.13	4.74E-01	0.44
7	MTTC_at				0.05	6.82E-01	-0.14	3.10E-01	-0.18	1.91E-01	0.07	3.94E-01	-0.05	5.99E-01	-0.12	2.32E-01	0.47
7	MTTF_at				-0.17	2.72E-01	-0.09	6.24E-01	0.08	6.79E-01	-0.14	2.67E-01	0.05	6.84E-01	0.19	1.91E-01	0.30
7	MTTG_at				0.38	2.14E-02	-0.03	8.92E-01	-0.40	4.67E-02	0.02	8.87E-01	0.05	7.07E-01	0.03	8.29E-01	0.28
7	MTTH_at				-0.38	1.89E-01	-0.16	6.44E-01	0.22	5.38E-01	0.15	5.06E-01	-0.02	9.21E-01	-0.17	5.12E-01	1.21
7	MTTK_x_at				-0.12	6.62E-01	-0.22	5.11E-01	-0.10	7.78E-01	0.07	7.37E-01	0.01	9.52E-01	-0.06	8.16E-01	0.73
7	MTTL1_at				-0.10	5.76E-01	-0.14	4.87E-01	-0.05	8.26E-01	0.23	8.94E-02	-0.03	8.31E-01	-0.26	1.02E-01	0.48
7	MTTL1_x_at				-0.09	5.85E-01	-0.12	5.30E-01	-0.03	8.69E-01	0.15	2.33E-01	-0.03	8.26E-01	-0.18	2.26E-01	0.49
7	MTTL2_at				0.11	7.27E-01	-0.10	7.85E-01	-0.21	5.86E-01	0.33	1.64E-01	0.02	9.27E-01	-0.31	2.69E-01	0.68
7	MTTM_at				-0.27	3.44E-01	-0.07	8.41E-01	0.20	5.68E-01	0.01	9.62E-01	0.03	8.88E-01	0.02	9.32E-01	0.94
7	MTTR_at				0.32	2.75E-02	-0.08	6.31E-01	-0.40	2.53E-02	0.08	4.94E-01	-0.01	9.08E-01	-0.09	4.93E-01	0.29
7	MTTS2_at				-0.51	6.41E-02	-0.18	5.83E-01	0.33	3.32E-01	0.14	5.23E-01	0.11	6.26E-01	-0.03	9.14E-01	1.15
7	MTTV_at				-0.17	3.52E-01	-0.14	5.13E-01	0.03	9.05E-01	0.33	2.38E-02	-0.03	8.29E-01	-0.36	3.42E-02	0.38
7	MTTY_at				0.20	1.96E-01	0.06	7.48E-01	-0.14	4.62E-01	0.35	3.32E-03	-0.04	7.77E-01	-0.39	5.88E-03	0.41
8	200887_s_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.34	7.96E-02	0.18	4.28E-01	0.52	3.00E-02	-0.70	5.53E-06	0.22	1.57E-01	0.92	4.30E-07	-0.44
8	201137_s_at	3115	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.01	9.21E-01	0.32	7.29E-02	0.30	9.87E-02	-0.37	1.37E-03	0.24	4.56E-02	0.61	9.57E-06	-0.15
8	202869_at	4938	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	-0.84	6.25E-05	0.13	5.88E-01	0.97	1.77E-04	-0.11	4.86E-01	-0.02	9.13E-01	0.09	6.20E-01	-0.96
8	203915_at	4283	CXCL9	chemokine (C-X-C motif) ligand 9	-0.66	6.66E-06	0.44	9.95E-03	1.10	3.27E-09	-0.37	1.06E-03	0.17	1.50E-01	0.53	5.76E-05	-0.06
8	203932_at	3109	HLA-DMB	major histocompatibility complex, class II, DM beta	0.10	3.52E-01	0.13	3.14E-01	0.03	8.26E-01	-0.27	1.38E-03	0.12	1.82E-01	0.38	1.08E-04	0.03
8	204103_at	6351	CCL4	chemokine (C-C motif) ligand 4	-0.63	1.20E-04	0.29	1.33E-01	0.91	7.41E-06	-0.11	3.63E-01	0.01	9.58E-01	0.12	4.11E-01	-0.15
8	204533_at	3627	CXCL10	chemokine (C-X-C motif) ligand 10	-0.46	3.36E-03	0.28	1.23E-01	0.74	1.44E-04	-0.21	7.98E-02	0.08	5.09E-01	0.29	3.80E-02	-0.36
8	204655_at	6352	CCL5	chemokine (C-C motif) ligand 5	-0.66	2.21E-07	0.19	2.04E-01	0.85	9.35E-08	-0.30	1.66E-03	0.15	1.45E-01	0.45	8.54E-05	-0.23
8	204972_at	4939	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	-0.28	5.58E-02	0.09	6.04E-01	0.38	4.16E-02	-0.10	3.69E-01	0.08	4.80E-01	0.19	1.63E-01	-0.67
8	205114_s_at		CCL3 /// CCL3L1 /// CCL3L3 /// LOC728830	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to C-C motif chemokine 3-like 1 precursor (Small-inducible cytokine A3-li	-0.27	9.70E-02	0.54	6.27E-03	0.81	9.09E-05	0.00	9.97E-01	0.03	8.00E-01	0.03	8.18E-01	0.02
8	208306_x_at	3123	HLA-DRB1	MHC class II HLA-DRB3 mRNA (HLA-DRB3*01012 allele)	0.08	4.87E-01	0.16	2.31E-01	0.08	5.50E-01	-0.30	6.94E-04	0.12	1.77E-01	0.42	5.22E-05	-0.13
8	208729_x_at	3106	HLA-B	major histocompatibility complex, class I, B	0.07	6.71E-01	0.39	5.59E-02	0.31	1.32E-01	-0.58	1.36E-05	0.22	1.08E-01	0.80	4.47E-07	-0.25

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
8	209312_x_at		HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histoco	0.07	5.84E-01	0.37	1.98E-02	0.30	6.93E-02	-0.33	1.73E-03	0.18	1.03E-01	0.51	4.83E-05	-0.16
8	209619_at	972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	0.24	4.06E-02	0.15	2.94E-01	-0.09	5.16E-01	-0.23	1.37E-02	0.28	3.72E-03	0.51	4.44E-06	-0.03
8	209969_s_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.71	1.70E-04	0.15	5.01E-01	0.86	2.43E-04	-0.48	9.92E-04	0.08	6.17E-01	0.56	1.18E-03	-0.68
8	210163_at	6373	CXCL11	chemokine (C-X-C motif) ligand 11	-0.31	4.70E-03	0.50	1.67E-04	0.81	1.13E-08	-0.18	3.29E-02	0.08	3.53E-01	0.26	8.48E-03	-0.14
8	210514_x_at	3135	HLA-G	major histocompatibility complex, class I, G	-0.10	4.06E-01	0.33	2.25E-02	0.43	4.34E-03	-0.42	1.20E-05	0.14	1.62E-01	0.55	9.42E-07	-0.04
8	210982_s_at	3122	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.20	1.58E-01	0.54	2.05E-03	0.34	6.20E-02	-0.33	3.31E-03	0.21	7.55E-02	0.54	5.67E-05	-0.06
8	211122_s_at	6373	CXCL11	chemokine (C-X-C motif) ligand 11	-0.24	2.45E-02	0.42	1.20E-03	0.66	1.44E-06	-0.17	3.98E-02	0.09	2.73E-01	0.27	6.66E-03	-0.23
8	211430_s_at		IGH@ /// IGHG1 /// IGHG2 /// IGHM /// IGHV4-31	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy v	-2.08	2.20E-06	0.83	1.05E-01	2.91	1.28E-07	-0.85	1.05E-02	0.78	2.54E-02	1.63	4.08E-05	-1.28
8	211528_x_at	3135	HLA-G	major histocompatibility complex, class I, G	0.08	5.45E-01	0.27	8.05E-02	0.19	2.29E-01	-0.50	9.99E-07	0.23	3.02E-02	0.73	3.00E-09	-0.17
8	211530_x_at	3135	HLA-G	major histocompatibility complex, class I, G	0.05	6.41E-01	0.20	1.22E-01	0.15	2.63E-01	-0.34	9.44E-05	-0.04	6.73E-01	0.30	2.82E-03	-0.07
8	211990_at	3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	-0.41	5.10E-02	-0.43	8.91E-02	-0.02	9.49E-01	-0.23	1.51E-01	0.22	2.02E-01	0.45	1.88E-02	-0.05
8	211991_s_at	3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.01	9.34E-01	0.29	7.16E-02	0.28	9.44E-02	-0.29	4.82E-03	0.25	2.30E-02	0.54	1.39E-05	-0.09
8	212671_s_at		HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2	0.07	7.63E-01	0.19	5.23E-01	0.11	7.09E-01	-0.27	1.63E-01	0.19	3.34E-01	0.46	4.12E-02	-0.26
8	213932_x_at	3105	HLA-A	major histocompatibility complex, class I, A	0.06	6.53E-01	0.04	8.04E-01	-0.02	9.02E-01	-0.44	1.59E-05	0.25	1.58E-02	0.69	1.50E-08	-0.10
8	214038_at	6355	CCL8	chemokine (C-C motif) ligand 8	-0.77	7.45E-07	0.42	2.11E-02	1.19	1.67E-09	-0.15	2.06E-01	0.06	6.11E-01	0.21	1.26E-01	-0.22
8	215193_x_at		HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histoco	0.04	7.78E-01	0.31	6.13E-02	0.27	1.14E-01	-0.34	1.37E-03	0.24	3.20E-02	0.58	5.42E-06	-0.07
8	215313_x_at	3105	HLA-A	major histocompatibility complex, class I, A	0.06	7.16E-01	0.11	5.73E-01	0.05	8.03E-01	-0.50	8.94E-05	0.28	3.48E-02	0.78	3.39E-07	-0.07
8	216231_s_at	567	B2M	beta-2-microglobulin	0.01	9.28E-01	0.08	5.84E-01	0.07	6.49E-01	-0.72	3.51E-12	0.27	9.39E-03	0.99	2.79E-15	-0.13
8	216598_s_at	6347	CCL2	chemokine (C-C motif) ligand 2	-0.16	2.92E-01	0.45	1.75E-02	0.61	1.85E-03	-0.14	2.54E-01	0.07	5.90E-01	0.21	1.47E-01	-0.17
8	217478_s_at	3108	HLA-DMA	major histocompatibility complex, class II, DM alpha	0.08	4.46E-01	0.03	7.96E-01	-0.05	7.15E-01	-0.18	3.74E-02	0.14	1.15E-01	0.32	1.65E-03	0.01
8	223220_s_at	83666	PARP9	poly (ADP-ribose) polymerase family, member 9	-0.23	1.17E-01	0.18	3.08E-01	0.41	2.53E-02	-0.20	7.99E-02	0.15	2.15E-01	0.35	9.80E-03	-0.71
8	224701_at	54625	PARP14	poly (ADP-ribose) polymerase family, member 14	-0.26	2.90E-02	0.13	3.73E-01	0.39	9.14E-03	-0.16	8.45E-02	0.06	5.12E-01	0.22	4.05E-02	-0.52
8	226736_at	91612	CHURC1	churchill domain containing 1	-0.16	5.80E-01	0.61	8.36E-02	0.77	3.50E-02	-0.14	5.40E-01	0.37	1.23E-01	0.51	5.81E-02	0.02
8	AFFX-HUMISGF3A/M97935_3_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.30	6.98E-02	0.09	6.42E-01	0.39	5.64E-02	-0.63	2.17E-06	0.20	1.37E-01	0.83	1.34E-07	-0.43
8	AFFX-HUMISGF3A/M97935_MA_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.17	1.87E-01	0.07	6.69E-01	0.24	1.40E-01	-0.33	1.32E-03	0.01	9.62E-01	0.34	5.31E-03	-0.48
8	AFFX-HUMISGF3A/M97935_MB_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	-0.21	2.22E-01	0.28	1.75E-01	0.48	2.27E-02	-0.59	1.34E-05	0.13	3.52E-01	0.72	6.67E-06	-0.61
9	1553297_a_at	1441	CSF3R	colony stimulating factor 3 receptor (granulocyte)	0.07	6.04E-01	-0.28	8.03E-02	-0.34	3.59E-02	0.03	7.37E-01	-0.04	6.94E-01	-0.08	5.24E-01	0.02
9	1555878_at	6229	RPS24	Ribosomal protein S24 (RPS24), transcript variant b, mRNA	0.17	1.86E-01	-0.03	8.55E-01	-0.20	2.14E-01	-0.01	9.25E-01	-0.04	7.34E-01	-0.03	8.23E-01	0.09
9	1555996_s_at	1974	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	0.19	2.50E-02	0.20	4.95E-02	0.01	9.33E-01	0.02	7.29E-01	-0.04	5.33E-01	-0.07	3.94E-01	0.23
9	1556035_s_at	7756	ZNF207	zinc finger protein 207	0.17	2.19E-01	0.15	3.58E-01	-0.02	9.16E-01	0.08	4.50E-01	-0.02	8.55E-01	-0.10	4.20E-01	0.14
9	200992_at	10527	IPO7	importin 7	0.12	1.23E-01	0.19	5.63E-02	0.06	5.46E-01	-0.11	9.29E-02	0.04	5.10E-01	0.15	4.40E-02	0.29
9	201064_s_at	8761	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	0.05	5.41E-01	0.05	5.76E-01	0.00	9.63E-01	0.07	2.33E-01	0.13	4.32E-02	0.06	4.22E-01	0.25
9	201441_at	1340	COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	-0.40	1.86E-03	-0.19	2.19E-01	0.21	1.75E-01	-0.06	5.25E-01	-0.04	6.77E-01	0.02	8.66E-01	0.31
9	201568_at	27089	UQCRQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	-0.14	2.12E-01	-0.05	6.97E-01	0.09	5.28E-01	-0.03	7.42E-01	0.06	5.07E-01	0.09	3.83E-01	0.29
9	201636_at	8087	FXR1	fragile X mental retardation, autosomal homolog 1	-0.31	7.91E-06	0.07	3.86E-01	0.38	1.00E-05	0.06	2.25E-01	-0.02	6.97E-01	-0.08	1.68E-01	0.14
9	201737_s_at	10299		membrane-associated ring finger (C3HC4) 6	0.07	6.35E-01	0.09	5.94E-01	0.02	8.96E-01	0.36	8.98E-04	0.05	6.40E-01	-0.31	1.49E-02	0.02
9	201812_s_at		C4orf46 /// TOMM7	chromosome 4 open reading frame 46 /// translocase of outer mitochondrial membrane 7 homolog (yeast)	-0.04	7.47E-01	-0.02	8.59E-01	0.01	9.29E-01	0.06	5.04E-01	0.00	9.86E-01	-0.06	5.79E-01	0.38
9	202090_s_at	10975	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	-0.22	6.18E-02	-0.14	3.04E-01	0.08	6.03E-01	-0.01	9.40E-01	-0.01	9.13E-01	0.00	9.73E-01	0.27
9	202481_at	9249	DHRS3	dehydrogenase/reductase (SDR family) member 3	-0.26	5.68E-03	-0.22	4.77E-02	0.04	7.37E-01	-0.09	2.21E-01	0.03	7.07E-01	0.11	1.69E-01	0.13
9	202961_s_at	9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	-0.19	9.34E-02	-0.11	4.23E-01	0.08	5.59E-01	-0.10	2.41E-01	-0.03	7.67E-01	0.07	4.62E-01	0.35
9	203385_at	1606	DGKA	diacylglycerol kinase, alpha 80kDa	0.01	8.83E-01	-0.01	9.39E-01	-0.02	8.48E-01	-0.01	8.85E-01	-0.03	6.72E-01	-0.02	7.98E-01	0.33
9	203386_at	9882	TBC1D4	TBC1 domain family, member 4	-0.05	5.79E-01	-0.18	1.13E-01	-0.13	2.78E-01	0.04	5.72E-01	0.02	7.74E-01	-0.02	8.22E-01	0.14
9	203387_s_at	9882	TBC1D4	TBC1 domain family, member 4	0.05	5.79E-01	-0.02	8.50E-01	-0.07	5.29E-01	-0.07	3.13E-01	0.05	5.45E-01	0.12	1.62E-01	0.03
9	204560_at	2289	FKBP5	FK506 binding protein 5	-0.01	9.40E-01	0.02	8.79E-01	0.03	8.36E-01	-0.01	9.42E-01	-0.20	7.66E-02	-0.19	1.27E-01	0.29
9	204777_s_at	4118	MAL	mal, T-cell differentiation protein	0.08	5.35E-01	-0.10	5.36E-01	-0.18	2.73E-01	0.05	6.22E-01	-0.03	8.03E-01	-0.08	5.20E-01	0.37
9	205251_at	8864	PER2	period homolog 2 (Drosophila)	0.35	8.29E-03	0.08	5.95E-01	-0.26	1.03E-01	0.21	4.24E-02	0.02	8.61E-01	-0.19	1.15E-01	0.26
9	205798_at	3575	IL7R	interleukin 7 receptor	-0.26	6.47E-02	0.02	9.17E-01	0.27	1.11E-01	0.01	9.29E-01	0.02	8.53E-01	0.01	9.29E-01	0.46
9	205859_at	9450	LY86	lymphocyte antigen 86	-0.07	4.71E-01	-0.15	1.92E-01	-0.08	4.97E-01	0.01	9.42E-01	-0.01	9.10E-01	-0.01	8.71E-01	0.30
9	205883_at	7704	ZBTB16	zinc finger and BTB domain containing 16	0.12	4.54E-01	-0.06	7.41E-01	-0.18	3.56E-01	0.02	9.00E-01	-0.08	5.15E-01	-0.10	4.90E-01	0.26
9	207335_x_at	521	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	-0.26	6.98E-02	-0.18	3.00E-01	0.08	6.39E-01	-0.08	4.71E-01	0.01	9.46E-01	0.09	5.00E-01	0.52
9	207794_at		CCR2 /// FLJ78302	chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2-like	-0.02	7.97E-01	0.04	7.14E-01	0.07	5.75E-01	-0.03	7.10E-01	0.00	9.76E-01	0.03	7.31E-01	0.22
9	209170_s_at	2824	GPM6B	glycoprotein M6B	0.31	9.33E-04	-0.23	3.78E-02	-0.54	4.76E-06	0.09	1.92E-01	-0.12	1.06E-01	-0.21	1.10E-02	0.12
9	209184_s_at	8660	IRS2	insulin receptor substrate 2	0.00	9.76E-01	0.27	7.68E-02	0.28	8.34E-02	0.00	9.73E-01	0.10	3.64E-01	0.09	4.34E-01	0.18

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					ADIPOSE TISSUE						MUSCLE						
					HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs. HIV+No ART		HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg		HIV+ART vs.
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change	P-value	Fold Change
9	209492_x_at	521	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	-0.23	1.47E-01	-0.15	4.06E-01	0.07	7.11E-01	-0.09	4.48E-01	0.03	8.30E-01	0.12	4.03E-01	0.56
9	209678_s_at	5584	PRKCI	protein kinase C, iota	-0.01	9.32E-01	0.00	9.84E-01	0.00	9.60E-01	0.08	2.10E-01	0.02	7.37E-01	-0.05	4.43E-01	0.28
9	210607_at	2323	FLT3LG	fms-related tyrosine kinase 3 ligand	0.03	7.70E-01	-0.03	8.02E-01	-0.06	6.33E-01	-0.05	4.99E-01	0.06	4.69E-01	0.11	2.22E-01	0.20
9	211663_x_at	5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	0.13	2.08E-01	-0.13	2.77E-01	-0.25	4.01E-02	0.18	1.90E-02	-0.03	7.52E-01	-0.21	2.28E-02	0.21
9	211919_s_at	7852	CXCR4	chemokine (C-X-C motif) receptor 4	-0.19	1.28E-01	0.16	2.75E-01	0.34	2.34E-02	0.02	8.07E-01	0.00	9.68E-01	-0.02	8.63E-01	0.11
9	211937_at	1975	EIF4B	eukaryotic translation initiation factor 4B	-0.26	1.57E-02	-0.06	6.31E-01	0.20	1.34E-01	0.01	8.87E-01	-0.05	5.33E-01	-0.06	4.97E-01	0.33
9	211938_at	1975	EIF4B	eukaryotic translation initiation factor 4B	0.39	1.74E-05	-0.02	8.21E-01	-0.41	2.12E-04	0.07	2.81E-01	0.04	5.31E-01	-0.03	7.20E-01	0.03
9	212773_s_at	9804	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	0.04	6.28E-01	0.02	8.08E-01	-0.02	8.76E-01	-0.03	6.39E-01	0.08	2.02E-01	0.11	1.24E-01	0.22
9	212843_at	4684	NCAM1	neural cell adhesion molecule 1	0.14	7.22E-02	-0.01	9.03E-01	-0.15	1.17E-01	0.02	6.92E-01	0.04	5.49E-01	0.01	8.42E-01	0.24
9	213093_at	5578	PRKCA	protein kinase C, alpha	0.18	6.28E-02	0.08	4.60E-01	-0.09	4.26E-01	0.08	3.03E-01	0.07	3.36E-01	0.00	9.87E-01	0.33
9	213846_at	1350	COX7C	cytochrome c oxidase subunit VIIc	-0.26	1.99E-02	-0.29	3.32E-02	-0.02	8.61E-01	-0.04	6.20E-01	0.03	7.54E-01	0.07	4.83E-01	0.33
9	214183_s_at	8277	TKTL1	transketolase-like 1	-0.04	6.64E-01	0.03	7.72E-01	0.08	5.29E-01	-0.03	6.98E-01	-0.02	7.99E-01	0.01	9.18E-01	0.07
9	218200_s_at	4708	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	-0.35	2.19E-03	-0.16	2.24E-01	0.18	1.84E-01	0.02	8.29E-01	0.00	9.87E-01	-0.02	8.65E-01	0.24
9	218273_s_at	54704	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	-0.27	2.30E-02	0.07	6.26E-01	0.34	2.15E-02	0.10	2.80E-01	0.04	6.44E-01	-0.05	6.12E-01	0.23
9	219024_at	59338	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	-0.10	2.37E-01	0.07	4.97E-01	0.17	1.08E-01	0.08	2.51E-01	-0.01	8.97E-01	-0.09	2.74E-01	0.27
9	221006_s_at	81609	SNX27	sorting nexin family member 27	-0.01	8.62E-01	-0.05	5.16E-01	-0.04	6.27E-01	0.16	3.66E-03	0.03	6.36E-01	-0.13	3.84E-02	0.22
9	221188_s_at	27141	CIDEB	cell death-inducing DFFA-like effector b	-0.01	9.33E-01	-0.08	3.83E-01	-0.07	4.39E-01	0.05	3.82E-01	0.01	9.20E-01	-0.04	5.13E-01	0.20
9	221860_at	3191	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.15	1.82E-01	0.01	9.56E-01	-0.14	3.06E-01	0.03	6.90E-01	-0.13	1.62E-01	-0.16	1.13E-01	0.21
9	222040_at		HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728844	-0.04	7.35E-01	-0.09	4.64E-01	-0.06	6.64E-01	0.03	7.32E-01	-0.04	6.82E-01	-0.06	5.11E-01	0.25
9	225107_at	3181	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	0.25	5.88E-02	0.17	2.89E-01	-0.08	6.12E-01	0.11	2.90E-01	0.00	9.84E-01	-0.11	3.58E-01	0.20
9	225204_at	160760	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	-0.20	3.22E-02	-0.05	6.81E-01	0.16	1.80E-01	-0.02	8.37E-01	-0.07	3.81E-01	-0.05	5.43E-01	0.26
9	225312_at	170622	COMMD6	COMM domain containing 6	0.06	5.40E-01	-0.03	8.00E-01	-0.08	4.60E-01	-0.08	2.71E-01	0.04	6.26E-01	0.12	1.70E-01	0.23
9	225413_at	84833	USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	-0.17	1.34E-01	-0.11	4.17E-01	0.06	6.67E-01	-0.21	2.07E-02	0.00	9.90E-01	0.21	4.72E-02	0.30
9	225523_at	116540	MRPL53	mitochondrial ribosomal protein L53	-0.16	2.09E-01	-0.15	3.21E-01	0.01	9.53E-01	0.00	9.64E-01	0.03	7.49E-01	0.04	7.45E-01	0.31
9	226218_at	3575	IL7R	interleukin 7 receptor	0.00	9.77E-01	-0.03	8.14E-01	-0.03	8.03E-01	0.00	9.60E-01	0.03	7.72E-01	0.02	8.28E-01	0.16
9	226452_at	5163	PDK1	pyruvate dehydrogenase kinase, isozyme 1	0.11	2.11E-01	-0.23	3.46E-02	-0.35	2.54E-03	-0.06	3.72E-01	-0.02	8.10E-01	0.05	5.86E-01	0.02
9	227722_at	6228	RPS23	ribosomal protein S23	0.11	3.89E-01	0.02	9.08E-01	-0.09	5.59E-01	0.14	1.35E-01	-0.01	9.06E-01	-0.16	1.69E-01	0.34
9	228007_at	387119	C6orf204	CDNA clone IMAGE:5265665	0.01	9.48E-01	0.05	6.41E-01	0.04	6.92E-01	0.06	3.52E-01	-0.03	6.43E-01	-0.10	2.28E-01	0.23
9	228157_at	7756	ZNF207	zinc finger protein 207	0.06	6.35E-01	0.08	6.11E-01	0.02	9.15E-01	0.03	8.04E-01	-0.05	6.35E-01	-0.08	5.25E-01	0.22
9	229253_at	117145	THEM4	thioesterase superfamily member 4	-0.01	9.12E-01	-0.08	4.12E-01	-0.07	4.82E-01	0.04	5.44E-01	0.06	3.66E-01	0.02	7.69E-01	0.27
9	231989_s_at	641298	LOC641298	PI-3-kinase-related kinase SMG-1	-0.16	1.32E-01	0.14	2.88E-01	0.30	2.59E-02	0.04	6.60E-01	-0.09	3.04E-01	-0.13	1.96E-01	0.15
9	235099_at	152189	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	0.17	3.19E-02	-0.20	3.56E-02	-0.37	2.15E-04	0.04	5.04E-01	0.03	6.18E-01	-0.01	9.03E-01	0.13
9	235735_at		---	---	-0.14	1.48E-01	0.05	6.72E-01	0.19	1.16E-01	-0.01	9.01E-01	-0.02	7.93E-01	-0.01	8.97E-01	0.19
9	238880_at	2971	GTF3A	general transcription factor IIIA	-0.10	2.85E-01	-0.04	7.10E-01	0.06	6.14E-01	0.03	7.01E-01	-0.02	8.05E-01	-0.05	5.84E-01	0.09
9	MTND1_at				-0.02	8.30E-01	0.01	9.17E-01	0.03	7.84E-01	0.01	8.12E-01	-0.01	9.15E-01	-0.02	7.65E-01	0.24
9	MTND1_s_at				0.01	9.25E-01	-0.03	7.30E-01	-0.03	6.83E-01	0.03	5.05E-01	0.01	8.16E-01	-0.02	7.20E-01	0.25
9	MTND4L_at				-0.02	7.11E-01	-0.05	5.00E-01	-0.03	7.24E-01	-0.06	2.15E-01	-0.03	5.99E-01	0.04	5.57E-01	0.24
9	MTND4L_x_at				-0.04	6.02E-01	-0.07	4.16E-01	-0.03	7.16E-01	-0.05	3.34E-01	-0.04	5.27E-01	0.02	7.97E-01	0.27
9	MTND5_at				0.06	5.90E-01	-0.09	4.83E-01	-0.15	2.67E-01	-0.11	1.98E-01	-0.02	8.21E-01	0.09	3.70E-01	0.33

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					PBMC			
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
1	1552509_a_at	146894	CD300LG	CD300 molecule-like family member g	8.42E-01	-0.01	9.22E-01	0.01	9.25E-01
1	1554574_a_at	1727	CYB5R3	cytochrome b5 reductase 3	4.83E-03	0.19	8.10E-02	-0.13	2.97E-01
1	1555725_a_at	8490	RGS5	regulator of G-protein signaling 5	5.99E-01	-0.03	7.99E-01	0.04	8.00E-01
1	1561180_at		---	---	6.86E-01	0.03	4.89E-01	0.05	3.27E-01
1	200602_at	351	APP	amyloid beta (A4) precursor protein	1.41E-07	0.07	4.37E-01	-0.42	2.64E-05
1	200603_at	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	7.77E-01	0.02	6.30E-01	0.04	4.93E-01
1	200693_at	10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	2.93E-04	0.02	7.16E-01	0.22	3.02E-04
1	200758_s_at	4779	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	3.60E-01	0.05	5.29E-01	0.11	1.65E-01
1	200762_at	1808	DPYSL2	dihydropyrimidinase-like 2	3.75E-01	0.07	3.19E-01	0.01	9.40E-01
1	200785_s_at		LOC100134190 /// LRP1	similar to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) /// low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	2.65E-03	-0.03	5.97E-01	-0.23	1.41E-03
1	200974_at	59	ACTA2	actin, alpha 2, smooth muscle, aorta	2.35E-01	0.06	7.13E-01	0.24	1.60E-01
1	201147_s_at	7078	TIMP3	TIMP metallopeptidase inhibitor 3	9.38E-01	0.00	9.83E-01	-0.01	9.29E-01
1	201162_at	3490	IGFBP7	insulin-like growth factor binding protein 7	3.57E-02	-0.07	4.96E-01	-0.29	1.23E-02
1	201163_s_at	3490	IGFBP7	insulin-like growth factor binding protein 7	8.86E-02	-0.01	9.15E-01	-0.19	9.99E-02
1	201304_at	4698	NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	6.12E-01	0.06	2.28E-01	0.08	1.26E-01
1	201481_s_at	5834	PYGB	phosphorylase, glycogen; brain	6.76E-01	0.06	2.20E-01	0.04	4.78E-01
1	201560_at	25932	CLIC4	chloride intracellular channel 4	5.13E-01	0.04	5.97E-01	-0.01	8.99E-01
1	201589_at	8243	SMC1A	structural maintenance of chromosomes 1A	1.79E-01	-0.02	6.87E-01	0.06	3.85E-01
1	201616_s_at	800	CALD1	caldesmon 1	1.19E-01	0.01	8.90E-01	-0.13	1.94E-01
1	202104_s_at	6687	SPG7	spastic paraplegia 7 (pure and complicated autosomal recessive)	7.06E-01	-0.06	2.86E-01	-0.08	1.97E-01
1	202274_at	72	ACTG2	actin, gamma 2, smooth muscle, enteric	9.41E-01	0.00	9.98E-01	-0.01	9.48E-01
1	202743_at	8503	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	1.96E-02	0.06	4.07E-01	0.25	4.46E-03
1	202917_s_at	6279	S100A8	S100 calcium binding protein A8	8.16E-01	0.08	6.83E-01	0.12	5.66E-01
1	202948_at	3554	IL1R1	interleukin 1 receptor, type I	5.73E-01	-0.01	8.39E-01	-0.05	4.88E-01
1	203044_at	22856	CHSY1	chondroitin sulfate synthase 1	3.58E-03	0.07	2.57E-01	0.26	2.97E-04
1	203666_at	6387	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	1.84E-01	0.01	8.48E-01	0.09	1.68E-01
1	203895_at	5332	PLCB4	phospholipase C, beta 4	6.93E-01	-0.02	8.05E-01	-0.04	5.63E-01
1	203896_s_at	5332	PLCB4	phospholipase C, beta 4	4.13E-01	0.02	7.29E-01	0.06	2.93E-01
1	204363_at	2152	F3	coagulation factor III (thromboplastin, tissue factor)	3.20E-01	-0.03	6.46E-01	0.03	6.18E-01
1	204368_at	6578	SLCO2A1	solute carrier organic anion transporter family, member 2A1	7.53E-01	-0.01	6.59E-01	0.00	9.16E-01
1	204422_s_at	2247	FGF2	fibroblast growth factor 2 (basic)	3.86E-01	-0.02	7.70E-01	0.03	5.95E-01
1	204567_s_at	9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	1.24E-01	-0.17	7.28E-02	-0.02	8.46E-01
1	204938_s_at	5350	PLN	phospholamban	8.10E-01	-0.02	8.78E-01	0.01	9.34E-01
1	204948_s_at	10468	FST	follistatin	7.29E-01	0.01	8.62E-01	-0.01	8.72E-01
1	205003_at	9732	DOCK4	dedicator of cytokinesis 4	7.19E-01	0.13	1.29E-01	0.16	9.49E-02
1	205525_at	800	CALD1	caldesmon 1	5.66E-01	-0.01	8.60E-01	0.02	7.14E-01
1	205700_at	8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	6.99E-01	0.01	8.93E-01	0.03	6.37E-01
1	205854_at	7289	TULP3	tubby like protein 3	2.61E-01	-0.08	6.22E-02	-0.13	7.86E-03
1	207016_s_at	8854	ALDH1A2	aldehyde dehydrogenase 1 family, member A2	4.03E-01	0.01	9.29E-01	0.06	4.01E-01
1	207431_s_at	8560	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	7.97E-01	-0.04	5.89E-01	-0.06	4.76E-01
1	207738_s_at	10787	NCKAP1	NCK-associated protein 1	1.88E-01	-0.03	5.79E-01	-0.12	9.17E-02
1	208655_at		---	---	6.98E-01	-0.02	7.35E-01	-0.04	5.13E-01
1	208683_at	824	CAPN2	calpain 2, (m/II) large subunit	4.74E-03	0.06	2.05E-01	0.21	2.61E-04
1	208694_at	5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	5.42E-01	-0.06	1.61E-01	-0.03	4.89E-01
1	209047_at	358	AQP1	aquaporin 1 (Colton blood group)	6.98E-01	0.06	5.51E-01	0.02	8.60E-01
1	209070_s_at	8490	RGS5	regulator of G-protein signaling 5	1.36E-01	-0.05	7.08E-01	-0.23	9.15E-02
1	209120_at	7026	NR2F2	nuclear receptor subfamily 2, group F, member 2	7.59E-01	0.02	8.24E-01	0.05	6.33E-01
1	209169_at	2824	GPM6B	glycoprotein M6B	8.42E-01	-0.04	2.93E-01	-0.05	2.65E-01
1	209295_at	8795	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1.32E-01	-0.02	6.89E-01	-0.10	8.49E-02
1	209297_at	6453	ITSN1	intersectin 1 (SH3 domain protein)	9.66E-01	-0.04	4.45E-01	-0.05	4.74E-01
1	209386_at	4071	TM4SF1	transmembrane 4 L six family member 1	9.65E-01	-0.02	8.14E-01	-0.03	8.04E-01
1	209387_s_at	4071	TM4SF1	transmembrane 4 L six family member 1	7.30E-01	0.06	4.86E-01	0.09	3.51E-01
1	209684_at	54453	RIN2	Ras and Rab interactor 2	9.63E-02	0.10	2.42E-01	-0.05	6.30E-01
1	210275_s_at	7763	ZFAND5	zinc finger, AN1-type domain 5	7.50E-01	-0.01	9.04E-01	0.01	8.55E-01
1	211559_s_at	901	CCNG2	cyclin G2	1.38E-01	-0.13	6.88E-02	-0.23	3.30E-03
1	211748_x_at	5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	1.33E-05	-0.34	2.00E-02	-1.01	5.34E-09
1	211922_s_at	847	CAT	catalase	9.35E-01	-0.18	7.26E-02	-0.19	9.55E-02
1	211959_at	3488	IGFBP5	insulin-like growth factor binding protein 5	9.01E-01	0.01	8.93E-01	0.02	8.16E-01
1	211964_at	1284	COL4A2	collagen, type IV, alpha 2	5.48E-01	0.04	6.76E-01	-0.02	8.60E-01
1	211980_at	1282	COL4A1	collagen, type IV, alpha 1	8.39E-01	-0.01	9.12E-01	0.01	9.31E-01
1	211981_at	1282	COL4A1	collagen, type IV, alpha 1	4.64E-01	-0.05	6.11E-01	0.02	8.29E-01
1	212143_s_at	3486	IGFBP3	insulin-like growth factor binding protein 3	2.62E-01	-0.04	5.67E-01	0.04	6.06E-01
1	212160_at	11260	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	1.27E-01	0.05	3.43E-01	0.14	2.65E-02
1	212192_at	115207	KCTD12	potassium channel tetramerisation domain containing 12	1.32E-01	0.05	5.11E-01	-0.07	4.29E-01
1	212224_at	216	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	3.39E-01	0.20	1.36E-01	0.07	6.48E-01
1	212230_at	8613	PPAP2B	phosphatidic acid phosphatase type 2B	6.35E-02	0.06	3.95E-01	0.20	1.51E-02
1	212344_at	23213	SULF1	sulfatase 1	6.34E-01	-0.01	7.46E-01	-0.03	4.71E-01
1	212538_at	23348	DOCK9	dedicator of cytokinesis 9	1.25E-01	-0.26	4.81E-03	-0.12	2.59E-01
1	212560_at	6653	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	5.60E-02	-0.30	4.50E-03	-0.50	2.88E-05
1	212950_at	221395	GPR116	G protein-coupled receptor 116	5.90E-01	0.00	9.90E-01	0.04	6.31E-01
1	212951_at	221395	GPR116	G protein-coupled receptor 116	6.69E-01	0.00	9.52E-01	0.03	6.58E-01
1	213222_at	23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	4.34E-01	-0.15	2.10E-02	-0.21	6.06E-03
1	213404_s_at	6009	RHEB	Ras homolog enriched in brain	2.39E-02	0.09	4.43E-02	0.18	1.57E-04
1	213415_at	1193	CLIC2	chloride intracellular channel 2	4.93E-02	0.05	3.50E-01	-0.06	3.32E-01
1	214853_s_at	6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	6.82E-01	0.09	6.16E-02	0.11	4.26E-02

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					PBMC			
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
1	215785_s_at	26999	CYFIP2	cytoplasmic FMR1 interacting protein 2	1.70E-02	-0.04	6.41E-01	0.19	7.66E-02
1	217757_at	2	A2M	alpha-2-macroglobulin	9.64E-01	0.03	7.67E-01	0.02	8.25E-01
1	217894_at	51133	KCTD3	potassium channel tetramerisation domain containing 3	7.98E-01	0.01	8.32E-01	0.02	6.74E-01
1	217966_s_at	116496	FAM129A	family with sequence similarity 129, member A	2.11E-01	0.22	2.39E-02	0.34	1.86E-03
1	217967_s_at	116496	FAM129A	family with sequence similarity 129, member A	1.39E-01	0.17	8.39E-02	0.32	4.29E-03
1	218236_s_at	23683	PRKD3	protein kinase D3	9.11E-01	0.01	9.22E-01	0.00	9.89E-01
1	218764_at	5583	PRKCH	protein kinase C, eta	1.25E-04	-0.07	3.96E-01	0.27	5.30E-03
1	219825_at	56603	CYP26B1	cytochrome P450, family 26, subfamily B, polypeptide 1	5.87E-01	0.02	7.71E-01	0.06	4.53E-01
1	220170_at	9457	FHL5	four and a half LIM domains 5	6.96E-01	0.02	8.06E-01	0.05	5.66E-01
1	221087_s_at	80833	APOL3	apolipoprotein L, 3	3.93E-03	0.14	2.79E-02	0.34	7.52E-06
1	222453_at	79901	CYBRD1	cytochrome b reductase 1	3.60E-02	-0.06	4.81E-01	-0.26	1.17E-02
1	222484_s_at	9547	CXCL14	chemokine (C-X-C motif) ligand 14	5.85E-01	0.02	8.31E-01	0.07	4.92E-01
1	223077_at	29766	TMOD3	tropomodulin 3 (ubiquitous)	1.97E-01	0.05	3.92E-01	0.12	5.40E-02
1	223449_at	57556	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	3.67E-01	0.01	8.07E-01	0.06	3.00E-01
1	224817_at	9644	SH3PXD2A	SH3 and PX domains 2A	1.08E-01	0.00	9.98E-01	0.07	1.43E-01
1	224894_at	10413	YAP1	Yes-associated protein 1, 65kDa	2.80E-01	0.00	9.95E-01	0.08	3.22E-01
1	225079_at	2013	EMP2	epithelial membrane protein 2	4.85E-01	0.00	9.83E-01	0.04	5.37E-01
1	225720_at	171024	SYNPO2	synaptopodin 2	3.97E-01	0.00	9.62E-01	0.09	4.16E-01
1	225721_at	171024	SYNPO2	synaptopodin 2	1.91E-01	-0.14	1.41E-01	-0.27	1.32E-02
1	226022_at	23328	SASH1	SAM and SH3 domain containing 1	4.11E-03	0.30	4.44E-03	-0.01	9.27E-01
1	226302_at	5205	ATP8B1	ATPase, class I, type 8B, member 1	7.65E-01	0.00	9.68E-01	0.02	8.13E-01
1	226420_at	2122	EVI1	ecotropic viral integration site 1	8.68E-01	-0.04	5.49E-01	-0.05	4.95E-01
1	226685_at	6645	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	1.51E-01	-0.11	1.11E-01	-0.01	9.14E-01
1	227095_at		---	---	4.79E-02	0.06	4.27E-01	-0.09	2.69E-01
1	227758_at	85004	RERG	RAS-like, estrogen-regulated, growth inhibitor	8.35E-01	0.02	6.91E-01	0.01	8.70E-01
1	227870_at	57722	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	4.61E-01	-0.02	8.09E-01	0.05	6.47E-01
1	228202_at	5350	PLN	Phospholamban, mRNA (cDNA clone MGC:12311 IMAGE:3934199)	8.25E-01	0.03	8.08E-01	0.06	6.77E-01
1	228434_at	153579	BTNL9	butyrophilin-like 9	2.62E-01	0.00	9.72E-01	0.11	2.92E-01
1	230250_at	5787	PTPRB	protein tyrosine phosphatase, receptor type, B	5.87E-01	-0.02	8.29E-01	0.03	7.62E-01
1	233734_s_at	114879	OSBPL5	oxysterol binding protein-like 5	1.52E-02	0.07	6.98E-02	-0.02	5.39E-01
1	238066_at	116362	RBP7	retinol binding protein 7, cellular	2.50E-02	-0.06	5.54E-01	-0.32	1.06E-02
1	37512_at	8630	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	4.86E-01	0.01	8.80E-01	0.05	4.43E-01
1	41644_at	23328	SASH1	SAM and SH3 domain containing 1	1.28E-01	0.11	1.08E-01	0.00	9.67E-01
2	1552584_at	3594	IL12RB1	interleukin 12 receptor, beta 1	6.36E-05	0.07	2.00E-01	0.30	2.54E-06
2	1554240_a_at	3683	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	1.26E-05	0.11	7.88E-02	0.38	6.51E-08
2	200675_at	975	CD81	CD81 molecule	1.62E-04	0.25	3.95E-04	0.52	3.01E-10
2	201301_s_at	307	ANXA4	annexin A4	2.74E-02	0.10	1.92E-01	0.27	1.73E-03
2	201761_at	10797	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	4.78E-02	0.06	4.90E-01	0.24	1.62E-02
2	201963_at	2180	ACSL1	acyl-CoA synthetase long-chain family member 1	5.50E-03	0.21	2.49E-02	0.48	9.80E-06
2	202073_at	10133	OPTN	optineurin	1.31E-03	0.09	2.24E-01	0.36	7.69E-05
2	202074_s_at	10133	OPTN	optineurin	7.73E-08	0.09	2.18E-01	0.51	4.10E-09
2	202345_s_at		FABP5 /// FABP5L2 /// FABP5L7	fatty acid binding protein 5 (psoriasis-associated) /// fatty acid binding protein 5-like 2 /// fatty acid binding protein 5-like 7	2.82E-04	0.27	2.55E-03	0.60	7.92E-09
2	202422_s_at	2182	ACSL4	acyl-CoA synthetase long-chain family member 4	1.28E-01	0.18	1.06E-02	0.28	3.13E-04
2	202430_s_at	5359	PLSCR1	phospholipid scramblase 1	7.70E-03	0.34	9.27E-04	0.61	1.90E-07
2	202688_at	8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1.30E-04	0.16	9.60E-02	0.54	1.18E-06
2	202705_at	9133	CCNB2	cyclin B2	1.87E-01	0.23	2.71E-04	0.32	1.25E-05
2	202761_s_at	23224	SYNE2	spectrin repeat containing, nuclear envelope 2	2.83E-05	-0.02	8.45E-01	0.39	2.44E-04
2	202763_at	836	CASP3	caspase 3, apoptosis-related cysteine peptidase	1.01E-07	0.08	6.36E-02	0.34	2.84E-10
2	202912_at	133	ADM	adrenomedullin	1.94E-04	0.04	7.08E-01	0.49	2.00E-04
2	203213_at	983	CDC2	cell division cycle 2, G1 to S and G2 to M	9.95E-02	0.23	9.92E-04	0.35	1.40E-05
2	204170_s_at	1164	CKS2	CDC28 protein kinase regulatory subunit 2	5.18E-04	0.07	3.57E-01	0.34	8.16E-05
2	204562_at	3662	IRF4	interferon regulatory factor 4	2.68E-09	0.01	8.10E-01	0.37	1.59E-08
2	204613_at	5336	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	7.32E-06	0.05	3.47E-01	0.33	1.15E-06
2	204781_s_at	355	FAS	Fas (TNF receptor superfamily, member 6)	5.12E-06	0.05	4.40E-01	0.38	1.61E-06
2	204858_s_at	1890	TYMP	thymidine phosphorylase	7.30E-04	0.33	2.35E-03	0.70	2.40E-08
2	205099_s_at	1230	CCR1	chemokine (C-C motif) receptor 1	3.17E-01	0.27	3.42E-03	0.36	5.07E-04
2	205241_at	9997	SCO2	SCO cytochrome oxidase deficient homolog 2 (yeast)	1.27E-05	0.22	1.46E-02	0.64	2.95E-09
2	205568_at	366	AQP9	aquaporin 9	1.56E-03	0.12	2.54E-01	0.47	1.20E-04
2	205590_at	10125	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	2.01E-02	-0.10	1.90E-01	0.08	3.32E-01
2	205768_s_at	11001	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	3.17E-05	0.13	2.25E-03	0.30	4.48E-10
2	205769_at	11001	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	1.04E-07	0.07	1.43E-01	0.33	1.84E-09
2	205801_s_at	25780	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	3.28E-07	0.09	1.42E-01	0.42	5.72E-09
2	205831_at	914	CD2	CD2 molecule	1.73E-03	0.07	2.66E-01	0.28	1.46E-04
2	205842_s_at	3717	JAK2	Janus kinase 2 (a protein tyrosine kinase)	1.00E-04	0.10	1.29E-01	0.39	1.60E-06
2	205988_at	8832	CD84	CD84 molecule	1.84E-04	0.11	2.87E-02	0.30	1.95E-07
2	205992_s_at	3600	IL15	interleukin 15	7.18E-02	0.18	1.76E-02	0.32	2.24E-04
2	206515_at	4051	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	9.67E-04	0.02	8.30E-01	0.34	1.40E-03
2	206991_s_at		CCR5 /// LOC727797	chemokine (C-C motif) receptor 5 /// C-C chemokine receptor type 5-like	2.28E-08	0.20	1.99E-02	0.71	5.94E-12
2	207008_at	3579	IL8RB	interleukin 8 receptor, beta	7.00E-04	-0.24	9.35E-02	0.27	1.00E-01
2	207181_s_at	840	CASP7	caspase 7, apoptosis-related cysteine peptidase	7.57E-04	0.20	4.98E-04	0.40	3.17E-09
2	207275_s_at	2180	ACSL1	acyl-CoA synthetase long-chain family member 1	9.64E-03	0.08	5.19E-01	0.43	3.56E-03
2	207536_s_at	3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	9.84E-09	0.09	1.96E-02	0.32	2.46E-12
2	207614_s_at	8454	CUL1	cullin 1	1.83E-10	0.03	4.85E-01	0.32	1.74E-10
2	207681_at	2833	CXCR3	chemokine (C-X-C motif) receptor 3	1.56E-07	0.16	3.57E-03	0.45	2.21E-12

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					PBMC				
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
2	207907_at	8740	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	9.97E-07	0.13	7.14E-03	0.38	5.25E-11
2	208002_s_at	11332	ACOT7	acyl-CoA thioesterase 7	7.49E-05	0.12	1.30E-02	0.33	1.86E-08
2	209091_s_at	51100	SH3GLB1	SH3-domain GRB2-like endophilin B1	8.47E-03	0.14	2.30E-02	0.31	1.53E-05
2	209197_at	23208	SYT11	synaptotagmin XI	2.12E-06	0.16	1.48E-03	0.41	1.01E-11
2	209369_at	306	ANXA3	annexin A3	3.08E-01	0.15	3.60E-01	0.31	8.29E-02
2	209593_s_at	27348	TOR1B	torsin family 1, member B (torsin B)	9.51E-08	0.05	3.63E-01	0.34	2.11E-08
2	209770_at	11119	BTN3A1	butyrophilin, subfamily 3, member A1	5.66E-06	0.06	4.04E-01	0.40	1.38E-06
2	210354_at	3458	IFNG	interferon, gamma	2.36E-11	0.18	9.21E-03	0.68	1.36E-15
2	212048_s_at	8565	YARS	tyrosyl-tRNA synthetase	2.33E-05	0.13	4.25E-03	0.32	8.08E-10
2	212203_x_at	10410	IFITM3	interferon induced transmembrane protein 3 (1-8U)	3.28E-04	0.12	1.64E-01	0.44	9.21E-06
2	212657_s_at	3557	IL1RN	interleukin 1 receptor antagonist	2.05E-01	0.25	1.68E-02	0.38	1.19E-03
2	212845_at	23034	SAMD4A	sterile alpha motif domain containing 4A	2.00E-03	0.15	4.80E-02	0.40	7.66E-06
2	213787_s_at	10682	EBP	emopamil binding protein (sterol isomerase)	2.77E-03	0.14	1.95E-02	0.32	2.82E-06
2	216565_x_at		---	---	9.11E-04	0.06	4.54E-01	0.31	2.54E-04
2	217677_at	59339	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	1.41E-11	0.01	7.63E-01	0.34	1.16E-10
2	217738_at	10135	NAMPT	nicotinamide phosphoribosyltransferase	1.09E-02	0.13	2.14E-01	0.42	7.16E-04
2	218085_at	51510	CHMP5	chromatin modifying protein 5	1.12E-06	0.13	2.55E-02	0.44	5.59E-10
2	218254_s_at	51128	SAR1B	SAR1 homolog B (S. cerevisiae)	8.99E-03	0.17	9.46E-03	0.34	4.80E-06
2	218397_at	55120	FANCL	Fanconi anemia, complementation group L	3.73E-06	0.17	7.72E-03	0.49	2.57E-10
2	219073_s_at	114884	OSBPL10	oxysterol binding protein-like 10	1.33E-03	0.10	2.35E-01	0.39	8.61E-05
2	219356_s_at	51510	CHMP5	chromatin modifying protein 5	2.22E-07	0.08	1.34E-01	0.38	3.39E-09
2	222154_s_at	26010	LOC26010	viral DNA polymerase-transactivated protein 6	1.42E-06	0.22	1.53E-02	0.68	2.86E-10
2	223502_s_at	10673	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	1.88E-01	0.13	1.79E-01	0.26	1.74E-02
2	225663_at	91452	ACBD5	acyl-Coenzyme A binding domain containing 5	3.69E-06	0.14	3.04E-03	0.37	5.71E-11
2	230464_at	53637	S1PR5	sphingosine-1-phosphate receptor 5	1.91E-02	0.08	4.01E-01	0.31	4.22E-03
2	231769_at	26270	FBXO6	F-box protein 6	3.19E-06	0.30	1.70E-04	0.68	7.47E-13
2	232629_at	60675	PROK2	prokineticin 2	1.02E-04	0.30	1.19E-02	0.78	2.33E-08
2	238327_at	440836	ODF3B	outer dense fiber of sperm tails 3B	2.27E-01	0.11	1.85E-01	0.21	2.36E-02
2	238600_at	152789	JAKMIP1	janus kinase and microtubule interacting protein 1	3.99E-05	0.19	5.55E-03	0.48	2.31E-09
2	241869_at	80830	APOL6	apolipoprotein L, 6	3.94E-05	0.20	4.35E-02	0.62	7.13E-08
2	241916_at		---	---	1.28E-01	0.04	4.02E-01	0.13	3.40E-02
2	242234_at	54739	XAF1	XIAP associated factor 1	1.65E-03	0.07	3.84E-01	0.35	3.08E-04
2	244261_at	163702	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	2.68E-07	0.20	4.52E-03	0.57	5.84E-12
2	AFFX-HUMISGF3A/M97935_5_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	7.30E-02	0.19	2.72E-03	0.30	2.49E-05
3	200657_at	292	SLC25A5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	5.18E-01	0.02	6.54E-01	-0.01	8.49E-01
3	200862_at	1718	DHCR24	24-dehydrocholesterol reductase	2.49E-02	0.04	7.46E-01	0.30	2.00E-02
3	201128_s_at	47	ACLY	ATP citrate lyase	2.62E-01	0.01	9.06E-01	0.15	2.61E-01
3	201489_at	10105	PPIF	peptidylprolyl isomerase F	4.14E-01	0.17	5.73E-02	0.10	3.42E-01
3	202022_at	230	ALDOC	aldolase C, fructose-bisphosphate	8.43E-01	-0.05	6.29E-01	-0.03	8.05E-01
3	202068_s_at	3949	LDLR	low density lipoprotein receptor	4.81E-04	0.07	5.40E-01	0.46	2.13E-04
3	202884_s_at	5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	5.59E-01	-0.01	8.93E-01	0.05	6.80E-01
3	203945_at	384	ARG2	arginase, type II	7.31E-01	0.02	7.60E-01	0.04	5.59E-01
3	204348_s_at		AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	2.71E-01	0.06	4.34E-01	-0.02	7.57E-01
3	204663_at	10873	ME3	malic enzyme 3, NADP(+)-dependent, mitochondrial	7.98E-01	-0.03	4.77E-01	-0.02	6.91E-01
3	205108_s_at	338	APOB	apolipoprotein B (including Ag(x) antigen)	8.36E-01	-0.02	7.62E-01	-0.01	9.36E-01
3	205334_at	6271	S100A1	S100 calcium binding protein A1	9.71E-01	0.04	6.94E-01	0.05	7.02E-01
3	206012_at	7044	LEFTY2	left-right determination factor 2	3.49E-01	0.00	9.96E-01	-0.03	3.91E-01
3	206210_s_at	1071	CETP	cholesteryl ester transfer protein, plasma	4.28E-01	0.02	7.90E-01	-0.04	6.27E-01
3	207096_at	6291	SAA4	serum amyloid A4, constitutive	9.93E-01	0.02	8.19E-01	0.02	8.46E-01
3	208607_s_at		SAA1 /// SAA2	serum amyloid A1 /// serum amyloid A2	8.61E-01	-0.04	8.64E-01	-0.08	7.56E-01
3	209146_at	6307	SC4MOL	sterol-C4-methyl oxidase-like	1.17E-04	0.11	1.96E-01	0.44	4.55E-06
3	209496_at	5919	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	7.12E-01	0.03	7.50E-01	-0.01	9.57E-01
3	209605_at	7263	TST	thiosulfate sulfurtransferase (rhodanese)	1.48E-02	-0.08	3.32E-01	-0.30	2.25E-03
3	210337_s_at	47	ACLY	ATP citrate lyase	2.12E-01	-0.08	4.86E-01	0.07	6.02E-01
3	210512_s_at	7422	VEGFA	vascular endothelial growth factor A	1.98E-01	0.08	3.71E-01	-0.04	7.03E-01
3	210949_s_at		EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	5.38E-01	-0.06	4.73E-01	-0.11	2.32E-01
3	211423_s_at	6309	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	2.27E-01	0.00	9.87E-01	0.09	2.65E-01
3	211708_s_at	6319	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	9.84E-01	0.02	9.40E-01	0.01	9.62E-01
3	212274_at	23175	LPIN1	lipin 1	8.15E-02	-0.10	2.57E-01	0.06	5.58E-01
3	218434_s_at	65985	AACS	acetoacetyl-CoA synthetase	7.35E-01	0.01	9.46E-01	0.06	7.12E-01
3	218856_at	27242	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	9.09E-02	-0.08	4.23E-01	-0.25	2.51E-02
3	222011_s_at	6950	TCP1	t-complex 1	3.00E-02	0.01	9.15E-01	0.13	3.84E-02
3	222351_at	5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	9.43E-01	0.02	8.65E-01	0.01	9.32E-01
3	223839_s_at		SCD /// SCDOS	stearoyl-CoA desaturase (delta-9-desaturase) /// stearoyl-CoA desaturase opposite strand	3.02E-01	0.05	7.61E-01	0.23	2.26E-01
3	224650_at	114569	MAL2	mal, T-cell differentiation protein 2	9.86E-01	-0.04	7.12E-01	-0.04	7.31E-01
3	224812_at	11112	HIBADH	3-hydroxyisobutyrate dehydrogenase	3.81E-02	-0.03	6.06E-01	-0.13	1.94E-02
3	228309_at		---	---	5.14E-01	0.01	9.30E-01	0.05	5.02E-01
3	234312_s_at	55902	ACSS2	acyl-CoA synthetase short-chain family member 2	1.61E-01	0.02	8.16E-01	-0.10	2.84E-01
4	1553575_at	4541	ND6	NADH dehydrogenase, subunit 6 (complex I)	4.30E-02	-0.22	1.26E-01	-0.52	1.55E-03
4	1566342_at	6648	SOD2	CDNA clone IMAGE:5301545	7.09E-01	0.06	6.29E-01	0.11	4.43E-01
4	208844_at	7419	VDAC3	voltage-dependent anion channel 3	6.55E-01	-0.02	8.63E-01	0.03	8.00E-01
4	213655_at		---	---	5.55E-01	0.01	9.38E-01	-0.05	6.40E-01
4	213736_at	1329	COX5B	Cytochrome c oxidase subunit Vb, mRNA (cDNA clone MGC:10622 IMAGE:3952882)	9.67E-01	-0.06	4.60E-01	-0.05	5.36E-01
4	216246_at		---	---	5.55E-01	-0.13	7.54E-02	-0.17	3.51E-02
4	217383_at	5230	PGK1	MRNA encoding phosphoglycerate kinase	3.90E-01	0.03	8.14E-01	0.16	3.22E-01
4	222027_at	64710	NUCKS1	CDNA clone IMAGE:4513453	4.08E-01	-0.14	2.23E-01	-0.25	6.76E-02

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					PBMC				
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
4	228435_at		---	---	4.38E-01	-0.02	8.31E-01	0.05	6.06E-01
4	228634_s_at	8531	CSDA	DNA-binding protein A (dbpA) gene, 3' end	8.80E-01	0.03	7.94E-01	0.04	7.13E-01
4	MTCYB_at				4.64E-01	-0.21	1.85E-01	-0.32	6.64E-02
4	MTND6_at				8.84E-02	-0.25	1.19E-01	-0.52	3.64E-03
4	MTTA_at				3.21E-01	0.16	6.49E-01	0.52	1.92E-01
4	MTTA_x_at				2.88E-01	0.20	5.55E-01	0.57	1.37E-01
4	MTTE_at				1.31E-01	-0.16	3.81E-01	-0.45	3.21E-02
4	MTTN_x_at				2.00E-01	-0.14	4.36E-01	-0.38	6.43E-02
4	MTTP_s_at				2.39E-02	-0.13	5.60E-01	-0.66	1.04E-02
4	MTTQ_at				1.16E-04	-0.33	1.21E-01	-1.17	1.66E-06
4	MTTS1_x_at				6.38E-01	-0.24	1.18E-01	-0.17	3.37E-01
4	MTTT_x_at				6.93E-01	-0.09	6.74E-01	-0.18	4.64E-01
4	MTTW_x_at				4.83E-02	-0.05	7.80E-01	-0.44	4.09E-02
5	1555229_a_at	716	C1S	complement component 1, s subcomponent	9.36E-01	-0.01	9.54E-01	0.00	9.82E-01
5	1555814_a_at	387	RHOA	ras homolog gene family, member A	7.37E-01	-0.04	7.04E-01	-0.08	5.20E-01
5	1557910_at	3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.62E-02	-0.09	5.45E-01	-0.48	6.64E-03
5	200604_s_at	5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	1.13E-04	0.02	8.83E-01	-0.50	6.59E-04
5	200641_s_at	7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	4.38E-02	-0.06	6.10E-01	-0.32	2.25E-02
5	200866_s_at	5660	PSAP	prosaposin	8.19E-01	0.16	1.07E-01	0.18	1.02E-01
5	201539_s_at	2273	FHL1	four and a half LIM domains 1	1.70E-01	-0.02	8.76E-01	-0.23	1.65E-01
5	208750_s_at	375	ARF1	ADP-ribosylation factor 1	9.02E-01	0.08	4.09E-01	0.07	5.34E-01
5	210317_s_at	7531	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	1.88E-04	0.09	5.27E-01	-0.45	4.01E-03
5	210338_s_at	3312	HSPA8	heat shock 70kDa protein 8	1.10E-01	-0.04	7.33E-01	0.14	2.47E-01
5	213872_at		---	---	6.39E-07	0.27	1.68E-01	-0.78	6.08E-04
5	214040_s_at	2934	GSN	gelsolin (amyloidosis, Finnish type)	4.41E-01	0.05	7.01E-01	-0.05	7.17E-01
5	214359_s_at	3326	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	2.20E-01	-0.03	6.97E-01	-0.15	1.45E-01
5	217294_s_at	2023	ENO1	enolase 1, (alpha)	4.62E-01	0.18	1.62E-01	0.27	5.70E-02
5	220477_s_at	29058	C20orf30	chromosome 20 open reading frame 30	8.12E-02	-0.02	8.10E-01	-0.18	7.20E-02
5	AFFX-HSAC07/X00351_5_at	60	ACTB	actin, beta	7.47E-01	0.13	3.48E-01	0.18	2.61E-01
5	AFFX-HSAC07/X00351_M_at	60	ACTB	actin, beta	7.83E-01	0.11	2.45E-01	0.14	2.00E-01
5	AFFX-HUMGAPDH/M33197_5_at	2597	GAPDH	glyceraldehyde-3-phosphate dehydrogenase	1.87E-01	0.12	1.46E-01	0.24	1.34E-02
6	1555058_a_at	9926	LPGAT1	lysophosphatidylglycerol acyltransferase 1	1.32E-01	0.01	9.25E-01	0.16	1.46E-01
6	1555938_x_at	7431	VIM	vimentin	7.78E-01	-0.14	1.67E-01	-0.11	3.32E-01
6	1557100_s_at	25831	HECTD1	HECT domain containing 1	8.67E-01	-0.09	1.37E-01	-0.08	2.43E-01
6	1557994_at	7273	TTN	titin	8.27E-01	0.02	8.84E-01	-0.01	9.44E-01
6	1558924_s_at	6249	CLIP1	CAP-GLY domain containing linker protein 1	2.65E-02	0.09	4.23E-01	0.35	6.62E-03
6	200702_s_at	57062	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	9.54E-01	0.03	7.31E-01	0.04	7.20E-01
6	201009_s_at	10628	TXNIP	thioredoxin interacting protein	4.45E-01	0.00	9.89E-01	-0.10	4.94E-01
6	201030_x_at	3945	LDHB	lactate dehydrogenase B	5.26E-01	-0.06	6.00E-01	-0.14	2.98E-01
6	201069_at	4313	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	5.88E-01	0.00	9.95E-01	-0.05	6.26E-01
6	201198_s_at	5707	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	7.79E-02	-0.04	4.53E-01	-0.13	2.38E-02
6	201465_s_at	3725	JUN	jun oncogene	2.58E-01	0.05	5.45E-01	-0.04	6.20E-01
6	201466_s_at	3725	JUN	jun oncogene	5.48E-01	0.01	9.54E-01	0.07	5.50E-01
6	201508_at	3487	IGFBP4	insulin-like growth factor binding protein 4	8.96E-01	-0.04	5.77E-01	-0.04	5.39E-01
6	201917_s_at	55186	SLC25A36	solute carrier family 25, member 36	3.06E-01	0.06	5.19E-01	0.16	1.33E-01
6	201968_s_at	5236	PGM1	phosphoglucomutase 1	8.46E-01	-0.04	5.16E-01	-0.06	4.51E-01
6	201996_s_at	23013	SPEN	spen homolog, transcriptional regulator (Drosophila)	1.81E-01	-0.02	8.33E-01	-0.15	1.61E-01
6	202118_s_at	8895	CPNE3	copine III	5.27E-01	-0.27	3.72E-02	-0.35	1.57E-02
6	202554_s_at	2947	GSTM3	glutathione S-transferase mu 3 (brain)	2.41E-01	-0.16	2.05E-01	-0.30	2.92E-02
6	202587_s_at	203	AK1	adenylate kinase 1	4.16E-01	-0.10	2.68E-01	-0.02	8.09E-01
6	202780_at	5019	OXCT1	3-oxoacid CoA transferase 1	1.75E-01	-0.09	3.91E-01	0.06	6.33E-01
6	202785_at	4701	NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	3.20E-01	-0.03	6.60E-01	-0.09	1.96E-01
6	202934_at	3099	HK2	hexokinase 2	2.67E-01	-0.17	2.33E-01	-0.01	9.63E-01
6	202942_at	2109	ETFB	electron-transfer-flavoprotein, beta polypeptide	3.88E-01	0.08	2.15E-01	0.02	7.52E-01
6	202947_s_at	2995	GYPC	glycophorin C (Gerbich blood group)	4.67E-01	0.01	9.45E-01	0.07	4.70E-01
6	203542_s_at	687	KLF9	Kruppel-like factor 9	4.97E-02	-0.06	4.93E-01	-0.23	1.71E-02
6	203548_s_at	4023	LPL	lipoprotein lipase	5.22E-02	0.07	6.04E-01	-0.19	1.89E-01
6	203549_s_at	4023	LPL	lipoprotein lipase	5.13E-02	0.07	5.94E-01	-0.18	1.91E-01
6	203683_s_at	7423	VEGFB	vascular endothelial growth factor B	9.89E-01	-0.03	6.86E-01	-0.03	7.10E-01
6	203722_at	8659	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	5.50E-01	0.03	7.22E-01	0.07	3.91E-01
6	203781_at	9553	MRPL33	mitochondrial ribosomal protein L33	1.26E-05	-0.03	5.89E-01	-0.33	9.12E-06
6	203851_at	3489	IGFBP6	insulin-like growth factor binding protein 6	7.68E-01	-0.01	9.21E-01	-0.05	7.21E-01
6	203936_s_at	4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	1.87E-01	-0.01	9.48E-01	0.14	2.52E-01
6	203946_s_at	384	ARG2	arginase, type II	5.88E-01	-0.02	8.95E-01	-0.09	5.42E-01
6	204174_at	241	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	3.89E-02	-0.08	3.26E-01	0.10	3.08E-01
6	204278_s_at	9166	EBAG9	estrogen receptor binding site associated, antigen, 9	3.15E-01	-0.02	6.89E-01	-0.06	2.05E-01
6	204388_s_at	4128	MAOA	monoamine oxidase A	7.93E-01	-0.01	9.76E-01	0.05	8.32E-01
6	204389_at	4128	MAOA	monoamine oxidase A	9.81E-01	-0.04	7.44E-01	-0.04	7.89E-01
6	204416_x_at	341	APOC1	apolipoprotein C-I	7.00E-01	-0.05	7.04E-01	-0.10	4.92E-01
6	204881_s_at	7357	UGCG	UDP-glucose ceramide glucosyltransferase	5.91E-04	-0.10	1.29E-01	-0.33	1.09E-05
6	204997_at	2819	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	4.51E-01	0.02	7.87E-01	-0.04	6.54E-01
6	205132_at	70	ACTC1	actin, alpha, cardiac muscle 1	8.64E-01	-0.03	8.22E-01	-0.01	9.66E-01

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Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
6	205145_s_at		LOC649851 /// MYL5	similar to Superfast myosin regulatory light chain 2 (MyLC-2) (MYLC2) (Myosin regulatory light chain 5) /// myosin, light chain 5, regulatory	8.18E-01	0.04	7.54E-01	0.01	9.45E-01
6	205200_at	7123	CLEC3B	C-type lectin domain family 3, member B	8.30E-02	0.06	5.13E-01	-0.11	3.15E-01
6	205404_at	3290	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	7.11E-01	-0.05	6.71E-01	-0.01	9.68E-01
6	205890_s_at		GABBR1 /// UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D	9.46E-01	0.05	3.41E-01	0.06	3.65E-01
6	205898_at	1524	CX3CR1	chemokine (C-X3-C motif) receptor 1	5.89E-02	0.10	2.05E-01	0.26	4.80E-03
6	206029_at	27063	ANKRD1	ankyrin repeat domain 1 (cardiac muscle)	7.91E-01	-0.01	9.39E-01	0.03	8.62E-01
6	206262_at	126	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	8.98E-01	-0.01	8.89E-01	-0.02	8.10E-01
6	206306_at	6263	RYR3	ryanodine receptor 3	8.56E-01	0.03	7.86E-01	0.05	6.85E-01
6	206372_at	4618	MYF6	myogenic factor 6 (herculin)	8.77E-01	-0.01	9.44E-01	0.01	9.37E-01
6	206407_s_at	6357	CCL13	chemokine (C-C motif) ligand 13	6.42E-01	0.04	6.79E-01	-0.01	9.56E-01
6	206453_s_at	57447	NDRG2	NDRG family member 2	4.67E-02	-0.06	2.51E-01	-0.18	4.99E-03
6	206717_at	4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	6.31E-01	-0.01	9.11E-01	0.04	7.35E-01
6	207057_at	9194	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	9.69E-01	0.09	5.24E-01	0.09	5.48E-01
6	207191_s_at	3671	ISLR	immunoglobulin superfamily containing leucine-rich repeat	5.37E-01	-0.03	5.31E-01	0.00	9.95E-01
6	207709_at	5563	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	6.47E-01	0.00	9.60E-01	-0.04	7.10E-01
6	207876_s_at	2318	FLNC	filamin C, gamma (actin binding protein 280)	8.25E-01	-0.07	3.61E-01	-0.05	5.41E-01
6	208610_s_at	23524	SRRM2	serine/arginine repetitive matrix 2	1.11E-02	-0.21	1.42E-01	-0.59	3.58E-04
6	208624_s_at	1981	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1.27E-05	0.02	7.38E-01	0.35	1.97E-05
6	208629_s_at	3030	HADHA	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	1.42E-02	0.01	9.09E-01	-0.18	3.26E-02
6	208711_s_at	595	CCND1	cyclin D1	7.65E-01	0.04	6.13E-01	0.02	8.60E-01
6	208747_s_at	716	C1S	complement component 1, s subcomponent	6.31E-01	-0.03	7.02E-01	-0.07	4.38E-01
6	208900_s_at	7150	TOP1	topoisomerase (DNA) I	3.49E-01	0.14	4.47E-02	0.07	3.49E-01
6	208998_at	7351	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	6.09E-01	0.16	8.81E-02	0.11	2.93E-01
6	209122_at	123	ADFP	adipose differentiation-related protein	7.93E-01	-0.06	4.32E-01	-0.04	6.46E-01
6	209160_at	8644	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	1.22E-01	-0.36	8.19E-03	-0.58	2.13E-04
6	209183_s_at	11067	C10orf10	chromosome 10 open reading frame 10	3.45E-01	-0.01	9.54E-01	0.09	4.19E-01
6	209257_s_at	9126	SMC3	structural maintenance of chromosomes 3	3.98E-05	0.06	4.69E-01	0.45	1.35E-05
6	209283_at	1410	CRYAB	crystallin, alpha B	3.47E-01	0.06	3.88E-01	0.13	1.06E-01
6	209335_at	1634	DCN	decorin	6.60E-01	-0.03	7.35E-01	-0.07	4.84E-01
6	209355_s_at	8613	PPAP2B	phosphatidic acid phosphatase type 2B	8.92E-01	0.01	8.69E-01	0.00	9.81E-01
6	209555_s_at	948	CD36	CD36 molecule (thrombospondin receptor)	2.34E-01	-0.10	5.73E-01	0.12	5.58E-01
6	209612_s_at	125	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	7.43E-01	0.01	8.86E-01	0.04	6.70E-01
6	209669_s_at	26135	SERBP1	SERPINE1 mRNA binding protein 1	1.10E-01	0.02	6.80E-01	0.12	6.91E-02
6	209924_at	6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	8.20E-01	0.00	9.74E-01	-0.04	8.13E-01
6	210069_at		CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	7.57E-01	-0.03	7.41E-01	0.00	9.90E-01
6	210070_s_at		CHKB /// CPT1B	choline kinase beta /// carnitine palmitoyltransferase 1B (muscle)	8.13E-01	-0.03	6.91E-01	-0.05	5.70E-01
6	210072_at	6363	CCL19	chemokine (C-C motif) ligand 19	9.66E-01	0.01	9.29E-01	0.01	9.06E-01
6	210284_s_at	23118	MAP3K7IP2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	2.83E-01	-0.23	1.68E-03	-0.15	6.55E-02
6	211149_at		LOC100130224 /// UTY	hypothetical protein LOC100130224 /// ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	9.53E-01	0.18	8.68E-02	0.18	1.16E-01
6	211169_s_at	5506	PPP1R3A	protein phosphatase 1, regulatory (inhibitor) subunit 3A	9.14E-01	-0.01	8.69E-01	-0.02	8.07E-01
6	211560_s_at	212	ALAS2	aminolevulinate, delta-, synthase 2	4.31E-01	0.00	9.61E-01	0.08	4.47E-01
6	211969_at	3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	5.92E-01	0.02	7.53E-01	-0.01	8.34E-01
6	212240_s_at	5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	5.08E-01	-0.15	1.60E-01	-0.22	6.52E-02
6	212922_s_at	56950	SMYD2	SET and MYND domain containing 2	5.39E-01	0.03	5.61E-01	0.07	2.83E-01
6	213564_x_at	3945	LDHB	lactate dehydrogenase B	7.16E-01	-0.06	6.52E-01	-0.11	4.65E-01
6	213880_at	8549	LGR5	leucine-rich repeat-containing G protein-coupled receptor 5	9.08E-01	-0.01	9.40E-01	-0.02	8.63E-01
6	214211_at	2495	FTH1	ferritin, heavy polypeptide 1	1.60E-01	0.11	2.60E-01	-0.03	7.76E-01
6	214305_s_at	23451	SF3B1	splicing factor 3b, subunit 1, 155kDa	9.82E-02	0.03	6.97E-01	-0.11	2.44E-01
6	214474_at	5565	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	6.14E-01	0.01	9.33E-01	-0.03	7.00E-01
6	214788_x_at	23109	DDN	dendrin	9.71E-01	-0.06	6.27E-01	-0.06	6.43E-01
6	215368_at	4703	NEB	nebulin	6.14E-01	-0.02	7.83E-01	0.02	8.29E-01
6	215795_at	57644	MYH7B	myosin, heavy chain 7B, cardiac muscle, beta	5.37E-01	-0.01	8.59E-01	0.03	6.85E-01
6	216438_s_at		TMSB4X /// TMSL3	thymosin beta 4, X-linked /// thymosin-like 3	5.34E-01	0.05	3.72E-01	0.08	1.75E-01
6	217626_at	1645	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	9.38E-01	0.01	9.29E-01	0.00	9.94E-01
6	217717_s_at	7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	5.02E-02	-0.12	5.67E-02	0.01	9.25E-01
6	217973_at	51181	DCXR	dicarbonyl/L-xylulose reductase	6.60E-01	-0.11	2.20E-01	-0.07	4.90E-01
6	218934_s_at	27129	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	7.40E-01	0.04	6.94E-01	0.00	9.63E-01
6	218959_at	3226	HOXC10	homeobox C10	8.01E-01	-0.02	9.01E-01	0.02	9.05E-01
6	221051_s_at	27231	ITGB1BP3	integrin beta 1 binding protein 3	9.00E-01	-0.01	9.64E-01	0.02	9.41E-01
6	221058_s_at	51192	CKLF	chemokine-like factor	1.33E-03	-0.13	5.51E-02	-0.35	5.91E-06
6	221295_at	1149	CIDEA	cell death-inducing DFFA-like effector a	9.08E-01	0.00	9.95E-01	0.01	9.21E-01
6	222407_s_at	64397	ZFP106	zinc finger protein 106 homolog (mouse)	5.29E-01	-0.12	1.45E-01	-0.07	4.69E-01
6	222538_s_at	26060	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	2.00E-01	-0.08	2.72E-01	0.02	8.46E-01
6	222586_s_at	114885	OSBPL11	oxysterol binding protein-like 11	9.51E-01	-0.05	5.28E-01	-0.05	5.38E-01
6	222725_s_at	54873	PALMD	palmdelphin	7.21E-01	-0.01	9.08E-01	-0.04	6.69E-01
6	223210_at	91612	CHURC1	churchill domain containing 1	1.79E-01	0.32	6.54E-03	0.16	2.26E-01

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					PBMC				
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
6	223465_at	10087	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	5.76E-01	0.11	8.44E-02	0.15	4.20E-02
6	223649_s_at	51629	SLC25A39	solute carrier family 25, member 39	7.09E-01	0.09	1.93E-01	0.07	4.13E-01
6	224330_s_at	51264	MRPL27	mitochondrial ribosomal protein L27	7.99E-01	0.10	6.75E-02	0.12	6.40E-02
6	224797_at	57561	ARRDC3	arrestin domain containing 3	8.35E-01	0.03	7.49E-01	0.01	9.25E-01
6	225207_at	5166	PDK4	pyruvate dehydrogenase kinase, isozyme 4	1.52E-01	-0.20	4.02E-01	-0.54	4.14E-02
6	225294_s_at	58485	TRAPPC1	trafficking protein particle complex 1	9.09E-06	0.09	2.22E-01	-0.25	2.37E-03
6	226096_at	252995	FNDC5	fibronectin type III domain containing 5	9.98E-01	0.02	8.60E-01	0.02	8.74E-01
6	226616_s_at	4731	NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	3.49E-02	0.02	8.20E-01	-0.19	8.46E-02
6	226875_at	139818	DOCK11	dedicator of cytokinesis 11	9.27E-03	-0.05	3.60E-01	0.09	1.15E-01
6	228057_at	115265	DDIT4L	DNA-damage-inducible transcript 4-like	5.06E-01	0.05	6.06E-01	0.13	2.88E-01
6	228766_at	948	CD36	CD36 molecule (thrombospondin receptor)	9.54E-01	-0.06	6.96E-01	-0.05	7.69E-01
6	228885_at	256691	MAMDC2	MAM domain containing 2	8.65E-01	0.01	9.36E-01	0.03	8.21E-01
6	229119_s_at	125150	ZSWIM7	zinc finger, SWIM-type containing 7	2.40E-01	-0.01	9.26E-01	-0.13	2.49E-01
6	231042_s_at		---	---	1.98E-02	0.00	9.83E-01	0.20	3.52E-02
6	231078_at		---	---	7.57E-01	0.01	8.78E-01	-0.01	8.84E-01
6	231274_s_at		---	---	1.68E-01	0.01	9.38E-01	0.12	1.86E-01
6	232311_at	567	B2M	Beta 2- mu =beta 2-microglobulin [human, SK-MEL-33 cells, mRNA Mutant, 433 nt]	9.82E-02	-0.03	5.19E-01	0.06	3.48E-01
6	235128_at	11346	SYNPO	synaptopodin	4.54E-01	-0.03	6.57E-01	0.02	7.74E-01
6	238909_at	6281	S100A10	Calpactin I light chain, 5'UTR region	7.71E-01	-0.11	9.51E-02	-0.13	8.13E-02
6	242903_at	3459	IFNGR1	interferon gamma receptor 1	6.88E-04	0.02	6.34E-01	-0.15	7.05E-03
6	32128_at	6362	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	8.01E-01	0.00	9.77E-01	-0.03	8.38E-01
6	34471_at	4626	MYH8	myosin, heavy chain 8, skeletal muscle, perinatal	6.84E-01	0.00	9.73E-01	0.05	6.89E-01
6	AFFX-HUMRGE/M10098_3_at		---	---	4.72E-02	-0.16	2.32E-01	-0.44	4.45E-03
6	AFFX-HUMRGE/M10098_5_at		---	---	9.98E-02	-0.31	1.44E-01	-0.66	5.61E-03
6	AFFX-HUMRGE/M10098_M_at		---	---	8.06E-01	-0.35	1.93E-02	-0.39	2.16E-02
6	MTCO1_at				1.86E-02	0.35	8.57E-03	0.03	8.45E-01
7	201251_at	5315	PKM2	pyruvate kinase, muscle	1.06E-02	0.12	3.45E-01	-0.21	1.32E-01
7	201540_at	2273	FHL1	four and a half LIM domains 1	1.22E-05	-0.27	3.57E-02	-0.85	1.37E-08
7	201938_at	8099	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	4.59E-05	0.09	2.02E-01	-0.22	8.10E-03
7	203817_at	2983	GUCY1B3	guanylate cyclase 1, soluble, beta 3	3.77E-02	0.08	5.09E-01	-0.18	1.88E-01
7	206390_x_at	5196	PF4	platelet factor 4	1.45E-02	-0.52	1.75E-02	-1.06	2.15E-05
7	207550_at	4352	MPL	myeloproliferative leukemia virus oncogene	1.60E-03	0.03	7.98E-01	-0.41	7.77E-03
7	207815_at	5197	PF4V1	platelet factor 4 variant 1	1.58E-01	-0.45	2.15E-02	-0.74	1.01E-03
7	210986_s_at	7168	TPM1	tropomyosin 1 (alpha)	9.84E-03	0.14	3.39E-01	-0.26	1.28E-01
7	212148_at	5087	PBX1	pre-B-cell leukemia homeobox 1	2.33E-02	-0.08	3.10E-01	-0.26	3.24E-03
7	212667_at	6678	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6.46E-02	0.04	7.23E-01	-0.18	1.70E-01
7	212687_at	3987	LIMS1	LIM and senescent cell antigen-like domains 1	3.67E-02	-0.06	3.90E-01	-0.21	8.09E-03
7	214146_s_at	5473	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	3.87E-02	-0.43	3.83E-02	-0.87	2.48E-04
7	215813_s_at	5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	4.20E-04	0.01	9.12E-01	-0.46	1.76E-03
7	217963_s_at	27018	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	6.46E-03	-0.28	3.90E-02	-0.65	2.35E-05
7	218711_s_at	8436	SDPR	serum deprivation response (phosphatidylserine binding protein)	1.33E-03	-0.23	1.62E-01	-0.77	4.09E-05
7	222717_at	8436	SDPR	serum deprivation response (phosphatidylserine binding protein)	1.25E-02	-0.32	1.38E-01	-0.87	3.95E-04
7	229830_at		---	---	1.48E-02	0.03	6.92E-01	-0.16	6.02E-02
7	230942_at	116173	CMTM5	CKLF-like MARVEL transmembrane domain containing 5	3.62E-03	0.04	7.85E-01	-0.40	1.55E-02
7	MTTC_at				2.67E-07	0.04	6.16E-01	-0.43	1.60E-05
7	MTTF_at				1.58E-02	-0.17	1.66E-01	-0.47	7.07E-04
7	MTTG_at				2.88E-02	-0.04	7.37E-01	-0.32	2.23E-02
7	MTTH_at				2.60E-07	-0.28	1.98E-01	-1.50	1.03E-08
7	MTTK_x_at				7.14E-04	-0.29	1.64E-01	-1.02	2.13E-05
7	MTTL1_at				4.24E-04	-0.24	6.70E-02	-0.72	2.22E-06
7	MTTL1_x_at				1.88E-04	-0.23	6.97E-02	-0.71	9.58E-07
7	MTTL2_at				4.56E-03	-0.38	1.01E-01	-1.05	7.11E-05
7	MTTM_at				3.78E-05	-0.36	1.02E-01	-1.30	3.53E-07
7	MTTR_at				9.35E-03	-0.07	5.45E-01	-0.36	3.85E-03
7	MTTS2_at				2.40E-07	-0.19	3.59E-01	-1.34	4.90E-08
7	MTTV_at				8.45E-03	-0.23	1.02E-01	-0.61	1.48E-04
7	MTTY_at				6.68E-04	0.03	7.85E-01	-0.38	4.04E-03
8	200887_s_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	3.78E-03	0.31	3.21E-02	0.75	8.87E-06
8	201137_s_at	3115	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	1.79E-01	0.12	2.72E-01	0.28	2.87E-02
8	202869_at	4938	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	9.13E-09	0.20	1.98E-01	1.16	4.05E-10
8	203915_at	4283	CXCL9	chemokine (C-X-C motif) ligand 9	5.88E-01	0.10	3.68E-01	0.16	1.97E-01
8	203932_at	3109	HLA-DMB	major histocompatibility complex, class II, DM beta	7.33E-01	0.00	9.94E-01	-0.03	7.61E-01
8	204103_at	6351	CCL4	chemokine (C-C motif) ligand 4	2.10E-01	0.10	4.01E-01	0.26	6.01E-02
8	204533_at	3627	CXCL10	chemokine (C-X-C motif) ligand 10	2.58E-03	0.49	4.39E-05	0.85	9.33E-10
8	204655_at	6352	CCL5	chemokine (C-C motif) ligand 5	1.77E-02	0.17	6.49E-02	0.40	1.84E-04
8	204972_at	4939	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	3.16E-08	0.20	6.86E-02	0.87	1.04E-10
8	205114_s_at		CCL3 /// CCL3L1 /// CCL3L3 /// LOC728830	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to C-C motif chemokine 3-like 1 precursor (Small-inducible cytokine A3-li	8.89E-01	0.16	1.93E-01	0.14	3.04E-01
8	208306_x_at	3123	HLA-DRB1	MHC class II HLA-DRB3 mRNA (HLA-DRB3*01012 allele)	1.35E-01	0.08	3.44E-01	0.21	2.85E-02
8	208729_x_at	3106	HLA-B	major histocompatibility complex, class I, B	5.29E-02	0.20	1.20E-01	0.45	1.88E-03

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					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
8	209312_x_at		HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histoco	1.19E-01	0.17	9.60E-02	0.33	4.12E-03
8	209619_at	972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	7.34E-01	0.18	4.05E-02	0.21	3.38E-02
8	209969_s_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	4.10E-06	0.47	8.87E-04	1.16	1.02E-11
8	210163_at	6373	CXCL11	chemokine (C-X-C motif) ligand 11	1.02E-01	0.15	6.40E-02	0.29	1.93E-03
8	210514_x_at	3135	HLA-G	major histocompatibility complex, class I, G	6.75E-01	0.05	5.42E-01	0.09	3.57E-01
8	210982_s_at	3122	HLA-DRA	major histocompatibility complex, class II, DR alpha	5.64E-01	0.10	3.63E-01	0.16	1.84E-01
8	211122_s_at	6373	CXCL11	chemokine (C-X-C motif) ligand 11	6.01E-03	0.14	8.04E-02	0.37	6.72E-05
8	211430_s_at		IGH@ /// IGHG1 /// IGHG2 /// IGHM /// IGHV4-31	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy v	1.44E-04	0.33	3.11E-01	1.61	1.63E-05
8	211528_x_at	3135	HLA-G	major histocompatibility complex, class I, G	7.90E-02	0.13	1.83E-01	0.30	5.82E-03
8	211530_x_at	3135	HLA-G	major histocompatibility complex, class I, G	3.87E-01	0.09	2.54E-01	0.17	7.31E-02
8	211990_at	3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	7.62E-01	0.06	6.93E-01	0.11	5.31E-01
8	211991_s_at	3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	4.00E-01	0.17	1.01E-01	0.25	2.70E-02
8	212671_s_at		HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2	1.83E-01	-0.26	1.64E-01	0.00	9.83E-01
8	213932_x_at	3105	HLA-A	major histocompatibility complex, class I, A	3.04E-01	0.10	2.95E-01	0.20	6.31E-02
8	214038_at	6355	CCL8	chemokine (C-C motif) ligand 8	5.64E-02	0.11	3.22E-01	0.34	9.34E-03
8	215193_x_at		HLA-DRB1 /// HLA-DRB2 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5 /// LOC100133484 /// LOC100133661 /// LOC100133811 /// LOC730415 /// RNASE2 /// ZNF749	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 2 (pseudogene) /// major histocompatibility complex, class II, DR beta 3 /// major histoco	4.91E-01	0.07	4.87E-01	0.14	2.15E-01
8	215313_x_at	3105	HLA-A	major histocompatibility complex, class I, A	6.04E-01	0.13	2.94E-01	0.19	1.61E-01
8	216231_s_at	567	B2M	beta-2-microglobulin	1.69E-01	0.06	5.36E-01	0.19	7.24E-02
8	216598_s_at	6347	CCL2	chemokine (C-C motif) ligand 2	1.68E-01	0.11	3.69E-01	0.27	4.10E-02
8	217478_s_at	3108	HLA-DMA	major histocompatibility complex, class II, DM alpha	8.82E-01	0.14	1.04E-01	0.12	1.90E-01
8	223220_s_at	83666	PARP9	poly (ADP-ribose) polymerase family, member 9	3.09E-09	0.31	5.66E-03	1.01	7.65E-14
8	224701_at	54625	PARP14	poly (ADP-ribose) polymerase family, member 14	5.97E-08	0.11	2.26E-01	0.63	3.51E-09
8	226736_at	91612	CHURC1	churchill domain containing 1	9.44E-01	0.67	2.96E-03	0.65	9.81E-03
8	AFFX-HUMISGF3A/M97935_3_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	1.06E-03	0.31	1.29E-02	0.74	4.49E-07
8	AFFX-HUMISGF3A/M97935_MA_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	5.65E-06	0.32	1.83E-03	0.80	4.33E-11
8	AFFX-HUMISGF3A/M97935_MB_at	6772	STAT1	signal transducer and activator of transcription 1, 91kDa	7.06E-06	0.26	4.79E-02	0.87	1.32E-08
9	1553297_a_at	1441	CSF3R	colony stimulating factor 3 receptor (granulocyte)	8.68E-01	-0.01	9.13E-01	-0.03	8.04E-01
9	1555878_at	6229	RPS24	Ribosomal protein S24 (RPS24), transcript variant b, mRNA	3.62E-01	-0.23	2.07E-02	-0.32	4.21E-03
9	1555996_s_at	1974	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	5.76E-04	-0.07	2.65E-01	-0.30	4.60E-05
9	1556035_s_at	7756	ZNF207	zinc finger protein 207	1.95E-01	-0.26	1.16E-02	-0.40	7.18E-04
9	200992_at	10527	IPO7	importin 7	8.49E-06	-0.06	3.60E-01	-0.34	1.47E-06
9	201064_s_at	8761	PABPC4	poly(A) binding protein, cytoplasmic 4 (inducible form)	5.28E-05	-0.13	2.91E-02	-0.38	4.81E-08
9	201441_at	1340	COX6B1	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	1.84E-03	-0.09	3.74E-01	-0.40	3.24E-04
9	201568_at	27089	UQCRQ	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa	1.22E-03	-0.05	5.32E-01	-0.35	5.01E-04
9	201636_at	8087	FXR1	fragile X mental retardation, autosomal homolog 1	7.40E-03	-0.15	2.80E-03	-0.30	7.27E-07
9	201737_s_at	10299		membrane-associated ring finger (C3HC4) 6	8.37E-01	-0.04	6.66E-01	-0.07	5.68E-01
9	201812_s_at		C4orf46 /// TOMM7	chromosome 4 open reading frame 46 /// translocase of outer mitochondrial membrane 7 homolog (yeast)	2.44E-05	-0.18	3.68E-02	-0.56	3.09E-08
9	202090_s_at	10975	UQCR	ubiquinol-cytochrome c reductase, 6.4kDa subunit	2.86E-03	-0.06	4.80E-01	-0.33	8.97E-04
9	202481_at	9249	DHRS3	dehydrogenase/reductase (SDR family) member 3	5.91E-02	-0.18	9.62E-03	-0.31	7.86E-05
9	202961_s_at	9551	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	6.73E-05	-0.02	8.31E-01	-0.37	1.33E-04
9	203385_at	1606	DGKA	diacylglycerol kinase, alpha 80kDa	3.49E-05	-0.24	1.41E-03	-0.57	2.55E-10
9	203386_at	9882	TBC1D4	TBC1 domain family, member 4	6.46E-02	-0.28	1.29E-04	-0.41	6.83E-07
9	203387_s_at	9882	TBC1D4	TBC1 domain family, member 4	6.58E-01	-0.34	3.08E-06	-0.38	5.73E-06
9	204560_at	2289	FKBP5	FK506 binding protein 5	7.21E-03	-0.05	6.33E-01	-0.34	4.23E-03
9	204777_s_at	4118	MAL	mal, T-cell differentiation protein	5.31E-04	-0.20	5.40E-02	-0.56	1.97E-06
9	205251_at	8864	PER2	period homolog 2 (Drosophila)	1.09E-02	0.00	9.88E-01	-0.26	1.95E-02
9	205798_at	3575	IL7R	interleukin 7 receptor	3.02E-05	-0.40	1.57E-04	-0.86	1.04E-11
9	205859_at	9450	LY86	lymphocyte antigen 86	4.33E-05	0.07	3.14E-01	-0.23	3.83E-03
9	205883_at	7704	ZBTB16	zinc finger and BTB domain containing 16	3.46E-02	-0.18	1.25E-01	-0.44	1.16E-03
9	207335_x_at	521	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	6.20E-06	-0.11	3.19E-01	-0.63	7.84E-07
9	207794_at		CCR2 /// FLJ78302	chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2-like	2.97E-03	-0.12	9.63E-02	-0.34	3.94E-05
9	209170_s_at	2824	GPM6B	glycoprotein M6B	8.92E-02	-0.06	3.82E-01	-0.18	2.08E-02
9	209184_s_at	8660	IRS2	insulin receptor substrate 2	7.37E-02	-0.13	1.90E-01	-0.31	5.62E-03

Supplemental Table. Genes identified by exploratory microarray analysis, organized by cluster.

					PBMC			
					HIV+No ART	HIV+ART vs. HIV Neg		HIV+No ART vs. HIV Neg	
Cluster	ProbeID	Entrez Gene	Gene Symbol	Gene Title	P-value	Fold Change	P-value	Fold Change	P-value
9	209492_x_at	521	ATP5I	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	6.17E-06	-0.14	2.24E-01	-0.70	3.17E-07
9	209678_s_at	5584	PRKCI	protein kinase C, iota	9.38E-06	-0.12	5.08E-02	-0.39	2.00E-08
9	210607_at	2323	FLT3LG	fms-related tyrosine kinase 3 ligand	8.45E-03	-0.11	1.43E-01	-0.30	2.62E-04
9	211663_x_at	5730	PTGDS	prostaglandin D2 synthase 21kDa (brain)	7.85E-03	-0.13	7.75E-02	-0.34	8.74E-05
9	211919_s_at	7852	CXCR4	chemokine (C-X-C motif) receptor 4	2.33E-01	-0.28	2.83E-03	-0.39	2.22E-04
9	211937_at	1975	EIF4B	eukaryotic translation initiation factor 4B	7.20E-05	-0.27	8.05E-04	-0.60	2.82E-10
9	211938_at	1975	EIF4B	eukaryotic translation initiation factor 4B	6.44E-01	-0.21	1.43E-03	-0.24	1.19E-03
9	212773_s_at	9804	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	3.68E-04	-0.12	4.13E-02	-0.35	8.06E-07
9	212843_at	4684	NCAM1	neural cell adhesion molecule 1	1.38E-04	-0.19	1.82E-03	-0.42	1.99E-09
9	213093_at	5578	PRKCA	protein kinase C, alpha	1.40E-05	-0.22	2.30E-03	-0.55	1.76E-10
9	213846_at	1350	COX7C	cytochrome c oxidase subunit VIIc	2.26E-04	-0.16	6.75E-02	-0.49	1.11E-06
9	214183_s_at	8277	TKTL1	transketolase-like 1	3.73E-01	-0.24	1.56E-03	-0.30	3.34E-04
9	218200_s_at	4708	NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	6.41E-03	-0.12	1.65E-01	-0.36	2.46E-04
9	218273_s_at	54704	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	1.22E-02	0.06	5.01E-01	-0.17	8.90E-02
9	219024_at	59338	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	1.16E-04	-0.12	6.07E-02	-0.39	4.34E-07
9	221006_s_at	81609	SNX27	sorting nexin family member 27	4.08E-05	-0.09	7.77E-02	-0.31	2.21E-07
9	221188_s_at	27141	CIDEB	cell death-inducing DFFA-like effector b	5.25E-04	-0.11	5.26E-02	-0.31	1.85E-06
9	221860_at	3191	HNRNPL	heterogeneous nuclear ribonucleoprotein L	1.45E-02	-0.18	3.25E-02	-0.39	5.17E-05
9	222040_at		HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728844	3.10E-03	-0.15	5.78E-02	-0.40	1.76E-05
9	225107_at	3181	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	5.09E-02	-0.24	1.95E-02	-0.44	1.51E-04
9	225204_at	160760	PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	5.41E-04	-0.11	1.26E-01	-0.37	9.35E-06
9	225312_at	170622	COMMD6	COMM domain containing 6	1.62E-03	-0.13	7.32E-02	-0.35	1.21E-05
9	225413_at	84833	USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	8.26E-04	-0.02	8.31E-01	-0.32	1.22E-03
9	225523_at	116540	MRPL53	mitochondrial ribosomal protein L53	1.42E-03	-0.09	3.19E-01	-0.40	1.76E-04
9	226218_at	3575	IL7R	interleukin 7 receptor	7.42E-02	-0.30	4.61E-04	-0.46	3.53E-06
9	226452_at	5163	PDK1	pyruvate dehydrogenase kinase, isozyme 1	7.52E-01	-0.13	6.22E-02	-0.15	5.24E-02
9	227722_at	6228	RPS23	ribosomal protein S23	5.18E-04	-0.13	1.63E-01	-0.47	1.49E-05
9	228007_at	387119	C6orf204	CDNA clone IMAGE:5265665	1.02E-03	-0.13	5.05E-02	-0.37	3.72E-06
9	228157_at	7756	ZNF207	zinc finger protein 207	3.52E-02	-0.19	7.24E-02	-0.41	5.29E-04
9	229253_at	117145	THEM4	thioesterase superfamily member 4	6.89E-05	-0.14	3.44E-02	-0.40	8.69E-08
9	231989_s_at	641298	LOC641298	PI-3-kinase-related kinase SMG-1	7.40E-02	-0.17	4.00E-02	-0.32	6.64E-04
9	235099_at	152189	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	3.89E-02	-0.11	6.78E-02	-0.23	5.51E-04
9	235735_at		---	---	1.25E-02	-0.13	6.78E-02	-0.32	1.27E-04
9	238880_at	2971	GTF3A	general transcription factor IIIA	2.19E-01	-0.25	3.26E-04	-0.34	2.14E-05
9	MTND1_at				1.29E-04	-0.15	1.03E-02	-0.39	2.43E-08
9	MTND1_s_at				3.09E-06	-0.12	2.06E-02	-0.36	1.13E-09
9	MTND4L_at				1.05E-05	-0.12	1.84E-02	-0.36	3.56E-09
9	MTND4L_x_at				8.90E-07	-0.13	1.75E-02	-0.40	2.20E-10
9	MTND5_at				1.30E-04	-0.08	3.41E-01	-0.41	1.83E-05