Supplemental Table 1. Differential gene expression (averages, Avg) in cultured endometrial stromal cells (T-HESC) under conditions (Ctl), treated with estrogen plus progesterone (E+P), treated with macrophage conditioned medium (Mph CM), or treated with E+P+Mph CM.[a]

GenBank Accession #	Description	Ctl Avg	E+P Avg	Mph CM	E+P+ MphCM	p value
	Signal Transduction					
NM_144497	A kinase (PRKA) anchor protein (gravin) 12 (AKAP12)	90.41	50.63	39.64	38.05	0.023
NM_005737	ADP-ribosylation factor-like 7 (ARL7)	1.43	1.18	2.78	1.32	0.024
NM_000682	adrenergic, alpha-2B-, receptor (ADRA2B)	1.41	1.90	6.80	10.76	0.018
NM_000683	adrenergic, alpha-2C-, receptor (ADRA2C)	3.76	15.91	1.11	3.81	0.015
NM_014840	AMP-activated protein kinase family member 5 (ARK5)	3.28	2.34	9.28	3.69	0.047
NM_000484	amyloid beta (A4) precursor protein (protease nexin-II) (APP)	44.47	26.38	28.65	20.42	0.025
NM_020350	angiotensin II receptor-associated protein (AGTRAP)	9.41	8.77	22.47	20.23	0.021
NM_018153	anthrax toxin receptor 1 (ANTXR1)	27.51	48.51	12.07	17.55	0.033
NM_001165	baculoviral IAP repeat-containing 3 (BIRC3)	0.31	0.37	1.92	1.20	0.047
NM_000623	bradykinin receptor B2 (BDKRB2)	59.53	35.75	20.98	26.34	0.023
NM_031908	C1q and tumor necrosis factor related protein 2 (C1QTNF2)	2.34	1.28	1.47	1.02	0.033
NM_001740	calbindin 2, 29kDa (calretinin) (CALB2)	0.83	0.87	12.85	4.56	0.022
NM_014478	calcitonin gene-related peptide-receptor component protein (RCP9)	3.58	2.21	2.29	1.50	0.042
NM_001896	casein kinase 2, alpha prime polypeptide (CSNK2A2)	17.39	18.19	7.87	8.54	0.030
NM_012121	CDC42 effector protein (Rho GTPase binding) 4 (CDC42EP4)	18.60	13.40	9.39	9.00	0.037
NM_001878	cellular retinoic acid binding protein 2 (CRABP2)	41.79	32.32	6.47	7.79	0.024
NM_015242	centaurin, delta 2 (CENTD2)	10.91	7.16	4.61	4.00	0.031
NM_001822	chimerin (chimaerin) 1 (CHN1)	95.69	81.08	48.49	32.45	0.043
NM_005242	coagulation factor II (thrombin) receptor-like 1 (F2RL1)	0.90	0.20	9.10	0.75	0.022
BC070085	colony stimulating factor 2 receptor, beta, low-affinity	1.60	0.51	20.84	6.07	0.026
NM_000760	colony stimulating factor 3 receptor (granulocyte) (CSF3R)	0.87	1.24	1.54	2.27	0.022
NM_001901	connective tissue growth factor (CTGF)	91.72	36.09	592.80	232.97	0.015
NM_016651	dapper homolog 1, antagonist of beta-catenin (DACT1)	3.32	1.53	8.59	1.95	0.020
NM_013989	deiodinase, iodothyronine, type II (DIO2)	1.44	1.99	9.49	3.56	0.014
NM_019074	delta-like 4 (DLL4)	1.58	1.93	3.63	3.35	0.030
NM_001388	developmentally regulated GTP binding protein 2 (DRG2)	2.74	2.38	1.19	1.27	0.026
NM_014421	dickkopf homolog 2 (DKK2)	5.78	1.17	0.47	1.01	0.015
NM_004417	dual specificity phosphatase 1 (DUSP1)	1.62	2.05	4.18	4.61	0.029
NM_004419	dual specificity phosphatase 5 (DUSP5)	1.47	1.32	2.80	5.92	0.015
NM_001953	endothelial cell growth factor 1 (platelet-derived) (ECGF1)	0.45	0.60	2.22	3.00	0.042

NM_005226	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3 (EDG3)	85.72	95.47	29.62	24.54	0.018
NM_004438	EphA4 (EPHA4)	6.10	4.90	2.23	2.53	0.043
NM_004444	EphB4 (EPHB4)	17.26	14.68	8.56	5.76	0.031
NM_004951	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) (EBI2)	0.94	0.31	3.04	0.80	0.023
NM_033136	fibroblast growth factor 1 (acidic) (FGF1)	1.24	0.73	3.32	1.96	0.034
NM_002006	fibroblast growth factor 2 (basic) (FGF2)	13.27	10.68	37.83	20.51	0.012
NM_004117	FK506 binding protein 5 (FKBP5)	0.28	1.96	0.57	1.88	0.031
NM_001459	fms-related tyrosine kinase 3 ligand (FLT3LG)	6.09	5.28	3.15	2.81	0.036
NM_153047	FYN oncogene related to SRC, FGR, YES (FYN)	82.73	69.82	31.33	51.18	0.034
NM_153442	G protein-coupled receptor 26 (GPR26)	1.58	1.79	3.68	4.40	0.026
NM_001505	G protein-coupled receptor 30 (GPR30)	2.08	1.72	0.85	0.43	0.042
NM_005458	G protein-coupled receptor 51 (GPR51)	5.58	6.20	12.02	14.30	0.034
NM_005684	G protein-coupled receptor 52 (GPR52)	1.21	1.63	2.27	3.56	0.032
NM_005308	G protein-coupled receptor kinase 5 (GRK5)	5.72	2.58	2.10	1.60	0.043
NM_014710	G protein-coupled receptor-associated sorting protein (GASP)	1.58	1.48	0.78	0.81	0.020
BC013576	GASP2 protein	24.17	14.10	13.62	9.84	0.031
NM_013372	gremlin 1 homolog, cysteine knot superfamily (GREM1)	2.79	2.08	16.70	14.21	0.028
NM_000557	growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5)	0.77	0.90	1.59	3.97	0.021
NM_016194	guanine nucleotide binding protein (G protein), beta 5 (GNB5)	47.81	22.79	17.01	14.99	0.038
NM_016315	GULP, engulfment adaptor PTB domain containing 1 (GULP1)	8.55	9.64	4.07	3.32	0.034
NM_007069	HRAS-like suppressor 3 (HRASLS3)	26.36	19.23	11.81	11.74	0.038
NM_022460	HS1-binding protein 3	9.95	6.85	4.25	5.29	0.044
NM_002192	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA)	17.49	17.04	84.96	48.10	0.022
NM_002222	inositol 1,4,5-triphosphate receptor, type 1 (ITPR1)	2.50	3.83	0.80	0.91	0.014
NM_002221	inositol 1,4,5-trisphosphate 3-kinase B (ITPKB)	3.79	2.46	2.19	1.87	0.037
NM_014214	inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2)	6.45	20.35	3.17	13.55	0.025
NM_198336	insulin induced gene 1 (INSIG1)	3.67	2.90	8.99	10.79	0.019
NM_000599	insulin-like growth factor binding protein 5 (IGFBP5)	0.47	0.77	2.77	1.26	0.049
NM_004972	Janus kinase 2 (a protein tyrosine kinase) (JAK2)	6.05	9.63	2.86	3.79	0.034
NM_006611	killer cell lectin-like receptor subfamily A, member 1 (KLRA1)	2.01	1.89	0.96	0.97	0.034
NM_015236	latrophilin 3 (LPHN3)	36.57	29.47	5.63	5.74	0.016
NM_006863	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1)	1.69	2.25	4.57	2.94	0.037
NM_014449	likely ortholog of mouse gene rich cluster, A gene (GRCA)	6.12	4.16	2.34	2.13	0.019
NM_032641	likely ortholog of mouse gene rich cluster, C9 gene (GRCC9)	9.26	8.06	4.47	4.54	0.045

NM_144641	likely ortholog of mouse protein phosphatase 2C eta	9.61	8.17	4.50	4.71	0.038
NM_030952	likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK)	2.10	1.50	4.25	5.03	0.029
NM_012320	lysophospholipase 3 (lysosomal phospholipase A2) (LYPLA3)	2.06	1.90	12.76	20.96	0.014
NM_199054	MAP kinase-interacting serine/threonine kinase 2 (MKNK2)	3.74	2.62	1.22	1.18	0.021
NM_145015	MAS-related GPR, member F (MRGPRF)	4.72	4.40	2.03	3.03	0.030
NM_000529	melanocortin 2 receptor (adrenocorticotropic hormone) (MC2R)	0.97	1.27	2.02	1.90	0.032
NM_002391	midkine (neurite growth-promoting factor 2) (MDK)	149.15	127.23	76.38	68.19	0.039
NM_001001931	mitochondrial tumor suppressor 1 (MTUS1)	23.80	7.41	8.10	5.04	0.039
NM_002754	mitogen-activated protein kinase 13 (MAPK13)	1.81	1.35	4.40	2.92	0.026
NM_145110	mitogen-activated protein kinase kinase 3 (MAP2K3)	9.47	6.16	20.41	19.41	0.022
NM_005204	mitogen-activated protein kinase kinase kinase 8 (MAP3K8)	1.55	1.23	4.61	11.32	0.013
NM_031419	molecule possessing ankyrin repeats induced by lipopolysaccharide (MAIL)	10.83	10.40	23.19	19.52	0.041
NM_002506	nerve growth factor, beta polypeptide (NGFB)	5.02	1.35	2.15	1.53	0.018
NM_006403	neural precursor cell expressed, developmentally down-regulated 9 (NEDD9)	0.84	0.94	2.28	1.34	0.019
NM_014284	neurochondrin (NCDN)	7.20	6.51	3.73	4.93	0.030
NM_139160	novel 583 KDA protein (LOC91614)	2.85	1.61	5.74	4.25	0.030
NM_002502	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) (NFKB2)	0.99	0.92	2.29	2.17	0.030
NM_020529	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA)	8.88	12.89	16.41	26.76	0.031
NM_004556	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE)	2.85	1.58	6.26	4.70	0.019
NM_005007	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1 (NFKBIL1)	20.23	17.89	9.57	10.26	0.036
NM_005126	nuclear receptor subfamily 1, group D, member 2 (NR1D2)	2.93	2.01	1.88	1.13	0.041
NM_021005	nuclear receptor subfamily 2, group F, member 2 (NR2F2)	12.88	7.19	6.13	5.45	0.024
NM_003999	oncostatin M receptor (OSMR)	2.20	8.17	7.95	6.91	0.041
NM_033014	osteoglycin (osteoinductive factor, mimecan) (OGN)	2.24	7.89	0.65	1.97	0.031
NM_000916	oxytocin receptor (OXTR)	6.73	5.81	29.80	26.53	0.020
NM_003711	phosphatidic acid phosphatase type 2A (PPAP2A)	80.83	110.17	23.13	28.42	0.015
NM_005028	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha (PIP5K2A)	1.64	1.44	0.82	0.77	0.035
NM_005019	phosphodiesterase 1A, calmodulin-dependent (PDE1A)	1.99	1.58	0.30	1.15	0.026
NM_006202	phosphodiesterase 4A, cAMP-specific (PDE4A)	6.60	5.72	2.87	3.17	0.026
NM_001083	phosphodiesterase 5A, cGMP-specific (PDE5A)	1.80	1.39	0.75	0.58	0.022
NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide (PIK3CD)	2.36	1.72	4.91	2.89	0.031

NM_002646	phosphoinositide-3-kinase, class 2, beta polypeptide (PIK3C2B)	6.62	5.10	1.58	1.97	0.026
NM_181523	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) (PIK3R1)	42.00	56.95	14.63	33.99	0.031
NM_003629	phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) (PIK3R3)	23.60	13.79	6.42	5.46	0.032
NM_019012	phosphoinositol 3-phosphate-binding protein-2 (PEPP2)	8.18	6.96	4.59	3.97	0.041
NM_002667	phospholamban (PLN)	0.40	0.55	15.36	4.48	0.012
NM_015192	phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1)	4.37	2.71	1.14	1.39	0.023
NM_020353	phospholipid scramblase 4 (PLSCR4)	29.06	18.17	12.38	12.85	0.039
NM_025208	platelet derived growth factor D (PDGFD)	4.50	8.02	0.93	2.76	0.026
NM_002609	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	21.53	16.34	10.76	11.65	0.030
NM_006622	polo-like kinase 2 (PLK2)	9.83	4.70	3.90	6.09	0.034
NM_153026	prickle-like 1 (PRICKLE1) [Wnt pathway]	71.53	54.57	48.16	32.39	0.042
NM_024897	progestin and adipoQ receptor family member VI (PAQR6)	2.28	3.21	1.00	1.26	0.034
NM_024430	proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2)	1.56	1.21	3.28	2.55	0.048
NM_020440	prostaglandin F2 receptor negative regulator (PTGFRN)	19.87	10.87	10.17	8.48	0.012
NM_002737	protein kinase C, alpha (PRKCA)	1.84	1.34	1.08	0.89	0.036
NM_006255	protein kinase C, eta (PRKCH)	0.62	0.96	1.81	2.35	0.039
NM_005398	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C)	41.40	22.30	13.06	15.23	0.037
BC067106	putative G protein coupled receptor	5.28	5.08	15.39	12.99	0.024
NM_016277	RAB23, member RAS oncogene family (RAB23)	69.28	78.58	31.33	40.69	0.014
NM_004794	RAB33A, member RAS oncogene family (RAB33A)	2.93	3.50	1.43	1.29	0.025
NM_022337	RAB38, member RAS oncogene family (RAB38)	1.54	0.68	0.51	0.98	0.038
NM_002867	RAB3B, member RAS oncogene family (RAB3B)	4.66	2.36	9.18	5.60	0.032
NM_006822	RAB40B, member RAS oncogene family (RAB40B)	13.07	12.64	3.89	5.19	0.022
NM_015149	ral guanine nucleotide dissociation stimulator-like 1 (RGL1)	30.39	10.33	10.41	9.81	0.032
NM_005739	RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1)	4.18	3.13	14.06	19.47	0.010
NM_004675	ras homolog gene family, member I (ARHI)	1.01	0.35	4.69	6.73	0.024
NM_022157	Ras-related GTP binding C (RRAGC)	3.66	2.69	1.73	1.96	0.031
NM_005854	receptor (calcitonin) activity modifying protein 2 (RAMP2)	2.41	2.77	1.16	1.21	0.045
NM_198230	regulator of G-protein signalling 12 (RGS12)	4.51	3.57	1.79	1.41	0.034
NM_002928	regulator of G-protein signalling 16 (RGS16)	0.64	0.79	2.38	5.24	0.027
NM_014059	response gene to complement 32 (RGC32)	28.12	23.67	60.89	120.97	0.022
NM_004585	retinoic acid receptor responder 3 (RARRES3)	26.32	20.31	8.85	10.66	0.049
NM_002899	retinol binding protein 1, cellular (RBP1)	16.66	15.66	10.73	8.14	0.028
NM_001175	Rho GDP dissociation inhibitor (GDI) beta (ARHGDIB)	9.51	6.45	18.90	14.20	0.024

NM_020809	Rho GTPase activating protein 20 (ARHGAP20)	22.24	25.79	8.43	7.14	0.033
NM_020824	Rho GTPase activating protein 21 (ARHGAP21)	6.42	4.52	3.17	2.49	0.023
NM_013427	Rho GTPase activating protein 6 (ARHGAP6)	11.18	15.17	1.90	5.51	0.013
NM_019555	Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3)	0.62	0.55	1.81	2.20	0.019
NM_004755	ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5)	6.07	3.58	1.32	0.81	0.020
NM_002961	S100 calcium binding protein A4 (S100A4)	52.98	76.21	18.22	30.20	0.024
NM_020796	sema domain, transmembrane domain, and cytoplasmic domain (semaphorin) 6A (SEMA6A)	7.51	5.65	0.96	2.20	0.015
NM_030754	serum amyloid A2 (SAA2)	2.77	3.17	3.98	23.65	0.037
NM_004657	serum deprivation response (phosphatidylserine binding protein) (SDPR)	5.59	5.51	2.08	2.02	0.030
NM_012309	SH3 and multiple ankyrin repeat domains 2 (SHANK2)	4.01	5.39	6.45	7.80	0.034
NM_004844	SH3-domain binding protein 5 (BTK-associated) (SH3BP5)	24.40	14.41	10.18	6.90	0.019
NM_020974	signal peptide, CUB domain, EGF-like 2 (SCUBE2)	7.58	8.80	3.32	3.32	0.028
NM_020808	signal-induced proliferation-associated 1 like 2 (SIPA1L2)	15.70	2.50	1.32	1.38	0.021
R02198	similar to blue-sensitive opsin	10.51	7.94	21.64	15.97	0.034
NM_172069	similar to PH (pleckstrin homology) domain	3.93	2.94	0.89	0.82	0.024
NM_177403	similar to RAB7, member RAS oncogene family (MGC9726)	4.47	3.23	1.16	1.64	0.023
NM_005585	SMAD, mothers against DPP homolog 6 (SMAD6)	3.95	2.71	2.01	1.62	0.036
NM_015385	sorbin and SH3 domain containing 1 (SORBS1)	0.95	1.39	0.95	3.77	0.047
NM_015180	spectrin repeat containing, nuclear envelope 2 (SYNE2)	3.52	1.94	1.80	1.13	0.021
NM_003127	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) (SPTAN1)	50.82	36.63	30.05	24.94	0.032
NM_006714	sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A)	34.87	32.65	9.87	14.03	0.018
NM_021972	sphingosine kinase 1 (SPHK1)	0.94	0.36	3.76	2.11	0.036
NM_005841	sprouty homolog 1, antagonist of FGF signaling (SPRY1)	3.95	1.80	1.23	1.03	0.046
NM_025106	SPRY domain-containing SOCS box protein SSB-1 (SSB1)	6.07	5.23	17.10	7.58	0.029
NM_006748	Src-like-adaptor (SLA)	0.51	0.36	2.13	3.79	0.047
NM_003714	stanniocalcin 2 (STC2)	5.08	3.23	12.17	30.62	0.020
NM_003955	suppressor of cytokine signaling 3	0.30	0.47	1.64	1.47	0.033
NM_016945	taste receptor, type 2, member 16 (TAS2R16)	2.66	2.93	6.88	7.13	0.027
NM_015173	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 (TBC1D1)	1.55	1.81	3.51	4.22	0.045
NM_170754	tensin like C1 domain containing phosphatase (TENC1)	7.41	5.97	3.37	4.08	0.036
NM_006531	tetratricopeptide repeat domain 10 (TTC10)	3.57	2.43	1.30	1.43	0.034
NM_003597	TGFB inducible early growth response 2 (TIEG2)	14.05	14.04	7.31	6.60	0.036

NM_021809	TGFB-induced factor 2 (TALE family homeobox) (TGIF2)	5.31	4.52	3.54	2.15	0.047
NM_003250	thyroid hormone receptor, alpha (v-erb-a oncogene homolog) (THRA)	8.94	7.48	2.76	3.70	0.013
NM_013381	thyrotropin-releasing hormone degrading ectoenzyme (TRHDE)	4.69	4.38	3.74	2.11	0.019
NM_006058	TNFAIP3 interacting protein 1 (TNIP1)	5.18	3.84	10.33	9.55	0.038
NM_005647	transducin (beta)-like 1X-linked (TBL1X)	27.86	19.94	10.25	11.60	0.026
NM_005077	transducin-like enhancer of split 1 (E(sp1) homolog) (TLE1)	38.46	26.59	14.02	17.16	0.036
NM_007005	transducin-like enhancer of split 4 (E(sp1) homolog) (TLE4)	12.80	8.10	7.67	4.92	0.021
NM_003239	transforming growth factor, beta 3 (TGFB3)	2.05	0.83	0.84	0.46	0.028
NM_005423	trefoil factor 2 (spasmolytic protein 1) (TFF2)	10.26	12.13	13.65	20.95	0.017
NM_025195	tribbles homolog 1 (TRIB1)	1.78	1.94	4.25	3.00	0.029
NM_021158	tribbles homolog 3 (TRIB3)	8.16	4.92	1.47	1.81	0.033
NM_016175	truncated calcium binding protein	20.27	19.53	9.49	11.33	0.026
NM_003326	tumor necrosis factor (ligand) superfamily, member 4 (TNFSF4)	5.87	4.68	24.52	11.21	0.013
NM_002546	tumor necrosis factor receptor superfamily 11b (TNFRSF11B)	1.92	1.72	10.15	4.67	0.013
NM_016639	tumor necrosis factor receptor superfamily, member 12A (TNFRSF12A)	40.73	18.11	127.28	75.70	0.019
NM_016639	tumor necrosis factor receptor superfamily, member 12A (TNFRSF12A)	20.47	9.99	68.26	41.42	0.022
NM_032871	tumor necrosis factor receptor superfamily, member 19-like (TNFRSF19L)	2.38	2.14	4.93	3.81	0.020
NM_032871	tumor necrosis factor receptor superfamily, member 19-like (TNFRSF19L)	0.95	0.81	2.09	1.16	0.021
NM_001066	tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B)	3.65	5.26	6.05	11.30	0.039
NM_014452	tumor necrosis factor receptor superfamily, member 21 (TNFRSF21)	15.69	13.42	33.55	38.88	0.039
NM_006290	tumor necrosis factor, alpha-induced protein 3 (TNFAIP3)	0.88	2.14	2.91	5.08	0.024
NM_006293	TYRO3 protein tyrosine kinase (TYRO3)	14.18	15.96	6.08	7.42	0.038
NM_005148	unc-119 homolog (UNC119)	7.38	6.15	3.68	3.71	0.025
NM_170744	unc-5 homolog B (UNC5B) [netrin receptor]	4.98	2.45	1.71	1.13	0.033
NM_005239	v-ets erythroblastosis virus E26 oncogene homolog 2 (ETS2)	5.09	4.98	2.42	4.42	0.026
NM_012323	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (MAFF)	1.86	1.35	5.50	3.82	0.023
NM_002350	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN)	1.34	1.11	2.67	3.03	0.014
NM_003882	WNT1 inducible signaling pathway protein 1 (WISP1)	0.88	0.65	2.43	3.76	0.019
	Proteases and related					
NM_033274	a disintegrin and metalloproteinase domain 19 (meltrin beta) (ADAM19)	1.91	1.41	4.35	2.16	0.034
NM_153202	a disintegrin and metalloproteinase domain 33 (ADAM33)	26.80	23.54	6.82	8.77	0.031
NM_003817	a disintegrin and metalloproteinase domain 7 (ADAM7)	1.21	1.18	1.98	3.36	0.012

NM_001109	a disintegrin and metalloproteinase domain 8 (ADAM8)	5.57	4.53	4.24	2.55	0.029
NM_006988	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1)	2.02	4.81	1.01	2.87	0.026
NM_007038	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (ADAMTS5)	31.10	48.86	9.96	14.69	0.022
NM_000070	calpain 3, (p94) (CAPN3)	2.64	2.67	1.32	1.52	0.036
NM_004079	cathepsin S (CTSS)	2.33	1.81	5.16	3.30	0.018
NM_016302	cereblon (CRBN)	47.98	38.67	18.66	19.66	0.035
NM_020169	latexin (LXN)	14.74	9.79	49.42	10.75	0.041
NM_002421	matrix metalloproteinase 1 (interstitial collagenase) (MMP1)	5.28	1.22	74.68	16.01	0.014
NM_002422	matrix metalloproteinase 3 (stromelysin 1) (MMP3)	1.75	1.70	78.19	25.54	0.022
NM_002658	plasminogen activator, urokinase (PLAU)	26.22	15.76	69.90	22.29	0.038
NM_002659	plasminogen activator, urokinase receptor (PLAUR)	13.82	9.59	50.82	26.94	0.024
NM_002575	serine (or cysteine) proteinase inhibitor, clade B2 (SERPINB2)	0.56	0.25	15.22	5.00	0.031
NM_004568	serine (or cysteine) proteinase inhibitor, clade B6 (SERPINB6)	32.53	23.77	18.84	16.32	0.033
NM_003784	serine (or cysteine) proteinase inhibitor, clade B7 (SERPINB7)	1.29	1.67	2.54	1.62	0.037
NM_000602	serine (or cysteine) proteinase inhibitor, clade E1 (plasminogen activator inhibitor type 1) (SERPINE1)	40.29	107.23	324.76	368.40	0.019
NM_006216	serine (or cysteine) proteinase inhibitor, clade E2 (plasminogen activator inhibitor type 1) (SERPINE2)	60.23	62.48	149.05	77.02	0.024
NM_197941	similar to A disintegrin and metalloproteinase with thrombospondin motifs 10 (ADAM-TS 10)	1.68	1.46	3.25	1.57	0.038
NM_021928	similar to signal peptidase SPC22/23	17.05	15.37	38.41	39.08	0.014
NM_003278	tetranectin (plasminogen binding protein) (TNA)	47.09	176.60	21.66	93.87	0.014
NM_006528	tissue factor pathway inhibitor 2 (TFPI2)	113.56	73.13	228.52	196.02	0.019
NM_000362	tissue inhibitor of metalloproteinase 3 (TIMP3)	4.20	5.94	1.85	2.12	0.030
	Steroid metabolism					
NM_001353	aldo-keto reductase family 1, member C1 (AKR1C1)	4.21	5.35	1.58	3.21	0.042
NM_004391	cytochrome P450, family 8, subfamily B, polypeptide 1 (CYP8B1)	2.25	2.38	4.08	4.48	0.015
NM_005525	hydroxysteroid (11-beta) dehydrogenase 1 (HSD11B1)	0.89	4.14	22.58	73.58	0.009
	Transcriptional regulation					
NM_004024	activating transcription factor 3 (ATF3)	1.86	1.14	7.72	7.50	0.012
NM_020183	aryl hydrocarbon receptor nuclear translocator-like 2 (ARNTL2)	1.35	1.10	6.07	3.82	0.014
NM_032827	atonal homolog 8 (ATOH8)	13.40	10.03	6.91	11.79	0.041
NM_003670	basic helix-loop-helix domain containing, class B, 2 (BHLHB2)	2.43	2.71	4.05	4.67	0.037

NM_013450	bromodomain adjacent to zinc finger domain, 2B (BAZ2B)	4.39	3.76	2.58	2.18	0.031
NM_007371	bromodomain containing 3 (BRD3)	14.04	11.66	7.62	6.15	0.033
NM_052854	cAMP responsive element binding protein 3-like 1 (CREB3L1)	28.53	19.97	15.20	12.87	0.033
NM_005195	CCAAT/enhancer binding protein (C/EBP), delta (CEBPD)	6.45	10.75	17.93	37.25	0.021
NM_001806	CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG)	7.71	6.11	2.03	2.14	0.043
NM_024300	coiled-coil-helix-coiled-coil-helix domain containing 7 (CHCHD7)	15.92	18.89	7.96	10.05	0.015
NM_016206	colon carcinoma related protein	3.47	3.73	5.82	8.36	0.047
NM_005093	core-binding factor, runt domain, alpha subunit 2; translocated to, 2 (CBFA2T2)	5.47	3.65	3.04	2.62	0.047
NM_012081	elongation factor, RNA polymerase II, 2 (ELL2)	5.53	3.82	11.26	13.18	0.022
NM_004098	empty spiracles homolog 2 (EMX2)	57.83	38.72	20.42	26.58	0.023
NM_015630	enhancer of polycomb homolog 2 (EPC2)	27.30	17.10	12.44	10.18	0.030
NM_005438	FOS-like antigen 1 (FOSL1)	3.82	2.68	9.56	6.51	0.026
NM_199135	FOXD4-like 2 (FOXD4L2)	2.03	1.58	0.90	0.66	0.017
NM_032638	GATA binding protein 2 (GATA2)	31.24	23.10	13.74	9.73	0.020
NM_005257	GATA binding protein 6 (GATA6)	2.99	1.81	11.74	6.18	0.030
NM_173537	GTF2I repeat domain containing 2 (GTF2IRD2)	10.59	9.45	4.12	4.05	0.026
NM_021973	heart and neural crest derivatives expressed 2 (HAND2)	26.17	33.79	12.76	27.48	0.042
X07290	HF12 gene	3.02	2.49	1.65	1.41	0.050
NM_145904	high mobility group AT-hook 1 (HMGA1)	8.07	5.41	19.52	12.31	0.023
NM_006037	histone deacetylase 4 (HDAC4)	10.26	8.20	3.27	3.16	0.022
NM_006735	homeo box A2 (HOXA2)	2.62	1.86	1.21	1.16	0.043
NM_019102	homeo box A5 (HOXA5)	17.75	12.70	7.17	7.35	0.038
NM_002147	homeo box B5 (HOXB5)	23.80	17.42	12.46	10.67	0.021
NM_002148	homeo box D10 (HOXD10)	30.24	25.52	11.38	10.47	0.014
NM_021192	homeo box D11 (HOXD11)	36.34	33.54	18.87	19.50	0.031
NM_181358	homeodomain interacting protein kinase 1 (HIPK1)	3.72	2.43	2.41	1.80	0.040
NM_139211	homeodomain-only protein (HOP)	0.53	0.58	4.23	4.65	0.050
NM_199072	I-mfa domain-containing protein (HIC)	24.86	24.35	10.17	14.52	0.018
NM_002167	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3)	4.93	5.10	18.37	13.45	0.018
AF251050	jerky	7.24	6.56	3.88	3.63	0.019
NM_002229	jun B proto-oncogene (JUNB)	3.89	3.51	8.00	6.11	0.029
NM_130469	jun dimerization protein 2 (JDP2)	56.79	40.33	22.60	24.47	0.026
NM_018664	Jun dimerization protein p21SNFT (SNFT)	1.04	0.94	2.47	3.29	0.026
NM_004235	Kruppel-like factor 4 (gut) (KLF4)	48.90	58.13	6.02	12.04	0.019
NM_015478	l(3)mbt-like (Drosophila) (L3MBTL)	1.78	1.78	0.89	0.91	0.012
NM_014583	LIM and cysteine-rich domains 1 (LMCD1)	1.34	1.12	5.13	5.86	0.020
NM_002397	MADS box transcription enhancer factor 2, polypeptide C (MEF2C)	2.41	1.07	1.19	1.11	0.049
NM_013446	makorin, ring finger protein, 1 (MKRN1)	15.47	13.14	7.97	7.91	0.035
NM_006800	male-specific lethal 3-like 1 (MSL3L1)	8.19	6.20	3.77	2.83	0.039
NM_005962	MAX interactor 1 (MXI1)	3.14	2.85	1.76	1.02	0.047

NM_004739	metastasis-associated gene family, member 2 (MTA2)	6.41	5.45	3.25	2.63	0.022
NM_006722	microphthalmia-associated transcription factor (MITF)	11.72	11.62	3.99	5.03	0.023
NM_014048	myocardin-related transcription factor B (MRTF-B)	5.44	3.45	3.05	2.69	0.031
NM_006167	NK3 transcription factor related, locus 1 (NKX3-1)	2.06	1.63	5.41	4.17	0.015
NM_003113	nuclear antigen Sp100 (SP100)	5.21	3.20	3.21	2.04	0.042
NM_005595	nuclear factor I/A (NFIA)	2.53	2.15	1.07	1.50	0.049
L22454	nuclear respiratory factor-1 (NRF-1)	2.37	1.45	1.45	1.18	0.012
NM_145260	odd-skipped homolog (ODD)	5.02	5.20	2.11	1.98	0.034
NM_053001	odd-skipped-related 2A protein (OSR2)	90.26	113.88	8.49	9.96	0.014
NM_033222	PC4 and SFRS1 interacting protein 1 (PSIP1)	9.00	5.73	5.31	4.28	0.029
NM_018313	polybromo 1 (PB1)	5.39	3.69	2.99	2.52	0.042
NM_020226	PR domain containing 8 (PRDM8)	6.32	6.57	2.97	3.33	0.039
NM_020524	pre-B-cell leukemia transcription factor interacting protein 1 (PBXIP1)	25.63	19.70	13.50	12.15	0.036
NM_006608	putative homeodomain transcription factor 1 (PHTF1)	7.54	5.67	4.74	3.58	0.040
AK122739	similar to dHand protein	49.62	64.33	13.82	44.46	0.012
AA977908	similar to homeobox protein HOX-D4	8.32	5.99	2.59	2.39	0.022
AK128624	similar to Zinc finger protein 29	3.89	4.06	2.69	1.78	0.036
R98102	similar to zinc finger protein 7	11.39	9.88	5.48	5.59	0.038
AK096536	similar to zinc finger protein 84	5.68	4.87	2.80	2.85	0.040
AF020276	spinocerebellar ataxia 7 (SCA7)	1.57	2.07	4.10	5.79	0.021
NM_003108	SRY (sex determining region Y)-box 11 (SOX11)	1.91	1.67	0.72	0.83	0.048
NM_006943	SRY (sex determining region Y)-box 12 (SOX12)	7.45	6.13	2.80	3.00	0.029
NM_003107	SRY (sex determining region Y)-box 4 (SOX4)	86.05	88.78	86.80	31.85	0.027
NM_005996	T-box 3 (ulnar mammary syndrome) (TBX3)	0.87	1.15	1.75	1.90	0.024
NM_003195	transcription elongation factor A (SII), 2 (TCEA2)	24.21	20.24	12.10	13.07	0.023
NM_006756	transcription elongation factor A 1 isoform 1	63.35	50.29	26.38	26.30	0.030
NM_207040	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12)	27.12	27.01	13.72	12.39	0.022
M77810	transcription factor GATA-2 (GATA-2)	2.37	1.39	1.00	0.66	0.039
NM_000474	twist homolog 1 (TWIST1)	49.90	34.10	18.51	21.61	0.028
NM_020861	zinc finger and BTB domain containing 2 (ZBTB2)	9.05	5.21	4.04	3.38	0.022
NM_032494	zinc finger CCCH type domain containing 8 (ZC3HDC8)	3.02	2.74	1.31	1.23	0.035
NM_021994	zinc finger protein (C2H2 type) 277 (ZNF277)	6.09	6.76	3.16	4.06	0.045
NM_018651	zinc finger protein 167 (ZNF167)	2.06	1.64	1.14	0.98	0.049
NM_194320	zinc finger protein 169 (ZNF169)	5.53	5.46	11.37	13.10	0.022
NM_003451	zinc finger protein 177 (ZNF177)	5.36	4.89	2.68	2.48	0.025
NM_201599	zinc finger protein 261 (ZNF261)	7.14	4.89	2.93	2.65	0.031
NM_012482	zinc finger protein 281 (ZNF281)	17.90	13.84	40.49	30.98	0.038
NM_020843	zinc finger protein 291 (ZNF291)	4.05	3.00	2.26	1.83	0.037
NM_005453	zinc finger protein 297 (ZNF297)	8.47	6.74	4.60	3.82	0.038
NM_006973	zinc finger protein 32 (KOX 30) (ZNF32)	20.16	21.49	10.34	11.40	0.042

NM_003407	zinc finger protein 36, C3H type, homolog (ZFP36)	11.10	14.77	12.26	23.19	0.047
NM_174945	zinc finger protein 575 (ZNF575)	23.26	16.67	6.11	8.18	0.022
NM_016535	zinc finger protein 581 (ZNF581)	15.75	15.48	6.99	7.46	0.031
BC044615	zinc finger protein 599	3.24	3.64	1.60	1.98	0.020
NM_020787	zinc finger protein 624 (ZNF624)	3.25	2.61	1.58	1.71	0.024
U17838	zinc finger protein RIZ mRNA	16.23	14.10	6.97	6.35	0.030
NM_006060	zinc finger protein, subfamily 1A, 1 (Ikaros) (ZNFN1A1)	2.28	3.55	4.51	3.51	0.034
NM_032367	zinc finger, BED domain containing 3 (ZBED3)	6.71	5.18	1.81	1.17	0.017
	Cytoskeleton					
NM_001101	actin, beta (ACTB)	55.19	50.01	115.56	133.76	0.031
NM_005139	annexin A3 (ANXA3)	2.44	1.92	1.13	0.87	0.025
NM_021149	coactosin-like 1 (COTL1)	2.96	2.28	6.36	4.93	0.026
NM_018662	disrupted in schizophrenia 1 (DISC1)	5.08	2.83	3.02	2.18	0.039
NM_023036	dynein, axonemal, intermediate polypeptide 2 (DNAI2)	5.60	6.07	11.29	13.79	0.019
NM_003462	dynein, axonemal, light intermediate polypeptide 1 (DNALI1)	4.83	4.46	2.42	2.88	0.046
NM_015033	formin binding protein 1 (FNBP1)	18.84	12.50	9.00	7.78	0.017
NM_017415	kelch-like 3 (KLHL3)	9.91	8.35	2.26	5.16	0.023
NM_031961	keratin associated protein 9-2 (KRTAP9-2)	1.48	2.39	3.40	3.35	0.034
NM_144722	KPL2 protein	2.08	1.60	0.63	1.25	0.039
NM_000426	laminin, alpha 2 (merosin) (LAMA2)	5.23	6.96	1.93	2.60	0.021
NM_002292	laminin, beta 2 (laminin S) (LAMB2)	36.08	28.42	17.90	15.81	0.035
NM_178428	late envelope protein 9 (LEP9)	1.44	1.41	5.22	4.81	0.026
NM_005379	myosin IA (MYO1A)	0.77	0.88	1.45	3.33	0.015
NM_013262	myosin regulatory light chain interacting protein (MYLIP)	19.80	14.48	6.39	10.78	0.034
NM_002477	myosin, light polypeptide 5, regulatory (MYL5)	14.01	10.89	5.20	7.94	0.033
M80899	novel protein AHNAK	43.20	36.31	16.25	13.81	0.021
NM_017668	nudE nuclear distribution gene E homolog 1(NDE1)	20.54	13.78	9.51	6.97	0.034
NM_000231	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein) (SGCG)	8.95	9.46	3.97	4.66	0.031
AK128036	similar to Keratin, type I cytoskeletal 18	19.81	6.53	43.24	15.58	0.016
NM_024803	tubulin, alpha-like 3 (TUBAL3)	11.47	9.44	22.55	17.58	0.012
NM_001069	tubulin, beta polypeptide (TUBB)	7.88	5.10	14.11	15.51	0.036
NM_178012	tubulin, beta polypeptide paralog	1.29	1.59	2.64	1.54	0.031
NM_016262	tubulin, epsilon 1 (TUBE1)	15.35	10.55	5.90	6.77	0.043
NM_017491	WD repeat domain 1 (WDR1)	9.78	8.88	17.92	19.24	0.026
	Defense/Immunity					
NM_203416	CD163 antigen (CD163)	0.21	0.34	0.40	2.50	0.045
NM_020404	CD164 sialomucin-like 1 (CD164L1)	179.27	168.40	93.02	98.92	0.015
NM_002985	chemokine (C-C motif) ligand 5 (CCL5)	0.84	1.20	2.58	7.44	0.014
NM_006273	chemokine (C-C motif) ligand 7 (CCL7)	3.14	1.56	9.26	8.71	0.017
NM_005623	chemokine (C-C motif) ligand 8 (CCL8)	0.28	0.71	0.90	9.40	0.036
NM_016557	chemokine (C-C motif) receptor-like 1 (CCRL1)	1.65	0.38	8.35	2.57	0.022
NM_002089	chemokine (C-X-C motif) ligand 2 (CXCL2)	0.28	0.11	0.91	5.40	0.035

NM_021010	defensin, alpha 5, Paneth cell-specific (DEFA5)	0.64	0.90	1.43	2.34	0.042
NM_005755	Epstein-Barr virus induced gene 3 (EBI3)	1.75	1.76	2.77	3.96	0.019
NM_207585	interferon (alpha, beta and omega) receptor 2 (IFNAR2)	4.16	3.01	9.86	8.30	0.014
NM_006332	interferon, gamma-inducible protein 30 (IFI30)	4.97	5.37	10.99	12.68	0.045
NM_001548	interferon-induced protein with tetratricopeptide repeats 1 (IFIT1)	12.23	8.20	5.33	3.94	0.019
NM_001547	interferon-induced protein with tetratricopeptide repeats 2 (IFIT2)	1.55	1.02	0.85	0.62	0.042
NM_000576	interleukin 1, beta (IL1B)	0.58	0.83	8.98	3.47	0.022
NM_000641	interleukin 11 (IL11)	0.82	0.56	1.69	0.52	0.043
NM_002189	interleukin 15 receptor, alpha (IL15RA)	2.07	2.19	9.45	7.99	0.017
NM_000600	interleukin 6 (interferon, beta 2) (IL6)	3.19	3.39	8.51	9.24	0.022
NM_002185	interleukin 7 receptor (IL7R)	2.31	2.99	7.72	12.87	0.038
NM_000584	interleukin 8 (IL8)	1.08	0.55	100.72	140.98	0.009
NM_001557	interleukin 8 receptor, beta (IL8RB)	1.17	1.04	1.90	2.47	0.026
NM_004221	natural killer cell transcript 4 (NK4)	3.17	2.92	51.21	46.97	0.013
AK094237	similar to MHC class I chain-related gene A protein	0.81	1.71	1.77	1.49	0.023
NM_025217	UL16 binding protein 2 (ULBP2)	4.23	3.70	9.86	7.65	0.018
	Cell cycle/cell death					
NM_001731	B-cell translocation gene 1, anti-proliferative (BTG1)	68.77	88.78	27.08	31.19	0.031
NM_004282	BCL2-associated athanogene 2 (BAG2)	25.58	33.92	11.89	13.51	0.013
NM_004305	bridging integrator 1 (BIN1)	16.01	12.18	6.76	4.76	0.025
NM_032996	caspase 9, apoptosis-related cysteine protease (CASP9)	12.26	10.05	6.06	6.11	0.024
NM_020739	cell cycle progression 8 protein (CPR8)	68.36	43.35	34.58	36.48	0.025
NM_015076	cyclin-dependent kinase (CDC2-like) 11 (CDK11)	19.62	13.58	9.09	7.78	0.030
NM_000076	cyclin-dependent kinase inhibitor 1C (p57, Kip2) (CDKN1C)	52.33	61.13	22.24	33.64	0.043
NM_004196	cyclin-dependent kinase-like 1 (CDC2-related kinase) (CDKL1)	2.88	3.81	1.04	1.19	0.024
NM_001321	cysteine and glycine-rich protein 2 (CSRP2)	50.84	27.88	175.90	113.55	0.025
NM_001343	disabled homolog 2, mitogen-responsive phosphoprotein (DAB2)	13.57	9.46	27.32	27.18	0.048
NM_019058	DNA-damage-inducible transcript 4 (DDIT4)	13.06	14.83	3.45	5.24	0.036
NM_145244	DNA-damage-inducible transcript 4-like (DDIT4L)	3.19	0.77	0.85	0.54	0.014
NM_002048	growth arrest-specific 1 (GAS1)	3.89	5.25	1.54	5.90	0.024
NM_201432	growth arrest-specific 7 (GAS7)	5.33	1.51	1.43	1.11	0.022
NM_003897	immediate early response 3 (IER3)	29.64	11.80	90.72	51.46	0.019
NM_022477	NDRG family member 3 (NDRG3)	19.16	16.13	9.58	8.93	0.043
NM_032510	par-6 partitioning defective 6 homolog gamma (PARD6G)	7.52	5.46	4.55	3.61	0.047
NM_003311	pleckstrin homology-like domain A2 (PHLDA2)	9.98	6.70	24.02	19.39	0.037
NM_025239	programmed cell death 1 ligand 2 (PDCD1LG2)	4.37	3.80	14.39	9.56	0.045
NM_145341	programmed cell death 4 (PDCD4)	9.42	10.28	4.00	3.97	0.014
NM_002727	proteoglycan 1, secretory granule (PRG1)	34.21	38.90	89.03	119.66	0.014

NM_015714	putative lymphocyte G0/G1 switch gene (G0S2)	2.45	8.95	17.54	30.77	0.017
NM_031459	sestrin 2 (SESN2)	11.06	7.98	5.42	4.76	0.037
H25717	similar to growth arrest and DNA-damage-inducible protein GADD153	4.73	3.54	1.75	1.81	0.013
NM_006542	S-phase response (cyclin-related) (SPHAR)	13.93	12.92	6.94	7.10	0.023
NM_025188	tripartite motif-containing 45 (TRIM45)	8.12	5.89	2.13	2.33	0.010
NM_033285	tumor protein p53 inducible nuclear protein 1 (TP53INP1)	36.91	31.72	17.17	14.06	0.026
NM_017523	XIAP associated factor-1 (HSXIAPAF1)	12.32	10.18	5.26	3.96	0.032
	Adhesion					
NM_181847	amphoterin induced gene 2 (AMIGO2)	1.43	0.92	16.42	9.25	0.013
NM_032457	BH-protocadherin (PCDH7)	7.19	4.34	1.95	2.80	0.044
NM_014343	claudin 15 (CLDN15)	2.47	1.90	1.06	1.21	0.049
NM_005545	immunoglobulin superfamily containing leucine-rich repeat (ISLR)	9.72	5.89	2.34	1.83	0.012
NM_181501	integrin, alpha 1 (ITGA1)	7.49	6.90	25.69	14.98	0.034
NM_000210	integrin, alpha 6 (ITGA6)	107.58	43.75	22.27	17.87	0.027
NM_014599	melanoma antigen, family D, 2 (MAGED2)	123.37	114.41	69.81	63.21	0.016
NM_138970	neurexin 3 (NRXN3)	9.23	22.75	28.02	30.34	0.037
NM_016522	neurotrimin (HNT)	2.59	1.10	7.32	3.12	0.032
NM_005014	osteomodulin (OMD)	3.75	14.94	1.43	2.75	0.018
NM_032961	protocadherin 10 (PCDH10)	4.63	2.58	2.20	1.87	0.044
NM_203487	protocadherin 9 (PCDH9)	2.24	1.35	0.52	0.42	0.027
NM_018931	protocadherin beta 11 (PCDHB11)	3.39	3.00	2.07	1.67	0.037
NM_019119	protocadherin beta 9 (PCDHB9)	3.81	3.76	2.28	1.73	0.035
NM_033130	sialic acid binding Ig-like lectin 10 (SIGLEC10)	1.52	1.44	2.65	3.52	0.021
AK091292	similar to cadherin-related tumor suppressor precursor	32.63	24.43	10.25	12.83	0.027
U60115	skeletal muscle LIM-protein FHL1	26.26	30.50	7.67	11.96	0.020
NM_016157	trophinin (TRO), transcript variant 3	14.46	9.58	7.13	5.00	0.026
	Extracellular matrix					
NM_017680	asporin (LRR class 1) (ASPN)	6.67	13.07	1.36	3.00	0.022
NM_001276	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1)	2.43	2.49	4.17	6.97	0.032
NM_004000	chitinase 3-like 2 (CHI3L2)	0.75	1.28	2.31	35.67	0.030
NM_080806	collagen, type XIII, alpha 1 (COL13A1)	4.61	2.27	16.15	8.89	0.015
NM_052846	elastin microfibril interfacer 3 (EMILIN3)	1.14	2.02	0.86	3.54	0.026
NM_001393	extracellular matrix protein 2, female organ and adipocyte specific (ECM2)	6.48	9.14	2.32	3.47	0.019
Y11711	Extracellular matrix protein collagen type XIV	32.45	41.95	10.33	13.75	0.024
NM_005558	ladinin 1 (LAD1)	4.88	4.84	8.18	9.65	0.026
NM_018192	leprecan-like 1 (LEPREL1)	1.52	1.06	9.88	4.28	0.046
NM_153267	MAM domain containing 2 (MAMDC2)	6.07	19.23	2.42	3.28	0.013
NM_030583	matrilin 2 (MATN2)	42.96	83.10	17.87	36.53	0.021
NM_002381	matrilin 3 (MATN3)	2.82	2.95	1.37	1.61	0.037
NM_000900	matrix Gla protein (MGP)	1.29	6.24	8.95	11.36	0.024
NM_002404	microfibrillar-associated protein 4 (MFAP4)	94.69	58.40	50.00	34.54	0.025
NM_032536	netrin G2 (NTNG2)	2.64	2.49	1.15	1.16	0.015
NM_182487	olfactomedin-like 2A (OLFML2A)	24.84	15.30	11.57	9.35	0.034

NM_015441	olfactomedin-like 2B (OLFML2B)	19.96	31.06	16.61	8.98	0.023
NM_020190	olfactomedin-like 3 (OLFML3)	25.72	23.22	11.11	12.15	0.027
NM_002160	tenascin C (hexabrachion) (TNC)	4.71	4.70	49.13	31.24	0.014
	Angiogenesis					
NM_133265	angiomotin (AMOT)	13.35	13.52	2.03	1.89	0.010
NM_139314	angiopoietin-like 4 (ANGPTL4)	8.90	6.47	0.97	0.96	0.019
NM_001704	brain-specific angiogenesis inhibitor 3 (BAI3)	2.23	4.01	0.24	0.61	0.037
NM_001554	cysteine-rich, angiogenic inducer, 61 (CYR61)	31.23	17.92	149.33	118.08	0.017
	Translation					
NM_003732	eukaryotic translation initiation factor 4E binding protein 3 (EIF4EBP3)	4.63	5.88	1.27	2.00	0.027
NM_183004	eukaryotic translation initiation factor 5 (EIF5)	29.16	22.64	19.09	12.26	0.024
NM_005801	putative translation initiation factor (SUI1)	206.11	198.03	106.22	124.00	0.033
	Oxidation/Reduction					
NM_001752	catalase (CAT)	3.88	6.22	1.35	1.79	0.030
NM_005952	metallothionein 1X (MT1X)	43.17	50.05	67.57	140.74	0.041
NM_016931	NADPH oxidase 4 (NOX4)	1.89	1.21	4.09	1.00	0.036
NM_181354	oxidation resistance 1 (OXR1)	16.38	11.90	8.84	6.39	0.045
NM_005410	selenoprotein P, plasma, 1 (SEPP1)	1.88	2.13	0.97	0.99	0.045
NM_000636	superoxide dismutase 2, mitochondrial (SOD2)	2.84	2.75	42.05	76.32	0.009
NM_004881	tumor protein p53 inducible protein 3 (TP53I3)	11.26	9.73	37.55	10.02	0.022
	Proteoglycans					
NM_004385	chondroitin sulfate proteoglycan 2 (versican) (CSPG2)	4.12	3.79	10.66	7.12	0.049
NM_004950	dermatan sulfate proteoglycan 3 (DSPG3)	1.83	0.98	1.02	0.76	0.036
NM_173462	papilin, proteoglycan-like sulfated glycoprotein (PAPLN)	1.20	10.42	0.51	3.21	0.018
NM_002998	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan) (SDC2)	37.82	17.66	11.54	10.39	0.042
	Chaperonins					
NM_014109	ATPase family, AAA domain containing 2 (ATAD2)	6.01	3.66	12.16	8.85	0.037
NM_005345	heat shock 70kDa protein 1A (HSPA1A)	37.65	24.13	18.61	20.04	0.024
BC063507	heat shock 70kDa protein 1B	38.77	28.71	17.56	18.69	0.041
NM_021979	heat shock 70kDa protein 2 (HSPA2)	5.24	5.36	4.59	14.08	0.012
NM_017870	heat shock 70kDa protein 5 binding protein 1 (HSPA5BP1)	3.21	2.66	8.78	4.65	0.037
BC050602	histone 1, H2ac	22.24	28.18	4.95	6.45	0.023
NM_003509	histone 1, H2ai (HIST1H2AI)	8.97	9.82	3.18	3.30	0.021
NM_021063	histone 1, H2bd (HIST1H2BD)	10.93	13.04	2.28	2.38	0.013
NM_018848	McKusick-Kaufman syndrome (MKKS)	9.44	6.76	4.88	4.86	0.041
	Ubiquitin system					
NM_012304	F-box and leucine-rich repeat protein 7 (FBXL7)	15.10	12.65	6.10	7.06	0.041
NM_024907	F-box protein 17 (FBXO17)	12.52	9.25	6.26	6.13	0.031

NM_183420	F-box protein 25 (FBXO25)	11.88	11.05	5.71	5.15	0.031
NM_183413	F-box protein 44 (FBXO44)	6.01	4.39	3.28	3.03	0.034
NM_018434	ring finger protein 130 (RNF130)	34.68	32.68	15.72	20.25	0.021
NM_007212	ring finger protein 2 (RNF2)	20.87	17.30	12.30	10.40	0.035
NM_030936	ring finger protein 32 (RNF32)	1.10	1.77	0.26	0.61	0.041
NM_032236	ubiquitin specific protease 48 (USP48)	41.90	27.68	25.59	21.29	0.032
NM_006357	ubiquitin-conjugating enzyme E2E 3 (UBE2E3)	90.53	63.71	39.55	33.73	0.022
NM_013282	ubiquitin-like, containing PHD and RING finger domains, 1 (UHRF1)	0.59	0.49	1.27	0.96	0.038
	Lipid metabolism					
NM_001122	adipose differentiation-related protein (ADFP)	20.13	27.78	8.24	14.09	0.022
NM_001645	apolipoprotein C-I (APOC1)	4.95	5.94	1.94	3.54	0.029
NM_000041	apolipoprotein E (APOE)	7.63	11.44	3.60	6.06	0.049
NM_001638	apolipoprotein F (APOF)	0.81	0.90	1.62	2.38	0.036
NM_019101	apolipoprotein M (APOM)	2.95	3.05	1.47	1.79	0.036
NM_030637	DDHD domain containing 1 (DDHD1)	4.27	3.57	2.27	1.99	0.027
NM_001442	fatty acid binding protein 4, adipocyte (FABP4)	15.19	6.41	7.14	12.85	0.018
NM_001444	fatty acid binding protein 5 (psoriasis-associated) (FABP5)	16.77	9.86	8.14	9.63	0.038
NM_203463	LAG1 longevity assurance homolog 6 (LASS6)	9.74	14.06	4.91	9.20	0.016
NM_005779	lipoma HMGIC fusion partner-like 2 (LHFPL2)	38.68	22.41	16.13	11.47	0.012
NM_000527	low density lipoprotein receptor (LDLR)	23.86	15.32	45.03	63.01	0.013
NM_002543	oxidised low density lipoprotein (lectin-like) receptor 1 (OLR1)	1.22	0.91	4.96	3.89	0.033
NM_017784	oxysterol binding protein-like 10 (OSBPL10)	3.58	2.53	1.53	1.39	0.036
W01427	similar to apolipoprotein AI regulatory protein-1	7.98	4.73	4.35	3.70	0.022
	Membrane proteins					
NM_153000	adenomatosis polyposis coli down-regulated 1 (APCDD1)	3.59	7.29	0.60	5.04	0.039
NM_197974	butyrophilin, subfamily 3, member A3 (BTN3A3)	9.22	6.60	4.46	3.20	0.029
NM_015416	cervical cancer 1 protooncogene (HCCR1)	15.06	17.37	7.57	8.56	0.042
NM_001410	EGF-like-domain, multiple 4 (EGFL4)	9.94	7.58	4.98	4.70	0.044
NM_030652	EGF-like-domain, multiple 8 (EGFL8)	3.09	2.53	1.38	1.39	0.045
NM_005512	glycoprotein A repetitions predominant (GARP)	1.77	1.40	4.70	4.33	0.029
NM_002231	kangai 1 (CD82 antigen) (KAI1)	4.85	5.31	13.03	11.14	0.037
NM_002306	lectin, galactoside-binding, soluble, 3 (galectin 3) (LGALS3)	146.90	106.18	72.18	91.30	0.033
NM_153377	leucine-rich repeats and immunoglobulin-like domains 3 (LRIG3)	14.35	11.57	7.43	9.95	0.026
NM_020962	likely ortholog of mouse neighbor of Punc E11 (NOPE)	6.73	4.77	3.61	2.59	0.039
NM_052858	MARVEL (membrane-associating) domain containing 3 (MRVLDC3)	1.50	1.55	2.88	3.09	0.037
NM_032623	ovary-specific acidic protein (OSAP)	19.93	10.39	8.97	6.58	0.022
NM_022361	popeye domain containing 3 (POPDC3)	3.05	3.24	7.24	7.48	0.026
NM_006054	reticulon 3 (RTN3)	21.23	17.94	9.71	8.79	0.033
AA463818	similar to 14 KDA transmembrane protein	1.19	1.70	5.54	8.70	0.011

NM_003156	stromal interaction molecule 1 (STIM1)	49.27	73.03	23.41	26.48	0.019
NM_004711	synaptogyrin 1 (SYNGR1)	7.68	6.13	3.54	3.67	0.026
NM_014220	transmembrane 4 superfamily member 1 (TM4SF1)	5.60	3.46	28.22	10.18	0.022
NM_014051	transmembrane protein 14A (TMEM14A)	30.32	31.03	12.56	18.06	0.013
NM_198276	transmembrane protein 17 (TMEM17)	11.49	10.43	4.39	5.62	0.026
NM_013390	transmembrane protein 2 (TMEM2)	5.16	3.97	16.91	11.99	0.017
	Protein-protein interaction					
NM_032548	ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1)	2.59	2.03	1.28	0.99	0.043
NM_005824	leucine rich repeat containing 17 (LRRC17)	32.47	36.57	9.00	3.08	0.012
NM_024512	leucine rich repeat containing 2 (LRRC2)	4.05	2.93	14.77	10.59	0.031
NM_020956	periaxin (PRX)	6.17	5.00	2.32	2.24	0.029
NM_014575	schwannomin interacting protein 1 (SCHIP1)	1.11	0.49	3.67	1.71	0.014
NM_012477	WW domain binding protein 1 (WBP1)	31.18	31.28	14.25	14.82	0.018
	Vesicle trafficking					
NM_012133	coatomer protein complex, subunit gamma 2 (COPG2)	5.55	4.68	2.16	3.05	0.042
NM_015219	exocyst complex component 7 (EXOC7)	73.09	50.37	40.88	38.22	0.035
NM_005803	flotillin 1 (FLOT1)	36.36	31.07	18.41	23.83	0.048
NM_152540	sec1 family domain containing 2 (SCFD2)	11.52	12.50	25.00	21.95	0.028
	Nucleic acid regulation					
NM_030594	cytoplasmic polyadenylation element binding protein 1 (CPEB1)	7.45	7.12	5.24	2.43	0.031
NM_133636	DNA helicase HEL308 (HEL308)	2.90	2.90	1.49	1.39	0.037
NM_003685	KH-type splicing regulatory protein (FUSE binding protein 2) (KHSRP)	7.09	5.37	2.40	2.04	0.016
NM_032485	MCM8 minichromosome maintenance deficient 8 (MCM8)	7.68	0.72	1.98	1.57	0.037
AA741024	similar to small nuclear ribonucleoprotein C	2.64	2.26	1.06	1.28	0.042
AK057417	similar to synaptonemal complex protein 1	1.84	2.15	3.05	4.35	0.041
NM_005870	sin3-associated polypeptide, 18kDa (SAP18)	12.27	11.19	6.34	6.77	0.029
NM_018070	single stranded DNA binding protein 3 (SSBP3)	6.28	7.47	2.62	4.40	0.041
NM_012239	sirtuin (silent mating type information regulation 2 homolog) 3 (SIRT3)	7.16	7.63	3.53	4.28	0.026
NM_006275	splicing factor, arginine/serine-rich 6 (SFRS6)	15.53	11.82	8.60	7.18	0.037
NM_022090	transposon-derived Buster3 transposase-like	2.09	2.08	1.04	1.13	0.034
NM_023010	UPF3 regulator of nonsense transcripts homolog B (UPF3B)	6.22	4.15	3.50	2.79	0.042
NM_000553	Werner syndrome (WRN)	4.74	3.01	3.10	2.32	0.040
	Enzymes/Metabolism					
NM_032592	1-aminocyclopropane-1-carboxylate synthase (PHACS)	14.32	14.19	4.50	7.21	0.014
NM_006187	2'-5'-oligoadenylate synthetase 3, 100kDa (OAS3)	2.67	4.08	7.15	12.53	0.041
NM_014362	3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH)	20.97	14.06	8.65	9.11	0.017
NM_003500	acyl-Coenzyme A oxidase 2, branched chain	13.83	13.65	5.52	7.60	0.049

	(ACOX2)					
NM_015833	adenosine deaminase, RNA-specific, B1 (ADARB1)	7.70	9.99	17.32	26.79	0.024
NM_000480	adenosine monophosphate deaminase (isoform E) (AMPD3)	10.59	7.86	43.37	38.54	0.017
NM_013410	adenylate kinase 3 (AK3)	0.76	1.00	1.27	1.91	0.014
NM_024758	agmatine ureohydrolase (agmatinase) (AGMAT)	0.85	0.71	1.46	1.97	0.030
NM_000692	aldehyde dehydrogenase 1 family, member B1 (ALDH1B1)	1.95	1.66	5.71	5.48	0.012
NM_000382	aldehyde dehydrogenase 3 family, member A2 (ALDH3A2)	2.39	2.56	0.97	1.23	0.029
NM_001159	aldehyde oxidase 1 (AOX1)	6.61	38.23	3.26	10.41	0.012
NM_020978	amylase, alpha 2B; pancreatic (AMY2B)	2.07	2.26	0.79	1.05	0.035
NM_000050	argininosuccinate synthetase (ASS)	26.39	32.10	6.07	14.56	0.022
NM_001218	carbonic anhydrase XII (CA12)	2.55	2.31	5.38	9.31	0.022
AJ578034	chondroitin synthase 2 (CHSY2)	1.45	1.26	2.38	3.36	0.038
NM_206808	citrate lyase beta like (CLYBL)	1.41	2.06	0.39	0.91	0.042
NM_001905	CTP synthase (CTPS)	9.26	5.11	18.41	12.81	0.017
NM_000791	dihydrofolate reductase (DHFR)	7.64	5.61	14.12	14.53	0.049
NM_012137	dimethylarginine dimethylaminohydrolase 1 (DDAH1)	16.15	11.29	44.77	40.60	0.024
NM_013974	dimethylarginine dimethylaminohydrolase 2 (DDAH2)	1.50	1.41	0.69	0.52	0.046
NM_006208	ectonucleotide pyrophosphatase/phosphodiesterase 1 (ENPP1)	5.44	9.44	1.39	1.82	0.016
NM_001976	enolase 3, (beta, muscle) (ENO3)	4.77	5.64	2.14	2.32	0.033
NM_001398	enoyl Coenzyme A hydratase 1, peroxisomal (ECH1)	35.78	32.53	14.98	17.68	0.025
NM_001439	exostoses (multiple)-like 2 (EXTL2)	49.72	34.14	25.01	20.55	0.050
NM_000507	fructose-1,6-bisphosphatase 1 (FBP1)	2.44	2.98	4.89	4.29	0.037
NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH)	6.36	12.27	5.65	14.81	0.022
NM_001001556	galactokinase 2 (GALK2)	4.57	5.19	7.56	9.75	0.036
NM_004121	gamma-glutamyltransferase-like activity 1 (GGTLA1)	0.95	1.37	3.41	5.01	0.036
NM_002065	glutamate-ammonia ligase (glutamine synthase) (GLUL)	37.91	60.66	29.80	79.23	0.019
NM_133443	glutamic pyruvate transaminase (alanine aminotransferase) 2 (GPT2)	7.45	7.13	3.83	3.20	0.031
NM_000167	glycerol kinase (GK)	1.17	0.72	5.12	5.85	0.011
NM_014291	glycine C-acetyltransferase (GCAT)	2.25	1.93	3.59	4.52	0.019
NM_002047	glycyl-tRNA synthetase (GARS)	109.38	95.52	51.81	54.23	0.036
NM_000189	hexokinase 2 (HK2)	1.96	1.39	7.00	5.65	0.022
NM_014509	kraken-like	2.38	2.31	1.01	1.45	0.041
NM_003937	kynureninase (L-kynurenine hydrolase) (KYNU)	0.43	0.75	1.16	1.94	0.020
NM_002299	lactase (LCT)	1.69	2.05	3.43	4.47	0.039
NM_005566	lactate dehydrogenase A (LDHA)	75.36	82.17	170.01	218.07	0.017
NM_006859	lipoic acid synthetase (LIAS)	13.29	16.22	5.40	5.70	0.015
NM_002317	lysyl oxidase (LOX)	63.09	68.20	125.28	93.18	0.030
NM_002402	mesoderm specific transcript homolog (MEST)	14.35	5.56	2.13	0.99	0.026

NM_052963	mitochondrial topoisomerase I (TOP1MT)	9.56	7.01	3.61	4.88	0.037
NM_007283	monoglyceride lipase (MGLL)	45.03	26.13	109.79	92.44	0.030
NM_016256	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (NAGPA)	31.47	31.17	15.28	18.56	0.047
NM_000903	NAD(P)H dehydrogenase, quinone 1 (NQO1)	7.12	4.96	3.29	3.90	0.041
NM_175614	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 147kDa (NDUFA11)	2.23	2.37	1.15	1.14	0.026
NM_006169	nicotinamide N-methyltransferase (NNMT)	57.83	88.96	325.79	461.39	0.014
NM_000269	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	19.05	14.82	37.70	32.03	0.014
NM_007169	phosphatidylethanolamine N-methyltransferase (PEMT)	14.11	27.04	9.01	13.43	0.014
NM_014338	phosphatidylserine decarboxylase (PISD)	6.53	11.49	6.19	15.79	0.029
NM_006623	phosphoglycerate dehydrogenase (PHGDH)	15.69	13.06	3.52	4.19	0.050
NM_002767	phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2)	5.65	4.88	3.07	2.56	0.039
NM_020200	phosphoribosyl transferase domain containing 1 (PRTFDC1)	3.45	3.09	1.73	1.48	0.032
NM_002863	phosphorylase, glycogen; liver (PYGL)	19.91	28.09	7.52	8.26	0.020
NM_005746	pre-B-cell colony enhancing factor 1 (PBEF1)	3.09	3.49	10.30	21.98	0.019
NM_016297	prenylcysteine oxidase 1 (PCYOX1)	25.86	25.26	8.93	10.47	0.013
NM_000947	primase, polypeptide 2A, 58kDa (PRIM2A)	13.67	8.47	8.44	6.22	0.029
NM_000935	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 (PLOD2)	1.54	1.42	5.21	3.55	0.041
NM_002611	pyruvate dehydrogenase kinase, isoenzyme 2 (PDK2)	5.46	4.04	2.23	1.85	0.031
NM_194431	ribonuclease, RNase A family, 4 (RNASE4)	7.06	10.09	3.40	4.44	0.026
NM_001033	ribonucleotide reductase M1 polypeptide (RRM1)	2.86	2.11	5.86	4.76	0.029
NM_001034	ribonucleotide reductase M2 polypeptide (RRM2)	8.63	5.86	20.38	15.89	0.049
NM_170694	serine hydrolase-like (SERHL)	1.69	1.90	3.11	3.58	0.022
NM_006513	seryl-tRNA synthetase (SARS)	47.77	37.81	21.45	17.95	0.031
NM_030965	sialyltransferase 7E (SIAT7E)	7.95	8.17	18.40	18.11	0.048
W67378	similar to aldehyde dehydrogenase, mitochondrial precursor	3.44	3.25	1.02	2.03	0.024
NM_198519	similar to Cytochrome c, somatic	6.07	5.86	2.25	3.39	0.049
AK023341	similar to Pre-B cell enhancing factor precursor	1.56	1.73	4.32	5.76	0.034
NM_019025	spermine oxidase (SMOX)	6.00	5.36	2.69	2.48	0.010
NM_013352	squamous cell carcinoma antigen recognized by T cells 2 (SART2)	7.79	5.14	17.76	10.86	0.022
NM_015170	sulfatase 1 (SULF1)	48.95	23.19	137.63	53.03	0.027
NM_021199	sulfide quinone reductase-like (SQRDL)	7.43	5.28	16.58	19.16	0.025
NM_024838	threonine synthase-like 1 (THNSL1)	7.76	8.69	2.91	4.27	0.017
NM_004613	transglutaminase 2 (C polypeptide) (TGM2)	7.18	10.13	14.74	20.92	0.023
NM_006351	translocase of inner mitochondrial membrane 44 homolog (TIMM44)	4.71	3.72	2.44	2.52	0.045
NM_006809	translocase of outer mitochondrial membrane 34 (TOMM34)	2.55	2.07	5.84	4.25	0.019
NM_004184	tryptophanyl-tRNA synthetase (WARS)	16.50	11.74	5.83	4.64	0.031
NM_003783	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	2.02	3.03	3.46	6.10	0.039

	(B3GALT2)					
NM_007210	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) (GALNT6)	3.35	3.21	6.01	6.65	0.043
NM_012474	uridine monophosphate kinase (UMPK)	2.59	1.83	6.46	3.70	0.027
NM_003364	uridine phosphorylase 1 (UPP1)	6.74	1.87	16.87	5.50	0.040
NM_005715	uronyl-2-sulfotransferase (UST)	15.60	10.75	7.56	7.01	0.020
NM_175907	zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2)	18.43	18.86	9.24	11.69	0.036
	Channels/Transporters					
NM_001681	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2)	15.95	9.80	36.62	32.52	0.028
NM_005603	ATPase, Class I, type 8B, member 1 (ATP8B1)	1.14	0.71	2.86	2.23	0.045
NM_130463	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G isoform 2 (ATP6V1G2)	2.68	2.06	0.68	0.83	0.028
NM_080282	ATP-binding cassette, sub-family A (ABC1), member 10 (ABCA10)	3.22	1.57	1.27	0.93	0.026
NM_080284	ATP-binding cassette, sub-family A (ABC1), member 6 (ABCA6)	2.42	1.59	0.96	0.66	0.036
NM_020038	ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3)	0.78	0.89	1.00	1.69	0.022
NM_004827	ATP-binding cassette, sub-family G (WHITE), member 2 (ABCG2)	4.37	4.97	8.15	10.73	0.021
NM_001289	chloride intracellular channel 2 (CLIC2)	2.18	1.93	1.00	1.02	0.049
NM_007235	exportin, tRNA (nuclear export receptor for tRNAs) (XPOT)	52.97	44.82	21.00	22.30	0.021
NM_017885	host cell factor C1 regulator 1 (XPO1 dependant) (HCFC1R1)	72.21	61.72	20.77	26.71	0.019
NM_006985	nuclear pore complex interacting protein (NPIP)	84.69	76.40	41.17	38.90	0.029
NM_014217	potassium channel, subfamily K, member 2 (KCNK2)	9.52	17.24	12.86	19.51	0.042
NM_172160	potassium voltage-gated channel, shaker-related subfamily, beta member 1 (KCNAB1)	7.43	6.24	5.02	3.25	0.033
NM_005549	potassium voltage-gated channel, shaker-related subfamily, member 10 (KCNA10)	1.53	1.59	3.82	4.88	0.034
NM_012281	potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2)	2.30	1.08	1.04	1.03	0.031
NM_003944	selenium binding protein 1 (SELENBP1)	6.86	8.51	3.16	3.66	0.042
AK025584	similar to 4F2 heavy chain	53.51	43.31	17.95	17.82	0.044
NM_012449	six transmembrane epithelial antigen of the prostate (STEAP)	0.55	0.70	2.51	6.29	0.019
NM_014191	sodium channel, voltage gated, type VIII, alpha (SCN8A)	3.44	2.89	6.53	9.37	0.026
NM_004171	solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2)	5.33	1.17	1.70	0.85	0.022
NM_005628	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5)	91.23	64.85	43.77	49.99	0.047

NM_001046	solute carrier family 12 (sodium/potassium/chloride transporters), member 2 (SLC12A2)	4.14	3.23	2.46	1.79	0.040
NM_004207	solute carrier family 16 (monocarboxylic acid transporters), member 3 (SLC16A3)	2.64	2.40	7.23	8.89	0.012
NM_004696	solute carrier family 16 (monocarboxylic acid transporters), member 4 (SLC16A4)	15.65	9.70	8.27	4.21	0.020
NM_006749	solute carrier family 20 (phosphate transporter), member 2 (SLC20A2)	6.85	3.90	14.92	7.86	0.026
NM_000387	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20 (SLC25A20)	3.79	3.44	1.87	1.73	0.036
NM_031481	solute carrier family 25 (mitochondrial carrier), member 18 (SLC25A18)	0.85	2.01	0.23	0.46	0.023
NM_024330	solute carrier family 27 (fatty acid transporter), member 3 (SLC27A3)	4.08	4.33	1.66	2.66	0.026
NM_015139	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1 (SLC35D1)	0.82	0.87	1.46	1.99	0.014
NM_014854	solute carrier family 35, member E2 (SLC35E2)	109.00	106.63	50.80	45.01	0.026
NM_014585	solute carrier family 40 (iron-regulated transporter), member 1 (SLC40A1)	3.20	3.79	0.62	1.37	0.009
NM_017836	solute carrier family 41, member 3 (SLC41A3)	10.10	7.35	4.65	4.74	0.026
NM_007332	transient receptor potential cation channel, subfamily A, member 1 (TRPA1)	0.58	0.28	2.36	1.91	0.010
BC046362	voltage-dependent calcium channel gamma subunit-like protein	1.62	2.67	0.46	0.77	0.033
	Unknown function					
NM_030802	C/EBP-induced protein (LOC81558)	2.03	2.03	1.02	1.14	0.034
NM_016053	CGI-116 protein (CGI-116)	10.79	10.16	5.13	5.88	0.018
NM_025214	CTCL tumor antigen se57-1 (SE57-1)	2.60	5.78	1.11	2.47	0.023
NM_020223	family with sequence similarity 20, member C (FAM20C)	10.27	6.15	24.23	20.01	0.022
NM_015916	family with sequence similarity 26, member B (FAM26B)	11.23	8.51	3.62	3.10	0.022
BC040073	H19, imprinted maternally expressed untranslated mRNA	13.16	16.85	3.75	6.19	0.041
NM_032853	melanoma associated antigen (mutated) 1 (MUM1)	14.20	9.93	9.00	6.76	0.035
AF220263	MOST2	7.95	5.39	3.73	2.63	0.049
NM_197955	normal mucosa of esophagus specific 1 (NMES1)	0.28	0.20	2.13	3.04	0.048
NM_031915	SET domain, bifurcated 2 (SETDB2)	6.82	6.24	2.69	2.95	0.038
NM_021967	small EDRK-rich factor 1A (telomeric) (SERF1A)	7.13	5.25	4.60	3.36	0.033

[a] Statistical differences in gene expression were calculated by GeneSpring 7.3.

Supplemental Table 2. Differential gene expression (averages, Avg, n=3) in cultured endometrial stromal cells (T-HESC) under control conditions (Ctl), in the presence of estrogen plus progesterone (E+P), treated with macrophage conditioned medium along (Mph CM), or treated with E+P+Mph CM.[a]

GenBank Accession #	Description	Ctl Avg	E+P Avg	Mph CM	E+P+ MphCM	p value
	Signal Transduction					
NM_000867	5-hydroxytryptamine (serotonin) receptor 2B (HTR2B)	63.80	18.47	43.05	30.13	0.034
NM_001946	dual specificity phosphatase 6 (DUSP6)	4.63	1.34	4.31	3.91	0.030
NM_206963	retinoic acid receptor responder (tazarotene induced) 1 (RARRES1)	4.10	1.21	7.43	3.65	0.025
NM_021643	tribbles homolog 2 (TRIB2)	25.81	8.28	18.35	12.65	0.017
NM_004787	slit homolog 2 (SLIT2)	7.15	2.48	3.82	1.98	0.022
NM_002924	regulator of G-protein signalling 7 (RGS7)	6.80	2.40	3.51	2.26	0.026
NM_002889	retinoic acid receptor responder (tazarotene induced) 2 (RARRES2)	97.17	38.21	161.32	61.02	0.037
NM_181784	sprouty-related, EVH1 domain containing 2 (SPRED2)	10.47	4.14	7.56	5.78	0.036
NM_004101	coagulation factor II (thrombin) receptor-like 2 (F2RL2)	3.32	1.38	2.45	0.93	0.017
NM_003507	frizzled homolog 7 (FZD7)	19.98	8.78	26.76	27.40	0.022
NM_007115	tumor necrosis factor, alpha-induced protein 6 (TNFAIP6)	22.91	10.15	20.21	21.73	0.017
NM_004431	EphA2 (EPHA2)	5.82	2.63	7.56	5.32	0.023
NM_170732	brain-derived neurotrophic factor (BDNF)	4.07	1.86	7.09	3.44	0.033
NM_005475	lymphocyte adaptor protein (LNK)	6.05	2.80	5.50	4.37	0.043
NM_203418	Down syndrome critical region gene 1 (DSCR1)	10.30	4.79	19.94	12.78	0.026
AW189008	similar to signal transducer and activator of transcription 1-α/β	2.14	1.01	2.40	2.46	0.037
NM_004073	polo-like kinase 3 (PLK3)	3.91	1.85	6.80	4.40	0.035
NM_001992	coagulation factor II (thrombin) receptor (F2R)	6.11	2.94	4.95	1.38	0.019
NM_018948	mitogen-inducible gene 6 (MIG-6)	1.76	3.92	1.39	2.14	0.024
NM_198569	G protein-coupled receptor 126 (GPR126)	2.24	5.10	1.29	1.69	0.022
NM_002923	regulator of G-protein signalling 2, 24kDa (RGS2)	8.71	23.45	5.33	4.55	0.041
NM_012242	dickkopf homolog 1 (DKK1) [Wnt pathway]	24.50	67.08	39.28	35.58	0.034
NM_016084	RAS, dexamethasone-induced 1 (RASD1)	1.00	3.28	0.85	0.87	0.012
NM_000618	insulin-like growth factor 1 (somatomedin C) (IGF1)	2.20	9.74	2.12	1.95	0.032
NM_001629	arachidonate 5-lipoxygenase-activating protein (ALOX5AP)	0.61	3.47	0.76	0.95	0.030
NM_002193	inhibin, beta B (activin AB beta polypeptide) (INHBB)	2.99	21.25	1.52	15.81	0.015
NM_000597	insulin-like growth factor binding protein 2 (36kD) (IGFBP2)	1.20	11.17	0.72	4.75	0.023
	Proteases and related					
NM_007289	membrane metallo-endopeptidase (MME)	2.13	4.84	3.44	7.92	0.048

NM_006587	corin, serine protease (CORIN)	4.16	29.63	2.25	20.48	0.012
	Transcriptional regulation					
NM_004454	ets variant gene 5 (ets-related molecule) (ETV5)	18.28	5.40	19.63	14.45	0.017
NM_002166	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2)	4.86	1.53	4.61	3.23	0.039
NM_002518	neuronal PAS domain protein 2 (NPAS2)	3.93	1.43	2.99	2.64	0.033
NM_003483	high mobility group AT-hook 2 (HMGA2)	20.30	7.58	32.31	22.34	0.019
NM_030762	basic helix-loop-helix domain containing, class B, 3 (BHLHB3)	2.40	1.08	1.53	1.18	0.026
BC033086	transcription factor 19 (SC1)	15.24	7.17	16.48	10.98	0.043
NM_080390	my048 protein (my048)	69.50	150.64	45.94	100.52	0.017
NM_198057	delta sleep inducing peptide, immunoreactor (DSIPI)	8.30	38.46	7.40	19.09	0.022
NM_006006	zinc finger protein 145 (Kruppel-like) (ZNF145)	0.76	7.66	0.83	6.44	0.013
	Cytoskeleton					
NM_012334	myosin X (MYO10)	8.28	2.28	10.13	3.36	0.022
NM_031957	keratin associated protein 1-5 (KRTAP1-5)	7.57	2.35	9.98	8.65	0.034
NM_031217	kinesin family member 18A	3.35	1.24	3.14	1.93	0.032
NM_015894	stathmin-like 3 (STMN3)	5.42	2.51	6.02	4.89	0.038
NM_020859	Shroom-related protein (ShrmL)	6.64	3.17	13.01	11.66	0.019
NM_004010	dystrophin (DMD)	4.75	13.07	6.60	7.02	0.021
	Defense/Immunity					
NM_004946	dedicator of cytokinesis 2 (DOCK2)	5.34	1.87	9.63	5.10	0.014
NM_000609	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1) (CXCL12)	99.29	49.70	76.34	64.81	0.041
	Cell cycle/cell death					
NM_199414	protein regulator of cytokinesis 1 (PRC1)	10.90	4.58	12.05	6.61	0.042
	Adhesion					
NM_014344	four jointed box 1 (FJX1)	50.50	11.66	45.66	17.48	0.033
NM_015419	adlican	8.31	2.98	9.24	6.75	0.038
NM_005602	claudin 11 (oligodendrocyte transmembrane protein) (CLDN11)	148.76	53.43	81.95	53.02	0.036
	Extracellular matrix					
NM_001850	collagen, type VIII, alpha 1 (COL8A1)	10.84	5.37	11.80	7.52	0.037
NM_001937	dermatopontin (DPT)	4.14	21.27	2.17	8.55	0.040
	Oxidation/Reduction					
NM_002084	glutathione peroxidase 3 (plasma) (GPX3)	0.72	1.45	0.79	8.40	0.050
	Ubiquitin system					
NM_005358	LIM domain only 7 (LMO7)	8.90	3.29	6.99	4.43	0.031
NM_020799	associated molecule with the SH3 domain of STAM (AMSH) like protein (AMSH-LP)	23.77	9.31	22.33	14.16	0.033

NM_014176	HSPC150 protein similar to ubiquitin-conjugating enzyme (HSPC150)	20.38	10.27	37.10	24.13	0.027
	Lipid metabolism					
NM_001647	apolipoprotein D (APOD)	1.83	4.20	0.98	2.04	0.045
	Membrane proteins					
NM_002522	neuronal pentraxin I (NPTX1)	40.92	2.22	68.46	22.48	0.009
NM_032812	plexin domain containing 2 (PLXDC2)	7.53	1.84	3.88	1.24	0.023
	Nucleic acid regulation					
NM_006739	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (MCM5)	4.99	2.26	8.24	7.07	0.032
NM_018518	MCM10 minichromosome maintenance deficient 10 (MCM10)	2.35	1.12	4.51	2.81	0.025
	Enzymes/Metabolism					
NM_032211	lysyl oxidase-like 4 (LOXL4)	39.02	7.68	30.53	13.39	0.013
NM_003033	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (SIAT4A)	12.72	5.28	13.03	8.80	0.023
NM_003358	UDP-glucose ceramide glucosyltransferase (UGCG)	13.55	6.63	23.80	22.61	0.030
NM_006926	surfactant, pulmonary-associated protein A2 (SFTPA2)	1.38	2.84	2.72	3.41	0.047
NM_001874	carboxypeptidase M (CPM)	13.26	39.73	11.50	45.04	0.027
NM_019886	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 (CHST7)	2.02	10.99	1.81	3.36	0.022
	Channels/Transporters					
NM_000519	hemoglobin, delta (HBD)	8.40	1.31	5.41	1.13	0.010
NM_005415	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1)	17.51	8.08	22.73	19.04	0.025
NM_002245	potassium channel, subfamily K, member 1 (KCNK1)	1.70	0.85	2.23	1.93	0.030
	Unknown function					
NM_017565	family with sequence similarity 20, member A (FAM20A)	20.34	8.66	21.44	25.02	0.019
NM_002616	period homolog 1 (PER1)	1.81	6.18	2.12	3.60	0.024

[a] Statistical differences in gene expression were calculated by GeneSpring 7.3.

Supplemental Table 3. Genes differentially expressed in T-HESC cells in response to both macrophage CM and monocyte CM[a].

GenBank	Gene Name	Fold MphCM[b]	Fold MonoCM[c]
NM_053001	Odd-skipped-related 2A protein (OSR2)	0.09	0.19
NM_032592	1-aminocyclopropane-1-carboxylate synthase (PHACS)	0.31	0.22
NM_153202	A disintegrin and metalloproteinase domain 33 (ADAM33)	0.25	0.4
NM_003500	Acyl-Coenzyme A oxidase 2, branched chain (ACOX2)	0.40	0.19
NM_000382	aldehyde dehydrogenase 3 family, member A2 (ALDH3A2)	0.41	0.3
NM_020978	Amylase, alpha 2B; pancreatic (AMY2B)	0.38	0.37
NM_133265	Angiomotin (AMOT)	0.15	0.07
NM_004282	BCL2-associated athanogene 2 (BAG2)	0.46	0.25
NM_001704	Brain-specific angiogenesis inhibitor 3 (BAI3)	0.11	0.05
NM_000070	Calpain 3, (p94) (CAPN3)	0.50	0.18
NM_001752	Catalase (CAT)	0.35	0.21
NM_020404	CD164 sialomucin-like 1 (CD164L1)	0.52	0.18
NM_001289	Chloride intracellular channel 2 (CLIC2)	0.46	0.24
NM_206808	Citrate lyase beta like (CLYBL)	0.28	0.31
NM_019058	DNA-damage-inducible transcript 4 (DDIT4)	0.26	0.21
NM_003462	dynein, axonemal, light intermediate polypeptide 1 (DNALI1)	0.50	0.38
NM_004438	EphA4 (EPHA4)	0.37	0.27
NM_001439	Exostoses (multiple)-like 2 (EXTL2)	0.50	0.31
NM_012304	F-box and leucine-rich repeat protein 7 (FBXL7)	0.40	0.15
NM_183420	F-box protein 25 (FBXO25)	0.48	0.33
NM_199135	FOXD4-like 2 (FOXD4L2)	0.44	0.13
NM_001505	G protein-coupled receptor 30 (GPR30)	0.41	0.1
NM_173537	GTF2I repeat domain containing 2 (GTF2IRD2)	0.39	0.19
NM_016315	GULP engulfment adaptor PTB domain containing 1 (GULP1)	0.48	0.2
NM_021973	Heart and neural crest derivatives expressed 2 (HAND2)	0.49	0.5
NM_199072	I-mfa domain-containing protein (HIC)	0.41	0.2
NM_002222	Inositol 1,4,5-triphosphate receptor, type 1 (ITPR1)	0.32	0.24
NM_014214	Inositol(myo)-1(or 4)-monophosphatase 2 (IMPA2)	0.49	0.36
NM_000210	Integrin, alpha 6 (ITGA6)	0.21	0.26
NM_017415	Kelch-like 3 (KLHL3)	0.23	0.14
NM_014509	Kraken-like (serine hydrolase-like 2) (SERHL2)	0.42	0.34
NM_005824	Leucine rich repeat containing 17 (LRRC17)	0.28	0.06
NM_006859	Lipoic acid synthetase (LIAS)	0.41	0.36
NM_145015	MAS-related GPR, member F (MRGPRF)	0.43	0.33
NM_016256	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase (NAGPA)	0.49	0.26
NM_022477	NDRG family member 3 (NDRG3)	0.50	0.36
NM_033014	osteoglycin (osteoinductive factor, mimecan) (OGN)	0.29	0.32
NM_005014	Osteomodulin (OMD)	0.38	0.24
NM_032623	Ovary-specific acidic protein (OSAP)	0.45	0.11
NM_003711	Phosphatidic acid phosphatase type 2A (PPAP2A)	0.29	0.24

NM_181523	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha) (PIK3R1)	0.35	0.23
NM_003629	Phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma) (PIK3R3)	0.27	0.06
NM_019012	Phosphoinositol 3-phosphate-binding protein-2 (PEPP2)	0.56	0.13
NM_002863	Phosphorylase, glycogen; liver (PYGL)	0.38	0.34
NM_016277	RAB23, member RAS oncogene family (RAB23)	0.45	0.49
NM_198230	regulator of G-protein signalling 12 (RGS12)	0.40	0.35
NM_020809	Rho GTPase activating protein 20 (ARHGAP20)	0.38	0.19
NM_013427	Rho GTPase activating protein 6 (ARHGAP6)	0.17	0.29
NM_004755	Ribosomal protein S6 kinase, 90kDa, polypeptide 5 (RPS6KA5)	0.22	0.36
NM_020796	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A)	0.13	0.08
NM_004657	Serum deprivation response (SDPR)	0.37	0.23
NM_004844	SH3-domain binding protein 5 (BTK-associated) (SH3BP5)	0.42	0.36
NM_198519	Similar to Cytochrome c, somatic	0.37	0.15
NM_024330	solute carrier family 27 (fatty acid transporter), member 3 (SLC27A3)	0.41	0.37
NM_014854	Solute carrier family 35, member E2 (SLC35E2)	0.47	0.29
NM_014585	solute carrier family 40, member 1 (SLC40A1)	0.19	0.11
NM_006714	Sphingomyelin phosphodiesterase, acid-like 3A (SMPDL3A)	0.28	0.15
NM_006275	Splicing factor, arginine/serine-rich 6 (SFRS6)	0.55	0.34
NM_006531	Tetratricopeptide repeat domain 10 (TTC10)	0.36	0.21
NM_003597	TGFB inducible early growth response 2 (TIEG2)	0.52	0.43
NM_024838	Threonine synthase-like 1 (THNSL1)	0.38	0.18
NM_005647	Transducin (beta)-like 1X-linked (TBL1X)	0.37	0.15
NM_005077	Transducin-like enhancer of split 1 (E(sp1) homolog) (TLE1)	0.36	0.28
NM_198276	Transmembrane protein 17 (TMEM17)	0.38	0.16
NM_025188	Tripartite motif-containing 45 (TRIM45)	0.26	0.15
NM_016175	Truncated calcium binding protein	0.47	0.2
NM_005715	Uronyl-2-sulfotransferase (UST)	0.48	0.23
NM_175907	Zinc binding alcohol dehydrogenase, domain containing 2 (ZADH2)	0.50	0.2
NM_003451	Zinc finger protein 177 (ZNF177)	0.50	0.27
NM_020843	Zinc finger protein 291 (ZNF291)	0.56	0.28
NM_006973	Zinc finger protein 32 (KOX 30) (ZNF32)	0.51	0.24
NM_174945	Zinc finger protein 575 (ZNF575)	0.26	0.2
NM_004419	Dual specificity phosphatase 5 (DUSP5)	1.90	30.15
NM_153000	Adenomatosis polyposis coli down-regulated 1 (APCDD1)	2.03	0.1
NM_001638	Apolipoprotein F (APOF)	2.00	4.31
NM_170665	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2)	2.30	2.92
NM_005242	Coagulation factor II (thrombin) receptor-like 1 (F2RL1)	10.11	5.66
NM_001343	disabled homolog 2 (DAB2)	2.01	2.33
NM_012081	elongation factor, RNA polymerase II, 2 (ELL2)	2.04	5.26
NM_005438	FOS-like antigen 1 (FOSL1)	2.50	6.54

NM_005458	G protein-coupled receptor 51 (GPR51)	2.15	4.99
NM_013372	Gremlin 1 homolog, cysteine knot superfamily (GREM1)	5.99	5.74
NM_145904	High mobility group AT-hook 1 (HMGA1)	2.42	7.02
NM_000599	Insulin-like growth factor binding protein 5 (IGFBP5)	5.89	3.97
NM_002189	Interleukin 15 receptor, alpha (IL15RA)	4.57	2.77
NM_000600	interleukin 6 (interferon, beta 2) (IL6)	2.67	2
NM_030952	likely ortholog of rat SNF1/AMP-activated protein kinase (SNARK)	2.02	1.85
NM_012320	lysophospholipase 3 (lysosomal phospholipase A2) (LYPLA3)	6.19	11.58
NM_002317	Lysyl oxidase (LOX)	1.99	3.97
NM_145110	Mitogen-activated protein kinase kinase 3 (MAP2K3)	2.16	5.31
NM_004221	Natural killer cell transcript 4 (NK4)	16.15	3.74
NM_002659	Plasminogen activator, urokinase receptor (PLAUR)	3.68	3.06
NM_002867	RAB3B, member RAS oncogene family (RAB3B)	1.97	4.13
NM_000636	Superoxide dismutase 2, mitochondrial (SOD2)	14.81	5.61
NM_006926	Surfactant, pulmonary-associated protein A2 (SFTPA2)	1.97	2.85
NM_006058	TNFAIP3 interacting protein 1 (TNIP1)	1.99	3.25
NM_012323	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) (MAFF)	2.96	5.1

[a] Statistical differences in gene expression were calculated with GeneSpring 7.3 software.

[b] Fold decrease or increase in T-HESC gene expression in response to macrophage CM compared to control.

[c] Fold decrease or increase in T-HESC gene expression in response to monocyte CM[12] compared to control.