

Appendix 3
(UCB1 MSCs in LECCM >> UCB1 MSCs in LECBM)

Gene	Mean 1	Mean 2	FoldDiff	p_SAM	Gene Name
MMP3	5.9361	9.6790	13.3884	1.67E-04	matrix metallopeptidase 3 (stromelysin 1, progelatinase)
ABI3BP	8.2281	11.5907	10.2862	6.52E-05	ABI family, member 3 (NESH) binding protein
C3	7.8510	11.1965	10.1646	1.09E-04	complement component 3
IL6	8.5551	11.8881	10.0771	4.57E-04	interleukin 6 (interferon, beta 2)
IL8	9.2103	12.4379	9.3674	1.38E-04	interleukin 8
EHF	4.0444	6.9202	7.3404	2.25E-04	ets homologous factor
PTGS2	8.2186	10.9596	6.6854	3.12E-04	prostaglandin-endoperoxidase synthase 2
RAB27B	7.7960	10.4961	6.4985	1.73E-03	RAB27B, member RAS oncogene family
MMP1	9.5535	12.2426	6.4493	2.97E-04	matrix metallopeptidase 1 (interstitial collagenase)
IL1B	6.1274	8.7905	6.3340	9.42E-05	interleukin 1, beta
TRPA1	4.7798	7.4049	6.1694	1.14E-03	transient receptor potential cation channel, subfamily A, member 1
SERPINB2	5.4503	7.9259	5.5621	7.97E-05	serpin peptidase inhibitor, clade B (ovalbumin), member 2
LCP1	5.1097	7.5550	5.4463	1.52E-04	lymphocyte cytosolic protein 1 (L-plastin)
CXCL1	9.6236	12.0660	5.4355	1.96E-04	chemokine (C-X-C motif) ligand 2
SNORA73A	7.8350	10.2041	5.1663	3.17E-03	small nucleolar RNA, H/ACA box 73A
CXCL6	6.8740	9.2199	5.0838	4.28E-04	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
KCNJ2	6.6156	8.8795	4.8029	2.83E-04	potassium inwardly-rectifying channel, subfamily J, member 2
MIR154	4.1791	6.3980	4.6554	1.23E-04	microRNA 154
NETO1	6.5571	8.7753	4.6532	5.58E-04	neuropilin (NRP) and tolloid (TLL)-like 1
TXN	7.3960	9.6072	4.6306	1.96E-03	thioredoxin
SNORD12C	3.5478	5.7045	4.4590	1.09E-03	small nucleolar RNA, C/D box 12C
IL7R	5.9428	8.0855	4.4160	2.81E-03	interleukin 7 receptor
CCL2	10.8654	12.9346	4.1966	5.73E-04	chemokine (C-C motif) ligand 2
LOC100271836	5.4531	7.5158	4.1776	3.70E-04	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene
PSME2	7.8322	9.8906	4.1651	6.02E-04	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
HSD11B1	5.8397	7.8762	4.1025	1.40E-03	hydroxysteroid (11-beta) dehydrogenase 1
LOC389906	4.7725	6.8089	4.1025	3.53E-03	hypothetical LOC389906
IL13RA2	4.0964	6.1296	4.0933	2.54E-04	interleukin 13 receptor, alpha 2
MIR199A1	2.7410	4.7694	4.0796	8.05E-04	microRNA 199a-1
TNFSF18	4.7361	6.7455	4.0262	4.29E-02	tumor necrosis factor (ligand) superfamily, member 18
TMEM132B	6.4580	8.4142	3.8805	2.10E-04	transmembrane protein 132B
SLC22A4	5.8046	7.7413	3.8285	6.16E-04	solute carrier family 22 (organic cation/ergothioneine transporter), member 4
TFPI2	9.4236	11.3293	3.7469	1.15E-03	tissue factor pathway inhibitor 2
RNPS1	7.3907	9.2783	3.7002	1.28E-03	RNA binding protein S1, serine-rich domain
ZC3H12C	6.6857	8.5585	3.6624	1.75E-03	zinc finger CCCH-type containing 12C
PLA2G4A	3.8255	5.6302	3.4937	1.33E-03	phospholipase A2, group IVA (cytosolic, calcium-dependent)
SLC7A14	5.8153	7.6105	3.4706	6.60E-04	solute carrier family 7 (cationic amino acid transporter) member 14
NEDD4	6.6954	8.4903	3.4699	3.72E-03	neural precursor cell expressed, developmentally

					down-regulated 4
RPS27L	7.4336	9.2230	3.4567	1.83E-03	ribosomal protein S27-like
CXCL2	6.5981	8.3825	3.4447	6.44E-03	chemokine (C-X-C motif) ligand 2
KYNU	5.1757	6.9393	3.3954	3.08E-03	kynureninase
PLAU	8.4400	10.2002	3.3876	3.41E-04	plasminogen activator, urokinase
NDUFV2	5.7193	7.4747	3.3762	8.34E-04	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
LIF	7.5402	9.2689	3.3141	2.68E-04	leukemia inhibitory factor (cholinergic differentiation factor)
TNFAIP6	5.6898	7.4023	3.2772	4.42E-04	tumor necrosis factor, alpha-induced protein 6
CASP1	4.0817	5.7793	3.2436	9.08E-03	caspase 1
ACSL4	6.9410	8.6378	3.2419	2.08E-03	acyl-CoA synthetase long-chain family member 4
CBWD2	2.4303	4.1211	3.2283	4.09E-02	COBW domain containing 2
GUSBL1	3.0717	4.7606	3.2241	5.27E-03	glucuronidase, beta-like 1
TIMM9	4.7981	6.4870	3.2240	1.30E-03	translocase of inner mitochondrial membrane 9 homolog (yeast)
STC1	9.9234	11.6079	3.2143	9.06E-04	stanniocalcin 1
SCD	8.7869	10.4694	3.2098	3.26E-04	stearoyl-CoA desaturase (delta-9-desaturase)
FADS1	8.9225	10.6022	3.2035	8.48E-04	fatty acid desaturase 1
LPXN	7.4206	9.0997	3.2023	1.25E-03	leupaxin
CHORDC1	5.1719	6.8384	3.1744	5.65E-03	cysteine and histidine-rich domain (CHORD) containing 1
LOC100132832	3.9734	5.6345	3.1626	1.56E-03	postmeiotic segregation increased 2-like 5-like
SNORA71D	9.1855	10.8419	3.1522	4.21E-03	small nucleolar RNA, H/ACA box 71D
COX7B	6.0278	7.6783	3.1394	1.91E-03	cytochrome c oxidase subunit VIIb
SNORD36B	5.5339	7.1825	3.1352	2.86E-03	small nucleolar RNA, C/D box 36B
CLDN1	9.3888	11.0318	3.1232	5.62E-03	claudin 1
VBP1	5.0972	6.7401	3.1229	4.50E-03	von Hippel-Lindau binding protein 1
MMP16	6.2829	7.9228	3.1163	5.00E-04	matrix metalloproteinase 16 (membrane-inserted)
NUDT5	6.8148	8.4451	3.0958	7.18E-04	nudix (nucleoside diphosphate linked moiety X)-type motif 5
IRAK3	4.1957	5.8200	3.0829	3.04E-03	interleukin-1 receptor-associated kinase 3
DPP4	8.5382	10.1450	3.0457	3.79E-03	dipeptidyl-peptidase 4
SNORD49A	2.7747	4.3793	3.0411	5.05E-03	small nucleolar RNA, C/D box 49A
GNG11	7.9484	9.5507	3.0363	3.96E-03	guanine nucleotide binding protein (G protein), gamma 11
PSG5	8.2015	9.7989	3.0259	4.69E-03	pregnancy specific beta-1-glycoprotein 5
UGCG	7.6538	9.2485	3.0202	1.72E-02	UDP-glucose ceramide glucosyltransferase
FAM103A1	4.9076	6.5003	3.0163	1.28E-02	family with sequence similarity 103, member A1
ARPC3	8.4422	10.0323	3.0107	2.33E-03	actin related protein 2/3 complex, subunit 3, 21kDa
CCDC55	6.4231	8.0124	3.0090	3.02E-03	coiled-coil domain containing 55
ZBTB8OS	5.8069	7.3934	3.0033	6.70E-03	zinc finger and BTB domain containing 8 opposite strand
CLN5	6.2907	7.8747	2.9979	6.46E-03	ceroid-lipofuscinosis, neuronal 5
POU2F2	7.5707	9.1490	2.9863	1.62E-03	POU class 2 homeobox 2
CDR1	6.4094	7.9774	2.9650	3.27E-03	cerebellar degeneration-related protein 1, 34kDa
GDF5	8.4439	10.0103	2.9616	5.87E-04	growth differentiation factor 5
NETO2	7.1234	8.6875	2.9568	5.33E-03	neuropilin (NRP) and tolloid (TLL)-like 2
LOC729013	6.6846	8.2427	2.9446	1.50E-03	hypothetical LOC729013
CXCL5	7.2186	8.7716	2.9342	6.40E-03	chemokine (C-X-C motif) ligand 5
APOO	7.3232	8.8710	2.9237	6.45E-04	apolipoprotein O
MIR24-2	4.2901	5.8312	2.9101	4.56E-03	microRNA 24-2

DHCR7	8.4705	10.0114	2.9097	6.31E-04	7-dehydrocholesterol reductase
FTH1	5.8636	7.3979	2.8966	2.47E-03	ferritin, heavy polypeptide 1
GDF15	9.5224	11.0506	2.8843	4.23E-03	growth differentiation factor 15
HIGD2A	8.0751	9.5876	2.8531	3.60E-03	HIG1 hypoxia inducible domain family, member 2A
MSC	7.4116	8.9235	2.8519	1.98E-03	musculin
HERC2P9	4.3155	5.8236	2.8443	3.92E-03	hect domain and RLD 2 pseudogene 9
ADD3	7.6501	9.1544	2.8369	2.44E-03	adducin 3 (gamma)
NME2P1	8.7041	10.2030	2.8264	1.44E-03	non-metastatic cells 2, protein (NM23B) expressed in, pseudogene 1
CTSS	4.5473	6.0425	2.8191	4.14E-03	cathepsin S
TMSL3	9.3106	10.8058	2.8190	9.79E-04	thymosin-like 3
USP16	6.8222	8.3092	2.8030	1.34E-02	ubiquitin specific peptidase 16
SNORA71A	5.7900	7.2732	2.7958	1.20E-03	small nucleolar RNA, H/ACA box 71A
STK32B	7.0075	8.4903	2.7949	7.61E-04	serine/threonine kinase 32B
LY96	6.1185	7.6005	2.7935	3.83E-02	lymphocyte antigen 96
GLIS3	8.4634	9.9436	2.7898	8.92E-04	GLIS family zinc finger 3
SNHG4	2.1803	3.6572	2.7834	3.58E-02	small nucleolar RNA host gene 4 (non-protein coding)
EIF3E	7.1214	8.5980	2.7829	5.28E-03	eukaryotic translation initiation factor 3, subunit E
SLC11A2	7.7399	9.2165	2.7829	1.18E-03	solute carrier fam.11 (proton-coupled divalent ion transporter), member 2
STC2	8.0431	9.5158	2.7755	3.95E-03	stanniocalcin 2
SLC38A6	6.0855	7.5576	2.7741	3.57E-03	solute carrier family 38, member 6
C9orf30	6.6809	8.1522	2.7727	1.72E-03	chromosome 9 open reading frame 30
ATP6V1D	6.3583	7.8260	2.7658	1.32E-02	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D
RPL36AL	6.5442	8.0091	2.7605	7.03E-04	ribosomal protein L36a-like
SNORD116-14	9.1037	10.5685	2.7604	1.14E-02	small nucleolar RNA, C/D box 116-14
HIST2H2BC	5.4272	6.8914	2.7590	5.21E-03	histone cluster 2, H2bc
CTSK	9.1315	10.5955	2.7587	4.31E-02	cathepsin K
LOC100506575	8.2180	9.6807	2.7563	6.24E-03	hypothetical LOC100506575
DDT	8.1575	9.6174	2.7510	2.07E-03	D-dopachrome tautomerase
HSPH1	7.6997	9.1588	2.7493	1.05E-02	heat shock 105kDa/110kDa protein 1
FST	10.0863	11.5401	2.7392	1.70E-03	follistatin
SLC7A2	6.7772	8.2279	2.7334	3.11E-03	solute carrier family 7 (cationic amino acid transporter) member 2
TOP2A	5.4891	6.9341	2.7227	8.37E-03	topoisomerase (DNA) II alpha 170kDa
AKR1B1	10.6878	12.1284	2.7142	1.08E-03	aldo-keto reductase family 1, member B1 (aldose reductase)
MIR224	2.8519	4.2897	2.7091	3.42E-02	microRNA 224
LOC729020	4.1328	5.5694	2.7067	5.86E-03	rcRPE
CASC4	8.7615	10.1964	2.7037	2.18E-03	cancer susceptibility candidate 4
TOM1L1	6.3548	7.7797	2.6849	2.75E-03	target of myb1 (chicken)-like 1
CDC26	6.1503	7.5745	2.6837	3.85E-03	cell division cycle 26 homolog (S. cerevisiae)
RELN	5.7785	7.1934	2.6663	6.31E-03	reelin
MTMR10	6.8891	8.3028	2.6643	3.41E-03	myotubularin related protein 10
C9orf21	6.6498	8.0615	2.6606	9.00E-03	chromosome 9 open reading frame 21
MRPL42	6.5000	7.8978	2.6350	3.32E-02	mitochondrial ribosomal protein L42
TIMM17A	6.6060	7.9984	2.6252	5.52E-03	translocase of inner mitochondrial membrane 17 homolog A (yeast)
SOD2	10.6416	12.0259	2.6104	1.52E-02	superoxide dismutase 2, mitochondrial
RPL12	8.5197	9.9040	2.6104	1.02E-03	ribosomal protein L12

TAF9B	7.8006	9.1827	2.6065	4.34E-03	TAF9B RNA polymerase II, TATA box binding protein-assoc.d factor, 31kDa
ZNF271	4.5158	5.8974	2.6056	1.21E-02	zinc finger protein 271
IFNAR1	6.8680	8.2486	2.6038	2.49E-02	interferon (alpha, beta and omega) receptor 1
NDUFB6	5.7482	7.1275	2.6015	4.12E-03	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
INSIG1	5.9711	7.3502	2.6012	2.30E-03	insulin induced gene 1
RPS12	7.2671	8.6395	2.5891	7.40E-03	ribosomal protein S12
SPA17	6.5362	7.9058	2.5840	1.67E-03	sperm autoantigenic protein 17
AKR1C1	5.0555	6.4180	2.5713	6.41E-03	aldo-keto reductase family 1, member C1
LOC100505506	8.2445	9.6002	2.5592	1.09E-02	barrier-to-autointegration factor-like
DNER	6.5789	7.9294	2.5500	6.82E-03	delta/notch-like EGF repeat containing
LOC100128252	7.9603	9.3044	2.5387	1.66E-03	hypothetical LOC100128252
EVI2B	4.0178	5.3598	2.5350	4.46E-03	ecotropic viral integration site 2B
ZNF75A	6.6290	7.9699	2.5330	1.24E-03	zinc finger protein 75a
BBIP1	7.0804	8.4180	2.5273	8.69E-03	BBSome interacting protein 1
MT1L	6.5873	7.9211	2.5207	6.56E-03	metallothionein 1L (gene/pseudogene)
PDP2	5.8506	7.1838	2.5196	1.36E-02	pyruvate dehydrogenase phosphatase catalytic subunit 2
EREG	8.7420	10.0730	2.5156	1.09E-02	epiregulin
SAT1	8.5612	9.8907	2.5132	4.75E-03	spermidine/spermine N1-acetyltransferase 1
MT1F	8.3908	9.7165	2.5066	2.43E-03	metallothionein 1F
FAM32A	6.8195	8.1450	2.5063	8.13E-03	family with sequence similarity 32, member A
RPSAP52	4.2522	5.5773	2.5056	3.70E-03	ribosomal protein SA pseudogene 52
RPS29	4.6552	5.9779	2.5013	8.44E-03	ribosomal protein S29
MKX	8.5954	9.9173	2.5000	1.70E-02	mohawk homeobox
SPRY2	7.5879	8.9073	2.4956	3.40E-03	sprouty homolog 2 (Drosophila)
TPX2	6.4438	7.7601	2.4903	4.33E-03	TPX2, microtubule-associated, homolog (Xenopus laevis)
SLC43A3	8.6786	9.9932	2.4873	5.50E-03	solute carrier family 43, member 3
PMAIP1	7.8517	9.1639	2.4832	1.46E-03	phorbol-12-myristate-13-acetate-induced protein 1
LOC100506394	6.9685	8.2788	2.4798	5.20E-03	hypothetical LOC100506394
#N/A	4.7962	6.1046	2.4765	2.02E-02	#N/A
TPCN1	9.6348	10.9395	2.4703	2.14E-03	two pore segment channel 1
TRIM37	6.7217	8.0215	2.4619	5.68E-03	tripartite motif containing 37
OSBPL8	7.6163	8.9151	2.4603	3.09E-02	oxysterol binding protein-like 8
C9orf6	7.5743	8.8719	2.4583	7.57E-03	chromosome 9 open reading frame 6
RASGRF2	7.0554	8.3514	2.4555	4.98E-03	Ras protein-specific guanine nucleotide-releasing factor 2
HIST1H3B	8.5227	9.8123	2.4445	1.18E-02	histone cluster 1, H3b
HIST2H2BE	7.3838	8.6709	2.4404	6.62E-03	histone cluster 2, H2be
SHC3	7.4211	8.7079	2.4398	2.40E-03	SHC (Src homology 2 domain containing) transforming protein 3
EFHA1	5.7952	7.0803	2.4370	1.88E-02	EF-hand domain family, member A1
C1QTNF1	9.2998	10.5835	2.4346	1.05E-03	C1q and tumor necrosis factor related protein 1
FAP	6.6521	7.9344	2.4324	1.94E-02	fibroblast activation protein, alpha
TRMT112	10.3472	11.6281	2.4299	1.86E-03	tRNA methyltransferase 11-2 homolog (S. cerevisiae)
LOC100130009	9.9766	11.2567	2.4285	3.50E-03	hypothetical protein LOC100130009
PSMA3	7.2375	8.5147	2.4238	1.06E-02	proteasome (prosome, macropain) subunit, alpha type, 3
SNHG1	6.8483	8.1235	2.4203	1.78E-02	small nucleolar RNA host gene 1 (non-protein coding)

SNAP23	8.0234	9.2958	2.4155	1.45E-02	synaptosomal-associated protein, 23kDa
TERC	6.3807	7.6481	2.4074	2.09E-03	telomerase RNA component
CASP4	8.1754	9.4425	2.4068	2.54E-03	caspase 4, apoptosis-related cysteine peptidase
DUSP6	8.0674	9.3322	2.4029	2.82E-03	dual specificity phosphatase 6
CCDC53	6.7970	8.0559	2.3932	1.59E-02	coiled-coil domain containing 53
HMGNI	6.8017	8.0602	2.3924	1.36E-02	high-mobility group nucleosome binding domain 1
GNS	9.5206	10.7772	2.3893	1.65E-02	glucosamine (N-acetyl)-6-sulfatase
LOC654342	8.5360	9.7906	2.3861	3.12E-03	lymphocyte-specific protein 1 pseudogene
CYB5R2	9.0892	10.3422	2.3833	2.12E-03	cytochrome b5 reductase 2
STAMBPL1	5.9137	7.1611	2.3742	2.17E-02	STAM binding protein-like 1
SVIL	8.5875	9.8332	2.3714	2.95E-03	supervillin
HMGA2	8.5483	9.7939	2.3710	1.04E-03	high mobility group AT-hook 2
FUNDC2	6.9069	8.1516	2.3696	1.26E-02	FUN14 domain containing 2
C2orf49	6.3556	7.6001	2.3693	2.08E-02	chromosome 2 open reading frame 49
IDH3A	8.7054	9.9498	2.3692	1.09E-02	isocitrate dehydrogenase 3 (NAD+) alpha
EIF3M	8.7306	9.9712	2.3630	9.15E-03	eukaryotic translation initiation factor 3, subunit M
DNAJC15	8.6051	9.8421	2.3572	6.69E-03	DnaJ (Hsp40) homolog, subfamily C, member 15
PIIF	8.9749	10.2086	2.3518	1.11E-03	peptidylprolyl isomerase F
PSMD12	7.2629	8.4935	2.3466	1.22E-02	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
SCFD1	5.8895	7.1185	2.3440	2.50E-02	sec1 family domain containing 1
KCNJ15	5.4449	6.6728	2.3422	2.31E-02	potassium inwardly-rectifying channel, subfamily J, member 15
MTHFD2L	5.4332	6.6602	2.3408	1.22E-02	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like
LOC541472	5.0858	6.3125	2.3403	3.05E-03	hypothetical LOC541472
NFKBIA	9.9484	11.1732	2.3373	2.88E-03	nuclear factor kappa light polypeptide gene enhancer in B-cells inhib., alpha
IRAK2	7.3221	8.5448	2.3339	1.53E-03	interleukin-1 receptor-associated kinase 2
MANSC1	6.7311	7.9487	2.3256	1.63E-03	MANSC domain containing 1
SEC11C	5.3362	6.5509	2.3209	2.31E-02	SEC11 homolog C (<i>S. cerevisiae</i>)
LOC389607	4.0745	5.2890	2.3206	1.83E-02	hypothetical LOC389607
SKA3	5.0217	6.2302	2.3109	1.38E-02	spindle and kinetochore associated complex subunit 3
BLOC1S1	8.0019	9.2098	2.3099	9.95E-03	biogenesis of lysosomal organelles complex-1, subunit 1
DLEU1	5.2267	6.4312	2.3045	2.38E-03	deleted in lymphocytic leukemia 1 (non-protein coding)
C16orf61	8.2591	9.4621	2.3023	1.99E-02	chromosome 16 open reading frame 61
TRPM7	6.7377	7.9407	2.3021	2.58E-02	transient receptor potential cation channel, subfamily M, member 7
SERPINB8	7.7520	8.9515	2.2965	1.36E-02	serpin peptidase inhibitor, clade B (ovalbumin), member 8
SYAP1	6.7983	7.9973	2.2959	8.60E-03	synapse associated protein 1
SUZ12	7.1547	8.3531	2.2948	2.06E-02	suppressor of zeste 12 homolog (<i>Drosophila</i>)
PRR11	5.7526	6.9501	2.2934	8.73E-03	proline rich 11
MIS12	6.0970	7.2889	2.2846	2.53E-03	MIS12, MIND kinetochore complex component, homolog (<i>S. pombe</i>)
PRRX1	10.0834	11.2744	2.2831	5.02E-03	paired related homeobox 1
TXNL4A	8.4535	9.6425	2.2799	2.99E-03	thioredoxin-like 4A
NCOA4	8.3554	9.5436	2.2787	9.34E-03	nuclear receptor coactivator 4
C18orf21	5.9091	7.0951	2.2752	1.06E-02	chromosome 18 open reading frame 21
ARHGAP11A	5.0547	6.2405	2.2749	4.86E-03	Rho GTPase activating protein 11A
#N/A	5.5811	6.7665	2.2743	5.23E-03	#N/A

HIST1H3C	8.6419	9.8257	2.2718	2.50E-03	histone cluster 1, H3c
SLIT2	8.1604	9.3442	2.2717	3.26E-02	slit homolog 2 (Drosophila)
TNFRSF11B	9.5097	10.6924	2.2700	1.05E-02	tumor necrosis factor receptor superfamily, member 11b
C13orf31	5.7861	6.9677	2.2681	1.26E-02	chromosome 13 open reading frame 31
PGAM4	6.1513	7.3295	2.2630	3.81E-03	phosphoglycerate mutase family member 4
LOC100505587	6.8078	7.9854	2.2620	1.12E-02	v-type proton ATPase subunit F-like
FYN	7.8899	9.0618	2.2530	8.15E-03	FYN oncogene related to SRC, FGR, YES
NUSAP1	6.0158	7.1859	2.2502	1.22E-02	nucleolar and spindle associated protein 1
ANXA7	7.8100	8.9792	2.2489	2.76E-03	annexin A7
PSMD11	8.1123	9.2798	2.2462	3.82E-03	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
LAMB3	7.2642	8.4315	2.2459	2.27E-03	laminin, beta 3
IARS	9.4428	10.6092	2.2444	2.13E-02	isoleucyl-tRNA synthetase
MTRNR2L2	5.5000	6.6663	2.2443	4.44E-02	MT-RNR2-like 2
HIST1H4E	9.3629	10.5285	2.2432	2.87E-02	histone cluster 1, H4e
CUL4B	7.8294	8.9892	2.2344	1.17E-02	cullin 4B
ESD	7.4928	8.6525	2.2341	6.23E-03	esterase D
XPOT	8.4932	9.6524	2.2334	2.15E-02	exportin, tRNA (nuclear export receptor for tRNAs)
RNF144B	6.4334	7.5921	2.2326	6.49E-03	ring finger protein 144B
SNORD60	3.3957	4.5537	2.2315	4.30E-03	small nucleolar RNA, C/D box 60
CAB39L	5.0633	6.2195	2.2287	9.85E-03	calcium binding protein 39-like
PTGES3	9.0033	10.1575	2.2257	4.24E-02	prostaglandin E synthase 3 (cytosolic)
PSMB3	8.8710	10.0249	2.2252	7.59E-03	proteasome (prosome, macropain) subunit, beta type, 3
UBE2V1	4.3200	5.4725	2.2230	7.17E-03	ubiquitin-conjugating enzyme E2 variant 1
LOC550643	8.2718	9.4233	2.2214	1.41E-02	hypothetical LOC550643
PITRM1	9.0595	10.2072	2.2156	3.76E-03	pitrilysin metallopeptidase 1
RNY5	4.9739	6.1179	2.2099	3.42E-02	RNA, Ro-associated Y5
KIAA0101	5.0076	6.1488	2.2057	2.92E-03	KIAA0101
NSF	8.5058	9.6458	2.2039	4.82E-03	N-ethylmaleimide-sensitive factor
SNORA67	7.3006	8.4401	2.2031	1.21E-02	small nucleolar RNA, H/ACA box 67
SCYL2	7.8312	8.9703	2.2024	2.44E-02	SCY1-like 2 (S. cerevisiae)
ADNP	8.1134	9.2509	2.2000	1.19E-02	activity-dependent neuroprotector homeobox
MIR100HG	8.2702	9.4072	2.1991	1.99E-02	mir-100-let-7a-2 cluster host gene (non-protein coding)
HINT1	7.5231	8.6591	2.1977	3.33E-03	histidine triad nucleotide binding protein 1
SNORD26	6.1917	7.3266	2.1961	2.96E-02	small nucleolar RNA, C/D box 26
GTF2A2	6.8384	7.9733	2.1960	4.89E-02	general transcription factor IIA, 2, 12kDa

Mean 1 = UCB1 MSCs grown in lens epithelial cell basal medium (LECBM)

Mean 2 = UCB1 MSCs grown in lens epithelial cell-conditioned medium (LECCM)

FoldDiff = Fold Difference

p-SAM = p-Significance Analysis of Microarrays