

Appendix 1
(UCB MSCs >> HCEC)

Gene	Mean 1	Mean 2	FoldDiff	p-SAM	Gene Name
GREM1	5.415	12.261	115.098	4.70E-05	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)
LPPR4	4.732	10.023	39.158	3.80E-04	lipid phosphate phosphatase-related protein type 4
MEIS1	4.010	8.963	30.977	2.40E-04	Meis homeobox 1
NLGN1	3.916	8.296	20.832	3.20E-04	neuroligin 1
SIX1	5.507	9.573	16.752	7.50E-05	SIX homeobox 1
CDK15	4.632	8.639	16.072	4.50E-05	cyclin-dependent kinase 15
ADAMTS2	7.168	10.962	13.869	3.80E-04	ADAM metalloproteinase with thrombospondin type 1 motif, 2
EPHA5	4.599	8.335	13.325	1.10E-04	EPH receptor A5
CREB3L1	6.636	10.368	13.284	6.50E-05	cAMP responsive element binding protein 3-like 1
EBF1	5.184	8.904	13.183	8.40E-04	early B-cell factor 1
MYOCD	5.172	8.872	12.989	2.50E-04	myocardin
BCAT1	6.553	10.193	12.467	1.30E-04	branched chain aminotransferase 1, cytosolic
SCUBE3	7.372	10.958	12.007	7.30E-04	signal peptide, CUB domain, EGF-like 3
LMOD1	5.727	9.265	11.614	7.00E-05	leiomodulin 1 (smooth muscle)
MYLK	5.721	9.253	11.564	1.40E-03	myosin light chain kinase
MEIS2	4.925	8.443	11.460	1.40E-04	Meis homeobox 2
ENPP2	6.193	9.671	11.141	4.50E-04	ectonucleotide pyrophosphatase/phosphodiesterase 2
TBX18	5.035	8.493	10.996	4.10E-04	T-box 18
COL1A1	9.516	12.962	10.892	1.10E-04	collagen, type I, alpha 1
OXTR	5.887	9.320	10.794	1.20E-04	oxytocin receptor
TSHZ3	5.328	8.707	10.398	4.90E-05	teashirt zinc finger homeobox 3
FBN2	6.483	9.837	10.224	1.10E-03	fibrillin 2
ABCC9	3.696	7.015	9.979	6.90E-04	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
ACTG2	8.819	12.075	9.555	1.60E-03	actin, gamma 2, smooth muscle, enteric
SLC14A1	4.379	7.547	8.992	1.70E-02	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
MAB21L1	4.385	7.511	8.734	2.10E-04	mab-21-like 1 (C. elegans)
TAGLN	8.602	11.692	8.517	4.60E-04	transgelin
SNTB1	6.853	9.903	8.280	1.60E-04	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)
PCDH10	7.238	10.279	8.236	1.40E-03	protocadherin 10
AFF3	5.715	8.749	8.190	1.40E-04	AF4/FMR2 family, member 3
ROR1	6.228	9.245	8.098	1.80E-04	receptor tyrosine kinase-like orphan receptor 1
CXCL12	6.792	9.805	8.072	2.40E-03	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
COL6A3	8.530	11.542	8.071	6.30E-04	collagen, type VI, alpha 3
VGLL3	7.103	10.109	8.036	1.30E-03	vestigial like 3 (Drosophila)
GCNT4	4.142	7.139	7.988	1.30E-04	glucosaminyl (N-acetyl) transferase 4, core 2 (beta-1,6-N-acetylglucosaminyltransferase)
ANLN	6.321	9.298	7.872	7.90E-04	anillin, actin binding protein
SLC8A1	5.339	8.312	7.855	6.00E-05	solute carrier family 8 (sodium/calcium exchanger), member 1
HIST1H3G	6.696	9.624	7.607	3.10E-04	histone cluster 1, H3g
COL4A1	7.064	9.979	7.541	1.40E-03	collagen, type IV, alpha 1
FAM26E	5.745	8.653	7.503	3.90E-04	family with sequence similarity 26, member E
UACA	6.961	9.860	7.460	5.80E-05	uveal autoantigen with coiled-coil domains and ankyrin repeats

COL6A2	8.558	11.441	7.377	1.20E-04	collagen, type VI, alpha 2
CNN1	6.309	9.190	7.363	5.40E-04	calponin 1, basic, smooth muscle
NID2	7.589	10.456	7.293	4.90E-04	nidogen 2 (osteonidogen)
PLK1	7.416	10.242	7.094	1.40E-04	polo-like kinase 1 (Drosophila)
ALPL	5.811	8.634	7.073	7.90E-03	alkaline phosphatase, liver/bone/kidney
UNQ3104	4.990	7.808	7.052	9.50E-05	ACAH3104
CRISPLD2	6.718	9.533	7.038	3.40E-04	cysteine-rich secretory protein LCCL domain containing 2
E2F7	6.092	8.867	6.842	7.60E-04	E2F transcription factor 7
PSG5	4.749	7.514	6.797	8.20E-03	pregnancy specific beta-1-glycoprotein 5
GFPT2	5.978	8.723	6.701	3.70E-04	glutamine-fructose-6-phosphate transaminase 2
AKAP12	7.147	9.880	6.649	1.90E-04	A kinase (PRKA) anchor protein 12
TPX2	6.738	9.460	6.599	2.80E-04	TPX2, microtubule-associated, homolog (Xenopus laevis)
LOC728264	5.563	8.274	6.549	1.60E-03	hypothetical LOC728264
ALPK2	5.344	8.041	6.485	8.10E-05	alpha-kinase 2
DLC1	6.026	8.694	6.357	3.30E-04	deleted in liver cancer 1
DLGAP5	5.317	7.913	6.044	7.40E-04	discs, large (Drosophila) homolog-associated protein 5
ITGA11	7.194	9.783	6.017	4.30E-02	integrin, alpha 11
COL4A2	7.782	10.368	6.006	2.80E-04	collagen, type IV, alpha 2
SFTA1P	3.504	6.086	5.985	4.30E-02	surfactant associated 1 (pseudogene)
KRTAP1-5	6.670	9.239	5.936	4.60E-04	keratin associated protein 1-5
MKI67	5.949	8.489	5.816	8.60E-04	antigen identified by monoclonal antibody Ki-67
HIST1H3B	7.970	10.508	5.807	1.10E-03	histone cluster 1, H3b
FGF5	7.001	9.531	5.777	1.10E-03	fibroblast growth factor 5
BRIP1	5.058	7.578	5.736	6.80E-04	BRCA1 interacting protein C-terminal helicase 1
CDC20	6.573	9.068	5.638	5.00E-04	cell division cycle 20 homolog (S. cerevisiae)
MSC	5.362	7.841	5.577	3.60E-03	musculin (activated B-cell factor-1)
KIF20A	6.201	8.674	5.549	9.90E-04	kinesin family member 20A
LAMA2	5.250	7.719	5.536	6.60E-04	laminin, alpha 2
OLFM2	8.593	11.061	5.533	5.60E-03	olfactomedin 2
BEX1	4.167	6.635	5.531	3.00E-03	brain expressed, X-linked 1
SPON2	6.329	8.797	5.530	1.90E-04	spondin 2, extracellular matrix protein
TMEM47	9.156	11.617	5.505	1.20E-03	transmembrane protein 47
ACTA2	9.700	12.160	5.503	6.10E-04	actin, alpha 2, smooth muscle, aorta
FMN2	5.531	7.985	5.478	1.30E-04	formin 2
CCNB2	5.673	8.108	5.407	3.30E-04	cyclin B2
SLC7A2	4.512	6.946	5.404	6.30E-05	solute carrier family 7 (cationic amino acid transporter), member 2
VCAM1	5.661	8.095	5.403	2.80E-03	vascular cell adhesion molecule 1
PBK	4.646	7.078	5.397	3.50E-04	PDZ binding kinase
IGF2BP1	5.474	7.898	5.368	5.60E-04	insulin-like growth factor 2 mRNA binding protein 1
BVES	7.276	9.697	5.357	5.30E-04	blood vessel epicardial substance
CENPF	5.189	7.585	5.262	9.00E-04	centromere protein F, 350/400ka (mitosin)
MEG3	7.223	9.596	5.183	6.60E-04	maternally expressed 3 (non-protein coding)
APOBEC3B	6.443	8.816	5.180	8.70E-04	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
NR2F2	7.410	9.769	5.134	7.70E-05	nuclear receptor subfamily 2, group F, member 2
LIFR	4.879	7.238	5.133	1.30E-03	leukemia inhibitory factor receptor alpha
CEP55	4.989	7.334	5.081	3.00E-04	centrosomal protein 55kDa

COL6A1	9.985	12.330	5.078	8.90E-04	collagen, type VI, alpha 1
TOP2A	6.187	8.530	5.077	6.50E-04	topoisomerase (DNA) II alpha 170kDa
KCNG1	5.816	8.155	5.058	2.50E-04	potassium voltage-gated channel, subfamily G, member 1
DIAPH3	5.292	7.626	5.045	2.40E-04	diaphanous homolog 3 (Drosophila)
TRPC4	5.210	7.535	5.010	1.90E-03	transient receptor potential cation channel, subfamily C, member 4
MXRA5	5.669	7.988	4.991	3.00E-02	matrix-remodelling associated 5
C9orf109	5.013	7.329	4.979	5.30E-03	chromosome 9 open reading frame 109
HOXD10	5.081	7.394	4.971	2.20E-02	homeobox D10
BUB1B	5.316	7.623	4.952	3.30E-04	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
GAS2L3	5.848	8.156	4.951	7.70E-04	growth arrest-specific 2 like 3
ZIC1	4.165	6.468	4.935	1.10E-02	Zic family member 1 (odd-paired homolog, Drosophila)
PABPC4L	4.570	6.858	4.886	1.50E-04	poly(A) binding protein, cytoplasmic 4-like
NXN	7.983	10.266	4.869	5.00E-04	nucleoredoxin
CASC5	5.186	7.466	4.854	3.50E-04	cancer susceptibility candidate 5
FAT4	5.773	8.043	4.826	7.60E-04	FAT tumor suppressor homolog 4 (Drosophila)
PHGDH	8.721	10.989	4.819	3.80E-04	phosphoglycerate dehydrogenase
MYL9	9.099	11.364	4.804	1.40E-04	myosin, light chain 9, regulatory
SPC25	3.018	5.272	4.769	6.90E-04	SPC25, NDC80 kinetochore complex component
SHCBP1	5.303	7.548	4.739	2.10E-04	SHC SH2-domain binding protein 1
VCAN	7.428	9.654	4.678	7.10E-03	versican
CKAP2L	5.133	7.348	4.642	2.40E-04	cytoskeleton associated protein 2-like
NOTCH3	7.794	10.001	4.616	1.10E-03	Notch homolog 3 (Drosophila)
ULBP1	6.441	8.644	4.604	1.90E-03	UL16 binding protein 1
CACNA2D1	6.654	8.857	4.603	1.70E-03	calcium channel, voltage-dependent, alpha 2/delta subunit 1
NCAPH	5.393	7.583	4.562	1.30E-04	non-SMC condensin I complex, subunit H
CDH6	5.320	7.509	4.560	2.00E-02	cadherin 6, type 2, K-cadherin (fetal kidney)
PDE1C	4.601	6.786	4.548	7.50E-03	phosphodiesterase 1C, calmodulin-dependent 70kDa
NCAM2	3.996	6.175	4.528	1.70E-04	neural cell adhesion molecule 2
ESCO2	5.714	7.882	4.493	1.20E-03	establishment of cohesion 1 homolog 2 (S. cerevisiae)
PDLIM1	8.048	10.204	4.458	1.90E-03	PDZ and LIM domain 1
KIF23	5.910	8.059	4.437	2.00E-04	kinesin family member 23
ADAMTS15	5.507	7.643	4.396	1.20E-03	ADAM metallopeptidase with thrombospondin type 1 motif, 15
TBX15	3.890	6.026	4.395	1.10E-02	T-box 15
PRR11	6.497	8.632	4.394	9.60E-04	proline rich 11
BUB1	5.947	8.078	4.381	6.50E-04	budding uninhibited by benzimidazoles 1 homolog (yeast)
EBF2	4.923	7.053	4.375	1.40E-02	early B-cell factor 2
MLF1IP	4.301	6.427	4.363	9.80E-04	MLF1 interacting protein
C1orf198	8.126	10.250	4.359	1.50E-03	chromosome 1 open reading frame 198
DSP	7.446	9.568	4.353	6.70E-03	desmoplakin
SGOL1	4.338	6.458	4.348	4.80E-04	shugoshin-like 1 (S. pombe)
CHAC1	7.966	10.082	4.334	1.00E-04	ChaC, cation transport regulator homolog 1 (E. coli)
HIST1H3C	8.706	10.821	4.330	8.20E-04	histone cluster 1, H3c
ZEB2	7.799	9.907	4.312	6.30E-04	zinc finger E-box binding homeobox 2
PDGFRB	9.114	11.221	4.309	1.70E-04	platelet-derived growth factor receptor, beta polypeptide
PRC1	6.828	8.934	4.306	2.90E-04	protein regulator of cytokinesis 1
TBX5	4.939	7.024	4.242	2.80E-02	T-box 5
DKK3	9.312	11.394	4.236	1.90E-03	dickkopf homolog 3 (Xenopus laevis)

FAM64A	5.831	7.914	4.236	2.60E-04	family with sequence similarity 64, member A
ZNF804A	5.513	7.596	4.235	3.90E-02	zinc finger protein 804A
HOXC10	3.827	5.909	4.233	3.70E-02	homeobox C10
CSPG4	6.609	8.688	4.225	3.30E-04	chondroitin sulfate proteoglycan 4
TK1	6.788	8.859	4.203	1.70E-04	thymidine kinase 1, soluble
GPC6	7.671	9.740	4.195	1.30E-02	glypican 6
NCAPG	5.152	7.210	4.166	7.40E-04	non-SMC condensin I complex, subunit G
ALDH1L2	7.649	9.706	4.160	4.20E-04	aldehyde dehydrogenase 1 family, member L2
OSR2	6.055	8.099	4.125	9.10E-04	odd-skipped related 2 (Drosophila)
TBX3	6.266	8.296	4.082	3.80E-02	T-box 3
GRIK2	6.241	8.268	4.075	1.00E-03	glutamate receptor, ionotropic, kainate 2
PSAT1	7.353	9.379	4.072	1.40E-03	phosphoserine aminotransferase 1
BST1	7.027	9.052	4.072	1.90E-03	bone marrow stromal cell antigen 1
BAALC	5.824	7.850	4.071	1.00E-03	brain and acute leukemia, cytoplasmic
KIF2C	5.064	7.087	4.063	1.90E-04	kinesin family member 2C
CHRM2	4.715	6.736	4.057	2.70E-02	cholinergic receptor, muscarinic 2
S100A3	5.395	7.414	4.053	2.10E-04	S100 calcium binding protein A3
MEF2C	5.463	7.481	4.049	3.60E-04	myocyte enhancer factor 2C
GPSM2	5.059	7.063	4.010	1.90E-04	G-protein signaling modulator 2 (AGS3-like, C. elegans)
MRV11	5.740	7.743	4.010	9.60E-05	murine retrovirus integration site 1 homolog
HIST1H3E	9.447	11.448	4.002	1.30E-03	histone cluster 1, H3e
HAPLN1	3.160	5.155	3.985	6.50E-03	hyaluronan and proteoglycan link protein 1
SKA3	5.266	7.259	3.981	6.60E-04	spindle and kinetochore associated complex subunit 3
CCNA2	7.135	9.128	3.981	3.60E-04	cyclin A2
TRIP13	5.719	7.710	3.973	5.50E-04	thyroid hormone receptor interactor 13
MEG8	5.862	7.846	3.955	3.90E-04	maternally expressed 8 (non-protein coding)
KIAA0101	5.579	7.549	3.917	1.30E-03	KIAA0101
ASPM	4.973	6.941	3.913	1.60E-03	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
ZNF608	5.369	7.325	3.881	8.40E-04	zinc finger protein 608
MELK	4.687	6.637	3.864	1.30E-04	maternal embryonic leucine zipper kinase
PRKCDBP	8.628	10.577	3.862	4.40E-04	protein kinase C, delta binding protein
FOXM1	6.789	8.736	3.854	4.00E-04	forkhead box M1
MYBL2	6.267	8.213	3.853	1.40E-04	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
ATP8B1	7.690	9.635	3.850	3.50E-03	ATPase, class I, type 8B, member 1
CDK1	4.533	6.470	3.831	5.10E-04	cyclin-dependent kinase 1
AK5	6.306	8.243	3.830	2.50E-03	adenylate kinase 5
FLT1	5.892	7.822	3.811	4.50E-03	fms-related tyrosine kinase 1
HIST1H2BM	8.938	10.863	3.796	9.90E-04	histone cluster 1, H2bm
CBS	7.971	9.894	3.793	5.60E-04	cystathionine-beta-synthase
TTK	4.027	5.946	3.784	5.70E-04	TTK protein kinase
LDB2	6.505	8.413	3.755	4.40E-04	LIM domain binding 2
ABLIM3	6.791	8.698	3.751	3.40E-04	actin binding LIM protein family, member 3
LOC400590	6.650	8.540	3.709	6.10E-04	hypothetical LOC400590
IQGAP3	5.898	7.788	3.707	2.90E-04	IQ motif containing GTPase activating protein 3
TGFB1I1	9.332	11.221	3.702	8.30E-05	transforming growth factor beta 1 induced transcript 1
LOX	9.725	11.603	3.676	5.10E-04	lysyl oxidase
NUF2	4.273	6.151	3.676	5.00E-04	NUF2, NCD80 kinetochore complex component

ITGA8	4.082	5.955	3.664	1.00E-03	integrin, alpha 8
SKA1	3.665	5.534	3.654	9.70E-05	spindle and kinetochore associated complex subunit 1
NEXN	7.121	8.988	3.647	3.80E-03	nexilin (F actin binding protein)
UHRF1	6.595	8.458	3.637	1.10E-03	ubiquitin-like with PHD and ring finger domains 1
NTF3	4.366	6.228	3.636	4.70E-04	neurotrophin 3
LRRK1	6.510	8.367	3.624	3.90E-04	leucine-rich repeat kinase 1
CENPI	5.022	6.875	3.613	4.40E-04	centromere protein I
KIF11	5.263	7.114	3.609	7.00E-04	kinesin family member 11
WNT2	4.438	6.287	3.604	2.90E-02	wingless-type MMTV integration site family member 2
HIST1H2AB	4.567	6.411	3.592	3.10E-02	histone cluster 1, H2ab
HIST1H2BH	7.102	8.941	3.578	3.70E-04	histone cluster 1, H2bh
PRR16	7.591	9.424	3.565	8.60E-05	proline rich 16
MGLL	6.684	8.516	3.561	1.60E-03	monoglyceride lipase
B3GALT2	3.130	4.954	3.541	1.60E-03	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
KLF4	5.886	7.699	3.513	3.10E-04	Kruppel-like factor 4 (gut)
TET1	5.234	7.037	3.490	2.00E-04	tet oncogene 1
GJC1	7.262	9.062	3.483	3.10E-03	gap junction protein, gamma 1, 45kDa
SNAI2	10.665	12.461	3.473	6.70E-04	snail homolog 2 (Drosophila)
TOX	7.116	8.909	3.466	3.80E-02	thymocyte selection-associated high mobility group box
EBF3	4.703	6.492	3.456	4.40E-02	early B-cell factor 3
DTL	6.142	7.930	3.453	9.90E-04	denticleless homolog (Drosophila)
CDCA8	5.699	7.480	3.437	2.30E-04	cell division cycle associated 8
KLF7	9.122	10.902	3.434	1.30E-03	Kruppel-like factor 7 (ubiquitous)
ITGB3	7.288	9.068	3.433	1.60E-03	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
C14orf139	6.782	8.559	3.428	1.30E-03	chromosome 14 open reading frame 139
SIX2	7.740	9.513	3.417	8.90E-04	SIX homeobox 2
FAM129A	6.670	8.440	3.412	3.80E-02	family with sequence similarity 129, member A
C14orf49	6.296	8.065	3.408	8.80E-04	chromosome 14 open reading frame 49
RBM3	9.702	11.465	3.396	4.80E-04	RNA binding motif (RNP1, RRM) protein 3
GDF6	5.491	7.250	3.383	1.90E-03	growth differentiation factor 6
NDC80	4.607	6.365	3.383	5.80E-04	NDC80 homolog, kinetochore complex component (S. cerevisiae)
JAZF1	7.972	9.711	3.337	3.10E-04	JAZF zinc finger 1
ARHGAP11A	5.764	7.502	3.335	9.20E-04	Rho GTPase activating protein 11A
XG	4.987	6.725	3.335	4.80E-02	Xg blood group
SYT14	5.609	7.343	3.326	2.60E-03	synaptotagmin XIV
TNFRSF19	5.882	7.614	3.321	2.10E-02	tumor necrosis factor receptor superfamily, member 19
PTN	5.666	7.394	3.312	7.60E-03	pleiotrophin
NUSAP1	6.368	8.095	3.310	8.50E-04	nucleolar and spindle associated protein 1
MYBL1	6.088	7.804	3.285	2.10E-03	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
C7orf58	6.384	8.099	3.284	2.10E-02	chromosome 7 open reading frame 58
HIST1H4F	7.098	8.811	3.277	4.60E-03	histone cluster 1, H4f
C10orf72	6.241	7.952	3.274	2.00E-03	chromosome 10 open reading frame 72
AR	6.026	7.734	3.267	1.00E-02	androgen receptor
HIST1H2AL	7.025	8.732	3.264	5.30E-04	histone cluster 1, H2al
SYNJ2	7.893	9.594	3.251	4.70E-04	synaptojanin 2
ASF1B	6.698	8.397	3.247	6.10E-04	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)

CENPE	3.960	5.658	3.244	1.60E-03	centromere protein E, 312kDa
CAMK4	4.125	5.816	3.229	7.80E-04	calcium/calmodulin-dependent protein kinase IV
CLDN11	9.224	10.911	3.220	4.70E-02	claudin 11
RELN	4.506	6.192	3.216	3.80E-03	reelin
RALGPS2	6.701	8.376	3.194	3.90E-03	Ral GEF with PH domain and SH3 binding motif 2
HOXA7	5.533	7.201	3.177	2.20E-02	homeobox A7
AHNAK	9.218	10.883	3.172	2.60E-03	AHNAK nucleoprotein
TINAGL1	6.383	8.043	3.161	2.50E-02	tubulointerstitial nephritis antigen-like 1
ARSJ	7.464	9.123	3.156	1.90E-03	arylsulfatase family, member J
MEOX2	5.686	7.341	3.150	4.70E-02	mesenchyme homeobox 2
ELFN1	6.344	7.998	3.148	5.10E-03	extracellular leucine-rich repeat, fibronectin type III domain
DACT1	6.528	8.178	3.137	1.70E-02	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)
PLEKHO1	7.015	8.665	3.137	2.00E-04	pleckstrin homology domain containing, family O member 1
APOLD1	7.207	8.856	3.135	2.90E-04	apolipoprotein L domain containing 1
CKB	7.262	8.910	3.135	1.10E-03	creatine kinase, brain
JAG1	8.293	9.940	3.131	5.50E-03	jagged 1 (Alagille syndrome)
DSEL	8.132	9.778	3.130	1.70E-03	dermatan sulfate epimerase-like
CCBE1	7.411	9.050	3.113	6.30E-03	collagen and calcium binding EGF domains 1
CDKN3	5.927	7.565	3.111	3.60E-03	cyclin-dependent kinase inhibitor 3
MOCOS	5.704	7.337	3.102	1.60E-03	molybdenum cofactor sulfurase
KIF15	3.957	5.587	3.095	7.10E-04	kinesin family member 15
TRHDE	6.980	8.609	3.093	2.70E-02	thyrotropin-releasing hormone degrading enzyme
SASH1	7.535	9.164	3.092	3.20E-04	SAM and SH3 domain containing 1

Mean 1 = Mean of HCEC Samples

Mean 2 = Mean of MSC Samples

FoldDiff = Fold Difference

p_SAM = p-Significance Analysis of Microarrays