

Supplemental Figures and Tables

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Line and subline name	Method used to generate subline	Passage analyzed	% nuclei with H3K27me3 foci
HSF-6	Start	57	40%
HSF-6 (1)	Colony pick	61	70%
HSF-6 (2)	Colony pick	61	30%
HSF-6 (3)	Colony pick	61	30%
HSF-6 (4)	Colony pick	61	70%
HSF-6 (5)	Colony pick	61	50%
HSF-6 (6)	Colony pick	61	50%
HSF-6 (7)	Colony pick	61	95%
HSF-6 (8)	Colony pick	61	95%
HSF-6 (9)	Colony pick	61	50%
HSF-6 (10)	Colony pick	61	95%
HSF-6 (S6)	Single cell	64	0%
HSF-6 (S7)	Single cell	64	0%
HSF-6 (S8)	Single cell	64	0%
HSF-6 (S9)	Single cell	64	0%
H9	Start	37	36%
H9 (1)	Colony pick	41	0%
H9 (2)	Colony pick	41	0%
H9 (3)	Colony pick	41	0%
H9 (4)	Colony pick	41	0%
H9 (5)	Colony pick	41	50%
H9 (6)	Colony pick	41	50%
H9 (7)	Colony pick	41	0%
H9 (8)	Colony pick	41	0%
H9 (9)	Colony pick	41	0%
H9 (10)	Colony pick	41	0%
HSF-6	Regular passaging	61	0%
H9	Regular passaging	41	0%

Supplemental Table 1: Percentage of nuclei in HSF-6 and H9 lines and sublines containing a single focal dot of H3K27me3.

Supplemental Figure Legends:

Supplemental Figure 1: Comparison of Cot 1/X chromosome FISH and H3K27me3/X chromosome FISH techniques for identifying XCI in female fibroblasts and hIPS21. **(A)** Female fibroblast nuclei stained with H3K27me3 and DAPI. Arrow indicates focal dot identified in n=328/328 nuclei **(B)** Female fibroblast demonstrating a single *XIST* focal dot in a DAPI stained nucleus indicating *XIST*-dependent XCI. **(C)** Cot1/X chromosome FISH of female fibroblasts, where one X chromosome is localized to a nuclear exclusion zone in n=18/18 nuclei (arrow). **(D)** H3K4me3/X chromosome FISH technique of female fibroblasts, one X chromosome localized to a nuclear exclusion zone in n=30/30 nuclei (arrow). **(E)** H3K4me3/X chromosome FISH of hIPS21 which was previously reported as exhibiting *XIST*-independent XCI in the self-renewing state shows one X chromosome to a nuclear exclusion zone (n=27 nuclei analyzed).

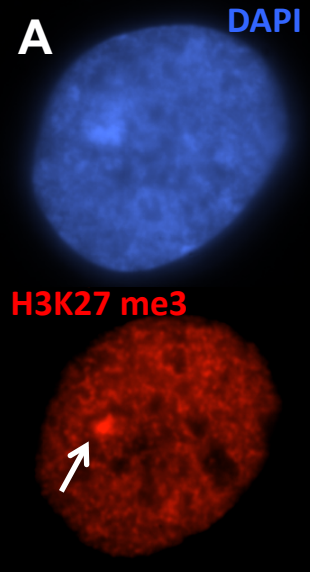
Supplemental Figure 2: Teratoma analysis in class III lines. **(A)** Teratomas were generated by transplantation into the testicles of immunocompromized mice. n= number of testicles that were transplanted. **(B)**. Representative image of endoderm, mesoderm and ectodermal lineages (arrow) identified in each of the tumors by histology.

Supplemental Figure 3: Karyotype and Flow cytometry of new UCLA hESC lines. **(A)** Karyotype was performed by Cell Line Genetics at the passage (p) indicated for all six hESC lines. **(B)** Flow cytometry was performed to evaluate TRA-1-81 and SSEA4 positive cells in all six hESC lines at the passage (p) indicated.

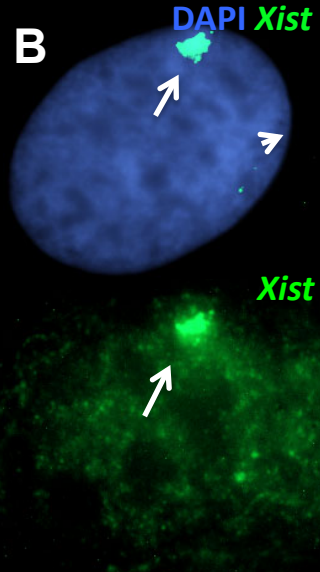
Supplemental Figure 4: Teratomas were generated from the six new UCLA lines as indicated. All lines generated teratomas with evidence of ectoderm, mesoderm and endoderm as shown in the representative picture. In UCLA5 n=4 replicates generated tumors, however n=2/4 developed cystic tumors with no solid regions for diagnosis of teratoma and n=2/4 developed solid tumors where representative lineages from ectoderm, endoderm and mesoderm could be identified. n=number of testicles transplanted.

Supplemental Figure 5: Images of the human blastocysts used to generate UCLA1-6 hESC lines. Images were taken within 24 hours of plating on MEFs

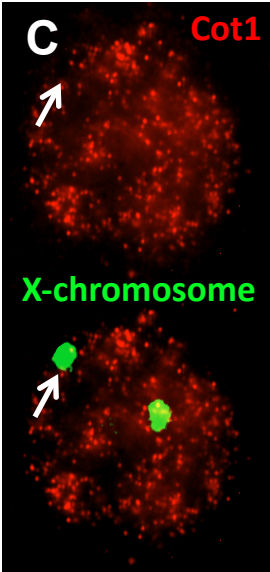
Human fibroblast



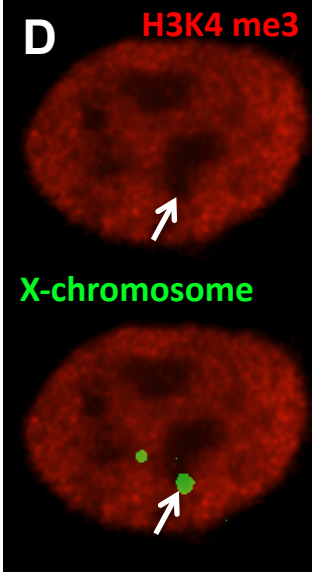
Human fibroblast



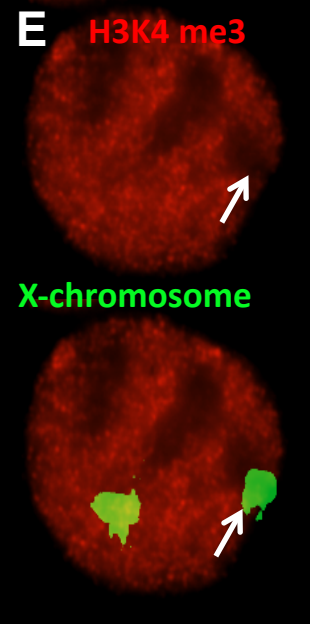
Human fibroblast



Human fibroblast



hiPS21



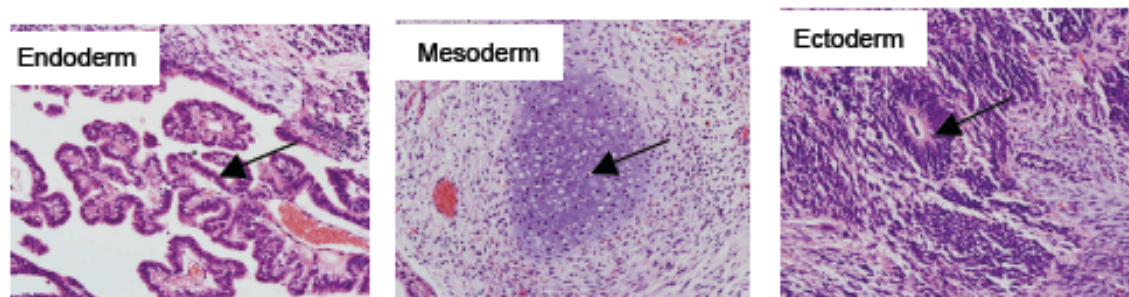
Supplemental figure 1

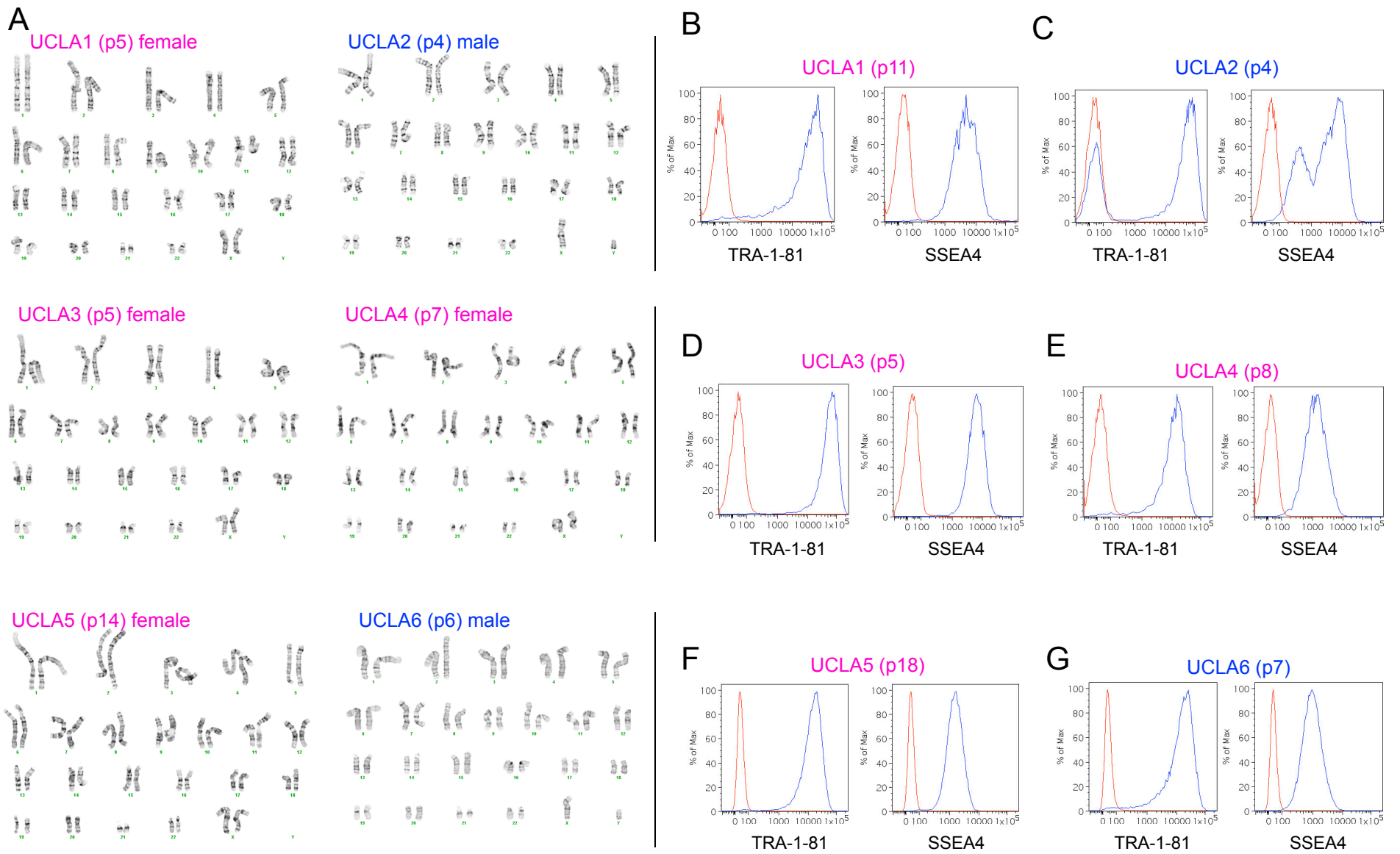
A

Line and Subline name	Differentiation in vivo	Result
HSF-6 (S7)	SCID-Beige testicles	4/4 teratomas
HSF-6 (S8)	SCID-Beige testicles	4/4 teratomas
HSF-6 (S9)	SCID-Beige testicles	4/4 teratomas
HSF-6	SCID-Beige testicles	4/4 teratomas
H9 (7)	SCID-Beige testicles	4/4 teratomas
H9 (8)	SCID-Beige testicles	4/4 teratomas
H9 (9)	SCID-Beige testicles	4/4 teratomas
H9	SCID-Beige testicles	4/4 teratomas

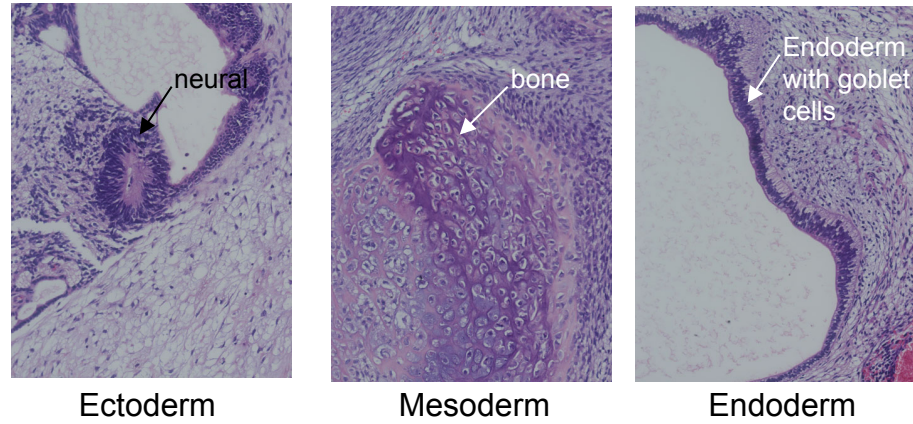
Table: Teratomas generated from class III hESC lines and sublines

B

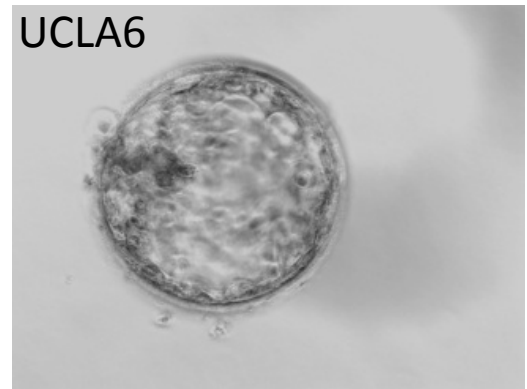
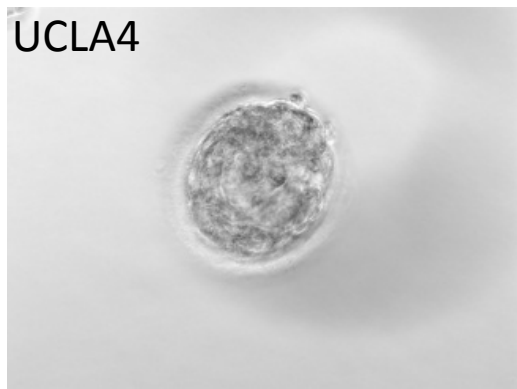
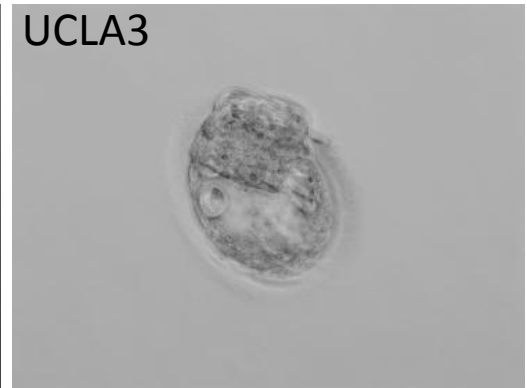
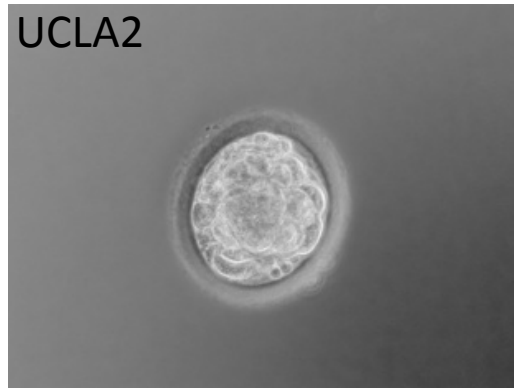
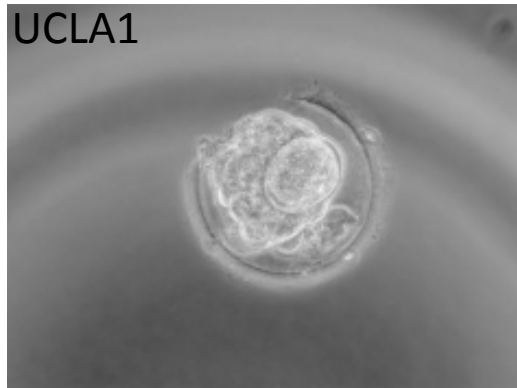




Supplemental Figure 3



Cell Line	Positive	Positive	Positive
UCLA1	n=4	n=4	n=4
UCLA2	n=2	n=2	n=2
UCLA3	n=2	n=2	n=2
UCLA4	n=2	n=2	n=2
UCLA5*	n=2/4	n=2/4	n=2/4
UCLA6	n=4	n=4	n=4



Supplemental Table 2: List of 170 differentially expressed gene accession numbers comparing HSF-6 (8) cultured with and without B+D. Red (negative numbers) indicate downregulated in B+D

probe set	gene	Accession	EntrezGene	Description	fold change	t statistic	P value
237911_at	Transcribed locus	BF057809		Hs.197683.0		51.77	13.268
235557_at	LOC150763: hypothetical protein LOC150763	AW082827		150763 Hs.146084.0		48.22	9.522
224997_x_at	H19: H19, imprinted maternally expressed untranslated mRNA	AL575306		283120 Hs.279525.0		36.14	12.681
39318_at	TCL1A: T-cell leukemia/lymphoma 1A	X82240		8115 4856700_RC		20.18	13.751
206994_at	CST4: cystatin S	NM_001899		1472 g4503108		20.02	15.593
242516_x_at	MGC27016: hypothetical protein MGC27016	AA934358		166863 Hs.126987.0		16.27	13.826
206224_at	CST1: cystatin SN	NM_001898		1469 g4503102		12.76	14.168
228949_at	GPR177: G protein-coupled receptor 177	AL534095		79971 Hs.250746.1		10.63	8.178
221958_s_at	GPR177: G protein-coupled receptor 177	AA775681		79971 Hs.250746.2		10.08	16.255
208555_x_at	CST2: cystatin SA	NM_001322		1470 g4503104		8.63	11.605
211276_at	TCEAL2: transcription elongation factor A (SII)-like 2	AF063606		140597 g12002041		8.47	8.414
220535_at	FAM90A1: family with sequence similarity 90, member A1	NM_018088		55138 g8922410		7.9	9.285
221916_at	NEFL: neurofilament, light polypeptide 68kDa	BF055311		4747 Hs.302689.1		7.68	8.827
209392_at	ENPP2: ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	L35594		5168 g537905		7.41	9.384
237552_at	CDNA clone IMAGE:4667929	BF056473		Hs.197042.0		7.31	5.37
215356_at	ECAT8: ES cell associated transcript 8	AK023134		91646 Hs.277014.0		6.29	10.731
221805_at	NEFL: neurofilament, light polypeptide 68kDa	AL537457		4747 Hs.211584.0		6.08	9.162
231460_at	Transcribed locus	AI702438		Hs.145533.0		6.08	11.386
214603_at	MAGEA2 /// MAGEA2B: melanoma antigen family A, 2 /// melanoma antigen family	U26271	266740 /// 4101	Hs.36980.0		5.98	6.981
210770_s_at	CACNA1A: calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	AF004884		773 g2213912		5.34	7.935
221690_s_at	NLRP2: NLR family, pyrin domain containing 2	AF298547		55655 g10198206		5.16	14.339
210839_s_at	ENPP2: ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	D45421		5168 g662289		4.82	11.001
221558_s_at	LEF1: lymphoid enhancer-binding factor 1	AF288571		51176 g9858157		4.77	6.857
228950_s_at	GPR177: G protein-coupled receptor 177	AL534095		79971 Hs.250746.1		4.42	10.121
1564413_at	Hs.2.396985.1	AK093435		Hs.2.396985.1		4.34	10.029
209604_s_at	GATA3: GATA binding protein 3	BC003070		2625 g13111765		4.13	7.311
205524_s_at	HAPLN1: hyaluronan and proteoglycan link protein 1	NM_001884		1404 g4503052		4.08	7.203
213238_at	ATP10D: ATPase, Class V, type 10D	AI478147		57205 Hs.173540.0		4	7.497
213258_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	BF511231		7035 Hs.288582.0		3.68	6.507
206390_x_at	PF4: platelet factor 4 (chemokine (C-X-C motif) ligand 4)	NM_002619		5196 g4505732		3.61	5.449
205710_at	LRP2: low density lipoprotein-related protein 2	NM_004525		4036 g6806918		3.51	6.595
213624_at	SMPDL3A: sphingomyelin phosphodiesterase, acid-like 3A	AA873600		10924 Hs.42945.0		3.42	9.857
223422_s_at	ARHGAP24: Rho GTPase activating protein 24	AI743534		83478 Hs.93589.0		3.36	8.505
210664_s_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834		7035 g4103170		3.29	6.72
212234_at	ASXL1: additional sex combs like 1 (Drosophila)	AL034550		171023 Hs.3686.0		3.23	11.492
209676_at	TFPI: tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	J03225		7035 g180545		3.21	5.783
209197_at	SYT11: synaptotagmin XI	AA626780		23208 Hs.74554.0		3.11	8.108
203881_s_at	DMD: dystrophin (muscular dystrophy, Duchenne and Becker types)	NM_004010		1756 g5032314		3.05	15.931
218445_at	H2AFY2: H2A histone family, member Y2	NM_018649		55506 g8923919		2.9	8.89
209280_at	MRC2: mannose receptor, C type 2	U58856		9902 g2209262		2.88	5.17
232191_at	C21orf105: chromosome 21 open reading frame 105	BC005107		90625 Hs.143375.0		2.88	5.927
202273_at	PDGFRB: platelet-derived growth factor receptor, beta polypeptide	NM_002609		5159 g4505682		2.87	6.67
204689_at	HHEX: hematopoietically expressed homeobox	NM_001529		3087 g10835016		2.85	11.144
205893_at	NLG1: neuroligin 1	NM_014932		22871 g7662469		2.7	5.768
201278_at	DAB2: disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	N21202		1601 Hs.81988.0		2.57	6.003
204073_s_at	C11orf9: chromosome 11 open reading frame 9	NM_013279		745 g7019334		2.57	6.604
238467_at	CDNA FLI41419 fis, clone BRHIP2002339	BE892293		Hs.127121.0		2.56	8.438
226113_at	ZNF436: zinc finger protein 436	AB051497		80818 Hs.293798.0		2.54	4.81
218297_at	C10orf97: chromosome 10 open reading frame 97	NM_024948		80013 g13376430		2.53	6.486
215933_s_at	HHEX: hematopoietically expressed homeobox	Z21533		3087 Hs.118651.1		2.5	6.864
212741_at	MAOA: monoamine oxidase A	AA923354		4128 Hs.183109.1		2.48	4.758
226756_at	CDNA FLI25556 fis, clone JTH02629	AA191741		Hs.29692.0		2.45	6.199
232636_at	SLITRK4: SLIT and NTRK-like family, member 4	AL080239		139065 Hs.272284.0		2.45	8.746
226725_at	SLFN5: Schlafen family member 5	AI435399		162394 Hs.14691.0		2.39	6.171
207826_s_at	ID3: inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_002167		3399 g10835060		2.38	10.636
212830_at	MEGF9: multiple EGF-like-domains 9	W68084		1955 Hs.5599.0		2.29	8.605
225855_at	EPB41L5: erythrocyte membrane protein band 4.1 like 5	AB046768		57669 Hs.6728.0		2.26	5.822
236840_at	C12orf56: chromosome 12 open reading frame 56	AI522132		115749 Hs.28700.0		2.25	7.389
209589_s_at	EPHB2: EPH receptor B2	AF025304		2048 g2739055		2.23	5.836
227290_at	CDNA FLI13598 fis, clone PLACE1009921	AU157881		Hs.60257.0		2.23	11.943
203295_s_at	ATP1A2: ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	AW440492		477 Hs.34114.0		2.2	8.022
202998_s_at	LOXL2: lysyl oxidase-like 2	NM_002318		4017 g4505010		2.18	4.852
224565_at	TncRNA: trophoblast-derived noncoding RNA	BE675516		283131 Hs.240443.0		2.16	5.607
212930_at	ATP2B1: ATPase, Ca++ transporting, plasma membrane 1	AW576457		490 Hs.20952.0		2.13	9.492
209530_at	CACNB3: calcium channel, voltage-dependent, beta 3 subunit	U07139		784 g463890		2.1	5.509
202007_at	NID1: nidogen 1	BF940043		4811 Hs.62041.0		2.09	6.877
236016_at	CDNA FLI38419 fis, clone FEBRA2009846	AI702962		Hs.127211.0		2.09	5.794
227911_at	ARHGAP28: Rho GTPase activating protein 28	AI935647		79822 Hs.183114.0		2.06	5.551
1556361_s_at	ANKRD13C: ankyrin repeat domain 13C	BC016937		81573 Hs.2.398143.1		2.06	7.042
205080_at	RARB: retinoic acid receptor, beta	NM_000965		5915 g4506420		2.04	6.041
213785_at	IPO9: importin 9	AW269792		55705 Hs.5010.0		2.02	5.093
222653_at	PNPO: pyridoxamine 5'-phosphate oxidase	AA005137		55163 Hs.267963.0		2.01	5.355
224826_at	RP5-1022P6.2: hypothetical protein KIAA1434	AK001947		56261 Hs.171917.1		2.01	11.6
202008_s_at	NID1: nidogen 1	NM_002508		4811 g4505394		2	5.931
226625_at	Hs.79059.1	AW193698		Hs.79059.1		1.98	6.452
221139_s_at	CSAD: cysteine sulfonic acid decarboxylase	NM_015989		51380 g7705333		1.97	7.809
235904_at	UGT3A1: UDP glucosyltransferase 3 family, polypeptide A1	AL135700		133688 Hs.132501.0		1.96	6.248
208073_x_at	TTC3: tetratricopeptide repeat domain 3	NM_003316		7267 g10835036		1.94	6.283
201539_s_at	FHL1: four and a half LIM domains 1	U29538		2273 g2078479		1.93	4.711
210645_s_at	TTC3: tetratricopeptide repeat domain 3	D83077		7267 g1304131		1.93	6.601
213333_at	MDH2: malate dehydrogenase 2, NAD (mitochondrial)	AL520774		4191 Hs.111076.1		1.93	7.806
204483_at	ENO3: enolase 3 (beta, muscle)	NM_001976		2027 g4503572		1.92	6.226
201473_at	JUNB: jun B proto-oncogene	NM_002229		3726 g4504808		1.88	6.87
201540_at	FHL1: four and a half LIM domains 1	NM_001449		2273 g4503720		1.87	5.129
205862_at	GREB1: GREB1 protein	NM_014668		9687 g7662187		1.87	8.585
219952_s_at	MCOLN1: mucopolin 1	NM_020533		57192 g10092596		1.86	6.729
222749_at	SUFU: suppressor of fused homolog (Drosophila)	AF159447		51684 g6689893		1.86	5.39
227120_at	FOXP4: forkhead box P4	AI673539		116113 Hs.199316.0		1.84	5.364
232202_at	CDNA: FLI21274 fis, clone COL01781	AK024927		Hs.152423.0		1.84	7.379
235940_at	C9orf64: chromosome 9 open reading frame 64	AW983691		84267 Hs.145809.0		1.84	5.978
215594_at	PTR2 mRNA for repetitive sequence	AU148611		Hs.296832.0		1.83	7.515
227860_at	CPXM1: carboxypeptidase X (M14 family), member 1	NM_019609		56265 Hs.177536.0		1.82	8.79

218208_at	PQLC1: PQ loop repeat containing 1	NM_025078	80148 g13376629	1.8	5.394	0.005714
224593_at	ZNF664: zinc finger protein 664	BE965646	144348 Hs.61976.0	1.8	5.557	0.009259
205347_s_at	TMSL8: thymosin-like 8	NM_021992	11013 g11496272	1.77	6.235	0.003572
210512_s_at	VEGFA: vascular endothelial growth factor A	AF022375	7422 g3719220	1.77	4.947	0.007883
201727_s_at	ELAVL1: ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	NM_001419	1994 g4503550	1.76	5.822	0.004335
226868_at	GLT8D3: glycosyltransferase 8 domain containing 3	BF977231	283464 Hs.173044.0	1.75	7.52	0.002678
201200_at	CREG1: cellular repressor of E1A-stimulated genes 1	NM_003851	8804 g4503036	1.74	6.086	0.004667
201650_at	KRT19: keratin 19	NM_002276	3880 g4504916	1.74	6.95	0.003423
202815_s_at	HEXIM1: hexamethylene bis-acetamide inducible 1	NM_006460	10614 g5453681	1.74	8.447	0.001632
207551_s_at	MSL3L1: male-specific lethal 3-like 1 (Drosophila)	NM_006800	10943 g5803103	1.74	5.316	0.006178
212195_at	IL6ST: Interleukin 6 signal transducer (gp130, oncostatin M receptor)	AL049265	3572 Hs.71968.0	1.73	6.903	0.002358
226786_at	RFX1: regulatory factor X, 1 (influences HLA class II expression)	BF507952	5989 Hs.73677.0	1.73	9.595	0.001692
213135_at	TIAM1: T-cell lymphoma invasion and metastasis 1	U90902	7074 Hs.82141.0	1.72	6.625	0.00273
202083_s_at	SEC14L1: SEC14-like 1 (S. cerevisiae)	AI017770	6397 Hs.75232.0	1.71	5.312	0.007319
202743_at	PIK3R3: phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	BE622627	8503 Hs.88051.0	1.71	6.49	0.003045
41387_r_at	JMJD3: jumonji domain containing 3	AB002344	23135 4861272_RC	1.7	5.309	0.006103
204944_at	PTPRG: protein tyrosine phosphatase, receptor type, G	NM_002841	5793 g11386168	1.69	4.802	0.009016
213146_at	JMJD3: jumonji domain containing 3	AA521267	23135 Hs.103915.0	1.69	6.114	0.004094
202931_x_at	BIN1: bridging integrator 1	NM_004305	274 g4757747	1.68	5.437	0.005553
225543_at	GTF3C4: general transcription factor IIIC, polypeptide 4, 90kDa	BF434224	9329 Hs.21734.0	1.68	5.626	0.001663
225864_at	FAM84B: family with sequence similarity 84, member B	AL039862	157638 Hs.49136.0	1.68	12.45	0.000254
235520_at	SUHW3: suppressor of hairy wing homolog 3 (Drosophila)	AA805654	55609 Hs.121668.0	1.68	11.296	0.000933
212980_at	USP34: ubiquitin specific peptidase 34	AL050376	9736 Hs.322645.0	1.66	4.865	0.009106
226713_at	CCDC50: coiled-coil domain containing 50	AI247881	152137 Hs.10198.0	1.66	5.692	0.005566
211107_s_at	AURKC: aurora kinase C	AB017332	6795 g4521232	1.64	5.219	0.00644
202447_at	DECR1: 2,4-dienoyl CoA reductase 1, mitochondrial	NM_001359	1666 g4503300	1.63	6.51	0.005614
226715_at	FOXK1: forkhead box K1	AW007319	221937 Hs.11556.0	1.63	7.096	0.005404
227559_at	Hs.5232.1	ALS21129	Hs.5232.1	1.63	5.121	0.009701
223043_at	TMEM85: transmembrane protein 85	AF151018	51234 g7106757	1.62	9.041	0.00083
200720_s_at	ACTR1A: ARP1 actin-related protein 1 homolog A, contractin alpha (yeast)	ALS32341	10121 Hs.153961.0	1.61	6.856	0.002893
218913_s_at	GMP1: GEM interacting protein	NM_016573	51291 g7706106	1.61	5.549	0.007898
224374_s_at	EMILIN2: elastin microfibril interfacer 2	AF270513	84034 g13661555	1.61	6.103	0.00419
225617_at	ODF2: outer dense fiber of sperm tails 2	AL138382	4957 Hs.129055.2	1.61	6.197	0.003449
41386_i_at	JMJD3: jumonji domain containing 3	AB002344	23135 4861272_RC	1.6	7.018	0.002316
208112_x_at	EHD1: EH-domain containing 1	NM_006795	10938 g5803008	1.59	6.513	0.002872
211980_at	COL4A1: collagen, type IV, alpha 1	AI922605	1282 Hs.119129.0	1.59	5.587	0.005114
223547_at	C14orf100: chromosome 14 open reading frame 100	AL038769	15528 Hs.170219.0	1.58	8.087	0.001305
212484_at	FAM89B: family with sequence similarity 89, member B	BF974389	23265 Hs.18686.0	1.57	6.076	0.004273
221954_at	C20orf111: Chromosome 20 open reading frame 111	AA160474	51526 Hs.75798.1	1.57	8.226	0.005339
1568629_s_at	PIK3R2: phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	BC033311	5296 Hs2.390523.1	1.57	6.565	0.003144
205823_at	RGS12: regulator of G-protein signaling 12	AI824113	6002 Hs.78281.0	1.56	6.326	0.005412
238041_at	Transcribed locus	AA151712	Hs.82572.1	1.56	6.035	0.007326
203329_at	PTPRM: protein tyrosine phosphatase, receptor type, M	NM_002845	5797 g4506318	1.55	6.983	0.002561
203943_at	KIF3B: kinesin family member 3B	NM_004798	9371 g4758645	1.54	5.075	0.007109
209039_x_at	EHD1: EH-domain containing 1	AF001434	10938 g2529706	1.54	6.304	0.003255
218853_s_at	MOSPD1: motile sperm domain containing 1	NM_019556	56180 g9506542	1.54	5.186	0.00701
224996_at	CDNA FLJ39064 fis, clone NT2RP7014583	N30209	Hs.332422.0	1.54	5.407	0.0059
205406_s_at	SPA17: sperm autoantigenic protein 17	NM_017425	53340 g8394342	1.53	5.112	0.006931
222221_x_at	EHD1: EH-domain containing 1	AY007161	10938 Hs.155119.2	1.53	7.118	0.002215
205002_at	AHDC1: AT hook, DNA binding motif, containing 1	NM_015699	27245 g7661559	1.52	5.419	0.007801
218699_at	RAB7L1: RAB7, member RAS oncogene family-like 1	BG338251	8934 Hs.115325.0	1.52	5.718	0.005165
226077_at	RNF145: ring finger protein 145	AL539442	153830 Hs.104893.0	1.52	12.745	0.000303
212905_at	CSTF2T: cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	AI872408	23283 Hs.21992.1	1.5	5.179	0.008063
227373_at	ATXN1L: ataxin 1-like	AW299653	342371 Hs.20787.0	1.5	5.923	0.004382
227656_at	C6orf70: chromosome 6 open reading frame 70	AW968493	55780 Hs.47546.0	1.5	5.761	0.004509
202005_at	ST14: suppression of tumorigenicity 14 (colon carcinoma)	NM_021978	6768 g11415039	-1.58	-5.331	0.007794
220615_s_at	MLSTD1: male sterility domain containing 1	NM_018099	55711 g8922433	-1.63	-6.496	0.003841
209615_s_at	PAK1: p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	U51120	5058 g1256421	-1.67	-14.176	0.000237
213010_at	PRKCDBP: protein kinase C, delta binding protein	AI088622	112464 Hs.85181.1	-1.7	-5.468	0.007638
219073_s_at	OSBPL10: oxysterol binding protein-like 10	NM_017784	114884 g8923336	-1.71	-5.375	0.006349
205229_s_at	COCH: coagulation factor C homolog, cochlin (Limulus polyphemus)	AA669336	1690 Hs.21016.0	-1.77	-8.122	0.001592
201058_s_at	MYL9: myosin, light chain 9, regulatory	NM_006097	10398 g5174602	-1.83	-6.453	0.00347
210999_s_at	GRB10: growth factor receptor-bound protein 10	U66065	2887 g1518100	-1.83	-10.351	0.00074
226370_at	KLHL15: kelch-like 15 (Drosophila)	BG149487	80311 Hs.61603.0	-1.89	-6.302	0.004331
226913_s_at	SOX8: SRY (sex determining region Y)-box 8	BF527050	30812 Hs.243678.0	-1.98	-5.549	0.005264
216905_s_at	ST14: suppression of tumorigenicity 14 (colon carcinoma)	U20428	6768 Hs.56937.1	-2	-7.114	0.005012
1554242_a_at	COCH: coagulation factor C homolog, cochlin (Limulus polyphemus)	BC007230	1690 Hs2.21016.2	-2.02	-7.047	0.002937
232553_at	PCYT1B: phosphate cytidylyltransferase 1, choline, beta	AI857508	9468 Hs.212482.0	-2.08	-4.915	0.008033
219032_x_at	OPN3: opsin 3 (encephalopsin, panopsin)	NM_014322	23596 g7657070	-2.1	-7.58	0.00307
235649_at	ADAMTS8: ADAM metalloproteinase with thrombospondin type 1 motif, 8	AW207389	11095 Hs.126758.0	-2.25	-7.094	0.002162
227846_at	GPR176: G protein-coupled receptor 176	AA526584	11245 Hs.55144.0	-2.38	-8.879	0.003939
226863_at	FAM110C: family with sequence similarity 110, member C	AI674565	642273 Hs.8379.0	-2.42	-9.89	0.00063
206673_at	GPR176: G protein-coupled receptor 176	NM_007223	11245 g6005771	-2.43	-6.91	0.002324
1554887_at	Hs2.375106.1	BC032716	Hs2.375106.1	-2.66	-8.714	0.001211
209496_at	RARRES2: retinoic acid receptor responder (tazarotene induced) 2	BC000069	5919 g12652642	-2.85	-9.965	0.001791
202771_at	FAM38A: family with sequence similarity 38, member A	NM_014745	9780 g7662013	-2.91	-9.669	0.001187
222033_s_at	FLT1: Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular perr	AA058828	2321 Hs.138671.2	-2.94	-11.662	0.000765
216915_s_at	PTPN12: protein tyrosine phosphatase, non-receptor type 12	SP69182	5782 Hs.62.1	-5.43	-6.742	0.005342

170 genes satisfied the comparison filtering criteria