Table A

Cell line	Passage (Δ)	Splitting	Doublings
human			
SAOS	38	1:20	164
LM5	36	1:20	156
HOS	41	1:200	314
143B	36	1:200	275
mouse			
Dunn	61	1:200	467
LM8	67	1:200	512

Table B

	Human		**Mouse**	
Chr.	**n**	**p(%)**	**n**	**p(%)**
1	2163	10.1	1331	5.8
2	1360	6.4	1891	8.2
3	1164	5.5	1101	4.8
4	819	3.8	1318	5.7
5	926	4.3	1340	5.8
6	1103	5.2	1247	5.4
7	1025	4.8	2004	8.7
8	774	3.6	1153	5
9	854	4	1339	4.9
10	837	3.9	1086	4.6
11	1353	6.3	1702	7.4
12	1093	5.1	771	3.3
13	382	1.8	916	4
14	668	3.1	868	3.8
15	669	3.1	878	3.8
16	883	4.1	746	3.3
17	1233	5.8	1118	4.8
18	321	1.5	571	2.5
19	1445	6.8	777	3.4
20	607	2.8	n.p.	n.p.
21	280	1.3	n.p.	n.p.
22	504	2.4	n.p.	n.p.
X	804	3.8	891	3.9
Y	72	0.3	26	0.1
Sum	**21339**		**23074**	
Average		**4.2**		**4.7**

Table C

Cyclin D1 (CCND1)
Forward primer: 5´- CCGTCCATGCGGAAGATC -3´
Reverse primer: 5´- ATGGCCAGCGGGAAGAC -3´

Integrin α_4 (ITGA4)
Forward primer: 5´- TTCGGAGCCAGCATACTACC -3´
Reverse primer: 5´- GCAGAATCAGACCGAAAAGC -3´

Parvin gamma (PARVG)
Forward primer: 5´- CTACCTCACTCCCAACTCTCCT -3´
Reverse primer: 5´- CTCAGTGTGCTCTTGGCATCCT -3´

Myosin regulatory light chain 10 (MYL10)
Forward primer: 5´- GGATTACAGGCACCGAGAAGAG -3´
Reverse primer: 5´- TGAGCCGAGATCATGCCATTGC -3´

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
Forward primer: 5´-AGGGCTGCTTTTAACTCTGGT-3′
Reverse primer: 5′-CCCCACTTGATTTTGGAGGGA-3′

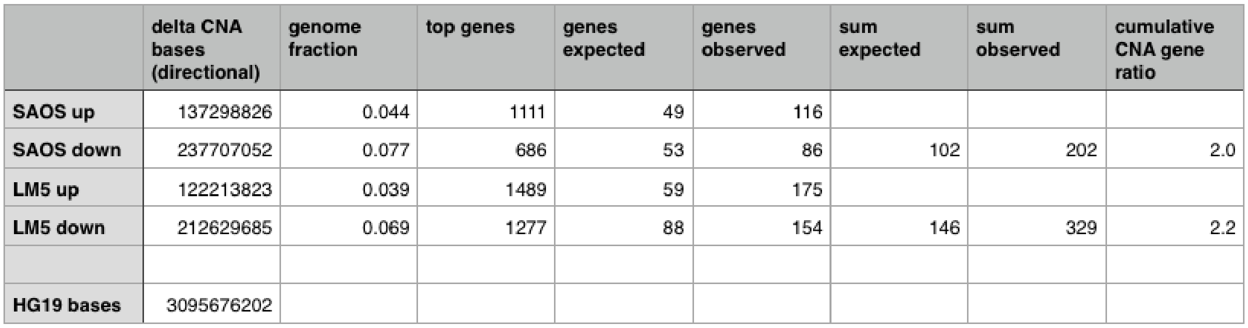
Table D

Serial *in vitro* passaging		
(up/down/total)	**n (up/down)**	**Affected chromosomes (up + down)**
SAOS (810/487/1297)	4 (2/2)	**1 (145)**; 5 (53); 6 (68); **12 (83)**
LM5 (1035/912/1947)	7 (3/4)	**4 (121)**; 9 (101); 10 (113); **12 (160)**; 14 (66); 18 (33); **21 (46)**
HOS (705/400/1105)	2 (0/2)	17 (49); 19 (79)
143B (338/92/430)	0	
Dunn (313/313/626)	3 (2/1)	9 (36); **14 (28); 18 (23)**
LM8 (327/338/665)	1 (1/0)	**X (58)**
Metastatic comparison		
LM5/SAOS (1283/1295/2578)	12 (6/6)	**1 (313); 2 (181); 4 (130); 5 (142); 6 (130); 7 (125)**; 8 (121); 10 (95); 16 (83); 19 (150); 21 (36); X (119)
143B/HOS (1833/1967/3800)	9 (5/4)	**1 (419); 3 (205)**; 6 (197); **10 (152)**; 13 (65); 15 (116); 17 (216); **18 (81); 20 (120)**
LM8/Dunn (1363/660/2029)	6 (4/2)	**4 (147)**; 6 (141); 9 (128); **12 (107); 16 (89); 18 (84)**

Table E

	SAOS					LM5		
	early	**late**	**late/early**			**early**	**late**	**late/early**
1q23.2-q42.13	normal	gain	gain					
					2p25.2-p25.1	normal	gain	gain
2q11.2	gain	normal	loss					
2q13	normal	loss	loss					
					2q37.3	gain	normal	loss
3q28-q29	gain	normal	loss		3q28	gain	normal	loss
					4p16.3-p16.1	normal	gain	gain
4q13.1-q13.3	gain	normal	loss					
					5p15.33	normal	gain	gain
					5p14.3	normal	gain	gain
					5p14.1	normal	gain	gain
6p21.32-p21.1	gain	normal	loss					
					7p21.1-p11.1	gain	normal	loss
7q36.1-q36.3	gain	normal	loss					
9p12-p11.1	normal	gain	gain					
9q21.13	gain	normal	loss		9q21.13	gain	normal	loss
9q21.33-q32	gain	normal	loss		9q21.31-q31.3	gain	normal	loss
					9q34.2-q34.3	gain	normal	loss
					10p	normal	loss	loss
12p13.33	loss	normal	gain		12p13.33	loss	normal	gain
12p13.32-p11.1	normal	gain	gain		12p13.32-p11.1	normal	gain	gain
14q22.3-q32.33	gain	normal	loss		14q22.3-q32.2	gain	normal	loss
18q23	normal	loss	loss					
19q13.11-q13.12	normal	gain	gain					
					21q	normal	gain	gain
Xp22.33-p21.2	gain	normal	loss		Xp22.33-p22.31	normal	gain	gain
Xq11.2-q27.1	gain	normal	loss					

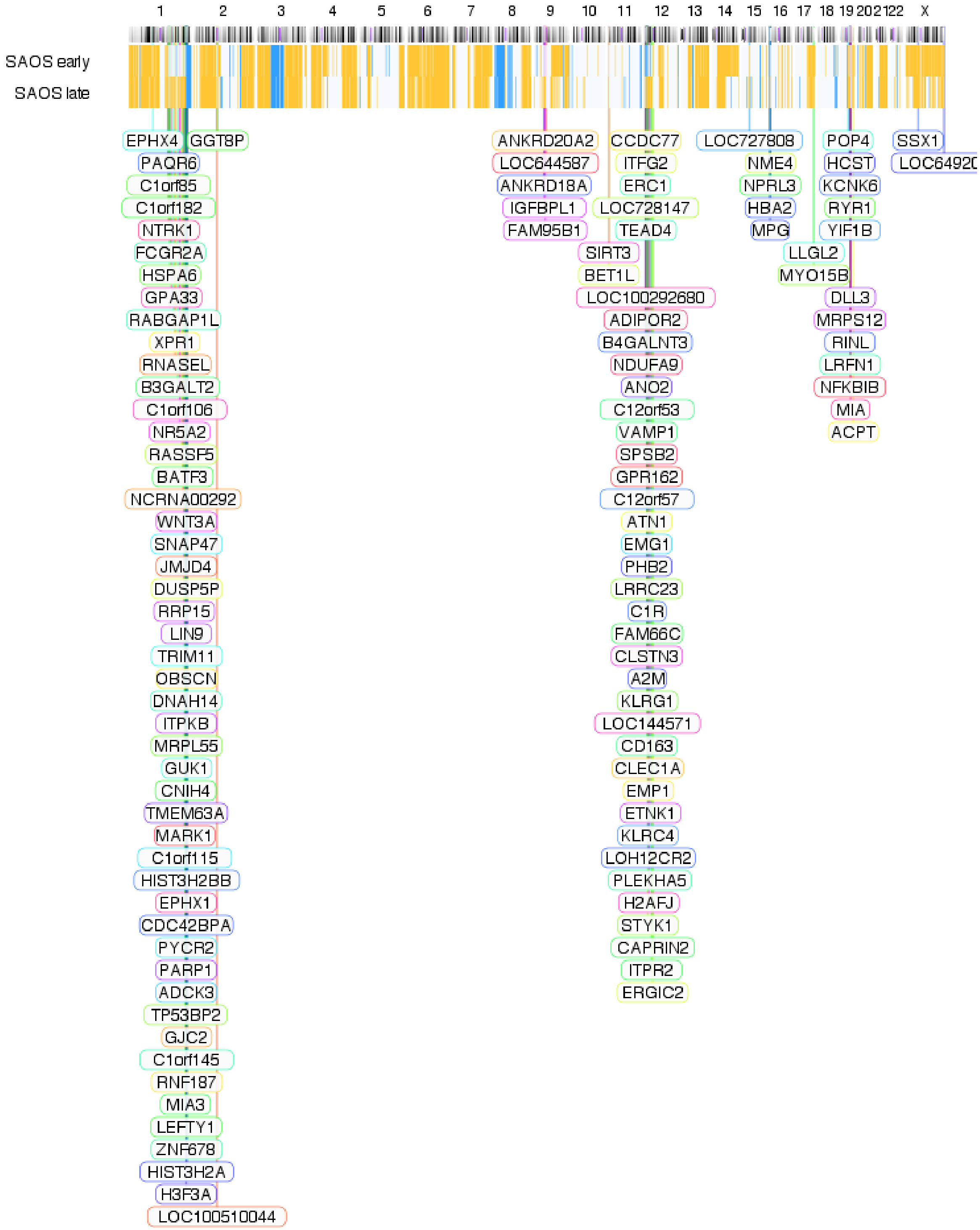
Table F



	delta CNA bases (directional)	genome fraction	top genes	genes expected	genes observed	sum expected	sum observed	cumulative CNA gene ratio
SAOS up	137298826	0.044	1111	49	116			
SAOS down	237707052	0.077	686	53	86	102	202	2.0
LM5 up	122213823	0.039	1489	59	175			
LM5 down	212629685	0.069	1277	88	154	146	329	2.2
HG19 bases	3095676202							

Figure 1

A)



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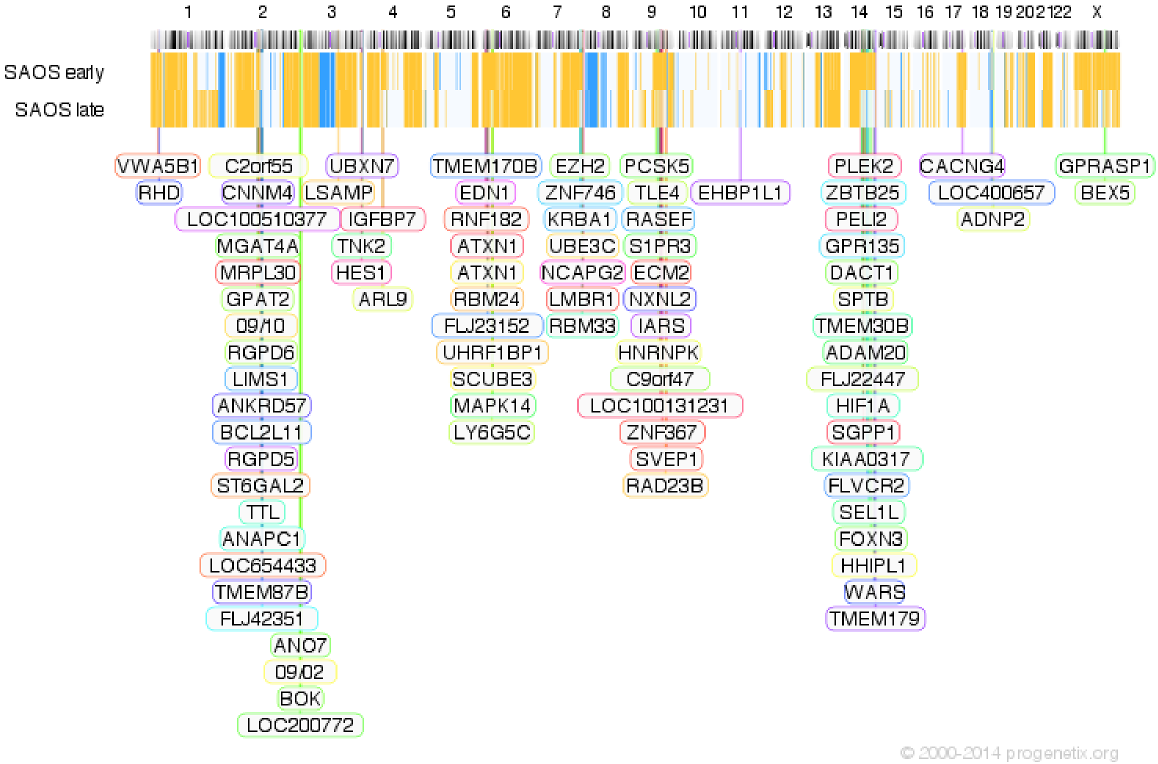
B)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EZH2
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KRBA1
UBE3C
NCAPG2
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FOXN3
HHIPL1
WARS
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CACNG4
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ADNP2
GPRASP1
BEX5
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C)

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LM5 late
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LMO3
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KLRAP1
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EMP1
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STK38L
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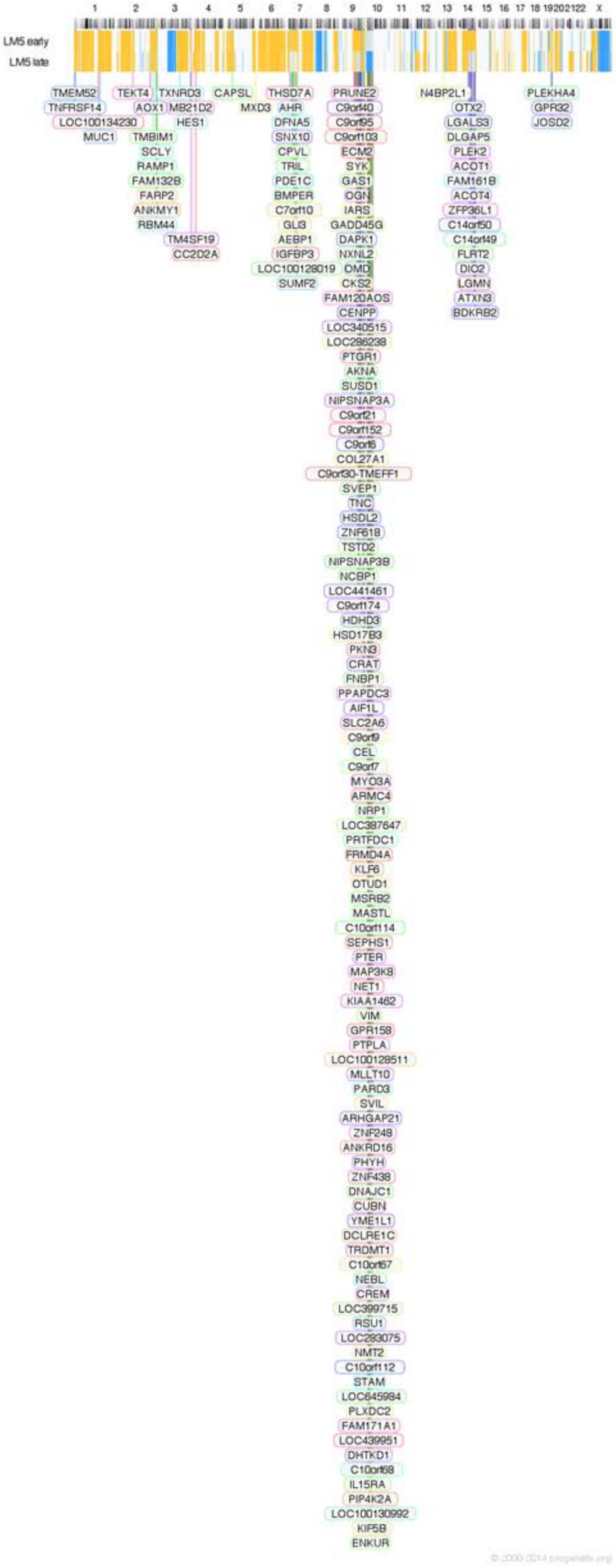
D)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LGMN
ATXN3
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PLEKHA4
GPR32
JOSD2
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Table G

	SAOS	LM5	LM5/SAOS
1q23.1-q23.2	normal	gain	gain
1q31.1-q31.3	normal	gain	gain
1q42.2-q44	loss	normal	gain
2q32.2-q33.1	gain	normal	loss
3p26.3-p14.3	gain	normal	loss
4q32.1-q34.3	gain	normal	loss
5p15.32-p13.3	normal	gain	gain
8q23.2-q23.3	gain	normal	loss
8q24.23-q24.3	gain	normal	loss
15q23-q24.1	normal	gain	gain
18p11.32	normal	loss	loss
18p11.31	normal	gain	gain
20p13-p12.3	normal	gain	gain
20p12.1	normal	gain	gain
20q13.12	gain	loss	loss
20q13.13-q13.33	gain	normal	loss
Xq	normal/gain	loss/normal	loss

Figure 2

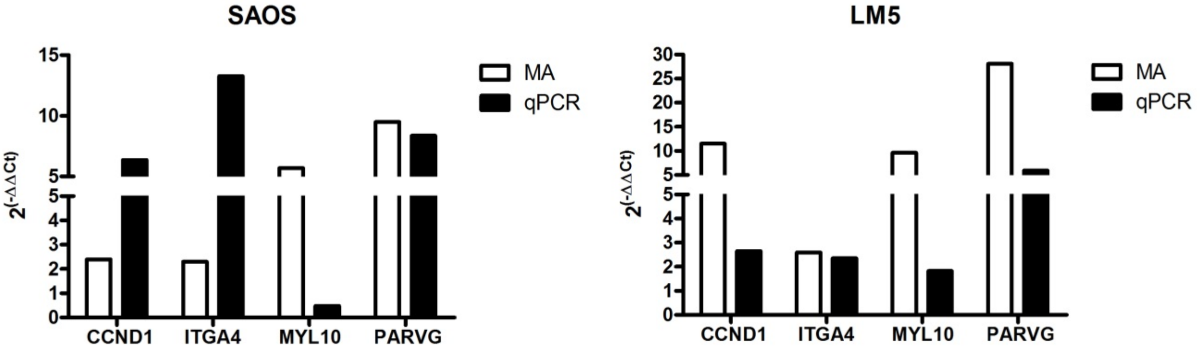

SAOS
LM5
$2^{(-\Delta\Delta Ct)}$
15
10
5
4
3
2
1
0
30
25
20
CCND1
ITGA4
MYL10
PARVG
□ MA
■ qPCR

Table H

			LM5/SAOS				
			L/L	L/E	E/L	E/E	Mean
Gene	**KEGG**	**Up-regulated in LM5**					
WNT1	7471	wingless-type MMTV integration site family, member 1	7	11.3	10.9	17.5	11.7
FIGF	2277	c-fos induced growth factor (vascular endothelial growth factor D)	4.9	8.9	7.8	14.1	8.9
PTCH1	5727	patched 1	9.5	11.5	5.3	3.8	7.5
RASSF5	83593	Ras association (RalGDS/AF-6) domain family member 5	6.4	14.3	2.2	4.9	7.0
FGF5	2250	fibroblast growth factor 5	5.5	3.7	6.9	4.8	5.2
FOXO1	2308	forkhead box O1	3	3.2	2.3	2.5	2.8
FH	2271	fumarate hydratase	2.2	2.6	2.3	2.7	2.5
		Down-regulated in LM5					
TCF7L1	83439	transcription factor 7-like 1 (T-cell specific, HMG-box)	100	100	100	100	100.0
PLCG2	5336	phospholipase C, gamma 2 (phosphatidylinositol-specific)	33.3	6.3	33.3	5.3	19.6
PPARG	5468	peroxisome proliferator-activated receptor gamma	11.1	14.3	16.7	20	15.5
FGF1	2246	fibroblast growth factor 1 (acidic)	2.1	4	20	33.3	14.9
KIT	3815	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	4.3	8.3	2.8	4.3	4.9
FZD8	8325	frizzled family receptor 8	4	5.6	3	4.2	4.2
STK4	6789	serine/threonine kinase 4	2.8	3.4	2.6	3.2	3.0

			LM8/Dunn				
			L/L	L/E	E/L	E/E	Mean
		Up-regulated in LM8					
EGFR	13649	epidermal growth factor receptor	25.9	19	75	57	44.2
DAPK2	13143	death-associated protein kinase 2	26.4	7.1	24	6.8	16.1
MMP2	17390	matrix metallopeptidase 2	10	7.2	13.5	10	10.2
WNT8B	22423	wingless related MMTV integration site 8b	14.1	8.1	12.1	5.9	10.1
BIRC3	11796	baculoviral IAP repeat-containing 3	6.7	10.3	7.3	10.5	8.7
PTCH2	19207	patched homolog 2	3.5	15.3	2.1	8.3	7.3
WNT1	22408	wingless-related MMTV integration site 1	8.5	6.1	7.7	5.5	7
MAPK1	26413	mitogen-activated protein kinase 1	2.3	7	2.4	7.3	4.8
CSF1R	12978	colony stimulating factor 1 receptor	5.1	5	4.4	3.9	4.6
GLI2	14633	GLI-Kruppel family member GLI2	3.8	4.4	4.3	4.8	4.3
PIAS1	56469	protein inhibitor of activated STAT 1	3.8	5	2.2	2.9	3.5
SUFU	24069	suppressor of fused homolog (Drosophila)	2.4	4.3	2.3	4.2	3.3
TRAF3	22031	TNF receptor-associated factor 3	3.1	3.5	2.6	3	3.1
FZD7	14369	frizzled homolog 7 (Drosophila)	3.2	3.2	2.5	2.1	2.8
		Down-regulated in LM8					
PDGFB	18591	platelet derived growth factor, B polypeptide	100	100	50	100	87.5
LAMA1	16772	laminin, alpha 1	111	50	9.1	5	43.8
VEGFC	22341	vascular endothelial growth factor C	33.3	100	5.3	10	37.2
PPARG	19016	peroxisome proliferator activated receptor gamma	50	10	50	10	30
LEF1	16842	lymphoid enhancer binding factor 1	10	33.3	50	20	28.3
KITL	17311	kit ligand	9.1	16.7	6.3	11.1	10.8
PLCG2	234779	phospholipase C, gamma 2	12.5	7.7	8.3	4.8	8.3
CSF2RA	12982	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-	5	10	7.7	10	8.2
ITGA3	16400	integrin alpha 3	6.3	6.3	4.3	4.3	5.3
PRKCC	18752	protein kinase C, gamma	6.7	2.4	6.3	2.2	4.4
NFKB1	18033	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1, p	4	3.8	2.7	2.6	3.3
STAT3	20848	signal transducer and activator of transcription 3	2.8	3.1	3.2	2.9	3
MITF	17342	microphthalmia-associated transcription factor	2.6	3.3	2.2	2.9	2.8
LAMA4	16775	laminin, alpha 4	2.9	3.2	2.1	2.4	2.7
MYC	17869	myelocytomatosis oncogene	2.5	2.8	2.1	2.2	2.4

			143B/HOS				
			L/L	L/E	E/L	E/E	Mean
		Up-regulated in 143B					
MMP1	4312	matrix metallopeptidase 1 (interstitial collagenase)	1087	649	716	433	721.3
RAC2	5880	rho family, small GTP binding protein Rac2	105	58.7	98.5	54.5	79.2
HHIP	64399	hedgehog interacting protein	19.9	31.4	34.7	57.2	35.8
FGF5	2250	fibroblast growth factor 5	42.9	17.9	50.9	22.1	33.5
WNT7A	7476	wingless-type MMTV integration site family, member 7A	18.5	16.6	17.4	15.7	17.1
BMP2	650	bone morphogenetic protein 2	4.3	33	3.3	26.5	16.8
COL4A6	1288	collagen, type IV, alpha 6	17.2	19	10.1	11	14.3
IL8	3576	interleukin 8	17.9	14.7	6	5.1	10.9
LAMB3	3914	laminin, beta 3	12.1	8.4	10.7	7.3	9.6
LEF1	51176	lymphoid enhancer-binding factor 1	2.2	16.7	2.2	17.1	9.6
FZD8	8325	frizzled family receptor 8	9.8	8.5	8.5	7.3	8.5
WNT7B	7477	wingless-type MMTV integration site family, member 7B	2.7	15.4	2.3	12.6	8.3
ITGA2	3673	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	10.5	10	5.4	5.5	7.9
PTGS2	5743	prostaglandin-endoperoxide synthase 2	7.6	7.7	4.9	5	6.3
FOS	2353	FBJ murine osteosarcoma viral oncogene homolog	6.4	6.9	4	4.2	5.4
FGF7	2252	fibroblast growth factor 7	3.7	7	3.4	6.7	5.2
TGFBR2	7048	transforming growth factor, beta receptor II (70/80kDa)	6.3	6.6	3.8	2.9	4.9
JUN	3725	jun proto-oncogene	4.5	4.6	4.1	4.2	4.4
BCL2	596	B-cell CLL/lymphoma 2	3	3.8	3.2	4.2	3.6
PIK3CG	5294	phosphoinositide-3-kinase, catalytic, gamma polypeptide	2.5	4.4	2.3	4	3.3
TCF7	6932	transcription factor 7 (T-cell specific, HMG-box)	2.2	4.3	2.4	3.1	3.0
NRAS	4893	neuroblastoma RAS viral (v-ras) oncogene homolog	2.3	2.1	3.6	3.1	2.8
WNT2B	7482	wingless-type MMTV integration site family, member 2B	2.9	2.9	2.4	2.4	2.7
CCNE2	9134	cyclin E2	2.3	2.4	2.6	2.7	2.5
MMP9	4318	matrix metallopeptidase 9	2.6	2.9	2.2	2.4	2.5
DVL1	1855	dishevelled, dsh homolog 1 (Drosophila)	2.2	2.5	2.1	2.1	2.2
		Down-regulated in 143B					
PDGFRB	5159	platelet-derived growth factor receptor, beta polypeptide	333	333	333	250	312
EGF	1950	epidermal growth factor	50	50	20	25	36
NOS2	4843	nitric oxide synthase 2, inducible	33.3	20	33.3	25	27.9
GLI1	2735	GLI family zinc finger 1	25	3.3	50	5.6	21
RUNX1T1	862	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	25	12.5	25	12.5	19
FN1	2335	fibronectin 1	7.7	8.3	10	11.1	9.3
STAT5A	6776	signal transducer and activator of transcription 5A	8.3	11.1	6.7	9.1	8.8
JUP	3728	junction plakoglobin	11.1	6.7	10	5.9	8.4
FLT3	2322	fms-related tyrosine kinase 3	11.1	6.3	7.1	4.2	7.2
LAMC3	10319	laminin, gamma 3	7.7	7.7	5.9	5.6	6.7
FOXO1	2308	forkhead box O1	4.2	7.1	4	6.7	5.5
FGF18	8817	fibroblast growth factor 18	8.3	3.7	6.7	3	5.4
TGFB2	7042	transforming growth factor, beta 2	5.6	6.7	4.2	5	5.3
FGF1	2246	fibroblast growth factor 1 (acidic)	5	7.1	2.9	4	5
ARAF	369	v-raf murine sarcoma 3611 viral oncogene homolog	5	5.9	3.7	4.3	5
COL4A1	1282	collagen, type IV, alpha 1	4.2	5.9	4	5.6	4.9
TRAF5	7188	TNF receptor-associated factor 5	3.7	4.3	4.8	5.6	4.6
PDGFB	5155	platelet-derived growth factor beta polypeptide	3.6	6.3	2.9	5	4.4
BMP4	652	bone morphogenetic protein 4	2.9	6.7	2.3	5.3	4.3
COL4A4	1286	collagen, type IV, alpha 4	3.6	2.5	6.7	4.3	4.3
PTCH1	5727	patched 1	4.2	4.3	4	4.2	4.2
FZD2	2535	frizzled family receptor 2	4.2	4	3.2	3	3.6
LAMA5	3911	laminin, alpha 5	3.2	2.4	4.5	3.6	3.4
TCF7L1	83439	transcription factor 7-like 1 (T-cell specific, HMG-box)	2.9	3.1	3.3	3.6	3.2
WNT3	7473	wingless-type MMTV integration site family, member 3	3.6	2.4	3.8	2.6	3.1
IKBKB	3551	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	3	2.5	2.7	2.3	3
ITGAV	3685	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	2.4	2.3	3.2	3.1	2.8
ARNT	405	aryl hydrocarbon receptor nuclear translocator	2.4	3.3	2.1	3	2.7
COL4A2	1284	collagen, type IV, alpha 2	2.6	2.8	2.7	2.9	2.7
ERBB2	2064	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2	2.5	2.2	3.1	2.8	2.7
CTNNA1	1495	catenin (cadherin-associated protein), alpha 1, 102kDa	2.6	2.6	2.3	2.4	2.5
LAMC1	3915	laminin, gamma 1 (formerly LAMB2)	2.2	2.6	2.3	2.7	2.4

Table I

SAOS_up	BMP2, BMP7, CCND1, DAAM2, DKK1, HHIP, IHH, NFATC1, WIF1, WNT3A, WNT6, WNT11
SAOS_down	NKD2, MAPK9, SFRP2
LM5_up	BMP6, CAMK2B, CCND1, DAAM2, GLI2, IHH, LRP5, PLCB1, PRKACG, PPP2R1B, SFRP1, WIF1, WNT6
LM5_down	BMP7, FZD7, GAS1, GLI3, LEF1, NFATC1, PRICKLE1, WNT2B
HOS_up	APC2, BMP2, BMP7, CCND2, CXXC4, FZD10, GLI1, LEF1, NFATC4, NKD2, PLCB1, WIF1, WNT3A, WNT4, WNT6, WNT7B, WNT10B, WNT11
HOS_down	
143B_up	APC, CXXC4, ROCK1, ROCK2
143B_down	
Dunn_up	CCND2, LEF1, PRICKLE1, RHOA, SFRP4, WIF1, WNT6, WNT10A
Dunn_down	
LM8_up	BMP7, CER1, MAPK10, SFRP4, TCF7L1, WNT11
LM8_down	DAAM2, FOSL1, FZD8, NFATC4, RAC3

Table J

	L/L	E/L	L/E	E/E	combined
LM5/SAOS					
Up-regulation					
Total	1613	1368	1848	1291	3174
HH	10 (1.8E-2)	6 (2.4E-1)	13 (5.1E-3)	10 (5.7E-3)	14 (6E-2)
WNT	16 (1.3E-1)	10 (5.5E-1)	17 (3.5E-1)	15 (6.9E-2)	23 (5.6E-1)
Down-regulation					
Total	1685	1634	1462	1215	2942
HH	7 (3.4E-1)	5 (6.8E-1)	4 (7.9E-1)	2 (9.7E-1)	8 (7.2E-1)
WNT	17 (2.1E-1	21 (1.9E-2)	15 (2.1E-1)	17 (1.4E-2)	30 (6.3E-2)
LM8/Dunn					
Up-regulation					
Total	2008	1324	3025	2067	4174
HH	8 (2E-1)	8 (3E-2)	13 (4.6E-2)	16 (9.5E-5)	19 (4.6E-3)
WNT	23 (1.2E-2)	15 (4E-2)	28 (5.2E-2)	27 (1.4E-3)	44 (6E-4)
Down-regulation					
Total	1376	944	3223	2021	4060
HH	4 (7.2E-1)	4 (4.4E-1)	7 (8.3E-1)	5 (7.5E-1)	11 (5.2E-1)
WNT	9 (8E-1)	6 (8.1E-1)	20 (8E-1)	8 (9.9E-1)	23 (8.8E-1)
143B/HOS					
Up-regulation					
Total	1725	1888	1863	1821	2914
HH	13 (2.1E-3)	13 (5.2E-3)	11 (2.2E-2)	9 (1.1E-1)	14 (3.1E-2)
WNT	21 (3E-2)	23 (2.6E-2)	24 (6E-3)	25 (2.8E-3	35 (3E-3)
Down-regulation					
Total	1999	2341	1954	2035	3342
HH	10 (1.1E-1)	12 (4.2E-2)	7 (4.6E-1)	8 (3.2E-1)	12 (2.5E-1)
WNT	19 (2.8E-1)	28 (8.2E-3)	14 (7.2E-1)	15 (6.5E-1)	29 (1.8E-1)

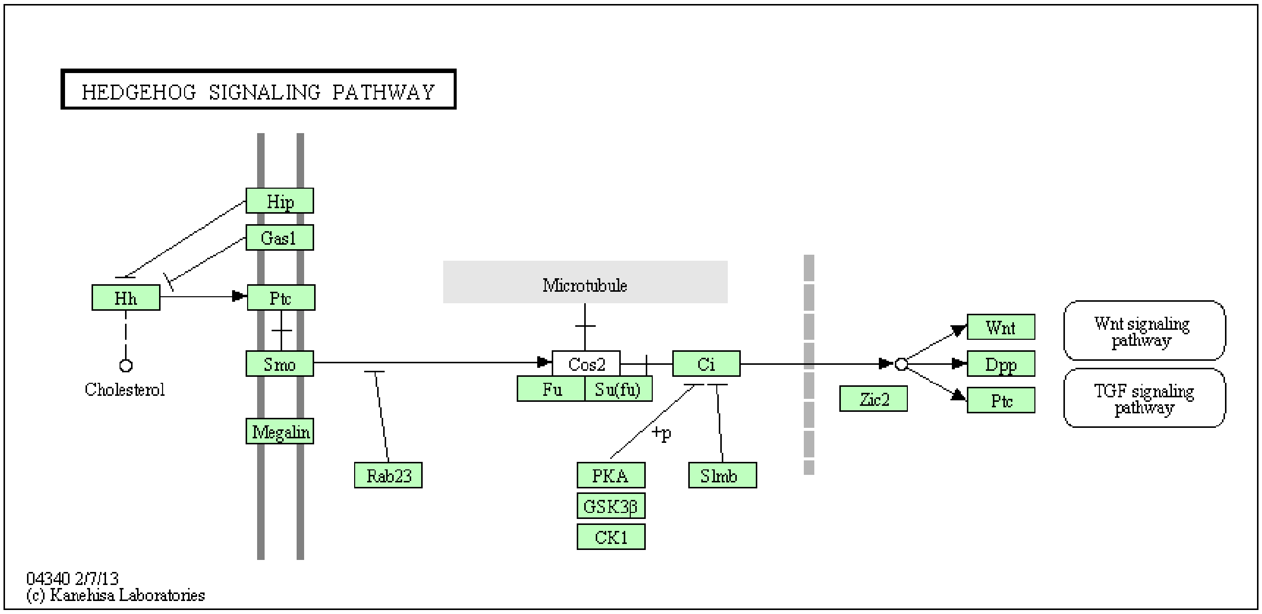
Table K

Up-regulated in LM5						
	L/L	**E/L**	**L/E**	**E/E**	**Mean**	**Comp.**
WIF1	124.2	19.2	468.1	67.1	169.7	4
IHH	21.2	1	58.5	2.8	20.9	3
PLCB1	23.9	4	26.1	4.1	14.5	4
WNT1	7	10.9	11.3	17.5	11.7	4
BMP6	17.4	3.2	15.8	2.8	9.8	4
NKD2	8.5	4.4	13.7	7.1	8.4	4
PTCH1	9.5	5.3	11.5	3.8	7.5	4
WNT6	5.8	1	14	2.4	5.8	3
DAAM2	2.8	0.9	11.7	3.6	4.8	3
NKD1	2.9	2.1	5.7	4.1	3.7	4
HHIP	2	2.5	4.3	5.3	3.5	3
GLI2	3.3	2	5.4	3.2	3.5	3
WNT10B	3.2	1.8	5.3	2.9	3.3	3
FZD7	2.6	5.3	1.4	2.8	3.0	3
WNT11	2.1	1.3	4.3	2.6	2.6	3
WNT5A	4	2.4	2.4	1.4	2.6	3
TCF7	2.2	1.8	2.9	2.4	2.3	3

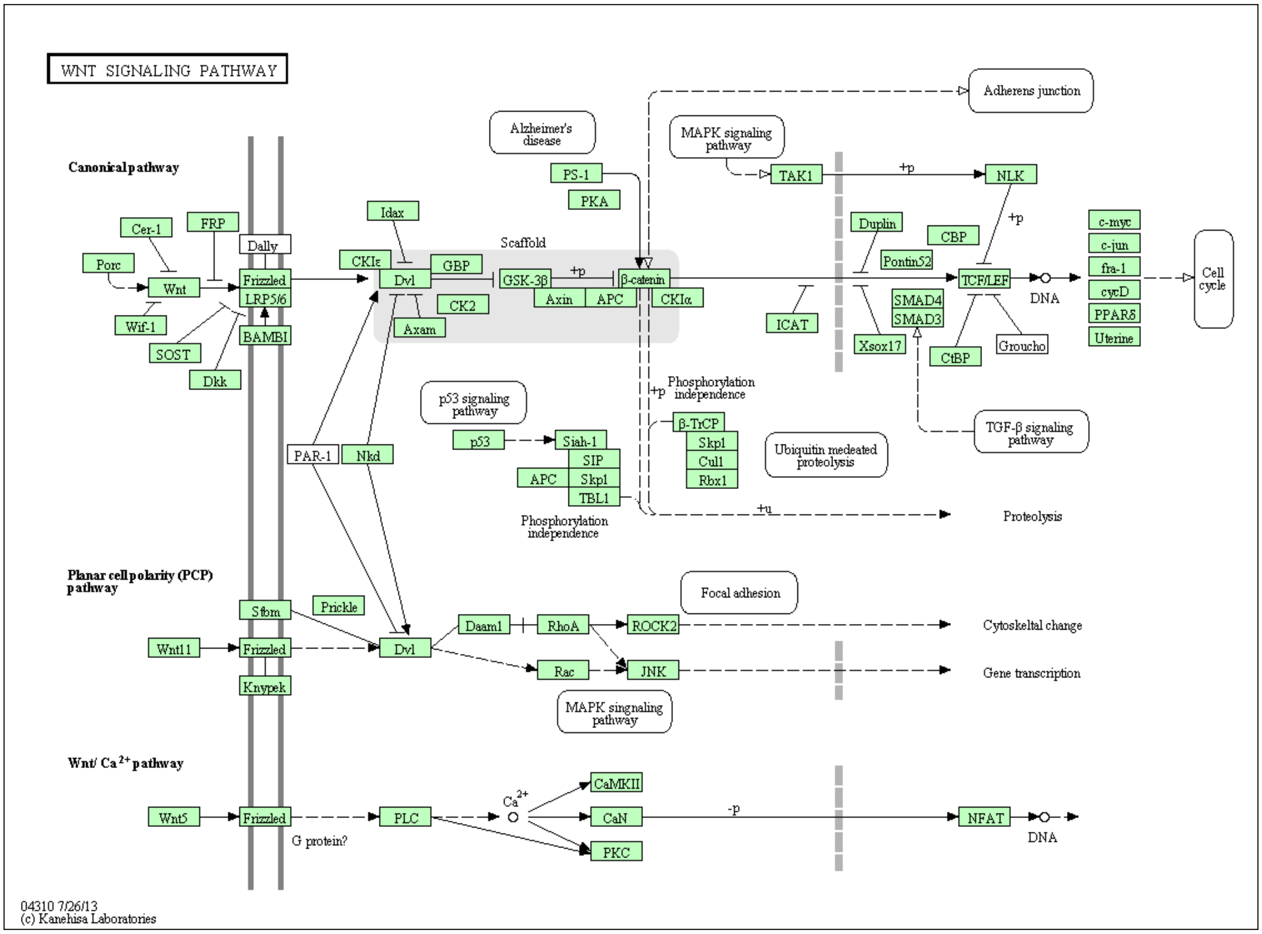
Up-regulated in 143B						
RAC2	105	98	59	55	79.3	4
HHIP	19.9	34.7	31.4	57	35.8	4
WNT7A	18.5	17.4	16.6	15.7	17.1	4
BMP2	4.3	3.3	33	26.5	16.8	4
LEF1	2.2	2.2	16.7	17.1	9.6	4
BMP6	6.8	6.2	13.1	12	9.5	4
BMP7	3.7	4.8	12.1	15	8.9	4
FZD8	9.8	8.5	8.5	7.3	8.5	4
WNT7B	2.7	2.3	15.4	12.6	8.3	4
DKK1	8.2	8.3	5.3	5.2	6.8	4
FOSL1	8	6.8	5.2	4.4	6.1	4
JUN	4.5	4.1	4.6	4.2	4.4	4
IHH	4.5	4.6	3.9	3.9	4.2	4
NKD1	2.7	3	4.2	4.8	3.7	4
TCF7	2.6	2.4	4.3	3.1	3.1	4
WNT10B	2.1	1.9	4.2	4	3.1	3
SOX17	2.1	2.2	3	3.3	2.7	4
WNT2B	2.9	2.4	2.9	2.4	2.7	4
PRKACB	3.1	2.3	3	2	2.6	3
SFRP1	2.6	1.9	3.1	2.2	2.5	3
CTNNBIP1	2.5	3	1.9	2.3	2.4	3
SUFU	2.1	2.1	2.7	2.3	2.3	3
DVL1	2.2	2.1	2.5	2.3	2.3	4
MYC	1.9	2.3	2.1	2.6	2.2	3

Up-regulated in LM8						
VANGL1	67.4	69.9	15.3	13.1	41.4	4
WNT8B	14.1	12.1	8.1	5.9	10.1	4
NFATC4	4.2	14.8	3.3	13.2	8.9	4
PPP2R5C	14.1	6	10	3.6	8.4	4
PTCH2	3.5	2.2	15.3	8.3	7.3	4
IHH	4.9	6.5	7.7	10	7.3	3
NKD2	11.9	12.2	2	2.2	7.1	3
WNT1	8.5	7.7	6.1	5.5	7.0	4
SFRP4	5.4	2.1	14.5	5.6	6.9	4
WNT11	4.5	2	11.8	4.5	5.7	3
GLI2	3.8	4.3	4.4	4.8	4.3	4
APC2	5.4	5.7	1.9	2.1	3.8	3
SUFU	2.4	2.3	4.3	4.2	3.3	4
DVL2	3.4	2.5	3.6	2.7	3.1	3
FZD7	3.2	2.5	3.2	2.1	2.8	4
WNT10B	2.7	2.2	2.8	2.3	2.5	3
TCF7	2.4	2.6	2	2.1	2.3	3

Figure 3



For gene list see: http://www.genome.jp/dbget-bin/www_bget?pathway+hsa04340



For gene list see: http://www.genome.jp/dbget-bin/www_bget?pathway+hsa04310