

ORIGINAL ARTICLE

DNA Microarray Analyses of Gene Expression in Human Mesenchymal Stem Cells Cultured in Osteogenic Differentiation Medium for 14 days

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SYNOPSIS

Mesenchymal stem cells are important for tissue engineering therapy because they can be seeded in scaffold materials, proliferated and differentiated into osteoblasts. The purpose of this study was to evaluate gene expressions of human mesenchymal stem cells cultured for 14 days in osteogenic differentiation medium that contained ascorbic acid, β -glycerol phosphate and dexamethasone, using 2.9k DNA microarray. It became evident that 198 genes were more than 10-fold up-regulated, but 395 genes were less than 0.1-fold down-regulated with respect to control genes. These 593 genes had wide varieties of biological significance. While ossification-related sialoprotein precursor and osteopontin genes were significantly up-regulated, cartilage-related chondroitin sulfate proteoglycan 2 and aggrecan 1 genes were also up-regulated. Some genes related to angiogenesis, TGF-beta receptor signaling pathway and cell differentiation were also considerably up-regulated. It was concluded that osteogenic differentiation medium differentiated mesenchymal stem cells into not only osteoblasts but also chondroblasts to facilitate endochondral ossification with vascular invasion in gene expression levels. The list of genes presented here could be used as a database for ossification studies of human mesenchymal stem cells that might be clinically useful.

Key words: *Mesenchymal stem cells, DNA-microarray, Osteogenic differentiation medium*

INTRODUCTION

In dental tissue engineering therapy, culture of mesenchymal stem cells collected from iliac-crest-derived bone marrow is regarded as one important clinical technique¹ because mesen-

chymal stem cells can be multiplied², seeded in bio-absorbable scaffold materials and differentiated into osteoblasts³⁻⁵. Osseous defects could be restored using the *ex vivo* formed complex of scaffold and osteoblasts⁶⁻⁸.

Osteogenic differentiation of stem cells and osteoblastic cells has often been induced by osteogenic differentiation medium, namely, alpha-minimum essential medium supplemented with 50 µg/ml ascorbic acid, 10mM Na beta-glycerophosphate and 10⁻⁸M dexamethasone^{9,10}. The role of this medium on gene expressions of mesenchymal stem cells has not been fully clarified, yet¹¹, although only several osteogenic differentiation marker genes such as osteopontin and bone sialo protein were examined by RT-PCR or real-time quantitative RT-PCR^{12,13}. The recent development of DNA microarray technology makes simultaneous analyses of many gene expressions possible^{14,15}.

In this study, we cultured commercial human mesenchymal stem cells in the osteogenic differentiation medium for 14 days, extracted total RNA, and conducted two-dye 2.9k oligo DNA microarray. Then, (1) we clarified genes whose expressions were significantly altered with respect to control genes, either up-regulated more than 10-fold or down-regulated less than 0.1-fold, and (2) revealed the expression levels of genes which belonged to 6 selected function and ontologies such as ossification, extracellular matrix (sensu Metazoa), cell differentiation, TGF-beta signaling pathway, angiogenesis, and collagen and aggrecan.

MATERIALS AND METHODS

Human mesenchymal stem cells (PT-2501, Takara, Tokyo, Japan) were cultured in two polystyrene dishes 125mm in diameter (168351, Nunc, Rochester, NY, U.S.A.) with 20 ml exclusive alpha-minimum essential medium supplemented with 10% exclusive mesenchymal cell growth supplement (serum portion, PT-4106, Takara, Tokyo, Japan) and 1% penicillin/streptomycin (PT-3238, Takara, Tokyo, Japan) (con-

trol medium) in a 5% CO₂ incubator at 37 °C. At sub-confluence, the cells (about 10⁷ cells) were collected from one dish by a plastic cell scraper following twice cell wash with PBS (-) solution. The cells on another dish were further cultured with fresh osteogenic differentiation medium consisting of control medium and three additives such as 50 µg /ml L (+) ascorbic acid (012-04802, Wako Chemical, Osaka, Japan), 10mM Na β-glycerophosphate (Sigma Chemical, St. Louis, MO, U.S.A.) and 10⁻⁸M dexamethasone (Sigma Chemical, St. Louis, MO, U.S.A.). After 14 days culture with osteogenic differentiation medium, the cells were collected by a cell scraper following twice cell wash with PBS (-) solution. For entire cell culture, the medium exchange was conducted every three days.

Total RNAs (at least 10 µg) were extracted from the cells using TRIZOL reagent (Invitrogen, Carlsbad, CA, U.S.A.). Genomic DNA was removed by DNase treatment (DNase I, 2215A, Takara, Tokyo, Japan). After isolation and purification, total RNAs of the test (i.e. culture with osteogenic differentiation medium for 14 days following sub-confluence) and control (i.e. culture with control medium until sub-confluence) cells were labeled by reverse transcription with nucleotides containing Cy-3 and Cy-5 fluorophores, respectively. For the hybridization, a human 2.9k (29,134) oligo DNA microarray chip (Sigma Genesis, Sapporo, Japan) was used. The labeling, microarray hybridization and scanning were conducted by Sigma Genesis (Sapporo, Japan) and DNA Chip Consortium (Hokkaido University, Sapporo, Japan). Signal intensities for each spot were corrected for background, and filtered out when corrected test and control intensities did not meet the re-

quirement that intensity > background + 2SD where SD = standard deviation of all background. Global normalization of test (Cy3) and control (Cy5) signals was conducted by "median ratio centering" method (ratio = (test intensity - background)/(control intensity - background))¹⁶.

We used a web-based microarray data analysis system (Genesifter Net, VizXlabs, Seattle, WA, U.S.A.), which clearly identified differentially expressed genes with biological significance, provided gene ontology¹⁷ and pathway report, and conducted gene clustering. The ratio (i.e. fold change) of normalized test signal versus normalized control signal was termed as fold change, and used as a scale to assess gene expression alterations in this study.

RESULTS

Out of total 29,134 genes scanned, 11,085 genes (38%) were eliminated due to low signals and absence of gene expression, and 18,049 genes (62%) were validated. Table 1 lists 198 genes of human mesenchymal stem cells whose expressions were more than 10 fold up-regulated by culture in osteogenic differentiation medium for 14 days with details of gene name, gene identifier (gene accession number), gene symbol, normalized test signal value (Test signal_norm) and fold change (=Test signal_norm / Control signal_norm). The genes in Table 1 are displayed by the fold change order from the largest (2.3E+6= 2,300,000 fold) to the least (1.0E+1=10 fold). Table 2 shows 395 genes of human mesenchymal stem cells whose expression were less than 1/10 (=0.1) fold down-regulated by culture in osteogenic differentiation medium for 14 days with details of gene name, gene identifier, gene symbol, normalized test signal value and fold change. The genes in Table 2 were arranged by the fold

change order from the lowest (3.4E-06= 0.0000034 fold) to the largest (1.0E-01= 0.1 fold). Gene ontology analysis of genes in Tables 1 and 2 by Gene-sifter Net clarified the following characteristics. In biological process ontologies; 94 genes were up-regulated (termed as +94) while 139 genes were down-regulated (termed as -139) in physiological process, +61 and -94 in metabolism, +58 and -93 in cellular process, +35 and -49 in cell communication, +31 and -44 in cell growth and or maintenance, +26 and -43 in signal transduction, +19 and -47 in nucleobase, nucleoside, nucleotide and nucleic acid metabolism, +25 and -27 in development, +25 and -26 in protein metabolism, +17 and -29 in transport, +13 and -30 in transcription, +11 and -28 in regulation of transcription, +10 and -28 in DNA-dependent transcription, +10 and -28 in DNA-dependent regulation of transcription, +17 and -19 in response to external stimulus, +12 and -20 in cell surface receptor linked signal transduction, +16 and -16 in protein modification, +16 and -12 in morphogenesis, +14 and -12 in response to biotic stimulus, +15 and -10 in organogenesis, +12 and -10 in lipid metabolism, +10 and -13 in to response to stress, +12 and -10 in cell proliferation, +9 and -12 in catabolism, +8 and -13 in intracellular signaling cascade, +10 and -10 in biosynthesis, +11 and -8 in immune response, +11 and -8 in defense response, +10 and -9 in macromolecule biosynthesis, and +9 and -9 in ion transport. In molecular function ontologies; 81 genes were up-regulated (+81) while 120 genes were down-regulated (-120), +49 and -59 in catalytic binding, +29 and -36 in metal ion binding, +27 and -34 in protein binding, +24 and -35 in signal transducer activity, +16 and -40 in nucleic acid binding, +15 and -24 in hydrolase activity, +12 and -26 in DNA binding, +14 and -23 in transporter

Table 1 198 genes of human mesenchymal stem cells whose expressions were up-regulated more than 10-fold by culture in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Contr ol signal_norm)
1	Scm-related gene containing four mbt domains (SFMBT), mRNA.	NM_016329	SFMBT1	6.5E+02	2.3E+06
2	hypothetical protein MGC10848 (MGC10848), mRNA.	NM_030569	ITIH5	5.1E+02	1.8E+06
3	integrin alpha 8 subunit mRNA, 3 end.	L36531	ITGA8	2.5E+02	8.9E+05
4	H.sapiens mRNA HTPCRX02 for olfactory receptor.	X64980	OR2L1P	2.4E+02	8.4E+05
5	Human mRNA for KIAA0378 gene, partial cds.	AB002376	C1orf1	1.9E+02	6.8E+05
6	fucosyltransferase 9 (alpha (1,3) fucosyltransferase) (FUT9), mRNA.	NM_006581	FUT9	1.7E+02	5.9E+05
7	numb homolog (Drosophila)-like (NUMBL), mRNA.	NM_004756	NUMBL	1.6E+02	5.6E+05
8	chondroitin beta1.4 N-acetylgalactosaminyltransferase (ChGn), mRNA.	NM_018371	ChGn	1.6E+02	5.5E+05
9	mRNA; cDNA DKFZp686J113 (from clone DKFZp686J113).	AL833544	SLC24A3	1.5E+02	5.5E+05
10	hypothetical protein MGC40579 (MGC40579), mRNA.	NM_152776	MGC40579	1.5E+02	5.3E+05
11	claudin 7 (CLDN7), mRNA.	NM_001307	CLDN7	1.5E+02	5.2E+05
12	hypothetical protein FLJ11235 (FLJ11235), mRNA.	NM_019033	-	1.4E+02	5.0E+05
13	cDNA FLJ39478 fis, clone PROST2013605.	AK096797	CDC91L1	1.4E+02	4.8E+05
14	cDNA FLJ37852 fis, clone BRSSN2014513.	AK095171	C10orf95	1.3E+02	4.6E+05
15	Human mRNA sequence.	M84507	IGHM	1.3E+02	4.6E+05
16	dentatorubral-pallidoluysian atrophy (atrophin-1) (DRPLA), mRNA.	NM_001940	DRPLA	1.3E+02	4.5E+05
17	musashi homolog 1 (Drosophila) (MSI1), mRNA.	NM_002442	MSI1	1.2E+02	4.3E+05
18	transient receptor potential cation channel, subfamily V, member 5 (TRPV5), mRNA.	NM_019841	TRPV5	1.2E+02	4.2E+05
19	cDNA FLJ32895 fis, clone TESTI2005060.	AK057457	LOC285498	1.1E+02	4.1E+05
20	Homo sapiens. Similar to KIAA1979 protein, clone MGC:45900 IMAGE:5095186, mRNA, complete cds.	BC033230	-	1.1E+02	4.1E+05
21	Ras-GTPase-activating protein SH3-domain-binding protein (G3BP), mRNA.	NM_005754	G3BP	1.1E+02	4.0E+05
22	DKFZP564O0823 protein (DKFZP564O0823), mRNA.	NM_015393	KFZP564O082	1.1E+02	4.0E+05
23	fibroblast growth factor 18 (FGF18), transcript variant 1, mRNA.	NM_003862	FGF18	1.1E+02	3.9E+05
24	ankyrin repeat domain 6 (ANKRD6), mRNA.	NM_014942	ANKRD6	1.1E+02	3.9E+05
25	mRNA for putative 14kD protein containing SHMT homology, clone pUS1215.	Y14488	SHMT1	1.1E+02	3.8E+05
26	Homo sapiens. Similar to RIKEN cDNA 1700003M02 gene, clone MGC:43118 IMAGE:5260875, mRNA, complete cds.	BC035083	C6orf165	1.1E+02	3.8E+05
27	glucokinase (hexokinase 4) regulatory protein (GCKR), mRNA.	NM_001486	GCKR	1.1E+02	3.8E+05
28	phospholipase A2, group IVA (cytosolic, calcium-dependent) (PLA2G4A), mRNA.	NM_024420	PLA2G4A	1.1E+02	3.8E+05
29	mRNA for KIAA1364 protein, partial cds.	AB037785	MICAL3	1.0E+02	3.7E+05
30	cDNA FLJ33371 fis, clone BRACE2005949.	AK090690	CD3Z	1.0E+02	3.7E+05
31	ATP-binding cassette, sub-family C (CFTR/MRP), member 12 (ABCC12), transcript variant C, mRNA.	NM_145189	ABCC12	1.0E+02	3.6E+05
32	Homo sapiens, clone IMAGE:4429392, mRNA, partial cds.	BC017721	-	1.0E+02	3.6E+05
33	ceruloplasmin (ferroxidase) (CP), mRNA.	NM_000096	CP	9.8E+01	3.5E+05
34	chemokine (C-C motif) ligand 17 (CCL17), mRNA.	NM_002987	CCL17	9.7E+01	3.4E+05
35	septin 2 (SEP2) mRNA, partial cds.	AF179995	8-Sep	9.7E+01	3.4E+05
36	Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila) (ZIC3), mRNA.	NM_003413	ZIC3	9.6E+01	3.4E+05
37	Human vacuolar ATPase (isoform HO68) mRNA, complete cds.	L09234	-	8.8E+01	3.1E+05
38	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), mRNA.	NM_001045	SLC6A4	8.8E+01	3.1E+05
39	601879681F1 NIH.MGC.55 cDNA clone IMAGE:4108316 5, mRNA sequence.	BF241821	PARG	8.6E+01	3.1E+05
40	spastic paraplegia 4 (autosomal dominant: spastin) (SPG4), mRNA.	NM_014946	SPG4	8.5E+01	3.0E+05
41	musashi homolog 2 (Drosophila) (MSI2), transcript variant 2, mRNA.	NM_170721	MSI2	8.2E+01	2.9E+05
42	carbonic anhydrase II (CA2), mRNA.	NM_000067	CA2	7.9E+01	2.8E+05
43	Homo sapiens, clone IMAGE:5265764, mRNA.	BC036525	KIAA1377	7.8E+01	2.8E+05
44	thioredoxin domain-containing (TXNDC), mRNA.	NM_030755	TXNDC	7.8E+01	2.8E+05
45	testis-specific kinase substrate (TSKS), mRNA.	NM_021733	TSKS	7.3E+01	2.6E+05
46	chorea acanthocytosis (CHAC), transcript variant A, mRNA.	NM_033305	VPS13A	7.2E+01	2.6E+05
47	sialoprotein precursor (IBSP) mRNA, complete cds.	J05213	IBSP	7.0E+01	2.5E+05
48	Homo sapiens. Similar to hypothetical protein FLJ20378, clone IMAGE:4822123, mRNA.	BC035402	SNRPN	7.0E+01	2.5E+05

49	rhabdoid tumor deletion region gene 1 (RTDR1), mRNA.	NM_014433	RTDR1	6.9E+01	2.5E+05
50	hypothetical protein FLJ30999 (FLJ30999), mRNA.	NM_152461	ERN1	6.9E+01	2.4E+05
51	O-acetyltransferase (CAS1), mRNA.	NM_022900	CAS1	6.8E+01	2.4E+05
52	hypothetical protein FLJ14981 (FLJ14981), mRNA.	NM_032868	FLJ14981	6.7E+01	2.4E+05
53	cDNA FLJ40386 fis, clone TESTI2036114.	AK097705	FBXO24	6.6E+01	2.3E+05
54	cDNA FLJ31725 fis, clone NT2RI2006716.	AK056287	-	6.5E+01	2.3E+05
55	immunoglobulin (CD79A) binding protein 1 (IGBP1), mRNA.	NM_001551	IGBP1	6.4E+01	2.3E+05
56	mRNA for SCCA2b, complete cds.	AB046400	SERPINB4	6.3E+01	2.2E+05
57	sterol O-acyltransferase 2 (SOAT2), mRNA.	NM_003578	SOAT2	6.2E+01	2.2E+05
58	plasminogen activator, urokinase (PLAU), mRNA.	NM_002658	PLAU	6.2E+01	2.2E+05
59	mRNA for KIAA1630 protein, partial cds.	AB046850	-	6.2E+01	2.2E+05
60	ALS2CR16 mRNA, complete cds.	AB053318	ALS2CR16	5.8E+01	2.0E+05
61	cDNA FLJ33784 fis, clone BRSSN2007819.	AK091103	-	5.7E+01	2.0E+05
62	Homo sapiens, clone IMAGE:4401608, mRNA.	BC041431	-	5.5E+01	2.0E+05
63	cDNA FLJ40157 fis, clone TESTI2014800, weakly similar to PROTEIN DISULFIDE ISOMERASE (EC 5.3.4.1).	AK097476	PDILT	5.5E+01	1.9E+05
64	insulin-like growth factor binding protein 5 (IGFBP5), mRNA.	NM_000599	IGFBP5	5.4E+01	1.9E+05
65	dystrophin related protein 2 (DRP2), mRNA.	NM_001939	DRP2	5.3E+01	1.9E+05
66	Homo sapiens, Similar to RIKEN cDNA 8430436A10 gene, clone MGC:21763 IMAGE:4706746, mRNA, complete cds.	BC012027	CYP2U1	5.2E+01	1.8E+05
67	Homo sapiens, clone IMAGE:5176738, mRNA.	BC040730	-	5.1E+01	1.8E+05
68	p65 protein (HSAJ2425), mRNA.	NM_017532	-	5.0E+01	1.8E+05
69	tripartite motif protein TRIM5 isoform beta (TRIM5) mRNA, complete cds; alternatively spliced.	AF220026	TRIM5	4.9E+01	1.8E+05
70	cDNA FLJ40319 fis, clone TESTI2030754.	AK097638	FLJ40319	4.8E+01	1.7E+05
71	cDNA FLJ37596 fis, clone BRCOC2008064.	AK094915	PTN	4.8E+01	1.7E+05
72	mRNA; cDNA DKFZp313P1931 (from clone DKFZp313P1931).	AL832095	CHIC1	4.7E+01	1.7E+05
73	opioid receptor, kappa 1 (OPRK1), mRNA.	NM_000912	OPRK1	4.5E+01	1.6E+05
74	osteoclast stimulating factor 1 (OSTF1), mRNA.	NM_012383	OSTF1	4.5E+01	1.6E+05
75	cDNA FLJ13112 fis, clone NT2RP3002587.	AK023174	-	4.4E+01	1.6E+05
76	hypothetical protein MGC2705 (MGC2705), mRNA.	NM_032701	SUV420H2	4.4E+01	1.5E+05
77	dihydrofolate reductase (DHFR), mRNA.	NM_000791	DHFR	4.3E+01	1.5E+05
78	insulin-like 6 (INSL6), mRNA.	NM_007179	INSL6	4.2E+01	1.5E+05
79	hypothetical protein FLJ14721 (FLJ14721), mRNA.	NM_032829	FLJ14721	4.1E+01	1.5E+05
80	p53-regulated apoptosis-inducing protein 1 (P53AIP1), mRNA.	NM_022112	P53AIP1	4.0E+01	1.4E+05
81	xylulokinase homolog (H. influenzae) (XYLB), mRNA.	NM_005108	XYLB	4.0E+01	1.4E+05
82	testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds.	AF000990	TTY1	4.0E+01	1.4E+05
83	Homo sapiens, clone MGC:35245 IMAGE:5172531, mRNA, complete	BC033502	PTPNS1L2	4.0E+01	1.4E+05
84	hypothetical protein FLJ20354 (FLJ20354), mRNA.	NM_017779	DEPDC1	3.9E+01	1.4E+05
85	cDNA FLJ25428 fis, clone TST05354.	AK058157	COL4A1	3.8E+01	1.3E+05
86	UI-H-BI4-aor-e-08-0-UI.s1 NCLCGAP_Sub8 cDNA clone IMAGE:3085911 3, mRNA sequence.	BF508849	-	3.6E+01	1.3E+05
87	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, mRNA.	NM_003101	SOAT1	3.5E+01	1.2E+05
88	hypothetical protein FLJ20802 (FLJ20802), mRNA.	NM_017959	-	3.4E+01	1.2E+05
89	myeloid/lymphoid or mixed-lineage leukemia3 (MLL3), mRNA.	NM_021230	MLL3	3.4E+01	1.2E+05
90	wx23e01.x1 NCI_CGAP_Kid11 cDNA clone IMAGE:2544504 3 similar to contains element MER35 repetitive element ;, mRNA sequence.	AW058560	-	3.3E+01	1.2E+05
91	inducible nitric oxide synthase (iNOS) mRNA, complete cds.	AF049656	-	3.1E+01	1.1E+05
92	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA.	NM_005239	ETS2	3.1E+01	1.1E+05
93	Human BRCA2 region, mRNA sequence CG014.	U50526	13CDNA73	3.1E+01	1.1E+05
94	cDNA FLJ40282 fis, clone TESTI2027562.	AK097601	PAK6	3.0E+01	1.1E+05
95	cDNA FLJ11597 fis, clone HEMBA1003856.	AK021659	DNMT2	2.8E+01	1.0E+05
96	G protein interaction factor 1-like mRNA sequence.	AF288405	DNCH2	2.8E+01	1.0E+05
97	chromosome 20 open reading frame 36 (C20orf36), mRNA.	NM_018257	C20orf36	2.8E+01	9.9E+04
98	monocarboxylate transporter 3 (SLC16A8), mRNA.	NM_013356	SLC16A8	2.7E+01	9.6E+04
99	Homo sapiens, protein phosphatase, clone MGC:33229 IMAGE:5269106, mRNA, complete cds.	BC035000	DUSP19	2.7E+01	9.5E+04
100	phosphodiesterase 6G, cGMP-specific, rod, gamma (PDE6G), mRNA.	NM_002602	PDE6G	2.4E+01	8.7E+04
101	Ets2 repressor factor (ERF), mRNA.	NM_006494	ERF	2.4E+01	8.6E+04
102	Homo sapiens, clone IMAGE:4837056, mRNA, partial cds.	BC034591	LOC284648	2.4E+01	8.4E+04
103	solute carrier family 23 (nucleobase transporters), member 1 (SLC23A1), mRNA.	NM_005116	SLC23A2	2.1E+01	7.4E+04
104	Fzr1 protein (FZR1), mRNA.	NM_016263	FZR1	2.1E+01	7.3E+04
105	small proline-rich protein 3 (SPRR3), mRNA.	NM_005416	SPRR3	2.0E+01	7.0E+04

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106	immunoglobulin superfamily, member 3 (IGSF3), mRNA.	NM_001542	IGSF3	1.9E+01	6.9E+04
107	putative protease inhibitor WAP9 (WAP9), mRNA.	NM_147198	WFDC9	1.9E+01	6.9E+04
108	mab-21-like 2 (C. elegans) (MAB21L2), mRNA.	NM_006439	MAB21L2	1.9E+01	6.8E+04
109	hypothetical protein BC002926 (LOC90379), mRNA.	NM_138353	-	1.9E+01	6.6E+04
110	FK506 binding protein 14, 22 kDa (FKBP14), mRNA.	NM_017946	FKBP14	1.9E+01	6.6E+04
111	cDNA FLJ34996 fis, clone OCBBF2011536.	AK092315	-	1.7E+01	6.0E+04
112	hypothetical protein BC000993 (LOC130026), mRNA.	NM_138468	ALS2CR15	1.7E+01	5.9E+04
113	ts96g04.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2239158 3. mRNA sequence.	AI917293	-	1.6E+01	5.6E+04
114	cDNA FLJ12097 fis, clone HEMBB1002617.	AK022159	UBE2E2	1.5E+01	5.5E+04
115	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 (HSD3B1), mRNA.	NM_000862	HSD3B1	1.5E+01	5.2E+04
116	hypothetical protein FLJ21432 (FLJ21432), mRNA.	NM_024551	ADIPOR2	1.4E+01	5.1E+04
117	chondrolectin (CHODL), mRNA.	NM_024944	CHODL	1.3E+01	4.7E+04
118	oxysterol binding protein-like 10 (OSBPL10), mRNA.	NM_017784	OSBPL10	1.3E+01	4.5E+04
119	hypothetical protein FLJ13154 (FLJ13154), mRNA.	NM_024598	FLJ13154	1.2E+01	4.1E+04
120	POU domain, class 2, associating factor 1 (POU2AF1), mRNA.	NM_006235	POU2AF1	1.2E+01	4.1E+04
121	myotubularin related protein 4 (MTMR4), mRNA.	NM_004687	MTMR4	1.1E+01	3.9E+04
122	cDNA FLJ33309 fis, clone BNGH42004538.	AK090628	-	1.1E+01	3.8E+04
123	interferon (alpha, beta and omega) receptor 1 (IFNAR1), mRNA.	NM_000629	IFNAR1	1.1E+01	3.7E+04
124	ATP-binding cassette, sub-family A (ABC1), member 7 (ABCA7), transcript variant 1, mRNA.	NM_019112	ABCA7	1.0E+01	3.7E+04
125	occludin (OCLN), mRNA.	NM_002538	OCLN	1.0E+01	3.6E+04
126	Homo sapiens. Similar to hypothetical protein MGC5149, clone IMAGE:3840062, mRNA.	BC010121	-	7.9E+00	2.8E+04
127	cDNA FLJ32896 fis, clone TESTI2005155.	AK057458	-	7.0E+00	2.5E+04
128	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA.	NM_003222	TFAP2C	6.3E+00	2.2E+04
129	cDNA FLJ35316 fis, clone PROST2011012.	AK092635	-	5.5E+00	1.9E+04
130	Homo sapiens, clone IMAGE:4829078, mRNA.	BC033355	LOC152024	5.2E+00	1.8E+04
131	CTL2 gene (CTL2), mRNA.	NM_020428	CTL2	3.8E+00	1.4E+04
132	neuroigin (KIAA1260), mRNA.	NM_020742	NLGN4X	1.3E+00	4.8E+03
133	mRNA; cDNA DKFZp7271051 (from clone DKFZp7271051); partial cds.	AL117478	GPSM1	1.2E+00	4.2E+03
134	cDNA FLJ12040 fis, clone HEMBB1001944.	AK022102	DBC1	1.2E+00	4.2E+03
135	phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA.	NM_003706	PLA2G4C	7.9E-01	2.8E+03
136	clone FLB2543.	AF113675	RAP80	2.3E+01	7.7E+02
137	oz21c12.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1675990 3 similar to contains element L1 repetitive element ;, mRNA sequence.	AI052253	LMO2	1.6E+02	6.8E+02
138	KIAA0449 protein (KIAA0449), mRNA.	NM_017596	-	1.1E+02	6.2E+02
139	found in inflammatory zone 3 (FIZZ3), mRNA.	NM_020415	RETN	1.6E+01	2.8E+02
140	mRNA; cDNA DKFZp686N1648 (from clone DKFZp686N1648).	AL833569	KLHL1	7.9E-02	2.8E+02
141	Homo sapiens, similar to dJ402N21.3 (novel protein with Immunoglobulin domains), clone IMAGE:5165468, mRNA.	BC028193	MAMDC1	8.1E+01	2.2E+02
142	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase 1) (B3GAT3), mRNA.	NM_012200	B3GAT3	7.3E+01	1.4E+02
143	scrapie responsive protein 1 (SCRG1), mRNA.	NM_007281	SCRG1	3.3E+03	6.9E+01
144	Human (clone Z149) retinal mRNA.	L23402	-	1.4E+02	6.9E+01
145	deoxynucleotidyltransferase, terminal (DNNT), mRNA.	NM_004088	DNNT	1.7E+02	6.7E+01
146	integrin, alpha 11 (ITGA11), mRNA.	NM_012211	ITGA11	2.3E+02	6.4E+01
147	single stranded DNA binding protein 4 (SSBP4), mRNA.	NM_032627	SSBP4	1.3E+02	5.2E+01
148	carcinoembryonic antigen-related cell adhesion molecule 4 (CEACAM4), mRNA.	NM_001817	-	3.7E+01	5.0E+01
149	mRNA for KIAA1866 protein, partial cds.	AB058769	FNDC1	3.3E+03	4.8E+01
150	unknown mRNA sequence.	AY010115	-	7.2E+01	4.4E+01
151	hypothetical protein FLJ31934 (FLJ31934), mRNA.	NM_152554	C6orf195	1.0E+01	4.2E+01
152	sterol carrier protein 2 (SCP2), mRNA.	NM_002979	SCP2	1.2E+02	3.5E+01
153	cDNA FLJ31115 fis, clone IMR322000418.	AK055677	KCNB2	9.1E+01	2.8E+01
154	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 (HSD3B2), mRNA.	NM_000198	HSD3B2	8.3E+01	2.7E+01
155	AGENCOURT_6394712 NIH_MGC_67 cDNA clone IMAGE:5494246 5, mRNA sequence.	BM450580	KIAA0650	4.1E+02	2.7E+01
156	guanylate cyclase activator 1C (GUCA1C), mRNA.	NM_005459	GUCA1C	1.1E+02	2.7E+01
157	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA.	NM_000582	SPP1	2.6E+02	2.5E+01

158	hypocretin (orexin) receptor 1 (HCRTR1), mRNA.	NM_001525	HCRTR1	2.5E+02	2.4E+01
159	Human thrombospondin mRNA.	M81339	THBS2	1.1E+04	2.2E+01
160	cDNA FLJ32201 fis, clone PLACE6002949.	AK056763	-	2.5E+03	2.1E+01
161	cancer/testis antigen 2 (CTAG2), mRNA.	NM_020994	CTAG2	3.4E+03	2.0E+01
162	secreted frizzled-related protein 4 (SFRP4), mRNA.	NM_003014	SFRP4	2.3E+03	1.8E+01
163	interleukin 6 (interferon, beta 2) (IL6), mRNA.	NM_000600	IL6	1.2E+03	1.8E+01
164	hypothetical protein HSPC242 (HSPC242), mRNA.	NM_016498	MTP18	1.1E+03	1.8E+01
165	hypothetical protein FLJ11082 (FLJ11082), mRNA.	NM_018317	TBC1D19	2.9E+02	1.7E+01
166	ganglioside-induced differentiation-associated protein 1 (GDAP1).	NM_018972	GDAP1	2.2E+01	1.7E+01
167	clone HM6003 T-cell receptor delta chain (TCRDV1) mRNA, partial	AF312279	-	2.9E+03	1.7E+01
168	adican (DKFZp564I1922), mRNA.	NM_015419	DKFZp564I1922	1.6E+03	1.7E+01
169	cDNA FLJ36200 fis, clone TESTI2028269	AK093519	-	1.4E+02	1.6E+01
170	mRNA; cDNA DKFZp667J039 (from clone DKFZp667J039).	AL833701	RP11-19J3.3	3.1E+01	1.5E+01
171	full length insert cDNA clone ZE04B05.	AF086519	FLJ35258	7.4E+02	1.5E+01
172	mRNA for KIAA1199 protein, partial cds.	AB033025	KIAA1199	1.9E+04	1.5E+01
173	similar to NMDA receptor-regulated gene 2 (mouse) (FLJ11896).	NM_024611	NARG2	7.0E+02	1.5E+01
174	cDNA FLJ20463 fis, clone KAT06143.	AK000470	LOC286434	1.2E+03	1.5E+01
175	UI-1-BC1p-ati-g-12-0-UI.s1 NCI_CGAP_PI3 cDNA clone UI-1-BC1p-ati-g-12-0-UI 3, mRNA sequence.	BQ011970	-	6.1E+02	1.5E+01
176	cDNA: FLJ21782 fis, clone HEP00266, highly similar to AF118063 PRO1400 mRNA.	AK025435	-	1.2E+02	1.4E+01
177	carbonyl reductase 3 (CBR3), mRNA.	NM_001236	CBR3	3.7E+02	1.4E+01
178	uncharacterized gastric protein ZG33P mRNA, partial cds.	AF264623	RERG	7.6E+01	1.4E+01
179	A kinase (PRKA) anchor protein 7 (AKAP7), transcript variant gamma, mRNA.	NM_016377	AKAP7	1.3E+03	1.4E+01
180	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 (LILRB2), mRNA.	NM_005874	LILRB2	1.1E+02	1.3E+01
181	ODZ3 (ODZ3) mRNA, partial cds.	AF195420	ODZ3	7.0E+01	1.3E+01
182	lysyl oxidase-like 2 (LOXL2), mRNA.	NM_002318	LOXL2	9.1E+03	1.3E+01
183	actin, alpha 2, smooth muscle, aorta (ACTA2), mRNA.	NM_001613	ACTA2	7.9E+03	1.3E+01
184	cDNA FLJ11319 fis, clone PLACE1010293.	AK002181	-	2.4E+02	1.3E+01
185	RNB6 (RNB6), mRNA.	NM_016337	EVL	3.6E+02	1.3E+01
186	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA.	NM_030955	ADAMTS12	3.5E+02	1.2E+01
187	cDNA FLJ25521 fis, clone CBR06845.	AK098387	-	9.2E+01	1.2E+01
188	lumican (LUM), mRNA.	NM_002345	LUM	9.0E+03	1.1E+01
189	chromosome 21 open reading frame 7 (C21orf7), mRNA.	NM_020152	C21orf7	3.9E+02	1.1E+01
190	adipose specific 2 (APM2), mRNA.	NM_006829	C10orf116	2.5E+03	1.1E+01
191	cDNA FLJ40856 fis, clone TRACH2016498, moderately similar to ZINC FINGER PROTEIN 184.	AK098175	ZNF283	2.1E+02	1.1E+01
192	CES hBr2 mRNA for brain carboxylesterase hBr2, complete cds.	AB025027	-	5.1E+01	1.1E+01
193	cDNA FLJ13803 fis, clone THYRO1000187.	AK023865	PRKCE	1.2E+02	1.1E+01
194	hypothetical protein BC019238 (LOC120379), mRNA.	NM_138789	LOC120379	1.4E+03	1.1E+01
195	hypothetical protein FLJ22672 (FLJ22672), mRNA.	NM_024897	PAGR6	2.1E+02	1.0E+01
196	KIAA1932 protein (KIAA1932), mRNA.	NM_052925	LENG8	5.3E+02	1.0E+01
197	cDNA FLJ25405 fis, clone TST02892.	AK058134	-	1.1E+02	1.0E+01
198	Human profilaggrin mRNA, 3 end.	M60502	FLG	8.6E+02	1.0E+01

Table 2 395 genes of human mesenchymal stem cells whose expressions were less than 0.1-fold down-regulated by culture in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change (=Test signal_norm/Control signal_norm)
1	ng32g04.s1 NCI_CGAP_Co3 cDNA clone IMAGE:936534 3, mRNA	AA524295	-	1.00E-03	3.4E-06
2	full length insert cDNA clone ZD63E04.	AF086354	PRND	1.00E-03	3.5E-06
3	cDNA FLJ34810 fis, clone NT2NE2006958.	AK092129	FAM19A1	1.00E-03	3.6E-06
4	Homo sapiens, clone IMAGE:5760168, mRNA.	BC039549	-	1.00E-03	3.8E-06
5	protein phosphatase 2A, regulatory subunit B (PR 53) (PPP2R4), mRNA.	NM_021131	PPP2R4	1.00E-03	3.9E-06
6	Homo sapiens, Similar to RIKEN cDNA 4921504I05 gene, clone IMAGE:5766894, mRNA.	BC038240	C6orf194	1.00E-03	4.0E-06
7	phosphotriesterase related (PTER), mRNA.	NM_030664	PTER	1.00E-03	4.3E-06
8	hypothetical protein HSU79252 (HSU79252), mRNA.	NM_013298	-	1.00E-03	4.3E-06
9	za23a04.r1 Soares fetal liver spleen 1NFLS cDNA clone IMAGE:293358 5, mRNA sequence.	N92035	-	1.00E-03	4.8E-06
10	APMCF1 protein (APMCF1), mRNA.	NM_021203	SRPRB	1.00E-03	5.1E-06
11	hypothetical protein FLJ10652 (FLJ10652), mRNA.	NM_018169	FLJ10652	1.00E-03	5.2E-06
12	SEC15 (S. cerevisiae)-like (SEC15L), mRNA.	NM_019053	SEC15L1	1.00E-03	5.3E-06
13	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1 (SERPINB1), mRNA.	NM_030666	SERPINB1	1.00E-03	5.3E-06
14	cDNA FLJ11617 fis, clone HEMBA1004045.	AK021679	ALMS1	1.00E-03	5.4E-06
15	cDNA FLJ34536 fis, clone HLUNG2008384.	AK091855	LOC283299	1.00E-03	5.5E-06
16	poliovirus receptor-related 2 (herpesvirus entry mediator B) (PVRL2),	NM_002856	PVRL2	1.00E-03	5.5E-06
17	Homo sapiens, Similar to RIKEN cDNA 2510006C20 gene, clone MGC:24001 IMAGE:4050858, mRNA, complete cds.	BC019239	LOC494143	1.00E-03	5.5E-06
18	Homo sapiens, Similar to RIKEN cDNA 5730409G15 gene, clone MGC:19636 IMAGE:2822323, mRNA, complete cds.	BC010084	SB153	1.00E-03	5.7E-06
19	cDNA FLJ39455 fis, clone PROST2010400, weakly similar to SPLICEOSOME ASSOCIATED PROTEIN 62.	AK096774	-	1.00E-03	5.8E-06
20	cDNA FLJ40521 fis, clone TESTI2046797.	AK097840	-	1.00E-03	6.1E-06
21	tx28f05.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2270913 3, mRNA	AI801879	-	1.00E-03	6.2E-06
22	Homo sapiens, clone IMAGE:5517530, mRNA.	BC033263	PVT1	1.00E-03	6.2E-06
23	colony stimulating factor 1 (macrophage) (CSF1), transcript variant 3,	NM_172211	CSF1	1.00E-03	6.4E-06
24	testis specific ankyrin-like protein 1 (LOC51281), mRNA.	NM_016552	ANKMY1	1.00E-03	6.4E-06
25	mRNA activated in tumor suppression, clone TSAP20.	AJ012500	-	1.00E-03	6.6E-06
26	chromosome 12 open reading frame 22 (C12orf22), mRNA.	NM_030809	C12orf22	1.00E-03	6.6E-06
27	cDNA FLJ13651 fis, clone PLACE1011452.	AK023713	-	1.00E-03	6.6E-06
28	Homo sapiens, Similar to hypothetical protein BC013995, clone MGC:47795 IMAGE:5742332, mRNA, complete cds.	BC038980	MYADML	1.00E-03	6.6E-06
29	hypothetical protein DKFZp434N0650 (DKFZp434N0650), mRNA.	NM_032261	C21orf56	1.00E-03	6.8E-06
30	hypothetical protein FLJ40201 (FLJ40201), mRNA.	NM_152607	FLJ40201	1.00E-03	7.0E-06
31	mRNA for KIAA1045 protein, partial cds.	AB028968	KIAA1045	1.00E-03	7.0E-06
32	hypothetical protein DKFZp547M109 (DKFZp547M109), mRNA.	NM_152742	GPC2	1.00E-03	7.0E-06
33	cDNA FLJ12230 fis, clone MAMMA1001186.	AK022292	ZNF346	1.00E-03	7.0E-06
34	mRNA; cDNA DKFZp762B2115 (from clone DKFZp762B2115).	AL832912	LOC200895	1.00E-03	7.0E-06
35	HSEZ6b protein mRNA, complete cds; alternatively spliced.	AF502129	SEZ6	1.00E-03	7.0E-06
36	pseudouridylate synthase 1 (PUS1), mRNA.	NM_025215	PUS1	1.00E-03	7.2E-06
37	cDNA FLJ34894 fis, clone NT2NE2017982.	AK092213	PTOV1	1.00E-03	7.2E-06
38	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R), mRNA.	NM_002386	MC1R	1.00E-03	7.3E-06
39	clone 23636 mRNA sequence.	AF052121	-	1.00E-03	7.4E-06
40	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member 4 (ILT7), mRNA.	NM_012276	ILT7	1.00E-03	7.5E-06
41	cDNA FLJ39726 fis, clone SMINT2015306.	AK097045	FLJ10385	1.00E-03	7.5E-06
42	mRNA; fetal brain cDNA 5 sequence.	AJ002784	-	1.00E-03	7.5E-06
43	partial mRNA; ID EE2-16E2.	AJ227904	-	1.00E-03	7.5E-06
44	zinc finger protein 275 (ZNF275), mRNA.	NM_020636	-	1.00E-03	8.0E-06
45	Homo sapiens, clone IMAGE:3447073, mRNA, partial cds.	BC000922	LOC400684	1.00E-03	8.0E-06
46	hypothetical protein MGC39389 (FLJ32384), mRNA.	NM_144608	FLJ32384	1.00E-03	8.2E-06
47	small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA.	NM_004596	SNRPA	1.00E-03	8.3E-06
48	cDNA FLJ11612 fis, clone HEMBA1004011.	AK021674	NFIA	1.00E-03	8.5E-06
49	hypothetical protein MGC15705 (MGC15705), mRNA.	NM_032757	-	1.00E-03	8.5E-06
50	Homo sapiens, clone IMAGE:3506202, mRNA, partial cds.	BC008335	DOCK6	1.00E-03	8.5E-06
51	cDNA FLJ38107 fis, clone D3OST2001669.	AK095426	-	1.00E-03	8.5E-06
52	mRNA; cDNA DKFZp686D1456 (from clone DKFZp686D1456).	AL833573	PHF6	1.00E-03	8.6E-06
53	spinophilin (SPINO), mRNA.	NM_032595	PPP1R9B	1.00E-03	8.6E-06
54	full length insert cDNA YU12H01.	AF075107	-	1.00E-03	8.7E-06

55	hypothetical protein FLJ32115 (FLJ32115), mRNA.	NM_152321	FLJ32115	1.00E-03	8.7E-06
56	chromosome 1 open reading frame 25 (C1orf25), mRNA.	NM_030934	C1orf25	1.00E-03	8.7E-06
57	T-cell receptor delta chain (TCRDV3J1) mRNA, partial cds.	U91203	-	1.00E-03	9.0E-06
58	cDNA FLJ37037 fis, clone BRACE2011611.	AK094356	LOC286382	1.00E-03	9.0E-06
59	full length insert cDNA clone YB64E03.	AF147370	-	1.00E-03	9.1E-06
60	DIP13 beta (DIP13B), mRNA.	NM_018171	DIP13B	1.00E-03	9.1E-06
61	testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds.	AF000991	TTY2	1.00E-03	9.2E-06
62	mRNA; cDNA DKFZp434E2221 (from clone DKFZp434E2221).	AL137458	-	1.00E-03	9.2E-06
63	hqp0376 protein mRNA, complete cds.	AF078844	-	1.00E-03	9.3E-06
64	mRNA sequence, IMAGE clone 446411.	AJ011980	LOC89231	1.00E-03	9.4E-06
65	clone TCRBV20S1.72 T-cell receptor beta chain (TCRBV20S1) mRNA, partial cds.	AF088765	-	1.00E-03	9.4E-06
66	AGENCOURT 6560067 NIH_MGC_119 cDNA clone IMAGE:5742052 5, mRNA sequence.	BM564038	-	1.00E-03	9.5E-06
67	cDNA FLJ40823 fis, clone TRACH2011093.	AK098142	-	1.00E-03	9.5E-06
68	cDNA FLJ35119 fis, clone PLACE6007482.	AK092438	FLJ35119	1.00E-03	9.5E-06
69	hypothetical protein FLJ32894 (FLJ32894), mRNA.	NM_144667	FLJ32894	1.00E-03	9.6E-06
70	ubiquitin specific protease (NY-REN-60), mRNA.	NM_032582	USP32	1.00E-03	9.7E-06
71	5-hydroxytryptamine (serotonin) receptor 2B (HTR2B), mRNA.	NM_000867	HTR2B	1.00E-03	9.7E-06
72	cDNA FLJ13558 fis, clone PLACE1007743.	AK023620	-	1.00E-03	9.7E-06
73	cDNA FLJ13401 fis, clone PLACE1001440.	AK023463	RALGPS1	1.00E-03	9.8E-06
74	T-box 22 (TBX22), mRNA.	NM_016954	TBX22	1.00E-03	9.9E-06
75	cDNA FLJ36617 fis, clone TRACH2016481.	AK093936	LOC284276	1.00E-03	1.0E-05
76	ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA.	NM_002003	FCN1	1.00E-03	1.0E-05
77	Homo sapiens, clone IMAGE:5288733, mRNA.	BC033974	ZFY	1.00E-03	1.0E-05
78	Homo sapiens, Similar to hect domain and RLD 2, clone IMAGE:4581928, mRNA.	BC018626	-	1.00E-03	1.0E-05
79	glycoprotein 2 (zymogen granule membrane) (GP2), mRNA.	NM_001502	GP2	1.00E-03	1.0E-05
80	full length insert cDNA clone YY72D01.	AF086051	-	1.00E-03	1.0E-05
81	Homo sapiens, clone IMAGE:5585678, mRNA.	BC035768	MSI2	1.00E-03	1.0E-05
82	kinesin family member C2-like (LOC90990), mRNA.	NM_145754	KIFC2	1.00E-03	1.0E-05
83	beta-1 adrenergic receptor mRNA, 3 UTR.	AF272890	ADRB1	1.00E-03	1.0E-05
84	602501387F1 NIH_MGC_75 cDNA clone IMAGE:4615101 5, mRNA	BG429688	-	1.00E-03	1.1E-05
85	Homo sapiens, clone IMAGE:5192696, mRNA.	BC040153	LOC339674	1.00E-03	1.1E-05
86	unc93 (C.elegans) homolog A (UNC93A), mRNA.	NM_018974	UNC93A	1.00E-03	1.1E-05
87	block of proliferation 1 (BOP1), mRNA.	NM_015201	BOP1	1.00E-03	1.1E-05
88	stromal cell-derived factor 2 (SDF2), mRNA.	NM_006923	SDF2	1.00E-03	1.1E-05
89	cDNA FLJ30234 fis, clone BRACE2001972.	AK054796	MLR1	1.00E-03	1.1E-05
90	Homo sapiens, similar to chlorophyll a/b-binding protein, clone MGC:46290 IMAGE:5763022, mRNA, complete cds.	BC039694	-	1.00E-03	1.1E-05
91	hypothetical protein FLJ10385 (FLJ10385), mRNA.	NM_018081	FLJ10385	1.00E-03	1.2E-05
92	centromere protein J (CENPJ), mRNA.	NM_018451	CENPJ	1.00E-03	1.2E-05
93	gastrin (GAS), mRNA.	NM_000805	GAS	1.00E-03	1.2E-05
94	hypothetical protein MGC12945 (MGC12945), mRNA.	NM_032318	HIATL2	1.00E-03	1.2E-05
95	mRNA for FLJ00052 protein, partial cds.	AK024460	SDS3	1.00E-03	1.2E-05
96	Homo sapiens, clone MGC:20904 IMAGE:4555434, mRNA, complete cds.	BC011943	SPPL3	1.00E-03	1.2E-05
97	transglutaminase 5 (TGM5), mRNA.	NM_004245	TGM5	1.00E-03	1.2E-05
98	full length insert cDNA clone YW19A06.	AF086015	NLGN1	1.00E-03	1.2E-05
99	hypothetical protein DJ667H12.2 (DJ667H12.2), mRNA.	NM_019605	SERTAD4	1.00E-03	1.2E-05
100	cDNA FLJ30835 fis, clone FEBRA2002109.	AK055397	-	1.00E-03	1.3E-05
101	H.sapiens mRNA for UV-B repressed sequence, HUR 8.	X98206	ARID1B	1.00E-03	1.3E-05
102	epithelial cell transforming sequence 2 oncogene (ECT2), mRNA.	NM_018098	ECT2	1.00E-03	1.3E-05
103	Human isolate HR001 T cell receptor V-beta complementarity determining region 3 mRNA, partial cds.	U55077	-	1.00E-03	1.3E-05
104	hypothetical protein PRO2831 (PRO2831), mRNA.	NM_018540	-	1.00E-03	1.3E-05
105	hsp70-interacting protein (HSPBP1), mRNA.	NM_012267	HSPBP1	1.00E-03	1.3E-05
106	cDNA: FLJ23108 fis, clone LNG07742.	AK026761	-	1.00E-03	1.3E-05
107	hypothetical protein FLJ31153 (FLJ31153), mRNA.	NM_144600	FLJ31153	1.00E-03	1.3E-05
108	hypothetical protein BC014602 (LOC130951), mRNA.	NM_138804	LOC130951	1.00E-03	1.3E-05
109	hypothetical protein FLJ13942 (FLJ13942), mRNA.	NM_024581	C6orf60	1.00E-03	1.4E-05
110	hypothetical protein FLJ22184 (FLJ22184), mRNA.	NM_025094	-	1.00E-03	1.4E-05
111	cDNA FLJ40589 fis, clone THYMU2009596.	AK097908	9-Sep	1.00E-03	1.4E-05
112	cDNA FLJ38062 fis, clone CTONG2014995.	AK095381	UGCG	1.00E-03	1.4E-05
113	cDNA FLJ37874 fis, clone BRSSN2018731, weakly similar to ANKYRIN 1.	AK095193	FLJ37874	1.00E-03	1.4E-05
114	mRNA; cDNA DKFZp313E1934 (from clone DKFZp313E1934).	AL832690	C6orf83	1.00E-03	1.4E-05
115	Williams-Beuren syndrome chromosome region 27 (WBSCR27), mRNA.	NM_152559	WBSCR27	1.00E-03	1.4E-05
116	misato (FLJ10504), mRNA.	NM_018116	FLJ10504	1.00E-03	1.4E-05
117	cDNA FLJ20112 fis, clone COL05405.	AK000119	MGC40405	1.00E-03	1.4E-05
118	RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA.	NM_002907	RECQL	1.00E-03	1.4E-05
119	hypothetical protein FLJ34917 (FLJ34917), mRNA.	NM_153263	ZNF549	1.00E-03	1.4E-05

120	cDNA FLJ32661 fis. clone TEST11000055, weakly similar to HOMEBOX PROTEIN SIX1.	AK057223	-	1.00E-03	1.5E-05
121	dead ringer (Drosophila)-like 2 (bright and dead ringer) (DRIL2), mRNA.	NM_006465	ARID3B	1.00E-03	1.5E-05
122	hypothetical protein FLJ20010 (FLJ20010), mRNA.	NM_019021	FLJ20010	1.00E-03	1.5E-05
123	mRNA for KIAA0869 protein, partial cds.	AB020676	KIBRA	1.00E-03	1.5E-05
124	cDNA FLJ35076 fis. clone PLACE6001712.	AK092395	RHBDL6	1.00E-03	1.5E-05
125	mRNA: cDNA DKFZp686L0519 (from clone DKFZp686L0519).	AL832482	MEIS2	1.00E-03	1.5E-05
126	UI-E-CK1-afk-g-20-0-UI.s2 UI-E-CK1 cDNA clone UI-E-CK1-afk-g-20-0-UI 3, mRNA sequence.	BM671360	BRUNOL4	1.00E-03	1.6E-05
127	cDNA FLJ37105 fis. clone BRACE2019510.	AK094424	VGLL4	1.00E-03	1.6E-05
128	prostate differentiation factor (PLAB), mRNA.	NM_004864	GDF15	1.00E-03	1.6E-05
129	5-hydroxytryptamine (serotonin) receptor 3A (HTR3A), mRNA.	NM_000869	HTR3A	1.00E-03	1.6E-05
130	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity 1, receptor for, beta polypeptide) (MS4A2), mRNA.	NM_000139	MS4A2	1.00E-03	1.6E-05
131	full length insert cDNA clone ZD98A02.	AF088075	-	1.00E-03	1.6E-05
132	mRNA: cDNA DKFZp667P1220 (from clone DKFZp667P1220).	AL833656	KIAA1596	1.00E-03	1.6E-05
133	mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA.	NM_002758	MAP2K6	1.00E-03	1.7E-05
134	we17a06.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:2341330 3, mRNA sequence.	AI697756	-	1.00E-03	1.7E-05
135	xv21d02.x1 Soares_NFL_T.GBC.S1 cDNA clone IMAGE:2813763 3, mRNA sequence.	AW303619	CDA08	1.00E-03	1.8E-05
136	lipocalin 2 (oncogene 24p3) (LCN2), mRNA.	NM_005564	LCN2	1.00E-03	1.8E-05
137	Homo sapiens, clone IMAGE:5303602, mRNA.	BC039434	U2AF1L2	1.00E-03	1.8E-05
138	erythrocyte membrane protein band 4.1 like 4A (EPB41L4A), mRNA.	NM_022140	EPB41L4A	1.00E-03	1.8E-05
139	cDNA FLJ35321 fis. clone PROST2012088.	AK092640	ADM2	1.00E-03	1.8E-05
140	cDNA FLJ12275 fis. clone MAMMA1001686.	AK022337	-	1.00E-03	1.8E-05
141	Homo sapiens, clone IMAGE:5269834, mRNA.	BC040593	-	1.00E-03	1.8E-05
142	full length insert cDNA clone YI72C08.	AF147400	-	1.00E-03	1.8E-05
143	cDNA FLJ40360 fis. clone TESTI2034401.	AK097679	-	1.00E-03	1.9E-05
144	Human tandem repeat region from facioscapulohumeral muscular dystrophy-associated mRNA clone cDNAdelta4.	U21072	-	1.00E-03	1.9E-05
145	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA.	NM_000963	PTGS2	1.00E-03	2.0E-05
146	T-cell receptor delta chain (TCRDV1J1) mRNA, partial cds.	U91141	-	1.00E-03	2.0E-05
147	kinesin family member 9 (KIF9), mRNA.	NM_022342	KIF9	1.00E-03	2.0E-05
148	hypothetical protein DKFZp434L142 (DKFZp434L142), mRNA.	NM_016613	DKFZp434L142	1.00E-03	2.0E-05
149	T-cell receptor delta chain (TCRDV1J1) mRNA, partial cds.	U91143	-	1.00E-03	2.0E-05
150	full length insert cDNA clone YY72H05.	AF088005	-	1.00E-03	2.0E-05
151	cDNA FLJ35056 fis. clone OCBFF2018581.	AK092375	-	1.00E-03	2.0E-05
152	engulfment and cell motility 3 (ced-12 homolog, C. elegans) (ELMO3).	NM_024712	ELMO3	1.00E-03	2.0E-05
153	HSPC163 protein (HSPC163), mRNA.	NM_014184	HSPC163	1.00E-03	2.1E-05
154	Homo sapiens, similar to RIKEN cDNA 1110018M03, clone MGC:24932 IMAGE:4938507, mRNA, complete cds.	BC026873	LOC387758	1.00E-03	2.1E-05
155	cDNA FLJ11832 fis. clone HEMBA1006566.	AK021894	ANK2	1.00E-03	2.1E-05
156	mRNA: cDNA DKFZp667I0318 (from clone DKFZp667I0318).	AL832283	-	1.00E-03	2.1E-05
157	partial mRNA; ID LG141-8A.	AJ227881	-	1.00E-03	2.1E-05
158	cDNA FLJ39665 fis. clone SMINT2007294.	AK096984	-	1.00E-03	2.2E-05
159	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 13 (SERPINB13), mRNA.	NM_012397	SERPINB13	1.00E-03	2.2E-05
160	Homo sapiens, clone IMAGE:4732808, mRNA.	BC029450	SLC33A1	1.00E-03	2.2E-05
161	Homo sapiens, clone IMAGE:4108565, mRNA, partial cds.	BC030635	-	1.00E-03	2.2E-05
162	metaxin 2 (MTX2), mRNA.	NM_006554	MTX2	1.00E-03	2.3E-05
163	Homo sapiens, clone IMAGE:5274185, mRNA.	BC040544	-	1.00E-03	2.3E-05
164	potassium channel, subfamily K, member 12 (KCNK12), mRNA.	NM_022055	KCNK12	1.00E-03	2.3E-05
165	603175427F1 NIH_MGC_121 cDNA clone IMAGE:5239687 5, mRNA sequence.	BI522474	-	1.00E-03	2.3E-05
166	leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA.	NM_021020	LZTS1	1.00E-03	2.3E-05
167	hypothetical protein MGC23980 (MGC23980), transcript variant 2, mRNA.	NM_145005	C9orf72	1.00E-03	2.3E-05
168	interleukin 28 receptor, alpha (interferon, lambda receptor) (IL28RA), transcript variant 1, mRNA.	NM_170743	IL28RA	1.00E-03	2.3E-05
169	cDNA FLJ36669 fis. clone UTERU2004015.	AK093988	LOC286299	1.00E-03	2.3E-05
170	cDNA FLJ34583 fis. clone KIDNE2008666.	AK091902	TMEM17	1.00E-03	2.4E-05
171	AGENCOURT_10425903 NIH_MGC_79 cDNA clone IMAGE:6663015 5, mRNA sequence.	BU929224	-	1.00E-03	2.4E-05
172	mRNA: cDNA DKFZp547E096 (from clone DKFZp547E096).	AL359603	GTF2IRD2	1.00E-03	2.4E-05
173	solute carrier family 15 (H+/peptide transporter), member 2 (SLC15A2), mRNA.	NM_021082	SLC15A2	1.00E-03	2.4E-05
174	ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA.	NM_007332	TRPA1	1.00E-03	2.5E-05
175	cDNA FLJ30210 fis. clone BRACE2001588.	AK054772	-	1.00E-03	2.5E-05
176	hypothetical protein FLJ20825 (FLJ20825), mRNA.	NM_017962	-	1.00E-03	2.5E-05

177	cDNA FLJ90572 fis. clone OVARC1001727.	AK075053	PLGB1	1.00E-03	2.5E-05
178	cDNA FLJ35018 fis. clone OCBFF2014386.	AK092337	-	1.00E-03	2.5E-05
179	mRNA, cDNA DKFZp451E1916 (from clone DKFZp451E1916).	AL832577	PHACTR3	1.00E-03	2.5E-05
180	zyxin (ZYG). mRNA.	NM_003461	ZYG	1.00E-03	2.5E-05
181	mRNA for KIAA2022 protein.	AB095942	KIAA2022	1.00E-03	2.5E-05
182	mRNA: cDNA DKFZp451E1618 (from clone DKFZp451E1618).	AL832630	-	1.00E-03	2.5E-05
183	cDNA FLJ33679 fis. clone BRAWH2002352.	AK090998	TCF7L2	1.00E-03	2.5E-05
184	AU125832 NT2RM4 cDNA clone NT2RM4002272 5. mRNA sequence.	AU125832	NANOG	1.00E-03	2.6E-05
185	hypothetical protein FLJ11535 (FLJ11535), mRNA.	NM_024888	FLJ11535	1.00E-03	2.6E-05
186	H.sapiens 5 mRNA of PECAM-1 molecule.	X96849	PECAM1	1.00E-03	2.6E-05
187	clone FLB5448 PRO1433 mRNA, complete cds.	AF130107	SLICK	1.00E-03	2.6E-05
188	cDNA FLJ35811 fis. clone TESTI2006045.	AK093130	LOC283129	1.00E-03	2.6E-05
189	cDNA FLJ12901 fis. clone NT2RP2004339.	AK022963	-	1.00E-03	2.6E-05
190	hypothetical protein MGC32020 (MGC32020), mRNA.	NM_152266	MGC32020	1.00E-03	2.7E-05
191	DNA (cytosine-5-)-methyltransferase 3 alpha (DNMT3A), mRNA.	NM_022552	DNMT3A	1.00E-03	2.7E-05
192	hypothetical protein FLJ22313 (FLJ22313), mRNA.	NM_022373	FLJ22313	1.00E-03	2.7E-05
193	cDNA FLJ37527 fis. clone BRCAN2011946.	AK094846	ELL3	1.00E-03	2.7E-05
194	Williams-Beuren syndrome chromosome region 17 (WBSR17), mRNA.	NM_022479	WBSR17	1.00E-03	2.7E-05
195	cDNA FLJ38601 fis. clone HEART2003781.	AK095920	BCAR3	1.00E-03	2.8E-05
196	Homo sapiens, clone IMAGE:4272661. mRNA.	BC015196	-	1.00E-03	2.8E-05
197	Homo sapiens, clone IMAGE:5301965. mRNA.	BC039413	TTC10	1.00E-03	2.9E-05
198	neurobeachin (NBEA), mRNA.	NM_015678	NBEA	1.00E-03	2.9E-05
199	colony stimulating factor 2 (granulocyte-macrophage) (CSF2), mRNA.	NM_000758	CSF2	1.00E-03	2.9E-05
200	Homo sapiens, clone IMAGE:4747257. mRNA.	BC039180	C9orf148	1.00E-03	2.9E-05
201	Homo sapiens, clone IMAGE:4332981. mRNA.	BC015999	-	1.00E-03	2.9E-05
202	mRNA full length insert cDNA clone EUROIMAGE 1019864.	AL109782	SIAT6	1.00E-03	2.9E-05
203	cargo selection protein (mannose 6 phosphate receptor binding protein) (TIP47), mRNA.	NM_005817	M6PRBP1	1.00E-03	2.9E-05
204	hypothetical protein FLJ22233 (FLJ22233), mRNA.	NM_024959	SLC24A6	1.00E-03	2.9E-05
205	Homo sapiens, clone MGC:13162 IMAGE:3010103, mRNA, complete cds.	BC006438	-	1.00E-03	2.9E-05
206	cDNA FLJ38312 fis. clone FCBBF3021506.	AK095631	FLJ43806	1.00E-03	2.9E-05
207	Human mRNA fragment for ceruloplasmin (aa 530-580).	X04136	CP	1.00E-03	3.0E-05
208	Homo sapiens. Similar to down-regulated by Ctnnb1, a, clone MGC:39518 IMAGE:5267063, mRNA, complete cds.	BC039295	MGC39518	1.00E-03	3.0E-05
209	Homo sapiens, clone IMAGE:3950788, mRNA.	BC018655	-	1.00E-03	3.0E-05
210	ATPase, Ca++ transporting, ubiquitous (ATP2A3), mRNA.	NM_005173	ATP2A3	1.00E-03	3.1E-05
211	cDNA FLJ35203 fis. clone PLACE6018441, moderately similar to Mus musculus peroxisomal long chain acyl-CoA thioesterase 1b (Pte1b) gene.	AK092522	ZNF545	1.00E-03	3.1E-05
212	clone IgM5588 immunoglobulin M heavy chain mRNA, partial cds.	AF267837	-	1.00E-03	3.1E-05
213	Cri-du-chat region mRNA, clone CSC8.	U52830	-	1.00E-03	3.1E-05
214	EST390979 MAGE resequences, MAGP cDNA, mRNA sequence.	AW978870	SMAD4	1.00E-03	3.1E-05
215	AGENCOURT_6393497 NIH_MGC_72 cDNA clone IMAGE:5528058 5, mRNA sequence.	BM450047	-	1.00E-03	3.1E-05
216	hypothetical protein DKFZp564D0478 (DKFZP564D0478), mRNA.	NM_032125	KFZP564D047	1.00E-03	3.2E-05
217	full length insert cDNA clone YT85E08.	AF085971	-	1.00E-03	3.2E-05
218	Homo sapiens, clone IMAGE:4821449. mRNA, partial cds.	BC030596	LOC400794	1.00E-03	3.3E-05
219	hypothetical protein BC014341 (LOC116123), mRNA.	NM_138784	LOC116123	1.00E-03	3.3E-05
220	myeloid leukemia factor 1 (MLF1), mRNA.	NM_022443	MLF1	1.00E-03	3.3E-05
221	solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA.	NM_003051	SLC16A1	1.00E-03	3.3E-05
222	UI-CF-FN0-aer-c-04-0-UI.s1 UI-CF-FN0 cDNA clone UI-CF-FN0-aer-c-04-0-UI 3. mRNA sequence.	BU609011	MGC33556	1.00E-03	3.3E-05
223	cDNA FLJ13665 fis. clone PLACE1011650.	AK023727	-	1.00E-03	3.3E-05
224	cDNA FLJ34816 fis. clone NT2NE2007877.	AK092135	-	1.00E-03	3.3E-05
225	om18a12.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1541374 3, mRNA sequence.	AA927867	-	1.00E-03	3.4E-05
226	mRNA for FLJ00409 protein.	AK090485	PIP5K2A	1.00E-03	3.4E-05
227	cDNA FLJ30556 fis. clone BRAWH2003832.	AK055118	PKNOX2	1.00E-03	3.4E-05
228	hypothetical protein FLJ25680 (FLJ25680), mRNA.	NM_153216	FLJ25680	1.00E-03	3.5E-05
229	dishevelled, dsh homolog 3 (Drosophila) (DVL3), mRNA.	NM_004423	DVL3	1.00E-03	3.5E-05
230	eyes absent homolog 3 (Drosophila) (EYA3), transcript variant 1, mRNA.	NM_001990	EYA3	1.00E-03	3.7E-05
231	603045296F1 NIH_MGC_116 cDNA clone IMAGE:5185775 5, mRNA sequence.	BI760398	-	1.00E-03	3.7E-05
232	cDNA FLJ31430 fis. clone NT2NE2000546.	AK055992	-	1.00E-03	3.7E-05
233	retina and anterior neural fold homeobox (RAX), mRNA.	NM_013435	RAX	1.00E-03	3.8E-05
234	neurogenin 1 (NEUROG1), mRNA.	NM_006161	NEUROG1	1.00E-03	3.8E-05
235	Homo sapiens, clone IMAGE:4824433. mRNA.	BC034426	-	1.00E-03	3.8E-05
236	Human protein-tyrosine phosphatase (hPTP1E) mRNA, 5UTR sequence.	U12131	PTPN13	1.00E-03	3.9E-05
237	solute carrier family 27 (fatty acid transporter), member 4 (SLC27A4),	NM_005094	SLC27A4	1.00E-03	3.9E-05
238	Homo sapiens, clone IMAGE:4295422. mRNA.	BC007114	B1	1.00E-03	3.9E-05
239	hypothetical protein FLJ30532 (FLJ30532), mRNA.	NM_144724	MARVELD2	1.00E-03	3.9E-05

240	mRNA: cDNA DKFZp666B224 (from clone DKFZp666B224).	AL833001	ELOVL5	1.00E-03	4.0E-05
241	mRNA: cDNA DKFZp313M2114 (from clone DKFZp313M2114).	AL832061	ARRB2	1.00E-03	4.0E-05
242	mRNA: cDNA DKFZp667E0314 (from clone DKFZp667E0314).	AL833364	LOC283314	1.00E-03	4.1E-05
243	olfactory receptor, family 1, subfamily A, member 1 (OR1A1), mRNA.	NM_014565	OR1A1	1.00E-03	4.2E-05
244	cDNA FLJ12003 fis, clone HEMBB1001537.	AK022065	RAB5A	1.00E-03	4.2E-05
245	cDNA FLJ25178 fis, clone CBR09176.	AK057907	-	1.00E-03	4.4E-05
246	Homo sapiens, clone IMAGE:3689998, mRNA.	BC021164	-	1.00E-03	4.4E-05
247	cDNA FLJ20762 fis, clone HEP00177.	AK000769	IGF2R	1.00E-03	4.5E-05
248	arfaptin 1 (HSU52521), mRNA.	NM_014447	ARFIP1	1.00E-03	4.6E-05
249	cDNA FLJ33341 fis, clone BRACE2002582.	AK090660	KIAA0493	1.00E-03	4.6E-05
250	hypothetical protein MGC16075 (MGC16075), mRNA.	NM_032761	-	1.00E-03	4.8E-05
251	PRO2738 mRNA, complete cds.	AF116712	-	1.00E-03	4.9E-05
252	putative glioblastoma cell differentiation-related (GDBR1), mRNA.	NM_016172	UBADC1	1.00E-03	5.0E-05
253	clone BGL3 mRNA sequence.	AY034471	-	1.00E-03	5.0E-05
254	sulfotransferase, estrogen-preferring (STE), mRNA.	NM_005420	SULT1E1	1.00E-03	5.0E-05
255	mRNA: cDNA DKFZp667H065 (from clone DKFZp667H065).	AL833184	P2RY8	1.00E-03	5.0E-05
256	Homo sapiens, clone IMAGE:3454421, mRNA.	BC010534	SEC15L2	1.00E-03	5.1E-05
257	deoxyribonuclease I (DNASE1), mRNA.	NM_005223	DNASE1	1.00E-03	5.2E-05
258	hyaluronoglucosaminidase 4 (HYAL4), mRNA.	NM_012269	HYAL4	1.00E-03	5.3E-05
259	clone FE1281 T-cell receptor delta chain (TCRDV1J1) mRNA, partial cds.	U90990	-	1.00E-03	5.3E-05
260	G-protein coupled receptor SALPR: somatostatin and angiotensin-like peptide receptor (SALPR), mRNA.	NM_016568	RLN3R1	1.00E-03	5.4E-05
261	sialyltransferase 8E (alpha-2, 8-polysialyltransferase) (SIAT8E), mRNA.	NM_013305	SIAT8E	1.00E-03	5.5E-05
262	zinc finger protein 205 (ZNF205), mRNA.	NM_003456	ZNF205	1.00E-03	5.6E-05
263	Homo sapiens, clone IMAGE:4827370, mRNA.	BC031948	FLJ13855	1.00E-03	5.6E-05
264	LIM domain binding 1 (LDB1), mRNA.	NM_003893	LDB1	1.00E-03	5.6E-05
265	cDNA FLJ37977 fis, clone CTONG2010276.	AK095296	-	1.00E-03	5.6E-05
266	AV762221 MDS cDNA clone MDS CBD08 5, mRNA sequence.	AV762221	NASP	1.00E-03	5.6E-05
267	full length insert cDNA clone YP75C01.	AF147422	KIAA1279	1.00E-03	5.6E-05
268	PP565 mRNA, complete cds.	AF258587	-	1.00E-03	5.7E-05
269	Kaiso (ZNF-kaiso), mRNA.	NM_006777	ZBTB33	1.00E-03	5.8E-05
270	matrix metalloproteinase 21 (MMP21), mRNA.	NM_147191	MMP21	1.00E-03	5.9E-05
271	G protein-coupled receptor MRGX1 (MRGX1), mRNA.	NM_147199	MRGX1	1.00E-03	5.9E-05
272	hypothetical protein FLJ12476 (FLJ12476), mRNA.	NM_022784	FLJ12476	1.00E-03	6.0E-05
273	KIAA1880 protein (KIAA1880), mRNA.	NM_152733	BTBD9	1.00E-03	6.1E-05
274	protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA.	NM_017431	PRKAG3	1.00E-03	6.2E-05
275	carboxypeptidase A5 (CPA5), mRNA.	NM_080385	CPA5	1.00E-03	6.2E-05
276	Homo sapiens. Similar to RIKEN cDNA 1200015N20 gene, clone MGC:33233 IMAGE:5270033, mRNA, complete cds.	BC036453	FAM13C1	1.00E-03	6.3E-05
277	protein kinase, cAMP-dependent, catalytic, beta (PRKACB), mRNA.	NM_002731	PRKACB	1.00E-03	6.3E-05
278	melanoma antigen, family A, 2, copy b (MAGEA2b), mRNA.	NM_153488	MAGEA2	1.00E-03	6.4E-05
279	NEU1 protein (ZNEU1), mRNA.	NM_016215	EGFL7	1.00E-03	6.5E-05
280	Homo sapiens, clone IMAGE:4792693, mRNA.	BC030088	-	1.00E-03	6.6E-05
281	cDNA FLJ36933 fis, clone BRACE2005329.	AK094252	-	1.00E-03	6.8E-05
282	602975268F1 NIH_MGC_12 cDNA clone IMAGE:5114537 5, mRNA	BI256378	LPHN1	1.00E-03	6.9E-05
283	Homo sapiens, clone IMAGE:5480214, mRNA.	BC041649	-	1.00E-03	7.0E-05
284	clone IgM5587-2 immunoglobulin M heavy chain mRNA, partial cds.	AF267836	-	1.00E-03	7.1E-05
285	Human BRCA2 region, mRNA sequence CG017.	U50524	LOC196549	1.00E-03	7.1E-05
286	UI-E-EJ0-ahf-m-23-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahf-m-23-0-UI 5, mRNA sequence.	BM711999	-	1.00E-03	7.2E-05
287	cut-like 1, CCAAT displacement protein (Drosophila) (CUTL1), mRNA.	NM_001913	CUTL1	1.00E-03	7.5E-05
288	hypothetical protein MGC21675 (MGC21675), mRNA.	NM_052861	MGC21675	1.00E-03	7.7E-05
289	HT001 protein (HT001), mRNA.	NM_014065	HT001	1.00E-03	7.7E-05
290	chromosome 14 open reading frame 69 (C14orf69), mRNA.	NM_152333	SLC25A29	1.00E-03	7.9E-05
291	huntingtin (Huntington disease) (HD), mRNA.	NM_002111	HD	1.00E-03	7.9E-05
292	cDNA FLJ38404 fis, clone FEBRA2008542.	AK095723	ADCYAP1	1.00E-03	7.9E-05
293	polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA.	NM_002689	POLA2	1.00E-03	8.1E-05
294	tubby like protein 3 (TULP3), mRNA.	NM_003324	TULP3	1.00E-03	8.2E-05
295	Homo sapiens, clone IMAGE:4838152, mRNA.	BC034596	-	1.00E-03	8.5E-05
296	hypothetical protein MGC4562 (MGC4562), mRNA.	NM_133375	MGC4562	1.00E-03	9.0E-05
297	protease, serine, 7 (enterokinase) (PRSS7), mRNA.	NM_002772	PRSS7	1.00E-03	9.3E-05
298	ring finger protein 38 (RNF38), mRNA.	NM_022781	RNF38	1.00E-03	9.5E-05
299	cDNA FLJ38995 fis, clone NT2RI2019826.	AK096314	KLRC4	1.00E-03	9.6E-05
300	serine protease inhibitor, Kazal type 5 (SPINK5), mRNA.	NM_006846	SPINK5	1.00E-03	9.7E-05
301	patched homolog (Drosophila) (PTCH), mRNA.	NM_000264	PTCH	1.00E-03	1.0E-04
302	cDNA FLJ35222 fis, clone PROST2000835.	AK092541	-	1.00E-03	1.0E-04
303	full length insert cDNA clone ZD48A05.	AF086288	-	1.00E-03	1.0E-04
304	Human pre-T/NK cell associated protein (1F6) mRNA, 3 end.	L17326	-	1.00E-03	1.0E-04
305	AGENCOURT_8344424 NIH_MGC_110 cDNA clone IMAGE:6251298 5, mRNA sequence.	BQ685117	7A5	1.00E-03	1.0E-04

306	602154006F1 NIH MGC 83 cDNA clone IMAGE:4295161 5. mRNA	BF679569	-	1.00E-03	1.1E-04
307	cDNA FLJ38413 fis. clone FEBRA2009478.	AK095732	CACNB4	1.00E-03	1.1E-04
308	Homo sapiens, similar to mannosidase, alpha, class 1B, member 1, clone IMAGE:3623379, mRNA.	BC018639	-	1.00E-03	1.1E-04
309	Homo sapiens, clone IMAGE:3944699, mRNA.	BC025328	-	1.00E-03	1.1E-04
310	hypothetical protein FLJ21156 (FLJ21156), mRNA.	NM_024602	FLJ21156	1.00E-03	1.1E-04
311	cDNA FLJ36875 fis. clone ASTRO2019039.	AK094194	TTC15	1.00E-03	1.2E-04
312	hypothetical protein DKFZp434G0522 (DKFZp434G0522), mRNA.	NM_017566	KLHDC4	1.00E-03	1.2E-04
313	cDNA FLJ40354 fis. clone TESTI2033641.	AK097673	RP11-529L18.	1.00E-03	1.2E-04
314	mRNA; cDNA DKFZp313F0131 (from clone DKFZp313F0131).	AL832090	NHLRC2	1.00E-03	1.3E-04
315	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A (MGAT4A), mRNA.	NM_012214	MGC52110	1.00E-03	1.3E-04
316	retinoic acid induced 14 (RAI14), mRNA.	NM_015577	RAI14	1.00E-03	1.4E-04
317	cDNA FLJ30474 fis. clone BRAWH1000116.	AK055036	-	1.00E-03	1.5E-04
318	Pseudoautosomal GTP-binding protein-like (PGPL), mRNA.	NM_012227	GTPBP6	1.00E-03	1.8E-04
319	AUT-like 2, cysteine endopeptidase (S. cerevisiae) (AUTL2), mRNA.	NM_052936	APG4A	1.00E-03	1.8E-04
320	heat shock protein 75 (TRAP1), mRNA.	NM_016292	TRAP1	1.00E-03	1.8E-04
321	cDNA FLJ31075 fis. clone HSYRA2001484.	AK055637	-	1.00E-03	1.9E-04
322	alkaline phosphatase, placental-like 2 (ALPPL2), mRNA.	NM_031313	ALPPL2	1.00E-03	1.9E-04
323	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA.	NM_000152	GAA	1.00E-03	1.9E-04
324	inositol 1,4,5-trisphosphate 3-kinase C (ITPKC), mRNA.	NM_025194	ITPKC	1.00E-03	1.9E-04
325	hypothetical protein MGC16025 (MGC16025), mRNA.	NM_032923	-	1.00E-03	2.1E-04
326	clone 24707 mRNA sequence.	AF055007	MARCH-III	1.00E-03	2.1E-04
327	tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency) (TTPA), mRNA.	NM_000370	TTPA	1.00E-03	2.2E-04
328	H.sapiens mRNA within CEPH Mega-YAC 788H12, clone 23.	Y12021	-	1.00E-03	2.2E-04
329	Homo sapiens, clone IMAGE:5273319, mRNA.	BC037872	-	1.00E-03	2.4E-04
330	cDNA FLJ33091 fis. clone TRACH2000660.	AK057653	-	1.00E-03	2.7E-04
331	clone pbvb327 T cell receptor beta chain mRNA, partial cds.	AY006156	-	1.00E-03	3.0E-04
332	Homo sapiens, clone IMAGE:5270538, mRNA.	BC036258	-	1.00E-03	3.1E-04
333	cDNA FLJ32931 fis. clone TESTI2007452.	AK057493	-	1.00E-03	3.3E-04
334	Human mRNA, Xq terminal portion.	D16468	-	1.00E-03	3.4E-04
335	hypothetical protein PRO2859 (PRO2859), mRNA.	NM_018543	-	1.00E-03	3.4E-04
336	cDNA FLJ90641 fis. clone PLACE1004028.	AK075122	PTPNS1	1.00E-03	3.6E-04
337	Homo sapiens, LOC146745, clone IMAGE:5298923, mRNA.	BC031286	LOC201243	1.00E-03	3.7E-04
338	cDNA FLJ35891 fis. clone TESTI2009217.	AK093210	-	1.00E-03	3.7E-04
339	MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA.	NM_005919	MEF2B	1.00E-03	4.5E-04
340	(clone RA-SIR 65SR-10-1) T cell receptor alpha chain (TCRA) mRNA, partial cds.	L42807	-	1.00E-03	4.5E-04
341	cDNA FLJ35683 fis. clone SPLEN2019131.	AK093002	-	1.00E-03	4.9E-04
342	glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 1, mRNA.	NM_001509	GPX5	1.00E-03	5.8E-04
343	glial cells missing homolog 2 (Drosophila) (GCM2), mRNA.	NM_004752	GCM2	1.00E-03	6.3E-04
344	chromosome 21 open reading frame 87 (C21orf87), mRNA.	NM_153455	-	1.00E-03	6.8E-04
345	mutant dystrophin mRNA, partial cds.	AF181286	IL1RAPL1	1.00E-03	8.0E-04
346	mRNA for KIAA1034 protein, partial cds.	AB028957	SATB2	1.60E-01	1.4E-03
347	Human mRNA for KIAA0251 gene, partial cds.	D87438	KIAA0251	1.00E-03	1.8E-03
348	Homo sapiens, clone IMAGE:4638364, mRNA.	BC027727	-	1.00E-03	2.0E-03
349	cDNA FLJ40501 fis. clone TESTI2045171.	AK097820	-	5.30E-01	2.7E-03
350	Homo sapiens, similar to ubiquitin-protein ligase, clone MGC:27112 IMAGE:4838835, mRNA, complete cds.	BC034982	HACE1	1.00E-03	3.6E-03
351	UI-CF-DU1-aa1-j-15-0-UI.s1 UI-CF-DU1 cDNA clone UI-CF-DU1-aa1-j-15-0-UI 3, mRNA sequence.	BU675922	-	2.80E+00	7.8E-03
352	cDNA FLJ38531 fis. clone HCHON2001050.	AK095850	LOC87769	1.10E+00	9.7E-03
353	cDNA: FLJ21733 fis. clone COLF1876.	AK025386	-	1.90E+00	1.1E-02
354	KIAA0133 gene product (KIAA0133), mRNA.	NM_014777	KIAA0133	4.10E+00	1.1E-02
355	urocortin (UCN), mRNA.	NM_003353	UCN	6.40E+00	1.6E-02
356	E2F transcription factor 5, p130-binding (E2F5), mRNA.	NM_001951	E2F5	2.10E+00	1.7E-02
357	hypothetical protein FLJ31842 (FLJ31842), mRNA.	NM_152487	FLJ31842	1.70E+00	1.9E-02
358	protease inhibitor 15 (P115), mRNA.	NM_015886	P115	1.80E+00	1.9E-02
359	pp8961 mRNA, complete cds.	AF318368	-	4.60E+00	2.6E-02
360	proline rich 4 (lacrima) (PROL4), mRNA.	NM_007244	PRR4	6.50E+00	2.7E-02
361	hypothetical protein HS747E2A (HS747E2A), mRNA.	NM_015370	HS747E2A	3.30E+00	3.2E-02
362	metallothionein 1B (functional) (MT1B), mRNA.	NM_005947	MT1B	1.50E+02	3.3E-02
363	serum amyloid A2 (SAA2), mRNA.	NM_030754	SAA2	1.90E+02	3.4E-02
364	cDNA FLJ10095 fis. clone HEMBA1002430.	AK000957	-	4.00E+00	3.6E-02
365	RGC32 protein (RGC32), mRNA.	NM_014059	RGC32	1.40E+02	3.6E-02
366	arrestin, beta 1 (ARRB1), transcript variant 1, mRNA.	NM_004041	ARRB1	3.70E+00	3.8E-02
367	MR4-TN0112-051000-105-b05 TN0112 cDNA, mRNA sequence.	BF885230	LRPPRC	4.10E+00	3.9E-02

368	serum amyloid A1 (SAA1), mRNA.	NM_000331	SAA1	1.80E+02	4.0E-02
369	AGENCOURT_8232538 Lupski_sympathetic_trunk cDNA clone IMAGE:6191646 5, mRNA sequence.	BQ719128	CHRN2	4.80E+00	4.0E-02
370	Human isolate HR027 T cell receptor V-beta complementarity determining region 3 mRNA, partial cds.	U55097	-	4.80E+00	4.3E-02
371	zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia) (ZNF145), mRNA.	NM_006006	ZBTB16	2.30E+02	4.4E-02
372	cDNA FLJ32381 fis, clone SKMUS1000067.	AK056943	-	1.50E+01	4.5E-02
373	guanine nucleotide binding protein (G protein), beta 5 (GNB5), transcript variant 2, mRNA.	NM_016194	GNB5	4.80E+01	5.7E-02
374	aldehyde oxidase 1 (AOX1), mRNA.	NM_001159	AOX1	2.20E+02	6.2E-02
375	ADMP (ADMP), mRNA.	NM_145035	ADMP	1.20E+01	6.3E-02
376	cDNA FLJ10940 fis, clone OVARC1001162.	AK001802	IGFBP7	1.30E+01	6.4E-02
377	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA.	NM_139314	ANGPTL4	2.90E+02	6.7E-02
378	mRNA for KIAA1958 protein.	AB075838	KIAA1958	1.50E+01	6.7E-02
379	hypothetical protein PRO1489 (PRO1489), mRNA.	NM_018584	CaMKIIalpha	2.30E+02	7.2E-02
380	cDNA FLJ11056 fis, clone PLACE1004691.	AK001918	-	6.70E+00	7.4E-02
381	cDNA FLJ30682 fis, clone FCBBF2000214.	AK055244	LOC284244	3.40E+00	7.5E-02
382	Homo sapiens, clone IMAGE:4830065, mRNA, partial cds.	BC030605	-	1.10E+01	7.6E-02
383	cDNA FLJ34549 fis, clone HLUNG2009253.	AK091868	LOC285713	2.30E+01	7.7E-02
384	Homo sapiens, clone IMAGE:5273088, mRNA.	BC041362	-	1.30E+01	7.8E-02
385	tissue inhibitor of metalloproteinase 4 (TIMP4), mRNA.	NM_003256	TIMP4	1.10E+02	7.9E-02
386	PERQ amino acid rich, with GYF domain 1 (PERQ1), mRNA.	NM_022574	PERQ1	7.70E+00	8.1E-02
387	cDNA FLJ33850 fis, clone CTONG2005615.	AK091169	TMEM30B	3.70E+00	8.3E-02
388	clone IgM5575 immunoglobulin M heavy chain mRNA, partial cds.	AF267839	-	1.20E+01	8.3E-02
389	cholecystokinin (CCK), mRNA.	NM_000729	CCK	1.80E+00	8.4E-02
390	cDNA: FLJ21157 fis, clone CAS09937.	AK024810	FNBP3	4.30E+01	8.8E-02
391	dickkopf homolog 1 (Xenopus laevis) (DKK1), mRNA.	NM_012242	DKK1	1.10E+03	8.8E-02
392	mRNA from chromosome 5q21-22, clone:FBR35.	AB002445	DCP2	9.70E+00	8.9E-02
393	cDNA FLJ12971 fis, clone NT2RP2005882.	AK023033	-	5.00E+00	8.9E-02
394	metallothionein 1L (MT1L), mRNA.	NM_002450	-	8.20E+02	9.1E-02
395	forkhead box O1A (rhabdomyosarcoma) (FOXO1A), mRNA.	NM_002015	FOXO1A	3.80E+02	1.0E-01

Table 3 31 genes classified in ossification of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Contr of signal_norm)
1	sialoprotein precursor (IBSP) mRNA, complete cds.	J05213	IBSP	9.8E-02	3.5E+02
2	osteoclast stimulating factor 1 (OSTF1), mRNA.	NM_012383	OSTF1	6.2E-02	2.2E+02
3	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA.	NM_000582	SPP1	3.6E-01	2.3E+01
4	secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA.	NM_003118	SPARC	3.6E+01	5.9E+00
5	runt-related transcription factor 2 (RUNX2), mRNA.	NM_004348	RUNX2	2.7E-01	3.6E+00
6	cDNA FLJ36223 fis, clone THYMU2000982.	AK093542	ANKH	1.9E-01	2.6E+00
7	cadherin 11, type 2, OB-cadherin (osteoblast) (CDH11), transcript variant 2, full length insert cDNA YN63H06.	NM_033664	-	9.1E+00	2.3E+00
8	amelogenin (X chromosome, amelogenesis imperfecta 1) (AMELX), mRNA.	AF075041	ANKH	2.2E-01	2.0E+00
9	hypothetical protein FKSG28 (FKSG28), mRNA.	NM_001142	AMELX	1.9E-01	1.6E+00
10	bone morphogenetic protein 1 (BMP1), transcript variant BMP1-3, mRNA.	NM_030929	KAZALD1	1.9E-01	1.6E+00
11	CBFA1/OSF2 transcription factor mRNA, partial cds.	NM_006129	BMP1	1.8E-01	1.3E+00
12	DKFZP586N2124 protein (DKFZP586N2124), mRNA.	AF053952	RUNX2	4.4E-01	1.3E+00
13	cDNA FLJ11424 fis, clone HEMBA1001026.	NM_015424	CHRD2	3.0E-01	1.2E+00
14	bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA.	AK021486	BMP5	2.2E-01	1.2E+00
15	likely ortholog of mouse and rat twist-related bHLH protein Dermo-1 (DERM1), mRNA.	NM_001202	BMP4	1.6E-01	1.2E+00
16	dentin matrix acidic phosphoprotein (DMP1), mRNA.	NM_057179	TWIST2	1.4E-01	1.1E+00
17	TRAF6-inhibitory zinc finger protein (TIZ), mRNA.	NM_004407	DMP1	1.6E-01	1.1E+00
18	ankylosis, progressive homolog (mouse) (ANKH), transcript variant 2, mRNA.	NM_138330	TIZ	1.9E-01	1.0E+00
19	bone morphogenetic protein 2 (BMP2), mRNA.	NM_054027	ANKH	3.7E-01	1.0E+00
20	full length insert cDNA clone YR30C05.	NM_001200	BMP2	1.6E-01	9.5E-01
21	alpha-2-HS-glycoprotein (AHSG), mRNA.	AF087960	RUNX2	2.3E-01	9.4E-01
22	bone morphogenetic protein 2 (osteogenic protein 2) (BMP8), mRNA.	NM_001622	AHSG	1.6E-01	9.2E-01
23	sclerosteosis (SOST), mRNA.	NM_001720	BMP8B	1.7E-01	9.2E-01
24	ameloblastin, enamel matrix protein (AMBN), mRNA.	NM_025237	SOST	7.9E-01	8.7E-01
25	histatin 3 (HTN3), mRNA.	NM_016519	AMBN	2.5E-01	8.3E-01
26	cDNA FLJ33715 fis, clone BRAWH2008577.	NM_000200	HTN3	6.0E-01	7.6E-01
27	histatin 1 (HTN1), mRNA.	AK091034	OSTF1	2.1E-01	7.4E-01
28	tuftelin 1 (TUFT1), mRNA.	NM_002159	HTN1	1.1E+00	6.3E-01
29	matrix Gla protein (MGP), mRNA.	NM_020127	TUFT1	9.4E-02	5.6E-01
30	tuftelin interacting protein 11 (TFIP11), mRNA.	NM_000900	MGP	5.0E-01	4.2E-01
31	tuftelin interacting protein 11 (TFIP11), mRNA.	NM_012143	TFIP11	1.5E+00	3.6E-01

Table 4 132 genes classified in extracellular matrix (sensu Metazoa) of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Control signal_norm)
1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA.	NM_000582	SPP1	3.6E-01	2.3E+01
2	Human thrombospondin mRNA.	M81339	THBS2	1.6E+01	2.1E+01
3	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 12 (ADAMTS12), mRNA.	NM_030955	ADAMTS12	4.8E-01	1.1E+01
4	lumican (LUM), mRNA.	NM_002345	LUM	1.3E+01	1.0E+01
5	cartilage associated protein (CRTAP), mRNA.	NM_006371	CRTAP	2.8E+00	7.6E+00
6	cartilage linking protein 1 (CRTLI), mRNA.	NM_001884	HAPLN1	3.3E+00	6.7E+00
7	fibrillin 1 (Marfan syndrome) (FBN1), mRNA.	NM_000138	FBN1	4.2E+00	5.5E+00
8	lysyl oxidase (LOX), mRNA.	NM_002317	LOX	3.2E+00	4.5E+00
9	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK), mRNA.	NM_004598	SPOCK	1.9E+01	4.5E+00
10	Microfibril-associated glycoprotein-2 (MAGP2), mRNA.	NM_003480	MFAP5	9.7E+00	4.4E+00
11	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (ADAMTS5), mRNA.	NM_007038	ADAMTS5	3.7E+00	4.3E+00
12	osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA.	NM_006475	POSTN	2.1E+01	3.8E+00
13	clone G4-10-3 mucin 4 (MUC4) mRNA, partial cds.	AF058804	MUC4	3.6E-01	3.7E+00
14	cDNA FLJ38586 fis, clone HCHON2009384.	AK095905	ADAMTS5	5.6E-01	3.7E+00
15	matrix metalloproteinase 13 (collagenase 3) (MMP13), mRNA.	NM_002427	MMP13	2.3E-01	3.5E+00
16	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA.	NM_004105	EFEMP1	1.7E+01	3.4E+00
17	matriin 2 (MATN2), transcript variant 1, mRNA.	NM_002380	MATN2	4.0E-01	3.4E+00
18	chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA.	NM_004385	CSPG2	1.5E+00	3.3E+00
19	hyaluronan synthase 1 (HAS1), mRNA.	NM_001523	HAS1	3.0E+00	3.0E+00
20	clone IMAGE:241742, mRNA sequence.	AF339802	GPC5	5.5E-01	3.0E+00
21	AU140984 PLACE4 cDNA clone PLACE4000606 5', mRNA sequence.	AU140984	VWF	1.7E-01	2.8E+00
22	full length insert cDNA clone YP42D06.	AF085885	IMP1	1.8E-01	2.7E+00
23	extracellular matrix protein 2, female organ and adipocyte specific (ECM2), mRNA.	NM_001393	ECM2	7.5E-01	2.6E+00
24	matrix metalloproteinase 20 (enamelysin) (MMP20), mRNA.	NM_004771	MMP20	2.7E-01	2.6E+00
25	latent transforming growth factor beta binding protein 2 (LTBP2), mRNA.	NM_000428	LTBP2	3.1E+01	2.6E+00
26	clone IMAGE:248602, mRNA sequence.	AF339805	GPC5	2.7E-01	2.3E+00
27	collagen, type VI, alpha 3 (COL6A3), transcript variant 1, mRNA.	NM_004369	COL6A3	2.2E+01	2.2E+00
28	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA.	NM_003254	TIMP1	4.7E+01	2.1E+00
29	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA.	NM_004530	MMP2	2.2E-01	2.0E+00
30	Human tenascin mRNA, partial CDS, AD1 type III repeat region.	M96686	TNC	4.2E-01	2.0E+00
31	fibronectin 1 (FN1), transcript variant 1, mRNA.	NM_002026	FN1	1.5E+00	2.0E+00
32	MSTP031 protein (MSTP031), mRNA.	NM_032035	-	7.3E+00	2.0E+00
33	zona pellucida glycoprotein 4 (ZP4), mRNA.	NM_021186	ZP4	2.5E-01	1.9E+00
34	microfibrillar-associated protein 4 (MFAP4), mRNA.	NM_002404	MFAP4	1.8E+00	1.9E+00
35	netrin 1 (NTN1), mRNA.	NM_004822	NTN1	2.2E-01	1.9E+00
36	biglycan (BGN), mRNA.	NM_001711	BGN	1.9E-01	1.8E+00
37	cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA.	NM_000095	COMP	1.3E+00	1.8E+00
38	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 13 (ADAMTS13), transcript variant 1,	NM_139025	ADAMTS13	2.0E-01	1.8E+00
39	transforming growth factor, beta-induced, 68kDa (TGFB1), mRNA.	NM_000358	TGFB1	1.1E+01	1.8E+00
40	fibulin 2 (FBLN2), mRNA.	NM_001998	FBLN2	2.8E+00	1.7E+00
41	proline arginine-rich end leucine-rich repeat protein (PRELP), mRNA.	NM_002725	PRELP	1.0E+00	1.7E+00
42	ADAMTS-like 1 (ADAMTSL1), transcript variant 3, mRNA.	NM_139264	ADAMTSL1	1.6E-01	1.7E+00
43	decorin (DCN), transcript variant A1, mRNA.	NM_001920	DCN	2.8E+01	1.6E+00
44	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA.	NM_001276	CHI3L1	1.6E-01	1.6E+00
45	proteoglycan link protein mRNA, complete cds.	AY037161	HAPLN3	6.2E-01	1.6E+00
46	amelogenin (X chromosome, amelogenesis imperfecta 1) (AMELX),	NM_001142	AMELX	1.9E-01	1.6E+00
47	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1 (cartilage-derived) (CLECSF1), mRNA.	NM_005752	CLECSF1	1.9E-01	1.6E+00
48	netrin G1f (KIAA0976), mRNA.	NM_014917	NTNG1	2.5E-01	1.5E+00
49	cDNA FLJ11443 fis, clone HEMBA1001330.	AK021505	GPC6	1.5E-01	1.5E+00
50	EMILIN-like protein EndoGlyx-1 (ENDOGLYX1), mRNA.	NM_024756	MMRN2	8.4E-01	1.5E+00
51	netrin G2 (KIAA1857), mRNA.	NM_032536	NTNG2	1.7E-01	1.5E+00
52	extracellular matrix protein 1 (ECM1), transcript variant 1, mRNA.	NM_004425	ECM1	1.3E+00	1.5E+00

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53	putative emu1 (LOC129080), mRNA.	NM_133455	EMID1	5.6E-01	1.5E+00
54	glypican 1 (GPC1), mRNA.	NM_002081	GPC1	1.0E+00	1.5E+00
55	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive) (SPG7), mRNA.	NM_003119	SPG7	1.7E-01	1.4E+00
56	collagen, type XVI, alpha 1 (COL16A1), mRNA.	NM_001856	COL16A1	2.6E+00	1.4E+00
57	latent transforming growth factor beta binding protein 4 (LTBP4), mRNA.	NM_003573	LTBP4	2.9E-01	1.4E+00
58	full length insert cDNA clone YX36D02.	AF087991	NTNG1	2.3E-01	1.4E+00
59	DiGeorge syndrome critical region gene 6 (DGCR6), mRNA.	NM_005675	DGCR6	5.1E-01	1.4E+00
60	connective tissue growth factor (CTGF), mRNA.	NM_001901	CTGF	1.4E+01	1.4E+00
61	dermatan sulfate proteoglycan 3 (DSPG3), mRNA.	NM_004950	DSPG3	2.2E-01	1.4E+00
62	elastin microfibril interface located protein (EMILIN), mRNA.	NM_007046	EMILIN1	7.0E-01	1.4E+00
63	tenascin C (hexabrachion) (TNC), mRNA.	NM_002160	TNC	3.3E-01	1.3E+00
64	specific granule protein (28 kDa) (SGP28), mRNA.	NM_006061	CRISP3	6.5E-01	1.3E+00
65	collagen triple helix repeat containing 1 (CTHRC1), mRNA.	NM_138455	CTHRC1	7.2E+00	1.3E+00
66	latent transforming growth factor beta binding protein 1 (LTBP1), mRNA.	NM_000627	LTBP1	4.7E+00	1.3E+00
67	glypican 4 (GPC4), mRNA.	NM_001448	GPC4	1.5E+00	1.2E+00
68	superoxide dismutase 3, extracellular (SOD3), mRNA.	NM_003102	SOD3	1.4E+00	1.2E+00
69	laminin, gamma 3 (LAMC3), mRNA.	NM_006059	LAMC3	2.8E-01	1.2E+00
70	clone IMAGE.205688, mRNA sequence.	AF339787	GPC5	3.3E-01	1.2E+00
71	mucin 4, tracheobronchial (MUC4), transcript variant 1, mRNA.	NM_018406	MUC4	1.8E-01	1.2E+00
72	microfibrillar-associated protein 1 (MFAP1), mRNA.	NM_005926	MFAP1	3.1E-01	1.2E+00
73	dystroglycan 1 (dystrophin-associated glycoprotein 1) (DAG1), mRNA.	NM_004393	DAG1	2.7E-01	1.1E+00
74	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA.	NM_000362	TIMP3	4.0E-01	1.1E+00
75	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA.	NM_006988	ADAMTS1	6.2E+00	1.1E+00
76	spondin 2, extracellular matrix protein (SPON2), mRNA.	NM_012445	SPON2	1.3E+00	1.1E+00
77	fibromodulin (FMOD), mRNA.	NM_002023	FMOD	3.5E+00	1.1E+00
78	keratocan (KERA), mRNA.	NM_007035	KERA	2.1E-01	1.1E+00
79	laminin, beta 3 (LAMB3), mRNA.	NM_000228	LAMB3	6.8E-01	1.1E+00
80	hypothetical protein FLJ14927 (FLJ14927), mRNA.	NM_032863	FRAS1	2.9E-01	1.1E+00
81	cDNA: FLJ22017 fis, clone HEP07429.	AK025670	NTN4	2.1E-01	1.1E+00
82	fibulin 5 (FBLN5), mRNA.	NM_006329	FBLN5	3.1E+00	1.1E+00
83	dentin matrix acidic phosphoprotein (DMP1), mRNA.	NM_004407	DMP1	1.6E-01	1.1E+00
84	von Willebrand factor (VWF), mRNA.	NM_000552	VWF	3.8E-01	1.0E+00
85	interphotoreceptor matrix proteoglycan 2 (IMPG2), mRNA.	NM_016247	IMPG2	9.7E-01	1.0E+00
86	spondin 1, (f-spondin) extracellular matrix protein (SPON1), mRNA.	NM_006108	SPON1	5.4E-01	1.0E+00
87	tissue inhibitor of metalloproteinase 2 (TIMP2), mRNA.	NM_003255	TIMP2	3.3E+00	9.8E-01
88	cDNA FLJ38522 fis, clone HCHON2000818.	AK095841	FBN1	4.9E-01	9.4E-01
89	tenascin XB (TNXB), transcript variant XB, mRNA.	NM_019105	TNXB	3.2E-01	9.4E-01
90	cDNA FLJ11419 fis, clone HEMBA1000985.	AK021481	GPC6	8.2E-02	9.2E-01
91	thrombospondin 3 (THBS3), mRNA.	NM_007112	THBS3	7.6E-01	9.2E-01
92	collagen, type IX, alpha 1 (COL9A1), transcript variant 1, mRNA.	NM_001851	COL9A1	2.2E-01	9.2E-01
93	netrin 2-like (chicken) (NTN2L), mRNA.	NM_006181	NTN2L	5.5E-01	9.2E-01
94	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA.	NM_000501	ELN	3.1E-01	9.2E-01
95	lectin, galactoside-binding, soluble, 3 binding protein (LGALS3BP),	NM_005567	LGALS3BP	1.8E-01	9.1E-01
96	microfibrillar-associated protein 2 (MFAP2), transcript variant 1, mRNA.	NM_017459	MFAP2	4.0E-01	9.1E-01
97	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (CILP), mRNA.	NM_003613	CILP	2.3E-01	9.1E-01
98	collagen, type XV, alpha 1 (COL15A1), mRNA.	NM_001855	COL15A1	2.9E-01	9.1E-01
99	pp14571 mRNA, complete cds.	AF318342	GPC1	7.6E-01	9.1E-01
100	matrilin 3 (MATN3) precursor, mRNA.	NM_002381	MATN3	1.3E-01	9.1E-01
101	UI-H-EZ1-bbi-e-16-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbi-e-16-0-UI 3', mRNA sequence.	CA418947	FLRT2	2.3E-01	9.0E-01
102	mRNA: cDNA DKFZp434A2410 (from clone DKFZp434A2410); partial	AL137580	EMILIN3	4.1E-01	9.0E-01
103	matrix metalloproteinase 16 (membrane-inserted) (MMP16), transcript variant 1, mRNA.	NM_005941	MMP16	1.8E-01	8.8E-01
104	fibulin 1 (FBLN1), transcript variant B, mRNA.	NM_006485	FBLN1	2.1E-01	8.7E-01
105	retinol binding protein 3, interstitial (RBP3), mRNA.	NM_002900	RBP3	2.9E-01	8.6E-01
106	Human tenascin-C mRNA, splice variant TNCfn-ad2, partial cds.	U88892	TNC	2.5E-01	8.6E-01
107	collagen, type VIII, alpha 1 (COL8A1), mRNA.	NM_001850	COL8A1	5.2E+00	8.6E-01
108	ameloblastin, enamel matrix protein (AMBN), mRNA.	NM_016519	AMBN	2.5E-01	8.3E-01
109	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2 (ADAMTS2), transcript variant 1, mRNA.	NM_014244	ADAMTS2	4.1E-01	8.2E-01
110	Usher syndrome 2A (autosomal recessive, mild) (USH2A), mRNA.	NM_007123	USH2A	4.3E-01	8.1E-01
111	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2), mRNA.	NM_004613	TGM2	9.9E-01	8.1E-01
112	wingless-type MMTV integration site family, member 3 (WNT3), mRNA.	NM_030753	WNT3	1.7E-01	8.0E-01
113	microfibrillar-associated protein 3 (MFAP3), mRNA.	NM_005927	MFAP3	5.3E-01	7.6E-01
114	wingless-type MMTV integration site family, member 3A (WNT3A),	NM_033131	WNT3A	1.2E+00	7.1E-01

115	brain link protein-1 (BRAL1), mRNA.	NM_021817	HAPLN2	4.8E-01	7.0E-01
116	clone IMAGE:297403, mRNA sequence.	AF339813	GPC6	4.0E-01	7.0E-01
117	matrix metalloproteinase 17 (membrane-inserted) (MMP17), mRNA.	NM_016155	MMP17	3.7E-01	6.9E-01
118	matrix metalloproteinase 23B (MMP23B), mRNA.	NM_006983	MMP23B	1.7E-01	6.6E-01
119	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), transcript variant 1,	NM_139155	ADAMTS14	6.4E-01	6.5E-01
120	clone IMAGE:212461, mRNA sequence.	AF339789	GPC6	1.6E-01	6.4E-01
121	glypican 6 (GPC6), mRNA.	NM_005708	GPC6	5.4E-01	6.1E-01
122	chondroadherin (CHAD), mRNA.	NM_001267	CHAD	1.1E+00	6.1E-01
123	EST381162 MAGE resequenes, MAGK cDNA, mRNA sequence.	AW969085	WNT3	1.3E-01	5.9E-01
124	tenascin R (restrictin, janusin) (TNR), mRNA.	NM_003285	TNR	9.6E-02	5.9E-01
125	matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA.	NM_002421	MMP1	1.7E-01	5.6E-01
126	osteomodulin (OMD), mRNA.	NM_005014	OMD	4.3E-01	5.2E-01
127	tectorin alpha (TECTA), mRNA.	NM_005422	TECTA	2.2E-01	5.0E-01
128	Homo sapiens, clone MGC:22244 IMAGE:4688190, mRNA, complete cds.	BC022258	VWF	1.5E-01	4.8E-01
129	tumor endothelial marker 1 precursor (TEM1), mRNA.	NM_020404	CD164L1	1.6E-01	4.5E-01
130	matrix Gla protein (MGP), mRNA.	NM_000900	MGP	5.0E-01	4.2E-01
131	extracellular glycoprotein EMILIN-2 precursor (EMILIN-2), mRNA.	NM_032048	EMILIN2	9.7E-02	9.7E-02
132	tissue inhibitor of metalloproteinase 4 (TIMP4), mRNA.	NM_003256	TIMP4	1.5E-01	7.2E-02

activity, +16 and -21 in transition metal ion binding, +15 and -21 in receptor activity, +16 and -16 in nucleotide activity, +18 and -14 in transferase activity, +7 and -23 in transcription regulator activity, +12 and -17 in zinc ion binding, +14 and -13 in purine nucleotide binding, +10 and -17 in enzyme regulator activity, +5 and -17 in transcription factor activity, +6 and -15 in transmembrane receptor activity, +12 and -9 in ATP binding, +12 and -9 in adeny nucleotide activity, and +10 and -9 in calcium ion binding. In cellular component ontologies; 252 genes were associated in cellular component, 239 were in cell, 160 were in intracellular, 111 were in membrane, 83 in nucleus, 83 were in integral to membrane, 79 were in cytoplasm, 44 were in plasma membrane, 30 were in integral to plasma membrane, 22 were in extracellular, 22 were in cell fraction, 19 were in extracellular region, 16 were in extracellular space, 14 were in membrane fraction, 14 were in cytoskeleton, and 12 in endoplasmic reticulum.

Table 3 lists 31 genes classified in ossification of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days in the fold change order from the largest to the least with details of gene name, gene

identifier, gene symbol, test signal_norm and fold change. Well-known osteogenic differentiation marker genes such as sialoprotein precursor (IBSP=integrin-binding bone sialoprotein), secreted phosphoprotein (SPP1), osteonectin (SPARC), runt-related transcription factor 2 (RUNX2) genes were up-regulated more than 2-fold while matrix Gla protein (MGP) gene was down-regulated less-than 0.5-fold. Further more, osteoclast stimulating factor 1 (OSTF1) and cadherin 11 (CDH11) genes were up-regulated 220-fold and 2.3-fold, respectively. BMP (BMP1, BMP2, BMP4 and BMP5) and dentin matrix acidic phosphoprotein (DMP1) genes, however, were not significantly altered by culture in osteogenic differentiation medium for 14 days with their fold changes lying between 0.5 and 1.5-folds (=not significantly altered range).

Table 4 lists 132 genes classified in extracellular matrix (sensu Metazoa) of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days by the fold change order from the largest to the least with details of gene name, gene identifier, gene symbol, test signal_norm and fold change. It was noted that not only additional osteoblast-related gene such as

Table 5 253 genes classified in cell differentiation of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Control signal_norm)
1	secreted frizzled-related protein 4 (SFRP4), mRNA.	NM_003014	SFRP4	3.2E+00	1.6E+01
2	interleukin 6 (interferon, beta 2) (IL6), mRNA.	NM_000600	IL6	1.7E+00	1.6E+01
3	Human profilaggrin mRNA, 3' end.	M60502	FLG	1.2E+00	9.3E+00
4	insulin-like growth factor binding protein 3 (IGFBP3), mRNA.	NM_000598	IGFBP3	1.3E+00	6.3E+00
5	cDNA FLJ11041 fis, clone PLACE1004405.	AK001903	INHBA	1.6E+01	6.1E+00
6	full length insert cDNA clone ZE12G05.	AF086552	SLIT3	2.2E+00	5.3E+00
7	HNC52-1-E4.R HNC (Human Normal Cartilage) cDNA, mRNA	BG924682	MBNL1	3.4E+00	4.8E+00
8	clone FBB7 Cri-du-chat critical region mRNA.	AF056426	SEMA5A	1.7E-01	4.5E+00
9	Homo sapiens, clone IMAGE:4186245, mRNA.	BC026731	EPAS1	2.6E-01	4.4E+00
10	inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA),	NM_002192	INHBA	6.9E+00	4.1E+00
11	gp130-like monocyte receptor (CRL3), mRNA.	NM_139017	IL31RA	1.4E+00	4.0E+00
12	cDNA FLJ36948 fis, clone BRACE2005719, weakly similar to NUCLEOPLASMIN.	AK094267	NPM2	1.3E+00	3.7E+00
13	mRNA, chromosome 1 specific transcript KIAA0490.	AB007959	NHLH2	3.9E-01	3.6E+00
14	doublecortin; lissencephaly, X-linked (doublecortin) (DCX), mRNA.	NM_000555	DCX	1.9E-01	3.5E+00
15	MAP/microtubule affinity-regulating kinase 2 (MARK2), transcript variant 1, mRNA.	NM_017490	MARK2	2.8E-01	3.3E+00
16	clone FBA6 Cri-du-chat region mRNA.	AF009269	SEMA5A	3.5E-01	3.1E+00
17	fibroblast growth factor 1 (acidic) (FGF1), transcript variant 1, mRNA.	NM_000800	FGF1	4.6E-01	3.0E+00
18	Homo sapiens, clone MGC:46562 IMAGE:5247719, mRNA, complete	BC036847	NEUROG2	1.8E-01	2.8E+00
19	clone TEC10 Cri-du-chat region mRNA.	AF009302	SEMA5A	2.7E-01	2.7E+00
20	clone OPA5 Cri-du-chat region mRNA.	AF009299	SEMA5A	1.3E-01	2.7E+00
21	basic helix-loop-helix domain containing, class B, 3 (BHLHB3), mRNA.	NM_030762	BHLHB3	6.7E-01	2.5E+00
22	mRNA for A-type microphthalmia associated transcription factor, complete cds.	AB006909	MITF	2.2E-01	2.5E+00
23	clone FB2C5 Cri-du-chat region mRNA.	AF009265	SEMA5A	1.2E+00	2.5E+00
24	neuroigin 1 (NLGN1), mRNA.	NM_014932	NLGN1	3.3E-01	2.5E+00
25	diaphanous homolog 2 (Drosophila) (DIAPH2), transcript variant 156, mRNA.	NM_006729	DIAPH2	4.6E-01	2.4E+00
26	bone morphogenetic protein 10 (BMP10), mRNA.	NM_014482	BMP10	2.7E-01	2.2E+00
27	pregnancy-associated plasma protein A (PAPPA), mRNA.	NM_002581	PAPPA	3.1E-01	2.2E+00
28	angiopoietin 2 (ANGPT2), mRNA.	NM_001147	ANGPT2	1.8E-01	2.1E+00
29	clone FBF3 Cri-du-chat region mRNA.	AF009282	SEMA5A	1.6E-01	2.1E+00
30	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mRNA.	NM_002019	FLT1	1.9E-01	2.1E+00
31	clone FBC9 Cri-du-chat region mRNA.	AF009274	SEMA5A	1.6E-01	2.1E+00
32	clone TUB2 Cri-du-chat region mRNA.	AF009316	SEMA5A	1.7E-01	2.1E+00
33	developmentally regulated RNA-binding protein 1 (DRB1), mRNA.	NM_152945	DRB1	3.3E-01	2.0E+00
34	clone TUC3 Cri-du-chat region mRNA.	AF009321	SEMA5A	1.1E+00	2.0E+00
35	bol, boule-like (Drosophila) (BOLL), mRNA.	NM_033030	BOLL	2.8E-01	2.0E+00
36	EST388566 MAGE resequences, MAGN cDNA, mRNA sequence.	AW976457	MBNL1	5.0E-01	1.9E+00
37	four and a half LIM domains 1 (FHL1), mRNA.	NM_001449	FHL1	4.2E+00	1.9E+00
38	hypothetical protein PRO2714 (PRO2714), mRNA.	NM_018534	NRP2	8.0E-01	1.9E+00
39	pro-melanin-concentrating hormone (PMCH), mRNA.	NM_002674	PMCH	1.7E+00	1.9E+00
40	Homo sapiens, clone IMAGE:3925349, mRNA.	BC033456	HILS1	2.2E-01	1.9E+00
41	S100 calcium binding protein A13 (S100A13), mRNA.	NM_005979	S100A13	3.4E+00	1.9E+00
42	chromosome 6 open reading frame 18 (C6orf18), mRNA.	NM_019052	C6orf18	2.1E-01	1.8E+00
43	vascular endothelial growth factor C (VEGFC), mRNA.	NM_005429	VEGFC	5.0E+00	1.8E+00
44	thioredoxin domain containing 3 (spermatzoa) (TXNDC3), mRNA.	NM_016616	TXNDC3	4.1E-01	1.8E+00
45	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase) (NME5), mRNA.	NM_003551	NME5	6.8E-01	1.7E+00
46	H1 histone family, member T (testis-specific) (H1FT), mRNA.	NM_005323	HIST1H1T	2.3E-01	1.7E+00
47	mRNA; cDNA DKFZp761G2123 (from clone DKFZp761G2123).	AL137424	SMURF1	3.2E-01	1.7E+00
48	deleted in azoospermia-like (DAZL), mRNA.	NM_001351	DAZL	3.0E-01	1.7E+00
49	midkine (neurite growth-promoting factor 2) (MDK), mRNA.	NM_002391	MDK	5.0E-01	1.7E+00
50	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (SEMA4D).	NM_006378	SEMA4D	2.5E-01	1.6E+00
51	mRNA for KIAA1625 protein, partial cds.	AB046845	SMURF1	4.5E-01	1.6E+00
52	Homo sapiens, clone IMAGE:3961600, mRNA.	BC021693	BOLL	1.9E-01	1.6E+00
53	hypothetical protein FKSG28 (FKSG28), mRNA.	NM_030929	KAZALD1	1.9E-01	1.6E+00
54	netrin G1f (KIAA0976), mRNA.	NM_014917	NTNG1	2.5E-01	1.5E+00
55	ribosomal protein S21 (RPS21), mRNA.	NM_001024	RPS21	2.4E+01	1.5E+00
56	mRNA for KIAA1568 protein, partial cds.	AB046788	ROBO2	3.0E-01	1.5E+00

57	netrin G2 (KIAA1857), mRNA.	NM_032536	NTNG2	1.7E-01	1.5E+00
58	Homo sapiens, clone IMAGE:5272221, mRNA.	BC041347	FLNB	2.3E-01	1.5E+00
59	cysteine and glycine-rich protein 2 (CSRP2), mRNA.	NM_001321	CSRP2	1.0E+00	1.5E+00
60	involucrin (IVL), mRNA.	NM_005547	IVL	1.5E-01	1.4E+00
61	endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA.	NM_001953	ECGF1	1.7E-01	1.4E+00
62	mitogen-activated protein kinase 12 (MAPK12), mRNA.	NM_002969	MAPK12	3.8E-01	1.4E+00
63	filamin B, beta (actin binding protein 278) (FLNB), mRNA.	NM_001457	FLNB	9.8E-01	1.4E+00
64	latent transforming growth factor beta binding protein 4 (LTBP4),	NM_003573	LTBP4	2.9E-01	1.4E+00
65	Homo sapiens, KIAA1445 protein, clone MGC:3430 IMAGE:3621447, mRNA, complete cds.	BC002776	SEMA5B	1.4E-01	1.4E+00
66	neuregulin 1 (NRG1), transcript variant HRG-beta2, mRNA.	NM_013957	NRG1	7.0E-01	1.4E+00
67	full length insert cDNA clone YX36D02.	AF087991	NTNG1	2.3E-01	1.4E+00
68	mal, T-cell differentiation protein (MAL), transcript variant a, mRNA.	NM_002371	MAL	2.8E-01	1.4E+00
69	cDNA FLJ13510 fis, clone PLACE1005146.	AK023572	EPAS1	1.5E-01	1.4E+00
70	clone 23698 mRNA sequence.	AF052094	EPAS1	3.3E+00	1.4E+00
71	bone morphogenetic protein 1 (BMP1), transcript variant BMP1-3, mRNA.	NM_006129	BMP1	1.8E-01	1.3E+00
72	transcription factor-like 5 (basic helix-loop-helix) (TCFL5), mRNA.	NM_006602	TCFL5	8.8E-01	1.3E+00
73	N-myc downstream regulated gene 1 (NDRG1), mRNA.	NM_006096	NDRG1	1.9E+00	1.3E+00
74	clone FBC10 Cri-du-chat region mRNA.	AF009272	SEMA5A	3.7E-01	1.3E+00
75	enabled homolog (Drosophila) (ENAH), mRNA.	NM_018212	ENAH	1.5E+01	1.3E+00
76	z170h11.s1 Soares fetal liver spleen_1NFLS.S1 cDNA clone IMAGE:436197 3', mRNA sequence.	AA703280	SERPINE2	1.5E+00	1.3E+00
77	DKFZP586N2124 protein (DKFZP586N2124), mRNA.	NM_015424	CHRDL2	3.0E-01	1.2E+00
78	Retina-derived POU-domain factor-1 (RPF-1), mRNA.	NM_007252	POU6F2	2.3E-01	1.2E+00
79	cDNA FLJ11424 fis, clone HEMBA1001026.	AK021486	BMP5	2.2E-01	1.2E+00
80	H.sapiens cyclin mRNA.	Z22780	CYLC1	1.8E-01	1.2E+00
81	neurogenic differentiation 1 (NEUROD1), mRNA.	NM_002500	NEUROD1	9.9E-02	1.2E+00
82	DC-specific transmembrane protein (DCSTAMP), mRNA.	NM_030788	TM7SF4	2.5E-01	1.2E+00
83	zinc-finger protein DZIP1 (DZIP1), mRNA.	NM_014934	DZIP1	1.0E+00	1.2E+00
84	bone morphogenetic protein 4 (BMP4), transcript variant 1, mRNA.	NM_001202	BMP4	1.6E-01	1.2E+00
85	myogenic factor 6 (herculin) (MYF6), mRNA.	NM_002469	MYF6	3.4E-01	1.2E+00
86	clone FBD10 Cri-du-chat region mRNA.	AF009275	SEMA5A	1.8E-01	1.2E+00
87	likely ortholog of mouse and rat twist-related bHLH protein Dermo-1 (DERMO1), mRNA.	NM_057179	TWIST2	1.4E-01	1.1E+00
88	vesicle-associated membrane protein 5 (myobrevin) (VAMP5), mRNA.	NM_006634	VAMP5	1.5E+00	1.1E+00
89	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE2), mRNA.	NM_006216	SERPINE2	1.9E+01	1.1E+00
90	mesenchymal stem cell protein DSC92 (NEUGRIN), mRNA.	NM_016645	NEUGRIN	3.1E-01	1.1E+00
91	ectodysplasin 1, anhidrotic receptor (EDAR), mRNA.	NM_022336	EDAR	1.5E-01	1.1E+00
92	cDNA FLJ13731 fis, clone PLACE3000142.	AK023793	JAG1	6.0E-01	1.1E+00
93	single-minded homolog 2 (Drosophila) (SIM2), transcript variant SIM2, mRNA.	NM_005069	SIM2	3.4E-01	1.1E+00
94	clone TUA4 Cri-du-chat region mRNA.	AF009311	SEMA5A	7.4E-01	1.1E+00
95	glucose transporter 14 short form (SLC2A14) mRNA, complete cds; alternatively spliced.	AF481878	SLC2A14	6.6E-01	1.1E+00
96	calcium/calmodulin-dependent protein kinase I (CAMK1), mRNA.	NM_003656	CAMK1	5.1E-01	1.1E+00
97	hematopoietic PBX-interacting protein (HPIP), mRNA.	NM_020524	PBXIP1	4.5E-01	1.1E+00
98	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA.	NM_014225	PPP2R1A	1.7E-01	1.0E+00
99	seven in absentia homolog 1 (Drosophila) (SIAH1), mRNA.	NM_003031	SIAH1	5.6E-01	1.0E+00
100	B-cell translocation gene 4 (BTG4), mRNA.	NM_017589	BTG4	2.4E-01	1.0E+00
101	cysteine and glycine-rich protein 3 (cardiac LIM protein) (CSRP3), mRNA.	NM_003476	CSRP3	5.3E-01	1.0E+00
102	von Hippel-Lindau syndrome (VHL), mRNA.	NM_000551	VHL	4.8E-01	1.0E+00
103	cDNA: FLJ21284 fis, clone COL01911.	AK024937	SMURF1	3.5E-01	1.0E+00
104	Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1), transcript variant long, mRNA.	NM_023034	WHSC1L1	5.2E-01	1.0E+00
105	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E (SEMA3E), mRNA.	NM_012431	SEMA3E	4.4E-01	1.0E+00
106	TRAF6-inhibitory zinc finger protein (TIZ), mRNA.	NM_138330	TIZ	1.9E-01	1.0E+00
107	paired box gene 4 (PAX4), mRNA.	NM_006193	PAX4	5.0E-01	1.0E+00
108	drebrin 1 (DBN1), transcript variant 2, mRNA.	NM_080881	DBN1	1.8E+00	1.0E+00
109	growth arrest-specific 7 (GAS7), transcript variant b, mRNA.	NM_005890	-	2.7E-01	9.9E-01
110	UI-E-CK1-abk-b-12-0-UI.s1 UI-E-CK1 cDNA clone UI-E-CK1-abk-b-12-0-UI 3', mRNA sequence.	BM661486	NTRK2	1.9E-01	9.9E-01
111	interleukin 11 (IL11), mRNA.	NM_000641	IL11	1.9E-01	9.9E-01
112	clone HEA7 Cri-du-chat region mRNA.	AF009285	SEMA5A	2.1E-01	9.9E-01
113	Homo sapiens, clone IMAGE:5590200, mRNA.	BC035781	-	1.6E+00	9.6E-01
114	Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA.	NM_003412	ZIC1	4.6E-01	9.6E-01

115	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant longest, mRNA.	NM_033071	SYNE1	2.0E+00	9.6E-01
116	bone morphogenetic protein 2 (BMP2), mRNA.	NM_001200	BMP2	1.6E-01	9.5E-01
117	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa (PAFAH1B1), mRNA.	NM_000430	PAFAH1B1	4.6E+00	9.5E-01
118	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain. (semaphorin) 5A (SEMA5A), mRNA.	NM_003966	SEMA5A	1.6E-01	9.5E-01
119	casein kinase 2, alpha prime polypeptide (CSNK2A2), mRNA.	NM_001896	CSNK2A2	9.0E-01	9.4E-01
120	nescient helix loop helix 1 (NHLH1), mRNA.	NM_005598	NHLH1	6.5E-01	9.4E-01
121	cDNA FLJ30779 fis, clone FEBRA2000815.	AK055341	DAB1	3.6E-01	9.3E-01
122	hypothetical protein MGC2601 (MGC2601), mRNA.	NM_024042	METRN	4.4E-01	9.3E-01
123	cDNA FLJ30384 fis, clone BRACE2008114.	AK054946	DTX1	6.0E-01	9.2E-01
124	bone morphogenetic protein 8 (osteogenic protein 2) (BMP8), mRNA.	NM_001720	BMP8B	1.7E-01	9.2E-01
125	Homo sapiens, clone MGC:9168 IMAGE:3876839, mRNA, complete	BC010857	UTP14C	1.8E-01	9.2E-01
126	collagen, type XV, alpha 1 (COL15A1), mRNA.	NM_001855	COL15A1	2.9E-01	9.1E-01
127	cDNA FLJ40167 fis, clone TESTI2016331.	AK097486	NTRK3	3.1E-01	9.1E-01
128	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), transcript variant 1, mRNA.	NM_021988	UBE2V1	6.4E-01	9.0E-01
129	pregnancy-induced growth inhibitor mRNA, complete cds.	AY037158	OKL38	5.2E-01	9.0E-01
130	neuropilin 1 (NRP1), mRNA.	NM_003873	NRP1	4.7E-01	9.0E-01
131	carnitine deficiency-associated gene expressed in ventricle 1 (CDV-1), mRNA.	NM_014055	CDV1	3.0E-01	8.9E-01
132	ras homolog gene family, member B (ARHB), mRNA.	NM_004040	RHOB	2.5E-01	8.8E-01
133	cDNA FLJ13880 fis, clone THYRO1001434.	AK023942	NRP2	1.1E+00	8.8E-01
134	zinc finger protein 3 (A8-51) (ZNF3), mRNA.	NM_032924	ZNF3	1.8E-01	8.7E-01
135	internexin neuronal intermediate filament protein, alpha (INA), mRNA.	NM_032727	INA	3.5E-01	8.6E-01
136	hypothetical protein DKFZp547J036 (DKFZp547J036), mRNA.	NM_032281	ELAVL3	3.8E-01	8.6E-01
137	bone morphogenetic protein receptor, type IB (BMPRI1B), mRNA.	NM_001203	BMPRI1B	2.9E-01	8.6E-01
138	delta-like 3 (Drosophila) (DLL3), mRNA.	NM_016941	DLL3	4.2E-01	8.5E-01
139	paired box gene 2 (PAX2), transcript variant a, mRNA.	NM_003987	PAX2	3.7E-01	8.5E-01
140	ephrin-B2 (EFNB2), mRNA.	NM_004093	EFNB2	5.0E-01	8.5E-01
141	ephrin-B3 (EFNB3), mRNA.	NM_001406	EFNB3	2.9E-01	8.4E-01
142	delta-like 1 (Drosophila) (DLL1), mRNA.	NM_005618	DLL1	2.3E-01	8.4E-01
143	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA.	NM_002715	PPP2CA	1.9E+00	8.2E-01
144	clone TUC1 Cri-du-chat region mRNA.	AF009320	SEMA5A	1.7E-01	8.2E-01
145	paired box gene 8 (PAX8), transcript variant PAX8C, mRNA.	NM_013952	PAX8	1.4E-01	8.1E-01
146	NDRG family member 2 (NDRG2), mRNA.	NM_016250	NDRG2	1.7E-01	8.1E-01
147	heat shock 70kDa protein 2 (HSPA2), mRNA.	NM_021979	HSPA2	2.3E-01	8.1E-01
148	endothelial differentiation-related factor 1 (EDF1), transcript variant alpha, mRNA.	NM_003792	EDF1	5.8E+00	8.0E-01
149	SH2 domain protein 2A (SH2D2A), mRNA.	NM_003975	SH2D2A	7.4E-01	8.0E-01
150	mRNA for silencer element, complete cds.	D50375	STMN2	1.8E+00	8.0E-01
151	slit homolog 1 (Drosophila) (SLIT1), mRNA.	NM_003061	SLIT1	8.2E-01	8.0E-01
152	interleukin 20 (IL20), mRNA.	NM_018724	IL20	2.9E-01	8.0E-01
153	CDK5 regulatory subunit associated protein 3 (CDK5RAP3), mRNA.	NM_025197	CDK5RAP3	9.1E-01	8.0E-01
154	IL-27 p28 subunit (P28), mRNA.	NM_145659	IL27	1.9E-01	7.9E-01
155	Homo sapiens, clone IMAGE:4825733, mRNA, partial cds.	BC032027	SLIT3	1.9E-01	7.9E-01
156	CDK5 regulatory subunit associated protein 2 (CDK5RAP2), mRNA.	NM_018249	CDK5RAP2	3.3E-01	7.9E-01
157	roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA.	NM_133631	ROBO1	2.2E-01	7.8E-01
158	myelin gene expression factor 2 (MEF-2), mRNA.	NM_016132	MYEF2	3.0E-01	7.8E-01
159	family with sequence similarity 12, member B (epididymal) (FAM12B), mRNA.	NM_022360	FAM12B	1.2E-01	7.8E-01
160	clone TUA9 Cri-du-chat region mRNA.	AF009315	SEMA5A	2.8E-01	7.8E-01
161	delta-like 4 (Drosophila) (DLL4), mRNA.	NM_019074	DLL4	5.9E-01	7.8E-01
162	mitogen-activated protein kinase kinase kinase kinase 1 (MAP4K1), mRNA.	NM_007181	MAP4K1	1.3E+00	7.8E-01
163	bridging integrator 1 (BIN1), transcript variant 1, mRNA.	NM_139343	BIN1	2.1E-01	7.7E-01
164	clone FBF1 Cri-du-chat region mRNA.	AF009281	SEMA5A	1.6E-01	7.7E-01
165	metallothionein-like 5, testis-specific (tesmin) (MTL5), mRNA.	NM_004923	MTL5	3.0E-01	7.7E-01
166	Homo sapiens, clone MGC:9657 IMAGE:3463997, mRNA, complete	BC011461	MITF	7.0E-01	7.7E-01
167	Zic family member 2 (odd-paired homolog, Drosophila) (ZIC2), mRNA.	NM_007129	ZIC2	1.2E+00	7.7E-01
168	toll-like receptor 3 (TLR3), mRNA.	NM_003265	TLR3	3.1E-01	7.7E-01
169	full length insert cDNA clone Y140H11.	AF085834	-	1.2E-01	7.6E-01
170	suppressor of cytokine signaling 5 (SOCS5), transcript variant 2.	NM_144949	SOCS5	3.9E+00	7.6E-01
171	single-minded homolog 1 (Drosophila) (SIM1), mRNA.	NM_005068	SIM1	2.1E-01	7.5E-01
172	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) (CD86), mRNA.	NM_006889	CD86	4.7E-01	7.5E-01
173	cDNA FLJ25687 fis, clone TST04292.	AK098553	SLIT3	1.6E-01	7.5E-01
174	jagged 2 (JAG2), transcript variant 1, mRNA.	NM_002226	JAG2	1.6E-01	7.5E-01

175	KIAA0076 gene product (KIAA0076), mRNA.	NM_014780	CUL7	4.2E-01	7.4E-01
176	glucocorticoid receptor DNA binding factor 1 (GRLF1), transcript variant 1, mRNA.	NM_024342	GRLF1	1.1E+00	7.4E-01
177	inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA.	NM_002193	INHBB	3.1E-01	7.3E-01
178	hypothetical protein FLJ13057 similar to germ cell-less (FLJ13057), mRNA.	NM_022471	GMCL1L	1.7E-01	7.3E-01
179	toll-like receptor 4 (TLR4), transcript variant 3, mRNA.	NM_003266	TLR4	7.9E-01	7.3E-01
180	small proline-rich protein 2A (SPRR2A), mRNA.	NM_005988	SPRR2A	3.1E-01	7.3E-01
181	cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 1, mRNA.	NM_001791	CDC42	5.1E-01	7.3E-01
182	jagged 1 (Alagille syndrome) (JAG1), mRNA.	NM_000214	JAG1	2.6E-01	7.2E-01
183	Homo sapiens, clone IMAGE:5223698, mRNA.	BC036874	SCUBE1	1.1E-01	7.2E-01
184	SFRS protein kinase 1 (SRPK1), mRNA.	NM_003137	SRPK1	7.1E-01	7.1E-01
185	clone IMAGE:451939, mRNA sequence.	AF339822	FLT1	2.0E-01	7.0E-01
186	FKBP-associated protein (FAP48), transcript variant 1, mRNA.	NM_053274	GLMN	6.9E-01	7.0E-01
187	epiregulin (EREG), mRNA.	NM_001432	EREG	9.0E-02	7.0E-01
188	NDRG family member 3 (NDRG3), mRNA.	NM_032013	NDRG3	1.7E-01	7.0E-01
189	AF15q14 protein (AF15Q14), mRNA.	NM_170589	AF15Q14	1.4E-01	6.9E-01
190	arachidonate 15-lipoxygenase, second type (ALOX15B), mRNA.	NM_001141	ALOX15B	3.1E-01	6.9E-01
191	NADP-dependent retinol dehydrogenase/reductase (RDHL), transcript variant C, mRNA.	NM_005771	DHRS9	2.0E-01	6.7E-01
192	v-ski sarcoma viral oncogene homolog (avian) (SKI), mRNA.	NM_003036	SKI	3.8E-01	6.7E-01
193	MR1-HN0070-020101-005-g08 HN0070 cDNA, mRNA sequence.	BG999677	UBE2V1	6.5E-01	6.7E-01
194	wingless-type MMTV integration site family, member 1 (WNT1),	NM_005430	WNT1	4.2E-01	6.6E-01
195	LIM homeobox transcription factor 1, beta (LMX1B), mRNA.	NM_002316	LMX1B	2.5E-01	6.5E-01
196	nerve growth factor receptor (TNFR superfamily, member 16) (NGFR), mRNA.	NM_002507	NGFR	2.2E-01	6.4E-01
197	placental growth factor, vascular endothelial growth factor-related protein (PGF), mRNA.	NM_002632	PGF	3.8E-01	6.3E-01
198	Notch homolog 3 (Drosophila) (NOTCH3), mRNA.	NM_000435	NOTCH3	2.5E-01	6.2E-01
199	secreted frizzled-related protein 1 (SFRP1), mRNA.	NM_003012	SFRP1	1.9E-01	6.1E-01
200	NDRG family member 4 (NDRG4), mRNA.	NM_020465	NDRG4	3.1E-01	6.1E-01
201	transcriptional coactivator tubedown-100 (TBDN100), transcript variant 1, mRNA.	NM_057175	NARG1	4.4E-01	6.1E-01
202	SKI-like (SKIL), mRNA.	NM_005414	SKIL	2.3E-01	6.0E-01
203	placenta-specific 3 (PLAC3), transcript variant 1, mRNA.	NM_020318	PAPPA2	3.4E-01	5.9E-01
204	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA.	NM_012479	YWHAG	3.2E-01	5.9E-01
205	growth arrest and DNA-damage-inducible, gamma (GADD45G),	NM_006705	GADD45G	6.9E-01	5.9E-01
206	mRNA; cDNA DKFz666E199 (from clone DKFz666E199).	AL833045	EFNA5	1.9E-01	5.9E-01
207	fibroblast growth factor 2 (basic) (FGF2), mRNA.	NM_002006	FGF2	1.6E+00	5.8E-01
208	protamine 2 (PRM2), mRNA.	NM_002762	PRM2	3.6E-01	5.8E-01
209	neurogenin 3 (NEUROG3), mRNA.	NM_020999	NEUROG3	3.7E-01	5.7E-01
210	zinc finger protein 313 (ZNF313), mRNA.	NM_018683	ZNF313	3.9E-01	5.7E-01
211	cyclin-dependent kinase 5, regulatory subunit 1 (p35) (CDK5R1),	NM_003885	CDK5R1	2.1E-01	5.6E-01
212	clone FB2A12 Cri-du-chat region mRNA.	AF009258	SEMA5A	2.4E-01	5.6E-01
213	tumor necrosis factor receptor superfamily, member 12A (TNFRSF12A), mRNA.	NM_016639	TNFRSF12A	1.5E+00	5.5E-01
214	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (PPP2R1B), mRNA.	NM_002716	PPP2R1B	6.1E-01	5.4E-01
215	male-enhanced antigen (MEA), mRNA.	NM_014623	MEA	1.8E+00	5.4E-01
216	CDK5 regulatory subunit associated protein 1 (CDK5RAP1), mRNA.	NM_016082	CDK5RAP1	7.0E-01	5.4E-01
217	UI-E-CK1-afh-1-24-0-ULs1 UI-E-CK1 cDNA clone UI-E-CK1-afh-1-24-0-UI 3', mRNA sequence.	BU729805	NANOS3	3.2E-01	5.3E-01
218	EDAR-associated death domain (EDARADD), transcript variant B,	NM_080738	EDARADD	2.0E-01	5.3E-01
219	interferon, gamma-inducible protein 16 (IFI16), mRNA.	NM_005531	IFI16	4.8E+00	5.3E-01
220	full length insert cDNA Y129A01.	AF075019	PAFAH1B1	3.5E-01	5.3E-01
221	hook1 protein (HOOK1), mRNA.	NM_015888	HOOK1	1.5E-01	5.3E-01
222	clone FB2A9 Cri-du-chat region mRNA.	AF009260	SEMA5A	2.2E-01	5.3E-01
223	ectodermal dysplasia 1, anhidrotic (ED1), mRNA.	NM_001399	EDA	2.3E-01	5.3E-01
224	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA.	NM_001731	BTG1	1.8E+00	5.1E-01
225	hypothetical protein FLJ10283 (FLJ10283), mRNA.	NM_018046	AGGF1	7.0E-01	5.1E-01
226	cDNA FLJ36094 fis, clone TEST12020717, highly similar to Human testis-specific protein (TSPY) mRNA.	AK093413	TSPY1	1.2E-01	5.1E-01
227	clone TUC12 Cri-du-chat region mRNA.	AF009319	SEMA5A	9.9E-02	5.0E-01
228	full length insert cDNA clone YQ07F12.	AF085898	FLNB	2.5E-01	4.9E-01
229	serine/threonine kinase 22B (spermiogenesis associated) (STK22B), mRNA.	NM_053006	STK22B	3.5E-01	4.8E-01
230	MGC4170 protein (MGC4170), mRNA.	NM_024312	MGC4170	8.0E-02	4.7E-01
231	glutaredoxin 2 (GLRX2), mRNA.	NM_016066	GLRX2	8.7E-01	4.6E-01
232	fibroblast growth factor 22 (FGF22), mRNA.	NM_020637	FGF22	7.9E-02	4.5E-01

233	growth arrest and DNA-damage-inducible, beta (GADD45B), mRNA.	NM_015675	GADD45B	7.2E+00	4.5E-01
234	interferon-related developmental regulator 1 (IFRD1), mRNA.	NM_001550	IFRD1	2.2E+00	4.4E-01
235	neurogenic differentiation 2 (NEUROD2), mRNA.	NM_006160	NEUROD2	2.4E-01	4.4E-01
236	matrix Gla protein (MGP), mRNA.	NM_000900	MGP	5.0E-01	4.2E-01
237	tumor protein p53 (Li-Fraumeni syndrome) (TP53), mRNA.	NM_000546	TP53	2.3E-01	4.1E-01
238	sperm associated antigen 6 (SPAG6), transcript variant 1, mRNA.	NM_012443	SPAG6	1.5E-01	4.1E-01
239	deltex homolog 1 (Drosophila) (DTX1), mRNA.	NM_004416	DTX1	2.3E+00	4.0E-01
240	sema domain, transmembrane domain (TM), and cytoplasmic domain. (semaphorin) 6B (SEMA6B), transcript variant SEMA6B.3, mRNA.	NM_032108	SEMA6B	2.5E-01	4.0E-01
241	Homo sapiens, clone IMAGE:4499056, mRNA, partial cds.	BC019583	POU6F2	1.5E-01	3.6E-01
242	tuftelin interacting protein 11 (TFIP11), mRNA.	NM_012143	TFIP11	1.5E+00	3.6E-01
243	Human filaggrin gene, partial cds.	M24355	FLG	1.6E-01	3.6E-01
244	myeloid cell leukemia sequence 1 (BCL2-related) (MCL1), mRNA.	NM_021960	MCL1	1.7E+00	3.4E-01
245	neuronal cell adhesion molecule (NRCAM), mRNA.	NM_005010	NRCAM	2.4E-02	2.4E-01
246	platelet factor 4 (chemokine (C-X-C motif) ligand 4) (PF4), mRNA.	NM_002619	PF4	2.4E-01	1.7E-01
247	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA.	NM_139314	ANGPTL4	4.1E-01	6.1E-02
248	NEU1 protein (ZNEU1), mRNA.	NM_016215	EGFL7	1.0E-06	4.2E-05
249	neurogenin 1 (NEUROG1), mRNA.	NM_006161	NEUROG1	1.0E-06	2.5E-05
250	myeloid leukemia factor 1 (MLF1), mRNA.	NM_022443	MLF1	1.0E-06	2.1E-05
251	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA.	NM_000963	PTGS2	1.0E-06	1.3E-05
252	full length insert cDNA clone YW19A06.	AF086015	NLGN1	1.0E-06	8.1E-06
253	colony stimulating factor 1 (macrophage) (CSF1), transcript variant 3, mRNA.	NM_172211	CSF1	1.0E-06	4.2E-06

osteoblast specific factor 2 (OSF-2)) gene but also many cartilage-related genes were more than 2-fold up-regulated which included cartilage associated protein (CRTAP), cartilage linking protein 1 (HAPLN1), chondroitin sulfate proteoglycan 2 (CSPG2) and hyaluronan synthase 1 (HAS1) genes. One adipocyte-related gene (extracellular matrix protein 2) was also more than 2-fold up-regulated.

Table 5 lists 253 genes classified in cell differentiation of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days by the fold change order from the largest to the least with details of gene name, gene identifier, gene symbol, test signal_norm and fold change. The top largest secreted frizzled-related protein 4 (SFRP4) gene was associated with osteogenesis-accelerating Wnt signaling pathway. The second largest interleukin 6 (IL6) gene had influence over neural stem cell differentiation. The third largest profilaggrin (FLG) gene played a role in epidermal differentiation.

Table 6 lists 64 genes classified in TGF-beta signaling pathway of human mesenchymal stem cells cultured in

osteogenic differentiation medium for 14 days by the fold change order from the largest to the least with details of gene name, gene identifier, gene symbol, test signal_norm and fold change. It was confirmed that transforming growth factor, beta1 (TGFB1) and transforming growth factor, beta receptor 1 (TGFB1) genes were up-regulated 1.5-fold and 2.0-fold, respectively. Thrombospondin 1 and 2 (THBS1 and THBS2) genes are strong activator of TGF-beta. Inhibin (INHBA) and MAD (SMAD3) genes facilitate embryo differentiation.

Table 7 lists 40 genes classified in angiogenesis of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days by the fold change order from the largest to the least with details of gene name, gene identifier, gene symbol, test signal_norm and fold change. Several genes were more than 1.5-fold up-regulated for angiogenesis, which included angiopoietin-like 3 (ANGPTL3), angiopoietin 2 (ANGPT2) and vascular endothelial growth factor (ECGF1) genes.

Table 8 lists 67 genes classified in collagen and aggrecan of human mesenchymal stem cells cultured in osteo

Table 6 64 genes classified in TGF-beta signaling pathway of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Control signal_norm)
1	Human thrombospondin mRNA.	M81339	THBS2	1.6E+01	2.1E+01
2	Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405.	AK001903	INHBA	1.6E+01	6.1E+00
3	Homo sapiens, clone IMAGE:5300951, mRNA.	BC039406	ROCK1	2.2E-01	4.4E+00
4	Homo sapiens inhibin, beta A (activin A, activin AB alpha polypeptide) (INHBA), mRNA.	NM_002192	INHBA	6.9E+00	4.1E+00
5	Homo sapiens thrombospondin 1 (THBS1), mRNA.	NM_003246	THBS1	9.6E+00	3.9E+00
6	Homo sapiens MAD, mothers against decapentaplegic homolog 3 (Drosophila) (MADH3), mRNA.	NM_005902	SMAD3	2.2E+00	2.3E+00
7	Homo sapiens chordin variant 2 (CHRD) mRNA, complete cds, alternatively	AF209930	CHRD	1.5E-01	2.2E+00
8	Homo sapiens inhibitor of DNA binding 4, dominant negative helix-loop-helix protein (ID4), mRNA.	NM_001546	ID4	7.0E-01	2.1E+00
9	Homo sapiens transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa) (TGFBRI), mRNA.	NM_004612	TGFBRI	2.1E+00	2.0E+00
10	Homo sapiens activin A receptor, type II (ACVR2), mRNA.	NM_001616	ACVR2	3.9E-01	1.9E+00
11	Homo sapiens cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) (COMP), mRNA.	NM_000095	COMP	1.3E+00	1.8E+00
12	Homo sapiens retinoblastoma-like 1 (p107) (RBL1), mRNA.	NM_002895	RBL1	2.5E-01	1.8E+00
13	Homo sapiens follistatin (FST), transcript variant FST317, mRNA.	NM_006350	FST	8.8E+00	1.7E+00
14	Homo sapiens mRNA, cDNA DKFZp761G2123 (from clone DKFZp761G2123).	AL137424	SMURF1	3.2E-01	1.7E+00
15	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA.	NM_002166	ID2	3.7E-01	1.7E+00
16	Homo sapiens decorin (DCN), transcript variant A1, mRNA.	NM_001920	DCN	2.8E+01	1.6E+00
17	Homo sapiens anti-Mullerian hormone receptor, type II (AMHR2), mRNA.	NM_020547	AMHR2	2.8E-01	1.6E+00
18	Homo sapiens activin A receptor, type I (ACVR1), mRNA.	NM_001105	ACVR1	2.7E-01	1.6E+00
19	Homo sapiens mRNA for KIAA1625 protein, partial cds.	AB046845	SMURF1	4.5E-01	1.6E+00
20	Homo sapiens transforming growth factor, beta 1 (Camurati-Engelmann disease) (TGFB1), mRNA.	NM_000660	TGFB1	2.9E-01	1.5E+00
21	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A), mRNA.	NM_004329	BMPRI1A	9.2E-01	1.4E+00
22	Homo sapiens inhibitor of DNA binding 3, dominant negative helix-loop-helix protein (ID3), mRNA.	NM_002167	ID3	1.1E+00	1.4E+00
23	Homo sapiens paired-like homeodomain transcription factor 2 (PITX2), transcript variant 3, mRNA.	NM_000325	PITX2	3.3E+00	1.4E+00
24	Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 2, mRNA.	NM_078487	CDKN2B	3.0E+00	1.4E+00
25	Homo sapiens cDNA FLJ32163 fis, clone PLACE6000371.	AK056725	ACVRL1	3.5E-01	1.3E+00
26	Homo sapiens E3 ubiquitin ligase SMURF2 (SMURF2), mRNA.	NM_022739	SMURF2	2.2E+00	1.2E+00
27	Homo sapiens cDNA FLJ11424 fis, clone HEMBA1001026.	AK021486	BMP5	2.2E-01	1.2E+00
28	Homo sapiens, clone IMAGE:4824737, mRNA.	BC039099	E2F5	9.1E-02	1.2E+00
29	Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 1.	NM_001202	BMP4	1.6E-01	1.2E+00
30	Homo sapiens, clone IMAGE:5239967, mRNA, partial cds.	BC033585	NODAL	1.2E-01	1.2E+00
31	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP), mRNA.	NM_004380	CREBBP	5.1E-02	1.1E+00
32	Homo sapiens ring-box 1 (RBX1), mRNA.	NM_014248	RBX1	1.7E+00	1.1E+00
33	AGENCOURT_6439576 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520419 5', mRNA sequence.	BM803754	BMPRI2	9.2E-01	1.0E+00
34	Homo sapiens cDNA: FLJ21284 fis, clone COL01911.	AK024937	SMURF1	3.5E-01	1.0E+00
35	Homo sapiens ras homolog gene family, member A (ARHA), mRNA.	NM_001664	RHOA	5.9E+00	1.0E+00
36	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA.	NM_005611	RBL2	1.3E+00	1.0E+00
37	Homo sapiens left-right determination, factor B (LEFTB), mRNA.	NM_020997	LEFTY1	1.9E-01	1.0E+00
38	Homo sapiens bone morphogenetic protein 2 (BMP2), mRNA.	NM_001200	BMP2	1.6E-01	9.5E-01
39	Homo sapiens endometrial bleeding associated factor (left-right determination, factor A; transforming growth factor beta superfamily) (EBAF), mRNA.	NM_003240	LEFTY2	2.8E-01	9.5E-01
40	Homo sapiens transcription factor Dp-1 (TFDP1), mRNA.	NM_007111	TFDP1	1.0E+00	9.3E-01
41	Homo sapiens thrombospondin 3 (THBS3), mRNA.	NM_007112	THBS3	7.6E-01	9.2E-01
42	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8),	NM_001720	BMP8B	1.7E-01	9.2E-01
43	Homo sapiens cDNA FLJ11950 fis, clone HEMBB1000826.	AK022012	BMPRI2	8.8E-02	9.0E-01
44	Homo sapiens bone morphogenetic protein receptor, type IB (BMPRI1B), mRNA.	NM_001203	BMPRI1B	2.9E-01	8.6E-01
45	Homo sapiens MAD, mothers against decapentaplegic homolog 1 (Drosophila) (MADH1), mRNA.	NM_005900	SMAD1	6.0E-01	8.4E-01
46	Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA), mRNA.	NM_002715	PPP2CA	1.9E+00	8.2E-01
47	Homo sapiens hypothetical protein BC012008 (LOC144467), mRNA.	NM_138473	SP1	2.4E-01	8.0E-01

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48	Homo sapiens Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA.	NM_004850	ROCK2	6.3E-01	7.8E-01
49	Homo sapiens interferon, gamma (IFNG), mRNA.	NM_000619	IFNG	1.6E-01	7.7E-01
50	Homo sapiens anti-Mullerian hormone (AMH), mRNA.	NM_000479	AMH	8.1E-01	7.4E-01
51	Homo sapiens inhibin, beta B (activin AB beta polypeptide) (INHBB), mRNA.	NM_002193	INHBB	3.1E-01	7.3E-01
52	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA.	NM_002748	MAPK6	2.1E-01	7.1E-01
53	Homo sapiens inhibin, beta C (INHBC), mRNA.	NM_005538	INHBC	4.9E-01	7.1E-01
54	Homo sapiens endosome-associated FYVE-domain protein (ENDOFIN), mRNA.	NM_014733	ZFYVE16	3.3E-01	6.4E-01
55	Homo sapiens ribosomal protein S6 kinase, 70kDa, polypeptide 2 (RPS6KB2),	NM_003952	RPS6KB2	1.6E-01	5.8E-01
56	Homo sapiens MAD, mothers against decapentaplegic homolog 4 (Drosophila) (MADH4), mRNA.	NM_005359	SMAD4	1.9E-01	5.6E-01
57	Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 1, mRNA.	NM_002745	MAPK1	1.2E+00	5.5E-01
58	Homo sapiens activin A receptor, type IIB (ACVR2B), mRNA.	NM_001106	ACVR2B	1.3E-01	5.4E-01
59	Homo sapiens MAD, mothers against decapentaplegic homolog 2 (Drosophila) (MADH2), mRNA.	NM_005901	SMAD2	5.3E-01	5.4E-01
60	AGENCOURT_8882236 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:6197923 5', mRNA sequence.	BQ954223	SMAD4	5.1E-01	5.4E-01
61	Homo sapiens MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA.	NM_004799	ZFYVE9	4.9E-01	5.3E-01
62	Homo sapiens protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform (PPP2CB), mRNA.	NM_004156	PPP2CB	2.8E+00	5.1E-01
63	AGENCOURT_7504507 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6049909 5', mRNA sequence.	BQ214665	EP300	1.1E-01	3.8E-01
64	Homo sapiens E2F transcription factor 5, p130-binding (E2F5), mRNA.	NM_001951	E2F5	2.9E-03	1.5E-02

Table 7 40 genes classified in angiogenesis of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Control signal_norm)
1	angiopoietin-like 3 (ANGPTL3), mRNA.	NM_014495	ANGPTL3	3.3E-01	4.9E+00
2	Homo sapiens, clone IMAGE:4186245, mRNA.	BC026731	EPAS1	2.6E-01	4.4E+00
3	fibroblast growth factor 1 (acidic) (FGF1), transcript variant 1, mRNA.	NM_000800	FGF1	4.6E-01	3.0E+00
4	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator (ARTS-1), mRNA.	NM_016442	ARTS-1	3.6E-01	2.4E+00
5	angiopoietin 2 (ANGPT2), mRNA.	NM_001147	ANGPT2	1.8E-01	2.1E+00
6	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) (FLT1), mRNA.	NM_002019	FLT1	1.9E-01	2.1E+00
7	hypothetical protein PRO2714 (PRO2714), mRNA.	NM_018534	NRP2	8.0E-01	1.9E+00
8	vascular endothelial growth factor C (VEGFC), mRNA.	NM_005429	VEGFC	5.0E+00	1.8E+00
9	keratin 1 (epidermolytic hyperkeratosis) (KRT1), mRNA.	NM_006121	KRT1	5.4E-01	1.6E+00
10	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A) (NPR1), mRNA.	NM_000906	NPR1	2.3E-01	1.6E+00
11	endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA.	NM_001953	ECGF1	1.7E-01	1.4E+00
12	cDNA FLJ13510 fis, clone PLACE1005146.	AK023572	EPAS1	1.5E-01	1.4E+00
13	clone 23698 mRNA sequence.	AF052094	EPAS1	3.3E+00	1.4E+00
14	tumor endothelial marker 7 precursor (TEM7), mRNA.	NM_020405	PLXDC1	2.8E-01	1.3E+00
15	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1 (SERPINF1), mRNA.	NM_002615	SERPINF1	3.5E+00	1.1E+00
16	cDNA FLJ13731 fis, clone PLACE3000142.	AK023793	JAG1	6.0E-01	1.1E+00
17	troponin I, cardiac (TNNI3), mRNA.	NM_000363	TNNI3	1.1E-01	1.1E+00
18	natriuretic peptide precursor B (NPPB), mRNA.	NM_002521	NPPB	3.7E-01	9.4E-01
19	collagen, type XV, alpha 1 (COL15A1), mRNA.	NM_001855	COL15A1	2.9E-01	9.1E-01
20	neuropilin 1 (NRP1), mRNA.	NM_003873	NRP1	4.7E-01	9.0E-01
21	ras homolog gene family, member B (ARHB), mRNA.	NM_004040	RHOB	2.5E-01	8.8E-01
22	cDNA FLJ13880 fis, clone THYRO1001434.	AK023942	NRP2	1.1E+00	8.8E-01
23	SH2 domain protein 2A (SH2D2A), mRNA.	NM_003975	SH2D2A	7.4E-01	8.0E-01
24	stabilin 1 (STAB1), mRNA.	NM_015136	STAB1	3.6E-01	7.6E-01
25	pp3859 mRNA, complete cds.	AF318349	ERBB2	2.1E+00	7.5E-01
26	jagged 1 (Alagille syndrome) (JAG1), mRNA.	NM_000214	JAG1	2.6E-01	7.2E-01
27	clone IMAGE:451939, mRNA sequence.	AF339822	FLT1	2.0E-01	7.0E-01
28	epiregulin (EREG), mRNA.	NM_001432	EREG	9.0E-02	7.0E-01
29	placental growth factor, vascular endothelial growth factor-related protein (PGF), mRNA.	NM_002632	PGF	3.8E-01	6.3E-01
30	transcriptional coactivator tubedown-100 (TBDN100), transcript variant 1, mRNA.	NM_057175	NARG1	4.4E-01	6.1E-01
31	interleukin 18 (interferon-gamma-inducing factor) (IL18), mRNA.	NM_001562	IL18	2.6E-01	5.8E-01
32	fibroblast growth factor 2 (basic) (FGF2), mRNA.	NM_002006	FGF2	1.6E+00	5.8E-01
33	tumor necrosis factor receptor superfamily, member 12A (TNFRSF12A),	NM_016639	NFRSF12	1.5E+00	5.5E-01
34	interleukin 17F (IL17F), transcript variant 2, mRNA.	NM_172343	-	1.6E-01	5.5E-01
35	B-cell translocation gene 1, anti-proliferative (BTG1), mRNA.	NM_001731	BTG1	1.8E+00	5.1E-01
36	type II transmembrane serine protease 6 (TMPRSS6), mRNA.	NM_153609	TMPRSS6	2.1E-01	5.1E-01
37	hypothetical protein FLJ10283 (FLJ10283), mRNA.	NM_018046	AGGF1	7.0E-01	5.1E-01
38	platelet factor 4 (chemokine (C-X-C motif) ligand 4) (PF4), mRNA.	NM_002619	PF4	2.4E-01	1.7E-01
39	angiopoietin-like 4 (ANGPTL4), transcript variant 1, mRNA.	NM_139314	ANGPTL4	4.1E-01	6.1E-02
40	NEU1 protein (ZNEU1), mRNA.	NM_016215	EGFL7	1.0E-06	4.2E-05

Table 8 67 genes classified in collagen and aggrecan of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days

No.	Gene Name	Gene Identifier	Gene symbol	Test signal_norm	Fold change(=Test signal_norm/Control signal_norm)
1	aggrecan 1 (chondroitin sulfate proteoglycan 1. large aggregating proteoglycan, antigen identified by monoclonal antibody A0122) (AGC1), transcript variant 2, mRNA.	NM_013227	AGC1	7.1E+00	7.7E+00
2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid hormone binding protein p55) (P4HB), mRNA.	NM_000918	P4HB	5.6E-01	5.5E+00
3	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA.	NM_000090	COL3A1	6.4E+00	5.0E+00
4	collagen, type I, alpha 1 (COL1A1), mRNA.	NM_000088	COL1A1	7.1E-01	4.8E+00
5	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II (P4HA2), mRNA.	NM_004199	P4HA2	1.4E+01	4.0E+00
6	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2 (SERPINH2), mRNA.	NM_001235	SERPINH1	9.8E-01	3.7E+00
7	matrix metalloproteinase 13 (collagenase 3) (MMP13), mRNA.	NM_002427	MMP13	2.3E-01	3.5E+00
8	cDNA FLJ11469 fis, clone HEMBA1001658.	AK021531	COL3A1	9.9E-01	3.2E+00
9	collagen, type IV, alpha 6 (COL4A6), transcript variant B, mRNA.	NM_033641	COL4A6	3.0E-01	3.1E+00
10	collagen, type V, alpha 2 (COL5A2), mRNA.	NM_000393	COL5A2	6.0E+00	2.9E+00
11	collagen, type IV, alpha 1 (COL4A1), mRNA.	NM_001845	COL4A1	5.5E+00	2.7E+00
12	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD), mRNA.	NM_000302	PLOD1	1.3E+01	2.7E+00
13	procollagen C-endopeptidase enhancer (PCOLCE), mRNA.	NM_002593	PCOLCE	7.7E+00	2.4E+00
14	collagen, type IV, alpha 2 (COL4A2), mRNA.	NM_001846	COL4A2	2.1E+00	2.2E+00
15	collagen, type VI, alpha 3 (COL6A3), transcript variant 1, mRNA.	NM_004369	COL6A3	2.2E+01	2.2E+00
16	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1), mRNA.	NM_003254	TIMP1	4.7E+01	2.1E+00
17	collagen, type XI, alpha 1 (COL11A1), transcript variant B, mRNA.	NM_080629	COL11A1	9.6E+00	2.1E+00
18	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) (MMP2), mRNA.	NM_004530	MMP2	2.2E-01	2.0E+00
19	collagen, type VI, alpha 2 (COL6A2), transcript variant 2C2, mRNA.	NM_001849	COL6A2	9.2E+00	2.0E+00
20	mRNA for FLJ00201 protein.	AK074129	COL8A2	1.6E+00	1.9E+00
21	full length insert cDNA clone ZC33A09.	AF086191	COL5A1	7.0E-01	1.8E+00
22	collagen, type V, alpha 1 (COL5A1), mRNA.	NM_000093	COL5A1	7.3E-01	1.8E+00
23	mRNA; cDNA DKFZp434L0823 (from clone DKFZp434L0823).	AL833965	P4HA3	6.3E-01	1.8E+00
24	KIAA1870 protein (KIAA1870), mRNA.	NM_032888	COL27A1	2.2E-01	1.7E+00
25	Homo sapiens, clone IMAGE:3892140, mRNA.	BC013423	P4HA2	7.1E-01	1.6E+00
26	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant VI, mRNA.	NM_080542	COLQ	3.2E-01	1.6E+00
27	cDNA FLJ11536 fis, clone HEMBA1002712.	AK021598	COL5A1	1.8E+00	1.5E+00
28	full length insert cDNA clone ZD50G09.	AF086302	COL14A1	4.5E-01	1.5E+00
29	collagen, type XXI, alpha 1 (COL21A1), mRNA.	NM_030820	COL21A1	6.3E-01	1.5E+00
30	collagen, type XVI, alpha 1 (COL16A1), mRNA.	NM_001856	COL16A1	2.6E+00	1.4E+00
31	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2), mRNA.	NM_000935	PLOD2	1.8E+00	1.4E+00
32	Homo sapiens, clone IMAGE:3506644, mRNA, partial cds.	BC005159	COL6A1	6.8E-01	1.4E+00
33	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I (P4HA1), mRNA.	NM_000917	P4HA1	5.2E-01	1.4E+00
34	Homo sapiens, Similar to RIKEN cDNA 1700051112 gene, clone MGC:24967 IMAGE:4933482, mRNA, complete cds.	BC019637	KIAA1510	4.5E-01	1.4E+00
35	collagen, type XVIII, alpha 1 (COL18A1), transcript variant 1, mRNA.	NM_030582	COL18A1	3.0E-01	1.4E+00
36	collagen triple helix repeat containing 1 (CTHRC1), mRNA.	NM_138455	CTHRC1	7.2E+00	1.3E+00
37	procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA.	NM_013363	PCOLCE2	4.0E-01	1.3E+00
38	cDNA FLJ11973 fis, clone HEMBB1001221.	AK022035	COL11A1	2.3E+00	1.3E+00
39	collagen, type XIII, alpha 1 (COL13A1), transcript variant 1, mRNA.	NM_005203	COL13A1	2.6E-01	1.3E+00
40	collagen, type I, alpha 2 (COL1A2), mRNA.	NM_000089	COL1A2	3.6E-01	1.2E+00
41	mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds.	AL137461	COL23A1	2.6E-01	1.2E+00
42	mRNA for KIAA1983 protein.	AB075863	CCBE1	5.8E-01	1.0E+00
43	collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA.	NM_000493	COL10A1	1.9E-01	9.3E-01
44	cDNA FLJ38793 fis, clone LIVER2003568.	AK096112	FCN2	7.3E-02	9.3E-01
45	collagen, type XIX, alpha 1 (COL19A1), mRNA.	NM_001858	COL19A1	3.5E-01	9.2E-01
46	collagen, type IX, alpha 1 (COL9A1), transcript variant 1, mRNA.	NM_001851	COL9A1	2.2E-01	9.2E-01
47	collagen, type XV, alpha 1 (COL15A1), mRNA.	NM_001855	COL15A1	2.9E-01	9.1E-01
48	cDNA FLJ40439 fis, clone TESTI2039867.	AK097758	COL10A1	1.5E-01	9.0E-01

49	collagen, type VIII, alpha 1 (COL8A1), mRNA.	NM_001850	COL8A1	5.2E+00	8.6E-01
50	Homo sapiens, clone IMAGE:4429946, mRNA.	BC015452	-	2.0E-01	8.3E-01
51	Homo sapiens, similar to collagen, clone IMAGE:5179937, mRNA.	BC032383	LOC147645	1.7E-01	7.9E-01
52	macrophage receptor with collagenous structure (MARCO), mRNA.	NM_006770	MARCO	5.1E-02	7.9E-01
53	collagen type XXIV, alpha 1 (COL24A1), mRNA.	NM_152890	COL24A1	2.1E-01	7.8E-01
54	adipose most abundant gene transcript 1 (APM1), mRNA.	NM_004797	ACDC	1.8E-01	7.2E-01
55	Homo sapiens, clone IMAGE:4111050, mRNA.	BC006310	COL27A1	2.1E-01	7.1E-01
56	Homo sapiens, clone IMAGE:5266441, mRNA.	BC036509	ACDC	1.5E-01	6.4E-01
57	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive) (COL7A1), mRNA.	NM_000094	COL7A1	1.1E+00	6.1E-01
58	collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital) (COL2A1), transcript variant 1, mRNA.	NM_001844	COL2A1	4.2E-01	5.9E-01
59	collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA.	NM_080680	COL11A2	9.7E-02	5.9E-01
60	collagen, type V, alpha 3 (COL5A3), mRNA.	NM_015719	COL5A3	2.3E-01	5.7E-01
61	on68b01.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1561801 3' similar to gb:M76729 PROCOLLAGEN ALPHA 1(V) CHAIN PRECURSOR (HUMAN);, mRNA sequence.	AA948539	LOC374395	3.2E-01	5.7E-01
62	matrix metalloproteinase 1 (interstitial collagenase) (MMP1), mRNA.	NM_002421	MMP1	1.7E-01	5.6E-01
63	collagen, type XII, alpha 1 (COL12A1), transcript variant long, mRNA.	NM_004370	COL12A1	1.0E-06	3.5E-03
64	ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA.	NM_002003	FCN1	1.0E-06	6.6E-06
65	Homo sapiens, similar to collagen, clone IMAGE:5179937, mRNA.	BC032383	LOC147645	1.7E-01	7.9E-01
66	Homo sapiens, Similar to RIKEN cDNA 1700051112 gene, clone MGC:24967 IMAGE:4933482, mRNA, complete cds.	BC019637	KIAA1510	4.5E-01	1.4E+00
67	on68b01.s1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:1561801 3' similar to gb:M76729 PROCOLLAGEN ALPHA 1(V) CHAIN PRECURSOR (HUMAN);, mRNA sequence.	AA948539	LOC374395	3.2E-01	5.7E-01

genic differentiation medium for 14 days by the fold change order from the largest to the least with details of gene name, gene identifier, gene symbol, test signal_norm and fold change. Both collagen type I, alpha 1 (COL1A1) gene abundant in bone and aggrecan 1 (AGC1) gene present in cartilage were up-regulated 4.8-fold and 7.7-fold, respectively. Many other collagen-related genes were up-regulated more than 2-fold, indicating that other connective tissues (e.g. tendon and ligament) were attempted to be produced.

DISCUSSION

Osteogenic differentiation medium used has been recognized as a world-wide standard medium for bone studies⁹, but yet the differentiation mechanism of stem cells and osteoblasts remains largely undefined and unknown at molecular and biochemical levels¹⁸) The safety of the use of osteogenic differentiation medium for human patients is not confirmed, yet, either. It seems, there-

fore, quite important to carry out genome-wide screening of genes of human mesenchymal stem cells exposed to osteogenic differentiation medium.

We selected 14 days as the culture period with osteogenic differentiation medium because most well-known osteogenic differentiation marker genes (e.g. osteopontin, bone sialo protein and osteocalcin genes) appear and peak in this middle-to-latter stage of osteogenic differentiation lineage from mesenchymal stem cells¹² and osteoblasts¹⁹. It is, of course, hoped to evaluate gene expressions of mesenchymal stem cells at different culture periods with osteogenic differentiation medium such as 7 and 21 days. The high cost to conduct DNA microarray analysis presently hindered these experiments. It was speculated that the expression of early-to-middle stage osteogenic differentiation marker genes such as alkaline phosphatase might increase at 7 days, peak at 14 days, but decline at 21 days^{12,14}. It was anticipated that expression of middle to later stage osteoblast marker genes

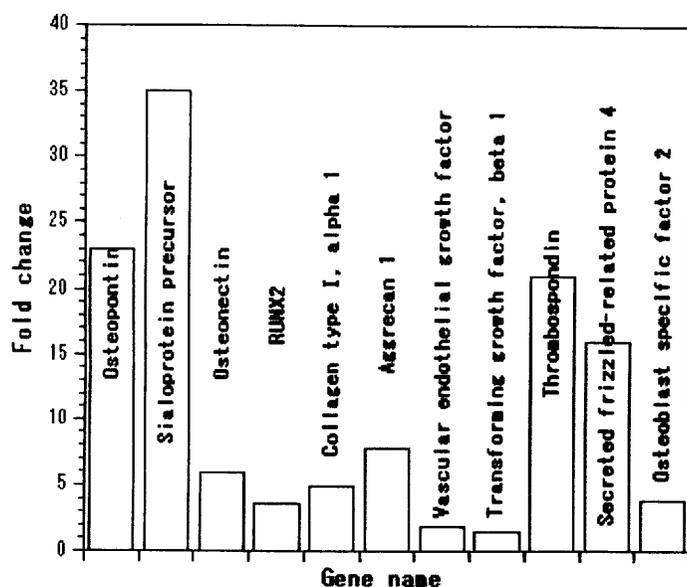


Fig. 1 The fold change of 11 selective genes of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days.

such as osteopontin might emerge at 7 days, peak at 14 days, but stagnate or decline at 21 days^{12,14}. It was hinted that matrix Gla protein (MGP) gene would be up-regulated and osteoblast-specific osteocalcin gene would appear¹². Expressions of other genes at 7 and 21 days might significantly differ from those at 14 days¹⁴, and need to be clarified in the near future.

It became clear from the results obtained that osteogenic differentiation medium differentiated human mesenchymal stem cells largely into osteoblasts with several characteristic phenotype genes such as those of sialoprotein precursor and osteopontin significantly up-regulated (Table 3), but simultaneously differentiated them into chondroblasts with their characteristic extracellular matrix genes such as those of chondroitin sulfate proteoglycan 2 and aggrecan 1 considerably up-regulated²⁰ (Tables 4 and 8). It should be noted that osteogenic differentiation medium also increased expressions of some genes classified in

extracellular matrix (sensu Metazoa) (Table 4), cell differentiation (Table 5), TGF-beta signaling pathway (Table 6), angiogenesis (Table 7), and collagen and aggrecan (Table 8). These results appear to reflect endochondral ossification²¹ from mesenchymal stem cells with vascular invasion. Fig. 1 shows the fold change of 11 selective genes of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days, reflecting endochondral ossification with vascular invasion.

This study has two clinical meanings. Table 1 might be a candidate sheet of new marker genes to assess the osteogenic differentiation of mesenchymal stem cells. The search of such genes is still continued²². It is still very difficult to collect and isolate pure human mesenchymal stem cells (only 0.01 to 1%) from aspirated bone marrows from the patients^{2,23}. For cell purification, it is very useful to use antibody of mesenchymal stem cells (e.g. CD44⁺ and CD74²²) coated with surfaces of later-collectable magnetic beads. Table 2 might provide new marker genes specific for mesenchymal stem cells²² as well.

In the brief summary, it can be stated that osteogenic differentiation medium not only facilitated osteogenic differentiation of mesenchymal stem cells but also chondrogenic differentiation in gene expression levels with up-regulation of many other genes related to angiogenesis, TGF-beta signaling pathway, other cell differentiation, and collagen and aggrecan synthesis. The role of the osteogenic differentiation medium could not be solely confined to

ossification, but could be associated with many other biological functions (thus, more complicated and systematic). Research is highly probable to confirm and compare with in protein levels the gene expressions of human mesenchymal stem cells cultured in osteogenic differentiation medium for 14 days in the near future.

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