Supplementary Table S8. Functional enrichment analyses of the differently expressed mRNAs from the proliferation high/low comparison.

Cluster number	Enrichment score	Term	Counts	Population hits	False discovery rate
1	9.97	Cell adhesion	43	700	0,0000
		Biological adhesion	43	701	0,0000
		Cell adhesion	23	422	0,0010
2	9.68	Secreted	76	1689	0,0000
		Extracellular region part	55	960	0,0000
		Signal	102	3250	0,0000
		Signal peptide	102	3250	0,0000
		Extracellular region	81	2010	0,0000
3	5.42	Cell migration	19	276	0,0026
		Cell motion	25	475	0,0047
		Localization of cell	19	307	0,0119
		Cell motility	19	307	0,0119
4	5.33	Extracellular matrix	25	241	0,0000
		Proteinaceous extracellular matrix	29	320	0,0000
		Collagen	12	35	0,0000
		Extracellular matrix	29	345	0,0000
		Collagen	15	95	0,0000
5	5.19	Skeletal system development	26	319	0,0000
		Bone development	14	123	0,0004
		Ossification	13	115	0,0012
		Cartilage development	9	74	0,0703
		Osteoblast differentiation	7	42	0,1363

The terms in the five first clusters, with enrichment scores, are shown (only the first five terms in clusters 2, 4 and 5).

The counts and population hits are the number of genes in the gene list and background gene list, respectively, mapping to a specific term.