Supplementary Table S5. Functional enrichment analyses of the differently expressed mRNAs from the tumorigenic high/low comparison.

Cluster number	Enrichment score	Term	Counts	Population hits	False discovery rate
1	5.69	Extracellular matrix	29	345	0,0000
		Extracellular region part	50	960	0,0000
		Signal	102	3250	0,0000
		Proteinaceous extracellular matrix	26	320	0,0000
		Signal peptide	102	3250	0,0000
2	5.20	Vasculature development	22	251	0,0001
		Blood vessel development	21	245	0,0003
		Blood vessel morphogenesis	16	211	0,0609
		Angiogenesis	10	148	6,3243
3	4.26	Extracellular matrix organization	13	104	0,0028
		Extracellular structure organization	14	163	0,0616
		Collagen fibril organization	5	29	4,8673
4	3.80	Growth factor binding	14	105	0,0005
		domain:IGFBP N-terminal	6	20	0,0391
		SM00121:IB	6	20	0,0373
		Insulin-like growth factor-binding protein, IGFBP	6	20	0,0491
		Insulin-like growth factor binding protein, N-terminal	5	12	0,0917
5	3.54	Skeletal system development	19	319	0,2113
		Ossification	11	115	0,2413
		Bone development	11	123	0,4196
		Osteoblast differentiation	6	42	2,8940

The terms in the five first clusters, with enrichment scores, are shown (only the first five terms in clusters 1 and 4).
The counts and population hits are the number of genes in the gene list and background gene list, respectively, mapping to a specific term.