

Supplementary Table S6. Functional enrichment analyses of the differently expressed mRNAs from the clonogenic high/low comparison.

Cluster number	Enrichment score	Term	Counts	Population hits	False discovery rate
1	4.04	Extracellular matrix	8	241	0,0002
		Extracellular region part	13	960	0,0005
		Proteinaceous extracellular matrix	8	320	0,0060
		Extracellular matrix	8	345	0,0098
		Secreted	13	1689	0,0207
2	2.82	Extracellular matrix	8	241	0,0002
		Collagen	5	35	0,0011
		Proteinaceous extracellular matrix	8	320	0,0060
		Extracellular matrix part	6	117	0,0063
		Extracellular matrix	8	345	0,0098
3	2.40	Regulation of blood pressure	4	100	1,8312
		Blood circulation	4	186	10,1410
		Circulatory system process	4	186	10,1410
4	2.16	Focal adhesion	6	201	0,1834
		Small cell lung cancer	3	84	20,5064
		Pathways in cancer	4	328	47,6286
5	1.87	Urogenital system development	4	110	2,4027
		Gland development	4	135	4,2684
		Tissue morphogenesis	4	180	9,3046
		Epithelium development	4	227	16,8330
		Kidney development	3	96	23,4571

The terms in the five first clusters, with enrichment scores, are shown (only the first five terms in clusters 1, 2 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.