

Supplementary Figure S3. Heatmap with Gene Ontology: Biological Functions analysis. Numbers in rows presents number of genes associated with particular function.

Biological Function	Cluster 1	Cluster 2
<i>signal transduction</i>	102	47
<i>positive regulation of transcription from RNA polymerase II promoter</i>	67	36
<i>positive regulation of GTPase activity</i>	53	7
<i>positive regulation of cell migration</i>	40	33
<i>response to drug</i>	35	17
<i>extracellular matrix organization</i>	33	40
<i>aging</i>	29	31
<i>protein phosphorylation</i>	28	42
<i>negative regulation of gene expression</i>	24	0
<i>phosphatidylinositol phosphorylation</i>	23	6
<i>positive regulation of smooth muscle cell proliferation</i>	22	5
<i>positive regulation of ERK1 and ERK2 cascade</i>	22	4
<i>MAPK cascade</i>	22	4
<i>response to hypoxia</i>	19	3
<i>activation of MAPK activity</i>	19	0
<i>cerebral cortex development</i>	18	17
<i>regulation of phosphatidylinositol 3-kinase signaling</i>	18	4
<i>platelet activation</i>	16	15
<i>collagen catabolic process</i>	15	26
<i>phosphatidylinositol-mediated signaling</i>	15	3
<i>positive regulation of phospholipase C activity</i>	15	2
<i>peptidyl-tyrosine phosphorylation</i>	14	3
<i>positive regulation of positive chemotaxis</i>	14	3
<i>positive regulation of nitric oxide biosynthetic process</i>	13	6
<i>cell adhesion</i>	13	0
<i>protein stabilization</i>	12	6
<i>chemotaxis</i>	12	0
<i>response to cold</i>	11	18
<i>positive regulation of MAP kinase activity</i>	11	9

<i>positive regulation of cell proliferation</i>	11	5
<i>cell adhesion mediated by integrin</i>	11	2
<i>cellular response to estradiol stimulus</i>	10	2
<i>nervous system development</i>	10	0
<i>positive regulation of gene expression</i>	10	0
<i>positive regulation of protein complex assembly</i>	9	2
<i>leukocyte chemotaxis</i>	9	0
<i>phosphatidylinositol-3-phosphate biosynthetic process</i>	9	0
<i>positive regulation of protein kinase B signaling</i>	9	0
<i>cell-matrix adhesion</i>	9	0
<i>temperature homeostasis</i>	8	12
<i>cellular response to insulin-like growth factor stimulus</i>	8	2
<i>sphingolipid biosynthetic process</i>	8	0
<i>insulin-like growth factor receptor signaling pathway</i>	8	0
<i>G-protein coupled acetylcholine receptor signaling pathway</i>	8	0
<i>positive regulation of protein phosphorylation</i>	7	12
<i>positive regulation of angiogenesis</i>	7	3
<i>positive regulation of developmental growth</i>	6	6
<i>release of sequestered calcium ion into cytosol</i>	6	3
<i>positive regulation of peptidyl-tyrosine phosphorylation</i>	6	3
<i>positive regulation of cell adhesion</i>	6	2
<i>response to muscle activity</i>	6	2
<i>negative regulation of protein phosphorylation</i>	6	0
<i>integrin-mediated signaling pathway</i>	6	0
<i>positive regulation of leukocyte migration</i>	6	0
<i>cellular glucose homeostasis</i>	6	0
<i>skeletal system development</i>	4	8
<i>response to superoxide</i>	4	8
<i>fatty acid oxidation</i>	4	2
<i>regulation of immunoglobulin secretion</i>	4	0
<i>glutamate receptor signaling pathway</i>	4	0
<i>regulation of smooth muscle contraction</i>	4	0

<i>cellular response to amino acid stimulus</i>	3	12
<i>positive regulation of cysteine-type endopeptidase activity involved in apoptotic process</i>	3	0
<i>positive regulation of endothelial cell migration</i>	3	0
<i>positive regulation of cell division</i>	3	0
<i>aorta smooth muscle tissue morphogenesis</i>	2	10
<i>positive regulation of glycolytic process</i>	2	4
<i>smooth muscle contraction</i>	2	4
<i>positive regulation of lipophagy</i>	2	0
<i>inositol phosphate biosynthetic process</i>	2	0
<i>regulation of phosphatidylinositol 3-kinase activity</i>	2	0
<i>regulation of establishment of endothelial barrier</i>	2	0
<i>positive regulation of protein kinase C signaling</i>	2	0
<i>tube formation</i>	2	0
<i>phosphatidylinositol metabolic process</i>	2	0
<i>sleep</i>	2	0
<i>cell migration involved in sprouting angiogenesis</i>	2	0
<i>positive regulation of blood vessel endothelial cell migration</i>	2	0
<i>positive regulation of focal adhesion assembly</i>	2	0

Supplementary Figure S4. Heatmap with Gene Ontology: Cellular Compartment analysis. Numbers in rows presents number of genes associated with particular function.

Cellular Compartment	Cluster 1	Cluster 2
<i>cytoplasm</i>	72	46
<i>membrane</i>	71	13
<i>extracellular region</i>	58	68
<i>extracellular space</i>	51	43
<i>cytosol</i>	48	0
<i>plasma membrane</i>	43	16
<i>Golgi apparatus</i>	42	34
<i>proteinaceous extracellular matrix</i>	23	36
<i>collagen trimer</i>	21	38
<i>extracellular matrix</i>	20	14
<i>external side of plasma membrane</i>	20	0
<i>receptor complex</i>	16	27
<i>cytoskeleton</i>	15	4
<i>intracellular</i>	15	0
<i>membrane raft</i>	14	3
<i>nuclear euchromatin</i>	12	2
<i>endoplasmic reticulum lumen</i>	11	40
<i>integral component of plasma membrane</i>	10	9
<i>extrinsic component of membrane</i>	9	0
<i>early endosome</i>	8	16
<i>endoplasmic reticulum</i>	8	0
<i>focal adhesion</i>	5	0
<i>lamellipodium</i>	4	8
<i>integrin complex</i>	4	0
<i>filopodium</i>	3	6
<i>cell-cell junction</i>	3	3
<i>intrinsic component of plasma membrane</i>	2	2
<i>CD40 receptor complex</i>	2	0
<i>collagen type IV trimer</i>	0	8
<i>organelle membrane</i>	0	6
<i>collagen type VI trimer</i>	0	4
<i>endosome membrane</i>	0	3