

**Supplementary Table 2.** Genes correlated to *EGFL7* expression present in each enriched gene ontology term

Gene ontology term	p-value	Genes
GO:0001525~angiogenesis	<.001	<i>ACVRL1, ROBO4, EGFL7, NOS3, TIE1, ECSCR, PLXDC1, RASIP1, DLL4, EMCN, SOX17, SOX18, MMRN2</i>
GO:0001570~vasculogenesis	<.001	<i>EGFL7, SOX17, SOX18, TIE1, RASIP1</i>
GO:0001946~lymphangiogenesis	<.001	<i>ACVRL1, SOX18, FLT4</i>
GO:0007220~Notch receptor processing	.001	<i>JAG2, DLL4, NOTCH4</i>
GO:0007043~cell-cell junction assembly	.002	<i>CLDN5, CDH5, GJA4</i>
GO:0001938~positive regulation of endothelial cell proliferation	.002	<i>ACVRL1, EGFL7, FLT4, PDGFB</i>
GO:0007179~transforming growth factor beta receptor signaling pathway	.004	<i>ACVRL1, CLDN5, CDH5, PDGFB</i>
GO:0001701~in utero embryonic development	.004	<i>JAG2, ACVRL1, SOX18, NOS3, TIE1</i>
GO:0045746~negative regulation of Notch signaling pathway	.005	<i>DLL4, EGFL7, PEAR1</i>
GO:0030198~extracellular matrix organization	.005	<i>FOXF2, VWF, LAMC3, PDGFB, ICAM2</i>
GO:0016337~single organismal cell-cell adhesion	.005	<i>CDH5, EMCN, ICAM2, ESAM</i>
GO:0001974~blood vessel remodeling	.005	<i>DLL4, ACVRL1, NOS3</i>
GO:0048866~stem cell fate specification	.007	<i>SOX17, SOX18</i>
GO:0045892~negative regulation of transcription, DNA-templated	.007	<i>FOXS1, FOXF2, SOX18, PDGFB, NOSTRIN, SOX7, TNFRSF4</i>
GO:0001568~blood vessel development	.008	<i>FOXS1, EGFL7, GJA4</i>
GO:0045893~positive regulation of transcription, DNA-templated	.009	<i>ACVRL1, SOX17, FOXF2, SOX18, NOTCH4, PDGFB, SOX7</i>
GO:0008015~blood circulation	.011	<i>DLL4, ACVRL1, ADORA2A</i>
GO:0003151~outflow tract morphogenesis	.011	<i>CLDN5, SOX17, SOX18</i>
GO:0008285~negative regulation of cell proliferation	.012	<i>DLL4, ACVRL1, CDH5, ADORA2A, NOS3, SOX7</i>
GO:0007189~adenylate cyclase-activating G-protein coupled receptor signaling pathway	.013	<i>PTGIR, ADORA2A, ADCY4</i>
GO:1903142~positive regulation of establishment of endothelial barrier	.014	<i>CLDN5, CDH5</i>
GO:0060214~endocardium formation	.014	<i>SOX17, SOX18</i>
GO:0018108~peptidyl-tyrosine phosphorylation	.016	<i>TIE1, FLT4, IL3RA, PDGFB</i>
GO:0060836~lymphatic endothelial cell differentiation	.017	<i>ACVRL1, SOX18</i>
GO:0045602~negative regulation of endothelial cell differentiation	.017	<i>ACVRL1, NOTCH4</i>
GO:0060956~endocardial cell differentiation	.017	<i>SOX17, SOX18</i>
GO:0016525~negative regulation of angiogenesis	.019	<i>TIE1, ECSCR, GPR4</i>
GO:0007155~cell adhesion	.021	<i>CDH5, EGFL7, VWF, LAMC3, ICAM2, SCARF1</i>
GO:0003209~cardiac atrium morphogenesis	.024	<i>DLL4, CCM2L</i>
GO:0035912~dorsal aorta morphogenesis	.027	<i>DLL4, ACVRL1</i>
GO:0072091~regulation of stem cell proliferation	.027	<i>SOX17, SOX18</i>
GO:0010544~negative regulation of platelet activation	.027	<i>NOS3, PDGFB</i>
GO:0001945~lymph vessel development	.027	<i>TMEM204, FLT4</i>
GO:0001955~blood vessel maturation	.027	<i>ACVRL1, CDH5</i>
GO:0043410~positive regulation of MAPK cascade	.032	<i>FLT4, PDGFB, TNFRSF4</i>
GO:0090051~negative regulation of cell migration involved in sprouting angiogenesis	.037	<i>DLL4, MMRN2</i>
GO:0001944~vasculature development	.040	<i>SOX18, FLT4</i>
GO:0001706~endoderm formation	.041	<i>SOX17, SOX7</i>
GO:0003016~respiratory system process	.044	<i>JAG2, FLT4</i>
GO:0043547~positive regulation of GTPase activity	.045	<i>RGS5, PTGIR, ARHGEF15, IL3RA, SH2D3C, PDGFB</i>

EGFL7, epidermal growth factor-like domain multiple 7.