

S4 Table. Enriched GO terms associated with Wnt3a targets

GO terms associted with up-regulated genes			
GO ID	Enriched Biological Process	No. genes	FDR
GO:0042127	regulation of cell proliferation	74	8.32E-16
GO:0048729	tissue morphogenesis	48	4.25E-15
GO:0048646	anatomical structure formation involved in morphogenesis	62	1.81E-14
GO:0001944	vasculature development	44	2.48E-14
GO:0007167	enzyme linked receptor protein signaling pathway	53	9.46E-14
GO:0051094	positive regulation of developmental process	61	1.03E-13
GO:0001525	angiogenesis	35	3.59E-13
GO:0009719	response to endogenous stimulus	70	3.59E-13
GO:0060485	mesenchyme development	27	4.59E-13
GO:0023057	negative regulation of signaling	58	2.73E-12
GO:0048585	negative regulation of response to stimulus	63	2.73E-12
GO:0051270	regulation of cellular component movement	46	2.75E-12
GO:0048762	mesenchymal cell differentiation	23	3.58E-12
GO:0040007	growth	52	3.58E-12
GO:0010648	negative regulation of cell communication	58	3.58E-12
GO:0030334	regulation of cell migration	42	5.47E-12
GO:0007267	cell-cell signaling	55	7.67E-12
GO:0048863	stem cell differentiation	27	8.20E-12
GO:2000145	regulation of cell motility	43	9.86E-12
GO:0040012	regulation of locomotion	45	1.01E-11
GO:0016477	cell migration	56	1.50E-11
GO:0009968	negative regulation of signal transduction	53	1.52E-11
GO:0090130	tissue migration	24	1.95E-11
GO:0071363	cellular response to growth factor stimulus	38	1.95E-11
GO:0009967	positive regulation of signal transduction	60	2.51E-11
GO:0070848	response to growth factor	38	6.73E-11
GO:0006928	movement of cell or subcellular component	68	7.07E-11
GO:0045597	positive regulation of cell differentiation	46	8.75E-11
GO:0051674	localization of cell	57	1.42E-10
GO:0048870	cell motility	57	1.42E-10
GO:0051093	negative regulation of developmental process	44	1.78E-10
GO:0000904	cell morphogenesis involved in differentiation	42	1.78E-10
GO:0008284	positive regulation of cell proliferation	44	2.45E-10
GO:0014031	mesenchymal cell development	20	3.04E-10
GO:0008285	negative regulation of cell proliferation	38	3.33E-10
GO:0040011	locomotion	63	3.88E-10
GO:0045595	regulation of cell differentiation	62	4.71E-10
GO:0048864	stem cell development	20	4.92E-10
GO:0023056	positive regulation of signaling	61	5.54E-10
GO:0010647	positive regulation of cell communication	61	9.31E-10
GO:0030335	positive regulation of cell migration	29	1.07E-09
GO:0040017	positive regulation of locomotion	30	1.11E-09

<i>GO:0010941</i>	<i>regulation of cell death</i>	60	<i>1.15E-09</i>
<i>GO:2000147</i>	<i>positive regulation of cell motility</i>	29	<i>1.99E-09</i>
<i>GO:0022610</i>	<i>biological adhesion</i>	57	<i>2.12E-09</i>
<i>GO:0007178</i>	<i>transmembrane receptor protein serine/threonine kinase signaling pathway</i>	25	<i>2.46E-09</i>
<i>GO:0051272</i>	<i>positive regulation of cellular component movement</i>	29	<i>3.41E-09</i>
<i>GO:0042981</i>	<i>regulation of apoptotic process</i>	56	<i>3.41E-09</i>
<i>GO:0060393</i>	<i>regulation of pathway-restricted SMAD protein phosphorylation</i>	12	<i>4.01E-09</i>
<i>GO:0007155</i>	<i>cell adhesion</i>	56	<i>4.38E-09</i>
<i>GO:0043067</i>	<i>regulation of programmed cell death</i>	56	<i>4.97E-09</i>
<i>GO:0012501</i>	<i>programmed cell death</i>	65	<i>4.97E-09</i>
<i>GO:0001932</i>	<i>regulation of protein phosphorylation</i>	53	<i>4.97E-09</i>
<i>GO:0060389</i>	<i>pathway-restricted SMAD protein phosphorylation</i>	12	<i>6.73E-09</i>
<i>GO:0006915</i>	<i>apoptotic process</i>	64	<i>7.15E-09</i>
<i>GO:0042325</i>	<i>regulation of phosphorylation</i>	55	<i>7.40E-09</i>
<i>GO:0001763</i>	<i>morphogenesis of a branching structure</i>	20	<i>1.56E-08</i>
<i>GO:0040008</i>	<i>regulation of growth</i>	35	<i>1.86E-08</i>
<i>GO:0014070</i>	<i>response to organic cyclic compound</i>	43	<i>2.61E-08</i>
<i>GO:0090092</i>	<i>regulation of transmembrane receptor protein serine/threonine kinase signaling pathway</i>	19	<i>3.08E-08</i>
<i>GO:0006468</i>	<i>protein phosphorylation</i>	63	<i>3.08E-08</i>
<i>GO:0002040</i>	<i>sprouting angiogenesis</i>	12	<i>3.25E-08</i>
<i>GO:0030178</i>	<i>negative regulation of Wnt signaling pathway</i>	18	<i>4.64E-08</i>
<i>GO:0090287</i>	<i>regulation of cellular response to growth factor stimulus</i>	20	<i>4.94E-08</i>
<i>GO:0009725</i>	<i>response to hormone</i>	42	<i>5.31E-08</i>
<i>GO:0010720</i>	<i>positive regulation of cell development</i>	30	<i>5.31E-08</i>
<i>GO:0051130</i>	<i>positive regulation of cellular component organization</i>	47	<i>8.21E-08</i>
<i>GO:0030111</i>	<i>regulation of Wnt signaling pathway</i>	22	<i>8.37E-08</i>
<i>GO:0007169</i>	<i>transmembrane receptor protein tyrosine kinase signaling pathway</i>	33	<i>1.01E-07</i>
<i>GO:0031399</i>	<i>regulation of protein modification process</i>	59	<i>1.34E-07</i>
<i>GO:0007389</i>	<i>pattern specification process</i>	27	<i>1.47E-07</i>
<i>GO:0051247</i>	<i>positive regulation of protein metabolic process</i>	54	<i>1.53E-07</i>
<i>GO:0030324</i>	<i>lung development</i>	18	<i>1.53E-07</i>
<i>GO:0019220</i>	<i>regulation of phosphate metabolic process</i>	57	<i>1.61E-07</i>
<i>GO:0032989</i>	<i>cellular component morphogenesis</i>	50	<i>1.61E-07</i>
<i>GO:0051216</i>	<i>cartilage development</i>	17	<i>1.69E-07</i>
<i>GO:0042327</i>	<i>positive regulation of phosphorylation</i>	40	<i>1.96E-07</i>
<i>GO:0023014</i>	<i>signal transduction by protein phosphorylation</i>	39	<i>1.96E-07</i>
<i>GO:0030029</i>	<i>actin filament-based process</i>	32	<i>1.96E-07</i>
<i>GO:0051174</i>	<i>regulation of phosphorus metabolic process</i>	57	<i>1.96E-07</i>
<i>GO:0043065</i>	<i>positive regulation of apoptotic process</i>	31	<i>2.04E-07</i>
<i>GO:0043068</i>	<i>positive regulation of programmed cell death</i>	31	<i>2.47E-07</i>
<i>GO:0031401</i>	<i>positive regulation of protein modification process</i>	45	<i>2.55E-07</i>
<i>GO:0010942</i>	<i>positive regulation of cell death</i>	32	<i>2.63E-07</i>
<i>GO:0048705</i>	<i>skeletal system morphogenesis</i>	18	<i>2.67E-07</i>

GO:0030278	regulation of ossification	17	2.94E-07
GO:1904035	regulation of epithelial cell apoptotic process	11	3.01E-07
GO:0060284	regulation of cell development	39	3.43E-07
GO:0000902	cell morphogenesis	47	3.72E-07
GO:0060688	regulation of morphogenesis of a branching structure	10	3.82E-07
GO:0061448	connective tissue development	19	4.02E-07
GO:0045765	regulation of angiogenesis	18	4.30E-07
GO:0071772	response to BMP	15	5.37E-07
GO:0071773	cellular response to BMP stimulus	15	5.37E-07
GO:1902531	regulation of intracellular signal transduction	56	5.72E-07
GO:0072132	mesenchyme morphogenesis	9	6.57E-07
GO:0006935	chemotaxis	28	6.83E-07
GO:0042330	taxis	28	7.31E-07
GO:0003002	regionalization	22	7.41E-07
GO:0032270	positive regulation of cellular protein metabolic process	50	7.77E-07
GO:0001503	ossification	23	7.77E-07
GO:0061061	muscle structure development	30	8.47E-07
GO:0010769	regulation of cell morphogenesis involved in differentiation	22	8.75E-07
GO:0030855	epithelial cell differentiation	30	9.90E-07
GO:0061035	regulation of cartilage development	10	1.06E-06
GO:0030155	regulation of cell adhesion	31	1.09E-06
GO:0048608	reproductive structure development	25	1.18E-06
GO:0010562	positive regulation of phosphorus metabolic process	41	1.25E-06
GO:0045937	positive regulation of phosphate metabolic process	41	1.25E-06
GO:0061458	reproductive system development	25	1.35E-06
GO:0071407	cellular response to organic cyclic compound	27	1.44E-06
GO:0016049	cell growth	27	1.48E-06
GO:0043627	response to estrogen	17	1.62E-06
GO:0001501	skeletal system development	26	1.73E-06
GO:0003156	regulation of animal organ formation	8	2.04E-06
GO:0045926	negative regulation of growth	18	2.25E-06
GO:0033993	response to lipid	38	2.37E-06
GO:0048545	response to steroid hormone	27	2.43E-06
GO:0090090	negative regulation of canonical Wnt signaling pathway	14	3.48E-06
GO:0030036	actin cytoskeleton organization	27	3.78E-06
GO:0010594	regulation of endothelial cell migration	12	4.17E-06
GO:0072089	stem cell proliferation	14	4.23E-06
GO:0048589	developmental growth	29	4.30E-06
GO:0060537	muscle tissue development	22	4.58E-06
GO:0072078	nephron tubule morphogenesis	10	5.21E-06
GO:0045667	regulation of osteoblast differentiation	12	5.76E-06
GO:0030198	extracellular matrix organization	20	6.05E-06
GO:0031589	cell-substrate adhesion	19	6.25E-06
GO:0043062	extracellular structure organization	20	6.26E-06
GO:0048666	neuron development	39	6.50E-06
GO:0051384	response to glucocorticoid	14	7.51E-06
GO:0045859	regulation of protein kinase activity	31	7.51E-06

<i>GO:0032355</i>	<i>response to estradiol</i>	13	<i>8.08E-06</i>
<i>GO:0090100</i>	<i>positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway</i>	11	<i>8.57E-06</i>

GO terms associated with down-regulated genes			
<i>GO ID</i>	<i>Enriched Biological Process</i>	<i>No. genes</i>	<i>FDR</i>
<i>GO:0022610</i>	<i>biological adhesion</i>	93	<i>1.44E-14</i>
<i>GO:0007155</i>	<i>cell adhesion</i>	89	<i>4.36E-13</i>
<i>GO:0030198</i>	<i>extracellular matrix organization</i>	39	<i>6.86E-13</i>
<i>GO:0043062</i>	<i>extracellular structure organization</i>	39	<i>6.86E-13</i>
<i>GO:0048514</i>	<i>blood vessel morphogenesis</i>	48	<i>2.09E-12</i>
<i>GO:0001525</i>	<i>angiogenesis</i>	42	<i>3.05E-11</i>
<i>GO:1903034</i>	<i>regulation of response to wounding</i>	42	<i>4.66E-11</i>
<i>GO:0001568</i>	<i>blood vessel development</i>	50	<i>4.66E-11</i>
<i>GO:0001944</i>	<i>vasculature development</i>	51	<i>4.85E-11</i>
<i>GO:0040011</i>	<i>locomotion</i>	90	<i>5.57E-11</i>
<i>GO:0032101</i>	<i>regulation of response to external stimulus</i>	64	<i>7.75E-11</i>
<i>GO:0051241</i>	<i>negative regulation of multicellular organismal process</i>	68	<i>9.4E-11</i>
<i>GO:0016477</i>	<i>cell migration</i>	74	<i>1.15E-10</i>
<i>GO:0006952</i>	<i>defense response</i>	86	<i>1.15E-10</i>
<i>GO:0080134</i>	<i>regulation of response to stress</i>	83	<i>1.87E-10</i>
<i>GO:0051674</i>	<i>localization of cell</i>	77	<i>3.87E-10</i>
<i>GO:0048870</i>	<i>cell motility</i>	77	<i>3.87E-10</i>
<i>GO:0030334</i>	<i>regulation of cell migration</i>	51	<i>7.26E-10</i>
<i>GO:0009611</i>	<i>response to wounding</i>	59	<i>1.67E-09</i>
<i>GO:0006928</i>	<i>movement of cell or subcellular component</i>	90	<i>2.47E-09</i>
<i>GO:0048585</i>	<i>negative regulation of response to stimulus</i>	78	<i>2.49E-09</i>
<i>GO:2000145</i>	<i>regulation of cell motility</i>	51	<i>6.98E-09</i>
<i>GO:0031347</i>	<i>regulation of defense response</i>	52	<i>6.98E-09</i>
<i>GO:0002682</i>	<i>regulation of immune system process</i>	76	<i>9.78E-09</i>
<i>GO:0040012</i>	<i>regulation of locomotion</i>	53	<i>1.49E-08</i>
<i>GO:0045087</i>	<i>innate immune response</i>	52	<i>1.9E-08</i>
<i>GO:0043207</i>	<i>response to external biotic stimulus</i>	57	<i>2.19E-08</i>
<i>GO:0051270</i>	<i>regulation of cellular component movement</i>	52	<i>3.1E-08</i>
<i>GO:0009607</i>	<i>response to biotic stimulus</i>	58	<i>3.43E-08</i>
<i>GO:0002237</i>	<i>response to molecule of bacterial origin</i>	31	<i>4.29E-08</i>
<i>GO:0001503</i>	<i>ossification</i>	33	<i>4.97E-08</i>
<i>GO:0006955</i>	<i>immune response</i>	76	<i>5.41E-08</i>
<i>GO:0009967</i>	<i>positive regulation of signal transduction</i>	73	<i>6.6E-08</i>
<i>GO:0010647</i>	<i>positive regulation of cell communication</i>	79	<i>8.59E-08</i>
<i>GO:0023056</i>	<i>positive regulation of signaling</i>	78	<i>1.08E-07</i>
<i>GO:0048589</i>	<i>developmental growth</i>	43	<i>2E-07</i>
<i>GO:0006935</i>	<i>chemotaxis</i>	39	<i>2.24E-07</i>
<i>GO:0030155</i>	<i>regulation of cell adhesion</i>	44	<i>2.36E-07</i>

GO:0042330	taxis	39	2.36E-07
GO:0051240	positive regulation of multicellular organismal process	75	3.03E-07
GO:0006954	inflammatory response	44	3.03E-07
GO:0009617	response to bacterium	39	4.13E-07
GO:0001816	cytokine production	43	5.56E-07
GO:0040007	growth	57	5.92E-07
GO:0050727	regulation of inflammatory response	28	7.12E-07
GO:1902533	positive regulation of intracellular signal transduction	52	8.16E-07
GO:0032722	positive regulation of chemokine production	12	8.31E-07
GO:0032103	positive regulation of response to external stimulus	27	1.2E-06
GO:0051093	negative regulation of developmental process	50	1.2E-06
GO:0030335	positive regulation of cell migration	32	1.31E-06
GO:0002684	positive regulation of immune system process	52	1.31E-06
GO:0009968	negative regulation of signal transduction	59	1.31E-06
GO:0040017	positive regulation of locomotion	33	1.82E-06
GO:0001817	regulation of cytokine production	39	1.98E-06
GO:0001501	skeletal system development	35	2.09E-06
GO:2000147	positive regulation of cell motility	32	2.27E-06
GO:0032496	response to lipopolysaccharide	27	2.35E-06
GO:0031589	cell-substrate adhesion	26	2.67E-06
GO:0050678	regulation of epithelial cell proliferation	26	2.8E-06
GO:0032642	regulation of chemokine production	13	3.51E-06
GO:0002687	positive regulation of leukocyte migration	16	3.58E-06
GO:0051272	positive regulation of cellular component movement	32	3.69E-06
GO:0001818	negative regulation of cytokine production	22	3.74E-06
GO:0045088	regulation of innate immune response	28	3.74E-06
GO:0042127	regulation of cell proliferation	73	3.93E-06
GO:0031349	positive regulation of defense response	30	4.57E-06
GO:0033993	response to lipid	52	4.57E-06
GO:0045824	negative regulation of innate immune response	10	4.94E-06
GO:1901700	response to oxygen-containing compound	71	4.94E-06
GO:1903036	positive regulation of response to wounding	19	4.94E-06
GO:0070374	positive regulation of ERK1 and ERK2 cascade	19	5.78E-06
GO:0045596	negative regulation of cell differentiation	40	6.42E-06
GO:0023057	negative regulation of signaling	61	6.66E-06
GO:0032602	chemokine production	13	6.78E-06
GO:0050776	regulation of immune response	47	8.32E-06
GO:0071346	cellular response to interferon-gamma	16	9.16E-06
GO:0002526	acute inflammatory response	17	9.84E-06
GO:0010648	negative regulation of cell communication	61	9.86E-06
GO:0048646	anatomical structure formation involved in morphogenesis	60	1.03E-05
GO:0060349	bone morphogenesis	13	1.07E-05
GO:0050920	regulation of chemotaxis	19	1.07E-05
GO:0010721	negative regulation of cell development	26	1.24E-05
GO:0044236	multicellular organism metabolic process	16	1.26E-05
GO:0034341	response to interferon-gamma	17	1.31E-05
GO:0044259	multicellular organismal macromolecule metabolic process	15	1.32E-05

GO:0048608	reproductive structure development	31	1.65E-05
GO:0030278	regulation of ossification	19	1.71E-05
GO:0050900	leukocyte migration	27	1.79E-05
GO:0061458	reproductive system development	31	1.89E-05
GO:0050729	positive regulation of inflammatory response	15	2.07E-05
GO:0048729	tissue morphogenesis	41	2.22E-05
GO:0002697	regulation of immune effector process	30	2.25E-05
GO:0048699	generation of neurons	66	2.29E-05
GO:0002252	immune effector process	44	2.37E-05
GO:0043410	positive regulation of MAPK cascade	32	2.65E-05
GO:0001763	morphogenesis of a branching structure	20	3.21E-05
GO:0002685	regulation of leukocyte migration	17	3.42E-05
GO:0046903	secretion	56	3.45E-05
GO:0008284	positive regulation of cell proliferation	46	3.53E-05
GO:0045765	regulation of angiogenesis	20	3.54E-05
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	20	3.74E-05
GO:0032963	collagen metabolic process	14	3.94E-05
GO:1901342	regulation of vasculature development	21	4.11E-05
GO:0044093	positive regulation of molecular function	76	4.21E-05
GO:0060828	regulation of canonical Wnt signaling pathway	20	4.57E-05
GO:0001649	osteoblast differentiation	19	4.73E-05
GO:0045595	regulation of cell differentiation	70	4.78E-05
GO:0010810	regulation of cell-substrate adhesion	17	5.65E-05
GO:0071345	cellular response to cytokine stimulus	38	6.26E-05
GO:0033002	muscle cell proliferation	17	0.000069
GO:0002683	negative regulation of immune system process	27	7.24E-05
GO:0030111	regulation of Wnt signaling pathway	23	7.38E-05
GO:0050921	positive regulation of chemotaxis	14	7.67E-05
GO:0001101	response to acid chemical	25	7.78E-05
GO:0045785	positive regulation of cell adhesion	27	8.59E-05
GO:0023014	signal transduction by protein phosphorylation	46	8.73E-05
GO:0048659	smooth muscle cell proliferation	14	9.56E-05
GO:0032940	secretion by cell	50	9.8E-05
GO:0070371	ERK1 and ERK2 cascade	21	0.000112
GO:1902531	regulation of intracellular signal transduction	71	0.000113
GO:0043408	regulation of MAPK cascade	38	0.000114
GO:0050679	positive regulation of epithelial cell proliferation	16	0.000115
GO:0010941	regulation of cell death	67	0.000119
GO:0051094	positive regulation of developmental process	57	0.000123
GO:0018108	peptidyl-tyrosine phosphorylation	25	0.000129
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	16	0.00013
GO:0071396	cellular response to lipid	32	0.000137
GO:0018212	peptidyl-tyrosine modification	25	0.000139
GO:0060350	endochondral bone morphogenesis	9	0.000151
GO:2000027	regulation of organ morphogenesis	20	0.000154
GO:0032490	detection of molecule of bacterial origin	5	0.000157
GO:0070372	regulation of ERK1 and ERK2 cascade	20	0.000161

GO:0001934	positive regulation of protein phosphorylation	45	0.000163
GO:0048771	tissue remodeling	16	0.000163
GO:0002009	morphogenesis of an epithelium	33	0.000178
GO:0031214	biomineral tissue development	14	0.000179
GO:0032680	regulation of tumor necrosis factor production	13	0.000179
GO:0045667	regulation of osteoblast differentiation	13	0.000179
GO:0030199	collagen fibril organization	8	0.00018
GO:0003006	developmental process involved in reproduction	37	0.000198
GO:0050778	positive regulation of immune response	35	0.000203
GO:0042327	positive regulation of phosphorylation	46	0.000215
GO:0042981	regulation of apoptotic process	62	0.000215
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	13	0.000223
GO:0048705	skeletal system morphogenesis	18	0.00023
GO:0044243	multicellular organismal catabolic process	10	0.000233
GO:0034097	response to cytokine	40	0.00024
GO:0050918	positive chemotaxis	9	0.000241
GO:0030282	bone mineralization	12	0.00025
GO:0098609	cell-cell adhesion	45	0.000252
GO:0042592	homeostatic process	69	0.000259
GO:0071295	cellular response to vitamin	7	0.000259
GO:1900046	regulation of hemostasis	11	0.000261
GO:0045089	positive regulation of innate immune response	21	0.000264
GO:0048660	regulation of smooth muscle cell proliferation	13	0.000268
GO:0071706	tumor necrosis factor superfamily cytokine production	13	0.000268
GO:0032757	positive regulation of interleukin-8 production	8	0.000269
GO:0043067	regulation of programmed cell death	62	0.000278
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	14	0.000292
GO:0003416	endochondral bone growth	6	0.000308
GO:0060348	bone development	16	0.000311
GO:0042325	regulation of phosphorylation	61	0.000315
GO:0051336	regulation of hydrolase activity	57	0.000325
GO:0050663	cytokine secretion	16	0.000325
GO:0032677	regulation of interleukin-8 production	9	0.000329
GO:0006915	apoptotic process	73	0.00033
GO:0010628	positive regulation of gene expression	72	0.000337
GO:0042116	macrophage activation	9	0.000363
GO:0010562	positive regulation of phosphorus metabolic process	49	0.000363
GO:0045937	positive regulation of phosphate metabolic process	49	0.000363
GO:0043085	positive regulation of catalytic activity	63	0.000368
GO:1901701	cellular response to oxygen-containing compound	45	0.000373
GO:0006024	glycosaminoglycan biosynthetic process	12	0.000373