Supplemental Table 1. Top 100 (of 588 total) biological pathways associated with LGALS3 RPPA network

#pathway ID	pathway description	observed gene count	false discovery rate
GO.0006468	protein phosphorylation	16	3.41E-10
GO.0007166	cell surface receptor signaling pathway	22	3.41E-10
GO.0032268	regulation of cellular protein metabolic process	22	1.00E-09
GO.0032270	pos. regulation of cellular protein metabolic process	18	1.07E-09
GO.0016310	phosphorylation	16	7.93E-09
GO.0030335	positive regulation of cell migration	11	1.36E-08
GO.0006952	defense response	17	1.86E-08
GO.0031325	positive regulation of cellular metabolic process	22	1.86E-08
GO.0071363	cellular response to growth factor stimulus	13	1.86E-08
GO.0070887	cellular response to chemical stimulus	20	3.24E-08
GO.0010604	pos. regulation of macromolecule metabolic process	21	4.17E-08
GO.0006796	phosphate-containing compound metabolic process	18	5.31E-08
GO.0002682	regulation of immune system process	16	7.88E-08
GO.0007167	enzyme linked receptor protein signaling pathway	14	7.88E-08
GO.0048522	positive regulation of cellular process	25	9.97E-08
GO.0048584	positive regulation of response to stimulus	18	1.07E-07
GO.0050776	regulation of immune response	13	1.70E-07
GO.0051272	pos. regulation of cellular component movement	10	1.79E-07
GO.0002376	immune system process	18	1.82E-07
GO.1902533	pos. regulation of intracellular signal transduction	13	1.92E-07
GO.0006464	cellular protein modification process	20	2.32E-07
GO.0034110	regulation of homotypic cell-cell adhesion	9	2.32E-07
GO.0008283	cell proliferation	12	2.71E-07
GO.2001233	regulation of apoptotic signaling pathway	10	2.92E-07
GO.1901699	cellular response to nitrogen compound	11	3.46E-07
GO.0010647	positive regulation of cell communication	16	4.08E-07
GO.0033043	regulation of organelle organization	14	4.08E-07
GO.0080135	regulation of cellular response to stress	12	4.63E-07
GO.0050865	regulation of cell activation	10	5.63E-07
GO.0060255	regulation of macromolecule metabolic process	26	5.65E-07
GO.0030155	regulation of cell adhesion	11	5.74E-07
GO.0045087	innate immune response	13	5.81E-07
GO.1902531	regulation of intracellular signal transduction	15	5.88E-07
GO.0035295	tube development	11	6.13E-07
GO.0080090	regulation of primary metabolic process	26	6.13E-07
GO.0001932	regulation of protein phosphorylation	14	7.44E-07
GO.0014070	response to organic cyclic compound	12	1.09E-06
GO.0048015	phosphatidylinositol-mediated signaling	7	1.14E-06
GO.0010821	regulation of mitochondrion organization	9	1.17E-06
GO.0002764	immune response-regulating signaling pathway	10	1.23E-06
GO.0038093	Fc receptor signaling pathway	8	1.23E-06
GO.0051239	regulation of multicellular organismal process	18	1.26E-06
GO.0006950	response to stress	21	1.44E-06
GO.0042325	regulation of phosphorylation	14	1.45E-06
GO.0071417	cellular response to organonitrogen compound	10	1.45E-06
GO.0031401	positive regulation of protein modification process	13	1.48E-06
GO.0051174	regulation of phosphorus metabolic process	15	1.48E-06
GO.0009888	tissue development	15	1.88E-06
GO.0009725	response to hormone	12	2.06E-06

GO.0006955	immune response	14	2.08E-06
GO.0045859	regulation of protein kinase activity	11	2.19E-06
GO.0071310	cellular response to organic substance	16	2.19E-06
GO.0031399	regulation of protein modification process	15	2.34E-06
GO.0002768	immune response-reg. cell surface receptor sig. pathway	9	2.43E-06
GO.0051338	regulation of transferase activity	12	2.43E-06
GO.0007169	transmembrane receptor protein tyr. kinase sig. pathway	11	2.46E-06
GO.0002694	regulation of leukocyte activation	9	2.92E-06
GO.0038095	Fc-epsilon receptor signaling pathway	7	3.37E-06
GO.0043065	positive regulation of apoptotic process	10	3.70E-06
GO.0051130	positive regulation of cellular component organization	13	3.72E-06
GO.0043549	regulation of kinase activity	11	3.77E-06
GO.0048545	response to steroid hormone	9	3.77E-06
GO.0008631	intrinsic apoptotic sig. path. response to oxidative stress	4	3.84E-06
GO.0002521	leukocyte differentiation	8	4.29E-06
GO.0048608	reproductive structure development	9	4.29E-06
GO.0051726	regulation of cell cycle	12	4.29E-06
GO.0061458	reproductive system development	9	4.53E-06
GO.0042493	response to drug	9	4.57E-06
GO.0036473	cell death in response to oxidative stress	4	4.58E-06
GO.0045937	positive regulation of phosphate metabolic process	12	4.63E-06
GO.0048513	organ development	18	5.66E-06
GO.0042127	regulation of cell proliferation	14	6.03E-06
GO.0030334	regulation of cell migration	10	6.47E-06
GO.0043408	regulation of MAPK cascade	10	6.47E-06
GO.0030099	myeloid cell differentiation	7	6.90E-06
GO.0001934	positive regulation of protein phosphorylation	11	7.37E-06
GO.2001234	negative regulation of apoptotic signaling pathway	7	7.51E-06
GO.0071495	cellular response to endogenous stimulus	12	7.57E-06
GO.0010638	positive regulation of organelle organization	10	8.07E-06
GO.0097305	response to alcohol	8	8.07E-06
GO.0002684	positive regulation of immune system process	11	8.58E-06
GO.0035556	intracellular signal transduction	15	1.02E-05
GO.0042327	positive regulation of phosphorylation	11	1.02E-05
GO.0009967	positive regulation of signal transduction	13	1.08E-05
GO.0019538	protein metabolic process	21	1.08E-05
GO.0032355	response to estradiol	6	1.08E-05
GO.0051249	regulation of lymphocyte activation	8	1.08E-05
GO.0043069	negative regulation of programmed cell death	11	1.12E-05
GO.0042592	homeostatic process	13	1.16E-05
GO.0010646	regulation of cell communication	18	1.24E-05
GO.0018193	peptidyl-amino acid modification	11	1.28E-05
GO.1901698	response to nitrogen compound	11	1.30E-05
GO.0050790	regulation of catalytic activity	16	1.45E-05
GO.0051094	positive regulation of developmental process	12	1.57E-05
GO.0042221	response to chemical	20	2.07E-05
GO.0032103	positive regulation of response to external stimulus	8	2.13E-05
GO.0002696	positive regulation of leukocyte activation	7	2.14E-05
GO.0031323	regulation of cellular metabolic process	24	2.18E-05
GO.0050863	regulation of T cell activation	7	2.18E-05
GO.0051384	response to glucocorticoid	6	2.18E-05

Supplemental Table 2. Top KEGG pathways (86 total) associated with LGALS3 RPPA network

#pathway ID	pathway description	observed gene count	false discovery rate
4151	PI3K-Akt signaling pathway	13	1.80E-12
5200	Pathways in cancer	13	1.80E-12
4510	Focal adhesion	10	1.54E-10
4666	Fc gamma R-mediated phagocytosis	8	1.54E-10
5215	Prostate cancer	8	1.54E-10
5221	Acute myeloid leukemia	7	3.16E-10
4066	HIF-1 signaling pathway	8	4.39E-10
4015	Rap1 signaling pathway	9	2.86E-09
5206	MicroRNAs in cancer	8	4.86E-09
5213	Endometrial cancer	6	9.84E-09
5210	Colorectal cancer	6	2.03E-08
4014	Ras signaling pathway	8	9.91E-08
5205	Proteoglycans in cancer	8	9.91E-08
4012	ErbB signaling pathway	6	1.60E-07
4370	VEGF signaling pathway	5	1.30E-06
4664	Fc epsilon RI signaling pathway	5	2.16E-06
5218	Melanoma	5	2.41E-06
5220	Chronic myeloid leukemia	5	2.41E-06
5161	Hepatitis B	6	2.61E-06
5222	Small cell lung cancer	5	5.84E-06
5202	Transcriptional misregulation in cancer	6	6.26E-06
5169	Epstein-Barr virus infection	6	1.37E-05
4722	Neurotrophin signaling pathway	5	2.32E-05
4919	Thyroid hormone signaling pathway	5	2.32E-05
5223	Non-small cell lung cancer	4	3.08E-05
4910	Insulin signaling pathway	5	4.23E-05
5212	Pancreatic cancer	4	4.50E-05
5214	Glioma	4	4.50E-05
5166	HTLV-I infection	6	5.25E-05
4662	B cell receptor signaling pathway	4	6.88E-05
4210	Apoptosis	4	0.000141
5216	Thyroid cancer	3	0.000141
5203	Viral carcinogenesis	5	0.000155
4064	NF-kappa B signaling pathway	4	0.00016
4915	Estrogen signaling pathway	4	0.000193
5219	Bladder cancer	3	0.000323
4670	Leukocyte transendothelial migration	4	0.000393
4068	FoxO signaling pathway	4	0.000484
4380	Osteoclast differentiation	4	0.000506
4650	Natural killer cell mediated cytotoxicity	4	0.000506
5160	Hepatitis C	4	0.000576
5162	Measles	4	0.00058
5014	Amyotrophic lateral sclerosis (ALS)	3	0.000672
4390	Hippo signaling pathway	4	0.000893
4730	Long-term depression	3	0.000997
4921	Oxytocin signaling pathway	4	0.000997
4022	cGMP-PKG signaling pathway	4	0.00111
4115	p53 signaling pathway	3	0.00138
5152	uberculosis	4	0.00144
4520	Adherens junction	3	0.00157
4062	Chemokine signaling pathway	4	0.00165
4350	TGF-beta signaling pathway	3	0.00201
4144	Endocytosis	4	0.00208
4914	Progesterone-mediated oocyte maturation	3	0.00208

4810	Regulation of actin cytoskeleton	4	0.0027
4912	GnRH signaling pathway	3	0.0027
4916	Melanogenesis	3	0.00349
4320	Dorso-ventral axis formation	2	0.00356
4114	Oocyte meiosis	3	0.00437
4668	TNF signaling pathway	3	0.00442
4725	Cholinergic synapse	3	0.00447
4010	MAPK signaling pathway	4	0.00492
5145	Toxoplasmosis	3	0.00494
4152	AMPK signaling pathway	3	0.00579
4110	Cell cycle	3	0.00598
4611	Platelet activation	3	0.00662
4310	Wnt signaling pathway	3	0.00794
4932	Non-alcoholic fatty liver disease (NAFLD)	3	0.00997
4630	Jak-STAT signaling pathway	3	0.0112
4930	Type II diabetes mellitus	2	0.0123
5010	Alzheimer s disease	3	0.013
5164	Influenza A	3	0.0133
4913	Ovarian steroidogenesis	2	0.0145
5416	Viral myocarditis	2	0.0173
4150	mTOR signaling pathway	2	0.0195
562	Inositol phosphate metabolism	2	0.0206
5211	Renal cell carcinoma	2	0.0223
5120	Epithelial cell signaling in Helicobacter pylori infection	2	0.0227
4917	Prolactin signaling pathway	2	0.0251
5100	Bacterial invasion of epithelial cells	2	0.0277
4070	Phosphatidylinositol signaling system	2	0.0311
4540	Gap junction	2	0.0346
4060	Cytokine-cytokine receptor interaction	3	0.0397
4750	Inflammatory mediator regulation of TRP channels	2	0.0428
4660	T cell receptor signaling pathway	2	0.0458
4620	Toll-like receptor signaling pathway	2	0.0479

Supplemental Table 3. Top 100 (of 535 total) biological pathways associated with CD74 RPPA network

#pathway ID	pathway description	observed gene count	false discovery rate
GO.0048011	neurotrophin TRK receptor signaling pathway	15	3.71E-16
GO.0071363	cellular response to growth factor stimulus	17	2.12E-14
GO.0050776	regulation of immune response	18	2.16E-14
GO.0038095	Fc-epsilon receptor signaling pathway	12	3.81E-14
GO.0070887	cellular response to chemical stimulus	24	3.81E-14
GO.0044344	cellular response to fibroblast growth factor stimulus	12	8.86E-14
GO.0002764	immune response-regulating signaling pathway	15	1.01E-13
GO.0045087	innate immune response	18	1.10E-13
GO.0048015	phosphatidylinositol-mediated signaling	11	1.34E-13
GO.0002768	immune response-reg. cell surface receptor sig. pathway	14	1.36E-13
GO.0048545	response to steroid hormone	14	2.80E-13
GO.0007169	transmembrane receptor protein tyr. kinase sig. pathway	16	5.03E-13
GO.0008543	fibroblast growth factor receptor signaling pathway	11	6.49E-13
GO.0006955	immune response	19	9.73E-13
GO.0060548	negative regulation of cell death	17	9.73E-13
GO.0071310	cellular response to organic substance	21	1.34E-12
GO.0033993	response to lipid	16	2.39E-12
GO.0006952	defense response	19	2.74E-12
GO.0007173	epidermal growth factor receptor signaling pathway	11	4.95E-12
GO.0071495	cellular response to endogenous stimulus	17	4.95E-12
GO.0010604	positive regulation of macromolecule metabolic process	23	4.98E-12
GO.0010941	regulation of cell death	19	5.16E-12
GO.0043066	negative regulation of apoptotic process	16	5.16E-12
GO.0051254	positive regulation of RNA metabolic process	19	5.16E-12
GO.0048585	negative regulation of response to stimulus	18	1.19E-11
GO.0071407	cellular response to organic cyclic compound	12	3.59E-11
GO.0045893	positive regulation of transcription, DNA-templated	18	3.65E-11
GO.0010628	positive regulation of gene expression	19	3.74E-11
GO.0014070	response to organic cyclic compound	15	4.13E-11
GO.0048523	negative regulation of cellular process	25	8.10E-11
GO.0051246	regulation of protein metabolic process	21	1.32E-10
GO.0051338	regulation of transferase activity	15	1.62E-10
GO.0031325	positive regulation of cellular metabolic process	22	1.75E-10
GO.1901700	response to oxygen-containing compound	17	1.78E-10
GO.0051247	positive regulation of protein metabolic process	17	3.79E-10
GO.0023057	negative regulation of signaling	16	4.12E-10
GO.0010648	negative regulation of cell communication	16	4.53E-10
GO.0032268	regulation of cellular protein metabolic process	20	4.53E-10
GO.0002376	immune system process	19	5.55E-10
GO.0042327	positive regulation of phosphorylation	14	1.22E-09
GO.0042325	regulation of phosphorylation	16	1.29E-09
GO.0009968	negative regulation of signal transduction	15	1.47E-09
GO.0032270	positive regulation of cellular protein metabolic process	16	1.76E-09
GO.0009725	response to hormone	14	1.79E-09
GO.0010033	response to organic substance	20	1.79E-09
GO.0010557	positive regulation of macromolecule biosynthetic process	17	2.95E-09
GO.0002682	regulation of immune system process	16	3.05E-09
GO.0042981	regulation of apoptotic process	16	3.96E-09
GO.0006357	regulation of transcription from RNA polymerase II promoter	17	5.00E-09
GO.0006950	response to stress	22	6.07E-09
GO.0097305	response to alcohol	10	6.27E-09
GO.0051252	regulation of RNA metabolic process	22	6.55E-09
GO.0031328	positive regulation of cellular biosynthetic process	17	7.39E-09
GO.0001934	positive regulation of protein phosphorylation	13	9.81E-09

GO.1901701	cellular response to oxygen-containing compound	13	9.81E-09
GO.0009966	regulation of signal transduction	19	1.04E-08
GO.0071396	cellular response to lipid	10	1.97E-08
GO.0048583	regulation of response to stimulus	21	3.01E-08
GO.0006355	regulation of transcription, DNA-templated	21	3.23E-08
GO.0048519	negative regulation of biological process	23	3.27E-08
GO.0009719	response to endogenous stimulus	15	5.14E-08
GO.0080134	regulation of response to stress	15	5.66E-08
GO.0048608	reproductive structure development	10	5.96E-08
GO.0051347	positive regulation of transferase activity	11	6.14E-08
GO.0065009	regulation of molecular function	19	6.14E-08
GO.0051726	regulation of cell cycle	13	6.20E-08
GO.0001932	regulation of protein phosphorylation	14	6.21E-08
GO.0061458	reproductive system development	10	6.21E-08
GO.0010468	regulation of gene expression	22	6.92E-08
GO.0042127	regulation of cell proliferation	15	8.66E-08
GO.0009891	positive regulation of biosynthetic process	16	9.10E-08
GO.0043627	response to estrogen	8	9.80E-08
GO.0003006	developmental process involved in reproduction	11	1.05E-07
GO.0006468	protein phosphorylation	12	1.22E-07
GO.0009894	regulation of catabolic process	12	1.47E-07
GO.0035556	intracellular signal transduction	16	1.52E-07
GO.0031399	regulation of protein modification process	15	2.23E-07
GO.0033554	cellular response to stress	15	3.19E-07
GO.0048522	positive regulation of cellular process	22	3.94E-07
GO.0044093	positive regulation of molecular function	15	5.06E-07
GO.0023051	regulation of signaling	18	5.46E-07
GO.0032870	cellular response to hormone stimulus	10	6.47E-07
GO.0007166	cell surface receptor signaling pathway	16	7.57E-07
GO.0097192	extrinsic apoptotic signaling pathway in absence of ligand	5	8.36E-07
GO.0010646	regulation of cell communication	18	1.19E-06
GO.0045944	pos. reg. of transcription from RNA polymerase II promoter	12	1.28E-06
GO.0042221	response to chemical	20	1.51E-06
GO.0022402	cell cycle process	12	1.86E-06
GO.0031401	positive regulation of protein modification process	12	1.88E-06
GO.0050790	regulation of catalytic activity	16	1.88E-06
GO.0009967	positive regulation of signal transduction	13	1.98E-06
GO.0044702	single organism reproductive process	12	2.04E-06
GO.0000278	mitotic cell cycle	11	2.13E-06
GO.0034097	response to cytokine	10	2.14E-06
GO.0033674	positive regulation of kinase activity	9	2.26E-06
GO.0007049	cell cycle	13	2.48E-06
GO.0009896	positive regulation of catabolic process	9	2.81E-06
GO.0048513	organ development	17	3.22E-06
GO.0045785	positive regulation of cell adhesion	8	3.41E-06
GO.0009628	response to abiotic stimulus	12	3.54E-06

Supplemental Table 4. Top KEGG pathways (83 total) associated with CD74 RPPA network

#pathway ID	pathway description	observed gene count	false discovery rate
5200	Pathways in cancer	14	7.11E-15
5213	Endometrial cancer	9	7.27E-15
5215	Prostate cancer	10	7.27E-15
5206	MicroRNAs in cancer	11	1.60E-14
4151	PI3K-Akt signaling pathway	12	4.74E-12
5223	Non-small cell lung cancer	7	1.16E-10
5161	Hepatitis B	8	1.83E-09
4012	ErbB signaling pathway	7	1.97E-09
4919	Thyroid hormone signaling pathway	7	1.63E-08
5212	Pancreatic cancer	6	1.63E-08
4115	p53 signaling pathway	6	2.21E-08
4510	Focal adhesion	8	2.21E-08
5220	Chronic myeloid leukemia	6	2.68E-08
5205	Proteoglycans in cancer	8	3.31E-08
5203	Viral carcinogenesis	7	2.54E-07
4722	Neurotrophin signaling pathway	6	4.86E-07
4110	Cell cycle	6	6.20E-07
4014	Ras signaling pathway	7	7.77E-07
5160	Hepatitis C	6	7.77E-07
5164	Influenza A	6	3.46E-06
5219	Bladder cancer	4	4.88E-06
5169	Epstein-Barr virus infection	6	6.74E-06
4066	HIF-1 signaling pathway	5	7.77E-06
4068	FoxO signaling pathway	5	1.59E-05
5221	Acute myeloid leukemia	4	2.07E-05
5162	Measles	5	2.10E-05
5210	Colorectal cancer	4	2.22E-05
4370	VEGF signaling pathway	4	2.46E-05
4010	MAPK signaling pathway	6	2.62E-05
5214	Glioma	4	2.62E-05
4662	B cell receptor signaling pathway	4	3.92E-05
4917	Prolactin signaling pathway	4	3.92E-05
5218	Melanoma	4	3.92E-05
4062	Chemokine signaling pathway	5	7.75E-05
5222	Small cell lung cancer	4	8.10E-05
4912	GnRH signaling pathway	4	9.06E-05
4114	Oocyte meiosis	4	0.000185
4380	Osteoclast differentiation	4	0.000336
4910	Insulin signaling pathway	4	0.000431
4921	Oxytocin signaling pathway	4	0.000727
5202	Transcriptional misregulation in cancer	4	0.000951
5120	Epithelial cell signaling in Helicobacter pylori infection	3	0.00104
5152	Tuberculosis	4	0.00104
4920	Adipocytokine signaling pathway	3	0.00109
5168	Herpes simplex infection	4	0.00109
5140	Leishmaniasis	3	0.00116
4520	Adherens junction	3	0.00119
4540	Gap junction	3	0.00192
4210	Apoptosis	3	0.00195
4916	Melanogenesis	3	0.00283
4660	T cell receptor signaling pathway	3	0.00295
4320	Dorso-ventral axis formation	2	0.0031
4620	Toll-like receptor signaling pathway	3	0.0031
5145	Toxoplasmosis	3	0.00411

4670	Leukocyte transendothelial migration	3	0.00414
5216	Thyroid cancer	2	0.00443
4650	Natural killer cell mediated cytotoxicity	3	0.00511
5020	Prion diseases	2	0.0076
4932	Non-alcoholic fatty liver disease (NAFLD)	3	0.00824
5010	Alzheimer s disease	3	0.0111
4020	Calcium signaling pathway	3	0.0129
5014	Amyotrophic lateral sclerosis (ALS)	2	0.0136
5016	Huntington s disease	3	0.0139
5134	Legionellosis	2	0.0148
5131	Shigellosis	2	0.0168
4730	Long-term depression	2	0.0171
4015	Rap1 signaling pathway	3	0.0183
5321	Inflammatory bowel disease (IBD)	2	0.019
4720	Long-term potentiation	2	0.0193
5211	Renal cell carcinoma	2	0.0196
5031	Amphetamine addiction	2	0.0199
4664	Fc epsilon RI signaling pathway	2	0.0202
3320	PPAR signaling pathway	2	0.0211
4914	Progesterone-mediated oocyte maturation	2	0.0279
5166	HTLV-I infection	3	0.0287
4512	ECM-receptor interaction	2	0.0313
4666	Fc gamma R-mediated phagocytosis	2	0.0323
4064	NF-kappa B signaling pathway	2	0.0326
4915	Estrogen signaling pathway	2	0.0358
5146	Amoebiasis	2	0.0438
4668	TNF signaling pathway	2	0.0448
4725	Cholinergic synapse	2	0.0451
4726	Serotonergic synapse	2	0.0461