

Supplementary Table 1 The total pathways of GO, KEGG and GSEA enrichment analysis of co-DEGs involved in gastric cancer

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferr oni	Benjam ini	FDR
GOTERM_BP_DIR ECT	GO:0030199~collagen fibril organization	10	4.405286344	2.08E-08	COMP, COL3A1, ADAMTS2, FOXC1, COL1A2, COL5A1, COL12A1, COL5A2, SERPINH1, P3H4	219	59	19157	14.82625184	3.01E-05	3.01E-05	2.98E-05
GOTERM_BP_DIR ECT	GO:0051301~cell division	20	8.810572687	7.76E-08	CENPW, UBE2C, RCC2, CDCA7, KIF14, NCAPG, NDC80, CDC25B, CDC20, CCNB2, TPX2, CCNB1, PRC1, NUF2, CDK1, NEK2, KIF2C, BUB1, MAD2L1, SPC25	219	380	19157	4.60394136	1.12E-04	5.62E-05	5.55E-05
GOTERM_BP_DIR ECT	GO:0030198~extracellular matrix organization	13	5.726872247	2.67E-07	OLFML2B, MMP7, MMP1, TNFRSF11B, COL3A1, ADAMTS2, COL1A2, COL5A1, COL4A1, COL5A2, COL4A5, COL8A1, COL10A1	219	158	19157	7.197300734	3.86E-04	1.29E-04	1.27E-04

GOTERM_BP_DIR ECT	GO:0001501~skeletal system development	12	5.286343612	3.61E-07	TEAD4, COL3A1, PKDCC, CDH11, COL10A1, TNFRSF11B, HOXA13, HOXC10	219	133	19157	7.892470903	5.22E-04	1.30E-04	1.29E-04
GOTERM_BP_DIR ECT	GO:0010273~detoxification of copper ion	6	2.643171806	7.19E-07	MT2A, MT1M, MT1G, MT1H, MT1X, MT1E	219	16	19157	32.80308219	0.001040412	2.08E-04	2.06E-04
GOTERM_BP_DIR ECT	GO:0006882~cellular zinc ion homeostasis	7	3.083700441	1.74E-06	MT2A, MT1M, SLC39A10, MT1G, MT1H, MT1X, MT1E	219	33	19157	18.55527882	0.002511927	3.85E-04	3.80E-04
GOTERM_BP_DIR ECT	GO:0045926~negative regulation of growth	6	2.643171806	1.86E-06	MT2A, MT1M, MT1G, MT1H, MT1X, MT1E	219	19	19157	27.62364816	0.002691351	3.85E-04	3.80E-04
GOTERM_BP_DIR ECT	GO:0007059~chromosome segregation	9	3.964757709	2.17E-06	TOP2A, CENPW, NUF2, HJURP, CENPN, NEK2, NDC80, DLGAP5, SPC25	219	75	19157	10.4969863	0.003134663	3.92E-04	3.88E-04
GOTERM_BP_DIR ECT	GO:0071294~cellular response to zinc ion	6	2.643171806	8.04E-06	MT2A, MT1M, MT1G, MT1H, MT1X, MT1E	219	25	19157	20.9939726	0.011579597	0.00129323	0.001278931
GOTERM_BP_DIR ECT	GO:0071280~cellular response to copper ion	6	2.643171806	1.73E-05	MT2A, MT1M, MT1G, MT1H, MT1X, MT1E	219	29	19157	18.09825224	0.024774381	0.002506889	0.002479169

GOTERM_BP_DIR ECT	GO:0007155~cell adhesion	20	8.810572687	1.91E-05	CNTNAP2, TROAP, 219 SIGLEC11, ITGA2, COL12A1, THY1, THBS2, CLDN1, ATP4B, COMP, VCAN, CDH3, COL5A1, FAP, CDH11, SPP1, ANOS1, COL8A1, CNTN3, ADA	552	19157	3.169379922	0.02733	0.00251	0.00248	3167	766	9822
GOTERM_BP_DIR ECT	GO:0007052~mitotic spindle organization	7	3.083700441	2.67E-05	STIL, CCNB1, KIF4A, 219 NUF2, NDC80, DLGAP5, SPC25	52	19157	11.7754654	0.03787	0.00321	0.00317	6205	5414	986
GOTERM_BP_DIR ECT	GO:0043588~skin development	6	2.643171806	7.66E-05	COMP, COL3A1, 219 ADAMTS2, COL5A1, CDH11, COL5A2	39	19157	13.45767475	0.10495	0.00852	0.00842	7228	3304	9059
GOTERM_BP_DIR ECT	GO:0071276~cellular response to cadmium ion	6	2.643171806	9.78E-05	MT2A, MT1M, MT1G, 219 MT1H, MT1X, MT1E	41	19157	12.80120281	0.13210	0.01011	0.01000	5265	2862	1041
GOTERM_BP_DIR ECT	GO:0048844~artery morphogenesis	5	2.202643172	1.45E-04	COMP, FOXC1, 219 PRRX1, APOE, HOXA13	24	19157	18.22393455	0.18935	0.01398	0.01382	6068	4412	9782
GOTERM_BP_DIR ECT	GO:0010971~positive regulation of G2/M transition of mitotic cell cycle	5	2.202643172	3.10E-04	CCNB1, RCC2, CDK1, 219 DTL, CDC25B	29	19157	15.08187687	0.36161	0.02776	0.02745	4071	1221	4255

GOTERM_BP_DIR ECT	GO:0008283~cell proliferation	9	3.964757709	3.26E-04	BOP1, CNTNAP2, 219 FOXC1, MELK, ITGA2, ESRRB, CDK1, BUB1, BYSL	150	19157	5.248493151	0.376460984	0.027761221	0.027454255
GOTERM_BP_DIR ECT	GO:0051382~kinetochore assembly	4	1.762114537	5.98E-04	CENPW, CENPN, 219 CENPA, DLGAP5	15	19157	23.32663623	0.579299153	0.048054261	0.047522907
GOTERM_BP_DIR ECT	GO:0046314~phosphocreatine biosynthetic process	3	1.321585903	0.001260263	CKMT2, CKM, CKB 219	5	19157	52.48493151	0.83894544	0.095978998	0.094917723
GOTERM_BP_DIR ECT	GO:1990573~potassium ion import across plasma membrane	5	2.202643172	0.001550415	ATP4B, ATP4A, 219 KCNE2, KCNJ15, KCNJ16	44	19157	9.940327937	0.8942569	0.112172508	0.110932176
GOTERM_BP_DIR ECT	GO:0006508~proteolysis	14	6.167400881	0.00166771	CPA2, CELA3B, CPB1, 219 MMP7, MMP1, PGC, LRP8, KLK11, CAPN13, CAPN9, FAP, PLAU, QPCT, OLR1	440	19157	2.783291822	0.910798754	0.114913176	0.113642539
GOTERM_BP_DIR ECT	GO:0042493~response to drug	11	4.845814978	0.002002008	ALDH3A1, CCNB1, 219 CDH3, SCNN1B, ITGA2, GAD1, CDK1, TNFRSF11B, LRP8, ADA, PGF	293	19157	3.284040083	0.945076451	0.131677517	0.130221511
GOTERM_BP_DIR ECT	GO:0000281~mitotic cytokinesis	5	2.202643172	0.003534397	ANLN, KIF4A, ECT2, 219 CENPA, CEP55	55	19157	7.95226235	0.994064903	0.222359653	0.219900943

GOTERM_BP_DIR ECT	GO:0001523~retinoid metabolic process	4	1.762114537	0.00386	AKR1B10, RDH12, 219 ADH7, LRP8	28	19157	12.49641226	0.99630	0.23273	0.23015
				01					3028	1892	8492
GOTERM_BP_DIR ECT	GO:0032964~collagen biosynthetic process	3	1.321585903	0.00440	COL5A1, SERPINH1, 219 P3H4	9	19157	29.15829528	0.99832	0.25482	0.25200
				2597					0123	2315	4653
GOTERM_BP_DIR ECT	GO:0051315~attachment of mitotic spindle microtubules to kinetochore	3	1.321585903	0.00662	NUF2, KIF2C, NDC80 219	11	19157	23.85678705	0.99993	0.36876	0.36469
				6127					4047	9477	186
GOTERM_BP_DIR ECT	GO:0006915~apoptotic process	15	6.607929515	0.00695	CHIA, DDIAS, 219 ZBTB16, CDCA7, TNFRSF11B, SULF1, COMP, TOX3, TPX2, MELK, SFRP5, FAM3B, CDK1, MAL, BUB1	582	19157	2.254507367	0.99995	0.37262	0.36850
				2914					9043	4686	4441
GOTERM_BP_DIR ECT	GO:0001525~angiogenesis	9	3.964757709	0.00751	PDGFRB, TMEM100, 219 FOXC1, CXCL8, ANGPT2, FAP, CXCL17, COL8A1, THY1	247	19157	3.187344019	0.99998	0.38816	0.38386
				1051					1854	037	8341
GOTERM_BP_DIR ECT	GO:0030510~regulation of BMP signaling pathway	3	1.321585903	0.00789	SFRP4, SFRP5, 219 HOXA13	12	19157	21.86872146	0.99998	0.39378	0.38943
				2069					9593	7053	2808
GOTERM_BP_DIR ECT	GO:0090181~regulation of cholesterol metabolic process	3	1.321585903	0.00925	ACADL, APOE, 219 FMO5	13	19157	20.18651212	0.99999	0.44652	0.44158
				7516					8583	0853	3511

GOTERM_BP_DIR ECT	GO:0006629~lipid metabolic process	8	3.524229075	0.00966	ALDH3A1, PLCXD3, 219 AADAC, VSIG2, ADHFE1, APOC1, FMO5, LRP8	207	19157	3.380671917	0.99999	0.45133	0.44634
				9193					9224	2957	2406
GOTERM_BP_DIR ECT	GO:0008608~attachment of spindle microtubules to kinetochore	3	1.321585903	0.01072	NUF2, NDC80, SPC25 219	14	19157	18.7446184	0.99999	0.48474	0.47938
				006					9833	7695	7665
GOTERM_BP_DIR ECT	GO:0045184~establishment of protein localization	4	1.762114537	0.01127	RCC2, ITGA2, KIF14, 219 CEP55	41	19157	8.534135204	0.99999	0.49435	0.48889
				4221					9926	7528	1239
GOTERM_BP_DIR ECT	GO:0030277~maintenance of gastrointestinal epithelium	3	1.321585903	0.01227	VSIG1, TFF2, TFF1 219	15	19157	17.49497717	0.99999	0.52250	0.51673
				7335					9983	8914	1345
GOTERM_BP_DIR ECT	GO:0001568~blood vessel development	4	1.762114537	0.01366	FOXS1, FOXC1, 219 COL1A2, COL5A1	44	19157	7.95226235	0.99999	0.55978	0.55359
				3738					9998	8664	8879
GOTERM_BP_DIR ECT	GO:0048566~embryonic digestive tract development	3	1.321585903	0.01392	PKDCC, CXCL8, ADA 219	16	19157	16.4015411	0.99999	0.55978	0.55359
				7016					9998	8664	8879
GOTERM_BP_DIR ECT	GO:0001666~response to hypoxia	7	3.083700441	0.01718	ALDH3A1, ANGPT2, 219 PLAU, ITGA2, NOX4, ADA, PGF	180	19157	3.401801116	1	0.66359	0.65625
				7302						0224	2668
GOTERM_BP_DIR ECT	GO:0035264~multicellular organism growth	5	2.202643172	0.01742	COMP, COL3A1, 219 STIL, PKDCC, SCNN1B	87	19157	5.02729229	1	0.66359	0.65625
				6696						0224	2668
GOTERM_BP_DIR ECT	GO:0006805~xenobiotic metabolic process	5	2.202643172	0.01809	CYP2C9, ALDH3A1, 219 AADAC, FMO5, SULT2A1	88	19157	4.970163968	1	0.67149	0.66406
				8316						3927	8977

GOTERM_BP_DIR ECT	GO:0048839~inner ear development	4	1.762114537	0.01924	PDGFRB, SPARC, 219 4447 ESRRB, HOXA13	50	19157	6.997990868	1	0.68243	0.67488
GOTERM_BP_DIR ECT	GO:0008284~positive regulation of cell proliferation	13	5.726872247	0.01956	PDGFRB, KIF14, LIFR, 219 899 PGF, HOXC10, CDC25B, CDC20, ALDH3A1, CCKBR, PRC1, GPER1, TIMP1, WNT2	534	19157	2.129538419	1	0.68243	0.67488
GOTERM_BP_DIR ECT	GO:0042572~retinol metabolic process	4	1.762114537	0.02027	AKR1B10, RDH12, 219 955 ADH1C, ADH7	51	19157	6.86077536	1	0.68243	0.67488
GOTERM_BP_DIR ECT	GO:0034097~response to cytokine	4	1.762114537	0.02027	COL3A1, SPARC, 219 955 LIFR, TIMP1	51	19157	6.86077536	1	0.68243	0.67488
GOTERM_BP_DIR ECT	GO:0007568~aging	7	3.083700441	0.02177	PDGFRB, ALDH3A1, 219 6695 KCNE2, MMP7, TIMP1, CLDN1, ADA	190	19157	3.222758952	1	0.69346	0.68579
GOTERM_BP_DIR ECT	GO:1903225~negative regulation of endodermal cell differentiation	2	0.881057269	0.02263	COL5A1, COL5A2 219 0395	2	19157	87.47488584	1	0.69346	0.68579
GOTERM_BP_DIR ECT	GO:0008315~meiotic G2/MI transition	2	0.881057269	0.02263	CCNB2, NDC80 219 0395	2	19157	87.47488584	1	0.69346	0.68579
GOTERM_BP_DIR ECT	GO:0043401~steroid hormone mediated signaling pathway	3	1.321585903	0.02348	GPER1, ESRRB, 219 2924 ESRRG	21	19157	12.49641226	1	0.69346	0.68579
GOTERM_BP_DIR ECT	GO:0035567~non-canonical Wnt signaling pathway	3	1.321585903	0.02348	SFRP4, FZD2, SFRP5 219 2924	21	19157	12.49641226	1	0.69346	0.68579

GOTERM_BP_DIR ECT	GO:0001556~oocyte maturation	3	1.321585903	0.02348	CCNB1, TRIP13, CDC25B	219	21	19157	12.49641226	1	0.69346	0.68579
				2924							513	7236
GOTERM_BP_DIR ECT	GO:0071230~cellular response to amino acid stimulus	4	1.762114537	0.02472	COL3A1, COL4A1, COL5A2	219	55	19157	6.36180988	1	0.70003	0.69229
				1316							2093	1586
GOTERM_BP_DIR ECT	GO:0010467~gene expression	4	1.762114537	0.02472	ANGPT2, SCNN1B, NOX4, APOE	219	55	19157	6.36180988	1	0.70003	0.69229
				1316							2093	1586
GOTERM_BP_DIR ECT	GO:0007417~central nervous system development	6	2.643171806	0.02523	VCAN, PTPRZ1, ZBTB16, DNER, MAL, SH3GL2	219	145	19157	3.619650449	1	0.70003	0.69229
				1752							2093	1586
GOTERM_BP_DIR ECT	GO:0042157~lipoprotein metabolic process	3	1.321585903	0.02564	APOC1, OLR1, APOE	219	22	19157	11.92839352	1	0.70003	0.69229
				0429							2093	1586
GOTERM_BP_DIR ECT	GO:0014911~positive regulation of smooth muscle cell migration	3	1.321585903	0.02787	PDGFRB, ITGA2, NOX4	219	23	19157	11.40976772	1	0.74695	0.73869
				5158							0998	1692
GOTERM_BP_DIR ECT	GO:0051216~cartilage development	4	1.762114537	0.03095	PRRX1, ZBTB16, TIMP1, SULF1	219	60	19157	5.831659056	1	0.80800	0.79907
				035							8517	4076
GOTERM_BP_DIR ECT	GO:0016477~cell migration	8	3.524229075	0.03127	PDGFRB, FOXC1, DEPDC1B, COL5A1, FSCN1, CDK1, PDILT, CTHRC1	219	263	19157	2.660833029	1	0.80800	0.79907
				0544							8517	4076
GOTERM_BP_DIR ECT	GO:0001701~in utero embryonic development	7	3.083700441	0.03201	TMEM100, CCNB2, COL3A1, FOXC1, STIL, CCNB1, LY6E	219	208	19157	2.943866351	1	0.81252	0.80353
				3147							1576	7233

GOTERM_BP_DIR ECT	GO:0006883~cellular sodium ion homeostasis	3	1.321585903	0.03256	ATP4B, ATP4A, 219	25	19157	10.4969863	1	0.81252	0.80353	
				8246	SCNN1B					1576	7233	
GOTERM_BP_DIR ECT	GO:0051987~positive regulation of attachment of spindle microtubules to kinetochore	2	0.881057269	0.03375	CCNB1, RCC2	219	3	19157	58.31659056	1	0.81402	0.80502
				3683						6324	5342	
GOTERM_BP_DIR ECT	GO:0034447~very-low-density lipoprotein particle clearance	2	0.881057269	0.03375	APOC1, APOE	219	3	19157	58.31659056	1	0.81402	0.80502
				3683						6324	5342	
GOTERM_BP_DIR ECT	GO:0007094~mitotic spindle assembly checkpoint	3	1.321585903	0.03502	TRIP13, BUB1, 219	26	19157	10.09325606	1	0.83078	0.82159	
				2671	MAD2L1					3682	7407	
GOTERM_BP_DIR ECT	GO:0048010~vascular endothelial growth factor receptor signaling pathway	3	1.321585903	0.03754	FOXC1, SULF1, PGF	219	27	19157	9.719431761	1	0.87628	0.86659
				6453						5755	6348	
GOTERM_BP_DIR ECT	GO:0007586~digestion	3	1.321585903	0.04013	CAPN9, GKN1, PGC	219	28	19157	9.372309198	1	0.89936	0.88942
				771						9836	518	
GOTERM_BP_DIR ECT	GO:0048041~focal adhesion assembly	3	1.321585903	0.04013	RCC2, ITGA2, THY1	219	28	19157	9.372309198	1	0.89936	0.88942
				771						9836	518	
GOTERM_BP_DIR ECT	GO:0048565~digestive tract development	3	1.321585903	0.04279	COL3A1, CCNB1, 219	29	19157	9.049126122	1	0.89936	0.88942	
				4597	CCKBR					9836	518	
GOTERM_BP_DIR ECT	GO:0009314~response to radiation	3	1.321585903	0.04279	COL3A1, ANGPT2, 219	29	19157	9.049126122	1	0.89936	0.88942	
				4597	AQP4					9836	518	
GOTERM_BP_DIR ECT	GO:0007057~spindle assembly involved in female meiosis I	2	0.881057269	0.04475	CCNB2, NDC80	219	4	19157	43.73744292	1	0.89936	0.88942
				0952						9836	518	

GOTERM_BP_DIR ECT	GO:0036018~cellular response to erythropoietin	2	0.881057269	0.04475	MT2A, MT1X	219	4	19157	43.73744292	1	0.89936	0.88942
				0952							9836	518
GOTERM_BP_DIR ECT	GO:0035989~tendon development	2	0.881057269	0.04475	COMP, COL5A1	219	4	19157	43.73744292	1	0.89936	0.88942
				0952							9836	518
GOTERM_BP_DIR ECT	GO:1905448~positive regulation of mitochondrial ATP synthesis coupled electron transport	2	0.881057269	0.04475	CCNB1, CDK1	219	4	19157	43.73744292	1	0.89936	0.88942
				0952							9836	518
GOTERM_BP_DIR ECT	GO:0048592~eye morphogenesis	2	0.881057269	0.04475	COL5A1, COL5A2	219	4	19157	43.73744292	1	0.89936	0.88942
				0952							9836	518
GOTERM_BP_DIR ECT	GO:0045851~pH reduction	2	0.881057269	0.04475	ATP4B, CCKBR	219	4	19157	43.73744292	1	0.89936	0.88942
				0952							9836	518
GOTERM_BP_DIR ECT	GO:0000132~establishment of mitotic spindle orientation	3	1.321585903	0.04829	CENPA, NDC80, MAD2L1	219	31	19157	8.465311533	1	0.95642	0.94585
				8034							5756	0212
GOTERM_BP_DIR ECT	GO:0021987~cerebral cortex development	4	1.762114537	0.04891	ASPM, CNTNAP2, COL3A1, KIF14	219	72	19157	4.85971588	1	0.95642	0.94585
				1891							5756	0212

GOTERM_CC_DIR	GO:0005615~extracellular space	61	26.8722467	6.57E-1	PIGR,	SPARC,	226	1906	20163	2.85531252	1.78E-1	1.78E-1	1.72E-1
ECT				4	OLFML2B,	CXCL8,					1	1	1
					COL12A1,	CXCL17,							
					COMP,	VMO1, PLAU,							
					CA2,	FAM3B,							
					COL10A1,	SOSTDC1,							
					CPXM1,	TIMP1,							
					CPA2,	CHIA, MMP7,							
					GPX3,	GKN1, BGN,							
					GKN2,	PGC, PGF,							
					SFRP4,	ALDH3A1,							
					VCAN,	COL4A1,							
					SCGB2A1,	SFRP5,							
					ANOS1,	COL4A5,							
					COL8A1,	TFF2, TFF1,							
					CELA3B,	CPB1,							
					TNFRSF11B,	LRP8,							
					SCUBE2,	SELENBP1,							
					CST2,	CHAD, SPP1,							
					SERPINH1,	CKB,							
					APOE,	WNT2,							
					CTHRC1,	LINGO1,							
					ANGPT2,	CKM,							
					SULF1,	KLK11,							
					ATP4A,	COL3A1,							
					COL1A2,	COL5A1,							

FAP, COL5A2, ADA

GOTERM_CC_DIR	GO:0031012~extracellular matrix	21	9.251101322	1.06E-1	LINGO1, OLFML2B, 226	256	20163	7.318566787	2.86E-0	1.43E-0	1.38E-0
ECT				1	MMP7, MMP1, BGN, TNFRSF11B, COMP, COL3A1, ADAMTS2, VCAN, COL1A2, COL5A1, COL4A1, COL5A2, CHAD, ANOS1, COL4A5, COL8A1, COL10A1, TIMP1, APOE			9	9	9	

GOTERM_CC_DIR	GO:0005576~extracellular region	57	25.11013216	5.21E-1	SPARC,	OLFML2B,	226	2116	20163	2.403288472	1.41E-0	4.70E-0	4.55E-0
ECT				0	CXCL8,	PSCA,					7	8	8
					COL12A1,	AQP4,							
					COMP,	LIPF,							
					ADAMTS2,	PLAU,							
					FAM3B,	COL10A1,							
					OLR1,	TIMP1,	CPA2,						
					CHIA,	MMP7,	GPX3,						
					MMP1,	GKN1,							
					MAMDC2,	BGN,	PGF,						
					SFRP4,	VCAN,							
					FNDC1,	COL4A1,							
					NRG4,	ANOS1,							
					COL4A5,	COL8A1,							
					TFF1,	LY6E,	PKDCC,						
					TNFRSF11B,	THY1,							
					THBS2,	PLA2G7,							
					SCUBE2,	PTPRZ1,							
					SPP1,	APOE,							
					METTL7A,	WNT2,							
					GPIHBP1,	CTHRC1,							
					ANGPT2,	B3GAT1,							
					GUCA2B,	COL3A1,							
					AKR1B10,	COL1A2,							
					COL5A1,	QPCT,							
					COL5A2,	APOC1,							

CNTN3

GOTERM_CC_DIR	GO:0005581~collagen trimer	12	5.286343612	7.15E-0	COL3A1,	COL1A2,	226	93	20163	11.51184699	1.94E-0	4.84E-0	4.68E-0
ECT				9	COL5A1,	COL4A1,					6	7	7
					MMP1,	COL12A1,							
					COL5A2,	SERPINH1,							
					COL10A1,	COL4A5,							
					TIMP1,	CTHRC1							
GOTERM_CC_DIR	GO:0000776~kinetochore	11	4.845814978	4.23E-0	CENPW,	NUF2,	226	141	20163	6.960176991	0.00114	2.30E-0	2.22E-0
ECT				6	HJURP,	KIF2C,					686	4	4
					CENPN,	NEK2,							
					CENPA,	BUB1,							
					NDC80,	MAD2L1,							

GOTERM_CC_DIR ECT	GO:0009986~cell surface	16	7.04845815	0.00524	PDGFRB, CNTNAP2, 226 3951 KCNE2, SPARC, MMP7, ITGA2, BGN, THY1, SULF1, LRP8, SCUBE2, SFRP4, FAP, PLAU, ANOS1, ADA	634	20163	2.251528433	0.75945	0.11842	0.11449
									5418	5887	2924
GOTERM_CC_DIR ECT	GO:0016324~apical plasma membrane	11	4.845814978	0.00872	ATP4B, PDGFRB, 226 4229 ASPM, ATP4A, SLC7A8, SCNN1B, MAL, NOX4, THY1, CLDN1, GPIHBP1	369	20163	2.659579826	0.90695	0.18186	0.17582
									1974	661	6759
GOTERM_CC_DIR ECT	GO:0045178~basal part of cell	3	1.321585903	0.01182	FAP, ITGA2, GKN2 226 9609	15	20163	17.84336283	0.96024	0.22898	0.22138
									1702	7428	268
GOTERM_CC_DIR ECT	GO:0005813~centrosome	13	5.726872247	0.01858	STIL, SNX10, NDC80, 226 2684 CDC25B, CDC20, ASPM, CCNB2, CCNB1, CDK1, NEK2, KIF2C, DTL, CEP55	540	20163	2.147812193	0.99380	0.31655	0.30604
									0494	8384	5375
GOTERM_CC_DIR ECT	GO:0005694~chromosome	8	3.524229075	0.02061	BOP1, PRC1, KIF4A, 226 805 TRIP13, ETV4, HOXA13, DTL, BYSL	245	20163	2.913202095	0.99646	0.31655	0.30604
									8022	8384	5375

GOTERM_CC_DIR GO:0016020~membrane

40	17.62114537	0.02081	CNTNAP2,	SPARC,	226	2518	20163	1.417264721	0.99665	0.31655	0.30604
ECT		8062	CSE1L,	KIF14,					8205	8384	5375
			NCAPG,	AQP4,							
			SNX10,	LRP8,							
			SELENBP1,	CCNB2,							
			CCNB1,	CDH3,							
			VSIG2,	NUF2,	OLR1,						
			APOE,	METTL7A,							
			BUB1,	SH3GL2,							
			CEP55,	PDGFRB,							
			ITGA2,	RCC2,							
			MAMDC2,	KCNJ15,							
			KCNJ16,	NDC80,	PGF,						
			BYSL,	VCAN,	MELK,						
			COL4A1,	KIF4A,							
			PXMP2,	CDH11,							
			CDK1,	COL4A5,							
			KIF2C,	SLC25A4,							
			ADA								

GOTERM_CC_DIR ECT	GO:0070062~extracellular exosome	36	15.85903084	0.02196	CLIC6, PIGR, PSCA, 226 6049 CSE1L, COL12A1, THY1, SLC5A5, SELENBP1, COMP, VMO1, AKR7A3, PLAU, CA2, GNG7, FAM3B, SPP1, CKB, APOE, TIMP1, GPR155, MEST, MMP7, GPX3, SYTL1, BGN, KRT7, GUCA2B, LIFR, KLK11, COL1A2, SCNN1B, QPCT, CDH11, CDK1, FSCN1, FBP2	2217	20163	1.448716874	0.99756	0.31655	0.30604	
									827	8384	5375	
GOTERM_CC_DIR ECT	GO:0097125~cyclin B1-CDK1 complex	2	0.881057269	0.02219	CCNB1, CDK1	226	2	20163	89.21681416	0.99771	0.31655	0.30604
				413					7213	8384	5375	
GOTERM_CC_DIR ECT	GO:0031225~anchored component of membrane	5	2.202643172	0.03587	PSCA, CNTN3, THY1, 226 119 GPIHBP1, LY6E	111	20163	4.018775413	0.99994	0.44638	0.43156	
									9812	6456	1813	
GOTERM_CC_DIR ECT	GO:0000793~condensed chromosome	3	1.321585903	0.03623	TOP2A, ESRRB, 226 8015 NCAPG	27	20163	9.912979351	0.99995	0.44638	0.43156	
									473	6456	1813	
GOTERM_CC_DIR ECT	GO:0034364~high-density lipoprotein particle	3	1.321585903	0.03623	APOC1, APOE, 226 8015 PLA2G7	27	20163	9.912979351	0.99995	0.44638	0.43156	
									473	6456	1813	

GOTERM_CC_DIR GO:0005737~cytoplasm
ECT

73	32.15859031	0.04220	CLIC6,	TOP2A,	226	5375	20163	1.211688825	0.99999	0.45755	0.44235
		7807	SPARC,	CSE1L,					1595	0374	4974
			MT1M,	YBX2,	MT1X,						
			AQP4,	CLDN1,							
			MT2A,	PAIP2B,							
			CAPN9,	AKR7A3,							
			CDH3,	CA2,	GPER1,						
			NEK2,	SH3GL2,							
			DLGAP5,	CEP55,							
			SULT2A1,	PDGFRB,							
			TEAD4,	CHIA,							
			APOBEC2,	KRT7,							
			ANXA10,	CDC25B,							
			SFRP4,	ASPM,							
			ALDH3A1,	MELK,							
			SLC7A8,	CDH11,							
			FSCN1,	MT1G,	MT1H,						
			KIF2C,	FBP2,	MT1E,						
			TRIM50,	TROAP,							
			HDC,	NCAPG,	ADH7,						
			PLA2G7,	CCNB2,							
			CCNB1,	APOE,	ECT2,						
			WNT2,	RPRM,							
			CTHRC1,	STIL,	FZD2,						
			ARHGEF37,	DDIAS,							
			HOMER2,	GAD1,							

IRX3, ESRRB, BYSL,
 CAPN13, CYP2C9,
 TPX2, PLCXD3, FAP,
 PRC1, KIF4A, PXMP2,
 CDK1, CDKN3,
 MAD2L1

GOTERM_CC_DIR	GO:0005783~endoplasmic reticulum	20	8.810572687	0.04320	PDIA2, KCNE2, 226	1112	20163	1.60461896	0.99999	0.45755	0.44235
ECT				9275	MAMDC2, P3H4,				367	0374	4974
					SNX10, THY1, SULF1,						
					FMO5, TMEM100,						
					ALDH3A1, COL1A2,						
					GPER1, APOC1,						
					SERPINH1, MAL,						
					PDILT, METTL7A,						

APOE, MEST, TMED6

GOTERM_CC_DIR ECT	GO:0033597~mitotic checkpoint complex		2	0.881057269	0.04389	CDC20, MAD2L1	226	4	20163	44.60840708	0.99999	0.45755	0.44235	
					7822						4792	0374	4974	
GOTERM_CC_DIR ECT	GO:0005588~collagen type V trimer		2	0.881057269	0.04389	COL5A1, COL5A2	226	4	20163	44.60840708	0.99999	0.45755	0.44235	
					7822						4792	0374	4974	
GOTERM_CC_DIR ECT	GO:0016323~basolateral plasma membrane		7	3.083700441	0.04898	SLC7A8, VSIG1, CA2,	226	235	20163	2.657522124	0.99999	0.49164	0.47532	
					3391	KCNJ16, AQP4,					8773	8105	0308	
						CLDN1, GPIHBP1								
GOTERM_MF_DIR ECT	GO:0005201~extracellular constituent	matrix	structural	14	6.167400881	7.23E-0	SPARC, BGN, THBS2,	217	138	18765	8.772791024	2.88E-0	2.88E-0	2.83E-0
						9	COMP, COL3A1,				6	6	6	
							COL1A2, COL5A1,							
							COL4A1, COL5A2,							
							ANOS1, COL4A5,							
							COL8A1, COL10A1,							
							CTHRC1							
GOTERM_MF_DIR ECT	GO:0030020~extracellular constituent conferring tensile strength	matrix	structural	9	3.964757709	1.87E-0	COL3A1, COL1A2,	217	41	18765	18.9822412	7.45E-0	3.72E-0	3.66E-0
						8	COL5A1, COL4A1,				6	6	6	
							COL12A1, COL5A2,							
							COL10A1, COL4A5,							
							COL8A1							

GOTERM_MF_DIR	GO:0048407~platelet-derived growth factor binding	5	2.202643172	5.29E-0	PDGFRB, COL3A1,	217	11	18765	39.30666108	0.00210	7.03E-0	6.91E-0
ECT				6	COL1A2, COL5A1,					805	4	4
					COL4A1							
GOTERM_MF_DIR	GO:0008270~zinc ion binding	23	10.13215859	4.29E-0	CPA2, TRIM50, CPB1,	217	865	18765	2.29932607	0.15740	0.04280	0.04205
ECT				4	MMP7, ADH1C,					697	8612	7583
					MMP1, MT1M,							
					ESRRB, MT1X,							
					ESRRG, MYRIP,							
					ADH7, ADAMTS2,							
					MT2A, CA2, QPCT,							
					MT1G, ZNF385B,							
					CPXM1, MT1H,							
					TIMP1, ADA, MT1E							
GOTERM_MF_DIR	GO:0004111~creatine kinase activity	3	1.321585903	0.00191	CKMT2, CKM, CKB	217	6	18765	43.23732719	0.53531	0.15313	0.15044
ECT				8971						9498	3922	7362
GOTERM_MF_DIR	GO:0005178~integrin binding	8	3.524229075	0.00265	COMP, COL3A1,	217	161	18765	4.296877236	0.65383	0.16960	0.16662
ECT				5189	COL5A1, PTPRZ1,					1474	2905	7416
					FAP, ITGA2, SPP1,							
					THY1							

GOTERM_MF_DIR GO:0005515~protein binding
ECT

164	72.24669604	0.00313	SPARC,	CSE1L,	217	12517	18765	1.133006576	0.71379	0.16960	0.16662
		0572	MT1M,	HJURP,					8057	2905	7416
			CXCL17,	AQP4,							
			MT1X,	CLDN1,							
			COMP,	CDC20,							
			PAIP2B,	MT2A,							
			AKR7A3,	VSIG1,							
			PLAU, PDK4, FAM3B,								
			NEK2,	SH3GL2,							
			SULT2A1,	PDGFRB,							
			PDIA2, CHIA, SYTL1,								
			KRT7, LIFR, ANXA10,								
			BHLHA15,	FRMD1,							
			PGF, CDC25B, SFRP4,								
			ALDH3A1,	MELK,							
			COL4A1,	SCNN1B,							
			ANOS1,	FSCN1,							
			COL8A1,	MAL,							
			MT1G, MT1H, MT1E,								
			LY6E, KCNE2, CPB1,								
			MAOA,	TROAP,							
			CDCA7,	NCAPG,							
			TNFRSF11B,	THY1,							
			SLC5A5,	SCUBE2,							
			CCNB2,	CCNB1,							
			RDH12,	ORC1,							

LDHD, SERPINH1,
APOE, ECT2, WNT2,
GPIHBP1, STIL, FZD2,
UBE2C, HOMER2,
ZBTB16, RCC2,
ESRRG, NDC80,
ATP4B, TPX2,
PLCXD3, AKR1B10,
COL1A2, COL5A1,
KIF4A, PXMP2,
CDK1, NOX4, ADA,
TOP2A, CNTNAP2,
CXCL8, KIF14, KRT23,
SNX10, HOXC10,
TMEM100, ACADL,
CA2, GPER1, DNER,
NUF2, COL10A1,
PMEPA1, OLR1,
TIMP1, DLGAP5,
CEP55, TEAD4,
MMP7, GPX3, ITGA2,
GKN1, MAMDC2,
BGN, GKN2, MYRIP,
ETV4, TOX3, VCAN,
CCKBR, SLC7A8,
NRG4, SCGB2A1,

TFF2, TFF1, KIF2C,
 MTFR2, SLC25A4,
 DTL, FBP2, TRIM50,
 FOXC1, HDC, THBS2,
 CENPA, LRP8,
 SELENBP1, CKMT2,
 CST2, PTPRZ1, GNG7,
 SPP1, CKB,
 METTL7A, MEST,
 BUB1, RPRM,
 LINGO1, CENPW,
 ANGPT2, PRRX1,
 CKM, GAD1,
 B3GAT1, KCNJ15,
 FAM189A2, GUCA2B,
 BYSL, BOP1, COL3A1,
 AADAC, FAP, PRC1,
 QPCT, APOC1,
 TRIP13, CDKN3,
 SPC25, MAD2L1

GOTERM_MF_DIR	GO:0004022~alcohol dehydrogenase (NAD) activity	3	1.321585903	0.00352	ADH1C, ADHFE1, 217	8	18765	32.42799539	0.75589	0.16960	0.16662
ECT				8038	ADH7				9696	2905	7416
GOTERM_MF_DIR	GO:0008201~heparin binding	8	3.524229075	0.00382	COMP, CXCL8, 217	172	18765	4.022076948	0.78332	0.16960	0.16662
ECT				5629	MMP7, COL5A1, ANOS1, APOE,				4273	2905	7416

THBS2, PGF

GOTERM_MF_DIR ECT	GO:0017147~Wnt-protein binding	4	1.762114537	0.00485	SFRP4, FZD2, SFRP5, 217 CTHRC1	30	18765	11.52995392	0.85663	0.17614	0.17305
				6172					0841	6588	6297
GOTERM_MF_DIR ECT	GO:0005496~steroid binding	4	1.762114537	0.00485	PDIA2, GPER1, 217 ESRRB, ESRRG	30	18765	11.52995392	0.85663	0.17614	0.17305
				6172					0841	6588	6297
GOTERM_MF_DIR ECT	GO:0050840~extracellular matrix binding	4	1.762114537	0.00533	SPARC, OLFML2B, 217 SPP1, BGN	31	18765	11.15801992	0.88150	0.17726	0.17415
				1372					7798	8117	815
GOTERM_MF_DIR ECT	GO:0050660~flavin adenine dinucleotide binding	5	2.202643172	0.00743	ACADL, MAOA, 217 LDHD, NOX4, FMO5	67	18765	6.453332416	0.94905	0.21185	0.20813
				355					7883	6172	9397
GOTERM_MF_DIR ECT	GO:0005518~collagen binding	5	2.202643172	0.00743	COMP, SPARC, 217 ITGA2, SERPINH1, P3H4	67	18765	6.453332416	0.94905	0.21185	0.20813
				355					7883	6172	9397
GOTERM_MF_DIR ECT	GO:0008301~DNA binding, bending	3	1.321585903	0.01600	TOP2A, FOXC1, 217 FOXD1	17	18765	15.26023313	0.99840	0.41568	0.40839
				8767					2281	577	3037
GOTERM_MF_DIR ECT	GO:0016491~oxidoreductase activity	8	3.524229075	0.01666	CYP2C9, ALDH3A1, 217 RDH12, ADH1C, MAOA, ADHFE1, NOX4, ADH7	228	18765	3.034198399	0.99877	0.41568	0.40839
				9104					771	577	3037
GOTERM_MF_DIR ECT	GO:0008289~lipid binding	7	3.083700441	0.01805	LIPF, SCUBE2, MELK, 217 MAL, APOE, SH3GL2, GPIHBP1	180	18765	3.362903226	0.99930	0.41617	0.40887
				262					3056	9694	8296

GOTERM_MF_DIR ECT	GO:0043395~heparan sulfate proteoglycan binding	3	1.321585903	0.01982	COMP, ITGA2, APOE	217	19	18765	13.6538928	0.99966	0.41617	0.40887
				8109						1472	9694	8296
GOTERM_MF_DIR ECT	GO:0004745~retinol dehydrogenase activity	3	1.321585903	0.01982	RDH12, ADH1C, ADH7	217	19	18765	13.6538928	0.99966	0.41617	0.40887
				8109						1472	9694	8296
GOTERM_MF_DIR ECT	GO:0001228~transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	12	5.286343612	0.02086	TEAD4, FOXC1, FOXD1, PRRX1, IRX3, ZBTB16, ESRRB, ESRRG, BHLHA15, ETV4, HOXA13, HOXC10	217	471	18765	2.203175908	0.99977	0.41617	0.40887
				1138						7735	9694	8296
GOTERM_MF_DIR ECT	GO:0008106~alcohol dehydrogenase (NADP+) activity	2	0.881057269	0.02288	ALDH3A1, AKR1B10	217	2	18765	86.47465438	0.99990	0.42402	0.41658
				9691						2838	6935	7866
GOTERM_MF_DIR ECT	GO:0004252~serine-type endopeptidase activity	7	3.083700441	0.02337	CELA3B, MMP7, FAP, PLAU, MMP1, ANOS1, KLK11	217	191	18765	3.169228171	0.99992	0.42402	0.41658
				9931						047	6935	7866
GOTERM_MF_DIR ECT	GO:0003707~steroid hormone receptor activity	3	1.321585903	0.02846	GPER1, ESRRB, ESRRG	217	23	18765	11.27930274	0.99999	0.49387	0.48521
				9242						0111	9457	4905
GOTERM_MF_DIR ECT	GO:0008900~hydrogen:potassium-exchanging ATPase activity	2	0.881057269	0.03413	ATP4B, ATP4A	217	3	18765	57.64976959	0.99999	0.51631	0.50725
				8203						9043	0195	2121
GOTERM_MF_DIR ECT	GO:0004031~aldehyde oxidase activity	2	0.881057269	0.03413	ADH7, FMO5	217	3	18765	57.64976959	0.99999	0.51631	0.50725
				8203						9043	0195	2121
GOTERM_MF_DIR ECT	GO:0005539~glycosaminoglycan binding	3	1.321585903	0.03576	VCAN, BGN, SULF1	217	26	18765	9.977844736	0.99999	0.51631	0.50725
				0167						951	0195	2121

GOTERM_MF_DIR	GO:0005242~inward rectifier potassium channel activity	3	1.321585903	0.03576	KCNE2, KCNJ15, KCNJ16	217	26	18765	9.977844736	0.99999	0.51631	0.50725
ECT				0167						951	0195	2121
GOTERM_MF_DIR	GO:0002020~protease binding	5	2.202643172	0.03623	COMP, COL3A1, COL1A2, FAP, TIMP1	217	108	18765	4.003456221	0.99999	0.51631	0.50725
ECT				2294						9597	0195	2121
GOTERM_MF_DIR	GO:0004181~metallocarboxypeptidase activity	3	1.321585903	0.04645	CPA2, CPB1, CPXM1	217	30	18765	8.647465438	0.99999	0.63920	0.62798
ECT				8407						9994	3602	9504
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	13	5.726872247	2.23E-0	CPA2, CELA3B, CPB1, COL12A1, COL3A1, COL1A2, SLC7A8, COL5A1, COL4A1, COL5A2, COL4A5, COL8A1, COL10A1	118	103	8142	8.708737864	4.11E-0	4.13E-0	4.02E-0
				8						6	6	6
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	8	3.524229075	2.57E-0	COMP, COL1A2, COL4A1, ITGA2, CHAD, SPP1, COL4A5, THBS2	118	88	8142	6.272727273	0.04614	0.02374	0.02310
				4						0355	4688	294
KEGG_PATHWAY	hsa04971:Gastric acid secretion	7	3.083700441	7.46E-0	ATP4B, ATP4A, KCNE2, CCKBR, CA2, KCNJ15, KCNJ16	118	76	8142	6.355263158	0.12836	0.04602	0.04478
				4						6524	7126	3149
KEGG_PATHWAY	hsa04978:Mineral absorption	6	2.643171806	0.00163	MT2A, MT1M, MT1G, MT1H, MT1X, MT1E	118	60	8142	6.9	0.26011	0.07269	0.07072
				5962						7176	0676	6063
KEGG_PATHWAY	hsa04110:Cell cycle	8	3.524229075	0.00218	CDC20, CCNB2, CCNB1, ORC1, CDK1, BUB1, CDC25B,	118	126	8142	4.380952381	0.33102	0.07269	0.07072
				248						9348	0676	6063

KEGG_PATHWAY	hsa04510:Focal adhesion	10	4.405286344	0.00235	MAD2L1	118	201	8142	3.432835821	0.35228	0.07269	0.07072
				7535	PDGFRB, COMP, COL1A2, COL4A1, ITGA2, CHAD, SPP1, COL4A5, THBS2, PGF					122	0676	6063
KEGG_PATHWAY	hsa00982:Drug metabolism - cytochrome P450	6	2.643171806	0.00365	CYP2C9, ALDH3A1, ADH1C, MAOA, ADH7, FMO5	118	72	8142	5.75	0.49040	0.09665	0.09403
				7106						6021	2091	9873
KEGG_PATHWAY	hsa00980:Metabolism of xenobiotics by cytochrome P450	6	2.643171806	0.00515	CYP2C9, ALDH3A1, AKR7A3, ADH1C, ADH7, SULT2A1	118	78	8142	5.307692308	0.61366	0.11922	0.11599
				5461						8104	0028	7865
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	5.286343612	0.01263	PDGFRB, COMP, ANGPT2, COL1A2, COL4A1, GNG7, ITGA2, CHAD, SPP1, COL4A5, THBS2, PGF	118	354	8142	2.338983051	0.90363	0.23924	0.23277
				4786						4999	5193	9107
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	2.643171806	0.01434	COL3A1, CXCL8, COL1A2, COL4A1, COL4A5, NOX4	118	100	8142	4.14	0.92996	0.23924	0.23277
				6014						6665	5193	9107
KEGG_PATHWAY	hsa00350:Tyrosine metabolism	4	1.762114537	0.01462	ALDH3A1, ADH1C, MAOA, ADH7	118	36	8142	7.666666667	0.93356	0.23924	0.23277
				8193						0813	5193	9107
KEGG_PATHWAY	hsa04914:Progesterone-mediated oocyte maturation	6	2.643171806	0.01551	CCNB2, CCNB1, CDK1, BUB1, CDC25B, MAD2L1	118	102	8142	4.058823529	0.94374	0.23924	0.23277
				8607						2265	5193	9107

KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	4.845814978	0.02045	PDGFRB, FZD2, COL4A1, CHAD, COL4A5, WNT2	COMP, COL1A2, ITGA2, SPP1, THBS2,	118	331	8142	2.29305136	0.97768	0.29107	0.28321
			4099								6811	7564	0603
KEGG_PATHWAY	hsa00330:Arginine and proline metabolism	4	1.762114537	0.03656	CKMT2, MAOA, CKB	CKM,	118	51	8142	5.411764706	0.99894	0.43641	0.42461
			6049								5035	0444	5568
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	6	2.643171806	0.03792	COL3A1, COL4A1, GNG7, COL4A5	COL1A2, MMP1,	118	129	8142	3.209302326	0.99918	0.43641	0.42461
			2368								593	0444	5568
KEGG_PATHWAY	hsa00340:Histidine metabolism	3	1.321585903	0.03922	ALDH3A1, HDC	MAOA,	118	22	8142	9.409090909	0.99936	0.43641	0.42461
			1515								5135	0444	5568
KEGG_PATHWAY	hsa04114:Oocyte meiosis	6	2.643171806	0.04010	CDC20, CCNB1, CDK1, BUB1, MAD2L1	CCNB2,	118	131	8142	3.160305344	0.99946	0.43641	0.42461
			2581								375	0444	5568

Supplementary Table 2 The pathways of GO, KEGG and GSEA enrichment analysis of co-DEGs correlated to the prognosis of gastric cancer

Category	Term	Count	P value	FDR
The list of BGN enriched pathways				
Category	Term	Count	PValue	FDR
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	36	0.021966049	0.306045375
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	4	0.005331372	0.17415815
GOTERM_MF_DIRECT	GO:0005539~glycosaminoglycan binding	3	0.035760167	0.507252121
The list of CEP55 enriched pathways				
Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis	5	0.003534397	0.219900943
GOTERM_BP_DIRECT	GO:0045184~establishment of protein localization	4	0.011274221	0.488891239
GOTERM_CC_DIRECT	GO:0030496~midbody	10	2.04E-04	0.006690576
GOTERM_CC_DIRECT	GO:0005813~centrosome	13	0.018582684	0.306045375
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	27	0.079551123	0.974501257
The list of COL1A2 enriched pathways				
Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	10	2.08E-08	2.98E-05
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	13	2.67E-07	1.27E-04
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	12	3.61E-07	1.29E-04
GOTERM_BP_DIRECT	GO:0001568~blood vessel development	4	0.013663738	0.553598879
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	4	0.024721316	0.692291586

GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	36	0.021966049	0.306045375
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	20	0.043209275	0.442354974
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0030020~extracellular matrix structural constituent conferring tensile strength	9	1.87E-08	3.66E-06
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0002020~protease binding	5	0.036232294	0.507252121
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	27	0.079551123	0.974501257
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	13	2.23E-08	4.02E-06
KEGG_PATHWAY	hsa04512:ECM-receptor interaction ECM-receptor	8	2.57E-04	0.02310294
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	0.014346014	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	6	0.037922368	0.424615568
KEGG_PATHWAY	hsa05146:Amoebiasis	5	0.05889645	0.557966365

The list of COL4A1 enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	13	2.67E-07	1.27E-04
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	4	0.024721316	0.692291586

GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	4	0.087632773	0.989626556
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005587~collagen type IV trimer	2	0.075557326	0.659111517
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0030020~extracellular matrix structural constituent conferring tensile strength	9	1.87E-08	3.66E-06
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	13	2.23E-08	4.02E-06
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	8	2.57E-04	0.02310294
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	0.014346014	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	6	0.037922368	0.424615568
KEGG_PATHWAY	hsa05146:Amoebiasis	5	0.05889645	0.557966365
The list of FZD2 enriched pathways				
Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	3	0.023482924	0.685797236
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	4	0.052306886	0.988623199

GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	4	0.087632773	0.989626556
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0017147~Wnt-protein binding	4	0.004856172	0.173056297
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603

The list of MAOA enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050660~flavin adenine dinucleotide binding	5	0.00743355	0.208139397
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	8	0.016669104	0.408393037
KEGG_PATHWAY	hsa00982:Drug metabolism - cytochrome	6	0.003657106	0.094039873
KEGG_PATHWAY	hsa00350:Tyrosine metabolism	4	0.014628193	0.232779107
KEGG_PATHWAY	hsa00330:Arginine and proline metabolism	4	0.036566049	0.424615568
KEGG_PATHWAY	hsa00340:Histidine metabolism	3	0.039221515	0.424615568

The list of PDGFRB enriched pathways

Category	Term	Count	PValue	FDR
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	9	0.007511051	0.383868341
GOTERM_BP_DIRECT	GO:0048839~inner ear development	4	0.019244447	0.67488456
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	13	0.01956899	0.67488456
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.021776695	0.685797236
GOTERM_BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	3	0.027875158	0.738691692
GOTERM_BP_DIRECT	GO:0016477~cell migration	8	0.031270544	0.799074076
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	4	0.076997858	0.989626556
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	8	0.082565364	0.989626556
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	11	0.008724229	0.175826759

GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_CC_DIRECT	GO:0043235~receptor complex	6	0.094810285	0.752736205
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416

The list of SPARC enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0048839~inner ear development	4	0.019244447	0.67488456
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	0.02027955	0.67488456
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	5	0.055959804	0.988623199
GOTERM_BP_DIRECT	GO:0033591~response to L-ascorbic acid	2	0.066373105	0.989626556
GOTERM_BP_DIRECT	GO:0001937~negative regulation of endothelial cell proliferation	3	0.072589622	0.989626556
GOTERM_BP_DIRECT	GO:0030324~lung development	4	0.083307091	0.989626556
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	4	0.005331372	0.17415815
GOTERM_MF_DIRECT	GO:0005518~collagen binding	5	0.00743355	0.208139397
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	14	0.089299914	0.984924623

The list of TIMP1 enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	13	0.01956899	0.67488456
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	0.02027955	0.67488456
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.021776695	0.685797236
GOTERM_BP_DIRECT	GO:0051216~cartilage	4	0.03095035	0.799074076

	development			
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	36	0.021966049	0.306045375
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	23	4.29E-04	0.042057583
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0002020~protease binding	5	0.036232294	0.507252121

The list of VCAN enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	12	3.61E-07	1.29E-04
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	20	1.91E-05	0.002489822
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	6	0.025231752	0.692291586
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0005539~glycosaminoglycan binding	3	0.035760167	0.507252121
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	14	0.089299914	0.984924623

Category	Term	Count	PValue	FDR
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The list of BGN enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	36	0.021966049	0.306045375

GOTERM_MF_DIRECT	GO:0005201~extracellular structural constituent	matrix	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0005515~protein binding		164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050840~extracellular binding	matrix	4	0.005331372	0.17415815
GOTERM_MF_DIRECT	GO:0005539~glycosaminoglycan binding		3	0.035760167	0.507252121

The list of CEP55 enriched pathways

Category	Term		Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0000281~mitotic cytokinesis		5	0.003534397	0.219900943
GOTERM_BP_DIRECT	GO:0045184~establishment of localization	protein	4	0.011274221	0.488891239
GOTERM_CC_DIRECT	GO:0030496~midbody		10	2.04E-04	0.006690576
GOTERM_CC_DIRECT	GO:0005813~centrosome		13	0.018582684	0.306045375
GOTERM_CC_DIRECT	GO:0016020~membrane		40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm		73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005515~protein binding		164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0042802~identical protein binding		27	0.079551123	0.974501257

The list of COL1A2 enriched pathways

Category	Term		Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization		10	2.08E-08	2.98E-05
GOTERM_BP_DIRECT	GO:0030198~extracellular organization	matrix	13	2.67E-07	1.27E-04
GOTERM_BP_DIRECT	GO:0001501~skeletal development	system	12	3.61E-07	1.29E-04
GOTERM_BP_DIRECT	GO:0001568~blood vessel development		4	0.013663738	0.553598879
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus		4	0.024721316	0.692291586
GOTERM_CC_DIRECT	GO:0005615~extracellular space		61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix		21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region		57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer		12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic lumen	reticulum	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome		36	0.021966049	0.306045375
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum		20	0.043209275	0.442354974
GOTERM_MF_DIRECT	GO:0005201~extracellular structural constituent	matrix	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0030020~extracellular structural constituent conferring tensile strength	matrix	9	1.87E-08	3.66E-06
GOTERM_MF_DIRECT	GO:0048407~platelet-derived factor binding	growth	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding		164	0.003130572	0.166627416

GOTERM_MF_DIRECT	GO:0002020~protease binding	5	0.036232294	0.507252121
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	27	0.079551123	0.974501257
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	13	2.23E-08	4.02E-06
KEGG_PATHWAY	hsa04512:ECM-receptor interaction ECM-receptor	8	2.57E-04	0.02310294
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107
KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	0.014346014	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	6	0.037922368	0.424615568
KEGG_PATHWAY	hsa05146:Amoebiasis	5	0.05889645	0.557966365

The list of COL4A1 enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	13	2.67E-07	1.27E-04
GOTERM_BP_DIRECT	GO:0071230~cellular response to amino acid stimulus	4	0.024721316	0.692291586
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	4	0.087632773	0.989626556
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005587~collagen type IV trimer	2	0.075557326	0.659111517
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0030020~extracellular matrix structural constituent conferring tensile strength	9	1.87E-08	3.66E-06
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
KEGG_PATHWAY	hsa04974:Protein digestion and absorption	13	2.23E-08	4.02E-06
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	8	2.57E-04	0.02310294
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107

KEGG_PATHWAY	hsa04933:AGE-RAGE signaling pathway in diabetic complications	6	0.014346014	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
KEGG_PATHWAY	hsa04926:Relaxin signaling pathway	6	0.037922368	0.424615568
KEGG_PATHWAY	hsa05146:Amoebiasis	5	0.05889645	0.557966365

The list of FZD2 enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	3	0.023482924	0.685797236
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	4	0.052306886	0.988623199
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	4	0.087632773	0.989626556
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0017147~Wnt-protein binding	4	0.004856172	0.173056297
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603

The list of MAOA enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050660~flavin adenine dinucleotide binding	5	0.00743355	0.208139397
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	8	0.016669104	0.408393037
KEGG_PATHWAY	hsa00982:Drug metabolism - cytochrome	6	0.003657106	0.094039873
KEGG_PATHWAY	hsa00350:Tyrosine metabolism	4	0.014628193	0.232779107
KEGG_PATHWAY	hsa00330:Arginine and proline metabolism	4	0.036566049	0.424615568
KEGG_PATHWAY	hsa00340:Histidine metabolism	3	0.039221515	0.424615568

The list of PDGFRB enriched pathways

Category	Term	Count	PValue	FDR
KEGG_PATHWAY	hsa04510:Focal adhesion	10	0.002357535	0.070726063
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	12	0.012634786	0.232779107
KEGG_PATHWAY	hsa05165:Human papillomavirus infection	11	0.020454099	0.283210603
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	9	0.007511051	0.383868341
GOTERM_BP_DIRECT	GO:0048839~inner ear development	4	0.019244447	0.67488456
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	13	0.01956899	0.67488456
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.021776695	0.685797236
GOTERM_BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	3	0.027875158	0.738691692

GOTERM_BP_DIRECT	GO:0016477~cell migration	8	0.031270544	0.799074076
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	4	0.076997858	0.989626556
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	8	0.082565364	0.989626556
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	11	0.008724229	0.175826759
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_CC_DIRECT	GO:0043235~receptor complex	6	0.094810285	0.752736205
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	5	5.29E-06	6.91E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416

The list of SPARC enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0048839~inner ear development	4	0.019244447	0.67488456
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	0.02027955	0.67488456
GOTERM_BP_DIRECT	GO:0016525~negative regulation of angiogenesis	5	0.055959804	0.988623199
GOTERM_BP_DIRECT	GO:0033591~response to L-ascorbic acid	2	0.066373105	0.989626556
GOTERM_BP_DIRECT	GO:0001937~negative regulation of endothelial cell proliferation	3	0.072589622	0.989626556
GOTERM_BP_DIRECT	GO:0030324~lung development	4	0.083307091	0.989626556
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0009986~cell surface	16	0.005243951	0.114492924
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	73	0.042207807	0.442354974
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	14	7.23E-09	2.83E-06
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	4	0.005331372	0.17415815
GOTERM_MF_DIRECT	GO:0005518~collagen binding	5	0.00743355	0.208139397
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	14	0.089299914	0.984924623

The list of TIMP1 enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	13	0.01956899	0.67488456
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	4	0.02027955	0.67488456
GOTERM_BP_DIRECT	GO:0007568~aging	7	0.021776695	0.685797236
GOTERM_BP_DIRECT	GO:0051216~cartilage development	4	0.03095035	0.799074076
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11

GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	12	7.15E-09	4.68E-07
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	0.003706704	0.088286952
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	36	0.021966049	0.306045375
GOTERM_MF_DIRECT	GO:0008270~zinc ion binding	23	4.29E-04	0.042057583
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0002020~protease binding	5	0.036232294	0.507252121

The list of VCAN enriched pathways

Category	Term	Count	PValue	FDR
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	12	3.61E-07	1.29E-04
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	20	1.91E-05	0.002489822
GOTERM_BP_DIRECT	GO:0007417~central nervous system development	6	0.025231752	0.692291586
GOTERM_CC_DIRECT	GO:0005615~extracellular space	61	6.57E-14	1.72E-11
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	21	1.06E-11	1.38E-09
GOTERM_CC_DIRECT	GO:0005576~extracellular region	57	5.21E-10	4.55E-08
GOTERM_CC_DIRECT	GO:0005788~endoplasmic reticulum lumen	15	9.76E-06	4.26E-04
GOTERM_CC_DIRECT	GO:0016020~membrane	40	0.020818062	0.306045375
GOTERM_MF_DIRECT	GO:0005515~protein binding	164	0.003130572	0.166627416
GOTERM_MF_DIRECT	GO:0005539~glycosaminoglycan binding	3	0.035760167	0.507252121
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	14	0.089299914	0.984924623
