

Table S2 The GO and KEGG results

	ONTOL OGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0030198	BP	GO:0030198	extracellular matrix organization	20/74	341/17653	6.86E-18	1.24E-14	9.51E-15	SPP1/VCAN/LUM/COL4A1/MMP7/LA MC2/ITGA2/COL1A2/COL1A1/HAS2/ COL3A1/COL6A3/FAP/THBS2/TGFB2 /THBS1/LOXL4/CCDC80/MMP19/SER PINE1	20
GO:0043062	BP	GO:0043062	extracellular structure organization	20/74	395/17653	1.20E-16	1.08E-13	8.29E-14	SPP1/VCAN/LUM/COL4A1/MMP7/LA MC2/ITGA2/COL1A2/COL1A1/HAS2/ COL3A1/COL6A3/FAP/THBS2/TGFB2 /THBS1/LOXL4/CCDC80/MMP19/SER PINE1	20
GO:0030574	BP	GO:0030574	collagen catabolic process	8/74	68/17653	3.91E-10	2.35E-07	1.81E-07	COL4A1/MMP7/COL1A2/COL1A1/CO L3A1/COL6A3/FAP/MMP19	8
GO:0032963	BP	GO:0032963	collagen metabolic process	9/74	124/17653	2.34E-09	1.06E-06	8.10E-07	COL4A1/MMP7/ITGA2/COL1A2/COL 1A1/COL3A1/COL6A3/FAP/MMP19	9
GO:0097529	BP	GO:0097529	myeloid leukocyte migration	10/74	177/17653	3.29E-09	1.19E-06	9.11E-07	CXCL8/CCL2/TGFB2/THBS1/CXCL6/ ANXA1/CCL20/SERPINE1/CXCL10/S AA1	10
GO:0050900	BP	GO:0050900	leukocyte migration	14/74	470/17653	7.85E-09	2.37E-06	1.81E-06	EPCAM/CXCL8/ITGA2/COL1A2/COL 1A1/CCL2/TGFB2/THBS1/CXCL6/AN XA1/CCL20/SERPINE1/CXCL10/SAA 1	14

GO:0030595	BP	GO:0030595	leukocyte chemotaxis	10/74	202/17653	1.17E-08	2.94E-06	2.26E-06	CXCL8/CCL2/TGFB2/THBS1/CXCL6/ ANXA1/CCL20/SERPINE1/CXCL10/S AA1	10
GO:0071621	BP	GO:0071621	granulocyte chemotaxis	8/74	105/17653	1.30E-08	2.94E-06	2.26E-06	CXCL8/CCL2/TGFB2/THBS1/CXCL6/ ANXA1/CCL20/SAA1	8
GO:0060326	BP	GO:0060326	cell chemotaxis	11/74	273/17653	1.75E-08	3.51E-06	2.69E-06	CXCL8/CCL2/TGFB2/THBS1/CXCL6/ ANXA1/CCL20/SERPINE1/CXCL10/S AA2/SAA1	11
GO:0097530	BP	GO:0097530	granulocyte migration	8/74	119/17653	3.50E-08	6.32E-06	4.85E-06	CXCL8/CCL2/TGFB2/THBS1/CXCL6/ ANXA1/CCL20/SAA1	8
GO:0030199	BP	GO:0030199	collagen fibril organization	6/74	47/17653	4.14E-08	6.80E-06	5.21E-06	LUM/COL1A2/COL1A1/COL3A1/TGF B2/LOXL4	6
GO:0002685	BP	GO:0002685	regulation of leukocyte migration	9/74	176/17653	5.02E-08	7.57E-06	5.80E-06	CXCL8/ITGA2/CCL2/THBS1/CXCL6/ ANXA1/CCL20/SERPINE1/CXCL10	9
GO:0030335	BP	GO:0030335	positive regulation of cell migration	13/74	486/17653	1.01E-07	1.40E-05	1.07E-05	CXCL8/LAMC2/ITGA2/COL1A1/HAS 2/TGFB2/THBS1/CXCL6/ANXA1/CCL 20/GPNMB/SERPINE1/CXCL10	13
GO:0001655	BP	GO:0001655	urogenital system development	10/74	316/17653	7.64E-07	9.87E-05	7.57E-05	EPCAM/COL4A1/CD24/HAS2/TGFB2/ GCNT4/PROM1/HPGD/ANXA1/GPC3	10
GO:0002687	BP	GO:0002687	positive regulation of leukocyte migration	7/74	123/17653	8.21E-07	9.89E-05	7.59E-05	CXCL8/ITGA2/THBS1/CXCL6/CCL20/ SERPINE1/CXCL10	7
GO:0071674	BP	GO:0071674	mononuclear cell migration	6/74	79/17653	9.63E-07	0.000108 845	8.35E-05	CCL2/THBS1/ANXA1/CCL20/SERPIN E1/CXCL10	6

GO:0002237	BP	GO:0002237	response to molecule of bacterial origin	10/74	345/17653	1.69E-06	0.000179751	0.000137827	ANKRD1/CXCL8/CD24/CCL2/HPGD/CXCL6/CCL20/SERPINE1/CYP1A2/CXCL10	10
GO:0030593	BP	GO:0030593	neutrophil chemotaxis	6/74	88/17653	1.82E-06	0.000183107	0.0001404	CXCL8/CCL2/TGFB2/CXCL6/CCL20/SAA1	6
GO:0072001	BP	GO:0072001	renal system development	9/74	280/17653	2.51E-06	0.000235403	0.000180499	EPCAM/COL4A1/CD24/HAS2/TGFB2/GCNT4/PROM1/HPGD/GPC3	9
GO:0009612	BP	GO:0009612	response to mechanical stimulus	8/74	209/17653	2.60E-06	0.000235403	0.000180499	ANKRD1/MMP7/ITGA2/COL1A1/COL3A1/THBS1/CXCL10/FOSB	8
GO:1990266	BP	GO:1990266	neutrophil migration	6/74	99/17653	3.63E-06	0.00031294	0.000239953	CXCL8/CCL2/TGFB2/CXCL6/CCL20/SAA1	6
GO:0050918	BP	GO:0050918	positive chemotaxis	5/74	59/17653	4.74E-06	0.000389275	0.000298483	CXCL8/ITGA2/GPNMB/SAA2/SAA1	5
GO:0071634	BP	GO:0071634	regulation of transforming growth factor beta production	4/74	28/17653	5.40E-06	0.00042425	0.000325301	LUM/CD24/TGFB2/THBS1	4
GO:0002548	BP	GO:0002548	monocyte chemotaxis	5/74	62/17653	6.06E-06	0.000451326	0.000346062	CCL2/ANXA1/CCL20/SERPINE1/CXCL10	5
GO:0071604	BP	GO:0071604	transforming growth factor beta production	4/74	29/17653	6.24E-06	0.000451326	0.000346062	LUM/CD24/TGFB2/THBS1	4
GO:0002688	BP	GO:0002688	regulation of leukocyte chemotaxis	6/74	111/17653	7.06E-06	0.000475264	0.000364417	CXCL8/CCL2/THBS1/CXCL6/SERPINE1/CXCL10	6
GO:0042698	BP	GO:0042698	ovulation cycle	5/74	64/17653	7.10E-06	0.000475264	0.000364417	MMP7/HAS2/TGFB2/ANXA1/MMP19	5

GO:0071222	BP	GO:0071222	cellular response to lipopolysaccharide	7/74	174/17653	8.27E-06	0.000533 953	0.000409418	ANKRD1/CXCL8/CCL2/CXCL6/CCL2 0/SERPINE1/CXCL10	7
GO:0032496	BP	GO:0032496	response to lipopolysaccharide	9/74	327/17653	8.83E-06	0.000550 405	0.000422033	ANKRD1/CXCL8/CCL2/HPGD/CXCL6 /CCL20/SERPINE1/CYP1A2/CXCL10	9
GO:0071219	BP	GO:0071219	cellular response to molecule of bacterial origin	7/74	182/17653	1.11E-05	0.000664 253	0.000509328	ANKRD1/CXCL8/CCL2/CXCL6/CCL2 0/SERPINE1/CXCL10	7
GO:0038065	BP	GO:0038065	collagen-activated signaling pathway	3/74	11/17653	1.14E-05	0.000664 253	0.000509328	COL4A1/ITGA2/COL1A1	3
GO:0032355	BP	GO:0032355	response to estradiol	6/74	125/17653	1.40E-05	0.000788 989	0.000604971	ITGA2/COL1A1/HPGD/ANXA1/AREG /CYP1A2	6
GO:0001822	BP	GO:0001822	kidney development	8/74	264/17653	1.45E-05	0.000791 994	0.000607275	EPCAM/CD24/HAS2/TGFB2/GCNT4/P ROM1/HPGD/GPC3	8
GO:0050921	BP	GO:0050921	positive regulation of chemotaxis	6/74	130/17653	1.75E-05	0.000928 628	0.000712042	CXCL8/ITGA2/THBS1/CXCL6/SERPI NE1/CXCL10	6
GO:0050920	BP	GO:0050920	regulation of chemotaxis	7/74	202/17653	2.18E-05	0.001125 188	0.000862758	CXCL8/ITGA2/CCL2/THBS1/CXCL6/S ERPINE1/CXCL10	7
GO:0071216	BP	GO:0071216	cellular response to biotic stimulus	7/74	204/17653	2.32E-05	0.001154 296	0.000885077	ANKRD1/CXCL8/CCL2/CXCL6/CCL2 0/SERPINE1/CXCL10	7
GO:0070098	BP	GO:0070098	chemokine-mediated signaling pathway	5/74	82/17653	2.40E-05	0.001154 296	0.000885077	CXCL8/CCL2/CXCL6/CCL20/CXCL10	5
GO:0044849	BP	GO:0044849	estrous cycle	3/74	14/17653	2.49E-05	0.001154 296	0.000885077	MMP7/HAS2/ANXA1	3

GO:0051917	BP	GO:0051917	regulation of fibrinolysis	3/74	14/17653	2.49E-05	0.001154 296	0.000885077	FAP/THBS1/SERPINE1	3
GO:0002690	BP	GO:0002690	positive regulation of leukocyte chemotaxis	5/74	87/17653	3.19E-05	0.001442 615	0.00110615	CXCL8/THBS1/CXCL6/SERPINE1/CXCL10	5
GO:0045785	BP	GO:0045785	positive regulation of cell adhesion	9/74	392/17653	3.70E-05	0.001632 268	0.00125157	VTGN1/ITGA2/CD24/HAS2/CCL2/TGFB2/ANXA1/CCDC80/SAA1	9
GO:0034612	BP	GO:0034612	response to tumor necrosis factor	8/74	305/17653	4.06E-05	0.001747 729	0.001340102	ANKRD1/CXCL8/COL1A1/HAS2/CCL2/THBS1/UBD/CCL20	8
GO:0050878	BP	GO:0050878	regulation of body fluid levels	10/74	499/17653	4.22E-05	0.001775 887	0.001361692	ITGA2/COL1A2/COL1A1/HAS2/COL3A1/FAP/THBS1/CFTR/SERPINE1/SAA1	10
GO:0022617	BP	GO:0022617	extracellular matrix disassembly	5/74	94/17653	4.63E-05	0.001904 433	0.001460258	SPP1/MMP7/LAMC2/FAP/MMP19	5
GO:0071560	BP	GO:0071560	cellular response to transforming growth factor beta stimulus	7/74	229/17653	4.85E-05	0.001949 563	0.001494862	ANKRD1/COL1A2/COL1A1/COL3A1/TGFB2/THBS1/HPGD	7
GO:0051591	BP	GO:0051591	response to cAMP	5/74	97/17653	5.39E-05	0.002082 669	0.001596923	COL1A1/CFTR/AREG/MMP19/FOSB	5
GO:0071559	BP	GO:0071559	response to transforming growth factor beta	7/74	233/17653	5.41E-05	0.002082 669	0.001596923	ANKRD1/COL1A2/COL1A1/COL3A1/TGFB2/THBS1/HPGD	7
GO:0043588	BP	GO:0043588	skin development	9/74	413/17653	5.55E-05	0.002088 91	0.001601708	ITGA2/COL1A2/COL1A1/KRT23/COL3A1/KRT19/TGFB2/KRT7/ANXA1	9

GO:1901568	BP	GO:1901568	fatty acid derivative metabolic process	6/74	162/17653	6.02E-05	0.002222 726	0.001704314	ELOVL7/CYP2C18/HPGD/ANXA1/CY P1A2/CYP2C19	6
GO:0033559	BP	GO:0033559	unsaturated fatty acid metabolic process	5/74	103/17653	7.18E-05	0.002595 744	0.001990332	CYP2C18/HPGD/ANXA1/CYP1A2/CY P2C19	5
GO:0007596	BP	GO:0007596	blood coagulation	8/74	341/17653	8.88E-05	0.003097 157	0.0023748	ITGA2/COL1A2/COL1A1/COL3A1/FA P/THBS1/SERPINE1/SAA1	8
GO:0019373	BP	GO:0019373	epoxygenase P450 pathway	3/74	21/17653	8.91E-05	0.003097 157	0.0023748	CYP2C18/CYP1A2/CYP2C19	3
GO:0007162	BP	GO:0007162	negative regulation of cell adhesion	7/74	255/17653	9.54E-05	0.003228 401	0.002475434	EPCAM/VTCN1/COL1A1/THBS1/AN XA1/GPNMB/SERPINE1	7
GO:0006690	BP	GO:0006690	icosanoid metabolic process	5/74	110/17653	9.81E-05	0.003228 401	0.002475434	CYP2C18/HPGD/ANXA1/CYP1A2/CY P2C19	5
GO:0007599	BP	GO:0007599	hemostasis	8/74	346/17653	9.82E-05	0.003228 401	0.002475434	ITGA2/COL1A2/COL1A1/COL3A1/FA P/THBS1/SERPINE1/SAA1	8
GO:0050817	BP	GO:0050817	coagulation	8/74	347/17653	0.000100 192	0.003234 772	0.002480318	ITGA2/COL1A2/COL1A1/COL3A1/FA P/THBS1/SERPINE1/SAA1	8
GO:0006023	BP	GO:0006023	aminoglycan biosynthetic process	5/74	113/17653	0.000111 423	0.003534 271	0.002709965	VCAN/LUM/HAS2/B3GNT5/GPC3	5
GO:0048247	BP	GO:0048247	lymphocyte chemotaxis	4/74	60/17653	0.000116 147	0.003620 591	0.002776152	CCL2/CCL20/CXCL10/SAA1	4
GO:0042738	BP	GO:0042738	exogenous drug catabolic process	3/74	24/17653	0.000134 339	0.004116 694	0.003156547	CYP2C18/CYP1A2/CYP2C19	3

GO:0071230	BP	GO:0071230	cellular response to amino acid stimulus	4/74	63/17653	0.000140 539	0.004234 907	0.003247189	COL4A1/COL1A2/COL1A1/COL3A1	4
GO:0045765	BP	GO:0045765	regulation of angiogenesis	8/74	366/17653	0.000144 669	0.004287 883	0.00328781	CXCL8/THBS2/TGFB2/THBS1/ANXA1/GPNMB/SERPINE1/CXCL10	8
GO:0070555	BP	GO:0070555	response to interleukin-1	6/74	192/17653	0.000153 495	0.004476 116	0.00343214	ANKRD1/CXCL8/HAS2/CCL2/ANXA1/CCL20	6
GO:0001503	BP	GO:0001503	ossification	8/74	371/17653	0.000158 756	0.004556 041	0.003493425	SPP1/VCAN/COL1A1/TGFB2/MGP/GP C3/AREG/GPNMB	8
GO:0042730	BP	GO:0042730	fibrinolysis	3/74	27/17653	0.000192 395	0.005435 168	0.004167511	FAP/THBS1/SERPINE1	3
GO:0071356	BP	GO:0071356	cellular response to tumor necrosis factor	7/74	287/17653	0.000198 064	0.005509 233	0.004224301	ANKRD1/CXCL8/COL1A1/HAS2/CCL2/THBS1/CCL20	7
GO:0001501	BP	GO:0001501	skeletal system development	9/74	493/17653	0.000211 946	0.005806 028	0.004451874	VCAN/LUM/COL1A2/COL1A1/HAS2/COL3A1/TGFB2/EFEMP1/MGP	9
GO:0046683	BP	GO:0046683	response to organophosphorus	5/74	131/17653	0.000222 839	0.006013 337	0.004610832	COL1A1/CFTR/AREG/MMP19/FOSB	5
GO:0031214	BP	GO:0031214	biomineral tissue development	5/74	133/17653	0.000239 104	0.006357 358	0.004874616	SPP1/COL1A1/MGP/GPC3/GPNMB	5
GO:1901342	BP	GO:1901342	regulation of vasculature development	8/74	396/17653	0.000247 282	0.006479 512	0.00496828	CXCL8/THBS2/TGFB2/THBS1/ANXA1/GPNMB/SERPINE1/CXCL10	8
GO:0071260	BP	GO:0071260	cellular response to mechanical stimulus	4/74	78/17653	0.000320 969	0.008290 166	0.00635663	ANKRD1/MMP7/ITGA2/COL1A1	4

GO:0031589	BP	GO:0031589	cell-substrate adhesion	7/74	319/17653	0.000376 076	0.009533 497	0.007309977	ITGA2/COL1A1/HAS2/COL3A1/THBS1/CCDC80/SERPINE1	7
GO:0014074	BP	GO:0014074	response to purine-containing compound	5/74	147/17653	0.000379 653	0.009533 497	0.007309977	COL1A1/CFTR/AREG/MMP19/FOSB	5
GO:0048246	BP	GO:0048246	macrophage chemotaxis	3/74	34/17653	0.000385 402	0.009545 299	0.007319026	CCL2/THBS1/SAA1	3
GO:1903035	BP	GO:1903035	negative regulation of response to wounding	4/74	85/17653	0.000445 655	0.010888 428	0.008348893	SPP1/FAP/THBS1/SERPINE1	4
GO:0010634	BP	GO:0010634	positive regulation of epithelial cell migration	5/74	154/17653	0.000469 814	0.011325 641	0.008684135	ITGA2/HAS2/TGFB2/THBS1/ANXA1	5
GO:0071675	BP	GO:0071675	regulation of mononuclear cell migration	3/74	38/17653	0.000536 83	0.012770 914	0.009792323	THBS1/SERPINE1/CXCL10	3
GO:0033273	BP	GO:0033273	response to vitamin	4/74	90/17653	0.000553 597	0.012998 741	0.009967013	SPP1/ITGA2/COL1A1/CXCL10	4
GO:1903034	BP	GO:1903034	regulation of response to wounding	5/74	161/17653	0.000575 251	0.013334 027	0.0102241	SPP1/FAP/THBS1/ANXA1/SERPINE1	5
GO:1905517	BP	GO:1905517	macrophage migration	3/74	40/17653	0.000624 954	0.014161 666	0.010858707	CCL2/THBS1/SAA1	3
GO:0014812	BP	GO:0014812	muscle cell migration	4/74	93/17653	0.000626 622	0.014161 666	0.010858707	ITGA2/HAS2/ANXA1/SERPINE1	4
GO:0061326	BP	GO:0061326	renal tubule development	4/74	94/17653	0.000652 412	0.014384 899	0.011029874	COL4A1/CD24/PROM1/GPC3	4

GO:0072676	BP	GO:0072676	lymphocyte migration	4/74	94/17653	0.000652 412	0.014384 899	0.011029874	CCL2/CCL20/CXCL10/SAA1	4
GO:0016525	BP	GO:0016525	negative regulation of angiogenesis	5/74	169/17653	0.000716 501	0.015607 645	0.011967436	THBS2/TGFB2/THBS1/SERPINE1/CXCL10	5
GO:0071347	BP	GO:0071347	cellular response to interleukin-1	5/74	170/17653	0.000735 829	0.015757 047	0.012081993	ANKRD1/CXCL8/HAS2/CCL2/CCL20	5
GO:0032905	BP	GO:0032905	transforming growth factor beta1 production	2/74	10/17653	0.000763 315	0.015757 047	0.012081993	LUM/THBS1	2
GO:0032908	BP	GO:0032908	regulation of transforming growth factor beta1 production	2/74	10/17653	0.000763 315	0.015757 047	0.012081993	LUM/THBS1	2
GO:0051918	BP	GO:0051918	negative regulation of fibrinolysis	2/74	10/17653	0.000763 315	0.015757 047	0.012081993	THBS1/SERPINE1	2
GO:0006022	BP	GO:0006022	aminoglycan metabolic process	5/74	172/17653	0.000775 651	0.015757 047	0.012081993	VCAN/LUM/HAS2/B3GNT5/GPC3	5
GO:2000181	BP	GO:2000181	negative regulation of blood vessel morphogenesis	5/74	172/17653	0.000775 651	0.015757 047	0.012081993	THBS2/TGFB2/THBS1/SERPINE1/CXCL10	5
GO:0032570	BP	GO:0032570	response to progesterone	3/74	45/17653	0.000884 205	0.017762 702	0.013619864	TGFB2/THBS1/FOSB	3
GO:1901343	BP	GO:1901343	negative regulation of vasculature development	5/74	179/17653	0.000927 813	0.018433 914	0.014134528	THBS2/TGFB2/THBS1/SERPINE1/CXCL10	5

GO:0007179	BP	GO:0007179	transforming growth factor beta receptor signaling pathway	5/74	182/17653	0.000999 415	0.019525 248	0.014971327	COL1A2/COL3A1/TGFB2/THBS1/HPGD	5
GO:0071622	BP	GO:0071622	regulation of granulocyte chemotaxis	3/74	47/17653	0.001004 341	0.019525 248	0.014971327	CXCL8/THBS1/CXCL6	3
GO:1901654	BP	GO:1901654	response to ketone	5/74	183/17653	0.001024 172	0.019698 966	0.015104529	SPP1/TGFB2/THBS1/CFTR/FOSB	5
GO:0048511	BP	GO:0048511	rhythmic process	6/74	276/17653	0.001052 619	0.019958 89	0.01530383	MMP7/HAS2/TGFB2/ANXA1/MMP19/SERPINE1	6
GO:0006024	BP	GO:0006024	glycosaminoglycan biosynthetic process	4/74	107/17653	0.001059 764	0.019958 89	0.01530383	VCAN/LUM/HAS2/GPC3	4
GO:0010755	BP	GO:0010755	regulation of plasminogen activation	2/74	12/17653	0.001113 463	0.020322 619	0.015582726	THBS1/SERPINE1	2
GO:0007565	BP	GO:0007565	female pregnancy	5/74	187/17653	0.001127 783	0.020322 619	0.015582726	SPP1/MMP7/ITGA2/HPGD/FOSB	5
GO:2000401	BP	GO:2000401	regulation of lymphocyte migration	3/74	49/17653	0.001134 338	0.020322 619	0.015582726	CCL2/CCL20/CXCL10	3
GO:0006721	BP	GO:0006721	terpenoid metabolic process	4/74	109/17653	0.001135 279	0.020322 619	0.015582726	GPC3/CYP1A2/CYP2C19/AKR1B10	4
GO:0043200	BP	GO:0043200	response to amino acid	4/74	109/17653	0.001135 279	0.020322 619	0.015582726	COL4A1/COL1A2/COL1A1/COL3A1	4
GO:0022407	BP	GO:0022407	regulation of cell-cell adhesion	7/74	388/17653	0.001192 176	0.021131 907	0.016203262	EPCAM/VTGN1/CD24/HAS2/CCL2/ANXA1/GPNMB	7

GO:0010810	BP	GO:0010810	regulation of cell-substrate adhesion	5/74	191/17653	0.001238 979	0.021535 411	0.016512655	COL1A1/HAS2/THBS1/CCDC80/SERPINE1	5
GO:0048545	BP	GO:0048545	response to steroid hormone	7/74	391/17653	0.001246 294	0.021535 411	0.016512655	SPP1/COL1A1/TGFB2/THBS1/ANXA1/AREG/FOSB	7
GO:0030195	BP	GO:0030195	negative regulation of blood coagulation	3/74	51/17653	0.001274 496	0.021535 411	0.016512655	FAP/THBS1/SERPINE1	3
GO:0072678	BP	GO:0072678	T cell migration	3/74	51/17653	0.001274 496	0.021535 411	0.016512655	CCL2/CCL20/CXCL10	3
GO:1900047	BP	GO:1900047	negative regulation of hemostasis	3/74	51/17653	0.001274 496	0.021535 411	0.016512655	FAP/THBS1/SERPINE1	3
GO:0070208	BP	GO:0070208	protein heterotrimerization	2/74	13/17653	0.001312 343	0.021768 037	0.016691025	COL1A2/COL1A1	2
GO:0072182	BP	GO:0072182	regulation of nephron tubule epithelial cell differentiation	2/74	13/17653	0.001312 343	0.021768 037	0.016691025	CD24/PROM1	2
GO:0032103	BP	GO:0032103	positive regulation of response to external stimulus	6/74	289/17653	0.001332 737	0.021905 355	0.016796316	CXCL8/ITGA2/THBS1/CXCL6/SERPINE1/CXCL10	6
GO:0019369	BP	GO:0019369	arachidonic acid metabolic process	3/74	53/17653	0.001425 108	0.023212 562	0.01779864	CYP2C18/CYP1A2/CYP2C19	3
GO:0090303	BP	GO:0090303	positive regulation of wound healing	3/74	54/17653	0.001504 422	0.024285 662	0.018621458	THBS1/ANXA1/SERPINE1	3

GO:0051770	BP	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	2/74	14/17653	0.001526 917	0.024430 671	0.018732646	CCL2/CCL20	2
GO:0001819	BP	GO:0001819	positive regulation of cytokine production	7/74	411/17653	0.001658 24	0.025825 629	0.019802255	LUM/VTCN1/THBS1/ANXA1/CCL20/ SERPINE1/SAA1	7
GO:1903037	BP	GO:1903037	regulation of leukocyte cell-cell adhesion	6/74	302/17653	0.001666 694	0.025825 629	0.019802255	VTCN1/CD24/HAS2/CCL2/ANXA1/GP NMB	6
GO:0033627	BP	GO:0033627	cell adhesion mediated by integrin	3/74	56/17653	0.001671 238	0.025825 629	0.019802255	ITGA2/TGFB2/SERPINE1	3
GO:0050819	BP	GO:0050819	negative regulation of coagulation	3/74	56/17653	0.001671 238	0.025825 629	0.019802255	FAP/THBS1/SERPINE1	3
GO:0001649	BP	GO:0001649	osteoblast differentiation	5/74	205/17653	0.001692 792	0.025937 012	0.01988766	SPP1/VCAN/COL1A1/AREG/GPNMB	5
GO:0070365	BP	GO:0070365	hepatocyte differentiation	2/74	15/17653	0.001757 053	0.026472 937	0.02029859	ITGA2/ANXA1	2
GO:0072160	BP	GO:0072160	nephron tubule epithelial cell differentiation	2/74	15/17653	0.001757 053	0.026472 937	0.02029859	CD24/PROM1	2
GO:0042476	BP	GO:0042476	odontogenesis	4/74	123/17653	0.001772 843	0.026490 086	0.02031174	COL1A2/COL1A1/TGFB2/SERPINE1	4
GO:0046394	BP	GO:0046394	carboxylic acid biosynthetic process	7/74	419/17653	0.001850 009	0.027416 531	0.021022107	VCAN/ELOVL7/HAS2/HPGD/ANXA1/ PSAT1/PFKFB3	7

GO:0016053	BP	GO:0016053	organic acid biosynthetic process	7/74	420/17653	0.001875 145	0.027563 111	0.0211345	VCAN/ELOVL7/HAS2/HPGD/ANXA1/PSAT1/PFKFB3	7
GO:0032102	BP	GO:0032102	negative regulation of response to external stimulus	6/74	310/17653	0.001901 743	0.027728 645	0.021261426	SPP1/FAP/CCL2/THBS1/SERPINE1/AA1	6
GO:0018149	BP	GO:0018149	peptide cross-linking	3/74	59/17653	0.001942 434	0.028095 368	0.021542617	COL3A1/THBS1/ANXA1	3
GO:0002683	BP	GO:0002683	negative regulation of immune system process	7/74	426/17653	0.002031 596	0.028966 633	0.022210675	VTCN1/COL3A1/CCL2/TGFB2/THBS1/ANXA1/GPNMB	7
GO:0010812	BP	GO:0010812	negative regulation of cell-substrate adhesion	3/74	60/17653	0.002038 555	0.028966 633	0.022210675	COL1A1/THBS1/SERPINE1	3
GO:0006720	BP	GO:0006720	isoprenoid metabolic process	4/74	128/17653	0.002050 735	0.028966 633	0.022210675	GPC3/CYP1A2/CYP2C19/AKR1B10	4
GO:0044706	BP	GO:0044706	multi-multicellular organism process	5/74	218/17653	0.002213 995	0.030769 872	0.02359334	SPP1/MMP7/ITGA2/HPGD/FOSB	5
GO:0045807	BP	GO:0045807	positive regulation of endocytosis	4/74	131/17653	0.002231 193	0.030769 872	0.02359334	ITGA2/CCL2/GPC3/SERPINE1	4
GO:0006027	BP	GO:0006027	glycosaminoglycan catabolic process	3/74	62/17653	0.002239 565	0.030769 872	0.02359334	VCAN/LUM/GPC3	3
GO:0071636	BP	GO:0071636	positive regulation of transforming growth factor beta production	2/74	17/17653	0.002263 492	0.030769 872	0.02359334	LUM/THBS1	2

GO:0090026	BP	GO:0090026	positive regulation of monocyte chemotaxis	2/74	17/17653	0.002263 492	0.030769 872	0.02359334	SERPINE1/CXCL10	2
GO:0010631	BP	GO:0010631	epithelial cell migration	6/74	324/17653	0.002372 664	0.031665 369	0.024279978	ITGA2/HAS2/FAP/TGFB2/THBS1/ANXA1	6
GO:0042737	BP	GO:0042737	drug catabolic process	4/74	134/17653	0.002422 331	0.031665 369	0.024279978	CYP2C18/MOXD1/CYP1A2/CYP2C19	4
GO:0061041	BP	GO:0061041	regulation of wound healing	4/74	134/17653	0.002422 331	0.031665 369	0.024279978	FAP/THBS1/ANXA1/SERPINE1	4
GO:1903036	BP	GO:1903036	positive regulation of response to wounding	3/74	64/17653	0.002452 472	0.031665 369	0.024279978	THBS1/ANXA1/SERPINE1	3
GO:0090132	BP	GO:0090132	epithelium migration	6/74	327/17653	0.002484 1	0.031665 369	0.024279978	ITGA2/HAS2/FAP/TGFB2/THBS1/ANXA1	6
GO:1903039	BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	5/74	224/17653	0.002490 408	0.031665 369	0.024279978	VTCN1/CD24/HAS2/CCL2/ANXA1	5
GO:0051767	BP	GO:0051767	nitric-oxide synthase biosynthetic process	2/74	18/17653	0.002539 535	0.031665 369	0.024279978	CCL2/CCL20	2
GO:0051769	BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic process	2/74	18/17653	0.002539 535	0.031665 369	0.024279978	CCL2/CCL20	2
GO:0061318	BP	GO:0061318	renal filtration cell differentiation	2/74	18/17653	0.002539 535	0.031665 369	0.024279978	CD24/PROM1	2
GO:0070633	BP	GO:0070633	transepithelial	2/74	18/17653	0.002539	0.031665	0.024279978	SLC12A2/CFTR	2

			transport			535	369			
GO:0072112	BP	GO:0072112	glomerular visceral epithelial cell differentiation	2/74	18/17653	0.002539 535	0.031665 369	0.024279978	CD24/PROM1	2
GO:2000696	BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	2/74	18/17653	0.002539 535	0.031665 369	0.024279978	CD24/PROM1	2
GO:0030858	BP	GO:0030858	positive regulation of epithelial cell differentiation	3/74	66/17653	0.002677 508	0.033157 081	0.025423775	CD24/PROM1/SERPINE1	3
GO:0090130	BP	GO:0090130	tissue migration	6/74	333/17653	0.002718 768	0.033439	0.025639942	ITGA2/HAS2/FAP/TGFB2/THBS1/ANXA1	6
GO:0007159	BP	GO:0007159	leukocyte cell-cell adhesion	6/74	335/17653	0.002800 58	0.033806 896	0.025922032	VTCN1/CD24/HAS2/CCL2/ANXA1/GPNMB	6
GO:0006833	BP	GO:0006833	water transport	2/74	19/17653	0.002830 622	0.033806 896	0.025922032	HAS2/CFTR	2
GO:0072311	BP	GO:0072311	glomerular epithelial cell differentiation	2/74	19/17653	0.002830 622	0.033806 896	0.025922032	CD24/PROM1	2
GO:0072073	BP	GO:0072073	kidney epithelium development	4/74	140/17653	0.002837 891	0.033806 896	0.025922032	EPCAM/CD24/PROM1/GPC3	4

GO:0007178	BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	6/74	336/17653	0.002842 173	0.033806 896	0.025922032	COL1A2/COL3A1/TGFB2/THBS1/HPG D/GPC3	6
GO:0006026	BP	GO:0006026	aminoglycan catabolic process	3/74	69/17653	0.003038 298	0.035903 552	0.02752968	VCAN/LUM/GPC3	3
GO:0071711	BP	GO:0071711	basement membrane organization	2/74	20/17653	0.003136 626	0.036824 808	0.028236069	COL4A1/LAMC2	2
GO:0008544	BP	GO:0008544	epidermis development	7/74	462/17653	0.003194 492	0.037219 535	0.028538733	LAMC2/KRT23/KRT19/TGFB2/KRT7/ EMP1/ANXA1	7
GO:0044344	BP	GO:0044344	cellular response to fibroblast growth factor stimulus	4/74	145/17653	0.003219 56	0.037219 535	0.028538733	CXCL8/COL1A1/CCL2/THBS1	4
GO:0050714	BP	GO:0050714	positive regulation of protein secretion	5/74	238/17653	0.003232 006	0.037219 535	0.028538733	ANKRD1/VTCN1/TGFB2/CFTR/SAA1	5
GO:0032652	BP	GO:0032652	regulation of interleukin-1 production	3/74	72/17653	0.003427 62	0.038115 958	0.029226081	ANXA1/CCL20/SAA1	3
GO:0048844	BP	GO:0048844	artery morphogenesis	3/74	72/17653	0.003427 62	0.038115 958	0.029226081	COL3A1/TGFB2/HPGD	3
GO:0061045	BP	GO:0061045	negative regulation of wound healing	3/74	72/17653	0.003427 62	0.038115 958	0.029226081	FAP/THBS1/SERPINE1	3
GO:0009713	BP	GO:0009713	catechol-containing compound biosynthetic process	2/74	21/17653	0.003457 421	0.038115 958	0.029226081	TGFB2/MOXD1	2

GO:0036499	BP	GO:0036499	PERK-mediated unfolded protein response	2/74	21/17653	0.003457 421	0.038115 958	0.029226081	CXCL8/CCL2	2
GO:0042423	BP	GO:0042423	catecholamine biosynthetic process	2/74	21/17653	0.003457 421	0.038115 958	0.029226081	TGFB2/MOXD1	2
GO:0071677	BP	GO:0071677	positive regulation of mononuclear cell migration	2/74	21/17653	0.003457 421	0.038115 958	0.029226081	SERPINE1/CXCL10	2
GO:0042129	BP	GO:0042129	regulation of T cell proliferation	4/74	149/17653	0.003549 059	0.038889 079	0.029818885	VTCN1/CD24/ANXA1/GPNMB	4
GO:0001818	BP	GO:0001818	negative regulation of cytokine production	5/74	245/17653	0.003657 238	0.039833 053	0.030542694	CD24/TGFB2/THBS1/ANXA1/GPNMB	5
GO:0014910	BP	GO:0014910	regulation of smooth muscle cell migration	3/74	74/17653	0.003703 361	0.040093 872	0.030742681	ITGA2/HAS2/SERPINE1	3
GO:0072010	BP	GO:0072010	glomerular epithelium development	2/74	22/17653	0.003792 88	0.040291 355	0.030894105	CD24/PROM1	2
GO:0090025	BP	GO:0090025	regulation of monocyte chemotaxis	2/74	22/17653	0.003792 88	0.040291 355	0.030894105	SERPINE1/CXCL10	2
GO:1901623	BP	GO:1901623	regulation of lymphocyte chemotaxis	2/74	22/17653	0.003792 88	0.040291 355	0.030894105	CCL2/CXCL10	2
GO:0071774	BP	GO:0071774	response to fibroblast growth factor	4/74	152/17653	0.003810 742	0.040291 355	0.030894105	CXCL8/COL1A1/CCL2/THBS1	4

GO:1903532	BP	GO:1903532	positive regulation of secretion by cell	6/74	361/17653	0.004040 769	0.042475 055	0.032568495	ANKRD1/SPP1/VTCN1/TGFB2/CFTR/SAA1	6
GO:0030193	BP	GO:0030193	regulation of blood coagulation	3/74	78/17653	0.004294 583	0.044624 169	0.034216366	FAP/THBS1/SERPINE1	3
GO:1900046	BP	GO:1900046	regulation of hemostasis	3/74	78/17653	0.004294 583	0.044624 169	0.034216366	FAP/THBS1/SERPINE1	3
GO:0030168	BP	GO:0030168	platelet activation	4/74	158/17653	0.004372 818	0.044920 764	0.034443786	COL1A2/COL1A1/COL3A1/SAA1	4
GO:0030203	BP	GO:0030203	glycosaminoglycan metabolic process	4/74	158/17653	0.004372 818	0.044920 764	0.034443786	VCAN/LUM/HAS2/GPC3	4
GO:0022408	BP	GO:0022408	negative regulation of cell-cell adhesion	4/74	159/17653	0.004471 639	0.045273 228	0.034714044	EPCAM/VTCN1/ANXA1/GPNMB	4
GO:0022409	BP	GO:0022409	positive regulation of cell-cell adhesion	5/74	257/17653	0.004477 646	0.045273 228	0.034714044	VTCN1/CD24/HAS2/CCL2/ANXA1	5
GO:0030728	BP	GO:0030728	ovulation	2/74	24/17653	0.004507 29	0.045273 228	0.034714044	HPGD/MMP19	2
GO:1903959	BP	GO:1903959	regulation of anion transmembrane transport	2/74	24/17653	0.004507 29	0.045273 228	0.034714044	THBS1/CFTR	2
GO:0031960	BP	GO:0031960	response to corticosteroid	4/74	160/17653	0.004571 959	0.045669 067	0.03501756	COL1A1/ANXA1/AREG/FOSB	4
GO:0002793	BP	GO:0002793	positive regulation of peptide secretion	5/74	259/17653	0.004626 156	0.045956 535	0.035237982	ANKRD1/VTCN1/TGFB2/CFTR/SAA1	5
GO:0006631	BP	GO:0006631	fatty acid metabolic process	6/74	372/17653	0.004672 905	0.046167 28	0.035399574	ELOVL7/CYP2C18/HPGD/ANXA1/CYP1A2/CYP2C19	6

GO:1901615	BP	GO:1901615	organic hydroxy compound metabolic process	7/74	497/17653	0.004759 271	0.046651 218	0.035770642	TGFB2/GCNT4/CFTR/MOXD1/PSAT1/APOF/AKR1B10	7
GO:0060415	BP	GO:0060415	muscle tissue morphogenesis	3/74	81/17653	0.004773 493	0.046651 218	0.035770642	ANKRD1/COL3A1/TGFB2	3
GO:0050927	BP	GO:0050927	positive regulation of positive chemotaxis	2/74	25/17653	0.004885 994	0.047239 985	0.036222089	CXCL8/ITGA2	2
GO:2000406	BP	GO:2000406	positive regulation of T cell migration	2/74	25/17653	0.004885 994	0.047239 985	0.036222089	CCL20/CXCL10	2
GO:0014909	BP	GO:0014909	smooth muscle cell migration	3/74	82/17653	0.004940 007	0.047256 785	0.036234971	ITGA2/HAS2/SERPINE1	3
GO:0032612	BP	GO:0032612	interleukin-1 production	3/74	82/17653	0.004940 007	0.047256 785	0.036234971	ANXA1/CCL20/SAA1	3
GO:0070482	BP	GO:0070482	response to oxygen levels	6/74	378/17653	0.005047 058	0.048026 741	0.036825348	ANKRD1/ITGA2/CD24/COL1A1/TGF B2/THBS1	6
GO:0062013	BP	GO:0062013	positive regulation of small molecule metabolic process	4/74	166/17653	0.005205 899	0.048245 057	0.036992746	HAS2/ANXA1/PFKFB3/CXCL10	4
GO:0006706	BP	GO:0006706	steroid catabolic process	2/74	26/17653	0.005278 866	0.048245 057	0.036992746	SPP1/CYP1A2	2
GO:0030194	BP	GO:0030194	positive regulation of blood coagulation	2/74	26/17653	0.005278 866	0.048245 057	0.036992746	THBS1/SERPINE1	2
GO:0031639	BP	GO:0031639	plasminogen activation	2/74	26/17653	0.005278 866	0.048245 057	0.036992746	THBS1/SERPINE1	2
GO:0042044	BP	GO:0042044	fluid transport	2/74	26/17653	0.005278	0.048245	0.036992746	HAS2/CFTR	2

						866	057			
GO:0050926	BP	GO:0050926	regulation of positive chemotaxis	2/74	26/17653	0.005278	0.048245	0.036992746	CXCL8/ITGA2	2
						866	057			
GO:1900048	BP	GO:1900048	positive regulation of hemostasis	2/74	26/17653	0.005278	0.048245	0.036992746	THBS1/SERPINE1	2
						866	057			
GO:0050818	BP	GO:0050818	regulation of coagulation	3/74	84/17653	0.005283	0.048245	0.036992746	FAP/THBS1/SERPINE1	3
						474	057			
GO:0010632	BP	GO:0010632	regulation of epithelial cell migration	5/74	269/17653	0.005421	0.049259	0.037770651	ITGA2/HAS2/TGFB2/THBS1/ANXA1	5
						824	583			
GO:0034330	BP	GO:0034330	cell junction organization	5/74	270/17653	0.005506	0.049777	0.03816798	LAMC2/ITGA2/CDH6/TGFB2/THBS1	5
						39	77			
GO:0031012	CC	GO:0031012	extracellular matrix	18/74	479/18698	3.19E-13	5.38E-11	4.49E-11	VCAN/LUM/COL4A1/MMP7/LAMC2/COL1A2/COL1A1/COL3A1/COL6A3/THBS2/TGFB2/THBS1/EFEMP1/MGP/CDC80/GPC3/MMP19/SERPINE1	18
GO:0005578	CC	GO:0005578	proteinaceous extracellular matrix	15/74	375/18698	1.61E-11	1.36E-09	1.14E-09	VCAN/LUM/COL4A1/MMP7/LAMC2/COL1A2/COL1A1/COL3A1/COL6A3/THBS2/EFEMP1/MGP/CCDC80/GPC3/MMP19	15
GO:0098644	CC	GO:0098644	complex of collagen trimers	5/74	20/18698	1.25E-08	7.06E-07	5.89E-07	LUM/COL4A1/COL1A2/COL1A1/COL3A1	5
GO:0044420	CC	GO:0044420	extracellular matrix component	8/74	119/18698	2.25E-08	9.52E-07	7.95E-07	LUM/COL4A1/LAMC2/COL1A2/COL1A1/COL3A1/THBS2/CCDC80	8

GO:0005583	CC	GO:0005583	fibrillar collagen trimer	4/74	12/18698	1.09E-07	3.08E-06	2.57E-06	LUM/COL1A2/COL1A1/COL3A1	4
GO:0098643	CC	GO:0098643	banded collagen fibril	4/74	12/18698	1.09E-07	3.08E-06	2.57E-06	LUM/COL1A2/COL1A1/COL3A1	4
GO:0005581	CC	GO:0005581	collagen trimer	6/74	88/18698	1.31E-06	3.16E-05	2.64E-05	LUM/COL4A1/COL1A2/COL1A1/COL3A1/COL6A3	6
GO:0005788	CC	GO:0005788	endoplasmic reticulum lumen	9/74	297/18698	2.55E-06	5.39E-05	4.50E-05	SPP1/VCAN/COL4A1/COL1A2/COL1A1/COL3A1/COL6A3/THBS1/GPC3	9
GO:0034364	CC	GO:0034364	high-density lipoprotein particle	3/74	27/18698	0.000162561	0.00305254	0.002547744	APOF/SAA2/SAA1	3
GO:0031091	CC	GO:0031091	platelet alpha granule	4/74	90/18698	0.000446554	0.006381661	0.005326331	THBS2/TGFB2/THBS1/SERPINE1	4
GO:0005604	CC	GO:0005604	basement membrane	4/74	92/18698	0.000485417	0.006381661	0.005326331	COL4A1/LAMC2/THBS2/CCDC80	4
GO:0034358	CC	GO:0034358	plasma lipoprotein particle	3/74	39/18698	0.000490897	0.006381661	0.005326331	APOF/SAA2/SAA1	3
GO:1990777	CC	GO:1990777	lipoprotein particle	3/74	39/18698	0.000490897	0.006381661	0.005326331	APOF/SAA2/SAA1	3
GO:0032994	CC	GO:0032994	protein-lipid complex	3/74	41/18698	0.000569357	0.006872956	0.005736382	APOF/SAA2/SAA1	3
GO:0009897	CC	GO:0009897	external side of plasma membrane	6/74	287/18698	0.000959171	0.010806655	0.009019569	VTCN1/ITGA2/CD24/THBS1/ANXA1/CXCL10	6
GO:0031093	CC	GO:0031093	platelet alpha granule lumen	3/74	67/18698	0.002377098	0.025108099	0.020955996	TGFB2/THBS1/SERPINE1	3
GO:0045177	CC	GO:0045177	apical part of cell	6/74	366/18698	0.003267575	0.03248354	0.027111768	EPCAM/SLC12A2/FAP/CFTR/PROM1/ANXA1	6

GO:1901681	MF	GO:1901681	sulfur compound binding	11/74	235/17548	3.91E-09	9.47E-07	6.96E-07	MMP7/LAMC2/ITGA2/THBS2/THBS1/CXCL6/CCDC80/GPC3/GPNMB/CXCL10/SAA1	11
GO:0008201	MF	GO:0008201	heparin binding	9/74	158/17548	2.07E-08	1.81E-06	1.33E-06	MMP7/LAMC2/THBS2/THBS1/CXCL6/CCDC80/GPNMB/CXCL10/SAA1	9
GO:0005539	MF	GO:0005539	glycosaminoglycan binding	10/74	215/17548	2.24E-08	1.81E-06	1.33E-06	VCAN/MMP7/LAMC2/THBS2/THBS1/CXCL6/CCDC80/GPNMB/CXCL10/SAA1	10
GO:0005201	MF	GO:0005201	extracellular matrix structural constituent	7/74	77/17548	3.37E-08	2.04E-06	1.50E-06	VCAN/LUM/COL4A1/COL1A2/COL1A1/COL3A1/MGP	7
GO:0048018	MF	GO:0048018	receptor ligand activity	13/74	472/17548	7.68E-08	3.72E-06	2.73E-06	SPP1/CXCL8/MACC1/CCL2/TGFB2/EFEMP1/CXCL6/AREG/CCL20/GPNMB/CXCL10/SAA2/SAA1	13
GO:0048407	MF	GO:0048407	platelet-derived growth factor binding	4/74	11/17548	9.40E-08	3.79E-06	2.79E-06	COL4A1/COL1A2/COL1A1/COL3A1	4
GO:0008009	MF	GO:0008009	chemokine activity	5/74	49/17548	1.92E-06	6.63E-05	4.88E-05	CXCL8/CCL2/CXCL6/CCL20/CXCL10	5
GO:0005125	MF	GO:0005125	cytokine activity	8/74	220/17548	3.98E-06	0.00012037	8.85E-05	SPP1/CXCL8/CCL2/TGFB2/CXCL6/AREG/CCL20/CXCL10	8
GO:0042379	MF	GO:0042379	chemokine receptor binding	5/74	66/17548	8.51E-06	0.000228698	0.000168116	CXCL8/CCL2/CXCL6/CCL20/CXCL10	5
GO:0043394	MF	GO:0043394	proteoglycan binding	4/74	38/17548	1.93E-05	0.000466878	0.000343203	ITGA2/THBS1/GPC3/GPNMB	4

GO:0050839	MF	GO:0050839	cell adhesion molecule binding	10/74	489/17548	3.74E-05	0.000823 417	0.000605296	EPCAM/ITGA2/CDH6/COL3A1/TES/FAP/THBS1/PROM1/ANXA1/GPNMB	10
GO:0045236	MF	GO:0045236	CXCR chemokine receptor binding	3/74	17/17548	4.69E-05	0.000946 148	0.000695515	CXCL8/CXCL6/CXCL10	3
GO:0005178	MF	GO:0005178	integrin binding	5/74	118/17548	0.000140 482	0.002615 119	0.00192238	ITGA2/COL3A1/FAP/THBS1/GPNMB	5
GO:0002020	MF	GO:0002020	protease binding	5/74	133/17548	0.000245 732	0.003964 483	0.0029143	COL1A2/COL1A1/COL3A1/FAP/SERPINE1	5
GO:0019838	MF	GO:0019838	growth factor binding	5/74	133/17548	0.000245 732	0.003964 483	0.0029143	COL4A1/COL1A2/COL1A1/COL3A1/THBS1	5
GO:0016712	MF	GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	3/74	31/17548	0.000297 252	0.004495 933	0.003304971	CYP2C18/CYP1A2/CYP2C19	3
GO:0042056	MF	GO:0042056	chemoattractant activity	3/74	34/17548	0.000392 143	0.005582 27	0.004103539	GPNMB/SAA2/SAA1	3
GO:0098631	MF	GO:0098631	cell adhesion mediator activity	3/74	40/17548	0.000635 816	0.008548 198	0.0062838	EPCAM/ITGA2/ANXA1	3
GO:0004497	MF	GO:0004497	monooxygenase activity	4/74	101/17548	0.000873 483	0.010883 873	0.008000759	CYP2C18/MOXD1/CYP1A2/CYP2C19	4

GO:0019825	MF	GO:0019825	oxygen binding	3/74	45/17548	0.000899 494	0.010883 873	0.008000759	CYP2C18/CYP1A2/CYP2C19	3
GO:0001664	MF	GO:0001664	G-protein coupled receptor binding	6/74	271/17548	0.000987 651	0.011381 504	0.008366569	CXCL8/CCL2/CXCL6/CCL20/CXCL10 /SAA1	6
GO:0005126	MF	GO:0005126	cytokine receptor binding	6/74	278/17548	0.001126 231	0.012388 544	0.009106846	CXCL8/CCL2/TGFB2/CXCL6/CCL20/ CXCL10	6
GO:0050840	MF	GO:0050840	extracellular matrix binding	3/74	52/17548	0.001371 622	0.014431 847	0.010608883	SPP1/ITGA2/THBS1	3
GO:0008391	MF	GO:0008391	arachidonic acid monooxygenase activity	2/74	17/17548	0.002290 103	0.022168 195	0.01629589	CYP2C18/CYP2C19	2
GO:0008392	MF	GO:0008392	arachidonic acid epoxygenase activity	2/74	17/17548	0.002290 103	0.022168 195	0.01629589	CYP2C18/CYP2C19	2
GO:0005518	MF	GO:0005518	collagen binding	3/74	63/17548	0.002384 29	0.022192 239	0.016313564	LUM/ITGA2/THBS1	3
GO:0098641	MF	GO:0098641	cadherin binding involved in cell-cell adhesion	2/74	19/17548	0.002863 808	0.025668 206	0.018868755	EPCAM/ANXA1	2
GO:0043395	MF	GO:0043395	heparan sulfate proteoglycan binding	2/74	20/17548	0.003173 349	0.027426 801	0.020161502	ITGA2/GPC3	2
GO:0001965	MF	GO:0001965	G-protein alpha-subunit binding	2/74	21/17548	0.003497 843	0.029188 895	0.021456821	RGS4/RGS1	2
GO:0046332	MF	GO:0046332	SMAD binding	3/74	74/17548	0.003765 452	0.029954 617	0.022019705	ANKRD1/COL1A2/COL3A1	3
GO:0070330	MF	GO:0070330	aromatase activity	2/74	22/17548	0.003837	0.029954	0.022019705	CYP2C18/CYP1A2	2

GO:0016705	MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	4/74	160/17548	0.004668692	0.03530698	0.025954239	CYP2C18/MOXD1/CYP1A2/CYP2C19	4
GO:0008083	MF	GO:0008083	growth factor activity	4/74	163/17548	0.004985021	0.036556823	0.026873001	MACC1/TGFB2/EFEMP1/AREG	4
GO:0001968	MF	GO:0001968	fibronectin binding	2/74	26/17548	0.005340152	0.03800932	0.027940736	THBS1/CCDC80	2
GO:0043236	MF	GO:0043236	laminin binding	2/74	28/17548	0.006177324	0.042711781	0.031397525	ITGA2/THBS1	2
GO:0015108	MF	GO:0015108	chloride transmembrane transporter activity	3/74	94/17548	0.007332919	0.04929351	0.036235769	SLC12A2/CFTR/CLIC6	3
GO:0098632	MF	GO:0098632	cell-cell adhesion mediator activity	2/74	31/17548	0.007537402	0.049298682	0.03623957	EPCAM/ANXA1	2
ID		Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count	
hsa04512	hsa04512	ECM-receptor interaction	9/41	88/8081	3.74E-10	4.41E-08	3.46E-08	6696/1282/3918/3673/1278/1277/1293/7058/7057	9	

hsa04933	hsa04933	AGE-RAGE signaling pathway in diabetic complications	8/41	100/8081	2.83E-08	1.67E-06	1.31E-06	3576/1282/1278/1277/1281/6347/7042/5054	8
hsa04510	hsa04510	Focal adhesion	9/41	201/8081	5.36E-07	1.94E-05	1.52E-05	6696/1282/3918/3673/1278/1277/1293/7058/7057	9
hsa05146	hsa05146	Amoebiasis	7/41	102/8081	6.56E-07	1.94E-05	1.52E-05	3576/1282/3918/1278/1277/1281/7042	7
hsa05144	hsa05144	Malaria	5/41	50/8081	4.68E-06	0.000110502	8.67E-05	3576/7058/6347/7042/7057	5
hsa04657	hsa04657	IL-17 signaling pathway	6/41	94/8081	6.83E-06	0.000128373	0.000100774	3576/6347/6372/6364/3627/2354	6
hsa04151	hsa04151	PI3K-Akt signaling pathway	10/41	354/8081	7.62E-06	0.000128373	0.000100774	6696/1282/3918/3673/1278/1277/1293/7058/7057/374	10
hsa05165	hsa05165	Human papillomavirus infection	9/41	331/8081	3.19E-05	0.000471013	0.000369751	6696/1282/3918/3673/1278/1277/1293/7058/7057	9
hsa05205	hsa05205	Proteoglycans in cancer	7/41	205/8081	6.59E-05	0.000864417	0.000678579	4060/3673/1278/1277/7042/7057/2719	7
hsa05323	hsa05323	Rheumatoid arthritis	5/41	93/8081	9.79E-05	0.001154895	0.000906608	3576/6347/7042/6372/6364	5

hsa04061	hsa04061	Viral protein interaction with cytokine and cytokine receptor	5/41	100/8081	0.000138 138	0.001481 84	0.00116326 4	3576/6347/6372/6364/3627	5
hsa04974	hsa04974	Protein digestion and absorption	5/41	103/8081	0.000158 839	0.001561 912	0.00122612 2	1282/1278/1277/1281/1293	5
hsa05142	hsa05142	Chagas disease	4/41	102/8081	0.001693 032	0.015367 518	0.01206370 7	3576/6347/7042/5054	4
hsa04668	hsa04668	TNF signaling pathway	4/41	112/8081	0.002385 73	0.020108 295	0.01578528	6347/6372/6364/3627	4
hsa04062	hsa04062	Chemokine signaling pathway	5/41	192/8081	0.002689 146	0.021154 619	0.01660665 9	3576/6347/6372/6364/3627	5
hsa04060	hsa04060	Cytokine-cytokine receptor interaction	6/41	295/8081	0.003442 699	0.023942 219	0.01879496 2	3576/6347/7042/6372/6364/3627	6
hsa04611	hsa04611	Platelet activation	4/41	124/8081	0.003449 303	0.023942 219	0.01879496 2	3673/1278/1277/1281	4
hsa04926	hsa04926	Relaxin signaling pathway	4/41	129/8081	0.003974 85	0.026057 352	0.02045537	1282/1278/1277/1281	4

