





**Supplementary Figure S2.** Box plots of expression values within all samples. (A) Expression of all samples before batch effects removal. (B) Expression values of all samples after batch effects removal. Y axis corresponds to normalized expression values.

**Supplementary Table S1.** Differential expressed lncRNAs.

RefSeq Accession	NOCODE Accession	Gene Symbol	CNCI Score	Chromosome Location	TD vs TC		GD vs GC	
					Fold change	P value	Fold change	P value
NR_029395.1	NONHSAT245052.1	IGLL3P	-0.08	chr22:25,318,25-7-25,320,227	17.18	3.33 E-05	5.81	1.25 E-02
NR_024448.2	NONHSAT083925.2	GUSBP1	-0.10	chr22:23,638,48-7-23,717,423	6.48	9.42 E-04	4.30	1.52 E-02
NR_038335.1	NONHSAT215593.1	CLU	-0.01	chr8:27,596,917-27,611,437	4.75	2.82 E-06	3.82	5.42 E-05
NR_045494.1	NONHSAT215593.1	CLU	-0.01	chr8:27,596,917-27,611,751	4.75	2.82 E-06	3.82	5.42 E-05
NR_130134.1	NA	ISG20	-0.02	chr5:35,856,849-35,879,603	3.83	6.39 E-05	2.33	1.52 E-02
NR_026691.1	NONHSAT160800.1	IL10RA	-0.06	chr11:117,986,3-91-118,001,483	3.41	3.72 E-06	3.20	1.10 E-05
NR_033390.1	NONRATT000579.2	TYROBP	-0.03	chr19:35,904,40-1-35,908,309	3.35	1.37 E-05	2.67	4.36 E-04

NR_029467	NONHSAT007472			chr1:169,690,66		7.16		2.96
.1	.2	SELL	-0.01	5-169,708,856	3.22	E-05	2.46	E-03
NR_120485	NONHSAT171153			chr15:88,635,63		3.45		7.28
.1	.1	IL7R	-0.08	7-88,656,344	2.33	E-04	3.45	E-07
NR_109871	NONMMUT00443	TRAF3IP		chr1:209,756,03		3.27		8.15
.1	5.2	3	-0.06	2-209,779,657	2.11	E-02	3.55	E-04

**Supplementary Table S2.** DEGs identified in human diabetic nephropathy

RefSeq Accession	Gene Symbol	GenBank ID	GD - GC		TD - TC	
			logFC	adj.P.Val	logFC	adj.P.Val
NM_000064.3	C3	718	2.99	4.81E-06	3.97	7.84E-09
NM_000089.3	COL1A2	1278	2.24	5.86E-07	2.63	1.75E-08
NM_000211.4	ITGB2	3689	1.51	3.27E-06	1.81	6.40E-08
NM_000358.2	TGFBI	7045	1.46	3.48E-04	1.77	1.30E-05
NM_000434.3	NEU1	4758	1.01	3.37E-03	1.15	4.59E-04
NM_000491.4	C1QB	713	2.26	2.48E-07	2.31	2.08E-07
NM_000560.3	CD53	963	1.86	2.30E-07	2.18	5.86E-09
NM_000582.2	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
NM_000587.3	C7	730	2.13	9.50E-06	1.63	3.65E-04
NM_000596.2	IGFBP1	3484	-2.02	1.72E-03	-1.17	4.91E-02
NM_000636.3	SOD2	6648	1.14	1.69E-05	1.49	6.26E-08
NM_000655.4	SELL	6402	1.30	2.96E-03	1.69	7.16E-05
NM_000689.4	ALDH1A1	216	1.32	1.74E-02	1.19	1.91E-02
NM_000693.3	ALDH1A3	220	1.05	7.92E-06	1.03	9.93E-06
NM_000732.4	CD3D	915	1.73	1.93E-05	1.22	1.37E-03
NM_000978.3	RPL23	9349	1.40	7.51E-03	1.13	1.87E-02
NM_001002029.3	C4B	721	1.33	1.88E-02	1.23	1.76E-02
NM_001002033.2	HN1	51155	1.24	3.65E-06	1.05	5.20E-05
NM_001002294.2	FMO3	2328	1.03	2.51E-03	1.29	8.85E-05
NM_001003927.2	EVI2A	2123	2.01	1.74E-05	2.83	9.40E-09
NM_001008389.2	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
NM_001008540.2	CXCR4	7852	1.17	9.38E-04	1.19	4.43E-04
NM_001024465.2	SOD2	6648	1.44	4.92E-06	1.78	6.05E-08
NM_001024466.2	SOD2	6648	1.42	6.21E-06	1.78	5.82E-08
NM_001034.3	RRM2	6241	1.58	1.86E-06	1.53	3.54E-06
NM_001040033.1	CD53	963	1.86	2.30E-07	2.18	5.86E-09
NM_001040058.1	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
NM_001040060.1	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
NM_001040651.1	CD3D	915	2.20	8.55E-06	1.69	3.26E-04
NM_001077654.2	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_001080494.3	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001081455.1	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
NM_001085.4	SERPINA3	12	2.55	2.26E-06	2.80	3.53E-07
NM_001098200.1	GPR18	2841	1.36	2.53E-04	1.12	1.37E-03

NM_001100431.1	VSIG4	11326	1.73	4.55E-08	1.32	1.79E-05
NM_0011102.3	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
NM_001122951.2	ACKR1	2532	1.15	7.79E-04	1.44	2.16E-05
NM_001123041.2	CCR2	729230	1.54	3.97E-04	2.50	4.70E-08
NM_001126336.2	VCAN	1462	1.18	6.85E-04	2.27	1.09E-09
NM_001127491.2	ITGB2	3689	1.51	3.27E-06	1.81	6.40E-08
NM_001130004.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
NM_001130005.1	ACTN1	87	1.23	1.24E-04	1.55	1.70E-06
NM_001130415.1	APOLD1	81575	-2.04	1.32E-04	-1.44	3.80E-03
NM_001130715.1	PLAC8	51316	1.06	3.08E-03	1.14	8.35E-04
NM_001130716.1	PLAC8	51316	1.29	9.40E-04	1.47	1.06E-04
NM_001143782.1	FKBP11	51303	1.00	1.50E-02	1.50	1.47E-04
NM_001144832.2	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001145459.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
NM_001145460.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
NM_001146590.1	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_001146627.1	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_001164097.1	VCAN	1462	1.18	6.85E-04	2.27	1.09E-09
NM_001164098.1	VCAN	1462	1.18	6.85E-04	2.27	1.09E-09
NM_001165931.1	RRM2	6241	1.58	1.86E-06	1.53	3.54E-06
NM_001173514.1	TYROBP	7305	1.42	4.36E-04	1.74	1.37E-05
NM_001173515.1	TYROBP	7305	1.42	4.36E-04	1.74	1.37E-05
NM_001177660.2	HABP2	3026	1.32	1.03E-03	1.14	2.66E-03
NM_001184830.1	VSIG4	11326	1.73	4.55E-08	1.32	1.79E-05
NM_001184831.1	VSIG4	11326	1.73	4.55E-08	1.32	1.79E-05
NM_001193289.1	APOBEC3A_B	100913187	1.11	5.72E-04	1.60	1.16E-06
NM_001193333.2	CORO1A	11151	1.64	1.04E-05	1.58	1.72E-05
NM_001199149.1	LTF	4057	3.34	2.54E-07	4.73	3.36E-11
NM_001199739.1	CTSS	1520	1.03	1.55E-04	1.58	2.73E-08
NM_001207024.1	M6PR	4074	1.01	3.76E-03	1.27	1.54E-04
NM_001242823.2	C4B_2	100293534	1.33	1.88E-02	1.23	1.76E-02
NM_001243266.1	MS4A4A	51338	2.62	3.35E-06	3.39	9.89E-09
NM_001243759.1	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
NM_001243962.1	HLA-DQB1	3119	1.39	5.28E-06	1.81	1.51E-08
NM_001247999.1	MS4A6A	64231	2.02	3.10E-08	2.14	1.08E-08
NM_001251829.1	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
NM_001251830.1	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
NM_001252204.1	C4A	720	1.33	1.88E-02	1.23	1.76E-02
NM_001255.2	CDC20	991	1.25	2.73E-06	1.05	4.81E-05
NM_001256030.1	CD48	962	1.29	1.29E-06	1.23	3.38E-06
NM_001256139.1	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
NM_001256140.1	CAPG	822	1.36	8.63E-04	1.18	2.06E-03
NM_001257403.1	VSIG4	11326	2.11	7.54E-08	1.90	1.17E-06
NM_001270411.1	APOBEC3B	9582	1.01	2.37E-04	1.20	1.30E-05

NM_001271606.1	BASP1	10409	1.04	4.29E-02	1.13	1.57E-02
NM_001278614.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
NM_001278736.1	CCL5	6352	1.80	2.56E-04	1.84	1.11E-04
NM_001282431.1	ARL4C	10123	1.65	2.42E-06	2.15	5.33E-09
NM_001286813.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_001286814.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_001286815.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_001286817.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_001287754.1	TRAF3IP3	80342	1.83	8.15E-04	1.08	3.27E-02
NM_001288609.1	HN1	51155	1.38	7.94E-06	1.21	5.41E-05
NM_001288610.1	HN1	51155	1.38	7.94E-06	1.21	5.41E-05
NM_001293815.1	ALDH1A3	220	1.05	7.92E-06	1.03	9.93E-06
NM_001297663.1	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001297664.1	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001297665.1	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001297666.1	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001297667.1	TTC39A	22996	1.16	5.48E-07	1.10	1.99E-06
NM_001303233.1	ISG20	3669	1.03	1.41E-02	1.24	1.52E-03
NM_001303234.1	ISG20	3669	1.03	1.41E-02	1.24	1.52E-03
NM_001303235.1	ISG20	3669	1.22	1.52E-02	1.94	6.39E-05
NM_001303236.1	ISG20	3669	1.12	1.17E-02	1.47	4.72E-04
NM_001303237.1	ISG20	3669	1.16	9.47E-03	1.50	3.72E-04
NM_001303238.1	ITGB2	3689	1.51	3.27E-06	1.81	6.40E-08
NM_001306129.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_001306130.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_001306131.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_001306132.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_0013111.4	CRIP1	1396	1.32	6.47E-03	1.54	7.45E-04
NM_001319173.1	FMO3	2328	1.03	2.51E-03	1.29	8.85E-05
NM_001319174.1	FMO3	2328	1.03	2.51E-03	1.29	8.85E-05
NM_001320638.1	CD53	963	1.86	2.30E-07	2.18	5.86E-09
NM_001320732.1	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
NM_001320733.1	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
NM_001320734.1	CAPG	822	1.60	1.10E-04	1.07	5.28E-03
NM_001321121.1	LTF	4057	3.34	2.54E-07	4.73	3.36E-11
NM_001321122.1	LTF	4057	3.34	2.54E-07	4.73	3.36E-11
NM_001322814.1	SOD2	6648	1.13	3.47E-05	1.49	1.40E-07
NM_001322815.1	SOD2	6648	1.13	3.92E-05	1.37	9.05E-07
NM_001322817.1	SOD2	6648	1.44	4.92E-06	1.78	6.05E-08
NM_001322819.1	SOD2	6648	1.14	1.69E-05	1.49	6.26E-08
NM_001322820.1	SOD2	6648	1.14	1.69E-05	1.49	6.26E-08
NM_001323.3	CST6	1474	1.06	1.25E-03	1.16	2.36E-04
NM_001326317.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326318.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04

NM_001326319.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326320.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326321.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326323.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326324.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326325.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326326.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326327.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326328.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326329.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326330.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326331.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326332.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326333.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326334.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326335.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326336.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326337.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326338.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326339.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326340.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326341.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326342.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326343.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326344.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326345.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326346.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326347.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326348.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001326349.1	CELF2	10659	1.05	5.83E-03	1.36	1.93E-04
NM_001328609.1	CD2	914	1.58	2.61E-06	1.33	4.24E-05
NM_001329903.1	SERPINF1	5176	1.55	2.44E-04	1.48	2.42E-04
NM_001329904.1	SERPINF1	5176	1.55	2.44E-04	1.48	2.42E-04
NM_001329905.1	SERPINF1	5176	1.55	2.44E-04	1.48	2.42E-04
NM_001331031.1	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_001331032.1	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_001331033.1	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_001347465.1	C1QA	712	2.05	1.14E-07	1.78	3.17E-06
NM_001347466.1	C1QA	712	2.05	1.14E-07	1.78	3.17E-06
NM_001347828.1	PDGFRA	5156	1.21	7.51E-03	1.65	1.35E-04
NM_001347829.1	PDGFRA	5156	1.21	7.51E-03	1.65	1.35E-04
NM_001347830.1	PDGFRA	5156	1.21	7.51E-03	1.65	1.35E-04
NM_001348056.1	CXCR4	7852	1.17	9.38E-04	1.19	4.43E-04
NM_001348059.1	CXCR4	7852	1.17	9.38E-04	1.19	4.43E-04

NM_001348060.1	CXCR4	7852	1.17	9.38E-04	1.19	4.43E-04
NM_001558.3	IL10RA	3587	1.68	1.10E-05	1.77	3.72E-06
NM_001710.5	CFB	629	1.79	4.77E-05	2.37	1.78E-07
NM_001747.3	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
NM_001765.2	CD1C	911	1.23	3.83E-08	1.24	6.10E-08
NM_001767.4	CD2	914	1.58	2.61E-06	1.33	4.24E-05
NM_001778.3	CD48	962	1.97	4.87E-07	2.19	6.10E-08
NM_001803.2	CD52	1043	2.10	6.89E-06	1.58	3.67E-04
NM_001831.3	CLU	1191	1.93	5.42E-05	2.25	2.82E-06
NM_001855.4	COL15A1	1306	1.19	1.95E-03	1.92	8.99E-07
NM_001870.3	CPA3	1359	2.09	4.16E-06	2.72	1.12E-08
NM_002001.3	FCER1A	2205	1.23	1.24E-06	1.52	9.58E-09
NM_002010.2	FGF9	2254	-1.66	1.87E-07	-1.15	1.47E-04
NM_002026.3	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_002036.3	ACKR1	2532	1.15	7.79E-04	1.44	2.16E-05
NM_002104.2	GZMK	3003	1.85	1.76E-05	1.50	2.71E-04
NM_002160.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
NM_002163.2	IRF8	3394	1.59	1.74E-05	1.88	5.95E-07
NM_002185.3	IL7R	3575	1.78	7.28E-07	1.22	3.45E-04
NM_002201.5	ISG20	3669	1.03	1.41E-02	1.24	1.52E-03
NM_002341.1	LTB	4050	1.86	3.83E-05	1.32	1.86E-03
NM_002343.5	LTF	4057	3.34	2.54E-07	4.73	3.36E-11
NM_002345.3	LUM	4060	2.66	3.17E-06	2.40	1.90E-05
NM_002423.4	MMP7	4316	2.47	5.28E-06	4.39	4.69E-12
NM_002438.3	MRC1	4360	1.48	1.10E-04	1.79	2.85E-06
NM_002615.6	SERPINF1	5176	1.55	2.44E-04	1.48	2.42E-04
NM_002738.6	PRKCB	5579	1.04	1.01E-03	1.08	3.54E-04
NM_002838.4	PTPRC	5788	1.40	4.39E-04	1.93	1.74E-06
NM_002888.3	RARRES1	5918	1.40	6.42E-06	1.09	2.37E-04
NM_002909.4	REG1A	5967	1.67	1.14E-04	1.44	4.75E-04
NM_002985.2	CCL5	6352	1.80	2.56E-04	1.84	1.11E-04
NM_002993.3	CXCL6	6372	2.38	3.20E-06	4.23	2.39E-12
NM_003107.2	SOX4	6659	1.18	2.42E-04	1.34	2.31E-05
NM_003182.2	TAC1	6863	1.76	2.04E-03	2.92	5.38E-07
NM_003247.3	THBS2	7058	2.05	1.79E-06	2.17	5.82E-07
NM_003263.3	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
NM_003332.3	TYROBP	7305	1.56	1.06E-04	1.76	1.08E-05
NM_003361.3	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
NM_003467.2	CXCR4	7852	1.17	9.38E-04	1.19	4.43E-04
NM_004079.4	CTSS	1520	1.03	1.55E-04	1.58	2.73E-08
NM_004132.4	HABP2	3026	1.32	1.03E-03	1.14	2.66E-03
NM_004205.4	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
NM_004244.5	CD163	9332	1.90	1.22E-07	2.11	1.45E-08
NM_004271.3	LY86	9450	1.15	6.17E-05	1.20	2.26E-05

NM_004288.4	CYTIP	9595	1.20	6.71E-03	1.30	1.70E-03
NM_004369.3	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
NM_004385.4	VCAN	1462	1.18	6.85E-04	2.27	1.09E-09
NM_004585.4	RARRES3	5920	1.43	2.66E-05	1.28	1.04E-04
NM_004900.4	APOBEC3B	9582	1.01	2.37E-04	1.20	1.30E-05
NM_004946.2	DOCK2	1794	1.24	1.49E-05	1.09	8.10E-05
NM_004951.4	GPR183	1880	1.41	2.86E-04	1.24	7.41E-04
NM_005022.3	PFN1	5216	1.30	7.77E-04	1.30	4.23E-04
NM_005292.3	GPR18	2841	1.36	2.53E-04	1.12	1.37E-03
NM_005556.3	KRT7	3855	1.24	6.01E-04	1.13	9.79E-04
NM_005615.4	RNASE6	6039	1.43	3.50E-07	1.57	6.10E-08
NM_005651.3	TDO2	6999	1.50	1.46E-05	1.12	6.08E-04
NM_005727.3	TSPAN1	10103	1.40	5.42E-03	1.26	6.70E-03
NM_005737.3	ARL4C	10123	1.65	2.42E-06	2.15	5.33E-09
NM_005849.3	IGSF6	10261	1.08	1.83E-03	1.38	4.90E-05
NM_006098.4	RACK1	10399	1.13	1.61E-03	1.08	1.38E-03
NM_006103.3	WFDC2	10406	2.18	1.35E-05	2.22	9.08E-06
NM_006144.3	GZMA	3001	2.00	2.73E-05	2.30	1.77E-06
NM_006169.2	NNMT	4837	2.59	2.07E-07	3.22	1.08E-09
NM_006206.5	PDGFRA	5156	1.21	7.51E-03	1.65	1.35E-04
NM_006274.2	CCL19	6363	1.97	2.31E-04	2.04	8.44E-05
NM_006317.4	BASP1	10409	1.04	4.29E-02	1.13	1.57E-02
NM_006398.3	UBD	10537	1.28	2.90E-03	1.70	5.08E-05
NM_006408.3	AGR2	10551	1.29	7.79E-04	1.98	4.80E-07
NM_006495.3	EVI2B	2124	1.66	9.96E-04	2.55	7.31E-07
NM_006762.2	LAPTM5	7805	1.52	4.87E-05	2.14	4.71E-08
NM_006894.5	FMO3	2328	1.03	2.51E-03	1.29	8.85E-05
NM_007074.3	CORO1A	11151	1.64	1.04E-05	1.58	1.72E-05
NM_007268.2	VSIG4	11326	1.73	4.55E-08	1.32	1.79E-05
NM_007293.2	C4A	720	1.33	1.88E-02	1.23	1.76E-02
NM_009588.1	LTB	4050	1.86	3.83E-05	1.32	1.86E-03
NM_013258.4	PYCARD	29108	1.64	8.59E-04	1.86	1.01E-04
NM_013996.2	TAC1	6863	1.76	2.04E-03	2.92	5.38E-07
NM_013997.2	TAC1	6863	1.76	2.04E-03	2.92	5.38E-07
NM_013998.2	TAC1	6863	1.76	2.04E-03	2.92	5.38E-07
NM_014210.3	EVI2A	2123	2.01	1.74E-05	2.83	9.40E-09
NM_014350.3	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
NM_014879.3	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
NM_015529.3	MOXD1	26002	2.02	4.93E-05	2.27	5.25E-06
NM_015675.3	GADD45B	4616	-1.40	2.68E-04	-1.30	4.09E-04
NM_015991.3	C1QA	712	2.05	1.14E-07	1.78	3.17E-06
NM_016562.3	TLR7	51284	1.33	2.44E-04	1.39	7.73E-05
NM_016619.2	PLAC8	51316	1.29	9.40E-04	1.47	1.06E-04
NM_018460.3	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05



NM_022349.3	MS4A6A	64231	2.02	3.10E-08	2.14	1.08E-08
NM_030817.2	APOLD1	81575	-2.04	1.32E-04	-1.44	3.80E-03
NM_031279.3	ETNPPL	64850	-1.38	1.84E-02	-2.24	6.91E-05
NM_032495.5	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
NM_033295.3	CASP1	834	1.16	2.56E-04	2.37	3.36E-11
NM_057166.4	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
NM_057167.3	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
NM_080921.3	PTPRC	5788	1.40	4.39E-04	1.93	1.74E-06
NM_139211.4	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
NM_139212.3	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
NM_144646.3	JCHAIN	3512	3.02	3.25E-06	4.22	1.09E-09
NM_145182.2	PYCARD	29108	1.64	8.59E-04	1.86	1.01E-04
NM_171997.2	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
NM_198125.2	TYROBP	7305	1.56	1.06E-04	1.76	1.08E-05
NM_203416.3	CD163	9332	2.00	2.45E-07	2.18	5.40E-08
NM_206963.1	RARRES1	5918	2.02	1.41E-07	1.75	3.75E-06
NM_212474.2	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_212476.2	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_212478.2	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NM_212482.2	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
NR_024448.2	GUSBP11	91316	2.11	1.52E-02	2.70	9.42E-04
NR_026691.1	IL10RA	3587	1.68	1.10E-05	1.77	3.72E-06
NR_029395.1	IGLL3P	91353	2.54	1.25E-02	4.10	3.33E-05
NR_029467.1	SELL	6402	1.30	2.96E-03	1.69	7.16E-05
NR_033390.1	TYROBP	7305	1.42	4.36E-04	1.74	1.37E-05
NR_038335.1	CLU	1191	1.93	5.42E-05	2.25	2.82E-06
NR_045494.1	CLU	1191	1.93	5.42E-05	2.25	2.82E-06
NR_109871.1	TRAF3IP3	80342	1.83	8.15E-04	1.08	3.27E-02
NR_120485.1	IL7R	3575	1.78	7.28E-07	1.22	3.45E-04
NR_130134.1	ISG20	3669	1.22	1.52E-02	1.94	6.39E-05
XM_005245625.1	CD48	962	2.65	3.72E-07	3.28	2.45E-09
XM_005246065.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_005246066.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_005246402.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005246405.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005246406.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005246409.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005246412.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005246414.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_005247686.4	RARRES1	5918	2.01	5.44E-08	1.76	1.57E-06
XM_005247922.3	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
XM_005247923.3	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
XM_005248299.3	IL7R	3575	1.78	7.28E-07	1.22	3.45E-04
XM_005249051.4	HLA-DQB2	3120	1.09	1.38E-04	1.19	2.37E-05

XM_005249581.4	AGR2	10551	1.29	7.79E-04	1.98	4.80E-07
XM_005251972.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_005251973.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_005251974.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_005251975.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_005253274.3	LOC101927562	101927562	-1.15	9.73E-03	-1.04	1.13E-02
XM_005253529.4	CD163	9332	2.04	1.58E-07	2.16	6.10E-08
XM_005254899.2	ISG20	3669	1.03	1.41E-02	1.24	1.52E-03
XM_005257946.3	EVI2B	2124	1.66	9.96E-04	2.55	7.31E-07
XM_005259642.1	VAV1	7409	1.06	5.97E-03	1.11	2.09E-03
XM_005262662.4	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_005265743.1	PDGFRA	5156	1.21	7.51E-03	1.65	1.35E-04
XM_005271721.4	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
XM_005271722.2	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
XM_006711472.3	PTPRC	5788	1.40	4.39E-04	1.93	1.74E-06
XM_006711473.3	PTPRC	5788	1.40	4.39E-04	1.93	1.74E-06
XM_006711474.3	PTPRC	5788	1.40	4.39E-04	1.93	1.74E-06
XM_006712253.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_006714211.2	JCHAIN	3512	3.02	3.25E-06	4.22	1.09E-09
XM_006714212.2	JCHAIN	3512	3.02	3.25E-06	4.22	1.09E-09
XM_006716284.2	CLU	1191	1.99	1.45E-04	2.46	2.87E-06
XM_006717096.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_006717097.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_006717098.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_006717101.3	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_006718661.2	MS4A6A	64231	2.02	3.10E-08	2.14	1.08E-08
XM_006719946.3	GPR18	2841	1.36	2.53E-04	1.12	1.37E-03
XM_006720488.3	ISG20	3669	1.03	1.41E-02	1.24	1.52E-03
XM_006724001.1	ITGB2	3689	1.51	3.27E-06	1.81	6.40E-08
XM_011509345.2	FMO3	2328	1.03	2.51E-03	1.29	8.85E-05
XM_011510018.2	TRAF3IP3	80342	1.89	1.19E-03	1.33	1.33E-02
XM_011510171.1	CD48	962	1.97	4.87E-07	2.19	6.10E-08
XM_011510574.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_011511479.2	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05
XM_011511483.1	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05
XM_011513340.2	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
XM_011513742.2	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_011513743.2	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_011513744.2	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_011513745.2	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_011518214.2	COL15A1	1306	1.19	1.95E-03	1.92	8.99E-07
XM_011518625.2	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_011518626.2	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_011518628.2	TNC	3371	1.54	2.36E-04	3.07	3.55E-11

XM_011518629.2	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_011521521.2	ISG20	3669	1.22	1.52E-02	1.94	6.39E-05
XM_011531925.1	JCHAIN	3512	3.02	3.25E-06	4.22	1.09E-09
XM_011531926.1	JCHAIN	3512	3.02	3.25E-06	4.22	1.09E-09
XM_011533122.1	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
XM_011533123.1	CAPG	822	1.46	1.43E-04	1.16	1.26E-03
XM_011534996.2	FGF9	2254	-1.66	1.87E-07	-1.15	1.47E-04
XM_011537265.2	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_011537266.2	ACTN1	87	1.21	2.93E-04	1.54	4.07E-06
XM_011537267.2	ACTN1	87	1.20	2.39E-04	1.50	4.38E-06
XM_011537268.2	ACTN1	87	1.21	2.93E-04	1.54	4.07E-06
XM_011538325.1	KRT7	3855	1.10	9.14E-03	1.48	2.53E-04
XM_011540460.2	TSPAN1	10103	1.36	1.28E-02	1.32	8.71E-03
XM_011542059.2	C1QB	713	2.30	4.05E-08	2.14	3.57E-07
XM_011542098.2	LAPTM5	7805	1.52	4.87E-05	2.14	4.71E-08
XM_011545714.2	CORO1A	11151	1.64	1.04E-05	1.58	1.72E-05
XM_011545934.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_011545935.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_011545936.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_011545937.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_011545938.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_011545940.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_017002867.1	CD48	962	2.39	3.47E-07	2.59	7.02E-08
XM_017003303.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_017003304.1	COL6A3	1293	2.34	4.92E-06	2.61	4.93E-07
XM_017003692.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_017003693.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_017003694.1	FN1	2335	1.23	7.92E-06	1.43	3.53E-07
XM_017004499.1	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05
XM_017004500.1	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05
XM_017005386.1	CYTIP	9595	1.20	6.71E-03	1.30	1.70E-03
XM_017007583.1	P2RY14	9934	1.43	1.38E-04	1.15	1.17E-03
XM_017008564.1	SPP1	6696	1.15	1.34E-03	1.05	1.90E-03
XM_017008571.1	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_017008572.1	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XM_017008728.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008729.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008730.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008731.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008732.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008733.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017008734.1	HOPX	84525	1.09	3.23E-02	2.49	8.99E-07
XM_017009327.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09
XM_017009328.1	TNFAIP8	25816	1.30	2.72E-04	2.23	4.58E-09

XM_017010714.1	MOXD1	26002	2.02	4.93E-05	2.27	5.25E-06
XM_017010715.1	MOXD1	26002	2.02	4.93E-05	2.27	5.25E-06
XM_017014678.1	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_017014679.1	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_017014680.1	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_017014681.1	TNC	3371	1.54	2.36E-04	3.07	3.55E-11
XM_017018124.1	MS4A6A	64231	2.02	3.10E-08	2.14	1.08E-08
XM_017018539.1	USP2	9099	-1.22	1.80E-02	-2.06	4.01E-05
XM_017018543.1	CD3D	915	1.73	1.93E-05	1.22	1.37E-03
XM_017019294.1	KRT7	3855	1.24	6.01E-04	1.13	9.79E-04
XM_017020405.1	GPR183	1880	1.41	2.86E-04	1.24	7.41E-04
XM_017021566.1	RNASE6	6039	1.43	3.50E-07	1.57	6.10E-08
XM_017021567.1	RNASE6	6039	1.43	3.50E-07	1.57	6.10E-08
XM_017021720.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021721.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021722.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021723.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021725.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021726.1	ACTN1	87	1.21	1.17E-04	1.49	2.33E-06
XM_017021727.1	ACTN1	87	1.21	2.93E-04	1.54	4.07E-06
XM_017021728.1	ACTN1	87	1.21	2.93E-04	1.54	4.07E-06
XM_017022147.1	ISG20	3669	1.12	1.17E-02	1.47	4.72E-04
XM_017022148.1	ISG20	3669	1.16	9.47E-03	1.50	3.72E-04
XM_017022885.1	CORO1A	11151	1.64	1.04E-05	1.58	1.72E-05
XM_017022886.1	CORO1A	11151	1.64	1.04E-05	1.58	1.72E-05
XM_017023199.1	IRF8	3394	1.59	1.74E-05	1.88	5.95E-07
XM_017023641.1	UMOD	7369	-1.56	1.94E-02	-1.63	7.69E-03
XM_017024761.1	PFN1	5216	1.30	1.65E-03	1.33	7.39E-04
XM_017026822.1	GADD45B	4616	-1.40	2.68E-04	-1.30	4.09E-04
XM_017028341.1	ITGB2	3689	1.51	3.27E-06	1.81	6.40E-08
XM_017029251.1	VSIG4	11326	2.11	7.54E-08	1.90	1.17E-06
XM_017030289.1	C4A	720	1.33	1.88E-02	1.23	1.76E-02
XR_001738850.1	ARHGAP15	55843	1.19	4.51E-05	1.10	9.53E-05
XR_001740228.1	RARRES1	5918	2.37	2.45E-09	1.97	4.36E-07
XR_001748699.1	KRT7	3855	1.24	6.01E-04	1.13	9.79E-04
XR_001748700.1	KRT7	3855	1.10	9.14E-03	1.48	2.53E-04
XR_925163.2	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06
XR_925165.1	TLR1	7096	1.01	1.00E-04	1.25	1.74E-06

**Supplementary Table S3.** Preservation score of modules derived from WGCNA

Module	MedianRank.pre s	MedianRank.qua l	Zsummary.pre s	Zsummary.qua l
black	10	14	29	37

blue	19	22	46	41
brown	16	20	49	55
cyan	5	10	20	18
darkgreen	4	15	12	10
darkred	2	3	13	15
gold	23	23	34	-0.62
green	21	21	30	38
greenyellow	18	19	18	16
grey	23	24	5.7	-1.8
grey60	22	12.5	11	11
lightcyan	15	11	13	15
lightgreen	3	4	14	16
lightyellow	11	7.5	12	13
magenta	10	8.5	18	24
midnightblue	8	6	13	16
pink	6	2	21	41
purple	12	18	17	17
red	11	12.5	34	46
royalblue	2	1	15	19
salmon	20	5	13	30
tan	6	8	23	21
turquoise	14	16.5	47	65
yellow	14	16.5	38	50

**Supplementary Table S4.** Functional enrichment of genes in significant modules

Module	Category	GO Term/Pathway	Gene count	Gene Ratio (%)	P Value	Fold Enrichment
lightcyan	BP	Cytokine secretion	3	21.43	7.09E-03	21.62
lightcyan	BP	Regulation of protein metabolic process	7	50.00	7.73E-03	3.31
lightcyan	BP	Blood vessel development	4	28.57	9.09E-03	8.26
lightcyan	BP	Regulation of cytokine production	4	28.57	9.13E-03	8.24
lightcyan	BP	Negative regulation of protein transport	3	21.43	9.59E-03	18.49
lightcyan	BP	Vasculature development	4	28.57	1.06E-02	7.80
lightcyan	BP	Negative regulation of establishment of protein localization	3	21.43	1.07E-02	17.49
lightcyan	BP	Cytokine production	4	28.57	1.17E-02	7.54
lightcyan	BP	Response to growth factor	4	28.57	1.18E-02	7.50
lightcyan	BP	Regulation of erk1 and erk2 cascade	3	21.43	1.56E-02	14.33
lightcyan	BP	Regulation of response to external stimulus	4	28.57	1.67E-02	6.60
lightcyan	BP	Negative regulation of response to stimulus	5	35.71	1.78E-02	4.34
lightcyan	BP	Regulation of immune effector process	3	21.43	2.57E-02	10.98
lightcyan	BP	Extracellular matrix organization	3	21.43	2.70E-02	10.68

lightcyan	BP	Extracellular structure organization	3	21.43	2.72E-02	10.65
lightcyan	BP	Circulatory system development	4	28.57	3.40E-02	5.03
lightcyan	BP	Cardiovascular system development	4	28.57	3.40E-02	5.03
lightcyan	BP	Positive regulation of cytokine production	3	21.43	3.53E-02	9.24
lightcyan	BP	Cell adhesion	5	35.71	3.64E-02	3.50
lightcyan	BP	Biological adhesion	5	35.71	3.68E-02	3.49
lightcyan	BP	Macrophage activation	2	14.29	3.76E-02	48.54
lightcyan	BP	Symbiosis, encompassing mutualism through parasitism	4	28.57	3.91E-02	4.77
lightcyan	BP	Interspecies interaction between organisms	4	28.57	3.91E-02	4.77
lightcyan	BP	Angiogenesis	3	21.43	4.00E-02	8.64
lightcyan	BP	Negative regulation of multicellular organismal process	4	28.57	4.10E-02	4.68
lightcyan	BP	Positive regulation of fibroblast proliferation	2	14.29	4.21E-02	43.25
lightcyan	BP	Cellular response to chemical stimulus	6	42.86	4.28E-02	2.69
lightcyan	BP	Negative regulation of transport	3	21.43	4.67E-02	7.93
lightcyan	BP	Regulation of signal transduction	6	42.86	4.79E-02	2.62
lightcyan	BP	Secretion	4	28.57	4.97E-02	4.33
lightcyan	CC	Extracellular matrix	6	42.86	2.17E-05	14.74
lightcyan	CC	Extracellular matrix component	4	28.57	9.19E-05	40.68
lightcyan	CC	Proteinaceous extracellular matrix	5	35.71	9.40E-05	18.03
lightcyan	CC	Cytoplasmic, membrane-bounded vesicle	6	42.86	9.47E-04	6.60
lightcyan	CC	Membrane-bounded vesicle	9	64.29	1.16E-03	3.24
lightcyan	CC	Cytoplasmic vesicle	6	42.86	1.37E-03	6.08
lightcyan	CC	Intracellular vesicle	6	42.86	1.38E-03	6.07
lightcyan	CC	Vesicle	9	64.29	1.52E-03	3.12
lightcyan	CC	Extracellular region part	9	64.29	1.90E-03	3.02
lightcyan	CC	Collagen trimer	3	21.43	2.32E-03	38.29
lightcyan	CC	Extracellular space	6	42.86	2.33E-03	5.41
lightcyan	CC	Extracellular region	9	64.29	6.20E-03	2.53
lightcyan	CC	Endomembrane system	8	57.14	9.95E-03	2.69
lightcyan	CC	Secretory granule	3	21.43	2.60E-02	10.91
lightcyan	CC	Secretory vesicle	3	21.43	4.24E-02	8.36
lightcyan	MF	Collagen binding	3	21.43	9.11E-04	60.87
lightcyan	MF	Growth factor binding	3	21.43	3.58E-03	30.43
lightcyan	MF	Transforming growth factor beta binding	2	14.29	1.13E-02	162.32
lightcyan	MF	Calcium ion binding	4	28.57	1.26E-02	7.24
black	BP	Immune response	28	16.37	2.63E-15	7.02
black	BP	Inflammatory response	23	13.45	8.94E-12	6.41
black	BP	Innate immune response	21	12.28	4.05E-09	5.16
black	BP	Cell adhesion	21	12.28	1.22E-08	4.83
black	BP	Chemokine-mediated signaling pathway	10	5.85	2.08E-08	14.87
black	BP	Cell chemotaxis	9	5.26	1.65E-07	14.62

black	BP	Chemotaxis	11	6.43	2.28E-07	9.52
black	BP	Adaptive immune response	11	6.43	1.37E-06	7.85
black	BP	Cell surface receptor signaling pathway	14	8.19	1.97E-06	5.40
black	BP	Leukocyte migration	10	5.85	2.27E-06	8.66
black	BP	Positive regulation of tumor necrosis factor production	7	4.09	4.93E-06	15.73
black	BP	Dendritic cell chemotaxis	5	2.92	1.63E-05	31.06
black	BP	Extracellular matrix organization	11	6.43	1.67E-05	5.93
black	BP	Neutrophil chemotaxis	7	4.09	3.60E-05	11.20
black	BP	Regulation of immune response	10	5.85	4.77E-05	5.93
black	BP	Regulation of cell shape	9	5.26	5.37E-05	6.79
black	BP	Lymphocyte chemotaxis	5	2.92	1.30E-04	18.86
black	BP	Response to lipopolysaccharide	9	5.26	1.63E-04	5.80
black	BP	Defense response to virus	9	5.26	1.69E-04	5.76
black	BP	T cell differentiation	5	2.92	1.71E-04	17.60
black	BP	Cellular response to interferon-gamma	6	3.51	1.95E-04	11.12
black	BP	Lipopolysaccharide-mediated signaling pathway	5	2.92	2.21E-04	16.50
black	BP	Positive regulation of erk1 and erk2 cascade	9	5.26	2.53E-04	5.43
black	BP	Regulation of inflammatory response	6	3.51	3.13E-04	10.06
black	BP	Integrin-mediated signaling pathway	7	4.09	3.44E-04	7.47
black	BP	Negative regulation of viral genome replication	5	2.92	5.30E-04	13.20
black	BP	Signal transduction	24	14.04	5.44E-04	2.18
black	BP	Interferon-gamma-mediated signaling pathway	6	3.51	5.47E-04	8.92
black	BP	Cellular response to interleukin-1	6	3.51	5.47E-04	8.92
black	BP	Cellular response to tumor necrosis factor	7	4.09	6.04E-04	6.72
black	BP	Monocyte chemotaxis	5	2.92	6.39E-04	12.57
black	BP	Cellular response to lipopolysaccharide	7	4.09	6.96E-04	6.54
black	BP	Positive regulation of tyrosine phosphorylation of stat protein	3	1.75	8.64E-04	63.37
black	BP	B cell receptor signaling pathway	5	2.92	1.66E-03	9.78
black	BP	Cellular calcium ion homeostasis	6	3.51	1.85E-03	6.81
black	BP	Humoral immune response	5	2.92	2.02E-03	9.26
black	BP	Positive regulation of t cell proliferation	5	2.92	2.44E-03	8.80
black	BP	Negative regulation of angiogenesis	5	2.92	2.76E-03	8.52
black	BP	Cell-cell signaling	9	5.26	2.82E-03	3.74
black	BP	Positive regulation of t cell migration	3	1.75	3.77E-03	31.68
black	BP	Immunological synapse formation	3	1.75	3.77E-03	31.68
black	BP	Positive regulation of i-kappab kinase/nf-kappab signaling	7	4.09	4.20E-03	4.59
black	BP	Positive regulation of macrophage chemotaxis	3	1.75	4.58E-03	28.80
black	BP	Platelet activation	6	3.51	4.63E-03	5.51
black	BP	Positive regulation of inflammatory response	5	2.92	4.96E-03	7.23

black	BP	Negative regulation of cell adhesion	4	2.34	5.02E-03	11.42
black	BP	Response to hypoxia	7	4.09	5.81E-03	4.30
black	BP	Macrophage chemotaxis	3	1.75	6.41E-03	24.37
black	BP	Cytokine-mediated signaling pathway	6	3.51	7.97E-03	4.84
black	BP	Positive regulation of interleukin-6 production	4	2.34	8.69E-03	9.39
black	BP	Positive regulation of interferon-gamma production	4	2.34	9.23E-03	9.18
black	BP	Skeletal system development	6	3.51	9.57E-03	4.63
black	BP	Positive regulation of monocyte chemotaxis	3	1.75	9.68E-03	19.80
black	BP	Phagocytosis	4	2.34	1.04E-02	8.80
black	BP	Negative regulation of apoptotic process	11	6.43	1.10E-02	2.55
black	BP	Defense response to bacterium	6	3.51	1.20E-02	4.37
black	BP	Positive regulation of t cell activation	3	1.75	1.22E-02	17.60
black	BP	Toll-like receptor 4 signaling pathway	3	1.75	1.22E-02	17.60
black	BP	Positive regulation of cell proliferation	11	6.43	1.28E-02	2.49
black	BP	Platelet degranulation	5	2.92	1.63E-02	5.13
black	BP	Positive regulation of nf-kappab import into nucleus	3	1.75	1.64E-02	15.09
black	BP	Response to ethanol	5	2.92	1.73E-02	5.03
black	BP	Cellular response to cytokine stimulus	3	1.75	1.80E-02	14.40
black	BP	Positive regulation of neutrophil chemotaxis	3	1.75	1.80E-02	14.40
black	BP	Positive regulation of interleukin-1 beta secretion	3	1.75	1.80E-02	14.40
black	BP	Apoptotic process	12	7.02	1.84E-02	2.24
black	BP	Fc receptor mediated stimulatory signaling pathway	2	1.17	1.87E-02	105.61
black	BP	Positive regulation of hematopoietic stem cell migration	2	1.17	1.87E-02	105.61
black	BP	Positive regulation of immune complex clearance by monocytes and macrophages	2	1.17	1.87E-02	105.61
black	BP	Bundle of his cell to purkinje myocyte communication	2	1.17	1.87E-02	105.61
black	BP	Osteoclast differentiation	3	1.75	1.96E-02	13.78
black	BP	Response to virus	5	2.92	2.02E-02	4.80
black	BP	Cellular defense response	4	2.34	2.06E-02	6.81
black	BP	Collagen catabolic process	4	2.34	2.24E-02	6.60
black	BP	G-protein coupled receptor signaling pathway	16	9.36	2.24E-02	1.88
black	BP	Leukocyte cell-cell adhesion	3	1.75	2.29E-02	12.67
black	BP	Positive regulation of angiogenesis	5	2.92	2.33E-02	4.59
black	BP	Positive regulation of apoptotic process	8	4.68	2.36E-02	2.82
black	BP	Tumor necrosis factor-mediated signaling pathway	5	2.92	2.53E-02	4.48
black	BP	Toll-like receptor signaling pathway	3	1.75	2.65E-02	11.73
black	BP	Negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	4	2.34	2.73E-02	6.12



black	BP	Negative regulation of endopeptidase activity	5	2.92	2.75E-02	4.36
black	BP	Myeloid dendritic cell activation involved in immune response	2	1.17	2.80E-02	70.41
black	BP	Positive regulation of type I hypersensitivity	2	1.17	2.80E-02	70.41
black	BP	Cellular response to triacyl bacterial lipopeptide	2	1.17	2.80E-02	70.41
black	BP	TLR2 signaling pathway	2	1.17	2.80E-02	70.41
black	BP	Cellular response to mechanical stimulus	4	2.34	2.93E-02	5.95
black	BP	Positive regulation of phagocytosis	3	1.75	3.03E-02	10.93
black	BP	Cellular response to fibroblast growth factor stimulus	3	1.75	3.22E-02	10.56
black	BP	Negative regulation of cell proliferation	9	5.26	3.39E-02	2.40
black	BP	Regulation of heart contraction	3	1.75	3.42E-02	10.22
black	BP	Extracellular matrix disassembly	4	2.34	3.49E-02	5.56
black	BP	Calcium ion transport	4	2.34	3.49E-02	5.56
black	BP	Brown fat cell differentiation	3	1.75	3.63E-02	9.90
black	BP	JAK-STAT cascade	3	1.75	3.63E-02	9.90
black	BP	Regulation of vascular endothelial growth factor production	2	1.17	3.71E-02	52.81
black	BP	Negative regulation of smooth muscle contraction	2	1.17	3.71E-02	52.81
black	BP	Neutrophil activation involved in immune response	2	1.17	3.71E-02	52.81
black	BP	T cell costimulation	4	2.34	3.72E-02	5.42
black	BP	Positive regulation of cytosolic calcium ion concentration	5	2.92	3.79E-02	3.94
black	BP	MyD88-dependent toll-like receptor signaling pathway	3	1.75	3.84E-02	9.60
black	BP	Negative regulation of T cell mediated cytotoxicity	2	1.17	4.62E-02	42.24
black	BP	Regulation of platelet activation	2	1.17	4.62E-02	42.24
black	BP	Interleukin-1 beta production	2	1.17	4.62E-02	42.24
black	BP	Proteolysis	10	5.85	4.70E-02	2.11
black	BP	Movement of cell or subcellular component	4	2.34	4.75E-02	4.91
black	BP	Complement activation	4	2.34	4.89E-02	4.86
black	CC	Extracellular region	43	25.15	1.41E-10	2.97
black	CC	Extracellular space	35	20.47	2.73E-08	2.89
black	CC	Integral component of plasma membrane	33	19.30	8.92E-07	2.59
black	CC	Cell surface	18	10.53	7.53E-06	3.69
black	CC	Plasma membrane	62	36.26	1.29E-05	1.67
black	CC	Extracellular exosome	45	26.32	9.95E-05	1.78
black	CC	External side of plasma membrane	10	5.85	1.30E-04	5.22
black	CC	Integral component of membrane	63	36.84	4.50E-03	1.36
black	CC	Early endosome	8	4.68	4.60E-03	3.88
black	CC	Extracellular matrix	9	5.26	5.24E-03	3.38
black	CC	Focal adhesion	10	5.85	8.71E-03	2.84
black	CC	Membrane raft	7	4.09	1.06E-02	3.78

black	CC	Platelet alpha granule lumen	4	2.34	1.31E-02	8.08
black	CC	Lysosome	7	4.09	1.61E-02	3.44
black	CC	Complement component C1 complex	2	1.17	1.78E-02	111.12
black	CC	Actin filament	4	2.34	2.05E-02	6.84
black	CC	Membrane	30	17.54	2.05E-02	1.52
black	CC	Proteinaceous extracellular matrix	7	4.09	3.36E-02	2.90
black	CC	Basement membrane	4	2.34	3.39E-02	5.63
black	CC	NLRP1 inflammasome complex	2	1.17	3.53E-02	55.56
black	CC	Immunological synapse	3	1.75	3.70E-02	9.80
black	CC	Collagen trimer	4	2.34	4.95E-02	4.83
black	MF	Chemokine activity	8	4.68	2.61E-07	18.01
black	MF	Heparin binding Transmembrane signaling receptor activity	10	5.85	1.46E-05	6.90
black	MF	Receptor activity	11	6.43	2.44E-05	5.67
black	MF	Protein homodimerization activity	10	5.85	1.56E-04	5.08
black	MF	Cysteine-type endopeptidase activity involved in apoptotic process	17	9.94	9.09E-04	2.57
black	MF	Serine-type endopeptidase activity	3	1.75	5.89E-03	25.46
black	MF	Serine-type endopeptidase inhibitor activity	8	4.68	8.39E-03	3.46
black	MF	Receptor binding	5	2.92	1.15E-02	5.69
black	MF	Integrin binding	9	5.26	1.47E-02	2.81
black	MF	IgE receptor activity	5	2.92	1.50E-02	5.25
black	MF	Cysteine-type endopeptidase inhibitor activity involved in apoptotic process	2	1.17	1.79E-02	110.33
black	MF	CCR chemokine receptor binding	3	1.75	1.80E-02	14.39
black	MF	Cell adhesion molecule binding	3	1.75	1.80E-02	14.39
black	MF	CCR2 chemokine receptor binding	4	2.34	1.84E-02	7.12
black	MF	Actin filament binding	2	1.17	2.68E-02	73.56
black	MF	Carbohydrate binding	5	2.92	3.15E-02	4.18
black	MF	Glycosphingolipid binding	6	3.51	3.23E-02	3.38
black	MF	Deoxycytidine deaminase activity	2	1.17	3.55E-02	55.17
black	MF	IgE binding	2	1.17	4.42E-02	55.17
black	KEGG	Pertussis	2	1.17	4.42E-02	44.13
black	KEGG	Staphylococcus aureus infection	9	5.26	3.87E-06	9.42
black	KEGG	Fc gamma R-mediated phagocytosis	8	4.68	4.31E-06	11.63
black	KEGG	Hematopoietic cell lineage	9	5.26	9.12E-06	8.41
black	KEGG	Chemokine signaling pathway	9	5.26	9.97E-06	8.31
black	KEGG	Cytokine-cytokine receptor interaction	12	7.02	1.88E-05	5.07
black	KEGG	Cell adhesion molecules (CAMs)	13	7.60	2.70E-05	4.44
black	KEGG	Tuberculosis	10	5.85	6.67E-05	5.53
black	KEGG	Phagosome	11	6.43	6.85E-05	4.88
black	KEGG	Malaria	10	5.85	1.19E-04	5.13
black	KEGG	Legionellosis	6	3.51	3.48E-04	9.62
black	KEGG	Leukocyte transendothelial migration	6	3.51	5.49E-04	8.72
black	KEGG		8	4.68	6.70E-04	5.32

black	KEGG	NF-kappa B signaling pathway	7	4.09	7.48E-04	6.32
black	KEGG	Rheumatoid arthritis	7	4.09	7.95E-04	6.25
black	KEGG	Leishmaniasis	6	3.51	1.91E-03	6.64
black	KEGG	TNF signaling pathway	7	4.09	2.09E-03	5.19
black	KEGG	Amoebiasis	7	4.09	2.09E-03	5.19
black	KEGG	Focal adhesion	9	5.26	4.23E-03	3.43
black	KEGG	ECM-receptor interaction	6	3.51	4.64E-03	5.42
black	KEGG	NOD-like receptor signaling pathway	5	2.92	4.90E-03	7.14
black	KEGG	Prion diseases	4	2.34	8.01E-03	9.52
black	KEGG	Primary immunodeficiency	4	2.34	8.71E-03	9.24
black	KEGG	Complement and coagulation cascades	5	2.92	1.09E-02	5.69
black	KEGG	Salmonella infection	5	2.92	2.03E-02	4.73
black	KEGG	Influenza A	7	4.09	2.20E-02	3.16
black	KEGG	Pathogenic Escherichia coli infection	4	2.34	2.60E-02	6.16
black	KEGG	Chagas disease (American trypanosomiasis)	5	2.92	4.17E-02	3.78
purple	BP	Cellular response to nutrient levels	6	14.29	3.30E-05	15.71
purple	BP	Cellular response to extracellular stimulus	6	14.29	7.34E-05	13.28
purple	BP	Cellular response to external stimulus	6	14.29	3.16E-04	9.72
purple	BP	Response to nutrient levels	6	14.29	2.40E-03	6.18
purple	BP	Cellular response to starvation	4	9.52	2.45E-03	14.48
purple	BP	Response to extracellular stimulus	6	14.29	3.29E-03	5.74
purple	BP	Protein maturation	5	11.90	3.61E-03	7.68
purple	BP	Response to acid chemical	5	11.90	3.95E-03	7.49
purple	BP	Response to starvation	4	9.52	5.46E-03	10.88
purple	BP	Renal sodium ion absorption	2	4.76	9.34E-03	208.13
purple	BP	Female pregnancy	4	9.52	9.47E-03	8.90
purple	BP	Response to organic substance	14	33.33	9.58E-03	2.07
purple	BP	Renal sodium ion transport	2	4.76	1.17E-02	166.50
purple	BP	Multi-multicellular organism process	4	9.52	1.38E-02	7.74
purple	BP	Proteolysis	10	23.81	1.45E-02	2.46
purple	BP	Protein processing	4	9.52	1.77E-02	7.06
purple	BP	Proteolysis involved in cellular protein catabolic process	6	14.29	1.79E-02	3.80
purple	BP	Cellular protein catabolic process	6	14.29	2.15E-02	3.62
purple	BP	Pyrimidine-containing compound salvage	2	4.76	2.78E-02	69.38
purple	BP	Pyrimidine nucleoside salvage	2	4.76	2.78E-02	69.38
purple	BP	Protein autoprocessing	2	4.76	3.00E-02	64.04
purple	BP	Cellular catabolic process	9	21.43	3.12E-02	2.32
purple	BP	Homeostatic process	9	21.43	3.42E-02	2.28
purple	BP	Renal absorption	2	4.76	3.46E-02	55.50
purple	BP	Hemoglobin metabolic process	2	4.76	3.46E-02	55.50
purple	BP	Nucleoside biosynthetic process	3	7.14	3.66E-02	9.68
purple	BP	Glycosyl compound biosynthetic process	3	7.14	3.77E-02	9.53

purple	BP	Nucleoside salvage	2	4.76	3.91E-02	48.97
purple	BP	Protein catabolic process	6	14.29	3.96E-02	3.08
purple	BP	Protein stabilization	3	7.14	4.03E-02	9.18
purple	BP	Establishment of mitochondrion localization	2	4.76	4.14E-02	46.25
purple	BP	Positive regulation of protein processing	2	4.76	4.36E-02	43.82
purple	BP	Innate immune response	6	14.29	4.42E-02	2.99
purple	BP	Ubiquitin-dependent protein catabolic process	5	11.90	4.51E-02	3.61
purple	BP	Protein activation cascade	3	7.14	4.58E-02	8.55
purple	BP	Positive regulation of protein maturation	2	4.76	4.58E-02	41.63
purple	BP	Myeloid cell differentiation	4	9.52	4.59E-02	4.85
purple	BP	Response to external stimulus	10	23.81	4.67E-02	2.01
purple	BP	Modification-dependent protein catabolic process	5	11.90	4.70E-02	3.56
purple	BP	Pyrimidine nucleoside catabolic process	2	4.76	4.81E-02	39.64
purple	BP	Inclusion body assembly	2	4.76	4.81E-02	39.64
purple	BP	Response to lipid	6	14.29	4.89E-02	2.90
purple	BP	Modification-dependent macromolecule catabolic process	5	11.90	4.90E-02	3.51
purple	CC	Extracellular space	11	26.19	4.79E-03	2.70
purple	CC	Membrane-bounded vesicle	17	40.48	2.48E-02	1.67
purple	CC	Hemoglobin complex	2	4.76	3.26E-02	59.05
purple	CC	Schmidt-Lanterman incisure	2	4.76	3.26E-02	59.05
purple	CC	Extracellular exosome	14	33.33	3.38E-02	1.76
purple	CC	Extracellular vesicle	14	33.33	3.51E-02	1.76
purple	CC	Extracellular organelle	14	33.33	3.52E-02	1.76
purple	CC	Compact myelin	2	4.76	4.32E-02	44.29
purple	CC	Apicolateral plasma membrane	2	4.76	4.58E-02	41.68
purple	MF	Misfolded protein binding	2	4.76	2.81E-02	68.62
purple	MF	Hydrolase activity	12	28.57	3.57E-02	1.90
purple	MF	Catalytic activity	21	50.00	4.37E-02	1.44

**Supplementary Table S5.** DEGs identified in mouse diabetic nephropathy

RefSeq Accession	Gene Symbol	GenBank ID	D - C (GSE20636)		GD - GC (GSE33744)	
			logFC	adj.P.Val	logFC	adj.P.Val
NM_001012335	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
NM_001012336	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
NM_001012766	Ear12	503845	0.71	3.72E-04	1.24	2.48E-05
NM_001025610	Ms4a7	109225	0.97	2.43E-06	1.35	4.29E-06
NM_001029937	Sec14l3	380683	-1.58	2.15E-10	-1.60	1.11E-09
NM_001034910	Defb42	619548	0.61	9.33E-05	0.92	9.10E-05
NM_001039150	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_001039151	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_001044384	Timp1	21857	0.62	1.51E-04	0.91	3.84E-03

NM_001111048	Fga	14161	0.59	5.89E-04	0.92	1.45E-03
NM_001111099	Cdkn1a	12575	1.02	1.48E-10	1.40	7.89E-16
NM_001145899	Slc15a2	57738	-0.64	1.44E-15	-0.83	2.19E-06
NM_001159986	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
NM_001161432	Eda2r	245527	0.64	1.54E-07	1.02	5.90E-10
NM_001164357	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
NM_001164358	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
NM_001166631	Havcr1	171283	0.98	7.29E-05	1.43	1.68E-04
NM_001166632	Havcr1	171283	0.98	7.29E-05	1.43	1.68E-04
NM_001177785	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_001177786	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_001177787	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_001199217	Slc38a3	76257	0.77	1.49E-08	0.87	1.97E-06
NM_001199218	Slc38a3	76257	0.77	1.49E-08	0.87	1.97E-06
NM_001204134	C1qtnf3	81799	-0.97	1.23E-11	-1.68	4.91E-11
NM_001204931	Reep6	70335	1.09	7.47E-10	0.83	5.12E-06
NM_001252330	Slc6a15	103098	-0.89	3.42E-11	-1.18	3.74E-11
NM_001253781	Prlr	19116	-1.13	6.00E-10	0.83	3.66E-06
NM_001276398	Ms4a7	109225	0.88	2.33E-05	1.35	4.96E-06
NM_001281830	Ifi2712a	76933	0.73	3.59E-03	1.10	1.83E-03
NM_001290273		66112	0.97	1.02E-07	1.52	2.61E-06
NM_001290558	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
NM_001291058	Cd68	12514	0.78	3.06E-06	1.22	1.48E-07
NM_001291481	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
NM_001291482	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
NM_001291483	Mdk	17242	-0.83	1.49E-11	-1.22	5.08E-12
NM_001294280	Timp1	21857	0.59	7.62E-04	0.92	3.42E-03
NM_001311132	Akr1c20	116852	-0.89	3.89E-10	0.69	2.65E-03
NM_001313963	Krt19	16669	0.67	7.78E-05	1.38	1.34E-06
NM_001320076	Mmp12	17381	0.64	6.98E-05	1.30	2.07E-04
NM_001320077	Mmp12	17381	0.64	6.98E-05	1.30	2.07E-04
NM_001347354	#N/A	#N/A	-0.67	6.64E-06	-1.68	7.61E-11
NM_007498	Atf3	11910	0.69	5.19E-05	0.65	3.26E-04
NM_007669	Cdkn1a	12575	1.02	1.48E-10	1.40	7.89E-16
NM_008176	Cxcl1	14825	0.80	1.38E-04	1.20	2.23E-04
NM_008256	Hmgcs2	15360	1.41	5.91E-05	1.74	1.81E-10
NM_008331	Ifit1	15957	0.67	7.96E-05	0.77	2.33E-03
NM_008471	Krt19	16669	0.67	7.78E-05	1.38	1.34E-06
NM_008491	Lcn2	16819	2.03	1.02E-08	3.20	3.53E-09
NM_008586	Mep1b	17288	-0.68	5.41E-09	-1.47	3.83E-06
NM_008605	Mmp12	17381	0.64	6.98E-05	1.30	2.07E-04
NM_008630	Mt2	17750	0.90	8.02E-07	0.65	2.58E-09
NM_008871	Serpine1	18787	0.73	9.44E-05	0.95	1.02E-08
NM_009139	Ccl6	20305	0.63	7.23E-05	1.31	2.13E-08

NM_009264	Sprr1a	20753	0.72	3.60E-04	0.98	4.68E-03
NM_009381	Thrsp	21835	-0.93	5.24E-04	0.76	4.21E-07
NM_009627	Adm	11535	0.69	4.38E-07	0.90	5.13E-10
NM_009778	C3	12266	1.91	1.92E-12	1.40	1.45E-06
NM_009827	Cckar	12425	-0.67	6.64E-06	-1.68	7.61E-11
NM_009851	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
NM_009899	Clca3a1	12722	0.70	2.05E-06	1.53	5.85E-12
NM_010006	Cyp2d9	13105	0.61	7.57E-04	-0.78	4.74E-03
NM_010493	Icam1	15894	0.60	3.35E-06	0.60	5.95E-07
NM_010594	Kap	16483	-0.83	4.61E-04	-1.32	1.34E-07
NM_010784	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
NM_011076	Abcb1a	18671	-0.60	5.93E-07	0.82	2.83E-07
NM_011169	Prlr	19116	-1.01	5.96E-11	0.76	4.75E-05
NM_011311	S100a4	20198	0.69	5.42E-08	0.82	1.07E-07
NM_011333	Ccl2	20296	0.68	9.82E-06	0.91	4.32E-04
NM_011338	Ccl9	20308	0.70	2.83E-05	1.16	6.60E-08
NM_011414	Slpi	20568	0.73	8.64E-05	2.23	7.83E-11
NM_011593	Timp1	21857	0.62	1.51E-04	0.91	3.84E-03
NM_011671	Ucp2	22228	0.91	1.58E-09	0.94	3.59E-11
NM_011825	Grem2	23893	0.74	2.56E-03	0.60	3.67E-03
NM_013468	Ankrd1	107765	0.97	3.05E-10	1.10	1.91E-09
NM_013602	Mt1	17748	0.62	6.36E-07	0.59	3.19E-10
NM_013697	Ttr	22139	-0.96	2.04E-04	-1.38	1.44E-02
NM_013750	Phlda3	27280	0.61	8.02E-11	0.78	3.98E-10
NM_017372	Lyz2	17105	1.06	2.18E-06	0.94	7.98E-07
NM_017388	Ear3	53876	0.82	4.96E-05	1.46	8.00E-08
NM_018816	Apom	55938	-0.73	3.64E-10	-0.68	1.59E-04
NM_020581	Angptl4	57875	1.15	6.19E-04	1.41	1.16E-09
NM_021274	Cxcl10	15945	0.97	1.58E-06	0.83	1.27E-04
NM_022018	Fam129a	63913	0.61	7.06E-05	1.09	5.69E-10
NM_023256	Krt20	66809	0.79	7.50E-06	1.14	6.49E-05
NM_023805	Slc38a3	76257	0.77	1.49E-08	0.87	1.97E-06
NM_025684	Nepn	66650	-0.70	9.45E-08	-0.74	2.18E-04
NM_027211	Anxa13	69787	-1.55	6.80E-15	-1.75	2.33E-14
NM_027762	Tchhl1	71325	0.72	1.34E-07	0.66	5.69E-03
NM_027836	Ms4a7	109225	0.88	2.33E-05	1.35	4.96E-06
NM_029083	Ddit4	74747	0.67	1.00E-04	0.60	5.70E-06
NM_029662	Mfsd2a	76574	-0.81	6.74E-07	-1.29	1.27E-05
NM_029796	Lrg1	76905	0.69	1.87E-04	1.34	1.94E-09
NM_029803	Ifi27l2a	76933	0.76	4.86E-03	0.99	2.33E-03
NM_030888	C1qtnf3	81799	-0.97	1.23E-11	-1.68	4.91E-11
NM_033354	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
NM_053215	Ugt2b37	112417	0.59	1.17E-04	-1.22	2.24E-08
NM_080845	Ftcd	14317	0.62	7.99E-10	0.68	2.02E-03

NM_133888	Smpdl3b	100340	0.95	1.17E-07	1.14	4.89E-08
NM_134248	Havcr1	171283	0.98	7.29E-05	1.43	1.68E-04
NM_138685	Wfdc15b	192201	-0.71	9.78E-12	-0.59	5.31E-05
NM_139292	Reep6	70335	1.09	7.47E-10	0.83	5.12E-06
NM_144785	Slc22a19	207151	-0.59	4.05E-08	-1.77	1.08E-07
NM_144856	Slc22a7	108114	-0.80	1.71E-08	-3.17	3.55E-14
NM_145424	BC089597	216454	-0.60	1.26E-09	0.83	6.71E-05
NM_146118	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
NM_172840	Vwa2	240675	-0.74	2.96E-11	-0.68	6.84E-07
NM_175158	Utp20	70683	0.94	1.11E-07	0.60	3.02E-09
NM_175328	Slc6a15	103098	-0.89	3.42E-11	-1.18	3.74E-11
NM_175540	Eda2r	245527	0.64	1.54E-07	1.02	5.90E-10
NM_177406	Cyp4a12a	277753	1.48	6.14E-10	-1.27	2.97E-09
NM_201360	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
NR_027641	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
NR_110993	Cd68	12514	0.78	3.06E-06	1.22	1.48E-07
NR_130895	Clca3a1	12722	0.70	2.05E-06	1.53	5.85E-12
XM_006496826	Grem2	23893	0.74	2.56E-03	0.60	3.67E-03
XM_006497049	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
XM_006497954	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
XM_006497955	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
XM_006497957	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
XM_006497958	Slc25a25	227731	0.60	8.91E-04	0.71	5.19E-06
XM_006498645	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
XM_006498646	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
XM_006498647	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
XM_006498649	Cd44	12505	0.84	6.71E-05	1.04	4.71E-06
XM_006501177	S100a4	20198	0.69	5.42E-08	0.82	1.07E-07
XM_006501178	S100a4	20198	0.69	5.42E-08	0.82	1.07E-07
XM_006503477	Mfsd2a	76574	-0.81	6.74E-07	-1.29	1.27E-05
XM_006503555	Abcb1a	18671	-0.60	5.93E-07	0.82	2.83E-07
XM_006503556	Abcb1a	18671	-0.60	5.93E-07	0.82	2.83E-07
XM_006507579	Ucp2	22228	0.91	1.58E-09	0.94	3.59E-11
XM_006512818	Nepn	66650	-0.70	9.45E-08	-0.74	2.18E-04
XM_006512819	Nepn	66650	-0.70	9.45E-08	-0.74	2.18E-04
XM_006512982	Slc6a15	103098	-0.87	6.35E-11	-1.15	2.05E-10
XM_006512983	Slc6a15	103098	-0.87	6.35E-11	-1.15	2.05E-10
XM_006512984	Slc6a15	103098	-0.87	6.35E-11	-1.15	2.05E-10
XM_006513215	Ftcd	14317	0.62	7.99E-10	0.68	2.02E-03
XM_006513216	Ftcd	14317	0.62	7.99E-10	0.68	2.02E-03
XM_006514077	Reep6	70335	1.09	7.47E-10	0.83	5.12E-06
XM_006516465	Akr1c20	116852	-0.89	3.89E-10	0.69	2.65E-03
XM_006516466	Akr1c20	116852	-0.89	3.89E-10	0.69	2.65E-03
XM_006520034	Prlr	19116	-1.01	5.96E-11	0.76	4.75E-05

XM_006520035	Prlr	19116	-1.01	5.96E-11	0.76	4.75E-05
XM_006520036	Prlr	19116	-1.01	5.96E-11	0.76	4.75E-05
XM_006520037	Prlr	19116	-1.01	5.96E-11	0.76	4.75E-05
XM_006521128	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
XM_006521129	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
XM_006521130	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
XM_006521131	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
XM_006521132	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10
XM_006526814	Slc22a19	207151	-0.59	4.05E-08	-1.77	1.08E-07
XM_006527090	Vwa2	240675	-0.74	2.96E-11	-0.68	6.84E-07
XM_006527091	Vwa2	240675	-0.74	2.96E-11	-0.68	6.84E-07
XM_006528025	Eda2r	245527	0.64	1.54E-07	1.02	5.90E-10
XM_006528026	Eda2r	245527	0.64	1.54E-07	1.02	5.90E-10
XM_006530752	Mt1	17748	0.62	4.45E-07	0.76	6.32E-11
XM_006532392	Havcr1	171283	0.97	7.65E-05	1.45	2.03E-04
XM_006532393	Havcr1	171283	0.98	7.29E-05	1.43	1.68E-04
XM_011239335	Mdk	17242	-1.05	1.41E-14	-1.28	9.88E-13
XM_011240004	Clca3a1	12722	0.70	2.05E-06	1.53	5.85E-12
XM_011243730	Sec14l3	380683	-1.52	2.71E-10	-1.60	1.62E-09
XM_011246258	C3	12266	1.91	1.92E-12	1.40	1.45E-06
XM_011248783	Havcr1	171283	0.97	7.65E-05	1.45	2.03E-04
XM_011248784	Havcr1	171283	0.97	7.65E-05	1.45	2.03E-04
XM_017312983	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
XM_017312984	Sec16b	89867	0.71	8.09E-11	0.83	1.83E-08
XM_017313160	Mmp12	17381	0.64	6.98E-05	1.30	2.07E-04
XM_017313682	Slc38a3	76257	0.77	1.49E-08	0.87	1.97E-06
XM_017318188	Slc22a26	236149	-1.26	6.41E-07	-0.97	3.33E-06
XM_017320448	Grem2	23893	0.74	2.56E-03	0.60	3.67E-03
XR_383836	C1qtnf3	81799	-0.97	1.23E-11	-1.68	4.91E-11
XR_871103	Slc38a3	76257	0.77	1.49E-08	0.87	1.97E-06
XR_875302	Cyp2d12	380997	-0.97	6.37E-06	-1.39	7.14E-10

**Supplementary Table S6.** Functional enrichment of DEGs identified in human diabetic nephropathy

Category	GO Term/Pathway	Gene count	Gene Ratio (%)	P Value	Fold Enrichment
BP	Defense response	49	38.28	3.04E-20	4.52
BP	Immune response	47	36.72	3.24E-18	4.24
BP	Immune system process	57	44.53	2.75E-17	3.24
BP	Innate immune response	32	25.00	1.31E-14	5.36
BP	Regulation of immune system process	39	30.47	8.77E-14	3.96
BP	Cell activation	32	25.00	1.29E-13	4.92



BP	Regulation of immune response	32	25.00	1.37E-13	4.91
BP	Response to stress	63	49.22	4.52E-13	2.40
BP	Positive regulation of immune system process	32	25.00	5.32E-13	4.66
BP	Immune effector process	28	21.88	1.45E-12	5.28
BP	Leukocyte activation	28	21.88	1.70E-12	5.25
BP	Positive regulation of immune response	26	20.31	1.03E-11	5.32
BP	Response to external stimulus	44	34.38	1.99E-11	2.97
BP	Inflammatory response	24	18.75	9.97E-11	5.27
BP	Adaptive immune response	20	15.63	1.21E-10	6.66
BP	Regulation of response to external stimulus	25	19.53	1.94E-10	4.85
BP	Leukocyte cell-cell adhesion	21	16.41	2.40E-10	5.98
BP	Humoral immune response	16	12.50	2.40E-10	9.03
BP	Biological adhesion	38	29.69	2.49E-10	3.12
BP	Activation of immune response	22	17.19	2.64E-10	5.60
BP	Positive regulation of response to stimulus	41	32.03	6.47E-10	2.83
BP	Cell adhesion	37	28.91	9.16E-10	3.05
BP	T cell aggregation	19	14.84	2.41E-09	5.96
BP	T cell activation	19	14.84	2.41E-09	5.96
BP	Lymphocyte aggregation	19	14.84	2.50E-09	5.95
BP	Response to other organism	25	19.53	3.16E-09	4.22
BP	Response to external biotic stimulus	25	19.53	3.16E-09	4.22
BP	Leukocyte aggregation	19	14.84	3.19E-09	5.86
BP	Lymphocyte activation	22	17.19	4.35E-09	4.79
BP	Single organism cell adhesion	24	18.75	4.91E-09	4.31
BP	Response to stimulus	91	71.09	5.03E-09	1.53
BP	Single organismal cell-cell adhesion	23	17.97	6.80E-09	4.44
BP	Myeloid leukocyte activation	12	9.38	7.46E-09	11.42
BP	Response to biotic stimulus	25	19.53	8.66E-09	4.01
BP	Leukocyte migration	17	13.28	9.60E-09	6.33
BP	Regulation of response to stimulus	54	42.19	1.93E-08	2.08

BP	Leukocyte mediated immunity	16	12.50	3.29E-08	6.29
BP	Positive regulation of leukocyte activation	15	11.72	4.30E-08	6.75
BP	Positive regulation of biological process	67	52.34	4.86E-08	1.77
BP	Acute inflammatory response	11	8.59	5.03E-08	11.15
BP	Positive regulation of cell activation	15	11.72	6.13E-08	6.56
BP	Regulation of response to stress	29	22.66	6.25E-08	3.16
BP	Response to organic substance	45	35.16	9.46E-08	2.23
BP	Lymphocyte mediated immunity Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	14	10.94	1.16E-07	6.87
BP	Complement activation	14	10.94	1.21E-07	6.85
BP	Regulation of defense response	10	7.81	1.44E-07	11.96
BP	Regulation of inflammatory response	20	15.63	2.72E-07	4.14
BP	Response to molecule of bacterial origin	14	10.94	3.53E-07	6.24
BP	Cell-cell adhesion	14	10.94	3.79E-07	6.20
BP	Regulation of cell activation	26	20.31	4.86E-07	3.13
BP	Regulation of immune effector process	17	13.28	4.93E-07	4.75
BP	Positive regulation of multicellular organismal process	14	10.94	5.21E-07	6.03
BP	Regulation of cytokine production	29	22.66	5.77E-07	2.84
BP	Positive regulation of cellular process	18	14.06	6.47E-07	4.37
BP	Regulation of acute inflammatory response	60	46.88	6.53E-07	1.77
BP	Positive regulation of lymphocyte activation	8	6.25	9.13E-07	15.13
BP	Protein activation cascade	13	10.16	9.21E-07	6.34
BP	Regulation of leukocyte activation	10	7.81	9.52E-07	9.58
BP	Cellular response to chemical stimulus	16	12.50	1.11E-06	4.78
BP	Regulation of lymphocyte activation Humoral immune response mediated by circulating immunoglobulin	41	32.03	1.13E-06	2.17
BP	Regulation of T cell activation	15	11.72	1.27E-06	5.11
BP	Cytokine production	9	7.03	1.29E-06	11.24
BP	Regulation of leukocyte cell-cell adhesion	13	10.16	1.42E-06	6.08
BP		18	14.06	2.20E-06	3.99
BP		13	10.16	2.28E-06	5.81

BP	Cell migration	25	19.53	2.39E-06	2.95
BP	Positive regulation of T cell activation	11	8.59	2.46E-06	7.33
BP	Regulation of cell adhesion	18	14.06	2.83E-06	3.92
BP	Regulation of biological process	101	78.91	3.08E-06	1.29
BP	Positive regulation of leukocyte cell-cell adhesion	11	8.59	3.43E-06	7.06
BP	Immunoglobulin mediated immune response	10	7.81	3.54E-06	8.18
BP	Regulation of complement activation	6	4.69	3.88E-06	24.69
BP	B cell mediated immunity	10	7.81	3.89E-06	8.09
BP	Leukocyte proliferation	12	9.38	4.88E-06	6.00
BP	Regulation of protein activation cascade	6	4.69	5.19E-06	23.32
BP	Cellular response to organic substance	35	27.34	5.31E-06	2.24
BP	Complement activation, classical pathway	8	6.25	6.53E-06	11.31
BP	Response to bacterium	16	12.50	6.96E-06	4.12
BP	Regulation of phagocytosis	7	5.47	7.83E-06	14.62
BP	Response to chemical	52	40.63	8.27E-06	1.77
BP	Cytokine-mediated signaling pathway	16	12.50	8.66E-06	4.04
BP	Regulation of multicellular organismal process	39	30.47	9.11E-06	2.05
BP	Regulation of tumor necrosis factor production	8	6.25	9.64E-06	10.66
BP	Cellular response to cytokine stimulus	18	14.06	9.77E-06	3.57
BP	Leukocyte chemotaxis	10	7.81	9.86E-06	7.21
BP	Regulation of proteolysis	18	14.06	1.01E-05	3.56
BP	Positive regulation of cell-cell adhesion	11	8.59	1.07E-05	6.21
BP	Cell proliferation	31	24.22	1.13E-05	2.33
BP	Regulation of tumor necrosis factor superfamily cytokine production	8	6.25	1.16E-05	10.37
BP	Cell chemotaxis	11	8.59	1.19E-05	6.13
BP	Response to cytokine	19	14.84	1.36E-05	3.32
BP	Tumor necrosis factor superfamily cytokine production	8	6.25	1.39E-05	10.09
BP	Positive regulation of phagocytosis	6	4.69	1.43E-05	19.08
BP	Proteolysis	29	22.66	1.51E-05	2.40
BP	Positive regulation of endocytosis	8	6.25	1.56E-05	9.91

BP	Biological regulation	103	80.47	1.58E-05	
CC	Extracellular region	71	55.47	5.35E-14	2.275480146
CC	Extracellular space	38	29.69	3.89E-13	3.899015832
CC	Extracellular region part	63	49.22	5.14E-13	2.406973673
CC	Membrane-bounded vesicle	57	44.53	5.98E-11	2.338761643
CC	Extracellular exosome	49	38.28	1.24E-10	2.58269921
CC	Extracellular vesicle	49	38.28	1.47E-10	2.569899993
CC	Extracellular organelle	49	38.28	1.49E-10	2.568990616
CC	Vesicle	57	44.53	2.85E-10	2.249671895
CC	Blood microparticle	11	8.59	8.49E-08	10.58304297
CC	Extracellular matrix component	10	7.81	1.96E-07	11.57520325
CC	Proteinaceous extracellular matrix	13	10.16	5.59E-06	5.335495349
CC	Extracellular matrix	15	11.72	1.25E-05	4.193281178
CC	Cell periphery	58	45.31	2.05E-05	1.634975437
CC	Basement membrane	7	5.47	4.25E-05	10.91724433
CC	Plasma membrane	55	42.97	1.06E-04	1.585089105
CC	Integral component of plasma membrane	25	19.53	1.89E-04	2.265483205
CC	Plasma membrane part	34	26.56	2.03E-04	1.911775505
CC	Intrinsic component of plasma membrane	25	19.53	3.41E-04	2.177580859
CC	Collagen trimer	6	4.69	6.15E-04	8.715447154
MF	Peptidase regulator activity	14	10.94	3.32E-09	9.260736677
MF	Serine-type endopeptidase activity	13	10.16	1.70E-07	7.418965517
MF	Serine-type peptidase activity	13	10.16	4.99E-07	6.708639032
MF	Serine hydrolase activity	13	10.16	5.59E-07	6.638021779
MF	Endopeptidase activity	16	12.50	1.34E-06	4.703866249
MF	Endopeptidase inhibitor activity	10	7.81	2.94E-06	8.363555291
MF	Endopeptidase regulator activity	10	7.81	3.89E-06	8.084770115
MF	Peptidase inhibitor activity	10	7.81	4.45E-06	7.9522329
MF	Enzyme regulator activity	21	16.41	1.19E-05	3.068316369
MF	Glycosaminoglycan binding	10	7.81	1.25E-05	6.996435676

MF	Molecular function regulator	25	19.53	1.95E-05	2.604256658
MF	Peptidase activity, acting on L-amino acid peptides	17	13.28	2.41E-05	3.49426505
MF	Peptidase activity	17	13.28	3.67E-05	3.375088206
MF	Receptor binding	25	19.53	4.08E-05	2.488472334
MF	Complement binding	4	3.13	3.23E-04	29.10517241
MF	Enzyme inhibitor activity	11	8.59	3.27E-04	4.115127205
MF	Transmembrane signaling receptor activity	21	16.41	5.07E-04	2.334639498
MF	Heparin binding	7	5.47	7.93E-04	6.366756466
MF	Transmembrane receptor activity	21	16.41	8.43E-04	2.24214461
MF	Molecular transducer activity	24	18.75	8.57E-04	2.078940887
MF	Receptor activity	24	18.75	8.57E-04	2.078940887
MF	Signaling receptor activity	21	16.41	1.36E-03	2.156699438
MF	Identical protein binding	20	15.63	2.00E-03	2.143238028
MF	Protein complex binding	14	10.94	2.14E-03	2.659741604
MF	Peptidase activator activity	4	3.13	2.18E-03	15.3185118
MF	Extracellular matrix structural constituent	5	3.91	2.38E-03	8.873528175
MF	Cysteine-type endopeptidase regulator activity involved in apoptotic process	4	3.13	2.72E-03	14.19764508
MF	Protein homodimerization activity	13	10.16	4.10E-03	2.591556448
MF	Sulfur compound binding	7	5.47	5.23E-03	4.372021607
MF	Protein dimerization activity	17	13.28	5.32E-03	2.132706599
MF	Cysteine-type endopeptidase activator activity involved in apoptotic process	3	2.34	5.85E-03	25.68103448
MF	Signal transducer activity	22	17.19	7.67E-03	1.815977859
MF	Peptidase activator activity involved in apoptotic process	3	2.34	8.07E-03	21.82887931
MF	Chemokine receptor binding	4	3.13	9.09E-03	9.239737274
MF	Carbohydrate binding	7	5.47	9.42E-03	3.858640282
MF	Collagen binding	4	3.13	9.49E-03	9.095366379
MF	Immunoglobulin binding	3	2.34	9.72E-03	19.84443574
MF	Hydrolase activity	28	21.88	1.49E-02	1.565395366
MF	Antigen binding	5	3.91	1.94E-02	4.850862069
MF	Enzyme activator activity	9	7.03	1.97E-02	2.651280888

MF	Cysteine-type endopeptidase activity	4	3.13	2.16E-02	6.690844233
MF	Cytokine receptor activity	4	3.13	2.36E-02	6.467816092
MF	Protein binding	85	66.41	2.52E-02	1.144706485
MF	Deoxycytidine deaminase activity	2	1.56	2.70E-02	72.76293103
MF	Serine-type endopeptidase inhibitor activity	4	3.13	2.86E-02	6.001066477
MF	CCR chemokine receptor binding	3	2.34	3.03E-02	10.91443966
MF	G-protein coupled receptor binding	6	4.69	3.13E-02	3.397490943
MF	Macromolecular complex binding	16	12.50	3.17E-02	1.782858953
MF	Cell adhesion molecule binding	8	6.25	3.83E-02	2.52539457
MF	Cytokine receptor binding	6	4.69	3.90E-02	3.198370595
MF	Chemokine activity	3	2.34	4.40E-02	8.909746657
MF	Protease binding	4	3.13	4.58E-02	4.975243148
MF	Retinal dehydrogenase activity	2	1.56	4.67E-02	41.57881773
KEGG	Pertussis	10	7.81	3.77E-08	13.352657
KEGG	Staphylococcus aureus infection	8	6.25	8.01E-07	14.83628556
KEGG	Complement and coagulation cascades	7	5.47	5.35E-05	10.15963033
KEGG	Focal adhesion	10	7.81	1.67E-04	4.861404249
KEGG	Systemic lupus erythematosus	8	6.25	3.19E-04	5.978801644
KEGG	Phagosome	8	6.25	7.11E-04	5.23633608
KEGG	ECM-receptor interaction	6	4.69	1.58E-03	6.906546727
KEGG	Tuberculosis	8	6.25	1.67E-03	4.526324408
KEGG	Prion diseases	4	3.13	4.03E-03	12.1387791
KEGG	Cytokine-cytokine receptor interaction	8	6.25	7.13E-03	3.483301827
KEGG	Chemokine signaling pathway	7	5.47	9.64E-03	3.768895122
KEGG	Rheumatoid arthritis	5	3.91	1.08E-02	5.690052701
KEGG	Cell adhesion molecules (CAMs)	6	4.69	1.26E-02	4.231475811
KEGG	Legionellosis	4	3.13	1.58E-02	7.41814278
KEGG	Regulation of actin cytoskeleton	7	5.47	1.71E-02	3.322343568
KEGG	Chagas disease (American trypanosomiasis)	5	3.91	1.89E-02	4.814659978
KEGG	PI3K-Akt signaling pathway	9	7.03	1.92E-02	2.612476371

KEGG	Amoebiasis	5	3.91	2.01E-02	4.723817337
KEGG	Influenza A	6	4.69	2.78E-02	3.453273363
KEGG	Leukocyte transendothelial migration	5	3.91	2.85E-02	4.243429133
KEGG	Natural killer cell mediated cytotoxicity	5	3.91	3.17E-02	4.104300309
KEGG	Primary immunodeficiency	3	2.34	4.37E-02	8.836317136
KEGG	Fc gamma R-mediated phagocytosis	4	3.13	4.94E-02	4.768806073

**Supplementary Table S7.** Functional enrichment of DEGs identified in mouse diabetic nephropathy

Category	GO Term/Pathway	Gene count	Gene Ratio (%)	P Value	Fold Enrichment
BP	Response to external stimulus	30	37.97	2.78E-09	3.27
BP	Response to stress	37	46.84	3.43E-09	2.64
BP	Defense response	22	27.85	1.33E-07	3.73
BP	Cellular response to cytokine stimulus	14	17.72	1.62E-07	6.49
BP	Response to cytokine	15	18.99	2.94E-07	5.59
BP	Response to nutrient levels	12	15.19	8.59E-07	7.01
BP	Response to extracellular stimulus	12	15.19	1.73E-06	6.52
BP	Response to other organism	17	21.52	1.74E-06	4.16
BP	Response to external biotic stimulus	17	21.52	1.76E-06	4.15
BP	Cellular response to interleukin-1	7	8.86	2.07E-06	18.31
BP	Response to organic substance	29	36.71	3.00E-06	2.45
BP	Response to biotic stimulus	17	21.52	3.50E-06	3.94
BP	Response to chemical	34	43.04	7.94E-06	2.08
BP	Response to interleukin-1	7	8.86	7.96E-06	14.53
BP	ERK1 and ERK2 cascade	9	11.39	8.92E-06	8.56
BP	Positive regulation of ERK1 and ERK2 cascade	8	10.13	9.54E-06	10.57
BP	Response to bacterium	13	16.46	1.08E-05	4.86
BP	Regulation of ERK1 and ERK2 cascade	9	11.39	1.17E-05	8.25
BP	Inflammatory response	12	15.19	2.51E-05	4.92
BP	Single-organism transport	28	35.44	2.60E-05	2.25
BP	Response to starvation	7	8.86	4.47E-05	10.72

BP	Cellular response to nutrient levels	7	8.86	5.46E-05	10.34
BP	Localization	39	49.37	6.99E-05	1.74
BP	Monocyte chemotaxis	5	6.33	7.37E-05	22.03
BP	Single-organism localization	28	35.44	7.87E-05	2.11
BP	Regulation of cell communication	25	31.65	9.39E-05	2.25
BP	Chemokine-mediated signaling pathway	5	6.33	1.03E-04	20.25
BP	Response to stimulus	52	65.82	1.03E-04	1.46
BP	Cellular response to external stimulus	8	10.13	1.03E-04	7.28
BP	Regulation of signaling	25	31.65	1.07E-04	2.24
BP	Signal transduction by p53 class mediator	6	7.59	1.09E-04	12.56
BP	Cellular response to organic substance	21	26.58	1.18E-04	2.51
BP	Regulation of signal transduction	23	29.11	1.26E-04	2.34
BP	Regulation of inflammatory response	8	10.13	1.29E-04	7.02
BP	Apoptotic process	19	24.05	1.31E-04	2.68
BP	Cellular response to extracellular stimulus	7	8.86	1.38E-04	8.75
BP	Defense response to other organism	11	13.92	1.39E-04	4.48
BP	Aging	8	10.13	1.63E-04	6.76
BP	Response to lipopolysaccharide	9	11.39	1.68E-04	5.65
BP	Negative regulation of endothelial cell apoptotic process	4	5.06	1.77E-04	35.88
BP	Regulation of response to external stimulus	12	15.19	1.91E-04	3.92
BP	Cell death	20	25.32	1.91E-04	2.51
BP	Transport	32	40.51	1.95E-04	1.86
BP	Positive regulation of phosphate metabolic process	14	17.72	2.04E-04	3.34
BP	Positive regulation of phosphorus metabolic process	14	17.72	2.04E-04	3.34
BP	Intrinsic apoptotic signaling pathway by p53 class mediator	5	6.33	2.04E-04	16.97
BP	Response to molecule of bacterial origin	9	11.39	2.13E-04	5.46
BP	Regulation of response to stimulus	27	34.18	2.19E-04	2.04
BP	Programmed cell death	19	24.05	2.46E-04	2.55
BP	Cytokine-mediated signaling pathway	8	10.13	2.87E-04	6.16
BP	Cellular response to tumor necrosis factor	6	7.59	2.99E-04	10.11



BP	Response to drug	9	11.39	3.57E-04	5.06
BP	Establishment of localization	32	40.51	3.61E-04	1.80
BP	Apoptotic signaling pathway	10	12.66	4.39E-04	4.32
BP	Response to lipid	13	16.46	4.40E-04	3.29
BP	Regulation of cell death	17	21.52	4.44E-04	2.64
BP	Myeloid leukocyte migration	6	7.59	4.51E-04	9.24
BP	Positive regulation of MAPK cascade	9	11.39	4.77E-04	4.84
BP	Response to tumor necrosis factor Intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	6	7.59	5.04E-04	9.02
BP	Regulation of defense response	4	5.06	5.16E-04	25.11
BP	Positive regulation of response to stimulus	10	12.66	5.67E-04	4.16
BP	Response to oxygen levels	18	22.78	5.92E-04	2.46
BP	Positive regulation of response to external stimulus	8	10.13	6.23E-04	5.42
BP	Positive regulation of protein phosphorylation	7	8.86	6.66E-04	6.51
BP	Regulation of endothelial cell apoptotic process	12	15.19	6.78E-04	3.37
BP	Ion transport	4	5.06	6.85E-04	22.83
BP	Cell migration	15	18.99	6.88E-04	2.78
BP	Negative regulation of epithelial cell apoptotic process	14	17.72	7.08E-04	2.93
BP	Cellular chemical homeostasis	4	5.06	7.31E-04	22.32
BP	Positive regulation of intracellular signal transduction	11	13.92	7.50E-04	3.63
BP	Cellular response to chemical stimulus	12	15.19	7.57E-04	3.33
BP	Positive regulation of defense response	22	27.85	7.65E-04	2.12
BP	Positive regulation of immune system process	7	8.86	7.91E-04	6.30
BP	Immune response	11	13.92	9.15E-04	3.53
BP	Single-organism metabolic process	14	17.72	9.18E-04	2.85
BP	Regulation of extrinsic apoptotic signaling pathway via death domain receptors	27	34.18	9.35E-04	1.86
BP	Endothelial cell apoptotic process	4	5.06	9.39E-04	20.50
BP	Response to wounding	4	5.06	9.39E-04	20.50
BP	Positive regulation of phosphorylation	9	11.39	9.50E-04	4.36
BP		12	15.19	9.81E-04	3.23

BP	Positive regulation of inflammatory response	5	6.33	9.85E-04	11.21
BP	Leukocyte chemotaxis	6	7.59	1.04E-03	7.69
BP	Response to hypoxia	7	8.86	1.13E-03	5.88
BP	Defense response to bacterium	7	8.86	1.17E-03	5.84
BP	Leukocyte migration	7	8.86	1.21E-03	5.80
BP	Response to endogenous stimulus	16	20.25	1.24E-03	2.50
BP	Regulation of MAPK cascade	10	12.66	1.26E-03	3.72
BP	Response to decreased oxygen levels	7	8.86	1.32E-03	5.71
BP	Positive regulation of monocyte chemotaxis	3	3.80	1.34E-03	53.82
BP	Regulation of phosphate metabolic process	16	20.25	1.45E-03	2.46
BP	Regulation of phosphorus metabolic process	16	20.25	1.45E-03	2.46
BP	MAPK cascade	10	12.66	1.48E-03	3.63
BP	Cellular response to starvation	5	6.33	1.48E-03	10.05
BP	Signal transduction by protein phosphorylation	10	12.66	1.54E-03	3.61
BP	Regulation of protein phosphorylation	14	17.72	1.58E-03	2.69
BP	Intracellular signal transduction	20	25.32	1.64E-03	2.11
BP	Regulation of apoptotic process	15	18.99	1.65E-03	2.54
BP	Positive regulation of biological process	34	43.04	1.67E-03	1.61
BP	Lymphocyte chemotaxis	4	5.06	1.69E-03	16.74
BP	Positive regulation of leukocyte migration	5	6.33	1.71E-03	9.66
BP	Positive regulation of cell communication	15	18.99	1.74E-03	2.53
BP	Negative regulation of cell communication	13	16.46	1.74E-03	2.81
BP	Multi-organism process	20	25.32	1.75E-03	2.10
BP	Negative regulation of signaling	13	16.46	1.79E-03	2.80
BP	Positive regulation of signal transduction	14	17.72	1.80E-03	2.65
BP	Positive regulation of signaling	15	18.99	1.81E-03	2.52
BP	Response to oxygen-containing compound	16	20.25	1.82E-03	2.41
BP	Regulation of programmed cell death	15	18.99	1.82E-03	2.51
BP	Cellular homeostasis	11	13.92	1.96E-03	3.19
BP	Cellular response to stress	16	20.25	2.04E-03	2.38

BP	Cell motility	14	17.72	2.06E-03	2.61
BP	Localization of cell	14	17.72	2.06E-03	2.61
BP	Negative regulation of signal transduction	12	15.19	2.06E-03	2.94
BP	Negative regulation of response to stimulus	14	17.72	2.09E-03	2.60
BP	Regulation of response to stress	13	16.46	2.17E-03	2.74
BP	Regulation of angiogenesis	6	7.59	2.26E-03	6.44
BP	Negative regulation of cell death	12	15.19	2.35E-03	2.89
BP	Cellular response to lipopolysaccharide	6	7.59	2.39E-03	6.36
BP	Regulation of intracellular signal transduction	15	18.99	2.54E-03	2.43
BP	Organic substance transport	20	25.32	2.61E-03	2.03
BP	Hormone transport	7	8.86	2.73E-03	4.94
BP	Cellular response to molecule of bacterial origin	6	7.59	2.76E-03	6.15
BP	Regulation of monocyte chemotaxis	3	3.80	2.76E-03	37.67
BP	Regulation of phosphorylation	14	17.72	3.00E-03	2.50
BP	Positive regulation of protein modification process	12	15.19	3.14E-03	2.79
BP	Regulation of epithelial cell apoptotic process	4	5.06	3.32E-03	13.22
BP	Extrinsic apoptotic signaling pathway via death domain receptors	4	5.06	3.32E-03	13.22
BP	Immune system process	19	24.05	3.42E-03	2.04
BP	Regulation of vasculature development	6	7.59	3.44E-03	5.84
BP	Negative regulation of apoptotic process	11	13.92	3.45E-03	2.95
BP	Response to temperature stimulus	5	6.33	3.54E-03	7.90
BP	Chemical homeostasis	12	15.19	3.59E-03	2.74
BP	Cell chemotaxis	6	7.59	3.62E-03	5.77
BP	Innate immune response	9	11.39	3.62E-03	3.52
BP	Cellular response to biotic stimulus	6	7.59	3.86E-03	5.69
BP	Negative regulation of programmed cell death	11	13.92	3.86E-03	2.90
BP	Response to glucocorticoid	5	6.33	3.95E-03	7.66
BP	Cellular metal ion homeostasis	8	10.13	4.16E-03	3.88
BP	Organ regeneration	4	5.06	4.26E-03	12.10
BP	Response to copper ion	3	3.80	4.30E-03	30.14

BP	Regulation of transport	16	20.25	4.35E-03	2.20
BP	Lymphocyte migration	4	5.06	4.40E-03	11.96
BP	Negative regulation of response to external stimulus	6	7.59	4.51E-03	5.48
BP	Positive regulation of metabolic process	22	27.85	4.59E-03	1.84
BP	Negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	3	3.80	4.65E-03	28.98
BP	Regulation of leukocyte migration	5	6.33	4.68E-03	7.30
BP	Response to hormone	10	12.66	4.73E-03	3.06
BP	Neutrophil chemotaxis	4	5.06	4.86E-03	11.55
BP	Cellular response to amino acid starvation	3	3.80	5.01E-03	27.90
BP	Positive regulation of leukocyte chemotaxis	4	5.06	5.01E-03	11.42
BP	Wound healing	7	8.86	5.18E-03	4.33
BP	Response to corticosteroid	5	6.33	5.60E-03	6.94
BP	Positive regulation of transport	11	13.92	5.68E-03	2.75
BP	Locomotion	14	17.72	6.07E-03	2.30
BP	Organic anion transport	6	7.59	6.14E-03	5.09
BP	Positive regulation of cellular process	30	37.97	6.24E-03	1.57
BP	Anion transport	7	8.86	6.30E-03	4.16
BP	Cellular response to endogenous stimulus	12	15.19	6.38E-03	2.53
BP	Response to heat	4	5.06	6.76E-03	10.25
BP	Cellular divalent inorganic cation homeostasis	7	8.86	7.11E-03	4.05
BP	Epithelial cell apoptotic process	4	5.06	7.34E-03	9.95
BP	Neutrophil migration	4	5.06	7.34E-03	9.95
BP	Angiogenesis	7	8.86	7.91E-03	3.96
BP	Cellular cation homeostasis	8	10.13	8.10E-03	3.42
BP	Cellular response to transforming growth factor beta stimulus	5	6.33	8.20E-03	6.22
BP	Small molecule metabolic process	15	18.99	8.25E-03	2.13
BP	Granulocyte chemotaxis	4	5.06	8.39E-03	9.48
BP	Metal ion homeostasis	8	10.13	8.39E-03	3.40
BP	Intrinsic apoptotic signaling pathway in response to DNA damage	4	5.06	8.60E-03	9.39
BP	Response to transforming growth factor beta	5	6.33	8.63E-03	6.13

BP	Female pregnancy	5	6.33	8.92E-03	6.07
BP	Cellular response to growth factor stimulus	8	10.13	9.00E-03	3.35
BP	Regulation of leukocyte chemotaxis	4	5.06	9.05E-03	9.22
BP	Regulation of immune system process	12	15.19	9.11E-03	2.41
BP	Divalent inorganic cation homeostasis	7	8.86	9.14E-03	3.84
BP	Cellular ion homeostasis	8	10.13	9.24E-03	3.34
BP	Regulation of protein modification process	14	17.72	9.61E-03	2.17
BP	Positive regulation of cell death	8	10.13	1.08E-02	3.24
BP	Response to growth factor	8	10.13	1.10E-02	3.22
BP	Positive regulation of cell proliferation	10	12.66	1.12E-02	2.66
BP	Granulocyte migration	4	5.06	1.15E-02	8.44
BP	Metal ion transport	9	11.39	1.17E-02	2.88
BP	Antibacterial humoral response	3	3.80	1.18E-02	17.94
BP	Interspecies interaction between organisms	8	10.13	1.25E-02	3.14
BP	Symbiosis, encompassing mutualism through parasitism	8	10.13	1.25E-02	3.14
BP	Regulation of calcium ion transport	5	6.33	1.29E-02	5.44
BP	Multi-multicellular organism process	5	6.33	1.33E-02	5.39
BP	Extrinsic apoptotic signaling pathway	5	6.33	1.35E-02	5.37
BP	Response to abiotic stimulus	11	13.92	1.38E-02	2.41
BP	Regulation of metal ion transport	6	7.59	1.39E-02	4.16
BP	Cell surface receptor signaling pathway	17	21.52	1.39E-02	1.87
BP	Antimicrobial humoral response	3	3.80	1.41E-02	16.38
BP	Negative regulation of endopeptidase activity	4	5.06	1.43E-02	7.79
BP	Positive regulation of cellular protein metabolic process	12	15.19	1.44E-02	2.26
BP	Regulation of hormone levels	7	8.86	1.48E-02	3.45
BP	Regulation of cellular protein metabolic process	17	21.52	1.50E-02	1.86
BP	Positive regulation of chemotaxis	4	5.06	1.52E-02	7.61
BP	Detoxification of copper ion	2	2.53	1.56E-02	125.57
BP	Stress response to copper ion	2	2.53	1.56E-02	125.57
BP	Movement of cell or subcellular component	14	17.72	1.58E-02	2.04

BP	Cation homeostasis	8	10.13	1.58E-02	3.00
BP	Positive regulation of angiogenesis	4	5.06	1.61E-02	7.44
BP	Response to organic cyclic compound	10	12.66	1.65E-02	2.50
BP	Protein phosphorylation	14	17.72	1.67E-02	2.02
BP	Positive regulation of ion transport	5	6.33	1.68E-02	5.02
BP	Inorganic ion homeostasis	8	10.13	1.78E-02	2.93
BP	Blood vessel morphogenesis	7	8.86	1.92E-02	3.26
BP	Positive regulation of apoptotic cell clearance	2	2.53	1.95E-02	100.46
BP	Response to toxic substance	4	5.06	1.98E-02	6.88
BP	DNA damage response, signal transduction by p53 class mediator	3	3.80	2.04E-02	13.45
BP	Response to gamma radiation	3	3.80	2.04E-02	13.45
BP	Monocarboxylic acid metabolic process	7	8.86	2.13E-02	3.18
BP	Response to ionizing radiation	4	5.06	2.16E-02	6.65
BP	Positive regulation of vasculature development	4	5.06	2.20E-02	6.61
BP	Defense response to Gram-negative bacterium	3	3.80	2.25E-02	12.77
BP	Cellular response to oxygen-containing compound	10	12.66	2.28E-02	2.36
BP	Positive regulation of protein metabolic process	12	15.19	2.28E-02	2.11
BP	Ion homeostasis	8	10.13	2.31E-02	2.78
BP	Intrinsic apoptotic signaling pathway	5	6.33	2.32E-02	4.55
BP	Stress response to metal ion	2	2.53	2.33E-02	83.71
BP	Detoxification of inorganic compound	2	2.53	2.33E-02	83.71
BP	Regulation of hydrolase activity	9	11.39	2.38E-02	2.52
BP	Cell communication	34	43.04	2.39E-02	1.37
BP	Positive regulation of calcium ion import	3	3.80	2.54E-02	11.96
BP	Regulation of extrinsic apoptotic signaling pathway	4	5.06	2.55E-02	6.24
BP	Cation transport	9	11.39	2.58E-02	2.48
BP	Regulation of ion transport	7	8.86	2.66E-02	3.02
BP	Cellular response to stimulus	38	48.10	2.68E-02	1.32
BP	Negative regulation of cellular process	26	32.91	2.71E-02	1.48
BP	Viral process	7	8.86	2.80E-02	2.98

BP	Cell activation	9	11.39	2.83E-02	2.44
BP	Cellular response to lipid	7	8.86	2.86E-02	2.97
BP	Multi-organism cellular process	7	8.86	2.90E-02	2.96
BP	Regulation of protein metabolic process	17	21.52	2.92E-02	1.72
BP	Positive regulation of cell migration	6	7.59	3.08E-02	3.38
BP	Signal transduction in response to DNA damage	3	3.80	3.17E-02	10.61
BP	Homeostatic process	13	16.46	3.30E-02	1.91
BP	Regulation of protein transport	8	10.13	3.38E-02	2.56
BP	Regulation of localization	17	21.52	3.40E-02	1.69
BP	Humoral immune response	4	5.06	3.43E-02	5.55
BP	Positive regulation of cell motility	6	7.59	3.48E-02	3.27
BP	Regulation of apoptotic cell clearance	2	2.53	3.48E-02	55.81
BP	Regulation of vasoconstriction	3	3.80	3.51E-02	10.05
BP	Negative regulation of biological process	27	34.18	3.58E-02	1.43
BP	Oxoacid metabolic process	8	10.13	3.65E-02	2.52
BP	Cellular response to drug	3	3.80	3.68E-02	9.78
BP	Positive regulation of cellular metabolic process	18	22.78	3.71E-02	1.63
BP	Cellular response to interferon-gamma	3	3.80	3.77E-02	9.66
BP	Positive regulation of cellular component movement	6	7.59	3.79E-02	3.19
BP	Positive regulation of locomotion	6	7.59	3.85E-02	3.18
BP	Positive regulation of heterotypic cell-cell adhesion	2	2.53	3.86E-02	50.23
BP	Blood vessel development	7	8.86	3.98E-02	2.74
BP	Positive regulation of macromolecule metabolic process	18	22.78	4.00E-02	1.62
BP	Regeneration	4	5.06	4.14E-02	5.15
BP	Signal transduction	31	39.24	4.20E-02	1.35
BP	Reproductive structure development	6	7.59	4.34E-02	3.08
BP	Regulation of chemotaxis	4	5.06	4.35E-02	5.05
BP	Negative regulation of angiogenesis	3	3.80	4.40E-02	8.86
BP	Reproductive system development	6	7.59	4.49E-02	3.04
BP	Cellular transition metal ion homeostasis	3	3.80	4.59E-02	8.66

BP	Cellular response to zinc ion	2	2.53	4.61E-02	41.86
BP	Establishment of blood-brain barrier	2	2.53	4.61E-02	41.86
BP	Regulation of establishment of protein localization	8	10.13	4.63E-02	2.39
BP	Negative regulation of blood vessel morphogenesis	3	3.80	4.69E-02	8.56
BP	Positive regulation of GTPase activity	4	5.06	4.79E-02	4.85
BP	Hormone secretion	5	6.33	4.79E-02	3.61
BP	Lipid metabolic process	10	12.66	4.80E-02	2.06
BP	Regulation of body fluid levels	5	6.33	4.84E-02	3.60
BP	Vasoconstriction	3	3.80	4.88E-02	8.37
BP	Phosphate-containing compound metabolic process	18	22.78	4.96E-02	1.58
BP	Vasculature development	7	8.86	4.96E-02	2.60
BP	Cell aging	3	3.80	4.98E-02	8.28
CC	Extracellular region	27	34.18	2.88E-10	4.09
CC	Extracellular space	25	31.65	4.09E-10	4.42
CC	Extracellular exosome	25	31.65	2.02E-05	2.48
CC	Integral component of plasma membrane	10	12.66	2.31E-02	2.36
MF	Chemokine activity	5	6.33	4.05E-05	25.60
MF	Chemokine receptor binding	5	6.33	9.78E-05	20.48
MF	Cytokine activity	7	8.86	3.19E-04	7.48
MF	Receptor binding	17	21.52	3.71E-04	2.67
MF	G-protein coupled receptor binding	7	8.86	7.44E-04	6.37
MF	Cytokine receptor binding	7	8.86	1.18E-03	5.83
MF	Secondary active transmembrane transporter activity	6	7.59	2.92E-03	6.07
MF	Active transmembrane transporter activity	7	8.86	4.17E-03	4.53
MF	Drug transporter activity	3	3.80	5.22E-03	27.30
MF	Enzyme inhibitor activity	7	8.86	5.40E-03	4.29
MF	Glycosaminoglycan binding	5	6.33	7.95E-03	6.27
MF	Peptidase inhibitor activity	5	6.33	1.13E-02	5.66
MF	CCR chemokine receptor binding	3	3.80	1.18E-02	17.98
MF	Transporter activity	12	15.19	1.19E-02	2.32



MF	Peptidase regulator activity	5	6.33	1.85E-02	4.88
MF	Symporter activity	4	5.06	2.02E-02	6.83
MF	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	3.80	2.13E-02	13.16
MF	Heparin binding	4	5.06	2.28E-02	6.51
MF	Substrate-specific transporter activity	10	12.66	2.67E-02	2.30
MF	Organic anion transmembrane transporter activity	3	3.80	4.29E-02	8.99
MF	Transmembrane transporter activity	9	11.39	4.36E-02	2.24
MF	Anion transmembrane transporter activity	4	5.06	4.36E-02	5.04
MF	Endopeptidase inhibitor activity	4	5.06	4.82E-02	4.84
KEGG	Chemokine signaling pathway	5	6.33	9.27E-03	5.79
KEGG	TNF signaling pathway	4	5.06	1.10E-02	8.33
KEGG	Complement and coagulation cascades	3	3.80	4.15E-02	8.96