

Supplementary Material

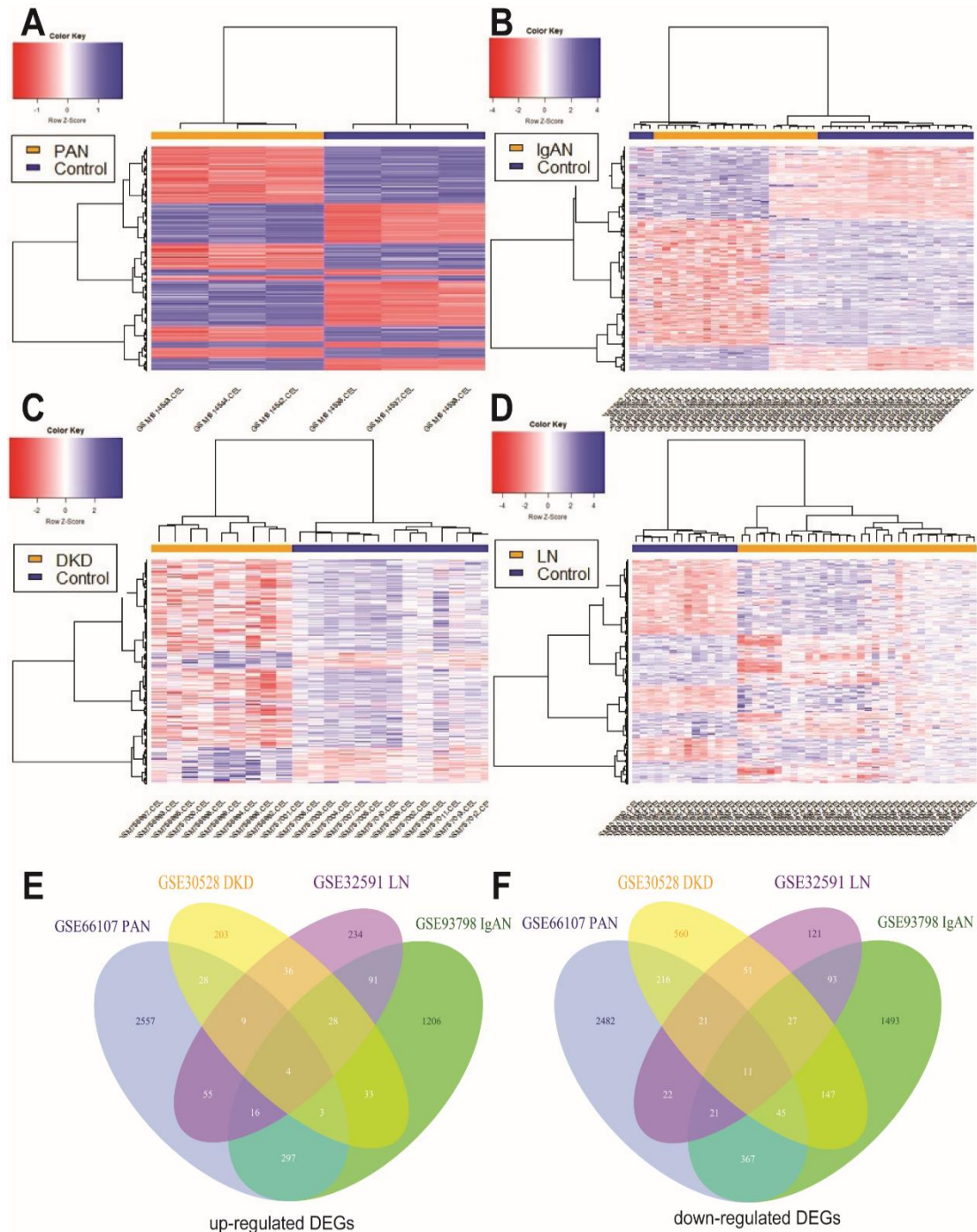
Weighted Gene Correlation Network Analysis (WGCNA) Detected Loss of MAGI2 Promotes Chronic Kidney Disease (CKD) by Podocyte Damage

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Supplementary Figure and legends

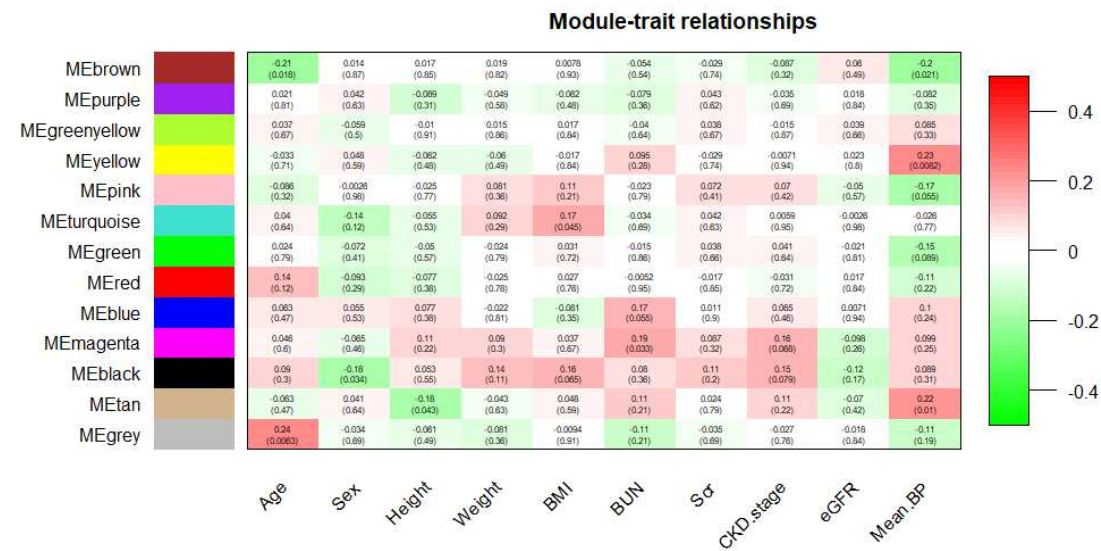
Supplementary Figure S1. Heatmaps and Venn plots of differentially expressed genes (DEGs) in various datasets.



Supplementary Figure S1. Heatmaps and Venn plots of differentially expressed genes (DEGs) in various datasets. (A) Heatmap of 6154 DEGs in injured podocytes induced by puromycin aminonucleoside (PAN). (B) Heatmap of 3882 DEGs in IgA nephropathy (IgAN). (C) Heatmap of 1422 DEGs in diabetic kidney disease (DKD). (D) Heatmap

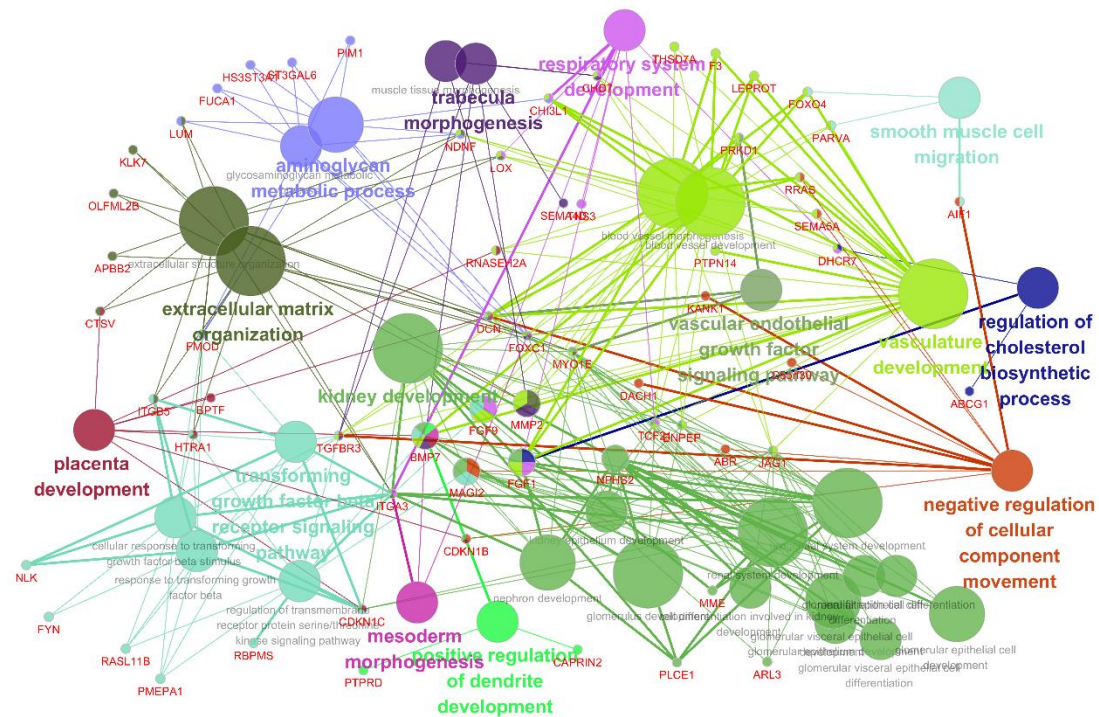
of 840 DEGs in lupus nephritis (LN). Each row represents a single gene, and each column represents a sample. The intensity of the color scheme is scaled to expression values, which are Z-score standardized per gene. The gradual color change from green to red represents the changing process from up-regulation to down-regulation. (E) Venn plot of all up-regulated DEGs. (F) Venn plot of all down-regulated DEGs.

Supplementary Figure S2. Correlation between modules and traits.



Supplementary Figure S2. Associations of modules and traits. The upper number in each cell refers to the correlation efficient of the given module in the trait, and the lower one is the corresponding p-value

Supplementary Figure S3. Gene ontology (GO) and KEGG analyses



Supplementary Figure S3. Gene ontology (GO) and KEGG analyses. Cytoscape functionally network visualization of BP terms and KEGG pathways, based on genes of the green module and created by the Cytoscape software v3.5.1 combined with ClueGO plug-in (v2.3.5)

Supplementary Materials

Supplementary Table S1. Top 50 upregulated and 50 downregulated genes after puromycin aminonucleoside (PAN) treatment in podocytes

Supplementary Table S2. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with IgA nephropathy (IgAN)

Supplementary Table S3. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with diabetic kidney disease (DKD)

Supplementary Table S4. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with lupus nephritis (LN)

Supplementary Table S5. Complete lists of genes for various modules

Supplementary Table S6. Gene ontology (GO) biological process (BP) terms of differentially expressed genes in each module (top 30 terms per module)

Supplementary Table S7. KEGG pathway terms of genes in each module

Supplementary Table S1. Top 50 upregulated and 50 downregulated genes after puromycin aminonucleoside (PAN) treatment in podocytes

upregulated genes				downregulated genes			
Gene	logFC	AveExpr	adj.P.Val	Gene	logFC	AveExpr	adj.P.Val
DDK1	5.569	9.938	3.93E-09	DTL	-6.735	8.047	8.93E-10
HIST1H2BG	4.741	8.558	7.38E-09	RRM2	-6.706	8.517	4.53E-09
C11orf96	4.613	8.036	5.66E-09	CCNE2	-6.366	8.411	4.53E-09
HIST1H1C	4.596	10.879	9.75E-09	ANLN	-6.339	8.140	1.25E-08
BLNK	4.311	7.669	2.59E-08	CEP55	-5.768	7.597	3.85E-08
HIST2H2AA3	4.296	12.045	4.53E-09	TOP2A	-5.730	7.504	4.42E-09
DOCK8	4.188	5.981	1.37E-08	VCAM1	-5.651	8.551	1.82E-09
LRRTM2	4.167	6.915	8.12E-08	BRIP1	-5.519	6.896	1.25E-07
FAM46C	3.962	6.672	3.74E-08	KIAA0101	-5.464	10.406	2.07E-09
HIST1H2BD	3.913	11.240	5.90E-09	CDK1	-5.454	8.885	3.25E-08
HIST2H2BE	3.850	9.415	2.59E-08	PBK	-5.409	7.185	6.21E-08
PCDH10	3.776	7.025	7.25E-09	ZNF367	-5.368	7.195	1.11E-08
AKR1B10	3.660	8.496	1.19E-07	APOBEC3B	-5.337	7.588	1.01E-08
GREB1	3.625	7.285	2.79E-08	ADAMTS3	-5.306	10.587	2.62E-09
CEACAM1	3.501	9.820	9.30E-09	SHCBP1	-5.298	6.799	1.06E-08
PTPN22	3.461	8.334	5.88E-08	DLGAP5	-5.278	6.365	3.04E-09
HES2	3.428	9.151	1.37E-08	FANCI	-5.217	8.479	2.26E-08
TMEM35	3.414	7.969	3.32E-08	NUSAP1	-5.119	8.677	9.91E-09
HIST1H2AE	3.384	7.806	6.63E-09	ASPM	-5.086	6.816	7.23E-09
FAM43A	3.378	7.439	2.72E-07	PRC1	-5.077	8.048	1.19E-07
PCDH9	3.366	8.633	1.18E-08	LMNB1	-5.067	8.478	4.51E-08
C4orf47	3.365	7.151	9.57E-08	NCAPG	-4.978	6.749	1.49E-08
GLS2	3.287	9.350	7.14E-08	CENPK	-4.959	8.275	2.16E-08
CES2	3.272	11.074	2.94E-08	MCM5	-4.920	8.069	2.13E-08
AF131215.8	3.247	8.104	8.05E-09	MCM6	-4.907	9.646	4.53E-09
FLCN	3.241	9.483	2.79E-08	CDT1	-4.897	7.301	2.27E-09
ASPA	3.226	8.892	1.76E-08	FUT9	-4.862	6.597	8.01E-09
RP11-196G18.24	3.198	7.699	1.05E-08	PRR11	-4.855	9.347	7.38E-09
DSEL	3.190	9.579	1.35E-08	POLE2	-4.824	7.765	2.24E-07
LINC00324	3.189	8.347	9.30E-09	RAD51AP1	-4.779	7.701	1.37E-08
EPPK1	3.151	9.587	8.01E-09	UHRF1	-4.775	9.014	7.38E-09
OSR2	3.110	7.549	7.25E-09	TTK	-4.767	6.456	1.39E-08
TNFSF15	3.096	7.757	5.98E-08	NCAPG2	-4.728	7.639	1.86E-08
SOX7	3.043	9.226	2.74E-08	TMEM163	-4.691	6.708	9.75E-09
CABYR	2.950	9.066	1.82E-07	PRIM1	-4.683	7.588	6.54E-08
DCLK1	2.932	7.997	2.43E-08	DEPDC1	-4.613	6.480	1.11E-08

HIST1H2BC	2.900	7.855	1.49E-08	GINS2	-4.578	8.192	6.10E-08
PODXL	2.898	9.190	9.91E-09	NEK2	-4.556	6.258	1.71E-08
SIAE	2.852	10.101	1.46E-08	CDC6	-4.544	7.371	3.33E-08
HSD17B3	2.827	6.652	8.04E-06	PRTFDC1	-4.515	7.878	9.30E-09
SIDT2	2.824	11.157	1.12E-08	TUBB2B	-4.510	8.492	1.37E-08
PLAC8	2.819	7.989	3.01E-08	GJB2	-4.496	6.329	1.18E-07
SLC2A5	2.816	6.469	4.59E-06	TNFRSF11B	-4.448	9.574	4.86E-08
TIPARP-AS1	2.814	6.616	7.17E-08	RBL1	-4.434	6.997	7.93E-07
SH3BP4	2.805	7.722	2.30E-07	TMEM97	-4.375	9.124	7.38E-09
ERV3-2	2.783	7.859	1.71E-08	BUB1	-4.368	6.619	3.04E-09
FAM196A	2.773	5.997	3.80E-07	HMMR	-4.354	7.316	9.30E-09
FAM84A	2.754	6.874	1.28E-07	NUF2	-4.329	6.097	3.05E-08
LAMP3	2.747	7.060	2.53E-06	LOC100506558	-4.309	8.659	2.43E-08
HIST1H3A	2.737	7.429	2.39E-08	GPR137C	-4.304	6.145	8.05E-09

Supplementary Table S2. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with IgA nephropathy (IgAN)

upregulated genes				downregulated genes			
Gene	logFC	AveExpr	adj.P.Val	Gene	logFC	AveExpr	adj.P.Val
TLN1	3.833	8.534	2.58E-04	FOS	-6.045	8.813	1.62E-15
HIST1H4E	3.509	7.510	7.41E-04	FOSB	-6.003	8.812	3.76E-18
GTF2I	3.447	6.982	2.30E-04	APOLD1	-4.087	9.411	2.64E-11
HIST1H4H	3.404	6.581	2.10E-04	CXCL2	-3.682	7.097	1.22E-09
PET100	3.290	7.843	2.37E-04	CD69	-3.349	6.815	7.11E-09
ZC3HAV1L	3.104	5.146	2.39E-04	EGR3	-3.250	7.708	4.18E-06
CD46	3.034	9.483	1.09E-04	NR4A2	-3.189	6.008	8.44E-11
LENG8	2.985	7.541	2.89E-05	SLC7A9	-3.174	7.893	3.87E-08
PFN1	2.954	8.389	2.88E-04	MAFF	-3.165	9.271	8.18E-09
AEBP1	2.950	9.412	4.15E-07	CEBPD	-3.102	9.656	7.91E-12
PNRC2	2.922	6.775	6.27E-04	RASD1	-3.067	8.580	2.86E-10
TMED2	2.831	8.420	2.23E-04	BRE-AS1	-2.985	6.254	4.02E-11
CALR	2.772	7.714	1.93E-04	TIPARP	-2.944	9.928	1.53E-09
ACTN4	2.753	8.824	8.25E-05	NR4A1	-2.853	7.764	2.13E-09
SP1	2.745	7.050	2.72E-04	CYP27B1	-2.851	5.859	6.27E-13
TAF9B	2.704	7.121	2.03E-04	AREG	-2.817	6.275	1.47E-05
RAMP2	2.631	8.637	9.53E-06	EGR1	-2.730	8.316	6.42E-12
ZNF460	2.598	6.105	3.79E-04	IGFBP1	-2.700	6.554	2.25E-05
HNRNPH1	2.523	6.508	4.70E-04	GDF15	-2.664	6.128	5.49E-12
CTNNB1	2.523	7.830	2.69E-04	SLC17A3	-2.560	7.659	5.11E-08
SLFN5	2.521	6.057	7.91E-06	FRMD4B	-2.510	7.374	7.33E-05
SLC9A3R2	2.519	6.289	1.61E-04	TNFAIP3	-2.500	8.206	7.10E-08
TAF15	2.460	9.103	3.23E-04	ERP27	-2.490	8.373	2.10E-07
CD74	2.452	9.427	1.94E-04	LINC00520	-2.477	6.359	1.10E-04
MALAT1	2.415	10.637	2.69E-04	HBEGF	-2.462	8.974	1.78E-07
HIPK3	2.355	7.500	3.04E-04	DIO1	-2.460	7.385	7.30E-07
C8orf4	2.308	10.109	2.64E-10	UQCRC1	-2.438	8.740	6.83E-05
ZNF33A	2.307	8.257	1.15E-04	CYP8B1	-2.427	6.087	8.68E-08
EPB41L2	2.293	7.156	2.23E-07	NFKBIZ	-2.424	8.292	5.06E-10
ITGB3	2.288	8.306	2.47E-04	DUSP1	-2.416	7.761	2.60E-17
BCL2L1	2.277	6.942	4.22E-04	RNF128	-2.402	6.939	1.39E-05
YWHAE	2.259	9.940	1.18E-03	SLC19A2	-2.365	7.109	3.22E-11
CSF1R	2.253	7.192	8.30E-10	RNF186	-2.338	6.742	1.29E-14
UGT1A6	2.253	5.248	1.79E-03	SPRY2	-2.333	8.351	1.66E-08
DDX3X	2.251	8.186	1.25E-03	HPD	-2.320	8.160	1.31E-07
AFF1	2.243	7.057	5.74E-04	NFIL3	-2.318	8.226	3.22E-11

LILRB2	2.234	6.327	4.18E-06	LINC00473	-2.286	5.308	2.76E-09
DDX17	2.220	8.901	5.60E-04	GPR160	-2.271	7.090	9.03E-05
PPFIBP1	2.199	8.626	8.20E-05	ACMSD	-2.257	7.498	1.52E-08
CBX5	2.197	8.911	1.78E-04	RPL22L1	-2.249	8.326	2.49E-04
ECM1	2.125	9.073	4.46E-08	LINC01003	-2.245	6.895	3.14E-04
APLNR	2.103	10.080	1.71E-06	FAM220A	-2.240	8.474	4.68E-04
P2RY1	2.099	6.003	5.39E-05	PLS1	-2.205	6.177	2.59E-06
ITGB8	2.094	9.253	2.80E-04	NCOA7	-2.205	9.709	2.81E-05
CDV3	2.083	9.013	4.01E-04	ECM2	-2.197	8.124	1.17E-03
IGFBP5	2.073	10.258	2.23E-05	UHRF2	-2.196	8.076	1.71E-03
ITGA6	2.067	8.740	1.78E-04	ZBTB21	-2.194	7.624	4.30E-05
UHMK1	2.058	8.580	6.63E-04	SOWAHC	-2.189	8.426	2.10E-08
FMNL3	2.057	6.507	9.09E-07	ARHGEF26-AS1	-2.187	6.045	2.50E-05
NFASC	2.056	9.366	7.74E-05	HSPB8	-2.186	10.173	1.65E-06

Supplementary Table S3. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with diabetic kidney disease (DKD)

upregulated genes				downregulated genes			
Gene	logFC	AveExpr	adj.P.Val	Gene	logFC	AveExpr	adj.P.Val
IGHA2	3.809	7.622	1.15E-02	CHI3L1	-3.586	9.600	1.10E-05
MIR8071-2	3.334	8.914	3.33E-02	TNNT2	-3.241	8.870	4.98E-06
IGLC1	3.186	9.325	4.57E-02	LPL	-3.199	9.551	3.13E-05
LOC101928916	2.825	8.943	2.51E-04	NDNF	-3.185	11.775	3.30E-04
IGK	2.716	10.232	2.33E-02	LRRC2	-3.166	7.985	6.48E-06
C3	2.678	8.121	1.84E-03	MAGI2	-3.137	9.899	1.30E-06
COL1A2	2.591	6.174	2.02E-04	PLCE1	-3.101	10.530	6.76E-06
JCHAIN	2.545	6.240	5.74E-03	PCOLCE2	-3.036	11.711	4.69E-04
LUM	2.375	8.712	6.81E-04	PRKAR2B	-3.016	9.228	7.43E-07
SERPINA3	2.325	6.633	1.43E-04	LOX	-2.974	7.447	8.57E-10
CXCL6	2.268	5.620	3.95E-03	NPHS1	-2.961	7.975	3.90E-07
CD52	2.232	5.668	1.29E-03	B3GALT2	-2.942	6.898	9.40E-07
COL6A3	2.208	6.839	5.44E-04	NFASC	-2.941	10.662	8.19E-05
C1QB	2.206	6.259	2.20E-05	PTPRO	-2.836	11.318	7.00E-04
ADH1B	2.180	7.149	4.07E-04	DPP6	-2.824	8.817	1.71E-06
MMP7	2.086	8.877	3.33E-03	TPPP3	-2.783	9.043	6.82E-05
C7	2.008	9.849	4.73E-04	MYLK3	-2.725	7.985	3.51E-04
THBS2	2.006	6.716	7.45E-04	SPOCK1	-2.724	10.901	1.16E-04
CD163	1.975	6.560	8.51E-05	SEMA3G	-2.706	10.310	5.35E-05
WFDC2	1.920	8.684	3.02E-03	NEBL	-2.698	11.971	2.10E-04
MOXD1	1.902	6.713	3.16E-04	PDPN	-2.697	8.633	1.78E-06
EVI2A	1.840	7.552	1.05E-03	FRY	-2.677	10.328	4.07E-05
GZMA	1.804	5.845	4.26E-03	PTGDS	-2.649	12.601	1.93E-04
OLFM4	1.793	5.156	1.76E-02	KLK6	-2.590	8.545	4.73E-06
ARL4C	1.774	7.160	2.64E-03	IGF1	-2.579	7.748	9.61E-04
TRBC1	1.772	6.927	8.87E-04	CA10	-2.545	7.846	2.28E-07
VTCN1	1.763	6.850	3.98E-04	TCF21	-2.542	9.826	1.39E-05
SERPINE2	1.762	9.882	2.30E-05	FGF1	-2.519	12.232	1.98E-03
TRAF3IP3	1.756	6.644	1.23E-02	NES	-2.516	10.998	1.13E-04
CCL5	1.719	6.484	5.47E-03	SYNPO	-2.509	10.363	9.15E-06
CFB	1.718	7.371	9.53E-04	F5	-2.496	8.673	4.88E-06
LTB	1.707	7.855	1.18E-02	SRGAP2C	-2.477	8.289	1.93E-05
LCK	1.690	5.949	9.07E-05	LGALS8	-2.438	9.986	8.57E-10
MARCKS	1.677	7.371	3.98E-03	SEMA5A	-2.435	9.480	9.55E-07
ALOX5	1.674	7.876	2.88E-02	IL13RA2	-2.408	8.945	1.00E-03
TAC1	1.671	5.578	4.80E-02	ATP10A	-2.391	9.322	1.82E-04

CD53	1.671	8.224	9.01E-04	DPYSL3	-2.367	8.407	2.99E-07
ABCA8	1.649	7.056	7.71E-03	MGAT5	-2.353	12.022	2.83E-05
CD3D	1.649	7.060	1.26E-03	CDC14A	-2.346	7.883	1.87E-05
LAPTM5	1.642	7.864	1.62E-02	EHD3	-2.337	9.154	1.14E-03
LEF1	1.610	6.368	8.87E-04	ZNF185	-2.337	9.913	4.66E-07
HGF	1.605	5.869	4.48E-03	APOD	-2.333	7.515	4.16E-04
IRF8	1.581	8.434	1.75E-03	WT1	-2.316	11.677	3.00E-04
VSIG4	1.573	6.761	1.60E-04	USP46	-2.298	8.261	2.29E-07
FN1	1.541	9.226	7.47E-05	ST3GAL6	-2.286	9.595	1.20E-05
LYZ	1.529	10.026	1.60E-02	GPRC5A	-2.278	9.577	1.87E-05
BLNK	1.508	6.964	3.13E-03	THSD7A	-2.266	10.019	6.76E-06
EVI2B	1.494	7.064	1.52E-02	NPHS2	-2.262	13.066	9.30E-03
CCR2	1.480	5.784	9.77E-03	ZDHHC6	-2.256	11.943	1.42E-05

Supplementary Table S4. Top 50 upregulated and 50 downregulated genes differently expressed in glomeruli of patients with lupus nephritis (LN)

upregulated genes				downregulated genes			
Gene	logFC	AveExpr	adj.P.Val	Gene	logFC	AveExpr	adj.P.Val
IFI44L	3.853	9.730	2.24E-12	UMOD	-2.897	9.800	8.50E-05
C1QA	3.541	8.170	2.15E-10	DEFB1	-2.390	9.269	1.09E-04
MS4A4A	3.329	7.060	6.75E-10	PCK1	-2.382	9.521	3.50E-05
TYROBP	3.297	8.863	3.15E-11	ALB	-2.226	7.516	1.54E-04
MX1	3.227	11.214	1.48E-12	TNNC1	-2.165	8.063	1.43E-04
IFI44	3.168	9.787	2.47E-16	MYL9	-2.144	10.867	1.22E-05
RSAD2	3.128	9.172	6.82E-09	CXCL14	-2.121	9.459	2.07E-04
C1QB	3.071	8.097	8.76E-08	HPD	-2.058	8.182	5.57E-04
CD163	2.957	8.619	2.01E-07	SIK1	-1.868	6.916	1.52E-07
CD53	2.935	9.874	3.15E-11	C1orf21	-1.648	7.966	4.82E-09
IFI6	2.881	11.694	1.23E-10	GSTA1	-1.645	9.657	1.09E-03
MX2	2.838	9.306	1.29E-11	SLC17A3	-1.635	8.860	3.99E-03
HERC6	2.794	9.047	9.13E-12	CYP27B1	-1.559	7.153	5.19E-05
ITGB2	2.748	8.177	1.99E-09	PLG	-1.546	8.822	2.27E-03
ISG15	2.709	10.338	3.71E-06	KNG1	-1.535	8.358	2.16E-03
OAS3	2.703	8.942	8.27E-11	TXNRD2	-1.528	8.883	6.05E-05
ISG20	2.690	8.366	1.48E-12	ALDH1L1	-1.491	7.984	2.39E-04
LYZ	2.646	8.830	2.32E-07	PDK4	-1.480	7.007	7.39E-06
HCK	2.639	8.391	6.56E-10	USP46	-1.457	8.545	4.14E-09
OAS2	2.591	8.294	1.38E-11	FXSD2	-1.414	8.927	7.39E-04
MS4A6A	2.518	8.583	3.64E-10	AOC1	-1.379	8.169	1.59E-02
FCER1G	2.506	9.321	9.17E-10	PRODH2	-1.372	9.593	3.20E-04
OAS1	2.503	10.075	5.87E-10	EPHX2	-1.349	8.713	1.19E-04
COL1A2	2.438	8.294	5.93E-08	CHI3L1	-1.344	11.184	3.39E-05
HERC5	2.415	8.066	1.16E-10	SDC1	-1.317	7.246	1.82E-04
C3AR1	2.400	8.713	1.59E-09	SLC27A2	-1.312	8.381	2.59E-03
XAF1	2.398	8.750	3.50E-11	SLC13A3	-1.310	8.694	1.51E-03
FCN1	2.378	8.469	1.42E-06	PHYHIP	-1.308	8.725	8.63E-05
PTPRC	2.319	7.321	4.64E-08	CRIP2	-1.307	9.369	2.14E-04
VSIG4	2.299	8.268	1.06E-06	G6PC	-1.292	4.964	1.94E-04
CD14	2.288	9.161	5.87E-10	DPYS	-1.279	8.091	1.80E-02
CD36	2.287	6.900	9.85E-06	CRYAA	-1.278	7.049	2.42E-05
CX3CR1	2.279	7.518	5.44E-08	USP11	-1.270	9.369	1.28E-07
LYN	2.245	8.287	1.16E-10	FABP1	-1.251	6.767	9.72E-04
IL10RA	2.239	7.598	2.74E-09	RASL11B	-1.246	10.691	3.16E-05
COL6A3	2.229	7.226	1.84E-06	DPEP1	-1.239	8.442	1.24E-04

IFIH1	2.188	7.896	2.83E-11	FGFR4	-1.235	6.982	3.77E-05
NETO2	2.179	7.566	1.92E-07	APOD	-1.227	9.847	2.85E-02
IFI27	2.166	11.761	1.48E-12	AZGP1	-1.219	6.771	1.37E-02
RNASE6	2.165	7.553	1.65E-07	TNNT2	-1.218	11.239	2.20E-04
LY96	2.156	6.717	3.04E-11	FAH	-1.190	7.597	1.72E-04
LCP1	2.087	8.813	4.75E-07	RHOBTB2	-1.180	7.842	9.29E-07
HCLS1	2.081	9.838	5.13E-10	PDE4B	-1.180	7.992	3.12E-07
IFIT1	2.044	10.861	8.01E-09	SERPINA5	-1.179	8.661	2.29E-02
EVI2B	2.032	6.571	9.14E-08	SLC22A6	-1.177	7.578	7.33E-03
CTSS	2.017	7.065	2.15E-10	SEMA3B	-1.172	9.872	1.39E-04
PYCARD	2.013	7.621	7.59E-11	CRISPLD2	-1.162	7.479	5.46E-03
CSTA	2.007	6.348	3.14E-10	PKP4	-1.153	6.818	1.23E-10
POSTN	2.001	11.112	8.82E-07	KRT18	-1.129	9.397	8.13E-03

Supplementary Table S5. Complete lists of genes for various modules

Genes in the turquoise module
PAPOLA NDUFV1 AKR7A2 ETFB 7-Mar BCKDHA PRKCZ OGFOD2 HAT1 AZIN1 COASY SOCS5 ARFIP1 UBE2B ILVBL MPST SENP6 TTC37 EFR3A TUFM CDC27 APEH KLHL9 MCAT PFKL CYC1 COQ4 ECSIT TRAPPC6A SLC25A44 PMM1 EBP RNF219 DR1 ACAA1 C21orf33 ZGPAT USP33 FBXW2 RPAP3 CAND1 SMARCA1 ASL HSD17B8 CPNE3 MRPL12 LIN7C CDC73 SH3GLB1 MTDH IDH3B ROGDI LONP1 SEC24B 10-Sep PSIP1 ECI1 SIGIRR GPS1 CCS IPO7 U2SURP SCAMP1 PPP2CA ACOT7 RECQL VPS26A GNAI3 PRKAR1A DPYD MLST8 RANBP2 SLC39A6 ZC3H14 EIF4E SEC23A ABI1 DUS1L ANGEL1 ACADVL EPS15 ARMCX1 ERGIC2 PSMD12 INSIG2 ANKRD12 AGFG1 RAB11FIP2 NFYB CLASP2 TANK RAB5A PCYT2 PPP2R5C CREBL2 AGGF1 MBNL1 PSMA3 SERINC1 MSRB2 ASF1A ATMIN SEC24D CHMP2B RHOQ NPLOC4 PPP1R2 C1GALT1C1 PLLP TMED10 ROBO1 PLS3 MTHFD1 AK055910 ACTR3 TXNDC9 ATP6AP2 RP2 UQCRC1 DNAJC10 SLC25A32 ACTR10 RASSF7 RASA1 CUL3 PSMD6 CUL9 PPP2R3C ATF1 PDHX KRR1 YES1 CD320 UBE3A URGCP CDKN2AIP PPM1B SRSF10 FBXO11 IARS ASCC3 OXR1 RNF14 C5orf22 KCTD3 DNAJB6 FAM208B STAG1 TRAPPC8 UBE2K PPP1CB MYL6B GTPBP4 PMVK ARF4 RAD23B RSF1 ACTL6A FKBP4 RNF11 USP1 ERBB2 GMFB HECA CLCN7 CNIH1 PMS1 DUS2 GRINA RAB21 GOLPH3 UHRF1BP1L C3orf18 LYPLA1 BNIP2 TRAM1 SGMS1 STRAP PEX16 SELT NFE2L2 SLC25A11 MIS12 TAB2 NEK4 ZNF302 DPY19L4 NPTN ME3 PRDX2 MTG1 STAM USP16 RNMTL1 GBAS NXPE3 FAM175B AKAP11 SLBP TRIP12 SPG20 FGGY PPP3CA RAB1A NIPA2 CPD APPL2 TOR1AIP1 TXN2 PHTF1 FAM208A RNF111 PDIA6 RFNG CDK17 OSTM1 MTM1 HPRT1 UBL3 NIPBL MMADHC MIIP ATP2B1 PRKACB PGM1 VAMP7 MAN2C1 UBR5 DEGS1 NBEA MGMT C12orf5 PDS5A CMAS ACSL3 PTDSS2 HMOX2 BIRC2 PPP6R2 FNDC3A IQGAP1 MINPP1 RAB2A SUMO1 ATOX1 INTS6 HS2ST1 TCEAL1 F2R RAB28 DDX18 WWTR1 DHX29 ANAPC10 NEMF PGAP2 RDX SMARCE1 MALT1 CHD9 NAE1 CEP57 GPATCH3 LRRC40 RB1 EXOC2 ACAP2 EXOC1 PTPLAD1 NAP1L3 ROCK1 DNTTIP2 PDS5B KIF2A MTMR2 NUP205 PANX1 NBN MPIRAD21 DOLPP1 SNTA1 ZEB2 NEK7 C12orf29 DCAF6 PALLD HNRNPR DHX40 GSS TRAPPC13 GGPS1 ATP2C1 TPD52 ATG9A TWSG1 CSNK1A1 STRN3 WWP1 PRRG1 UBQLN2 TRMT11 RCHY1 PDXK RPRD1A ANP32E RAP1GDS1 SRBD1 RPF1 MFSD1 NAP1L2 ATG5 SMAP1 UTP3 REV3L VMP1 PRPF4B SUPT6H HNRNPD NCBP2 BCOR CAST DLG3 QKI FANCL TEX261 ELMO2 GBE1 PUM2 KRCC1 NUP98 SNAPC3 CNBP DNAJA1 SUZ12 MRPS12 IFRD2 CSE1L TMOD3 CCNC ARMC8 SUPT7L ATP11B TMEM41B RECK ARL2 BTN2A1 TOLLIP WDR73 CBX3 RMI1 SUPV3L1 ZC3H7A KLHDC3 RHOT1 ADNP VEZF1 DMXL2 IARS2 PBX3 H2AFV CHD1 WTAP CASP7 MFN1 GULP1 RBBP7 KAT5 RCBTB1 UFL1 LMBRD1 MRPS30 VWA9 B3GALNT1 ACP2 DEK CCT8 WBP5 EDEM3 SDCBP SUB1 CLIP1 GCC2 SMC5 IPO4 SSR1 G3BP2 HSD17B10 TASP1 BECN1 GPALPP1 NUP37 DDB1 MPHOSPH10 NDC1 ZZZ3 ARPC2 PTP4A2 NRAS TMEM135 POLE3 MARK3 USO1 CIR1 DHRS12 KIF16B BRIX1 ZFAND5 TMEM177 ATXN1 ZNF638 PERP WDR6 TXNRD1 PCF11 PRMT3 SYNCRIP WAC WDR91 TTC31 COMMD10 STAM2 TCEB1 DESI2 SPR EIF4A2 CNIH4 EIF3A RBPJ FAM172A ZNF337 UNC50 LDB1 ENOPH1 SGCE TBL1XR1 ZNF692 DIMT1 SSBP1 TNKS2 POT1 SERP1 SUN1 LMBR1L UFM1 DNAJC11 NUP153 RFC1 ZNF23 GTDC1 AGPS ERBB2IP RIOK2

PAXIP1 STAU2 SRP54 ZNF217 NR1H3 CASD1 RAC1 KIAA0368 RRN3 TP53BP2
ANKRD27 ZNHIT6 STRADA SSBP2 C19orf53 ZNF184 ATAD2B BAG2 XRCC5 POGK
ARMCX2 SOCS2 ACTR2 CRKL ATP10D EMC2 ZCCHC10 SEC11A ZMYM4 UBA2
HNRNPM CTBP2 UBE2D3 HNRNPA3 SEC24A CHMP5 SMC6 CLPX TRPC1 PSMD1
UTP11L NGRN ASUN TCTA MICU2 GNB1 CNOT8 AASDHPPT MED6 SMC4 MAPRE2
CLTC ARHGAP5 ATP5G3 GSK3A CBR4 NUCB2 TSPYL5 MAPK9 PAK4 LARP4 RNF38
NDST2 IMPAD1 TLR3 GNL2 TIMM44 YWHAZ GPN3 ATG13 HBP1 CAAP1 KAT8 CAP1
LOC100129361 DERL1 ZBTB11 TMA16 FZD6 KCTD12 ABHD3 TMEM50B ZNF112 GAA
MTPAP TMEM33 ARF1 BZW2 AP1S1 PCBP1 ZNF143 CCDC59 FAM179B KHSRP
ARMCX5 ARHGEF5 PSMD7 CDC23 PCIF1 KIAA0196 GAPVD1 ANXA5 BAG5 DDX46
CALM1 CAP2 MAT2B NOL8 MPDZ GNAI1 EIF3B RLF MOK UBE2D2 PPP4R1 KIAA0907
PGK1 HMG20A LGR4 NPC1 EXTL2 TDRD7 STX6 CD59 ARL6IP1 RRAS2 ALG13
EIF4EBP1 MORC3 NMD3 SURF1 ALCAMN4BP2L2 RIT1 ZCCHC2 MBIP ZNF277 MAPK1
SPATA2L DCUN1D4 METAP1 NAA50 MATN3 PCM1 SCRIN3 PPP1R3D IDH3A ARCN1
HDGFRP3 PSME3 CREB1 GNA12 LRIG1 KLHL2 DDHD2 CTTN PIK3R4 ITSN1 CAPRIN1
NSF GNE PDE6D MED23 USP9X HSPA14 MTMR6 NUDT9 ORC3 HNRNPA2B1 MATR3
RPAP1 MYOF PKN2 FTSJ3 ATP6V0C PIGA ATG12 UPF3B LRP12 MED4 NAA35
KIAA0430 GSPT2 PTEN HUS1 SPAG9 PPP1CC UROS DSC2 PAPSS1 RYK RRAGB PROS1
RNF4 RBM34 SS18 IFT57 TMEM194A ZMPSTE24 SPARC COMMD8 UBE4A UGCG
FBXO28 SRSF3 PGAP1 AGTPBP1 RBM38 GPI SMPD1 STAMBP TRIM5 GIT1 RABGEF1
PELO IK ZNF146 SNX16 FXR1 SNX7 HIPK1 ZNF24 ZDHHC17 MANSC1 AZI2 SLC35A1
CTSC TMEM57 TOM1 KDM7A PLSCR4 TMEM53 ALG6 TRIM26 FAHD2A RBM28 CREM
TRDMT1 CIB2 HLTF ZCCHC8 CERS2 MLEC DARS PIGV SETD2 SUCLA2 PNN HADHA
EXOSC9 DAZAP2 LXN BNIP1 TUBGCP3 CACTIN PDCD2 ZNF529 ZNF83 ZNF14 TIA1
PLOD2 CRYZL1 METTL18 ZNF204P ABI2 TMEM159 PDCD6 FSTL1 COG5 WDTC1 DUT
SLC1A5 NUP107 TRAF3 DNAJC1 BTA1F1 REEP5 EPM2AIP1 IFT81 MAN1A2 USF2
YTHDC2 TERF1 ZNF274 PIGN RMDN1 GJA1 CENPQ MFF PSMG1 SNX5 XRCC4 CPEB3
KLF10 FBL PEX2 ANKMY2 SLC25A6 CCT4 DHX15 LEPROTL1 PAFAH2 HIGD1A IPO5
CAMSAP2 C1orf27 SPATS2L OSMR FURIN PRPS1 HAUS3 ZNF415 SIRT3 GYG1 UBA6
DNAJC8 ZNF767P DHRS7 MLLT3 CDK19 MFN2 CSTF2T PLEKHA5 SACM1L KATNBL1
ACIN1 ZNF180 RTEL1 GNL3 CBLL1 NUPL1 ZMYM2 TXNL1 PPIF CREB3L2 RALA
PIEZO2 ASPH MAGEH1 GGCT SIRT1 CLK1 GCLM NUP54 C2CD3 NMT2 SPRY1
TMEM8A NEK1 WDR3 PPARG UBR7 CEBPZ CAPN1 ELOVL5 SLC38A2 ZNF200 PSPC1
PDCD6IP TPBG APPL1 TMPO RTN4 SERPINB1 MTF2 TBCE AKAP10 RNF7 PHLPP2
CTNNAL1 GRSF1 VIM CCNH IL10RB PAK1IP1 BPGM CEP135 ID4 PSD3 FRMD4B
ST6GAL1 ORC5 NOL7 RAB22A ASNSD1 MAPK14 MID2 ZFAND1 SLC30A5 KDSR
SCML1 MRE11A FAM131A DNAJA2 ADK CDK16 RAB36 DICER1 SGPP1 TSPYL1
SLC2A10 PCNP PSMD11 METTL3 OPN3 POLR2H ATXN3 ANGPT1 PLA2G16 IRAK3
BTN2A2 SUCO VCPKMT ZNF75D KIF22 RPA1 RPS6 C6orf106 DMTN RAD50 YKT6 ZYX
AFF1 IMP3 ZNF468 RIPK2 ERC2 MSANTD2 ELF2 SPATA5L1 CKAP4 ERI2 DDX42 UAP1
PA2G4 EFTUD1 DIEXF USP7 FRZB TLK1 NSL1 UGGT1 VAPA GOLGA1 IKBKAP PSMA5
C11orf58 ANKRD49 TTLL5 SDPR ZNF384 B4GALT4 PBRM1 MCM9 SEPHS1 SSR3 CHUK
TTF2 DNAJC13 GPBP1L1 HNRNPL TP53BP1 COMMD9 TEFM CETN3 KAL1 MSH2
MTERF3 FXR2 ETV5 SAFB2 AKAP12 TFPI WSB2 TLR4 WDR37 PARP8 CHCHD3 OBSL1

RMDN3 GSE1 TRPS1 ETAA1 EMC8 ANKRD10 SSH3 WDR41 RNGTT NIPSNAP3B YIPF3 VPS54 AMFR LIPT1 CYP1B1 C3orf14 PPIC CRNKL1 MPP3 OPA1 ZNF516 FIG4 BBS9 MFSD5 TTC30A RABGGTB YEATS4 ZNF688 ETV7 8-Mar CMAHP MRPL2 SRSF4 NBR1 SRRM2 NACC2 ULK2 RFC4 PDE8A ENO1 GNS TIPRL MAGED2 IRS1 PAXBP1 CPOX ARHGAP29 R3HDM1 NPAT ZNF330 PGS1 TFB1M TULP4 HDAC4 TMEM168 ZNF571 PTPN2 OAZ2 AFAP1 PCSK5 OSBPL9 ALG9 SRSF8 ATP2B4 CEP162 FBXO17 C21orf59 SHROOM2 TM9SF1 DLGAP4 LSM5 TMEM106C VPS8 MRPL18 PDCL MLH1 RAPGEF2 PNISR TM9SF3 POLB FGD6 PALB2 PRKRA CHST2 SRP19 MGAT4B RAP2A FAM149B1 SMARCC1 BC033323 GLCE ASCC1 SNRNP25 PAPOLG TNFRSF10B HIST2H2BE TSC22D1 OGFOD1 TRIM32 ZC3H13 POLR3F ATG4A CUL5 KIAA0100 SIGMAR1 EIF4A3 CEP63 RALGAPB SYBU PTPN1 SH2B2 RBM12B METTL17 STX2 LRRC42 NCAPD3 THUMPD2 PTC3 CCBL2 PLAGL2 IGFBP7 NEK9 TUG1 KDM6A COMMD4 NET1 DMPK MBOAT7 CRIPT NT5C2 GUCY1A3 SIKE1 CNOT4 HSPB11 HFE AHSA1 ERAP1 GSAP SYNRG MRPS28 MAP1A SLC25A20 OLA1 CASZ1 RPP14 VAMP4 SPTAN1 AMMECR1 PTPLA PRDX1 REC8 STS HOXC6 RNH1 KIF3A SEMA3C ARNTL FAM134A XBP1 ZKSCAN7 PKNX1 UBA1 TP53BP1 MAP3K12 ING1 PSMD5 IKZF4 ANKHD1 CAMTA1 ATRNL1 ZFAND3 PRKX HMGXB3 NUBPL ZW10 TAF5 GBF1 SNX3 FOCAD WNT5A CCNL1 MAP3K5 UBE4B BANK1 TCF7L2 GPATCH2 AGL ZKSCAN1 SENP5 ZNF292 BACH2 BLCAP KDM4B SLC7A1 THNSL2 CMC4 ZBTB14 KRBOX4 GTF2H1 RPP30 GNLS1 HPS1 PPME1 LARP4B MOSPD2 WIP1 APAF1 SMG7 ZNF26 CDO1 KRT10 HERC2 PPA1 ECM2 ECD GPX7 MAP2 ZNF195 YIPF1 GATA3 TUSC2 CCRN4L CCDC92 RBM39 SOS1 ZNF84 BHLHB9 RNF44 SCPEP1 MGP JRKL ROBO4 ING2 DROSHA PRPF3 ELOVL6 GART PPP1R3C ACP6 UBXN8 GINS3 FGF2 P4HA1 ZNF202 HSPH1 SLC35E1 CLK2 ABCF3 HTR2B LTBP1 PFDN4 RFK IL1RL1 SRRD ZBTB43 SIN3B FLOT1 MCMBP EFCAB14 GOSR2 PLCB4 TLE1 TRO RFX7 SPATA7 HNRNPUL1 HSPBAP1 ITGB3BP RANBP10 ZBTB16 CRT3 MPZL2 DYRK1A RPGRIP1L ADCY3 POLG2 IFT52 ZFP36L1 ARIH2 DGKA ZNF197 PANK3

Genes in the blue module

TSR3 PSMB6 EFEMP2 C19orf60 NOSIP BAD NME3 PUF60 DDX49 VPS51 CUEDC2 KARS EDF1 FBXL15 NDUFA13 APRT FAM50A ASMTL PGLS SSNA1 EXOSC4 MRPL23 NAA10 DDRGK1 NDUFS7 SEC24C SARS KEAP1 LSM7 TSPAN4 VPS16 EIF3G BRMS1 DNAJB2 COG4 RBM10 ATRAID POMT1 FARSA SERPINB6 PSMB3 IFT20 EIF2B5 HRAS BIN3 SNRPD2 NARF PQBP1 RHOC MIF PES1 CSRP1 RARRES2 IMPDH2 WDR45 IRGQ BCL7C S100A6 CLDN5 PFDN5 PIEZO1 SAP30BP FAM160B2 BCAT2 KIAA0232 STX10 HIFX MEPCE CLTB AP2M1 NADSYN1 SDHAF1 COX7A1 POLR2L ATP6AP1 NTHL1 MRPS34 RNF187 MAN1B1 WRAP73 TNIP1 CHMP2A MBD3 PSMC3 PIH1D1 GPN1 CTSD ETHE1 UNC45A LEPRE1 PLEKHM2 CD2BP2 SPSB3 COPS3 COPZ1 LSM2 RRP8 LMNA FBXW4 WDR13 ING4 CYBA SAC3D1 C9orf16 FBXL12 CCT7 SPINT2 BST2 GOLGA5 FDXR DDX23 ARPC4 IP6K2 HAUS7 TRAPPC2L GID8 EDEM2 EMC9 DDX54 PFN1 SSR4 CCDC22 ZNF593 LIMS2 TCF7L1 RHOBTB2 QSOX1 TFPT RBM6 TXNRD2 OSGEP C8orf33 TCF12 KDM1A TMEM115 C9orf3 ARRB1 PSMG2 GUSB PPP4C TUBA1A MGAT1 RABEP2 NUDC ADCK2 PCNT TEO2 SLC38A10 RER1 MORC2 KATNB1 FZD2 TMEM127 ST5 SF1 INTS5 RANGAP1 PHYHIP POGZ SP3 PSMD8 SUPT5H IRAK1 NPR1 FAM134C EHD1 SLTM XPOT CRIP2 INTS1 PI4KB PTRF FGFR4 CBY1

SLC10A3 S100A13 TCEA2 NR1H2 HMCES HSBP1 RPL3 RABAC1 ATG2A ZSWIM8
POMGNT1 TFIP11 APOOL MUL1 EVL LAMTOR2 PRCC SQRDL AP5S1 USP11
AP001062.7 SAFB DCTN5 BAG1 TNFRSF14 MAP3K4 FAM65A REV1 HGS TESK1
IGFBP2 MUM1 UPP1 SEMA3B RCN2 9-Sep RABGGTA VGLL4 PSMB1 TRADD ARFGAP1
EIF2AK3 MAD1L1 FAM13B CD63 PNKP TEAD4 ARHGDIA SSR2 COTL1 SNRNP35
MFSD10 HOXD1 CCHCR1 S100A4 TMEM131 PTPN7 AVEN PPP2R5B GCN1L1 EXOC7
HYOU1 DOHH PBXIP1 ATP5I WDR83OS CSTB EDEM1 ELAVL1 EXT2 RALB MCM5
RSBN1 SMARCD2 AP5M1 NCK1 LMCD1 XPO7 DCUN1D2 URI1 CDC42EP2 ADIPOR1
PSMD4 PARP1 FLNC FOXJ2 SGSH TACC2 AK1 MRPS17 DLD HCCS ROM1 EIF2B4
SART1 STAT5A TCF25 ZFPL1 CTBS FKBP3 TCEB2 ITPR1 PPM1A MAP3K3 SS18L2
TRIM37 7-Sep MTRR AACS CDK9 PSMA1 DOLK SCP2 SNX17 EIF4G1 RNF40 IL11RA
B3GNT1 TRIM33 TBC1D1 EMC3 LRRC47 NAA15 ACVR1 ERLIN1 SEC61G EML3
METTL22 ERCC1 PUM1 ARPC5L TIMM10B BRD9 C6orf47 ZNF227 MGAT2 R3HCC1
MYO1C B9D1 NFKBIE CLN3 EHD4 PLXNB2 GPHN ERI3 GAS1 AEBP1 TUBA4A APOL2
DAAM1 DAPK3 SLC5A3 FUBP3 HIF1AN DFNA5 ACTR6 C2CD5 ETNK1 CPSF4 IGFBP4
SF3A3 HERPUD1 ABT1 PLOD3 PGM3 RNF138 JTB MSL2 MAP4K3 C1orf174 DAPK1
HMG20B FBXW11 WDFY3 MICAL1 POLG PVR ZPR1 ANAPC15 CSNK2A2 SFXN3
TMEM251 ZNF268 ATG4B TUBB BCS1L SPTLC1 ATP5F1 PEX3 KLK6 RAPGEF3 ARNT
PRPF39 KDM5A GNA11 SRRM1 5-Mar PSMA2 NOTCH2 UCHL5 SLC36A1 EHBP1 VASH1
LAMP2 TCEB3 YIF1A CNM3 CRIP1 SLC25A46 ATF5 DLG5 LAMTOR3 NARS GCC1
DDX5 DHX30 GPN2 PAICS TRAM2 IGFBP6 TSPAN15 SOS2 STIP1 EXOSC7 EDRF1 UBA5
PLA2G4C GOLGB1 SLC20A1 CEP164 KLHDC10 HMGB2 AKIP1 BAP1 TRIM2 NCOA4
DGCR14 ZDHHC13 SECISBP2L PIP5K1C PSEN1 WDYHV1 YY1AP1 POLA2 ZNF512B
PHKB KBTBD4 LRRC6 DESI1 KLHL21 UBE2G2 MRFAP1L1 MPPE1 STX17 ABCC1
TMEM165 MMP28 RRBP1 GOLGA3 ZSCAN18 HMGXB4 HSDL2 NUP85 TP53TG1 EIF1B
CEBPA TSNAX OAT COPS2 RNF34 ZNF12 FAF1 PHF10 NSD1 TMCC1 C2orf42 ANKRD40
EMC1 MAN2A1 SPIN1 MRPL3 YTHDF1 MRPL39 LGALS1 CDC37L1 AKAP9 SAMD14
DMXL1 G6PC3 ZNF500 DET1 XPO1 NNT GABARAPL1 DRG1 ACTR1A ELP4 C10orf76
NME4 MXI1 OSBPL1A AGA NEK3 AUP1 PPID MPRIP ECHDC1 C12orf4 NT5DC2
ARHGEF11 PELI2 PRPF38B CDK5RAP1 GPC1 MED27 DOPEY1 LRRFIP2 VPS13A TKT
BCL6 ZNF32 COPZ2 CCDC93 SIRT7 PRR14 NKRF ABCF2 M6PR RPLP2 SIK3 DNAJB12
MICAL2 ATF7IP2 LPCAT3 PIN1 RRP1B ATG14 AES EGLN1 AK057978 APOO SLC25A3
PDZD2 CEPT1 KIAA1109 KLHL24 GSTP1 BFSP1 TNFRSF1A NAT9 TBC1D22A TBC1D9B
FBXL5 AGAP1 NDUFAB1 CD248 SMARCB1 LZTR1 C9orf78 EIF3H NOP10 LTBR
DYNC1H1 EML2 RHOB DTYMK PINLYP TUBB4B ACVR2A AGRN SZRD1 RPP38
SLC46A3 FAM174B ZNF764 NDUFC1 ERMP1 ST3GAL1 ZNF140 CDKL3 GNG12 DHX8
UBTF ZC3H7B YAP1 CSAD TGS1 LANCL2 UBXN1 MAPKAP1 SETD6 PEX10 CLK4
MFAP1 LRRC20 PYROXD1 ZFPM2 TP73-AS1 VPS52 RRAGC PIK3CD WBSCR22 ACLY
JUP ADCY9 RBM23 IGFLR1 TBCD COL7A1 UBIAD1 TUBG1 PVRL3 WDR5B DTNA
POLR3B DNAJC6 UBAP1 ISCU VDAC3 CHP1 RPL22 ALDH18A1 ETFDH TSR1 STAT3
LRBA IFRD1 HIGD2A RITA1 TIMM22 PDE10A ERAL1 RAB5C TSSC1 RPA3 COX10
GALK2 PHLDA1 VASP HOMER1 SVIL C1orf123 CACYBP ANO10 IPP ZNF43 OXCT1
TBC1D8B NARS2 PIP5K1B NBAS MCUR1 PPP2R1A H1F0 LRRFIP1 DMTF1 SLC4A7
CANT1 NASP PIGZ TRIM45 SEPP1 ANAPC13 ORA12 FBXO2 STX16 PTBP2 KLF6 UEVLD

CARD10 OFD1 ATP5S EIF2AK1 SLC11A2 CYB561D2 TPP1 NDUFB3 TTC19 ETV1 ABL1
MFSD9 MBD2 ZSCAN32 CYP7B1 AAGAB MSH3 SMAD5 GUF1 RPL15 CASK ZNF394
FADS2 TCFL5 ZC2HC1A ARSJ CLASP1 NDUFA1 STK24 MED20 ZNF175 PSMD3 PEG3
SMARCA4 MNS1 FTO SLC35C2 NOP14 RBMX2 CYP39A1 LINC00312 KIAA0895 MIEF1
C11orf57 PPP1R11 ZNF419 CYR61 OSGIN2 NKTR AMPD3 CNIH3 AVL9 LAMA2 ZFP36L2
LINC01278 MGEA5 OTUD4 HIST1H1C RNMT LIMD1 WASF1 PARG FMO2 UPF3A
APH1B

Genes in the brown module

**GLYAT HGD SLC22A6 SLC13A3 MSRA AZGP1 PBLD KHK BHMT2 APOM PIPOX
KCNJ15 SLC47A1 CRYL1 DAO DPYS XPNPEP2 PEPD SLC7A9 PCK2 CRYM DIO1
LRRC19 ALDH8A1 ALDH6A1 ADH6 AGMAT SLC27A2 AKR7A3 UPB1 HRSP12 FMO1
ACAT1 HADH DDAH1 CUBN HAO2 SLC13A1 DDC IMPA2 ACADL SUGCT GJB1 BBOX1
USH1C GBA3 PLG SUCLG1 TMEM176A PXMP2 HPD ECHDC3 TLN2 SLC3A1 FABP1
SULT1C2 ABAT BHMT ANPEP SLC17A1 ALDH1L1 CES2 COLEC11 GIPC2 ACSM3 AFM
AKR1A1 SH3GL2 ALDOB IL17RB SLC10A2 SLC1A1 NQO2 KCNK5 DPEP1 ACO1 SDC1
AKR1C3 GATM PRODH2 QPRT TM4SF5 GOT1 GSTA1 PCCALGALS2 SLC34A1 SLC22A5
TMEM176B FBP1 RNF186 SLCO4C1 PPARGC1A ANK3 GLDC ACSM5 SLC17A3 AOC1
HDHD3 AHCY MT1G QDPR SH3YL1 CRYAA GGH SLC37A4 SLC39A4 RAB11FIP3
ABHD6 LPPR1 ACOX2 TPMT SLC16A4 DNPH1 TST SEPHS2 EPHX2 CAMK2N1 GLS
CDH16 GRAMD1C MACROD1 GPX3 FMO4 ESRRG COQ9 NOX4 SLC7A7 PCBP2 PCK1
ACADM G6PC KL MAOA CLDN10 TRHDE ARG2 MAOB ECI2 UGT2A3 ENOSF1 EPCAM
KCNJ16 MT1F MSRB1 WLS ASB13 CFI EMX2 HRG WWC1 ACO2 CYB5A CLMN HIBCH
FHIT HMGCL LACTB2 ARSE HSD17B14 PDZK1IP1 ALDH1B1 ANK2 POLDIP2 DIP2C
ALDH1A1 ALB AMT PLS1 VDR IDH1 MCCC1 KMO CRYZ MAL GLUD1 TACO1
SERPINA5 KCNJ1 CTH NFS1 PHGDH SLC6A8 BIN1 RBKS DNAJC12 KNG1 TOX3
ADCK3 PNPO GPR137B SLC22A4 CRAT F2RL1 ACP5 PRR5 RAB29 SLC22A18 ALPL
PTPN3 OR7E14P DEFB1 NR1H4 CLDN8 MDH1 DLEU1 DDX10 2-Mar GRB14 NINL
LRPPRC COBLL1 ACOX1 GALE METTL1 SLC12A6 DERA CAT SSX2IP EPB41L1 IDH2
LLGL2 EPB41L3 ELF4 HSPA4L MAN1C1 PDK2 MTCH2 DHTKD1 CXCL14 KIF13B
MRPS35 FHOD3 CALB1 CNNM2 C2orf47 NECAP2 MUC1 ACSL1 IGSF3 MPC2 MPC1
SELENBP1 ATP6V0E2 RETSAT MYOM2 HLF C14orf105 MTRF1 AOX1 FSCN1 MIPEP
PRUNE2 PPA2 DHRS11 SETD3 CHN1 PTER MICB GALNT14 C11orf71 NIT1 AFG3L2
PPP2R3A TUBB6 FAM149A ABLIM1 EGF MCCC2 IFITM2 UMOD PRDX3 KLC1 DSE
ALDH9A1 TFAP2A HK1 TOR1B IPO13 SLC1A4 MAP7D1 FNBP1 PGRMC1 PAK2 PLD1
HADHB TYRP1 DUSP22 LRRC8D CCNG1 AUTS2 SLCO3A1 PLP2 PCBD1 RRAGD
WFDC2 ASB9 RSU1 NDEL1 NUDT4 REEP4 ATP1A1 TRA2B CLU TBCB FAM13A PARM1
PAPPA2 FANCC PLEKHO1 ACPP BCHE ERBB3 FDX1 SHC1 ATP5A1 S100A2 CDR2L
SUCLG2 TIMP1 CCNB1IP1 LPCAT1 CASC1 GNB2 UBR4 RAB31 DENND5A METTL21B
CTSA SATB2 TEX30 ZHX3 PHF21A UBE2I MAF POLD3 ASNS TPP2 SFRP1 FEZ1 C4orf27
HEATR1 RHBDF2 ARSB HIST1H2BD GRPEL1 SRD5A1 GLB1L MPP1 PIAS3 C1orf216
MFAP3 ARHGAP24 CUL2 NUDT13 TMEM39B PANK2 PPP1R16B FAM102A DCK SNIP1
MAP1S LETMD1 LETM1 PCNA WASF2 ARHGEF10 UBE2D4 SH3BP5 NFIB NKIRAS2
PXDN IMPDH1 GLUD2 CD81 TFDP2 TAF11 DBI SRSF7 UQCRB FTH1 DEPTOR FAM184A
DYNLT1 ANP32B CA2 SNRPF CASP8AP2 DRAP1 GPR124 TRAF5 MRPL34 TNIP2 CISD1**

RAI14 KYNU FANCE PPFIBP2 RFTN1 MOCS1 TOR4A GNAI2 TPK1 RASGRP2 PDGFA
TRAFD1 TMEM43 TRIOBP CD9 C6orf62 UIMC1 HMOX1 KIT CSGALNACT2 MCAM
ENO2 TRIM24 COX15 PSMD13 SLC35D1 JOSD1 NDUFA2 C5 SHANK2 ENDOD1
C21orf62 PDLIM7 SLC12A7 CYP2C9 LDLRAD4 NEDD4L MBD4 SLC16A7 LYRM1
UBE3C ARHGEF10L MTHFD2 UQCRC2 WDR12 PDGFRB RHOBTB1 NAP1L1 OGFRL1
GYS1 ZBED8 TAGLN2 PEX5 OLFML1 NXT1 DDB2 DHRS1 MAN1A1 ELF1 WHSC1 PIBF1
ORMDL2 AQP2 CCT6B RBCK1 GLUL PIK3C3 TBPL1 FECH SNRPB ADH5 ARHGEF9
VWA1 GAR1 FKBP14 KANK2 FBXO5 HDAC1 NRCAM GALNT2 VSTM4 PTTG1IP ZNF7
MYO6 DZIP3 NCSTN TFB2M FAM57A ADRM1 MRPL57 MUS81 TTC27 CYP3A5
HNRNPA0 LOC728392 ICK PLAG1 TWIST1 WWP2 PFAS CDKN1A VRK1 PSPH WRN
CD69 C14orf159 FUT8 RELA KIAA0930 GMNN NFKBIA CCDC28A GGA2 SAE1 ZNF423
DNASE1L1 METTL4 CCDC90B SERPINB9 IDH3G FZD1 ZNF224 CSTF3 FRAT1 VCL
CTNS CDIP1 TMEM254 PPP3CB OXSM SDF2L1 ERAP2

Genes in the yellow module

**CD53 TYROBP FCER1G ITGB2 IL10RA CTSS HCK EVI2A RAC2 PTPRC HCLS1
CYBB** GPR65 CD14 PYCARD IGSF6 THEMIS2 SAMSN1 TLR2 CD86 MS4A4A CSTA
TNFRSF1B CLEC7A LAPTM5 BID LYN CCR1 LCP2 C1QA BCL2A1 MS4A6A C1QB IRF8
PTPRE FGR CASP1 CD163 LILRB2 CYTIP ADA CSF1R CD52 FCN1 PILRA PLA2G7 SRGN
LST1 CD36 VSIG4 LY96 MNDA ADAP2 SH3BGRL3 PLAUR MARCKS SOD2 NAGK PTX3
ISG20 PTPN6 SASH3 NMI LYZ ENTPD1 STK10 PLAC8 ALOX5 IFI16 RNASET2 BASP1
MAN2B1 TNFAIP3 LIPA CELF2 BAZ1A ARPC1B CCL4 PRKCB CPVL FAM49B BIRC3
HLA-DRA S100A11 CXCR4 RAB27A PID1 IL1B RAP2B ZCCHC6 NADK CRLF3 PSTPIP2
CASP4 CALHM2 APOBEC3G NAMPT HN1 PHLDA2 GCA FGL2 CSK KIAA1551 PKP4
MAP3K8 CXCL8 LMNB1 ADRB2 CCL5 ARL4C SECTM1 SPHK1 SLA MERTK CCRL2
GZMA GALNT7 CCR2 BBS1 CX3CR1 TRPV2 WDR1 LAP3 CCL2 IFNGR2 CASP8 CHFR
TRIM38 LTB PYGL FUT4 SNN SLC39A8 TPCN1 CD74 TUBA1B ADCY7 HLA-DRB1 ///
HLA-DRB1 RNF130 MCL1 CD83 KLHL7 GZMB LYRM9 FABP4 FAS ICAM1 MAP3K7CL
TMEM246 PRF1 STK17B CCDC109B SP140L GRN PLA2G4A PTGS2 TNFAIP6 CYTH1
PSMC4 YARS LRMP LY75 CD40 SLFN12 HNRNPF PROCR RND3 LRRC59 POPDC2 GNB5
MARCKSL1 PDGFRA C15orf39 WWOX OAZ1 ANKRD28 FKBP11 MLYCD SFT2D2 PFKM
UTP18 BMP2K DOCK1 THTPA INSIG1 TALDO1 ATXN7L3B ZFP36 S100A12 PFKFB3
TP53 BCL10 VPS13D SLC26A4 GALT SLAMF1 BCAS3 SIDT2 C11orf49 CST3 COL15A1
MED28 COLGALT1 UNC13B POLR2D EGFL6 WIPI2 IL7 KIZ PIK3IP1 PPP1R9A IL15
HLA-DQB1 NFKB1 ERBB4 TCTN2 CCDC176 MYO5C NUP214 INSR EDNRA CREG1
WDR77 C6orf48 RBL1 NAGA UBFD1 CTIF ARL4D SQSTM1 CXCL10 EDNRB OTUD3
NOV CPPED1

Genes in the green module

**NEBL MME PLCE1 ST3GAL6 CLIC5 NDNF ZDHHC6 MAGI2 IQGAP2 KANK1
MYO1E** FGF1 ARHGAP19 CDC42EP3 PDLIM2 MPP5 FRY FOXC1 FAM134B TJP1 TYRO3
MCM6 CTDSPL NLK DACH1 TCF21 THSD7A DPP6 CCDC91 FYN F3 PCOLCE2 PTPRD
KLK7 LOX MAN2A2 CRIM1 TGFB3R3 TPPP3 SEMA5A BLNK CDKN1C NES HTRA1
PARVA EXPH5 APBB2 GABARAPL2 B3GALT2 CAPG PRKAR2B SEMA3G WWC3 CA10
LEPROT GHR MAPK13 SMCO4 C16orf80 FAM98A 11-Sep TNS3 PGRMC2 SCAPER
HEBP1 ARL3 NPHS2 DAAM2 STX7 PIM1 STON1 CAND2 PDLIM5 BST1 NDN WASF3

KBTBD11 LRRC2 RRAS FARP2 CD200 PRKD1 ZNF185 AIF1 BMP7 MGAT5 AP3M2
CDKN1B FAXDC2 ATXN10 GRK5 ABCG1 MYOZ1 NDRG1 FXYD1 CR1 ITGA3 OPTN
ZNF16 NDRG2 OLFML2B HS3ST3A1 HOMER3 DCN PMEPA1 PSEN2 ARHGEF40
PPP2R2B ITGB5 RASL11B LRRC1 LANCL1 NUDT15 DDN ADH1B GM2A FBXL7 FUCA1
C1orf21 MMP2 NEDD9 LUM ABCA8 GSTA4 NPR2 APPBP2 NR3C2 CSPP1 6-Sep JAG1
NQO1 MDM1 SLC17A5 CLEC16A SMIM7 SLC48A1 C5orf30 CARKD FBXO21 KPNB1
WT1-AS FNBP1L FMO3 PI4KA RAMP3 PTDSS1 BBX ENPEP PTPN14 F5 ARHGEF17
FBXO9 RABGAP1L ERVMER34-1 CHD7 FAM206A VKORC1 UBAP2 TCEAL2 EFEMP1
TRIM68 BSDC1 GTF3A FGF9 CHI3L1 CEP104 NPAS3 COG7 KIF2C ACACA SRR FOXO4
CLCN4 ABR IGKC CBLB CLUAP1 RNLS FAM127B RBPMS JAKMIP2 DTX4 STAT4 DIS3
ZSCAN31 USP12 KIF1B RIC3 PTGDS TSR2 RARRES3 CTSV DCPS FMOD ZBTB18 CA11
BPTF TOX NUCB1 DHCR7 TEAD3 LPIN1 JARID2 SH3BGR SLC7A6 SFMBT1 RNASEH2A
SEMA4D USP25 CAPRIN2 GEMIN4

Genes in the red module

UGGT2 ME1 BTBD1 ARHGEF12 AMIGO2 KIAA0040 ENPP4 LGALS8 SULF1 SNCA
ARHGEF3 MYO1B ATP2A2 SPOCK1 MYOZ2 MEGF9 SLK CD2AP PON2 DNAJB9
HSPA13 PTGER4 ATP10A CD47 TUSC3 HIVEP2 HIST1H4H CLCN3 CAPN2 CORO2B
FAM114A1 SDC2 CCSER2 GALT DSTN KDELR3 DYNLT3 GADD45A USP46 YIPF6 PAM
TMEM45A RCAN1 ENTPD4 TMCO3 GDE1 WRB TSPAN2 RPS6KA1 SLC25A4 BACE1
MYO1D PJA1 ANXA2 LRP10 PARD3 KAT2B CERS6 COLGALT2 DCTD GPR107 PIGK
MACF1 LHFP GMDS MYH9 PTK2 BEX4 ERP44 APC ITFG1 CPQ ITGAV BCR EMC7
PLBD1 SCRNI ATP9A PDE4DIP MAPK10 HOXA1 TCTN1 PNMA2 NXN BBS4 PIGB
SYNJ2 NPR3 FAT1 ECM1 LEPREL1 HMGN3 COL4A5 ZNF106 FCHSD2 PDE4B HTATIP2
COMT GNPTAB UNG CCDC68 STXBP1 CLN5 ARHGAP28 MRS2 COQ10B BEAN1
RNF103 OS9 LOC730101 CITED2 FAM189A2 MAPKAPK3 VAT1 UCHL1 TIPARP
FAM168A HABP4 RC3H2 SNX24 FKBP1B DYNC1I1 COPS4 HIST1H2AC RPL37A CEP112
TMEM231 GGCX PSENEN SNX19 IPPK TMEM14A AXL GGNBP2 PIGO BCAR3 KCNH2
PLD3 PLEKHB1 PTPN13 GABRA2 CTGF USP14 ETF1 HPGD KPNA1 SMAD2 GYPC
RAB20 SEPWI VAPB INPP5F KCNS3 SYNM HSPA2 TMEM185B ANXA2P1 DHRS7B
GLRB KLHL18 LRPAP1 MCTP2 CXXC1 NDUFA4 C14orf1 DPYSL3 CYB5B ATP8A2
OLAH HIVEP1 BCL2L13 SMYD2 AHI1 TRIP4 ZNF226 C9orf9 VLDLR C2orf43 GATAD2A
PAMR1 CXCL12 ECE1 ATP1A2 CELSR2 PIGH EGR3 MR1 SAR1A PER2 NAGPA DMD
TMEM51 AP1G1 CNTN1 RQCD1

Genes in the black module

PRKCH PECAM1 MMRN2 GIMAP4 CDH5 TCF4 GIMAP6 CD34 S1PR1 MFNG ELTD1
GNG11 RNF144A EML1 MEF2C CLIC2 TIE1 ENG SH2B3 PDE2A LMO2 KIAA1462
TMEM47 SNRK ARHGAP25 SCARF1 TAL1 LPAR6 CLEC2B A2M RIN2 WAPAL CALCRL
ZCCHC24 FLI1 DCHS1 PPAP2A MYCT1 IL4R GMFG PIK3C2B JAG2 CD93 APLNR
DUSP11 IL15RA HLX HLA-B JADE3 ITM2A CDH13 FLT4 LIFR GPR4 HYAL2 PAPD7
CARD8 CEACAM1 HEPH SLC35G2 SGK1 ELMO1 GNA14 TBC1D8 MN1 CLEC1A
NOTCH1 CALCOCO2 VANGL1 CCND1 ITPKB PRCP HEY1 DPYSL2 WFDC1 STARD13
SATB1 HOXB6 KDM3A AGTR1 HLA-C TMEM109 NR1N1 LDLR ID2 TSPAN14 TBC1D15
4-Sep TFPI2 PCDH17 GAS2 MGST2 GATA2 FCN3 SMTN HES1 KCNMB4 VSIG10 PTGS1
SOSTDC1

Genes in the pink module

TROVE2 SCAF11 PRRC2C TTF1 RBMS1 ASXL2 ZBTB20 SUV420H1 THOC2 SOBP DPP8 ZNF148 NCOA1 KIF5B TAOX3 MYLK ADD3 RYBP RALBP1 DENND1B MYO9A ATRX HMBOX1 MAFG SNTB2 RBFOX2 ATXN7 DLC1 ANKRD11 TRIM44 AKAP13 ZMYND8 ZNF91 BRD2 SKAP2 PLEKHA1 TNPO1 USP47 DKFZP586I1420 GLG1 PSMC2 TBL1X SERTAD2 CELF1 ZC3HAV1 DCLRE1C TNPO3 BC036778 ESF1 TMEM87A RNASEH1 FOXO1 STAG2 PHIP ZFR TBC1D5 CUX1 RABGAP1 EPB41L5 EPRS JADE1 ATXN2 AK096592 ZNF395 TTC28 HOXA7 DCAF16 BRD4 ZBTB38 DCAF7 GOSR1 MIS18A NFATC2IP ZNF44 FKBP2 RAPGEF6 TTBK2 ZNF264 RHOBTB3 DDX27 FICD KLF9 RBMS3 DFFA MTIF2 TRIM28 NOLC1

Genes in the magenta module

PCDH12 ICAM2 PPM1F RNASE1 ARHGEF15 HMHA1 KLF2 SEC14L1 RAMP2 NPDC1 APOL3 FUT1 CD97 WARS CCDC85B PIK3R3 SNAI2 INPP5K PTPRM MAP3K11 GAS6 IRF1 PRKD2 HLA-E HHEX DUSP7 INPP5A CX3CL1 PIP4K2A PSMB8 EPHB4 TLE2 SEMA4C PPP1R13B TBX3 EFNB2 CCDC69 PKN1 STOM MAP3K6 VWA5A C2CD2 NCALD PARVB HOXB7 FZD4 PPWD1 SEMA3F CNOT2 BRE NME5 NPY1R TIAM1 TACC1 LUZP1 ROCK2 KIAA0391 TOM1L1 PIK3CB HOXB5 GFOD2 RGS3 ZMIZ1 MRPL15 TPRKB EGR1 CDK14 ERP29 SPSB1 GCFC2

Genes in the purple module

BICC1 PFKP PAX8 ANXA3 ADAMTS3 CDH2 DSP GPR56 GPR126 SOX9 VCAM1 RAPIGAP MET C3 PROM1 SACS PLAUI MXRA5 FLNB EFNA5 UPK1B HRH1 RBBP8 ANXA4 SLPI GTF2IRD1 MEST RELN TPM1 LTBP2 CAV1 NAV2 OXTR TNFRSF11B CAV2 CXCL1 HN1L FSTL3 MREG FBN2 GDF15 ARNT2 CEBPD MTCL1 KLF5 ITPA PDGFRL SLC39A14 PDGFC TNFRSF12A ANKRD6 C7 CRTAC1 SCCPDH PEG10 TRIL SPARCL1 FANCG

Genes in the greenyellow module

CDK1 NUSAP1 PBK CENPF GINS1 HMMR RAD51AP1 ECT2 DYRK2 HIF1A COL1A2 PCZWINT MYL3 POLE2 MAD2L1 SPTB CBF3 COL5A2 CBX7 CCNB1 FANCI ALS2CL TUBA1C TES CHEK1 MYBL1 FEN1 MCM2 ENAH IGFBP1 RFC3 PTH1R CDKN2C GSPT1 CCNE2 UGDH KIAA0101 SAT1 STK17A DONSON CYB561 TFRC ABCA1 COL3A1 OLR1 CCBL1 RACGAP1 RAB11FIP1 FAM216A TGFBI SIRPA TAF1D ADSL ARHGEF18 MYOM1 TECPR2

Genes in the tan module

RSAD2 IFI44 MX1 HERC6 OAS3 IFI44L OAS2 IFI6 IFIT3 XAF1 SP110 UBE2L6 ISG15 IFITM1 SP100 TRIM22 PARP12 IFI27 IRF7 LY6E TRIM21 IFIT5 SAMD9 C19orf66 PSMB9 SLC15A3 ADAR OASL TAP1 IRF9 TMEM140 IFI35 BTN3A3 ACSL5 OAS1 HCP5 B2M FARP1 PLA1A GCH1 CMTR1 PML TRIM14 TAP2 GVINP1 TUFT1 TTC39A RNF114 EFHD1 ZAK FAM111A IDO1

Supplementary Table S6. Gene ontology (GO) biological process (BP) terms of differentially expressed genes in each module (top 30 terms per module, Count: The number of Genes involved in the term; %: Percentage (involved genes/total genes); P-Value: Modified Fisher Exact P-value)

GO NO.	BP Term	Count	%	PValue
turquoise module				
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	36	3.013	1.19E-07
GO:0006888	ER to Golgi vesicle-mediated transport	31	2.594	1.43E-07
GO:0098609	cell-cell adhesion	40	3.347	2.77E-06
GO:0016032	viral process	42	3.515	5.33E-06
GO:0007062	sister chromatid cohesion	21	1.757	9.71E-06
GO:1900034	regulation of cellular response to heat	17	1.423	2.19E-05
GO:0051292	nuclear pore complex assembly	7	0.586	2.68E-05
GO:0000398	mRNA splicing, via spliceosome	32	2.678	5.12E-05
GO:0006511	ubiquitin-dependent protein catabolic process	28	2.343	5.35E-05
GO:0006406	mRNA export from nucleus	19	1.590	7.63E-05
GO:0051301	cell division	43	3.598	1.03E-04
GO:0016569	covalent chromatin modification	20	1.674	1.26E-04
GO:0048208	COPII vesicle coating	14	1.172	1.28E-04
GO:0006396	RNA processing	18	1.506	1.68E-04
GO:0016925	protein sumoylation	20	1.674	2.02E-04
GO:0008380	RNA splicing	25	2.092	2.04E-04
GO:0010467	gene expression	12	1.004	2.13E-04
GO:0042752	regulation of circadian rhythm	12	1.004	2.59E-04
GO:0015031	protein transport	45	3.766	3.76E-04
GO:0000209	protein polyubiquitination	25	2.092	9.37E-04
GO:0006914	autophagy	20	1.674	1.04E-03
GO:0016567	protein ubiquitination	40	3.347	1.27E-03
GO:0006397	mRNA processing	24	2.008	1.45E-03
GO:0006521	regulation of cellular amino acid metabolic process	11	0.921	1.50E-03
GO:0006457	protein folding	24	2.008	1.56E-03
GO:0007067	mitotic nuclear division	30	2.510	1.70E-03
GO:0035666	TRIF-dependent toll-like receptor signaling pathway	8	0.669	1.76E-03
GO:0000226	microtubule cytoskeleton organization	13	1.088	2.04E-03
GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	21	1.757	2.34E-03
GO:0006303	double-strand break repair via nonhomologous end joining	12	1.004	2.36E-03
blue module				
GO:0043488	regulation of mRNA stability	16	0.014	9.33E-06
GO:0000086	G2/M transition of mitotic cell cycle	18	0.016	2.13E-05
GO:0015031	protein transport	32	0.028	1.52E-04

GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	18	0.016	1.65E-04
GO:0038061	NIK/NF-kappaB signaling	11	0.010	2.05E-04
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	13	0.012	2.12E-04
GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	10	0.009	6.59E-04
GO:0006521	regulation of cellular amino acid metabolic process	9	0.008	6.91E-04
GO:0006888	ER to Golgi vesicle-mediated transport	16	0.014	1.36E-03
GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	10	0.009	1.58E-03
GO:0090090	negative regulation of canonical Wnt signaling pathway	16	0.014	1.63E-03
GO:0033209	tumor necrosis factor-mediated signaling pathway	13	0.012	2.01E-03
GO:0030433	ER-associated ubiquitin-dependent protein catabolic process	9	0.008	2.05E-03
GO:0006886	intracellular protein transport	20	0.018	2.07E-03
GO:0000910	cytokinesis	8	0.007	2.29E-03
GO:0090263	positive regulation of canonical Wnt signaling pathway	13	0.012	2.32E-03
GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	10	0.009	2.55E-03
GO:0031145	anaphase-promoting complex-dependent catabolic process	10	0.009	3.32E-03
GO:1902661	positive regulation of glucose mediated signaling pathway	3	0.003	4.35E-03
GO:0050852	T cell receptor signaling pathway	14	0.012	4.84E-03
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	17	0.015	5.50E-03
GO:0002223	stimulatory C-type lectin receptor signaling pathway	11	0.010	7.33E-03
GO:0036498	IRE1-mediated unfolded protein response	8	0.007	7.38E-03
GO:0090240	positive regulation of histone H4 acetylation	3	0.003	8.47E-03
GO:1904382	mannose trimming involved in glycoprotein ERAD pathway	3	0.003	8.47E-03
GO:0043044	ATP-dependent chromatin remodeling	5	0.004	1.08E-02
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	7	0.006	1.10E-02
GO:0000398	mRNA splicing, via spliceosome	17	0.015	1.25E-02
GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	5	0.004	1.26E-02
GO:0042176	regulation of protein catabolic process	4	0.004	1.51E-02
brown module				
GO:0055114	oxidation-reduction process	53	0.065	3.80E-13
GO:0008152	metabolic process	22	0.027	1.25E-08
GO:0006635	fatty acid beta-oxidation	11	0.013	3.18E-07
GO:0006099	tricarboxylic acid cycle	9	0.011	9.99E-07
GO:0006094	gluconeogenesis	9	0.011	2.84E-05
GO:0015811	L-cystine transport	4	0.005	8.86E-05
GO:0006520	cellular amino acid metabolic process	8	0.010	1.17E-04
GO:0006541	glutamine metabolic process	6	0.007	1.95E-04
GO:0006102	isocitrate metabolic process	4	0.005	2.17E-04

GO:0051289	protein homotetramerization	9	0.011	2.76E-04
GO:0042493	response to drug	21	0.026	4.42E-04
GO:0007588	excretion	7	0.009	5.54E-04
GO:0071363	cellular response to growth factor stimulus	7	0.009	1.60E-03
GO:0006805	xenobiotic metabolic process	9	0.011	1.62E-03
GO:0009083	branched-chain amino acid catabolic process	5	0.006	1.76E-03
GO:0009267	cellular response to starvation	7	0.009	2.02E-03
GO:0019254	carnitine metabolic process, CoA-linked	3	0.004	2.36E-03
GO:0002576	platelet degranulation	10	0.012	2.61E-03
GO:0006637	acyl-CoA metabolic process	5	0.006	3.11E-03
GO:0006081	cellular aldehyde metabolic process	4	0.005	3.15E-03
GO:0000096	sulfur amino acid metabolic process	4	0.005	3.15E-03
GO:0006559	L-phenylalanine catabolic process	4	0.005	3.15E-03
GO:0007016	cytoskeletal anchoring at plasma membrane	4	0.005	3.15E-03
GO:0030855	epithelial cell differentiation	8	0.010	3.62E-03
GO:0098869	cellular oxidant detoxification	8	0.010	3.62E-03
GO:0006069	ethanol oxidation	4	0.005	4.11E-03
GO:0006107	oxaloacetate metabolic process	4	0.005	4.11E-03
GO:0006538	glutamate catabolic process	3	0.004	4.63E-03
GO:0000302	response to reactive oxygen species	6	0.007	4.66E-03
GO:0010288	response to lead ion	4	0.005	5.24E-03
yellow module				
GO:0006954	inflammatory response	38	0.112	3.25E-22
GO:0006955	immune response	31	0.092	2.34E-14
GO:0071222	cellular response to lipopolysaccharide	17	0.050	1.19E-12
GO:0006915	apoptotic process	30	0.089	2.26E-10
GO:0007165	signal transduction	40	0.118	2.77E-08
GO:0007267	cell-cell signaling	18	0.053	3.25E-08
GO:0031663	lipopolysaccharide-mediated signaling pathway	8	0.024	1.35E-07
GO:0045087	innate immune response	22	0.065	1.78E-07
GO:0070098	chemokine-mediated signaling pathway	10	0.030	3.05E-07
GO:0051092	positive regulation of NF-kappaB transcription factor activity	12	0.036	1.18E-06
GO:0090026	positive regulation of monocyte chemotaxis	6	0.018	1.31E-06
GO:0050727	regulation of inflammatory response	9	0.027	1.39E-06
GO:0032760	positive regulation of tumor necrosis factor production	8	0.024	2.15E-06
GO:0007166	cell surface receptor signaling pathway	16	0.047	2.73E-06
GO:0060333	interferon-gamma-mediated signaling pathway	9	0.027	3.49E-06
GO:0006935	chemotaxis	11	0.033	3.96E-06
GO:0050729	positive regulation of inflammatory response	9	0.027	4.32E-06
GO:0008284	positive regulation of cell proliferation	20	0.059	9.83E-06

GO:0006968	cellular defense response	8	0.024	1.43E-05
GO:0070374	positive regulation of ERK1 and ERK2 cascade	12	0.036	1.68E-05
GO:0045429	positive regulation of nitric oxide biosynthetic process	7	0.021	1.73E-05
GO:0030593	neutrophil chemotaxis	8	0.024	2.16E-05
GO:0050766	positive regulation of phagocytosis	6	0.018	3.10E-05
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	9	0.027	3.31E-05
GO:0071260	cellular response to mechanical stimulus	8	0.024	3.50E-05
GO:0031295	T cell costimulation	8	0.024	6.44E-05
GO:0071356	cellular response to tumor necrosis factor	9	0.027	8.76E-05
GO:0030168	platelet activation	9	0.027	1.20E-04
GO:0050852	T cell receptor signaling pathway	10	0.030	1.28E-04
GO:0030890	positive regulation of B cell proliferation	6	0.018	1.36E-04
green module				
GO:0022617	extracellular matrix disassembly	6	0.018	1.66E-03
GO:0032835	glomerulus development	3	0.009	4.31E-03
GO:0072015	glomerular visceral epithelial cell development	3	0.009	5.34E-03
GO:0060411	cardiac septum morphogenesis	3	0.009	5.34E-03
GO:0071526	semaphorin-plexin signaling pathway	4	0.012	5.97E-03
GO:0035556	intracellular signal transduction	12	0.037	6.06E-03
GO:0030198	extracellular matrix organization	8	0.024	6.82E-03
GO:0030199	collagen fibril organization	4	0.012	9.53E-03
GO:0045766	positive regulation of angiogenesis	6	0.018	9.71E-03
GO:0030324	lung development	5	0.015	1.06E-02
GO:0001525	angiogenesis	8	0.024	1.33E-02
GO:0051781	positive regulation of cell division	4	0.012	1.58E-02
GO:0001822	kidney development	5	0.015	1.61E-02
GO:0006886	intracellular protein transport	8	0.024	1.76E-02
GO:0010976	positive regulation of neuron projection development	5	0.015	1.81E-02
GO:0042326	negative regulation of phosphorylation	3	0.009	2.10E-02
GO:0043547	positive regulation of GTPase activity	13	0.040	2.64E-02
GO:0001764	neuron migration	5	0.015	3.09E-02
GO:0007181	transforming growth factor beta receptor complex assembly	2	0.006	3.34E-02
GO:0048843	negative regulation of axon extension involved in axon guidance	3	0.009	3.43E-02
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	4	0.012	3.54E-02
GO:0051384	response to glucocorticoid	4	0.012	3.69E-02
GO:0018146	keratan sulfate biosynthetic process	3	0.009	3.93E-02
GO:0007219	Notch signaling pathway	5	0.015	4.10E-02
GO:0046449	creatinine metabolic process	2	0.006	4.43E-02
GO:0072006	nephron development	2	0.006	4.43E-02

GO:0034698	response to gonadotropin	2	0.006	4.43E-02
GO:0071514	genetic imprinting	2	0.006	4.43E-02
GO:0007417	central nervous system development	5	0.015	4.67E-02
GO:0048010	vascular endothelial growth factor receptor signaling pathway	4	0.012	4.76E-02
red module				
GO:0001921	positive regulation of receptor recycling	4	0.013	3.42E-04
GO:0048010	vascular endothelial growth factor receptor signaling pathway	5	0.016	6.11E-03
GO:0051893	regulation of focal adhesion assembly	3	0.010	1.25E-02
GO:0007179	transforming growth factor beta receptor signaling pathway	5	0.016	1.42E-02
GO:0010881	regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	3	0.010	1.56E-02
GO:0008344	adult locomotory behavior	4	0.013	1.57E-02
GO:0019229	regulation of vasoconstriction	3	0.010	1.72E-02
GO:0007229	integrin-mediated signaling pathway	5	0.016	1.81E-02
GO:0045963	negative regulation of dopamine metabolic process	2	0.006	2.01E-02
GO:0048259	regulation of receptor-mediated endocytosis	2	0.006	2.01E-02
GO:0051946	regulation of glutamate uptake involved in transmission of nerve impulse	2	0.006	2.01E-02
GO:0045332	phospholipid translocation	3	0.010	2.06E-02
GO:0006509	membrane protein ectodomain proteolysis	3	0.010	2.06E-02
GO:0009612	response to mechanical stimulus	4	0.013	2.19E-02
GO:0001764	neuron migration	5	0.016	2.20E-02
GO:0001525	angiogenesis	7	0.022	2.61E-02
GO:0007274	neuromuscular synaptic transmission	3	0.010	2.82E-02
GO:0006506	GPI anchor biosynthetic process	3	0.010	2.82E-02
GO:0007412	axon target recognition	2	0.006	3.01E-02
GO:0007417	central nervous system development	5	0.016	3.37E-02
GO:0071260	cellular response to mechanical stimulus	4	0.013	3.53E-02
GO:0030073	insulin secretion	3	0.010	3.91E-02
GO:0033299	secretion of lysosomal enzymes	2	0.006	3.99E-02
GO:0070830	bicellular tight junction assembly	3	0.010	4.14E-02
GO:0010632	regulation of epithelial cell migration	2	0.006	4.96E-02
black module				
GO:0045747	positive regulation of Notch signaling pathway	5	0.033	2.68E-05
GO:0007155	cell adhesion	11	0.073	1.56E-04
GO:0003273	cell migration involved in endocardial cushion formation	3	0.020	1.66E-04
GO:0001525	angiogenesis	8	0.053	1.82E-04
GO:0002040	sprouting angiogenesis	4	0.027	3.04E-04
GO:0007165	signal transduction	17	0.113	3.58E-04
GO:0048667	cell morphogenesis involved in neuron differentiation	3	0.020	4.11E-04

GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	4	0.027	4.28E-04
GO:0042127	regulation of cell proliferation	7	0.047	4.49E-04
GO:0003208	cardiac ventricle morphogenesis	3	0.020	9.76E-04
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	12	0.080	1.45E-03
GO:0048715	negative regulation of oligodendrocyte differentiation	3	0.020	1.48E-03
GO:0048711	positive regulation of astrocyte differentiation	3	0.020	1.48E-03
GO:0090051	negative regulation of cell migration involved in sprouting angiogenesis	3	0.020	1.48E-03
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	14	0.093	1.92E-03
GO:0003198	epithelial to mesenchymal transition involved in endocardial cushion formation	3	0.020	2.09E-03
GO:0006909	phagocytosis	4	0.027	2.10E-03
GO:0003203	endocardial cushion morphogenesis	3	0.020	3.18E-03
GO:0030097	hemopoiesis	4	0.027	3.78E-03
GO:0048661	positive regulation of smooth muscle cell proliferation	4	0.027	3.96E-03
GO:0010629	negative regulation of gene expression	5	0.033	6.06E-03
GO:0050729	positive regulation of inflammatory response	4	0.027	6.85E-03
GO:0090102	cochlea development	3	0.020	7.11E-03
GO:0045648	positive regulation of erythrocyte differentiation	3	0.020	7.11E-03
GO:0030334	regulation of cell migration	4	0.027	7.11E-03
GO:0001558	regulation of cell growth	4	0.027	8.81E-03
GO:0007389	pattern specification process	3	0.020	9.60E-03
GO:0007156	homophilic cell adhesion via plasma membrane adhesion molecules	5	0.033	9.92E-03
GO:0043542	endothelial cell migration	3	0.020	1.03E-02
GO:0060412	ventricular septum morphogenesis	3	0.020	1.03E-02
pink module				
GO:0006351	transcription, DNA-templated	24	0.167	3.31E-05
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	16	0.111	6.10E-05
GO:0045892	negative regulation of transcription, DNA-templated	9	0.063	2.77E-03
GO:0045893	positive regulation of transcription, DNA-templated	8	0.056	1.21E-02
GO:0016569	covalent chromatin modification	4	0.028	1.73E-02
GO:0006974	cellular response to DNA damage stimulus	5	0.035	1.81E-02
GO:0006357	regulation of transcription from RNA polymerase II promoter	7	0.049	1.97E-02
GO:0051056	regulation of small GTPase mediated signal transduction	4	0.028	2.70E-02
GO:0016070	RNA metabolic process	2	0.014	4.26E-02
GO:0042147	retrograde transport, endosome to Golgi	3	0.021	4.38E-02
magenta module				
GO:0045892	negative regulation of transcription, DNA-templated	9	0.084	5.30E-04
GO:0001570	vasculogenesis	4	0.038	1.21E-03
GO:0006661	phosphatidylinositol biosynthetic process	4	0.038	1.34E-03
GO:0060337	type I interferon signaling pathway	4	0.038	1.78E-03

GO:0010628	positive regulation of gene expression	6	0.056	2.99E-03
GO:0048013	ephrin receptor signaling pathway	4	0.038	4.13E-03
GO:0001701	in utero embryonic development	5	0.047	5.32E-03
GO:0043507	positive regulation of JUN kinase activity	3	0.028	6.01E-03
GO:0006468	protein phosphorylation	7	0.066	7.14E-03
GO:0007155	cell adhesion	7	0.066	7.37E-03
GO:0000187	activation of MAPK activity	4	0.038	7.57E-03
GO:0007257	activation of JUN kinase activity	3	0.028	8.93E-03
GO:0061299	retina vasculature morphogenesis in camera-type eye	2	0.019	2.23E-02
GO:0016525	negative regulation of angiogenesis	3	0.028	2.27E-02
GO:0090090	negative regulation of canonical Wnt signaling pathway	4	0.038	2.33E-02
GO:0048010	vascular endothelial growth factor receptor signaling pathway	3	0.028	2.99E-02
GO:0030335	positive regulation of cell migration	4	0.038	3.18E-02
GO:0016055	Wnt signaling pathway	4	0.038	3.32E-02
GO:0009952	anterior/posterior pattern specification	3	0.028	3.63E-02
GO:0060055	angiogenesis involved in wound healing	2	0.019	3.69E-02
GO:0046855	inositol phosphate dephosphorylation	2	0.019	4.05E-02
GO:0045893	positive regulation of transcription, DNA-templated	6	0.056	4.37E-02
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	3	0.028	4.67E-02
GO:0009887	organ morphogenesis	3	0.028	4.67E-02
purple module				
GO:0090090	negative regulation of canonical Wnt signaling pathway	5	0.053	1.73E-03
GO:0007165	signal transduction	11	0.117	3.05E-03
GO:0045907	positive regulation of vasoconstriction	3	0.032	4.56E-03
GO:0007417	central nervous system development	4	0.043	6.43E-03
GO:0019065	receptor-mediated endocytosis of virus by host cell	2	0.021	9.44E-03
GO:0061041	regulation of wound healing	2	0.021	1.26E-02
GO:0072289	metanephric nephron tubule formation	2	0.021	1.26E-02
GO:0032496	response to lipopolysaccharide	4	0.043	1.50E-02
GO:0070836	caveola assembly	2	0.021	1.57E-02
GO:0001666	response to hypoxia	4	0.043	1.70E-02
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	3	0.032	1.74E-02
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	3	0.032	1.79E-02
GO:0030198	extracellular matrix organization	4	0.043	2.39E-02
GO:0043410	positive regulation of MAPK cascade	3	0.032	2.70E-02
GO:0000075	cell cycle checkpoint	2	0.021	2.81E-02
GO:0042981	regulation of apoptotic process	4	0.043	2.96E-02
GO:0006954	inflammatory response	5	0.053	3.14E-02
GO:0032355	response to estradiol	3	0.032	3.35E-02

GO:0098911	regulation of ventricular cardiac muscle cell action potential	2	0.021	3.42E-02
GO:0030857	negative regulation of epithelial cell differentiation	2	0.021	3.42E-02
GO:0043206	extracellular fibril organization	2	0.021	3.72E-02
GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	2	0.021	3.72E-02
GO:0006957	complement activation, alternative pathway	2	0.021	4.03E-02
GO:0016337	single organismal cell-cell adhesion	3	0.032	4.05E-02
GO:0010001	glial cell differentiation	2	0.021	4.33E-02
GO:0006955	immune response	5	0.053	4.36E-02
greenyellow module				
GO:0006260	DNA replication	7	0.074	1.01E-05
GO:0000082	G1/S transition of mitotic cell cycle	6	0.064	1.87E-05
GO:0051301	cell division	7	0.074	8.73E-04
GO:0006281	DNA repair	6	0.064	9.31E-04
GO:0000070	mitotic sister chromatid segregation	3	0.032	2.90E-03
GO:0006270	DNA replication initiation	3	0.032	4.73E-03
GO:0000722	telomere maintenance via recombination	3	0.032	4.73E-03
GO:0007093	mitotic cell cycle checkpoint	3	0.032	4.73E-03
GO:0030199	collagen fibril organization	3	0.032	6.97E-03
GO:0051726	regulation of cell cycle	4	0.042	7.41E-03
GO:0000086	G2/M transition of mitotic cell cycle	4	0.042	9.73E-03
GO:0001501	skeletal system development	4	0.042	9.73E-03
GO:0071230	cellular response to amino acid stimulus	3	0.032	1.00E-02
GO:0042493	response to drug	5	0.053	1.64E-02
GO:0030574	collagen catabolic process	3	0.032	1.80E-02
GO:0042127	regulation of cell proliferation	4	0.042	2.16E-02
GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3	0.032	2.19E-02
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	2	0.021	2.23E-02
GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	3	0.032	2.49E-02
GO:0030198	extracellular matrix organization	4	0.042	2.51E-02
GO:0031145	anaphase-promoting complex-dependent catabolic process	3	0.032	2.67E-02
GO:0035023	regulation of Rho protein signal transduction	3	0.032	2.80E-02
GO:0055015	ventricular cardiac muscle cell development	2	0.021	3.17E-02
GO:0007179	transforming growth factor beta receptor signaling pathway	3	0.032	3.53E-02
GO:0001833	inner cell mass cell proliferation	2	0.021	3.79E-02
GO:0007062	sister chromatid cohesion	3	0.032	4.34E-02
GO:0006271	DNA strand elongation involved in DNA replication	2	0.021	4.72E-02
GO:0007095	mitotic G2 DNA damage checkpoint	2	0.021	4.72E-02
GO:0014850	response to muscle activity	2	0.021	4.72E-02

tan module				
GO:0060337	type I interferon signaling pathway	17	0.307	2.34E-28
GO:0051607	defense response to virus	17	0.307	2.72E-21
GO:0045071	negative regulation of viral genome replication	10	0.180	9.64E-16
GO:0060333	interferon-gamma-mediated signaling pathway	11	0.199	3.37E-15
GO:0009615	response to virus	12	0.217	6.30E-15
GO:0034341	response to interferon-gamma	5	0.090	5.03E-07
GO:0034340	response to type I interferon	4	0.072	6.68E-07
GO:0002481	antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent	3	0.054	1.53E-04
GO:0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	3	0.054	1.53E-04
GO:0045087	innate immune response	8	0.144	1.55E-04
GO:0032897	negative regulation of viral transcription	3	0.054	5.62E-04
GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	4	0.072	2.97E-03
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	3	0.054	3.04E-03
GO:0060700	regulation of ribonuclease activity	2	0.036	5.47E-03
GO:0046967	cytosol to ER transport	2	0.036	5.47E-03
GO:0006955	immune response	6	0.108	5.70E-03
GO:0034097	response to cytokine	3	0.054	8.92E-03
GO:0019060	intracellular transport of viral protein in host cell	2	0.036	1.36E-02
GO:0019941	modification-dependent protein catabolic process	2	0.036	1.36E-02
GO:0015833	peptide transport	2	0.036	1.36E-02
GO:0000209	protein polyubiquitination	4	0.072	1.39E-02
GO:0006952	defense response	3	0.054	1.45E-02
GO:0032020	ISG15-protein conjugation	2	0.036	1.63E-02
GO:0002489	antigen processing and presentation of endogenous peptide antigen via MHC class Ib via ER pathway, TAP-dependent	2	0.036	1.63E-02
GO:0002591	positive regulation of antigen processing and presentation of peptide antigen via MHC class I	2	0.036	1.63E-02
GO:0002485	antigen processing and presentation of endogenous peptide antigen via MHC class I via ER pathway, TAP-dependent	2	0.036	1.63E-02
GO:0035457	cellular response to interferon-alpha	2	0.036	2.44E-02
GO:0070206	protein trimerization	2	0.036	2.44E-02

Supplementary Table S7. KEGG pathway terms of genes in each module (Count: The number of Genes involved in the term; %: Percentage (involved genes/total genes); P-Value: Modified Fisher Exact P-value)

Module	Term	Count	%	PValue
turquoise	hsa04141:Protein processing in endoplasmic reticulum	32	2.678	9.31E-07
turquoise	hsa04120:Ubiquitin mediated proteolysis	27	2.259	3.71E-06
turquoise	hsa03015:mRNA surveillance pathway	18	1.506	2.19E-04
turquoise	hsa04071:Sphingolipid signaling pathway	21	1.757	3.15E-04
turquoise	hsa04910:Insulin signaling pathway	22	1.841	7.91E-04
turquoise	hsa03013:RNA transport	25	2.092	1.22E-03
turquoise	hsa05131:Shigellosis	12	1.004	5.42E-03
turquoise	hsa04728:Dopaminergic synapse	18	1.506	9.86E-03
turquoise	hsa03008:Ribosome biogenesis in eukaryotes	13	1.088	2.11E-02
turquoise	hsa03430:Mismatch repair	6	0.502	2.15E-02
turquoise	hsa04150:mTOR signaling pathway	10	0.837	2.16E-02
turquoise	hsa04114:Oocyte meiosis	15	1.255	2.37E-02
turquoise	hsa03040:Spliceosome	17	1.423	2.85E-02
turquoise	hsa04130:SNARE interactions in vesicular transport	7	0.586	3.22E-02
turquoise	hsa04261:Adrenergic signaling in cardiomyocytes	18	1.506	3.24E-02
turquoise	hsa03050:Proteasome	8	0.669	3.59E-02
turquoise	hsa03420:Nucleotide excision repair	8	0.669	4.90E-02
turquoise	hsa04144:Endocytosis	27	2.259	4.92E-02
blue	hsa03050:Proteasome	9	0.008	3.77E-04
blue	hsa04141:Protein processing in endoplasmic reticulum	17	0.015	1.62E-03
blue	hsa05221:Acute myeloid leukemia	9	0.008	1.97E-03
blue	hsa05130:Pathogenic Escherichia coli infection	8	0.007	4.69E-03
blue	hsa04142:Lysosome	12	0.011	1.13E-02
blue	hsa05010:Alzheimer's disease	14	0.012	2.17E-02
blue	hsa05169:Epstein-Barr virus infection	15	0.013	2.56E-02
blue	hsa03013:RNA transport	14	0.012	2.57E-02
blue	hsa04540:Gap junction	9	0.008	2.86E-02
blue	hsa00230:Purine metabolism	14	0.012	3.03E-02
blue	hsa04932:Non-alcoholic fatty liver disease (NAFLD)	12	0.011	4.81E-02
blue	hsa00190:Oxidative phosphorylation	11	0.010	4.85E-02
blue	hsa03040:Spliceosome	11	0.010	4.85E-02
blue	hsa05160:Hepatitis C	11	0.010	4.85E-02
brown	hsa01100:Metabolic pathways	116	0.142	1.15E-22
brown	hsa01200:Carbon metabolism	27	0.033	8.57E-14
brown	hsa01130:Biosynthesis of antibiotics	34	0.042	4.50E-12
brown	hsa00280:Valine, leucine and isoleucine degradation	14	0.017	1.52E-08

brown	hsa00380:Tryptophan metabolism	12	0.015	2.15E-07
brown	hsa00630:Glyoxylate and dicarboxylate metabolism	10	0.012	4.55E-07
brown	hsa04146:Peroxisome	16	0.020	5.44E-07
brown	hsa00071:Fatty acid degradation	12	0.015	6.20E-07
brown	hsa00020:Citrate cycle (TCA cycle)	10	0.012	1.25E-06
brown	hsa00260:Glycine, serine and threonine metabolism	11	0.013	1.58E-06
brown	hsa00350:Tyrosine metabolism	10	0.012	5.21E-06
brown	hsa00330:Arginine and proline metabolism	11	0.013	1.75E-05
brown	hsa04964:Proximal tubule bicarbonate reclamation	8	0.010	1.80E-05
brown	hsa01230:Biosynthesis of amino acids	13	0.016	2.41E-05
brown	hsa00010:Glycolysis / Gluconeogenesis	12	0.015	4.68E-05
brown	hsa00640:Propanoate metabolism	8	0.010	7.34E-05
brown	hsa00410:beta-Alanine metabolism	8	0.010	1.47E-04
brown	hsa00982:Drug metabolism - cytochrome P450	11	0.013	2.67E-04
brown	hsa01210:2-Oxocarboxylic acid metabolism	6	0.007	3.63E-04
brown	hsa00360:Phenylalanine metabolism	6	0.007	3.63E-04
brown	hsa00220:Arginine biosynthesis	6	0.007	8.25E-04
brown	hsa03320:PPAR signaling pathway	10	0.012	1.06E-03
brown	hsa00340:Histidine metabolism	6	0.007	1.63E-03
brown	hsa00250:Alanine, aspartate and glutamate metabolism	7	0.009	2.06E-03
brown	hsa01212:Fatty acid metabolism	8	0.010	2.35E-03
brown	hsa00650:Butanoate metabolism	6	0.007	3.44E-03
brown	hsa04978:Mineral absorption	7	0.009	8.33E-03
brown	hsa00471:D-Glutamine and D-glutamate metabolism	3	0.004	8.60E-03
brown	hsa00830:Retinol metabolism	8	0.010	1.27E-02
brown	hsa00310:Lysine degradation	7	0.009	1.49E-02
brown	hsa00270:Cysteine and methionine metabolism	6	0.007	1.51E-02
brown	hsa00790:Folate biosynthesis	4	0.005	1.54E-02
brown	hsa00620:Pyruvate metabolism	6	0.007	1.86E-02
brown	hsa00910:Nitrogen metabolism	4	0.005	2.65E-02
brown	hsa00983:Drug metabolism - other enzymes	6	0.007	3.21E-02
brown	hsa00051:Fructose and mannose metabolism	5	0.006	3.43E-02
brown	hsa00040:Pentose and glucuronate interconversions	5	0.006	4.98E-02
yellow	hsa04064:NF-kappa B signaling pathway	15	0.044	2.46E-10
yellow	hsa05152:Tuberculosis	18	0.053	1.01E-08
yellow	hsa04060:Cytokine-cytokine receptor interaction	20	0.059	1.55E-08
yellow	hsa04668:TNF signaling pathway	14	0.041	3.39E-08
yellow	hsa05323:Rheumatoid arthritis	13	0.038	3.52E-08
yellow	hsa05416:Viral myocarditis	11	0.033	4.35E-08
yellow	hsa04620:Toll-like receptor signaling pathway	13	0.038	2.88E-07

yellow	hsa05140:Leishmaniasis	11	0.033	3.78E-07
yellow	hsa04621:NOD-like receptor signaling pathway	10	0.030	3.98E-07
yellow	hsa05133:Pertussis	11	0.033	6.40E-07
yellow	hsa04062:Chemokine signaling pathway	16	0.047	7.94E-07
yellow	hsa05332:Graft-versus-host disease	8	0.024	1.31E-06
yellow	hsa04650:Natural killer cell mediated cytotoxicity	13	0.038	1.34E-06
yellow	hsa05164:Influenza A	15	0.044	1.96E-06
yellow	hsa05330:Allograft rejection	8	0.024	2.99E-06
yellow	hsa05168:Herpes simplex infection	15	0.044	3.56E-06
yellow	hsa05134:Legionellosis	9	0.027	3.96E-06
yellow	hsa05145:Toxoplasmosis	12	0.036	6.41E-06
yellow	hsa04940:Type I diabetes mellitus	8	0.024	7.27E-06
yellow	hsa05142:Chagas disease (American trypanosomiasis)	11	0.033	1.31E-05
yellow	hsa05144:Malaria	8	0.024	2.09E-05
yellow	hsa05320:Autoimmune thyroid disease	8	0.024	3.12E-05
yellow	hsa05132:Salmonella infection	9	0.027	9.78E-05
yellow	hsa04666:Fc gamma R-mediated phagocytosis	9	0.027	1.07E-04
yellow	hsa04672:Intestinal immune network for IgA production	7	0.021	1.59E-04
yellow	hsa05150:Staphylococcus aureus infection	7	0.021	3.46E-04
yellow	hsa04145:Phagosome	11	0.033	3.48E-04
yellow	hsa05169:Epstein-Barr virus infection	12	0.036	4.99E-04
yellow	hsa04623:Cytosolic DNA-sensing pathway	7	0.021	8.70E-04
yellow	hsa05321:Inflammatory bowel disease (IBD)	7	0.021	8.70E-04
yellow	hsa05200:Pathways in cancer	17	0.050	1.40E-03
yellow	hsa05310:Asthma	5	0.015	1.78E-03
yellow	hsa04380:Osteoclast differentiation	9	0.027	2.12E-03
yellow	hsa05202:Transcriptional misregulation in cancer	10	0.030	2.78E-03
yellow	hsa04640:Hematopoietic cell lineage	7	0.021	3.76E-03
yellow	hsa04210:Apoptosis	6	0.018	4.58E-03
yellow	hsa05166:HTLV-I infection	12	0.036	5.38E-03
yellow	hsa04664:Fc epsilon RI signaling pathway	6	0.018	6.79E-03
yellow	hsa05162:Measles	8	0.024	8.95E-03
yellow	hsa04913:Ovarian steroidogenesis	5	0.015	1.06E-02
yellow	hsa05146:Amoebiasis	7	0.021	1.09E-02
yellow	hsa05130:Pathogenic Escherichia coli infection	5	0.015	1.22E-02
yellow	hsa04514:Cell adhesion molecules (CAMs)	8	0.024	1.26E-02
yellow	hsa04923:Regulation of lipolysis in adipocytes	5	0.015	1.68E-02
yellow	hsa04071:Sphingolipid signaling pathway	7	0.021	1.91E-02
yellow	hsa05020:Prion diseases	4	0.012	1.99E-02
yellow	hsa05143:African trypanosomiasis	4	0.012	1.99E-02

yellow	hsa04370:VEGF signaling pathway	5	0.015	2.23E-02
yellow	hsa05131:Shigellosis	5	0.015	2.61E-02
yellow	hsa04066:HIF-1 signaling pathway	6	0.018	2.92E-02
yellow	hsa05120:Epithelial cell signaling in Helicobacter pylori infection	5	0.015	3.02E-02
yellow	hsa05322:Systemic lupus erythematosus	7	0.021	3.08E-02
yellow	hsa04662:B cell receptor signaling pathway	5	0.015	3.32E-02
yellow	hsa04660:T cell receptor signaling pathway	6	0.018	3.51E-02
yellow	hsa04010:MAPK signaling pathway	10	0.030	3.60E-02
yellow	hsa04020:Calcium signaling pathway	8	0.024	3.86E-02
yellow	hsa05161:Hepatitis B	7	0.021	4.28E-02
yellow	hsa04612:Antigen processing and presentation	5	0.015	4.49E-02
green	hsa05205:Proteoglycans in cancer	8	0.024	1.06E-02
green	hsa04520:Adherens junction	5	0.015	1.06E-02
green	hsa04015:Rap1 signaling pathway	8	0.024	1.36E-02
green	hsa04068:FoxO signaling pathway	6	0.018	2.32E-02
red	hsa00563:Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	4	0.013	2.57E-03
red	hsa04142:Lysosome	6	0.019	1.10E-02
red	hsa04141:Protein processing in endoplasmic reticulum	7	0.022	1.11E-02
red	hsa05200:Pathways in cancer	10	0.032	2.98E-02
red	hsa05010:Alzheimer's disease	6	0.019	3.89E-02
black	hsa04330:Notch signaling pathway	4	0.027	3.20E-03
black	hsa04514:Cell adhesion molecules (CAMs)	5	0.033	1.13E-02
black	hsa04270:Vascular smooth muscle contraction	4	0.027	3.73E-02
pink	hsa04919:Thyroid hormone signaling pathway	3	0.021	3.84E-02
magenta	hsa04360:Axon guidance	6	0.056	5.98E-04
magenta	hsa04070:Phosphatidylinositol signaling system	5	0.047	1.94E-03
magenta	hsa00562:Inositol phosphate metabolism	4	0.038	6.78E-03
magenta	hsa04062:Chemokine signaling pathway	5	0.047	1.84E-02
magenta	hsa04024:cAMP signaling pathway	5	0.047	2.26E-02
magenta	hsa05205:Proteoglycans in cancer	5	0.047	2.33E-02
magenta	hsa04810:Regulation of actin cytoskeleton	5	0.047	2.77E-02
magenta	hsa04923:Regulation of lipolysis in adipocytes	3	0.028	3.76E-02
magenta	hsa04550:Signaling pathways regulating pluripotency of stem cells	4	0.038	4.10E-02
purple	hsa04510:Focal adhesion	6	0.064	1.06E-03
purple	hsa05202:Transcriptional misregulation in cancer	5	0.053	3.82E-03
purple	hsa05205:Proteoglycans in cancer	5	0.053	7.09E-03
purple	hsa04610:Complement and coagulation cascades	3	0.032	2.94E-02
purple	hsa05100:Bacterial invasion of epithelial cells	3	0.032	3.68E-02
purple	hsa04015:Rap1 signaling pathway	4	0.043	4.74E-02

greenyellow	hsa04110:Cell cycle	7	0.074	1.23E-05
greenyellow	hsa03030:DNA replication	4	0.042	4.79E-04
greenyellow	hsa04115:p53 signaling pathway	4	0.042	2.93E-03
greenyellow	hsa04512:ECM-receptor interaction	4	0.042	6.12E-03
greenyellow	hsa05166:HTLV-I infection	5	0.053	2.36E-02
tan	hsa05164:Influenza A	9	0.162	2.12E-08
tan	hsa05168:Herpes simplex infection	9	0.162	3.15E-08
tan	hsa05162:Measles	7	0.126	1.94E-06
tan	hsa05160:Hepatitis C	5	0.090	6.09E-04
tan	hsa04612:Antigen processing and presentation	3	0.054	2.19E-02