

SUPPLEMENTARY TABLES

Supplementary Table 15. 21 pathways enriched by using MAGMA gene-set analysis based on the KEGG pathway resource.

Pathway Name	Gene Number	Beta	MAGMA-based P values	KOBAS-based P values (genes from the discovery stage)
Pyruvate metabolism	38	0.35	4.88E-03	5.70E-02
Acute myeloid leukemia	53	0.28	5.67E-03	1.03E-02
Toxoplasmosis	121	0.20	6.47E-03	6.68E-04
Type II diabetes mellitus	44	0.30	9.75E-03	3.13E-03
Neurotrophin signaling pathway	121	0.17	9.91E-03	8.91E-04
RIG-I-like receptor signaling pathway	62	0.27	1.09E-02	5.87E-02
B cell receptor signaling pathway	70	0.20	1.55E-02	4.15E-03
Adipocytokine signaling pathway	64	0.22	1.69E-02	5.68E-02
Natural killer cell mediated cytotoxicity	128	0.16	1.81E-02	5.60E-05
VEGF signaling pathway	73	0.20	2.11E-02	1.32E-03
Insulin signaling pathway	127	0.14	2.46E-02	1.93E-03
Toll-like receptor signaling pathway	95	0.18	2.55E-02	2.26E-03
Jak-STAT signaling pathway	142	0.14	2.69E-02	4.68E-03
Drug metabolism - cytochrome P450	71	0.23	2.70E-02	4.98E-05
mTOR signaling pathway	45	0.21	3.08E-02	8.13E-04
Prostate cancer	85	0.16	3.42E-02	3.44E-02
Pancreatic cancer	66	0.16	4.16E-02	6.88E-02
Hepatitis C	128	0.12	4.62E-02	1.87E-04
Metabolism of xenobiotics by cytochrome P450	71	0.20	4.74E-02	4.90E-04

Supplementary Table 16. The proportion of multiple layers of evidence in constructed GGI network using the GeneMANIA tool.

ID	Evidence of interactions	Proportions
1	Co-expression links	71.52%
2	Predicted links	19.09%
3	Physical interactions	8.44%
4	Pathways	0.39%
5	Genetic interactions	0.31%
6	Shared protein domains	0.23%
7	Co-localization	0.02%

Supplementary Table 17. Differential expression analysis of 26 candidate genes between infected cells and uninfected cells based on the GSE133803 data.

Gene	GSM3927531 (infected cells)	GSM3927532 (infected cells)	GSM3927533 (infected cells)	GSM3927534 (uninfected cells)	GSM3927535 (uninfected cells)	GSM3927536 (uninfected cells)	P values (t-test)
<i>RPS23</i>	9.91	9.69	9.47	12.03	12.05	12.02	5.45E-05
<i>RPS5</i>	11.52	11.14	11.08	13.08	13.16	13.02	2.11E-04
<i>CLN8</i>	6.74	6.85	6.77	7.78	7.78	7.76	8.18E-06
<i>SPATA20</i>	10.15	9.77	9.63	10.97	11.02	10.95	1.98E-03
<i>CDC16</i>	11.36	11.11	11.05	12.33	12.45	12.22	5.63E-04
<i>TMEM99</i>	9.40	9.42	9.09	10.31	10.37	10.11	2.00E-03
<i>LIG3</i>	7.90	7.65	7.67	8.51	8.49	8.35	1.86E-03
<i>RRM1</i>	10.49	10.24	10.00	11.13	11.16	11.12	3.24E-03
<i>SCAPER</i>	8.10	8.04	7.96	8.44	8.41	8.45	8.84E-04
<i>ZNF266</i>	6.78	6.76	6.74	6.77	7.17	7.24	0.110
<i>RCN3</i>	11.07	10.79	10.91	11.37	11.51	11.31	8.73E-03
<i>CARD9</i>	7.13	7.39	7.09	7.55	7.44	7.43	5.48E-02
<i>TBRG4</i>	8.66	8.24	8.44	8.74	8.77	8.63	0.111
<i>ZNF502</i>	7.62	7.67	7.30	7.84	7.75	7.68	0.143
<i>ZNF197</i>	6.96	7.05	6.91	7.06	7.25	7.18	5.40E-02
<i>NUDT13</i>	7.06	6.77	6.96	7.03	7.27	6.96	0.281
<i>HDAC10</i>	7.14	6.78	6.88	7.05	7.06	6.98	0.424
<i>TDRKH</i>	6.91	6.69	6.77	6.64	6.77	6.89	0.833
<i>PDK1</i>	7.24	7.13	7.04	7.13	7.26	6.95	0.825
<i>CDK10</i>	6.77	6.74	6.59	6.68	6.59	6.68	0.494
<i>DHX57</i>	6.70	6.81	6.69	6.64	6.80	6.59	0.475
<i>NPHP4</i>	8.00	7.78	7.86	7.87	7.82	7.62	0.318
<i>ZNF354A</i>	7.29	7.26	7.49	7.24	7.34	7.09	0.293
<i>FCHO1</i>	6.77	6.90	6.65	6.42	6.75	6.67	0.267
<i>MAP1S</i>	10.71	10.32	10.30	9.81	9.88	9.71	1.01E-02
<i>HIATL1</i>	10.41	10.42	10.37	8.24	8.31	8.24	1.83E-07

Note: The P values were calculated by using the Student's t test.