

**Supplementary Table S4.** Summary of functional enrichment in the network generated from initial miR-TF selected genes (for complete details, see Supplementary File 6).

Description	Observed	Background	Strength	FDR
<b>Biological process (GO)</b>				
Positive regulation of cellular biosynthetic process	16	2005	0.89	4.04E-09
Positive regulation of transcription, DNA-templated	14	1587	0.94	2.39E-08
Interleukin-1-mediated signaling pathway	6	96	1.79	4.58E-07
I- $\kappa$ B kinase/NF- $\kappa$ B signaling	5	74	1.82	8.10E-06
Negative regulation of cell death	10	999	0.99	8.19E-06
NIK/NF- $\kappa$ B signaling	5	81	1.78	1.13E-05
Negative regulation of apoptotic signaling pathway	6	232	1.4	4.45E-05
Regulation of type I interferon production	5	130	1.58	7.45E-05
Fc-epsilon receptor signaling pathway	4	115	1.53	0.0011
Regulation of canonical Wnt signaling pathway	5	291	1.23	0.0015
Response to cytokine	8	1101	0.85	0.0012
Pattern recognition receptor signaling pathway	4	125	1.5	0.0013
Positive regulation of protein ubiquitination	4	126	1.49	0.0014
Regulation of innate immune response	5	301	1.21	0.0017
Negative regulation of NF- $\kappa$ B transcription factor activity	3	85	1.54	0.0077
Toll-like receptor signaling pathway	3	100	1.47	0.0109
<b>Molecular function (GO)</b>				
Transcription regulatory region sequence-specific DNA binding	9	1028	0.93	0.0007
RNA polymerase II transcription regulatory region sequence-specific DNA binding	8	878	0.95	0.0007
DNA-binding transcription activator activity, RNA polymerase II-specific	7	449	1.18	0.0007
Chromatin binding	7	570	1.08	0.0007
DNA-binding transcription factor activity	9	1238	0.85	0.0007
Transcription factor binding	8	672	1.07	0.0007
Ubiquitin protein ligase binding	6	296	1.3	0.0007
Transcription regulator activity	11	1657	0.81	0.0007
$\beta$ -catenin binding	3	86	1.53	0.0189
<b>Local network cluster (STRING)</b>				
Canonical NF- $\kappa$ B pathway, and NF- $\kappa$ B/Dorsal	6	12	2.69	4.45E-08
<b>KEGG pathway</b>				
Chemokine signaling pathway	5	186	1.42	5.62E-05
RIG-I-like receptor signaling pathway	4	70	1.75	5.62E-05
B cell receptor signaling pathway	4	78	1.7	5.62E-05
Th1 and Th2 cell differentiation	4	87	1.65	6.47E-05
IL-17 signaling pathway	4	92	1.63	6.59E-05
NF- $\kappa$ B signaling pathway	4	101	1.59	7.65E-05
Toll-like receptor signaling pathway	4	101	1.59	7.65E-05
T cell receptor signaling pathway	4	101	1.59	7.65E-05
TNF signaling pathway	4	112	1.54	8.84E-05

Reactome pathway				
Activation of NF- $\kappa$ B in B cells	6	65	1.96	1.18E-06
I $\kappa$ BA variant leads to EDA-ID	4	7	2.75	1.79E-06
Interleukin-1 signaling	6	99	1.77	3.25E-06
Fc $\epsilon$ RI mediated NF- $\kappa$ B activation	5	80	1.79	2.77E-05
TRAF6 mediated NF- $\kappa$ B activation	4	24	2.21	2.77E-05
Toll Like Receptor 3 (TLR3) Cascade	5	92	1.73	3.42E-05
Downstream TCR signaling	5	91	1.73	3.42E-05
TRAF6 mediated induction of NF- $\kappa$ B and MAP kinases upon TLR7/8 or 9 activation	5	89	1.74	3.42E-05
TAK1 activates NF- $\kappa$ B by phosphorylation and activation of IKKs complex	4	32	2.09	3.44E-05
CLEC7A (Dectin-1) signaling	5	96	1.71	3.44E-05
TRIF(TICAM1)-mediated TLR4 signaling	5	96	1.71	3.44E-05
NF- $\kappa$ B is activated and signals survival	3	13	2.35	0.00024
Adaptive Immune System	7	743	0.96	0.0023
Signaling by WNT	5	296	1.22	0.0041
Immune System	9	1956	0.65	0.0173
Protein domains and features (InterPro)				
NF- $\kappa$ B/Dorsal	3	5	2.77	0.0015
NF- $\kappa$ B IPT domain	3	5	2.77	0.0015
Rel homology domain (RHD), DNA-binding domain	3	10	2.47	0.0019
Rel homology dimerization domain	3	10	2.47	0.0019
Rel homology domain (RHD), DNA-binding domain superfamily	3	10	2.47	0.0019
p53-like transcription factor, DNA-binding	3	44	1.82	0.0467