

Supplementary Table S2. Summary of functional enrichment in the network generated from initial PPIN selected genes (for complete details, see Supplementary File 4).

Description	Observed	Background	Strength	FDR
Biological process (GO)				
Proteasome-mediated ubiquitin-dependent protein catabolic process	10	323	1.29	3.02E-07
Proteolysis	15	1256	0.88	3.42E-07
Macromolecule catabolic process	13	1058	0.89	5.19E-06
Organonitrogen compound catabolic process	13	1070	0.88	5.40E-06
Regulation of canonical Wnt signaling pathway	6	291	1.11	0.0016
I- κ B kinase/NF- κ B signaling	4	74	1.53	0.0017
NIK/NF- κ B signaling	4	81	1.49	0.0022
Interleukin-1-mediated signaling pathway	4	96	1.42	0.0034
β -catenin-TCF complex assembly	3	29	1.81	0.0034
Stress-activated MAPK cascade	4	107	1.37	0.0047
Molecular function (GO)				
β -catenin binding	6	86	1.64	3.18E-05
Ubiquitin conjugating enzyme activity	4	40	1.8	0.0017
Transcription factor binding	8	672	0.88	0.0089
Ubiquitin protein ligase binding	6	296	1.11	0.0089
Enzyme binding	13	2239	0.56	0.0122
Local network cluster (STRING)				
Canonical NF- κ B pathway, and NF- κ B/Dorsal	4	12	2.32	0.0449
KEGG pathway				
Ubiquitin mediated proteolysis	8	135	1.57	2.05E-08
Cell cycle	7	120	1.57	2.13E-07
Wnt signaling pathway	5	154	1.31	0.00027
MAPK signaling pathway	5	288	1.04	0.0025
Th1 and Th2 cell differentiation	3	87	1.34	0.0073
IL-17 signaling pathway	3	92	1.31	0.0082
NF- κ B signaling pathway	3	101	1.27	0.0095
Toll-like receptor signaling pathway	3	101	1.27	0.0095
Th17 cell differentiation	3	101	1.27	0.0095
T cell receptor signaling pathway	3	101	1.27	0.0095
Reactome pathway				
Adaptive Immune System	11	743	0.97	0.00012
Signal Transduction	18	2741	0.62	0.00012
Immune System	16	1956	0.71	0.00012
CLEC7A (Dectin-1) signaling	6	96	1.6	0.00012
Antigen processing: Ubiquitination & Proteasome degradation	8	304	1.22	0.00012
Inactivation of APC/C via direct inhibition of the APC/C complex	4	20	2.1	0.00015
Fc ϵ RI signaling	5	129	1.39	0.0021
Innate immune system	10	1025	0.79	0.0024

Interleukin-1 family signaling	5	136	1.37	0.0024
Activation of NF- κ B in B cells	4	65	1.59	0.0034
FCERI mediated NF- κ B activation	4	80	1.5	0.0058
Degradation of beta-catenin by the destruction complex	4	81	1.49	0.0059
TRAF6 mediated induction of NF- κ B and MAP kinases upon TLR7/8 or 9 activation	4	89	1.45	0.0071
Toll Like Receptor 3 (TLR3) Cascade	4	92	1.44	0.0072
Interleukin-1 signaling	4	99	1.41	0.0073
Protein domains and features (InterPro)				
NF- κ B/Dorsal	3	5	2.58	0.0035
Ubiquitin-conjugating enzyme E2	4	38	1.82	0.0035
Ubiquitin-conjugating enzyme, active site	4	25	2	0.0035
Rel homology domain, conserved site	3	5	2.58	0.0035
NF- κ B IPT domain	3	5	2.58	0.0035
Rel homology domain (RHD), DNA-binding domain	3	10	2.28	0.005
Rel homology dimerisation domain	3	10	2.28	0.005
Rel homology domain (RHD), DNA-binding domain superfamily	3	10	2.28	0.005
Ubiquitin-conjugating enzyme/RWD-like	4	53	1.68	0.0062