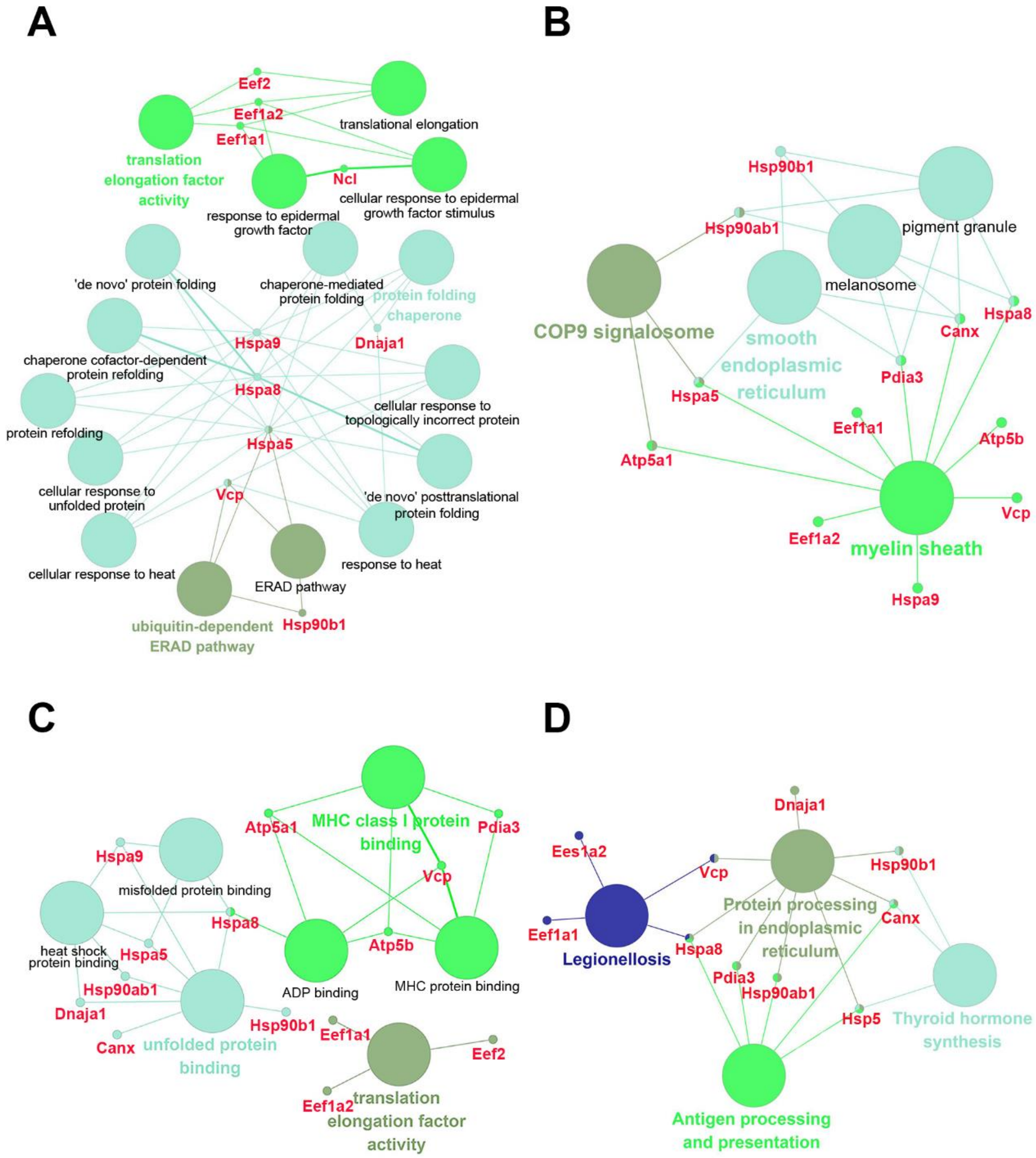

Supplemental figure 1: **Enrichment analysis of the most significant module of PPI network. A.** Biological process enrichment. **B.** Cellular component enrichment. **C.** Molecular function enrichment. **D.** KEGG pathway enrichment. GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Supplemental Table 1. Top 10 functions and pathways enriched by GO and KEGG analyses of all proteins.

ID	Term	Associated genes (%)	P Value	P Value corrected with Benjamini-Hochberg
Biological process (BP)				
GO:0032482	endoplasmic reticulum to cytosol transport	16.67	3.91E-08	2.88E-07
GO:0034605	retrograde protein transport, ER to cytosol	16.67	3.91E-08	2.88E-07
GO:0006888	structural constituent of cytoskeleton	8.45	1.06E-07	6.11E-07
GO:0010595	ubiquitin-dependent ERAD pathway	8.45	1.06E-07	6.11E-07
GO:0006487	ubiquitin-dependent ERAD pathway	8.45	1.06E-07	6.11E-07
GO:0070670	acylglycerol metabolic process	5.07	2.96E-07	1.50E-06
GO:0071353	neutral lipid metabolic process	4.93	3.59E-07	1.71E-06
GO:0070849	lipid droplet organization	21.05	3.61E-07	1.62E-06
GO:0071364	protein exit from endoplasmic reticulum	10.87	3.61E-07	1.54E-06
GO:0006414	ERAD pathway	6.19	6.82E-07	2.76E-06
Cellular component (CC)				
GO:0005811	lipid droplet	16.85	2.46E-22	1.99E-20
GO:0043209	myelin sheath	5.44	6.32E-13	2.56E-11
GO:0048770	pigment granule	5.98	9.55E-08	5.95E-07
GO:0042470	melanosome	5.98	9.55E-08	5.95E-07
GO:0048770	pigment granule	5.98	9.55E-08	5.95E-07
GO:0042470	melanosome	5.98	9.55E-08	5.95E-07
GO:0034098	VCP-NPL4-UFD1 AAA ATPase complex	33.33	2.61E-06	8.80E-06
GO:0034098	VCP-NPL4-UFD1 AAA ATPase complex	33.33	2.61E-06	8.80E-06
GO:0000786	nucleosome	4.72	3.31E-06	1.03E-05
GO:0005790	smooth endoplasmic reticulum	9.52	9.86E-06	2.75E-05
Molecular function (MF)				
GO:0001882	nucleoside binding	3.33	1.03E-11	2.79E-10
GO:0005525	GTP binding	3.39	4.41E-11	8.93E-10
GO:0032550	purine ribonucleoside binding	3.21	9.01E-11	1.46E-09
GO:0001883	purine nucleoside binding	3.18	1.02E-10	1.37E-09
GO:0032549	ribonucleoside binding	3.18	1.02E-10	1.37E-09
GO:0019001	guanyl nucleotide binding	3.10	1.45E-10	1.67E-09
GO:0032561	guanyl ribonucleotide binding	3.10	1.45E-10	1.67E-09

ID	Term	Associated genes (%)	P Value	P Value corrected with Benjamini-Hochberg
GO:0044389	ubiquitin-like protein ligase binding	3.31	1.65E-09	1.67E-08
GO:0031625	ubiquitin protein ligase binding	3.19	1.22E-08	1.10E-07
GO:0042288	MHC class I protein binding	18.52	2.23E-08	1.81E-07
KEGG pathway				
KEGG:04141	Protein processing in endoplasmic reticulum	6.13	5.75E-08	5.75E-07
KEGG:04540	Gap junction	6.98	1.56E-05	7.78E-05
KEGG:05322	Systemic lupus erythematosus	4.90	2.97E-05	9.89E-05
KEGG:05134	Legionellosis	8.62	3.01E-05	7.53E-05
KEGG:04145	Phagosome	3.87	1.33E-04	2.65E-04
KEGG:00100	Steroid biosynthesis	15.79	2.17E-04	3.62E-04
KEGG:04612	Antigen processing and presentation	5.49	2.61E-04	3.73E-04
KEGG:05034	Alcoholism	3.02	1.53E-03	1.91E-03
KEGG:00564	Glycerophospholipid metabolism	4.12	3.24E-03	3.60E-03
KEGG:04918	Thyroid hormone synthesis	4.11	1.10E-02	1.10E-02

GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Supplemental Table 2. Top 10 proteins with the highest degrees, betweenness and closeness.

No.	**Protein**	**Degree**	**Protein**	**Betweenness**	**Protein**	**Closeness**
1	Hsp90ab1	21	Hsp90ab1	0.22733206	Alg2	1
2	Hspa8	20	Hspa8	0.14978058	Dhrs1	1
3	Canx	17	Hist2h3c2	0.11454919	Hsp90ab1	0.51724138
4	Hspa5	17	Canx	0.11131336	Hspa8	0.51282051
5	Hspa9	16	Faf2	0.10550396	Hspa5	0.49180328
6	Eef1a1	15	Aup1	0.1020381	Canx	0.48780488
7	Hsp90b1	15	Tubb5	0.09105492	Vcp	0.47244094
8	Atp5b	15	Hspa5	0.0771835	Hsp90b1	0.47244094
9	Faf2	14	Plin2	0.07100355	Eef1a1	0.46153846
10	Vcp	14	Acta2	0.07027218	Atp5b	0.45454545

Supplemental Table 3. Enrichment analysis of sub-network1.

ID	Term	Associated genes (%)	P Value	P Value corrected with Benjamini-Hochberg
Biological process (BP)				
GO:0044183	protein folding chaperone	16.00	2.01E-09	3.02E-08
GO:0009408	response to heat	3.82	2.35E-08	1.76E-07
GO:0061077	chaperone-mediated protein folding	6.56	8.18E-08	4.09E-07
GO:0034605	cellular response to heat	5.41	1.79E-07	6.72E-07
GO:0003746	translation elongation factor activity	13.64	4.34E-07	1.30E-06
GO:0035967	cellular response to topologically incorrect	3.92	6.55E-07	1.64E-06
GO:0042026	protein refolding	9.68	1.26E-06	2.71E-06
GO:0051085	chaperone cofactor-dependent protein	9.38	1.39E-06	2.61E-06
GO:0051084	'de novo' posttranslational protein folding	8.11	2.18E-06	3.63E-06
GO:0006458	'de novo' protein folding	7.89	2.36E-06	3.54E-06
GO:0006414	translational elongation	5.77	6.15E-06	8.39E-06
GO:0071364	cellular response to epidermal growth factor	4.62	1.21E-05	1.51E-05
GO:0030433	ubiquitin-dependent ERAD pathway	4.23	1.58E-05	1.82E-05
GO:0070849	response to epidermal growth factor	4.23	1.58E-05	1.82E-05
GO:0034620	cellular response to unfolded protein	3.75	2.26E-05	2.42E-05
GO:0036503	ERAD pathway	3.09	4.03E-05	4.03E-05
Cellular component (CC)				
GO:0043209	myelin sheath	4.18	7.12E-17	2.85E-16
GO:0048770	pigment granule	4.27	1.29E-08	2.57E-08
GO:0042470	melanosome	4.27	1.29E-08	2.57E-08
GO:0005790	smooth endoplasmic reticulum	9.52	1.72E-08	2.29E-08
GO:0008180	COP9 signalosome	7.89	2.31E-06	2.31E-06
Molecular function (MF)				
GO:0051082	unfolded protein binding	6.36	5.58E-13	3.90E-12
GO:0042288	MHC class I protein binding	14.81	2.94E-09	1.03E-08
GO:0042287	MHC protein binding	9.30	2.05E-08	4.79E-08
GO:0043531	ADP binding	8.70	2.71E-08	4.74E-08
GO:0031072	heat shock protein binding	3.14	6.63E-08	9.28E-08
GO:0051787	misfolded protein binding	15.00	3.35E-07	3.90E-07
GO:0003746	translation elongation factor activity	13.64	4.52E-07	4.52E-07

ID	Term	Associated genes (%)	P Value	P Value corrected with Benjamini-Hochberg
KEGG pathway				
KEGG:04141	Protein processing in endoplasmic reticulum	4.91	4.81E-11	1.92E-10
KEGG:04612	Antigen processing and presentation	5.49	2.54E-07	5.09E-07
KEGG:04918	Thyroid hormone synthesis	4.11	2.17E-04	2.17E-04
KEGG:05134	Legionellosis	6.90	1.99E-06	2.65E-06

GO, gene ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.