

# Table S1

Supplementary Table 1. Primers for qPCR.

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')	TaqMan probe (5' to 3')
<i>Pparγ</i>	CTGCTCCACACTATGAAGACA T	TGCAGGTTCTACTTTGATCG C	/FAM/AGCTGACCC/ZEN/AATGGTTGCTGATTACA/IABkFQ/
<i>Cebpa</i>	ACAAGAACAGCAACGAGTAC C	TCATTGTCACTGGTCAACTC C	/FAM/CGCAAGAGC/ZEN/CGAGATAAAGCCAAAC/IABkFQ/ /FAM/
<i>Ap2</i>	AAATCACCGCAGACGACAG	CCTTTCATAACACATTCCAC CAC	TGAAGAGCA/ZEN/TCATAACCCTAGATGGCG/IABkFQ/ /
<i>Leptin</i>	GTGCCTATCCAGAAAGTCCA G	AATGAAGTCCAAGCCAGTGA	/FAM/ACCGACTGC/ZEN/GTGTGTGAAATGTCA/IABkFQ/ /56-
<i>AdipoQ</i>	GCAGGATTAAGAGGAACAGG AG	TGTCTGTACGATTGTCAGTG G	FAM/ACGACACCA/ZEN/AAAGGGCTCAGGAT/3IABkFQ/ Q/
<i>36b4</i>	TTATAACCCTGAAGTGCTCGA C	CGCTTGTACCCATTGATGAT G	/FAM/AGGCCCTGC/ZEN/ACTCTCGCTT/IABkFQ/

Table S2

Supplementary Table 2. Top 60 genes of upregulation and down regulation

Upregulation (Total: 826 genes)				Downregulation (Total: 725 genes)			
	log 2 Fold Change (3D/2D)	Gene symbol	Gene biotype		log 2 Fold Change (3D/2D)	Gene symbol	Gene biotype
1	9.00	Selp	protein_coding	-8.01	Ogn	protein_coding	
2	8.94	U90926	protein_coding	-7.93	Tinag	protein_coding	
3	7.85	Ranbp3l	protein_coding	-7.44	Inmt	protein_coding	
4	7.82	Plin1	protein_coding	-7.12	Pgm5	protein_coding	
5	7.66	Ccr1	protein_coding	-7.06	Rnf112	protein_coding	
6	7.56	Rab15	protein_coding	-6.79	1500015O10Rik	protein_coding	
7	7.00	Gm16548	lincRNA	-6.78	Omd	protein_coding	
8	6.98	Gm567	lincRNA	-6.76	Angptl7	protein_coding	
9	6.89	Lgr6	protein_coding	-6.48	Bmp4	protein_coding	
10	6.89	Gucy2g	protein_coding	-6.34	Fhod3	protein_coding	
11	6.89	Saa3	protein_coding	-6.17	Cpa1	protein_coding	
12	6.83	Ing4	protein_coding	-6.14	9130208D14Rik	unprocessed_pseudogene	
13	6.83	Nos2	protein_coding	-6.13	Itgbl1	protein_coding	
14	6.80	Tnn	protein_coding	-6.08	Trhde	protein_coding	
15	6.63	Accsl	protein_coding	-6.04	Tek	protein_coding	
16	6.60	Camp	protein_coding	-6.01	Fgf14	protein_coding	
17	6.58	Gm43609	TEC	-5.77	Ifi2712a	protein_coding	
18	6.52	Hr	protein_coding	-5.73	Slc4a10	protein_coding	
19	6.49	Myo1g	protein_coding	-5.69	Igf2	protein_coding	
20	6.49	Rasgrp2	protein_coding	-5.67	Aldh1a7	protein_coding	
21	6.44	Stfa3	protein_coding	-5.5	Optc	protein_coding	
22	6.43	Snord43	miRNA	-5.45	Nkain2	protein_coding	
23	6.36	Gm37309	TEC	-5.36	Clec3b	protein_coding	
24	6.32	Cd79a	protein_coding	-5.32	Rgag1	protein_coding	
25	6.32	Chad	protein_coding	-5.25	Ctsc	protein_coding	
26	6.26	Nppb	protein_coding	-5.15	Aldh1a1	protein_coding	
27	6.26	Gm14508	antisense	-5.15	Sult1a1	protein_coding	
28	6.25	Ngef	protein_coding	-4.72	Chrdl1	protein_coding	
29	6.2	Cyth4	protein_coding	-4.69	Ccl6	protein_coding	
30	6.18	Cck	protein_coding	-4.62	Agtr2	protein_coding	
31	6.14	Gm16587	antisense	-4.56	Fmod	protein_coding	
32	6.13	2700080J24Rik	TEC	-4.55	Krt8	protein_coding	
33	6.11	Slco4a1	protein_coding	-4.43	Gm42922	TEC	
34	6.07	Notumos	antisense	-4.43	Prex2	protein_coding	
35	6.07	Spink6	protein_coding	-4.41	Nrk	protein_coding	
36	5.98	Ces1f	protein_coding	-4.41	Prokr1	protein_coding	
37	5.93	Kcnk10	protein_coding	-4.41	Me3	protein_coding	
38	5.93	Gm26621	processed_transcript	-4.37	Adm	protein_coding	
39	5.93	Lce1f	protein_coding	-4.36	Actr3b	protein_coding	
40	5.93	Mir155hg	lincRNA	-4.33	H19	lincRNA	
41	5.93	Gm26514	lincRNA	-4.3	Dchs2	protein_coding	
42	5.92	Hsbp1l1	protein_coding	-4.29	Gm27786	misc_RNA	
43	5.86	Lcn2	protein_coding	-4.25	Bnc1	protein_coding	
44	5.85	RP23-14P17.5	sense_intronic	-4.16	Gpihbp1	protein_coding	
45	5.85	Il23r	protein_coding	-4.15	Cpz	protein_coding	
46	5.85	Ucn2	protein_coding	-4.15	Krt7	protein_coding	
47	5.85	Scg5	protein_coding	-4.07	Sorbs2	protein_coding	
48	5.85	Gm26789	lincRNA	-4.01	Mylk3	protein_coding	
49	5.85	2310007B03Rik	protein_coding	-3.96	Gm16559	antisense	
50	5.84	Lrg1	protein_coding	-3.96	Myl9	protein_coding	
51	5.84	Rdh8	protein_coding	-3.95	Sdpr	protein_coding	
52	5.77	Greb1	protein_coding	-3.91	Mlana	protein_coding	
53	5.77	Atp13a4	protein_coding	-3.88	Col11a1	protein_coding	
54	5.77	Vipr2	protein_coding	-3.88	Adh1	protein_coding	
55	5.77	Rnf183	protein_coding	-3.86	Mfap5	protein_coding	
56	5.77	Gm37755	TEC	-3.84	Gm27483	misc_RNA	
57	5.76	Pla2g4b	protein_coding	-3.82	Cdh26	protein_coding	
58	5.76	Gm43702	TEC	-3.81	Sema5b	protein_coding	
59	5.67	Mroh4	protein_coding	-3.76	Gm14434	protein_coding	
60	5.67	Snora34	snoRNA	-3.7	Efemp1	protein_coding	

# Table S3

Supplementary Table 3. Possible upstream regulators by IPA upstream analysis

Upstream Regulator	Exp Fold Change	Molecule Type	Predicted Activation State	Activation z-score	p-value of overlap
TNF		cytokine	Activated	4.882	2.53E-55
lipopolysaccharide		chemical drug	Activated	3.541	5.27E-54
PDGF BB		complex	Activated	5.740	1.95E-50
TGF 1	↑ 1.143	growth factor		1.960	1.61E-48
STAT3	↑ 1.029	transcription regulator	Activated	4.465	1.83E-47
dexamethasone		chemical drug	Inhibited	-3.535	4.10E-46
AGT	↑ 1.301	growth factor		1.722	2.87E-44
beta-estradiol		chemical-endogenous	Activated	2.178	4.27E-43
IFNG		cytokine		1.452	2.24E-42
IL1		cytokine	Activated	4.239	7.93E-41
KRAS		enzyme	Activated	3.919	5.68E-36
tretinoin		chemical-endogenous		0.701	1.32E-35
CG		complex		0.728	2.23E-35
IL6	↑ 3.458	cytokine	Activated	4.804	7.10E-35
NFKBIA		transcription regulator		1.145	1.92E-31
HRAS		enzyme	Activated	3.153	2.51E-31
TP53		transcription regulator		-1.913	3.26E-31
JUN		transcription regulator	Activated	3.603	1.04E-29
CTNNB1		transcription regulator		0.348	1.83E-29
U0126		chemical drug	Inhibited	-3.583	2.20E-28
IL10RA		transmembrane receptor		-1.573	4.15E-28
poly rI:C-RNA		biologic drug		0.805	4.20E-28
FOS	↑ 1.512	transcription regulator	Activated	3.086	5.01E-28
SB203580		chemical drug	Inhibited	-3.908	2.08E-27
TAZ		enzyme		-0.765	2.57E-27
Tgf		group		1.004	3.07E-27
IGF1		growth factor	Activated	4.333	4.89E-27
IKBKB		kinase		1.505	4.90E-27
YAP1		transcription regulator		-0.181	1.66E-26
WNT3A		cytokine		0.531	2.02E-26
OSM		cytokine	Activated	3.136	3.80E-26
G protein		group		-1.722	3.87E-26
ESR2		ligand-dependent nuclear receptor	Activated	2.027	4.41E-26
CHUK		kinase		1.880	1.19E-25
KDM1A		enzyme		0.895	2.69E-25
MYC	↑ 1.548	transcription regulator		0.041	2.95E-25
GNA15		enzyme			8.09E-25
PPARGC1A		transcription regulator	Activated	2.038	1.76E-24
PNPT1		enzyme	Activated	4.518	1.98E-24
cardiotoxin		chemical-other	Activated	2.268	2.42E-24
CITED2		transcription regulator		0.676	2.54E-24
IL17A		cytokine	Activated	4.552	2.63E-24
Alpha catenin		group		-0.148	2.70E-24
IFNB1		cytokine	Inhibited	-4.301	3.94E-24
NFkB(complex)		complex	Activated	4.280	4.43E-24
Ige		complex	Activated	4.217	5.64E-24
STAT1		transcription regulator	Inhibited	-2.142	7.53E-24
cycloheximide		chemical reagent		0.803	1.25E-23
IKBKG		kinase		0.450	1.87E-23
LY294002		chemical drug	Inhibited	-2.622	2.14E-23

Figure S1

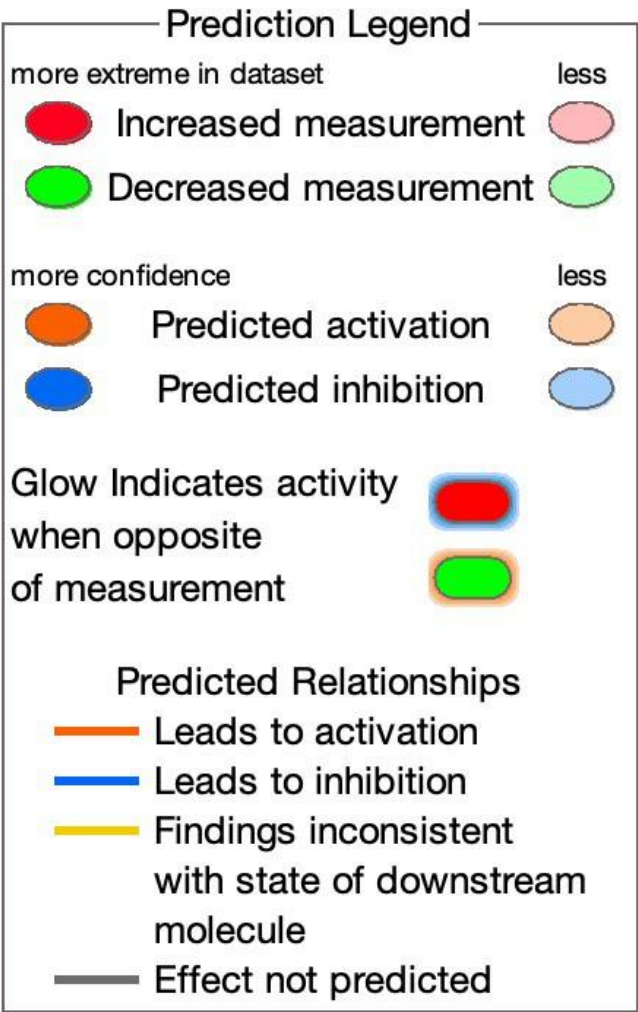


Figure S1: Prediction Legend.

Figure S2

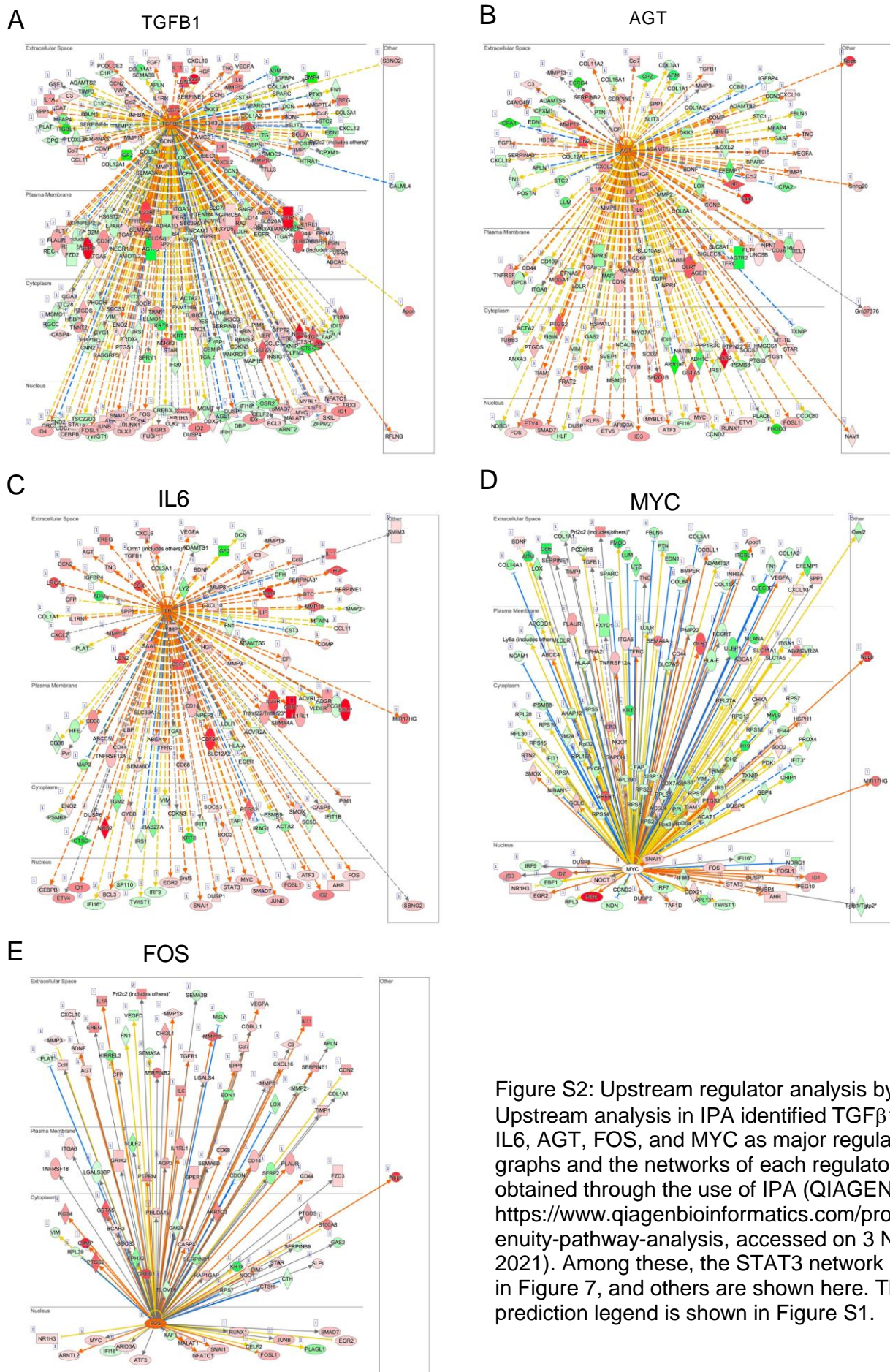
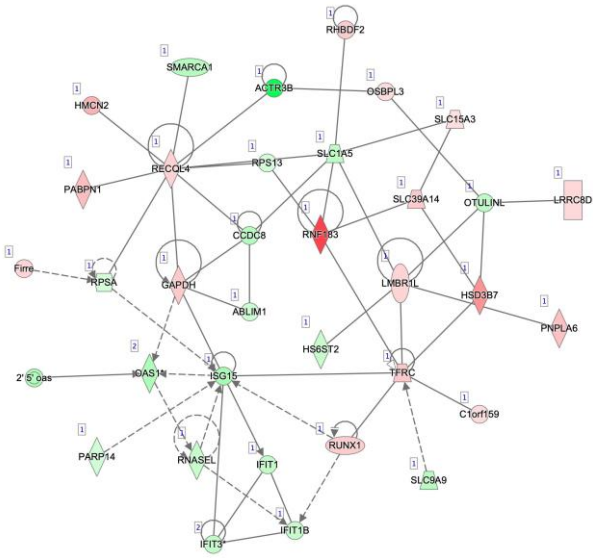


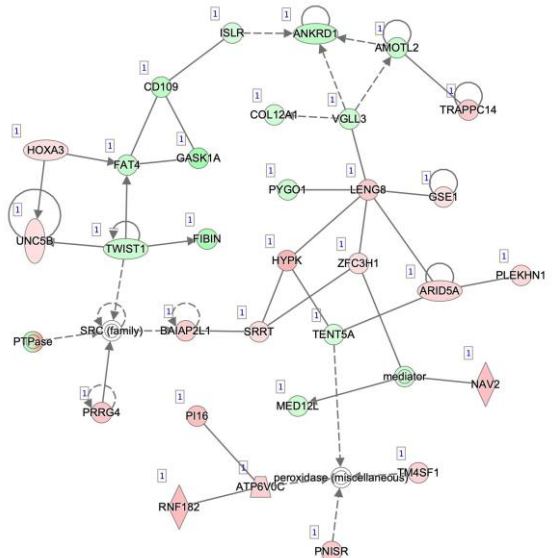
Figure S2: Upstream regulator analysis by IPA. Upstream analysis in IPA identified TGF $\beta$ 1, STAT3, IL6, AGT, FOS, and MYC as major regulators. The graphs and the networks of each regulator were obtained through the use of IPA (QIAGEN Inc., <https://www.qiagenbioinformatics.com/products/ingenuity-pathway-analysis>, accessed on 3 November 2021). Among these, the STAT3 network is shown in Figure 7, and others are shown here. The prediction legend is shown in Figure S1.

## Figure S3A

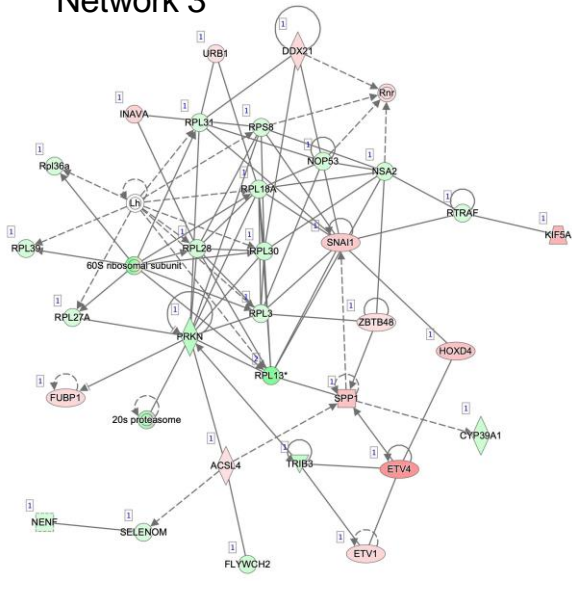
## Network 1



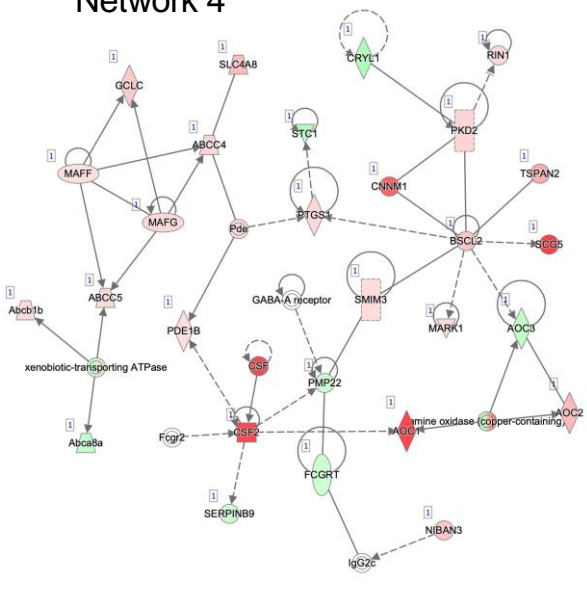
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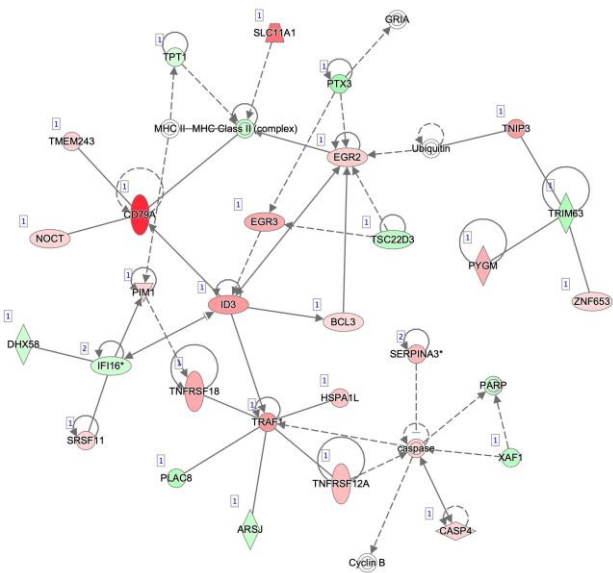
### Network 3



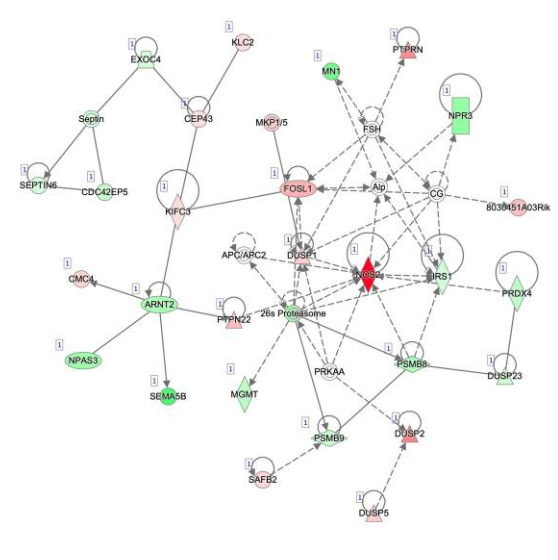
## Network 4



## Network 6

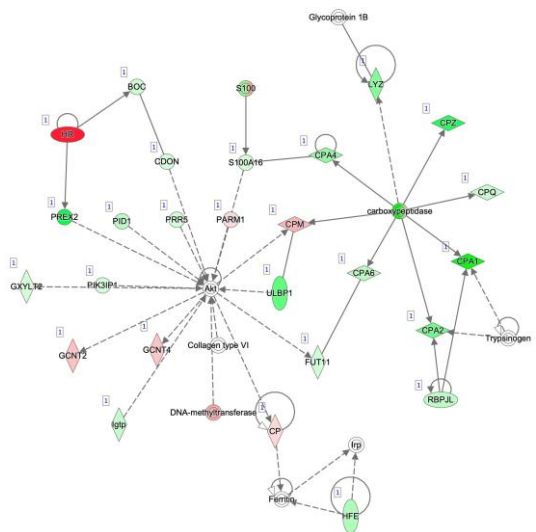


## Network 8

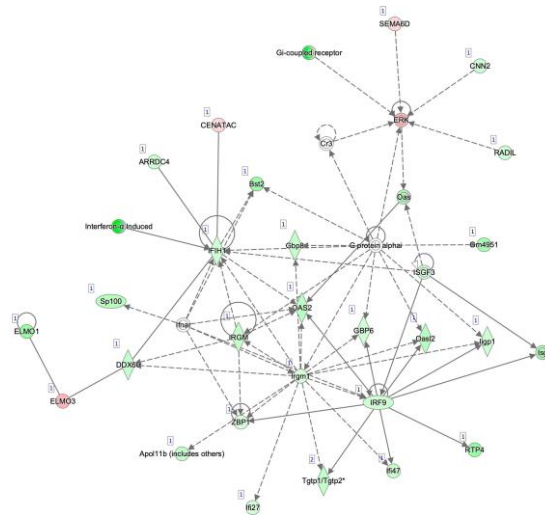


### Figure S3B

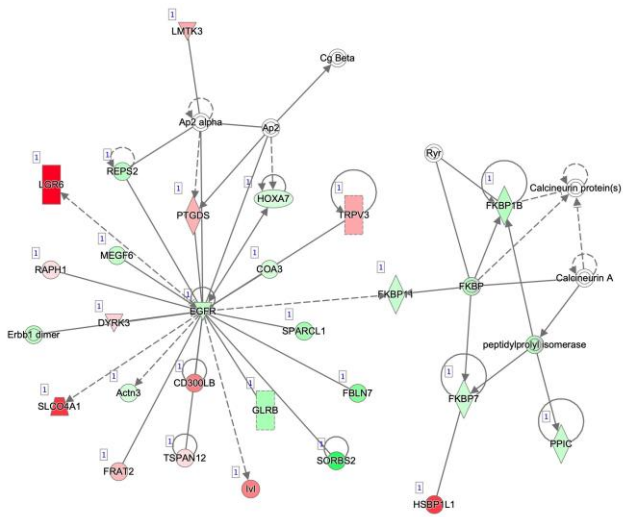
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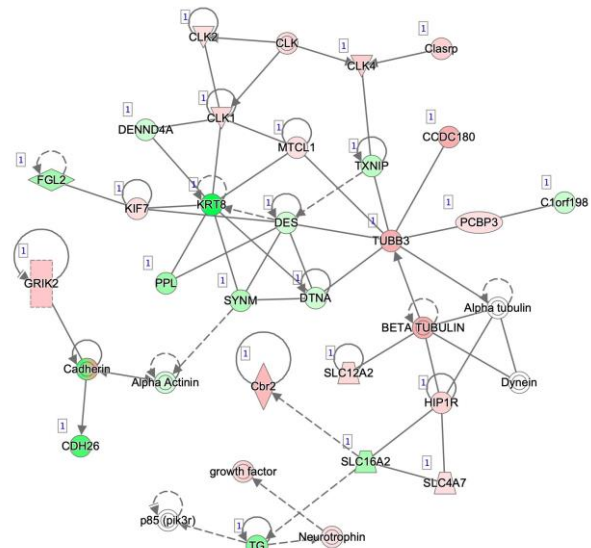
## Network 11



## Network 12



## Network 13



## Network 14

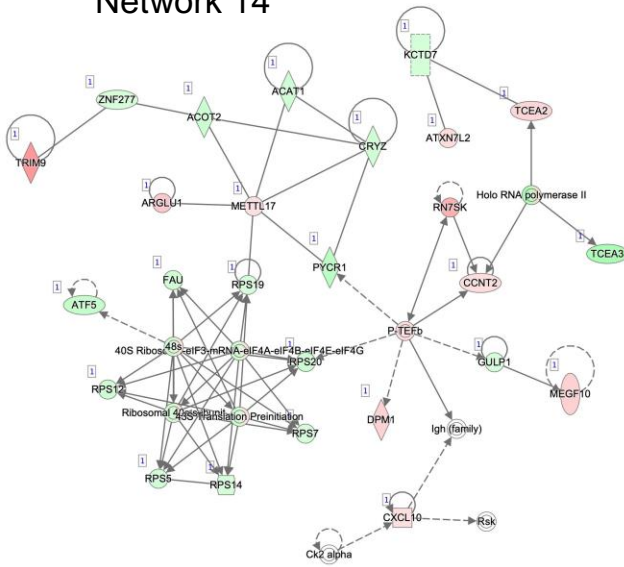
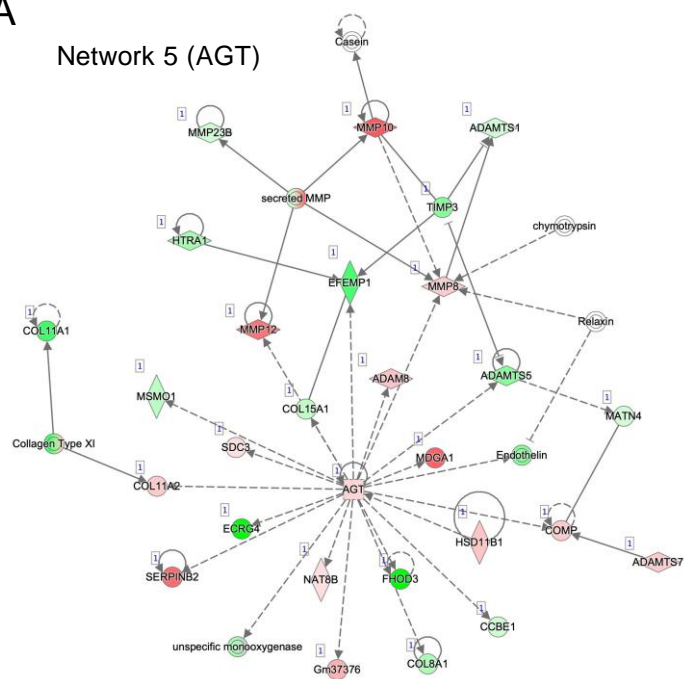


Figure S3: Top 14 causal networks of diseases and functions with IPA network score more than 30 (A: networks 1, 2, 3, 4, 6 and 8, B: networks 9, 11, 12, 13, and 14). Prediction legend is shown in Figure S1.

# Figure S4

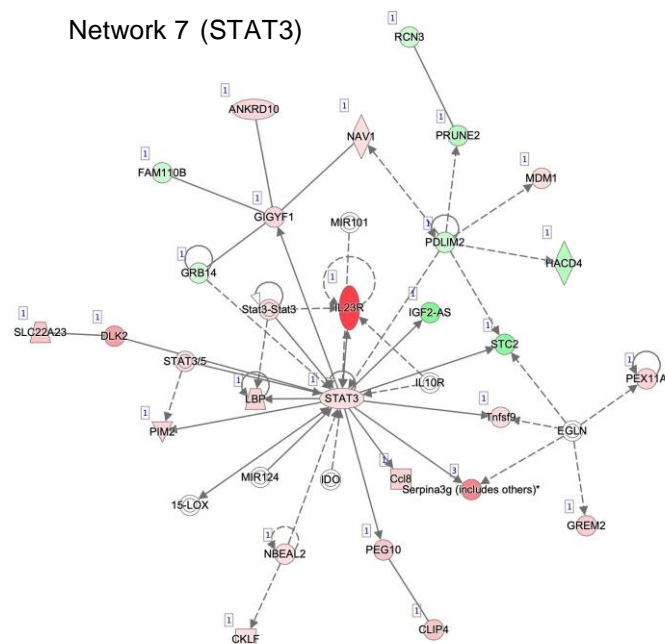
A

Network 5 (AGT)



B

Network 7 (STAT3)



C

Network 10 (TGFB1)

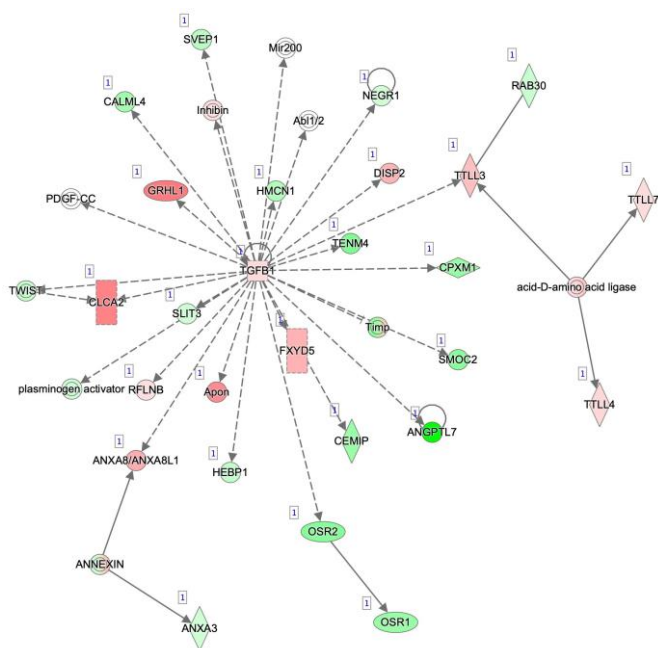


Figure S4: Causal networks related to AGT (network 5, A), STAT3 (network 7, B), and TGF $\beta$ 1 (network 10, C). The prediction legend is shown in Figure S1.