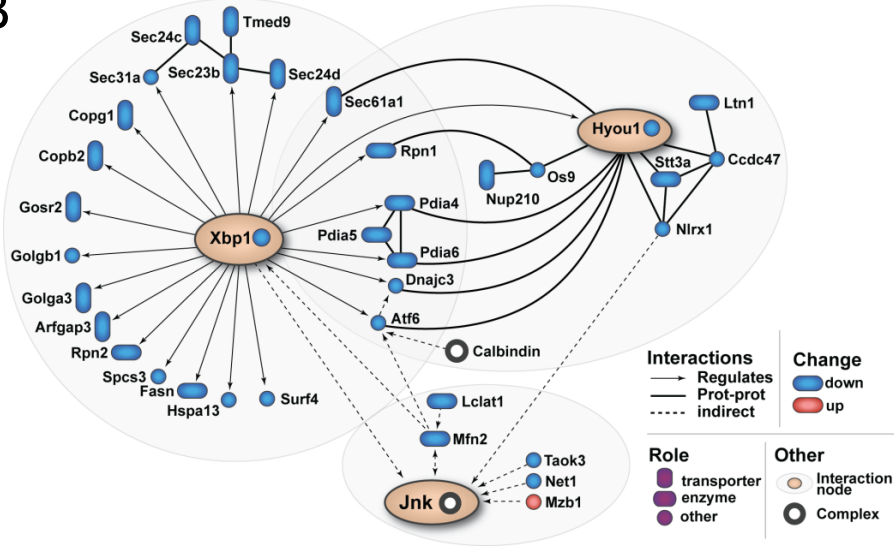


A

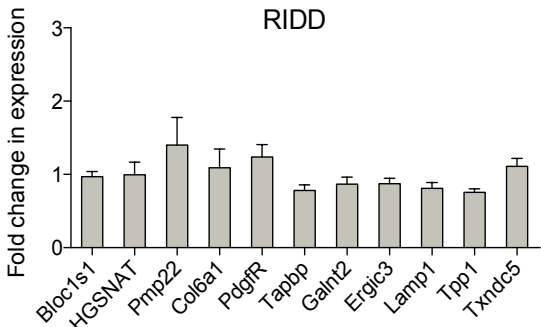
Regulator	Type	Fold	Targets	p	Prediction	Z
XBP1	TF	-1.84	24	1x10 ⁻⁹	Inhibited	-3.17
MKL2	TF		15	2x10 ⁻⁹	Inhibited	-3.16
TGFB1	GF		95	3x10 ⁻¹³	Inhibited	-2.73
SRF	TF		26	2x10 ⁻⁷	Inhibited	-2.71
CD38	enzyme		18	2x10 ⁻⁷	Inhibited	-2.35
MKL1	TF	-1.55	16	7x10 ⁻⁸	Inhibited	-2.33
ITK	kinase	1.80	13	1x10 ⁻⁷	Activated	2.02
NCR1	receptor	2.87	6	7x10 ⁻⁸	Activated	2.22
IL2	cytokine		48	1x10 ⁻¹⁴	Activated	2.77

TF = transcription factor, GF = growth factor, Z=prediction Z-score

B



C



D

Functional cluster	GO terms	Description	Enr	P	FDR	N	%↓
Carbohydrate metabolic process	GO:0044262	cellular carbohydrate metabolic process	2.2	0.0006	1%	24	96%
	GO:0005975	carbohydrate metabolic process	1.9	0.0013	2%	29	97%
Protein localization and transport	GO:0045184	establishment of protein localization	1.7	0.0022	3%	37	78%
	GO:0015031	protein transport	1.7	0.0034	5%	36	81%
	GO:0008104	protein localization	1.6	0.0067	9%	39	77%
Regulation of cell communication	GO:0010646	regulation of cell communication	1.6	0.0034	5%	41	68%
Lipid metabolic process	GO:0006629	lipid metabolic process	1.6	0.0094	13%	36	67%

Enr=enrichment fold, N=number of involved genes, % ↓ =% of involved genes that are down regulated