

Table S3:

The content of the uploaded files including significant protein is used as the input list for generation of biological networks using Transcription Regulation algorithm with default settings. This is a variant of the shortest paths algorithm with main parameters relative saturation of networks with canonical pathways. These networks are built on the fly and unique for the uploaded data. In this workflow the networks are prioritized based on the number of fragments of canonical pathways on the network.

No	Key network objects	p-Value	zScore	gScore
1	SP1 (Homo sapiens)	2.44e-232	122.54	122.54
2	c-Myc (Homo sapiens)	5.02e-180	108.13	108.13
3	p53 (Homo sapiens)	4.87e-124	89.89	89.89
4	HNF4-alpha (Homo sapiens)	4.87e-124	89.89	89.89
5	Androgen receptor (Homo sapiens)	6.80e-102	81.47	81.47
6	c-Jun (Homo sapiens)	7.09e-91	76.91	76.91
7	AP-1 (Homo sapiens)	7.09e-91	76.91	76.91
8	NF-kB (Homo sapiens)	1.77e-86	75.01	75.01
9	ESR1 (nuclear) (Homo sapiens)	2.78e-84	74.04	74.04
10	HIF1A (Homo sapiens)	1.39e-64	64.69	64.69
11	GCR-alpha (Homo sapiens)	2.11e-62	63.57	63.57
12	YY1 (Homo sapiens)	4.79e-58	61.26	61.26
13	CREB1 (Homo sapiens)	7.18e-56	60.07	60.07
14	GATA-1 (Homo sapiens)	1.07e-53	58.86	58.86
15	C/EBPbeta (Homo sapiens)	1.59e-51	57.62	57.62
16	MYOD (Homo sapiens)	2.36e-49	56.36	56.36
17	HSF1 (Homo sapiens)	3.47e-47	55.07	55.07
18	STAT1 (Homo sapiens)	3.47e-47	55.07	55.07
19	C/EBPalpha (Homo sapiens)	7.43e-43	52.39	52.39
20	Oct-3/4 (Homo sapiens)	7.43e-43	52.39	52.39
21	GATA-3 (Homo sapiens)	7.43e-43	52.39	52.39
22	ROR-alpha (Homo sapiens)	7.43e-43	52.39	52.39
23	RelA (p65 NF-kB subunit) (Homo sapiens)	1.08e-40	51.00	51.00
24	SP3 (Homo sapiens)	1.08e-40	51.00	51.00
25	EGR1 (Homo sapiens)	1.08e-40	51.00	51.00
26	SF1 (Homo sapiens)	1.56e-38	49.57	49.57
27	PPAR-gamma (Homo sapiens)	1.56e-38	49.57	49.57

28	AP-2A (Homo sapiens)	1.56e-38	49.57	49.57
29	ETS1 (Homo sapiens)	1.56e-38	49.57	49.57
30	SMAD4 (Homo sapiens)	1.56e-38	49.57	49.57