Suppl. Report 1. Transcription Regulation Workflow Report

Server: *portal.genego.com*
Date: *2010-12-01*
Name: *University of Miami - Andreev*
Login: *umiami17*

Experiments

1.		Sign_Cons_GG_112310

Figure 1. The experiments uploaded for comparative analysis

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Selected networks built from active experiments

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The gene content of the uploaded files 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 of 1. relative enrichment with the uploaded data, and 2. 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	GO Processes	Total nodes	Root nodes	Pathways	p-Value	zScore	gScore
1	SP1	regulation of biological quality (42.0%), response to abiotic stimulus (24.0%), response to organic substance (34.0%), response to chemical stimulus (44.0%), homeostatic process (28.0%)	50	49	0	7.01e-122	116.27	116.27
2	c-Myc	cellular process (91.9%), cellular metabolic process (73.0%), organ development (40.5%), positive regulation of macromolecule metabolic process (29.7%), positive regulation of cellular metabolic process (29.7%)	37	36	0	7.86e-89	99.29	99.29
3	HNF4-alpha	response to stress (35.3%), wound healing (11.8%), translational elongation (8.8%), Golgi to vacuole transport (2.9%), developmental process (44.1%)	34	33	0	2.83e-81	94.94	94.94
4	p53	regulation of cell death (52.0%), regulation of apoptosis (48.0%), regulation of programmed cell death (48.0%), positive regulation of apoptosis (36.0%), positive regulation of programmed cell death (36.0%)	27	26	0	9.53e-64	83.93	83.93
5	ESR1 (nuclear)	double-strand break repair via nonhomologous end joining (11.1%), response to ionizing radiation (16.7%), non-recombinational repair (11.1%), response to X-ray (11.1%), cellular response to chemical stimulus (27.8%)	18	17	0	1.95e-41	67.20	67.20
6	YY1	translational elongation (28.6%), negative regulation of cellular metabolic process (50.0%), negative regulation of metabolic process (50.0%), negative regulation of protein	14	13	0	1.30e-31	58.27	58.27

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		amino acid dephosphorylation (14.3%), negative regulation of dephosphorylation (14.3%)						
7	NF-kB	response to inorganic substance (30.8%), response to cadmium ion (15.4%), pattern recognition receptor signaling pathway (15.4%), developmental growth (23.1%), response to organic substance (46.2%)	13	12	0	3.62e-29	55.81	55.81
8	c-Jun	response to inorganic substance (41.7%), response to chemical stimulus (66.7%), response to hydrogen peroxide (25.0%), response to reactive oxygen species (25.0%), negative regulation of protein modification process (25.0%)	12	11	0	9.98e-27	53.25	53.25
9	ETS1	positive regulation of apoptosis (50.0%), positive regulation of programmed cell death (50.0%), positive regulation of cell death (50.0%), regulation of apoptosis (58.3%), regulation of programmed cell death (58.3%)	12	11	0	9.98e-27	53.25	53.25
10	Androgen receptor	catecholamine uptake involved in synaptic transmission (16.7%), dopamine uptake (16.7%), cell death (50.0%), death (50.0%), adult locomotory behavior (25.0%)	12	11	0	9.98e-27	53.25	53.25
11	RelA (p65 NF-kB subunit)	regulation of response to stress (45.5%), response to hydrogen peroxide (27.3%), regulation of response to stimulus (45.5%), liver development (27.3%), hepaticobiliary system development (27.3%)	11	10	0	2.72e-24	50.56	50.56
12	NRF2	catecholamine uptake involved in synaptic transmission (18.2%), dopamine uptake (18.2%), oxygen and reactive oxygen species metabolic process (27.3%), dopamine transport (18.2%), cellular metabolic process (100.0%)	11	10	0	2.72e-24	50.56	50.56
13	C/EBPbeta	positive regulation of apoptosis (50.0%), positive regulation of programmed cell death (50.0%), positive regulation of cell death (50.0%), regulation of apoptosis (50.0%), regulation of programmed cell death (50.0%)	10	9	0	7.30e-22	47.72	47.72
14	HSF1	posttranscriptional regulation of gene expression (40.0%), cellular component movement (50.0%), regulation of translation (30.0%), regulation of apoptosis (50.0%), regulation of programmed cell death (50.0%)	10	9	0	7.30e-22	47.72	47.72
15	Oct-1	double-strand break repair via nonhomologous end joining	10	9	0	7.30e-		

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		(22.2%), non-recombinational repair (22.2%), axon cargo transport (22.2%), microtubule-based transport (22.2%), telomere maintenance (22.2%)				22	47.72	47.72
16	NF-Y	skeletal muscle tissue regeneration (20.0%), developmental growth (30.0%), regulation of macromolecule biosynthetic process (70.0%), tissue regeneration (20.0%), regulation of cellular biosynthetic process (70.0%)	10	9	0	7.30e-22	47.72	47.72
17	Oct-3/4	multicellular organismal process (100.0%), system development (77.8%), anatomical structure development (77.8%), response to mineralocorticoid stimulus (22.2%), multicellular organismal development (77.8%)	9	8	0	1.93e-19	44.71	44.71
18	RARalpha	negative regulation of cellular protein metabolic process (44.4%), negative regulation of protein metabolic process (44.4%), regulation of cellular protein metabolic process (55.6%), regulation of protein metabolic process (55.6%), striated muscle cell differentiation (33.3%)	9	8	0	1.93e-19	44.71	44.71
19	p73	positive regulation of apoptosis (62.5%), positive regulation of programmed cell death (62.5%), positive regulation of cell death (62.5%), negative regulation of protein amino acid dephosphorylation (25.0%), negative regulation of dephosphorylation (25.0%)	8	7	0	5.02e-17	41.49	41.49
20	AP-2A	hyperosmotic salinity response (25.0%), hyperosmotic response (25.0%), response to salt stress (25.0%), response to abiotic stimulus (50.0%), response to osmotic stress (25.0%)	8	7	0	5.02e-17	41.49	41.49

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1. SP1.

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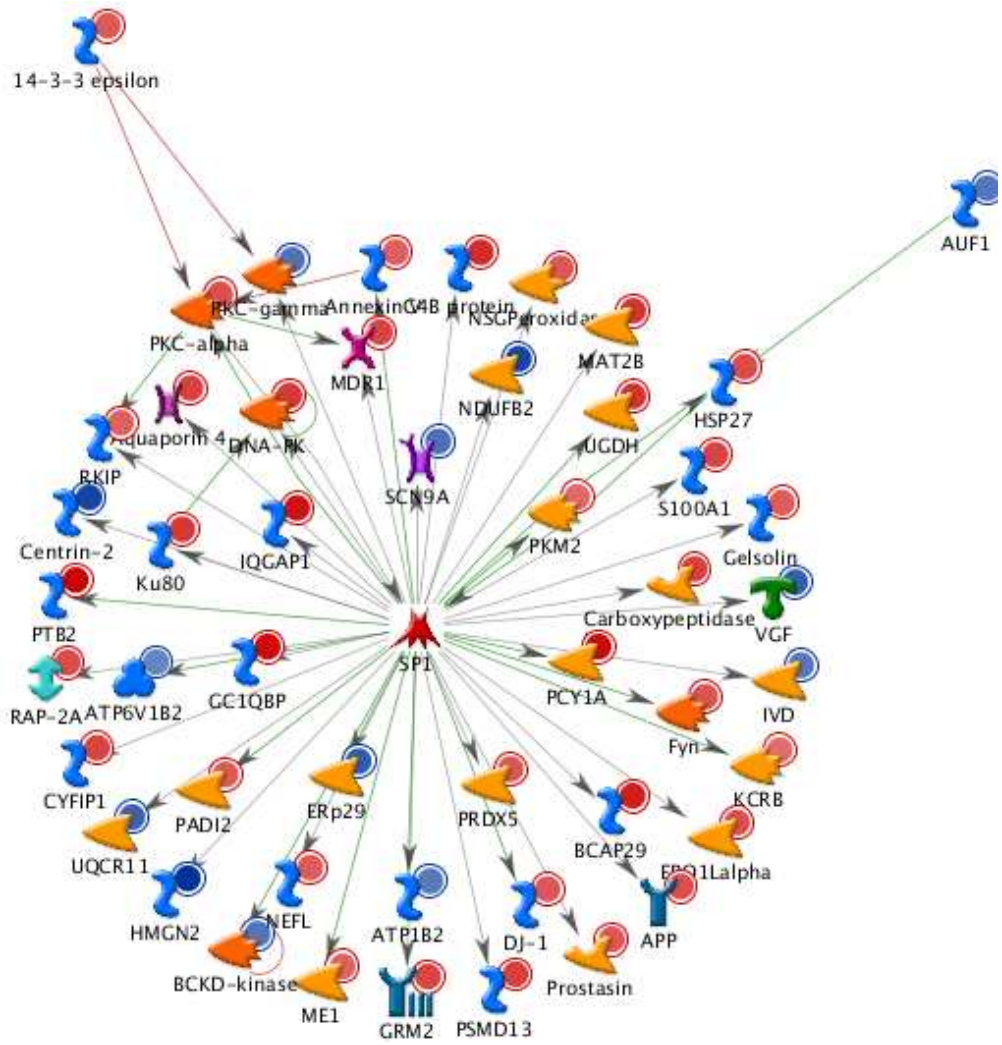

Figure 2. The top scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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indicates mixed expression for the gene between files or between multiple tags for the same gene.

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2. c-Myc.

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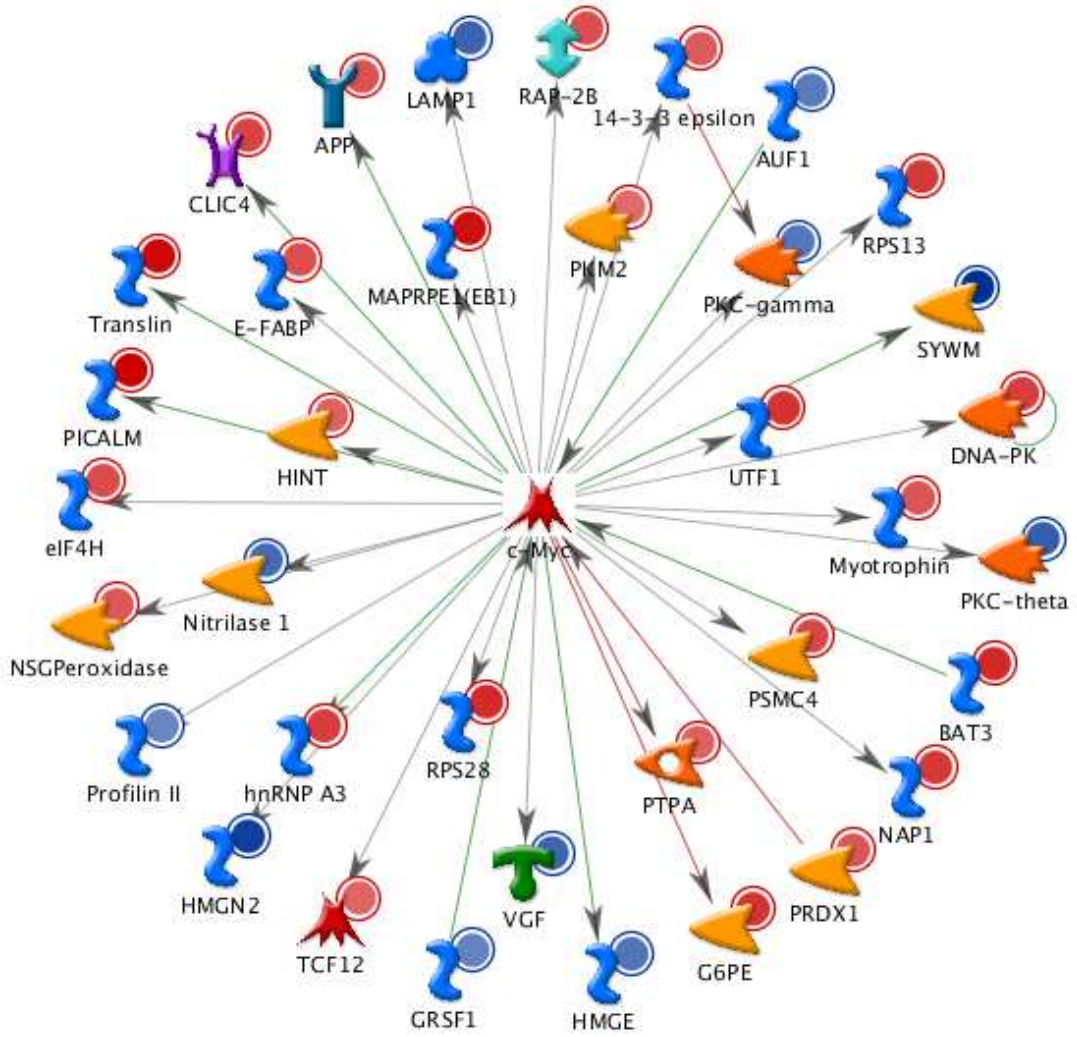

Figure 3. The second scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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3. HNF4-alpha.

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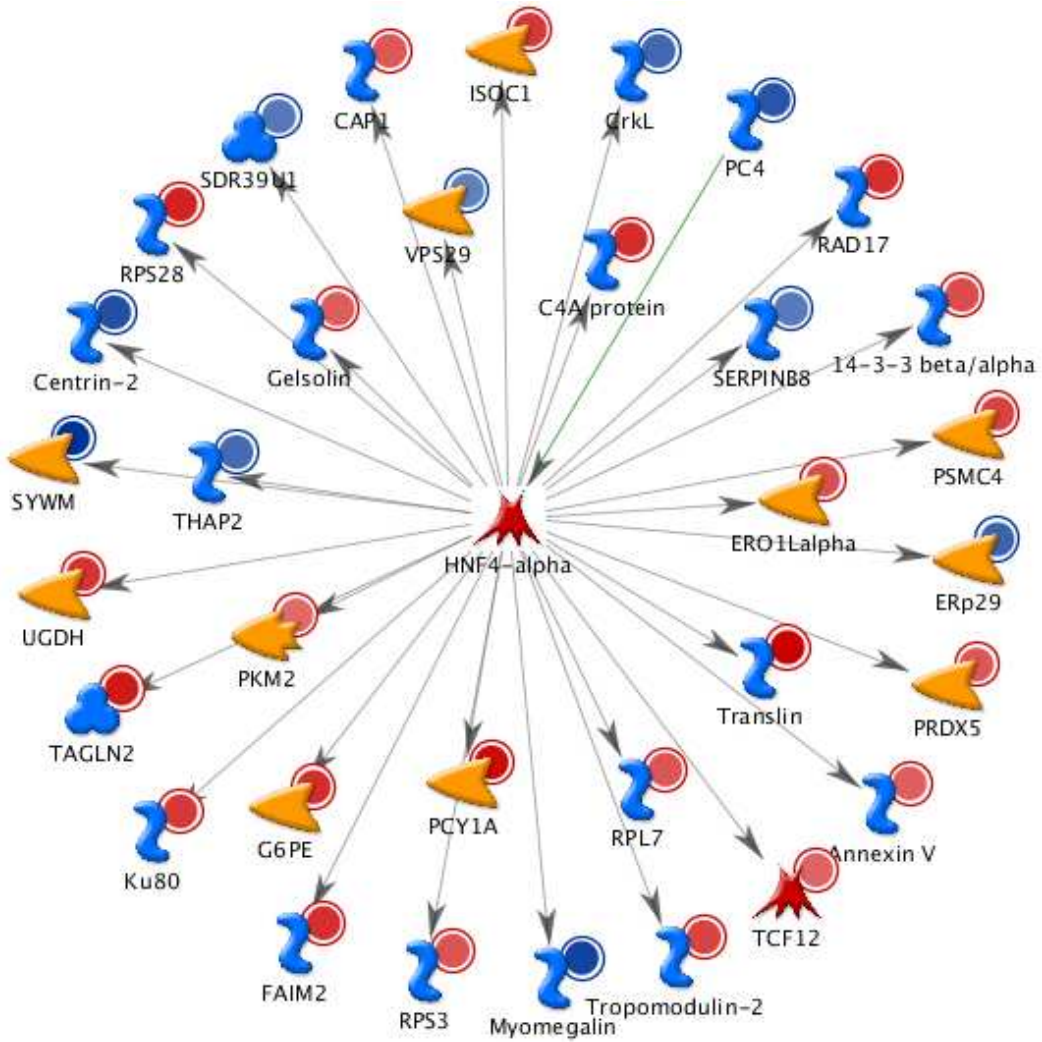

Figure 4. The third scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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4. p53.

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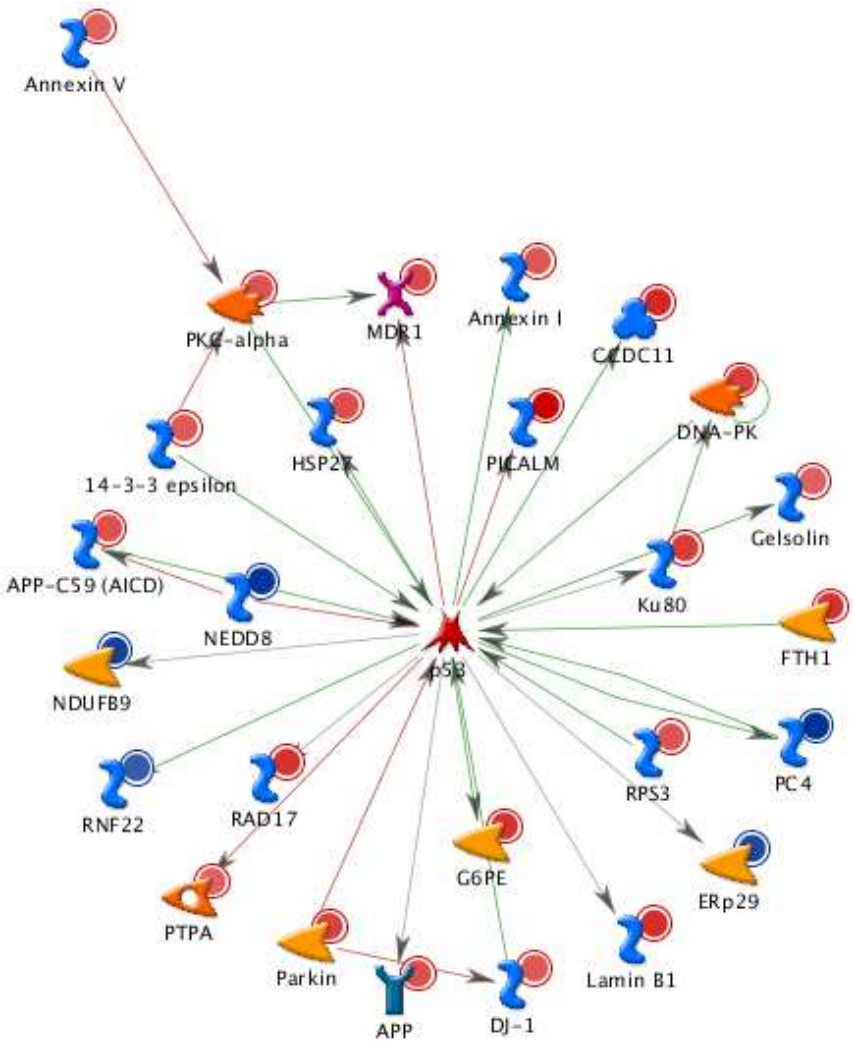

Figure 5. The fourth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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5. ESR1 (nuclear).

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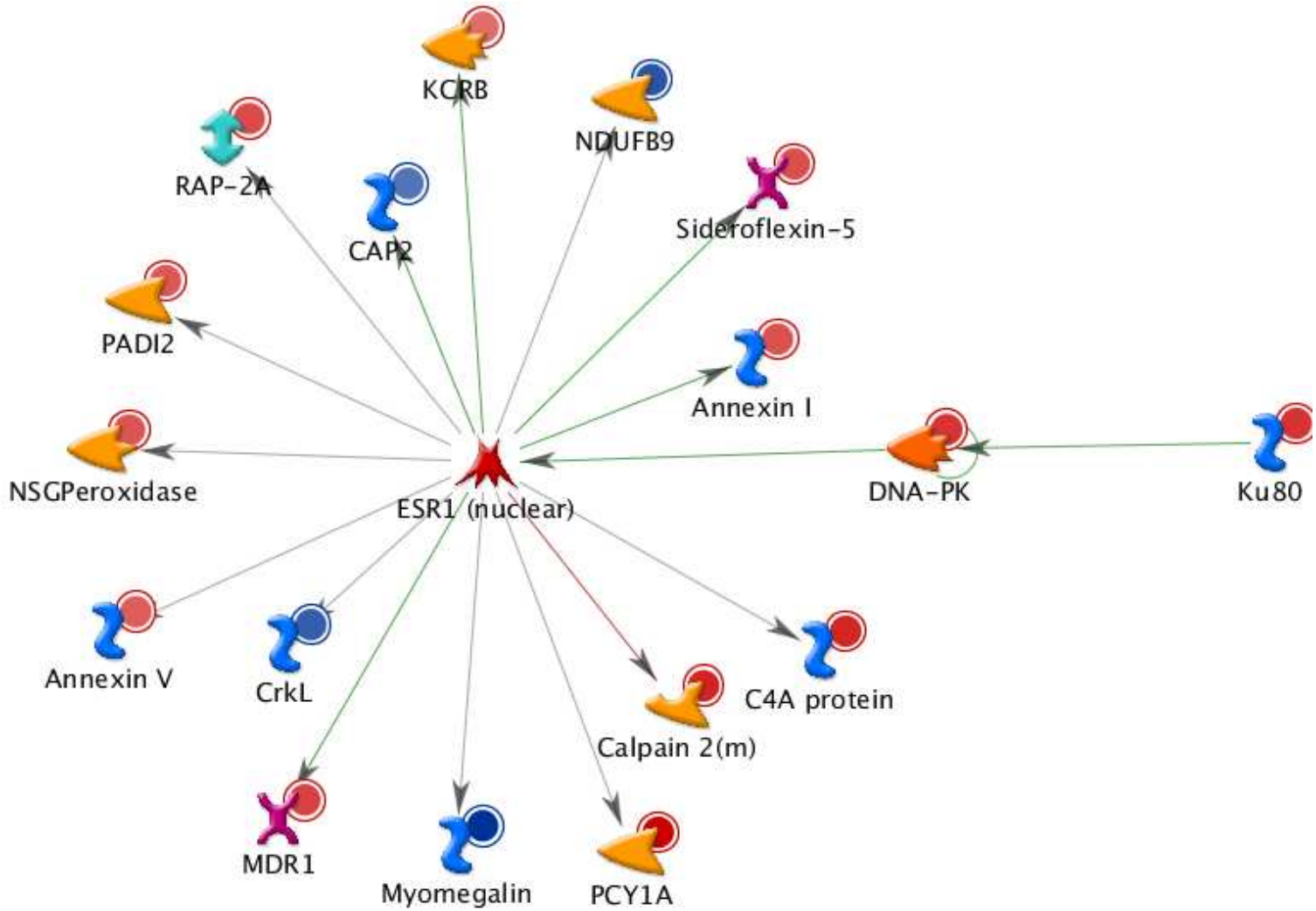

Figure 6. The fifth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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6. YY1.

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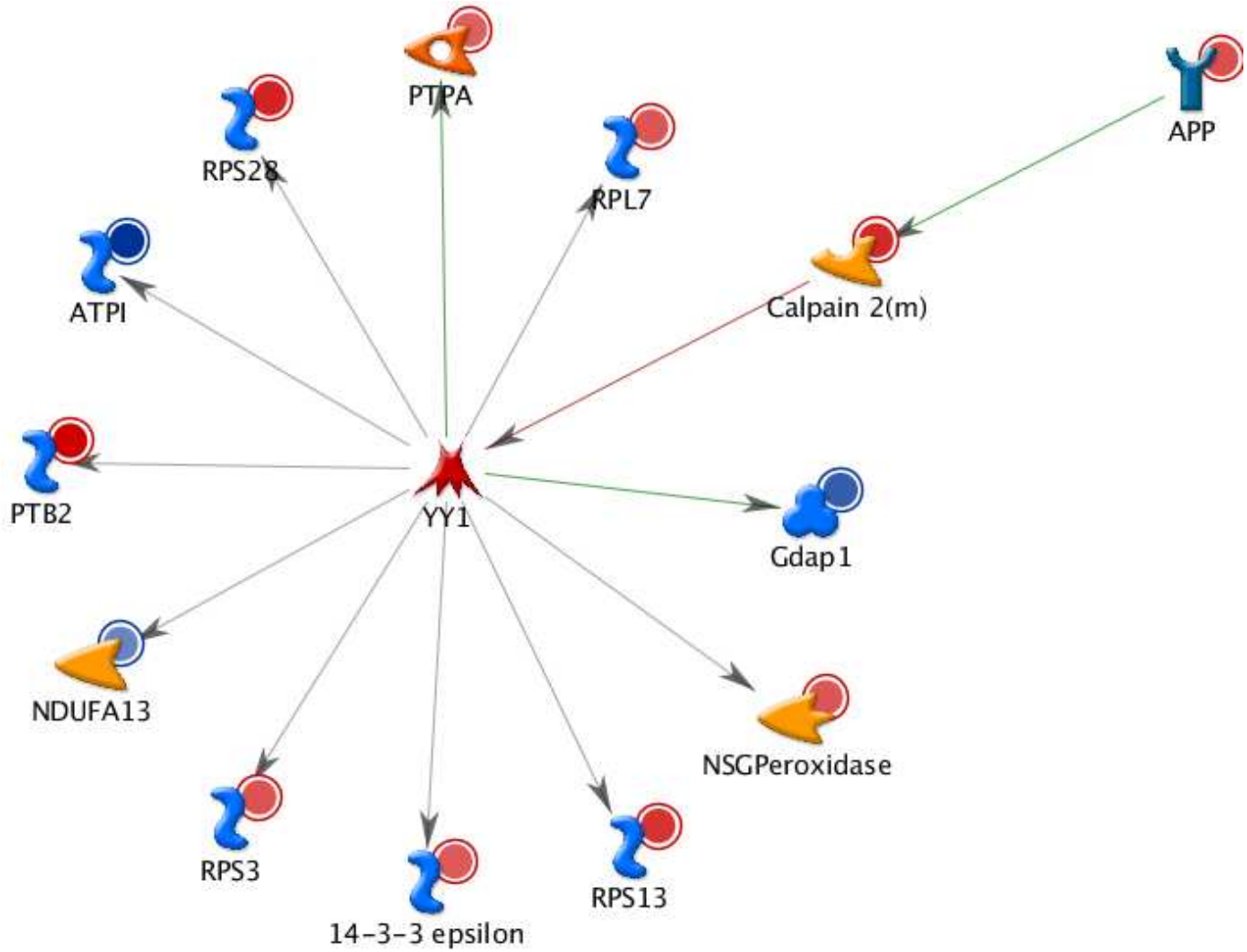

Figure 7. The sixth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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7. NF-kB.

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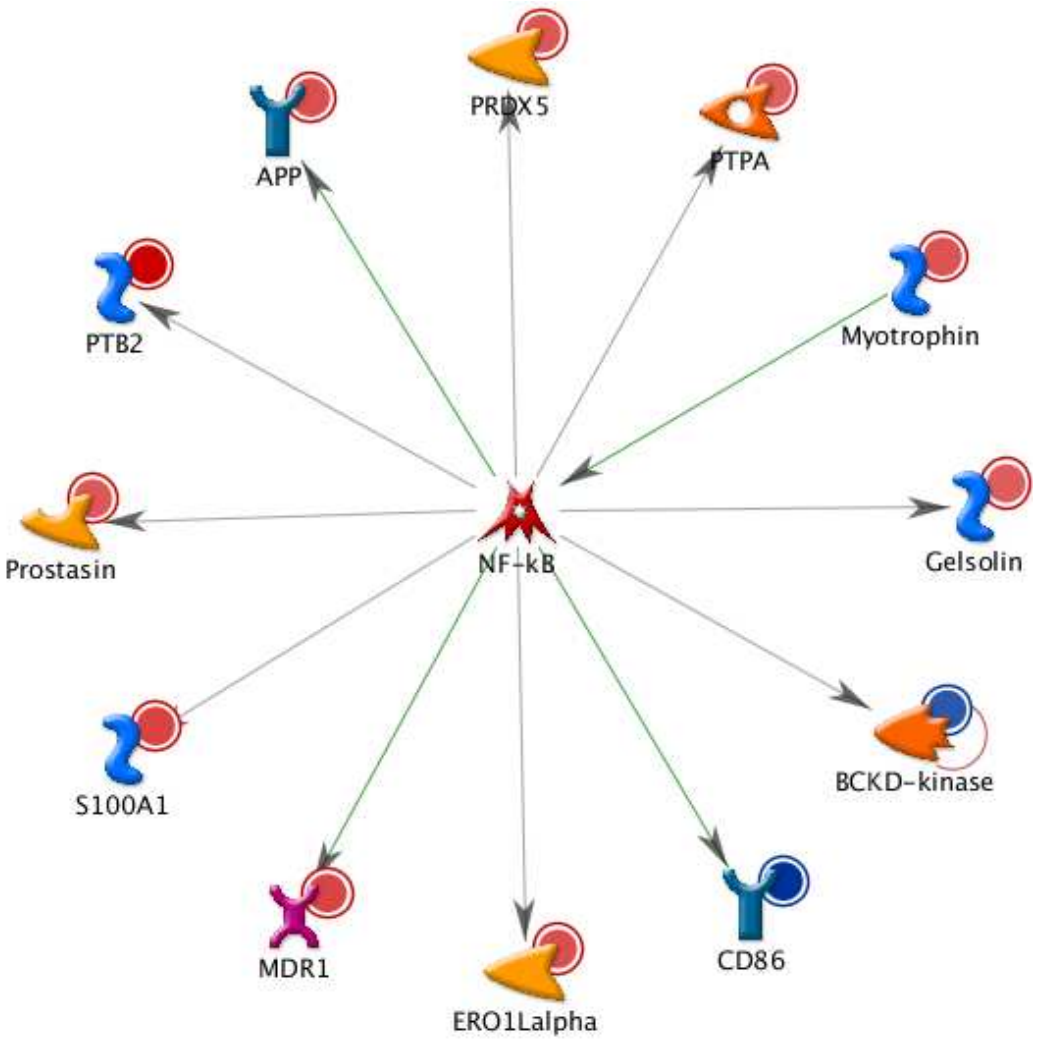

Figure 8. The seventh scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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8. c-Jun.

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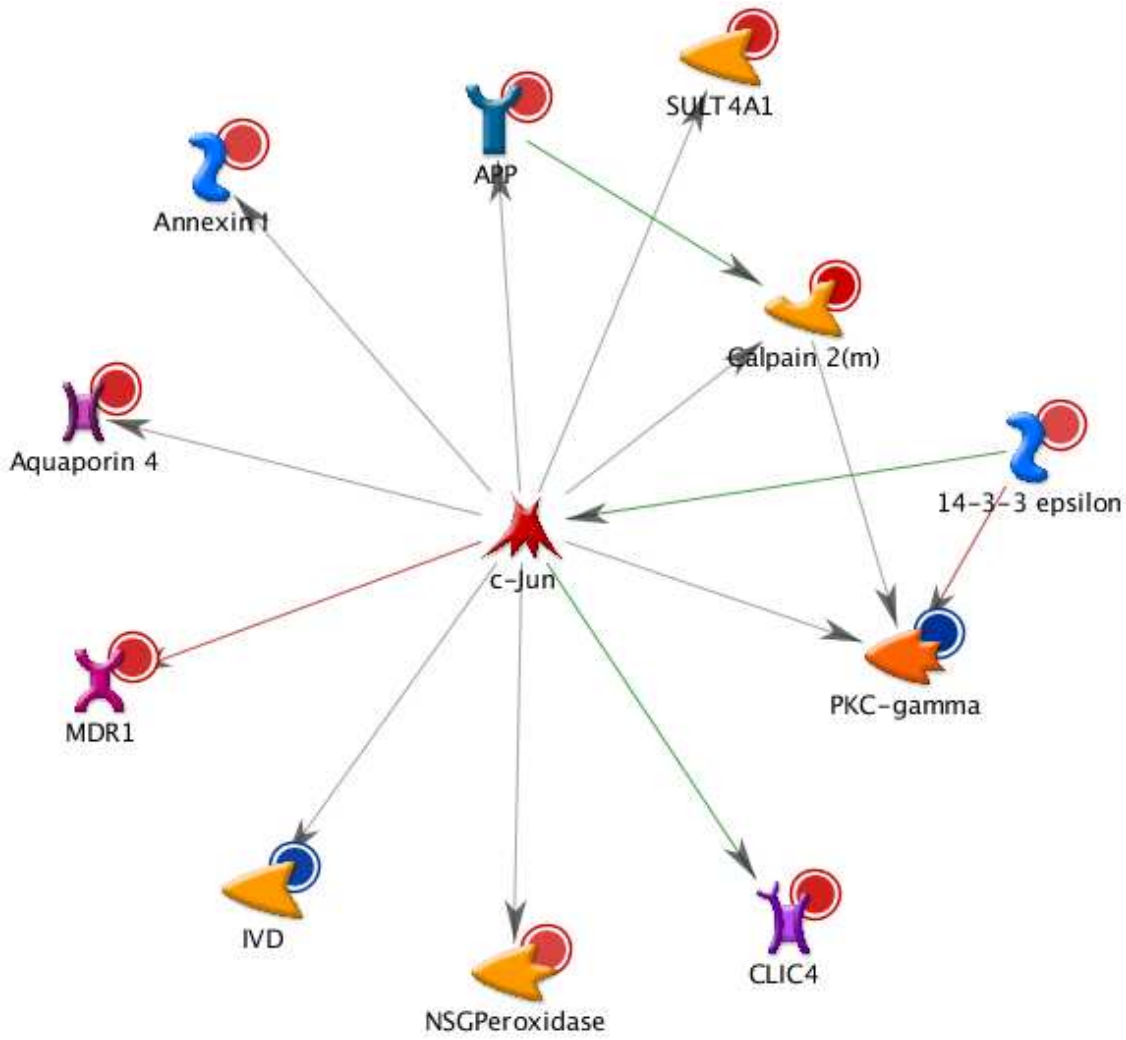

Figure 9. The eighth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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9. ETS1.

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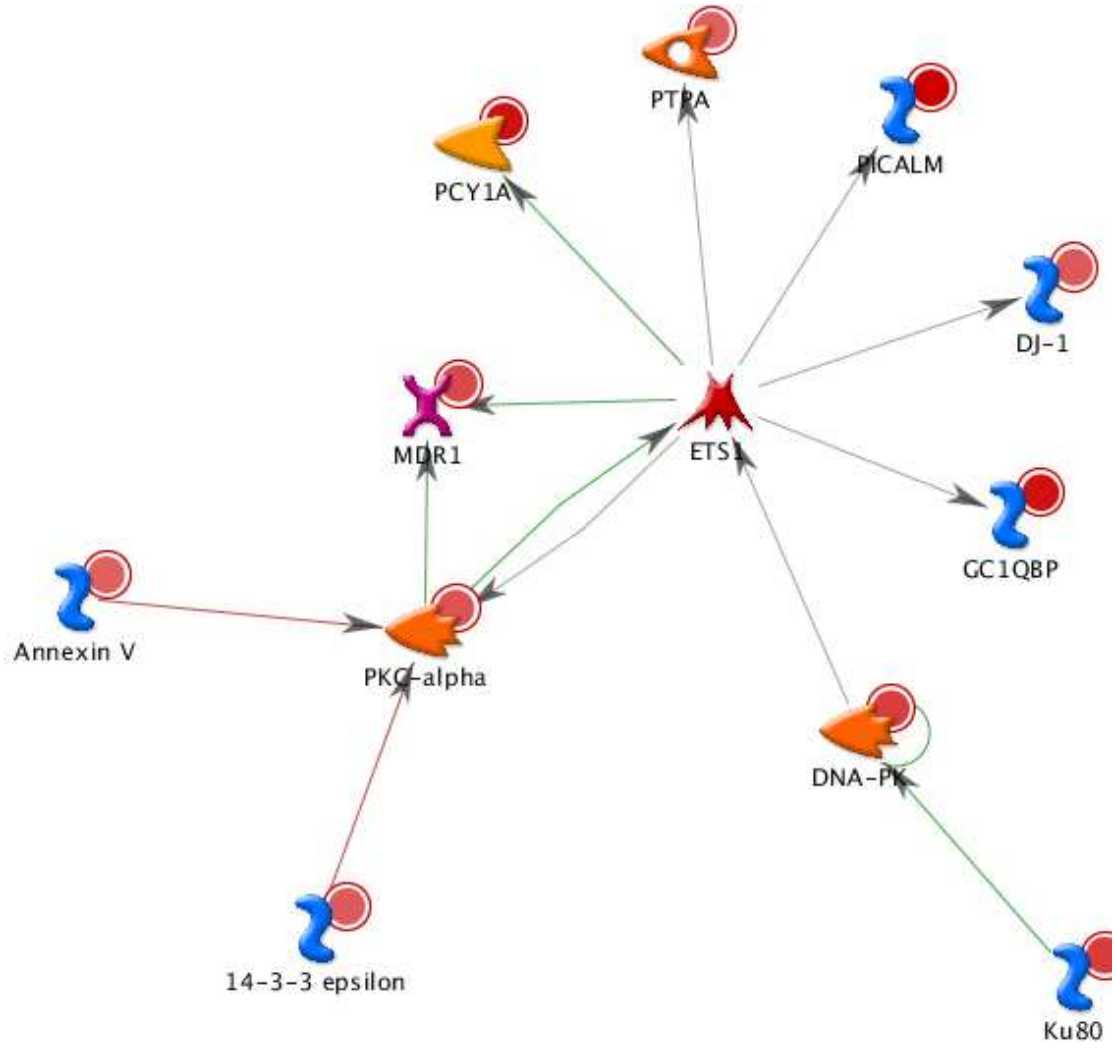

Figure 10. The ninth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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10. Androgen receptor.

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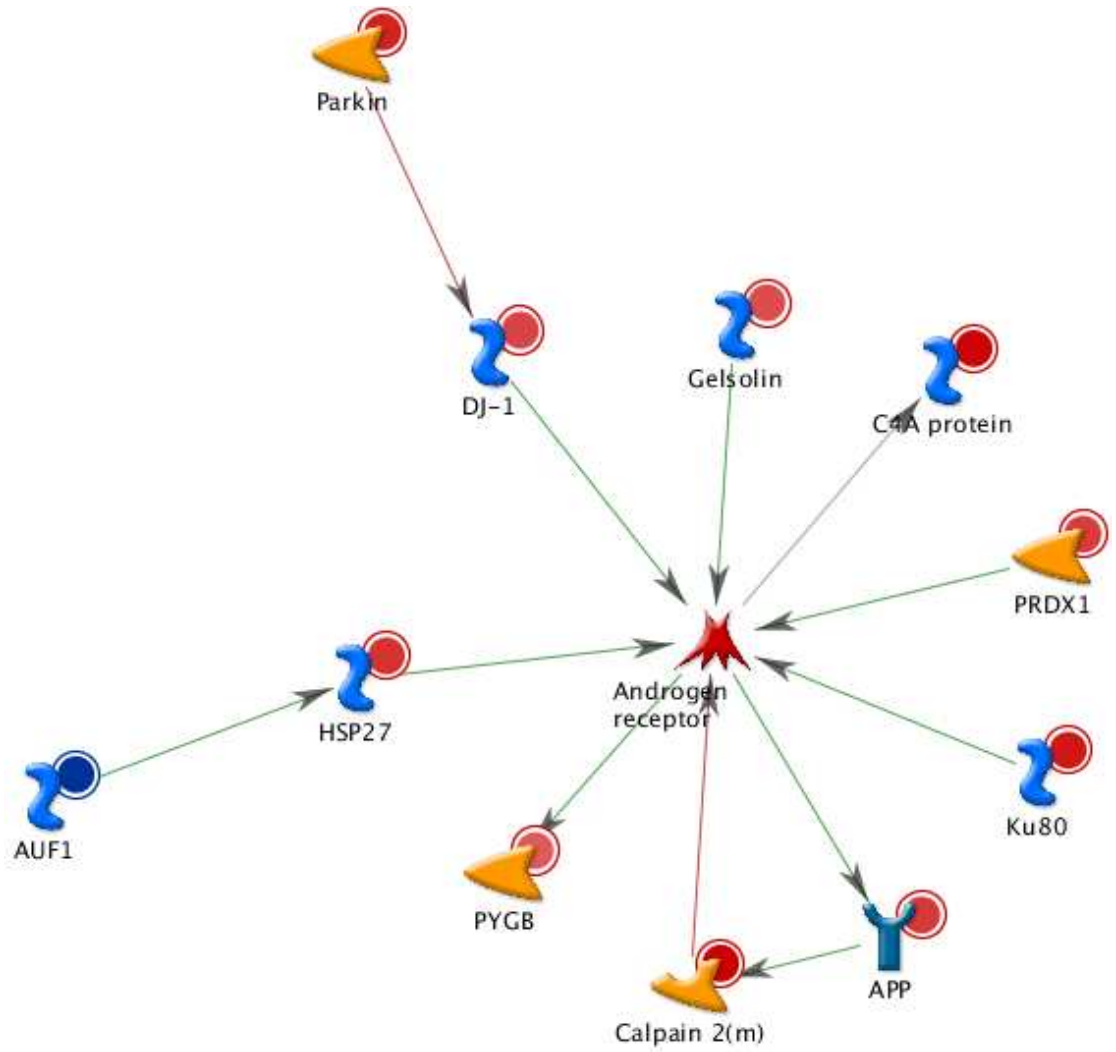

Figure 11. The tenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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11. RelA (p65 NF-kB subunit).

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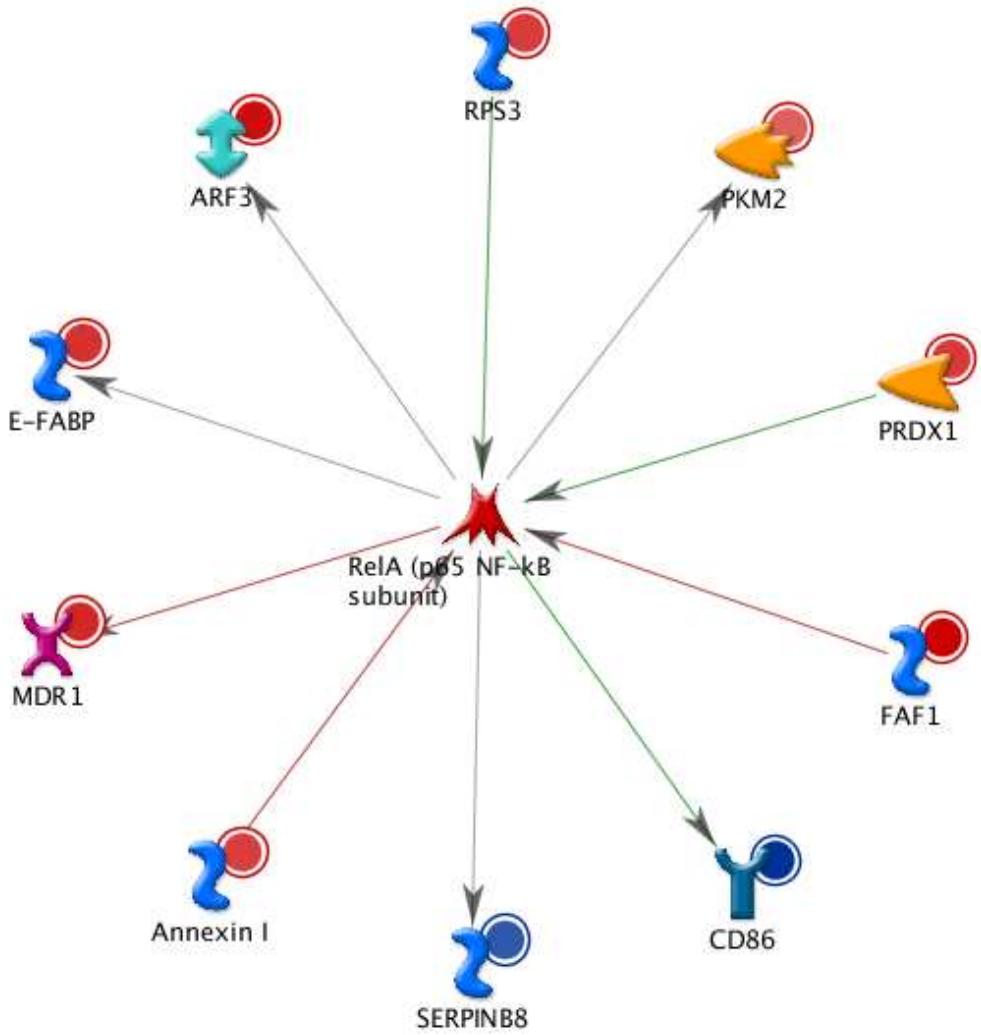

Figure 12. The eleventh scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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12. NRF2.

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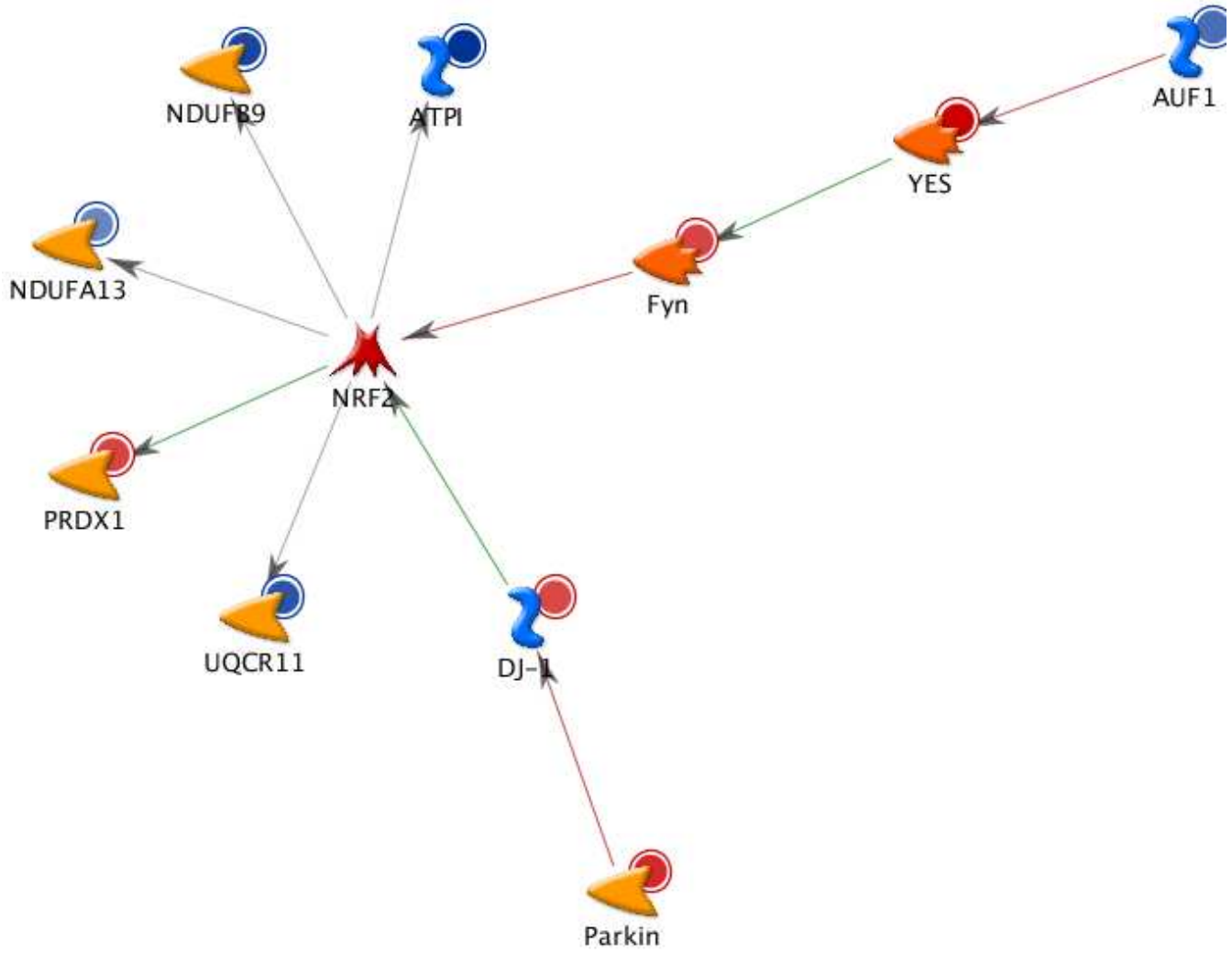

Figure 13. The twelfth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color

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13. C/EBPbeta.

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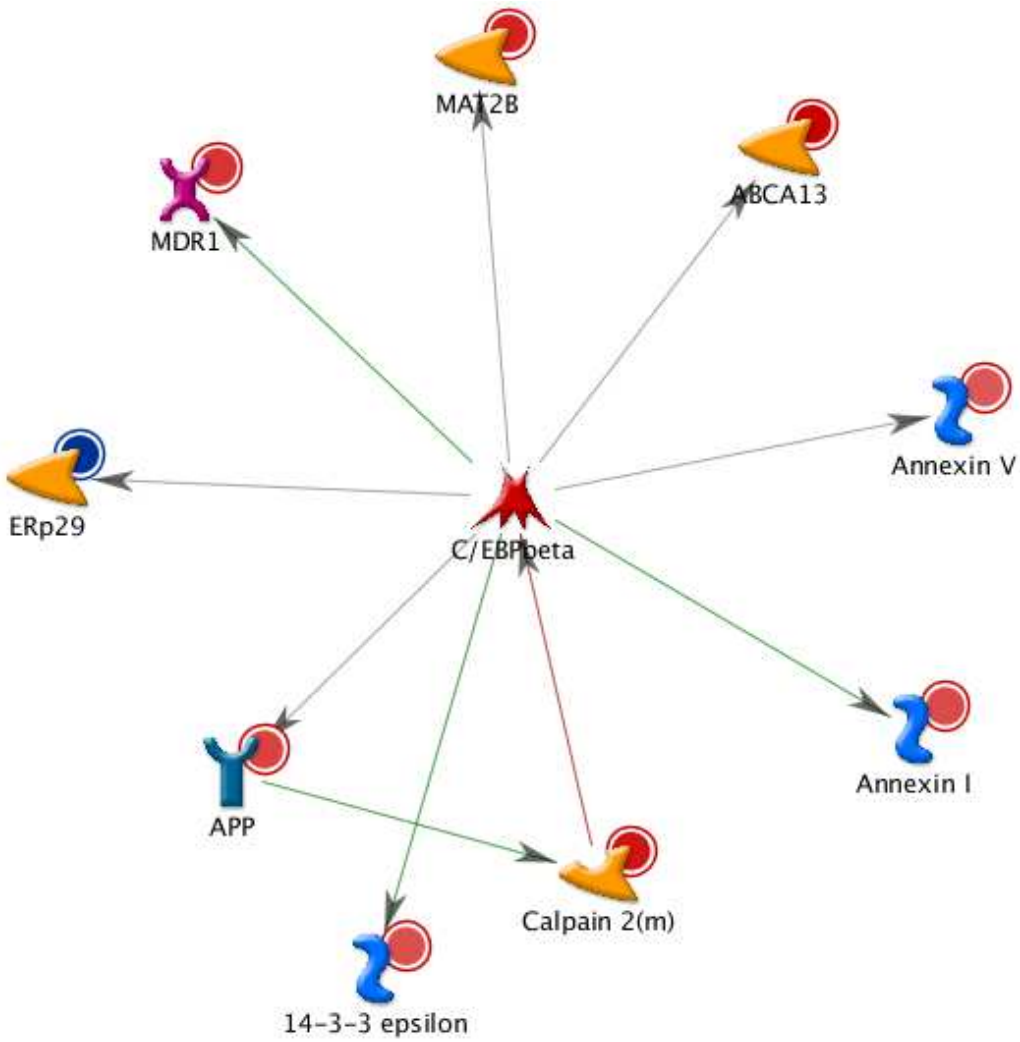

Figure 14. The thirteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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14. HSF1.

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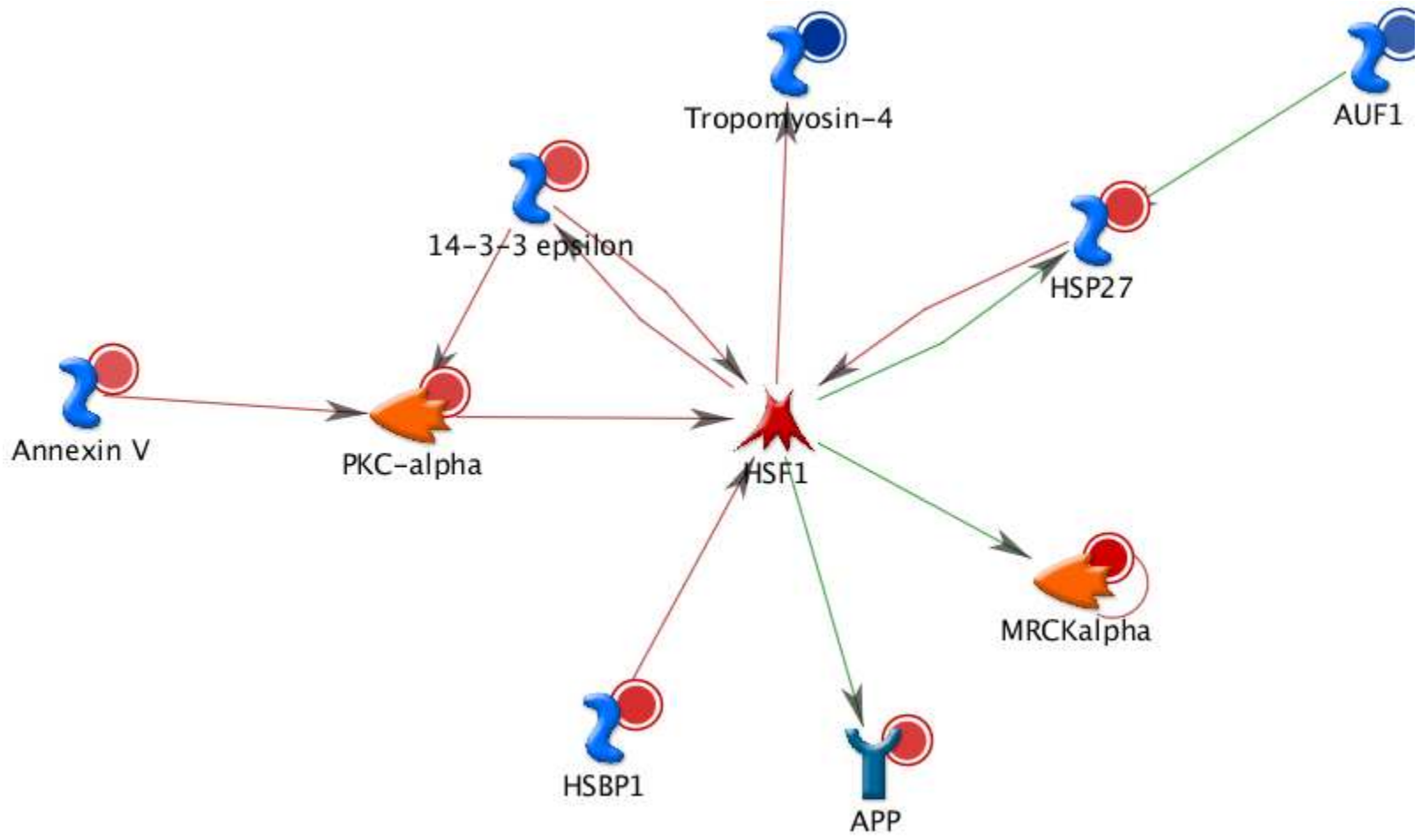

Figure 15. The fourteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The 'checkerboard' color indicates mixed expression for the gene between files or between multiple tags for the same gene.

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15. Oct-1.

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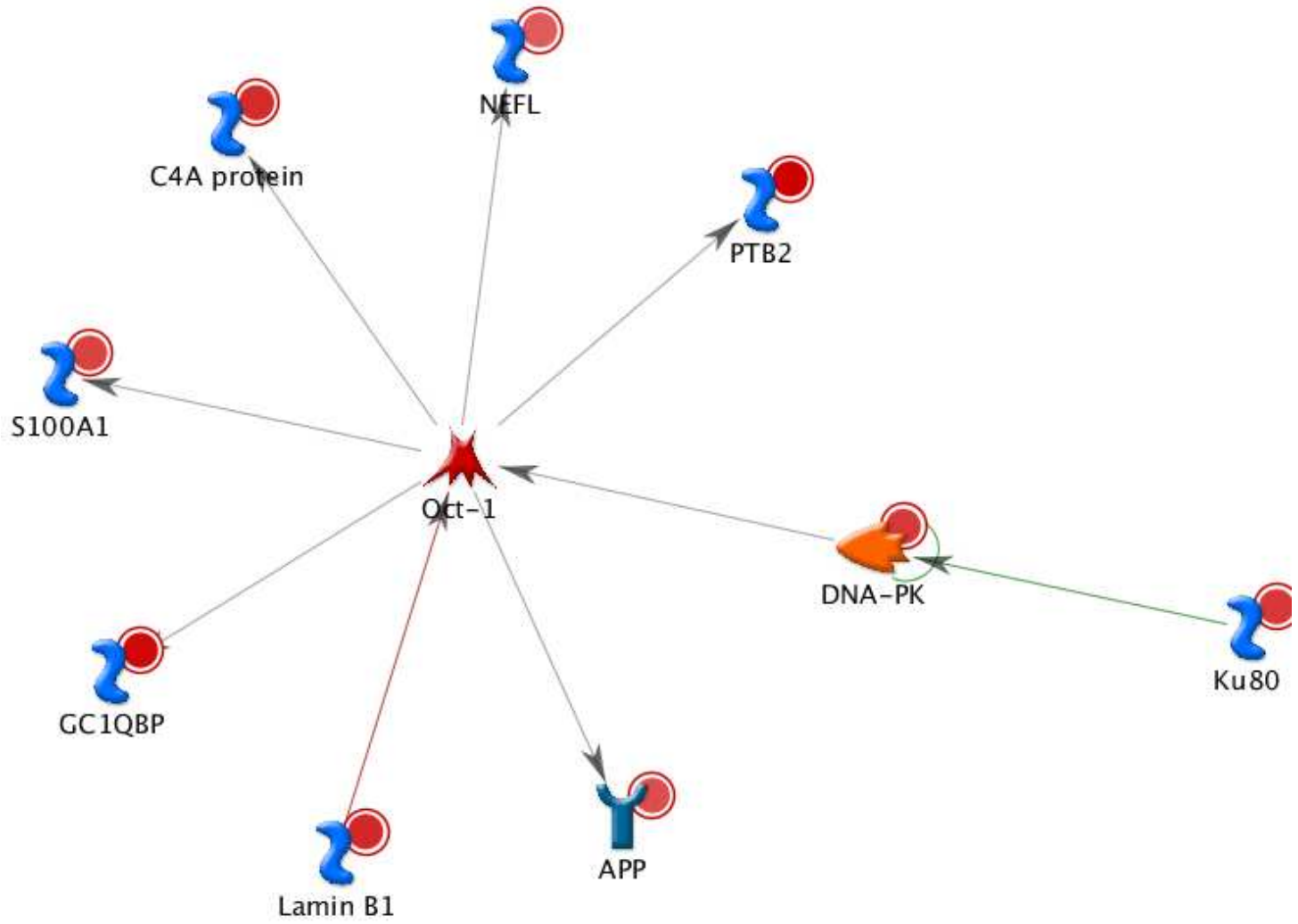

Figure 16. The fifteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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16. NF-Y.

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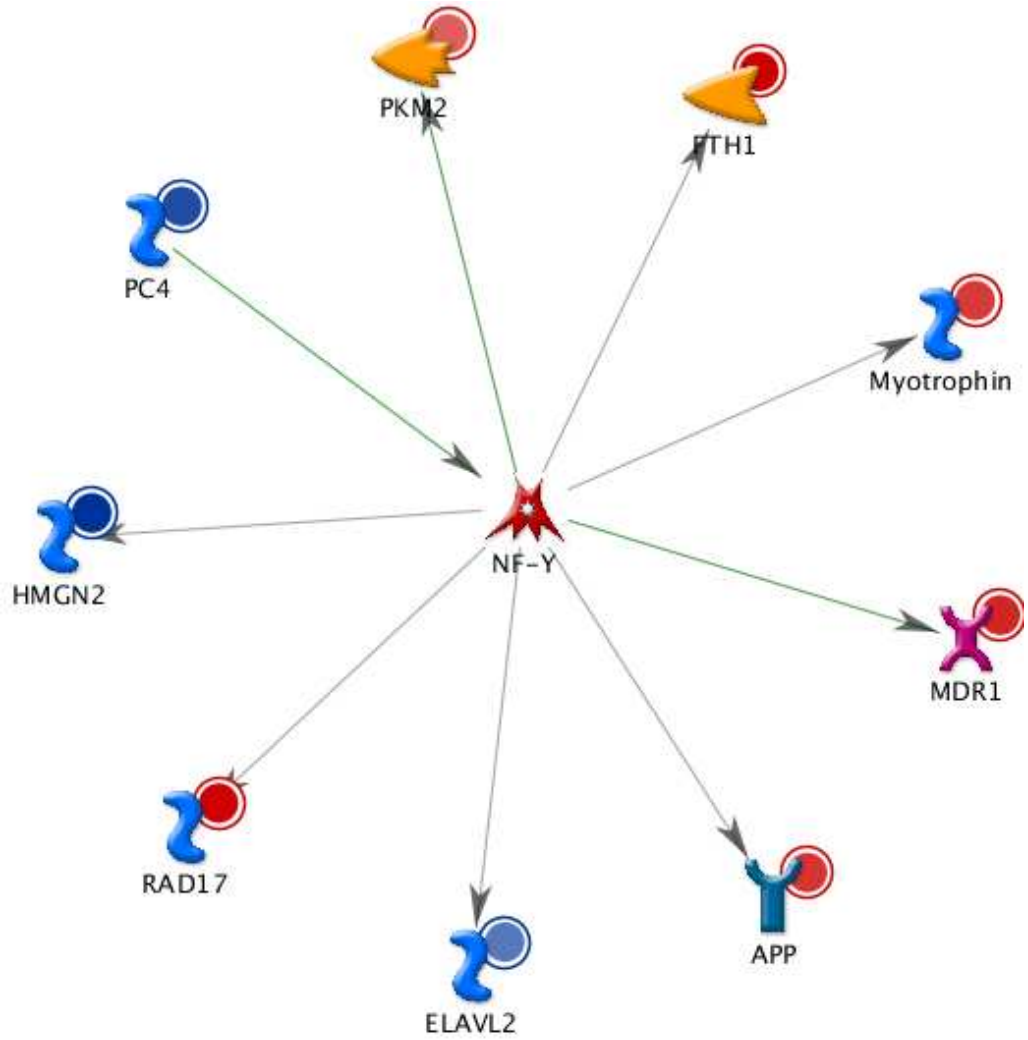

Figure 17. The sixteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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17. Oct-3/4.

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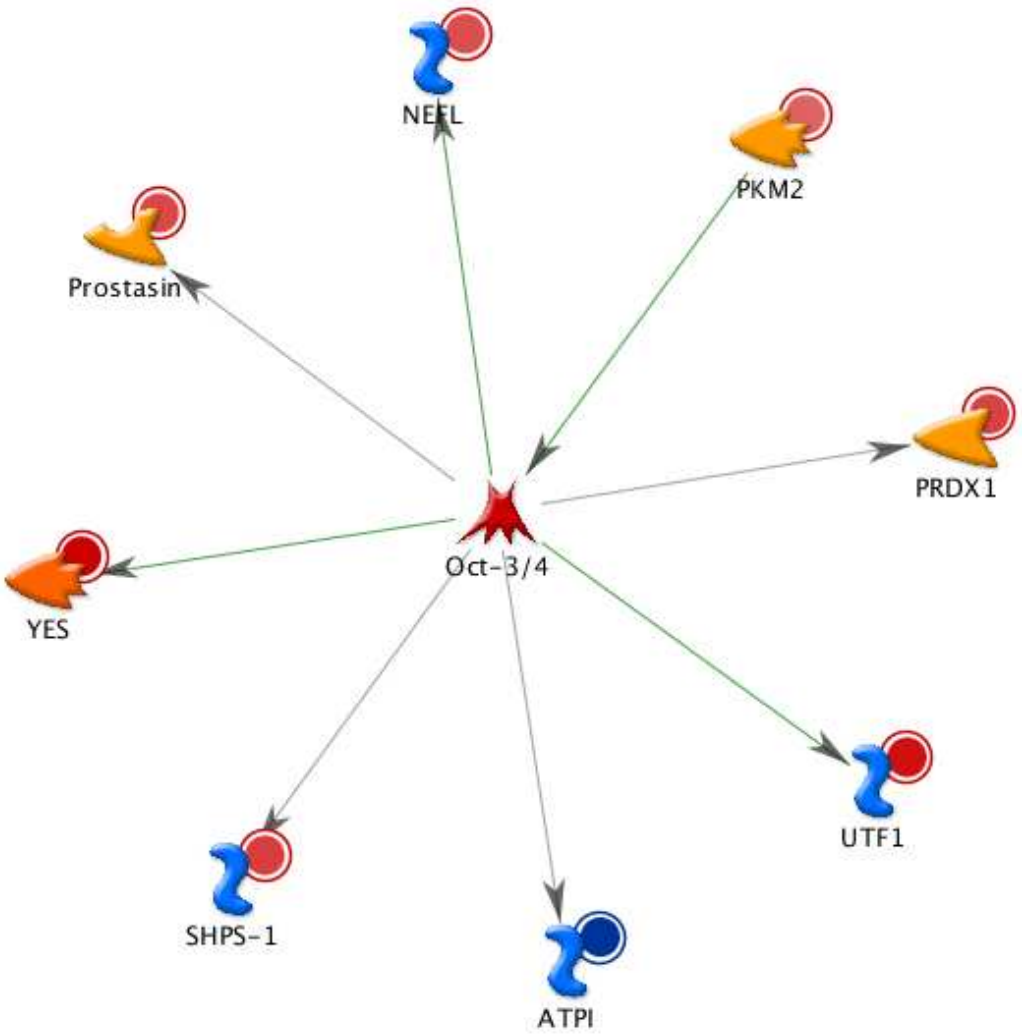

Figure 18. The seventeenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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18. RARalpha.

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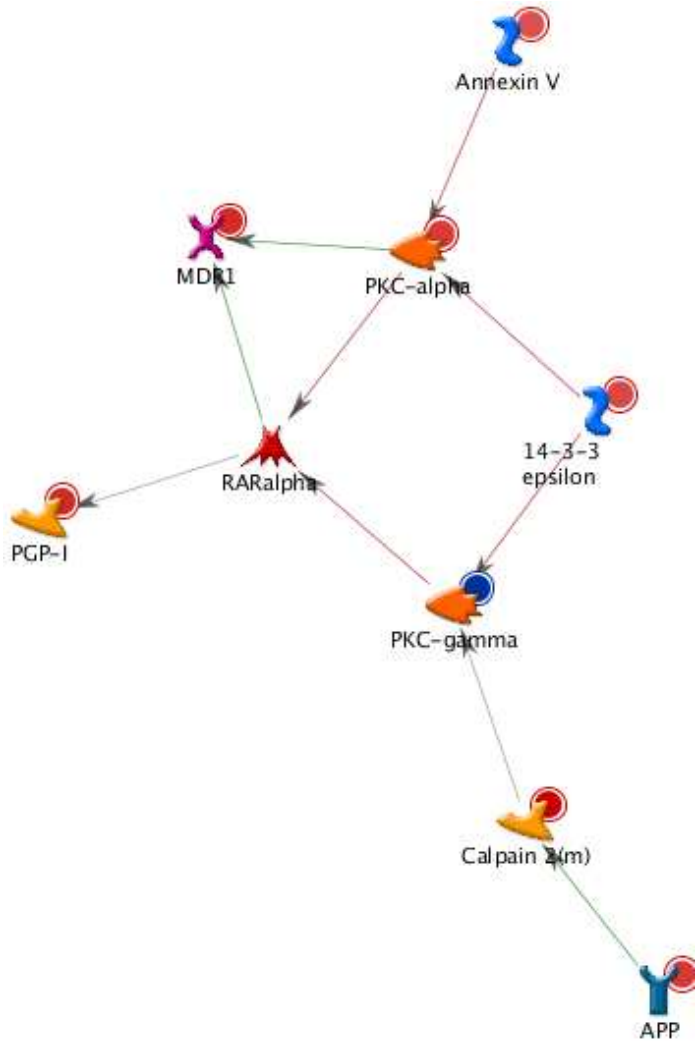

Figure 19. The eighteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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19. p73.

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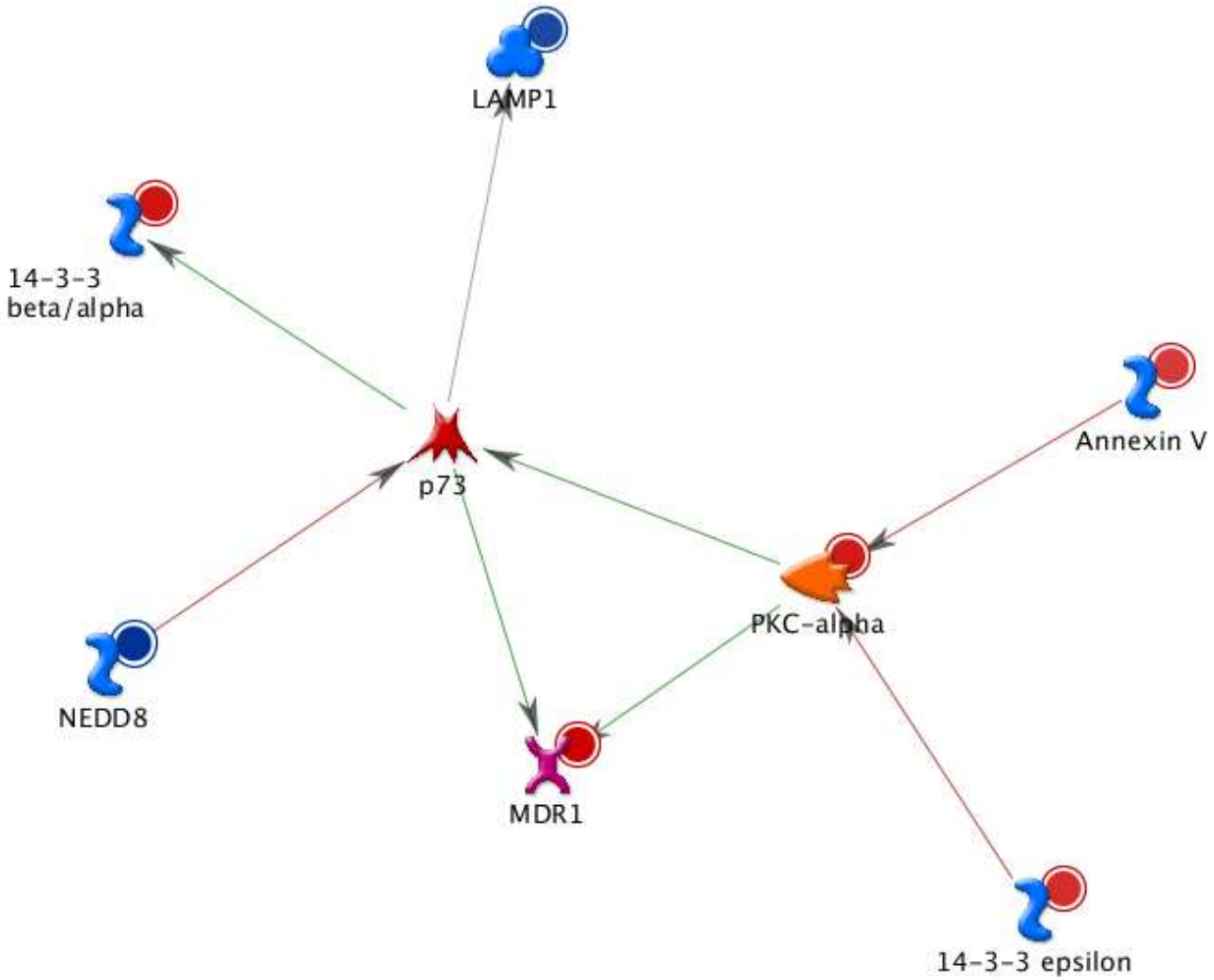

Figure 20. The nineteenth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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20. AP-2A.

(TOC)

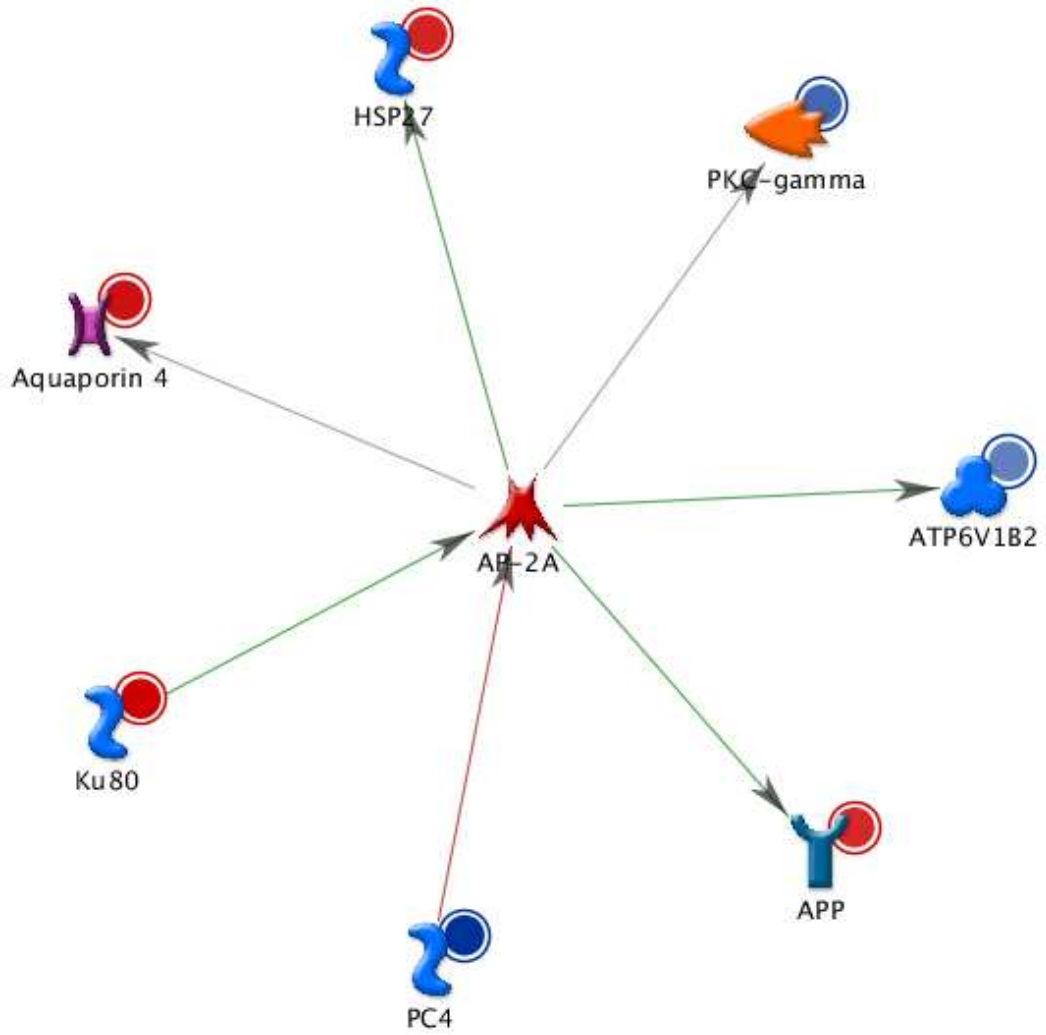

Figure 21. The twentieth scored (by the number of pathways) network from active experiments. Thick cyan lines indicate the fragments of canonical pathways. Up-regulated genes are marked with red circles; down-regulated with blue circles. The

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'checkerboard' color indicates mixed expression for the gene between files or between multiple tags for the same gene.

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