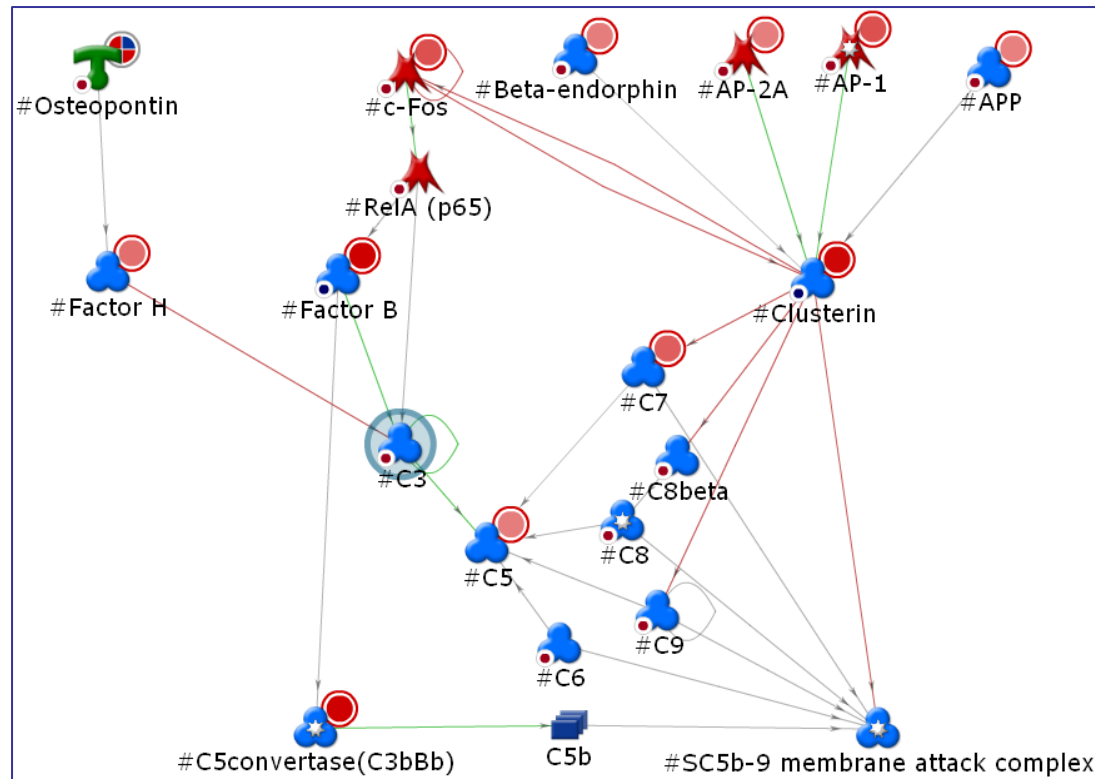
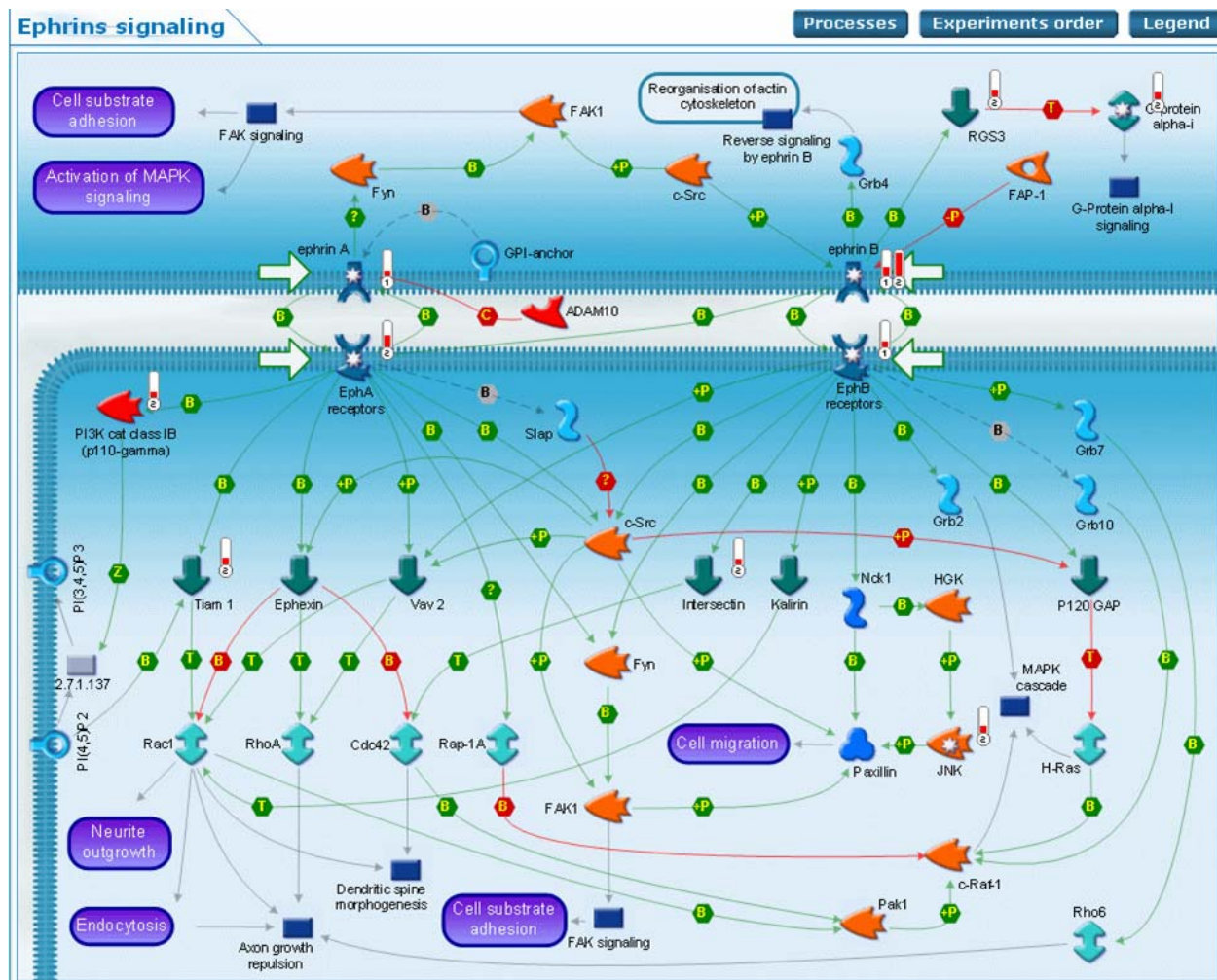
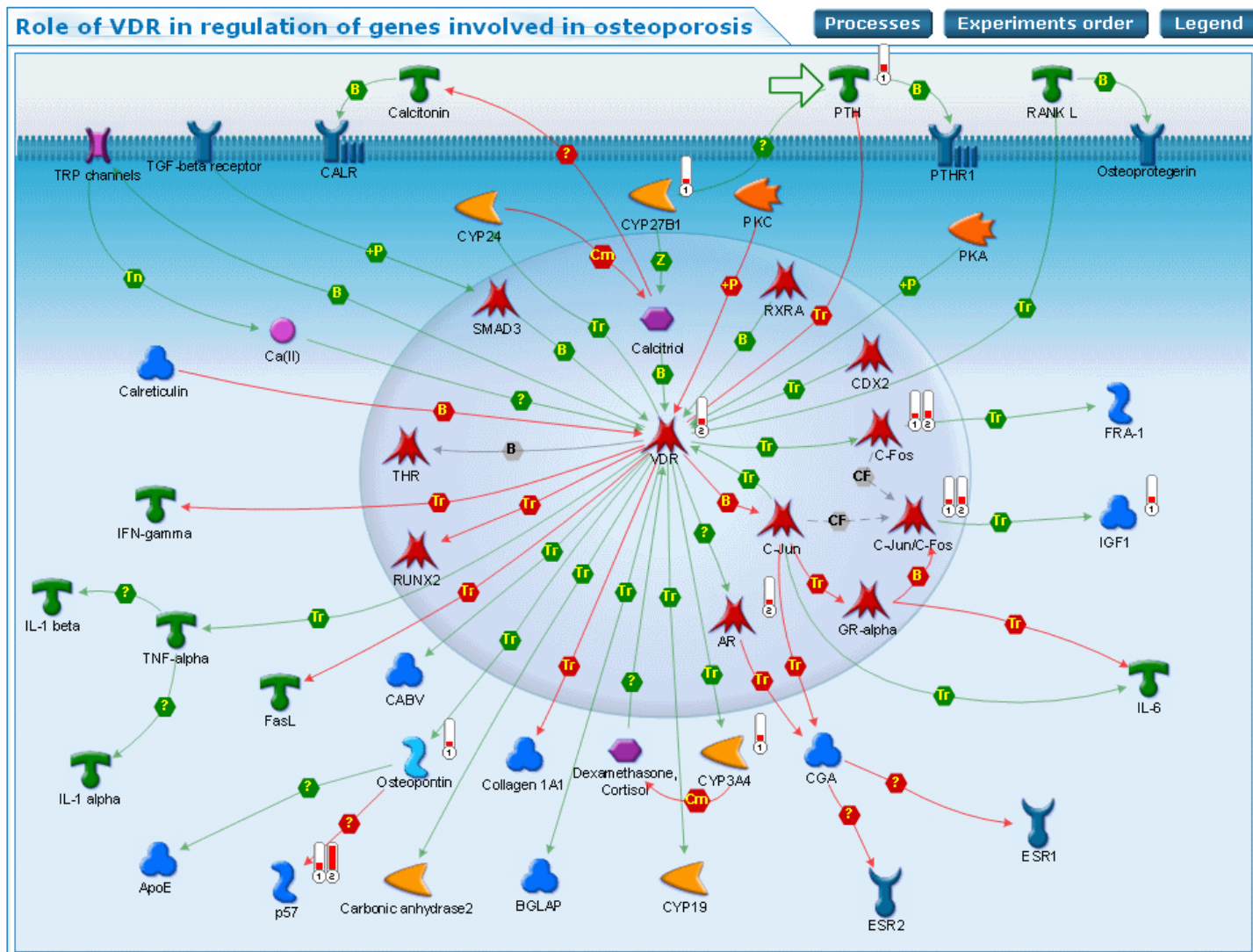




Supplement Figure 1. The shortest paths (SP) network built using up-regulated genes from GO process “complement activation” as the input list. Red frames indicate expression change in the combined file; blue – in the donor Group 1; green – in the donor Group 2. transcriptional activation of Factor H, Factor B, Clusterin and C3 was also confirmed at the level of protein accumulation.





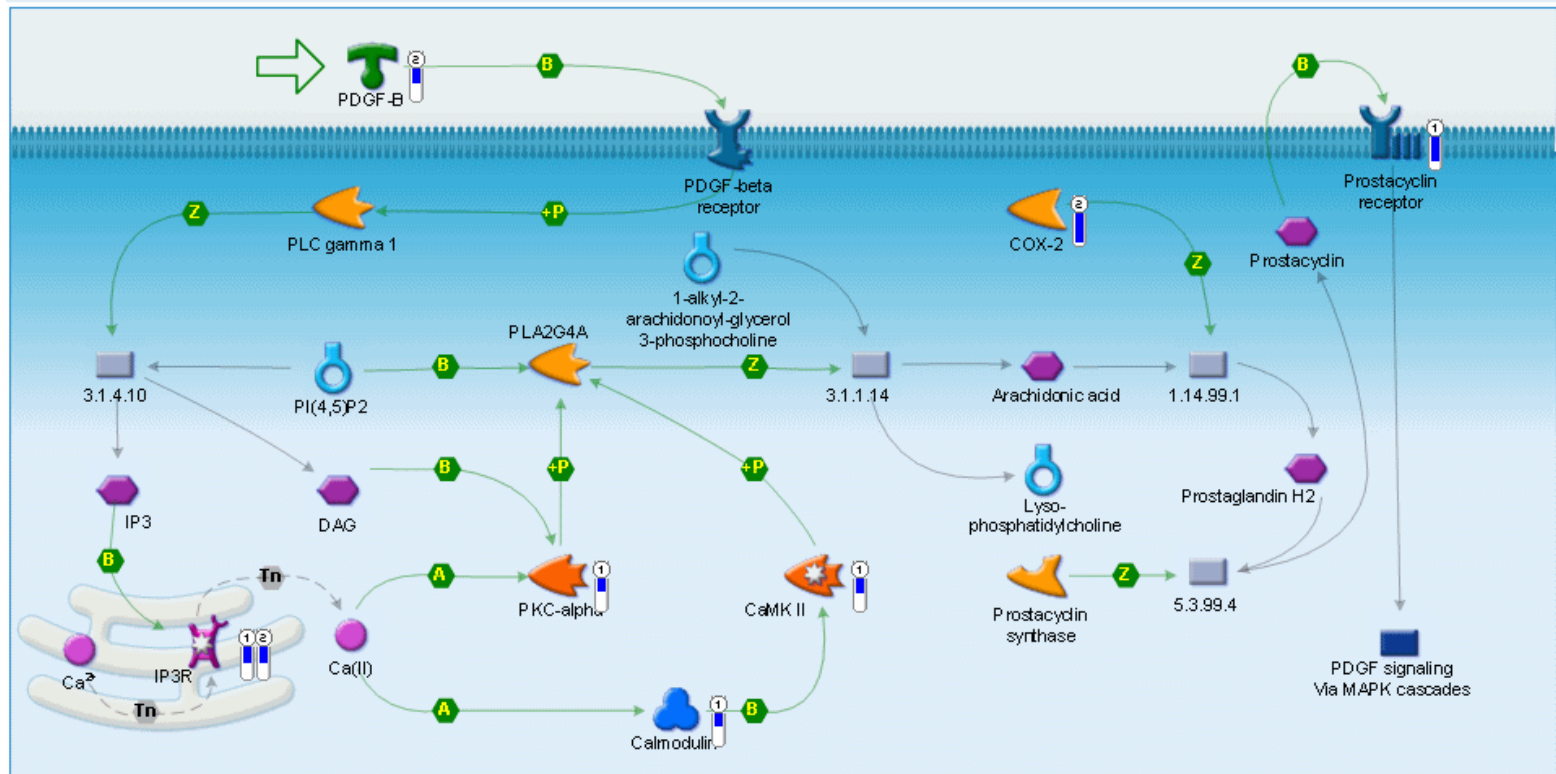
Supplement Figure 4. Activated VDR signaling shown on a standard signaling pathway map from MetaCore. The major participants are c-Fos (up-regulated in both groups), AR (donor group 2), p57 (both donor groups), osteopontin (group 1) and cytochromes CYP27B1 and CYP3A4. Gene expression level indicators: 1, donor Group1; 2, donor Group 2

PDGF activation of prostacyclin synthesis

Processes

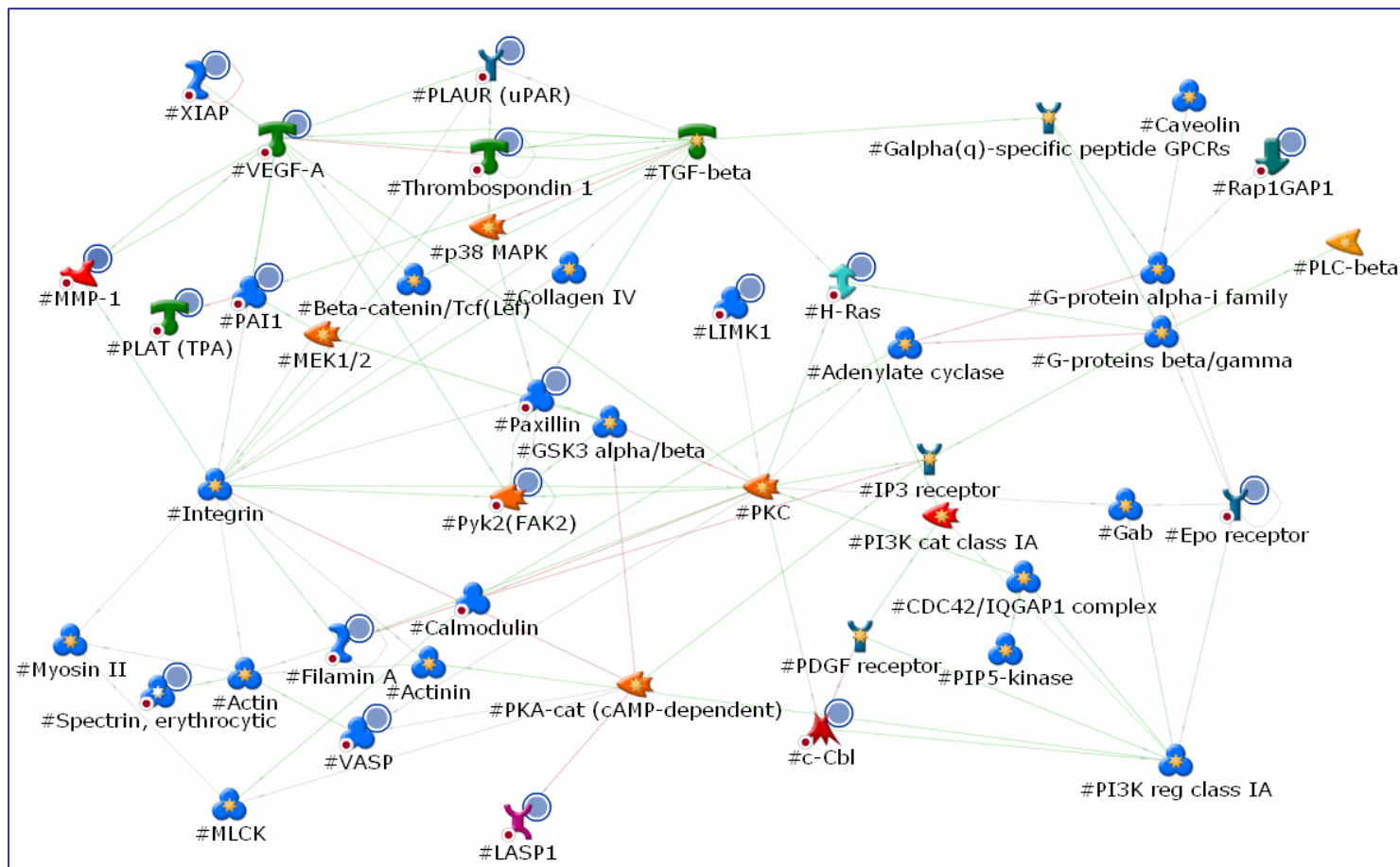
Experiments order

Legend



Supplement Figure 6. PDGF signaling was the highest scored (lowest p-values) pathway maps for down-regulated genes. Gene expression level indicators: 1, donor Group1; 2, donor Group 2

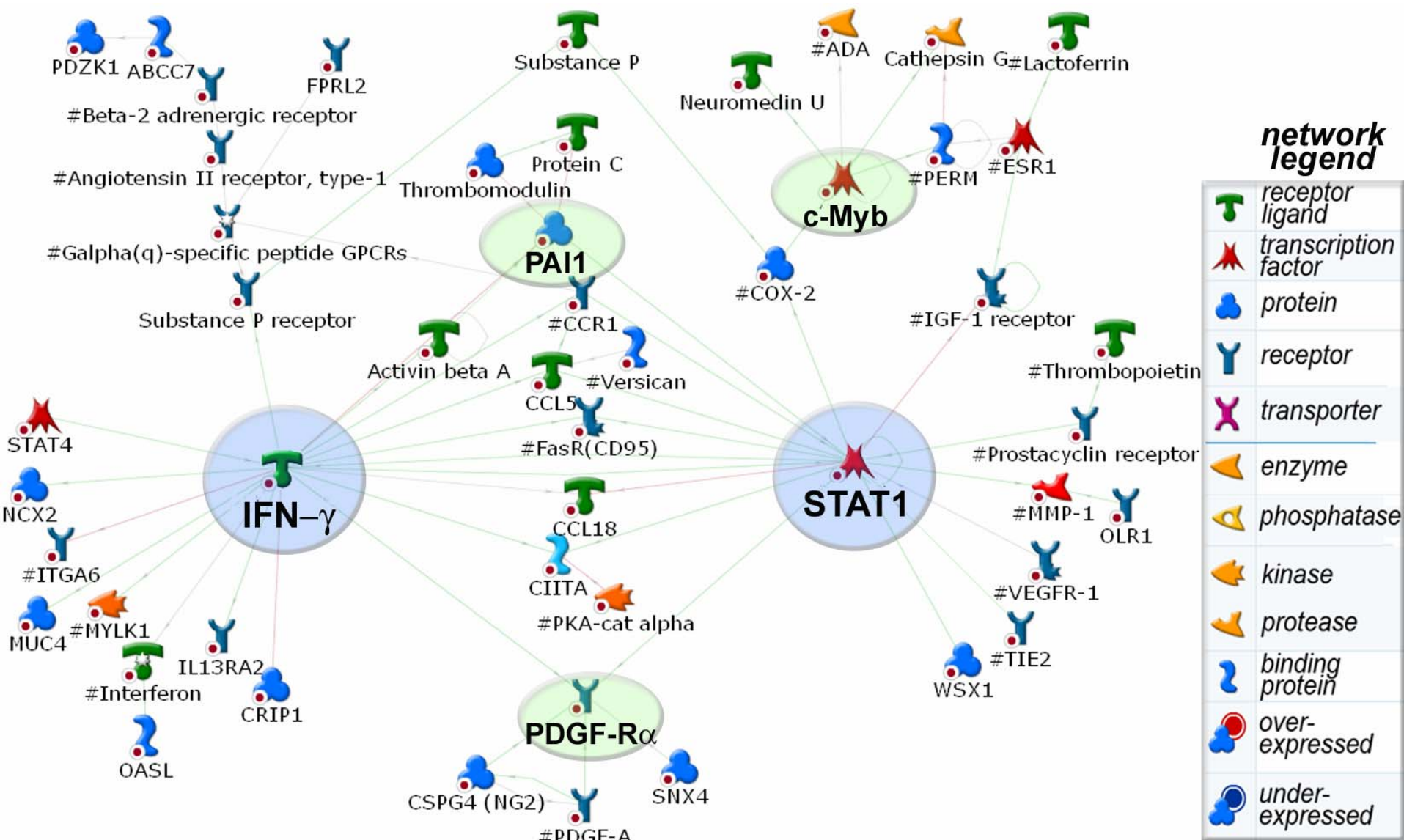
A



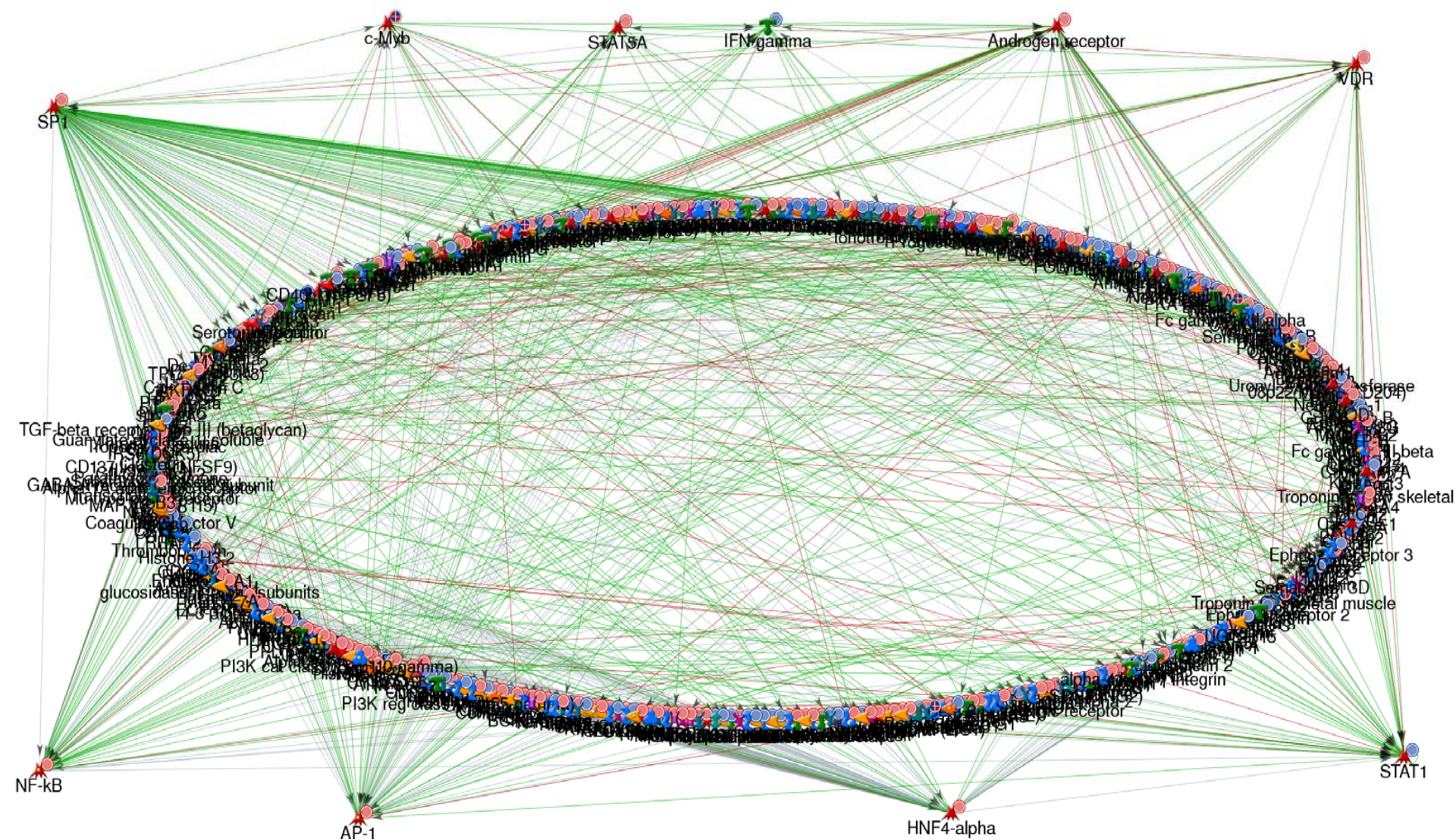
B

1	☐	signal transduction	35.29	5.853e-16
2	☐	cell adhesion	32.77	4.825e-30
3	☐	integrin-mediated signaling pathway	26.89	1.703e-44
4	☐	cell-matrix adhesion	25.21	2.078e-42
5	☐	development	24.37	5.754e-15
6	☐	regulation of progression through cell cycle	21.01	2.237e-17
7	☐	protein amino acid phosphorylation	20.17	1.692e-13
8	☐	cell migration	13.45	2.460e-21
9	☐	blood coagulation	10.92	8.332e-14
10	☐	negative regulation of cell differentiation	10.08	1.552e-18
11	☐	blood vessel development	9.24	4.650e-16
12	☐	cell-substrate junction assembly	6.72	3.792e-14

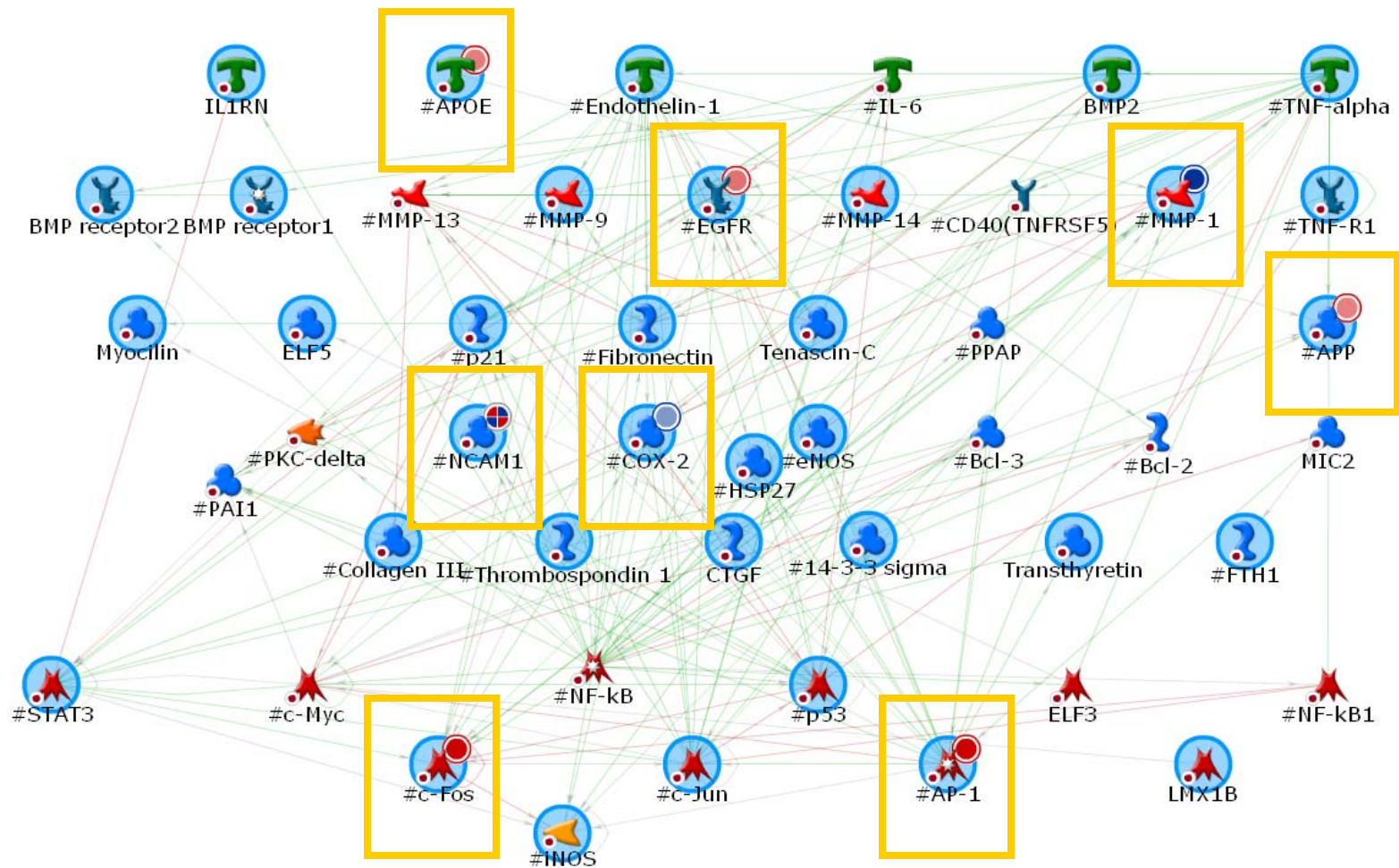
Supplement Figure 7. A. DI network for the negatively regulated genes retrieved from the top 12 scored pathway maps (fold change > 1.5). The color density of the blue indicator circles reflects the degree of downregulation; the expression data is shown from the donor groups 1 and 2 combined data set . **B.** Top 12 GO processes for the gene content of the network.



Supplement Figure 9. A direct interactions (DI) network for the downregulated genes from the combined (donor groups 1 and 2) data set. The highly connected hubs are marked with blue circles, four less connected ones with green oval. The full legend of symbols used as network and map objects is shown in Supplement Table II.



Supplement Figure 11. The DI network for the combined transcriptomic and proteomic data set interconnected 488 nodes that changed (>2.5 fold, both up- and down-regulated) in glaucomatous ONHAs. Top 12 major hubs are shown at the periphery. Subunits of NF- κ B (c-Rel and NF- κ B1) and AP-1 (c-Fos, c-Jun, JunD) are grouped together.



Supplement Figure 13. Proximity analysis using the AN algorithm revealed the DE (framed nodes with red and blue indicator circles) genes among close neighbors of the genes from the G-set (labeled with light blue circles)

