Supplementary file:
Interfacing cellular networks of *S. cerevisiae* and *E. coli*: Connecting dynamic and genetic information

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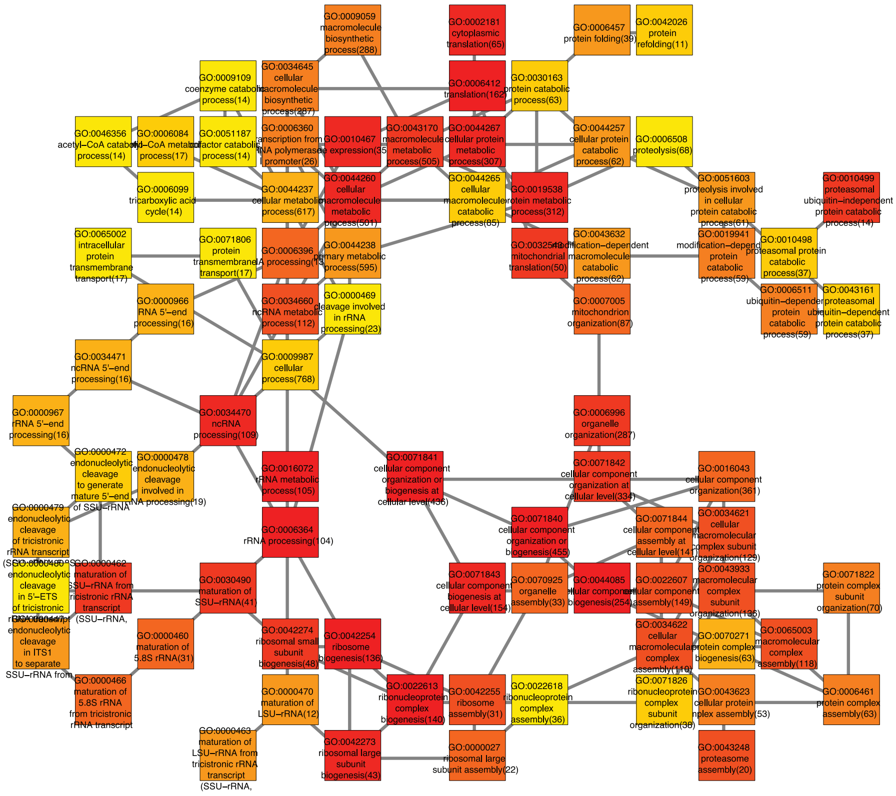
A) GEA GRN-PPN interface (S. cerevisiae)



B) GEA GRN-TRN interface (S. cerevisiae)

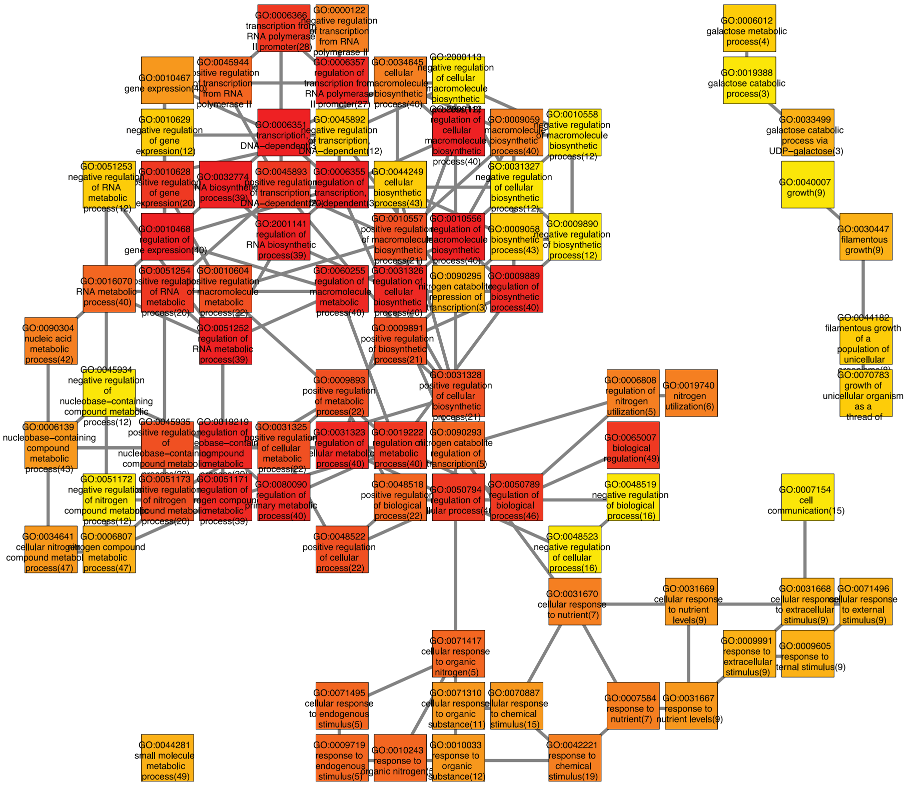


Figure 1: Gene Ontology Biological Process enrichment analysis of the *S. cerevisiae* A) GRN-PPN interface (785 genes, 82 terms $p_{fdr} \leq 0.01$) and B) GRN-TRN interface (64 genes, 86 terms $p_{fdr} \leq 0.01$).

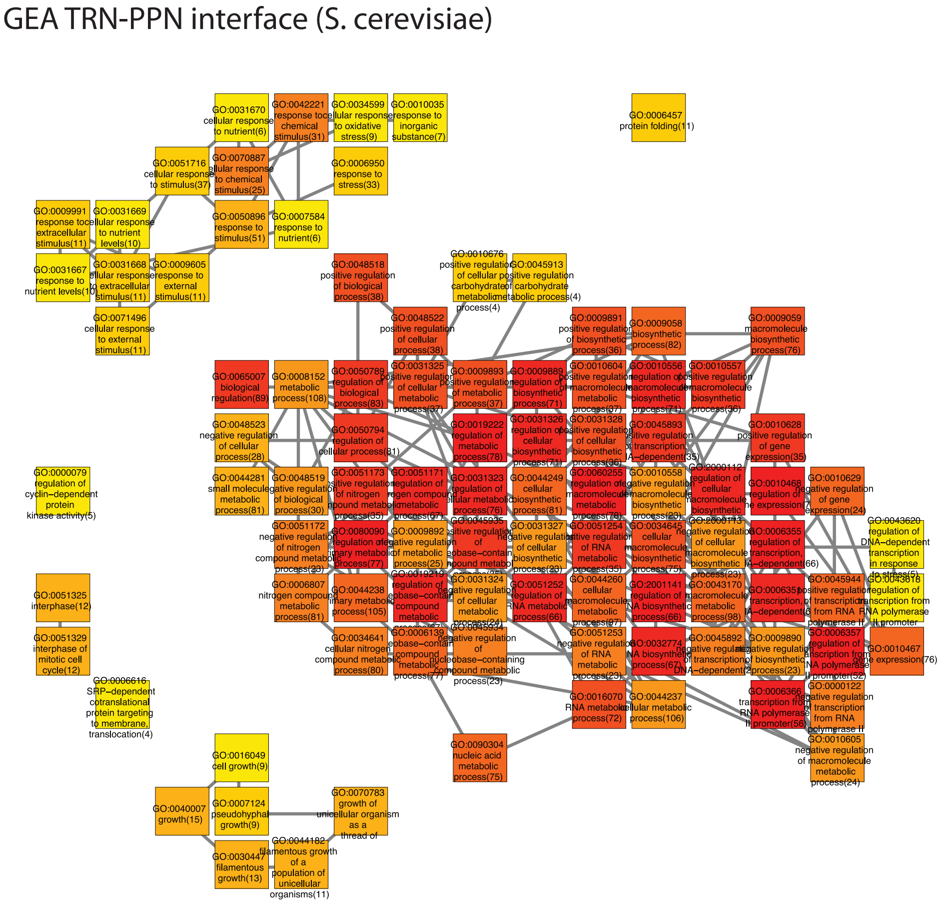
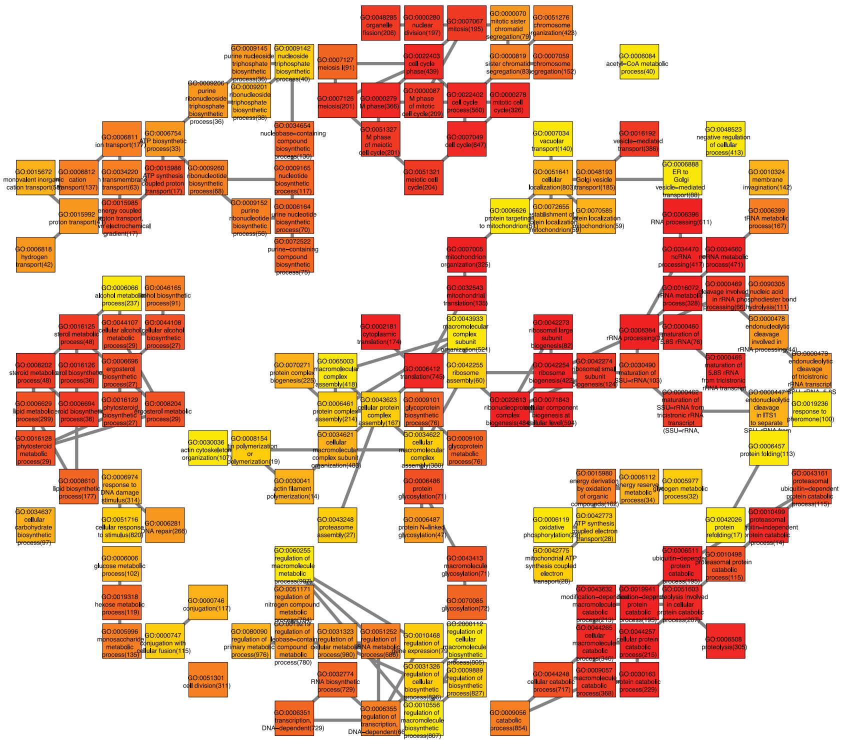


Figure 2: Gene Ontology Biological Process enrichment analysis of the *S. cerevisiae* TRN-PPN interface (115 genes, 96 terms $p_{fdr} \leq 0.01$).

A) GPEA GRN-PPN (S. cerevisiae)



B) GPEA GRN-TRN (S. cerevisiae)

B) GPEA TRN-PPN (S. cerevisiae)

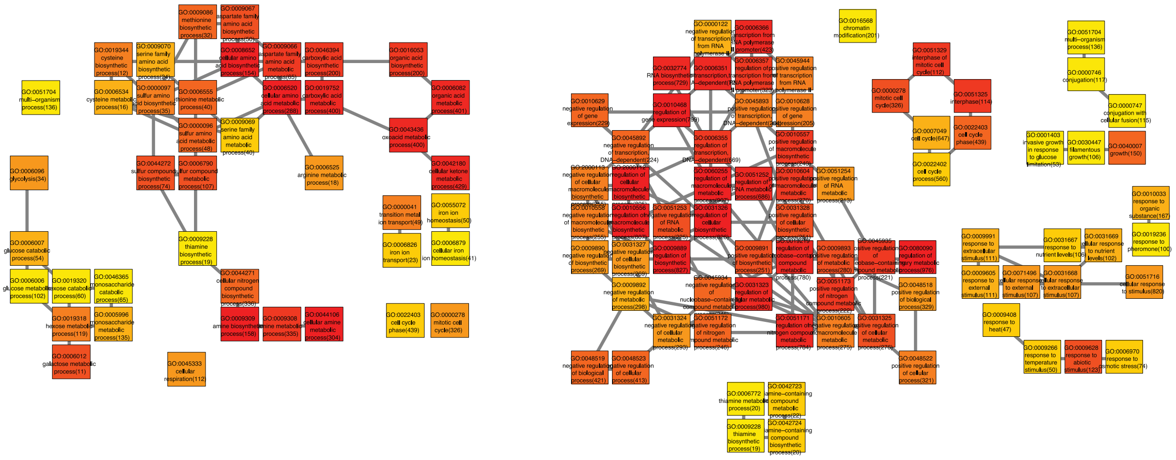


Figure 3: Gene Pair enrichment analysis of the *S. cerevisiae* GRN, PPN and TRN network. Shown are the shared significant Gene Ontology terms for A) GRN-PPN (top 150 terms from 249 $p_{bonf} \leq 10e-4$) B) GRN-TRN 42 terms ($p_{bonf} \leq 10e-4$) and C) TRN-PPN 75 terms ($p_{bonf} \leq 10e-4$). In brackets after the term name shown the number of edges in the respective term for network 1 and network 2.

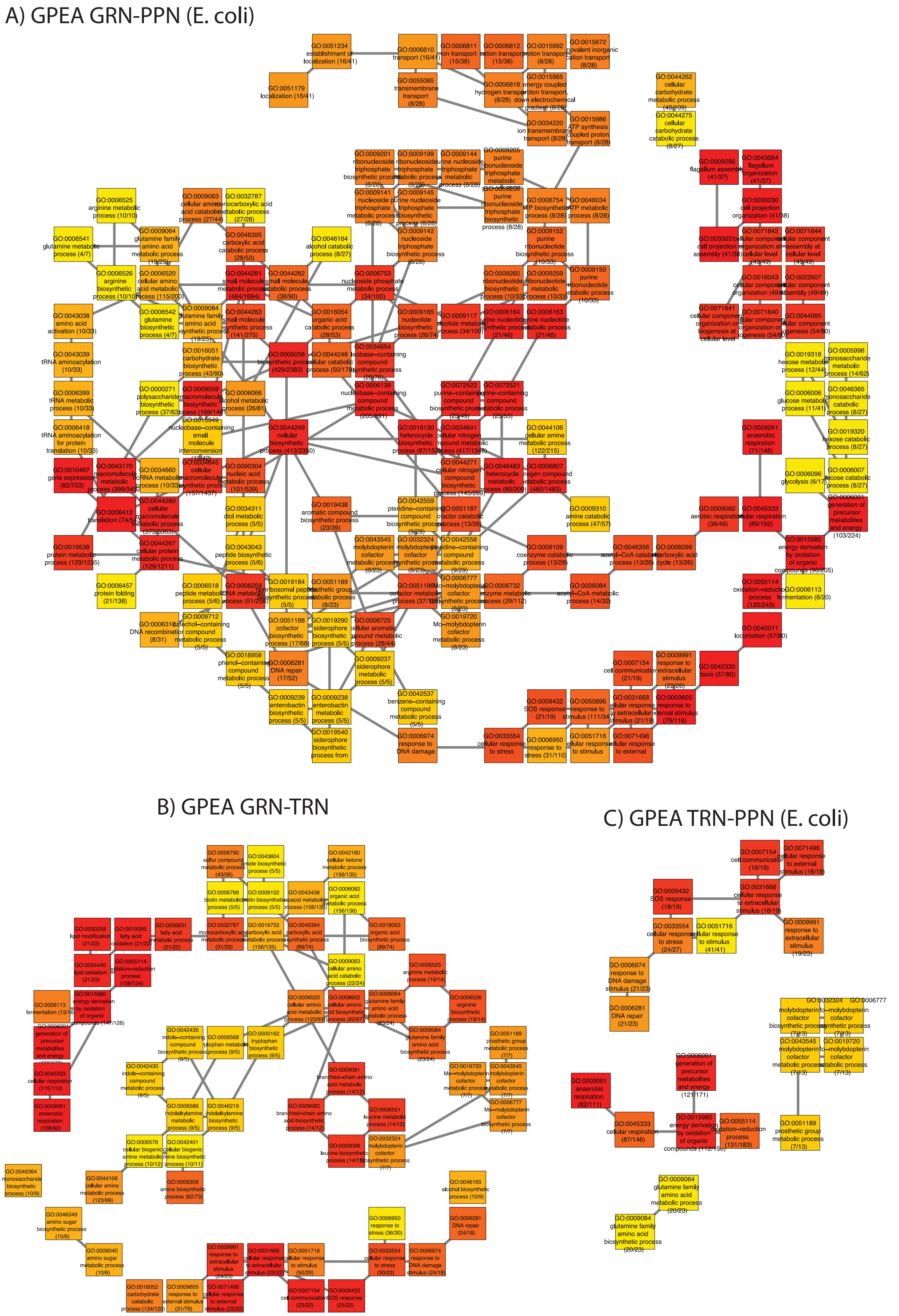


Figure 4: Gene Pair enrichment analysis of the *E. coli* GRN, PPN and TRN network. Shown are the shared significant Gene Ontology terms for A) GRN-PPN (151 terms $p_{bonf} \leq 10e-4$) B) GRN-TRN 63 terms ($p_{bonf} \leq 10e-4$) and C) TRN-PPN 21 terms ($p_{bonf} \leq 10e-4$). In brackets after the term name shown the number of edges in the respective term for network 1 and network 2.

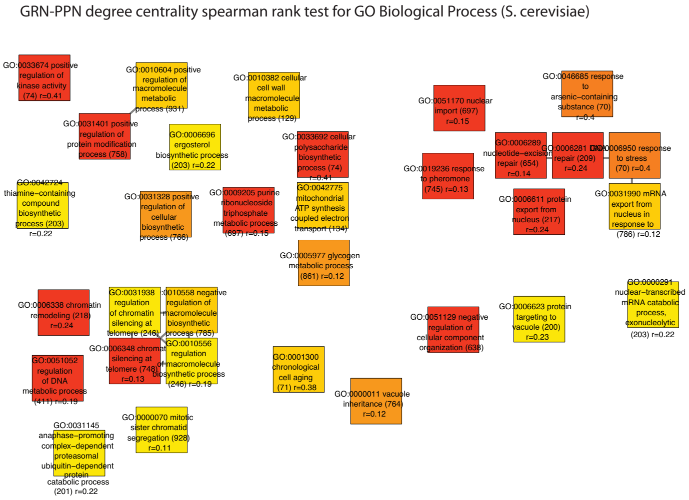


Figure 5: GRN-PPN degree centrality Spearman's rank test for GO Biological Process (*S. cerevisiae*). In brackets shown the number of genes shared between both networks of the corresponding GO term sub-networks and the centrality Spearman's correlation coefficient ρ. Color gradient (red to yellow) denote the rank of the 32 shown terms with $p_{fdr} \leq 0.05$.