

Figure 1. Significantly changed transcripts associated with proliferation related ontology vs. the control condition: (A) positive proliferation and (B) negative proliferation.

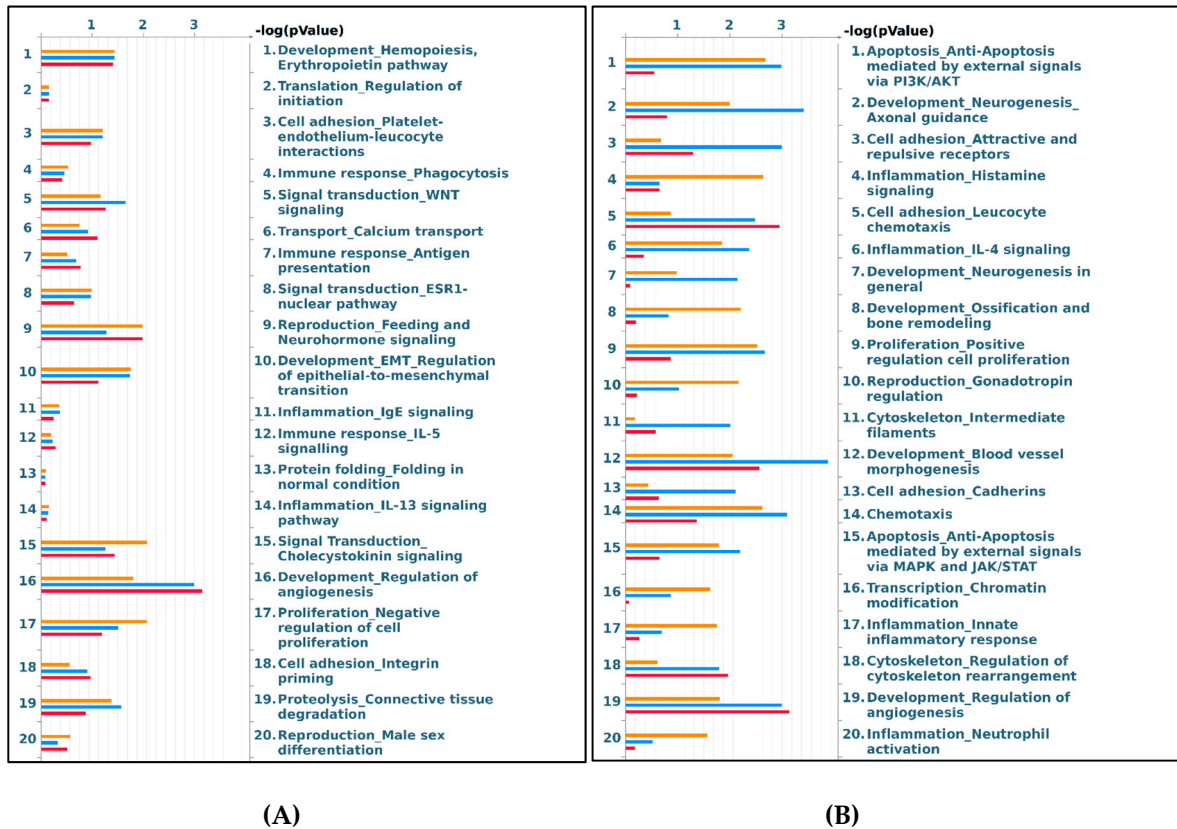


Figure 2. The most statistically affected genetic networks either shared (Supplementary Figure S2A) or uniquely changed (Supplementary Figure S2B) between conditions: orange for IL2, blue for IL7, and red for IL15.