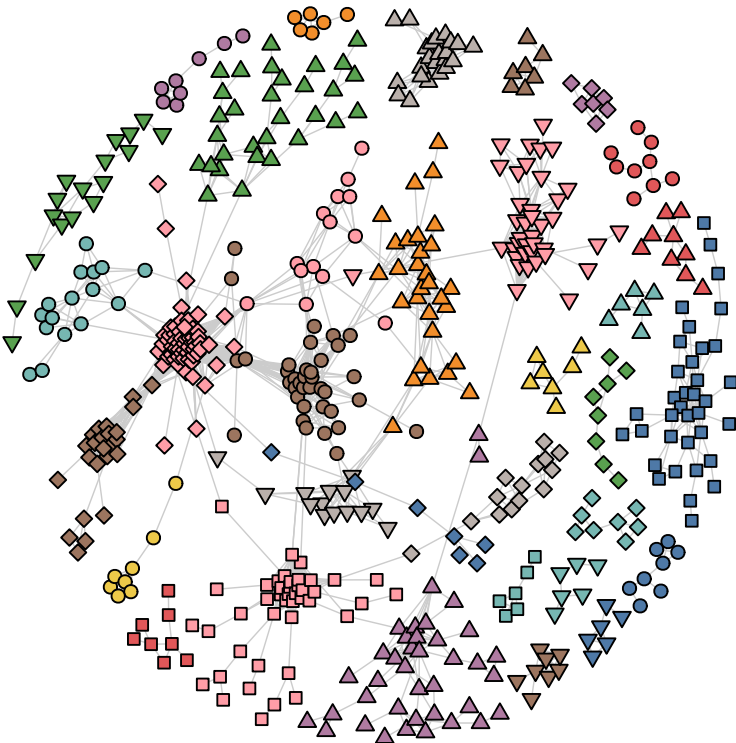


Common Reactome pathways, transcriptomes

vertices: n = 570, edges: n = 3149

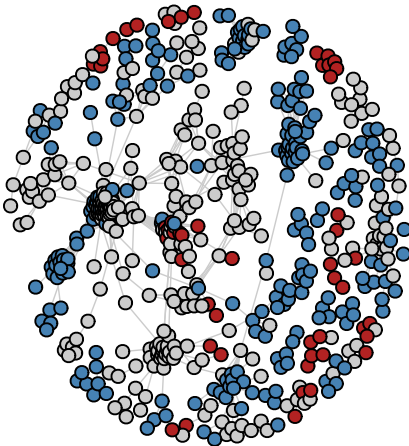
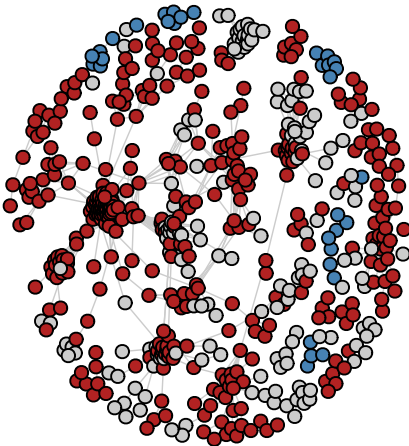
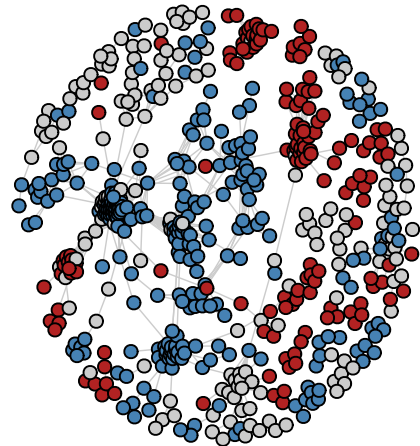


- | | |
|--|---|
| ◇ dermatan, chondroitin | ◇ fatty acid oxidation |
| ◇ WNT, NOTCH, HEDGEHOG, RUNX
TCR, IL1, antigen, DNA | ▽ mitochondria/peroxisomes |
| ● cell cycle checkpoints | ● bile acids |
| ▽ HIV infection, FGFR2 | ◇ xenobiotics |
| ■ EGFR/ERBB, RAS, PI3K
MET, EPOR, PDGFR, KIT | ▽ cell death, TNF signaling |
| ▲ inflammatomes, TLR, NFκB, ERK | ◆ CD28 and PD-1 |
| ▲ vesicles, cell junctions | ▲ small GTPases |
| ● chromatin, epigenetics, WNT | ● TCA and OXPHOS |
| ▲ DNA damage/repair, telomeres | ▲ coagulation |
| ● apoptosis, BH3-only | ▲ FGFR signaling |
| ▽ GPCR, ADP, Ca2+ signaling | ■ keratan sulfate |
| ▽ RNA processing | ● TP53, DNA damage/repair
cell cycle checkpoints |
| ● phospholipids | ■ integrin, laminin, MET |
| ◆ FC/scavenger receptors | ▲ IL6/27/35 and MAPK |
| ■ RNA metabolism, glucose
IFN/JAK/STAT | ◆ IL2/3/9/15/21 |
| ▲ collagen, ECM | ▽ NEF and WNT5A |
| ● cell cycle, mitosis | |

Reactome pathways, cluster #1

Reactome pathways, cluster #2

Reactome pathways, cluster #3



regulation
vs cohort mean ● upregulated ● downregulated ○ ns