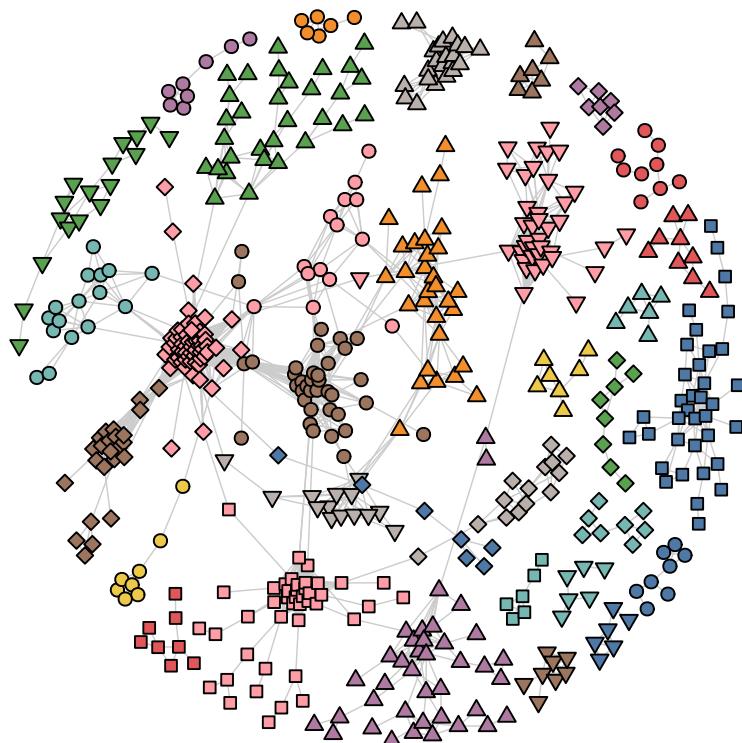


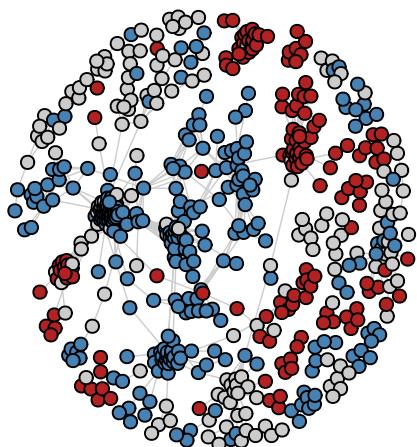
Common Reactome pathways, transcriptomes

vertices: n = 570, edges: n = 3149

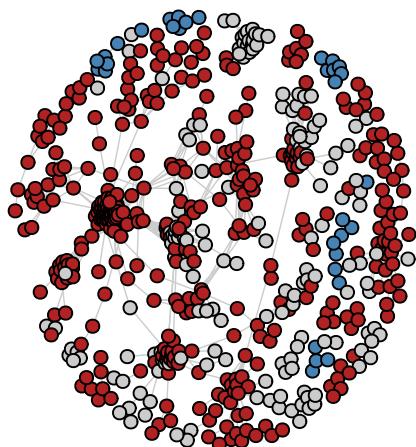


- ◊ dermatan, chondroitin
- ◊ fatty acid oxidation
- ◊ WNT, NOTCH, HEDGEHOG, RUNX
- ◊ mitochondria/peroxisomes
- ◊ cell cycle checkpoints
- ◊ bile acids
- ◊ xenobiotics
- ◊ cell death, TNF signaling
- ◊ CD28 and PD-1
- ◊ vesicles, cell junctions
- ◊ small GTPases
- ◊ TCA and OXPHOS
- ◊ apoptosis, BH3-only
- ◊ coagulation
- ◊ FGFR signaling
- ◊ keratan sulfate
- ◊ TP53, DNA damage/repair cell cycle checkpoints
- ◊ integrin, laminin, MET
- ◊ RNA processing
- ◊ phospholipids
- ◊ 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

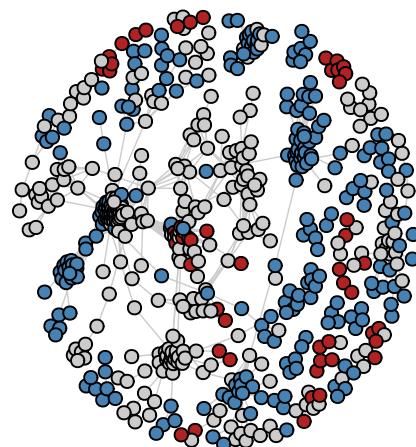
Reactome pathways, cluster #1



Reactome pathways, cluster #2



Reactome pathways, cluster #3



regulation
vs cohort mean

● upregulated

● downregulated

○ ns