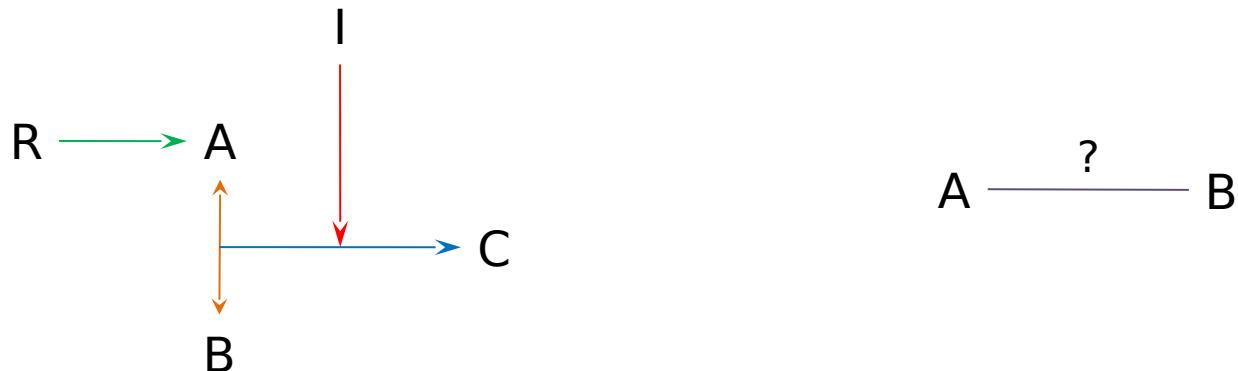
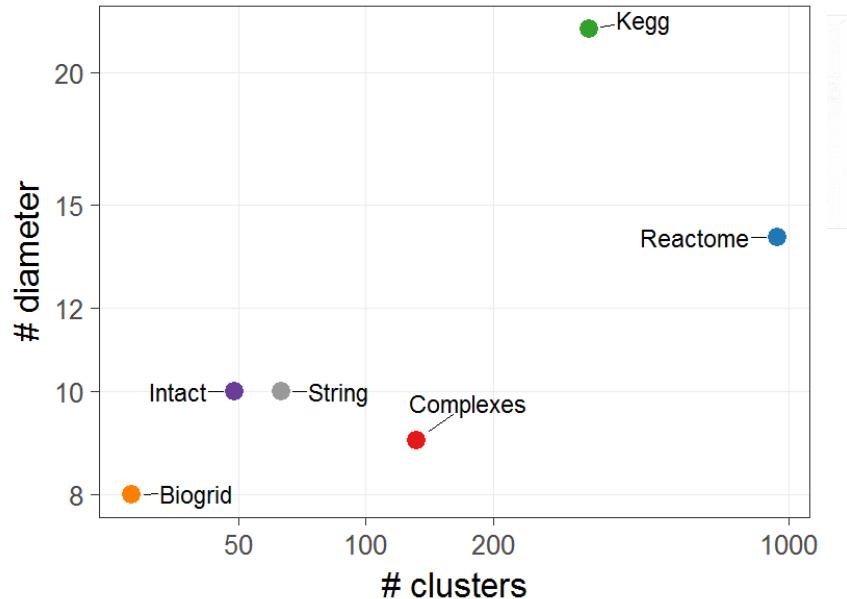
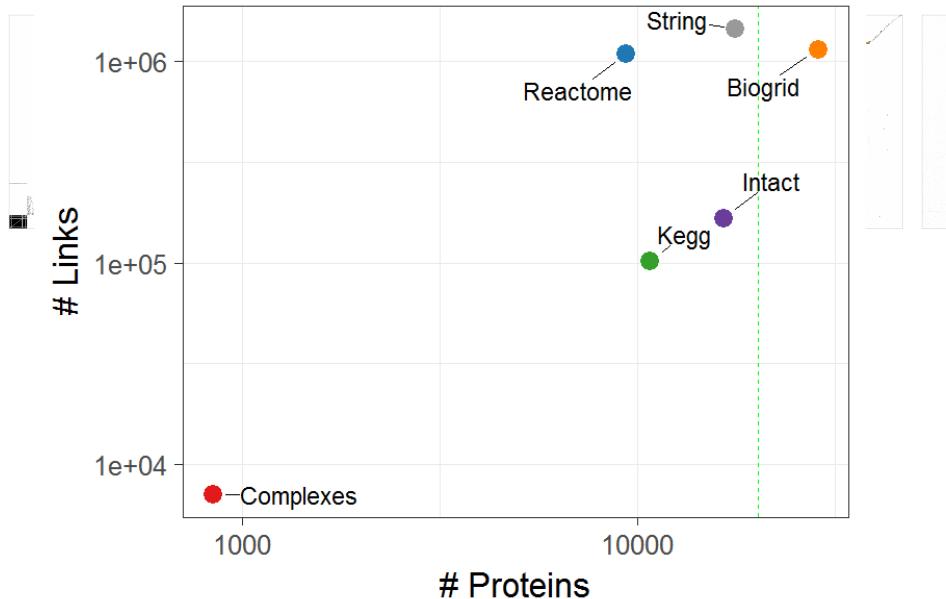


How do our maps look like?

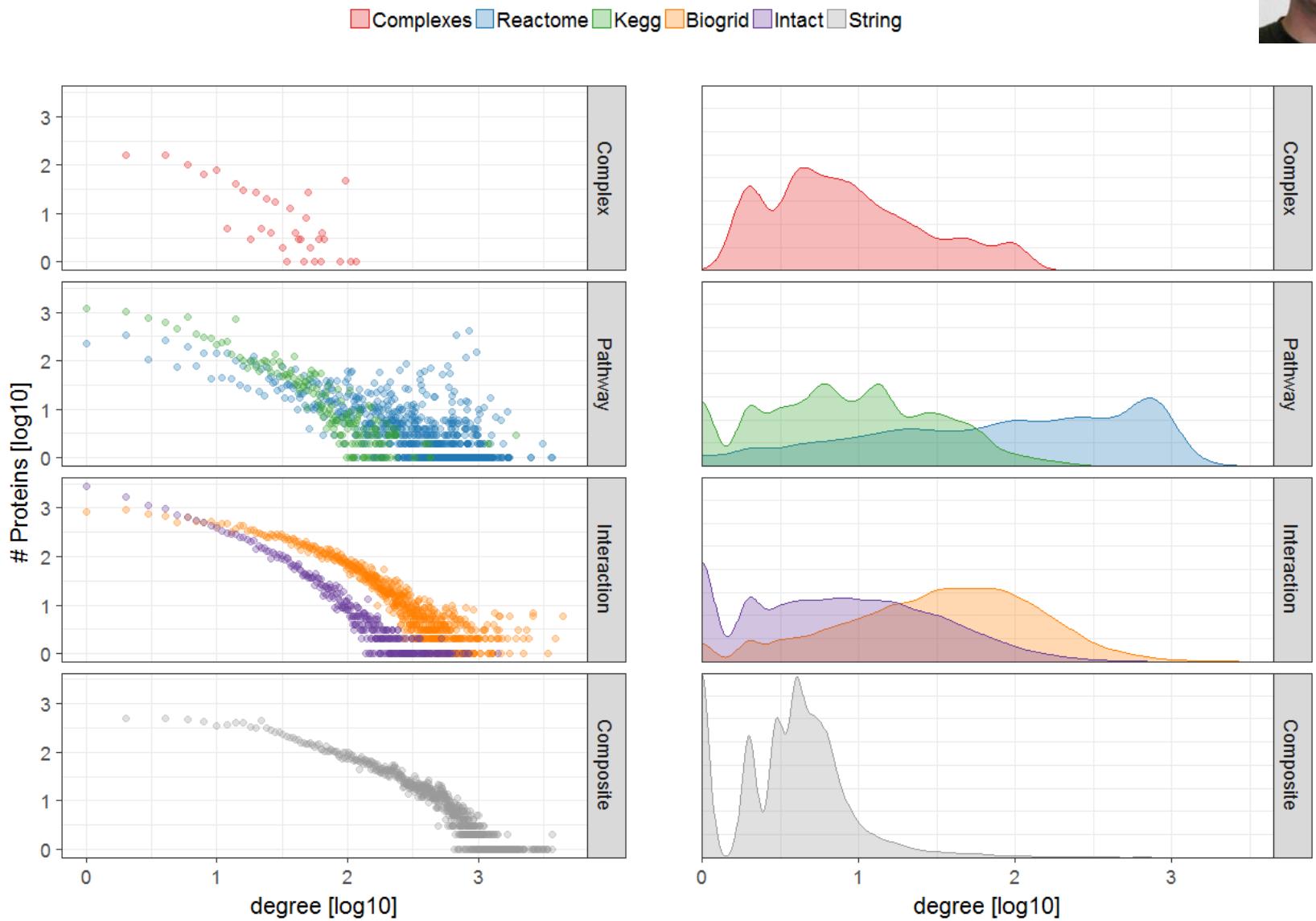


- Proteins only – human only
- One canonical isoform – proteoform per gene

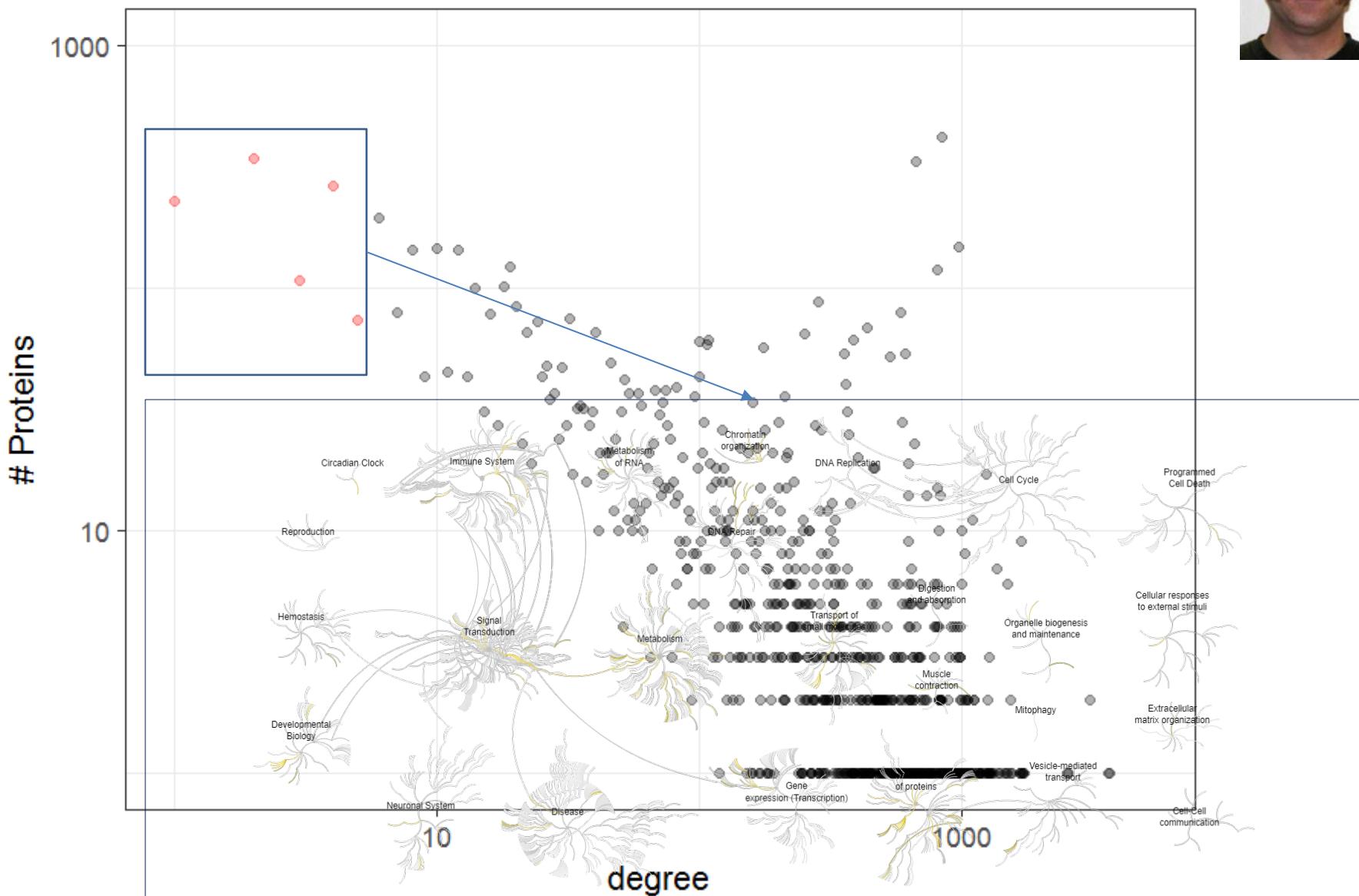
How do our maps look like?



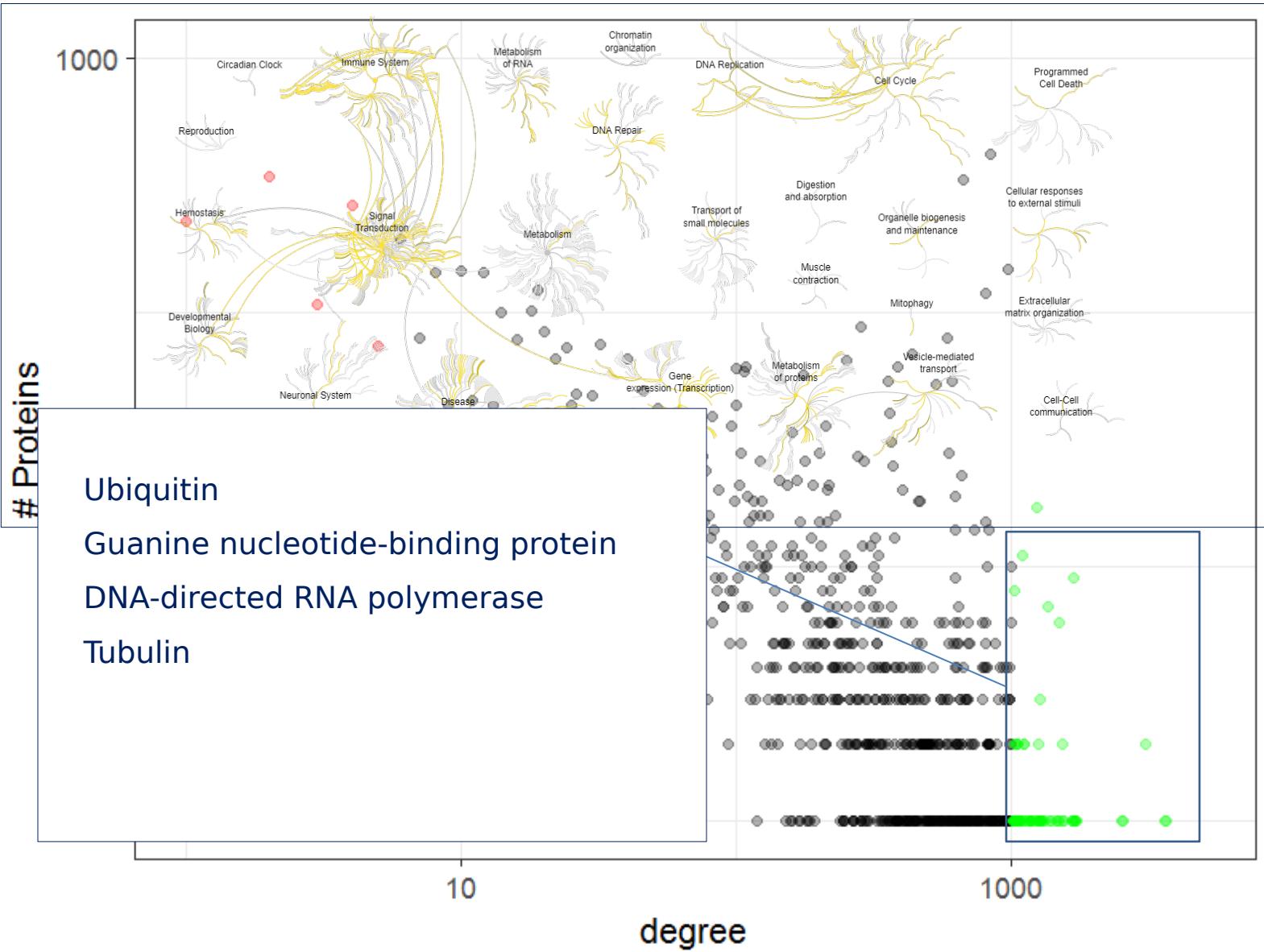
How do our maps look like?



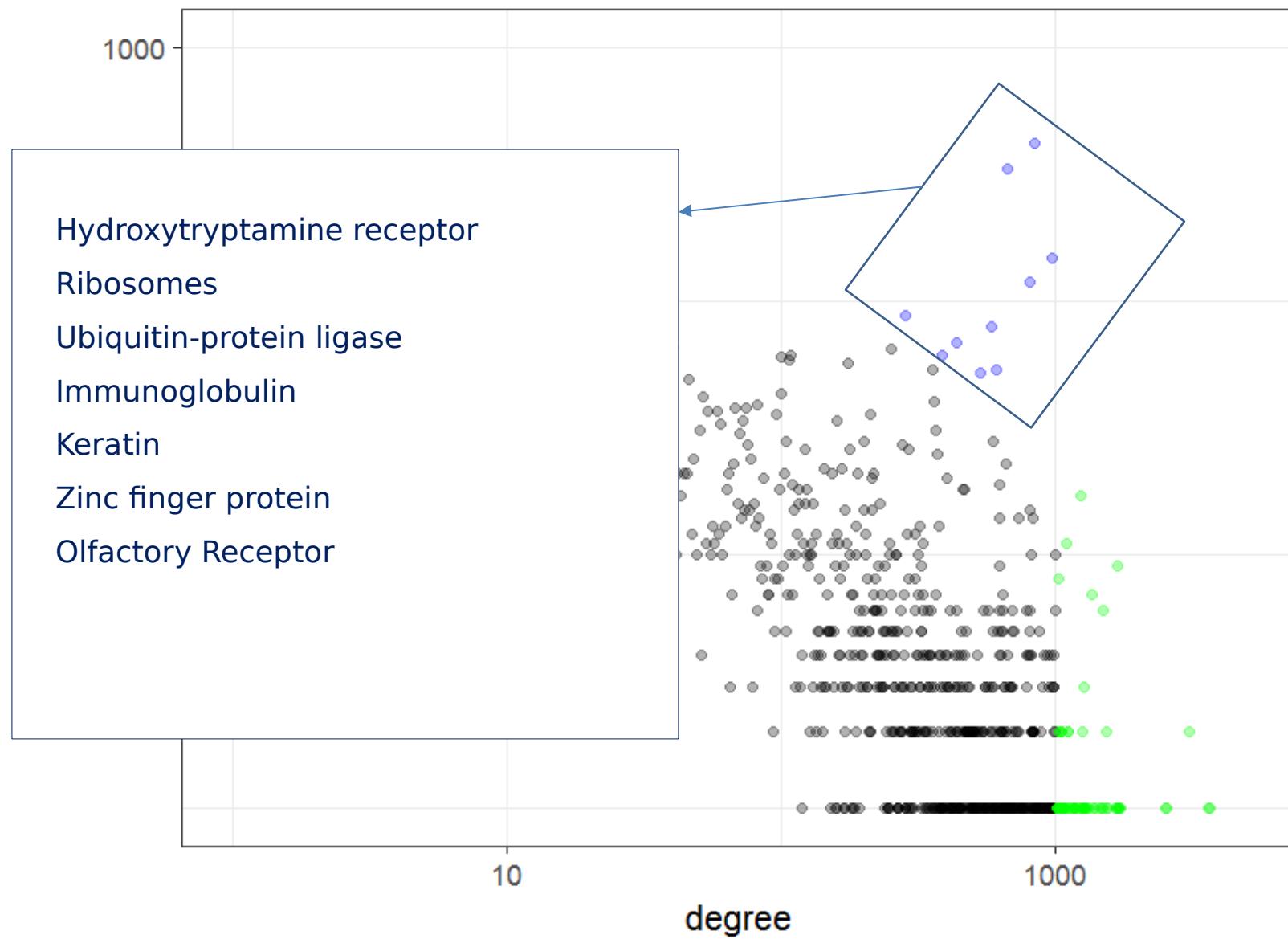
Proteins of Interest



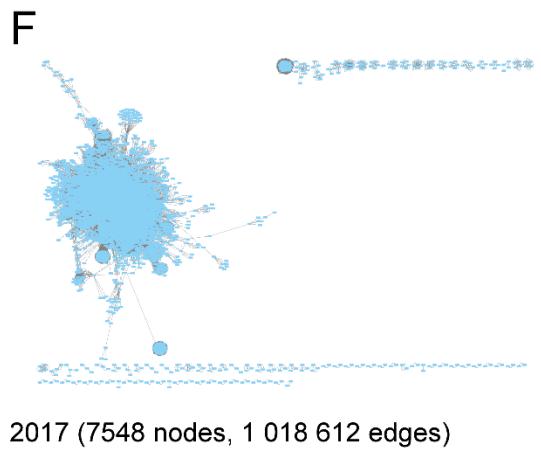
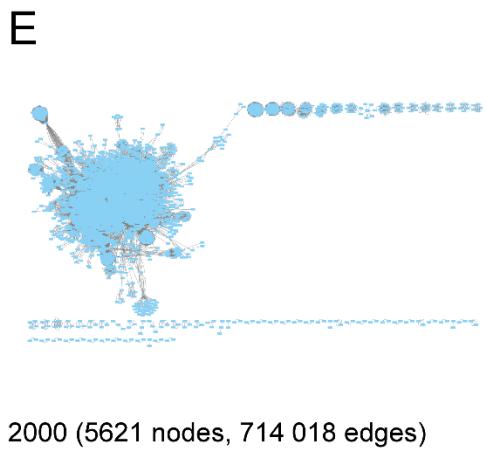
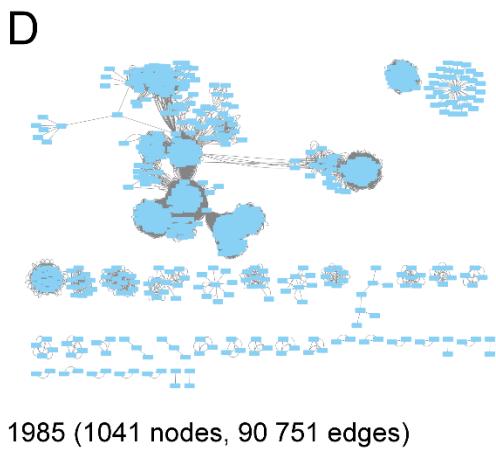
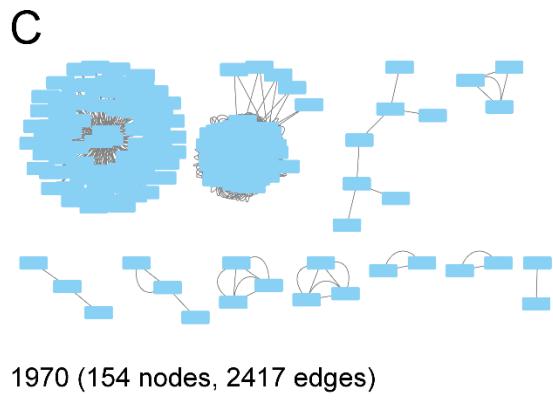
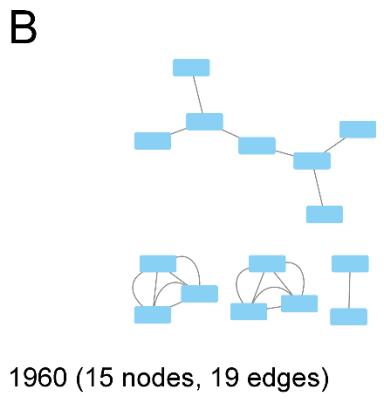
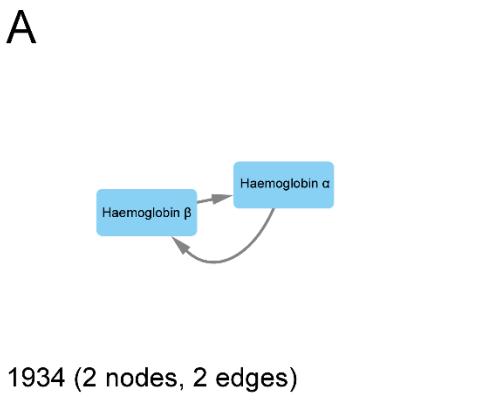
Proteins of Interest



Proteins of Interest



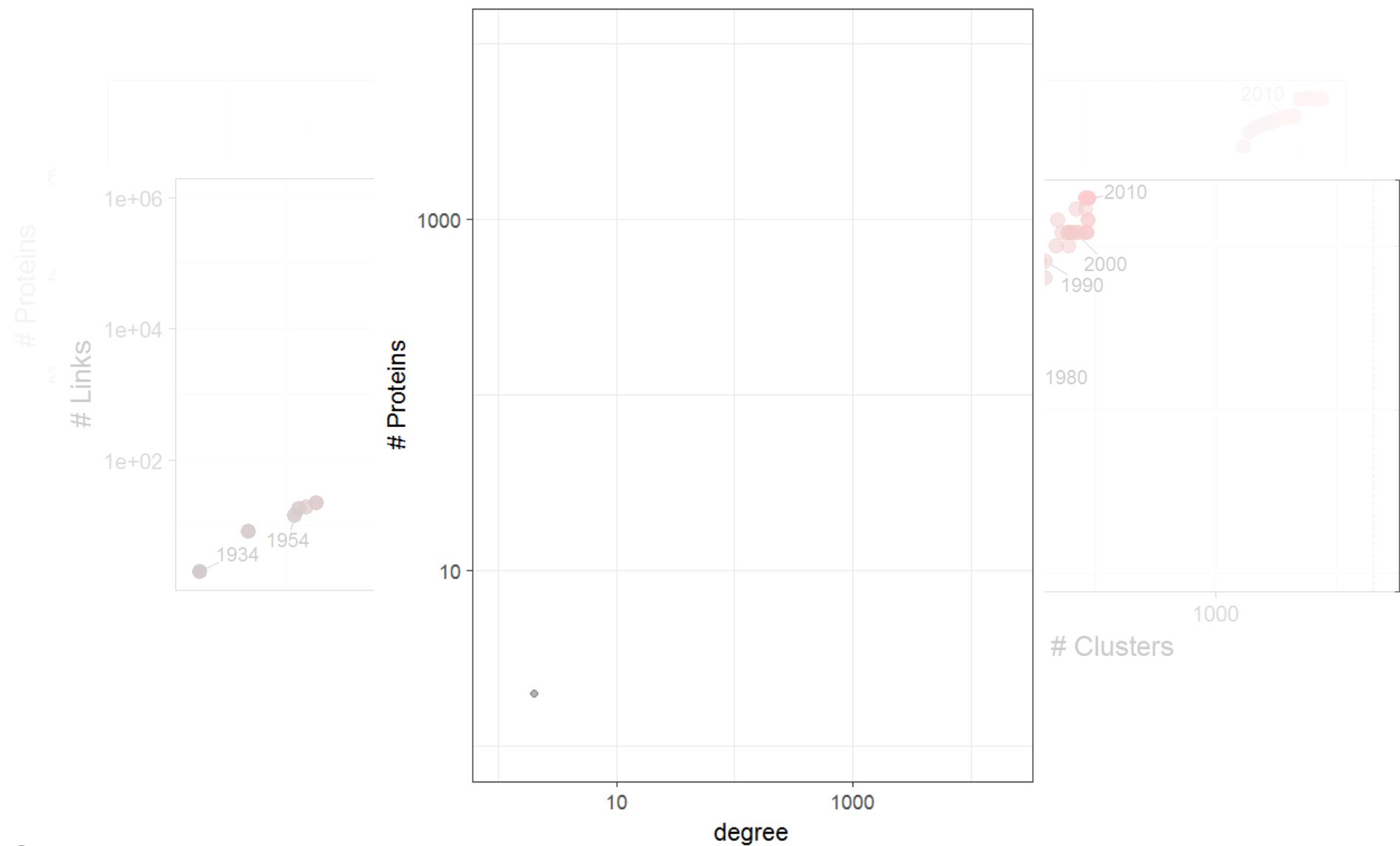
Pathway archeology



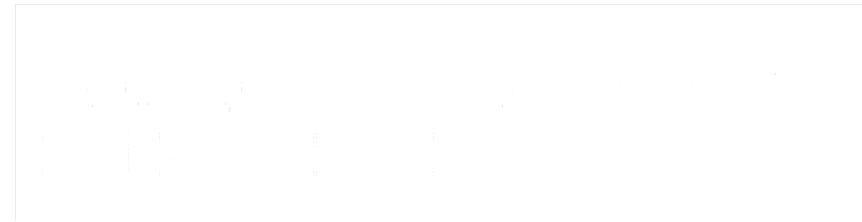
Pathway archeology



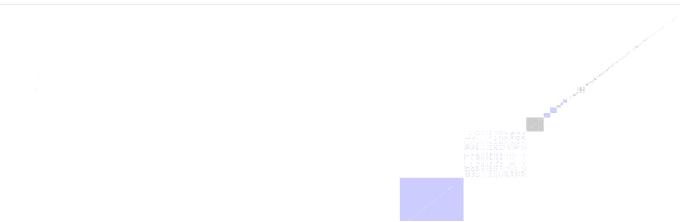
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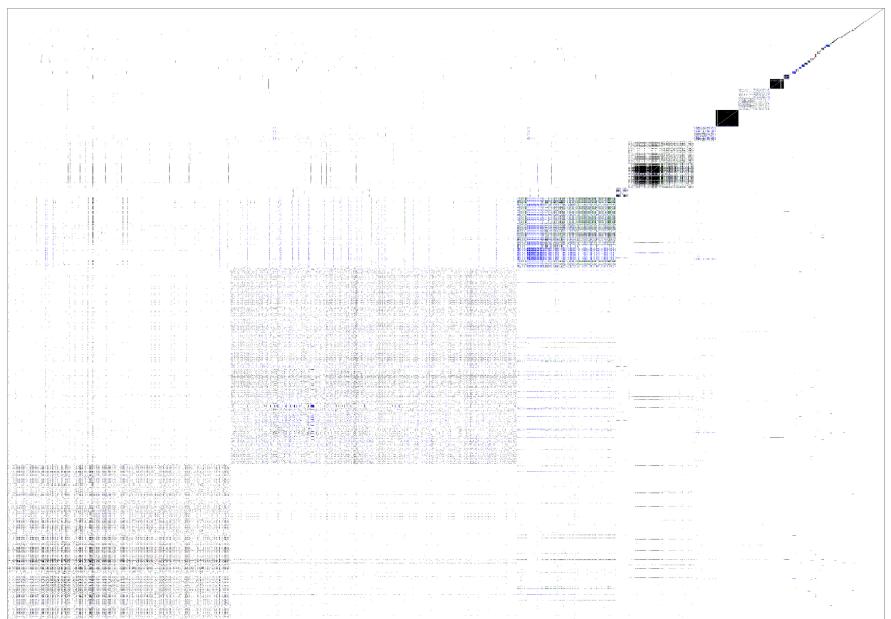
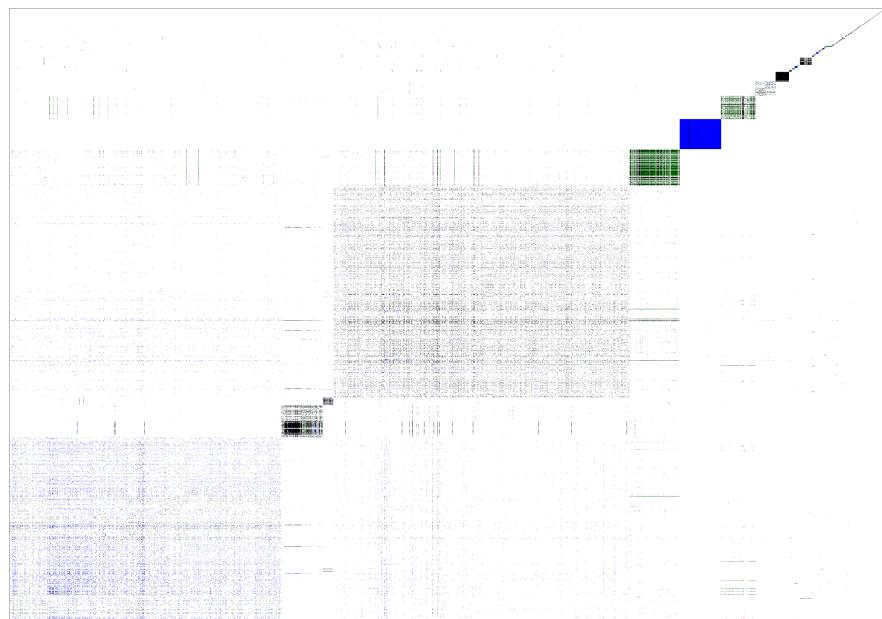
Tissue - Cell Specificity



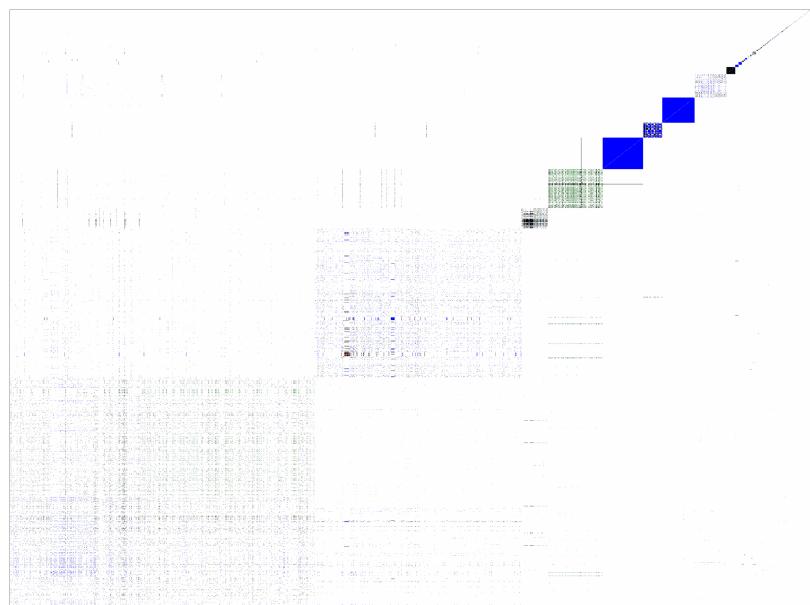
A-549 cell - RNA



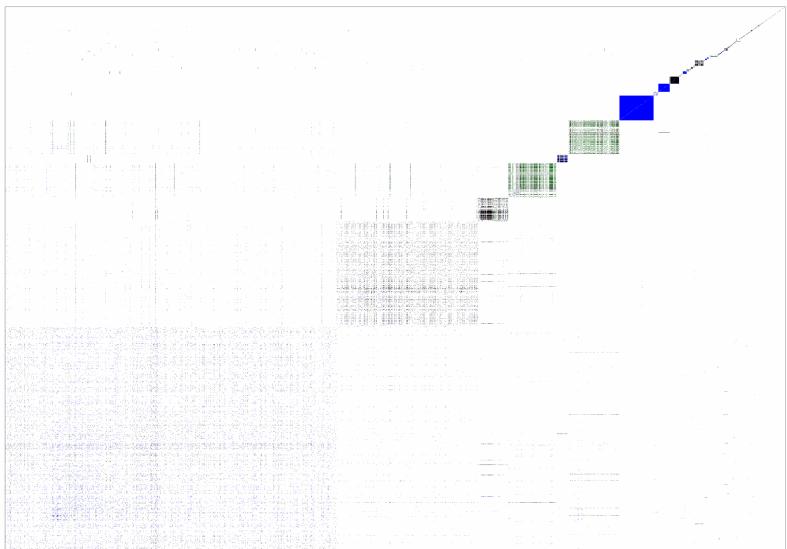
A-549 cell - Protein



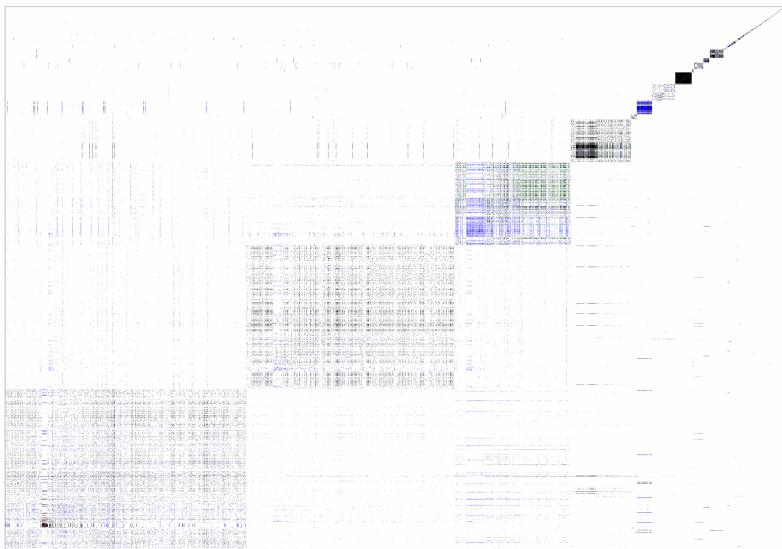
Tissue - Cell Specificity



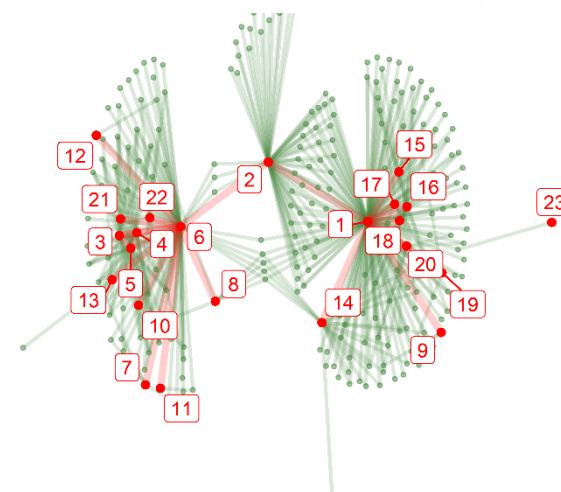
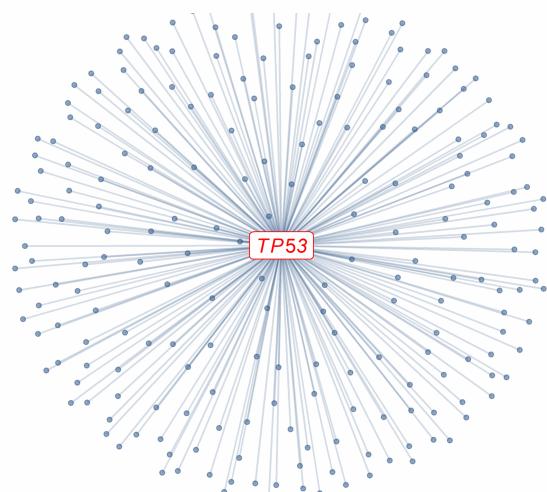
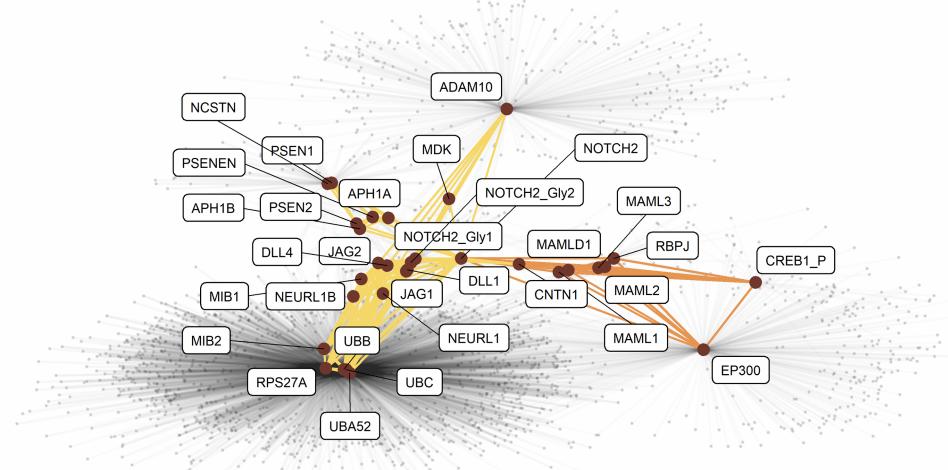
testis - RNA



testis - Protein



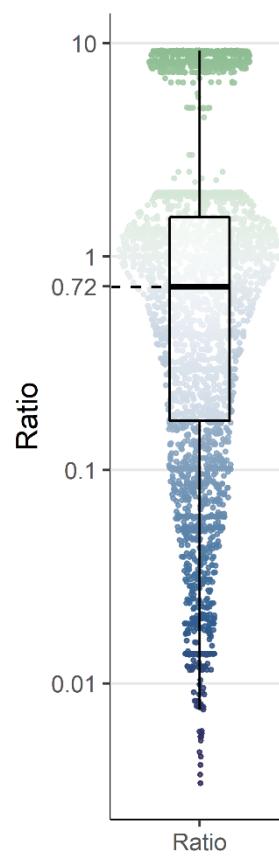
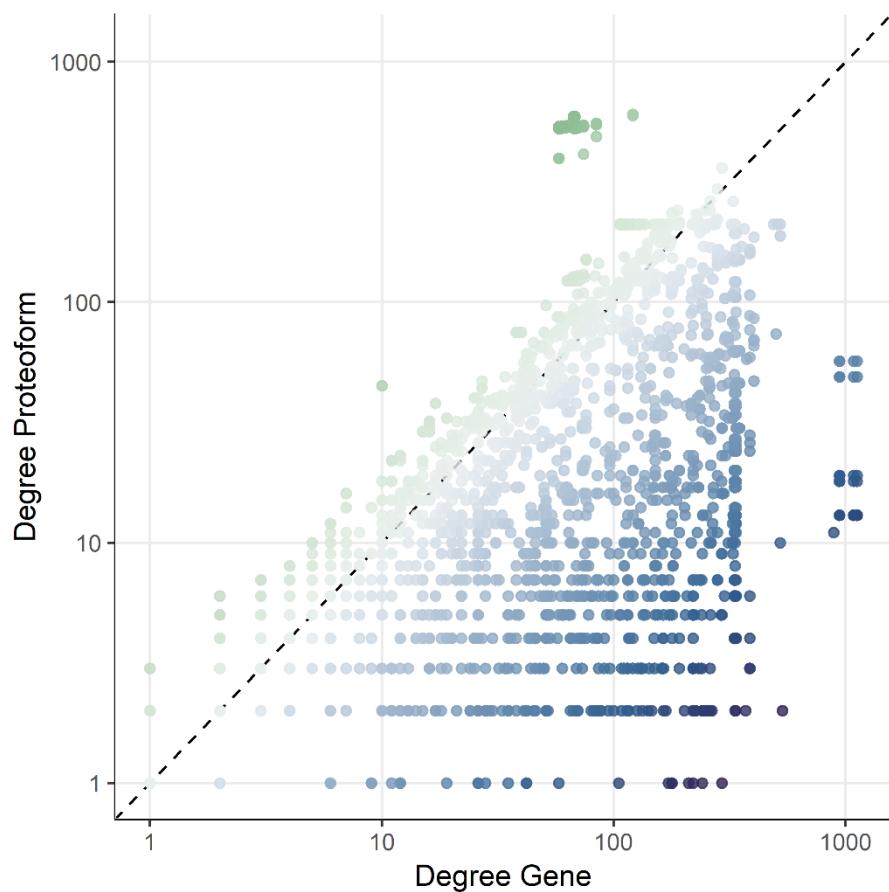
Proteoform Networks



→ Try it!

github.com/PathwayAnalysisPlatform/PathwayMatcher

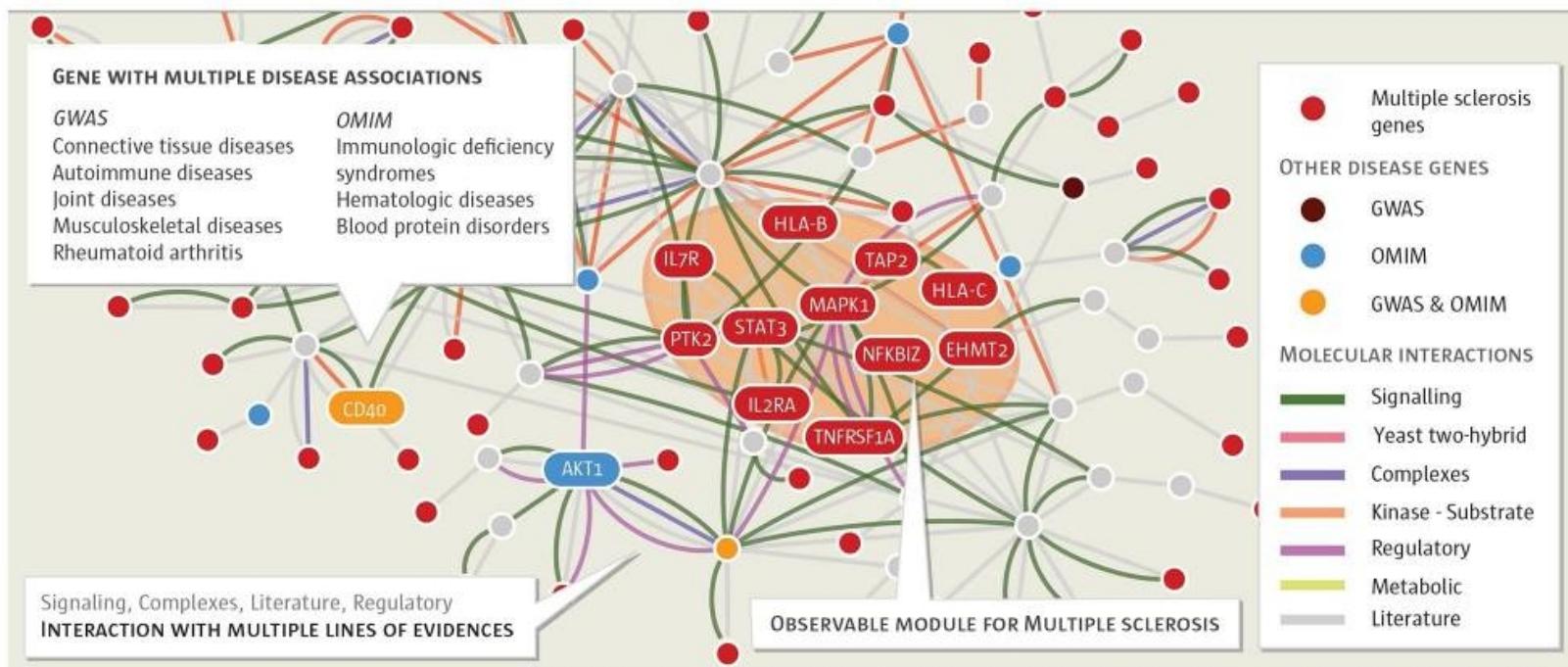
Different Topology



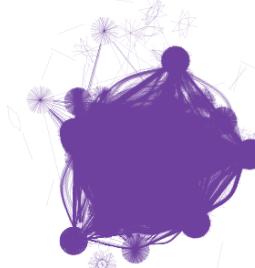
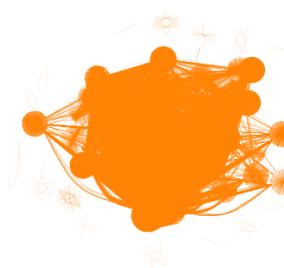
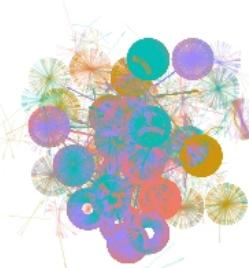
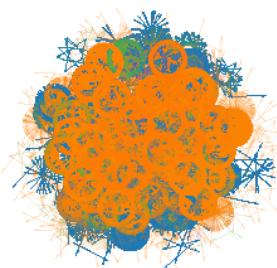
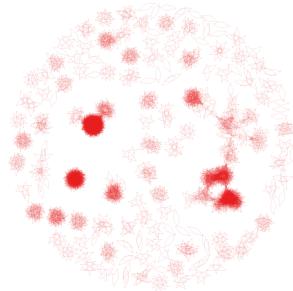
PTM-mediated Network Organization



D BUILDING THE INTERACTOME



Take home message



- No one database/algorithm fits all
- Be aware about internal structure prior to analysis
- Be careful about underlying object models and identifiers
- Use the right level of granularity - coverage for your analyses
- Be sceptical, always QC in details