Clustering modENCODE expressions of genes and ncRNAs in embryo development, and studying modular network influence of ncRNAs

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Species	Developmental stages	Protein-coding genes*	Non-coding RNAs*	Co-expression modules**
Worm (C. elegans)	111	9114	855	69
Fly (D. mel.)	50	8340	357	46

* >80% valid samples, coeff. of variance > 1 in the modENCODE finalized datasets in June 2012

** clustering via weighted gene co-expression network analysis (WGCNA)

Observations:

1. *Modules enriched w/ ncRNAs (red circles)*
2. *Influential ncRNAs (high network centrality) exist in modules NOT enriched with ncRNAs (blue circles)*

Worm (C. elegans)

Fly (D. mel.)