ncRNA Networks

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TF Out-degree Hubs in TF-Coding Gene Network	TF Out-degree Hubs in TF-ncRNA Network
- MAX	RAD21
- ELF1	MAX
- YY1	FOXA1
- E2F6	ELF1
- HEY1	PU1
- EGR1	YY1
- SIN3AK20	HDAC2
- HDAC2	SP1
- POU2F2	USF1
- OCT2	NFKB

Common Out-degree Hub: MAX

- it has 293 targets, miRNA is highly enriched with p-value less that 1.0e-6
- rRNA is under-represented with p-value 0.017
- All the other classes of ncRNAs don't have significant statistics

Properties of In-degree Hubs

- snoRNAs are highly enriched in top 10% of targets with the largest no. of TF regulators

- under-represented in top 10% targets: misc_RNA, rRNA, snRNA

- If I choose top 20% of targets with highest in-degrees, I got the same conclusion

TFs: Coding Gene vs. ncRNA

- No significant difference between in-degree distributions for different types of ncRNAs

ncRNA associated (top 5):
- BRF2 subunit of RNA polymerase III
- POU5F1 embryonic development
- BRF1 subunit of RNA polymerase III
- BDP1 subunit of RNA polymerase III
- BATF Basic leucine zipper transcription factor, ATF-like
- ESR1   estrogen receptor 1

TFs: Coding Gene vs. ncRNA

Coding Gene associated (top 10):
- BAF155
- ZBTB7A
- KAP1
- RFX5
- JUN
- STAT1
- NR2C2
- CFOS
- STAT3
- ELK4

Network Motifs

- Modify Koon-Kiu's script for motif analysis
- Look for motifs such as