|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Regulatory Network Property** | ***E.coli*1** | **Yeast1** | **Worm2** | **Fly3** | **Human** |
| Non-Random hierarchy structure | Yes | Yes | Yes | Yes | Yes |
| More bottlenecks (highest betweenness/degree centrality) in middle level | Yes | Yes | Yes | N/A | Yes |
| TFs at top level have more PPI partners | Yes | Yes | No | N/A | Yes |
| Higher levels TFs are more influential | Yes | Yes | Yes | N/A | Yes |
| Lower level TFs are more essential | Yes | Yes | Yes | N/A | N/A |
| Two classes of miRNAs (those regulating TFs and those regulated by TFs) | - | - | Yes | N/A | Yes |
| TFs on bottom level have fewer miRNA regulators | - | - | Yes | N/A | Yes |
| TFs on bottom level have fewer miRNA targets | - | - | N/A | Yes | Yes |
| Fraction of upward edges | N/A | N/A | N/A | 8% | 7% |
| TFs at top of hierarchy under greater negative selection | Yes4,5 | Yes4,5 | N/A | N/A | Yes4 |
| TFs with greater out degree (i.e. more targets) under greater negative selection | Yes6 | N/A | N/A | N/A | Yes |
| Allelicty of TFs positively correlated with degree centrality | N/A | N/A | N/A | N/A | Yes |

1 H Yu, M Gerstein (2006). Proc Natl Acad Sci U S A 103: 14724-31. 2 Gerstein et al. (2011). Science 330: 1775-87. 3 modENCODE Consortium et al. (2011). Science. 2010 Dec 24;330(6012):1787-97. 4 N Bhardwaj, KK Yan, MB Gerstein (2010). Proc Natl Acad Sci U S A 107: 6841-6. 5 N Bhardwaj, PM Kim, MB Gerstein (2010). Sci Signal 3: ra79. 6 Y Xia, EA Franzosa, MB Gerstein (2009). PLoS Comput Biol 5: e1000413.

Supplementary Table XXX. We compare the properties of human regulatory network with corresponding results for regulatory networks for *E.coli*, yeast (*S.cerevisiae*), worm (*C.elegans*), fly (*D.melanogaster*) and human. For the most part the results from this paper are consistent with the comparable results from other species. Dashes indicate results that are non relevant, while N/A indicates results that are not available.

Sample text for discussion in paper:

We compared the properties of the human regulatory network with similar results from other model organisms (see Supplementary Table XXX). Most of the properties that can be compared agree such the non-random structure of the hierarchy, TFs at the top layer being under the most constraint, properties of miRNA-TFs interactions. We find that TFs at the top of hierarchy have the most interaction partners (protein-protein-interactions, phosphorylation partners) consistent with *E.coli* and *S.cerevisiae* but not with *C.elegans*.