

Title: Evolutionarily Conserved Regulatory Programs

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Despite the diversity of metazoans, common structures and mechanisms can be found in species from a wide variety of taxonomic groups. The stages of metazoan tissue development have been well researched, but the underlying regulatory mechanisms are not understood well. Precise spatial and temporal control of transcription through gene regulatory network is vital for correct tissue development and specialization. The *cis*-regulatory regions of genes and the corresponding transcription factors are major components of this network, and motif over-representation analysis of co-expressed gene sets is often employed to determine the responsible transcription factors. Studies have shown that transcription factor binding profiles tend to be highly conserved even over long evolutionary distances, and with large-scale projects such as ENCODE and modENCODE, it has become feasible to examine transcriptional regulation through comparative genomics. Recently, we have developed oPOSSUM 3, the latest update to the regulatory motif over-representation analysis tool set. Using this system and publicly available co-expressed gene sets, we perform comparative analyses of the regulatory programs among evolutionarily divergent species, including human, fruit fly, and nematode, and examine the extent of conservation in major regulatory programs.