Animal developmental patterning is an vastly complex and intricate process, requiring the integration of multiple temporally and spatially variant signals to define the transcription profile of each cell. Groucho, a transcriptional corepressor, plays a central role in this process in *Drosophila*. Groucho is thought to repress gene expression primarily through its recruitment to the genome through the action of multiple DNA binding factors. While Groucho is ubiquitously expressed in the early fly embryo, these factors are not, so Groucho mediated expression becomes dependent on the presence and concentration of these recruiting elements. Despite the broad importance of Groucho in fly development, a full picture of its regulatory network in the developing embryo has yet to be established. To this end, we have undertaken a multiomics approach to identify Groucho targets during three discrete stages of embryonic development. At each stage, we have analyzed the embryonic transcriptome of wild-type and Groucho mutant embryos. Additionally, we have utilized high-throughput sequencing of chromatin-associated RNAs (Nascent-seq) to confirm transcriptional rates at each timepoint. Groucho ChIP-seq provides information about the dynamics of the localization of Groucho to the chromatin in wild-type embryos. By combining these data sources, we established a temporally discrete high-confidence set of Groucho regulated genes, illuminating Groucho's multiple roles in developmental processes. Groucho appears to be involved in the regulation of hundreds of genes at each stage, a significant proportion of which are regulatory genes themselves, reinforcing the idea that Groucho is a highly-connected node or hub in the developmental regulatory network. Groucho's recruitment is highly dynamic, with a widespread transition in genomic localization occurring in 4 to 6.4 hours post embryo deposition. Human homologs of Groucho have been shown to act as both coactivators and corepressors, Drosophila Gro appears to be a dedicated repressor. While Groucho has long been considered to be a long-range corepressor, often binding thousands of base pairs away from its target genes, we find that this is not an obligate condition for repression, as actively repressing Groucho is often bound directly adjacent to transcription start sites. Furthermore, while Groucho is known to oligomerize *in vivo*, the role and necessity of this oligomerization in repression remains unknown. We find that, while Groucho can bind over large portions of the genome, possibly through self-association, most binding events are more spatially constricted, though clustering of peaks is apparent at multiple genomic loci. Around some classes of regulated genes, Groucho exhibits binding to both distal and proximal regions, perhaps indicative of Groucho serving a role in bringing distant portions of the genome in close proximity.

* Drosophila Groucho dedicated is likely a dedicated repressor
* Groucho targets are often developmental regulators themselves – i.e., Groucho is a master regulator of developmental regulators.
* Nascent-seq/RNA-seq comparison suggests that regulation of Gro targets may occur in different ways…
* Groucho localizes to both enhancers and transcriptional start sites – perhaps mediating communication between the elements