



Supplemental Figure 4: Associations between biological processes derived by functional mapping. As a validation of the system's ability to derive known biology by means of functional mapping, a focus on the process of cell fate commitment predicts it to be associated with a cluster of cell development and differentiation processes. Arrow width indicates the strength of predicted association, and border thickness indicates the internal cohesiveness of each process in the integrated genomic data. For example, when we focus on the process of cell fate commitment, we predict associations with many specific processes of cell differentiation and development; many of these relationships represent known biology and thus serve as a validation of the computational method. Several of these associations are driven by proteins known to be involved in multiple processes, e.g. the association with gastrulation involves many shared genes including *TGFB2*, *BMP4*, *TBX6*, and *TRIM15*. On the other hand, an apparently similar association with axis specification is driven mainly by genes not yet cataloged as involved in a cell fate decision (e.g. *TDGF1*, *T*, *MDFI*, etc.) These predicted associations are based on a combination of proteins known to participate in multiple processes and on data-driven predicted relationships; additional novel associations can be explored for other biological processes using the HEFaM interface.