

Supp Fig S5: CMINT chromatin modules identified in the hematopoiesis lineage. **A.** Heatmaps of 16 chromatin modules numbered from 0-15, obtained from CMINT applied to the hematopoietic system. Signal value for each mark was calculated for each modification in 2000bp windows. Each row in each heatmap represents 1 region each column represents one histone modification. Red: enriched, white: depleted. Height of each module is roughly proportional to the number of regions within it. **B.** ORegAnno cis-regulatory enrichment of selected factors based on enrichment in 12 out of the 15 cell types in specific modules on the left and for each cell type indicated on the top. The number next to each element is the module (in any cell type) that has the enrichment for the element. Color bar represents $-\log(\text{p-value})$ of enrichment of binding sites in a particular module. Additional enrichments for individual modules are shown in **Supp Fig S8**.

