Additional file 13: Figure S11: **Input data is available for less well studied loci.** (A) Browser view of the *Slc25a37* (mitoferrin) locus. (B-D) ChIP-seq and DNase-seq data for mouse erythroid (Ter119+) cells across the same region. Red lines show the pile-up of reads, and black points indicate the positions of binding sites identified by peak-calling. CTCF data is from Ref. (14); DNase and histone modification data is from Ref. (56). (E-G) ChIP-seq and DNase-seq data for mouse ES cells across the same region. Data from the ENCODE project (58).