

Supplementary Figure S2: Saturation analysis plots. We randomly selected ten different subsets of reads corresponding to different percentages of the total reads (10%, 20%, 30%,..., 100%) for each cell type from the merged TCF7L2 ChIP-seq datasets and called peaks on each subset using the BELT program. These analyses showed that for each cell type the peak numbers reach saturation when the peaks are identified from subsets of peaks above 80% of the total reads for that cell type.

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