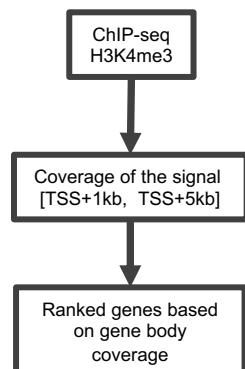
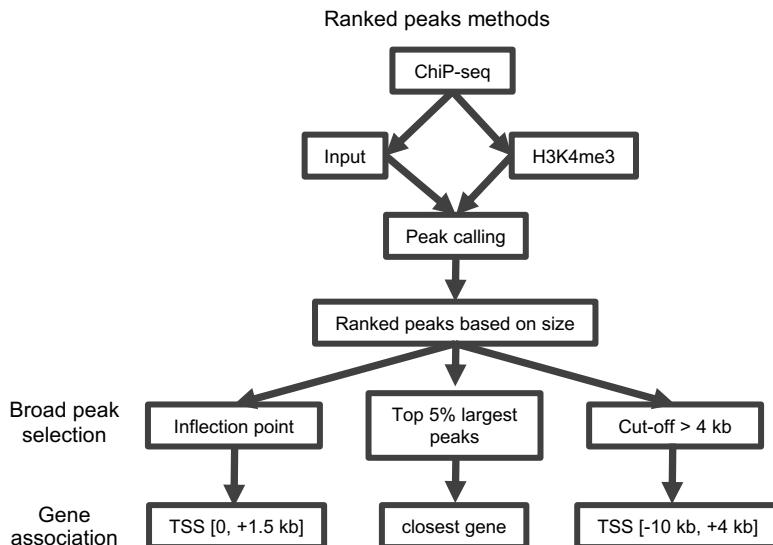


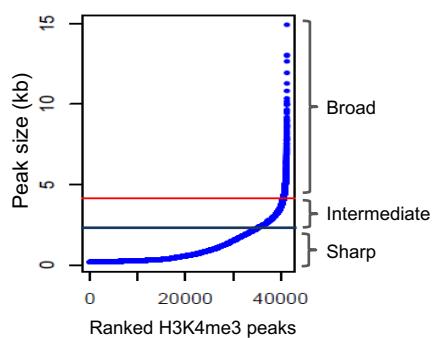
ACoverage method
(Pekowska et al. 2011)**B****C**

Ref.

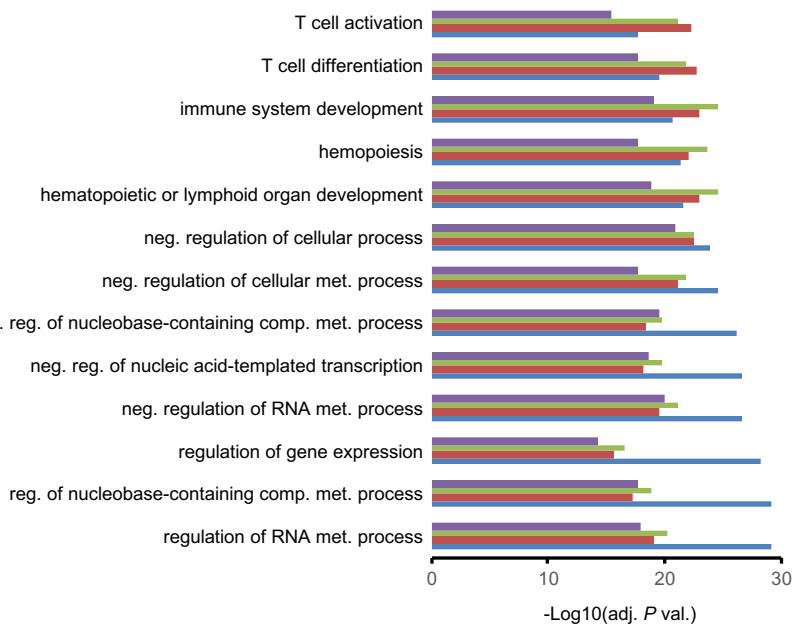
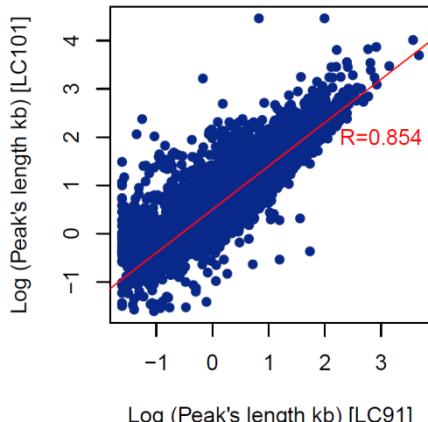
This study

Benayoun et al. 2014

Chen et al. 2015

**D**

■ Benayoun et al. 2014 ■ Chen et al. 2015 ■ Inf. point ■ coverage

**E**

Supplemental Figure S1: Comparison between the different approaches to identify broad H3K4me3 domain-associated genes. A) Strategy based on the coverage of H3K4me3 ChIP-seq signal. B) Strategies based on size-ranked H3K4me3 peaks using MACS2. C) Schematic representation of the identification of broad H3K4me3 domains, intermediate and sharp peaks based on the high (red line) and low (grey line) inflection points. D) Top 5 enriched GO-terms for Biological Process obtained with the different strategies using H3K4me3 ChIP-seq from LC thymocytes. E) Correlation between two experimental replicates of H3K4me3 ChIP-seq from LC thymocytes.