**S2 Table.** **Information about published datasets used in this study and downloaded from the NCBI Gene Expression Omnibus.**

| Sample | Reference | Source or GEO ID |
|---|---|---|
| CapStarr-seq in P5424 cells | [1] | GSE63732 |
| RNA-seq from P5424 cells | [2] | GSE120655 |
| ChIP-seq ETS1 from DP thymocytes | [3] | GSE29362 |
| ChIP-seq Runx1 from DP thymocytes | [4] | GSE45014 |
| ChIP-seq GATA3 from DP thymocytes | [5] | GSE20898 |
| ChIP-seq Ikaros from DP thymocytes | [6] | GSE61148 |
| ChIP-seq TCF1 from DP thymocytes | [1] | GSE63732 |
| ChIP-seq HEB from DP thymocytes | [1] | GSE63732 |
| ChIP-seq H3K27ac from DP thymocytes | [4] | GSE45014 |
| ChIP-seq H3K4me3 from DP thymocytes | [3] | GSE29362 |
| ChIP-seq Pol II from DP thymocytes | [3] | GSE29362 |
| DNase I from DP thymocytes | [1] | GSE63732 |
| ChIP-seq CTCF from DP thymocyte | [7] | GSE27214 |
| 4C-seq in DP thymocytes | [8] | GSE137417 |
| ChIP-seq from human thymocytes (Blueprint consortium) | [9] | http://dcc.blueprint-epigenome.eu<br>Direct track hub:<br>http://genome-euro.ucsc.edu/cgi-bin/hgTracks?hubUrl=https://raw.githubusercontent.com/guillaumecharbonnier/mw-cieslak2019/master/src/hub/hub.txt&genome=hg19 |
| Normalised RNA-seq data from mouse hematopoietic populations (ImmGen consortium) | [10] | www.immgen.org |
| Processed ATAC-seq data from mouse hematopoietic populations (ImmGen consortium) | [11] | GSE100738 |

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