

Description of Additional Supplementary Files

Supplementary Data 1

Expression programs detected by NMF in each of the 42 cell lines analyzed.

Supplementary Data 2

Expression programs derived from NMF.

Supplementary Data 3

TF clusters revealed by scATAC-seq.

Supplementary Data 4

TFs sorted with the motif enriched in the peaks of heterogeneous accessibility.

Supplementary Data 5

The distribution of ecDNA in all cell lines.