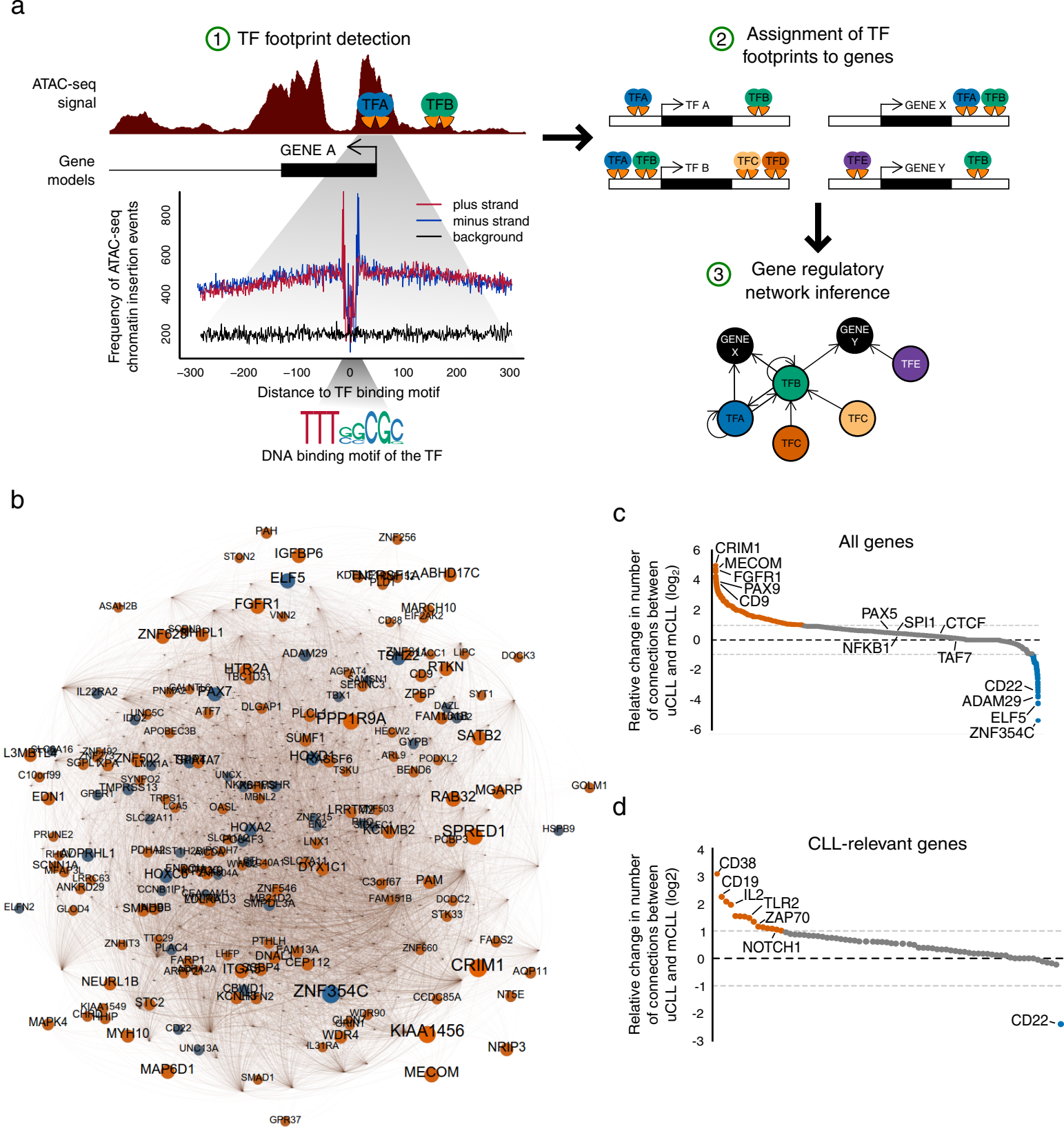
a
1 TF footprint detection
ATAC-seq signal
TFA
TFB
Gene models
GENE A
Frequency of ATAC-seq chromatin insertion events
plus strand
minus strand
background
Distance to TF binding motif
DNA binding motif of the TF
2 Assignment of TF footprints to genes
TF A
GENE X
TF B
GENE Y
TFC
TFD
TFE
3 Gene regulatory network inference
GENE X
GENE Y
TFE
TFB
TFA
TFC
b
c
All genes
Relative change in number of connections between uCLL and mCLL (log2)
CRIM1
MECOM
FGFR1
PAX9
CD9
PAX5
SPI1
CTCF
NFKB1
TAF7
CD22
ADAM29
ELF5
ZNF354C
d
CLL-relevant genes
CD38
CD19
IL2
TLR2
ZAP70
NOTCH1
CD22