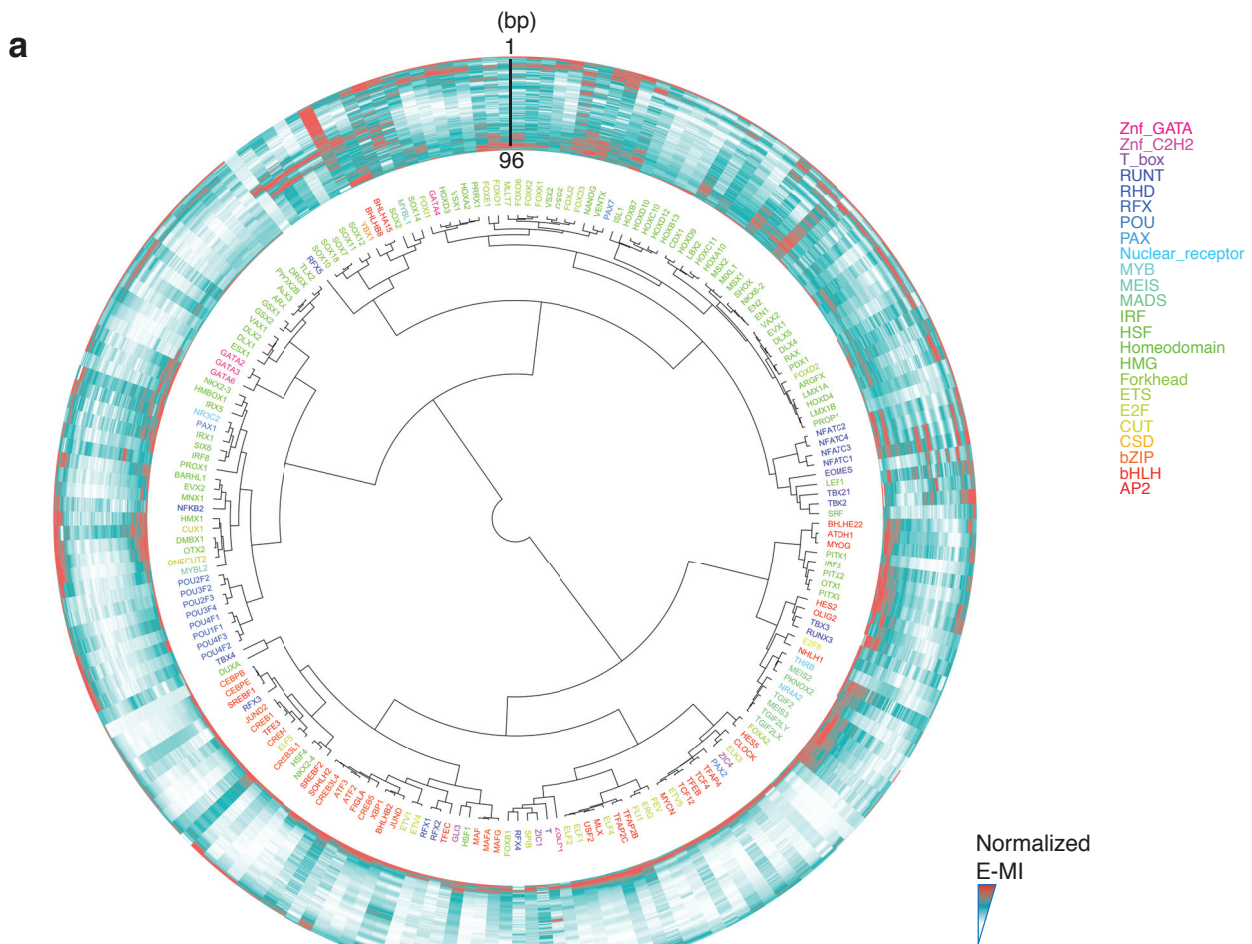
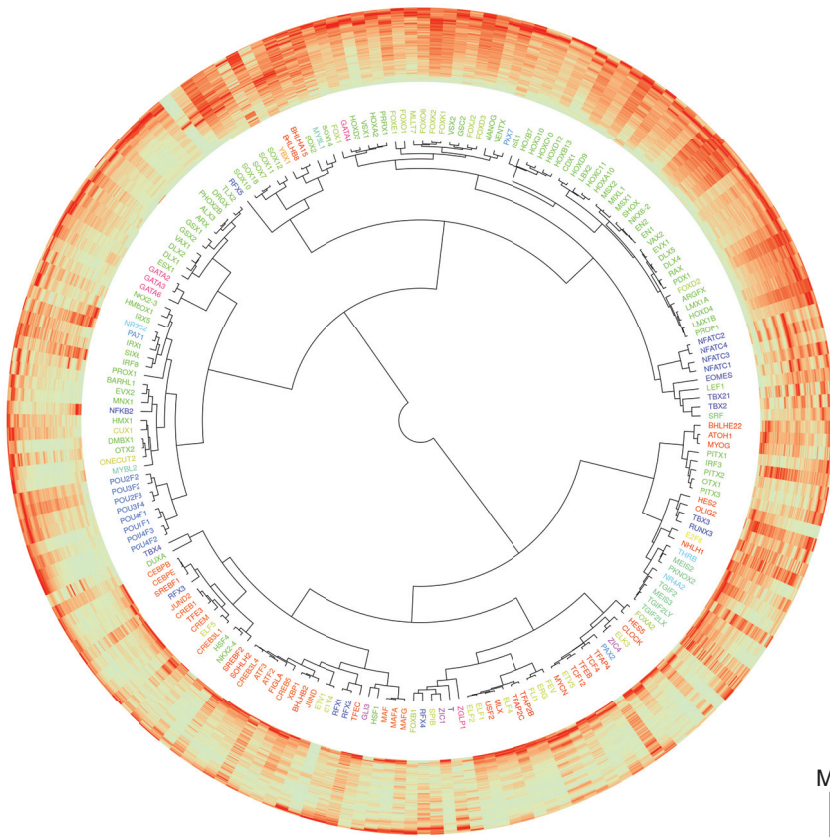


In the motif matching, 20-bp-long primary motifs generated with an automatic pipeline were used, see **Methods** for details. All discovered motifs are also illustrated in the following pages.

Supplementary Data 2 | Motif-based analysis for NCAP-SELEX. a, Due to the fixed adaptors of the SELEX ligand, TFs may also have positional preferences in the HT-SELEX library (**Extended Data Fig. 6a**). To more clearly visualize the positional preferences induced by nucleosome, the E-MI diagonals from NCAP-SELEX are normalized against those from the corresponding HT-SELEX. Specifically, the E-MI diagonal of each library is first divided by its total strength, then E-MI difference between the NCAP- and HT-SELEX libraries were calculated, and linearly normalized to (0,1) for each TF. TFs are arranged according to the E-MI clustering in **Fig. 3a** for comparison. The colouring scheme for TF families is indicated. **b**, Motif matching results for NCAP-SELEX with the 147-bp ligand (lig147). TFs are arranged according to the E-MI clustering in **Fig. 3a** to facilitate comparison. The motif matching result is oriented radially and scaled for each TF. **c**, Motif hits ratio (log scale) between the bound and the unbound cycle 5 libraries. The hits of each library were normalized by number of total reads of the library. TFs are arranged according to the clustering in **Fig. 5a** for comparison. **d**, Motif matching results of NCAP-SELEX with the 200-bp ligand (lig200). TFs are arranged according to the E-MI clustering in **Extended Data Fig. 2a** for comparison.



b

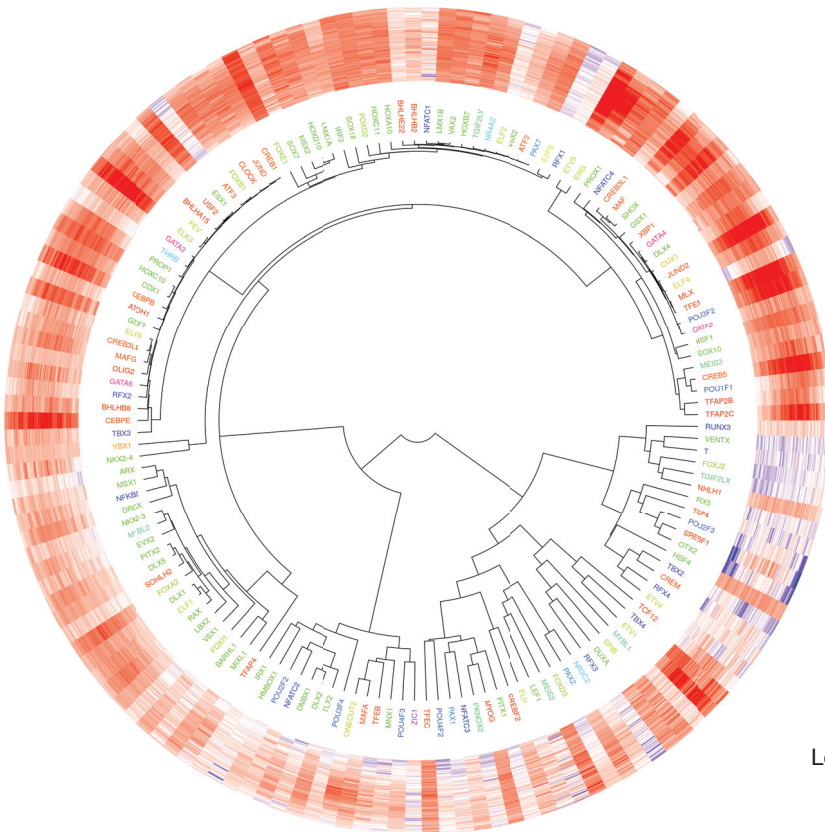


Motif hits



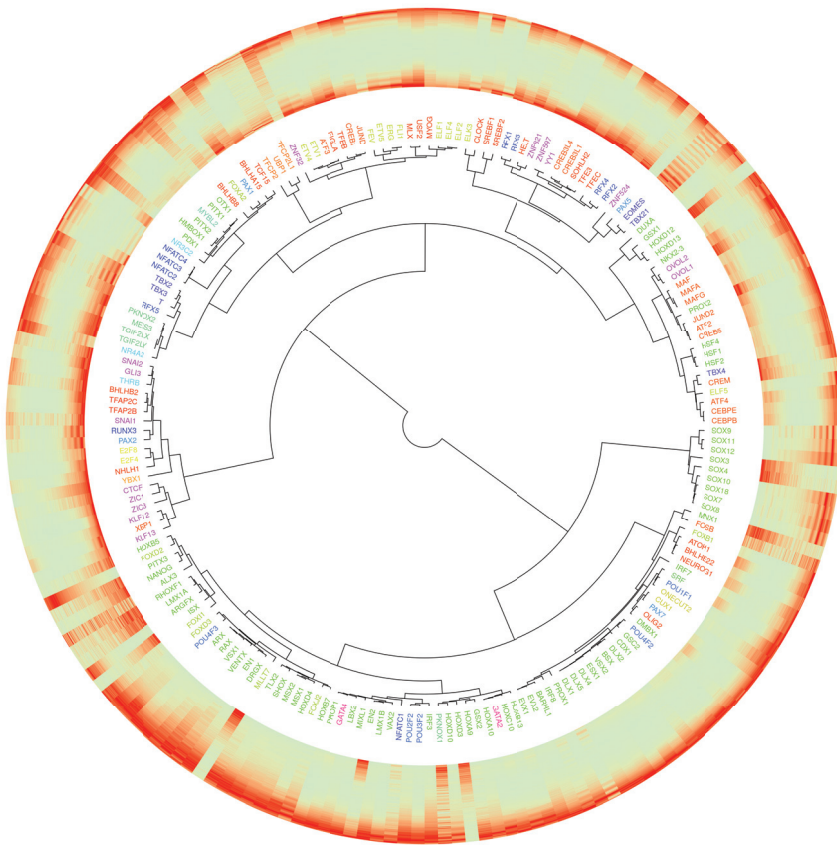
- Znf_GATA
- Znf_C2H2
- T_box
- RUNT
- RHD
- RFX
- POU
- PAX
- Nuclear_receptor
- MYB
- MEIS
- MADS
- IRF
- HSF
- Homeodomain
- HMG
- Forkhead
- ETS
- E2F
- CUT
- CSD
- bZIP
- bHLH
- AP2

c



1.67
0
-0.62
 $\text{Log}_2(\text{Hits}_{\text{unbound}}/\text{Hits}_{\text{bound}})$

d



- Znf_GATA
- Znf_C2H2
- T_box
- RUNT
- RHD
- RFX
- POU
- PAX
- Nuclear_receptor
- MYB
- MEIS
- MADS
- IRF
- HSF
- Homeodomain
- HMG
- Forkhead
- ETS
- E2F
- CUT
- CSD
- bZIP
- bHLH
- AP2

Motif hits



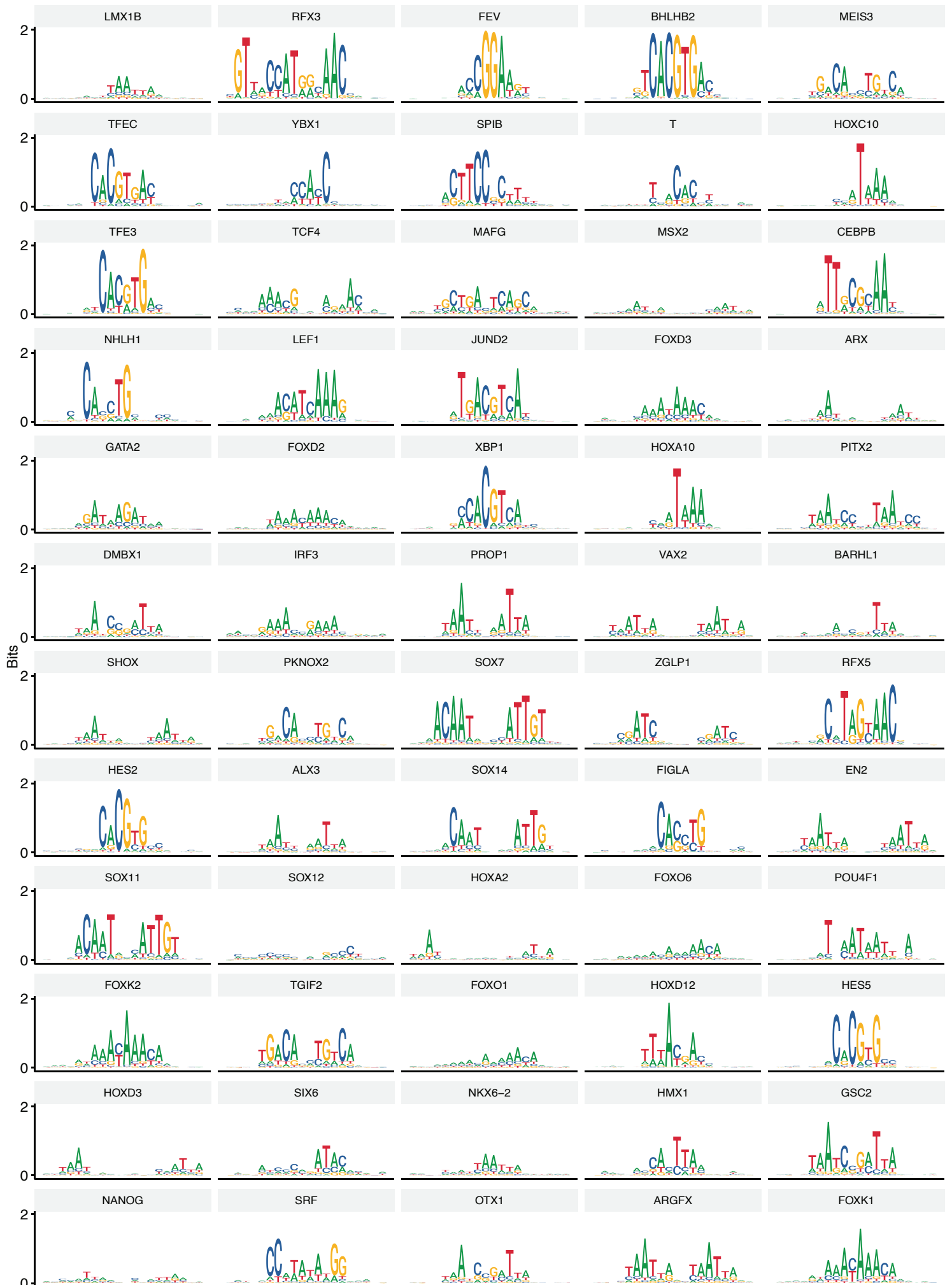
Automatic primary motif discovery (NCAP-SELEX, lig147)



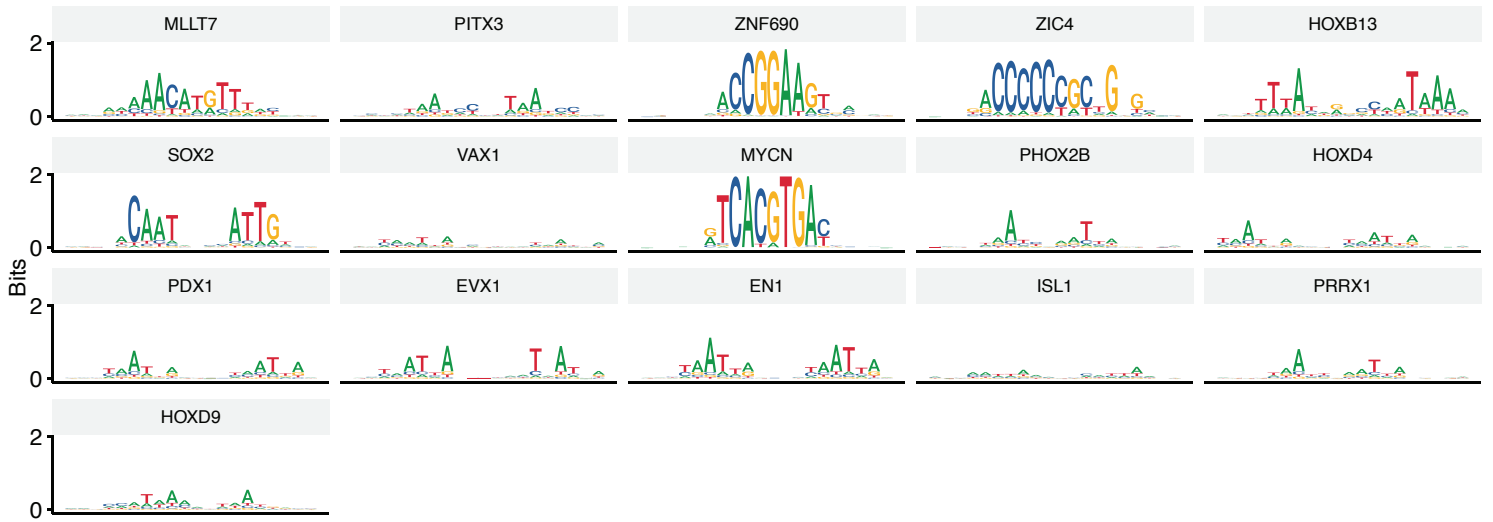
Automatic primary motif discovery (NCAP-SELEX, lig147)



Automatic primary motif discovery (NCAP-SELEX, lig147)



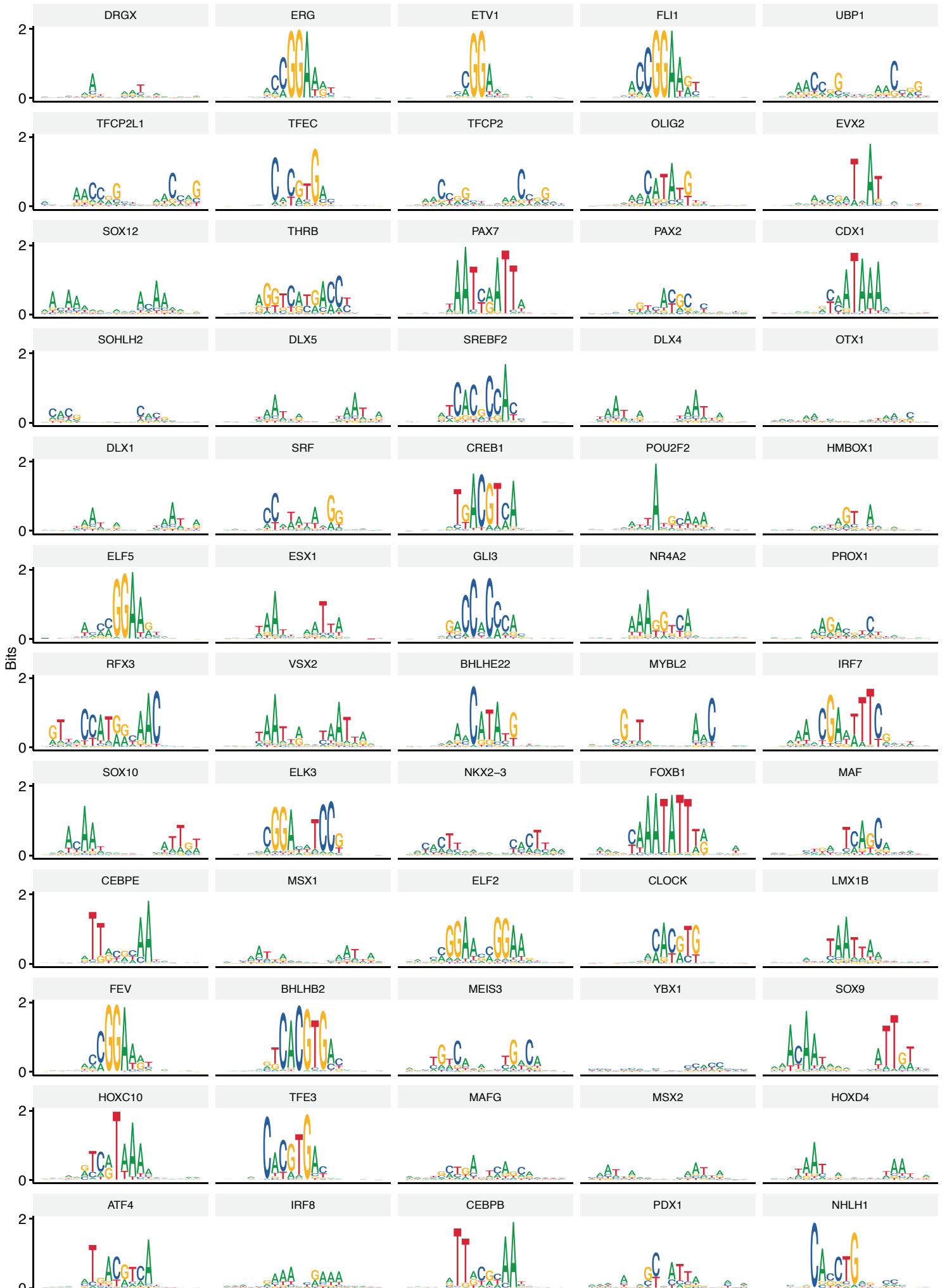
Automatic primary motif discovery (NCAP-SELEX, lig147)



Automatic primary motif discovery (NCAP-SELEX, lig200)



Automatic primary motif discovery (NCAP-SELEX, lig200)



Automatic primary motif discovery (NCAP-SELEX, lig200)



Automatic primary motif discovery (NCAP-SELEX, lig200)

