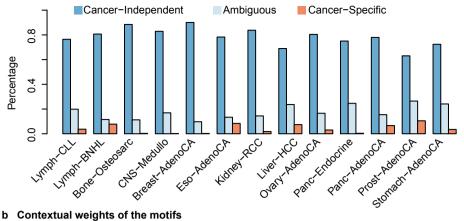
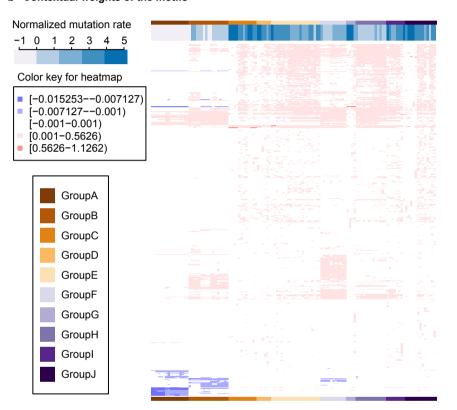
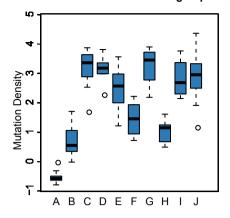
a Percentages of regions in each category



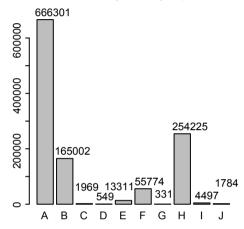
b Contextual weights of the motifs



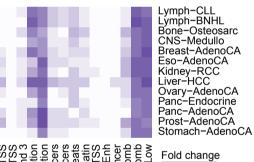
c Normalized mutation rates in groups



d The numbers of regions in groups



e Fold changes in group A



Active TSS
Flanking Active TSS
Transcr: at gene 5 and 3
Strong transcription
Weak transcription
Genic enhancers
Enhancers
ZNF genes & repeats
Heterochromatin
Bivalent/Poised TSS
Flanking Bivalent TSS/Enh
Bivalent Enhancer
Repressed PolyComb
Weak Repressed PolyComb
Quiescent/Low

