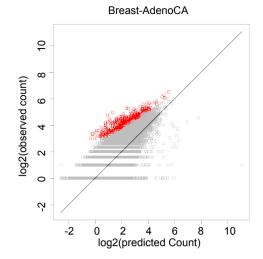
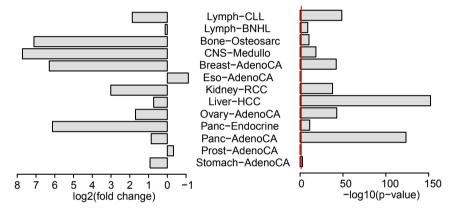
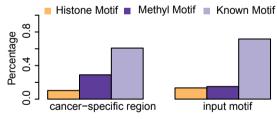
#### a The cancer-specific regions



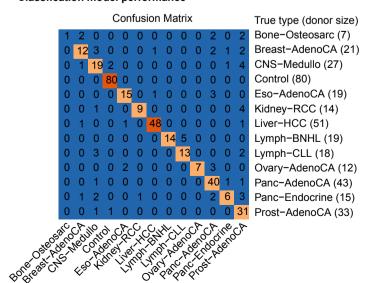
## c The motif disruption rates in the 13 tumors



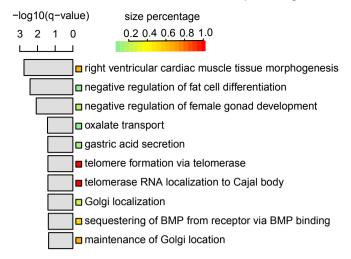
# e The percentages of motif types in cancer-specific regions



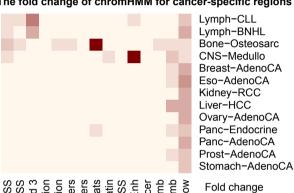
### f Classfication model performance



#### b The enriched GO terms for Breast-AdenoCA specific regions



## d The fold change of chromHMM for cancer-specific regions



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

