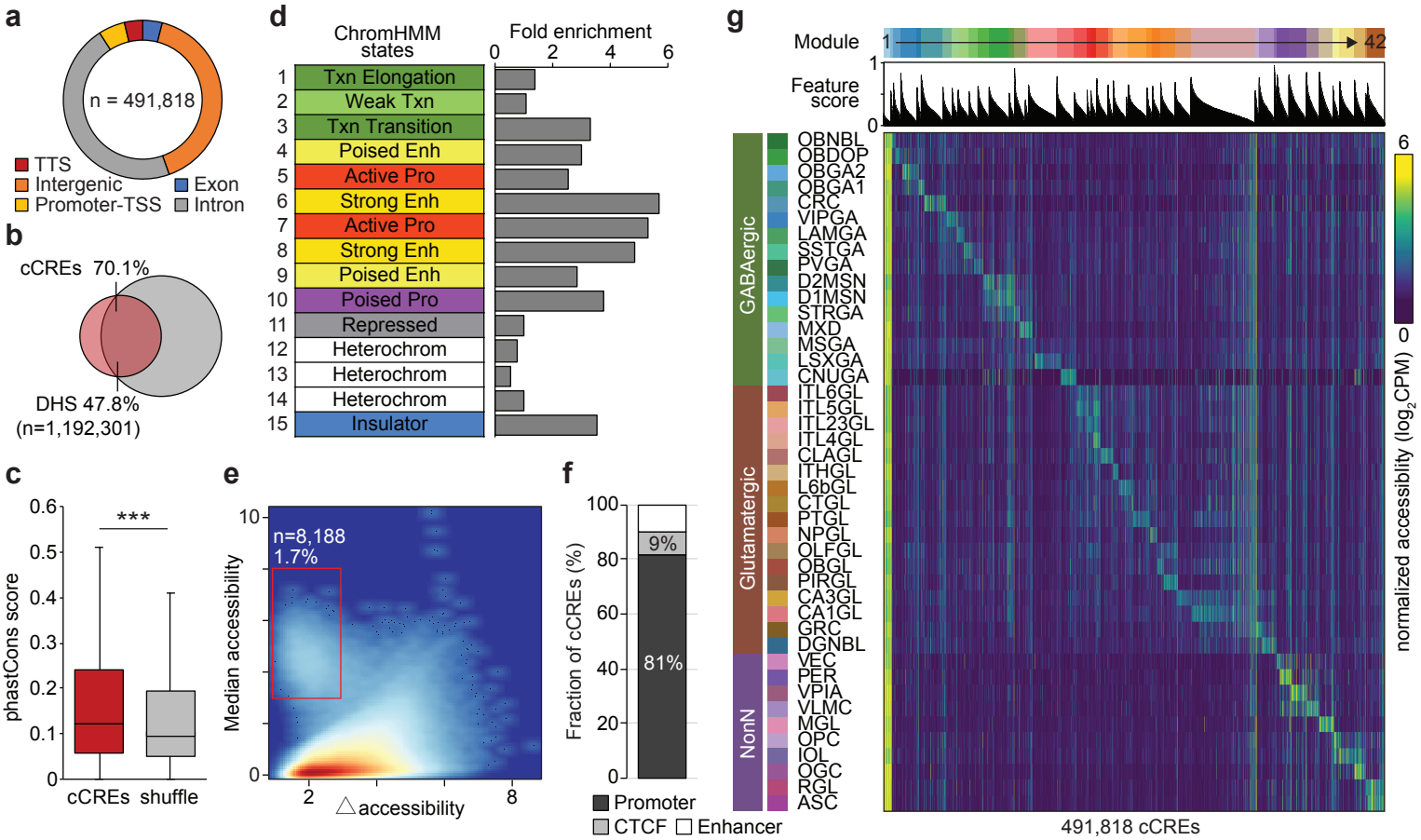
Figure 2


a
n = 491,818
TTS
Intergenic
Promoter-TSS
Exon
Intron
b
cCREs 70.1%
DHS 47.8%
(n=1,192,301)
c
***
phastCons score
cCREs
shuffle
d
ChromHMM states
Fold enrichment
1 Txn Elongation
2 Weak Txn
3 Txn Transition
4 Poised Enh
5 Active Pro
6 Strong Enh
7 Active Pro
8 Strong Enh
9 Poised Enh
10 Poised Pro
11 Repressed
12 Heterochrom
13 Heterochrom
14 Heterochrom
15 Insulator
e
n=8,188
1.7%
Median accessibility
△accessibility
f
Fraction of cCREs (%)
9%
81%
Promoter
CTCF
Enhancer
g
Module
Feature score
GABAergic
Glutamatergic
NonN
OBNBL
OBDOP
OBGA2
OBGA1
CRC
VIPGA
LAMGA
SSTGA
PVGA
D2MSN
D1MSN
STRGA
MXD
MSGA
LSXGA
CNUGA
ITL6GL
ITL5GL
ITL23GL
ITL4GL
CLAGL
ITHGL
L6bGL
CTGL
PTGL
NPGL
OLFGL
OBGL
PIRGL
CA3GL
CA1GL
GRC
DGNBL
VEC
PER
VPIA
VLMC
MGL
OPC
IOL
OGC
RGL
ASC
491,818 cCREs
normalized accessibility (log2CPM)