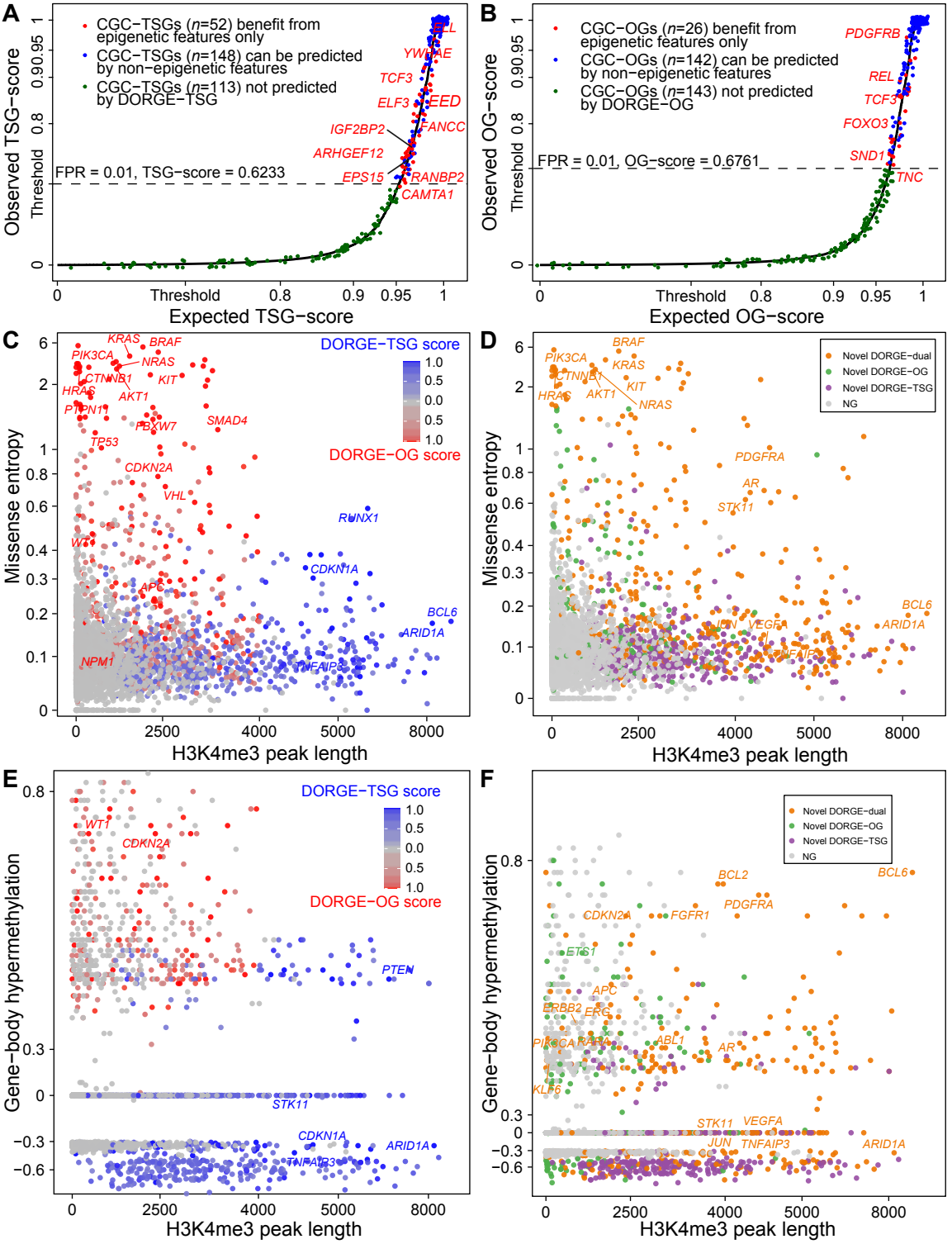
A
CGC−TSGs (n=52) benefit from epigenetic features only
CGC−TSGs (n=148) can be predicted by non−epigenetic features
CGC−TSGs (n=113) not predicted by DORGE−TSG
FPR = 0.01, TSG−score = 0.6233
Threshold
Observed TSG−score
Expected TSG−score
REL
YWHAE
TCF3
ELF3
EED
IGF2BP2
FANCC
ARHGEF12
EPS15
RANBP2
CAMTA1
B
CGC−OGs (n=26) benefit from epigenetic features only
CGC−OGs (n=142) can be predicted by non−epigenetic features
CGC−OGs (n=143) not predicted by DORGE−OG
FPR = 0.01, OG−score = 0.6761
Observed OG−score
Expected OG−score
PDGFRB
REL
TCF3
FOXO3
SND1
TNC
C
DORGE−TSG score
DORGE−OG score
Missense entropy
H3K4me3 peak length
KRAS
BRAF
PIK3CA
NRAS
CTNNB1
KIT
HRAS
AKT1
PTPN11
PBX/W7
SMAD4
TP53
CDKN2A
VHL
RUNX1
WT1
CDKN1A
APC
BCL6
ARID1A
NPM1
TNFAIP3
D
Novel DORGE−dual
Novel DORGE−OG
Novel DORGE−TSG
NG
PDGFRA
AR
STK11
VEGFA
E
Gene−body hypermethylation
PTEN
STK11
F
BCL2
FGFR1
ETS1
ERBB2
ERG
ABL1
KLF6
JUN