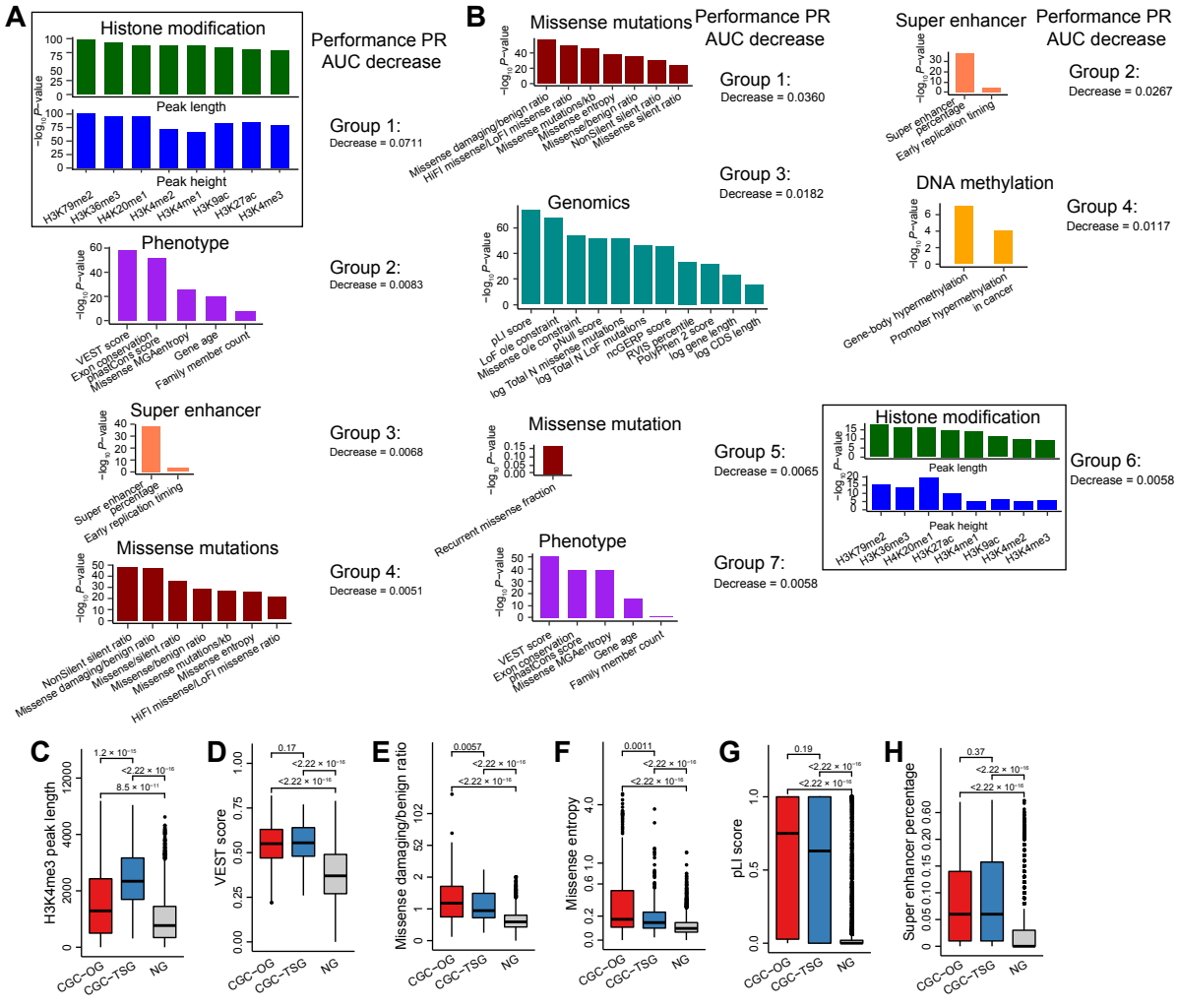
A
Histone modification
Peak length
Peak height
H3K79me2
H3K36me3
H4K20me1
H3K4me2
H3K4me1
H3K9ac
H3K27ac
H3K4me3
Phenotype
VEST score
Exon conservation
phastCons score
Missense MGAentropy
Gene age
Family member count
Super enhancer
Super enhancer percentage
Early replication timing
Missense mutations
NonSilent silent ratio
Missense damaging/benign ratio
Missense/silent ratio
Missense/benign ratio
Missense mutations/kb
Missense entropy
HiFI missense/LoFI missense ratio
Performance PR AUC decrease
Group 1:
Decrease = 0.0711
Group 2:
Decrease = 0.0083
Group 3:
Decrease = 0.0068
Group 4:
Decrease = 0.0051
B
Missense mutations
Missense damaging/benign ratio
HiFI missense/LoFI missense ratio
Missense mutations/kb
Missense entropy
Missense/benign ratio
NonSilent silent ratio
Missense silent ratio
Group 1:
Decrease = 0.0360
Super enhancer
Super enhancer percentage
Early replication timing
Group 2:
Decrease = 0.0267
Group 3:
Decrease = 0.0182
Genomics
pLI score
LoF o/e constraint
Missense o/e constraint
pNull score
log Total N missense mutations
log Total N LoF mutations
ncGERP score
RVIS percentile
PolyPhen 2 score
log gene length
log CDS length
DNA methylation
Gene-body hypermethylation
Promoter hypermethylation
in cancer
Group 4:
Decrease = 0.0117
Missense mutation
Recurrent missense fraction
Group 5:
Decrease = 0.0065
Histone modification
Group 6:
Decrease = 0.0058
Phenotype
Group 7:
Decrease = 0.0058
C
H3K4me3 peak length
1.2 × 10^-15
<2.22 × 10^-16
8.5 × 10^-11
D
VEST score
0.17
<2.22 × 10^-16
<2.22 × 10^-16
E
Missense damaging/benign ratio
0.0057
<2.22 × 10^-16
<2.22 × 10^-16
F
Missense entropy
0.0011
<2.22 × 10^-16
<2.22 × 10^-16
G
pLI score
0.19
<2.22 × 10^-16
<2.22 × 10^-16
H
Super enhancer percentage
0.37
<2.22 × 10^-16
<2.22 × 10^-16
CGC−OG
CGC−TSG
NG