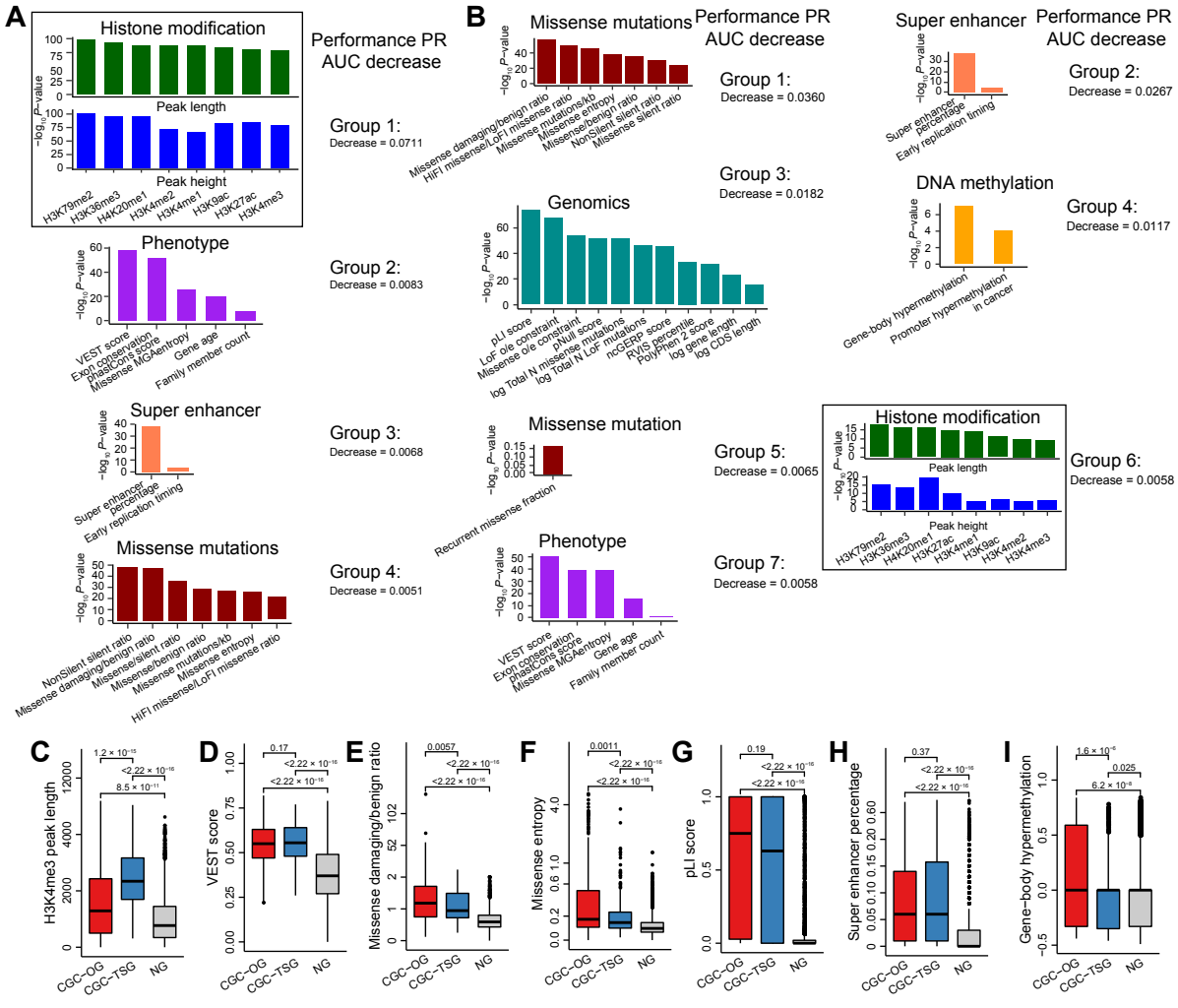
A
Histone modification
Peak length
Peak height
H3K79me2
H3K36me3
H4K20me1
H3K4me2
H3K4me1
H3K9ac
H3K27ac
H3K4me3
Performance PR AUC decrease
Group 1:
Decrease = 0.0711
Phenotype
VEST score
Exon conservation
phastCons score
Missense MGAentropy
Gene age
Family member count
Group 2:
Decrease = 0.0083
Super enhancer
Super enhancer percentage
Early replication timing
Group 3:
Decrease = 0.0068
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
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
Genomics
pLI score
LoF o/e constraint
Missense o/e constraint
pNull score
Missense mutations
log Total N missense mutations
log Total N LoF mutations
ncGERP score
RVIS percentile
PolyPhen 2 score
log gene length
log CDS length
Group 3:
Decrease = 0.0182
Missense mutation
Recurrent missense fraction
Phenotype
VEST score
Exon conservation
phastCons score
Missense MGAentropy
Gene age
Family member count
Group 7:
Decrease = 0.0058
Super enhancer
Super enhancer percentage
Early replication timing
Group 2:
Decrease = 0.0267
DNA methylation
Gene-body hypermethylation
Promoter hypermethylation
in cancer
Group 4:
Decrease = 0.0117
Histone modification
Peak length
Peak height
H3K79me2
H3K36me3
H4K20me1
H3K27ac
H3K4me1
H3K9ac
H3K4me2
H3K4me3
Group 5:
Decrease = 0.0065
Group 6:
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
I
Gene−body hypermethylation
1.6 × 10^-5
0.025
6.2 × 10^-6
CGC−OG
CGC−TSG
NG