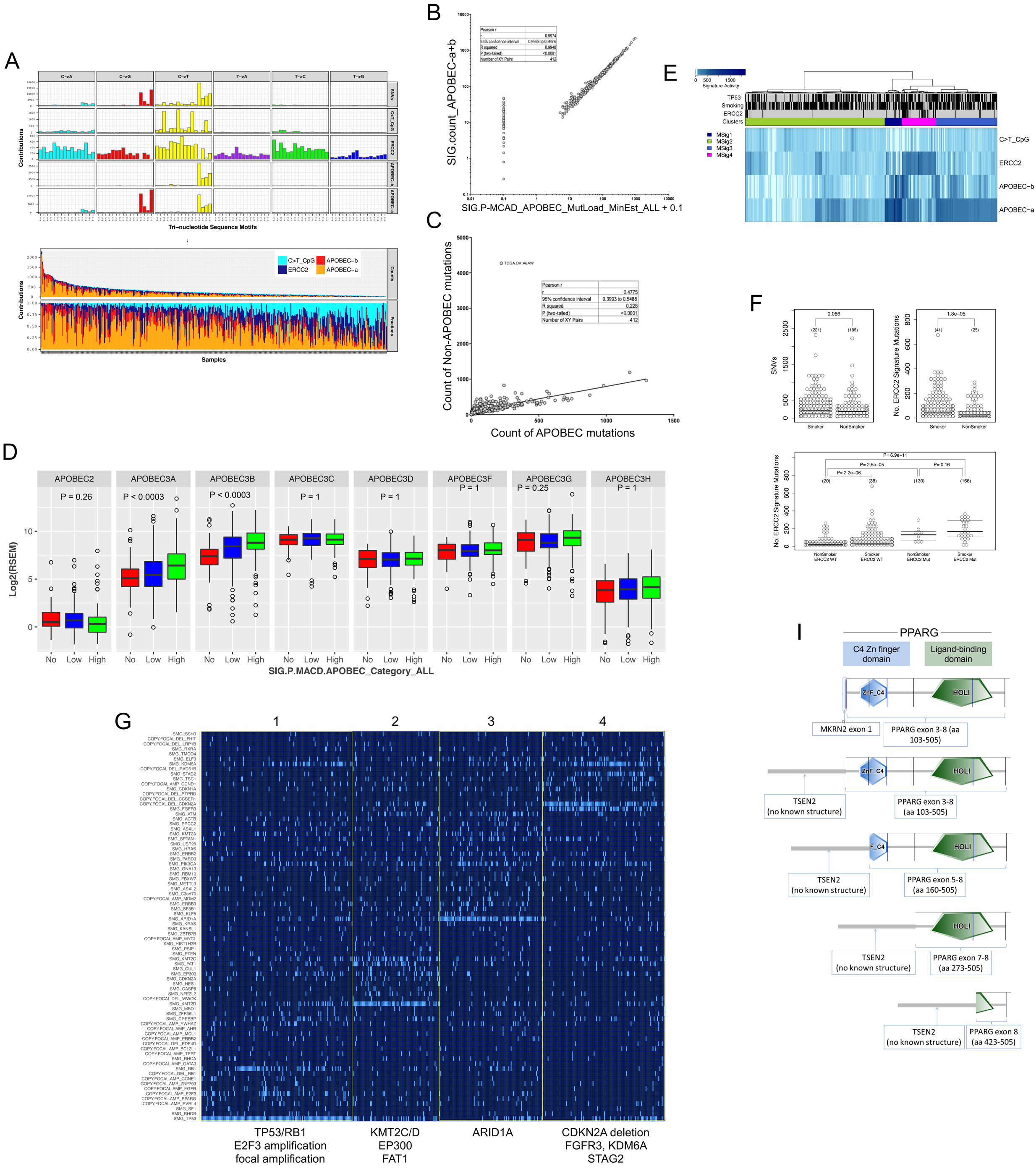
A
C->A
C->G
C->T
T->A
T->C
T->G
SNVs
C>T_CpG
ERCC2
APOBEC-b
APOBEC-a
Contributions
Tri-nucleotide Sequence Motifs
C>T_CpG
ERCC2
APOBEC-b
APOBEC-a
Counts
Fractions
Samples
B
SIG.count_APOBEC-a+b
SIG.P-MCAD_APOBEC_MutLoad_MinEst_ALL + 0.1
Pearson r
r 0.9974
95% confidence interval 0.9968 to 0.9978
R squared 0.9948
P (two-tailed) <0.0001
Number of XY Pairs 412
C
Count of Non-APOBEC mutations
Count of APOBEC mutations
TCGA.DK.A6AW
Pearson r
r 0.4775
95% confidence interval 0.3993 to 0.5488
R squared 0.228
P (two-tailed) <0.0001
Number of XY Pairs 412
D
APOBEC2
APOBEC3A
APOBEC3B
APOBEC3C
APOBEC3D
APOBEC3F
APOBEC3G
APOBEC3H
P = 0.26
P < 0.0003
P < 0.0003
P = 1
P = 1
P = 1
P = 0.25
P = 1
Log2(RSEM)
No
Low
High
SIG.P.MACD.APOBEC_Category_ALL
E
Signature Activity
TP53
Smoking
ERCC2
Clusters
MSig1
MSig2
MSig3
MSig4
C>T_CpG
ERCC2
APOBEC-b
APOBEC-a
F
SNVs
Smoker
NonSmoker
0.066
(221)
(185)
No. ERCC2 Signature Mutations
1.8e-05
(41)
(25)
P= 6.9e-11
P= 2.5e-05
P= 0.16
P= 2.2e-06
(20)
(38)
(130)
(166)
NonSmoker ERCC2 WT
Smoker ERCC2 WT
NonSmoker ERCC2 Mut
Smoker ERCC2 Mut
G
1
2
3
4
TP53/RB1
E2F3 amplification
focal amplification
KMT2C/D
EP300
FAT1
ARID1A
CDKN2A deletion
FGFR3, KDM6A
STAG2
H
Cluster
Normalized strength of association of genetic alterations to MutCN clusters
1.00
0.00
I
PPARG
C4 Zn finger domain
Ligand-binding domain
ZnF_C4
HOLI
MKRN2 exon 1
PPARG exon 3-8 (aa 103-505)
TSEN2 (no known structure)
PPARG exon 3-8 (aa 103-505)
F_C4
PPARG exon 5-8 (aa 160-505)
PPARG exon 7-8 (aa 273-505)
PPARG exon 8 (aa 423-505)