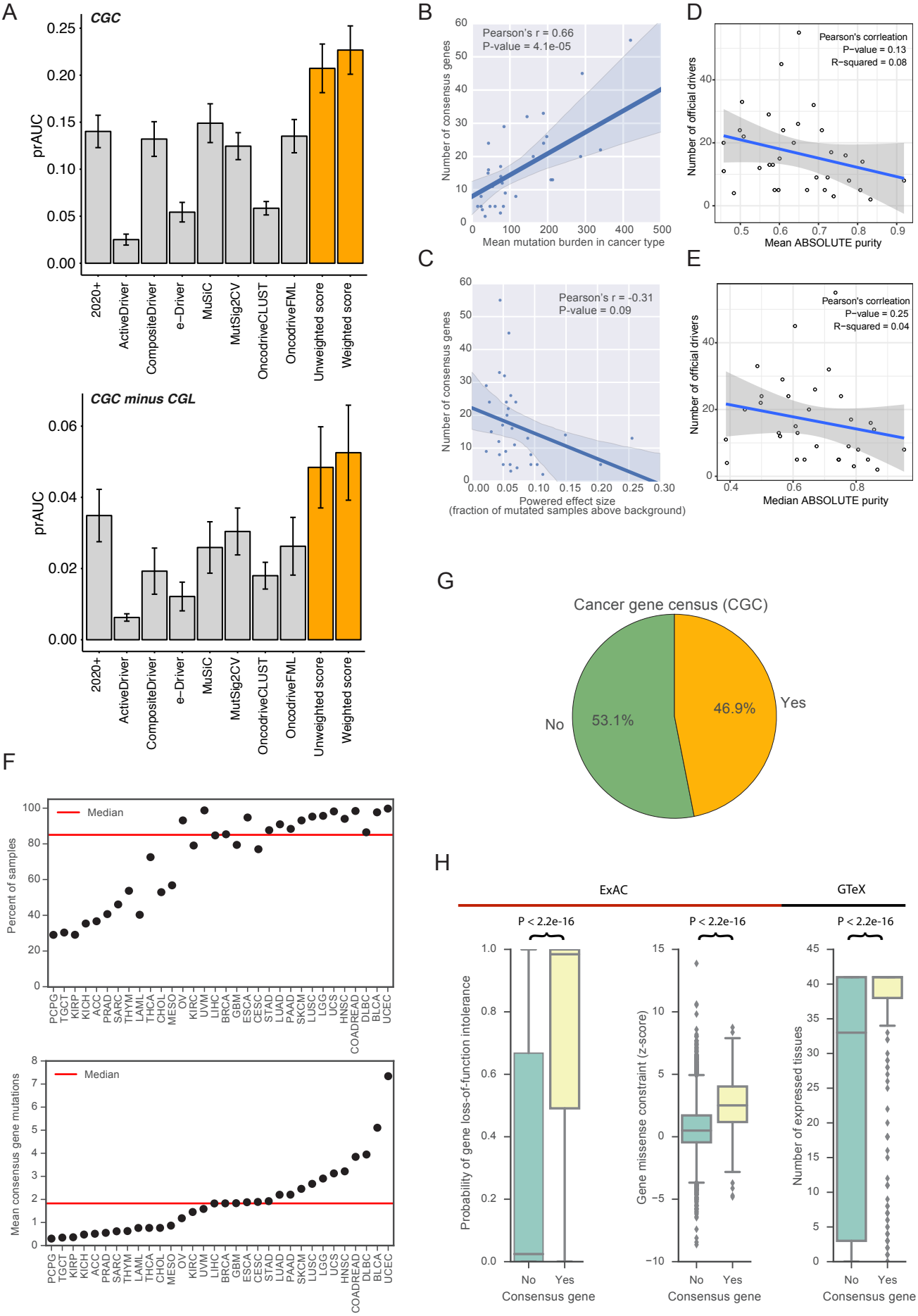
Figure S3


A
CGC
prAUC
2020+
ActiveDriver
CompositeDriver
e−Driver
MuSiC
MutSig2CV
OncodriveCLUST
OncodriveFML
Unweighted score
Weighted score
CGC minus CGL
B
Pearson's r = 0.66
P-value = 4.1e-05
Number of consensus genes
Mean mutation burden in cancer type
C
Pearson's r = -0.31
P-value = 0.09
Powered effect size
(fraction of mutated samples above background)
D
Pearson's correlation
P−value = 0.13
R−squared = 0.08
Number of official drivers
Mean ABSOLUTE purity
E
Pearson's correlation
P−value = 0.25
R−squared = 0.04
Median ABSOLUTE purity
G
Cancer gene census (CGC)
No
53.1%
46.9%
Yes
F
Median
Percent of samples
Mean consensus gene mutations
PCPG TGCT KIRP KICH ACC PRAD SARC THYM LAML THCA CHOL MESO OV KIRC UVM LIHC BRCA GBM ESCA CESC STAD LUAD PAAD SKCM LUSC LGG UCS HNSC COADREAD DLBC BLCA UCEC
H
ExAC
GTeX
P < 2.2e-16
Probability of gene loss-of-function intolerance
Gene missense constraint (z-score)
Number of expressed tissues
No
Yes
Consensus gene