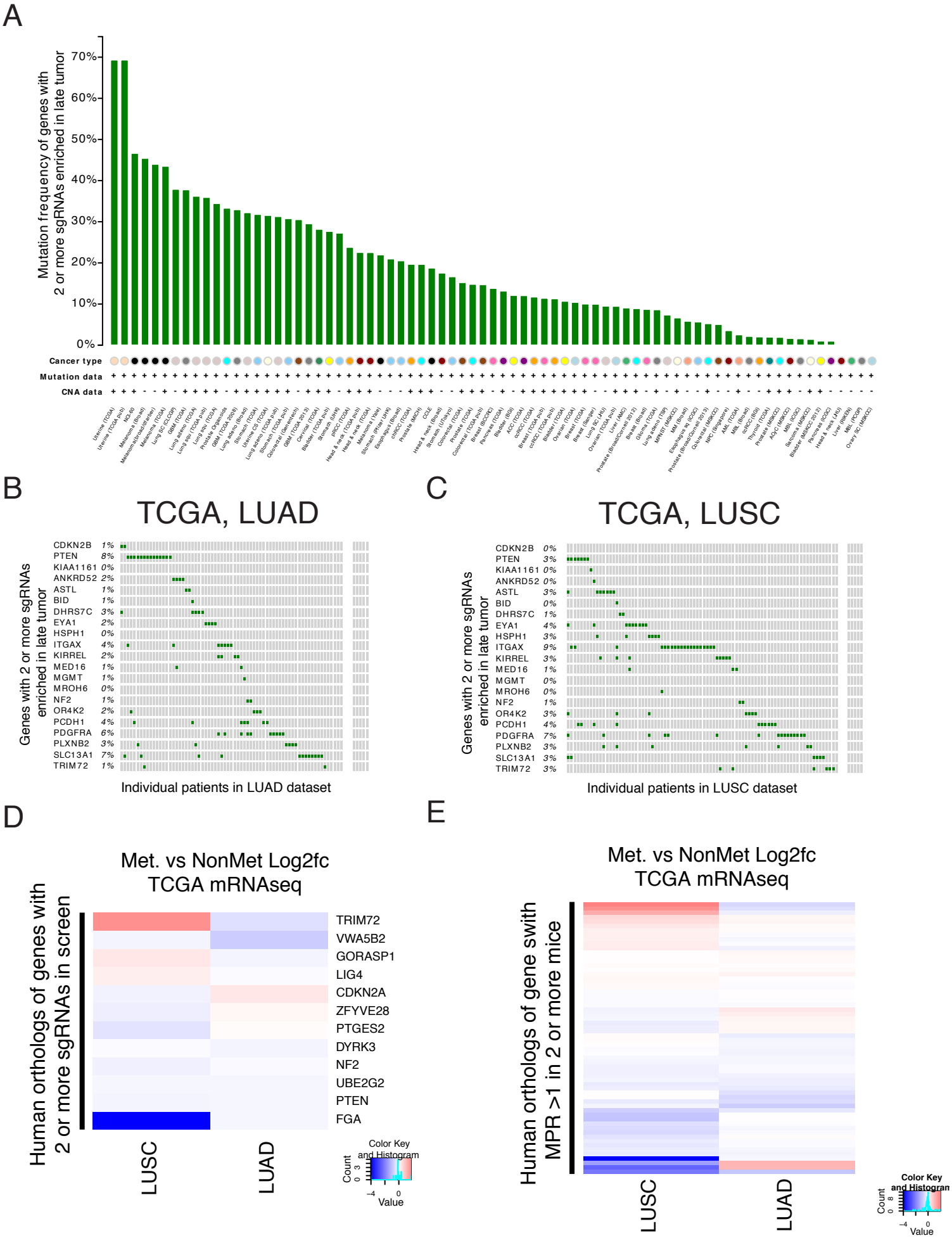
A
Mutation frequency of genes with 2 or more sgRNAs enriched in late tumor
70%
60%
50%
40%
30%
20%
10%
0%
Cancer type
Mutation data
CNA data
B
TCGA, LUAD
Genes with 2 or more sgRNAs enriched in late tumor
CDKN2B 1%
PTEN 8%
KIAA1161 0%
ANKRD52 2%
ASTL 1%
BID 1%
DHRS7C 3%
EYA1 2%
HSPH1 0%
ITGAX 4%
KIRREL 2%
MED16 1%
MGMT 1%
MROH6 0%
NF2 1%
OR4K2 2%
PCDH1 4%
PDGFRA 6%
PLXNB2 3%
SLC13A1 7%
TRIM72 1%
Individual patients in LUAD dataset
C
TCGA, LUSC
Genes with 2 or more sgRNAs enriched in late tumor
CDKN2B 0%
PTEN 3%
KIAA1161 0%
ANKRD52 0%
ASTL 3%
BID 0%
DHRS7C 1%
EYA1 4%
HSPH1 3%
ITGAX 9%
KIRREL 3%
MED16 1%
MGMT 0%
MROH6 0%
NF2 1%
OR4K2 3%
PCDH1 4%
PDGFRA 7%
PLXNB2 3%
SLC13A1 3%
TRIM72 3%
Individual patients in LUSC dataset
D
Met. vs NonMet Log2fc
TCGA mRNAseq
Human orthologs of genes with 2 or more sgRNAs in screen
TRIM72
VWA5B2
GORASP1
LIG4
CDKN2A
ZFYVE28
PTGES2
DYRK3
NF2
UBE2G2
PTEN
FGA
LUSC
LUAD
Color Key and Histogram
Count
Value
E
Met. vs NonMet Log2fc
TCGA mRNAseq
Human orthologs of gene swith MPR >1 in 2 or more mice
LUSC
LUAD
Color Key and Histogram
Count
Value

Figure S5