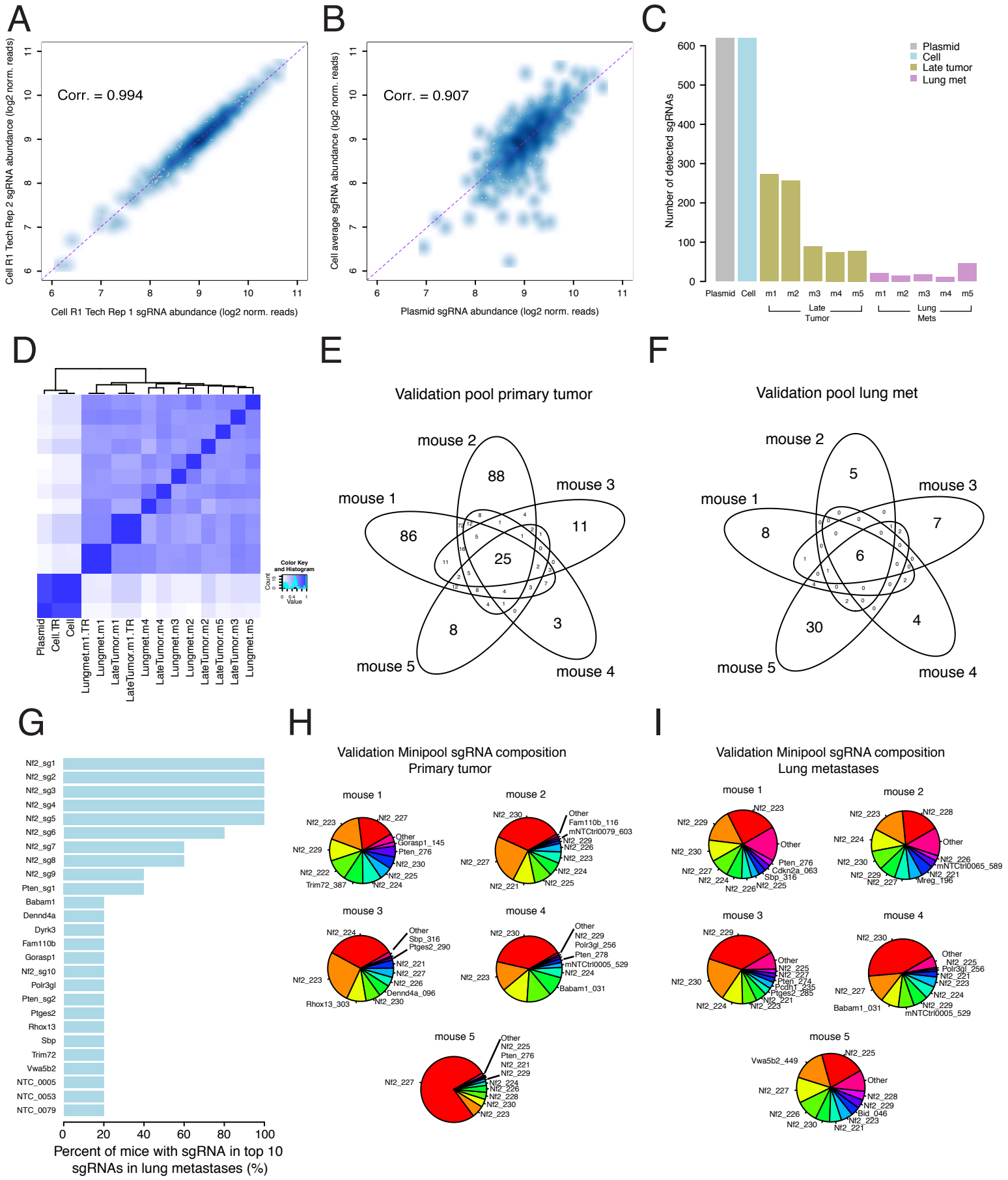
A
Corr. = 0.994
Cell R1 Tech Rep 2 sgRNA abundance (log2 norm. reads)
Cell R1 Tech Rep 1 sgRNA abundance (log2 norm. reads)
B
Corr. = 0.907
Cell average sgRNA abundance (log2 norm. reads)
Plasmid sgRNA abundance (log2 norm. reads)
C
Plasmid
Cell
Late tumor
Lung met
Number of detected sgRNAs
Plasmid Cell m1 m2 m3 m4 m5 m1 m2 m3 m4 m5
Late Tumor
Lung Mets
D
Color Key and Histogram
Count
Value
Plasmid
Cell.TR
Cell
Lungmet.m1.TR
Lungmet.m1
LateTumor.m1
LateTumor.m1.TR
Lungmet.m4
LateTumor.m4
Lungmet.m3
Lungmet.m2
LateTumor.m2
LateTumor.m5
LateTumor.m3
Lungmet.m5
E
Validation pool primary tumor
mouse 1
mouse 2
mouse 3
mouse 4
mouse 5
F
Validation pool lung met
mouse 1
mouse 2
mouse 3
mouse 4
mouse 5
G
Nf2_sg1
Nf2_sg2
Nf2_sg3
Nf2_sg4
Nf2_sg5
Nf2_sg6
Nf2_sg7
Nf2_sg8
Nf2_sg9
Pten_sg1
Babam1
Dennd4a
Dyrk3
Fam110b
Gorasp1
Nf2_sg10
Polr3gl
Pten_sg2
Ptges2
Rhox13
Sbp
Trim72
Vwa5b2
NTC_0005
NTC_0053
NTC_0079
Percent of mice with sgRNA in top 10 sgRNAs in lung metastases (%)
H
Validation Minipool sgRNA composition
Primary tumor
mouse 1
mouse 2
mouse 3
mouse 4
mouse 5
I
Validation Minipool sgRNA composition
Lung metastases
mouse 1
mouse 2
mouse 3
mouse 4
mouse 5

# Figure S7