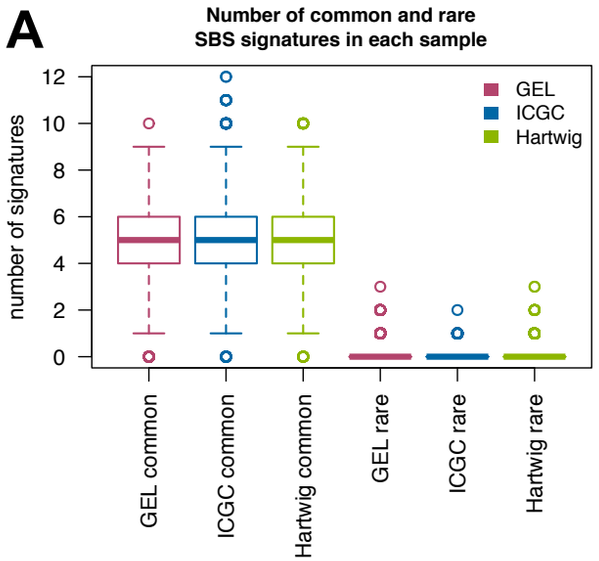
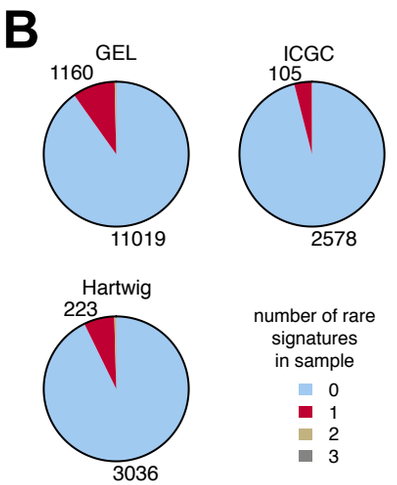
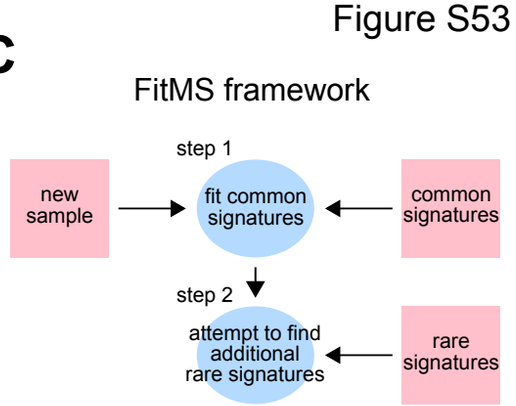
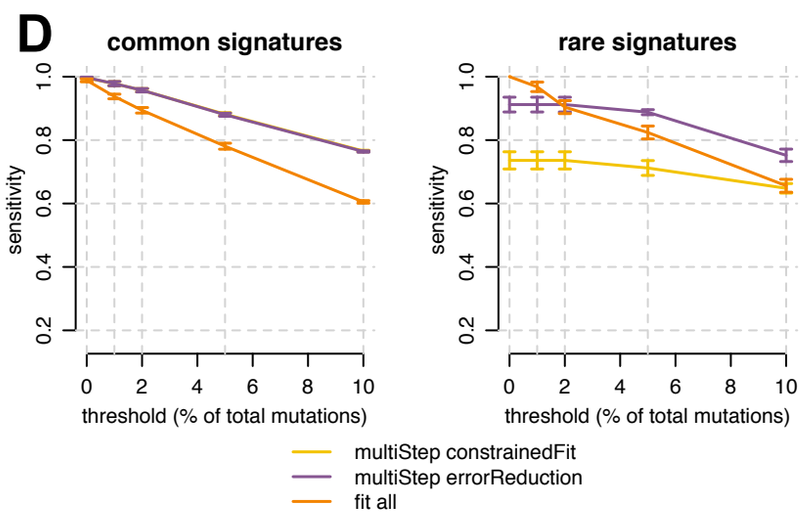
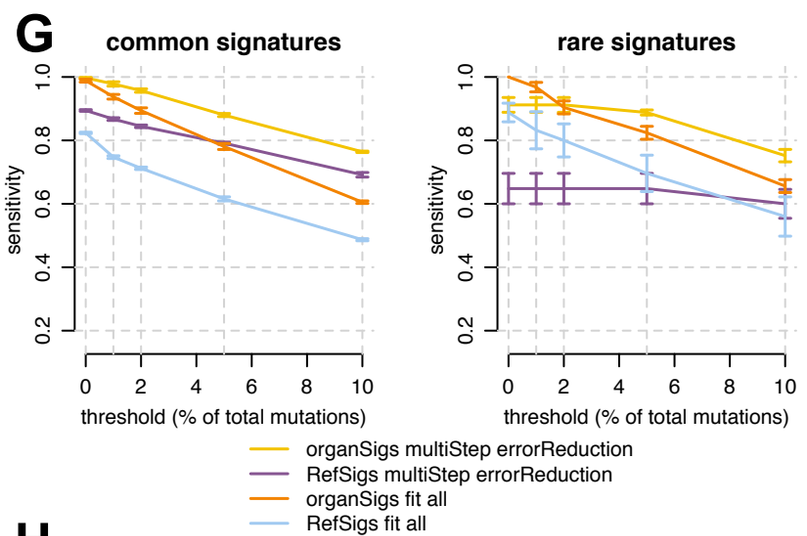
Figure S53

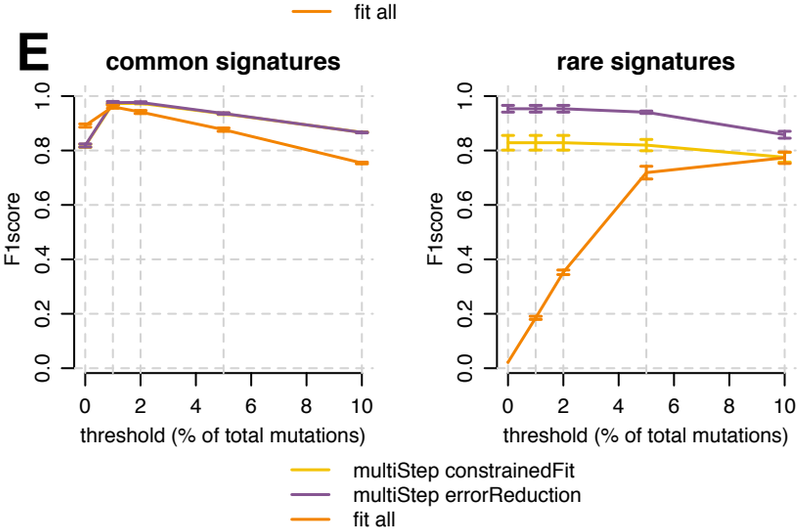

A
Number of common and rare
SBS signatures in each sample
number of signatures
GEL
ICGC
Hartwig
GEL common
ICGC common
Hartwig common
GEL rare
ICGC rare
Hartwig rare

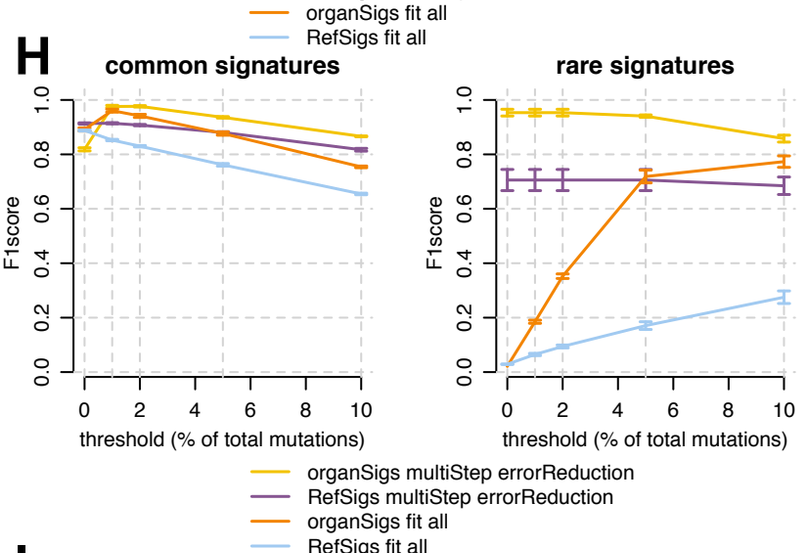

B
GEL
1160
11019
ICGC
105
2578
Hartwig
223
3036
number of rare
signatures
in sample
0
1
2
3

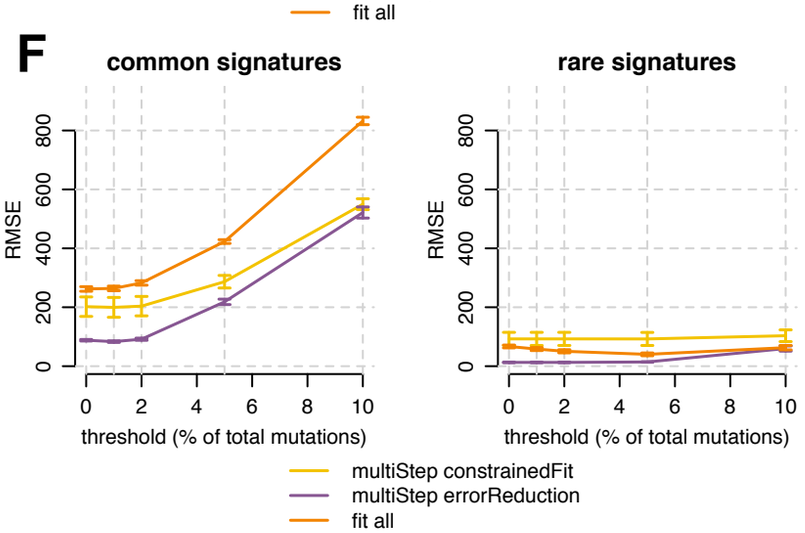

C
FitMS framework
step 1
new
sample
fit common
signatures
common
signatures
step 2
attempt to find
additional
rare signatures
rare
signatures

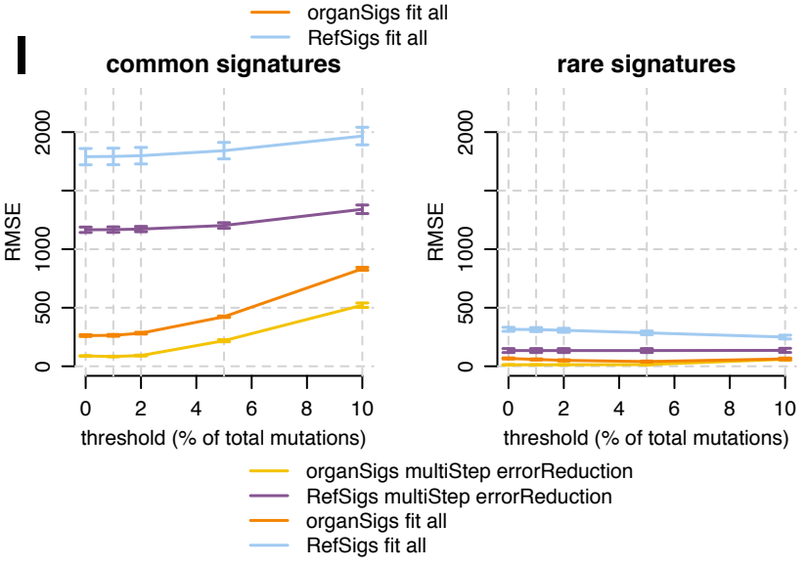

D
common signatures
rare signatures
sensitivity
threshold (% of total mutations)
multiStep constrainedFit
multiStep errorReduction
fit all


G
common signatures
rare signatures
sensitivity
threshold (% of total mutations)
organSigs multiStep errorReduction
RefSigs multiStep errorReduction
organSigs fit all
RefSigs fit all


E
common signatures
rare signatures
F1score
threshold (% of total mutations)
multiStep constrainedFit
multiStep errorReduction
fit all


H
common signatures
rare signatures
F1score
threshold (% of total mutations)
organSigs multiStep errorReduction
RefSigs multiStep errorReduction
organSigs fit all
RefSigs fit all


F
common signatures
rare signatures
RMSE
threshold (% of total mutations)
multiStep constrainedFit
multiStep errorReduction
fit all


I
common signatures
rare signatures
RMSE
threshold (% of total mutations)
organSigs multiStep errorReduction
RefSigs multiStep errorReduction
organSigs fit all
RefSigs fit all