Proportion truncating
Proportion deleterious
0.0
0.2
0.4
0.6
0.8
0.00
0.25
0.50
0.75
1.00
agrC
agrA
yjbH
xpaC
SAUSA300_0603
mgrA
SAUSA300_1856
purR
stp1
SAUSA300_1613
vraG
sucA
SAUSA300_2399
accB
dat
SAUSA300_2133
saeR
mprF
rpsJ
walR
Median PROVEAN score
2.5
0.0
−2.5
−5.0
−7.5
Number of mutations
5
10
15
20