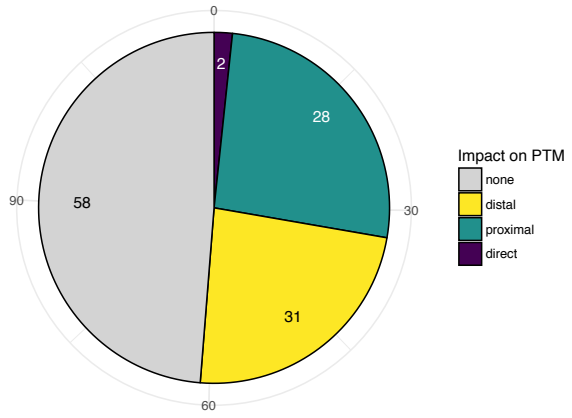
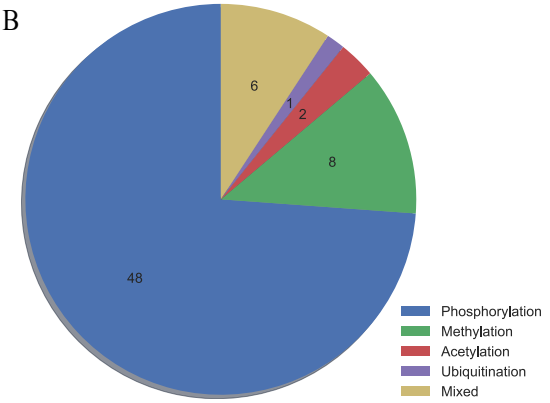
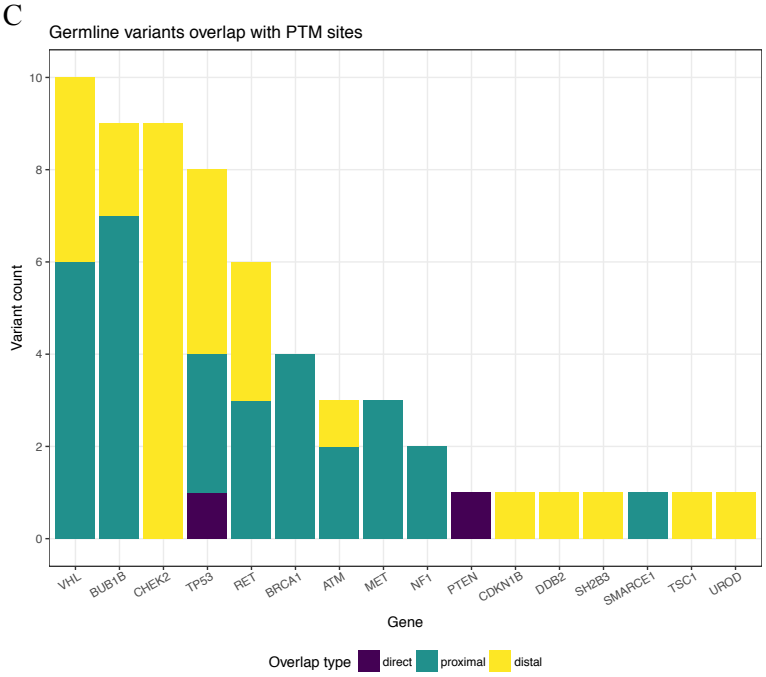
A


0
30
60
90
2
28
31
58
Impact on PTM
none
distal
proximal
direct

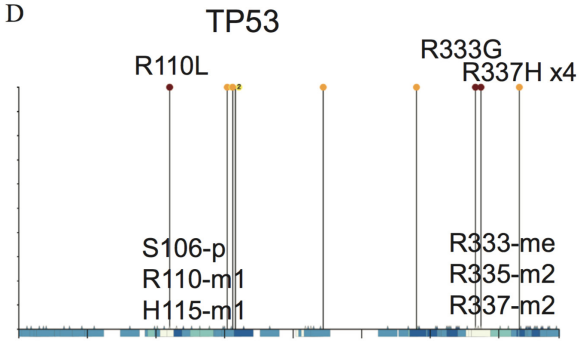
B


6
1
2
8
48
Phosphorylation
Methylation
Acetylation
Ubiquitination
Mixed

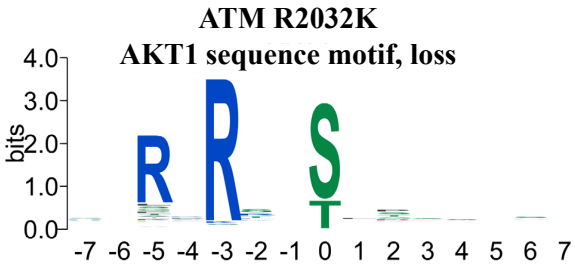
C

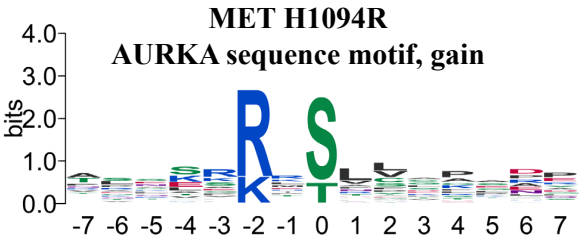

Germline variants overlap with PTM sites
Variant count
0
2
4
6
8
10
VHL
BUB1B
CHEK2
TP53
RET
BRCA1
ATM
MET
NF1
PTEN
CDKN1B
DDB2
SH2B3
SMARCE1
TSC1
UROD
Gene
Overlap type
direct
proximal
distal

D


TP53
R110L
R333G
R337H x4
S106-p
R110-m1
H115-m1
R333-me
R335-m2
R337-m2

E


ATM R2032K
AKT1 sequence motif, loss
bits
4.0
3.0
2.0
1.0
0.0
-7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7


MET H1094R
AURKA sequence motif, gain
bits
4.0
3.0
2.0
1.0
0.0
-7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7