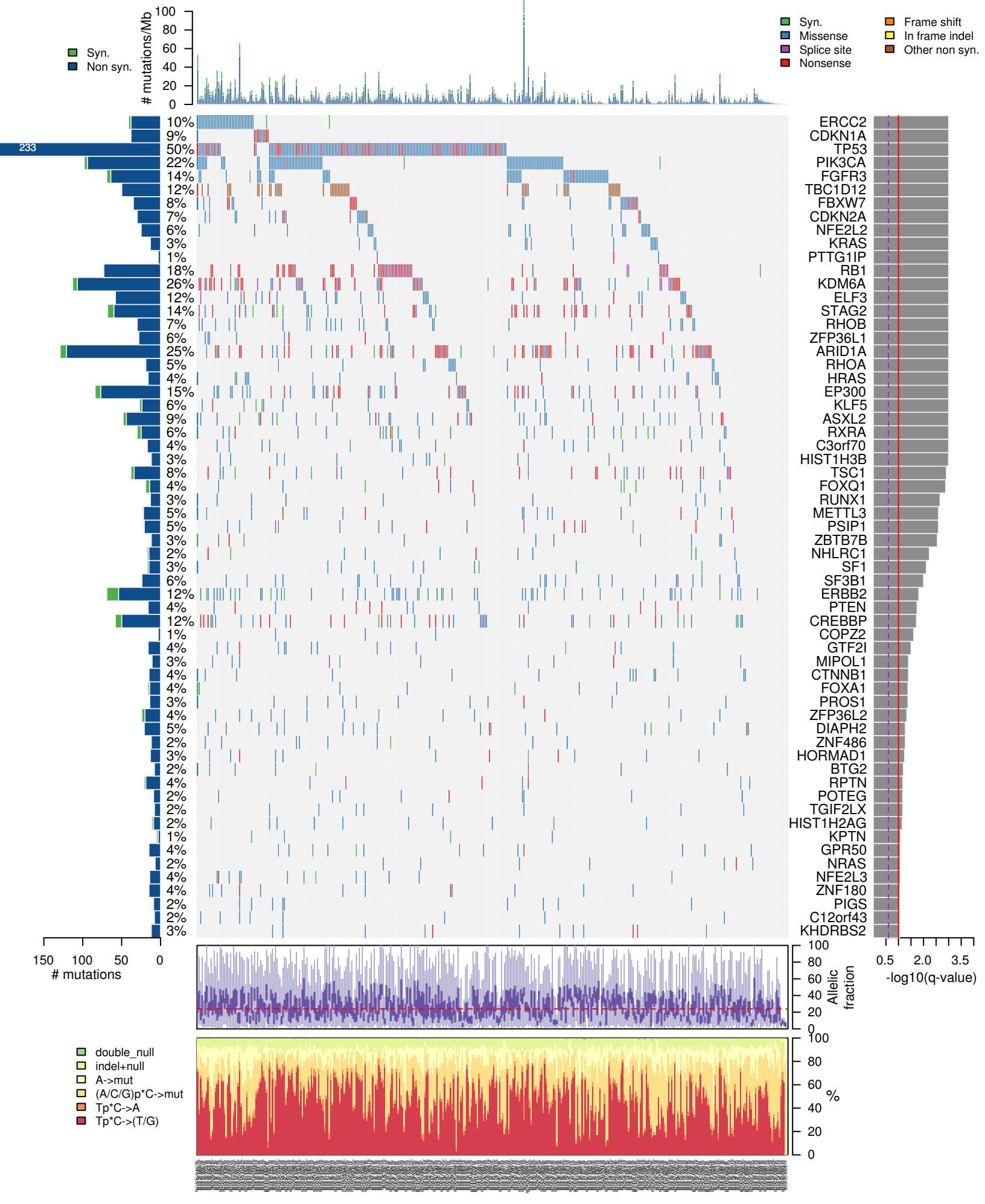
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
233
10%
9%
50%
22%
14%
12%
8%
7%
6%
3%
1%
18%
26%
12%
14%
7%
6%
25%
5%
4%
15%
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2%
3%
ERCC2
CDKN1A
TP53
PIK3CA
FGFR3
TBC1D12
FBXW7
CDKN2A
NFE2L2
KRAS
PTTG1IP
RB1
KDM6A
ELF3
STAG2
RHOB
ZFP36L1
ARID1A
RHOA
HRAS
EP300
KLF5
ASXL2
RXRA
C3orf70
HIST1H3B
TSC1
FOXQ1
RUNX1
METTL3
PSIP1
ZBTB7B
NHLRC1
SF1
SF3B1
ERBB2
PTEN
CREBBP
COPZ2
GTF2I
MIPOL1
CTNNB1
FOXA1
PROS1
ZFP36L2
DIAPH2
ZNF486
HORMAD1
BTG2
RPTN
POTEG
TGIF2LX
HIST1H2AG
KPTN
GPR50
NRAS
NFE2L3
ZNF180
PIGS
C12orf43
KHDRBS2
150
100
50
0
mutations
0.5
2.0
3.5
-log10(q-value)
Allelic fraction
double_null
indel+null
A->mut
(A/C/G)p*C->mut
Tp*C->A
Tp*C->(T/G)
%