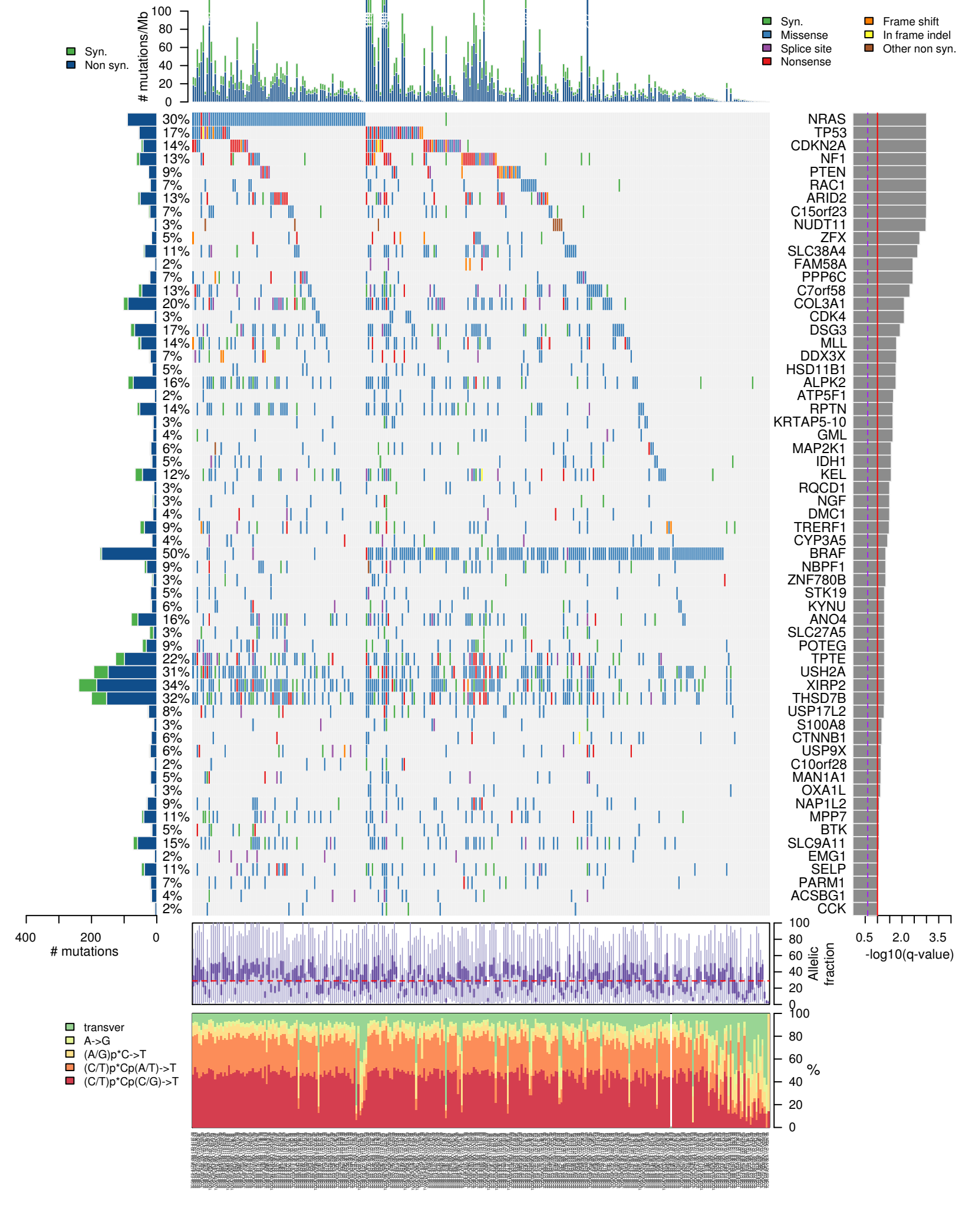
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
30%
17%
14%
13%
9%
7%
13%
7%
3%
5%
11%
2%
7%
13%
20%
3%
17%
14%
7%
5%
16%
2%
14%
3%
4%
6%
5%
12%
3%
3%
4%
9%
4%
50%
9%
3%
5%
6%
16%
3%
9%
22%
31%
34%
32%
8%
3%
6%
6%
2%
5%
3%
9%
11%
5%
15%
2%
11%
7%
4%
2%
NRAS
TP53
CDKN2A
NF1
PTEN
RAC1
ARID2
C15orf23
NUDT11
ZFX
SLC38A4
FAM58A
PPP6C
C7orf58
COL3A1
CDK4
DSG3
MLL
DDX3X
HSD11B1
ALPK2
ATP5F1
RPTN
KRTAP5-10
GML
MAP2K1
IDH1
KEL
RQCD1
NGF
DMC1
TRERF1
CYP3A5
BRAF
NBPF1
ZNF780B
STK19
KYNU
ANO4
SLC27A5
POTEG
TPTE
USH2A
XIRP2
THSD7B
USP17L2
S100A8
CTNNB1
USP9X
C10orf28
MAN1A1
OXA1L
NAP1L2
MPP7
BTK
SLC9A11
EMG1
SELP
PARM1
ACSBG1
CCK
400
200
0
mutations
0.5
2.0
3.5
-log10(q-value)
Allelic fraction
transver
A->G
(A/G)p*C->T
(C/T)p*Cp(A/T)->T
(C/T)p*Cp(C/G)->T
%