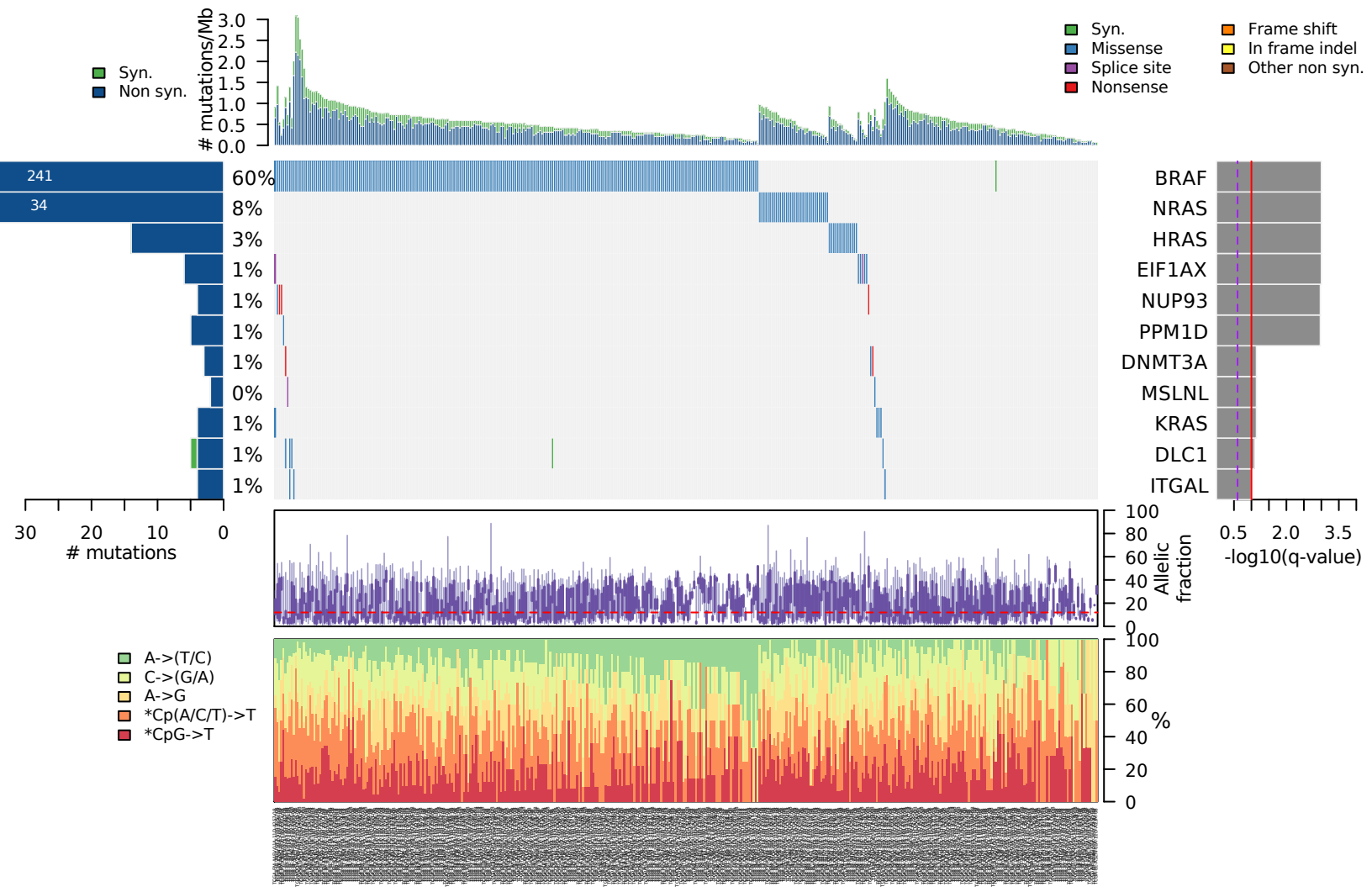
Syn.
Non syn.
mutations/Mb
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
241
34
60%
8%
3%
1%
1%
1%
1%
0%
1%
1%
1%
30
20
10
0
mutations
BRAF
NRAS
HRAS
EIF1AX
NUP93
PPM1D
DNMT3A
MSLNL
KRAS
DLC1
ITGAL
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
Allelic fraction
A->(T/C)
C->(G/A)
A->G
*Cp(A/C/T)->T
*CpG->T
100
80
60
40
20
0
%