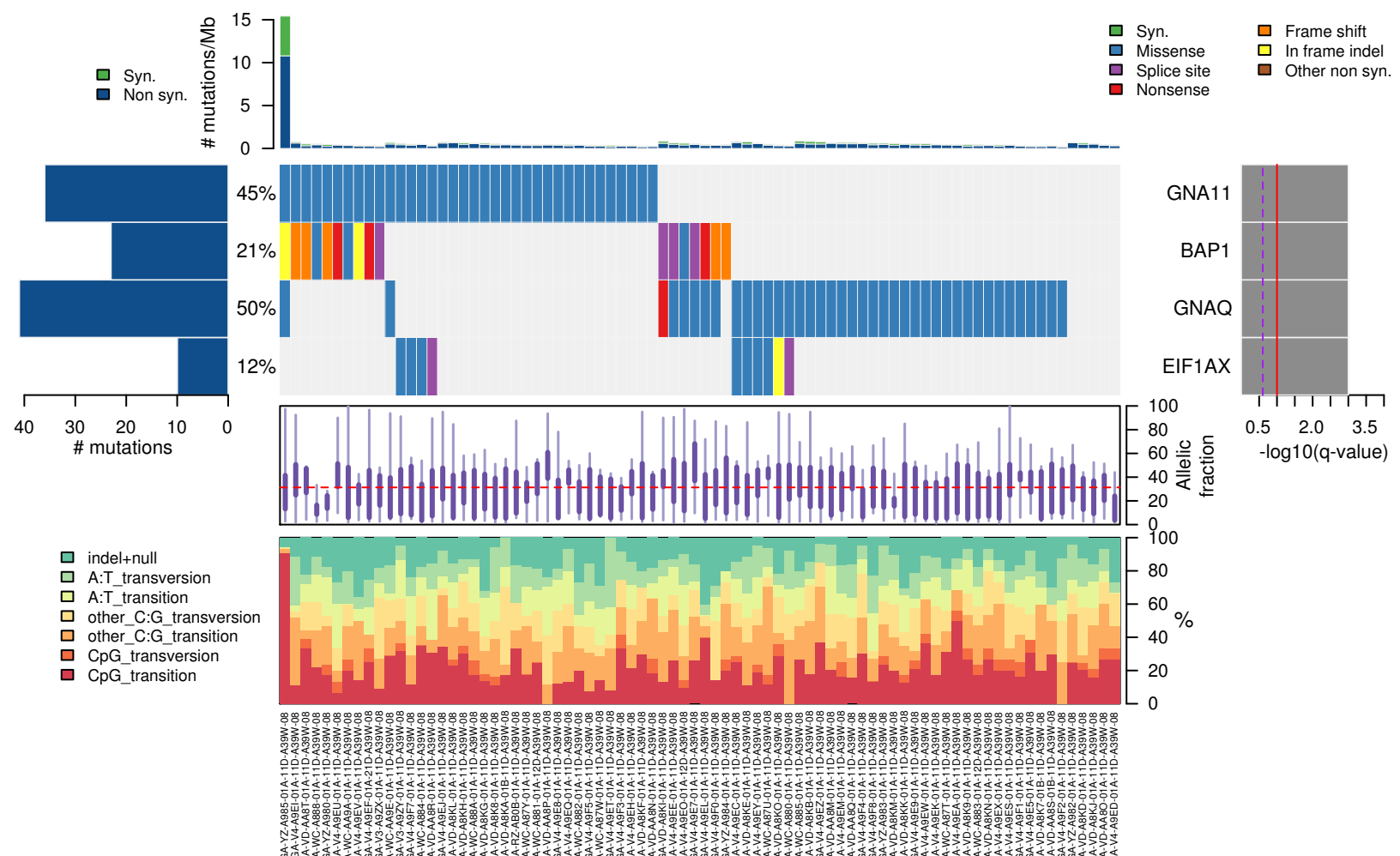
Syn.
Non syn.
mutations/Mb
15
10
5
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
45%
21%
50%
12%
GNA11
BAP1
GNAQ
EIF1AX
40
30
20
10
0
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
Allelic fraction
indel+null
A:T_transversion
A:T_transition
other_C:G_transversion
other_C:G_transition
CpG_transversion
CpG_transition
%