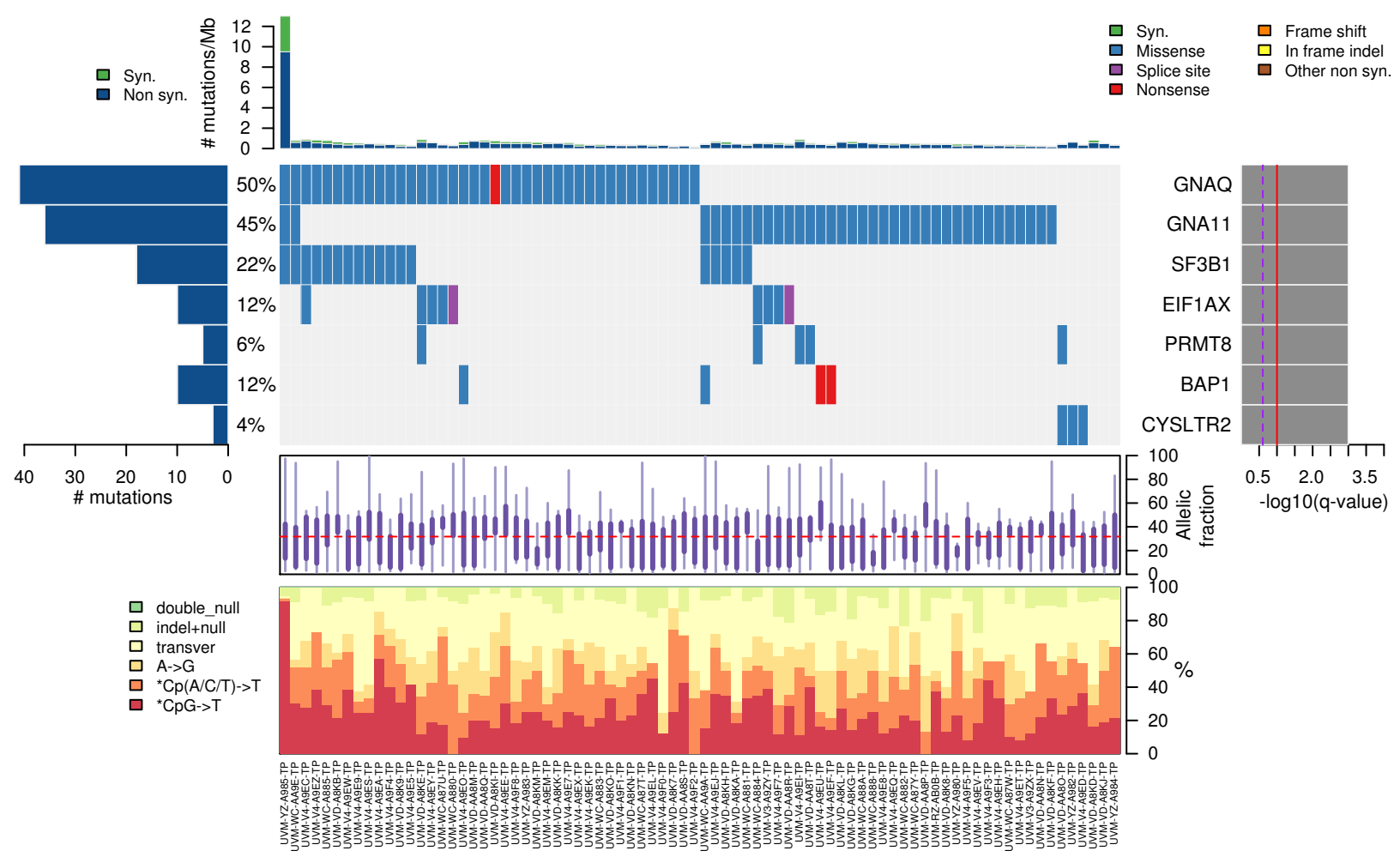
Syn.
Non syn.
mutations/Mb
12
10
8
6
4
2
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
50%
45%
22%
12%
6%
12%
4%
GNAQ
GNA11
SF3B1
EIF1AX
PRMT8
BAP1
CYSLTR2
40
30
20
10
0
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
Allelic fraction
double_null
indel+null
transver
A->G
*Cp(A/C/T)->T
*CpG->T
%