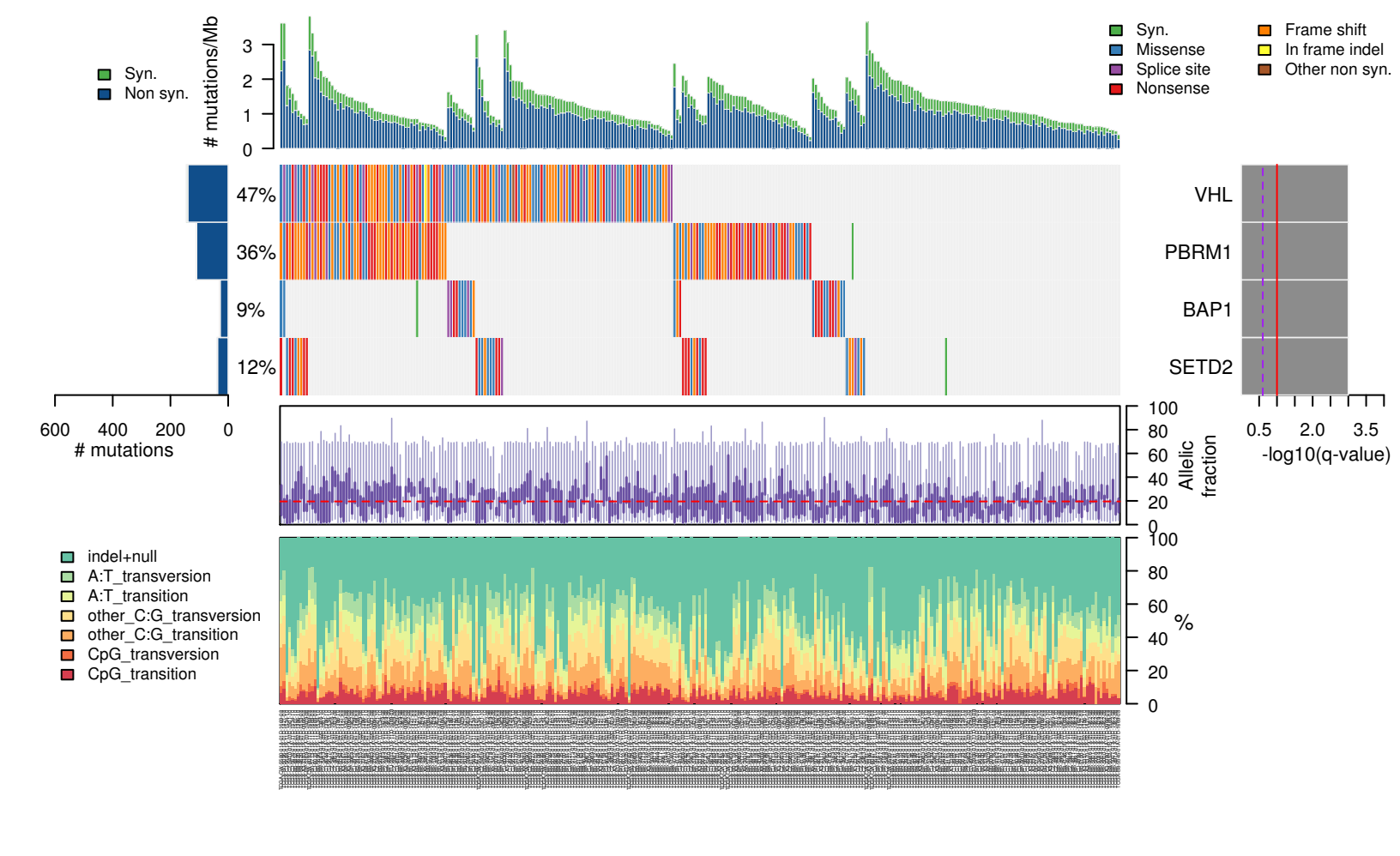
Syn.
Non syn.
mutations/Mb
3
2
1
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
47%
36%
9%
12%
VHL
PBRM1
BAP1
SETD2
600
400
200
0
mutations
100
80
60
40
20
0
Allelic fraction
0.5
2.0
3.5
-log10(q-value)
indel+null
A:T_transversion
A:T_transition
other_C:G_transversion
other_C:G_transition
CpG_transversion
CpG_transition
%