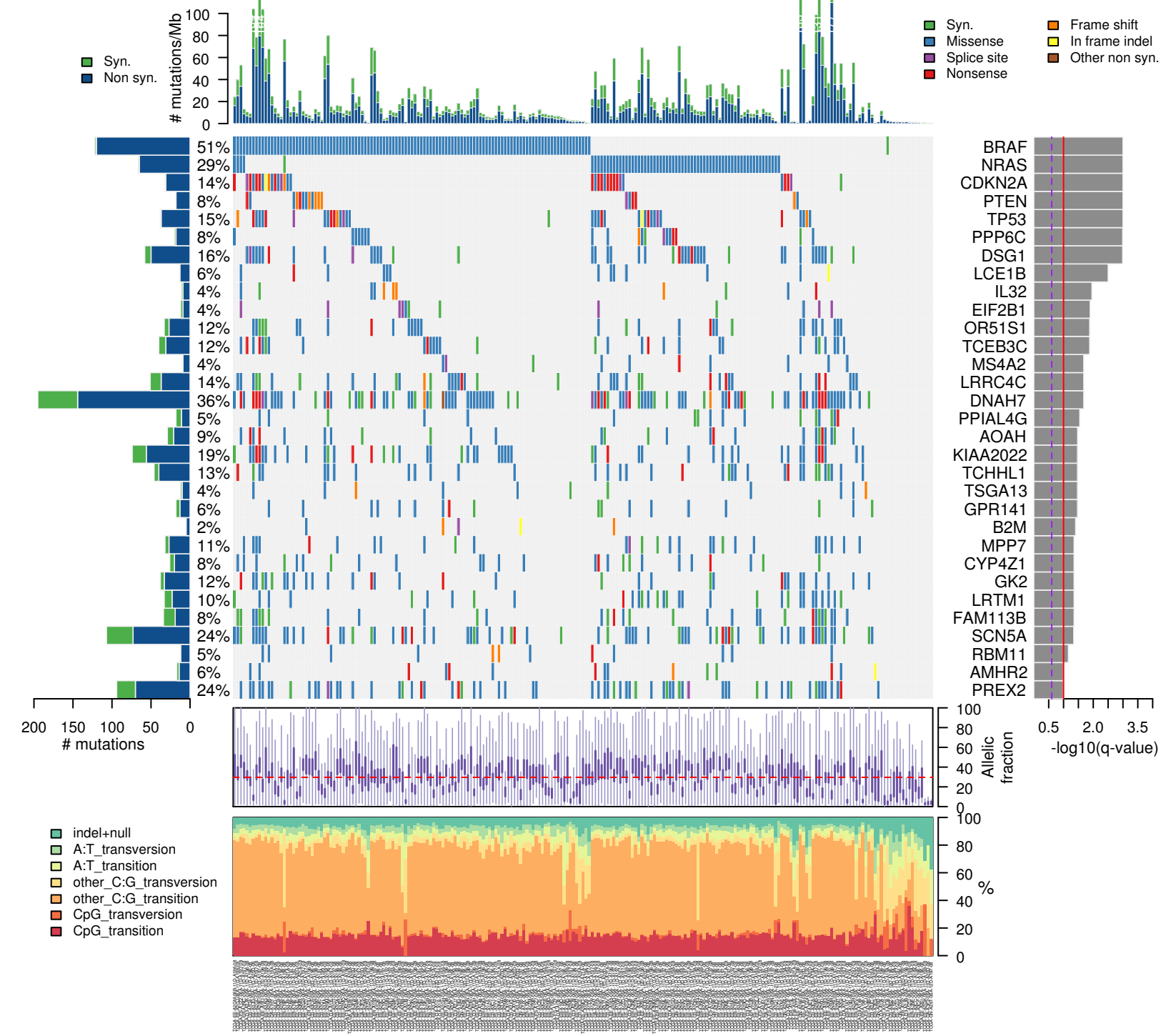
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
51%
29%
14%
8%
15%
8%
16%
6%
4%
4%
12%
12%
4%
14%
36%
5%
9%
19%
13%
4%
6%
2%
11%
8%
12%
10%
8%
24%
5%
6%
24%
BRAF
NRAS
CDKN2A
PTEN
TP53
PPP6C
DSG1
LCE1B
IL32
EIF2B1
OR51S1
TCEB3C
MS4A2
LRRC4C
DNAH7
PPIAL4G
AOAH
KIAA2022
TCHHL1
TSGA13
GPR141
B2M
MPP7
CYP4Z1
GK2
LRTM1
FAM113B
SCN5A
RBM11
AMHR2
PREX2
200
150
100
50
0
mutations
0.5
2.0
3.5
-log10(q-value)
Allelic fraction
indel+null
A:T_transversion
A:T_transition
other_C:G_transversion
other_C:G_transition
CpG_transversion
CpG_transition
%