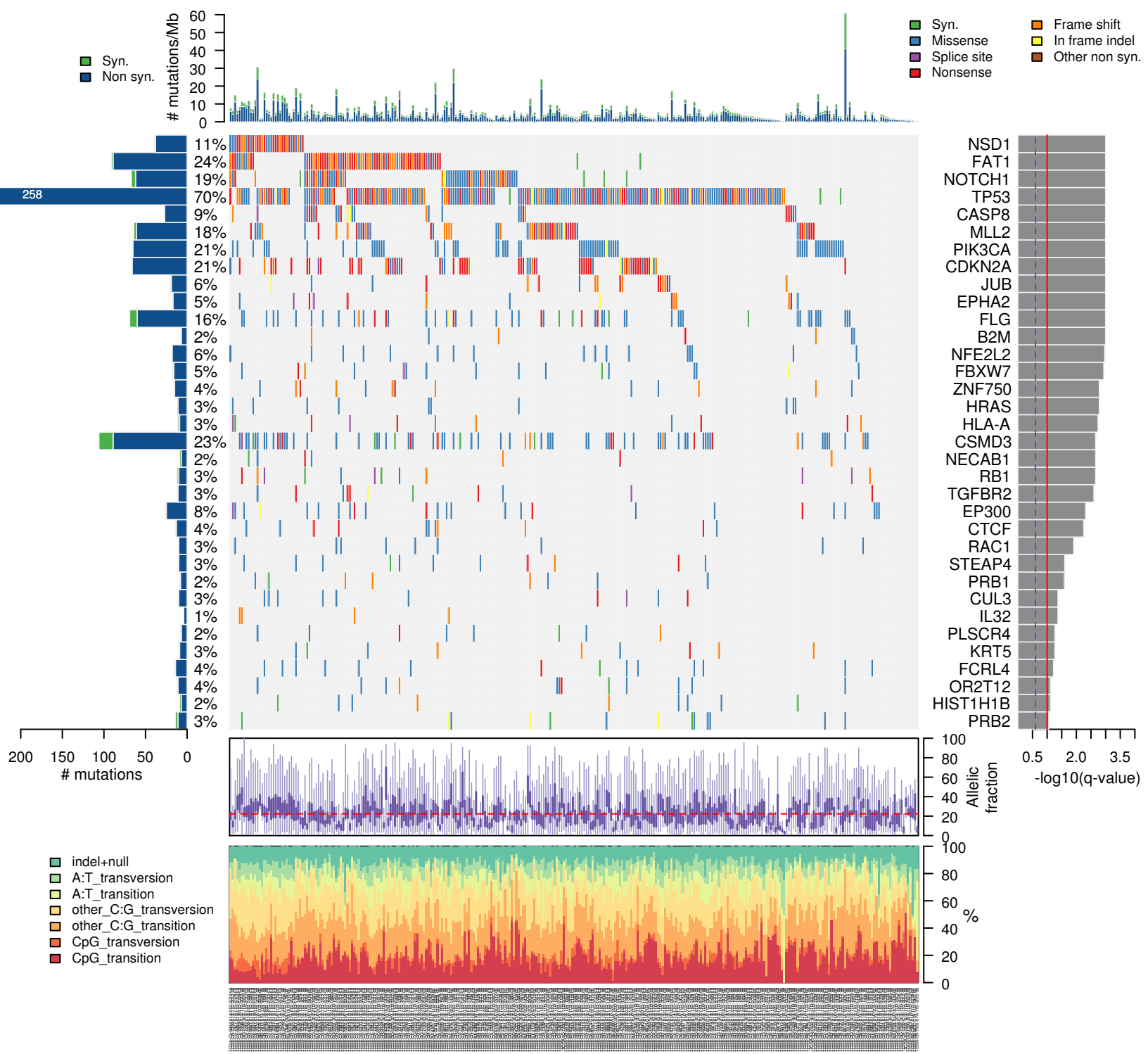
Syn.
Non syn.
mutations/Mb
60
50
40
30
20
10
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
11%
24%
19%
258
70%
9%
18%
21%
21%
6%
5%
16%
2%
6%
5%
4%
3%
3%
23%
2%
3%
3%
8%
4%
3%
3%
2%
3%
1%
2%
3%
4%
4%
2%
3%
NSD1
FAT1
NOTCH1
TP53
CASP8
MLL2
PIK3CA
CDKN2A
JUB
EPHA2
FLG
B2M
NFE2L2
FBXW7
ZNF750
HRAS
HLA-A
CSMD3
NECAB1
RB1
TGFBR2
EP300
CTCF
RAC1
STEAP4
PRB1
CUL3
IL32
PLSCR4
KRT5
FCRL4
OR2T12
HIST1H1B
PRB2
200
150
100
50
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
100
80
60
40
20
0
%