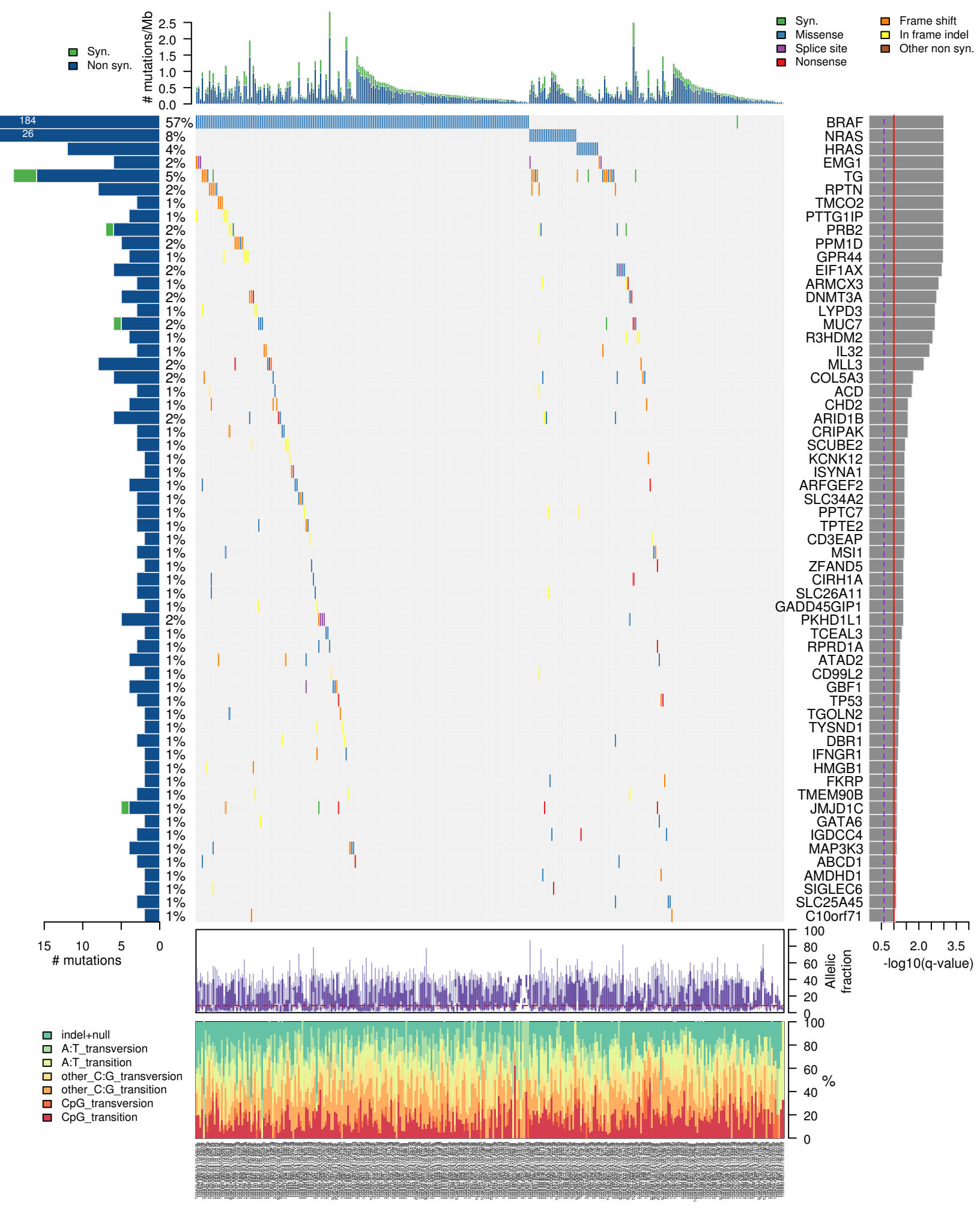
Syn.
Non syn.
mutations/Mb
2.5
2.0
1.5
1.0
0.5
0.0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
184
26
57%
8%
4%
2%
5%
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BRAF
NRAS
HRAS
EMG1
TG
RPTN
TMCO2
PTTG1IP
PRB2
PPM1D
GPR44
EIF1AX
ARMCX3
DNMT3A
LYPD3
MUC7
R3HDM2
IL32
MLL3
COL5A3
ACD
CHD2
ARID1B
CRIPAK
SCUBE2
KCNK12
ISYNA1
ARFGEF2
SLC34A2
PPTC7
TPTE2
CD3EAP
MSI1
ZFAND5
CIRH1A
SLC26A11
GADD45GIP1
PKHD1L1
TCEAL3
RPRD1A
ATAD2
CD99L2
GBF1
TP53
TGOLN2
TYSND1
DBR1
IFNGR1
HMGB1
FKRP
TMEM90B
JMJD1C
GATA6
IGDCC4
MAP3K3
ABCD1
AMDHD1
SIGLEC6
SLC25A45
C10orf71
15
10
5
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
%