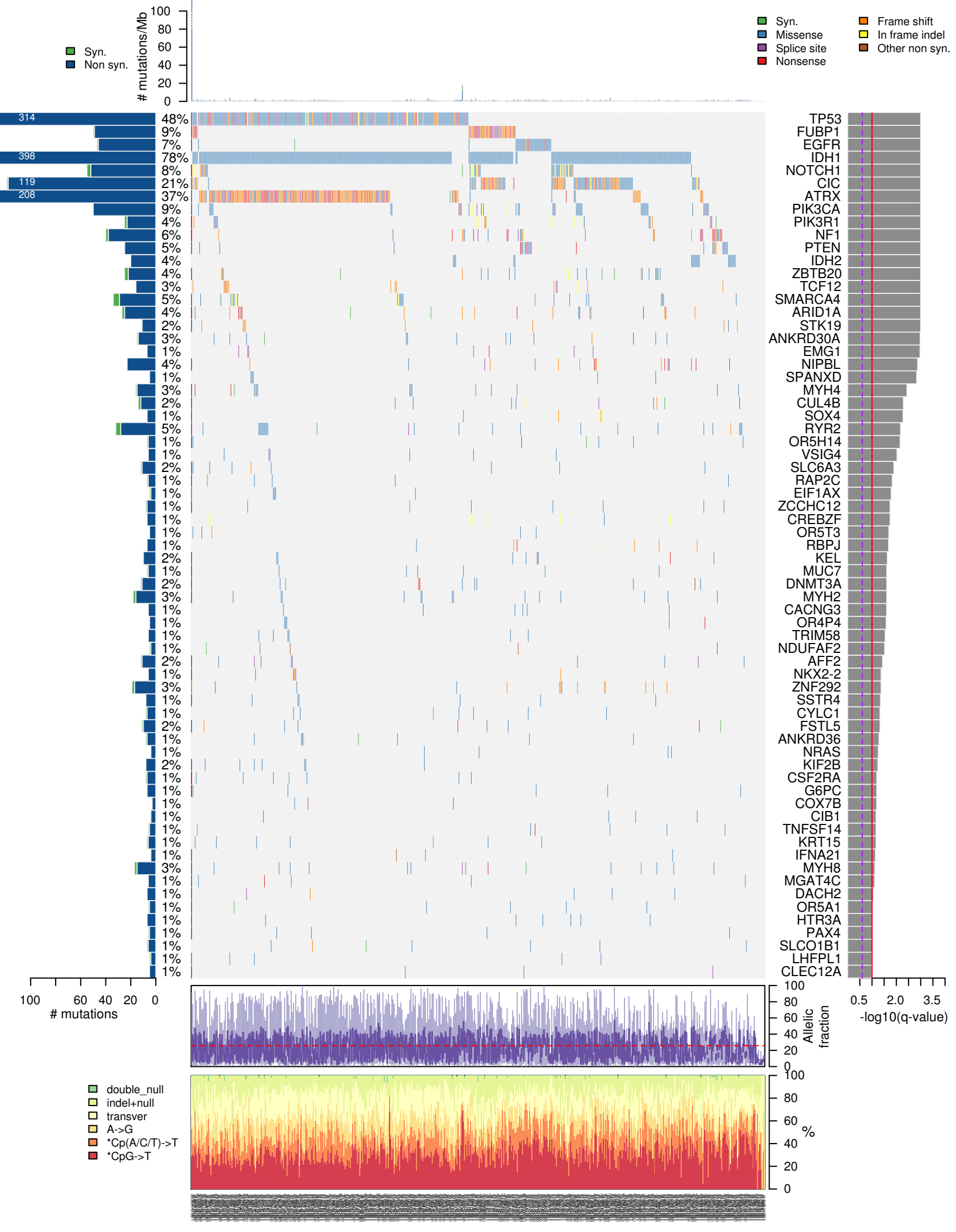

mutations/Mb
100
80
60
40
20
0
Syn.
Non syn.
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
314
398
119
208
48%
9%
7%
78%
8%
21%
37%
9%
4%
6%
5%
4%
4%
3%
5%
4%
2%
3%
1%
4%
1%
3%
2%
1%
5%
1%
1%
2%
1%
1%
1%
1%
1%
2%
1%
2%
3%
1%
1%
1%
1%
2%
1%
3%
1%
1%
2%
1%
1%
1%
1%
1%
1%
1%
1%
3%
1%
1%
1%
1%
1%
1%
1%
1%
TP53
FUBP1
EGFR
IDH1
NOTCH1
CIC
ATRX
PIK3CA
PIK3R1
NF1
PTEN
IDH2
ZBTB20
TCF12
SMARCA4
ARID1A
STK19
ANKRD30A
EMG1
NIPBL
SPANXD
MYH4
CUL4B
SOX4
RYR2
OR5H14
VSIG4
SLC6A3
RAP2C
EIF1AX
ZCCHC12
CREBZF
OR5T3
RBPJ
KEL
MUC7
DNMT3A
MYH2
CACNG3
OR4P4
TRIM58
NDUFAF2
AFF2
NKX2-2
ZNF292
SSTR4
CYLC1
FSTL5
ANKRD36
NRAS
KIF2B
CSF2RA
G6PC
COX7B
CIB1
TNFSF14
KRT15
IFNA21
MYH8
MGAT4C
DACH2
OR5A1
HTR3A
PAX4
SLCO1B1
LHFPL1
CLEC12A
100
80
60
40
20
0
mutations
0.5
2.0
3.5
-log10(q-value)
Allelic fraction
double_null
indel+null
transver
A->G
*Cp(A/C/T)->T
*CpG->T
%