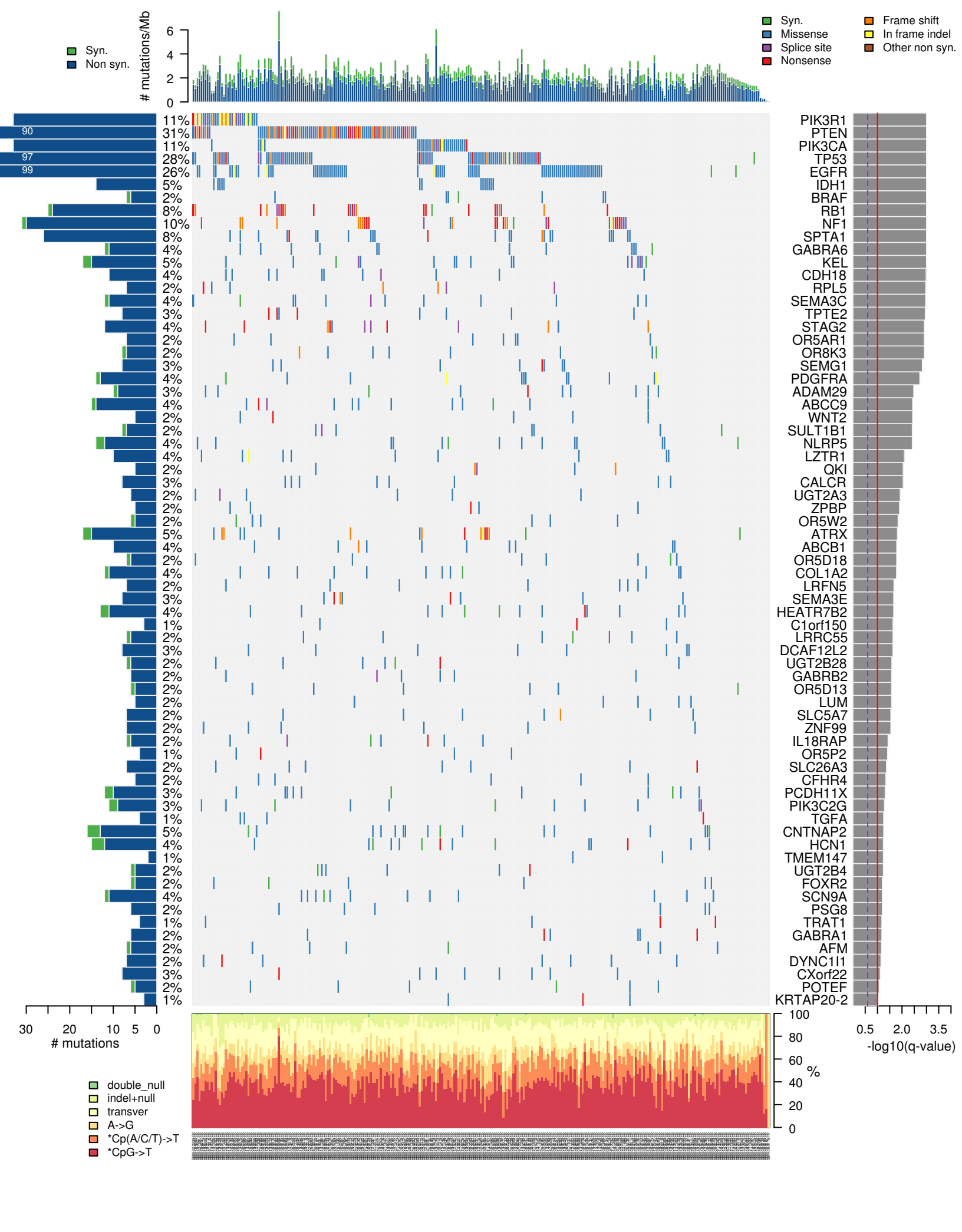
Syn.
Non syn.
mutations/Mb
6
4
2
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
11%
31%
11%
28%
26%
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1%
90
97
99
PIK3R1
PTEN
PIK3CA
TP53
EGFR
IDH1
BRAF
RB1
NF1
SPTA1
GABRA6
KEL
CDH18
RPL5
SEMA3C
TPTE2
STAG2
OR5AR1
OR8K3
SEMG1
PDGFRA
ADAM29
ABCC9
WNT2
SULT1B1
NLRP5
LZTR1
QKI
CALCR
UGT2A3
ZPBP
OR5W2
ATRX
ABCB1
OR5D18
COL1A2
LRFN5
SEMA3E
HEATR7B2
C1orf150
LRRC55
DCAF12L2
UGT2B28
GABRB2
OR5D13
LUM
SLC5A7
ZNF99
IL18RAP
OR5P2
SLC26A3
CFHR4
PCDH11X
PIK3C2G
TGFA
CNTNAP2
HCN1
TMEM147
UGT2B4
FOXR2
SCN9A
PSG8
TRAT1
GABRA1
AFM
DYNC1I1
CXorf22
POTEF
KRTAP20-2
30
20
10
5
0
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
%
double_null
indel+null
transver
A->G
*Cp(A/C/T)->T
*CpG->T