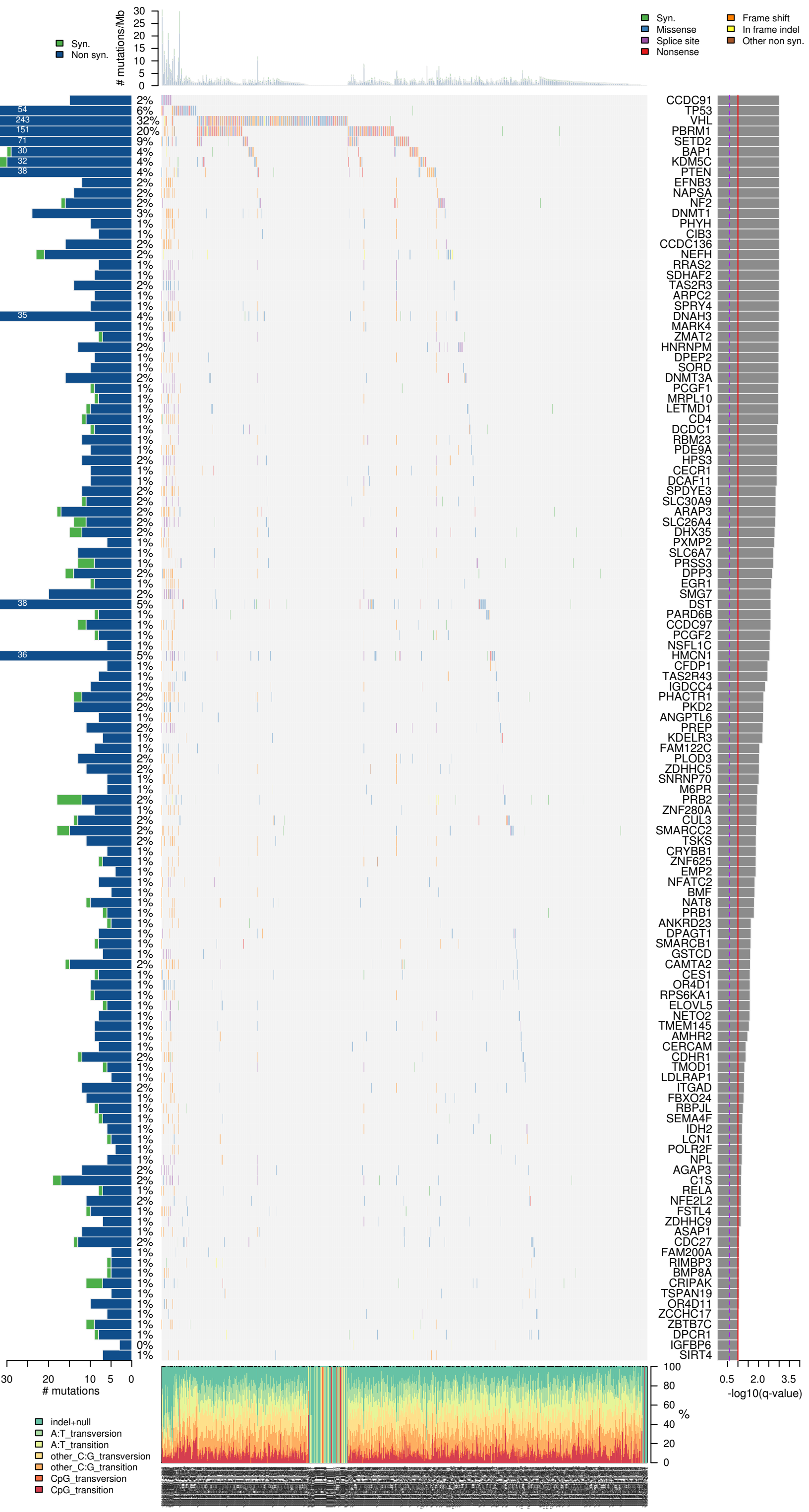
Syn.
Non syn.
mutations/Mb
30
25
20
15
10
5
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
54
243
151
71
30
32
38
35
38
36
CCDC91 2%
TP53 6%
VHL 32%
PBRM1 20%
SETD2 9%
BAP1 4%
KDM5C 4%
PTEN 4%
EFNB3 2%
NAPSA 2%
NF2 2%
DNMT1 3%
PHYH 1%
CIB3 1%
CCDC136 2%
NEFH 2%
RRAS2 1%
SDHAF2 1%
TAS2R3 2%
ARPC2 1%
SPRY4 1%
DNAH3 4%
MARK4 1%
ZMAT2 1%
HNRNPM 2%
DPEP2 1%
SORD 1%
DNMT3A 2%
PCGF1 1%
MRPL10 1%
LETMD1 1%
CD4 1%
DCDC1 1%
RBM23 1%
PDE9A 1%
HPS3 2%
CECR1 1%
DCAF11 1%
SPDYE3 2%
SLC30A9 2%
ARAP3 2%
SLC26A4 2%
DHX35 2%
PXMP2 1%
SLC6A7 1%
PRSS3 1%
DPP3 2%
EGR1 1%
SMG7 2%
DST 5%
PARD6B 1%
CCDC97 1%
PCGF2 1%
NSFL1C 1%
HMCN1 5%
CFDP1 1%
TAS2R43 1%
IGDCC4 1%
PHACTR1 2%
PKD2 2%
ANGPTL6 1%
PREP 2%
KDELR3 1%
FAM122C 1%
PLOD3 2%
ZDHHC5 2%
SNRNP70 1%
M6PR 1%
PRB2 2%
ZNF280A 1%
CUL3 2%
SMARCC2 2%
TSKS 2%
CRYBB1 1%
ZNF625 1%
EMP2 1%
NFATC2 1%
BMF 1%
NAT8 1%
PRB1 1%
ANKRD23 1%
DPAGT1 1%
SMARCB1 1%
GSTCD 1%
CAMTA2 2%
CES1 1%
OR4D1 1%
RPS6KA1 1%
ELOVL5 1%
NETO2 1%
TMEM145 1%
AMHR2 1%
CERCAM 1%
CDHR1 2%
TMOD1 1%
LDLRAP1 1%
ITGAD 2%
FBXO24 1%
RBPJL 1%
SEMA4F 1%
IDH2 1%
LCN1 1%
POLR2F 1%
NPL 1%
AGAP3 2%
C1S 2%
RELA 1%
NFE2L2 2%
FSTL4 1%
ZDHHC9 1%
ASAP1 1%
CDC27 2%
FAM200A 1%
RIMBP3 1%
BMP8A 1%
CRIPAK 1%
TSPAN19 1%
OR4D11 1%
ZCCHC17 1%
ZBTB7C 1%
DPCR1 1%
IGFBP6 0%
SIRT4 1%
30
20
10
5
0
mutations
0.5
2.0
3.5
-log10(q-value)
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
%