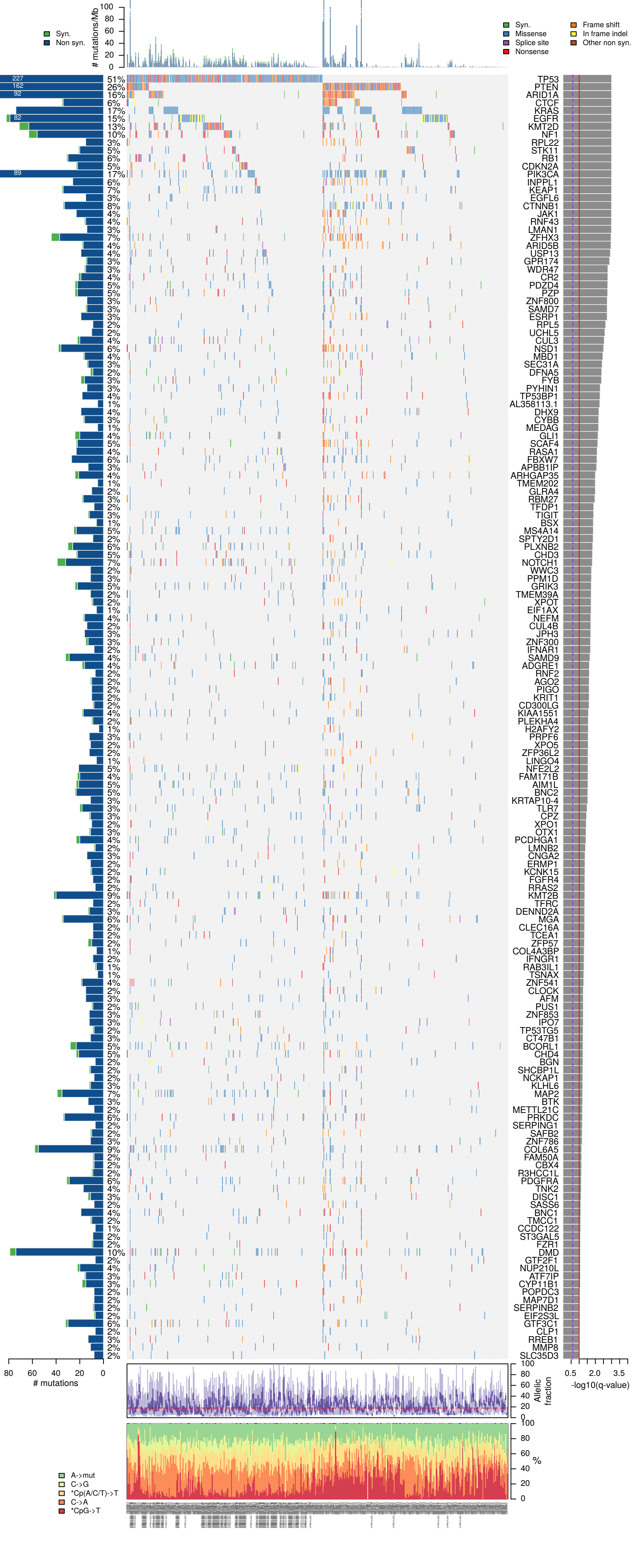
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
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92
82
89
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TP53
PTEN
ARID1A
CTCF
KRAS
EGFR
KMT2D
NF1
RPL22
STK11
RB1
CDKN2A
PIK3CA
INPPL1
KEAP1
EGFL6
CTNNB1
JAK1
RNF43
LMAN1
ZFHX3
ARID5B
USP13
GPR174
WDR47
CR2
PDZD4
PZP
ZNF800
SAMD7
ESRP1
RPL5
UCHL5
CUL3
NSD1
MBD1
SEC31A
DFNA5
FYB
PYHIN1
TP53BP1
AL358113.1
DHX9
CYBB
MEDAG
GLI1
SCAF4
RASA1
FBXW7
APBB1IP
ARHGAP35
TMEM202
GLRA4
RBM27
TFDP1
TIGIT
BSX
MS4A14
SPTY2D1
PLXNB2
CHD3
NOTCH1
WWC3
PPM1D
GRIK3
TMEM39A
XPOT
EIF1AX
NEFM
CUL4B
JPH3
ZNF300
IFNAR1
SAMD9
ADGRE1
RNF2
AGO2
PIGO
KRIT1
CD300LG
KIAA1551
PLEKHA4
H2AFY2
PRPF6
XPO5
ZFP36L2
LINGO4
NFE2L2
FAM171B
AIM1L
BNC2
KRTAP10-4
TLR7
CPZ
XPO1
OTX1
PCDHGA1
LMNB2
CNGA2
ERMP1
KCNK15
FGFR4
RRAS2
KMT2B
TFRC
DENND2A
MGA
CLEC16A
TCEA1
ZFP57
COL4A3BP
IFNGR1
RAB3IL1
TSNAX
ZNF541
CLOCK
AFM
PUS1
ZNF853
IPO7
TP53TG5
CT47B1
BCORL1
CHD4
BGN
SHCBP1L
NCKAP1
KLHL6
MAP2
BTK
METTL21C
PRKDC
SERPING1
SAFB2
ZNF786
COL6A5
FAM50A
CBX4
R3HCC1L
PDGFRA
TNK2
DISC1
SASS6
BNC1
TMCC1
CCDC122
ST3GAL5
FZR1
DMD
GTF2F1
NUP210L
ATF7IP
CYP11B1
POPDC3
MAP7D1
SERPINB2
EIF2S3L
GTF3C1
CLP1
RREB1
MMP8
SLC35D3
80
60
40
20
0
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
Allelic fraction
100
80
60
40
20
0
%
A->mut
C->G
*Cp(A/C/T)->T
C->A
*CpG->T