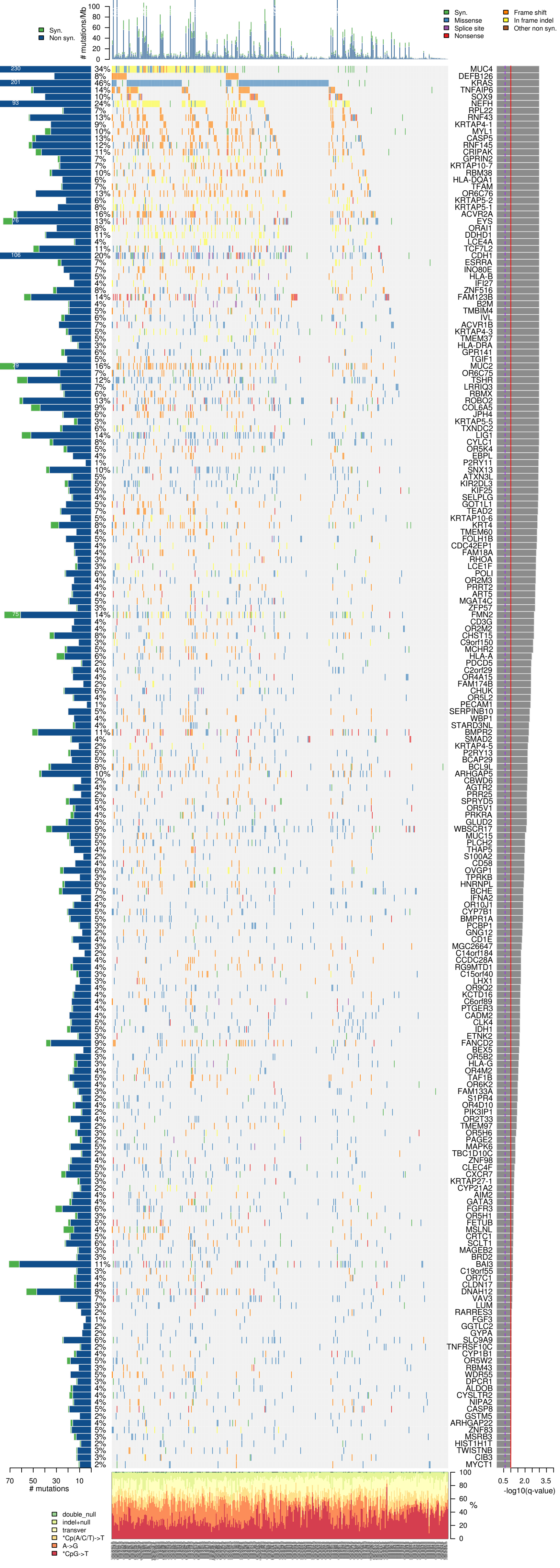
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
MUC4
DEFB126
KRAS
TNFAIP6
SOX9
NEFH
RPL22
RNF43
KRTAP4-1
MYL1
CASP5
RNF145
CRIPAK
GPRIN2
KRTAP10-7
RBM38
HLA-DQA1
TFAM
OR6C76
KRTAP5-2
KRTAP5-1
ACVR2A
EYS
ORAI1
DDHD1
LCE4A
TCF7L2
CDH1
ESRRA
INO80E
HLA-B
IFI27
ZNF516
FAM123B
B2M
TMBIM4
IVL
ACVR1B
KRTAP4-3
TMEM37
HLA-DRA
GPR141
TGIF1
MUC2
OR6C75
TSHR
LRRIQ3
RBMX
ROBO2
COL6A5
JPH4
KRTAP5-5
TXNDC2
LIG1
CYLC1
OR5K4
EBPL
P2RY11
SNX13
ATXN3L
KIR2DL3
KIF25
SELPLG
GOT1L1
TEAD2
KRTAP10-6
KRT4
TMEM60
FOLH1B
CDC42EP1
FAM18A
RHOA
LCE1F
POLI
OR2M3
PRRT2
ART5
MGAT4C
ZFP57
FMN2
CD3G
OR2M2
CHST15
C9orf150
MCHR2
HLA-A
PDCD5
C2orf29
OR4A15
FAM174B
CHUK
OR5L2
PECAM1
SERPINB10
WBP1
STARD3NL
BMPR2
SMAD2
KRTAP4-5
P2RY13
BCAP29
BCL9L
ARHGAP5
CBWD6
AGTR2
PRR25
SPRYD5
OR5V1
PRKRA
GLUD2
WBSCR17
MUC15
PLCH2
THAP5
S100A2
CD58
OVGP1
TPRKB
HNRNPL
BCHE
IFNA2
OR10J1
CYP7B1
BMPR1A
PCBP1
GNG12
CD1E
MGC26647
C14orf184
CCDC28A
RG9MTD1
C15orf40
LHX1
OR9Q2
KCTD16
C6orf89
PTGER3
CADM2
CLK4
IDH1
ETNK2
FANCD2
BEX5
OR5B2
HLA-G
OR4M2
TAF1B
OR6K2
FAM133A
S1PR4
OR4D10
PIK3IP1
OR2T33
TMEM97
OR5H6
PAGE2
MAPK6
TBC1D10C
ZNF98
CLEC4F
CXCR7
KRTAP27-1
CYP21A2
AIM2
GATA3
FGFR3
OR5H1
FETUB
MSLNL
CRTC1
SCLT1
MAGEB2
BRD2
BAI3
C19orf55
OR7C1
CLDN17
DNAH12
VAV3
LUM
RARRES3
FGF3
GGTLC2
GYPA
SLC9A9
TNFRSF10C
CYP1B1
OR5W2
RBM43
WDR55
DPCR1
ALDOB
CYSLTR2
NIPA2
CASP8
GSTM5
ARHGAP22
ZNF83
MSRB3
HIST1H1T
TWISTNB
CIB3
MYCT1
70
50
30
10
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
%
double_null
indel+null
transver
*Cp(A/C/T)->T
A->G
*CpG->T