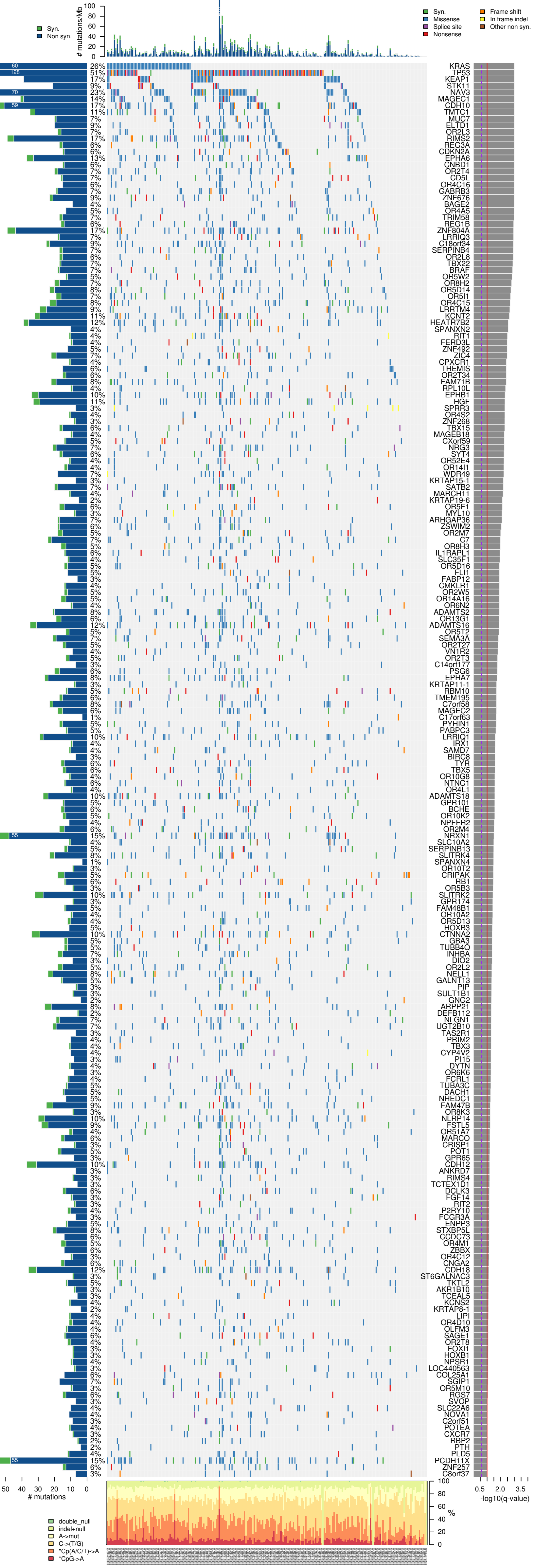
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
KRAS 26% 60
TP53 51% 128
KEAP1 17%
STK11 9%
NAV3 23% 70
MAGEC1 14%
CDH10 17% 59
TMTC1 11%
MUC7 7%
ELTD1 9%
OR2L3 7%
RIMS2 17%
REG3A 6%
CDKN2A 6%
EPHA6 13%
CNBD1 6%
OR2T4 7%
CD5L 7%
OR4C16 6%
GABRB3 7%
ZNF676 9%
BAGE2 4%
OR4A5 5%
TRIM58 7%
REG1B 6%
ZNF804A 17%
LRRIQ3 7%
C18orf34 9%
SERPINB4 7%
OR2L8 6%
TBX22 7%
BRAF 7%
OR5W2 5%
OR8H2 7%
OR5D14 8%
OR5I1 7%
OR4C15 8%
LRRTM4 9%
KCNT2 11%
HEATR7B2 12%
SPANXN2 4%
RIT1 4%
FERD3L 4%
ZNF492 5%
ZIC4 7%
CPXCR1 4%
THEMIS 6%
OR2T34 6%
FAM71B 8%
RPL10L 4%
EPHB1 10%
HGF 11%
SPRR3 3%
OR4S2 4%
ZNF268 3%
TBX15 6%
MAGEB18 4%
CXorf59 5%
NRG3 7%
SYT4 6%
OR52E4 4%
OR14I1 4%
WDR49 7%
KRTAP15-1 3%
SATB2 7%
MARCH11 4%
KRTAP19-6 2%
OR5F1 6%
MYL10 3%
ARHGAP36 7%
ZSWIM2 6%
OR2M7 5%
C7 7%
OR8H3 5%
IL1RAPL1 6%
SLC35F1 4%
OR5D16 5%
FLI1 5%
FABP12 3%
CMKLR1 4%
OR2W5 5%
OR14A16 5%
OR6N2 4%
ADAMTS2 8%
OR13G1 6%
ADAMTS16 12%
OR5T2 5%
SEMA3A 7%
OR2T27 5%
VN1R2 4%
OR2T3 5%
C14orf177 3%
PSG6 6%
EPHA7 8%
KRTAP11-1 3%
RBM10 5%
TMEM195 6%
C7orf58 8%
MAGEC2 6%
C17orf63 1%
PYHIN1 5%
PABPC3 5%
LRRIQ1 10%
IRX1 4%
SAMD7 4%
BIRC8 3%
TYR 6%
TBX5 6%
OR10G8 4%
NTNG1 6%
OR4L1 4%
ADAMTS18 10%
GPR101 5%
BCHE 6%
OR10K2 5%
NPFFR2 4%
OR2M4 6%
NRXN1 15% 55
SLC10A2 4%
SERPINB13 5%
SLITRK4 8%
SPANXN4 1%
OR10T2 3%
CRIPAK 5%
RB1 6%
OR5B3 3%
SLITRK2 10%
GPR174 3%
FAM48B1 5%
OR10A2 4%
OR5D13 4%
HOXB3 5%
CTNNA2 10%
GBA3 5%
TUBB4Q 5%
INHBA 7%
DIO2 3%
OR2L2 5%
NELL1 8%
GALNT13 5%
PIP 3%
SULT1B1 3%
GNG2 2%
ARPP21 8%
DEFB112 2%
NLGN1 7%
UGT2B10 7%
TAS2R1 3%
PRIM2 4%
TBX3 4%
CYP4V2 4%
PI15 3%
DYTN 4%
OR6K6 3%
FCRL1 4%
TUBA3C 5%
DACH1 5%
NHEDC1 5%
FAM47B 9%
OR8K3 3%
NLRP14 10%
FSTL5 9%
OR51A7 4%
MARCO 6%
CRISP1 3%
POT1 5%
GPR65 3%
CDH12 10%
ANKRD7 3%
RIMS4 3%
TCTEX1D1 3%
DCLK3 6%
FGF14 3%
RIT2 3%
P2RY10 4%
FCGR3A 3%
ENPP3 5%
STXBP5L 8%
CCDC73 6%
OR4M1 5%
ZBBX 6%
OR4C12 3%
CNGA2 6%
CDH18 12%
ST6GALNAC3 3%
TKTL2 5%
AKR1B10 3%
TCEAL5 3%
KCNS2 4%
KRTAP8-1 2%
LIPI 4%
OR4D10 4%
OLFM3 4%
SAGE1 6%
OR2T8 4%
FOXI1 3%
HOXB1 3%
NPSR1 4%
LOC440563 3%
COL25A1 6%
SGIP1 7%
OR5M10 3%
RGS7 6%
SVOP 3%
SLC22A6 4%
NOVA1 4%
C2orf51 3%
POTEA 4%
CXCR7 3%
RBP2 2%
PTH 2%
PLD5 4%
PCDH11X 15% 55
ZNF257 6%
C8orf37 3%
50 40 30 20 10 0
mutations
0.5 2.0 3.5
-log10(q-value)
100
80
60
40
20
0
%
double_null
indel+null
A->mut
C->(T/G)
*Cp(A/C/T)->A
*CpG->A