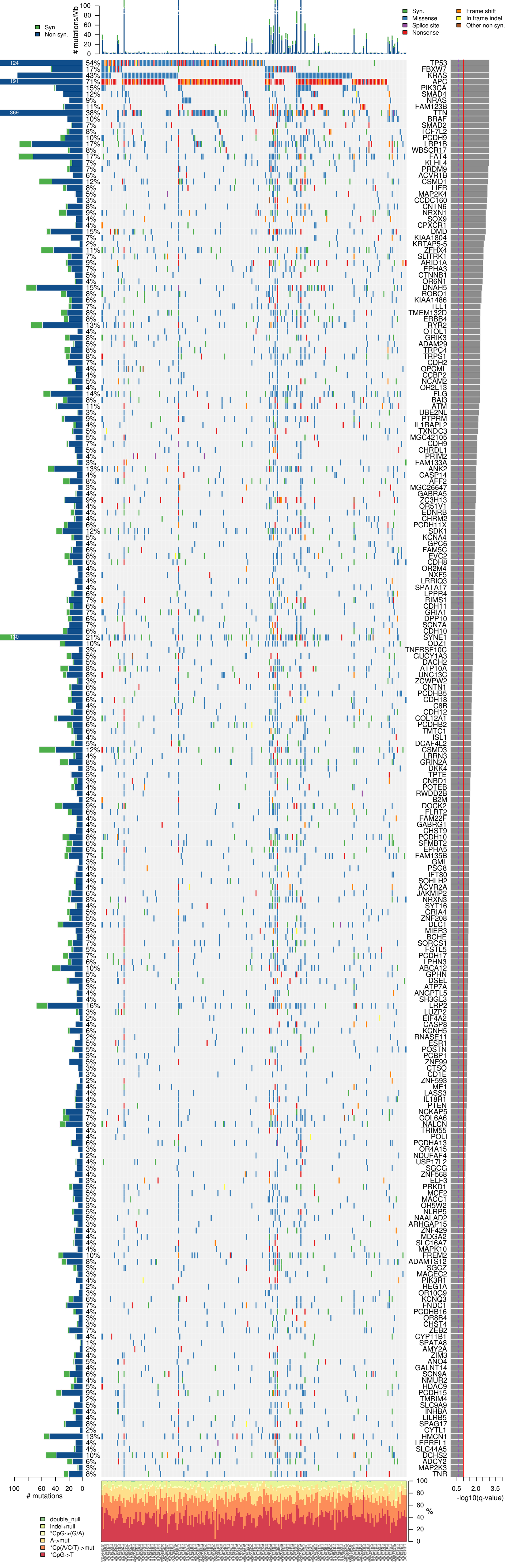
Syn.
Non syn.
mutations/Mb
100
80
60
40
20
0
Syn.
Missense
Splice site
Nonsense
Frame shift
In frame indel
Other non syn.
124
191
369
130
TP53 54%
FBXW7 17%
KRAS 43%
APC 71%
PIK3CA 15%
SMAD4 12%
NRAS 9%
FAM123B 11%
TTN 38%
BRAF 10%
SMAD2 7%
TCF7L2 8%
PCDH9 10%
LRP1B 17%
WBSCR17 8%
FAT4 17%
KLHL4 7%
PRDM9 7%
ACVR1B 6%
CSMD1 12%
LIFR 8%
MAP2K4 5%
CCDC160 3%
CNTN6 8%
NRXN1 9%
SOX9 4%
CPXCR1 4%
DMD 15%
KIAA1804 7%
KRTAP5-5 2%
ZFHX4 11%
SLITRK1 7%
ARID1A 9%
EPHA3 7%
CTNNB1 5%
OR6N1 4%
DNAH5 15%
ROBO1 8%
KIAA1486 6%
TLL1 7%
TMEM132D 8%
ERBB4 8%
RYR2 13%
OTOL1 4%
GRIK3 8%
ADAM29 5%
TRPC4 8%
TRPS1 8%
CDH2 7%
OPCML 4%
CCBP2 4%
NCAM2 5%
OR2L13 4%
FLG 14%
BAI3 8%
ATM 11%
UBE2NL 3%
PTPRM 9%
IL1RAPL2 4%
TXNDC3 5%
MGC42105 5%
CDH9 7%
CHRDL1 5%
PRIM2 4%
FAM133A 3%
ANK2 13%
CASP14 4%
AFF2 8%
MGC26647 3%
GABRA5 4%
ZC3H13 9%
OR51V1 4%
EDNRB 4%
CHRM2 4%
PCDH11X 6%
SDK1 12%
KCNA4 5%
GPC6 4%
FAM5C 6%
EVC2 8%
CDH8 6%
OR2M4 4%
NXF5 3%
LRRIQ3 4%
SPATA17 4%
LPPR4 6%
RIMS1 7%
CDH11 6%
GRIA1 7%
DPP10 6%
SCN7A 7%
CDH10 6%
SYNE1 21%
ODZ1 10%
TNFRSF10C 3%
GUCY1A3 5%
DACH2 5%
ATP10A 8%
UNC13C 8%
ZCWPW2 3%
CNTN1 6%
PCDHB5 6%
CDH18 6%
C8B 4%
CDH12 6%
COL12A1 9%
PCDHB2 6%
TMTC1 6%
ISL1 4%
DCAF4L2 5%
CSMD3 12%
LRRN3 4%
GRIN2A 8%
DKK4 3%
TPTE 5%
CNBD1 3%
POTEB 4%
RWDD2B 4%
B2M 2%
DOCK2 9%
FLRT2 6%
FAM22F 4%
GABRG1 4%
CHST9 4%
PCDH10 8%
SFMBT2 6%
EPHA5 6%
FAM135B 7%
GML 3%
PSG8 4%
IFT80 4%
SOHLH2 4%
ACVR2A 4%
JAKMIP2 6%
NRXN3 8%
SYT16 4%
GRIA4 5%
ZNF208 5%
DLC1 9%
MIER3 5%
BCHE 4%
SORCS1 7%
FSTL5 5%
PCDH17 7%
LPHN3 6%
ABCA12 10%
GPHN 5%
DSEL 6%
ATP7A 3%
ANGPTL5 4%
SH3GL3 4%
LRP2 16%
LUZP2 3%
EIF4A2 2%
CASP8 4%
KCNH5 6%
RNASE11 2%
ESR1 5%
POSTN 5%
PCBP1 3%
ZNF99 5%
CTSO 3%
CD1E 3%
ZNF593 2%
ME1 4%
LASS3 4%
IL18R1 4%
PTEN 3%
NCKAP5 7%
COL6A6 7%
NALCN 9%
TRIM55 4%
POLI 4%
PCDHA13 6%
OR4A15 3%
NDUFAF4 2%
USP17L2 4%
SGCG 3%
ZNF568 4%
ELF3 3%
PRKD1 5%
MCF2 5%
MACC1 5%
OR5W2 3%
NLRP5 5%
NAALAD2 5%
ARHGAP15 3%
ZNF429 4%
MDGA2 4%
SLC16A7 4%
MAPK10 4%
FREM2 10%
ADAMTS12 8%
SGCZ 3%
MAGEC2 3%
PIK3R1 4%
REG1A 2%
OR10G9 3%
KCNQ3 6%
FNDC1 7%
PCDHB16 4%
OR8B4 3%
CHST4 3%
ZEB2 7%
CYP11B1 4%
SPATA8 1%
AMY2A 2%
ZIM3 4%
ANO4 5%
GALNT14 4%
SCN9A 6%
NMUR2 4%
HDAC9 5%
PCDH15 9%
TMBIM4 2%
SLC9A9 5%
INHBA 4%
LILRB5 4%
SPAG17 8%
CYTL1 2%
HMCN1 13%
LEPREL1 4%
SLC44A5 4%
DCHS2 10%
ADCY2 6%
MAP2K3 3%
TNR 8%
100
60
40
20
0
mutations
0.5
2.0
3.5
-log10(q-value)
100
80
60
40
20
0
%
double_null
indel+null
*CpG->(G/A)
A->mut
*Cp(A/C/T)->mut
*CpG->T