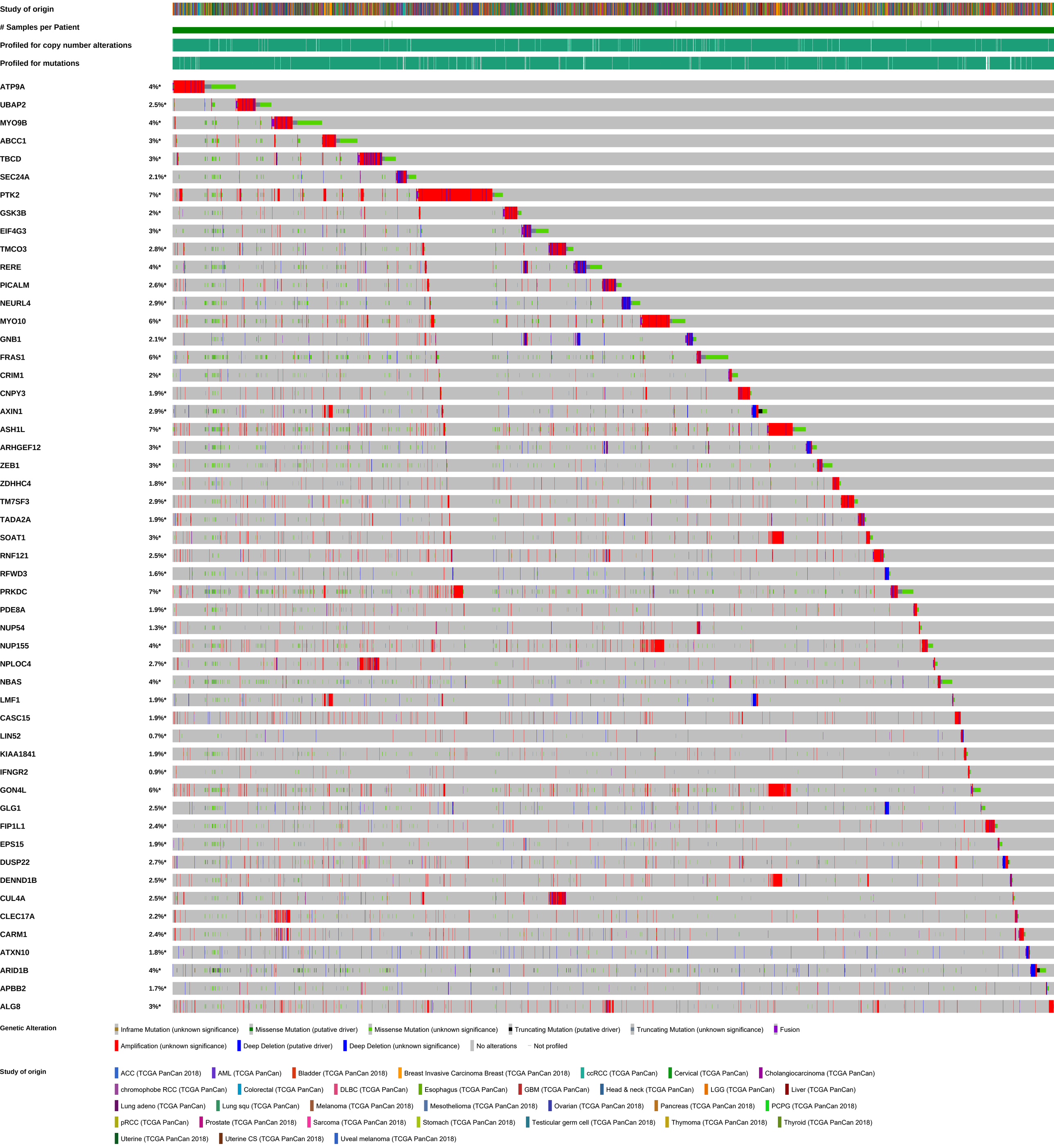
Study of origin
Samples per Patient
Profiled for copy number alterations
Profiled for mutations
ATP9A 4%*
UBAP2 2.5%*
MYO9B 4%*
ABCC1 3%*
TBCD 3%*
SEC24A 2.1%*
PTK2 7%*
GSK3B 2%*
EIF4G3 3%*
TMCO3 2.8%*
RERE 4%*
PICALM 2.6%*
NEURL4 2.9%*
MYO10 6%*
GNB1 2.1%*
FRAS1 6%*
CRIM1 2%*
CNPY3 1.9%*
AXIN1 2.9%*
ASH1L 7%*
ARHGEF12 3%*
ZEB1 3%*
ZDHHC4 1.8%*
TM7SF3 2.9%*
TADA2A 1.9%*
SOAT1 3%*
RNF121 2.5%*
RFWD3 1.6%*
PRKDC 7%*
PDE8A 1.9%*
NUP54 1.3%*
NUP155 4%*
NPLOC4 2.7%*
NBAS 4%*
LMF1 1.9%*
CASC15 1.9%*
LIN52 0.7%*
KIAA1841 1.9%*
IFNGR2 0.9%*
GON4L 6%*
GLG1 2.5%*
FIP1L1 2.4%*
EPS15 1.9%*
DUSP22 2.7%*
DENND1B 2.5%*
CUL4A 2.5%*
CLEC17A 2.2%*
CARM1 2.4%*
ATXN10 1.8%*
ARID1B 4%*
APBB2 1.7%*
ALG8 3%*
Genetic Alteration
Inframe Mutation (unknown significance)
Missense Mutation (putative driver)
Missense Mutation (unknown significance)
Truncating Mutation (putative driver)
Truncating Mutation (unknown significance)
Fusion
Amplification (unknown significance)
Deep Deletion (putative driver)
Deep Deletion (unknown significance)
No alterations
Not profiled
Study of origin
ACC (TCGA PanCan 2018)
AML (TCGA PanCan)
Bladder (TCGA PanCan 2018)
Breast Invasive Carcinoma Breast (TCGA PanCan 2018)
ccRCC (TCGA PanCan)
Cervical (TCGA PanCan)
Cholangiocarcinoma (TCGA PanCan)
chromophobe RCC (TCGA PanCan)
Colorectal (TCGA PanCan)
DLBC (TCGA PanCan)
Esophagus (TCGA PanCan)
GBM (TCGA PanCan)
Head & neck (TCGA PanCan)
LGG (TCGA PanCan)
Liver (TCGA PanCan)
Lung adeno (TCGA PanCan)
Lung squ (TCGA PanCan)
Melanoma (TCGA PanCan 2018)
Mesothelioma (TCGA PanCan 2018)
Ovarian (TCGA PanCan 2018)
Pancreas (TCGA PanCan 2018)
PCPG (TCGA PanCan 2018)
pRCC (TCGA PanCan)
Prostate (TCGA PanCan 2018)
Sarcoma (TCGA PanCan 2018)
Stomach (TCGA PanCan 2018)
Testicular germ cell (TCGA PanCan 2018)
Thymoma (TCGA PanCan 2018)
Thyroid (TCGA PanCan 2018)
Uterine (TCGA PanCan 2018)
Uterine CS (TCGA PanCan 2018)
Uveal melanoma (TCGA PanCan 2018)
Samples per Patient
0
2
Profiled for copy number alterations
Yes
No
Profiled for mutations
Yes
No