

BPA-3 - BPA-3-high_conf_snvs

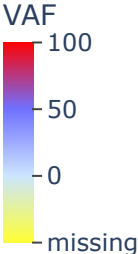
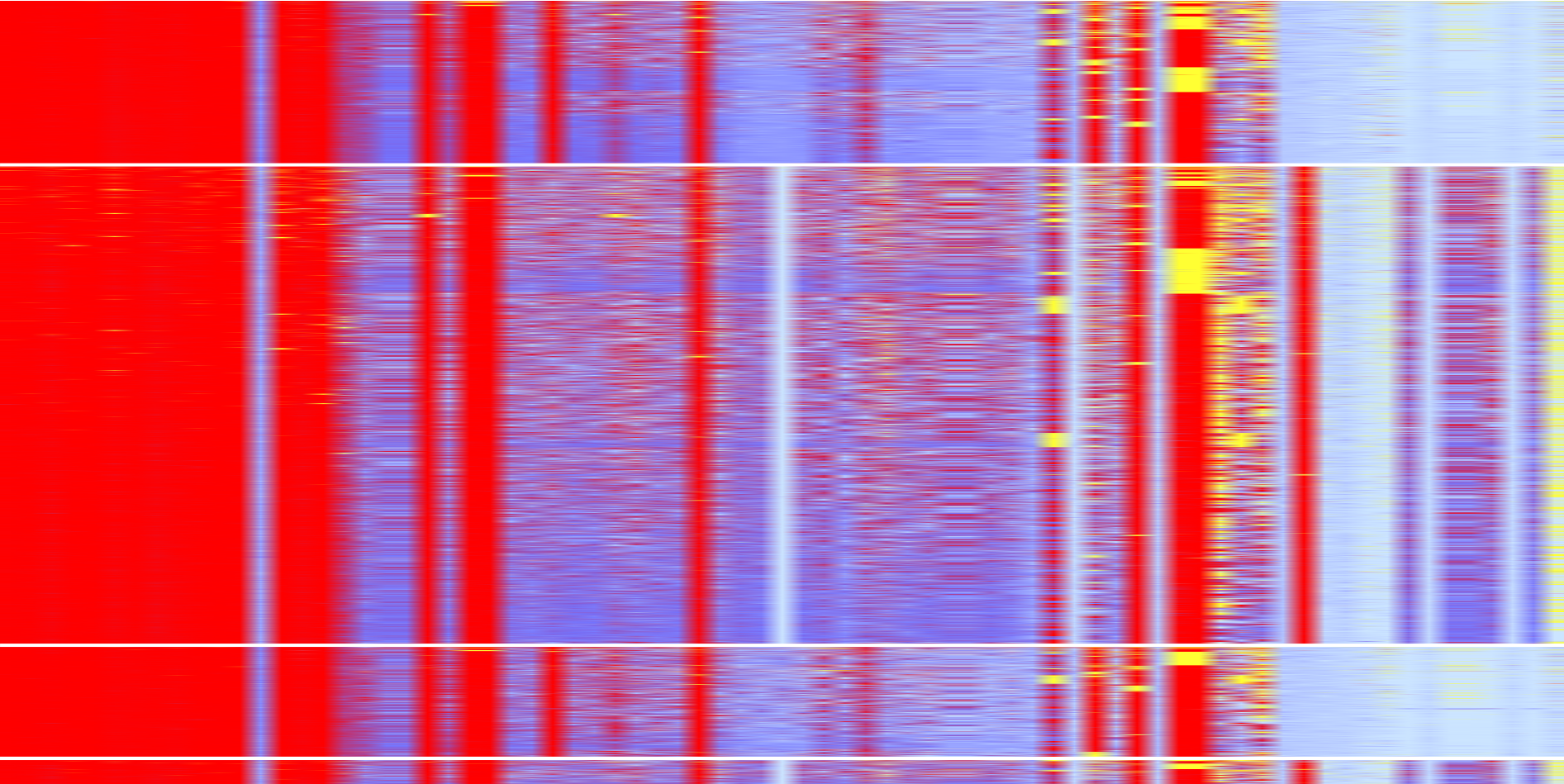
7493 cells, 75 features

CN_clone-4 20.9%

CN_clone-3 61.3%

CN_clone-2 14.4%

CN_clone-1 3.3%



PIK3CA intron_variant
FANCI p.Gly1302=
BMPR1B intron_variant
CHEK2 intron_variant
MGMT p.Leu84Phe
MGMT p.Leu53=
MLH3 intron_variant
FLT1 p.Tyr1273=
MTOR p.Ile313Thr
ERCC3 p.Ser90Phe
TGFBRT intron_variant
BMPR2 intron_variant
TP53 intron_variant
KMT2C intron_variant
BMPR1A p.Pro2Thr
MEN1 p.Asp418=
SETD2 intron_variant
PLXNB2 p.Lys318Glu
PLXNB2 intron_variant
BMPR1B intron_variant
BRCA2 p.Leu1521=
MUS81 p.Arg350Trp
AKT1 intron_variant
KMT2C intron_variant
MEN1 p.His433=
SPTA1 p.Cys1568Arg
RNFA43 p.Ile47Val
ACVR2A p.Pro118=
PAK5 intron_variant
PAK5 intron_variant
TP63 intron_variant
ERBB2 p.Ile655Val
PTPR1 intron_variant
MTOR p.Ala1577=
PAXIP1 p.Ala458dup
PAXIP1 p.Pro415=
RPL22 intron_variant
ARID1B p.Ser2117=
SLX4 intron_variant
AKT2 intron_variant
DNMT3B intron_variant
STK11 intron_variant
BMPR1A intron_variant
BMPR1A intron_variant
AURKA intron_variant
RECQL5 p.Asp480Gly
KMT2C p.Pro4033=
KMT2C p.Thr1636=
PARP2 intron_variant
TP53 intron_variant
GNAS p.Ile828=
PARP4 intron_variant
PARP4 p.Ser534=
TTK intron_variant
RECQL5 p.Tyr471=
DNMT3B p.Asp627=
DNMT3B intron_variant
KMT2D p.Gly2493=
RICTOR intron_variant
TP53 p.Pro72Arg
EPHA2 intron_variant
HFM1 p.Ile117Val
ERBB2 intron_variant
PBRM1 intron_variant
RPL22 intron_variant
KRAS p.Arg161=
MTOR p.Asn999=
FAT1 p.Gln2933Pro
KAT5 intron_variant
KDR intron_variant
CDKN2A_3_prime_UTR_variant
PARP1 intron_variant
CARD11 intron_variant
TP53 intron_variant
CUL5_5_prime_UTR_variant

