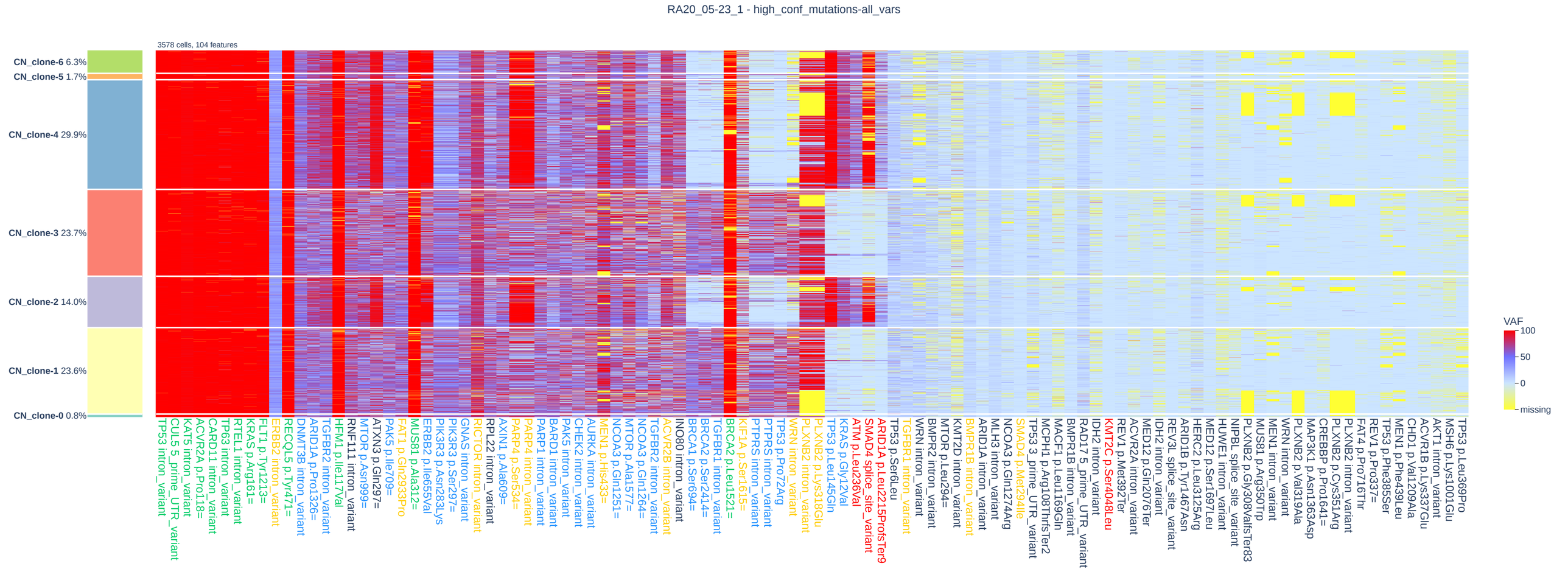
RA20_05-23_1 - high_conf_mutations-all_vars
3578 cells, 104 features
CN_clone-6 6.3%
CN_clone-5 1.7%
CN_clone-4 29.9%
CN_clone-3 23.7%
CN_clone-2 14.0%
CN_clone-1 23.6%
CN_clone-0 0.8%
TP53 intron_variant
CUL5 5_prime_UTR_variant
KAT5 intron_variant
ACVR2A p.Pro118=
CARD11 intron_variant
TP63 intron_variant
RTEL1 intron_variant
KRAS p.Arg161=
FLT1 p.Tyr1213=
ERBB2 intron_variant
RECQL5 p.Tyr471=
DNMT3B intron_variant
ARID1A p.Pro1326=
TGFBR2 intron_variant
HFM1 p.Ile117Val
RNF111 intron_variant
MTOR p.Asn999=
ATXN3 p.Gln297=
PAK5 p.Ile709=
FAT1 p.Gln2933Pro
MUS81 p.Ala312=
ERBB2 p.Ile655Val
PIK3R3 p.Asn283Lys
PIK3R3 p.Ser297=
GNAS intron_variant
RICTOR intron_variant
RPL22 intron_variant
AXIN1 p.Ala609=
PARP4 p.Ser534=
PARP4 intron_variant
PARP1 intron_variant
BARD1 intron_variant
PAK5 intron_variant
CHEK2 intron_variant
AURKA intron_variant
MEN1 p.His433=
NCOA3 p.Gln1251=
MTOR p.Ala1577=
NCOA3 p.Gln1264=
TGFBR2 intron_variant
ACVR2B intron_variant
INO80 intron_variant
BRCA1 p.Ser694=
BRCA2 p.Ser2414=
TGFBR1 intron_variant
BRCA2 p.Leu1521=
KIF1A p.Ser1615=
PTPRS intron_variant
TP53 p.Pro72Arg
TGFBR1 intron_variant
TP53 p.Ser6Leu
ARID1A p.Leu2215ProfsTer9
SMAD4 splice_site_variant
ATM p.Leu236Val
KRAS p.Gly12Val
TP53 p.Leu145Gln
PLXNB2 p.Lys318Glu
WRN intron_variant
KMT2D intron_variant
MTOR p.Leu294=
BMPR2 intron_variant
WRN intron_variant
MLH3 intron_variant
ARID1A intron_variant
NCOA3 p.Gln1274Arg
SMAD4 p.Met294Ile
TP53 3_prime_UTR_variant
MCPH1 p.Arg108ThrfsTer2
MACF1 p.Leu1169Gln
BMPR1B intron_variant
RAD17 5_prime_UTR_variant
IDH2 intron_variant
KMT2C p.Ser4048Leu
REV1 p.Met392Ter
ACVR2A intron_variant
MED12 p.Gln2076Ter
IDH2 intron_variant
REV3L splice_site_variant
ARID1B p.Tyr1467Asn
HERC2 p.Leu3125Arg
MED12 p.Ser1697Leu
HUWE1 intron_variant
NIPBL splice_site_variant
PLXNB2 p.Gly308ValfsTer83
MUS81 p.Arg350Trp
MEN1 intron_variant
WRN intron_variant
PLXNB2 p.Val319Ala
MAP3K1 p.Asn1363Asp
CREBBP p.Pro1641=
PLXNB2 intron_variant
PLXNB2 p.Cys351Arg
FAT4 p.Pro716Thr
REV1 p.Pro337=
TP53 p.Phe385Ser
MEN1 p.Phe439Leu
CHD1 p.Val1209Ala
ACVR1B p.Lys337Glu
AKT1 intron_variant
MSH6 p.Lys1001Glu
TP53 p.Leu369Pro
VAF
100
50
0
missing