

RA19\_21 - RA19\_21-high\_conf\_snvs

6035 cells, 82 features

CN\_clone-5 7.3%

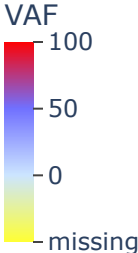
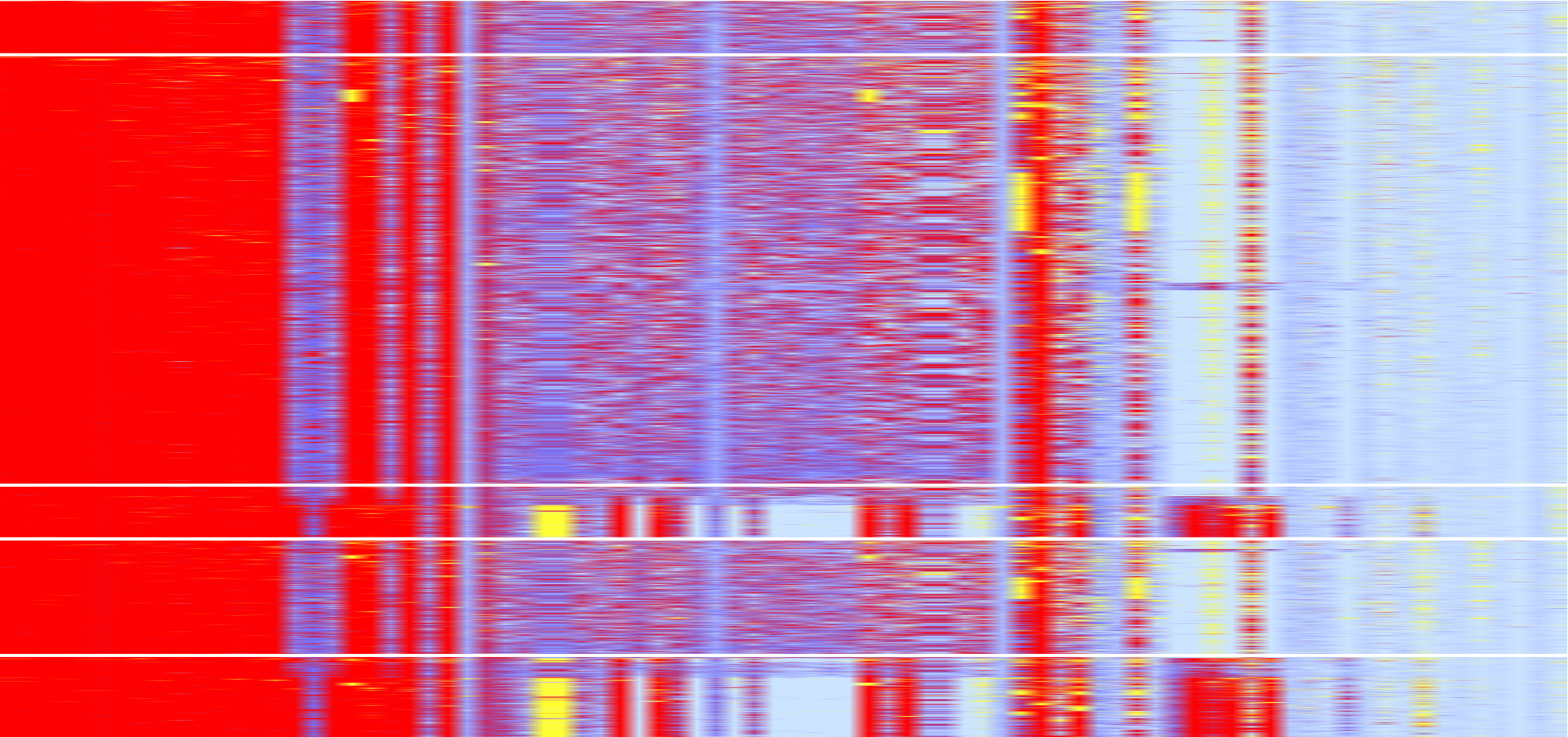
CN\_clone-4 58.5%

CN\_clone-3 7.3%

CN\_clone-2 0.0%

CN\_clone-1 15.8%

CN\_clone-0 11.1%



ARID1A intron variant  
ARID1A p.His544Arg  
CTNNA2 p.Arg136His  
MLH3 intron variant  
BMPR2 intron variant  
BMPR1B intron variant  
PAXIP1 p.Gln413del  
NCOA3 p.Gln1255=  
PAXIP1 p.Gln434del  
FAT3 intron variant  
TGFBRI intron variant  
PIK3CA p.Glu545Lys  
SMAD4 p.Met294Ile  
TP53 p.Ser6Leu  
BMPR1B intron variant  
SMAD2 p.Ser306Ter  
SMAD4 p.Trp524Ter  
RREB1 p.Ala429=  
IRF6 p.Arg84His  
RNF43 p.Arg337Ter  
KRAS p.Gln61His  
BMPR2 intron variant  
MEN1 p.Asp418=  
KMT2C intron variant  
CTNNA3 intron variant  
MED12 p.Pro1310=  
MUS81 p.Ala312=  
BRCA2 p.Leu1521=  
MEN1 p.His433=  
SMAD4 intron variant  
WRN intron variant  
CHEK2 intron variant  
PTPRS intron variant  
PTPRS intron variant  
RNFE43 p.Arg117His  
TGFBRI intron variant  
RECQL5 p.Asp480Gly  
PAK5 p.Ile709=  
PTPRD p.Ala1194=  
RPL22 intron variant  
BRCA2 p.Ser2414=  
RREB1 p.His338=  
FAT1 p.Gln2933Pro  
KMT2C intron variant  
FLT1 p.Tyr1213=  
PIK3CA intron variant  
EPHA2 intron variant  
SPEN intron variant  
PARP4 intron variant  
BARDD1 intron variant  
TTK intron variant  
CDKN2A\_3\_prime\_UTR\_variant  
CDKN2A\_3\_prime\_UTR\_variant  
TGFBRI intron variant  
ATXN3 p.Gln297=  
RICTOR intron variant  
SMAD4 intron variant  
SMAD4 intron variant  
MTOR p.Ala1577=  
EHMT2 intron variant  
TP53 p.Pro722Arg  
KMT2D p.Gly2493=  
HEM1 p.Ile117Val  
RECQL5 p.Tyr471=  
DNMT3B intron variant  
SPTA1 p.Cys1568Arg  
BRCA1 p.Ser694=  
PARP4 p.Ser534=  
AURKA intron variant  
FANCI p.Gly1302=  
PARP1 intron variant  
KRAS p.Arg161=  
TP63 intron variant  
PBRM1 intron variant  
MTOR p.Asn999=  
SMARCA4 intron variant  
REV3L p.Val3064Ile  
REV3L p.Arg3073=  
CUL5\_5\_prime\_UTR\_variant  
TP53 intron variant  
PIK3R3 p.Asn283Lys  
PIK3R3 p.Ser297=