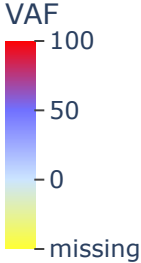
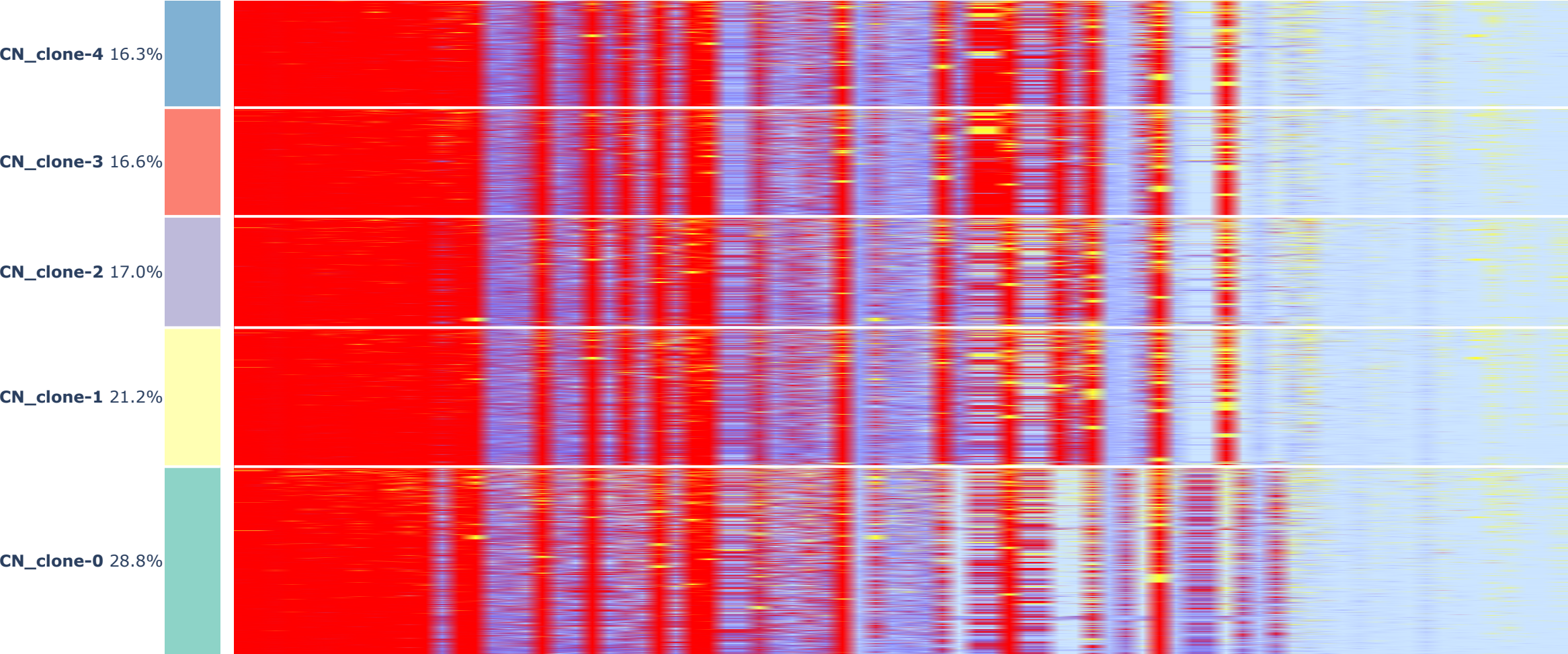


RA15\_06 - high\_conf\_snvs\_pre\_condor\_clone\_assignment

4977 cells, 80 features



G2E3 p.Ser456=  
ARHGAP35 p.Ser1127Pro  
DNMT3A p.Leu889Pro  
MYC p.Ser362Cys  
ARID1B intron variant  
FLT1 p.Phe1228Ser  
REV1 p.Met392Ter  
TGFBFR1 intron variant  
RAD17 splice site variant  
ATM intron variant  
CTNNB1 intron variant  
MCPH1 p.Arg108ThrfsTer2  
MLH3 intron variant  
SMAD4 p.Met294Ile  
PAXIP1 p.Gln413del  
TP53 p.Ser6Leu  
BMPR2 intron variant  
PBRM1 intron variant  
KMT2C intron variant  
ARID1B p.Ile2014=  
SMAD4 p.Arg420Cys  
TP53 intron variant  
BMPR1B intron variant  
BRCA2 p.Leu1521=  
KRAS p.Gly12Val  
BRAD1 intron variant  
SMAD4 intron variant  
AKT1 intron variant  
ARID1A p.Asp1975ValfsTer23  
TP53 p.Gln136Glu  
PTPRS intron variant  
PTPRS intron variant  
TP53 p.Pro72Arg  
PARP4 intron variant  
PARP4 p.Ser534=  
RTEL1 intron variant  
WRN intron variant  
NUF2 intron variant  
CHEK2 p.Glu84=  
SPTA1 p.Cys1568Arg  
RECQL5 p.Asp480Gly  
SMAD4 intron variant  
TGFBFR2 intron variant  
POLN p.Gln121His  
AURKA intron variant  
KDR intron variant  
RNF43 p.Ile47Val  
RICTOR intron variant  
PAK5 intron variant  
PAK5 intron variant  
TTK intron variant  
MTOR p.Ala1577=  
EPHA2 intron variant  
HFM1 p.Ile117Val  
AXIN1 p.Ala609=  
TGFBFR1 intron variant  
NCOA3 p.Gln1264=  
FLT1 p.Tyr1213=  
NCOA3 p.Gln1251=  
RNF43 p.Arg343His  
MUS81 p.Ala312=  
PAK5 p.Ile709=  
SLX4 intron variant  
BRCA1 p.Ser694=  
RECQL5 p.Tyr471=  
KMT2D p.Gly2493=  
TGFBFR2 intron variant  
KRAS p.Arg161=  
TP63 intron variant  
CARD11 intron variant  
TP53 intron variant  
PARP1 intron variant  
FANCI p.Gly1302=  
MTOR p.Asn999=  
FAT1 p.Gln2933Pro  
CUL5 prime\_UTR\_variant  
KAT5 intron variant  
PK3R3 p.Asn283Lys  
PK3R3 p.Ser297=