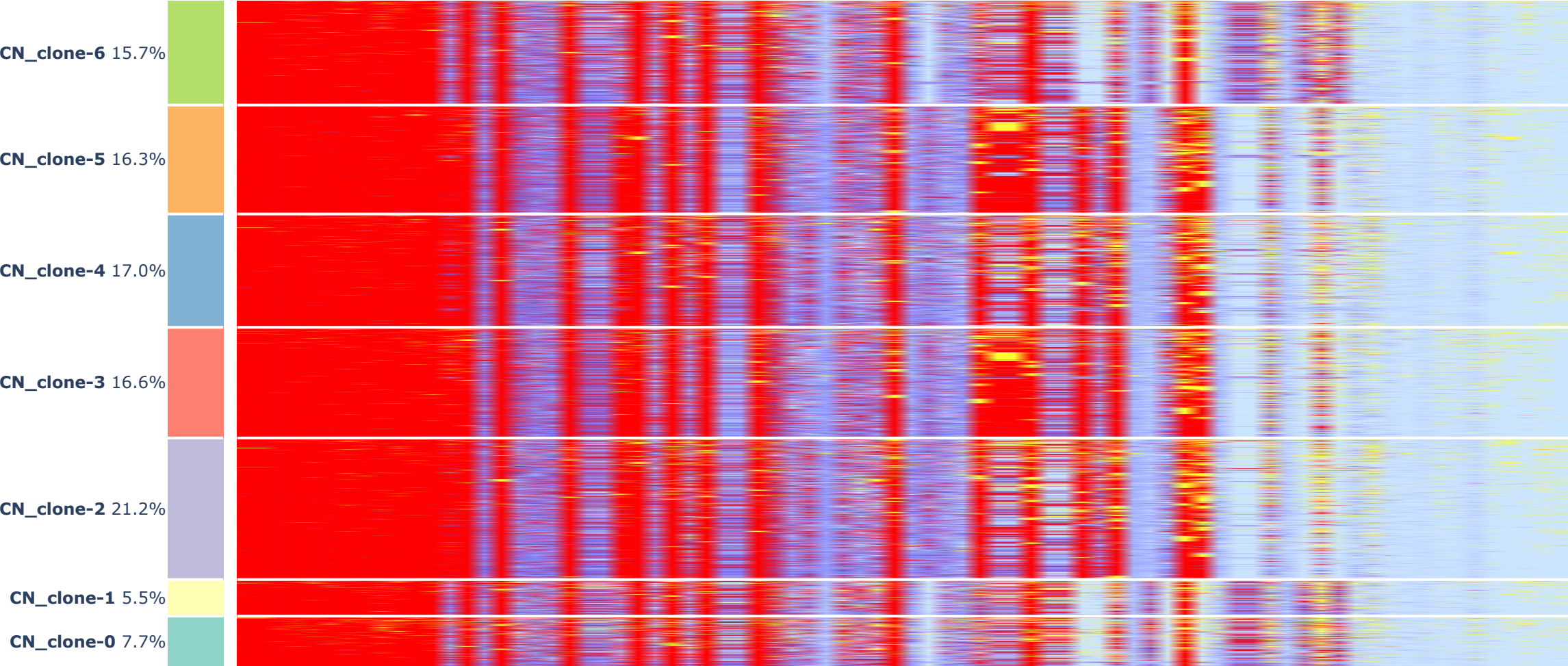


RA15_06 - RA15_06-high_conf_snvs

4977 cells, 78 features



G2E3 p. Ser456=
DNMT3A p. Leu889Pro
MYC p. Ser362Cys
FLT1 p. Phe1228Ser
TGFBF1 intron variant
RAD17 splice site variant
CTNNB1 intron variant
MCPH1 p. Arg108ThrfsTer2
MLH3 intron variant
SMAD4 p. Met294Ile
PAXIP1 p. Gln413del
TP53 p. Ser6Leu
BMPR2 intron variant
BMR1 intron variant
POLE intron variant
ARID1B p. Ile2014=
KMT2C intron variant
NRAS p. Ala59Gly
TP53 intron variant
TP53 intron variant
BMPR1B intron variant
SMAD4 p. Arg420Cys
BRCA2 p. Leu1521=
KRAS p. Gly12Val
BARD1 intron variant
SMAD4 intron variant
AKT1 intron variant
ARID1A p. Asp1975ValfsTer23
TP53 p. Gln136Glu
PTPRS intron variant
PTPRS intron variant
TP53 p. Pro722Arg
PARP4 intron variant
PARP4 p. Ser534=
WRN intron variant
NFE2 intron variant
CHEK2 p. Glu84=
RTEL1 intron variant
SPTA1 p. Cys1568Arg
TGFBF2 intron variant
RECQL5 p. Asp480Gly
POLN p. Gln121His
AURKA intron variant
SMAD4 intron variant
KDR intron variant
RNF43 p. Ile47Val
RICTOR intron variant
TTK intron variant
PAK5 intron variant
PAK5 intron variant
MTOR p. Ala1577=
EPHA2 intron variant
HFM1 p. Ile117Val
AXIN1 p. Ala609=
FLT1 p. Tyr1213=
TGFBF1 intron variant
NCOA3 p. Gln1264=
NCOA3 p. Gln1251=
MUS81 p. Ala312=
RNF43 p. Arg343His
SLX4 intron variant
PAK5 p. Ile709=
RECQL5 p. Tyr471=
BRCA1 p. Ser694=
KMT2D p. Gly2493=
TGFBF2 intron variant
KRAS p. Arg161=
TP53 intron variant
CARD11 intron variant
TP63 intron variant
MTOR p. Asn999=
PARP1 intron variant
FANCI p. Gly1302=
FAT1 p. Gln2933Pro
CUL5 prime UTR variant
KAT5 intron variant
PIK3R3 p. Ser297=
PIK3R3 p. Asn283Lys

