

RA19\_02 - high\_conf\_snvs\_pre\_condor\_clone\_assignment

4762 cells, 76 features

CN\_clone-3 14.5%

CN\_clone-2 23.7%

CN\_clone-1 18.8%

CN\_clone-0 43.0%

SACS p.Ala424Val  
FANCD2 intron\_variant  
CHD4 intron\_variant  
WRN intron\_variant  
CTNNB1 intron\_variant  
CDH1 intron\_variant  
PIK3CA intron\_variant  
NCOA3 p.Gln1274Arg  
REV3L splice site\_variant  
BMPR1B intron\_variant  
NCOA3 p.Gln1255=  
RICTOR intron\_variant  
SMAD4 p.Met294Ile  
FAT3 intron\_variant  
TGFBFR1 intron\_variant  
SETD2 intron\_variant  
EHMT2 intron\_variant  
NRAS p.Ala59Gly  
INO80 intron\_variant  
TP53 p.Pro72Arg  
SMAD4 intron\_variant  
PTPRD p.Ala1194=  
BRCA2 p.Leu1521=  
RREB1 p.Ala429=  
SMAD4 intron\_variant  
INPL1 p.Leu204=  
AKT1 intron\_variant  
PLXNB2 intron\_variant  
PLXNB2 p.Lys318Glu  
SMAD4 p.Ser144Ter  
MUS81 p.Ala312=  
MUS81 intron\_variant  
KRAS p.Gly12Val  
TP53 p.Ser241Cys  
SPTA1 p.Cys1568Arg  
RREB1 p.His338=  
AXIN1 p.Ala609=  
PARP4 intron\_variant  
PARP4 p.Ser534=  
RTEL1 intron\_variant  
PMS2 p.Arg20Gln  
MTOR p.Ala1577=  
FANCA intron\_variant  
BMPR1A intron\_variant  
PTPRS intron\_variant  
PTPRS intron\_variant  
BRCA2 p.Ser2414=  
IDH1 p.Gly105=  
WRN intron\_variant  
KAT5 intron\_variant  
HEM1 p.Ile117Val  
HEM1 p.Ser115Pro  
RECQL5 p.Tyr471=  
DNMT3B intron\_variant  
ELT1 p.Tyr1213=  
FANCI p.Gly1302=  
RPL22 intron\_variant  
RICTOR intron\_variant  
PAK5 p.Ile709=  
TGFBFR1 intron\_variant  
FAT1 p.Gln2933Pro  
RNF43 p.His697=  
TGFBFR2 p.Asn389=  
TP53 intron\_variant  
TP53 intron\_variant  
TP63 intron\_variant  
BRCA1 p.Ser694=  
PBRM1 intron\_variant  
MTOR p.Asn999=  
KRAS p.Arg161=  
CARD11 intron\_variant  
PIK3R3 p.Asn283Lys  
PIK3R3 p.Ser297=  
TP53 intron\_variant  
CUL5\_5\_prime\_UTR\_variant  
RNF111 intron\_variant

