

M07 - M07-high_conf_snvs

3993 cells, 63 features

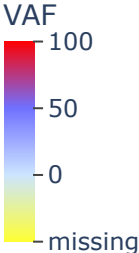
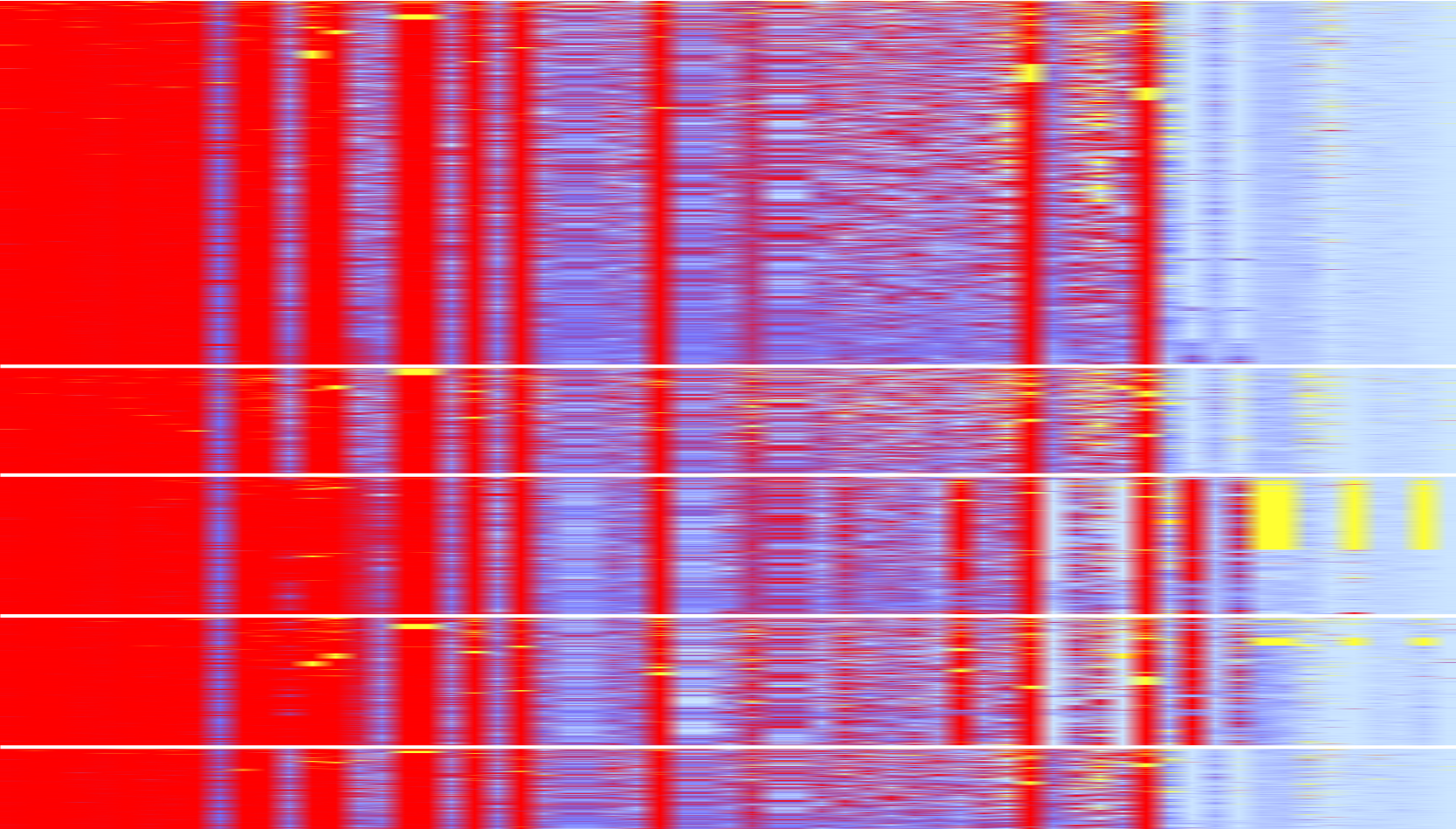
CN_clone-6 44.1%

CN_clone-5 13.1%

CN_clone-2 17.0%

CN_clone-1 15.8%

CN_clone-0 10.0%



FANCD2 intron_variant
SMAD4 intron_variant
BMPR1B intron_variant
ATXN3 p.Gln305del
SMAD4 p.Met294Ile
FAT3 intron_variant
BMPR2 intron_variant
SMAD4 intron_variant
SMAD4 intron_variant
KRAS p.Gly12Asp
KMT2C intron_variant
TP53 p.Cys242Tyr
SPRED1 5_prime_UTR_variant
BRCA2 p.Leu152T=
RECQL5 p.Asp480Gly
STK11 intron_variant
MUS81 p.Ala312=
BRCA1 p.Ser694=
AKT1 intron_variant
GATA6 p.Gly15Arg
AURKA intron_variant
RNF43 p.Ile47Val
RPL22 intron_variant
PBRM1 intron_variant
TP63 intron_variant
PARP2 intron_variant
CHEK2 intron_variant
RPL22 intron_variant
PARP4 intron_variant
PARP4 p.Ser534=
RICTOR intron_variant
RNF111 intron_variant
CDKN2A 3_prime_UTR_variant
CDKN2A 3_prime_UTR_variant
TP53 p.Pro72Arg
RTEL1 intron_variant
ACVR2B intron_variant
PIK3R3 p.Ser297=
PIK3R3 p.Asn283Lys
CARD11 intron_variant
MTOR p.Ala1577=
KMT2D p.Gly2493=
HFM1 p.Ile117Val
POLN p.Gln121His
PTPRS intron_variant
PTPRS intron_variant
RAD51AP1 p.Ser223=
MYC p.Asn26Ser
RECQL5 p.Tyr471=
NKK2-1 5_prime_UTR_variant
TP53 p.Pro222=
TTK intron_variant
KRAS p.Arg161=
SPTA1 p.Cys1568Arg
FLT1 p.Tyr1213=
FANCI p.Gly1302=
MTOR p.Asn999=
ACVR2A p.Pro118=
KAT5 intron_variant
FAT1 p.Gln2933Pro
TP53 intron_variant
CUL5 5_prime_UTR_variant
DNMT3B intron_variant

