

Indels → ...

Sequencing Data
(bcf.vcf output of bcftools mpileup)

SNPs

on masterlist?

YES

potential cluster!!

varfreq < 20%

varfreq > 20%

is it even necessary
to distinguish
here???

on BCFtool call
list?

NO

YES

in frequency cluster?

YES

NO

Recombination

semi safe

check in previous/ next timestep, if clusters overlap and how varfreq changes!

in frequency cluster?

NO

YES

Recombination

safe

NO

potential de novo mutation

varfreq < 20%

varfreq > 20%

on GATK list?

YES

NO

De Novo

semi safe de novo mutation!

check in previous/ next timestep, if mutation is real

on BCFtool call/
GATK list?

NO

YES

De Novo

relatively safe de novo mutation!

keep for comparison
with later timepoints

keep for comparison
with later timepoints