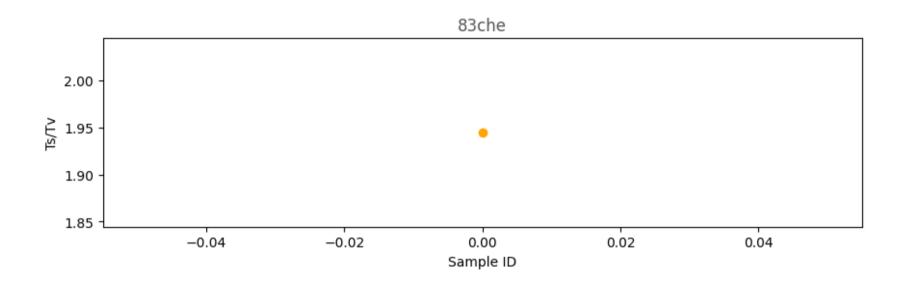
Summary Numbers

| | SNPs | | | indels | | MNPs | others | | |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | |
| 83che | 4,065,728 | 1.94 | 1.95 | 936,036 | _ | 0 | 0 | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | |

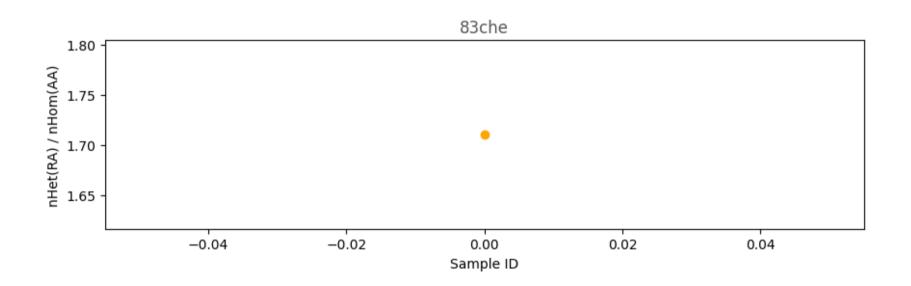
| | singl | etons (A | multiallelic | | |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 83che | 63.1% | 1.92 | 67.2% | 92,673 | 2,041 |

- 83che../ngc/projects2/gm/data/archive/2022/variants/snv/83cheritf-103891071749-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220713_A01176_AHMWJGDSX3-RHGM_LABKA_WGSA KUT-WGSAKUT04612_22RKG016697x01_snv_germline_raw.haplotype_caller.vcf.gz

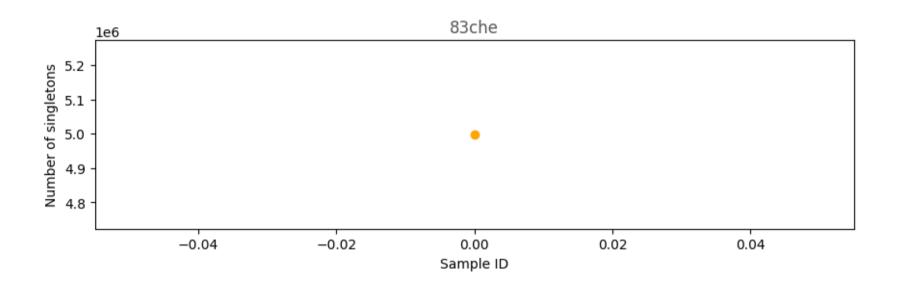
Ts/Tv by sample



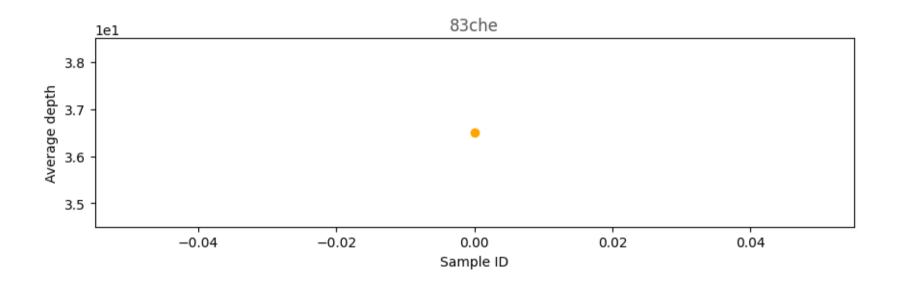
Hets vs non-ref Homs by sample



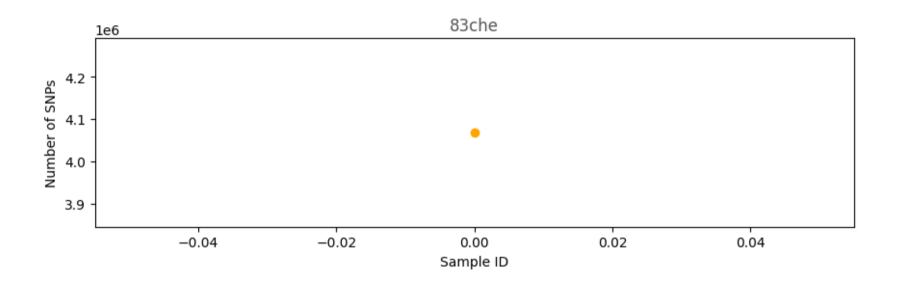
Singletons by sample (hets and homs)



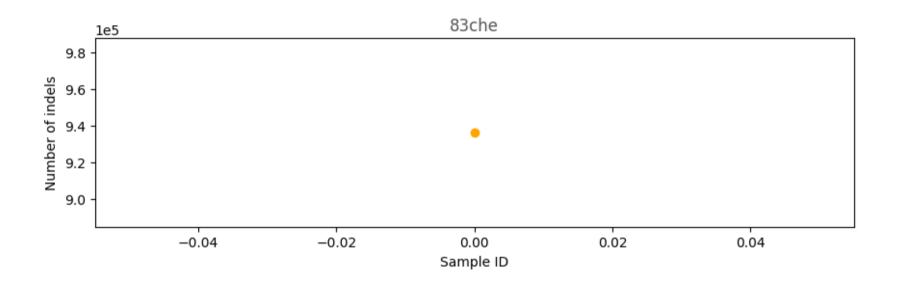
Average depth by sample



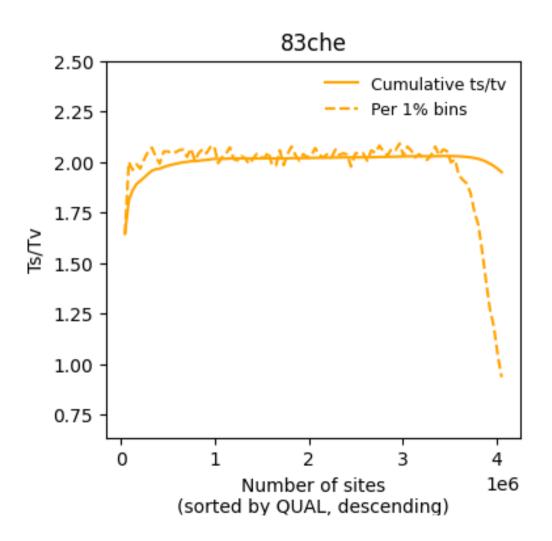
Number of SNPs by sample



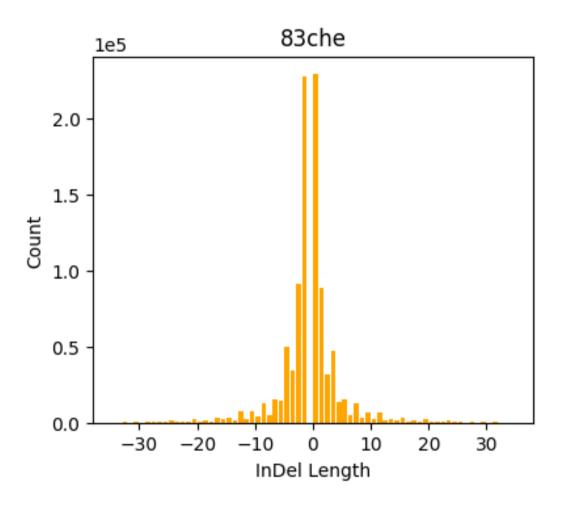
Number of indels by sample



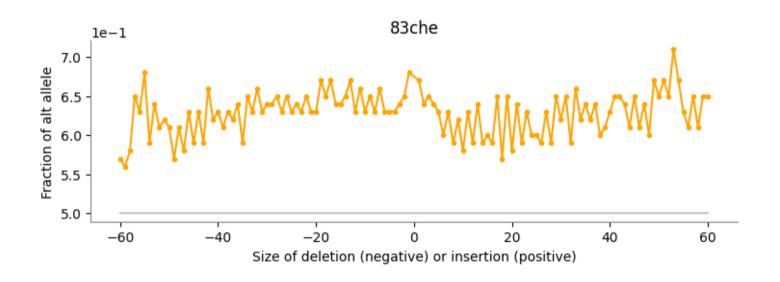
Ts/Tv stratified by QUAL



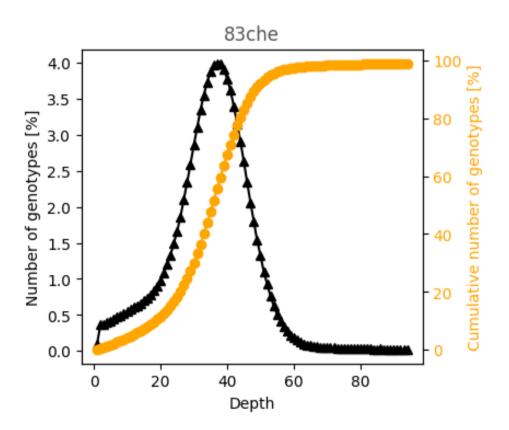
Indel distribution



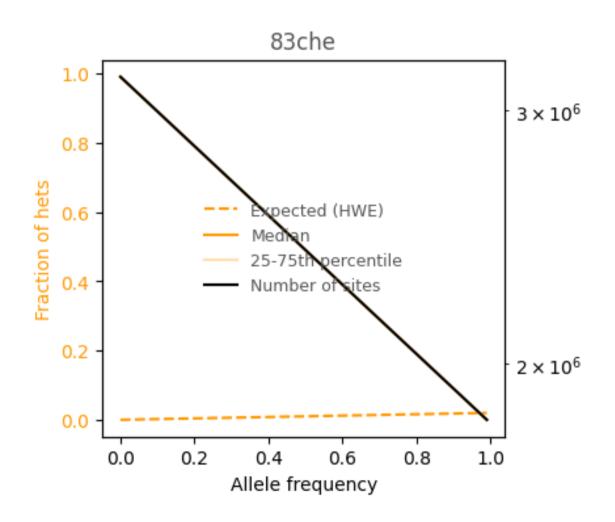
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

