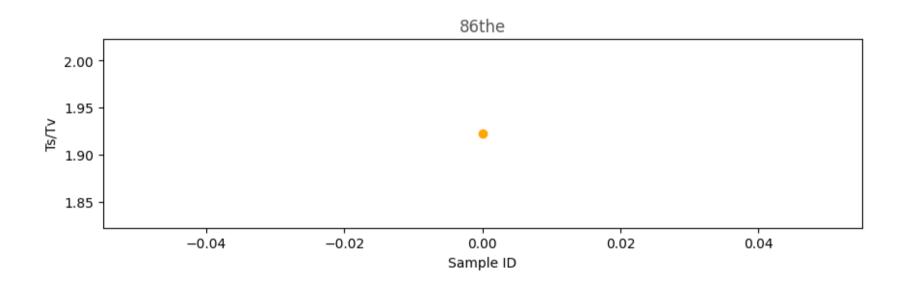
Summary Numbers

| | SNPs | | | indels | | MNPs | others | | |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | |
| 86the | 4,085,304 | 1.92 | 1.93 | 955,312 | _ | 0 | 0 | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | |

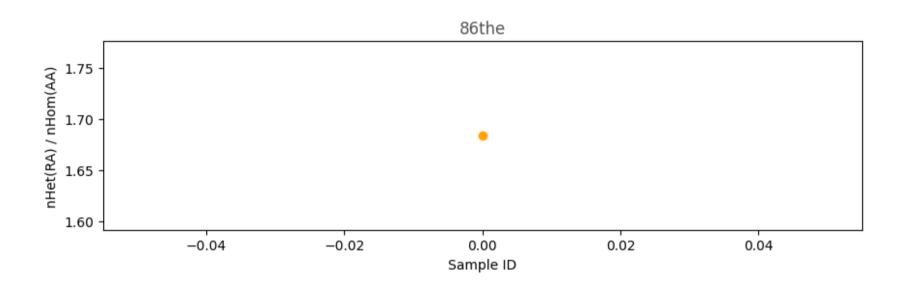
| | singl | etons (A | multiallelic | | |
|---------|-------|----------|--------------|---------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 86the | 62.8% | 1.89 | 67.6% | 102,274 | 2,105 |

- 86the.. /ngc/projects2/gm/data/archive/2022/variants/snv/86theotom-103880395033-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00922-220622_A00559_AHKCKKDSX3-EXT_LAB KA_NGCWGS-NGCWGS04526_22RKG012638x01_snv_germline_raw.haplotype_caller.vcf.gz

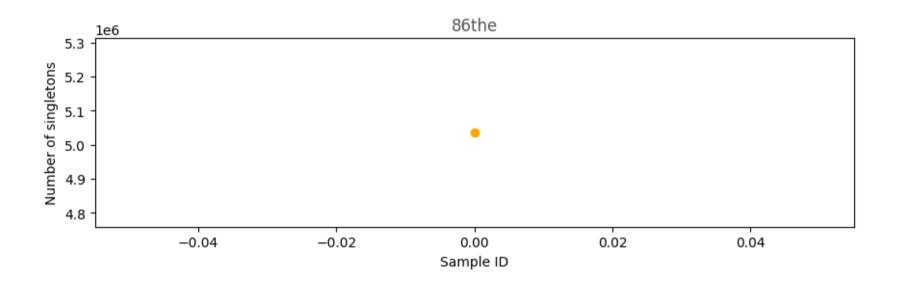
Ts/Tv by sample



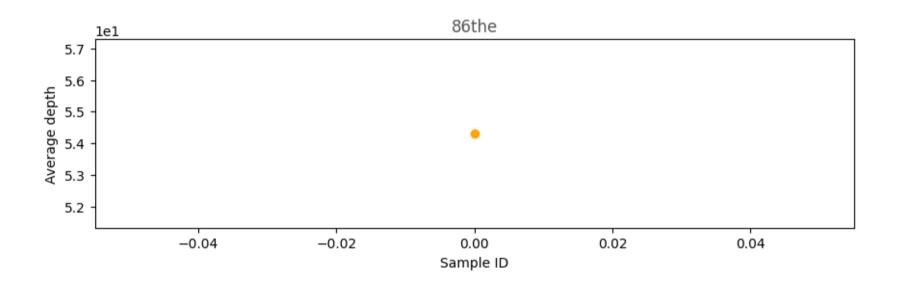
Hets vs non-ref Homs by sample



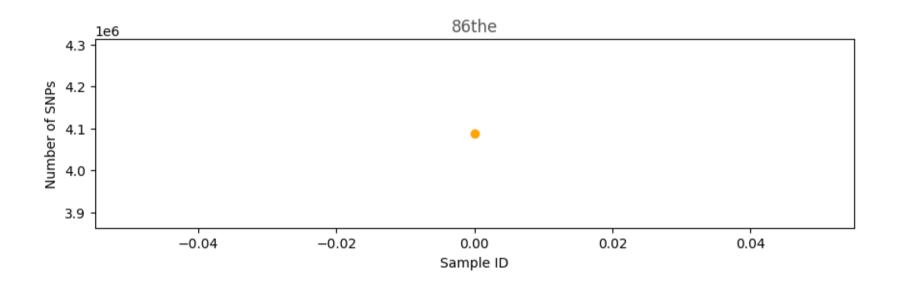
Singletons by sample (hets and homs)



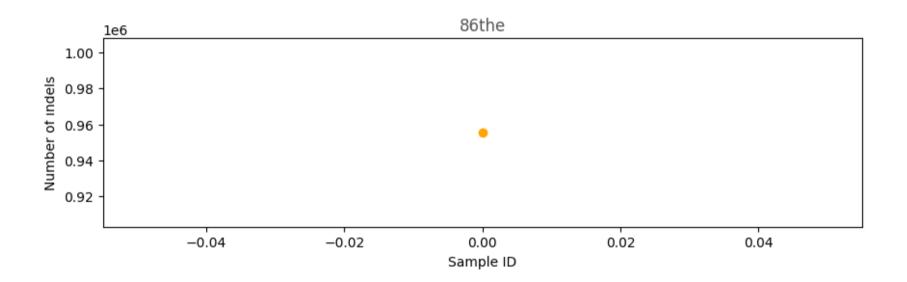
Average depth by sample



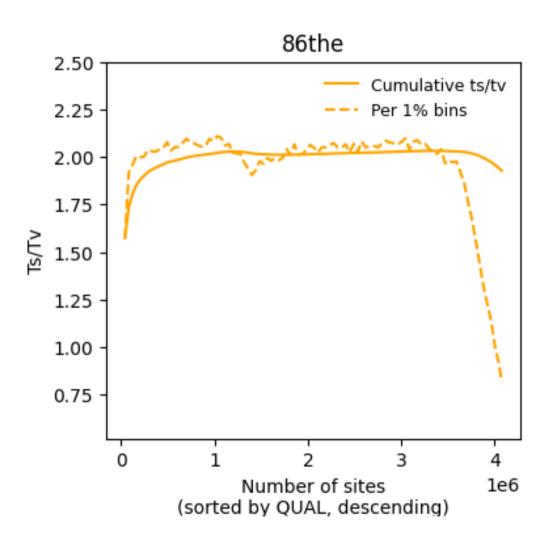
Number of SNPs by sample



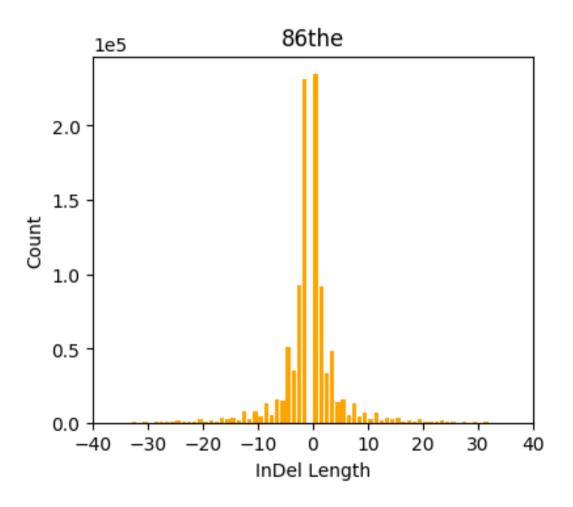
Number of indels by sample



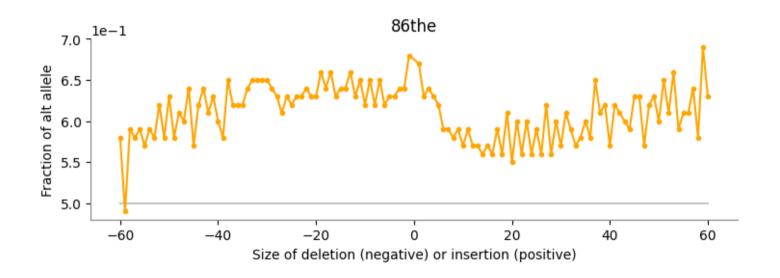
Ts/Tv stratified by QUAL



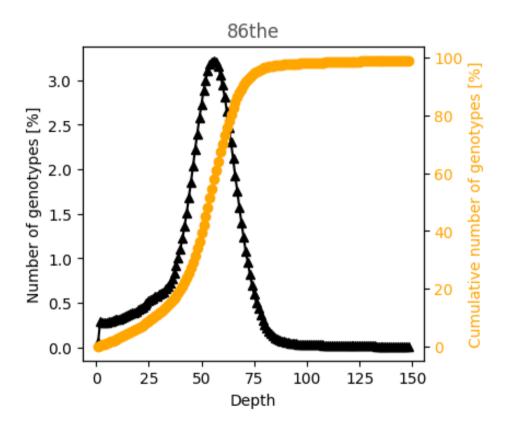
Indel distribution



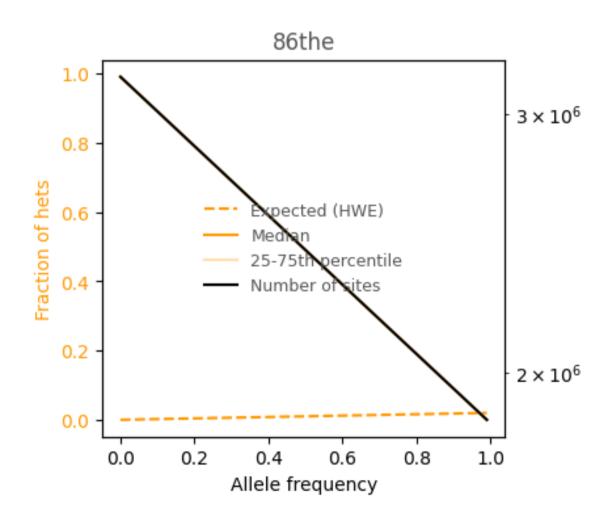
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

