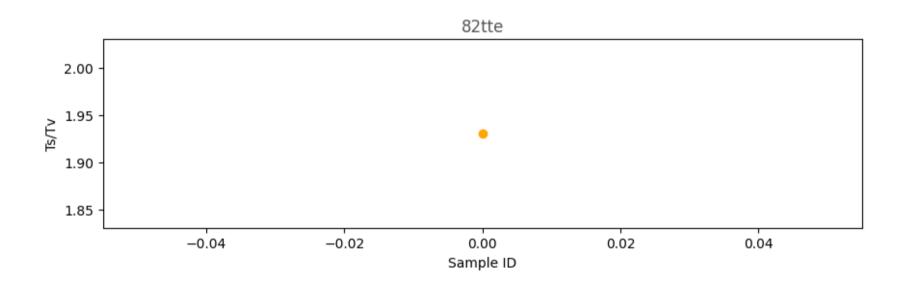
Summary Numbers

| | SNPs | | | indels | | MNPs | others | | | |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | | |
| 82tte | 4,046,942 | 1.93 | 1.94 | 935,253 | - | 0 | 0 | | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | | |

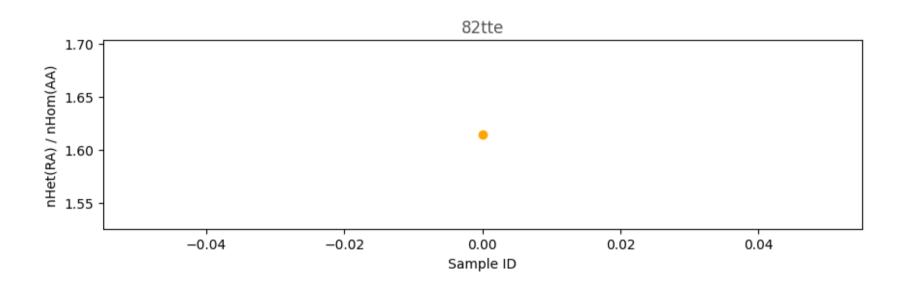
| | singl | etons (A | multiallelic | | |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 82tte | 61.8% | 1.90 | 66.1% | 94,363 | 2,126 |

- 82tte .. /ngc/projects2/gm/data/archive/2022/variants/snv/82ttesatm-103900270067-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01078-220817_A00559_AHNKFVDSX3-EXT_LAB KA_NGCWGS-NGCWGS04803_snv_germline_raw.haplotype_caller.vcf.gz

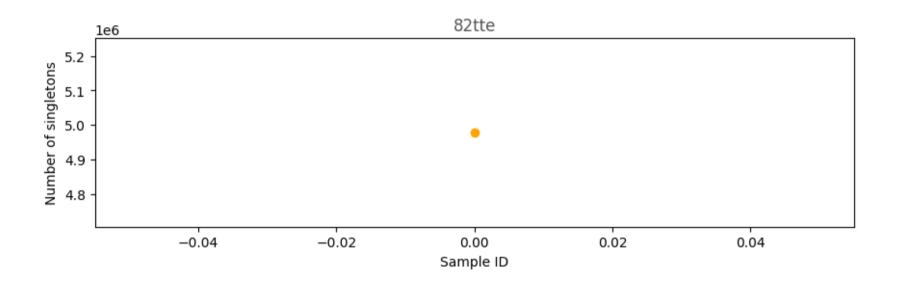
Ts/Tv by sample



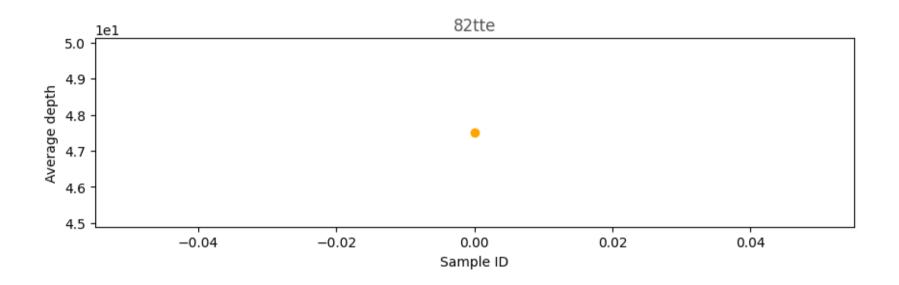
Hets vs non-ref Homs by sample



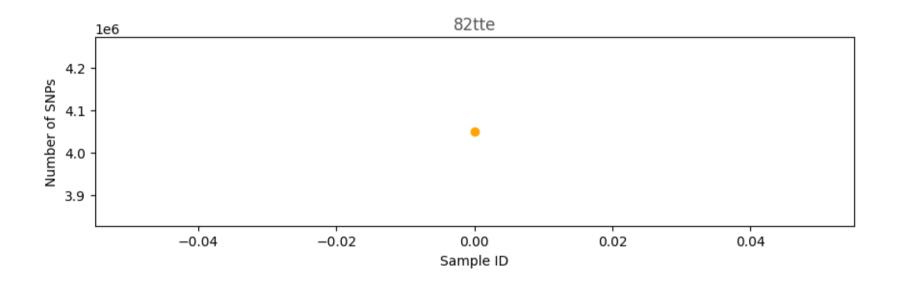
Singletons by sample (hets and homs)



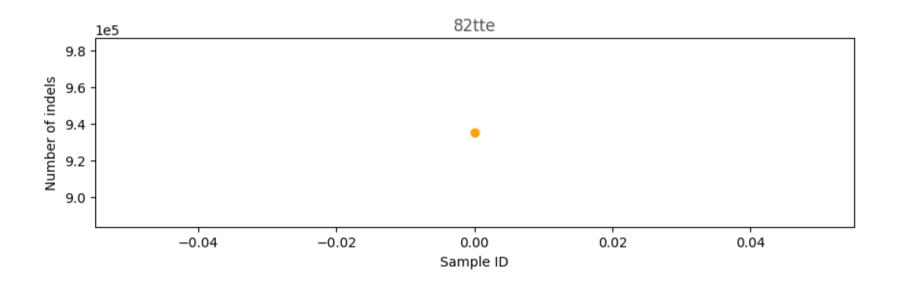
Average depth by sample



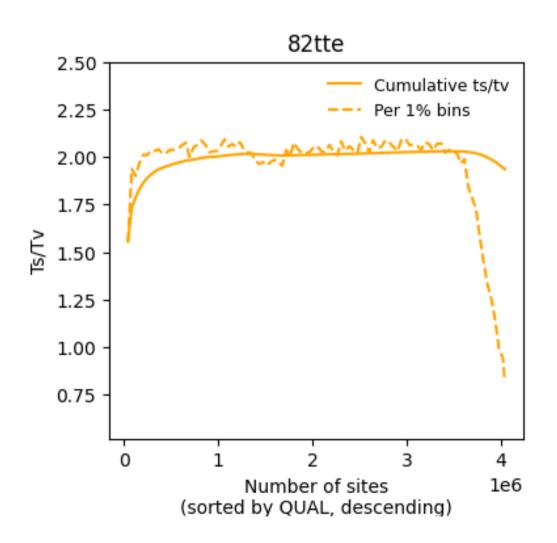
Number of SNPs by sample



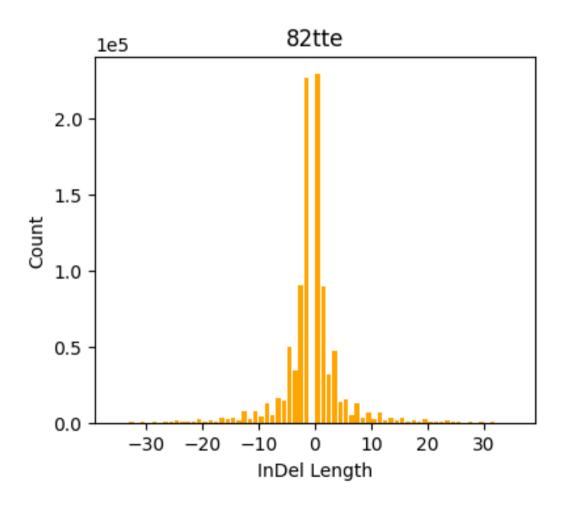
Number of indels by sample



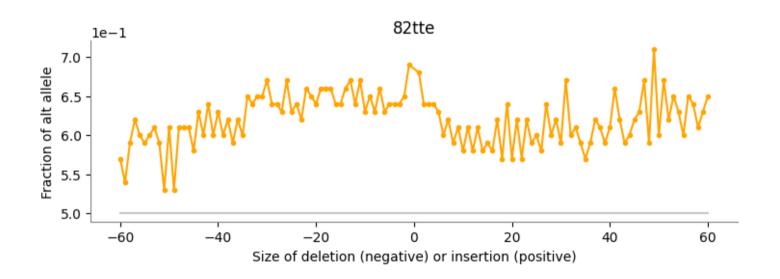
Ts/Tv stratified by QUAL



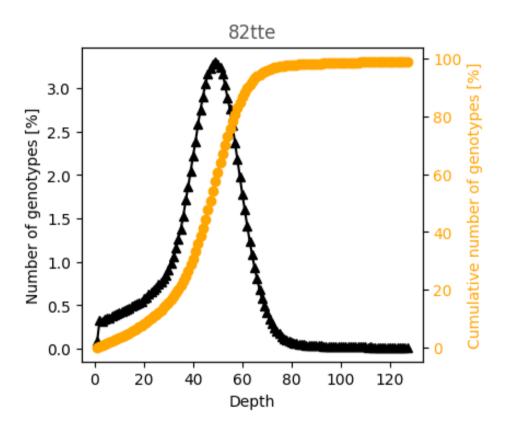
Indel distribution



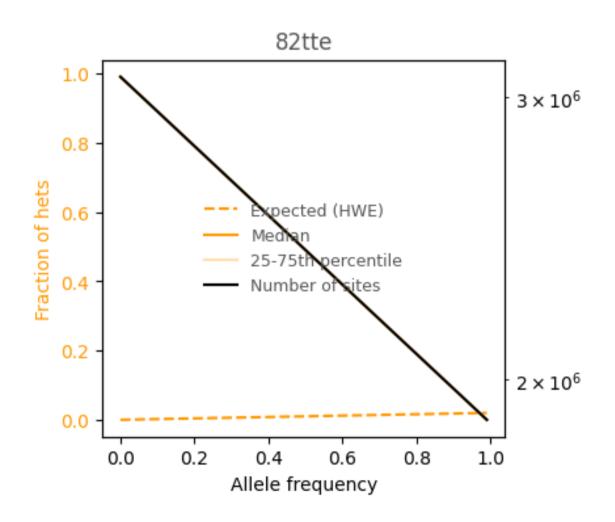
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

