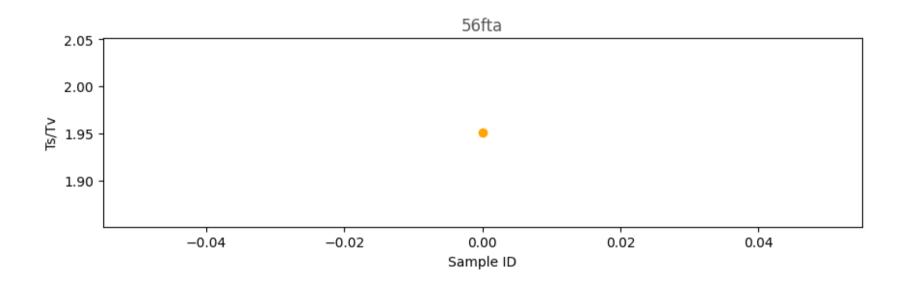
Summary Numbers

| | SNPs | | | indels | | MNPs | others | | |
|----------------------------------|-----------|-------|-----------|-----------|------|------|--------|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | |
| 56fta | 4,729,322 | 1.95 | 1.96 | 1,087,430 | - | 0 | 0 | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | |

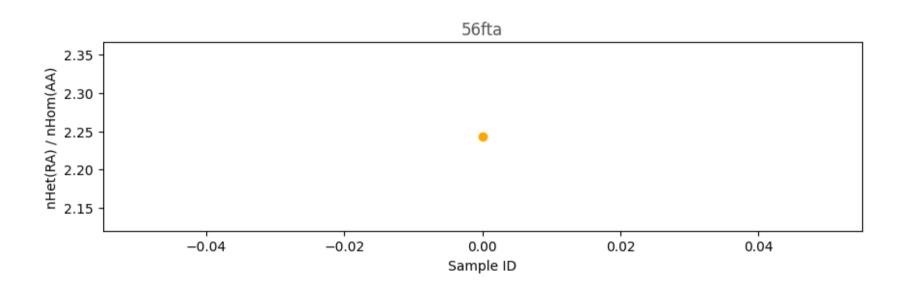
| | singl | etons (A | multiallelic | | |
|---------|-------|----------|--------------|---------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 56fta | 69.2% | 1.94 | 74.8% | 134,229 | 2,837 |

- 56fta .. /ngc/projects2/gm/data/archive/2022/variants/snv/56ftalerf-103782976175-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-211103_A01466_BHT575DSX2-RHGM_LABKA_WGS-WGS03285_snv_germline_raw.haplotype_caller.vcf.gz

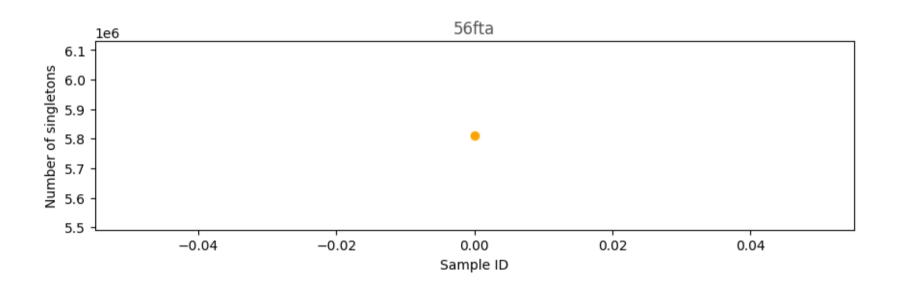
Ts/Tv by sample



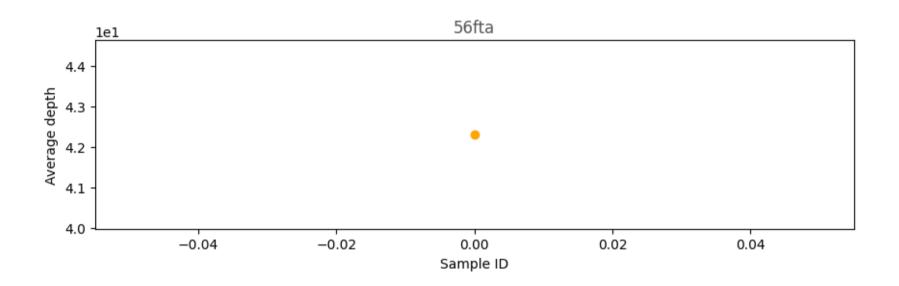
Hets vs non-ref Homs by sample



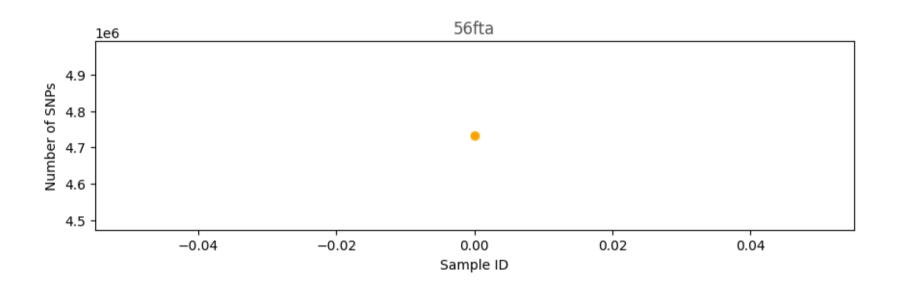
Singletons by sample (hets and homs)



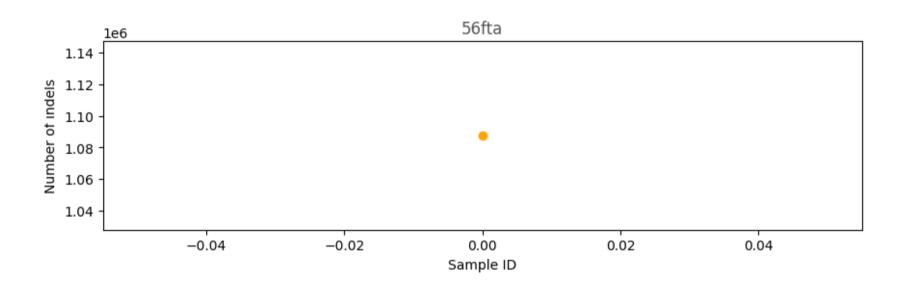
Average depth by sample



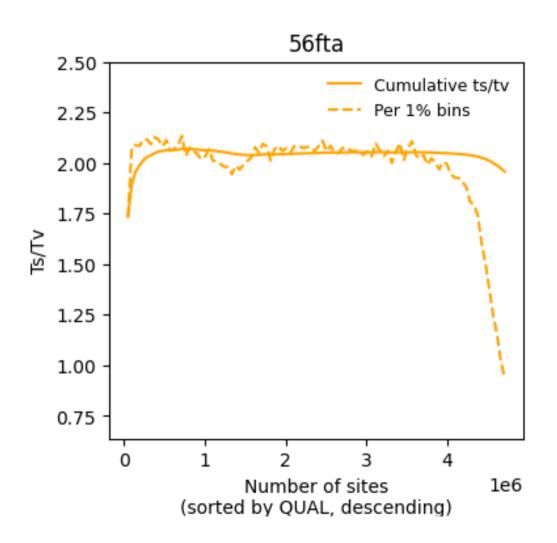
Number of SNPs by sample



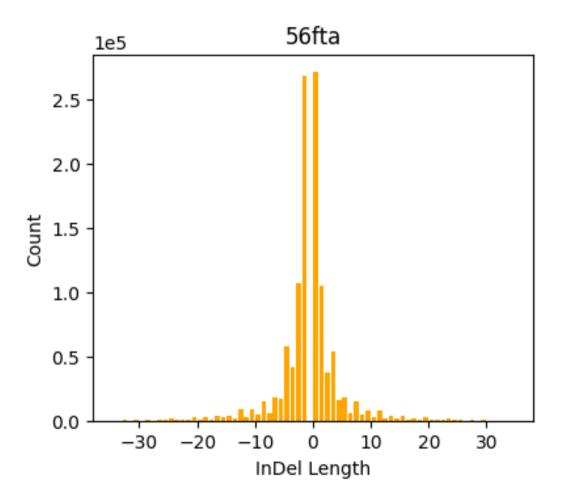
Number of indels by sample



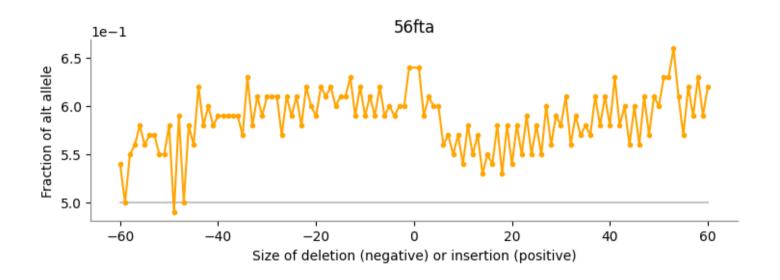
Ts/Tv stratified by QUAL



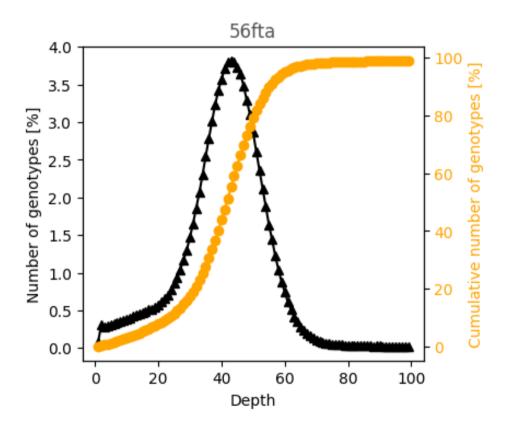
Indel distribution



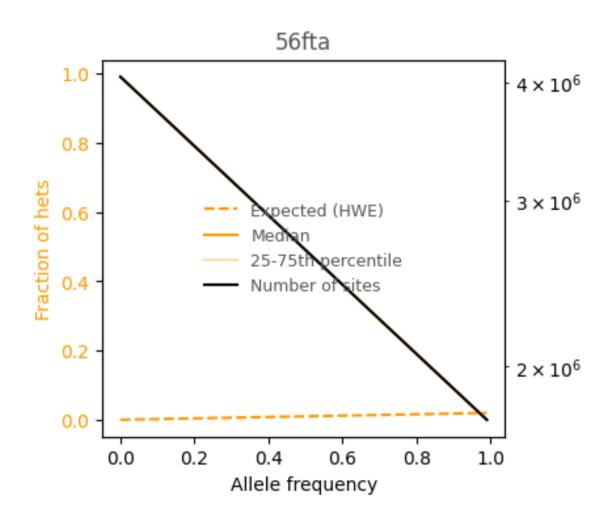
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

