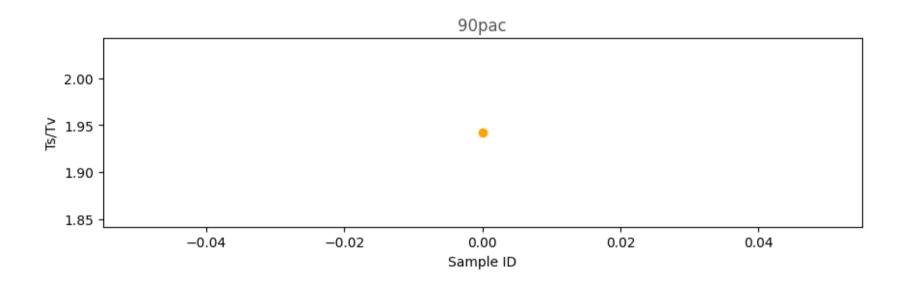
Summary Numbers

| | SNPs | | | indels | | MNPs | others | | | |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | | |
| 90pac | 4,064,448 | 1.94 | 1.95 | 948,877 | _ | 0 | 0 | | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | | |

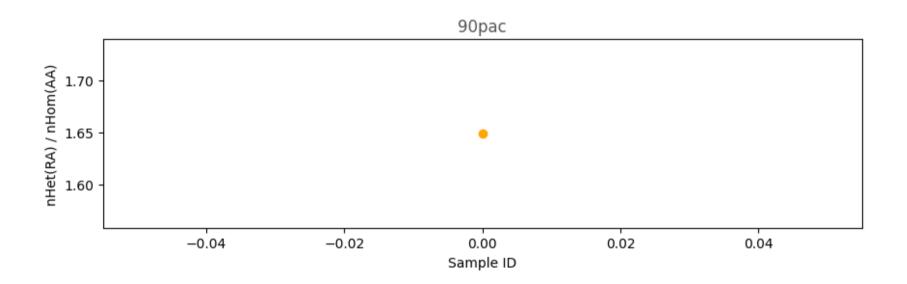
| | singl | etons (A | multiallelic | | |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 90pac | 62.3% | 1.92 | 67.2% | 98,353 | 2,038 |

- 90pac .. /ngc/projects2/gm/data/archive/2022/variants/snv/90pacomaf-103909637117-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01690-220921_A01961_AHY2KCDSX3-EXT_LAB KA_NGCWGS-NGCWGS05376_snv_germline_raw.haplotype_caller.vcf.gz

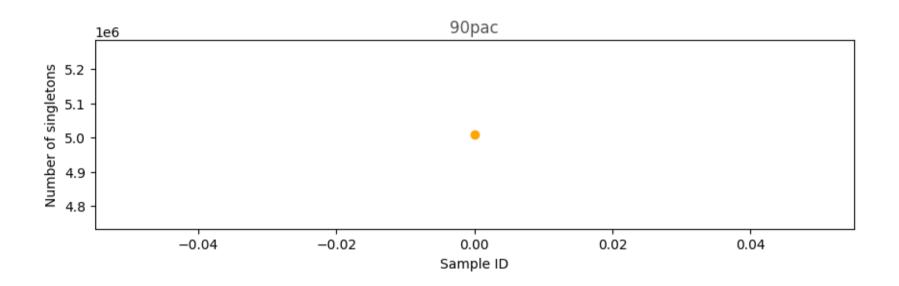
Ts/Tv by sample



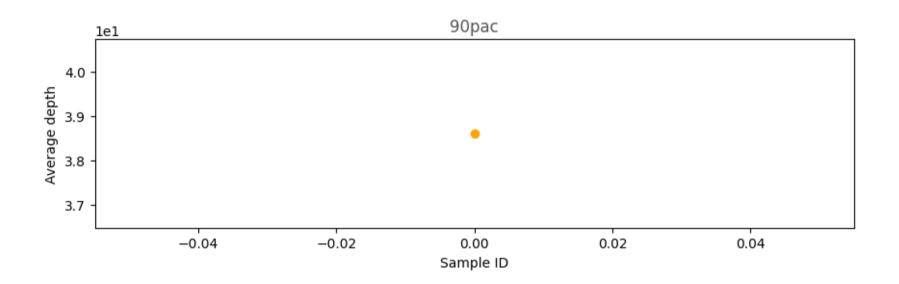
Hets vs non-ref Homs by sample



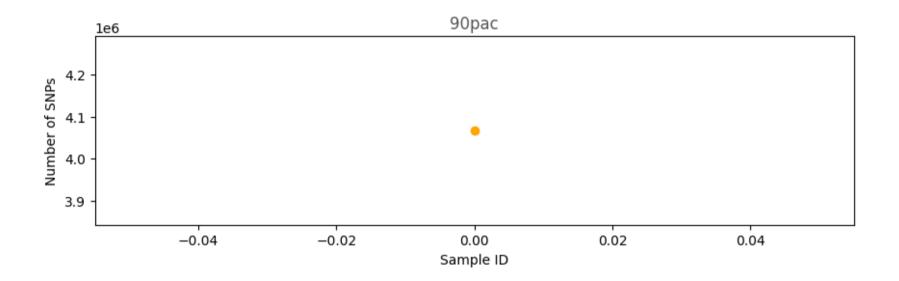
Singletons by sample (hets and homs)



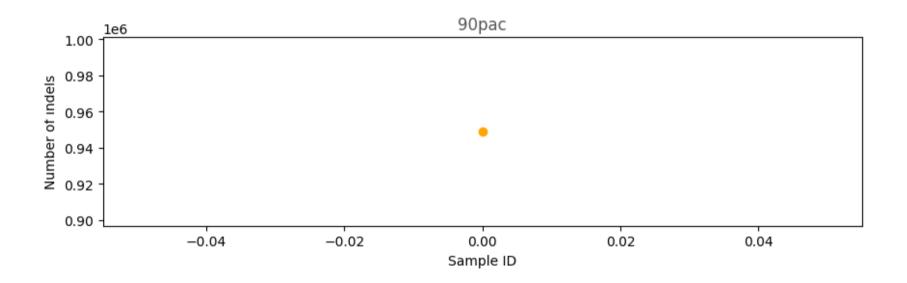
Average depth by sample



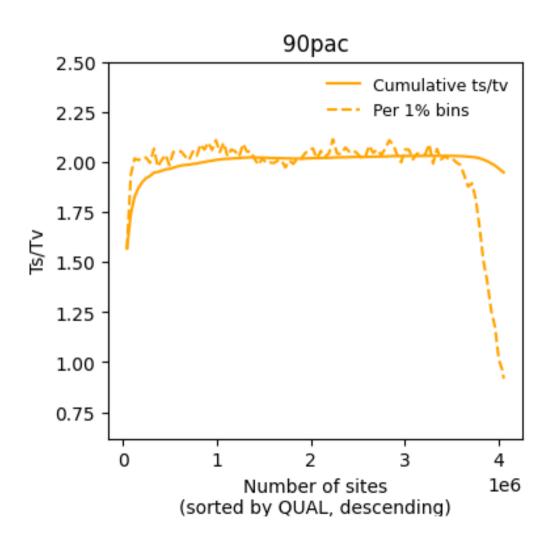
Number of SNPs by sample



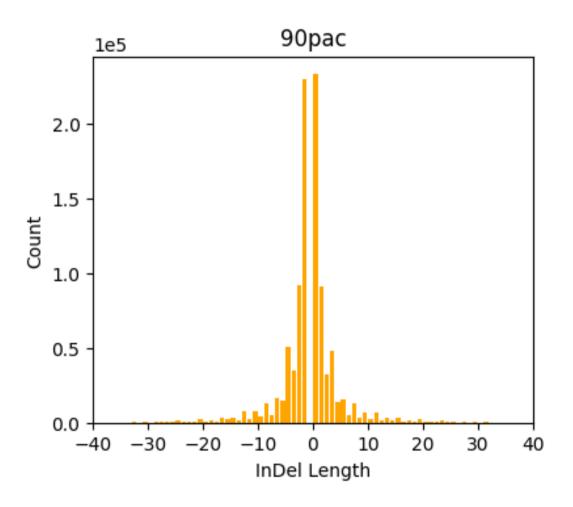
Number of indels by sample



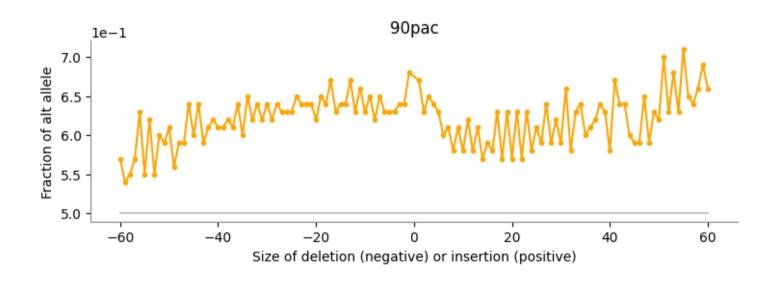
Ts/Tv stratified by QUAL



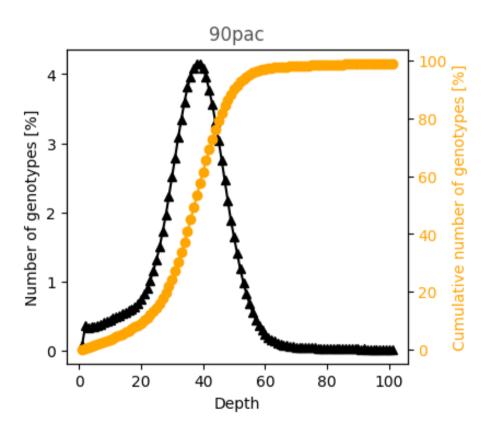
Indel distribution



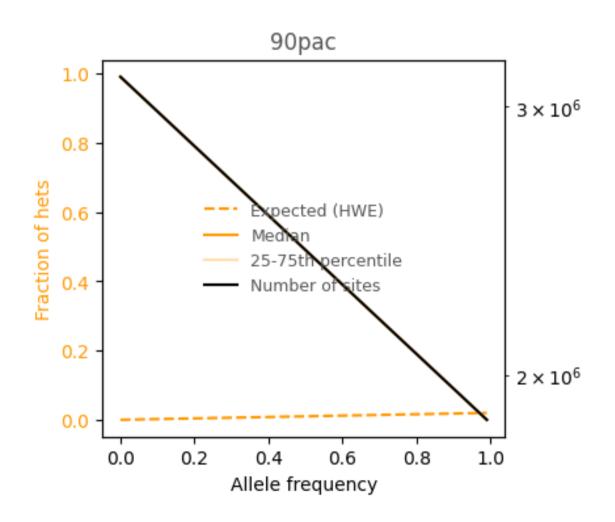
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

