

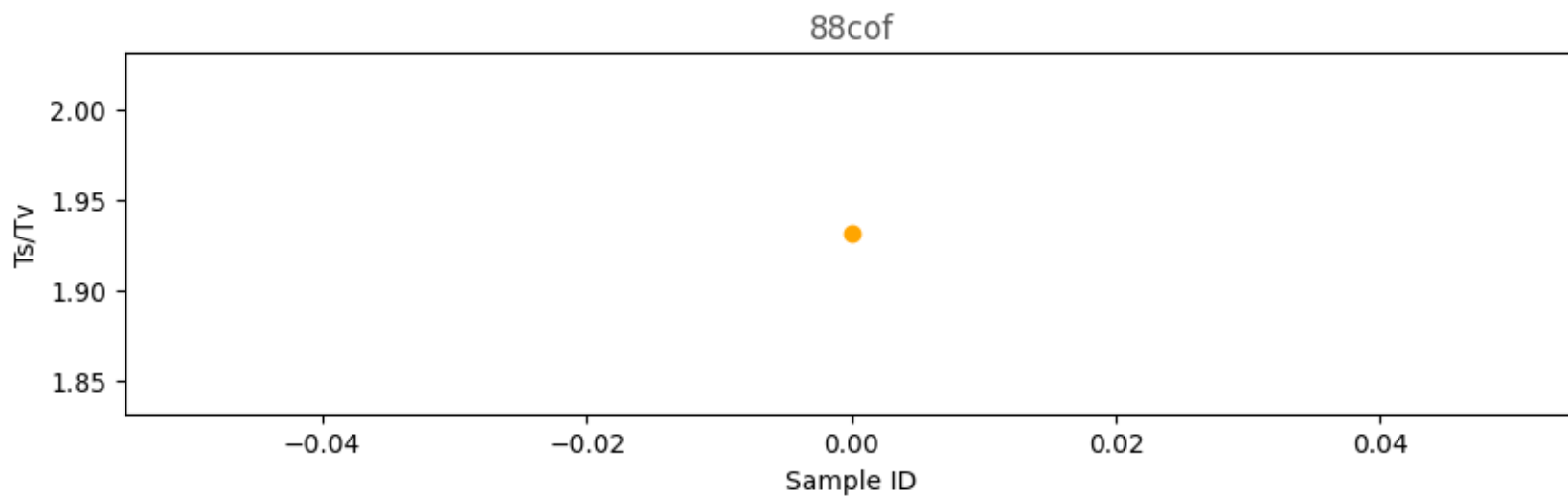
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 88cof | 4,133,799 | 1.93 | 1.94 | 969,416 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

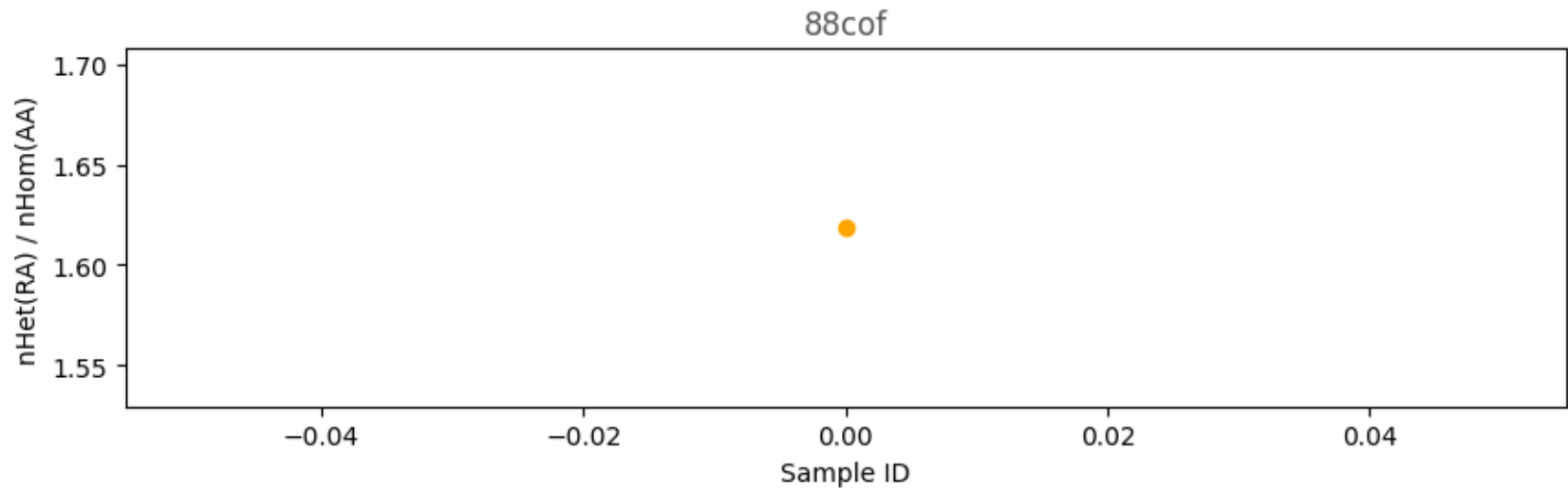
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 88cof | 61.8% | 1.90 | 67.3% | 105,501 | 2,222 |

- 88cof .. /ngc/projects2/gm/data/archive/2022/variants/snv/88coffjof-103794036563-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00360-211019_A01411_BHHHY3DSX2-EXT_LAB
KA_NGCWGS-NGCWGS00259_21RKG023577x01_snv_germline_raw.haplotype_caller.vcf.gz

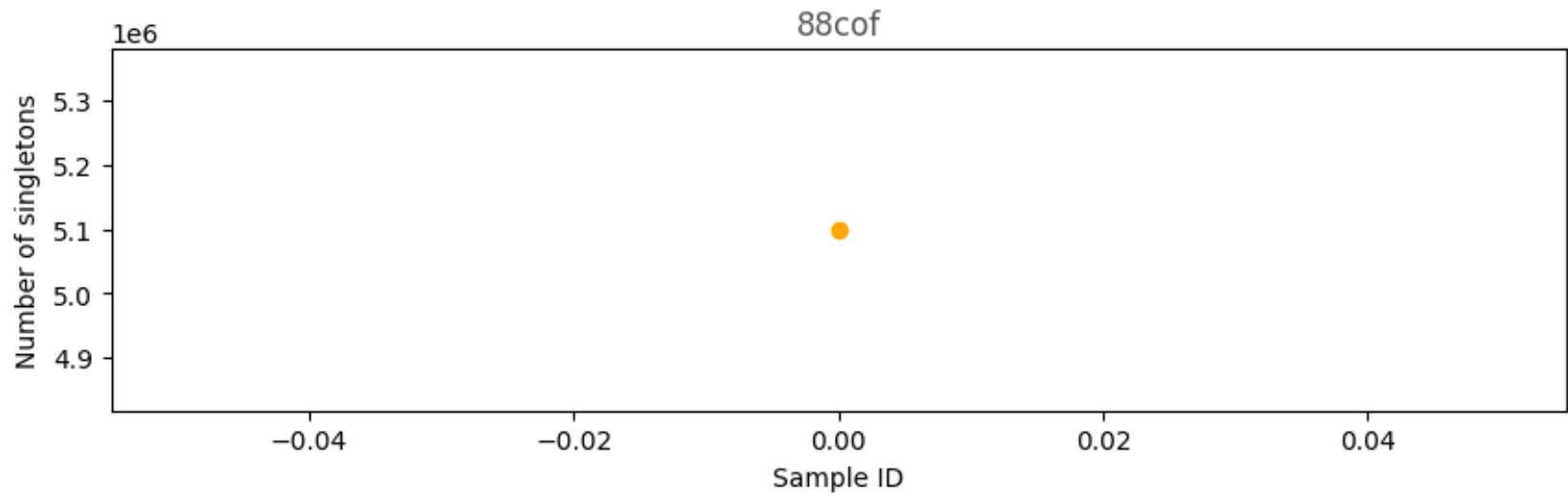
Ts/Tv by sample



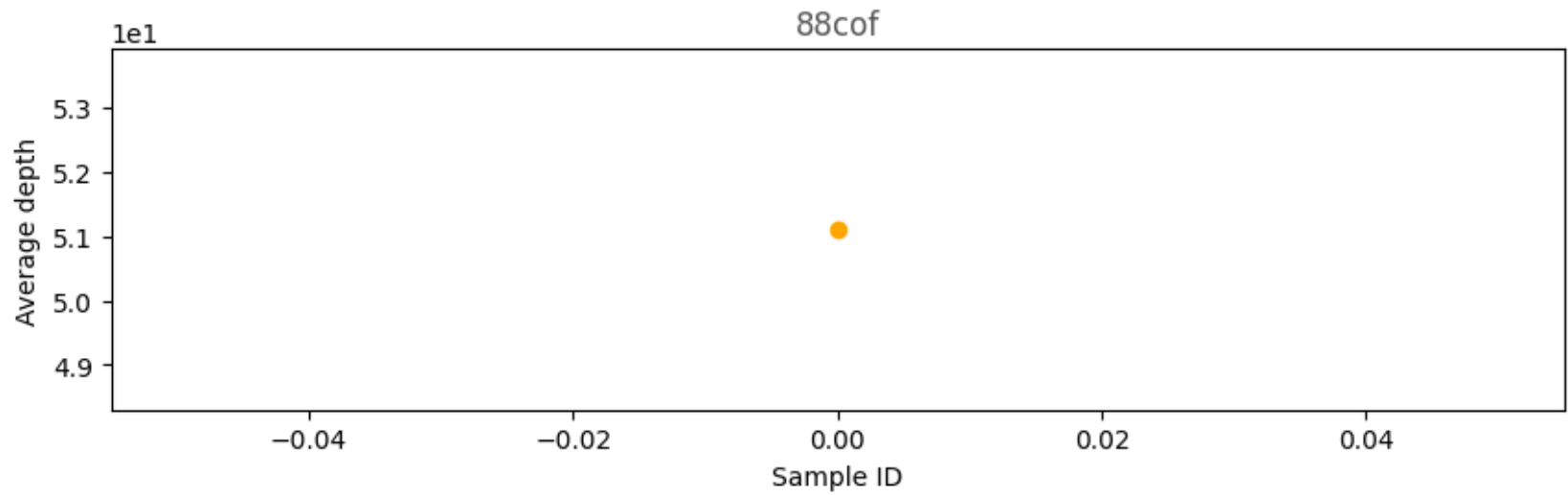
Hets vs non-ref Homs by sample



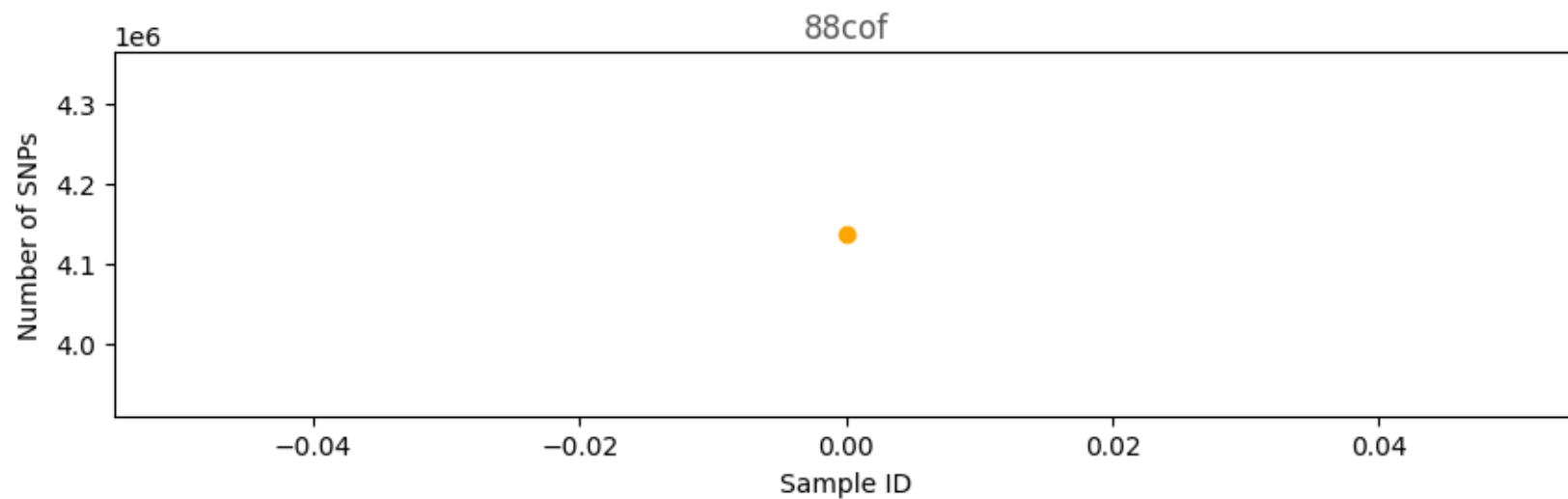
Singletons by sample (hets and homs)



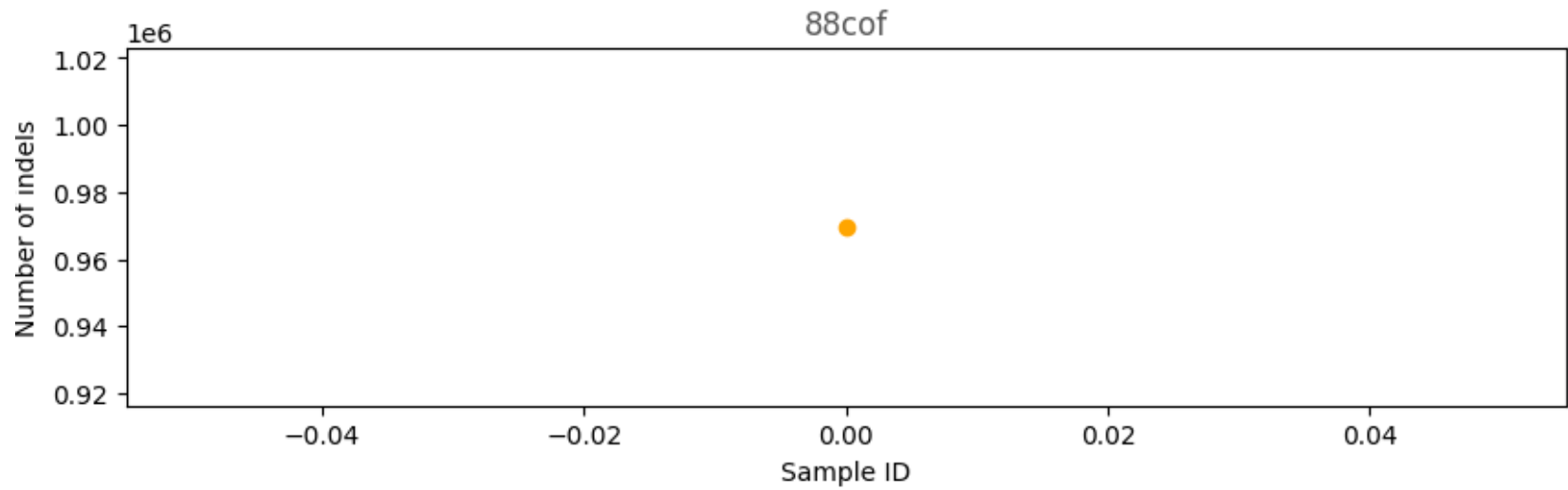
Average depth by sample



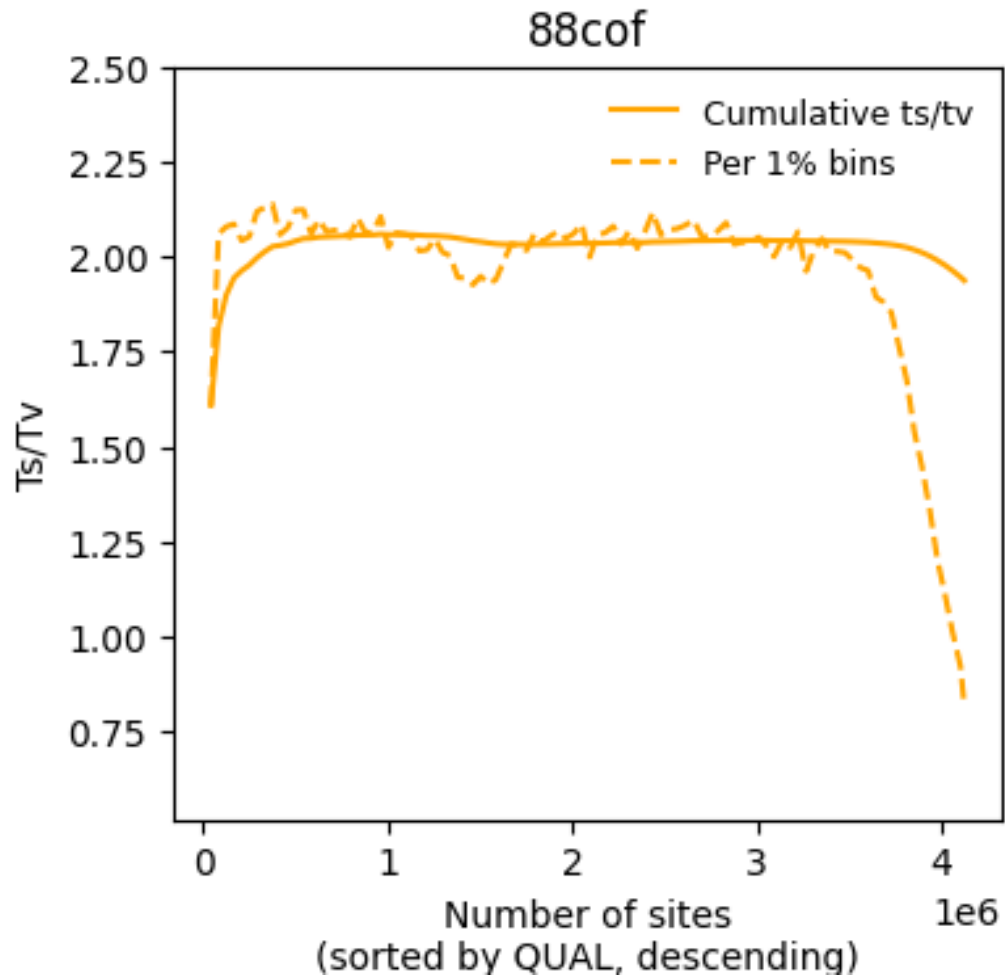
Number of SNPs by sample



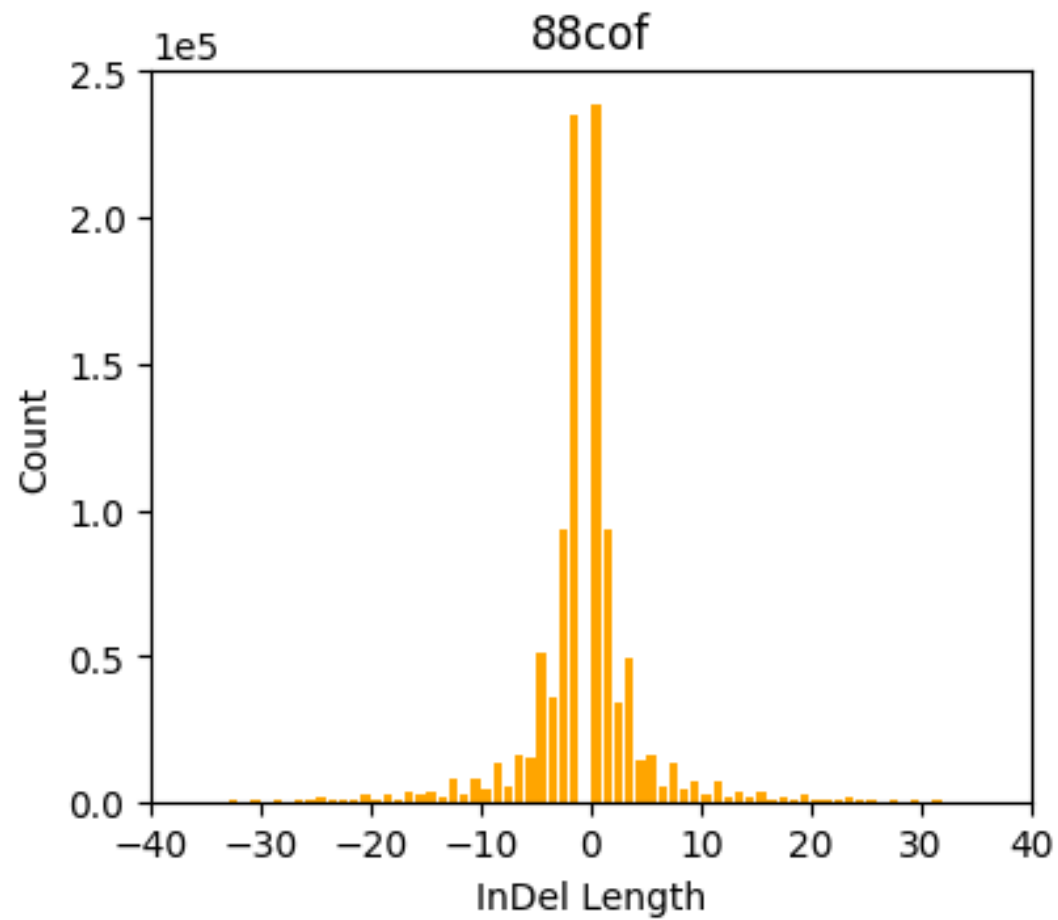
Number of indels by sample



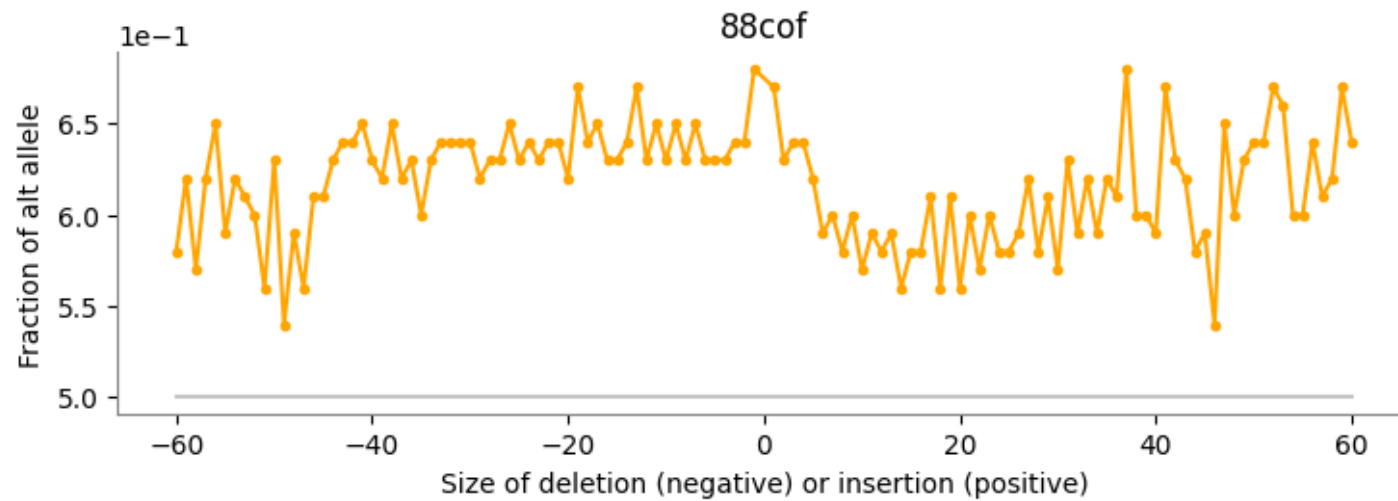
Ts/Tv stratified by QUAL



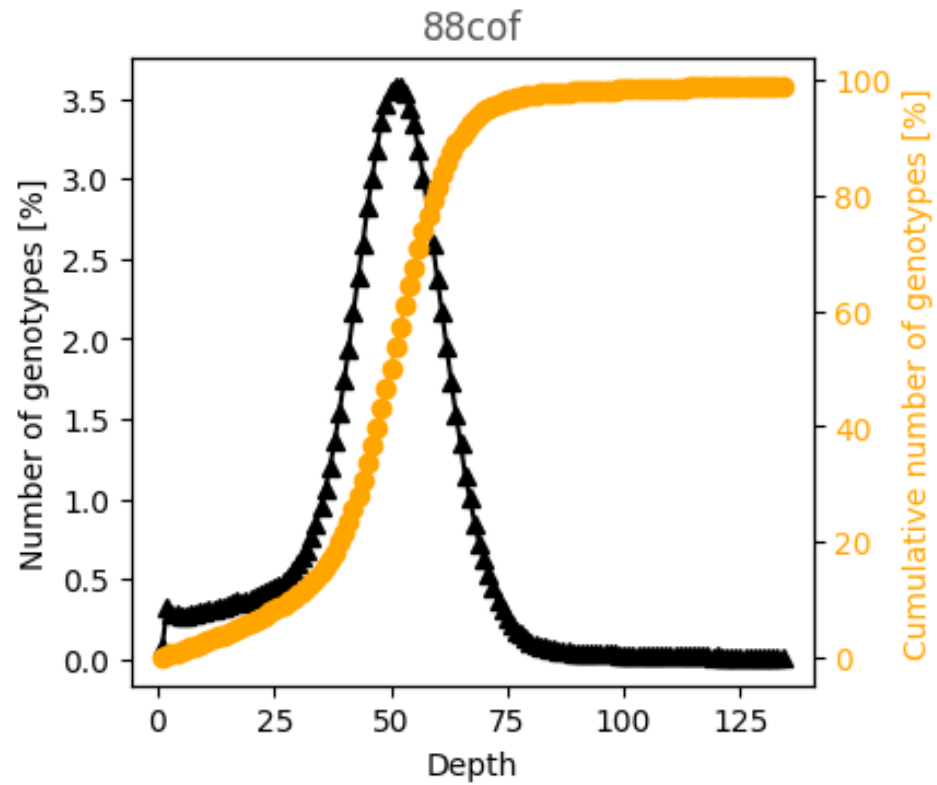
Indel distribution



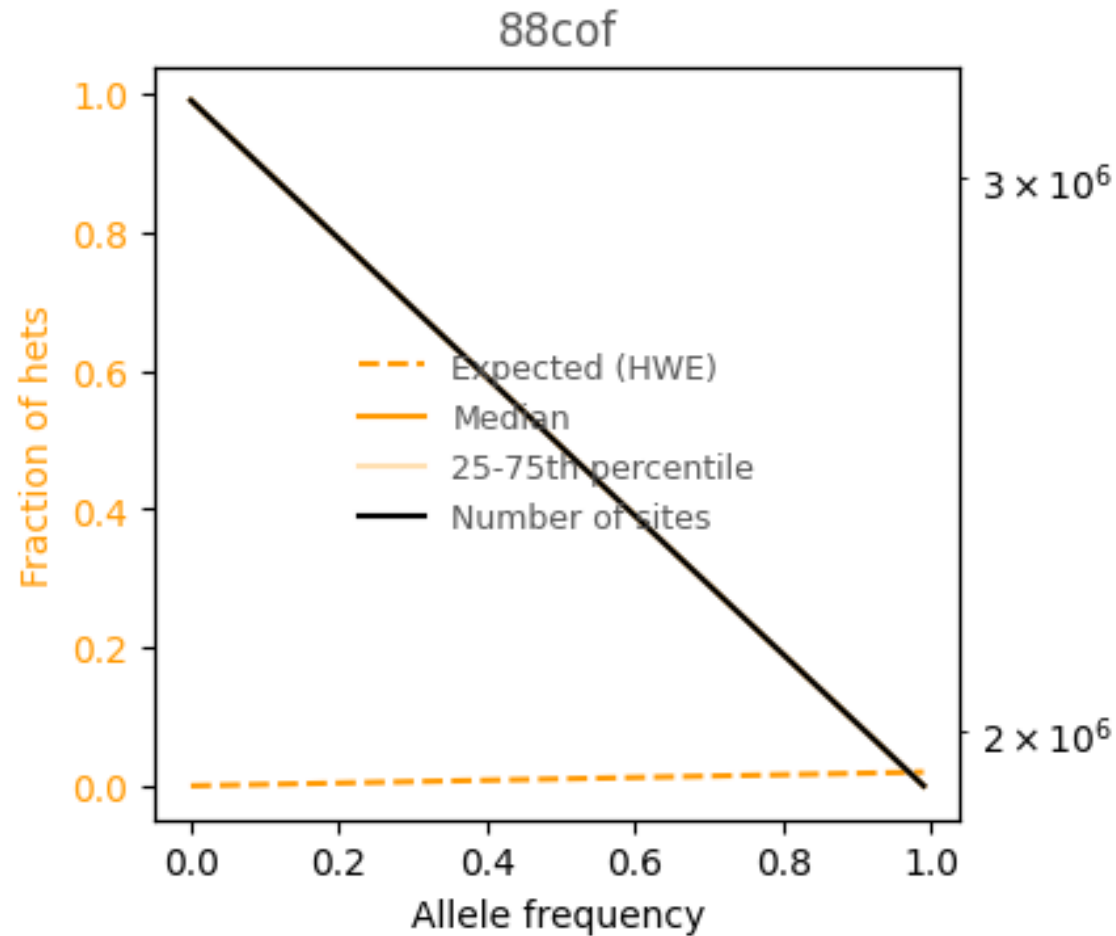
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

