# Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|---|---|---|---|---|---|---|---|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 86cee | 4,042,570 | 1.95 | 1.96 | 953,319 | – | 0 | 0 |
| | | | | | * frameshift ratio: out/(out+in) | | |

| Callset | singletons (AC=1) | | | multiallelic | |
|---|---|---|---|---|---|
| | SNPs | ts/tv | indels | sites | SNPs |
| 86cee | 62.4% | 1.92 | 67.4% | 101,942 | 1,727 |

- 86cee .. `/ngc/projects2/gm/data/archive/2022/variants/snv/86ceemiem-103825443498-Normal_B`
  `lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00494-220119_A01176_AH2CTLDSX3-EXT_LAB`
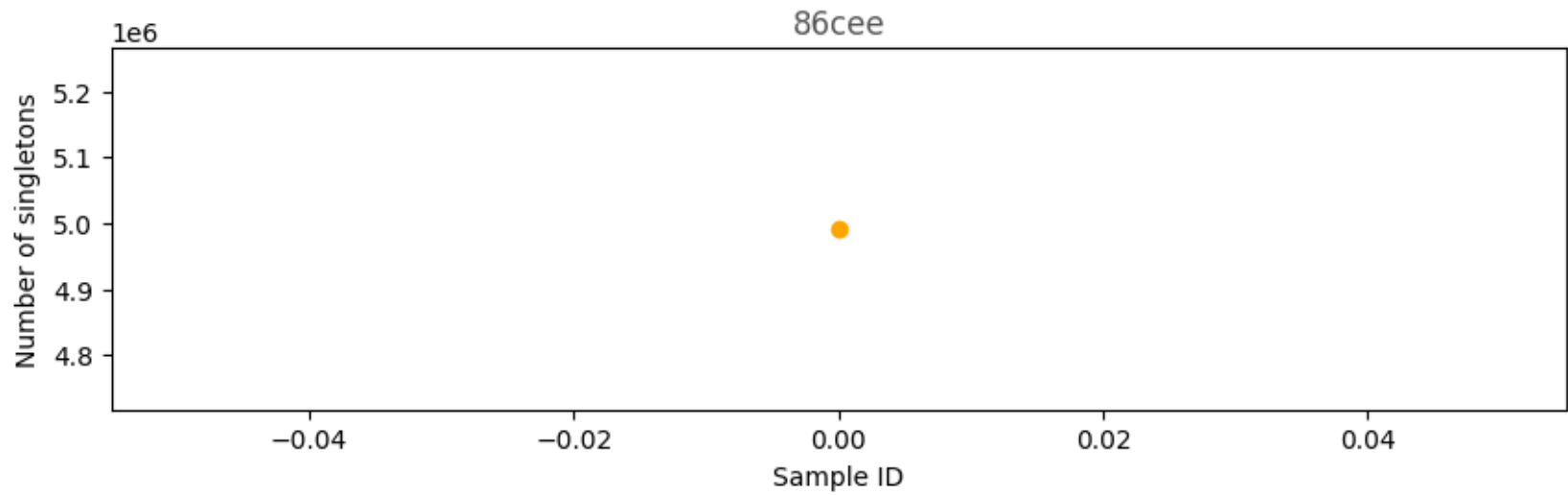  `KA_NGCWGS-NGCWGS03667_21RKG028439x01_snv_germline_raw.haplotype_caller.vcf.gz`
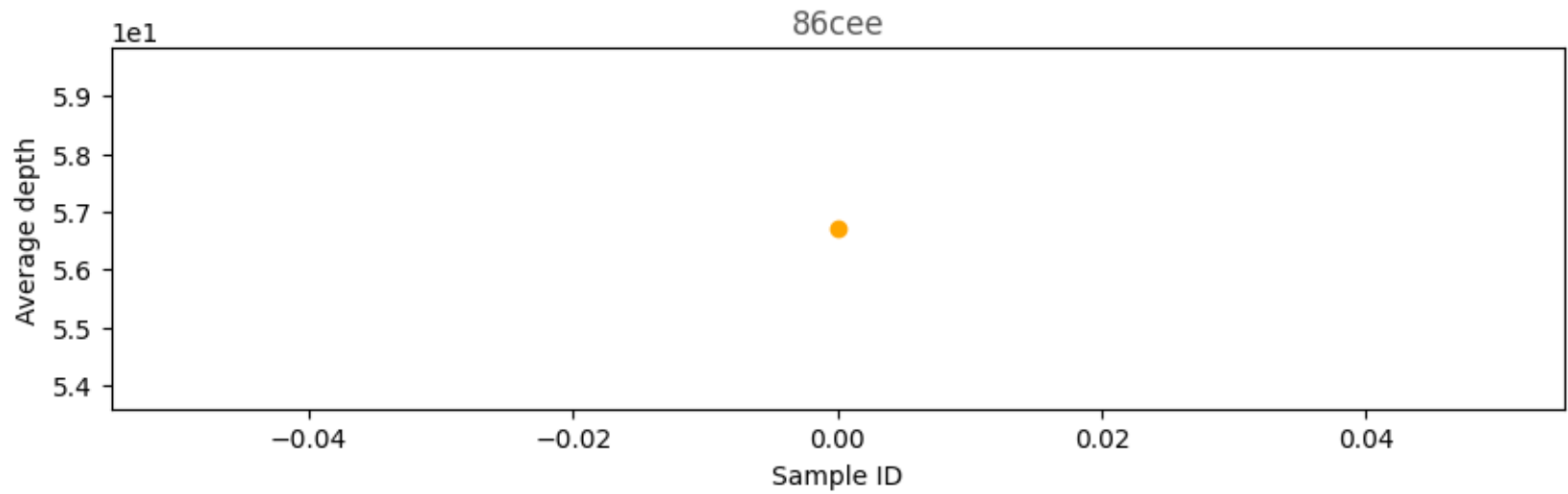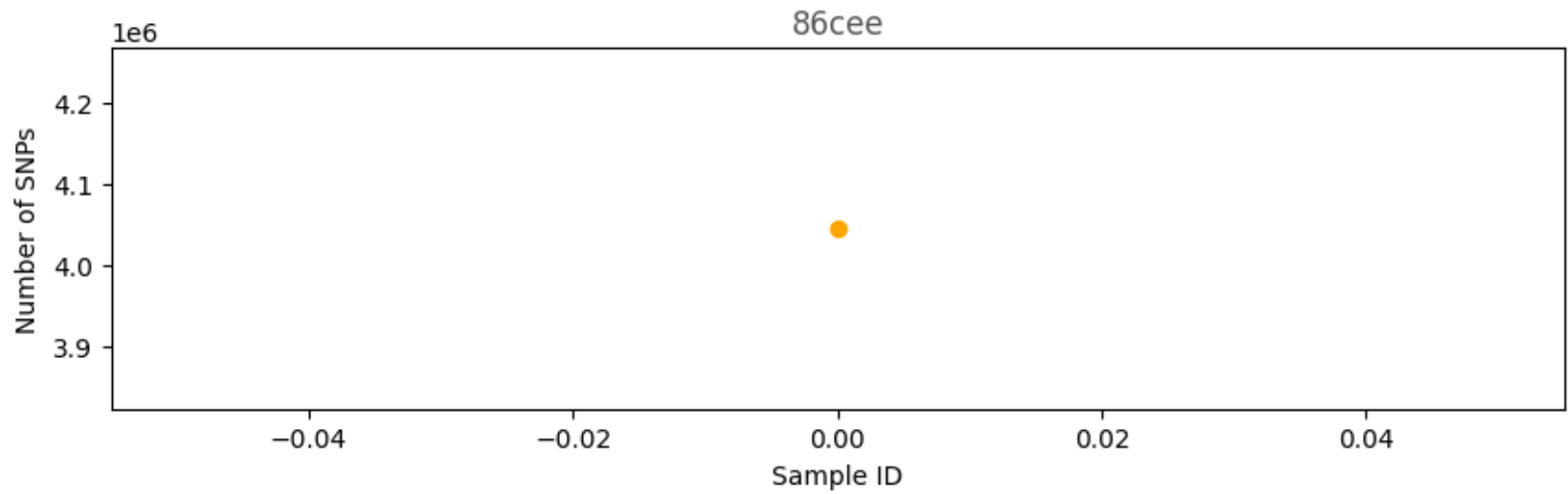
# Ts/Tv by sample
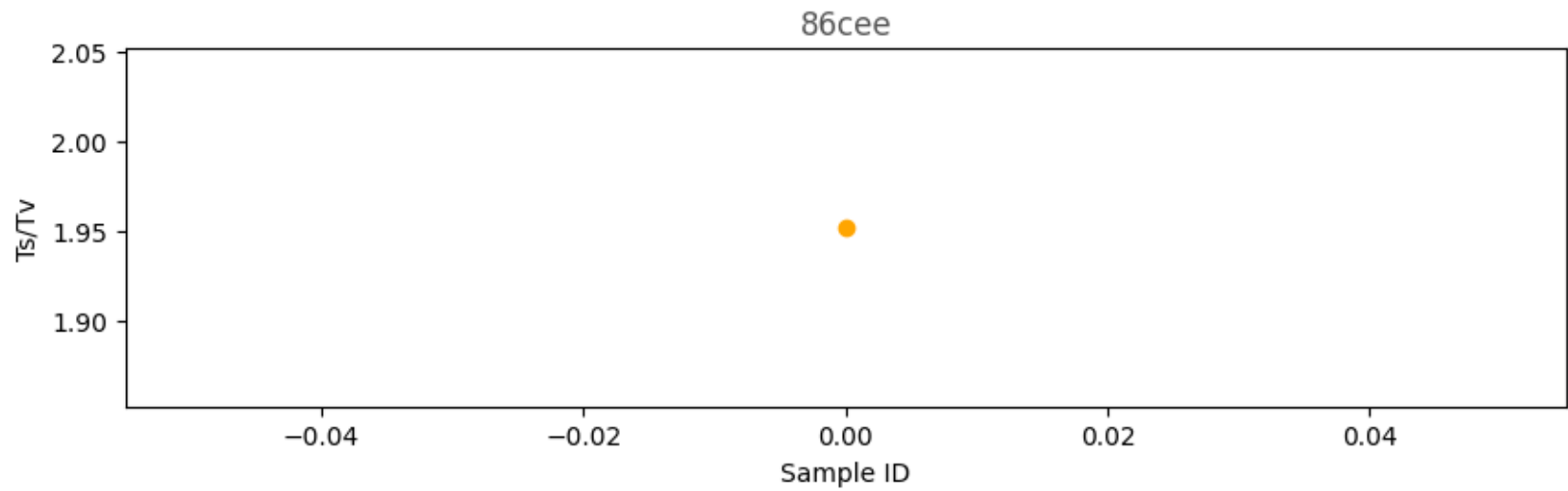
# Hets vs non-ref Homs by sample
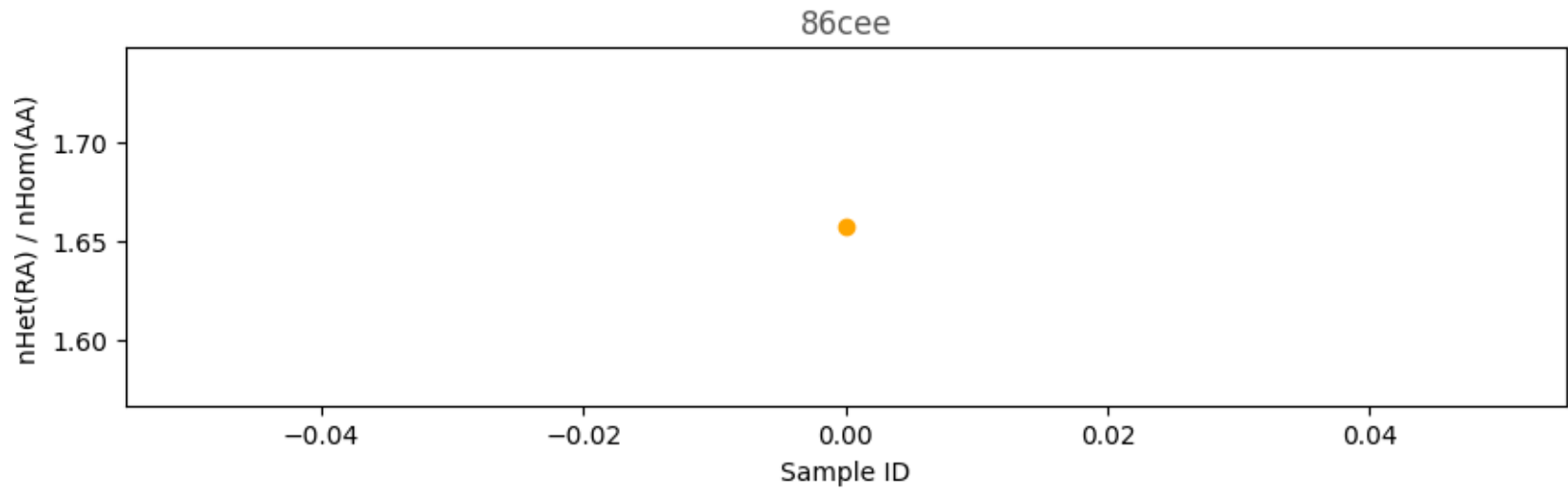
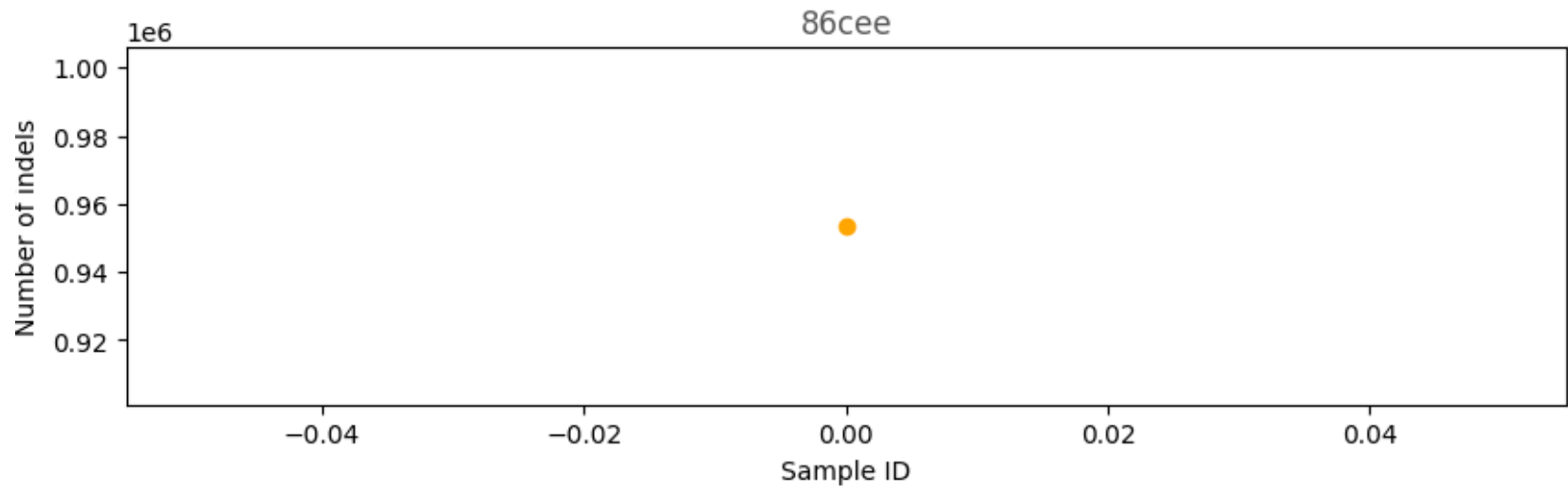# Singletons by sample (hets and homs)
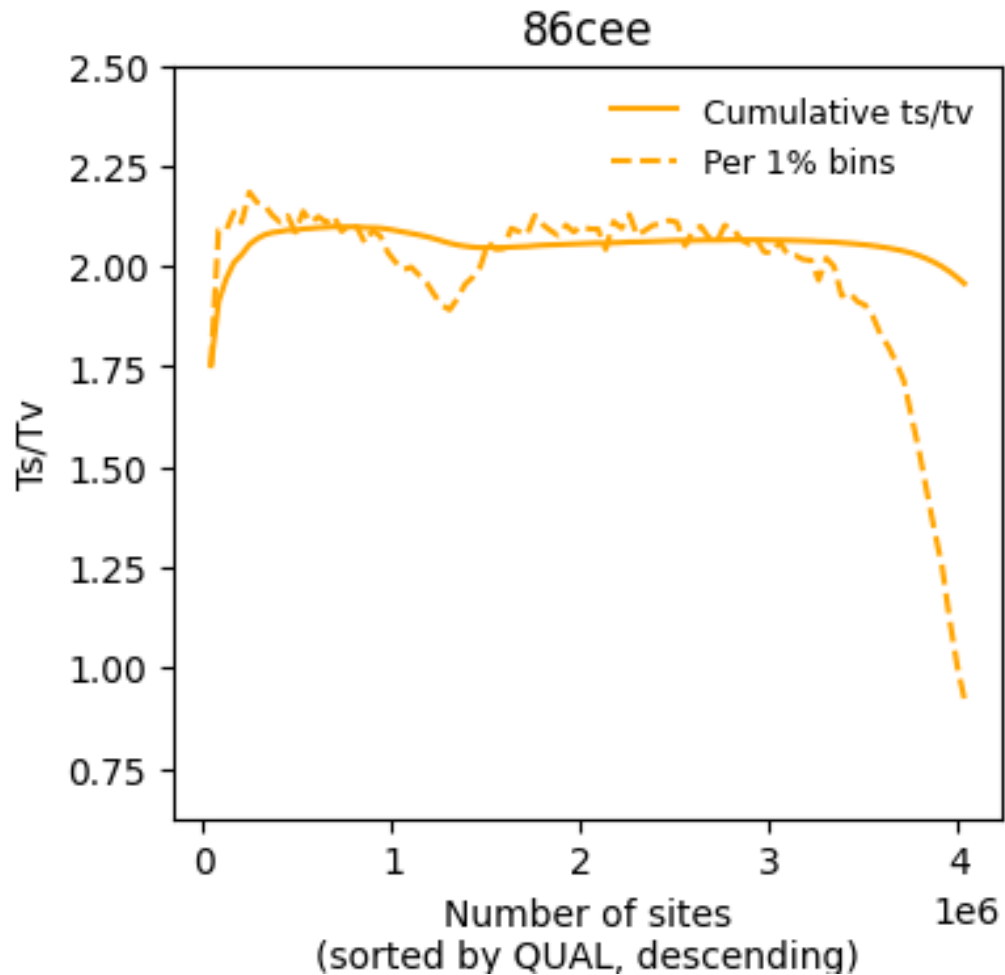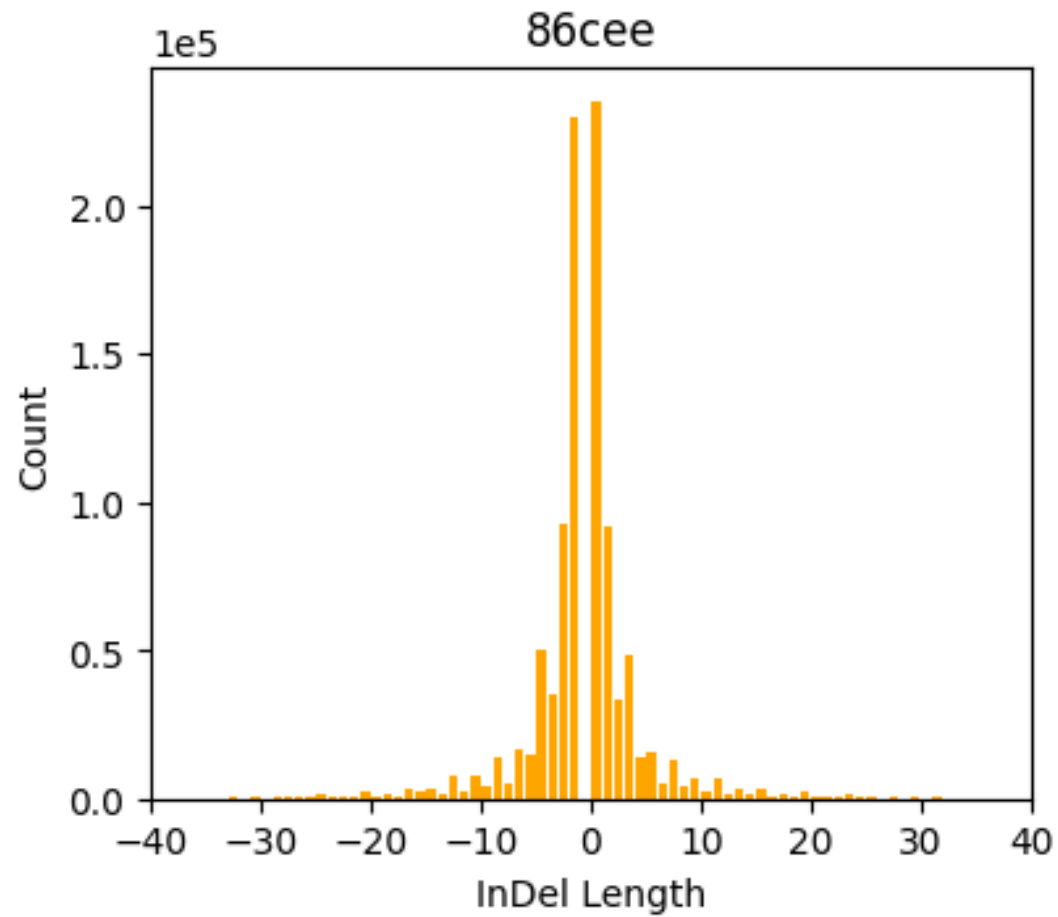
# Average depth by sample

# Number of SNPs by sample

# Number of indels by sample

# Ts/Tv stratified by QUAL

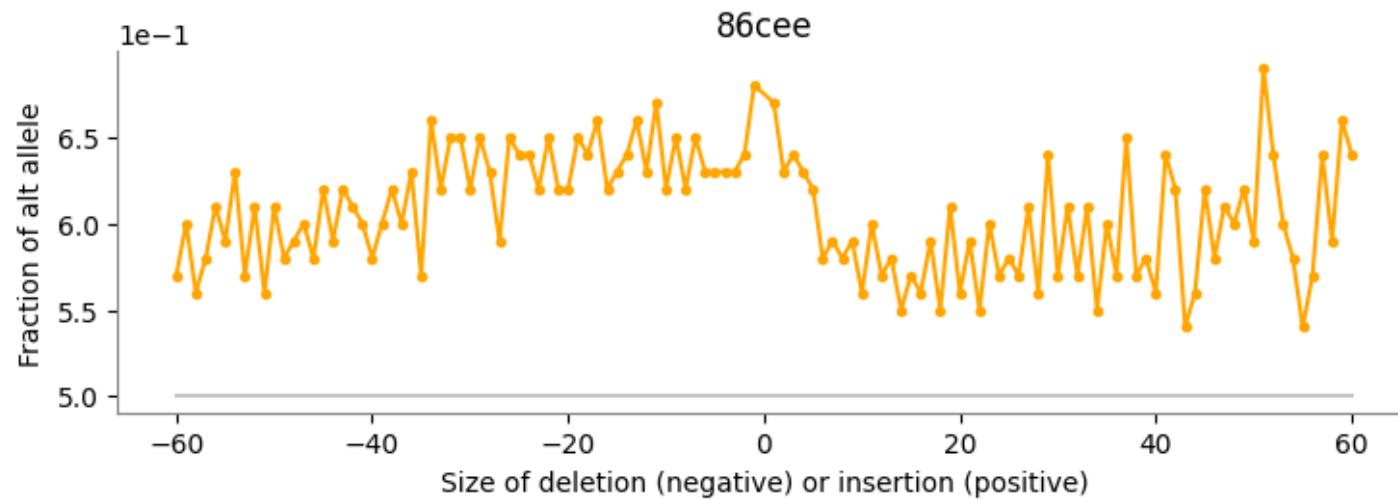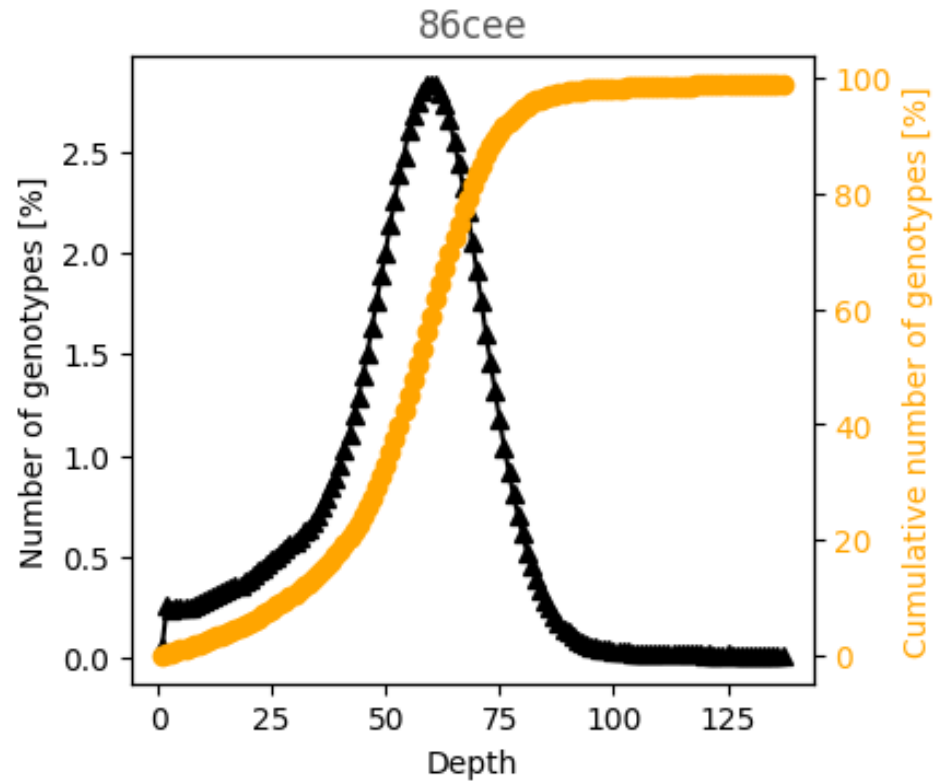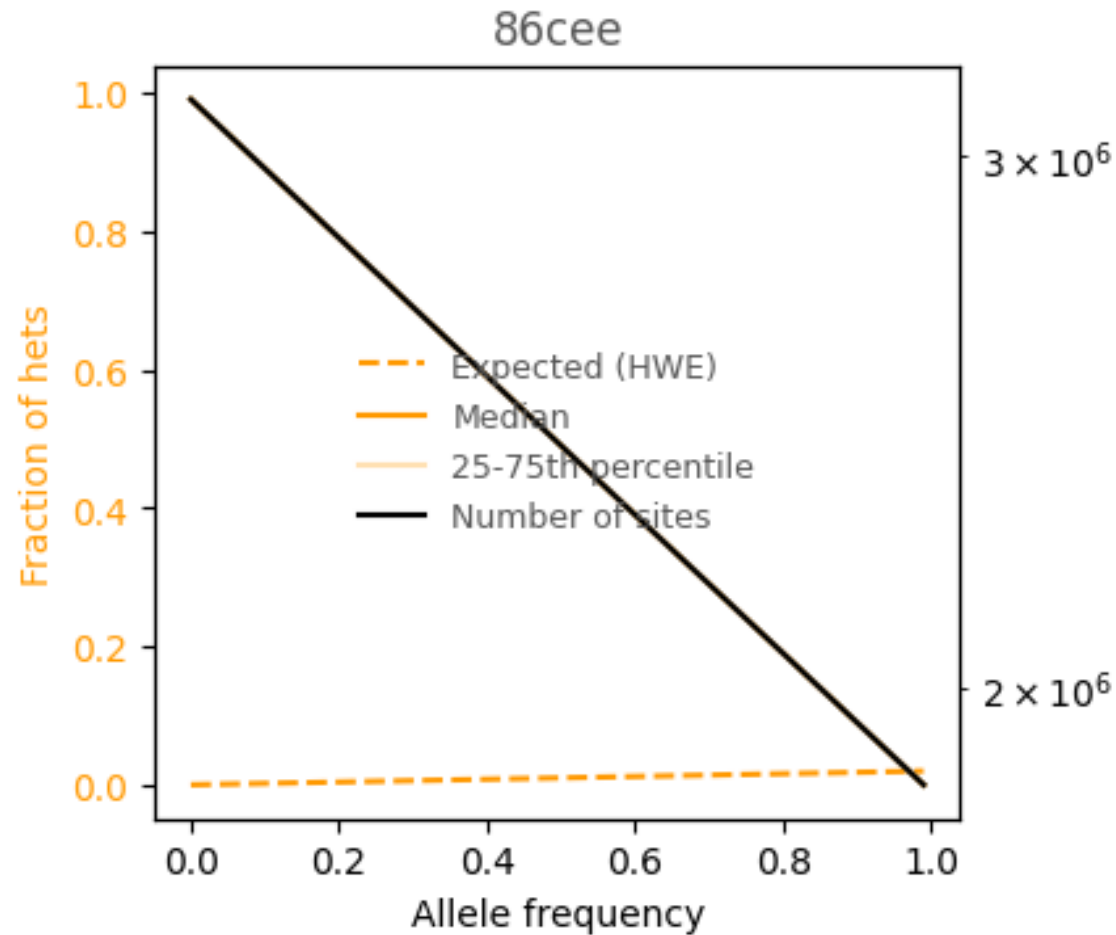# Indel distribution

# Fraction of alternate indel allele

# Depth distribution

# Number of HETs by AF

# Substitution types