Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
88cud	4,059,037	1.93	1.93	938,278	–	0	0
					* frameshift ratio: out/(out+in)		

Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
88cud	61.9%	1.89	66.3%	95,178	2,033

- 88cud .. `/ngc/projects2/gm/data/archive/2022/variants/snv/88cudithm-103858958837-Normal_B`
  `lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220413_A00559_BHGNWNDSX3-RHGM_LABKA_WGSA`
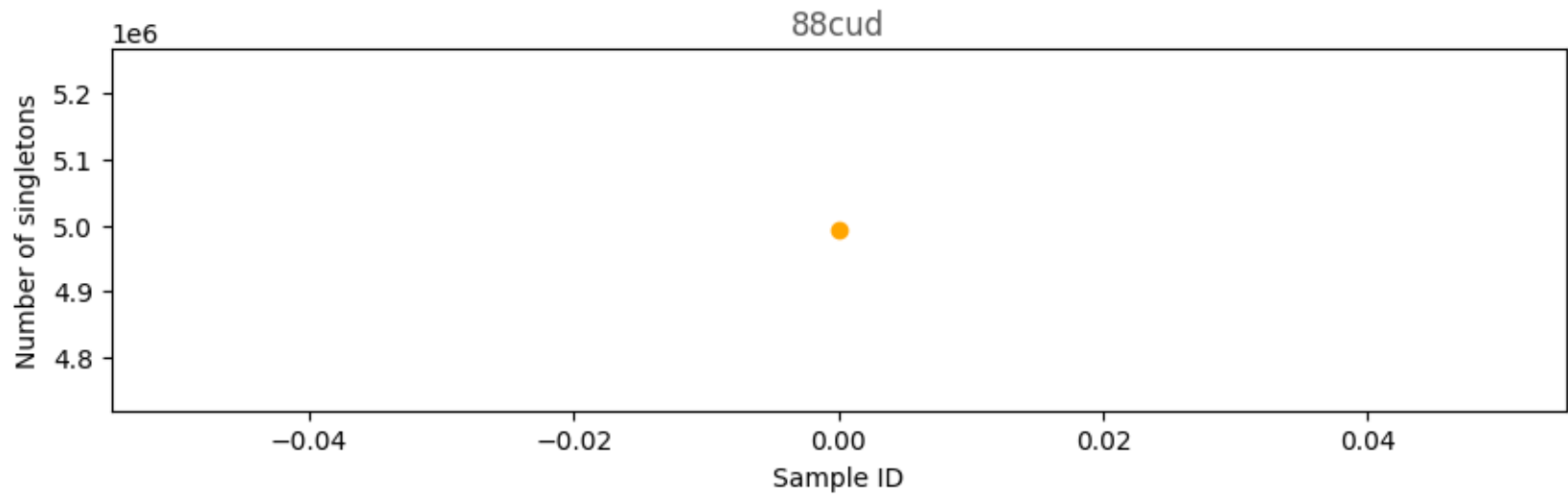 `KUT-WGSAKUT04129_22RKG008895x01_snv_germline_raw.haplotype_caller.vcf.gz`
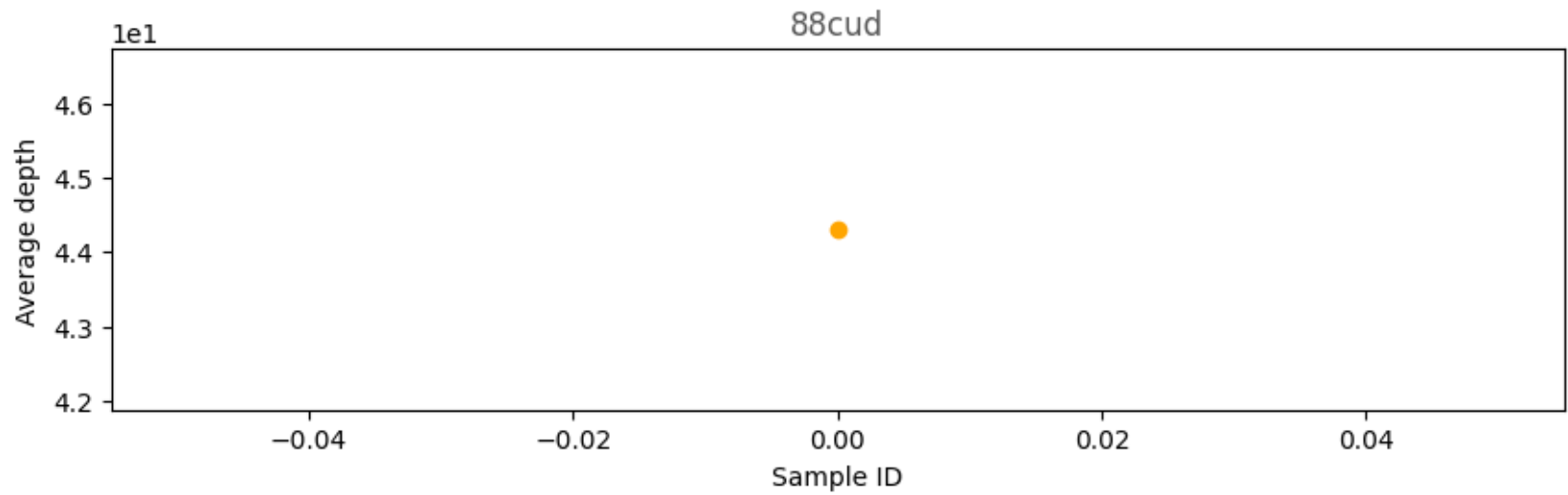
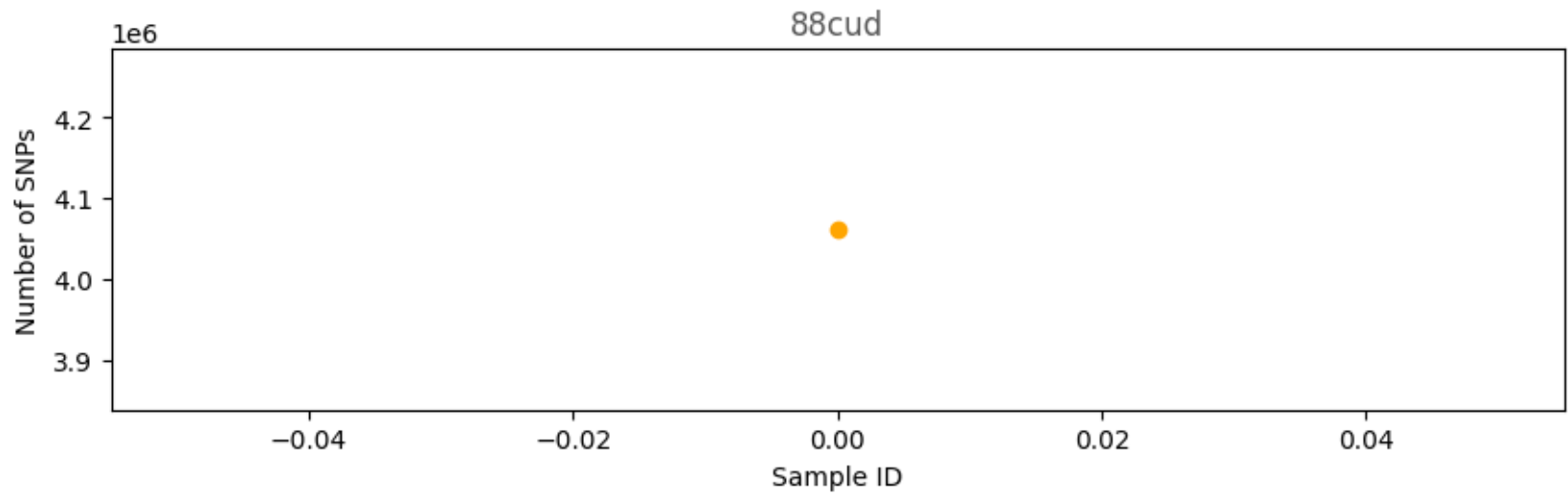# Ts/Tv by sample
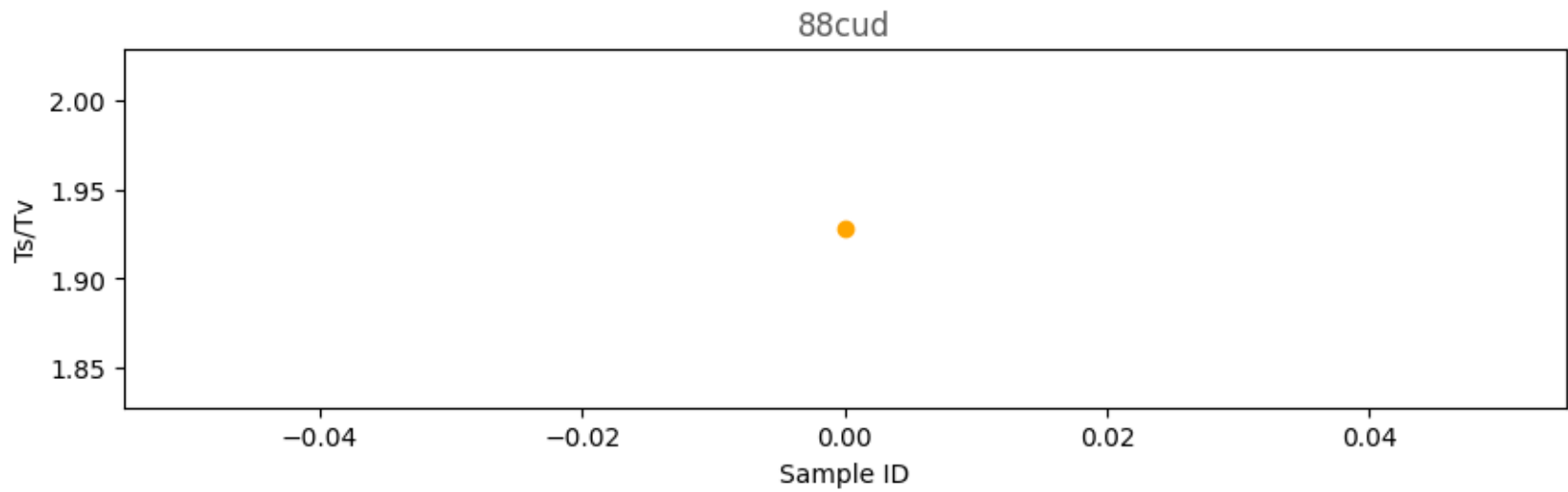
Hets vs non-ref Homs by sample
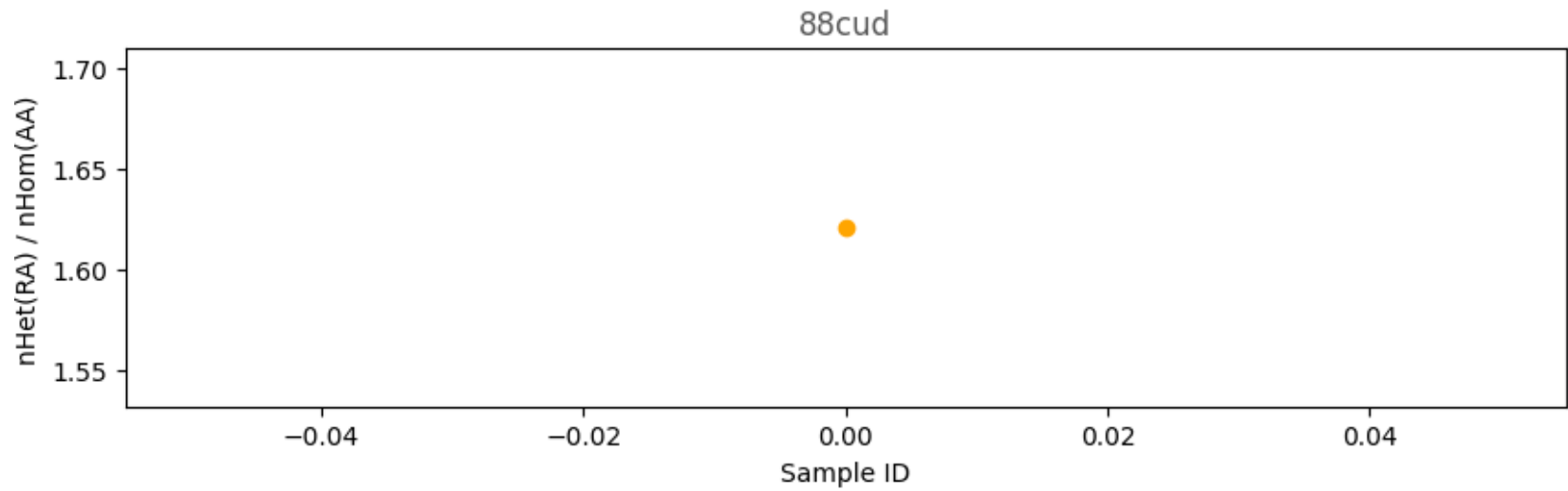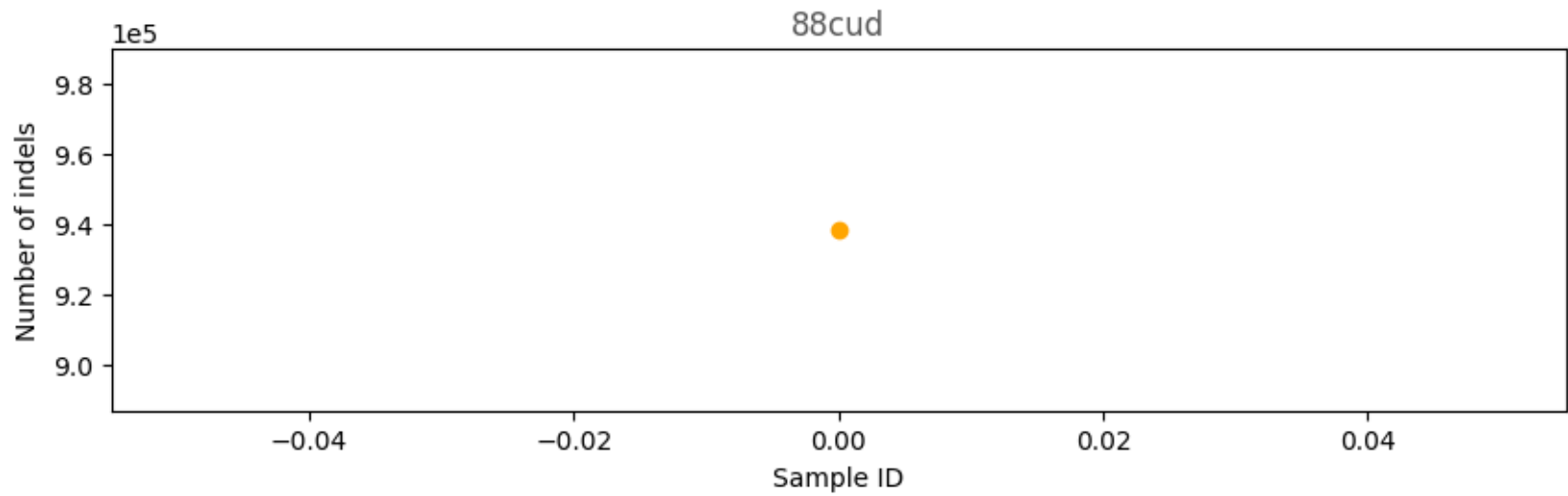
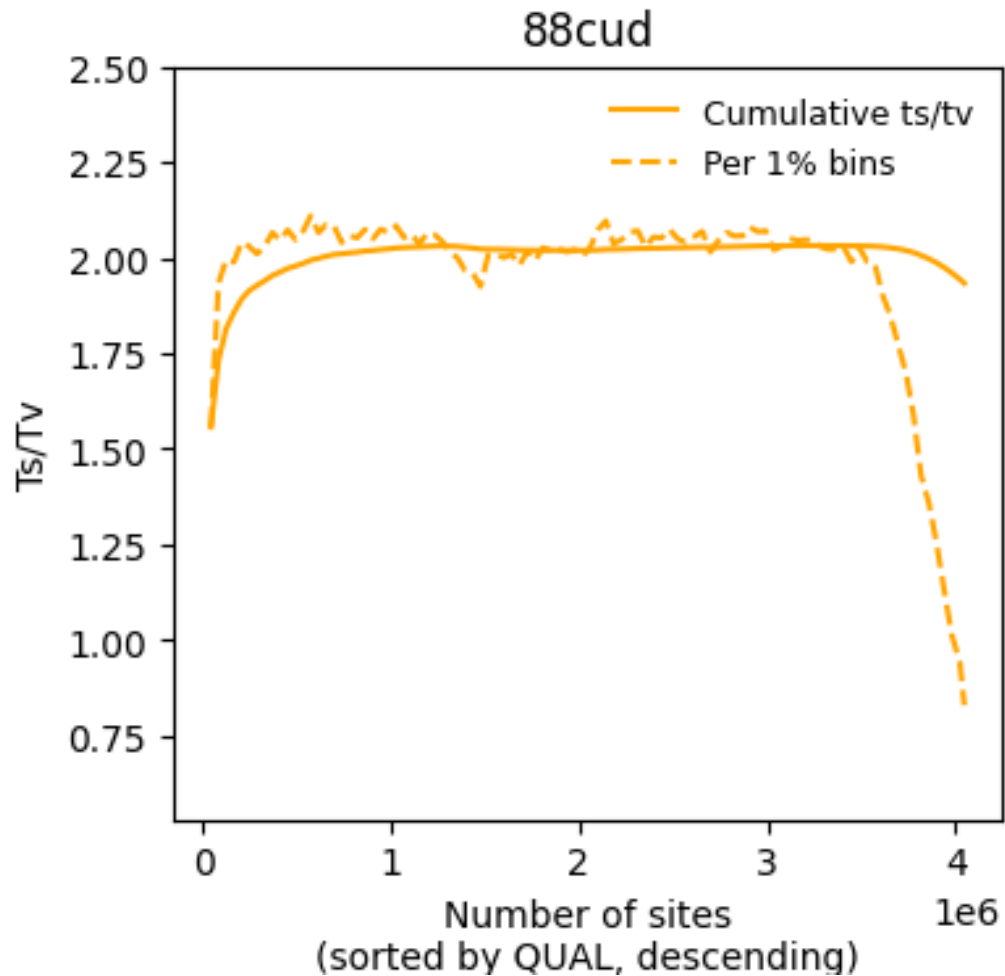# Singletons by sample (hets and homs)
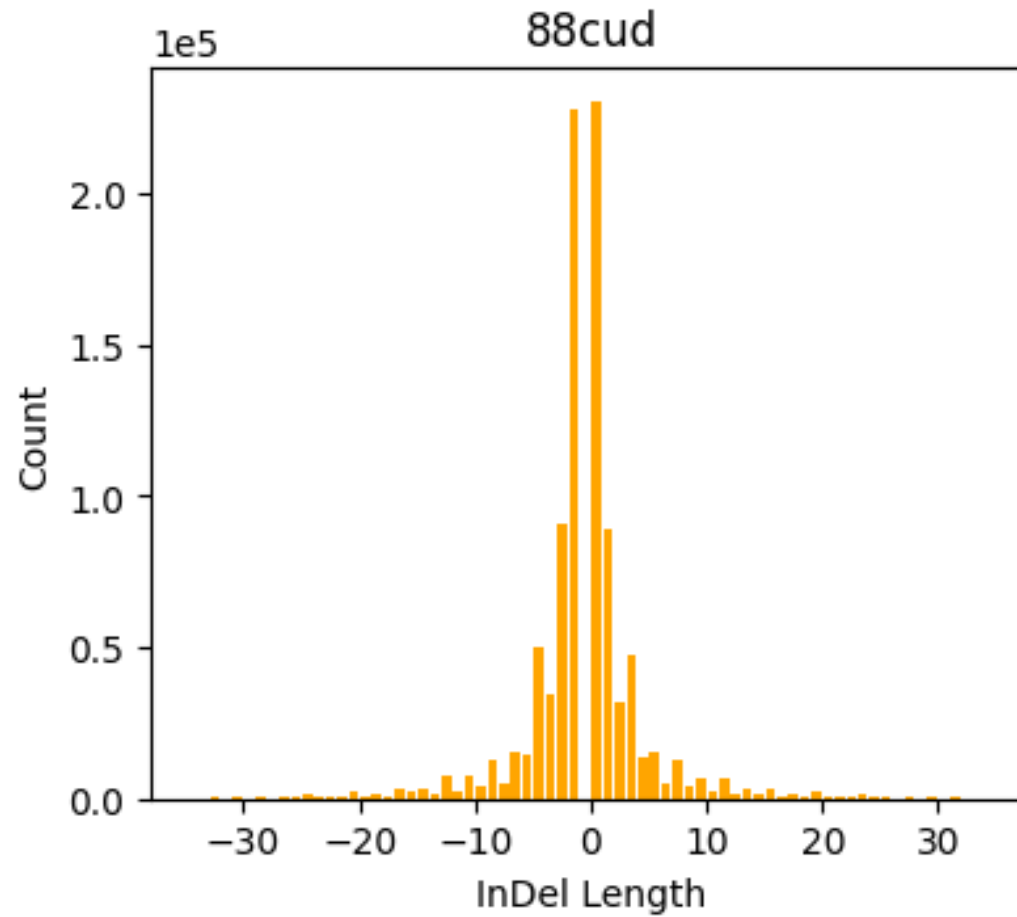
Average depth by sample
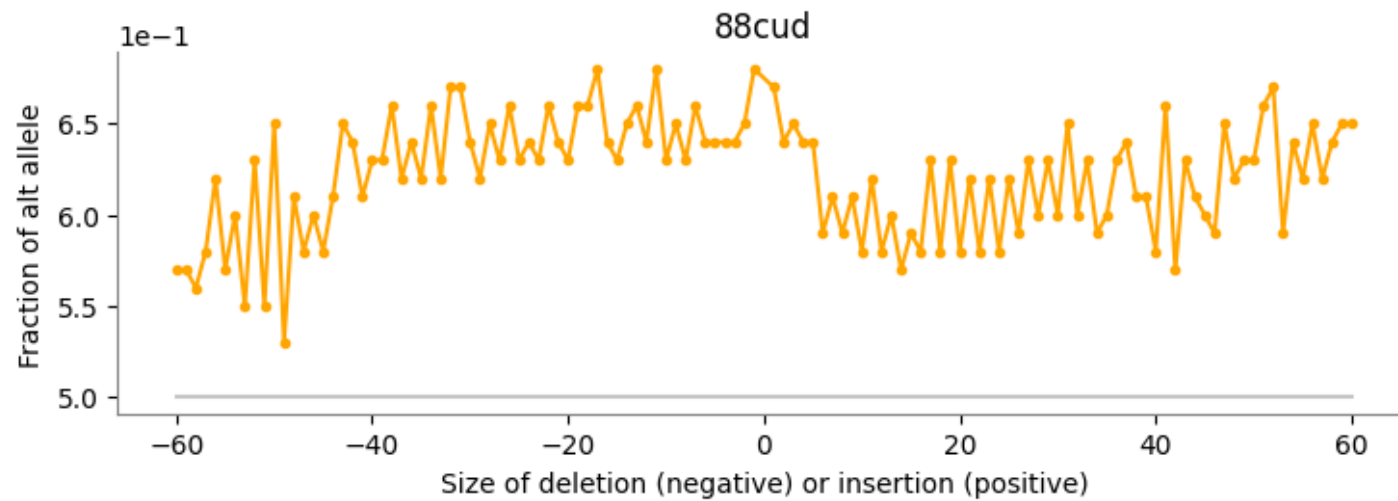
Number of SNPs by sample

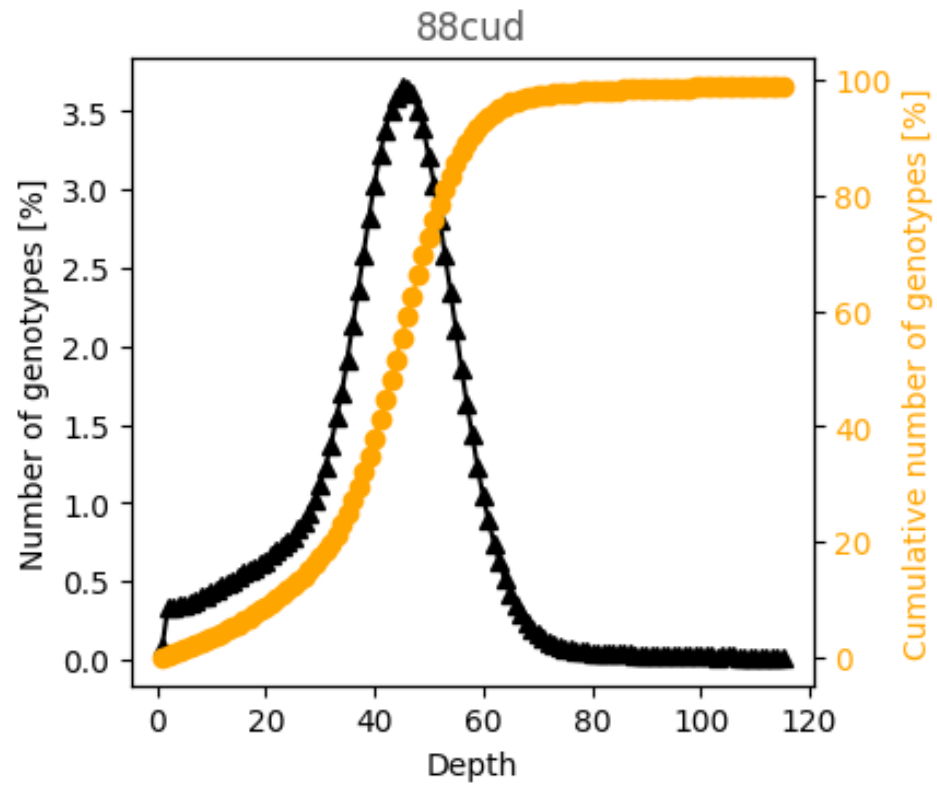# Number of indels by sample

Ts/Tv stratified by QUAL

88cud

Indel distribution

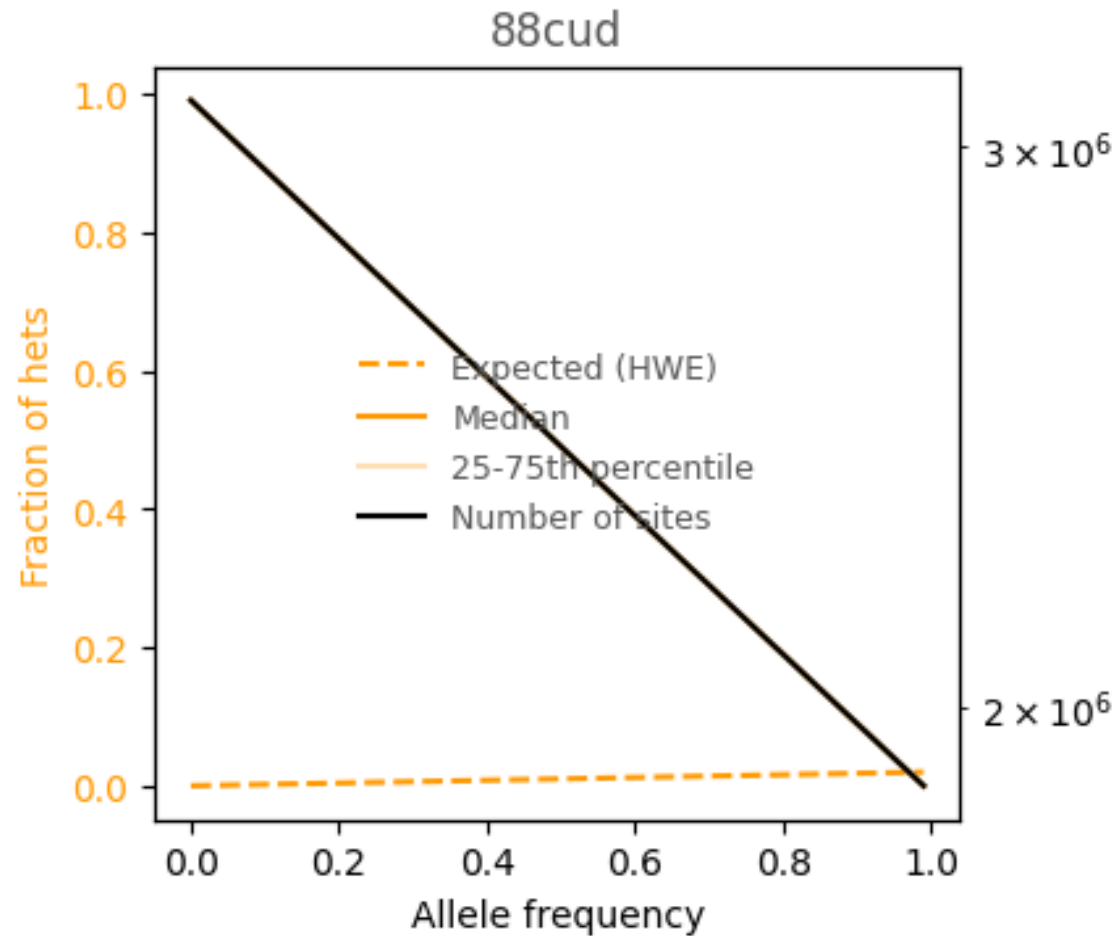# Fraction of alternate indel allele

Depth distribution

Number of HETs by AF

88cud

Substitution types