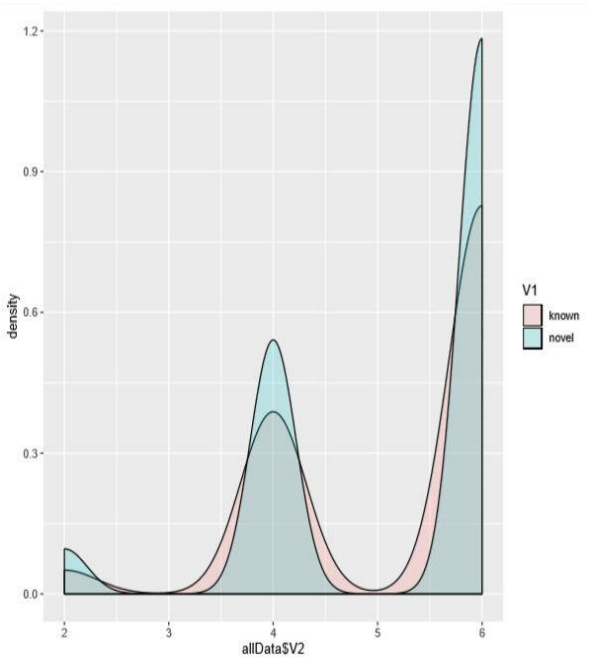
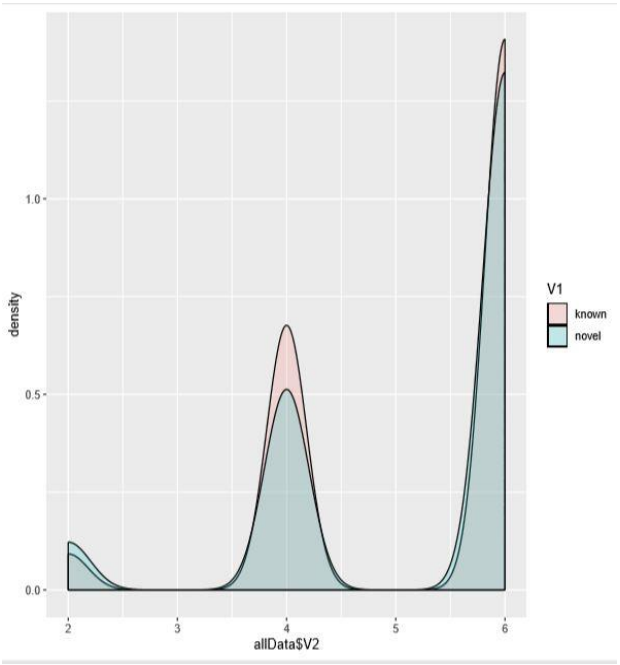
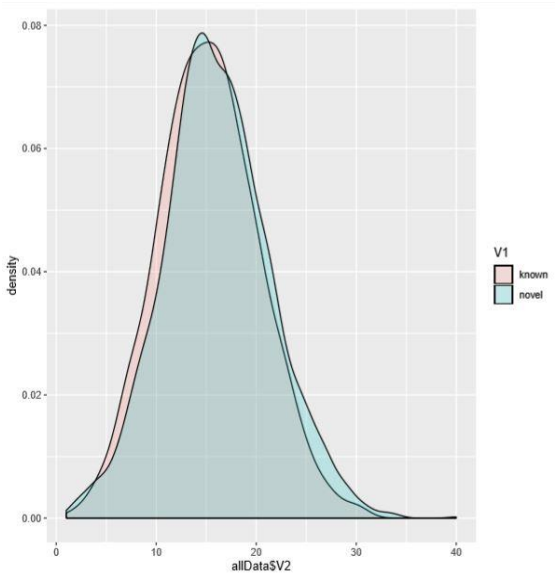
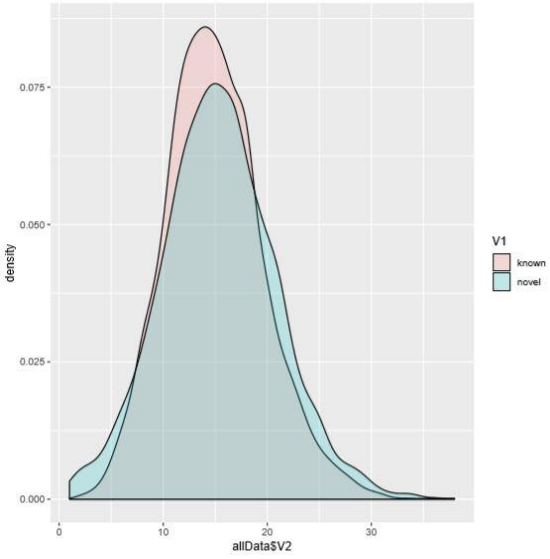
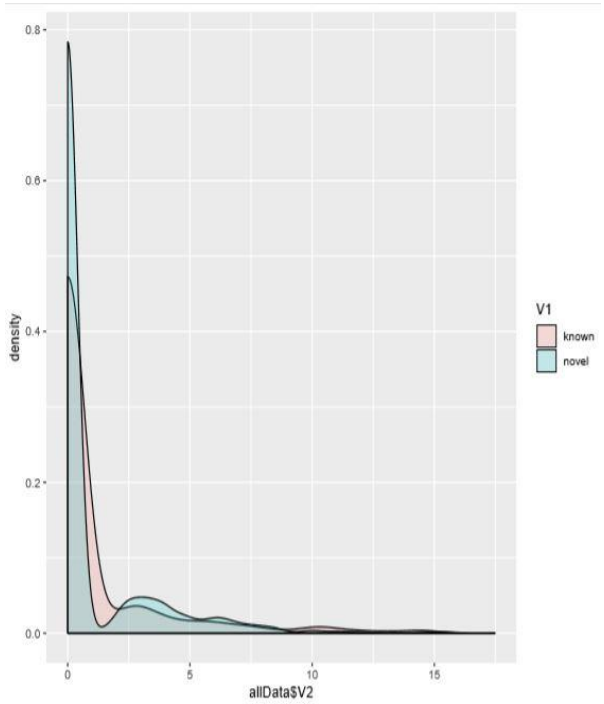
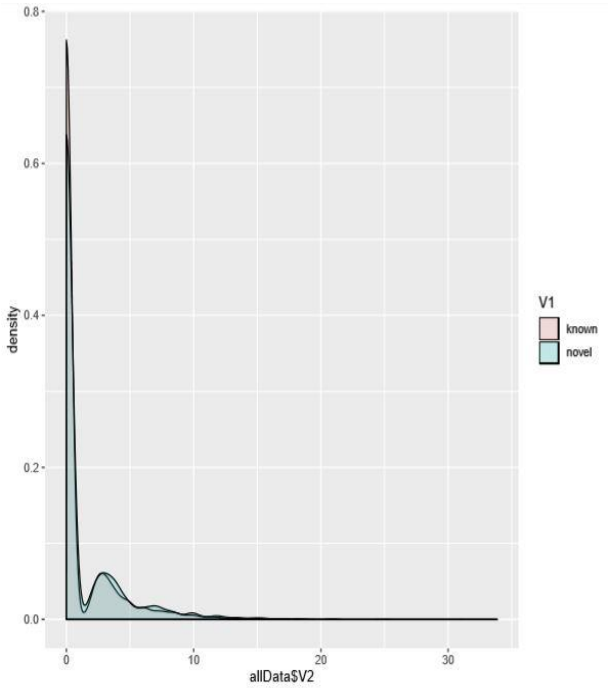
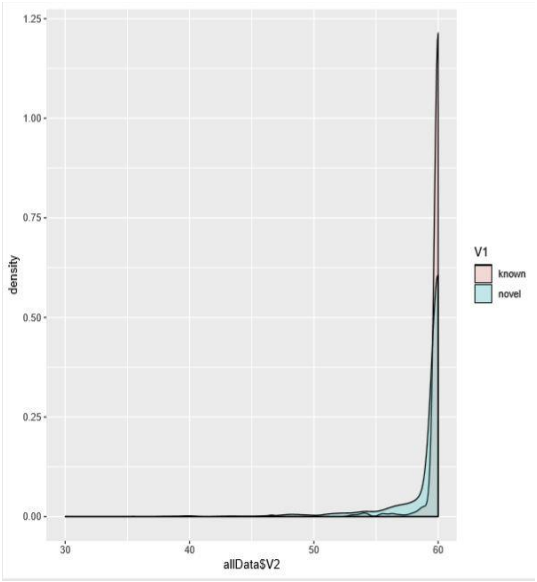
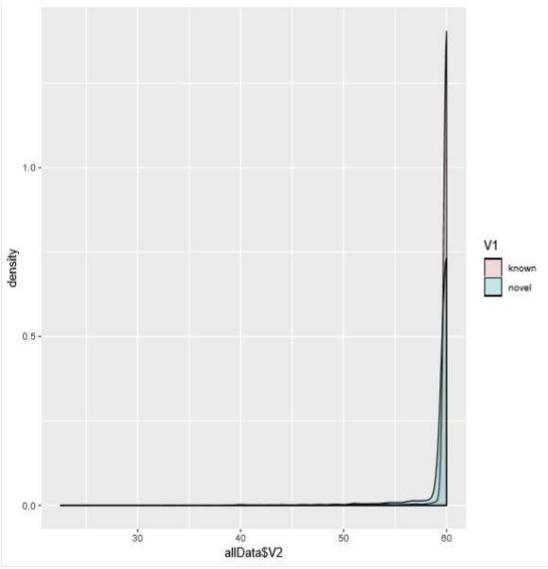
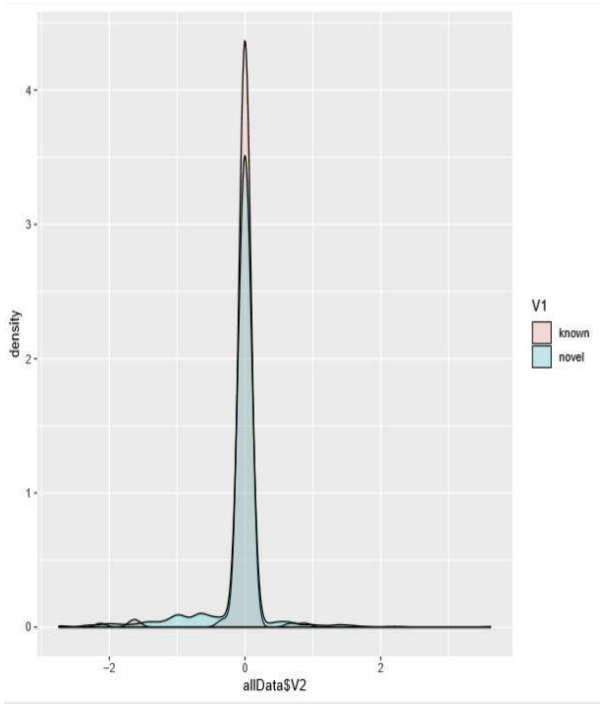
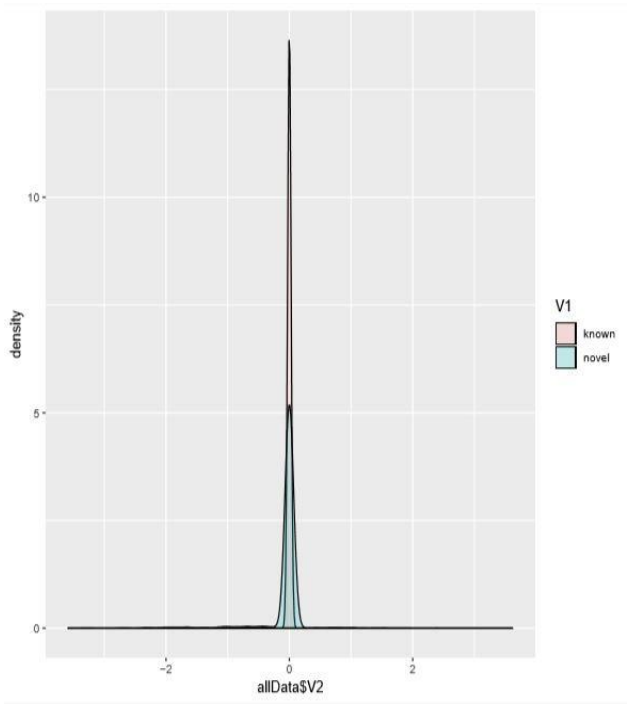
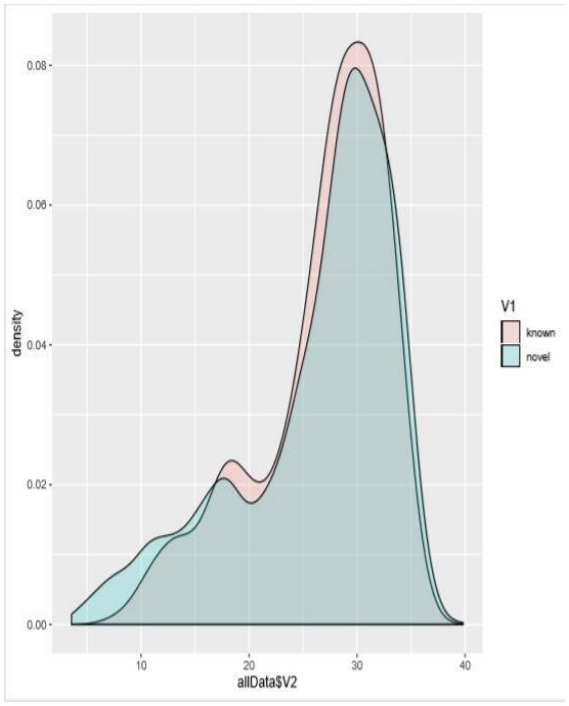
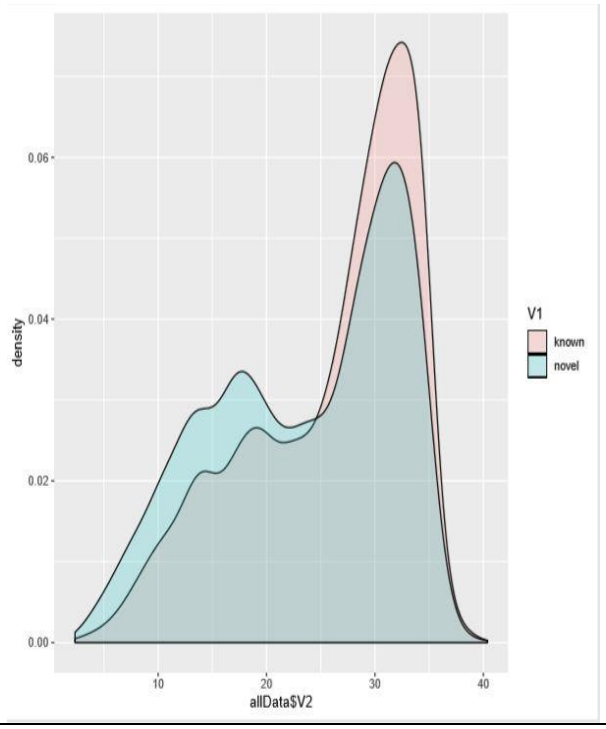
Working on R script (using test data "wget https://de.cyverse.org/dl/d/3CE425D7-ECDE-46B8-AB7F-FAF07048AD42/samples.tar.gz") to get figures for SNPs and INDELS before and after base recalibration as we supposed to move on the pipeline of dataset of Trisomy 21 and reach to VCF statistics till filtration, but unfortunately we couldn't because the number of annotated variants equal to zero.

	INDELS	SNPS
AN		
DP		

FS	 density allData$V2 V1 known novel	 density allData$V2 V1 known novel
MQ	 density allData$V2 V1 known novel	 density allData$V2 V1 known novel

MQ RankSum		
QD		

ReadPos-RankSum