<https://software.broadinstitute.org/gatk/documentation/tooldocs/current/picard_vcf_GenotypeConcordance.php>

java -jar picard.jar GenotypeConcordance \\

CALL\_VCF=input.vcf \\

CALL\_SAMPLE=sample\_name \\

O=gc\_concordance.vcf \\

TRUTH\_VCF=truth\_set.vcf \\

TRUTH\_SAMPLE=sample\_in\_truth \\

INTERVALS=confident.interval\_list \\

MISSING\_SITES\_HOM\_REF = true