The details regarding the WES assay in terms of sequencing information or variant calling information

Sequencing platform: DNBSEQ-T7

Library preparation reagents: Hieff NGS Ultima Pro DNA Library Prep Kit for Illumina SSELXT CRE V4

Sequencing specification: paired-end 150 bp depth >100x

Raw data filtering standard: Q30 ≥ 85%

fq quality control software: fastp, using the default parameters of the software

Comparison software: sentieon bwa mem uses the default parameters of the software

Deduplication method: gatk MarkDuplicates

Parameter：--OPTICAL\_DUPLICATE\_PIXEL\_DISTANCE 2500 --ASSUME\_SORT

\_ORDER "coordinate" --CLEAR\_DT false --CREATE\_MD5\_FILE true

Coefficient of variation：gatk parameter -T HaplotypeCaller -rf NotPrimaryAlignment -rf MaxInsertSize -maxInsert 1000 -rf BadCigar -rf BadMate --min\_mapping

\_quality\_score 20 -rf MateSameStrand --min\_base\_quality\_score 15

SNP parameter of filtration：QD < 2.0 || FS > 60.0 || MQ < 30.0, DP < 4

INDEL parameter of filtration：QD < 2.0 || FS > 200.0, DP < 4