
Low Pass Whole Genome Sequencing Method

1 Experimental Procedure

1.1 Sample Quality Control

Please refer to Novogene's QC report for methods of sample quality control.

1.2 Library Preparation and Sequencing

The genomic DNA sample was fragmented into short fragments. These DNA fragments were then end-polished, A-tailed, and ligated with full-length adapters for Illumina sequencing before further size selection. PCR amplification was then conducted unless specified as PCR-free. Purification was then conducted through the AMPure XP system (Beverly). The resulting library was assessed on the Agilent Fragment Analyzer System (Agilent) and quantified to 1.5nM through Qubit (Thermo Fisher Scientific) and qPCR.

The qualified libraries were pooled and sequenced on Illumina platforms, according to the effective library concentration and data amount required.

2 Bioinformatics Analysis

2.1 Raw Data

The original fluorescence image files obtained from the Illumina platform were transformed into short reads (raw data) by base-calling and these short reads were recorded in the FASTQ format, which contains sequences and the corresponding sequencing quality information.

2.2 Data Quality Control

It was the sequence artifacts, including reads containing adapter contamination, low-quality nucleotides, and unrecognizable nucleotide (N), that undoubtedly set the barrier for the subsequent reliable bioinformatics analysis. Therefore, quality control is an essential step to mitigate these obstacles and could be applied to guarantee meaningful downstream analysis.

The steps of data processing were as follows:

- (1) Discard a pair of reads if either one of them contains adapter contamination (>10 nucleotides aligned to the adapter, allowing $\leq 10\%$ mismatches);
- (2) Discard a pair of reads if more than 10% of bases are uncertain (read as N) in either one of the reads;
- (3) Discard a pair of reads if the proportion of low quality (Phred quality <5) bases is over 50% in either one of the reads.

Total reads number, raw data, error rate, and percentage of reads with Q30 (the percent of bases with Phred-scaled quality scores greater than 30) were calculated and summarized. After which, filtered reads were used as clean data for subsequent analysis.

2.3 Sequence Alignment

Clean data were mapped to the reference genome (b37/hg19/hg38) by Burrows-Wheeler Aligner (BWA) software (Li et al., 2018) to generate BAM files. Subsequently, Sambamba (Tarasov et al., 2015) was used to sort BAM files according to chromosome position. Picard tools (The Quick Start is available online: <https://broadinstitute.github.io/picard/>) were then utilized to merge BAM files and mark duplicate reads.

2.4 Variant Detection

2.4.1 Germline Mutation Detection

GATK (DePristo et al., 2011) was used to do the SNP and InDel joint calling, while the ichor-CNA was used to call germline CNV. Then the IMPUTE version 2 (Howie et al., 2009) was carried to do the genotype imputation and haplotype phasing

2.5 Annotation

ANNOVAR (Wang et al., 2010) was used to perform variant annotation. Annotation contents refer to protein-coding changes, genomic regions affected by the variants, allele frequency, deleterious prediction, etc. The main databases used were as follows:

Genes and regions annotation

RefSeq (O'Leary et al., 2016) and Gencode (Frankish et al., 2021) databases were used to find genomic regions affected by variants and possible changes in the protein. We annotated the features of the genomic regions affected by the variants, such as cytoband, small RNA, conserved mammalian microRNA regulatory target sites, conservative regions of vertebrates, transcription factor binding sites, repeats, etc.

Databases with frequency annotation

The established databases, such as 1000 Genomes (1000 Genomes Project Consortium) (Abecasis et al., 2012), Exome Aggregation Consortium (ExAC) (Kobayashi et al., 2017), Genome Aggregation Database (gnomAD) (Pio et al., 2021) and exome sequencing project (ESP), were all used to find alternative allele frequencies in the populations that were reported. There are a great number of common polymorphism sites in the human population, while many deleterious variants are rare or of low frequency.

Databases and scores with conservative and deleterious annotation

SIFT (Ng et al., 2003), PolyPhen (Adzhubei et al., 2013), MutationAssessor (Reva et al., 2011), LRT (Chun et al., 2009), and CADD (Rentzsch et al., 2019) scores were used to predict the deleterious mutations. GERP++ (Huber et al., 2020) scores were used to evaluate the conservation of mutations. SIFT, Polyphen2, MutationTaster (Steinhaus et al., 2021), LRT, MutationAssessor, and FATHMM (Shihab et al., 2013) were all used to predict whether an amino acid substitution affected protein function. SiPhy (Garber et al., 2009), phyloP (Pollard et al., 2010), GERP++, and CADD were all used to predict the conservative level of the site. It should be noted that the conservation scores only consider the conservative level at the current site, but

not the one involved in the nucleotide identity. Therefore, synonymous and non-synonymous variants at the same site will have the same scores. These scores are used for finding functionally important sites, which means that variants that confer increased susceptibility would score well.

Databases with cancer and disease-related annotation

dbSNP (Sherry et al., 2001), COSMIC (Tate et al., 2019), OMIM (Hamosh et al., 2005), GWAS Catalog (Buniello et al., 2019), and HGMD (Stenson et al., 2020) were used to find reported information of the variants.

Databases with functional and pathway annotation

Gene Ontology (Lee et al., 2004), KEGG (Kanehisa et al., 2000), Reactome (Jassal et al., 2020), and PID (Schaefer et al., 2009) databases were applied to provide functional or pathway annotation.

3 References

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