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BASECLEAR

Project code/Order number

096903

Date of Report

May-23-2018

Authorization

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Sequencing*



Next Generation Sequencing project

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Project 96903
Client John Bouwman
Date May-23-2018 14:17

1. Introduction

This report contains a detailed overview of your next-generation sequencing experiment. The data and results apply to the following samples:

	Illumina demultiplexing
ILC-oral-1	X
ILC-oral-2	X
ILC-oral-3	X
ILC-oral-4	X
ILC-oral-5	X

2. Download of data and analysis files

Order placed via the order-portal

The data and analysis results can be downloaded via the [order-portal](#) after login with your credentials.

Other - Please contact us via info@baseclear.com to obtain a username and password.

The secure FTP server can be accessed using a FTPs client (e.g. FileZilla). After installation, open the program and login with your username/password combination.

FTP connection details:

Host	ftps.baseclear.com
Port	990
Protocol	FTP – File Transfer Protocol
Encryption	Require implicit FTP over TLS

3. Illumina demultiplexing

Single-end or paired-end sequence reads were generated using the Illumina HiSeq2500 or MiSeq system.

FASTQ read sequence files were generated using bcl2fastq2 version 2.18. Initial quality assessment was based on data passing the Illumina Chastity filtering. Subsequently, reads containing PhiX control signal were removed using an in-house filtering protocol. In addition, reads containing (partial) adapters were clipped (up to a minimum read length of 50 bp). The second quality assessment was based on the remaining reads using the FASTQC quality control tool version 0.11.5.

The final quality scores per sample are provided as enclosure.

4. Results

A summary of the results is provided below. Sequence and project data are recorded digitally in our secure database and stored for backup purposes only. Data is stored for a period of two months. The result files which have been generated within this project for each analysis are as follows:

Illumina demultiplexing

The files are stored in the "raw_sequences" folder and include:

- The compressed sequence reads in FASTQ format (*.filt.fastq.gz)
- A text file containing the MD5 checksum (fingerprint) of each gzipped FASTQ file ("md5sum_*.txt")

Illumina demultiplexing report

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Summary of the results - Illumina demultiplexing report

Statistics after demultiplexing and filtering

Sample name	Number of reads	Average quality	Yield
ILC-oral-1	72697	34.67	43
ILC-oral-2	74142	33.36	44
ILC-oral-3	81206	34.56	48
ILC-oral-4	62084	34.16	37
ILC-oral-5	73715	33.41	44