

Sequencing statistics ATAC-seq 006_0235

Diagenode Epigenomics Services

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Introduction

This document describes the statistics obtained after sequencing of 6 samples on Novaseq 6000, running NovaSeq Control Software 1.7.5, RTA v3.4.4, and bcl2fastq2.20 v2.20.0.422.

Sequencing statistics.

The sequencing statistics of the samples are shown in table 1 and display:

- Number of read pairs: the number of read pairs obtained for each sample.
- Q30: the percentage of bases with a quality score greater or equal to 30.
- Mean Qual: the average quality score of all bases sequenced for each sample. This includes R1 and R2.

Table 1: Sequencing statistics

Sample_Name	Sample_ID	Number of read pairs	Q30	Mean Qual
006-CTL01-1	006_0235_001	46,680,365	94.71	36.10
006-TAM01-2	006_0235_002	43,674,790	91.27	35.55
006-CTL02-3	006_0235_003	54,472,758	94.31	36.04
006-TAM02-4	006_0235_009	59,461,012	94.87	36.14
006-WNT01-5	006_0235_005	42,086,934	93.48	35.91
006-WNT02-6	006_0235_006	41,494,951	94.38	36.04

Files

The following files are provided with this document:

1. fastq: directory containing the original reads from the sequencing in fastq gzip compressed format.

Data Download

You may download these files via SFTP transfer with the following credentials:

- IP address: 94.140.182.196
- port: 3022
- username: pgarcia
- password: M6!15pA\$

Our SFTP server is accessible via the command line or via a graphical client like [FileZilla](#).

IMPORTANT: Generated files will be available for download during 1 month and stored for an additional period of 3 months on Diagenode's servers. We recommend that you keep backed-up copies of the files.