

Project Overview

J.Lundeberg_14_01

Project Information

| | |
|------------------------------|--|
| User Project Name | 140117_Rapid_Ventana_TdT |
| NGI Project Name | J.Lundeberg_14_01 |
| NGI Project ID | P955 |
| User Contact | jlundeberg@ki.se |
| NGI Application Type | Finished Library (No best practice analysis) |
| Samples & Lanes | 1 sample, 2 lanes |
| Project Status | Sequencing Finished |
| Order Dates | <i>Order received:</i> 2014-01-10, <i>Contract received:</i> 2014-01-15, <i>Samples received:</i> 2014-01-20, <i>Queue date:</i> 2014-01-23, <i>All data delivered:</i> 2014-04-02, <i>Report Date:</i> 2014-12-02 |
| UPPMAX Project ID | b2011007 |
| UPPNEX project path | /proj/b2011007/INBOX/J.Lundberg_14 |
| Reference Genome | Human, hg19 |
| Minimum ordered reads | 200 million |

Methods

Library construction

- A) Library was prepared using the “650 bp insert standard DNA (Illumina TruSeq DNA)” protocol and clustering was done by cBot.

Sequencing

- A) All samples were sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup. The Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale used is Sanger / phred33 / Illumina 1.8+.

Data Flow

All data (demultiplexed) from the instrument are collected and transferred securely to a storage server with well established pipeline.

Data Processing:

A set of standard quality checks were performed to assure that all sequenced data meet NGI guaranteed quality / quantity. All analysis are carried out in UPPMAX servers before delivering the raw data.

Swedac Accreditation

The National Genomics Infrastructure is accredited by [Swedac](#). This means that our services are subject to highly stringent quality control procedures, so that you can be sure that your data is of excellent quality.

| | |
|---------------------|-------------------------|
| Library preparation | ✗ Not Swedac Accredited |
| Sequencing data | ✓ Swedac Accredited |
| Data flow | ✓ Swedac Accredited |
| Data processing | ✓ Swedac Accredited |

Sample Info

| NGI ID | User ID | Index | Lib Prep |
|----------|--------------------------|------------------|----------|
| P955_101 | 140117_Rapid_Ventana_TdT | Index 8 (ACTTGA) | A |

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Yield Overview

| Sample | Lib QC | Avg. FS | ≥ Q30 | # Reads | Status |
|-----------|--------|---------|--------|----------|--------|
| P955_101b | Passed | 350 bp | 59.34% | 105.66 M | Passed |

- *Lib QC*: Reception control library quality control step

- *Avg. FS*: Average fragment size.
- $\geq Q30$: Percentage of bases above quality score Q30 for the sample.
- *# Reads*: Millions of reads sequenced.

Run Info

| Date | FC id | Lane | Clusters | % PhiX | $\geq Q30$ | % Unique | Method |
|--------|-------------|------|----------|--------|------------|----------|--------|
| 140123 | B-H8A63ADXX | 1 | 66.88 M | 0.52% | 58.70% | 80.51% | A |
| 140123 | B-H8A63ADXX | 2 | 65.89 M | 0.56% | 57.15% | 78.32% | A |

- *FC id*: Position on flowcell - Flowcell ID.
- $\geq Q30$: Percentage of bases above quality score Q30 on the lane.
- *Unique*: Percentage of reads recovered after demultiplexing.
- *Method*: Sequencing method used. See above for description.

General Information

Naming conventions

The data is delivered in FastQ format using Illumina 1.8 quality scores. There will be one file for the forward reads and one file for the reverse reads (if the run was a paired-end run).

The naming of the files follow the convention:

[LANE]_[DATE]_[POSITION][FLOWCELL]_[NGI-NAME]_[READ].fastq.gz

Data access at UPPMAX

Data from the sequencing will be uploaded to the UPPNEX (UPPMAX Next Generation sequence Cluster Storage, uppmx.uu.se), from which the user can access it. You can find the data in the INBOX folder of the UPPNEX project, which was created for you when your order was placed:

/proj/b2011007/INBOX/J.Lundberg_14

If you have problems accessing your data, please contact SciLifeLab genomics_support@scilifelab.se. If you have questions regarding UPPNEX, please contact support@uppmx.uu.se.

Acknowledgements

In publications based on data from the work covered by this contract, the authors must acknowledge SciLifeLab, NGI and Uppmax:

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Further Help

If you have any queries, please get in touch at genomics_support@scilifelab.se.