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	jlundberg@ki.se
NGI Application Type	Finished Library (No best practice analysis)
Samples & Lanes	1 sample, 2 lanes
Project Status	Sequencing Finished
Order Dates	*Order received:* 2014-01-10, *Contract received:* 2014-01-15, *Samples received:* 2014-01-20, *Queue date:* 2014-01-23, *All data delivered:* 2014-04-02, *Report Date:* 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 transfered 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

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.
- ≥ *Q30:* Percentage of bases above quality score Q30 for the sample.
- *# Reads:* Millions of reads sequenced.

Run Info

Date	FC id	Lane	Clusters	% PhiX	≥ Q30	% Unique	Method
2014-01-23	B-H8A63ADXX	1	66.88 M	0.52%	58.70%	80.51%	A
2014-01-23	B-H8A63ADXX	2	65.89 M	0.56%	57.15%	78.32%	A

- *FC id:* Position on flowcell - Flowcell ID.
- *≥ 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, uppmax.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@uppmax.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.