Project overview

Project **J.Lundeberg_14_01(140117_Rapid_Ventana_TdT)** with 1 sample(s) is sequenced and all raw data with analysis data(if applicable) have been delivered to UPPMAX project ID **b2011007**. Project was run on flowcell(s) 130517_SN7001301_0086_AD259NACXX. Please follow through the report for elobrated overview.

Report name: J.Lundberg_14_01_project_summary

Date: April 2, 2014

Issued by: SP

Project duration: 2014-01-23 to 2014-04-02

Project status

Sequencing finished.

User contact details

jlundberg@ki.se

Order Information

Field	Info
Project name	J.Lundberg_14_01
Project id	P955
Application	Finished library
Run setup	2x101
Best practice analysis	No
Lanes ordered	2
Number of samples	1
Reference Genome	Other
Minimum ordered reads(M)	None
Order received	2014-01-10
Contract received	2014-01-15
Samples received	2014-01-20
Queue date	2014-01-23
UPPNEX id	b2011007
UPPNEX project path	/proj/b2011007/INBOX/J.Lundberg_14_01
All data delivered	2014-04-02

Methods

- *Library contructions:*
  - **A:** Library was prepared using "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.

Methods used	Swedac accredited
Library preparation	✗
Sequencing data	✓
Data flow	✓
Data processing	✓

Sample Info

SciLife ID	Submitted ID	Index	Lib Prep
P955_101	140117_Rapid_Ventana_TdT	Index 8 (ACTTGA)	A

Yield overview

Sample	Lib QC	Avg. FS(bp)	Q30(%)	MSequenced	Status
P955_101	✓	350	59.34	105.66	✓

* **Abrevations:** *Lib QC*: Recepetion control, *Avg. FS*: Average Fragment Size, *Q30*: Percentage of bases above quality score Q30 for the sample, *MSequenced*: Millions reads sequenced.

Run Info

Date	Pos-FCid	Lane	Clusters(M)	PhiX(%)	Q30(%)	DRecovery(%)	SMethod
140123	B-H8A63ADXX	1	66.88	0.52	58.70	80.51	A
140123	B-H8A63ADXX	2	65.89	0.56	57.15	78.32	A

* **Abrevations:** *Pos-FCid:* Position of flowcell-Flowcell ID, *Q30(%):* Percentage of bases above quality score Q30 on the lane, *DRecovery*: Percentage of reads recovered after demultiplexing.

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]_[SCILIFE NAME]_[READ].fastq.gz

Data access at UPPMAX

Data from the sequencing will be uploaded to the UPPNEX (UPPMAX Next Generation sequence Cluster Storage, www.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, e.g.

/proj/b2013000/INBOX/J.Doe_13_01

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

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Regards

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