

Project status note

SciLifeLab Stockholm

July 15, 2015

Project name

A.Blomberg_15_01 (Clone of Fucus vesiculosus - DNA)

UPPNEX project id

b2011228

Sequence data directories

/proj/b2011228/INBOX/A.Blomberg_15_01/

Flowcells Delivered

150521_AC6VGLANXX

Samples

ScilifeID	SubmittedID	BarcodeSeq	MSequenced	MOrdered
P1887_101	Fves11	NoIndex	265.653467	188

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]_[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.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, 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@uppmx.uu.se.

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