Project status note

SciLifeLab Stockholm

2015-02-16

Project name

N.Street_14_08 (Cone development - mRNA)

UPPNEX project id

b2015052

Sequence data directories

/proj/b2015052/INBOX/N.Street_14_08

Samples

ScilifeID	SubmittedID	BarcodeSeq	MSequenced	MOrdered
P1387_101	Pab.M1-09-12.TR0001	TCCGGAGA-TATAGCCT	19.34	11.28
P1387_102	Pab.M1-10-08.TR0001	TCCGGAGA-ATAGAGGC	21.93	11.28
P1387_103	Pab.M2-09-12.TR0001	TCCGGAGA-CCTATCCT	20.03	11.28
P1387_104	Pab.M3-09-12.TR0001	TCCGGAGA-GGCTCTGA	17.68	11.28
P1387_105	Pab.M4-09-12.TR0001	TCCGGAGA-AGGCGAAG	20.42	11.28
P1387_106	Pab.M5-09-12.TR0001	TCCGGAGA-TAATCTTA	22.41	11.28
P1387_107	Pab.M2-10-08.TR0001	TCCGGAGA-CAGGACGT	25.22	11.28
P1387_108	Pab.M4-10-08.TR0001	TCCGGAGA-GTACTGAC	18.78	11.28
P1387_109	Pab.M3-10-08.TR0001	CGCTCATT-TATAGCCT	18.38	11.28
P1387_110	Pab.M5-10-08.TR0001	CGCTCATT-ATAGAGGC	19.04	11.28
P1387_111	Pab.F2-10-08.TR0001	CGCTCATT-CCTATCCT	18.37	11.28
P1387_112	Pab.F3-10-08.TR0001	CGCTCATT-GGCTCTGA	22.13	11.28
P1387_113	Pab.F1-09-12.TR0001	CGCTCATT-AGGCGAAG	19.43	11.28
P1387_114	Pab.F4-09-12.TR0001	CGCTCATT-TAATCTTA	21.84	11.28
P1387_115	Pab.F1-10-08.TR0001	CGCTCATT-CAGGACGT	25.13	11.28
P1387_116	Pab.F2-09-12.TR0001	CGCTCATT-GTACTGAC	22.66	11.28
P1387_117	Pab.F4-10-08.TR0001	GAGATTCC-TATAGCCT	20.52	11.28
P1387_118	Pab.F5-09-12.TR0001	GAGATTCC-ATAGAGGC	21.66	11.28
P1387_119	Pab.V4-10-08.TR0001	GAGATTCC-CCTATCCT	16.47	11.28
P1387_120	Pab.V5-10-08.TR0001	GAGATTCC-GGCTCTGA	19.55	11.28
P1387_121	Pab.F5-10-08.TR0001	GAGATTCC-AGGCGAAG	22.70	11.28

P1387_122	Pab.F3-09-12.TR0001	GAGATTCC-TAATCTTA	21.50	11.28
P1387_123	Pab.V3-10-08.TR0001	GAGATTCC-CAGGACGT	28.27	11.28
P1387_124	Pab.V2-10-08.TR0001	GAGATTCC-GTACTGAC	19.10	11.28
P1387_125	Pab.V1-10-08.TR0001	ATTCAGAA-TATAGCCT	19.21	11.28

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.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.

Acknowledgement

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