Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1031/140619_BC47HDACXX

Sample

P1260_1031 / G4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.02 (86.43% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1007/140619_BC47HDACXX

Sample

P1260_1007 / G1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.18 (93.31% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1025/140619_BC47HDACXX

Sample

P1260_1025 / A4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

13.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.04 (93.28% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1004/140619_BC47HDACXX

Sample

P1260_1004 / D1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.4 million read pairs in lane with PhiX error rate 0.27%. Average quality score 35.64 (91.51% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1017/140619_BC47HDACXX

Sample

P1260_1017 / A3_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.7 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.26 (93.80% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1006/140619_BC47HDACXX

Sample

P1260_1006 / F1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.8 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.07 (92.87% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1016/140619_BC47HDACXX

Sample

P1260_1016 / H2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.32 (93.81% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1010/140619_BC47HDACXX

Sample

P1260_1010 / B2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

1.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.17 (93.21% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1002/140619_BC47HDACXX

Sample

P1260_1002 / B1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

1.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.47 (94.31% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1001/140619_BC47HDACXX

Sample

P1260_1001 / A1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.42 (94.24% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1028/140619_BC47HDACXX

Sample

P1260_1028 / D4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

8.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.19 (87.23% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1015/140619_BC47HDACXX

Sample

P1260_1015 / G2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.37 (93.98% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1019/140619_BC47HDACXX

Sample

P1260_1019 / C3_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.7 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.04 (92.74% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1012/140619_BC47HDACXX

Sample

P1260_1012 / D2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.34 (93.81% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1005/140619_BC47HDACXX

Sample

P1260_1005 / E1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 35.99 (92.62% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1033/140619_BC47HDACXX

Sample

P1260_1033 / A5_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

15.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 35.91 (92.61% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1022/140619_BC47HDACXX

Sample

P1260_1022 / F3_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 33.27 (84.13% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1009/140619_BC47HDACXX

Sample

P1260_1009 / A2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.32 (93.82% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1018/140619_BC47HDACXX

Sample

P1260_1018 / B3_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.7 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.23 (93.65% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1032/140619_BC47HDACXX

Sample

P1260_1032 / H4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

17.3 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.33 (93.96% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1011/140619_BC47HDACXX

Sample

P1260_1011 / C2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

1.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.65 (94.99% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1029/140619_BC47HDACXX

Sample

P1260_1029 / E4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

1.0 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.95 (89.25% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1021/140619_BC47HDACXX

Sample

P1260_1021 / E3_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

9.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 33.99 (86.54% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1027/140619_BC47HDACXX

Sample

P1260_1027 / C4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.2 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.03 (86.79% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1024/140619_BC47HDACXX

Sample

P1260_1024 / H3_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.7 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.54 (88.34% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1008/140619_BC47HDACXX

Sample

P1260_1008 / H1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

1.9 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.17 (93.34% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1003/140619_BC47HDACXX

Sample

P1260_1003 / C1_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.3 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.05 (92.88% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1013/140619_BC47HDACXX

Sample

P1260_1013 / E2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

2.7 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.05 (92.85% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1023/140619_BC47HDACXX

Sample

P1260_1023 / G3_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

5.4 million read pairs in lane with PhiX error rate 0.27%. Average quality score 35.13 (90.29% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1026/140619_BC47HDACXX

Sample

P1260_1026 / B4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

7.6 million read pairs in lane with PhiX error rate 0.27%. Average quality score 33.74 (85.87% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1014/140619_BC47HDACXX

Sample

P1260_1014 / F2_Debaryomyces. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 36.31 (93.79% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1020/140619_BC47HDACXX

Sample

P1260_1020 / D3_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

3.5 million read pairs in lane with PhiX error rate 0.27%. Average quality score 34.94 (89.54% bases >= Q30).

Raw data delivery note

SciLifeLab Stockholm

August 12, 2014

Project name

A.Blomberg_14_03 (Debaryomyces/Skeletonema - Nextera XT)

UPPNEX project id

b2011228

Flow cell id

BC47HDACXX

Lane

8

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1030/140619_BC47HDACXX

Sample

P1260_1030 / F4_skeletonema. Ordered amount: N/A million read pairs.

Method

Clustered using cBot and sequenced on HiSeq2500 (HiSeq Control Software 2.0.12.0/RTA 1.17.21.3) with a 2x101 setup in HighOutput mode. Bcl to Fastq conversion was performed using bcl2Fastq v1.8.3 from the CASAVA software suite. The quality scale is Sanger / phred33 / Illumina 1.8+.

Results

14.6 million read pairs in lane with PhiX error rate 0.27%. Average quality score 35.79 (92.19% bases >= Q30).