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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1004/140716_AH9BY4ADXX

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 RapidRun 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

1.6 million read pairs in lane with PhiX error rate 0.235%. Average quality score 35.34 (90.48% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1025/140716_AH9BY4ADXX

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 RapidRun 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

12.4 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.30 (94.00% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1030/140716_AH9BY4ADXX

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 RapidRun 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

12.3 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.16 (93.32% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1003/140716_AH9BY4ADXX

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 RapidRun 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

2.2 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.18 (93.20% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1019/140716_AH9BY4ADXX

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 RapidRun 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

2.0 million read pairs in lane with PhiX error rate 0.235%. Average quality score 35.70 (91.58% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1022/140716_AH9BY4ADXX

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 RapidRun 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

5.1 million read pairs in lane with PhiX error rate 0.235%. Average quality score 32.88 (82.99% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1005/140716_AH9BY4ADXX

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 RapidRun 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

2.1 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.11 (92.95% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1027/140716_AH9BY4ADXX

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 RapidRun 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

4.4 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.60 (88.79% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1023/140716_AH9BY4ADXX

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 RapidRun 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

4.6 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.89 (89.41% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1006/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 36.20 (93.20% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1033/140716_AH9BY4ADXX

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 RapidRun 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

12.8 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.21 (93.51% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1012/140716_AH9BY4ADXX

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 RapidRun 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

2.1 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.32 (93.67% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1002/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 36.72 (94.95% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1021/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 33.71 (85.61% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1010/140716_AH9BY4ADXX

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 RapidRun 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

1.3 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.36 (93.75% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1031/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 33.90 (86.19% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1020/140716_AH9BY4ADXX

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 RapidRun 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

3.1 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.29 (87.32% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1032/140716_AH9BY4ADXX

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 RapidRun 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

14.2 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.66 (94.88% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1013/140716_AH9BY4ADXX

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 RapidRun 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

1.8 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.15 (93.15% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1028/140716_AH9BY4ADXX

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 RapidRun 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

6.9 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.46 (88.12% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1015/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 36.51 (94.37% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1024/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 34.25 (87.37% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1026/140716_AH9BY4ADXX

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 RapidRun 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

6.8 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.32 (87.90% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1008/140716_AH9BY4ADXX

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 RapidRun 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

1.3 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.33 (93.71% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1011/140716_AH9BY4ADXX

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 RapidRun 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

0.77 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.91 (95.73% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1007/140716_AH9BY4ADXX

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 RapidRun 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

2.3 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.27 (93.49% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1016/140716_AH9BY4ADXX

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 RapidRun 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

2.6 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.50 (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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1001/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 36.46 (94.20% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1017/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 35.97 (92.67% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1014/140716_AH9BY4ADXX

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 RapidRun 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

2.2 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.52 (94.42% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1029/140716_AH9BY4ADXX

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 RapidRun 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

0.99 million read pairs in lane with PhiX error rate 0.235%. Average quality score 34.86 (88.97% 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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1018/140716_AH9BY4ADXX

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 RapidRun 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

2.6 million read pairs in lane with PhiX error rate 0.235%. Average quality score 36.16 (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

AH9BY4ADXX

Lane

1

Sequence data directory

/proj/b2011228/INBOX/A.Blomberg_14_03/P1260_1009/140716_AH9BY4ADXX

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 RapidRun 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 0.235%. Average quality score 36.36 (93.85% bases >= Q30).