**CWTL1\_24**

=== Summary ===

Total reads processed: 8,193,596

Reads with adapters: 1,209,592 (14.8%)

Reads written (passing filters): 8,193,596 (100.0%)

Total basepairs processed: 610,750,140 bp

Quality-trimmed: 342,854 bp (0.1%)

Total written (filtered): 608,928,011 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 1209592 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.3%

C: 25.8%

G: 17.9%

T: 20.0%

none/other: 0.1%

Overview of removed sequences

length count expect max.err error counts

1 1083077 2048399.0 0 1083077

2 38775 512099.8 0 38775

3 72963 128024.9 0 72963

4 11108 32006.2 0 11108

5 2856 8001.6 0 2856

6 222 2000.4 0 222

7 4 500.1 0 4

9 4 31.3 0 0 4

10 4 7.8 1 0 4

11 6 2.0 1 0 6

12 7 0.5 1 0 7

19 2 0.1 1 0 2

21 1 0.1 1 1

25 1 0.1 1 0 1

31 1 0.1 1 0 1

33 1 0.1 1 1

35 1 0.1 1 0 1

36 1 0.1 1 0 1

38 1 0.1 1 0 1

42 1 0.1 1 0 1

48 1 0.1 1 0 1

52 1 0.1 1 0 1

53 1 0.1 1 0 1

55 1 0.1 1 0 1

57 2 0.1 1 0 2

58 1 0.1 1 0 1

60 1 0.1 1 0 1

62 4 0.1 1 0 4

63 4 0.1 1 0 4

64 4 0.1 1 0 4

65 6 0.1 1 0 6

66 18 0.1 1 0 18

67 118 0.1 1 0 118

68 82 0.1 1 0 82

69 25 0.1 1 0 25

70 14 0.1 1 0 14

71 12 0.1 1 0 12

72 26 0.1 1 0 26

73 28 0.1 1 0 28

74 92 0.1 1 0 92

75 115 0.1 1 0 115

RUN STATISTICS FOR INPUT FILE: ./RawData/17978L1\_S1\_L001\_R2\_001.fastq

=============================================

8193596 sequences processed in total

**CWTL2\_24**

=== Summary ===

Total reads processed: 6,430,711

Reads with adapters: 953,168 (14.8%)

Reads written (passing filters): 6,430,711 (100.0%)

Total basepairs processed: 479,338,490 bp

Quality-trimmed: 242,897 bp (0.1%)

Total written (filtered): 477,887,530 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 953168 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 35.8%

C: 26.1%

G: 18.4%

T: 19.7%

none/other: 0.1%

Overview of removed sequences

length count expect max.err error counts

1 851028 1607677.8 0 851028

2 33107 401919.4 0 33107

3 57302 100479.9 0 57302

4 8291 25120.0 0 8291

5 2212 6280.0 0 2212

6 163 1570.0 0 163

7 2 392.5 0 2

9 4 24.5 0 1 3

10 4 6.1 1 0 4

11 5 1.5 1 0 5

12 3 0.4 1 0 3

14 1 0.1 1 0 1

17 1 0.1 1 0 1

24 1 0.1 1 0 1

25 1 0.1 1 1

29 1 0.1 1 0 1

33 1 0.1 1 0 1

35 1 0.1 1 0 1

36 1 0.1 1 0 1

48 2 0.1 1 0 2

57 2 0.1 1 0 2

58 1 0.1 1 0 1

60 2 0.1 1 0 2

61 4 0.1 1 0 4

62 5 0.1 1 0 5

63 5 0.1 1 0 5

64 6 0.1 1 0 6

65 19 0.1 1 0 19

66 24 0.1 1 0 24

67 200 0.1 1 0 200

68 171 0.1 1 0 171

69 54 0.1 1 0 54

70 31 0.1 1 0 31

71 22 0.1 1 0 22

72 33 0.1 1 0 33

73 86 0.1 1 0 86

74 181 0.1 1 0 181

75 191 0.1 1 0 191

RUN STATISTICS FOR INPUT FILE: ./RawData/17978L2\_S2\_L001\_R2\_001.fastq

=============================================

6430711 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 2059 (0.03%)

**CWTL3\_24**

=== Summary ===

Total reads processed: 7,349,998

Reads with adapters: 1,071,089 (14.6%)

Reads written (passing filters): 7,349,998 (100.0%)

Total basepairs processed: 547,269,718 bp

Quality-trimmed: 135,888 bp (0.0%)

Total written (filtered): 545,837,570 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 1071089 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.4%

C: 27.0%

G: 17.0%

T: 19.6%

none/other: 0.0%

Overview of removed sequences

length count expect max.err error counts

1 948106 1837499.5 0 948106

2 47314 459374.9 0 47314

3 64482 114843.7 0 64482

4 7972 28710.9 0 7972

5 2682 7177.7 0 2682

6 208 1794.4 0 208

7 14 448.6 0 14

8 2 112.2 0 2

9 9 28.0 0 1 8

10 23 7.0 1 0 23

11 13 1.8 1 0 13

12 5 0.4 1 0 5

13 3 0.1 1 0 3

14 5 0.1 1 0 5

15 5 0.1 1 3 2

16 2 0.1 1 0 2

17 4 0.1 1 2 2

18 6 0.1 1 3 3

19 17 0.1 1 9 8

20 5 0.1 1 2 3

21 13 0.1 1 5 8

23 2 0.1 1 0 2

24 5 0.1 1 2 3

25 11 0.1 1 8 3

26 3 0.1 1 2 1

27 4 0.1 1 4

29 5 0.1 1 5

30 1 0.1 1 1

31 3 0.1 1 2 1

32 12 0.1 1 10 2

38 1 0.1 1 0 1

39 1 0.1 1 0 1

42 1 0.1 1 1

45 1 0.1 1 1

46 1 0.1 1 0 1

47 2 0.1 1 1 1

48 1 0.1 1 1

51 1 0.1 1 0 1

62 1 0.1 1 0 1

63 1 0.1 1 0 1

65 2 0.1 1 0 2

66 3 0.1 1 0 3

67 22 0.1 1 0 22

68 34 0.1 1 0 34

69 14 0.1 1 0 14

70 5 0.1 1 0 5

71 4 0.1 1 0 4

72 5 0.1 1 0 5

73 8 0.1 1 0 8

74 22 0.1 1 0 22

75 23 0.1 1 0 23

RUN STATISTICS FOR INPUT FILE: ./RawData/17978WT\_S1\_L001\_R2\_001.fastq

=============================================

7349998 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 1025 (0.01%)

**CWTD1\_24**

=== Summary ===

Total reads processed: 4,445,054

Reads with adapters: 650,329 (14.6%)

Reads written (passing filters): 4,445,054 (100.0%)

Total basepairs processed: 331,346,529 bp

Quality-trimmed: 156,121 bp (0.0%)

Total written (filtered): 330,308,396 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 650329 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.9%

C: 25.2%

G: 17.5%

T: 20.1%

none/other: 0.2%

Overview of removed sequences

length count expect max.err error counts

1 581574 1111263.5 0 581574

2 20740 277815.9 0 20740

3 39339 69454.0 0 39339

4 5305 17363.5 0 5305

5 1677 4340.9 0 1677

6 103 1085.2 0 103

7 2 271.3 0 2

9 1 17.0 0 0 1

10 3 4.2 1 0 3

11 2 1.1 1 0 2

12 4 0.3 1 0 4

15 1 0.1 1 0 1

16 1 0.1 1 0 1

17 1 0.1 1 0 1

20 1 0.1 1 0 1

24 2 0.1 1 0 2

25 1 0.1 1 0 1

34 1 0.1 1 0 1

35 1 0.1 1 0 1

37 1 0.1 1 0 1

39 1 0.1 1 0 1

42 2 0.1 1 0 2

43 1 0.1 1 0 1

48 1 0.1 1 0 1

49 1 0.1 1 0 1

53 1 0.1 1 0 1

55 1 0.1 1 0 1

58 2 0.1 1 0 2

59 1 0.1 1 0 1

60 1 0.1 1 0 1

61 4 0.1 1 0 4

62 1 0.1 1 0 1

63 4 0.1 1 0 4

64 10 0.1 1 0 10

65 19 0.1 1 0 19

66 21 0.1 1 0 21

67 331 0.1 1 0 331

68 286 0.1 1 0 286

69 107 0.1 1 0 107

70 65 0.1 1 0 65

71 33 0.1 1 0 33

72 66 0.1 1 0 66

73 97 0.1 1 0 97

74 286 0.1 1 0 286

75 227 0.1 1 0 227

RUN STATISTICS FOR INPUT FILE: ./RawData/Abaumannii17978D1\_S1\_L001\_R2\_001.fastq

=============================================

4445054 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 2305 (0.05%)

**CWTD3\_24**

=== Summary ===

Total reads processed: 4,643,737

Reads with adapters: 685,045 (14.8%)

Reads written (passing filters): 4,643,737 (100.0%)

Total basepairs processed: 346,122,443 bp

Quality-trimmed: 223,719 bp (0.1%)

Total written (filtered): 344,466,671 bp (99.5%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 685045 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.8%

C: 24.9%

G: 17.3%

T: 19.6%

none/other: 1.3%

Overview of removed sequences

length count expect max.err error counts

1 602991 1160934.2 0 602991

2 23178 290233.6 0 23178

3 42356 72558.4 0 42356

4 5766 18139.6 0 5766

5 1799 4534.9 0 1799

6 113 1133.7 0 113

7 1 283.4 0 1

8 2 70.9 0 2

10 2 4.4 1 0 2

11 5 1.1 1 0 5

12 3 0.3 1 0 3

14 1 0.1 1 0 1

15 1 0.1 1 0 1

21 1 0.1 1 1

24 1 0.1 1 0 1

25 2 0.1 1 1 1

27 1 0.1 1 0 1

29 1 0.1 1 0 1

34 1 0.1 1 0 1

35 6 0.1 1 0 6

36 1 0.1 1 0 1

43 1 0.1 1 0 1

44 4 0.1 1 0 4

45 1 0.1 1 0 1

51 2 0.1 1 0 2

55 3 0.1 1 0 3

56 1 0.1 1 0 1

57 5 0.1 1 0 5

58 3 0.1 1 0 3

59 4 0.1 1 0 4

60 4 0.1 1 0 4

61 11 0.1 1 0 11

62 15 0.1 1 0 15

63 20 0.1 1 0 20

64 47 0.1 1 0 47

65 71 0.1 1 0 71

66 142 0.1 1 0 142

67 1613 0.1 1 0 1613

68 1793 0.1 1 0 1793

69 572 0.1 1 0 572

70 282 0.1 1 0 282

71 219 0.1 1 0 219

72 298 0.1 1 0 298

73 590 0.1 1 0 590

74 1749 0.1 1 0 1749

75 1363 0.1 1 0 1363

RUN STATISTICS FOR INPUT FILE: ./RawData/Abaumannii17978D2\_S2\_L001\_R2\_001.fastq

=============================================

4643737 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 10235 (0.22%)

**CWTD3\_24**

=== Summary ===

Total reads processed: 4,724,054

Reads with adapters: 693,826 (14.7%)

Reads written (passing filters): 4,724,054 (100.0%)

Total basepairs processed: 352,135,791 bp

Quality-trimmed: 213,212 bp (0.1%)

Total written (filtered): 350,709,093 bp (99.6%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 693826 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 37.0%

C: 24.7%

G: 17.5%

T: 20.0%

none/other: 0.8%

Overview of removed sequences

length count expect max.err error counts

1 613253 1181013.5 0 613253

2 23248 295253.4 0 23248

3 44281 73813.3 0 44281

4 5492 18453.3 0 5492

5 1928 4613.3 0 1928

6 87 1153.3 0 87

7 3 288.3 0 3

8 2 72.1 0 2

9 1 18.0 0 0 1

10 1 4.5 1 0 1

11 5 1.1 1 0 5

12 3 0.3 1 0 3

16 1 0.1 1 0 1

17 1 0.1 1 0 1

19 1 0.1 1 0 1

22 1 0.1 1 0 1

23 1 0.1 1 0 1

24 1 0.1 1 0 1

25 1 0.1 1 0 1

29 1 0.1 1 0 1

34 1 0.1 1 0 1

35 3 0.1 1 0 3

39 1 0.1 1 0 1

43 3 0.1 1 0 3

44 1 0.1 1 0 1

45 3 0.1 1 0 3

46 1 0.1 1 0 1

47 3 0.1 1 0 3

51 2 0.1 1 0 2

52 2 0.1 1 0 2

53 1 0.1 1 0 1

56 2 0.1 1 0 2

57 4 0.1 1 0 4

58 1 0.1 1 0 1

59 2 0.1 1 0 2

60 3 0.1 1 0 3

61 6 0.1 1 0 6

62 5 0.1 1 0 5

63 10 0.1 1 0 10

64 32 0.1 1 0 32

65 44 0.1 1 0 44

66 127 0.1 1 0 127

67 979 0.1 1 0 979

68 1117 0.1 1 0 1117

69 404 0.1 1 0 404

70 192 0.1 1 0 192

71 156 0.1 1 0 156

72 204 0.1 1 0 204

73 370 0.1 1 0 370

74 1046 0.1 1 0 1046

75 789 0.1 1 0 789

RUN STATISTICS FOR INPUT FILE: ./RawData/Abaumannii17978D3\_S3\_L001\_R2\_001.fastq

=============================================

4724054 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 6706 (0.14%)

**CBlsAL1\_24**

=== Summary ===

Total reads processed: 6,597,640

Reads with adapters: 981,545 (14.9%)

Reads written (passing filters): 6,597,640 (100.0%)

Total basepairs processed: 491,786,461 bp

Quality-trimmed: 257,190 bp (0.1%)

Total written (filtered): 490,266,417 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 981545 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 35.4%

C: 25.5%

G: 18.9%

T: 20.1%

none/other: 0.1%

Overview of removed sequences

length count expect max.err error counts

1 876083 1649410.0 0 876083

2 35381 412352.5 0 35381

3 58218 103088.1 0 58218

4 7960 25772.0 0 7960

5 2329 6443.0 0 2329

6 183 1610.8 0 183

7 5 402.7 0 5

9 1 25.2 0 0 1

10 2 6.3 1 0 2

11 4 1.6 1 0 4

12 7 0.4 1 0 7

15 2 0.1 1 2

21 1 0.1 1 1

24 1 0.1 1 0 1

27 1 0.1 1 1

35 1 0.1 1 0 1

36 1 0.1 1 0 1

37 1 0.1 1 1

42 1 0.1 1 1

44 1 0.1 1 0 1

47 1 0.1 1 1

48 1 0.1 1 0 1

51 1 0.1 1 0 1

52 1 0.1 1 0 1

56 1 0.1 1 0 1

57 1 0.1 1 0 1

59 2 0.1 1 0 2

60 2 0.1 1 0 2

61 2 0.1 1 0 2

62 1 0.1 1 0 1

63 9 0.1 1 0 9

64 10 0.1 1 0 10

65 17 0.1 1 0 17

66 44 0.1 1 0 44

67 257 0.1 1 0 257

68 217 0.1 1 0 217

69 65 0.1 1 0 65

70 35 0.1 1 0 35

71 35 0.1 1 0 35

72 47 0.1 1 0 47

73 82 0.1 1 0 82

74 255 0.1 1 0 255

75 276 0.1 1 0 276

RUN STATISTICS FOR INPUT FILE: ./RawData/17978mutL2\_S4\_L001\_R2\_001.fastq

=============================================

6597640 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 2453 (0.04%)

**CBlsAL2\_24**

=== Summary ===

Total reads processed: 8,813,889

Reads with adapters: 1,269,992 (14.4%)

Reads written (passing filters): 8,813,889 (100.0%)

Total basepairs processed: 656,477,326 bp

Quality-trimmed: 164,472 bp (0.0%)

Total written (filtered): 654,776,924 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 1269992 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 35.7%

C: 27.1%

G: 17.3%

T: 20.0%

none/other: 0.0%

Overview of removed sequences

length count expect max.err error counts

1 1123350 2203472.2 0 1123350

2 58565 550868.1 0 58565

3 75861 137717.0 0 75861

4 8626 34429.3 0 8626

5 2979 8607.3 0 2979

6 207 2151.8 0 207

7 9 538.0 0 9

9 2 33.6 0 0 2

10 34 8.4 1 0 34

11 17 2.1 1 1 16

12 9 0.5 1 0 9

13 1 0.1 1 0 1

14 7 0.1 1 1 6

15 4 0.1 1 0 4

16 8 0.1 1 4 4

17 8 0.1 1 3 5

18 7 0.1 1 5 2

19 14 0.1 1 10 4

20 5 0.1 1 2 3

21 13 0.1 1 9 4

22 4 0.1 1 4

23 9 0.1 1 7 2

24 6 0.1 1 4 2

25 10 0.1 1 8 2

26 5 0.1 1 3 2

27 7 0.1 1 5 2

29 2 0.1 1 2

30 2 0.1 1 1 1

31 2 0.1 1 2

32 15 0.1 1 13 2

33 6 0.1 1 5 1

34 7 0.1 1 5 2

38 1 0.1 1 0 1

40 1 0.1 1 1

42 2 0.1 1 2

43 2 0.1 1 0 2

45 1 0.1 1 1

49 1 0.1 1 0 1

50 2 0.1 1 2

57 1 0.1 1 0 1

59 2 0.1 1 0 2

63 1 0.1 1 1

64 2 0.1 1 0 2

66 2 0.1 1 0 2

67 37 0.1 1 1 36

68 37 0.1 1 0 37

69 10 0.1 1 0 10

70 3 0.1 1 0 3

71 4 0.1 1 0 4

72 2 0.1 1 0 2

73 13 0.1 1 0 13

74 31 0.1 1 0 31

75 36 0.1 1 0 36

RUN STATISTICS FOR INPUT FILE: ./RawData/17978mut\_S2\_L001\_R2\_001.fastq

=============================================

8813889 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 1339 (0.02%)

**CBlsAL3\_24**

=== Summary ===

Total reads processed: 3,637,060

Reads with adapters: 546,871 (15.0%)

Reads written (passing filters): 3,637,060 (100.0%)

Total basepairs processed: 271,088,711 bp

Quality-trimmed: 152,133 bp (0.1%)

Total written (filtered): 270,218,601 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 546871 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.4%

C: 25.4%

G: 18.6%

T: 19.3%

none/other: 0.2%

Overview of removed sequences

length count expect max.err error counts

1 487970 909265.0 0 487970

2 18624 227316.2 0 18624

3 33445 56829.1 0 33445

4 4341 14207.3 0 4341

5 1432 3551.8 0 1432

6 101 888.0 0 101

7 1 222.0 0 1

10 1 3.5 1 0 1

11 3 0.9 1 0 3

12 4 0.2 1 0 4

24 1 0.1 1 0 1

30 1 0.1 1 0 1

36 1 0.1 1 0 1

44 1 0.1 1 0 1

49 1 0.1 1 0 1

55 1 0.1 1 0 1

60 2 0.1 1 0 2

61 2 0.1 1 0 2

62 2 0.1 1 0 2

63 6 0.1 1 0 6

64 6 0.1 1 0 6

65 8 0.1 1 0 8

66 27 0.1 1 0 27

67 172 0.1 1 0 172

68 124 0.1 1 0 124

69 46 0.1 1 0 46

70 32 0.1 1 0 32

71 30 0.1 1 0 30

72 35 0.1 1 0 35

73 70 0.1 1 0 70

74 177 0.1 1 0 177

75 204 0.1 1 0 204

RUN STATISTICS FOR INPUT FILE: ./RawData/17978mutL1\_S3\_L001\_R2\_001.fastq

=============================================

3637060 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 1643 (0.05%)

**CBlsAD1\_24**

=== Summary ===

Total reads processed: 4,844,897

Reads with adapters: 603,103 (12.4%)

Reads written (passing filters): 4,844,897 (100.0%)

Total basepairs processed: 361,082,330 bp

Quality-trimmed: 55,451 bp (0.0%)

Total written (filtered): 359,964,864 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 603103 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 26.6%

C: 32.0%

G: 13.3%

T: 27.3%

none/other: 0.8%

Overview of removed sequences

length count expect max.err error counts

1 538519 1211224.2 0 538519

2 21305 302806.1 0 21305

3 31776 75701.5 0 31776

4 5432 18925.4 0 5432

5 1121 4731.3 0 1121

6 51 1182.8 0 51

7 19 295.7 0 19

9 2 18.5 0 0 2

10 2 4.6 1 0 2

11 1 1.2 1 0 1

12 3 0.3 1 0 3

14 2 0.1 1 0 2

16 1 0.1 1 1

17 1 0.1 1 1

18 1 0.1 1 0 1

19 1 0.1 1 1

22 1 0.1 1 0 1

25 1 0.1 1 0 1

32 1 0.1 1 1

36 1 0.1 1 0 1

37 1 0.1 1 1

44 1 0.1 1 1

57 1 0.1 1 0 1

59 2 0.1 1 0 2

60 1 0.1 1 0 1

61 2 0.1 1 0 2

62 5 0.1 1 0 5

63 6 0.1 1 0 6

64 2 0.1 1 0 2

65 1 0.1 1 0 1

66 5 0.1 1 0 5

67 8 0.1 1 0 8

68 10 0.1 1 0 10

69 17 0.1 1 0 17

70 30 0.1 1 0 30

71 58 0.1 1 0 58

72 198 0.1 1 0 198

73 1434 0.1 1 0 1434

74 2706 0.1 1 1 2705

75 374 0.1 1 0 374

RUN STATISTICS FOR INPUT FILE: ./RawData/AbaumanniiBlsAD1\_S4\_L001\_R1\_001.fastq

=============================================

4844897 sequences processed in total

The length threshold of paired-end sequences gets evaluated later on (in the validation step)

Writing report to '/Users/hopekirby/Desktop/Acinetobacter Baumanii/RNAseqPhrB/Clean/CBlsAD1\_24/AbaumanniiBlsAD1\_S4\_L001\_R2\_001.fastq\_trimming\_report.txt'

SUMMARISING RUN PARAMETERS

==========================

Input filename: ./RawData/AbaumanniiBlsAD1\_S4\_L001\_R2\_001.fastq

Trimming mode: paired-end

Trim Galore version: 0.6.6

Cutadapt version: 3.5

Number of cores used for trimming: 1

Quality Phred score cutoff: 20

Quality encoding type selected: ASCII+33

Adapter sequence: 'AGATCGGAAGAGC' (Illumina TruSeq, Sanger iPCR; auto-detected)

Maximum trimming error rate: 0.1 (default)

Minimum required adapter overlap (stringency): 1 bp

Minimum required sequence length for both reads before a sequence pair gets removed: 20 bp

Running FastQC on the data once trimming has completed

Cutadapt seems to be fairly up-to-date (version 3.5). Setting -j -j 1

Writing final adapter and quality trimmed output to AbaumanniiBlsAD1\_S4\_L001\_R2\_001\_trimmed.fq

>>> Now performing quality (cutoff '-q 20') and adapter trimming in a single pass for the adapter sequence: 'AGATCGGAAGAGC' from file ./RawData/AbaumanniiBlsAD1\_S4\_L001\_R2\_001.fastq <<<

This is cutadapt 3.5 with Python 3.8.8

Command line parameters: -j 1 -e 0.1 -q 20 -O 1 -a AGATCGGAAGAGC ./RawData/AbaumanniiBlsAD1\_S4\_L001\_R2\_001.fastq

Processing reads on 1 core in single-end mode ...

Finished in 30.60 s (6 µs/read; 9.50 M reads/minute).

=== Summary ===

Total reads processed: 4,844,897

Reads with adapters: 706,998 (14.6%)

Reads written (passing filters): 4,844,897 (100.0%)

Total basepairs processed: 361,116,785 bp

Quality-trimmed: 187,665 bp (0.1%)

Total written (filtered): 359,744,090 bp (99.6%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 706998 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 35.5%

C: 25.8%

G: 18.4%

T: 19.7%

none/other: 0.7%

Overview of removed sequences

length count expect max.err error counts

1 616408 1211224.2 0 616408

2 35438 302806.1 0 35438

3 42810 75701.5 0 42810

4 5939 18925.4 0 5939

5 1503 4731.3 0 1503

6 101 1182.8 0 101

7 6 295.7 0 6

9 1 18.5 0 0 1

10 2 4.6 1 0 2

11 1 1.2 1 0 1

12 4 0.3 1 0 4

16 1 0.1 1 0 1

18 1 0.1 1 0 1

19 1 0.1 1 0 1

20 1 0.1 1 0 1

21 1 0.1 1 0 1

24 2 0.1 1 0 2

25 1 0.1 1 1

26 1 0.1 1 0 1

33 1 0.1 1 0 1

35 5 0.1 1 0 5

38 1 0.1 1 0 1

43 2 0.1 1 0 2

52 1 0.1 1 0 1

55 1 0.1 1 0 1

56 2 0.1 1 0 2

57 3 0.1 1 0 3

58 2 0.1 1 0 2

59 3 0.1 1 0 3

60 5 0.1 1 0 5

61 3 0.1 1 0 3

62 1 0.1 1 0 1

63 14 0.1 1 0 14

64 27 0.1 1 0 27

65 33 0.1 1 0 33

66 79 0.1 1 0 79

67 880 0.1 1 0 880

68 972 0.1 1 0 972

69 287 0.1 1 0 287

70 150 0.1 1 0 150

71 117 0.1 1 0 117

72 178 0.1 1 0 178

73 306 0.1 1 0 306

74 958 0.1 1 0 958

75 745 0.1 1 0 745

RUN STATISTICS FOR INPUT FILE: ./RawData/AbaumanniiBlsAD1\_S4\_L001\_R2\_001.fastq

=============================================

4844897 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 5865 (0.12%)

**CBlsAD2\_24**

=== Summary ===

Total reads processed: 9,092,973

Reads with adapters: 1,330,227 (14.6%)

Reads written (passing filters): 9,092,973 (100.0%)

Total basepairs processed: 677,769,181 bp

Quality-trimmed: 367,681 bp (0.1%)

Total written (filtered): 675,163,360 bp (99.6%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 1330227 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 36.4%

C: 25.2%

G: 17.9%

T: 19.8%

none/other: 0.7%

Overview of removed sequences

length count expect max.err error counts

1 1167606 2273243.2 0 1167606

2 57228 568310.8 0 57228

3 82845 142077.7 0 82845

4 9844 35519.4 0 9844

5 3230 8879.9 0 3230

6 224 2220.0 0 224

7 8 555.0 0 8

9 1 34.7 0 0 1

10 1 8.7 1 0 1

11 9 2.2 1 0 9

12 7 0.5 1 0 7

13 1 0.1 1 0 1

15 1 0.1 1 1

18 2 0.1 1 0 2

19 2 0.1 1 0 2

20 1 0.1 1 1

21 1 0.1 1 0 1

23 1 0.1 1 0 1

24 1 0.1 1 0 1

25 2 0.1 1 2

31 1 0.1 1 0 1

32 2 0.1 1 2

33 2 0.1 1 1 1

34 1 0.1 1 1

35 3 0.1 1 0 3

36 2 0.1 1 0 2

41 1 0.1 1 0 1

43 2 0.1 1 0 2

44 4 0.1 1 1 3

45 1 0.1 1 0 1

47 1 0.1 1 0 1

48 1 0.1 1 0 1

49 1 0.1 1 0 1

50 2 0.1 1 0 2

51 2 0.1 1 0 2

52 5 0.1 1 0 5

53 1 0.1 1 0 1

54 2 0.1 1 0 2

55 1 0.1 1 0 1

56 1 0.1 1 0 1

57 6 0.1 1 0 6

58 5 0.1 1 0 5

59 11 0.1 1 0 11

60 11 0.1 1 1 10

61 20 0.1 1 0 20

62 22 0.1 1 0 22

63 54 0.1 1 0 54

64 83 0.1 1 0 83

65 123 0.1 1 0 123

66 221 0.1 1 0 221

67 1877 0.1 1 0 1877

68 1381 0.1 1 0 1381

69 489 0.1 1 0 489

70 279 0.1 1 0 279

71 215 0.1 1 0 215

72 326 0.1 1 0 326

73 585 0.1 1 0 585

74 1723 0.1 1 0 1723

75 1745 0.1 1 0 1745

RUN STATISTICS FOR INPUT FILE: ./RawData/BlsAD2\_S1\_L001\_R2\_001.fastq

=============================================

9092973 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 11035 (0.12%)

**CBlsAD3\_24**

=== Summary ===

Total reads processed: 10,763,452

Reads with adapters: 1,471,933 (13.7%)

Reads written (passing filters): 10,763,452 (100.0%)

Total basepairs processed: 802,371,385 bp

Quality-trimmed: 314,170 bp (0.0%)

Total written (filtered): 800,168,668 bp (99.7%)

=== Adapter 1 ===

Sequence: AGATCGGAAGAGC; Type: regular 3'; Length: 13; Trimmed: 1471933 times

Minimum overlap: 1

No. of allowed errors:

1-9 bp: 0; 10-13 bp: 1

Bases preceding removed adapters:

A: 34.9%

C: 24.9%

G: 19.3%

T: 20.9%

none/other: 0.1%

Overview of removed sequences

length count expect max.err error counts

1 1296458 2690863.0 0 1296458

2 62461 672715.8 0 62461

3 92210 168178.9 0 92210

4 16213 42044.7 0 16213

5 2802 10511.2 0 2802

6 193 2627.8 0 193

7 7 656.9 0 7

10 4 10.3 1 0 4

11 8 2.6 1 0 8

12 11 0.6 1 0 11

13 2 0.2 1 0 2

18 1 0.2 1 0 1

19 2 0.2 1 1 1

27 4 0.2 1 1 3

30 1 0.2 1 1

36 1 0.2 1 0 1

50 1 0.2 1 0 1

52 1 0.2 1 0 1

56 1 0.2 1 0 1

57 1 0.2 1 0 1

59 1 0.2 1 0 1

60 2 0.2 1 0 2

61 5 0.2 1 0 5

62 5 0.2 1 0 5

63 8 0.2 1 0 8

64 6 0.2 1 0 6

65 10 0.2 1 0 10

66 35 0.2 1 0 35

67 296 0.2 1 0 296

68 263 0.2 1 0 263

69 87 0.2 1 0 87

70 46 0.2 1 0 46

71 49 0.2 1 0 49

72 51 0.2 1 0 51

73 112 0.2 1 0 112

74 296 0.2 1 0 296

75 279 0.2 1 0 279

RUN STATISTICS FOR INPUT FILE: ./RawData/BlsAD3\_S2\_L001\_R2\_001.fastq

=============================================

10763452 sequences processed in total

Number of sequence pairs removed because at least one read was shorter than the length cutoff (20 bp): 2687 (0.02%)