



9. A

10.

11, 12

13 15

16

(1)

(2)

A

(G)

3' ACE

D A

A

E



2.2 3' ACE (DNA
A
E)

1. 3' ACE (DNA (-
F)[®]).
2. Note 1
3. H F (F)

2.3.2 NGS Data Quality Checks

1. F₁ C (//) 18 .
2. (//) 19 .
3. EA (//) 20 .
4. A H (//) 21 .

2.3.3 De Novo Transcriptome Assembly

1. (//) 17 .
2. E 22 .
3. B 23 .
4. E G (//) 24 .
5. E (//) 25 .
6. CD-HI (//) 26 .

2.3.4 Toxin Gene Identification and Expression Quantification

1. A + (// B 279690/) 27 .
2. DIA D (//)

- 3. EA (// /) 40 ,
- 4. GI (// /) 41 .

3 Methods

3.1 NAI

- 1. A 100 500 (1 50) 1 I I 10 100 () .
- 2. I 5
- 3. A 200
- 4. C 15
- 5. I 2 3
- 6. G 12,000 × 4 °C 15
- 7. (50%) . B
- 8. A 500 100%
- 9. I 10
- 10. G 12,000 × 4 °C 10
- 11. A () .
- 12. 1 75%
- 13. G 7500 × 4 °C 5
- 14. A 300 100% 40 3

15. F₁ ... -20 °C
16. G₁ ... 10,000 × ... 15 ... 4 °C.
17. ... 10'
18. A₁ 10 16 ... Note
4 ... A

3.2 3' ACE (...
A ... DNA
E ...):

3' ACE ...
3' ACE ... F₁ ...

2. H z 10 μ z 70 μ z 0.5 μ z ...

19. F
D
20. I 30
21. H 20, 42 °C,
22. I 2 1 B₂
23. I 60 37 °C
24. 200
25. 37 °C
(16 18)
26. 4 °C
27. GE - E
2 B₊ (I
) E A
42
28. 37 °C
29. I C 5
30. 200
E GE - E 7 6

3.3 N -G
(NG)
:
C D N

G

(E)

2. (E) I
(>150)
EA (E A) 20
A H (F A H) 21

3. I
A
20 21 //

Box 1 Abridged Pipeline Example Commands. A few command examples are given; documentation for each program should be referenced for all command arguments and parameters, and only examples are provided. All CPU/thread arguments should be modified based on computing resources:

```
#####
### FASTQC example command ###
#####
SYNOPSIS
```

Usage:

```
fastqc seqfile1 seqfile2.. seqfileN
fastqc [-o outputdir] [--(no)extract] [-f fastq|bam|sam]
[-c contami nant file] seqfile1.. seqfileN
```

```
fastqc RAWDATA_PAIR_1.fastq.gz RAWDATA_PAIR_2.fastq.gz -o
OUTPUT_DIRECTORY
```

```
#####
### TRIMMOMATIC example command ###
#####
SYNOPSIS
```

Usage:

```
PE [-threads <threads>] [-phred33|-phred64] [-trimlog
<trimLogFile>] [-quiet] [-validepairs] [-basein <inputBase> |
<inputFile1> <inputFile2>] [-baseout <outputBase> | <outputFile1P>
<outputFile1U> <outputFile2P> <outputFile2U>] <trimmer1>..
```

or:

```
SE [-threads <threads>] [-phred33|-phred64] [-trimlog
<trimLogFile>] [-quiet] <inputFile> <outputFile> <trimmer1>..
```

```
java -jar trimmomatic-0.35.jar PE -threads 4 -phred33 RAWDATA_
PAIR_1.fastq.gz RAWDATA_PAIR_2.fastq.gz OUTPUT_R1-paired.fastq
OUTPUT_R1-unpaired.fastq OUTPUT_R2-paired.fastq OUTPUT_R2-
unpaired.fastq ILLUMINACLIP:TruSeq3-PE-2.fa:2:40:15 SLIDINGWI N-
DOW:4:15 LEADING:20 TRAILING:20 MINLEN:50 HEADCROP:9
```

```
#####
### PEAR example command ###
#####
SYNOPSIS
```

Usage:

```
pear <options>
```

Standard (mandatory) :

- f, --forward-fastq <str> Forward paired-end FASTQ file.
- r, --reverse-fastq <str> Reverse paired-end FASTQ file.
- o, --output <str> Output filename.

```
pear -f INPUT_R1-paired.fastq -r INPUT_R2-paired.fastq -o  
OUTPUT_NAME
```

```
#####  
### FLASH example command ###  
#####
```

SYNOPSIS

Usage:

```
flash [OPTIONS] MATES_1.FASTQ MATES_2.FASTQ  
flash [OPTIONS] --interleaved-input (MATES.FASTQ | -)  
flash [OPTIONS] --tab-delimited-input (MATES.TAB | -)
```

```
flash -o OUTPUT_PREFIX -t 5 INPUT_R1-paired.fastq INPUT_R2-paired.  
fastq -r 140 -f 350 -s 50 -d OUTPUT_DIRECTORY
```

```
#####  
### TRINITY example command ###  
#####
```

SYNOPSIS

#Usage:

```
# --seqType <string>: type of reads: ('fa' or 'fq')  
#  
# --max_memory <string>: suggested max memory to use by Trinity where  
# limiting can be enabled. (jellyfish, sorting, etc)  
# provided in Gb of RAM, i.e. '--max_memory 10G'  
#  
# If paired reads:  
# --left <string>: left reads, one or more file names #(separated by  
# commas, no spaces)  
# --right <string>: right reads, one or more file names #(separated by  
# commas, no spaces)  
#  
# Or, if unpaired reads:  
# --single <string>: single reads, one or more file names, #comma-
```

```
# --samples_file <string> tab-delimited text file #indicating
biological replicaterelationships.
#ex.
#cond_A cond_A_rep1 A_rep1_left.fq A_rep1_right.fq
#cond_A cond_A_rep2 A_rep2_left.fq A_rep2_right.fq
#cond_B cond_B_rep1 B_rep1_left.fq B_rep1_right.fq
#cond_B cond_B_rep2 B_rep2_left.fq B_rep2_right.fq
#
```

```
Trinity --seqType fq --max_memory 50G --left INPUT_R1-paired.fastq.
gz --right INPUT_R2-paired.fastq.gz --CPU 6 --full_cleanup --min_
contig_length 100 --verbose
```

```
#####
### CD- HIT example command ###
#####
SYNOPSIS
```

Usage:

```
cd-hit-est [Options]
```

```
cd-hit-est -i INPUT_SEQUENCE -o OUTPUT_SEQUENCE -c 1 -n 8
```

```
#####
### BLAST+ example command ###
#####
SYNOPSIS
```

Usage:

```
blastx [-h] [-help] [-import_search_strategy filename]
[-export_search_strategy filename] [-task task_name] [-db
database_name]
[-dbsize num_letters] [-glist filename] [-seqdlst filename]
[-negative_glist filename] [-entrez_query entrez_query]
[-db_soft_mask filtering_algorithm] [-db_hard_mask
filtering_algorithm]
[-subject subject_input_file] [-subject_loc range] [-query
input_file]
[-out output_file] [-eval ue eval ue] [-word_size int_value]
[-gapopen open_penalty] [-gapext end end_penalty]
[-qcov_hsp_per float_value] [-max_hsps int_value]
[-xdrop_ungap float_value] [-xdrop_gap float_value]
[-xdrop_gap_final float_value] [-searchspint_value]
[-sum_stats bool_value] [-max_intron_length length] [-seg
SEG_options]
```

```
[-soft_masking soft_masking] [-matrix matrix_name]
[-threshold float_value] [-culling_limit int_value]
[-best_hit_overhang float_value] [-best_hit_score_edge
float_value]
[-window_size int_value] [-ungapped] [-lcase_masking] [-query_lo
range]
[-strand strand] [-parse_deflines] [-query_encode int_value]
[-outfmt format] [-show_gis] [-num_descriptions int_value]
[-num_alignments int_value] [-line_length line_length] [-html]
[-max_target_seqs num_sequences] [-num_threads int_value]
[-remote]
[-comp_based_stats compo] [-use_sw_tback] [-version]
```

```
blastx -query INPUT_SEQUENCE -db nr -max_target_seqs 3 -num_threads
8 -outfmt '6 std stitle' -out Blastx_nr_outfmt6
```

```
#####
### RSEM example command ###
#####
```

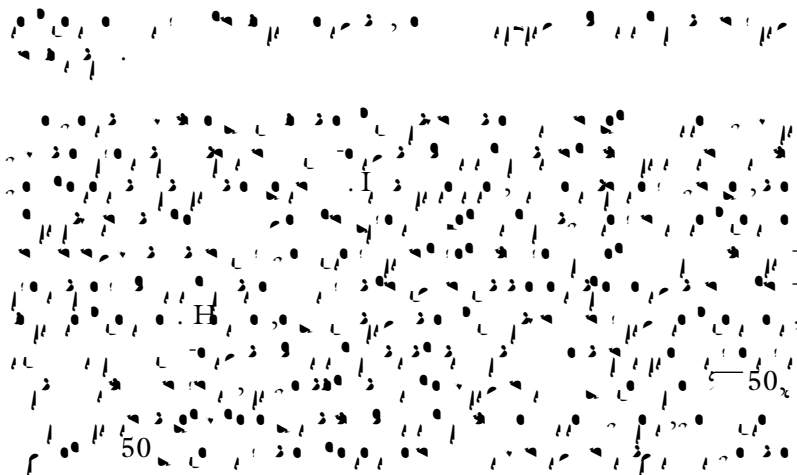
SYNOPSIS

Usage:

```
rsem-prepare-reference [options] reference_fast_file
(s) reference_name
rsem-calculate-expression [options] upstream_read_file
(s) reference_name sample_name
rsem-calculate-expression [options] --paired-end upstream_read_
file(s) downstream_read_file(s) reference_name sample_name
rsem-calculate-expression [options] --alignments [--paired-end]
```


24 (A)

3.3.4 Toxin Gene
Identification and
Expression Quantification



$E(A/B) = 2$ 31
 $B/B = 2$ 32
 $E(B) = 2$
 $E(A/B) = 48$

3.4

$68, 69$
 70
 13 A
 71
 E
 72
 ω
 $\omega < 1$
 $\omega = 1$

BEB 8
 7
 χ^2
 A 24
 A
 H 77 H
 A
 H D
 38 D 78

3.5 H. -
 I

A
 (/)
 G-C, /

FA A

2. A

(FD)

87. F

FD 88

A

89

(AF) 89 91

92

BA 93

AF

AI (E 94

A I)

A

(-H C) 95

I

I

/

(

A

/

A

96 B

97

This block contains a complex musical score with multiple staves. It includes annotations 'A', '96 B', and '97'. The notation is dense and appears to be a form of musical shorthand or a specific dialect of musical notation.

4 Notes

1.

(A)

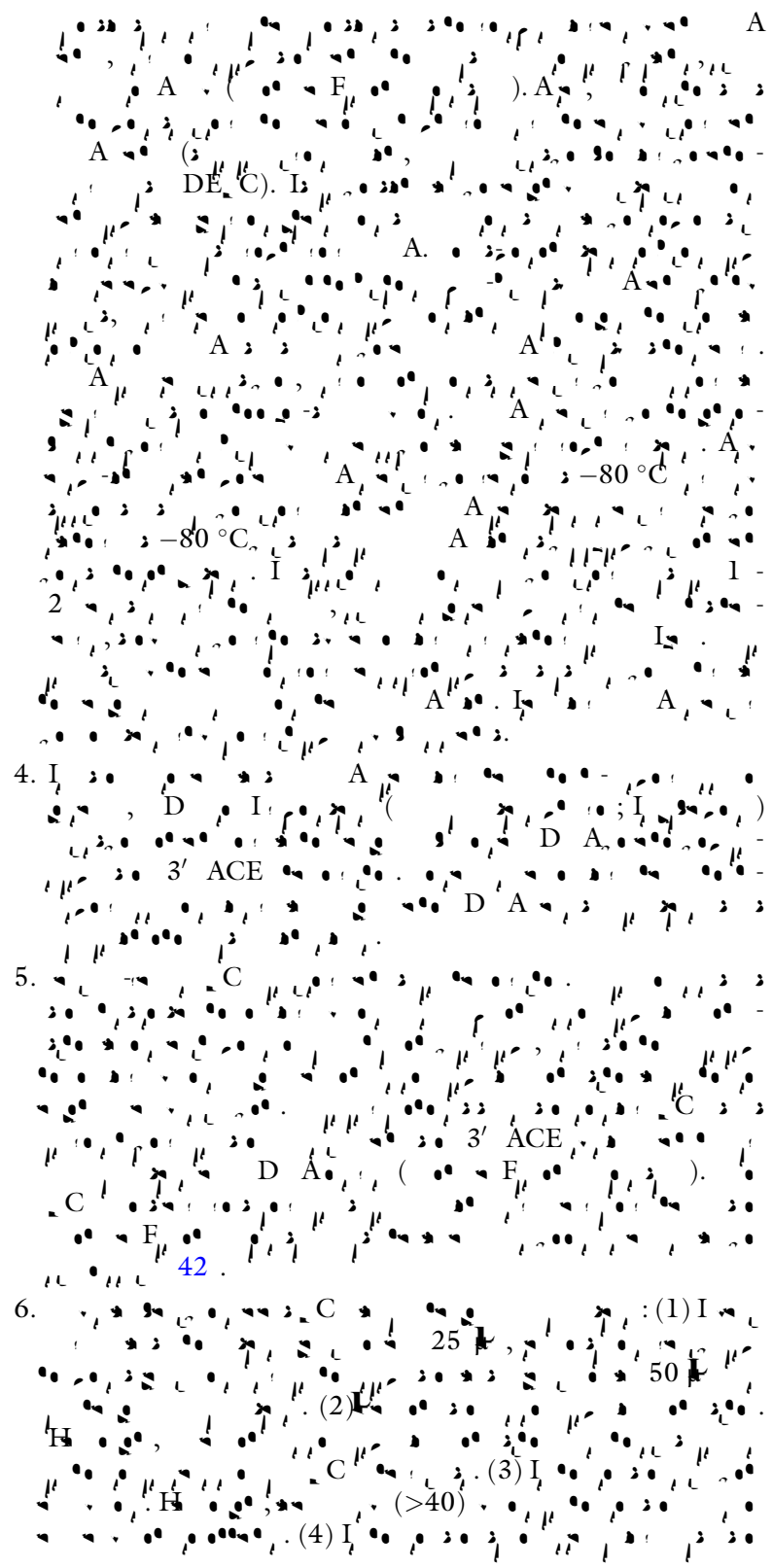
(2016)

C ACE.

2. I G 50°C.

3. A

This block contains a complex musical score with multiple staves. It includes annotations '1.', '(A)', '(2016)', 'C ACE.', '2. I G 50°C.', and '3. A'. The notation is dense and appears to be a form of musical shorthand or a specific dialect of musical notation.



68 °C

(5) D A C 1:2
 1:10 D A C

7. A B A

8. A B I
 (A I) B B A (A)
 28 18 98 7 8
 A I

The image shows musical notation for three numbered items. Item 5 consists of two staves of music with notes and rests, and is labeled with '68 °C', '(5)', 'D A C 1:2', and '1:10 D A C'. Item 7 is a single staff of music labeled '7.' and 'A B A'. Item 8 is a single staff of music labeled '8.', '(A I) B B A (A)', and '28 18 98 7 8 A I'. The notation includes various note values, rests, and dynamic markings.

38. D 300, 300 AF, E 300 D 300
300 (2010) D 300 2010: 300
300 300 300 300 300 300

- 62. (2013) A, E, B, C, G, 14:465
- 63. F, D, C, E, H, E, A, 29, 37, 39
- 64. F, D, G, E, A, C, GA, B, A (2016), 44(D1):D279 D285
- 65. H, A, A, A, A, B, D, B, B, C, E, G, D, D, D, F, D, F, G, H, D, H, D, E, I, A, C, B, C, H, D, C, AF, C, A, D, CH, C, (2012) I, 2011: 40:D306 D312
- 66. C (2017), (3):230 240
- 67. A, BA, C, B (2008), 5(7):621 628
- 68. (2015), 11(10):1005596
- 69. EA, H, G, EC, G, C, CE, I, H, GF, A, A, F, BG (2014) I, 99:68 83
- 70. D, B, A, E, C, B (2011) A, 57(5):657 671
- 71. A, D, A, B, A, A (2017)

- G, B, E, 9(10):2640 2649
- 72. A, A, F, BG (2013), E, A, A, E, 5(11):2172 2208
- 73. (1998), HI -1, 148(3):929 936
- 74. (2000), E, 51:423 432
- 75. (2005) B, B, E, (4):1107 1118
- 76. (2005) E, B, E, 22(12):2472 2479
- 77. F, D, (2005) H, 21(5):676 679
- 78. F, D (2005) D, B, (10):2531 2533
- 79. C, A, C, A, C, C, (2018), 10(9):E373
- 80. (1988), G, 1:92 101
- 81. D, A, G, (2003), F, (4):405 411
- 82. A, D, C, A, C, (2015) G, 121:28 43
- 83. D, EE (2017), 5, 3249
- 84. D, C, EE, (2012), C, B

