RNA-seq analysis with reference

- mapping reads to reference sequence
- comparison of different dataset

load data to server

- open terminal
- load reads data to server

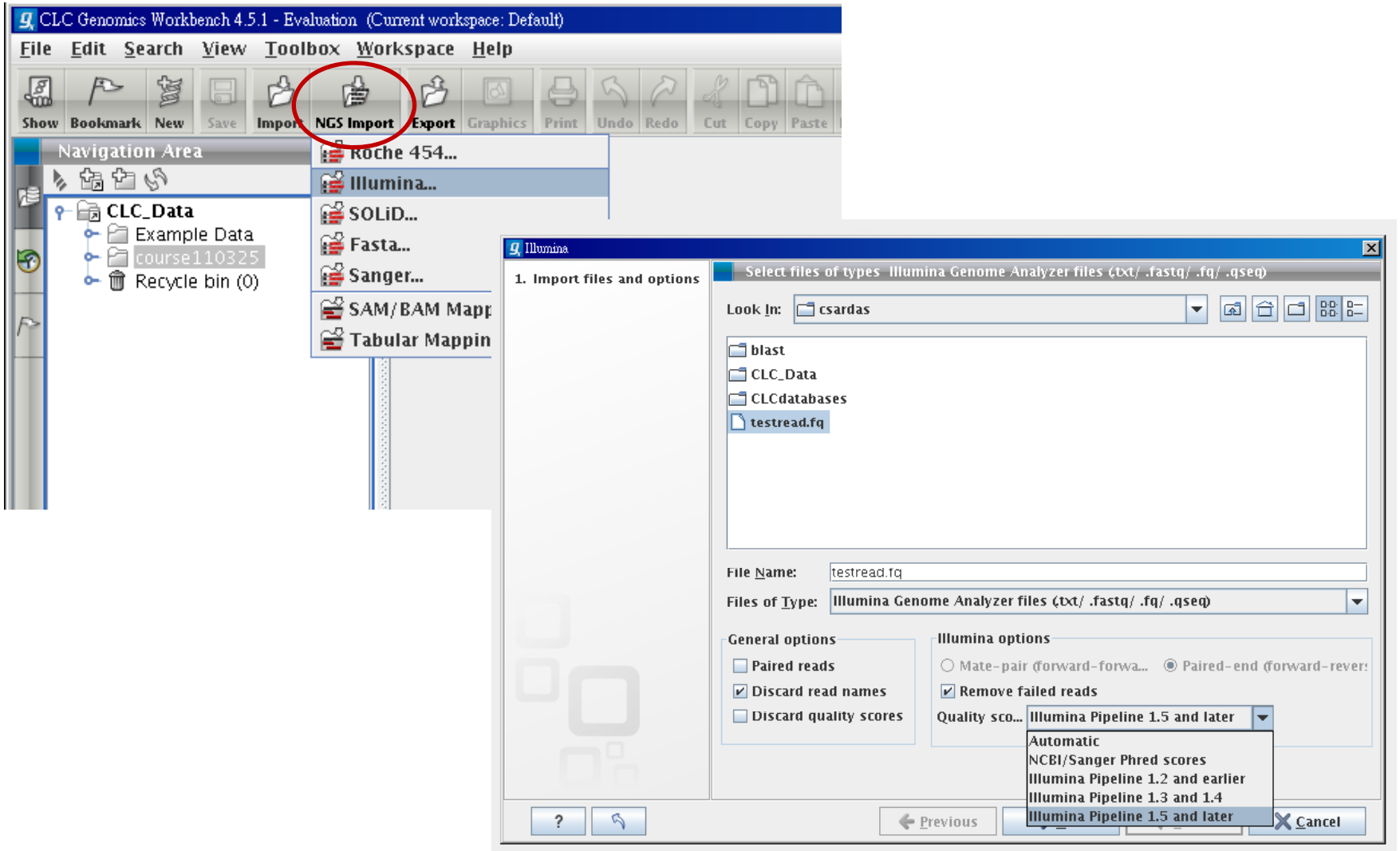
```
wget   http://163.25.92.61/course/testread.fq
```

- load & extract reference sequence to server
  - 59672 cds sequence

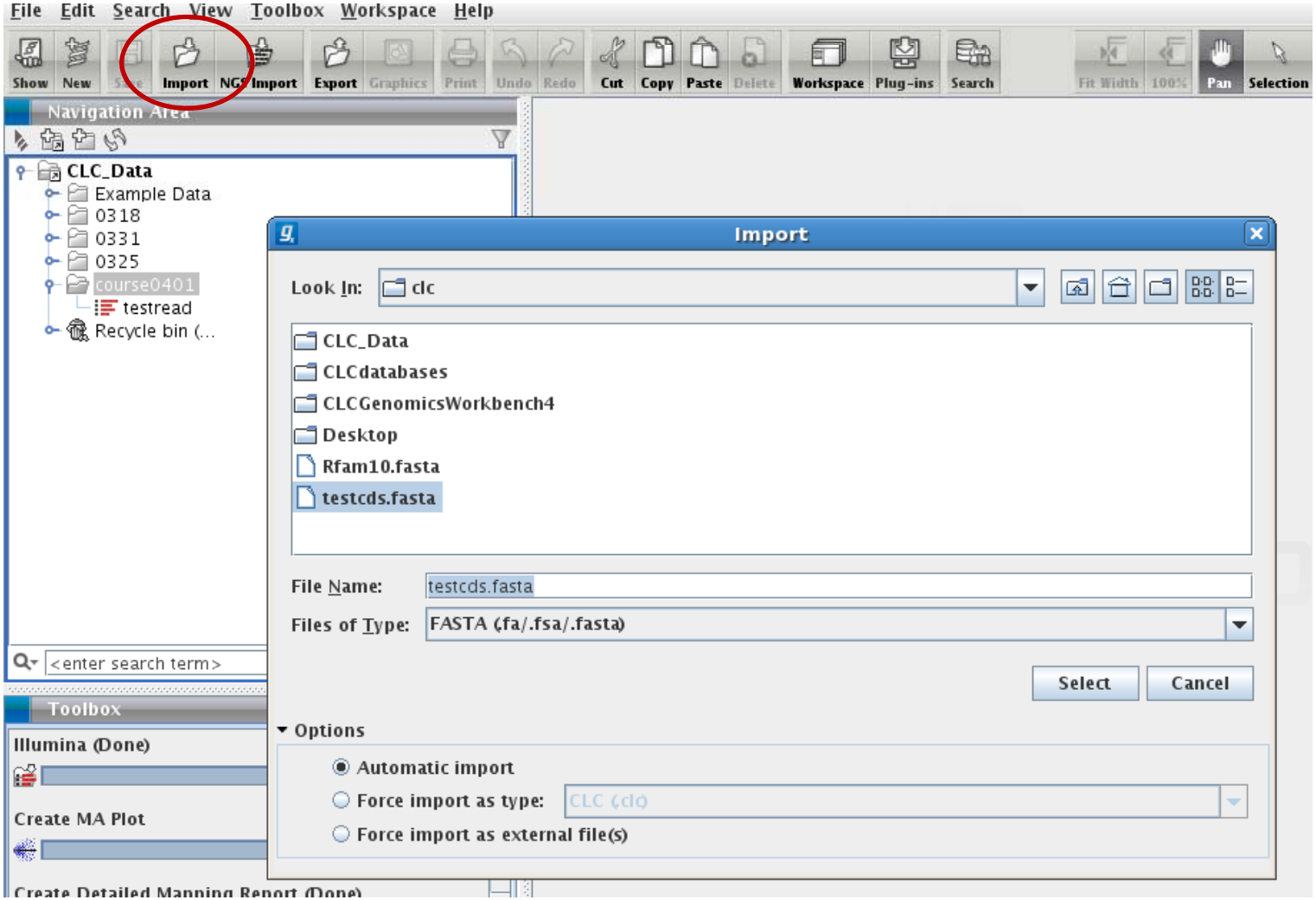
```
wget   http://163.25.92.61/course/testcds.fasta.gz

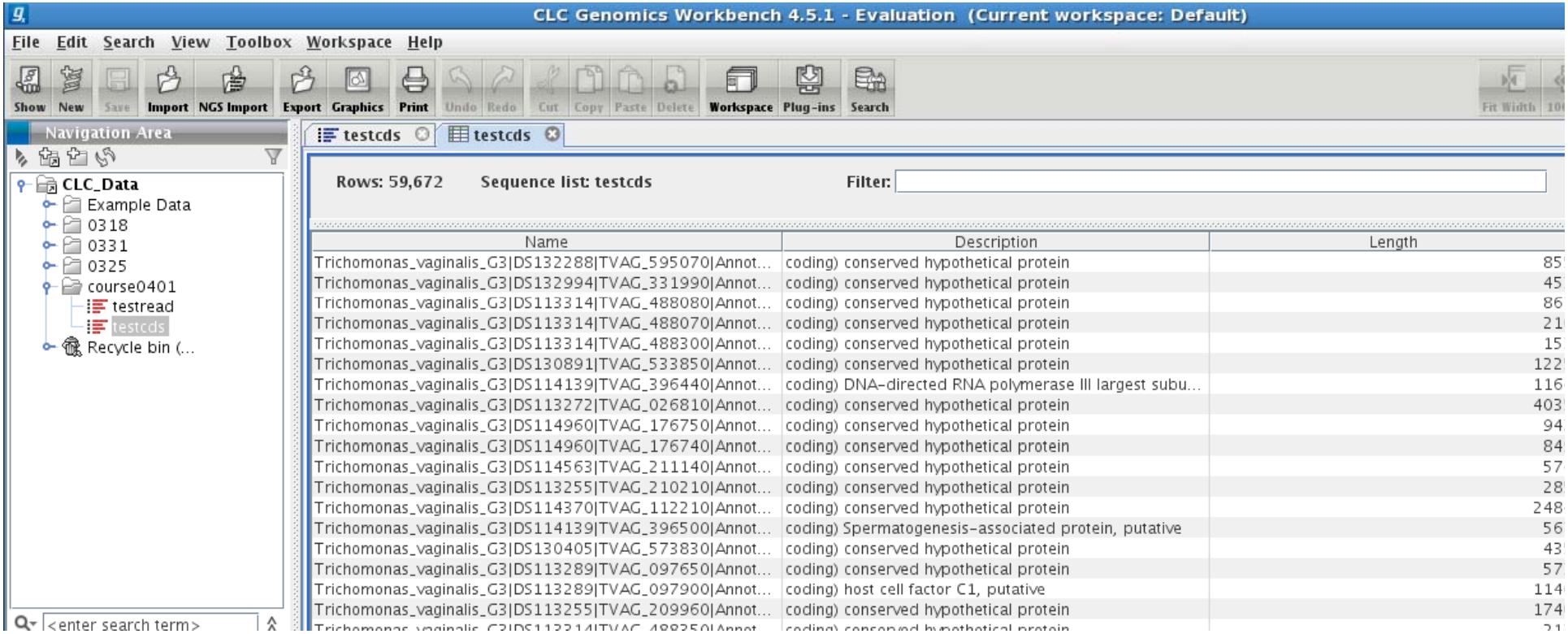
gunzip    testcds.fasta.gz
```

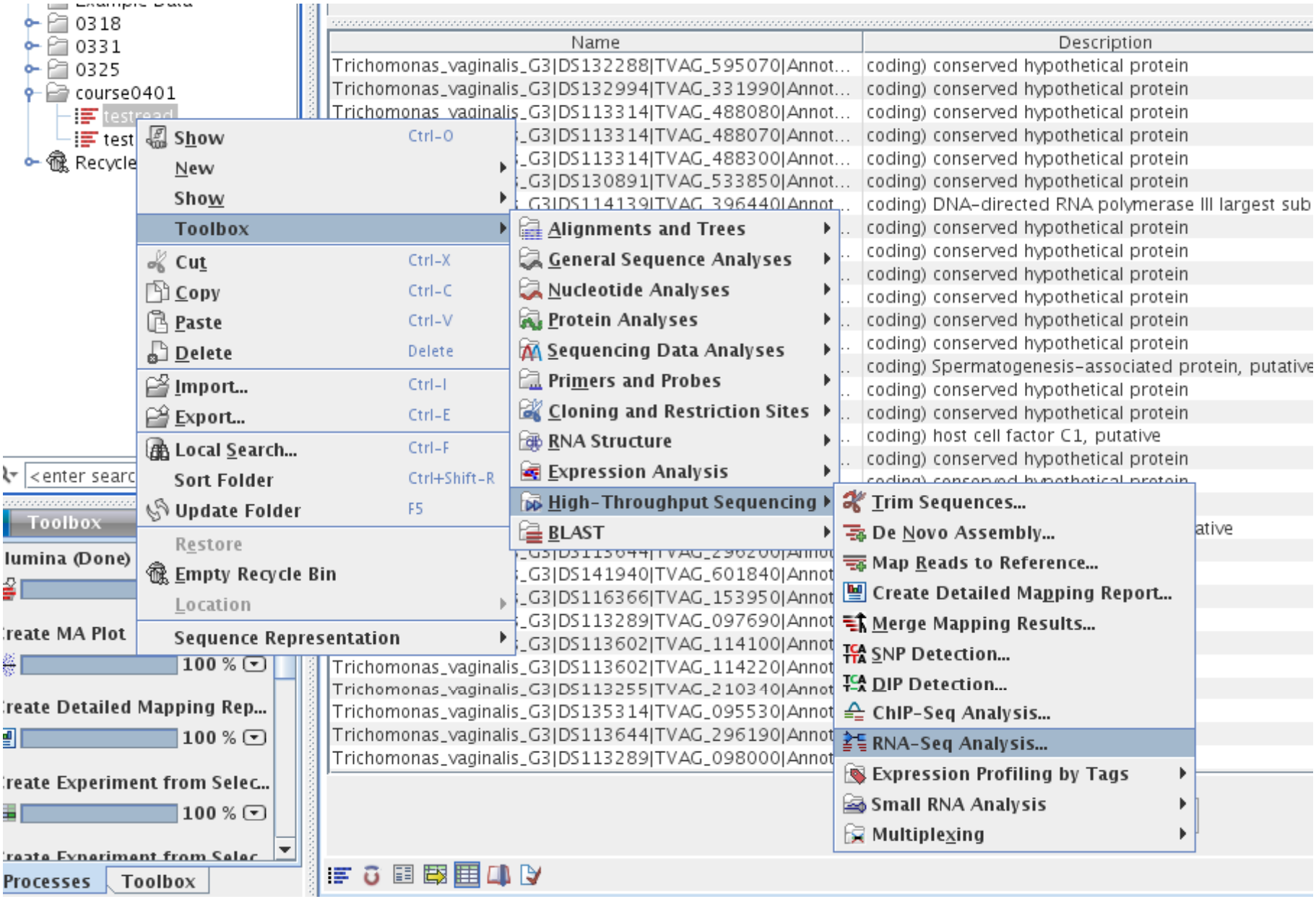
import reads data



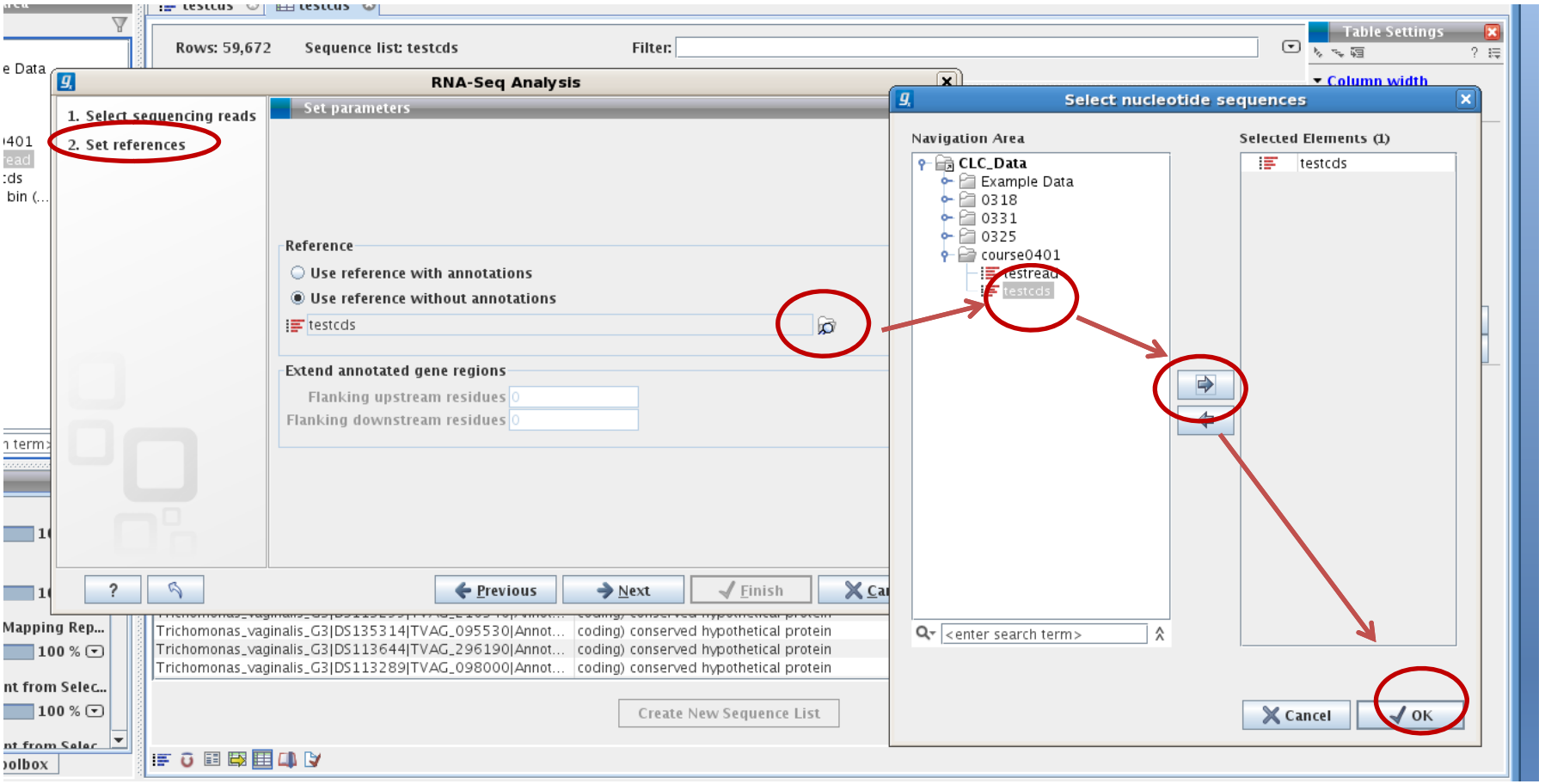
import reference data

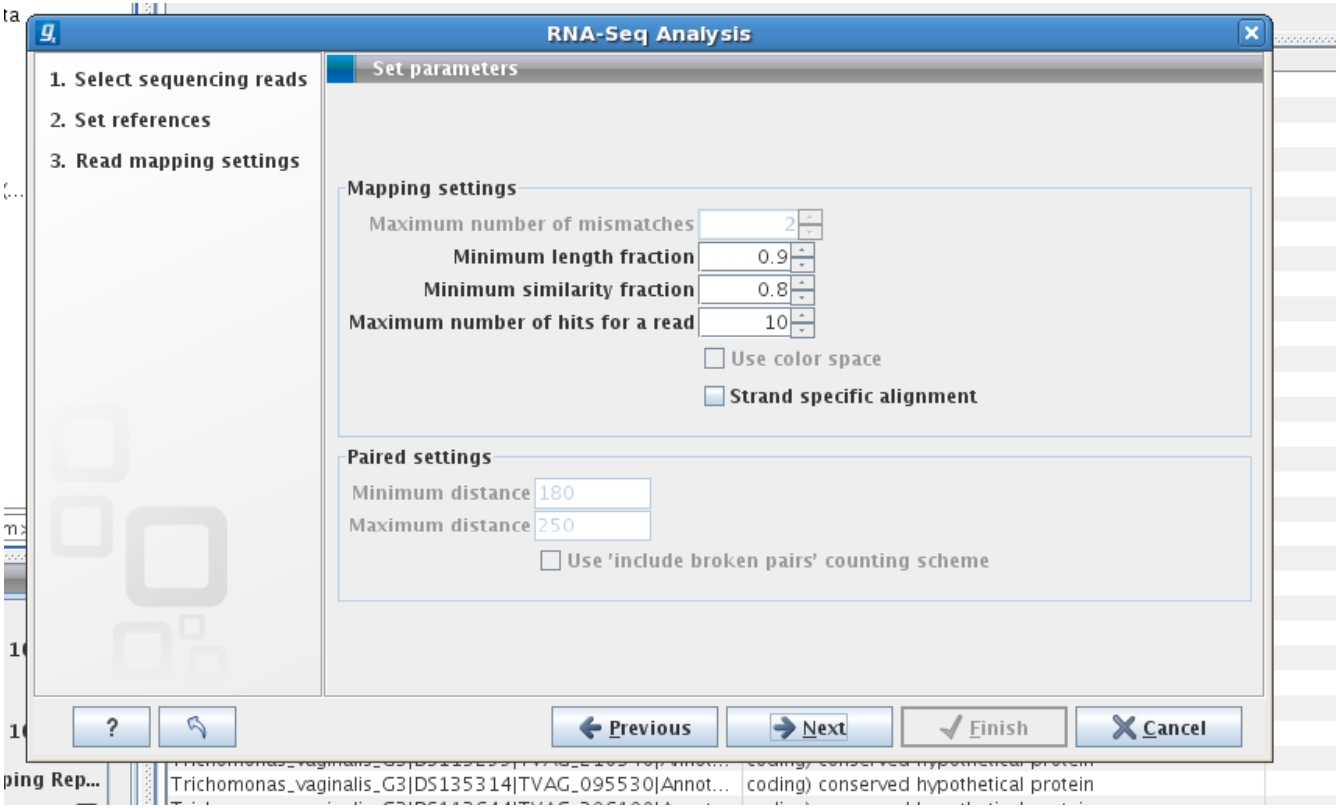


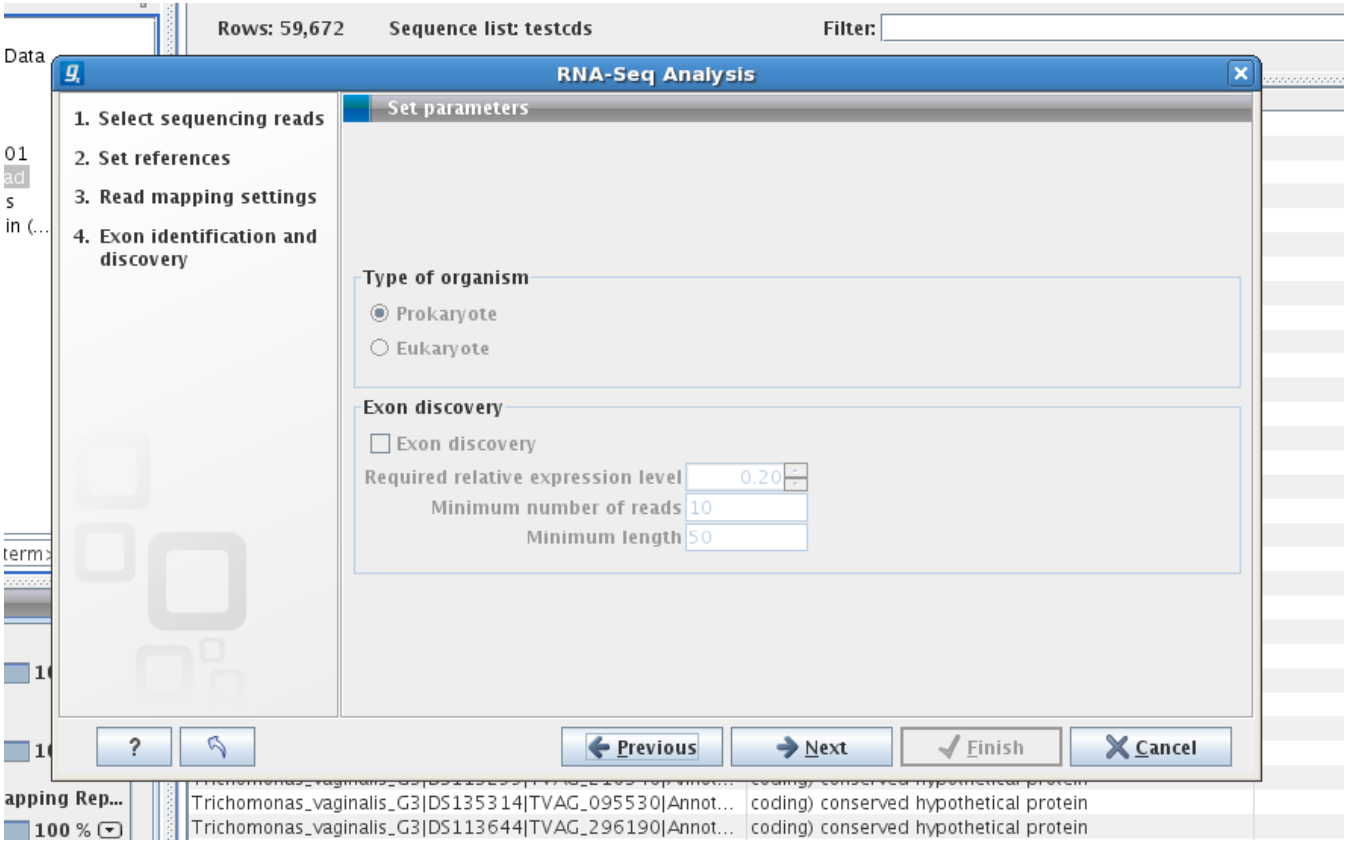

CLC Genomics Workbench 4.5.1 - Evaluation (Current workspace: Default)
File Edit Search View Toolbox Workspace Help
Show New Save Import NGS Import Export Graphics Print Undo Redo Cut Copy Paste Delete Workspace Plug-ins Search Fit Width
Navigation Area
CLC_Data
Example Data
0318
0331
0325
course0401
testread
testcds
Recycle bin (...
<enter search term>
testcds
testcds
Rows: 59,672
Sequence list: testcds
Filter:
Name
Description
Length
Trichomonas_vaginalis_G3|DS132288|TVAG_595070|Annot... coding) conserved hypothetical protein 85
Trichomonas_vaginalis_G3|DS132994|TVAG_331990|Annot... coding) conserved hypothetical protein 45
Trichomonas_vaginalis_G3|DS113314|TVAG_488080|Annot... coding) conserved hypothetical protein 86
Trichomonas_vaginalis_G3|DS113314|TVAG_488070|Annot... coding) conserved hypothetical protein 21
Trichomonas_vaginalis_G3|DS113314|TVAG_488300|Annot... coding) conserved hypothetical protein 15
Trichomonas_vaginalis_G3|DS130891|TVAG_533850|Annot... coding) conserved hypothetical protein 122
Trichomonas_vaginalis_G3|DS114139|TVAG_396440|Annot... coding) DNA-directed RNA polymerase III largest subu... 116
Trichomonas_vaginalis_G3|DS113272|TVAG_026810|Annot... coding) conserved hypothetical protein 403
Trichomonas_vaginalis_G3|DS114960|TVAG_176750|Annot... coding) conserved hypothetical protein 94
Trichomonas_vaginalis_G3|DS114960|TVAG_176740|Annot... coding) conserved hypothetical protein 84
Trichomonas_vaginalis_G3|DS114563|TVAG_211140|Annot... coding) conserved hypothetical protein 57
Trichomonas_vaginalis_G3|DS113255|TVAG_210210|Annot... coding) conserved hypothetical protein 28
Trichomonas_vaginalis_G3|DS114370|TVAG_112210|Annot... coding) conserved hypothetical protein 248
Trichomonas_vaginalis_G3|DS114139|TVAG_396500|Annot... coding) Spermatogenesis-associated protein, putative 56
Trichomonas_vaginalis_G3|DS130405|TVAG_573830|Annot... coding) conserved hypothetical protein 43
Trichomonas_vaginalis_G3|DS113289|TVAG_097650|Annot... coding) conserved hypothetical protein 57
Trichomonas_vaginalis_G3|DS113289|TVAG_097900|Annot... coding) host cell factor C1, putative 114
Trichomonas_vaginalis_G3|DS113255|TVAG_209960|Annot... coding) conserved hypothetical protein 174

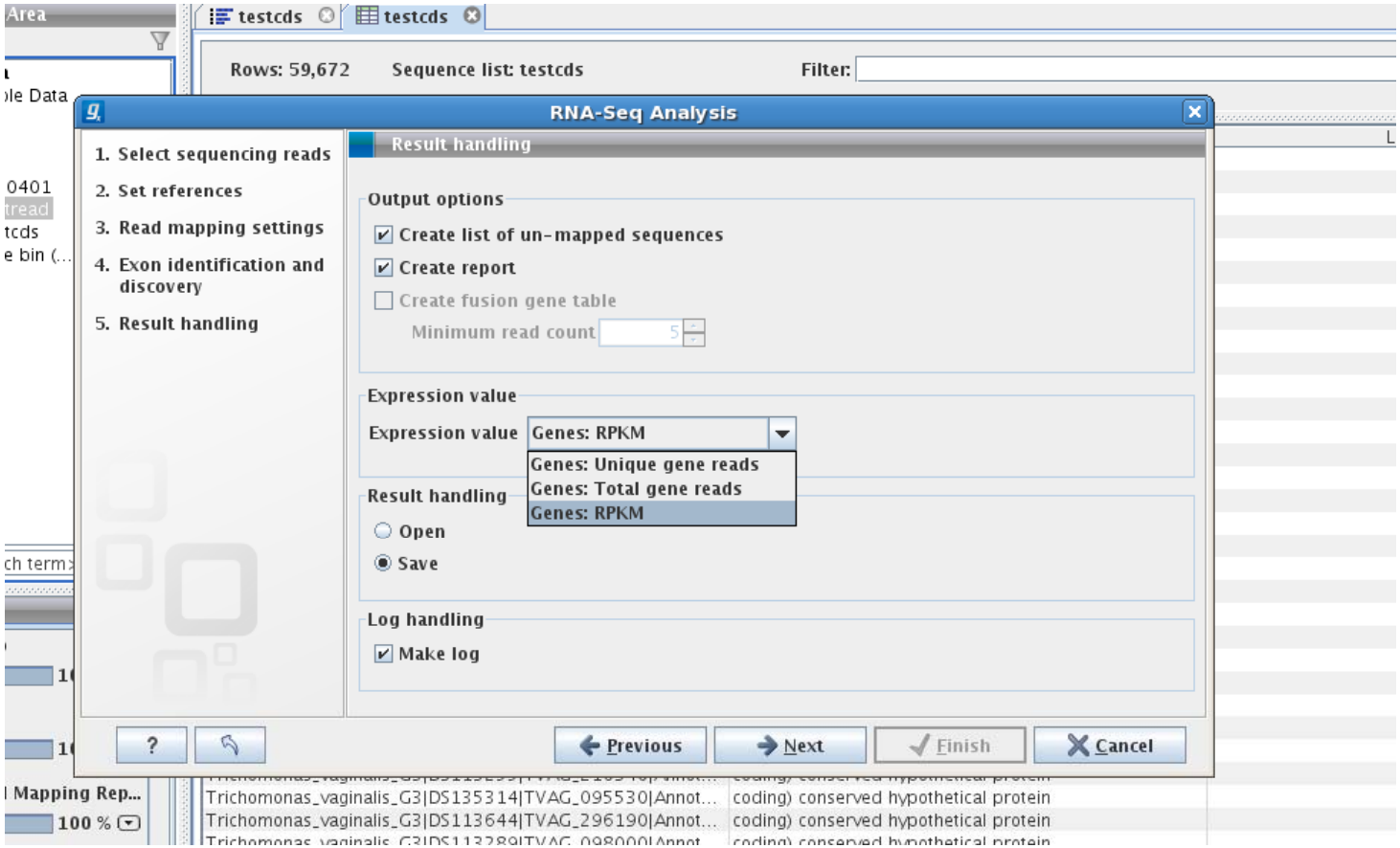

0318
0331
0325
course0401
test
Recycle
Show Ctrl-O
New
Show
Toolbox
Cut Ctrl-X
Copy Ctrl-C
Paste Ctrl-V
Delete Delete
Import... Ctrl-I
Export... Ctrl-E
Local Search... Ctrl-F
Sort Folder Ctrl+Shift-R
Update Folder F5
Restore
Empty Recycle Bin
Location
Sequence Representation
Alignments and Trees
General Sequence Analyses
Nucleotide Analyses
Protein Analyses
Sequencing Data Analyses
Primers and Probes
Cloning and Restriction Sites
RNA Structure
Expression Analysis
High-Throughput Sequencing
BLAST
Trim Sequences...
De Novo Assembly...
Map Reads to Reference...
Create Detailed Mapping Report...
Merge Mapping Results...
SNP Detection...
DIP Detection...
ChIP-Seq Analysis...
RNA-Seq Analysis...
Expression Profiling by Tags
Small RNA Analysis
Multiplexing
Name
Description
Trichomonas_vaginalis_G3|DS132288|TVAG_595070|Annot... coding) conserved hypothetical protein
Trichomonas_vaginalis_G3|DS132994|TVAG_331990|Annot... coding) conserved hypothetical protein
Trichomonas_vaginalis_G3|DS113314|TVAG_488080|Annot... coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) DNA-directed RNA polymerase III largest sub
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) Spermatogenesis-associated protein, putative
coding) conserved hypothetical protein
coding) conserved hypothetical protein
coding) host cell factor C1, putative
coding) conserved hypothetical protein
Trichomonas_vaginalis_G3|DS141940|TVAG_601840|Annot
Trichomonas_vaginalis_G3|DS116366|TVAG_153950|Annot
Trichomonas_vaginalis_G3|DS113289|TVAG_097690|Annot
Trichomonas_vaginalis_G3|DS113602|TVAG_114100|Annot
Trichomonas_vaginalis_G3|DS113602|TVAG_114220|Annot
Trichomonas_vaginalis_G3|DS113255|TVAG_210340|Annot
Trichomonas_vaginalis_G3|DS135314|TVAG_095530|Annot
Trichomonas_vaginalis_G3|DS113644|TVAG_296190|Annot
Trichomonas_vaginalis_G3|DS113289|TVAG_098000|Annot
<enter searc
Toolbox
lumina (Done)
reate MA Plot
100 %
reate Detailed Mapping Rep...
100 %
reate Experiment from Selec...
100 %
Processes
Toolbox

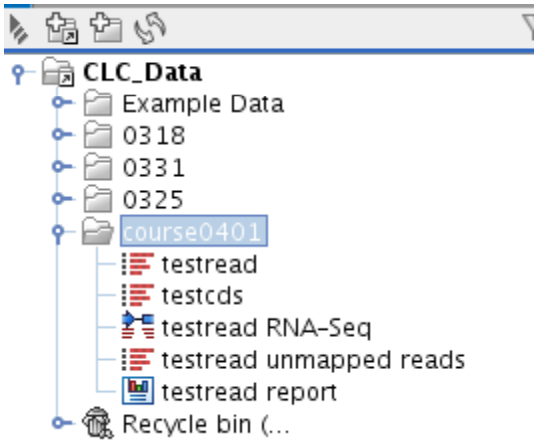
select reference sequence



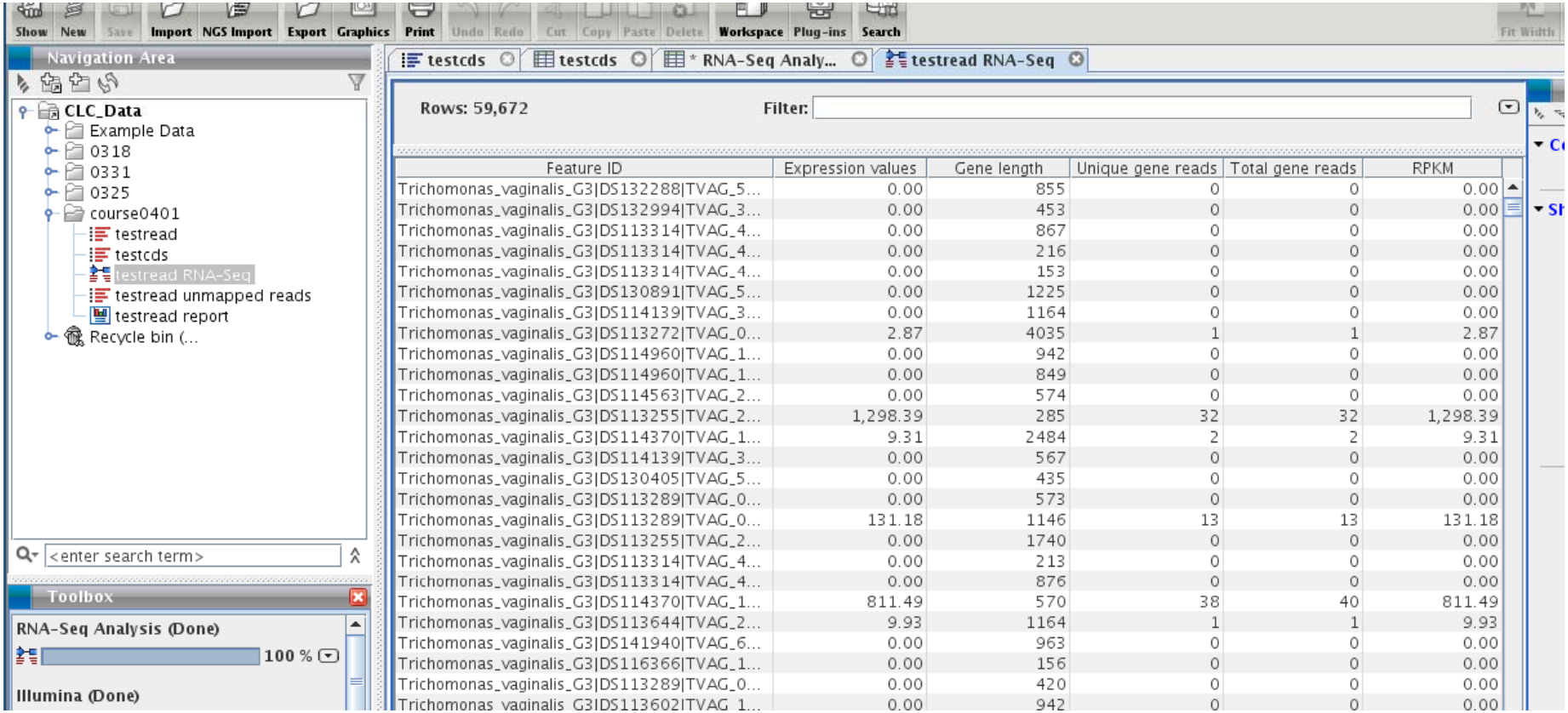

RNA-Seq Analysis
1. Select sequencing reads
2. Set references
3. Read mapping settings
Set parameters
Mapping settings
Maximum number of mismatches
2
Minimum length fraction
0.9
Minimum similarity fraction
0.8
Maximum number of hits for a read
10
Use color space
Strand specific alignment
Paired settings
Minimum distance
180
Maximum distance
250
Use 'include broken pairs' counting scheme
?
Previous
Next
Finish
Cancel
Trichomonas_vaginalis_G3|DS135314|TVAG_095530|Annot...
coding) conserved hypothetical protein

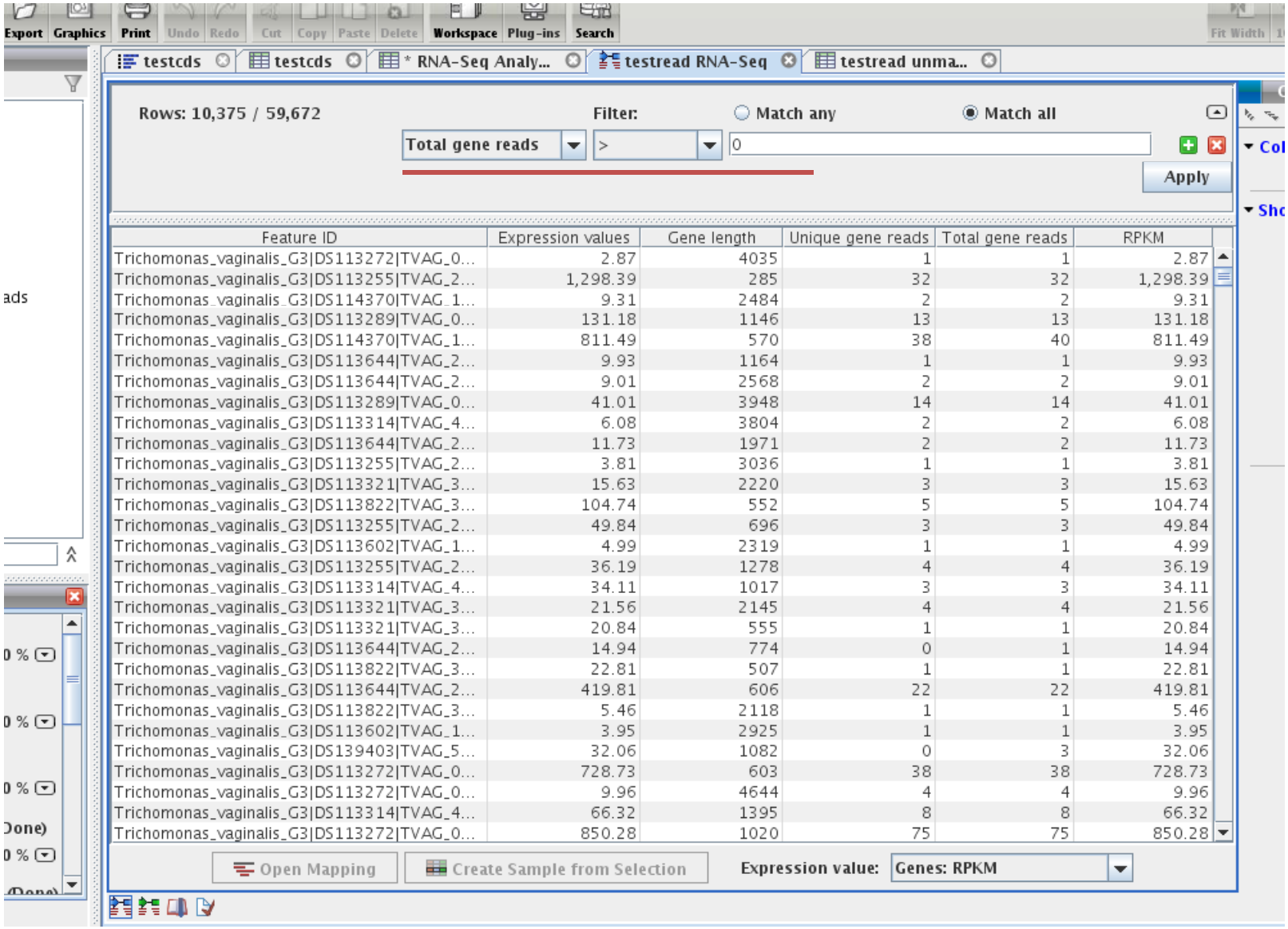

Rows: 59,672
Sequence list: testcds
Filter:
RNA-Seq Analysis
1. Select sequencing reads
2. Set references
3. Read mapping settings
4. Exon identification and discovery
Set parameters
Type of organism
Prokaryote
Eukaryote
Exon discovery
Exon discovery
Required relative expression level
0.20
Minimum number of reads
10
Minimum length
50
Previous
Next
Finish
Cancel
Trichomonas_vaginalis_G3|DS135314|TVAG_095530|Annot...
coding) conserved hypothetical protein
Trichomonas_vaginalis_G3|DS113644|TVAG_296190|Annot...
coding) conserved hypothetical protein


testcds
testcds
Rows: 59,672
Sequence list: testcds
Filter:
RNA-Seq Analysis
1. Select sequencing reads
2. Set references
3. Read mapping settings
4. Exon identification and discovery
5. Result handling
Result handling
Output options
Create list of un-mapped sequences
Create report
Create fusion gene table
Minimum read count
5
Expression value
Expression value
Genes: RPKM
Genes: Unique gene reads
Genes: Total gene reads
Genes: RPKM
Result handling
Open
Save
Log handling
Make log
Previous
Next
Finish
Cancel
Trichomonas_vaginalis_G3|DS135314|TVAG_095530|Annot...
coding) conserved hypothetical protein
Trichomonas_vaginalis_G3|DS113644|TVAG_296190|Annot...
coding) conserved hypothetical protein
Mapping Rep...
100 %

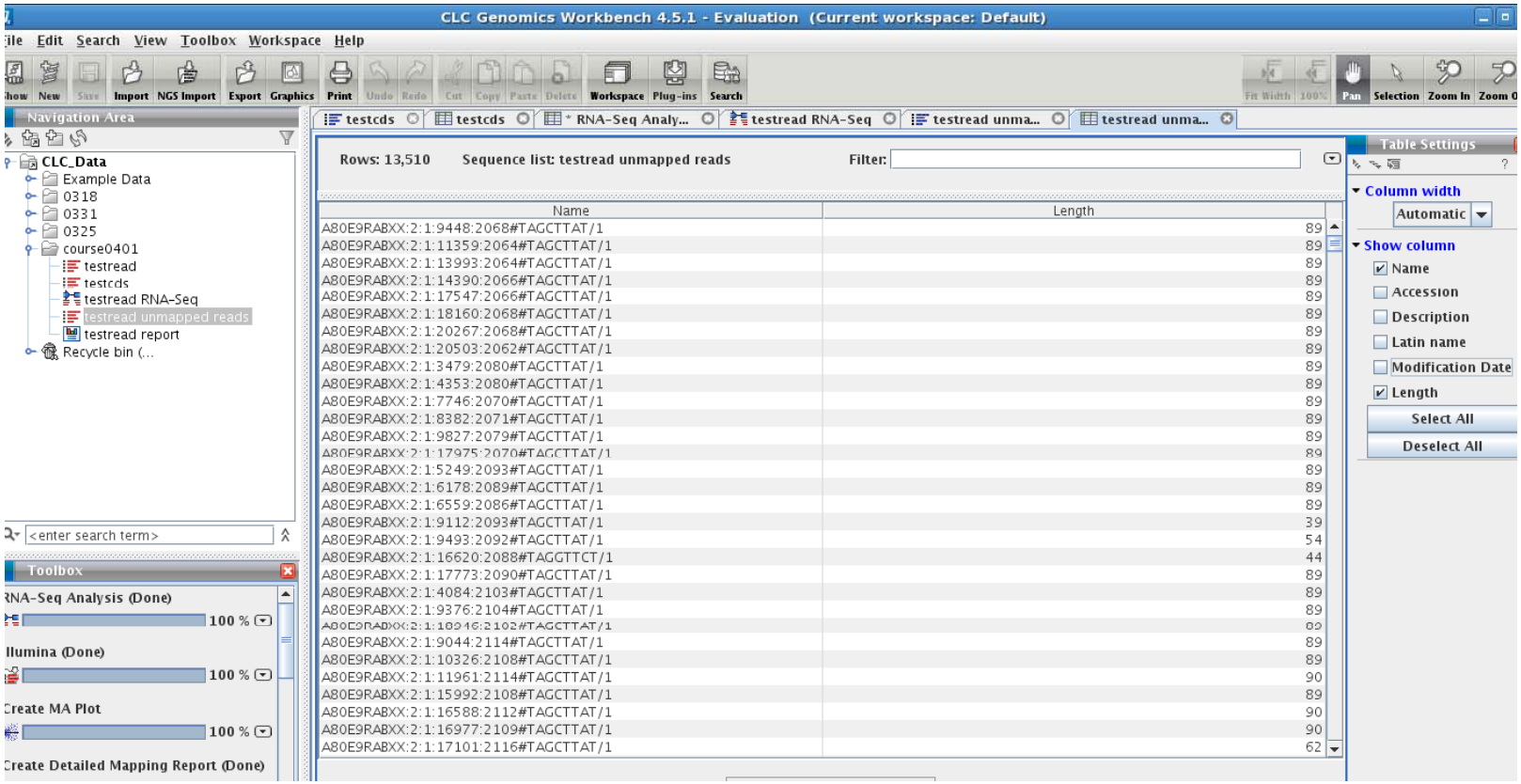

CLC_Data
Example Data
0318
0331
0325
course0401
testread
testcds
testread RNA-Seq
testread unmapped reads
testread report
Recycle bin (...

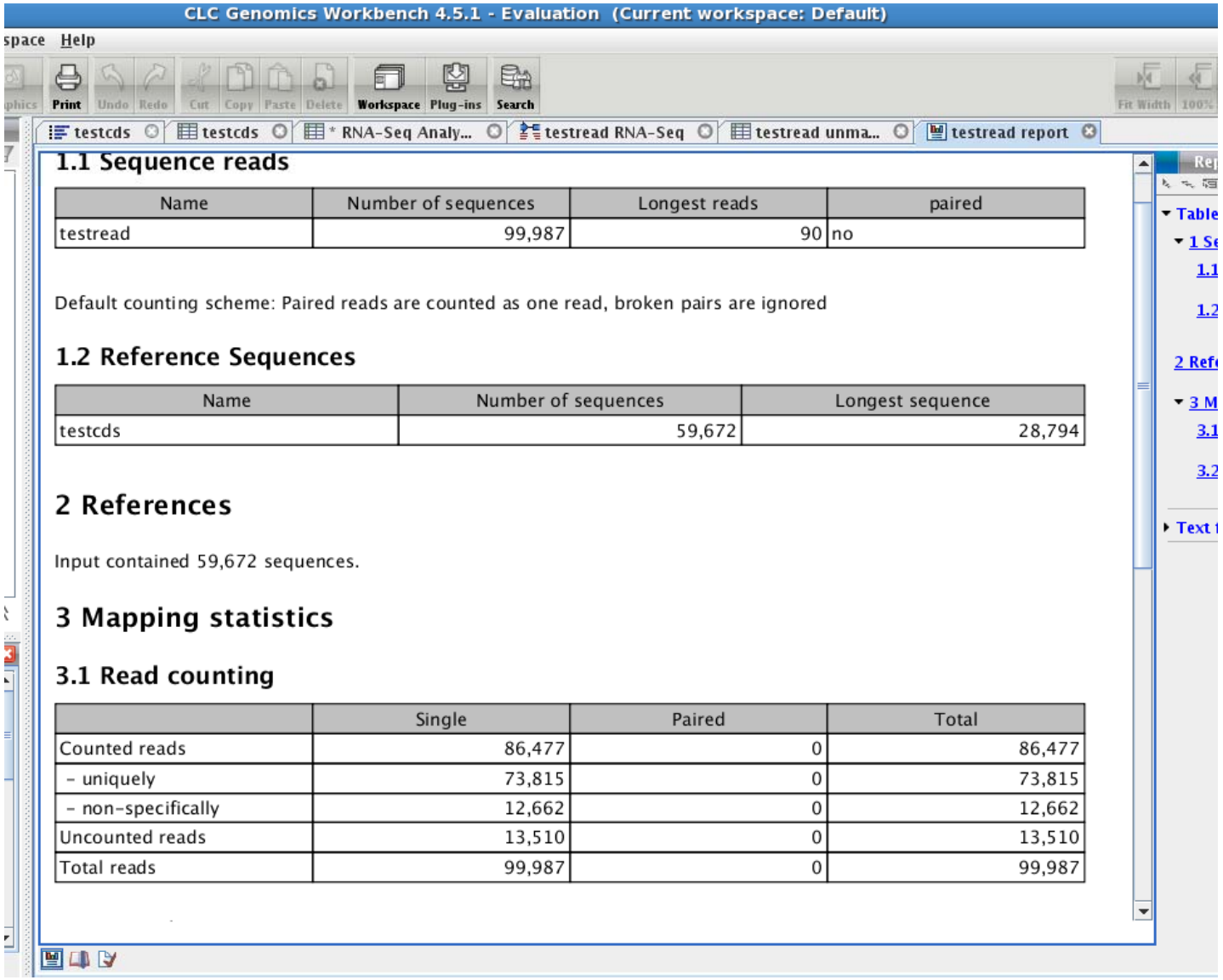
mapping results

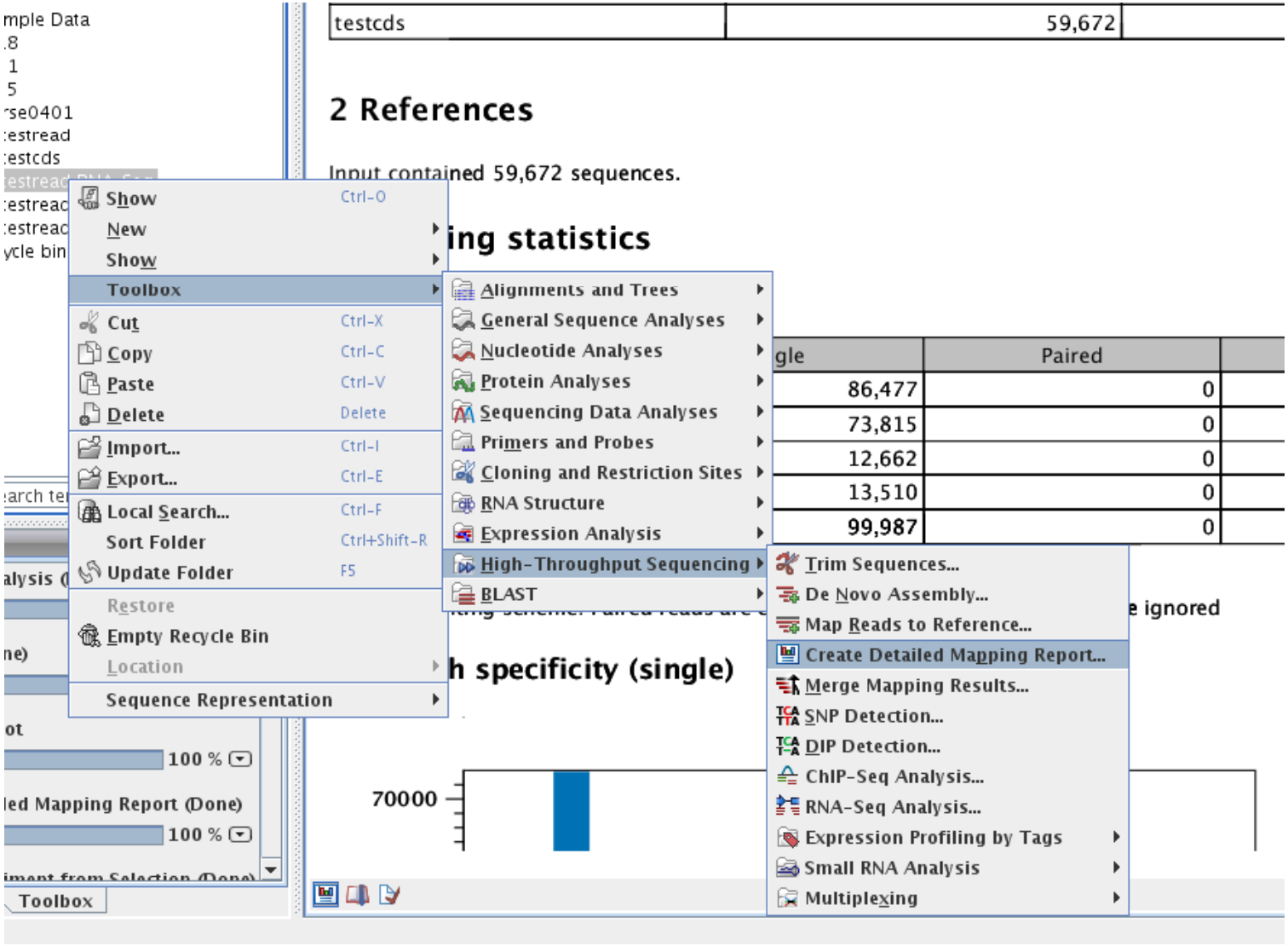



Export
Graphics
Print
Undo
Redo
Cut
Copy
Paste
Delete
Workspace
Plug-ins
Search
Fit Width
testcds
testcds
* RNA-Seq Analy...
testread RNA-Seq
testread unma...
Rows: 10,375 / 59,672
Filter:
Match any
Match all
Total gene reads
>
0
Apply
Feature ID
Expression values
Gene length
Unique gene reads
Total gene reads
RPKM
Trichomonas_vaginalis_G3|DS113272|TVAG_0... 2.87 4035 1 1 2.87
Trichomonas_vaginalis_G3|DS113255|TVAG_2... 1,298.39 285 32 32 1,298.39
Trichomonas_vaginalis_G3|DS114370|TVAG_1... 9.31 2484 2 2 9.31
Trichomonas_vaginalis_G3|DS113289|TVAG_0... 131.18 1146 13 13 131.18
Trichomonas_vaginalis_G3|DS114370|TVAG_1... 811.49 570 38 40 811.49
Trichomonas_vaginalis_G3|DS113644|TVAG_2... 9.93 1164 1 1 9.93
Trichomonas_vaginalis_G3|DS113644|TVAG_2... 9.01 2568 2 2 9.01
Trichomonas_vaginalis_G3|DS113289|TVAG_0... 41.01 3948 14 14 41.01
Trichomonas_vaginalis_G3|DS113314|TVAG_4... 6.08 3804 2 2 6.08
Trichomonas_vaginalis_G3|DS113644|TVAG_2... 11.73 1971 2 2 11.73
Trichomonas_vaginalis_G3|DS113255|TVAG_2... 3.81 3036 1 1 3.81
Trichomonas_vaginalis_G3|DS113321|TVAG_3... 15.63 2220 3 3 15.63
Trichomonas_vaginalis_G3|DS113822|TVAG_3... 104.74 552 5 5 104.74
Trichomonas_vaginalis_G3|DS113255|TVAG_2... 49.84 696 3 3 49.84
Trichomonas_vaginalis_G3|DS113602|TVAG_1... 4.99 2319 1 1 4.99
Trichomonas_vaginalis_G3|DS113255|TVAG_2... 36.19 1278 4 4 36.19
Trichomonas_vaginalis_G3|DS113314|TVAG_4... 34.11 1017 3 3 34.11
Trichomonas_vaginalis_G3|DS113321|TVAG_3... 21.56 2145 4 4 21.56
Trichomonas_vaginalis_G3|DS113321|TVAG_3... 20.84 555 1 1 20.84
Trichomonas_vaginalis_G3|DS113644|TVAG_2... 14.94 774 0 1 14.94
Trichomonas_vaginalis_G3|DS113822|TVAG_3... 22.81 507 1 1 22.81
Trichomonas_vaginalis_G3|DS113644|TVAG_2... 419.81 606 22 22 419.81
Trichomonas_vaginalis_G3|DS113822|TVAG_3... 5.46 2118 1 1 5.46
Trichomonas_vaginalis_G3|DS113602|TVAG_1... 3.95 2925 1 1 3.95
Trichomonas_vaginalis_G3|DS139403|TVAG_5... 32.06 1082 0 3 32.06
Trichomonas_vaginalis_G3|DS113272|TVAG_0... 728.73 603 38 38 728.73
Trichomonas_vaginalis_G3|DS113272|TVAG_0... 9.96 4644 4 4 9.96
Trichomonas_vaginalis_G3|DS113314|TVAG_4... 66.32 1395 8 8 66.32
Trichomonas_vaginalis_G3|DS113272|TVAG_0... 850.28 1020 75 75 850.28
Open Mapping
Create Sample from Selection
Expression value:
Genes: RPKM

unmapped list




CLC Genomics Workbench 4.5.1 - Evaluation (Current workspace: Default)
Help
Print
Undo
Redo
Cut
Copy
Paste
Delete
Workspace
Plug-ins
Search
Fit Width
testcds
testcds
* RNA-Seq Analy...
testread RNA-Seq
testread unma...
testread report
1.1 Sequence reads
Name | Number of sequences | Longest reads | paired
testread | 99,987 | 90 | no
Default counting scheme: Paired reads are counted as one read, broken pairs are ignored
1.2 Reference Sequences
Name | Number of sequences | Longest sequence
testcds | 59,672 | 28,794
2 References
Input contained 59,672 sequences.
3 Mapping statistics
3.1 Read counting
| Single | Paired | Total
Counted reads | 86,477 | 0 | 86,477
- uniquely | 73,815 | 0 | 73,815
- non-specifically | 12,662 | 0 | 12,662
Uncounted reads | 13,510 | 0 | 13,510
Total reads | 99,987 | 0 | 99,987


testcds
59,672
2 References
Input contained 59,672 sequences.
ing statistics
gle
Paired
86,477
0
73,815
0
12,662
0
13,510
0
99,987
0
ignored
h specificity (single)
70000
Show Ctrl-O
New
Show
Toolbox
Cut Ctrl-X
Copy Ctrl-C
Paste Ctrl-V
Delete Delete
Import... Ctrl-I
Export... Ctrl-E
Local Search... Ctrl-F
Sort Folder Ctrl+Shift-R
Update Folder F5
Restore
Empty Recycle Bin
Location
Sequence Representation
Alignments and Trees
General Sequence Analyses
Nucleotide Analyses
Protein Analyses
Sequencing Data Analyses
Primers and Probes
Cloning and Restriction Sites
RNA Structure
Expression Analysis
High-Throughput Sequencing
BLAST
Trim Sequences...
De Novo Assembly...
Map Reads to Reference...
Create Detailed Mapping Report...
Merge Mapping Results...
SNP Detection...
DIP Detection...
ChIP-Seq Analysis...
RNA-Seq Analysis...
Expression Profiling by Tags
Small RNA Analysis
Multiplexing
100 %
100 %
Toolbox

testcds | testcds | * RNA-Seq Analy... | testread RNA-Seq | testread unma... | testrea

1 Summary

Reference count	59,672
Type	Reference mapping
Total reference length	54,925,344
GC contents in %	35.49
Total read count	86,477
Mean read length	86.26
Total read length	7,459,314

2 References

2.1 Reference coverage

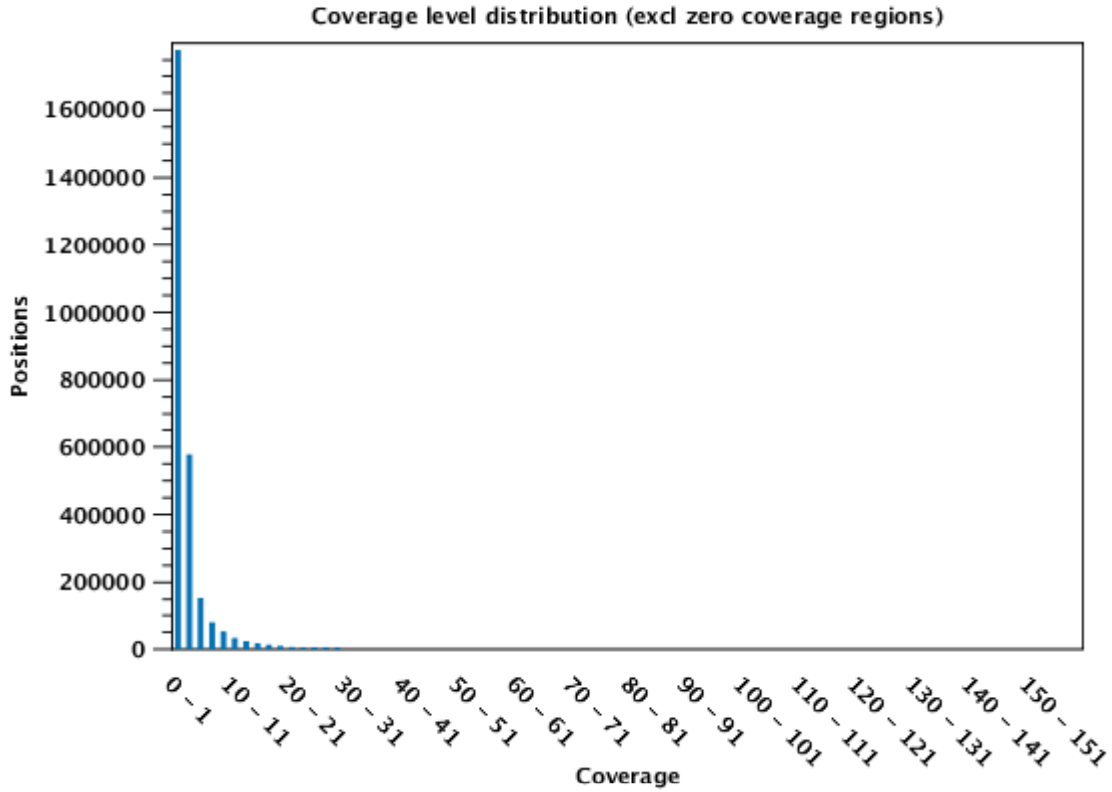
Total reference length	54,925,344
% GC	35.49
Total consensus length	2,780,514
Fraction of reference covered	0.05

2.2 Coverage statistics

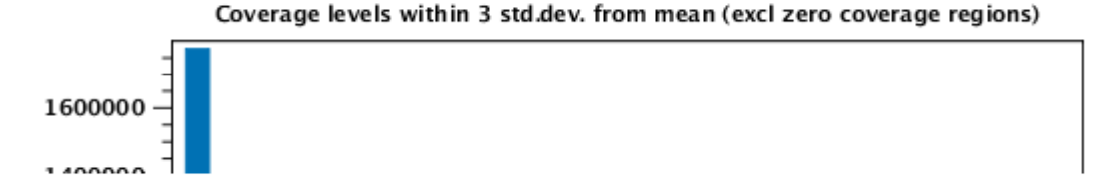
Total reference length	54,925,344
Minimum coverage	0
Maximum coverage	158
Average coverage	0.14
Standard deviation	1.30
Minimum excl zero coverage regions	1
Average excl. zero coverage regions	2.68

54,593,556 positions have coverage between 0 and 4.
331,788 positions have coverage above 4 (not shown in graph).

2.4 Coverage level distribution (excl zero coverage regions)



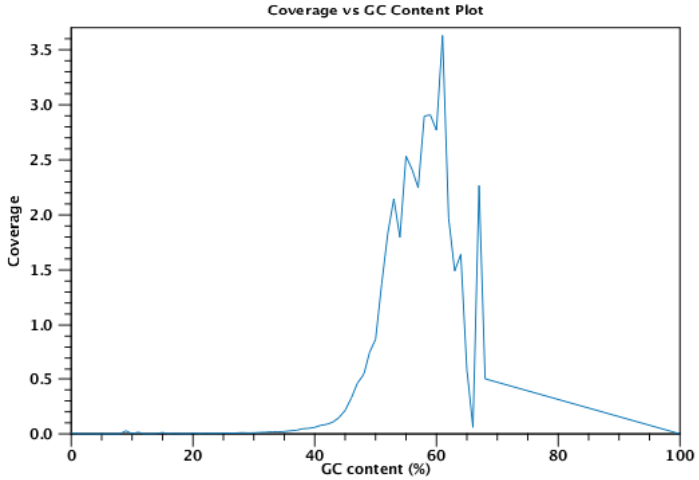
52,144,885 positions have zero coverage (not shown in graph).



2.5 Zero coverage regions

Count	81,660
Minimum length	1
Maximum length	27,312
Mean length	638.56
Standard deviation	751.99
Total length	52,144,885
Regions	

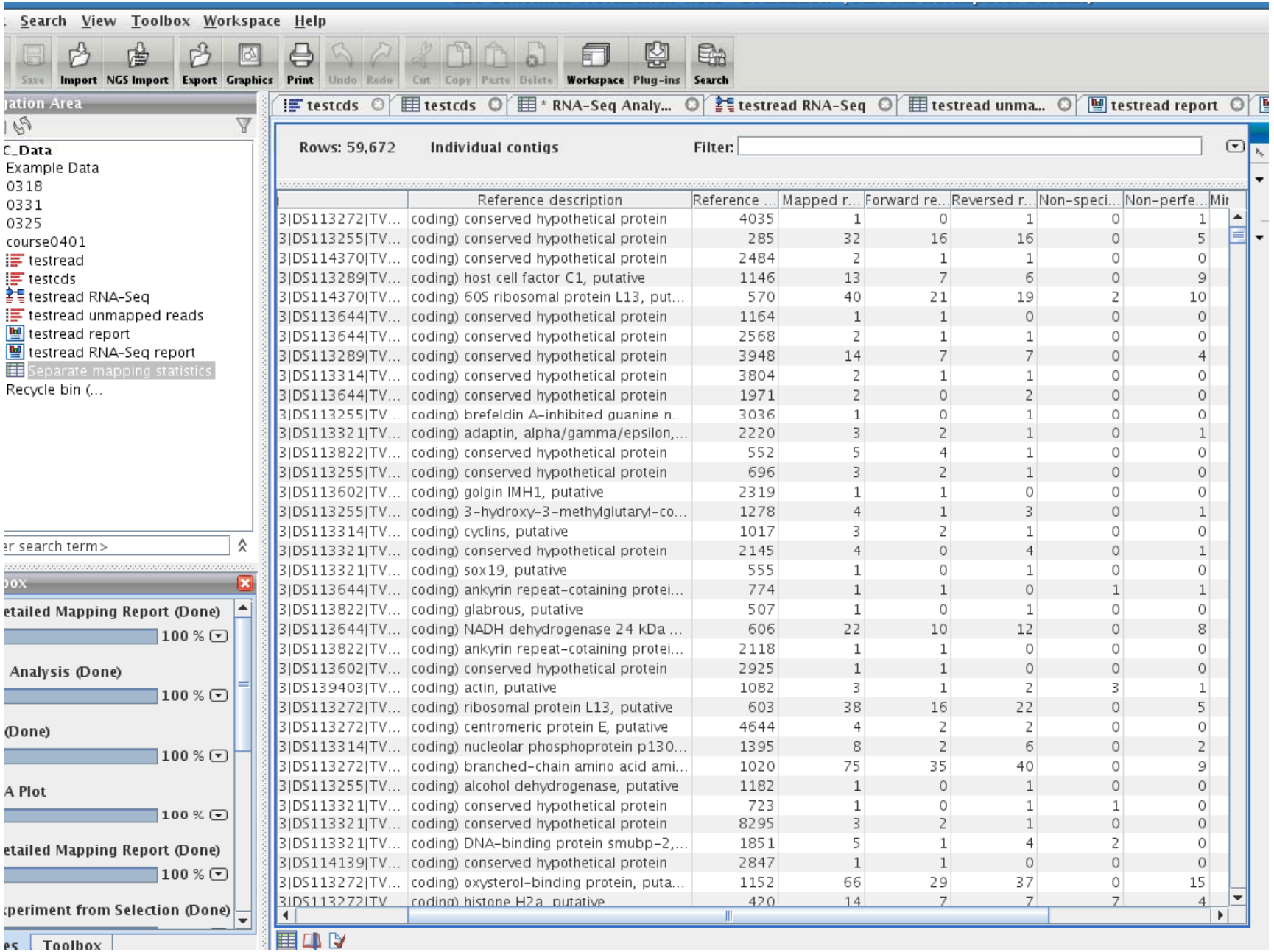
2.6 Coverage vs GC Content Plot



The plot displays, for each GC content level (0–100%), the mean read coverage of 100bp reference segments with that GC content.

3 Mapped reads

3.1 All mapped reads

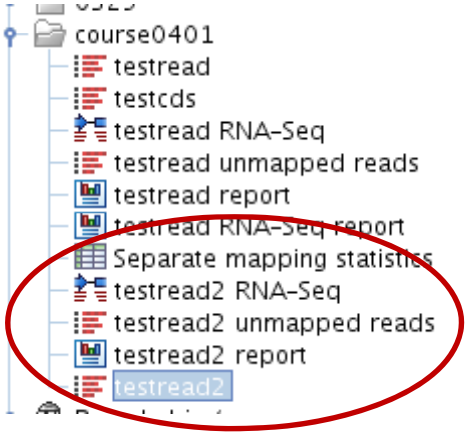

Search View Toolbox Workspace Help
Save Import NGS Import Export Graphics Print Undo Redo Cut Copy Paste Delete Workspace Plug-ins Search
gation Area
C_Data
Example Data
0318
0331
0325
course0401
testread
testcds
testread RNA-Seq
testread unmapped reads
testread report
testread RNA-Seq report
Separate mapping statistics
Recycle bin (...
er search term>
box
etailed Mapping Report (Done)
100 %
Analysis (Done)
100 %
(Done)
100 %
A Plot
100 %
etailed Mapping Report (Done)
100 %
periment from Selection (Done)
es Toolbox
testcds
testcds
* RNA-Seq Analy...
testread RNA-Seq
testread unma...
testread report
Rows: 59,672
Individual contigs
Filter:
Reference description
Reference ...
Mapped r...
Forward re...
Reversed r...
Non-speci...
Non-perfe...
Mir
3|DS113272|TV... coding) conserved hypothetical protein 4035 1 0 1 0 1
3|DS113255|TV... coding) conserved hypothetical protein 285 32 16 16 0 5
3|DS114370|TV... coding) conserved hypothetical protein 2484 2 1 1 0 0
3|DS113289|TV... coding) host cell factor C1, putative 1146 13 7 6 0 9
3|DS114370|TV... coding) 60S ribosomal protein L13, put... 570 40 21 19 2 10
3|DS113644|TV... coding) conserved hypothetical protein 1164 1 1 0 0 0
3|DS113644|TV... coding) conserved hypothetical protein 2568 2 1 1 0 0
3|DS113289|TV... coding) conserved hypothetical protein 3948 14 7 7 0 4
3|DS113314|TV... coding) conserved hypothetical protein 3804 2 1 1 0 0
3|DS113644|TV... coding) conserved hypothetical protein 1971 2 0 2 0 0
3|DS113255|TV... coding) brefeldin A-inhibited guanine n... 3036 1 0 1 0 0
3|DS113321|TV... coding) adaptin, alpha/gamma/epsilon,... 2220 3 2 1 0 1
3|DS113822|TV... coding) conserved hypothetical protein 552 5 4 1 0 0
3|DS113255|TV... coding) conserved hypothetical protein 696 3 2 1 0 0
3|DS113602|TV... coding) golgin IMH1, putative 2319 1 1 0 0 0
3|DS113255|TV... coding) 3-hydroxy-3-methylglutaryl-co... 1278 4 1 3 0 1
3|DS113314|TV... coding) cyclins, putative 1017 3 2 1 0 0
3|DS113321|TV... coding) conserved hypothetical protein 2145 4 0 4 0 1
3|DS113321|TV... coding) sox19, putative 555 1 0 1 0 0
3|DS113644|TV... coding) ankyrin repeat-cotaining protei... 774 1 1 0 1 1
3|DS113822|TV... coding) glabrous, putative 507 1 0 1 0 0
3|DS113644|TV... coding) NADH dehydrogenase 24 kDa ... 606 22 10 12 0 8
3|DS113822|TV... coding) ankyrin repeat-cotaining protei... 2118 1 1 0 0 0
3|DS113602|TV... coding) conserved hypothetical protein 2925 1 1 0 0 0
3|DS139403|TV... coding) actin, putative 1082 3 1 2 3 1
3|DS113272|TV... coding) ribosomal protein L13, putative 603 38 16 22 0 5
3|DS113272|TV... coding) centromeric protein E, putative 4644 4 2 2 0 0
3|DS113314|TV... coding) nucleolar phosphoprotein p130... 1395 8 2 6 0 2
3|DS113272|TV... coding) branched-chain amino acid ami... 1020 75 35 40 0 9
3|DS113255|TV... coding) alcohol dehydrogenase, putative 1182 1 0 1 0 0
3|DS113321|TV... coding) conserved hypothetical protein 723 1 0 1 1 0
3|DS113321|TV... coding) conserved hypothetical protein 8295 3 2 1 0 0
3|DS113321|TV... coding) DNA-binding protein smubp-2,... 1851 5 1 4 2 0
3|DS114139|TV... coding) conserved hypothetical protein 2847 1 1 0 0 0
3|DS113272|TV... coding) oxysterol-binding protein, puta... 1152 66 29 37 0 15
3|DS113272|TV... coding) histone H2a, putative 420 14 7 7 7 4

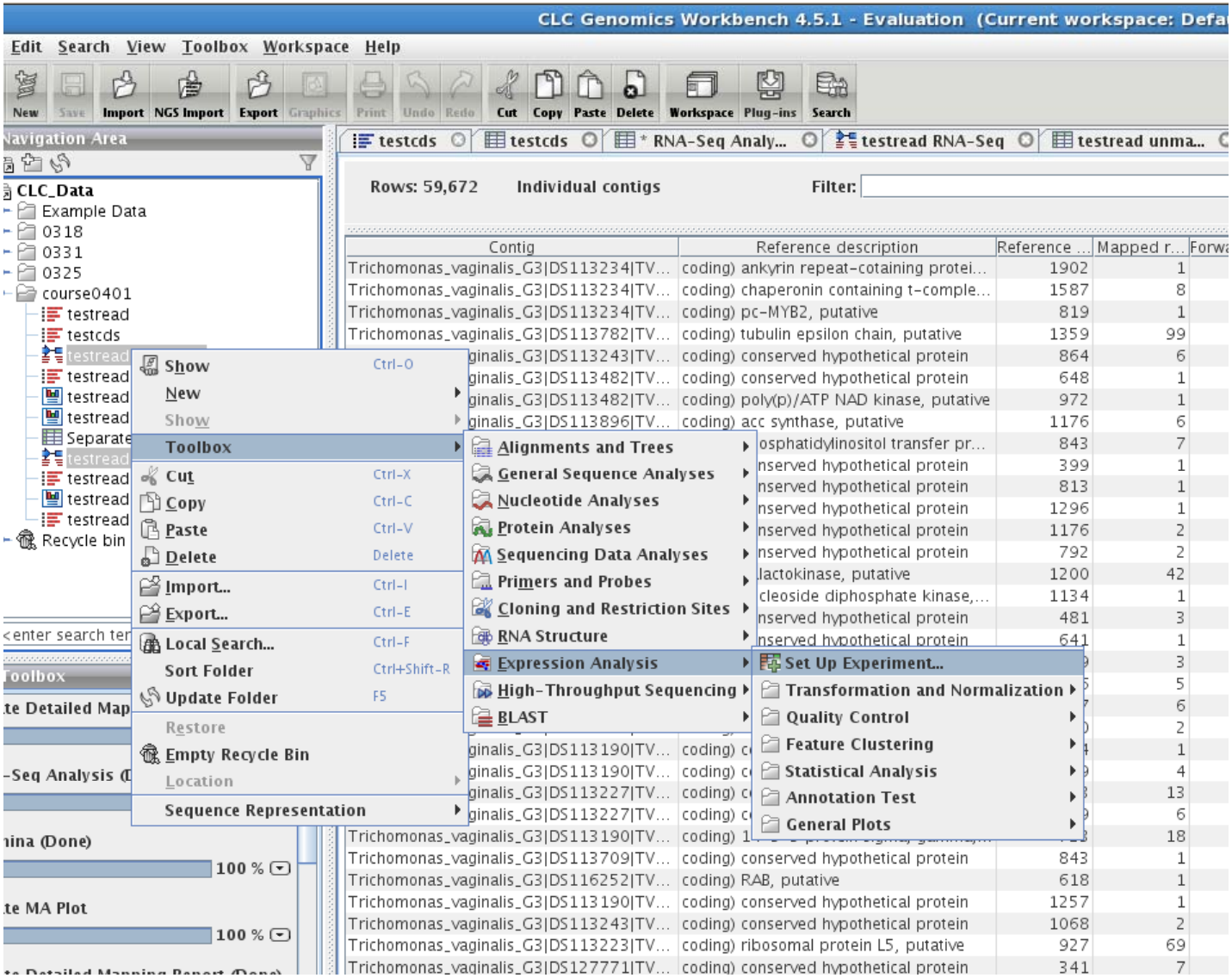
exercise

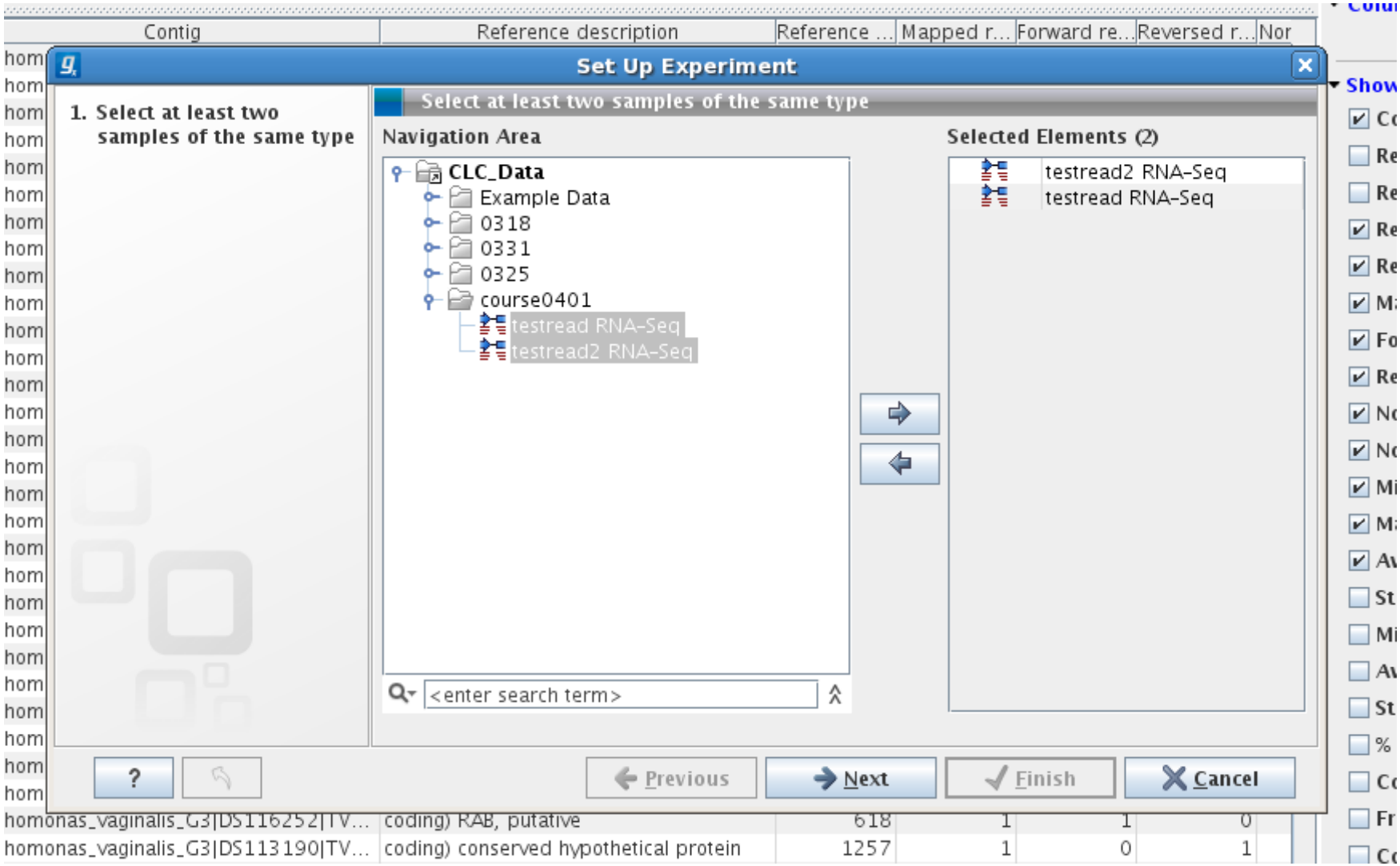
- get testread2

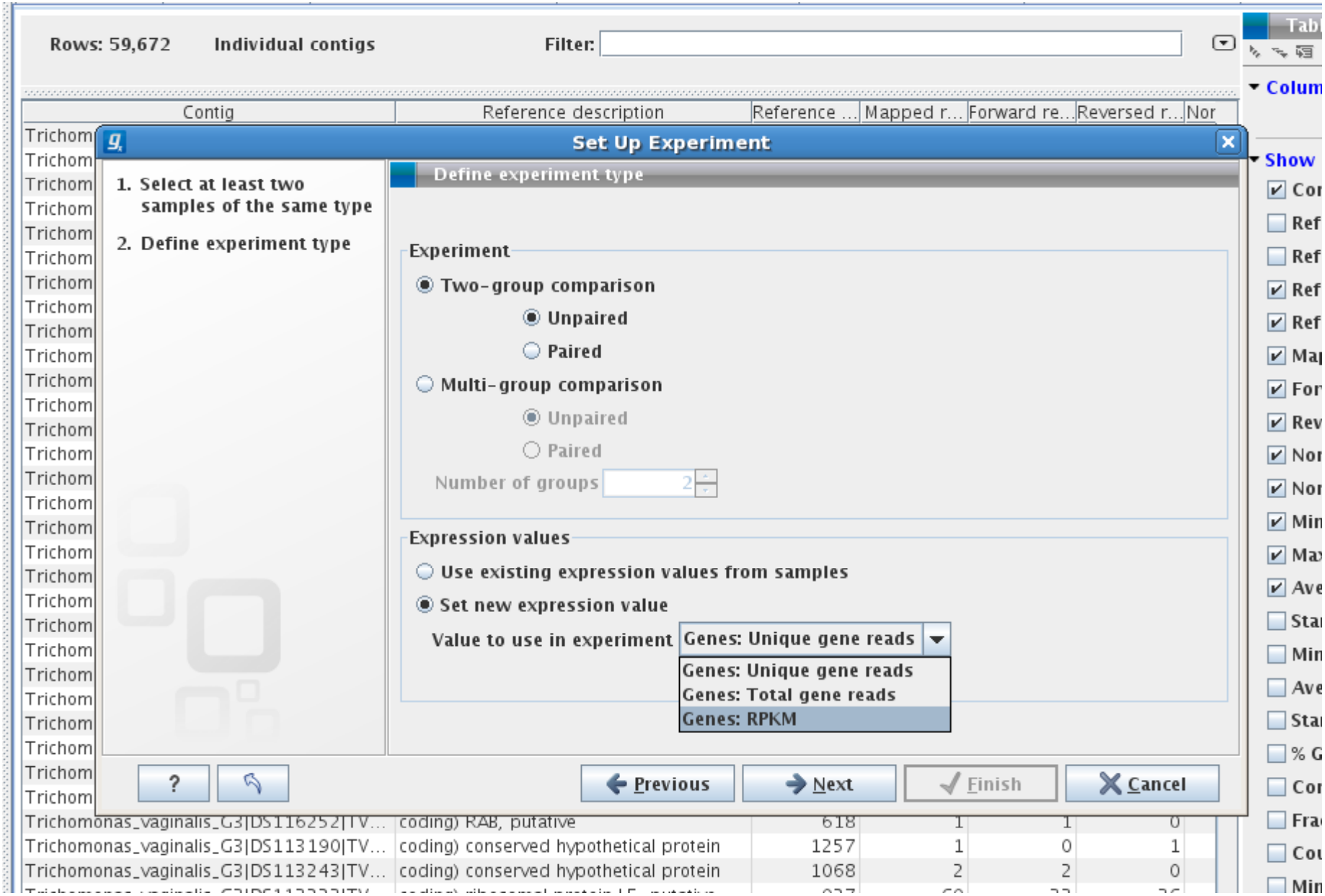
```
wget   http://163.25.92.61/course/testread2.fq
```

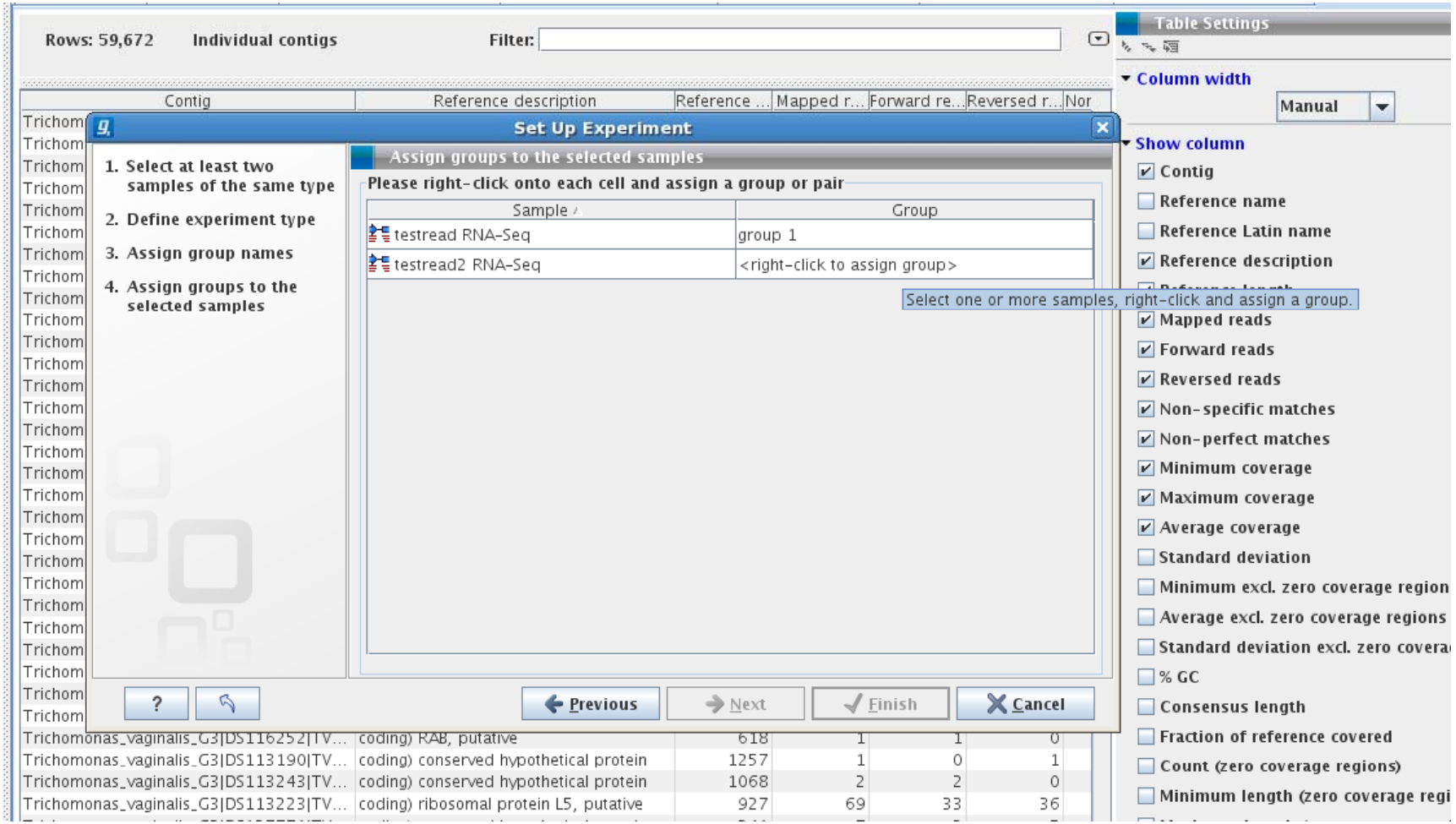
- do above works

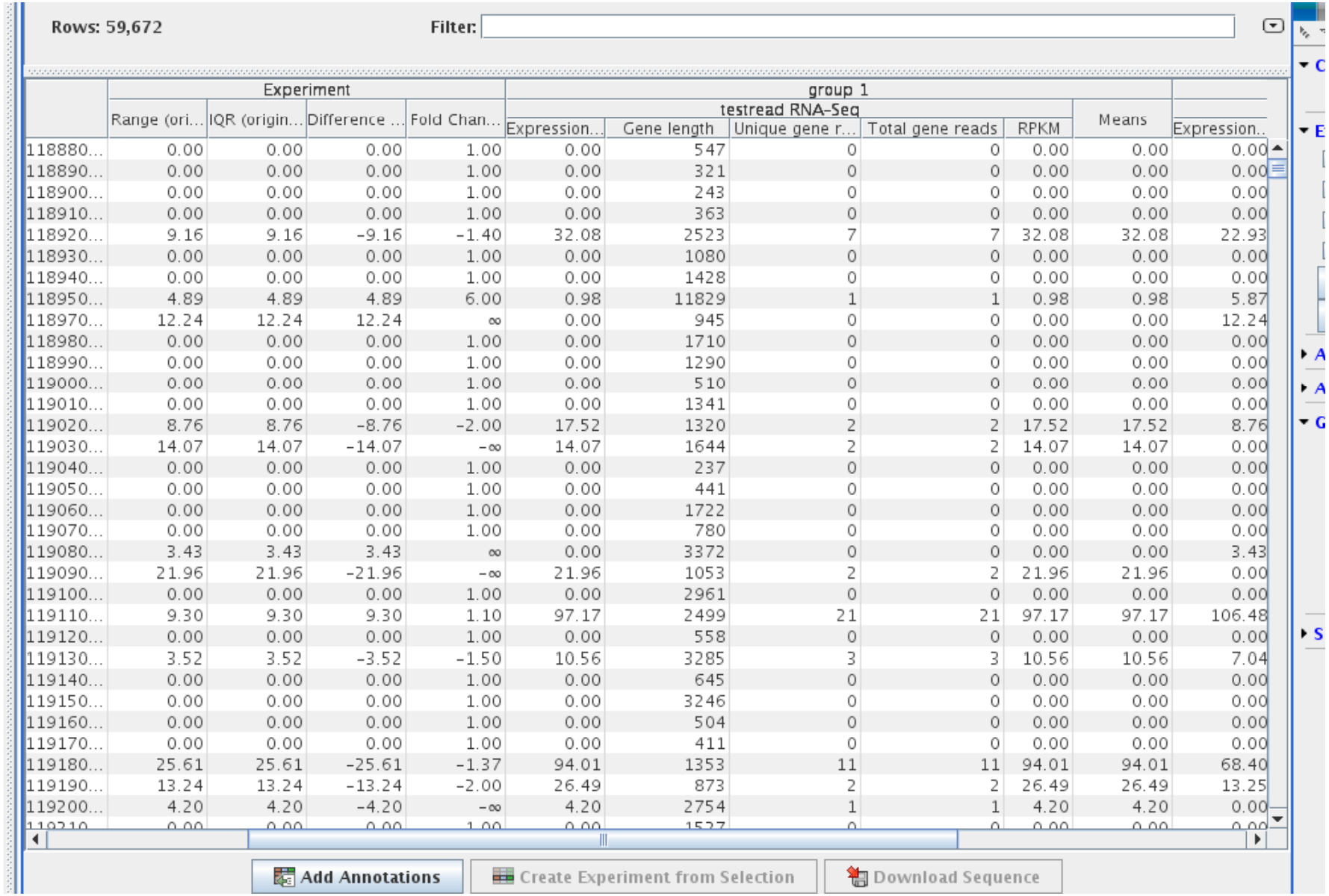



CLC Genomics Workbench 4.5.1 - Evaluation (Current workspace: Defa
Edit Search View Toolbox Workspace Help
New Save Import NGS Import Export Graphics Print Undo Redo Cut Copy Paste Delete Workspace Plug-ins Search
Navigation Area
CLC_Data
Example Data
0318
0331
0325
course0401
testread
testcds
testread
testread
testread
testread
Separate
testread
testread
testread
testread
Recycle bin
testcds
testcds
* RNA-Seq Analy...
testread RNA-Seq
testread unma...
Rows: 59,672
Individual contigs
Filter:
Contig
Reference description
Reference ...
Mapped r...
Trichomonas_vaginalis_G3|DS113234|TV... coding) ankyrin repeat-cotaining protei... 1902 1
Trichomonas_vaginalis_G3|DS113234|TV... coding) chaperonin containing t-comple... 1587 8
Trichomonas_vaginalis_G3|DS113234|TV... coding) pc-MYB2, putative 819 1
Trichomonas_vaginalis_G3|DS113782|TV... coding) tubulin epsilon chain, putative 1359 99
ginalis_G3|DS113243|TV... coding) conserved hypothetical protein 864 6
ginalis_G3|DS113482|TV... coding) conserved hypothetical protein 648 1
ginalis_G3|DS113482|TV... coding) poly(p)/ATP NAD kinase, putative 972 1
ginalis_G3|DS113896|TV... coding) acc synthase, putative 1176 6
osphatidylinositol transfer pr... 843 7
nserved hypothetical protein 399 1
nserved hypothetical protein 813 1
nserved hypothetical protein 1296 1
nserved hypothetical protein 1176 2
nserved hypothetical protein 792 2
lactokinase, putative 1200 42
cleoside diphosphate kinase,... 1134 1
nserved hypothetical protein 481 3
nserved hypothetical protein 641 1
Trichomonas_vaginalis_G3|DS113709|TV... coding) conserved hypothetical protein 843 1
Trichomonas_vaginalis_G3|DS116252|TV... coding) RAB, putative 618 1
Trichomonas_vaginalis_G3|DS113190|TV... coding) conserved hypothetical protein 1257 1
Trichomonas_vaginalis_G3|DS113243|TV... coding) conserved hypothetical protein 1068 2
Trichomonas_vaginalis_G3|DS113223|TV... coding) ribosomal protein L5, putative 927 69
Trichomonas_vaginalis_G3|DS127771|TV... coding) conserved hypothetical protein 341 7
Show Ctrl-O
New
Show
Toolbox
Cut Ctrl-X
Copy Ctrl-C
Paste Ctrl-V
Delete Delete
Import... Ctrl-I
Export... Ctrl-E
Local Search... Ctrl-F
Sort Folder Ctrl+Shift-R
Update Folder F5
Restore
Empty Recycle Bin
Location
Sequence Representation
Alignments and Trees
General Sequence Analyses
Nucleotide Analyses
Protein Analyses
Sequencing Data Analyses
Primers and Probes
Cloning and Restriction Sites
RNA Structure
Expression Analysis
High-Throughput Sequencing
BLAST
Set Up Experiment...
Transformation and Normalization
Quality Control
Feature Clustering
Statistical Analysis
Annotation Test
General Plots
<enter search ter
Toolbox
te Detailed Map
-Seq Analysis (
nina (Done)
100 %
te MA Plot
100 %


Contig
Reference description
Reference ...
Mapped r...
Forward re...
Reversed r...
Nor
Set Up Experiment
1. Select at least two samples of the same type
Select at least two samples of the same type
Navigation Area
CLC_Data
Example Data
0318
0331
0325
course0401
testread RNA-Seq
testread2 RNA-Seq
<enter search term>
Selected Elements (2)
testread2 RNA-Seq
testread RNA-Seq
?
Previous
Next
Finish
Cancel
homonas_vaginalis_G3|DS116252|TV...
coding) RAB, putative
618
1
1
0
homonas_vaginalis_G3|DS113190|TV...
coding) conserved hypothetical protein
1257
1
0
1


Rows: 59,672
Individual contigs
Filter:
Contig
Reference description
Reference ...
Mapped r...
Forward re...
Reversed r...
Nor
Set Up Experiment
1. Select at least two samples of the same type
2. Define experiment type
Define experiment type
Experiment
Two-group comparison
Unpaired
Paired
Multi-group comparison
Unpaired
Paired
Number of groups
2
Expression values
Use existing expression values from samples
Set new expression value
Value to use in experiment
Genes: Unique gene reads
Genes: Unique gene reads
Genes: Total gene reads
Genes: RPKM
Previous
Next
Finish
Cancel
Trichomonas_vaginalis_G3|DS116252|TV...
coding) RAB, putative
618
1
1
0
Trichomonas_vaginalis_G3|DS113190|TV...
coding) conserved hypothetical protein
1257
1
0
1
Trichomonas_vaginalis_G3|DS113243|TV...
coding) conserved hypothetical protein
1068
2
2
0


Rows: 59,672
Individual contigs
Filter:
Contig
Reference description
Reference ...
Mapped r...
Forward re...
Reversed r...
Nor
Set Up Experiment
1. Select at least two samples of the same type
2. Define experiment type
3. Assign group names
4. Assign groups to the selected samples
Assign groups to the selected samples
Please right-click onto each cell and assign a group or pair
Sample
Group
testread RNA-Seq
group 1
testread2 RNA-Seq
<right-click to assign group>
Select one or more samples, right-click and assign a group.
Previous
Next
Finish
Cancel
Trichomonas_vaginalis_G3|DS116252|TV... coding) RAB, putative 618 1 1 0
Trichomonas_vaginalis_G3|DS113190|TV... coding) conserved hypothetical protein 1257 1 0 1
Trichomonas_vaginalis_G3|DS113243|TV... coding) conserved hypothetical protein 1068 2 2 0
Trichomonas_vaginalis_G3|DS113223|TV... coding) ribosomal protein L5, putative 927 69 33 36
Table Settings
Column width
Manual
Show column
Contig
Reference name
Reference Latin name
Reference description
Mapped reads
Forward reads
Reversed reads
Non-specific matches
Non-perfect matches
Minimum coverage
Maximum coverage
Average coverage
Standard deviation
Minimum excl. zero coverage region
Average excl. zero coverage regions
Standard deviation excl. zero covera
% GC
Consensus length
Fraction of reference covered
Count (zero coverage regions)
Minimum length (zero coverage regi



Rows: 59,672 Filter:

	Experiment				group 1						
					testread RNA-Seq					Means	
	Range (ori...	IQR (origin...	Difference ...	Fold Chan...	Expression...	Gene length	Unique gene r...	Total gene reads	RPKM		Expression..
118880...	0.00	0.00	0.00	1.00	0.00	547	0	0	0.00	0.00	0.00
118890...	0.00	0.00	0.00	1.00	0.00	321	0	0	0.00	0.00	0.00
118900...	0.00	0.00	0.00	1.00	0.00	243	0	0	0.00	0.00	0.00
118910...	0.00	0.00	0.00	1.00	0.00	363	0	0	0.00	0.00	0.00
118920...	9.16	9.16	-9.16	-1.40	32.08	2523	7	7	32.08	32.08	22.93
118930...	0.00	0.00	0.00	1.00	0.00	1080	0	0	0.00	0.00	0.00
118940...	0.00	0.00	0.00	1.00	0.00	1428	0	0	0.00	0.00	0.00
118950...	4.89	4.89	4.89	6.00	0.98	11829	1	1	0.98	0.98	5.87
118970...	12.24	12.24	12.24	∞	0.00	945	0	0	0.00	0.00	12.24
118980...	0.00	0.00	0.00	1.00	0.00	1710	0	0	0.00	0.00	0.00
118990...	0.00	0.00	0.00	1.00	0.00	1290	0	0	0.00	0.00	0.00
119000...	0.00	0.00	0.00	1.00	0.00	510	0	0	0.00	0.00	0.00
119010...	0.00	0.00	0.00	1.00	0.00	1341	0	0	0.00	0.00	0.00
119020...	8.76	8.76	-8.76	-2.00	17.52	1320	2	2	17.52	17.52	8.76
119030...	14.07	14.07	-14.07	-∞	14.07	1644	2	2	14.07	14.07	0.00
119040...	0.00	0.00	0.00	1.00	0.00	237	0	0	0.00	0.00	0.00
119050...	0.00	0.00	0.00	1.00	0.00	441	0	0	0.00	0.00	0.00
119060...	0.00	0.00	0.00	1.00	0.00	1722	0	0	0.00	0.00	0.00
119070...	0.00	0.00	0.00	1.00	0.00	780	0	0	0.00	0.00	0.00
119080...	3.43	3.43	3.43	∞	0.00	3372	0	0	0.00	0.00	3.43
119090...	21.96	21.96	-21.96	-∞	21.96	1053	2	2	21.96	21.96	0.00
119100...	0.00	0.00	0.00	1.00	0.00	2961	0	0	0.00	0.00	0.00
119110...	9.30	9.30	9.30	1.10	97.17	2499	21	21	97.17	97.17	106.48
119120...	0.00	0.00	0.00	1.00	0.00	558	0	0	0.00	0.00	0.00
119130...	3.52	3.52	-3.52	-1.50	10.56	3285	3	3	10.56	10.56	7.04
119140...	0.00	0.00	0.00	1.00	0.00	645	0	0	0.00	0.00	0.00
119150...	0.00	0.00	0.00	1.00	0.00	3246	0	0	0.00	0.00	0.00
119160...	0.00	0.00	0.00	1.00	0.00	504	0	0	0.00	0.00	0.00
119170...	0.00	0.00	0.00	1.00	0.00	411	0	0	0.00	0.00	0.00
119180...	25.61	25.61	-25.61	-1.37	94.01	1353	11	11	94.01	94.01	68.40
119190...	13.24	13.24	-13.24	-2.00	26.49	873	2	2	26.49	26.49	13.25
119200...	4.20	4.20	-4.20	-∞	4.20	2754	1	1	4.20	4.20	0.00
119210...	0.00	0.00	0.00	1.00	0.00	1527	0	0	0.00	0.00	0.00

Add Annotations | Create Experiment from Selection | Download Sequence