Table of contents

1. RNA-Seq analysis

1.1 Read count statistics

For paired data, there are two reads in a pair.

The table is based on 24 samples.

Sample name	Read count	Single, mapped (%)	Single, not mapped (%)	Paired, mapped pairs (%)
AM24_1_1 (RNA-Seq report)	68,335,142	-	-	87.42
AM24_2_1 (RNA-Seq report)	74,985,334	-	-	87.37
AM24_3_1 (RNA-Seq report)	72,532,630	-	-	87.43
AM24_INF_1_1 (RNA-Seq report)	61,353,514	-	-	83.28
AM24_INF_2_1 (RNA-Seq report)	69,617,668	-	-	87.09
AM24_INF_3_1 (RNA-Seq report)	78,821,566	-	-	85.99
AM48_1_1 (RNA-Seq report)	61,369,580	-	-	87.14
AM48_2_1 (RNA-Seq report)	71,775,658	-	-	87.12
AM48_3_1 (RNA-Seq report)	64,580,534	-	-	87.72
AM48_INF_1_1 (RNA-Seq report)	73,683,698	-	-	86.35
AM48_INF_2_1 (RNA-Seq report)	72,071,366	-	-	87.31
AM48_INF_3_1 (RNA-Seq report)	64,205,784	-	-	87.62
NM24_1_1 (RNA-Seq report)	66,999,768	-	-	86.72
NM24_2_1 (RNA-Seq report)	75,204,118	-	-	87.34
NM24_3_1 (RNA-Seq report)	74,066,174	-	-	87.01
NM24_INF_1_1 (RNA-Seq report)	77,584,150	-	-	87.06
NM24_INF_2_1 (RNA-Seq report)	74,866,314	-	-	86.98

Sample name	Read count	Single, mapped (%)	Single, not mapped (%)	Paired, mapped pairs (%)
NM24_INF_3_1 (RNA-Seq report)	73,043,502	-	-	87.13
NM48_1_1 (RNA-Seq report)	71,842,400	-	-	87.05
NM48_2_1 (RNA-Seq report)	66,196,090	-	-	86.13
NM48_3_1 (RNA-Seq report)	71,053,948	-	-	86.95
NM48_INF_1_1 (RNA-Seq report)	68,044,224	-	-	85.45
NM48_INF_2_1 (RNA-Seq report)	71,826,926	-	-	86.69
NM48_INF_3_1 (RNA-Seq report)	61,368,712	-	-	86.90
Minimum	61,353,514.00	-	-	83.28
Median	71,801,292.00	-	-	87.05
Maximum	78,821,566.00	-	-	87.72
Mean	70,226,200.00	-	-	86.80
Standard deviation	5,054,908.86	-	-	0.92

Sample name	Paired, broken pairs (%)	Paired, not mapped (%)
AM24_1_1 (RNA-Seq report)	1.98	10.60
AM24_2_1 (RNA-Seq report)	2.44	10.19
AM24_3_1 (RNA-Seq report)	2.51	10.07
AM24_INF_1_1 (RNA-Seq report)	2.08	14.63
AM24_INF_2_1 (RNA-Seq report)	2.87	10.04
AM24_INF_3_1 (RNA-Seq report)	2.93	11.07
AM48_1_1 (RNA-Seq report)	2.80	10.06
AM48_2_1 (RNA-Seq report)	2.01	10.87
AM48_3_1 (RNA-Seq report)	2.45	9.82
AM48_INF_1_1 (RNA-Seq report)	2.62	11.03
AM48_INF_2_1 (RNA-Seq report)	2.05	10.64

Sample name	Paired, broken pairs (%)	Paired, not mapped (%)
AM48_INF_3_1 (RNA-Seq report)	2.34	10.04
NM24_1_1 (RNA-Seq report)	2.55	10.73
NM24_2_1 (RNA-Seq report)	2.68	9.97
NM24_3_1 (RNA-Seq report)	2.60	10.39
NM24_INF_1_1 (RNA-Seq report)	2.45	10.50
NM24_INF_2_1 (RNA-Seq report)	2.37	10.65
NM24_INF_3_1 (RNA-Seq report)	2.38	10.49
NM48_1_1 (RNA-Seq report)	2.10	10.86
NM48_2_1 (RNA-Seq report)	3.00	10.88
NM48_3_1 (RNA-Seq report)	2.98	10.08
NM48_INF_1_1 (RNA-Seq report)	3.15	11.40
NM48_INF_2_1 (RNA-Seq report)	3.13	10.18
NM48_INF_3_1 (RNA-Seq report)	2.89	10.21
Minimum	1.98	9.82
Median	2.53	10.49
Maximum	3.15	14.63
Mean	2.56	10.64
Standard deviation	0.36	0.95

	Outliers
Paired, mapped pairs (%)	AM24_INF_1_1 (RNA-Seq report), NM48_INF_1_1 (RNA-Seq report)
Paired, not mapped (%)	AM24_INF_1_1 (RNA-Seq report)

1.2 Fragment counting statistics

An intact pair is counted as one, broken pairs are ignored.

The table is based on 24 samples.

Sample name	Mapped to genes (%)	Mapped to exons (%)	Mapped to intergenic (%)
AM24_1_1 (RNA-Seq report)	93.26	87.06	6.74
AM24_2_1 (RNA-Seq report)	93.49	87.08	6.51
AM24_3_1 (RNA-Seq report)	93.43	86.69	6.57
AM24_INF_1_1 (RNA-Seq report)	93.69	87.04	6.31
AM24_INF_2_1 (RNA-Seq report)	93.79	86.92	6.21
AM24_INF_3_1 (RNA-Seq report)	93.89	87.21	6.11
AM48_1_1 (RNA-Seq report)	94.00	86.82	6.00
AM48_2_1 (RNA-Seq report)	93.32	87.36	6.68
AM48_3_1 (RNA-Seq report)	94.11	86.90	5.89
AM48_INF_1_1 (RNA-Seq report)	94.05	87.71	5.95
AM48_INF_2_1 (RNA-Seq report)	93.37	87.18	6.63
AM48_INF_3_1 (RNA-Seq report)	93.64	87.18	6.36
NM24_1_1 (RNA-Seq report)	93.52	87.15	6.48
NM24_2_1 (RNA-Seq report)	93.82	86.84	6.18
NM24_3_1 (RNA-Seq report)	93.67	87.06	6.33
NM24_INF_1_1 (RNA-Seq report)	93.69	87.01	6.31
NM24_INF_2_1 (RNA-Seq report)	93.41	86.82	6.59
NM24_INF_3_1 (RNA-Seq report)	93.80	87.06	6.20
NM48_1_1 (RNA-Seq report)	93.29	87.06	6.71
NM48_2_1 (RNA-Seq report)	93.61	86.96	6.39
NM48_3_1 (RNA-Seq report)	93.94	87.03	6.06
NM48_INF_1_1 (RNA-Seq report)	94.16	88.09	5.84
NM48_INF_2_1 (RNA-Seq report)	93.96	87.01	6.04
NM48_INF_3_1 (RNA-Seq report)	94.20	87.67	5.80
Minimum	93.26	86.69	5.80
Median	93.69	87.06	6.31
Maximum	94.20	88.09	6.74
Mean	93.71	87.12	6.29

Sample name	Mapped to genes (%)	Mapped to exons (%)	Mapped to intergenic (%)
Standard deviation	0.29	0.31	0.29

	Outliers
Mapped to exons (%)	AM48_INF_1_1 (RNA-Seq report), NM48_INF_1_1 (RNA-Seq report), NM48_INF_3_1 (RNA-Seq report)

1.3 Spike-in quality control

No data available

1.4 Strand specificity

The table is based on 24 samples.

Sample name	Strand specific setting	Forward reads mapped (%)	Reverse reads mapped (%)	Ignored reads (wrong strand) (%)
AM24_1_1 (RNA-Seq report)	Reverse	0	100	1.08
AM24_2_1 (RNA-Seq report)	Reverse	0	100	1.37
AM24_3_1 (RNA-Seq report)	Reverse	0	100	1.28
AM24_INF_1_1 (RNA-Seq report)	Reverse	0	100	1.03
AM24_INF_2_1 (RNA-Seq report)	Reverse	0	100	1.38
AM24_INF_3_1 (RNA-Seq report)	Reverse	0	100	1.35
AM48_1_1 (RNA-Seq report)	Reverse	0	100	1.11
AM48_2_1 (RNA-Seq report)	Reverse	0	100	1.04
AM48_3_1 (RNA-Seq report)	Reverse	0	100	1.16
AM48_INF_1_1 (RNA-Seq report)	Reverse	0	100	1.18
AM48_INF_2_1 (RNA-Seq report)	Reverse	0	100	0.97
AM48_INF_3_1 (RNA-Seq report)	Reverse	0	100	1.26
NM24_1_1 (RNA-Seq report)	Reverse	0	100	1.45
NM24_2_1 (RNA-Seq report)	Reverse	0	100	1.30

Sample name	Strand specific setting	Forward reads mapped (%)	Reverse reads mapped (%)	Ignored reads (wrong strand) (%)
NM24_3_1 (RNA-Seq report)	Reverse	0	100	1.33
NM24_INF_1_1 (RNA-Seq report)	Reverse	0	100	1.60
NM24_INF_2_1 (RNA-Seq report)	Reverse	0	100	1.43
NM24_INF_3_1 (RNA-Seq report)	Reverse	0	100	1.22
NM48_1_1 (RNA-Seq report)	Reverse	0	100	1.09
NM48_2_1 (RNA-Seq report)	Reverse	0	100	1.34
NM48_3_1 (RNA-Seq report)	Reverse	0	100	1.31
NM48_INF_1_1 (RNA-Seq report)	Reverse	0	100	1.17
NM48_INF_2_1 (RNA-Seq report)	Reverse	0	100	1.24
NM48_INF_3_1 (RNA-Seq report)	Reverse	0	100	1.07
Minimum	-	0.00	100.00	0.97
Median	-	0.00	100.00	1.25
Maximum	-	0.00	100.00	1.60
Mean	-	0.00	100.00	1.24
Standard deviation	-	0.00	0.00	0.16

1.5 Adapter read-through

The table is based on 24 samples.

Sample name	Estimated % containing read-through adapters
AM24_1_1 (RNA-Seq report)	2.52
AM24_2_1 (RNA-Seq report)	2.26
AM24_3_1 (RNA-Seq report)	2.03
AM24_INF_1_1 (RNA-Seq report)	2.31
AM24_INF_2_1 (RNA-Seq report)	1.86
AM24_INF_3_1 (RNA-Seq report)	1.78
AM48_1_1 (RNA-Seq report)	1.90
AM48_2_1 (RNA-Seq report)	2.53
AM48_3_1 (RNA-Seq report)	2.03
AM48_INF_1_1 (RNA-Seq report)	1.97
AM48_INF_2_1 (RNA-Seq report)	2.39

Sample name	Estimated % containing read-through adapters
AM48_INF_3_1 (RNA-Seq report)	2.12
NM24_1_1 (RNA-Seq report)	2.13
NM24_2_1 (RNA-Seq report)	1.90
NM24_3_1 (RNA-Seq report)	2.24
NM24_INF_1_1 (RNA-Seq report)	2.06
NM24_INF_2_1 (RNA-Seq report)	2.26
NM24_INF_3_1 (RNA-Seq report)	2.45
NM48_1_1 (RNA-Seq report)	2.54
NM48_2_1 (RNA-Seq report)	2.22
NM48_3_1 (RNA-Seq report)	2.07
NM48_INF_1_1 (RNA-Seq report)	2.13
NM48_INF_2_1 (RNA-Seq report)	2.01
NM48_INF_3_1 (RNA-Seq report)	2.07
Minimum	1.78
Median	2.12
Maximum	2.54
Mean	2.16
Standard deviation	0.22

1.6 Distribution of biotypes

The table is based on 24 samples.

Sample name	unknown
AM24_1_1 (RNA-Seq report)	100
AM24_2_1 (RNA-Seq report)	100
AM24_3_1 (RNA-Seq report)	100
AM24_INF_1_1 (RNA-Seq report)	100
AM24_INF_2_1 (RNA-Seq report)	100
AM24_INF_3_1 (RNA-Seq report)	100
AM48_1_1 (RNA-Seq report)	100
AM48_2_1 (RNA-Seq report)	100
AM48_3_1 (RNA-Seq report)	100
AM48_INF_1_1 (RNA-Seq report)	100
AM48_INF_2_1 (RNA-Seq report)	100
AM48_INF_3_1 (RNA-Seq report)	100
NM24_1_1 (RNA-Seq report)	100
NM24_2_1 (RNA-Seq report)	100
NM24_3_1 (RNA-Seq report)	100
NM24_INF_1_1 (RNA-Seq report)	100

Sample name	unknown
NM24_INF_2_1 (RNA-Seq report)	100
NM24_INF_3_1 (RNA-Seq report)	100
NM48_1_1 (RNA-Seq report)	100
NM48_2_1 (RNA-Seq report)	100
NM48_3_1 (RNA-Seq report)	100
NM48_INF_1_1 (RNA-Seq report)	100
NM48_INF_2_1 (RNA-Seq report)	100
NM48_INF_3_1 (RNA-Seq report)	100
Minimum	100.00
Median	100.00
Maximum	100.00
Mean	100.00
Standard deviation	0.00

1.7 Transcript length coverage

The table is based on 24 samples.

Sample name	Expected coverage bias	Difference between average 3' and 5' normalized counts	Reads mapping to transcripts that are longer than 10,000 bp (%)
AM24_1_1 (RNA-Seq report)	Unbiased	4.75	0.05
AM24_2_1 (RNA-Seq report)	Unbiased	9.25	0.05
AM24_3_1 (RNA-Seq report)	Unbiased	7.50	0.05
AM24_INF_1_1 (RNA-Seq report)	Unbiased	2.72	0.06
AM24_INF_2_1 (RNA-Seq report)	Unbiased	7.48	0.05
AM24_INF_3_1 (RNA-Seq report)	Unbiased	11.36	0.04
AM48_1_1 (RNA-Seq report)	Unbiased	2.59	0.05
AM48_2_1 (RNA-Seq report)	Unbiased	4.75	0.06
AM48_3_1 (RNA-Seq report)	Unbiased	0.44	0.06
AM48_INF_1_1 (RNA-Seq report)	Unbiased	10.39	0.07
AM48_INF_2_1 (RNA-Seq report)	Unbiased	6.25	0.06
AM48_INF_3_1 (RNA-Seq report)	Unbiased	12.50	0.05
NM24_1_1 (RNA-Seq report)	Unbiased	8.90	0.04
NM24_2_1 (RNA-Seq report)	Unbiased	5.81	0.06
NM24_3_1 (RNA-Seq report)	Unbiased	8.59	0.04

Sample name	Expected coverage bias	Difference between average 3' and 5' normalized counts	Reads mapping to transcripts that are longer than 10,000 bp (%)
NM24_INF_1_1 (RNA-Seq report)	Unbiased	8.53	0.05
NM24_INF_2_1 (RNA-Seq report)	Unbiased	9.73	0.05
NM24_INF_3_1 (RNA-Seq report)	Unbiased	1.05	0.06
NM48_1_1 (RNA-Seq report)	Unbiased	10.71	0.04
NM48_2_1 (RNA-Seq report)	Unbiased	5.79	0.06
NM48_3_1 (RNA-Seq report)	Unbiased	1.84	0.07
NM48_INF_1_1 (RNA-Seq report)	Unbiased	11.28	0.08
NM48_INF_2_1 (RNA-Seq report)	Unbiased	2.69	0.07
NM48_INF_3_1 (RNA-Seq report)	Unbiased	5.16	0.08
Minimum	-	0.44	0.04
Median	-	6.87	0.06
Maximum	-	12.50	0.08
Mean	-	6.67	0.06
Standard deviation	-	3.55	0.01

	Outliers
Reads mapping to transcripts that are longer than 10,000 bp (%)	NM48_INF_1_1 (RNA-Seq report), NM48_INF_3_1 (RNA-Seq report)

History for:

AM24_1_1 (Combined report)

Combine Reports 1.1
30 Jun 2023 10:53:55

Version:	CLC Genomics Workbench 23.0.4
Modified by:	markop
Show summary information as plots	No
Include tables for outliers	Yes
Comments:	

Originates from:

	AM24_1_1 (RNA-Seq report)
	AM24_2_1 (RNA-Seq report)
	AM24_3_1 (RNA-Seq report)
	AM24_INF_1_1 (RNA-Seq report)
	AM24_INF_2_1 (RNA-Seq report)
	AM24_INF_3_1 (RNA-Seq report)
	AM48_1_1 (RNA-Seq report)
	AM48_2_1 (RNA-Seq report)
	AM48_3_1 (RNA-Seq report)
	AM48_INF_1_1 (RNA-Seq report)
	AM48_INF_2_1 (RNA-Seq report)
	AM48_INF_3_1 (RNA-Seq report)
	NM24_1_1 (RNA-Seq report)
	NM24_2_1 (RNA-Seq report)
	NM24_3_1 (RNA-Seq report)
	NM24_INF_1_1 (RNA-Seq report)
	NM24_INF_2_1 (RNA-Seq report)
	NM24_INF_3_1 (RNA-Seq report)
	NM48_1_1 (RNA-Seq report)
	NM48_2_1 (RNA-Seq report)
	NM48_3_1 (RNA-Seq report)
	NM48_INF_1_1 (RNA-Seq report)
	NM48_INF_2_1 (RNA-Seq report)
	NM48_INF_3_1 (RNA-Seq report)