

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

Report generated on 2024-02-23, 19:34 EST based on data in: /athena/cayuga_0019/scratch/mij4011/homework/project/processed_fastqc_results

General Statistics

☐ Copy table ☐ Configure	e columns	Scatter plot	■ Violin plo	Showing ⁸⁰ / ₈	$_{0}$ rows and $^{3}/_{6}$ columns.	
Sample Name	% Dups		% GC		M Seqs	
SRR21190736_1_trimmed	53.6%	ed	44%		31.1 M	
SRR21190736_2_trimmed	51.8%	red	44%		31.1 M	
SRR21190737_1_trimmed	54.9%	ed	44%		32.0 M	
SRR21190737_2_trimmed	52.7%	ed	44%		32.0 M	
SRR21190738_1_trimmed	57.2%	d	43%		31.1 M	
SRR21190738_2_trimmed	56.2%	ed .	43%		31.1 M	
SRR21190739_1_trimmed	58.7%	d	43%		29.8 M	
SRR21190739_2_trimmed	56.9%	d	43%		29.8 M	
SRR21190740_1_trimmed	57.3%	d	43%		33.7 M	
SRR21190740_2_trimmed	56.0%	ed :	43%		33.7 M	
SRR21190741_1_trimmed	56.3%	ed :	45%		37.0 M	
SRR21190741_2_trimmed	54.9%	ed	45%		37.0 M	
SRR21190742_1_trimmed	52.3%	red	44%		28.5 M	
SRR21190742_2_trimmed	50.1%	ved	43%		28.5 M	
SRR21190743_1_trimmed	51.7%	red	43%		29.9 M	
SRR21190743_2_trimmed	49.7%	ved	43%		29.9 M	
SRR21190744_1_trimmed	51.0%	ved .	44%		28.8 M	
SRR21190744_2_trimmed	48.9%	ved	44%		28.8 M	
SRR21190745_1_trimmed	51.9%	red	44%		29.8 M	
SRR21190745_2_trimmed	49.8%	ved	44%		29.8 M	

Sample Name	% Dups		% GC	M Seqs	
SRR21190746_1_trimmed	47.5%	ved	44%	36.7 M	
SRR21190746_2_trimmed	45.5%	oved	44%	36.7 M	
SRR21190747_1_trimmed	43.6%	oved	43%	31.7 M	
SRR21190747_2_trimmed	41.3% n	oved	43%	31.7 M	
SRR21190748_1_trimmed	52.6%	ed 'ed	44%	33.1 M	
SRR21190748_2_trimmed	50.6%	/ed	44%	33.1 M	
SRR21190749_1_trimmed	43.8%	oved	44%	33.3 M	
SRR21190749_2_trimmed	41.3% 1	oved	44%	33.3 M	
SRR21190750_1_trimmed	48.0%	ved	44%	35.0 M	
SRR21190750_2_trimmed	46.0%	oved	44%	35.0 M	
SRR21190751_1_trimmed	43.6%	oved	42%	31.9 M	
SRR21190751_2_trimmed	41.7% 1	oved	42%	31.9 M	
SRR21190752_1_trimmed	38.6% n	oved	43%	27.4 M	
SRR21190752_2_trimmed	35.5% m	oved	42%	27.4 M	
SRR21190753_1_trimmed	41.8% 1	oved	43%	35.5 M	
SRR21190753_2_trimmed	39.4% n	oved	43%	35.5 M	
SRR21190754_1_trimmed	42.4%	oved	42%	35.1 M	
SRR21190754_2_trimmed	40.1% n	oved	42%	35.1 M	
SRR21190755_1_trimmed	46.4%	oved	42%	35.5 M	
SRR21190755_2_trimmed	44.0%	oved	42%	35.5 M	
SRR21190756_1_trimmed	51.5%	/ed	46%	32.1 M	
SRR21190756_2_trimmed	50.8%	/ed	46%	32.1 M	
SRR21190757_1_trimmed	46.8%	oved	45%	21.9 M	
SRR21190757_2_trimmed	44.4%	oved	45%	21.9 M	
SRR21190758_1_trimmed	49.4%	ved	45%	28.9 M	
SRR21190758_2_trimmed	45.5%	oved	46%	28.9 M	
SRR21190759_1_trimmed	48.3%	ved	45%	26.4 M	
SRR21190759_2_trimmed	46.7%	oved	45%	26.4 M	
SRR21190760_1_trimmed	49.8%	ved	45%	30.4 M	
SRR21190760_2_trimmed	48.1%	ved	45%	30.4 M	

Sample Name	% Dups		% GC	M Seqs	
SRR21190761_1_trimmed	52.7%	ed 'ed	42%	26.9 M	
SRR21190761_2_trimmed	51.3%	/ed	42%	26.9 M	
SRR21190762_1_trimmed	46.0%	oved	45%	24.8 M	
SRR21190762_2_trimmed	44.9%	oved	45%	24.8 M	
SRR21190763_1_trimmed	47.7%	ved	45%	25.5 M	
SRR21190763_2_trimmed	45.9%	oved	45%	25.5 M	
SRR21190764_1_trimmed	57.3%	d	46%	33.3 M	
SRR21190764_2_trimmed	56.4%	;d	46%	33.3 M	
SRR21190765_1_trimmed	57.0%	d	45%	33.6 M	
SRR21190765_2_trimmed	57.0%	d	45%	33.6 M	
SRR21190766_1_trimmed	54.2%	ed	46%	35.8 M	
SRR21190766_2_trimmed	52.3%	red	46%	35.8 M	
SRR21190767_1_trimmed	52.2%	red	46%	32.8 M	
SRR21190767_2_trimmed	51.1%	/ed	46%	32.8 M	
SRR21190768_1_trimmed	54.1%	ed	46%	33.6 M	
SRR21190768_2_trimmed	52.9%	ed	46%	33.6 M	
SRR21190769_1_trimmed	53.2%	ed	46%	33.0 M	
SRR21190769_2_trimmed	52.0%	red red	46%	33.0 M	
SRR21190770_1_trimmed	56.3%	•d	46%	27.1 M	
SRR21190770_2_trimmed	53.4%	ed	46%	27.1 M	
SRR21190771_1_trimmed	51.8%	red red	45%	29.2 M	
SRR21190771_2_trimmed	50.8%	/ed	45%	29.2 M	
SRR21190772_1_trimmed	50.1%	ved	45%	28.7 M	
SRR21190772_2_trimmed	48.7%	ved	45%	28.7 M	
SRR21190773_1_trimmed	49.1%	ved	45%	26.0 M	
SRR21190773_2_trimmed	47.3%	ved	45%	26.0 M	
SRR21190774_1_trimmed	51.5%	/ed	45%	31.8 M	
SRR21190774_2_trimmed	49.9%	ved	45%	31.8 M	
SRR21190775_1_trimmed	51.2%	/ed	45%	33.2 M	
SRR21190775_2_trimmed	49.1%	ved	45%	33.2 M	

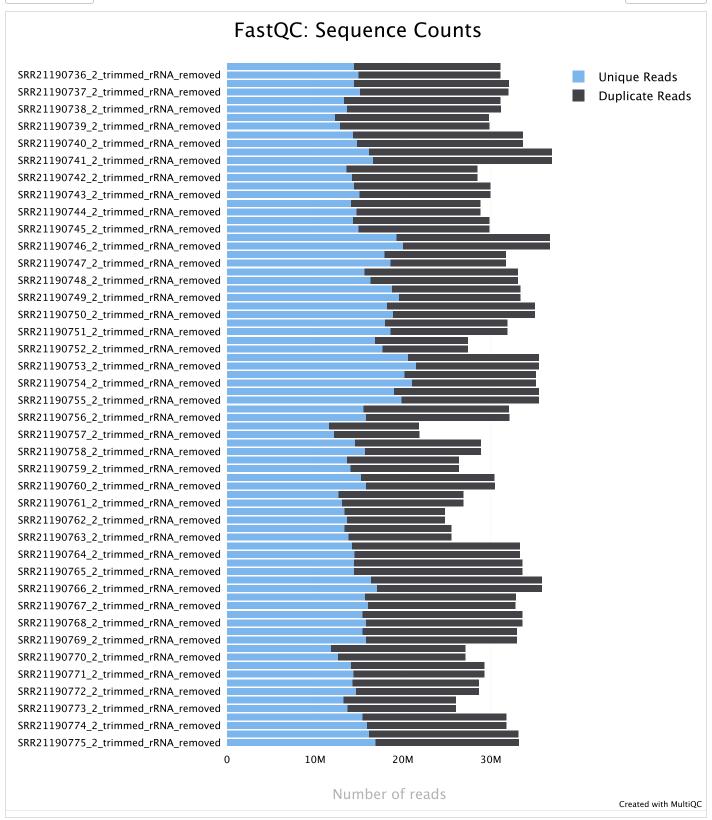
FastQC Version: 0.12.1

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

Sequence counts for each sample. Duplicate read counts are an estimate only.

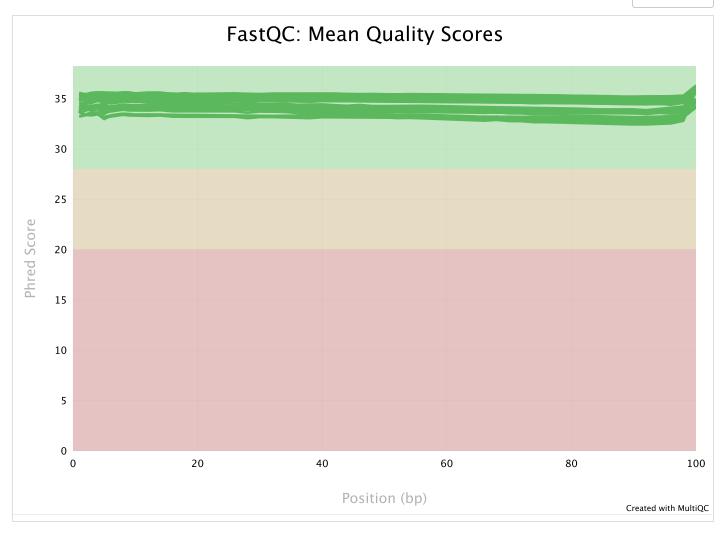
Percentages Export Plot



Sequence Quality Histograms

80

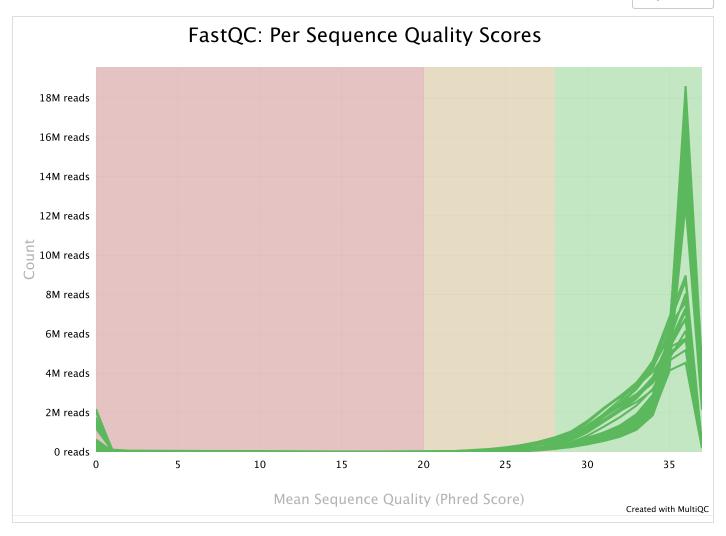
The mean quality value across each base position in the read.



Per Sequence Quality Scores



The number of reads with average quality scores. Shows if a subset of reads has poor quality.

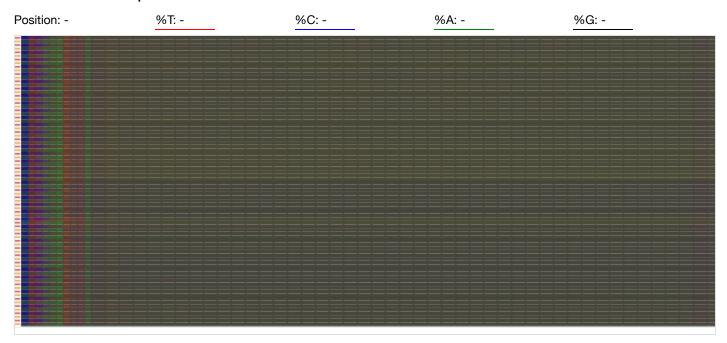


Per Base Sequence Content

The proportion of each base position for which each of the four normal DNA bases has been called.

Click a sample row to see a line plot for that dataset.

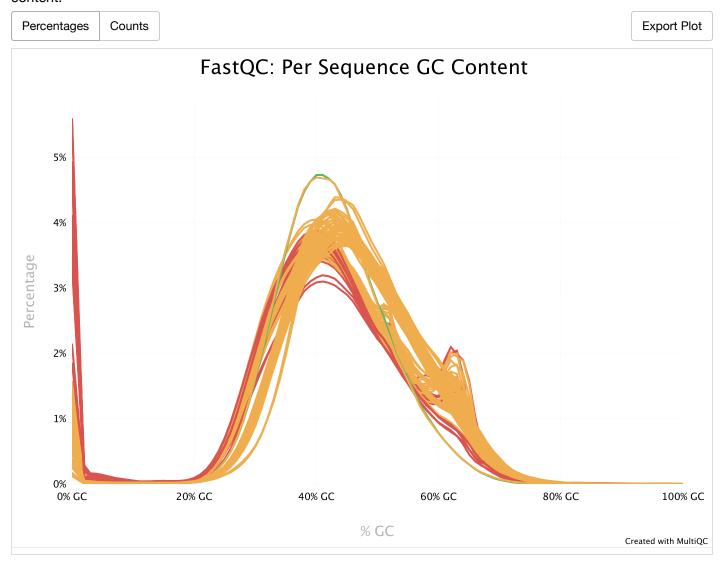
• Rollover for sample name



Per Sequence GC Content



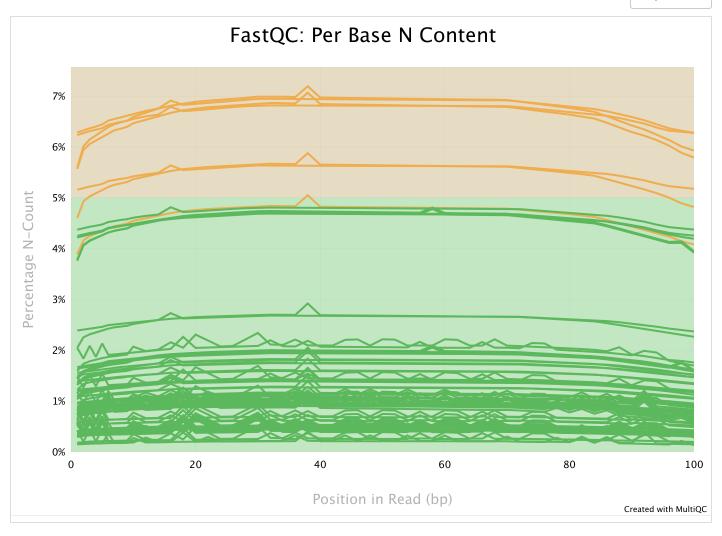
The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.



Per Base N Content



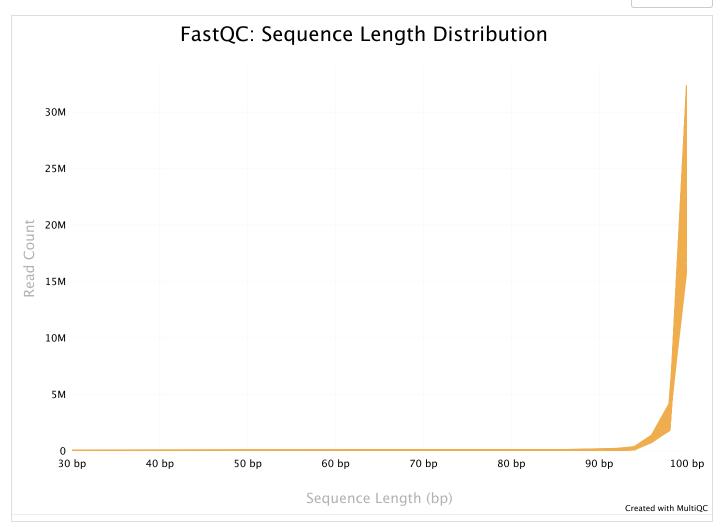
The percentage of base calls at each position for which an N was called.



Sequence Length Distribution

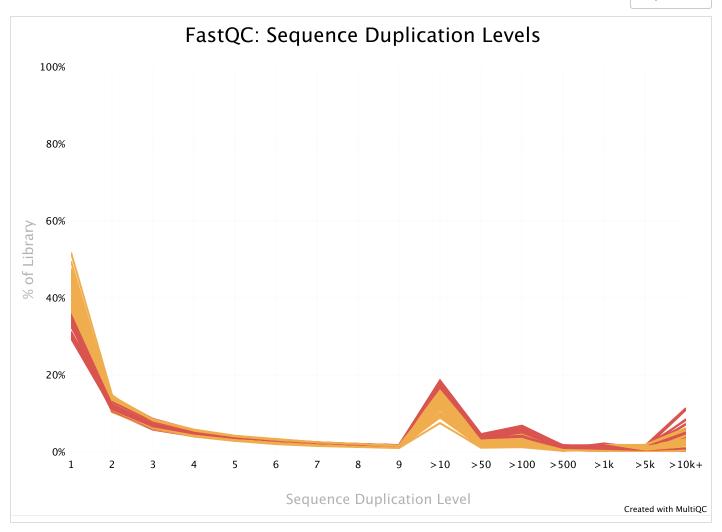


The distribution of fragment sizes (read lengths) found. See the FastQC help



Sequence Duplication Levels

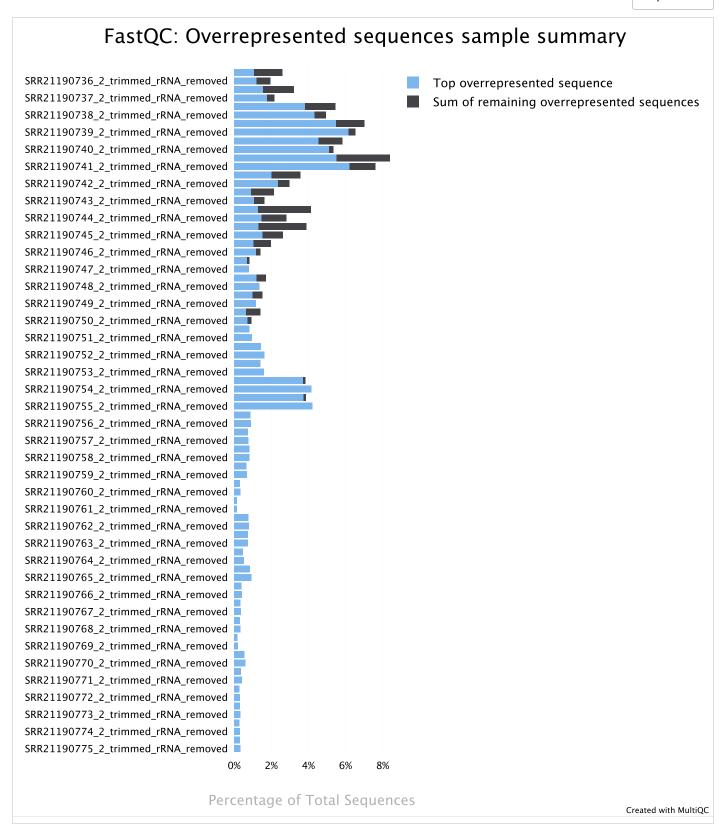
The relative level of duplication found for every sequence.



Overrepresented sequences by sample

The total amount of overrepresented sequences found in each library.

verrepresented sequences by sample



Top overrepresented sequences

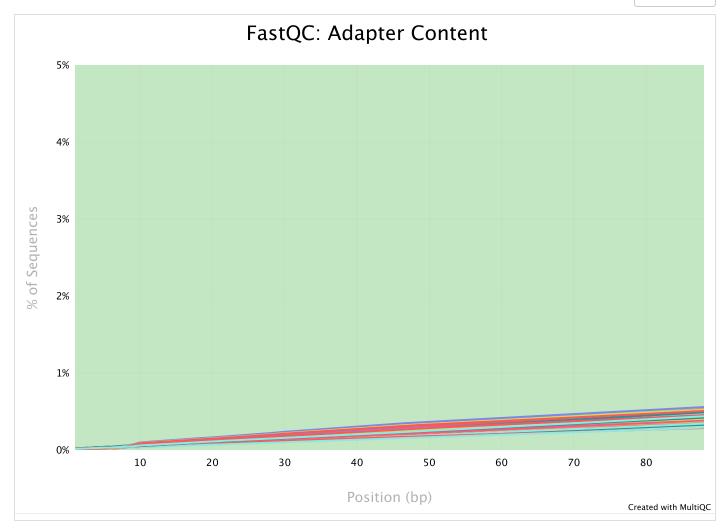
Top overrepresented sequences across all samples. The table shows 20 most overrepresented sequences across all samples, ranked by the number of samples they occur in.

S Copy table Sit Configure columns Sit Scatter plot Ex Violin plot Showing 20/20 rows and 3/3 columns. Overrepresented sequence Samples Occurrences % of all reads NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN		,	,		.,		
SEQUENCE NNNNNNNNNNNNNNNNNNNN 80 36 208 925 1.4578% GTCTGGAGTCTTGGAAG(15 ACTACCCTACGTTCT %TAGAAATGGACC 0.0401% CTCCGTTTCCGACCTGG(14 GGTTCACCCCTCCTT, GGCAACCTGGTGGT 0.0424% CCCCTCCTTAGGCAACCT 14 TAGCCCCCCGCTCCC &GGAGGTCACCCATAT 0.0360% CTGGAGTCTTGGAAGCT1 14 TACCCTACGTTCTCC TAGAAATGGACCT 0.0360% CCCTCCTTAGGCAACCT 12 GGTCCCCCGCTCCC &GGAGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTG(11 CCGCACCTCCCT TAGAAATGGACCTT 0.0256% CCTCCTTAGGCAACCTG(11 CCGCACCTCCCT TAGACAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTG(10 GTCCCCCGCTCCCG GGAGGTCACCATATT 0.0176% CCGTGGCGCGTGCCTGT 10 CCCCAGCTACTCGGGAGGGTCACCATATT 0.0176% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGGTGAGC 0.0181% CATCTGTCACCCCATTGA 9 CCCAGCTACTCGGGAGGGTGAGCA 0.0165% GTTCTGGGCTGTAGTGCC 9 TATGCCGATCGGGTGTCCGCCACCTACTTCGG AGCTCACTCGGAGGGTTGATT 0.0106% CTCAGGCTGGCTGCAC 7 TCTGTCACCCCATTGATCGCCACCTACTTCGG AGCTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	Copy table	III Configure	e columns	■ Scatter plot	■ Violin plot	Showing ²⁰ / ₂₀	rows and $^3/_3$ columns.
GTCTGGAGTCTTGGAAG(15 ACTACCCTACGTTCT SCTAGAAATGGACC 0.0401% CTCCGTTTCCGACCTGG(14 GGTTCACCCCTCCTT, IGGCAACCTGGTGGT 0.0424% CCCCTCCTTAGGCAACCT 14 FGGTCCCCCGCTCCC GGGAGGTCACCATAT 0.0360% CTGGAGTCTTGGAAGCTI 14 TACCCTACGTTCTCC FACAGATGGACCTT 0.0302% CCTCCTTAGGCAACCT (12 GGTCCCCCGCTCCC GGGAGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTG(11)CGGTTCACCCCTCCT FAGGCAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTG(10)GTCCCCCGCTCCCG GGAGGTCACCATATT 0.0176% CCGTGGCGCGTGCCTGT 10 CCCCAGCTACTCGGGAGGCTGAGGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGCGTTCATCGGGAGGCTGAGG 0.0181% GGTGGCGCGTGCCTGTA 9 CCCAGCTACTCGGGAGGCTGAGGA 0.0165% GTTCTGGGCTGTAGTGC(9 FATGCCGATCGGGAGGCTGAGGA 0.0165% GTTCTGGGCTGTAGTGC(9 FATGCCGATCGGGTGTCCGGCAGCTTGATTCGG 0.0149% GGGCGATCTGGCTGCAA 7 TCTGTCACCCCATTGATCGGCAGGTTGATT 0.0106% CCTTAGGCAACCTGGTG(6 CCCCCGCTCCCGGGAGGTCACCATATTGATG 0.0107% CCTTAGGCAACCTGGTG(6 CCCCCGCTCCCGGGAGGTCACCATATTGATG 0.0107% CTCAGGCTGGAGTGCAG GGCTATTCACAGGCGCGATCGCCACTACTGATC 0.0088% GTGGCTATTCACAGGCGG SATCCCCACTACTGATCAGCCCGGAGGTTTTGA 0.00075% CCGGTGGCGCGTGCCTGT. GTCCCAGCTACTCGGGAGGCTGAGGAGGTTTGA 0.00075% CCGGTGGCGCGTGCCTGT. GTCCCAGCTACTCGGGAGGCTGAGGGAGGTTTGA 0.00075% CCCAGCTACTCGGGAGG TGCCCAGCTACTCGGGAGGGTTGAGGTGCAGGGTGCAGGGAGGTCCCCAGGAGGTTTGA 0.00075% CCCAGCTACTCGGGAGGGTGCCCTGT. GTCCCAGCTACTCGGGAGGCCTTGAGGTGGGAGG 0.00085% CCCAGCTACTCGGGAGG TGCAGGAGGTTCCAGGAGGTT 0.00075%	-	ted	Samples		Occurrences	3	% of all reads
CTCCGTTTCCGACCTGG(14 GGTTCACCCCTCCTT, GGEARACCTGGTGGT 0.0424% CCCCTCCTTAGGCAACCT 14 FGGTCCCCCGGTCCC GGGAGGTCACCATAT 0.0360% CTGGAGTCTTGGAAGCTI 14 TACCCTACGTTCTCC FAEARATGGACCTT 0.0302% CCCTCCTTAGGCAACCT 12 GGTCCCCCGCTCCCG GGAGGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTG 11 CCGGTTCACCCCTCCT FAEARATGGACCTT 0.0256% CCTCCTTAGGCAACCTG 10 GTCCCCCGCTCCCG GGAGGGTCACCATATT 0.0246% CCTCCTTAGGCAACCTG 10 GTCCCCCGCTCCCG GGAGGGTCACCATATTG 0.0176% CGGTGGCGCGTGCCTGT 10 FCCCAGCTACTCGGGAGGGTCAGCAGGGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGGGTGAAGCTGGAGG 0.0165% GTTCTGGGCTGTAGTGC 9 FATGCCGATCTCGGGAGGGTTGATT 0.0166% GTTCTGGGCTGTAGTGC 9 FATGCCGATCGGGTGTCCGGCACTACTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 TCTGTCACCCCATTGATCGCCACCATATTGATG 0.0106% CCTTAGGCAACCTGGTG 6 CCCCCCGCTCCCGGGAGGGTCACCATATTGATG 0.0107% CTCAGGCTGGAGTGCAG GGCTATTCACAGGCGCGATCGGCACTACTTGATC 0.0088% CTCAGGCTGGAGTGCAG GGCTATTCACAGGCGCGATCGGAGGAGTTTTGA 0.0075% CGGTGGCCGTGCCTGT GTCCCACCATACTCGGGAGGGTTGATT 0.0075% CGGTGGCCGCTGCCTG SATCCCACTACTCGGGAGGGTTGAGGAGG 0.0085% CCCAGCTACTCGGGAGG STGAGGCTGGAGGATCCCATATTGAGG 0.0085% CCCAGCTACTCGGGAGG STGAGGCTGGAGGATCCCATACTCAGGAGGT 0.0085%	NNNNNNNN	INNNNNNI	80		36 208 925		1.4578%
CCCCTCCTTAGGCAACC: 14 TGGTCCCCGGCTCCC@GGAGGTCACCATAT 0.0360% CTGGAGTCTTGGAAGCTI 14 TACCCTACGTTCTCCTACAGATGGACCTT 0.0302% CCCTCCTTAGGCAACCTC 12 GGTCCCCCGCTCCCGGGAGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTGC 11 CCGGTTCACCCCTCCTTAGGCGAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTGC 10 GTCCCCCGCTCCCGGGAGGTCACCATATTG 0.0176% CGGTGGCGCGTGCCTGT. 10 TCCCAGCTACTCGGGAGGTCACCATATTG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGGTGAGGA 0.0185% GTTCTGGGCTGTAGTGCC 9 TATGCCGATCGGGAGGGTGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 TATGCCGATCGGGTGTCCGGGAGGGTTGATTCGG 0.0149% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	GTCTGGAGT	CTTGGAAG	15 ACT	ACCCTACGTTCT	PETACAAAT	GGACC	0.0401%
CTGGAGTCTTGGAAGCTI 14 >TACCCTACGTTCTCC FACAGATGGACCTT 0.0302% CCCTCCTTAGGCAACCTC 12 GGTCCCCCGCTCCCC GGAGGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTG(11 >CGGTTCACCCCTCCT FAGGGAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTG(10 >GTCCCCCGGTCCCGG GAGGGTCACCATATTG 0.0176% CGGTGGCGCGTGCCTGT. 10 TCCCAGCTACTCGGGAGGCTGAGGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGCFGAGTCTGGCGC 0.0137% GGTGGCGCGTGCCTGTA: 9 CCCAGCTACTCGGGAGGTGAGGAGGCTGGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 IATGCCGATCGGGTGCCCAGCTTAAGTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 TCTGTCACCCCATTGATCGCCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNN 6 INNNNNNNNNNNNNNNNNNNN	стссатттс	CGACCTGG	14 GGTT	ГСАССССТССТТ	GGCAACCT	GGTGGT	0.0424%
CCCTCCTTAGGCAACCT(12 GGTCCCCGGTCCCGGGAGGTCACCATATT 0.0256% GCTCCGTTTCCGACCTG(11)CGGTTCACCCCTCCTTAGGCGAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTG(10)GTCCCCCGCTCCCGGGAGGTCACCATATTG 0.0176% CGGTGGCGCGTGCCTGT, 10 TCCCAGCTACTCGGGAGGCTGGAGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGGTGAGCTGGAGG 0.0137% GGTGGCGCGTGCCTGTA 9 CCCAGCTACTCGGGAGGTGAGCTGGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 FATGCCGATCGGGTGTCGGGAGGATTGATT 0.0149% GGGCGATCTGGCTGCGA 7 \TCTGTCACCCCATTGATCGGCGAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	ССССТССТТА	AGGCAACC	14 FGGT	сссссстсс	C GGGAGGTC	ACCATAT	0.0360%
GCTCCGTTTCCGACCTG(11):CGGTTCACCCCTCCT MAGGGAACCTGGTGG 0.0246% CCTCCTTAGGCAACCTG(10):GTCCCCGCTCCCGC MAGGTCACCATATTG 0.0176% CGGTGGCGCGTGCCTGT. 10 FCCCAGCTACTCGGGAGGCTGGAGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGCTGATCTGGCAGGC 0.0137% GGTGGCGCGTGCCTGTA 9 CCCAGCTACTCGGGAGGTTGATCGGCTGGAGGA 0.0165% GTTCTGGGCTGTAGTGC(9 FATGCCGATCGGGAGGTTGATCGGCTGGAGGA 0.0165% GGGCGATCTGGCTGCGA 7 TCTGTCACCCCATTGATCGCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	CTGGAGTCT	TGGAAGCT	14 CTAC	CCTACGTTCTC	TACAAATGG	ACCTT	0.0302%
CCTCCTTAGGCAACCTG(10 AGTCCCCCGCTCCCGC CAGGGTCACCATATTG	CCCTCCTTAC	GCAACCT	12 GGTC	CCCCGCTCCC	GGAGGTCAG	CCATATT	0.0256%
CGGTGGCGCGTGCCTGT. 10 TCCCAGCTACTCGGGAGGCTGGAGG 0.0181% CATCTGTCACCCCATTGA 9 GCCAGGGTTGATTCGGGTGATCTGGCTGGC 0.0137% GGTGGCGCGTGCCTGTA 9 CCCAGCTACTCGGGAGGGTGAGGCTGGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 TATGCCGATCGGGTGTCGGCACTAGTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 TCTGTCACCCCATTGATCGCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	GCTCCGTTTC	CCGACCTG	11 CGG	TTCACCCCTCCT	TAGGOAACC	тддтдд	0.0246%
CATCTGTCACCCATTGA 9 GCCAGGGTTGATTCGGGTGATCGGCTGGC 0.0137% GGTGGCGCGTGCCTGTA 9 CCCAGCTACTCGGGAGGGTGAGGAGGAGGCTGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 IATGCCGATCGGGTGTCGGCACTAAGTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 ITCTGTCACCCCATTGATCGCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	CCTCCTTAG	GCAACCTG	10;GTCC	CCCGCTCCCG	GATGGT CAC	CATATTG	0.0176%
GGTGGCGCTGCCTGTA 9 CCCAGCTACTCGGGAGGGTGAGGAGGCTGAGGA 0.0165% GTTCTGGGCTGTAGTGCC 9 FATGCCGATCGGGTGTCGGCGACTAAGTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 TCTCTGTCACCCCATTGATCGGCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNN 6INNNNNNNNNNNNNNNNNNNNNNN	ССССССССССССССССССССССССССССССССССССССС	стасстат	10 TCCC/	AGCTACTCGGGA	4GGCTGAGG	CTGGAGG	0.0181%
GTTCTGGGCTGTAGTGCC 9 FATGCCGATCGGGTGTC GGCAETAAGTTCGG 0.0149% GGGCGATCTGGCTGCGA 7 TCTGTCACCCCATTGAT GGCCAGGGTTGATT 0.0106% CNNNNNNNNNNNNNNN 6INNNNNNNNNNNNNNNNNNNNN	CATCTGTCAC	CCCATTGA	9 GCCA	GGGTTGATTCG	GCTGATCTGG	СТССС	0.0137%
GGGCGATCTGGCTGCGA 7 ITCTGTCACCCCATTGAT CCCCAGGGGTTGATT 0.0106% CNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	GGTGGCGCG	TGCCTGTA	9 CCCAC	GCTACTCGGGAC	G G G G T G A G G C T	FGGAGGA	0.0165%
CONNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	GTTCTGGGC	TGTAGTGC	9 FATGC	CGATCGGGTGTC	COOCACTAAC	STTCGG	0.0149%
CCTTAGGCAACCTGGTG(6'CCCCCGCTCCCGGGAGGTCATCCATATTGATG 0.0107% CTCAGGCTGGAGTGCAG 5GGCTATTCACAGGCGCGATCCATACTGATC 0.0088% GTGGCTATTCACAGGCGC 5ATCCCACTACTGATCAGCACGGGAGTTTTGA 0.0075% CGGTGGCGCGTGCCTGT 5GTCCCAGCTACTCGGGAGGCTTGAGGTGGGAGG 0.0085% CCCAGCTACTCGGGAGG 5TGAGGCTGGAGGATCGCTTGAGGTCCAGGAGTT 0.0071%	GGGCGATCT	GGCTGCGA	7 ITCTGT	CACCCCATTGA	T CCCC AGGG	TTGATT	0.0106%
CTCAGGCTGGAGTGCAG 5GGCTATTCACAGGCGCGATCCCACTACTGATC 0.0088% GTGGCTATTCACAGGCGC SATCCCACTACTGATCAGCACGGGAGTTTTGA 0.0075% CGGTGGCGCGTGCCTGT 5GTCCCAGCTACTCGGGAGGCCTGAGGTGGGAGG 0.0085% CCCAGCTACTCGGGAGG 5TGAGGCTGGAGGATCGCTTGAGGTCCAGGAGTT 0.0071%	CNNNNNNN	INNNNNNI	6 INNNNN	NNNNNNNNN		INNNNNNN	0.0102%
GTGGCTATTCACAGGCG(SATCCCACTACTGATCAGCACGGGAGTTTTGA 0.0075% CGGTGGCGCGTGCCTGT, SGTCCCAGCTACTCGGGAGGCTTGAGGTGGGAGG 0.0085% CCCAGCTACTCGGGAGG 5TGAGGCTGGAGGATCGCTTGGAGTCCAGGAGTT 0.0071%	CCTTAGGCA	ACCTGGTG	6.CCCC	CGCTCCCGGGA	GEFCACCATA	TTGATG	0.0107%
CGGTGGCGCGTGCCTGT. 5GTCCCAGCTACTCGGGAGGCTGAGGTGGAGGG 0.0085% CCCAGCTACTCGGGAGG 5TGAGGCTGGAGGATCGCTTGAGGTCCAGGAGTT 0.0071%	CTCAGGCTG	GAGTGCAG	5GGCTAT	TCACAGGCGCG	ATIC CECACTA	CTGATC	0.0088%
CCCAGCTACTCGGGAGG 5TGAGGCTGGAGGATCGCTTGGAGTCCAGGAGTT 0.0071%	GTGGCTATTC	ACAGGCG	SATCCC	ACTACTGATCAC	CACGGGAG	TTTTGA	0.0075%
	ССССССССССССССССССССССССССССССССССССССС	стасстат	5GTCCC/	AGCTACTCGGGA	AGGOTGAGGT	ГGGGAGG	0.0085%
GCTCAGGCTGGAGTGCA 4TGGCTATTCACAGGCGCGATGGCCACTACTGAT 0.0073%	CCCAGCTAC	TCGGGAGG	5TGAGG	CTGGAGGATCG	CTTGAGTCCA	AGGAGTT	0.0071%
	GCTCAGGCT	GGAGTGCA	4TGGCTA	ATTCACAGGCGC	GATEECACT	ACTGAT	0.0073%

Adapter Content



The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.



Status Checks

Status for each FastQC section showing whether results seem entirely normal (green), slightly abnormal (orange) or very unusual (red).

Export Plot Min: 0 Max: 1 FastQC: Status Checks SRR21190736 1 trimmed rRNA removed SRR21190737_1_trimmed_rRNA_removed SRR21190738_1_trimmed_rRNA_removed SRR21190739_1_trimmed_rRNA_removed SRR21190740_1_trimmed_rRNA_removed SRR21190741_1_trimmed_rRNA_removed SRR21190742_1_trimmed_rRNA_removed SRR21190743_1_trimmed_rRNA_removed SRR21190744_1_trimmed_rRNA_removed SRR21190745_1_trimmed_rRNA_removed SRR21190746_1_trimmed_rRNA_removed SRR21190747_1_trimmed_rRNA_removed SRR21190748_1_trimmed_rRNA_removed SRR21190749_1_trimmed_rRNA_removed SRR21190750_1_trimmed_rRNA_removed $SRR21190751_1_trimmed_rRNA_removed$ SRR21190752_1_trimmed_rRNA_removed SRR21190753_1_trimmed_rRNA_removed $SRR21190754_1_trimmed_rRNA_removed$ SRR21190755_1_trimmed_rRNA_removed SRR21190756_1_trimmed_rRNA_removed SRR21190757_1_trimmed_rRNA_removed SRR21190758_1_trimmed_rRNA_removed SRR21190759 1 trimmed rRNA removed SRR21190760_1_trimmed_rRNA_removed SRR21190761_1_trimmed_rRNA_removed SRR21190762_1_trimmed_rRNA_removed SRR21190763_1_trimmed_rRNA_removed $SRR21190764_1_trimmed_rRNA_removed$ SRR21190765_1_trimmed_rRNA_removed SRR21190766_1_trimmed_rRNA_removed ${\sf SRR21190767_1_trimmed_rRNA_removed}$ SRR21190768_1_trimmed_rRNA_removed SRR21190769_1_trimmed_rRNA_removed SRR21190770_1_trimmed_rRNA_removed SRR21190771_1_trimmed_rRNA_removed SRR21190772_1_trimmed_rRNA_removed SRR21190773 1 trimmed rRNA removed SRR21190774_1_trimmed_rRNA_removed SRR21190775_1_trimmed_rRNA_removed Per Base Per Per Per Base NS equence Seque No særre presen Meddapter StatisticsSequenceSequenceSequence Content Length DuplicationequencesContent Ouality ContentGC Content Distribution Levels Quality

Scores

Created with MultiOC

Software Versions

Software Versions lists versions of software tools extracted from file contents.

Copy table

Software	Version
FastQC	0.12.1

MultiQC v1.20 - Written by Phil Ewels, available on GitHub.

This report uses <u>HighCharts</u>, <u>jQuery</u>, <u>jQuery UI</u>, <u>Bootstrap</u>, <u>FileSaver.js</u> and <u>clipboard.js</u>.

