

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 09:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163095.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1163095 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163095.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 09:48:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163095.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	86,425,608
Mapped reads	84,997,510 / 98.35%
Unmapped reads	1,428,098 / 1.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	401,340 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	54,105,839 / 62.6%
Duplication rate	51.63%
Clipped reads	32,284,194 / 37.35%

2.2. ACGT Content

Number/percentage of A's	1,846,269,776 / 24.14%
Number/percentage of C's	1,982,069,000 / 25.91%
Number/percentage of T's	1,796,487,273 / 23.49%
Number/percentage of G's	2,023,526,297 / 26.46%
Number/percentage of N's	289,556 / 0%
GC Percentage	52.37%

2.3. Coverage

Mean	2.471

Standard Deviation	38.5218
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2.4. Mapping Quality

Mean Mapping Quality	48.66
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2.5. Mismatches and indels

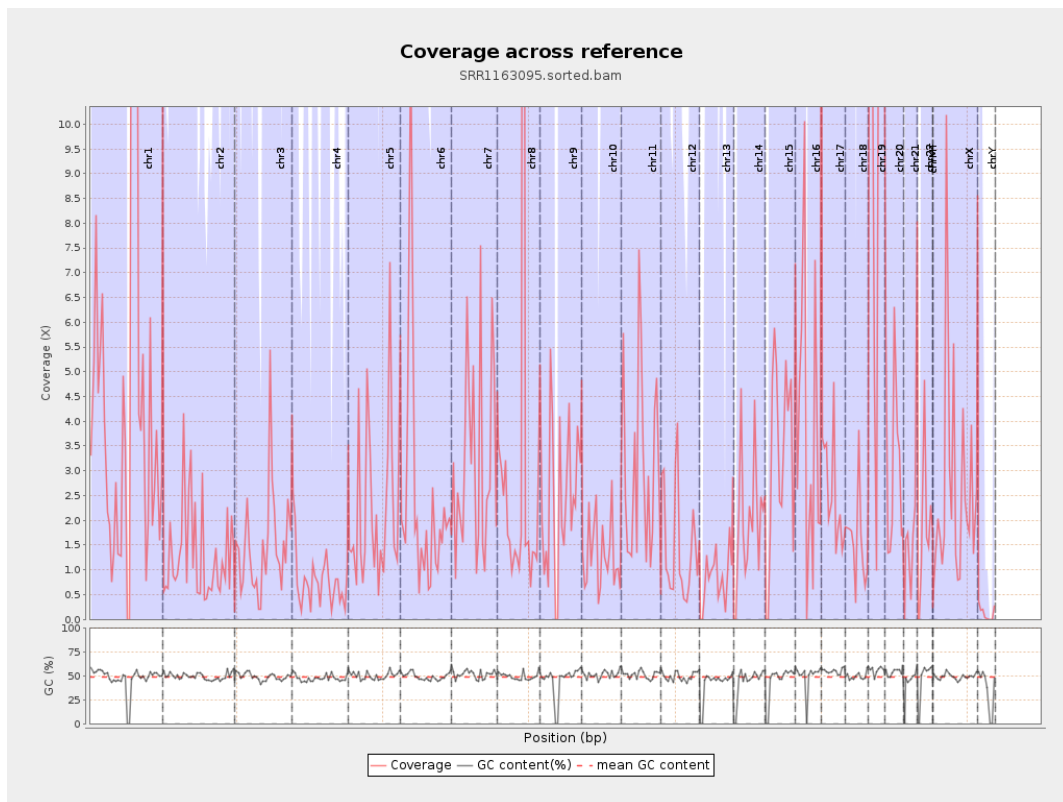
General error rate	0.38%
Mismatches	28,605,576
Insertions	478,977
Mapped reads with at least one insertion	0.56%
Deletions	384,444
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.83%

2.6. Chromosome stats

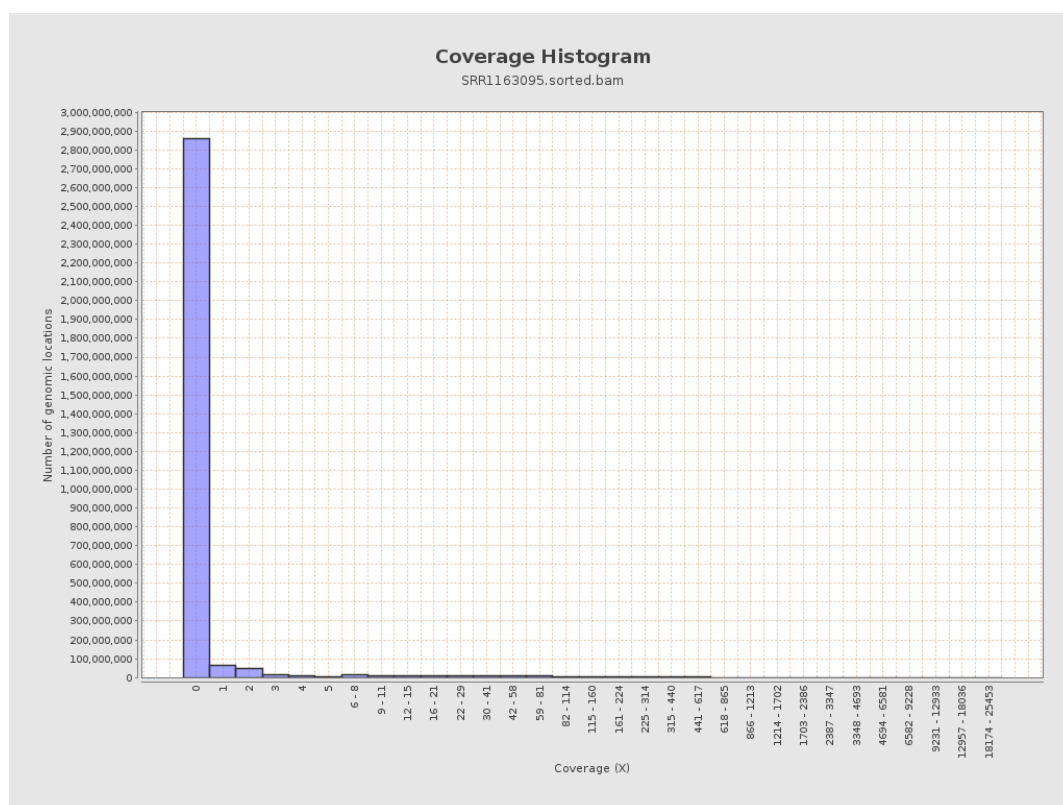
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1156183104	4.6386	50.9629
chr2	243199373	317968593	1.3074	18.4146
chr3	198022430	294698556	1.4882	19.1294
chr4	191154276	149404096	0.7816	13.8492
chr5	180915260	417479287	2.3076	38.7306
chr6	171115067	401760392	2.3479	29.5876
chr7	159138663	505190042	3.1745	43.5059

chr8	146364022	483355917	3.3024	89.0049
chr9	141213431	337366461	2.3891	28.23
chr10	135534747	177595783	1.3103	24.909
chr11	135006516	412707084	3.0569	32.224
chr12	133851895	200384822	1.4971	18.5665
chr13	115169878	100160943	0.8697	13.8277
chr14	107349540	215258268	2.0052	24.3195
chr15	102531392	329870634	3.2173	32.5246
chr16	90354753	347119091	3.8417	37.855
chr17	81195210	210760413	2.5957	27.5344
chr18	78077248	123623609	1.5833	21.05
chr19	59128983	666794296	11.2769	105.381
chr20	63025520	191255069	3.0346	33.1335
chr21	48129895	99488900	2.0671	40.8998
chr22	51304566	91516492	1.7838	21.8907
chrMT	16571	3647	0.2201	0.6703
chrX	155270560	412232365	2.6549	38.312
chrY	59373566	7312353	0.1232	7.3448

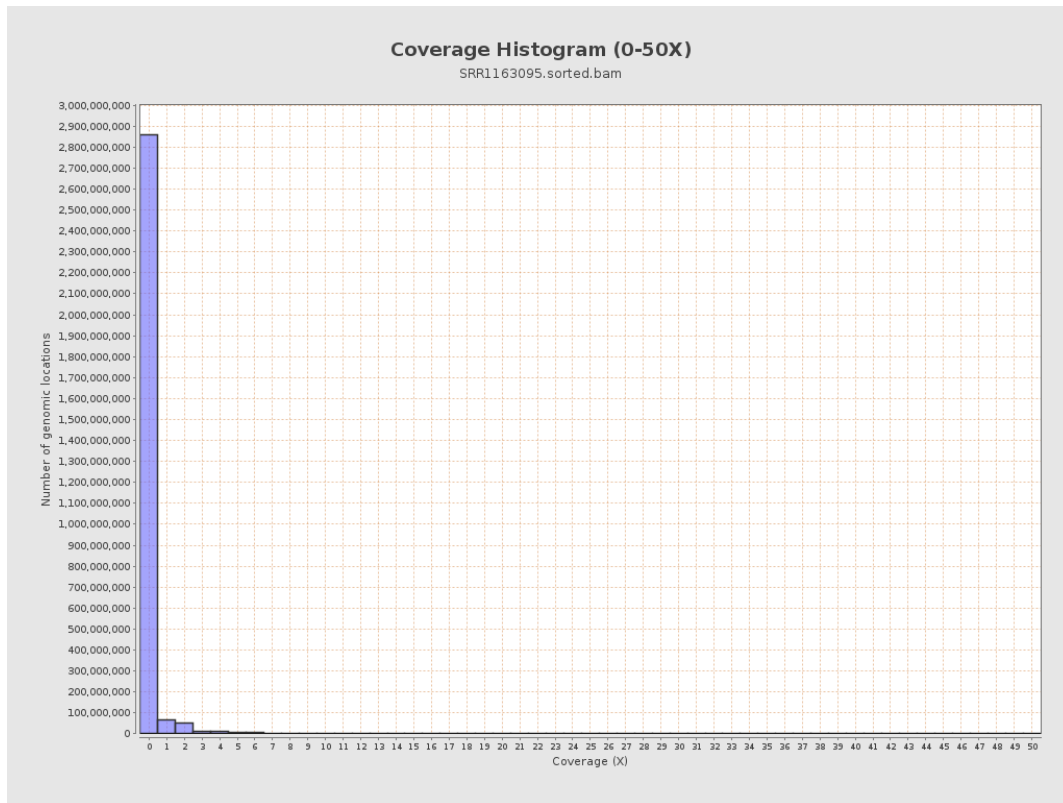
3. Results : Coverage across reference



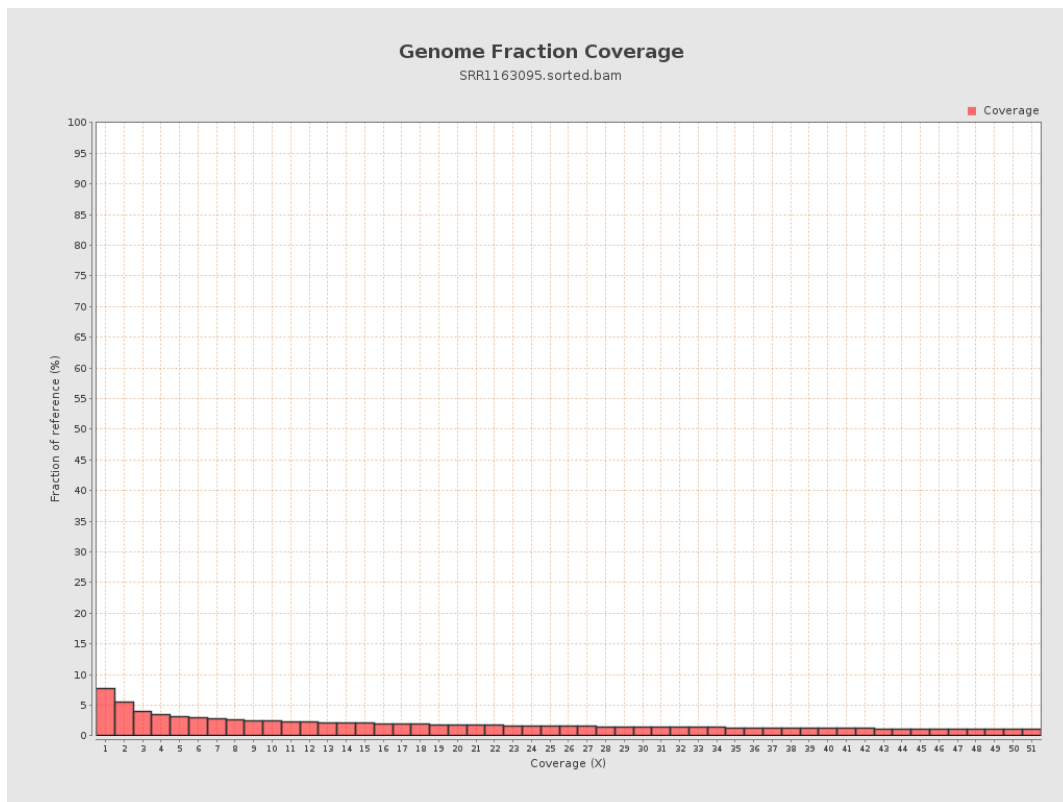
4. Results : Coverage Histogram



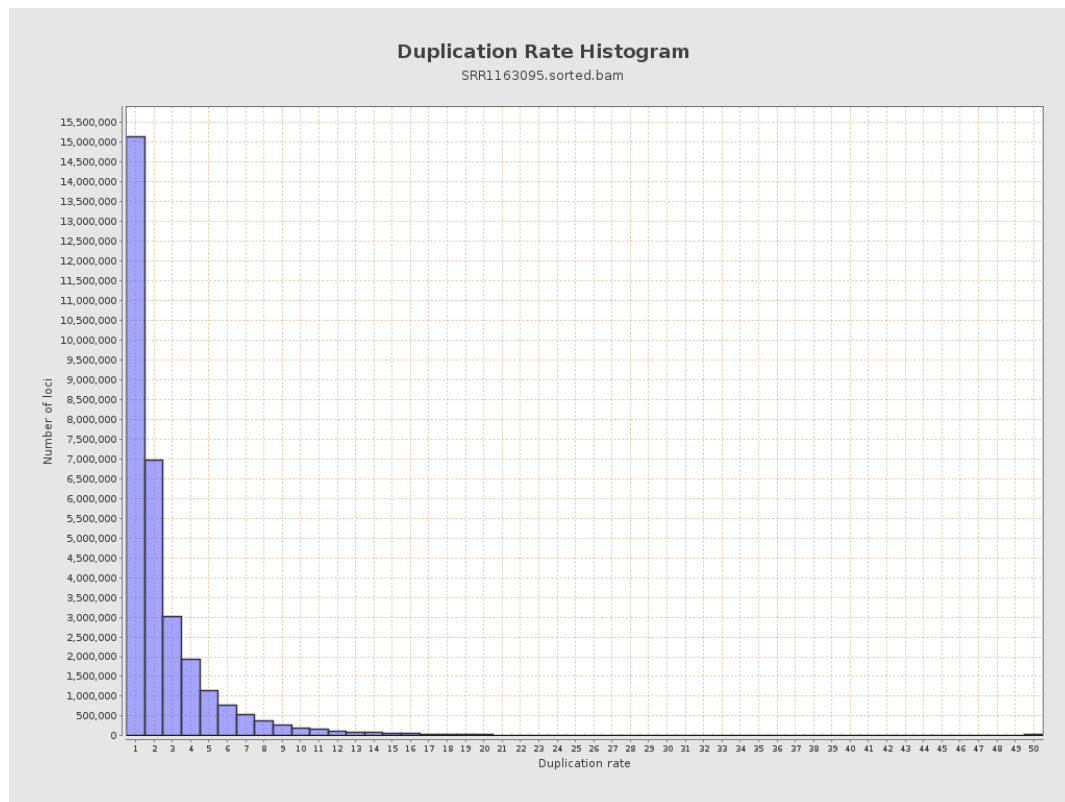
5. Results : Coverage Histogram (0-50X)



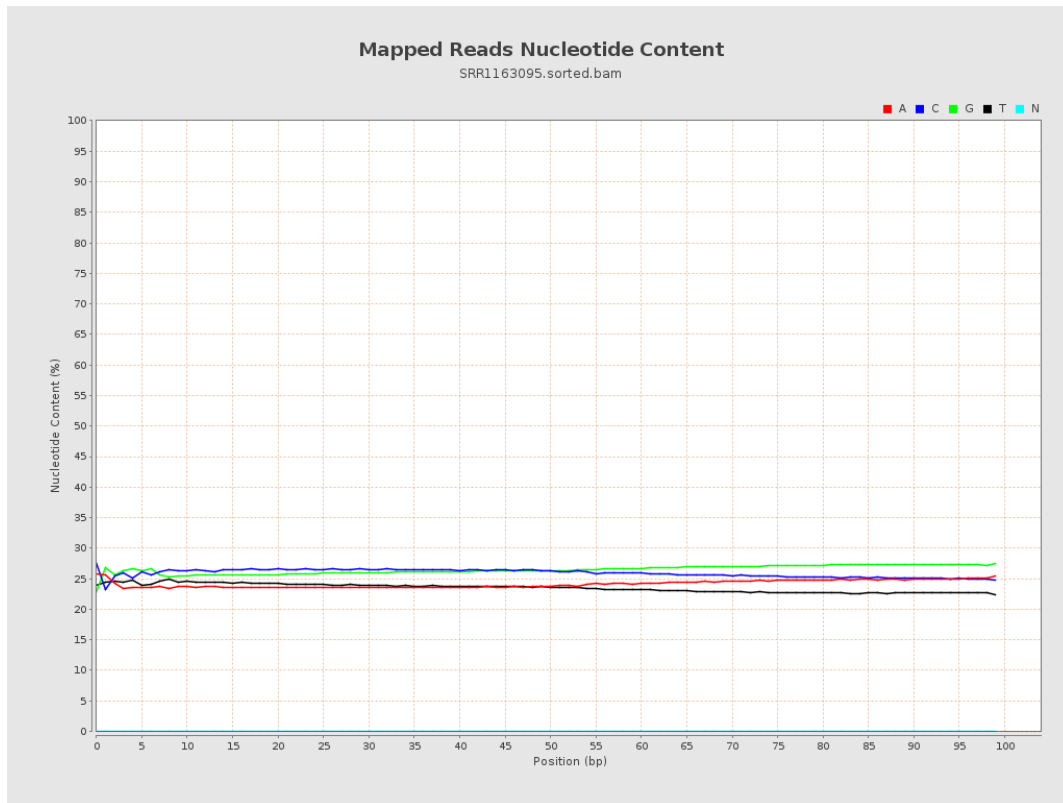
6. Results : Genome Fraction Coverage



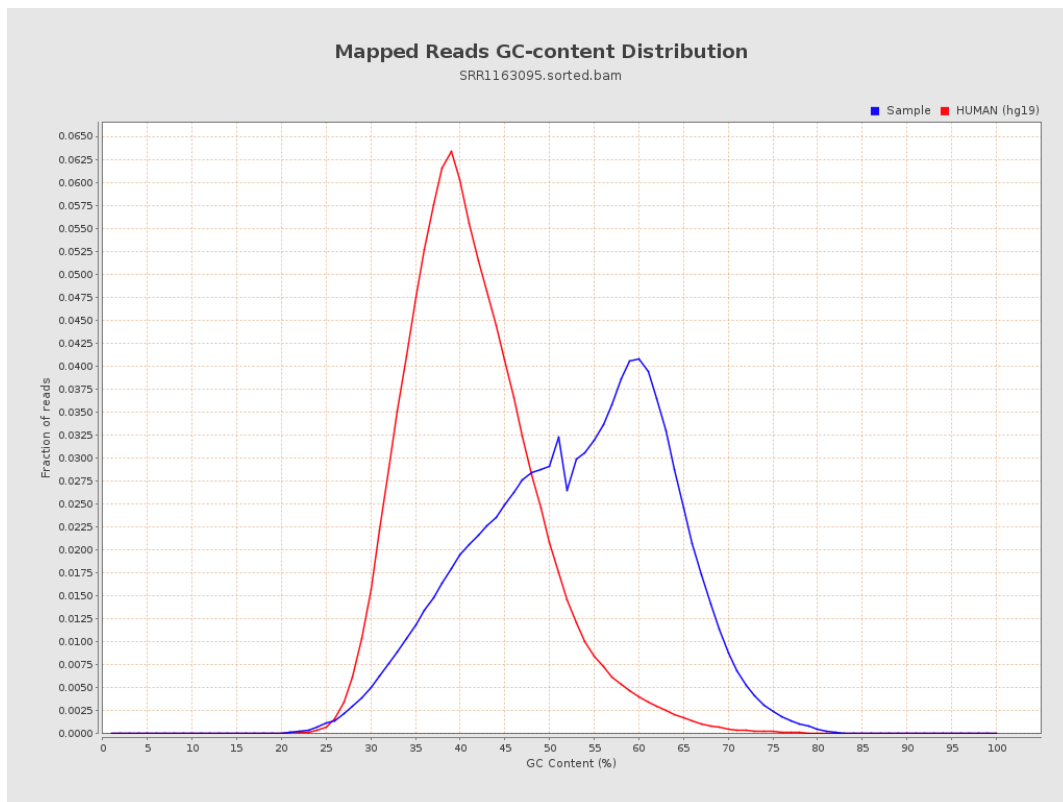
7. Results : Duplication Rate Histogram



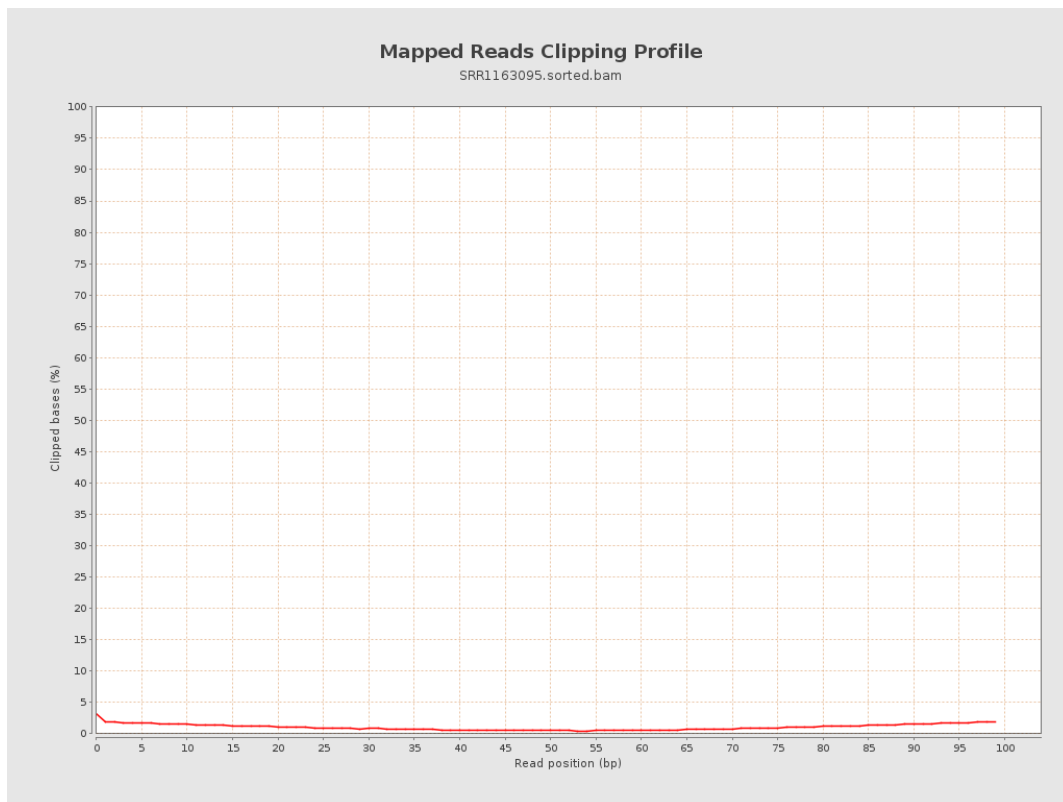
8. Results : Mapped Reads Nucleotide Content



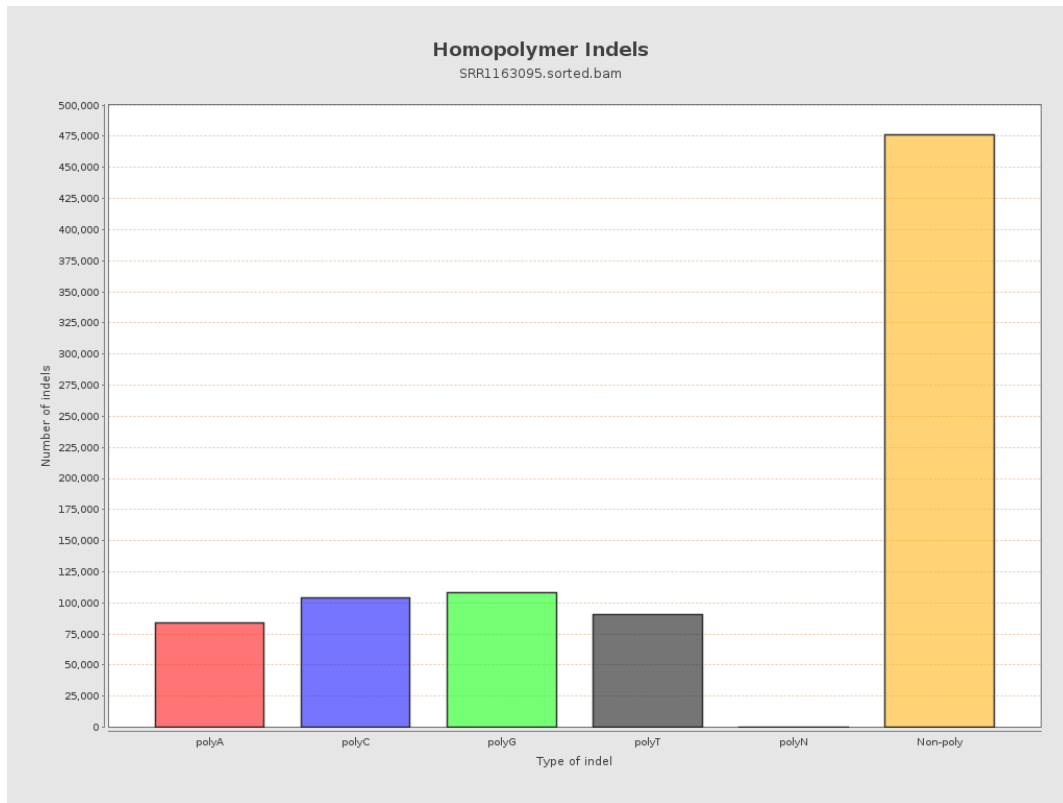
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

