

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 06:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153395.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_SRR1153395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153395.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 06:01:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153395.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,389,698
Mapped reads	47,981,297 / 99.16%
Unmapped reads	408,401 / 0.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	311,901 / 0.64%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	26,898,212 / 55.59%
Duplication rate	44.19%
Clipped reads	22,899,760 / 47.32%

2.2. ACGT Content

Number/percentage of A's	1,076,555,068 / 26.16%
Number/percentage of C's	989,479,843 / 24.05%
Number/percentage of T's	1,112,570,258 / 27.04%
Number/percentage of G's	934,617,633 / 22.71%
Number/percentage of N's	1,854,105 / 0.05%
GC Percentage	46.76%

2.3. Coverage

Mean	1.3295

Standard Deviation	14.1709
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2.4. Mapping Quality

Mean Mapping Quality	49.84
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2.5. Mismatches and indels

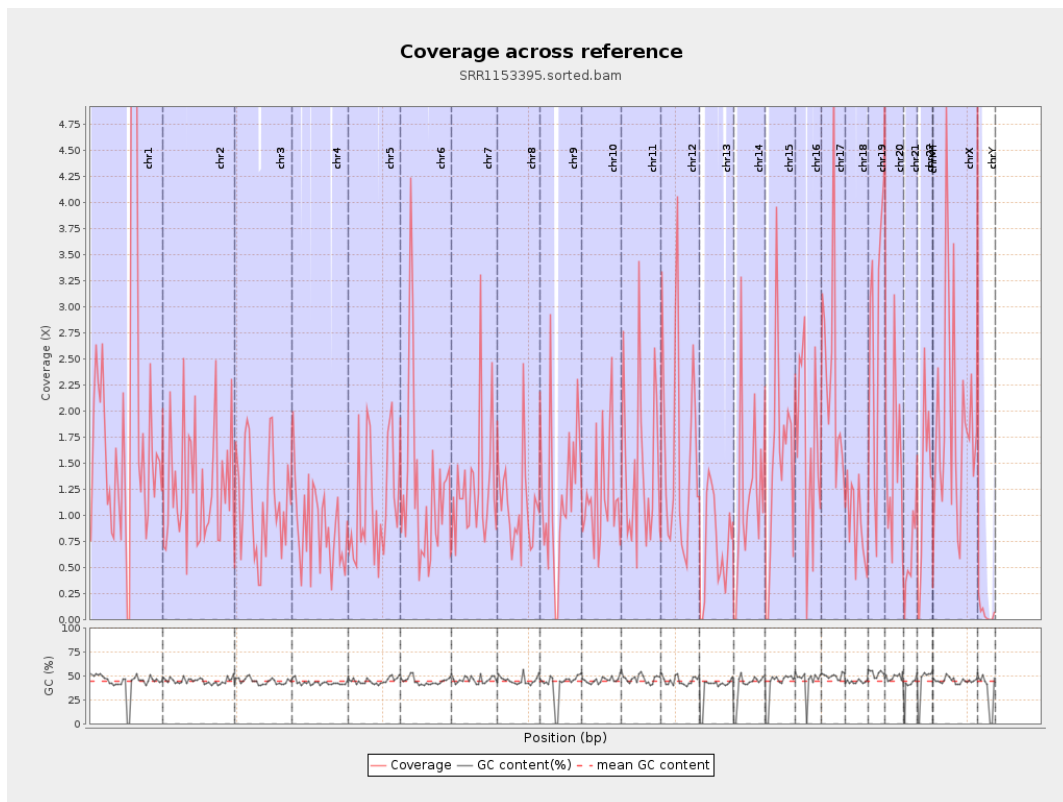
General error rate	0.26%
Mismatches	9,999,985
Insertions	448,910
Mapped reads with at least one insertion	0.93%
Deletions	365,078
Mapped reads with at least one deletion	0.75%
Homopolymer indels	49.3%

2.6. Chromosome stats

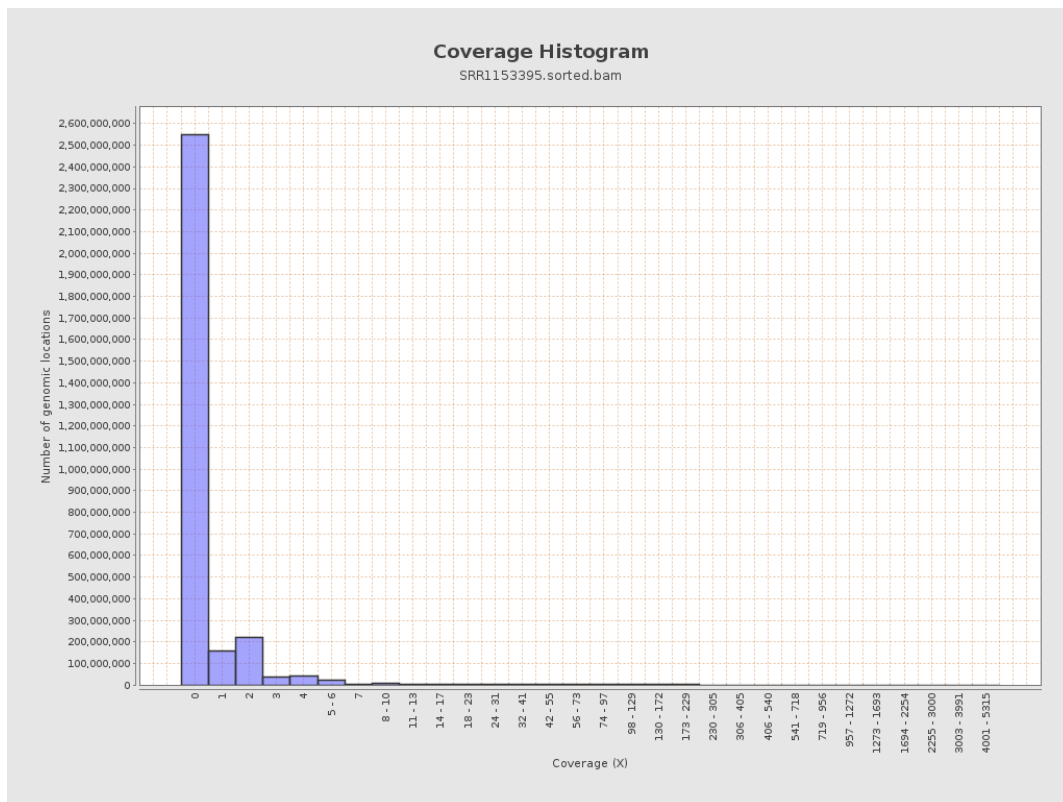
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	456233636	1.8304	19.8077
chr2	243199373	311069759	1.2791	13.3354
chr3	198022430	223328014	1.1278	11.492
chr4	191154276	169103239	0.8846	9.4741
chr5	180915260	203550063	1.1251	12.5648
chr6	171115067	212085307	1.2394	14.0795
chr7	159138663	201480503	1.2661	12.8617

chr8	146364022	158024318	1.0797	13.0045
chr9	141213431	164378608	1.164	12.9014
chr10	135534747	163279031	1.2047	11.1924
chr11	135006516	195701414	1.4496	14.1238
chr12	133851895	220229142	1.6453	15.9511
chr13	115169878	81165302	0.7047	8.4556
chr14	107349540	127042964	1.1835	12.6781
chr15	102531392	150386835	1.4667	14.0233
chr16	90354753	148424304	1.6427	14.6193
chr17	81195210	192662071	2.3728	20.3751
chr18	78077248	72432364	0.9277	10.1983
chr19	59128983	167030966	2.8249	21.218
chr20	63025520	93427798	1.4824	15.5958
chr21	48129895	32232798	0.6697	7.4747
chr22	51304566	66154679	1.2895	13.3689
chrMT	16571	4929	0.2974	1.1285
chrX	155270560	302914067	1.9509	19.7536
chrY	59373566	3484642	0.0587	2.8212

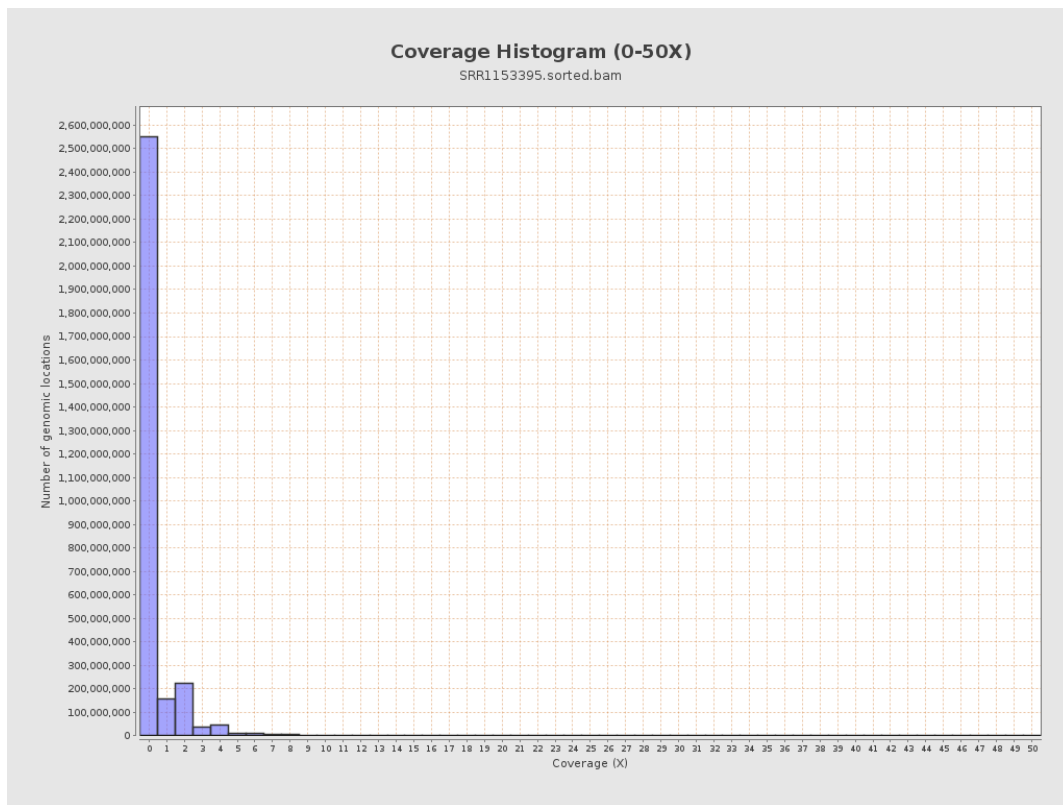
3. Results : Coverage across reference



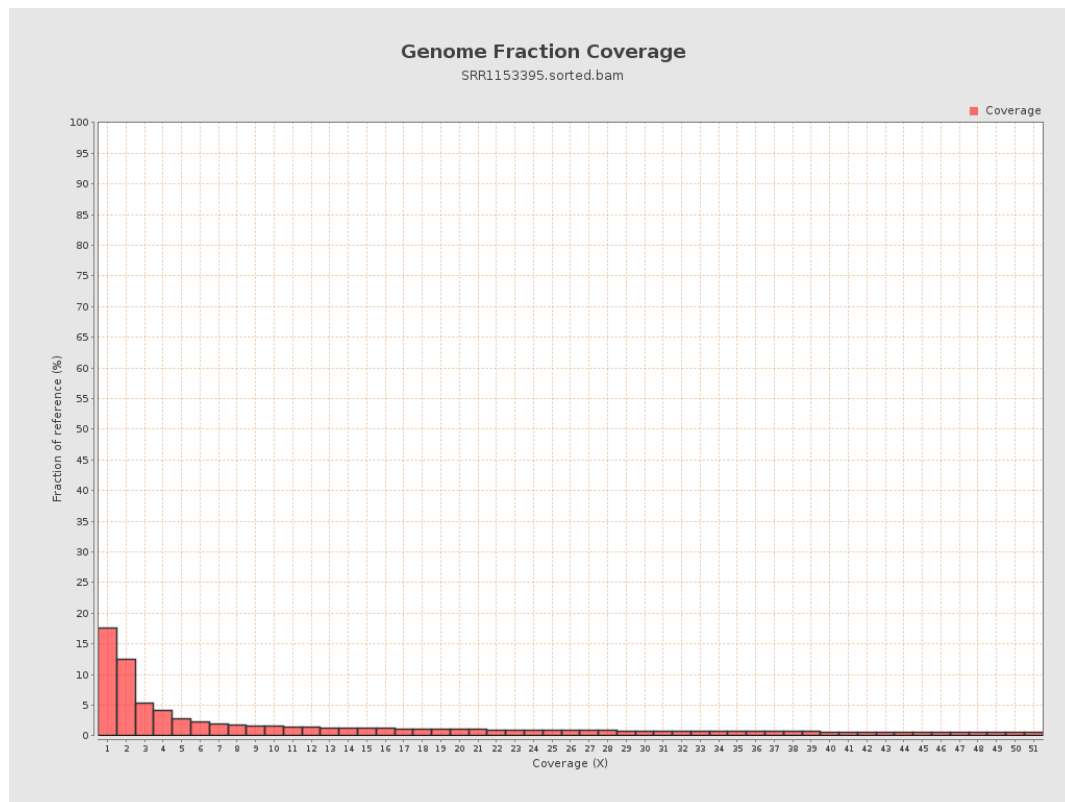
4. Results : Coverage Histogram



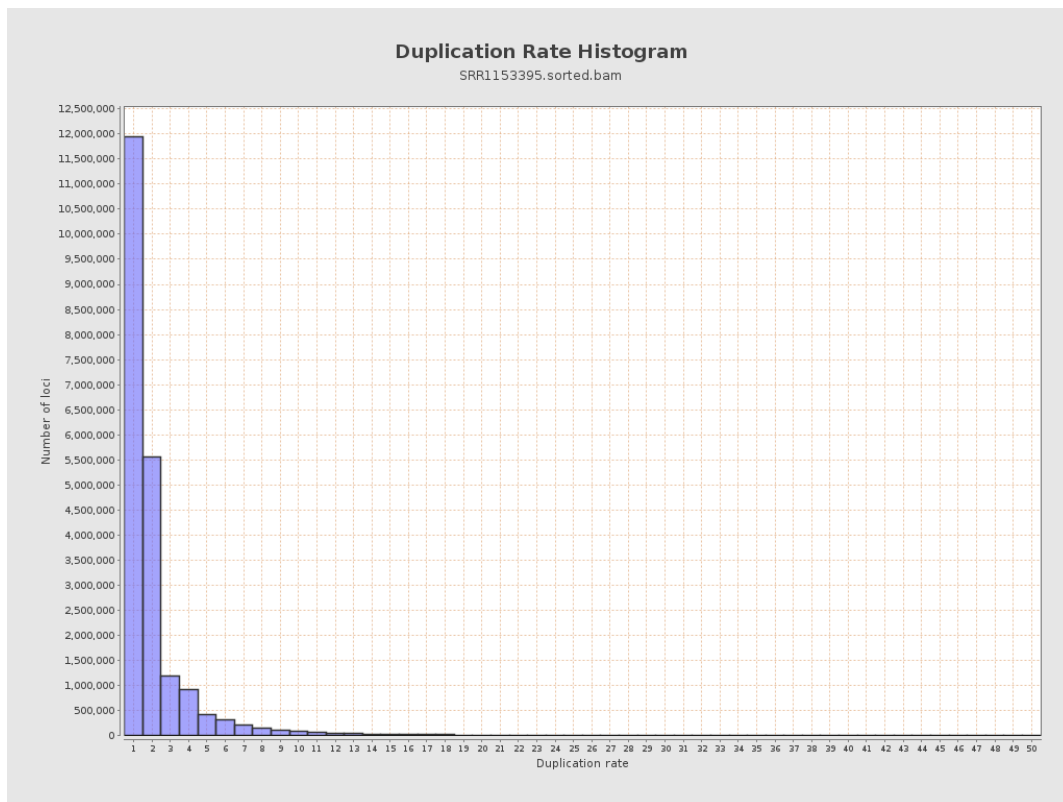
5. Results : Coverage Histogram (0-50X)



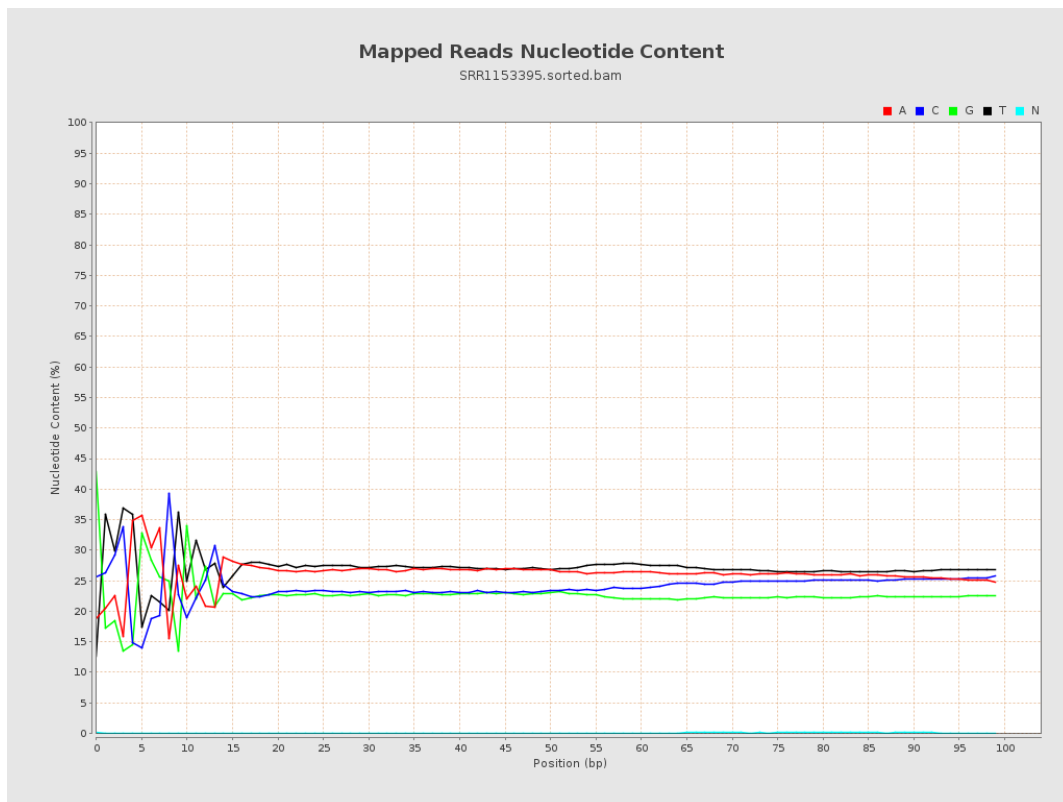
6. Results : Genome Fraction Coverage



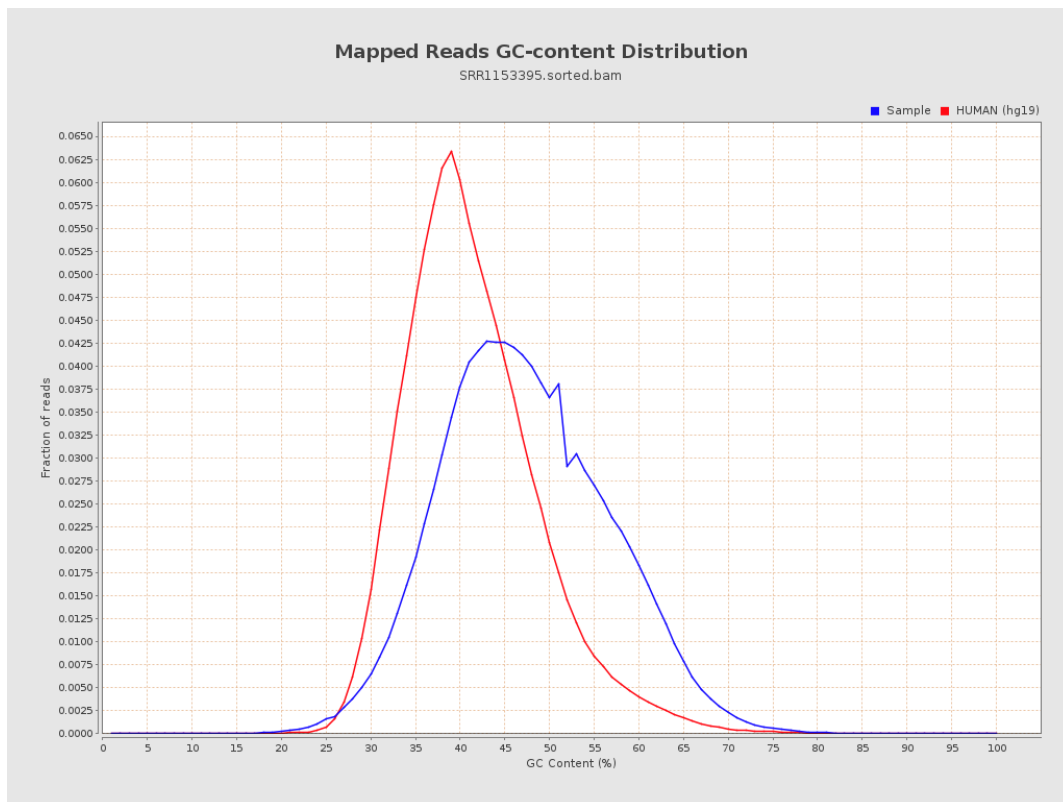
7. Results : Duplication Rate Histogram



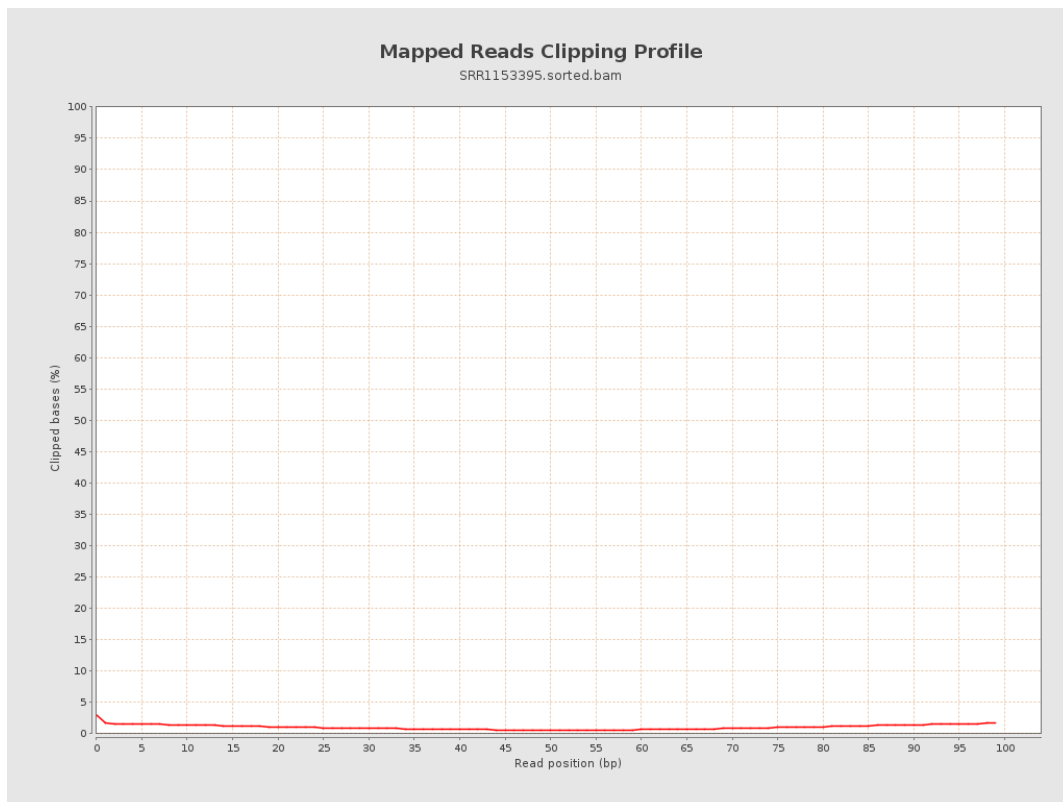
8. Results : Mapped Reads Nucleotide Content



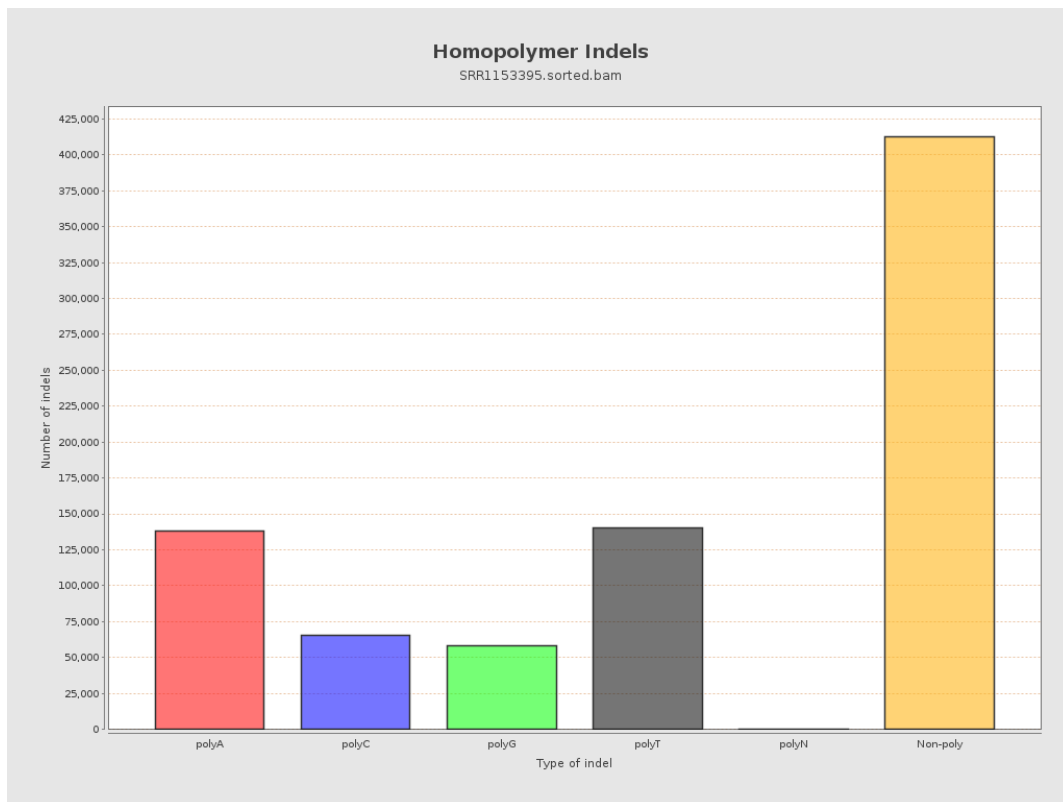
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

