

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251079.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_SRR10251079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:35:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,265,113
Mapped reads	4,029,842 / 94.48%
Unmapped reads	235,271 / 5.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,765 / 0.79%
Read min/max/mean length	30 / 80 / 80.28
Duplicated reads (estimated)	818,083 / 19.18%
Duplication rate	17.64%
Clipped reads	606,412 / 14.22%

2.2. ACGT Content

Number/percentage of A's	91,361,637 / 29.33%
Number/percentage of C's	61,900,711 / 19.87%
Number/percentage of T's	92,437,289 / 29.67%
Number/percentage of G's	65,828,233 / 21.13%
Number/percentage of N's	2,556 / 0%
GC Percentage	41%

2.3. Coverage

Mean	0.1007

Standard Deviation	1.1756
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2.4. Mapping Quality

Mean Mapping Quality	47.8
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2.5. Mismatches and indels

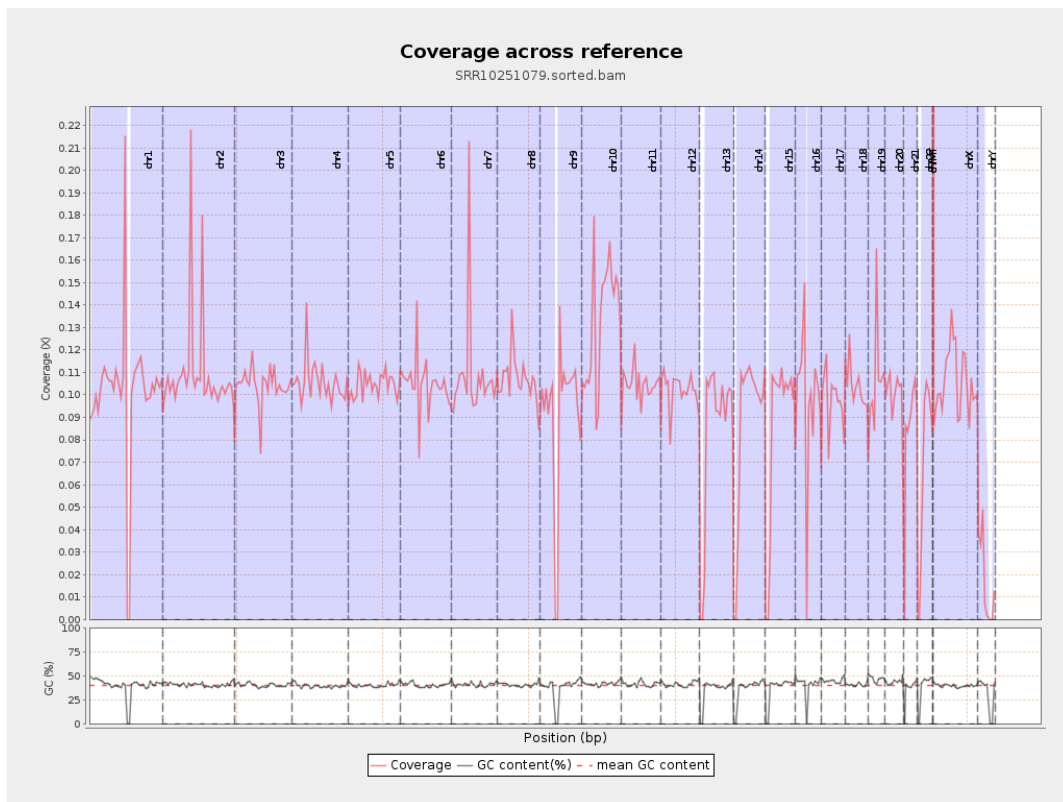
General error rate	0.64%
Mismatches	1,913,463
Insertions	39,042
Mapped reads with at least one insertion	0.95%
Deletions	115,689
Mapped reads with at least one deletion	2.82%
Homopolymer indels	44.77%

2.6. Chromosome stats

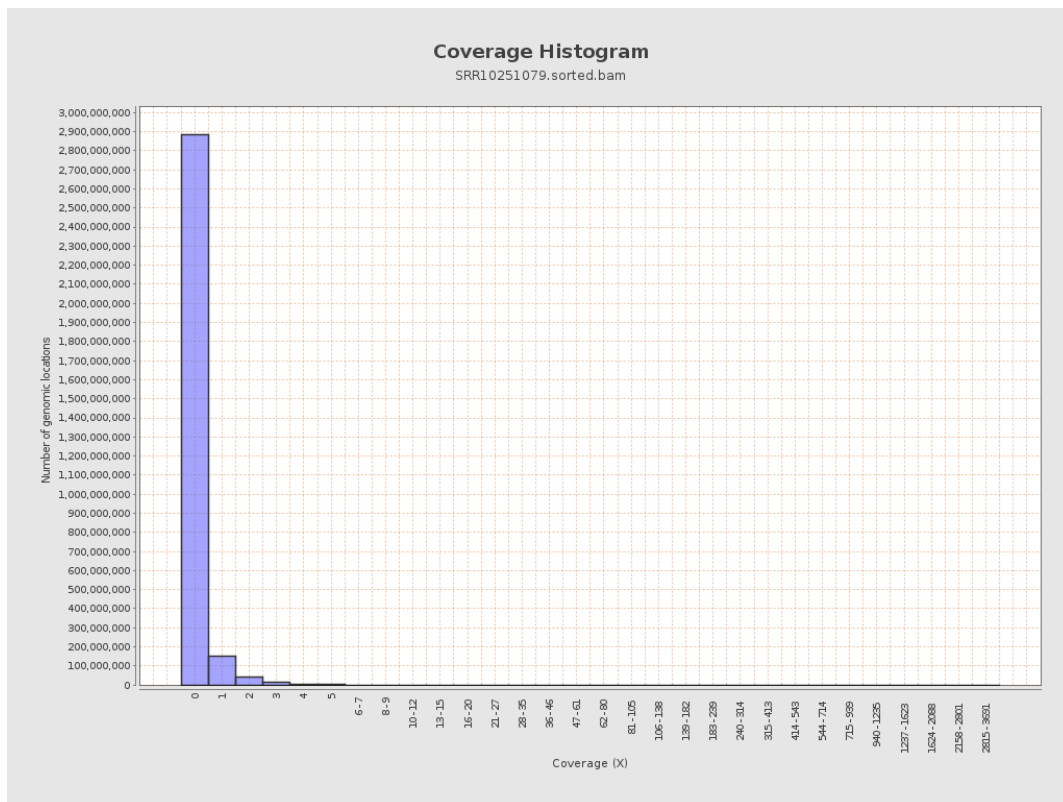
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25239517	0.1013	2.5332
chr2	243199373	26715109	0.1098	1.419
chr3	198022430	20600984	0.104	0.4463
chr4	191154276	20266016	0.106	0.5349
chr5	180915260	18922291	0.1046	0.4636
chr6	171115067	17894241	0.1046	0.6394
chr7	159138663	17221432	0.1082	1.8029

chr8	146364022	15636459	0.1068	0.7519
chr9	141213431	12997255	0.092	1.5639
chr10	135534747	17928785	0.1323	1.0873
chr11	135006516	14114083	0.1045	0.6746
chr12	133851895	13736912	0.1026	0.4627
chr13	115169878	9623233	0.0836	0.3896
chr14	107349540	9451856	0.088	0.6773
chr15	102531392	8673061	0.0846	0.3962
chr16	90354753	8665075	0.0959	0.8383
chr17	81195210	8012824	0.0987	0.5761
chr18	78077248	8128699	0.1041	1.3801
chr19	59128983	6332666	0.1071	2.3379
chr20	63025520	6354802	0.1008	0.4982
chr21	48129895	4092289	0.085	0.4642
chr22	51304566	3503128	0.0683	0.3874
chrMT	16571	231836	13.9905	8.4594
chrX	155270560	16400412	0.1056	0.5539
chrY	59373566	993650	0.0167	0.9966

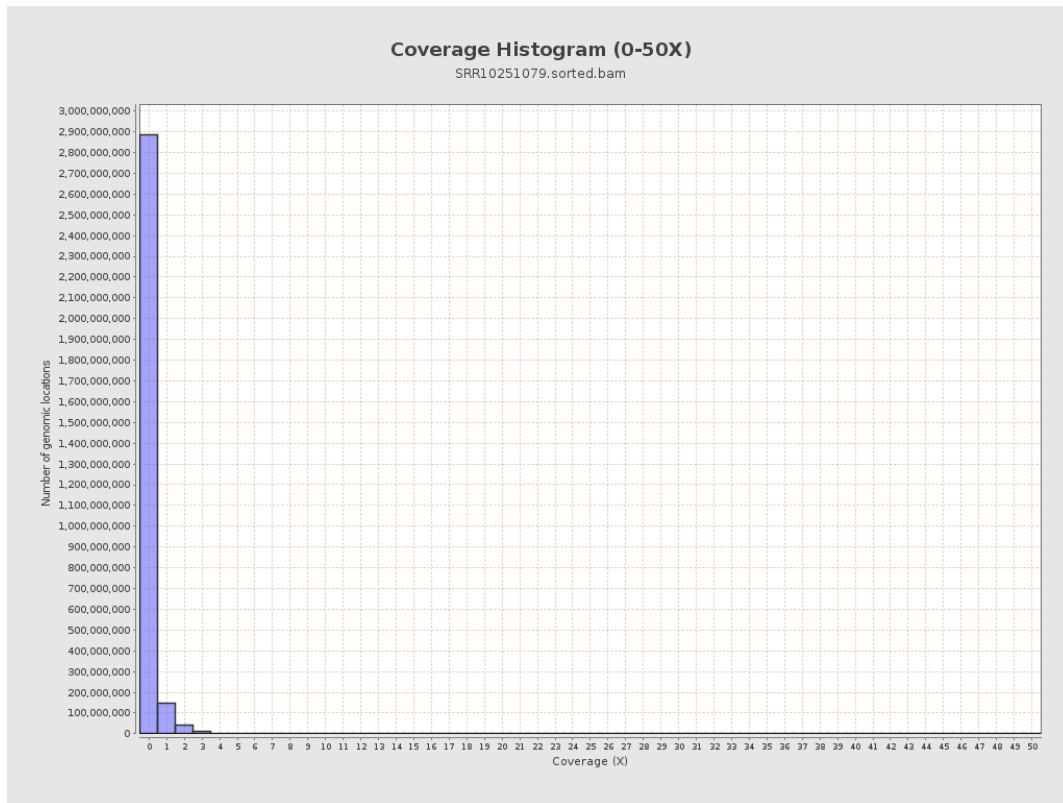
3. Results : Coverage across reference



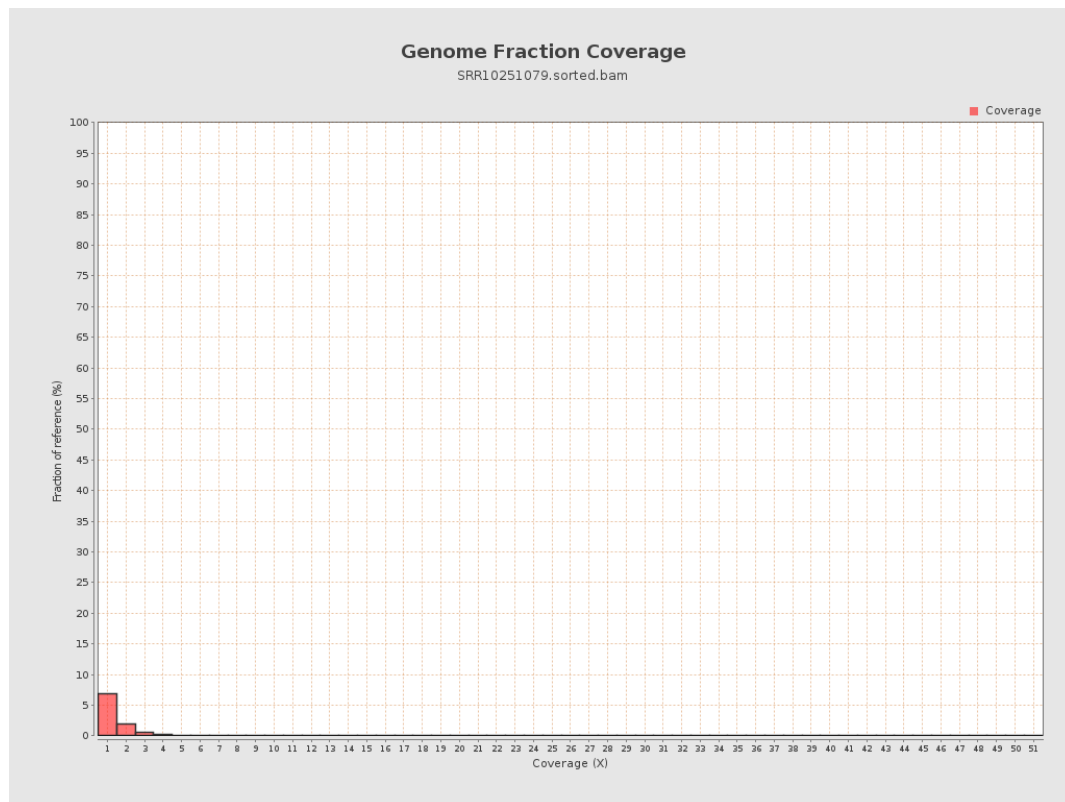
4. Results : Coverage Histogram



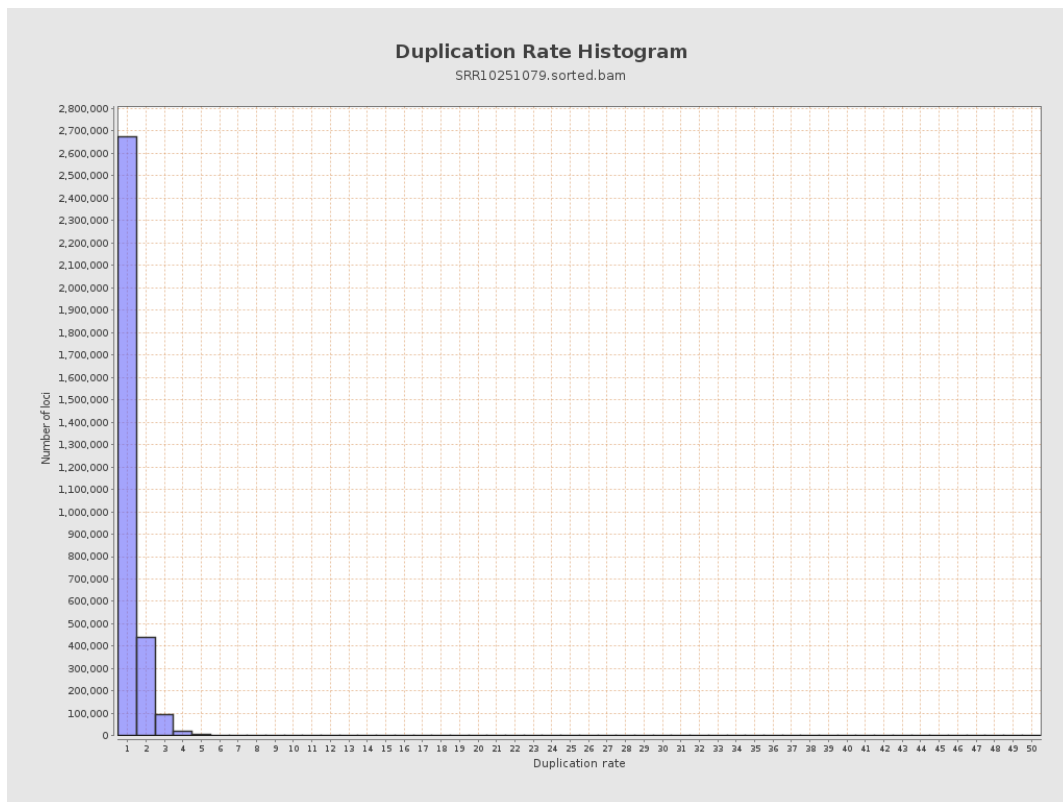
5. Results : Coverage Histogram (0-50X)



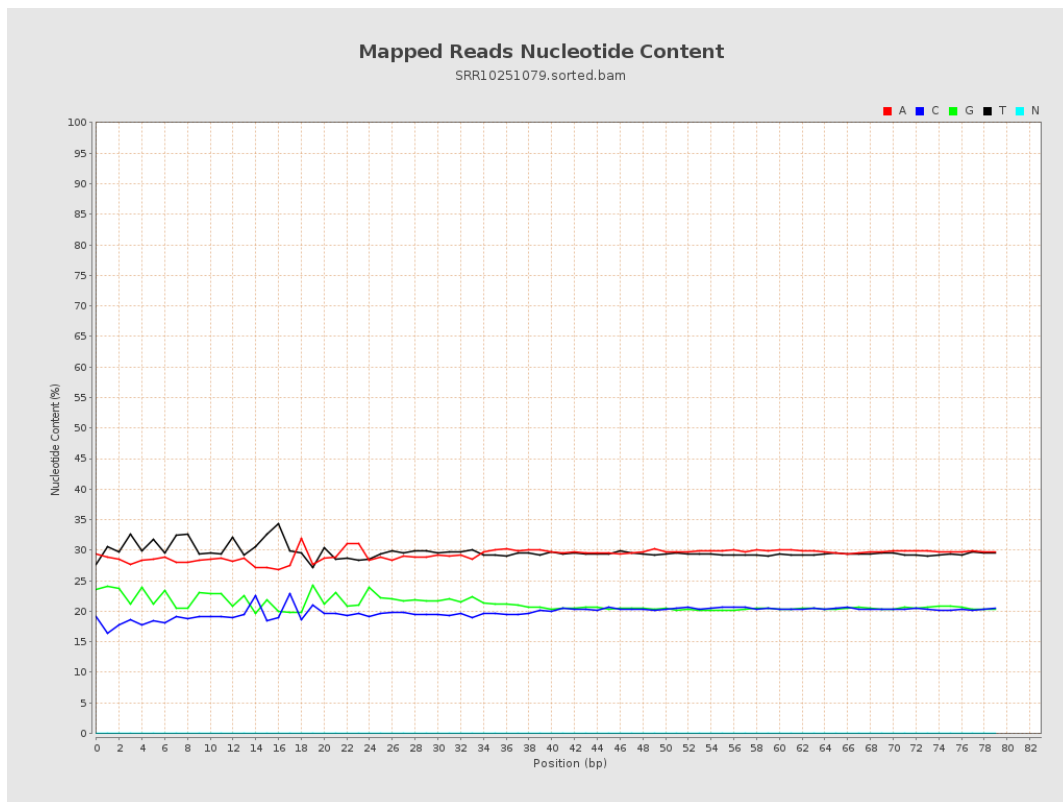
6. Results : Genome Fraction Coverage



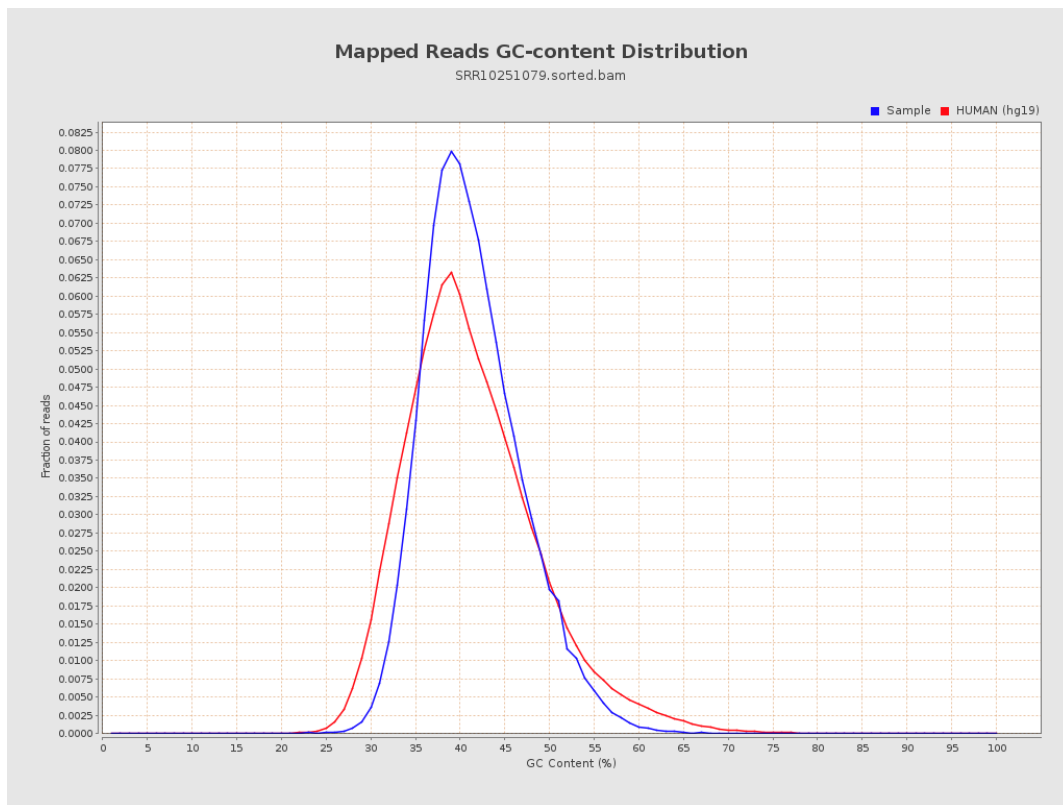
7. Results : Duplication Rate Histogram



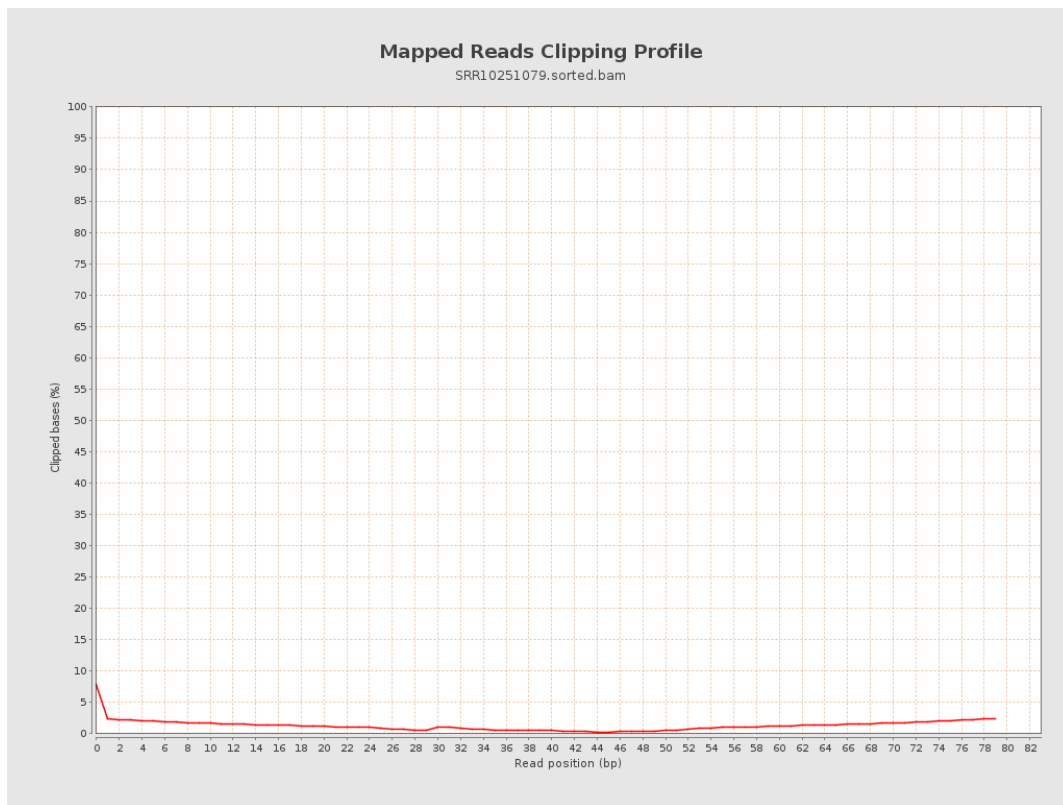
8. Results : Mapped Reads Nucleotide Content



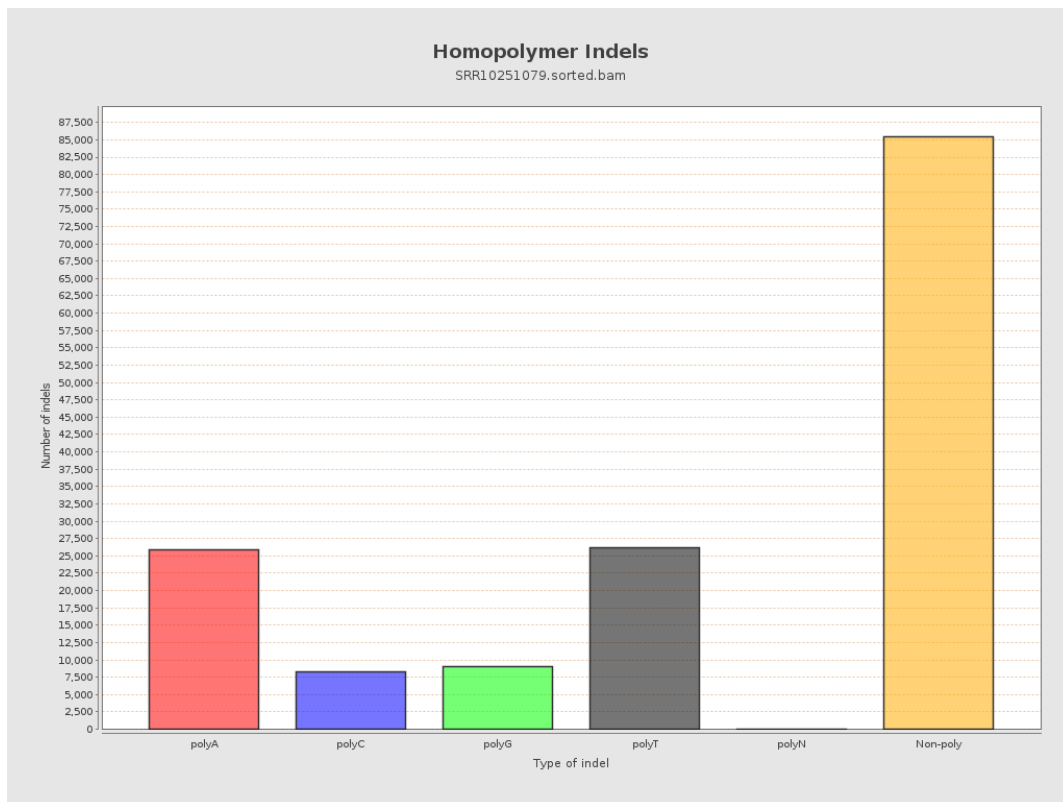
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

