

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:15:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251063.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_SRR10251063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:15:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,438,006
Mapped reads	3,312,455 / 96.35%
Unmapped reads	125,551 / 3.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,740 / 0.84%
Read min/max/mean length	30 / 80 / 80.3
Duplicated reads (estimated)	635,500 / 18.48%
Duplication rate	16.97%
Clipped reads	463,387 / 13.48%

2.2. ACGT Content

Number/percentage of A's	74,793,324 / 29.12%
Number/percentage of C's	51,325,105 / 19.98%
Number/percentage of T's	75,929,678 / 29.56%
Number/percentage of G's	54,776,210 / 21.33%
Number/percentage of N's	21,476 / 0.01%
GC Percentage	41.31%

2.3. Coverage

Mean	0.083

Standard Deviation	0.8154
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2.4. Mapping Quality

Mean Mapping Quality	48.07
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2.5. Mismatches and indels

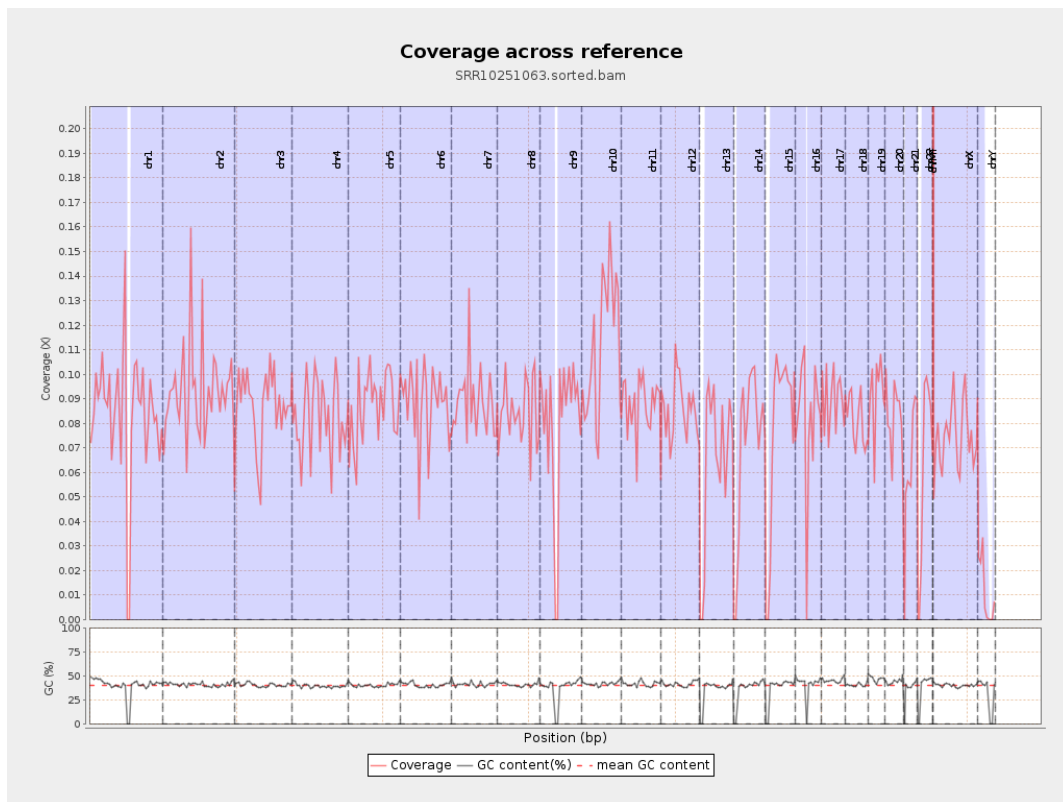
General error rate	0.59%
Mismatches	1,447,009
Insertions	31,322
Mapped reads with at least one insertion	0.93%
Deletions	85,870
Mapped reads with at least one deletion	2.55%
Homopolymer indels	45.7%

2.6. Chromosome stats

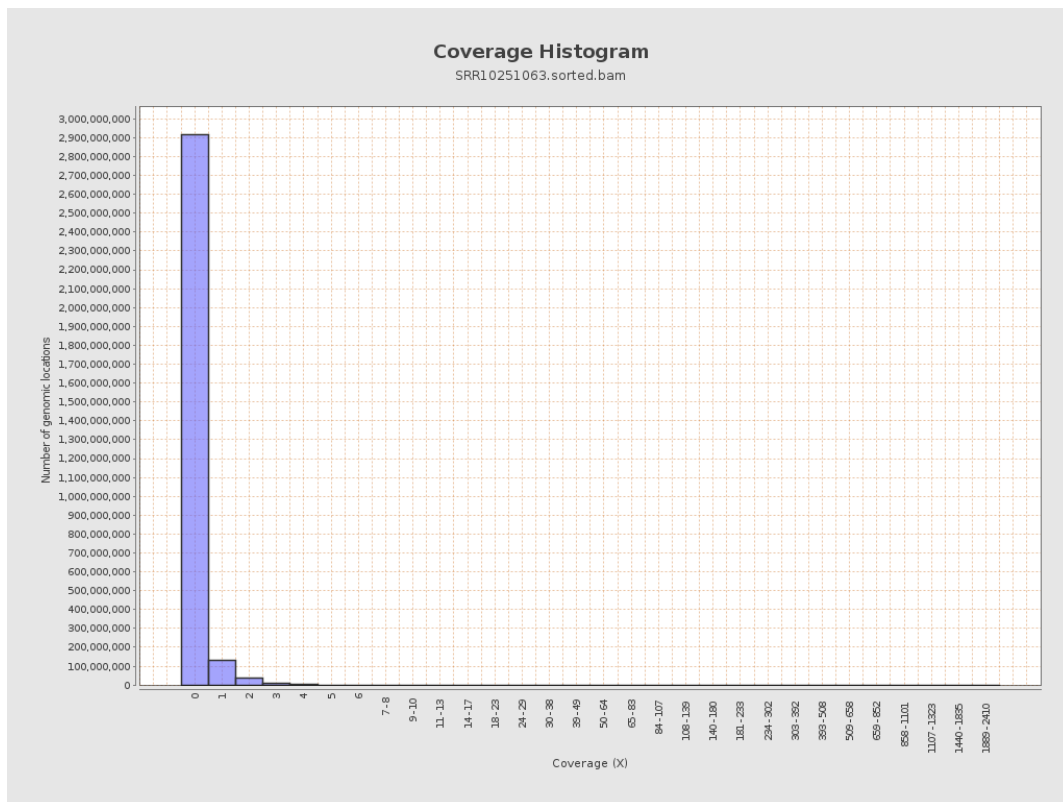
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20936732	0.084	1.666
chr2	243199373	22741376	0.0935	1.0652
chr3	198022430	17127531	0.0865	0.3953
chr4	191154276	15745744	0.0824	0.4482
chr5	180915260	15818810	0.0874	0.4139
chr6	171115067	15014008	0.0877	0.472
chr7	159138663	14046696	0.0883	1.1334

chr8	146364022	12287035	0.0839	0.5476
chr9	141213431	11225330	0.0795	0.8431
chr10	135534747	15300302	0.1129	0.8287
chr11	135006516	11839212	0.0877	0.542
chr12	133851895	11607793	0.0867	0.4065
chr13	115169878	7465353	0.0648	0.3367
chr14	107349540	7771214	0.0724	0.5645
chr15	102531392	7689291	0.075	0.3659
chr16	90354753	7237644	0.0801	0.667
chr17	81195210	7330734	0.0903	0.4917
chr18	78077248	6357742	0.0814	1.0306
chr19	59128983	5403528	0.0914	1.5954
chr20	63025520	5179974	0.0822	0.438
chr21	48129895	3059342	0.0636	0.3747
chr22	51304566	3225389	0.0629	0.3489
chrMT	16571	277920	16.7715	10.1493
chrX	155270560	11639910	0.075	0.4379
chrY	59373566	670632	0.0113	0.7423

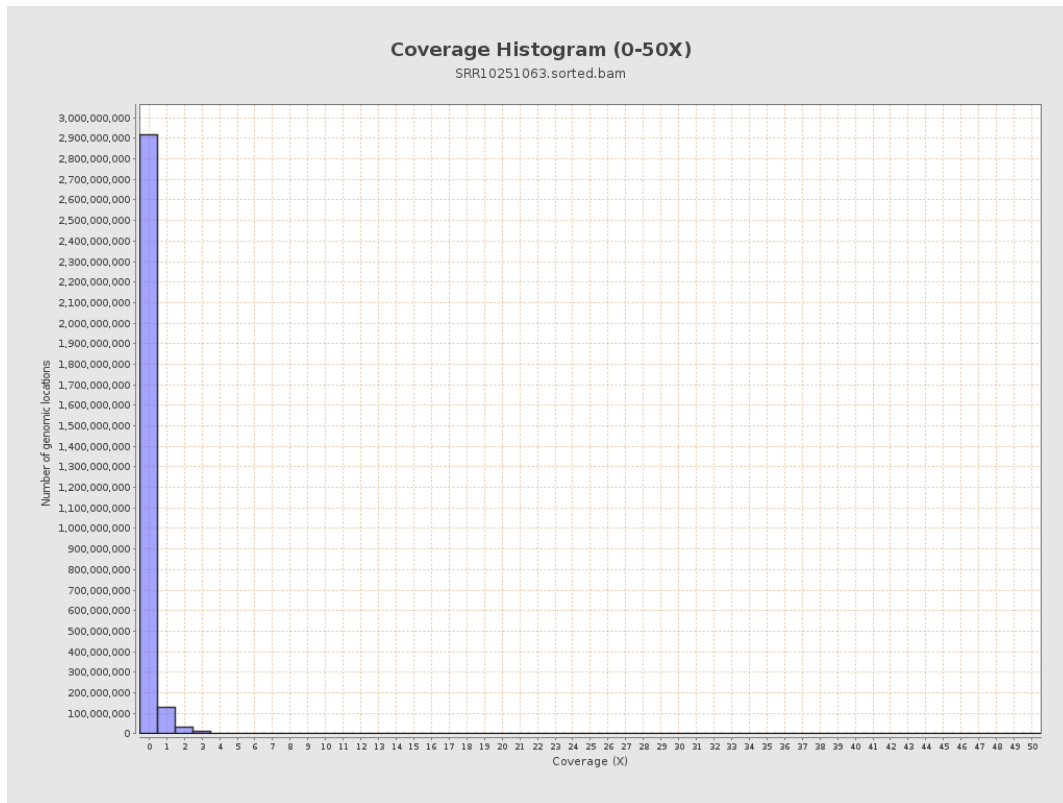
3. Results : Coverage across reference



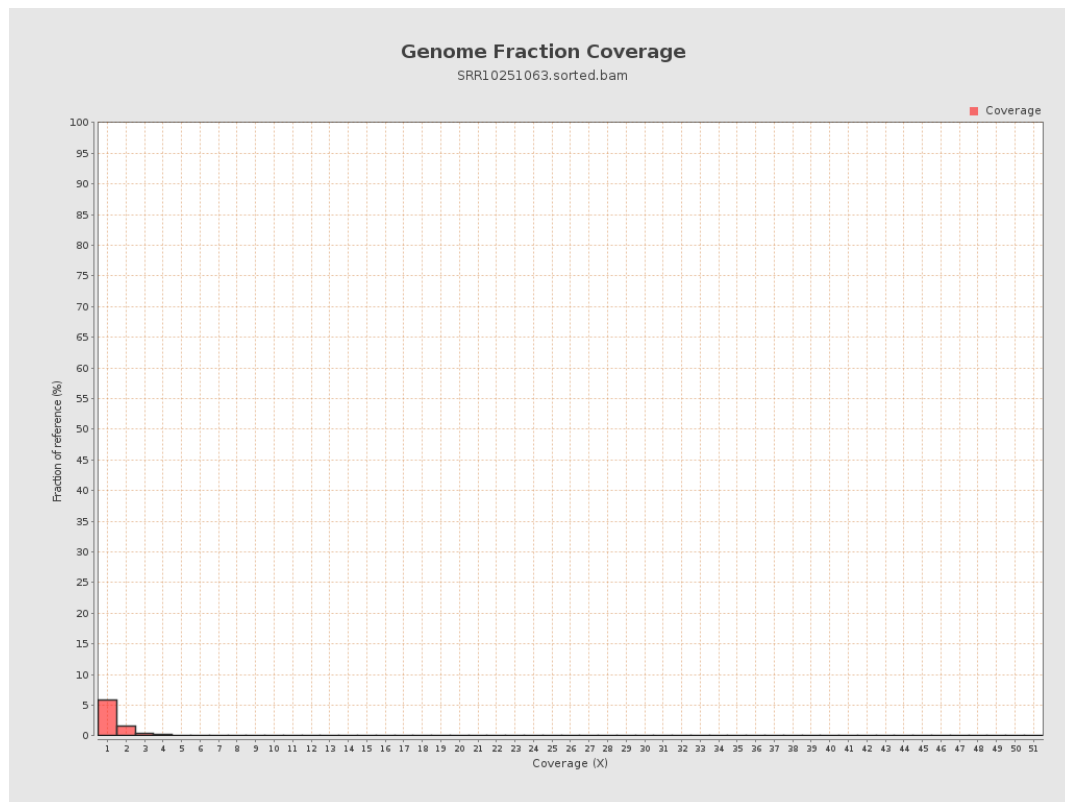
4. Results : Coverage Histogram



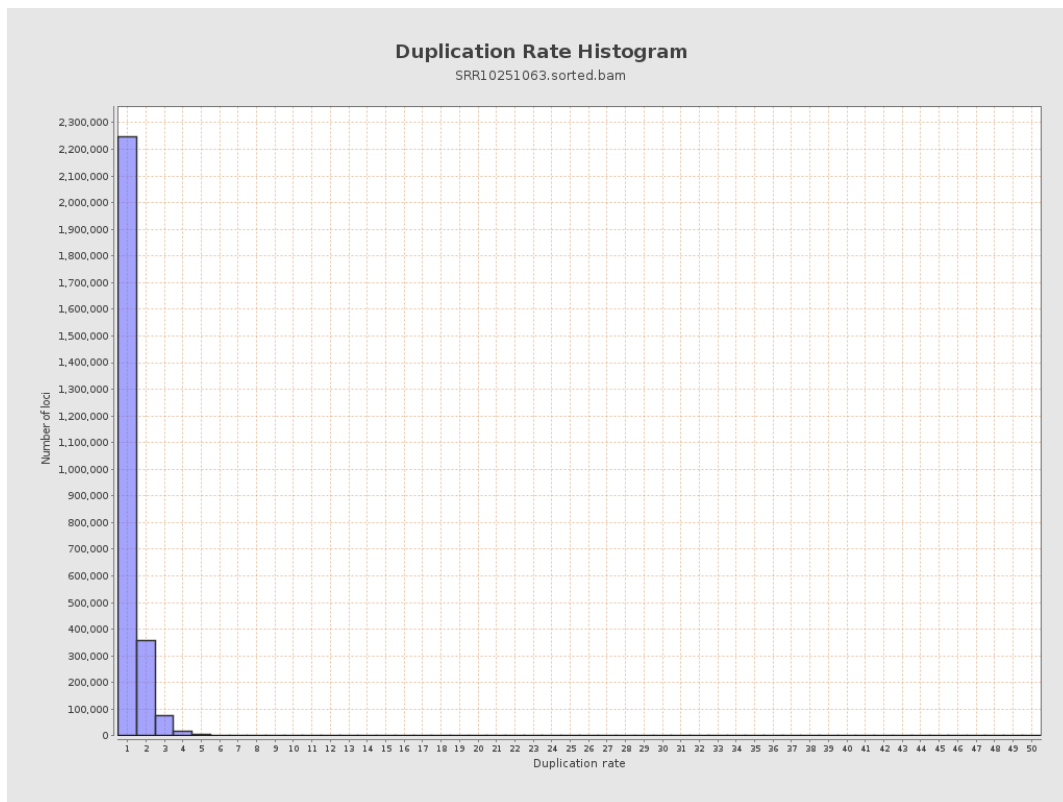
5. Results : Coverage Histogram (0-50X)



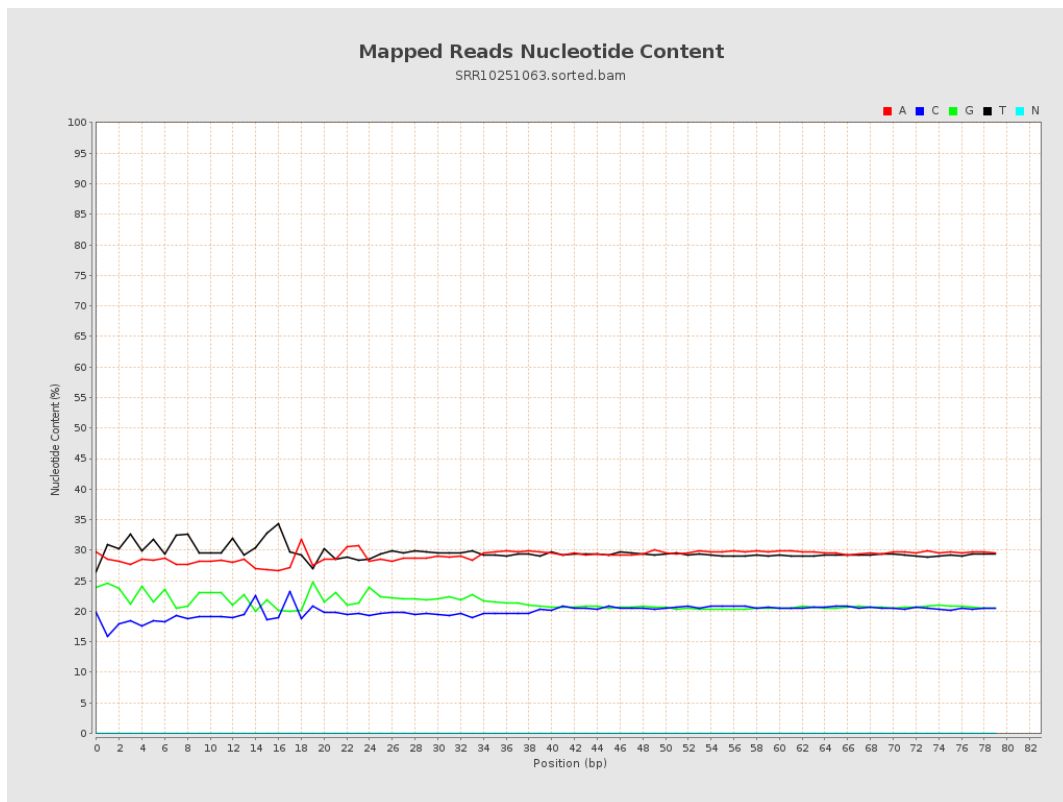
6. Results : Genome Fraction Coverage



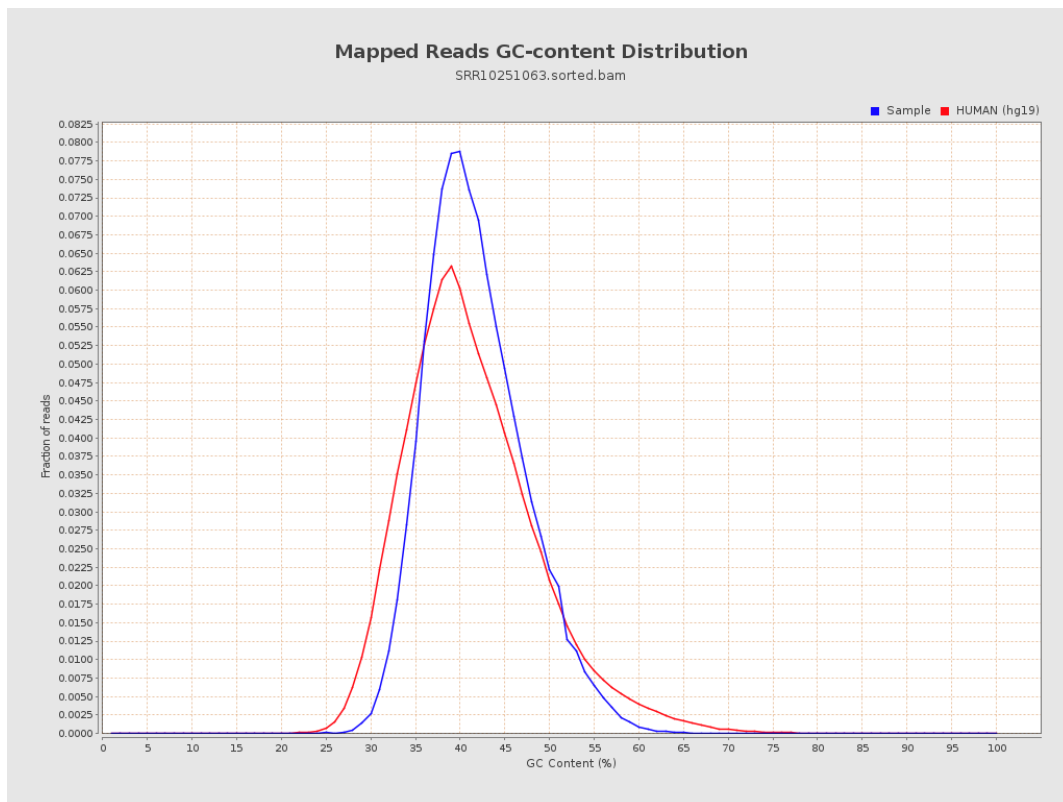
7. Results : Duplication Rate Histogram



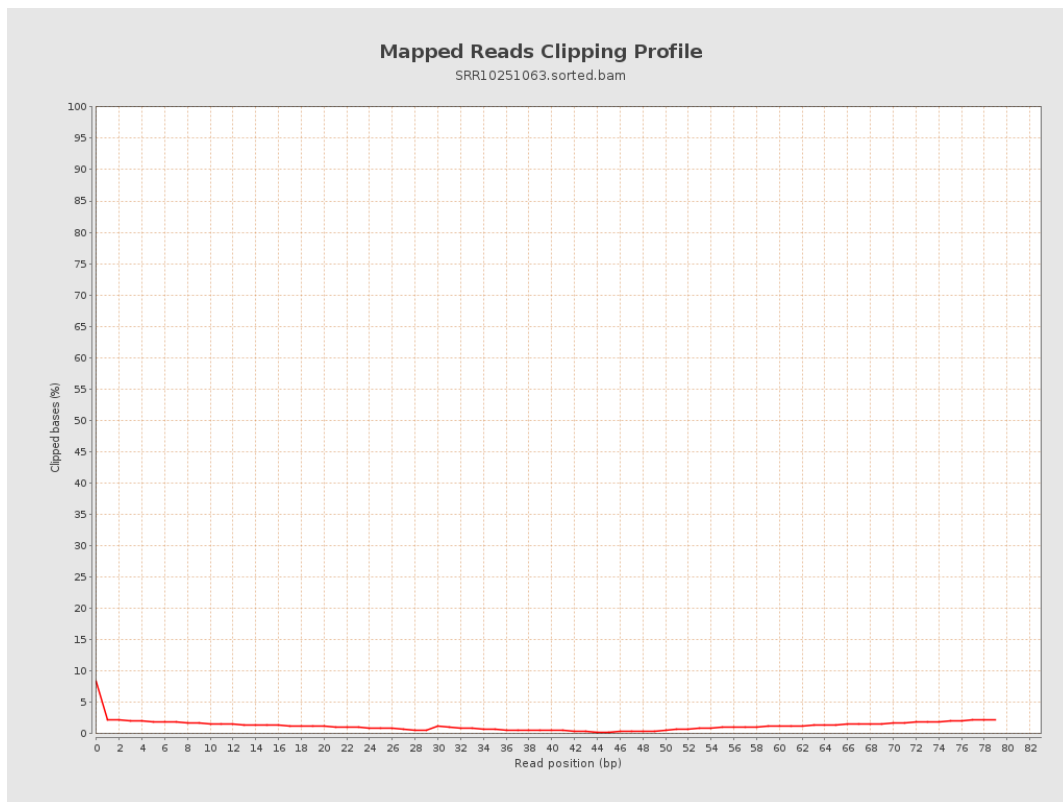
8. Results : Mapped Reads Nucleotide Content



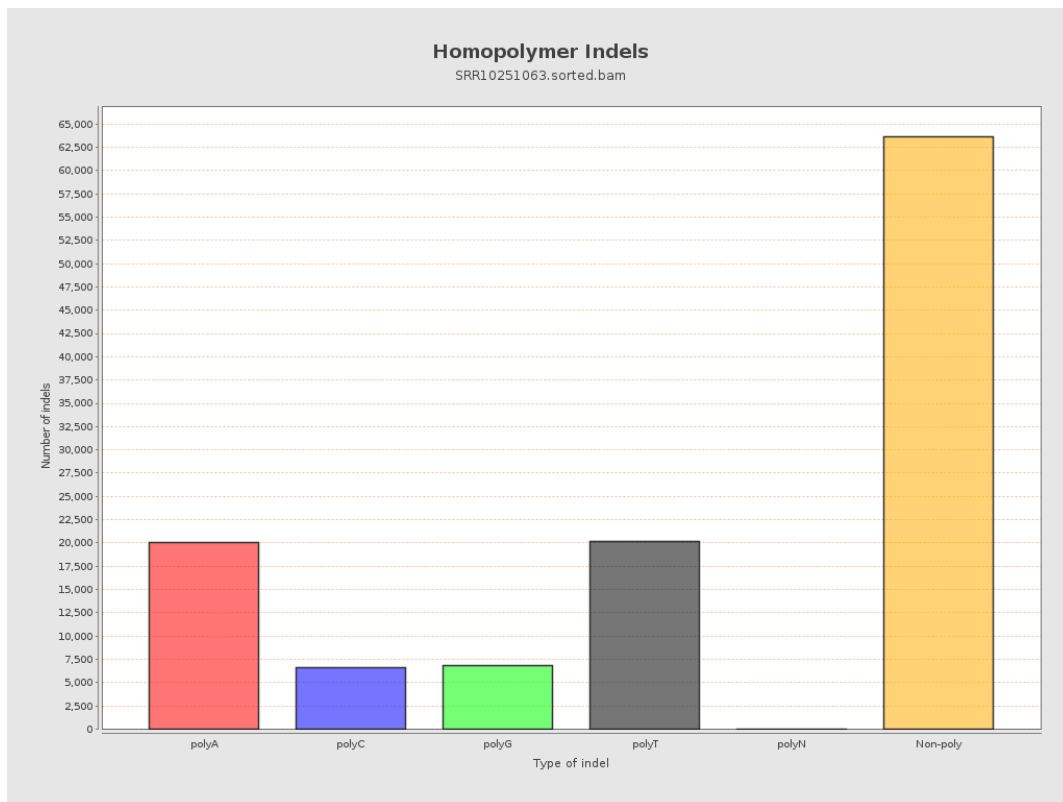
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

