

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251064.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_SRR10251064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:22:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,382,021
Mapped reads	3,282,104 / 97.05%
Unmapped reads	99,917 / 2.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,642 / 0.88%
Read min/max/mean length	30 / 80 / 80.31
Duplicated reads (estimated)	655,376 / 19.38%
Duplication rate	17.39%
Clipped reads	447,851 / 13.24%

2.2. ACGT Content

Number/percentage of A's	74,519,204 / 29.23%
Number/percentage of C's	50,951,747 / 19.98%
Number/percentage of T's	75,386,490 / 29.57%
Number/percentage of G's	54,076,072 / 21.21%
Number/percentage of N's	19,878 / 0.01%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0824

Standard Deviation	0.9714
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2.4. Mapping Quality

Mean Mapping Quality	48.1
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2.5. Mismatches and indels

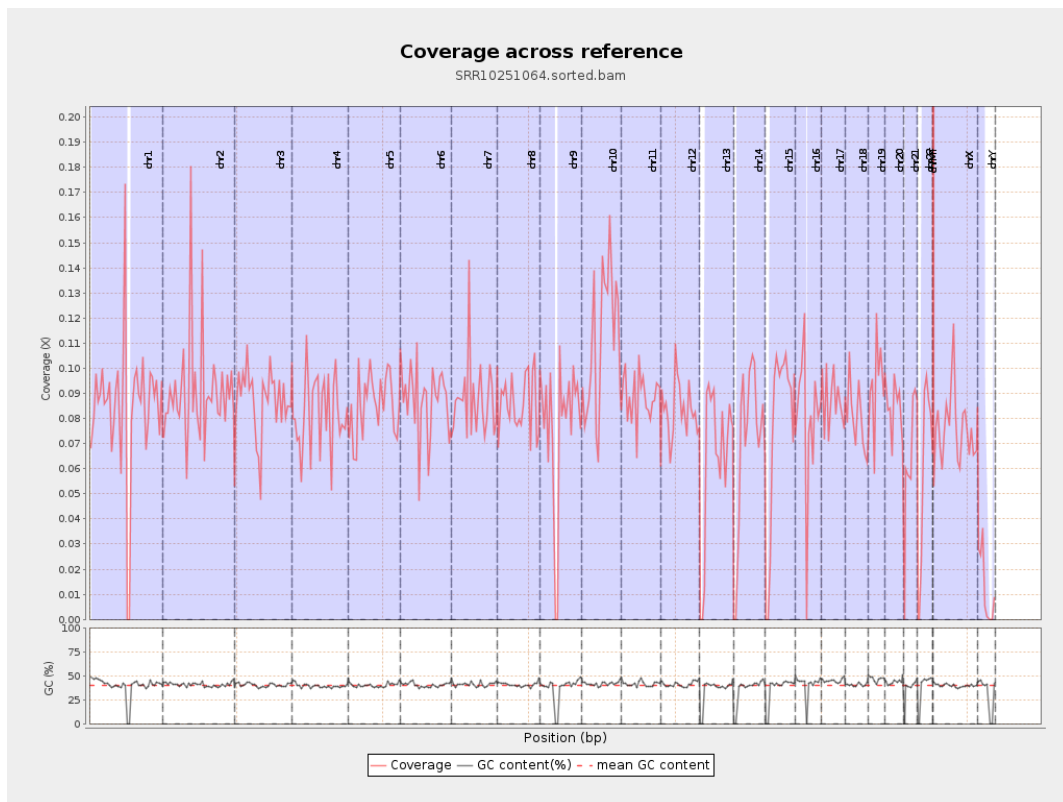
General error rate	0.61%
Mismatches	1,484,661
Insertions	32,384
Mapped reads with at least one insertion	0.97%
Deletions	84,497
Mapped reads with at least one deletion	2.53%
Homopolymer indels	45.52%

2.6. Chromosome stats

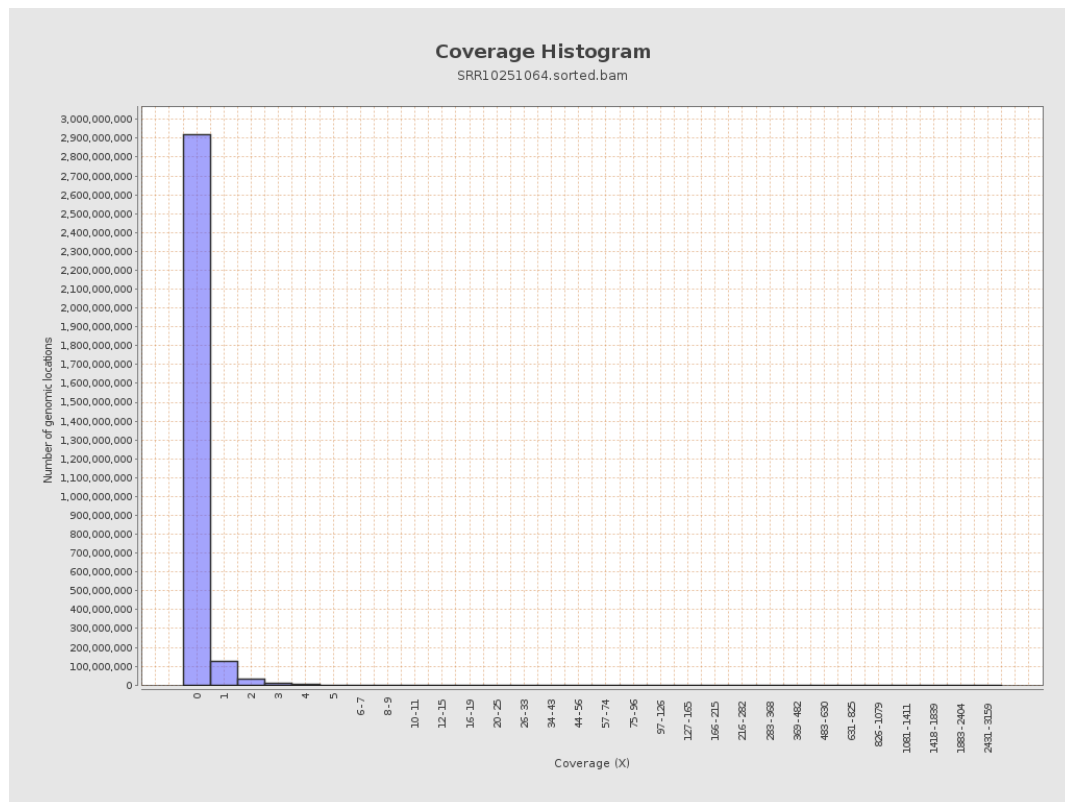
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21080096	0.0846	2.1596
chr2	243199373	22161064	0.0911	1.2344
chr3	198022430	17178556	0.0868	0.4014
chr4	191154276	15717413	0.0822	0.4728
chr5	180915260	15566612	0.086	0.4161
chr6	171115067	14844678	0.0868	0.5215
chr7	159138663	13893761	0.0873	1.2302

chr8	146364022	12480776	0.0853	0.6423
chr9	141213431	10843614	0.0768	1.0062
chr10	135534747	14990280	0.1106	0.9075
chr11	135006516	11954739	0.0885	0.6002
chr12	133851895	11269997	0.0842	0.4128
chr13	115169878	7388276	0.0642	0.3389
chr14	107349540	7668717	0.0714	0.6489
chr15	102531392	7704412	0.0751	0.3716
chr16	90354753	7161050	0.0793	0.7513
chr17	81195210	7093160	0.0874	0.5103
chr18	78077248	6286198	0.0805	1.2074
chr19	59128983	5521131	0.0934	2.028
chr20	63025520	5280599	0.0838	0.45
chr21	48129895	3175210	0.066	0.395
chr22	51304566	3079952	0.06	0.3602
chrMT	16571	192326	11.6062	7.2247
chrX	155270560	11828443	0.0762	0.4648
chrY	59373566	743413	0.0125	0.8481

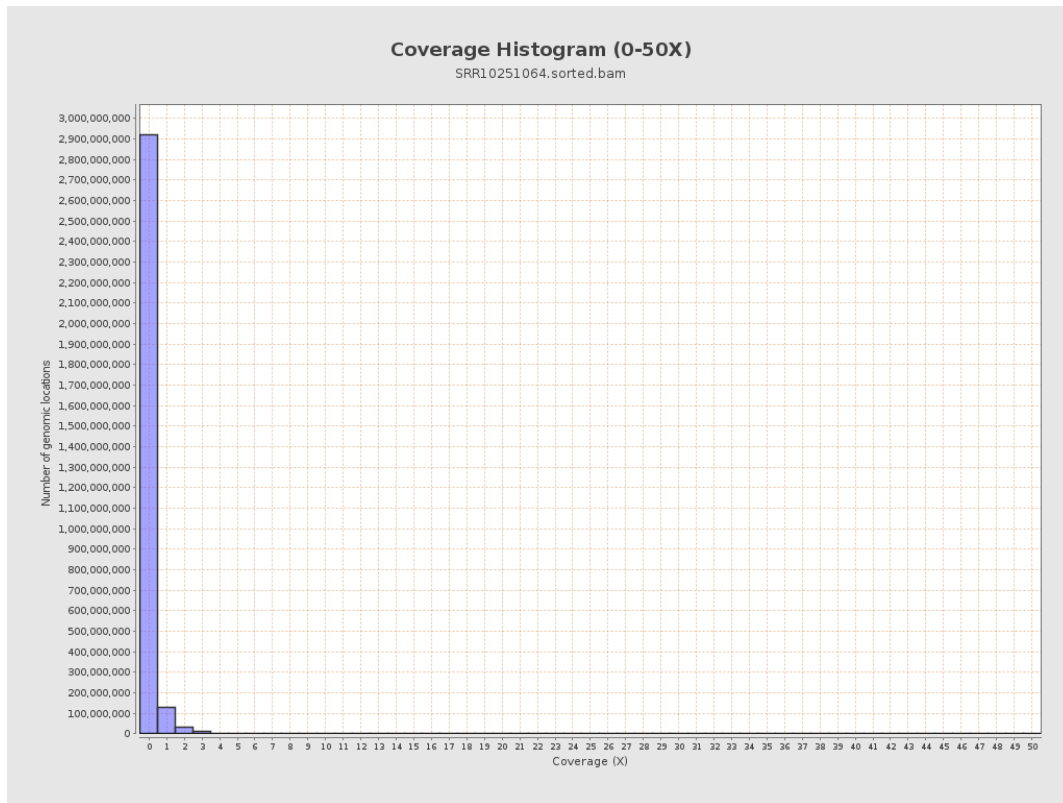
3. Results : Coverage across reference



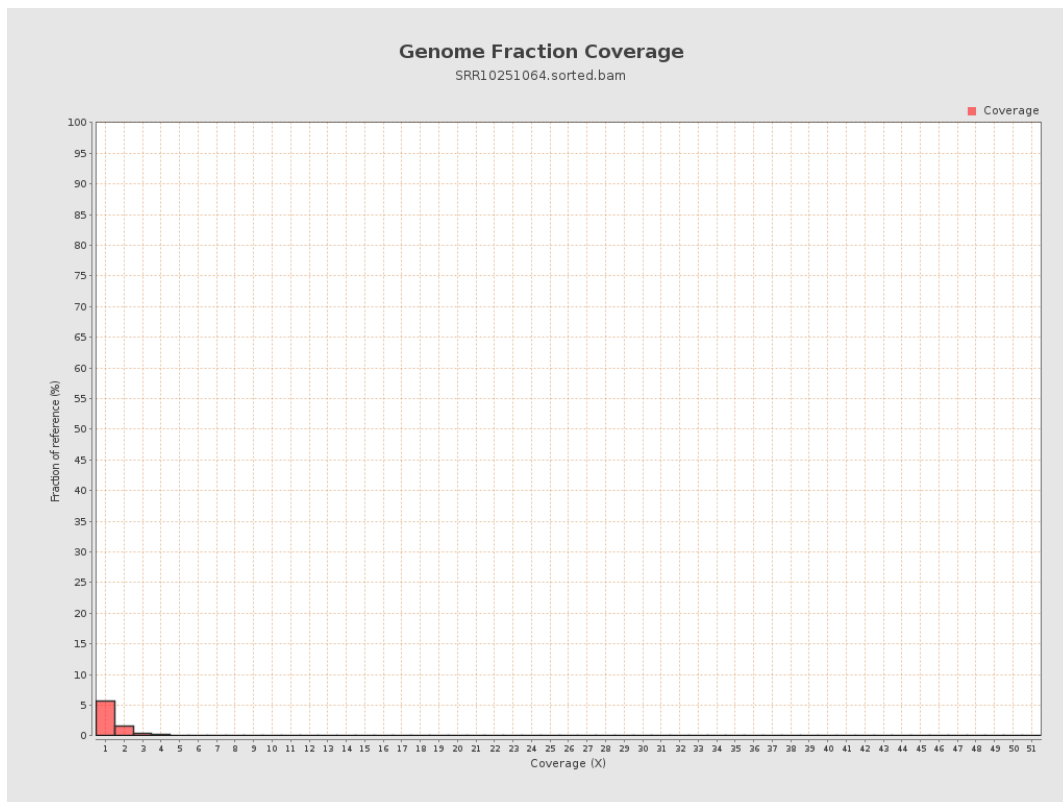
4. Results : Coverage Histogram



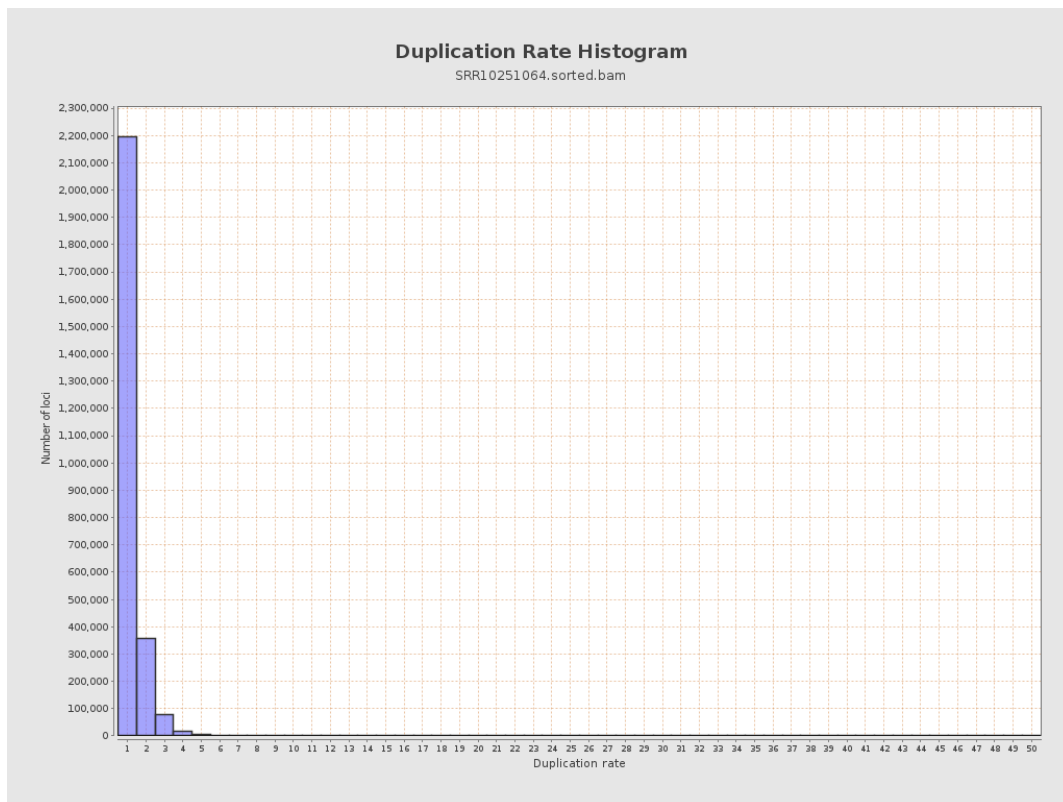
5. Results : Coverage Histogram (0-50X)



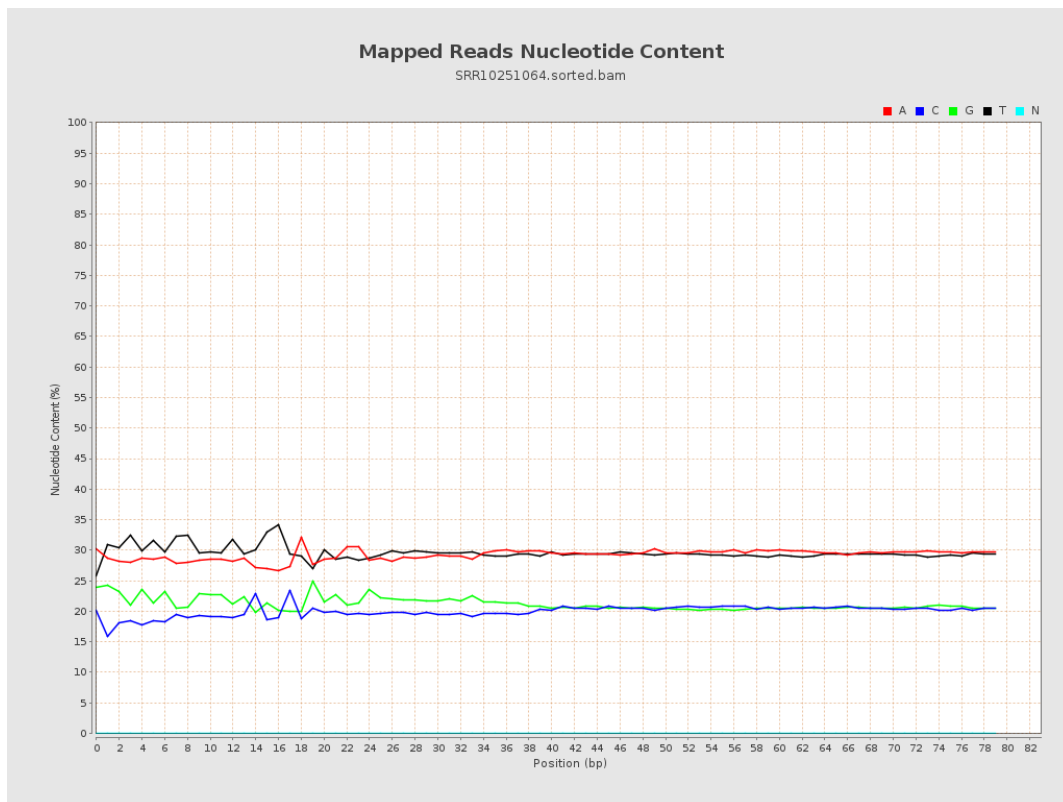
6. Results : Genome Fraction Coverage



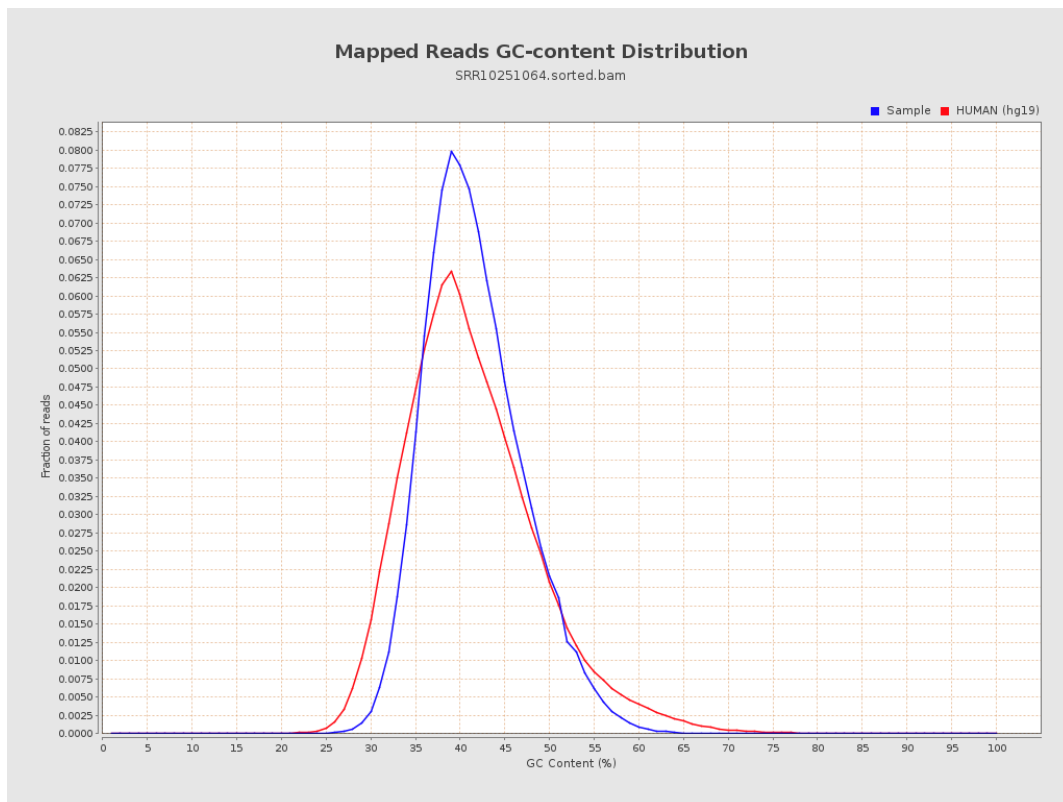
7. Results : Duplication Rate Histogram



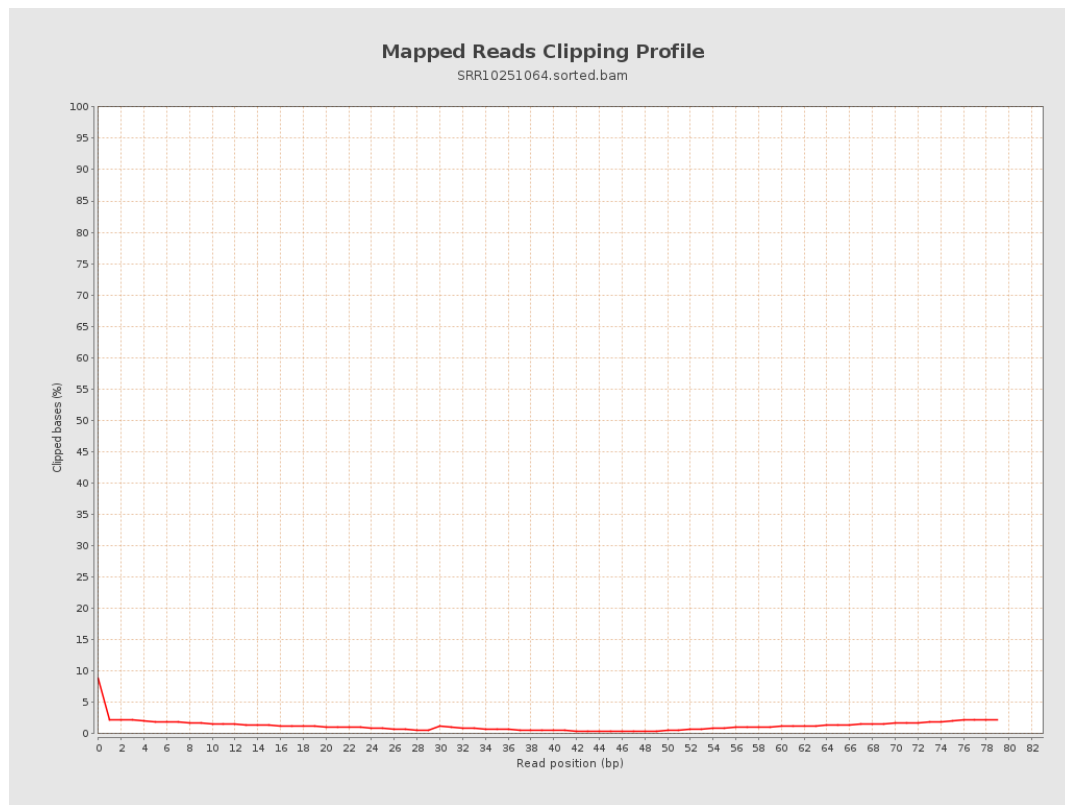
8. Results : Mapped Reads Nucleotide Content



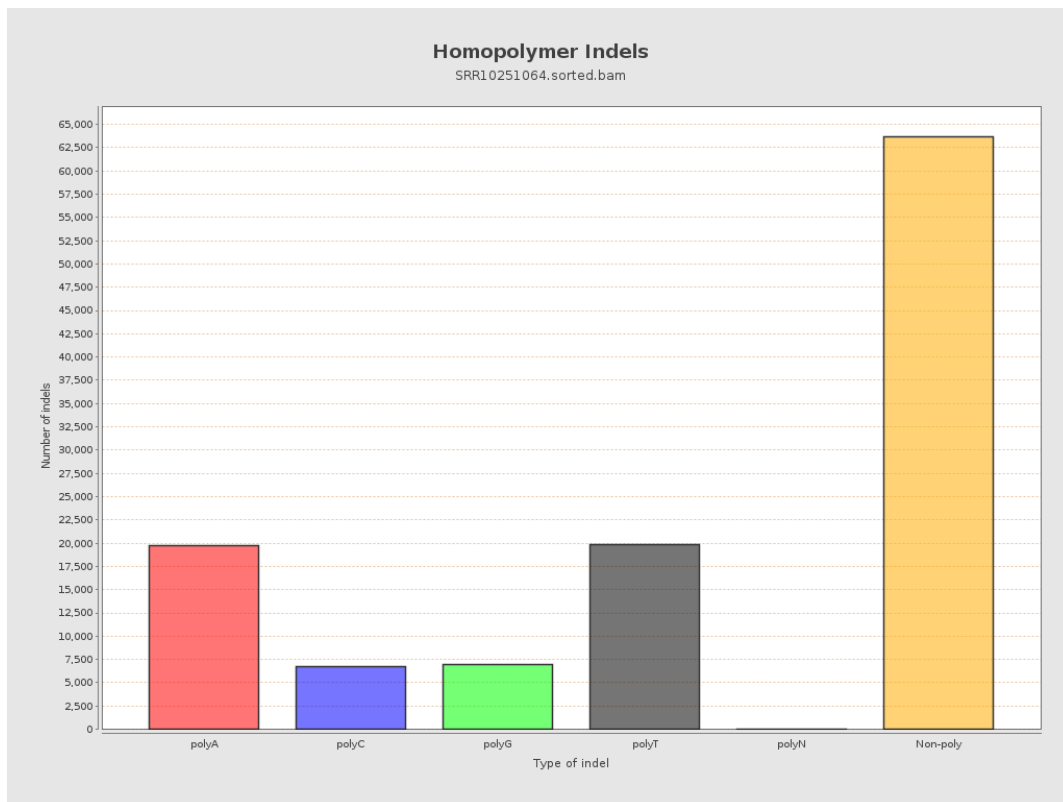
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

