

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:06:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081051.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_SRR3081051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:06:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,651,773
Mapped reads	1,163,717 / 70.45%
Unmapped reads	488,056 / 29.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,999 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	32,408 / 1.96%
Duplication rate	2.42%
Clipped reads	674,515 / 40.84%

2.2. ACGT Content

Number/percentage of A's	20,359,616 / 28.36%
Number/percentage of C's	13,651,700 / 19.02%
Number/percentage of T's	21,794,781 / 30.36%
Number/percentage of G's	15,978,497 / 22.26%
Number/percentage of N's	953 / 0%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.1954
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2.4. Mapping Quality

Mean Mapping Quality	45.9
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2.5. Mismatches and indels

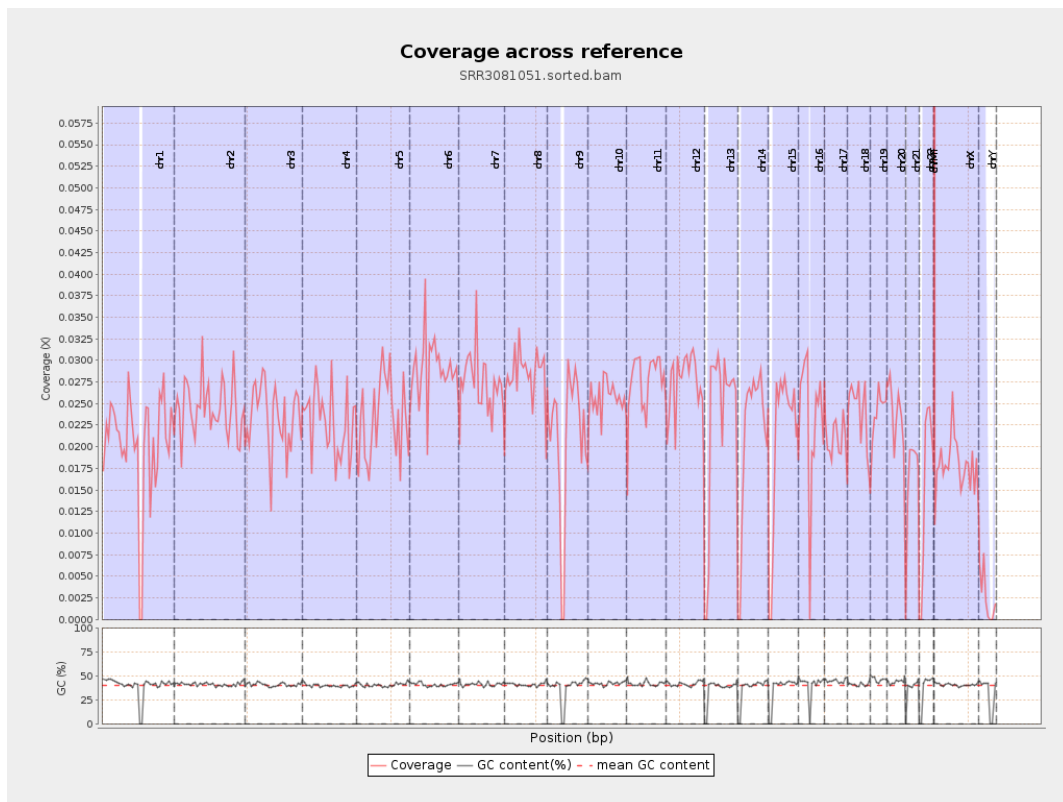
General error rate	0.74%
Mismatches	520,317
Insertions	4,614
Mapped reads with at least one insertion	0.39%
Deletions	13,328
Mapped reads with at least one deletion	1.13%
Homopolymer indels	47.44%

2.6. Chromosome stats

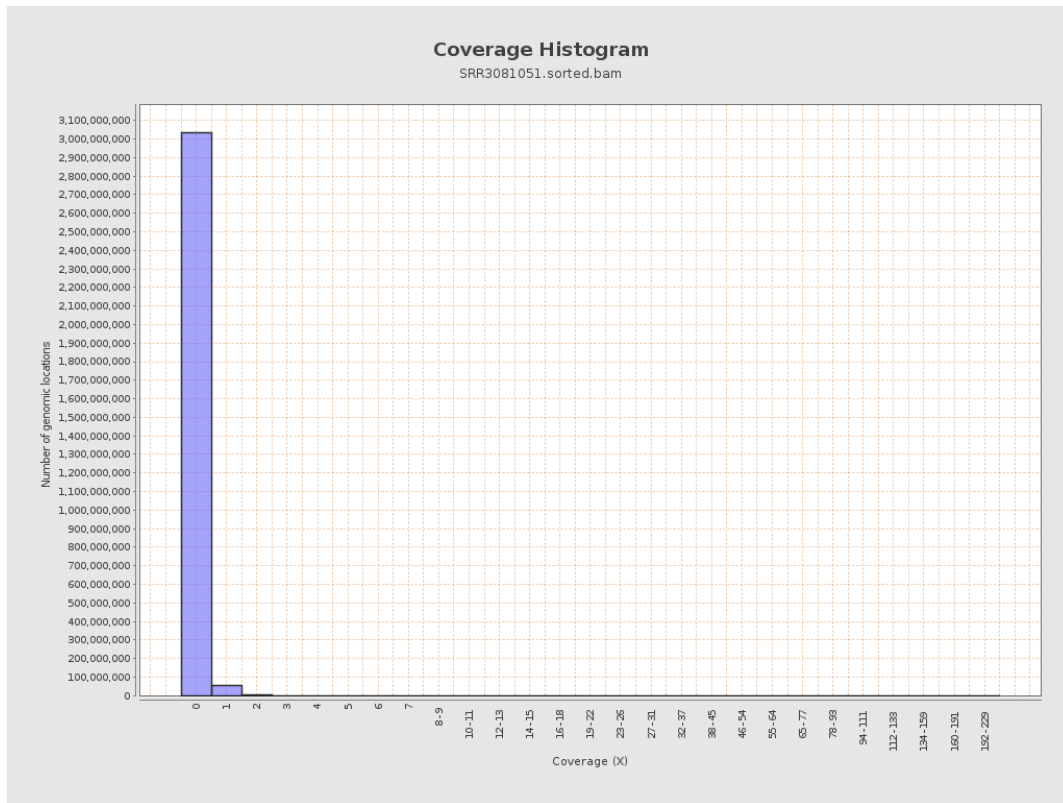
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5102621	0.0205	0.2298
chr2	243199373	5956638	0.0245	0.201
chr3	198022430	4630303	0.0234	0.1687
chr4	191154276	4366439	0.0228	0.1695
chr5	180915260	4226716	0.0234	0.1691
chr6	171115067	4953934	0.029	0.2138
chr7	159138663	4367989	0.0274	0.2785

chr8	146364022	4152089	0.0284	0.2314
chr9	141213431	2982409	0.0211	0.1813
chr10	135534747	3478262	0.0257	0.1891
chr11	135006516	3742622	0.0277	0.2064
chr12	133851895	3662823	0.0274	0.1836
chr13	115169878	2654450	0.023	0.1675
chr14	107349540	2280235	0.0212	0.1637
chr15	102531392	2135327	0.0208	0.1644
chr16	90354753	2065270	0.0229	0.1717
chr17	81195210	1688318	0.0208	0.1678
chr18	78077248	1897690	0.0243	0.2897
chr19	59128983	1417960	0.024	0.2161
chr20	63025520	1469354	0.0233	0.1698
chr21	48129895	796887	0.0166	0.1472
chr22	51304566	806306	0.0157	0.137
chrMT	16571	30188	1.8217	1.612
chrX	155270560	2794397	0.018	0.1556
chrY	59373566	149158	0.0025	0.0633

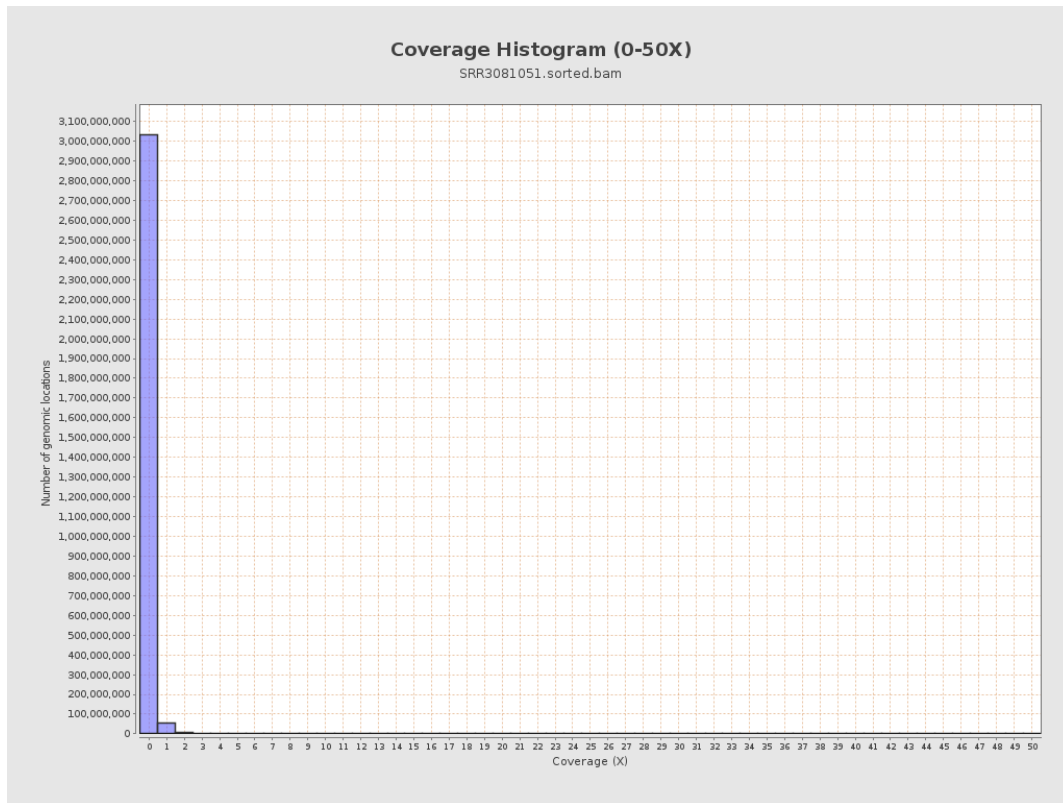
3. Results : Coverage across reference



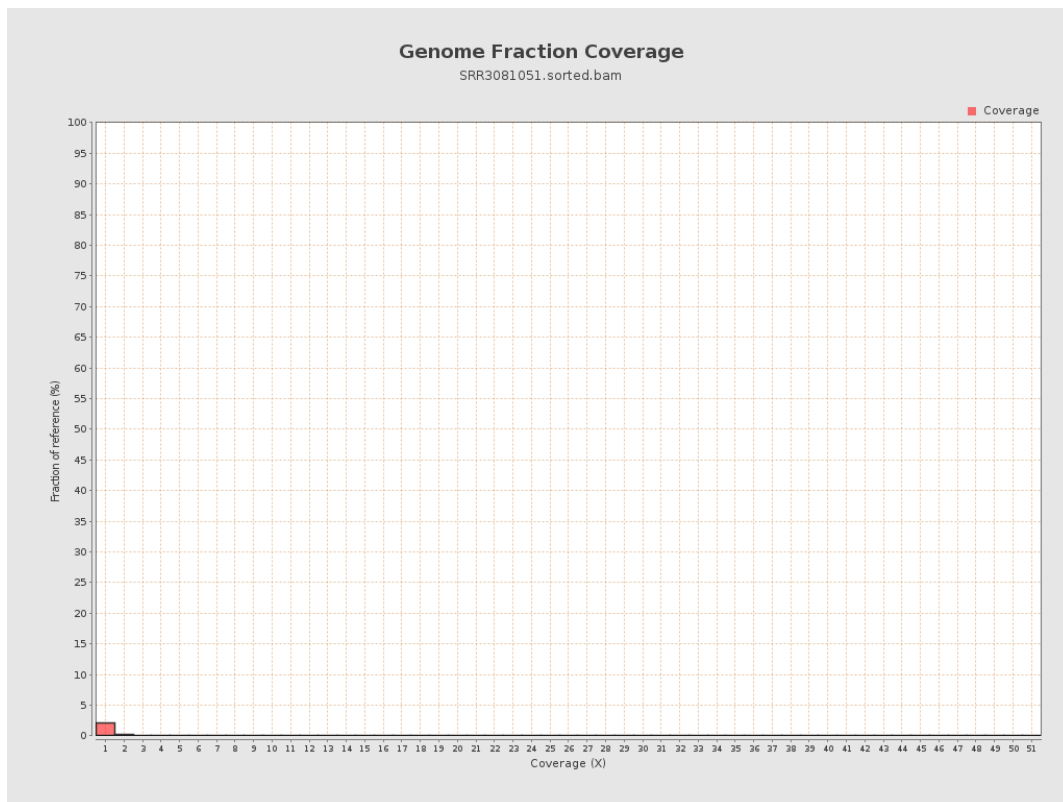
4. Results : Coverage Histogram



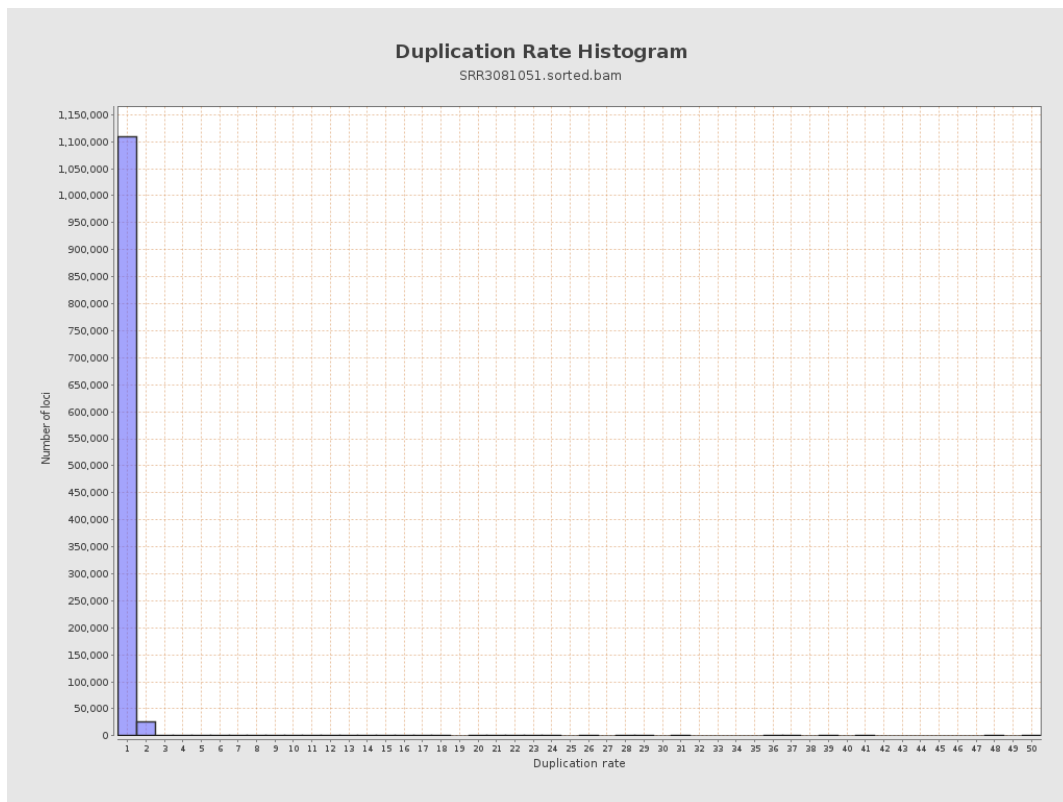
5. Results : Coverage Histogram (0-50X)



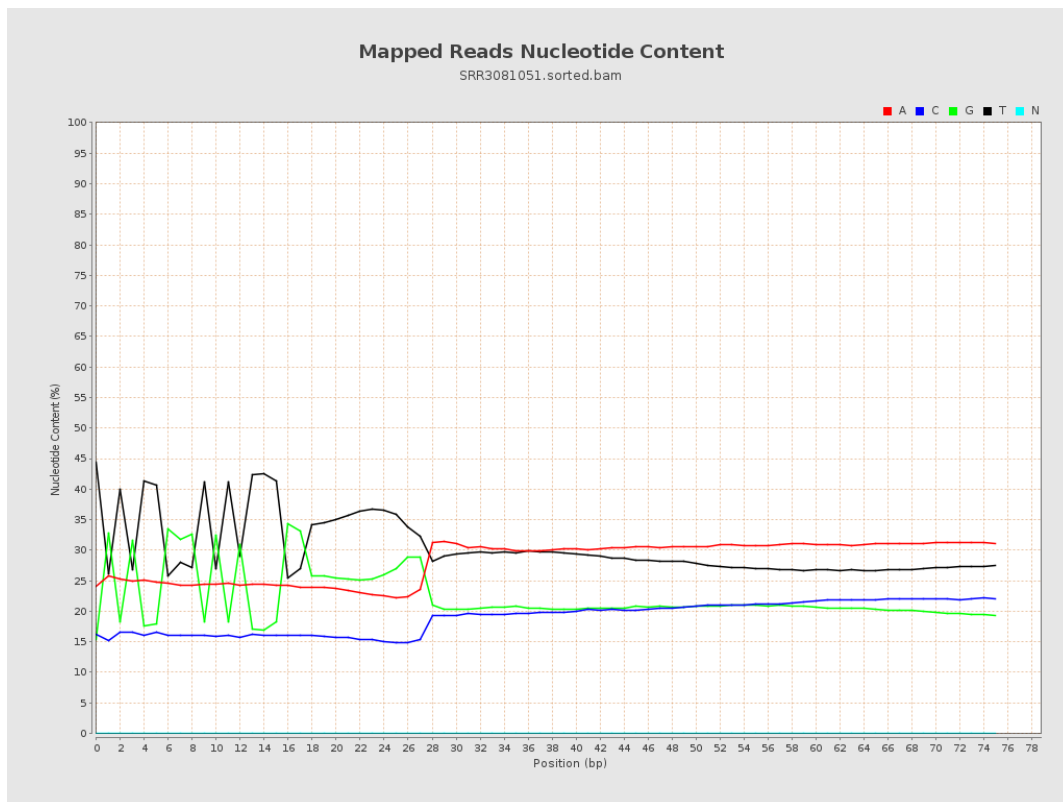
6. Results : Genome Fraction Coverage



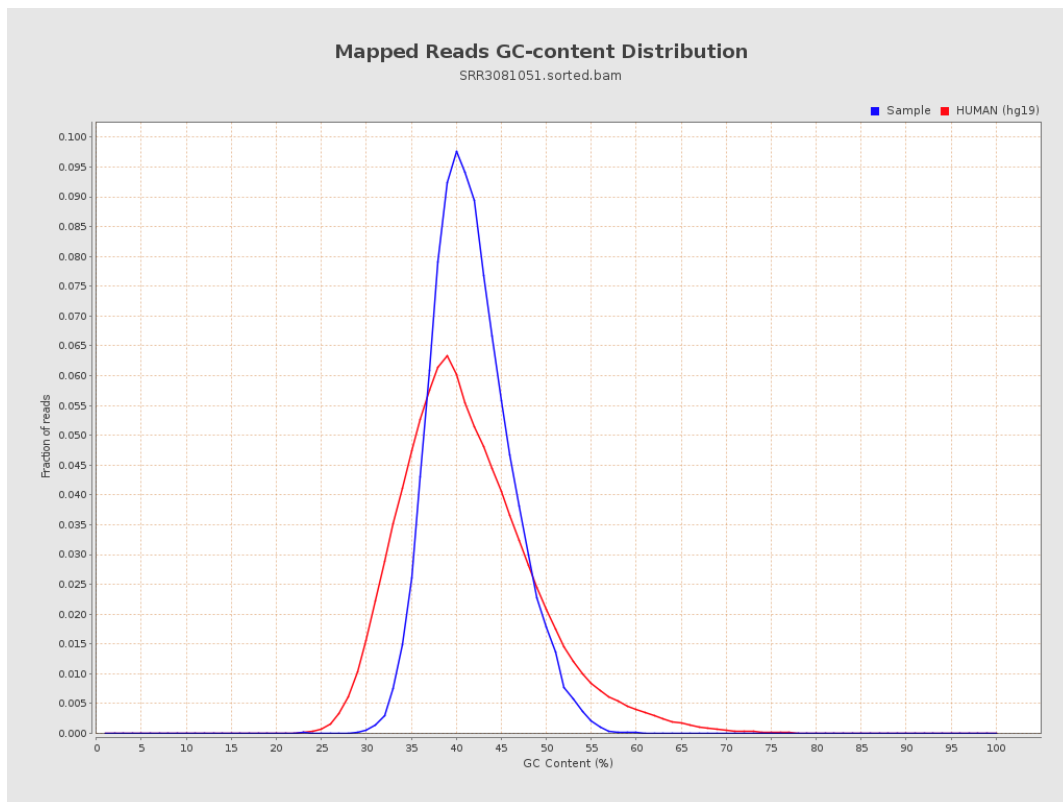
7. Results : Duplication Rate Histogram



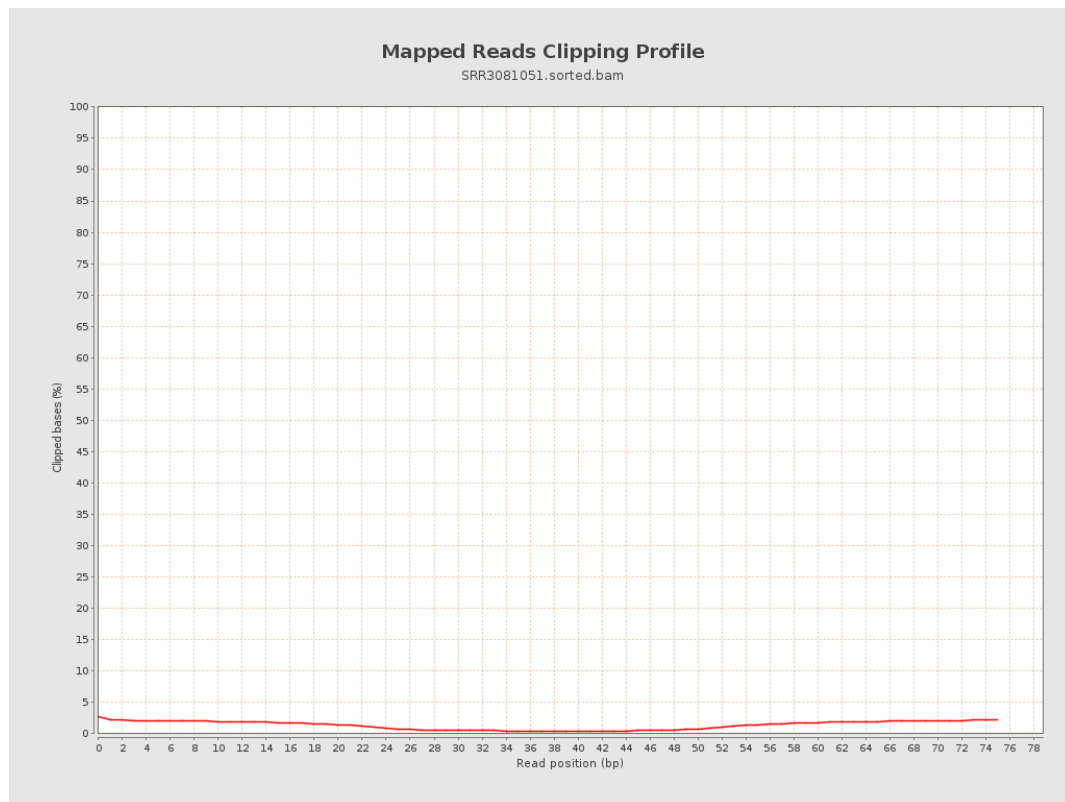
8. Results : Mapped Reads Nucleotide Content



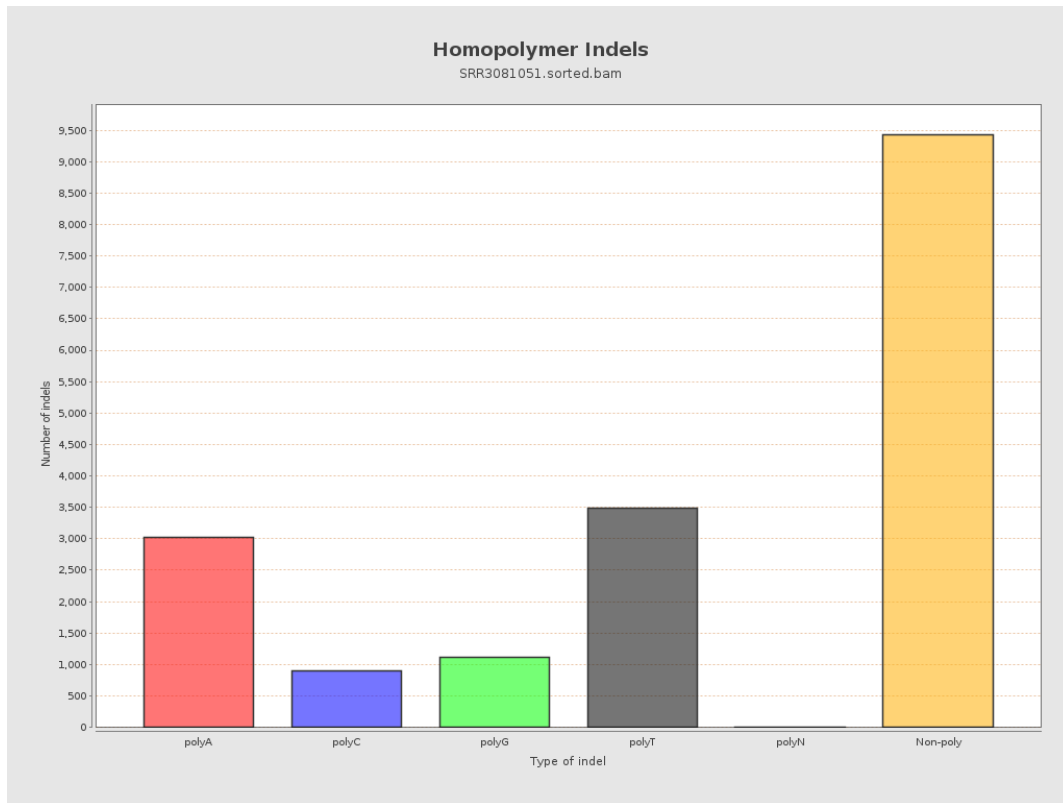
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

