

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 12:06:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251072.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_SRR10251072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 12:06:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,172,811
Mapped reads	3,982,783 / 95.45%
Unmapped reads	190,028 / 4.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,607 / 0.69%
Read min/max/mean length	30 / 80 / 80.25
Duplicated reads (estimated)	943,430 / 22.61%
Duplication rate	20.91%
Clipped reads	513,106 / 12.3%

2.2. ACGT Content

Number/percentage of A's	89,825,703 / 29.05%
Number/percentage of C's	61,685,344 / 19.95%
Number/percentage of T's	91,429,672 / 29.56%
Number/percentage of G's	66,315,787 / 21.44%
Number/percentage of N's	2,781 / 0%
GC Percentage	41.39%

2.3. Coverage

Mean	0.1

Standard Deviation	1.081
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	48.2
----------------------	------

2.5. Mismatches and indels

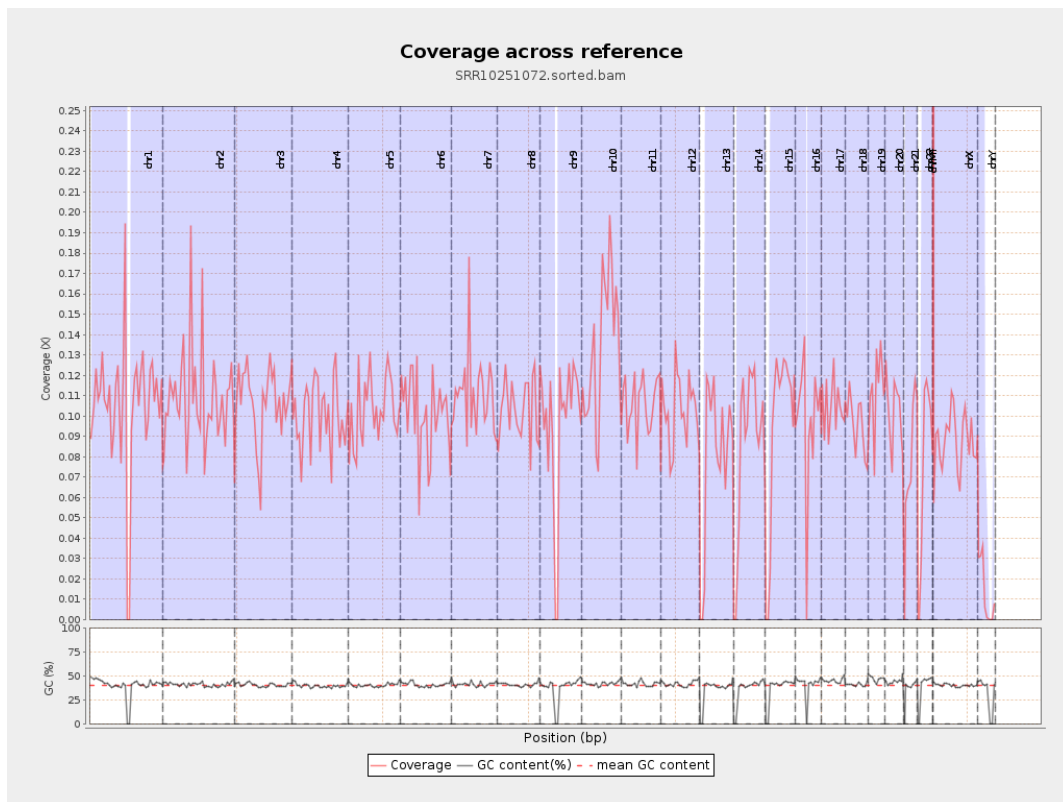
General error rate	0.6%
Mismatches	1,770,332
Insertions	37,418
Mapped reads with at least one insertion	0.92%
Deletions	109,664
Mapped reads with at least one deletion	2.71%
Homopolymer indels	45.02%

2.6. Chromosome stats

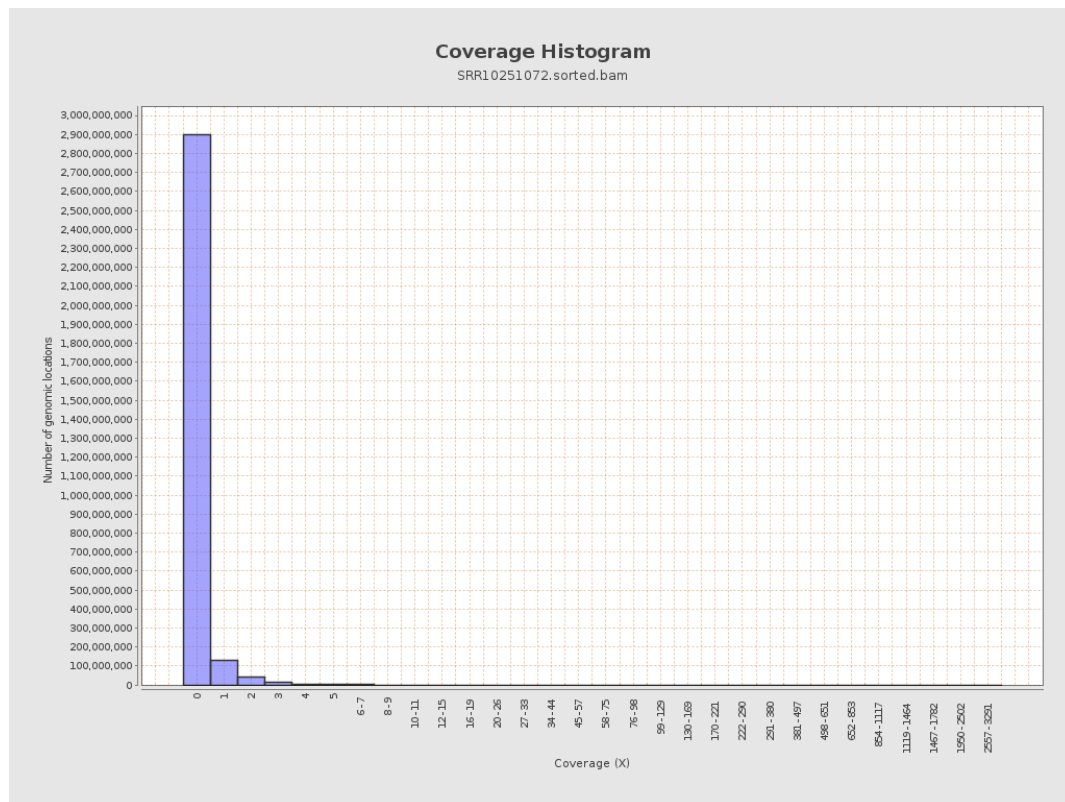
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26192679	0.1051	2.2982
chr2	243199373	26595021	0.1094	1.4282
chr3	198022430	21052328	0.1063	0.4799
chr4	191154276	19180985	0.1003	0.5384
chr5	180915260	18711881	0.1034	0.4921
chr6	171115067	17214120	0.1006	0.5971
chr7	159138663	17572652	0.1104	1.58

chr8	146364022	15051828	0.1028	0.6615
chr9	141213431	13506941	0.0956	1.0768
chr10	135534747	18202616	0.1343	1.0762
chr11	135006516	14259547	0.1056	0.6668
chr12	133851895	13938251	0.1041	0.492
chr13	115169878	9183600	0.0797	0.4064
chr14	107349540	9378754	0.0874	0.7289
chr15	102531392	9465231	0.0923	0.441
chr16	90354753	8762429	0.097	0.8829
chr17	81195210	8545493	0.1052	0.5692
chr18	78077248	7516540	0.0963	1.2366
chr19	59128983	6624066	0.112	2.1747
chr20	63025520	6372915	0.1011	0.5215
chr21	48129895	3730362	0.0775	0.4299
chr22	51304566	3848502	0.075	0.4258
chrMT	16571	111343	6.7191	5.5859
chrX	155270560	13642134	0.0879	0.5227
chrY	59373566	796001	0.0134	0.9431

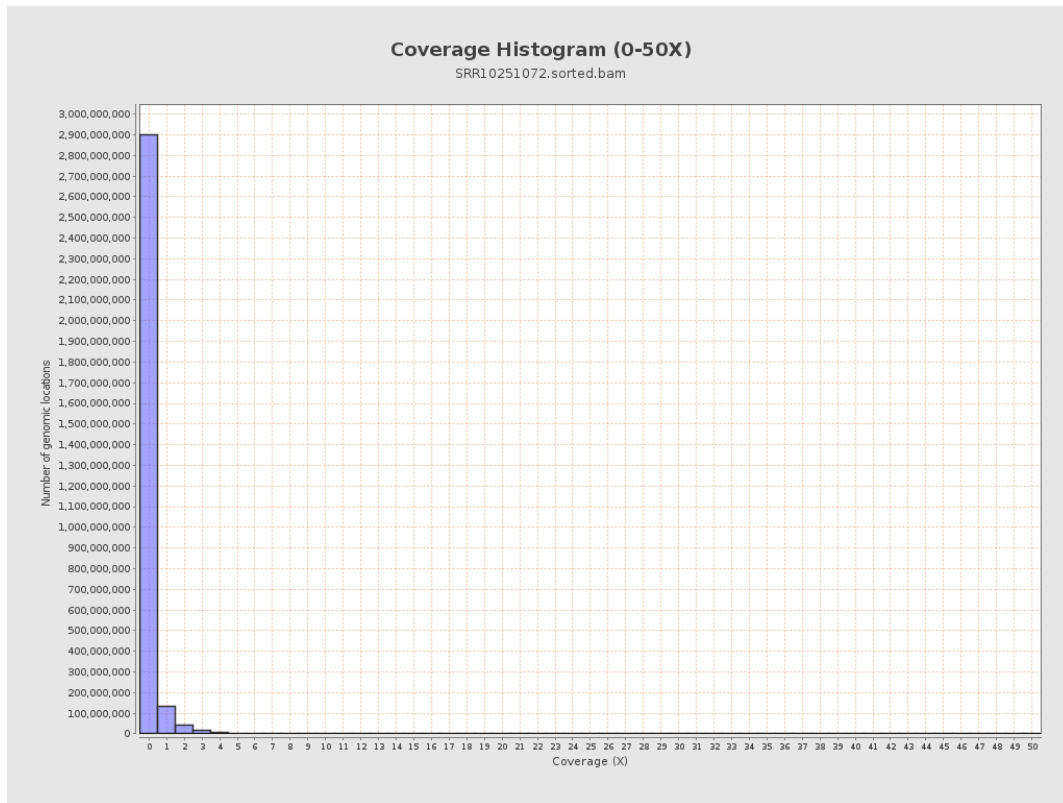
3. Results : Coverage across reference



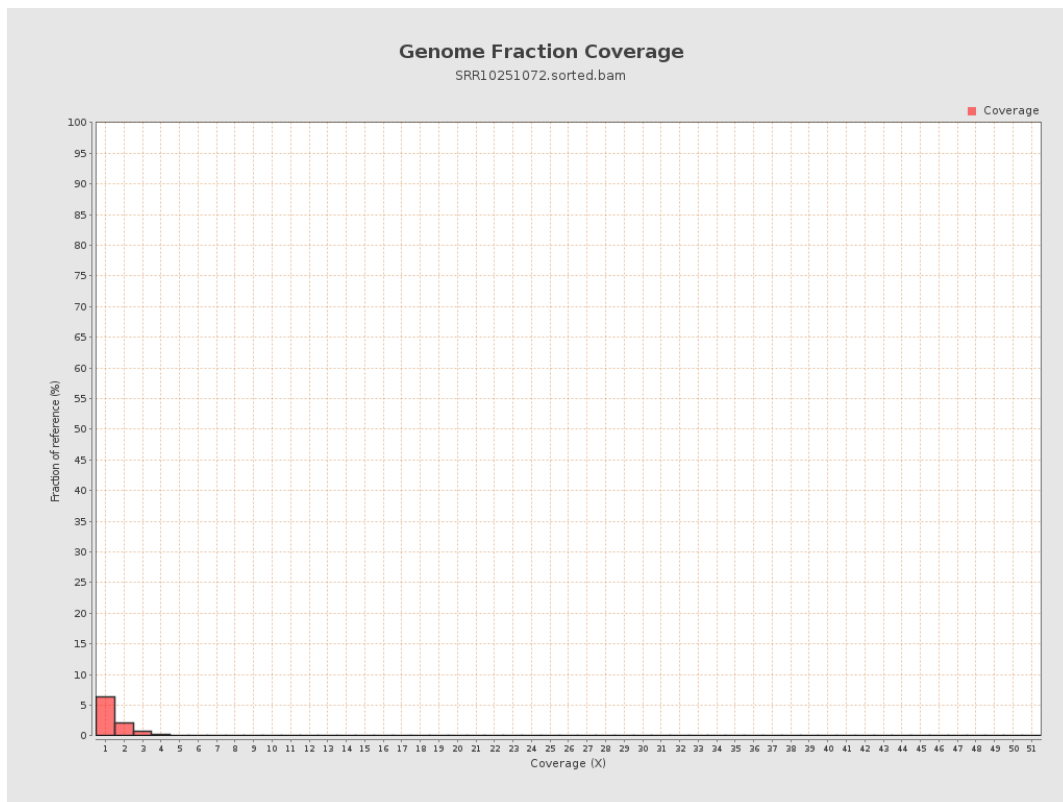
4. Results : Coverage Histogram



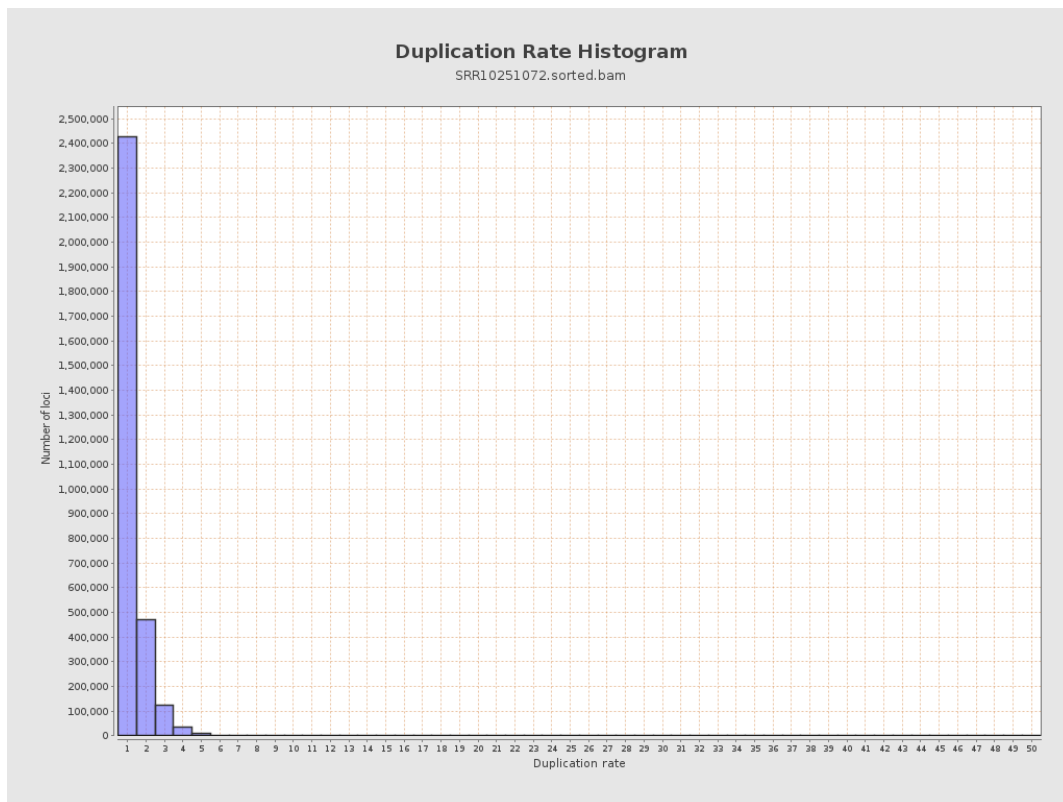
5. Results : Coverage Histogram (0-50X)



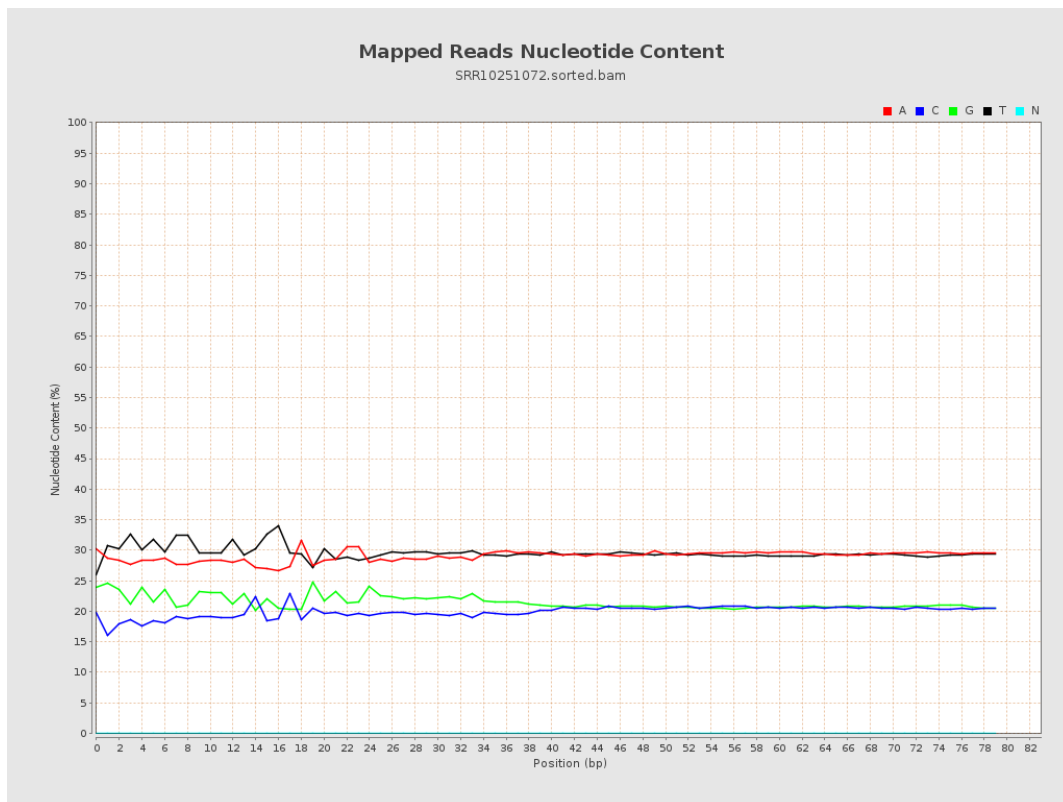
6. Results : Genome Fraction Coverage



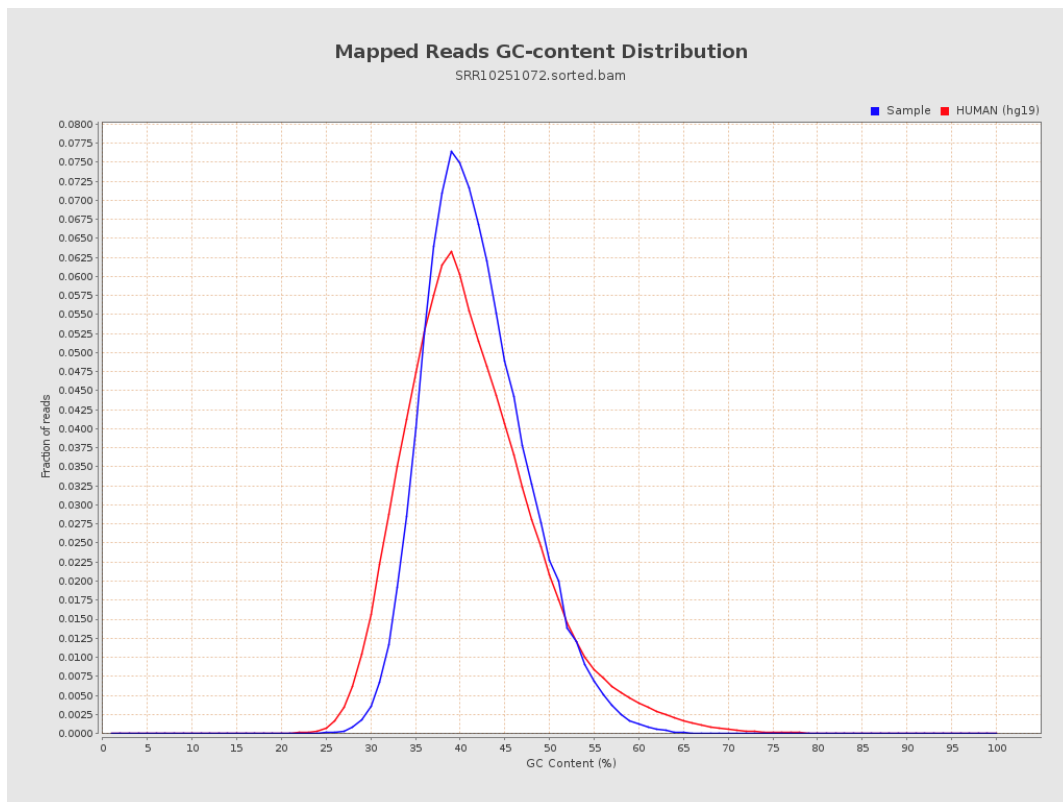
7. Results : Duplication Rate Histogram



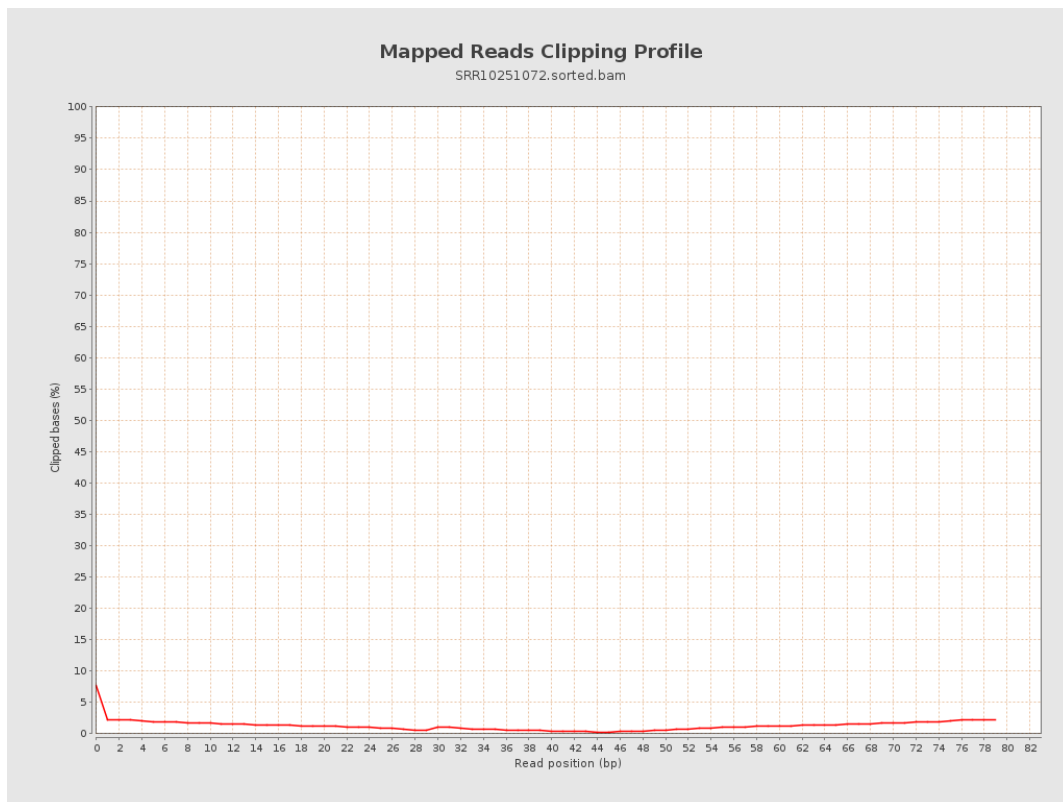
8. Results : Mapped Reads Nucleotide Content



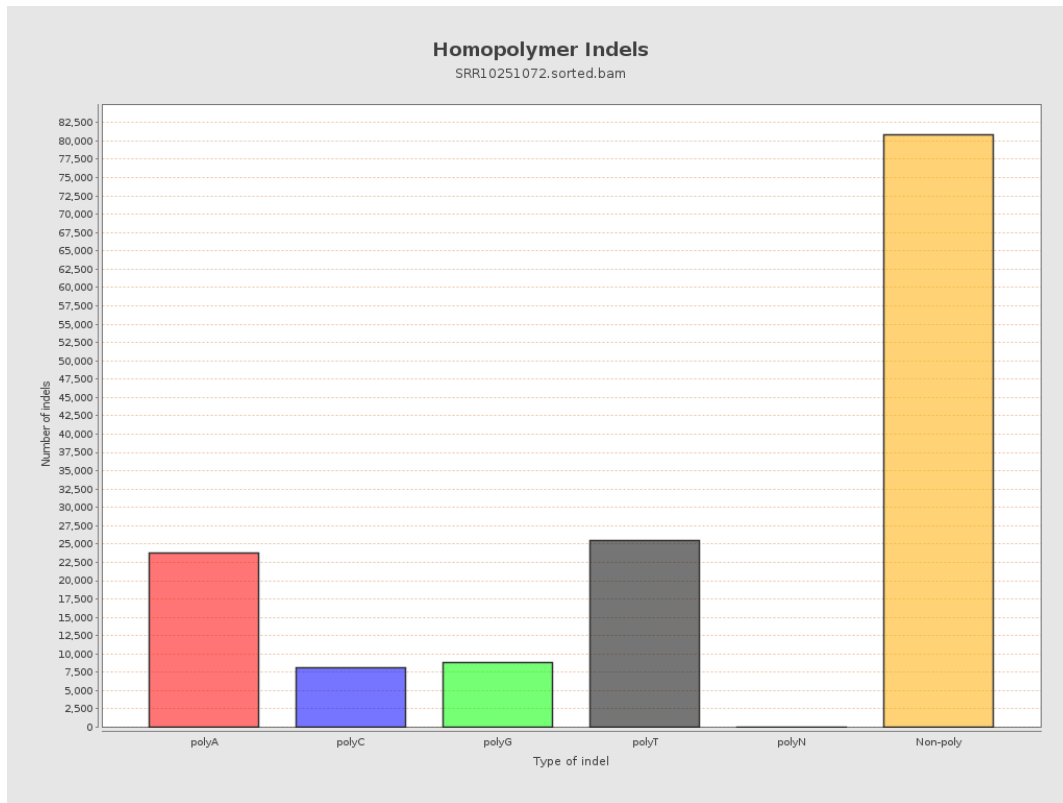
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

