

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:24:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084862.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_SRR3084862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:24:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,972,464
Mapped reads	1,691,356 / 85.75%
Unmapped reads	281,108 / 14.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,255 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	73,590 / 3.73%
Duplication rate	2.99%
Clipped reads	594,302 / 30.13%

2.2. ACGT Content

Number/percentage of A's	34,130,872 / 29.18%
Number/percentage of C's	21,547,670 / 18.42%
Number/percentage of T's	36,790,707 / 31.46%
Number/percentage of G's	24,470,284 / 20.92%
Number/percentage of N's	18,333 / 0.02%
GC Percentage	39.35%

2.3. Coverage

Mean	0.0378

Standard Deviation	0.5044
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2.4. Mapping Quality

Mean Mapping Quality	45.61
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2.5. Mismatches and indels

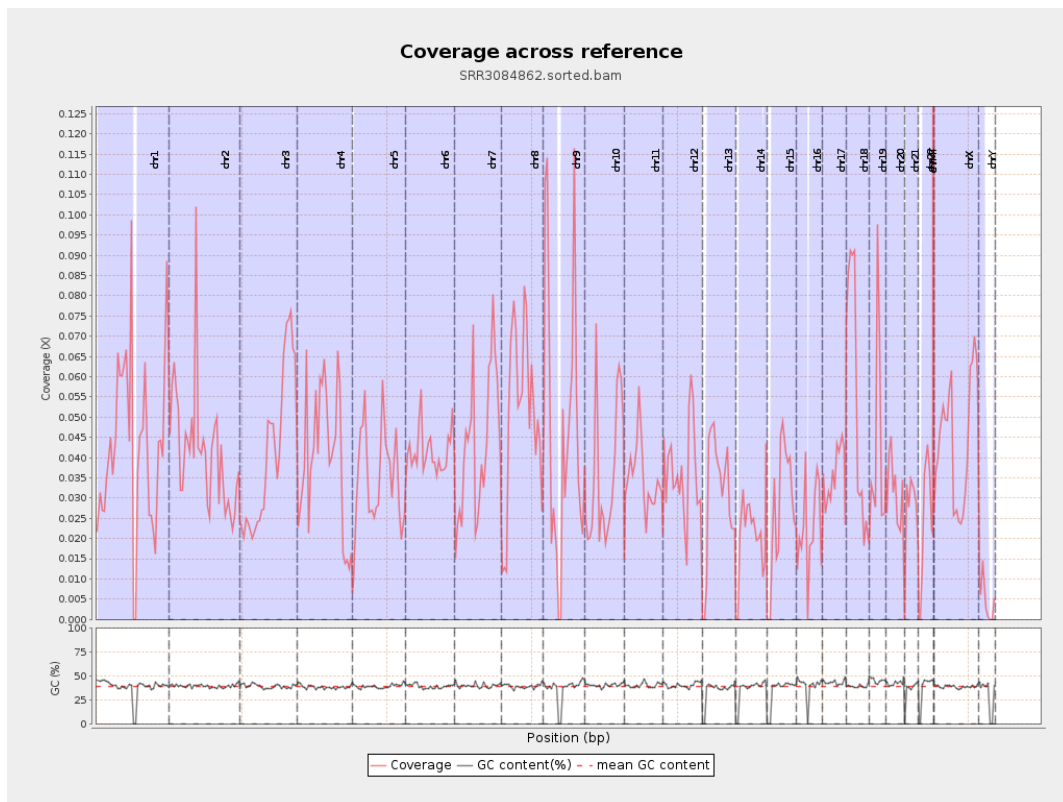
General error rate	0.94%
Mismatches	1,086,547
Insertions	10,197
Mapped reads with at least one insertion	0.6%
Deletions	27,819
Mapped reads with at least one deletion	1.63%
Homopolymer indels	47.14%

2.6. Chromosome stats

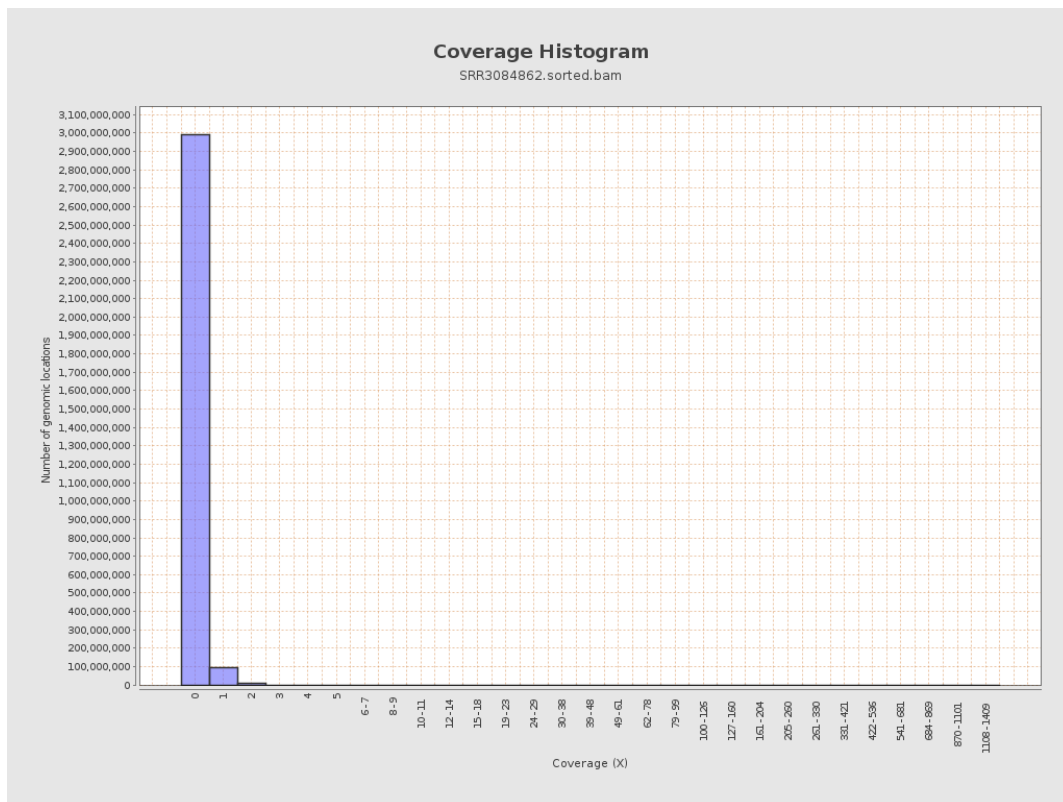
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10732475	0.0431	1.1921
chr2	243199373	10111955	0.0416	0.5115
chr3	198022430	8129583	0.0411	0.2216
chr4	191154276	7602662	0.0398	0.2239
chr5	180915260	6374623	0.0352	0.2249
chr6	171115067	7103191	0.0415	0.2371
chr7	159138663	6931165	0.0436	0.4293

chr8	146364022	7360889	0.0503	0.8628
chr9	141213431	6601922	0.0468	0.4245
chr10	135534747	4744130	0.035	0.372
chr11	135006516	4636369	0.0343	0.3584
chr12	133851895	4880879	0.0365	0.2175
chr13	115169878	3481485	0.0302	0.1858
chr14	107349540	2122544	0.0198	0.1911
chr15	102531392	2814290	0.0274	0.1803
chr16	90354753	2060725	0.0228	0.2277
chr17	81195210	2916434	0.0359	0.2389
chr18	78077248	4187888	0.0536	0.8848
chr19	59128983	2538414	0.0429	0.6371
chr20	63025520	1998335	0.0317	0.2277
chr21	48129895	1304078	0.0271	0.1959
chr22	51304566	1219748	0.0238	0.1648
chrMT	16571	12107	0.7306	0.9332
chrX	155270560	6867765	0.0442	0.2828
chrY	59373566	273282	0.0046	0.1116

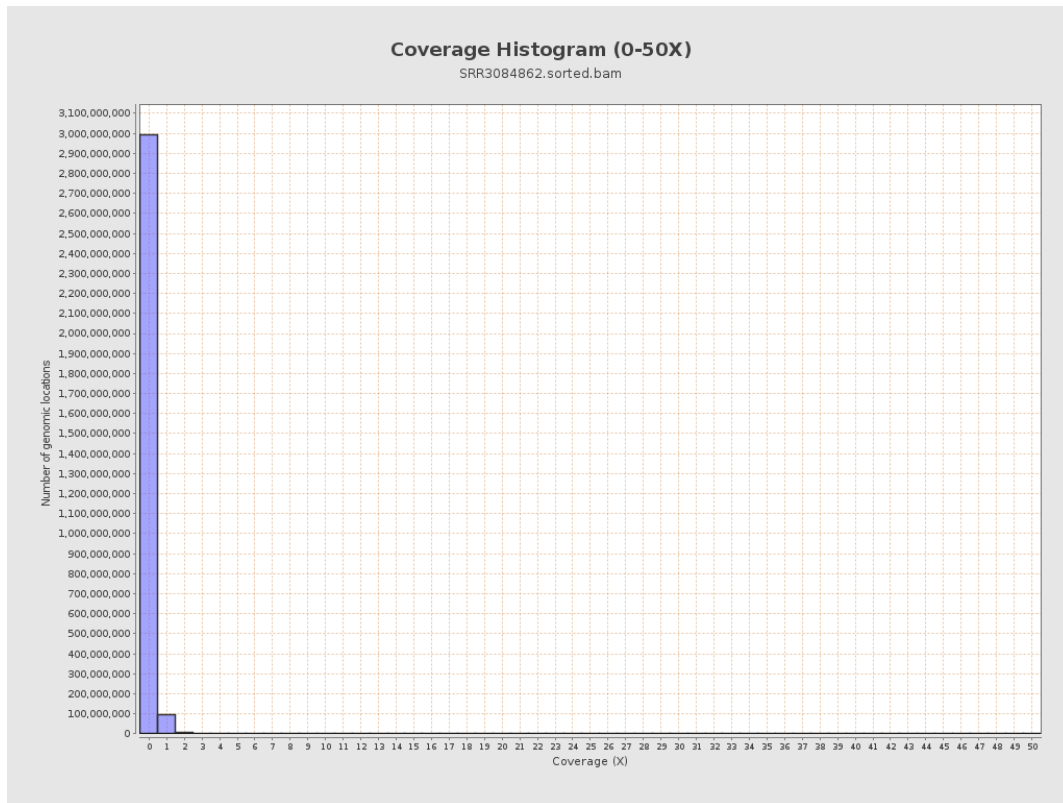
3. Results : Coverage across reference



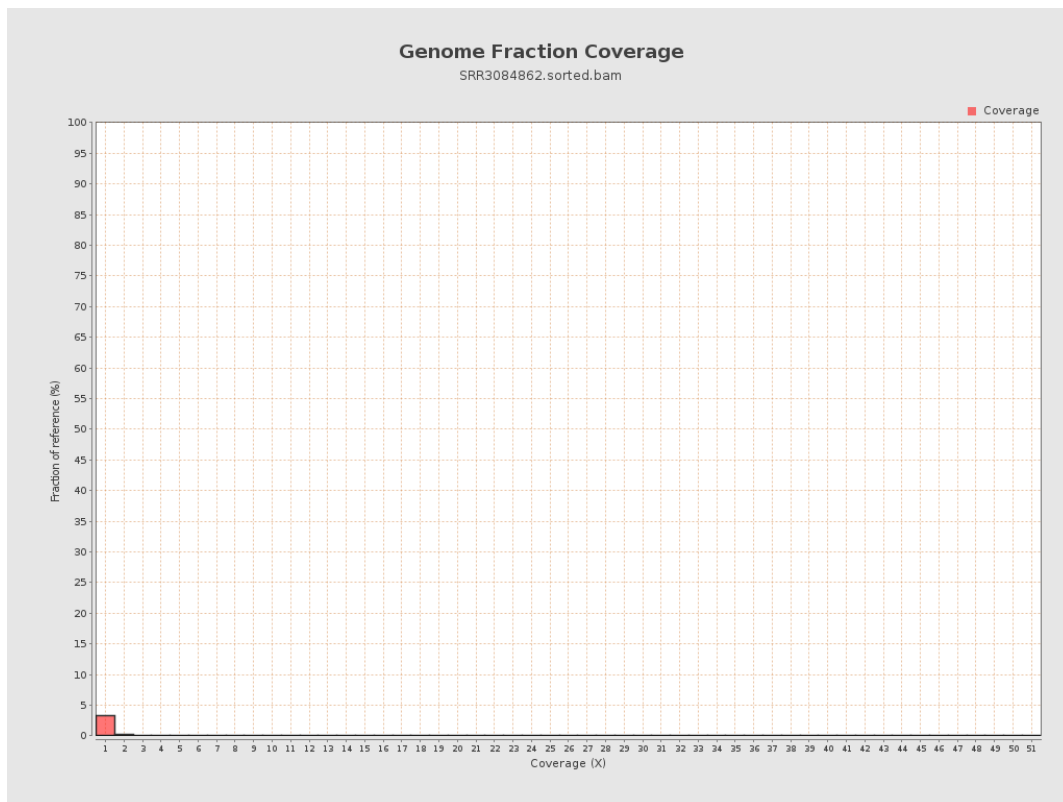
4. Results : Coverage Histogram



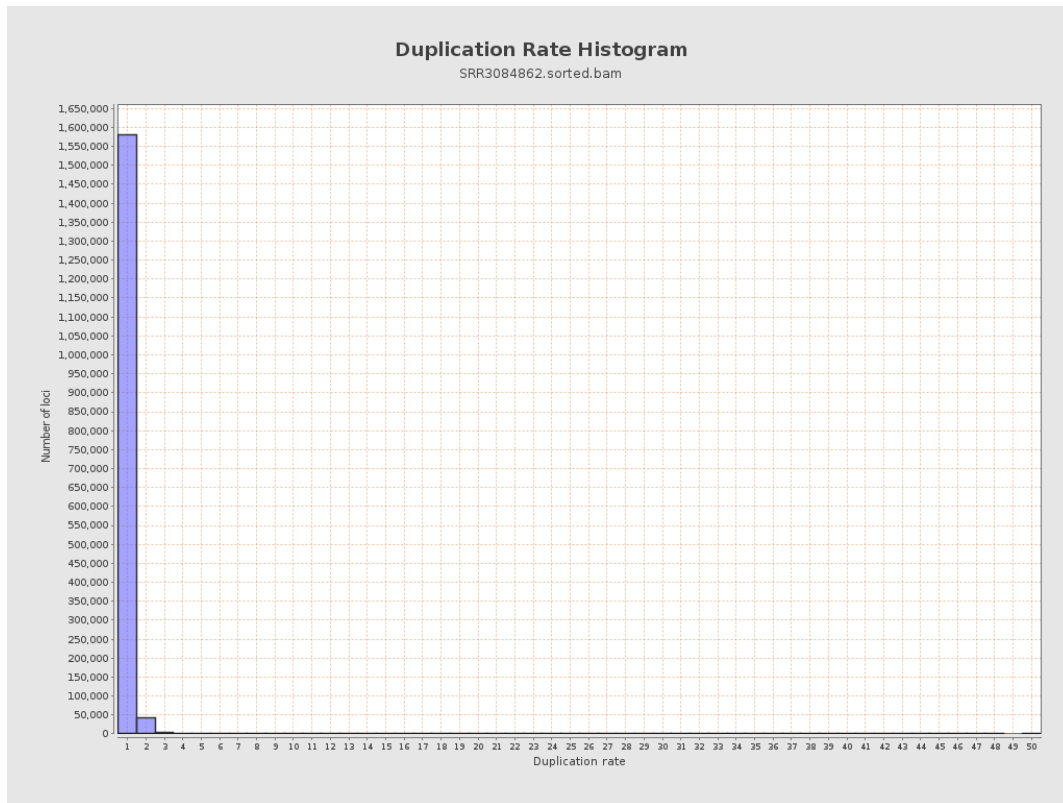
5. Results : Coverage Histogram (0-50X)



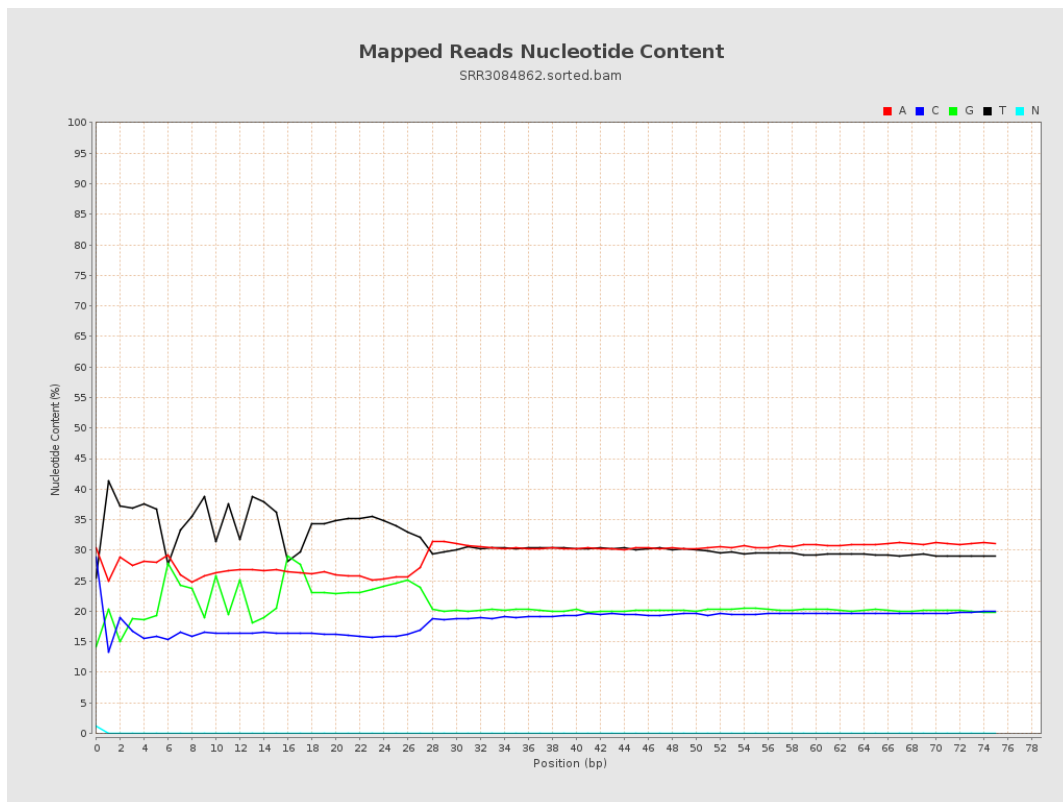
6. Results : Genome Fraction Coverage



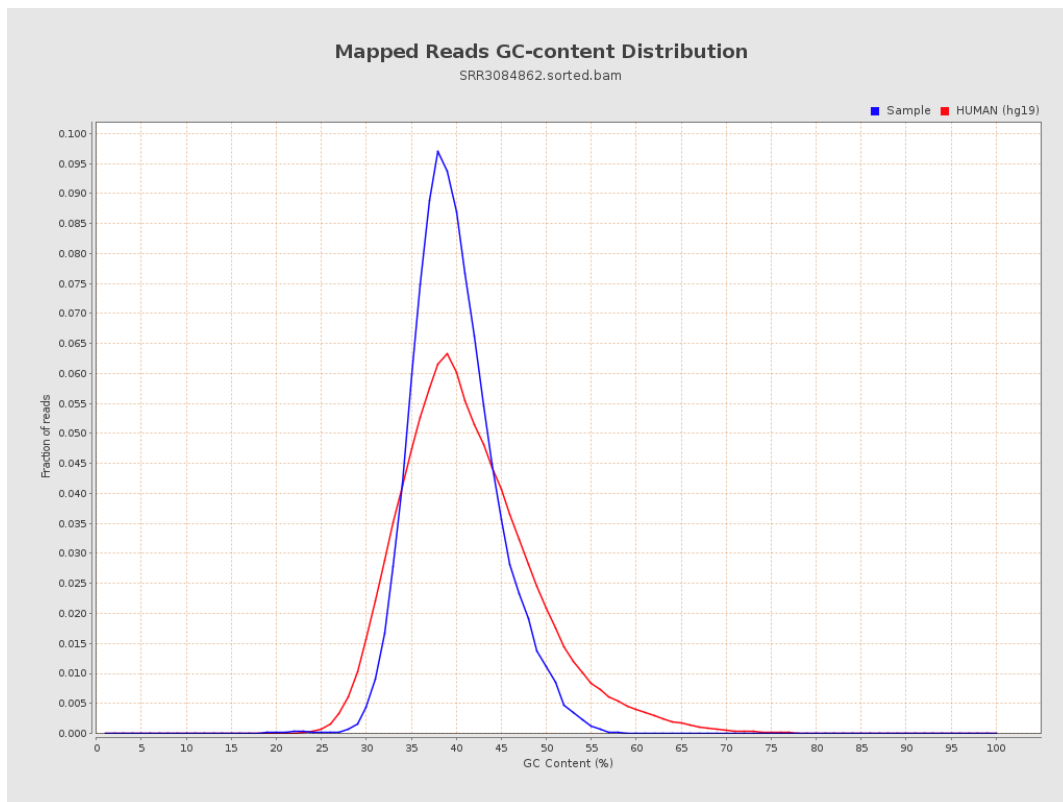
7. Results : Duplication Rate Histogram



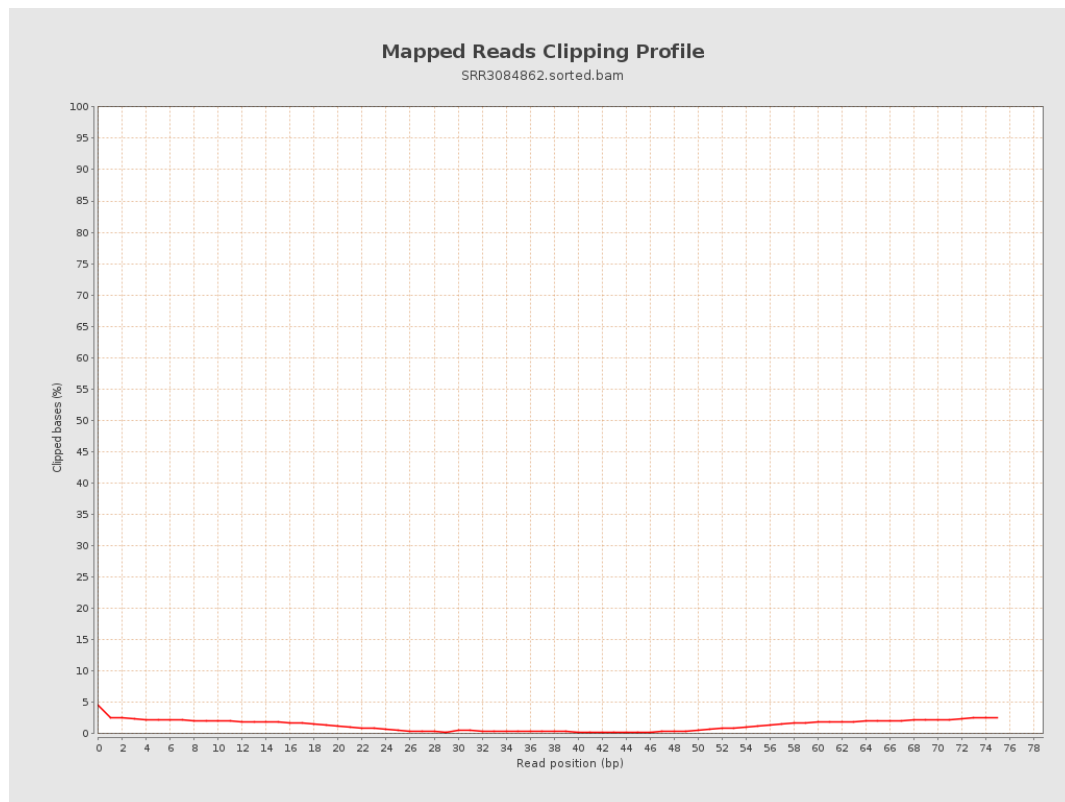
8. Results : Mapped Reads Nucleotide Content



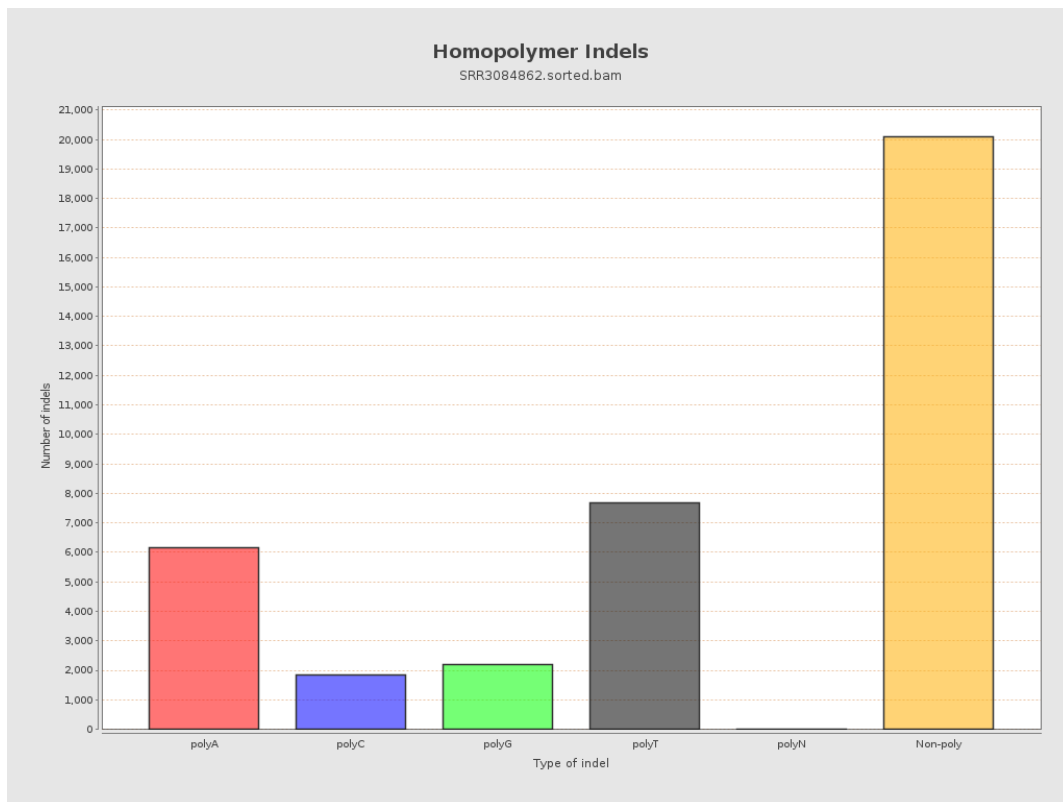
9. Results : Mapped Reads GC-content Distribution



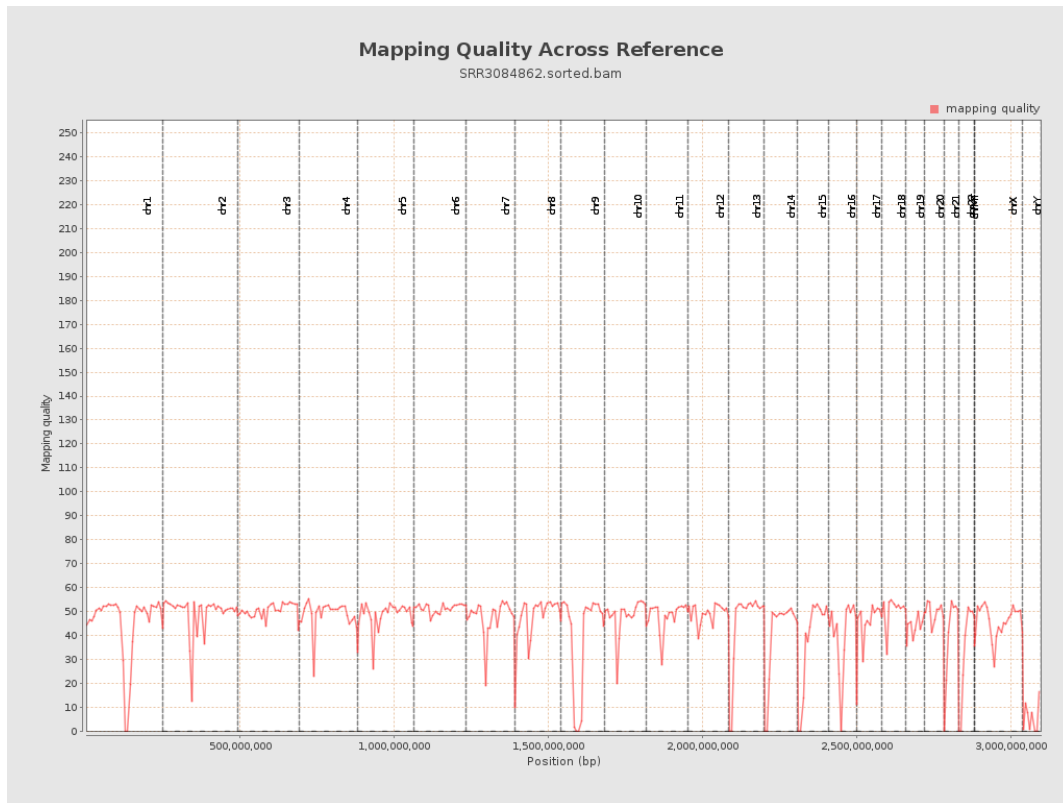
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

