Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:49:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084872.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_SRR3084872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084872.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:49:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,809
Mapped reads	1,748,992 / 86.12%
Unmapped reads	281,817 / 13.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,655 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	69,288 / 3.41%
Duplication rate	3.07%
Clipped reads	608,237 / 29.95%

2.2. ACGT Content

Number/percentage of A's	35,206,031 / 29.11%
Number/percentage of C's	22,253,123 / 18.4%
Number/percentage of T's	38,302,519 / 31.67%
Number/percentage of G's	25,171,487 / 20.81%
Number/percentage of N's	19,282 / 0.02%
GC Percentage	39.21%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3933

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

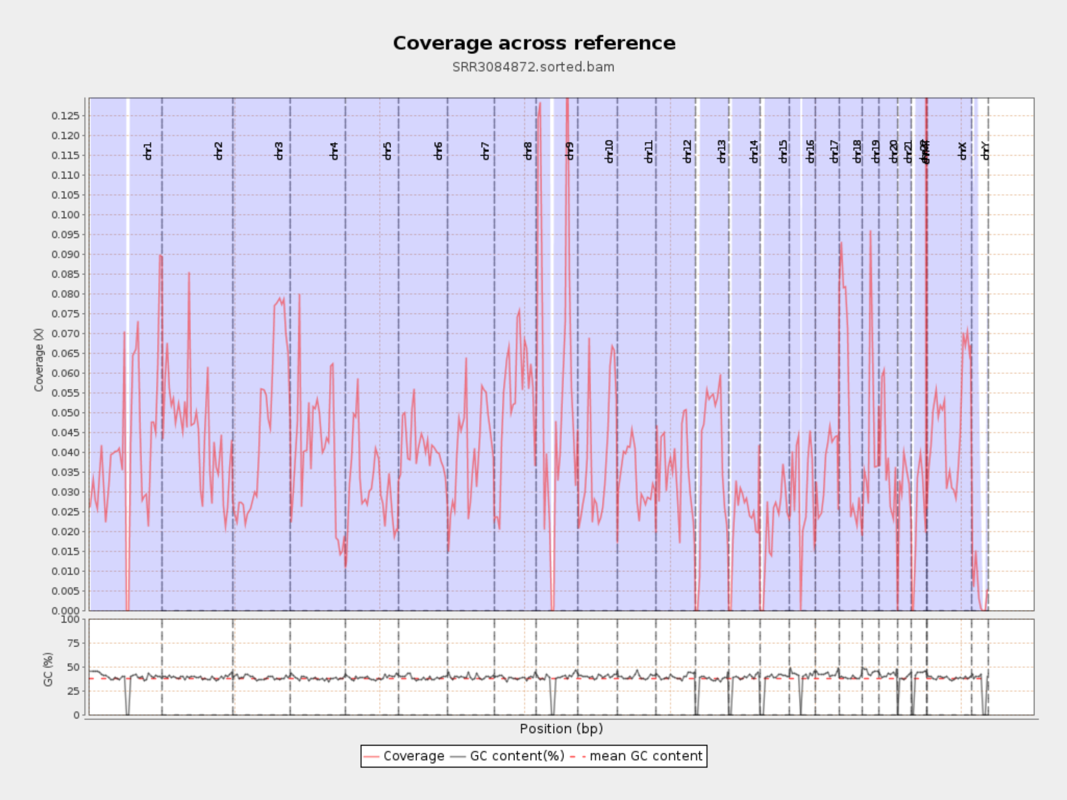
General error rate	0.9%
Mismatches	1,070,175
Insertions	10,465
Mapped reads with at least one insertion	0.59%
Deletions	26,582
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.76%

2.6. Chromosome stats

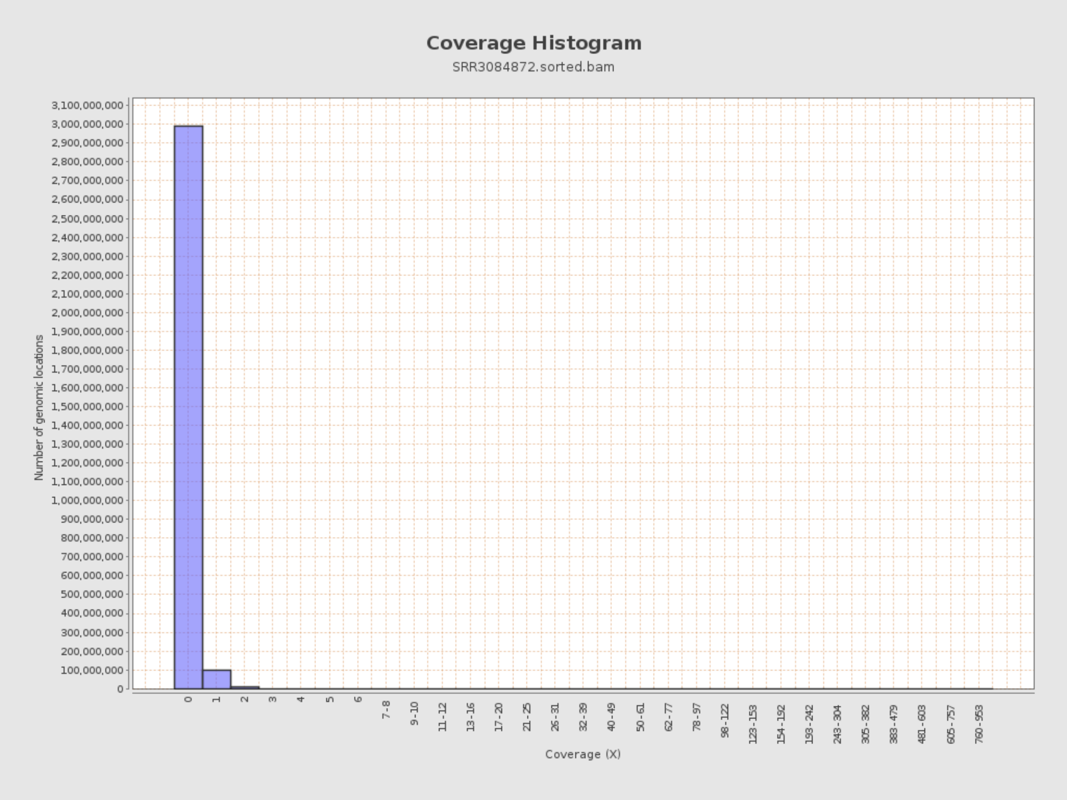
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9982534	0.0401	0.8336
chr2	243199373	10911938	0.0449	0.4139
chr3	198022430	9231939	0.0466	0.2368
chr4	191154276	7646066	0.04	0.2311
chr5	180915260	5742222	0.0317	0.2033
chr6	171115067	7015855	0.041	0.2297
chr7	159138663	6451613	0.0405	0.3473

chr8	146364022	7725855	0.0528	0.661
chr9	141213431	8074079	0.0572	0.3898
chr10	135534747	5109776	0.0377	0.3467
chr11	135006516	4465802	0.0331	0.2796
chr12	133851895	4857208	0.0363	0.2118
chr13	115169878	4408136	0.0383	0.2121
chr14	107349540	2405460	0.0224	0.1793
chr15	102531392	2147309	0.0209	0.157
chr16	90354753	2703537	0.0299	0.2248
chr17	81195210	2945676	0.0363	0.2183
chr18	78077248	3900526	0.05	0.6873
chr19	59128983	2718509	0.046	0.4872
chr20	63025520	2409917	0.0382	0.2245
chr21	48129895	1418668	0.0295	0.2025
chr22	51304566	1159930	0.0226	0.162
chrMT	16571	32767	1.9774	1.7021
chrX	155270560	7248645	0.0467	0.2586
chrY	59373566	285180	0.0048	0.1154

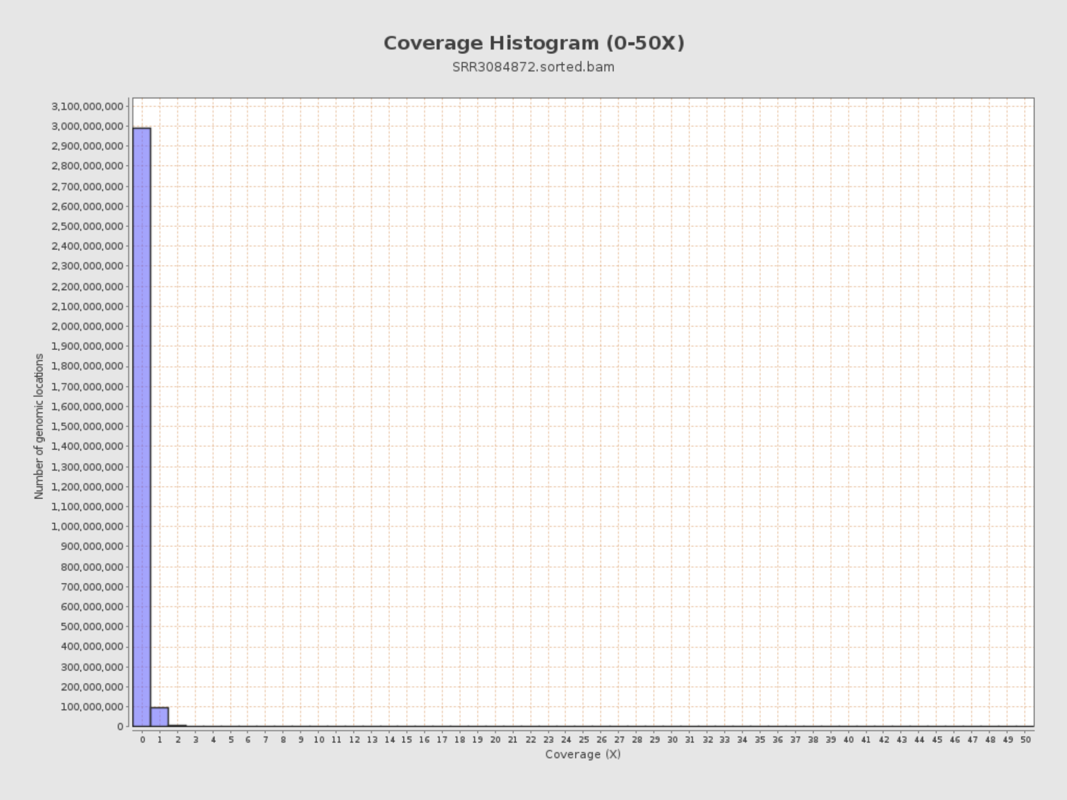
3. Results : Coverage across reference



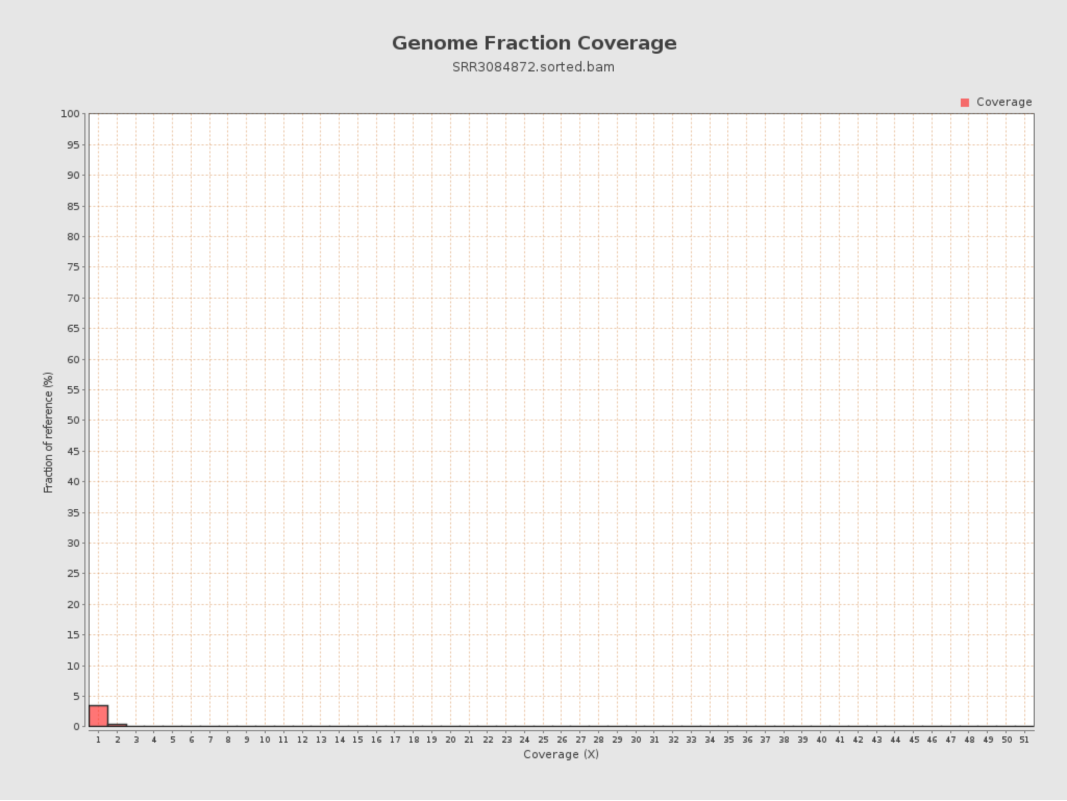
4. Results : Coverage Histogram



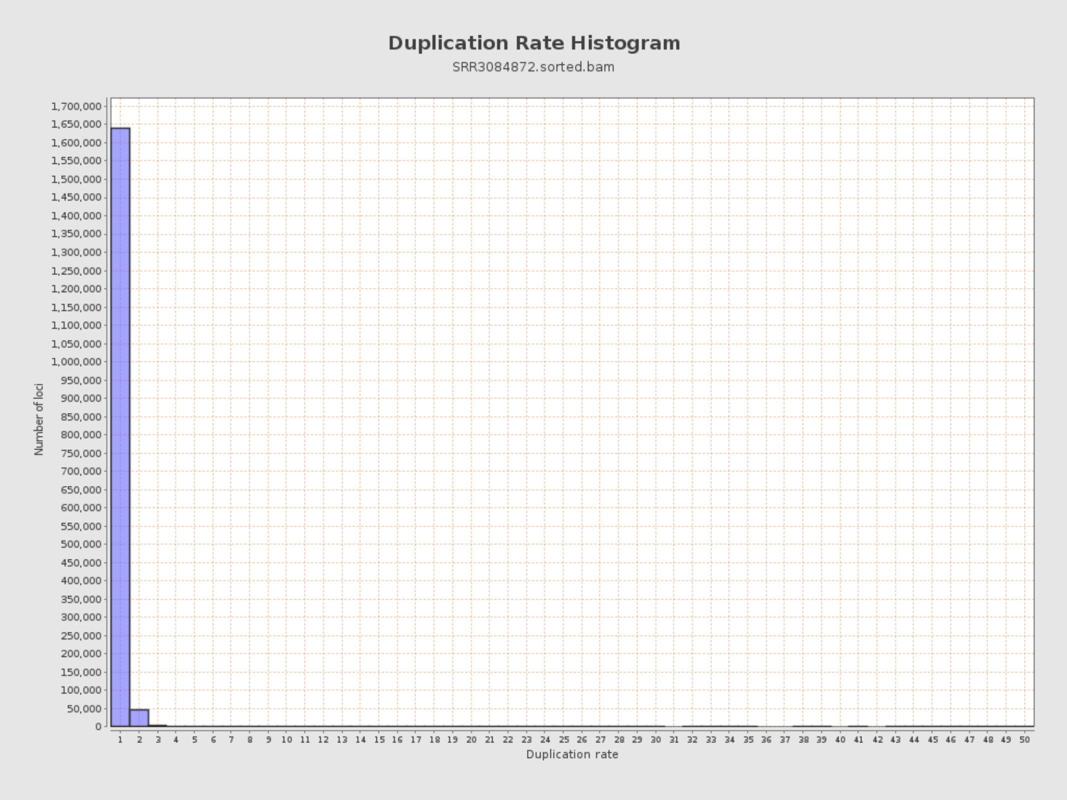
5. Results : Coverage Histogram (0-50X)



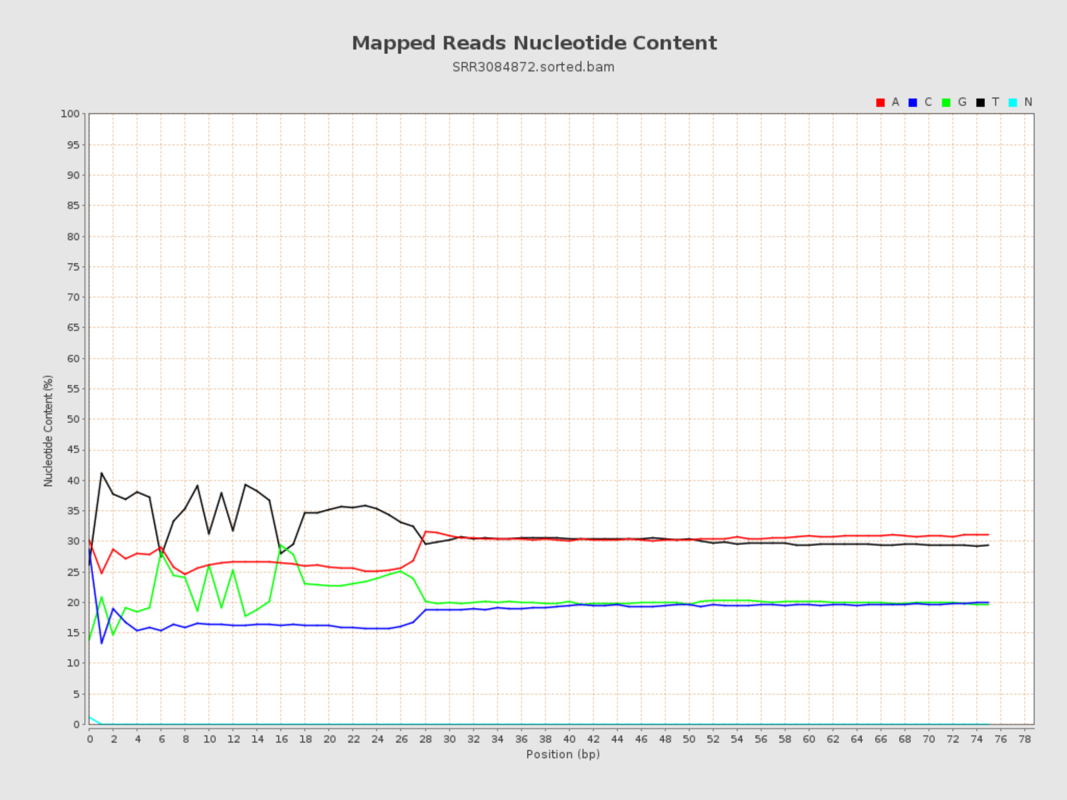
6. Results : Genome Fraction Coverage



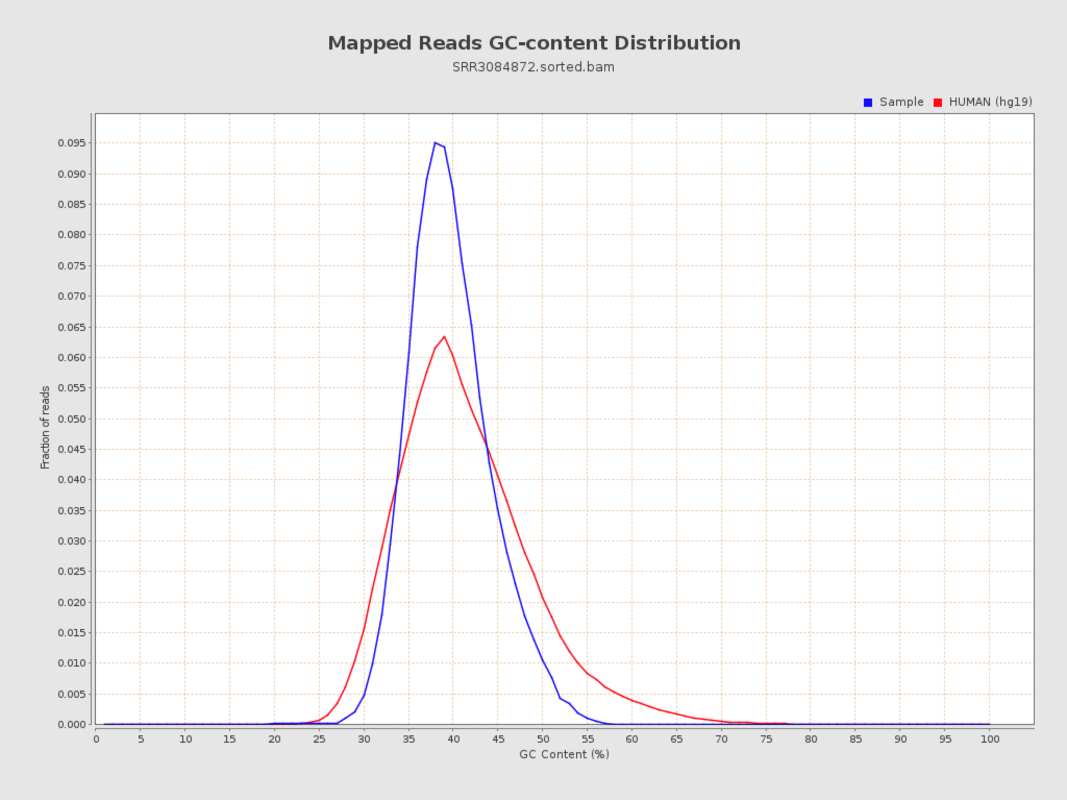
7. Results : Duplication Rate Histogram



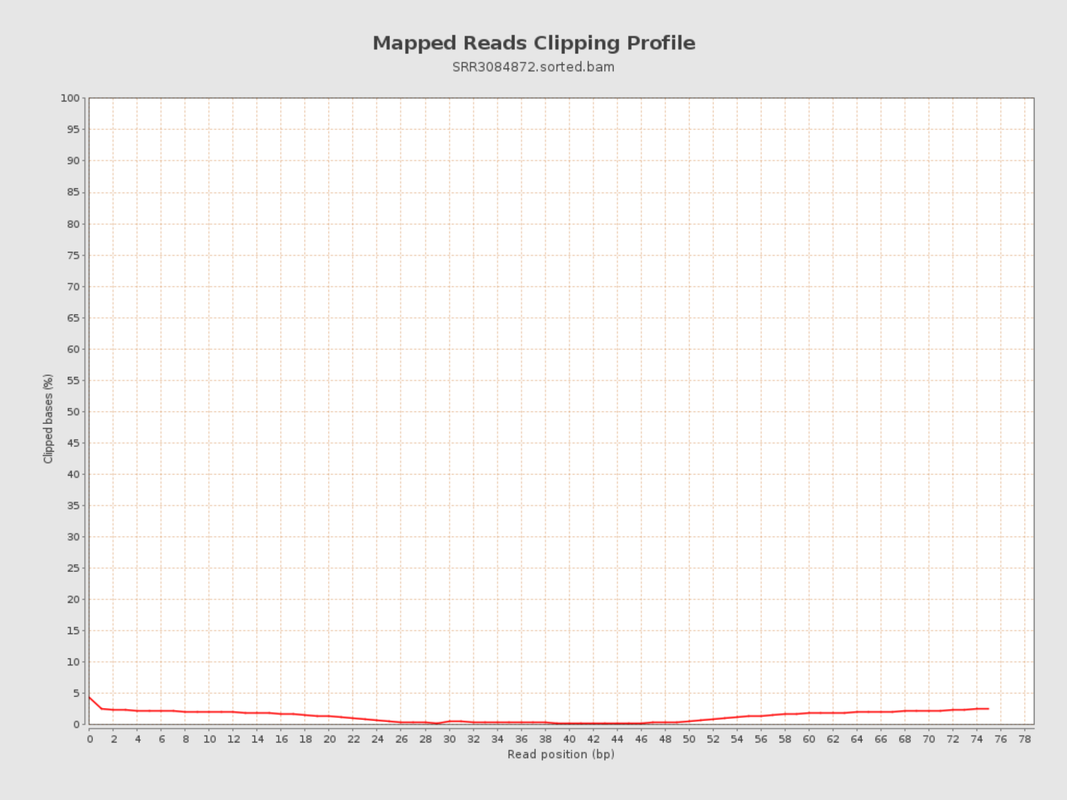
8. Results : Mapped Reads Nucleotide Content



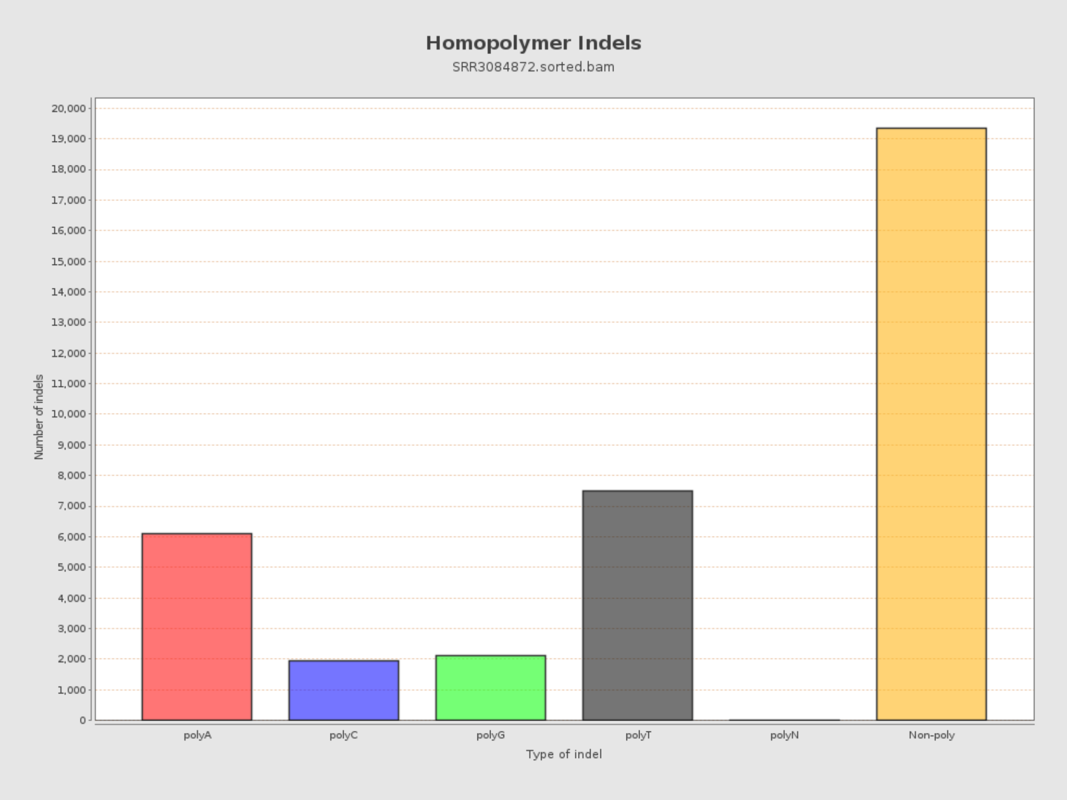
9. Results : Mapped Reads GC-content Distribution



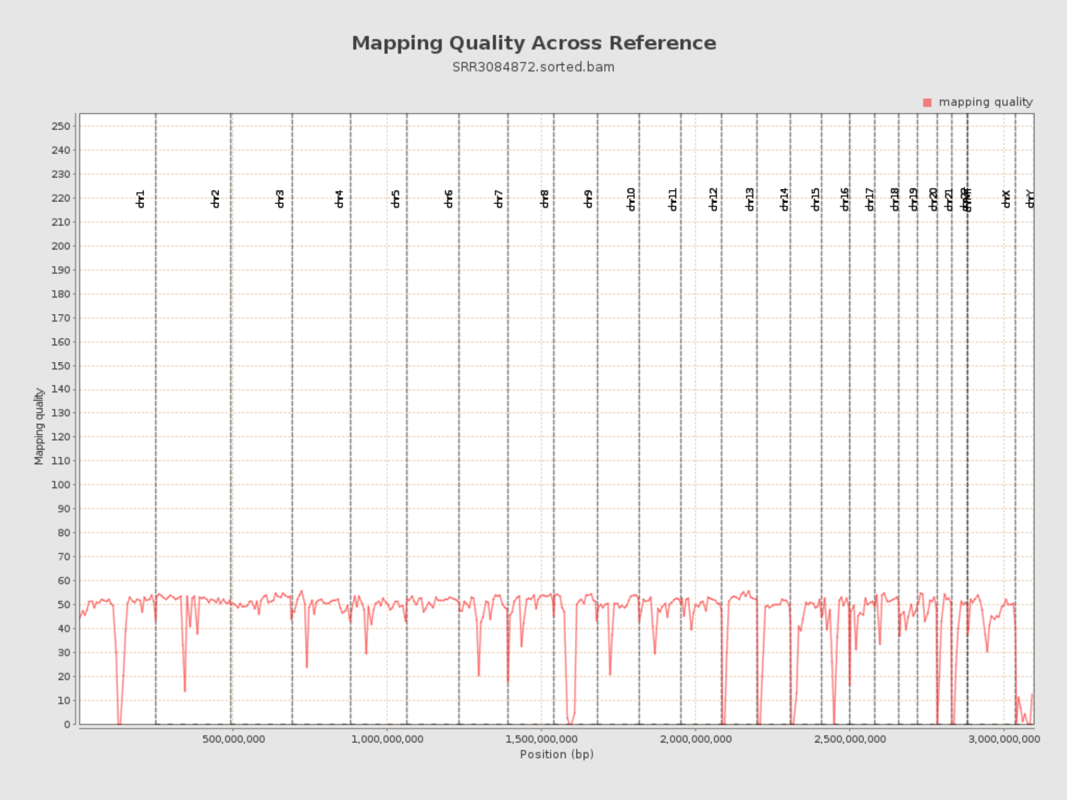
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram