Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:45:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082756.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_SRR3082756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:45:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,374,296
Mapped reads	2,694,148 / 79.84%
Unmapped reads	680,148 / 20.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,220 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	102,059 / 3.02%
Duplication rate	2.79%
Clipped reads	1,245,374 / 36.91%

2.2. ACGT Content

Number/percentage of A's	50,953,967 / 28.3%
Number/percentage of C's	32,731,305 / 18.18%
Number/percentage of T's	57,718,347 / 32.06%
Number/percentage of G's	38,622,771 / 21.45%
Number/percentage of N's	9,400 / 0.01%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0582

Standard Deviation	0.4823

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

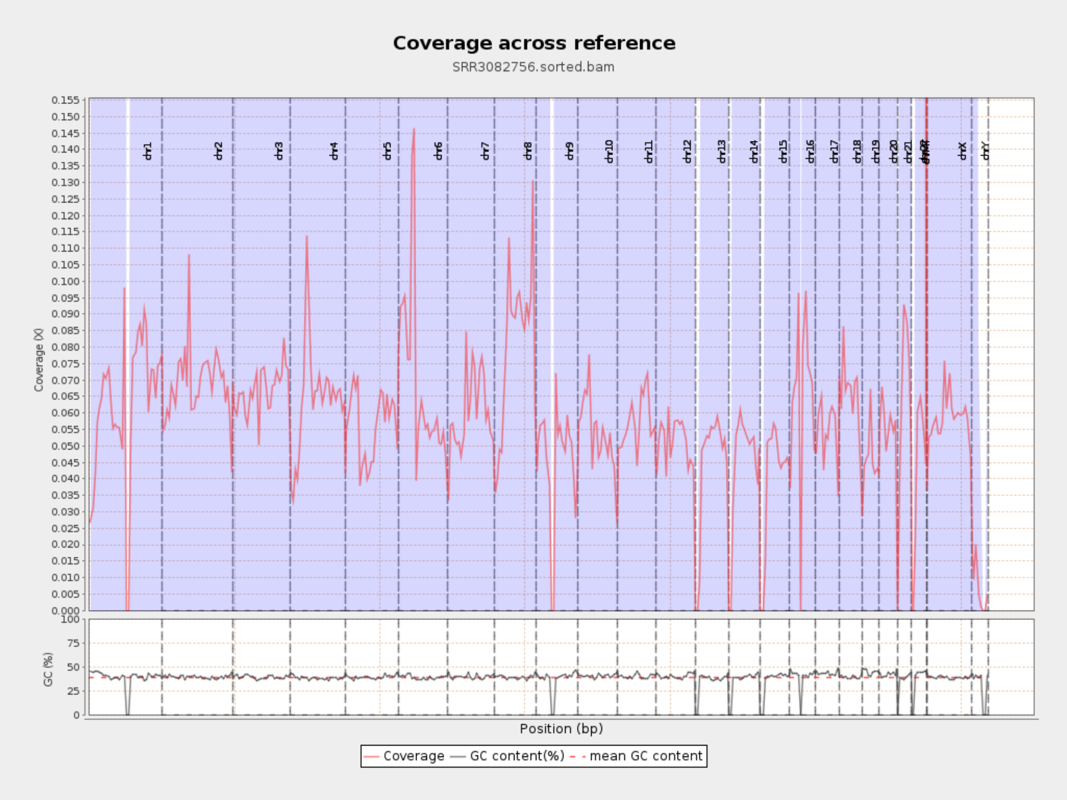
General error rate	0.96%
Mismatches	1,697,926
Insertions	16,171
Mapped reads with at least one insertion	0.59%
Deletions	40,822
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.01%

2.6. Chromosome stats

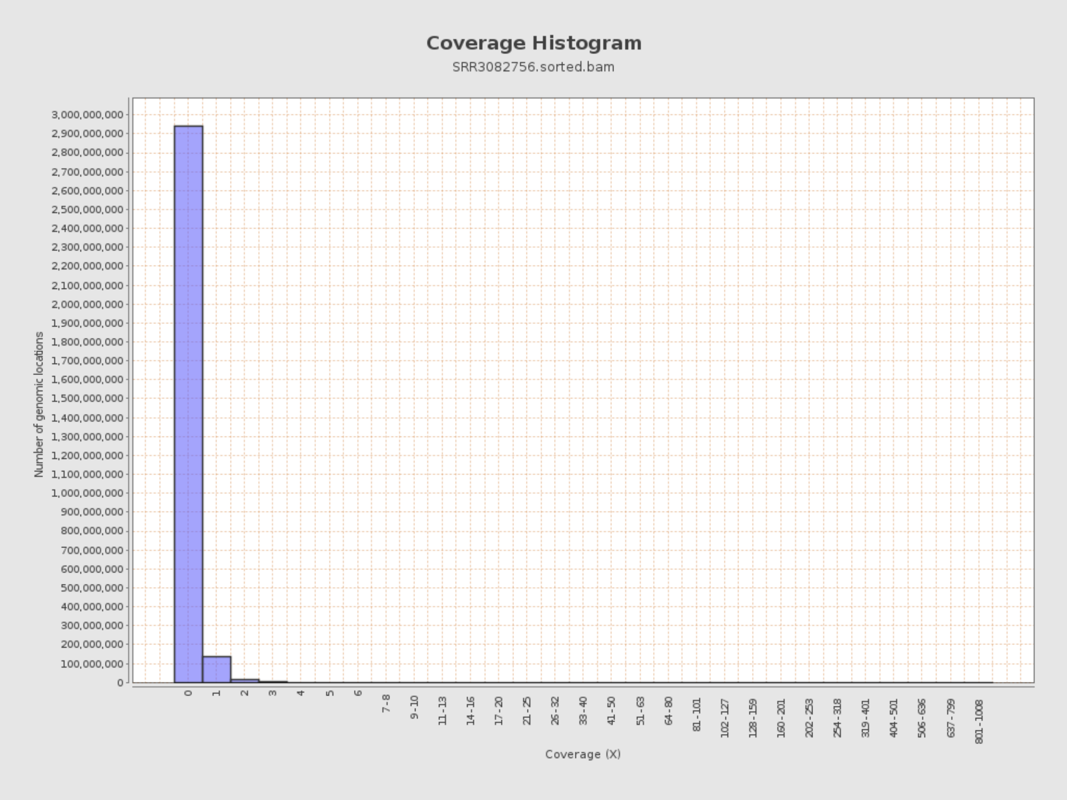
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15533475	0.0623	0.9067
chr2	243199373	16803561	0.0691	0.568
chr3	198022430	13272823	0.067	0.2872
chr4	191154276	12291227	0.0643	0.2919
chr5	180915260	10242698	0.0566	0.2678
chr6	171115067	11938595	0.0698	0.4102
chr7	159138663	9678600	0.0608	0.4964

chr8	146364022	11861960	0.081	0.7028
chr9	141213431	6441093	0.0456	0.4537
chr10	135534747	7378668	0.0544	0.3662
chr11	135006516	7647636	0.0566	0.395
chr12	133851895	6821496	0.051	0.2618
chr13	115169878	5008660	0.0435	0.2312
chr14	107349540	4718597	0.044	0.2843
chr15	102531392	4053628	0.0395	0.2216
chr16	90354753	5929154	0.0656	0.3543
chr17	81195210	4354334	0.0536	0.31
chr18	78077248	5127866	0.0657	1.0112
chr19	59128983	2760341	0.0467	0.6248
chr20	63025520	3527205	0.056	0.2848
chr21	48129895	3068788	0.0638	0.3038
chr22	51304566	2071650	0.0404	0.2235
chrMT	16571	152485	9.2019	6.3282
chrX	155270560	9025857	0.0581	0.3156
chrY	59373566	394877	0.0067	0.1411

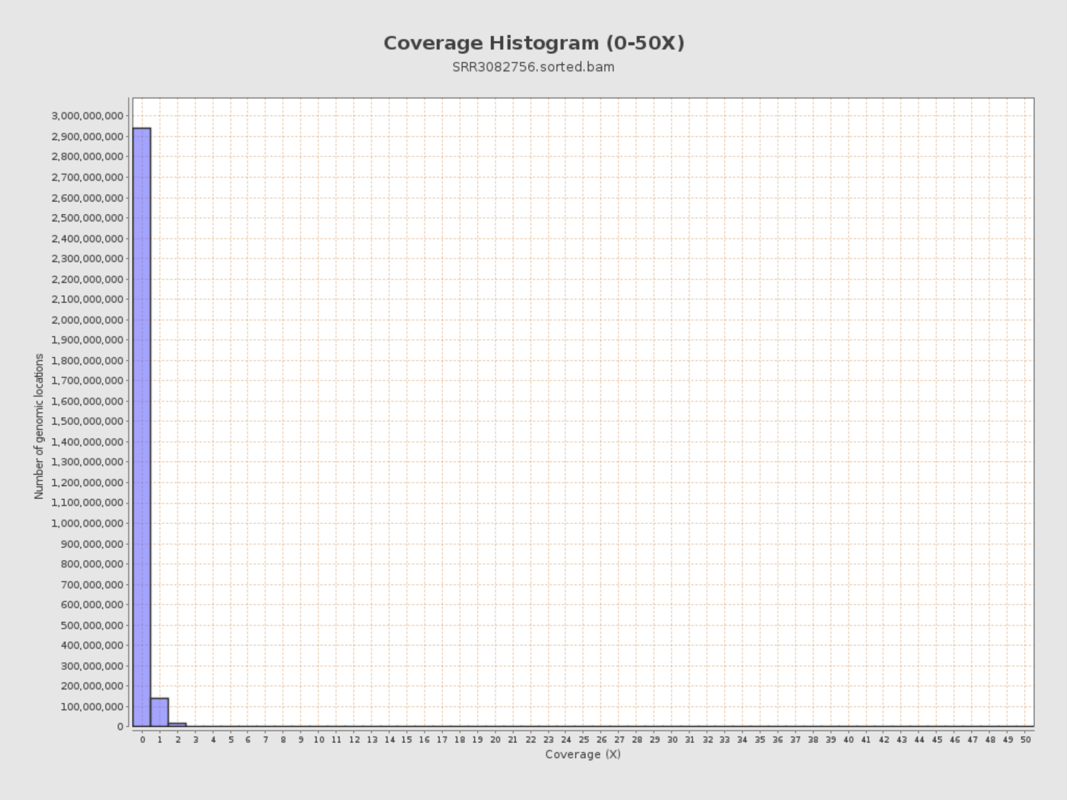
3. Results : Coverage across reference



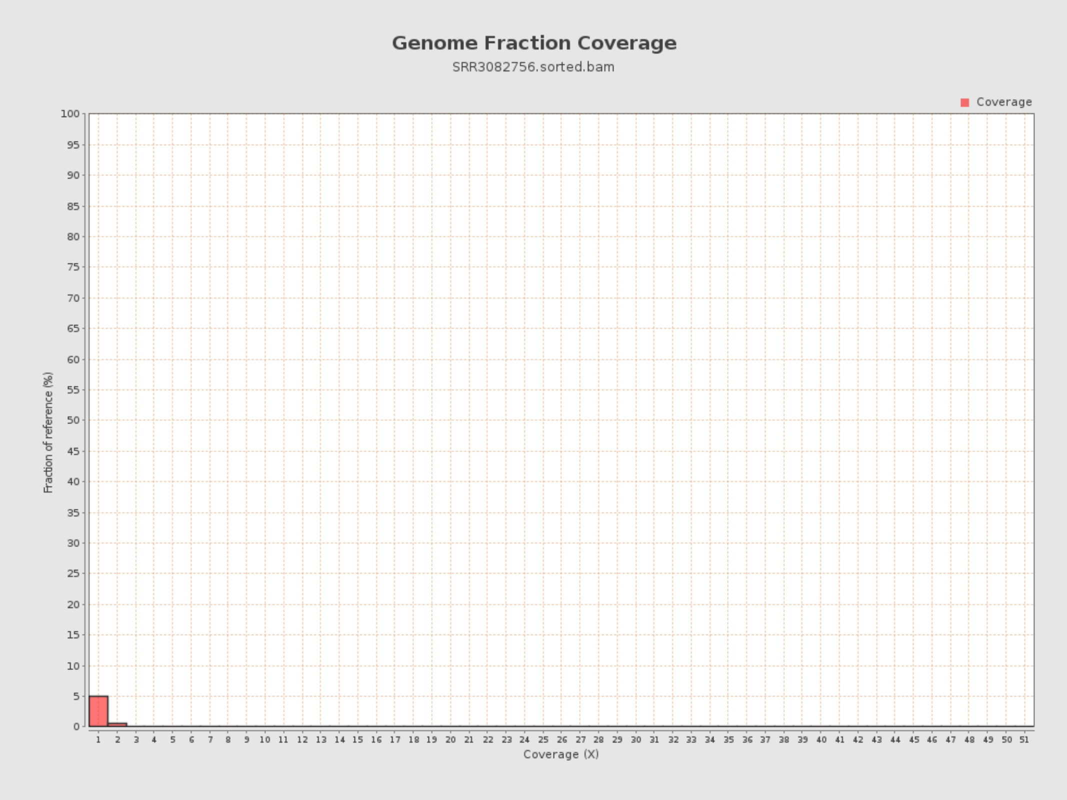
4. Results : Coverage Histogram



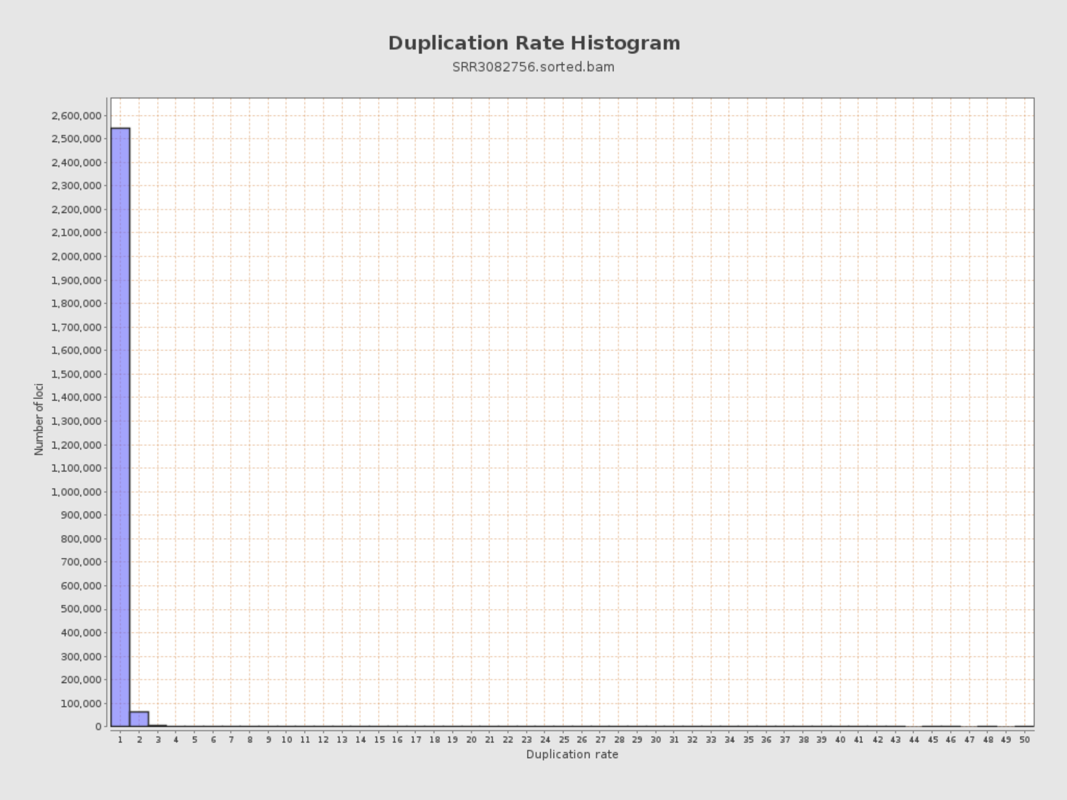
5. Results : Coverage Histogram (0-50X)



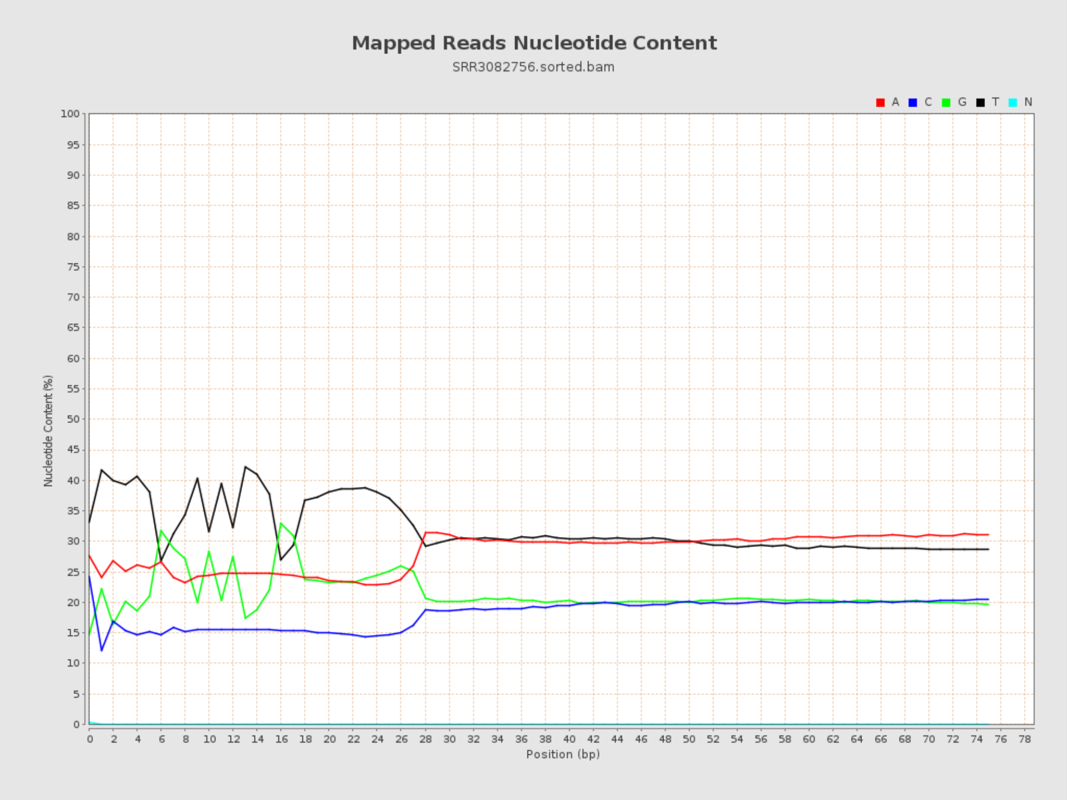
6. Results : Genome Fraction Coverage



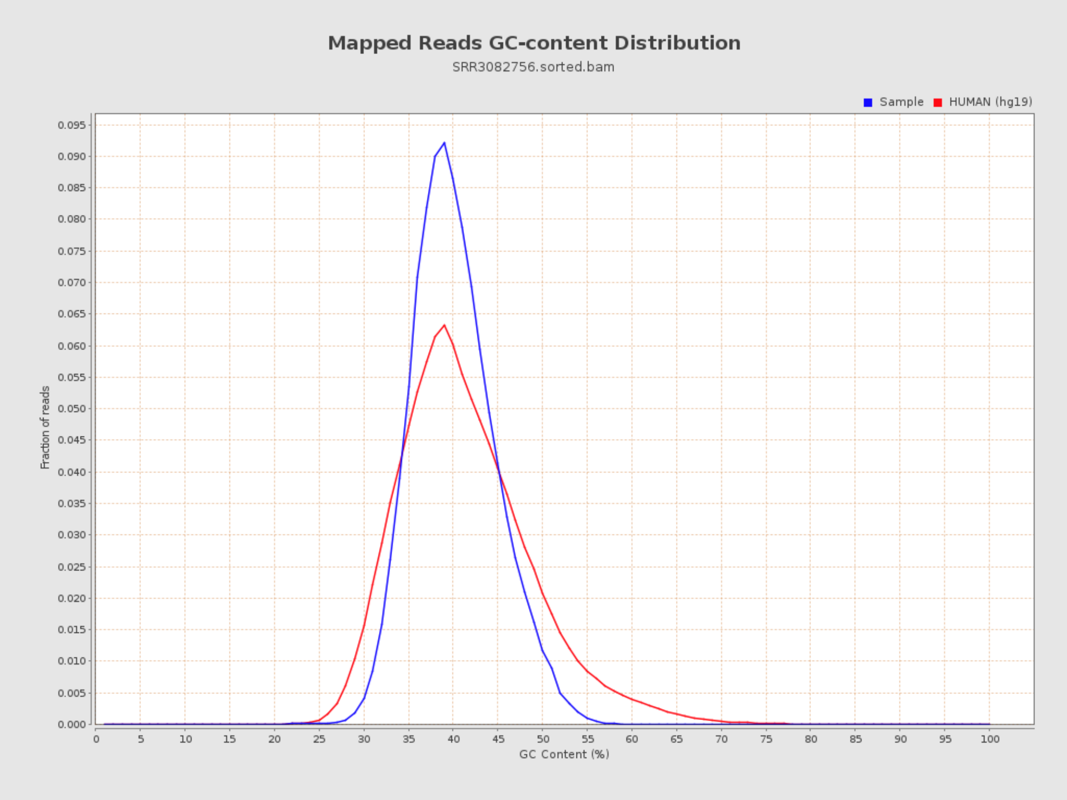
7. Results : Duplication Rate Histogram



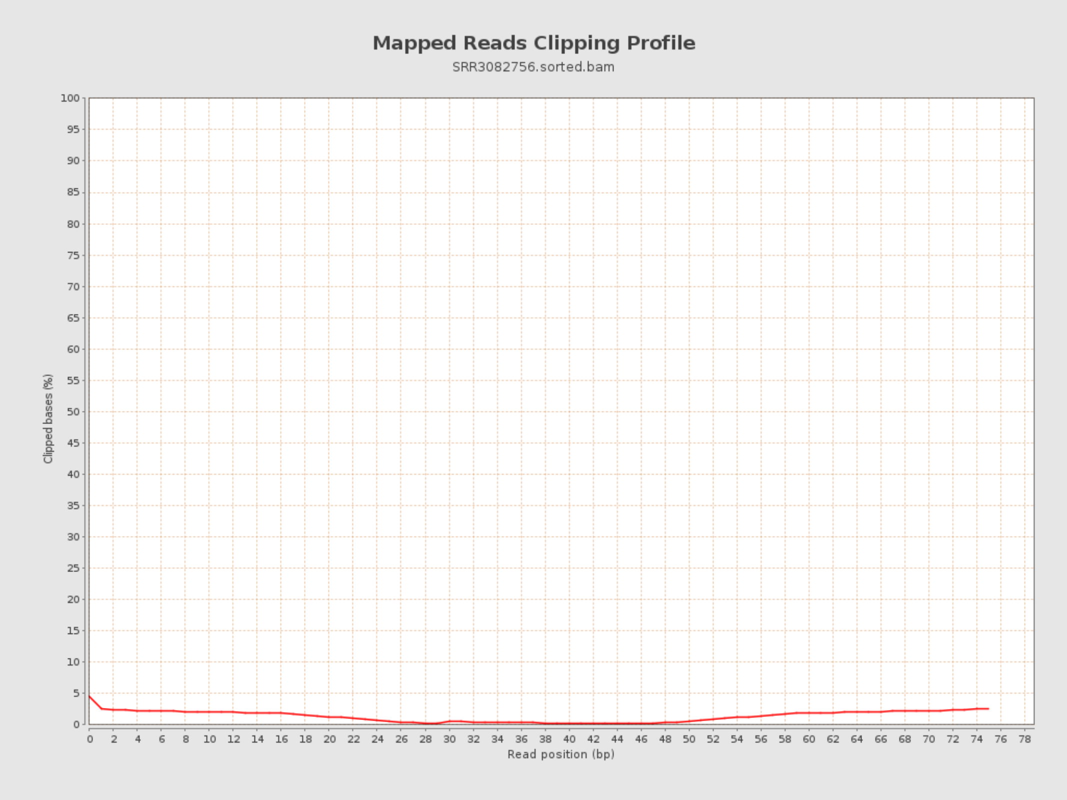
8. Results : Mapped Reads Nucleotide Content



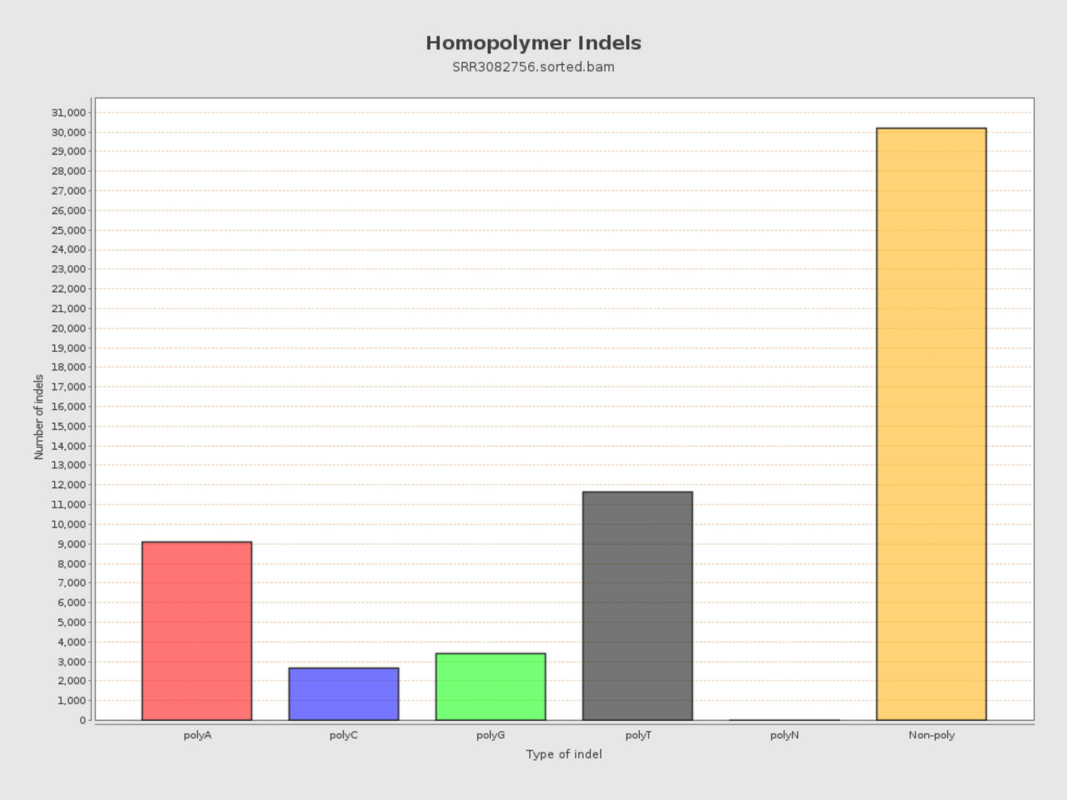
9. Results : Mapped Reads GC-content Distribution



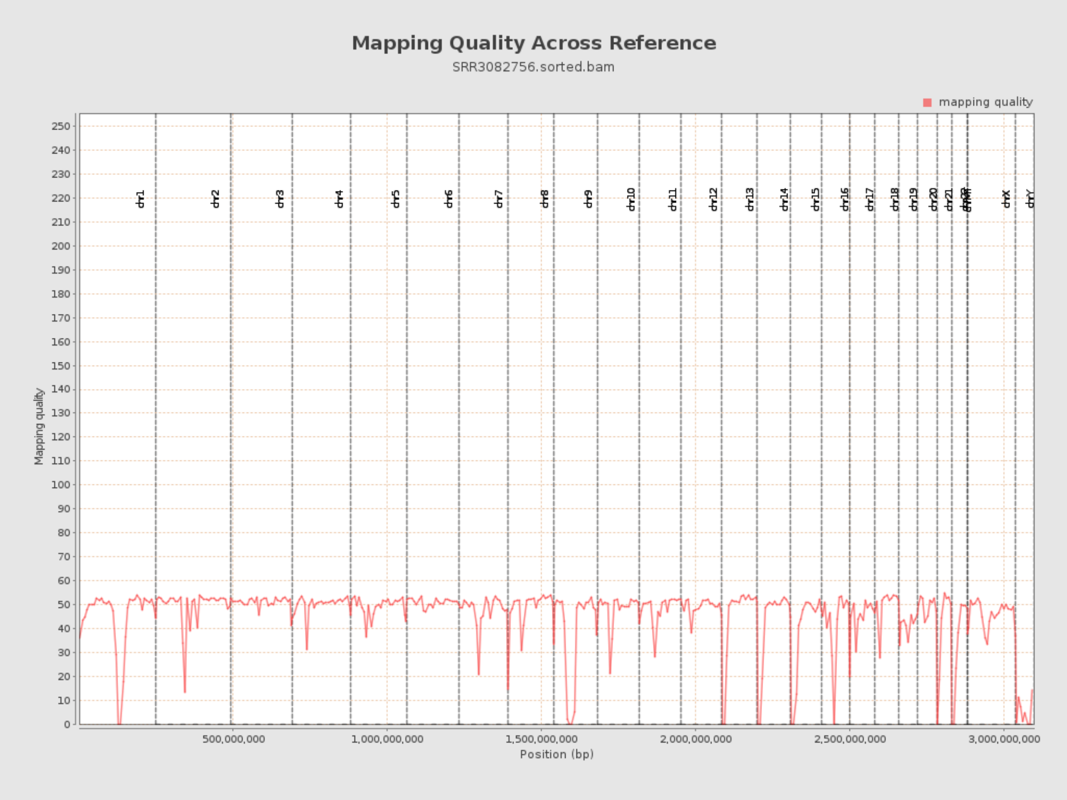
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram