Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:32:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082961.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_SRR3082961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082961.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:32:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,506,845
Mapped reads	2,700,768 / 77.01%
Unmapped reads	806,077 / 22.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,045 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	121,508 / 3.46%
Duplication rate	3.18%
Clipped reads	1,085,025 / 30.94%

2.2. ACGT Content

Number/percentage of A's	51,788,297 / 28.24%
Number/percentage of C's	33,840,237 / 18.45%
Number/percentage of T's	58,401,917 / 31.85%
Number/percentage of G's	39,330,550 / 21.45%
Number/percentage of N's	18,027 / 0.01%
GC Percentage	39.9%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.5695

2.4. Mapping Quality

Mean Mapping Quality	46.18

2.5. Mismatches and indels

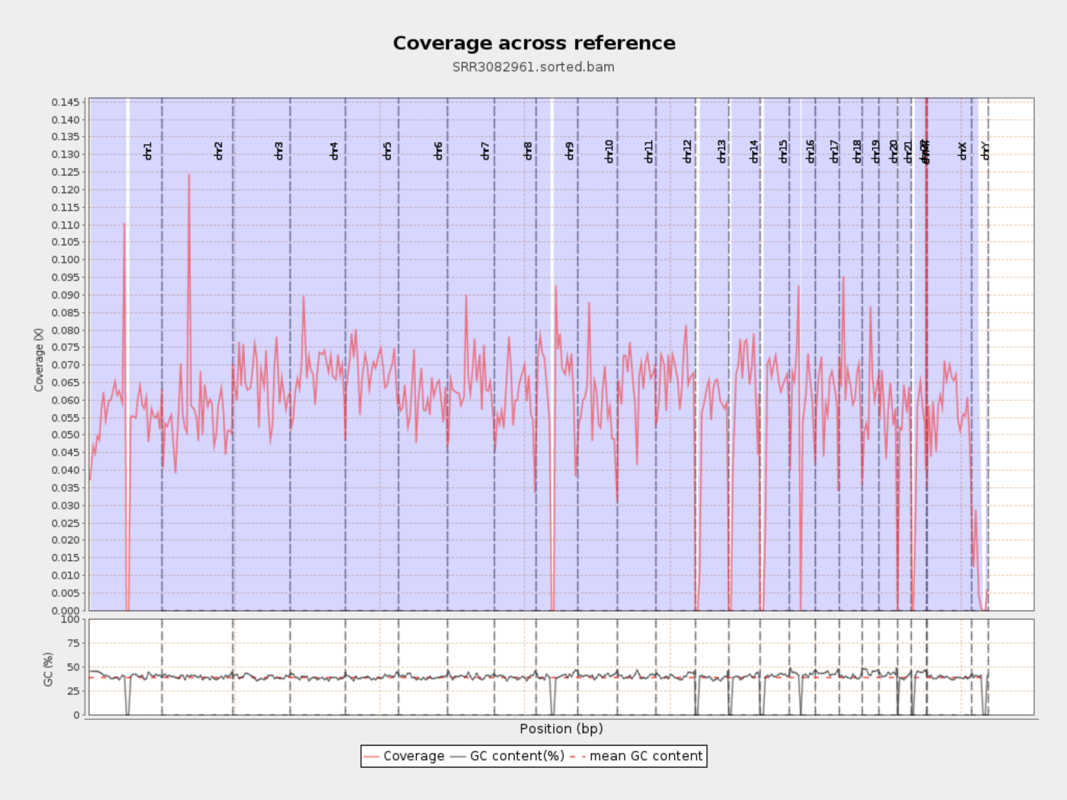
General error rate	0.98%
Mismatches	1,767,027
Insertions	17,459
Mapped reads with at least one insertion	0.64%
Deletions	44,696
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.33%

2.6. Chromosome stats

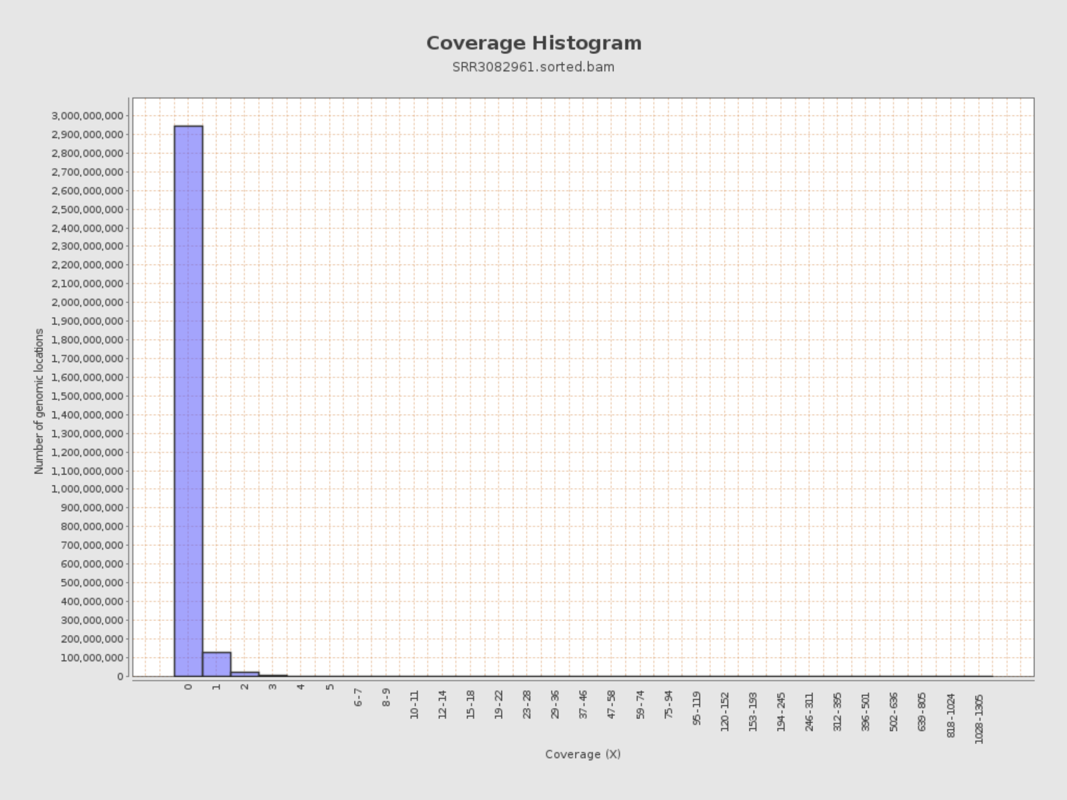
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13528189	0.0543	1.1243
chr2	243199373	13768291	0.0566	0.6737
chr3	198022430	12849755	0.0649	0.2999
chr4	191154276	12989560	0.068	0.3351
chr5	180915260	12499826	0.0691	0.3147
chr6	171115067	10294210	0.0602	0.3303
chr7	159138663	10398111	0.0653	0.5568

chr8	146364022	8684322	0.0593	0.671
chr9	141213431	8713099	0.0617	0.6498
chr10	135534747	7924108	0.0585	0.4312
chr11	135006516	8878382	0.0658	0.4627
chr12	133851895	8909289	0.0666	0.3193
chr13	115169878	5786159	0.0502	0.2625
chr14	107349540	6197016	0.0577	0.3427
chr15	102531392	5575081	0.0544	0.2765
chr16	90354753	5325353	0.0589	0.4277
chr17	81195210	4843566	0.0597	0.3736
chr18	78077248	5213517	0.0668	1.3093
chr19	59128983	3588688	0.0607	0.7457
chr20	63025520	3511106	0.0557	0.2921
chr21	48129895	2421099	0.0503	0.3192
chr22	51304566	2086572	0.0407	0.233
chrMT	16571	21979	1.3264	1.427
chrX	155270560	8961200	0.0577	0.3613
chrY	59373566	488649	0.0082	0.2477

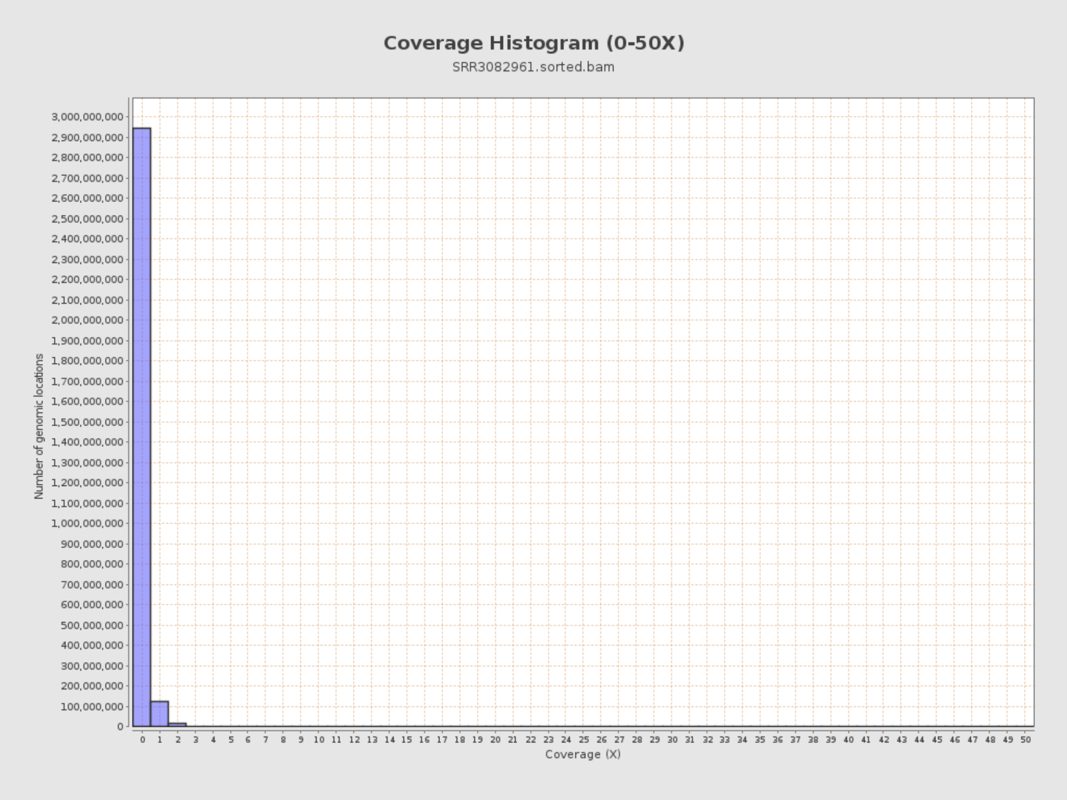
3. Results : Coverage across reference



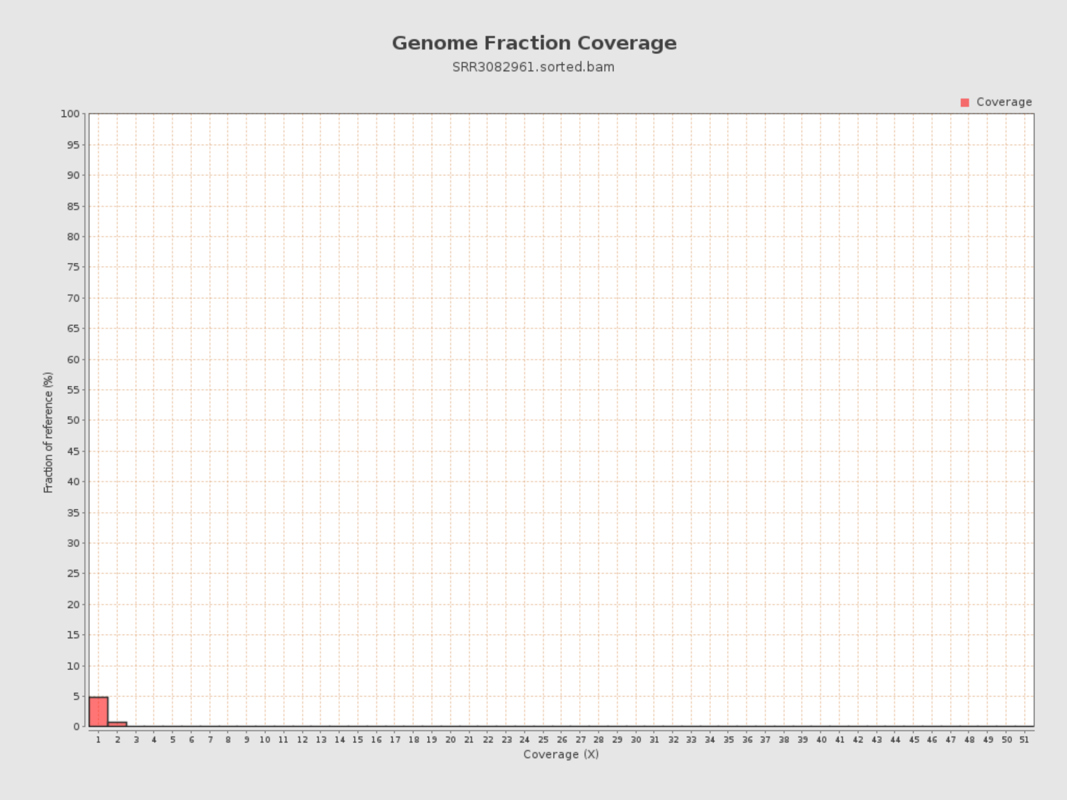
4. Results : Coverage Histogram



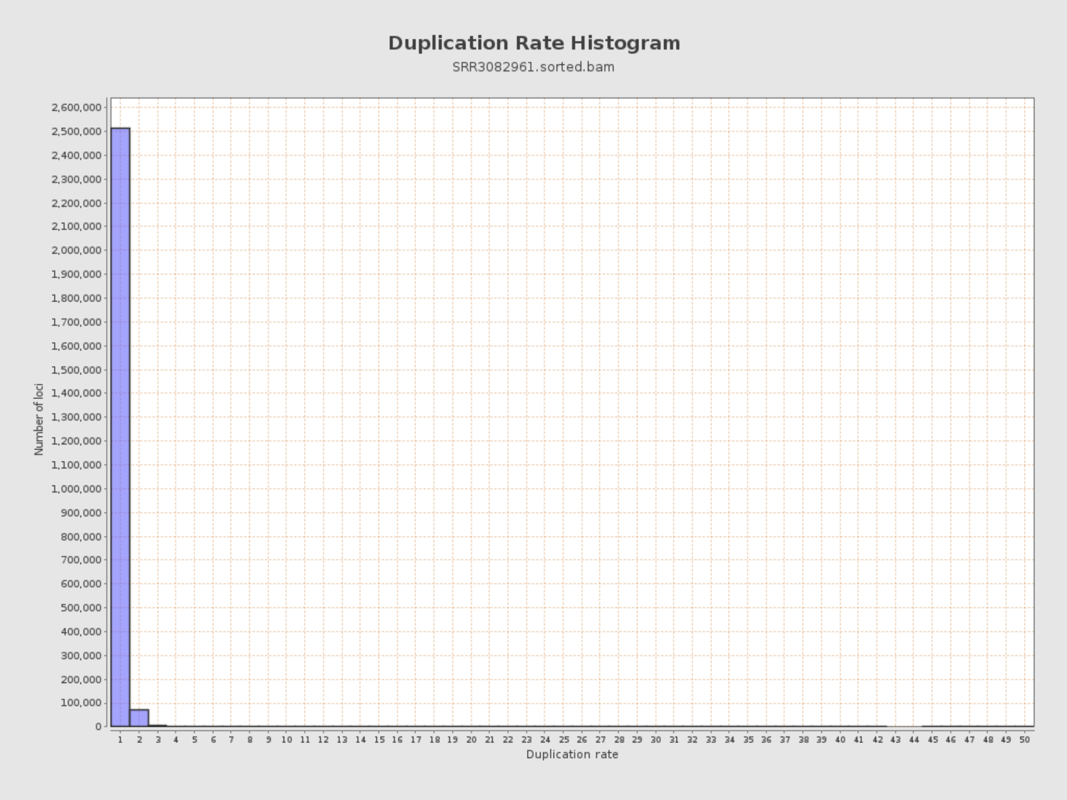
5. Results : Coverage Histogram (0-50X)



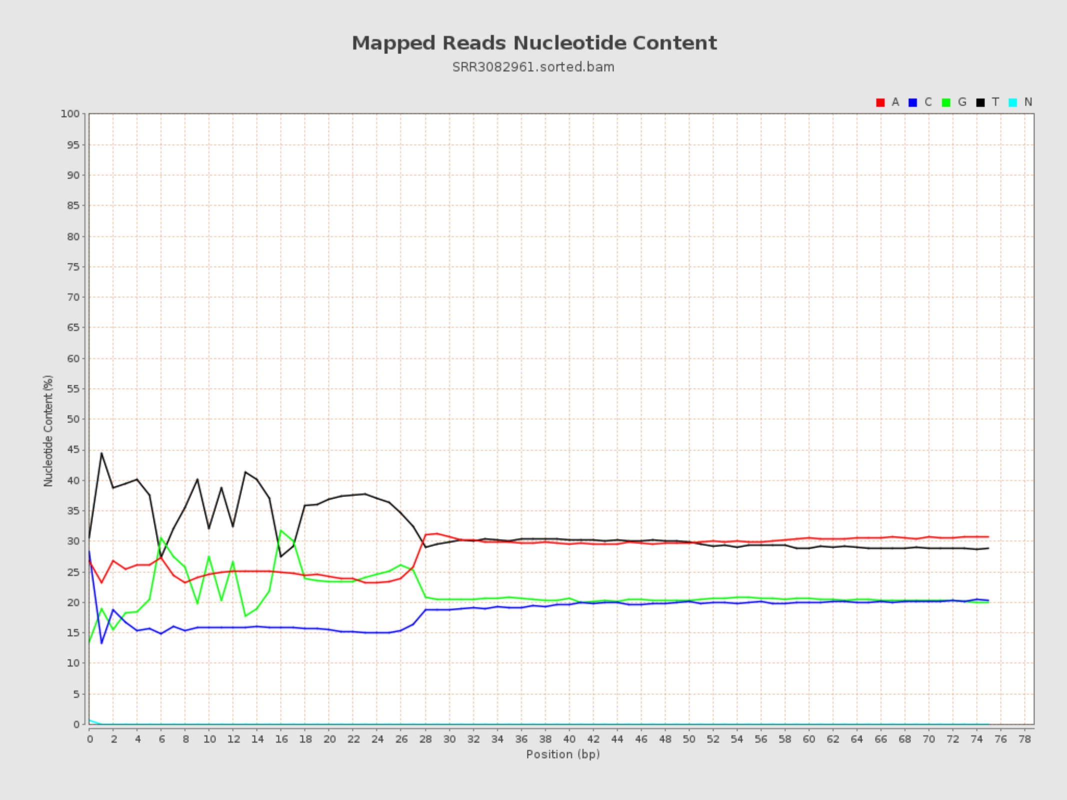
6. Results : Genome Fraction Coverage



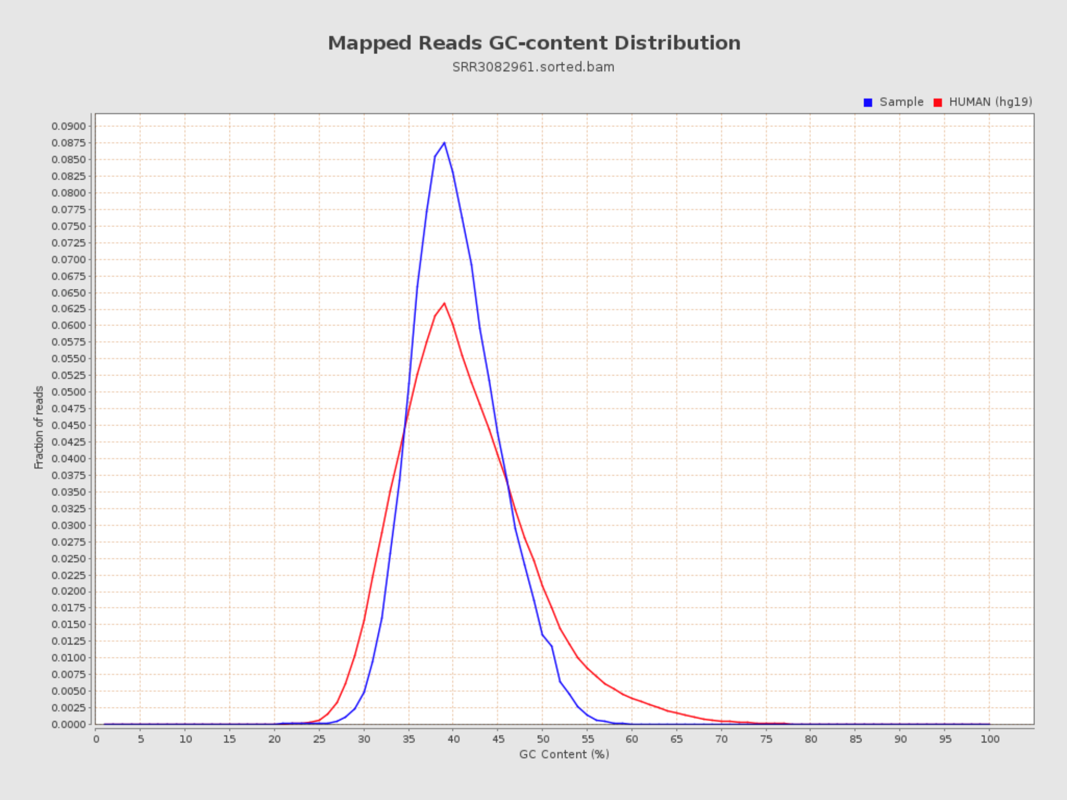
7. Results : Duplication Rate Histogram



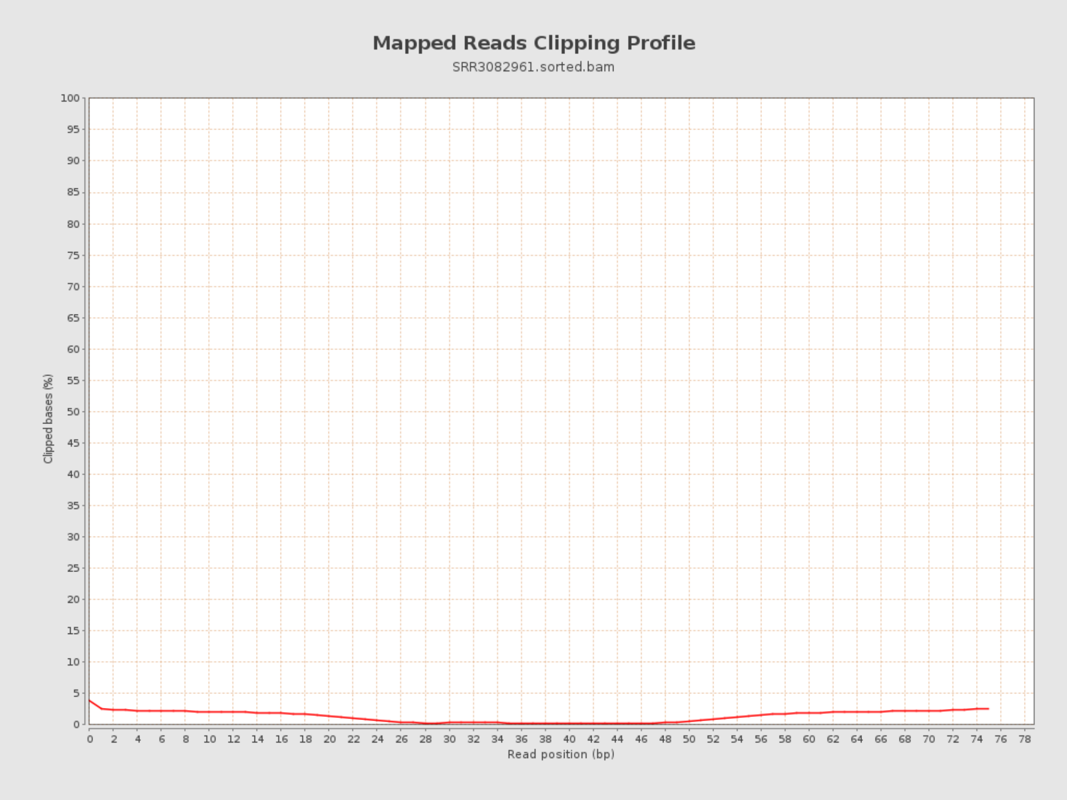
8. Results : Mapped Reads Nucleotide Content



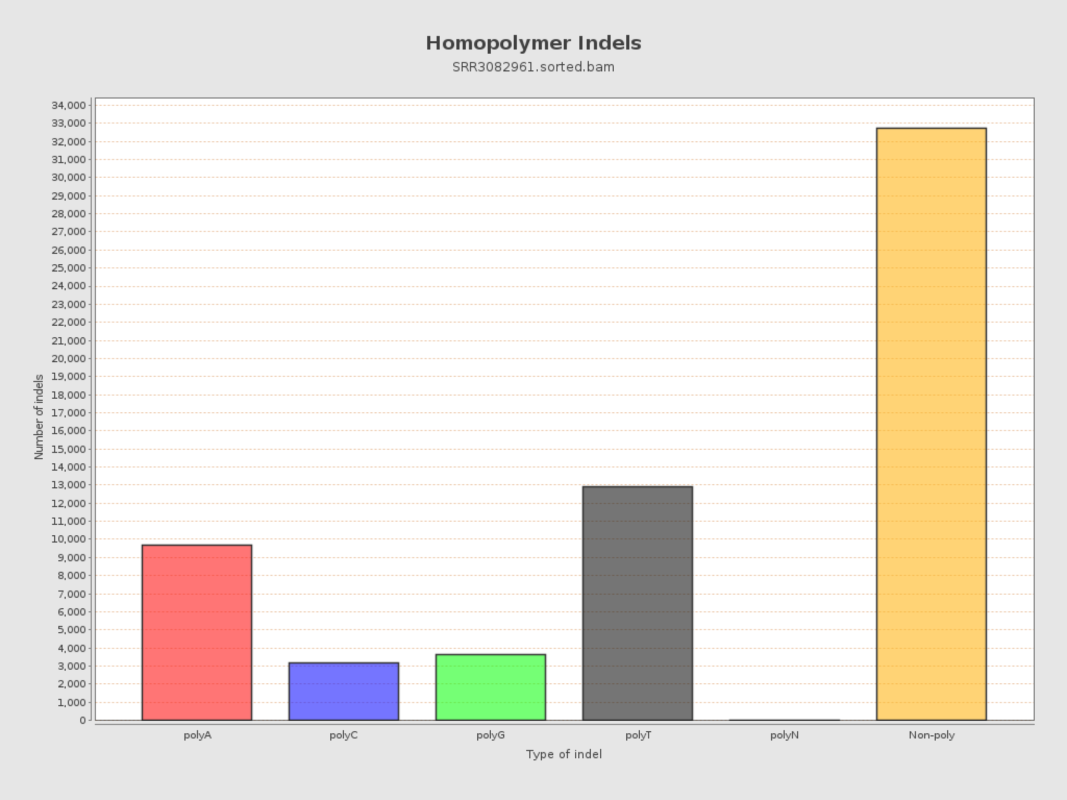
9. Results : Mapped Reads GC-content Distribution



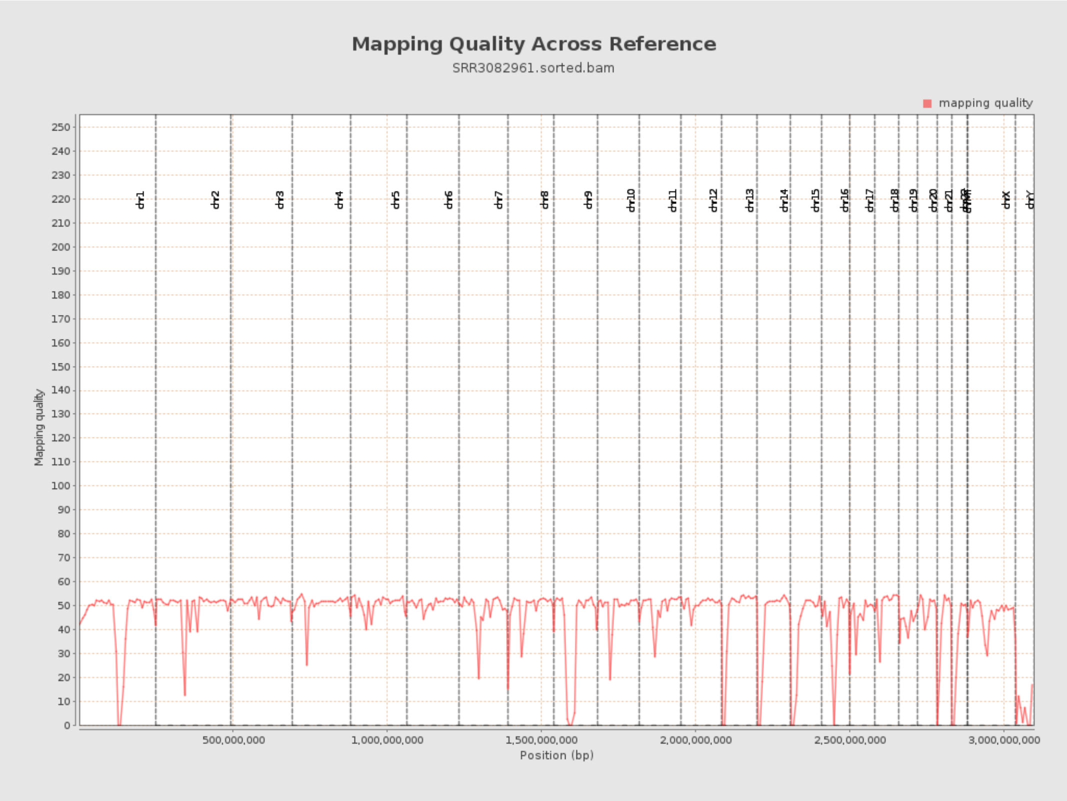
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram