Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:53:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082969.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_SRR3082969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:53:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,531,706
Mapped reads	3,042,839 / 86.16%
Unmapped reads	488,867 / 13.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,210 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	186,697 / 5.29%
Duplication rate	5.12%
Clipped reads	1,429,708 / 40.48%

2.2. ACGT Content

Number/percentage of A's	55,012,531 / 27.35%
Number/percentage of C's	36,293,091 / 18.05%
Number/percentage of T's	65,292,188 / 32.47%
Number/percentage of G's	44,494,737 / 22.12%
Number/percentage of N's	19,720 / 0.01%
GC Percentage	40.17%

2.3. Coverage

Mean	0.065

Standard Deviation	0.4607

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

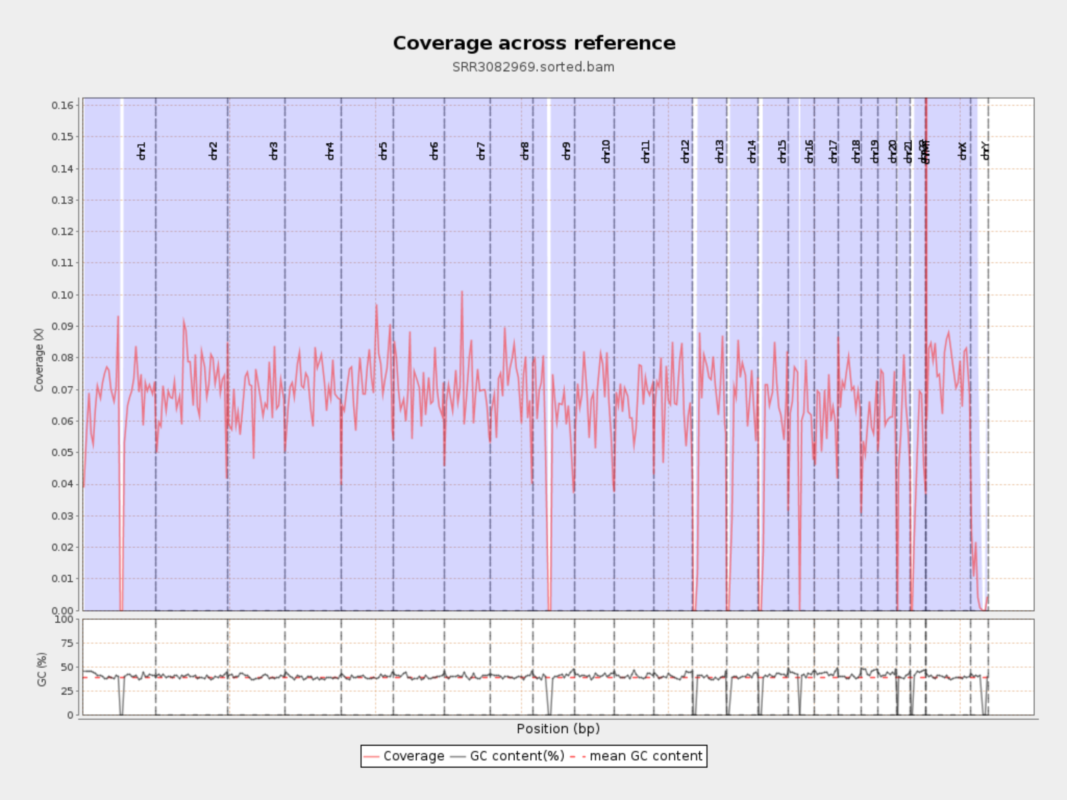
General error rate	0.87%
Mismatches	1,725,950
Insertions	15,914
Mapped reads with at least one insertion	0.52%
Deletions	43,970
Mapped reads with at least one deletion	1.43%
Homopolymer indels	48.38%

2.6. Chromosome stats

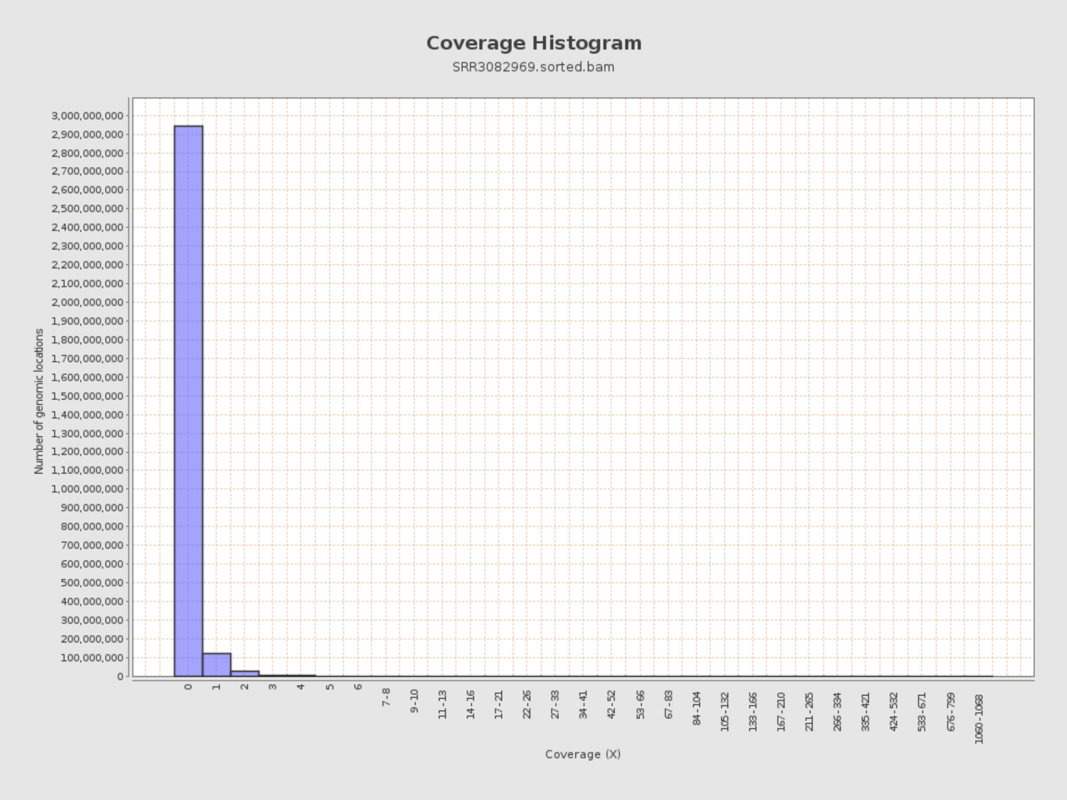
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15937881	0.0639	0.6796
chr2	243199373	17192785	0.0707	0.6158
chr3	198022430	13210016	0.0667	0.3285
chr4	191154276	13627464	0.0713	0.3513
chr5	180915260	13196463	0.0729	0.3486
chr6	171115067	11933573	0.0697	0.3755
chr7	159138663	11083274	0.0696	0.6602

chr8	146364022	10327464	0.0706	0.5128
chr9	141213431	8119060	0.0575	0.4701
chr10	135534747	9098714	0.0671	0.3714
chr11	135006516	8981931	0.0665	0.404
chr12	133851895	9102946	0.068	0.3376
chr13	115169878	7115541	0.0618	0.32
chr14	107349540	6250766	0.0582	0.3262
chr15	102531392	5652598	0.0551	0.3002
chr16	90354753	5255007	0.0582	0.347
chr17	81195210	4945823	0.0609	0.3364
chr18	78077248	5553210	0.0711	0.8162
chr19	59128983	3403434	0.0576	0.5508
chr20	63025520	4105268	0.0651	0.3385
chr21	48129895	2572513	0.0534	0.3119
chr22	51304566	2081580	0.0406	0.2536
chrMT	16571	76783	4.6336	4.9291
chrX	155270560	11914051	0.0767	0.3876
chrY	59373566	449047	0.0076	0.1571

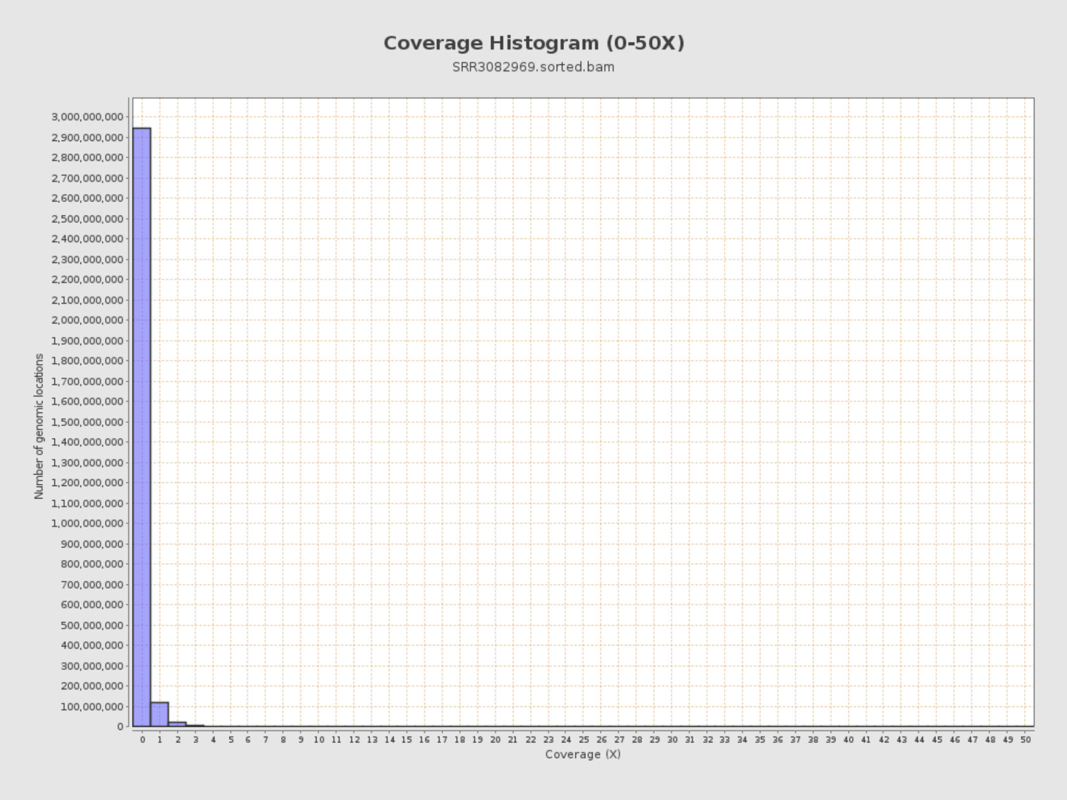
3. Results : Coverage across reference



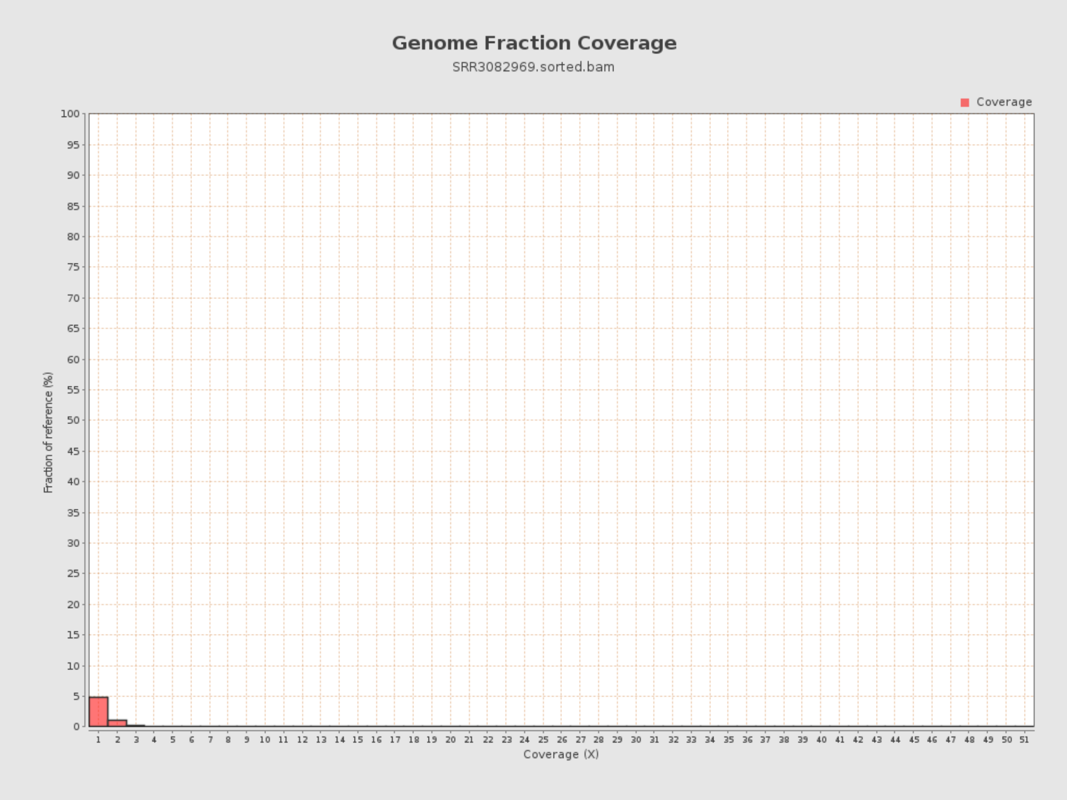
4. Results : Coverage Histogram



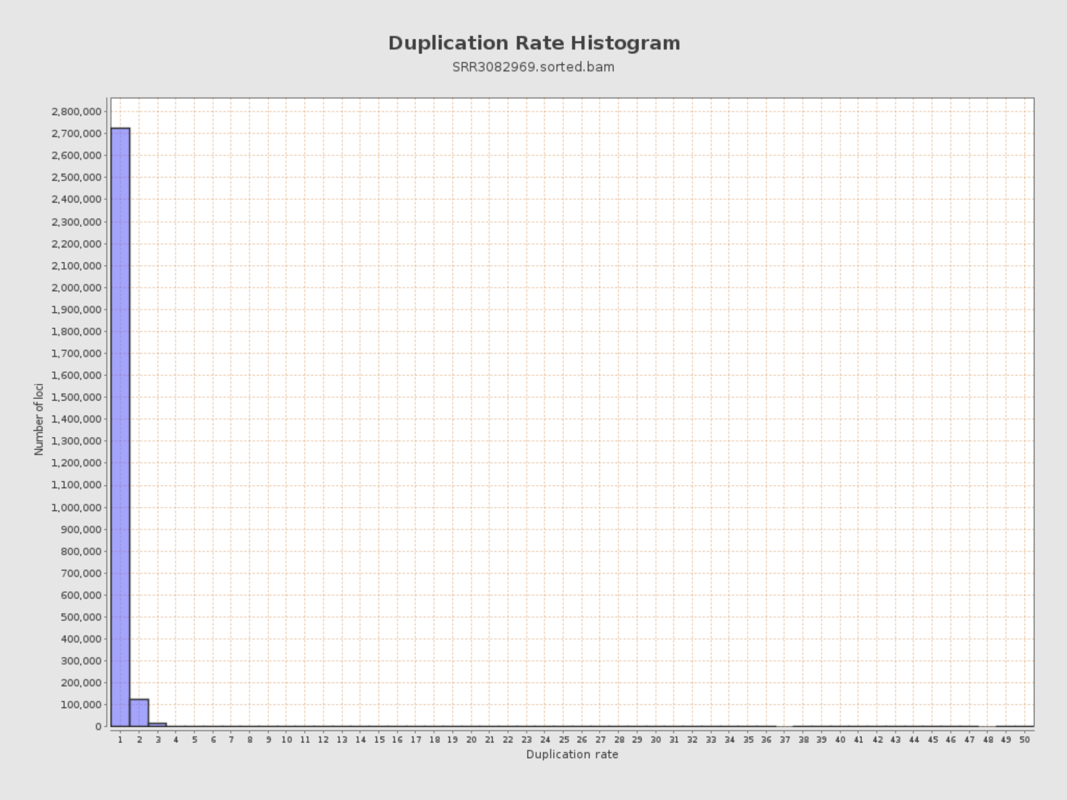
5. Results : Coverage Histogram (0-50X)



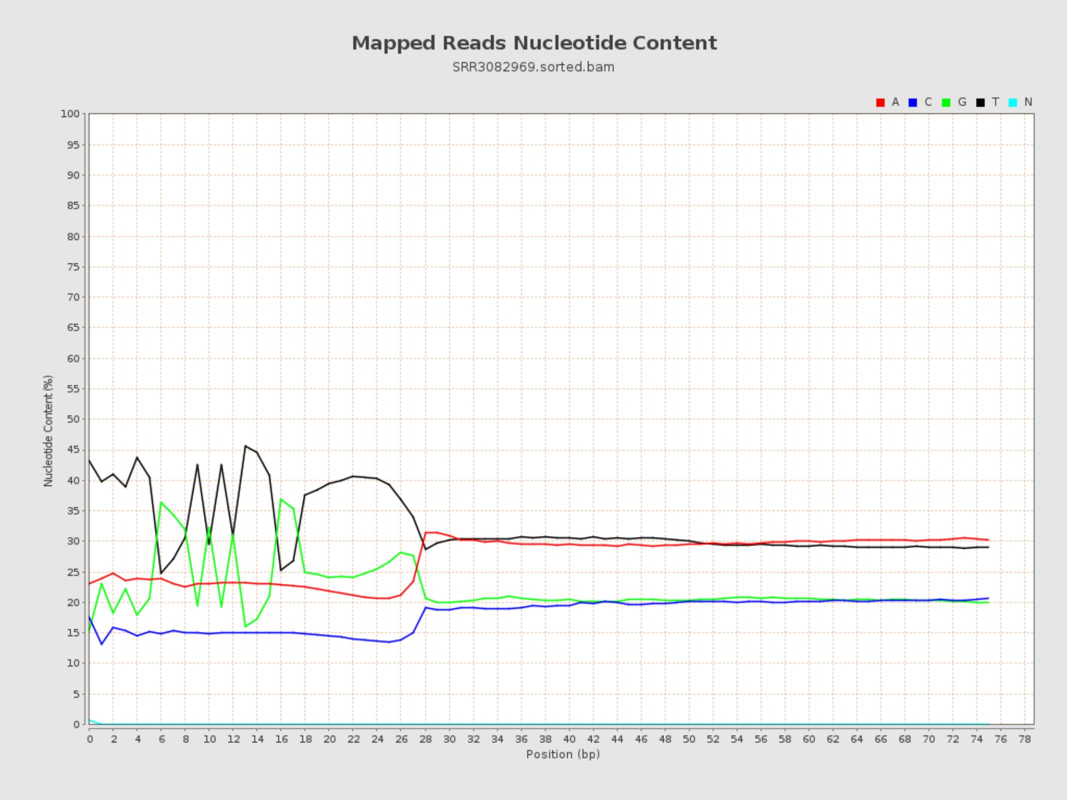
6. Results : Genome Fraction Coverage



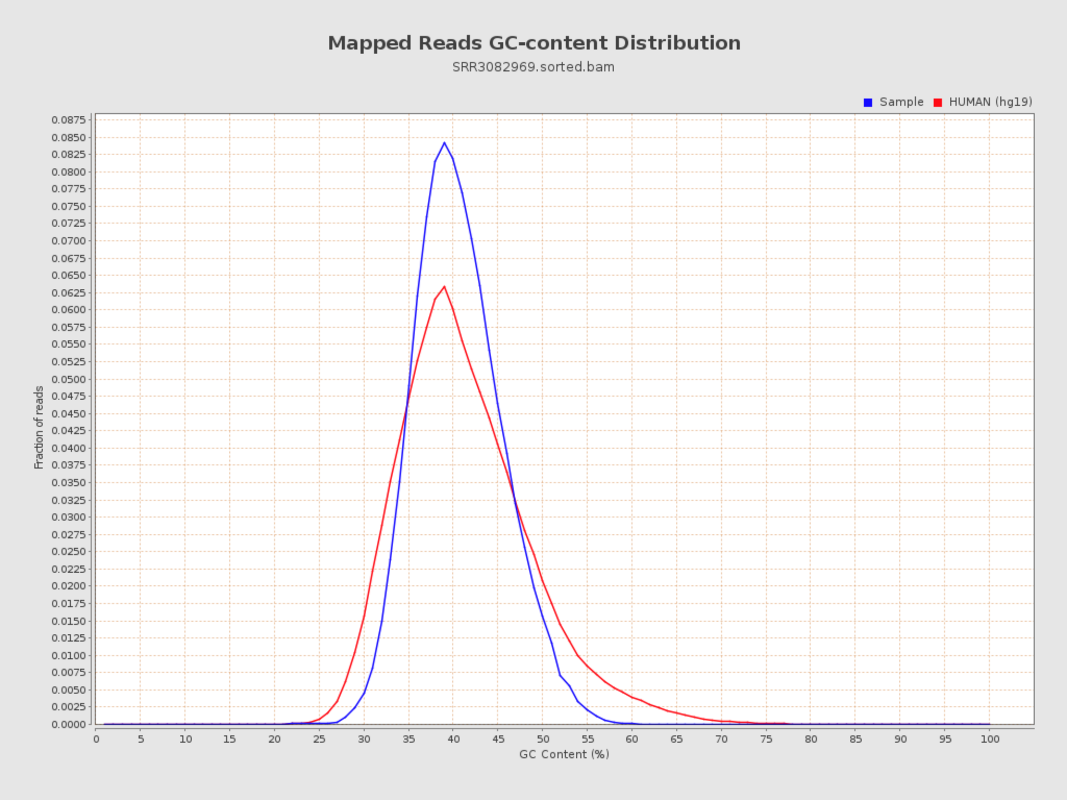
7. Results : Duplication Rate Histogram



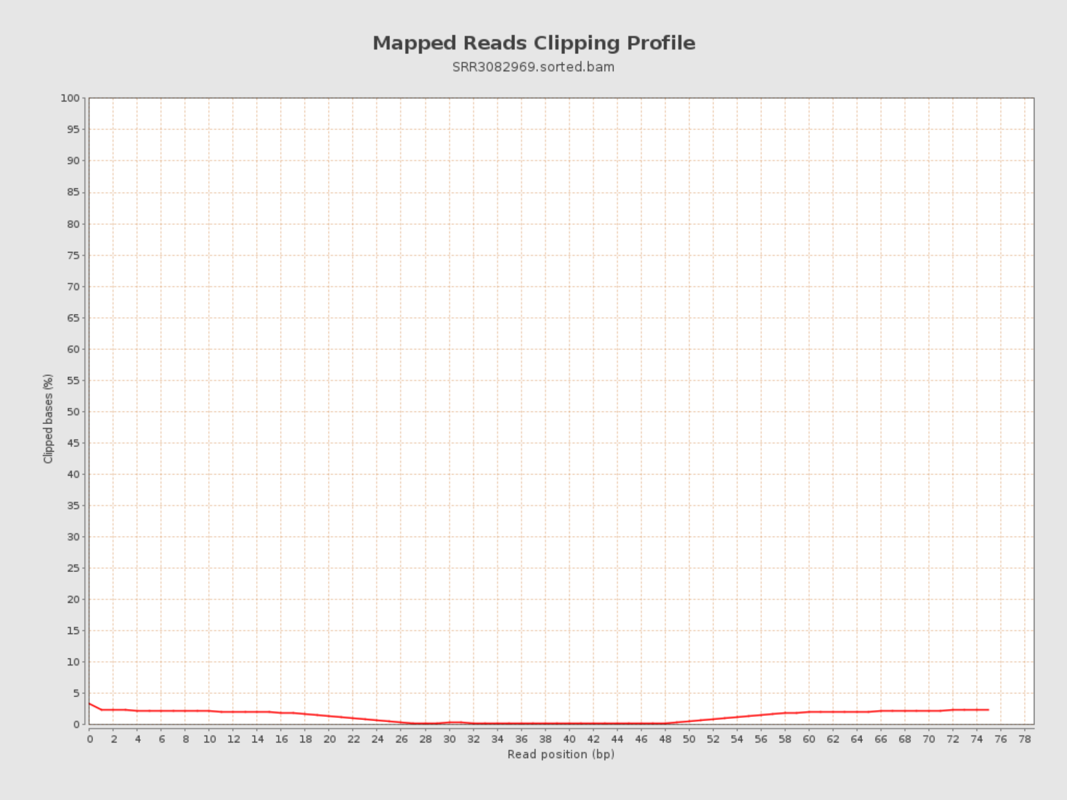
8. Results : Mapped Reads Nucleotide Content



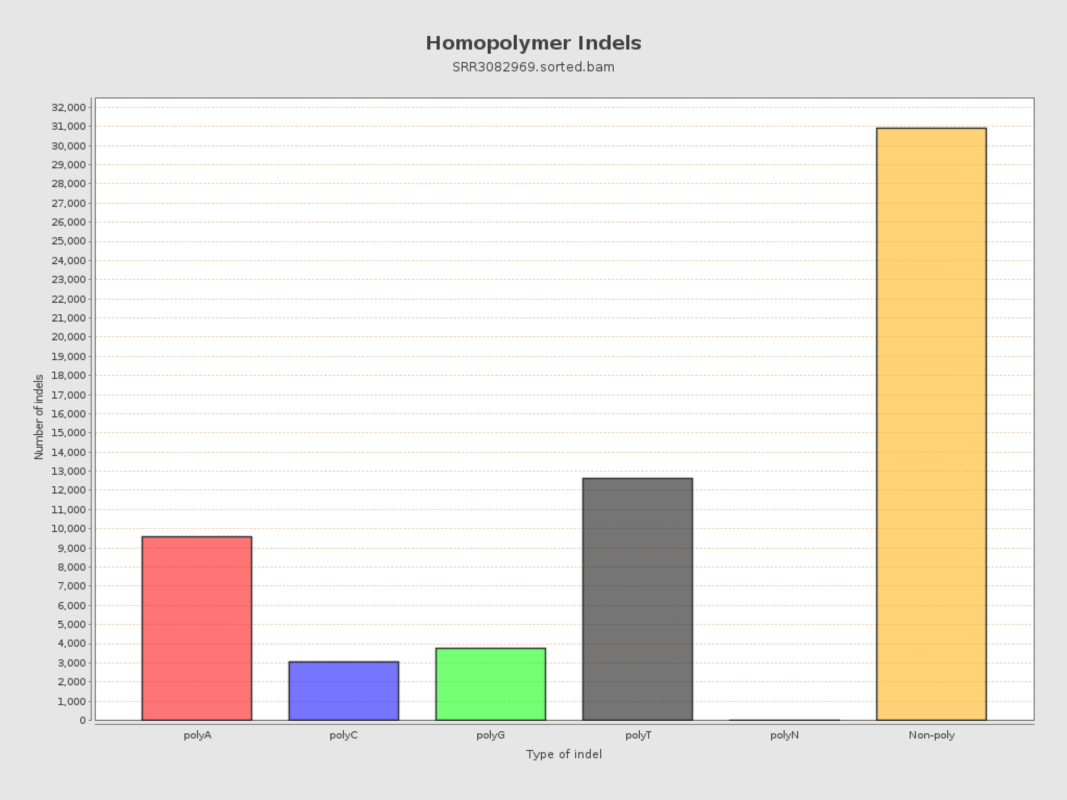
9. Results : Mapped Reads GC-content Distribution



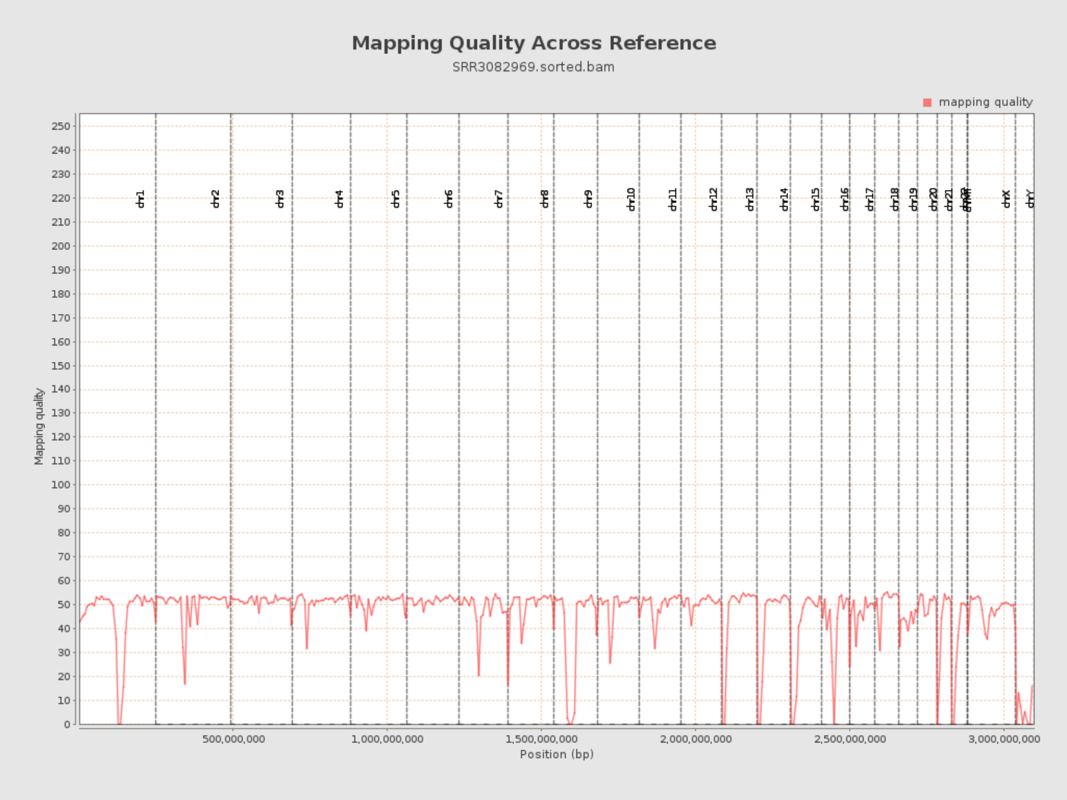
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram