Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:19:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524406.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_SRR10524406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524406.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:19:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,178,948
Mapped reads	3,777,339 / 90.39%
Unmapped reads	401,609 / 9.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,587 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	257,739 / 6.17%
Duplication rate	5.02%
Clipped reads	3,781,445 / 90.49%

2.2. ACGT Content

Number/percentage of A's	57,824,978 / 25.98%
Number/percentage of C's	43,544,815 / 19.56%
Number/percentage of T's	69,162,676 / 31.07%
Number/percentage of G's	52,027,374 / 23.37%
Number/percentage of N's	29,623 / 0.01%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0719

Standard Deviation	0.6627

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

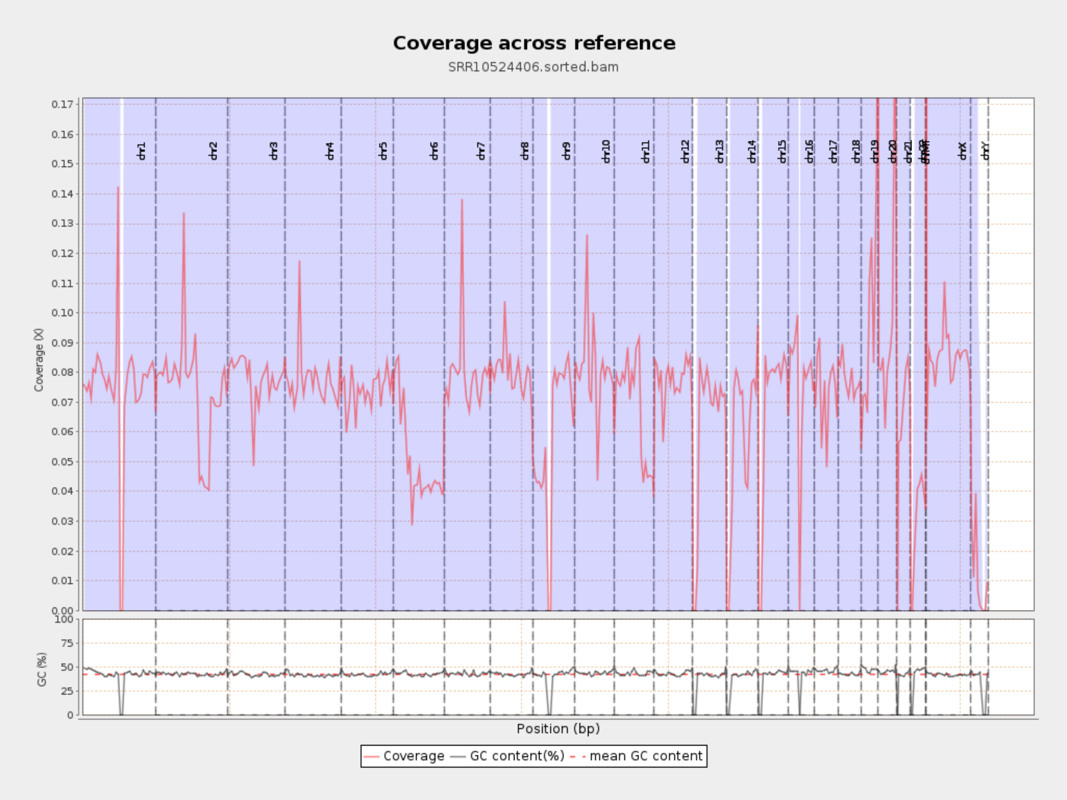
General error rate	0.5%
Mismatches	1,074,556
Insertions	16,537
Mapped reads with at least one insertion	0.44%
Deletions	41,018
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.48%

2.6. Chromosome stats

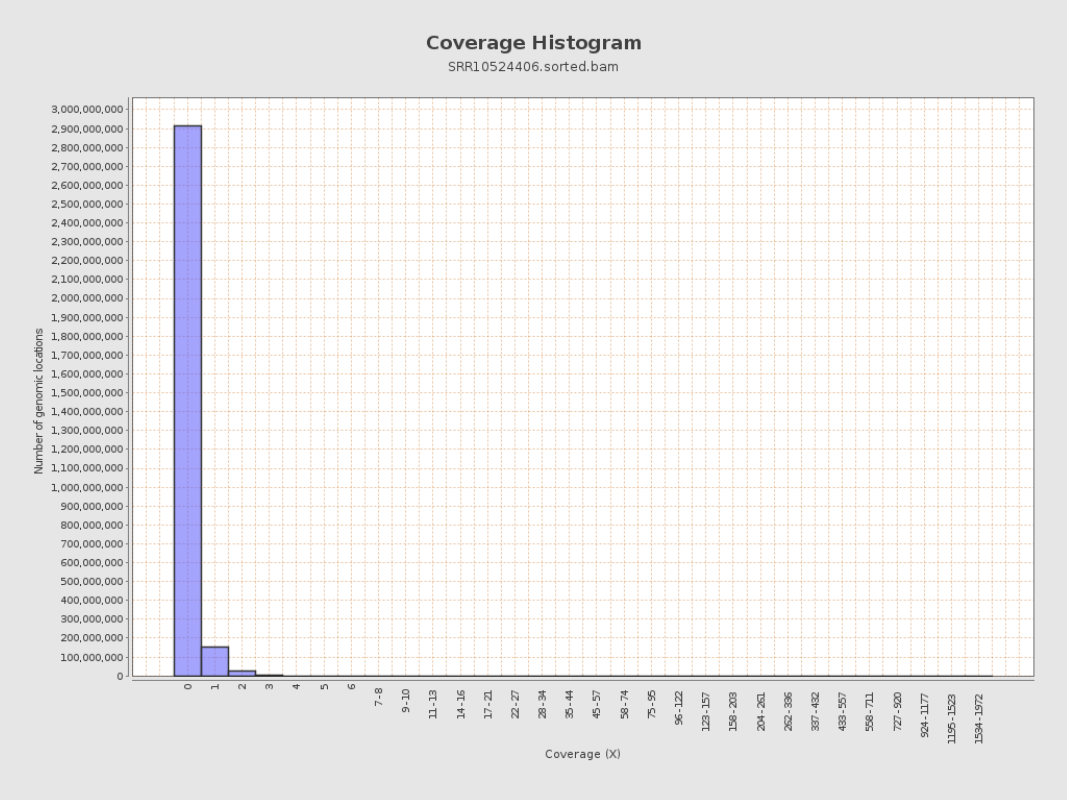
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18701255	0.075	1.5438
chr2	243199373	18066786	0.0743	0.6991
chr3	198022430	15435391	0.0779	0.3291
chr4	191154276	14878777	0.0778	0.4045
chr5	180915260	13432482	0.0742	0.325
chr6	171115067	8588276	0.0502	0.3082
chr7	159138663	12754168	0.0801	0.9738

chr8	146364022	11735954	0.0802	0.587
chr9	141213431	8226426	0.0583	0.4574
chr10	135534747	11056202	0.0816	0.5429
chr11	135006516	9192614	0.0681	0.489
chr12	133851895	10460289	0.0781	0.3504
chr13	115169878	7187907	0.0624	0.2961
chr14	107349540	6202212	0.0578	0.3042
chr15	102531392	6823849	0.0666	0.3075
chr16	90354753	6696575	0.0741	0.3533
chr17	81195210	5972758	0.0736	0.3878
chr18	78077248	6091763	0.078	0.9051
chr19	59128983	6006524	0.1016	0.9802
chr20	63025520	6223109	0.0987	0.3967
chr21	48129895	3091411	0.0642	0.364
chr22	51304566	1527176	0.0298	0.202
chrMT	16571	412609	24.8995	13.3636
chrX	155270560	13204635	0.085	0.4204
chrY	59373566	685373	0.0115	0.2981

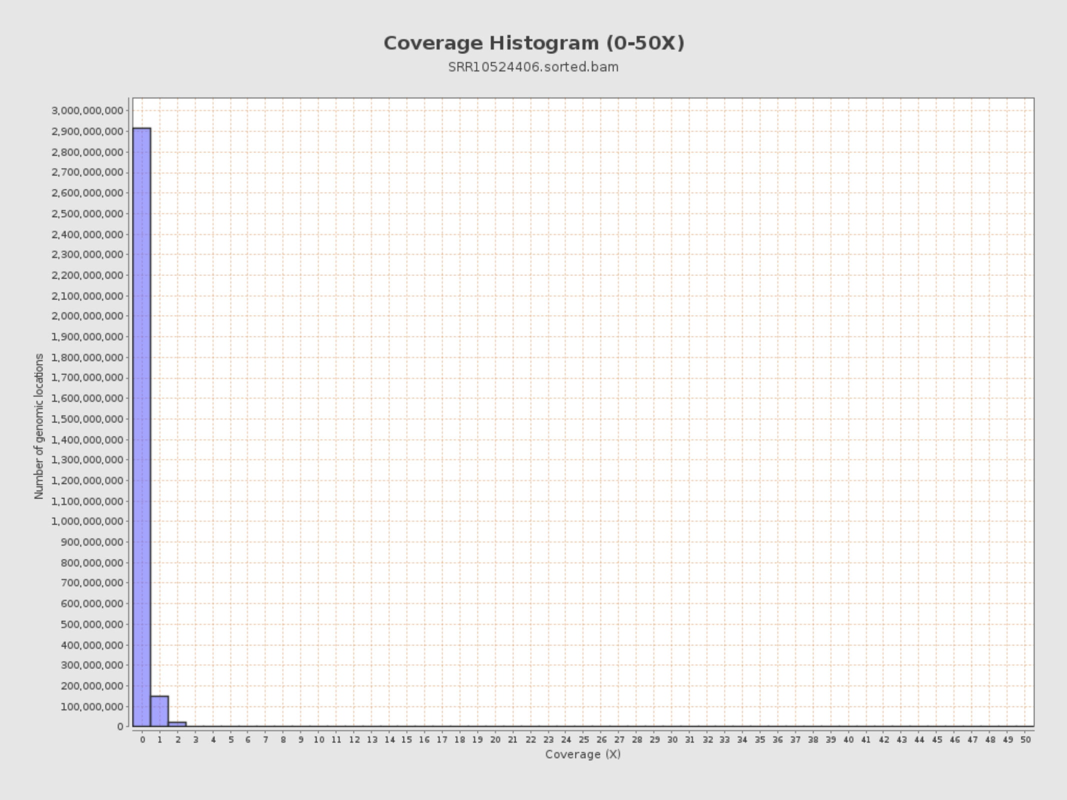
3. Results : Coverage across reference



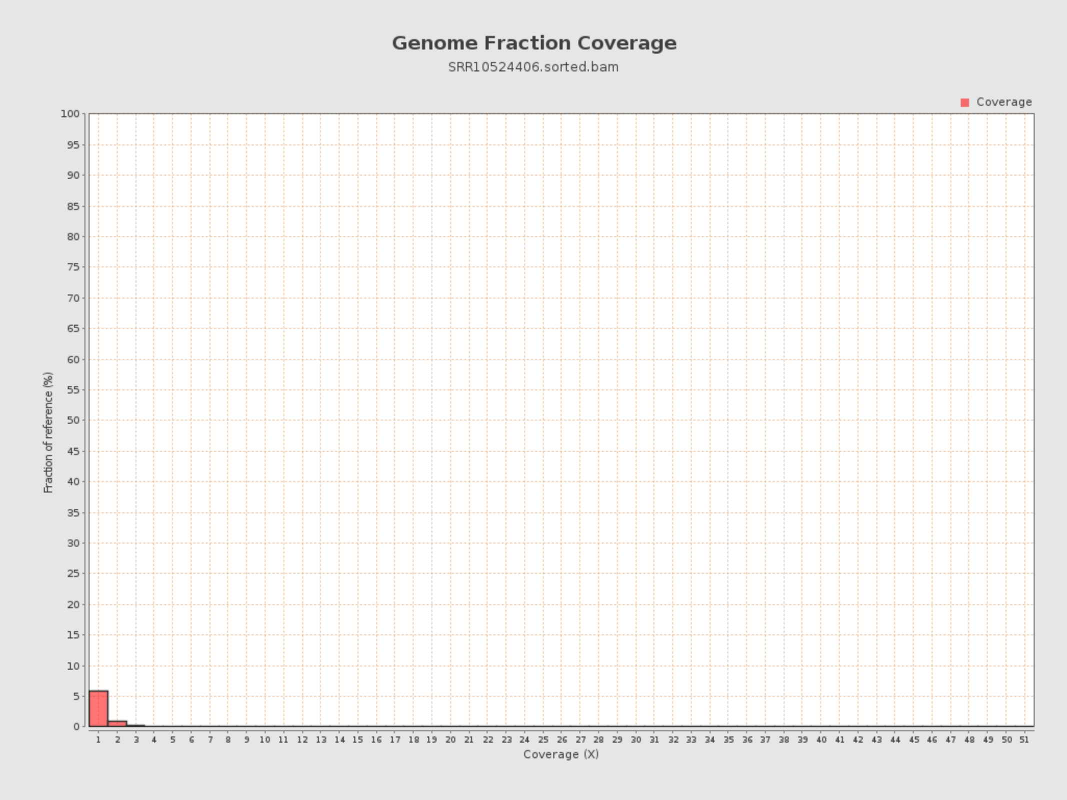
4. Results : Coverage Histogram



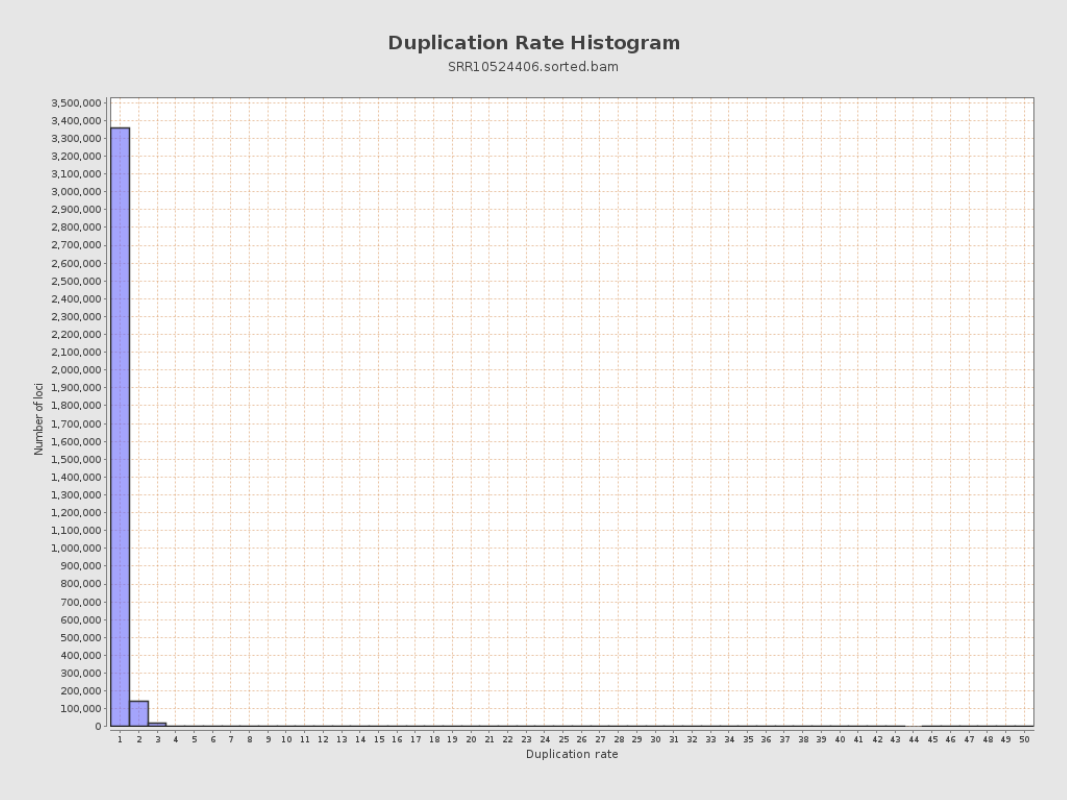
5. Results : Coverage Histogram (0-50X)



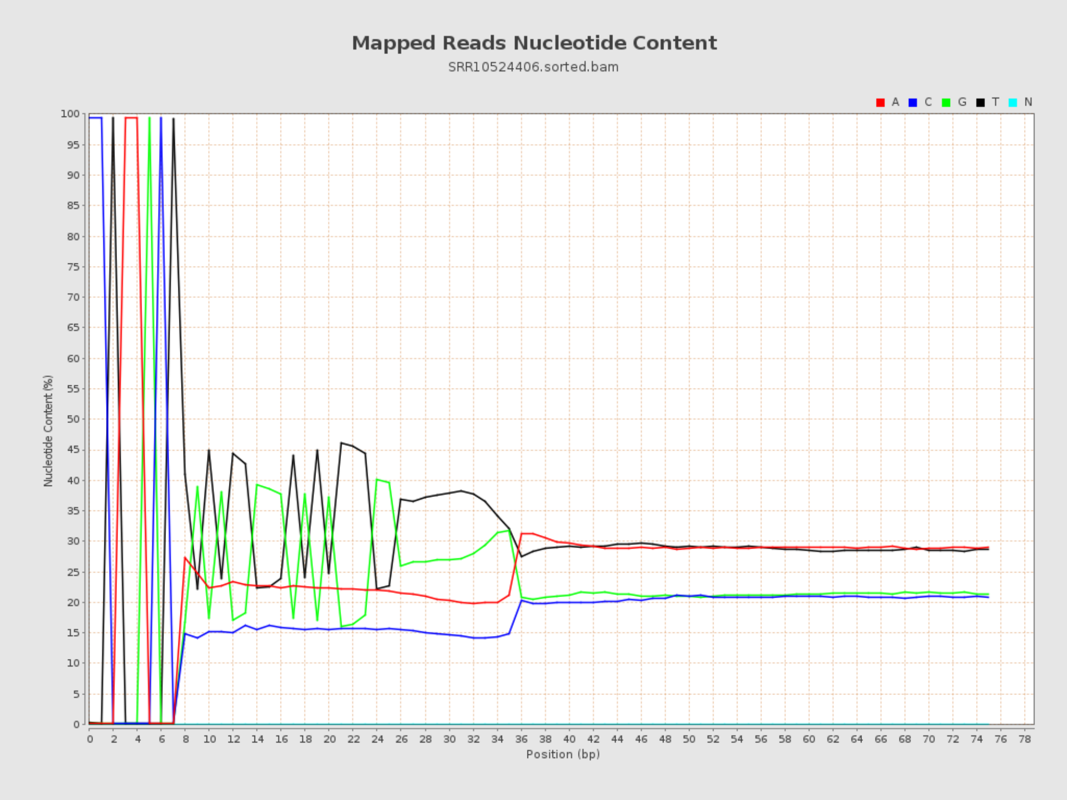
6. Results : Genome Fraction Coverage



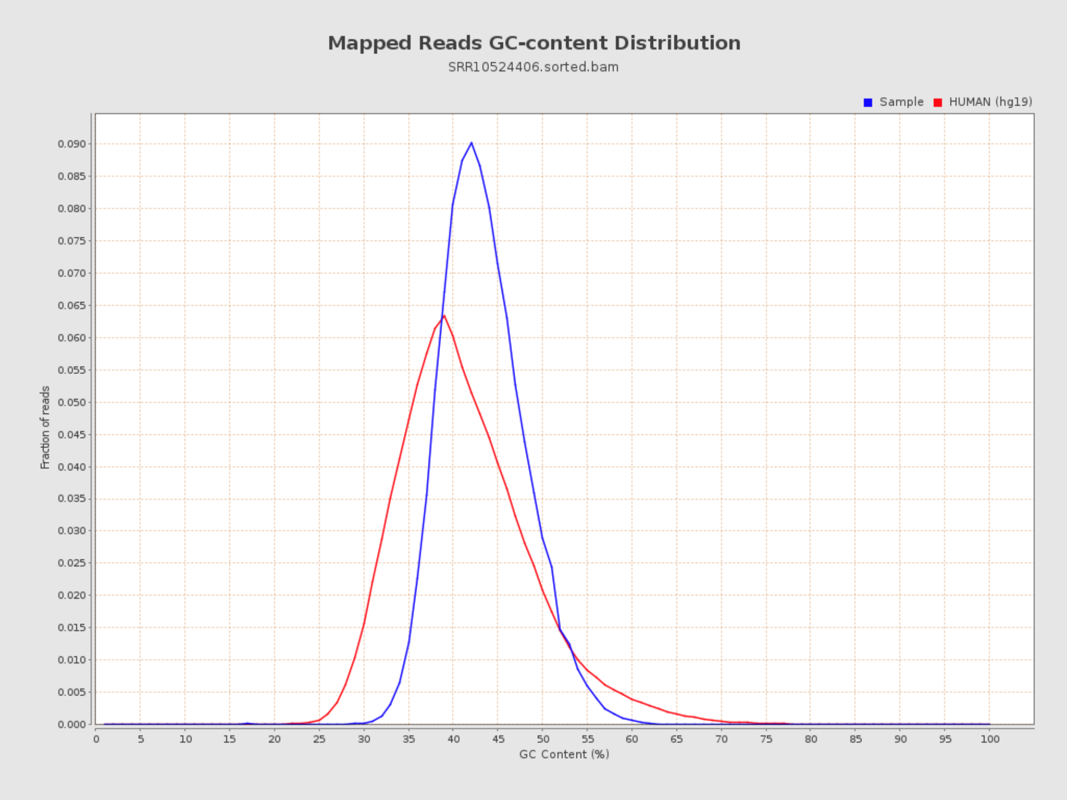
7. Results : Duplication Rate Histogram



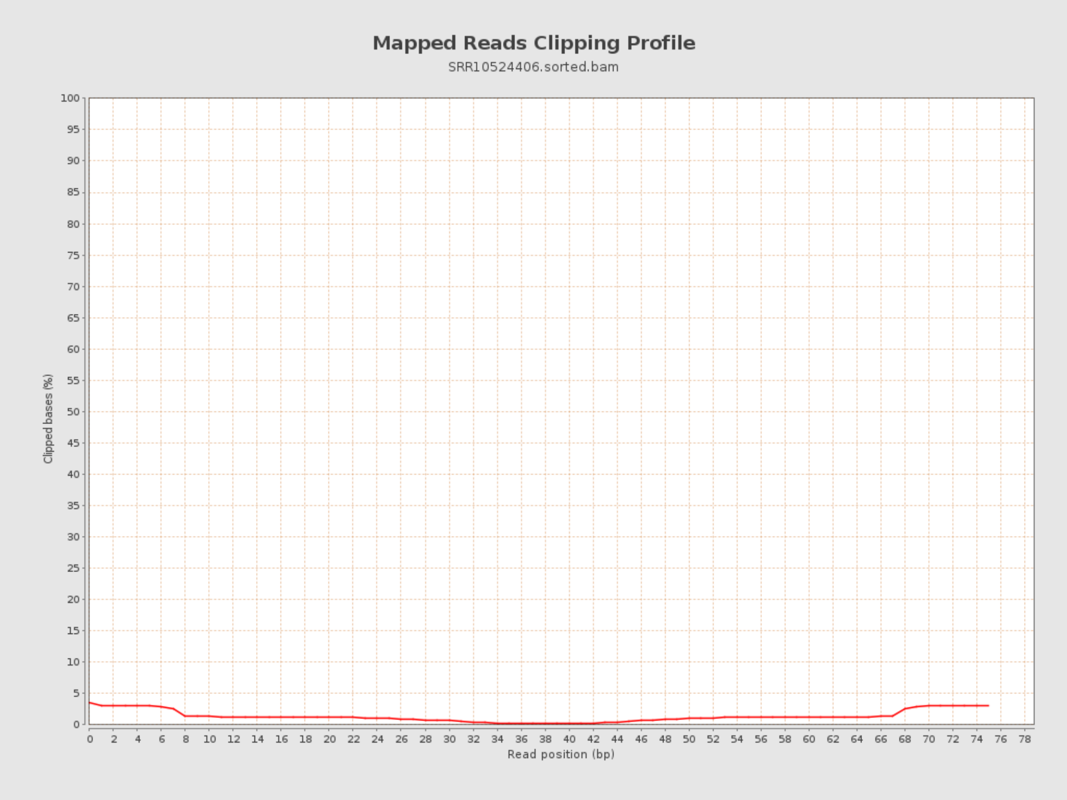
8. Results : Mapped Reads Nucleotide Content



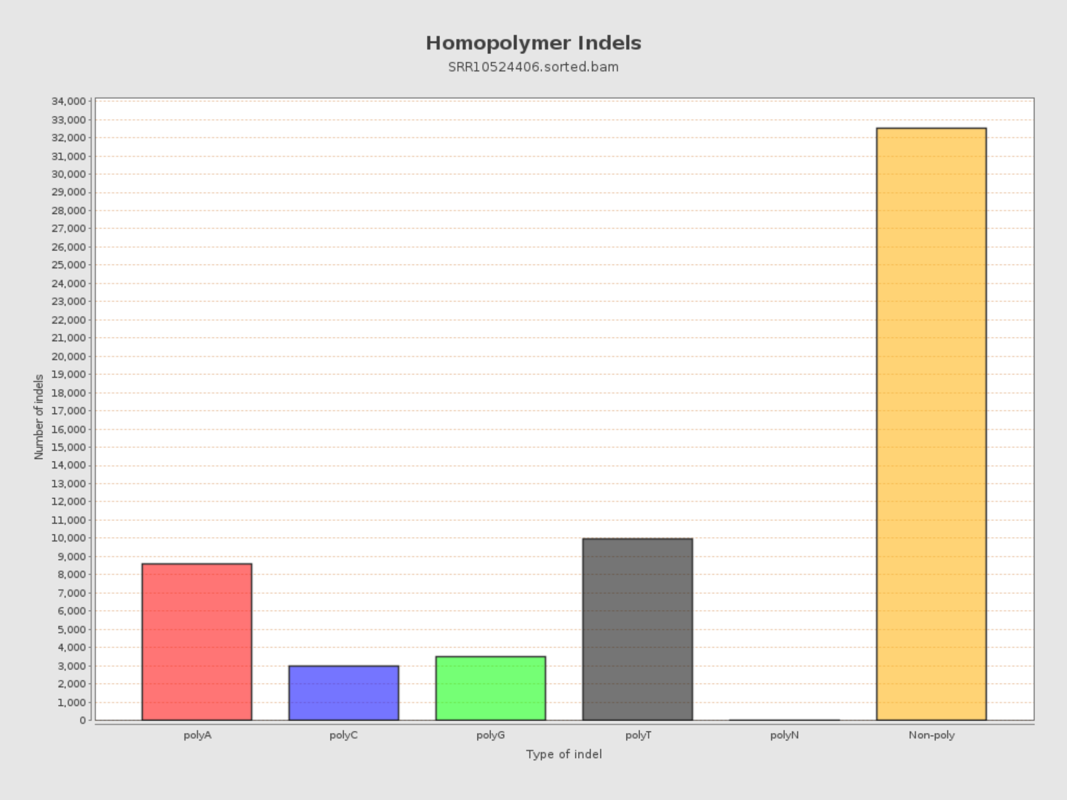
9. Results : Mapped Reads GC-content Distribution



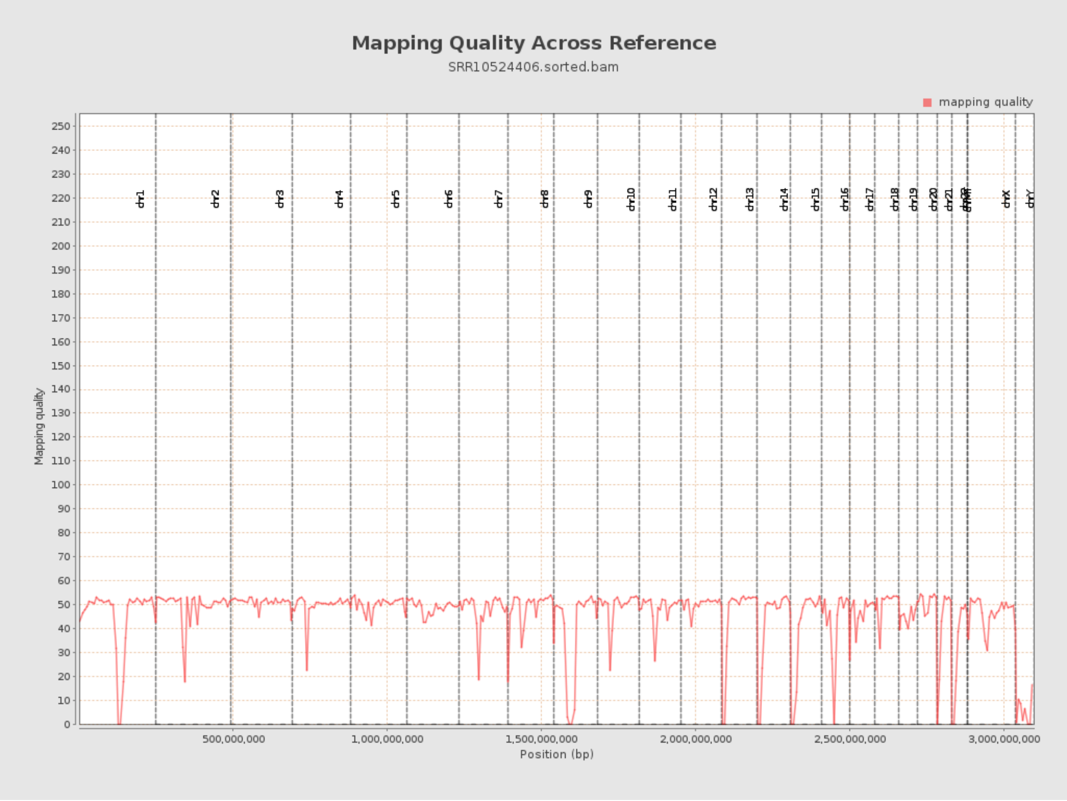
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram