Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:55:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524396.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_SRR10524396 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524396.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:55:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524396.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,744,602
Mapped reads	1,613,910 / 92.51%
Unmapped reads	130,692 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,268 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	64,099 / 3.67%
Duplication rate	2.94%
Clipped reads	1,618,493 / 92.77%

2.2. ACGT Content

Number/percentage of A's	24,431,174 / 25.82%
Number/percentage of C's	18,519,854 / 19.57%
Number/percentage of T's	29,422,567 / 31.09%
Number/percentage of G's	22,253,352 / 23.51%
Number/percentage of N's	11,770 / 0.01%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.3119

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

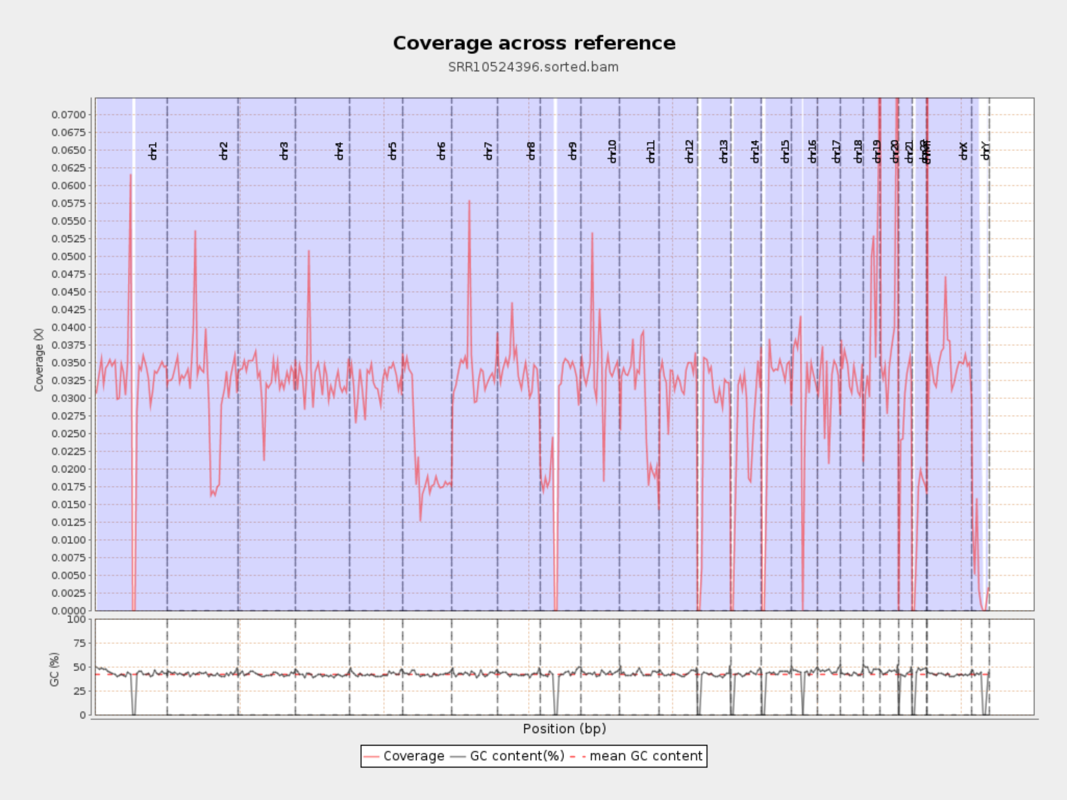
General error rate	0.5%
Mismatches	459,411
Insertions	5,809
Mapped reads with at least one insertion	0.36%
Deletions	16,799
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.62%

2.6. Chromosome stats

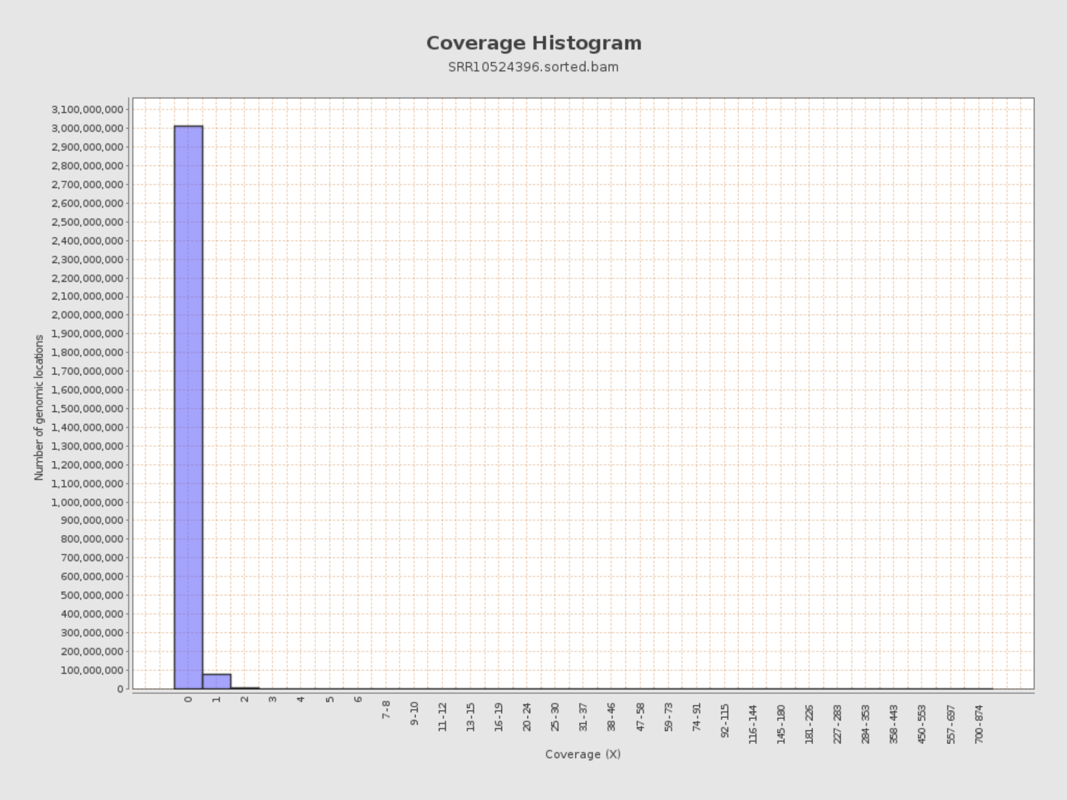
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7996362	0.0321	0.6766
chr2	243199373	7639393	0.0314	0.343
chr3	198022430	6532462	0.033	0.1967
chr4	191154276	6329208	0.0331	0.2219
chr5	180915260	5829146	0.0322	0.195
chr6	171115067	3698390	0.0216	0.1745
chr7	159138663	5452795	0.0343	0.43

chr8	146364022	5001917	0.0342	0.276
chr9	141213431	3528258	0.025	0.2225
chr10	135534747	4671246	0.0345	0.2783
chr11	135006516	3982314	0.0295	0.24
chr12	133851895	4394715	0.0328	0.2018
chr13	115169878	3089290	0.0268	0.1785
chr14	107349540	2625531	0.0245	0.1761
chr15	102531392	2898456	0.0283	0.1818
chr16	90354753	2819042	0.0312	0.2004
chr17	81195210	2571531	0.0317	0.2123
chr18	78077248	2598590	0.0333	0.3912
chr19	59128983	2611836	0.0442	0.4685
chr20	63025520	2648813	0.042	0.23
chr21	48129895	1310814	0.0272	0.1974
chr22	51304566	662133	0.0129	0.122
chrMT	16571	61509	3.7118	2.9258
chrX	155270560	5433195	0.035	0.2272
chrY	59373566	278501	0.0047	0.1275

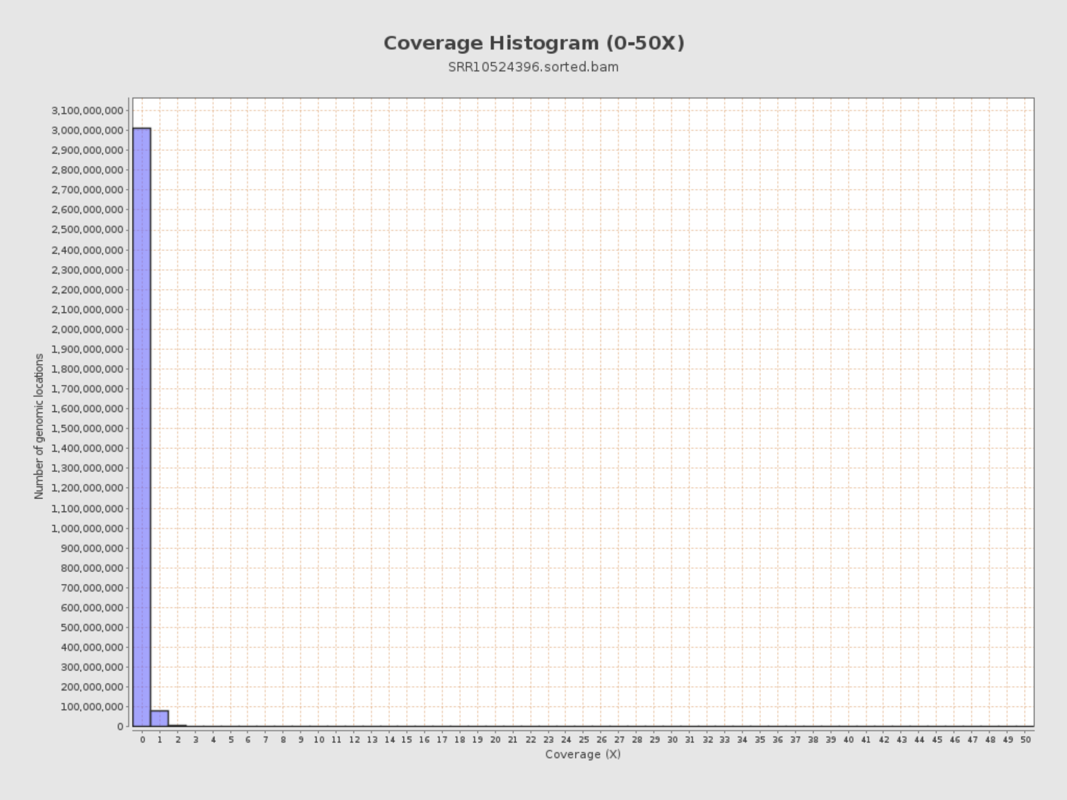
3. Results : Coverage across reference



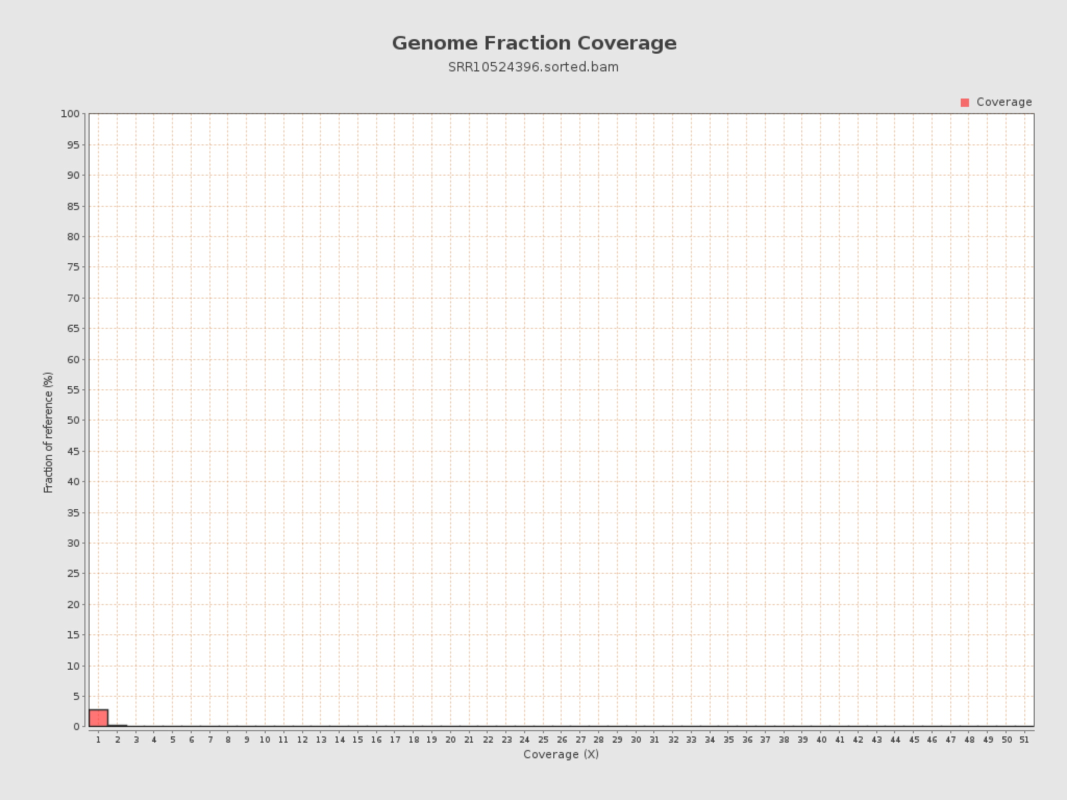
4. Results : Coverage Histogram



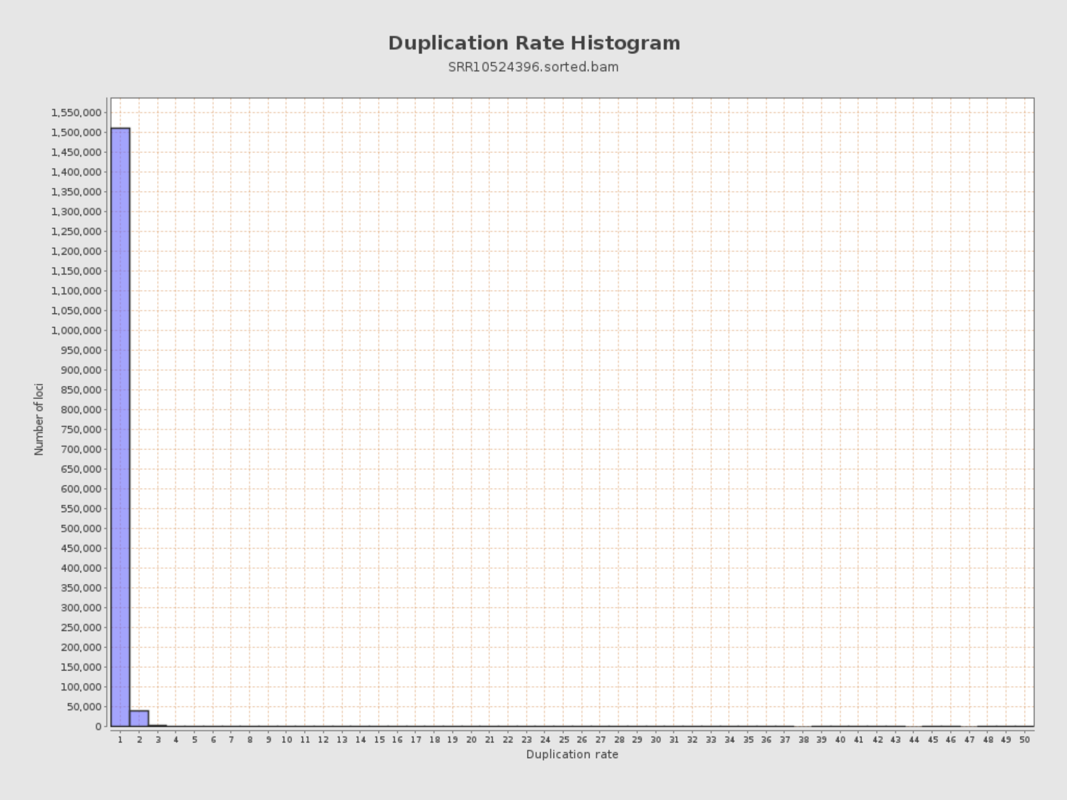
5. Results : Coverage Histogram (0-50X)



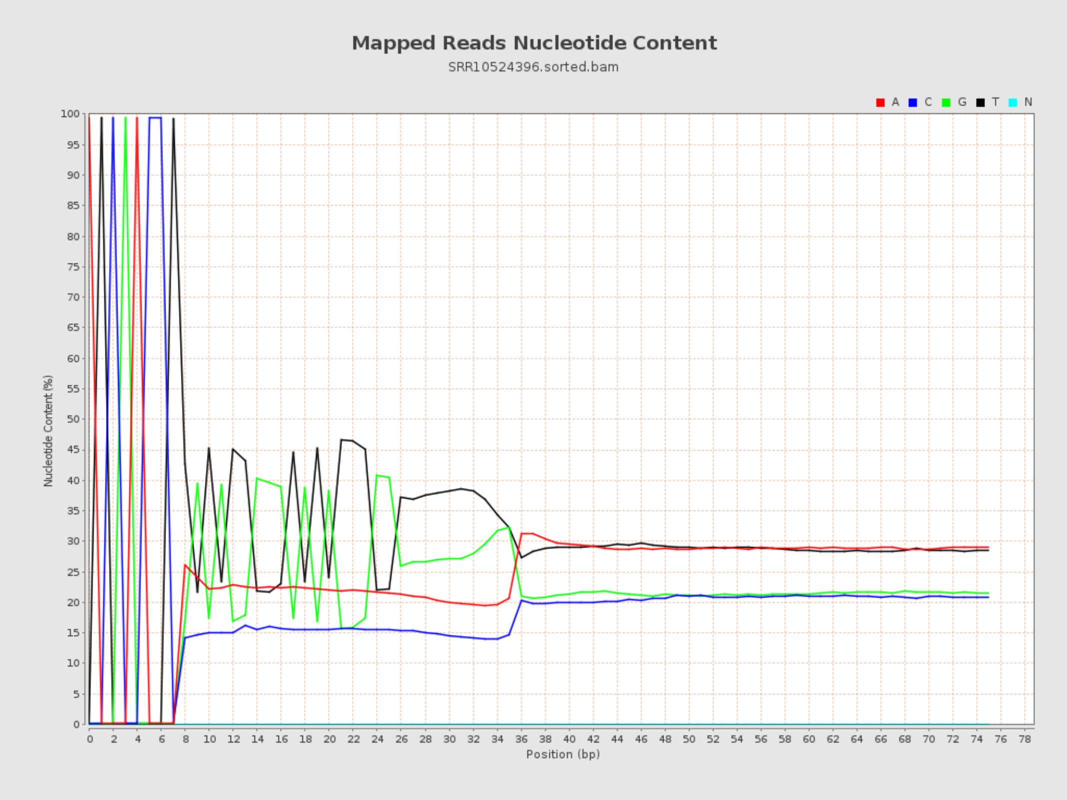
6. Results : Genome Fraction Coverage



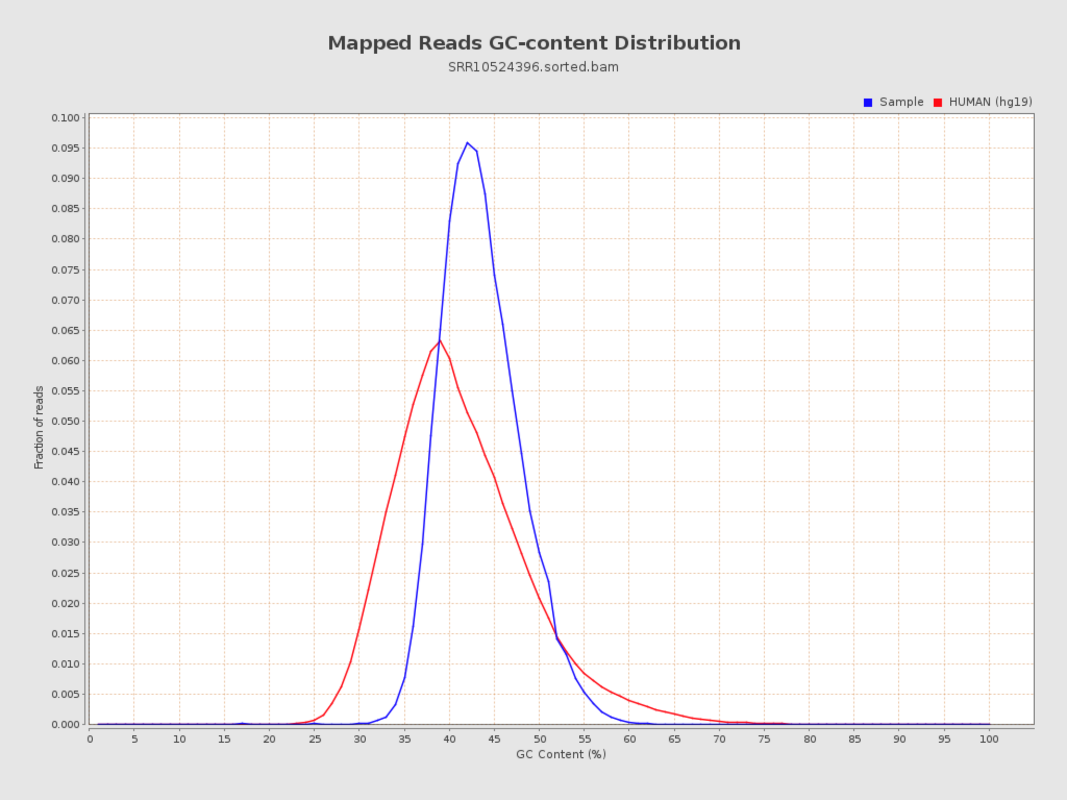
7. Results : Duplication Rate Histogram



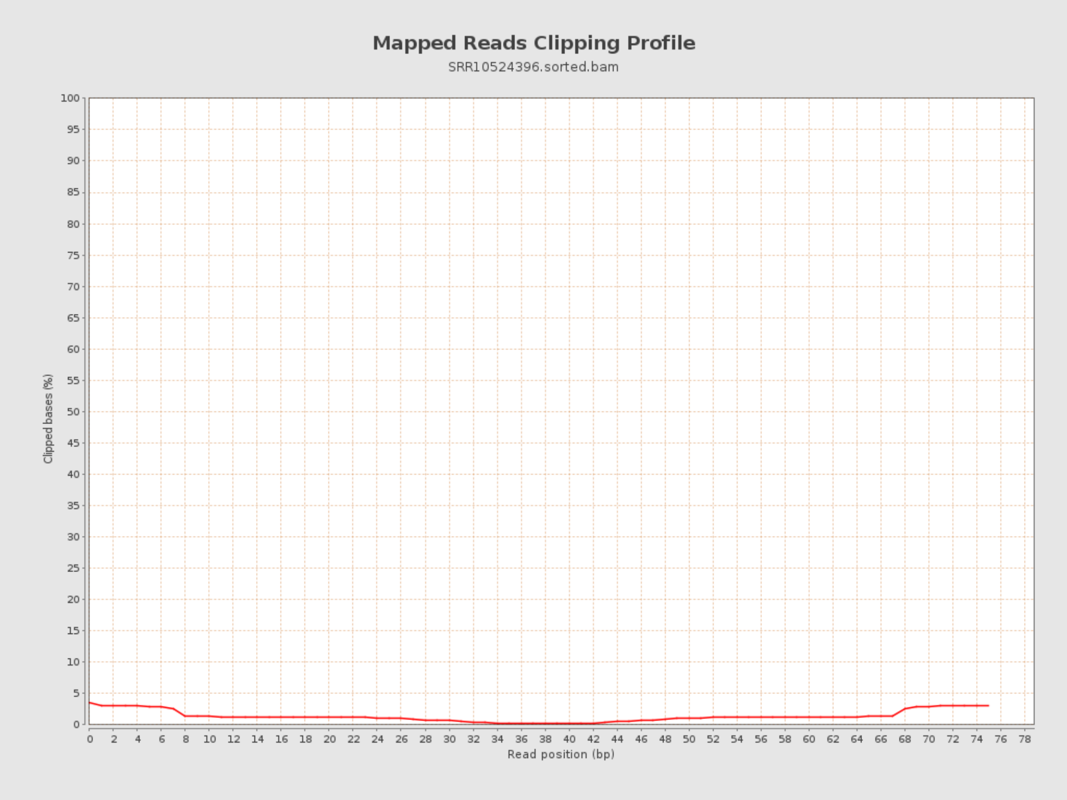
8. Results : Mapped Reads Nucleotide Content



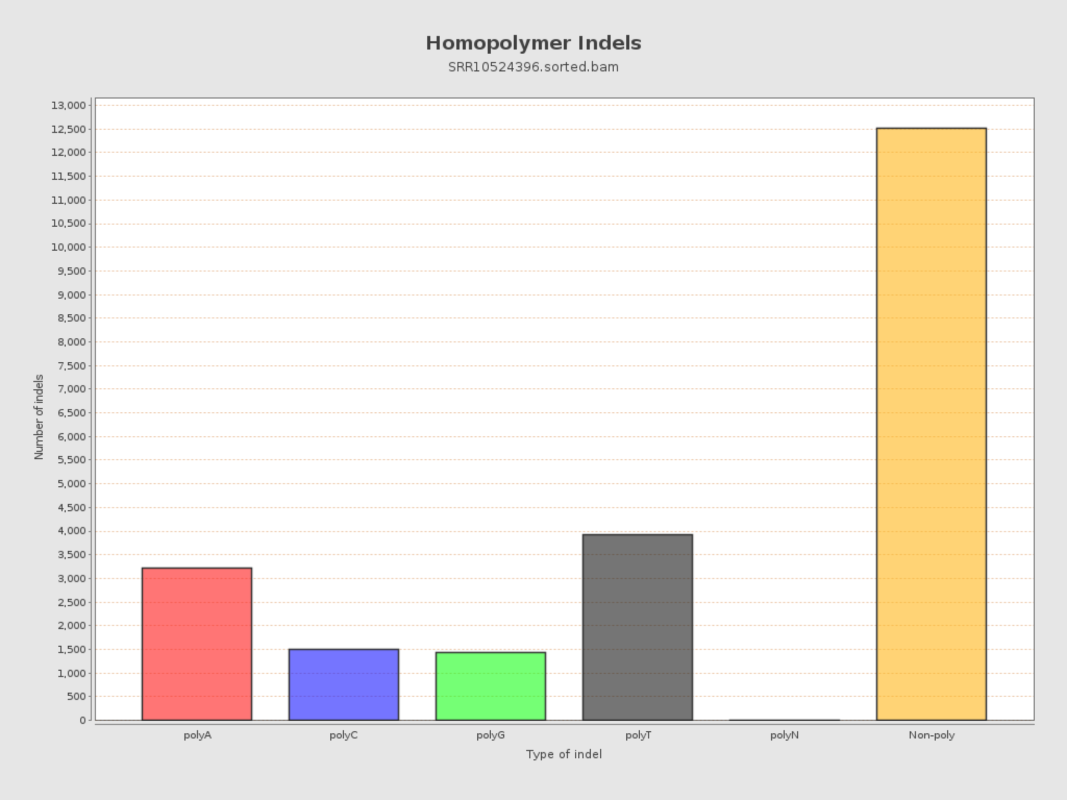
9. Results : Mapped Reads GC-content Distribution



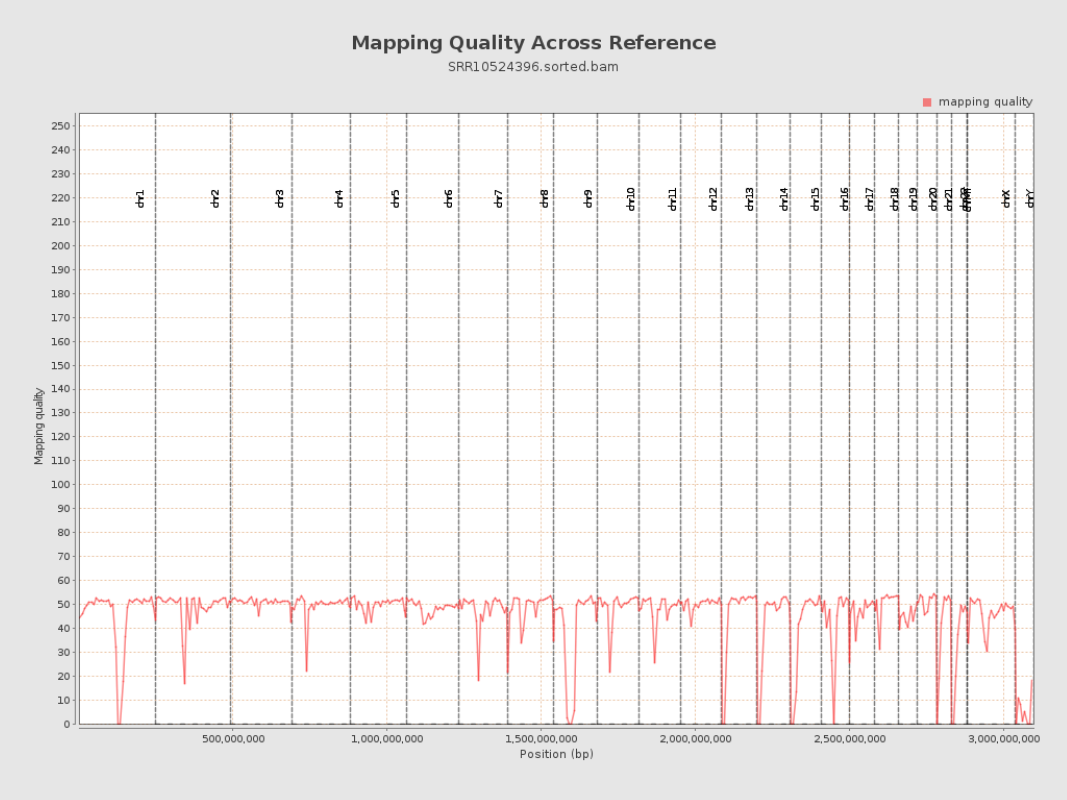
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram