Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:08:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524622.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_SRR10524622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524622.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:08:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,201,922
Mapped reads	2,928,335 / 91.46%
Unmapped reads	273,587 / 8.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,872 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	126,809 / 3.96%
Duplication rate	3.03%
Clipped reads	2,936,743 / 91.72%

2.2. ACGT Content

Number/percentage of A's	43,521,712 / 25.85%
Number/percentage of C's	33,059,373 / 19.63%
Number/percentage of T's	52,435,684 / 31.14%
Number/percentage of G's	39,365,981 / 23.38%
Number/percentage of N's	4,748 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.4544

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

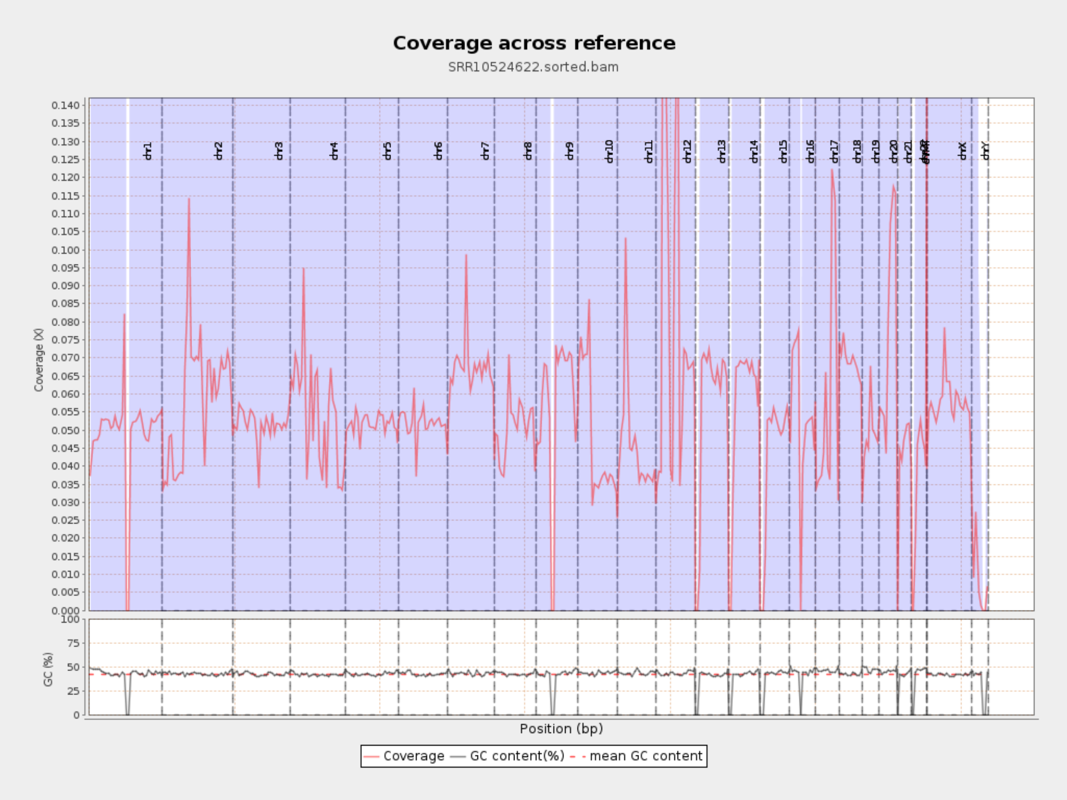
General error rate	0.49%
Mismatches	809,943
Insertions	9,013
Mapped reads with at least one insertion	0.31%
Deletions	25,902
Mapped reads with at least one deletion	0.88%
Homopolymer indels	43.75%

2.6. Chromosome stats

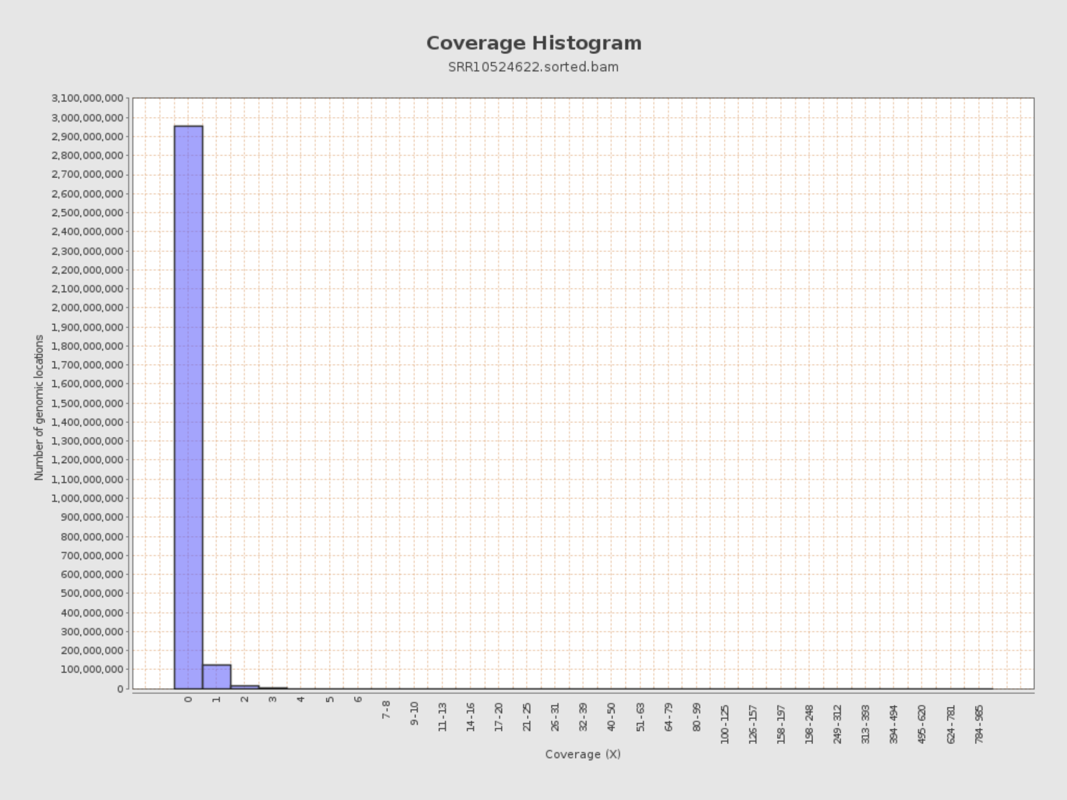
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12149751	0.0487	0.8004
chr2	243199373	14445901	0.0594	0.5282
chr3	198022430	10194043	0.0515	0.2571
chr4	191154276	10398379	0.0544	0.3203
chr5	180915260	9368374	0.0518	0.2631
chr6	171115067	8888921	0.0519	0.2988
chr7	159138663	10777846	0.0677	0.6454

chr8	146364022	7418013	0.0507	0.4347
chr9	141213431	7971529	0.0565	0.4813
chr10	135534747	6537694	0.0482	0.4332
chr11	135006516	6219719	0.0461	0.3799
chr12	133851895	11393094	0.0851	0.3852
chr13	115169878	6423421	0.0558	0.2672
chr14	107349540	5989581	0.0558	0.31
chr15	102531392	4350560	0.0424	0.24
chr16	90354753	4853000	0.0537	0.3052
chr17	81195210	4613526	0.0568	0.2873
chr18	78077248	5424359	0.0695	0.885
chr19	59128983	2890667	0.0489	0.6272
chr20	63025520	4974786	0.0789	0.3379
chr21	48129895	2033157	0.0422	0.286
chr22	51304566	1704509	0.0332	0.204
chrMT	16571	2381	0.1437	0.3908
chrX	155270560	8927863	0.0575	0.3576
chrY	59373566	479771	0.0081	0.1895

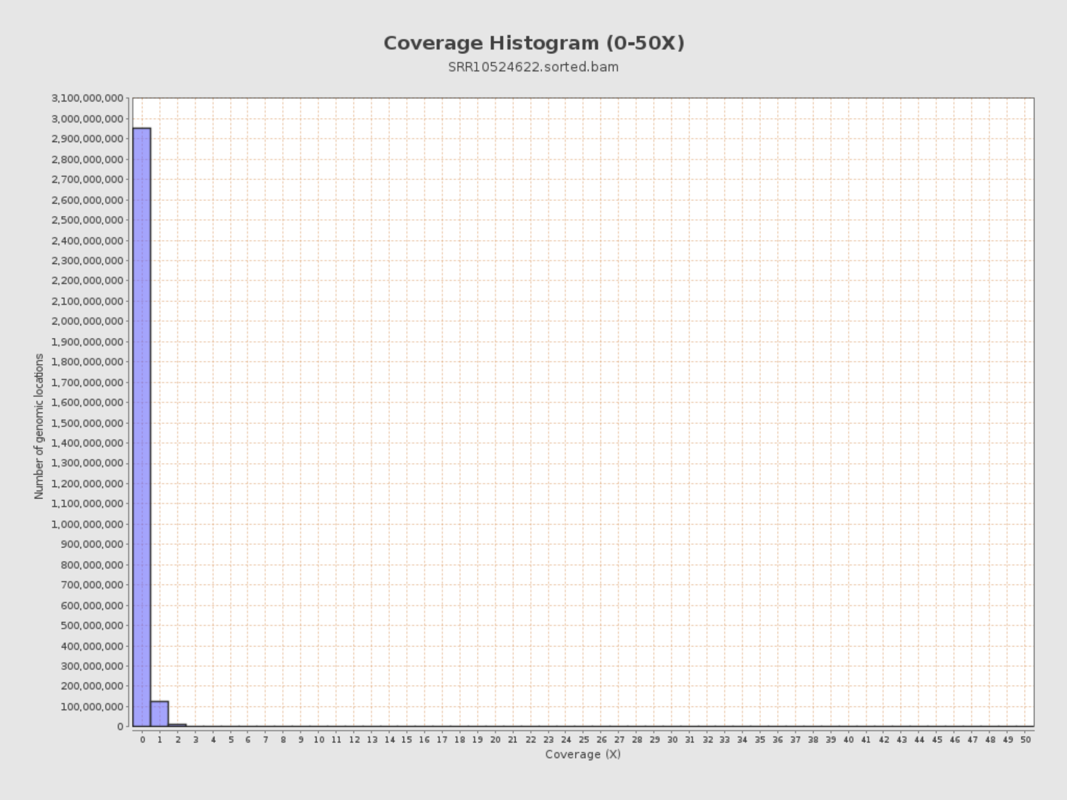
3. Results : Coverage across reference



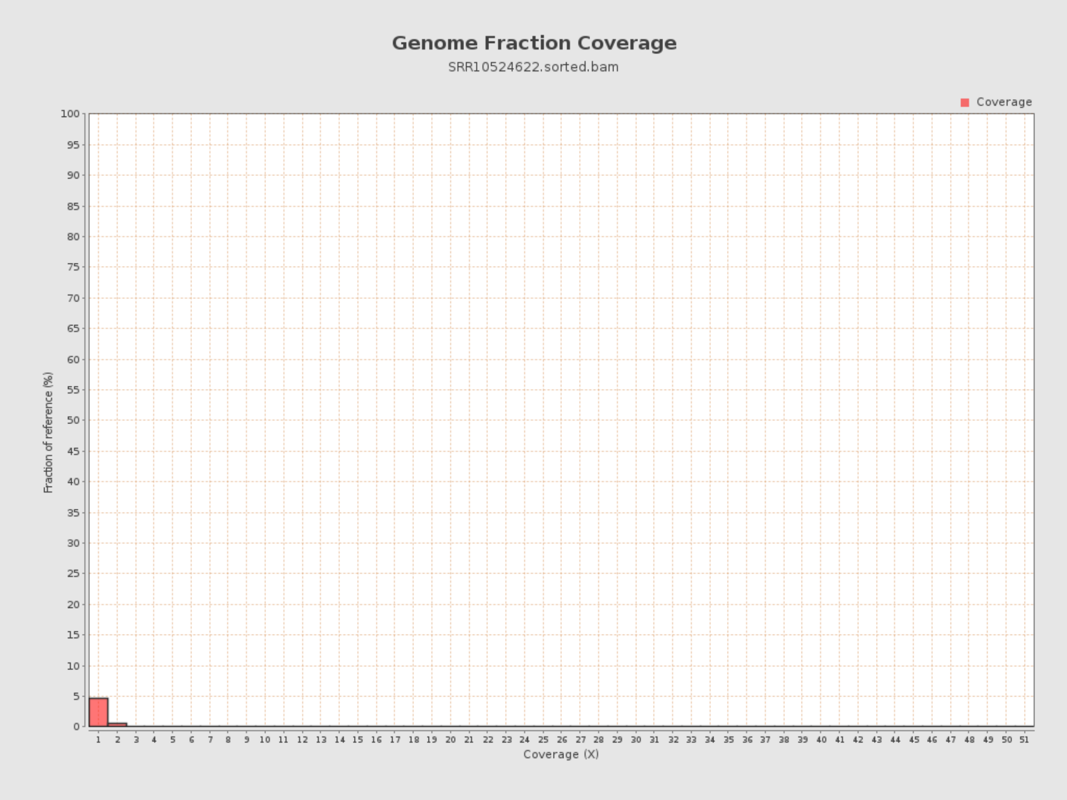
4. Results : Coverage Histogram



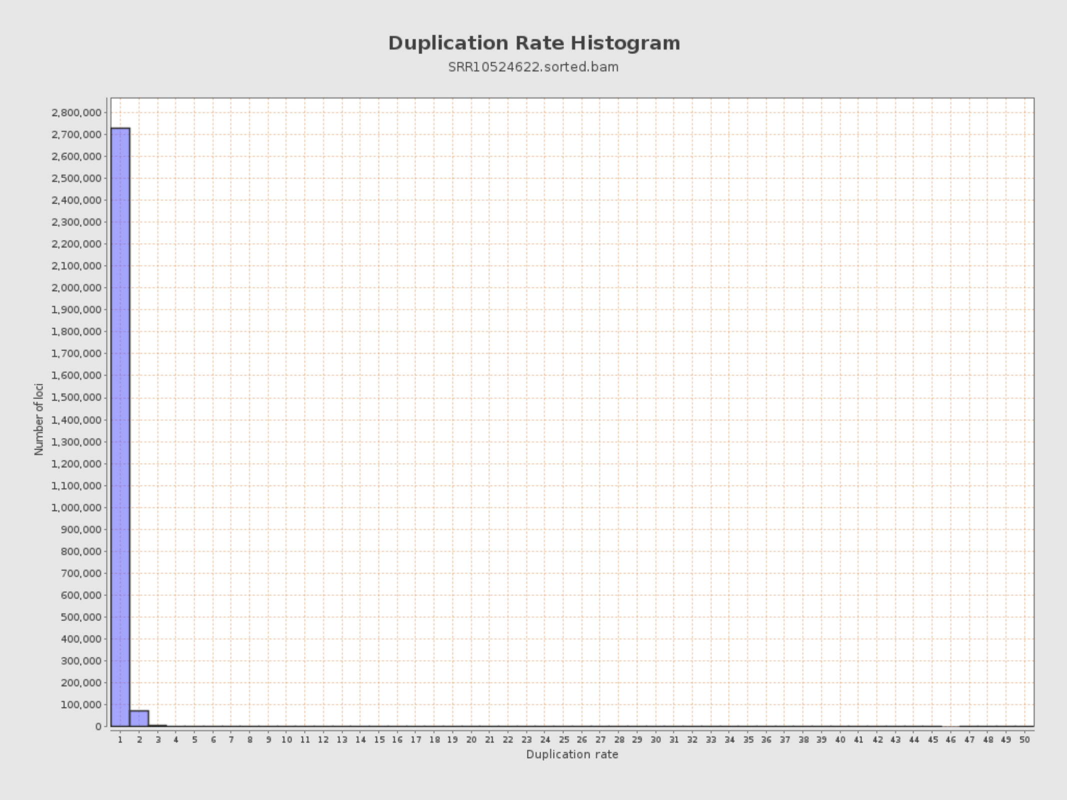
5. Results : Coverage Histogram (0-50X)



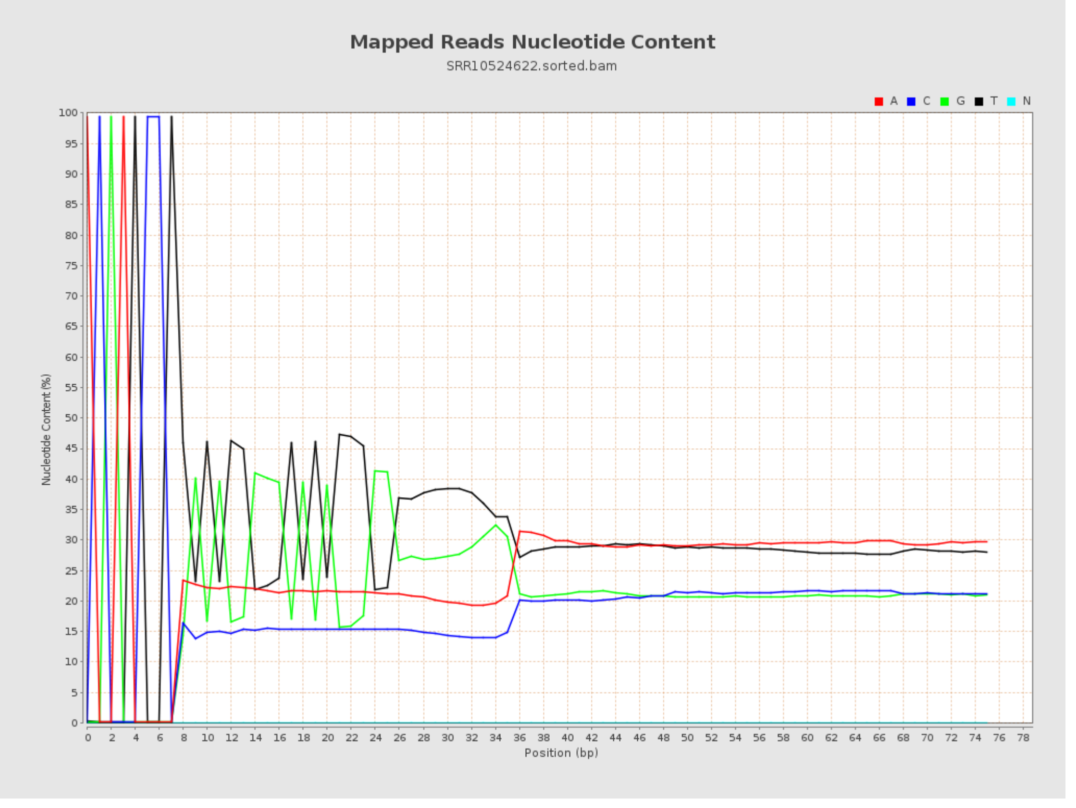
6. Results : Genome Fraction Coverage



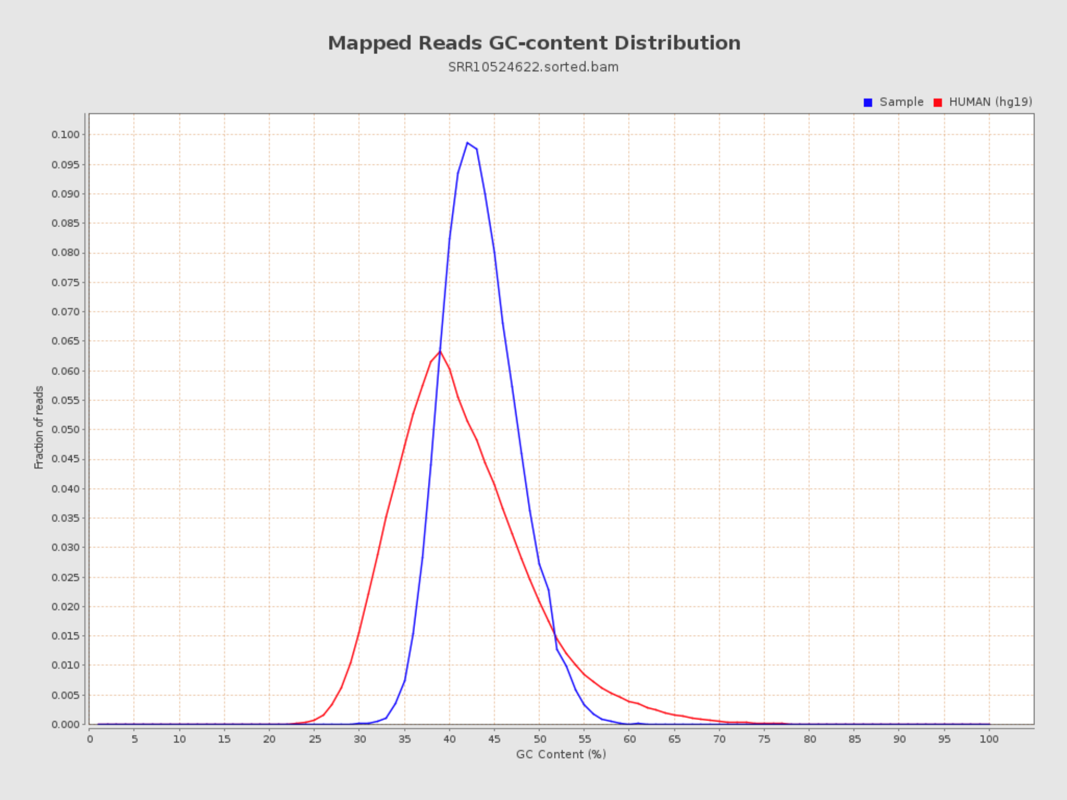
7. Results : Duplication Rate Histogram



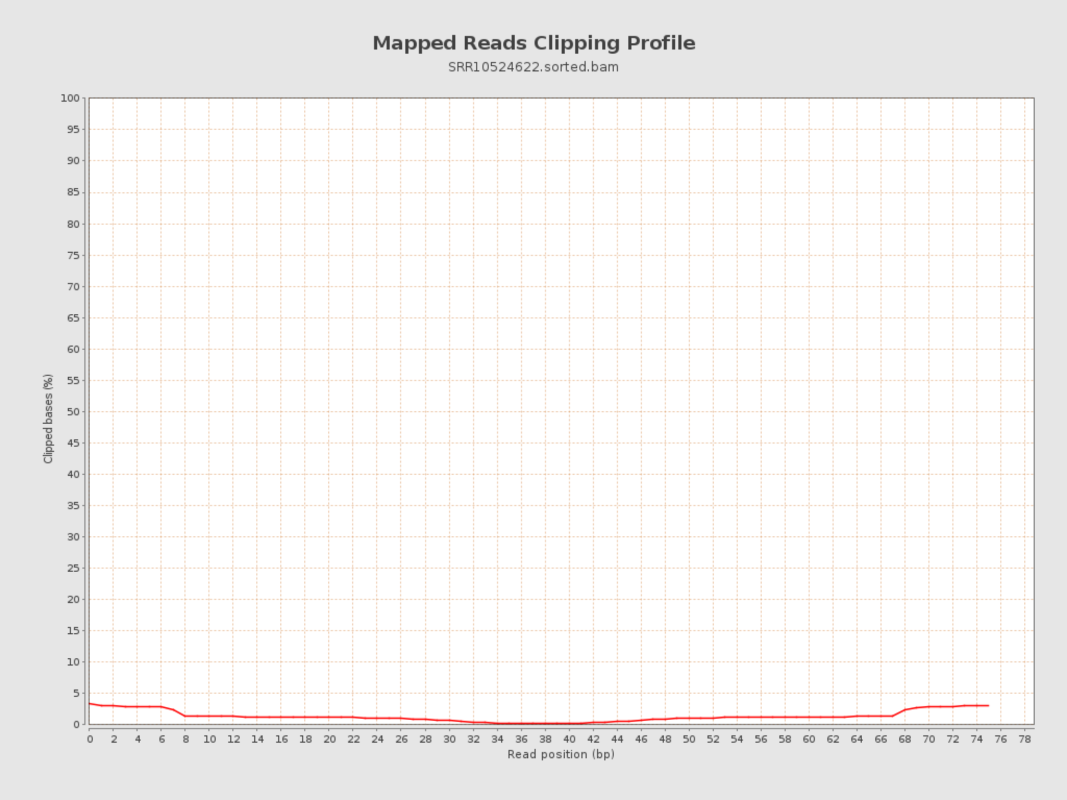
8. Results : Mapped Reads Nucleotide Content



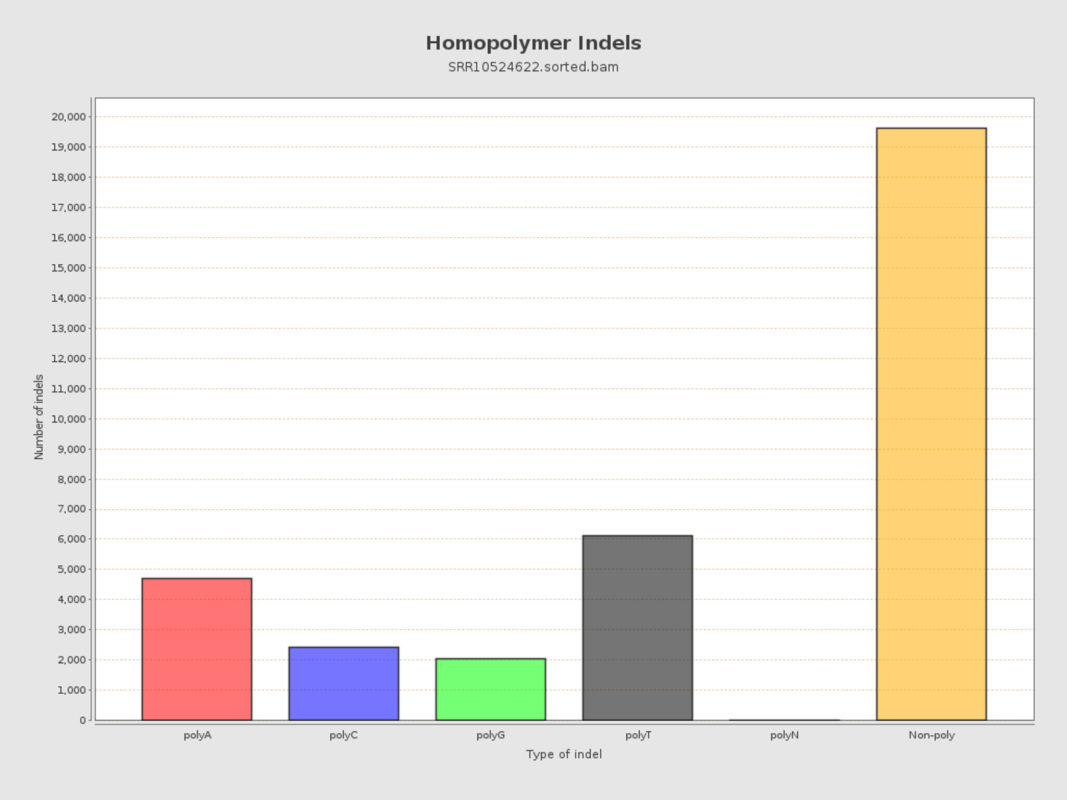
9. Results : Mapped Reads GC-content Distribution



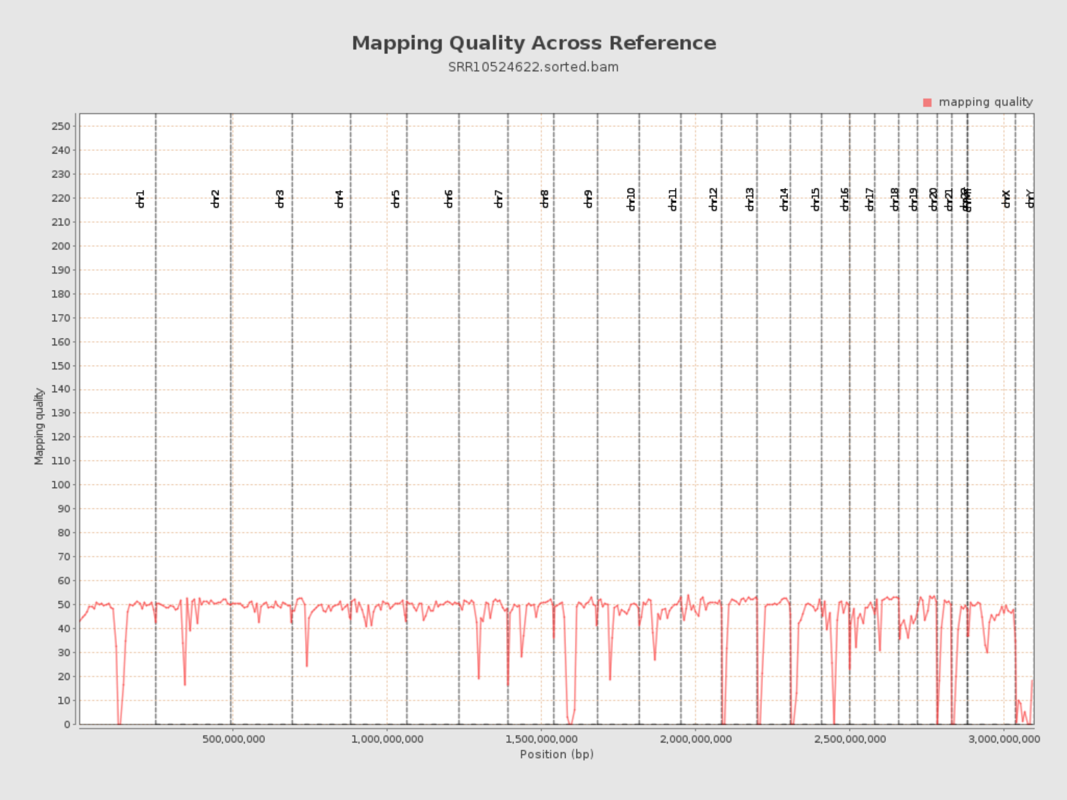
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram