Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:41:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524789.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_SRR10524789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,648,687
Mapped reads	1,501,948 / 91.1%
Unmapped reads	146,739 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,798 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,979 / 3.09%
Duplication rate	2.41%
Clipped reads	1,505,876 / 91.34%

2.2. ACGT Content

Number/percentage of A's	22,614,049 / 25.62%
Number/percentage of C's	16,239,952 / 18.4%
Number/percentage of T's	27,153,973 / 30.76%
Number/percentage of G's	22,255,156 / 25.21%
Number/percentage of N's	1,912 / 0%
GC Percentage	43.61%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2924

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

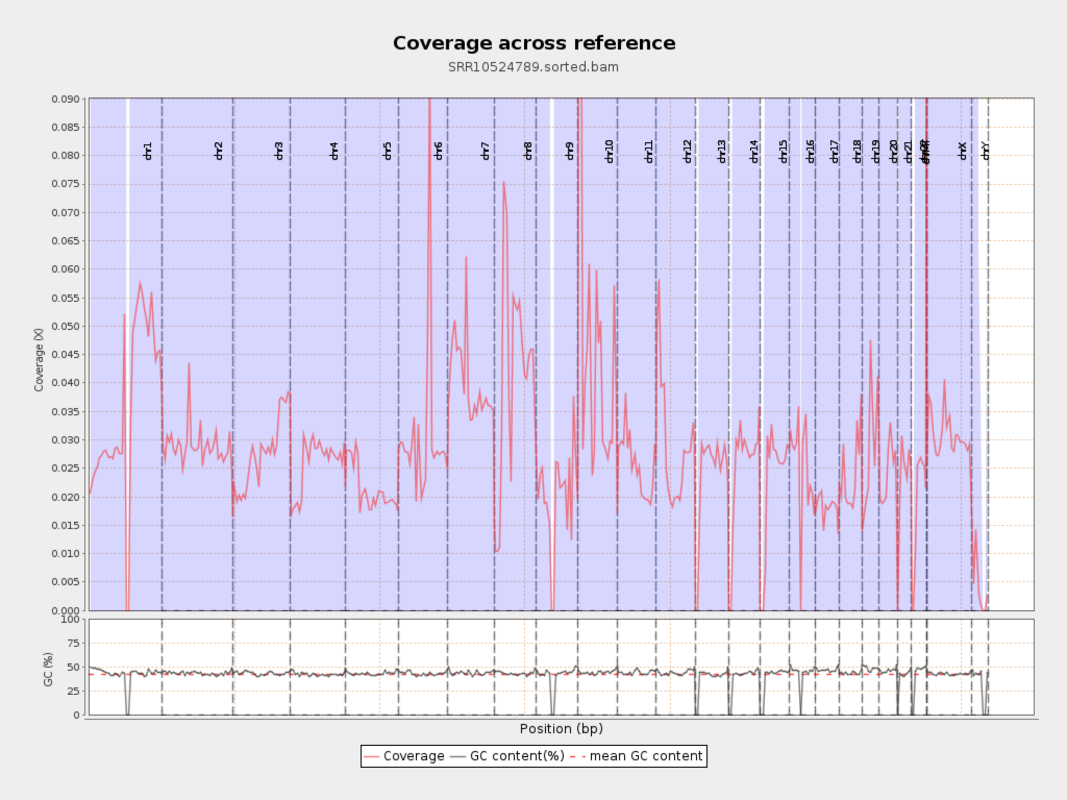
General error rate	0.56%
Mismatches	481,621
Insertions	5,279
Mapped reads with at least one insertion	0.35%
Deletions	18,724
Mapped reads with at least one deletion	1.24%
Homopolymer indels	45.72%

2.6. Chromosome stats

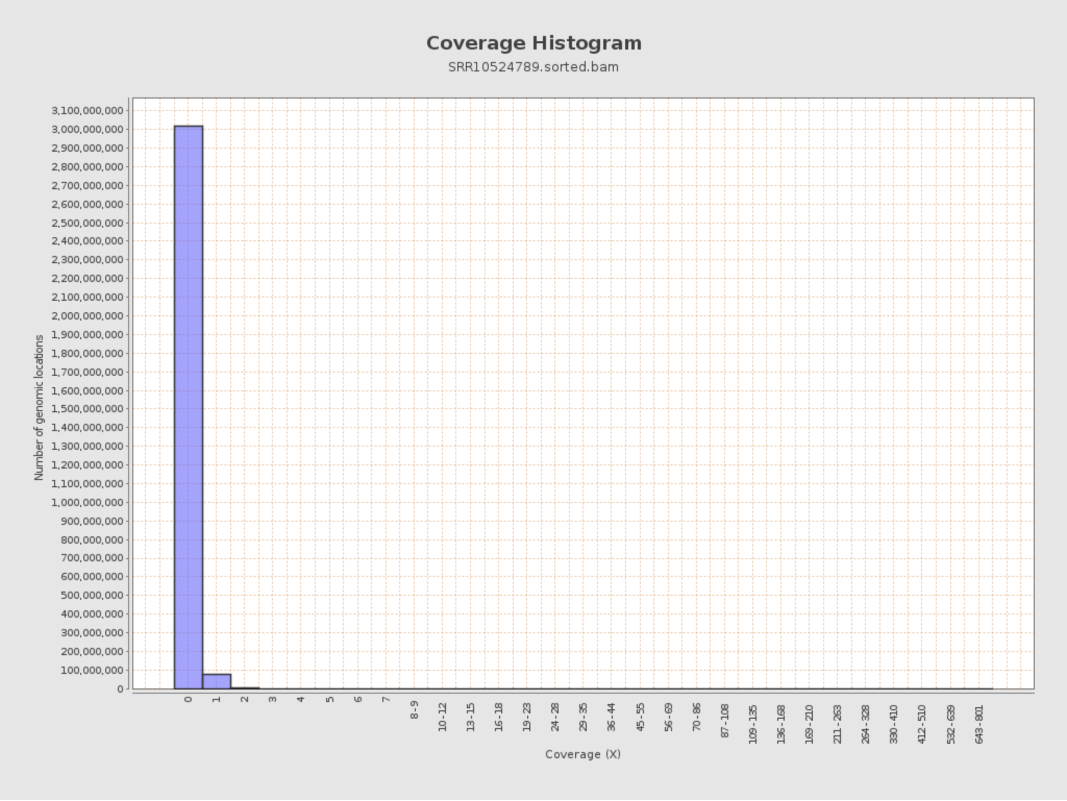
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8926020	0.0358	0.5593
chr2	243199373	7060419	0.029	0.3541
chr3	198022430	5432535	0.0274	0.1809
chr4	191154276	4941283	0.0258	0.1815
chr5	180915260	3891024	0.0215	0.1581
chr6	171115067	5343935	0.0312	0.2132
chr7	159138663	6434576	0.0404	0.4839

chr8	146364022	6033038	0.0412	0.3137
chr9	141213431	2818699	0.02	0.1976
chr10	135534747	6547644	0.0483	0.3386
chr11	135006516	3443645	0.0255	0.225
chr12	133851895	3898119	0.0291	0.1862
chr13	115169878	2736318	0.0238	0.1671
chr14	107349540	2622883	0.0244	0.1708
chr15	102531392	2303208	0.0225	0.1619
chr16	90354753	2213206	0.0245	0.1869
chr17	81195210	1471438	0.0181	0.149
chr18	78077248	1866922	0.0239	0.4079
chr19	59128983	1715314	0.029	0.3755
chr20	63025520	1511457	0.024	0.1684
chr21	48129895	1111214	0.0231	0.1713
chr22	51304566	919568	0.0179	0.1431
chrMT	16571	3209	0.1937	0.4552
chrX	155270560	4794099	0.0309	0.2026
chrY	59373566	255352	0.0043	0.118

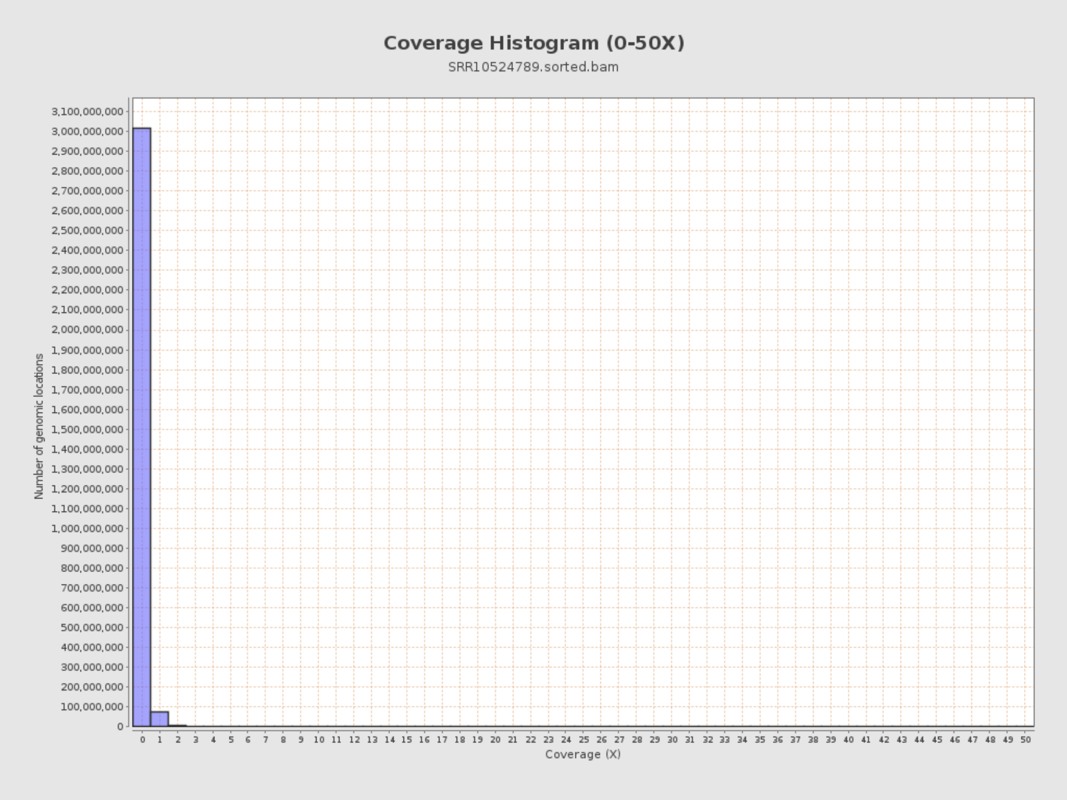
3. Results : Coverage across reference



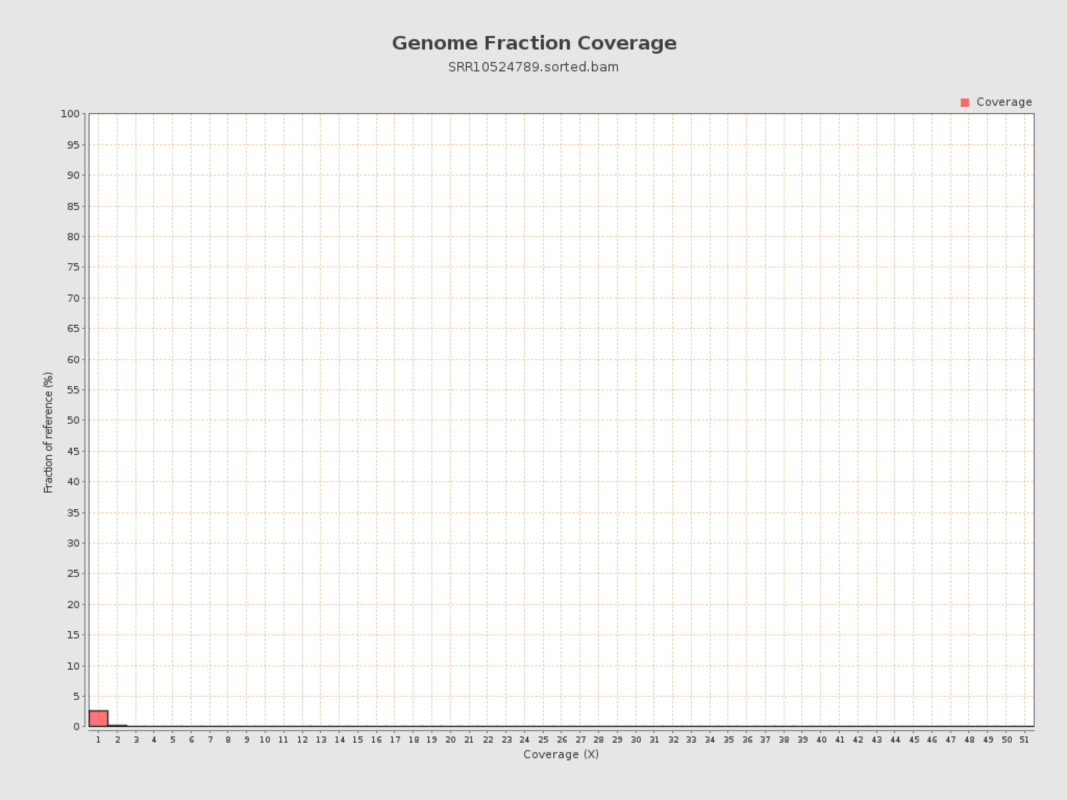
4. Results : Coverage Histogram



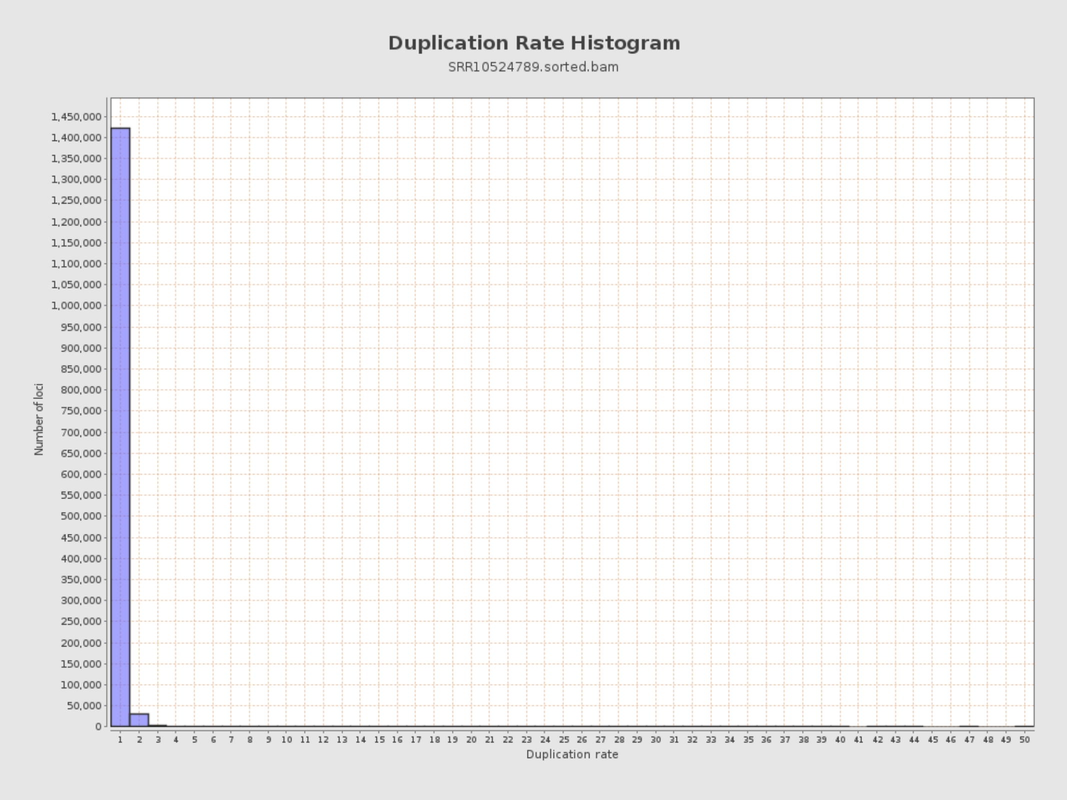
5. Results : Coverage Histogram (0-50X)



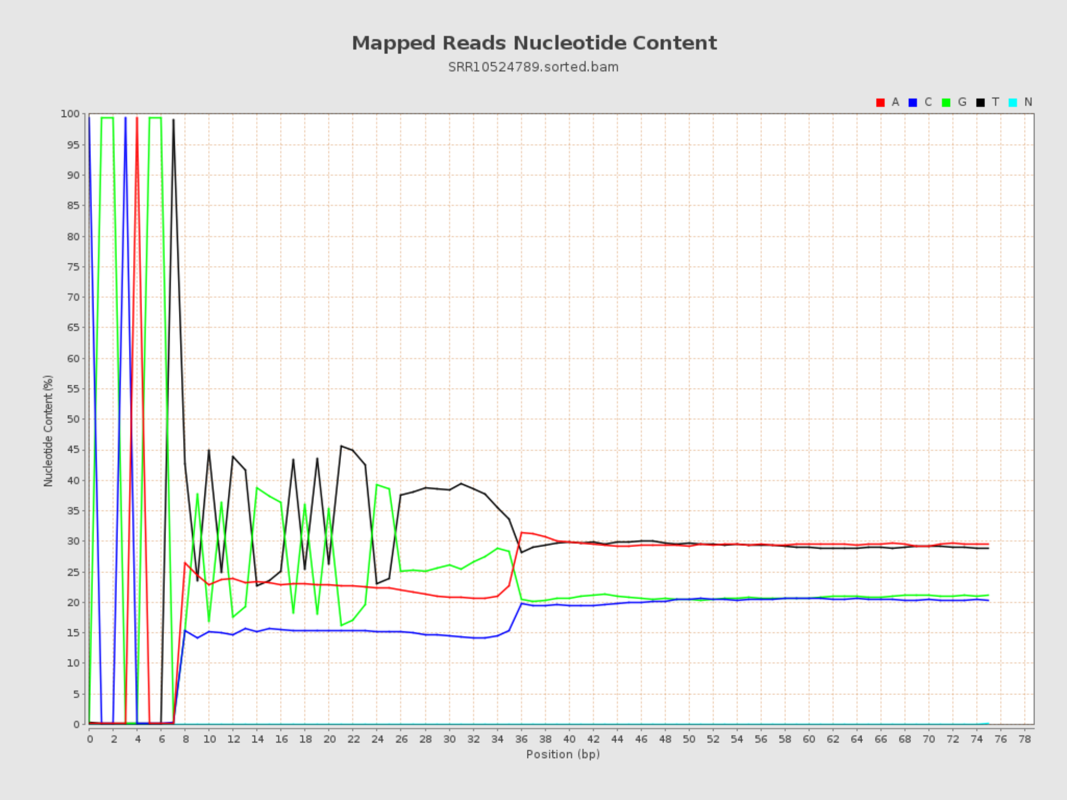
6. Results : Genome Fraction Coverage



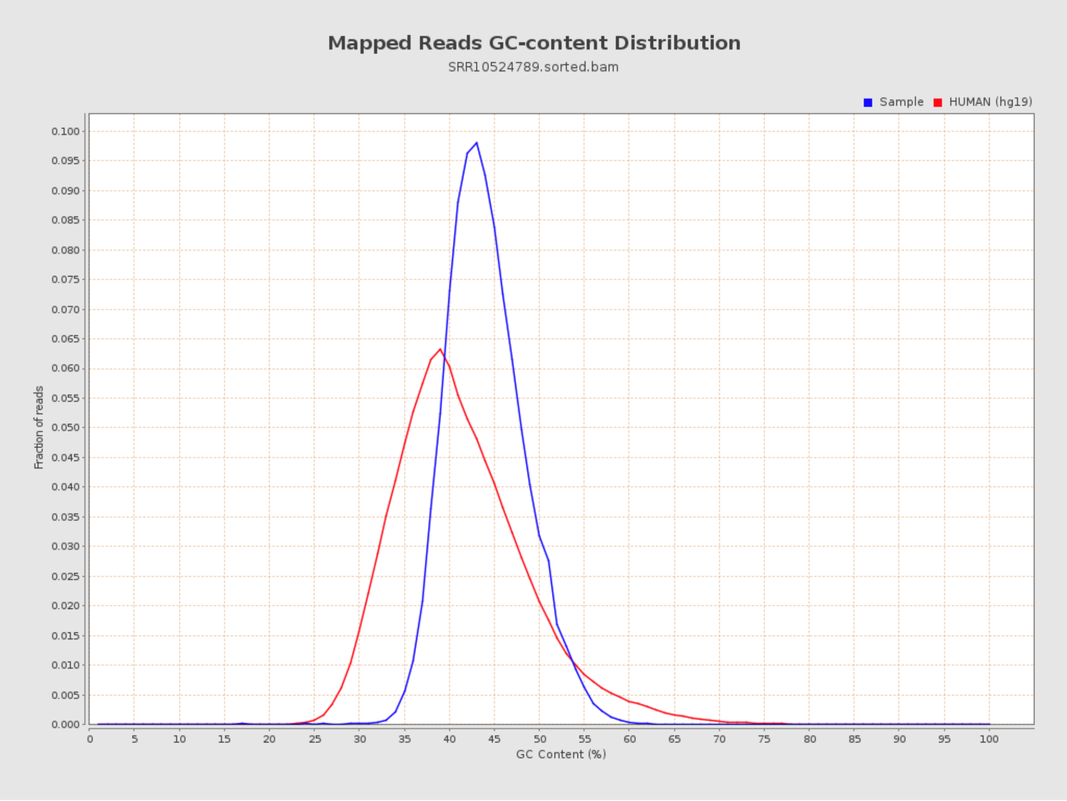
7. Results : Duplication Rate Histogram



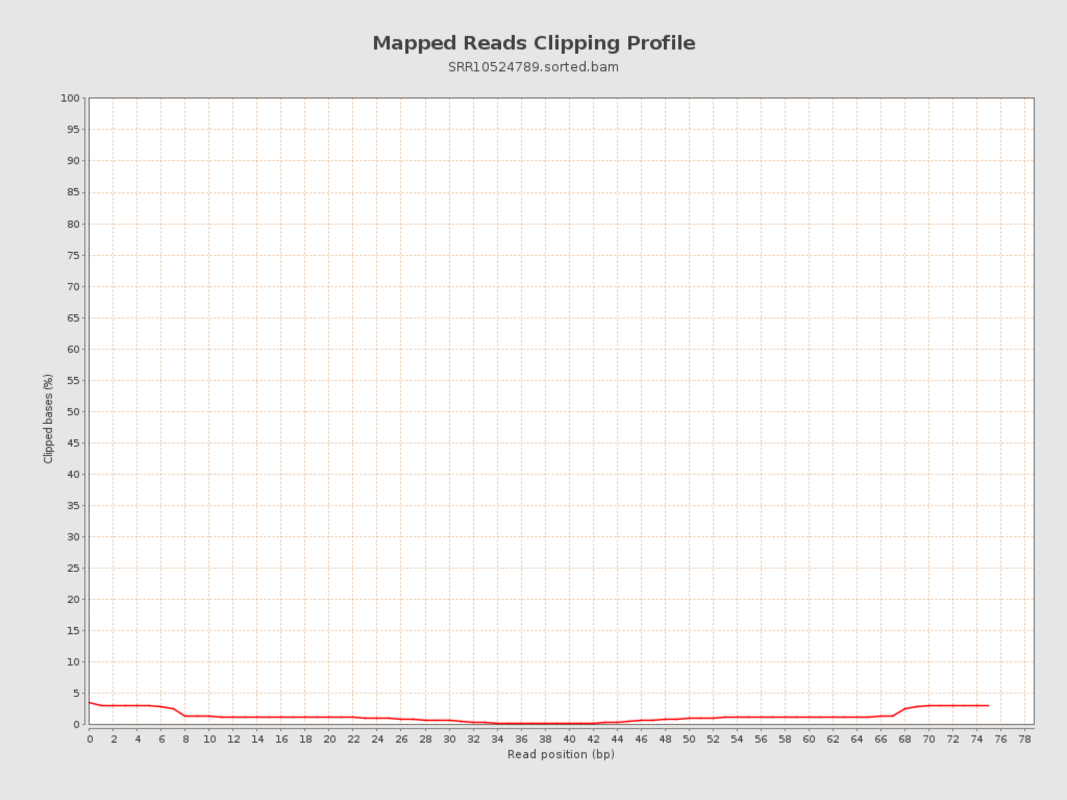
8. Results : Mapped Reads Nucleotide Content



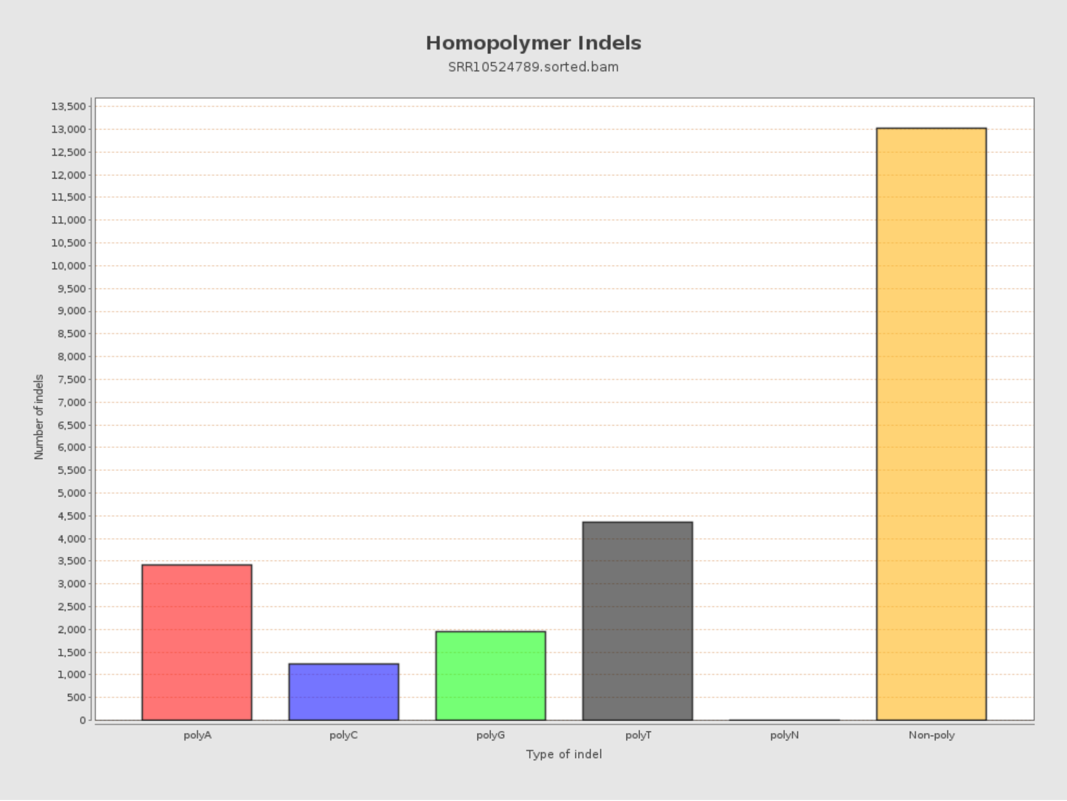
9. Results : Mapped Reads GC-content Distribution



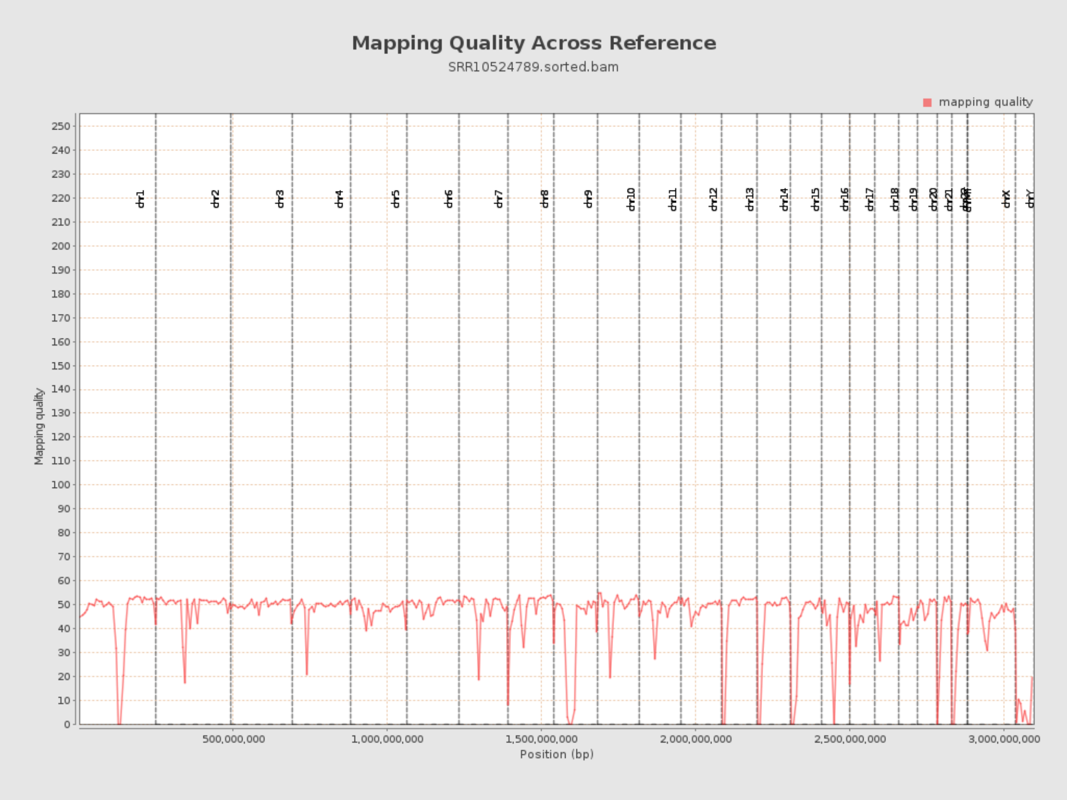
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram