Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:53:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524506.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_SRR10524506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524506.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:52:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524506.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	642,143
Mapped reads	592,933 / 92.34%
Unmapped reads	49,210 / 7.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,358 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	15,836 / 2.47%
Duplication rate	2.11%
Clipped reads	592,838 / 92.32%

2.2. ACGT Content

Number/percentage of A's	8,545,769 / 24.77%
Number/percentage of C's	6,395,837 / 18.54%
Number/percentage of T's	11,104,155 / 32.19%
Number/percentage of G's	8,449,679 / 24.49%
Number/percentage of N's	777 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1359

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

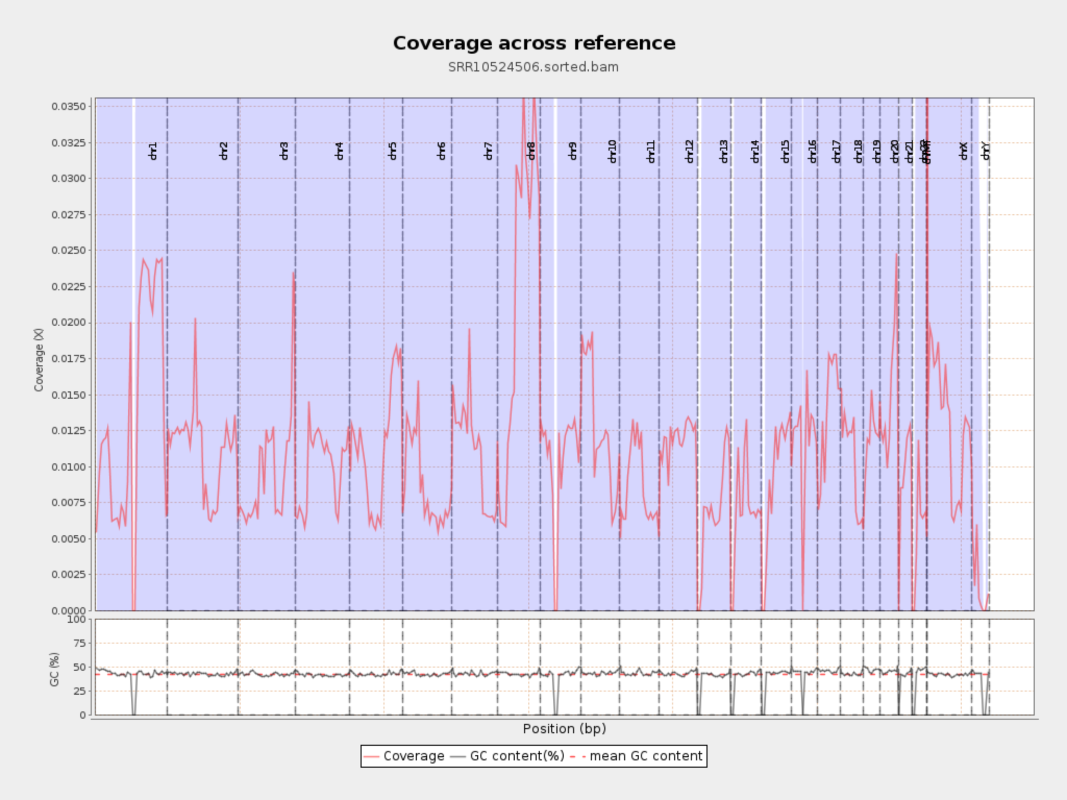
General error rate	0.47%
Mismatches	158,443
Insertions	2,401
Mapped reads with at least one insertion	0.4%
Deletions	6,372
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.46%

2.6. Chromosome stats

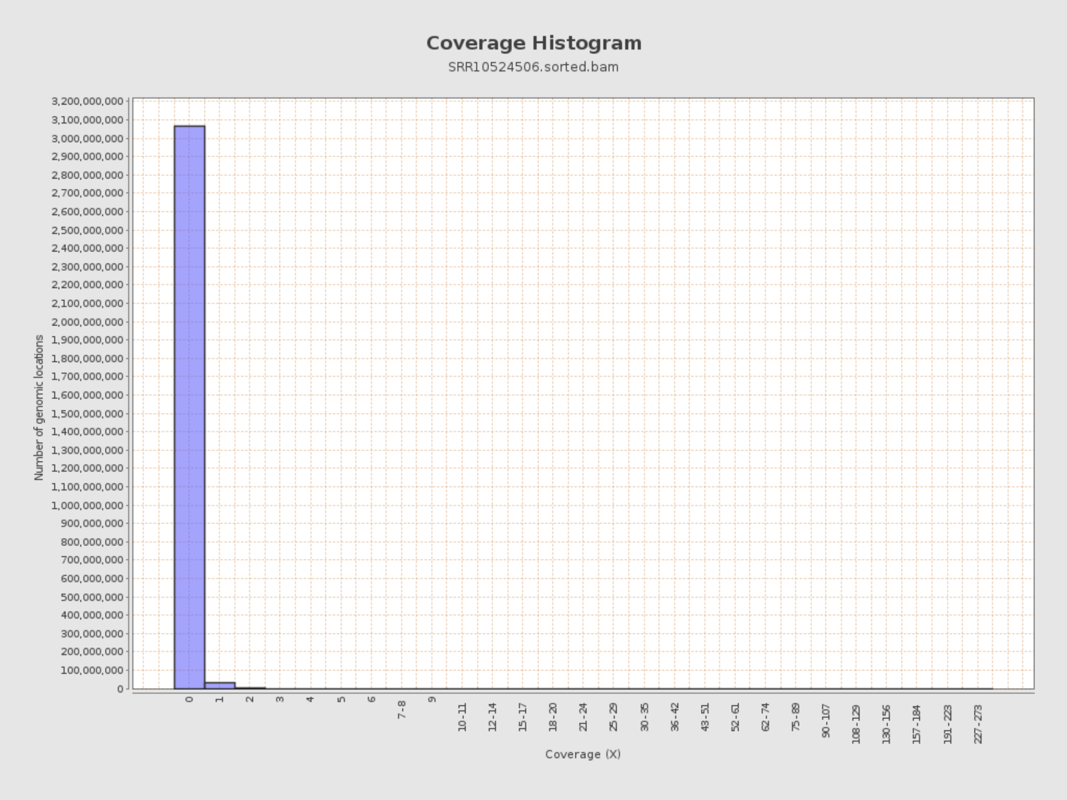
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3360287	0.0135	0.2208
chr2	243199373	2750536	0.0113	0.1489
chr3	198022430	1892964	0.0096	0.1028
chr4	191154276	1900188	0.0099	0.1101
chr5	180915260	2071543	0.0115	0.1125
chr6	171115067	1483617	0.0087	0.1086
chr7	159138663	1763251	0.0111	0.1626

chr8	146364022	3249525	0.0222	0.1665
chr9	141213431	1461434	0.0103	0.1221
chr10	135534747	1756697	0.013	0.1373
chr11	135006516	1174679	0.0087	0.1245
chr12	133851895	1598409	0.0119	0.1147
chr13	115169878	793172	0.0069	0.0876
chr14	107349540	744867	0.0069	0.0889
chr15	102531392	934776	0.0091	0.1014
chr16	90354753	1044923	0.0116	0.1175
chr17	81195210	1120464	0.0138	0.1265
chr18	78077248	821257	0.0105	0.1775
chr19	59128983	710368	0.012	0.1641
chr20	63025520	960975	0.0152	0.131
chr21	48129895	461087	0.0096	0.1064
chr22	51304566	287093	0.0056	0.0783
chrMT	16571	14118	0.852	1.0545
chrX	155270560	2045943	0.0132	0.1271
chrY	59373566	104943	0.0018	0.0585

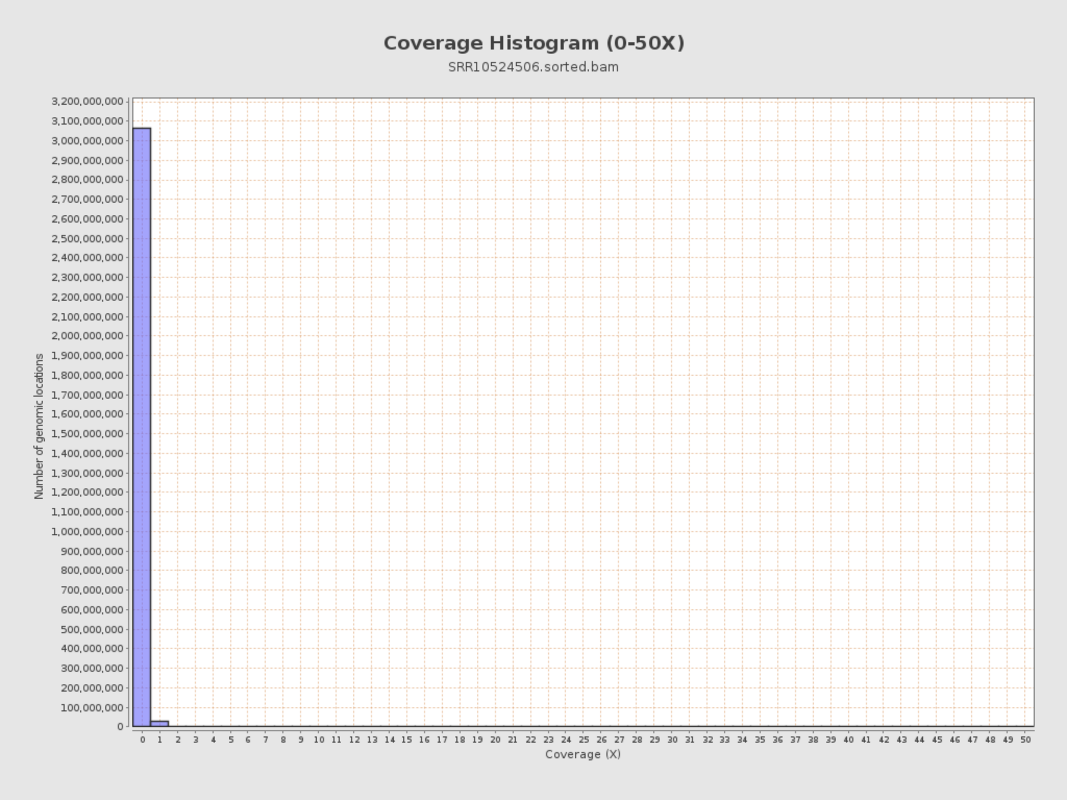
3. Results : Coverage across reference



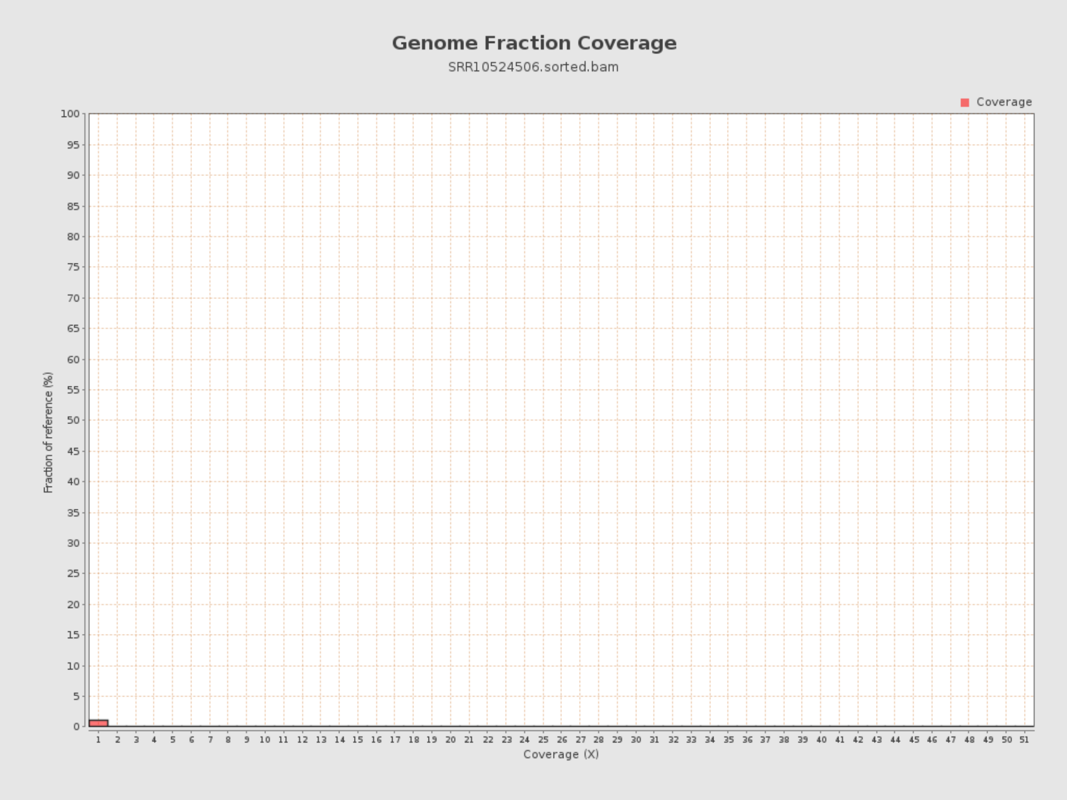
4. Results : Coverage Histogram



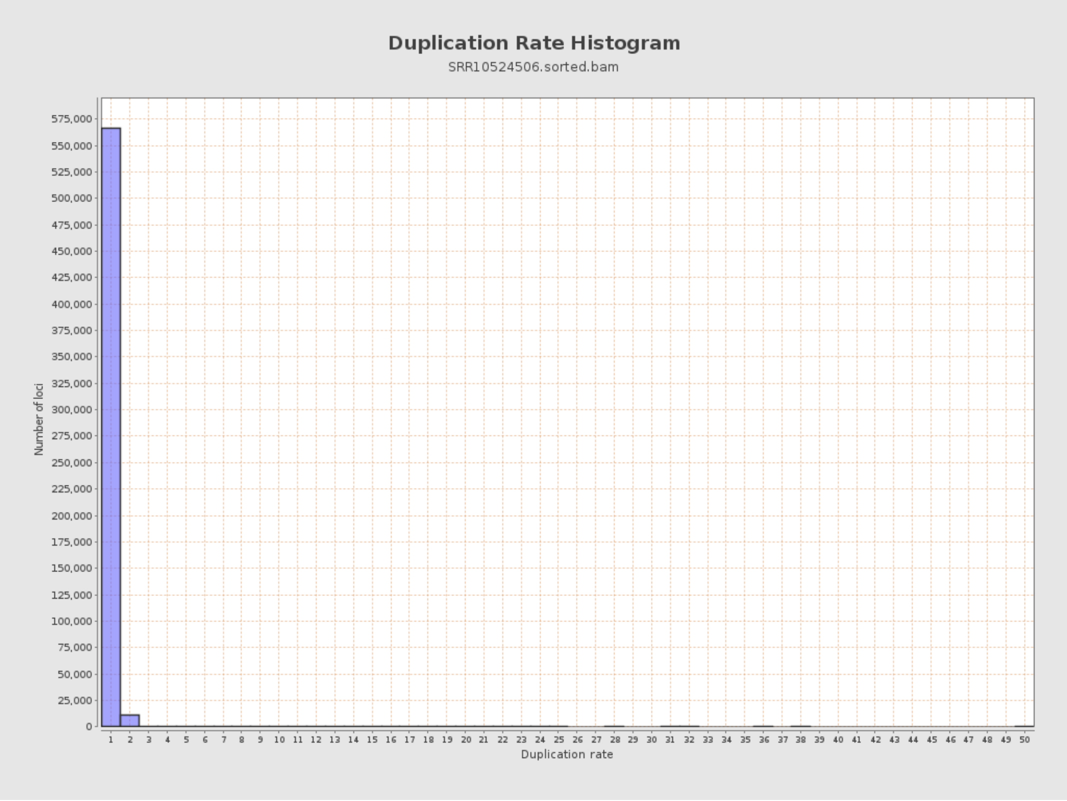
5. Results : Coverage Histogram (0-50X)



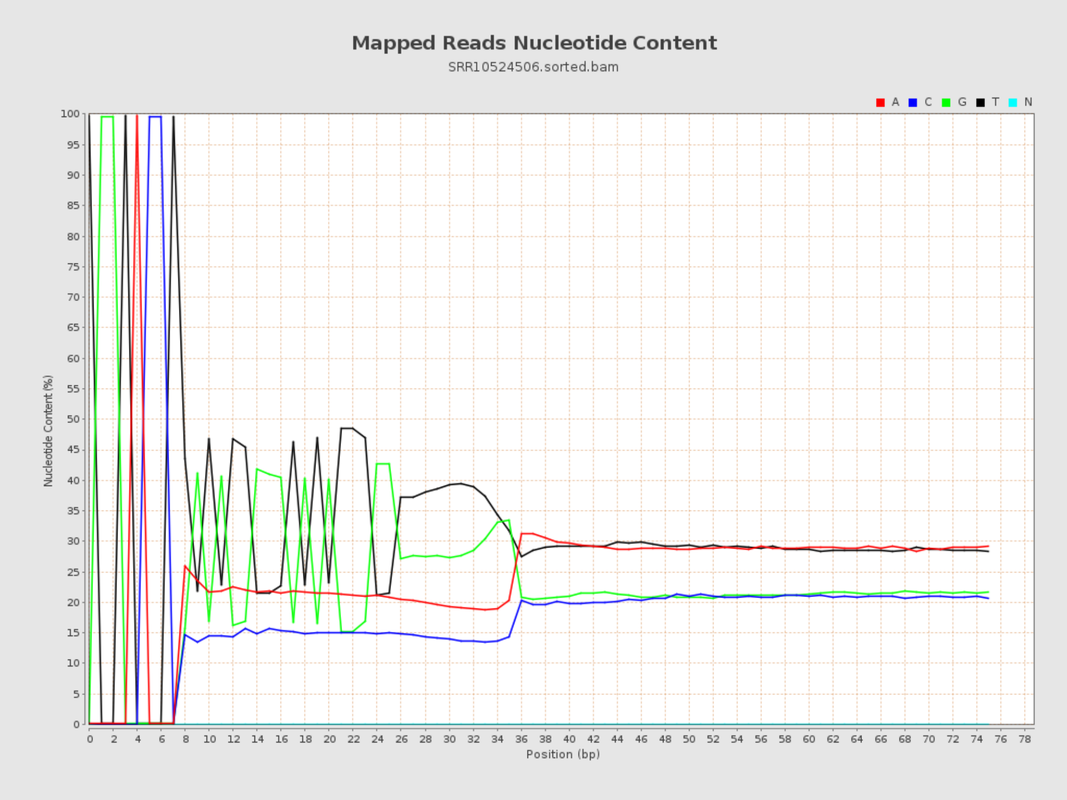
6. Results : Genome Fraction Coverage



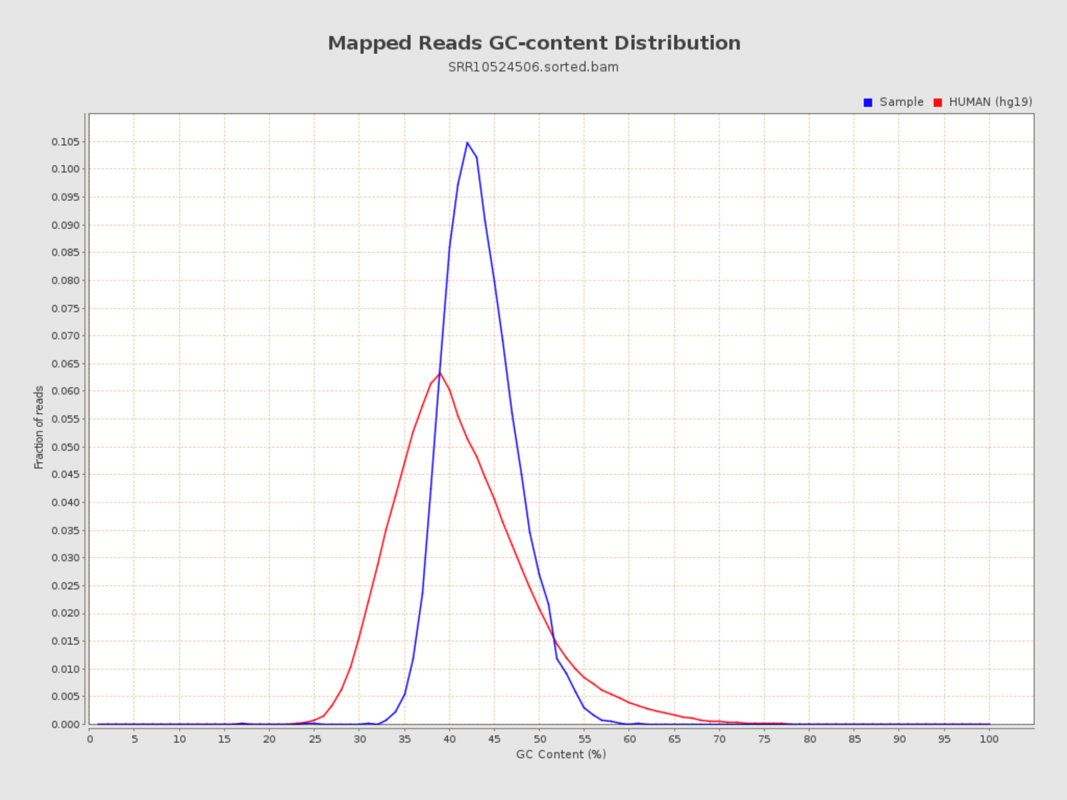
7. Results : Duplication Rate Histogram



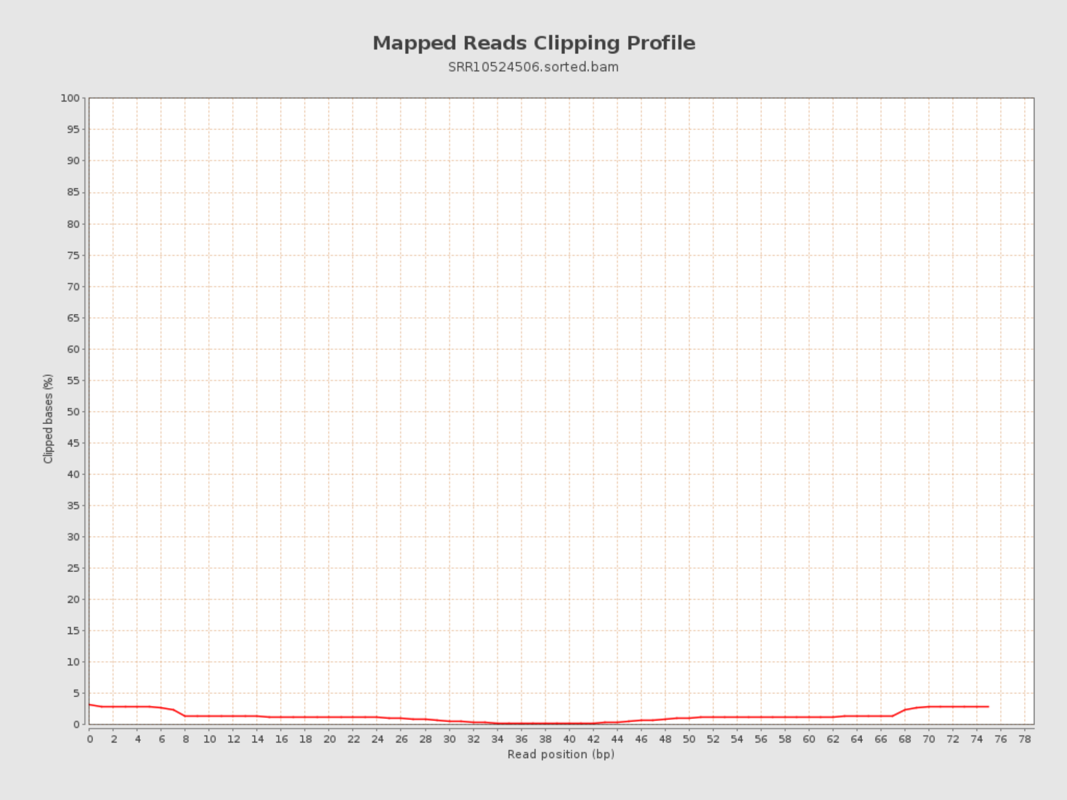
8. Results : Mapped Reads Nucleotide Content



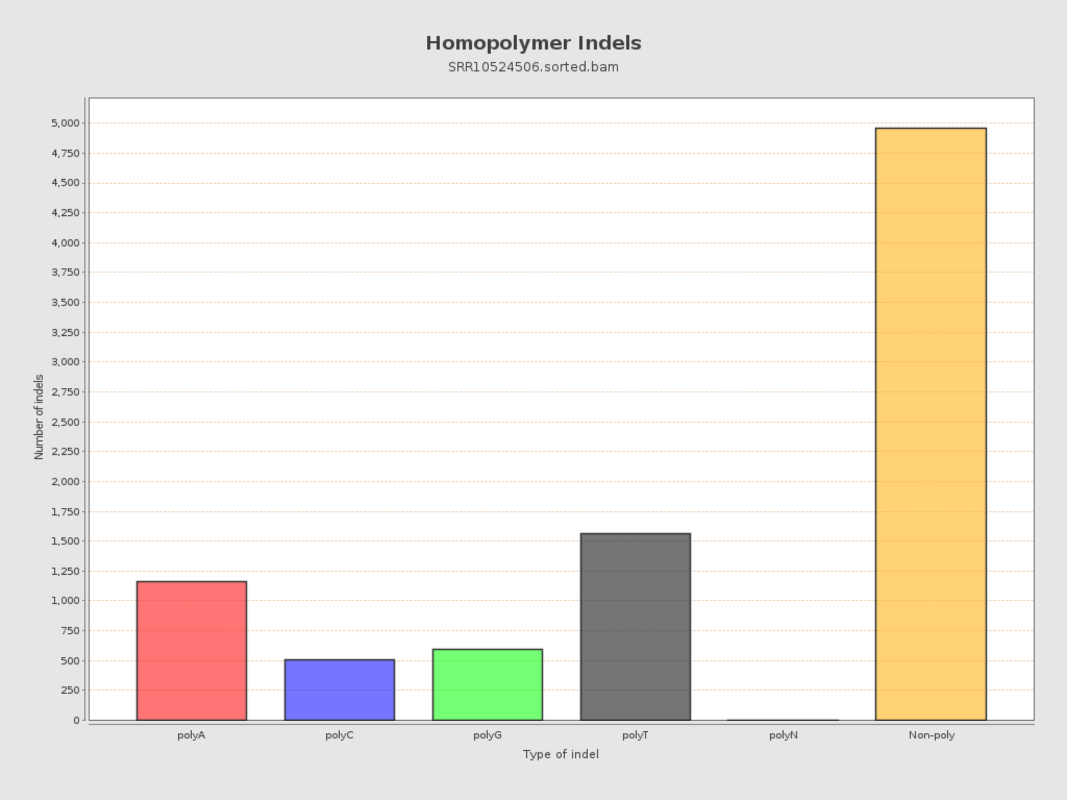
9. Results : Mapped Reads GC-content Distribution



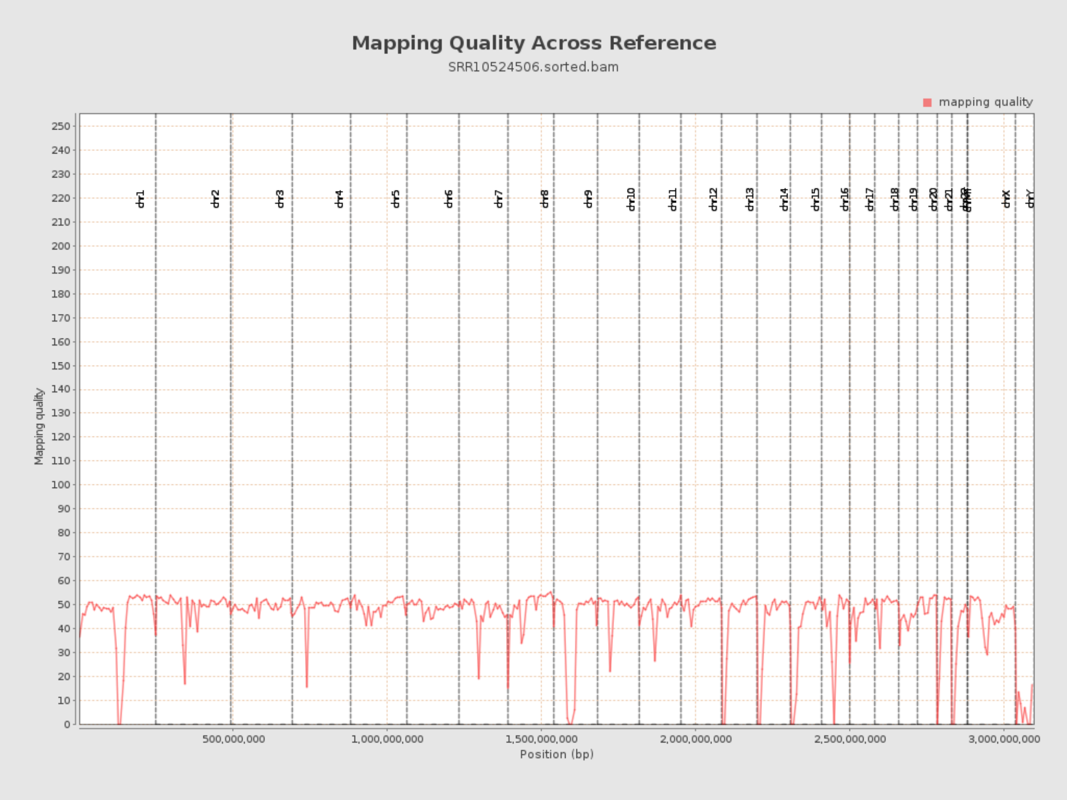
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram