Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:20:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524549.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_SRR10524549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524549.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:20:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,197,048
Mapped reads	1,032,039 / 86.22%
Unmapped reads	165,009 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,239 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	110,737 / 9.25%
Duplication rate	8.08%
Clipped reads	1,036,744 / 86.61%

2.2. ACGT Content

Number/percentage of A's	13,660,007 / 23.33%
Number/percentage of C's	10,848,320 / 18.53%
Number/percentage of T's	18,956,815 / 32.38%
Number/percentage of G's	15,079,619 / 25.76%
Number/percentage of N's	859 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.2311

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

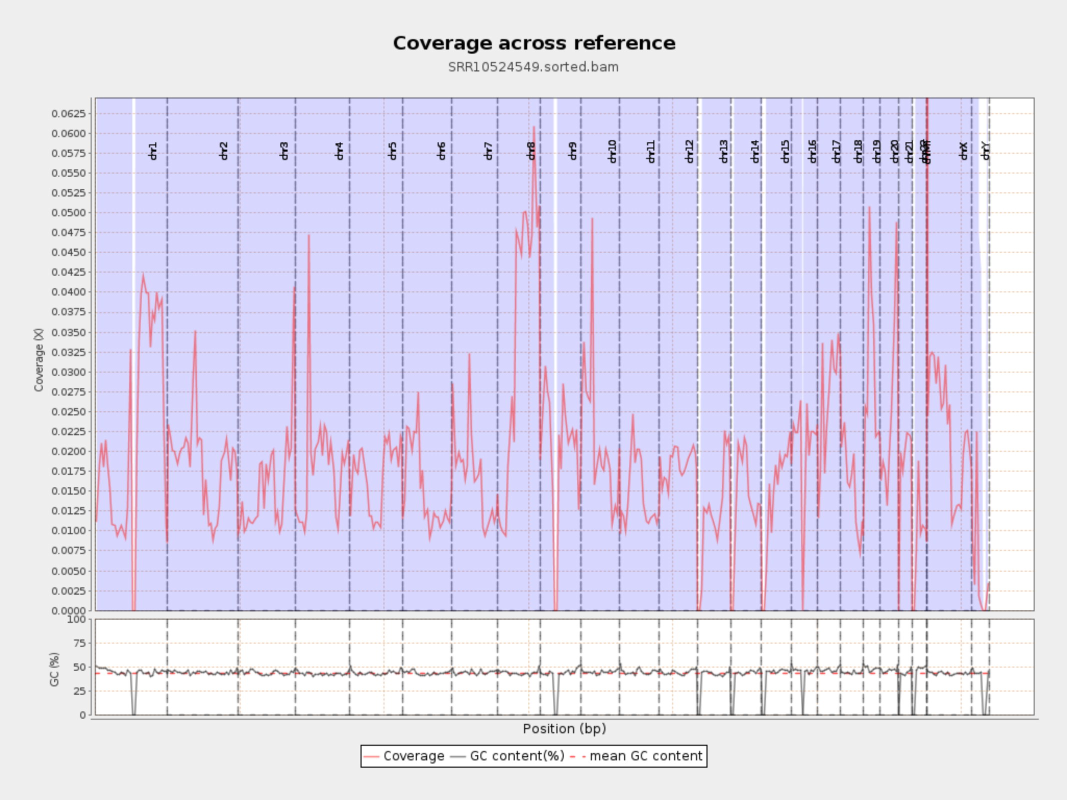
General error rate	0.59%
Mismatches	336,548
Insertions	3,428
Mapped reads with at least one insertion	0.33%
Deletions	13,687
Mapped reads with at least one deletion	1.31%
Homopolymer indels	43.16%

2.6. Chromosome stats

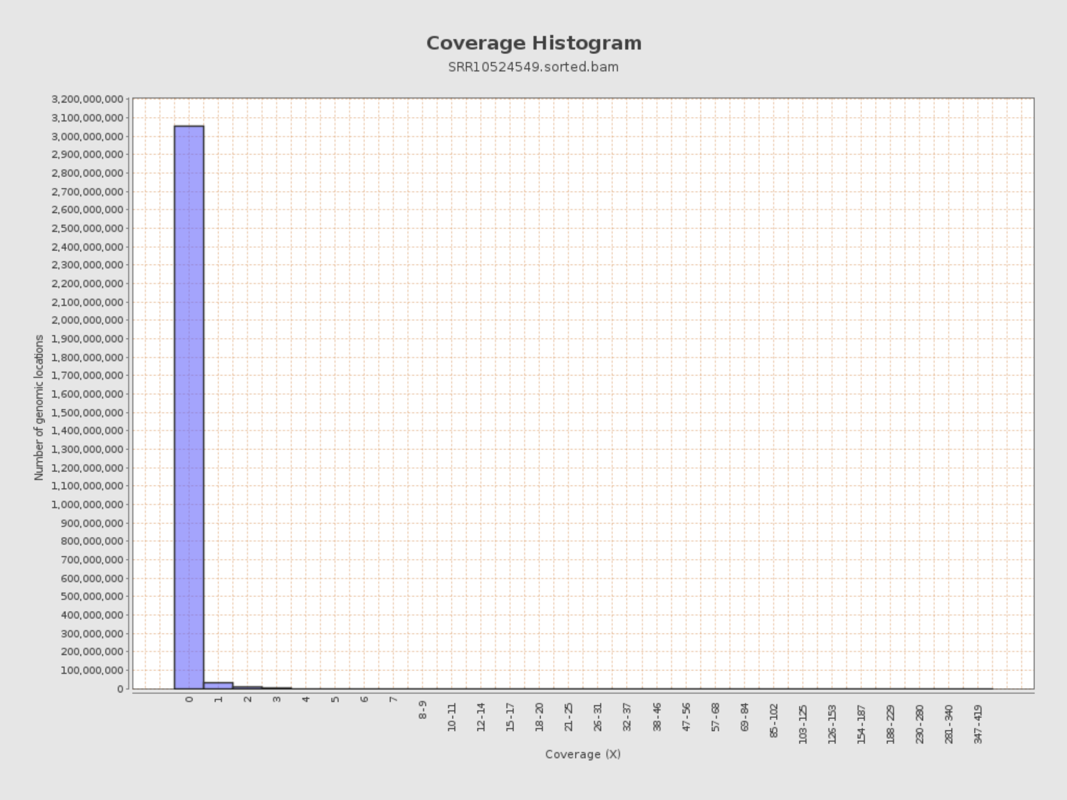
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5540417	0.0222	0.3474
chr2	243199373	4562872	0.0188	0.2831
chr3	198022430	3080127	0.0156	0.1625
chr4	191154276	3497316	0.0183	0.2227
chr5	180915260	3094374	0.0171	0.1692
chr6	171115067	2600464	0.0152	0.179
chr7	159138663	2734234	0.0172	0.2392

chr8	146364022	5136460	0.0351	0.2771
chr9	141213431	2839316	0.0201	0.204
chr10	135534747	2969159	0.0219	0.2939
chr11	135006516	1985646	0.0147	0.1887
chr12	133851895	2459055	0.0184	0.1763
chr13	115169878	1382472	0.012	0.1418
chr14	107349540	1467882	0.0137	0.1544
chr15	102531392	1442218	0.0141	0.154
chr16	90354753	1804167	0.02	0.1927
chr17	81195210	2139502	0.0264	0.2581
chr18	78077248	1220981	0.0156	0.2964
chr19	59128983	1784319	0.0302	0.2866
chr20	63025520	1609299	0.0255	0.2138
chr21	48129895	892949	0.0186	0.2225
chr22	51304566	459234	0.009	0.1222
chrMT	16571	17820	1.0754	1.3884
chrX	155270560	3557136	0.0229	0.2079
chrY	59373566	291619	0.0049	0.2166

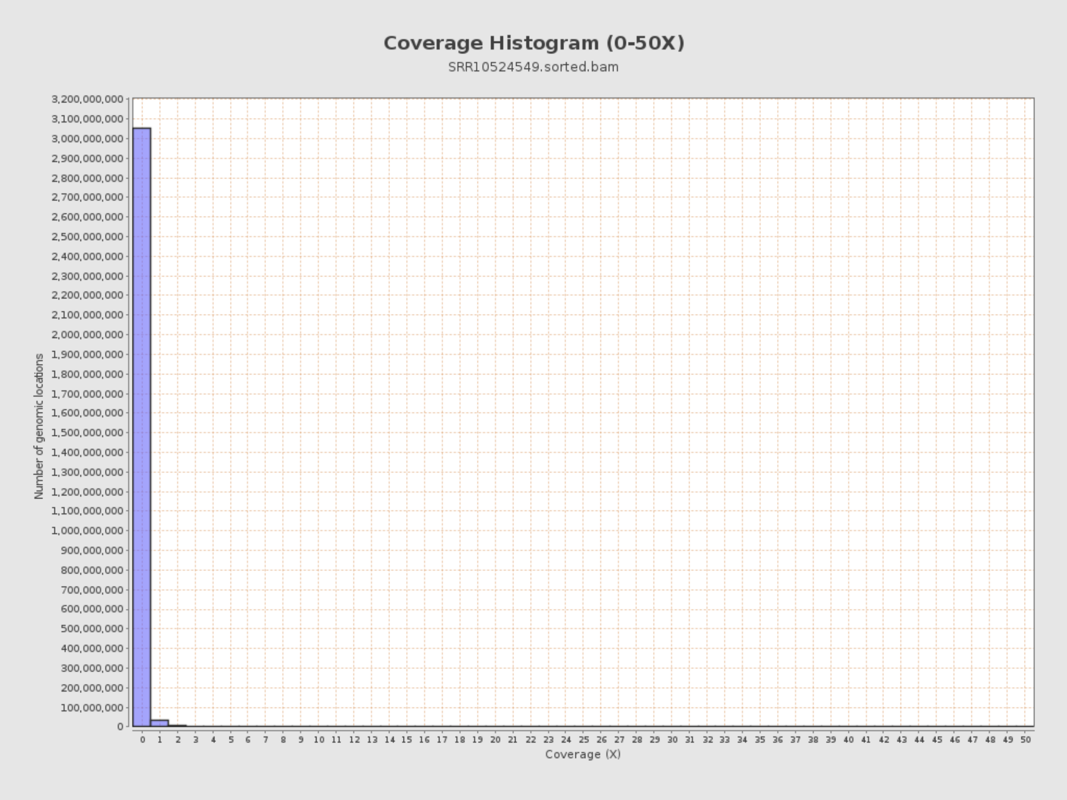
3. Results : Coverage across reference



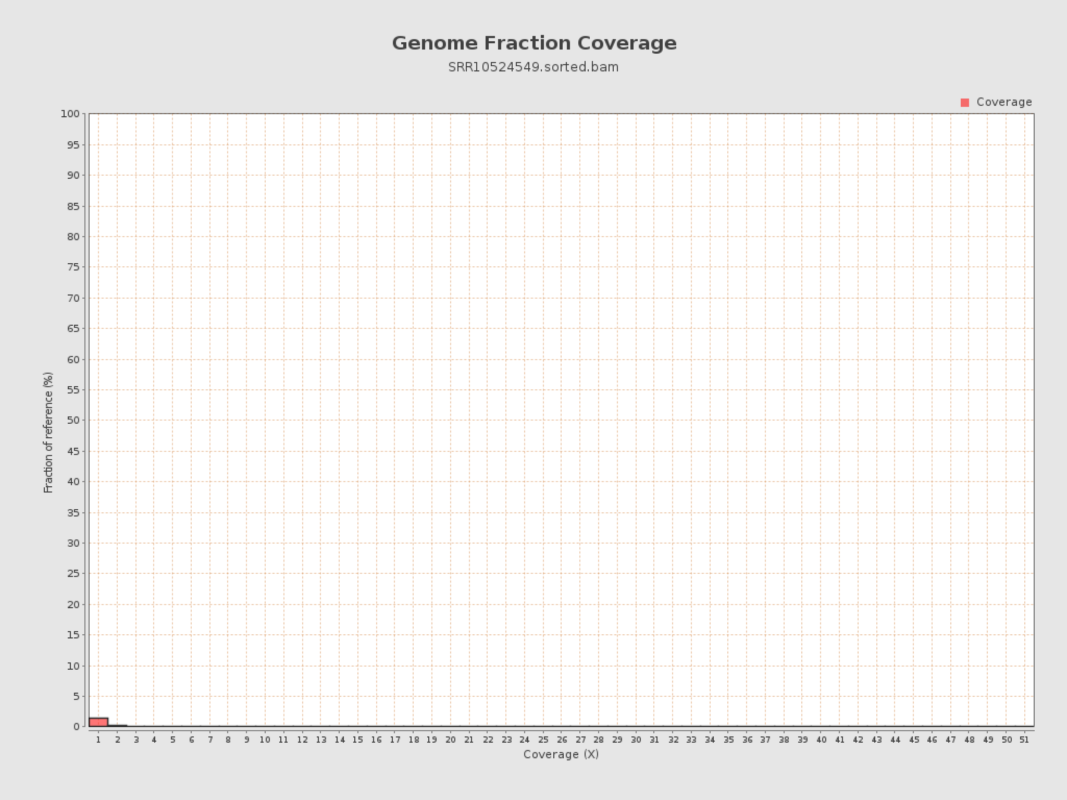
4. Results : Coverage Histogram



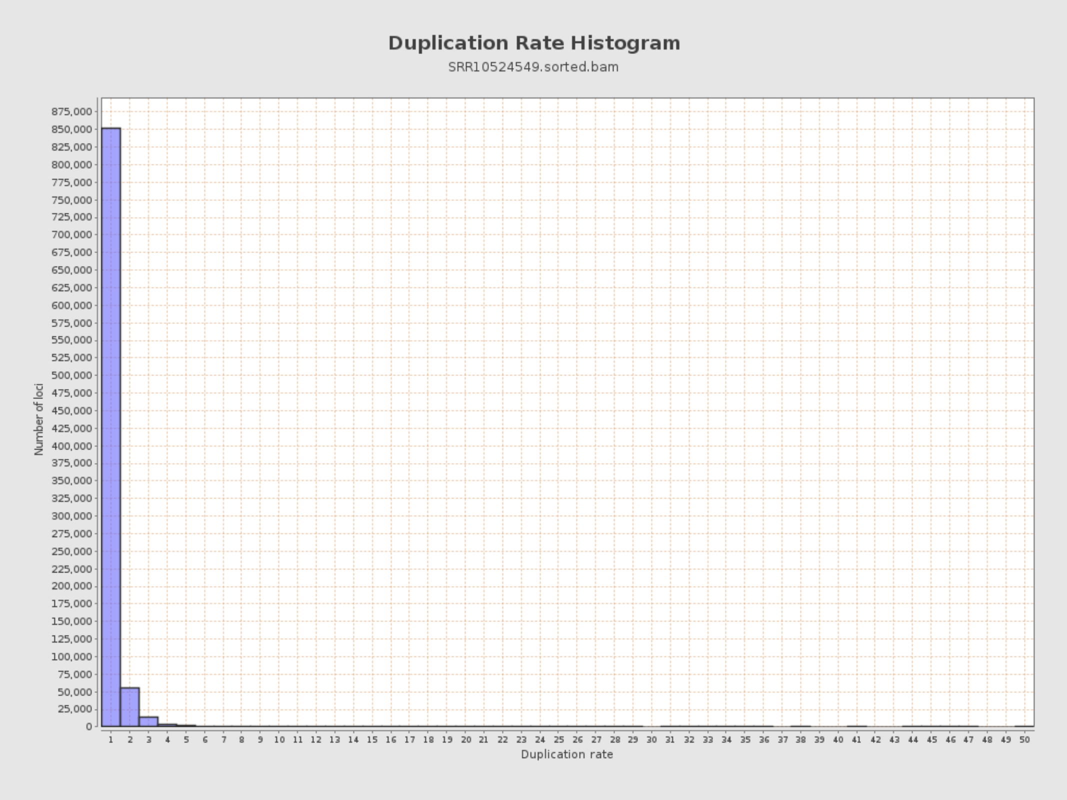
5. Results : Coverage Histogram (0-50X)



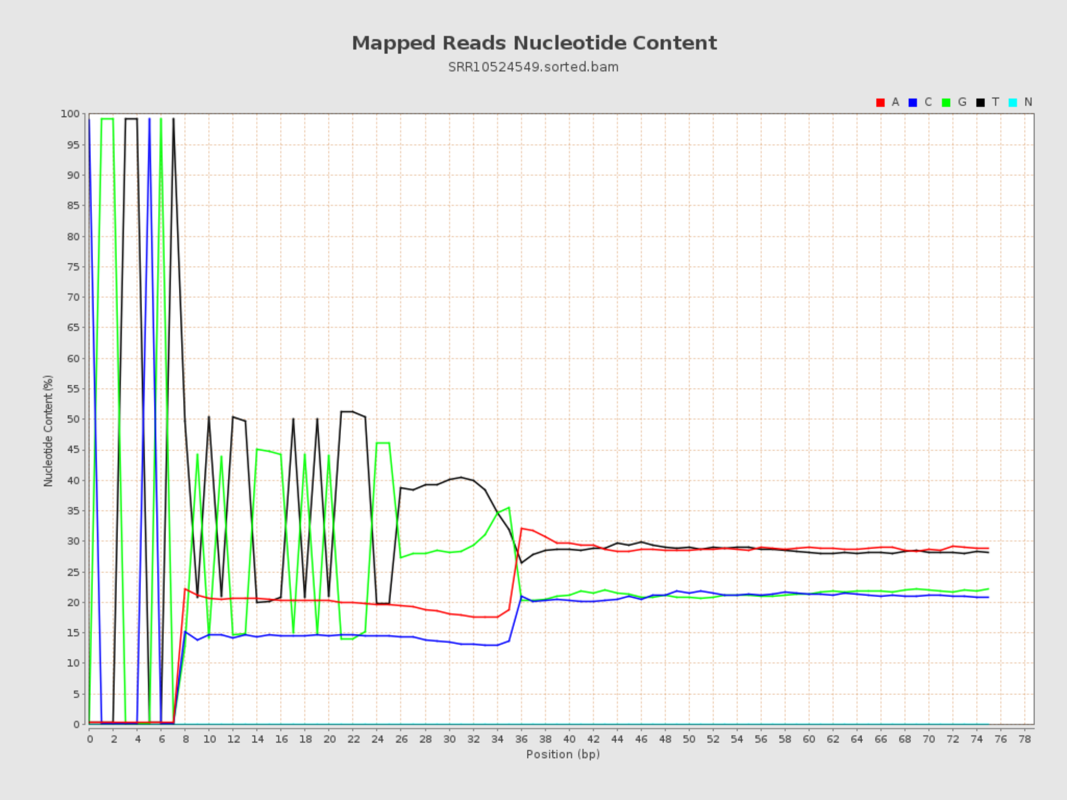
6. Results : Genome Fraction Coverage



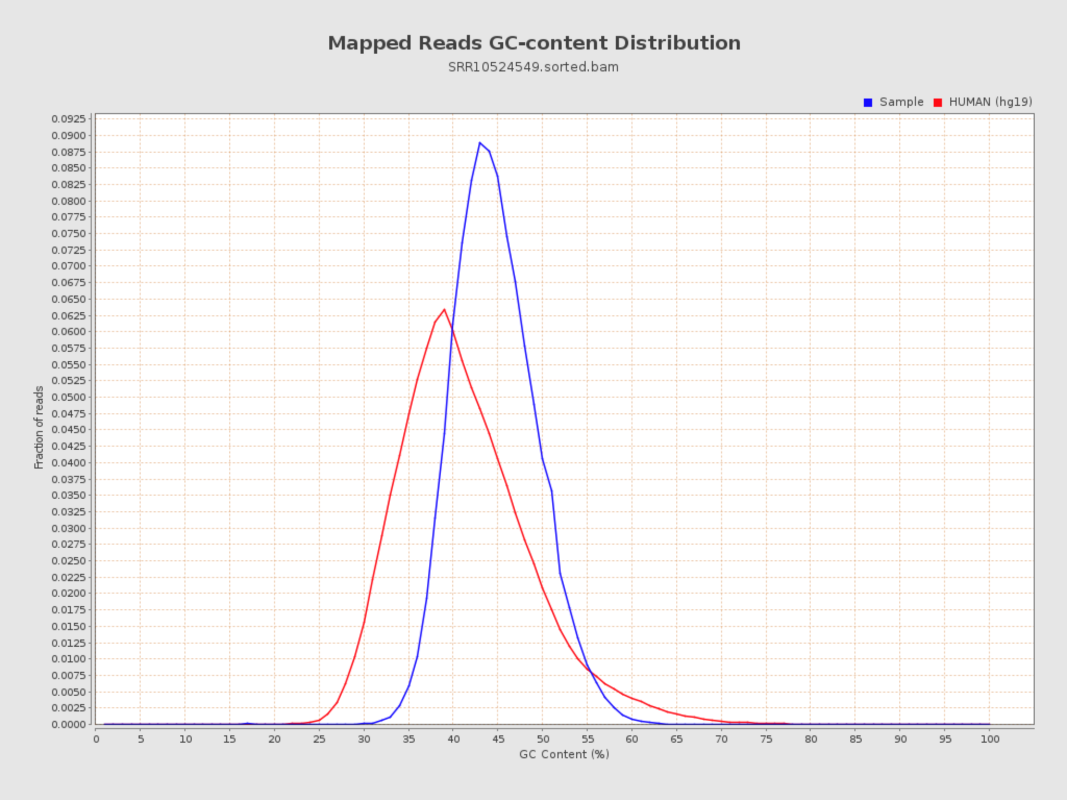
7. Results : Duplication Rate Histogram



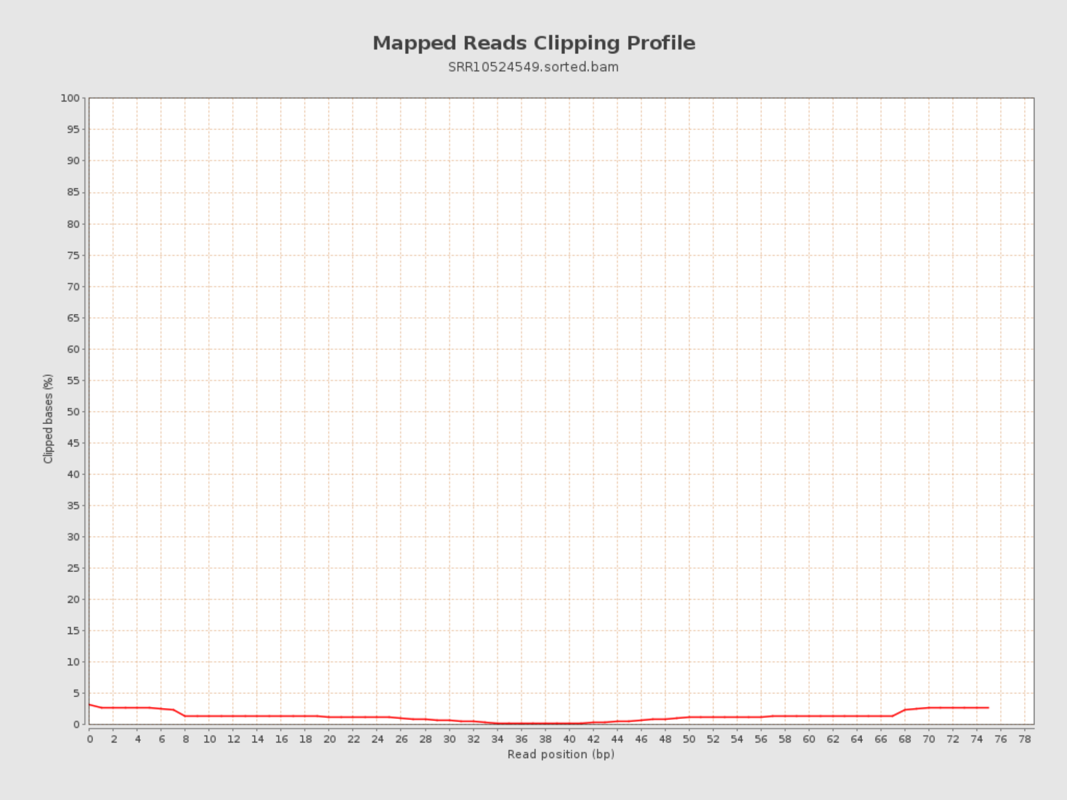
8. Results : Mapped Reads Nucleotide Content



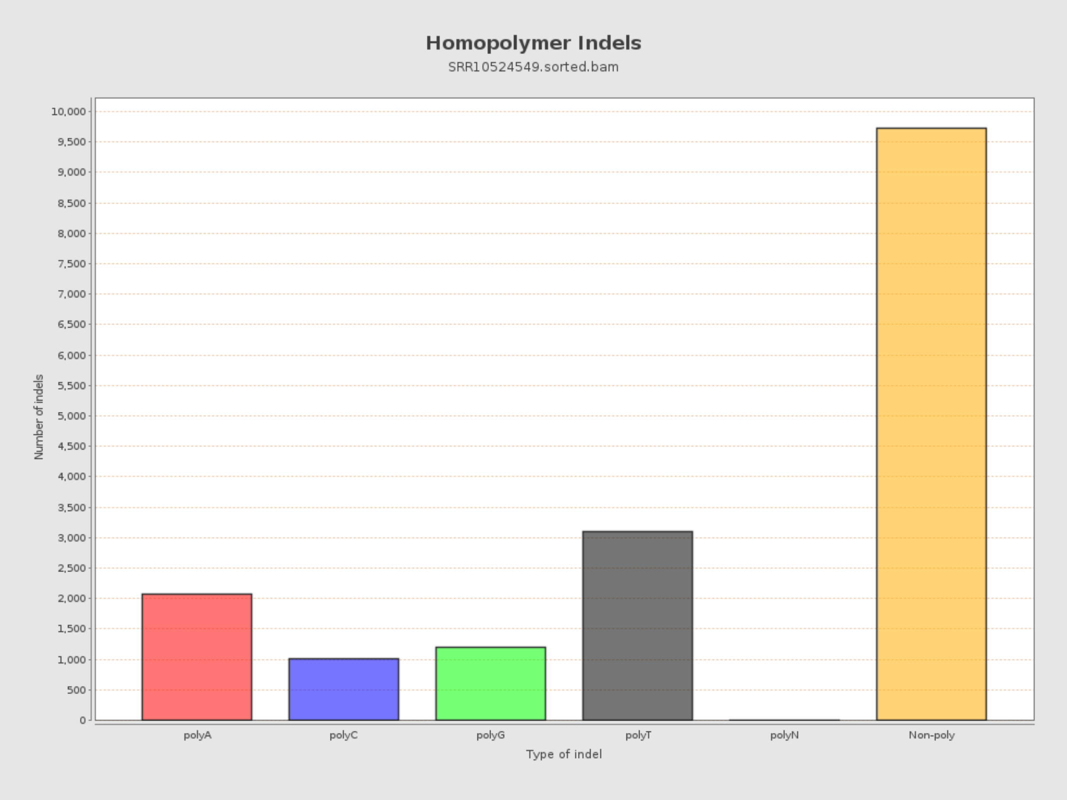
9. Results : Mapped Reads GC-content Distribution



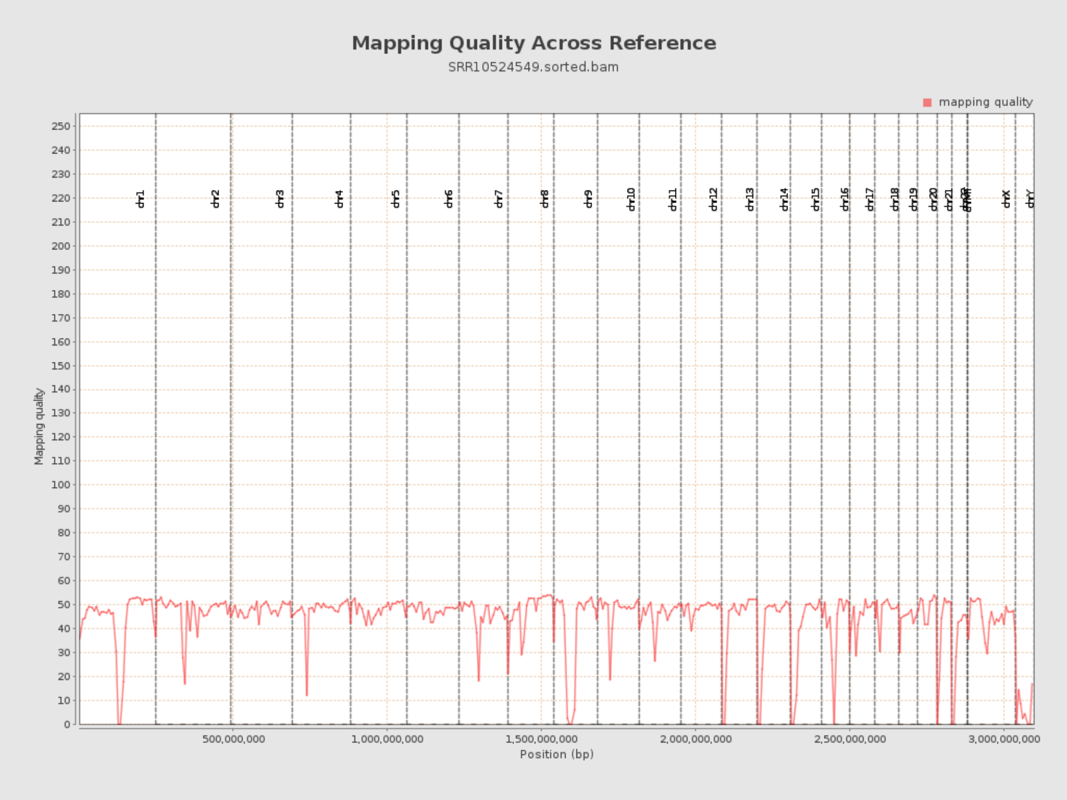
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram