Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:19:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524357.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_SRR10524357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524357.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:19:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	717,200
Mapped reads	634,811 / 88.51%
Unmapped reads	82,389 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,518 / 1.19%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	12,884 / 1.8%
Duplication rate	1.09%
Clipped reads	641,679 / 89.47%

2.2. ACGT Content

Number/percentage of A's	8,667,948 / 23.84%
Number/percentage of C's	6,810,710 / 18.73%
Number/percentage of T's	11,648,671 / 32.04%
Number/percentage of G's	9,223,820 / 25.37%
Number/percentage of N's	5,198 / 0.01%
GC Percentage	44.1%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1663

2.4. Mapping Quality

Mean Mapping Quality	41.16

2.5. Mismatches and indels

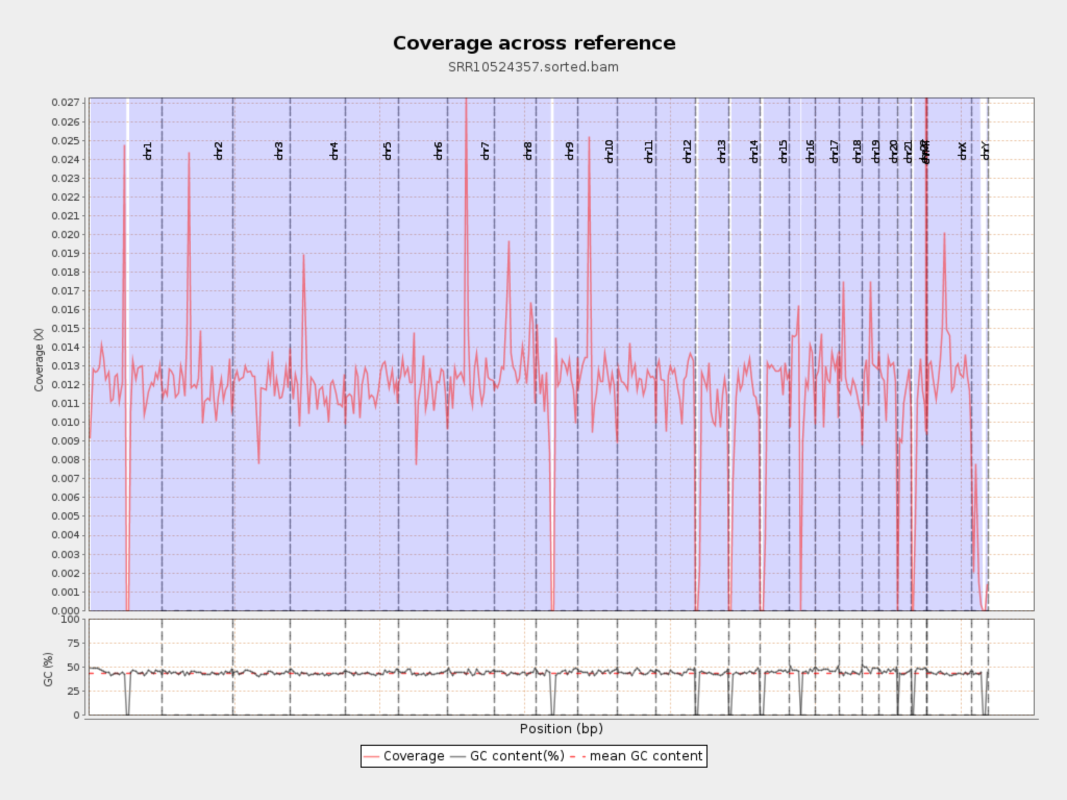
General error rate	0.54%
Mismatches	191,160
Insertions	2,729
Mapped reads with at least one insertion	0.43%
Deletions	5,972
Mapped reads with at least one deletion	0.93%
Homopolymer indels	40%

2.6. Chromosome stats

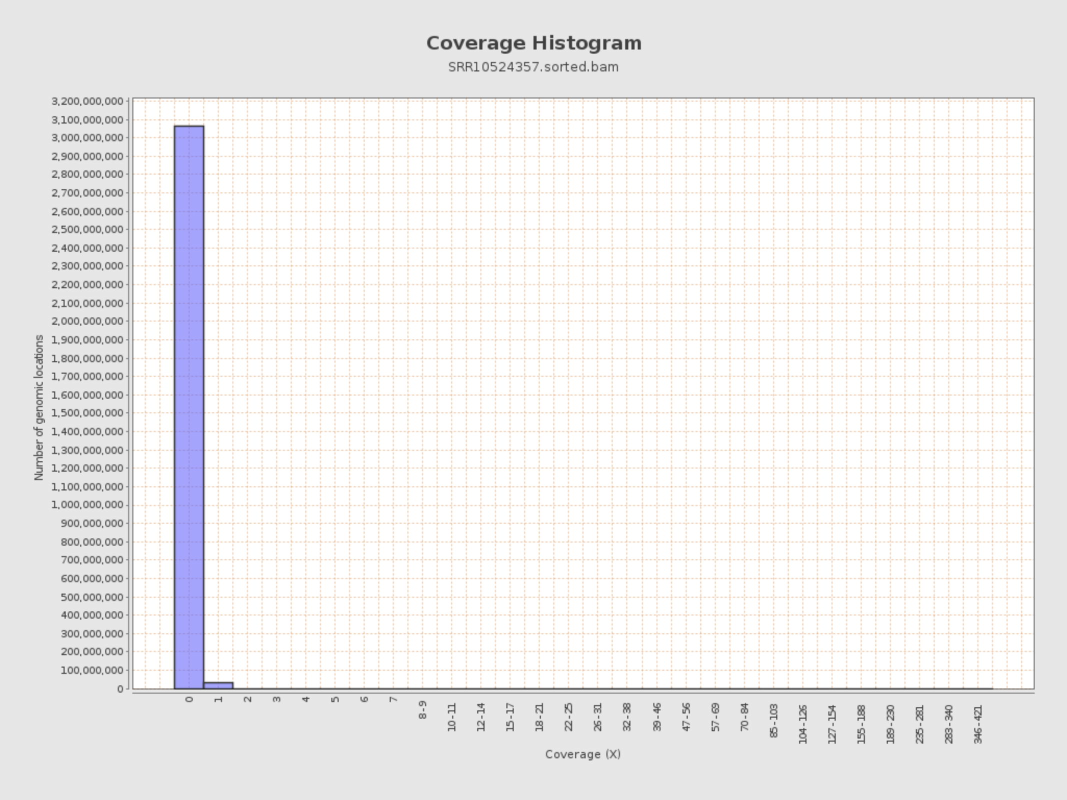
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2946476	0.0118	0.318
chr2	243199373	3006258	0.0124	0.1818
chr3	198022430	2382621	0.012	0.1131
chr4	191154276	2273177	0.0119	0.1204
chr5	180915260	2157017	0.0119	0.1135
chr6	171115067	2059758	0.012	0.1198
chr7	159138663	2075281	0.013	0.2362

chr8	146364022	1984180	0.0136	0.1553
chr9	141213431	1530203	0.0108	0.1389
chr10	135534747	1747502	0.0129	0.1516
chr11	135006516	1659006	0.0123	0.1461
chr12	133851895	1638464	0.0122	0.1169
chr13	115169878	1095704	0.0095	0.0997
chr14	107349540	1088305	0.0101	0.1146
chr15	102531392	1051542	0.0103	0.1049
chr16	90354753	1075119	0.0119	0.1214
chr17	81195210	1021200	0.0126	0.1218
chr18	78077248	968116	0.0124	0.2699
chr19	59128983	776475	0.0131	0.2065
chr20	63025520	767627	0.0122	0.1163
chr21	48129895	470072	0.0098	0.1066
chr22	51304566	420989	0.0082	0.0927
chrMT	16571	11321	0.6832	0.93
chrX	155270560	2033129	0.0131	0.1336
chrY	59373566	126432	0.0021	0.0698

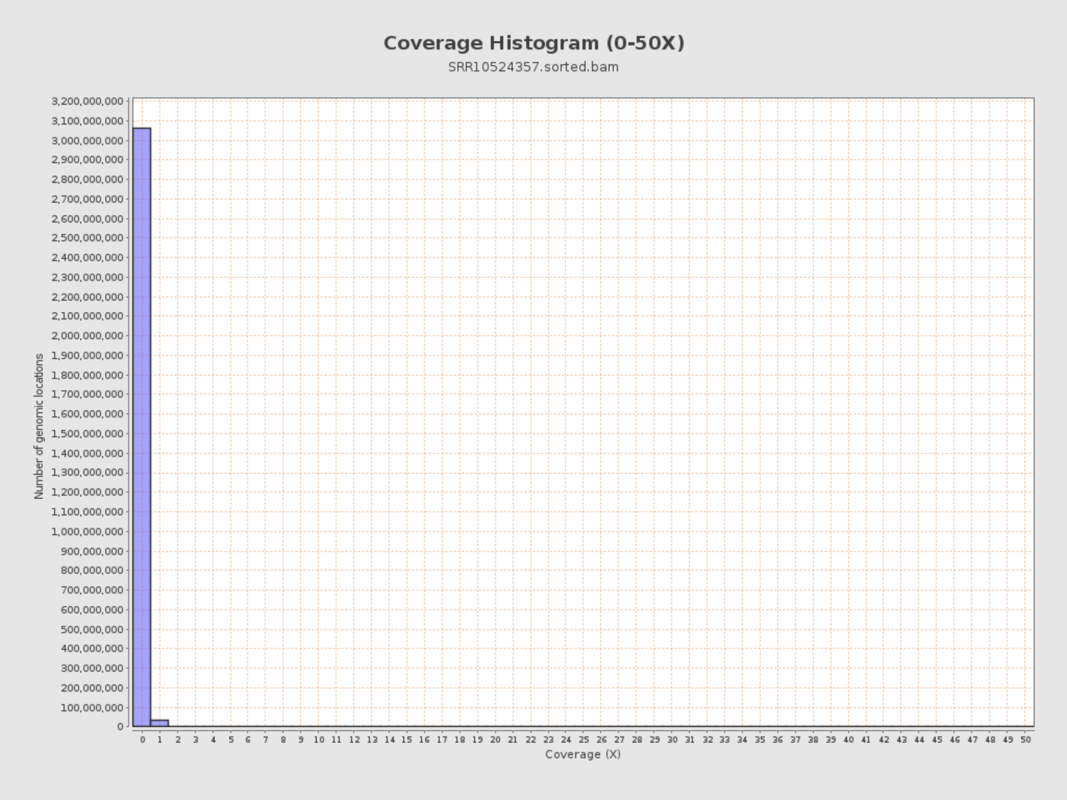
3. Results : Coverage across reference



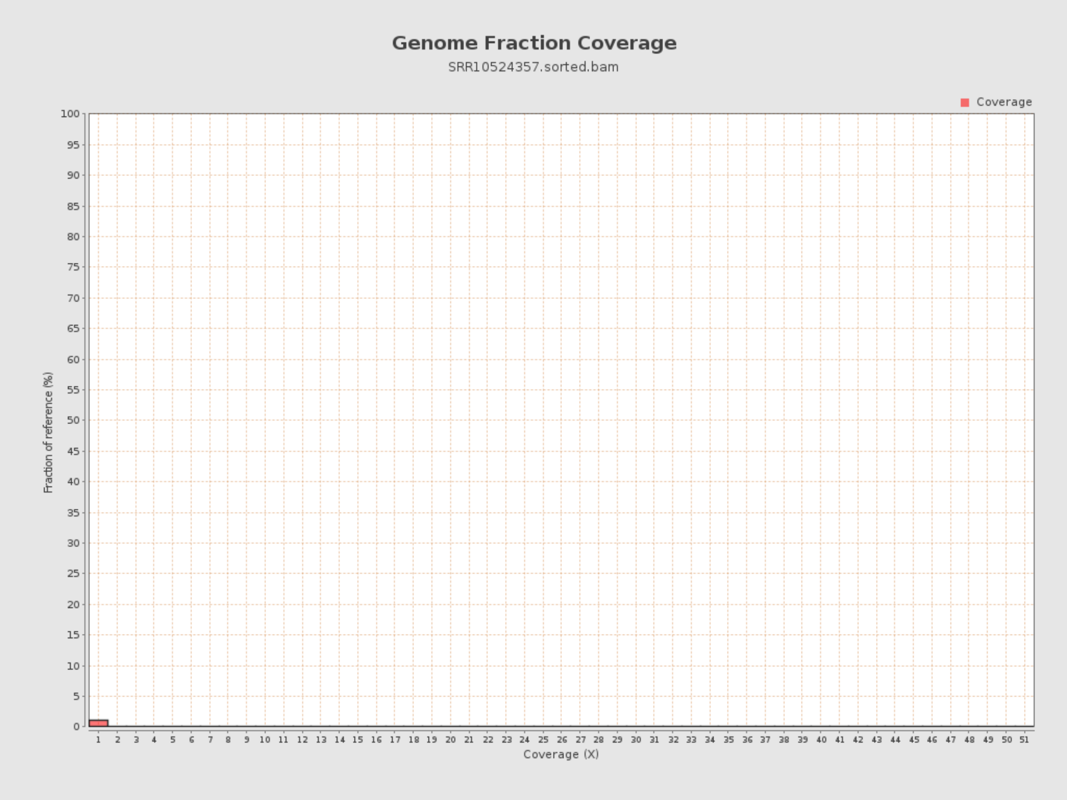
4. Results : Coverage Histogram



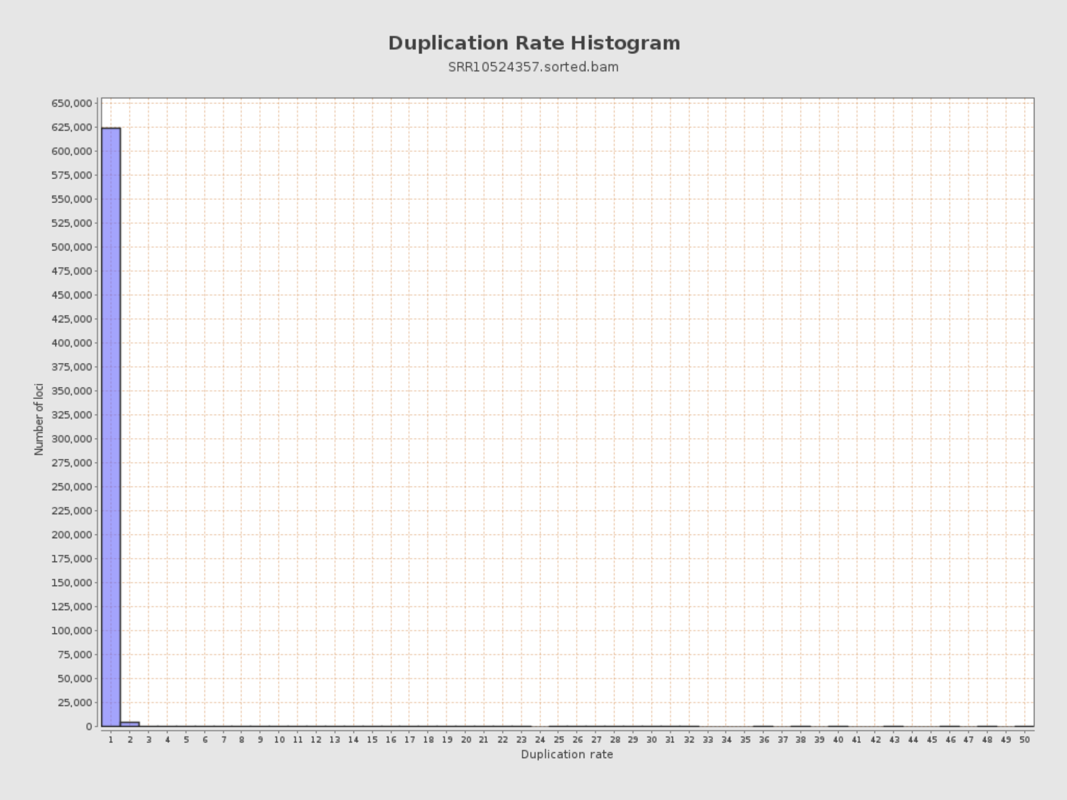
5. Results : Coverage Histogram (0-50X)



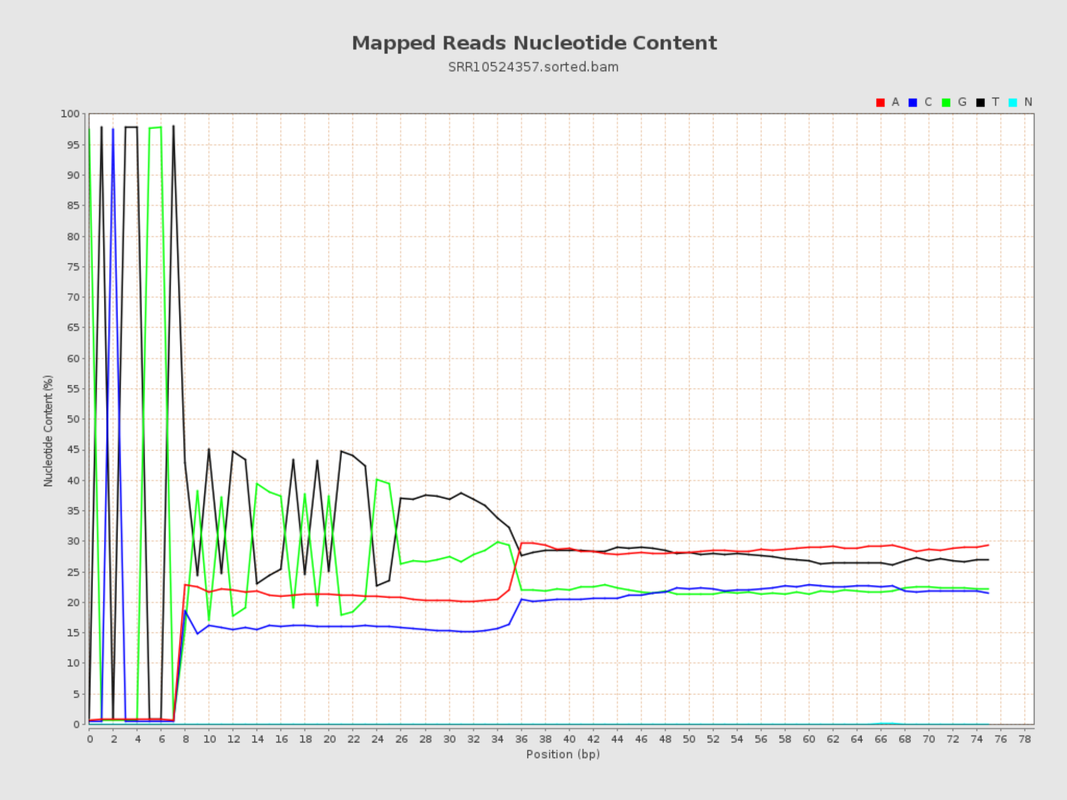
6. Results : Genome Fraction Coverage



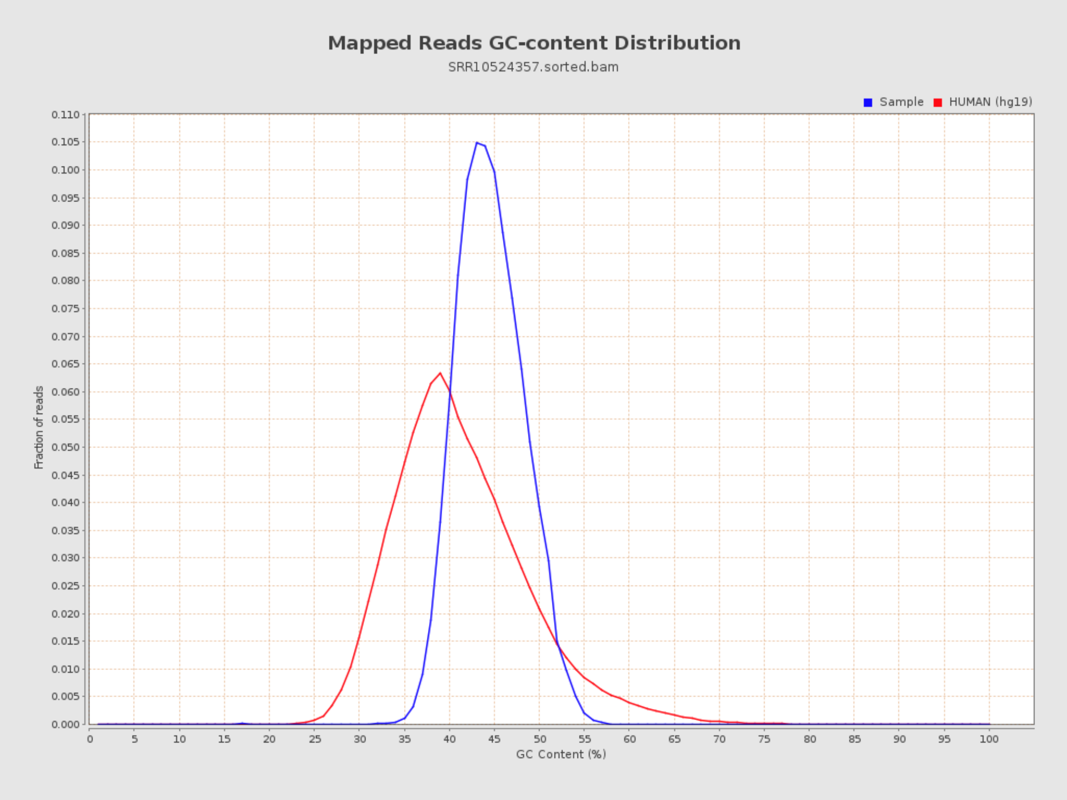
7. Results : Duplication Rate Histogram



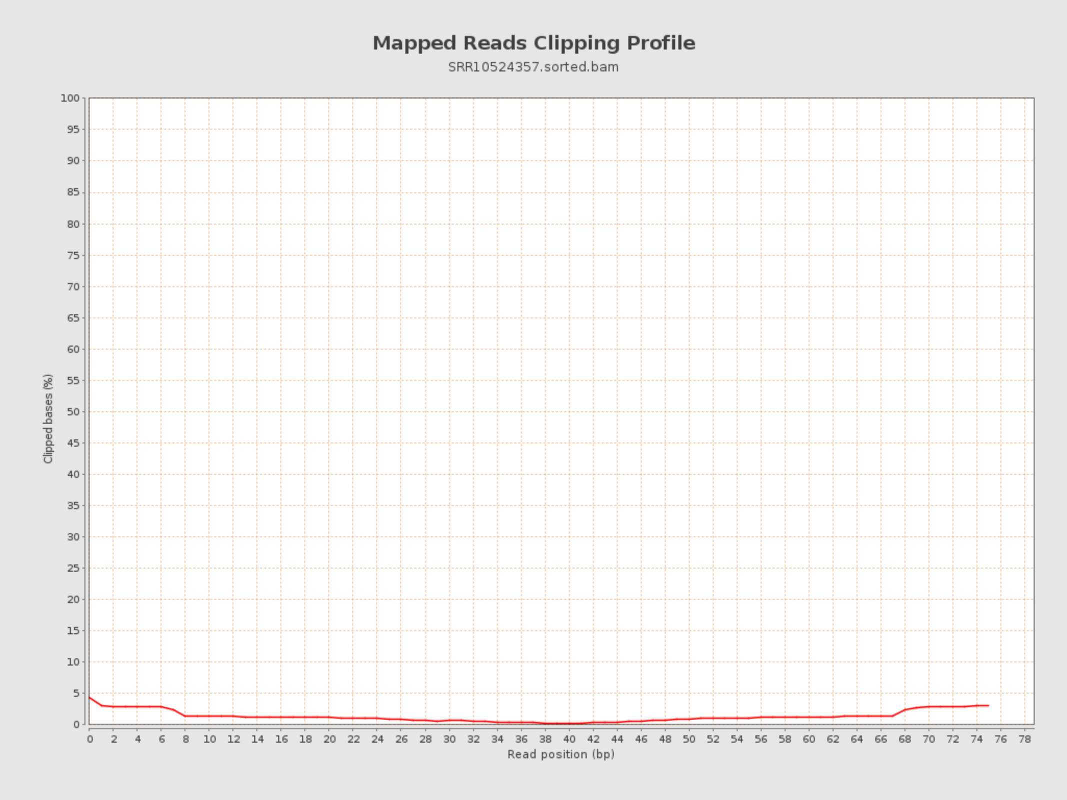
8. Results : Mapped Reads Nucleotide Content



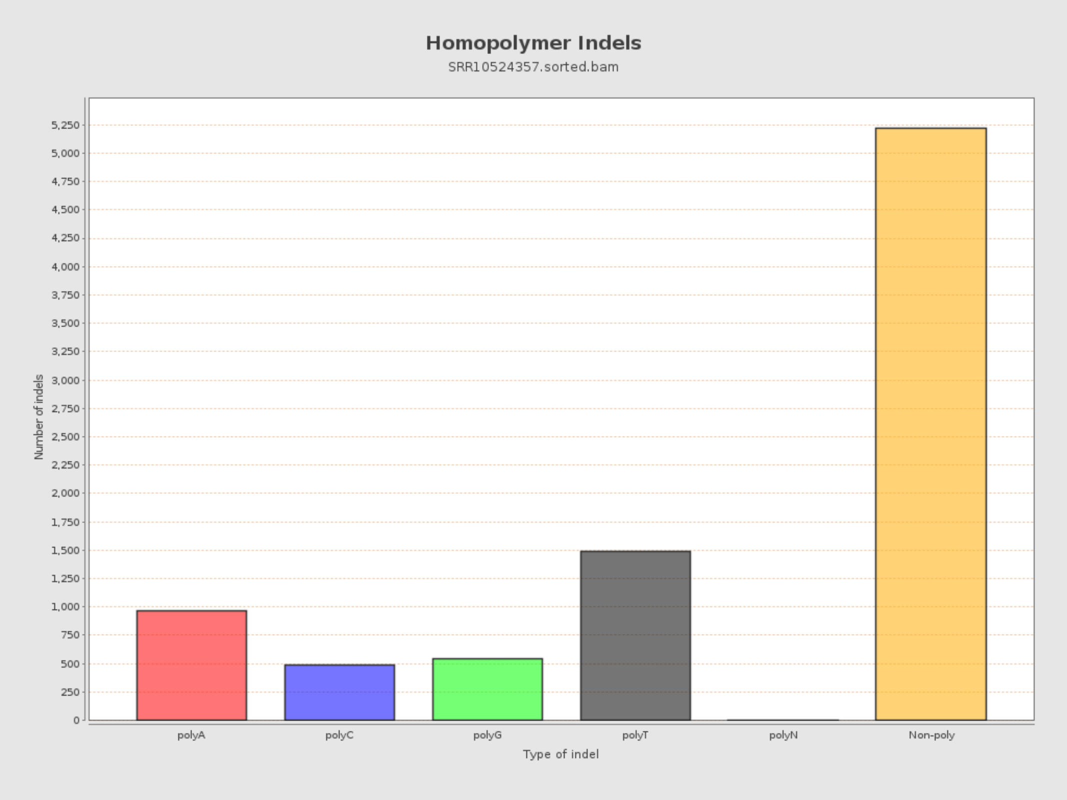
9. Results : Mapped Reads GC-content Distribution



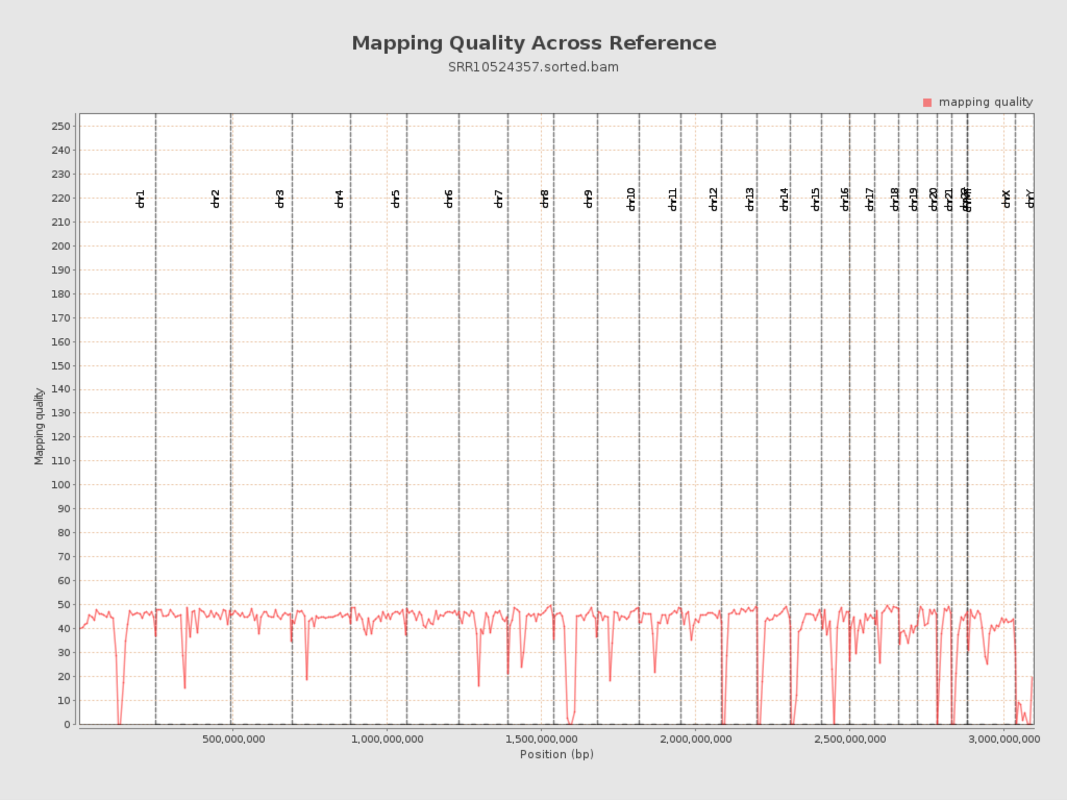
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram