Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:26:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524756.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_SRR10524756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:26:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,119,030
Mapped reads	1,016,737 / 90.86%
Unmapped reads	102,293 / 9.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,355 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,598 / 2.47%
Duplication rate	2.05%
Clipped reads	1,019,097 / 91.07%

2.2. ACGT Content

Number/percentage of A's	14,526,833 / 24.86%
Number/percentage of C's	11,914,554 / 20.39%
Number/percentage of T's	17,761,151 / 30.4%
Number/percentage of G's	14,216,314 / 24.33%
Number/percentage of N's	7,268 / 0.01%
GC Percentage	44.72%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.1798

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

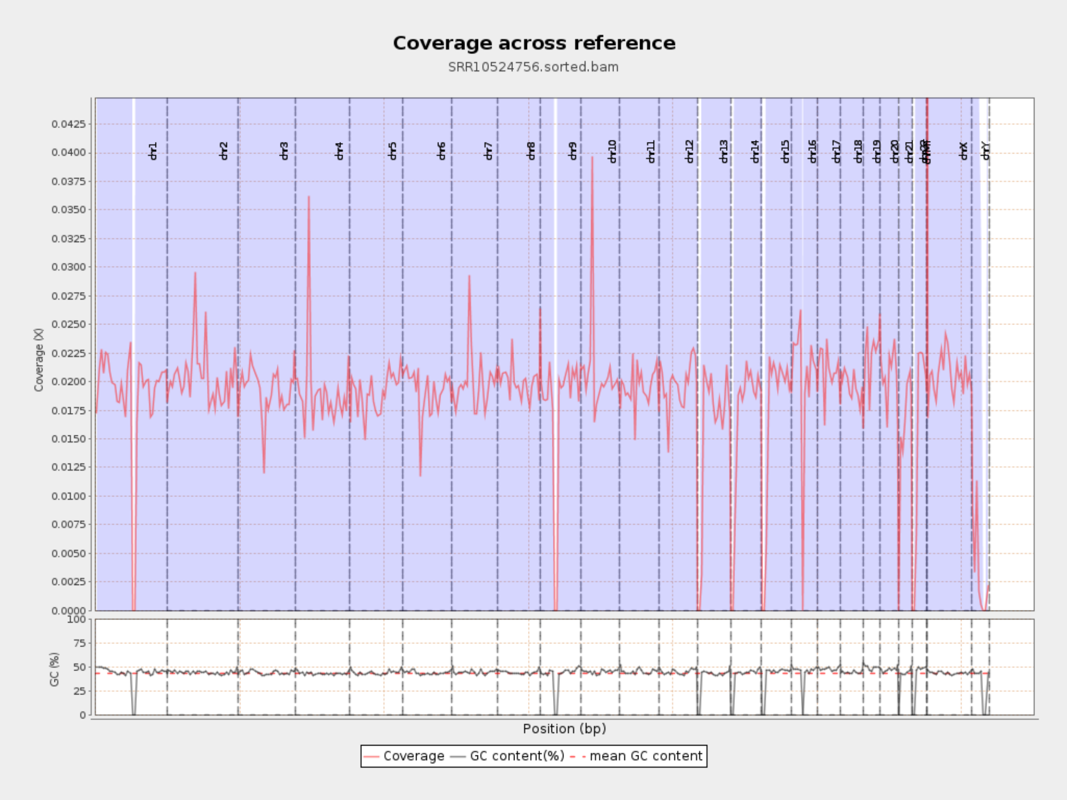
General error rate	0.51%
Mismatches	292,344
Insertions	3,566
Mapped reads with at least one insertion	0.35%
Deletions	11,561
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.53%

2.6. Chromosome stats

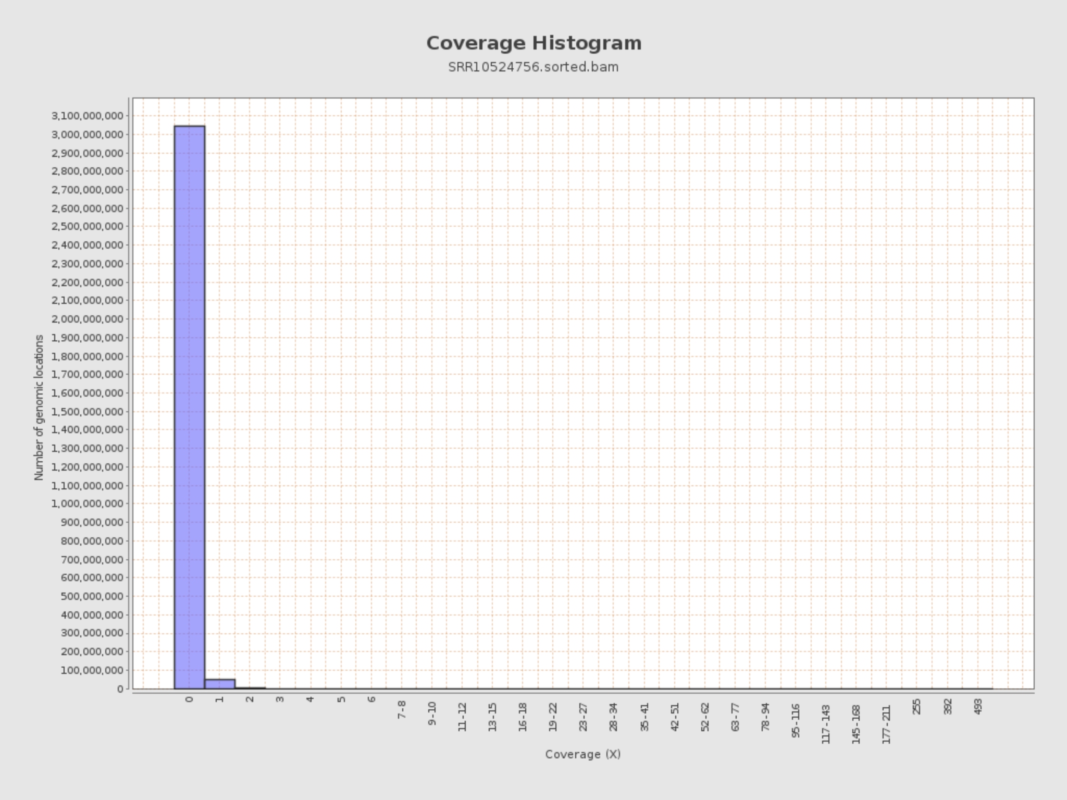
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4667117	0.0187	0.2133
chr2	243199373	4975740	0.0205	0.2671
chr3	198022430	3802278	0.0192	0.1498
chr4	191154276	3671573	0.0192	0.1648
chr5	180915260	3469249	0.0192	0.1481
chr6	171115067	3272562	0.0191	0.1558
chr7	159138663	3179757	0.02	0.2139

chr8	146364022	2918418	0.0199	0.1658
chr9	141213431	2486701	0.0176	0.162
chr10	135534747	2842592	0.021	0.2143
chr11	135006516	2654362	0.0197	0.1686
chr12	133851895	2651798	0.0198	0.1512
chr13	115169878	1799620	0.0156	0.1334
chr14	107349540	1757677	0.0164	0.1393
chr15	102531392	1708195	0.0167	0.1385
chr16	90354753	1812178	0.0201	0.1637
chr17	81195210	1703667	0.021	0.159
chr18	78077248	1532824	0.0196	0.2372
chr19	59128983	1315134	0.0222	0.1986
chr20	63025520	1291315	0.0205	0.1595
chr21	48129895	759993	0.0158	0.1457
chr22	51304566	771587	0.015	0.1312
chrMT	16571	6745	0.407	0.6792
chrX	155270560	3199691	0.0206	0.1615
chrY	59373566	194346	0.0033	0.0973

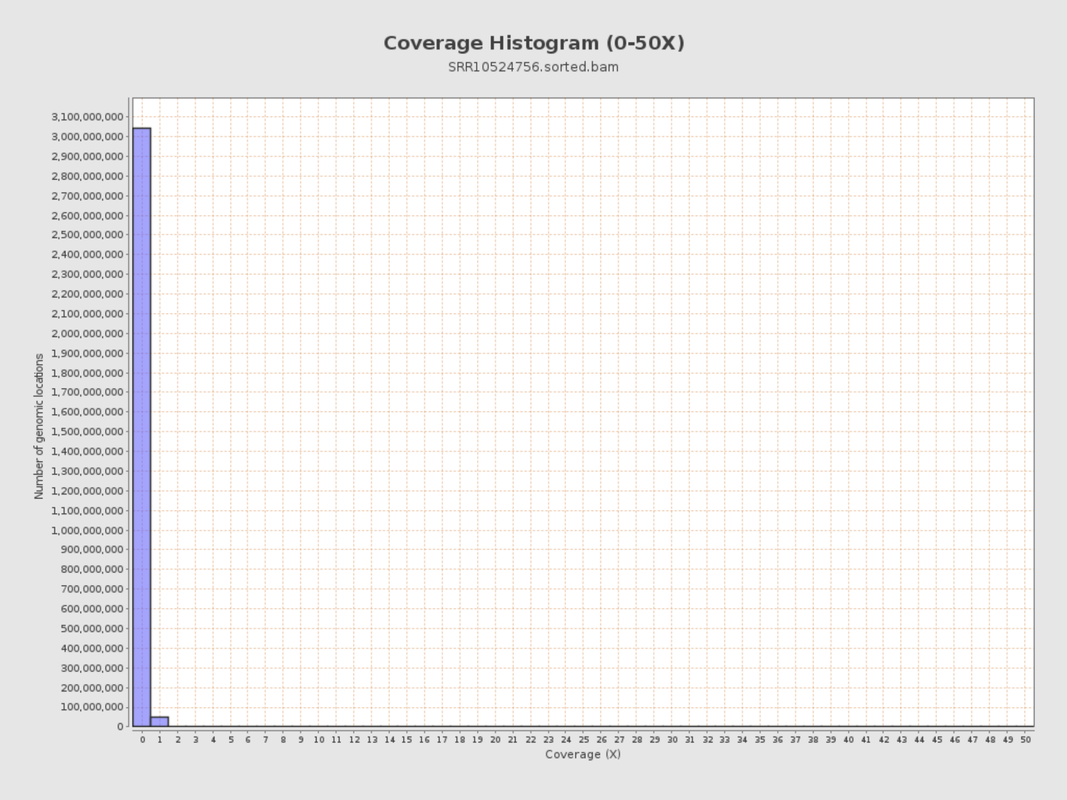
3. Results : Coverage across reference



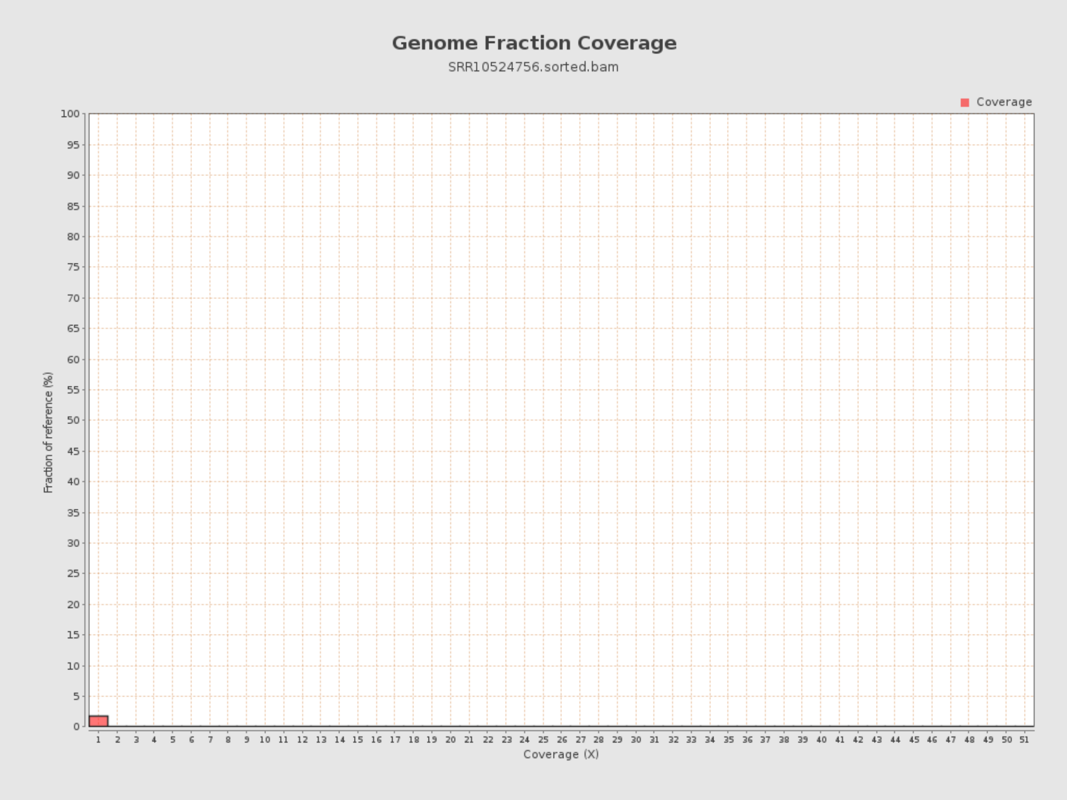
4. Results : Coverage Histogram



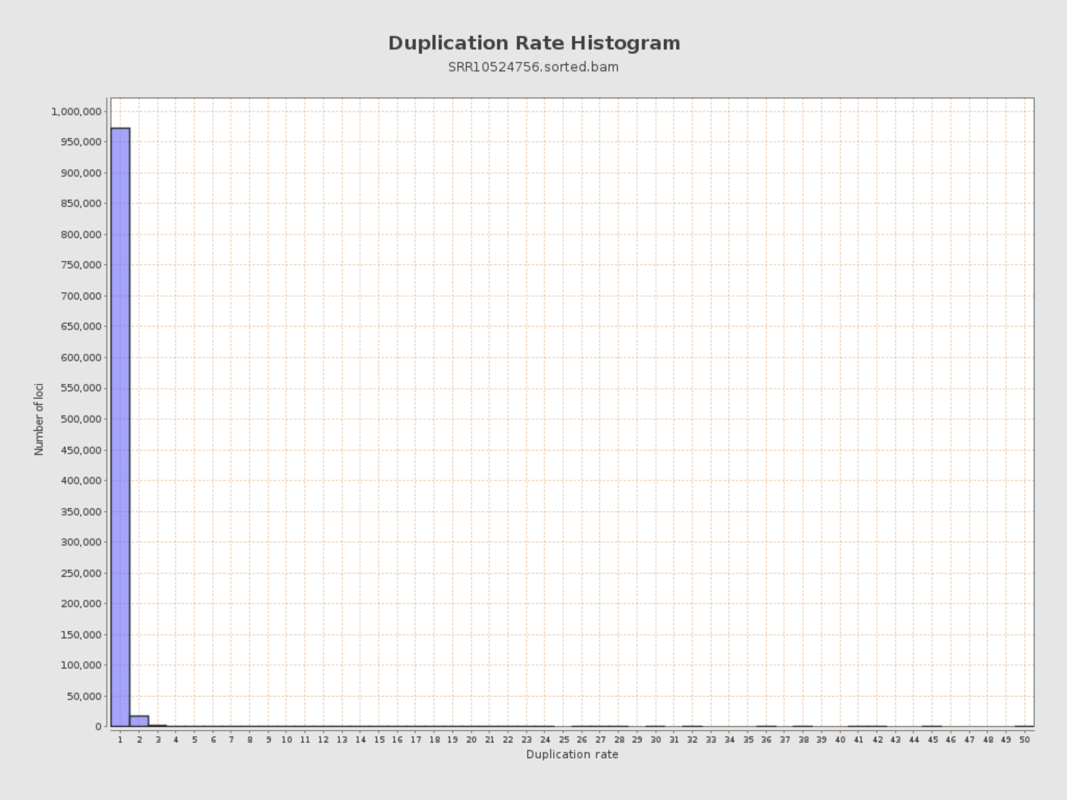
5. Results : Coverage Histogram (0-50X)



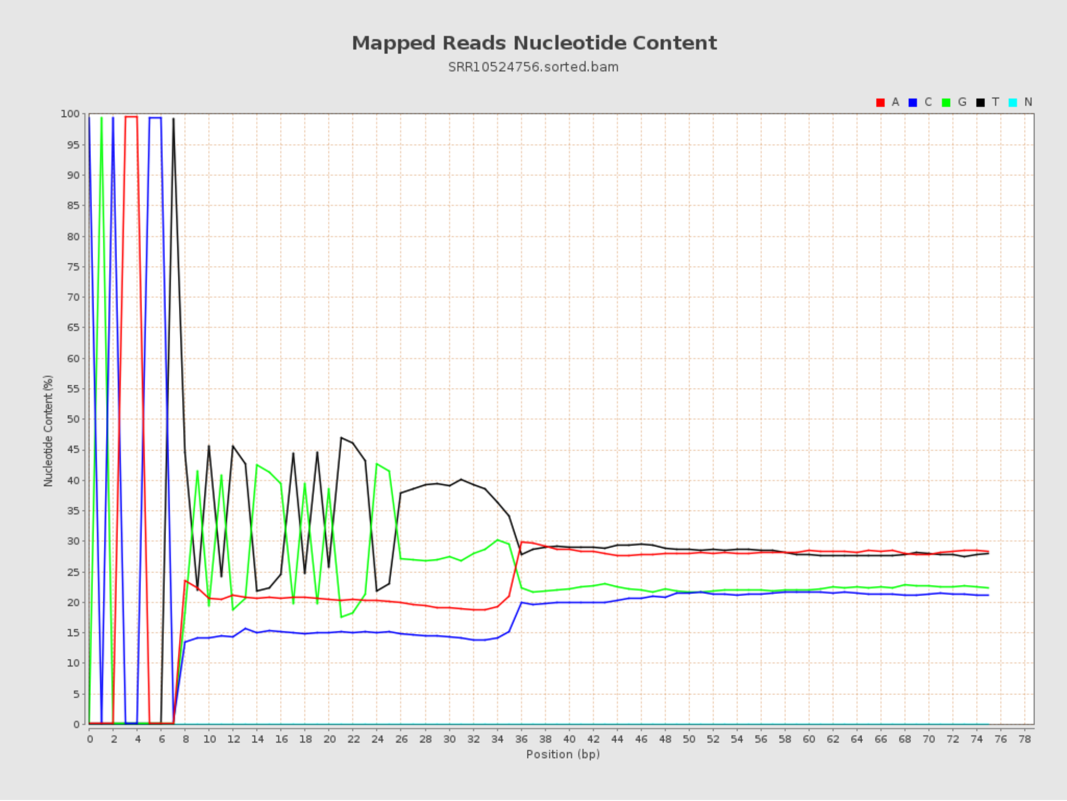
6. Results : Genome Fraction Coverage



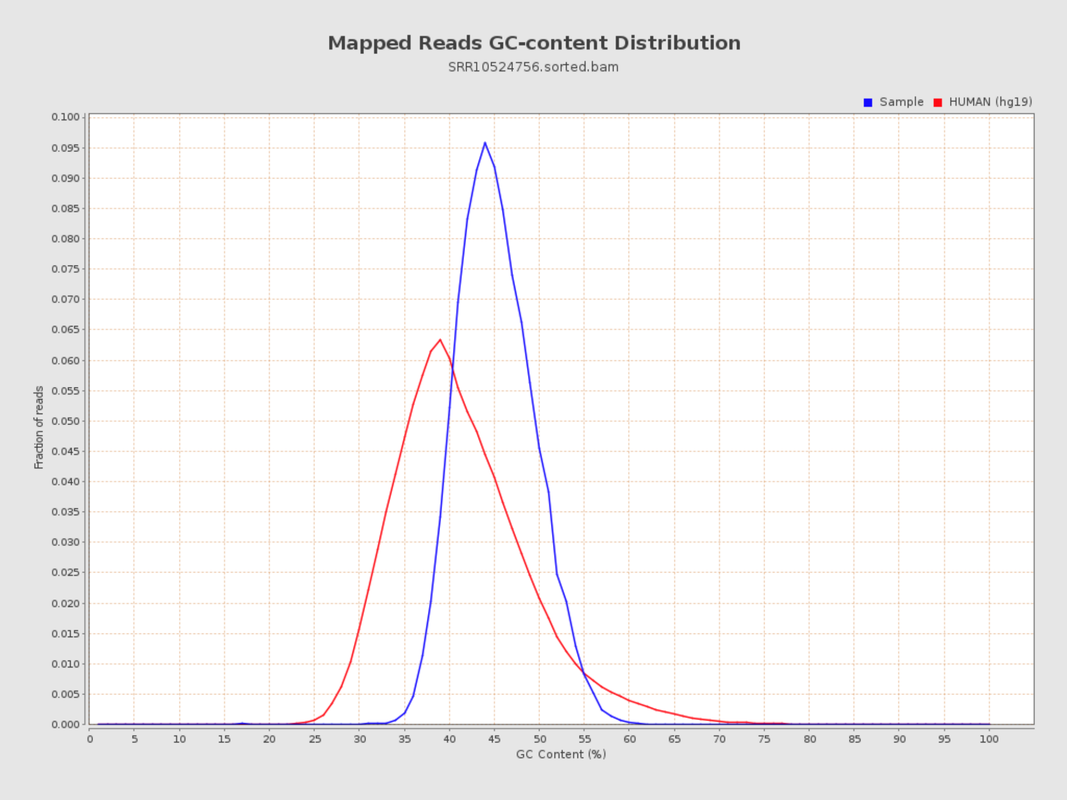
7. Results : Duplication Rate Histogram



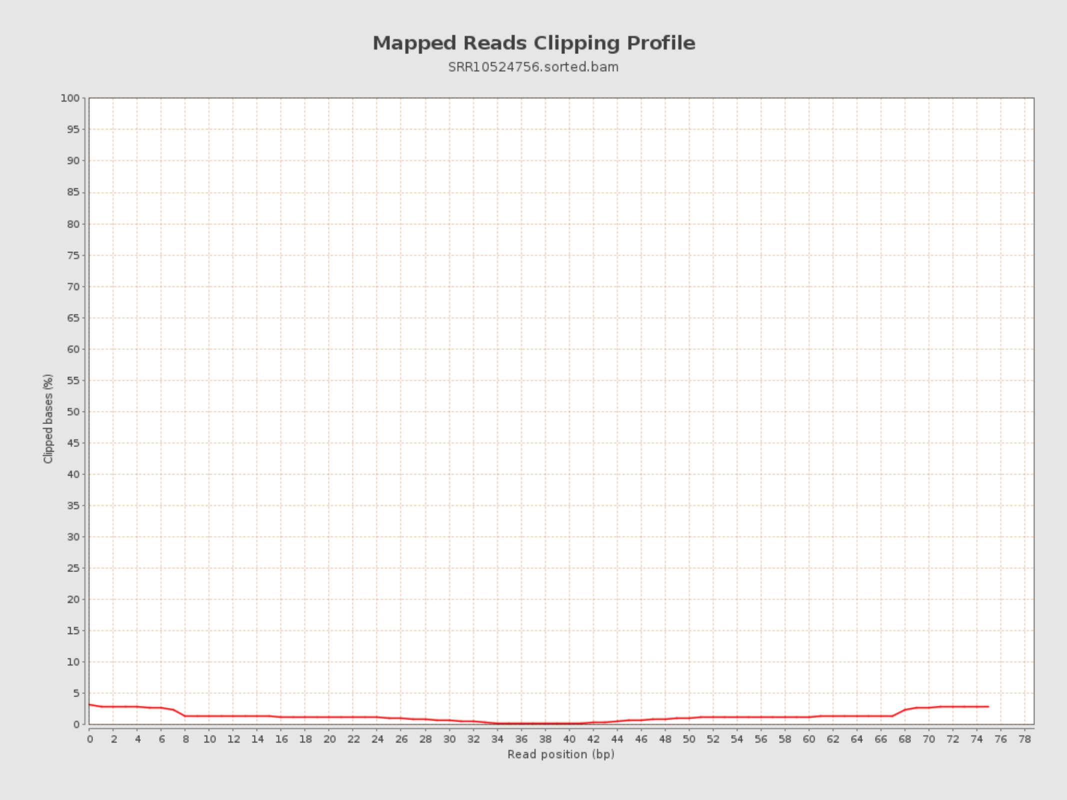
8. Results : Mapped Reads Nucleotide Content



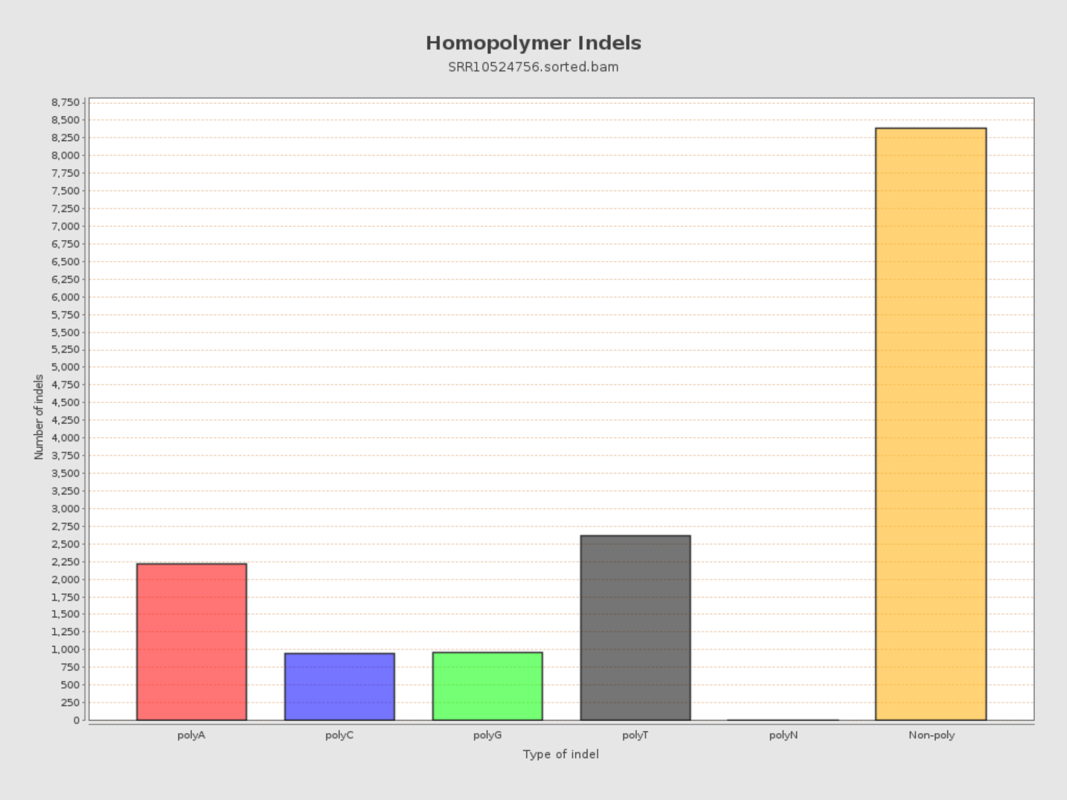
9. Results : Mapped Reads GC-content Distribution



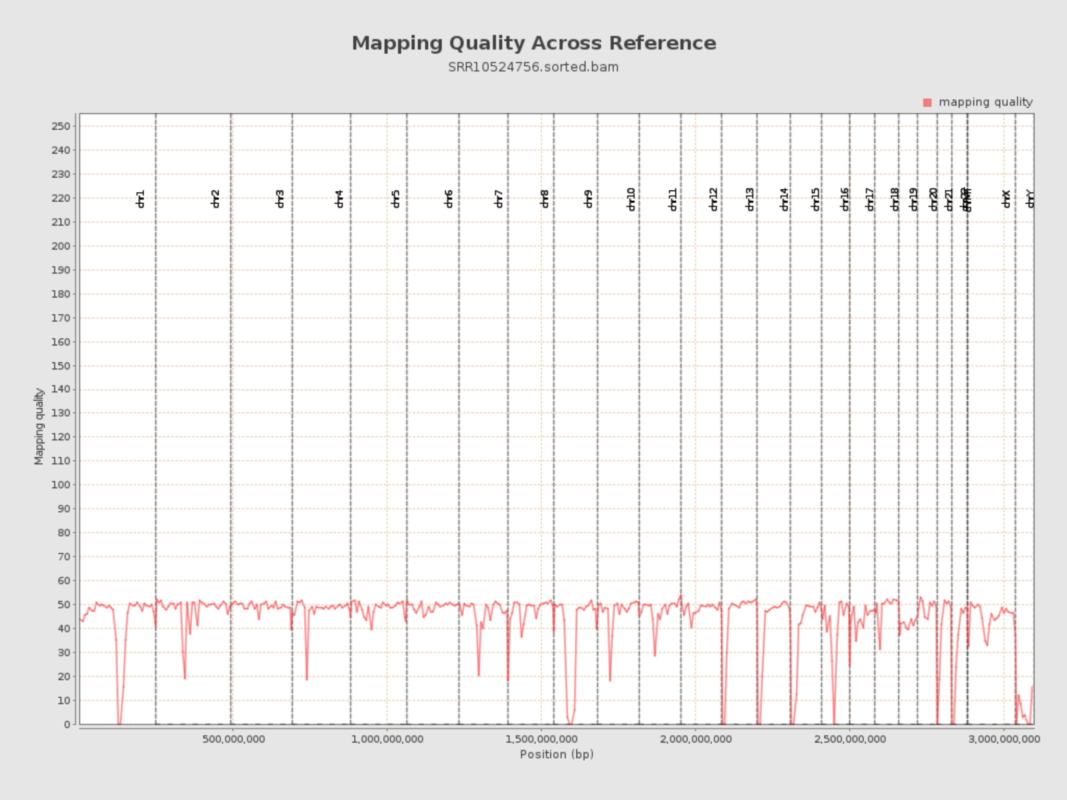
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram