Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:45:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524764.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_SRR10524764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:45:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,269,937
Mapped reads	1,159,479 / 91.3%
Unmapped reads	110,458 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,528 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,716 / 3.28%
Duplication rate	2.78%
Clipped reads	1,163,306 / 91.6%

2.2. ACGT Content

Number/percentage of A's	16,503,933 / 24.95%
Number/percentage of C's	11,592,354 / 17.52%
Number/percentage of T's	20,948,239 / 31.67%
Number/percentage of G's	17,095,977 / 25.84%
Number/percentage of N's	8,753 / 0.01%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0214

Standard Deviation	0.2042

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

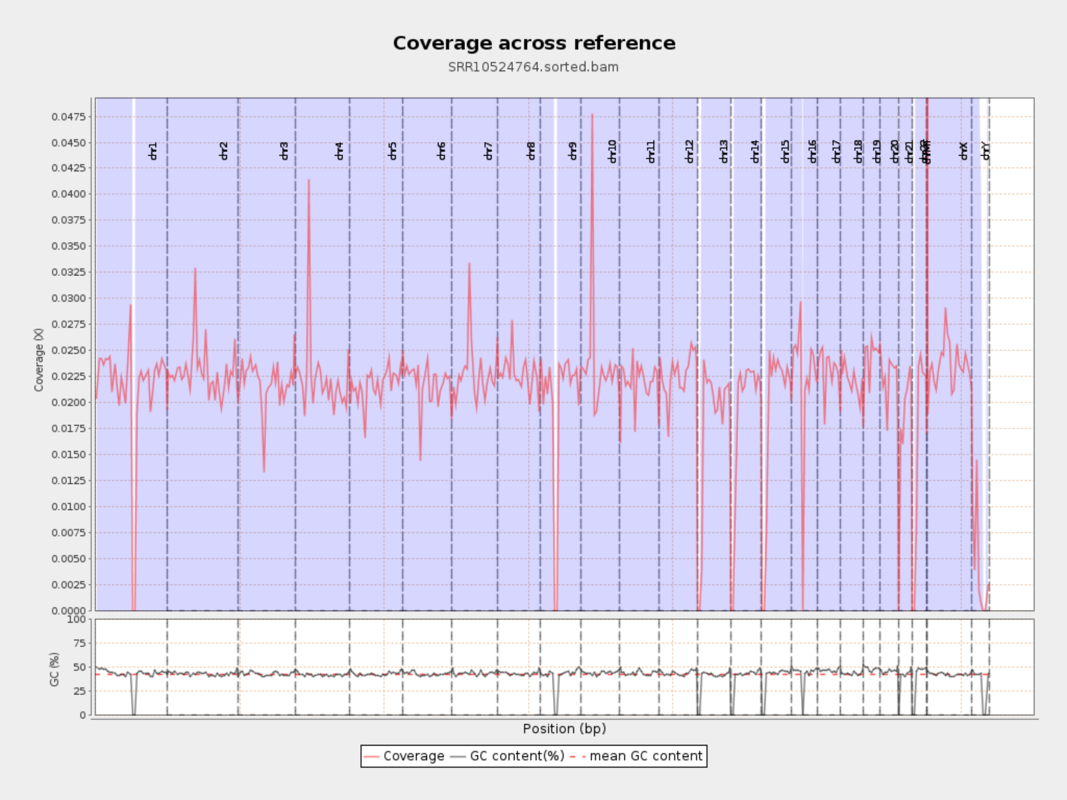
General error rate	0.51%
Mismatches	332,084
Insertions	3,949
Mapped reads with at least one insertion	0.34%
Deletions	13,114
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.73%

2.6. Chromosome stats

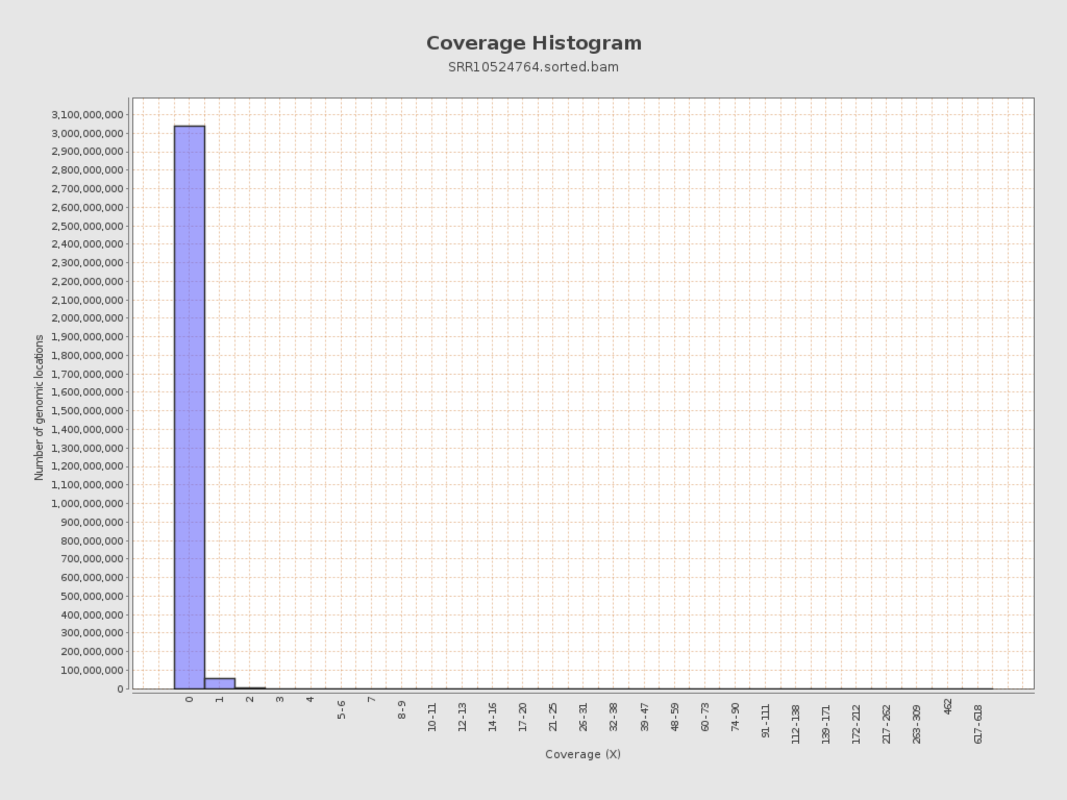
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5295003	0.0212	0.266
chr2	243199373	5588929	0.023	0.3115
chr3	198022430	4321126	0.0218	0.1614
chr4	191154276	4285232	0.0224	0.1831
chr5	180915260	3936187	0.0218	0.1597
chr6	171115067	3745876	0.0219	0.1715
chr7	159138663	3622170	0.0228	0.2425

chr8	146364022	3325392	0.0227	0.197
chr9	141213431	2812869	0.0199	0.1805
chr10	135534747	3237624	0.0239	0.246
chr11	135006516	2990092	0.0221	0.1828
chr12	133851895	3028333	0.0226	0.1655
chr13	115169878	2026379	0.0176	0.1433
chr14	107349540	1991487	0.0186	0.151
chr15	102531392	1922132	0.0187	0.1494
chr16	90354753	1978678	0.0219	0.1752
chr17	81195210	1873457	0.0231	0.1717
chr18	78077248	1726572	0.0221	0.2603
chr19	59128983	1442256	0.0244	0.2356
chr20	63025520	1404170	0.0223	0.1675
chr21	48129895	870793	0.0181	0.1592
chr22	51304566	818980	0.016	0.1382
chrMT	16571	29933	1.8063	1.716
chrX	155270560	3662986	0.0236	0.1765
chrY	59373566	233952	0.0039	0.1204

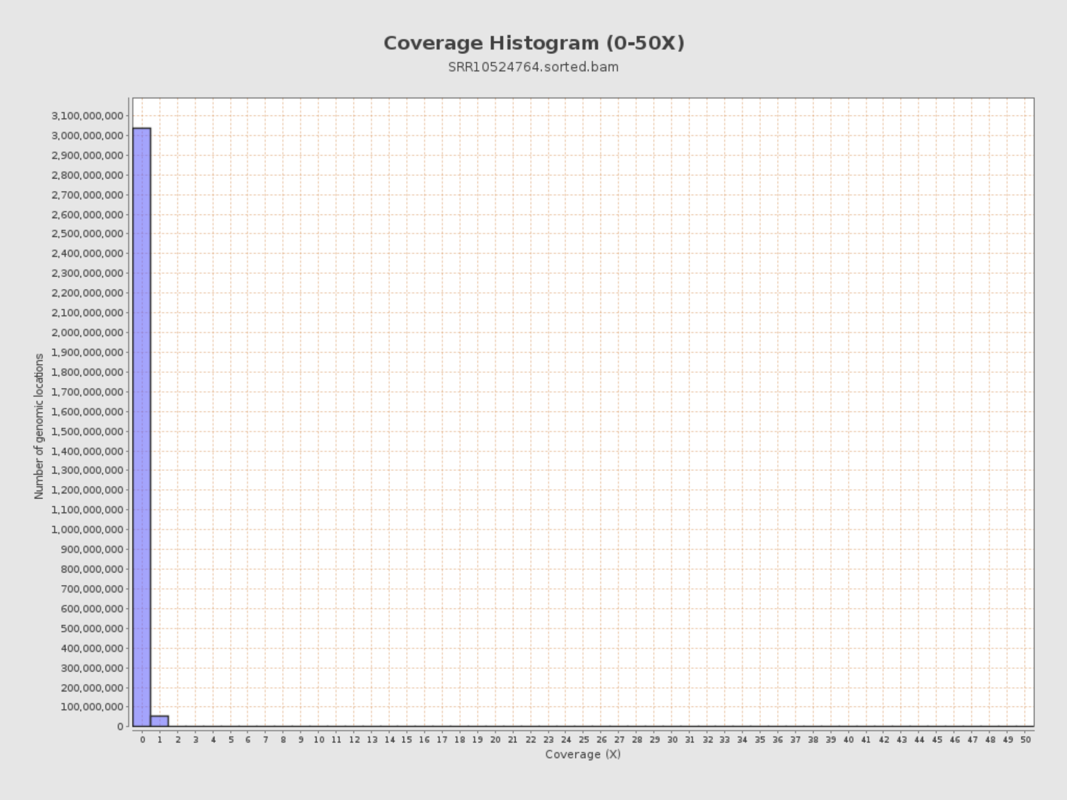
3. Results : Coverage across reference



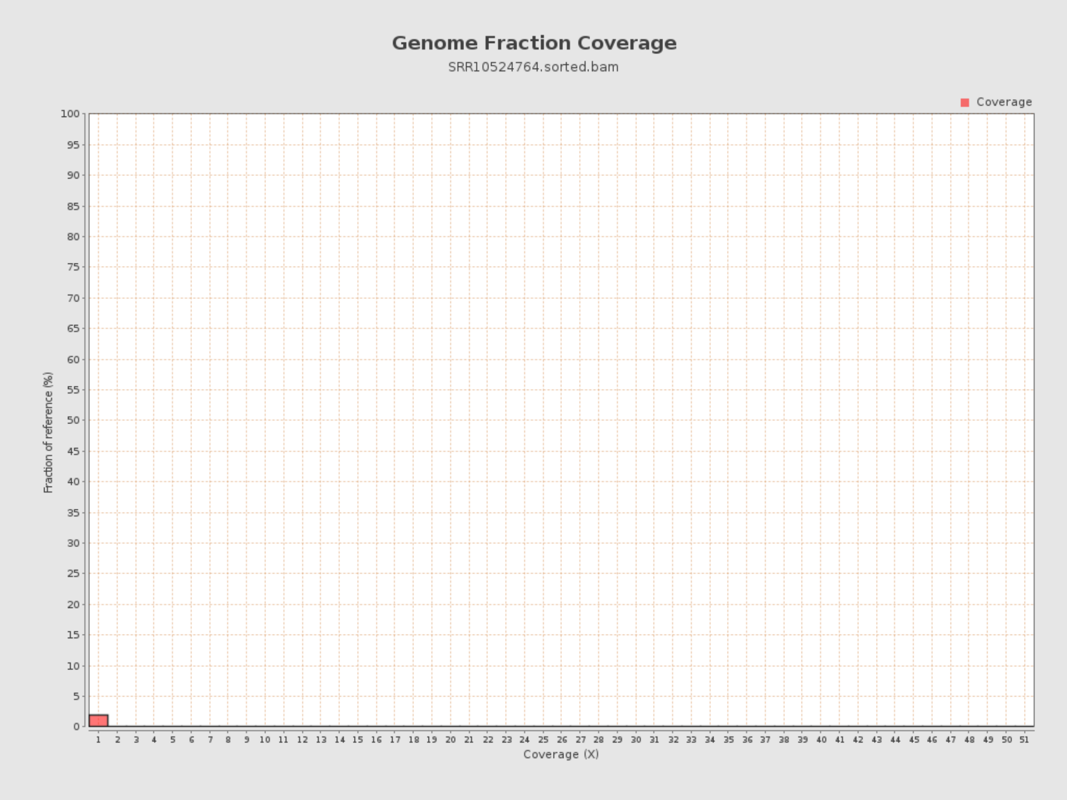
4. Results : Coverage Histogram



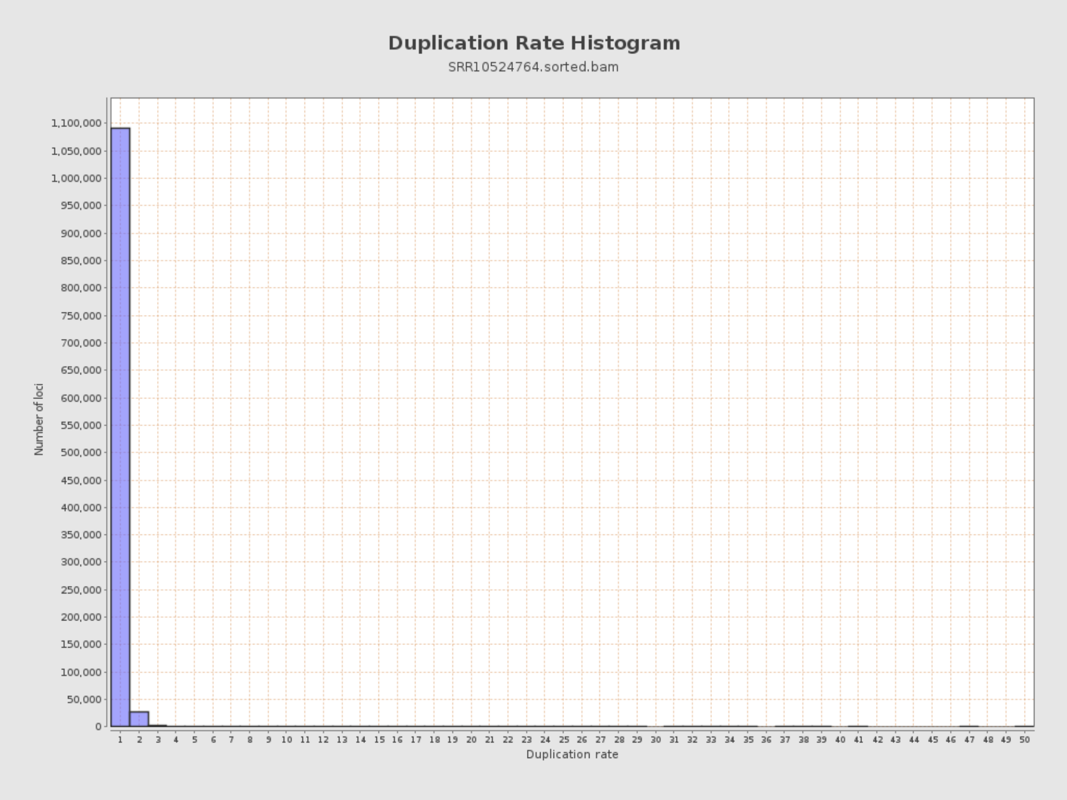
5. Results : Coverage Histogram (0-50X)



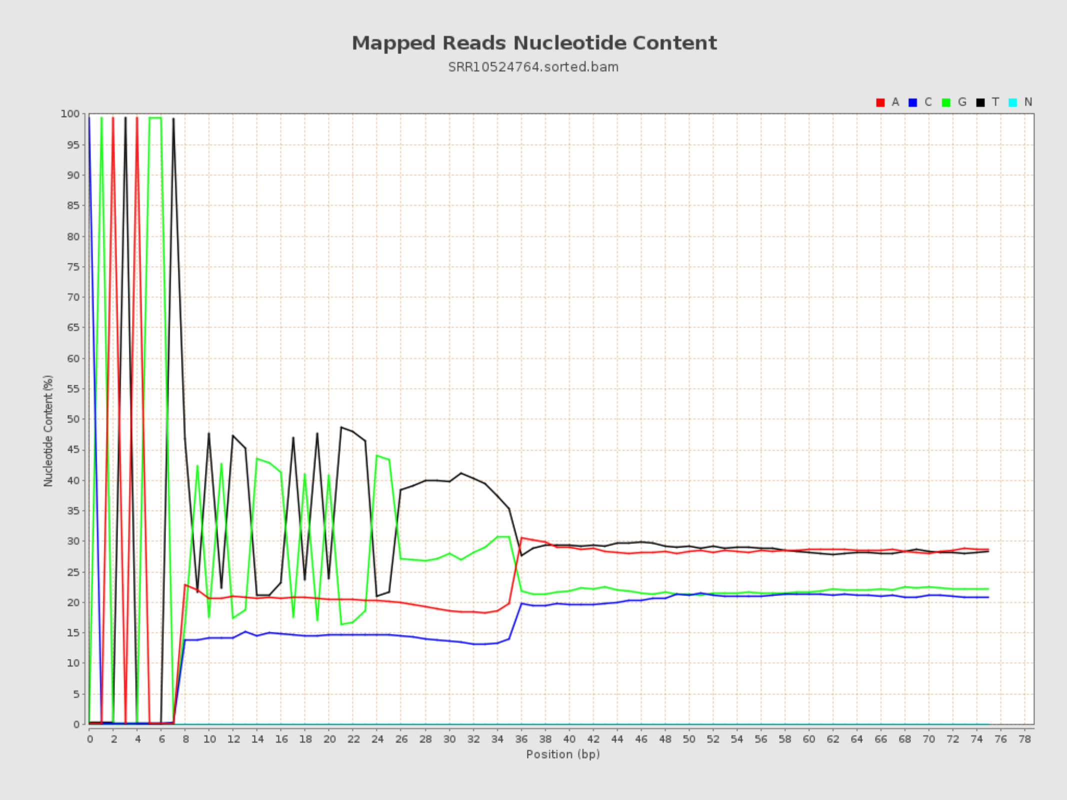
6. Results : Genome Fraction Coverage



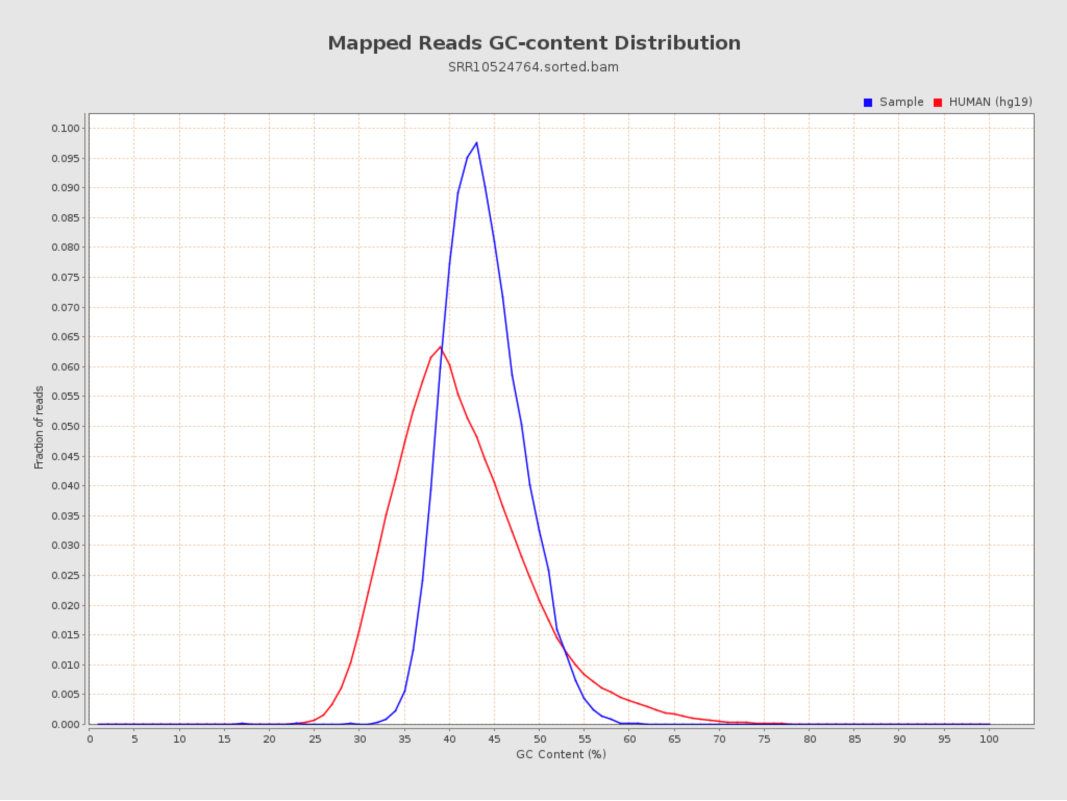
7. Results : Duplication Rate Histogram



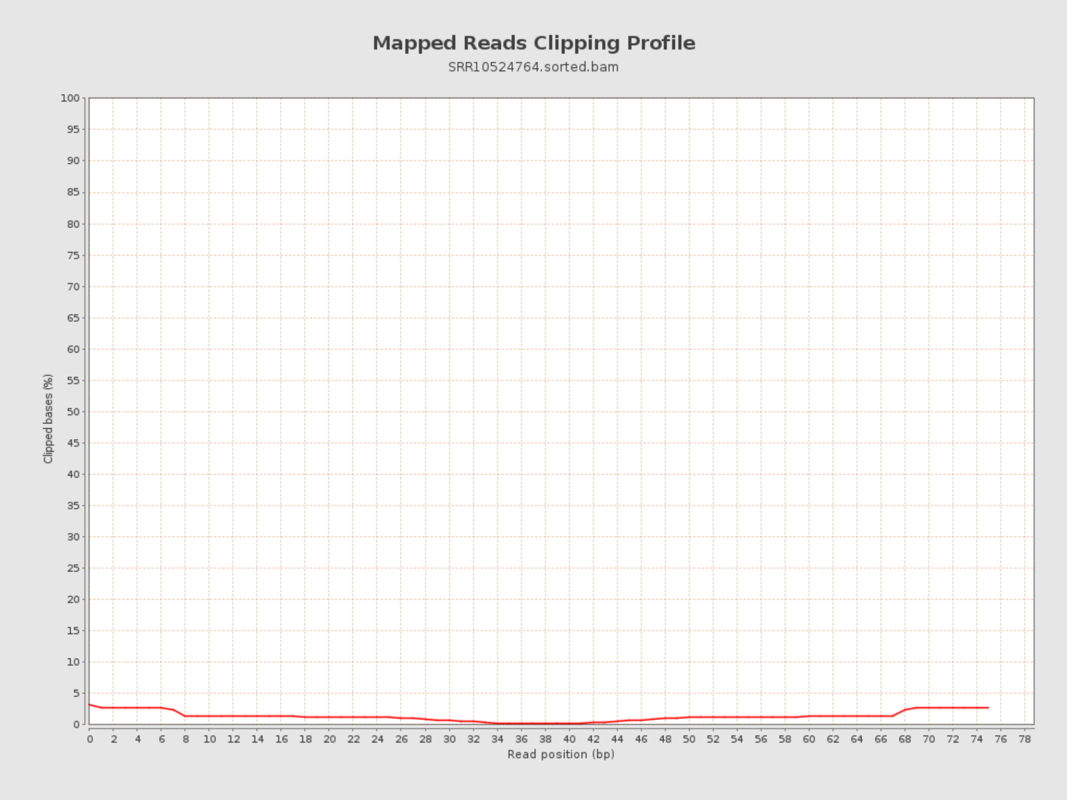
8. Results : Mapped Reads Nucleotide Content



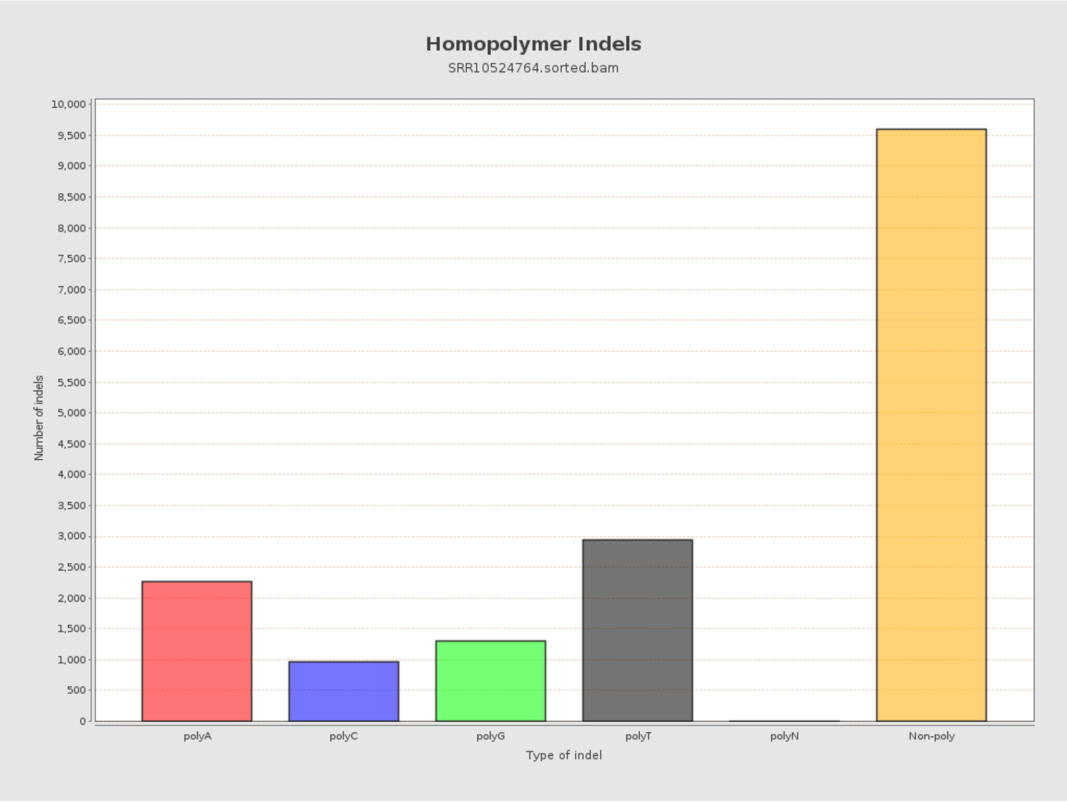
9. Results : Mapped Reads GC-content Distribution



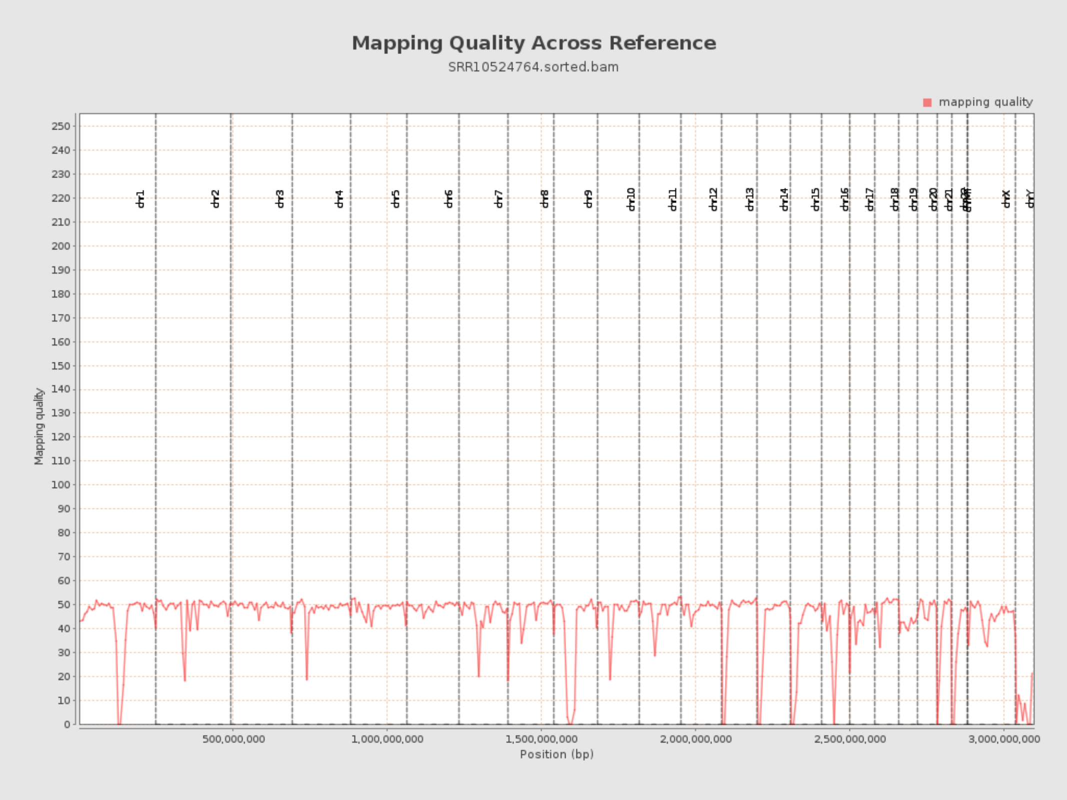
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram