Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:48:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524504.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_SRR10524504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524504.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:48:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524504.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,774
Mapped reads	1,315,372 / 92.97%
Unmapped reads	99,402 / 7.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,067 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	50,430 / 3.56%
Duplication rate	2.94%
Clipped reads	1,318,114 / 93.17%

2.2. ACGT Content

Number/percentage of A's	18,785,998 / 24.3%
Number/percentage of C's	15,057,786 / 19.48%
Number/percentage of T's	23,983,804 / 31.03%
Number/percentage of G's	19,465,335 / 25.18%
Number/percentage of N's	1,639 / 0%
GC Percentage	44.66%

2.3. Coverage

Mean	0.025

Standard Deviation	0.2425

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

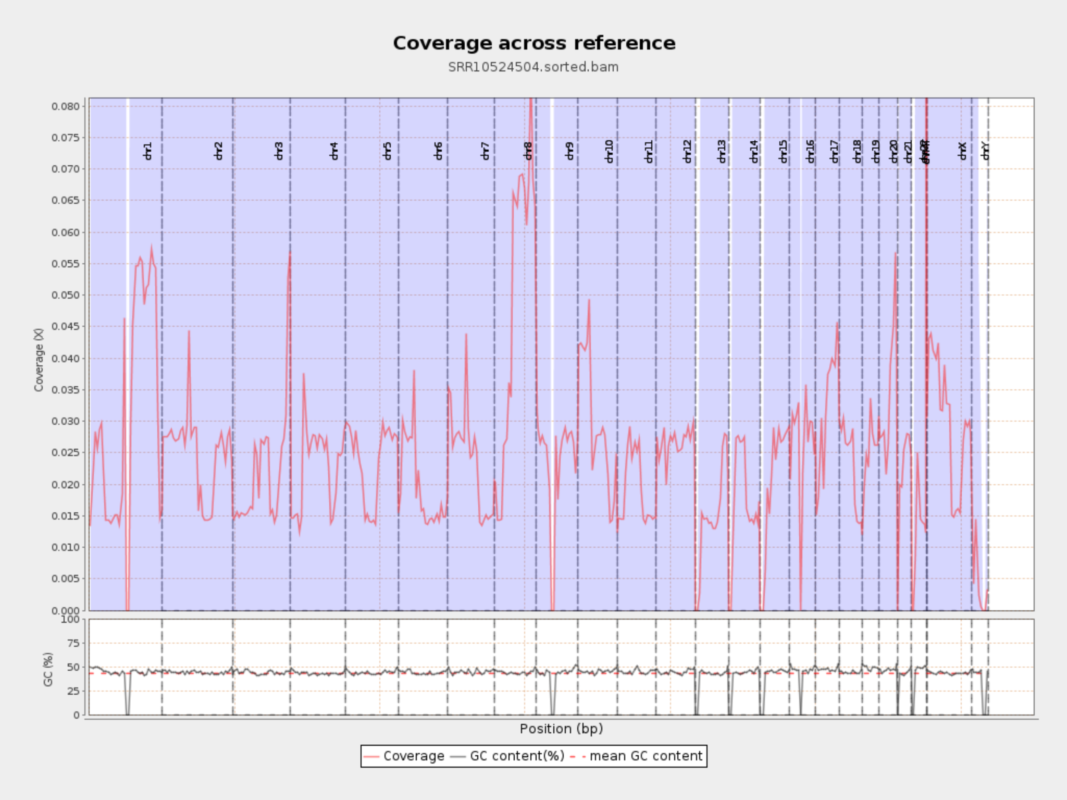
General error rate	0.48%
Mismatches	359,801
Insertions	4,051
Mapped reads with at least one insertion	0.31%
Deletions	14,246
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.42%

2.6. Chromosome stats

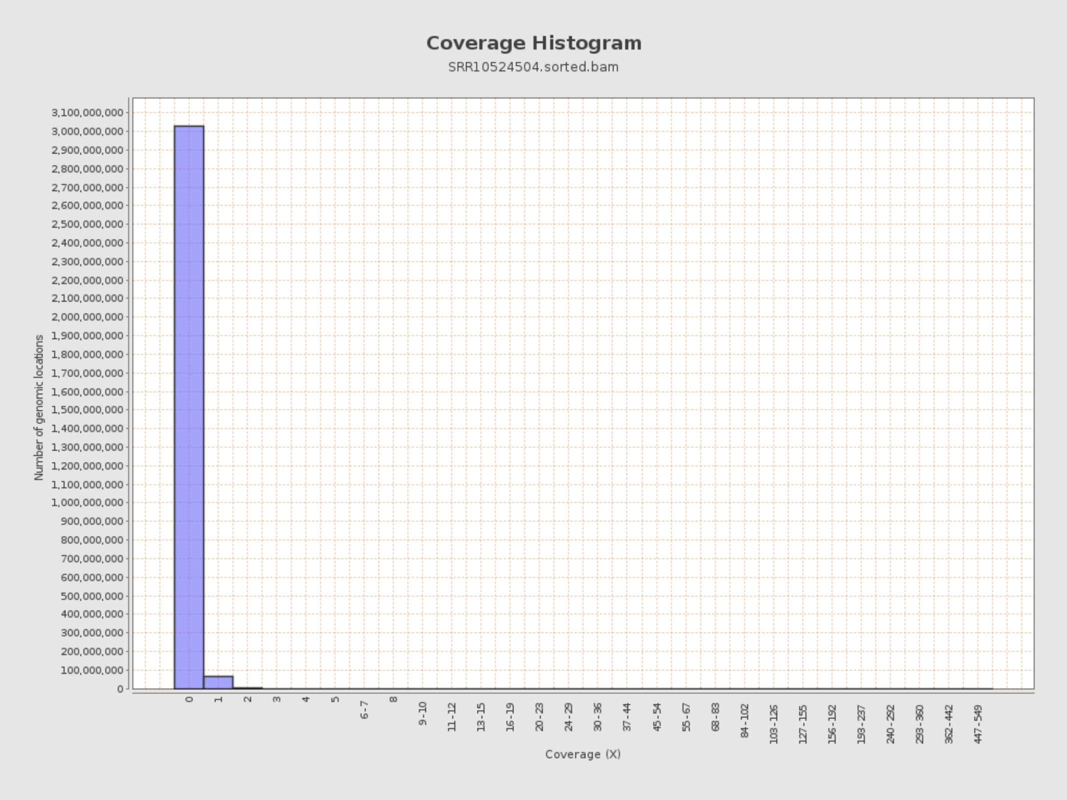
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7734189	0.031	0.4458
chr2	243199373	6108126	0.0251	0.256
chr3	198022430	4282966	0.0216	0.162
chr4	191154276	4342077	0.0227	0.183
chr5	180915260	4297657	0.0238	0.1679
chr6	171115067	3355225	0.0196	0.1909
chr7	159138663	3834449	0.0241	0.3128

chr8	146364022	7180924	0.0491	0.2762
chr9	141213431	3252215	0.023	0.214
chr10	135534747	4063330	0.03	0.2593
chr11	135006516	2603152	0.0193	0.214
chr12	133851895	3560090	0.0266	0.1776
chr13	115169878	1708943	0.0148	0.1344
chr14	107349540	1837914	0.0171	0.1471
chr15	102531392	2053480	0.02	0.1591
chr16	90354753	2388723	0.0264	0.1886
chr17	81195210	2604470	0.0321	0.2062
chr18	78077248	1820742	0.0233	0.3449
chr19	59128983	1503695	0.0254	0.3018
chr20	63025520	2179804	0.0346	0.2052
chr21	48129895	1059611	0.022	0.1729
chr22	51304566	611223	0.0119	0.1175
chrMT	16571	5655	0.3413	0.6538
chrX	155270560	4676520	0.0301	0.2085
chrY	59373566	254108	0.0043	0.1188

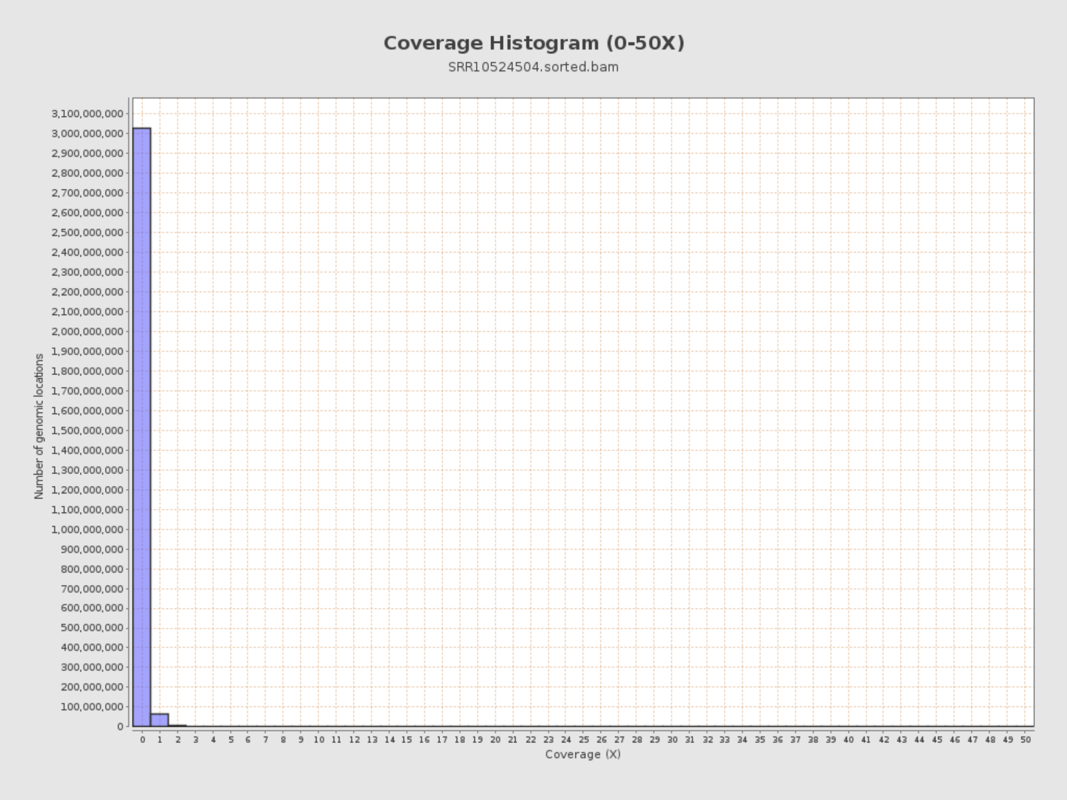
3. Results : Coverage across reference



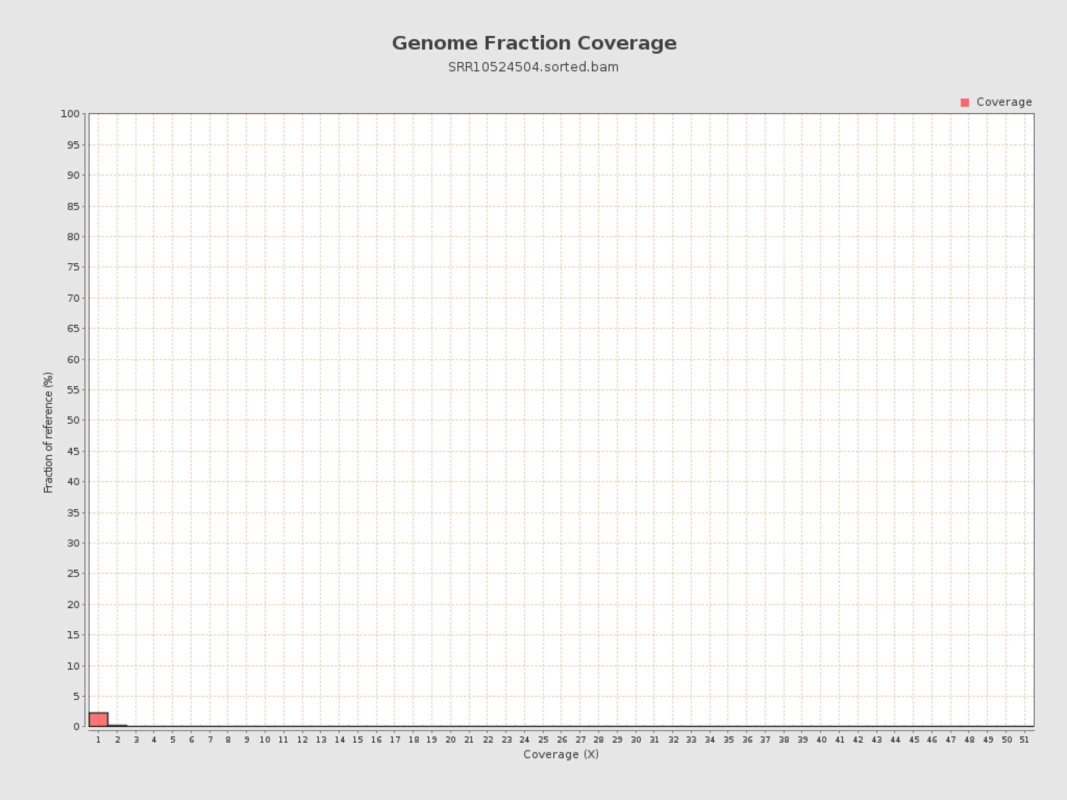
4. Results : Coverage Histogram



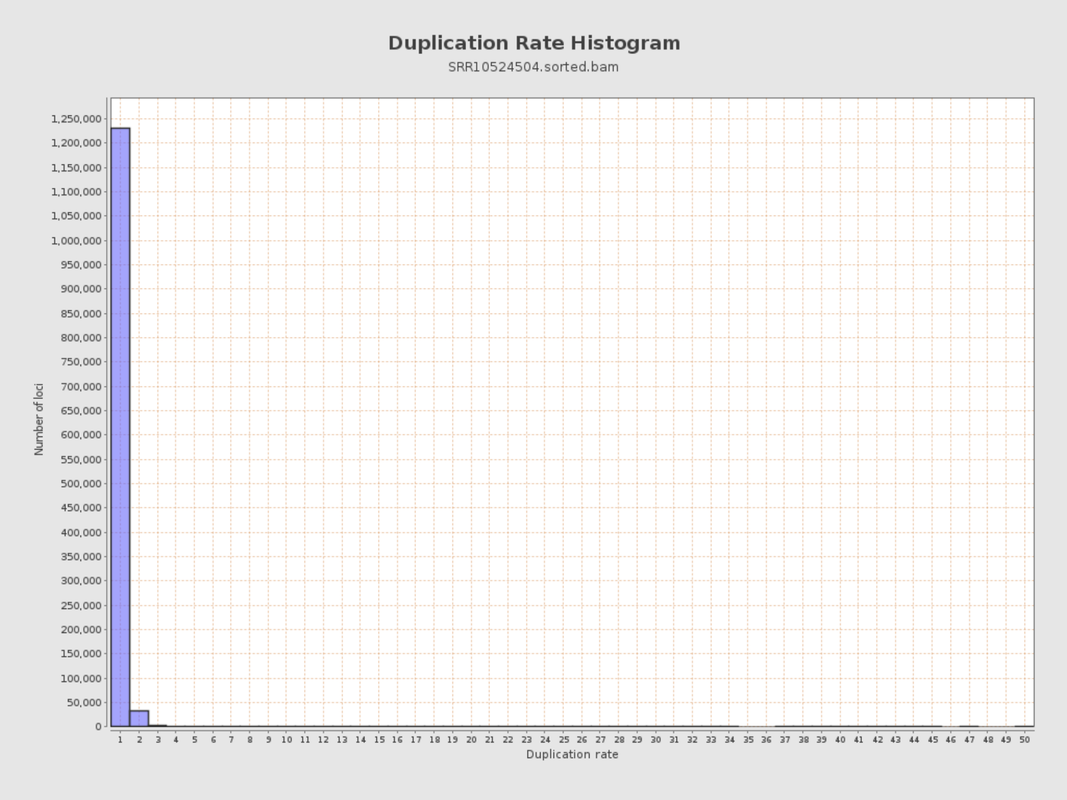
5. Results : Coverage Histogram (0-50X)



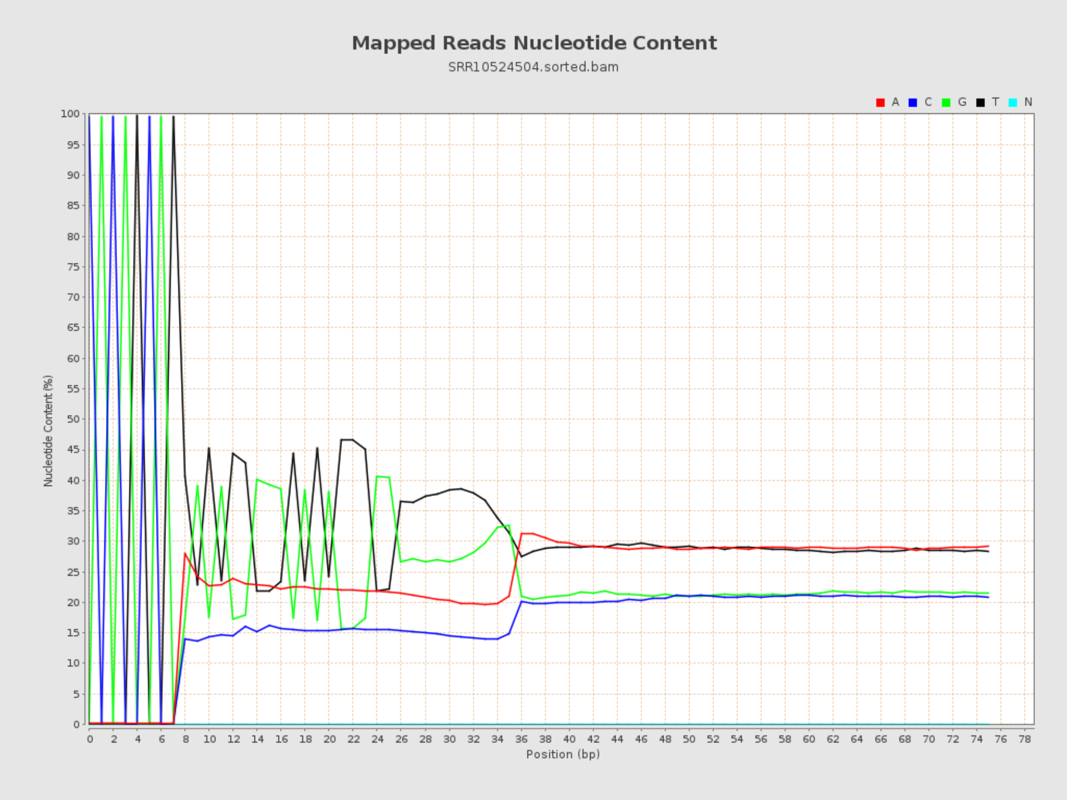
6. Results : Genome Fraction Coverage



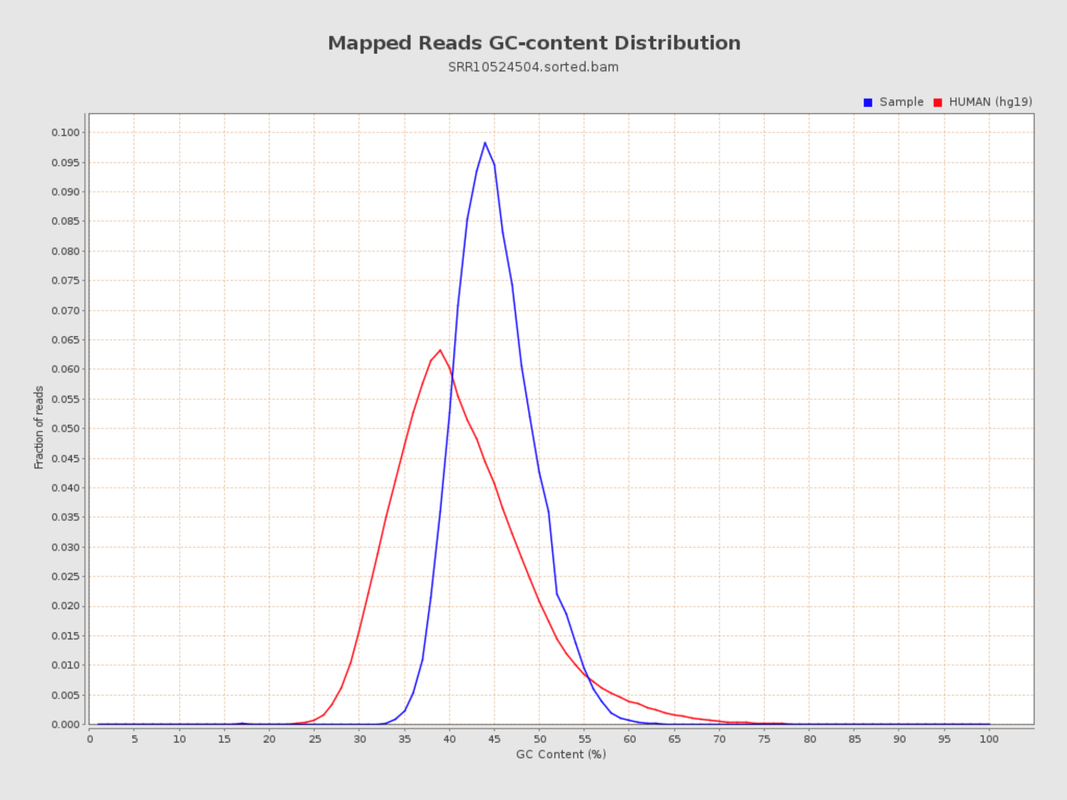
7. Results : Duplication Rate Histogram



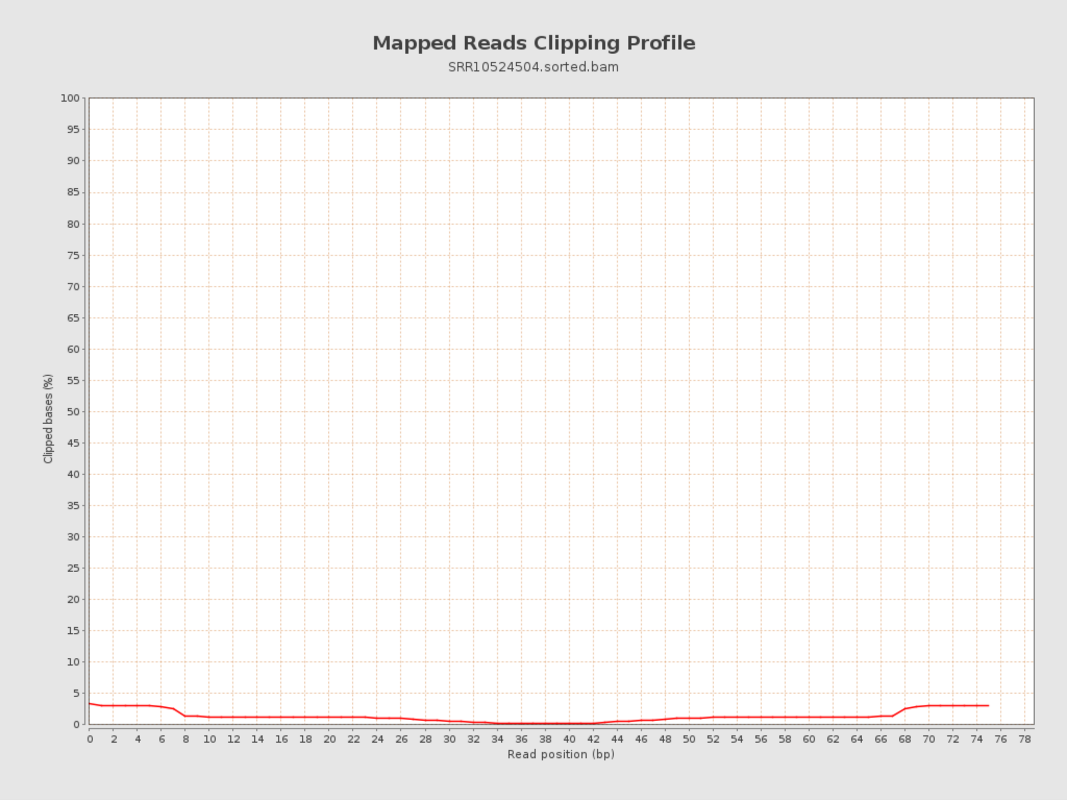
8. Results : Mapped Reads Nucleotide Content



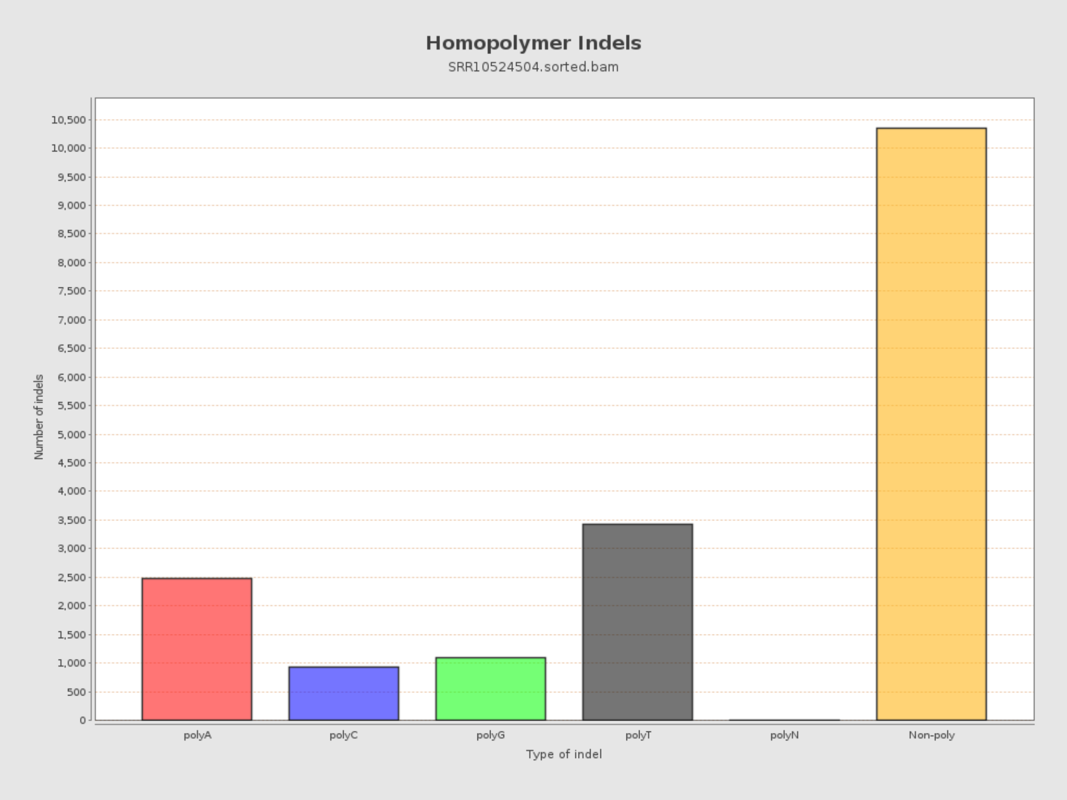
9. Results : Mapped Reads GC-content Distribution



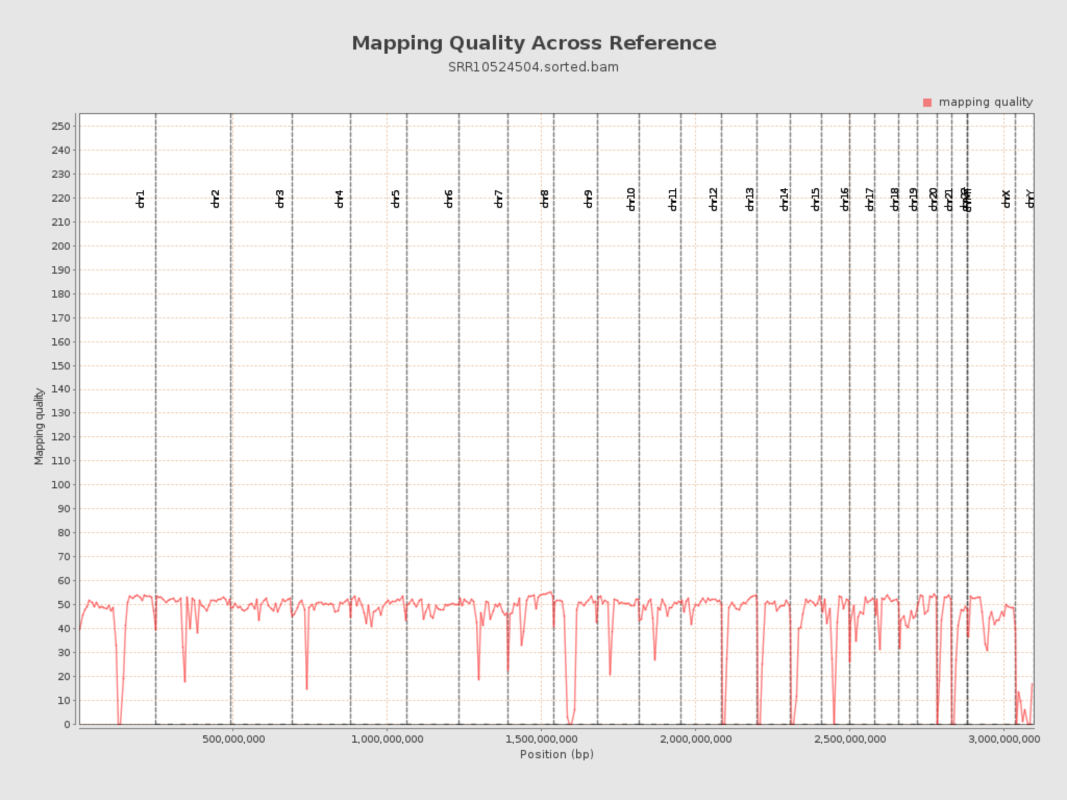
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram