Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:05:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524285.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_SRR10524285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:05:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,442,201
Mapped reads	2,245,951 / 91.96%
Unmapped reads	196,250 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,896 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	120,402 / 4.93%
Duplication rate	4%
Clipped reads	2,247,681 / 92.04%

2.2. ACGT Content

Number/percentage of A's	35,210,519 / 26.79%
Number/percentage of C's	23,144,081 / 17.61%
Number/percentage of T's	41,345,053 / 31.46%
Number/percentage of G's	31,723,479 / 24.14%
Number/percentage of N's	17,860 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.4091

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

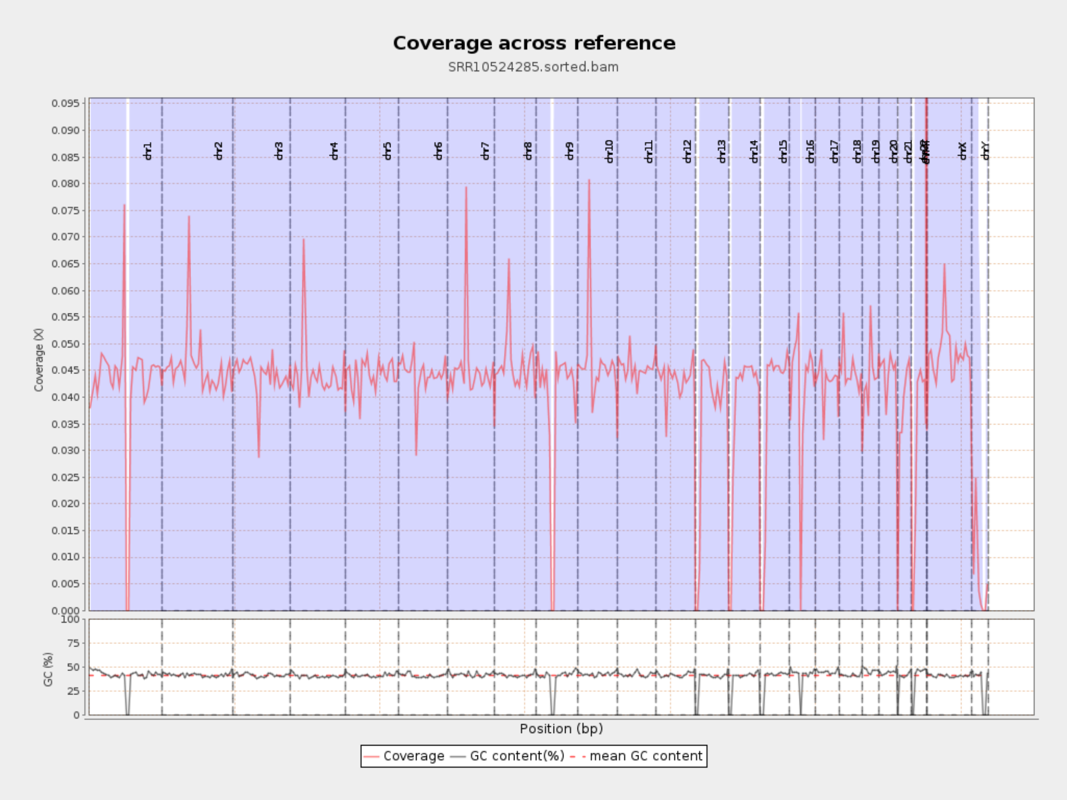
General error rate	0.51%
Mismatches	650,468
Insertions	9,353
Mapped reads with at least one insertion	0.41%
Deletions	24,594
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.81%

2.6. Chromosome stats

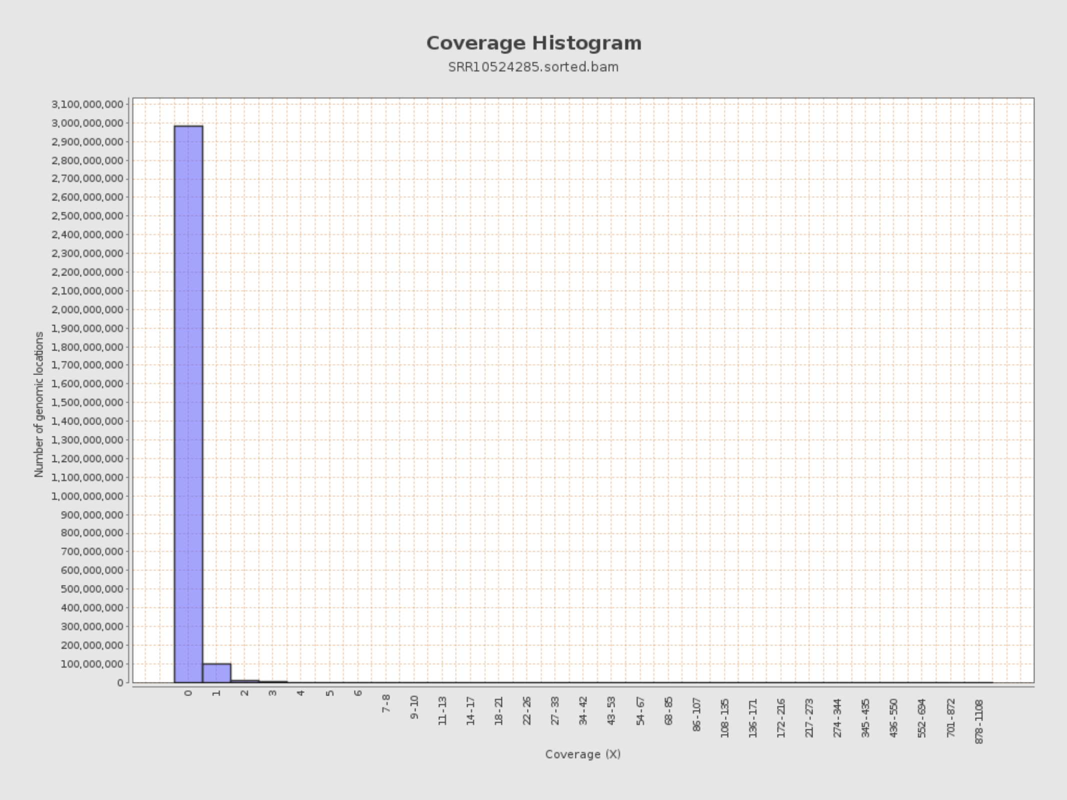
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10588267	0.0425	0.8437
chr2	243199373	11140307	0.0458	0.4266
chr3	198022430	8726640	0.0441	0.2353
chr4	191154276	8463261	0.0443	0.278
chr5	180915260	7980225	0.0441	0.2397
chr6	171115067	7573211	0.0443	0.2637
chr7	159138663	7265926	0.0457	0.5651

chr8	146364022	6770663	0.0463	0.3986
chr9	141213431	5488210	0.0389	0.3665
chr10	135534747	6320330	0.0466	0.3666
chr11	135006516	6095879	0.0452	0.3706
chr12	133851895	5795806	0.0433	0.2429
chr13	115169878	4135587	0.0359	0.2135
chr14	107349540	4022500	0.0375	0.2318
chr15	102531392	3784808	0.0369	0.2183
chr16	90354753	3775489	0.0418	0.254
chr17	81195210	3470688	0.0427	0.2583
chr18	78077248	3525495	0.0452	0.7409
chr19	59128983	2583077	0.0437	0.5293
chr20	63025520	2798658	0.0444	0.2449
chr21	48129895	1744315	0.0362	0.2524
chr22	51304566	1542256	0.0301	0.1941
chrMT	16571	23950	1.4453	1.4504
chrX	155270560	7461154	0.0481	0.2919
chrY	59373566	403515	0.0068	0.1854

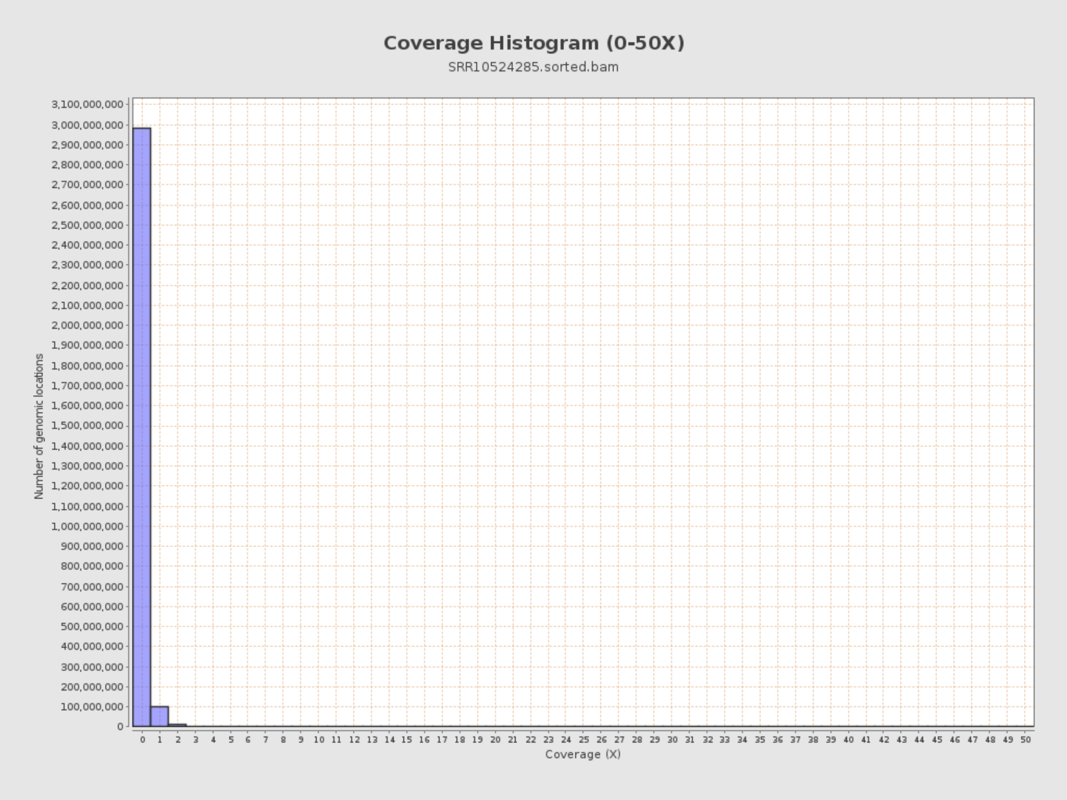
3. Results : Coverage across reference



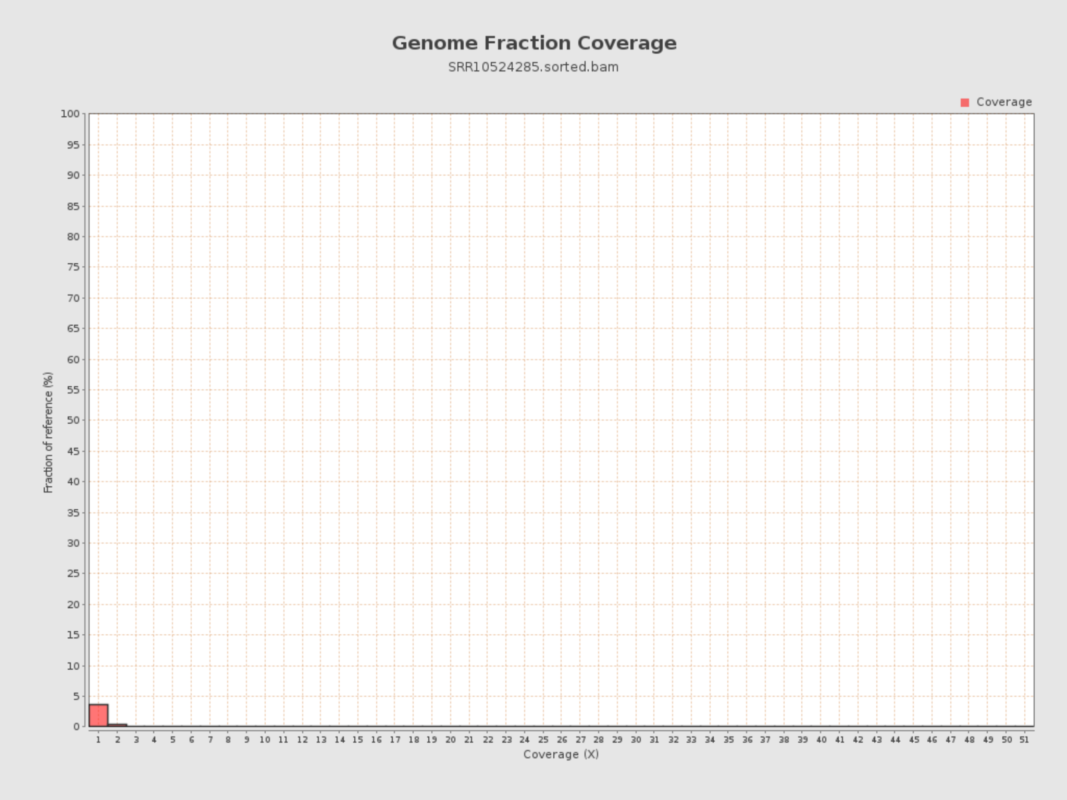
4. Results : Coverage Histogram



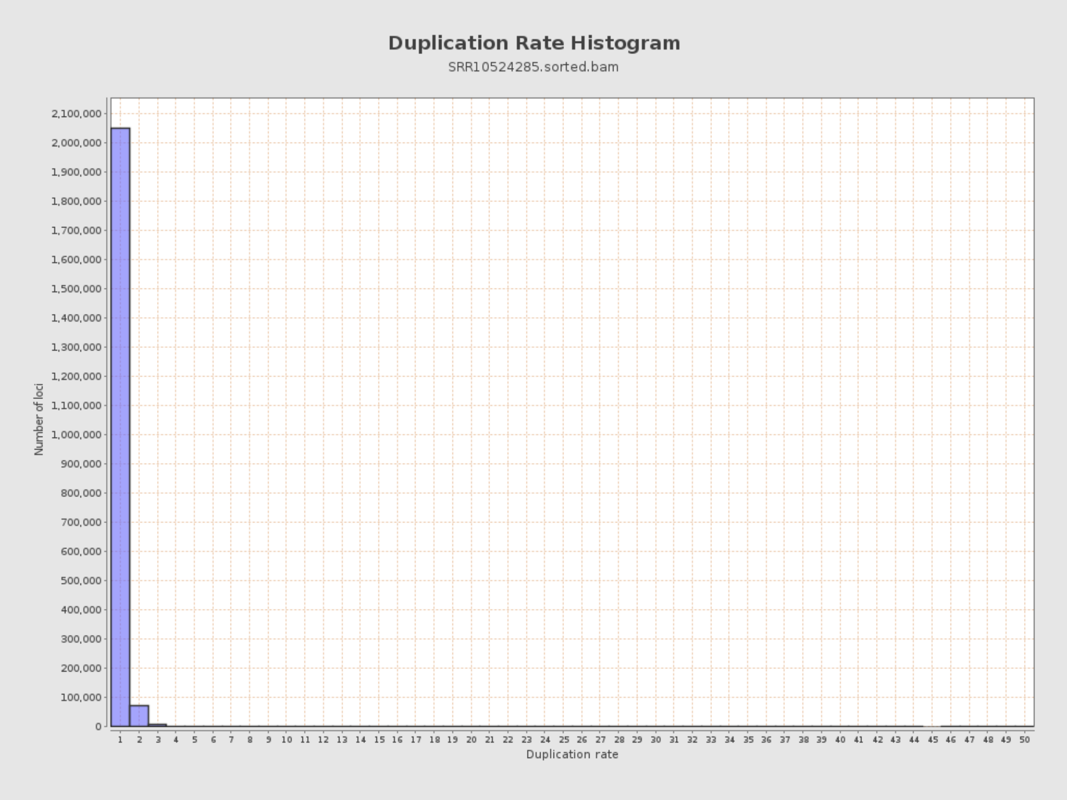
5. Results : Coverage Histogram (0-50X)



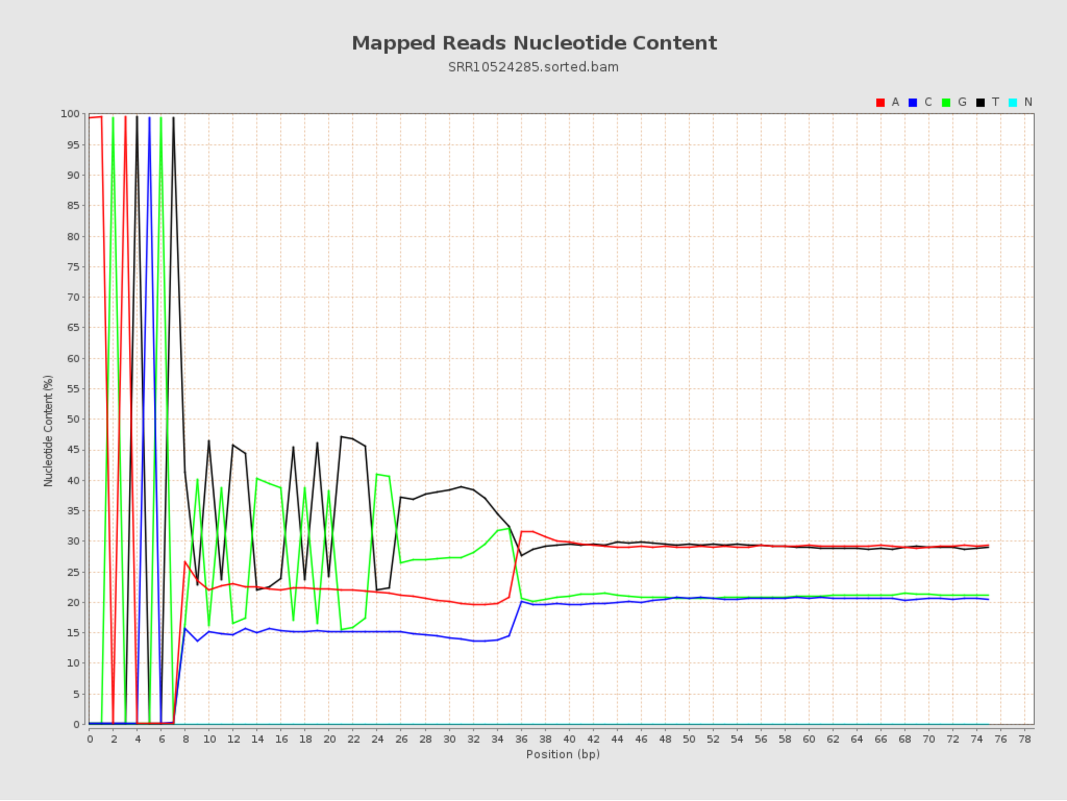
6. Results : Genome Fraction Coverage



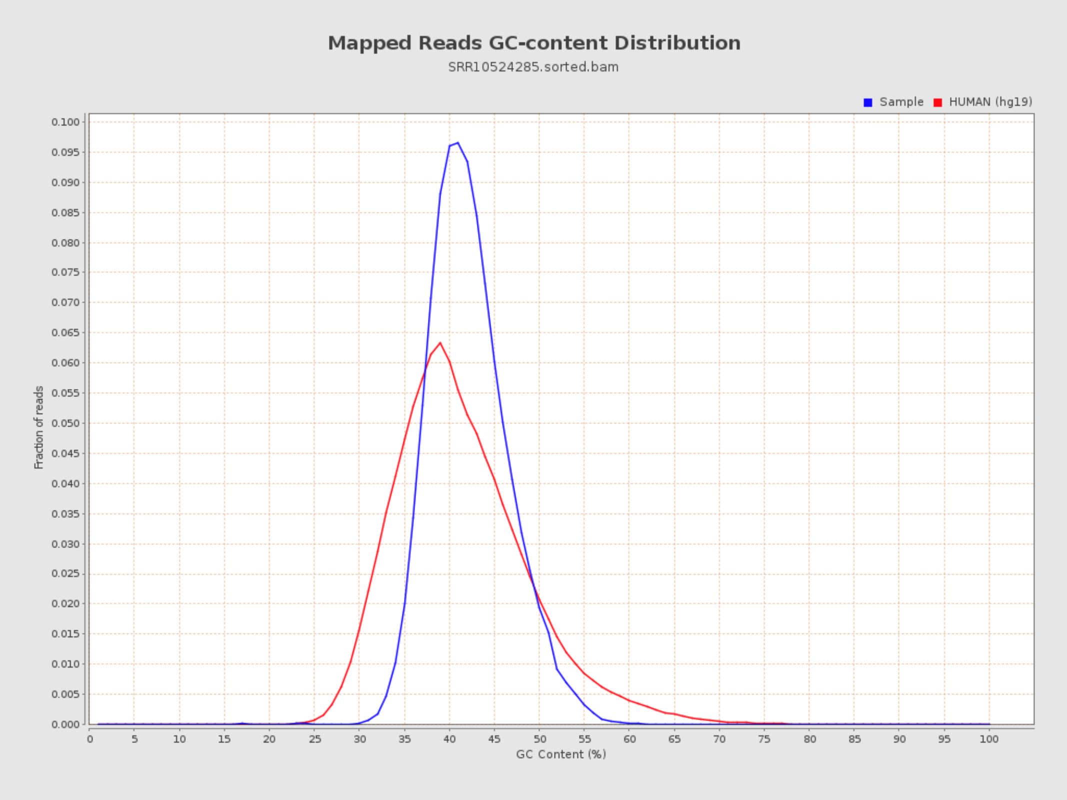
7. Results : Duplication Rate Histogram



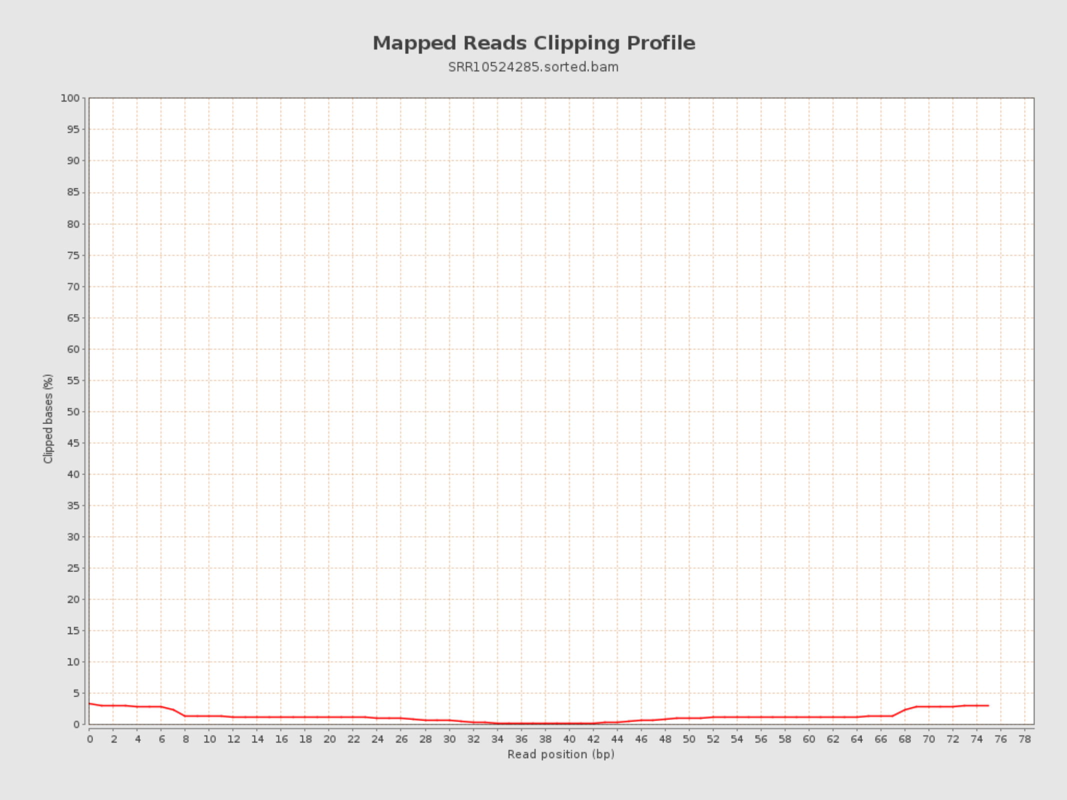
8. Results : Mapped Reads Nucleotide Content



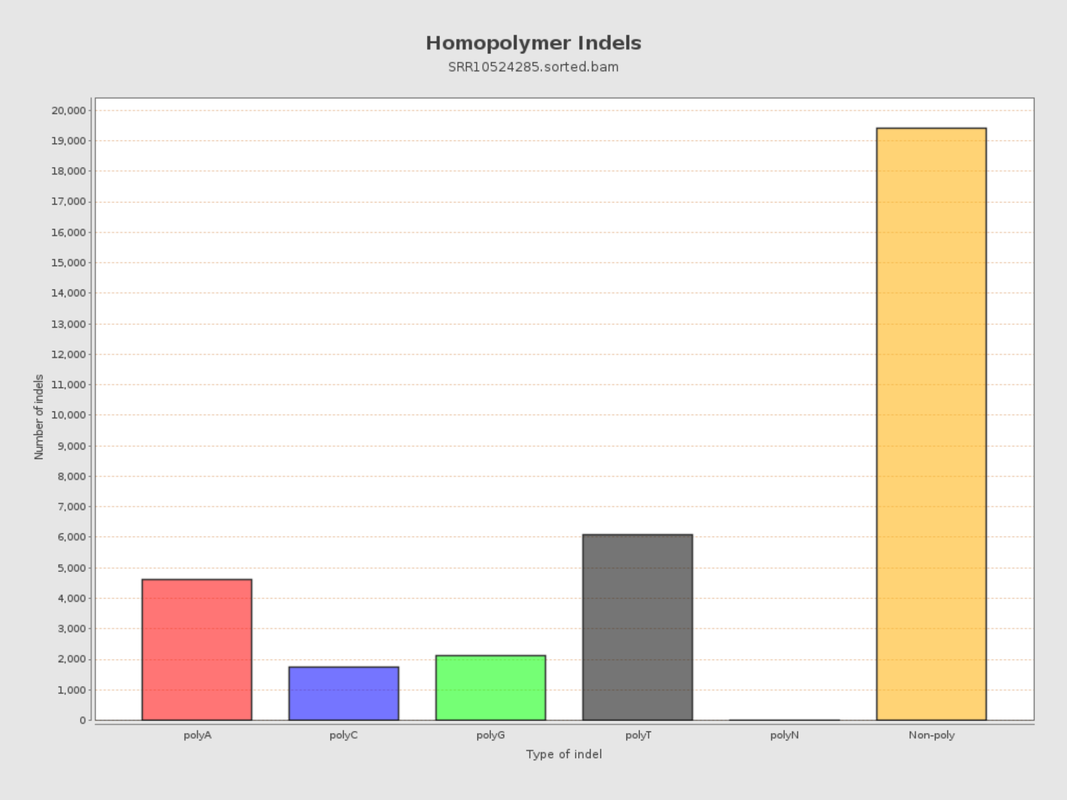
9. Results : Mapped Reads GC-content Distribution



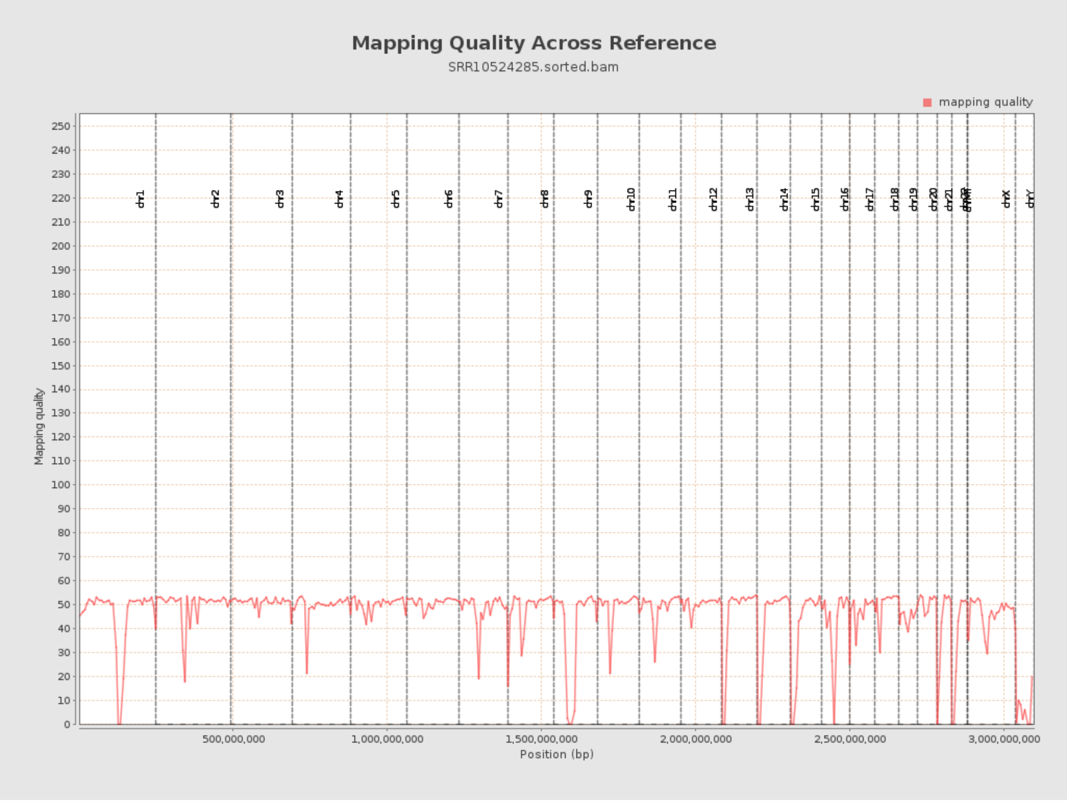
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram