Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:02:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525251.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_SRR10525251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:02:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,223,197
Mapped reads	1,122,319 / 91.75%
Unmapped reads	100,878 / 8.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,417 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	34,997 / 2.86%
Duplication rate	2.31%
Clipped reads	1,124,553 / 91.94%

2.2. ACGT Content

Number/percentage of A's	16,161,951 / 24.82%
Number/percentage of C's	12,431,533 / 19.09%
Number/percentage of T's	20,754,828 / 31.87%
Number/percentage of G's	15,768,738 / 24.22%
Number/percentage of N's	1,381 / 0%
GC Percentage	43.31%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2205

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

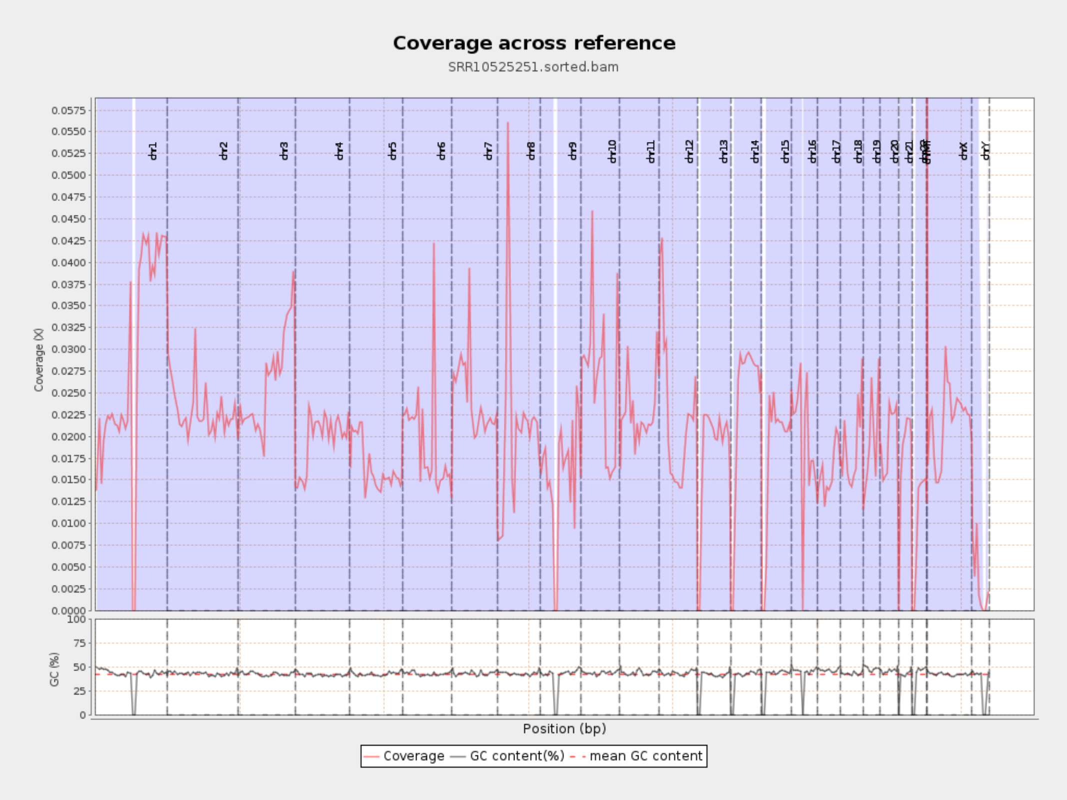
General error rate	0.51%
Mismatches	326,074
Insertions	4,366
Mapped reads with at least one insertion	0.39%
Deletions	13,209
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.66%

2.6. Chromosome stats

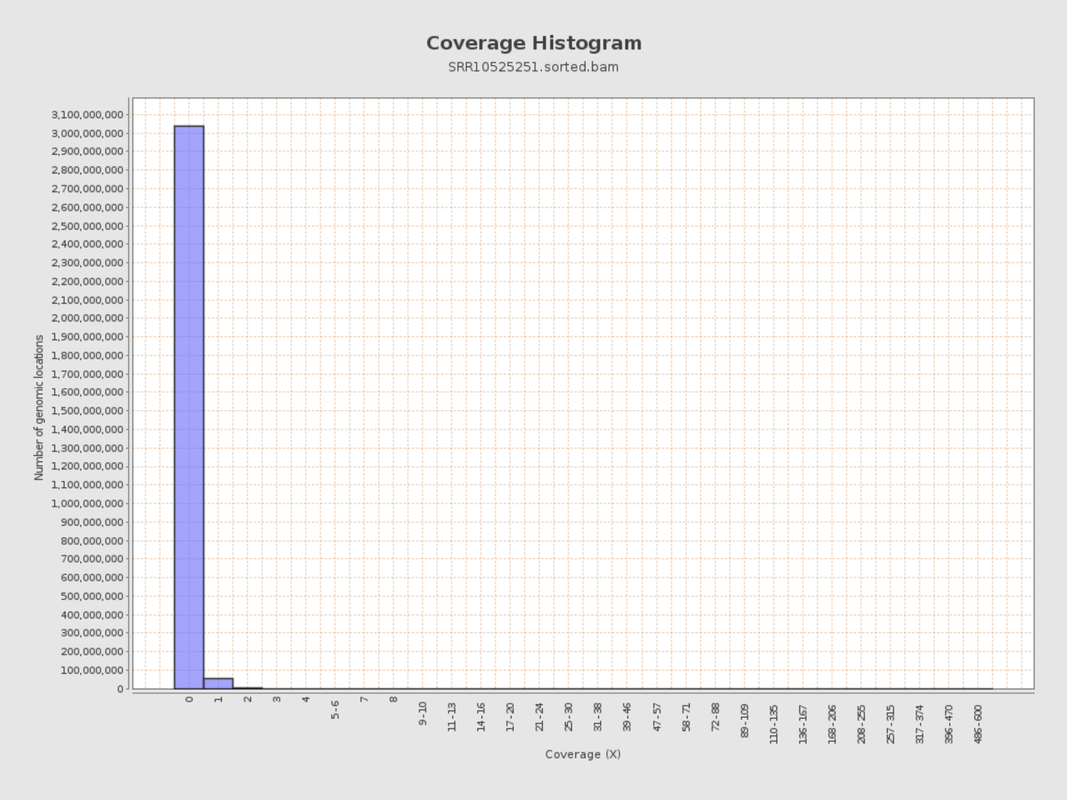
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7101161	0.0285	0.3979
chr2	243199373	5571433	0.0229	0.2906
chr3	198022430	5180339	0.0262	0.1726
chr4	191154276	3770914	0.0197	0.1559
chr5	180915260	2996519	0.0166	0.1373
chr6	171115067	3341916	0.0195	0.164
chr7	159138663	3910653	0.0246	0.3001

chr8	146364022	3103652	0.0212	0.2207
chr9	141213431	2184445	0.0155	0.1628
chr10	135534747	3605893	0.0266	0.2365
chr11	135006516	3049755	0.0226	0.1879
chr12	133851895	3016172	0.0225	0.1607
chr13	115169878	2086032	0.0181	0.1444
chr14	107349540	2520336	0.0235	0.1662
chr15	102531392	1809744	0.0177	0.1434
chr16	90354753	1760785	0.0195	0.1603
chr17	81195210	1311095	0.0161	0.14
chr18	78077248	1437297	0.0184	0.3024
chr19	59128983	1159235	0.0196	0.268
chr20	63025520	1237209	0.0196	0.1504
chr21	48129895	863587	0.0179	0.153
chr22	51304566	526444	0.0103	0.1075
chrMT	16571	1371	0.0827	0.3052
chrX	155270560	3405463	0.0219	0.1688
chrY	59373566	188385	0.0032	0.0932

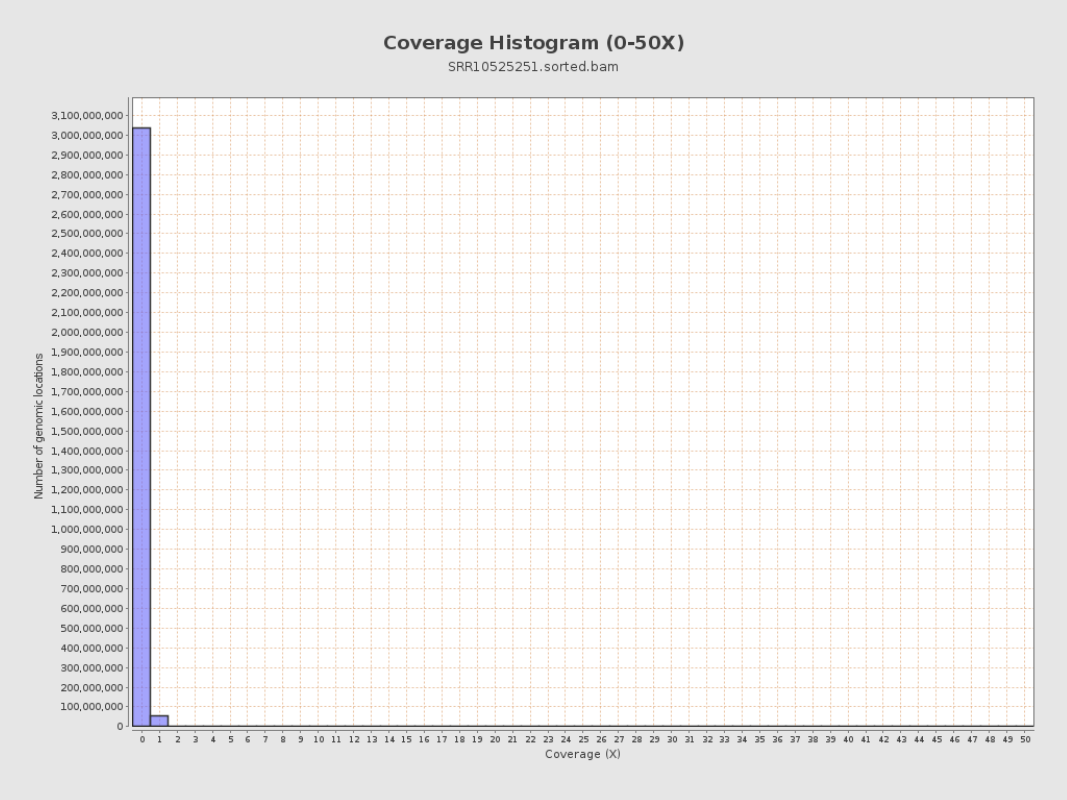
3. Results : Coverage across reference



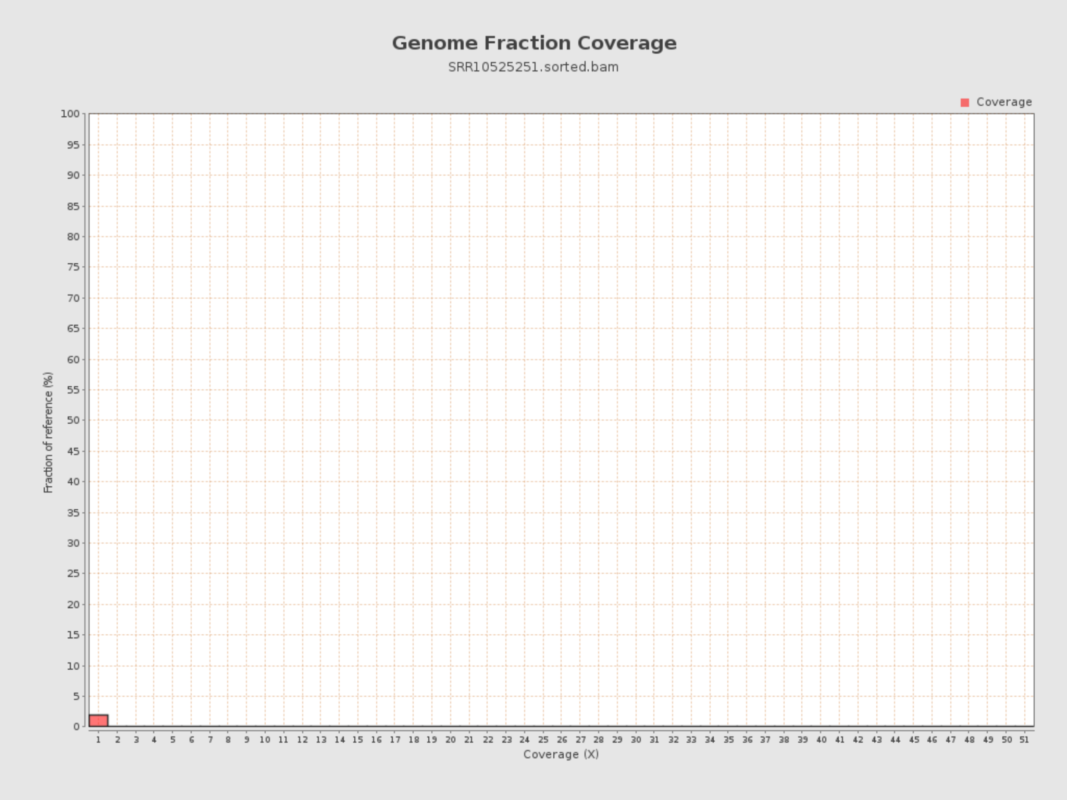
4. Results : Coverage Histogram



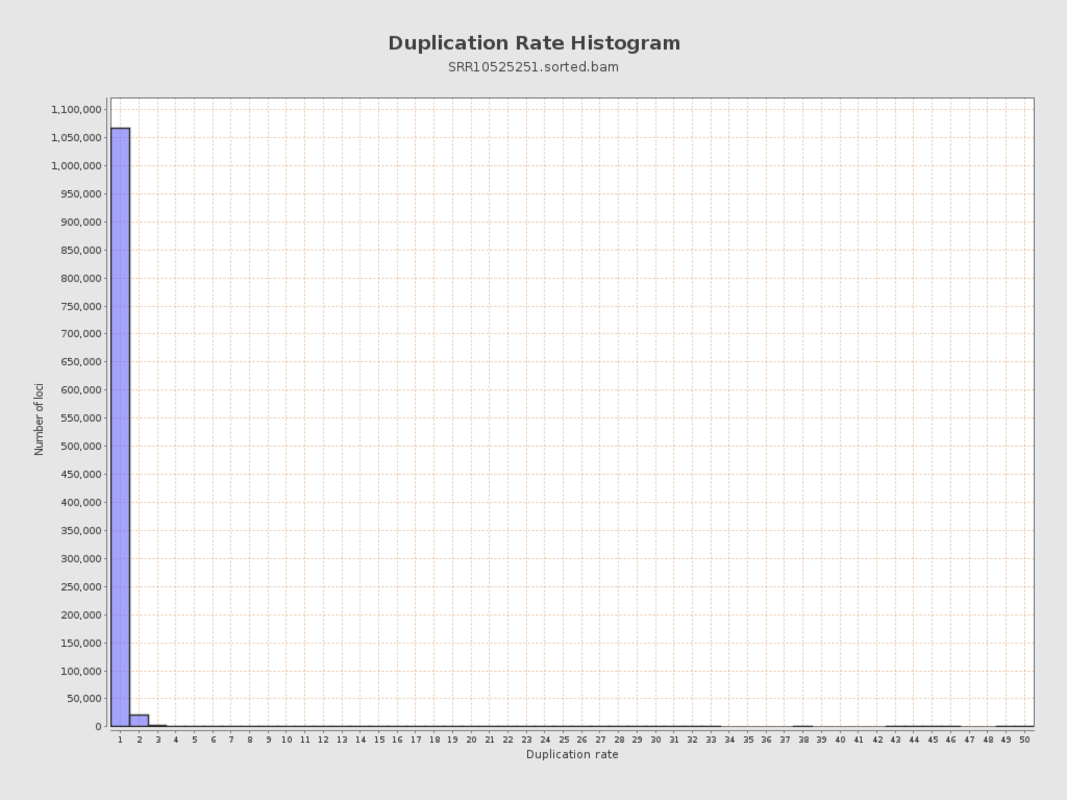
5. Results : Coverage Histogram (0-50X)



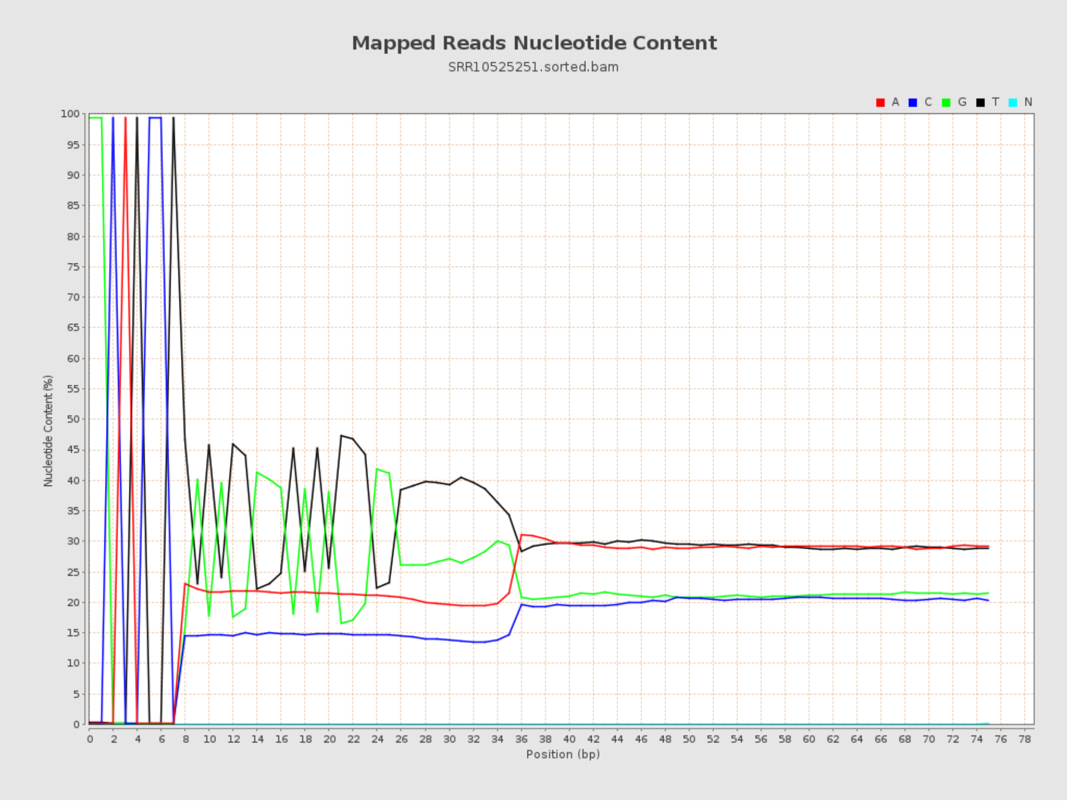
6. Results : Genome Fraction Coverage



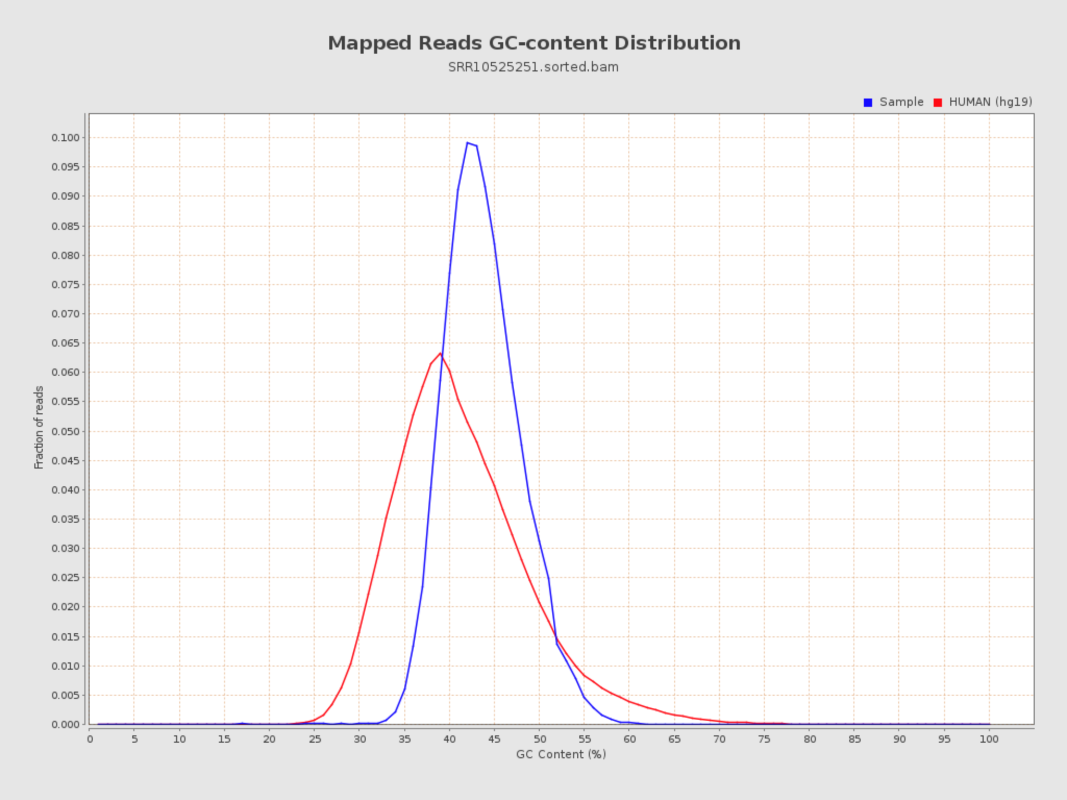
7. Results : Duplication Rate Histogram



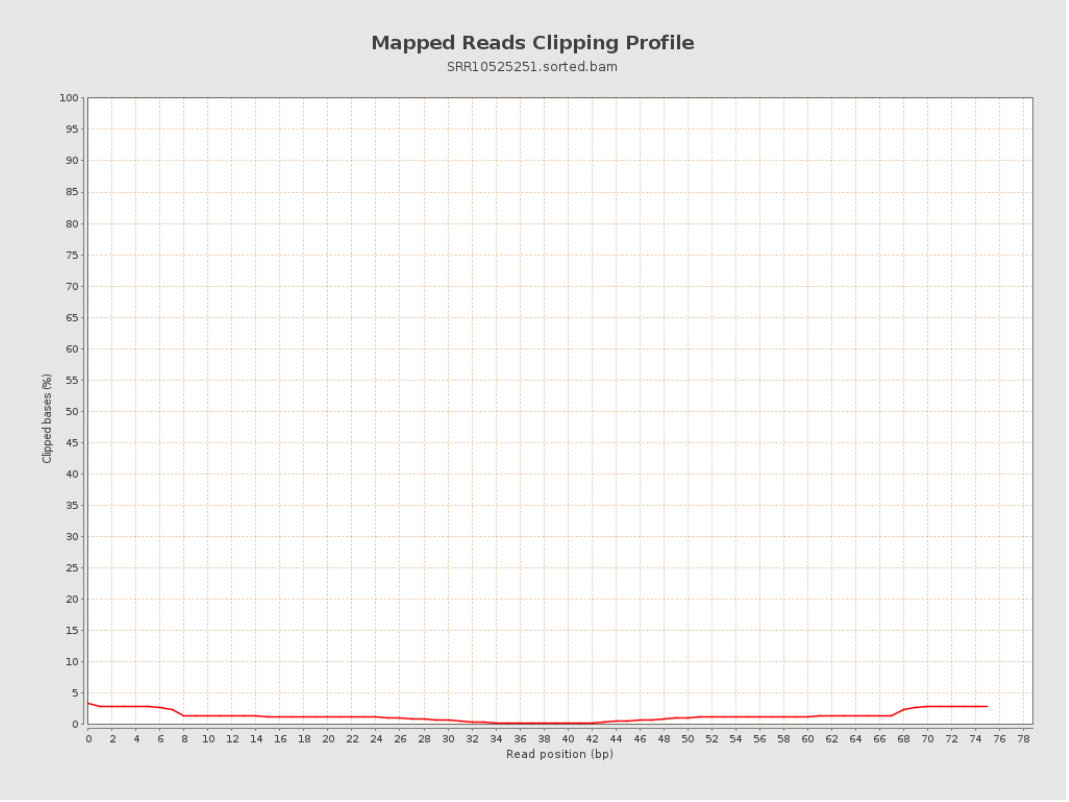
8. Results : Mapped Reads Nucleotide Content



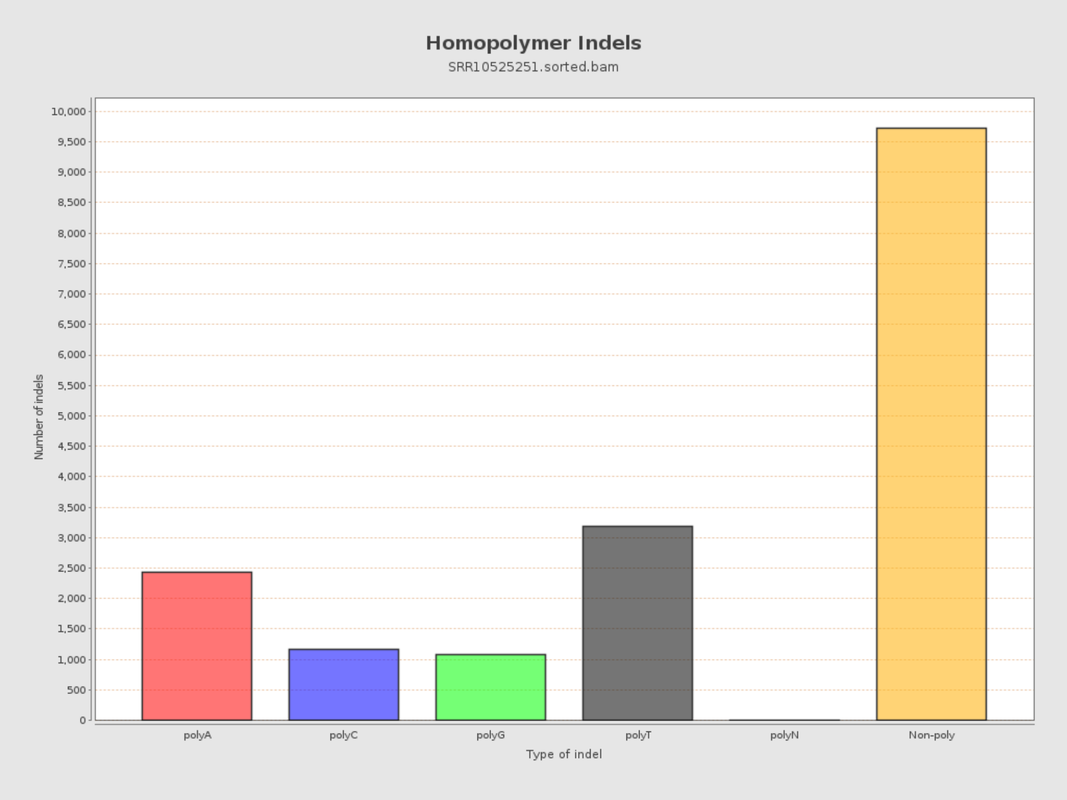
9. Results : Mapped Reads GC-content Distribution



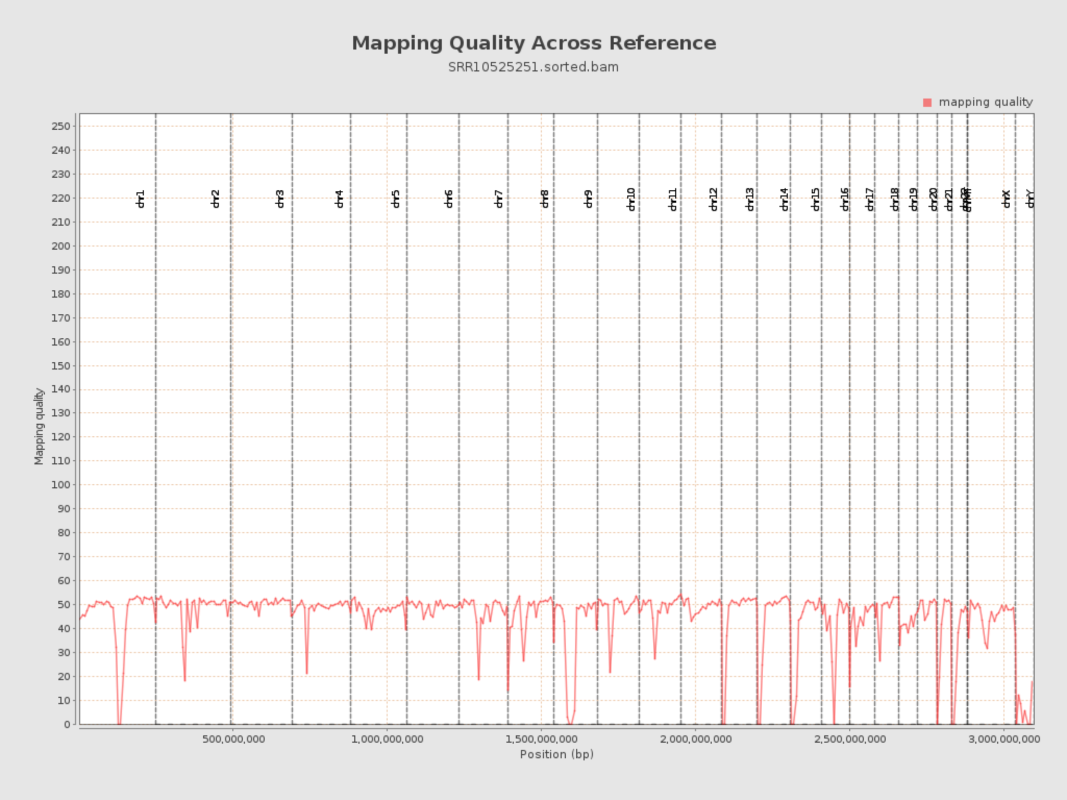
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram