Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:15:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716756.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_SRR9716756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:15:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	711,497
Mapped reads	631,903 / 88.81%
Unmapped reads	79,594 / 11.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,494 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	15,200 / 2.14%
Duplication rate	1.85%
Clipped reads	632,322 / 88.87%

2.2. ACGT Content

Number/percentage of A's	9,022,943 / 24.77%
Number/percentage of C's	7,066,973 / 19.4%
Number/percentage of T's	12,048,308 / 33.07%
Number/percentage of G's	8,294,768 / 22.77%
Number/percentage of N's	1,121 / 0%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.138

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

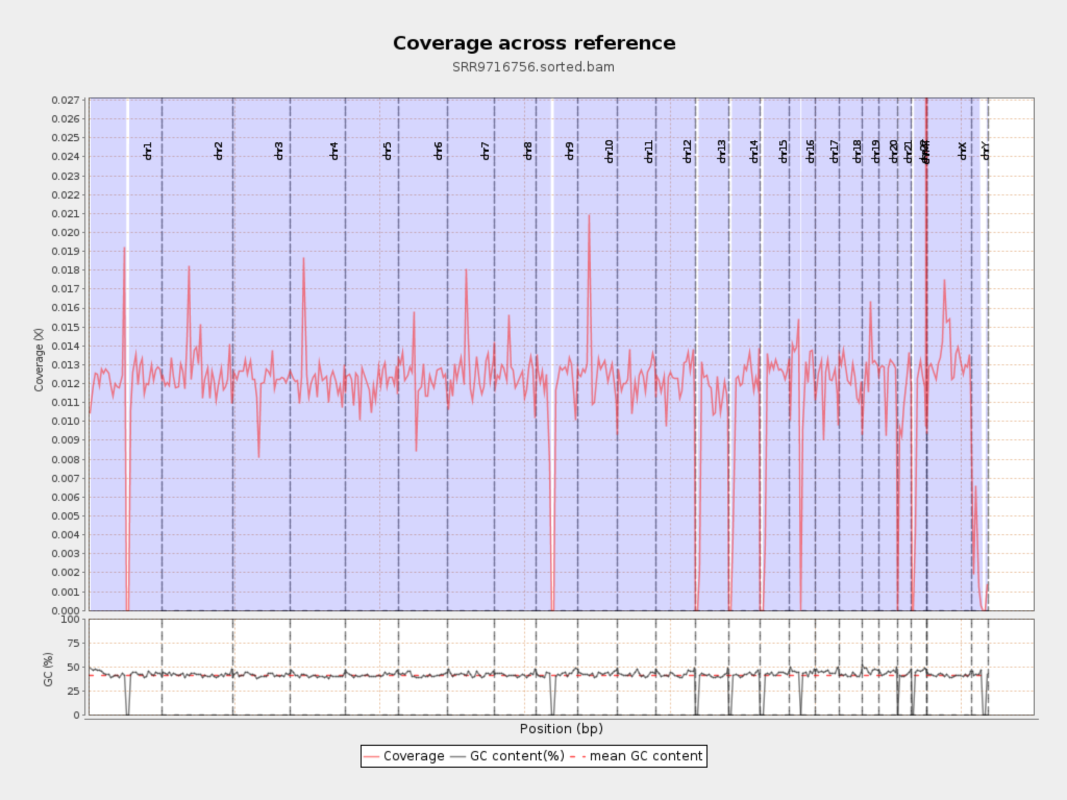
General error rate	0.53%
Mismatches	187,772
Insertions	2,537
Mapped reads with at least one insertion	0.4%
Deletions	6,996
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.24%

2.6. Chromosome stats

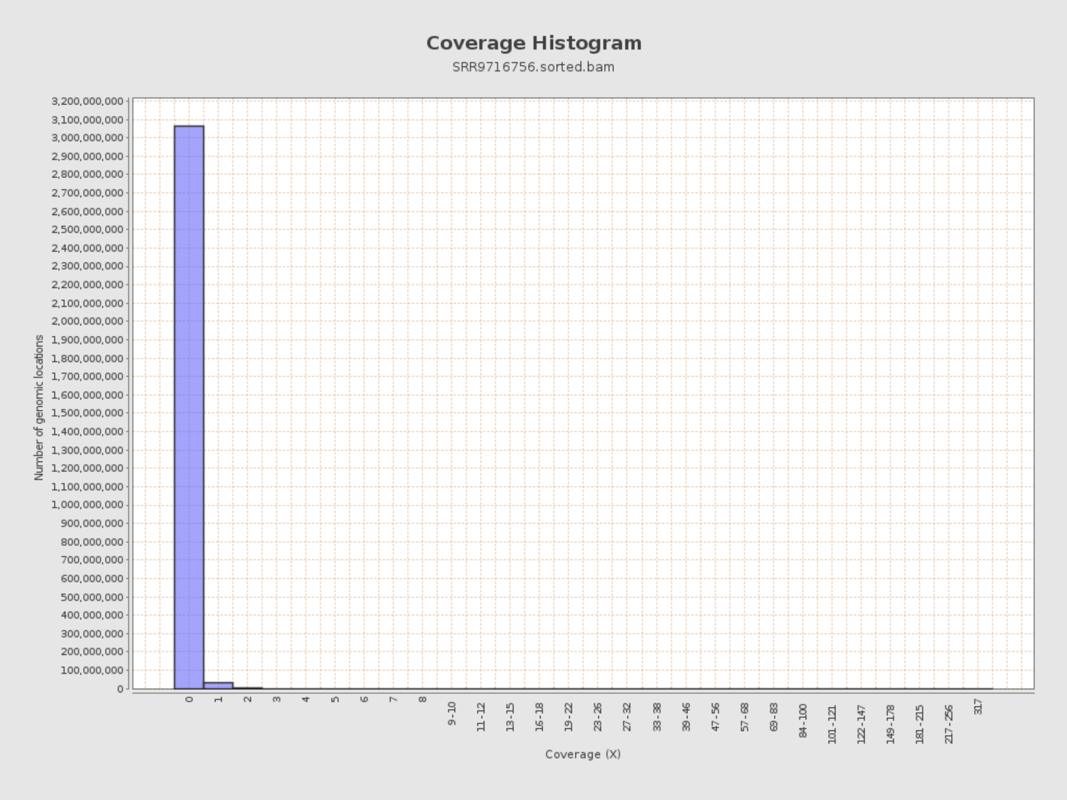
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2918668	0.0117	0.2118
chr2	243199373	3080521	0.0127	0.1762
chr3	198022430	2426392	0.0123	0.1162
chr4	191154276	2355142	0.0123	0.12
chr5	180915260	2179578	0.012	0.1147
chr6	171115067	2117041	0.0124	0.1276
chr7	159138663	2020771	0.0127	0.1501

chr8	146364022	1826836	0.0125	0.1342
chr9	141213431	1514431	0.0107	0.1223
chr10	135534747	1748592	0.0129	0.1359
chr11	135006516	1655956	0.0123	0.1262
chr12	133851895	1645093	0.0123	0.1168
chr13	115169878	1122434	0.0097	0.1038
chr14	107349540	1098831	0.0102	0.1071
chr15	102531392	1060641	0.0103	0.1066
chr16	90354753	1071818	0.0119	0.1165
chr17	81195210	972568	0.012	0.1164
chr18	78077248	969631	0.0124	0.1773
chr19	59128983	765753	0.013	0.1705
chr20	63025520	779641	0.0124	0.1174
chr21	48129895	490153	0.0102	0.1114
chr22	51304566	435746	0.0085	0.0964
chrMT	16571	2856	0.1723	0.4157
chrX	155270560	2072255	0.0133	0.1268
chrY	59373566	113715	0.0019	0.0611

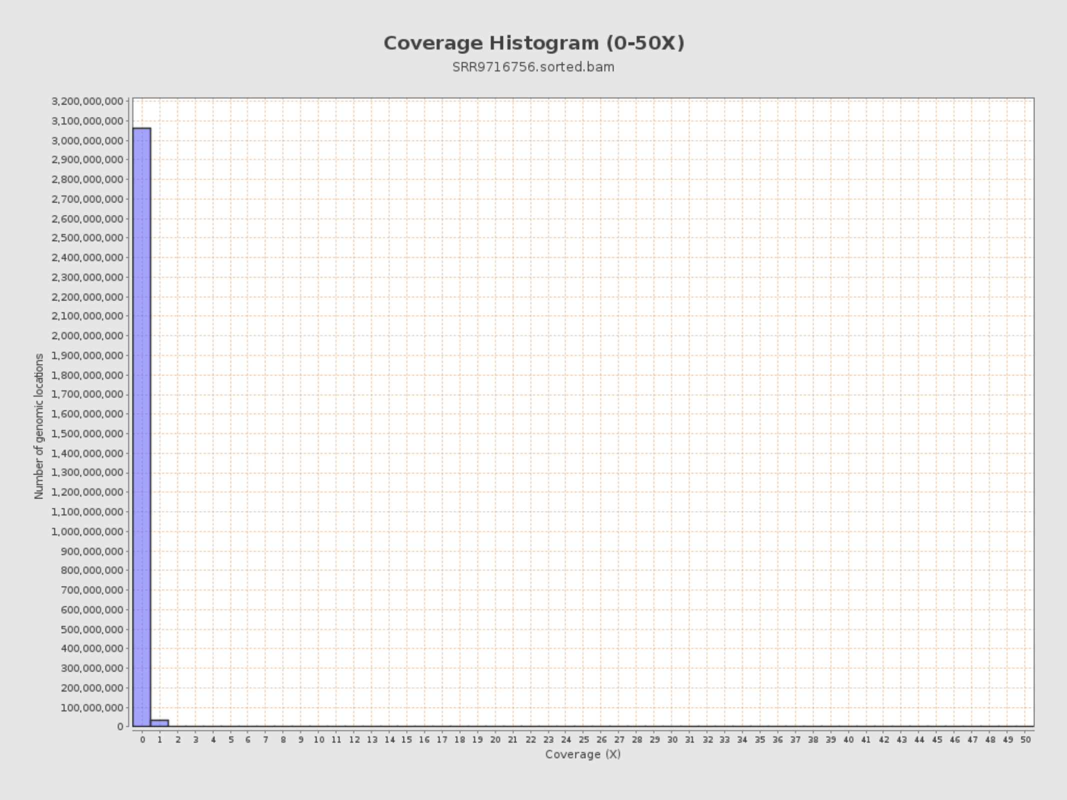
3. Results : Coverage across reference



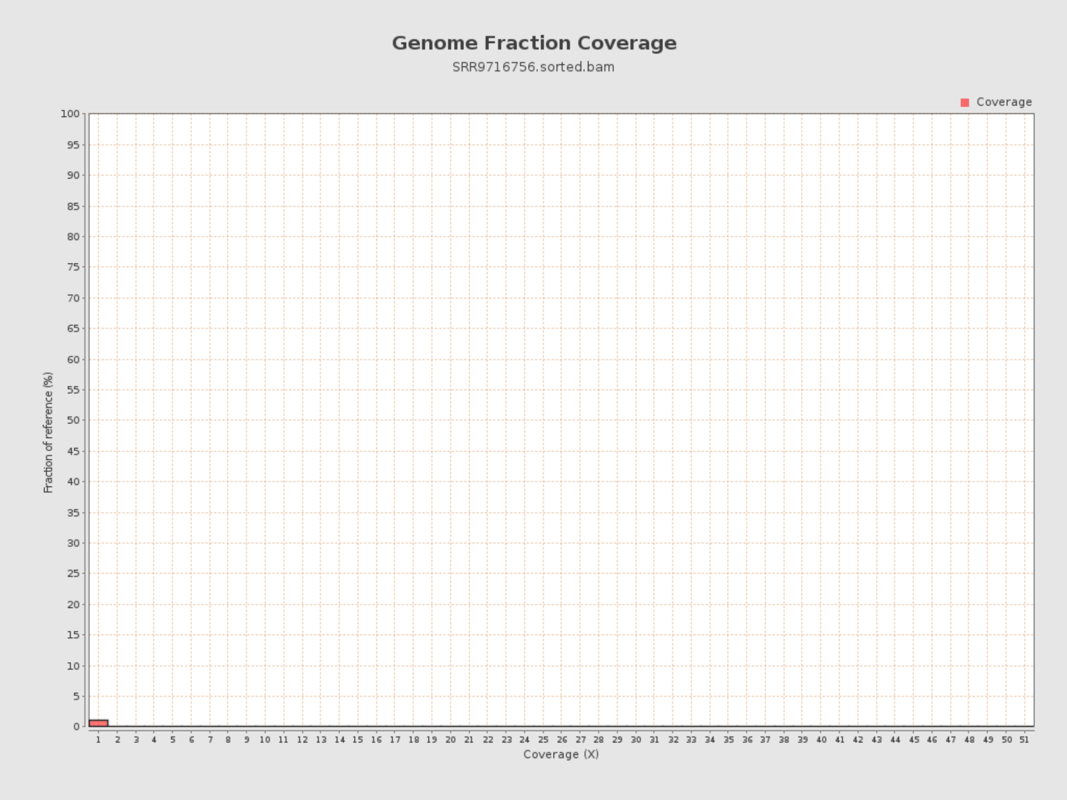
4. Results : Coverage Histogram



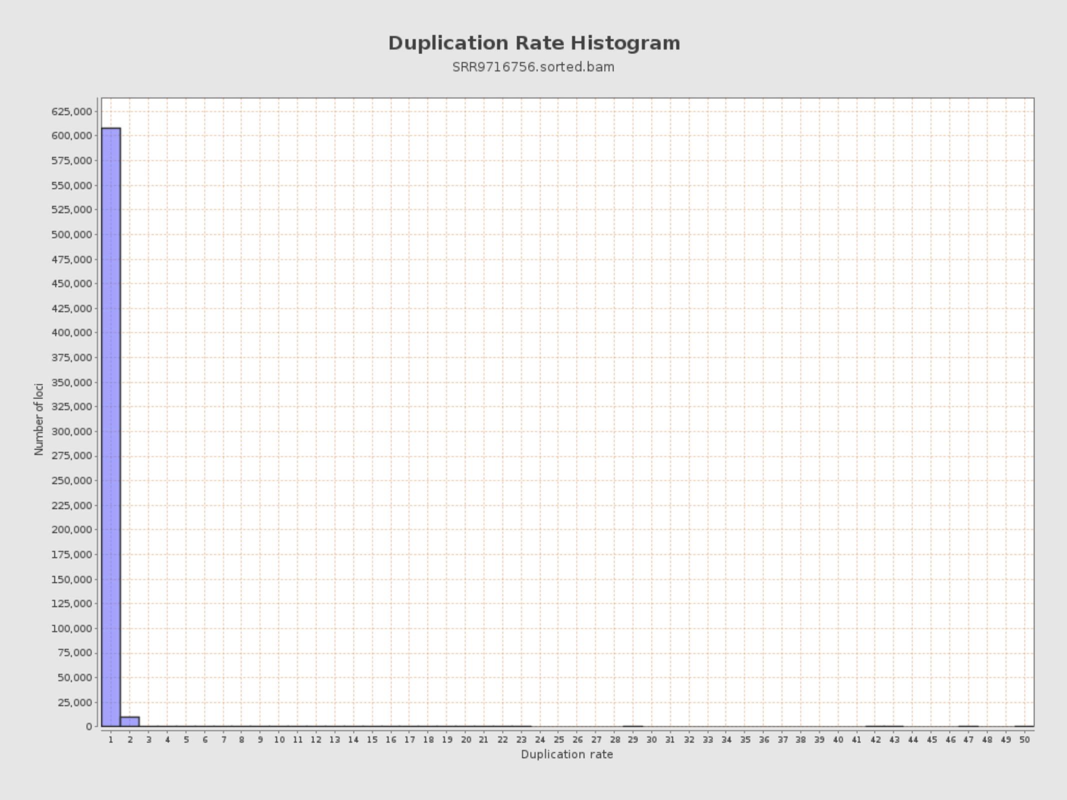
5. Results : Coverage Histogram (0-50X)



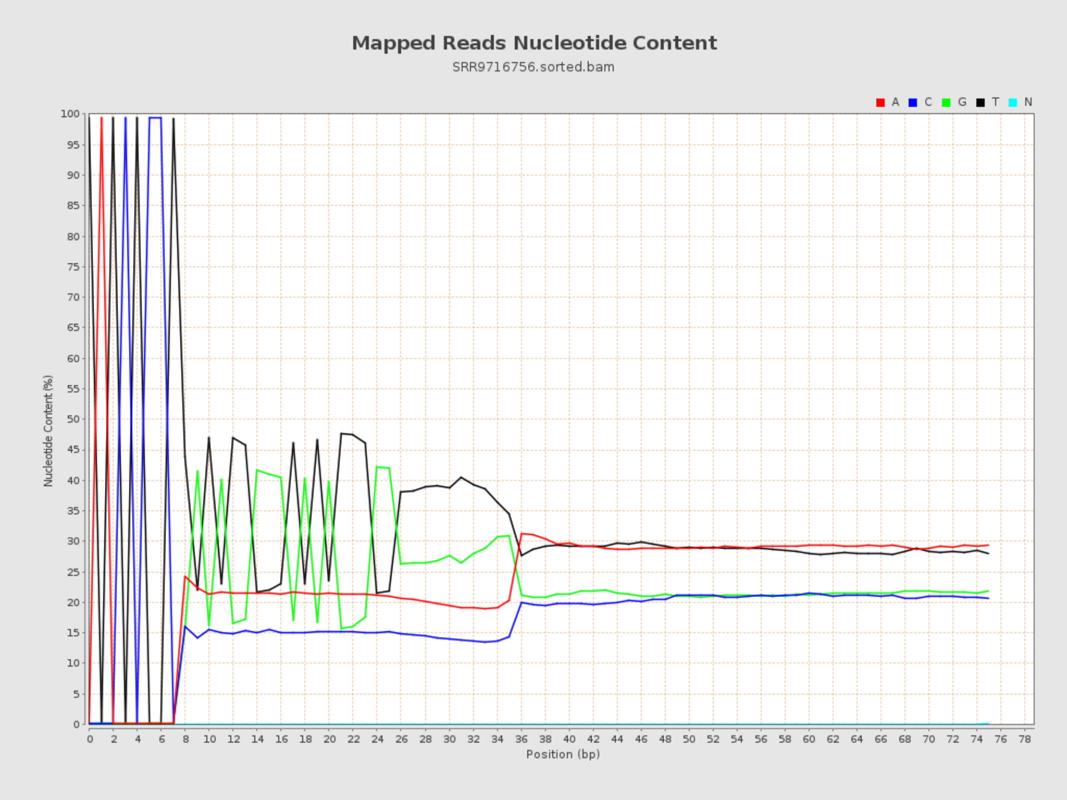
6. Results : Genome Fraction Coverage



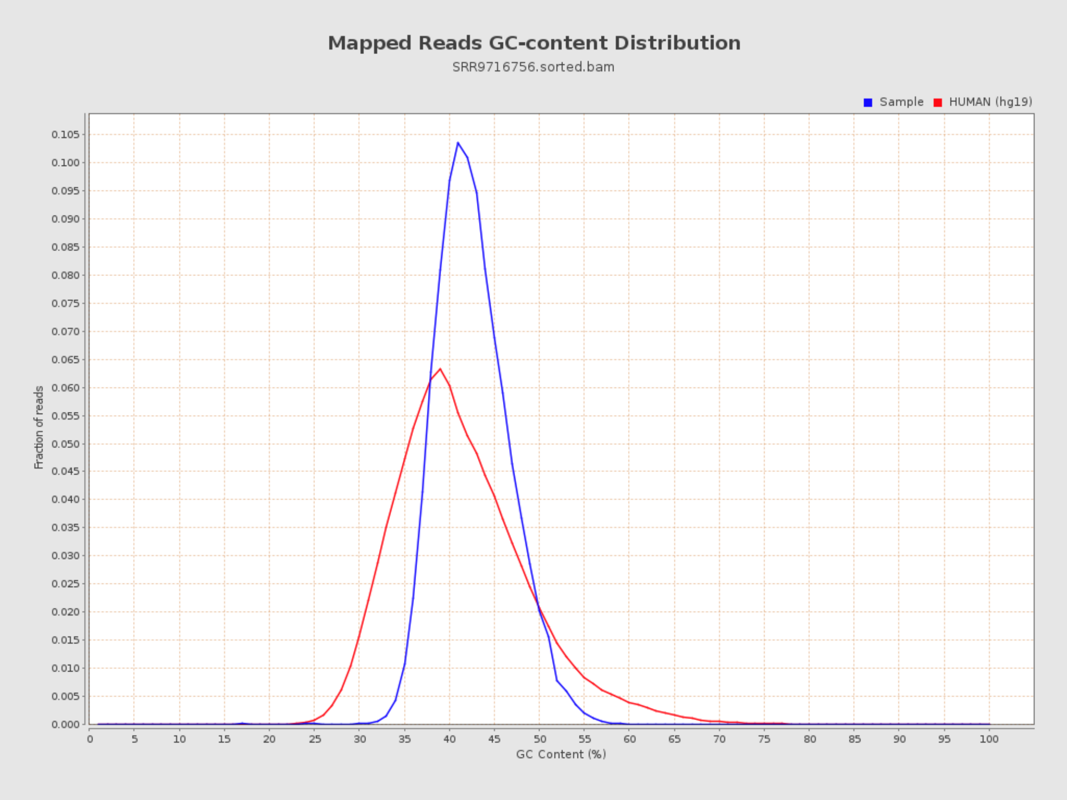
7. Results : Duplication Rate Histogram



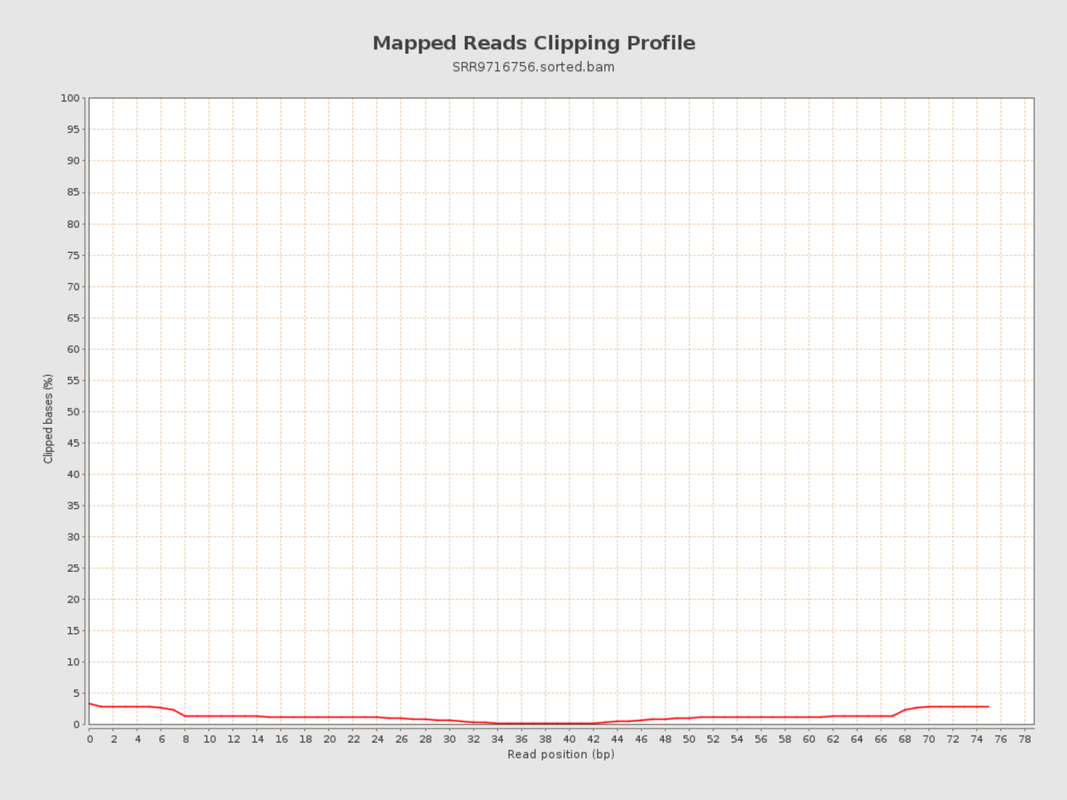
8. Results : Mapped Reads Nucleotide Content



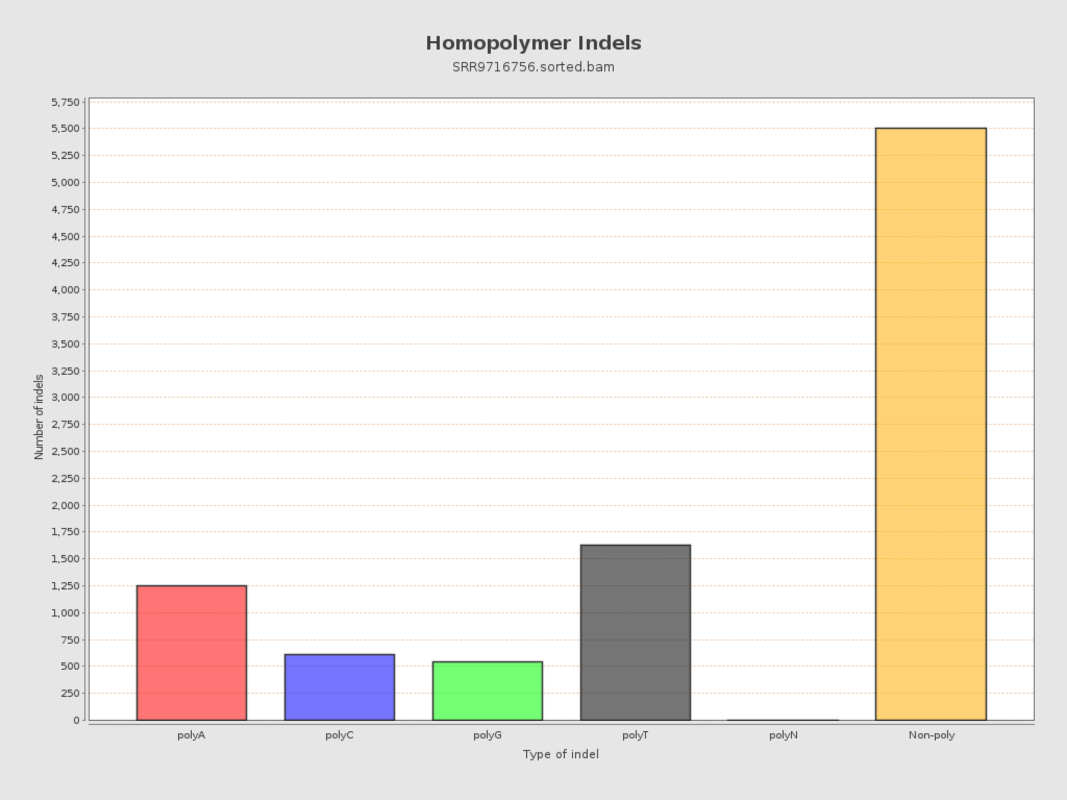
9. Results : Mapped Reads GC-content Distribution



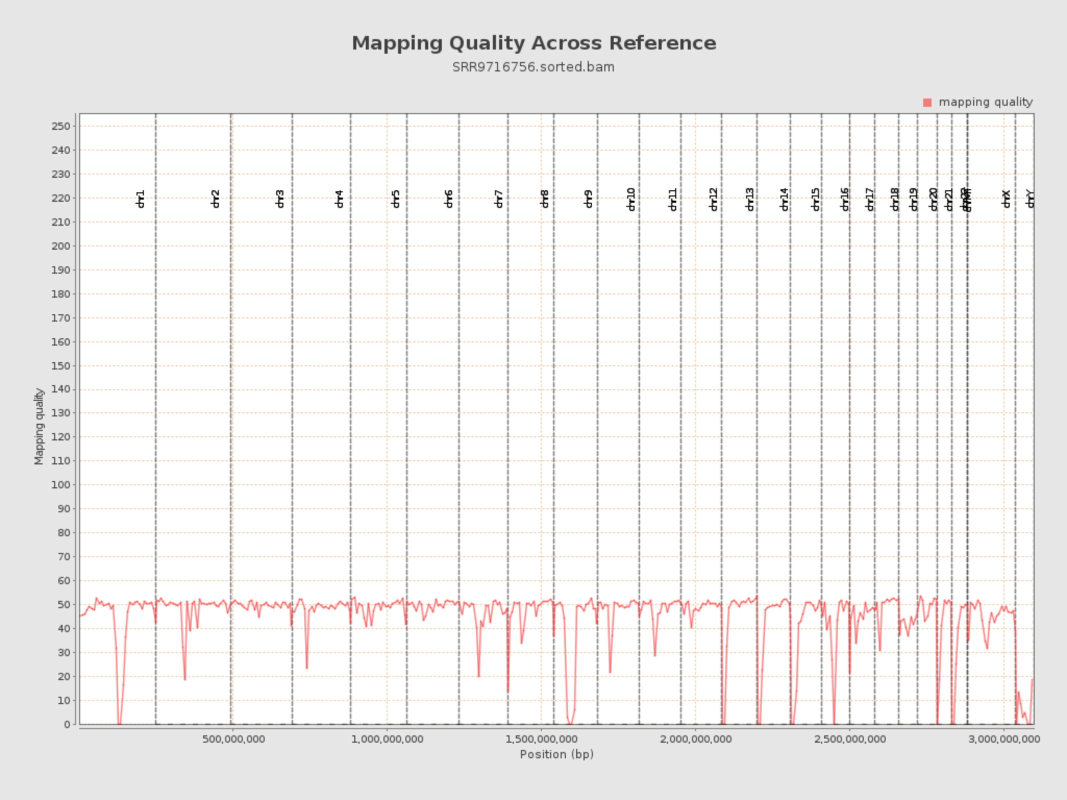
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram