Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716757.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_SRR9716757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716757.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:17:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	465,375
Mapped reads	419,157 / 90.07%
Unmapped reads	46,218 / 9.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,196 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	7,523 / 1.62%
Duplication rate	1.39%
Clipped reads	420,234 / 90.3%

2.2. ACGT Content

Number/percentage of A's	6,241,406 / 25.7%
Number/percentage of C's	4,550,348 / 18.74%
Number/percentage of T's	7,797,807 / 32.11%
Number/percentage of G's	5,692,849 / 23.44%
Number/percentage of N's	684 / 0%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0078

Standard Deviation	0.1057

2.4. Mapping Quality

Mean Mapping Quality	45.33

2.5. Mismatches and indels

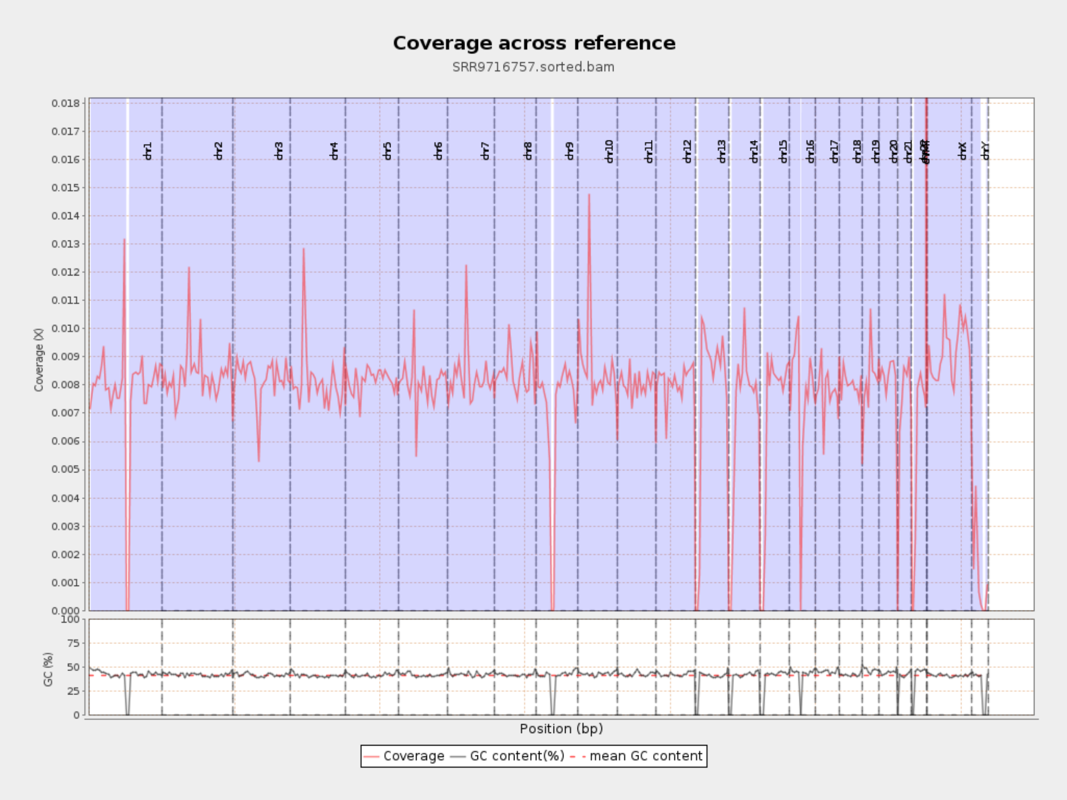
General error rate	0.52%
Mismatches	124,137
Insertions	1,642
Mapped reads with at least one insertion	0.39%
Deletions	4,620
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.01%

2.6. Chromosome stats

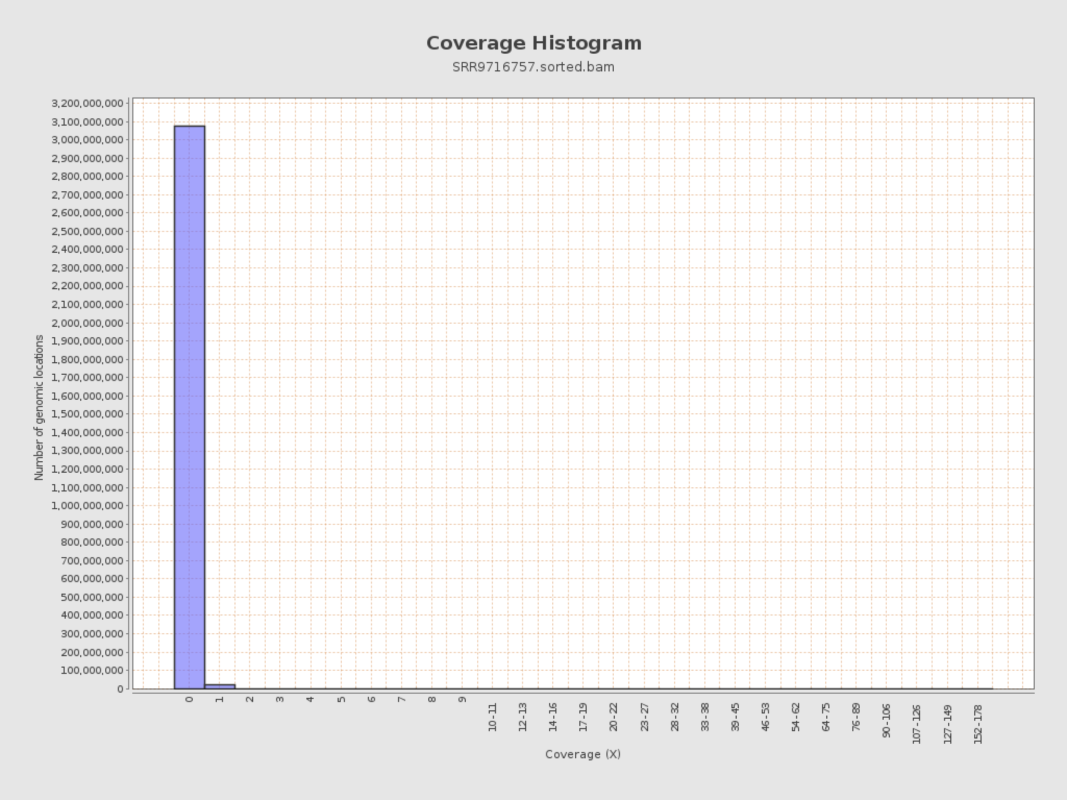
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1930568	0.0077	0.1549
chr2	243199373	2043602	0.0084	0.1223
chr3	198022430	1621978	0.0082	0.0933
chr4	191154276	1556838	0.0081	0.0952
chr5	180915260	1479177	0.0082	0.0931
chr6	171115067	1384173	0.0081	0.0977
chr7	159138663	1328417	0.0083	0.1169

chr8	146364022	1231014	0.0084	0.1034
chr9	141213431	980312	0.0069	0.0928
chr10	135534747	1178624	0.0087	0.1086
chr11	135006516	1081881	0.008	0.0994
chr12	133851895	1085207	0.0081	0.0931
chr13	115169878	861846	0.0075	0.0895
chr14	107349540	732889	0.0068	0.0865
chr15	102531392	696692	0.0068	0.0851
chr16	90354753	692802	0.0077	0.0925
chr17	81195210	625990	0.0077	0.0918
chr18	78077248	629632	0.0081	0.1355
chr19	59128983	487783	0.0082	0.1196
chr20	63025520	520399	0.0083	0.0946
chr21	48129895	341738	0.0071	0.0898
chr22	51304566	280914	0.0055	0.0761
chrMT	16571	13269	0.8007	0.9814
chrX	155270560	1426458	0.0092	0.1024
chrY	59373566	78218	0.0013	0.0491

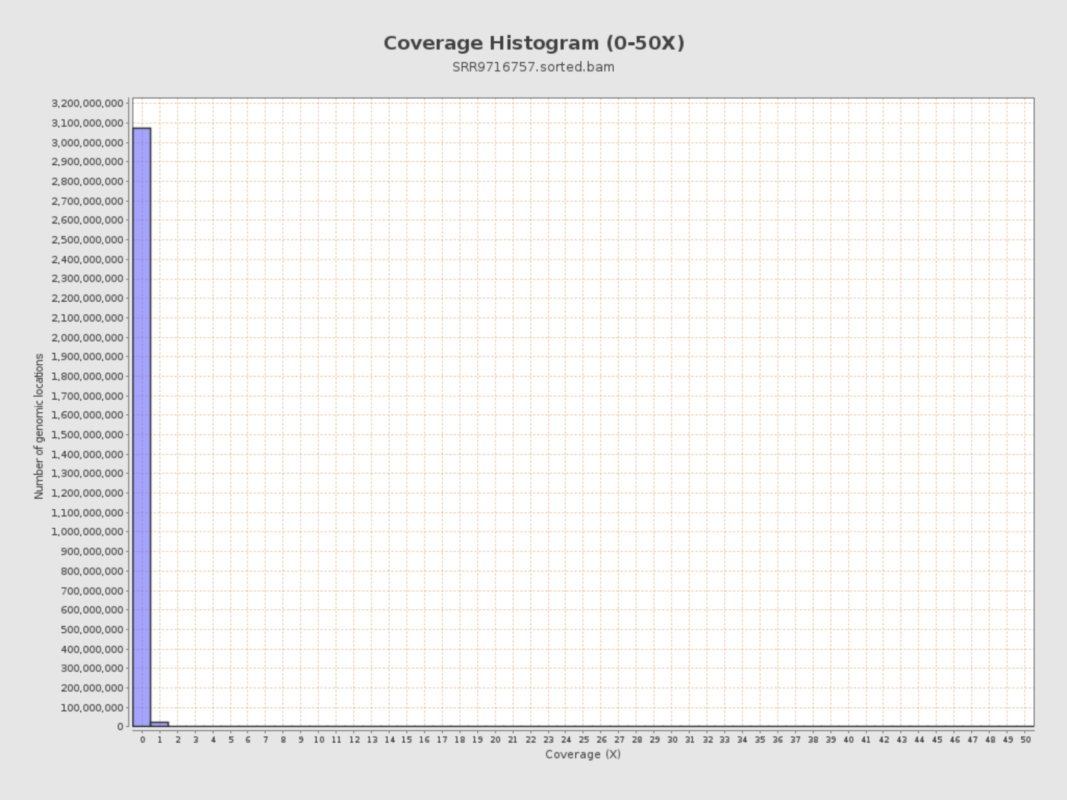
3. Results : Coverage across reference



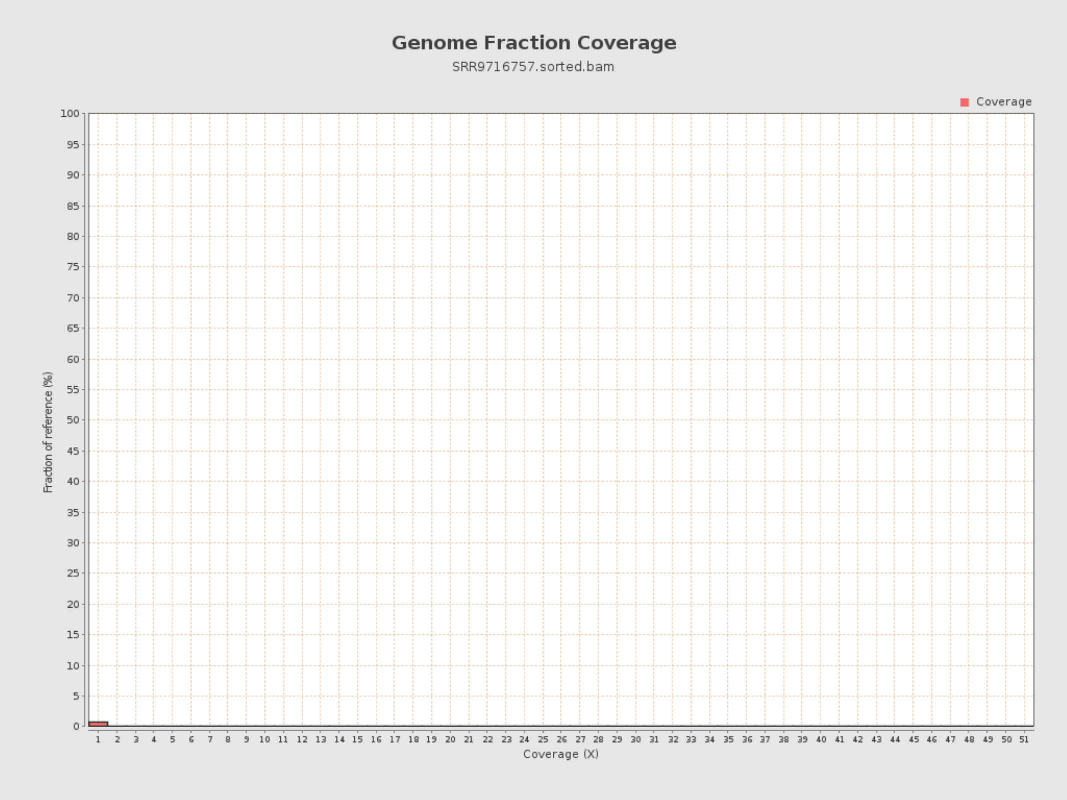
4. Results : Coverage Histogram



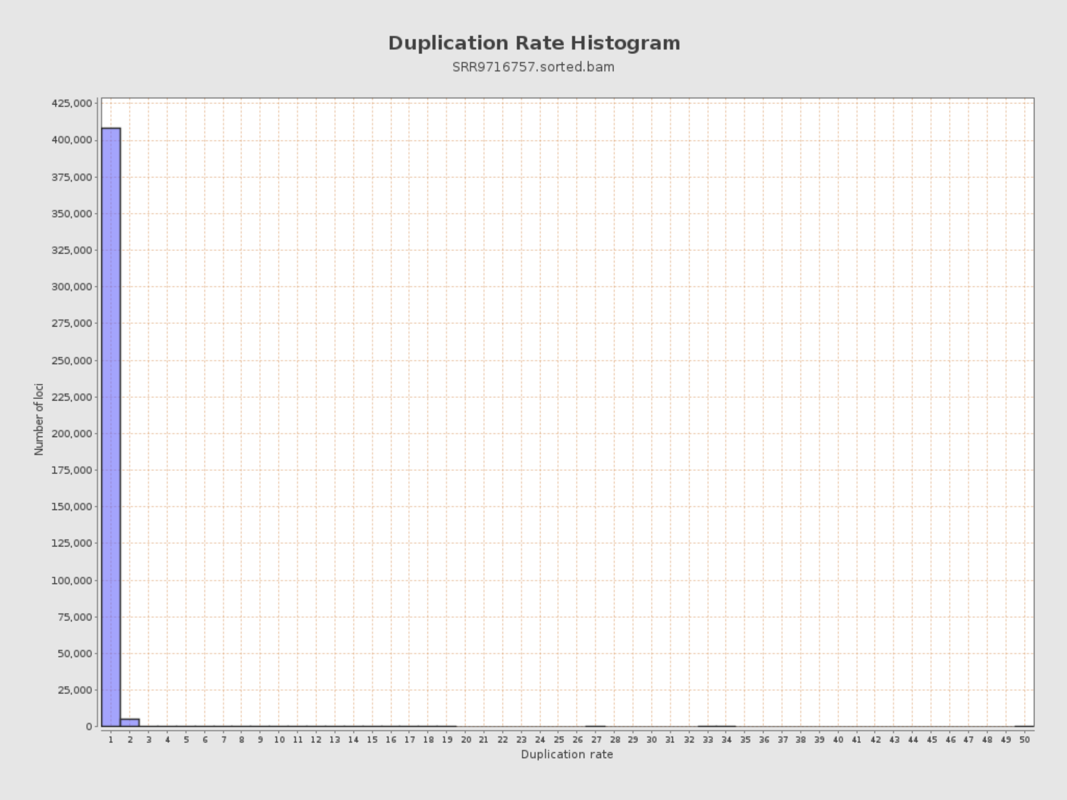
5. Results : Coverage Histogram (0-50X)



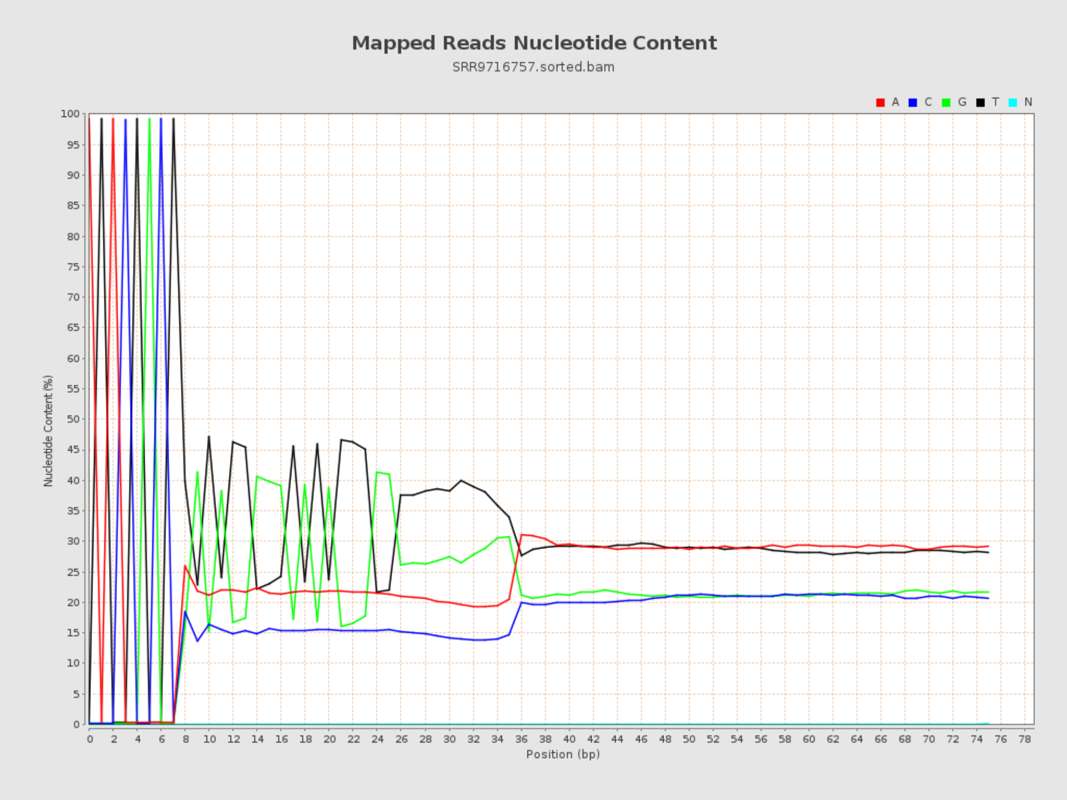
6. Results : Genome Fraction Coverage



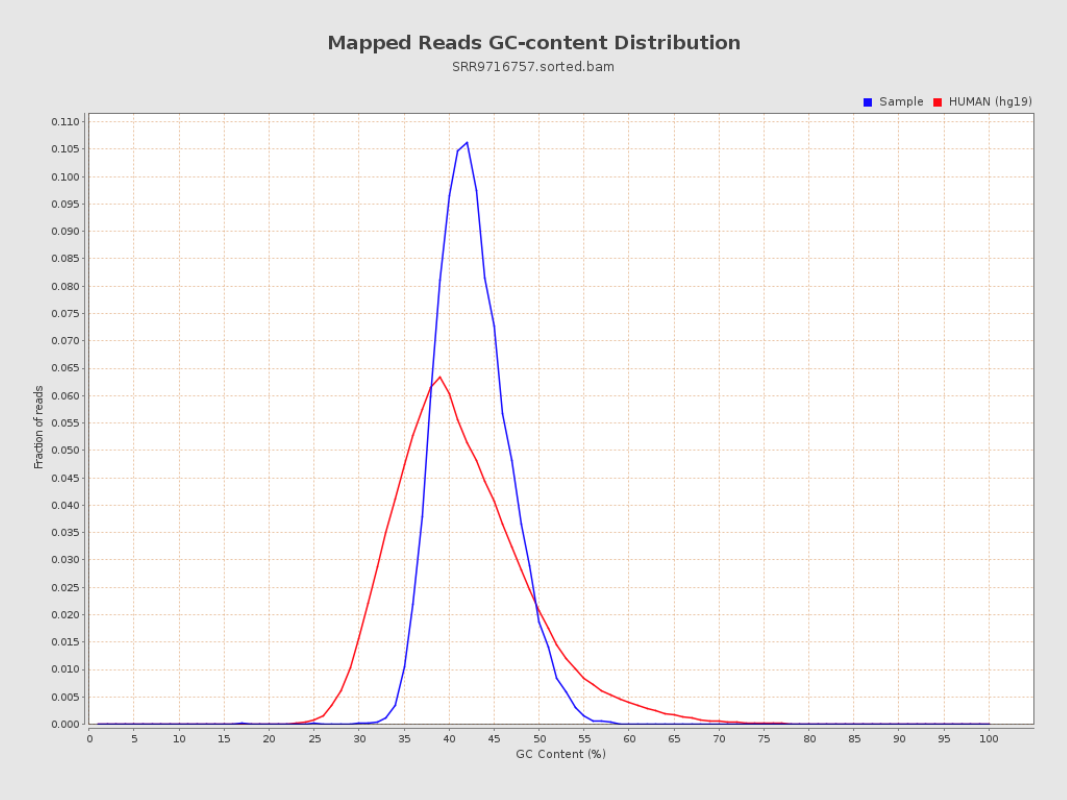
7. Results : Duplication Rate Histogram



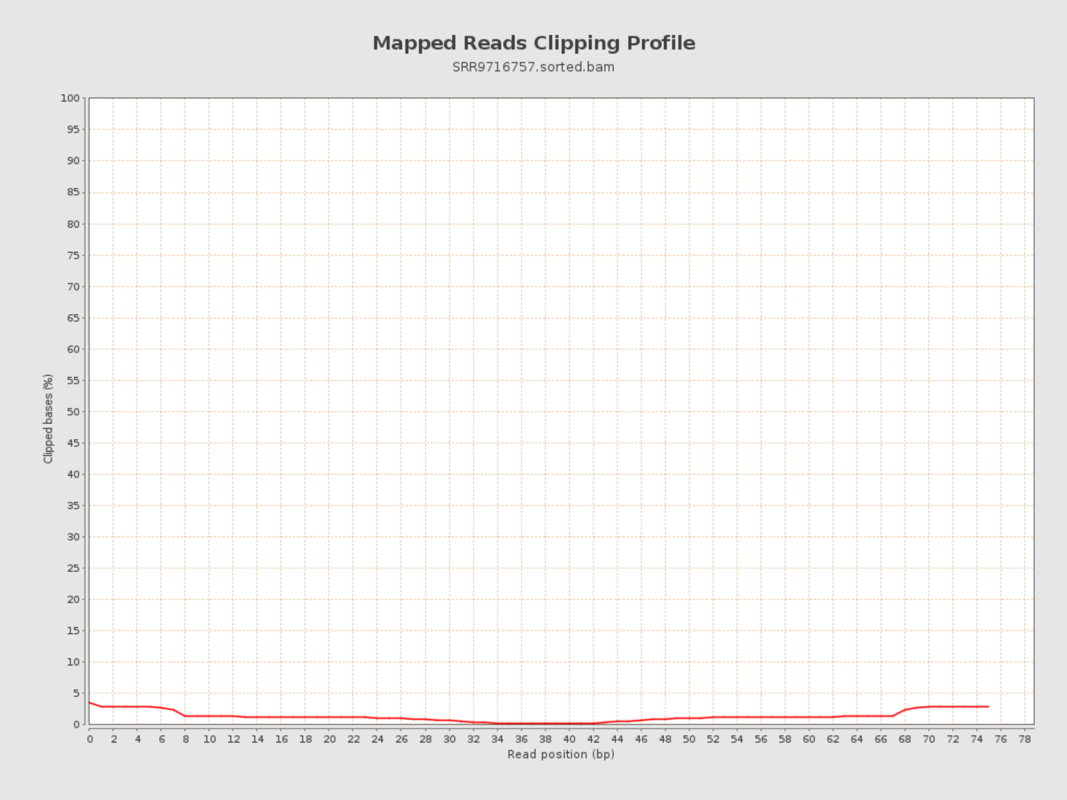
8. Results : Mapped Reads Nucleotide Content



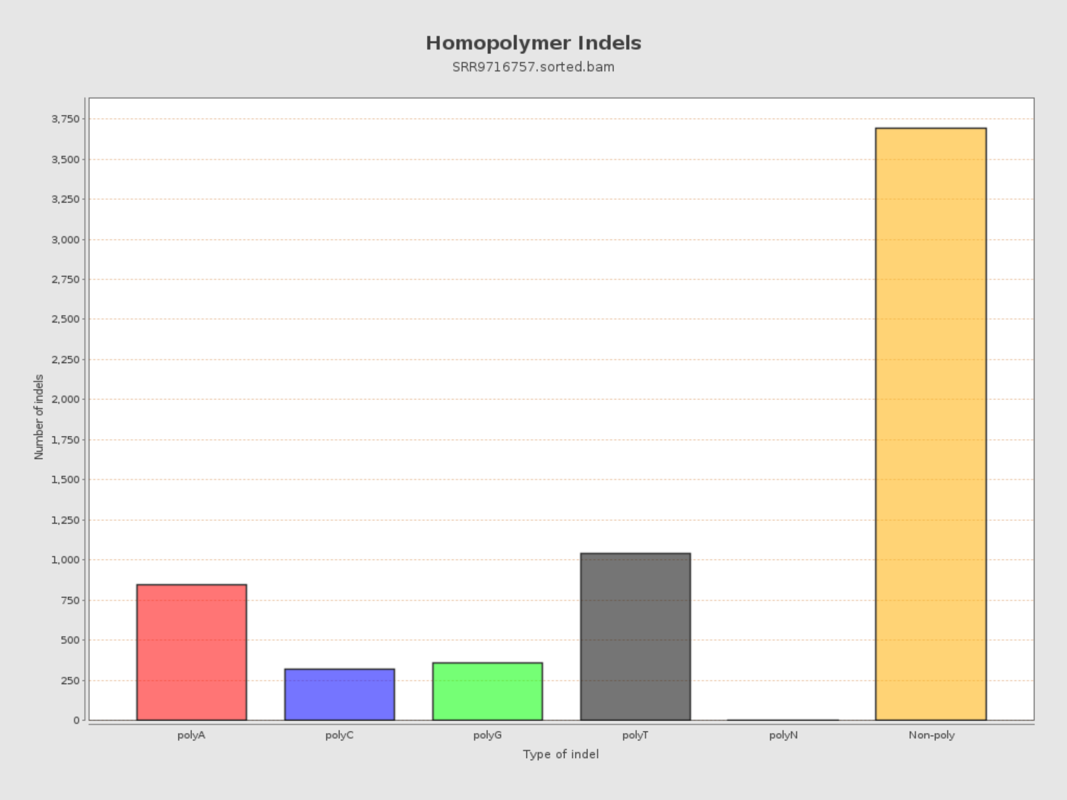
9. Results : Mapped Reads GC-content Distribution



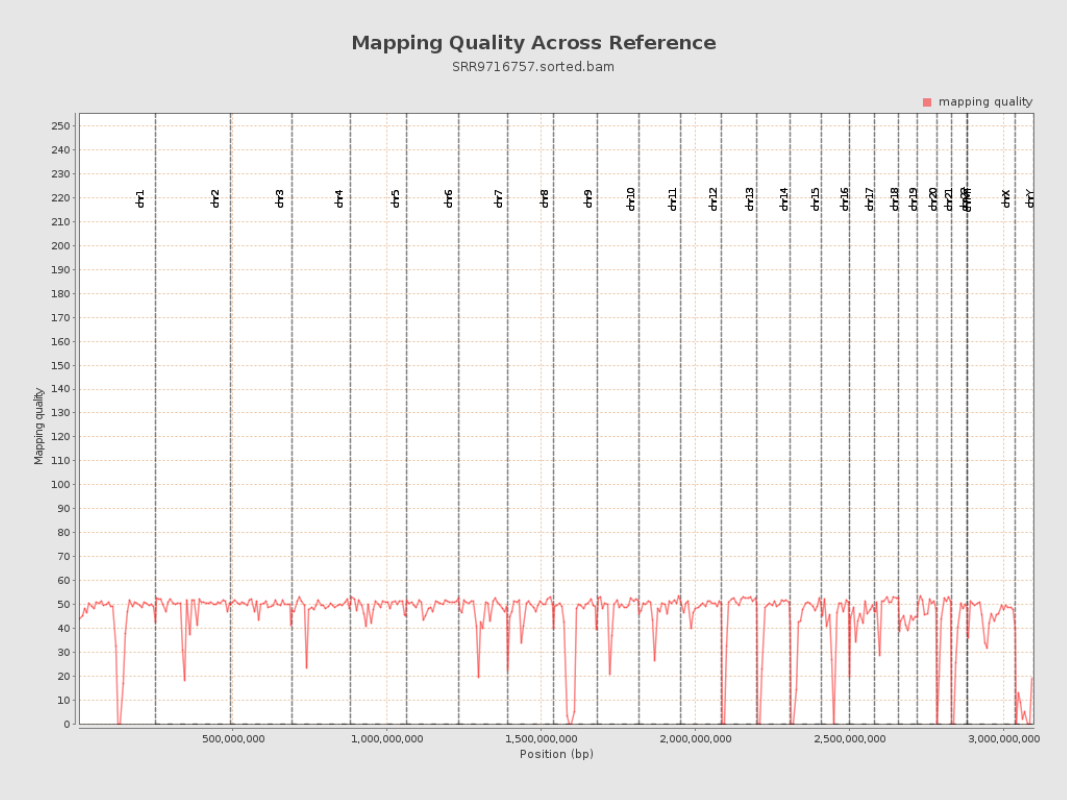
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram