Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:00:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716750.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_SRR9716750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:00:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	853,463
Mapped reads	535,409 / 62.73%
Unmapped reads	318,054 / 37.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	551 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	30,922 / 3.62%
Duplication rate	5.16%
Clipped reads	535,188 / 62.71%

2.2. ACGT Content

Number/percentage of A's	5,779,770 / 20.24%
Number/percentage of C's	5,104,523 / 17.88%
Number/percentage of T's	9,421,785 / 33%
Number/percentage of G's	8,243,245 / 28.87%
Number/percentage of N's	424 / 0%
GC Percentage	46.75%

2.3. Coverage

Mean	0.0092

Standard Deviation	0.1133

2.4. Mapping Quality

Mean Mapping Quality	43.43

2.5. Mismatches and indels

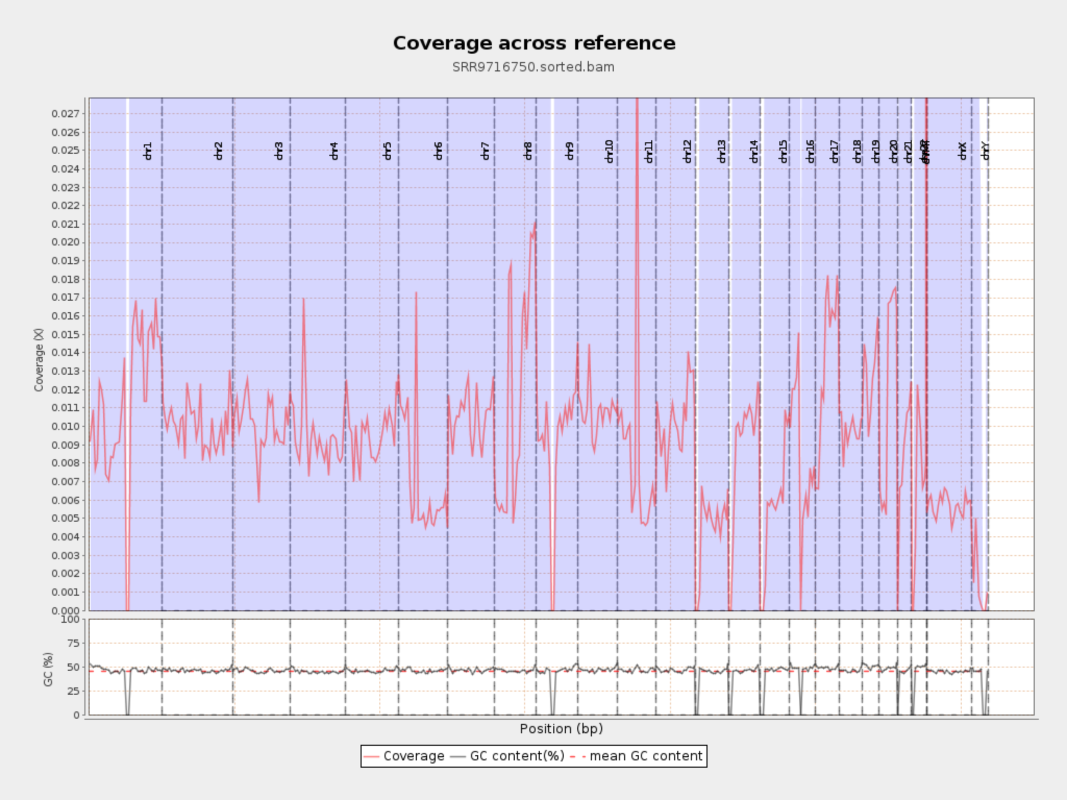
General error rate	0.64%
Mismatches	180,949
Insertions	1,640
Mapped reads with at least one insertion	0.31%
Deletions	4,127
Mapped reads with at least one deletion	0.76%
Homopolymer indels	42.01%

2.6. Chromosome stats

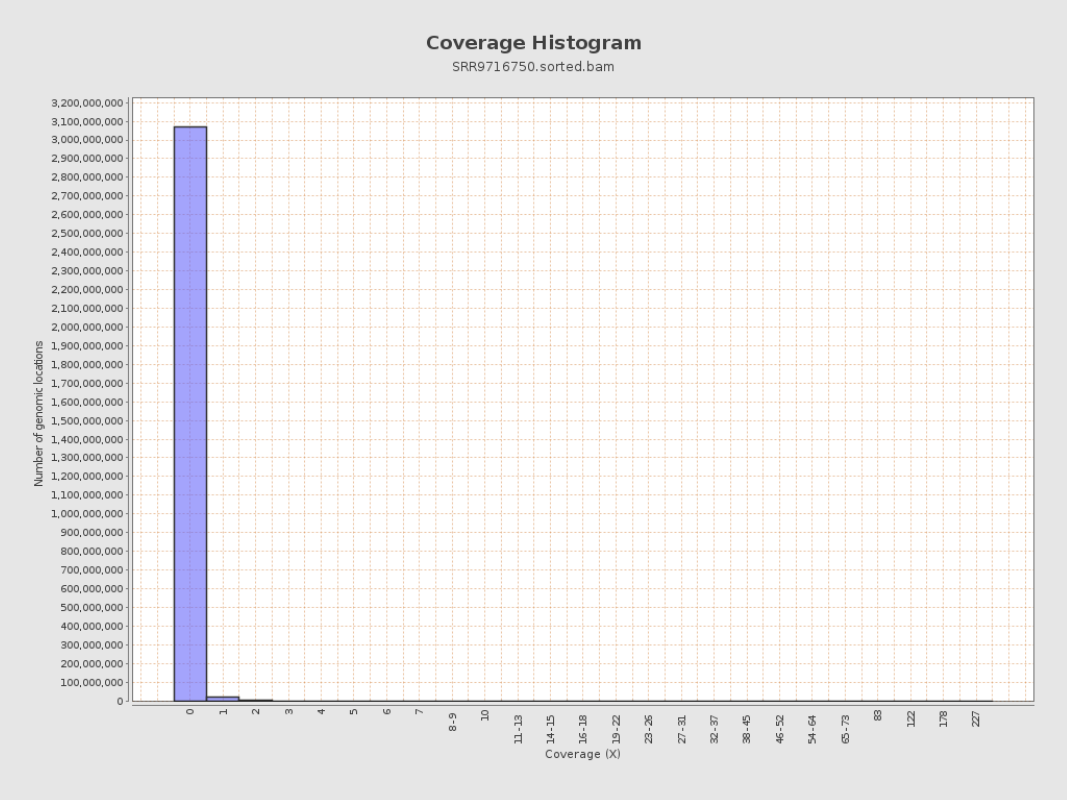
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2797775	0.0112	0.1273
chr2	243199373	2453658	0.0101	0.1441
chr3	198022430	1995882	0.0101	0.11
chr4	191154276	1802766	0.0094	0.1106
chr5	180915260	1735105	0.0096	0.1082
chr6	171115067	1218715	0.0071	0.1002
chr7	159138663	1674521	0.0105	0.124

chr8	146364022	1719955	0.0118	0.122
chr9	141213431	1266523	0.009	0.1084
chr10	135534747	1459013	0.0108	0.1244
chr11	135006516	1197793	0.0089	0.1098
chr12	133851895	1385277	0.0103	0.1131
chr13	115169878	504547	0.0044	0.0732
chr14	107349540	928345	0.0086	0.1029
chr15	102531392	571459	0.0056	0.0824
chr16	90354753	752409	0.0083	0.1055
chr17	81195210	1134429	0.014	0.1333
chr18	78077248	760301	0.0097	0.1184
chr19	59128983	752483	0.0127	0.1392
chr20	63025520	747187	0.0119	0.1244
chr21	48129895	401767	0.0083	0.1051
chr22	51304566	319140	0.0062	0.0891
chrMT	16571	7754	0.4679	0.7241
chrX	155270560	889132	0.0057	0.0844
chrY	59373566	80843	0.0014	0.0516

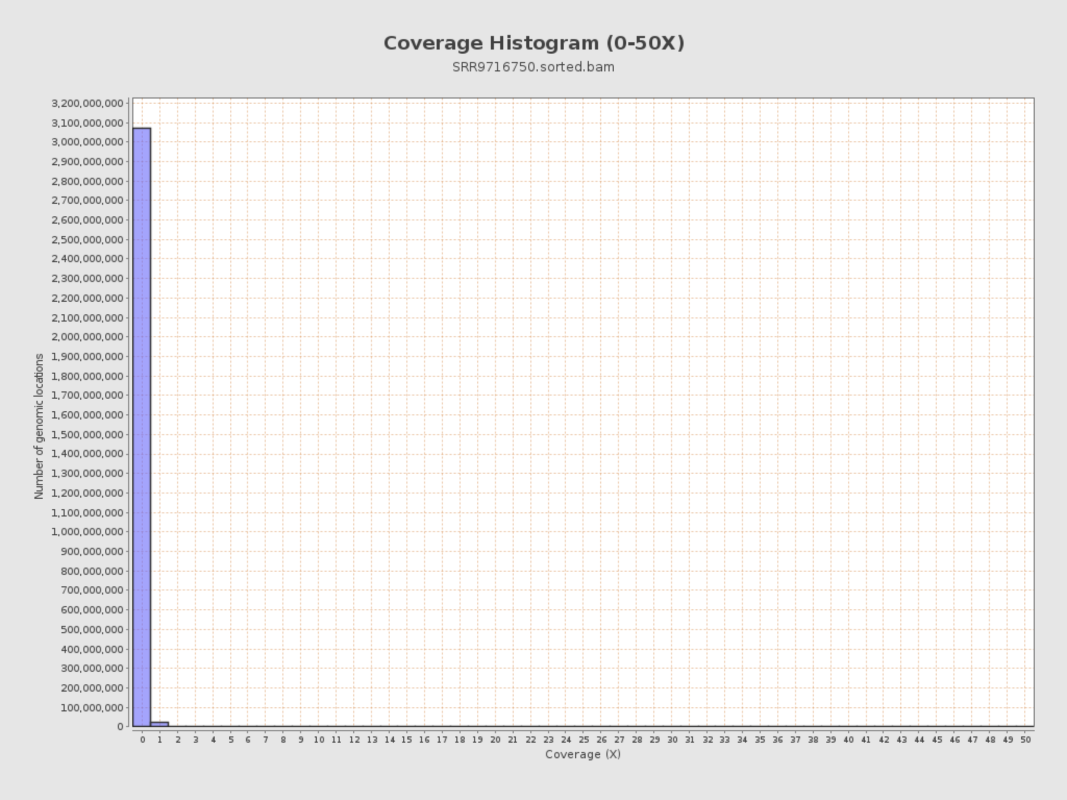
3. Results : Coverage across reference



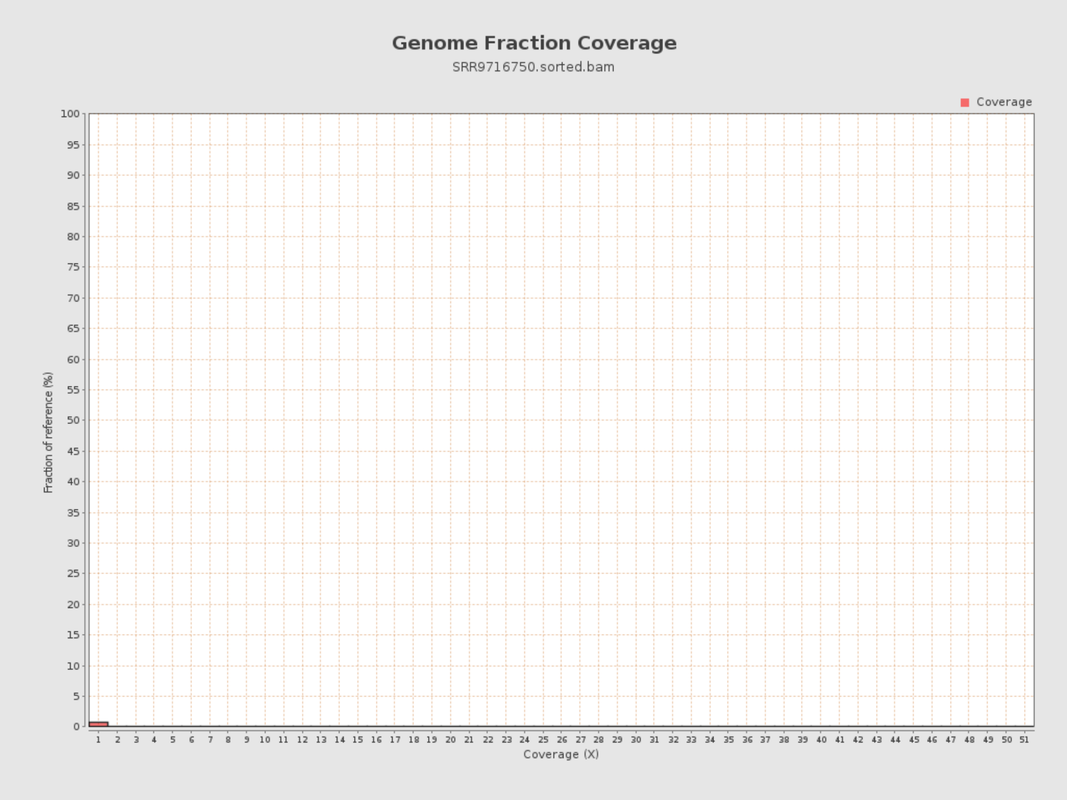
4. Results : Coverage Histogram



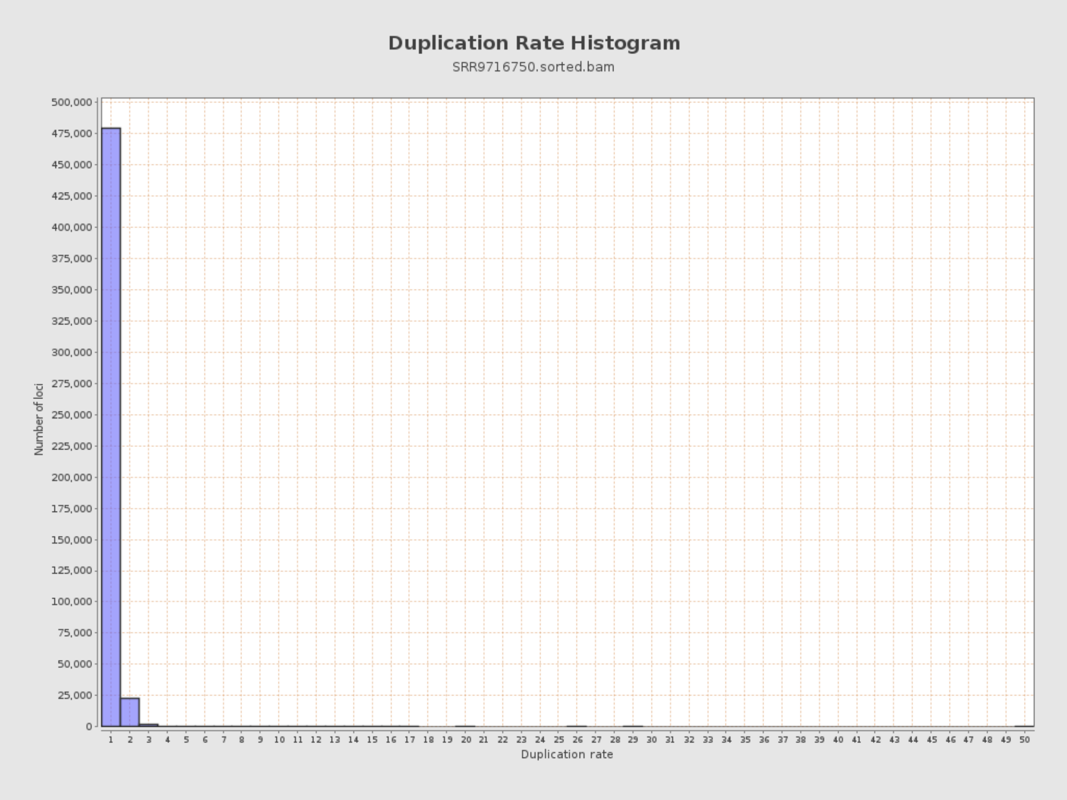
5. Results : Coverage Histogram (0-50X)



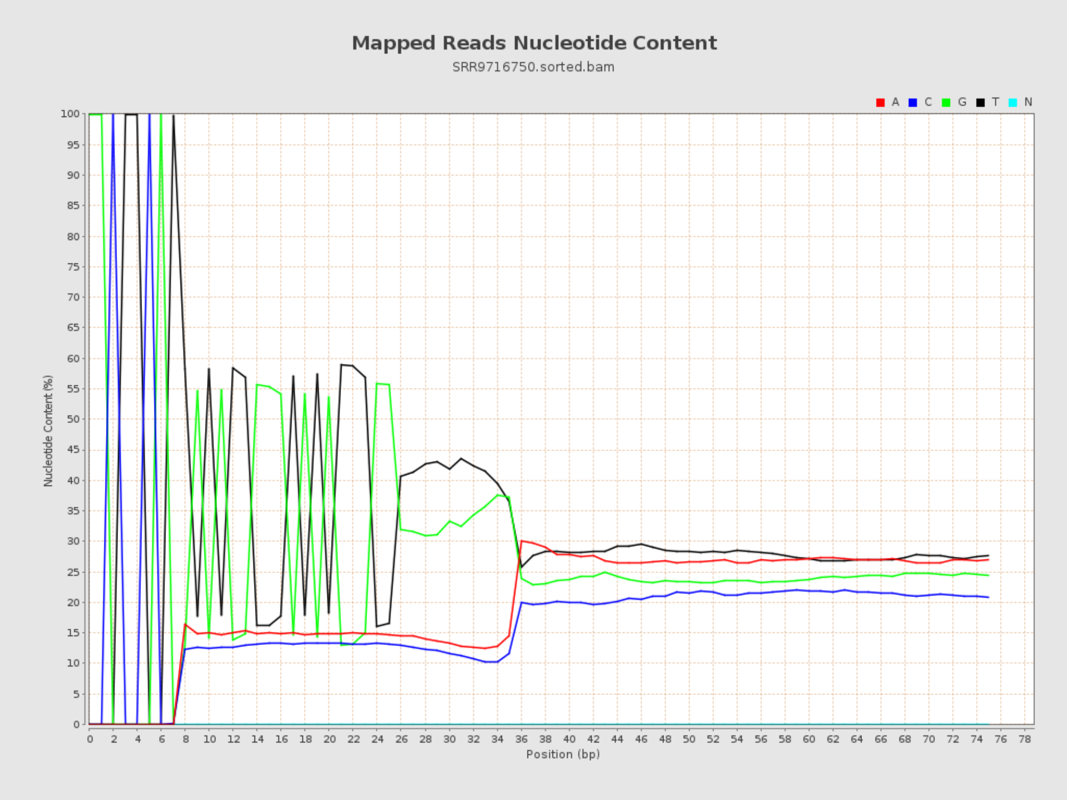
6. Results : Genome Fraction Coverage



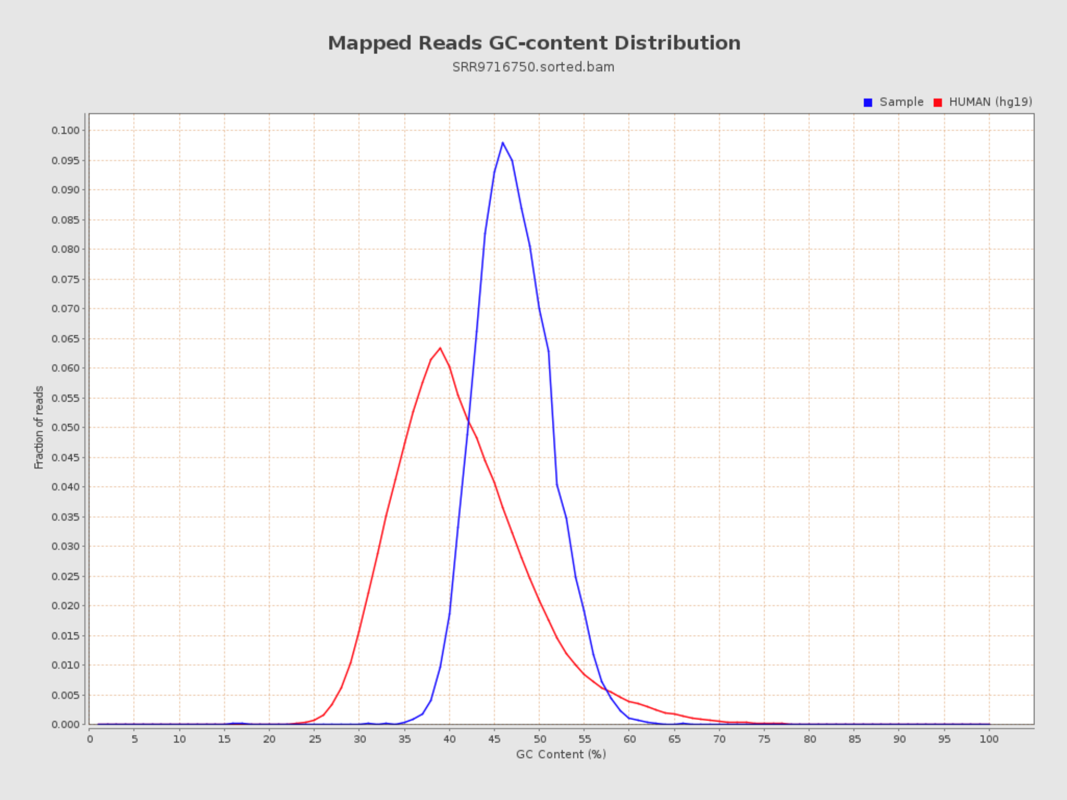
7. Results : Duplication Rate Histogram



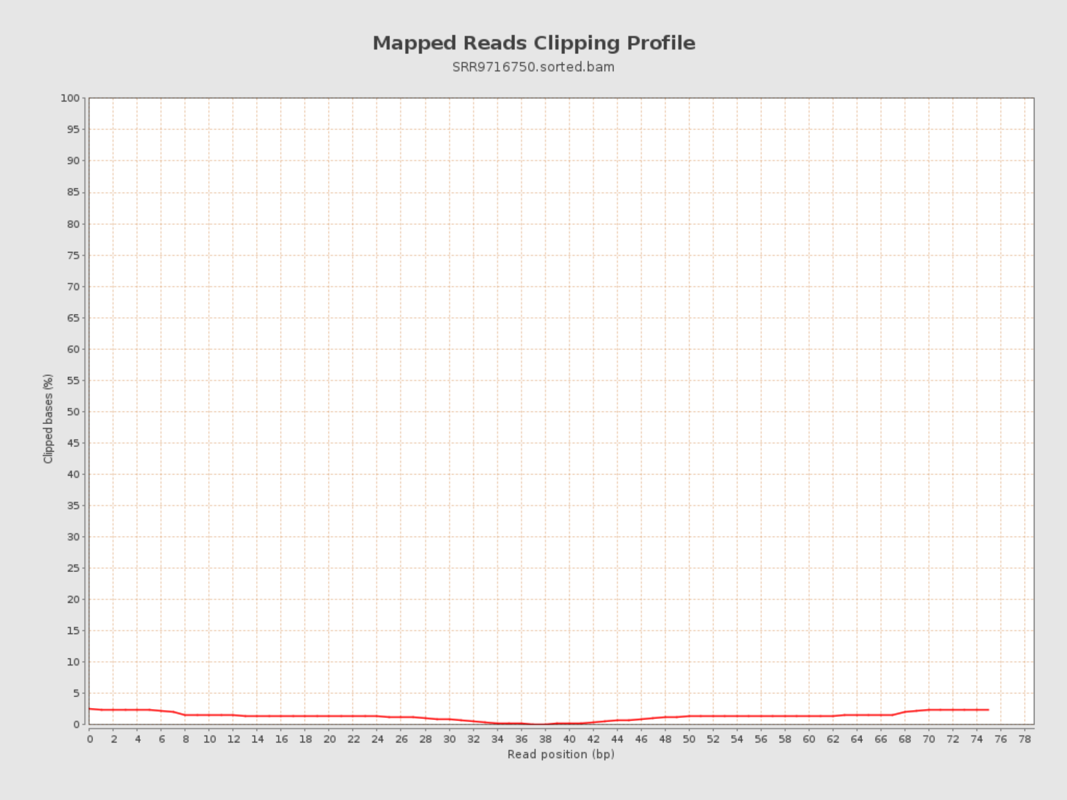
8. Results : Mapped Reads Nucleotide Content



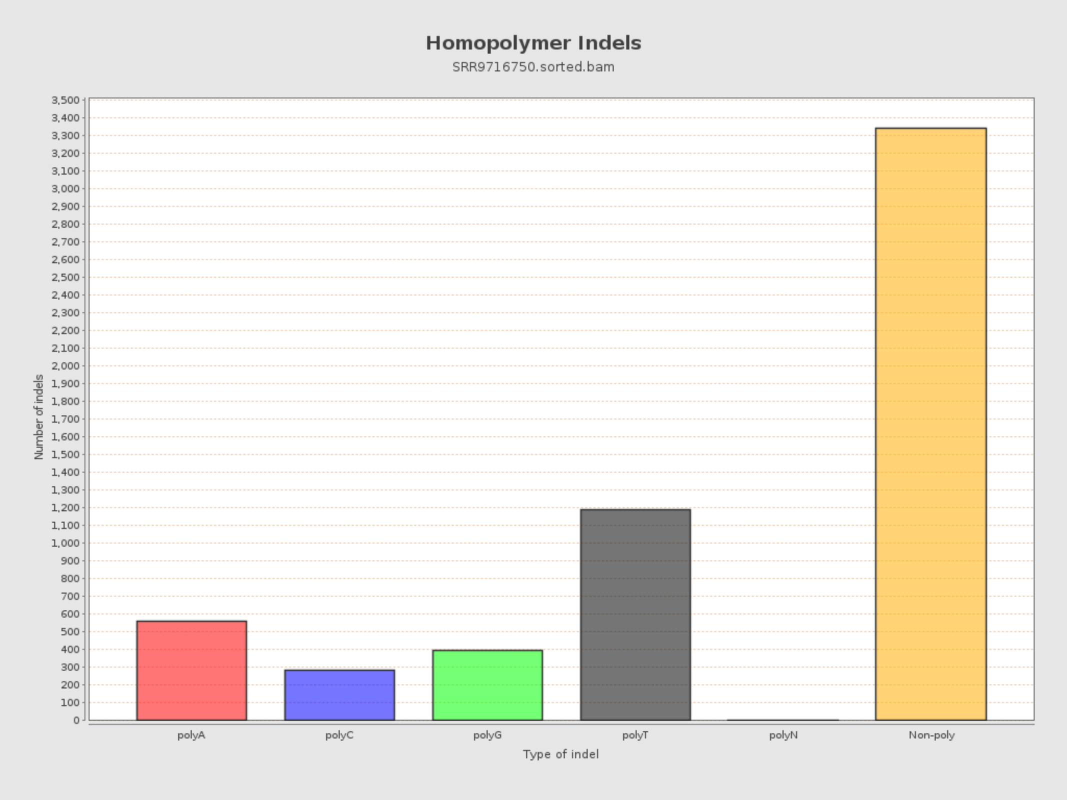
9. Results : Mapped Reads GC-content Distribution



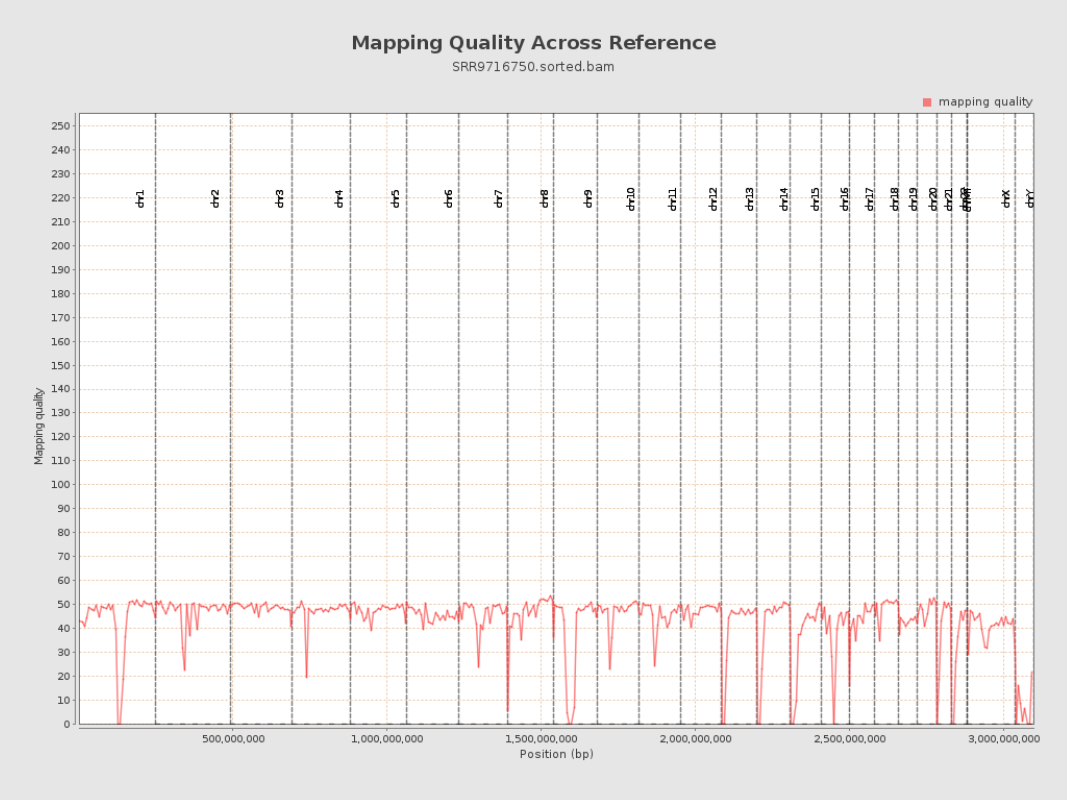
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram