Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:02:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716872.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_SRR9716872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716872.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:02:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,450
Mapped reads	337,483 / 78.22%
Unmapped reads	93,967 / 21.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	549 / 0.13%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	14,088 / 3.27%
Duplication rate	3.79%
Clipped reads	337,353 / 78.19%

2.2. ACGT Content

Number/percentage of A's	3,819,526 / 21.19%
Number/percentage of C's	3,243,007 / 17.99%
Number/percentage of T's	5,896,638 / 32.72%
Number/percentage of G's	5,063,517 / 28.09%
Number/percentage of N's	323 / 0%
GC Percentage	46.09%

2.3. Coverage

Mean	0.0058

Standard Deviation	0.0849

2.4. Mapping Quality

Mean Mapping Quality	43.76

2.5. Mismatches and indels

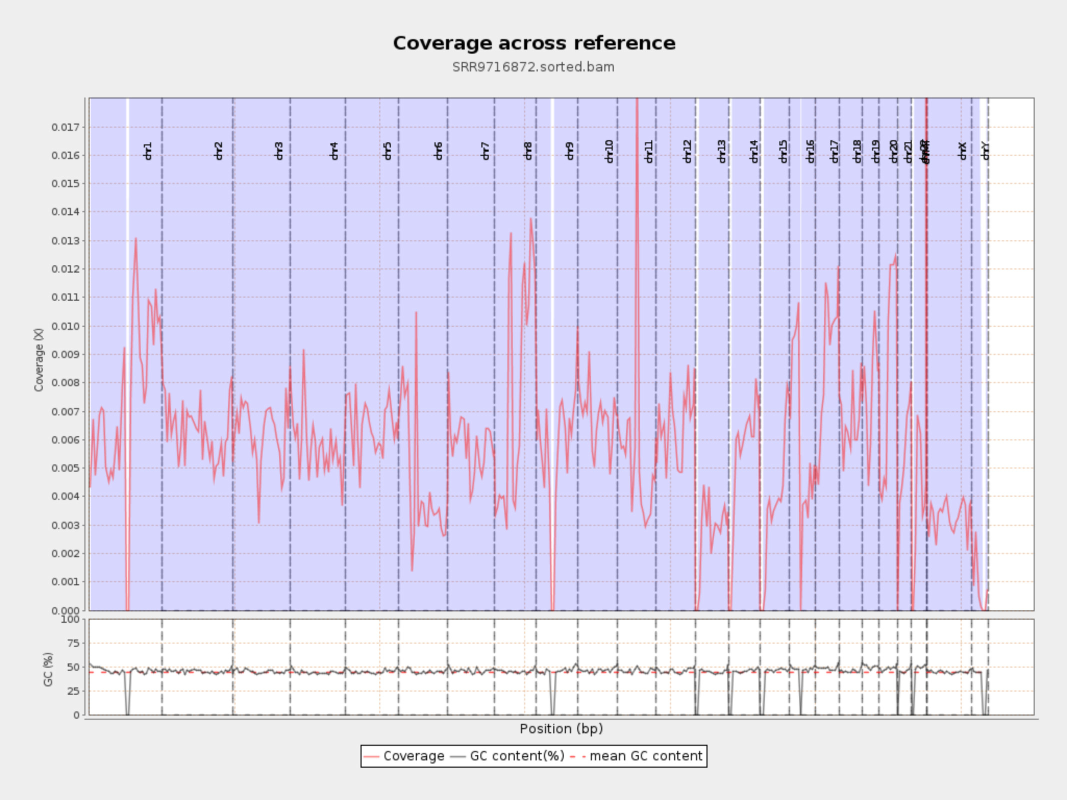
General error rate	0.66%
Mismatches	116,152
Insertions	1,125
Mapped reads with at least one insertion	0.33%
Deletions	2,653
Mapped reads with at least one deletion	0.78%
Homopolymer indels	39.97%

2.6. Chromosome stats

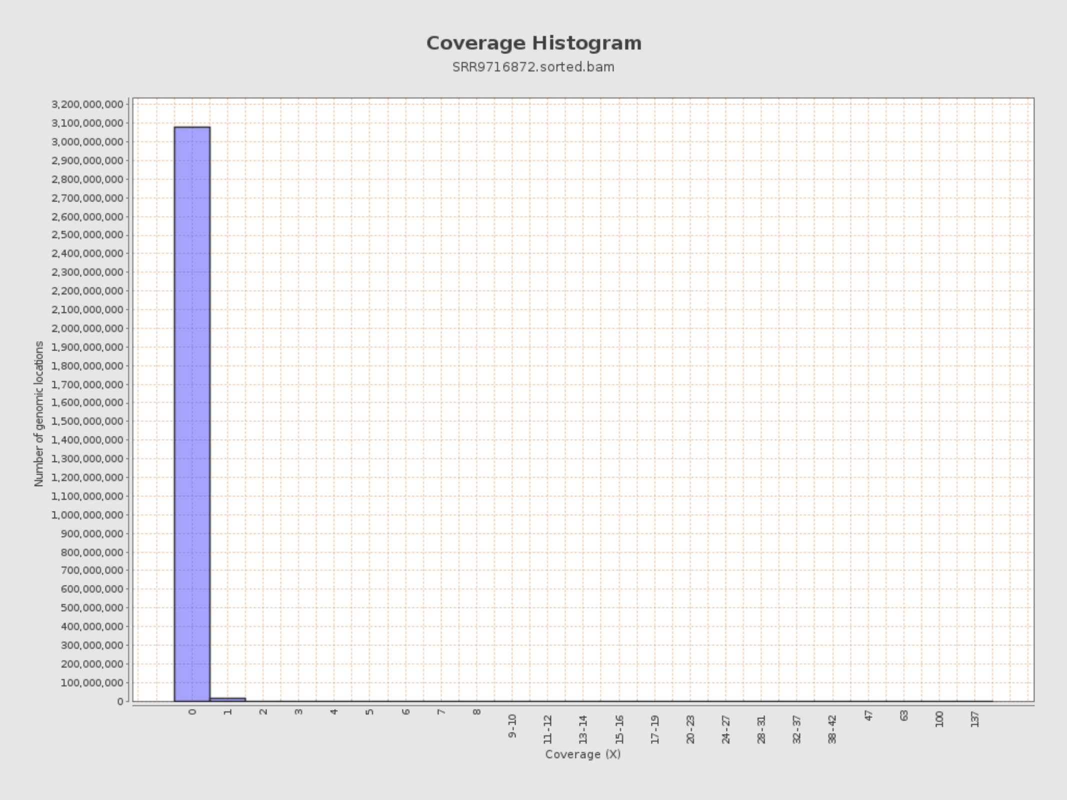
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1824095	0.0073	0.0963
chr2	243199373	1531602	0.0063	0.1017
chr3	198022430	1233864	0.0062	0.0847
chr4	191154276	1102940	0.0058	0.0819
chr5	180915260	1168352	0.0065	0.086
chr6	171115067	770286	0.0045	0.0753
chr7	159138663	920852	0.0058	0.0826

chr8	146364022	1137584	0.0078	0.0957
chr9	141213431	768754	0.0054	0.0793
chr10	135534747	918882	0.0068	0.0929
chr11	135006516	776865	0.0058	0.0844
chr12	133851895	872441	0.0065	0.0862
chr13	115169878	308019	0.0027	0.0553
chr14	107349540	572404	0.0053	0.0786
chr15	102531392	372952	0.0036	0.0644
chr16	90354753	537580	0.0059	0.0846
chr17	81195210	718223	0.0088	0.1017
chr18	78077248	515631	0.0066	0.0901
chr19	59128983	455783	0.0077	0.1065
chr20	63025520	525429	0.0083	0.0998
chr21	48129895	250146	0.0052	0.0782
chr22	51304566	180772	0.0035	0.0644
chrMT	16571	2865	0.1729	0.4606
chrX	155270560	513170	0.0033	0.0611
chrY	59373566	48189	0.0008	0.0348

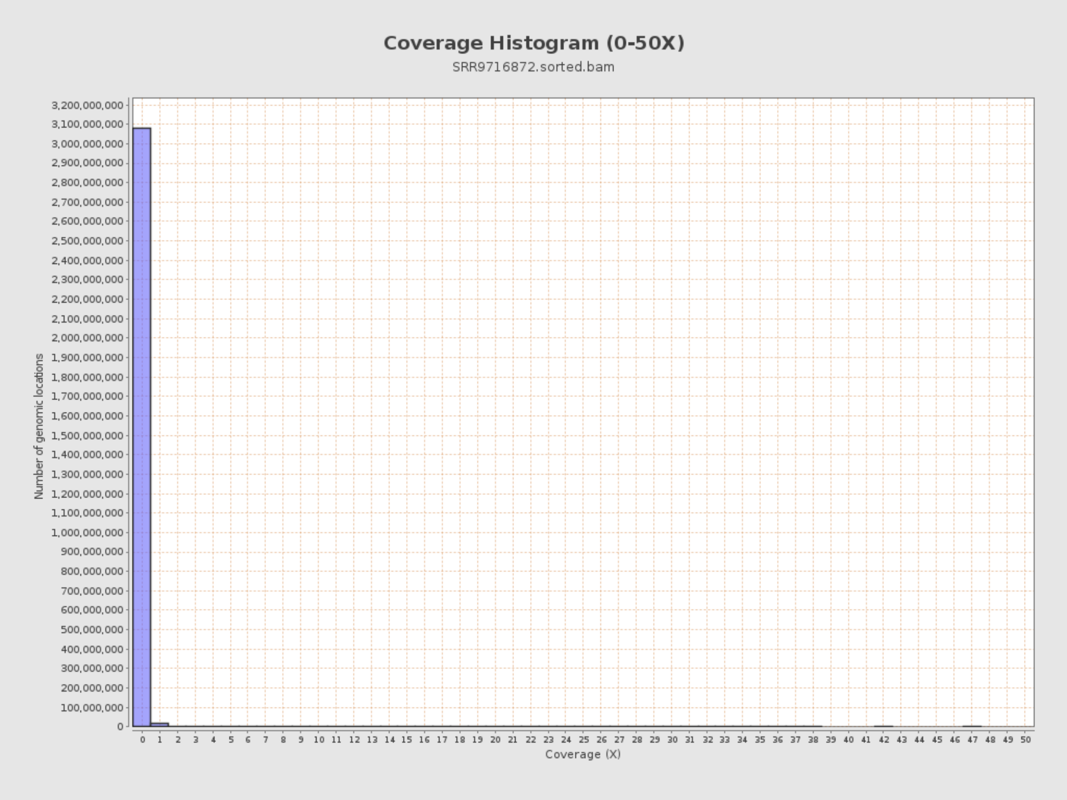
3. Results : Coverage across reference



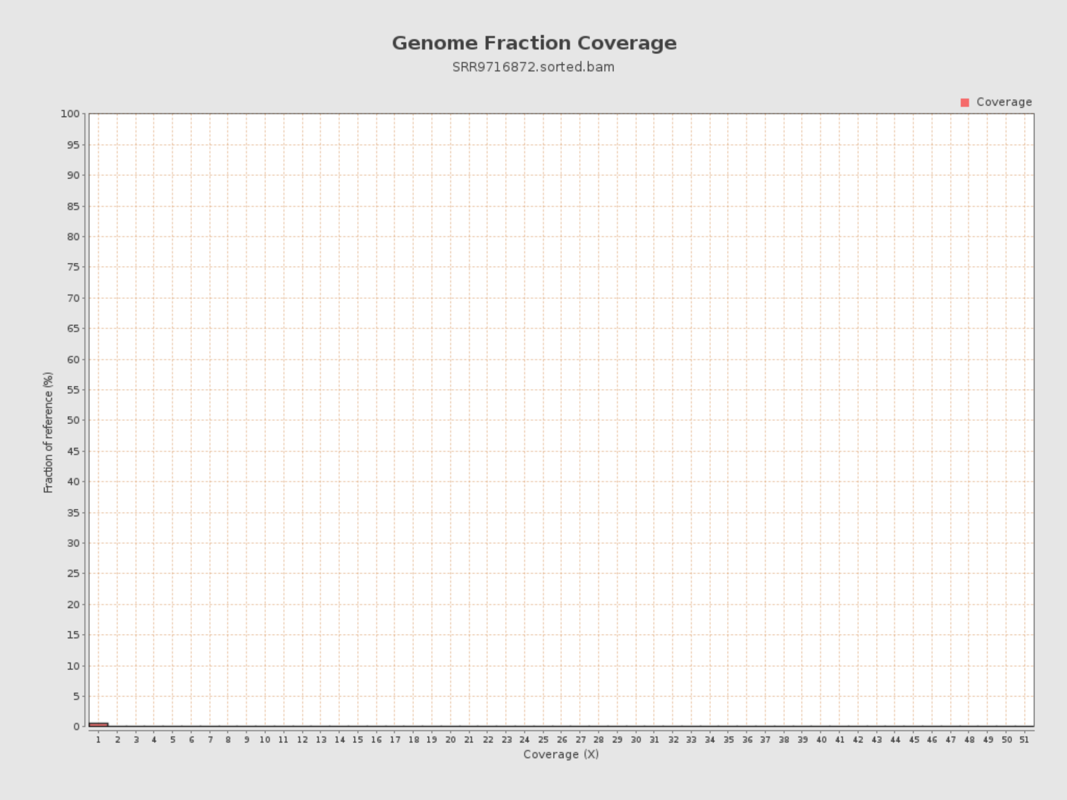
4. Results : Coverage Histogram



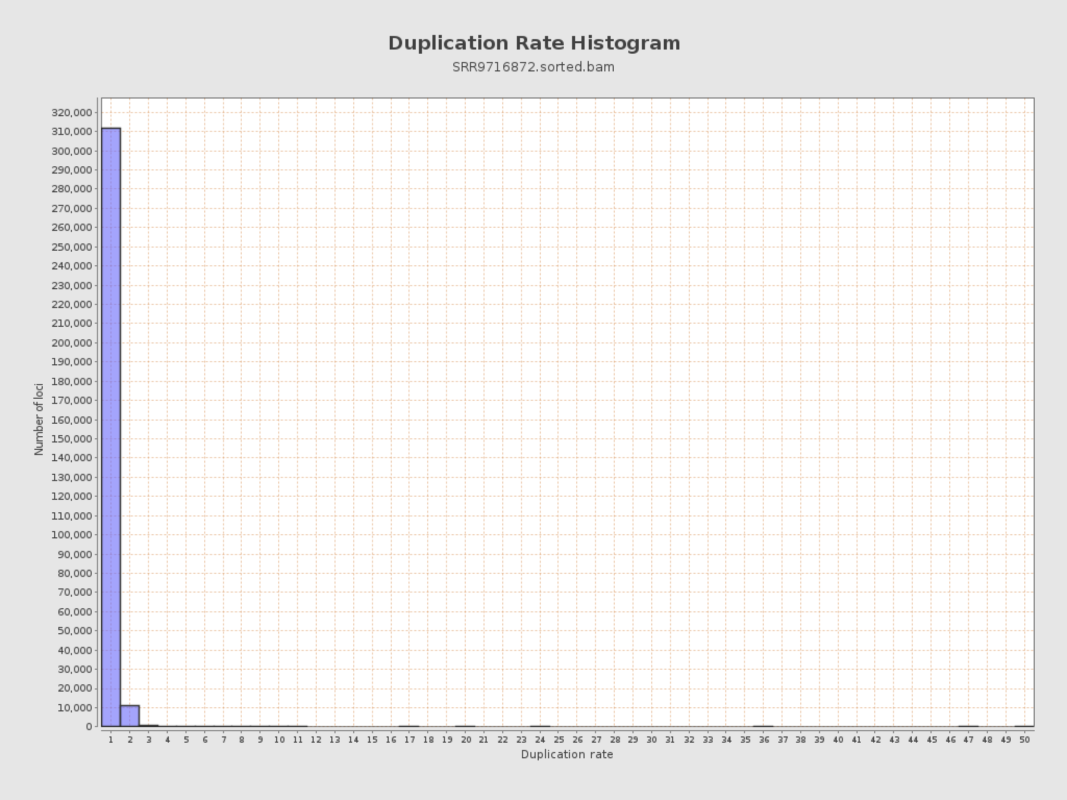
5. Results : Coverage Histogram (0-50X)



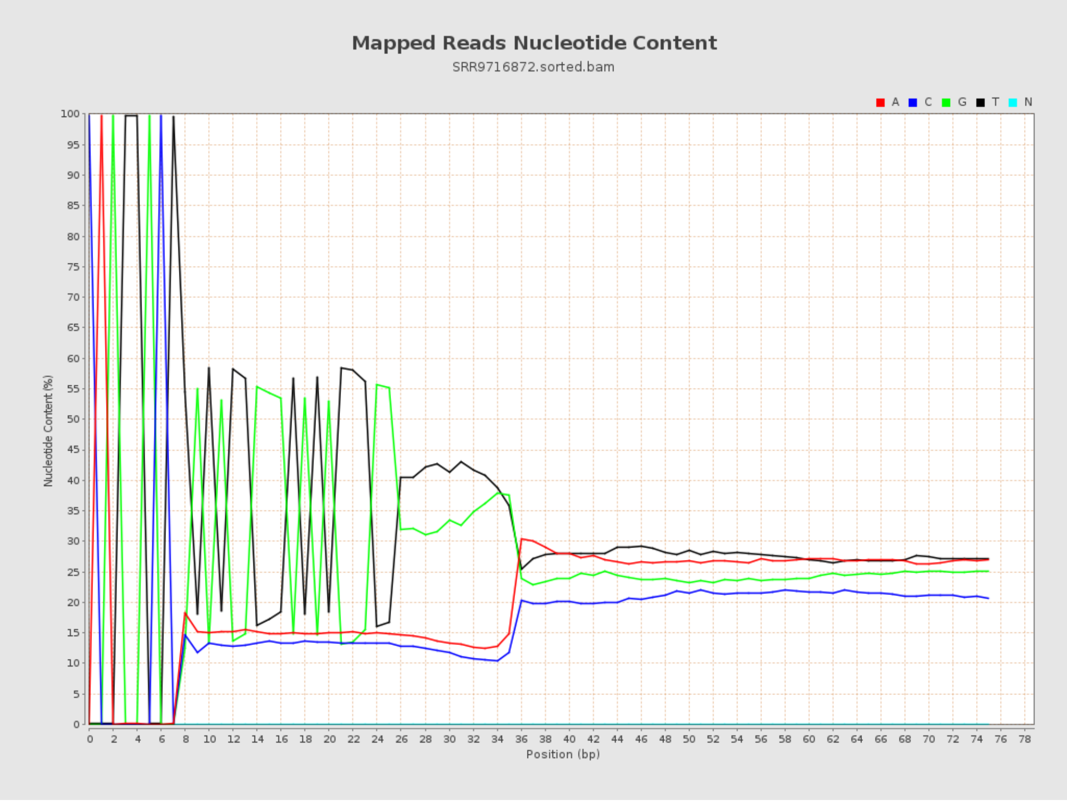
6. Results : Genome Fraction Coverage



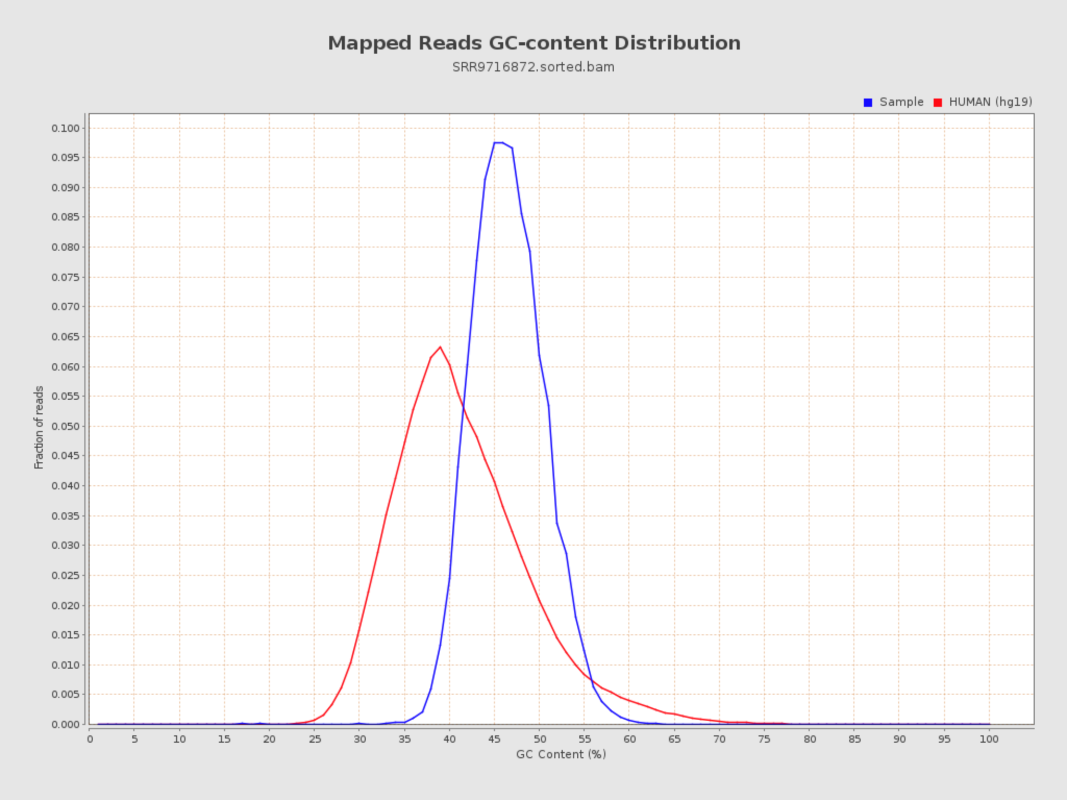
7. Results : Duplication Rate Histogram



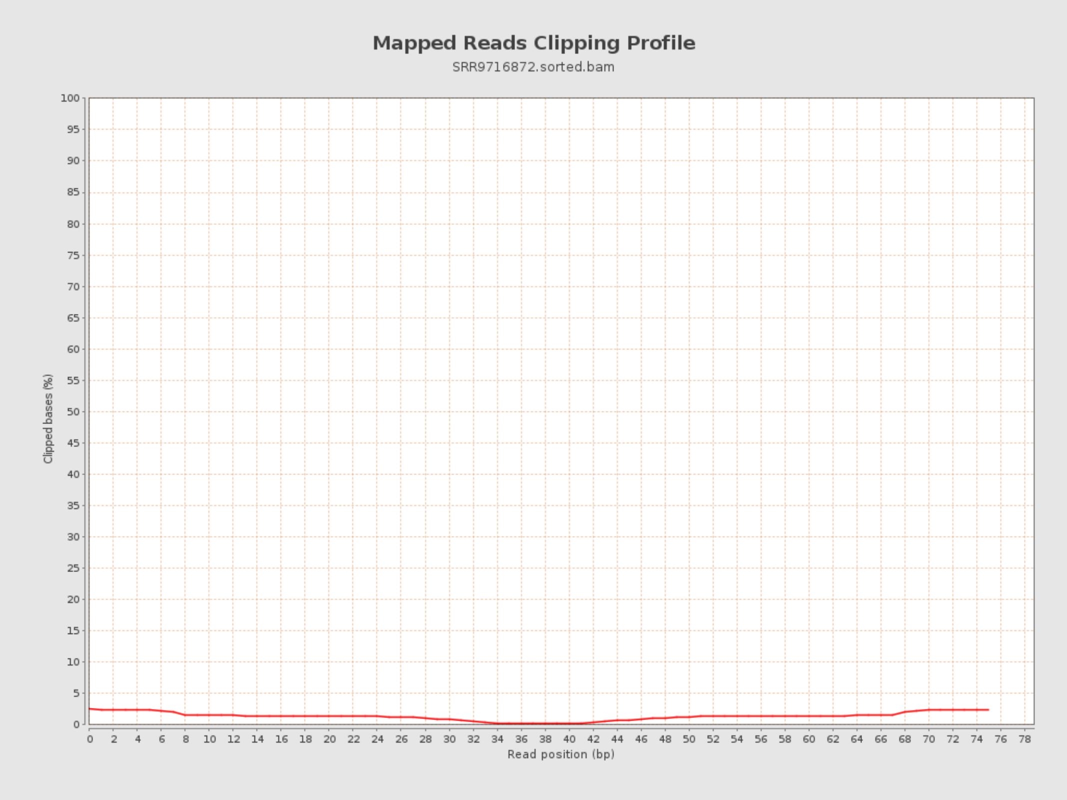
8. Results : Mapped Reads Nucleotide Content



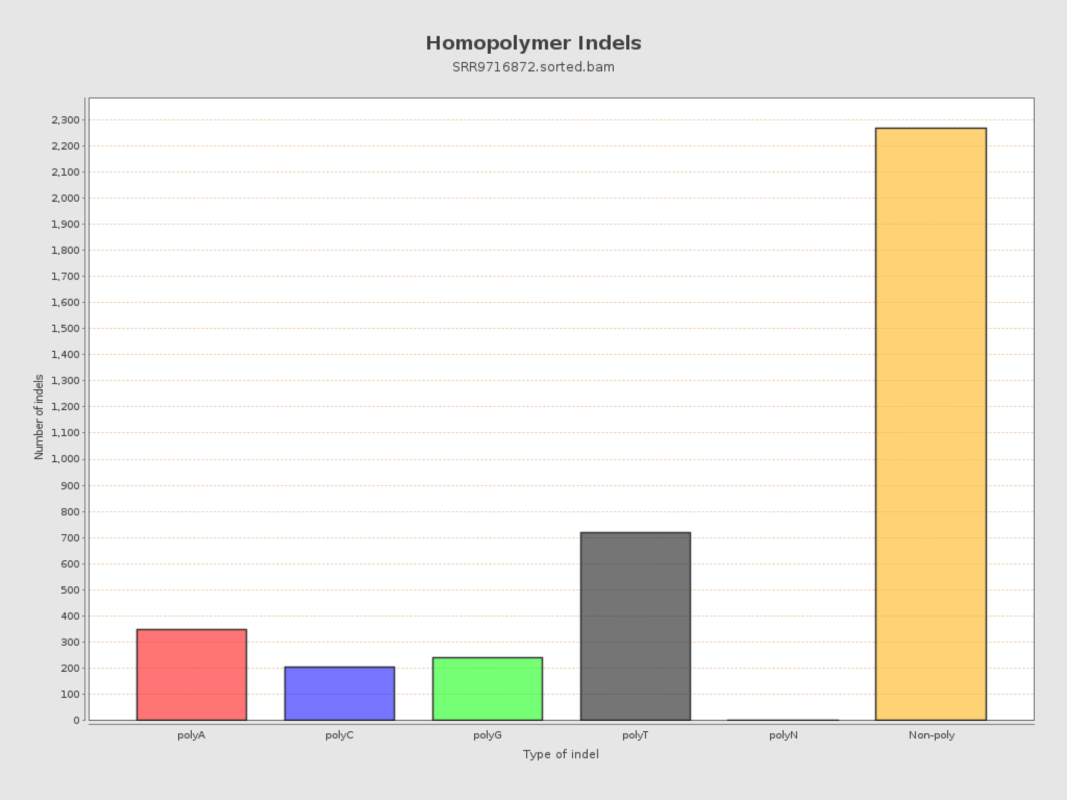
9. Results : Mapped Reads GC-content Distribution



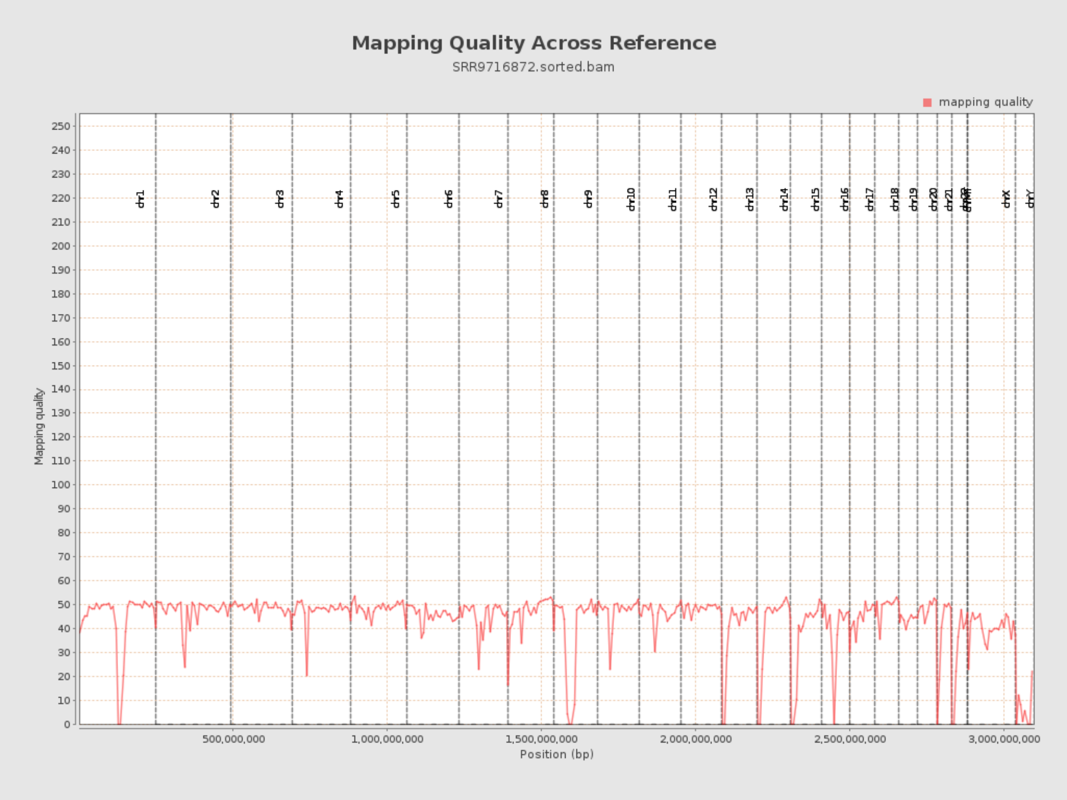
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram