Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:49:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716185.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_SRR9716185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:49:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	536,881
Mapped reads	478,693 / 89.16%
Unmapped reads	58,188 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,267 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	11,125 / 2.07%
Duplication rate	1.76%
Clipped reads	479,866 / 89.38%

2.2. ACGT Content

Number/percentage of A's	6,812,685 / 25.1%
Number/percentage of C's	5,233,780 / 19.28%
Number/percentage of T's	8,504,198 / 31.33%
Number/percentage of G's	6,589,614 / 24.28%
Number/percentage of N's	370 / 0%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1189

2.4. Mapping Quality

Mean Mapping Quality	43.44

2.5. Mismatches and indels

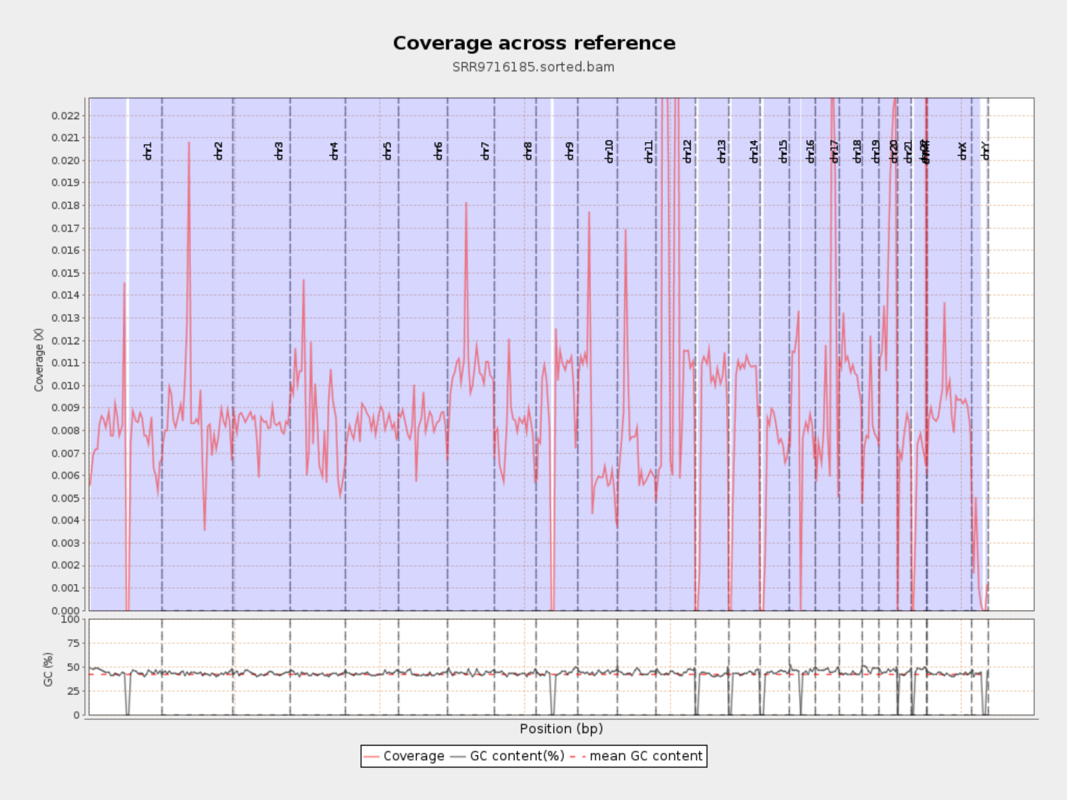
General error rate	0.57%
Mismatches	152,008
Insertions	1,815
Mapped reads with at least one insertion	0.38%
Deletions	4,713
Mapped reads with at least one deletion	0.98%
Homopolymer indels	41.8%

2.6. Chromosome stats

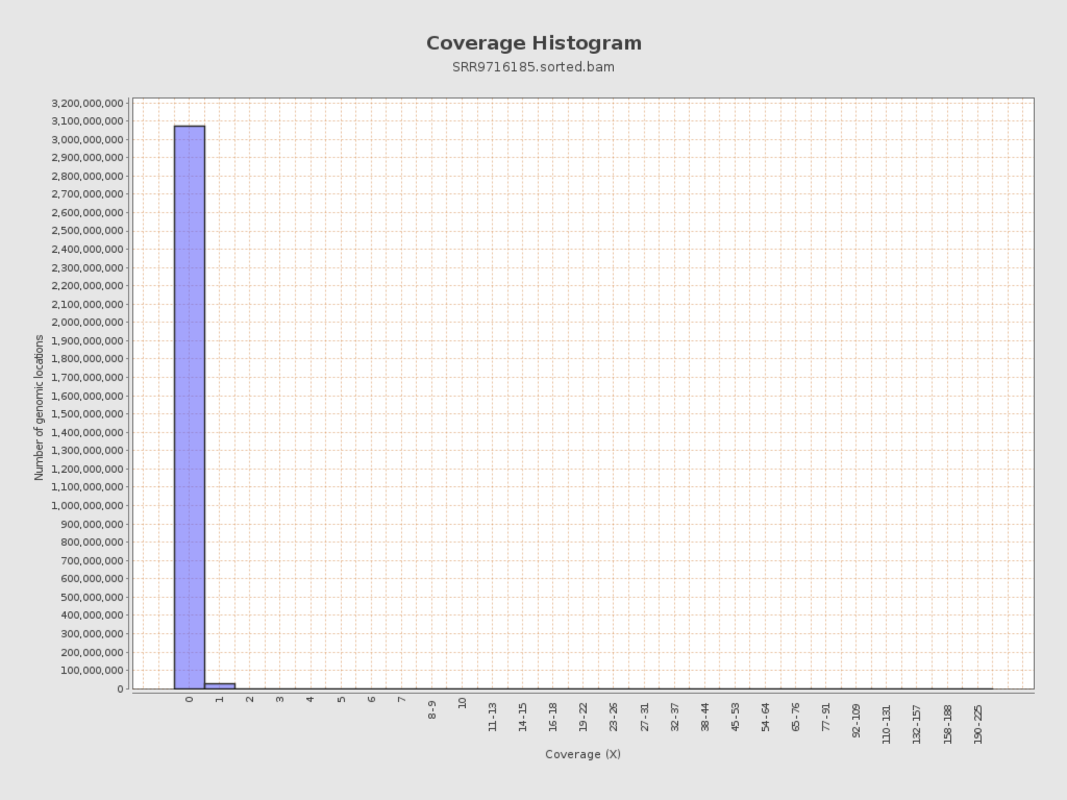
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1863875	0.0075	0.1758
chr2	243199373	2123942	0.0087	0.1284
chr3	198022430	1642789	0.0083	0.0939
chr4	191154276	1643555	0.0086	0.0998
chr5	180915260	1503023	0.0083	0.095
chr6	171115067	1431488	0.0084	0.0985
chr7	159138663	1734525	0.0109	0.1456

chr8	146364022	1179763	0.0081	0.1078
chr9	141213431	1264206	0.009	0.1226
chr10	135534747	1057624	0.0078	0.1187
chr11	135006516	1009130	0.0075	0.1029
chr12	133851895	1992642	0.0149	0.1305
chr13	115169878	1017887	0.0088	0.0966
chr14	107349540	957165	0.0089	0.1001
chr15	102531392	652011	0.0064	0.0821
chr16	90354753	784045	0.0087	0.0999
chr17	81195210	849970	0.0105	0.107
chr18	78077248	848160	0.0109	0.1832
chr19	59128983	482609	0.0082	0.1486
chr20	63025520	1003768	0.0159	0.1317
chr21	48129895	332226	0.0069	0.0903
chr22	51304566	263958	0.0051	0.0737
chrMT	16571	2688	0.1622	0.4276
chrX	155270560	1420901	0.0092	0.1062
chrY	59373566	86658	0.0015	0.0485

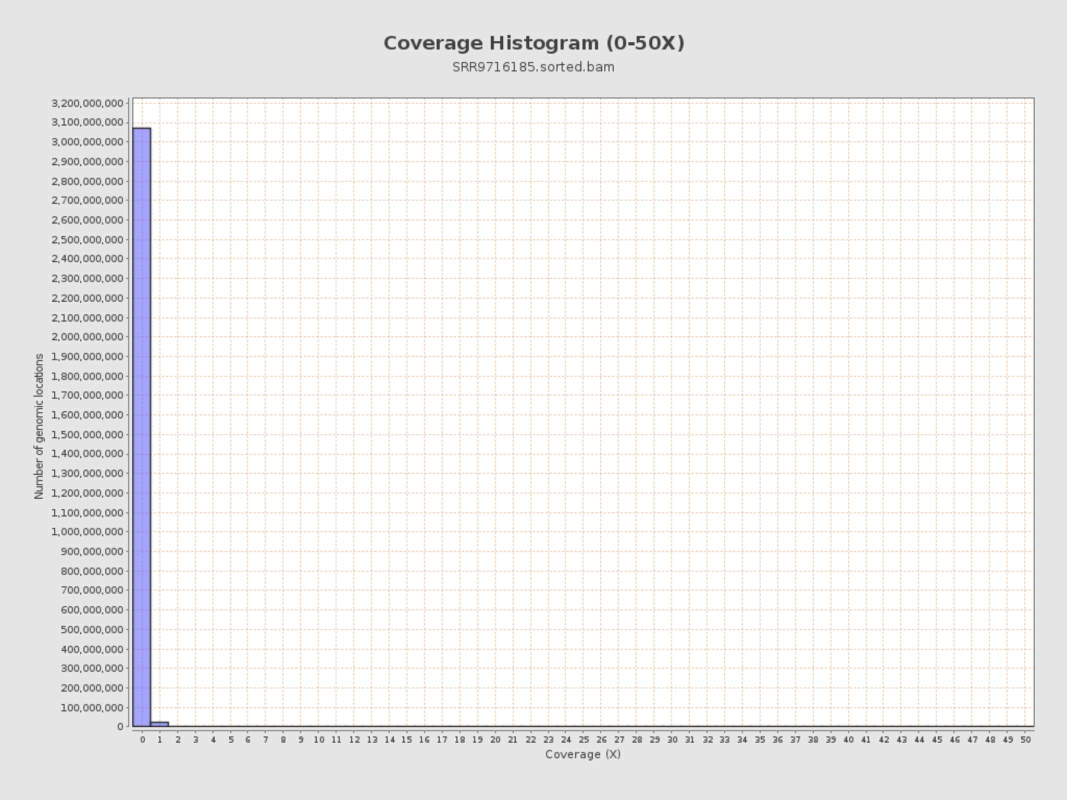
3. Results : Coverage across reference



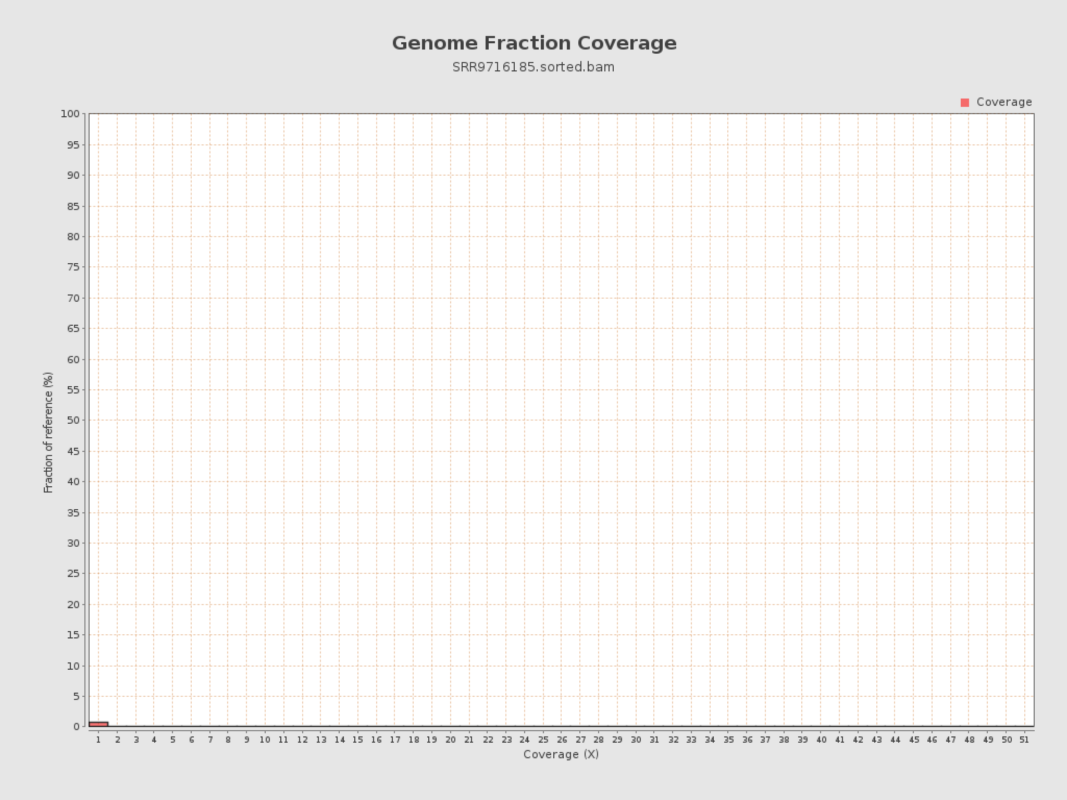
4. Results : Coverage Histogram



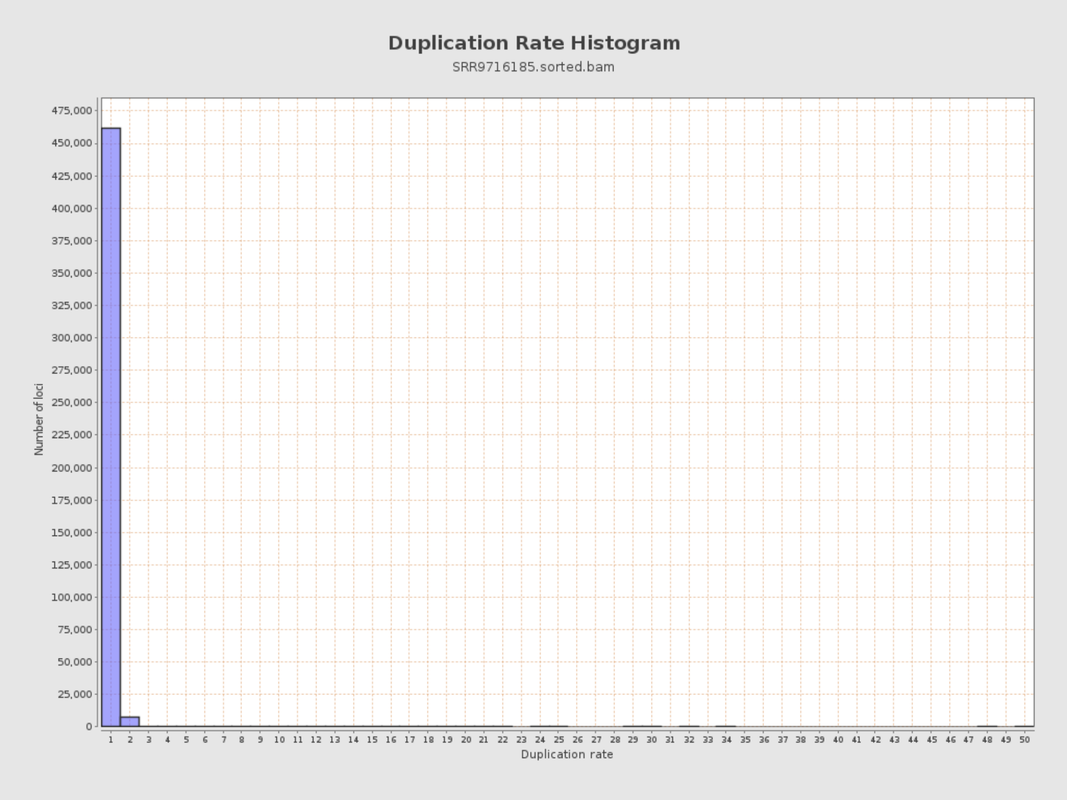
5. Results : Coverage Histogram (0-50X)



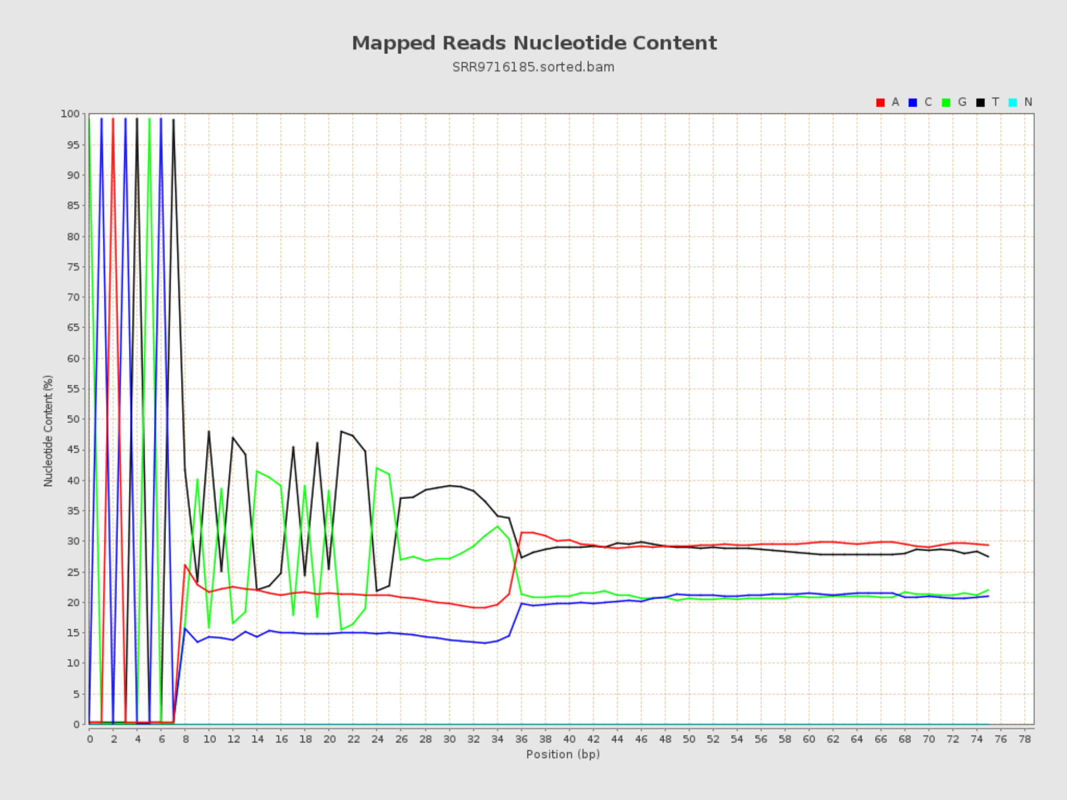
6. Results : Genome Fraction Coverage



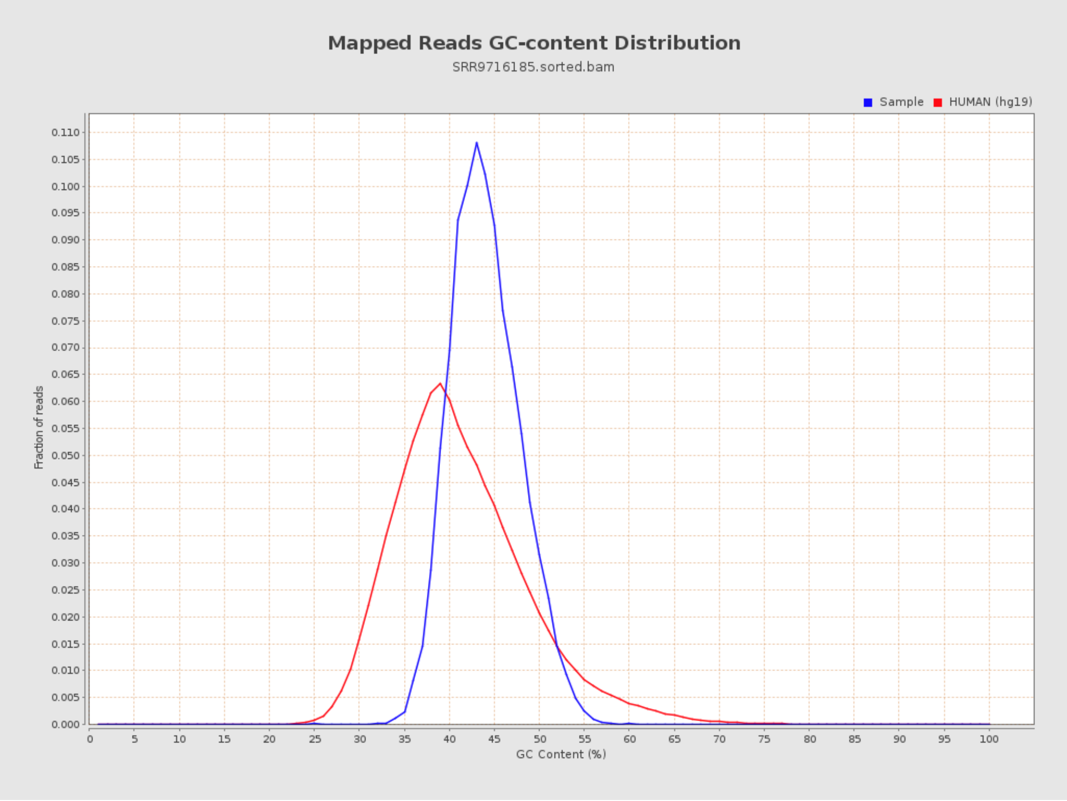
7. Results : Duplication Rate Histogram



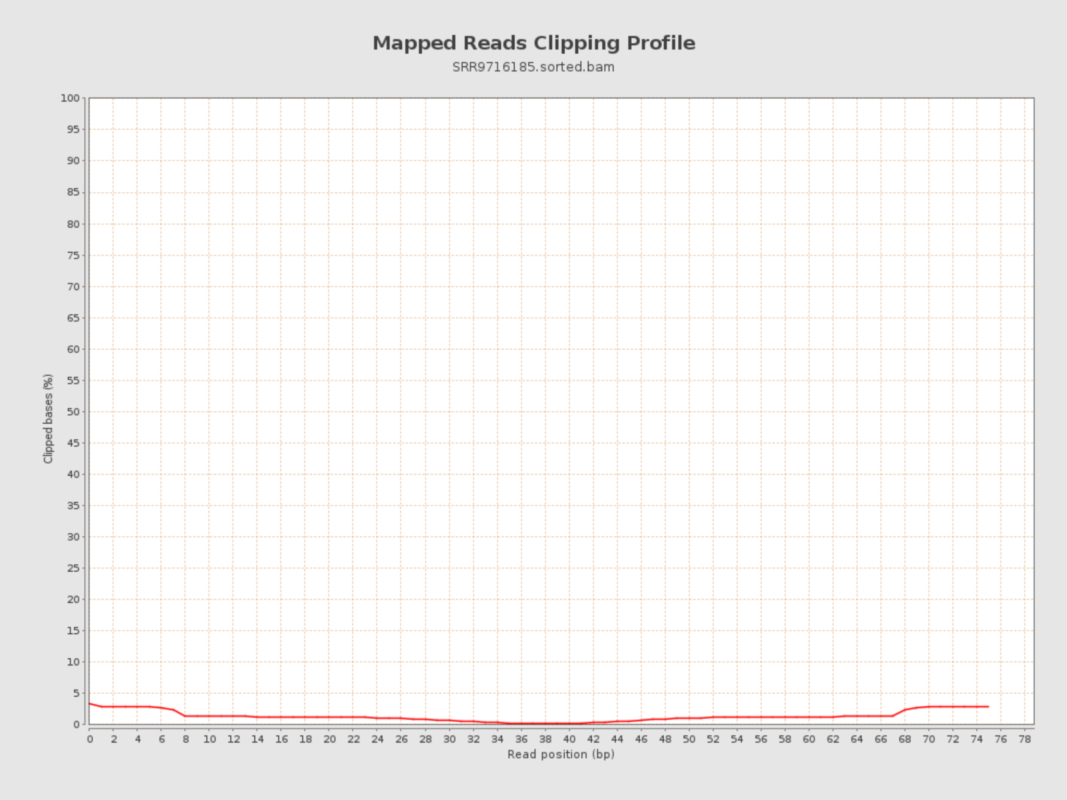
8. Results : Mapped Reads Nucleotide Content



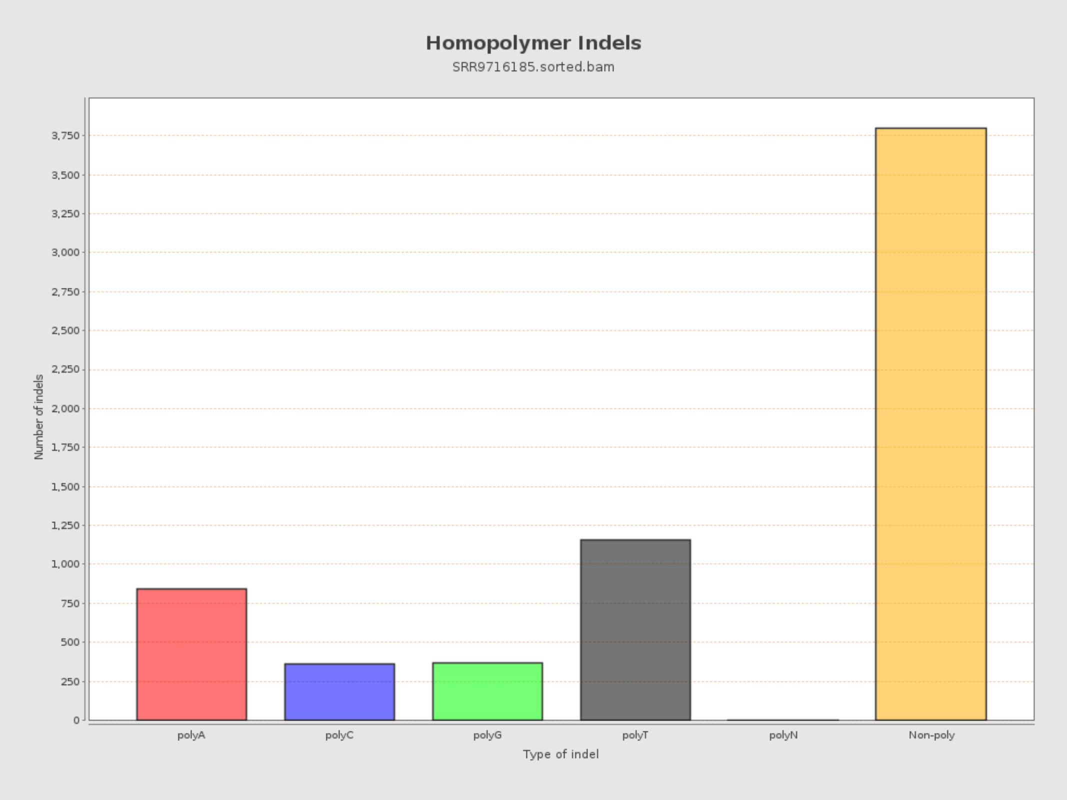
9. Results : Mapped Reads GC-content Distribution



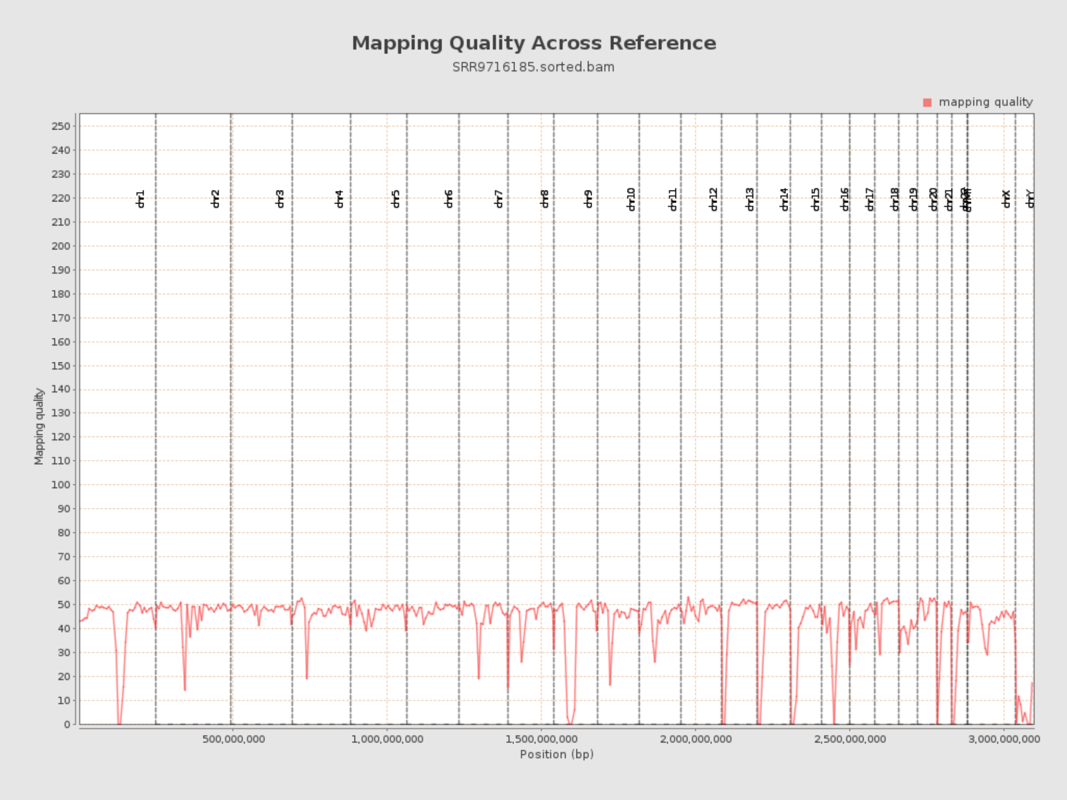
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram