Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:40:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716822.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_SRR9716822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:40:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,207,460
Mapped reads	957,273 / 79.28%
Unmapped reads	250,187 / 20.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,036 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	73,556 / 6.09%
Duplication rate	6.71%
Clipped reads	956,700 / 79.23%

2.2. ACGT Content

Number/percentage of A's	10,532,611 / 20.83%
Number/percentage of C's	9,861,801 / 19.5%
Number/percentage of T's	15,891,078 / 31.42%
Number/percentage of G's	14,283,654 / 28.25%
Number/percentage of N's	961 / 0%
GC Percentage	47.75%

2.3. Coverage

Mean	0.0163

Standard Deviation	0.1682

2.4. Mapping Quality

Mean Mapping Quality	43.14

2.5. Mismatches and indels

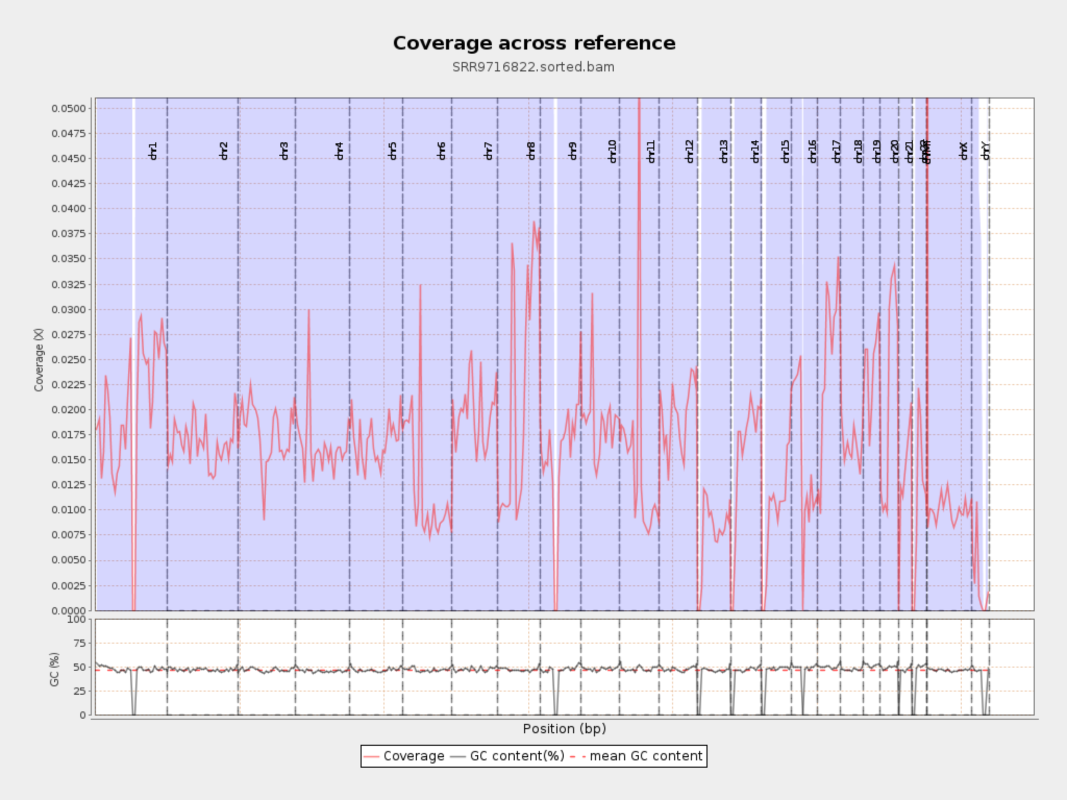
General error rate	0.66%
Mismatches	328,287
Insertions	3,024
Mapped reads with at least one insertion	0.31%
Deletions	7,792
Mapped reads with at least one deletion	0.81%
Homopolymer indels	40.83%

2.6. Chromosome stats

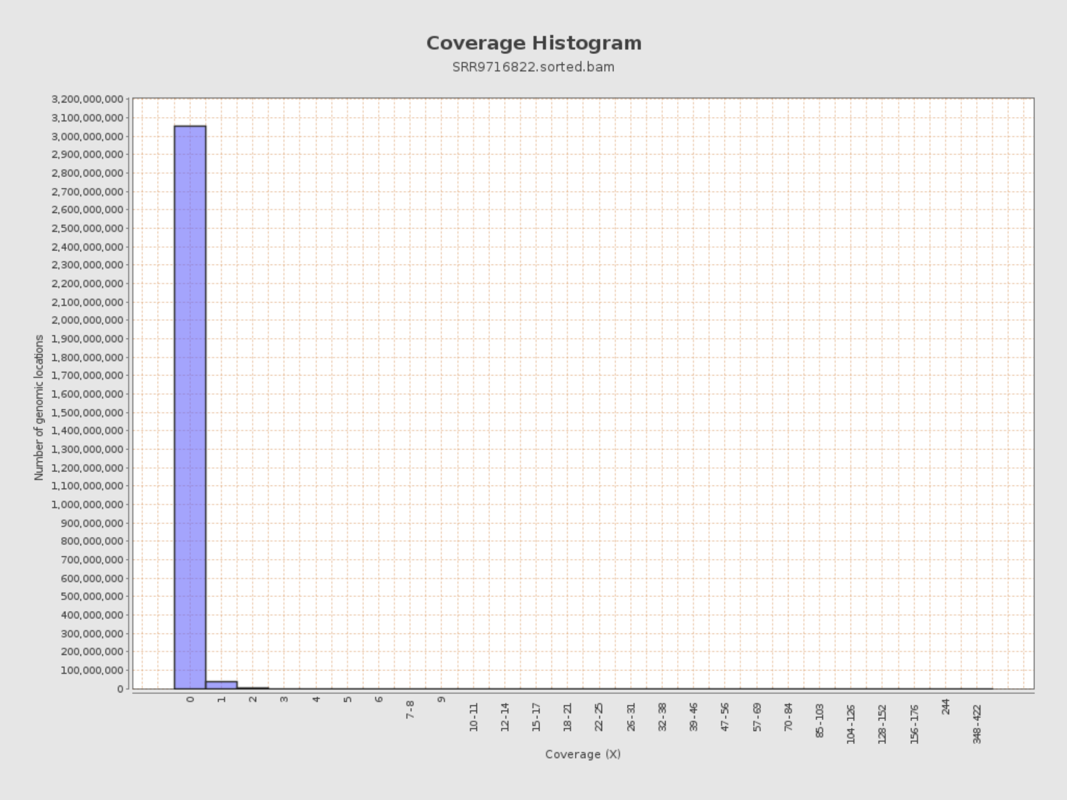
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4982582	0.02	0.2011
chr2	243199373	4044199	0.0166	0.2306
chr3	198022430	3491688	0.0176	0.1531
chr4	191154276	3159420	0.0165	0.1567
chr5	180915260	3067633	0.017	0.1489
chr6	171115067	2111635	0.0123	0.1457
chr7	159138663	3135139	0.0197	0.1907

chr8	146364022	3208002	0.0219	0.1764
chr9	141213431	2114194	0.015	0.1511
chr10	135534747	2565016	0.0189	0.1952
chr11	135006516	2076147	0.0154	0.1596
chr12	133851895	2589610	0.0193	0.1605
chr13	115169878	871742	0.0076	0.0996
chr14	107349540	1648541	0.0154	0.1441
chr15	102531392	998678	0.0097	0.1131
chr16	90354753	1348450	0.0149	0.1492
chr17	81195210	2047266	0.0252	0.1901
chr18	78077248	1276098	0.0163	0.1755
chr19	59128983	1426888	0.0241	0.2252
chr20	63025520	1380070	0.0219	0.1752
chr21	48129895	665138	0.0138	0.1419
chr22	51304566	581880	0.0113	0.1241
chrMT	16571	73225	4.4189	3.4695
chrX	155270560	1555188	0.01	0.1186
chrY	59373566	164952	0.0028	0.094

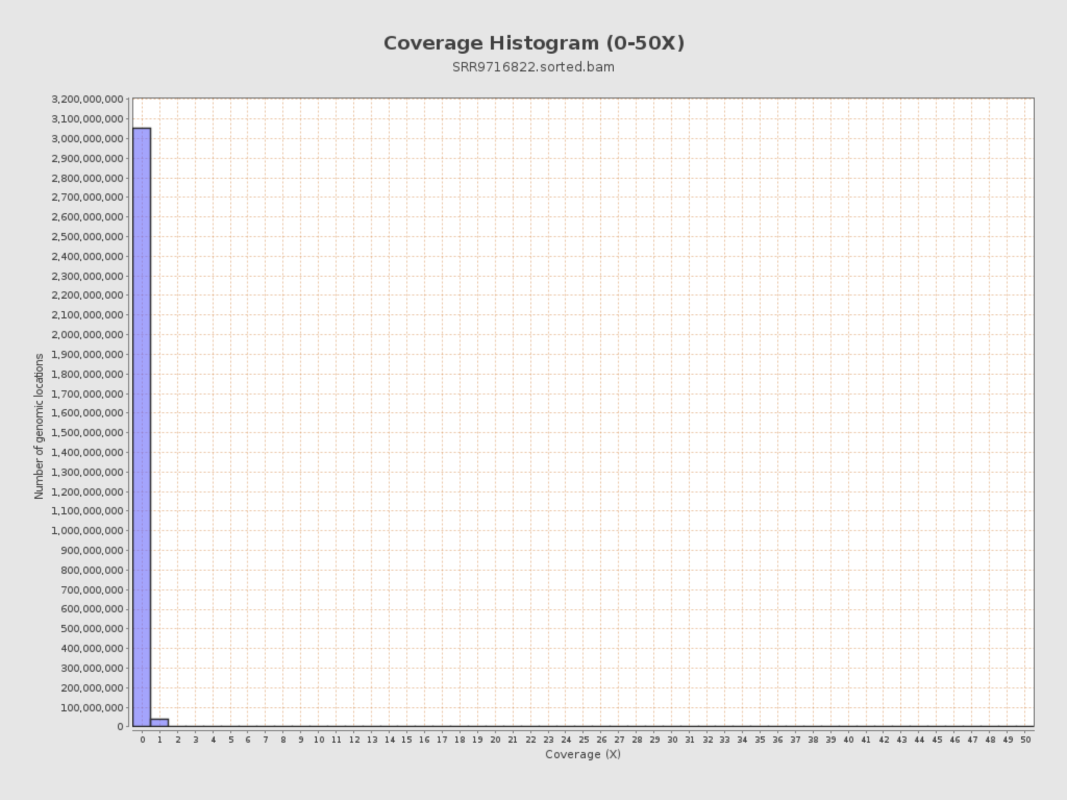
3. Results : Coverage across reference



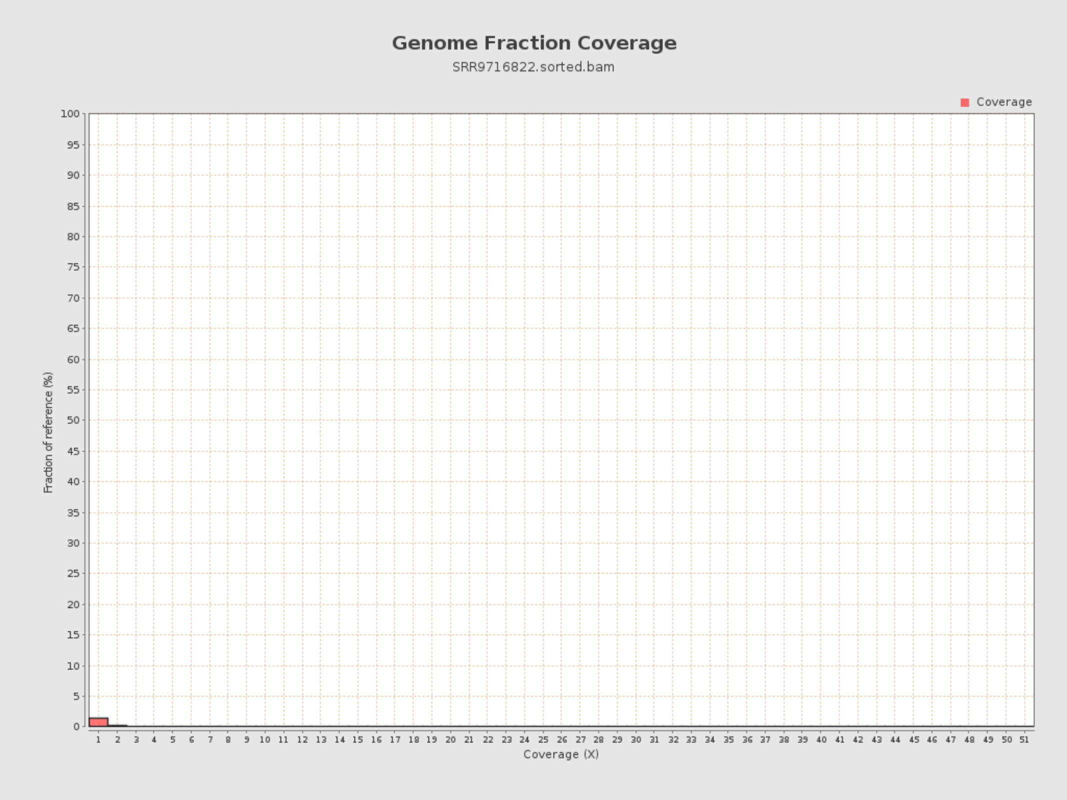
4. Results : Coverage Histogram



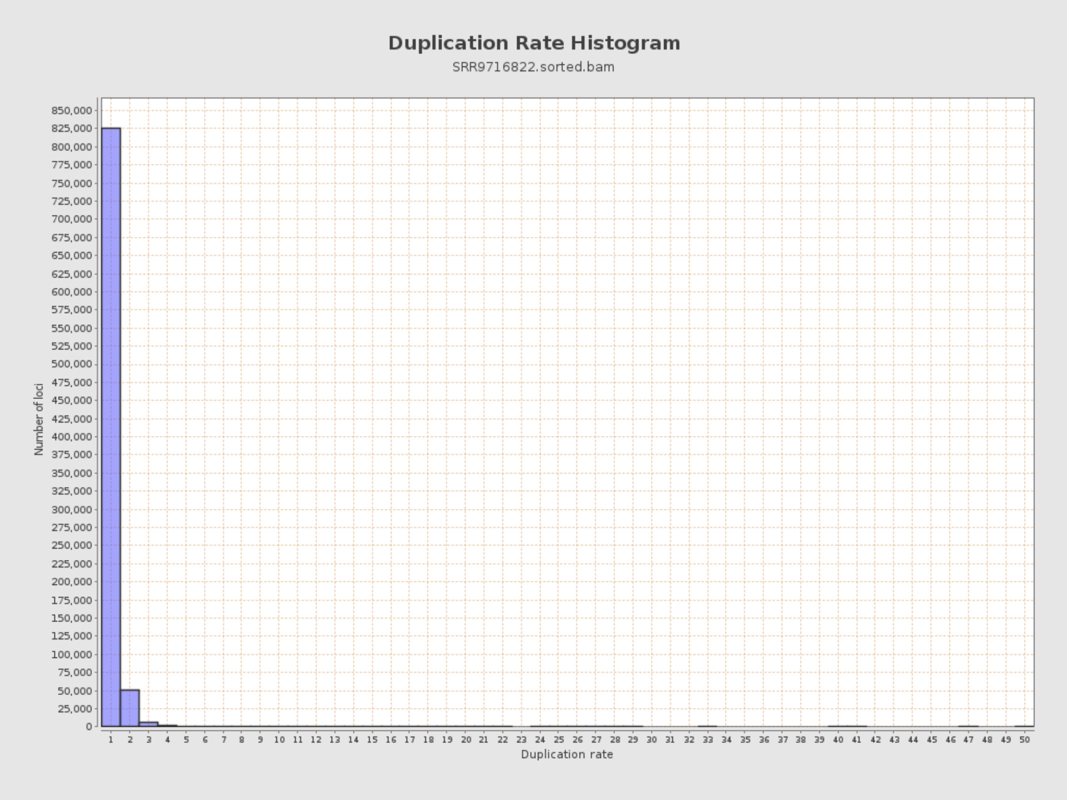
5. Results : Coverage Histogram (0-50X)



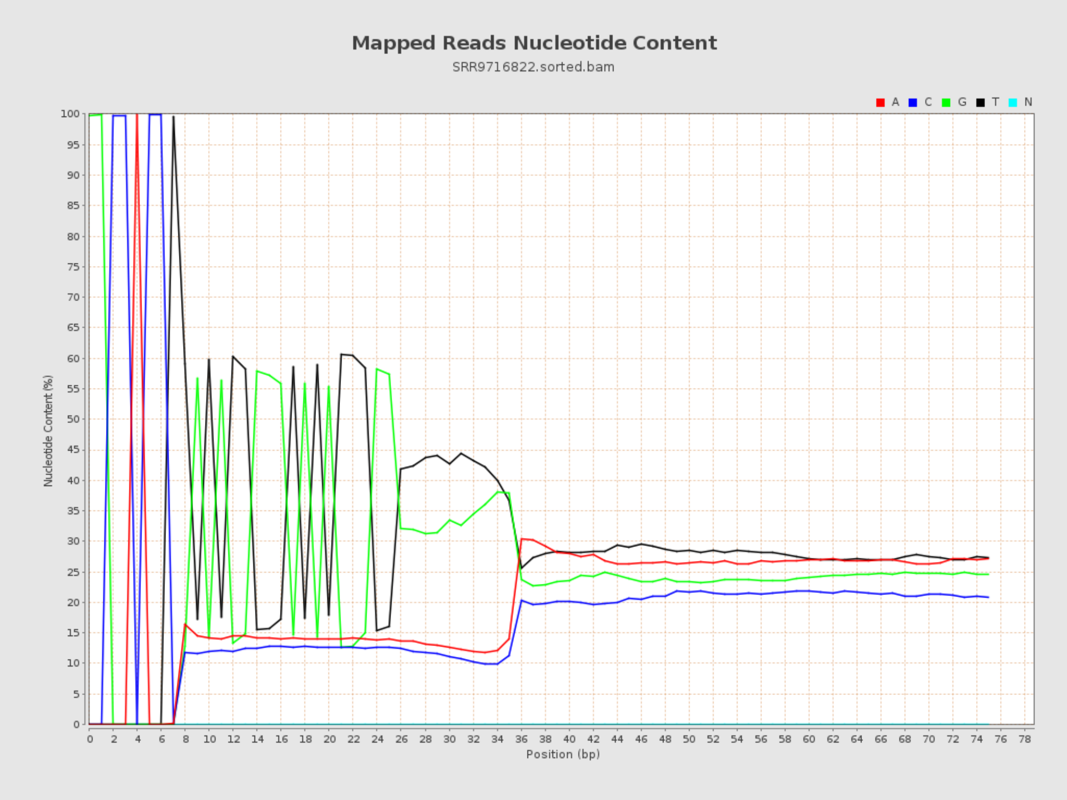
6. Results : Genome Fraction Coverage



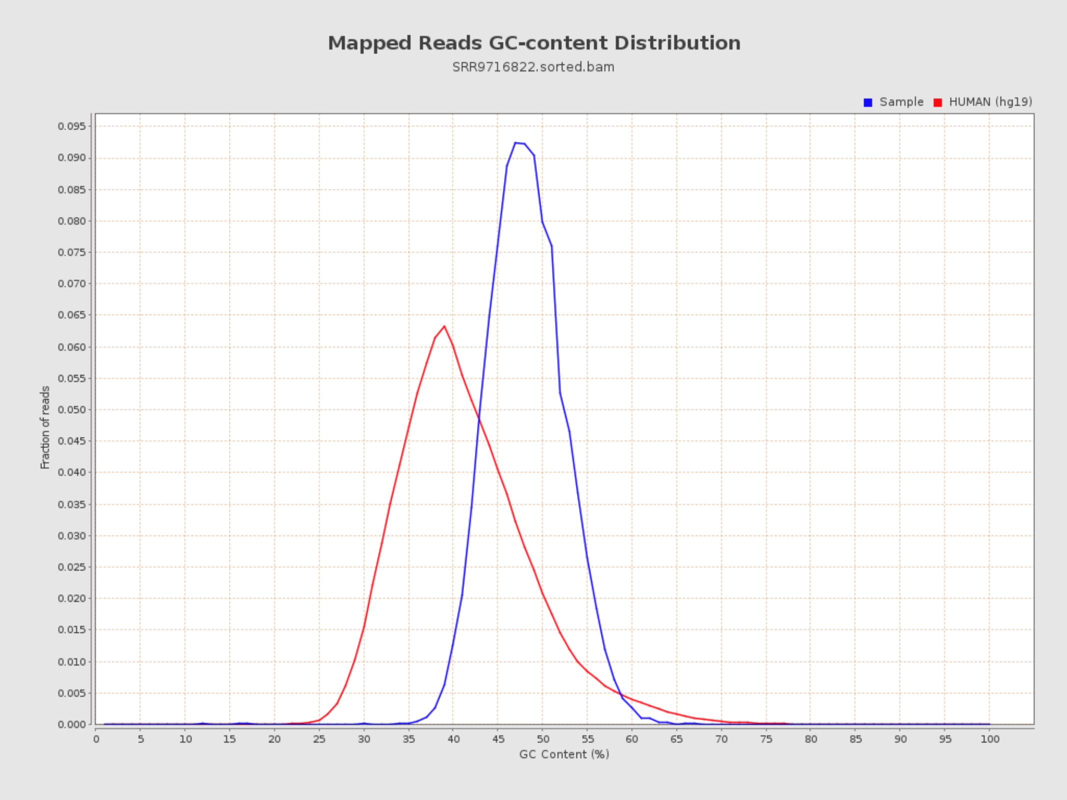
7. Results : Duplication Rate Histogram



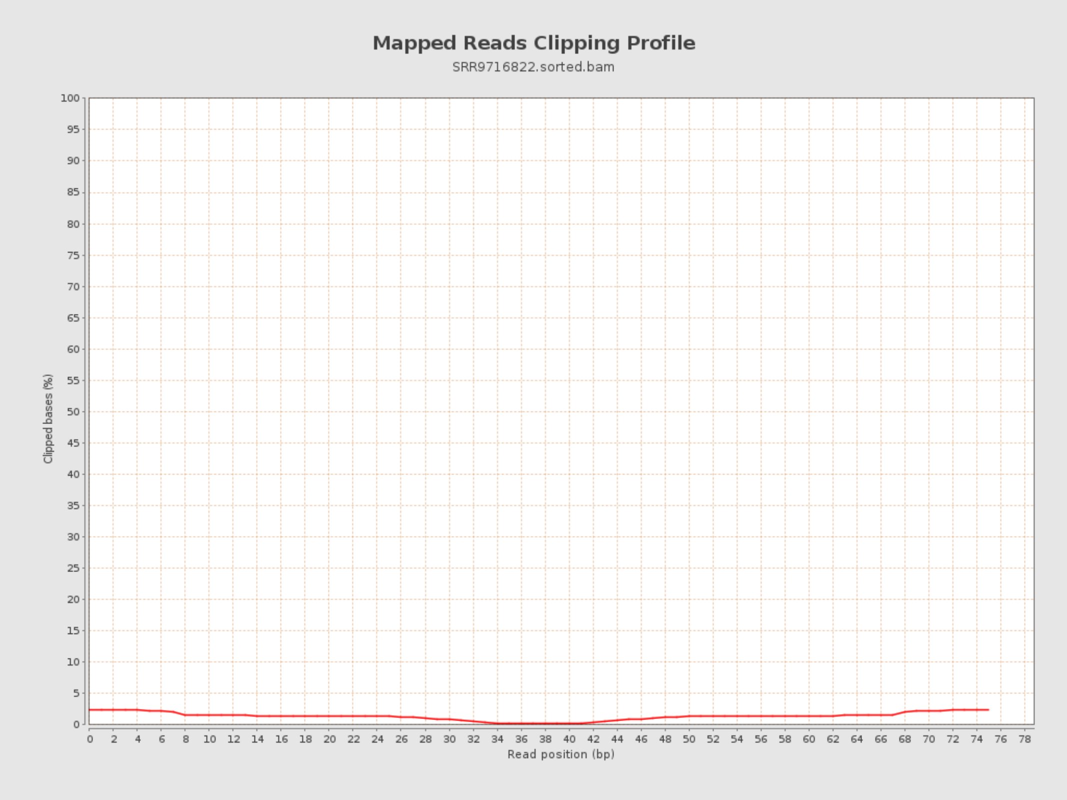
8. Results : Mapped Reads Nucleotide Content



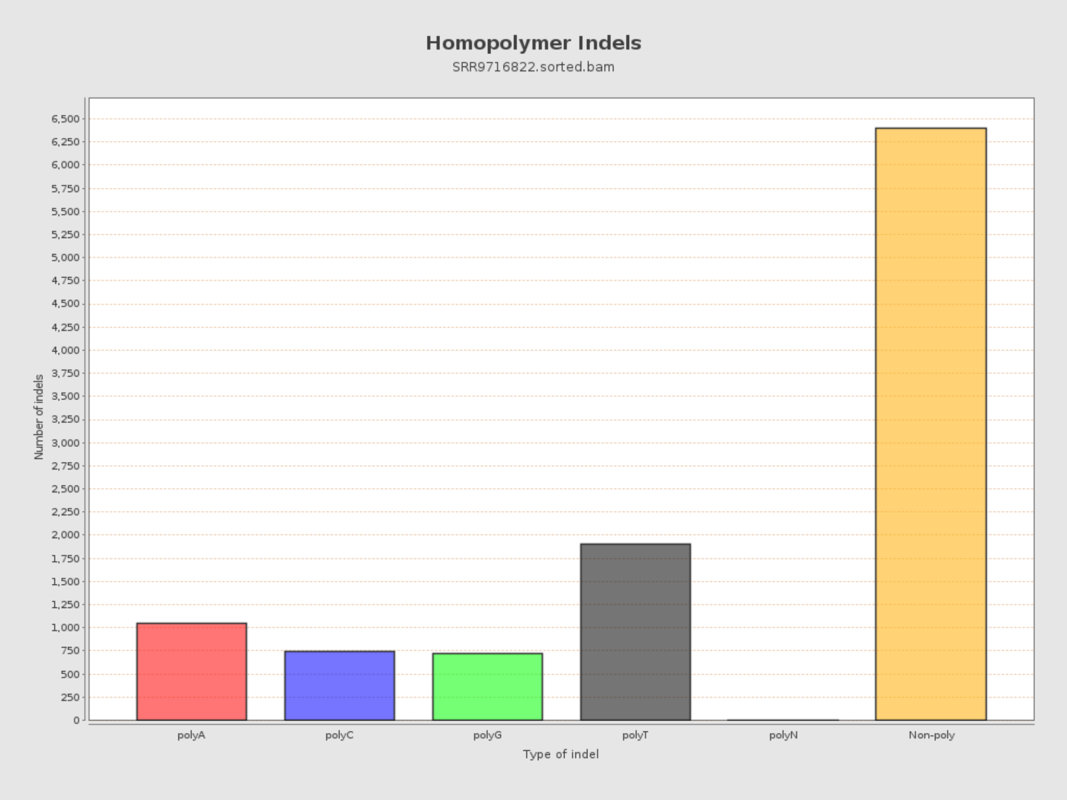
9. Results : Mapped Reads GC-content Distribution



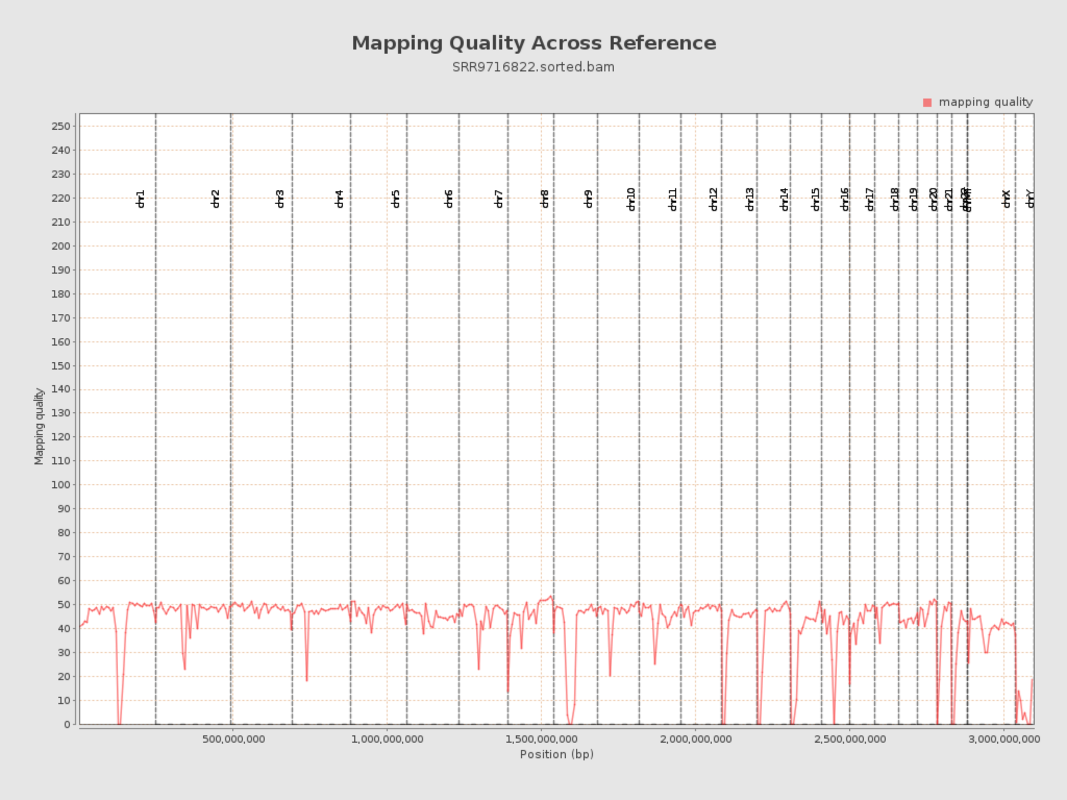
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram