Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:29:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716762.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_SRR9716762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:29:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,348,702
Mapped reads	1,149,418 / 85.22%
Unmapped reads	199,284 / 14.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,072 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	24,233 / 1.8%
Duplication rate	1.53%
Clipped reads	1,151,583 / 85.38%

2.2. ACGT Content

Number/percentage of A's	14,860,717 / 23.33%
Number/percentage of C's	13,462,262 / 21.13%
Number/percentage of T's	19,013,829 / 29.85%
Number/percentage of G's	16,369,663 / 25.69%
Number/percentage of N's	1,604 / 0%
GC Percentage	46.83%

2.3. Coverage

Mean	0.0206

Standard Deviation	0.1802

2.4. Mapping Quality

Mean Mapping Quality	39.76

2.5. Mismatches and indels

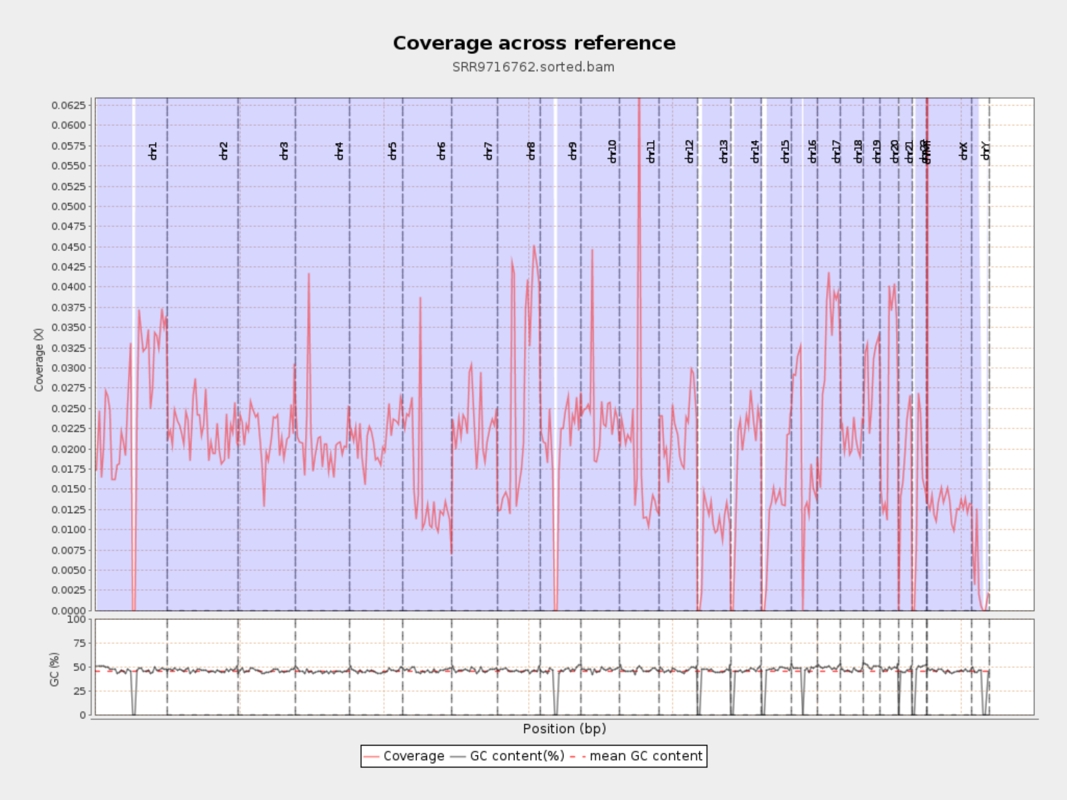
General error rate	0.53%
Mismatches	328,909
Insertions	3,916
Mapped reads with at least one insertion	0.34%
Deletions	10,033
Mapped reads with at least one deletion	0.87%
Homopolymer indels	35.43%

2.6. Chromosome stats

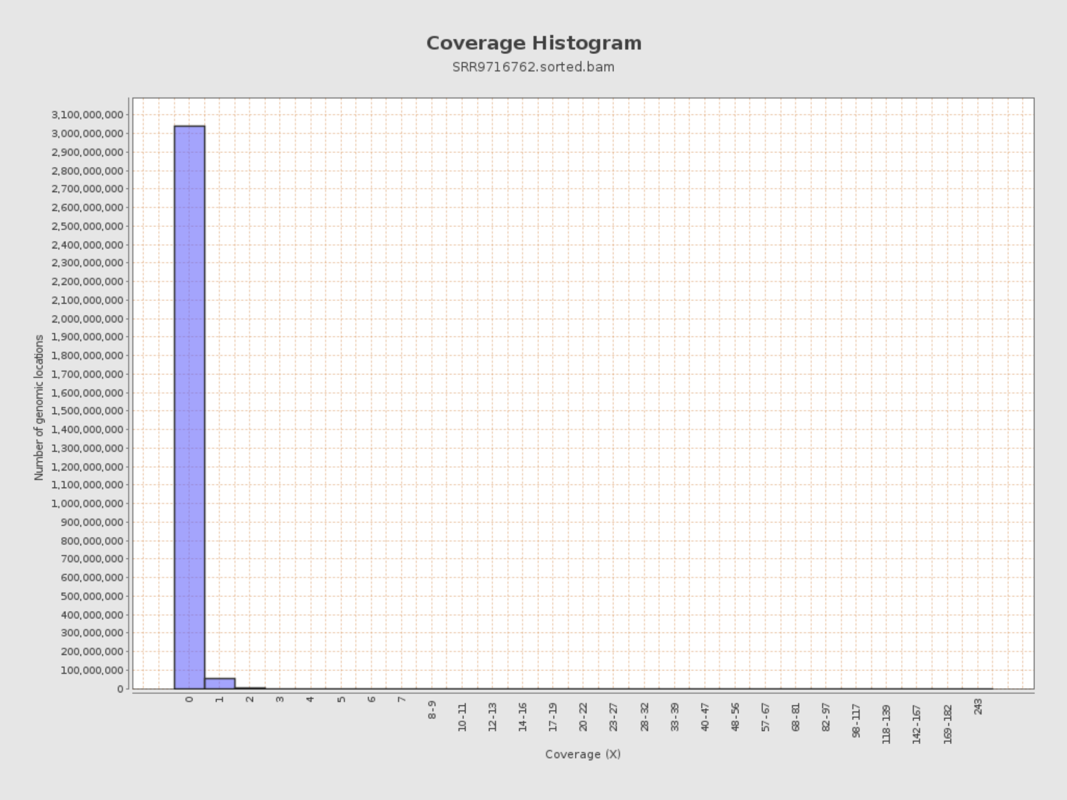
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6269635	0.0252	0.2232
chr2	243199373	5425670	0.0223	0.2138
chr3	198022430	4329430	0.0219	0.1655
chr4	191154276	4057181	0.0212	0.181
chr5	180915260	3879189	0.0214	0.1591
chr6	171115067	2678457	0.0157	0.1395
chr7	159138663	3677386	0.0231	0.2068

chr8	146364022	3906150	0.0267	0.1864
chr9	141213431	2793227	0.0198	0.1667
chr10	135534747	3328135	0.0246	0.2499
chr11	135006516	2689094	0.0199	0.1855
chr12	133851895	2996956	0.0224	0.1639
chr13	115169878	1125144	0.0098	0.1071
chr14	107349540	2051742	0.0191	0.1531
chr15	102531392	1277467	0.0125	0.1215
chr16	90354753	1733263	0.0192	0.1599
chr17	81195210	2602276	0.032	0.2053
chr18	78077248	1654852	0.0212	0.2024
chr19	59128983	1753244	0.0297	0.2148
chr20	63025520	1652208	0.0262	0.1817
chr21	48129895	882919	0.0183	0.1606
chr22	51304566	725510	0.0141	0.1317
chrMT	16571	24676	1.4891	1.8278
chrX	155270560	2010348	0.0129	0.1338
chrY	59373566	200601	0.0034	0.1057

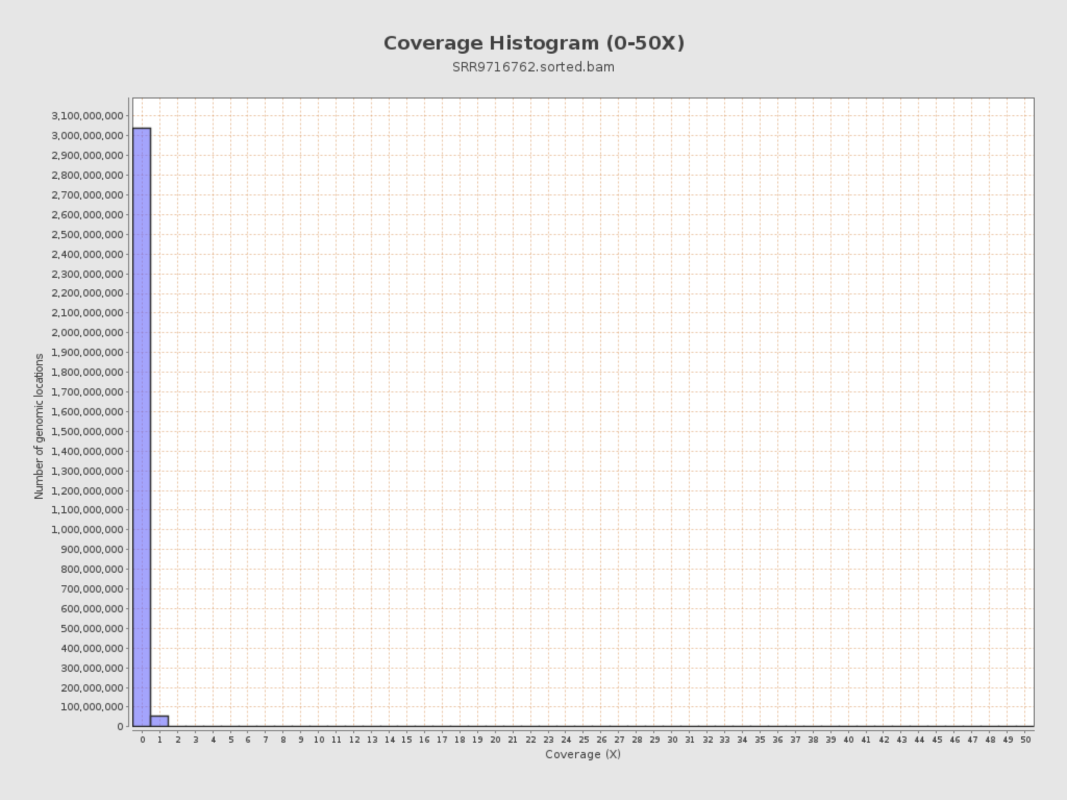
3. Results : Coverage across reference



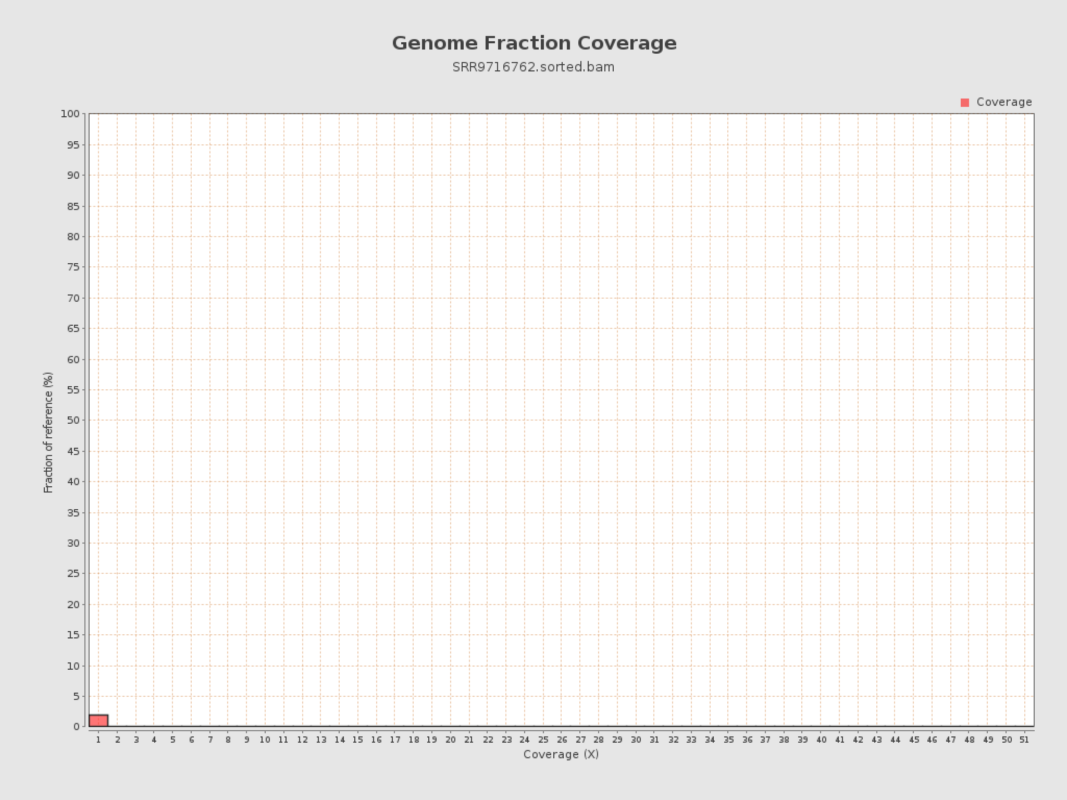
4. Results : Coverage Histogram



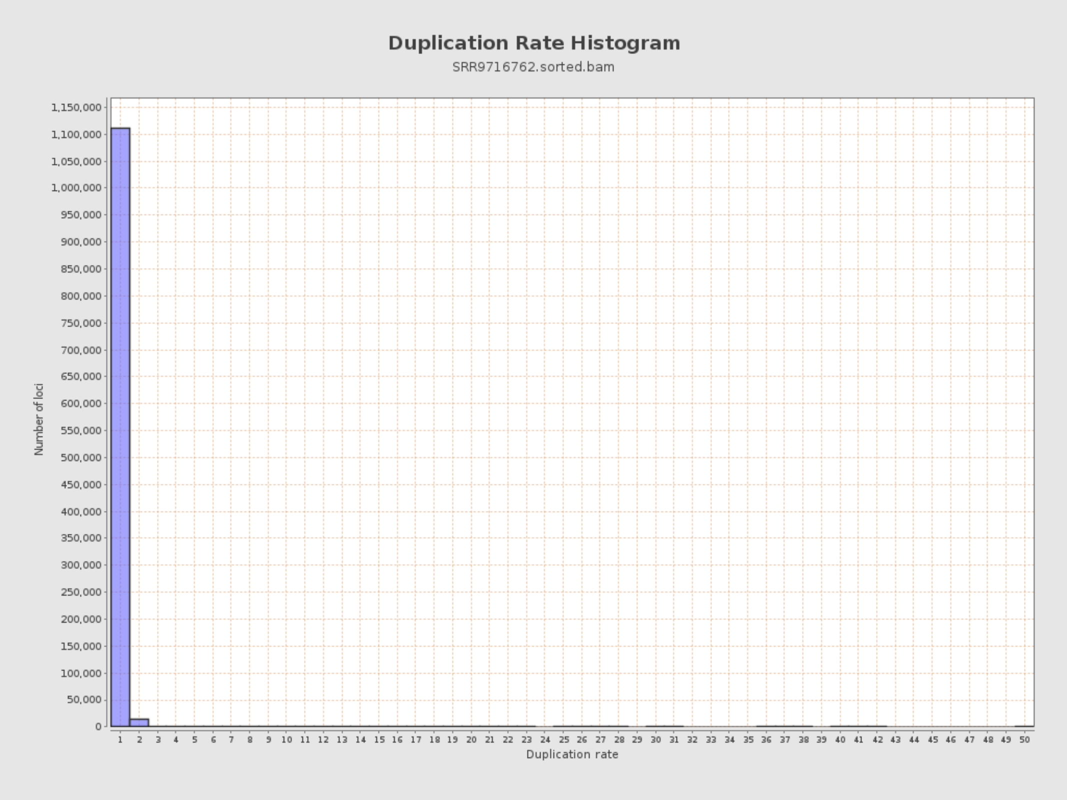
5. Results : Coverage Histogram (0-50X)



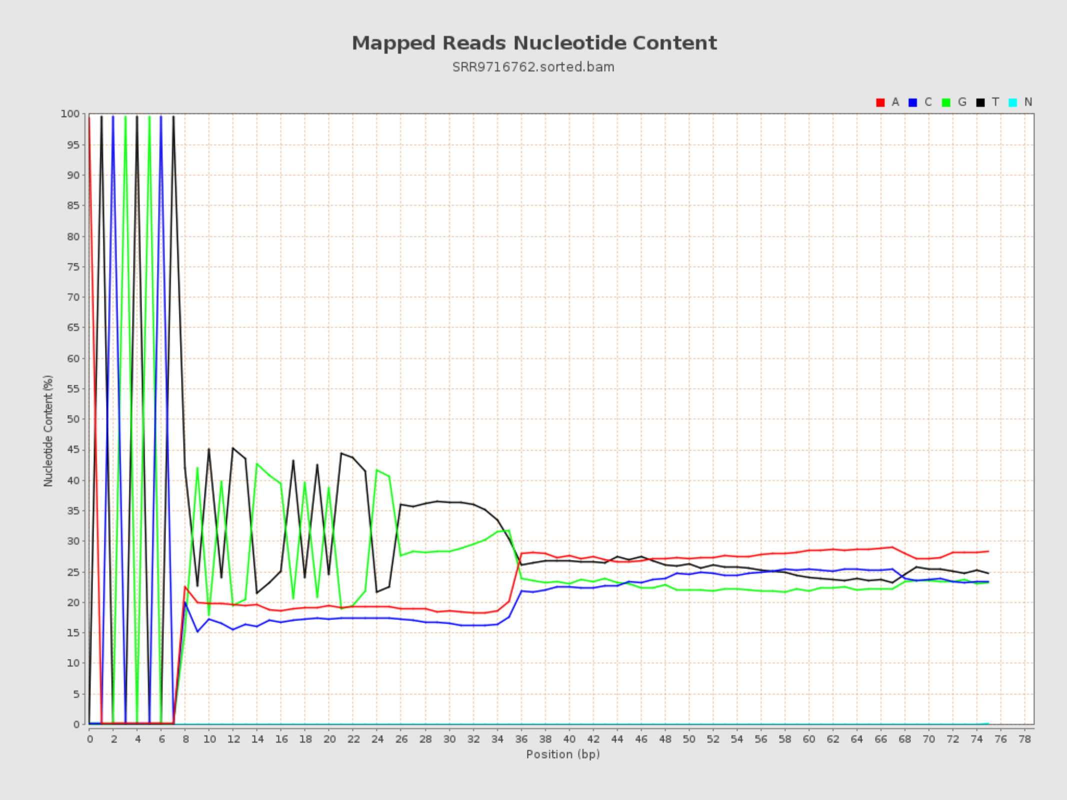
6. Results : Genome Fraction Coverage



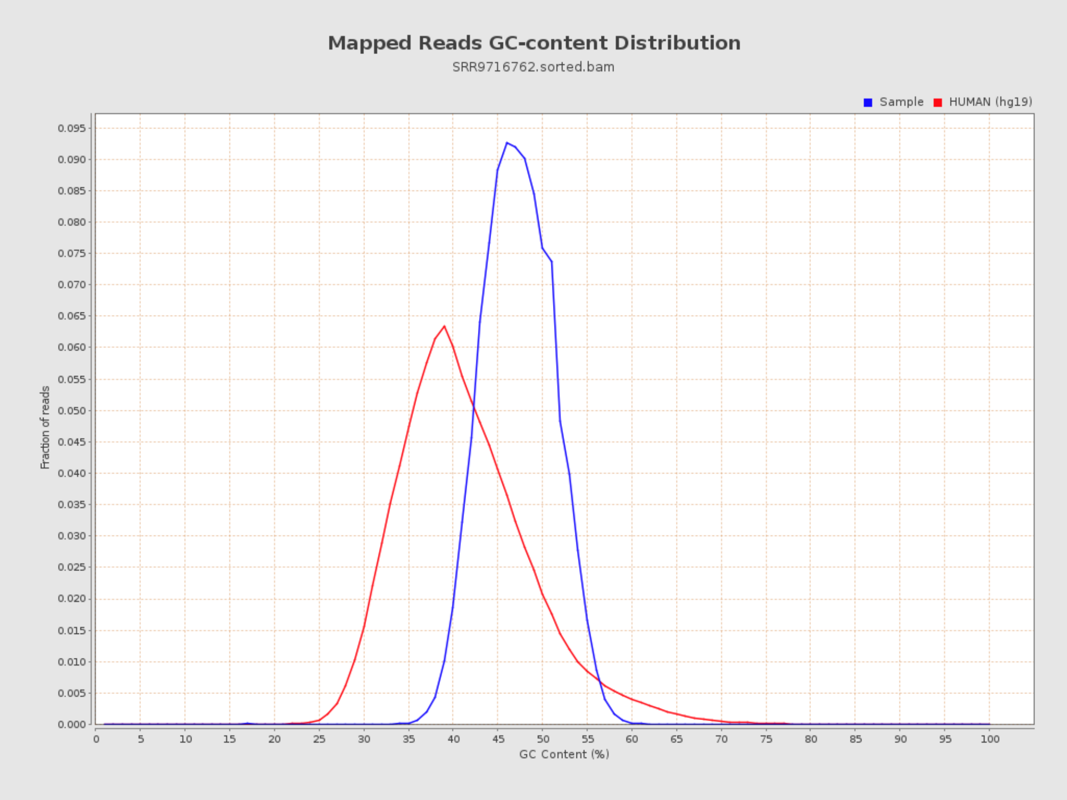
7. Results : Duplication Rate Histogram



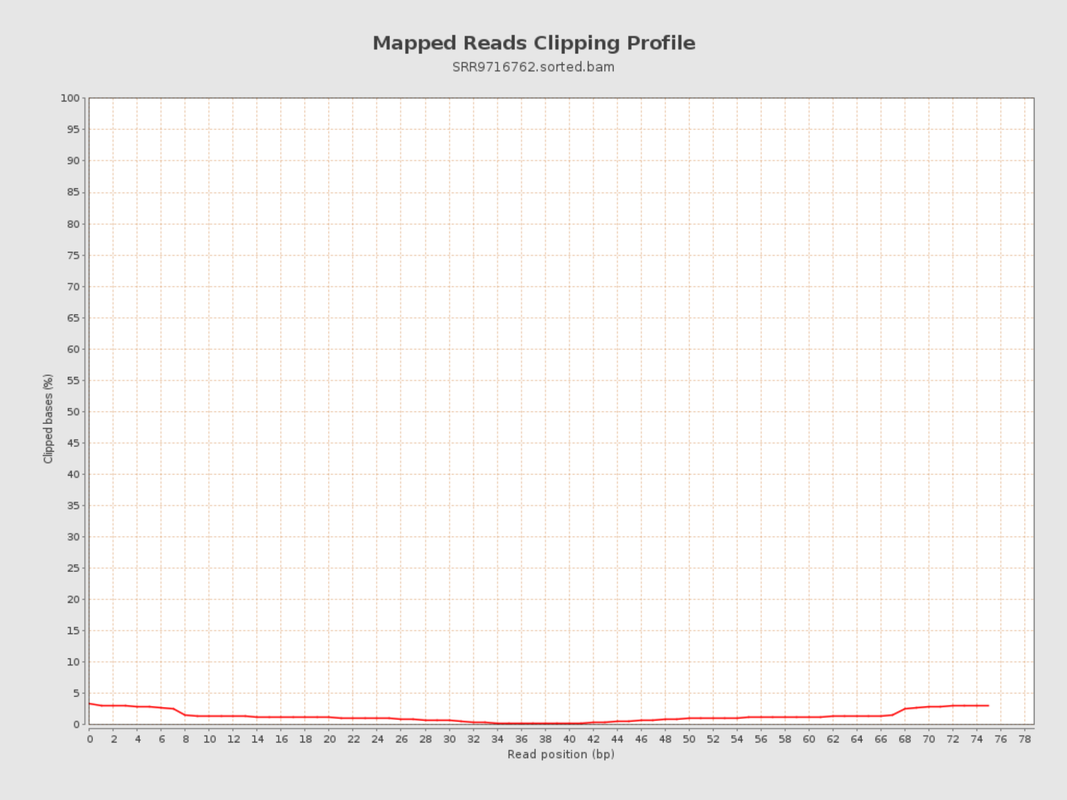
8. Results : Mapped Reads Nucleotide Content



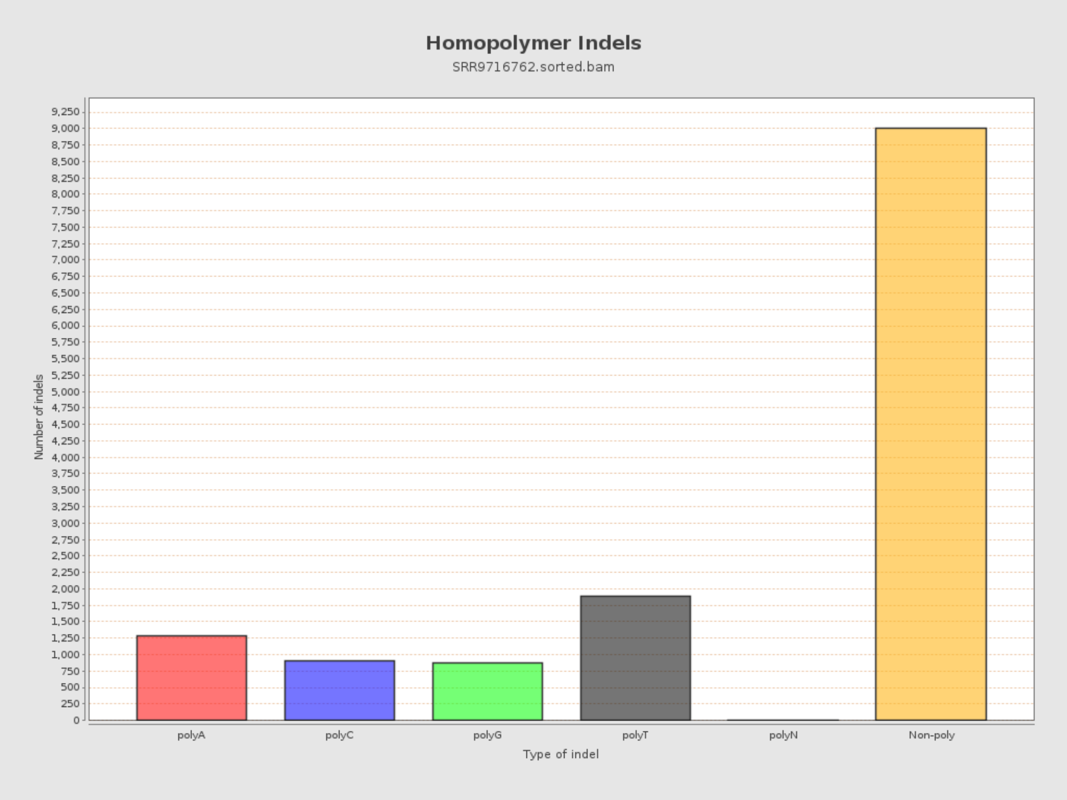
9. Results : Mapped Reads GC-content Distribution



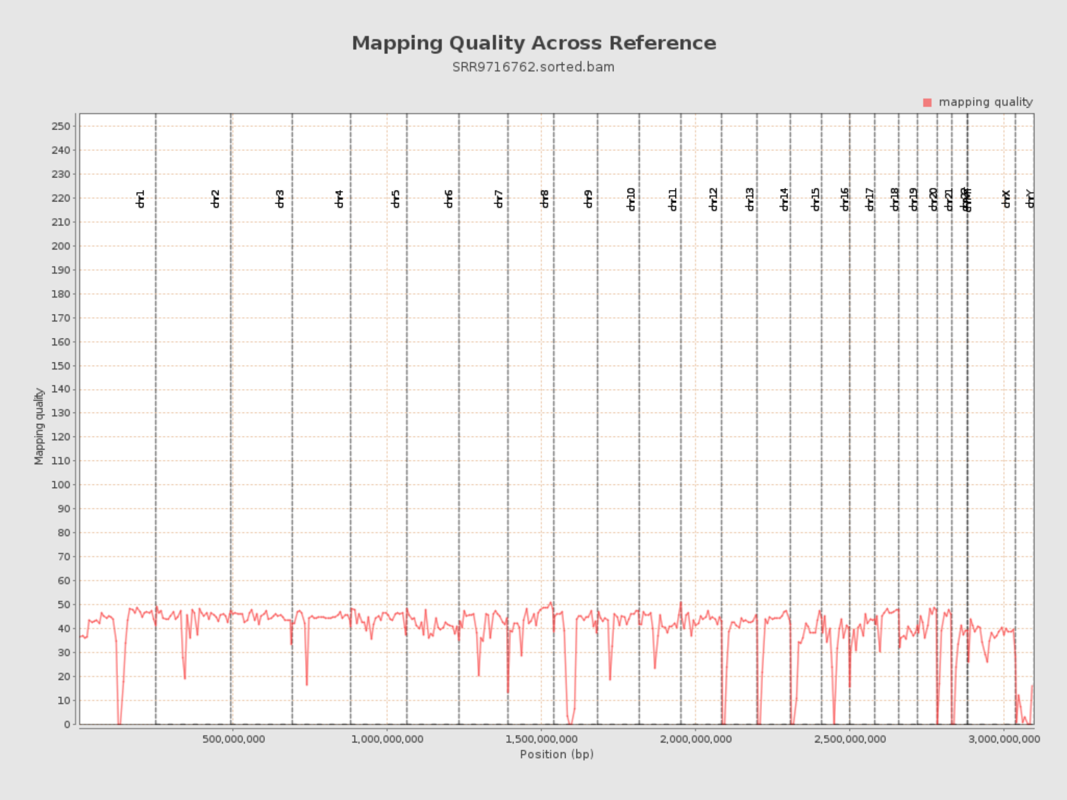
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram