Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 04:51:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716672.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_SRR9716672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 04:51:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,134,139
Mapped reads	994,313 / 87.67%
Unmapped reads	139,826 / 12.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,667 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	23,087 / 2.04%
Duplication rate	1.64%
Clipped reads	995,111 / 87.74%

2.2. ACGT Content

Number/percentage of A's	14,212,493 / 25.26%
Number/percentage of C's	10,384,331 / 18.46%
Number/percentage of T's	18,180,701 / 32.31%
Number/percentage of G's	13,483,791 / 23.97%
Number/percentage of N's	342 / 0%
GC Percentage	42.42%

2.3. Coverage

Mean	0.0182

Standard Deviation	0.1854

2.4. Mapping Quality

Mean Mapping Quality	43.68

2.5. Mismatches and indels

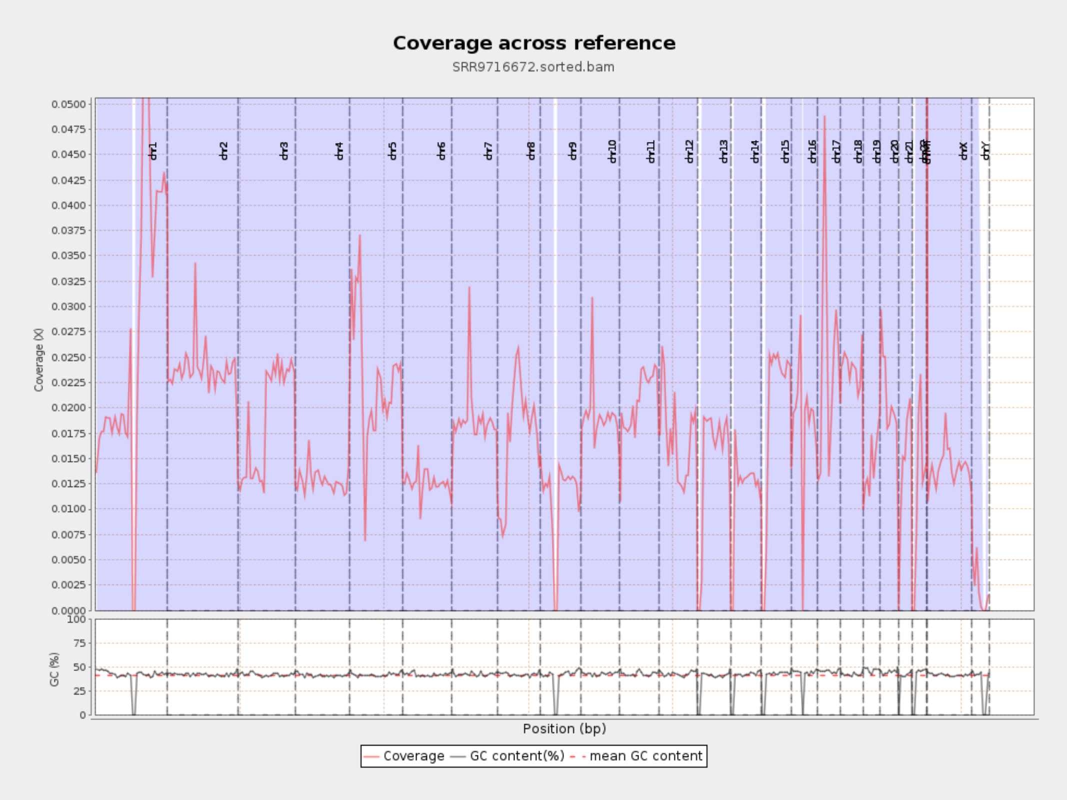
General error rate	0.53%
Mismatches	289,204
Insertions	3,812
Mapped reads with at least one insertion	0.38%
Deletions	10,221
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.41%

2.6. Chromosome stats

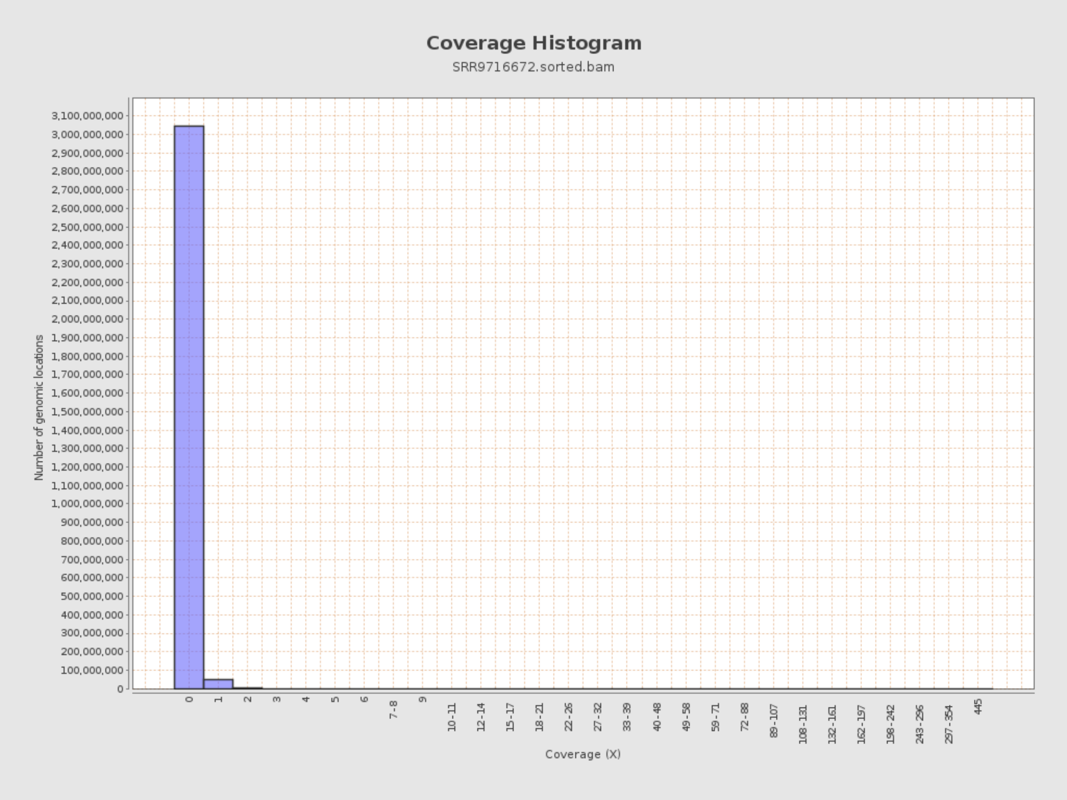
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6739157	0.027	0.2886
chr2	243199373	5812747	0.0239	0.2608
chr3	198022430	3724316	0.0188	0.1447
chr4	191154276	2449645	0.0128	0.1229
chr5	180915260	4165401	0.023	0.1594
chr6	171115067	2156527	0.0126	0.133
chr7	159138663	3027985	0.019	0.2446

chr8	146364022	2568183	0.0175	0.159
chr9	141213431	1571790	0.0111	0.1402
chr10	135534747	2619264	0.0193	0.1848
chr11	135006516	2809134	0.0208	0.1951
chr12	133851895	2263940	0.0169	0.1377
chr13	115169878	1700035	0.0148	0.1275
chr14	107349540	1245701	0.0116	0.1162
chr15	102531392	2010500	0.0196	0.1527
chr16	90354753	1661278	0.0184	0.1511
chr17	81195210	2045749	0.0252	0.1765
chr18	78077248	1867863	0.0239	0.2924
chr19	59128983	854837	0.0145	0.2102
chr20	63025520	1322820	0.021	0.1532
chr21	48129895	707585	0.0147	0.1299
chr22	51304566	622490	0.0121	0.1155
chrMT	16571	1762	0.1063	0.3464
chrX	155270560	2205596	0.0142	0.1456
chrY	59373566	123202	0.0021	0.0572

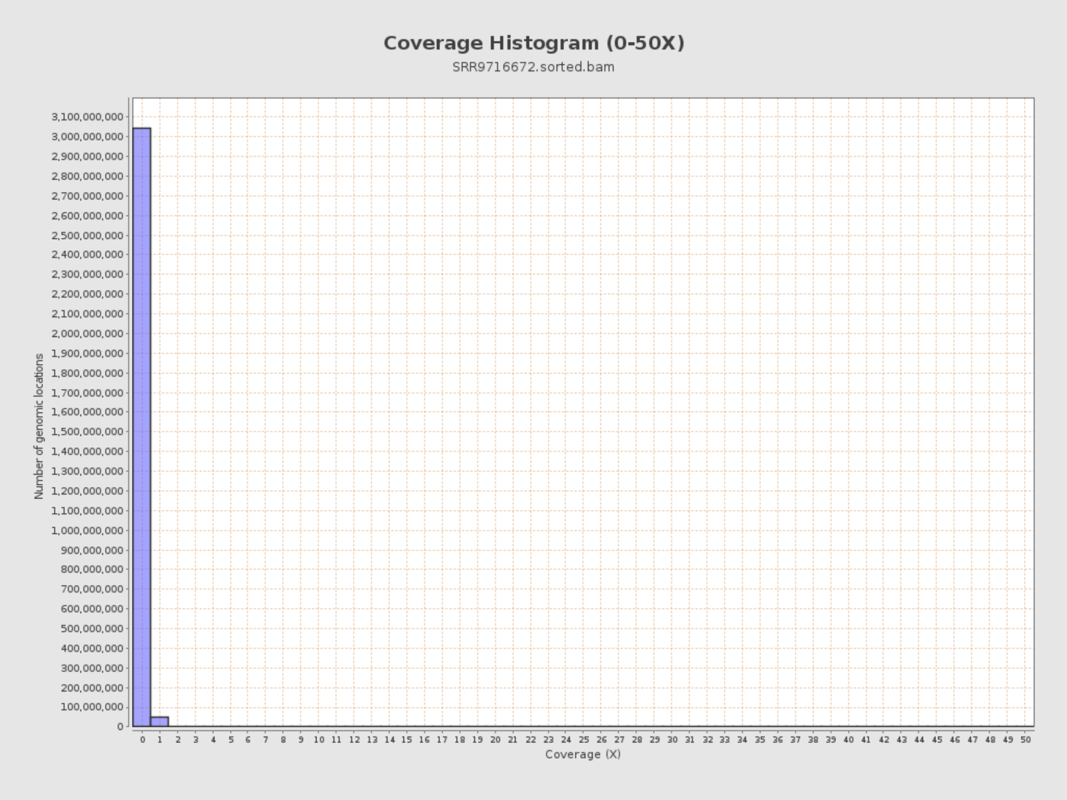
3. Results : Coverage across reference



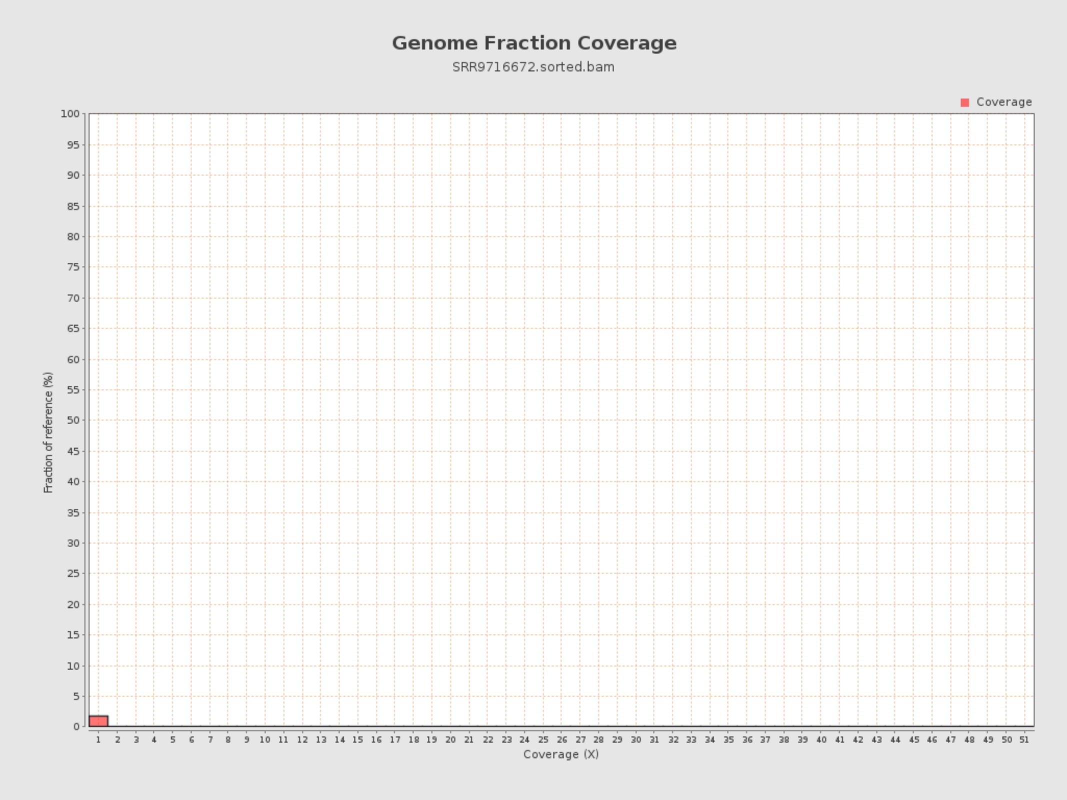
4. Results : Coverage Histogram



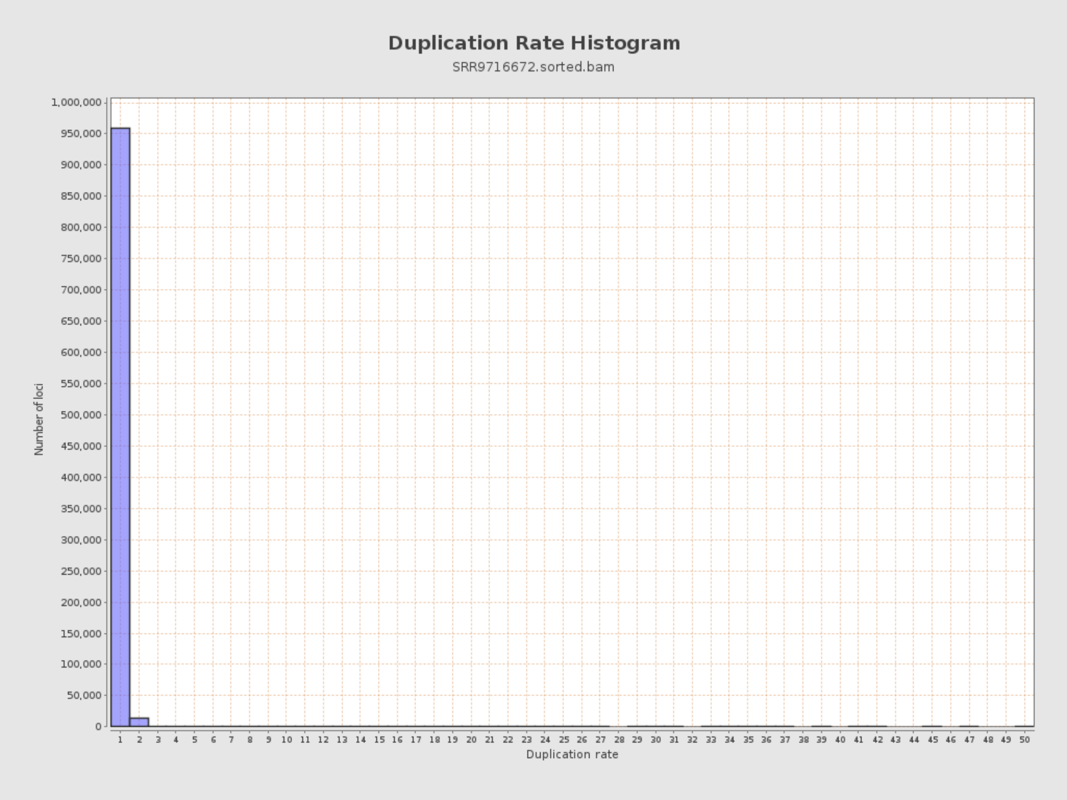
5. Results : Coverage Histogram (0-50X)



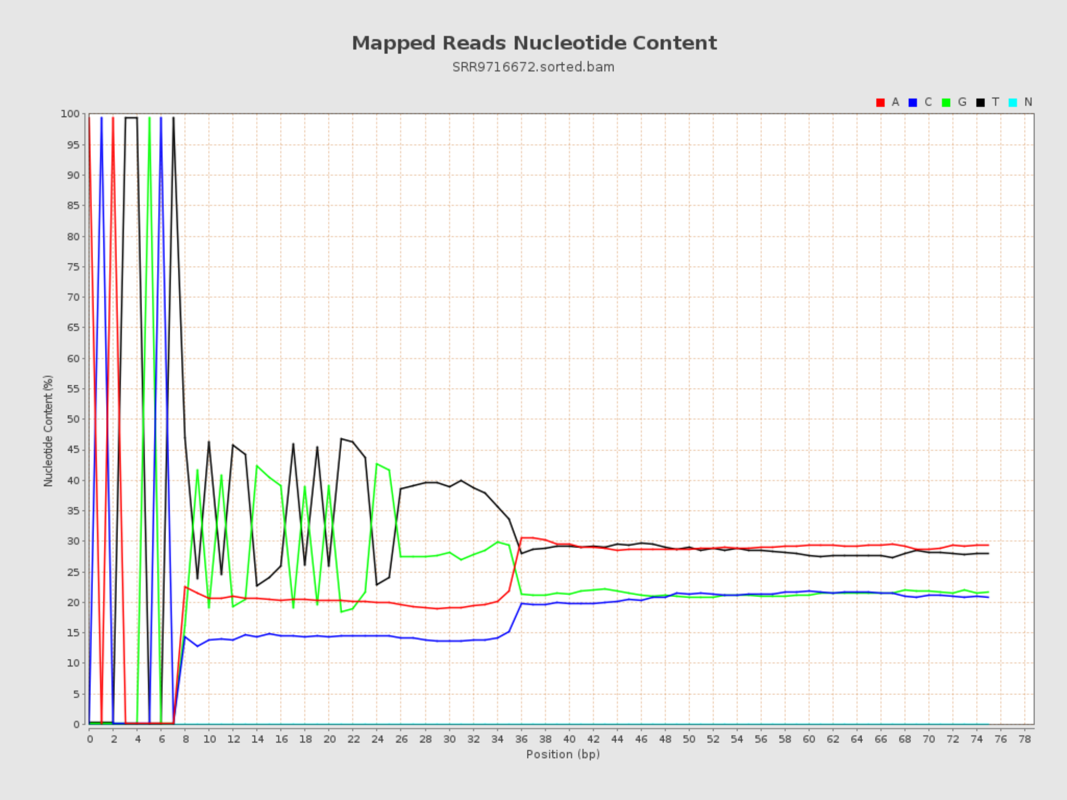
6. Results : Genome Fraction Coverage



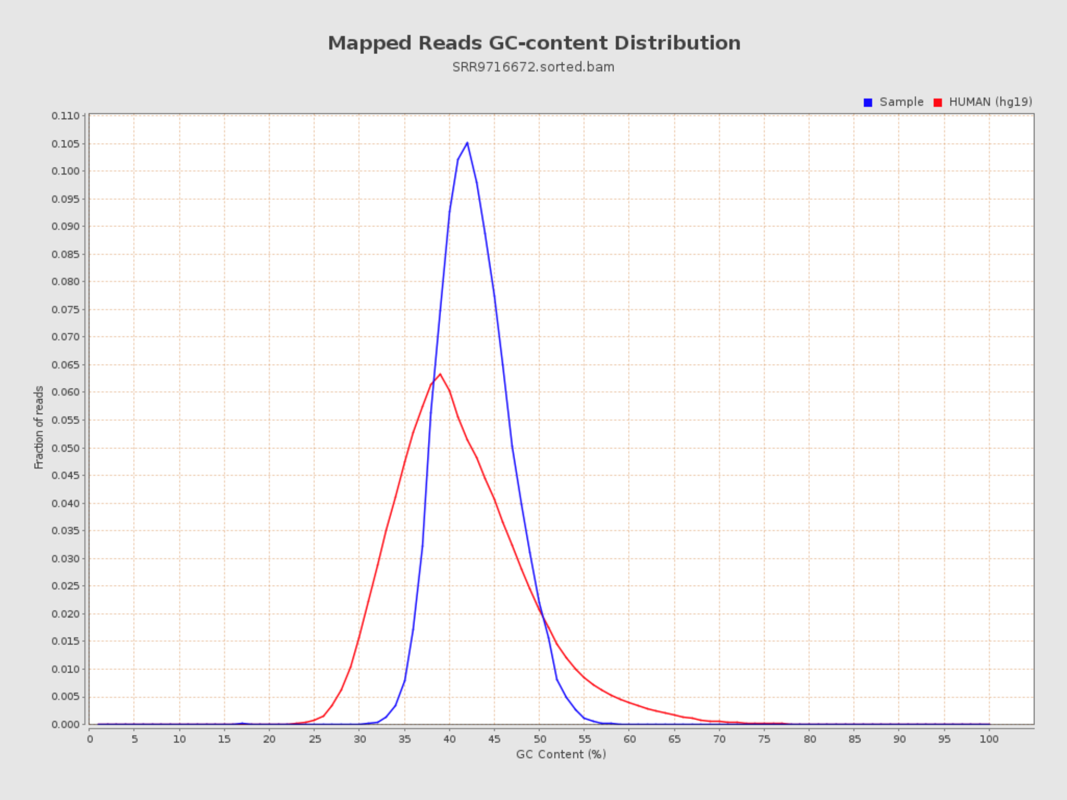
7. Results : Duplication Rate Histogram



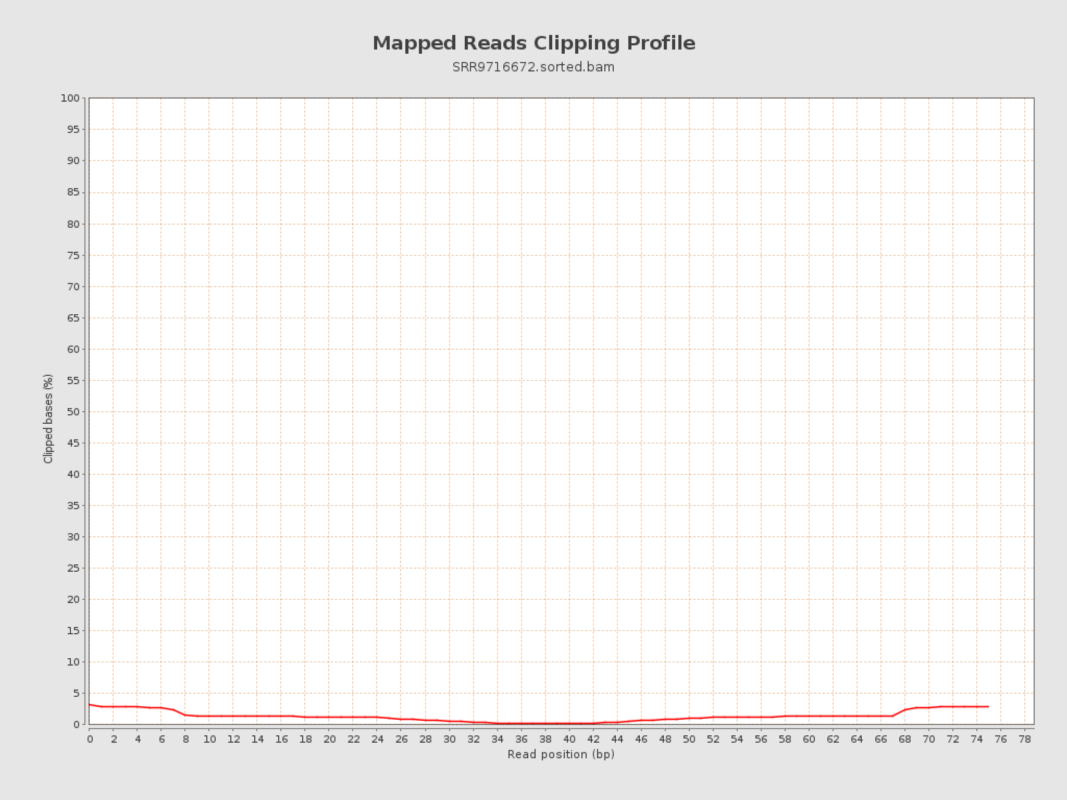
8. Results : Mapped Reads Nucleotide Content



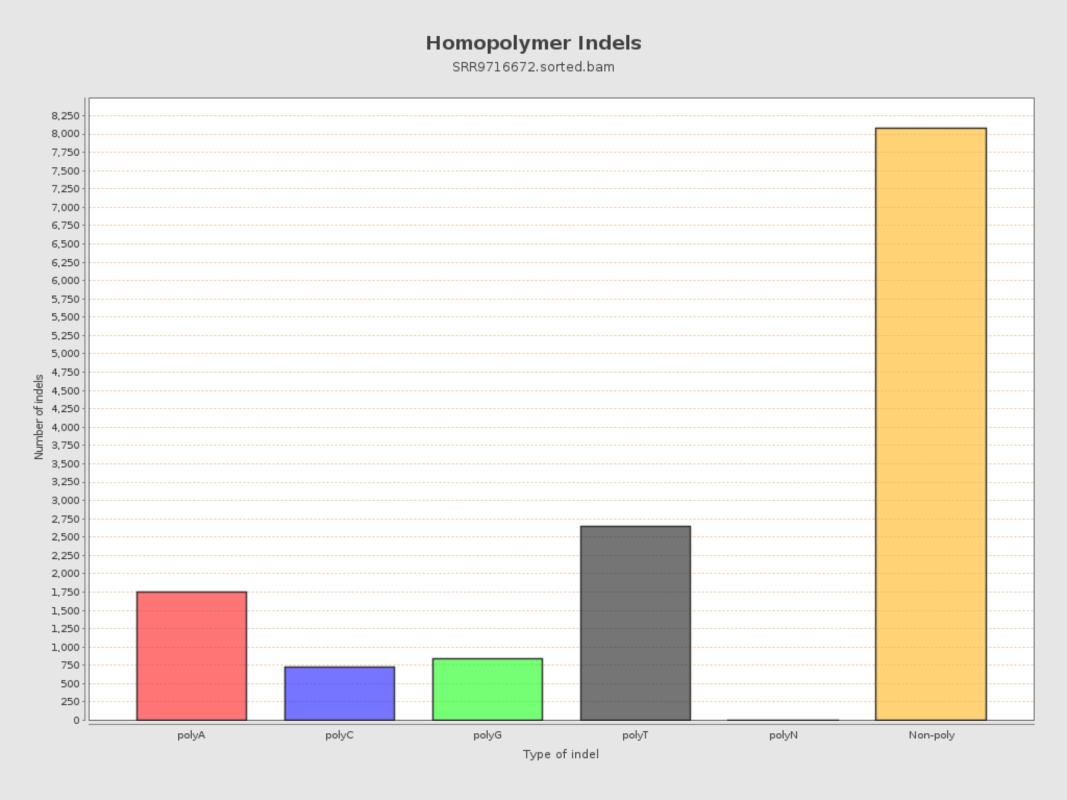
9. Results : Mapped Reads GC-content Distribution



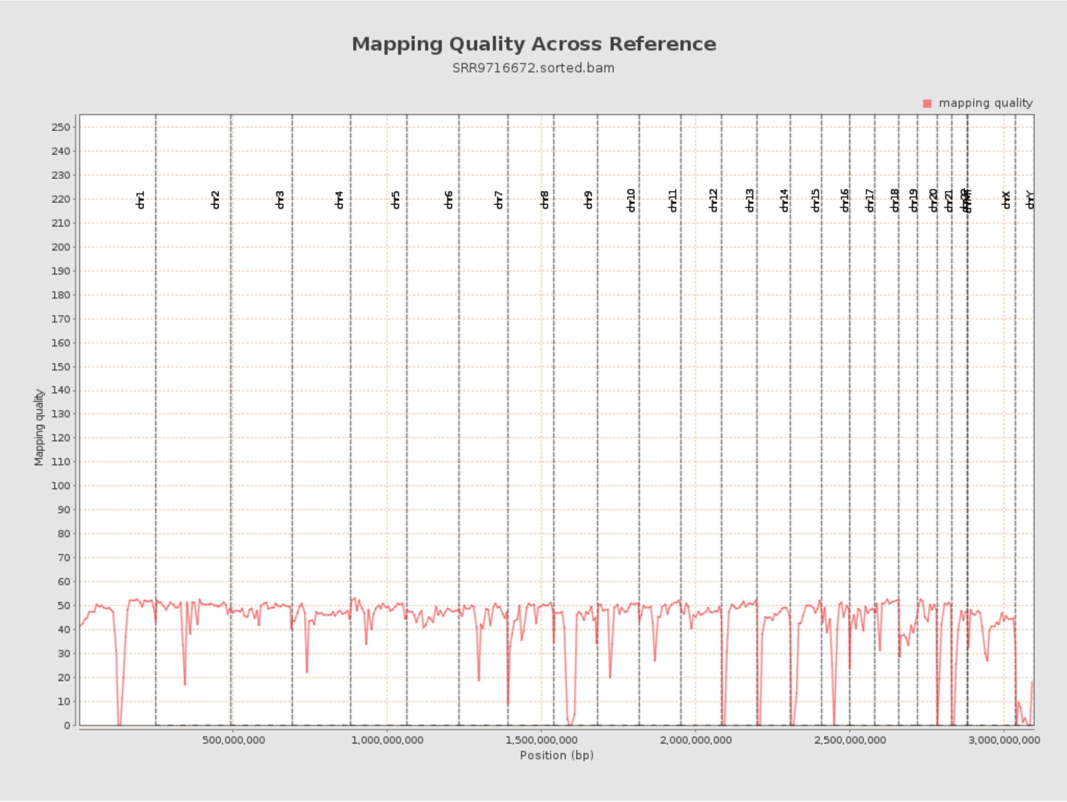
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram