Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:47:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716617.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_SRR9716617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716617.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:47:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,671,747
Mapped reads	3,235,364 / 88.12%
Unmapped reads	436,383 / 11.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,801 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	127,432 / 3.47%
Duplication rate	2.83%
Clipped reads	3,242,003 / 88.3%

2.2. ACGT Content

Number/percentage of A's	43,290,802 / 23.71%
Number/percentage of C's	36,235,531 / 19.84%
Number/percentage of T's	56,827,786 / 31.12%
Number/percentage of G's	46,245,415 / 25.33%
Number/percentage of N's	1,383 / 0%
GC Percentage	45.17%

2.3. Coverage

Mean	0.059

Standard Deviation	0.4181

2.4. Mapping Quality

Mean Mapping Quality	41.83

2.5. Mismatches and indels

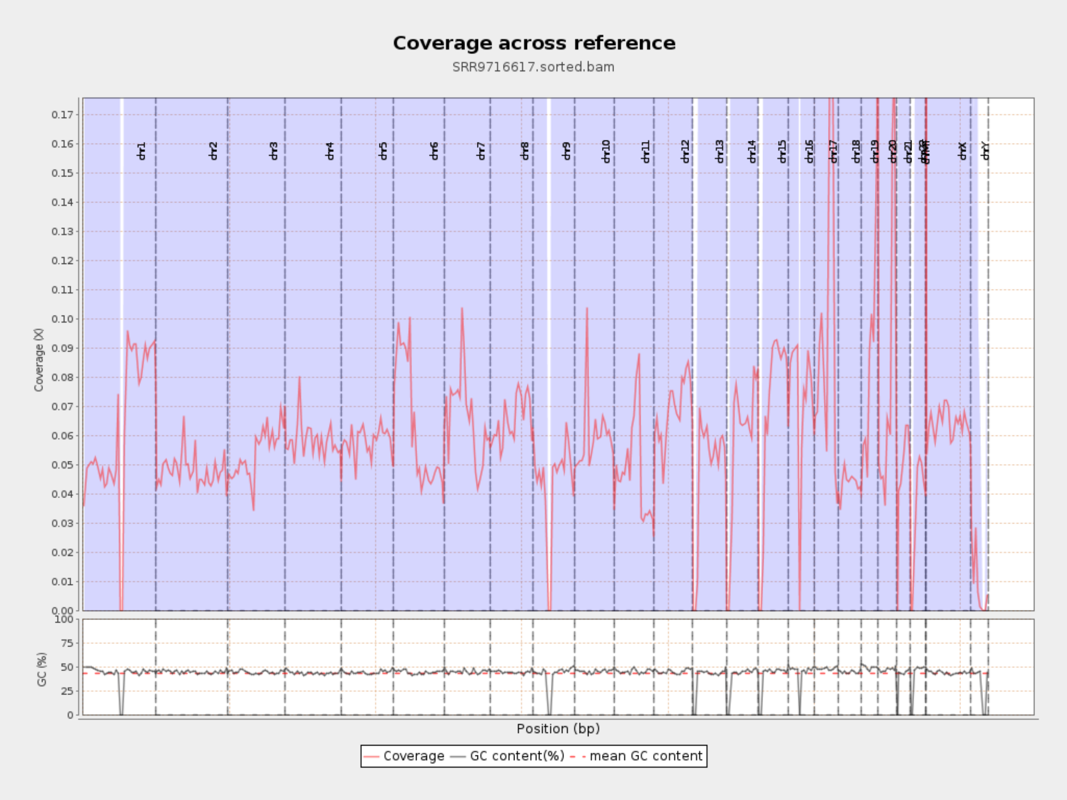
General error rate	0.53%
Mismatches	954,292
Insertions	11,668
Mapped reads with at least one insertion	0.36%
Deletions	33,270
Mapped reads with at least one deletion	1.02%
Homopolymer indels	40.25%

2.6. Chromosome stats

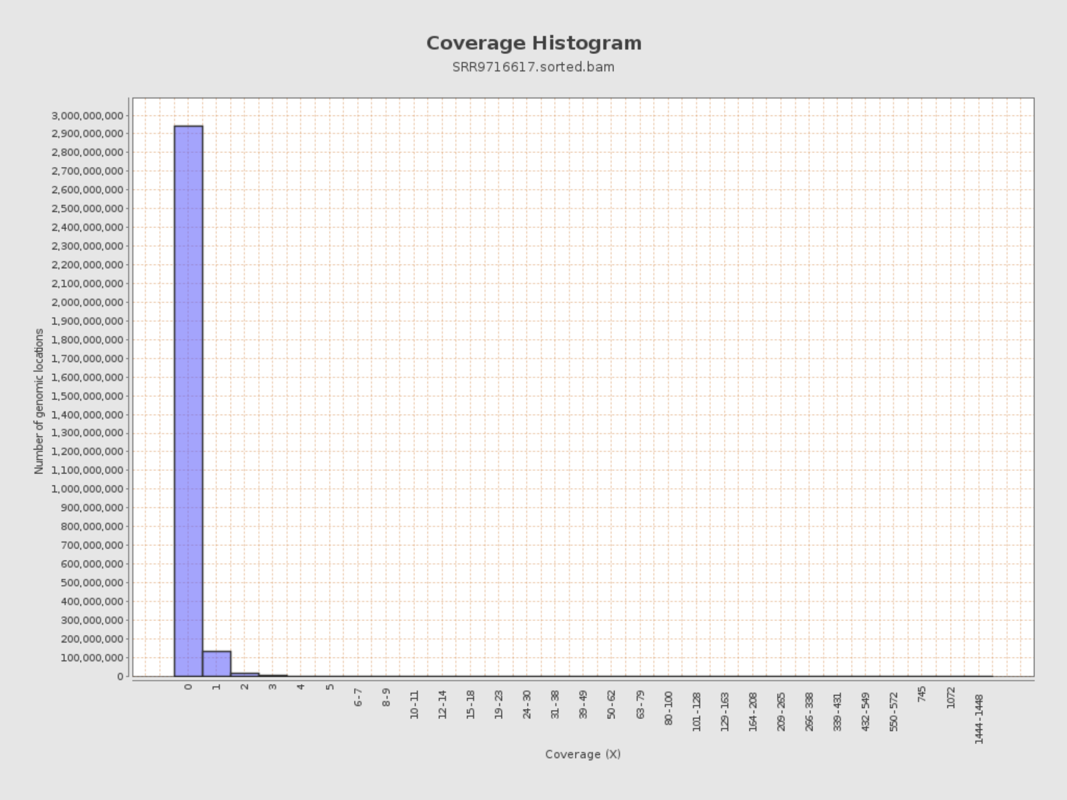
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15575601	0.0625	0.5367
chr2	243199373	11703237	0.0481	0.6393
chr3	198022430	10654438	0.0538	0.2783
chr4	191154276	11202099	0.0586	0.3096
chr5	180915260	10511016	0.0581	0.2795
chr6	171115067	10779214	0.063	0.3867
chr7	159138663	10529794	0.0662	0.6549

chr8	146364022	9569709	0.0654	0.3848
chr9	141213431	6154856	0.0436	0.311
chr10	135534747	8091912	0.0597	0.5095
chr11	135006516	6486867	0.048	0.3538
chr12	133851895	9286126	0.0694	0.3144
chr13	115169878	5550510	0.0482	0.2569
chr14	107349540	6233081	0.0581	0.3032
chr15	102531392	6823833	0.0666	0.3195
chr16	90354753	6479664	0.0717	0.3446
chr17	81195210	8397521	0.1034	0.4152
chr18	78077248	3420419	0.0438	0.5283
chr19	59128983	5263142	0.089	0.5435
chr20	63025520	5351335	0.0849	0.3717
chr21	48129895	2307378	0.0479	0.2847
chr22	51304566	1751282	0.0341	0.2182
chrMT	16571	9670	0.5835	1.4742
chrX	155270560	9988405	0.0643	0.3319
chrY	59373566	532037	0.009	0.2231

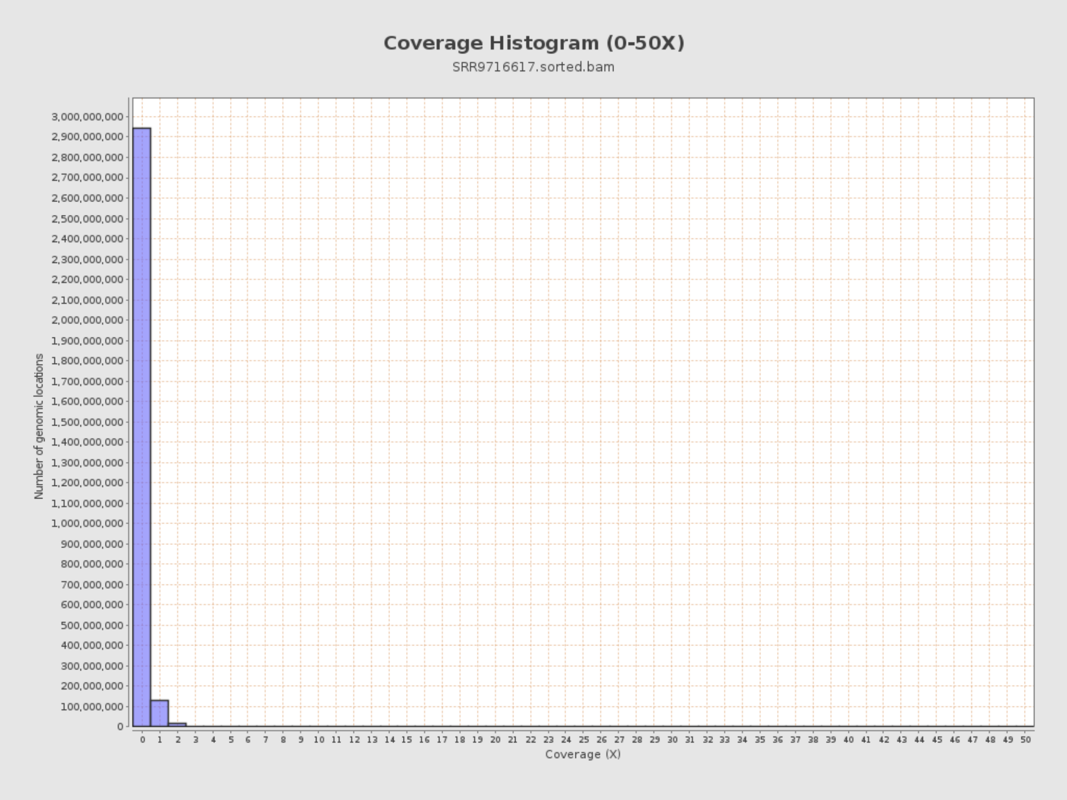
3. Results : Coverage across reference



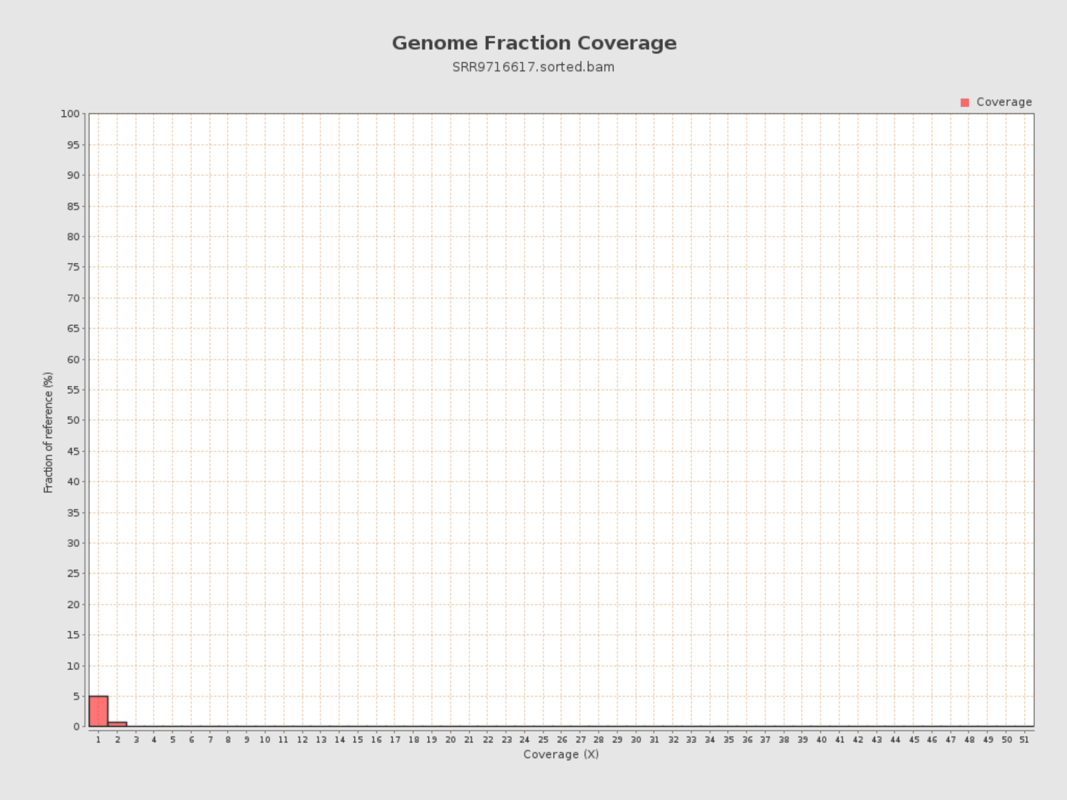
4. Results : Coverage Histogram



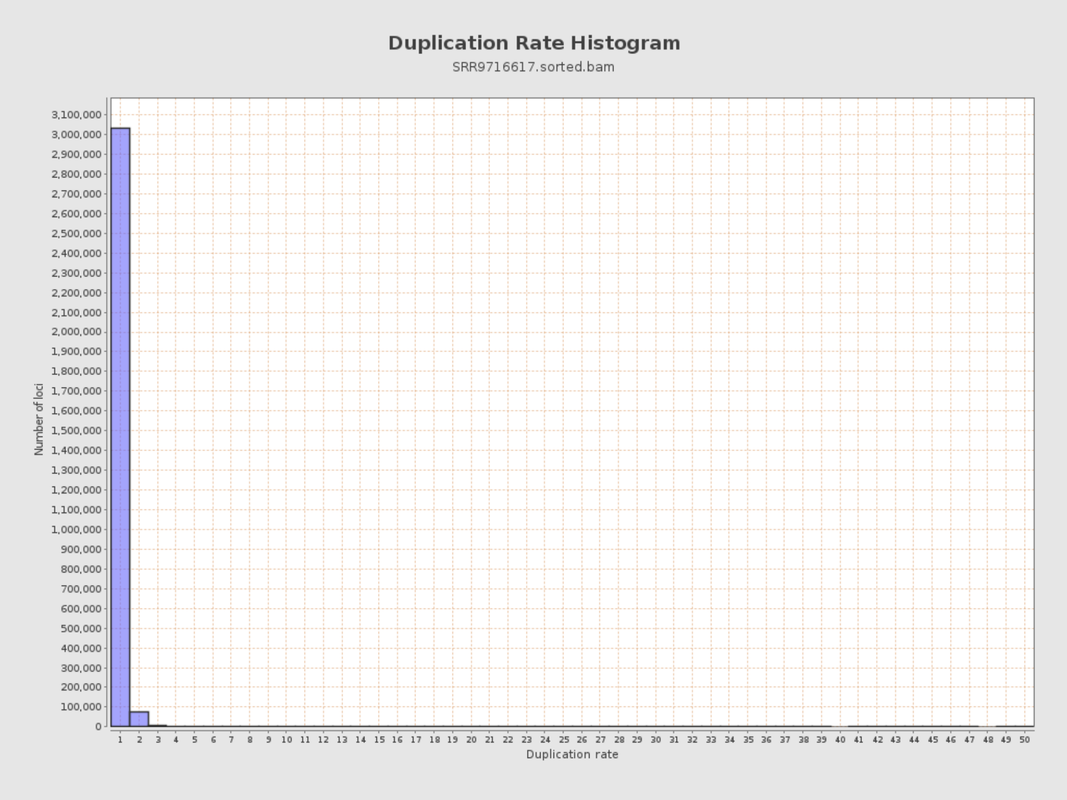
5. Results : Coverage Histogram (0-50X)



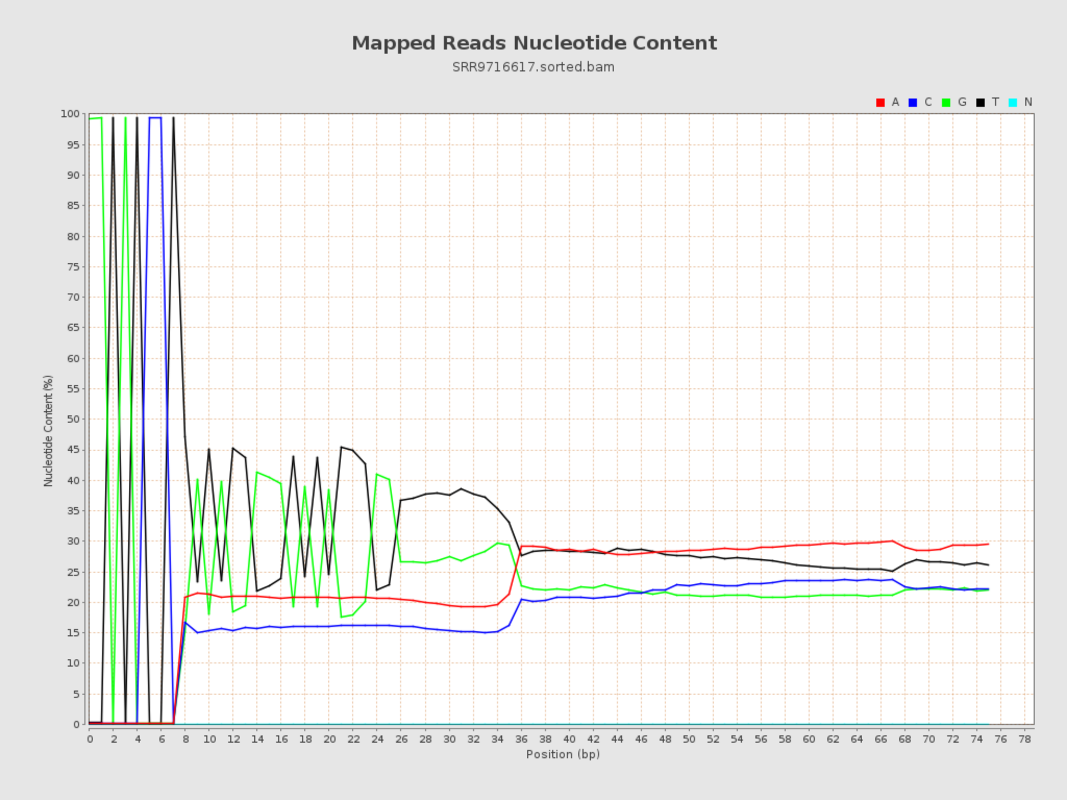
6. Results : Genome Fraction Coverage



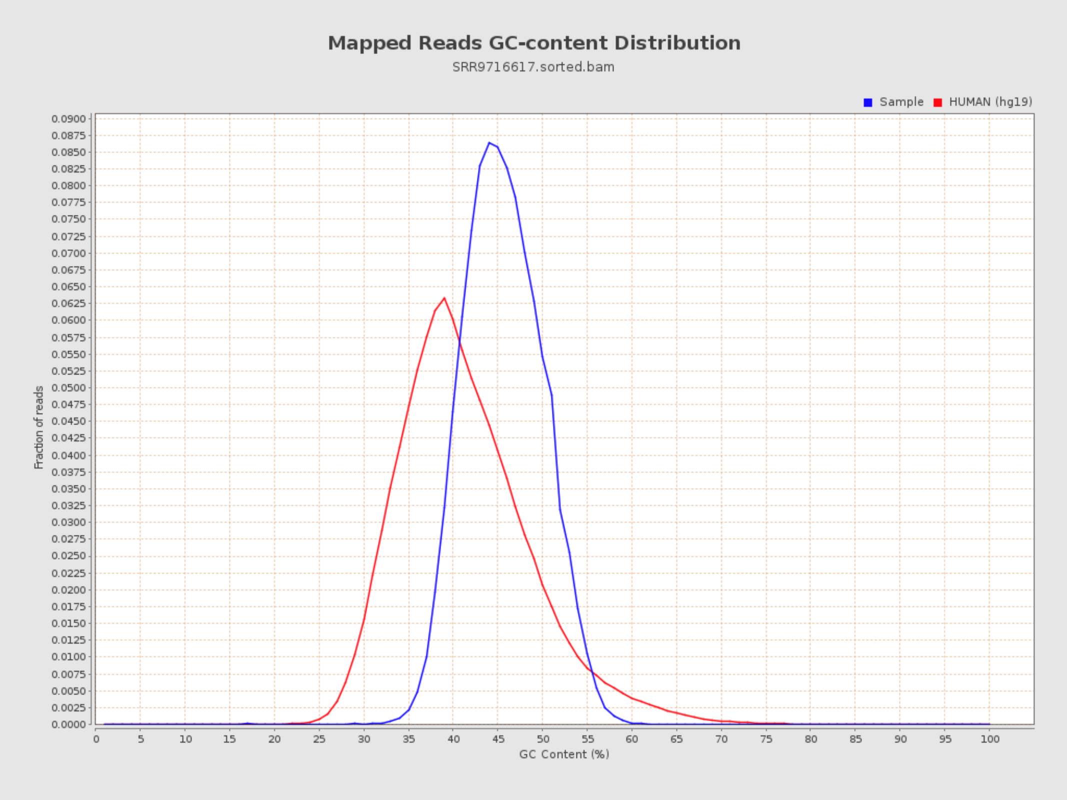
7. Results : Duplication Rate Histogram



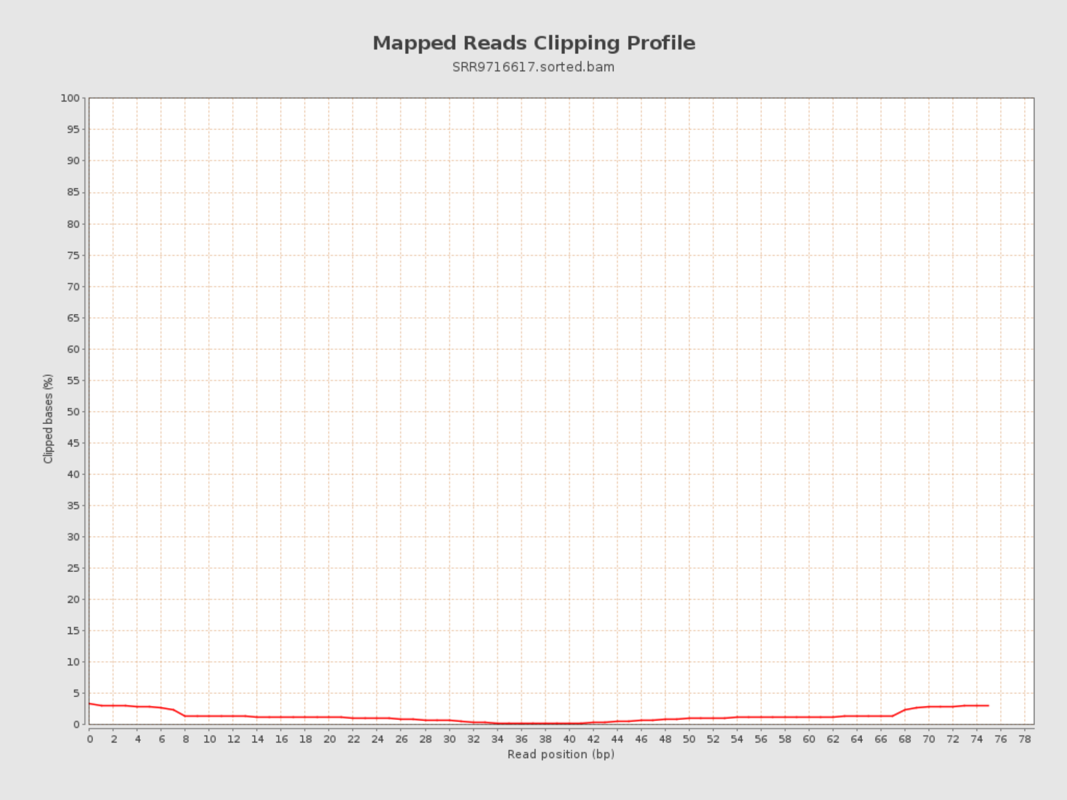
8. Results : Mapped Reads Nucleotide Content



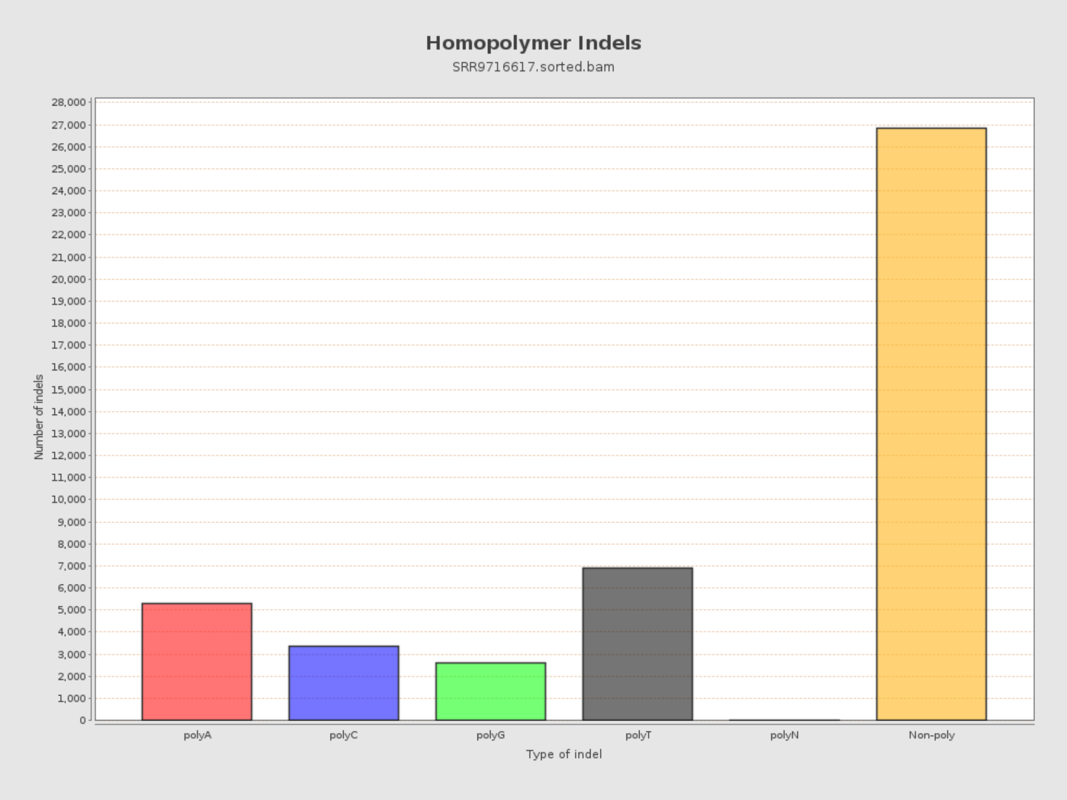
9. Results : Mapped Reads GC-content Distribution



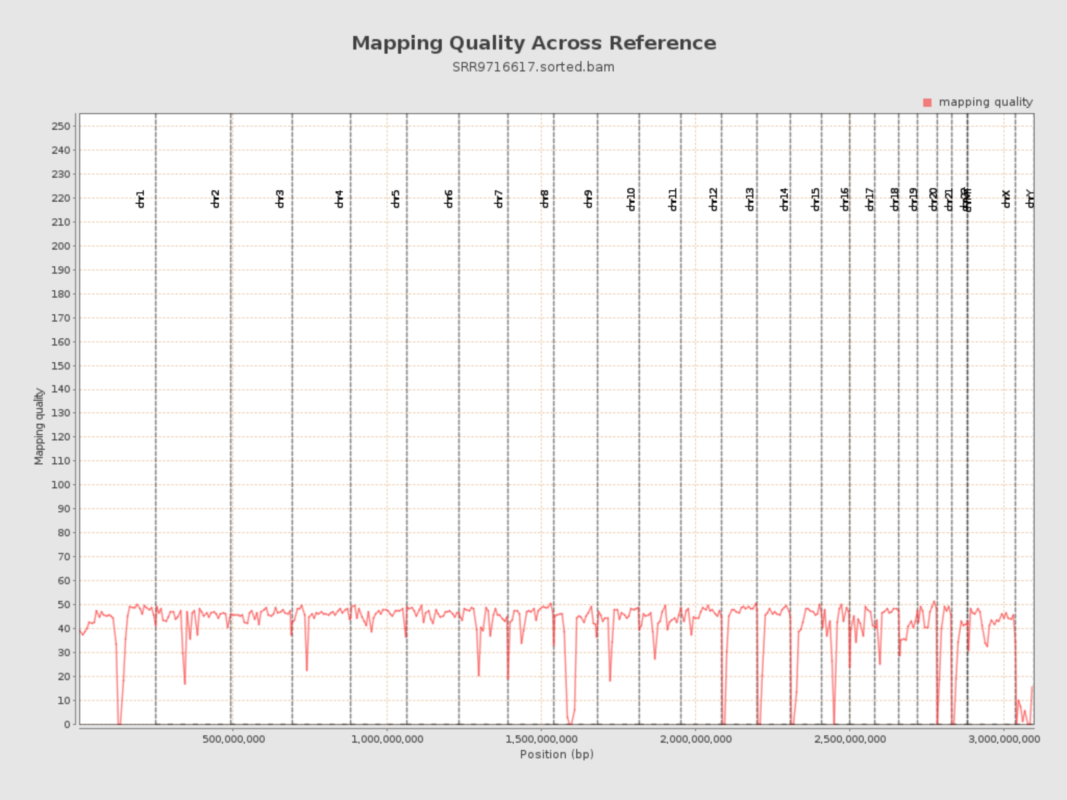
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram