Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:27:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716610.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_SRR9716610 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716610.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:27:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716610.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,041,055
Mapped reads	3,622,713 / 89.65%
Unmapped reads	418,342 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	96,932 / 2.4%
Read min/max/mean length	30 / 101 / 101.87
Duplicated reads (estimated)	172,717 / 4.27%
Duplication rate	3.31%
Clipped reads	3,712,561 / 91.87%

2.2. ACGT Content

Number/percentage of A's	72,804,886 / 26.6%
Number/percentage of C's	57,344,697 / 20.95%
Number/percentage of T's	80,919,145 / 29.57%
Number/percentage of G's	62,592,017 / 22.87%
Number/percentage of N's	33,330 / 0.01%
GC Percentage	43.82%

2.3. Coverage

Mean	0.0884

Standard Deviation	0.6802

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

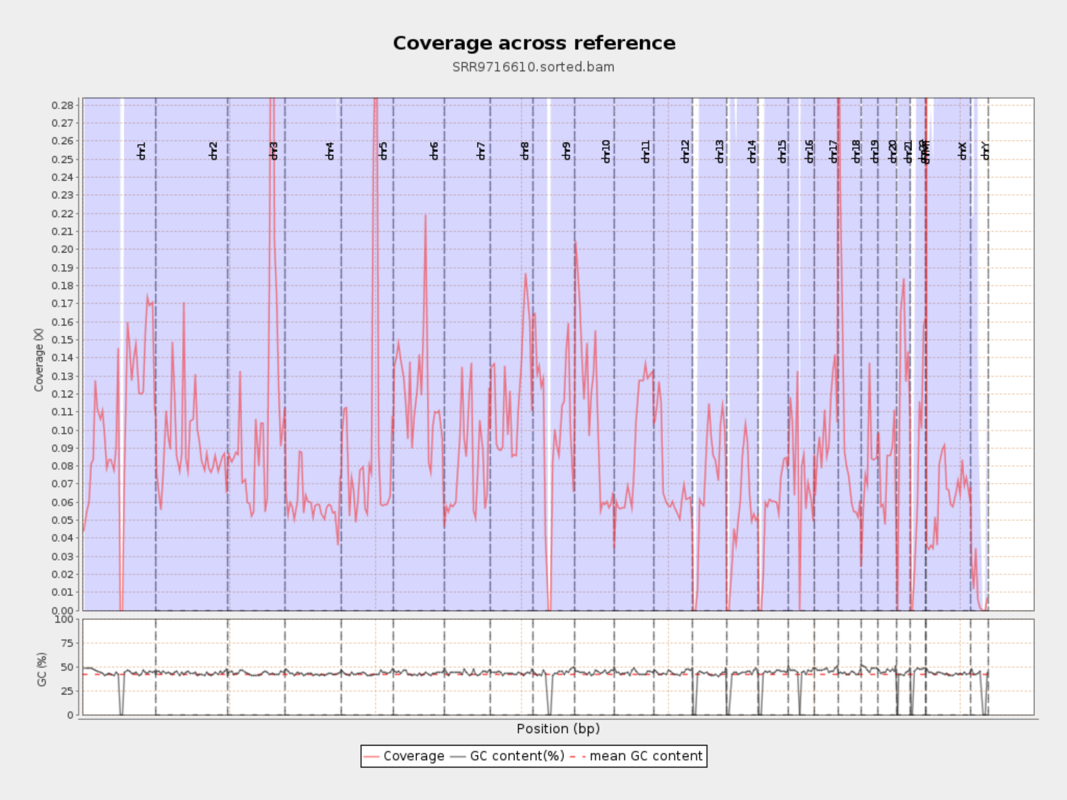
General error rate	0.78%
Mismatches	2,080,171
Insertions	23,717
Mapped reads with at least one insertion	0.65%
Deletions	58,874
Mapped reads with at least one deletion	1.6%
Homopolymer indels	39.85%

2.6. Chromosome stats

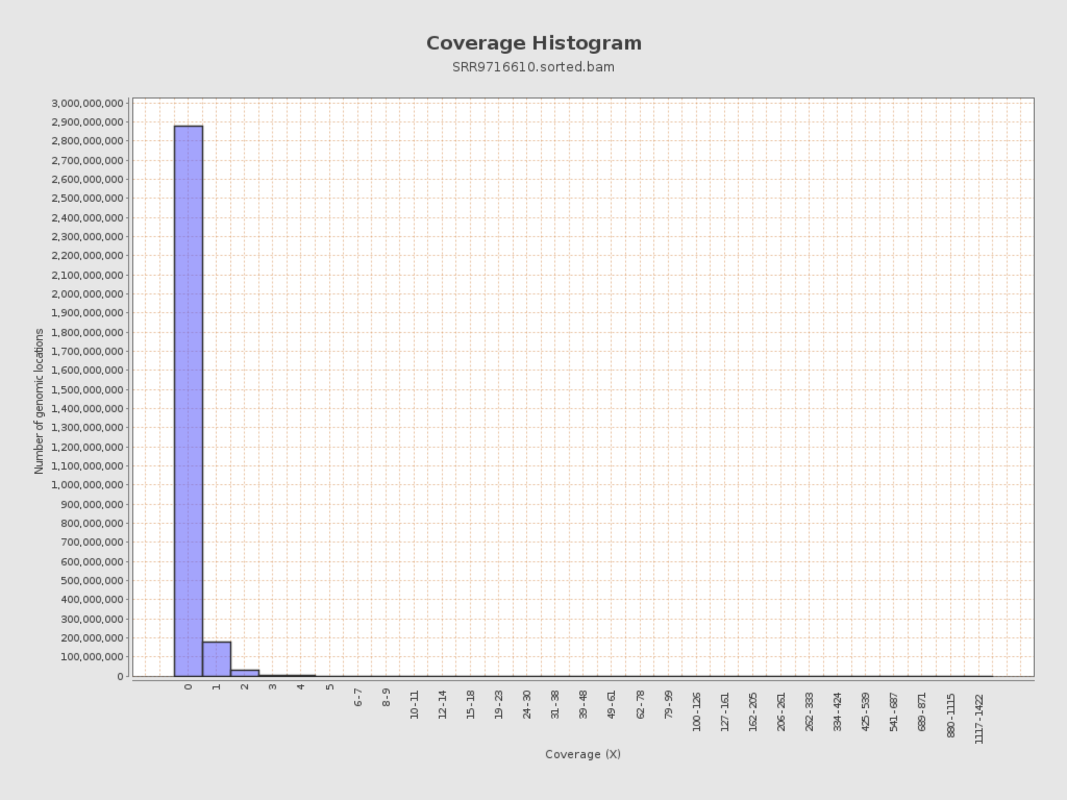
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26285895	0.1055	1.1877
chr2	243199373	22293451	0.0917	1.0505
chr3	198022430	22130165	0.1118	0.4228
chr4	191154276	11340788	0.0593	0.3428
chr5	180915260	16836815	0.0931	0.3809
chr6	171115067	20672429	0.1208	0.5366
chr7	159138663	13008644	0.0817	0.8981

chr8	146364022	17660226	0.1207	0.8258
chr9	141213431	14048932	0.0995	0.6238
chr10	135534747	15092755	0.1114	0.6728
chr11	135006516	12304373	0.0911	0.5402
chr12	133851895	9674597	0.0723	0.3295
chr13	115169878	8360975	0.0726	0.321
chr14	107349540	5589529	0.0521	0.3401
chr15	102531392	5455847	0.0532	0.2791
chr16	90354753	6802078	0.0753	0.3884
chr17	81195210	8202253	0.101	0.4621
chr18	78077248	8286847	0.1061	1.1498
chr19	59128983	4843494	0.0819	0.9329
chr20	63025520	4919930	0.0781	0.3922
chr21	48129895	5774785	0.12	0.4595
chr22	51304566	3826764	0.0746	0.3388
chrMT	16571	141462	8.5367	6.2193
chrX	155270560	9629385	0.062	0.4219
chrY	59373566	615211	0.0104	0.314

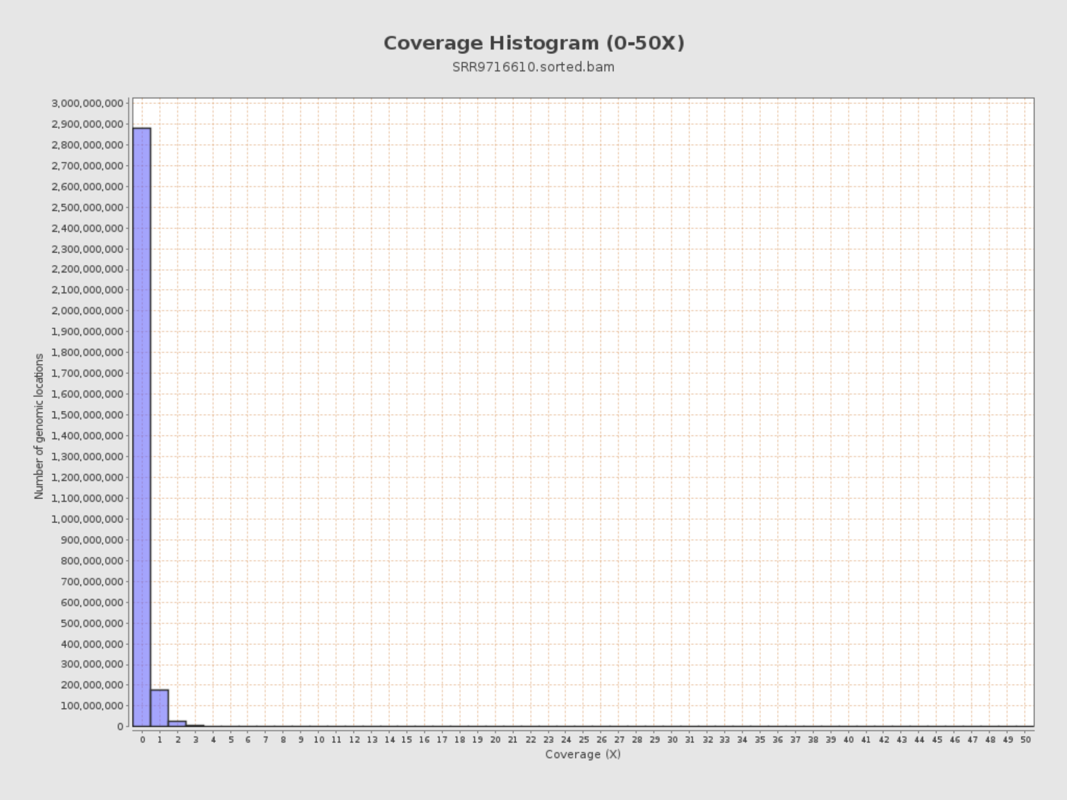
3. Results : Coverage across reference



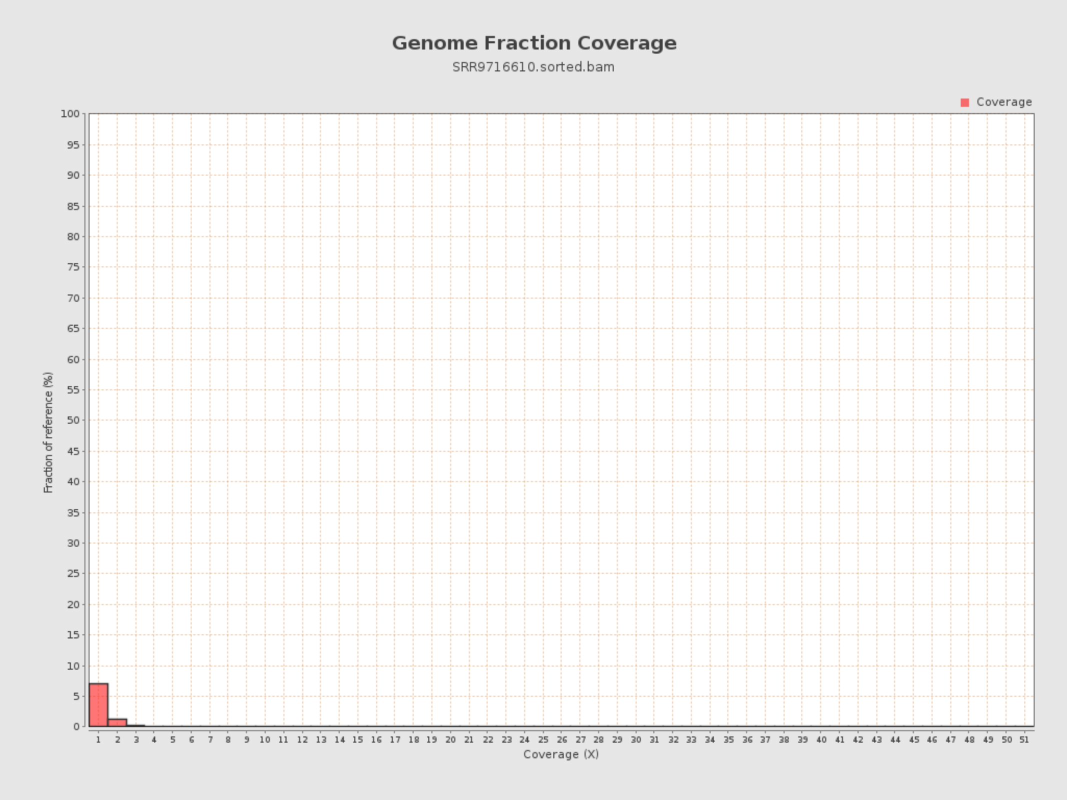
4. Results : Coverage Histogram



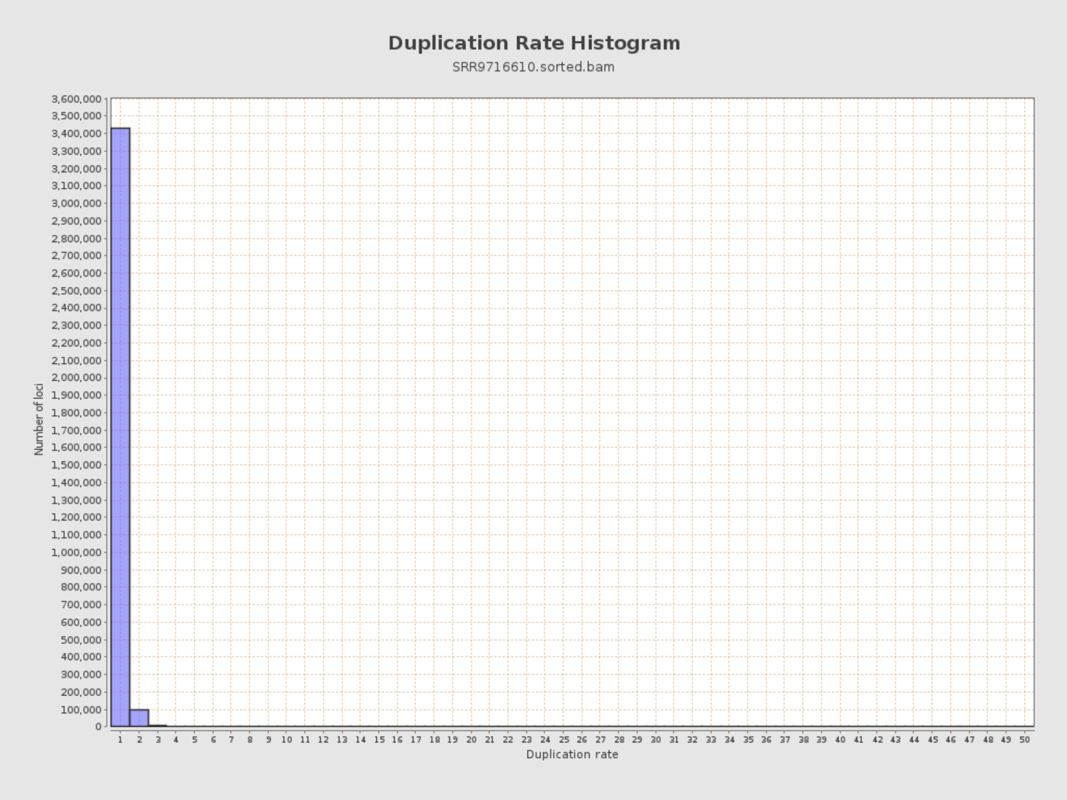
5. Results : Coverage Histogram (0-50X)



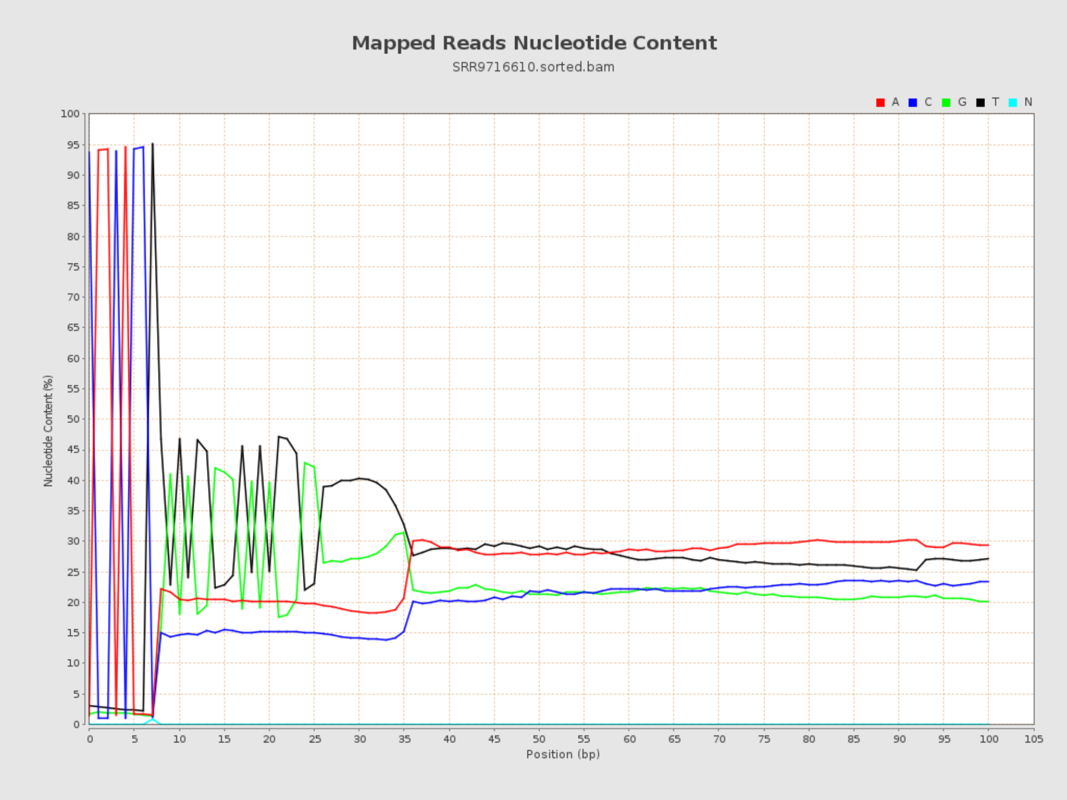
6. Results : Genome Fraction Coverage



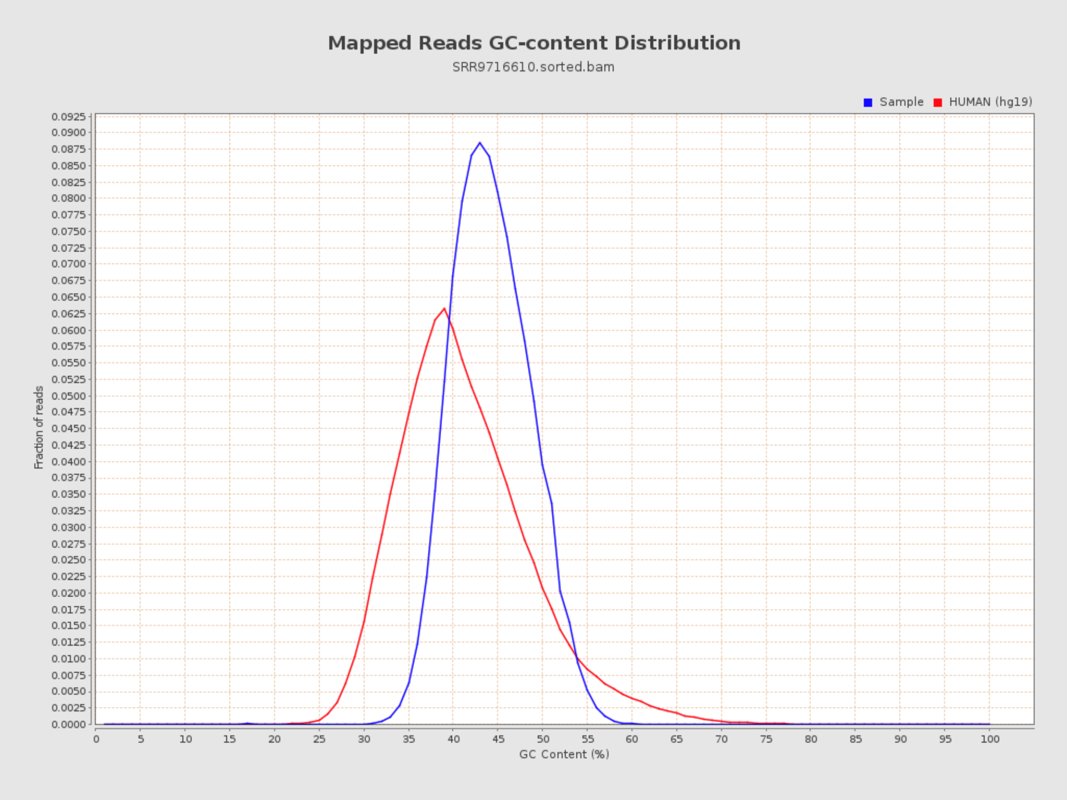
7. Results : Duplication Rate Histogram



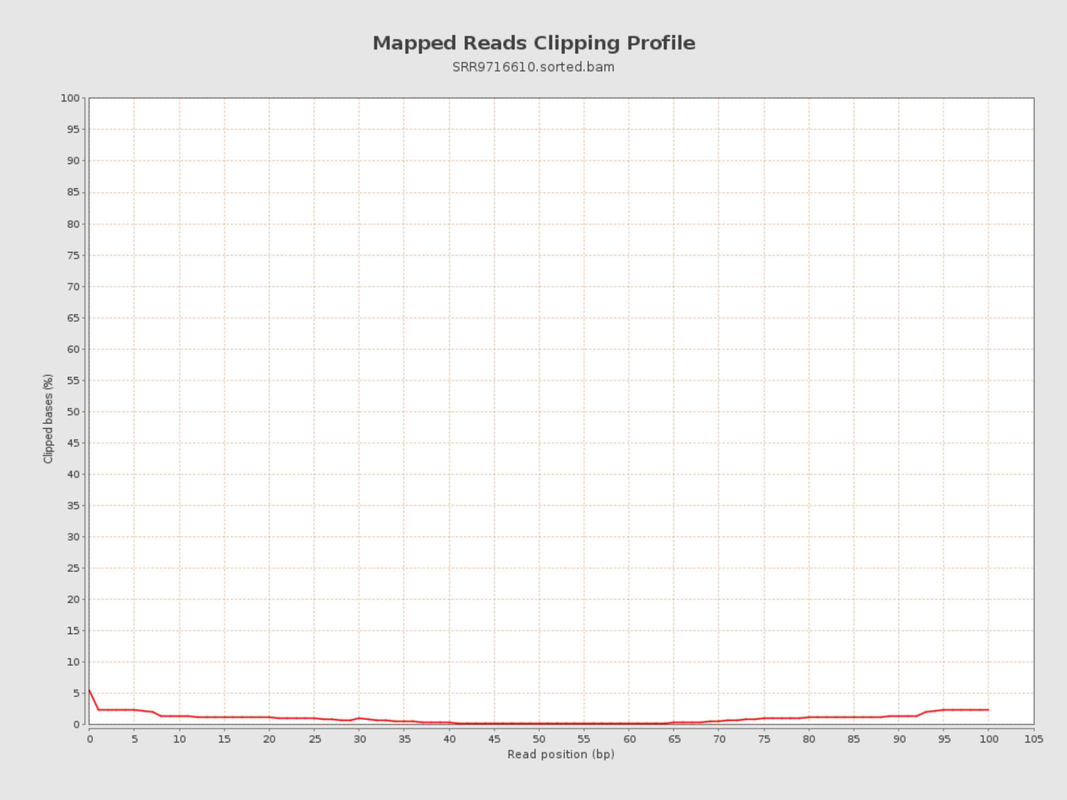
8. Results : Mapped Reads Nucleotide Content



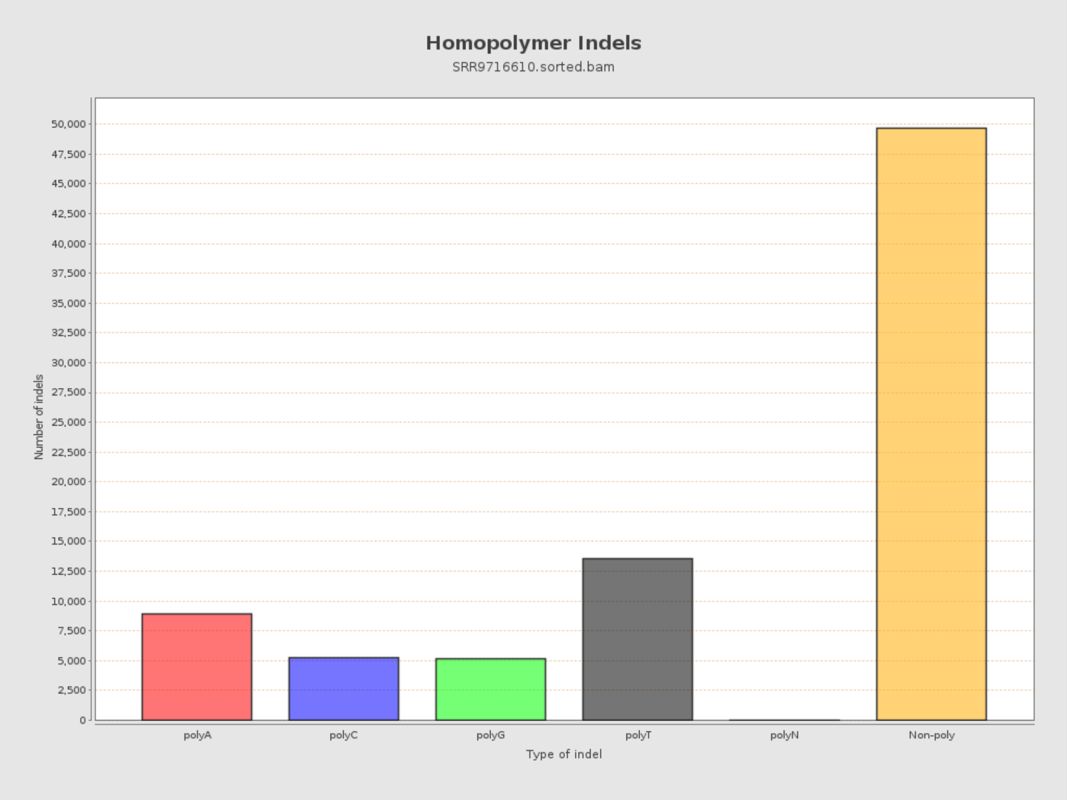
9. Results : Mapped Reads GC-content Distribution



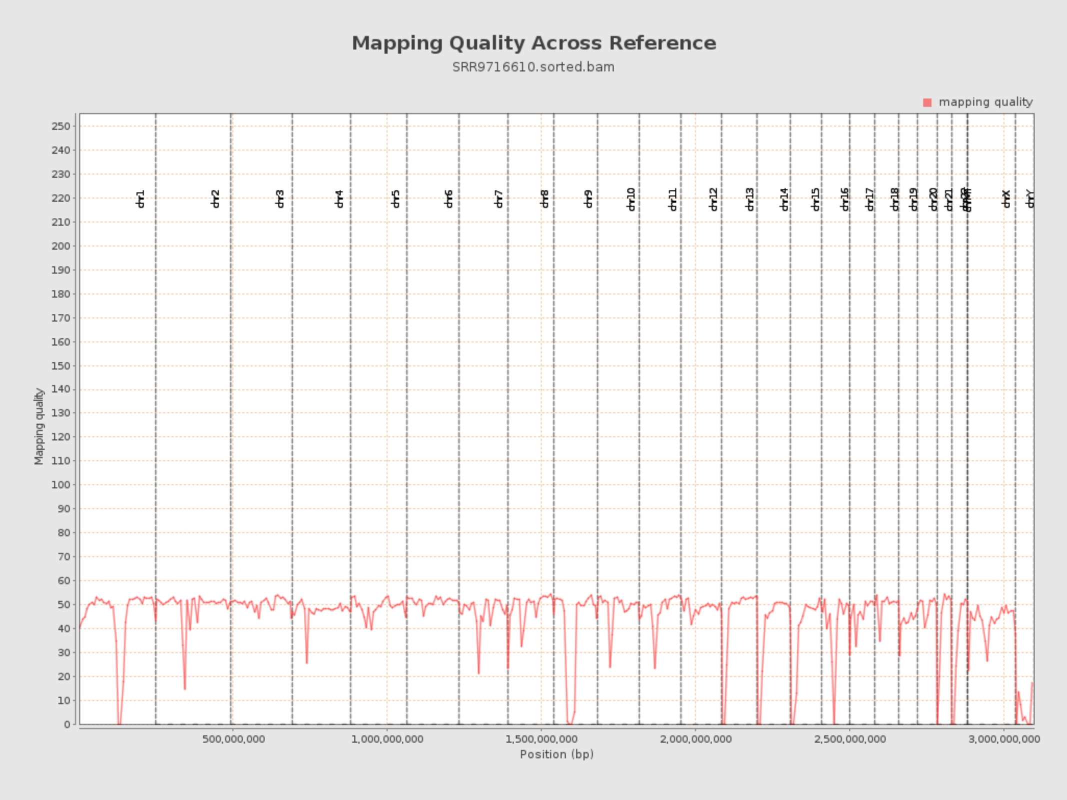
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram