Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:40:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716161.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_SRR9716161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:40:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,507,559
Mapped reads	3,166,109 / 90.27%
Unmapped reads	341,450 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,800 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	161,110 / 4.59%
Duplication rate	3.71%
Clipped reads	3,170,101 / 90.38%

2.2. ACGT Content

Number/percentage of A's	48,122,065 / 26.55%
Number/percentage of C's	33,774,136 / 18.63%
Number/percentage of T's	55,052,911 / 30.37%
Number/percentage of G's	44,314,579 / 24.45%
Number/percentage of N's	2,801 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0586

Standard Deviation	0.5031

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

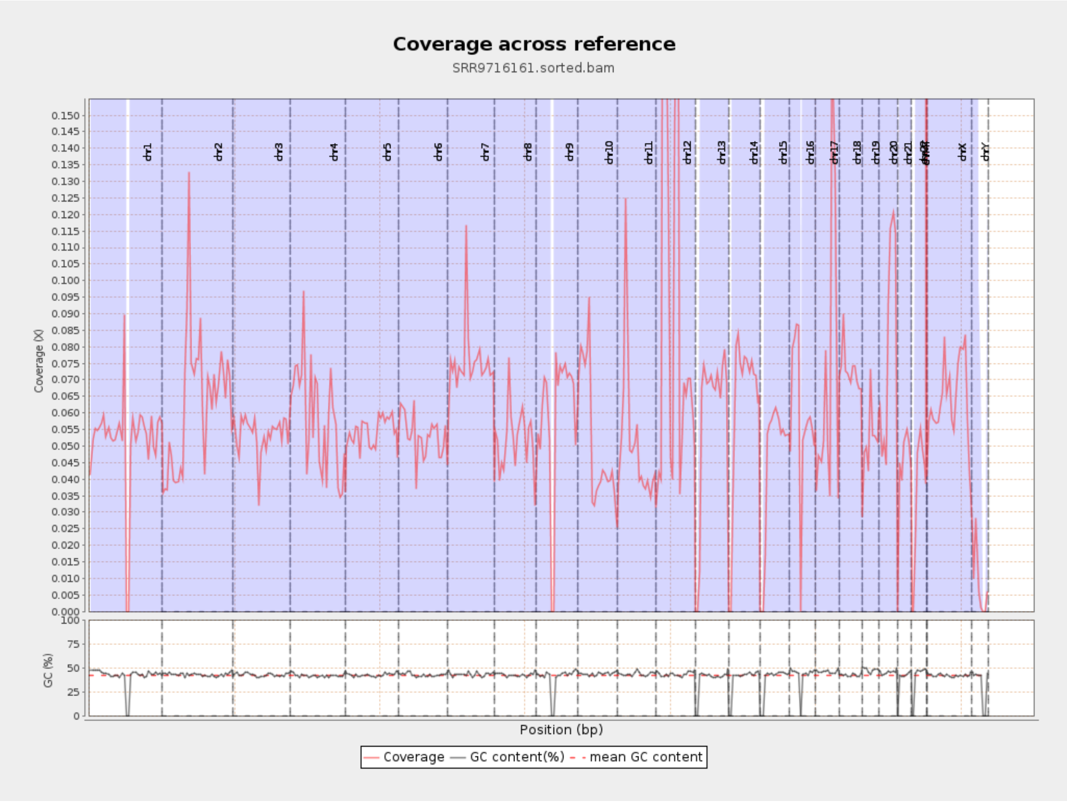
General error rate	0.55%
Mismatches	974,412
Insertions	13,450
Mapped reads with at least one insertion	0.42%
Deletions	28,586
Mapped reads with at least one deletion	0.9%
Homopolymer indels	40.9%

2.6. Chromosome stats

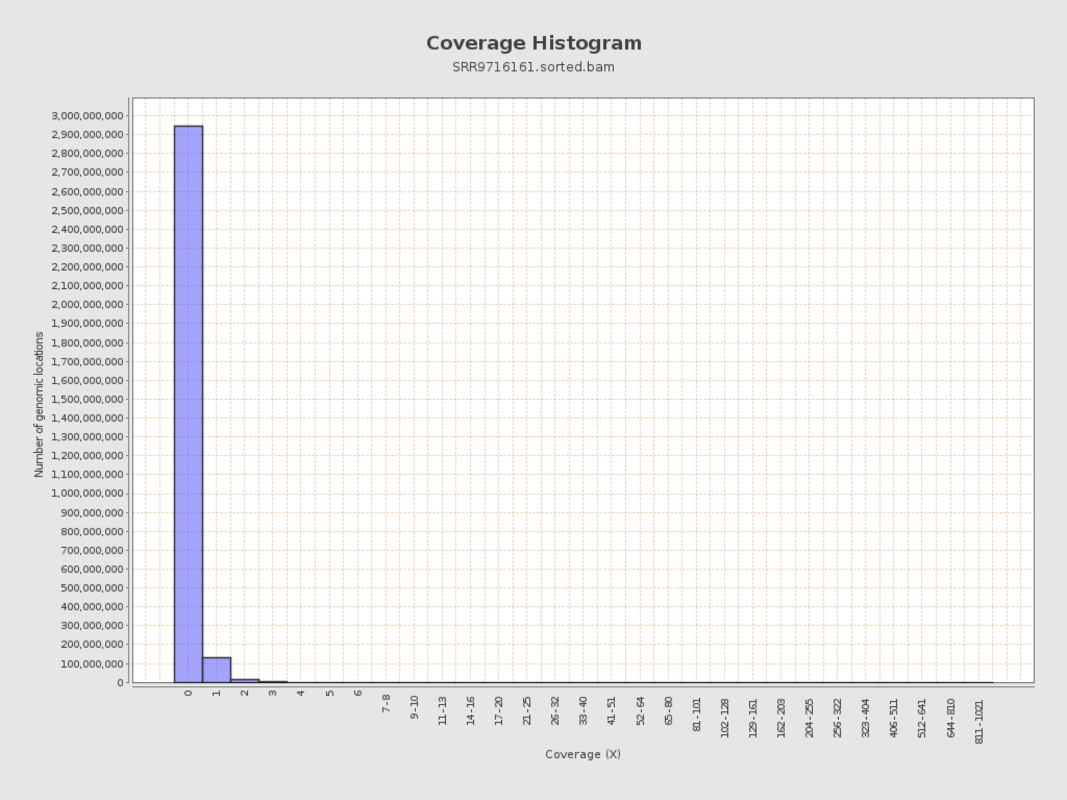
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12885836	0.0517	0.8183
chr2	243199373	15401901	0.0633	0.617
chr3	198022430	10611798	0.0536	0.2668
chr4	191154276	11215052	0.0587	0.3259
chr5	180915260	9851874	0.0545	0.2756
chr6	171115067	9084314	0.0531	0.3159
chr7	159138663	12021556	0.0755	0.7447

chr8	146364022	7636293	0.0522	0.4349
chr9	141213431	8291371	0.0587	0.5846
chr10	135534747	7033676	0.0519	0.453
chr11	135006516	6929918	0.0513	0.4353
chr12	133851895	13135123	0.0981	0.4422
chr13	115169878	6712150	0.0583	0.2788
chr14	107349540	6682232	0.0622	0.3506
chr15	102531392	4648245	0.0453	0.2481
chr16	90354753	5404775	0.0598	0.3371
chr17	81195210	5612165	0.0691	0.3259
chr18	78077248	5711627	0.0732	1.1323
chr19	59128983	3083826	0.0522	0.6675
chr20	63025520	5093144	0.0808	0.3546
chr21	48129895	2082421	0.0433	0.3076
chr22	51304566	1759003	0.0343	0.2106
chrMT	16571	27445	1.6562	1.7245
chrX	155270560	9883622	0.0637	0.3922
chrY	59373566	514864	0.0087	0.1875

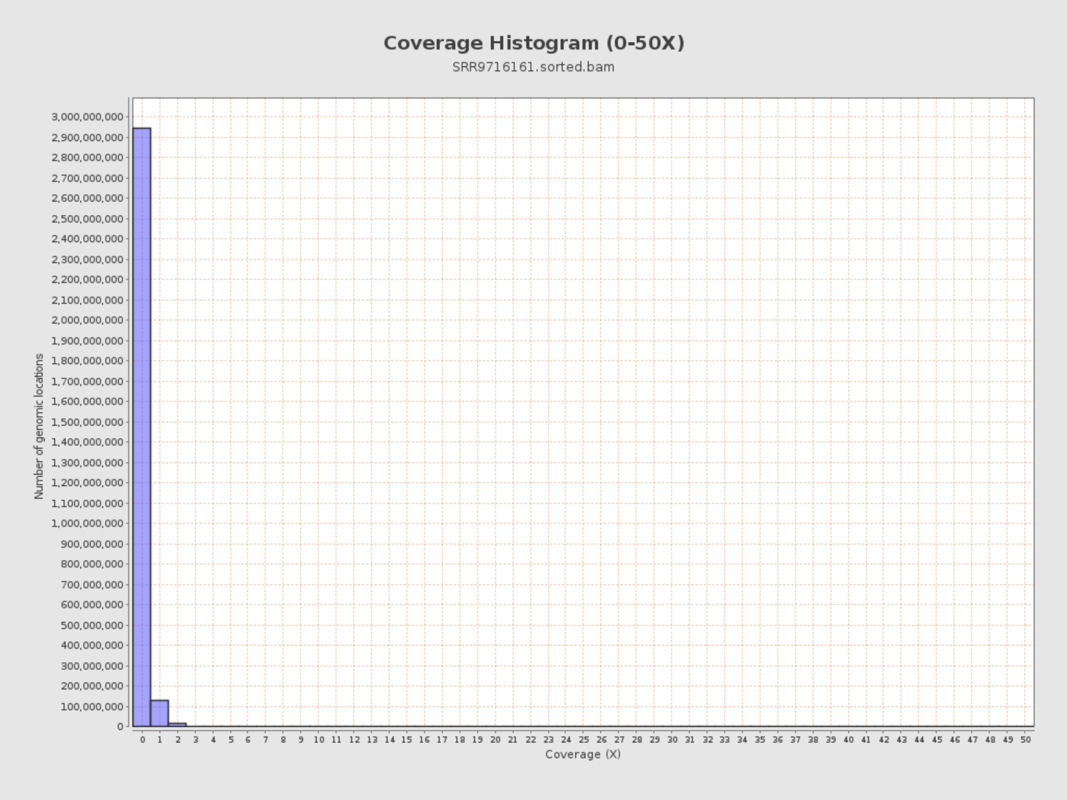
3. Results : Coverage across reference



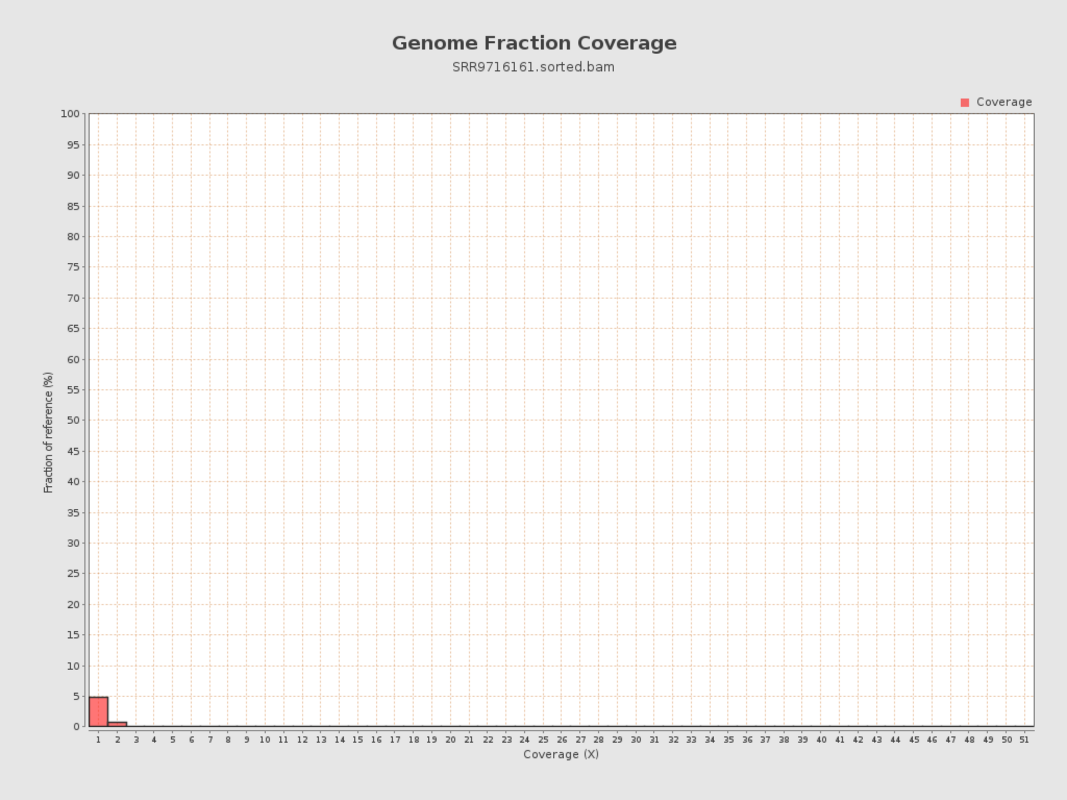
4. Results : Coverage Histogram



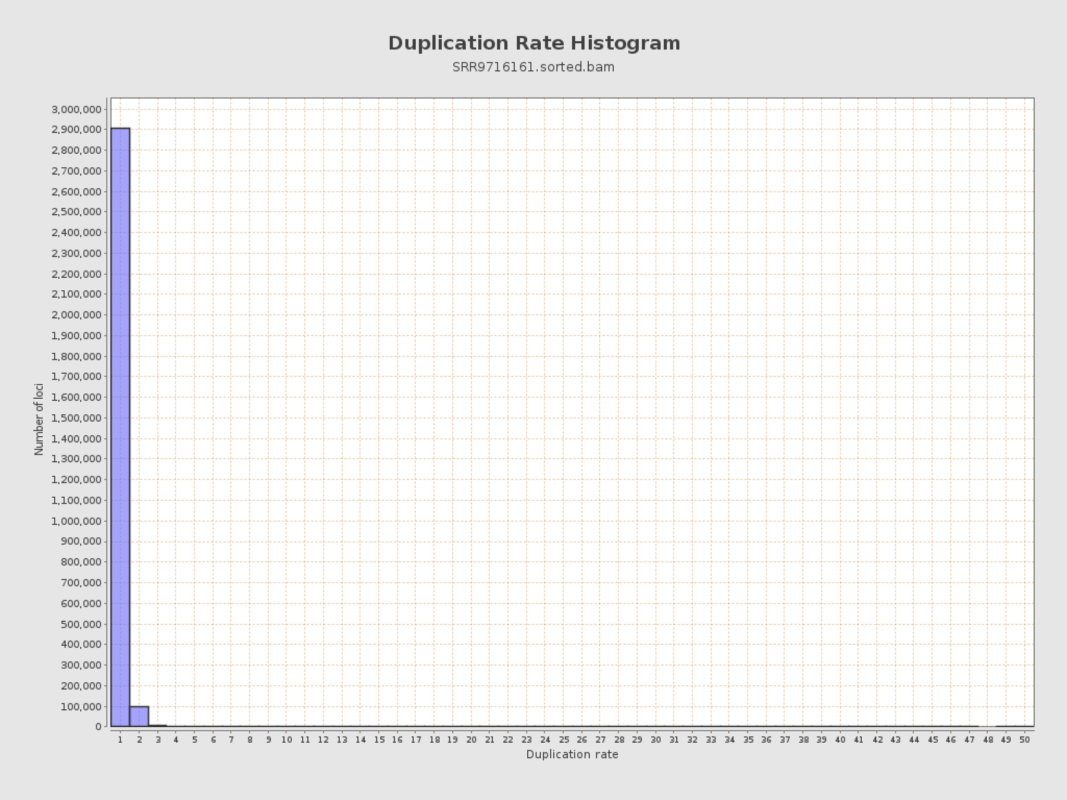
5. Results : Coverage Histogram (0-50X)



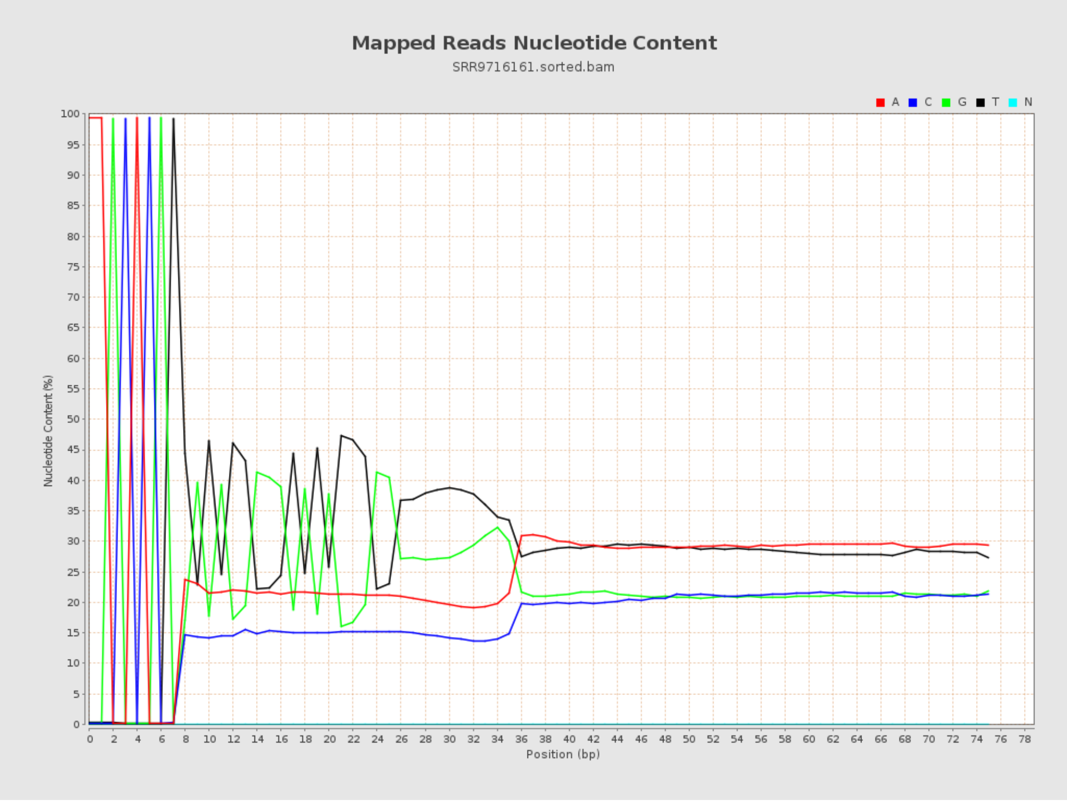
6. Results : Genome Fraction Coverage



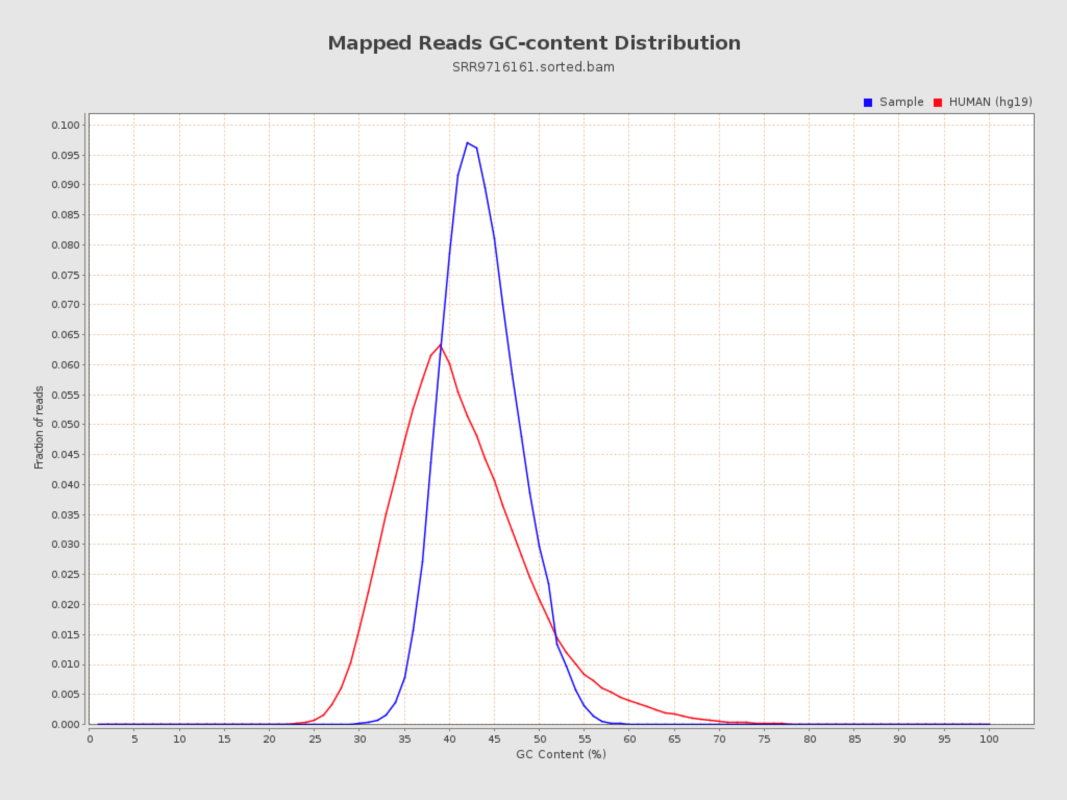
7. Results : Duplication Rate Histogram



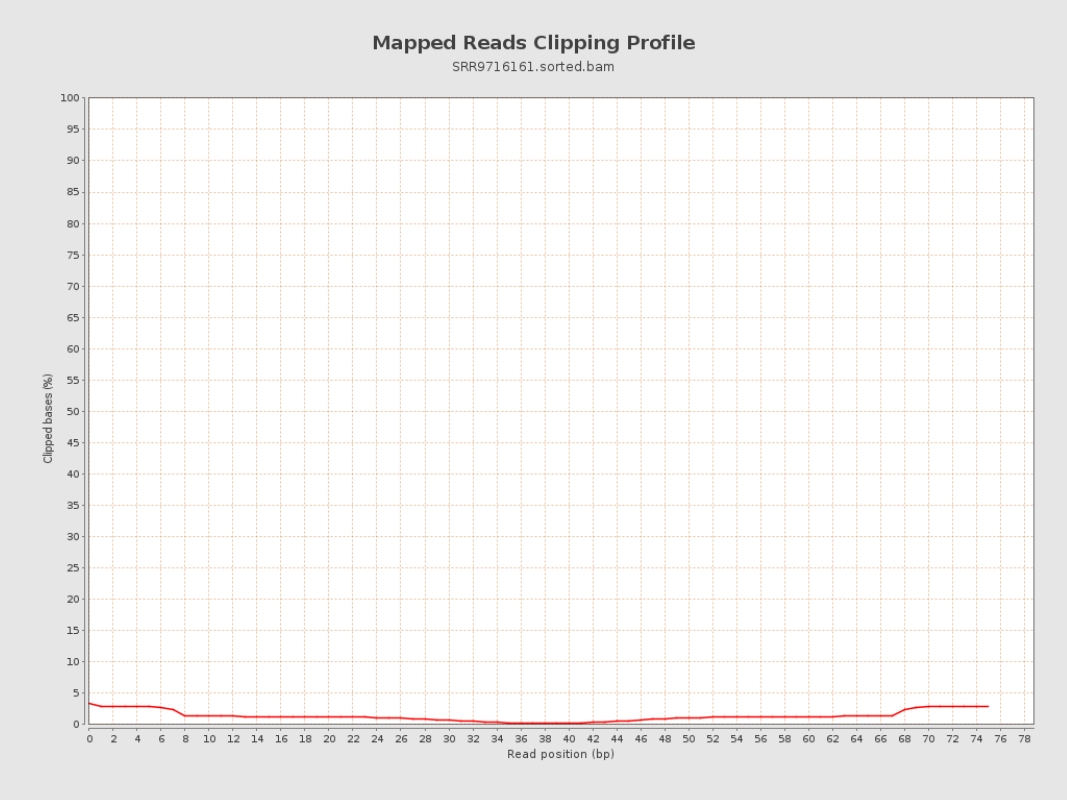
8. Results : Mapped Reads Nucleotide Content



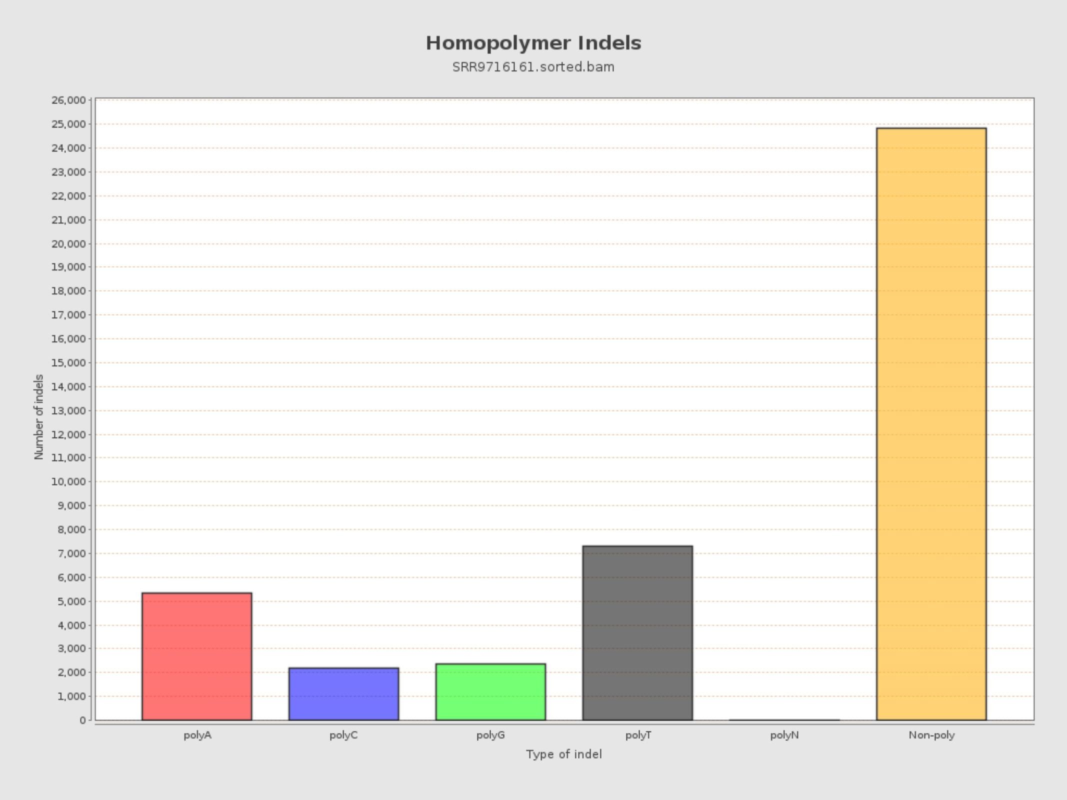
9. Results : Mapped Reads GC-content Distribution



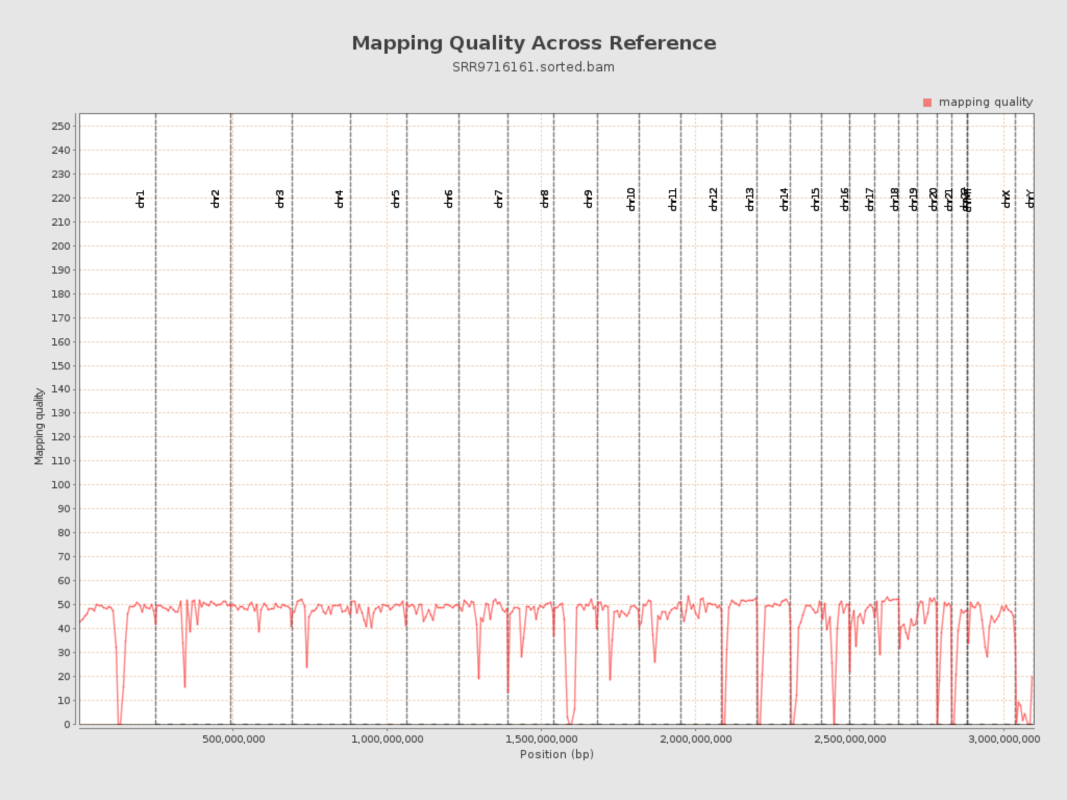
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram