Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716677.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_SRR9716677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:24:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,164,782
Mapped reads	2,852,985 / 90.15%
Unmapped reads	311,797 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,290 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	126,153 / 3.99%
Duplication rate	3.29%
Clipped reads	2,855,920 / 90.24%

2.2. ACGT Content

Number/percentage of A's	40,989,281 / 24.88%
Number/percentage of C's	32,309,410 / 19.61%
Number/percentage of T's	51,570,582 / 31.31%
Number/percentage of G's	39,863,857 / 24.2%
Number/percentage of N's	1,280 / 0%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0532

Standard Deviation	0.3866

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

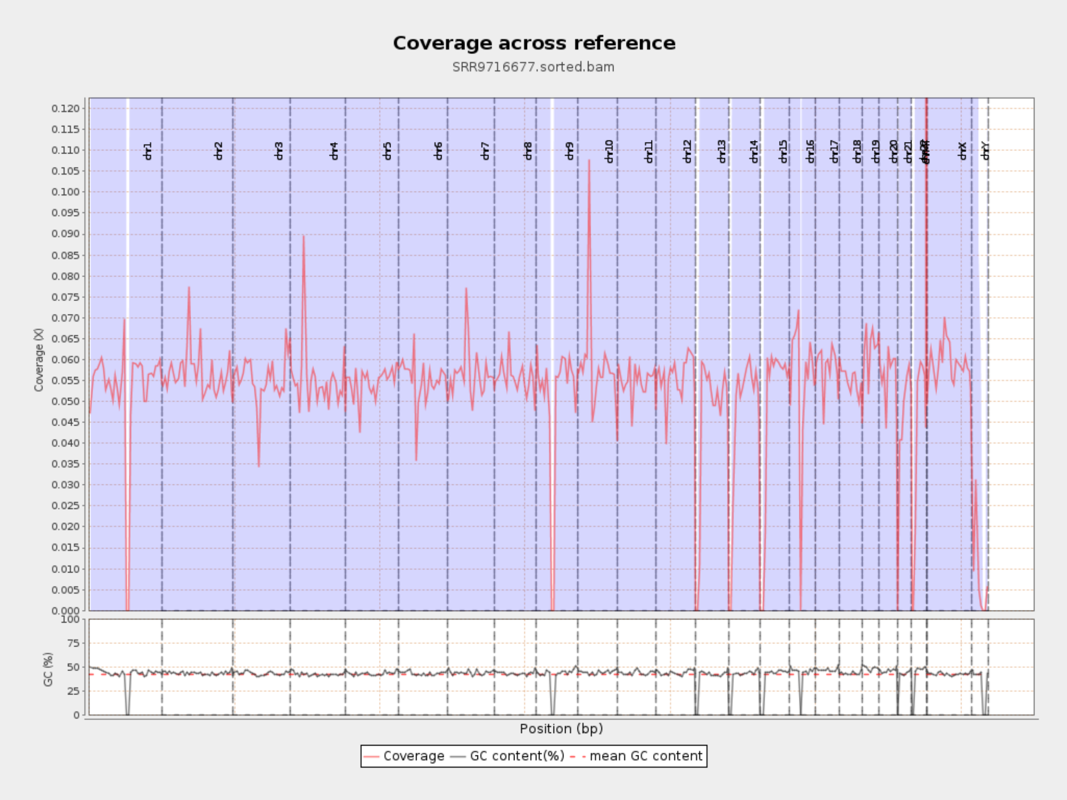
General error rate	0.53%
Mismatches	858,592
Insertions	11,506
Mapped reads with at least one insertion	0.4%
Deletions	32,383
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.49%

2.6. Chromosome stats

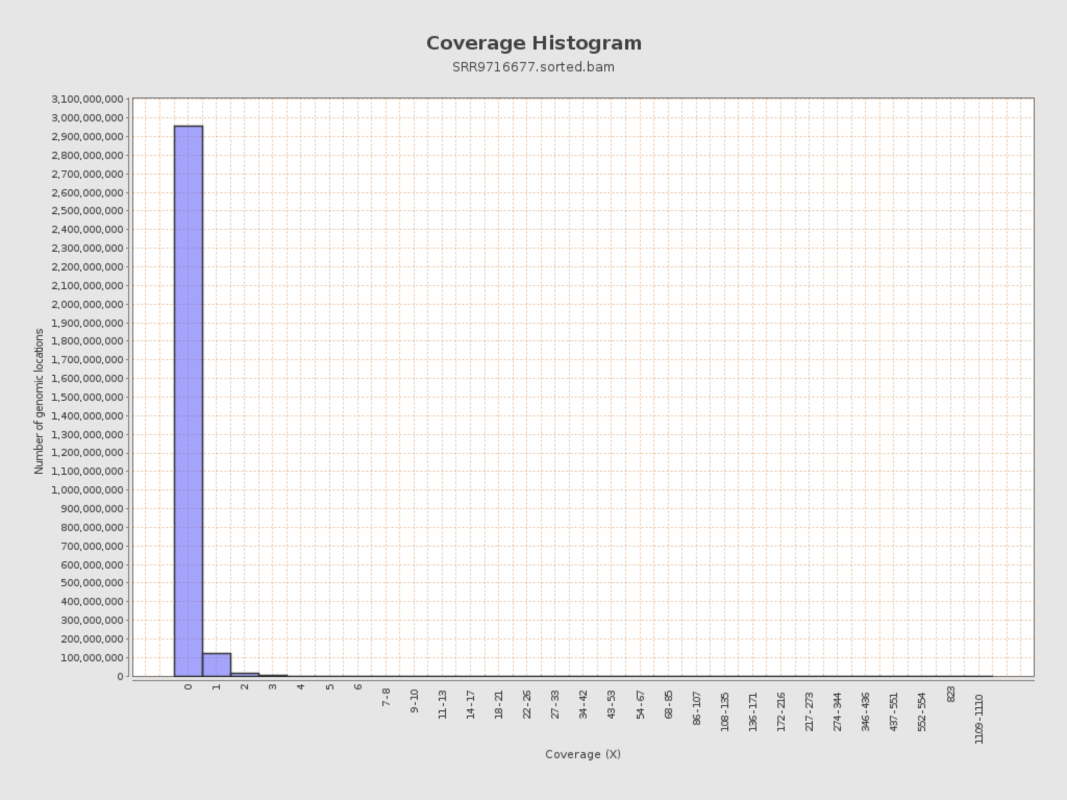
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13092003	0.0525	0.5239
chr2	243199373	13839287	0.0569	0.5763
chr3	198022430	10895992	0.055	0.277
chr4	191154276	10556925	0.0552	0.3237
chr5	180915260	9867793	0.0545	0.2719
chr6	171115067	9423666	0.0551	0.3291
chr7	159138663	9030668	0.0567	0.4997

chr8	146364022	8166144	0.0558	0.3862
chr9	141213431	6967977	0.0493	0.3231
chr10	135534747	7988527	0.0589	0.5007
chr11	135006516	7391640	0.0548	0.3492
chr12	133851895	7502323	0.056	0.2806
chr13	115169878	5147900	0.0447	0.2464
chr14	107349540	4923457	0.0459	0.269
chr15	102531392	4843688	0.0472	0.2642
chr16	90354753	4950125	0.0548	0.3085
chr17	81195210	4708268	0.058	0.2997
chr18	78077248	4306665	0.0552	0.5794
chr19	59128983	3684935	0.0623	0.4632
chr20	63025520	3555439	0.0564	0.2895
chr21	48129895	2170269	0.0451	0.2914
chr22	51304566	2010518	0.0392	0.2327
chrMT	16571	59256	3.5759	2.7712
chrX	155270560	9180802	0.0591	0.317
chrY	59373566	521658	0.0088	0.265

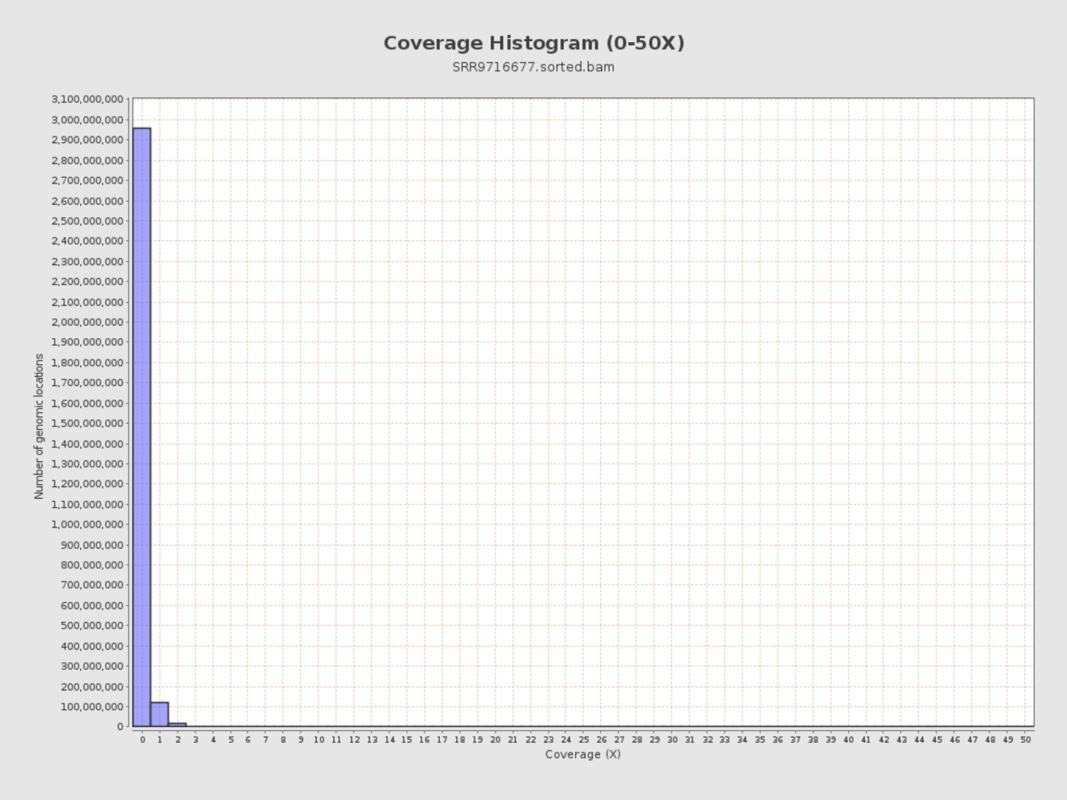
3. Results : Coverage across reference



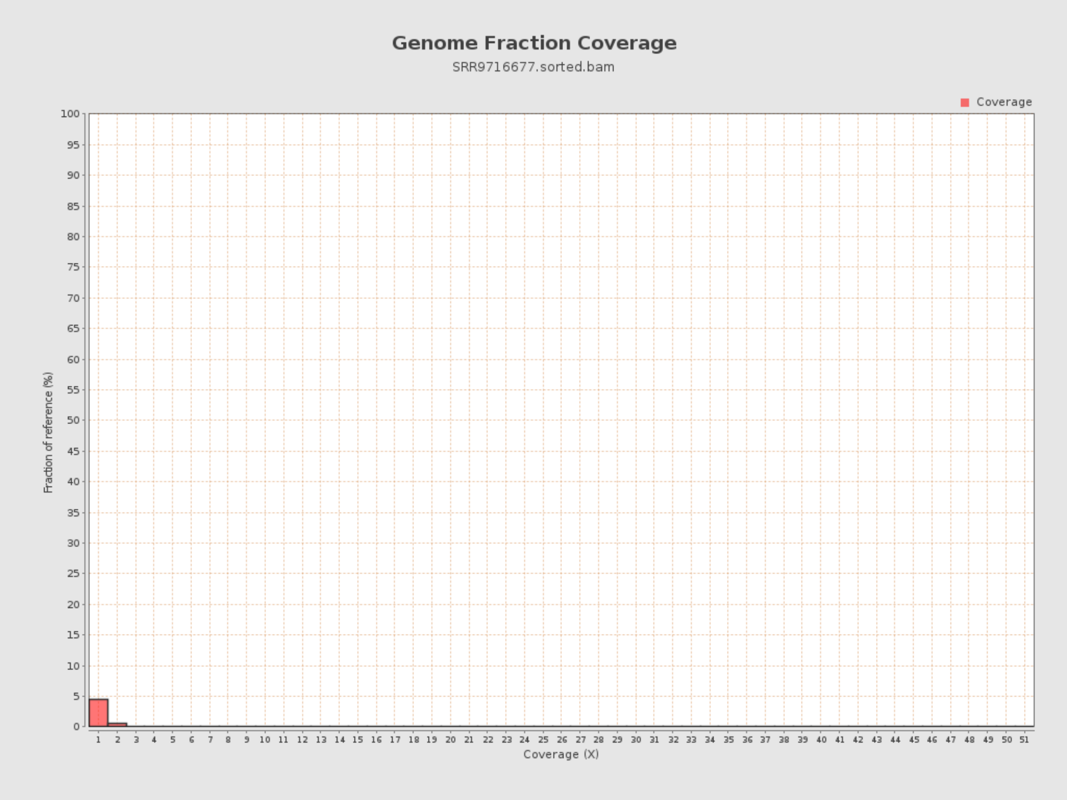
4. Results : Coverage Histogram



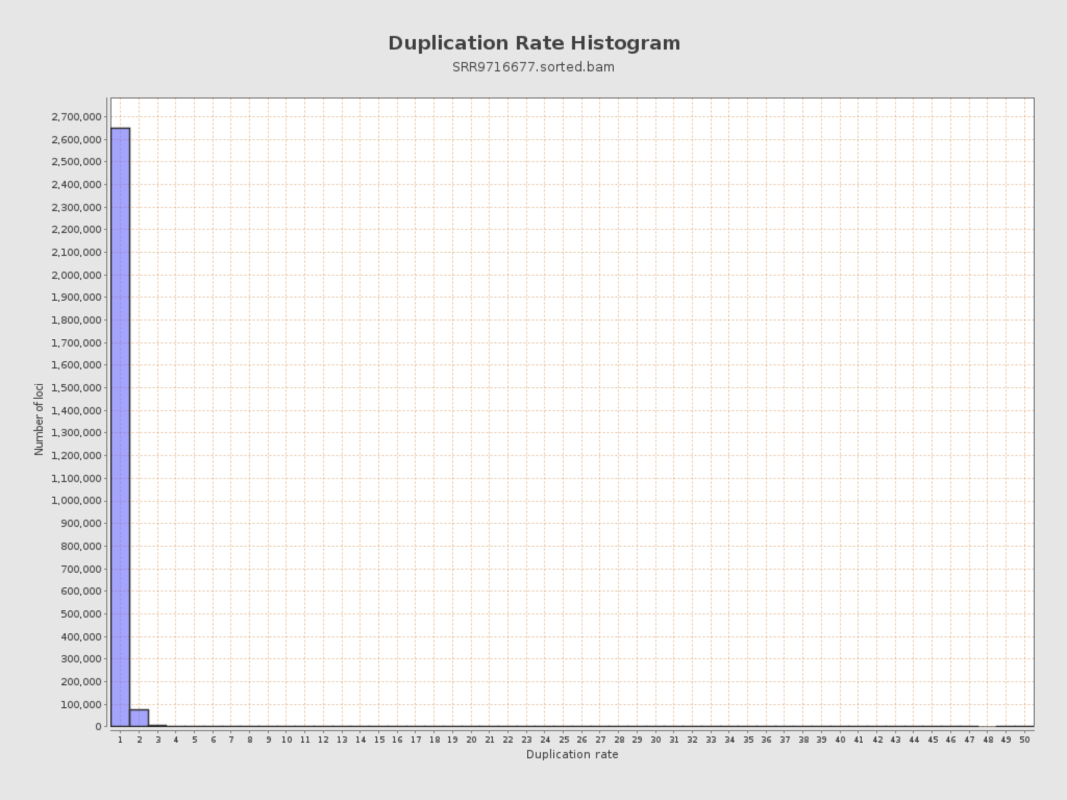
5. Results : Coverage Histogram (0-50X)



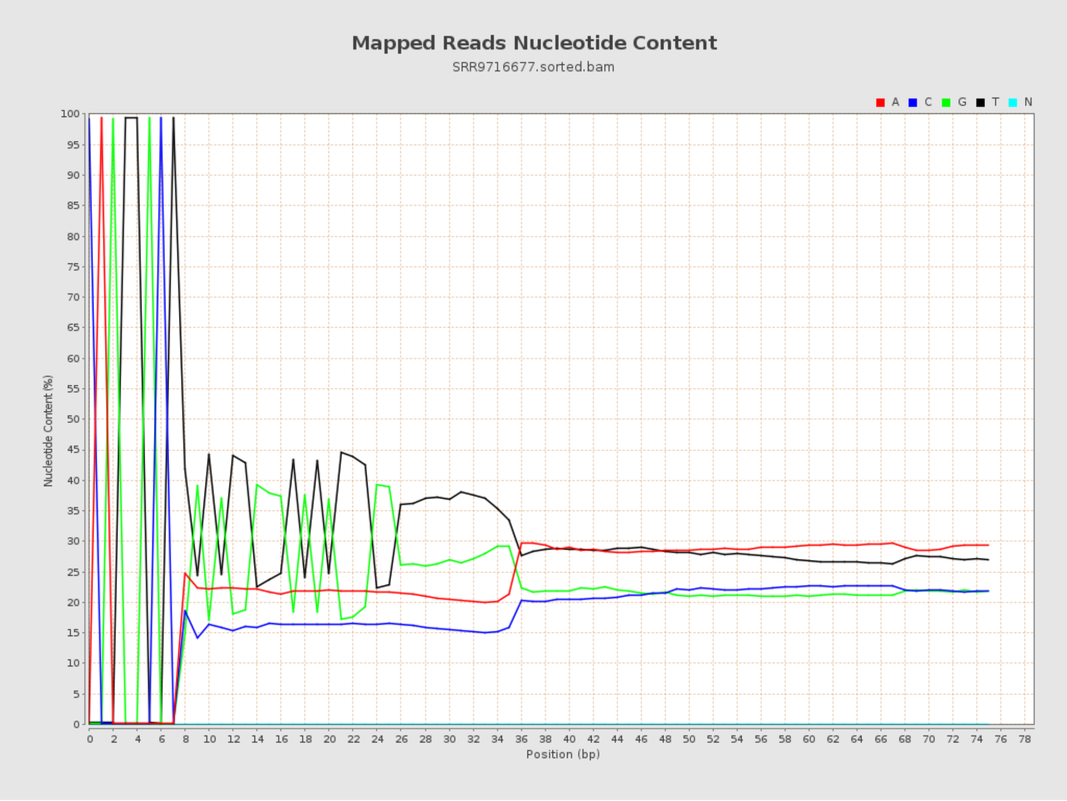
6. Results : Genome Fraction Coverage



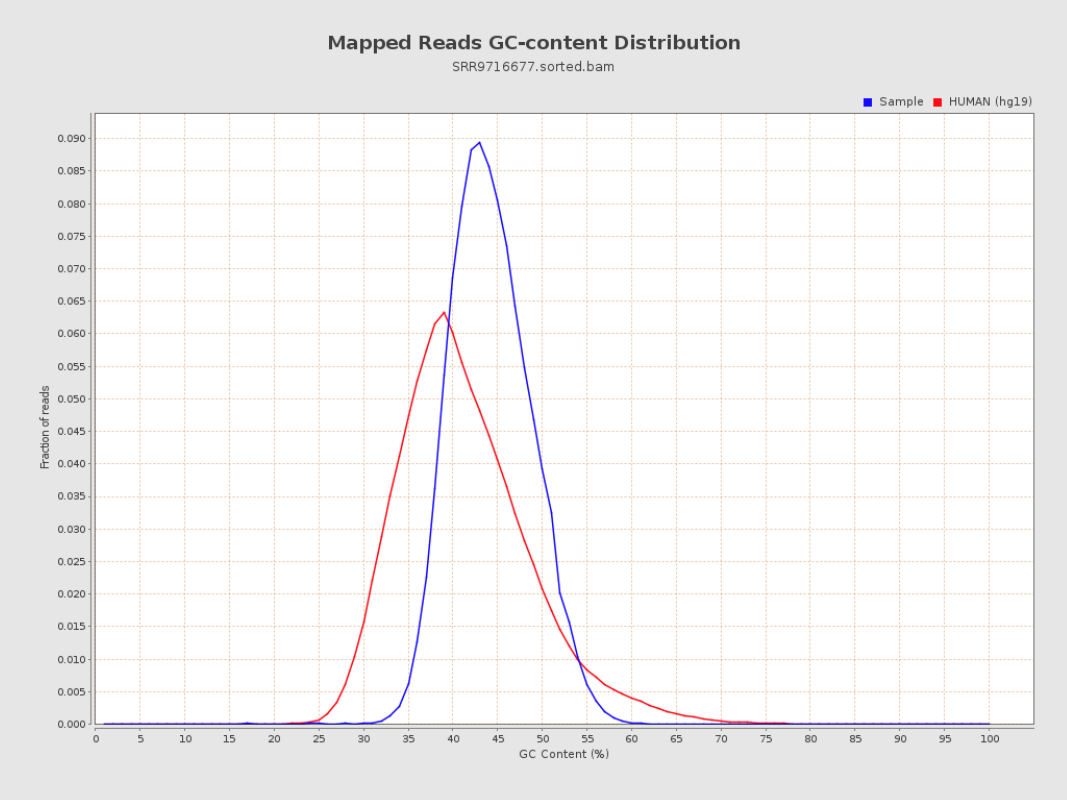
7. Results : Duplication Rate Histogram



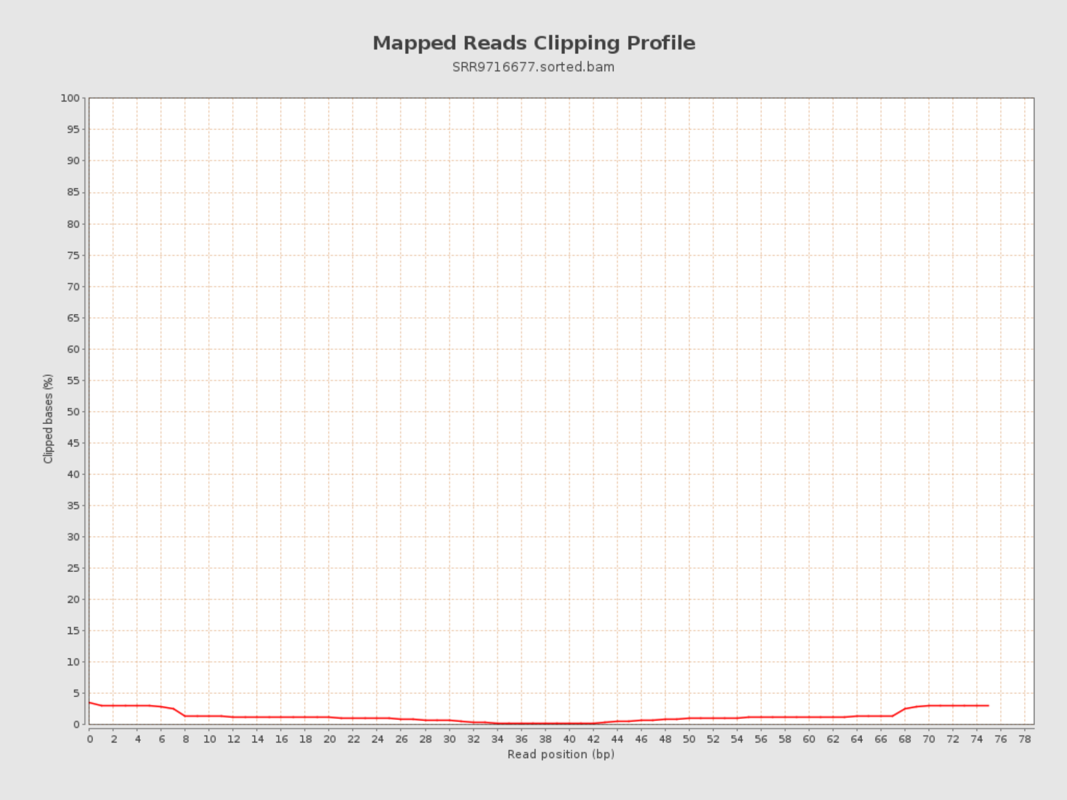
8. Results : Mapped Reads Nucleotide Content



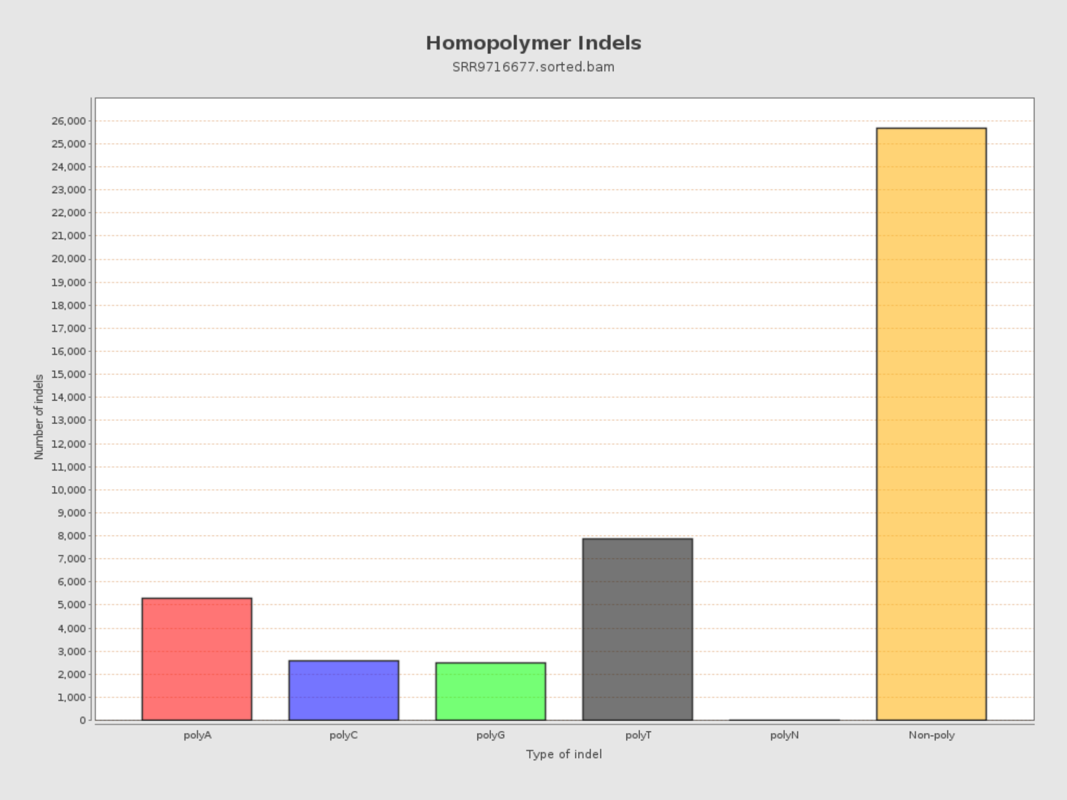
9. Results : Mapped Reads GC-content Distribution



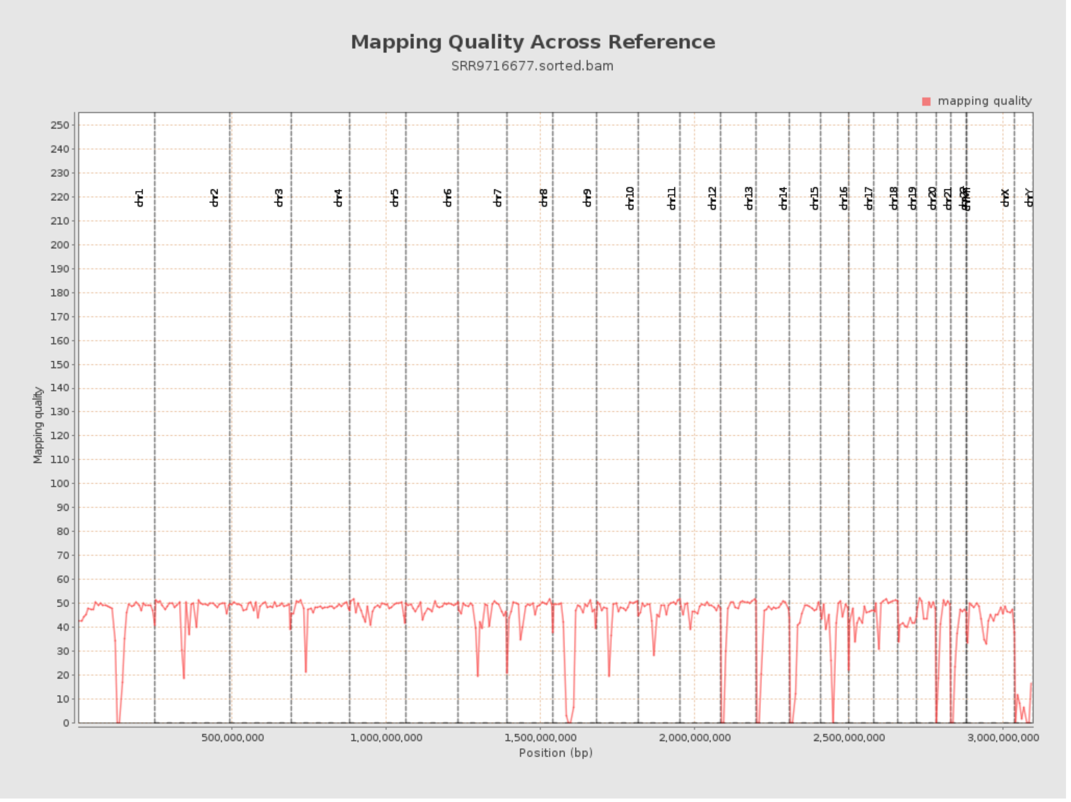
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram