Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:29:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716997.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_SRR9716997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716997.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:29:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,102,307
Mapped reads	2,744,926 / 88.48%
Unmapped reads	357,381 / 11.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,255 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	129,365 / 4.17%
Duplication rate	3.54%
Clipped reads	2,748,775 / 88.6%

2.2. ACGT Content

Number/percentage of A's	41,143,351 / 26.09%
Number/percentage of C's	29,165,212 / 18.49%
Number/percentage of T's	48,650,082 / 30.85%
Number/percentage of G's	38,754,796 / 24.57%
Number/percentage of N's	1,159 / 0%
GC Percentage	43.07%

2.3. Coverage

Mean	0.051

Standard Deviation	0.3792

2.4. Mapping Quality

Mean Mapping Quality	44.01

2.5. Mismatches and indels

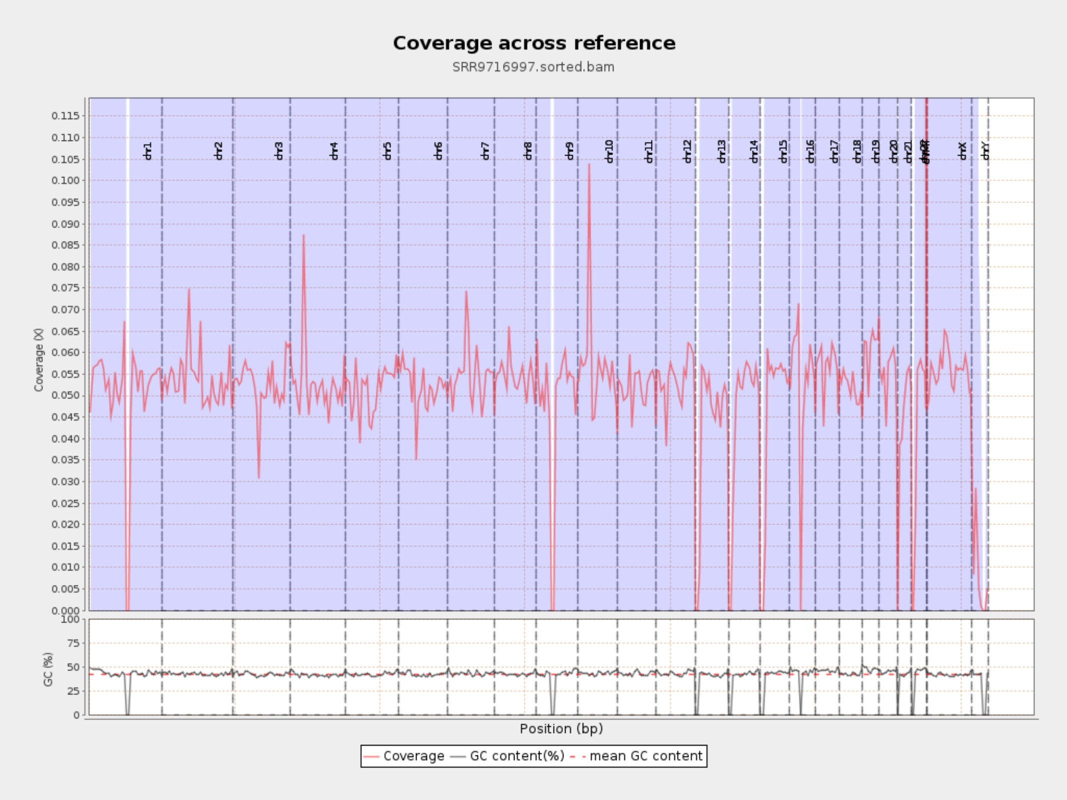
General error rate	0.54%
Mismatches	823,380
Insertions	10,933
Mapped reads with at least one insertion	0.4%
Deletions	29,032
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.41%

2.6. Chromosome stats

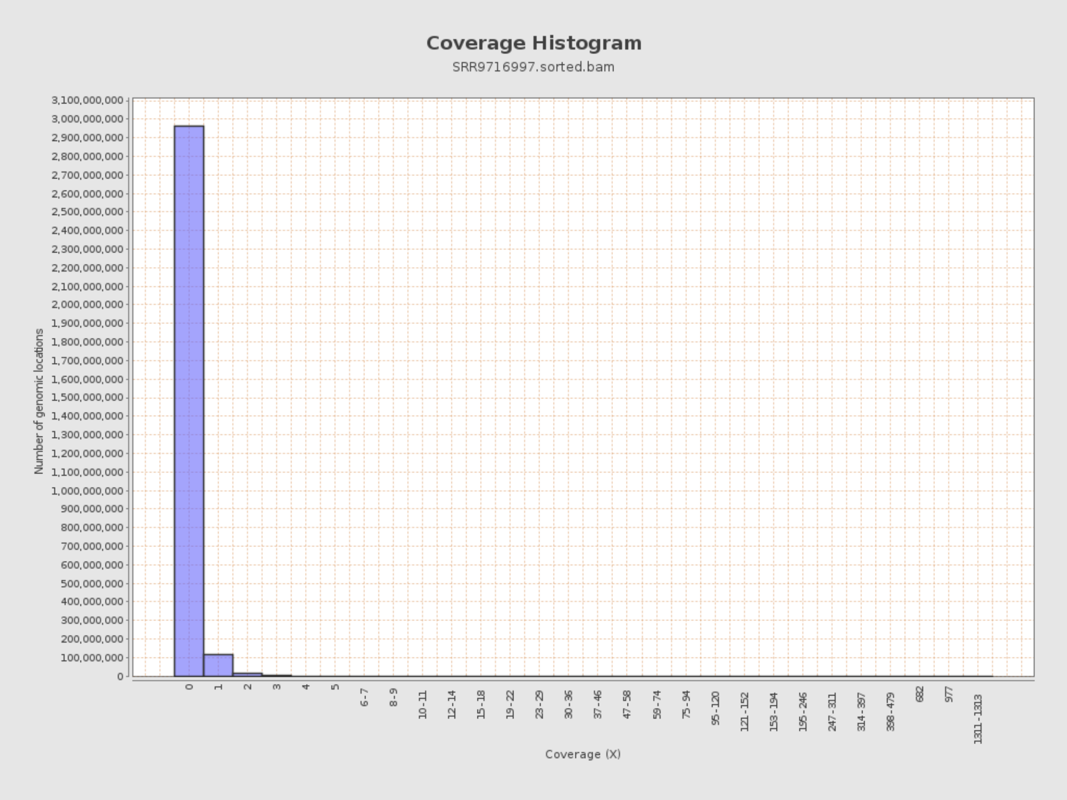
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12559781	0.0504	0.4801
chr2	243199373	13104870	0.0539	0.6263
chr3	198022430	10389081	0.0525	0.2716
chr4	191154276	10057789	0.0526	0.3187
chr5	180915260	9316676	0.0515	0.2648
chr6	171115067	8927981	0.0522	0.3152
chr7	159138663	8727827	0.0548	0.4667

chr8	146364022	7980718	0.0545	0.3852
chr9	141213431	6637789	0.047	0.3242
chr10	135534747	7739718	0.0571	0.4791
chr11	135006516	7011041	0.0519	0.3407
chr12	133851895	7225476	0.054	0.275
chr13	115169878	4819548	0.0418	0.2383
chr14	107349540	4841921	0.0451	0.2674
chr15	102531392	4637038	0.0452	0.2557
chr16	90354753	4808843	0.0532	0.3032
chr17	81195210	4587526	0.0565	0.2928
chr18	78077248	4076849	0.0522	0.5339
chr19	59128983	3585815	0.0606	0.4415
chr20	63025520	3458881	0.0549	0.2886
chr21	48129895	2101499	0.0437	0.2888
chr22	51304566	1991793	0.0388	0.2335
chrMT	16571	23823	1.4376	1.5427
chrX	155270560	8657669	0.0558	0.3084
chrY	59373566	491219	0.0083	0.2373

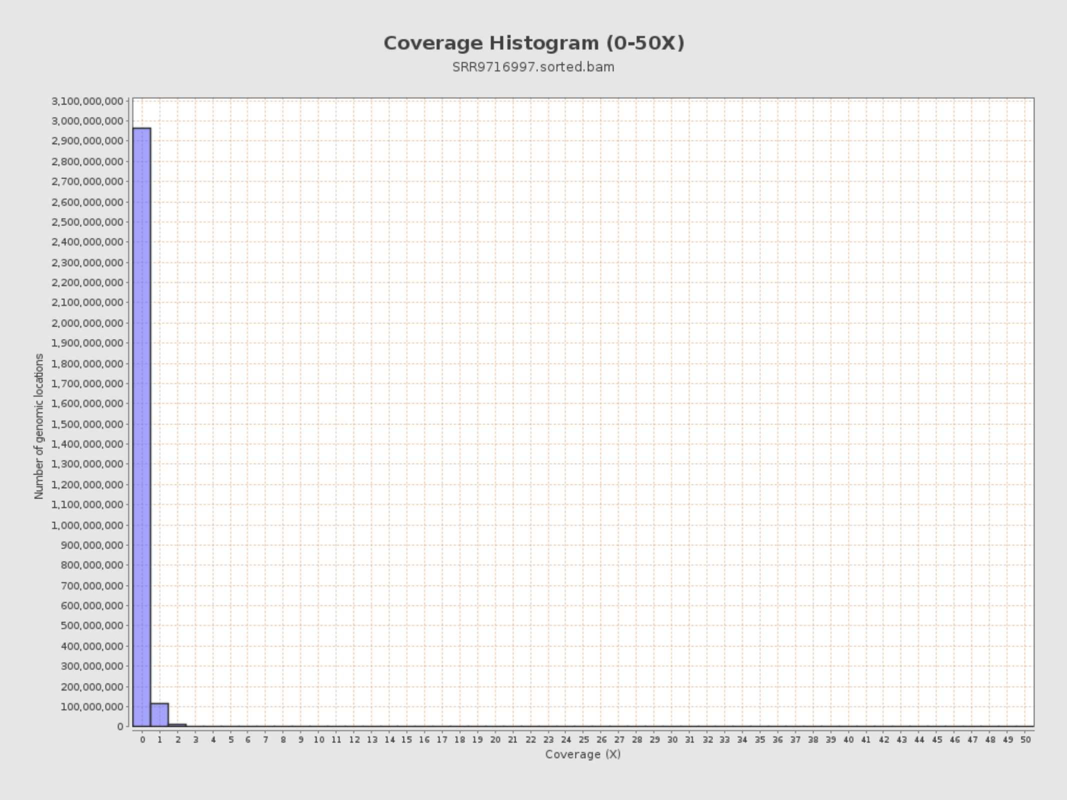
3. Results : Coverage across reference



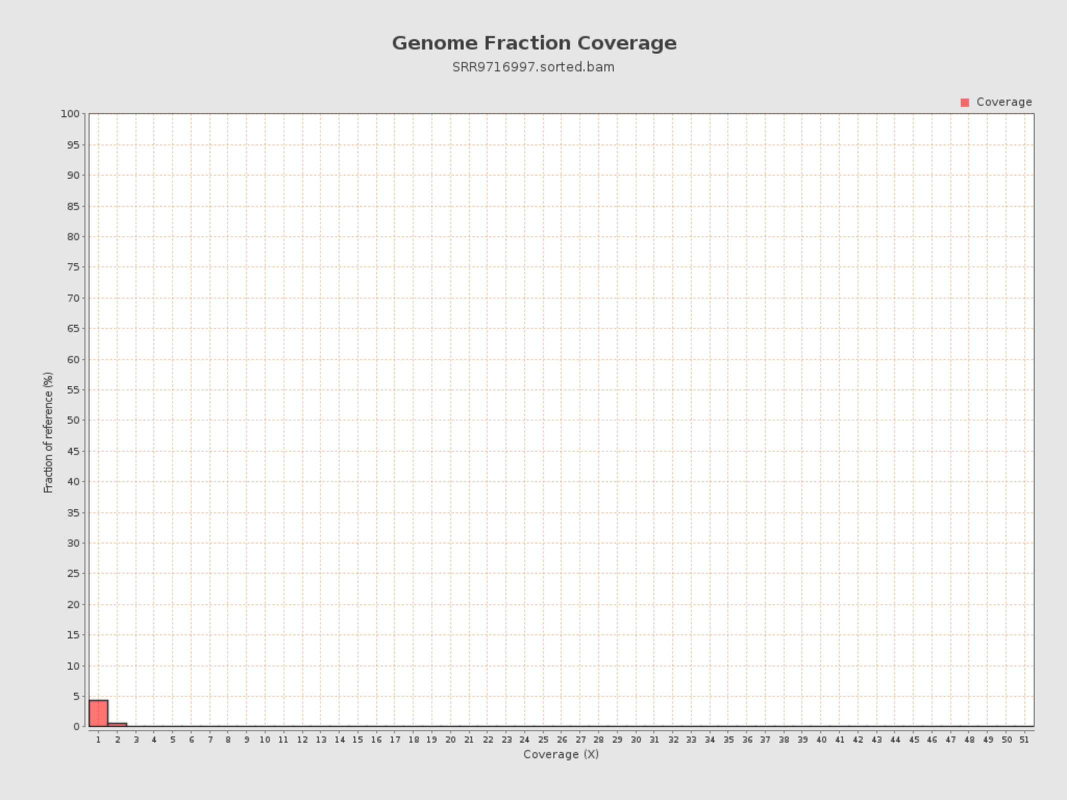
4. Results : Coverage Histogram



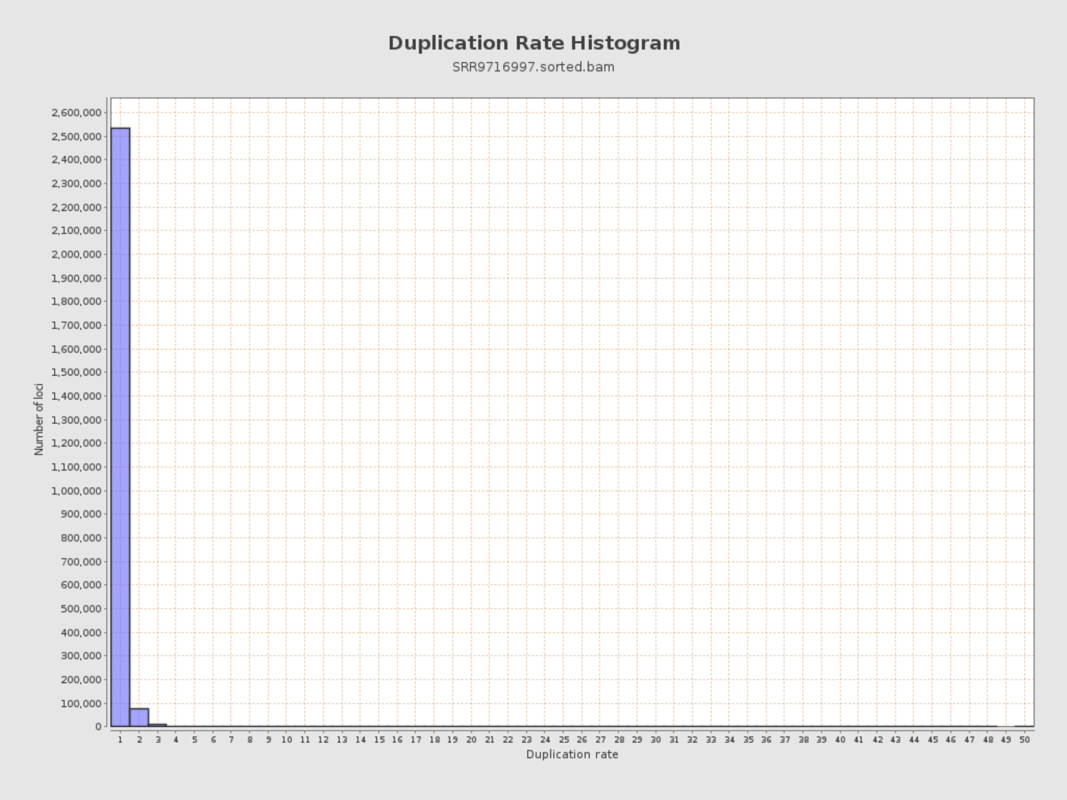
5. Results : Coverage Histogram (0-50X)



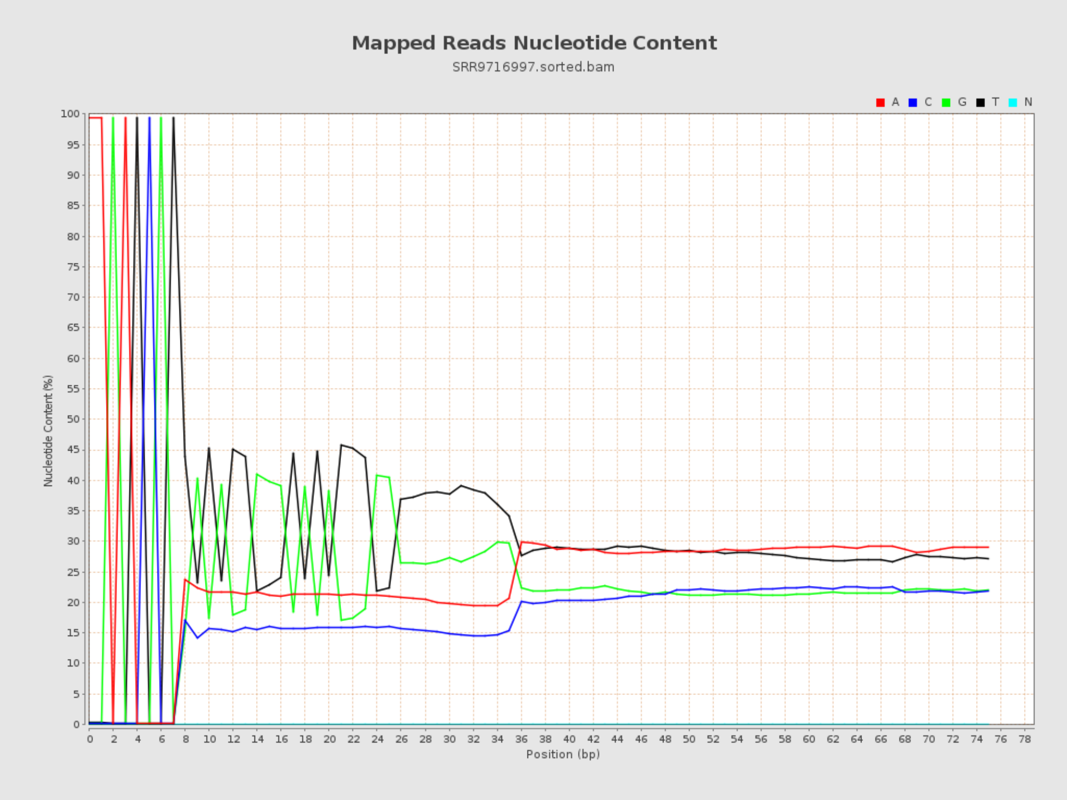
6. Results : Genome Fraction Coverage



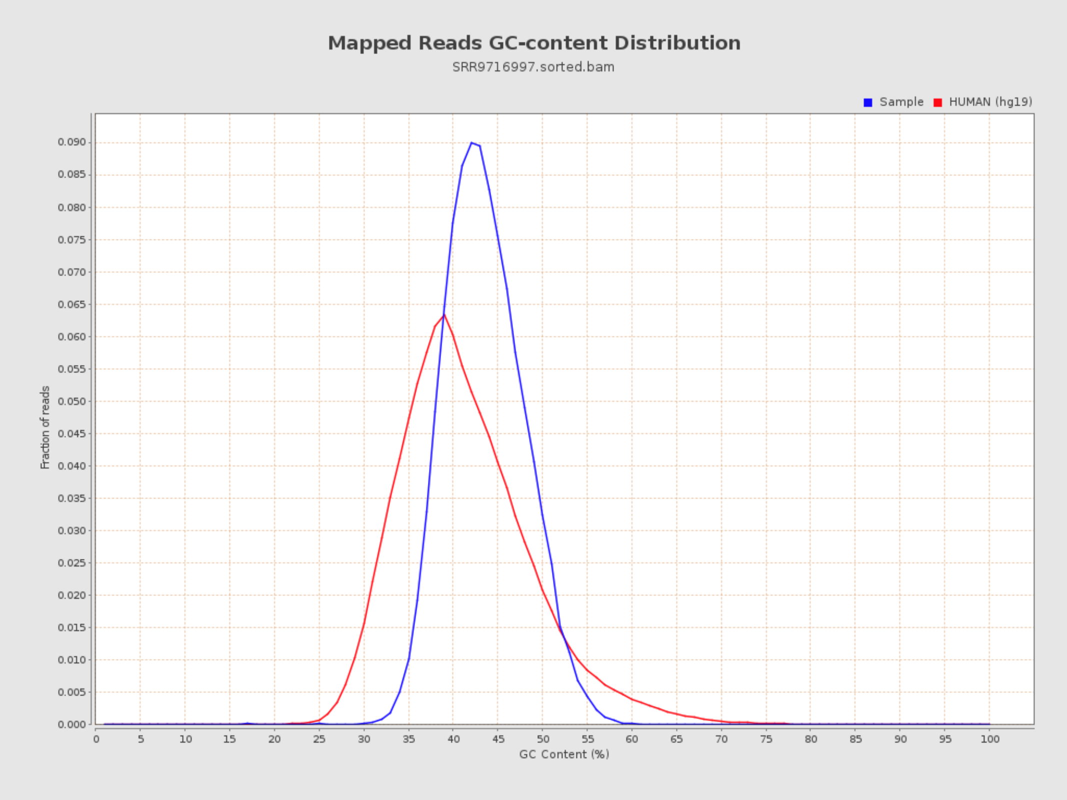
7. Results : Duplication Rate Histogram



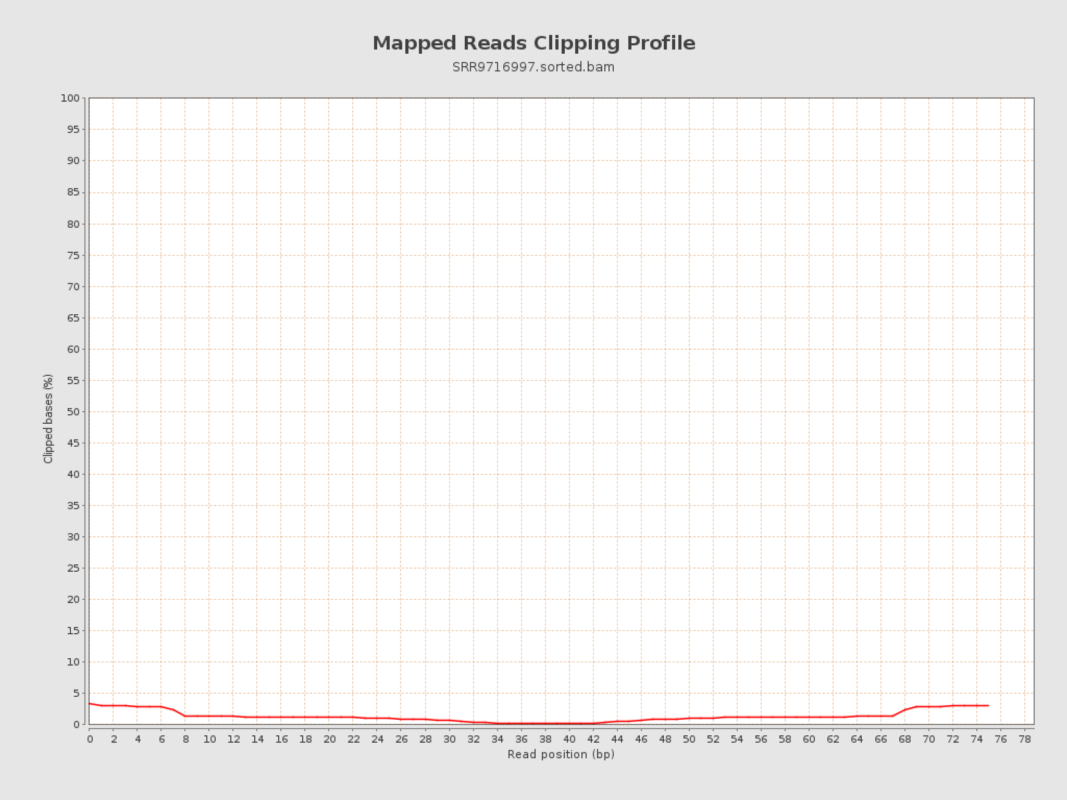
8. Results : Mapped Reads Nucleotide Content



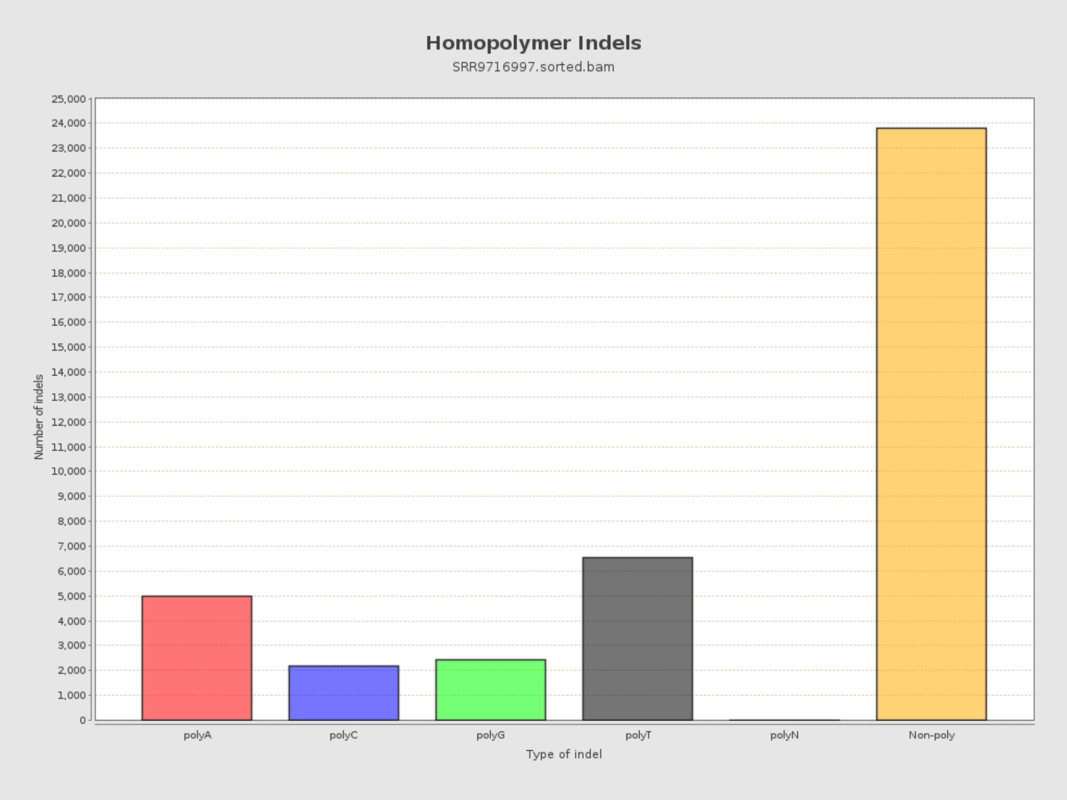
9. Results : Mapped Reads GC-content Distribution



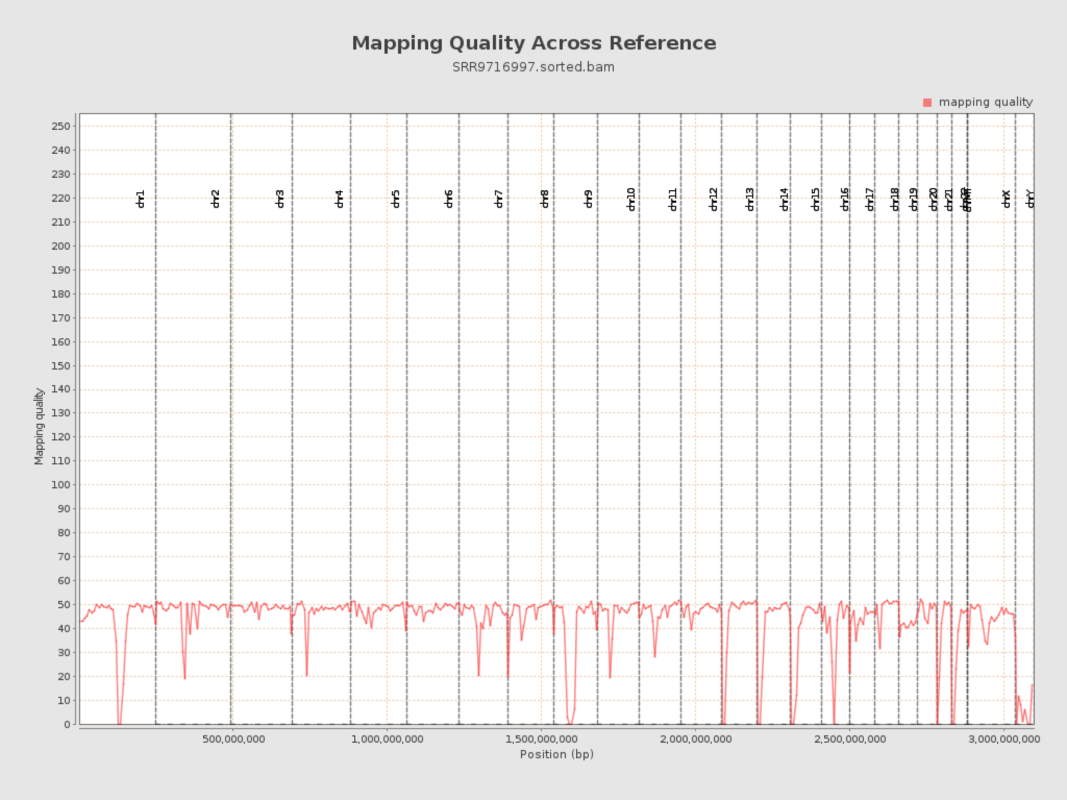
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram