Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:04:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716903.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_SRR9716903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716903.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:04:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,903,679
Mapped reads	2,692,529 / 68.97%
Unmapped reads	1,211,150 / 31.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,098 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	158,845 / 4.07%
Duplication rate	4.6%
Clipped reads	2,705,013 / 69.29%

2.2. ACGT Content

Number/percentage of A's	41,735,800 / 26.67%
Number/percentage of C's	29,564,478 / 18.89%
Number/percentage of T's	47,475,523 / 30.33%
Number/percentage of G's	37,733,107 / 24.11%
Number/percentage of N's	1,985 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.3902

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

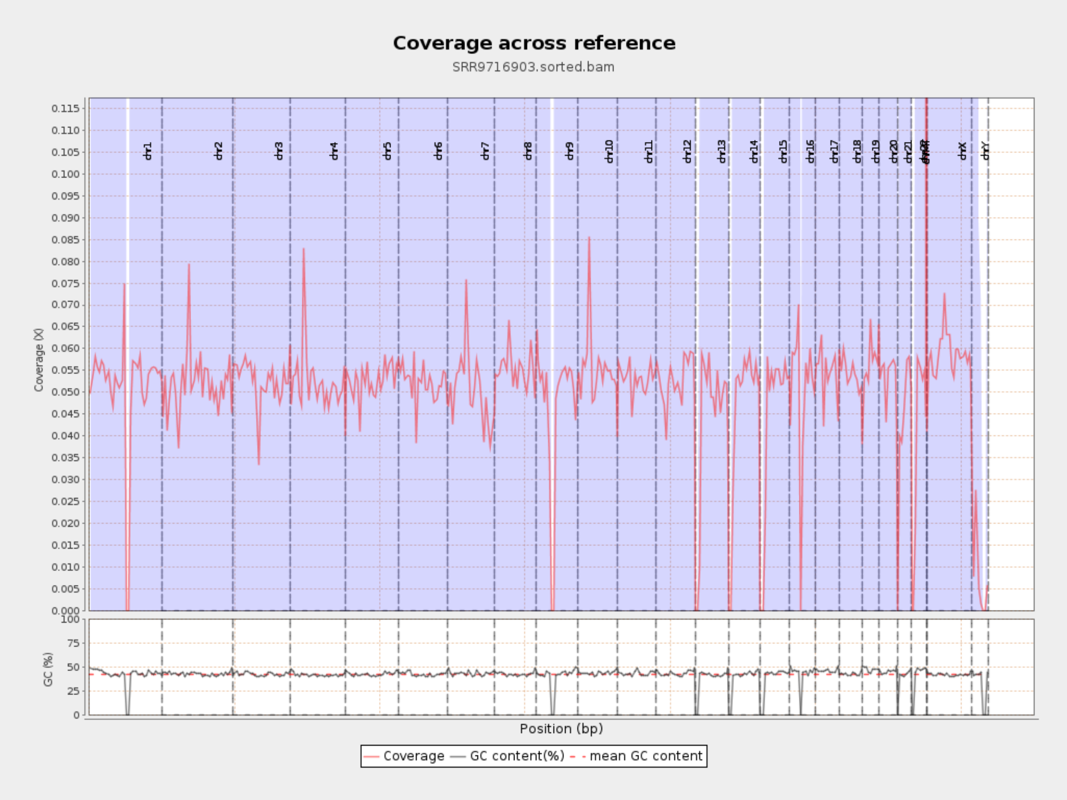
General error rate	0.51%
Mismatches	781,061
Insertions	10,702
Mapped reads with at least one insertion	0.4%
Deletions	26,007
Mapped reads with at least one deletion	0.96%
Homopolymer indels	40.05%

2.6. Chromosome stats

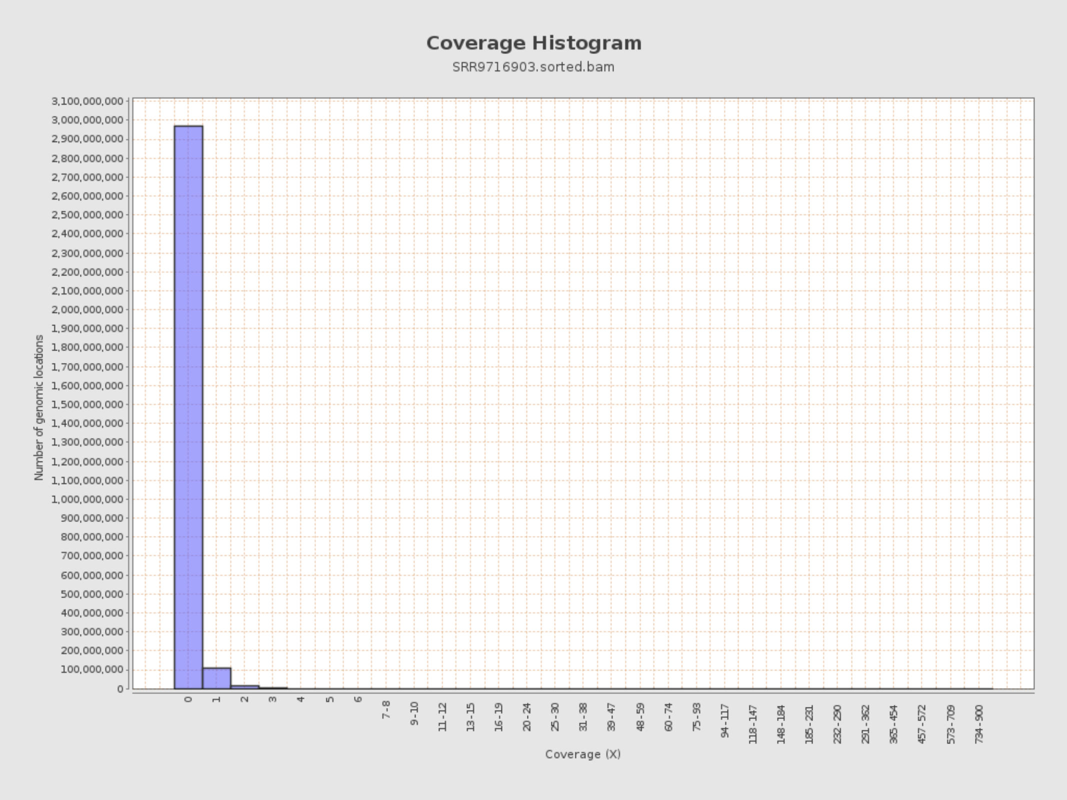
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12657070	0.0508	0.673
chr2	243199373	12686914	0.0522	0.5066
chr3	198022430	10382536	0.0524	0.2715
chr4	191154276	10023524	0.0524	0.3163
chr5	180915260	9518084	0.0526	0.2718
chr6	171115067	8952947	0.0523	0.297
chr7	159138663	8070377	0.0507	0.4592

chr8	146364022	8102016	0.0554	0.4158
chr9	141213431	6478651	0.0459	0.3229
chr10	135534747	7550532	0.0557	0.4071
chr11	135006516	7145640	0.0529	0.3517
chr12	133851895	7073172	0.0528	0.2773
chr13	115169878	4980491	0.0432	0.2487
chr14	107349540	4893351	0.0456	0.263
chr15	102531392	4496692	0.0439	0.2593
chr16	90354753	4549189	0.0503	0.2825
chr17	81195210	4379968	0.0539	0.3078
chr18	78077248	4258903	0.0545	0.5963
chr19	59128983	3340136	0.0565	0.5245
chr20	63025520	3379346	0.0536	0.2828
chr21	48129895	2103117	0.0437	0.2858
chr22	51304566	1948356	0.038	0.2302
chrMT	16571	31584	1.906	1.8839
chrX	155270560	9069123	0.0584	0.3211
chrY	59373566	480602	0.0081	0.2028

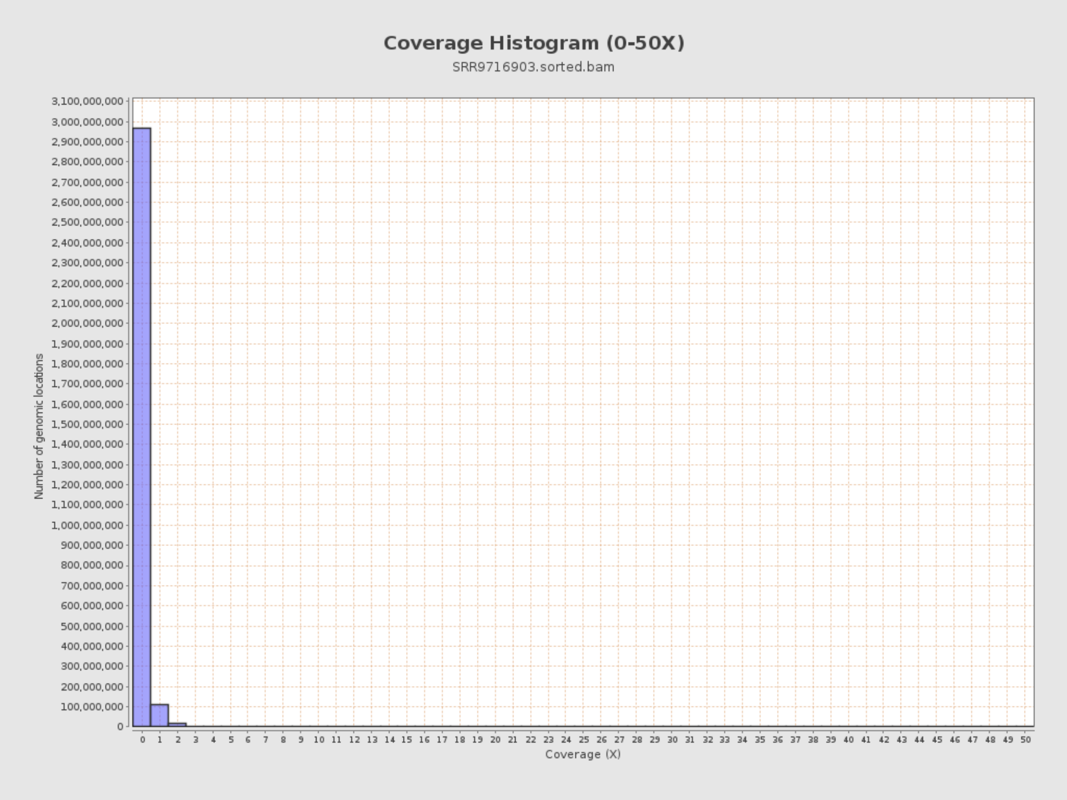
3. Results : Coverage across reference



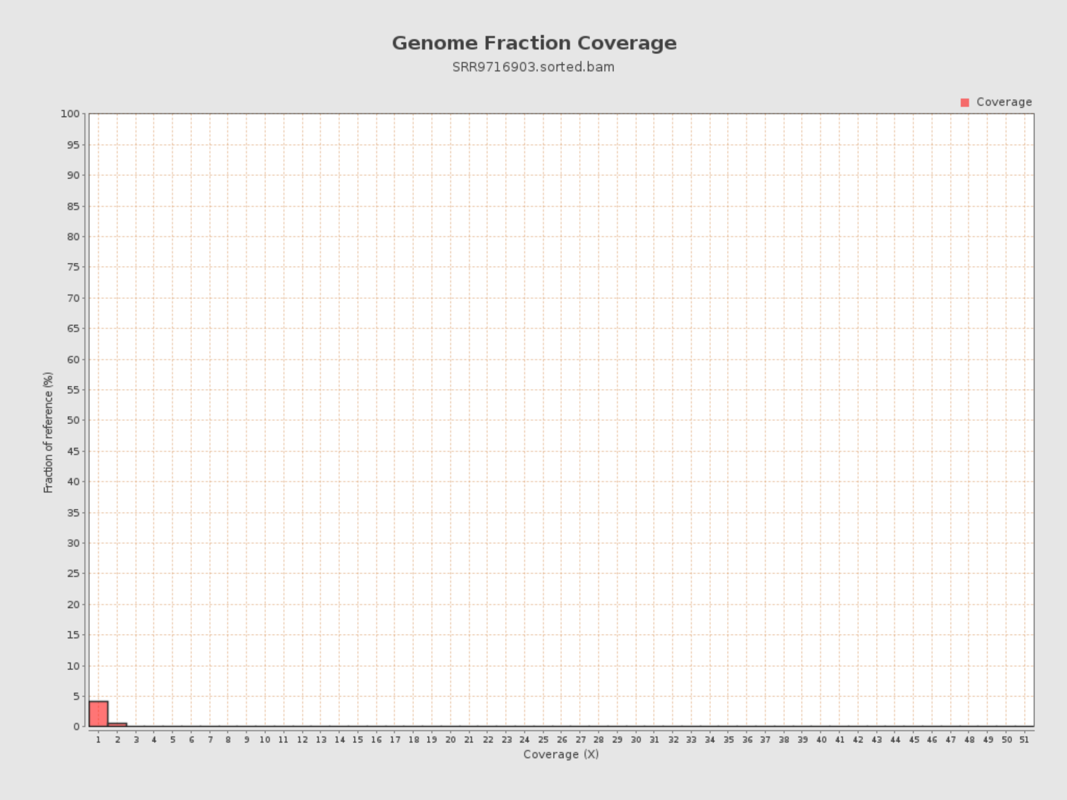
4. Results : Coverage Histogram



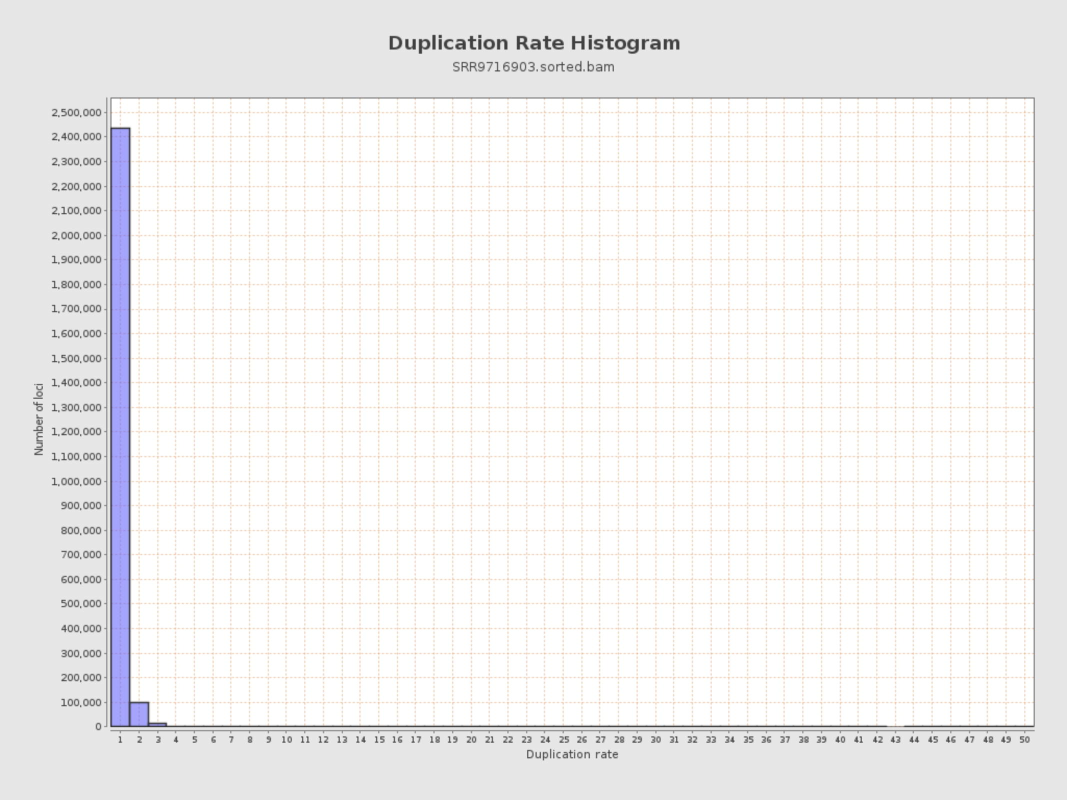
5. Results : Coverage Histogram (0-50X)



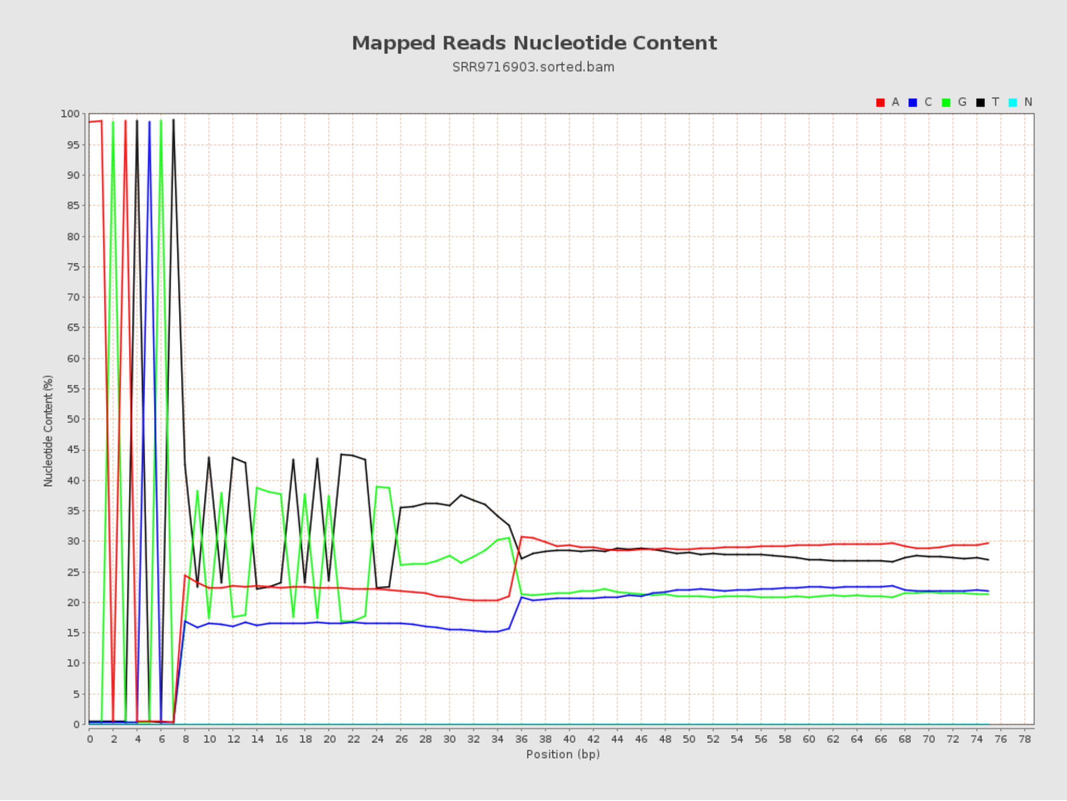
6. Results : Genome Fraction Coverage



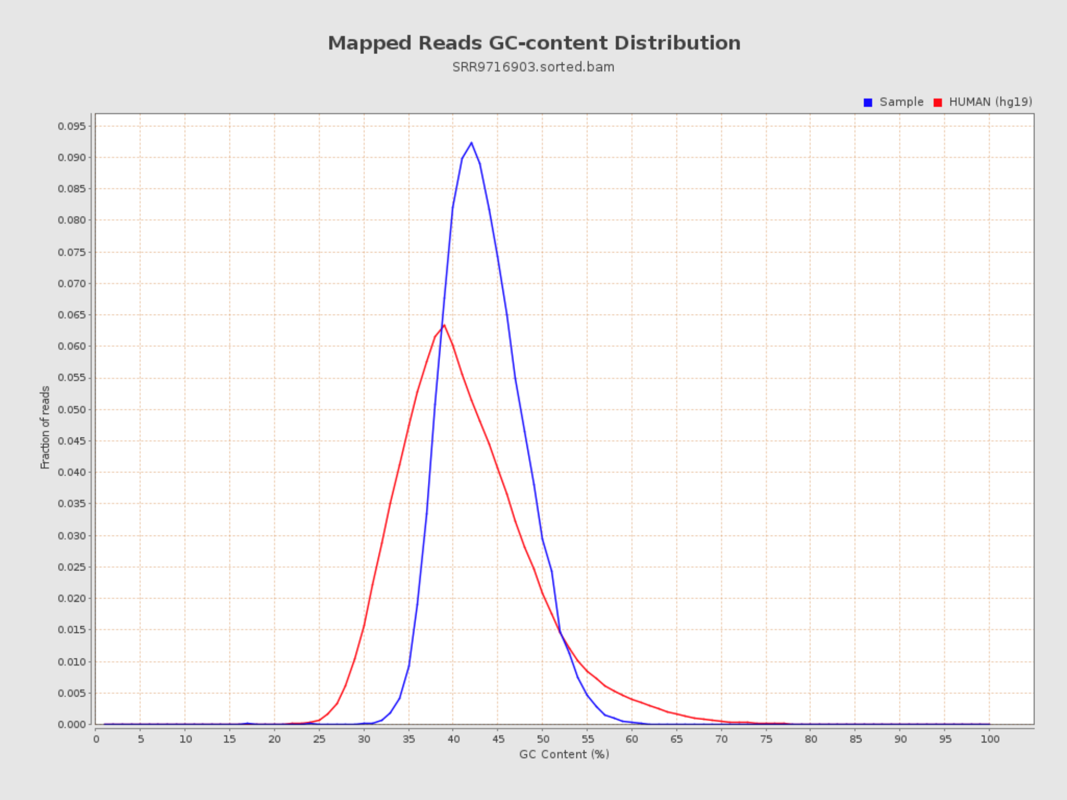
7. Results : Duplication Rate Histogram



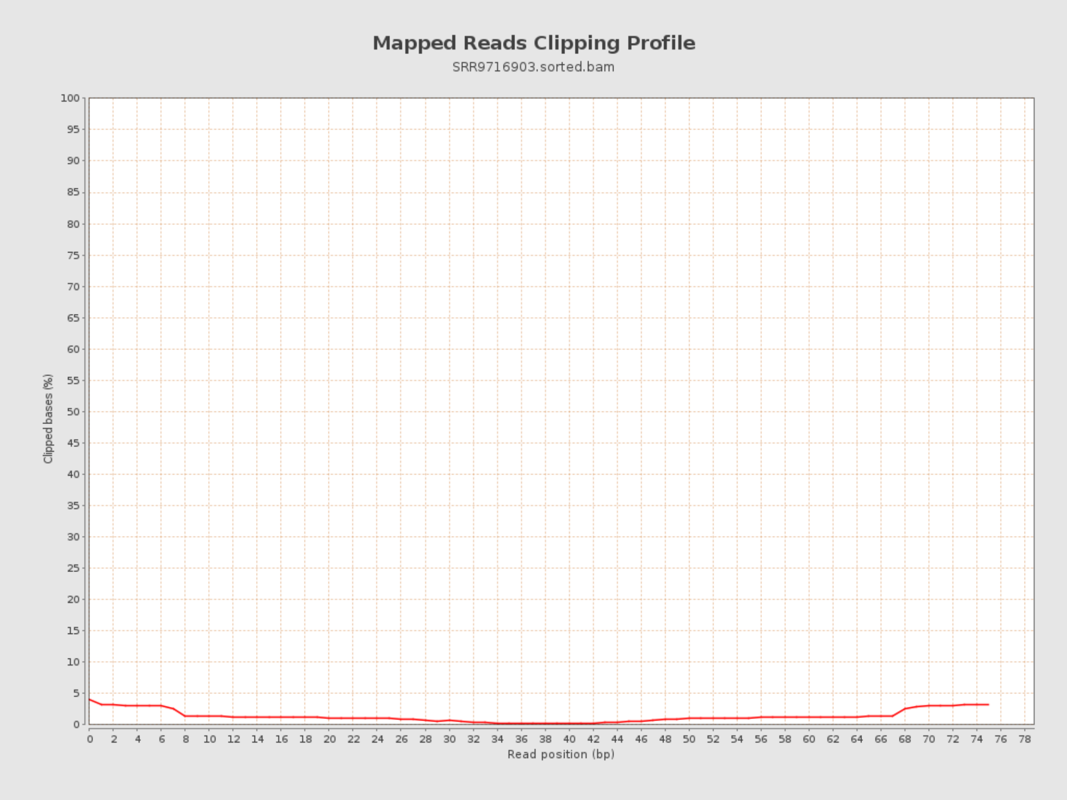
8. Results : Mapped Reads Nucleotide Content



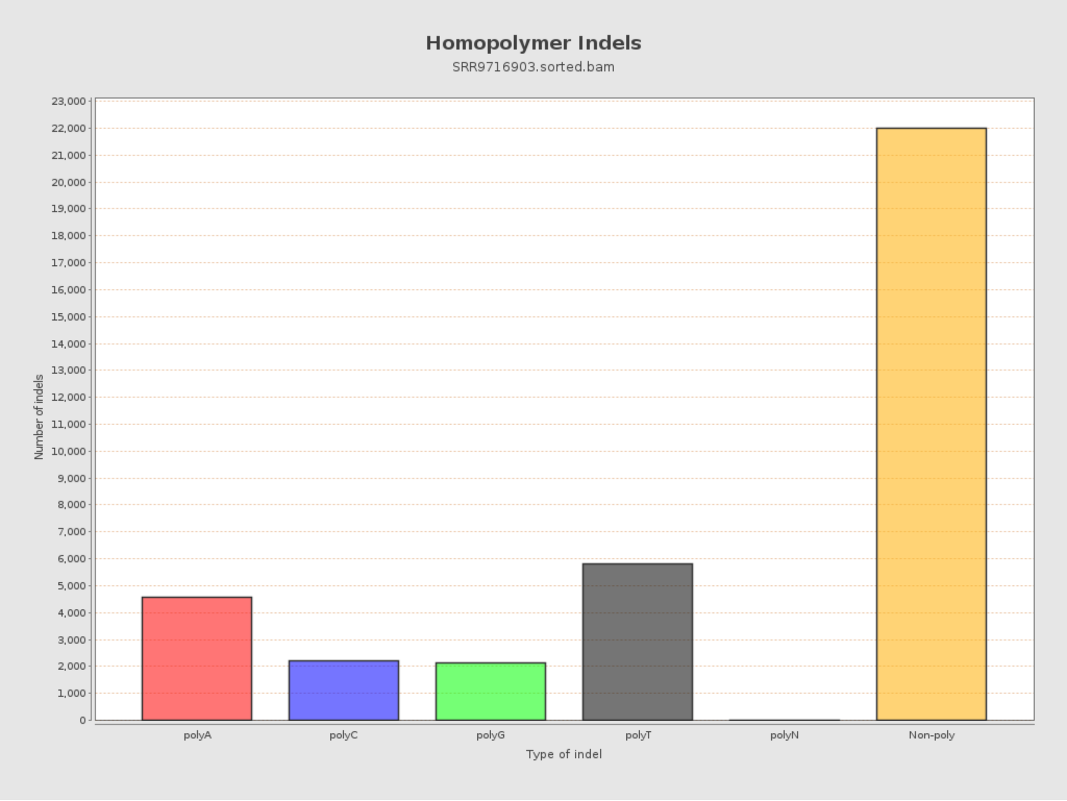
9. Results : Mapped Reads GC-content Distribution



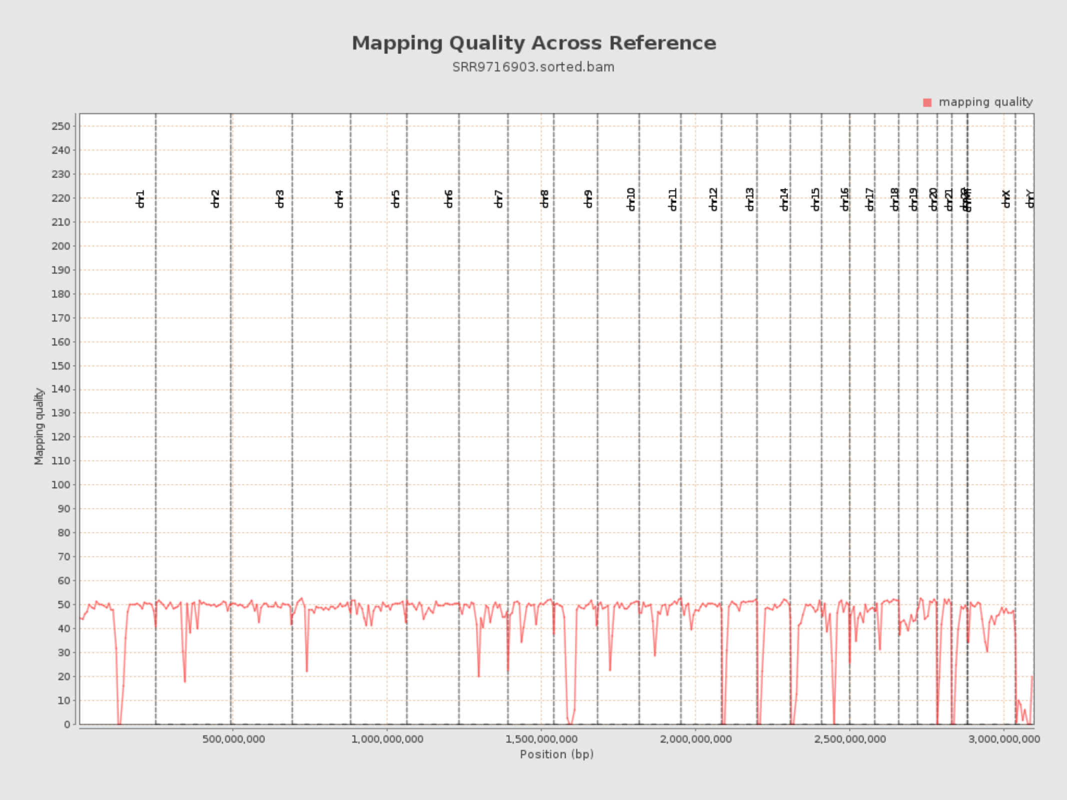
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram