Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:26:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716996.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_SRR9716996 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716996.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:26:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716996.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,411,934
Mapped reads	1,255,348 / 88.91%
Unmapped reads	156,586 / 11.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,042 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	41,235 / 2.92%
Duplication rate	2.34%
Clipped reads	1,259,309 / 89.19%

2.2. ACGT Content

Number/percentage of A's	18,368,889 / 25.42%
Number/percentage of C's	13,157,384 / 18.21%
Number/percentage of T's	23,148,782 / 32.04%
Number/percentage of G's	17,575,342 / 24.33%
Number/percentage of N's	1,019 / 0%
GC Percentage	42.54%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2425

2.4. Mapping Quality

Mean Mapping Quality	43.26

2.5. Mismatches and indels

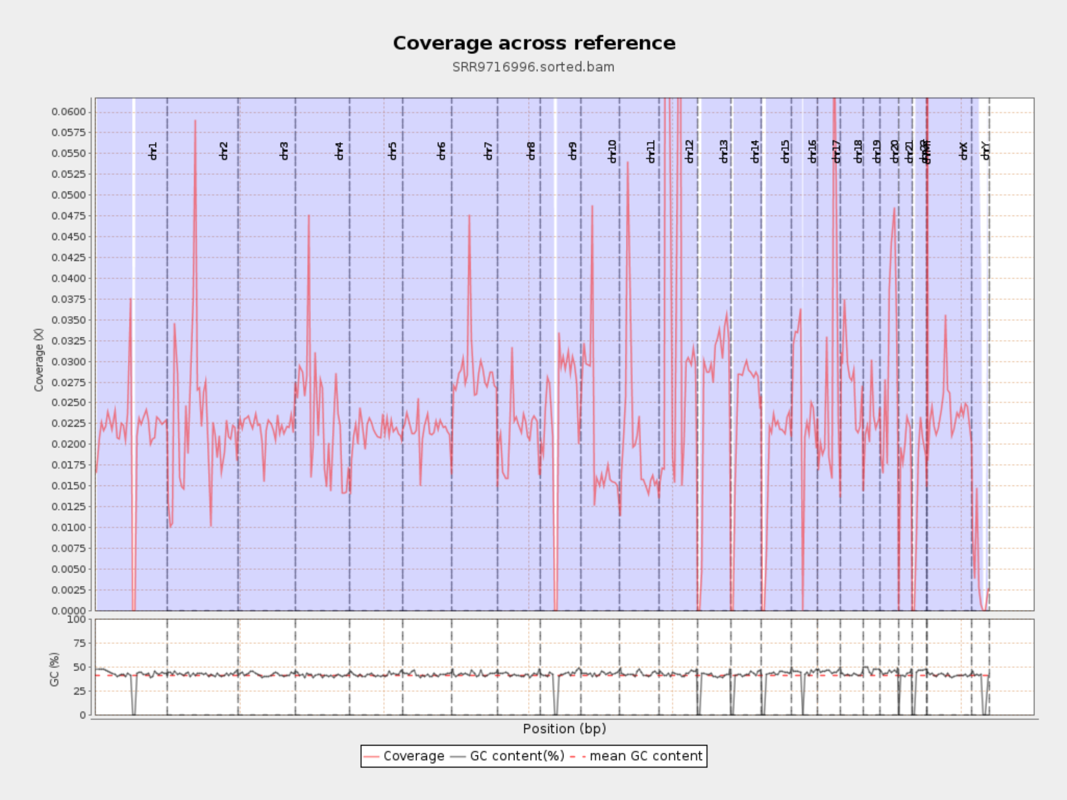
General error rate	0.57%
Mismatches	403,681
Insertions	5,140
Mapped reads with at least one insertion	0.41%
Deletions	11,901
Mapped reads with at least one deletion	0.94%
Homopolymer indels	41.39%

2.6. Chromosome stats

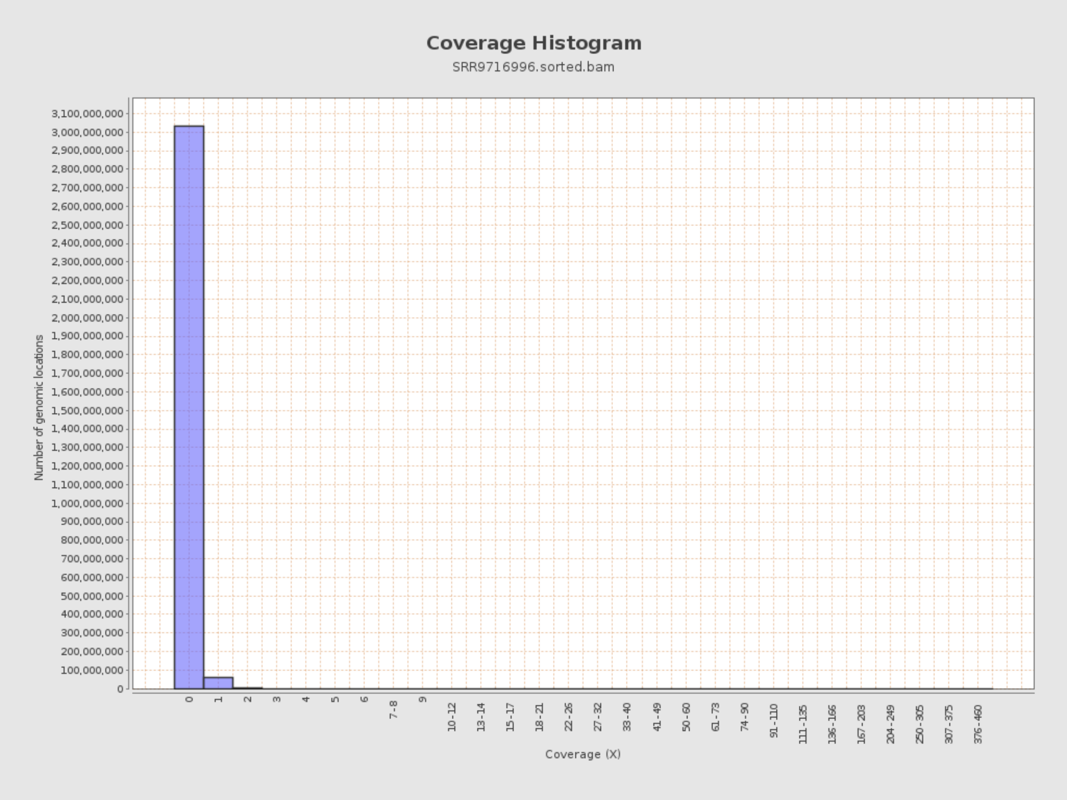
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5277184	0.0212	0.3863
chr2	243199373	5436365	0.0224	0.2799
chr3	198022430	4361750	0.022	0.1584
chr4	191154276	4424784	0.0231	0.1885
chr5	180915260	3920724	0.0217	0.1584
chr6	171115067	3722010	0.0218	0.1674
chr7	159138663	4608873	0.029	0.3218

chr8	146364022	3142968	0.0215	0.2133
chr9	141213431	3367051	0.0238	0.2584
chr10	135534747	2881437	0.0213	0.2652
chr11	135006516	2807679	0.0208	0.1968
chr12	133851895	5427171	0.0405	0.2346
chr13	115169878	2987775	0.0259	0.1703
chr14	107349540	2551788	0.0238	0.1862
chr15	102531392	1851770	0.0181	0.143
chr16	90354753	2196028	0.0243	0.1862
chr17	81195210	2280642	0.0281	0.1846
chr18	78077248	2153976	0.0276	0.4723
chr19	59128983	1348925	0.0228	0.3239
chr20	63025520	1949497	0.0309	0.1963
chr21	48129895	877023	0.0182	0.172
chr22	51304566	730330	0.0142	0.126
chrMT	16571	8633	0.521	0.7794
chrX	155270560	3720617	0.024	0.195
chrY	59373566	236789	0.004	0.1105

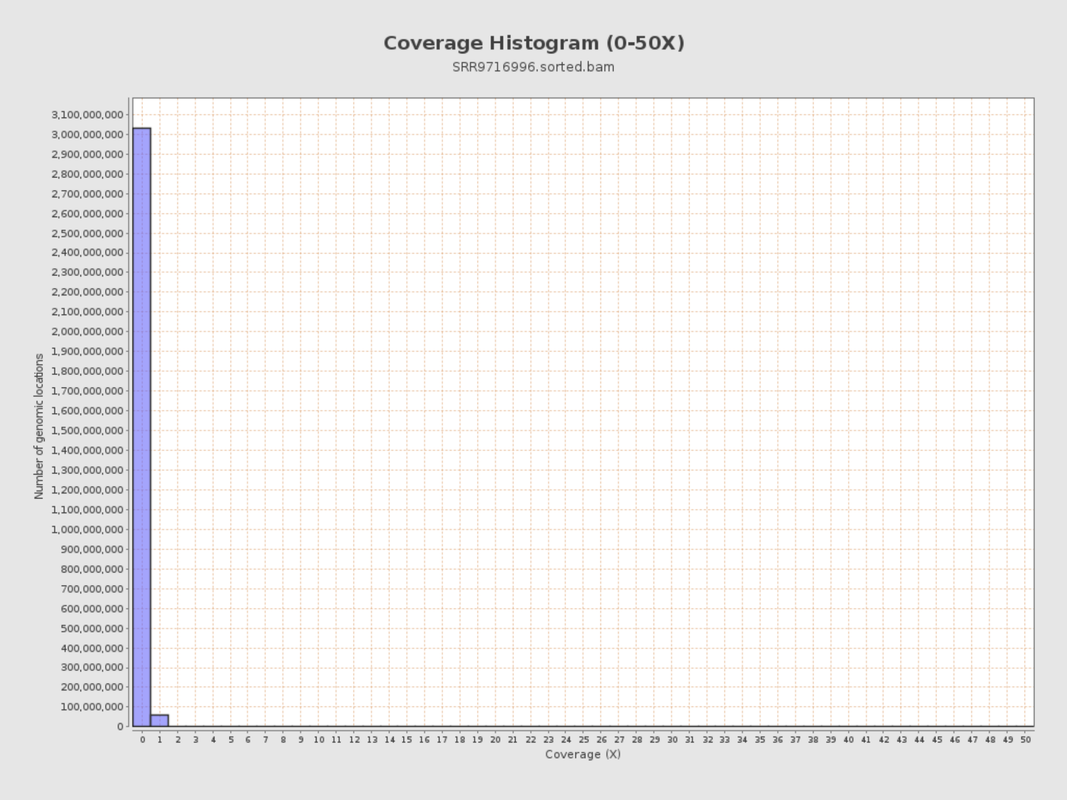
3. Results : Coverage across reference



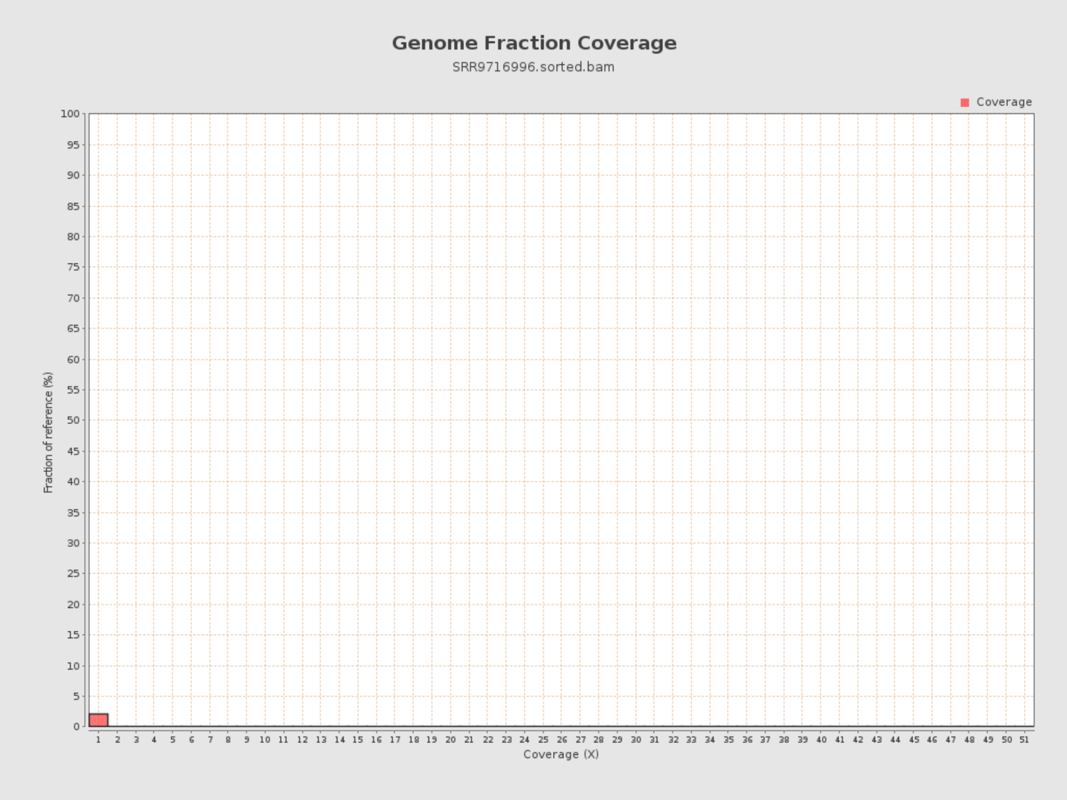
4. Results : Coverage Histogram



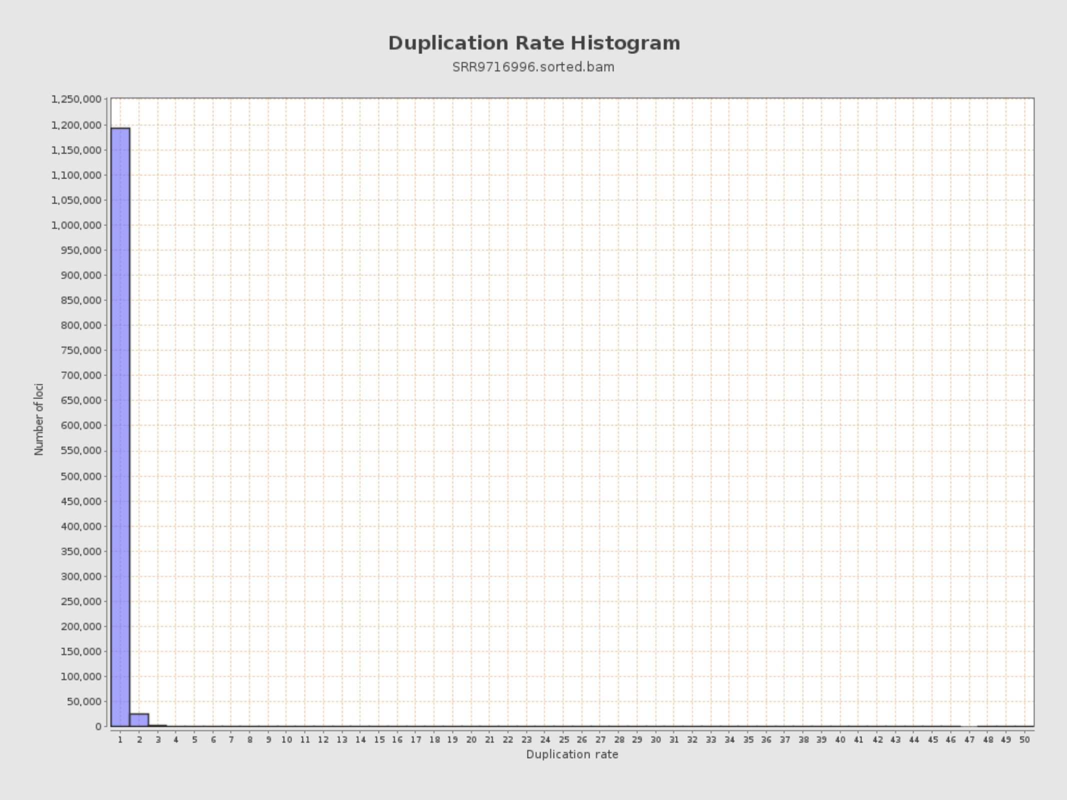
5. Results : Coverage Histogram (0-50X)



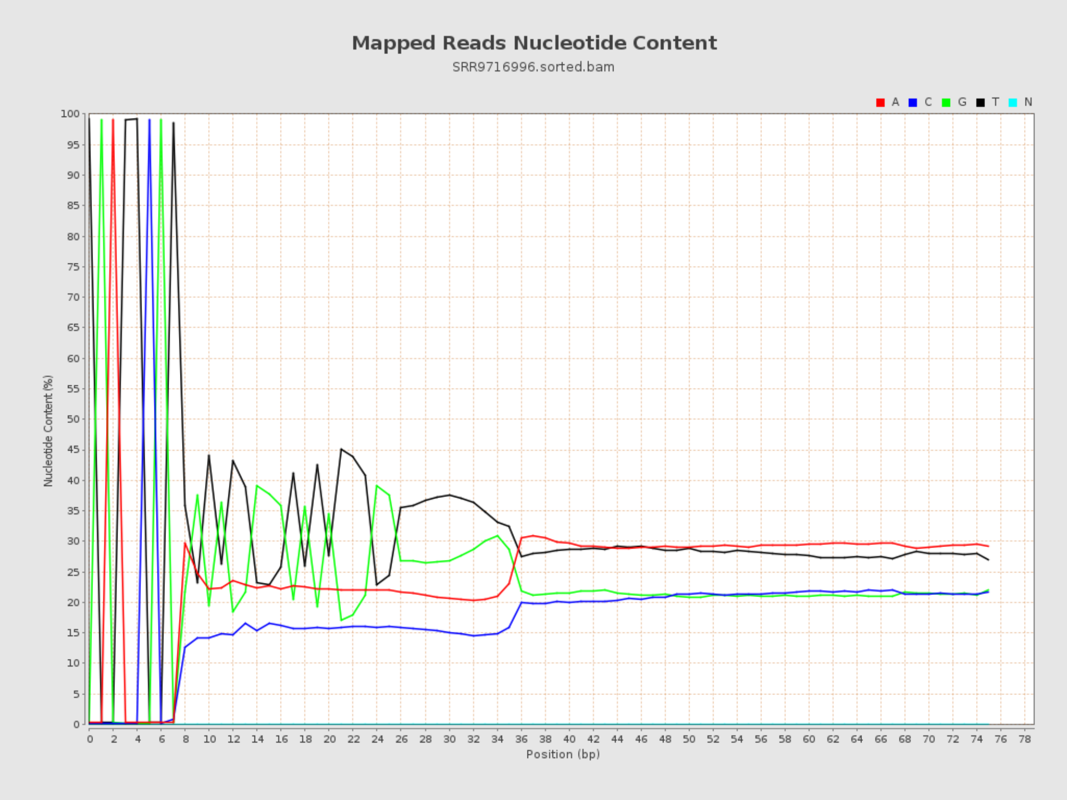
6. Results : Genome Fraction Coverage



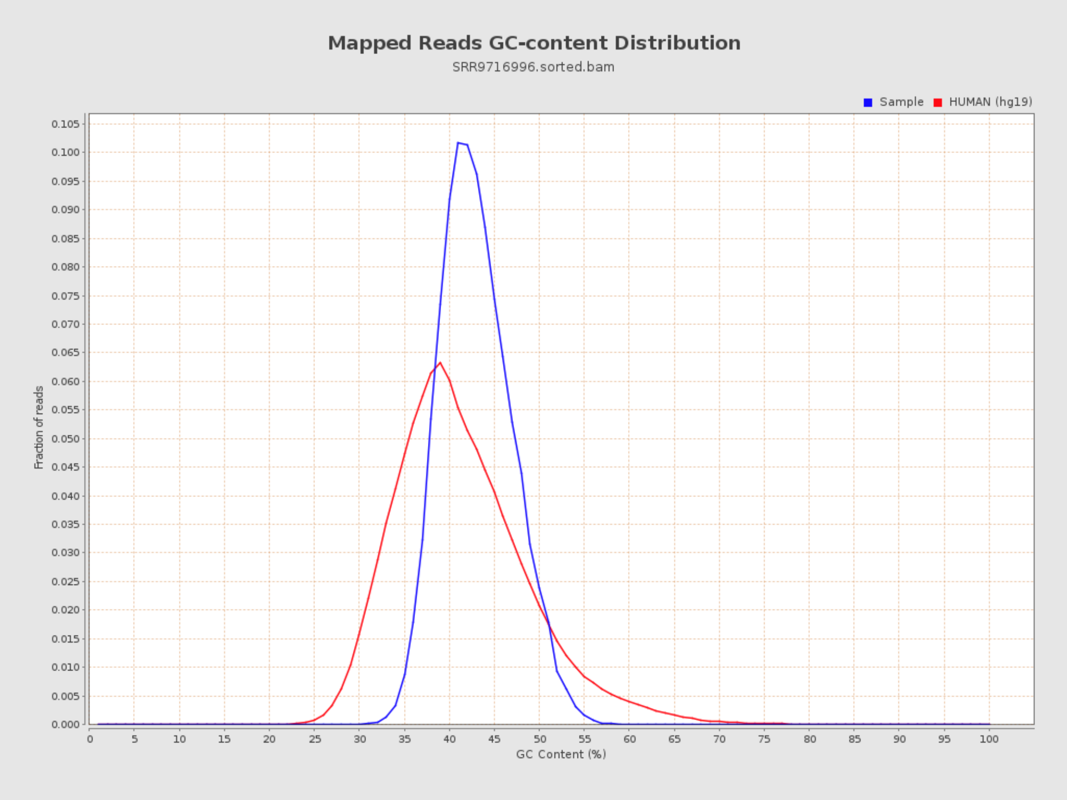
7. Results : Duplication Rate Histogram



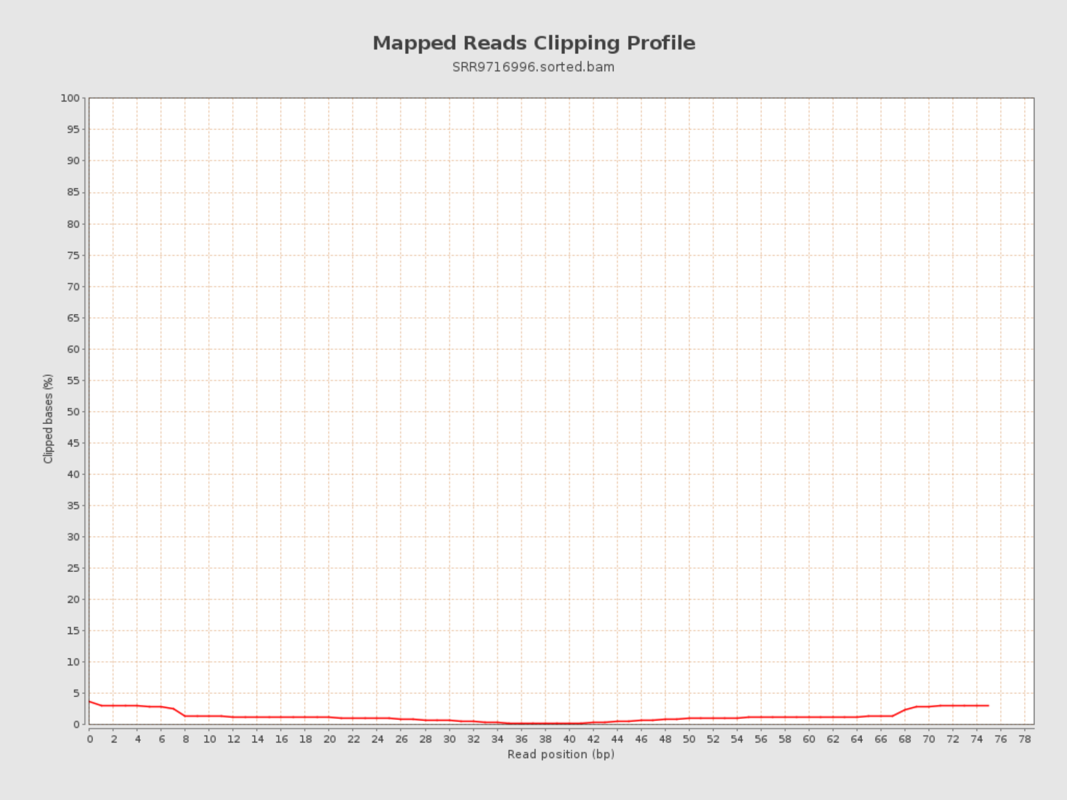
8. Results : Mapped Reads Nucleotide Content



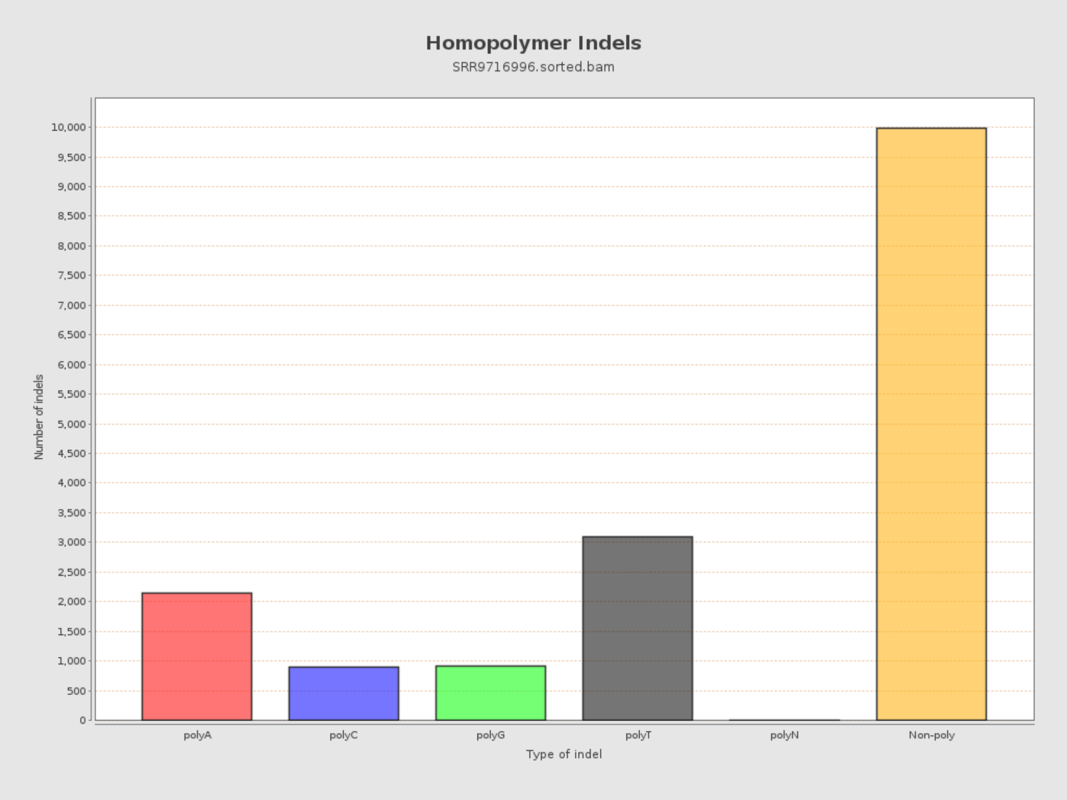
9. Results : Mapped Reads GC-content Distribution



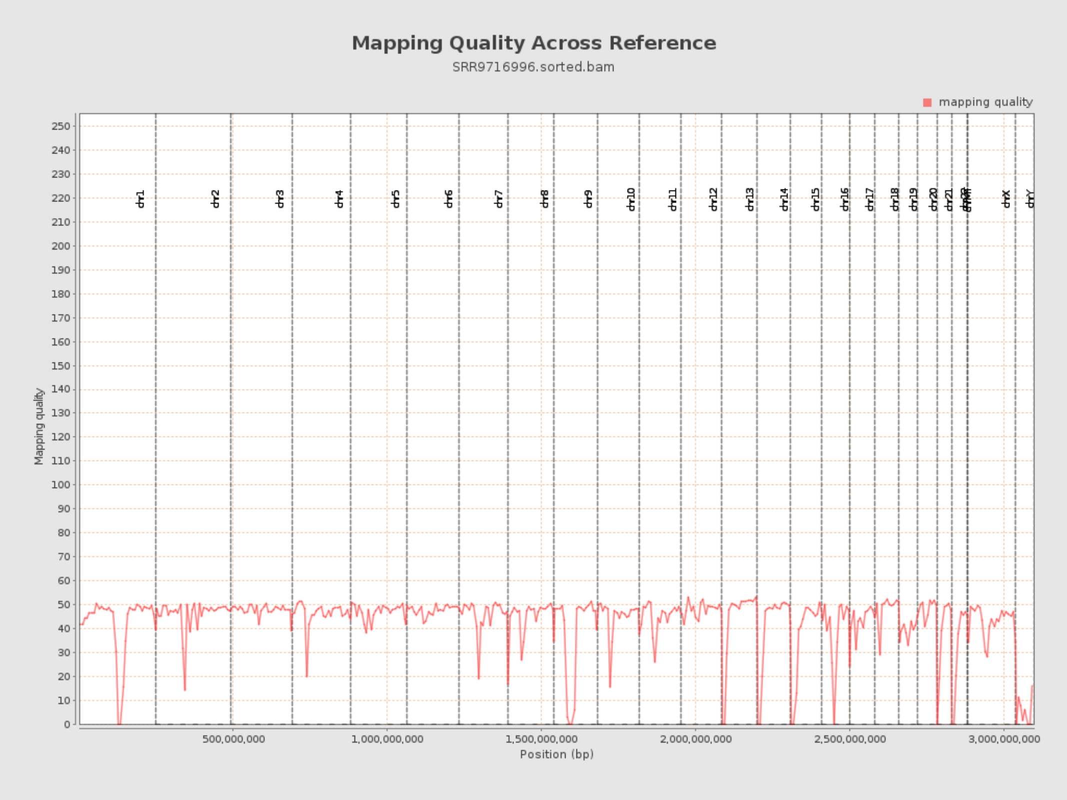
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram