Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:39:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716636.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_SRR9716636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:39:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,234,190
Mapped reads	1,128,547 / 91.44%
Unmapped reads	105,643 / 8.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,605 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,117 / 3.33%
Duplication rate	2.64%
Clipped reads	1,129,178 / 91.49%

2.2. ACGT Content

Number/percentage of A's	16,389,540 / 25.16%
Number/percentage of C's	12,013,407 / 18.44%
Number/percentage of T's	21,212,745 / 32.57%
Number/percentage of G's	15,516,497 / 23.82%
Number/percentage of N's	1,315 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2206

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

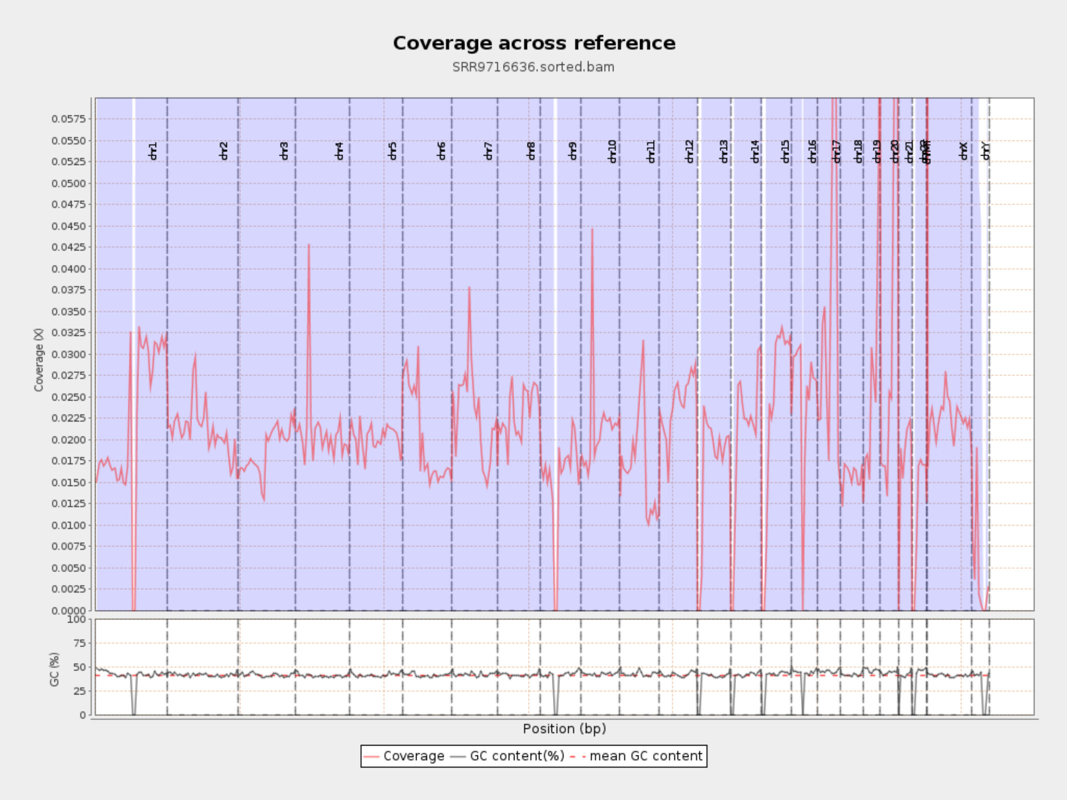
General error rate	0.53%
Mismatches	333,698
Insertions	5,507
Mapped reads with at least one insertion	0.49%
Deletions	13,036
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.54%

2.6. Chromosome stats

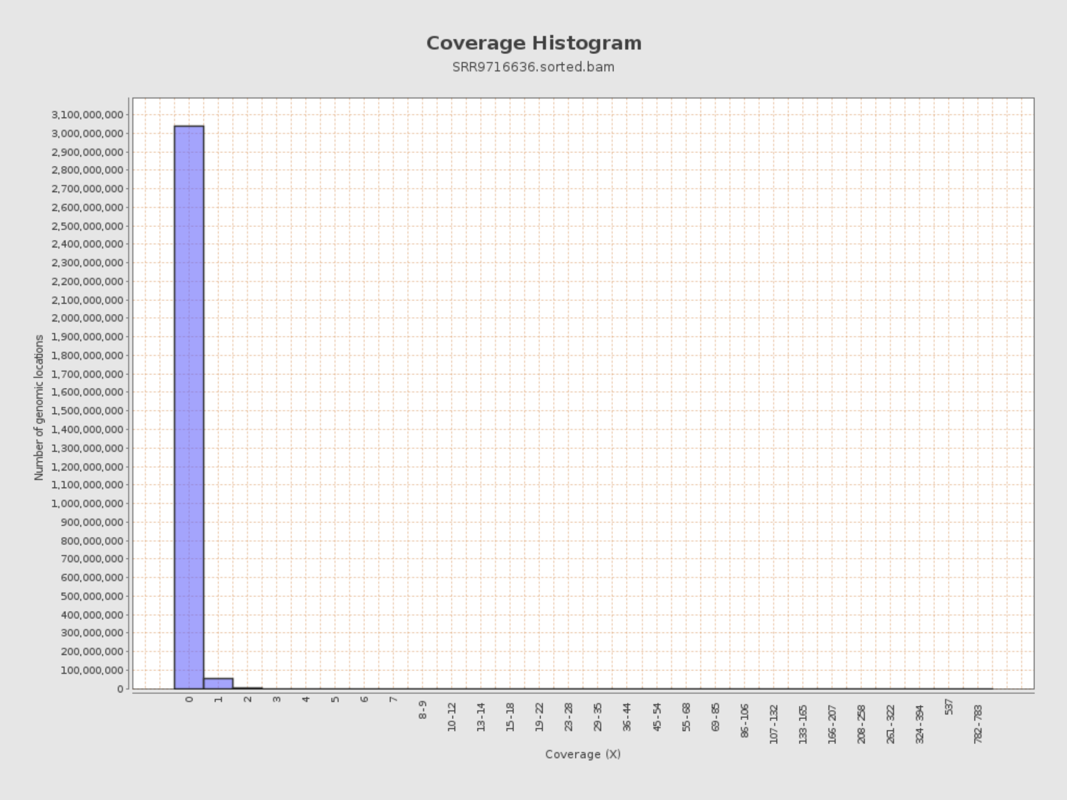
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5465007	0.0219	0.3176
chr2	243199373	5143067	0.0211	0.3464
chr3	198022430	3705695	0.0187	0.1477
chr4	191154276	4016902	0.021	0.1902
chr5	180915260	3660335	0.0202	0.1531
chr6	171115067	3457984	0.0202	0.1742
chr7	159138663	3684665	0.0232	0.2613

chr8	146364022	3400654	0.0232	0.2761
chr9	141213431	2166042	0.0153	0.1604
chr10	135534747	2916293	0.0215	0.245
chr11	135006516	2323257	0.0172	0.1672
chr12	133851895	3224729	0.0241	0.1677
chr13	115169878	1938723	0.0168	0.1399
chr14	107349540	2200408	0.0205	0.1565
chr15	102531392	2418197	0.0236	0.1645
chr16	90354753	2237449	0.0248	0.1746
chr17	81195210	2875663	0.0354	0.2082
chr18	78077248	1216137	0.0156	0.2325
chr19	59128983	1684212	0.0285	0.2615
chr20	63025520	2192818	0.0348	0.2075
chr21	48129895	846225	0.0176	0.1791
chr22	51304566	610559	0.0119	0.1165
chrMT	16571	16296	0.9834	1.1945
chrX	155270560	3490249	0.0225	0.1709
chrY	59373566	263064	0.0044	0.2066

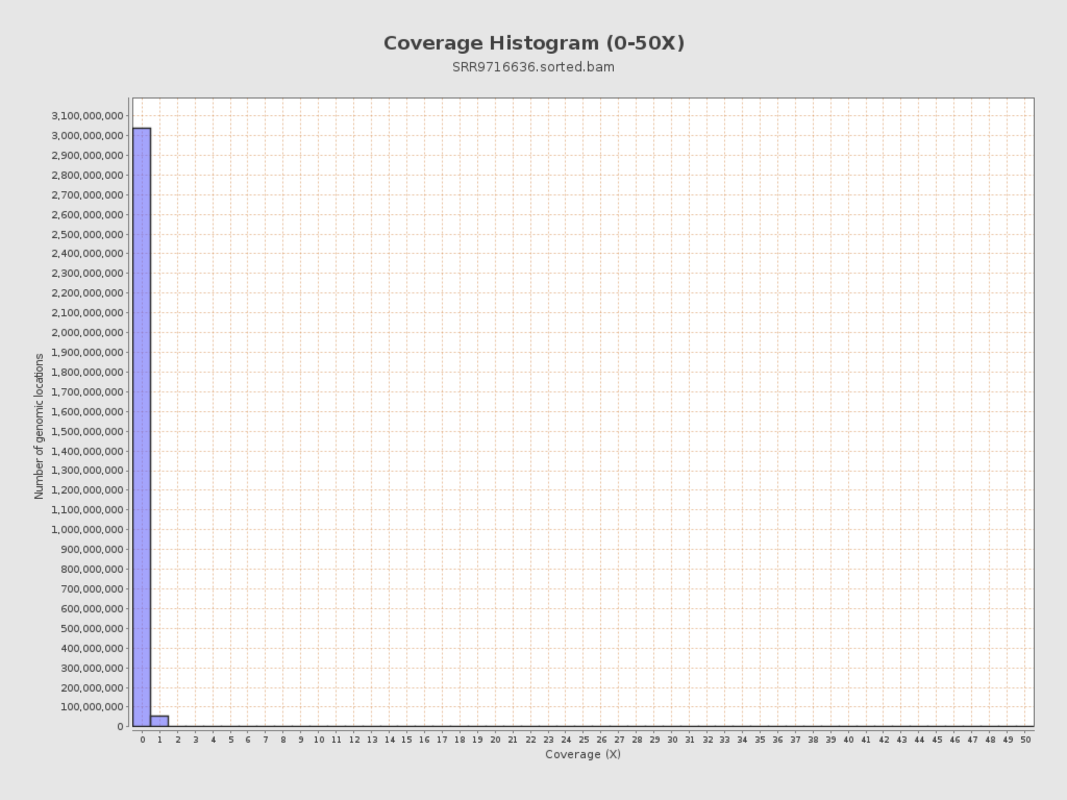
3. Results : Coverage across reference



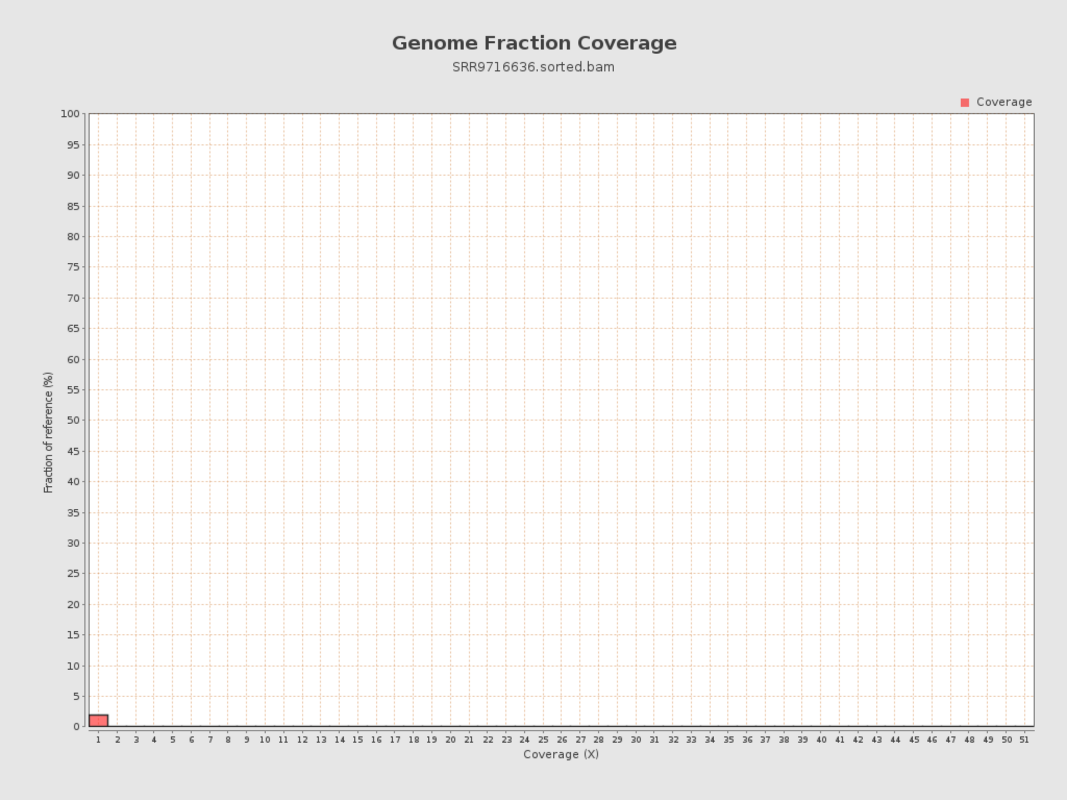
4. Results : Coverage Histogram



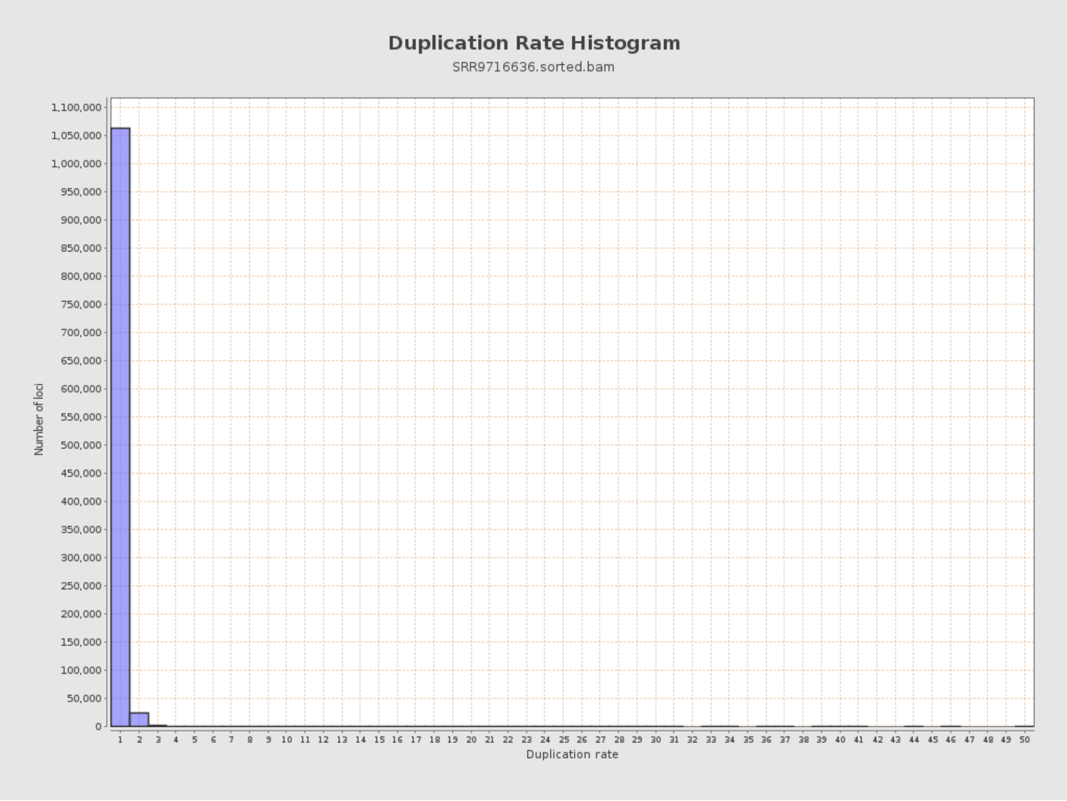
5. Results : Coverage Histogram (0-50X)



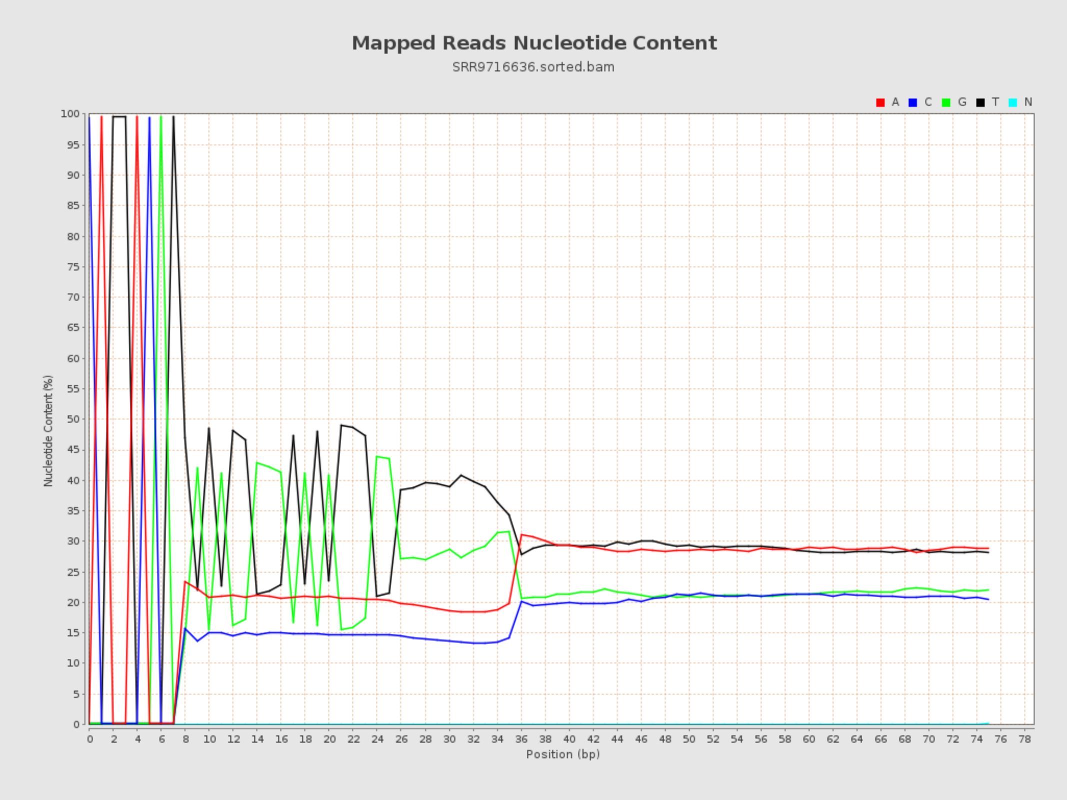
6. Results : Genome Fraction Coverage



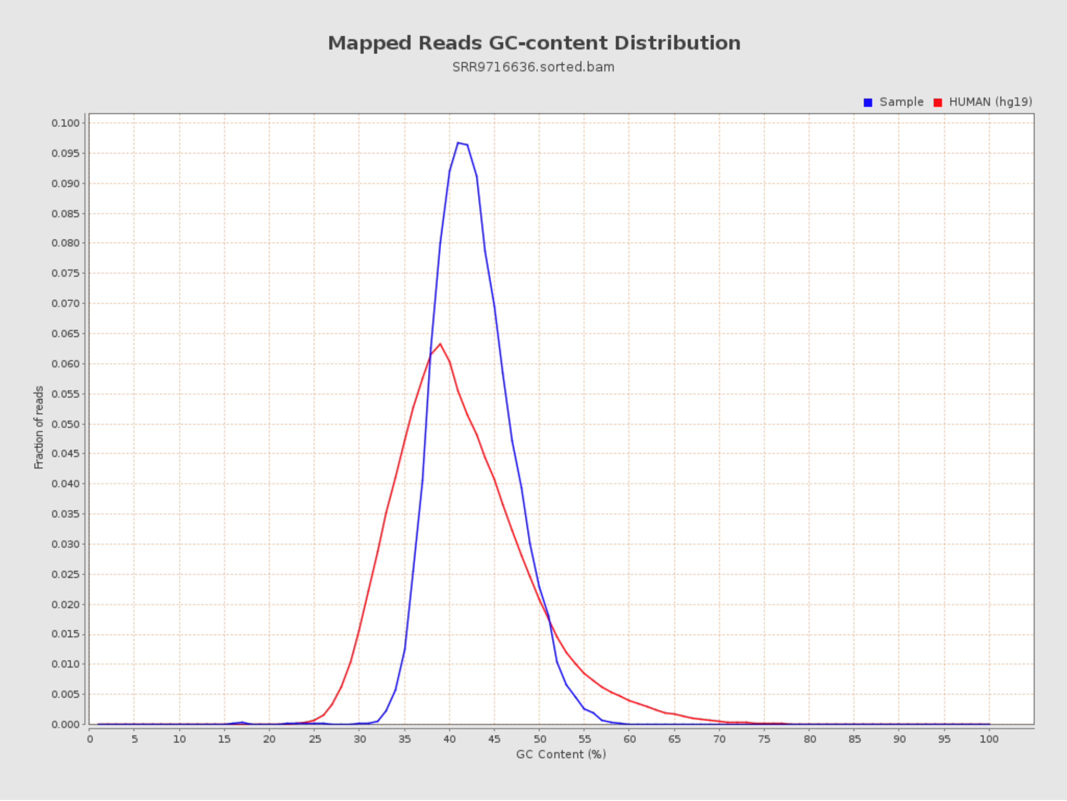
7. Results : Duplication Rate Histogram



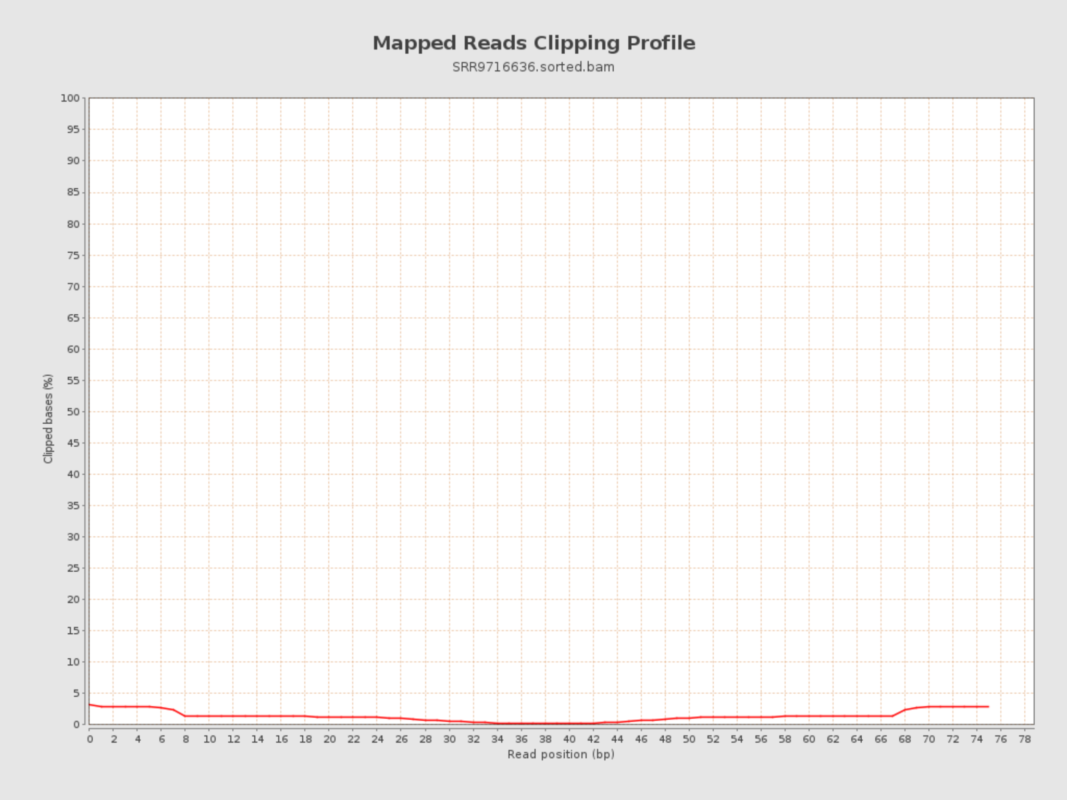
8. Results : Mapped Reads Nucleotide Content



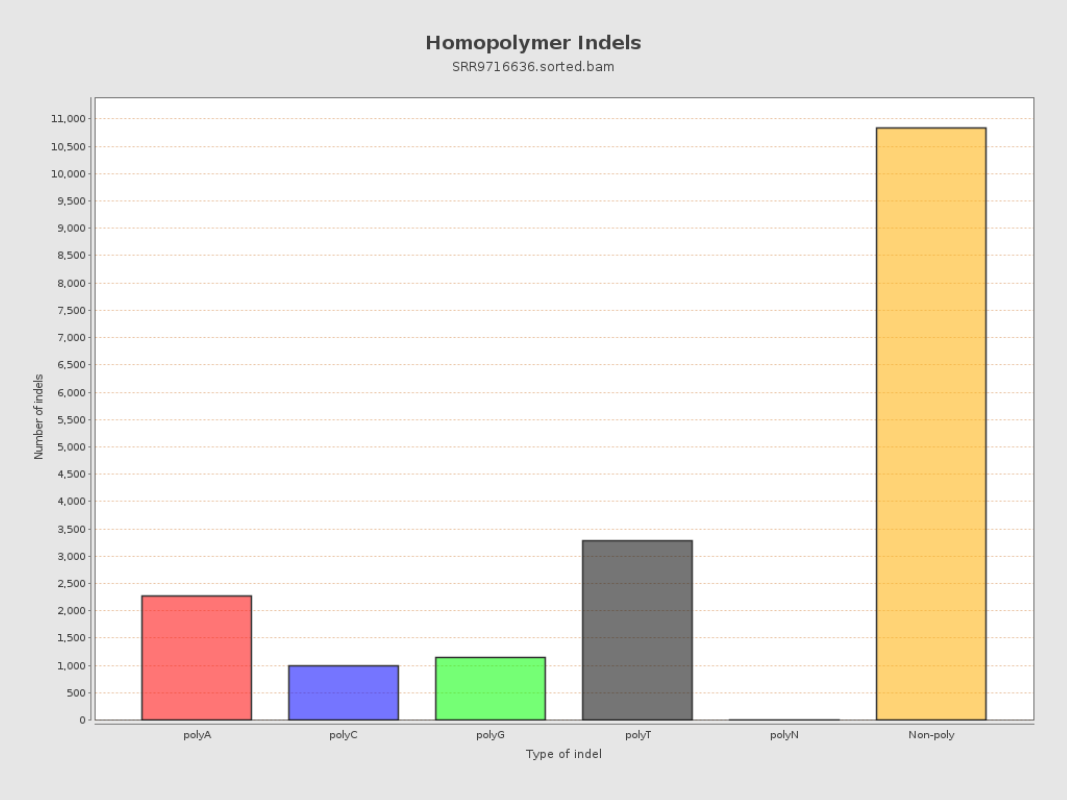
9. Results : Mapped Reads GC-content Distribution



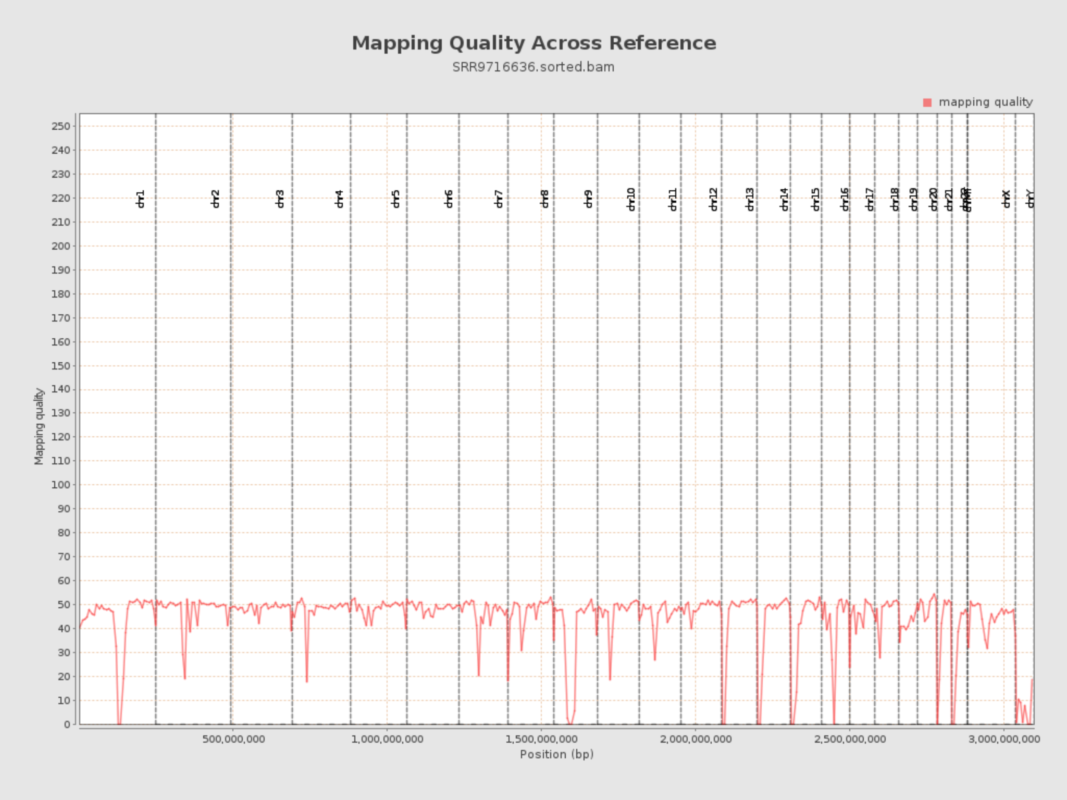
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram