Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:03:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716873.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_SRR9716873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716873.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,037,659
Mapped reads	911,097 / 87.8%
Unmapped reads	126,562 / 12.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,839 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	22,909 / 2.21%
Duplication rate	1.91%
Clipped reads	910,305 / 87.73%

2.2. ACGT Content

Number/percentage of A's	12,884,498 / 24.79%
Number/percentage of C's	8,578,713 / 16.51%
Number/percentage of T's	17,015,480 / 32.74%
Number/percentage of G's	13,496,234 / 25.97%
Number/percentage of N's	566 / 0%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.169

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

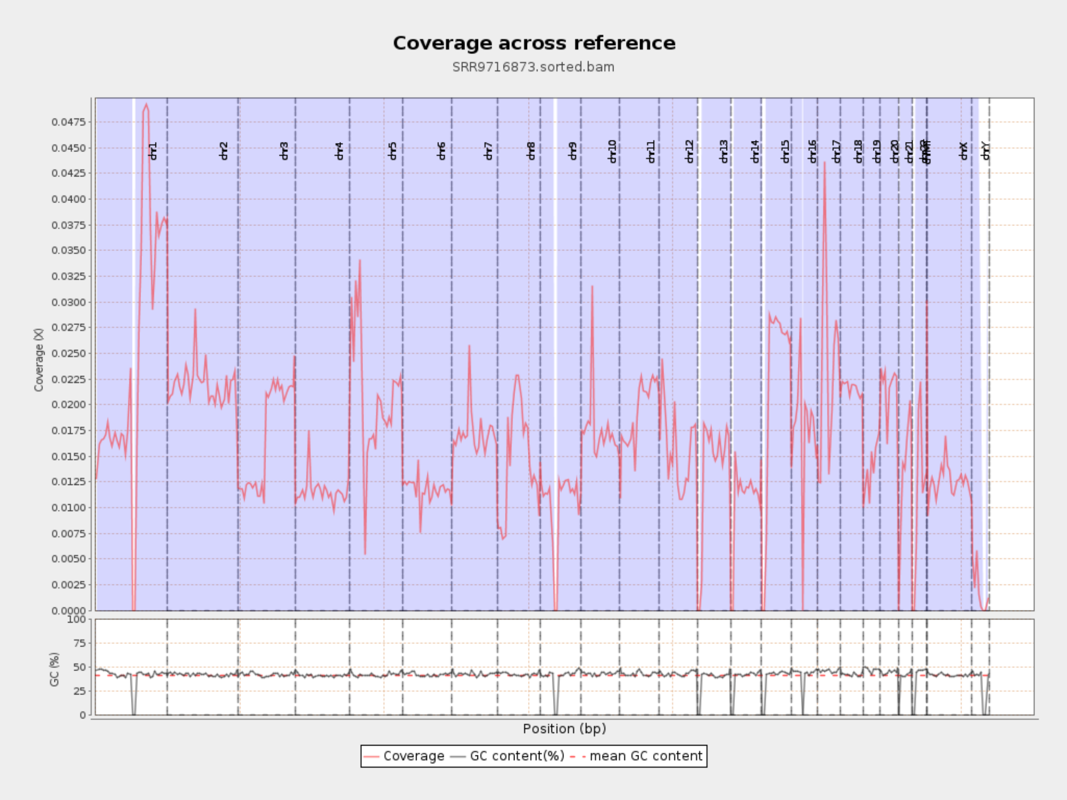
General error rate	0.51%
Mismatches	260,025
Insertions	3,582
Mapped reads with at least one insertion	0.39%
Deletions	10,130
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.47%

2.6. Chromosome stats

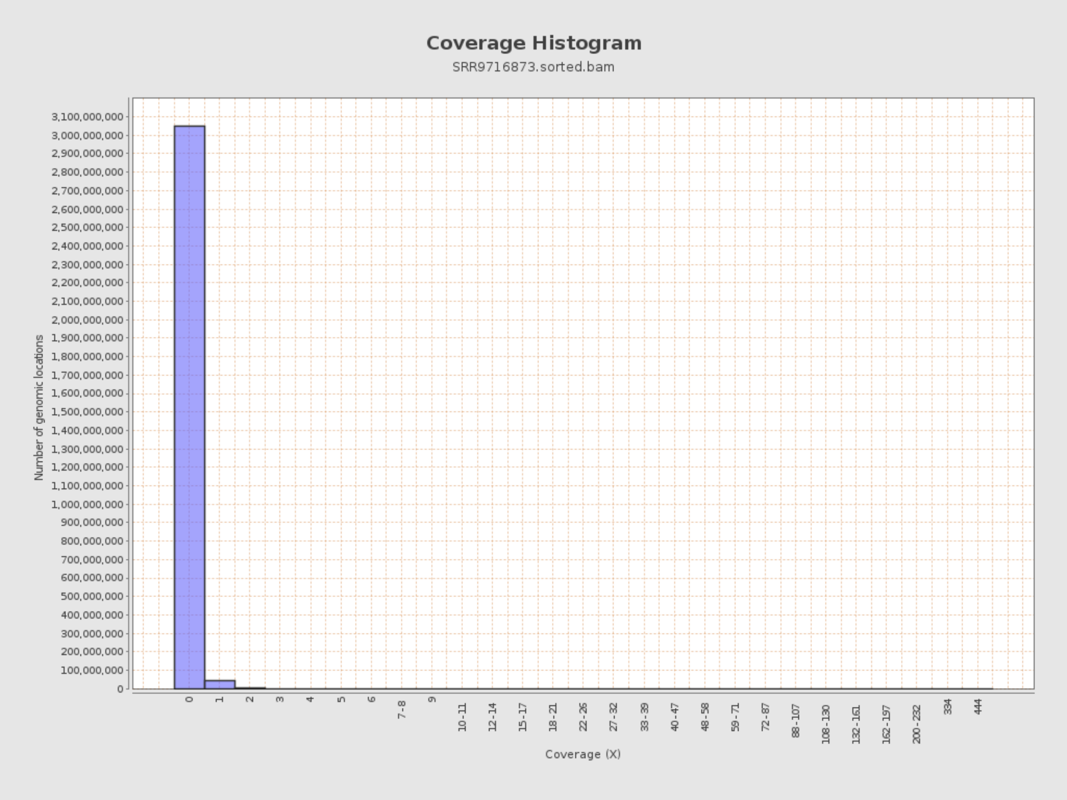
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6127356	0.0246	0.2308
chr2	243199373	5336284	0.0219	0.2485
chr3	198022430	3334429	0.0168	0.1389
chr4	191154276	2228661	0.0117	0.1179
chr5	180915260	3793355	0.021	0.153
chr6	171115067	2009578	0.0117	0.1307
chr7	159138663	2745660	0.0173	0.207

chr8	146364022	2190533	0.015	0.1464
chr9	141213431	1441843	0.0102	0.1318
chr10	135534747	2400595	0.0177	0.1912
chr11	135006516	2605687	0.0193	0.1728
chr12	133851895	2095333	0.0157	0.1323
chr13	115169878	1564161	0.0136	0.1238
chr14	107349540	1129285	0.0105	0.1127
chr15	102531392	2268905	0.0221	0.1583
chr16	90354753	1572523	0.0174	0.1499
chr17	81195210	1958479	0.0241	0.1715
chr18	78077248	1688623	0.0216	0.246
chr19	59128983	826940	0.014	0.1766
chr20	63025520	1353487	0.0215	0.1553
chr21	48129895	655667	0.0136	0.1248
chr22	51304566	590347	0.0115	0.113
chrMT	16571	500	0.0302	0.1711
chrX	155270560	1960082	0.0126	0.1372
chrY	59373566	113117	0.0019	0.0558

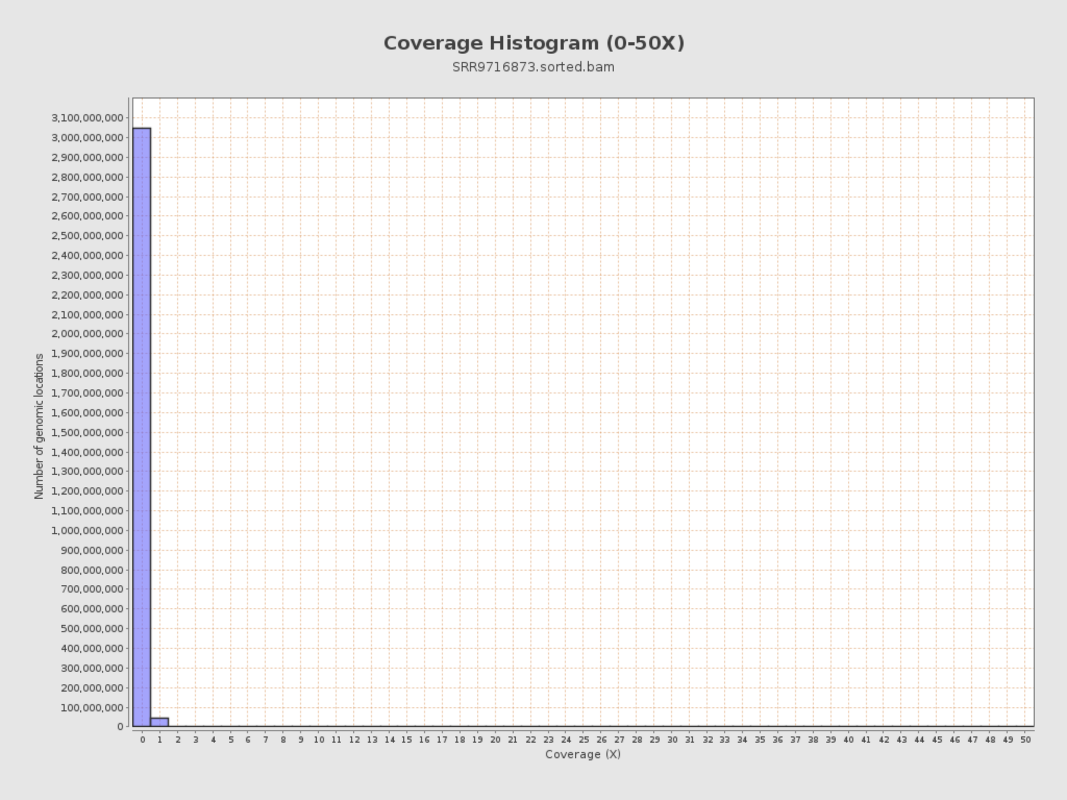
3. Results : Coverage across reference



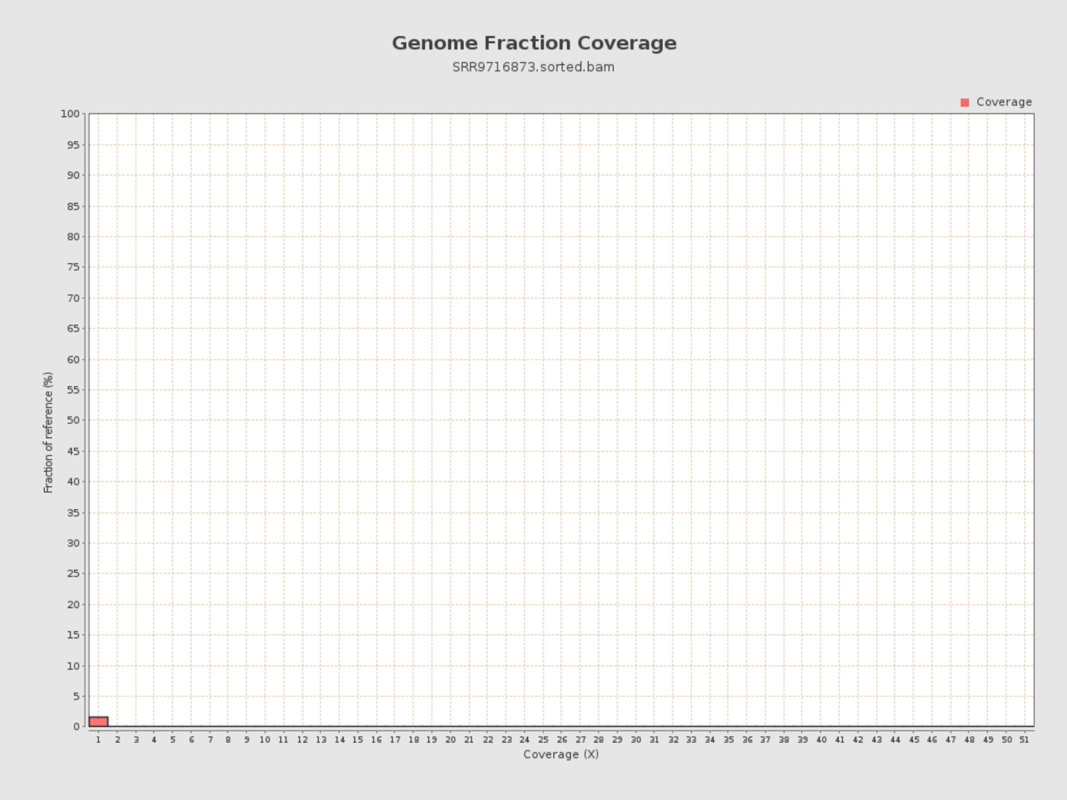
4. Results : Coverage Histogram



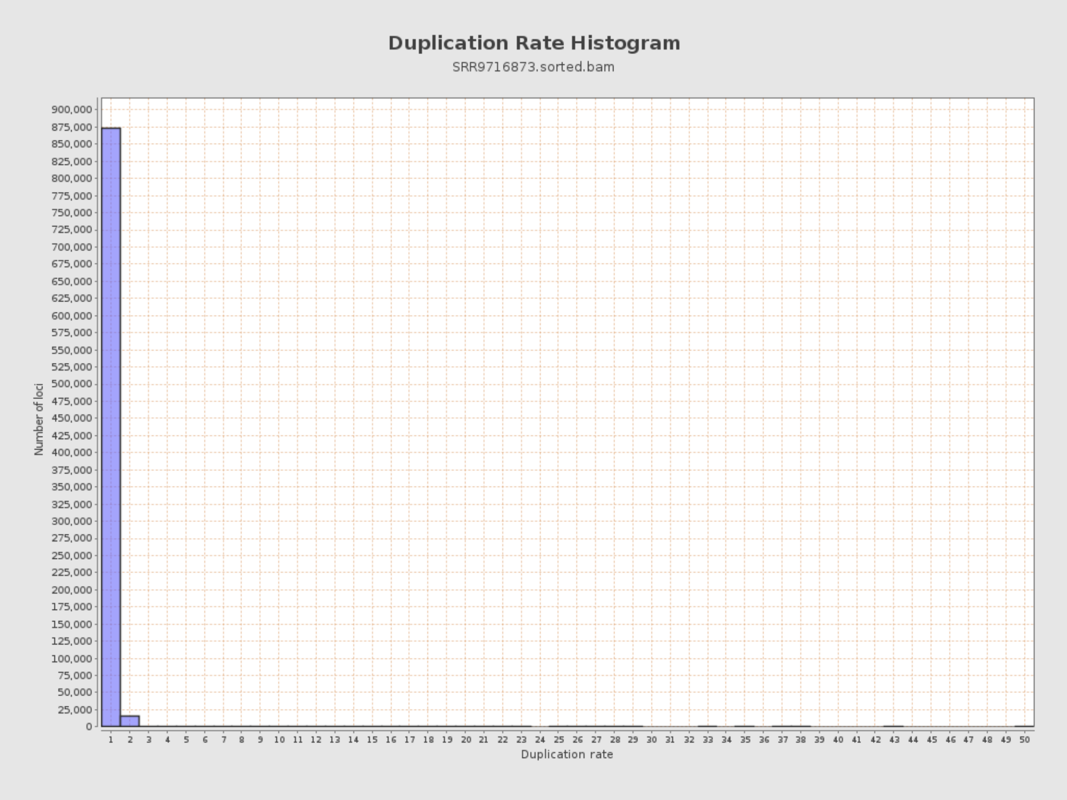
5. Results : Coverage Histogram (0-50X)



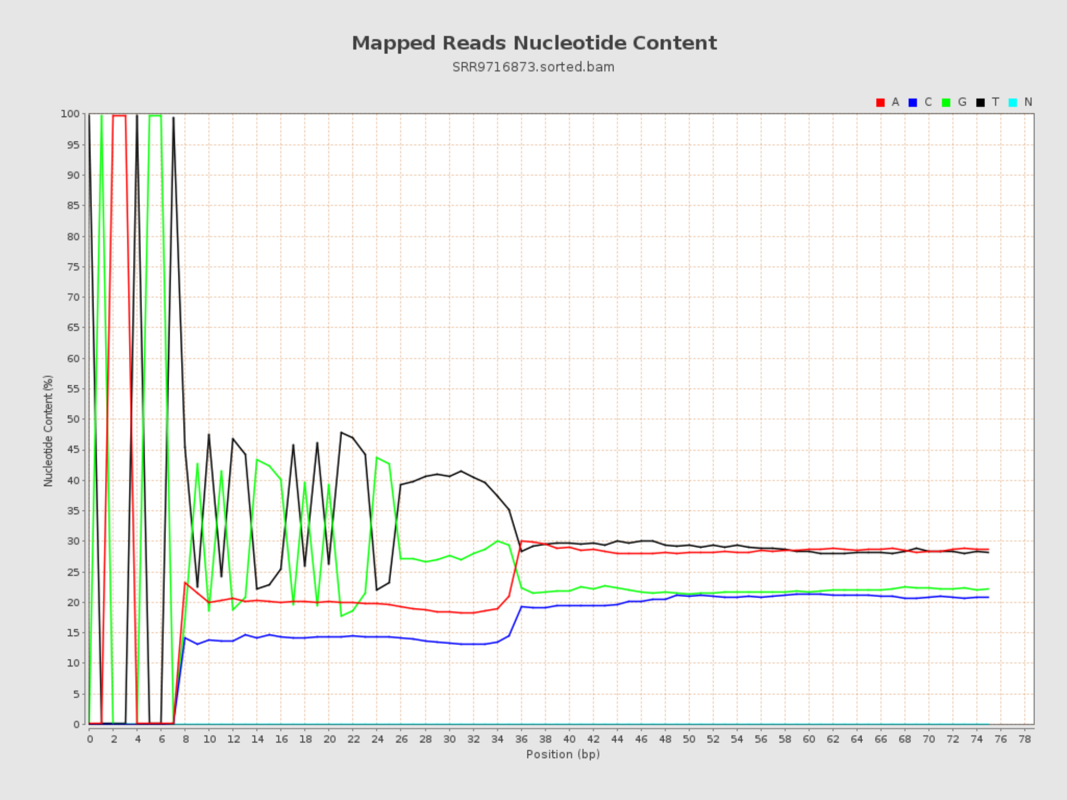
6. Results : Genome Fraction Coverage



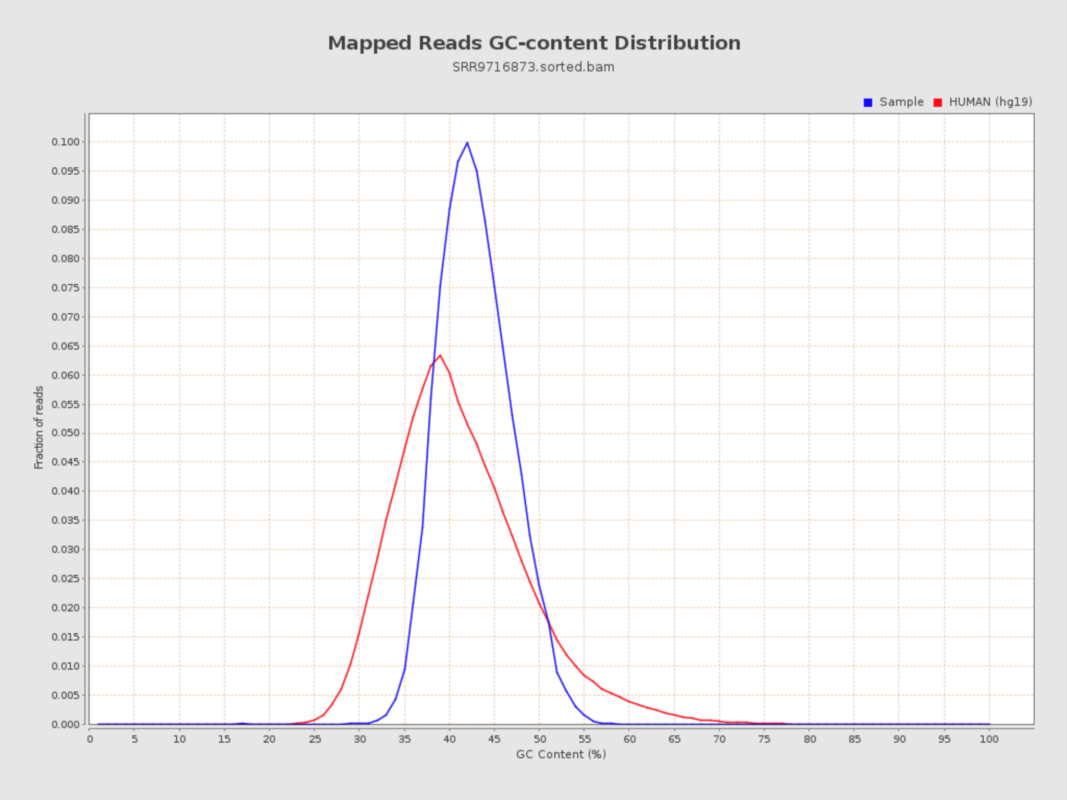
7. Results : Duplication Rate Histogram



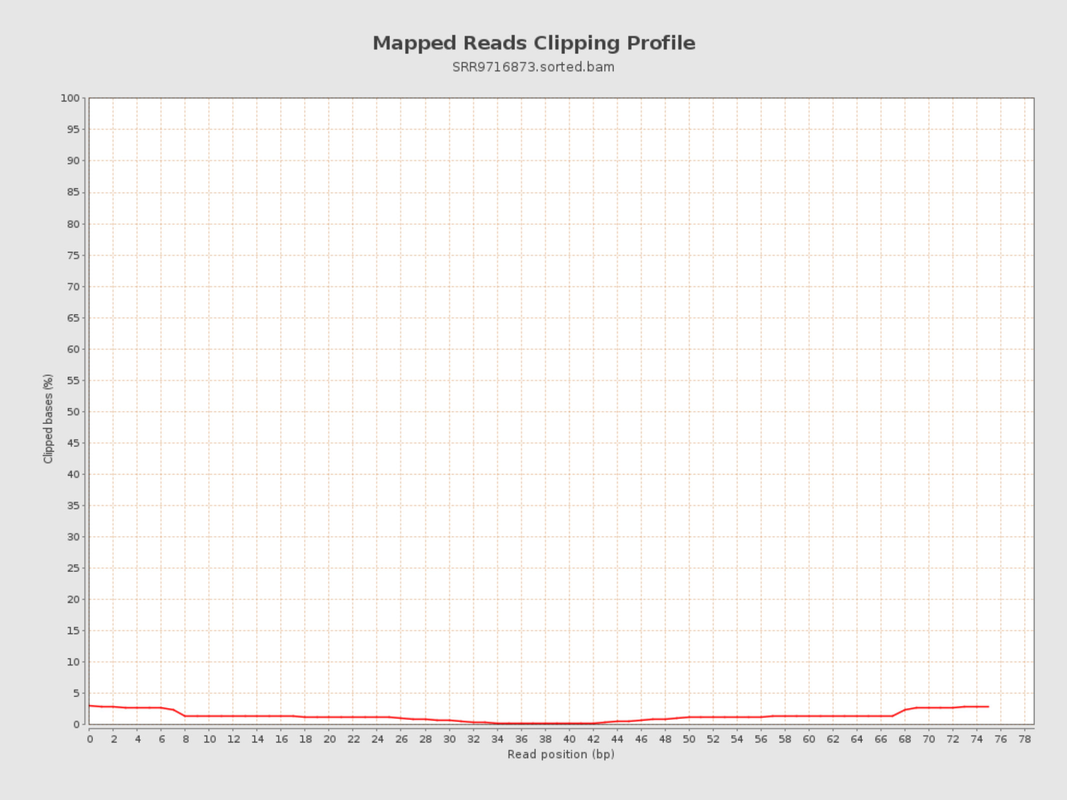
8. Results : Mapped Reads Nucleotide Content



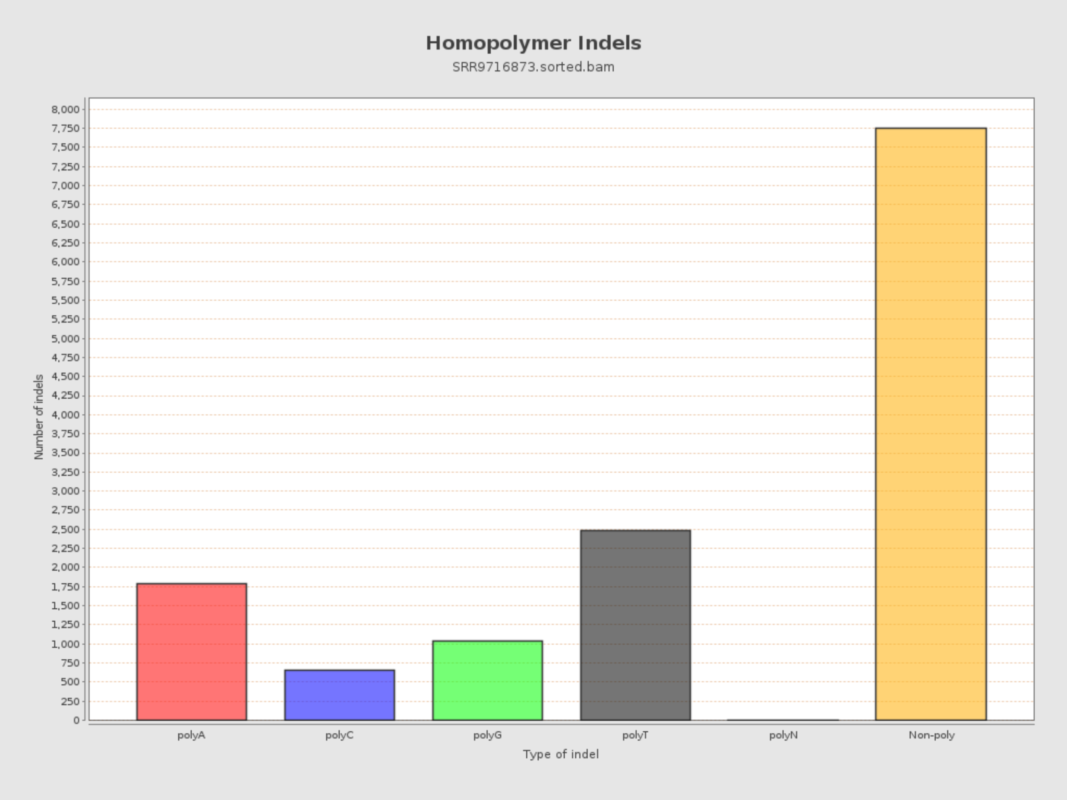
9. Results : Mapped Reads GC-content Distribution



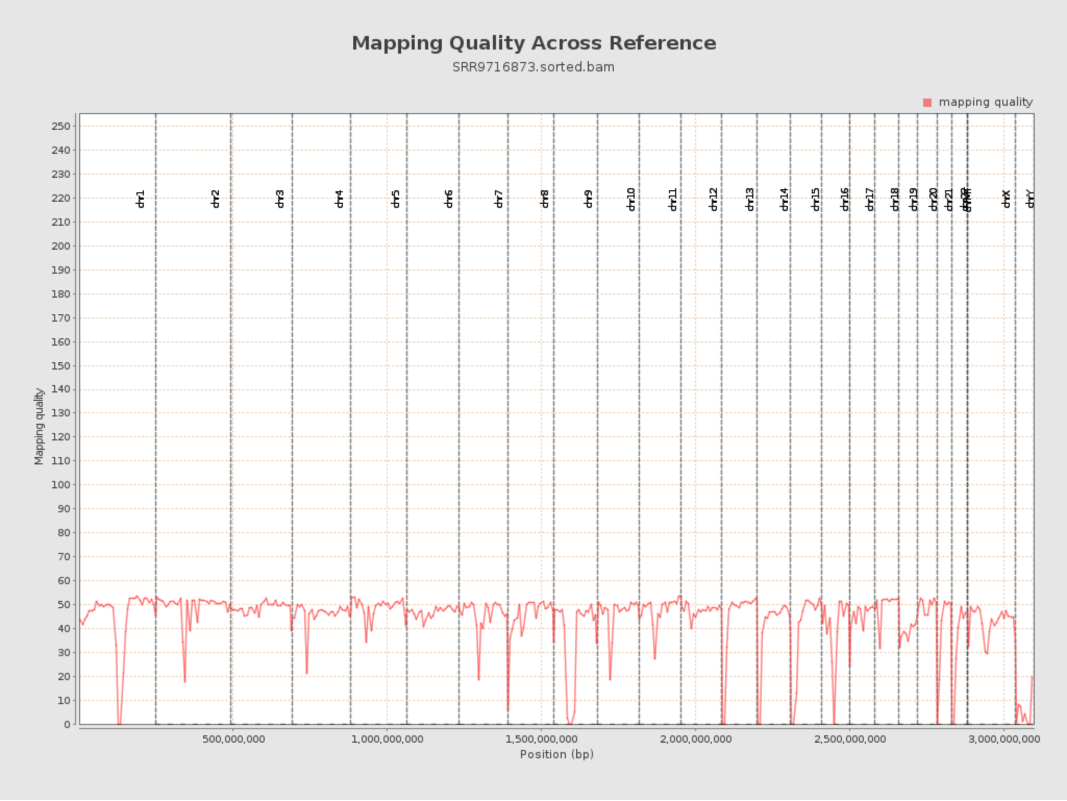
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram