Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:35:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717093.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_SRR9717093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:35:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,077,778
Mapped reads	1,910,207 / 91.94%
Unmapped reads	167,571 / 8.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,067 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	101,786 / 4.9%
Duplication rate	4.21%
Clipped reads	1,917,197 / 92.27%

2.2. ACGT Content

Number/percentage of A's	28,080,964 / 25.02%
Number/percentage of C's	20,878,845 / 18.61%
Number/percentage of T's	34,254,015 / 30.52%
Number/percentage of G's	29,001,878 / 25.84%
Number/percentage of N's	867 / 0%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.3097

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

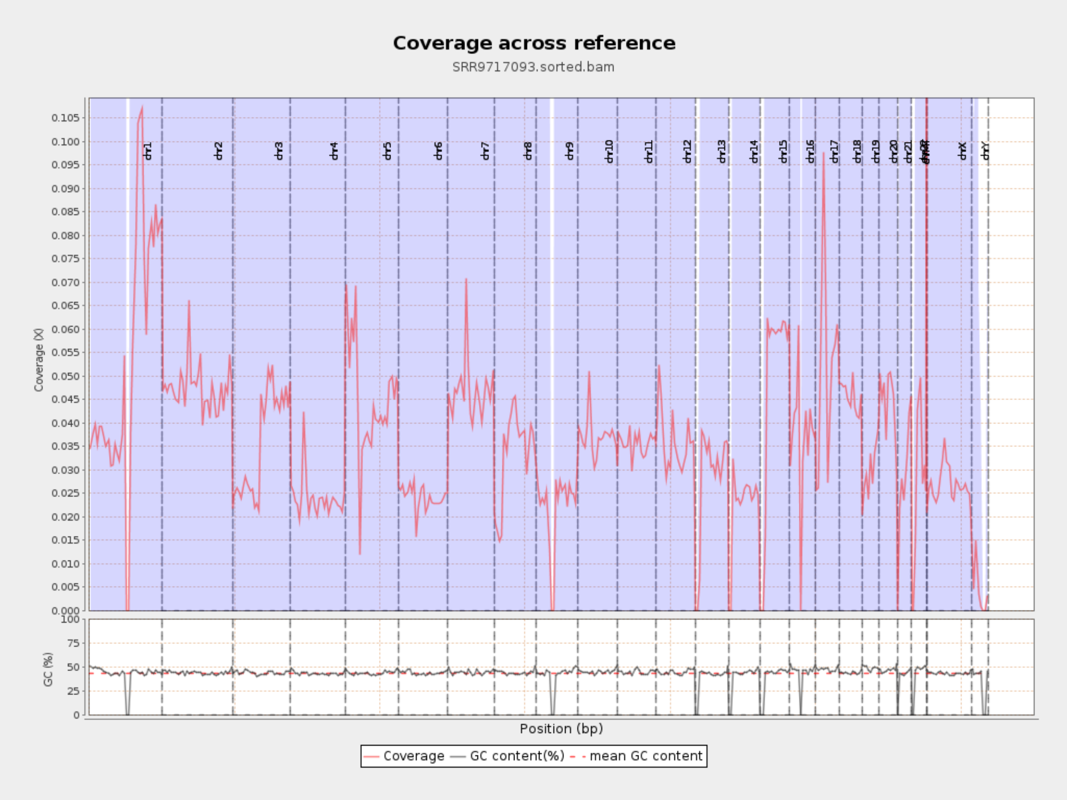
General error rate	0.51%
Mismatches	553,676
Insertions	7,786
Mapped reads with at least one insertion	0.41%
Deletions	19,437
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.58%

2.6. Chromosome stats

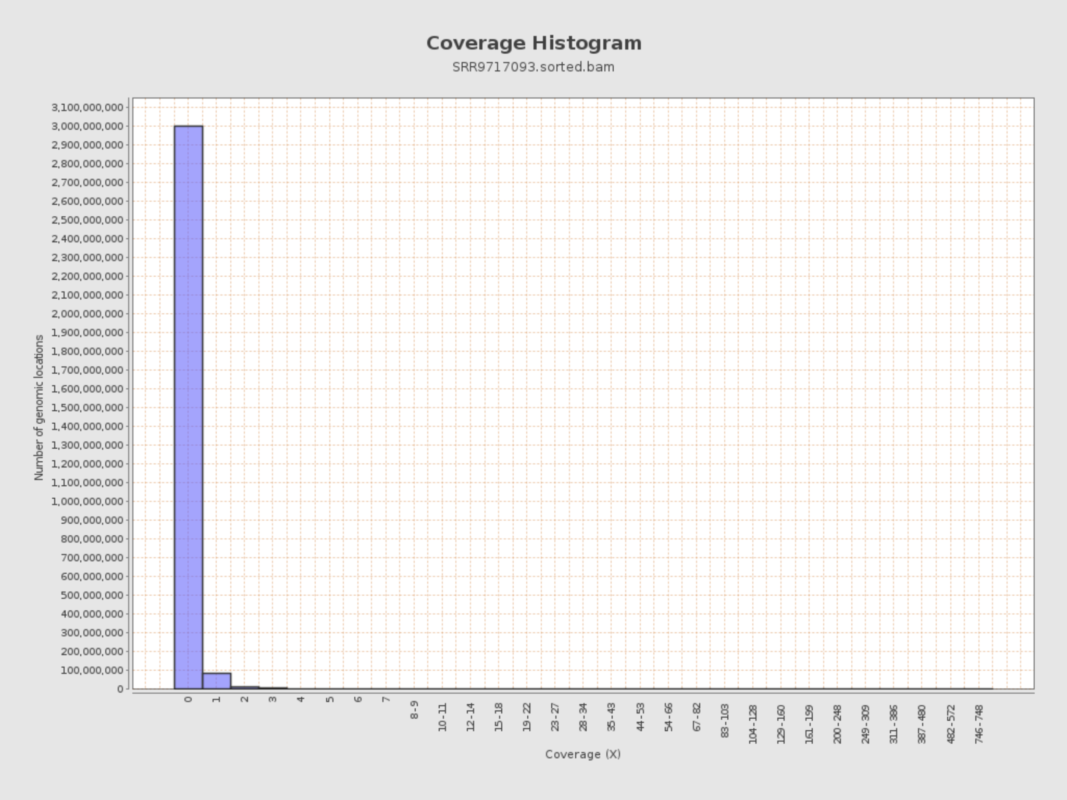
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13288212	0.0533	0.4884
chr2	243199373	11557892	0.0475	0.4261
chr3	198022430	7088628	0.0358	0.216
chr4	191154276	4557365	0.0238	0.2062
chr5	180915260	8101618	0.0448	0.2434
chr6	171115067	4126502	0.0241	0.1941
chr7	159138663	7479526	0.047	0.4986

chr8	146364022	4917993	0.0336	0.3
chr9	141213431	3060753	0.0217	0.2255
chr10	135534747	5030448	0.0371	0.2806
chr11	135006516	4796889	0.0355	0.2988
chr12	133851895	4774152	0.0357	0.2183
chr13	115169878	3216899	0.0279	0.1913
chr14	107349540	2377771	0.0221	0.1789
chr15	102531392	4947185	0.0483	0.2524
chr16	90354753	3340679	0.037	0.233
chr17	81195210	4294611	0.0529	0.2876
chr18	78077248	3563893	0.0456	0.5085
chr19	59128983	1780979	0.0301	0.3628
chr20	63025520	2805599	0.0445	0.246
chr21	48129895	1372831	0.0285	0.2109
chr22	51304566	1326303	0.0259	0.1831
chrMT	16571	2989	0.1804	0.477
chrX	155270560	4175861	0.0269	0.2134
chrY	59373566	261844	0.0044	0.1229

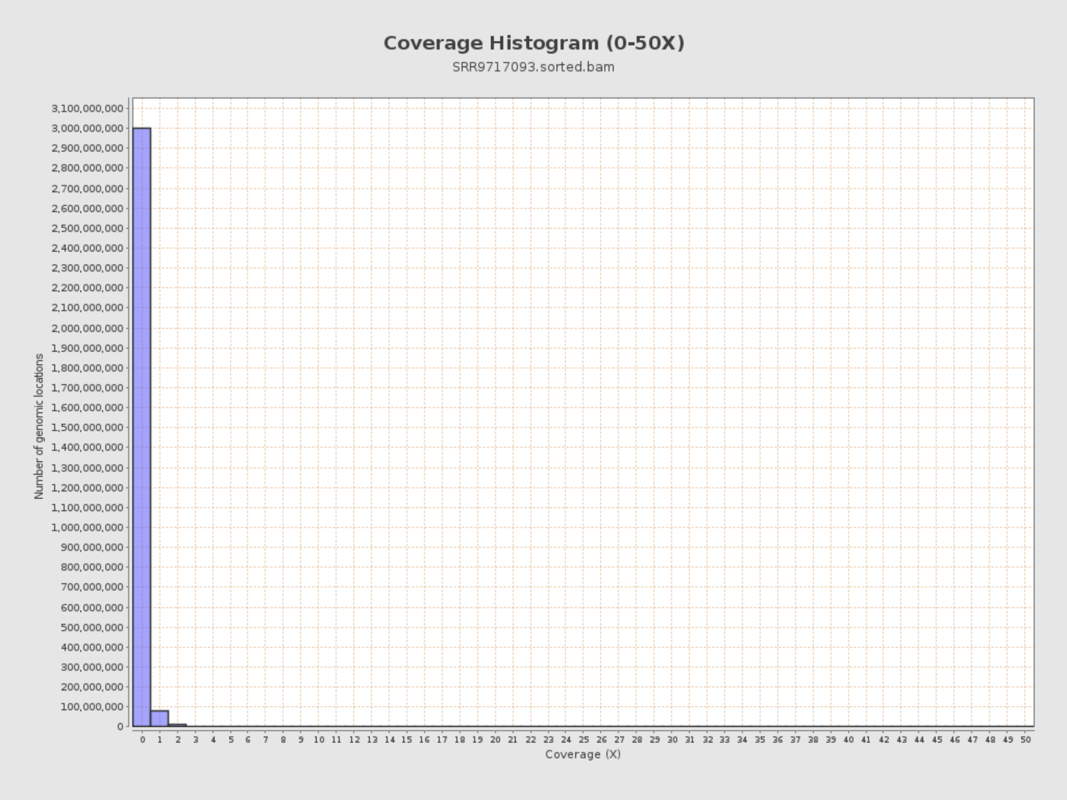
3. Results : Coverage across reference



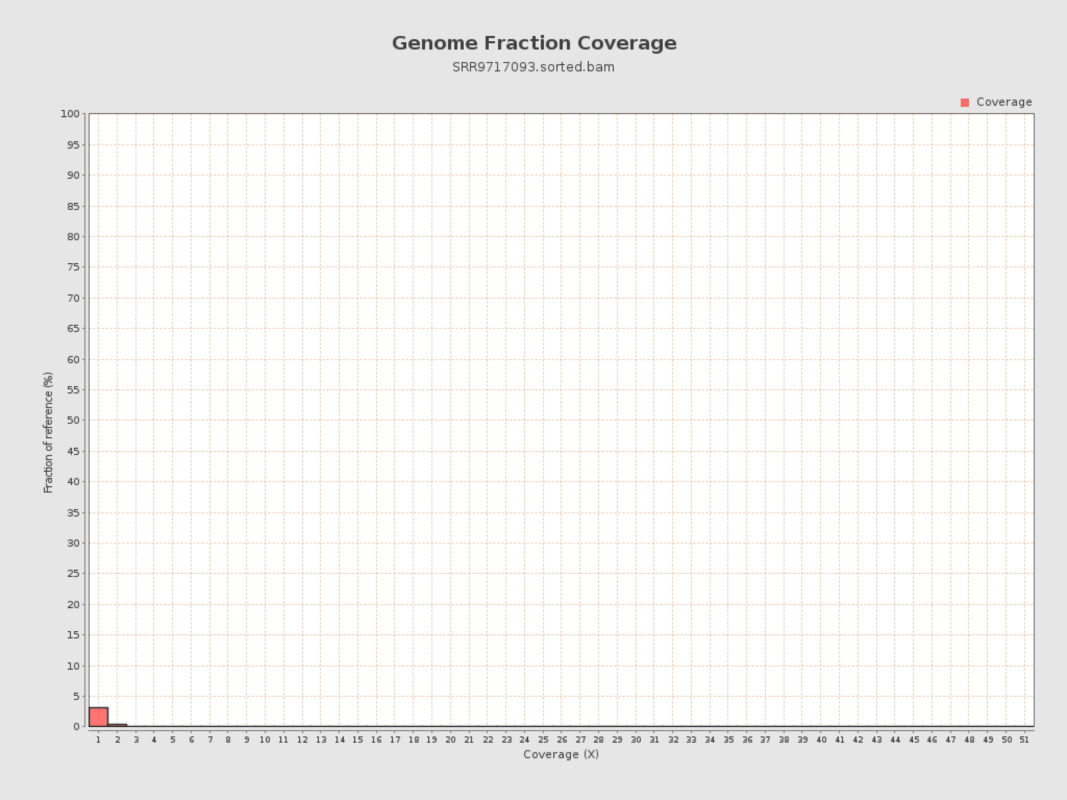
4. Results : Coverage Histogram



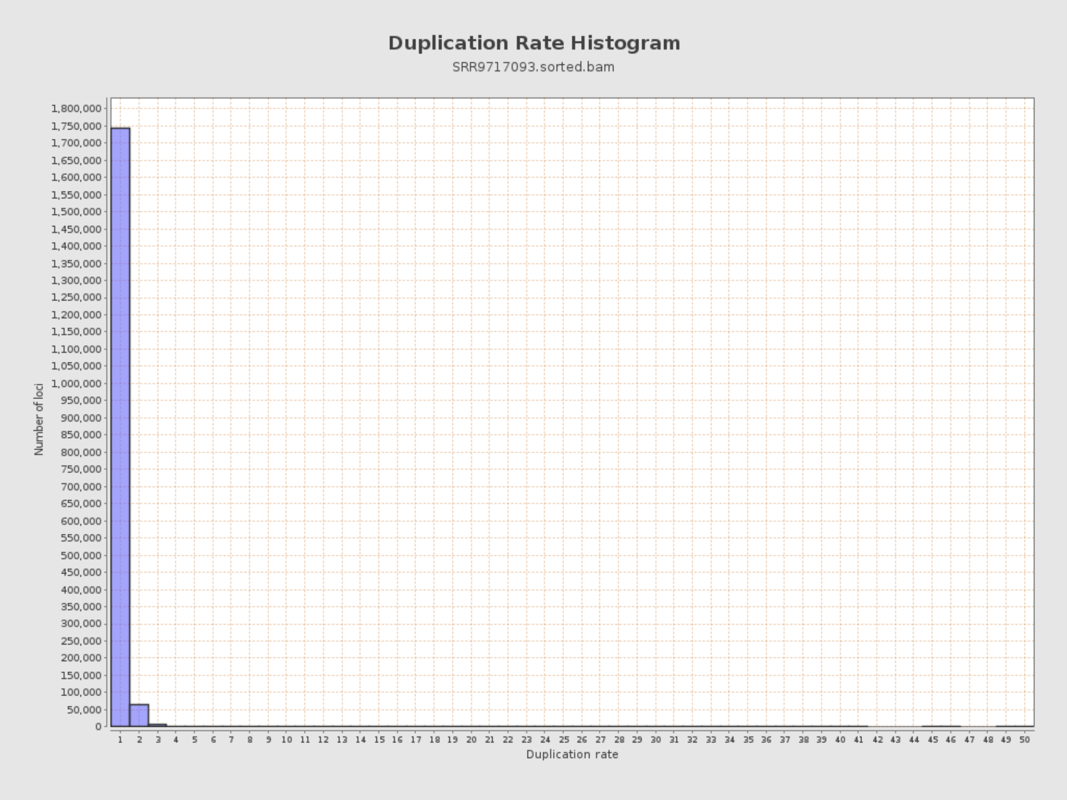
5. Results : Coverage Histogram (0-50X)



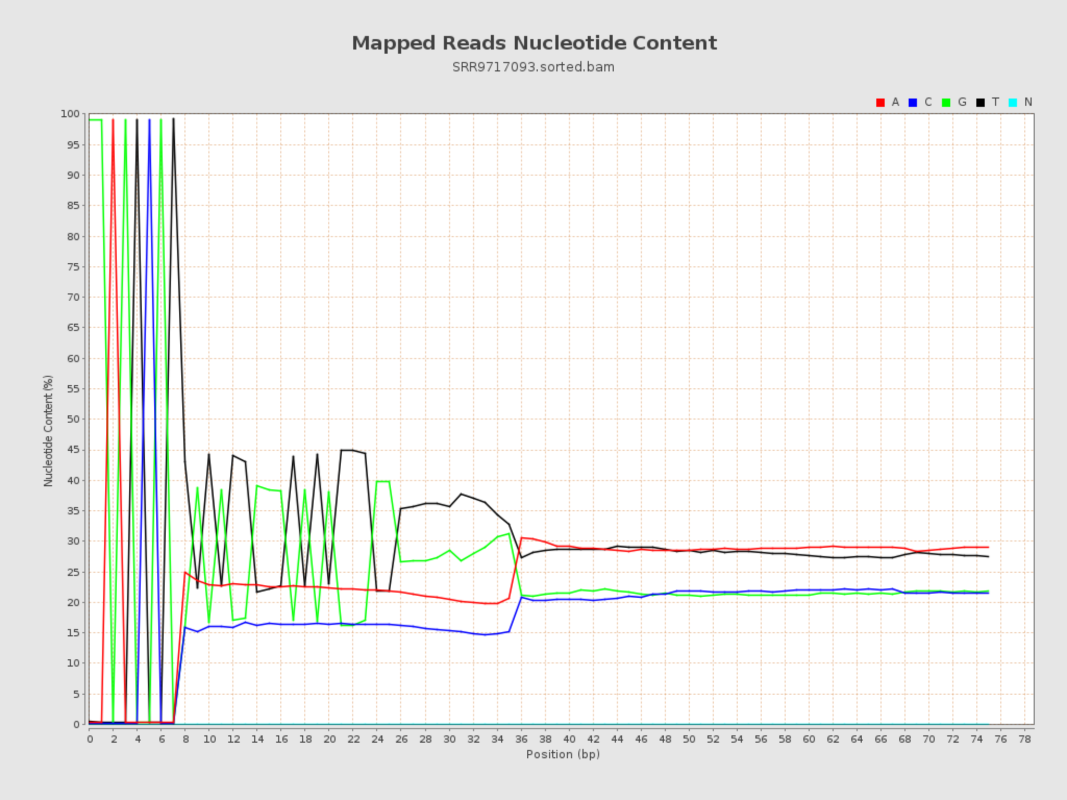
6. Results : Genome Fraction Coverage



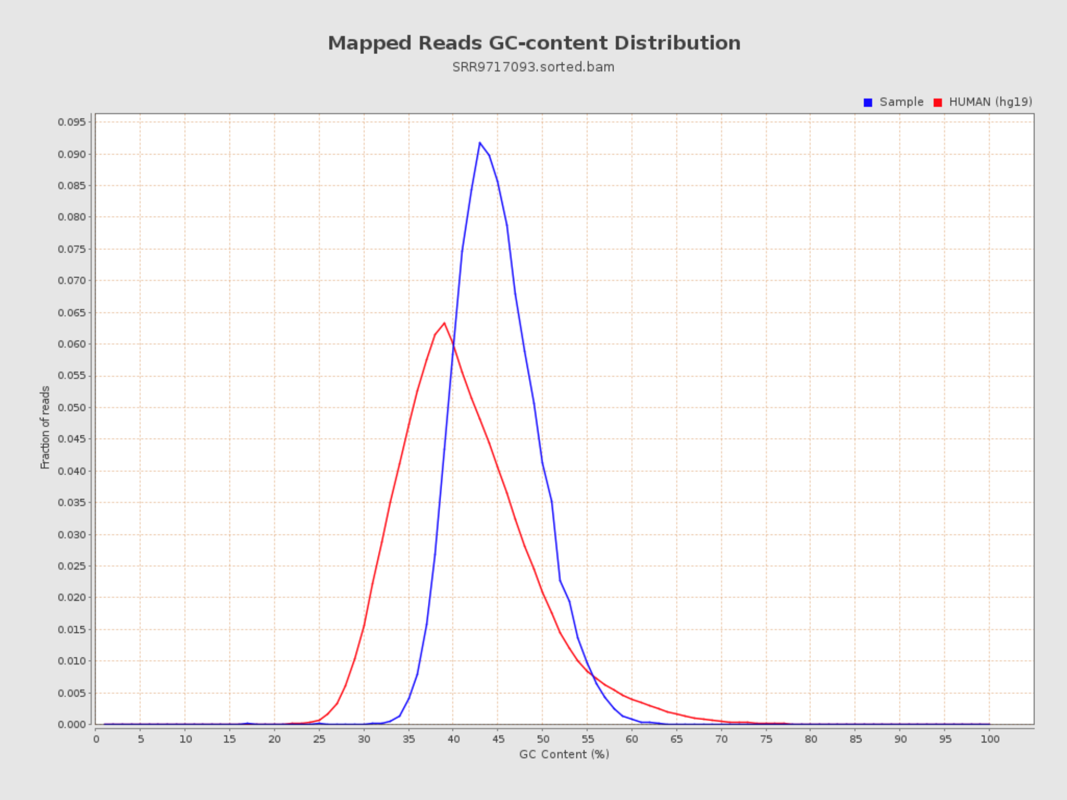
7. Results : Duplication Rate Histogram



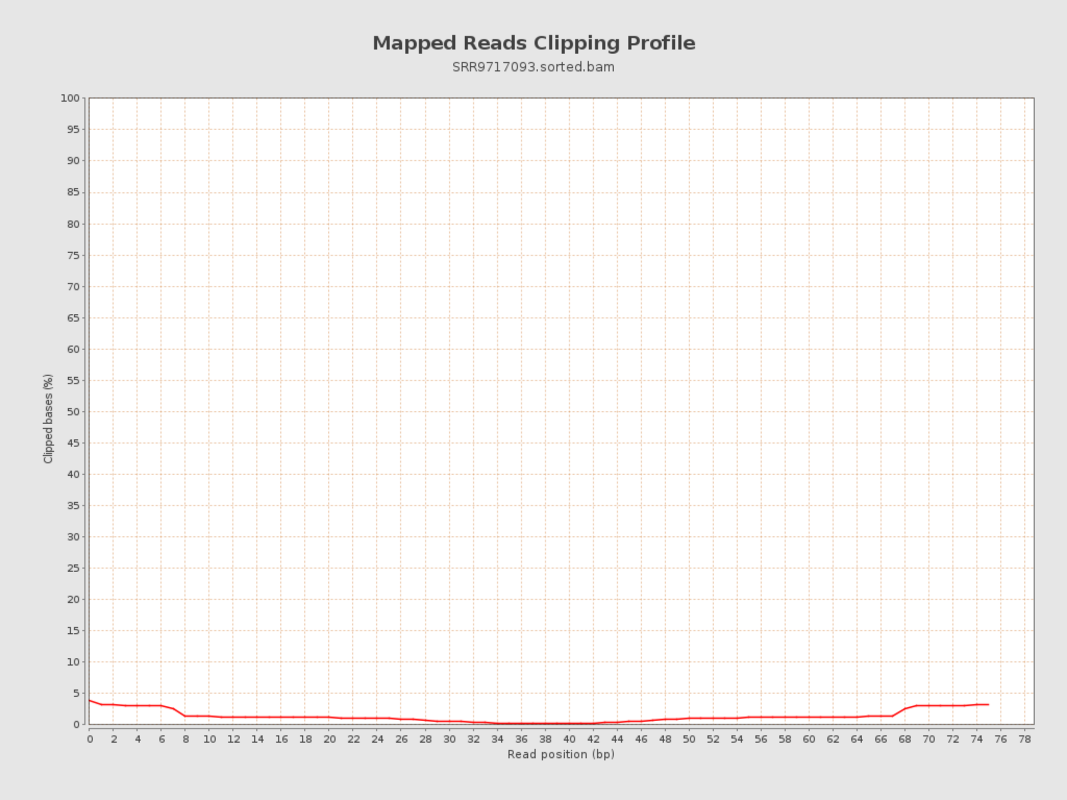
8. Results : Mapped Reads Nucleotide Content



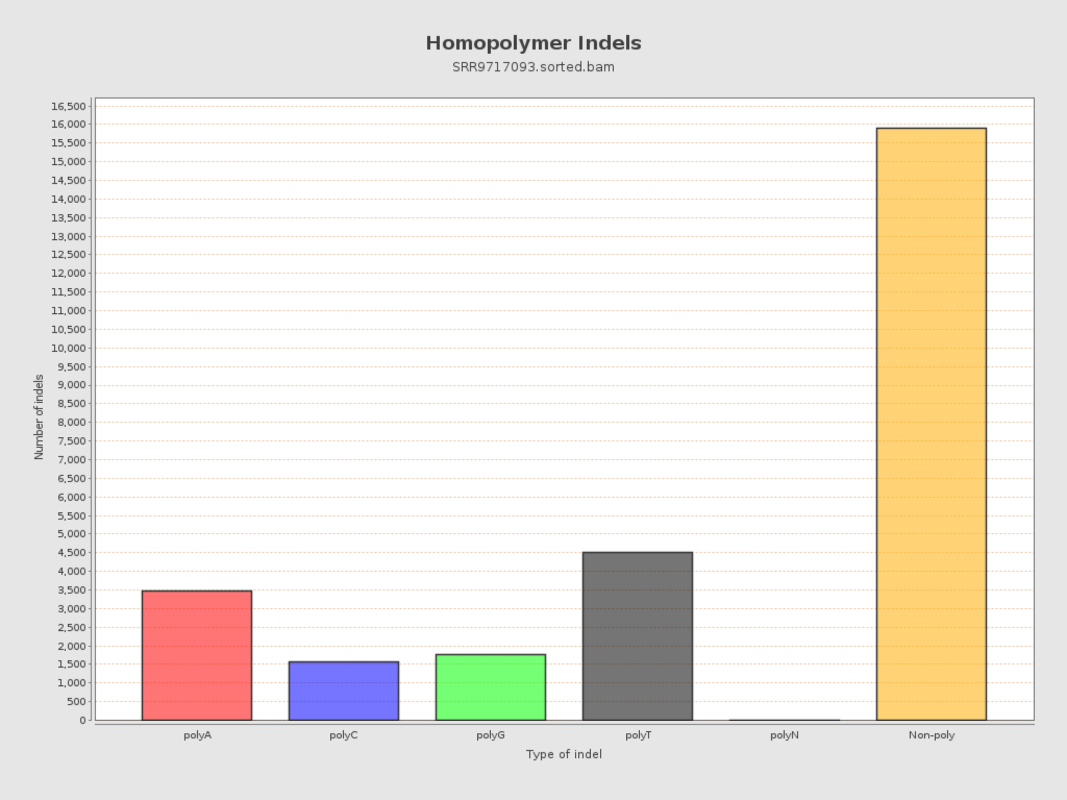
9. Results : Mapped Reads GC-content Distribution



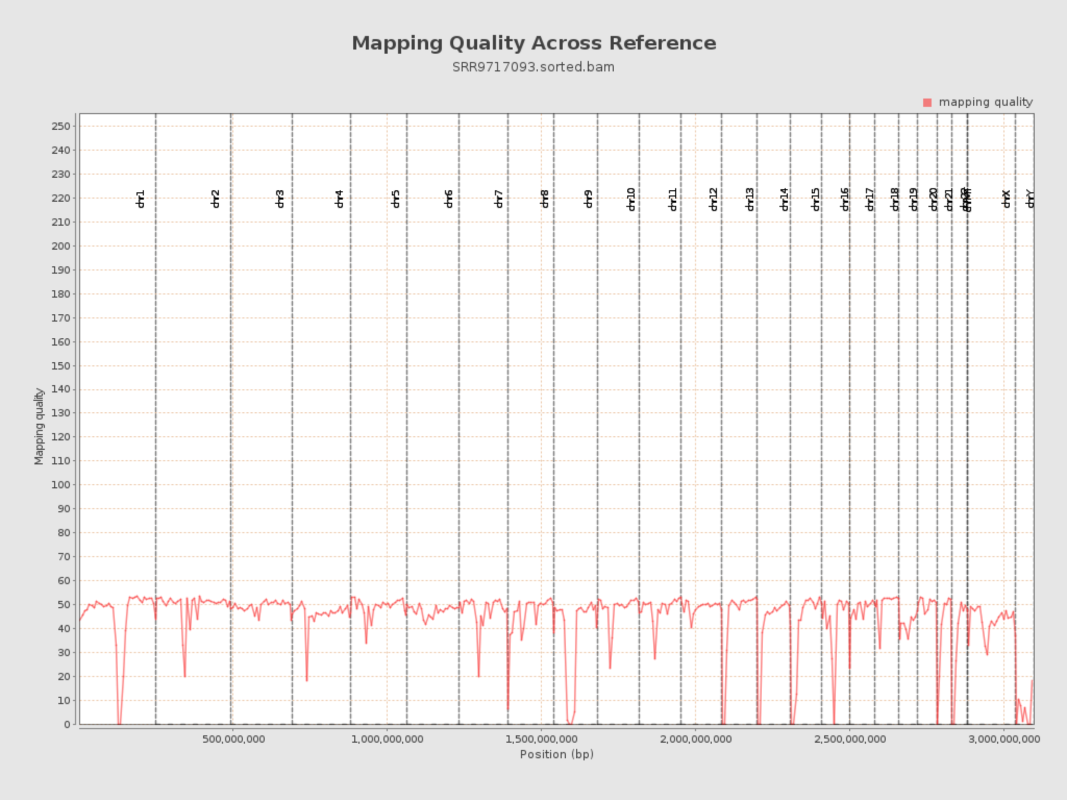
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram