Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:36:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716779.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_SRR9716779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:36:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,537,301
Mapped reads	1,266,323 / 82.37%
Unmapped reads	270,978 / 17.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,159 / 1.96%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	31,425 / 2.04%
Duplication rate	1.62%
Clipped reads	1,294,264 / 84.19%

2.2. ACGT Content

Number/percentage of A's	24,337,435 / 25.43%
Number/percentage of C's	19,125,888 / 19.98%
Number/percentage of T's	29,129,085 / 30.44%
Number/percentage of G's	23,104,275 / 24.14%
Number/percentage of N's	11,681 / 0.01%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2687

2.4. Mapping Quality

Mean Mapping Quality	46.19

2.5. Mismatches and indels

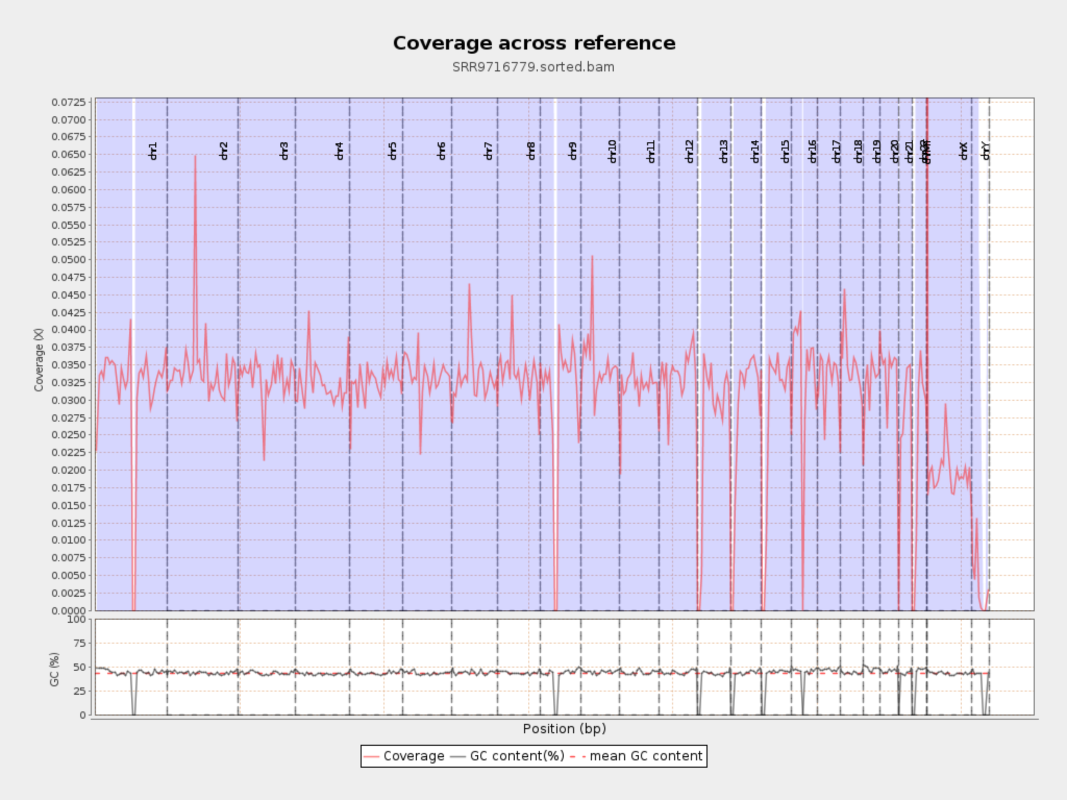
General error rate	0.74%
Mismatches	694,979
Insertions	8,168
Mapped reads with at least one insertion	0.64%
Deletions	20,198
Mapped reads with at least one deletion	1.57%
Homopolymer indels	41.06%

2.6. Chromosome stats

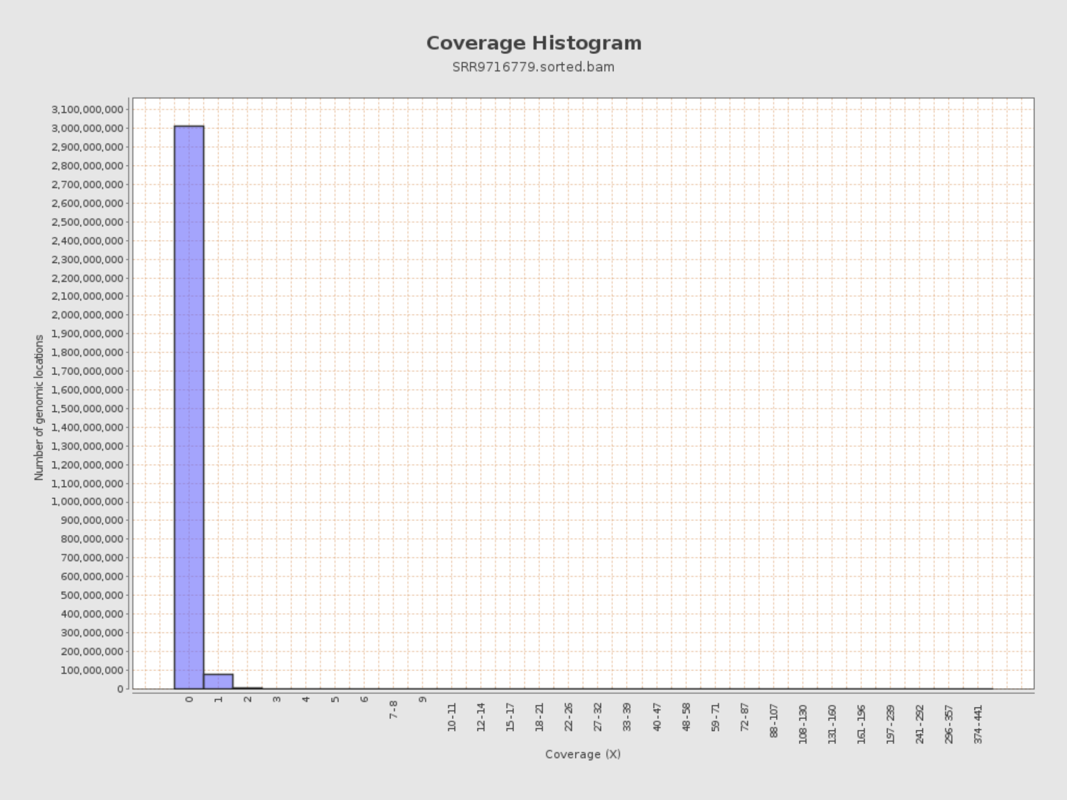
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7797652	0.0313	0.309
chr2	243199373	8397626	0.0345	0.3883
chr3	198022430	6566272	0.0332	0.1977
chr4	191154276	6198937	0.0324	0.208
chr5	180915260	5953787	0.0329	0.1998
chr6	171115067	5703461	0.0333	0.2219
chr7	159138663	5315763	0.0334	0.3267

chr8	146364022	4942787	0.0338	0.3314
chr9	141213431	4230470	0.03	0.2844
chr10	135534747	4740469	0.035	0.2808
chr11	135006516	4358782	0.0323	0.2859
chr12	133851895	4508995	0.0337	0.2036
chr13	115169878	3035150	0.0264	0.1759
chr14	107349540	2987031	0.0278	0.2113
chr15	102531392	2827464	0.0276	0.1813
chr16	90354753	2953004	0.0327	0.2204
chr17	81195210	2667014	0.0328	0.2133
chr18	78077248	2756471	0.0353	0.5317
chr19	59128983	1952747	0.033	0.287
chr20	63025520	2132021	0.0338	0.2075
chr21	48129895	1289307	0.0268	0.1918
chr22	51304566	1145031	0.0223	0.1644
chrMT	16571	7968	0.4808	0.913
chrX	155270560	3062445	0.0197	0.1977
chrY	59373566	212743	0.0036	0.1128

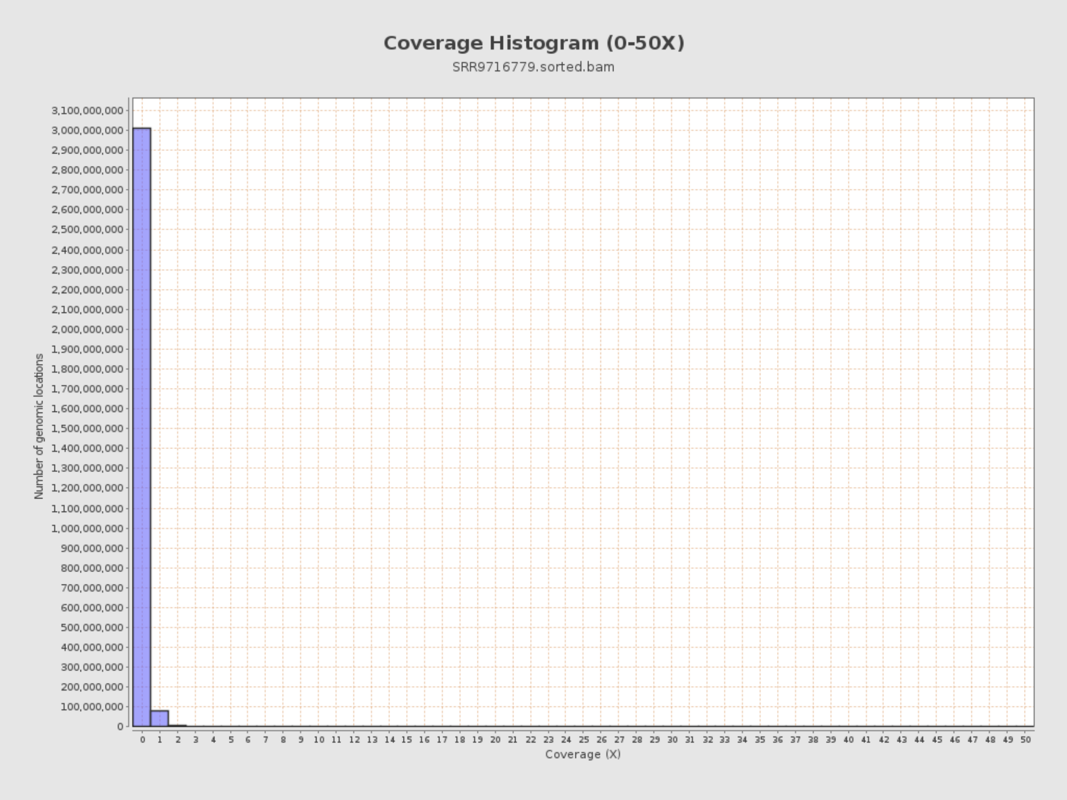
3. Results : Coverage across reference



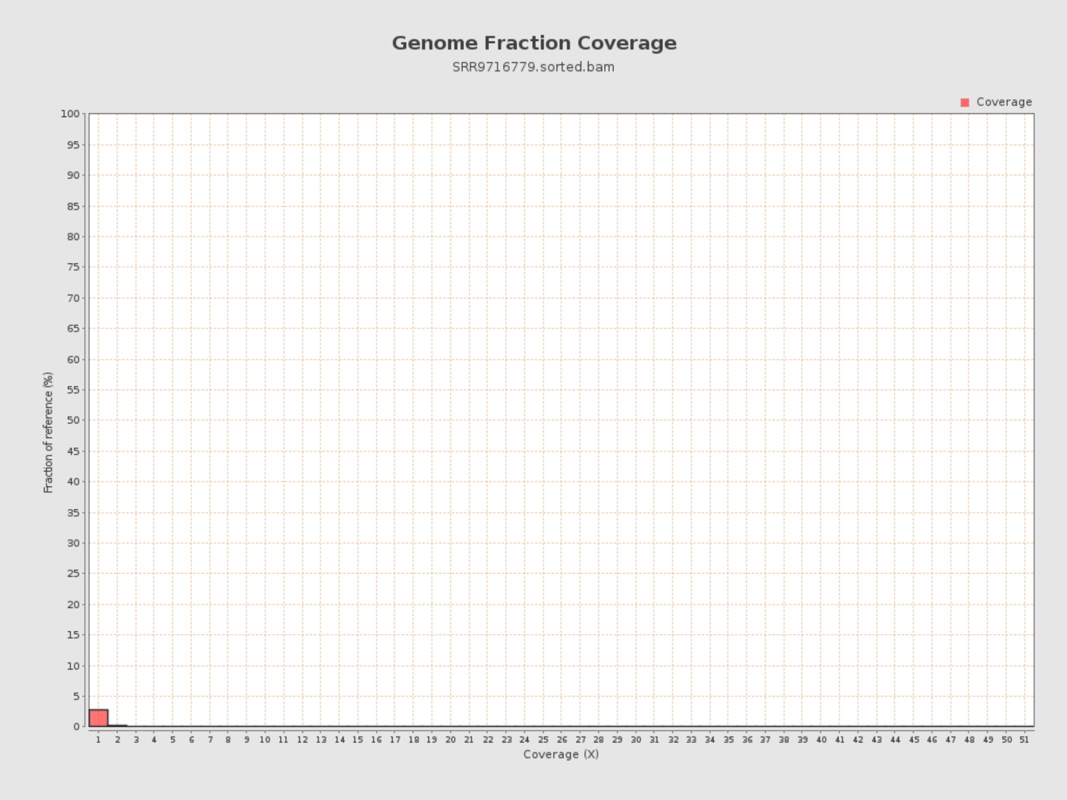
4. Results : Coverage Histogram



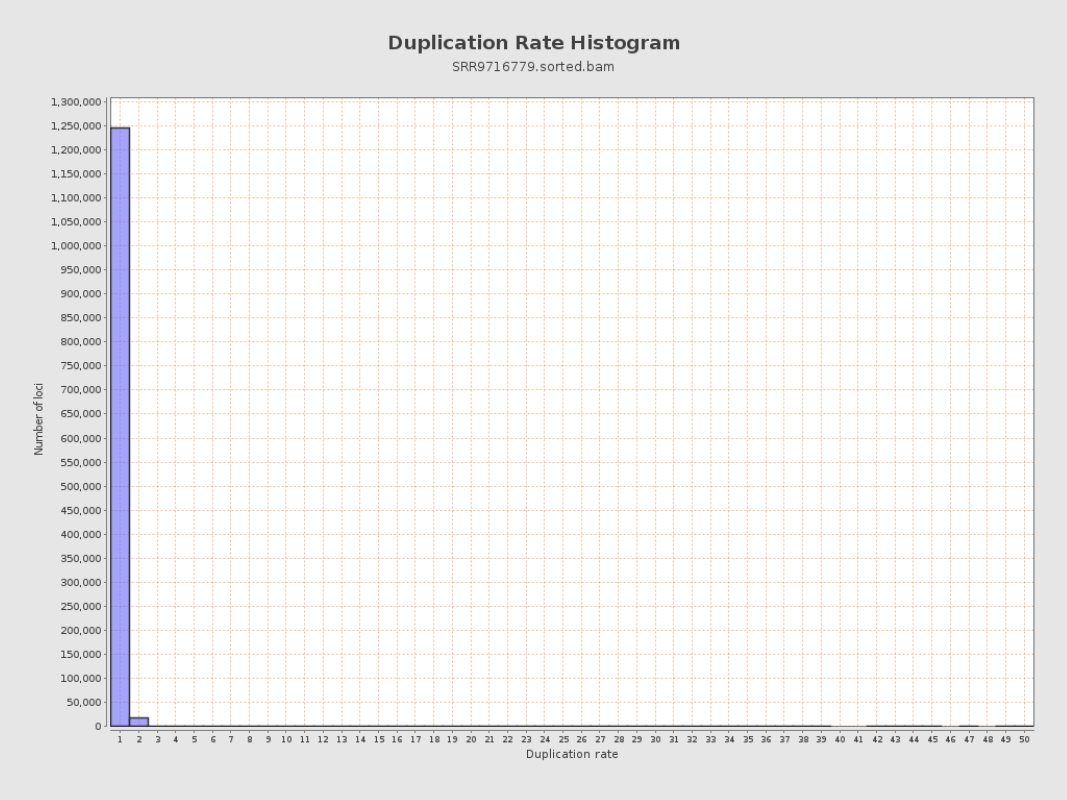
5. Results : Coverage Histogram (0-50X)



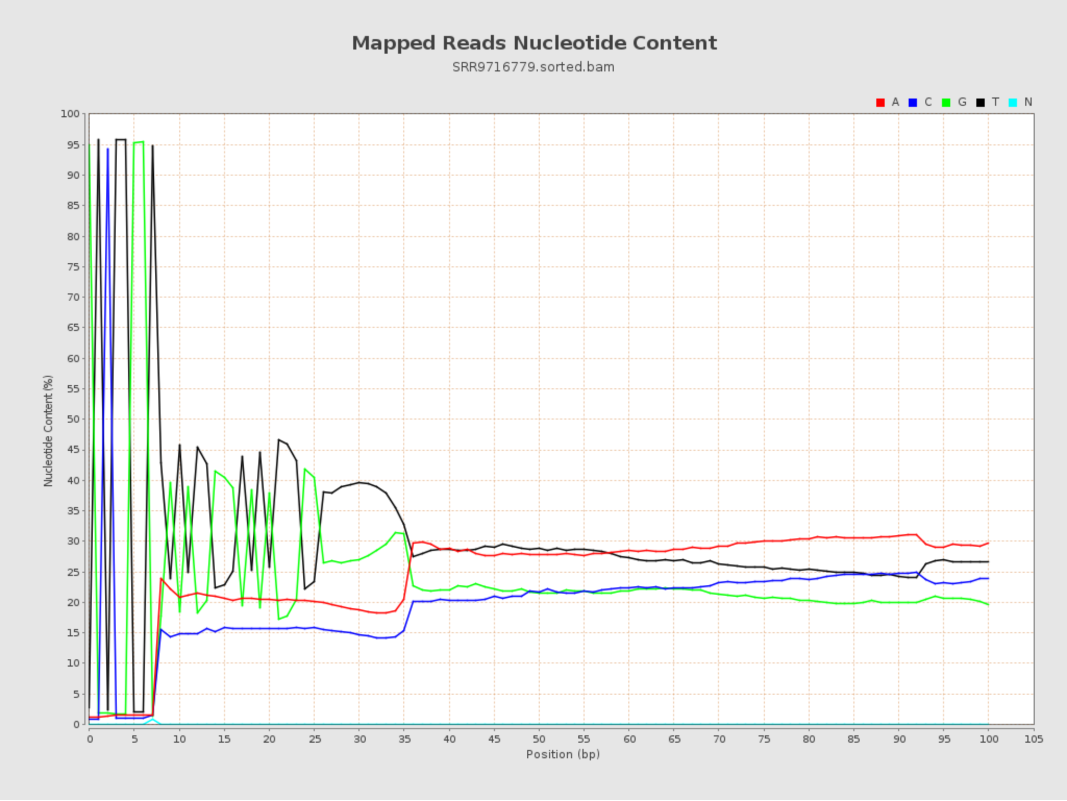
6. Results : Genome Fraction Coverage



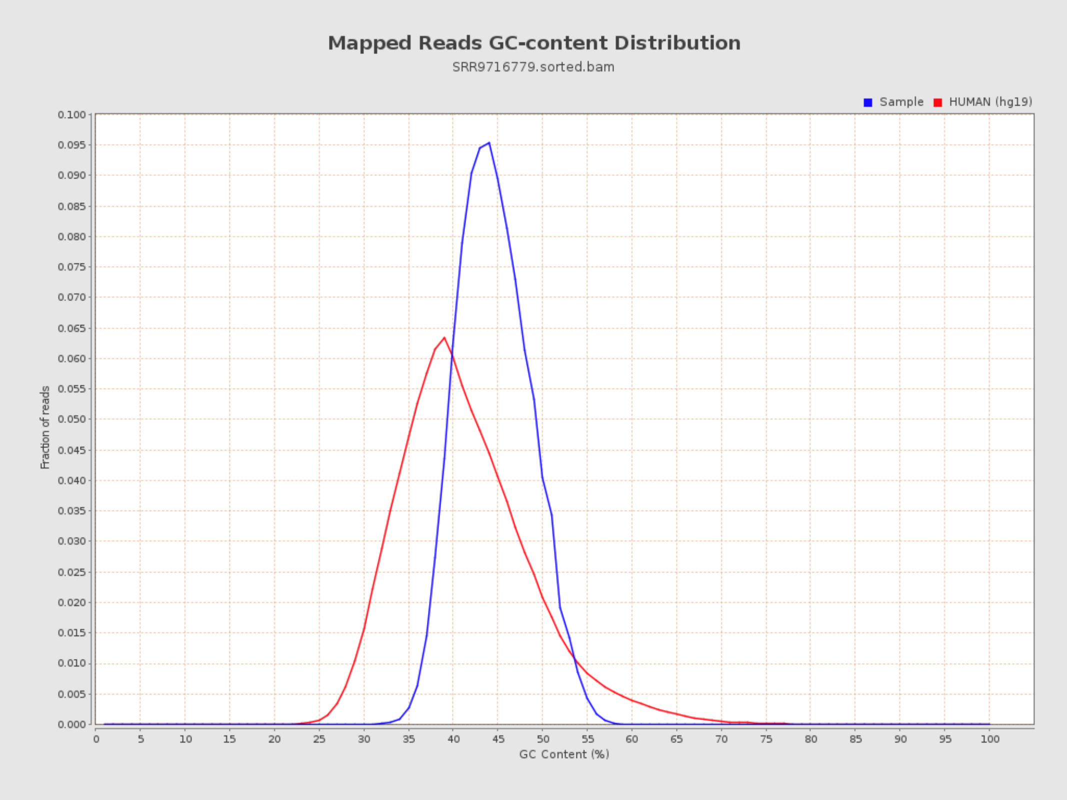
7. Results : Duplication Rate Histogram



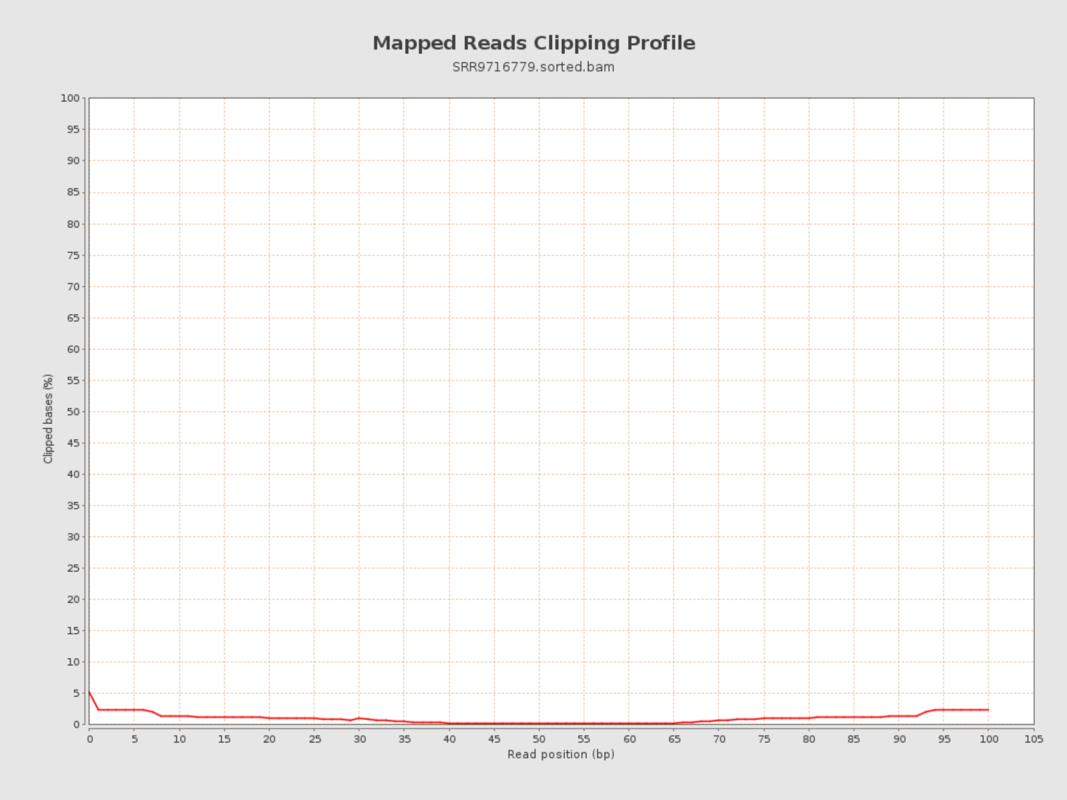
8. Results : Mapped Reads Nucleotide Content



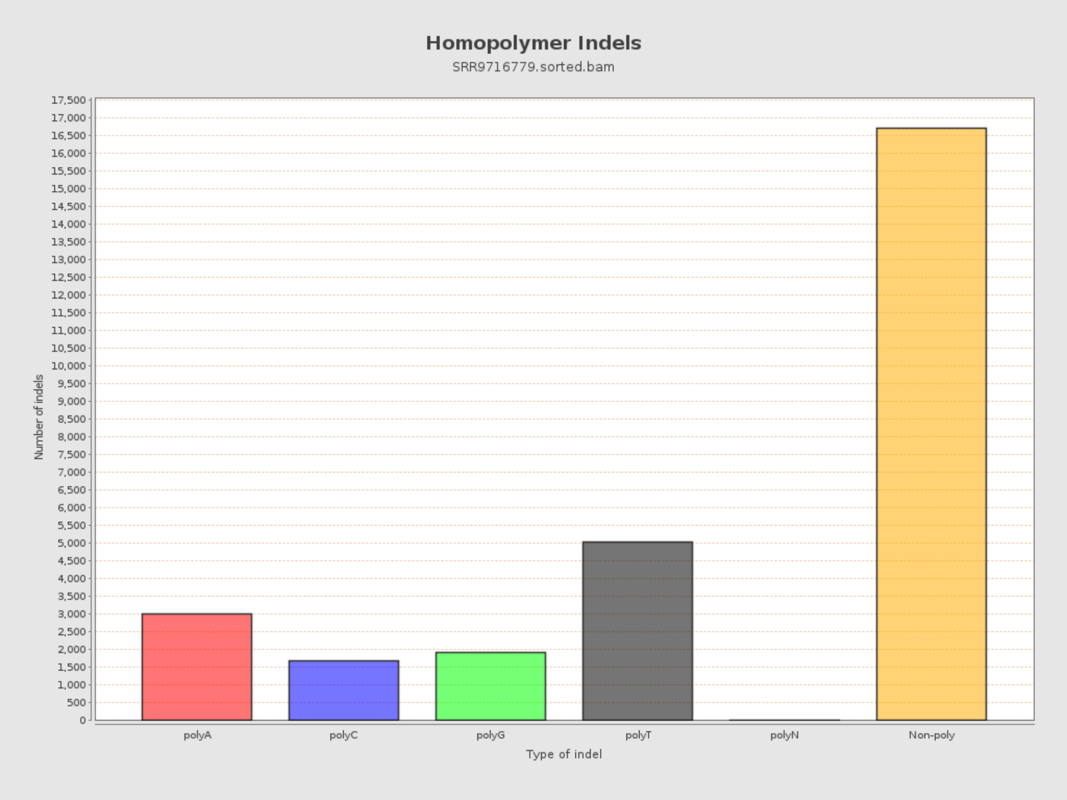
9. Results : Mapped Reads GC-content Distribution



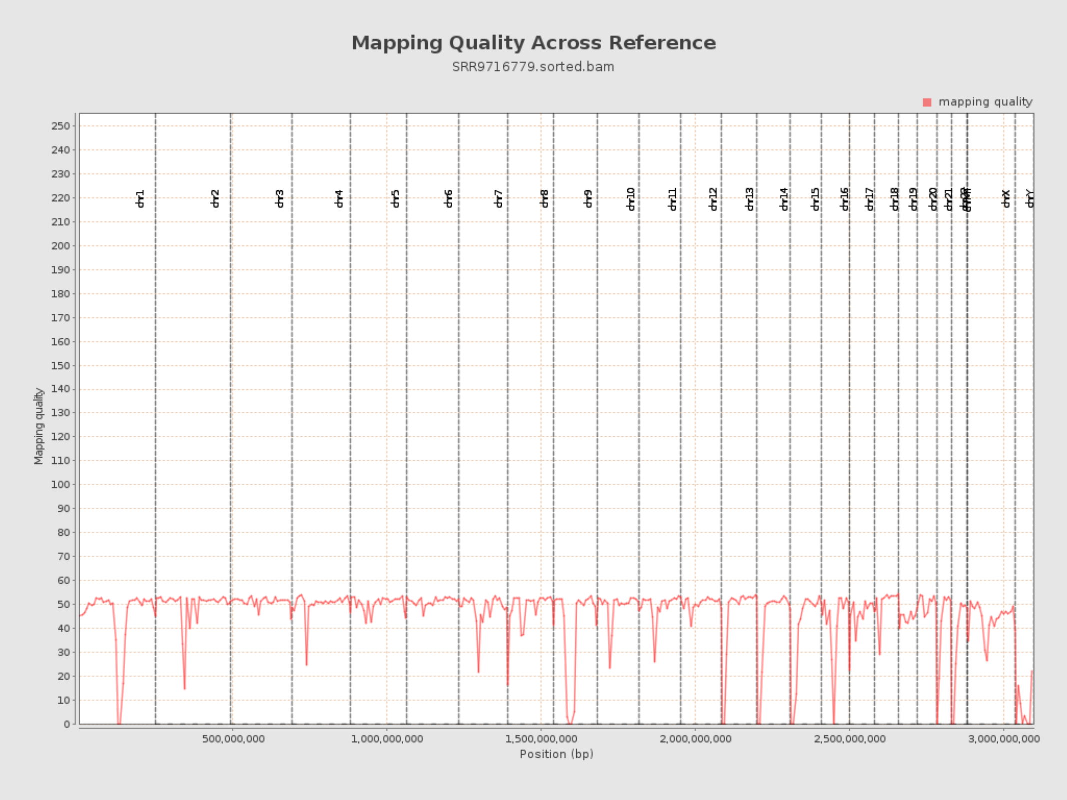
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram