Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:13:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716773.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_SRR9716773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:13:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,063,796
Mapped reads	1,929,772 / 93.51%
Unmapped reads	134,024 / 6.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,446 / 2.25%
Read min/max/mean length	30 / 101 / 101.81
Duplicated reads (estimated)	95,339 / 4.62%
Duplication rate	3.79%
Clipped reads	1,972,735 / 95.59%

2.2. ACGT Content

Number/percentage of A's	35,972,645 / 24.41%
Number/percentage of C's	29,673,857 / 20.13%
Number/percentage of T's	44,573,008 / 30.24%
Number/percentage of G's	37,149,953 / 25.21%
Number/percentage of N's	5,559 / 0%
GC Percentage	45.34%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.3924

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

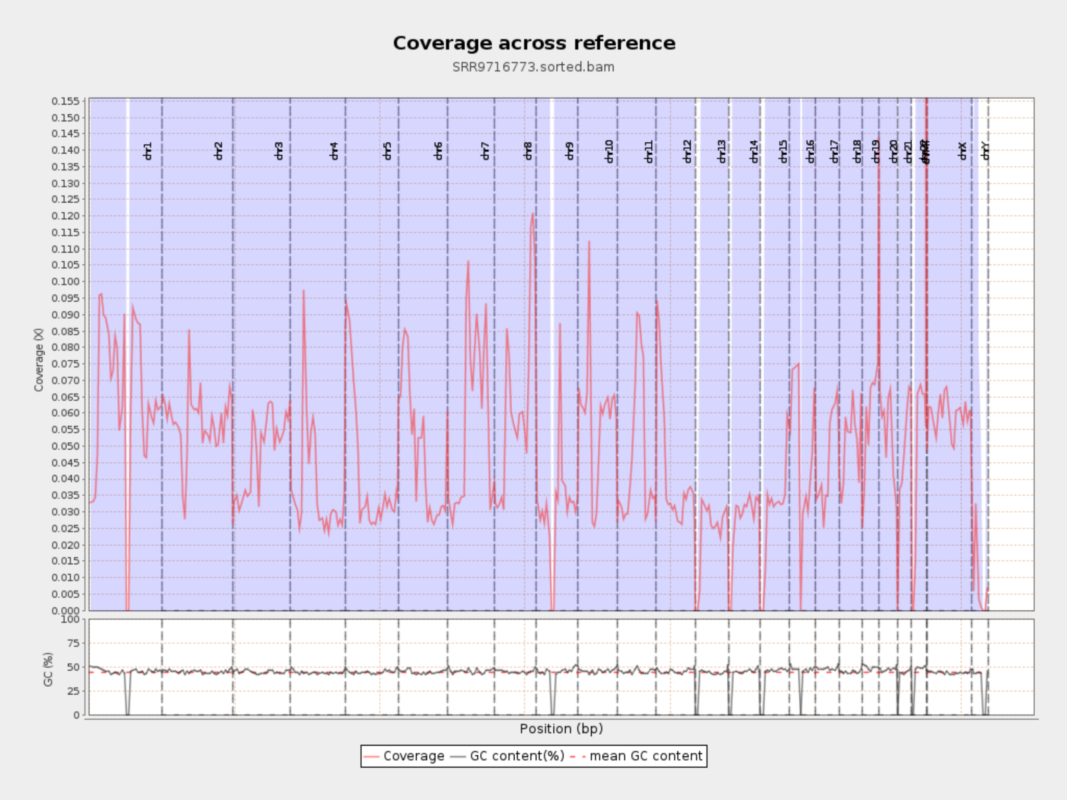
General error rate	0.68%
Mismatches	965,890
Insertions	12,671
Mapped reads with at least one insertion	0.65%
Deletions	28,816
Mapped reads with at least one deletion	1.47%
Homopolymer indels	39.33%

2.6. Chromosome stats

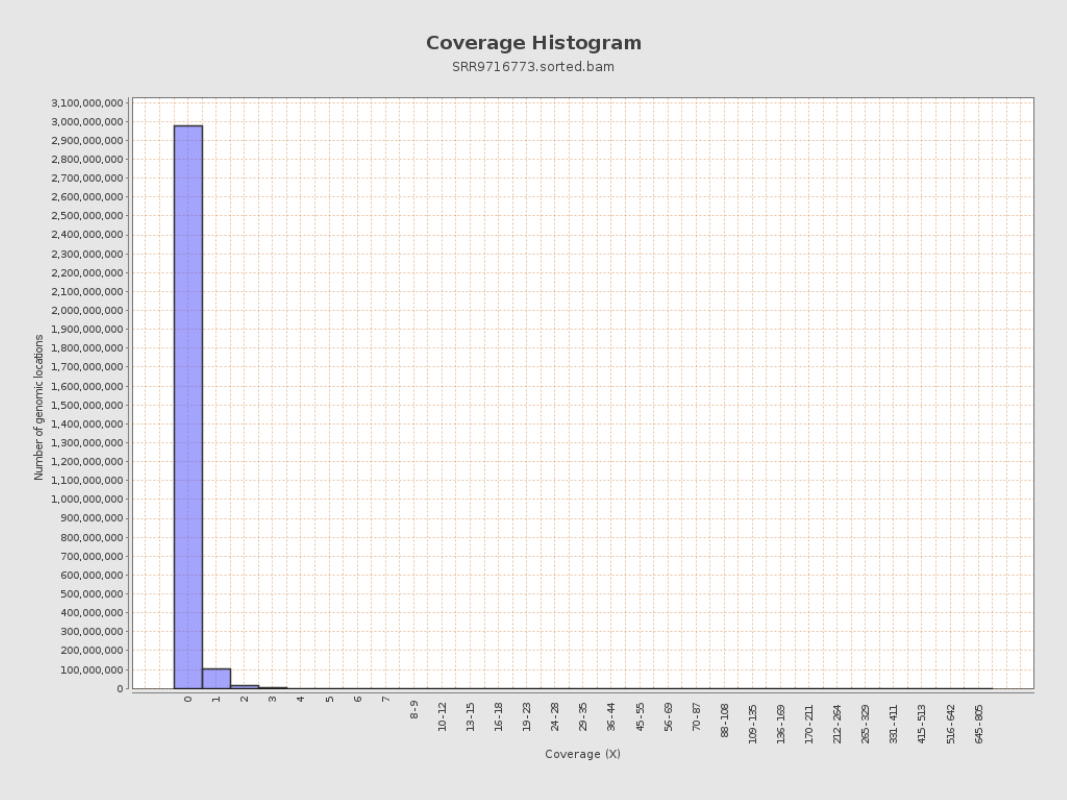
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15986648	0.0641	0.7421
chr2	243199373	13887080	0.0571	0.4209
chr3	198022430	9491454	0.0479	0.2585
chr4	191154276	7082092	0.037	0.3376
chr5	180915260	7579242	0.0419	0.2419
chr6	171115067	8234812	0.0481	0.2795
chr7	159138663	9283646	0.0583	0.5385

chr8	146364022	9135625	0.0624	0.4148
chr9	141213431	4448265	0.0315	0.2714
chr10	135534747	7927292	0.0585	0.5473
chr11	135006516	6313591	0.0468	0.3315
chr12	133851895	5721127	0.0427	0.2428
chr13	115169878	2756224	0.0239	0.1769
chr14	107349540	2879504	0.0268	0.2071
chr15	102531392	3030486	0.0296	0.1982
chr16	90354753	4502931	0.0498	0.2832
chr17	81195210	3719361	0.0458	0.2817
chr18	78077248	3978772	0.051	0.4165
chr19	59128983	3697932	0.0625	0.539
chr20	63025520	3370799	0.0535	0.2886
chr21	48129895	2276376	0.0473	0.3224
chr22	51304566	2283603	0.0445	0.2558
chrMT	16571	137125	8.275	5.9187
chrX	155270560	9208741	0.0593	0.3049
chrY	59373566	501162	0.0084	0.3001

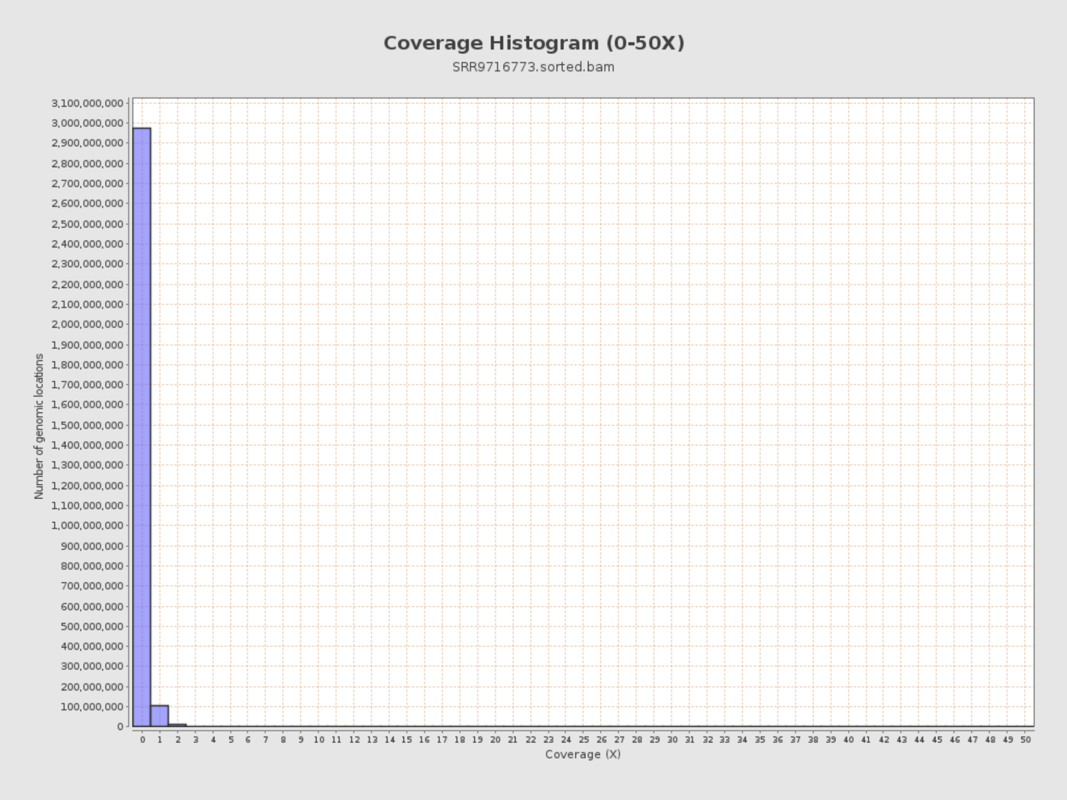
3. Results : Coverage across reference



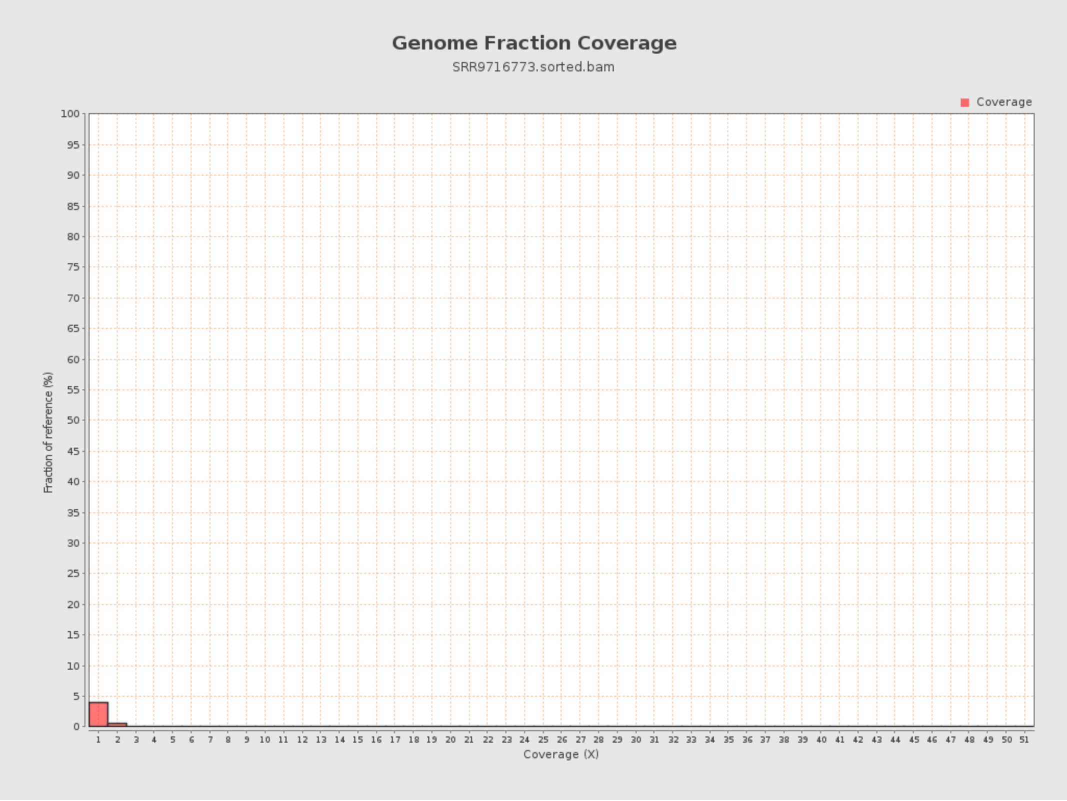
4. Results : Coverage Histogram



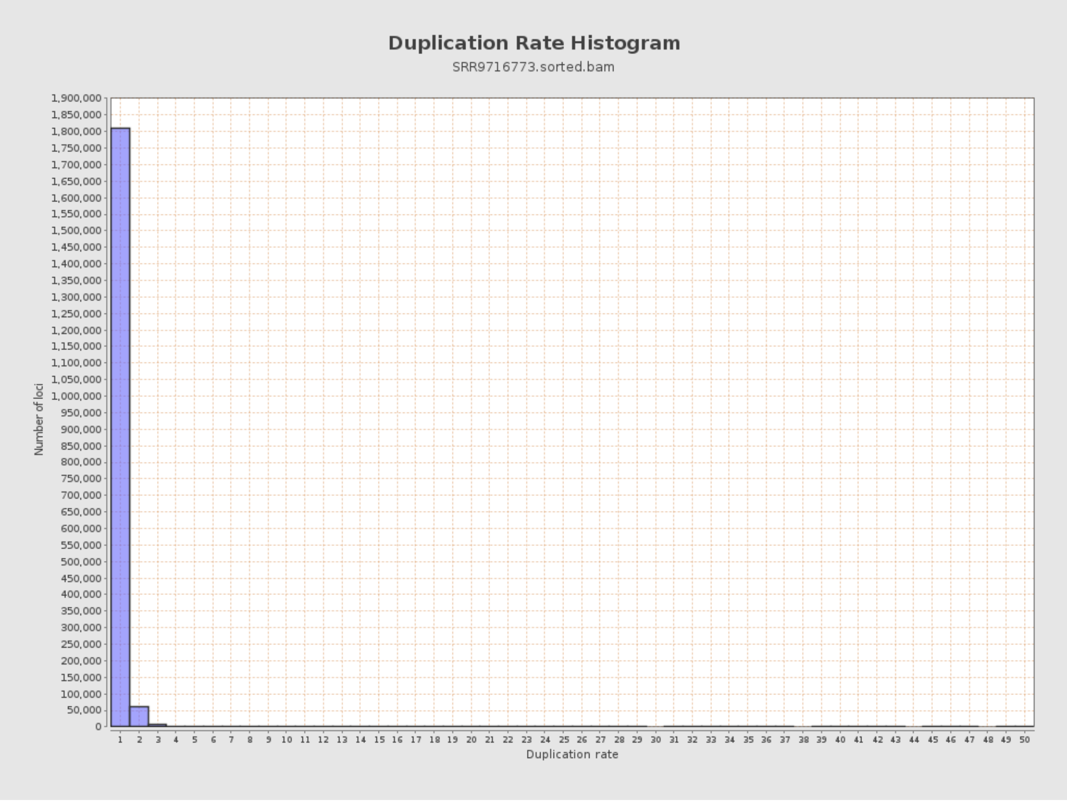
5. Results : Coverage Histogram (0-50X)



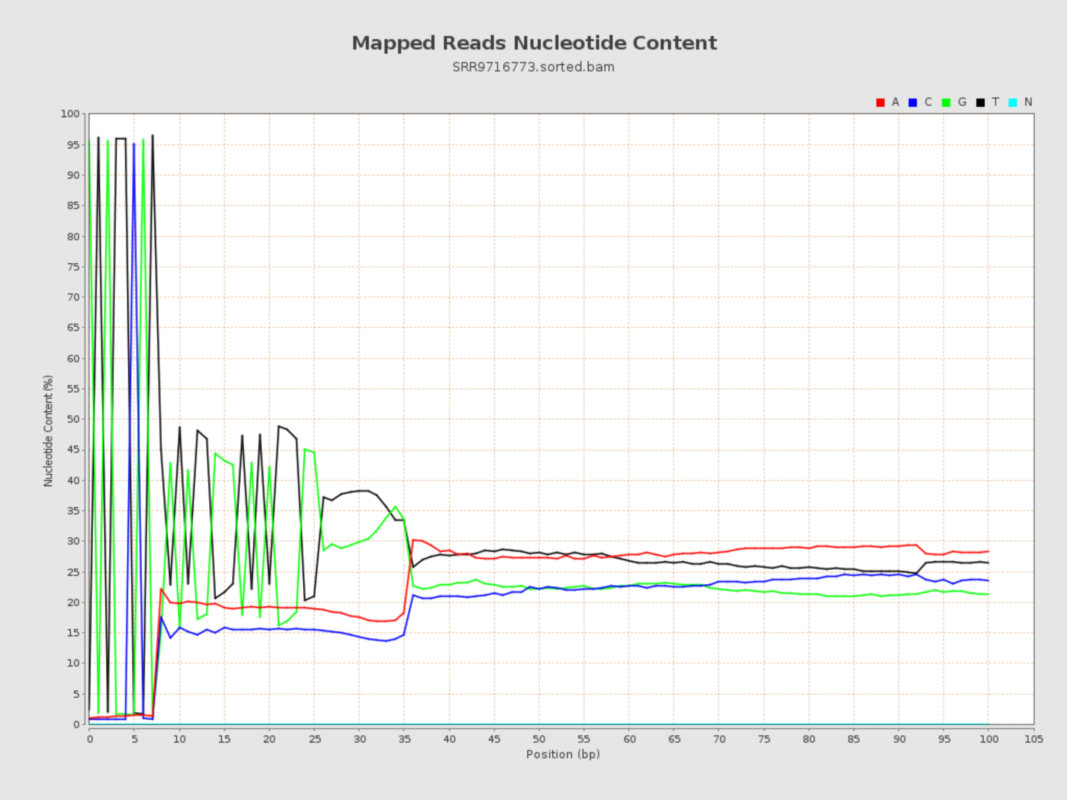
6. Results : Genome Fraction Coverage



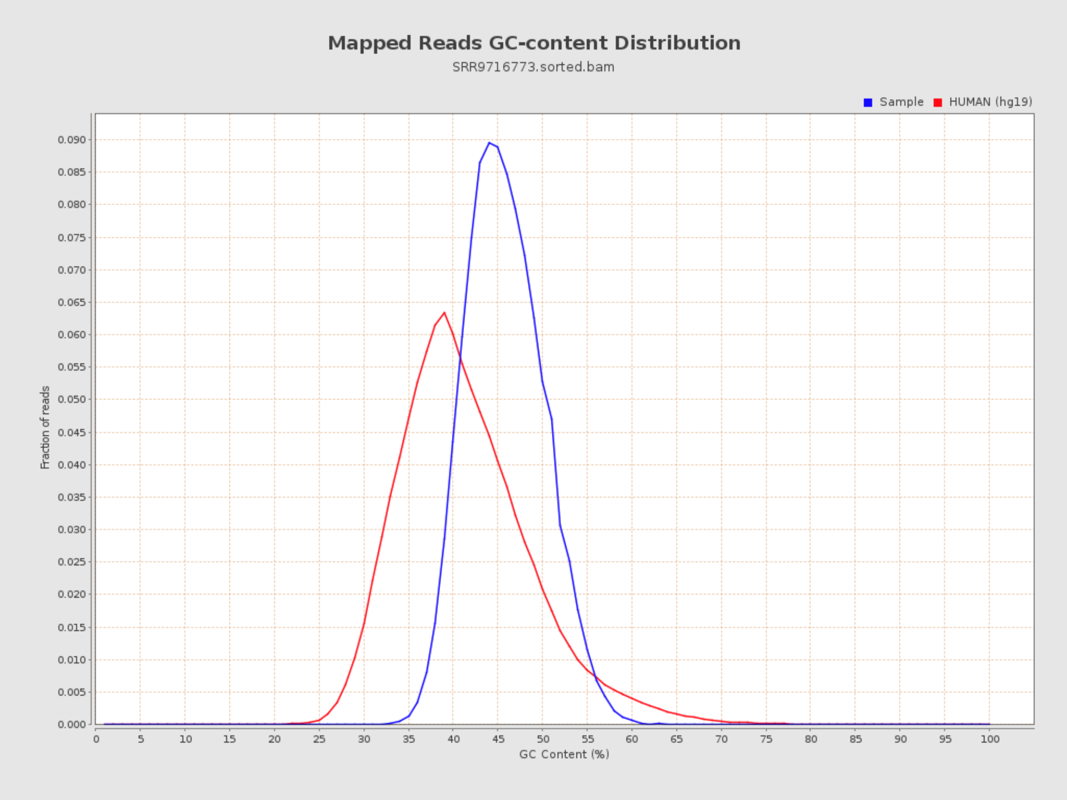
7. Results : Duplication Rate Histogram



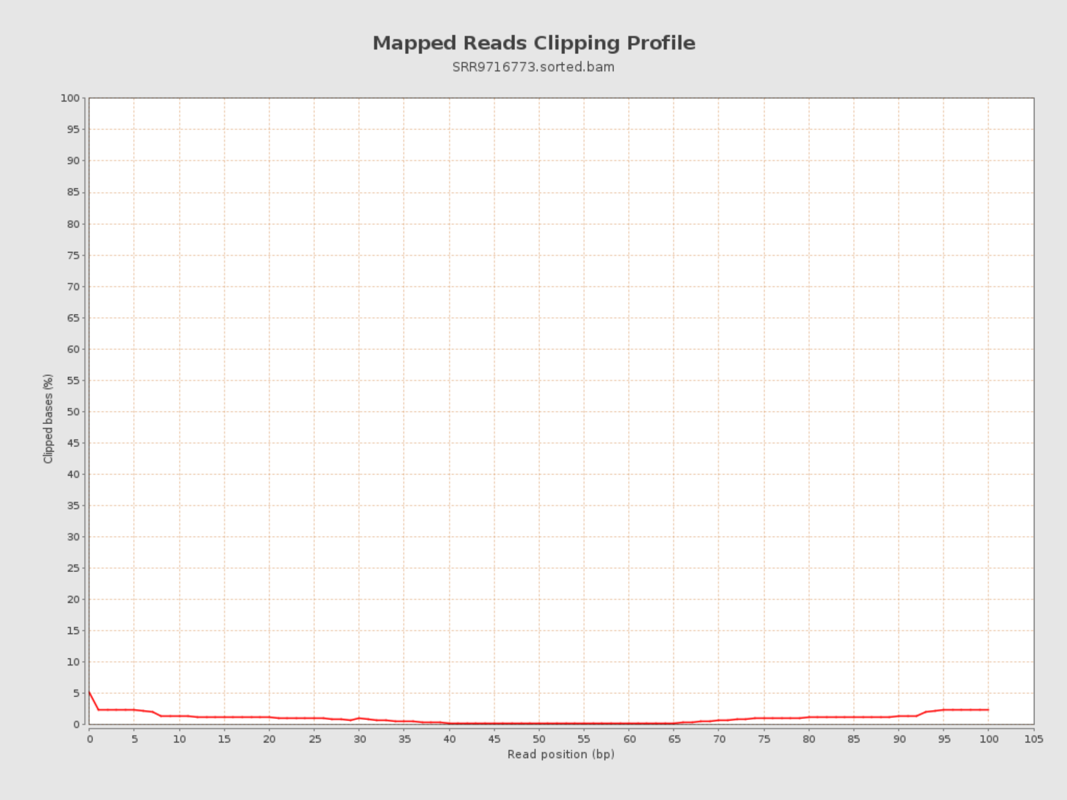
8. Results : Mapped Reads Nucleotide Content



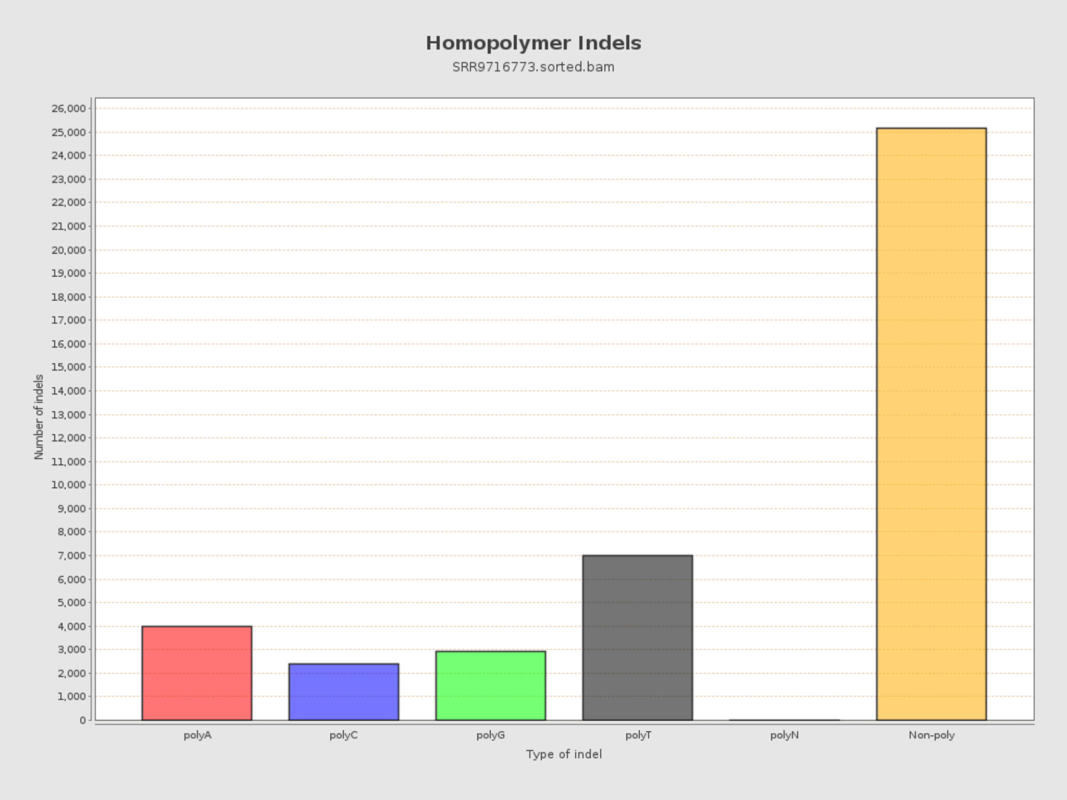
9. Results : Mapped Reads GC-content Distribution



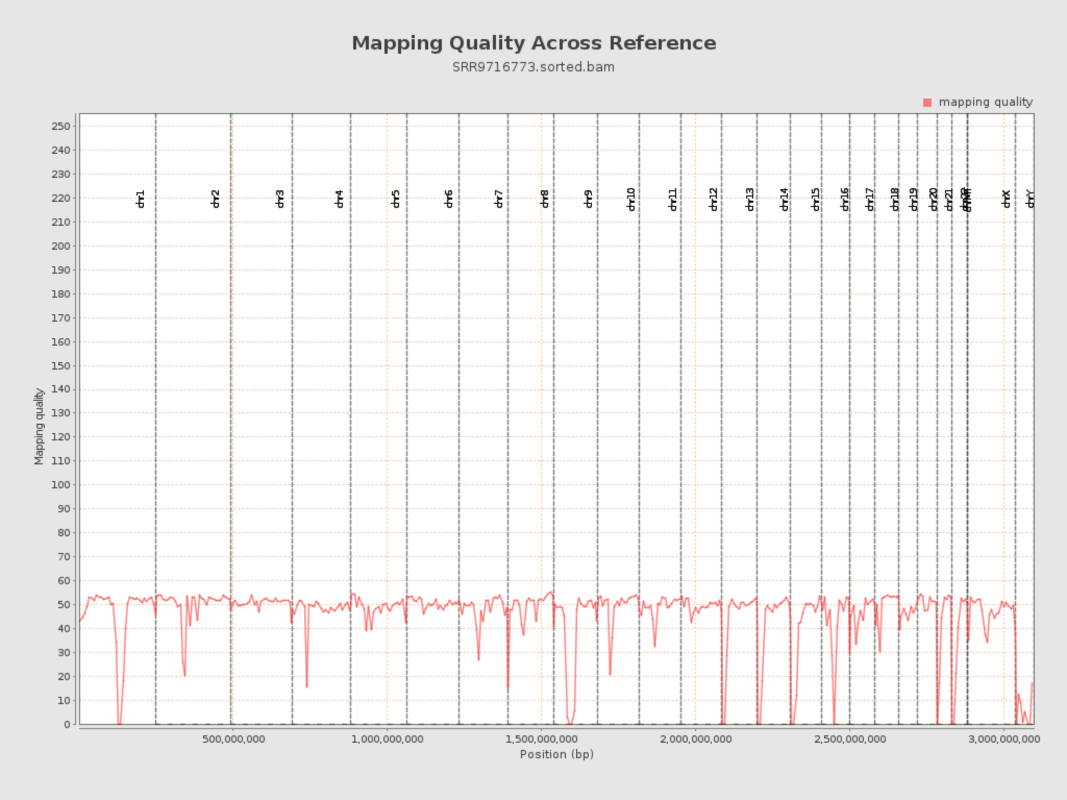
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram