Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:33:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716778.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_SRR9716778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:33:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,471,565
Mapped reads	1,374,659 / 93.41%
Unmapped reads	96,906 / 6.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,344 / 2.33%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	50,980 / 3.46%
Duplication rate	2.79%
Clipped reads	1,406,263 / 95.56%

2.2. ACGT Content

Number/percentage of A's	25,411,701 / 24.17%
Number/percentage of C's	21,513,797 / 20.46%
Number/percentage of T's	31,455,153 / 29.92%
Number/percentage of G's	26,749,829 / 25.44%
Number/percentage of N's	4,126 / 0%
GC Percentage	45.91%

2.3. Coverage

Mean	0.034

Standard Deviation	0.2745

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

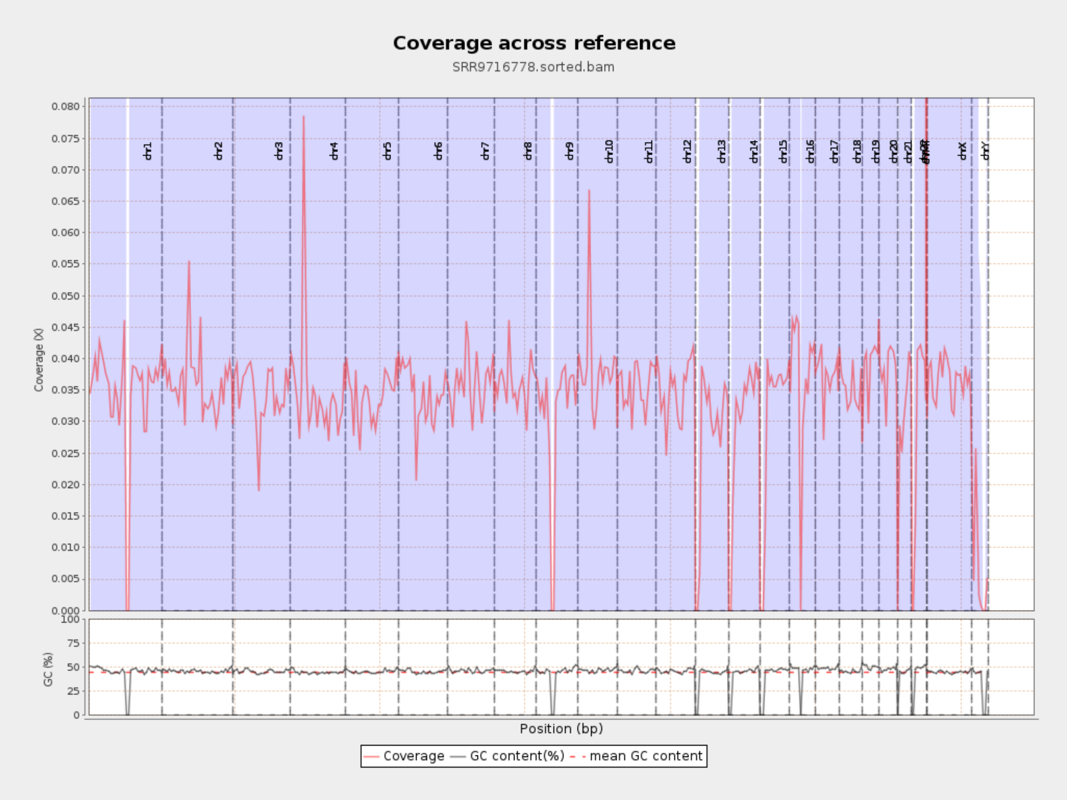
General error rate	0.7%
Mismatches	711,020
Insertions	9,526
Mapped reads with at least one insertion	0.68%
Deletions	22,470
Mapped reads with at least one deletion	1.6%
Homopolymer indels	38.42%

2.6. Chromosome stats

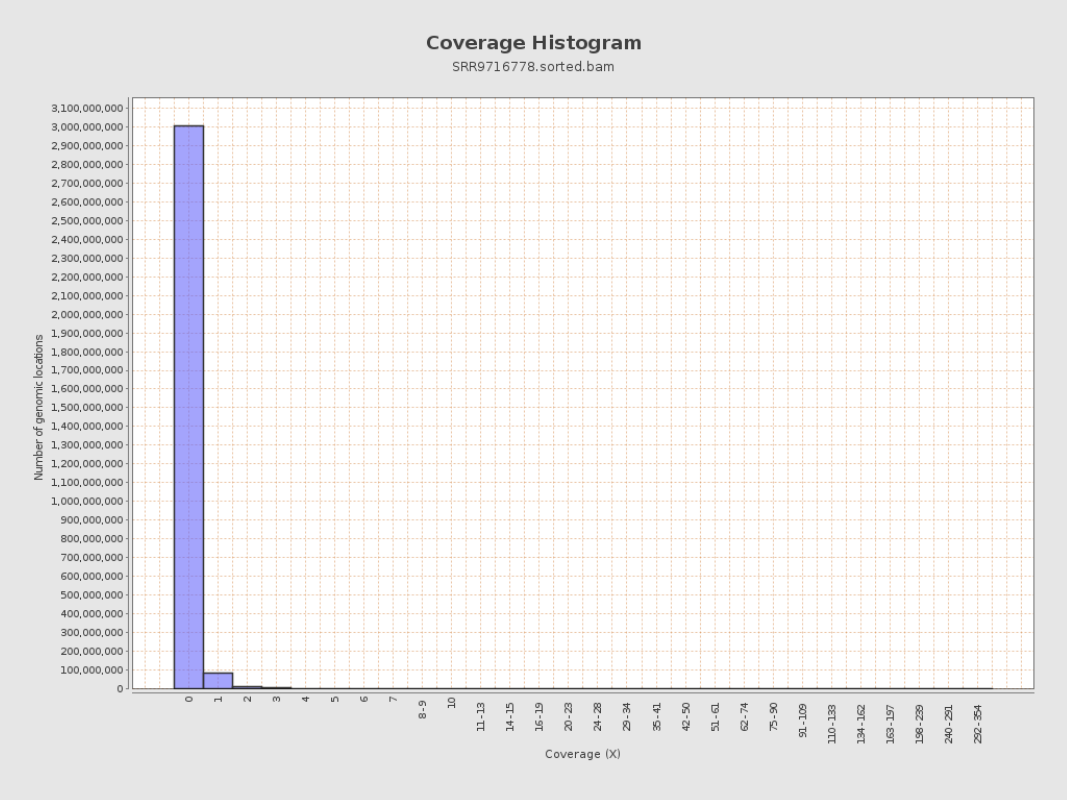
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8547247	0.0343	0.3662
chr2	243199373	8857552	0.0364	0.3055
chr3	198022430	6803441	0.0344	0.2051
chr4	191154276	6633113	0.0347	0.2976
chr5	180915260	6147215	0.034	0.2052
chr6	171115067	5892874	0.0344	0.2161
chr7	159138663	5729982	0.036	0.3388

chr8	146364022	5300723	0.0362	0.2698
chr9	141213431	4325532	0.0306	0.2514
chr10	135534747	5219833	0.0385	0.3895
chr11	135006516	4780169	0.0354	0.2918
chr12	133851895	4698184	0.0351	0.211
chr13	115169878	3137077	0.0272	0.1844
chr14	107349540	3146144	0.0293	0.211
chr15	102531392	3073266	0.03	0.1934
chr16	90354753	3345825	0.037	0.2337
chr17	81195210	3015788	0.0371	0.2425
chr18	78077248	2756001	0.0353	0.3792
chr19	59128983	2303563	0.039	0.2889
chr20	63025520	2405069	0.0382	0.2386
chr21	48129895	1442623	0.03	0.2514
chr22	51304566	1437913	0.028	0.1915
chrMT	16571	107408	6.4817	4.8773
chrX	155270560	5697016	0.0367	0.2325
chrY	59373566	377671	0.0064	0.2593

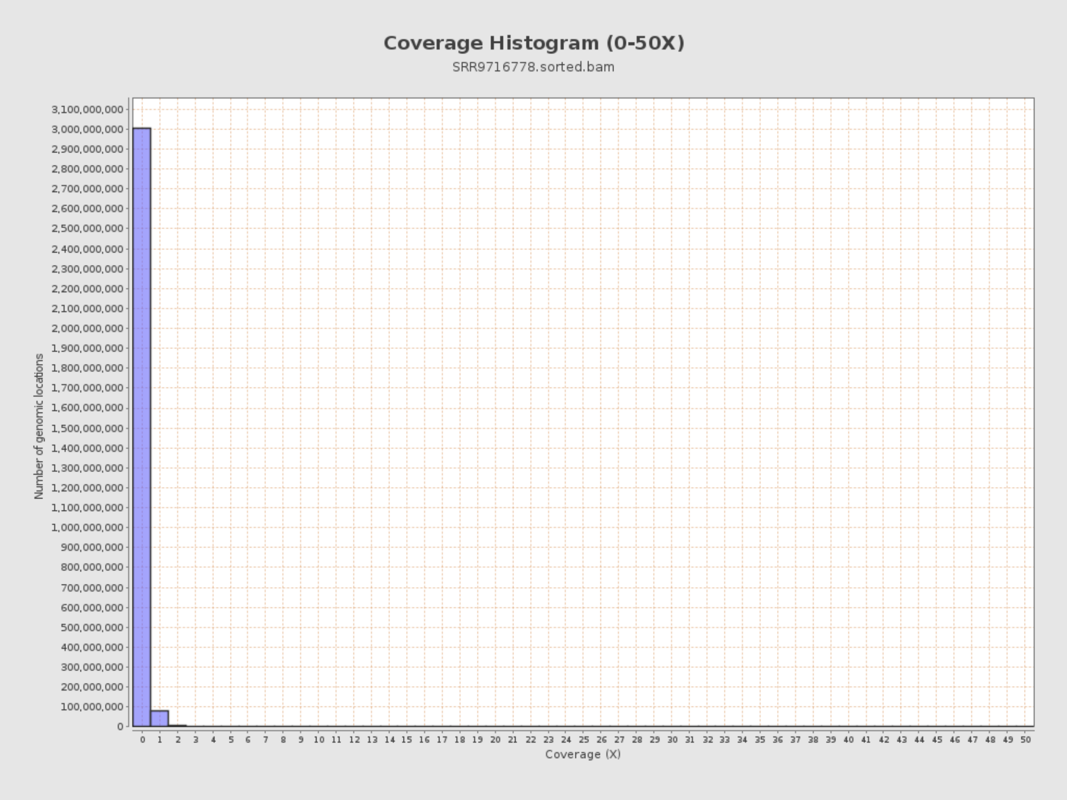
3. Results : Coverage across reference



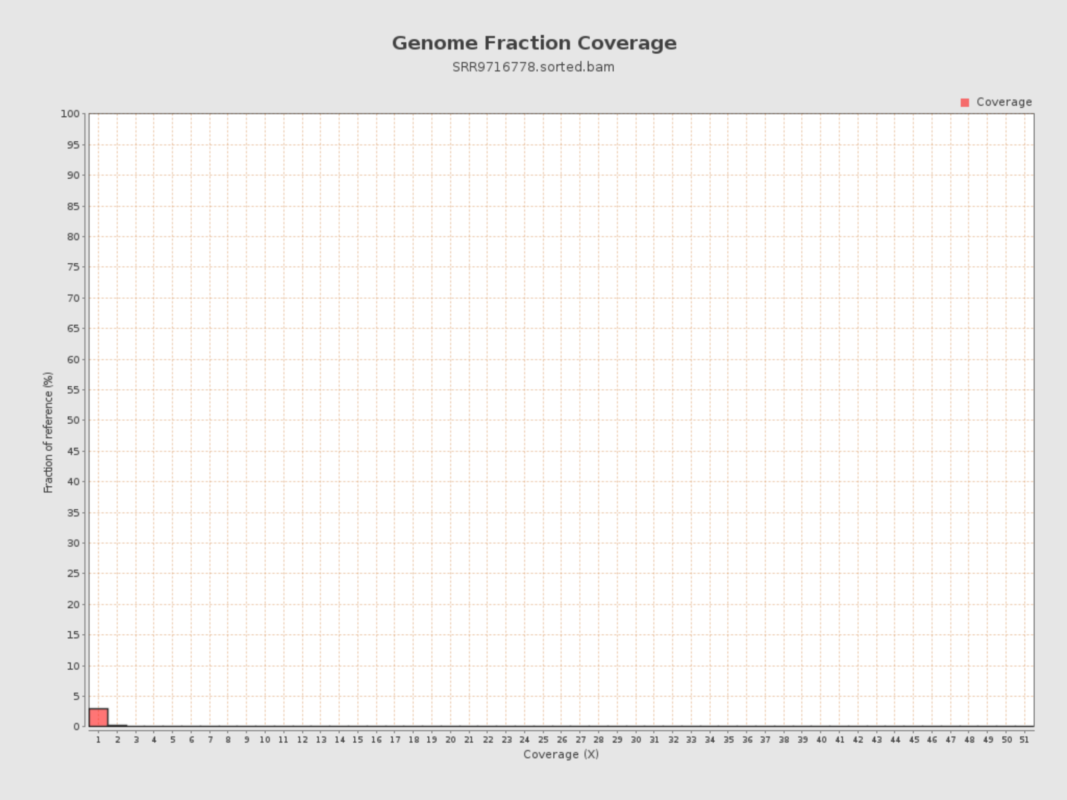
4. Results : Coverage Histogram



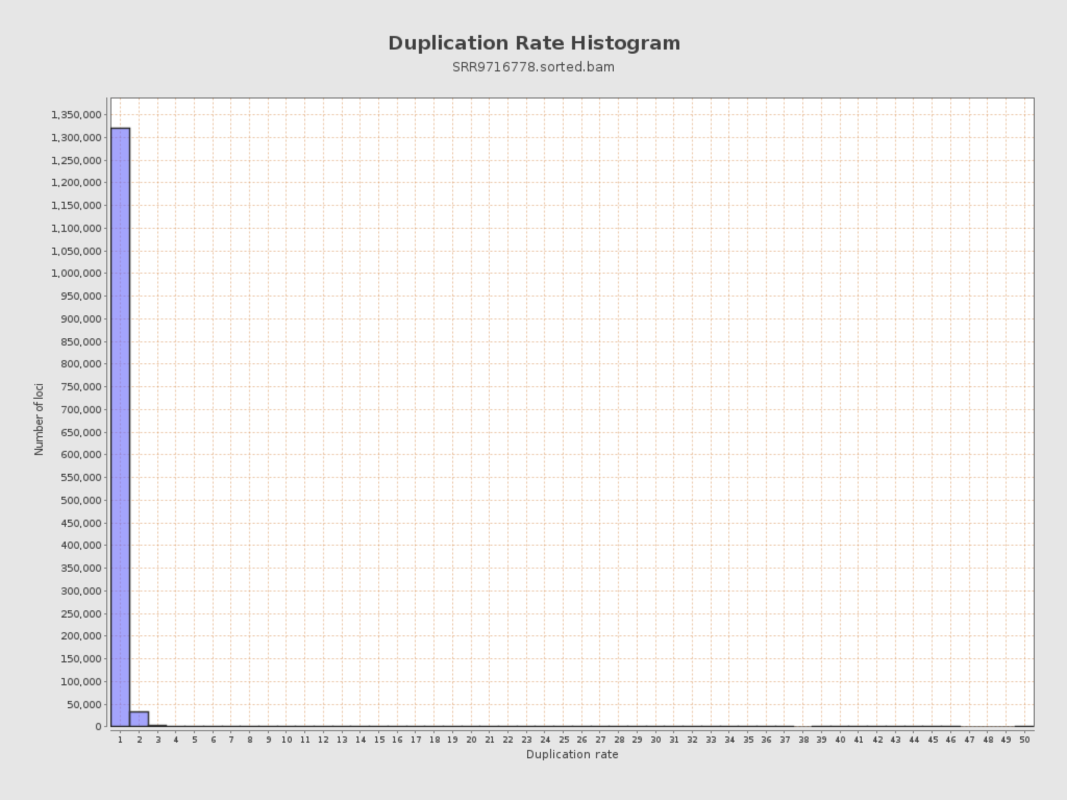
5. Results : Coverage Histogram (0-50X)



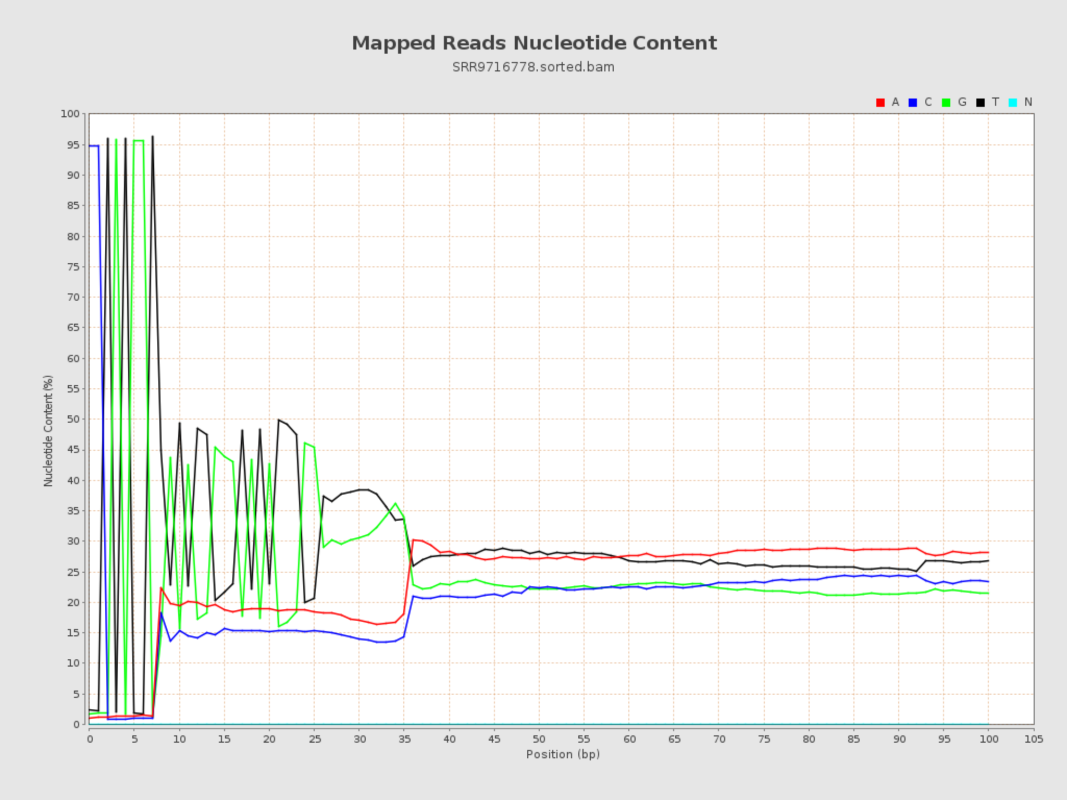
6. Results : Genome Fraction Coverage



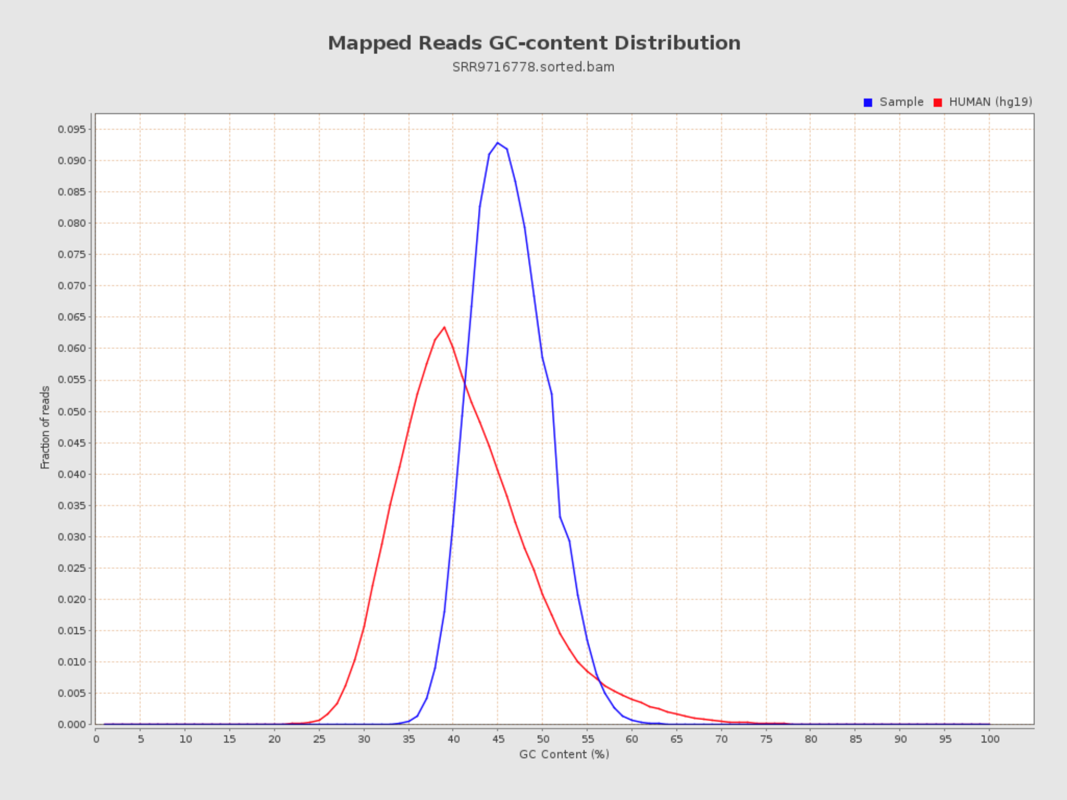
7. Results : Duplication Rate Histogram



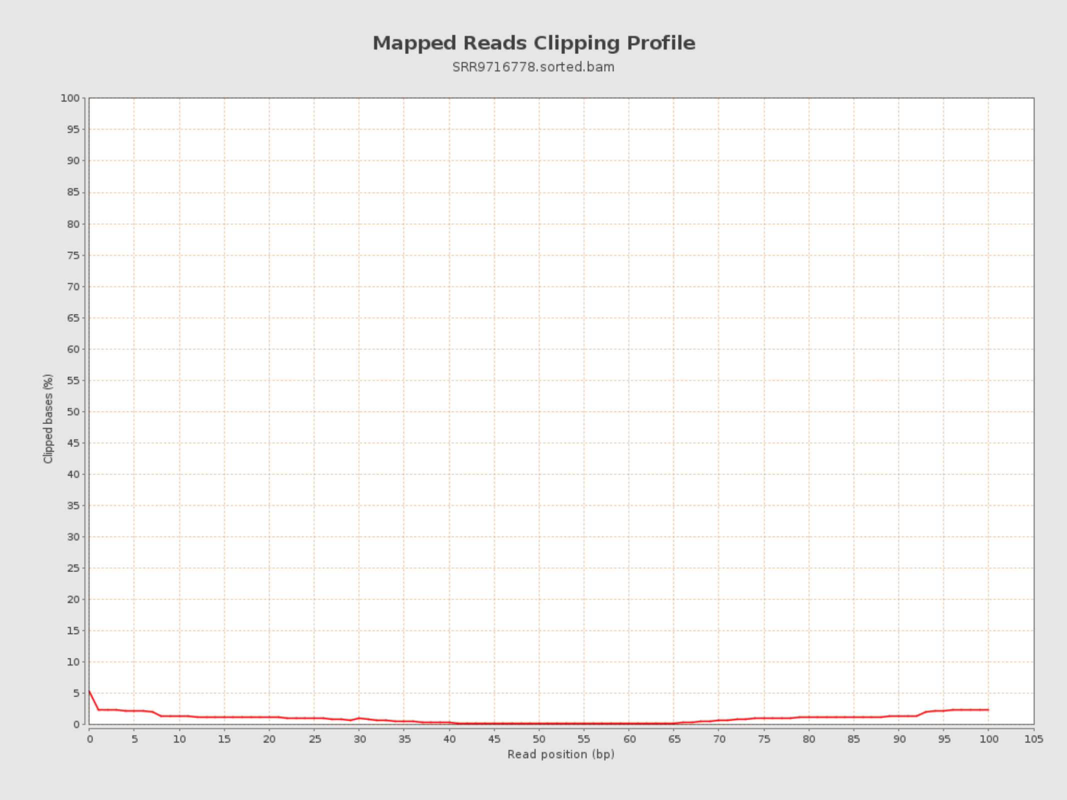
8. Results : Mapped Reads Nucleotide Content



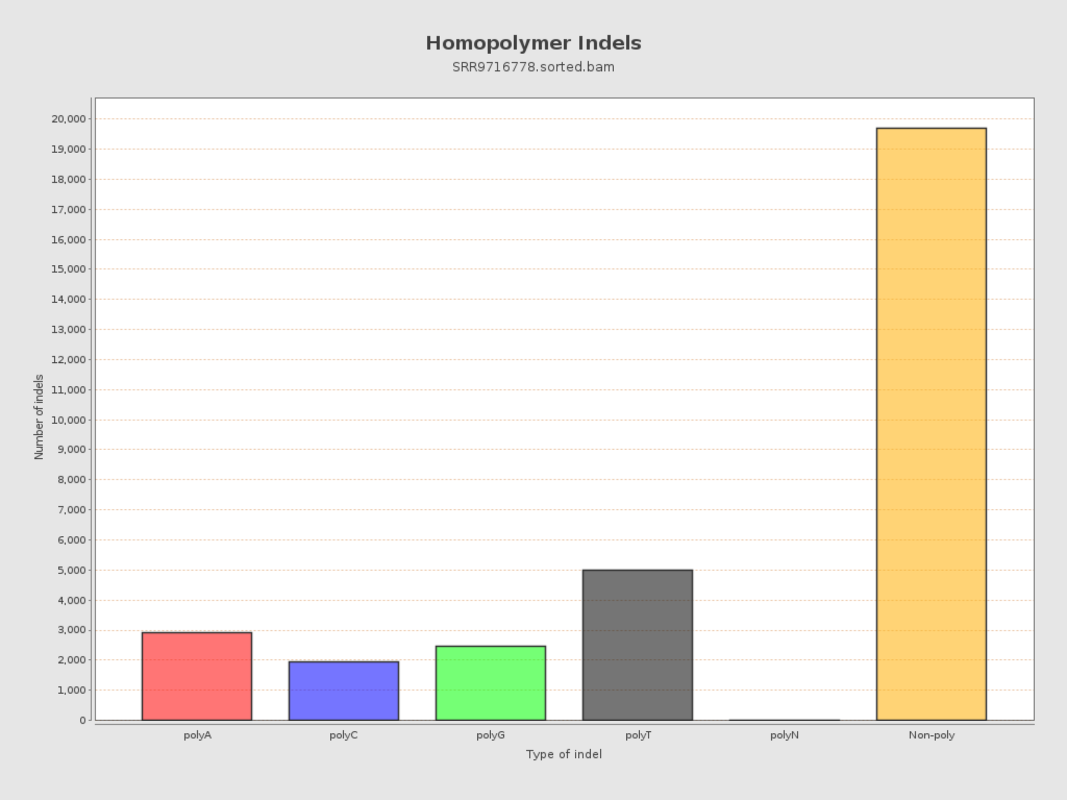
9. Results : Mapped Reads GC-content Distribution



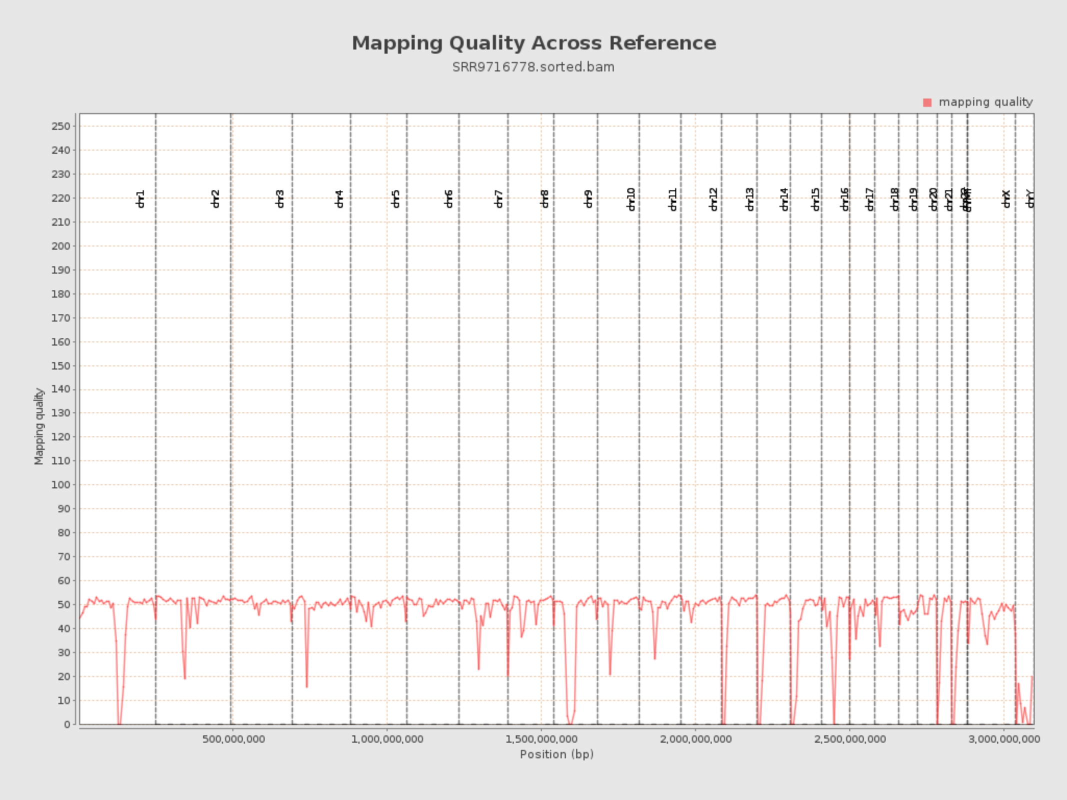
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram