Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 11:30:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716777.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_SRR9716777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 11:30:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,095,267
Mapped reads	1,025,344 / 93.62%
Unmapped reads	69,923 / 6.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,455 / 1.78%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	36,627 / 3.34%
Duplication rate	2.73%
Clipped reads	1,042,434 / 95.18%

2.2. ACGT Content

Number/percentage of A's	19,427,668 / 24.66%
Number/percentage of C's	15,716,800 / 19.95%
Number/percentage of T's	23,964,245 / 30.42%
Number/percentage of G's	19,675,979 / 24.97%
Number/percentage of N's	2,630 / 0%
GC Percentage	44.92%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2513

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

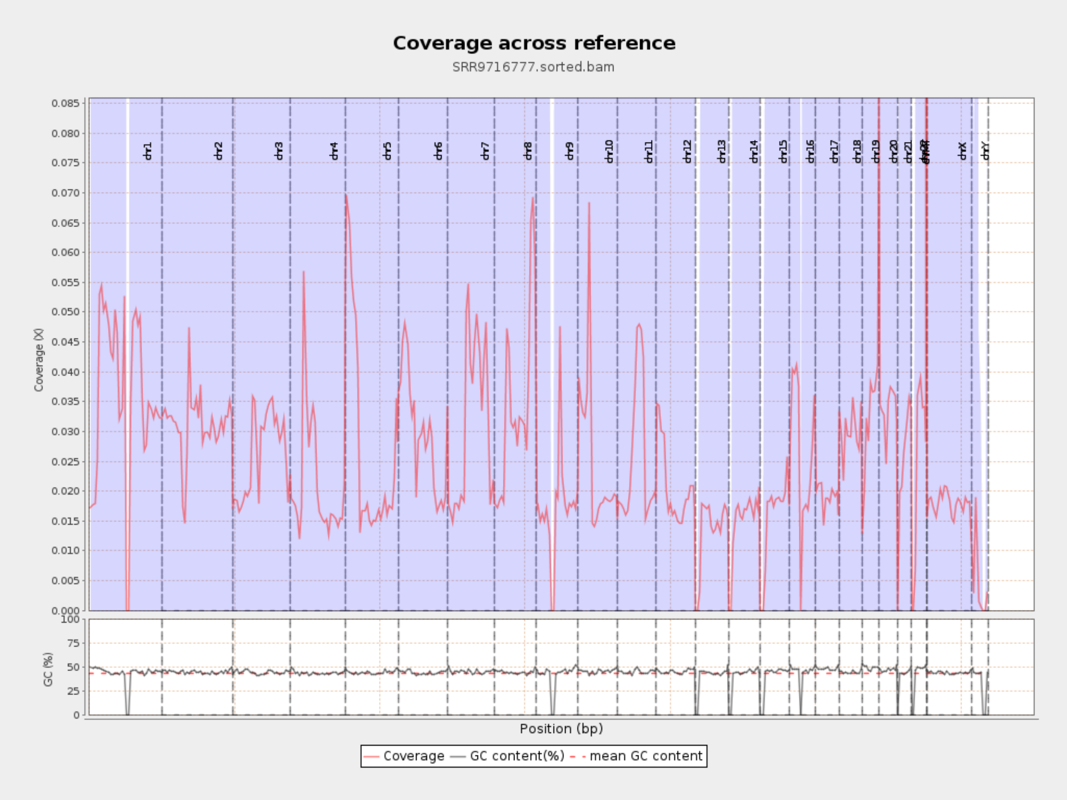
General error rate	0.67%
Mismatches	506,910
Insertions	7,078
Mapped reads with at least one insertion	0.68%
Deletions	14,698
Mapped reads with at least one deletion	1.41%
Homopolymer indels	39.03%

2.6. Chromosome stats

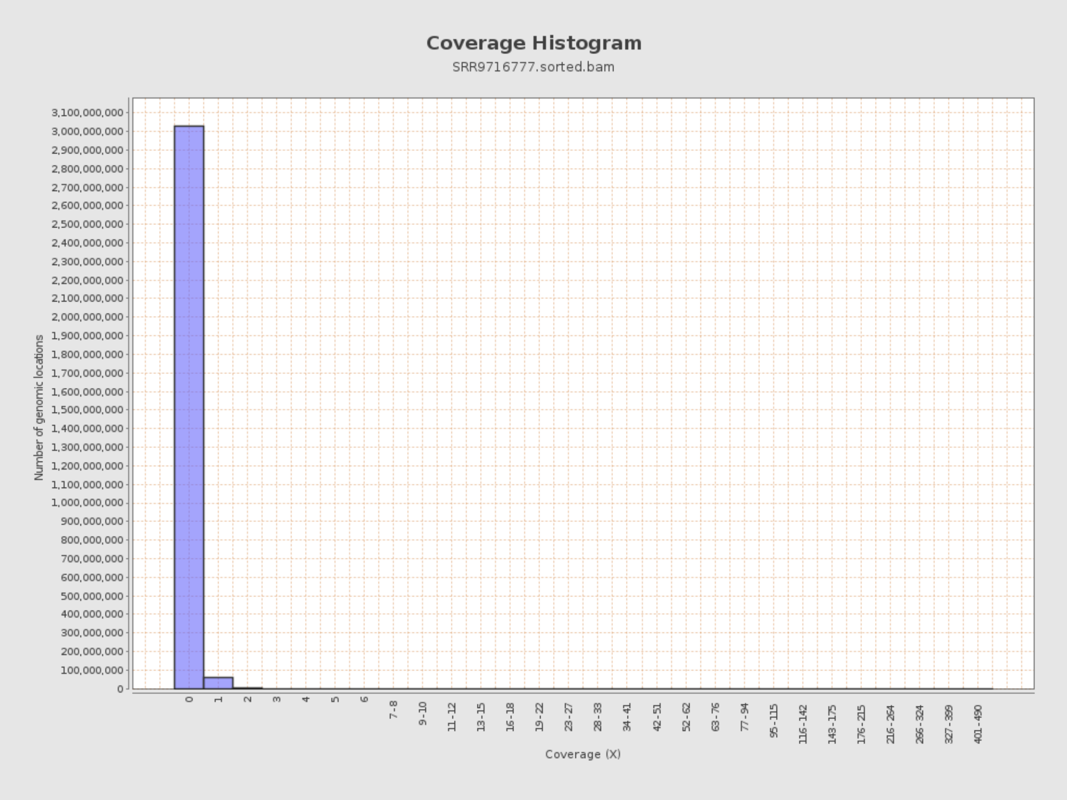
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9013164	0.0362	0.4734
chr2	243199373	7588120	0.0312	0.2654
chr3	198022430	5219034	0.0264	0.1841
chr4	191154276	4019060	0.021	0.2266
chr5	180915260	4999959	0.0276	0.186
chr6	171115067	5065960	0.0296	0.199
chr7	159138663	5046132	0.0317	0.3078

chr8	146364022	5058859	0.0346	0.2698
chr9	141213431	2409019	0.0171	0.1729
chr10	135534747	3428651	0.0253	0.3418
chr11	135006516	3490321	0.0259	0.2248
chr12	133851895	2786058	0.0208	0.16
chr13	115169878	1522937	0.0132	0.125
chr14	107349540	1556401	0.0145	0.1399
chr15	102531392	1595211	0.0156	0.1362
chr16	90354753	2433452	0.0269	0.1931
chr17	81195210	1546723	0.019	0.1697
chr18	78077248	2340271	0.03	0.2654
chr19	59128983	2029451	0.0343	0.3378
chr20	63025520	2123039	0.0337	0.2114
chr21	48129895	1209405	0.0251	0.2125
chr22	51304566	1220515	0.0238	0.1741
chrMT	16571	75119	4.5332	3.4671
chrX	155270560	2792214	0.018	0.156
chrY	59373566	249238	0.0042	0.1863

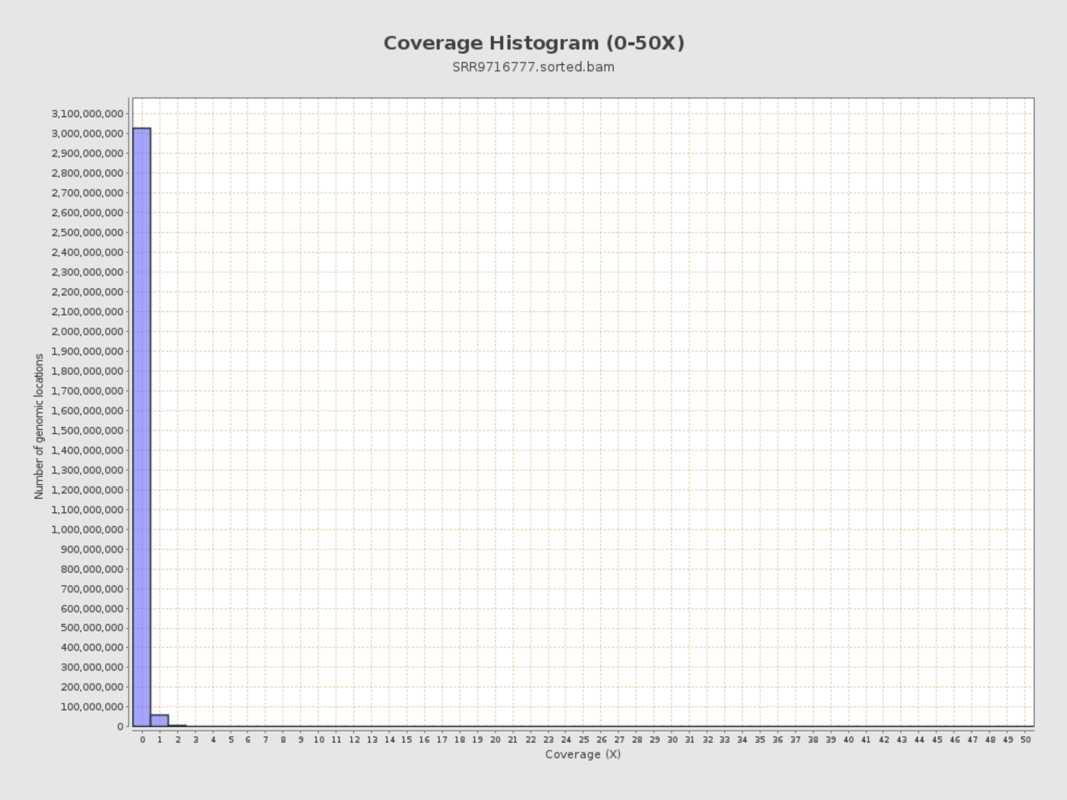
3. Results : Coverage across reference



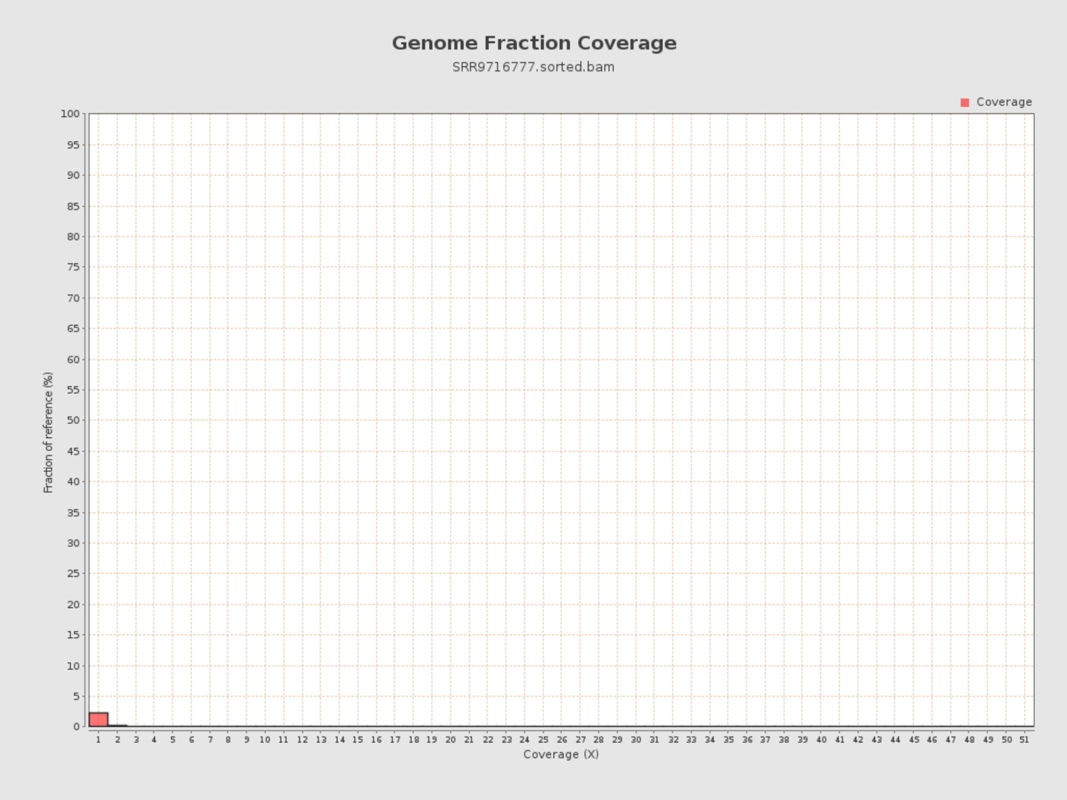
4. Results : Coverage Histogram



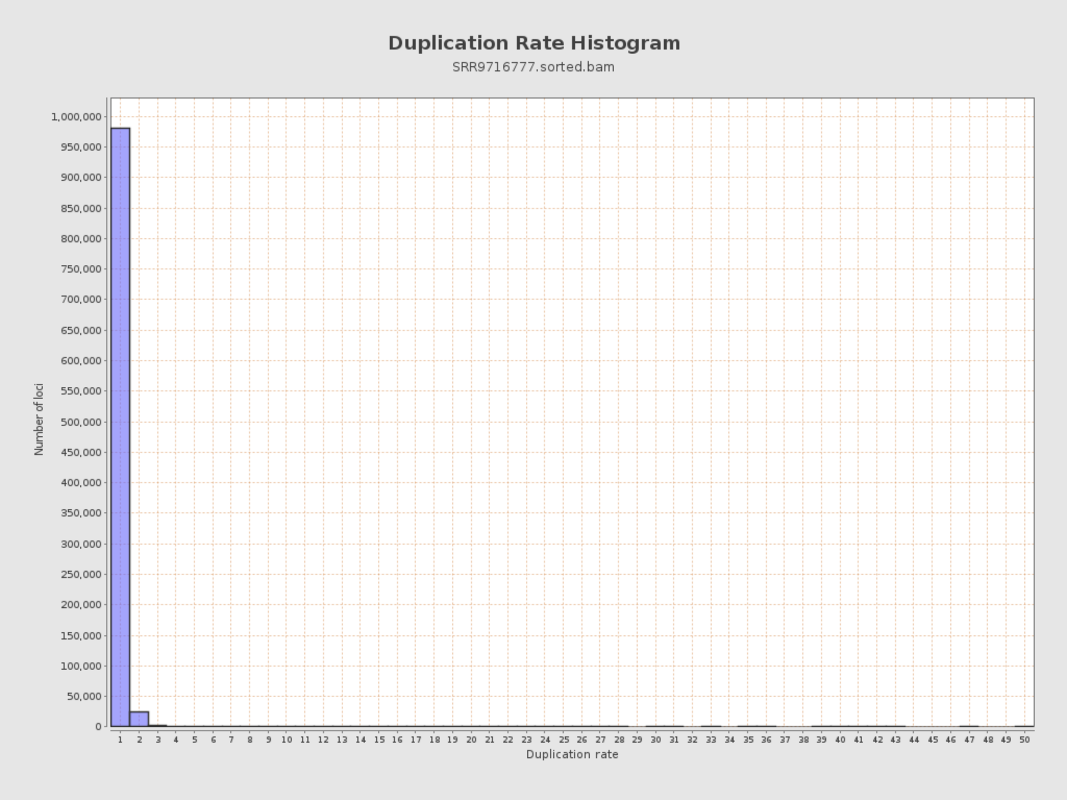
5. Results : Coverage Histogram (0-50X)



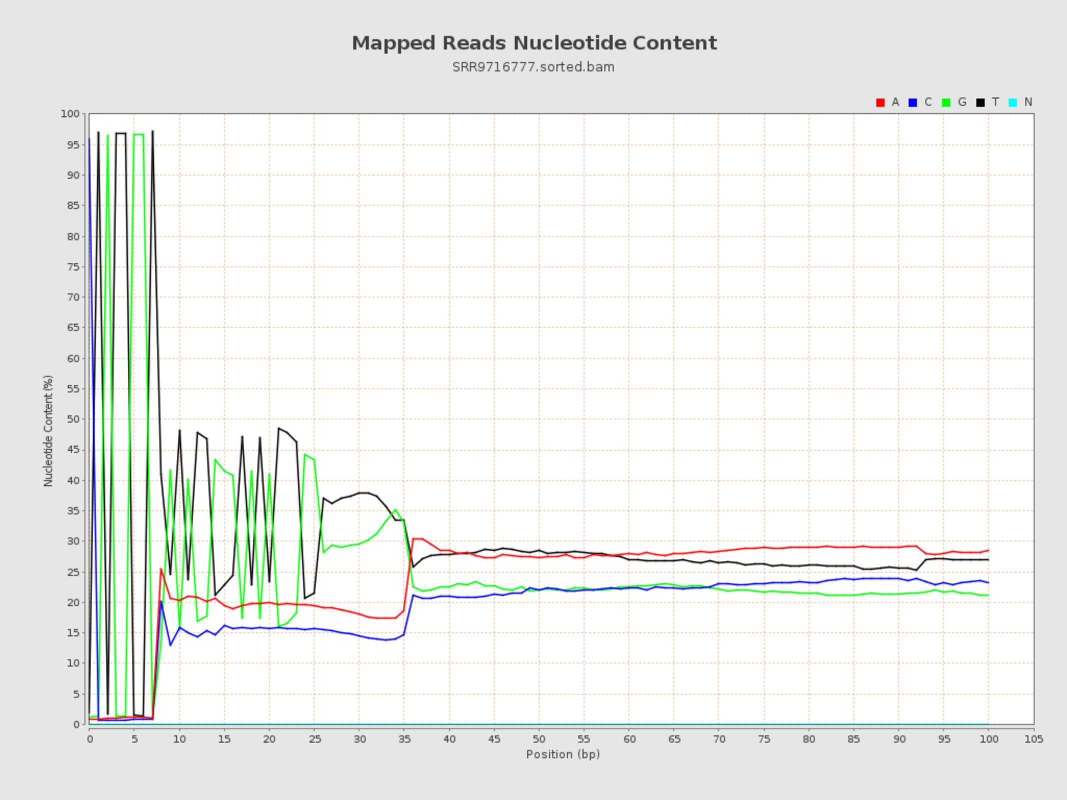
6. Results : Genome Fraction Coverage



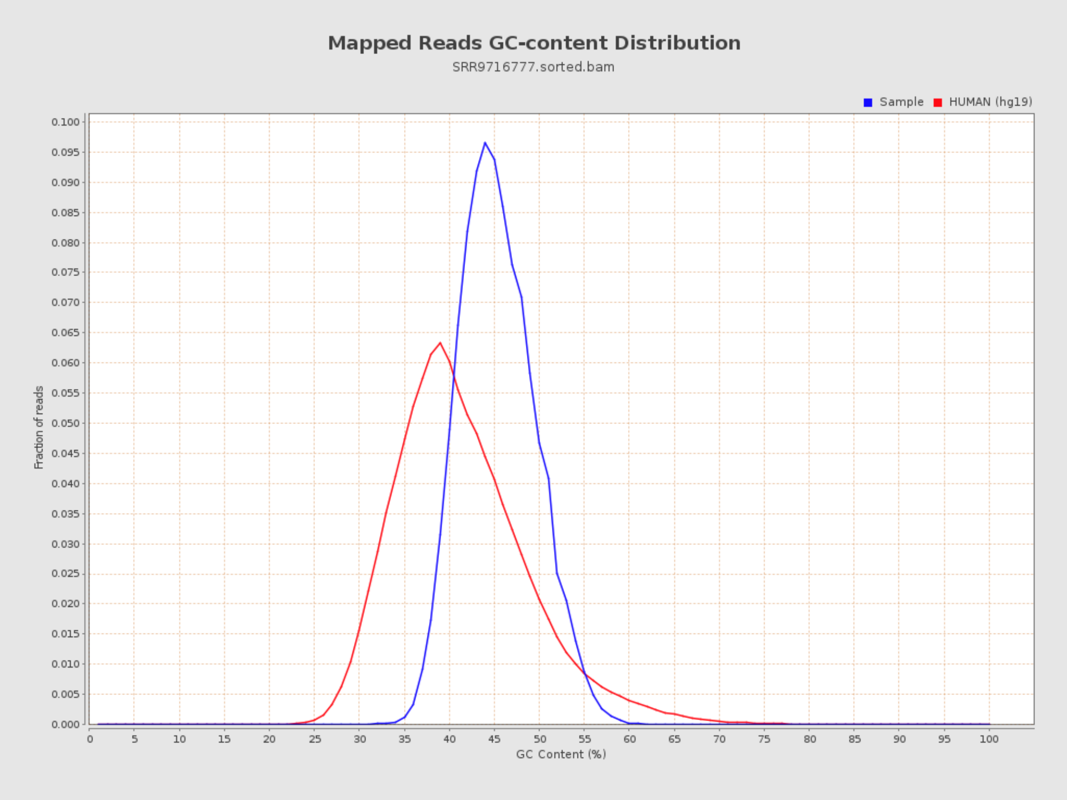
7. Results : Duplication Rate Histogram



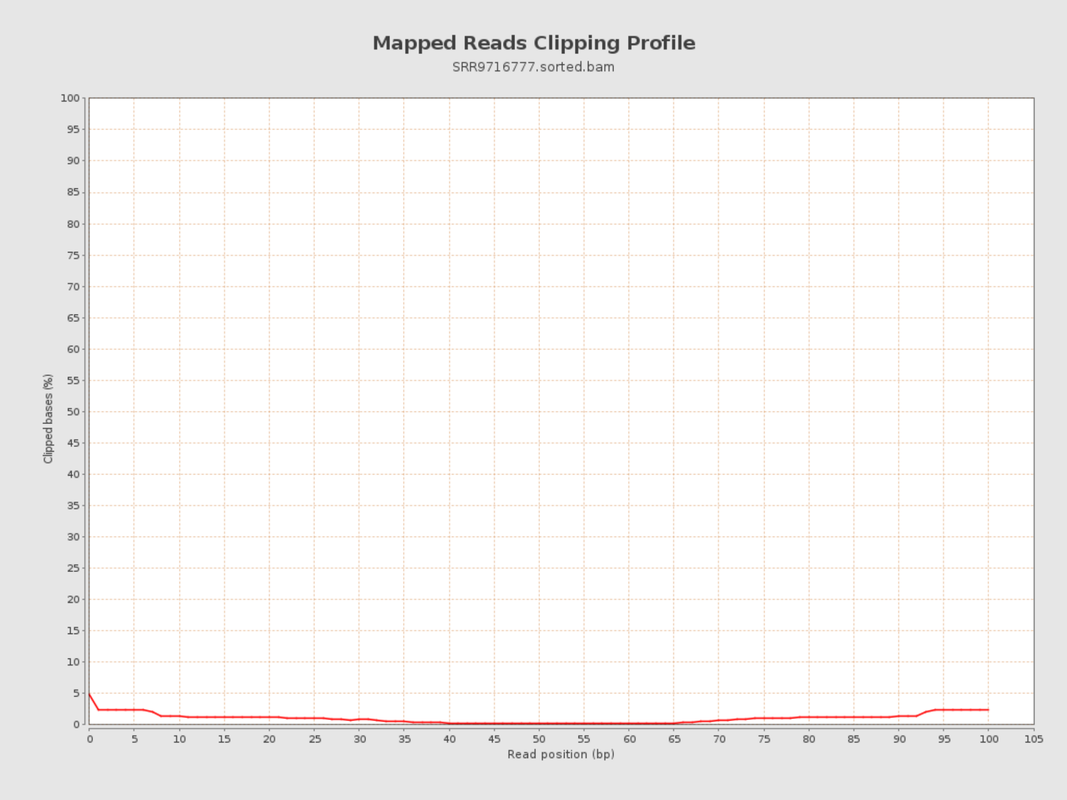
8. Results : Mapped Reads Nucleotide Content



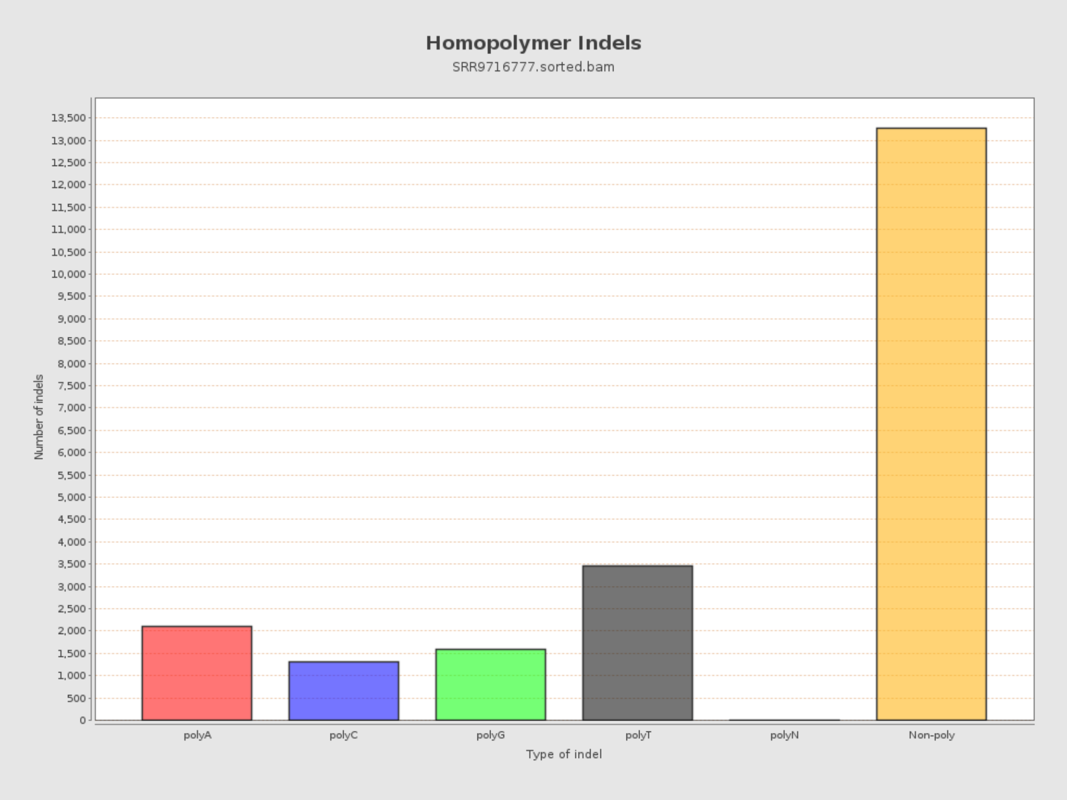
9. Results : Mapped Reads GC-content Distribution



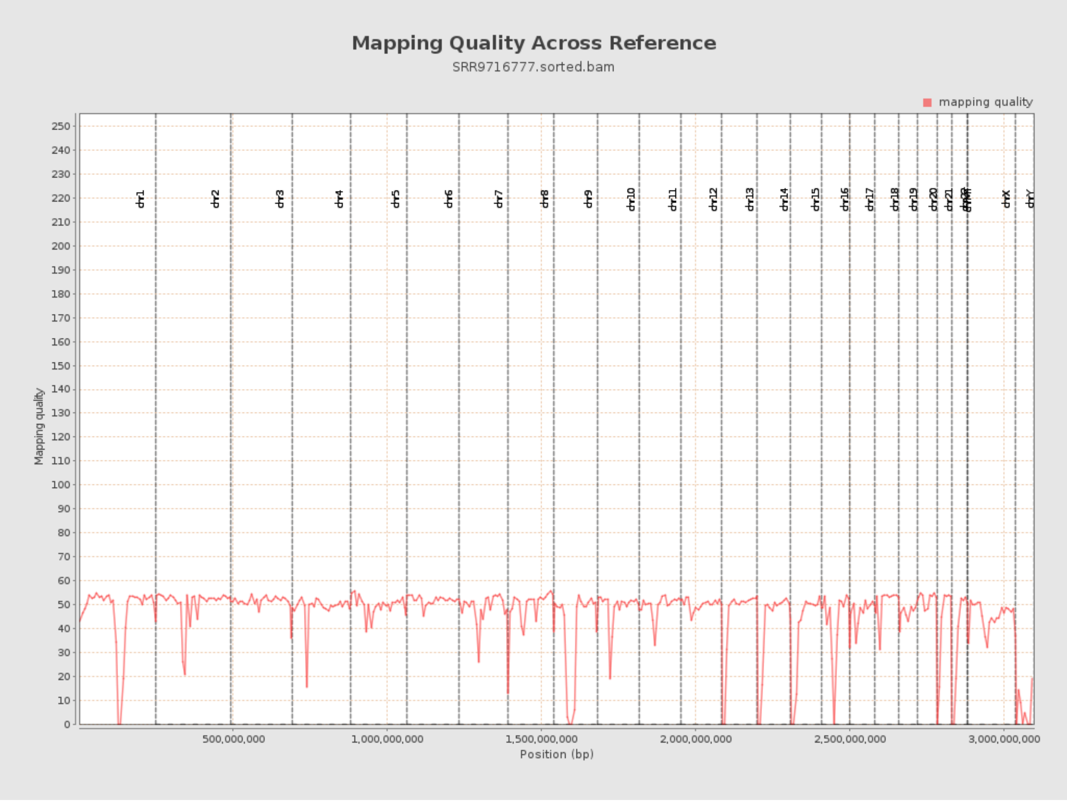
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram