Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:26:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083779.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_SRR3083779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:26:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,422,102
Mapped reads	1,428,599 / 58.98%
Unmapped reads	993,503 / 41.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,563 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	45,883 / 1.89%
Duplication rate	2.71%
Clipped reads	821,915 / 33.93%

2.2. ACGT Content

Number/percentage of A's	25,430,852 / 28.39%
Number/percentage of C's	16,995,090 / 18.97%
Number/percentage of T's	27,356,047 / 30.54%
Number/percentage of G's	19,802,168 / 22.1%
Number/percentage of N's	1,071 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2293

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

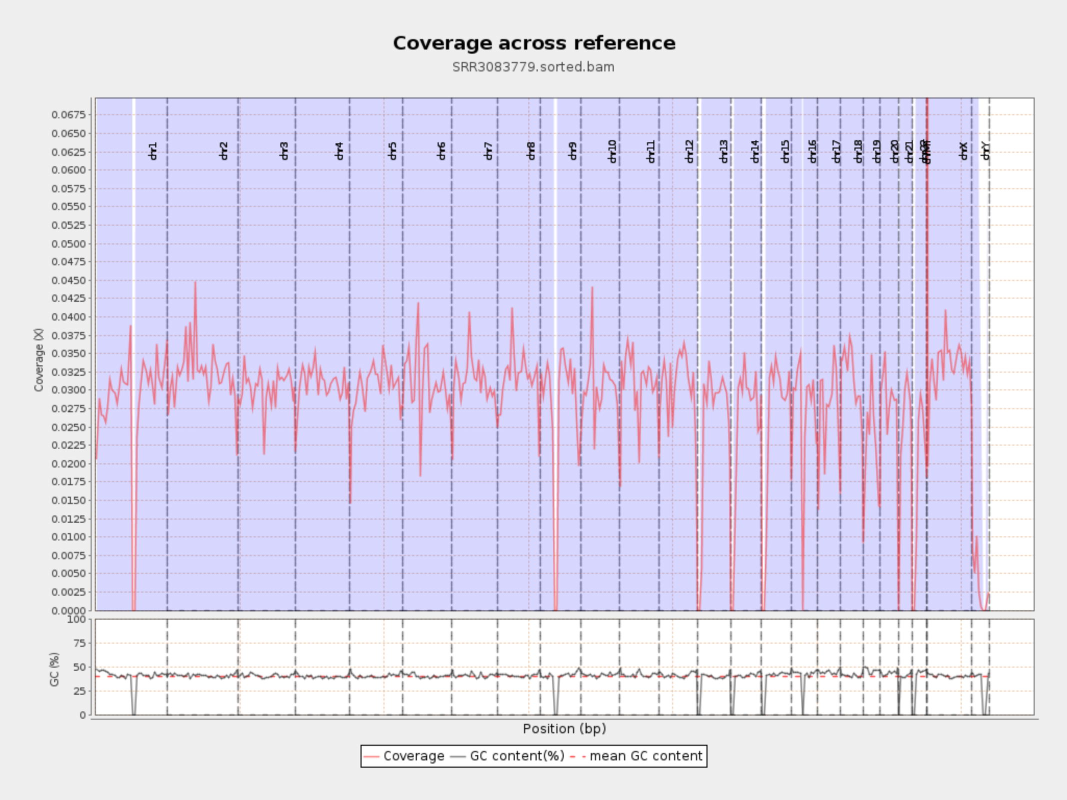
General error rate	0.83%
Mismatches	734,441
Insertions	6,426
Mapped reads with at least one insertion	0.45%
Deletions	18,386
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.3%

2.6. Chromosome stats

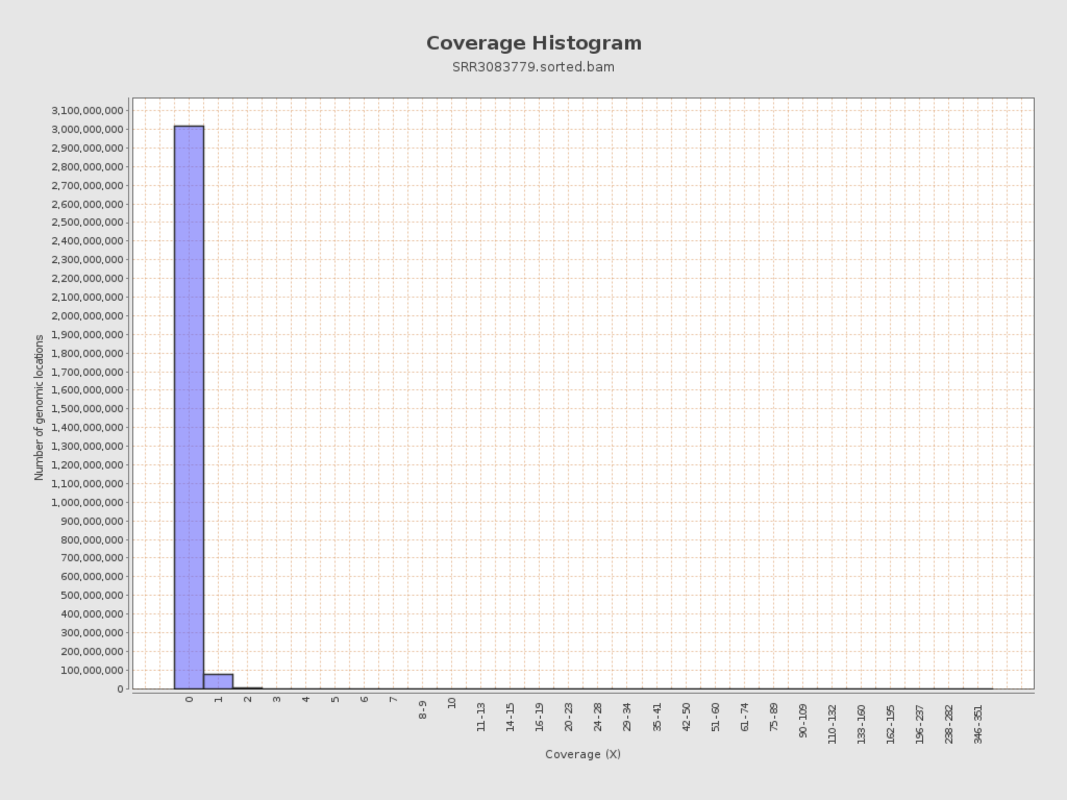
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7098365	0.0285	0.3114
chr2	243199373	7898738	0.0325	0.2806
chr3	198022430	6013225	0.0304	0.1894
chr4	191154276	5882696	0.0308	0.1934
chr5	180915260	5579694	0.0308	0.1905
chr6	171115067	5297401	0.031	0.2176
chr7	159138663	4973805	0.0313	0.2717

chr8	146364022	4636786	0.0317	0.2434
chr9	141213431	3869271	0.0274	0.2218
chr10	135534747	4115228	0.0304	0.2442
chr11	135006516	4211297	0.0312	0.2145
chr12	133851895	4133917	0.0309	0.1921
chr13	115169878	2867364	0.0249	0.1714
chr14	107349540	2657002	0.0248	0.1754
chr15	102531392	2590229	0.0253	0.1741
chr16	90354753	2386545	0.0264	0.1864
chr17	81195210	2186751	0.0269	0.1873
chr18	78077248	2512473	0.0322	0.3881
chr19	59128983	1358622	0.023	0.2506
chr20	63025520	1815356	0.0288	0.1879
chr21	48129895	1184094	0.0246	0.1764
chr22	51304566	913591	0.0178	0.1442
chrMT	16571	67468	4.0715	2.9113
chrX	155270560	5163272	0.0333	0.2113
chrY	59373566	201433	0.0034	0.0797

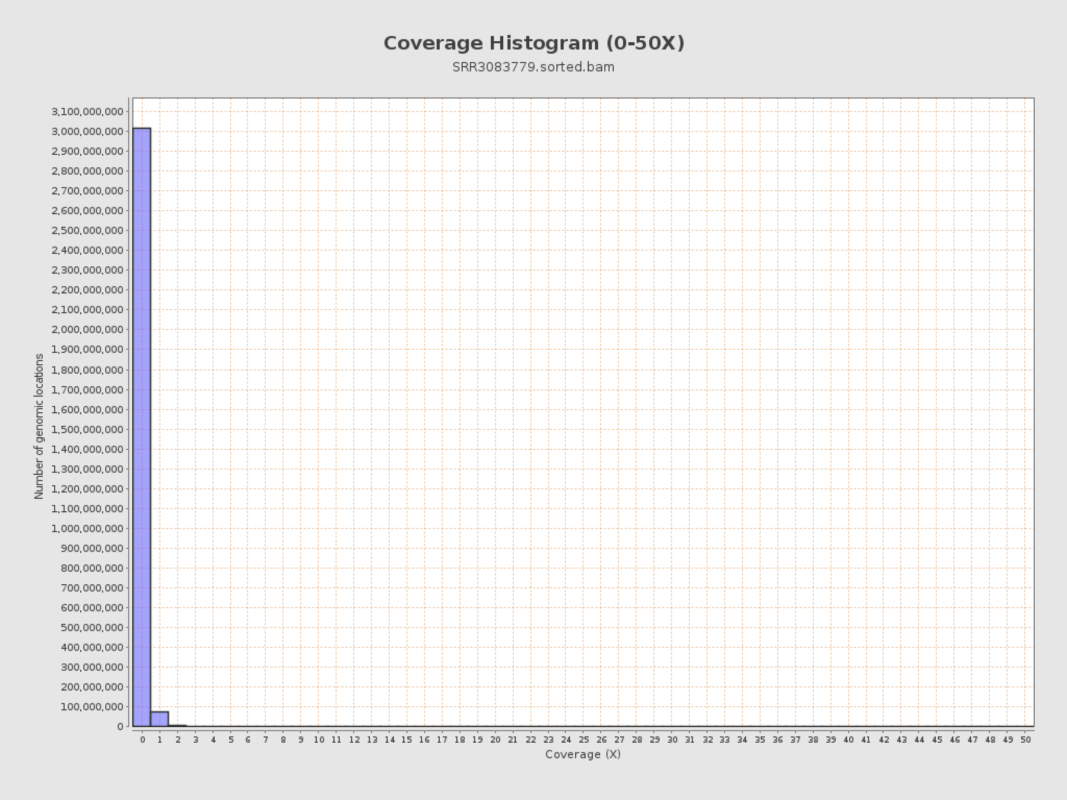
3. Results : Coverage across reference



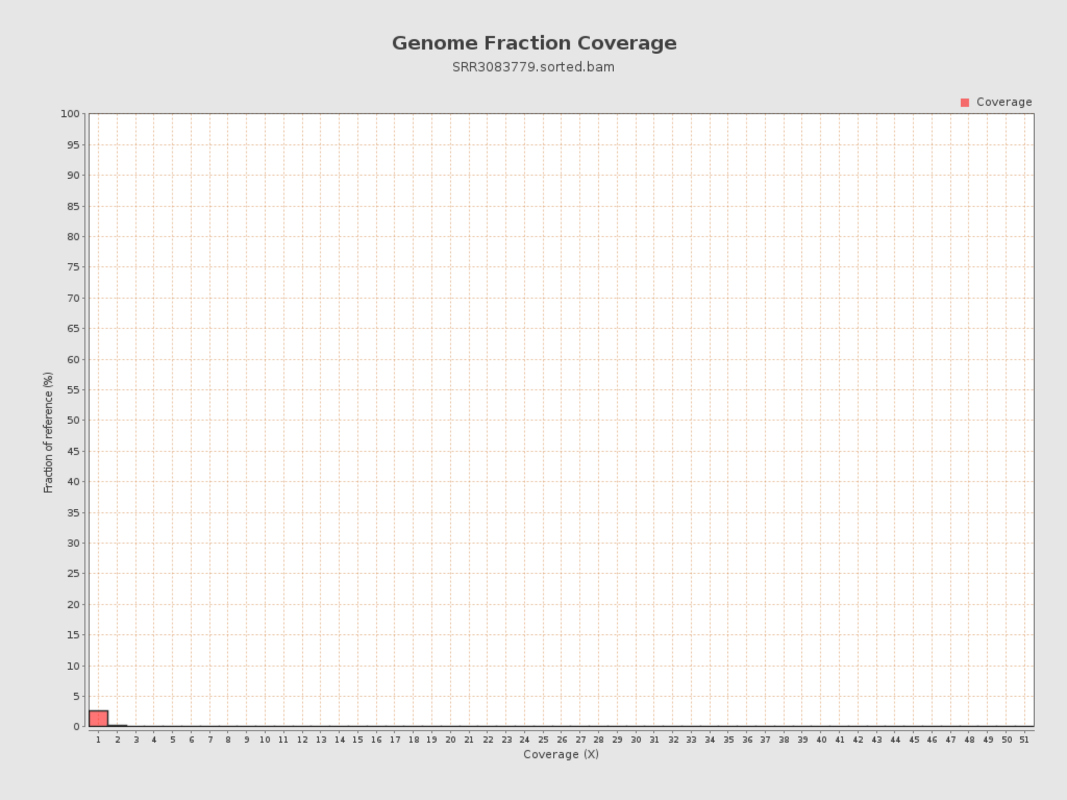
4. Results : Coverage Histogram



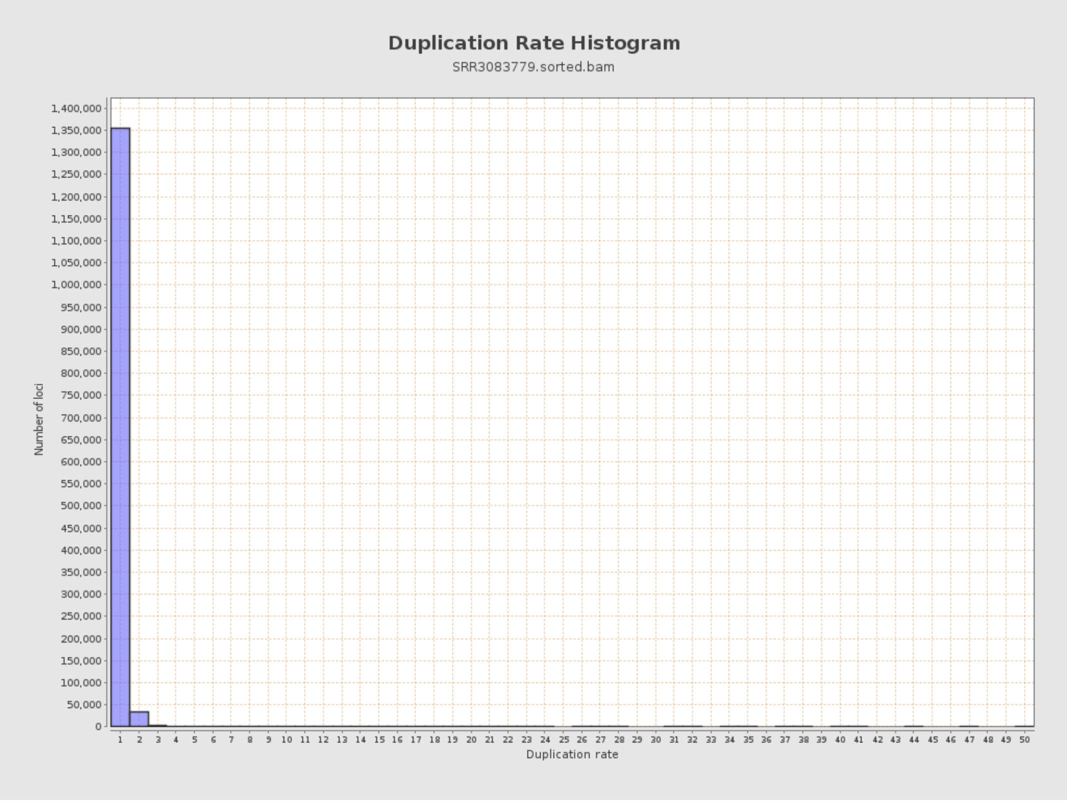
5. Results : Coverage Histogram (0-50X)



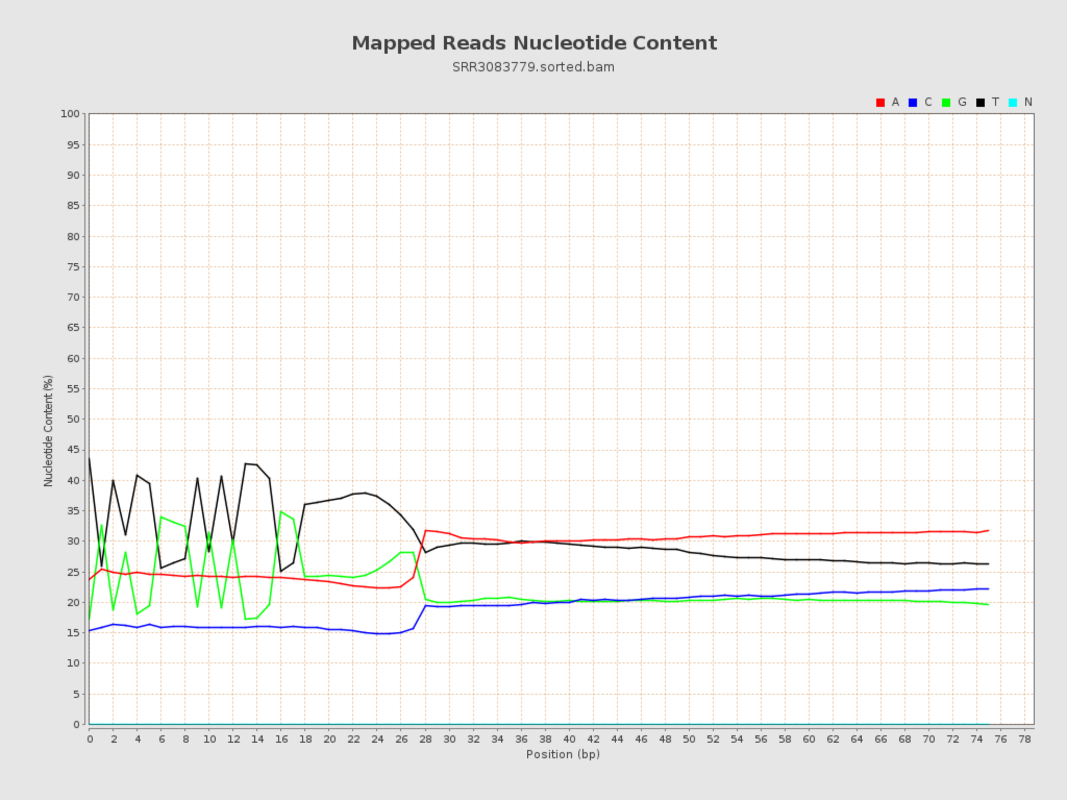
6. Results : Genome Fraction Coverage



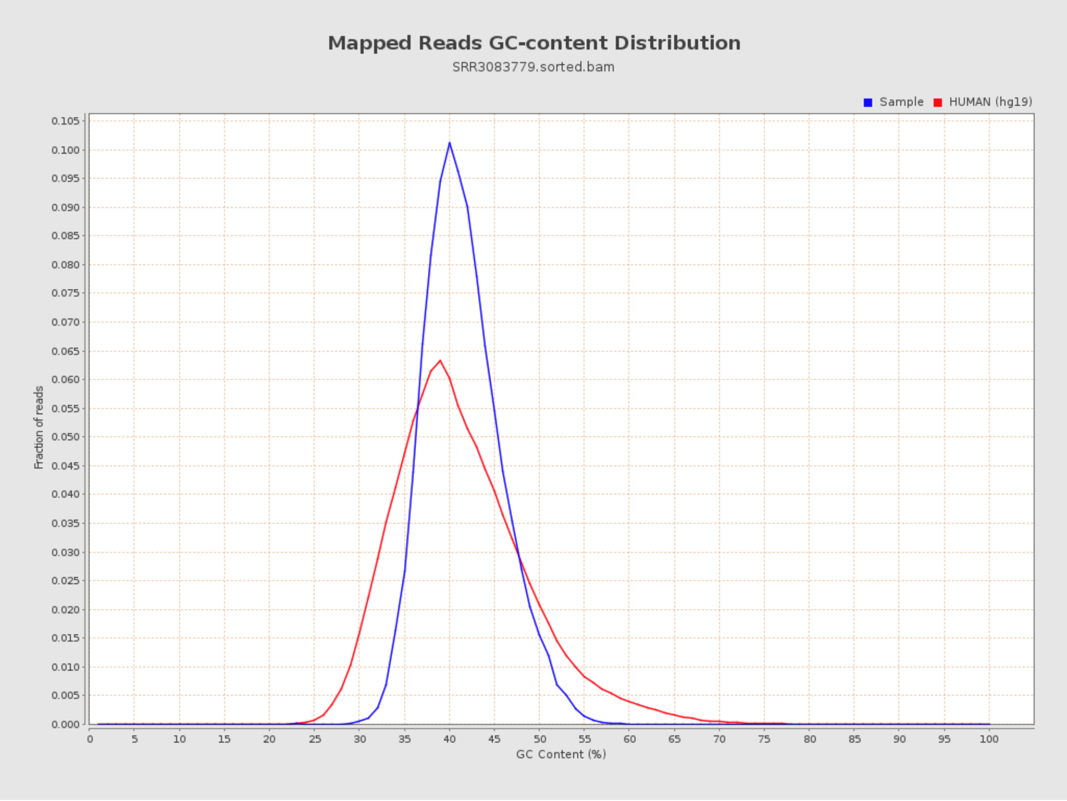
7. Results : Duplication Rate Histogram



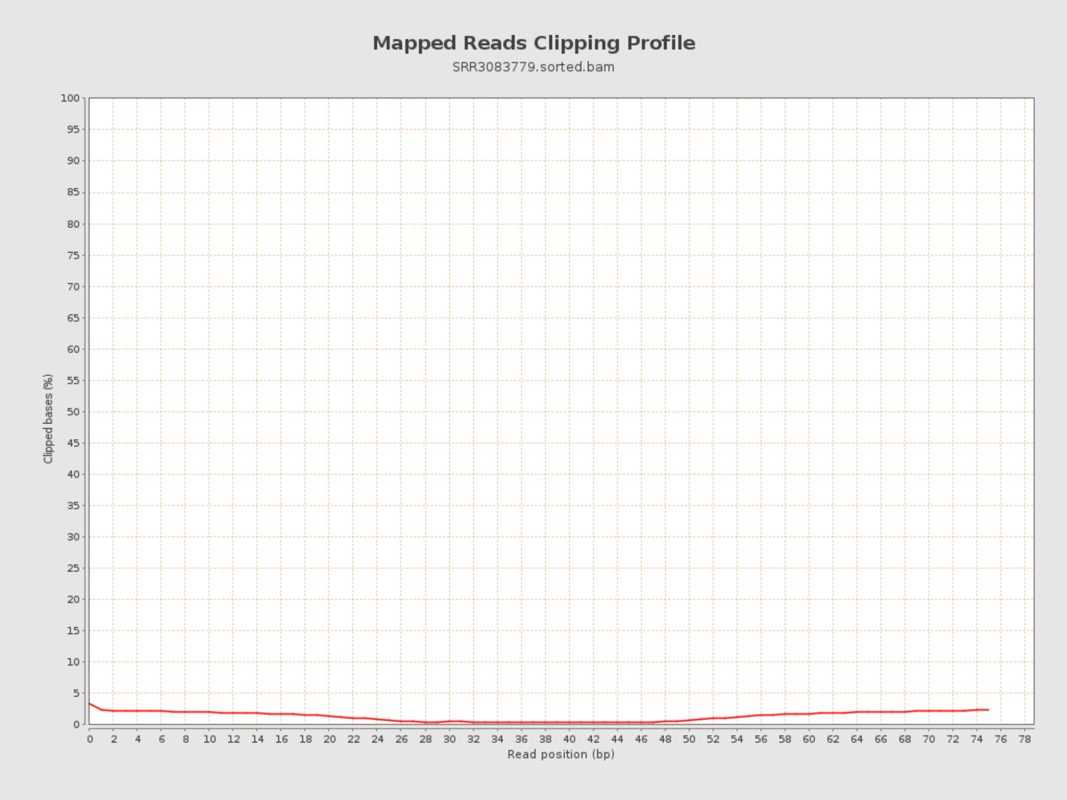
8. Results : Mapped Reads Nucleotide Content



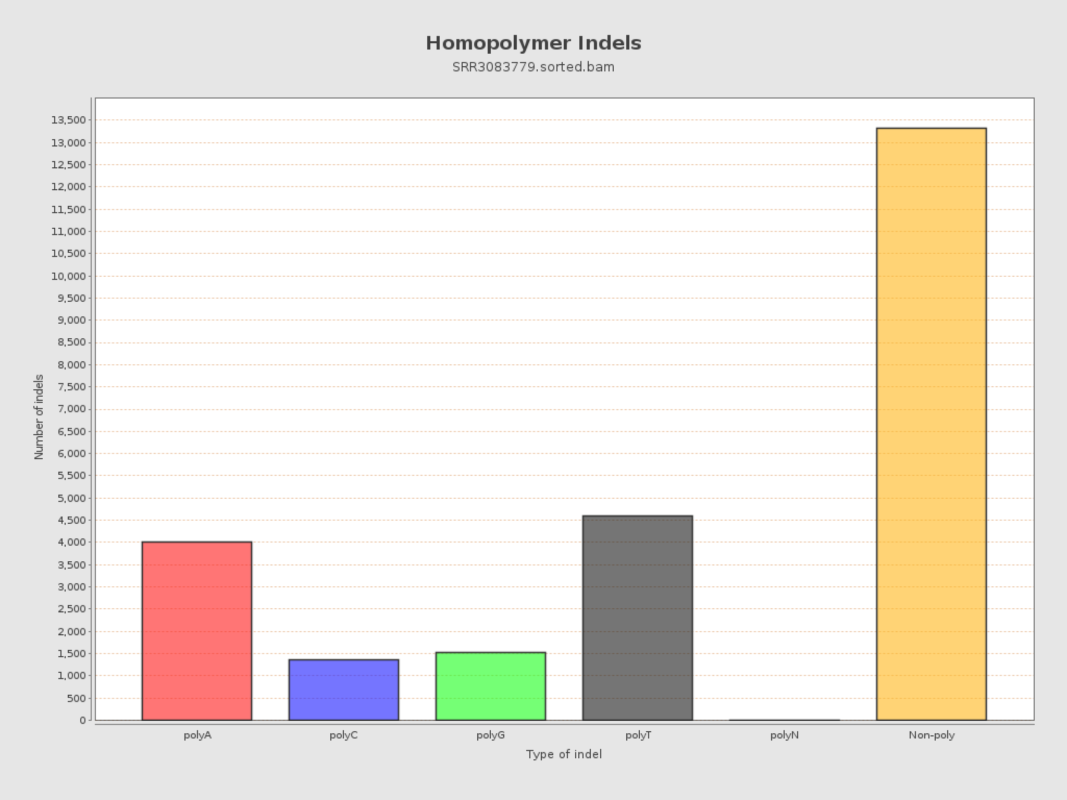
9. Results : Mapped Reads GC-content Distribution



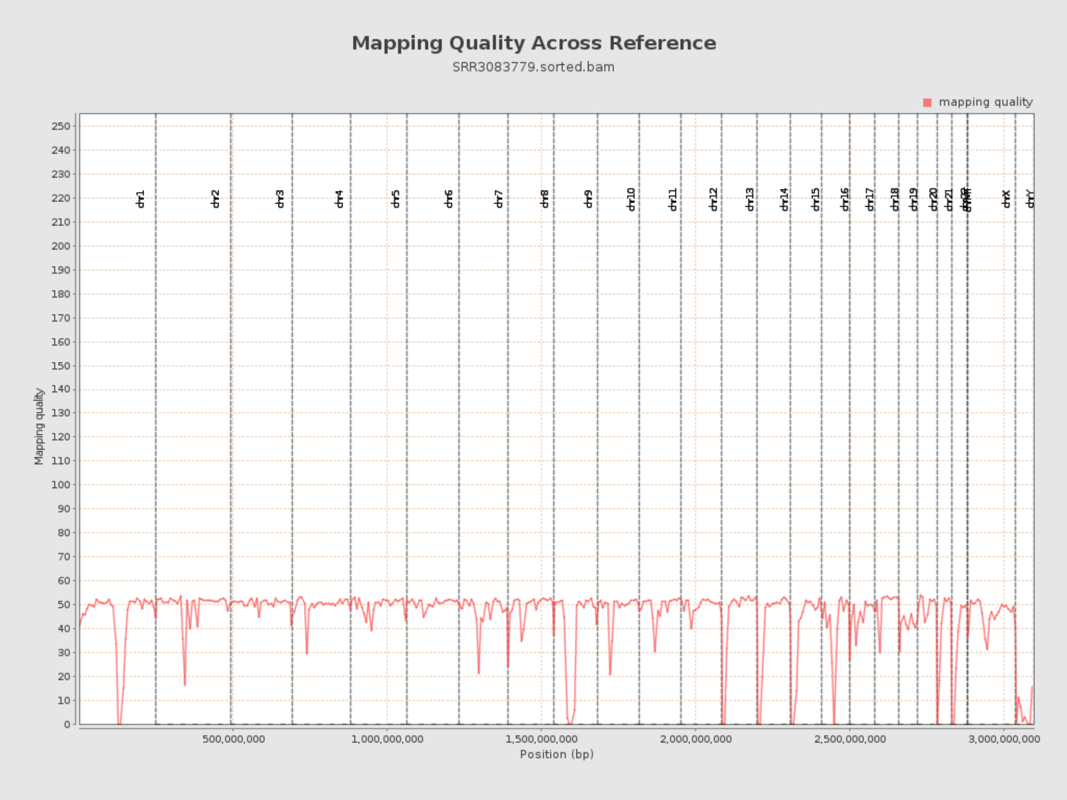
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram