Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 14:22:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779083.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_SRR1779083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779083_1.fastq.gz SRR1779083_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 14:22:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,135,572
Mapped reads	25,337,863 / 96.95%
Unmapped reads	797,709 / 3.05%
Mapped paired reads	25,337,863 / 96.95%
Mapped reads, first in pair	12,770,614 / 48.86%
Mapped reads, second in pair	12,567,249 / 48.08%
Mapped reads, both in pair	25,038,572 / 95.8%
Mapped reads, singletons	299,291 / 1.15%
Secondary alignments	0
Supplementary alignments	143,197 / 0.55%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	822,139 / 3.15%
Duplication rate	2.92%
Clipped reads	1,880,998 / 7.2%

2.2. ACGT Content

Number/percentage of A's	772,488,009 / 30.57%
Number/percentage of C's	489,711,757 / 19.38%
Number/percentage of T's	764,846,622 / 30.27%
Number/percentage of G's	499,235,727 / 19.76%
Number/percentage of N's	851,258 / 0.03%

GC Percentage	39.13%

2.3. Coverage

Mean	0.8165
Standard Deviation	2.1238

2.4. Mapping Quality

Mean Mapping Quality	53.56

2.5. Insert size

Mean	76,777.32
Standard Deviation	2,657,100.5
P25/Median/P75	152 / 207 / 284

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	11,691,321
Insertions	211,169
Mapped reads with at least one insertion	0.82%
Deletions	256,532
Mapped reads with at least one deletion	0.99%
Homopolymer indels	46.19%

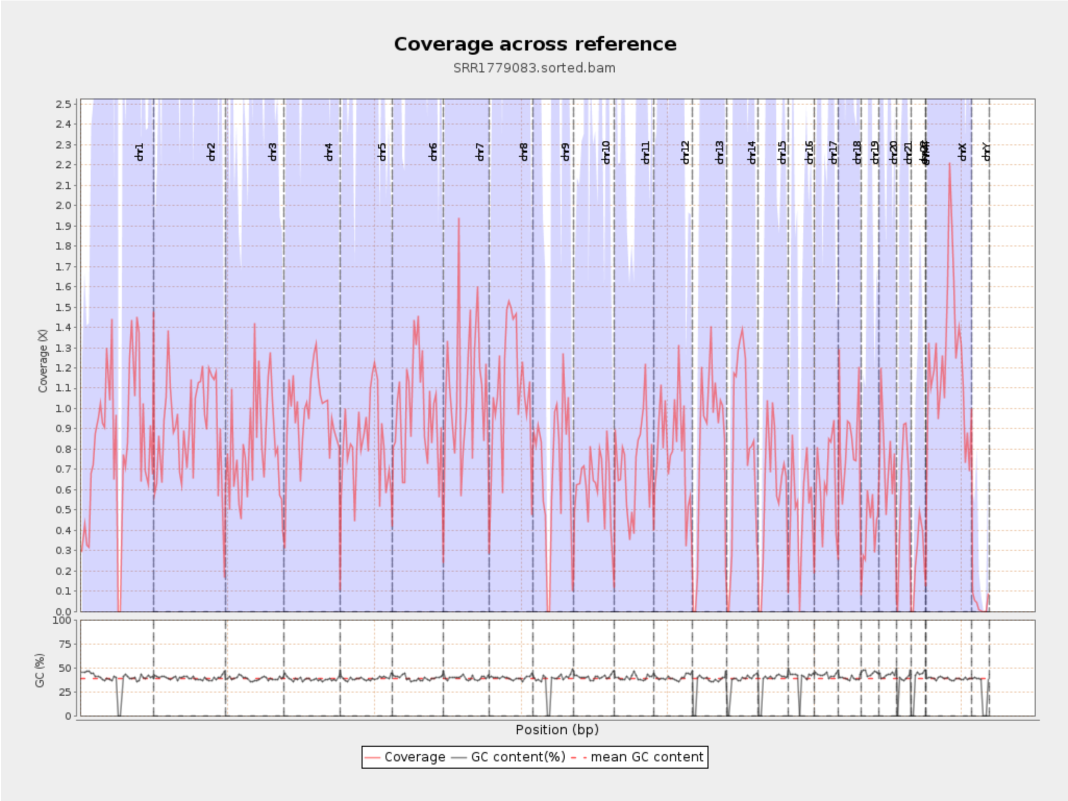
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

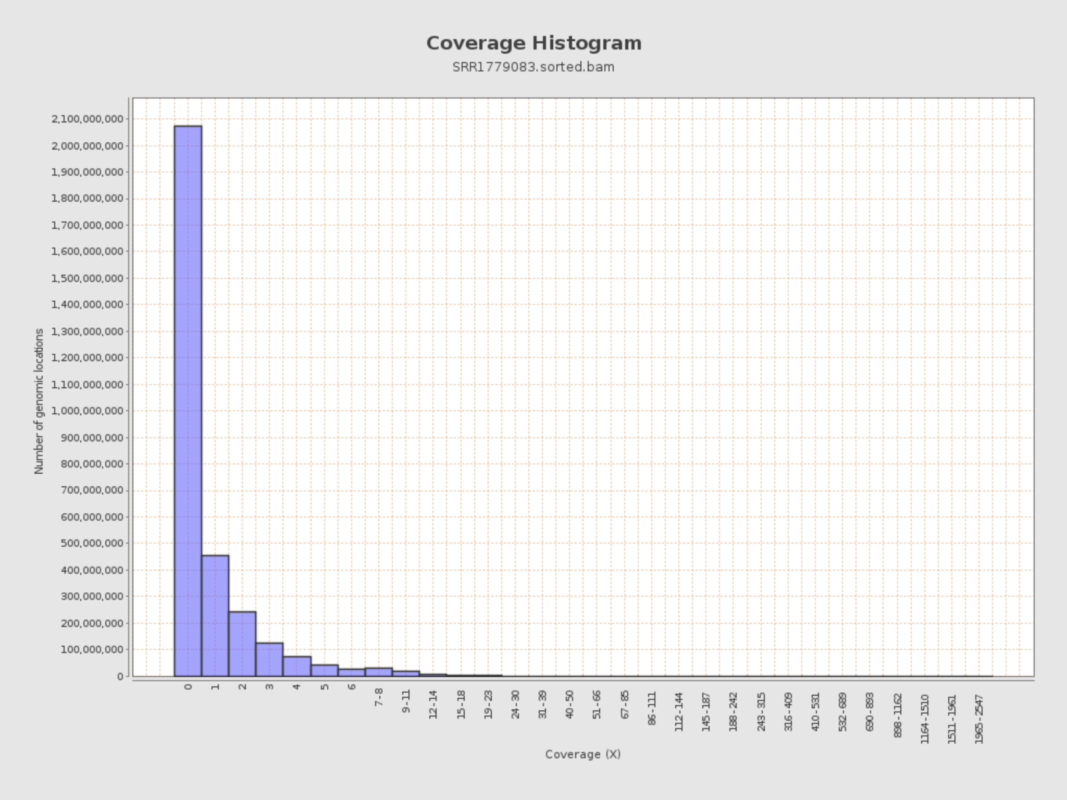
		bases	coverage	deviation
chr1	249250621	206160622	0.8271	3.2137
chr2	243199373	221503150	0.9108	2.0516
chr3	198022430	161854866	0.8174	1.7372
chr4	191154276	186814780	0.9773	1.9058
chr5	180915260	149288812	0.8252	1.6949
chr6	171115067	169983973	0.9934	1.9601
chr7	159138663	171091347	1.0751	2.5862
chr8	146364022	163551072	1.1174	1.9985
chr9	141213431	95984510	0.6797	1.8221
chr10	135534747	84878072	0.6262	3.6817
chr11	135006516	96438234	0.7143	1.5763
chr12	133851895	107662388	0.8043	1.7827
chr13	115169878	97499049	0.8466	1.745
chr14	107349540	88377666	0.8233	1.8227
chr15	102531392	61435640	0.5992	1.554
chr16	90354753	44093385	0.488	1.2855
chr17	81195210	50423912	0.621	1.7071
chr18	78077248	64826771	0.8303	1.8752
chr19	59128983	23788256	0.4023	2.0664
chr20	63025520	45888378	0.7281	1.5329
chr21	48129895	29124311	0.6051	1.4972
chr22	51304566	12882620	0.2511	0.863
chrMT	16571	2088	0.126	0.4448
chrX	155270560	192107082	1.2372	2.3413

chrY	59373566	2046028	0.0345	0.4323

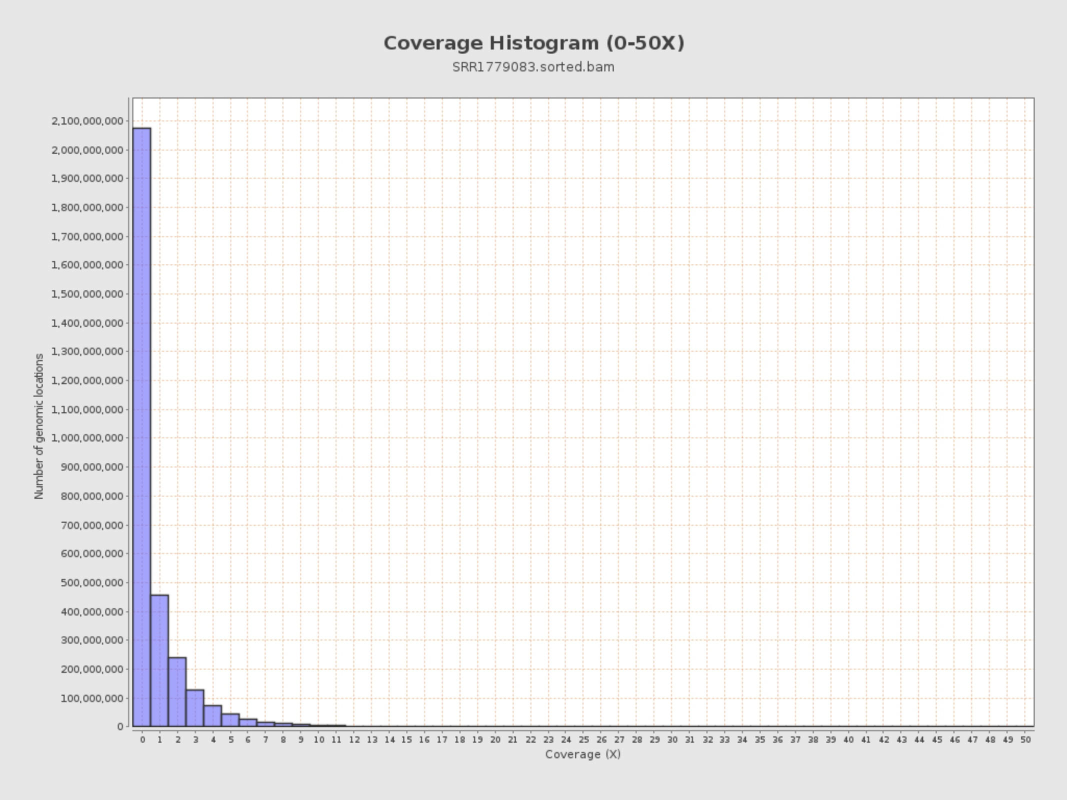
3. Results : Coverage across reference



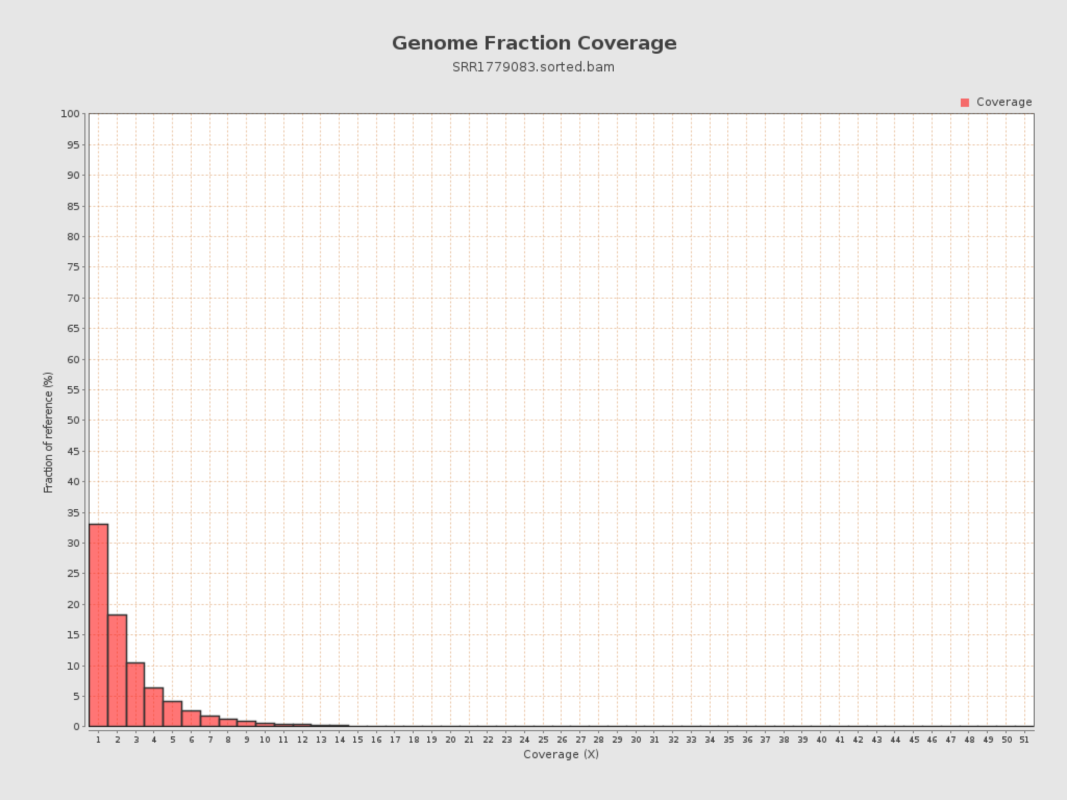
4. Results : Coverage Histogram



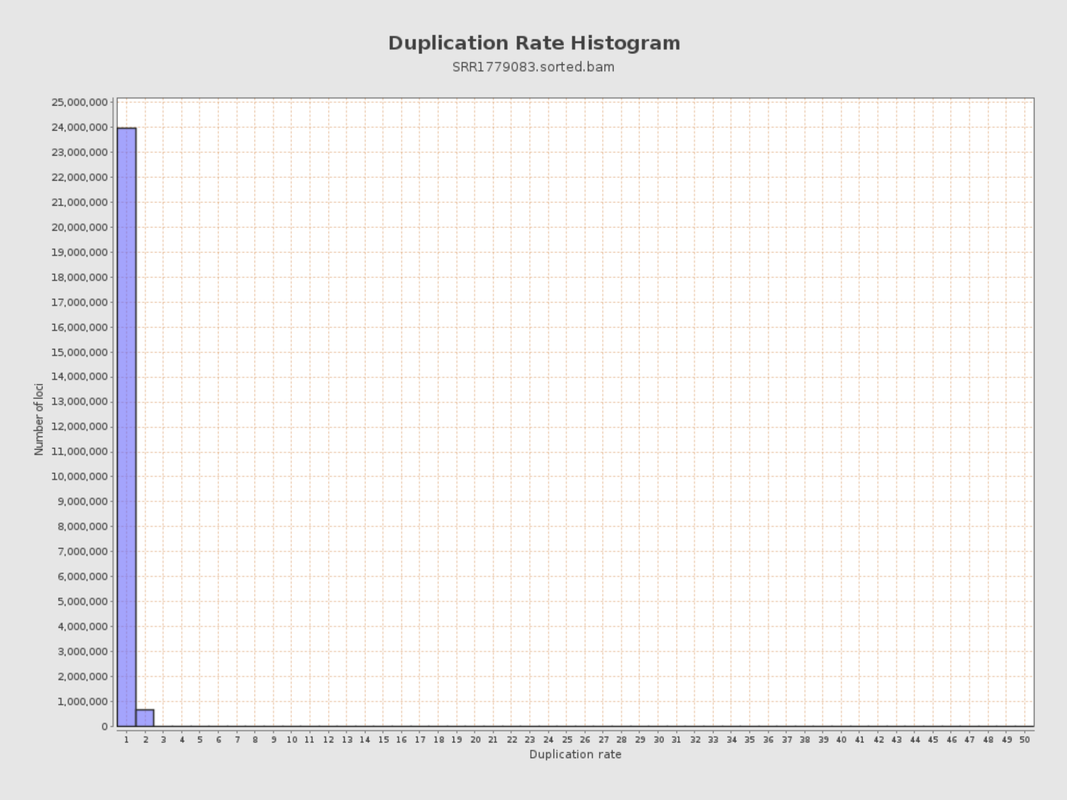
5. Results : Coverage Histogram (0-50X)



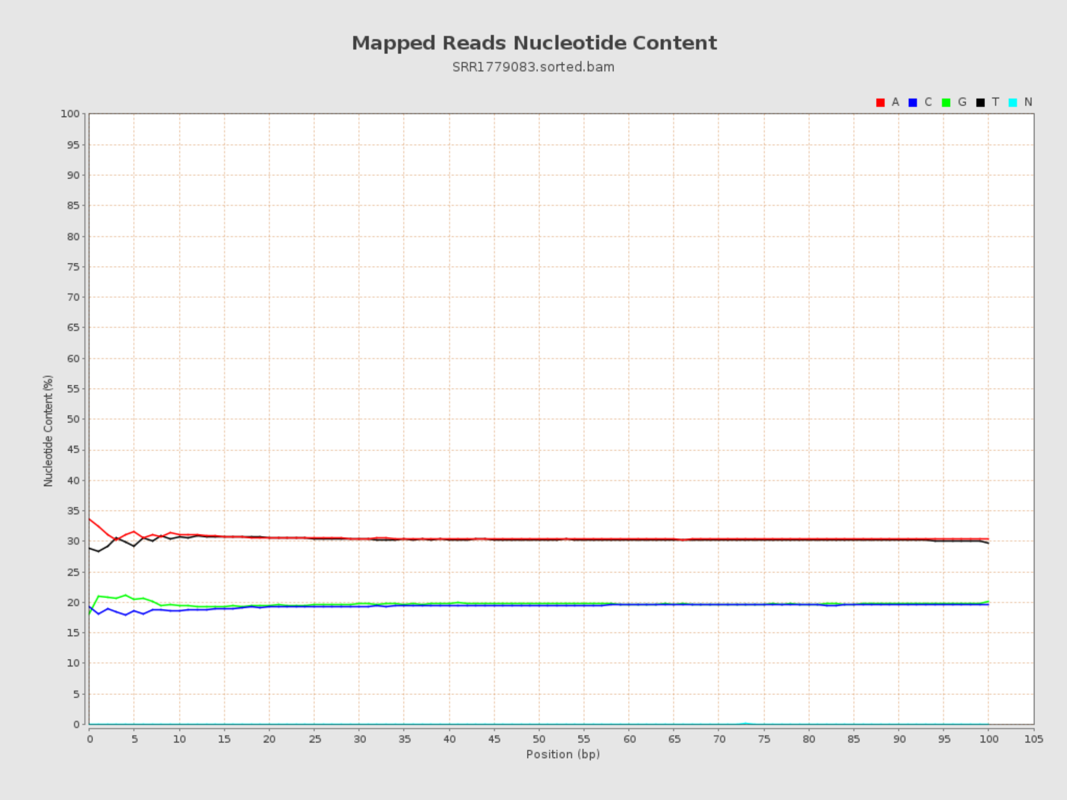
6. Results : Genome Fraction Coverage



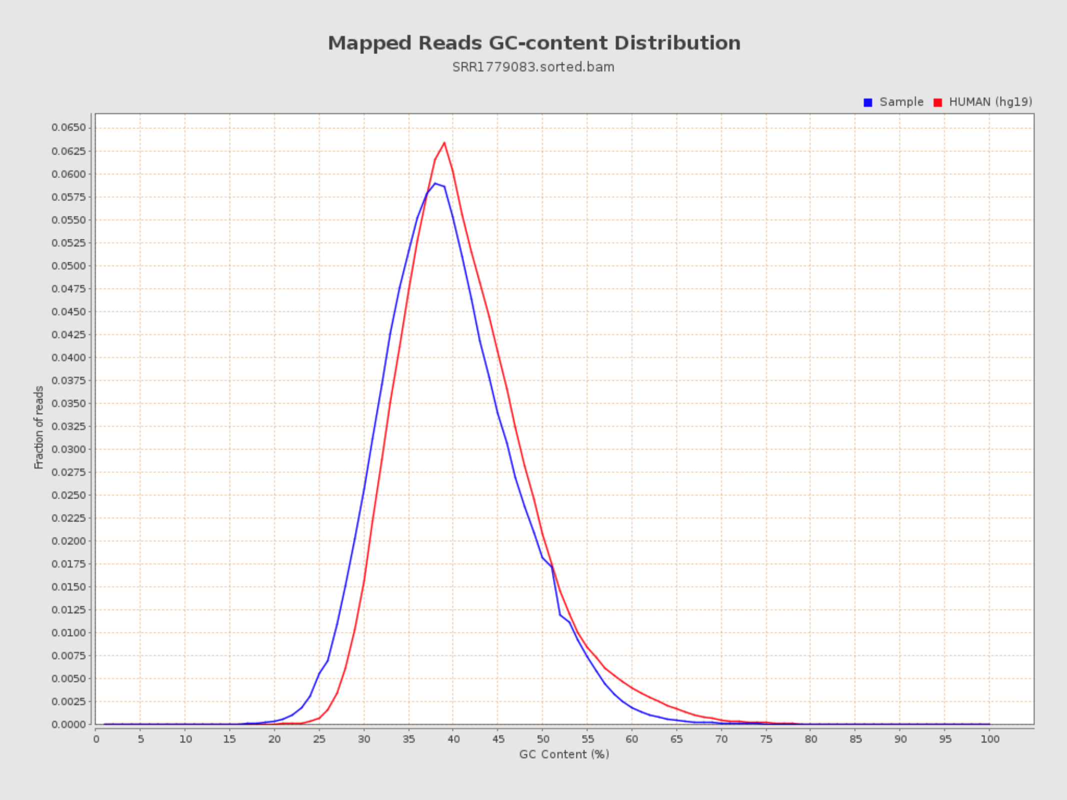
7. Results : Duplication Rate Histogram



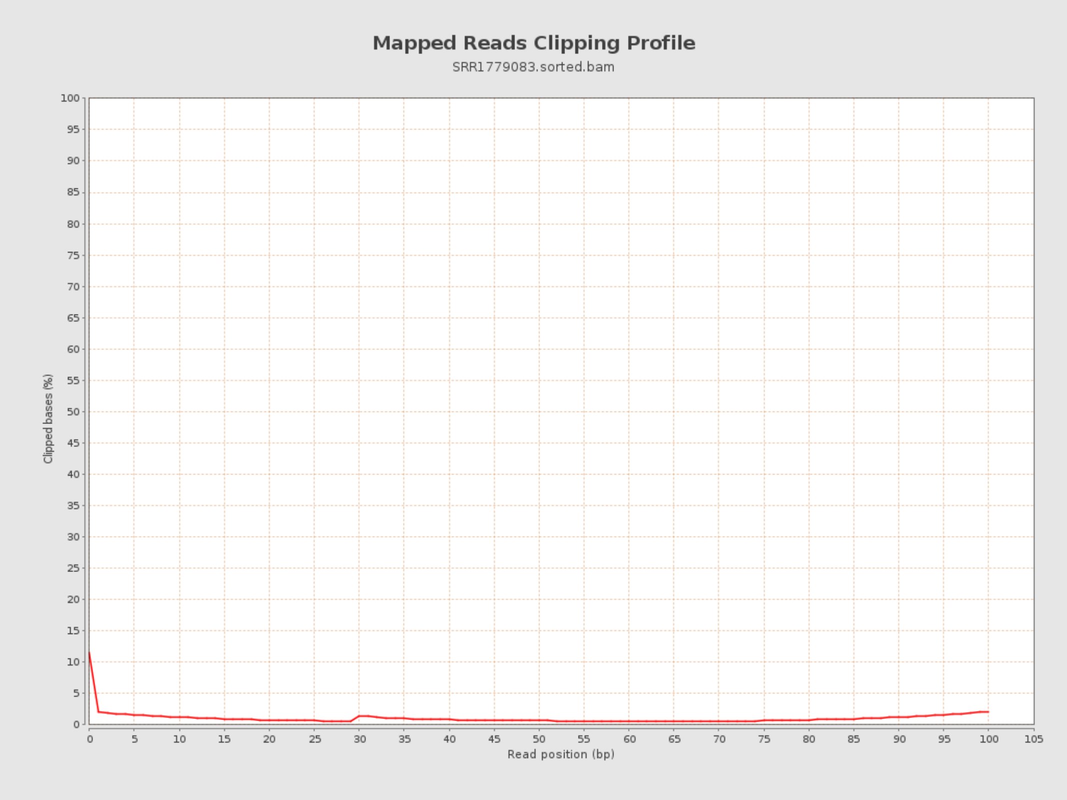
8. Results : Mapped Reads Nucleotide Content



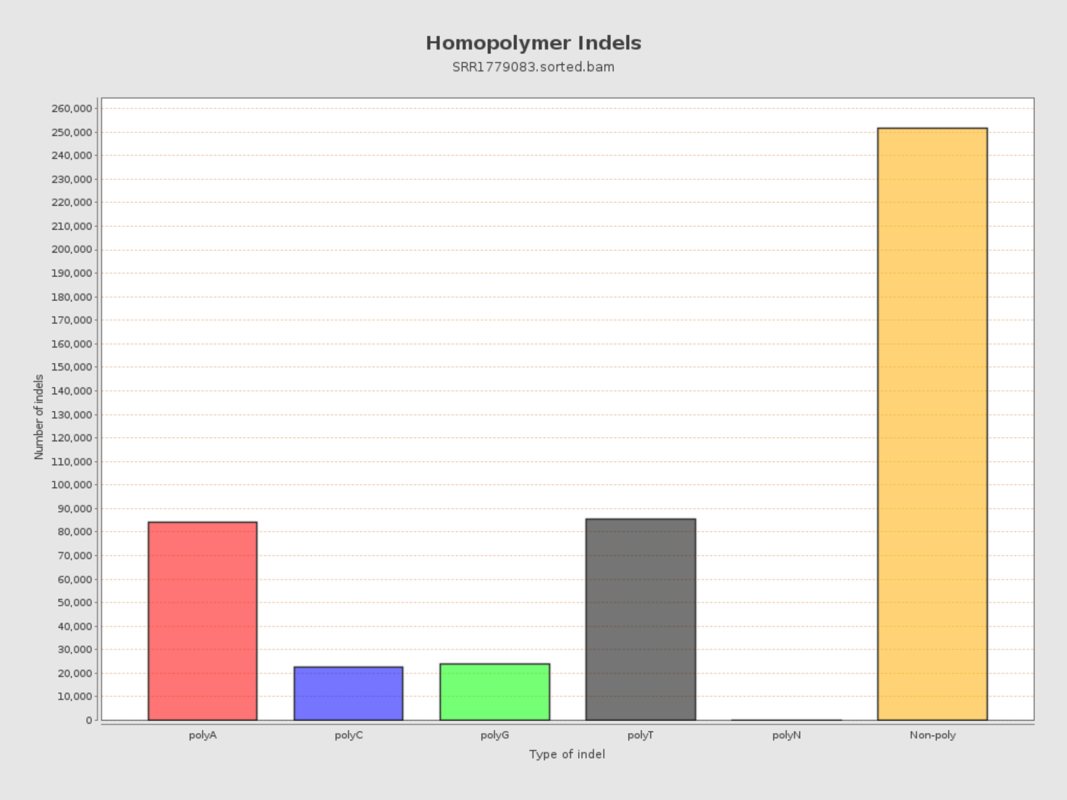
9. Results : Mapped Reads GC-content Distribution



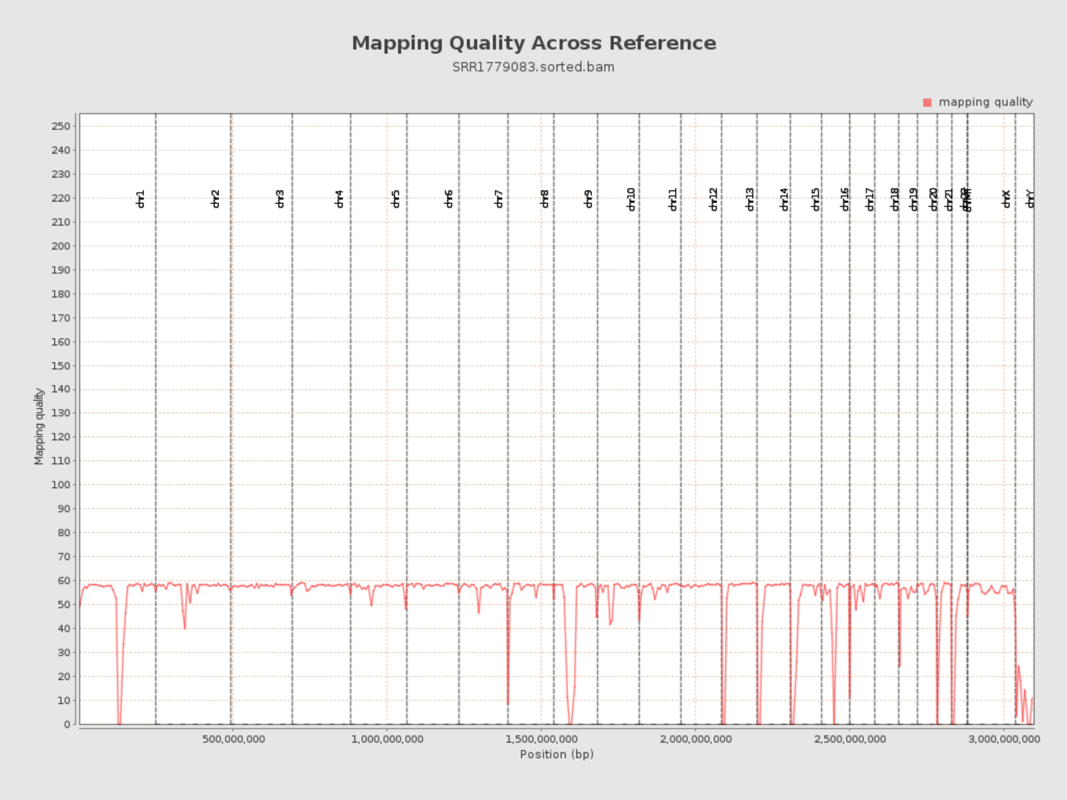
10. Results : Mapped Reads Clipping Profile



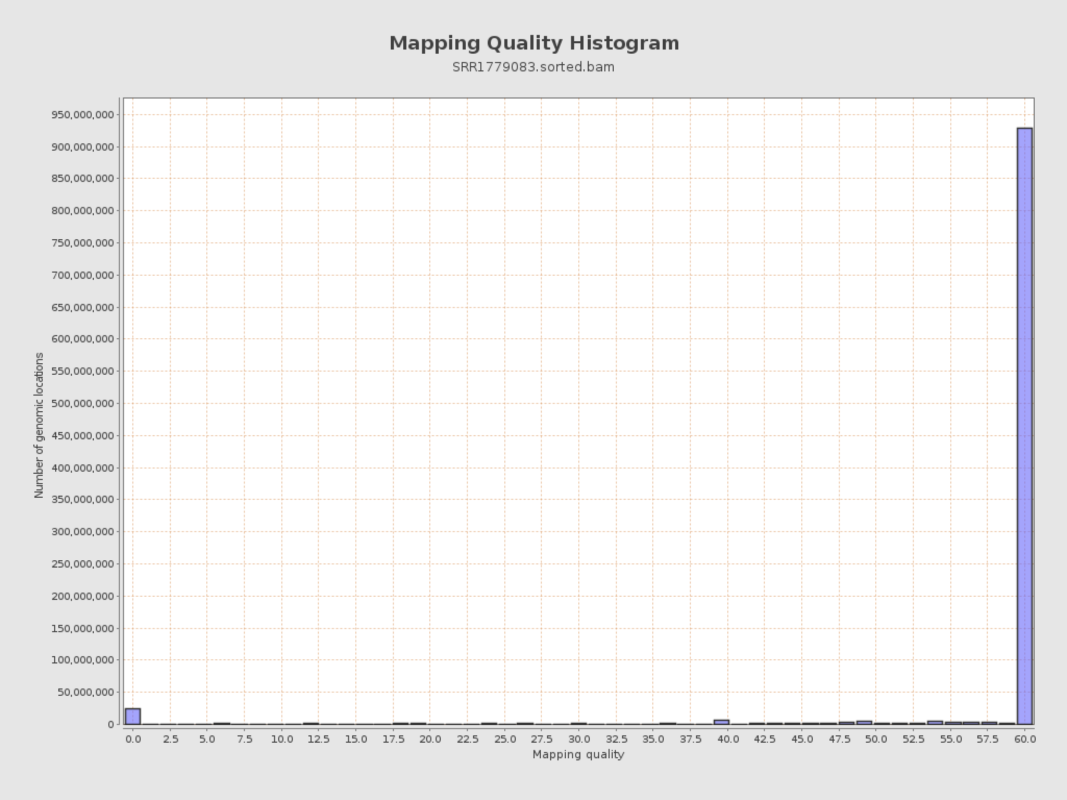
11. Results : Homopolymer Indels



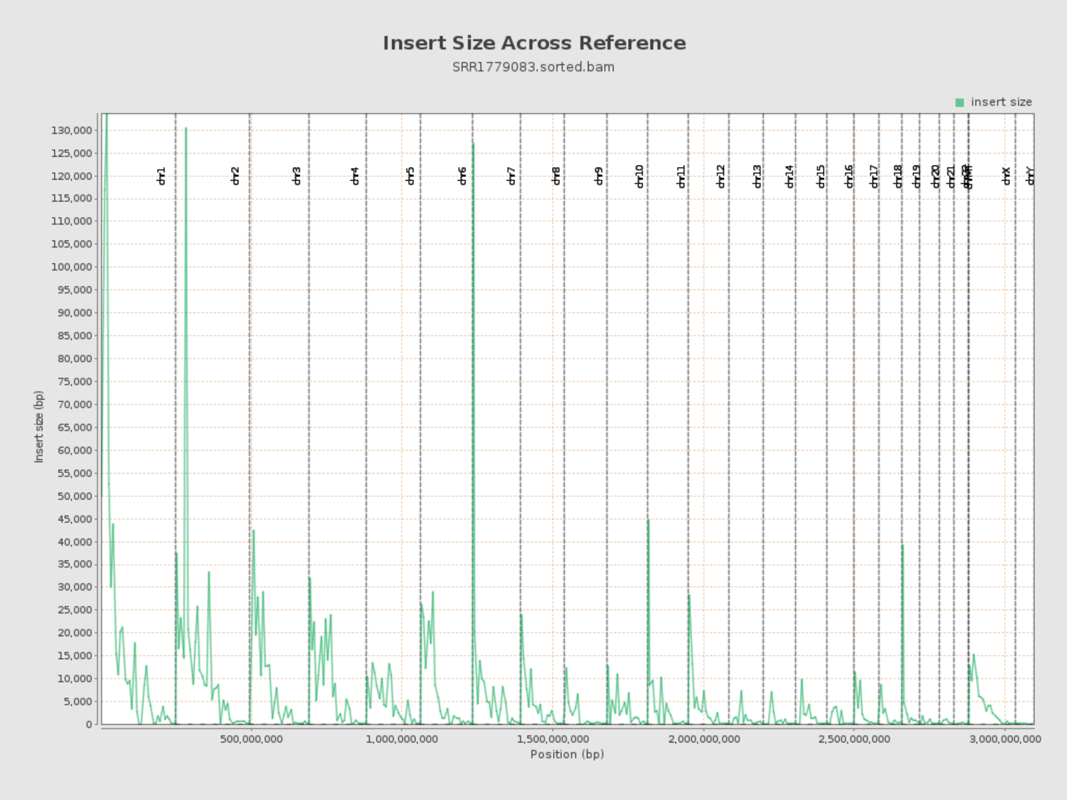
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram