Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:21:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779390.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_SRR1779390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779390_1.fastq.gz SRR1779390_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:21:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,160,078
Mapped reads	6,955,698 / 75.93%
Unmapped reads	2,204,380 / 24.07%
Mapped paired reads	6,955,698 / 75.93%
Mapped reads, first in pair	3,519,841 / 38.43%
Mapped reads, second in pair	3,435,857 / 37.51%
Mapped reads, both in pair	6,818,070 / 74.43%
Mapped reads, singletons	137,628 / 1.5%
Secondary alignments	0
Supplementary alignments	35,764 / 0.39%
Read min/max/mean length	30 / 80 / 80.14
Duplicated reads (estimated)	271,696 / 2.97%
Duplication rate	3.36%
Clipped reads	586,523 / 6.4%

2.2. ACGT Content

Number/percentage of A's	171,982,287 / 31.21%
Number/percentage of C's	99,545,767 / 18.07%
Number/percentage of T's	163,508,583 / 29.68%
Number/percentage of G's	115,835,958 / 21.02%
Number/percentage of N's	115,432 / 0.02%

GC Percentage	39.09%

2.3. Coverage

Mean	0.178
Standard Deviation	0.81

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Insert size

Mean	48,853.45
Standard Deviation	2,074,293.31
P25/Median/P75	220 / 334 / 511

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	3,563,943
Insertions	52,744
Mapped reads with at least one insertion	0.75%
Deletions	60,451
Mapped reads with at least one deletion	0.86%
Homopolymer indels	46.94%

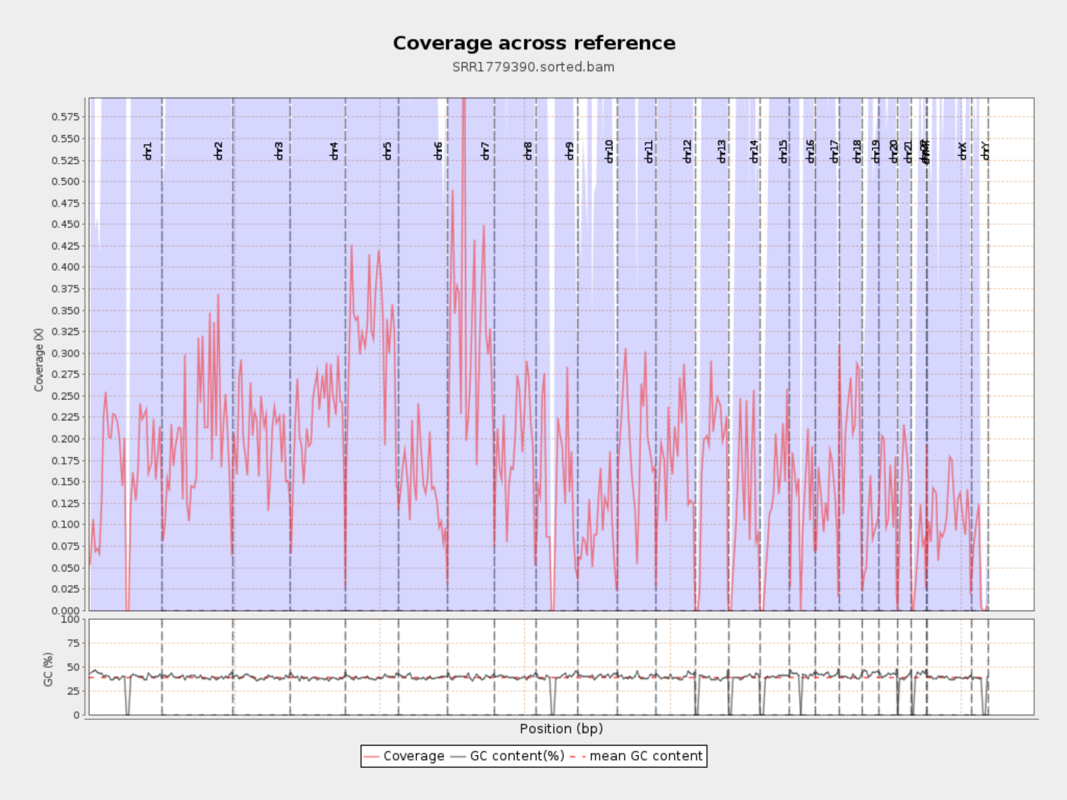
2.7. Chromosome stats

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

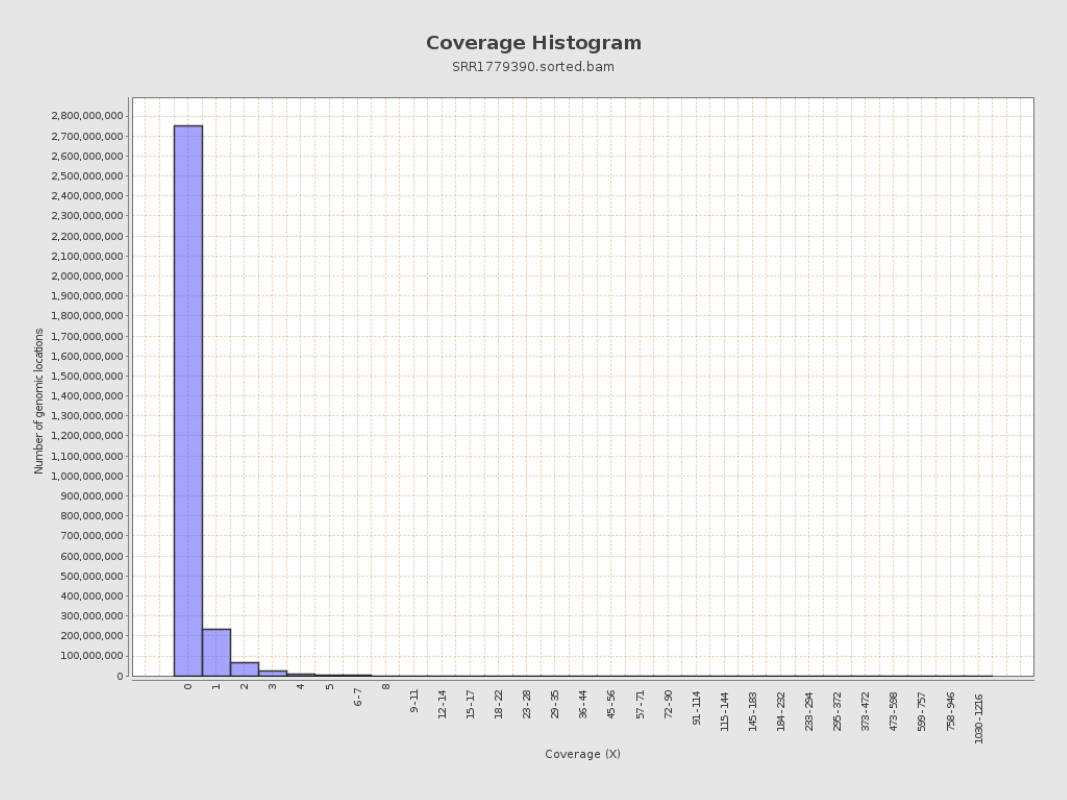
		bases	coverage	deviation
chr1	249250621	40575423	0.1628	1.2462
chr2	243199373	49035650	0.2016	0.8362
chr3	198022430	40256446	0.2033	0.6861
chr4	191154276	43104007	0.2255	0.8031
chr5	180915260	57966817	0.3204	0.866
chr6	171115067	24795276	0.1449	0.6091
chr7	159138663	54559580	0.3428	1.1446
chr8	146364022	28127757	0.1922	0.6735
chr9	141213431	20135829	0.1426	0.6431
chr10	135534747	13234593	0.0976	1.1438
chr11	135006516	26412752	0.1956	0.6811
chr12	133851895	23781649	0.1777	0.6381
chr13	115169878	20374721	0.1769	0.7869
chr14	107349540	13691153	0.1275	0.56
chr15	102531392	12825733	0.1251	0.5581
chr16	90354753	11609244	0.1285	0.5741
chr17	81195210	9857628	0.1214	0.5692
chr18	78077248	17206525	0.2204	0.8644
chr19	59128983	5328045	0.0901	1.1261
chr20	63025520	9067320	0.1439	0.5633
chr21	48129895	6339518	0.1317	0.5559
chr22	51304566	2922971	0.057	0.4071
chrMT	16571	3186	0.1923	0.513
chrX	155270560	17235160	0.111	0.5044

chrY	59373566	2665653	0.0449	0.3493

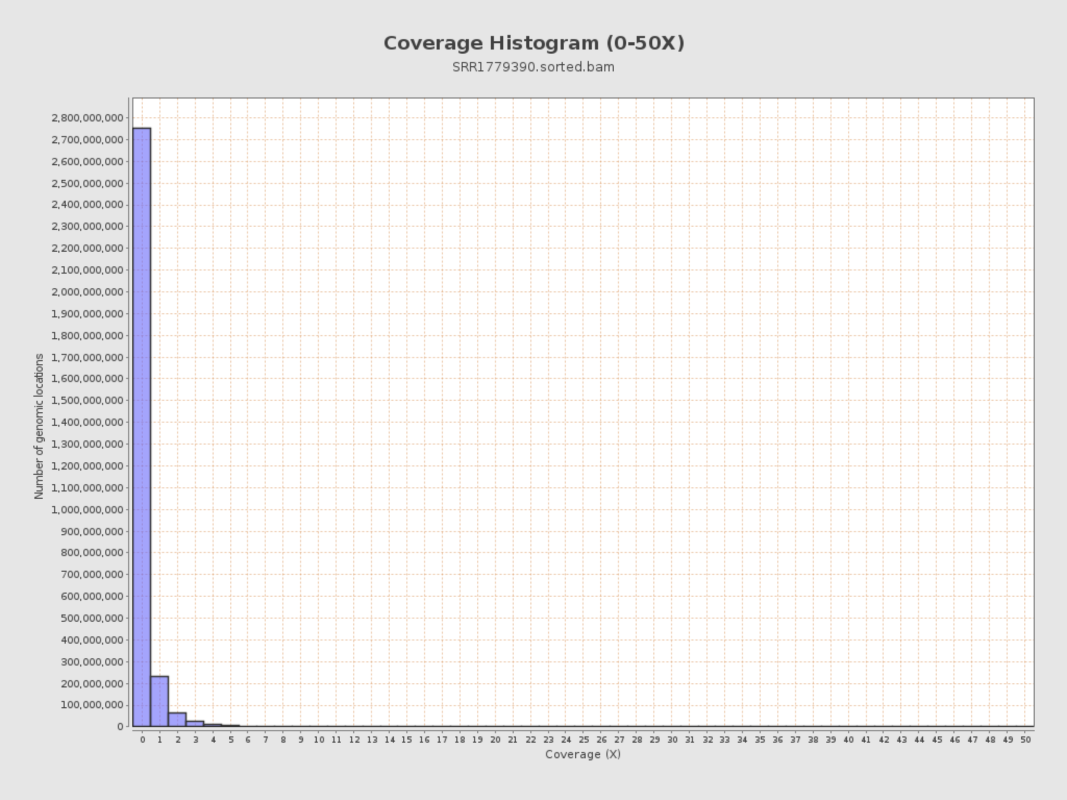
3. Results : Coverage across reference



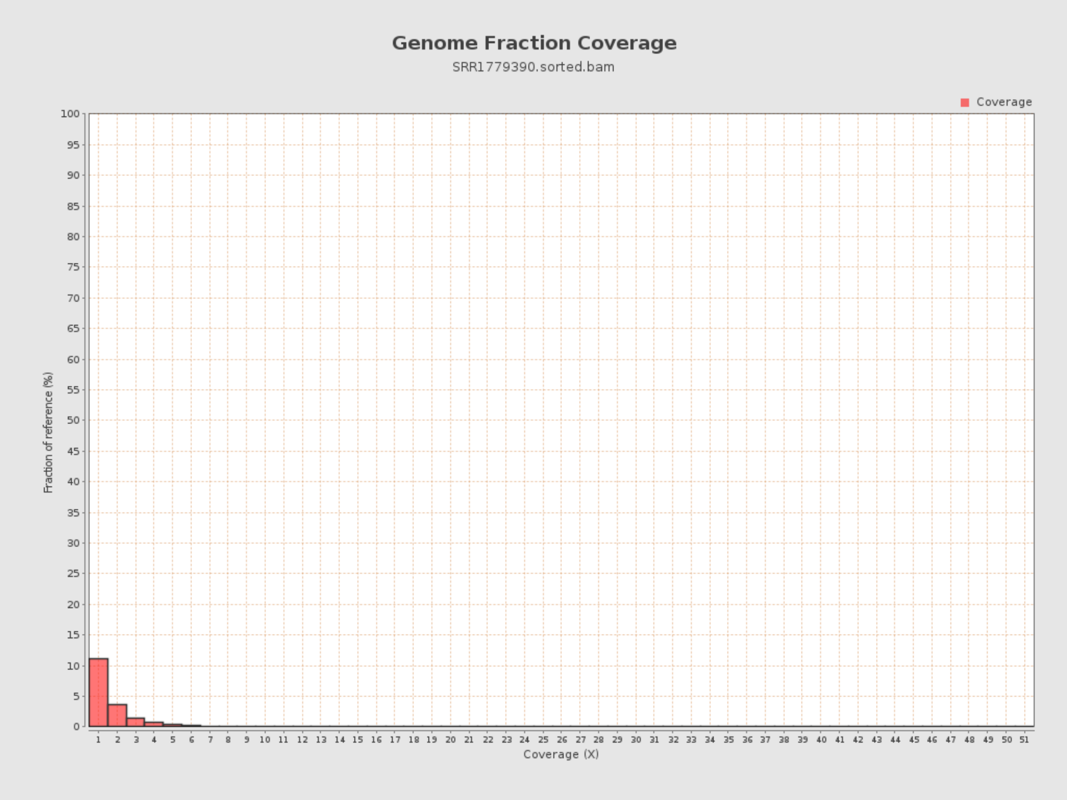
4. Results : Coverage Histogram



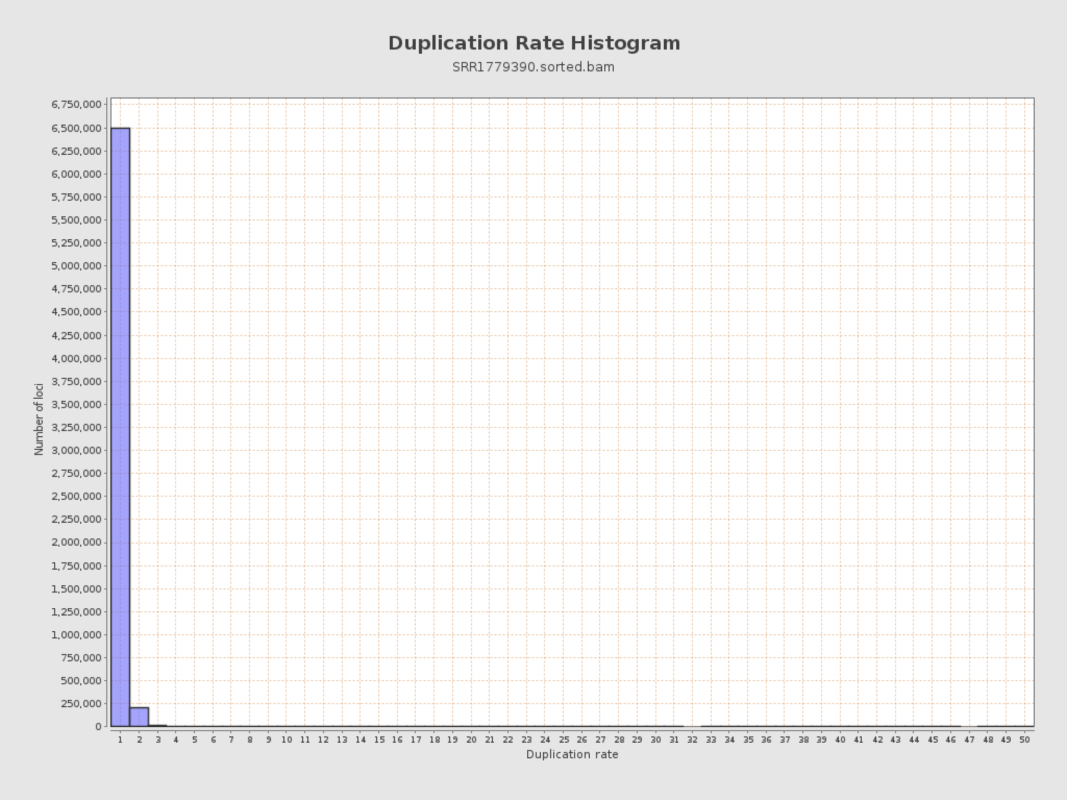
5. Results : Coverage Histogram (0-50X)



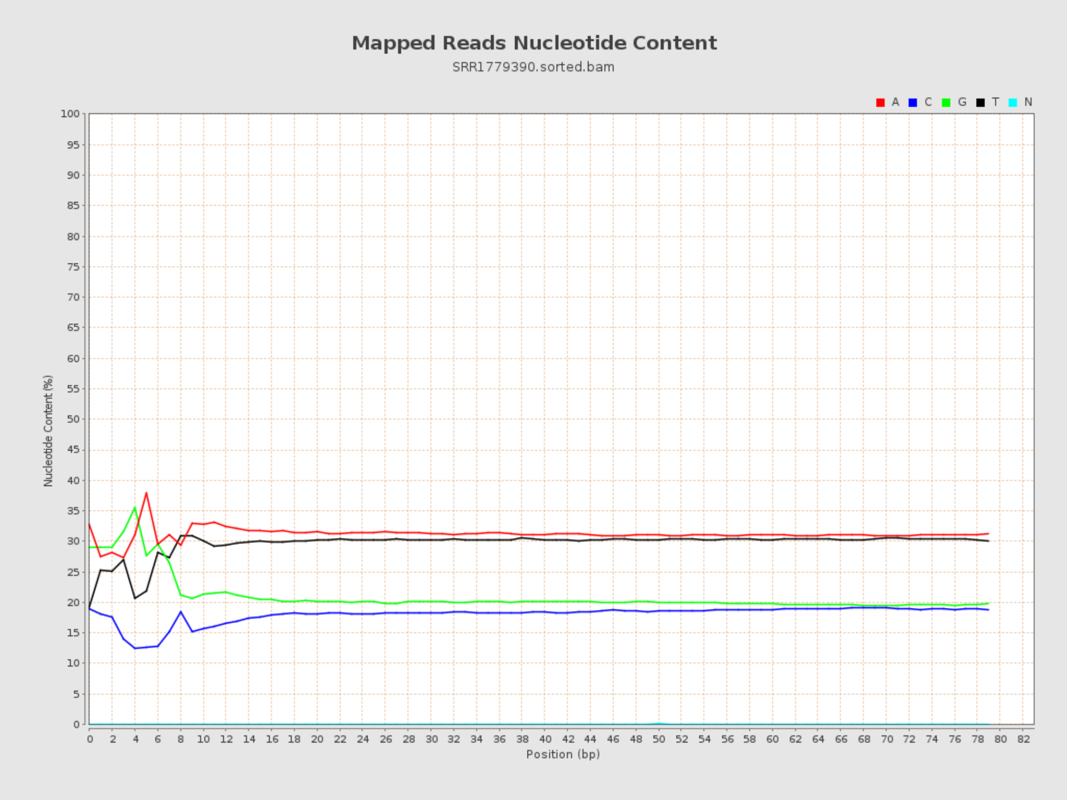
6. Results : Genome Fraction Coverage



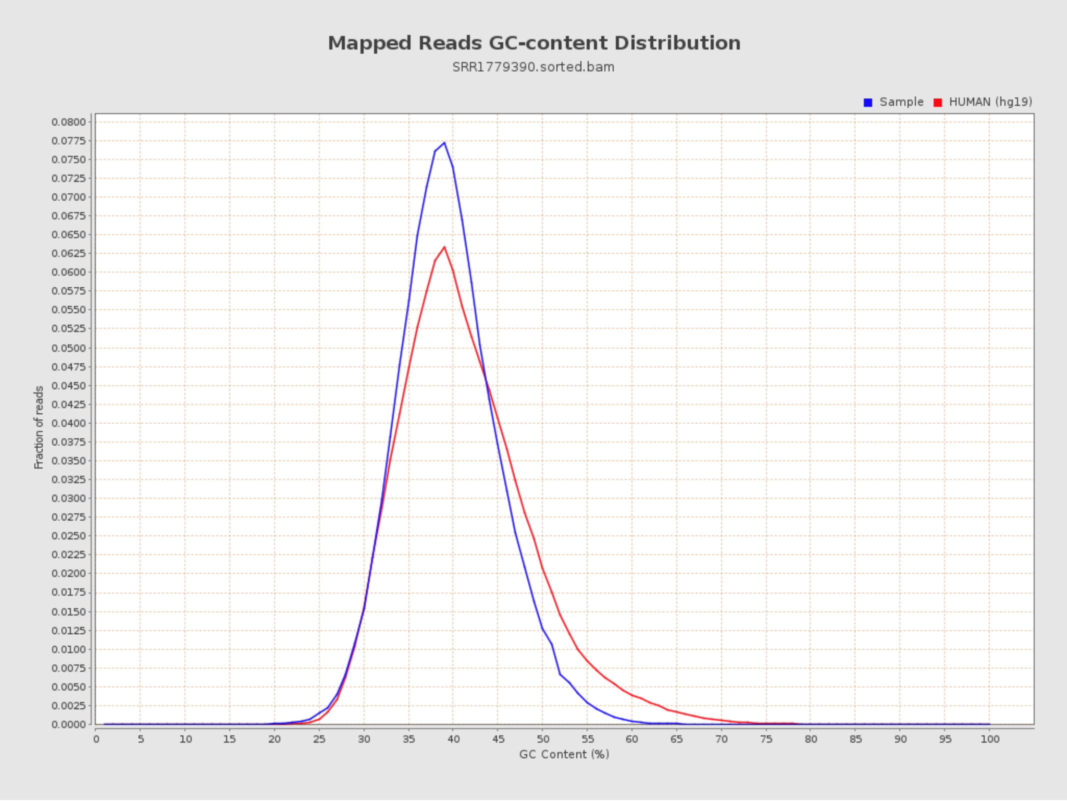
7. Results : Duplication Rate Histogram



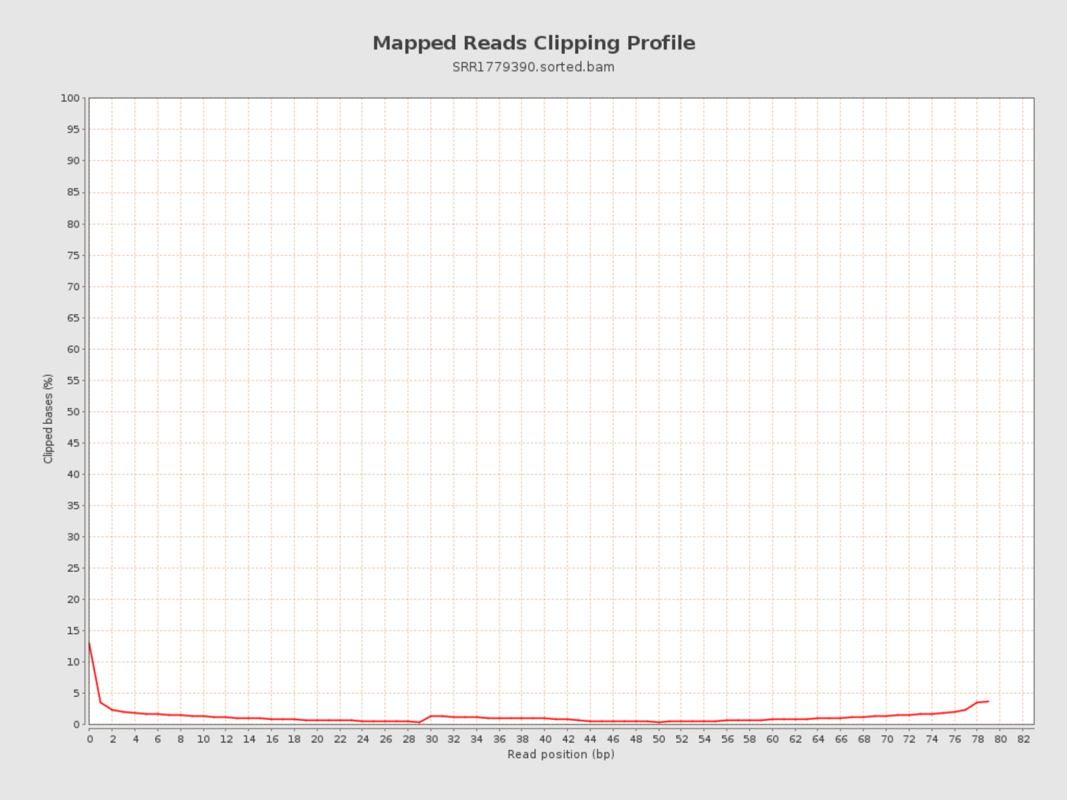
8. Results : Mapped Reads Nucleotide Content



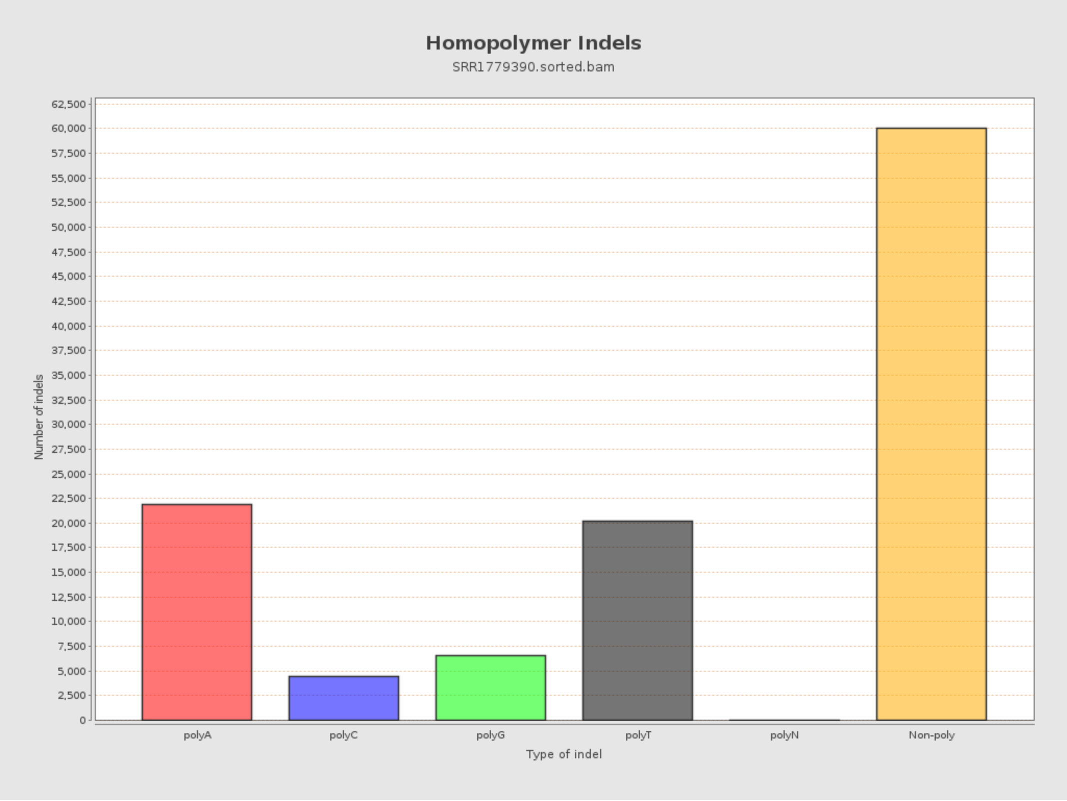
9. Results : Mapped Reads GC-content Distribution



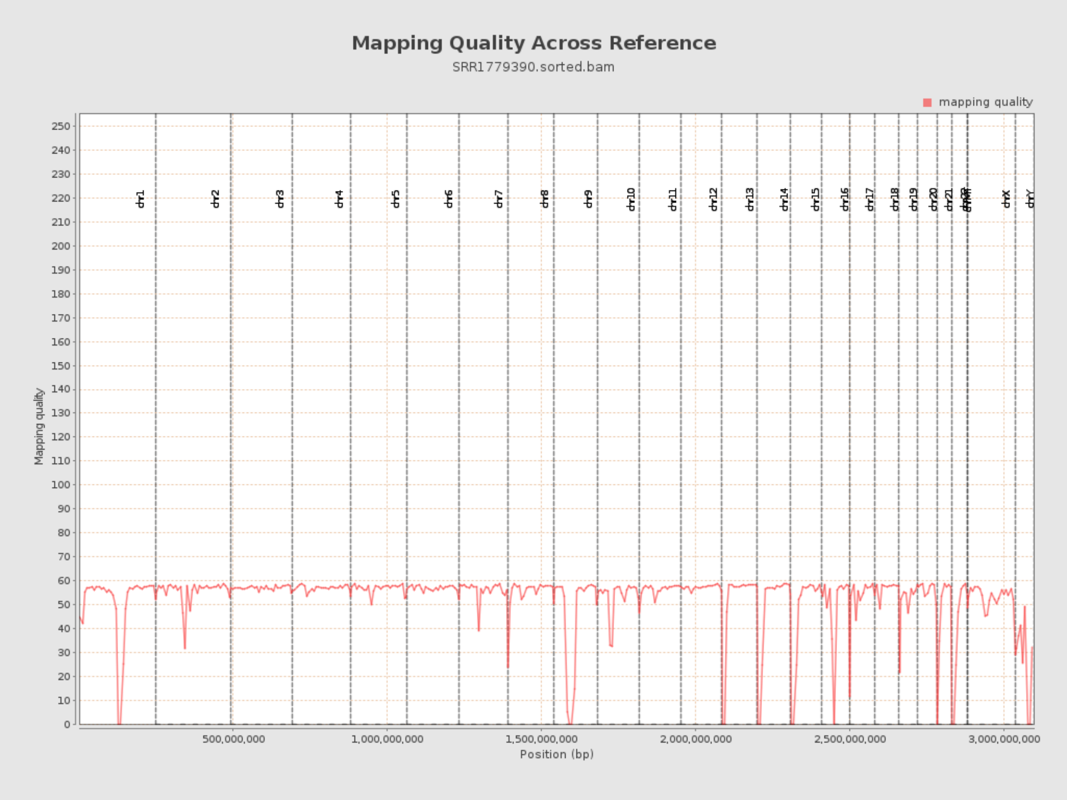
10. Results : Mapped Reads Clipping Profile



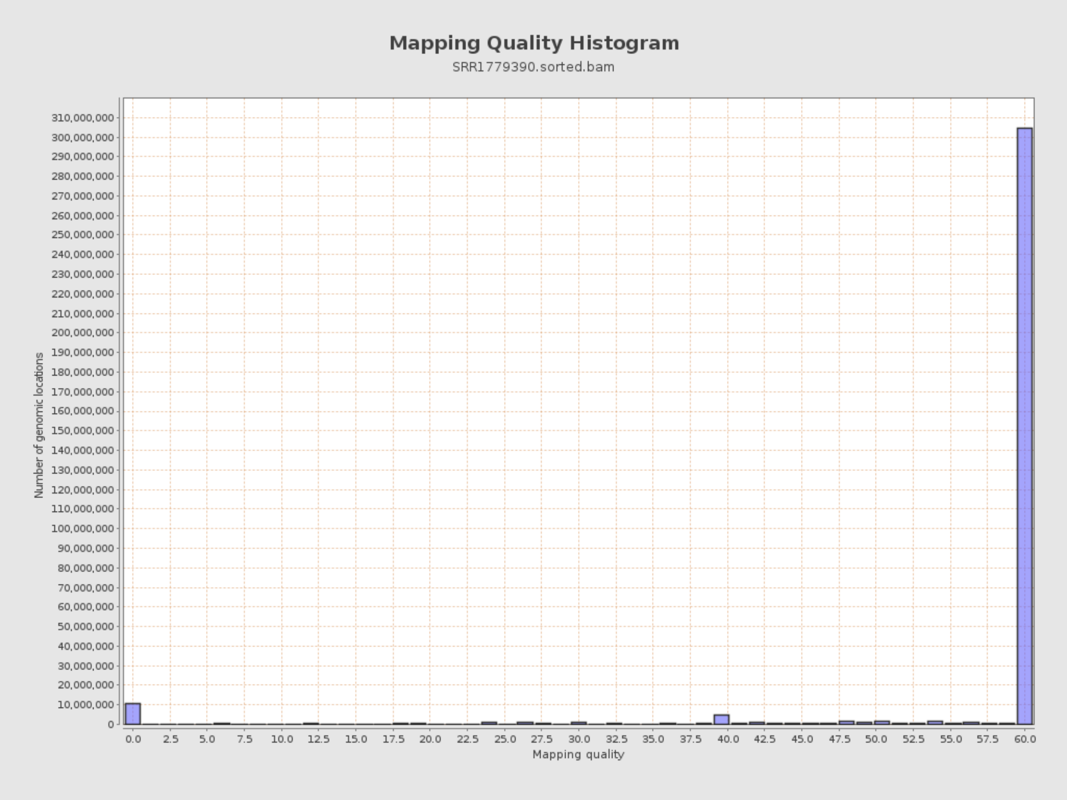
11. Results : Homopolymer Indels



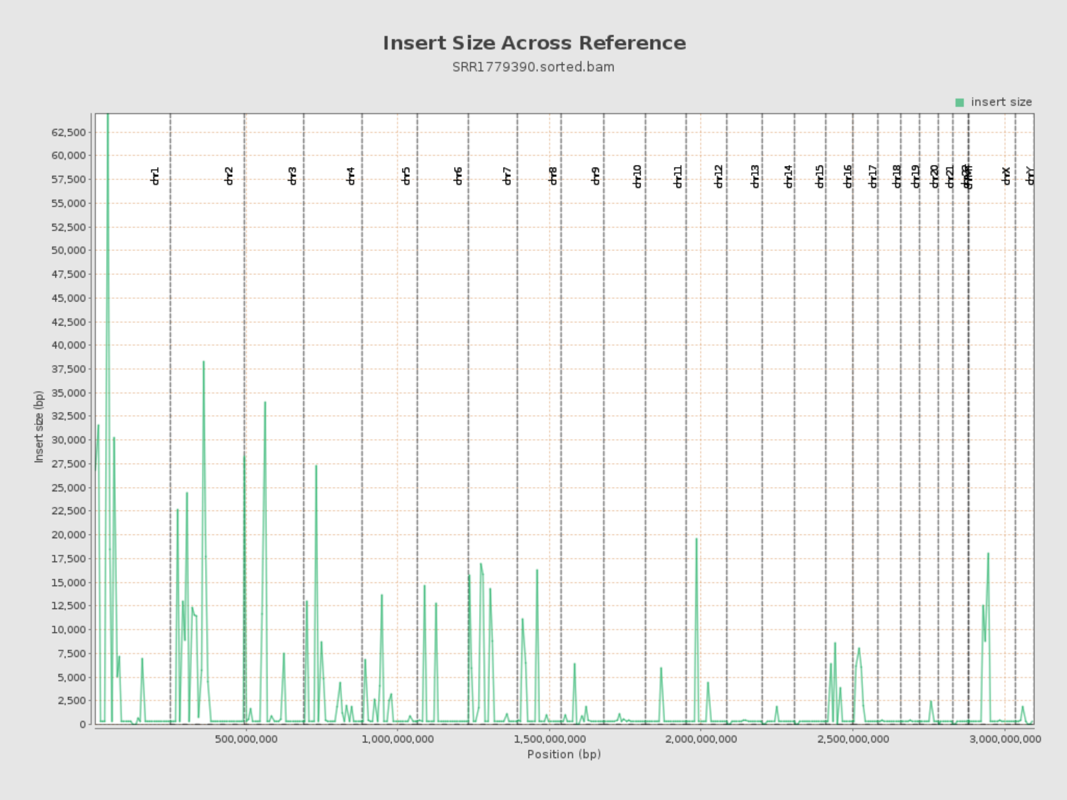
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram