Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 00:24:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779098.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_SRR1779098 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779098_1.fastq.gz SRR1779098_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 00:24:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779098.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,356,658
Mapped reads	26,290,783 / 96.1%
Unmapped reads	1,065,875 / 3.9%
Mapped paired reads	26,290,783 / 96.1%
Mapped reads, first in pair	13,257,929 / 48.46%
Mapped reads, second in pair	13,032,854 / 47.64%
Mapped reads, both in pair	25,948,456 / 94.85%
Mapped reads, singletons	342,327 / 1.25%
Secondary alignments	0
Supplementary alignments	145,692 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	1,149,661 / 4.2%
Duplication rate	3.72%
Clipped reads	1,986,950 / 7.26%

2.2. ACGT Content

Number/percentage of A's	799,398,956 / 30.5%
Number/percentage of C's	508,763,217 / 19.41%
Number/percentage of T's	794,869,206 / 30.33%
Number/percentage of G's	516,743,652 / 19.72%
Number/percentage of N's	1,062,804 / 0.04%

GC Percentage	39.13%

2.3. Coverage

Mean	0.8468
Standard Deviation	2.9

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	62,294.82
Standard Deviation	2,381,195.2
P25/Median/P75	148 / 201 / 276

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	11,120,009
Insertions	220,404
Mapped reads with at least one insertion	0.83%
Deletions	272,637
Mapped reads with at least one deletion	1.02%
Homopolymer indels	46.2%

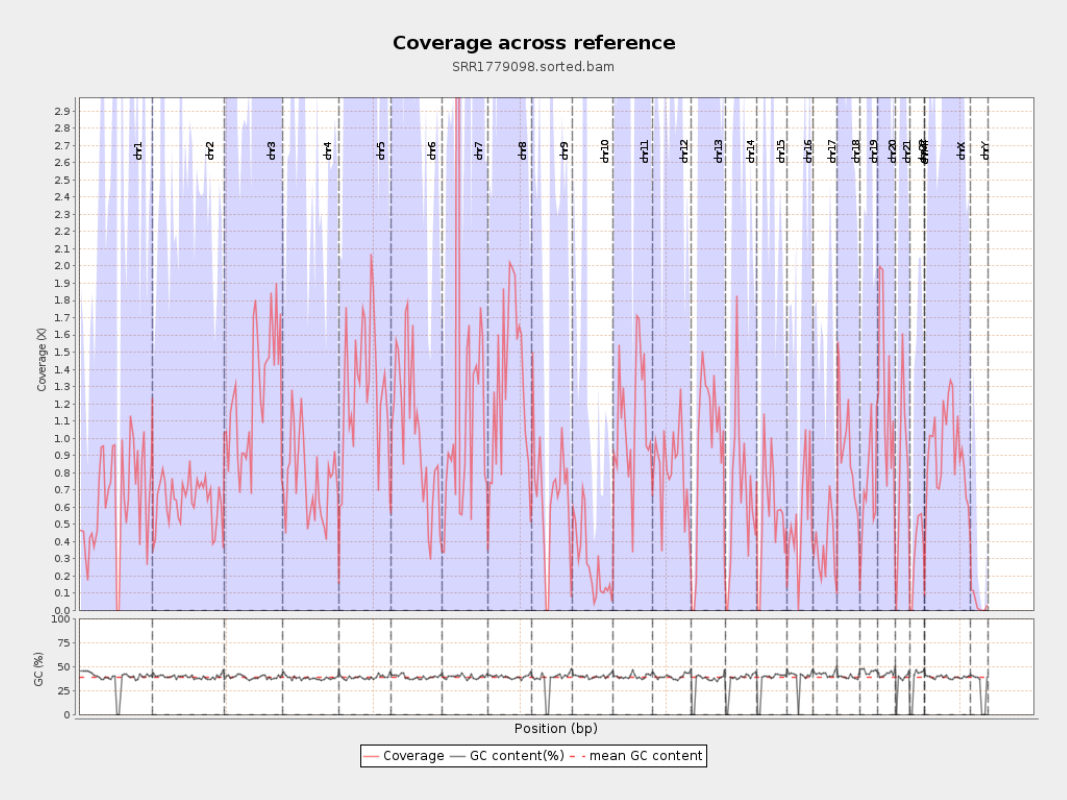
2.7. Chromosome stats

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

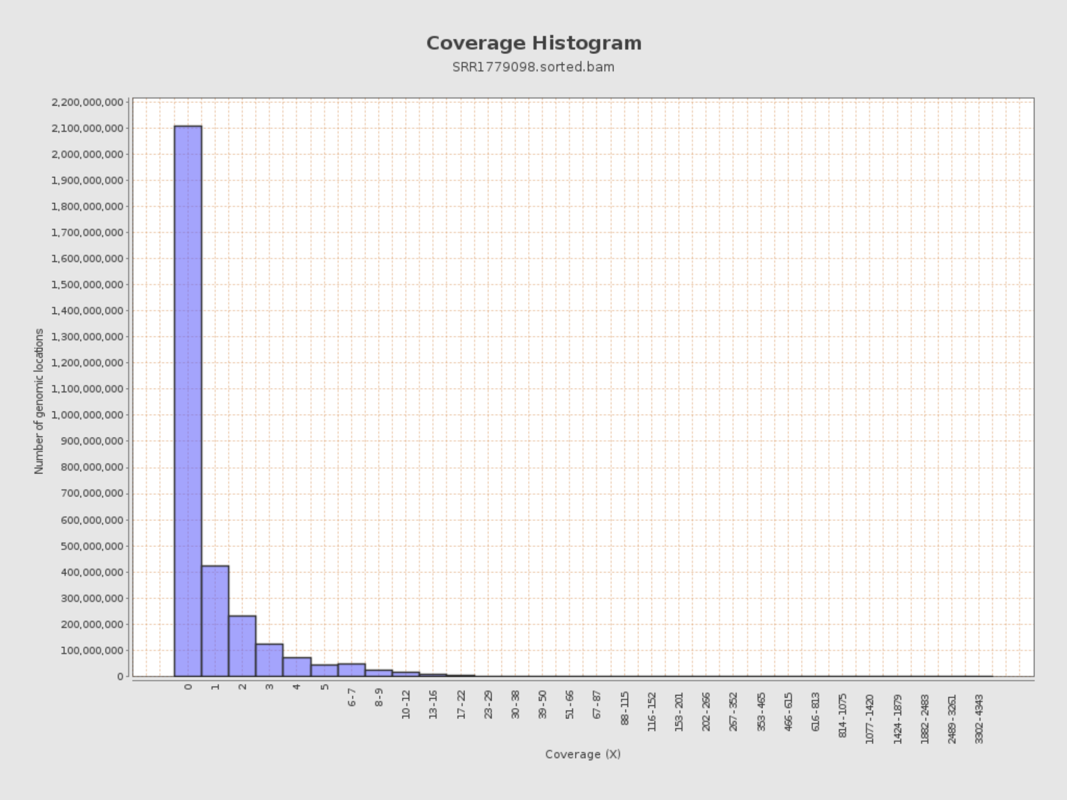
		bases	coverage	deviation
chr1	249250621	159553620	0.6401	4.8126
chr2	243199373	155232319	0.6383	1.945
chr3	198022430	248856888	1.2567	2.2615
chr4	191154276	145928077	0.7634	1.7128
chr5	180915260	227558058	1.2578	2.2405
chr6	171115067	174294836	1.0186	2.1952
chr7	159138663	216983699	1.3635	6.6967
chr8	146364022	194226317	1.327	2.3954
chr9	141213431	90986026	0.6443	1.8155
chr10	135534747	37316450	0.2753	4.4759
chr11	135006516	147897371	1.0955	2.1291
chr12	133851895	108552325	0.811	1.863
chr13	115169878	110862457	0.9626	2.06
chr14	107349540	73089130	0.6809	1.6648
chr15	102531392	56788628	0.5539	1.5558
chr16	90354753	46448239	0.5141	1.4307
chr17	81195210	29202799	0.3597	1.1916
chr18	78077248	72512434	0.9287	2.069
chr19	59128983	41354550	0.6994	3.0083
chr20	63025520	78315642	1.2426	2.3837
chr21	48129895	41352753	0.8592	1.9616
chr22	51304566	17341760	0.338	1.0703
chrMT	16571	1367	0.0825	0.3739
chrX	155270560	144531871	0.9308	2.0288

chrY	59373566	2260358	0.0381	0.6144

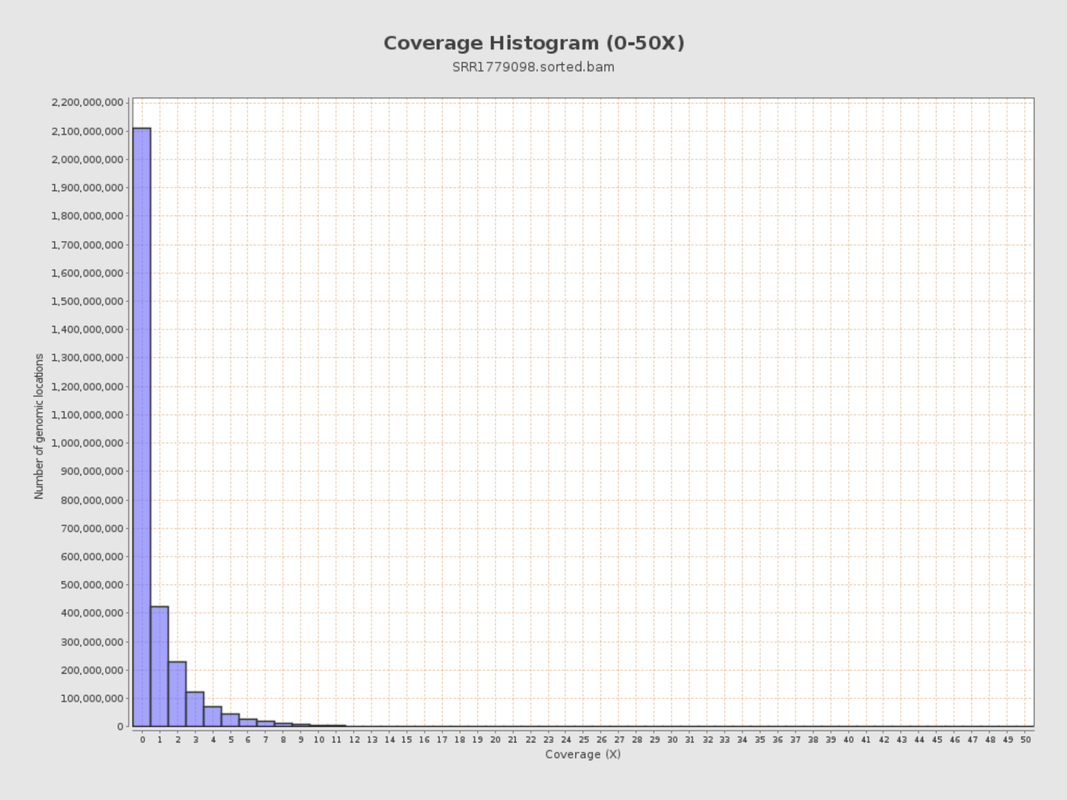
3. Results : Coverage across reference



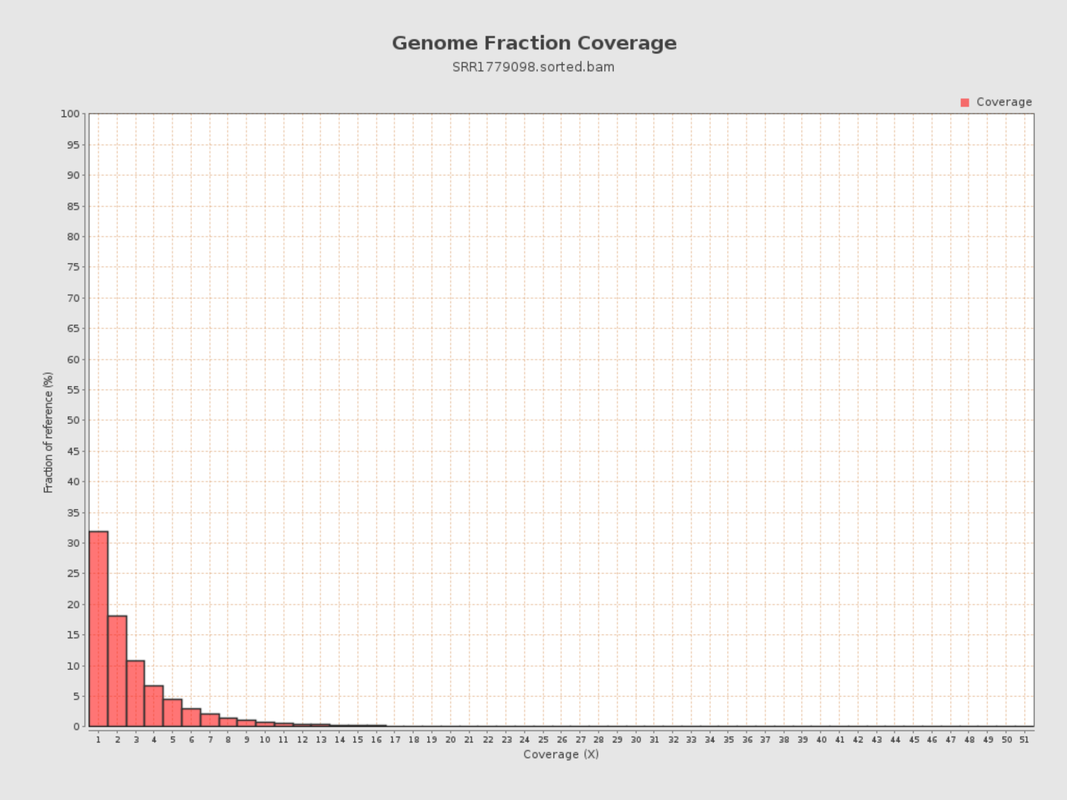
4. Results : Coverage Histogram



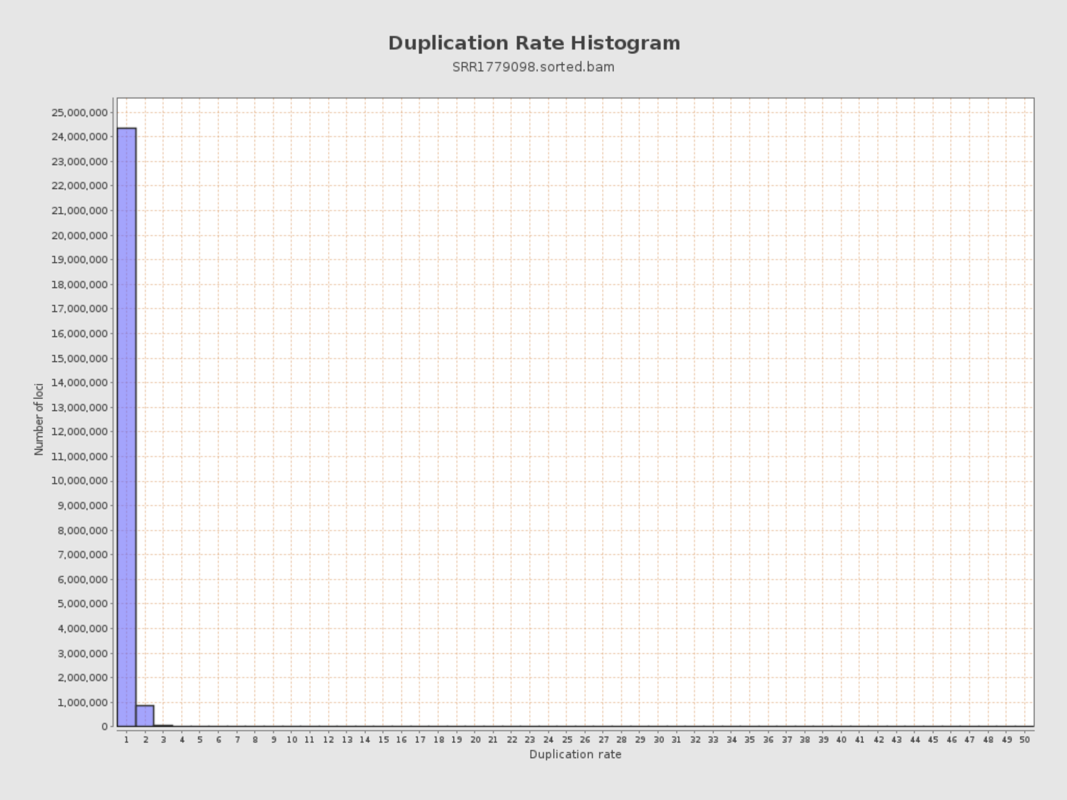
5. Results : Coverage Histogram (0-50X)



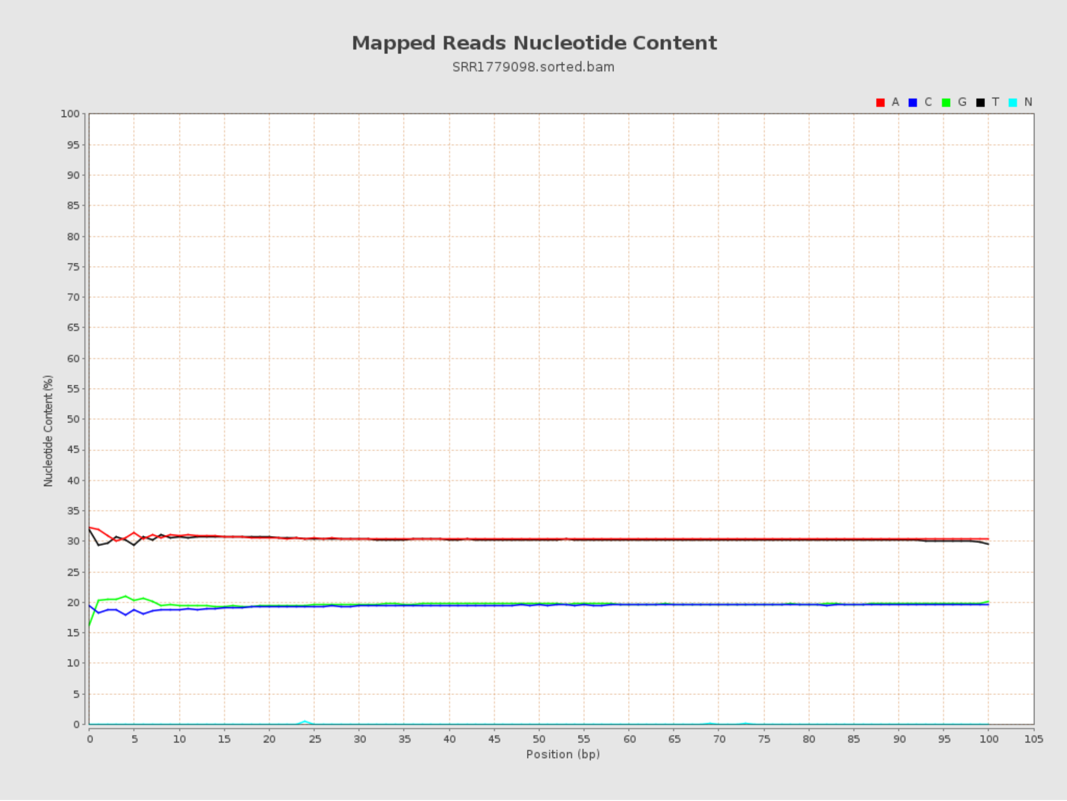
6. Results : Genome Fraction Coverage



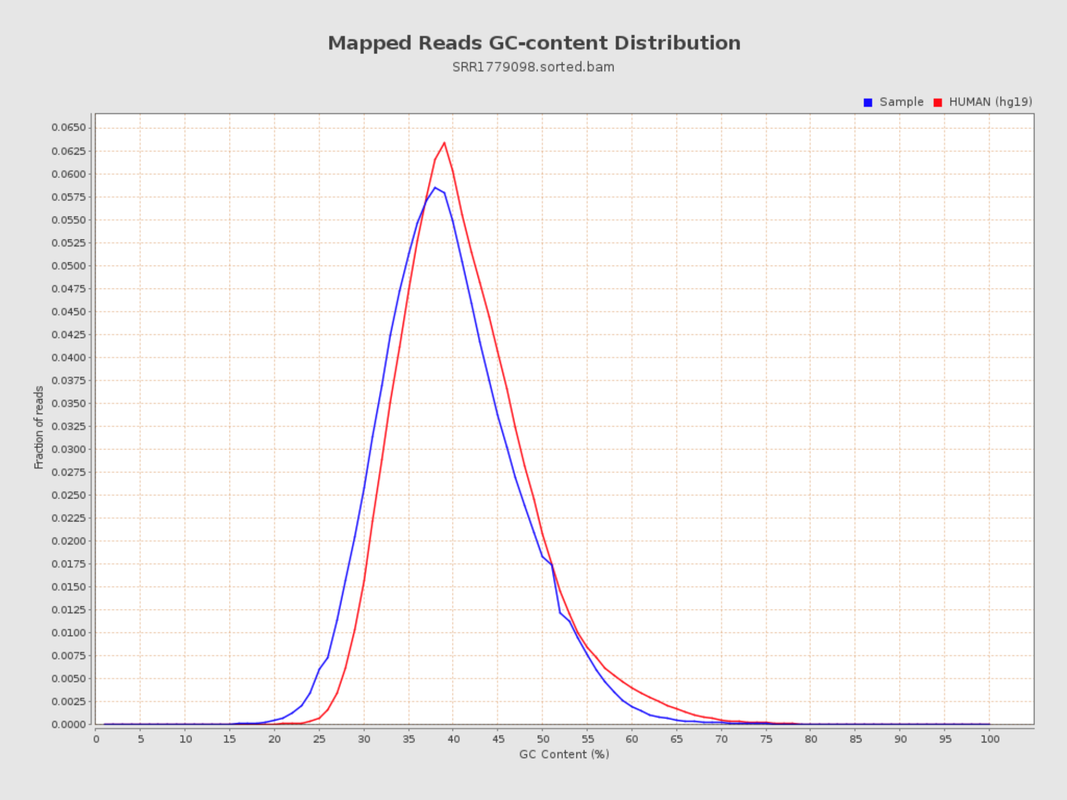
7. Results : Duplication Rate Histogram



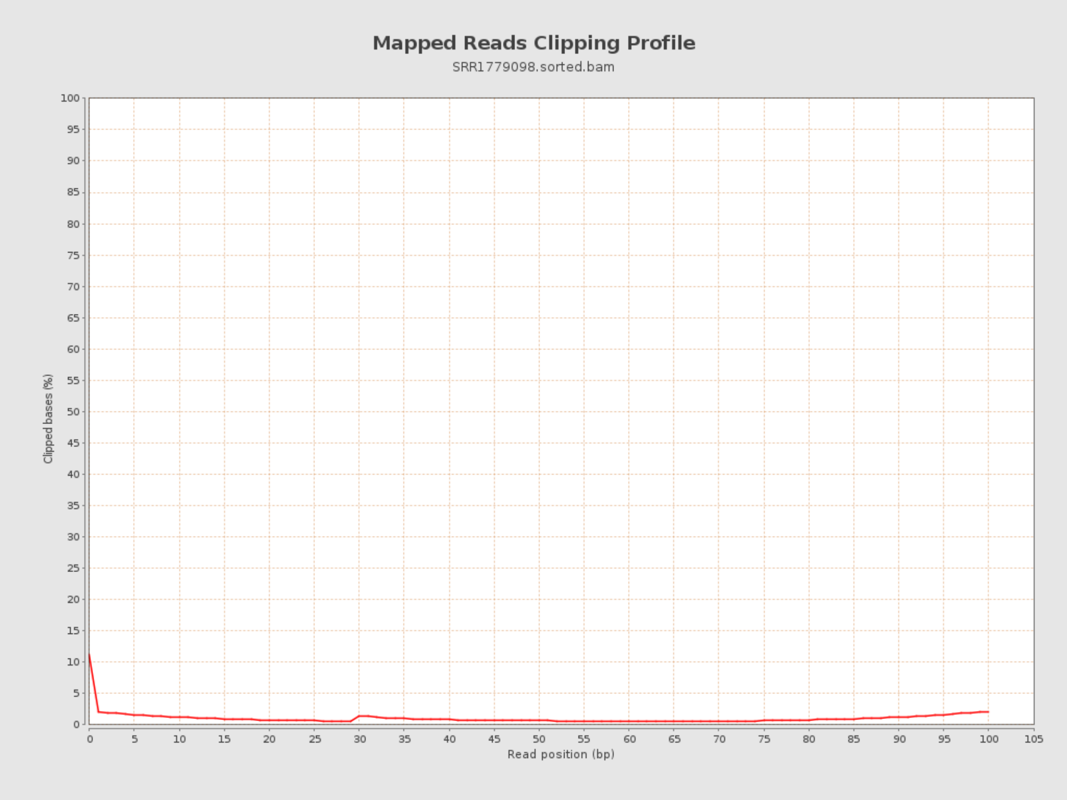
8. Results : Mapped Reads Nucleotide Content



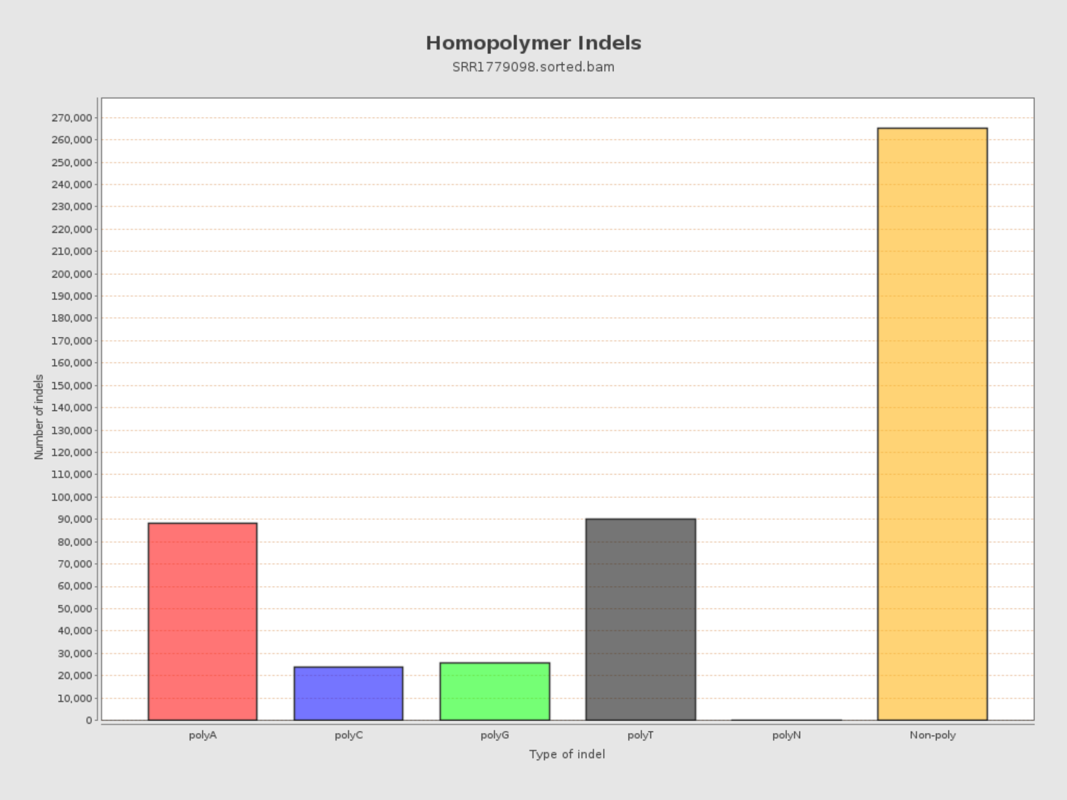
9. Results : Mapped Reads GC-content Distribution



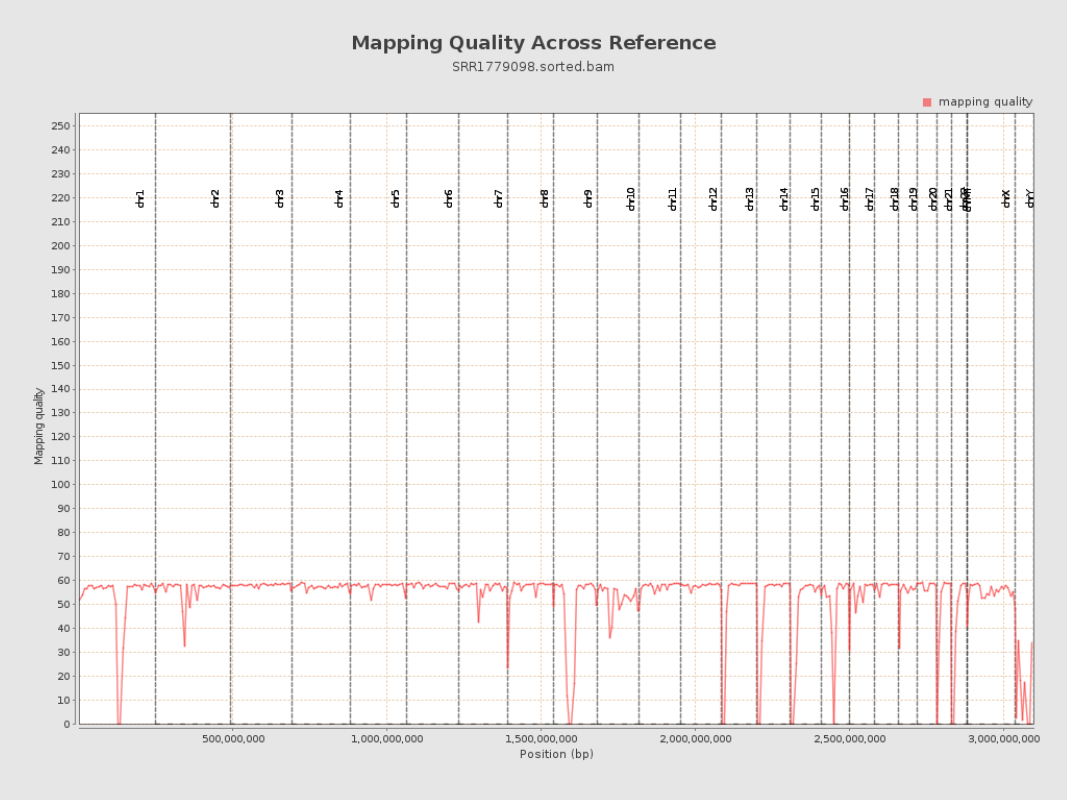
10. Results : Mapped Reads Clipping Profile



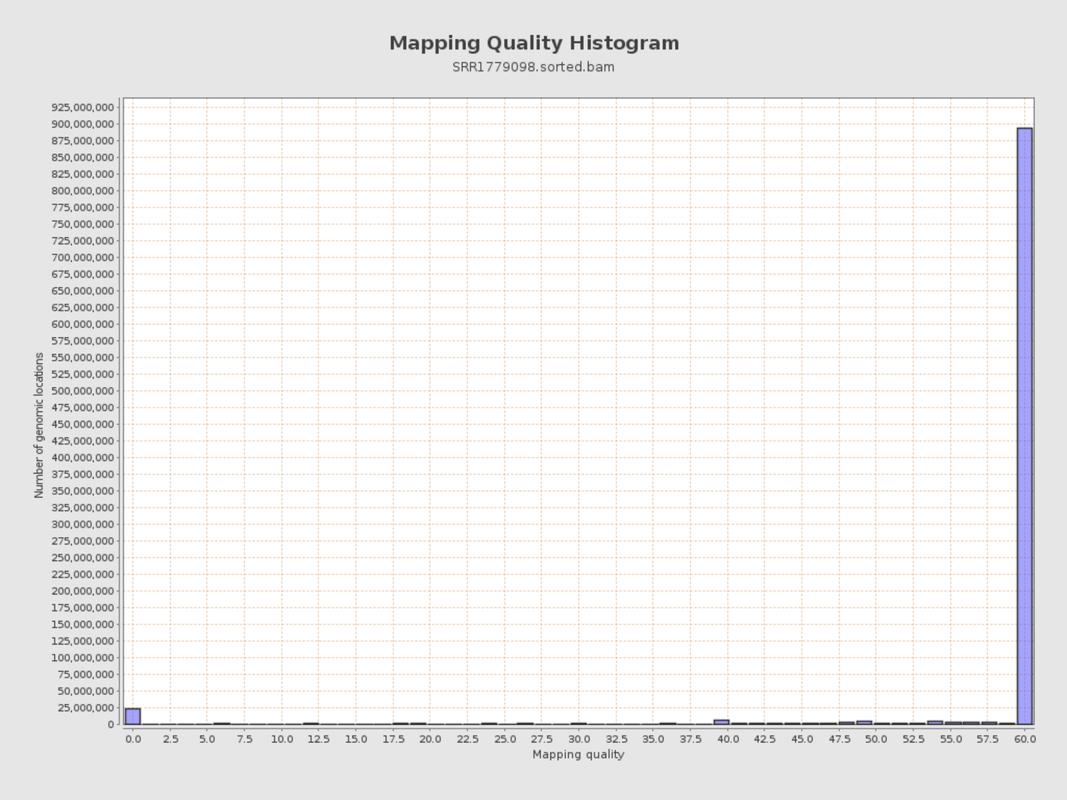
11. Results : Homopolymer Indels



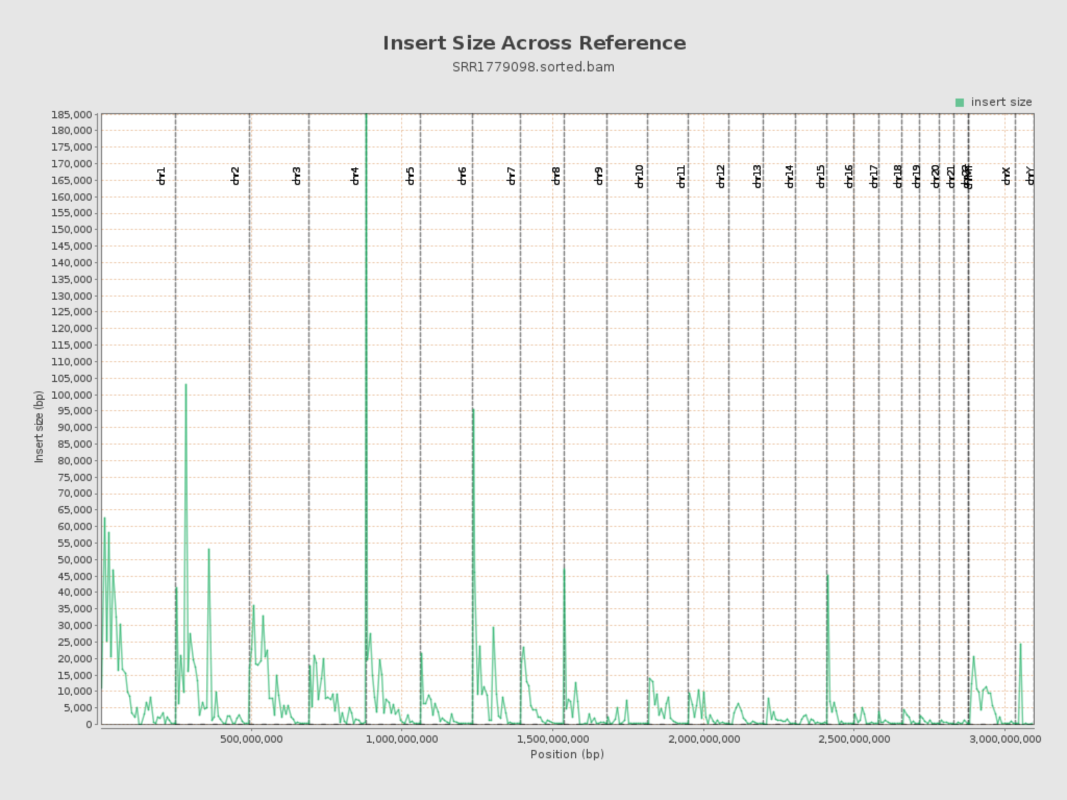
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram