Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 15:38:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779085.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_SRR1779085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779085_1.fastq.gz SRR1779085_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 15:38:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,641,044
Mapped reads	29,330,060 / 92.7%
Unmapped reads	2,310,984 / 7.3%
Mapped paired reads	29,330,060 / 92.7%
Mapped reads, first in pair	14,918,816 / 47.15%
Mapped reads, second in pair	14,411,244 / 45.55%
Mapped reads, both in pair	28,650,584 / 90.55%
Mapped reads, singletons	679,476 / 2.15%
Secondary alignments	0
Supplementary alignments	195,374 / 0.62%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	923,228 / 2.92%
Duplication rate	2.32%
Clipped reads	1,915,895 / 6.06%

2.2. ACGT Content

Number/percentage of A's	884,496,723 / 30.23%
Number/percentage of C's	573,253,527 / 19.59%
Number/percentage of T's	878,508,139 / 30.03%
Number/percentage of G's	588,448,805 / 20.11%
Number/percentage of N's	957,185 / 0.03%

GC Percentage	39.71%

2.3. Coverage

Mean	0.9453
Standard Deviation	3.4954

2.4. Mapping Quality

Mean Mapping Quality	53.88

2.5. Insert size

Mean	55,788.4
Standard Deviation	2,284,034.15
P25/Median/P75	238 / 302 / 377

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	16,921,593
Insertions	291,690
Mapped reads with at least one insertion	0.98%
Deletions	334,000
Mapped reads with at least one deletion	1.12%
Homopolymer indels	47.31%

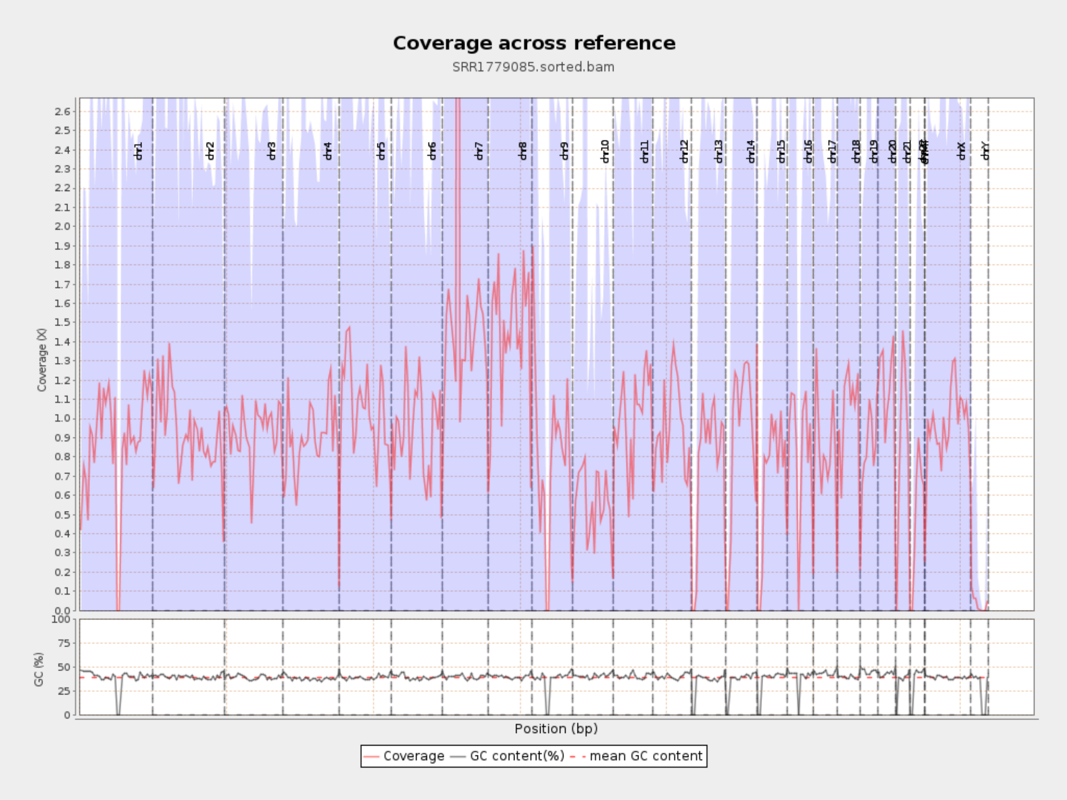
2.7. Chromosome stats

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

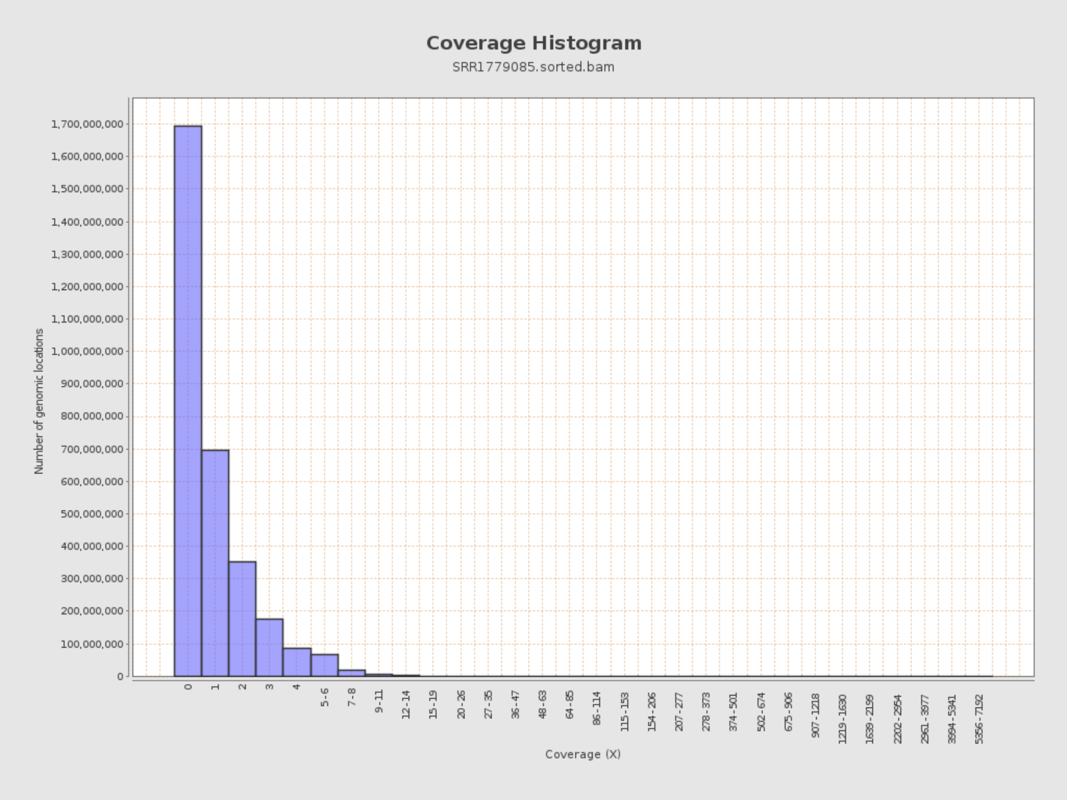
		bases	coverage	deviation
chr1	249250621	219555995	0.8809	7.8248
chr2	243199373	223941635	0.9208	2.2054
chr3	198022430	186261604	0.9406	1.391
chr4	191154276	172479341	0.9023	1.5082
chr5	180915260	187562186	1.0367	1.4724
chr6	171115067	164230010	0.9598	1.7036
chr7	159138663	285773640	1.7958	6.8916
chr8	146364022	212395026	1.4511	1.9309
chr9	141213431	112919321	0.7996	2.3677
chr10	135534747	76416002	0.5638	6.5379
chr11	135006516	137276525	1.0168	1.553
chr12	133851895	126229490	0.9431	1.5445
chr13	115169878	88768988	0.7708	1.334
chr14	107349540	97202156	0.9055	1.4666
chr15	102531392	70145129	0.6841	1.3689
chr16	90354753	72382830	0.8011	1.408
chr17	81195210	66749986	0.8221	2.4198
chr18	78077248	82020443	1.0505	2.5825
chr19	59128983	49024204	0.8291	5.0506
chr20	63025520	73290266	1.1629	1.6954
chr21	48129895	42323588	0.8794	1.5429
chr22	51304566	25378110	0.4947	1.089
chrMT	16571	4663	0.2814	0.6439
chrX	155270560	151959680	0.9787	1.6012

chrY	59373566	2113197	0.0356	0.4927

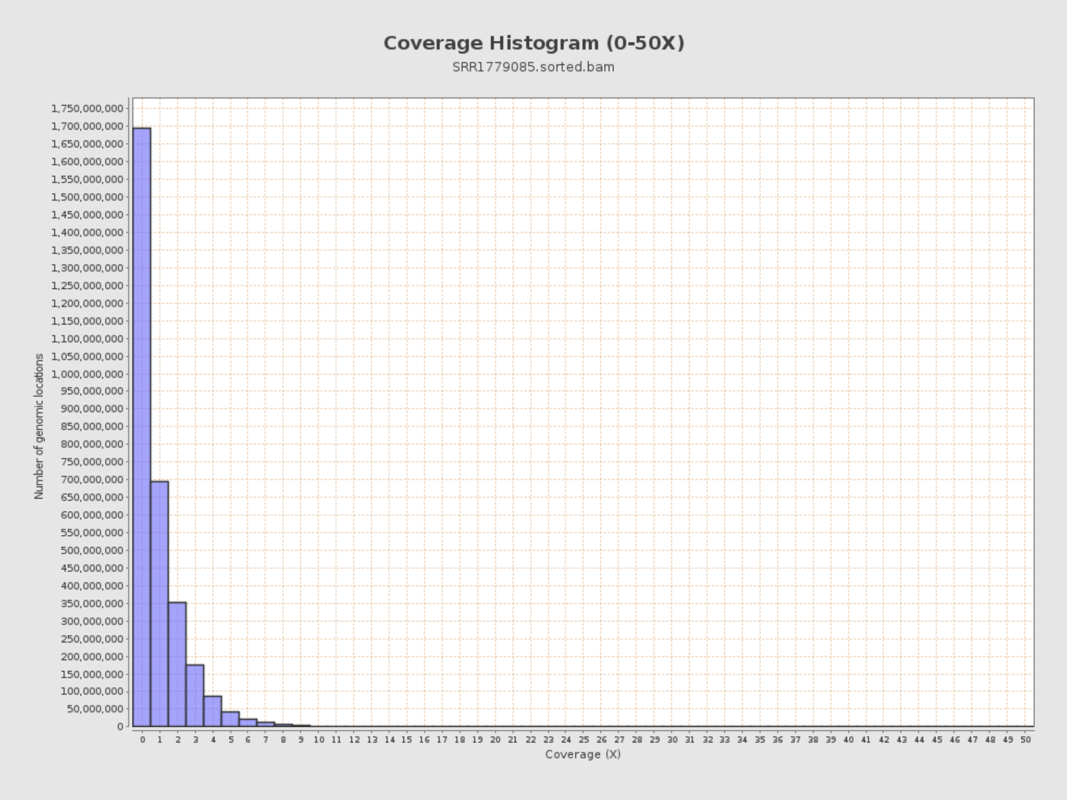
3. Results : Coverage across reference



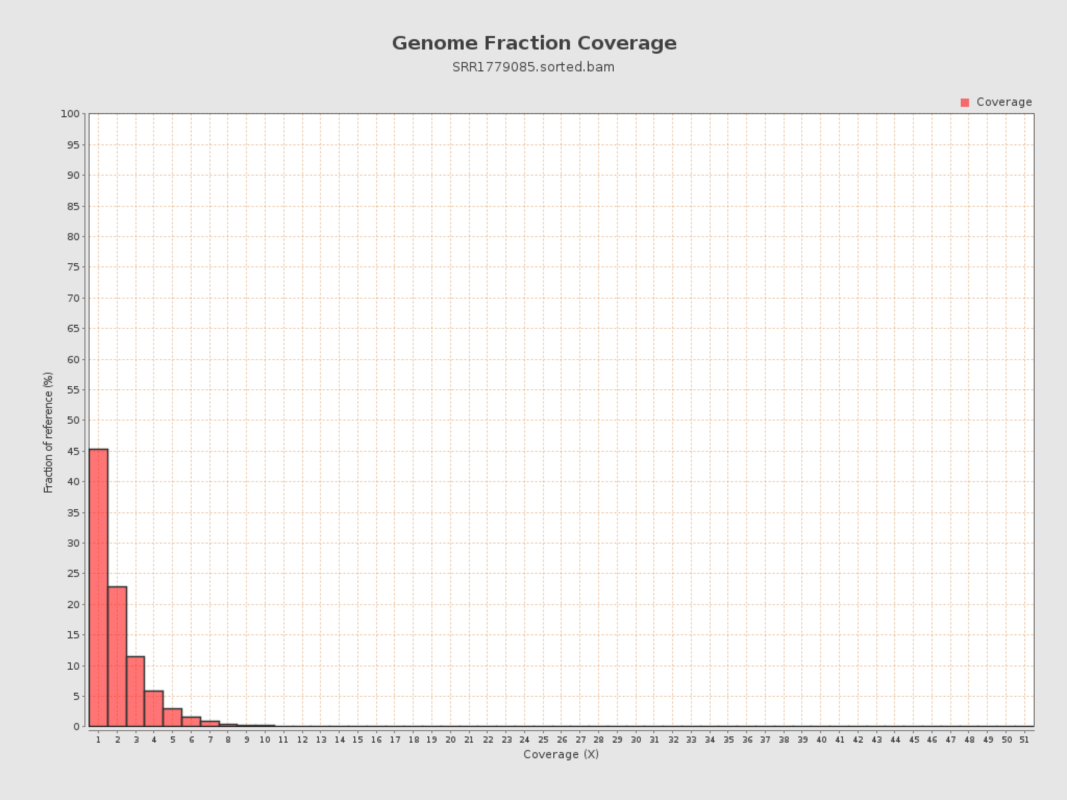
4. Results : Coverage Histogram



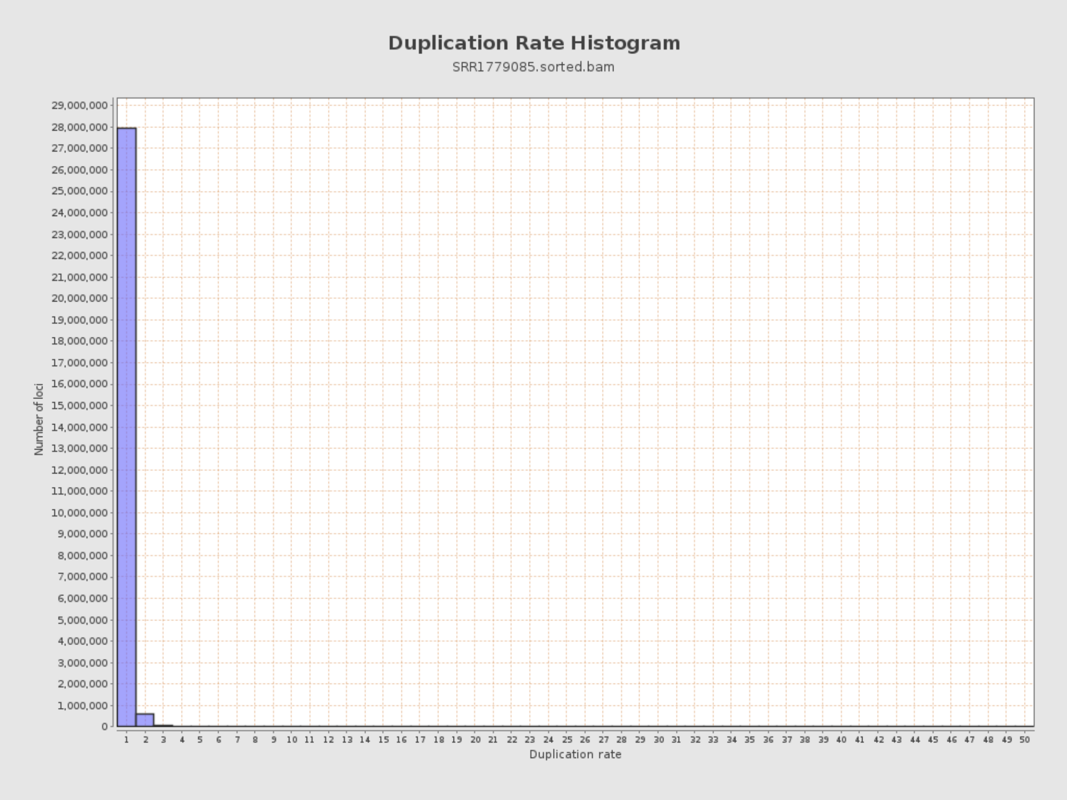
5. Results : Coverage Histogram (0-50X)



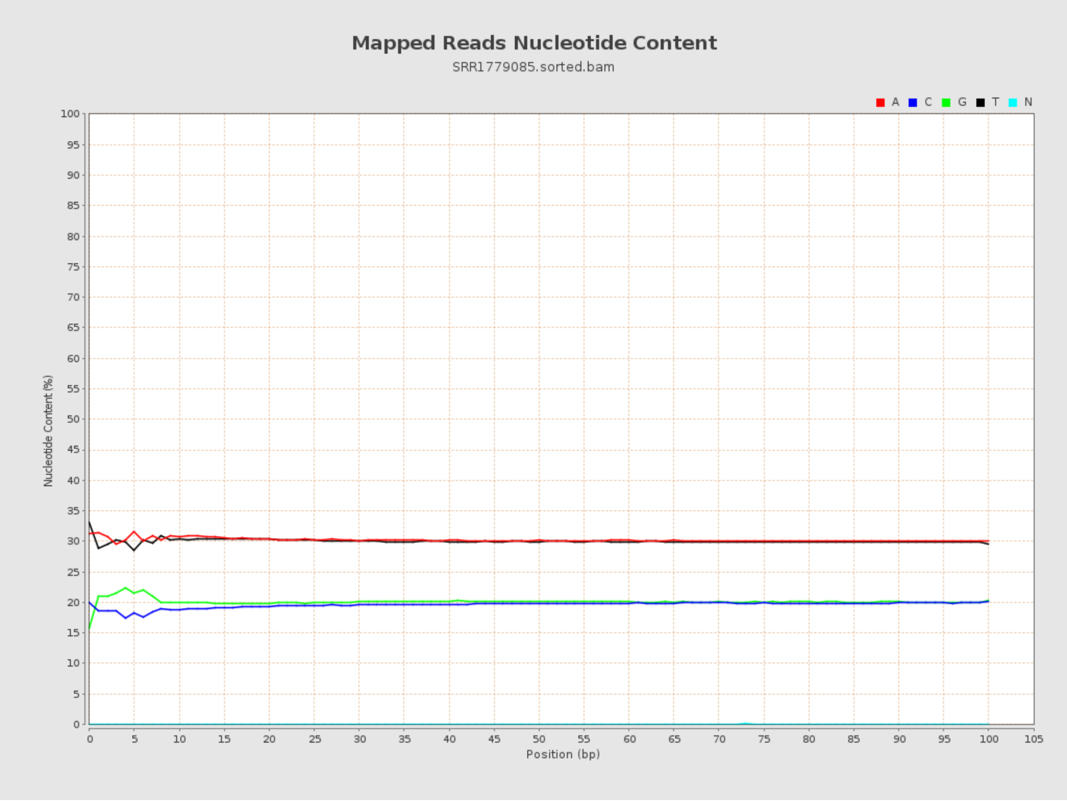
6. Results : Genome Fraction Coverage



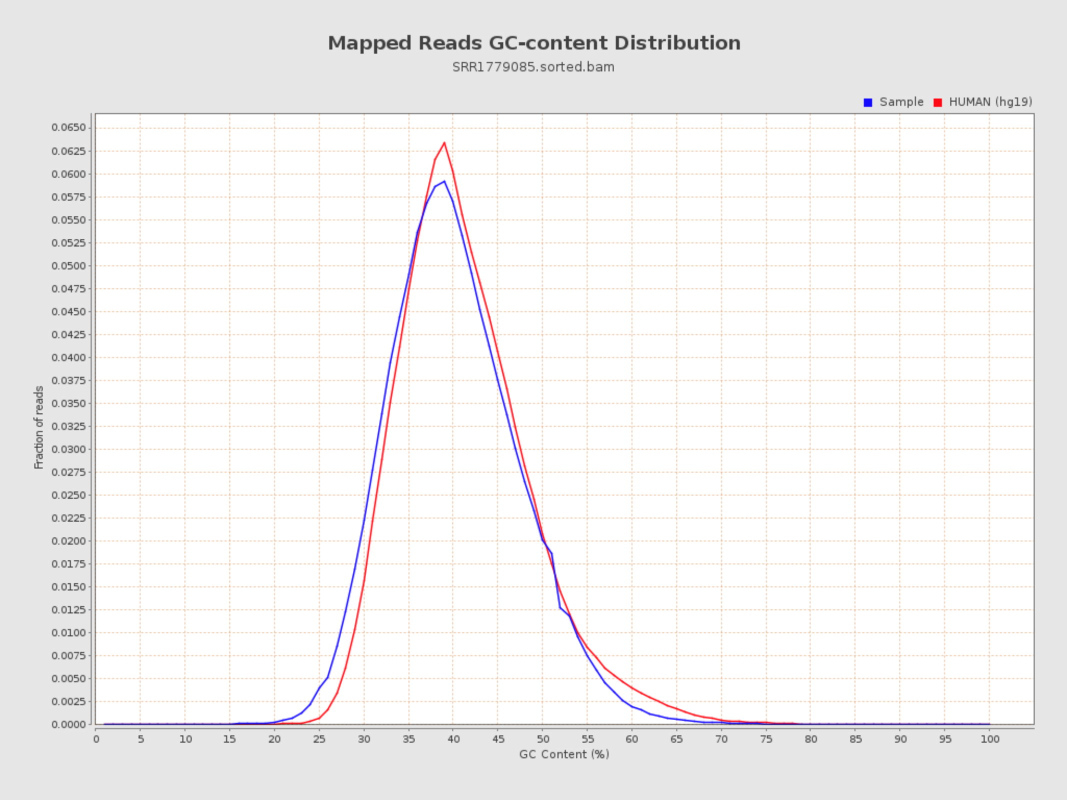
7. Results : Duplication Rate Histogram



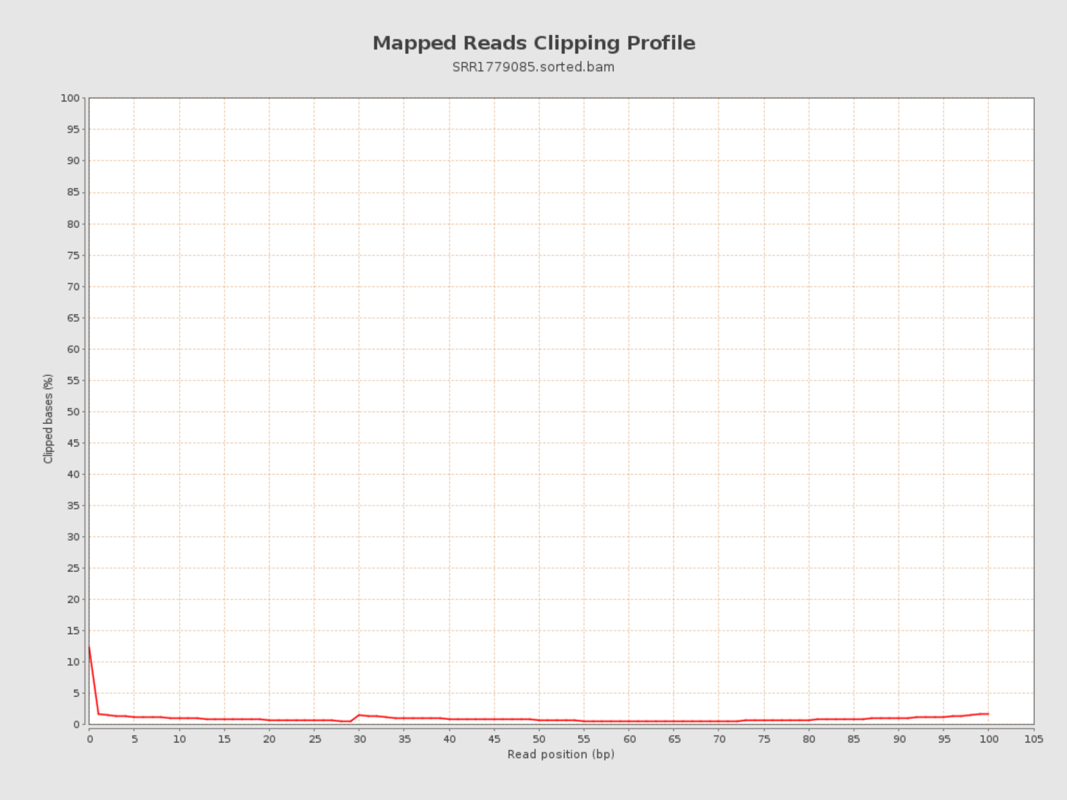
8. Results : Mapped Reads Nucleotide Content



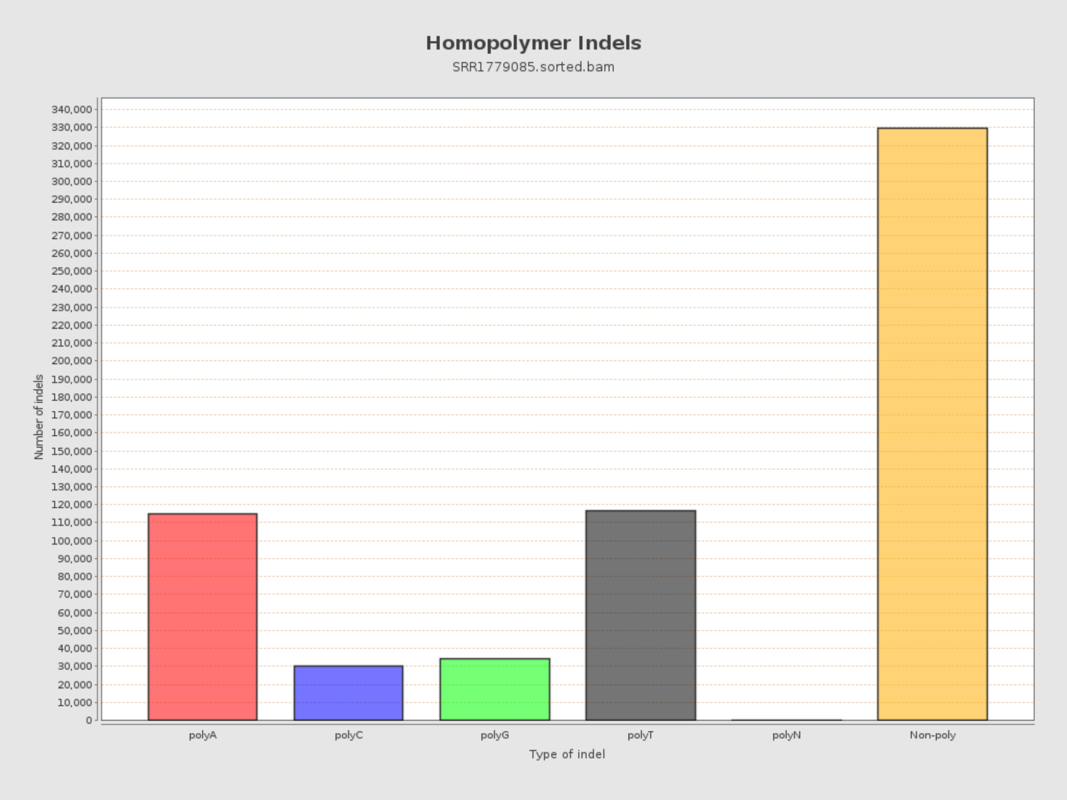
9. Results : Mapped Reads GC-content Distribution



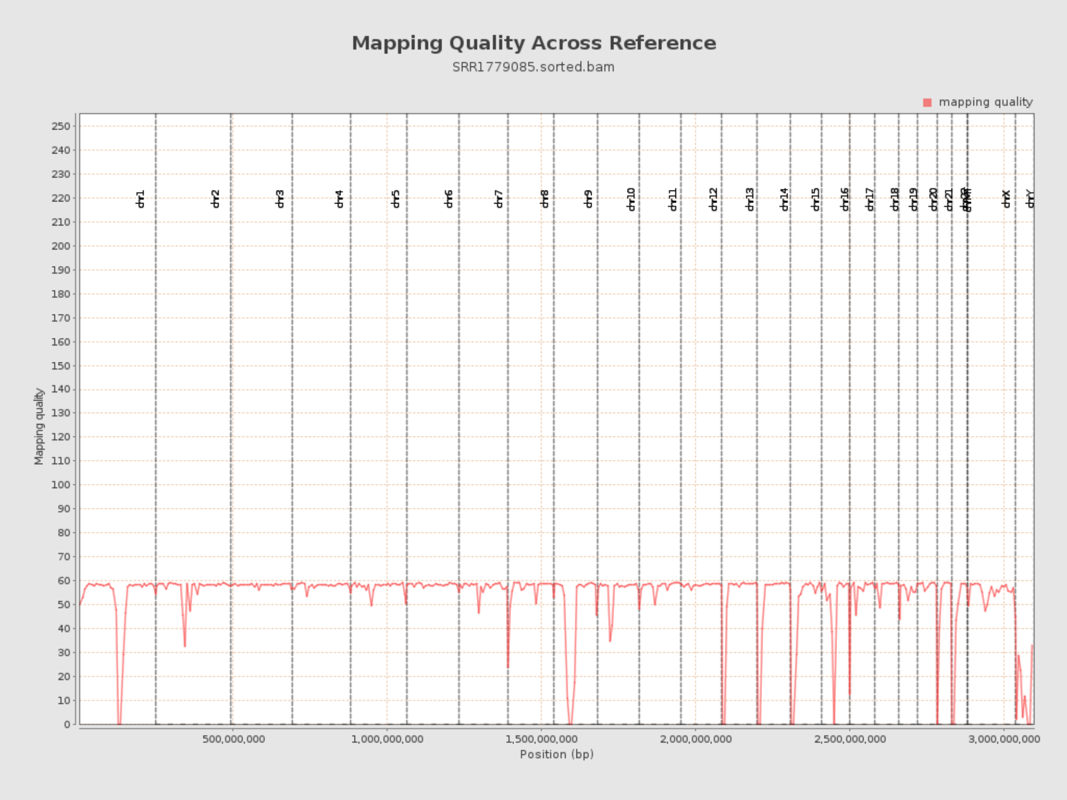
10. Results : Mapped Reads Clipping Profile



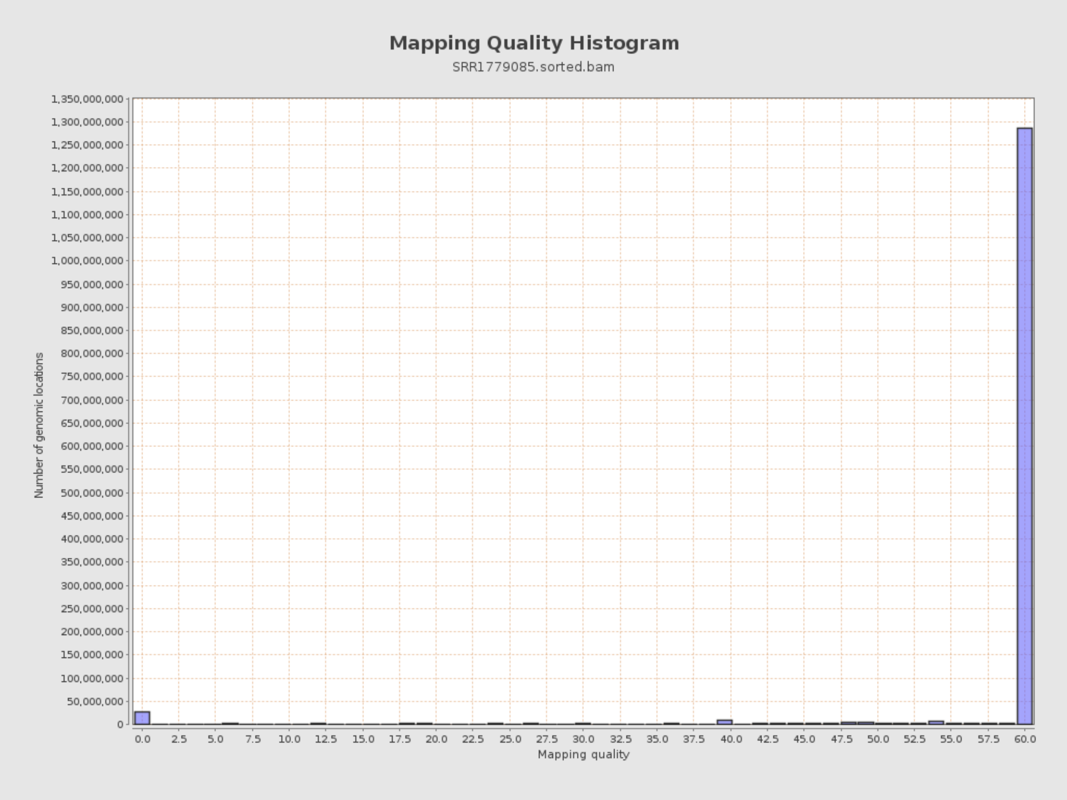
11. Results : Homopolymer Indels



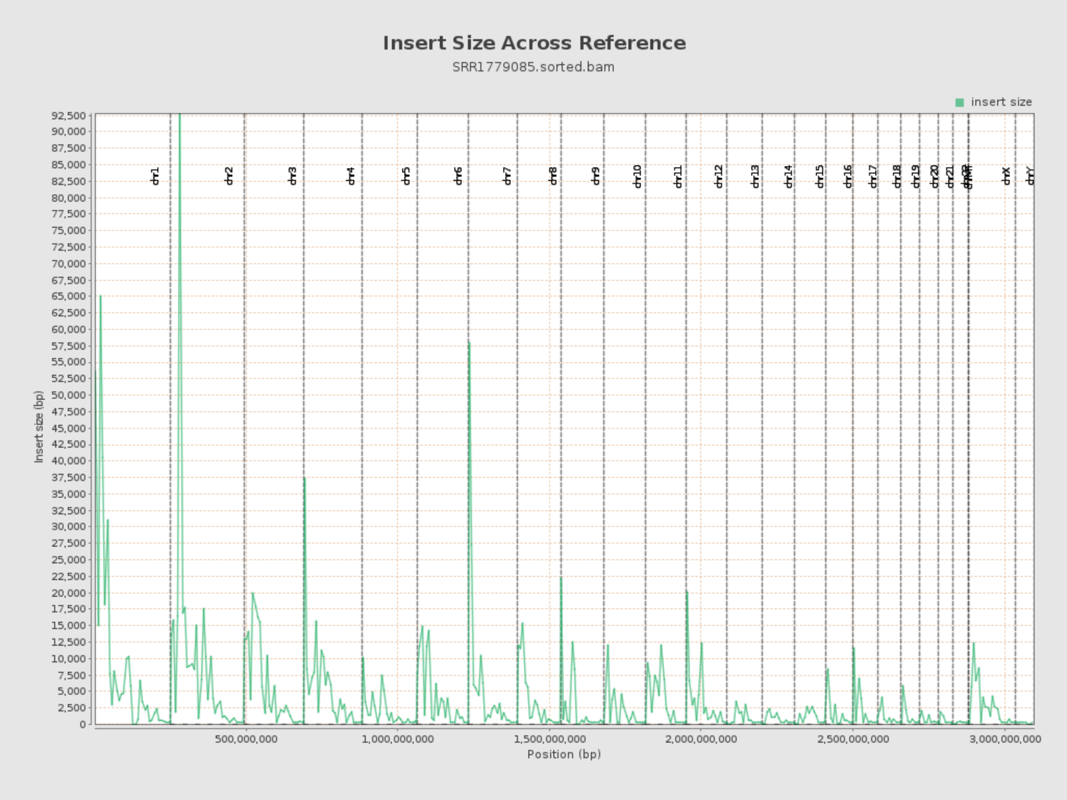
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram