Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 01:06:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779099.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_SRR1779099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779099_1.fastq.gz SRR1779099_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 01:06:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,691,036
Mapped reads	16,974,733 / 95.95%
Unmapped reads	716,303 / 4.05%
Mapped paired reads	16,974,733 / 95.95%
Mapped reads, first in pair	8,543,411 / 48.29%
Mapped reads, second in pair	8,431,322 / 47.66%
Mapped reads, both in pair	16,788,522 / 94.9%
Mapped reads, singletons	186,211 / 1.05%
Secondary alignments	0
Supplementary alignments	96,248 / 0.54%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	533,467 / 3.02%
Duplication rate	2.79%
Clipped reads	1,355,481 / 7.66%

2.2. ACGT Content

Number/percentage of A's	517,698,001 / 30.61%
Number/percentage of C's	327,023,431 / 19.33%
Number/percentage of T's	513,102,372 / 30.34%
Number/percentage of G's	332,902,428 / 19.68%
Number/percentage of N's	683,000 / 0.04%

GC Percentage	39.02%

2.3. Coverage

Mean	0.5465
Standard Deviation	1.6571

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	82,677.1
Standard Deviation	2,741,618.41
P25/Median/P75	146 / 199 / 274

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	7,083,147
Insertions	141,744
Mapped reads with at least one insertion	0.82%
Deletions	175,188
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.51%

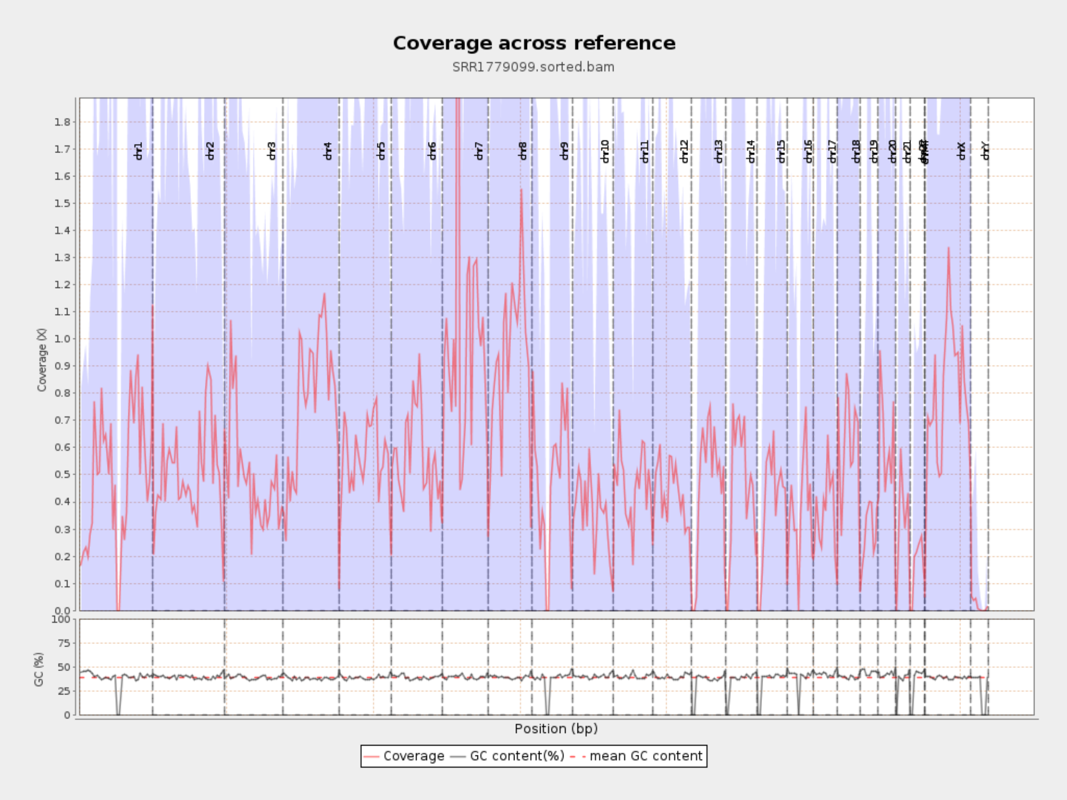
2.7. Chromosome stats

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

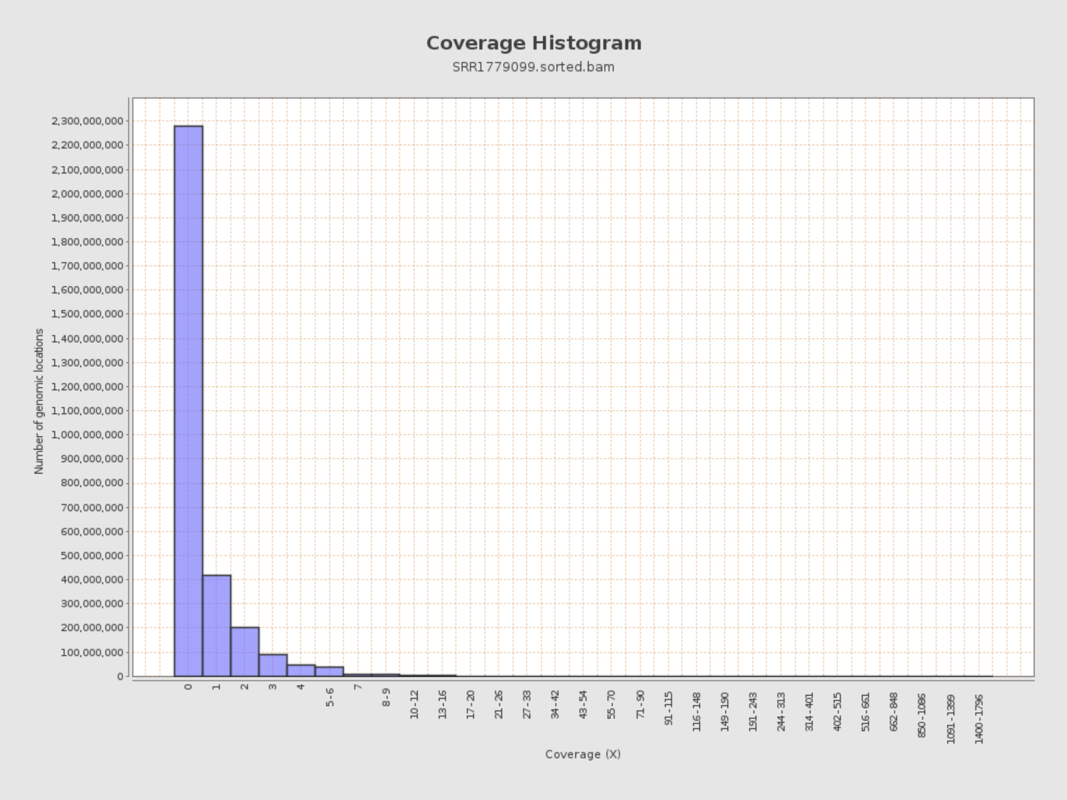
		bases	**coverage**	**deviation**
chr1	249250621	123914034	0.4971	2.1977
chr2	243199373	123762396	0.5089	1.4056
chr3	198022430	96900307	0.4893	1.1369
chr4	191154276	148763682	0.7782	1.5354
chr5	180915260	100727460	0.5568	1.2062
chr6	171115067	98982230	0.5785	1.2616
chr7	159138663	166517829	1.0464	3.3689
chr8	146364022	139544033	0.9534	1.6455
chr9	141213431	65760230	0.4657	1.2469
chr10	135534747	49041011	0.3618	2.9453
chr11	135006516	62287959	0.4614	1.1349
chr12	133851895	57444614	0.4292	1.0782
chr13	115169878	53634542	0.4657	1.1265
chr14	107349540	48891840	0.4554	1.1341
chr15	102531392	39762248	0.3878	1.0963
chr16	90354753	31945169	0.3536	1.0156
chr17	81195210	29044863	0.3577	1.2961
chr18	78077248	48569695	0.6221	1.3527
chr19	59128983	16498622	0.279	1.4556
chr20	63025520	37359996	0.5928	1.3496
chr21	48129895	16667992	0.3463	0.9825
chr22	51304566	8519542	0.1661	0.664
chrMT	16571	811	0.0489	0.2601
chrX	155270560	126205118	0.8128	1.6385

chrY	59373566	1053540	0.0177	0.2805

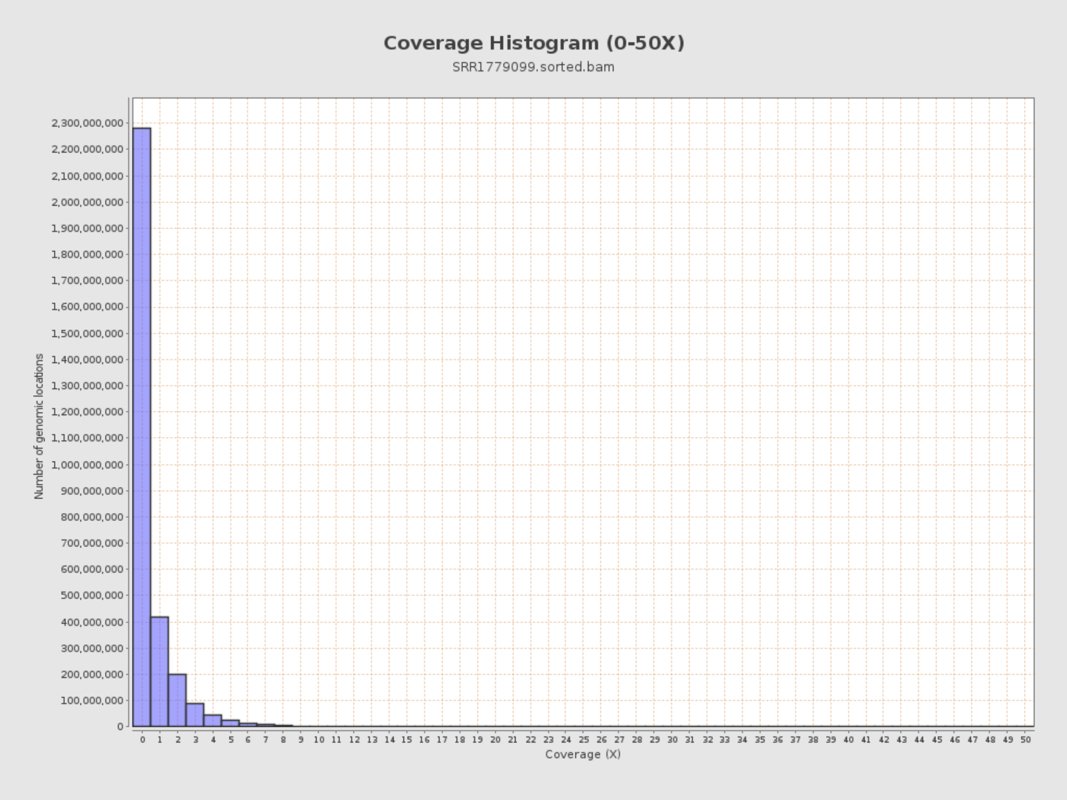
3. Results : Coverage across reference



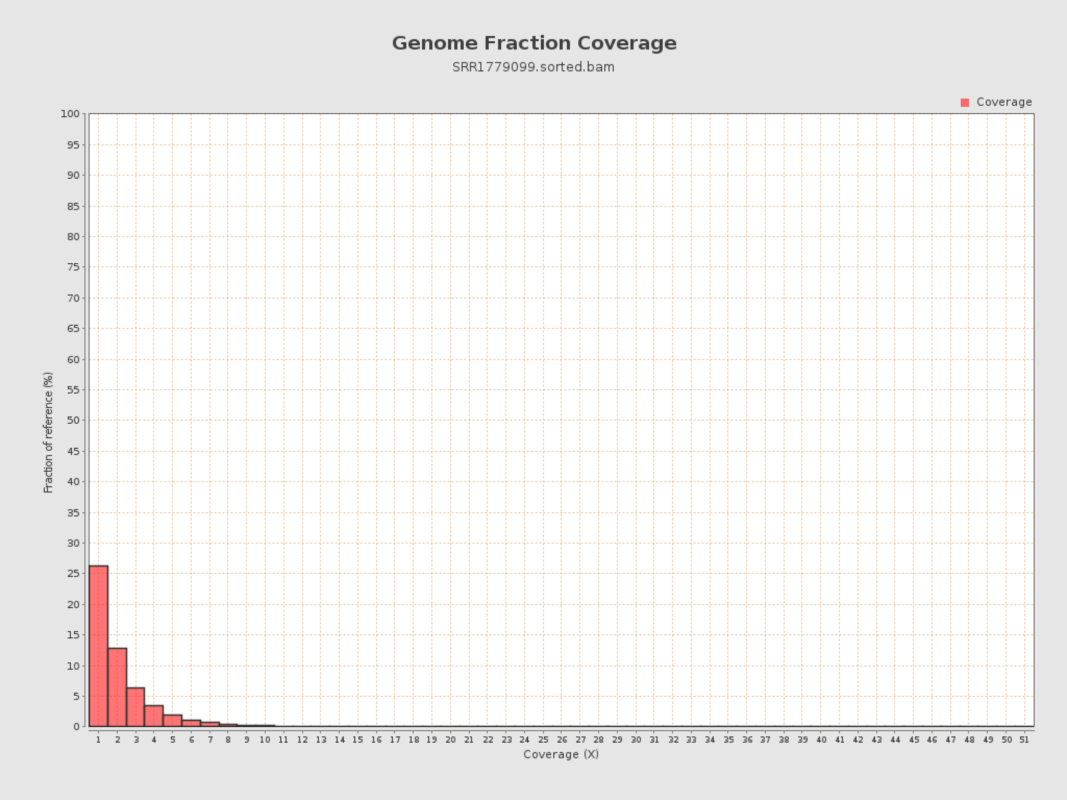
4. Results : Coverage Histogram



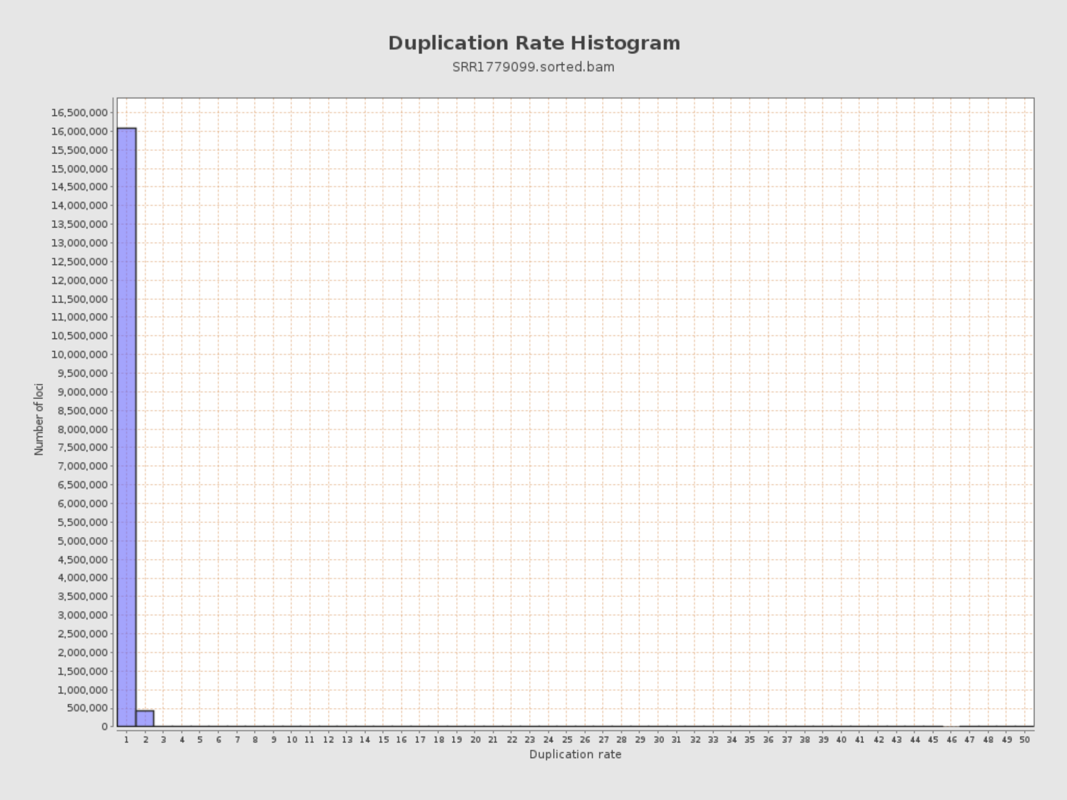
5. Results : Coverage Histogram (0-50X)



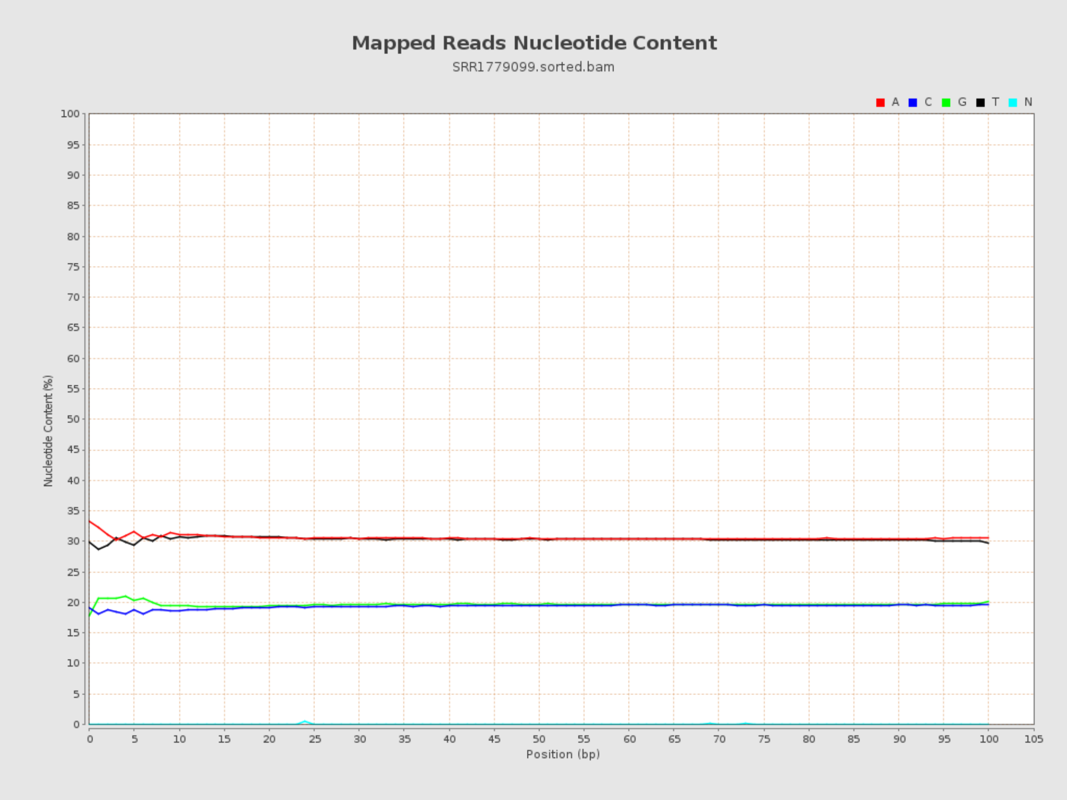
6. Results : Genome Fraction Coverage



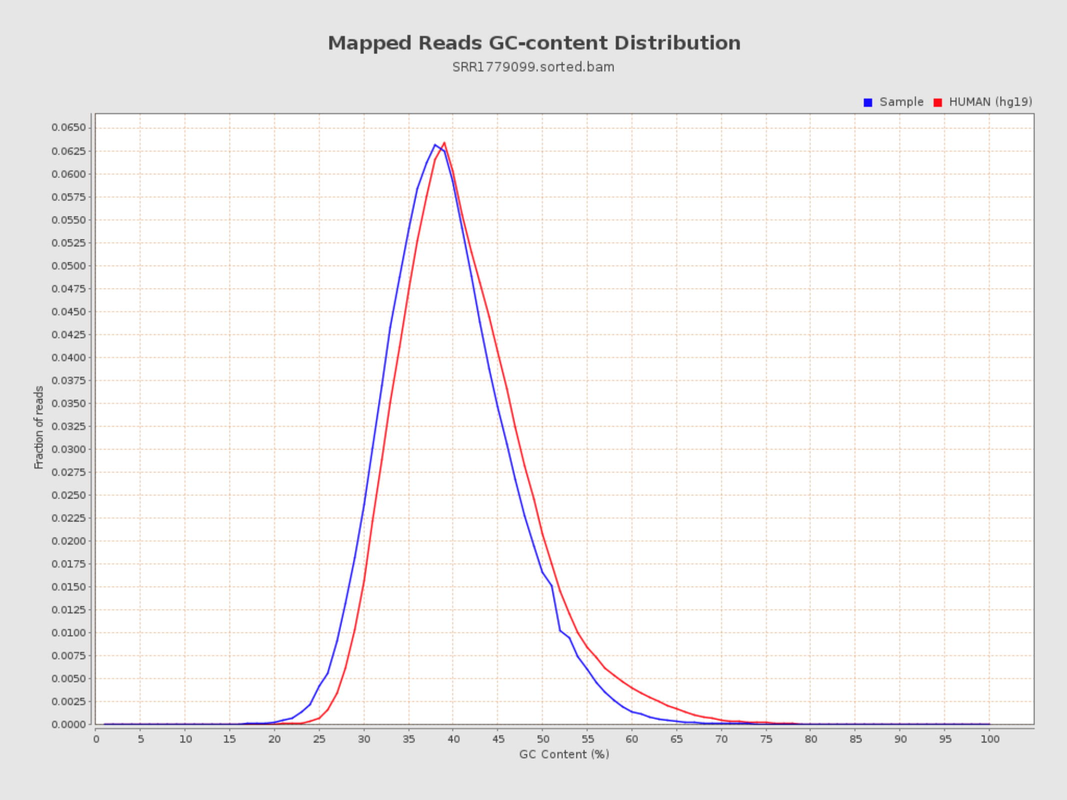
7. Results : Duplication Rate Histogram



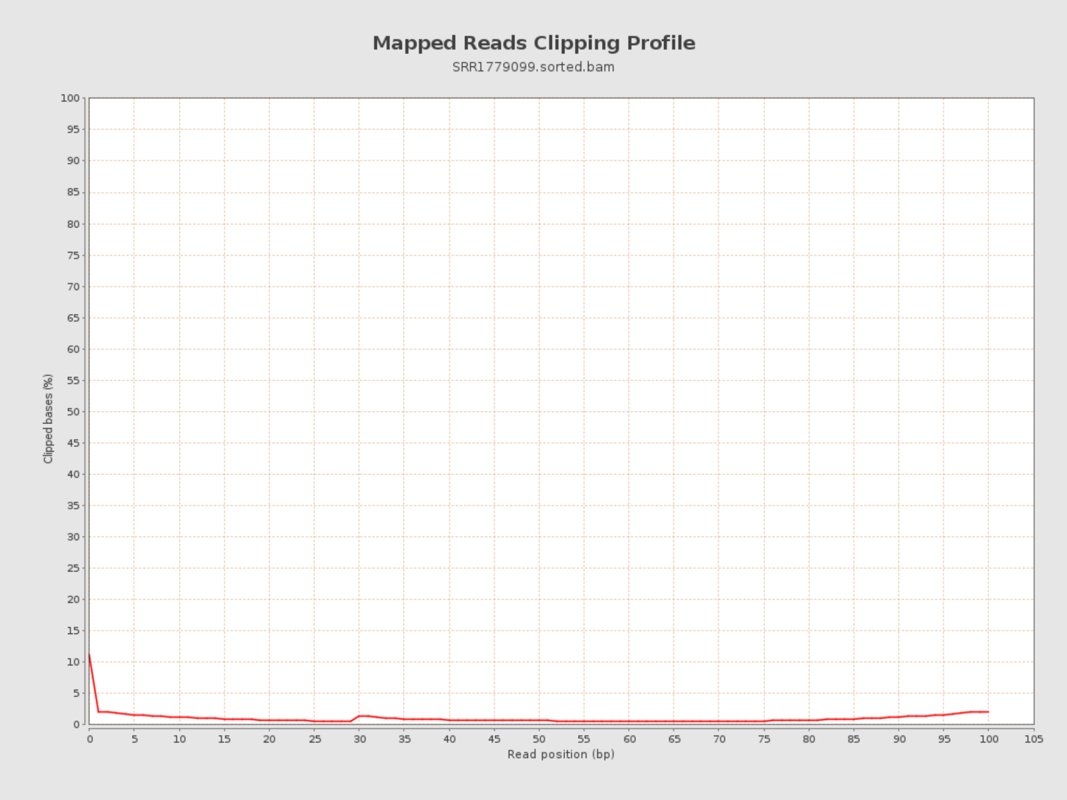
8. Results : Mapped Reads Nucleotide Content



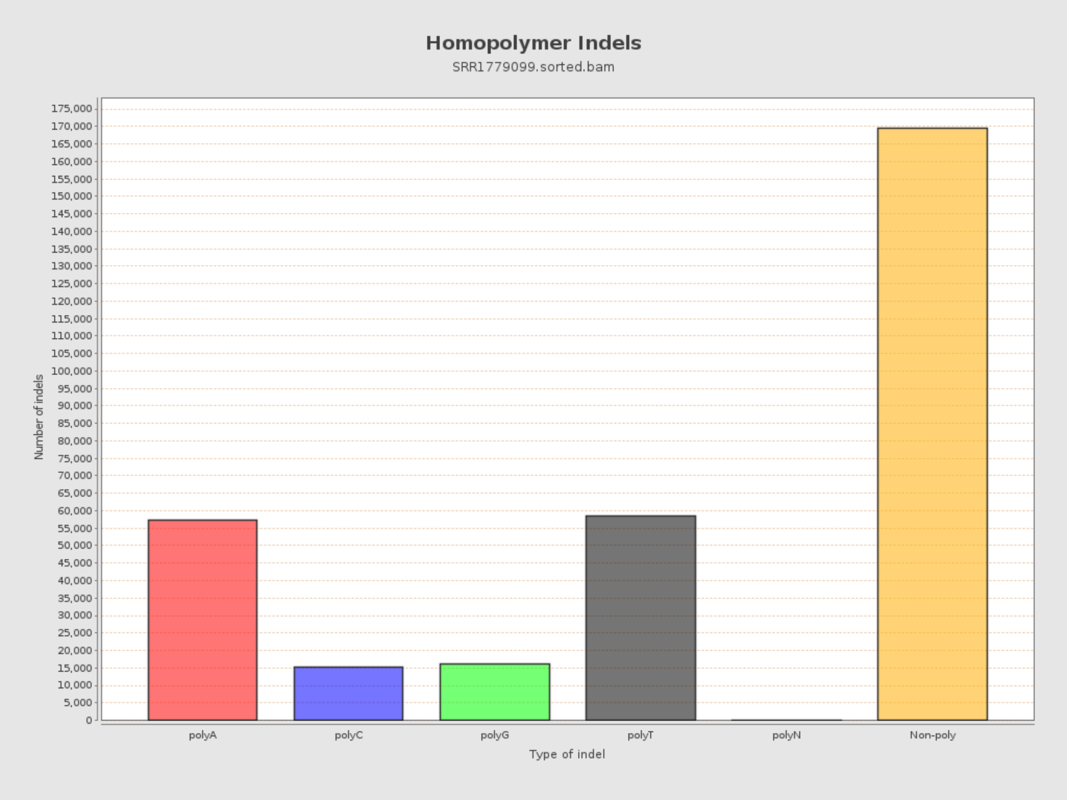
9. Results : Mapped Reads GC-content Distribution



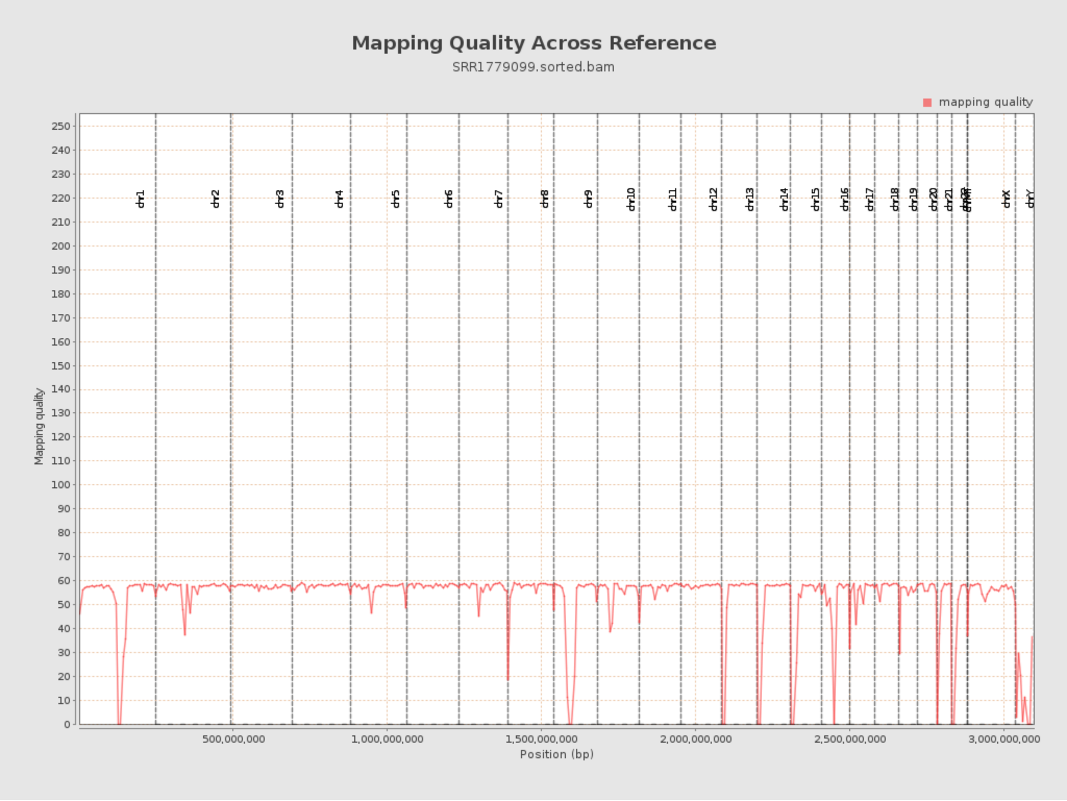
10. Results : Mapped Reads Clipping Profile



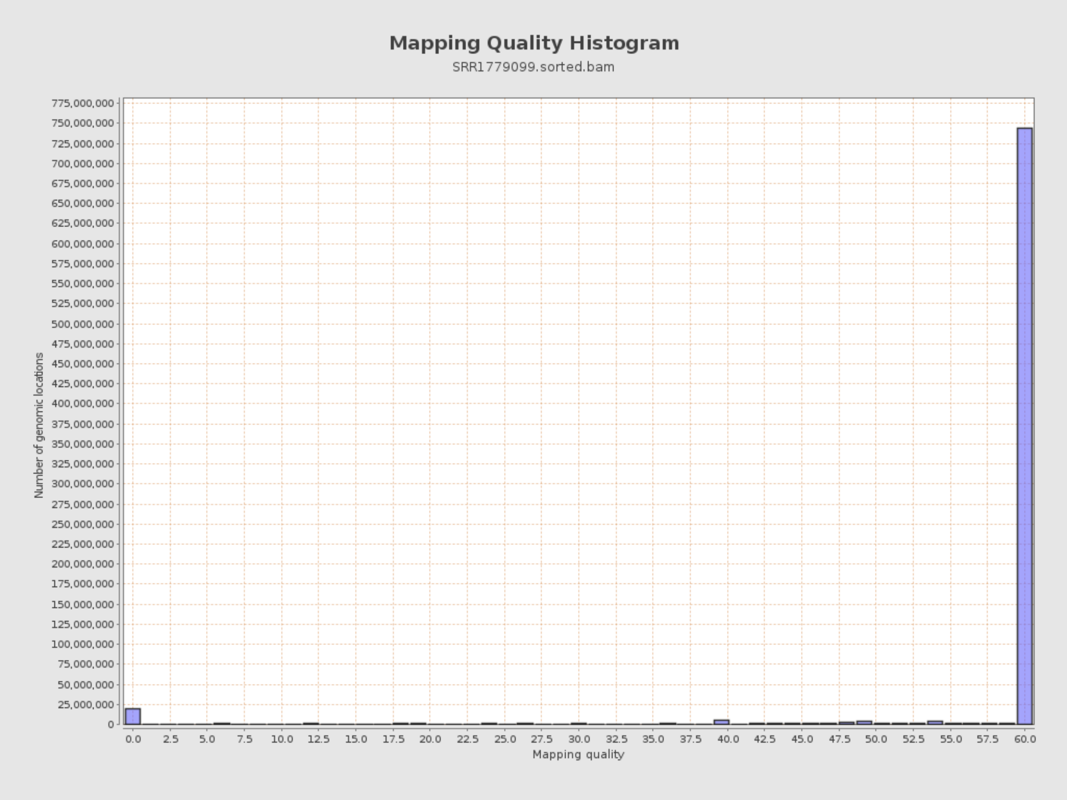
11. Results : Homopolymer Indels



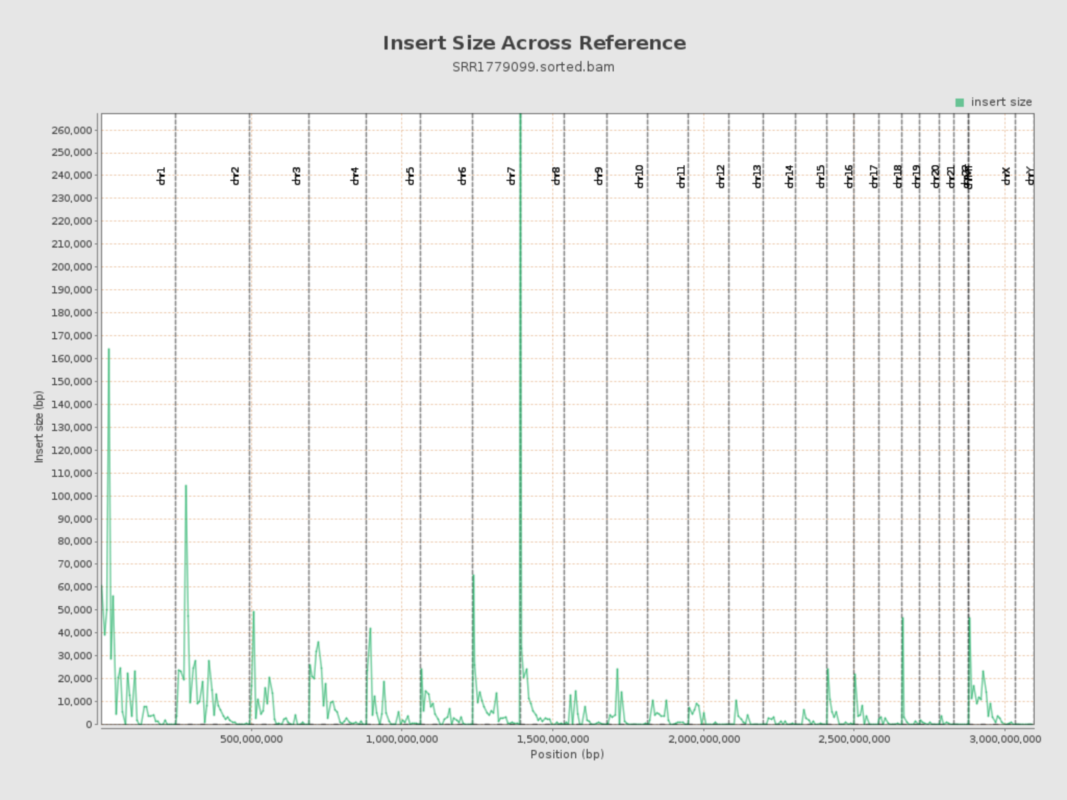
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram