Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 21:17:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779407.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_SRR1779407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779407_1.fastq.gz SRR1779407_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 21:17:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,092,418
Mapped reads	14,713,886 / 97.49%
Unmapped reads	378,532 / 2.51%
Mapped paired reads	14,713,886 / 97.49%
Mapped reads, first in pair	7,402,362 / 49.05%
Mapped reads, second in pair	7,311,524 / 48.45%
Mapped reads, both in pair	14,595,746 / 96.71%
Mapped reads, singletons	118,140 / 0.78%
Secondary alignments	0
Supplementary alignments	51,195 / 0.34%
Read min/max/mean length	30 / 80 / 80.12
Duplicated reads (estimated)	540,294 / 3.58%
Duplication rate	3.29%
Clipped reads	578,182 / 3.83%

2.2. ACGT Content

Number/percentage of A's	356,579,687 / 30.47%
Number/percentage of C's	228,426,415 / 19.52%
Number/percentage of T's	350,811,791 / 29.98%
Number/percentage of G's	234,093,718 / 20.01%
Number/percentage of N's	258,512 / 0.02%

GC Percentage	39.53%

2.3. Coverage

Mean	0.3781
Standard Deviation	1.4928

2.4. Mapping Quality

Mean Mapping Quality	53.42

2.5. Insert size

Mean	97,341.34
Standard Deviation	2,947,579.64
P25/Median/P75	145 / 185 / 235

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,798,205
Insertions	102,683
Mapped reads with at least one insertion	0.69%
Deletions	116,465
Mapped reads with at least one deletion	0.78%
Homopolymer indels	47.14%

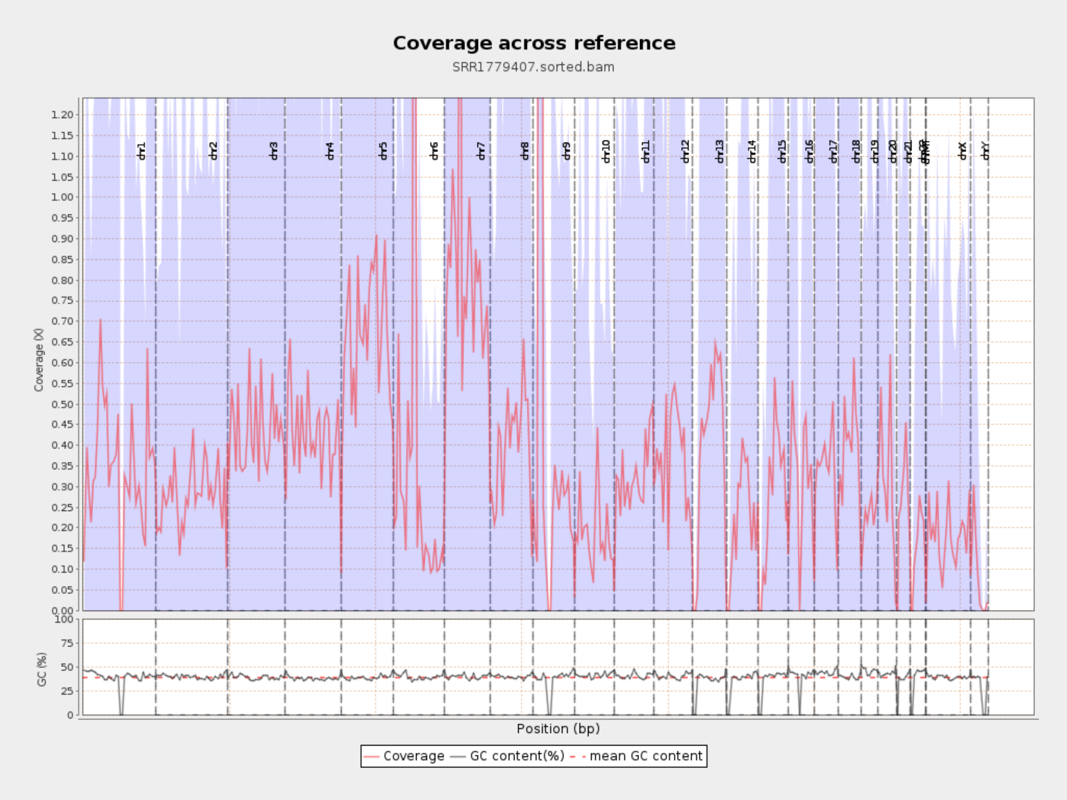
2.7. Chromosome stats

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

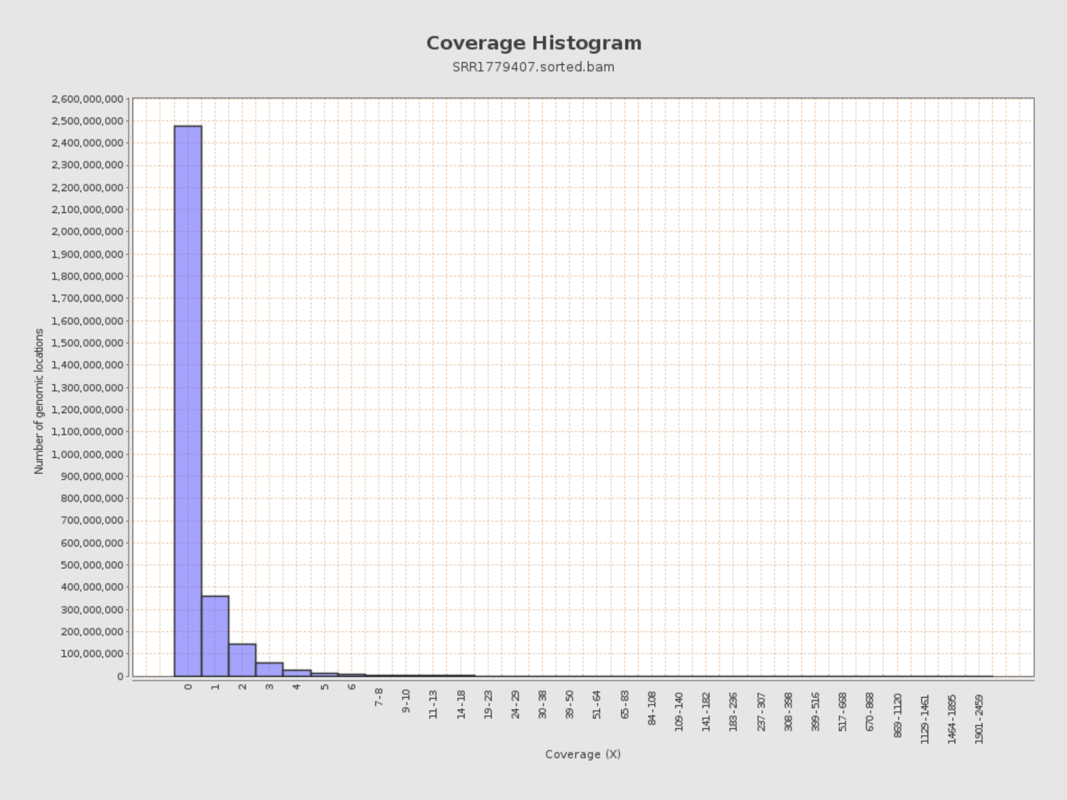
		bases	coverage	deviation
chr1	249250621	84931718	0.3407	2.7176
chr2	243199373	67423659	0.2772	0.8777
chr3	198022430	85617573	0.4324	0.9769
chr4	191154276	82007584	0.429	0.9664
chr5	180915260	120044786	0.6635	1.2164
chr6	171115067	57707142	0.3372	1.7554
chr7	159138663	132327380	0.8315	2.2728
chr8	146364022	58854791	0.4021	0.9966
chr9	141213431	88030055	0.6234	2.7999
chr10	135534747	25723665	0.1898	1.7526
chr11	135006516	43680748	0.3235	0.9451
chr12	133851895	49375669	0.3689	0.9272
chr13	115169878	46910045	0.4073	0.9376
chr14	107349540	23846085	0.2221	0.7059
chr15	102531392	27025946	0.2636	0.7744
chr16	90354753	28275460	0.3129	0.8501
chr17	81195210	28495884	0.351	0.936
chr18	78077248	31596351	0.4047	1.4075
chr19	59128983	13707985	0.2318	1.9222
chr20	63025520	20180796	0.3202	0.8578
chr21	48129895	12793314	0.2658	0.7871
chr22	51304566	8047981	0.1569	0.6004
chrMT	16571	320	0.0193	0.1376
chrX	155270560	28486431	0.1835	0.6351

chrY	59373566	5319195	0.0896	0.4624

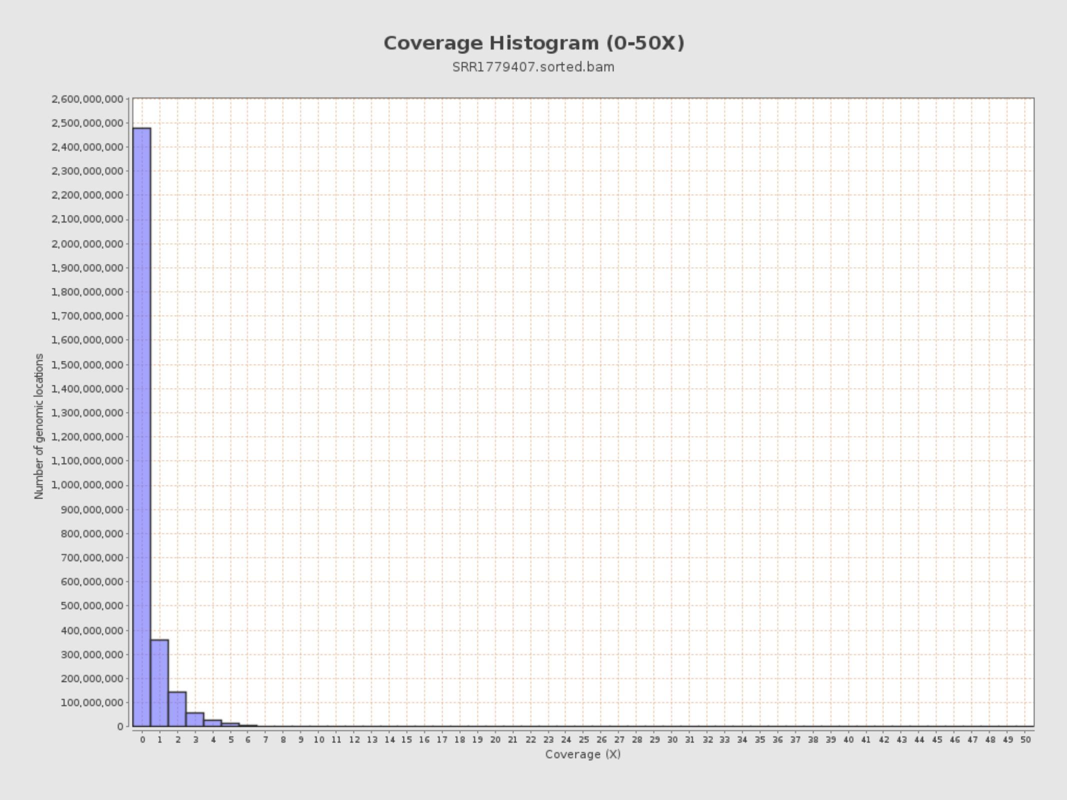
3. Results : Coverage across reference



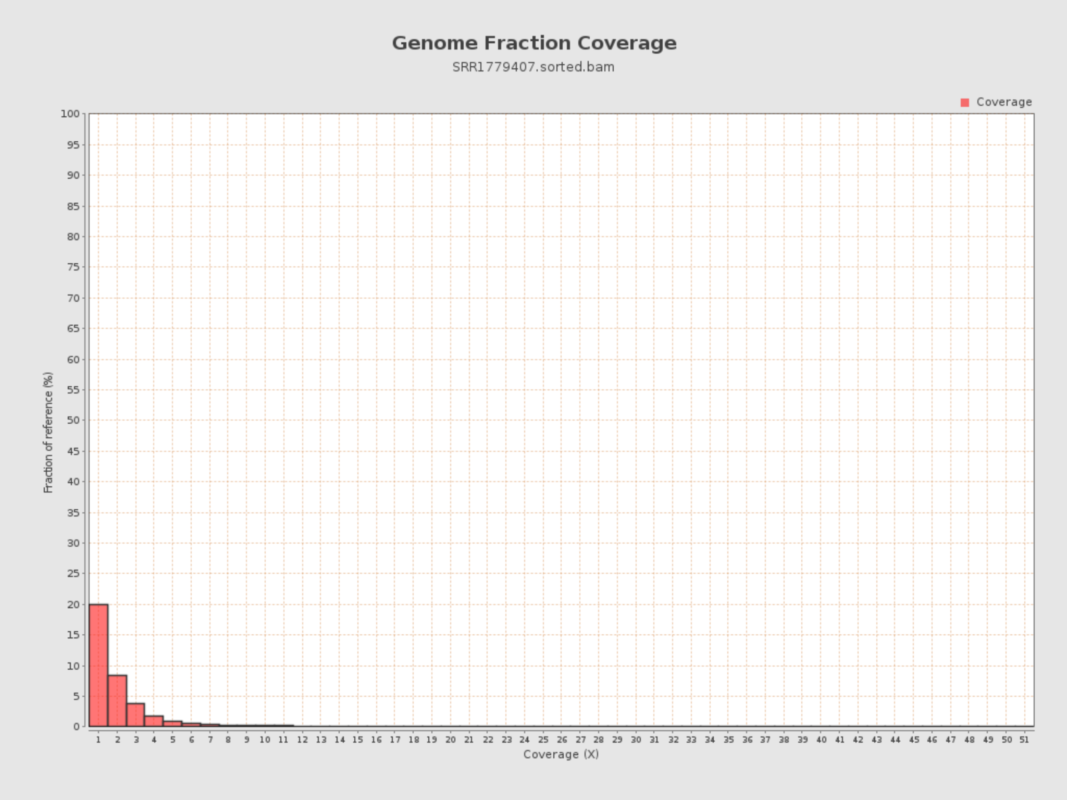
4. Results : Coverage Histogram



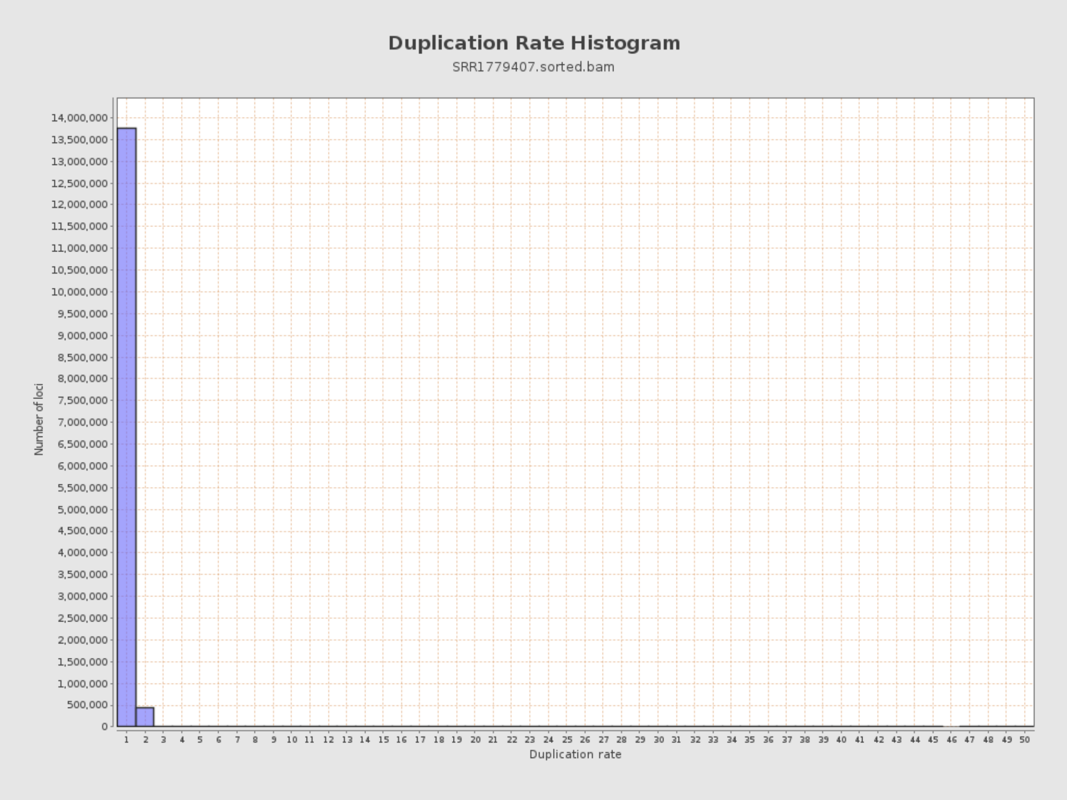
5. Results : Coverage Histogram (0-50X)



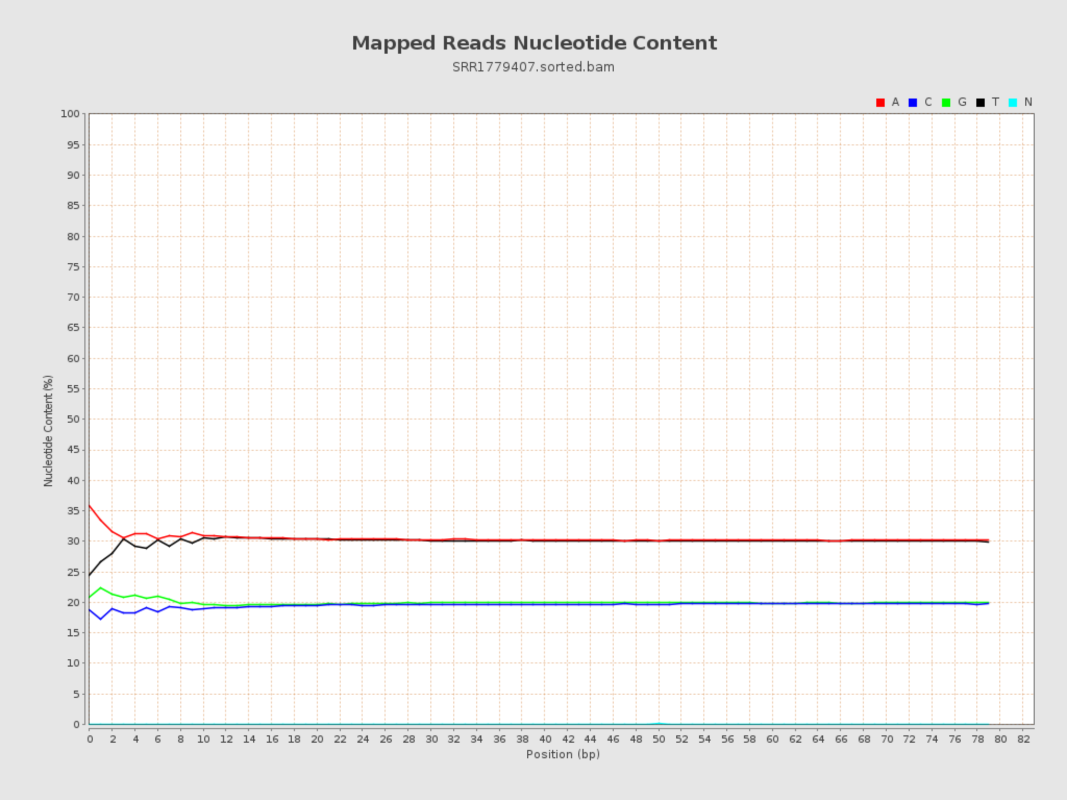
6. Results : Genome Fraction Coverage



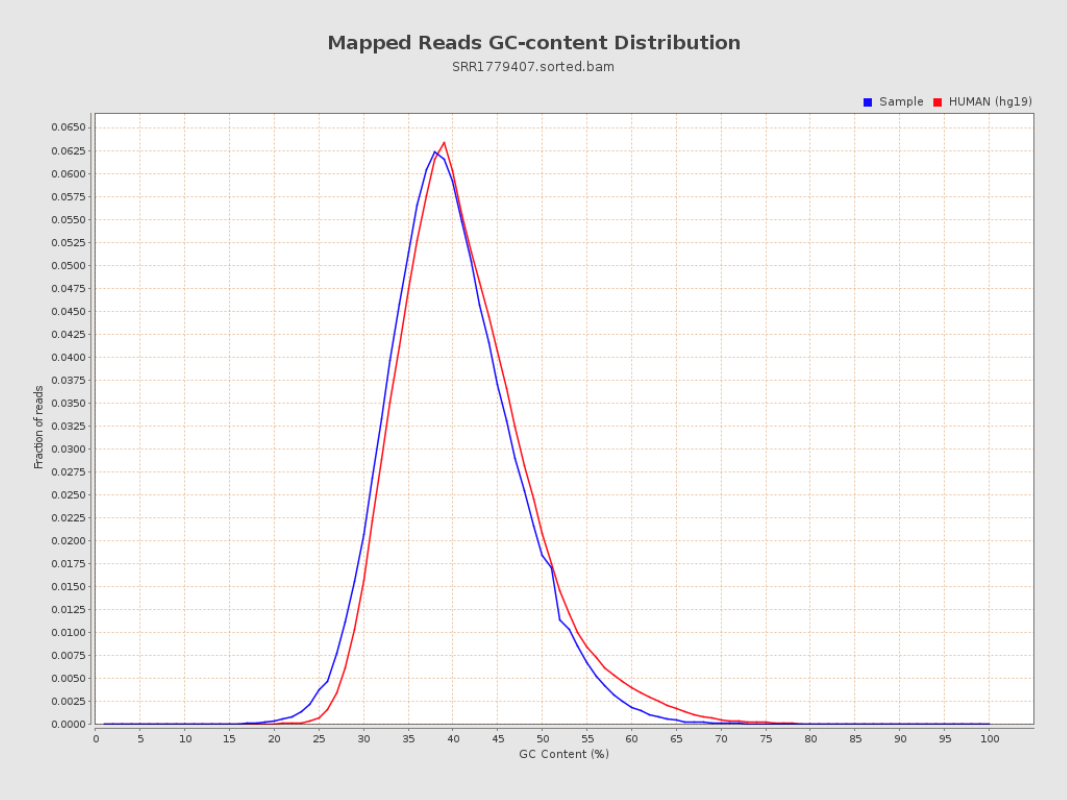
7. Results : Duplication Rate Histogram



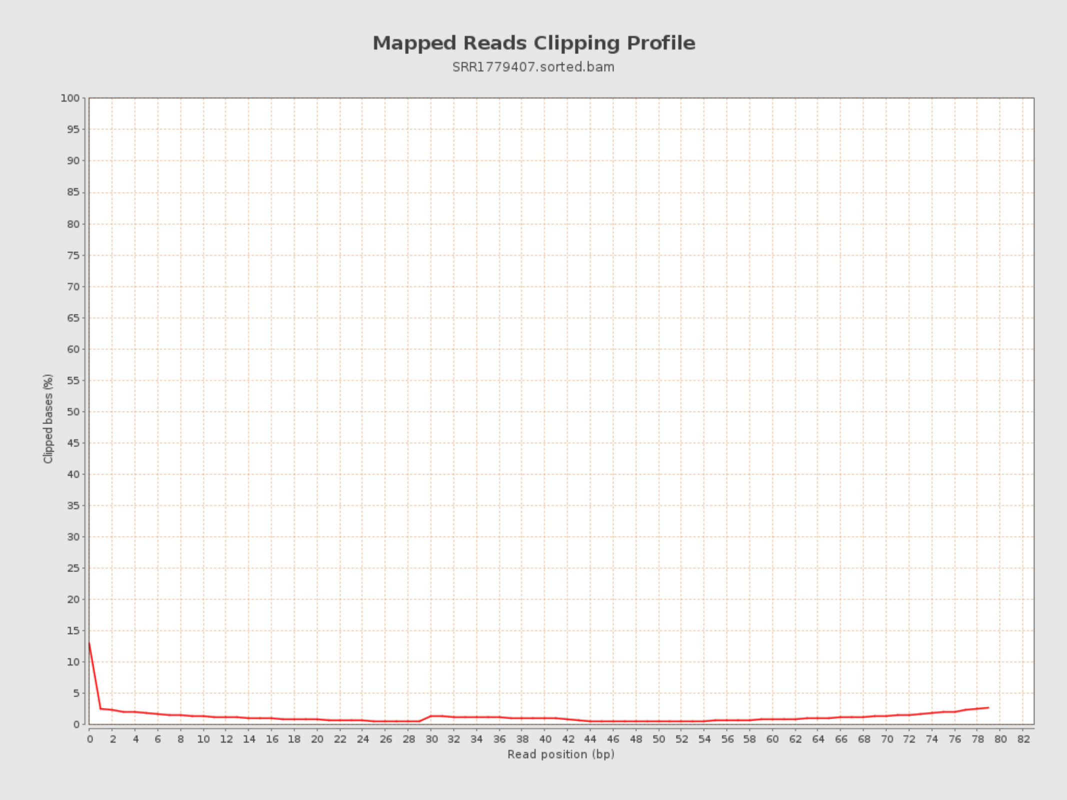
8. Results : Mapped Reads Nucleotide Content



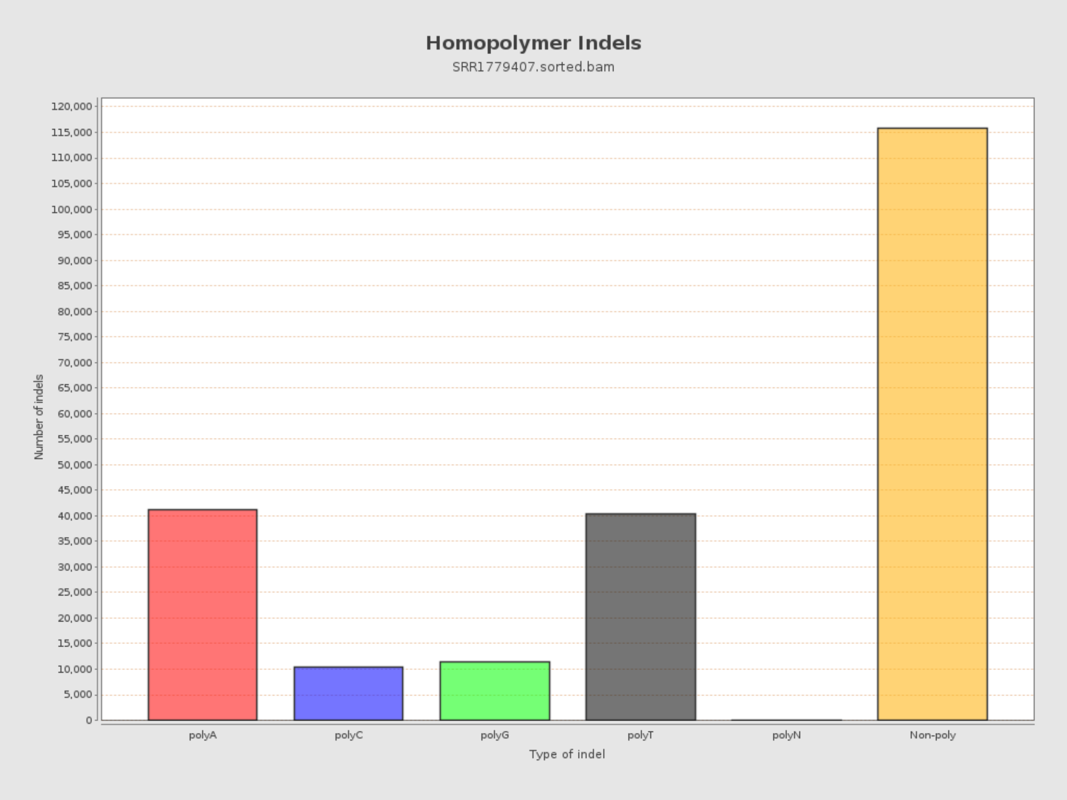
9. Results : Mapped Reads GC-content Distribution



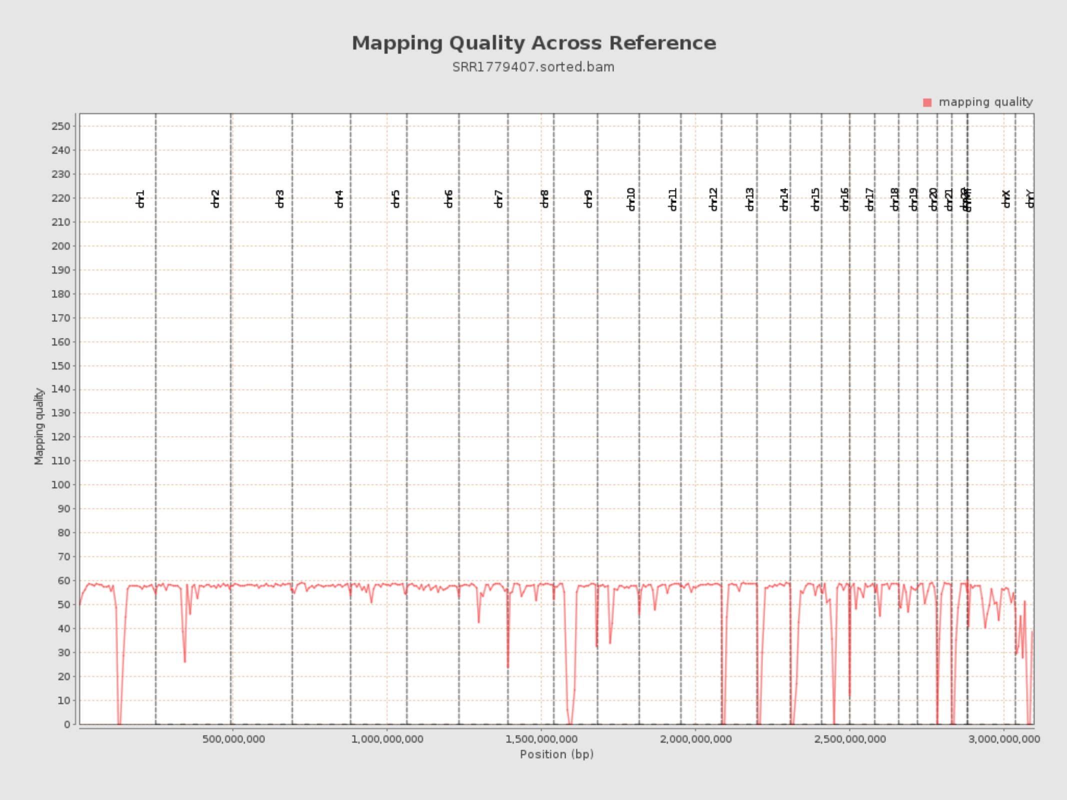
10. Results : Mapped Reads Clipping Profile



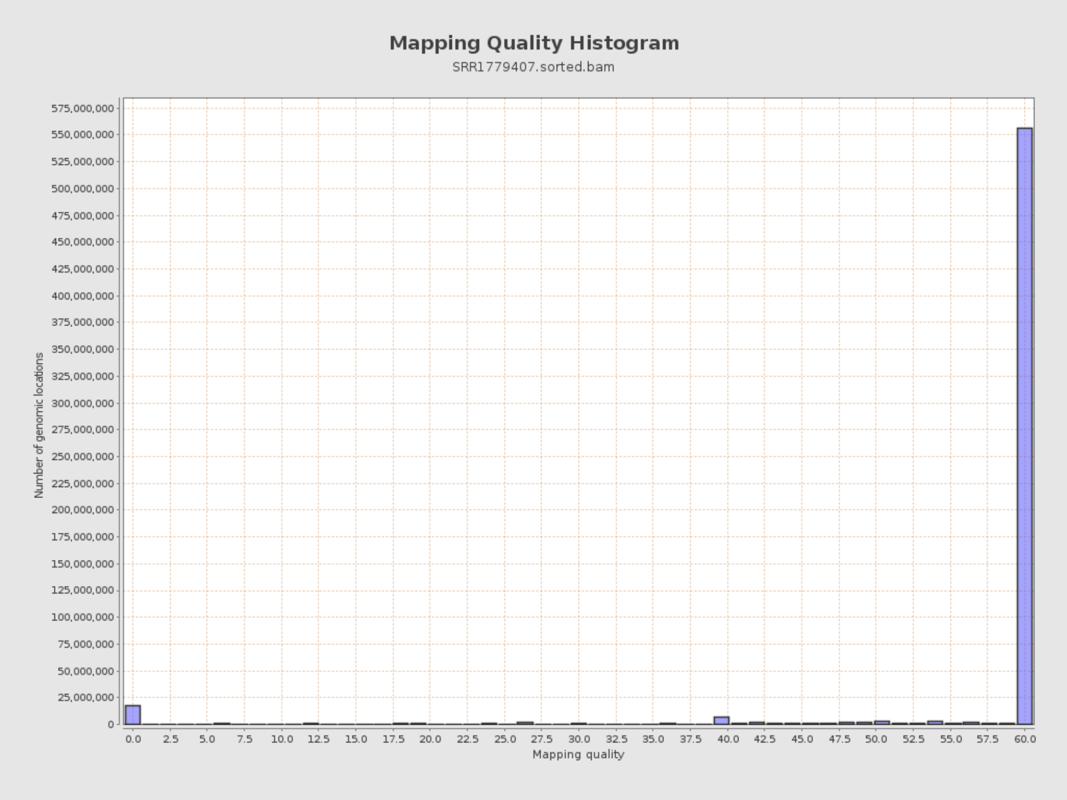
11. Results : Homopolymer Indels



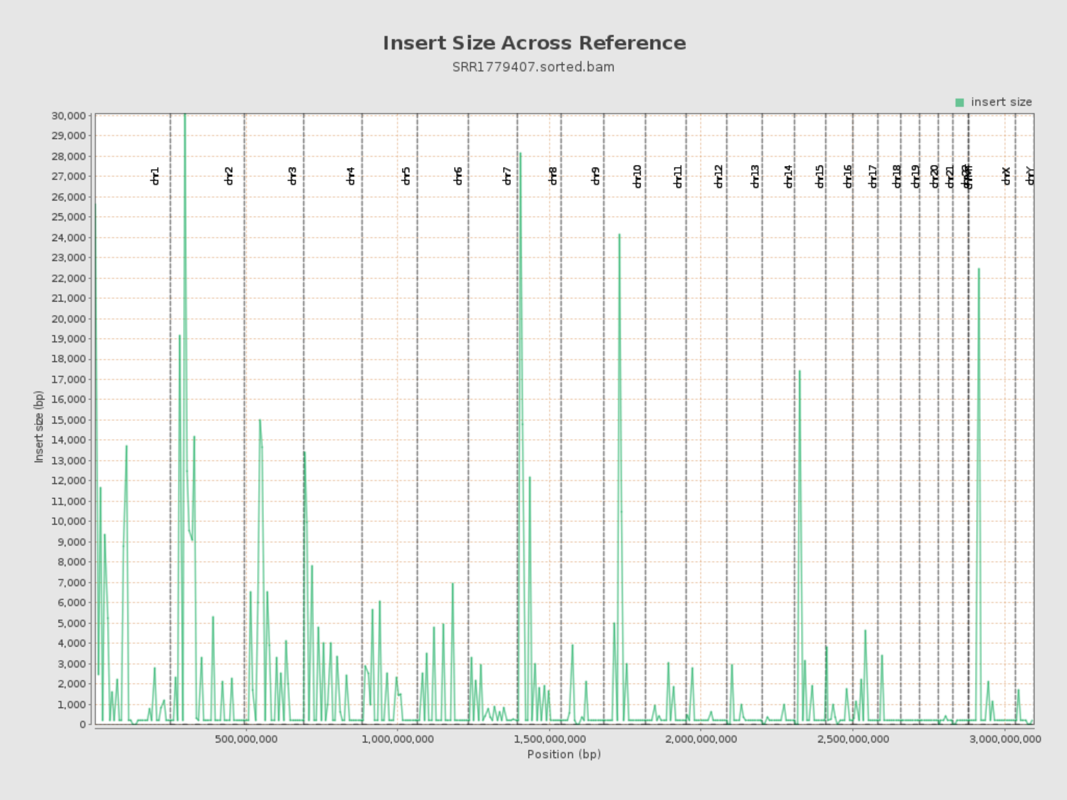
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram