Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 18:52:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779226.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_SRR1779226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779226_1.fastq.gz SRR1779226_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 18:52:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,764,110
Mapped reads	8,457,627 / 96.5%
Unmapped reads	306,483 / 3.5%
Mapped paired reads	8,457,627 / 96.5%
Mapped reads, first in pair	4,262,236 / 48.63%
Mapped reads, second in pair	4,195,391 / 47.87%
Mapped reads, both in pair	8,377,994 / 95.59%
Mapped reads, singletons	79,633 / 0.91%
Secondary alignments	0
Supplementary alignments	19,907 / 0.23%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	108,219 / 1.23%
Duplication rate	1.15%
Clipped reads	292,192 / 3.33%

2.2. ACGT Content

Number/percentage of A's	205,754,272 / 30.58%
Number/percentage of C's	129,724,483 / 19.28%
Number/percentage of T's	205,219,946 / 30.5%
Number/percentage of G's	131,929,516 / 19.61%
Number/percentage of N's	129,669 / 0.02%

GC Percentage	38.89%

2.3. Coverage

Mean	0.2174
Standard Deviation	0.7647

2.4. Mapping Quality

Mean Mapping Quality	53

2.5. Insert size

Mean	44,590.76
Standard Deviation	1,990,378.99
P25/Median/P75	146 / 198 / 272

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	2,614,356
Insertions	49,993
Mapped reads with at least one insertion	0.59%
Deletions	62,994
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.62%

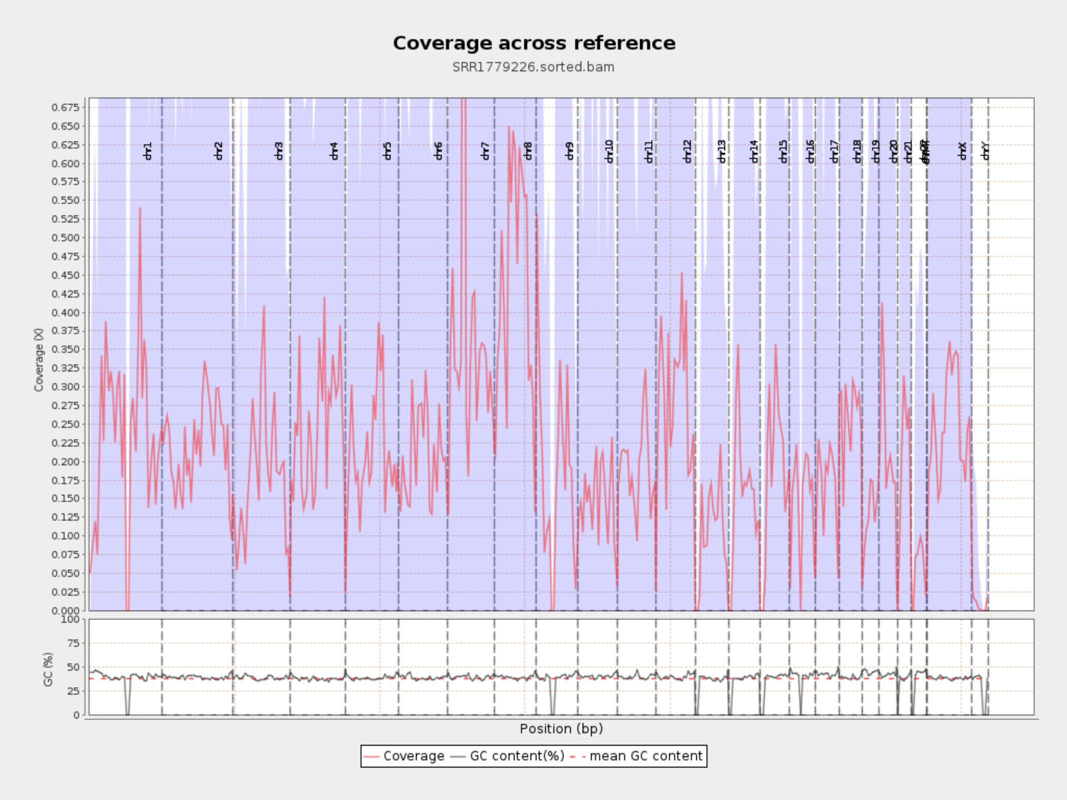
2.7. Chromosome stats

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

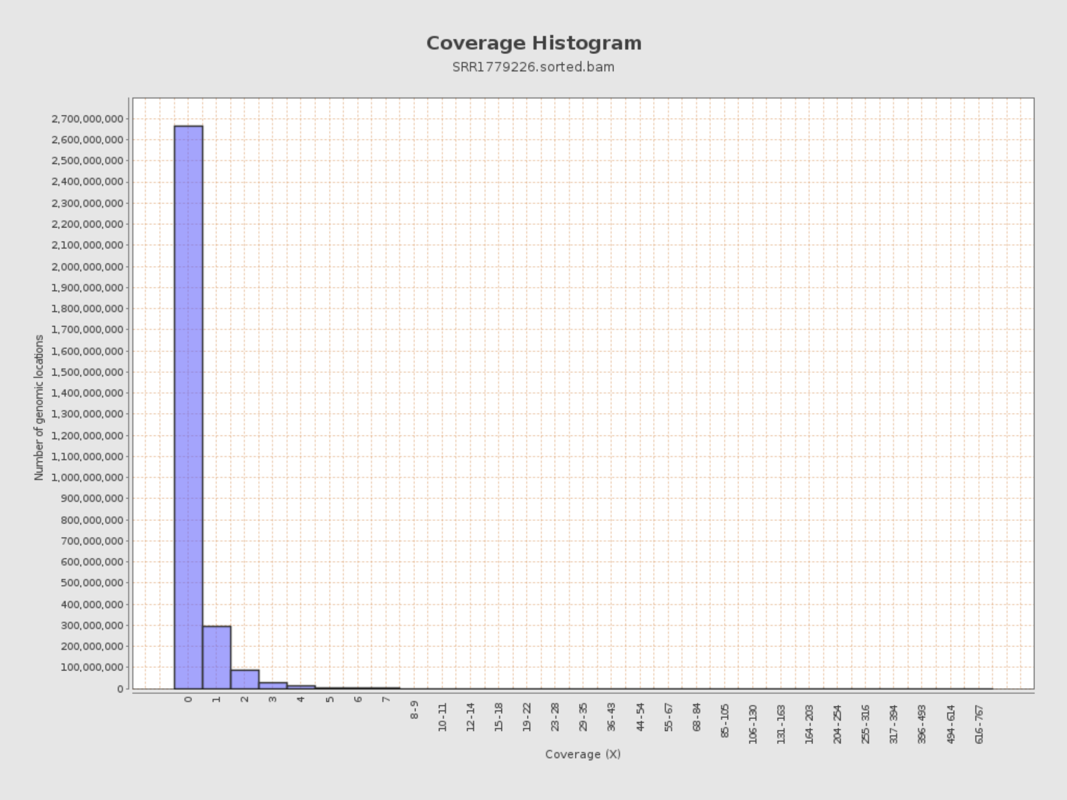
		bases	coverage	deviation
chr1	249250621	58600354	0.2351	1.043
chr2	243199373	53832422	0.2214	0.647
chr3	198022430	35880157	0.1812	0.5918
chr4	191154276	47699981	0.2495	0.7159
chr5	180915260	38647625	0.2136	0.638
chr6	171115067	35660276	0.2084	0.633
chr7	159138663	60566685	0.3806	1.3752
chr8	146364022	64878224	0.4433	0.9541
chr9	141213431	25076799	0.1776	0.609
chr10	135534747	20529355	0.1515	1.061
chr11	135006516	25698089	0.1903	0.6033
chr12	133851895	38372388	0.2867	0.7426
chr13	115169878	12026965	0.1044	0.4185
chr14	107349540	16862560	0.1571	0.5574
chr15	102531392	18824716	0.1836	0.6014
chr16	90354753	13248391	0.1466	0.5101
chr17	81195210	13424918	0.1653	0.5697
chr18	78077248	20704839	0.2652	0.7478
chr19	59128983	7713573	0.1305	0.7092
chr20	63025520	14101027	0.2237	0.6526
chr21	48129895	9197532	0.1911	0.5939
chr22	51304566	2922388	0.057	0.3007
chrMT	16571	882	0.0532	0.3339
chrX	155270560	37902911	0.2441	0.7231

chrY	59373566	514962	0.0087	0.1266

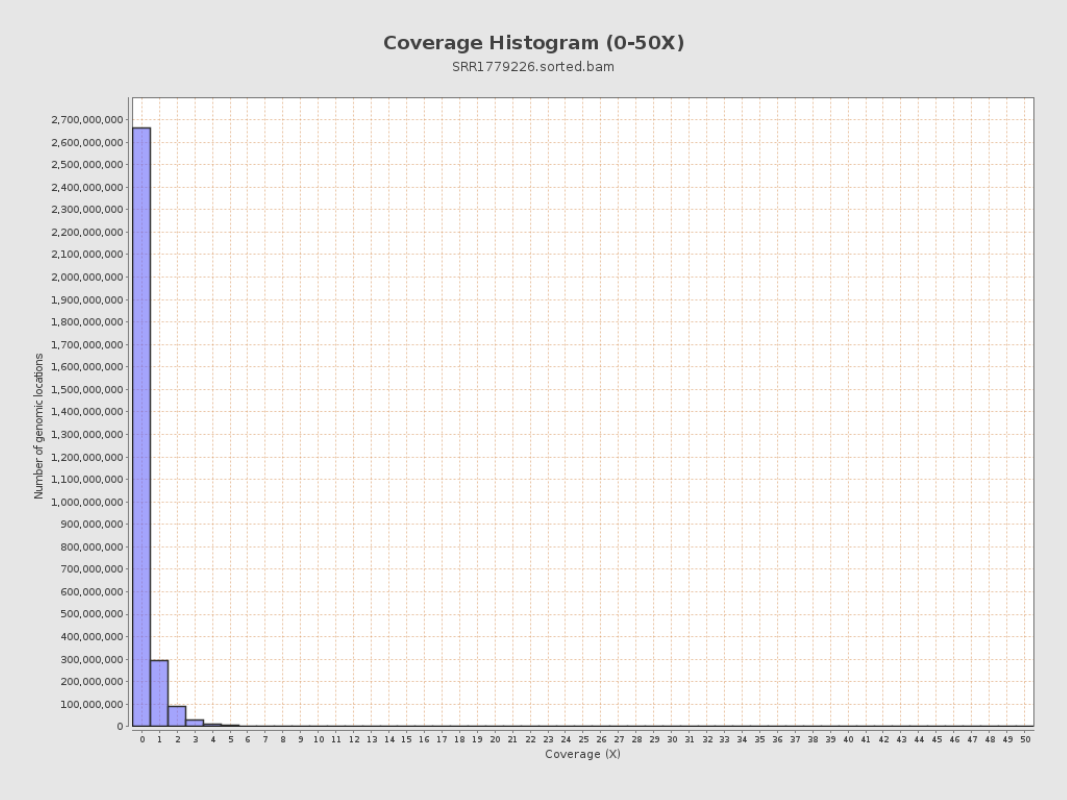
3. Results : Coverage across reference



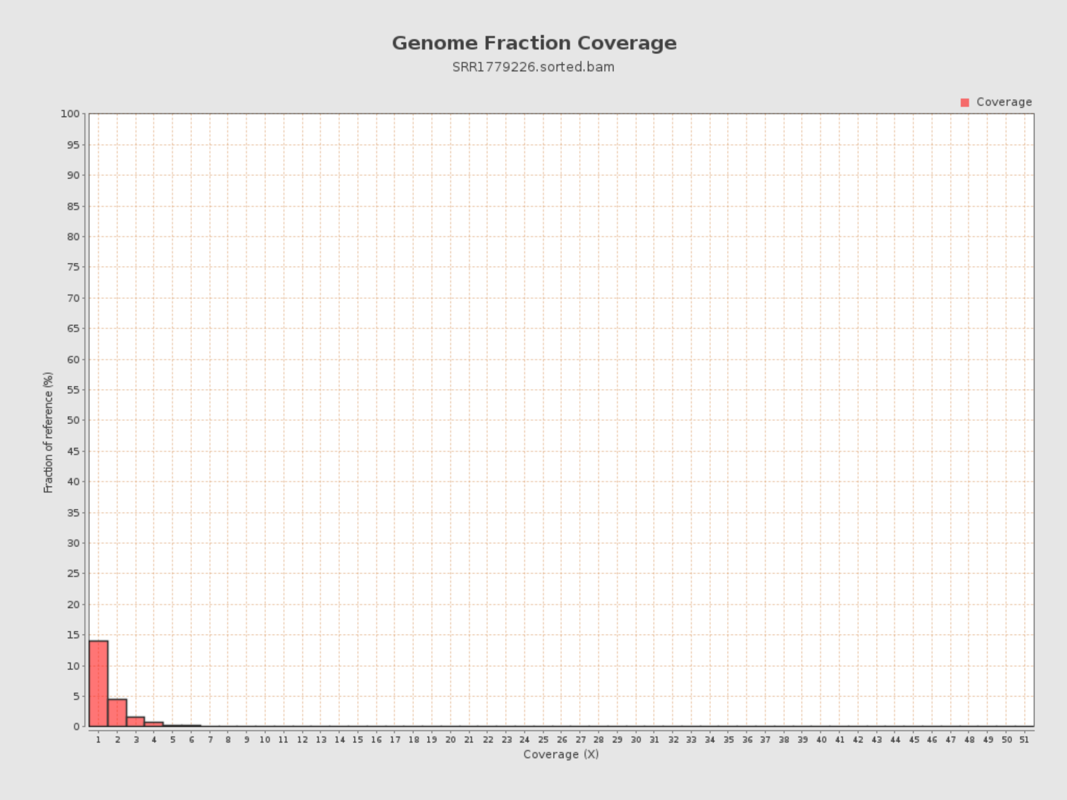
4. Results : Coverage Histogram



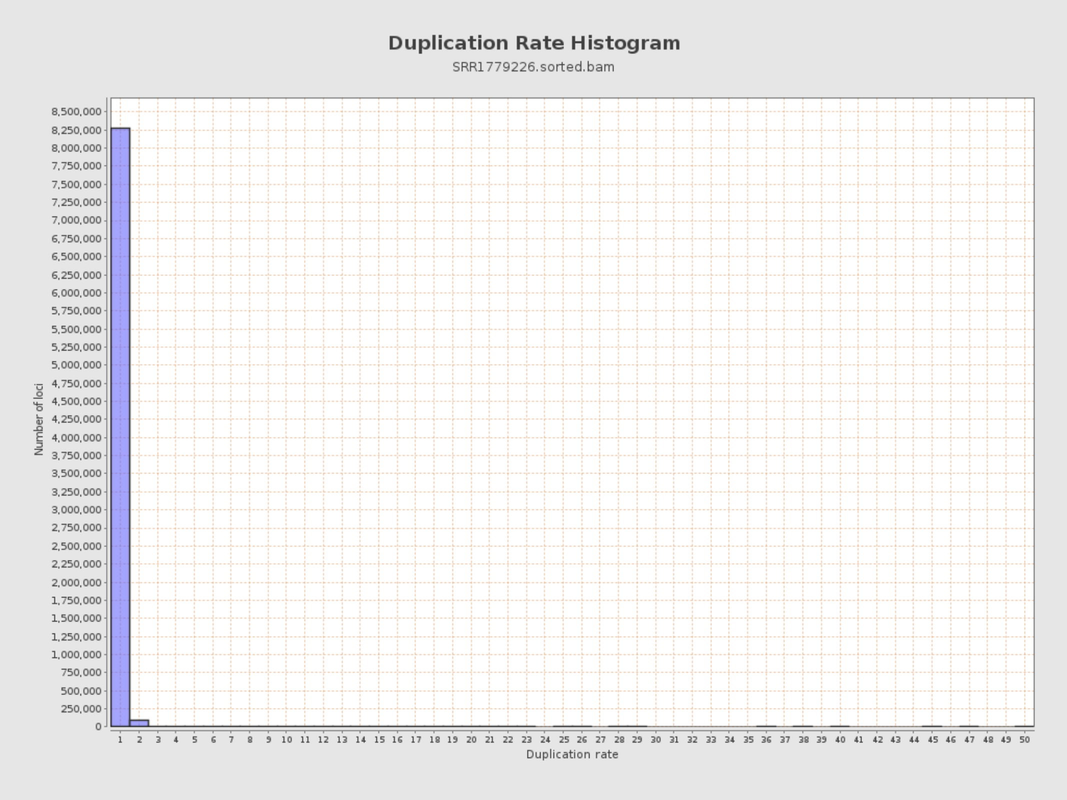
5. Results : Coverage Histogram (0-50X)



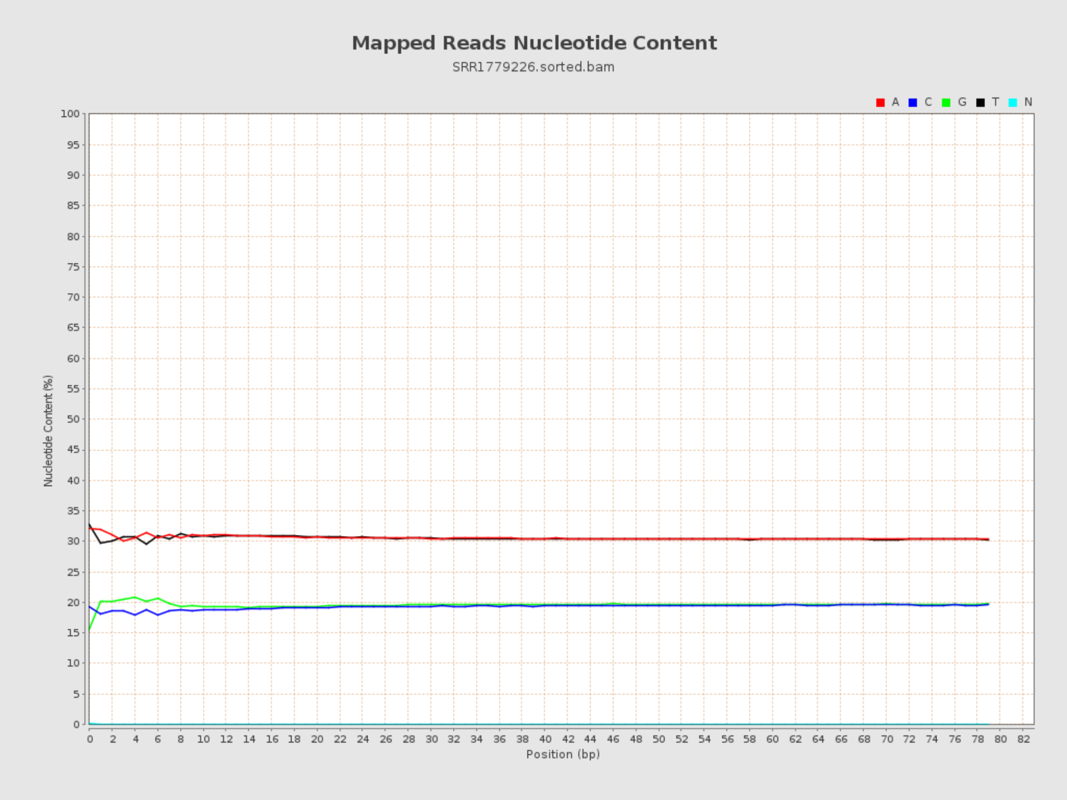
6. Results : Genome Fraction Coverage



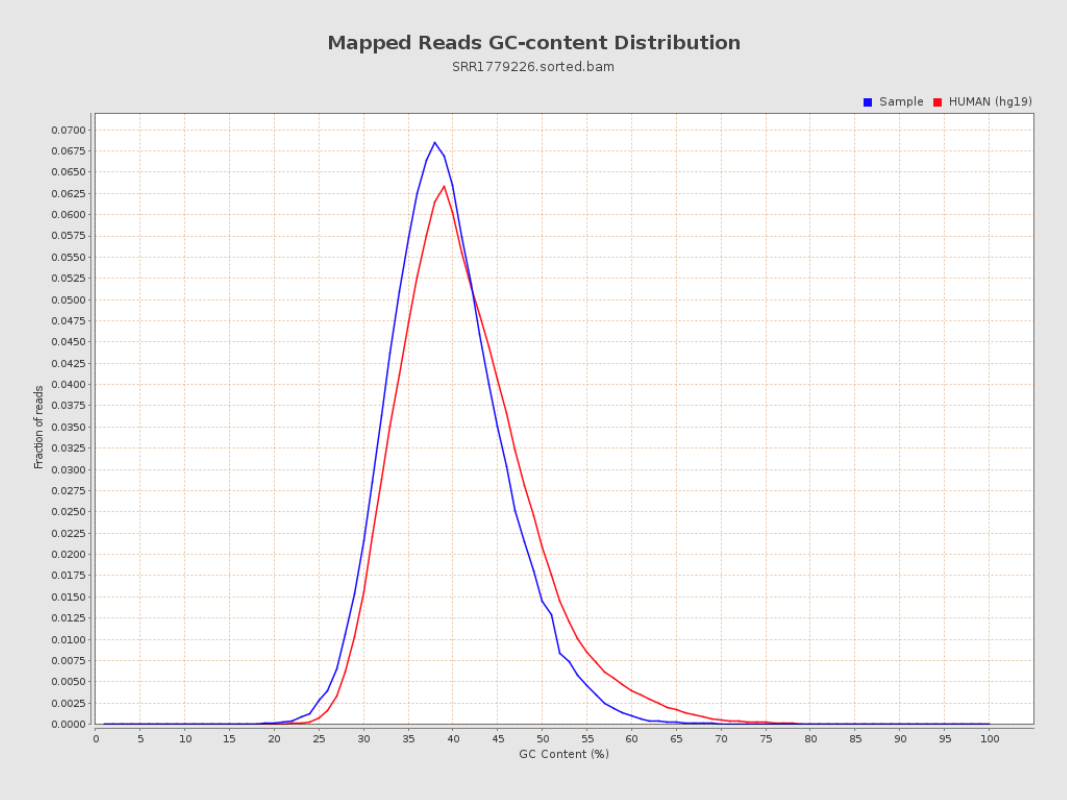
7. Results : Duplication Rate Histogram



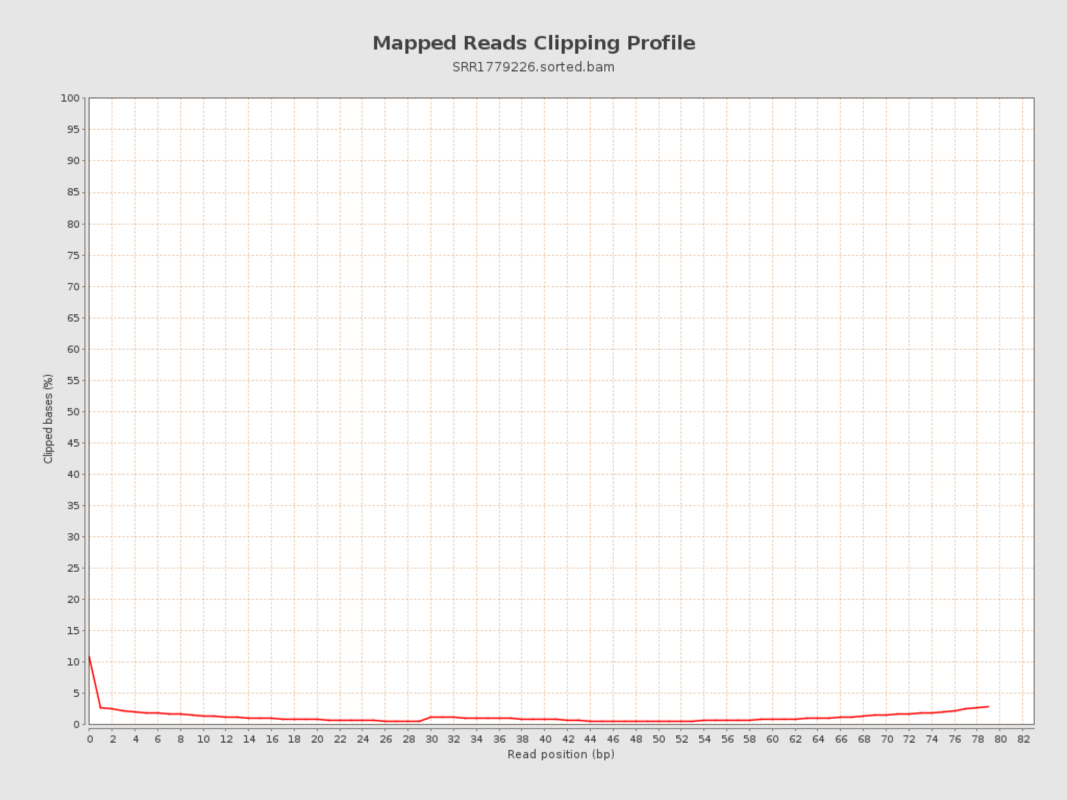
8. Results : Mapped Reads Nucleotide Content



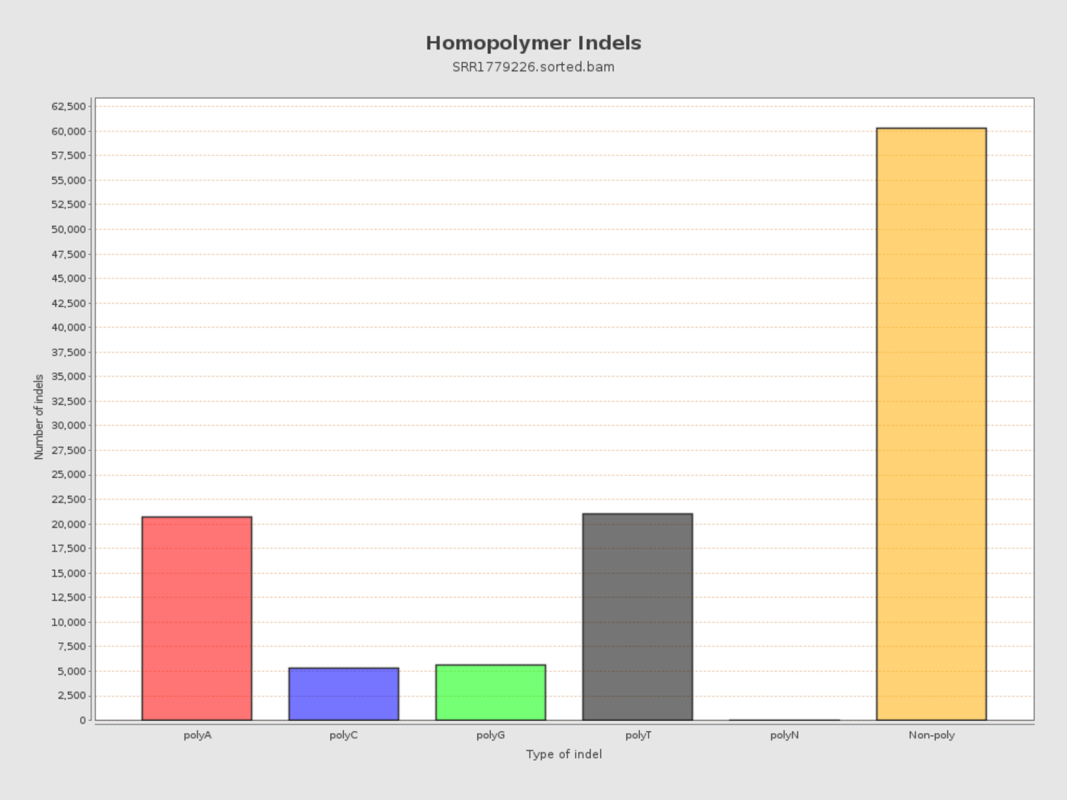
9. Results : Mapped Reads GC-content Distribution



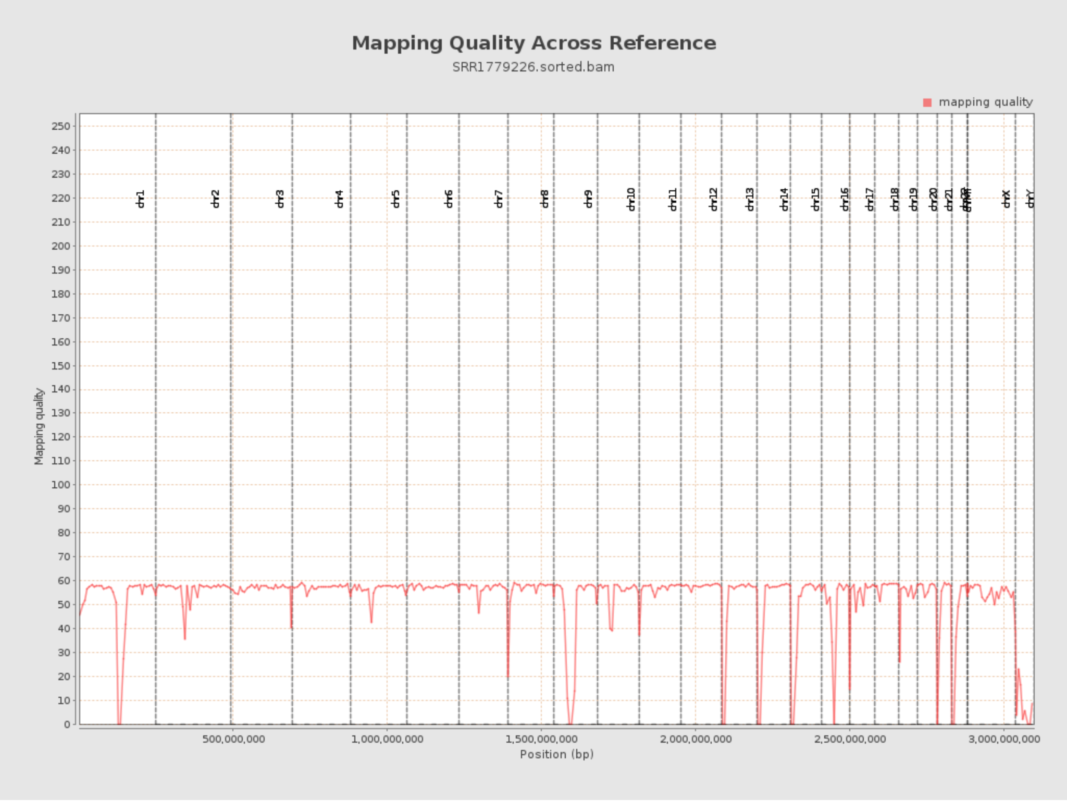
10. Results : Mapped Reads Clipping Profile



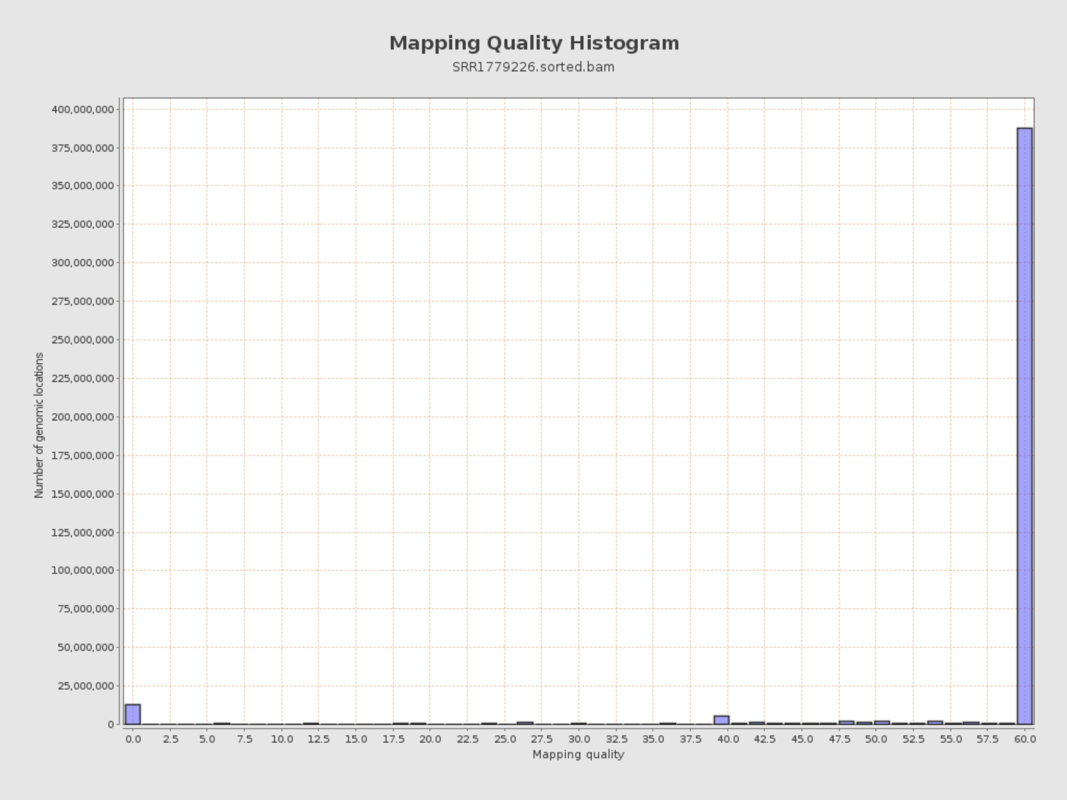
11. Results : Homopolymer Indels



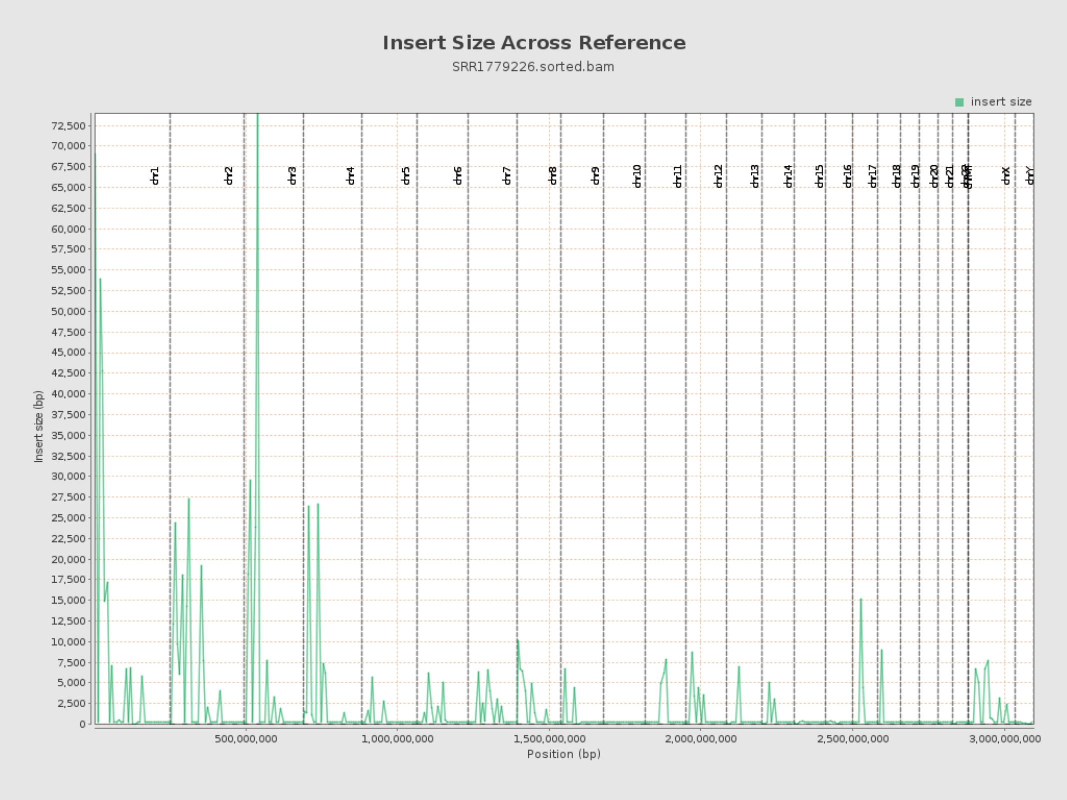
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram