Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 02:20:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779298.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_SRR1779298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779298_1.fastq.gz SRR1779298_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 02:20:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,505,720
Mapped reads	42,868,651 / 96.32%
Unmapped reads	1,637,069 / 3.68%
Mapped paired reads	42,868,651 / 96.32%
Mapped reads, first in pair	21,551,879 / 48.42%
Mapped reads, second in pair	21,316,772 / 47.9%
Mapped reads, both in pair	42,565,564 / 95.64%
Mapped reads, singletons	303,087 / 0.68%
Secondary alignments	0
Supplementary alignments	107,395 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	3,077,333 / 6.91%
Duplication rate	6.63%
Clipped reads	1,317,868 / 2.96%

2.2. ACGT Content

Number/percentage of A's	1,051,540,502 / 30.81%
Number/percentage of C's	650,554,943 / 19.06%
Number/percentage of T's	1,046,439,604 / 30.66%
Number/percentage of G's	663,311,439 / 19.44%
Number/percentage of N's	909,485 / 0.03%

GC Percentage	38.5%

2.3. Coverage

Mean	1.1026
Standard Deviation	3.7726

2.4. Mapping Quality

Mean Mapping Quality	52.96

2.5. Insert size

Mean	36,377.68
Standard Deviation	1,784,379.61
P25/Median/P75	155 / 211 / 288

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	11,700,173
Insertions	245,338
Mapped reads with at least one insertion	0.57%
Deletions	309,975
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.71%

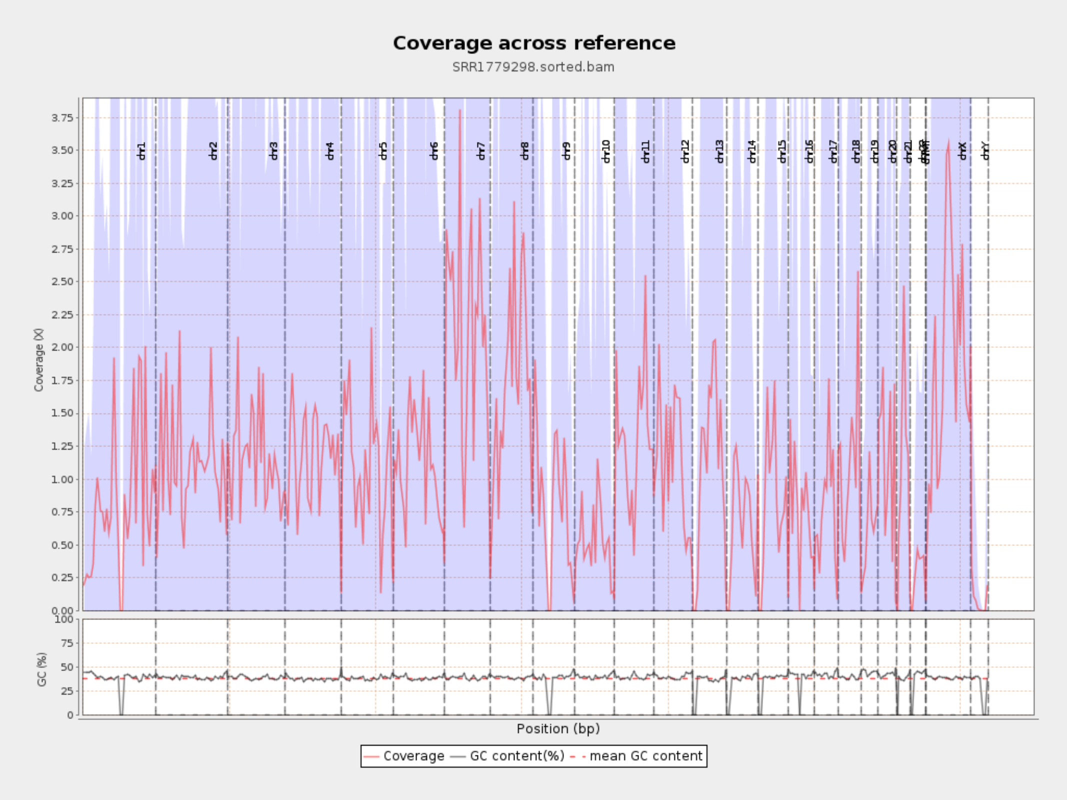
2.7. Chromosome stats

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

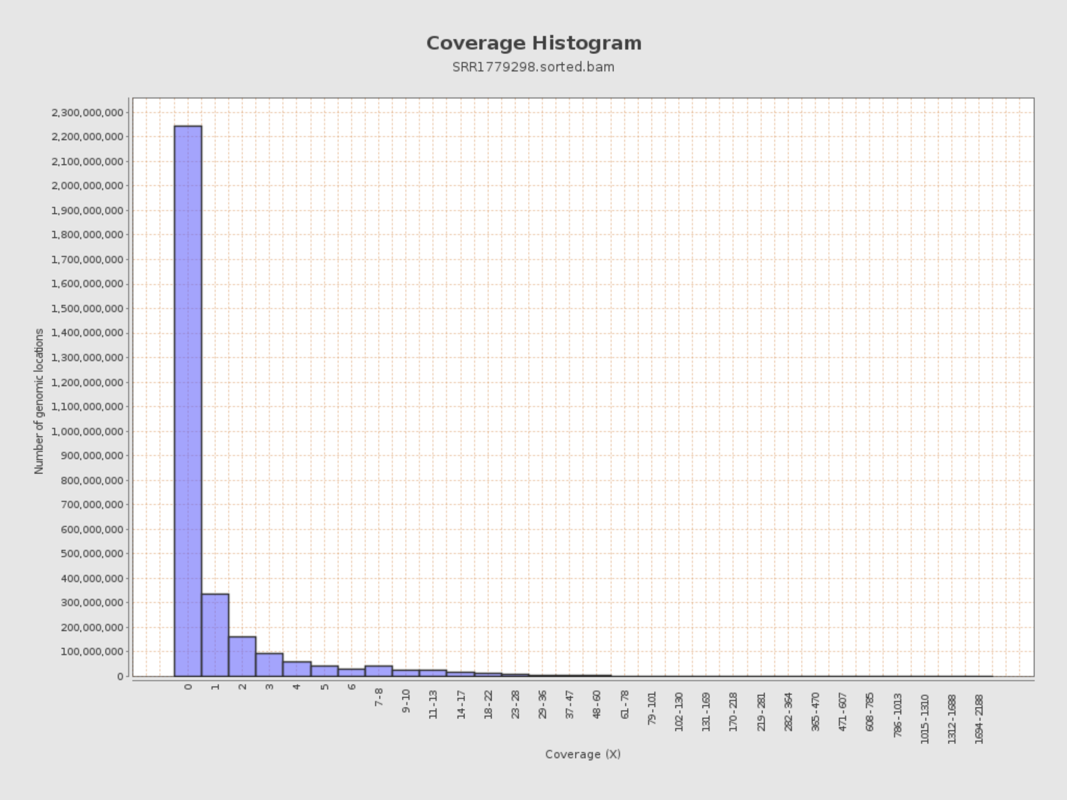
		bases	coverage	deviation
chr1	249250621	203108759	0.8149	3.7446
chr2	243199373	273026504	1.1226	3.3545
chr3	198022430	232339885	1.1733	3.5581
chr4	191154276	225522015	1.1798	3.3675
chr5	180915260	195315655	1.0796	3.3275
chr6	171115067	195533408	1.1427	3.7153
chr7	159138663	333673759	2.0967	5.6745
chr8	146364022	256384311	1.7517	4.5419
chr9	141213431	115880103	0.8206	2.8114
chr10	135534747	72275176	0.5333	3.9151
chr11	135006516	175853597	1.3026	4.2121
chr12	133851895	149523593	1.1171	3.5132
chr13	115169878	129382559	1.1234	3.4662
chr14	107349540	70574447	0.6574	2.5919
chr15	102531392	85727826	0.8361	2.9955
chr16	90354753	66038454	0.7309	2.7715
chr17	81195210	64765157	0.7976	3.1147
chr18	78077248	85336733	1.093	3.7813
chr19	59128983	37136002	0.6281	2.5796
chr20	63025520	74555774	1.1829	3.6084
chr21	48129895	50682789	1.053	3.5843
chr22	51304566	14732067	0.2871	1.1542
chrMT	16571	2410	0.1454	0.3905
chrX	155270560	301371401	1.9409	5.822

chrY	59373566	4652951	0.0784	0.8809

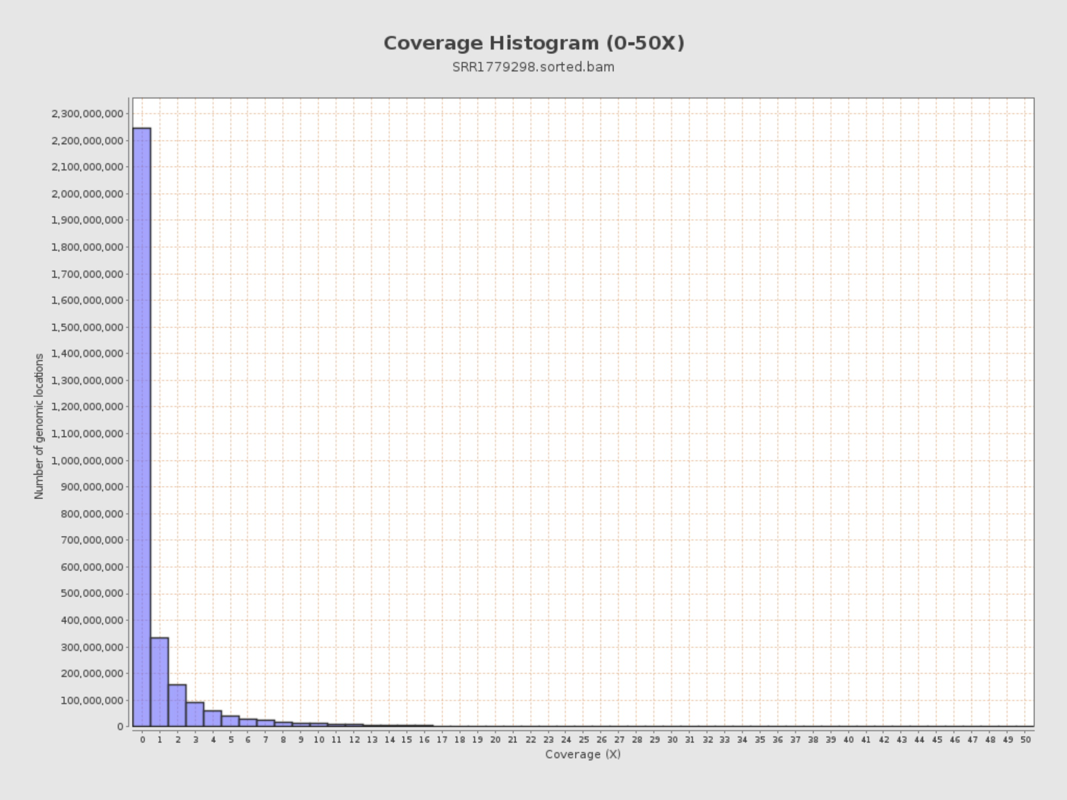
3. Results : Coverage across reference



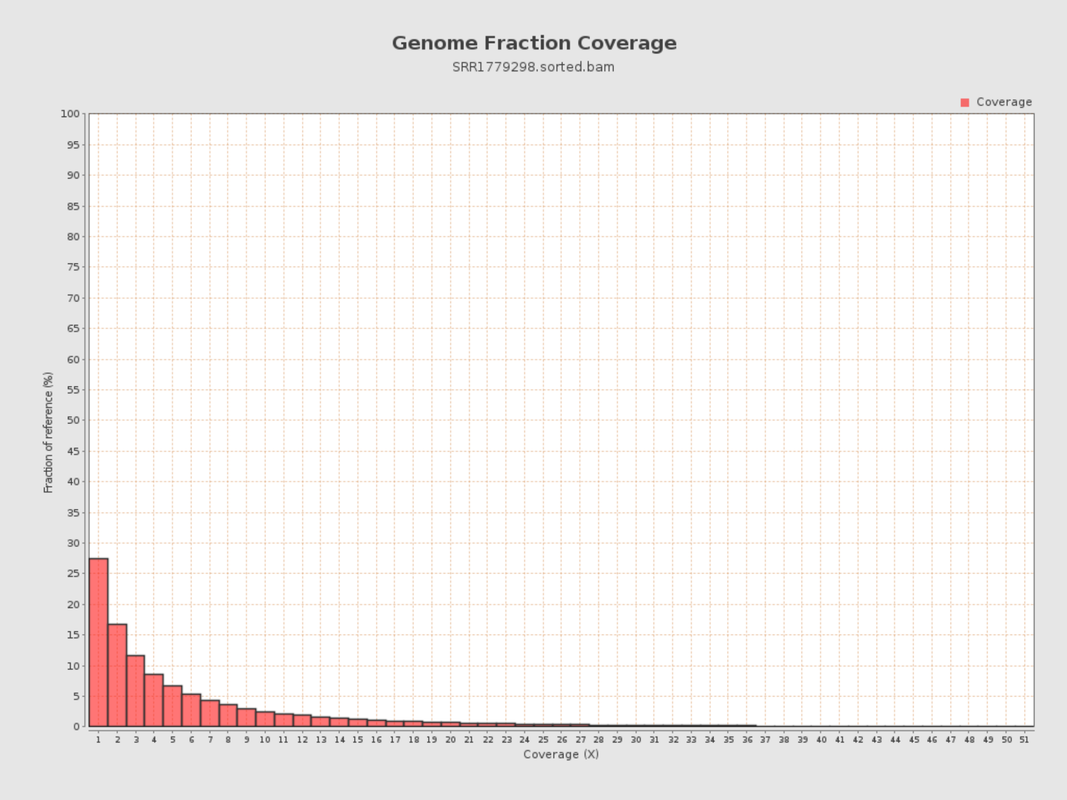
4. Results : Coverage Histogram



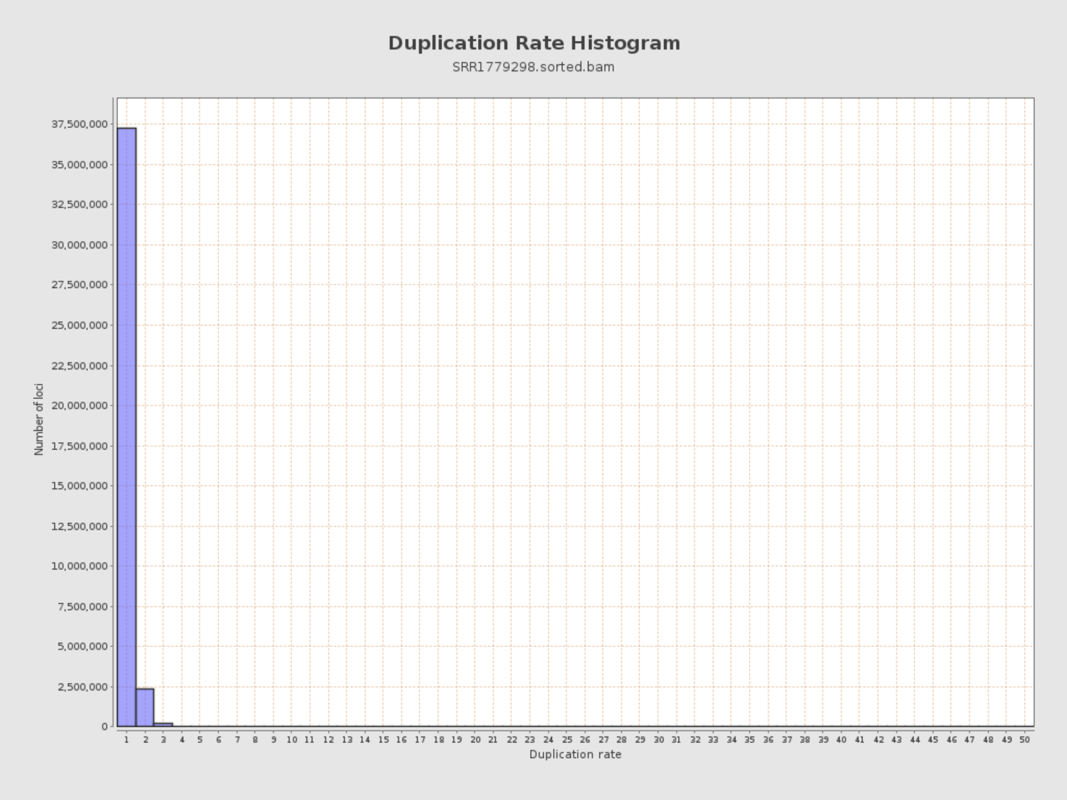
5. Results : Coverage Histogram (0-50X)



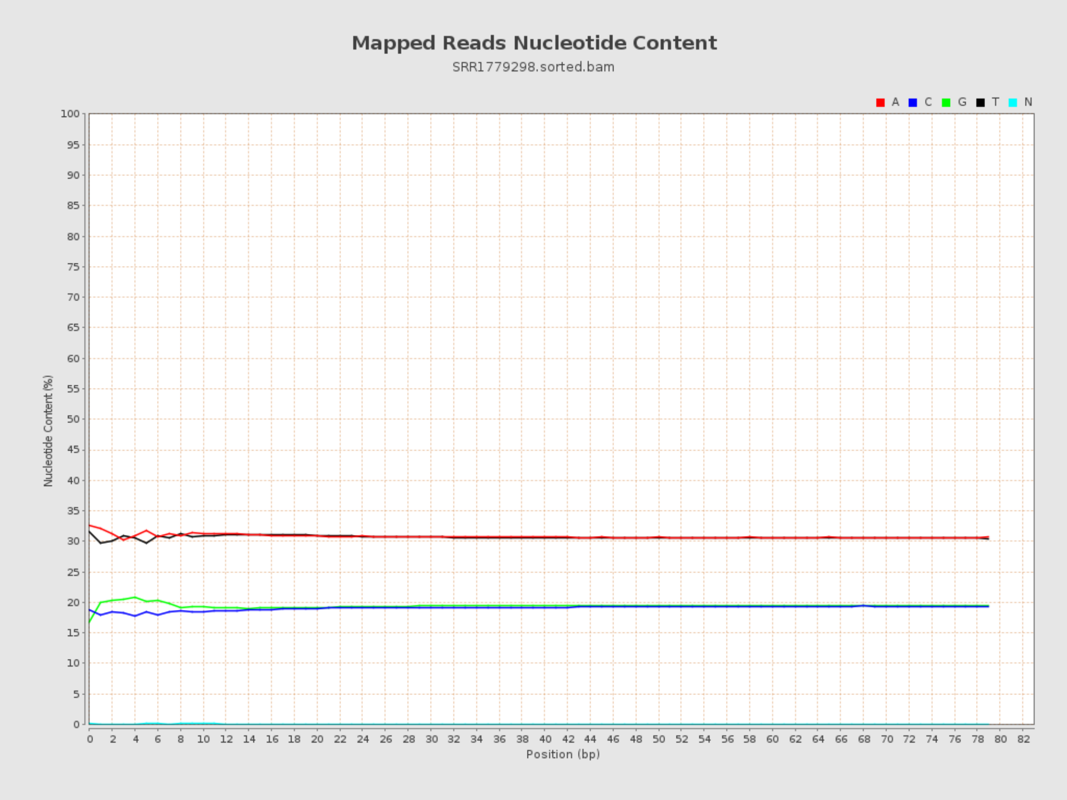
6. Results : Genome Fraction Coverage



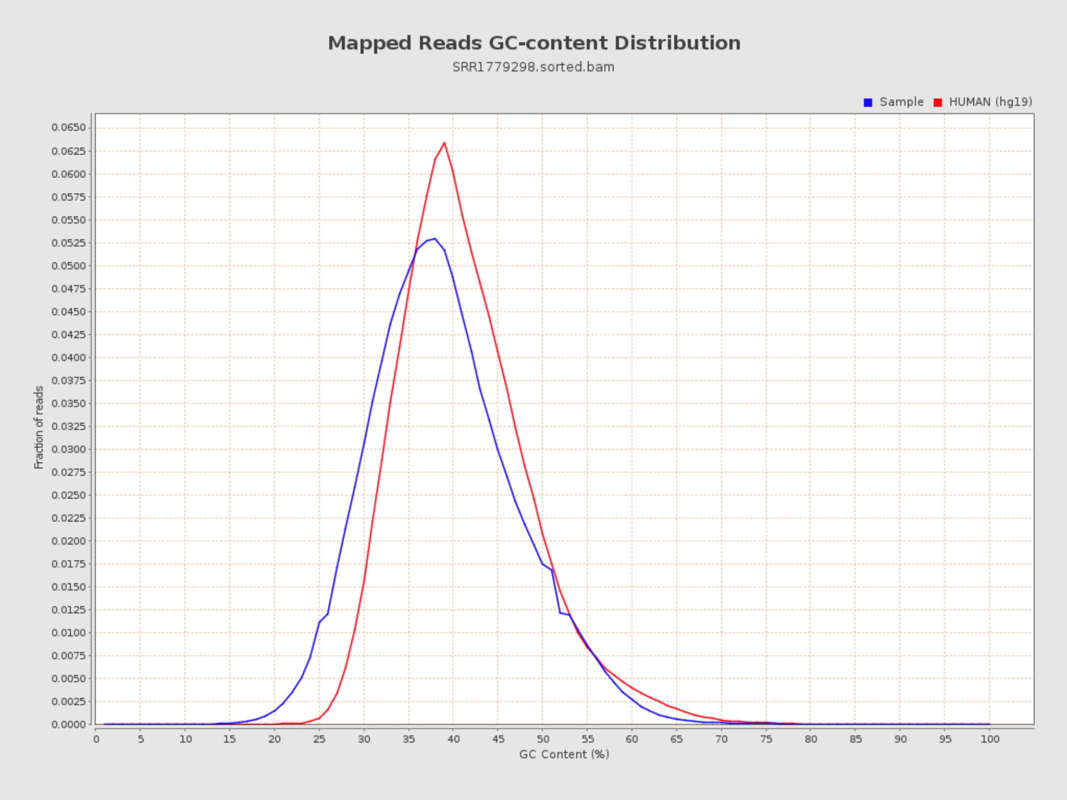
7. Results : Duplication Rate Histogram



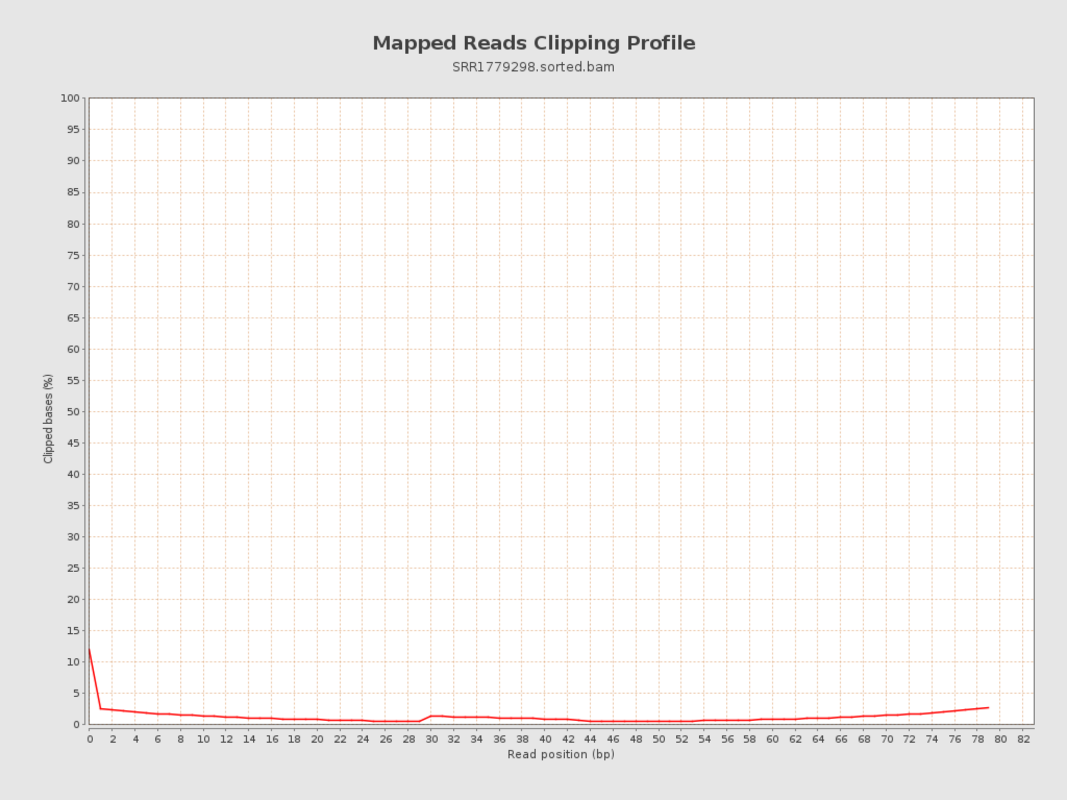
8. Results : Mapped Reads Nucleotide Content



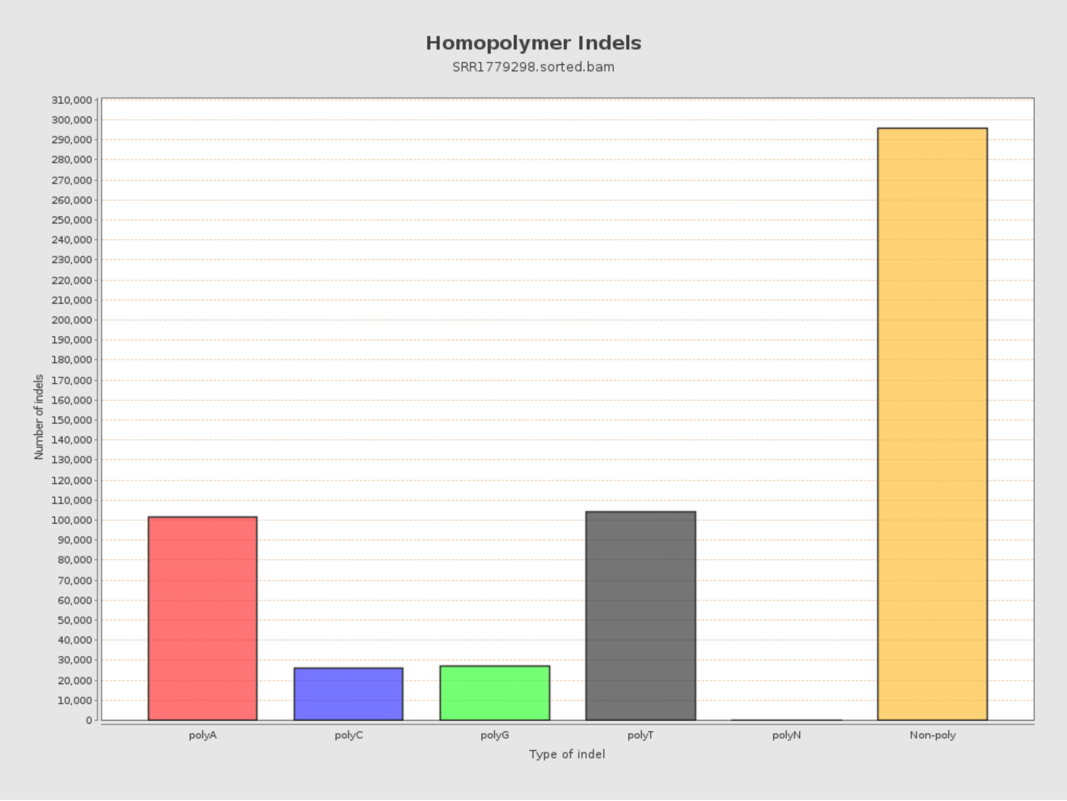
9. Results : Mapped Reads GC-content Distribution



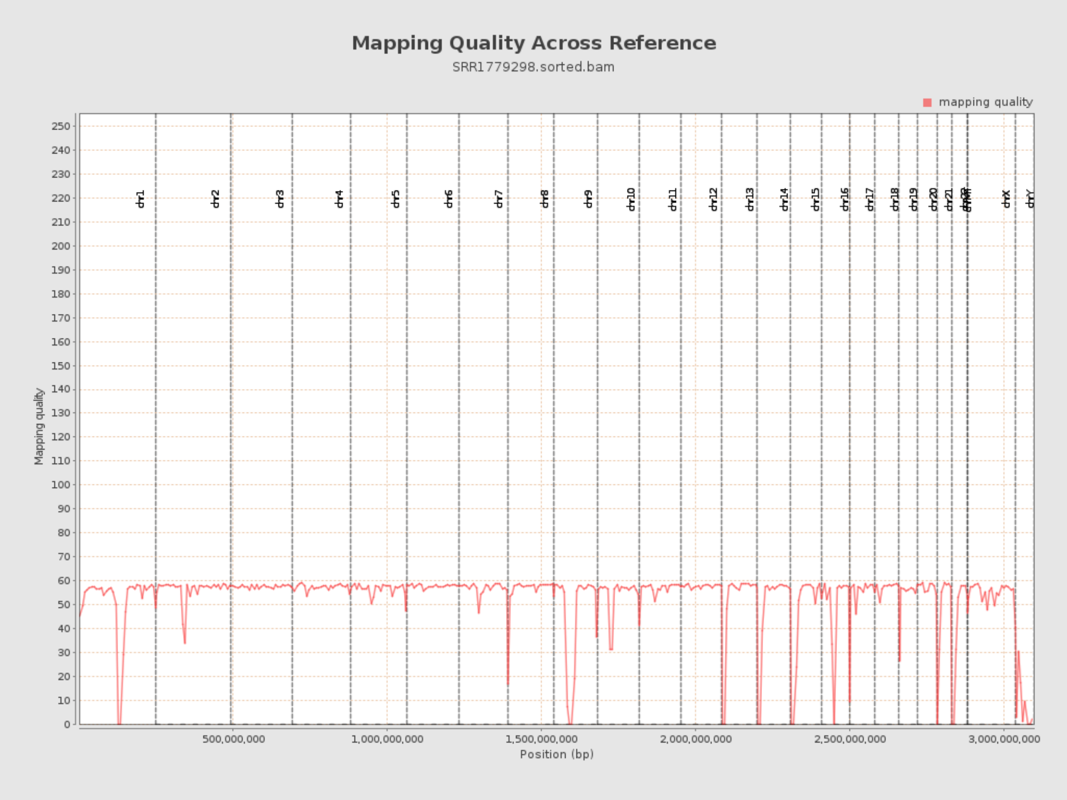
10. Results : Mapped Reads Clipping Profile



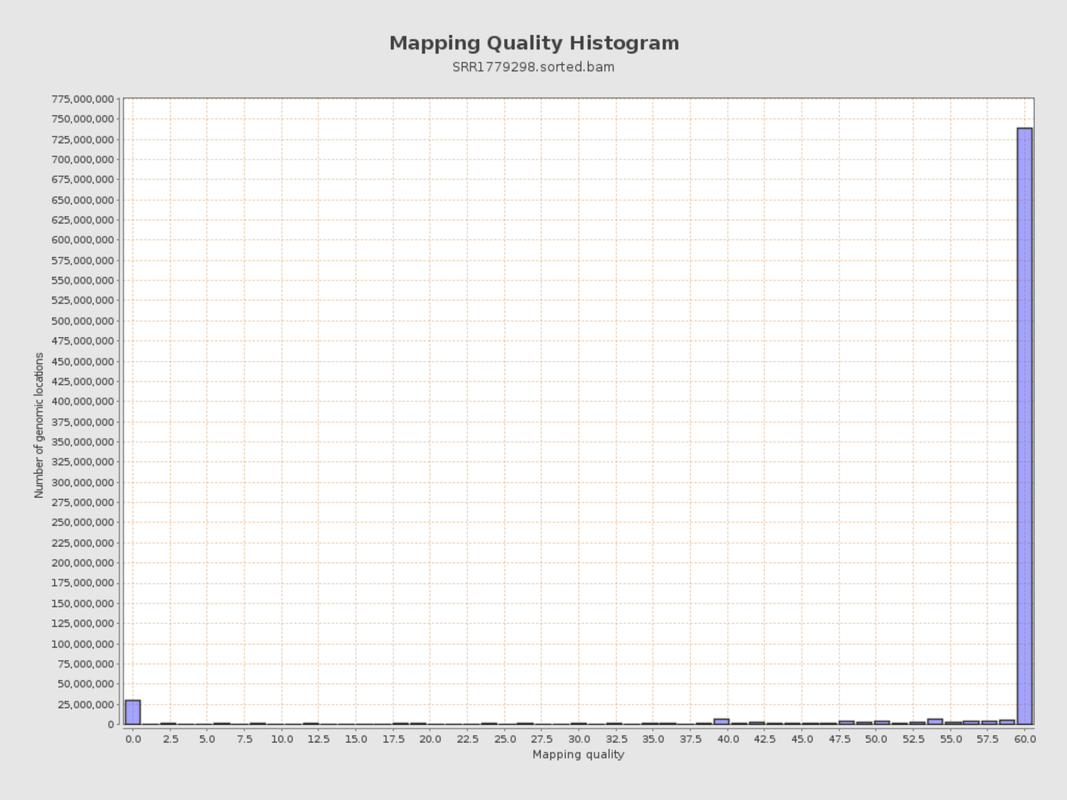
11. Results : Homopolymer Indels



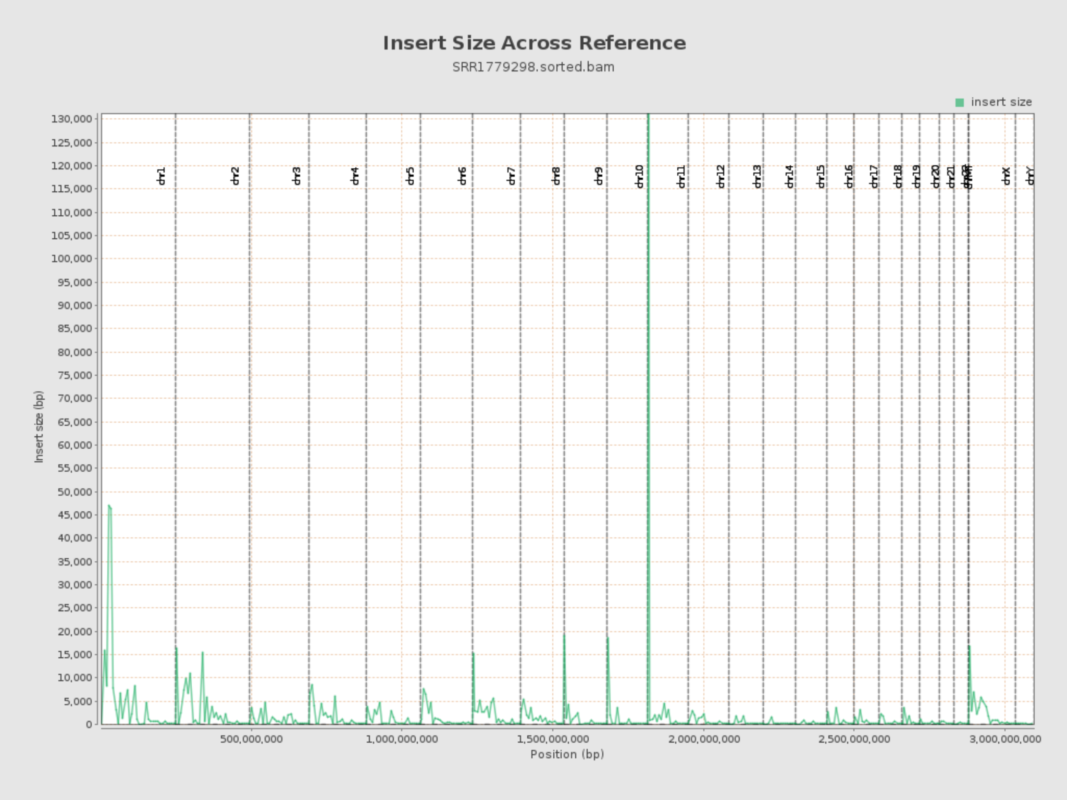
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram