Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 21:39:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779409.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_SRR1779409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779409_1.fastq.gz SRR1779409_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 21:39:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,913,022
Mapped reads	14,567,888 / 97.69%
Unmapped reads	345,134 / 2.31%
Mapped paired reads	14,567,888 / 97.69%
Mapped reads, first in pair	7,340,855 / 49.22%
Mapped reads, second in pair	7,227,033 / 48.46%
Mapped reads, both in pair	14,428,550 / 96.75%
Mapped reads, singletons	139,338 / 0.93%
Secondary alignments	0
Supplementary alignments	52,064 / 0.35%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	483,066 / 3.24%
Duplication rate	2.99%
Clipped reads	574,818 / 3.85%

2.2. ACGT Content

Number/percentage of A's	354,069,150 / 30.57%
Number/percentage of C's	225,786,484 / 19.49%
Number/percentage of T's	346,313,516 / 29.9%
Number/percentage of G's	231,906,106 / 20.02%
Number/percentage of N's	256,152 / 0.02%

GC Percentage	39.51%

2.3. Coverage

Mean	0.3743
Standard Deviation	1.4577

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	176,707.78
Standard Deviation	4,022,838.1
P25/Median/P75	142 / 181 / 231

2.6. Mismatches and indels

General error rate	0.34%
Mismatches	3,768,936
Insertions	100,347
Mapped reads with at least one insertion	0.68%
Deletions	117,134
Mapped reads with at least one deletion	0.79%
Homopolymer indels	47.28%

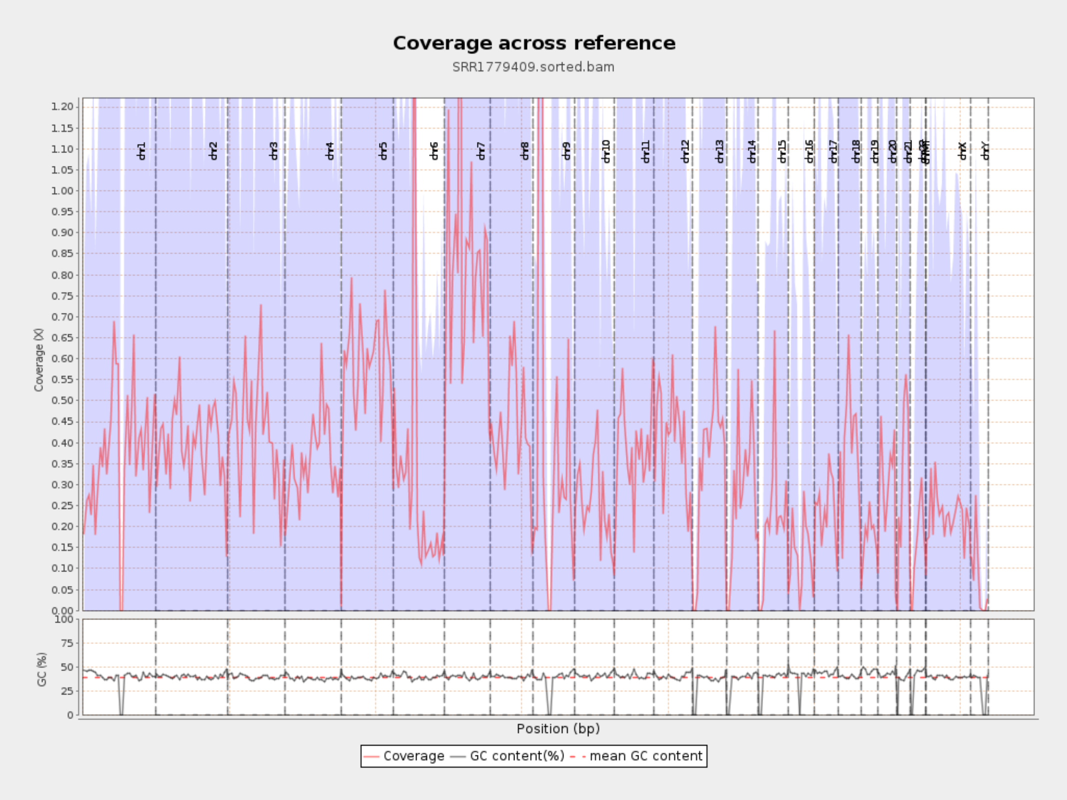
2.7. Chromosome stats

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

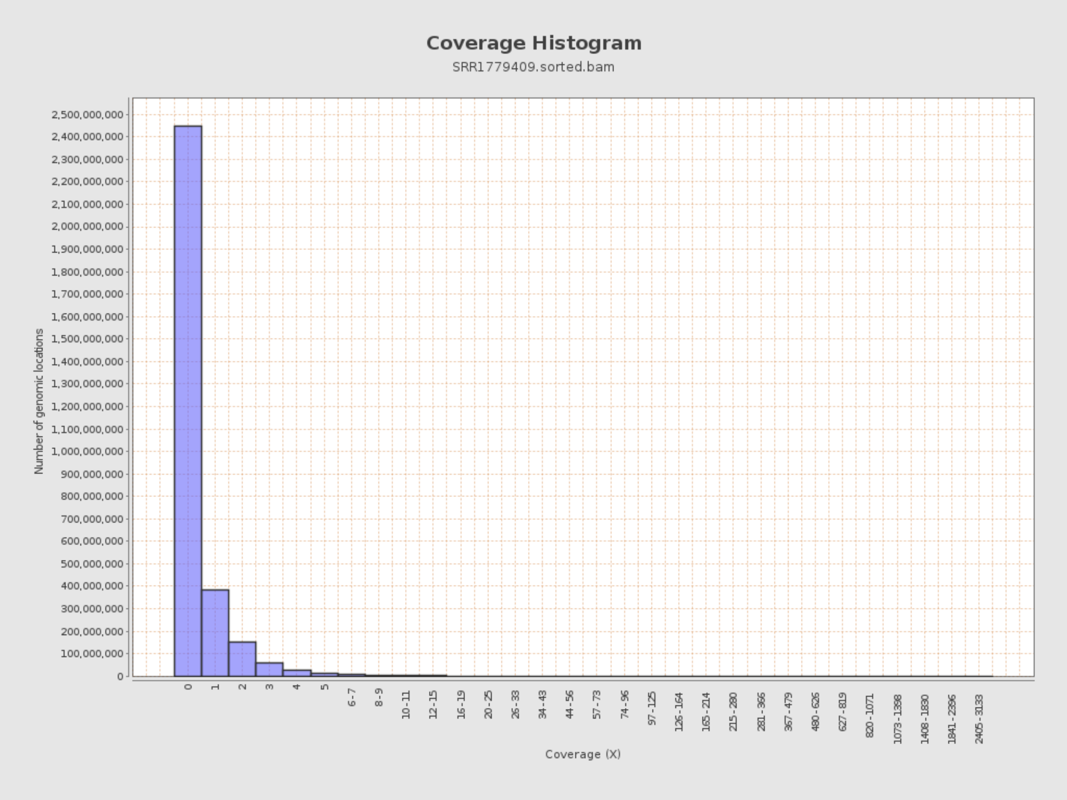
		bases	coverage	deviation
chr1	249250621	92614660	0.3716	3.3483
chr2	243199373	97047375	0.399	0.9579
chr3	198022430	84022510	0.4243	0.942
chr4	191154276	69338154	0.3627	0.855
chr5	180915260	104697547	0.5787	1.0945
chr6	171115067	50650830	0.296	1.1481
chr7	159138663	136074219	0.8551	2.2312
chr8	146364022	64434848	0.4402	0.9671
chr9	141213431	68125419	0.4824	1.7742
chr10	135534747	35994479	0.2656	1.6072
chr11	135006516	51616333	0.3823	0.9441
chr12	133851895	53666540	0.4009	0.9278
chr13	115169878	40807855	0.3543	0.8529
chr14	107349540	30919839	0.288	0.792
chr15	102531392	21965883	0.2142	0.688
chr16	90354753	11737087	0.1299	0.5451
chr17	81195210	20387772	0.2511	0.778
chr18	78077248	30653396	0.3926	1.029
chr19	59128983	10368320	0.1754	1.9564
chr20	63025520	19869168	0.3153	0.823
chr21	48129895	15287791	0.3176	0.8877
chr22	51304566	8407154	0.1639	0.6145
chrMT	16571	1390	0.0839	0.4307
chrX	155270560	35304065	0.2274	0.6966

chrY	59373566	4581832	0.0772	0.404

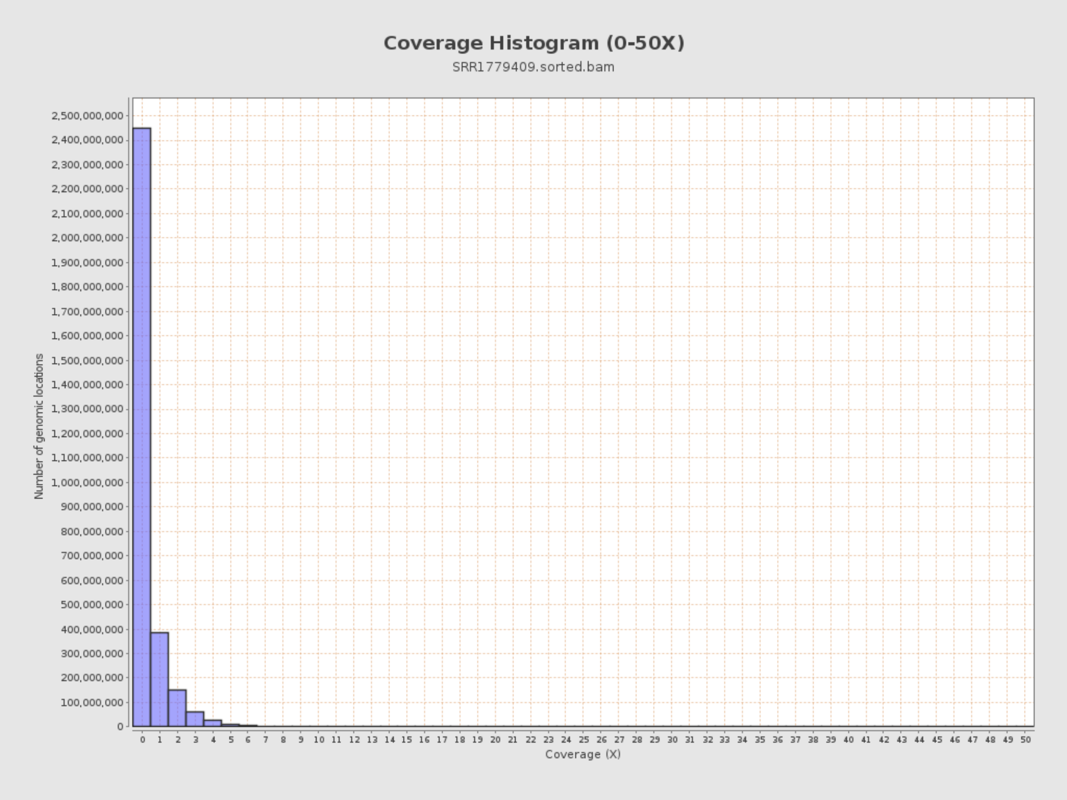
3. Results : Coverage across reference



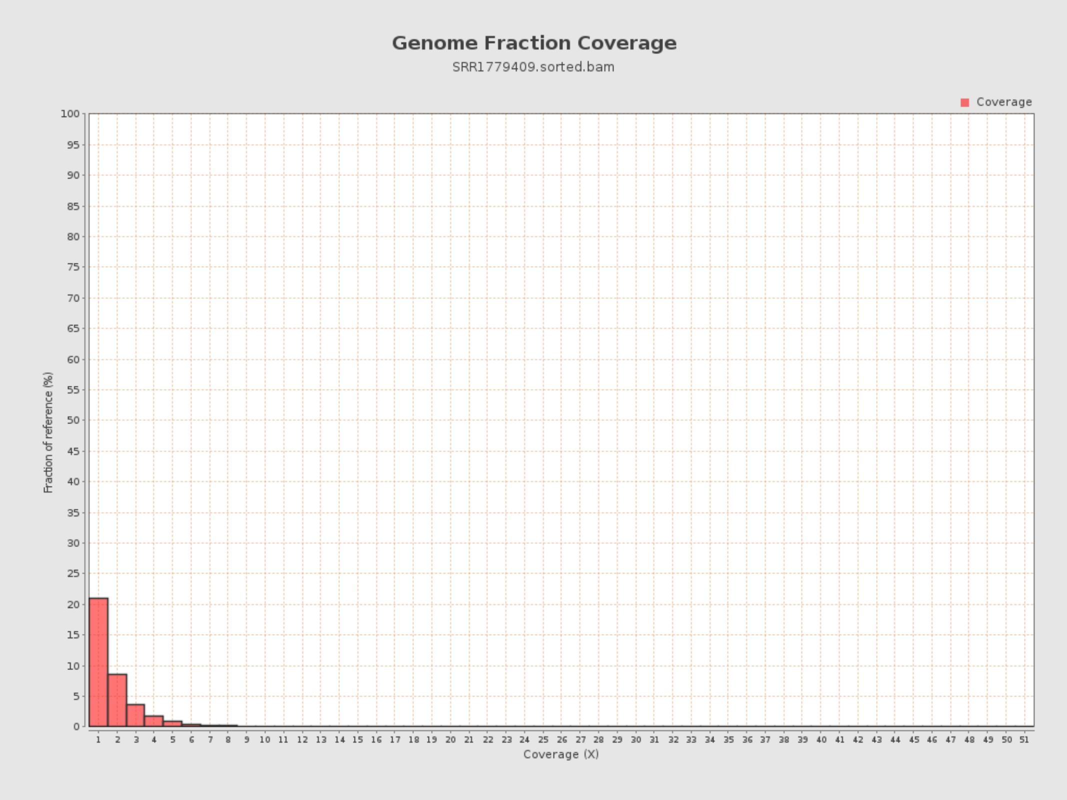
4. Results : Coverage Histogram



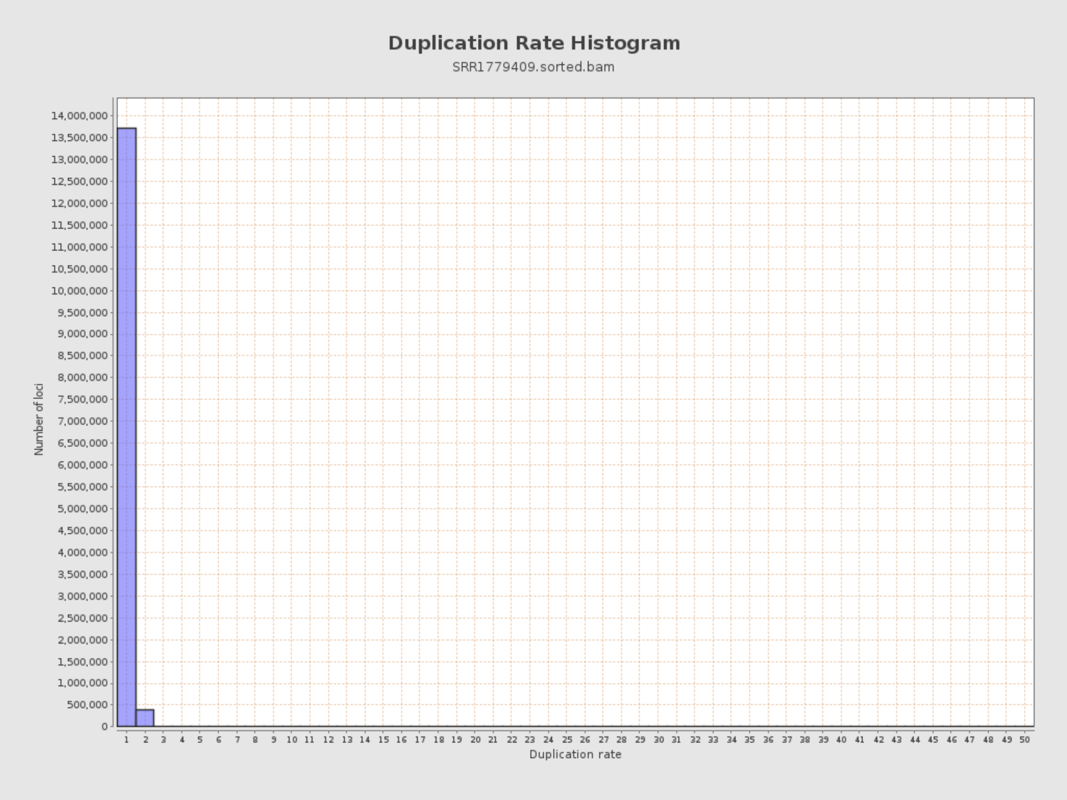
5. Results : Coverage Histogram (0-50X)



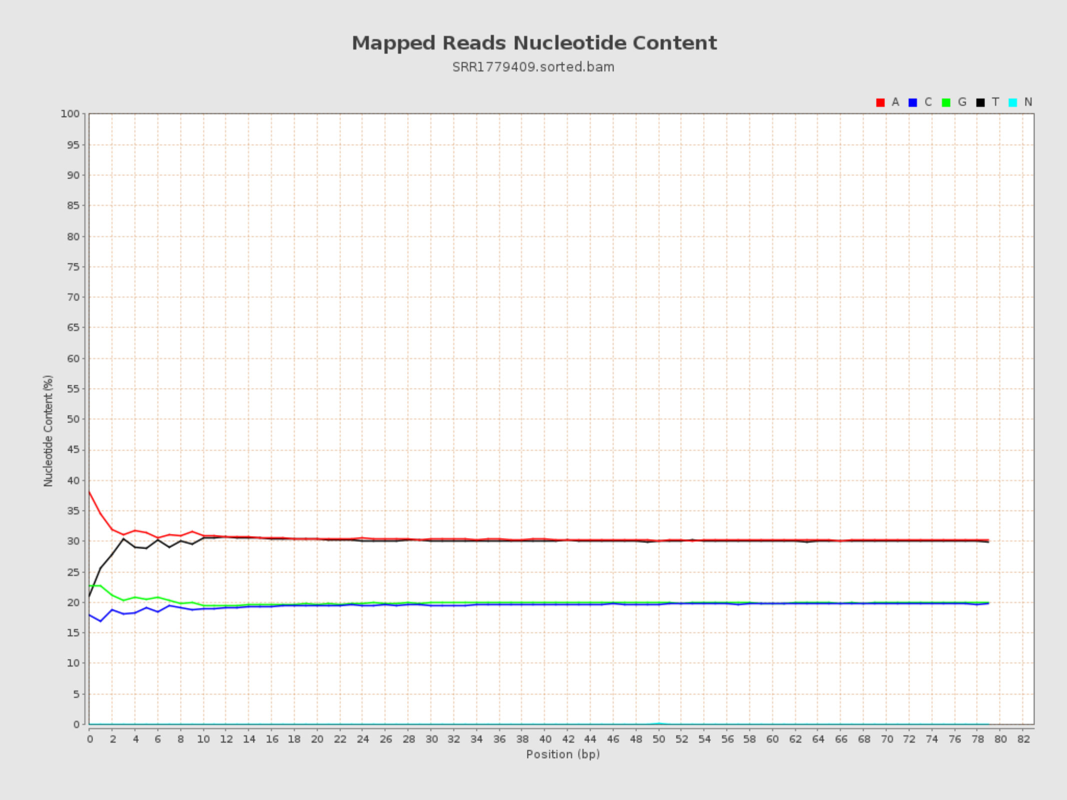
6. Results : Genome Fraction Coverage



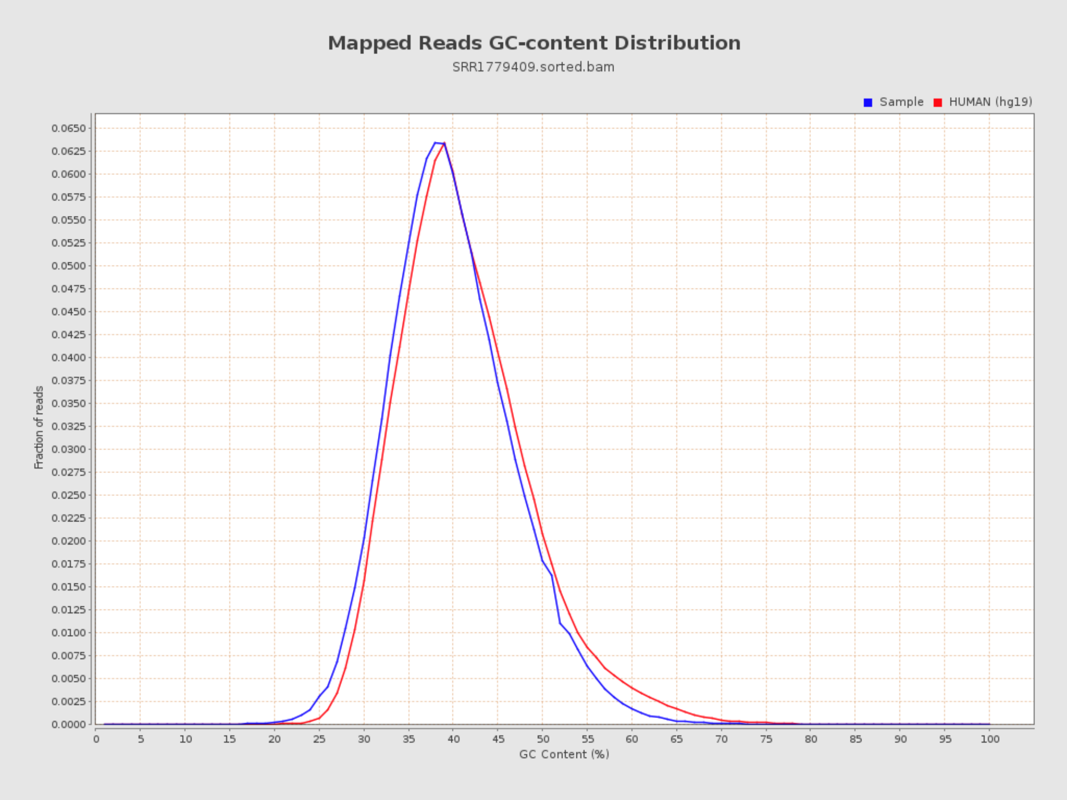
7. Results : Duplication Rate Histogram



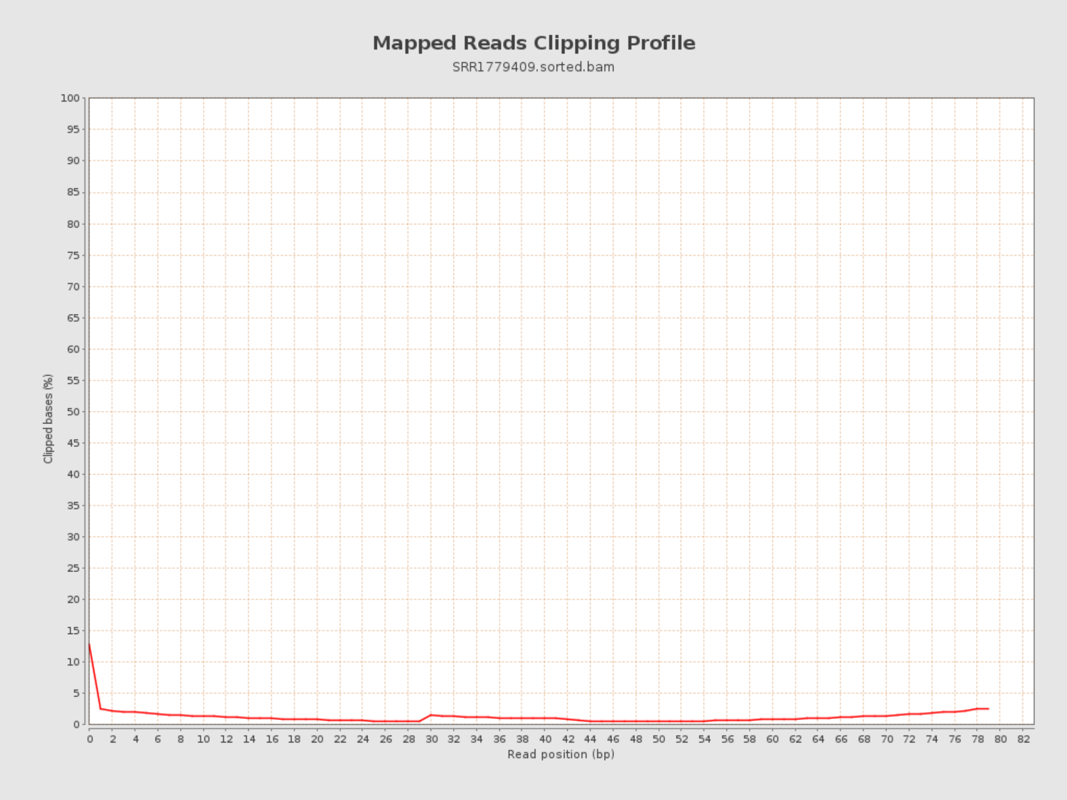
8. Results : Mapped Reads Nucleotide Content



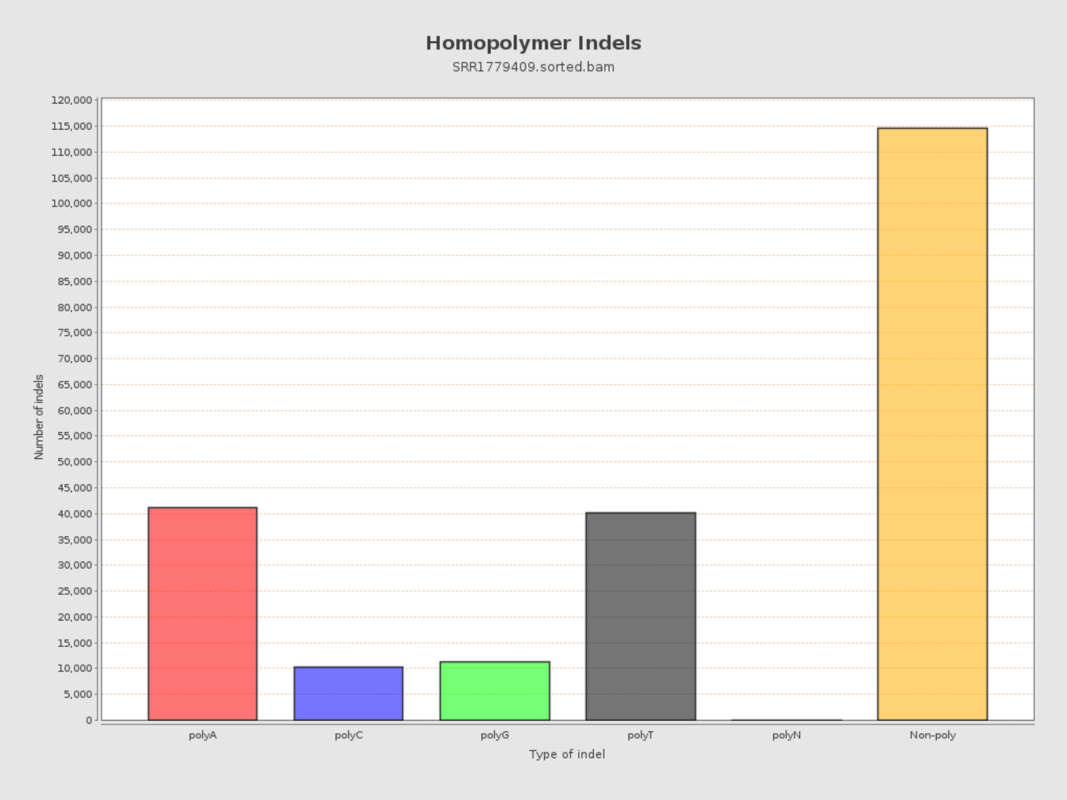
9. Results : Mapped Reads GC-content Distribution



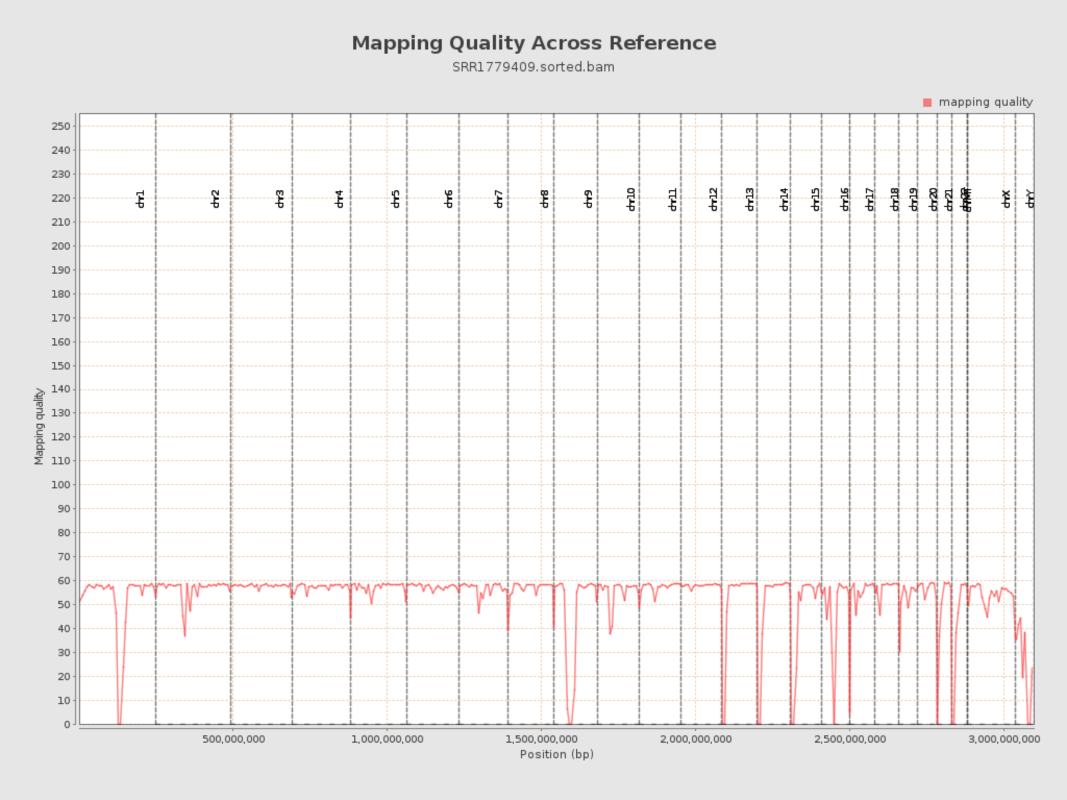
10. Results : Mapped Reads Clipping Profile



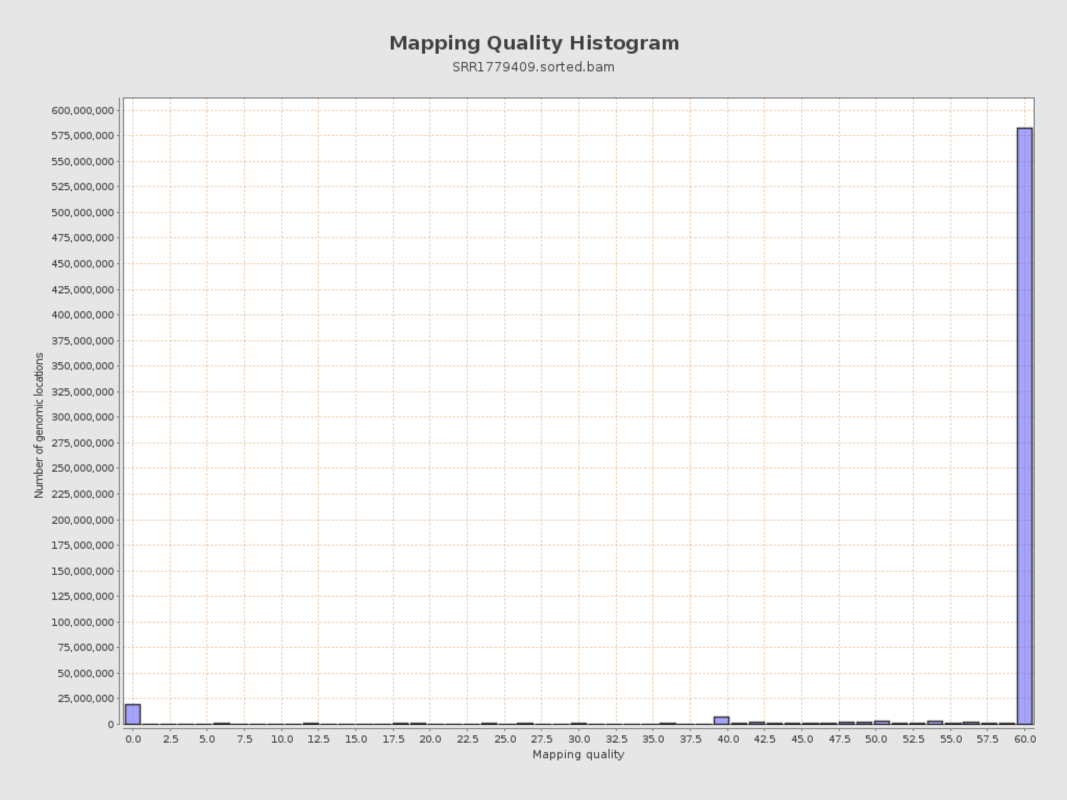
11. Results : Homopolymer Indels



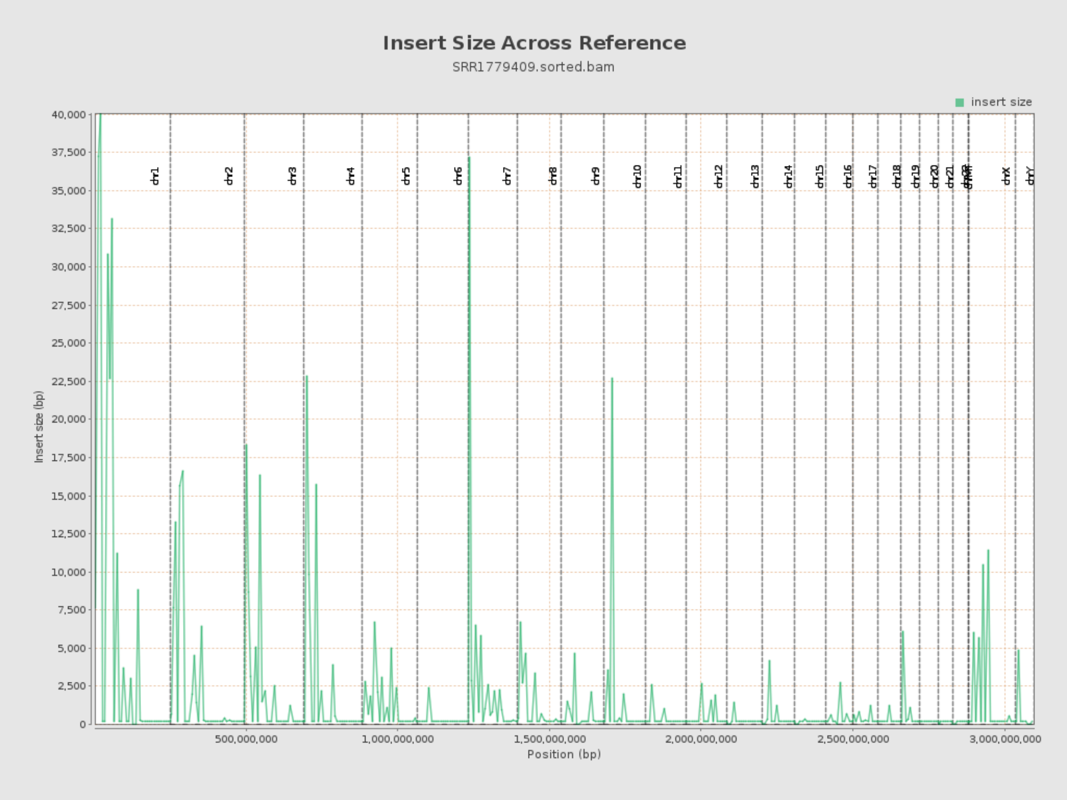
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram