Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 06:04:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779308.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_SRR1779308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779308_1.fastq.gz SRR1779308_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 06:04:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,536,992
Mapped reads	16,546,035 / 94.35%
Unmapped reads	990,957 / 5.65%
Mapped paired reads	16,546,035 / 94.35%
Mapped reads, first in pair	8,395,466 / 47.87%
Mapped reads, second in pair	8,150,569 / 46.48%
Mapped reads, both in pair	16,269,724 / 92.77%
Mapped reads, singletons	276,311 / 1.58%
Secondary alignments	0
Supplementary alignments	42,460 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	687,125 / 3.92%
Duplication rate	3.82%
Clipped reads	523,103 / 2.98%

2.2. ACGT Content

Number/percentage of A's	406,639,568 / 30.88%
Number/percentage of C's	249,658,210 / 18.96%
Number/percentage of T's	406,289,239 / 30.86%
Number/percentage of G's	253,804,911 / 19.28%
Number/percentage of N's	345,587 / 0.03%

GC Percentage	38.24%

2.3. Coverage

Mean	0.4254
Standard Deviation	1.7762

2.4. Mapping Quality

Mean Mapping Quality	52.72

2.5. Insert size

Mean	39,123.53
Standard Deviation	1,858,669.11
P25/Median/P75	160 / 214 / 292

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,627,128
Insertions	95,694
Mapped reads with at least one insertion	0.57%
Deletions	123,517
Mapped reads with at least one deletion	0.74%
Homopolymer indels	47.01%

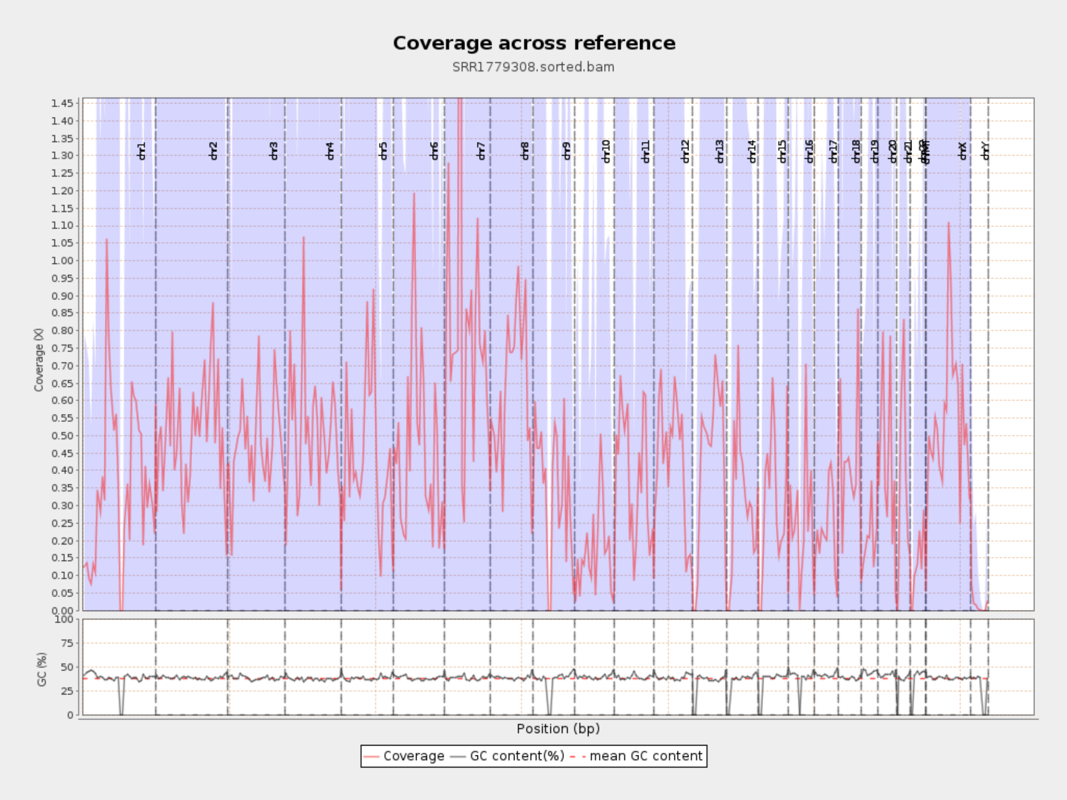
2.7. Chromosome stats

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

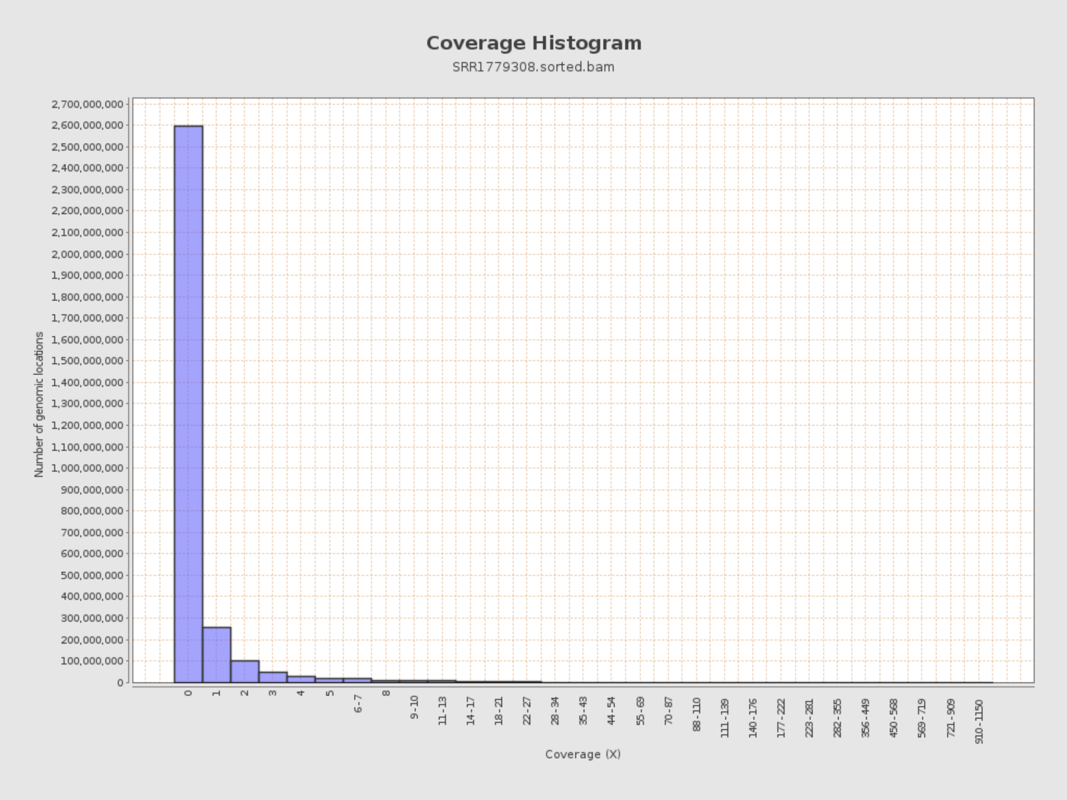
		bases	coverage	deviation
chr1	249250621	89165193	0.3577	1.7524
chr2	243199373	123124595	0.5063	1.7435
chr3	198022430	94683369	0.4781	1.6705
chr4	191154276	99106531	0.5185	1.758
chr5	180915260	78687597	0.4349	1.6275
chr6	171115067	81519358	0.4764	1.929
chr7	159138663	135292045	0.8502	3.2766
chr8	146364022	93564462	0.6393	1.9378
chr9	141213431	49091357	0.3476	1.3873
chr10	135534747	22764670	0.168	2.288
chr11	135006516	52636932	0.3899	1.6477
chr12	133851895	57120320	0.4267	1.6439
chr13	115169878	49699673	0.4315	1.4353
chr14	107349540	32837826	0.3059	1.2017
chr15	102531392	30902423	0.3014	1.278
chr16	90354753	22538556	0.2494	1.1235
chr17	81195210	19207754	0.2366	1.1355
chr18	78077248	34367423	0.4402	1.6595
chr19	59128983	12501388	0.2114	1.1949
chr20	63025520	27835753	0.4417	1.6745
chr21	48129895	16774897	0.3485	1.3598
chr22	51304566	6940168	0.1353	0.8431
chrMT	16571	936	0.0565	0.2353
chrX	155270560	85715593	0.552	1.9204

chrY	59373566	909315	0.0153	0.2173

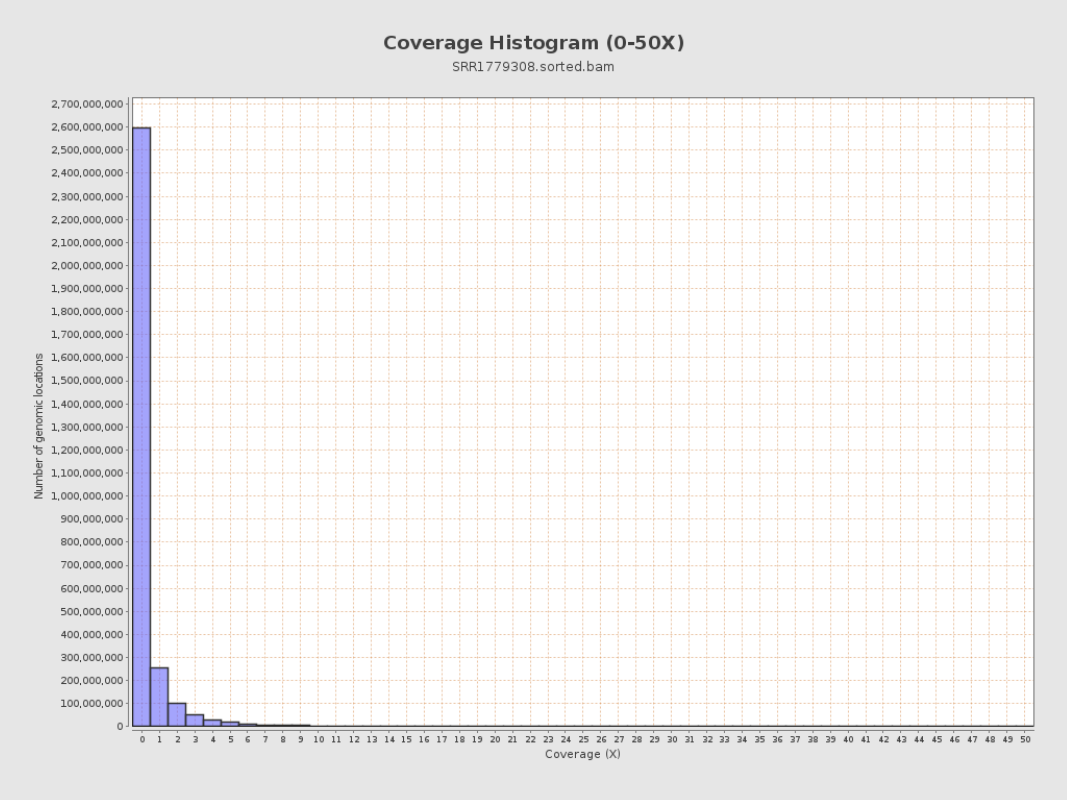
3. Results : Coverage across reference



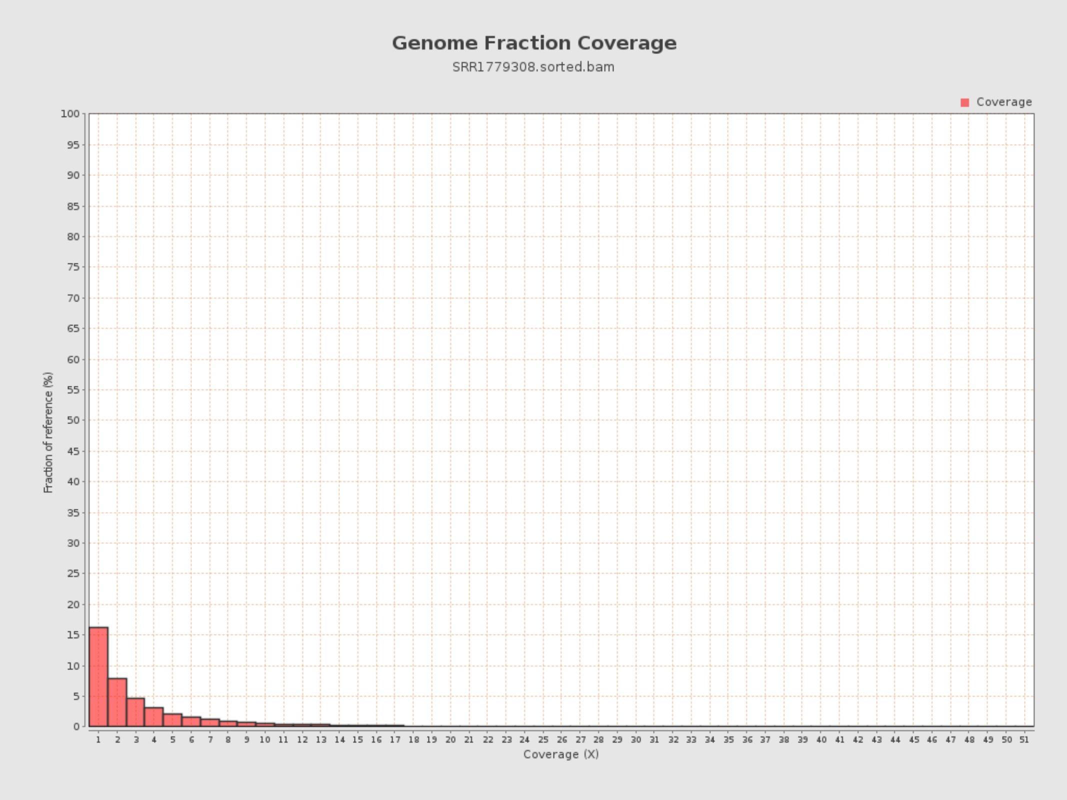
4. Results : Coverage Histogram



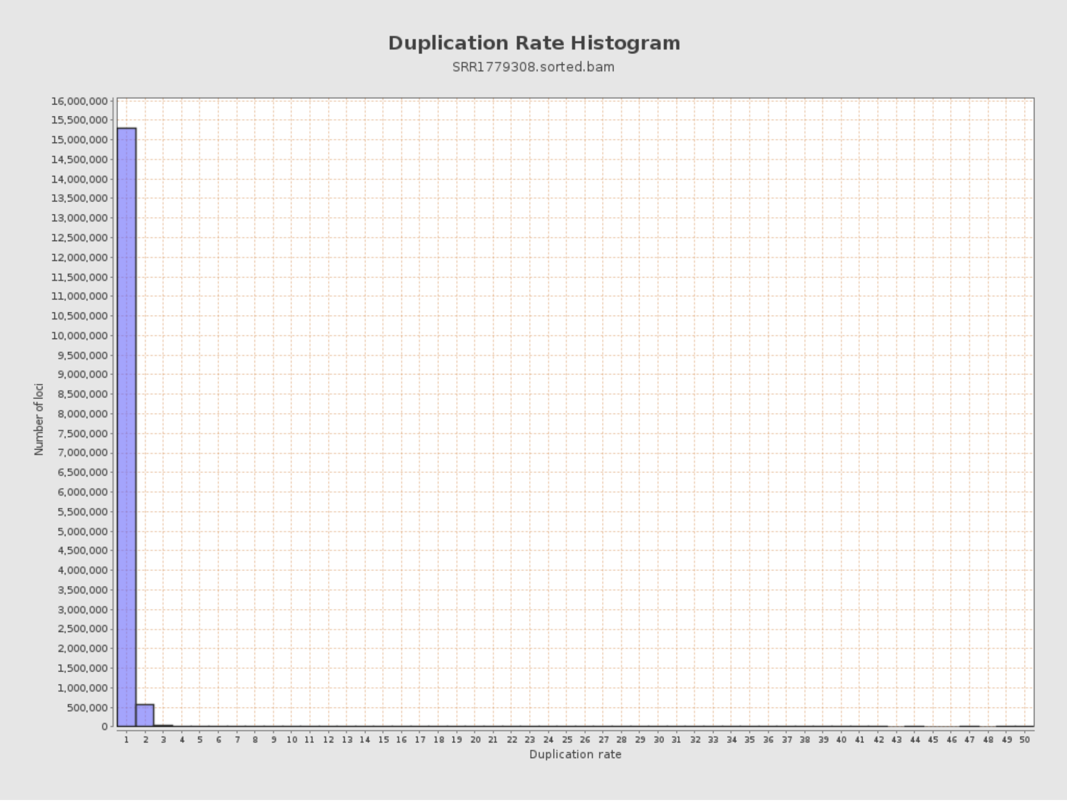
5. Results : Coverage Histogram (0-50X)



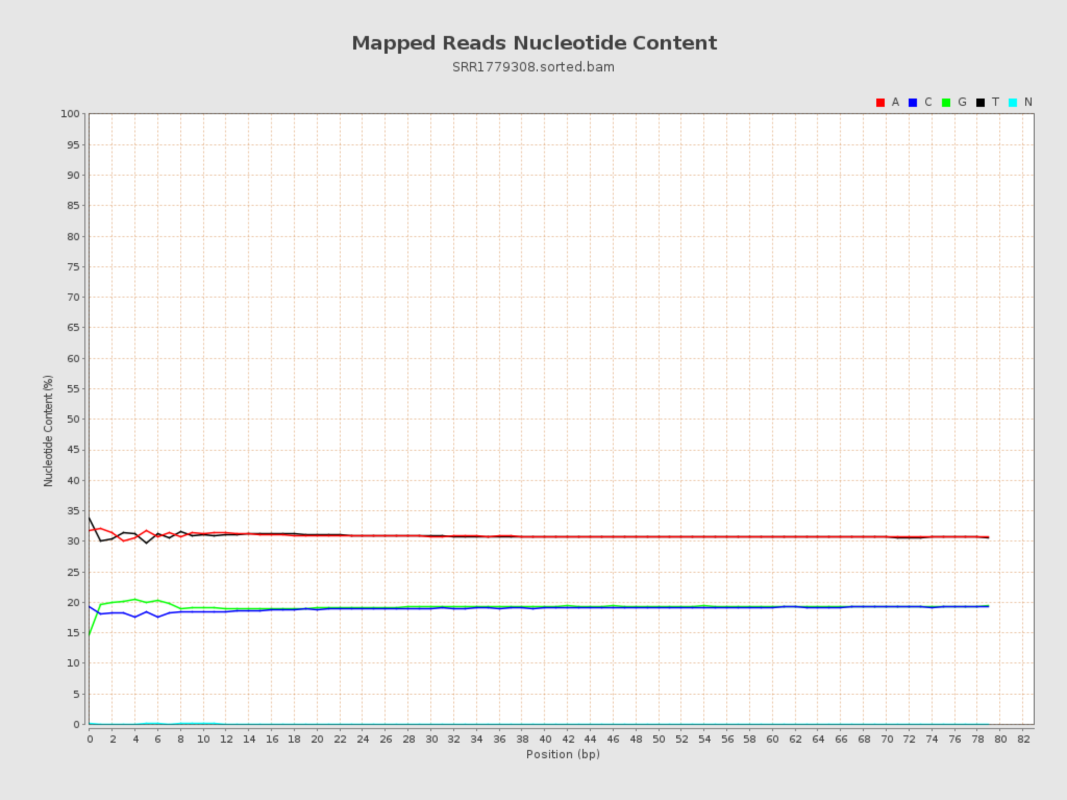
6. Results : Genome Fraction Coverage



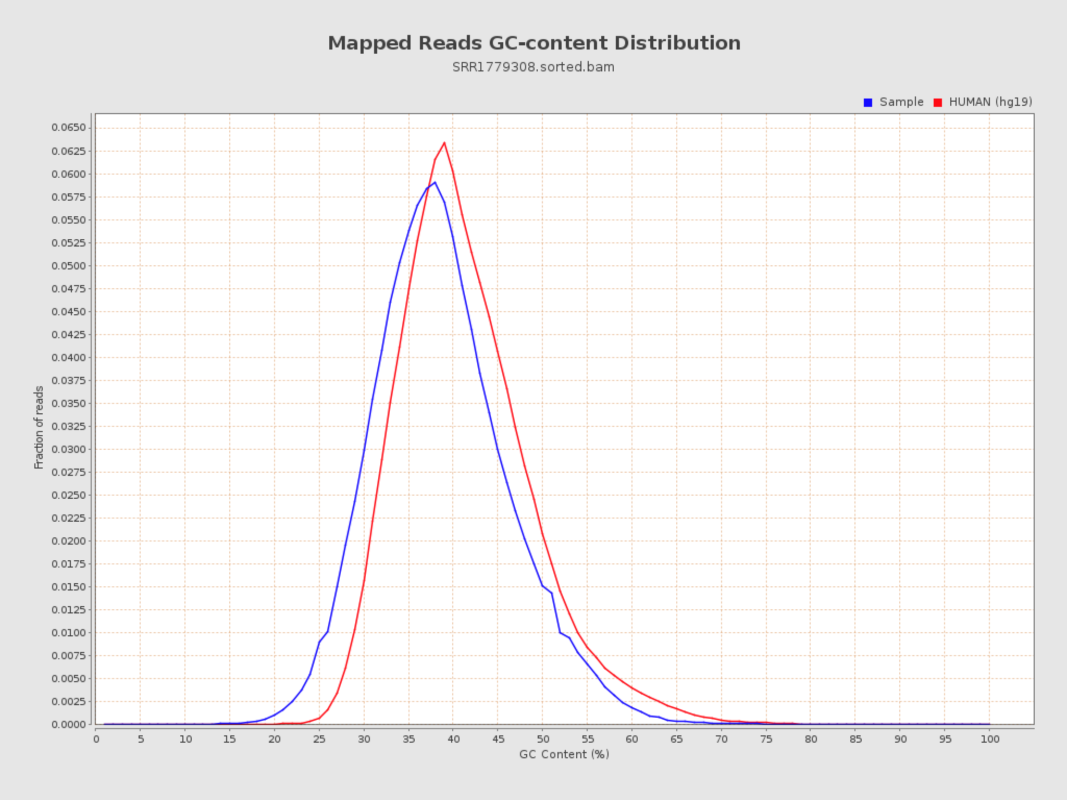
7. Results : Duplication Rate Histogram



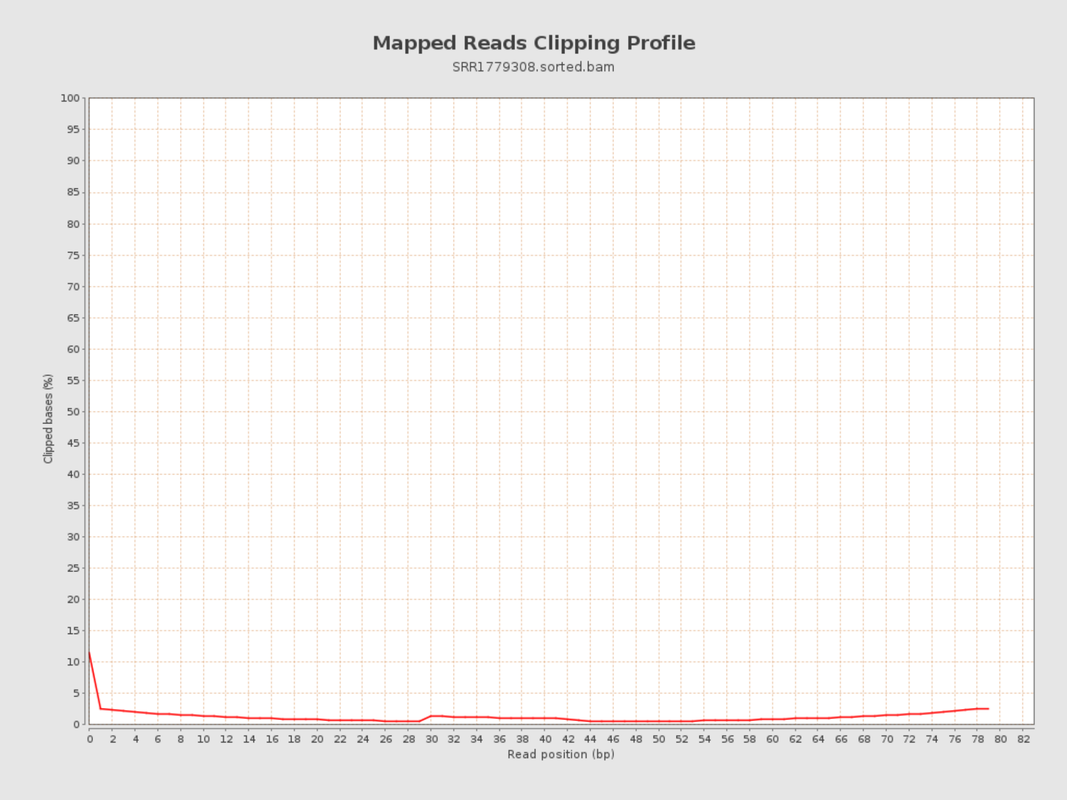
8. Results : Mapped Reads Nucleotide Content



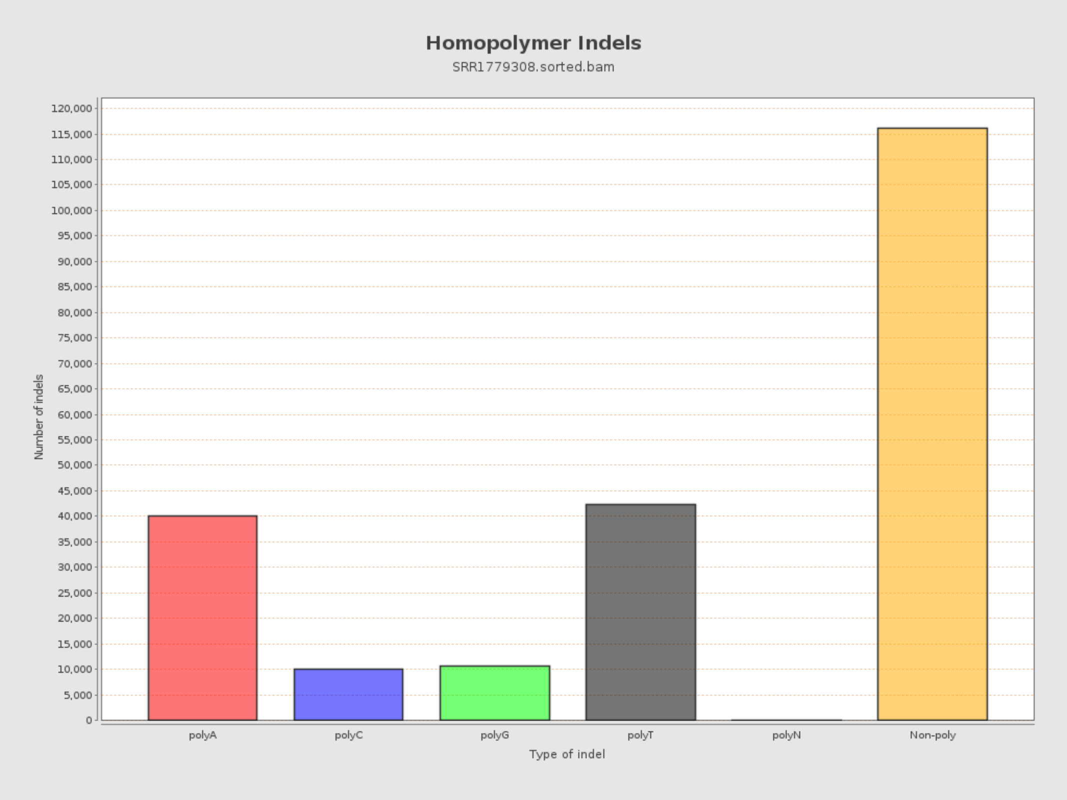
9. Results : Mapped Reads GC-content Distribution



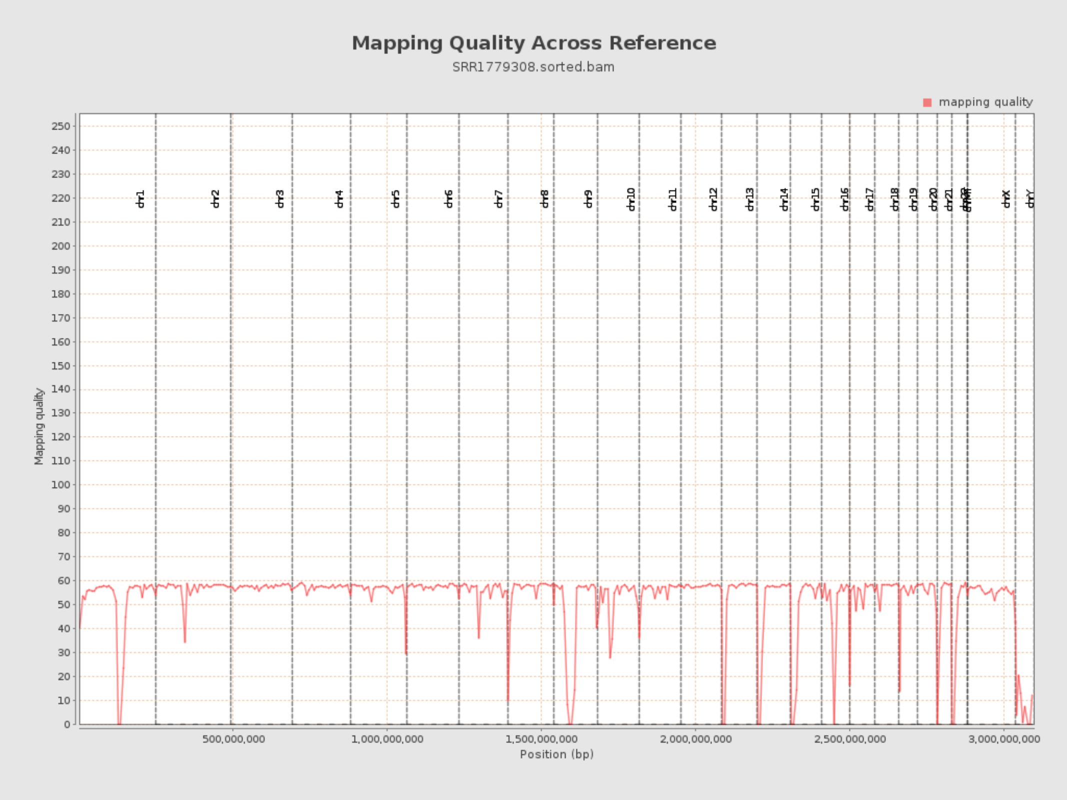
10. Results : Mapped Reads Clipping Profile



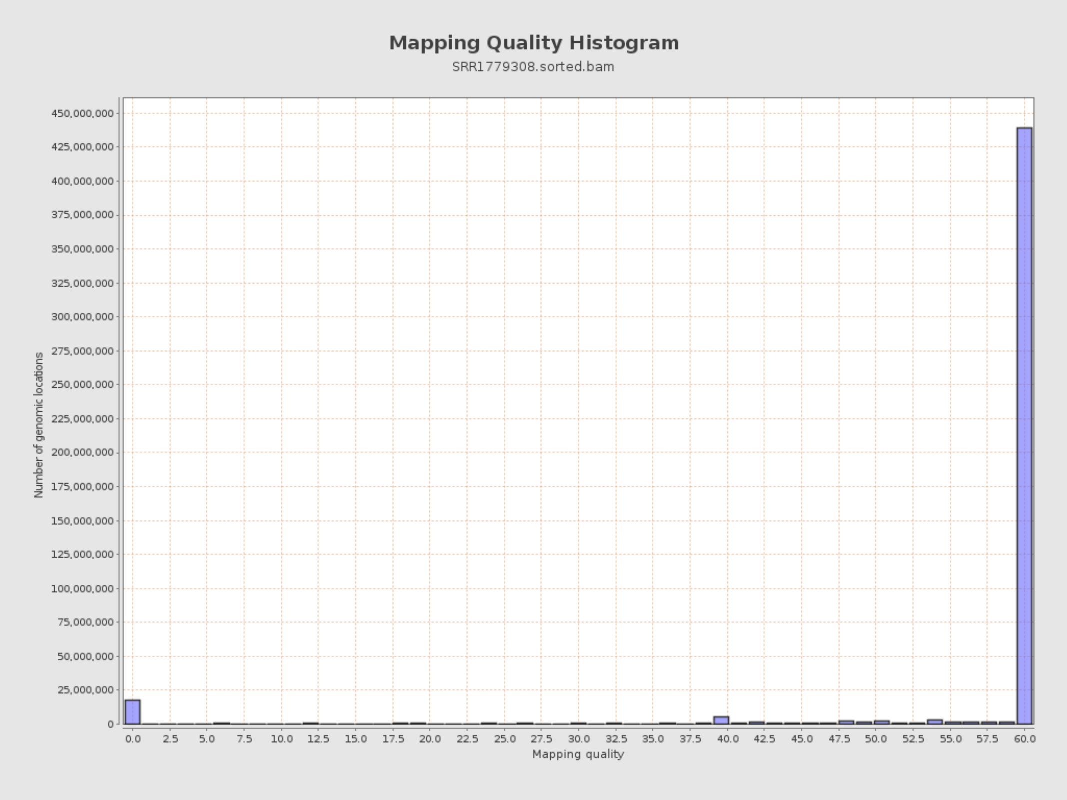
11. Results : Homopolymer Indels



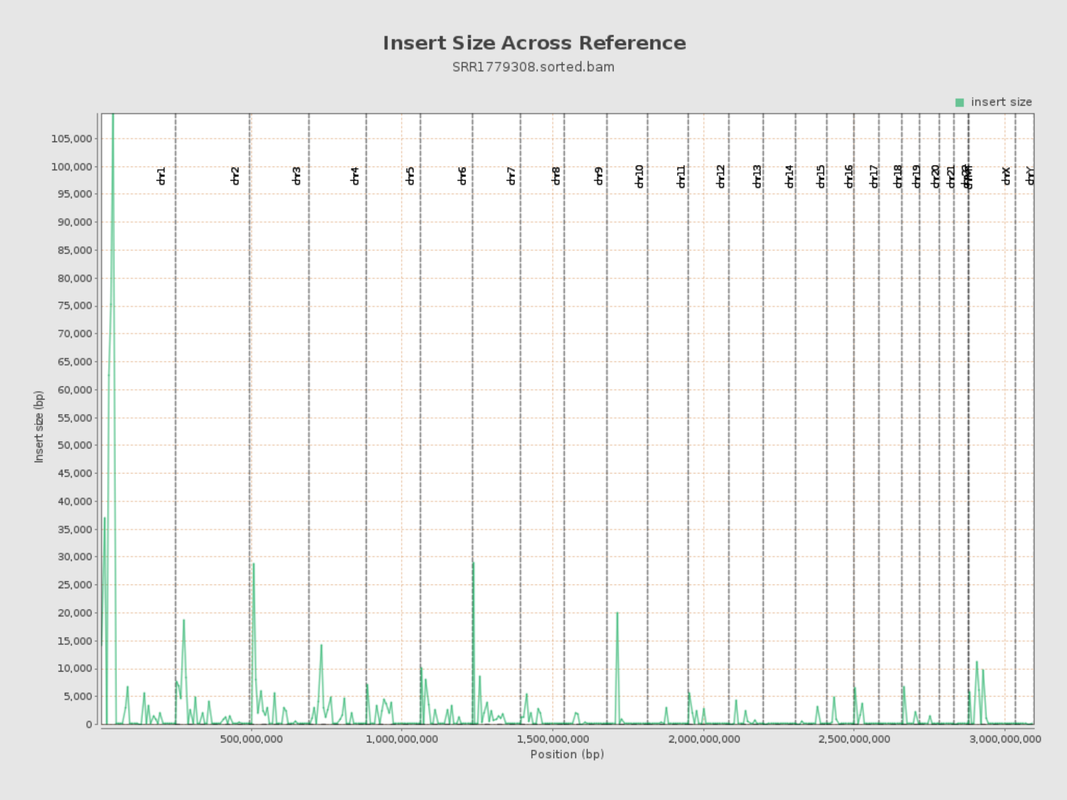
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram