Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/02 10:55:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438295.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_SRR8438295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438295_1.fastq.gz SRR8438295_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jan 02 10:55:06 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	714,225,630
Mapped reads	711,676,393 / 99.64%
Unmapped reads	2,549,237 / 0.36%
Mapped paired reads	711,676,393 / 99.64%
Mapped reads, first in pair	356,151,408 / 49.87%
Mapped reads, second in pair	355,524,985 / 49.78%
Mapped reads, both in pair	709,817,614 / 99.38%
Mapped reads, singletons	1,858,779 / 0.26%
Secondary alignments	0
Supplementary alignments	13,081,194 / 1.83%
Read min/max/mean length	28 / 151 / 146.28
Duplicated reads (estimated)	328,469,524 / 45.99%
Duplication rate	43.19%
Clipped reads	127,513,887 / 17.85%

2.2. ACGT Content

Number/percentage of A's	31,278,208,705 / 30.32%
Number/percentage of C's	20,548,254,913 / 19.92%
Number/percentage of T's	29,757,110,162 / 28.85%
Number/percentage of G's	21,572,694,164 / 20.91%
Number/percentage of N's	770,370 / 0%

GC Percentage	40.83%

2.3. Coverage

Mean	33.3326
Standard Deviation	106.4936

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	49,154.59
Standard Deviation	2,168,322.19
P25/Median/P75	207 / 270 / 364

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	528,952,444
Insertions	13,385,348
Mapped reads with at least one insertion	1.85%
Deletions	11,995,697
Mapped reads with at least one deletion	1.65%
Homopolymer indels	48.49%

2.7. Chromosome stats

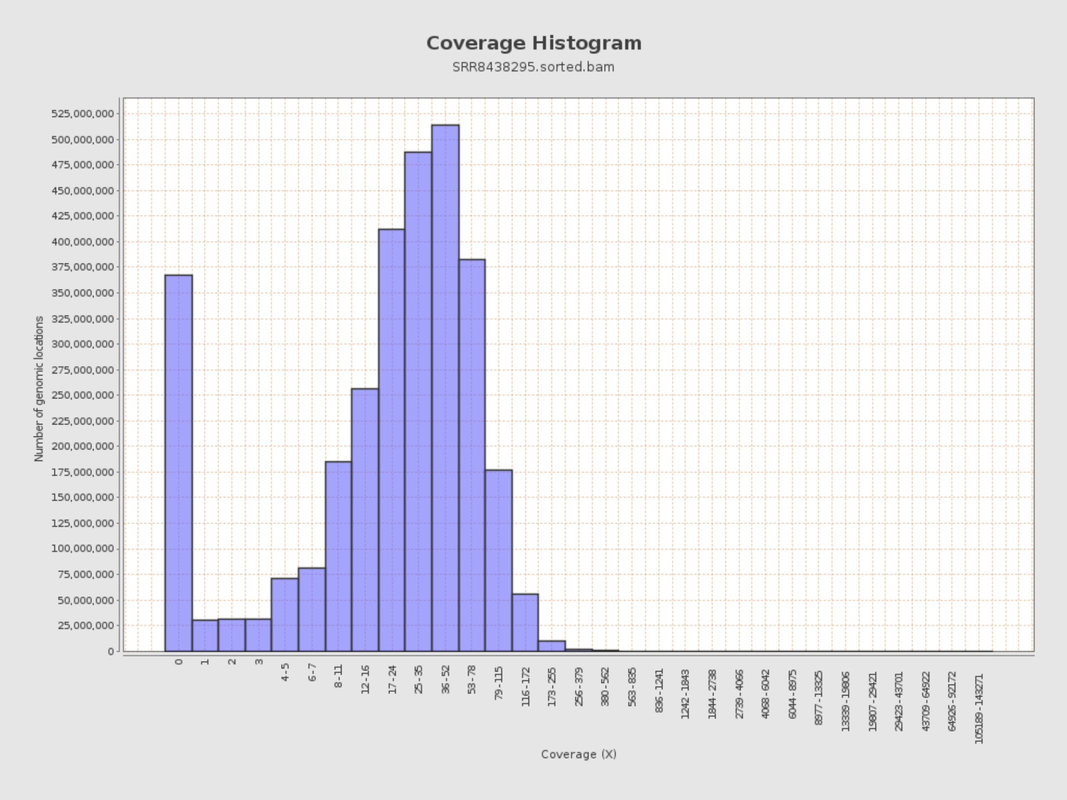
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	7898418717	31.6887	34.802
chr2	243199373	8489731449	34.9085	125.0908
chr3	198022430	7764864633	39.212	31.2191
chr4	191154276	7339719419	38.3968	30.6405
chr5	180915260	6535156101	36.1227	30.4752
chr6	171115067	6335283018	37.0235	33.071
chr7	159138663	6178604220	38.8253	32.4536
chr8	146364022	6173380668	42.1783	33.2781
chr9	141213431	4618651542	32.7069	38.8455
chr10	135534747	5233239105	38.6118	41.0808
chr11	135006516	4145950039	30.7093	30.5536
chr12	133851895	4442273719	33.188	29.4613
chr13	115169878	3410023864	29.6086	29.9149
chr14	107349540	3011075008	28.0493	30.5219
chr15	102531392	3139785866	30.6227	33.1724
chr16	90354753	2531380215	28.016	44.6726
chr17	81195210	2438344374	30.0306	35.2908
chr18	78077248	2711894241	34.7335	31.834
chr19	59128983	1703516325	28.8102	31.6687
chr20	63025520	2339394280	37.1182	34.2773
chr21	48129895	1409358783	29.2824	34.7459
chr22	51304566	1102416383	21.4877	30.8601
chrMT	16571	634181730	38,270.5769	15,350.5651
chrX	155270560	3117915008	20.0805	19.8493

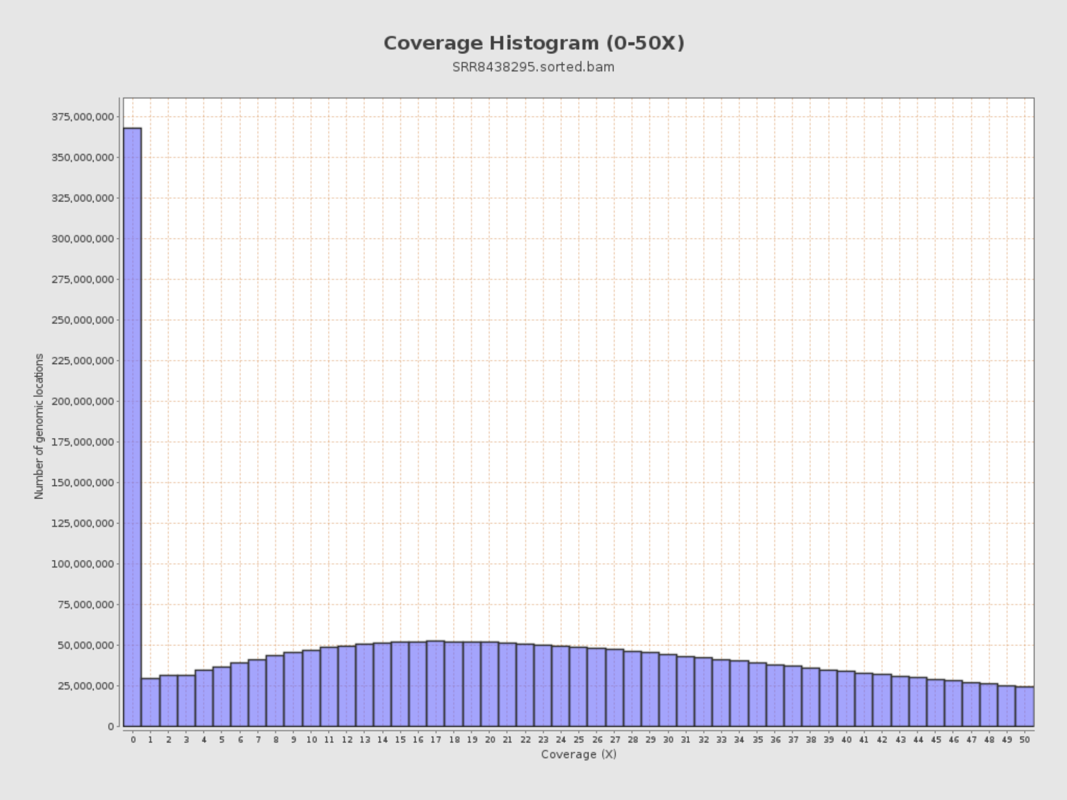
chrY	59373566	482968957	8.1344	22.7564

3. Results : Coverage across reference

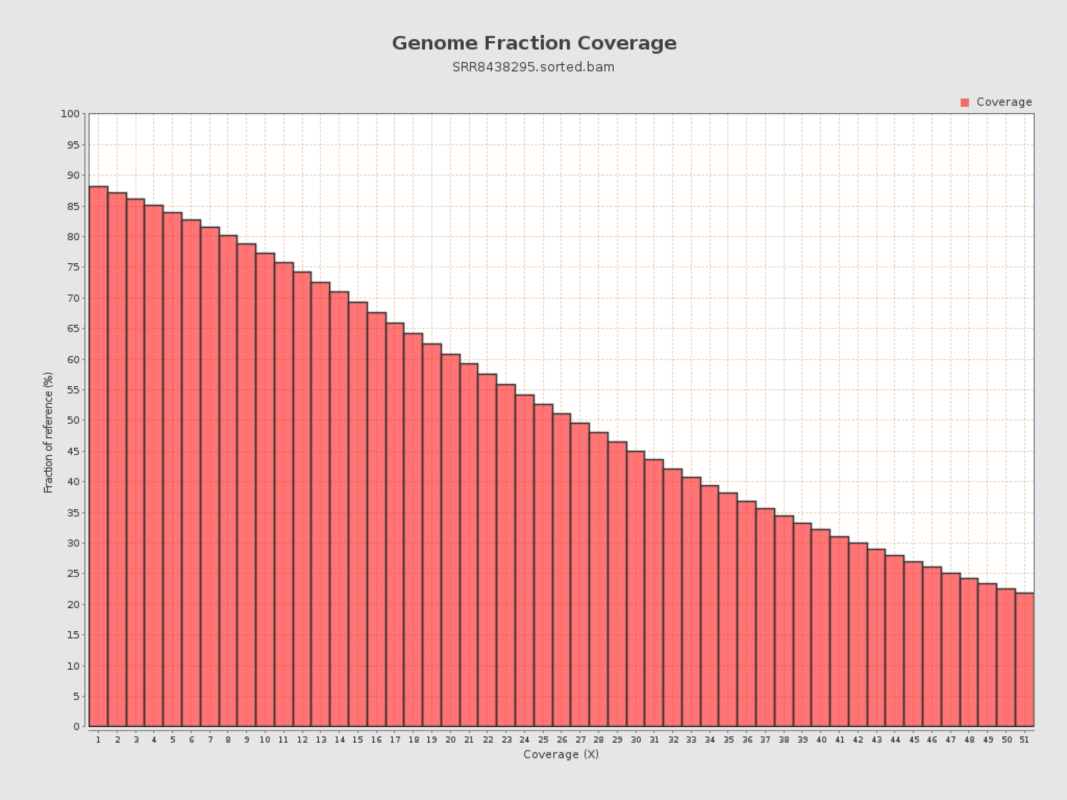
4. Results : Coverage Histogram



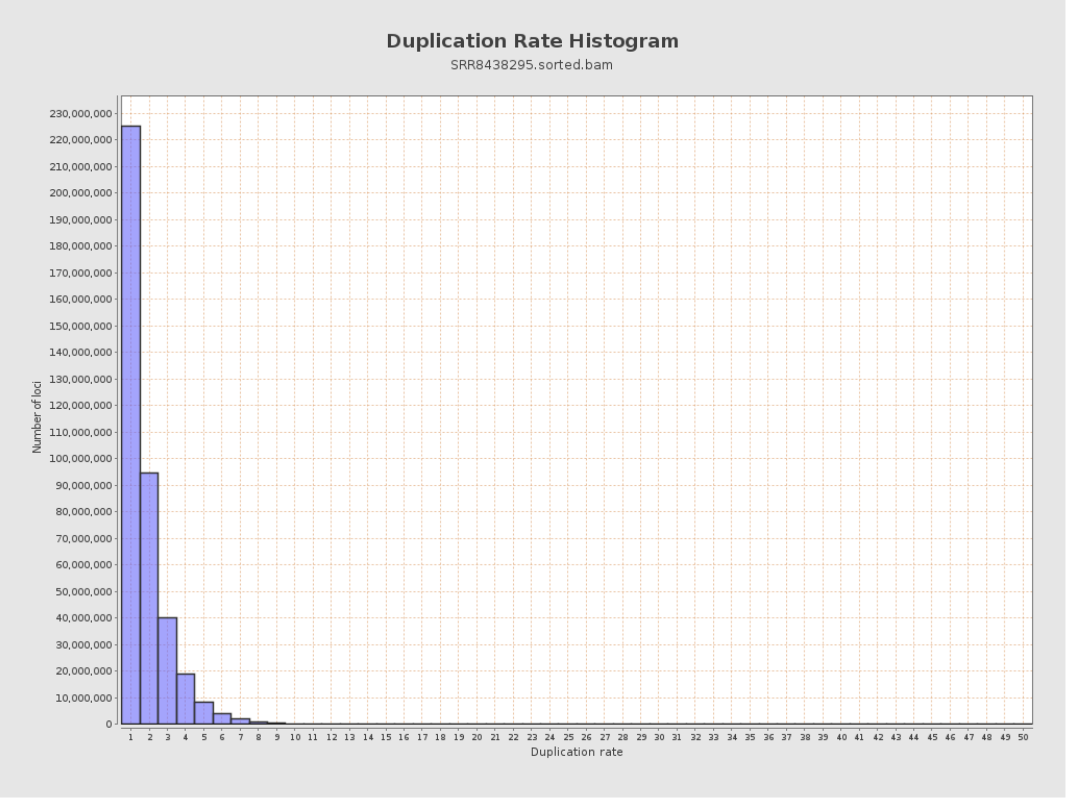
5. Results : Coverage Histogram (0-50X)



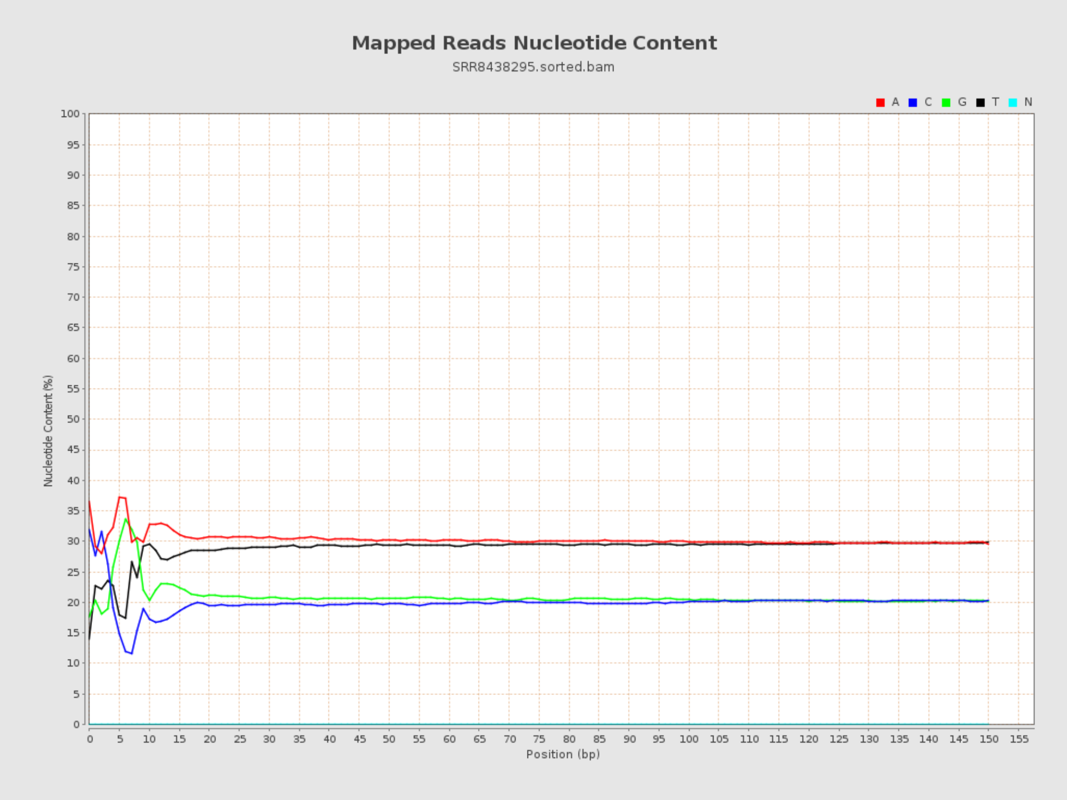
6. Results : Genome Fraction Coverage



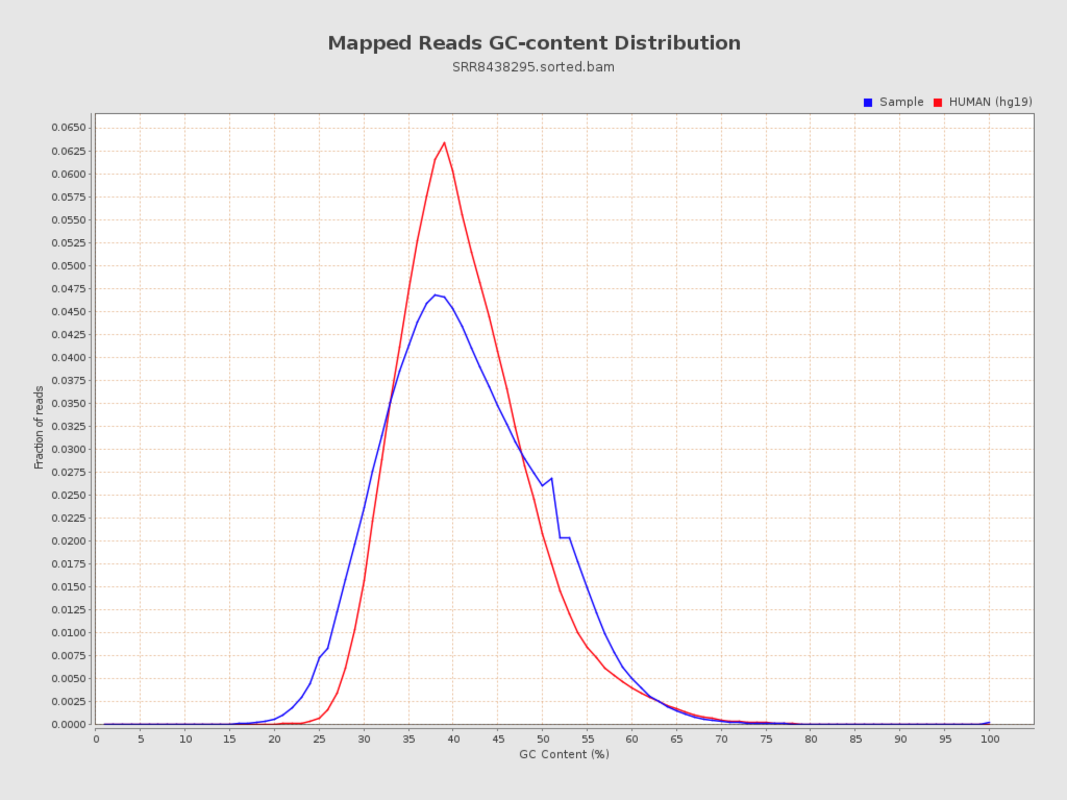
7. Results : Duplication Rate Histogram



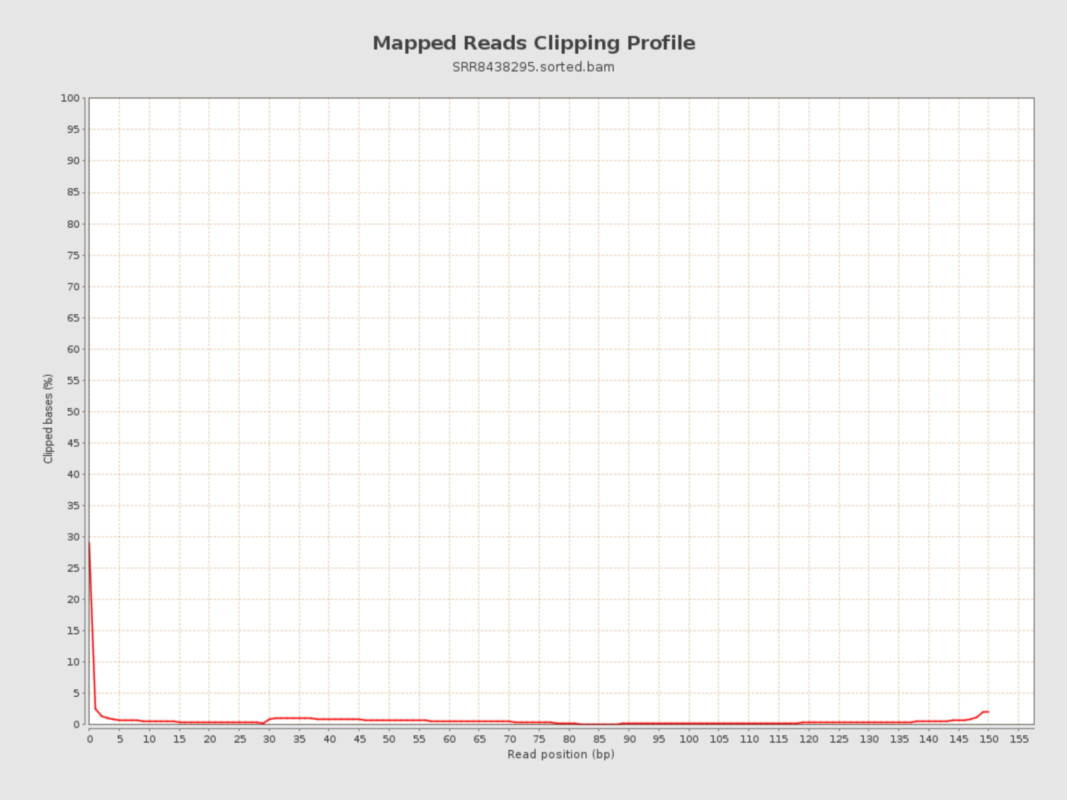
8. Results : Mapped Reads Nucleotide Content



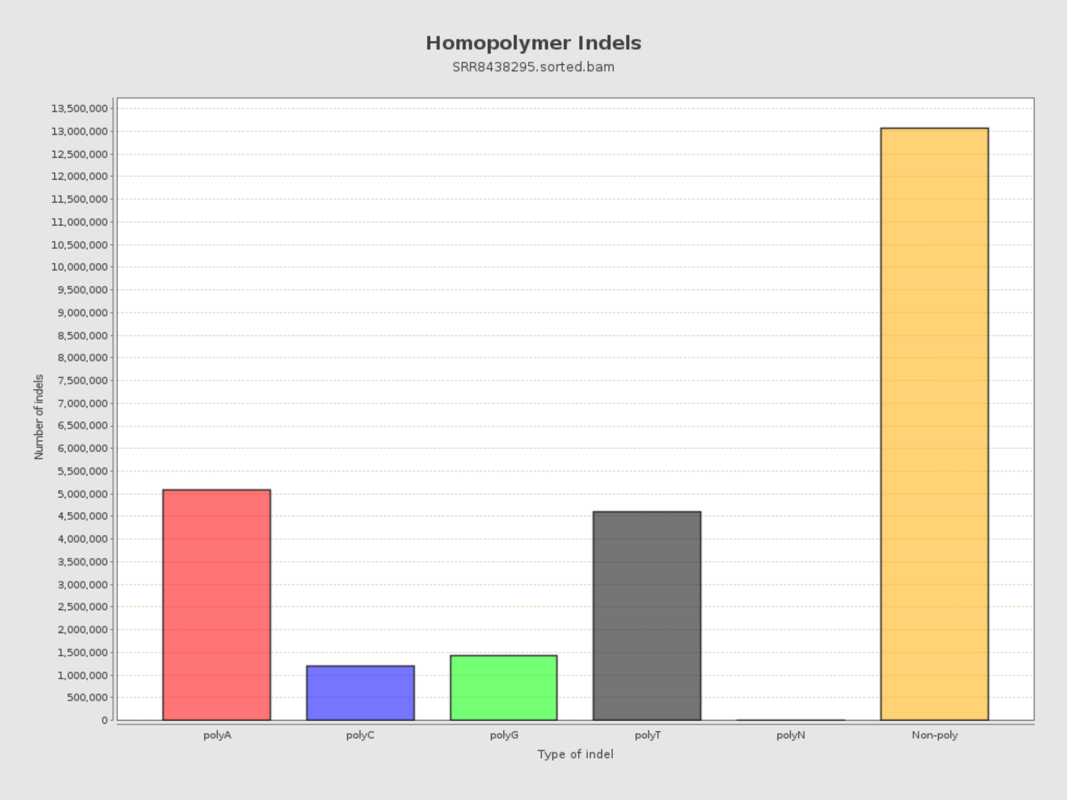
9. Results : Mapped Reads GC-content Distribution



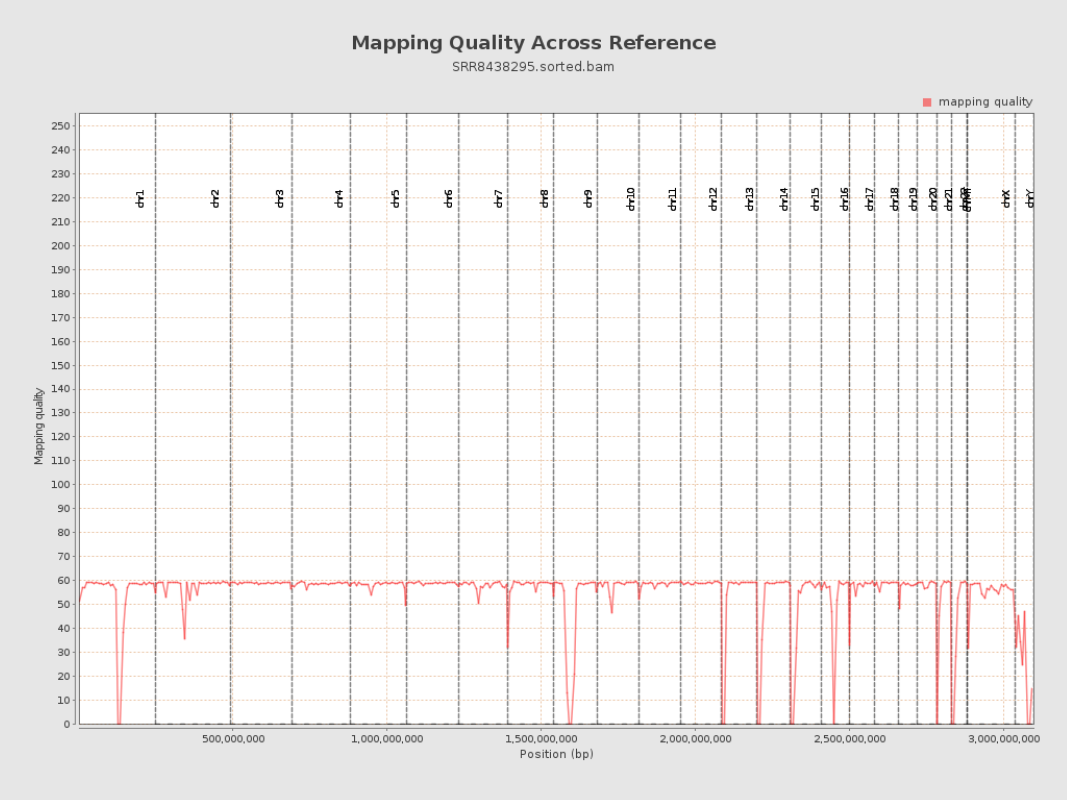
10. Results : Mapped Reads Clipping Profile



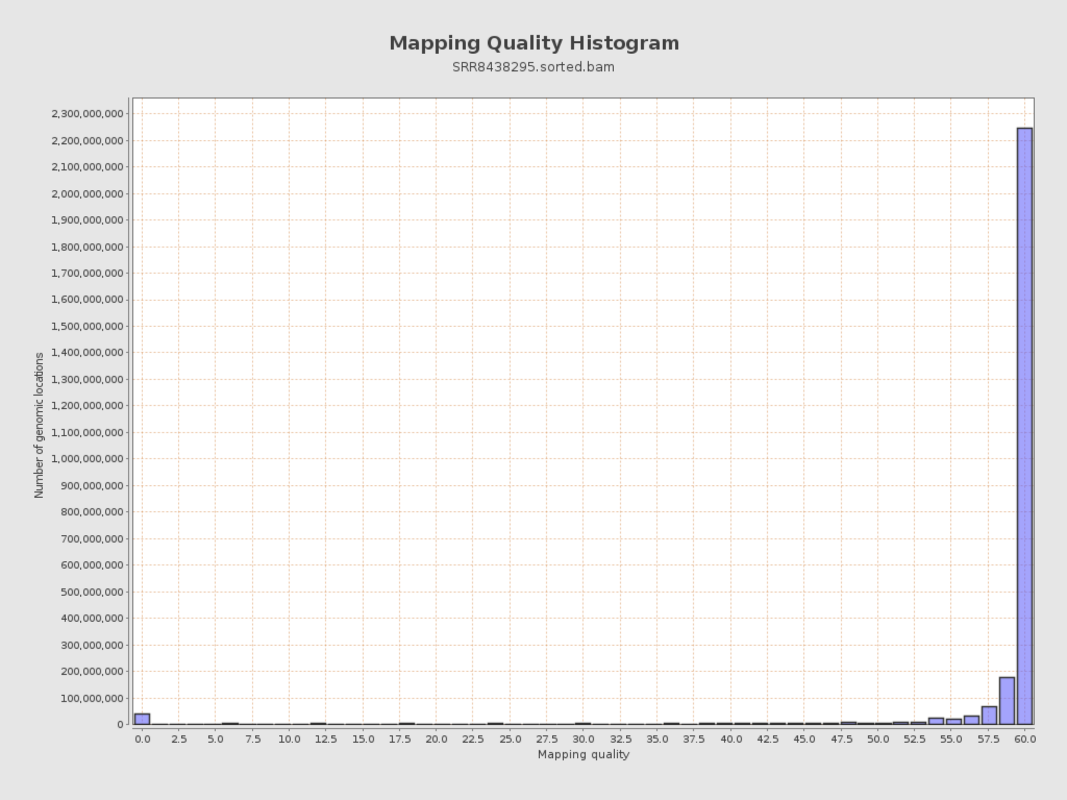
11. Results : Homopolymer Indels



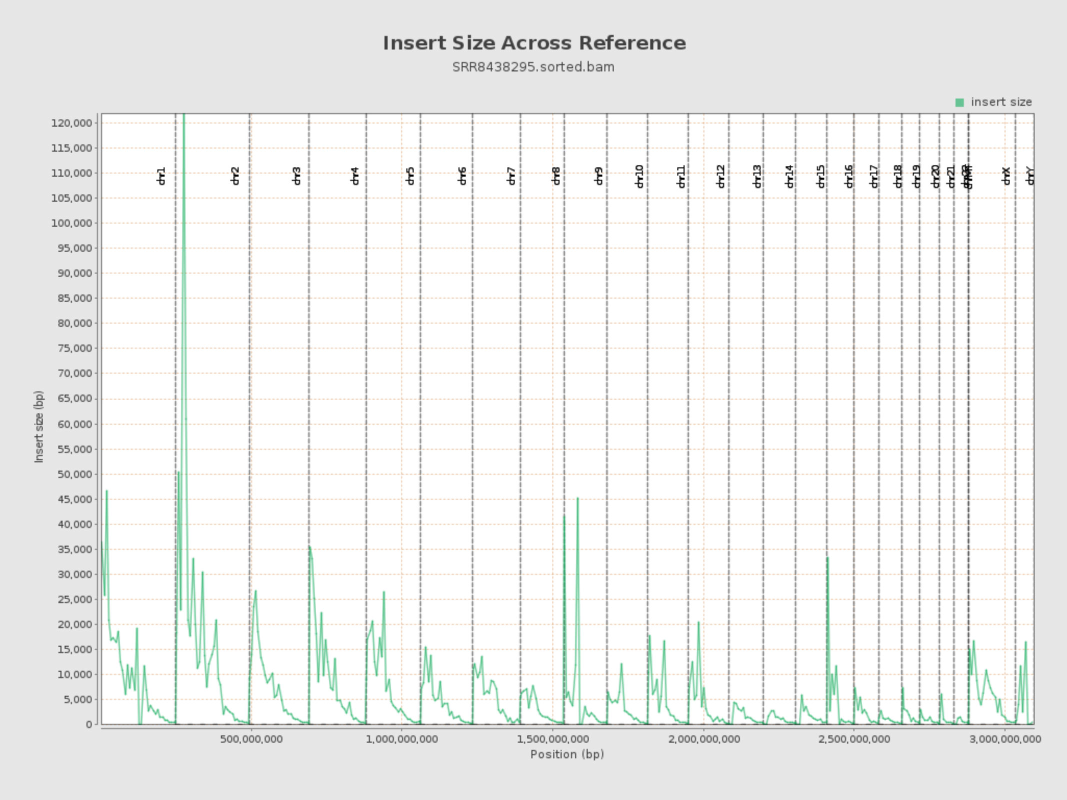
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram