Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/31 12:17:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438291.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_SRR8438291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438291_1.fastq.gz SRR8438291_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 31 12:17:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	703,325,588
Mapped reads	701,179,152 / 99.69%
Unmapped reads	2,146,436 / 0.31%
Mapped paired reads	701,179,152 / 99.69%
Mapped reads, first in pair	350,700,128 / 49.86%
Mapped reads, second in pair	350,479,024 / 49.83%
Mapped reads, both in pair	699,705,910 / 99.49%
Mapped reads, singletons	1,473,242 / 0.21%
Secondary alignments	0
Supplementary alignments	11,569,711 / 1.65%
Read min/max/mean length	28 / 151 / 145.34
Duplicated reads (estimated)	339,716,271 / 48.3%
Duplication rate	45.6%
Clipped reads	129,951,961 / 18.48%

2.2. ACGT Content

Number/percentage of A's	30,550,907,872 / 30.26%
Number/percentage of C's	20,176,426,979 / 19.98%
Number/percentage of T's	29,225,887,551 / 28.95%
Number/percentage of G's	21,014,774,625 / 20.81%
Number/percentage of N's	621,525 / 0%

GC Percentage	40.8%

2.3. Coverage

Mean	32.6246
Standard Deviation	83.4599

2.4. Mapping Quality

Mean Mapping Quality	55.14

2.5. Insert size

Mean	39,426.64
Standard Deviation	1,937,538.76
P25/Median/P75	180 / 232 / 308

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	514,660,025
Insertions	12,616,301
Mapped reads with at least one insertion	1.77%
Deletions	11,163,279
Mapped reads with at least one deletion	1.57%
Homopolymer indels	48.28%

2.7. Chromosome stats

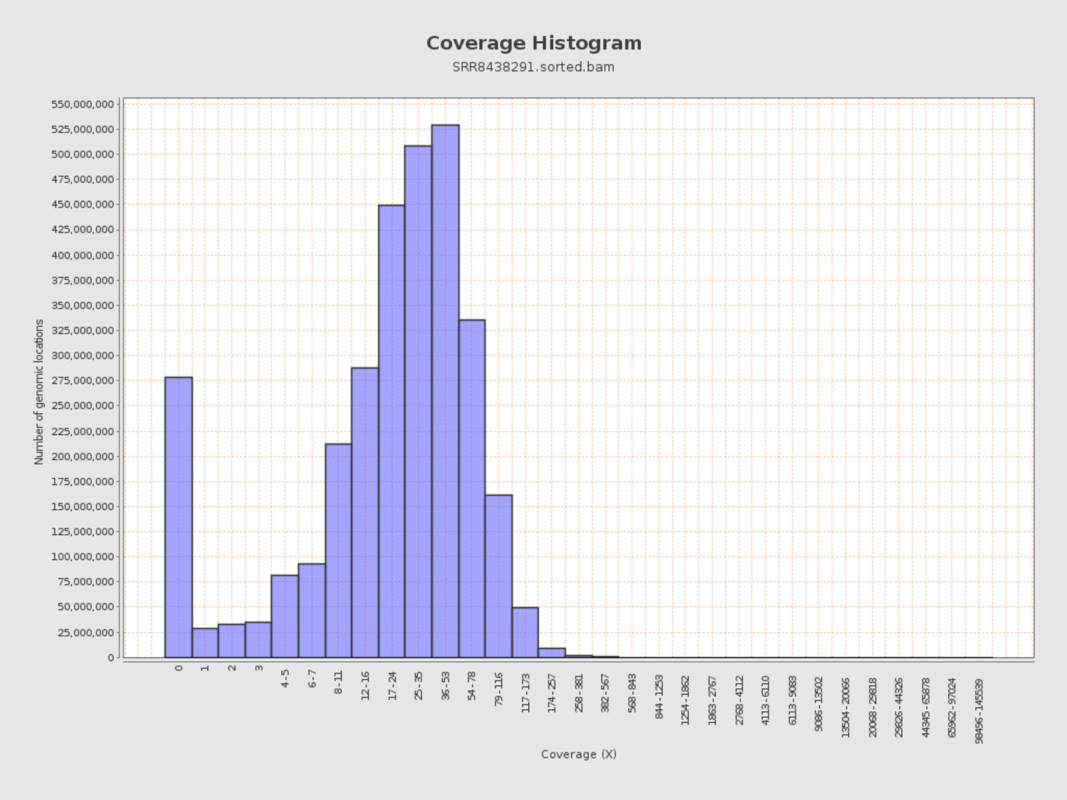
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	**coverage**	**deviation**
chr1	249250621	8271242452	33.1844	33.8557
chr2	243199373	8918776744	36.6727	130.2843
chr3	198022430	7070450393	35.7053	56.2629
chr4	191154276	6796591176	35.5555	29.237
chr5	180915260	6427762582	35.5291	30.373
chr6	171115067	6209515440	36.2885	30.876
chr7	159138663	5340618360	33.5595	29.9964
chr8	146364022	5387341996	36.8078	31.0225
chr9	141213431	4412837485	31.2494	35.358
chr10	135534747	4835483464	35.6771	36.6969
chr11	135006516	4964659942	36.7735	32.3415
chr12	133851895	4768149323	35.6226	30.0787
chr13	115169878	3574304152	31.0351	30.0286
chr14	107349540	3268404042	30.4464	31.0186
chr15	102531392	2856934838	27.864	30.8324
chr16	90354753	2567807703	28.4192	49.642
chr17	81195210	2425382445	29.871	37.1806
chr18	78077248	2801795849	35.8849	31.6576
chr19	59128983	1565891241	26.4826	74.0782
chr20	63025520	2156636645	34.2185	32.2719
chr21	48129895	1285119986	26.7011	38.6222
chr22	51304566	1002301291	19.5363	28.3873
chrMT	16571	444941579	26,850.6173	10,365.0904
chrX	155270560	3170094803	20.4166	21.1603

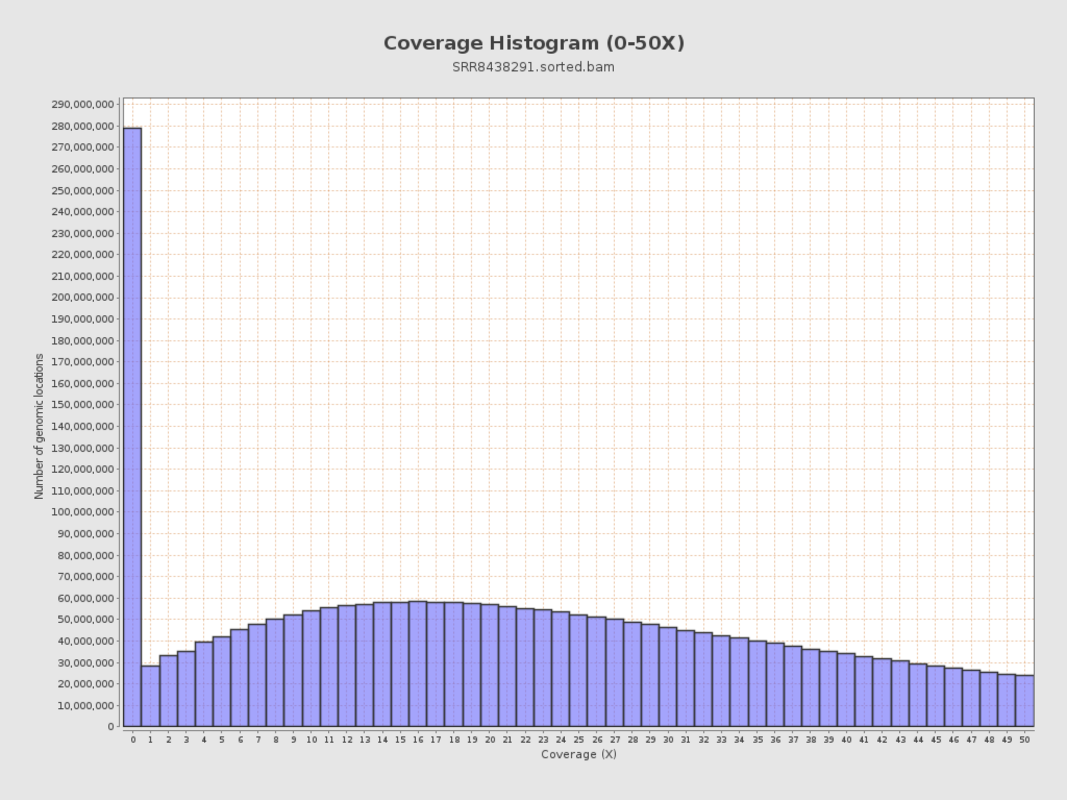
chrY	59373566	472888033	7.9646	25.799

3. Results : Coverage across reference

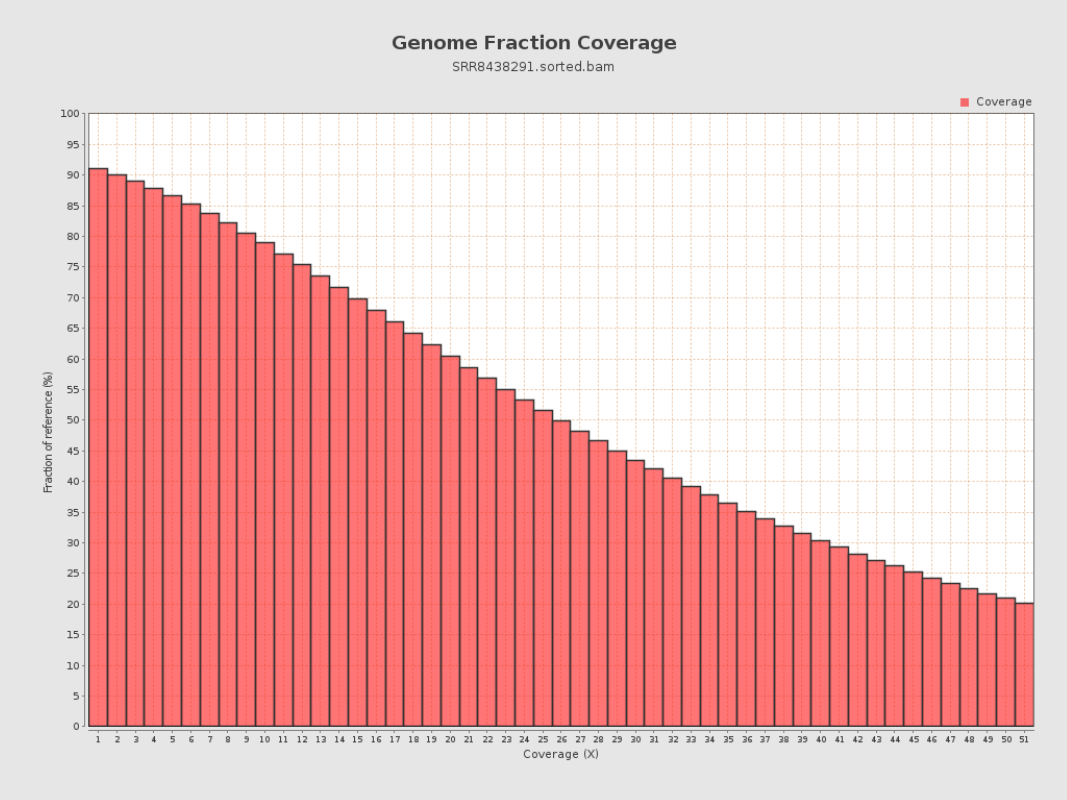
4. Results : Coverage Histogram



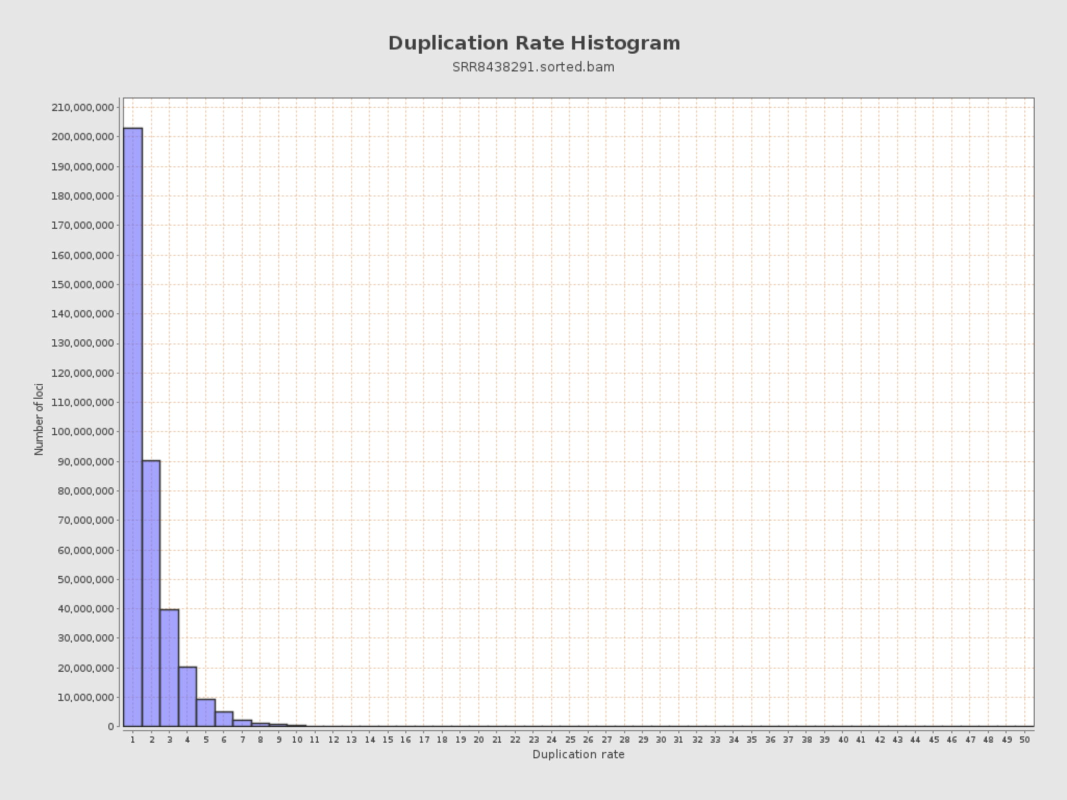
5. Results : Coverage Histogram (0-50X)



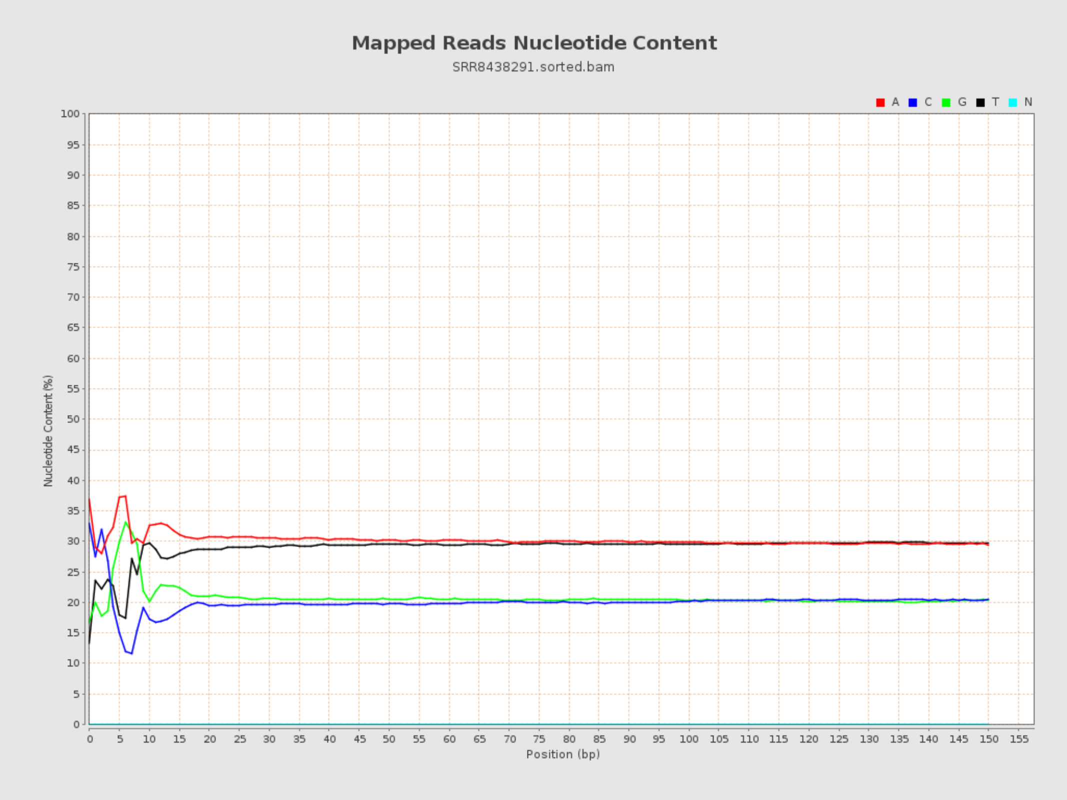
6. Results : Genome Fraction Coverage



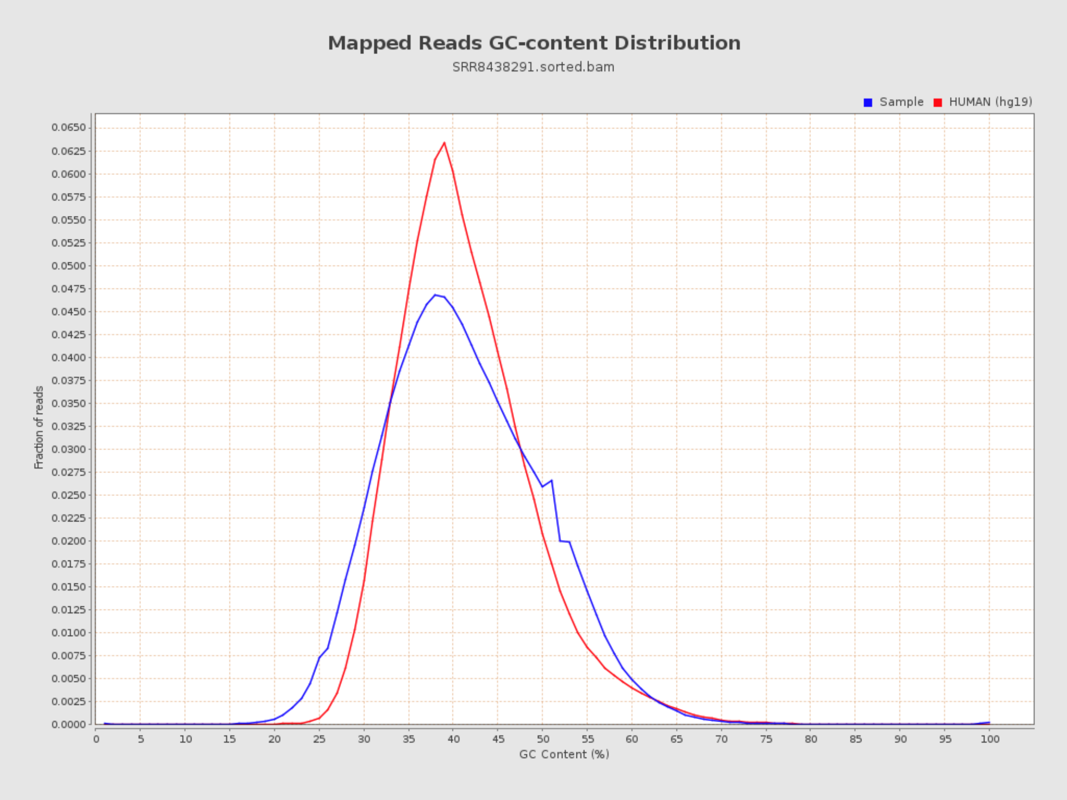
7. Results : Duplication Rate Histogram



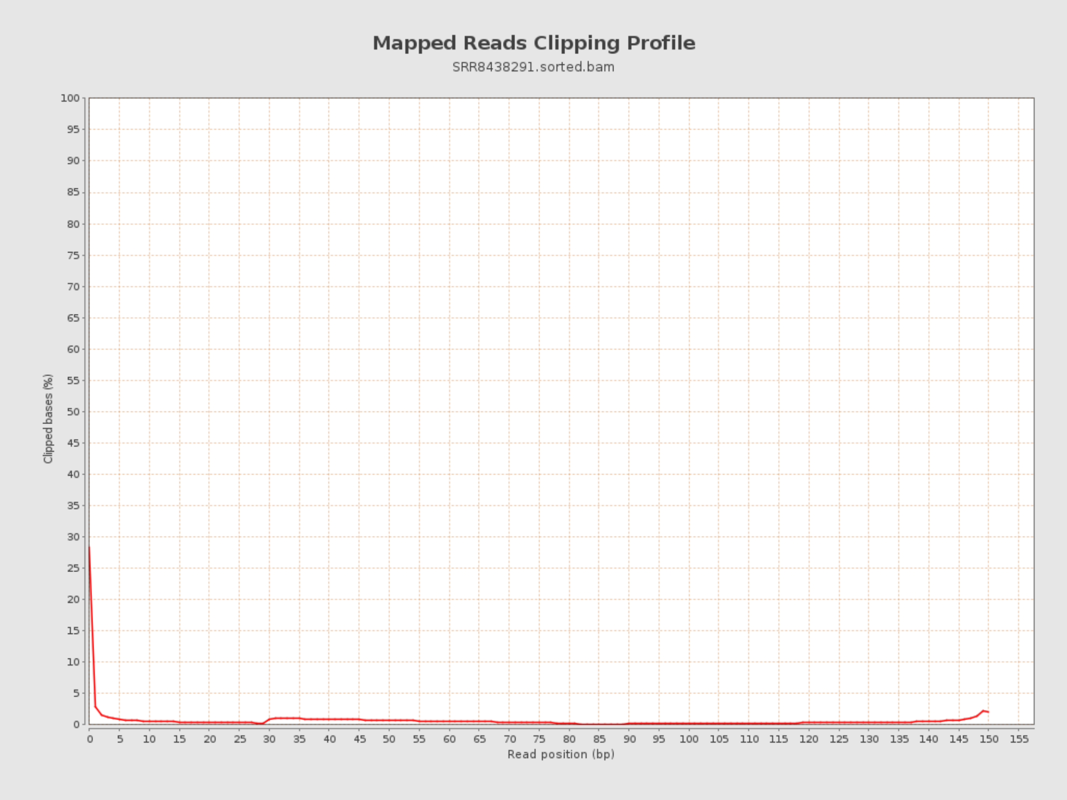
8. Results : Mapped Reads Nucleotide Content



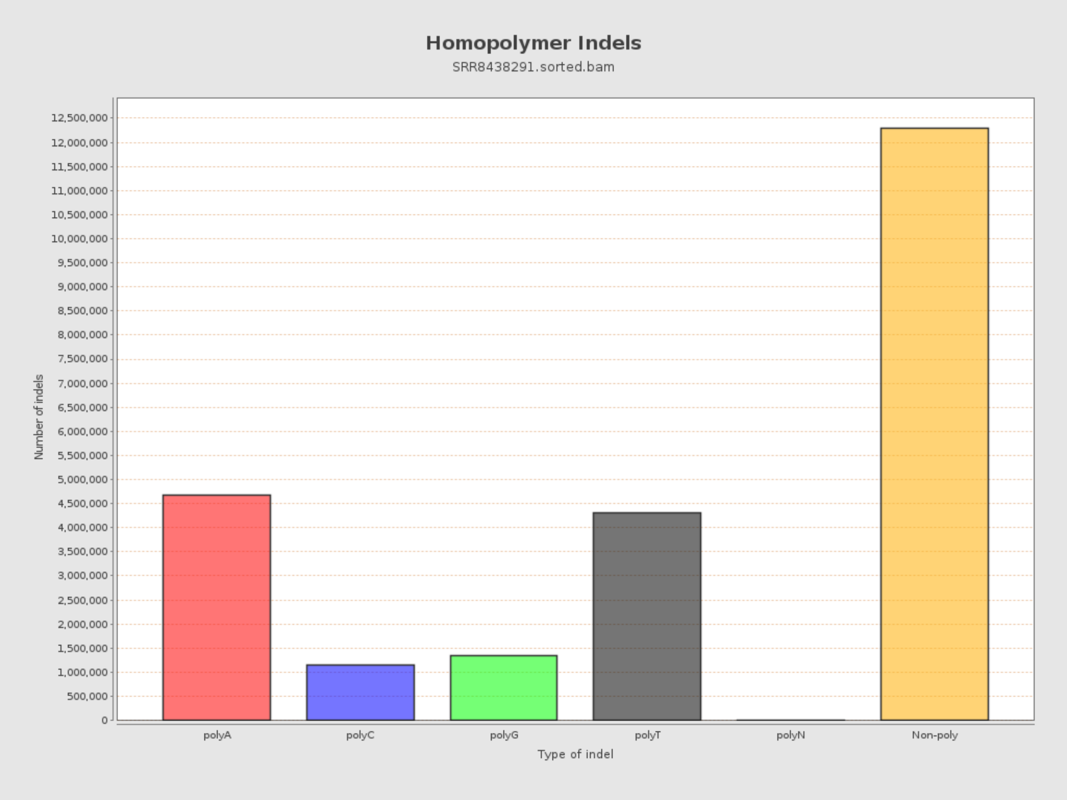
9. Results : Mapped Reads GC-content Distribution



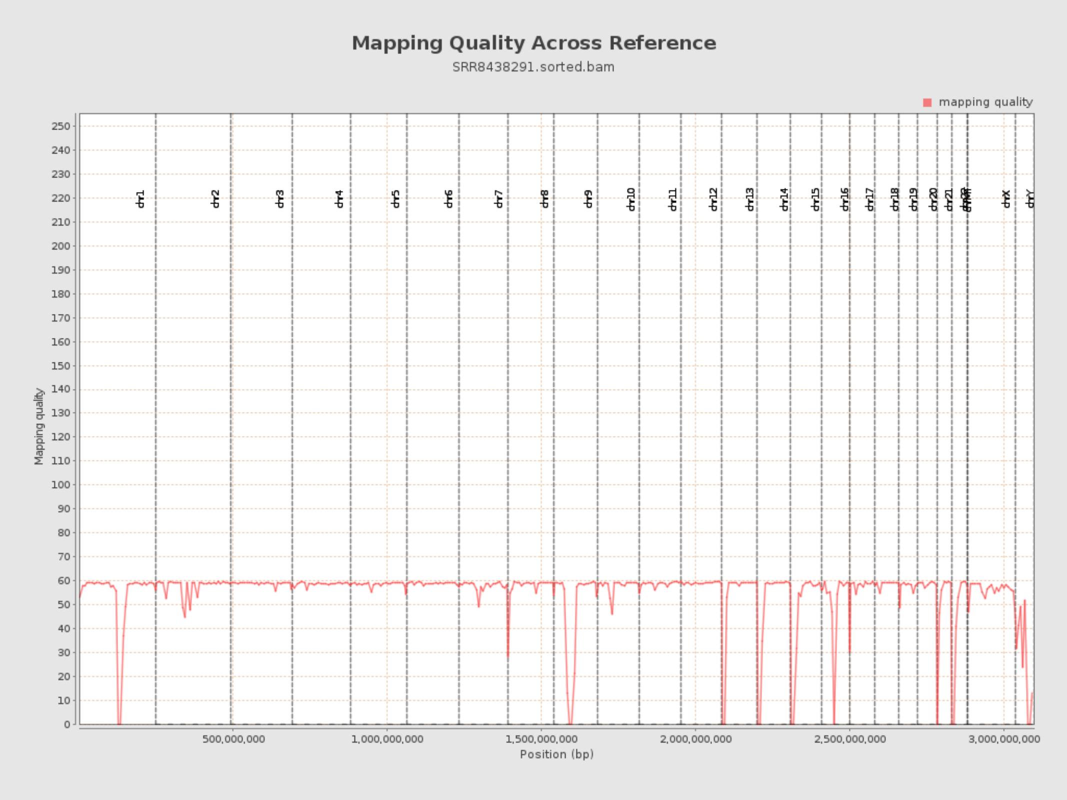
10. Results : Mapped Reads Clipping Profile



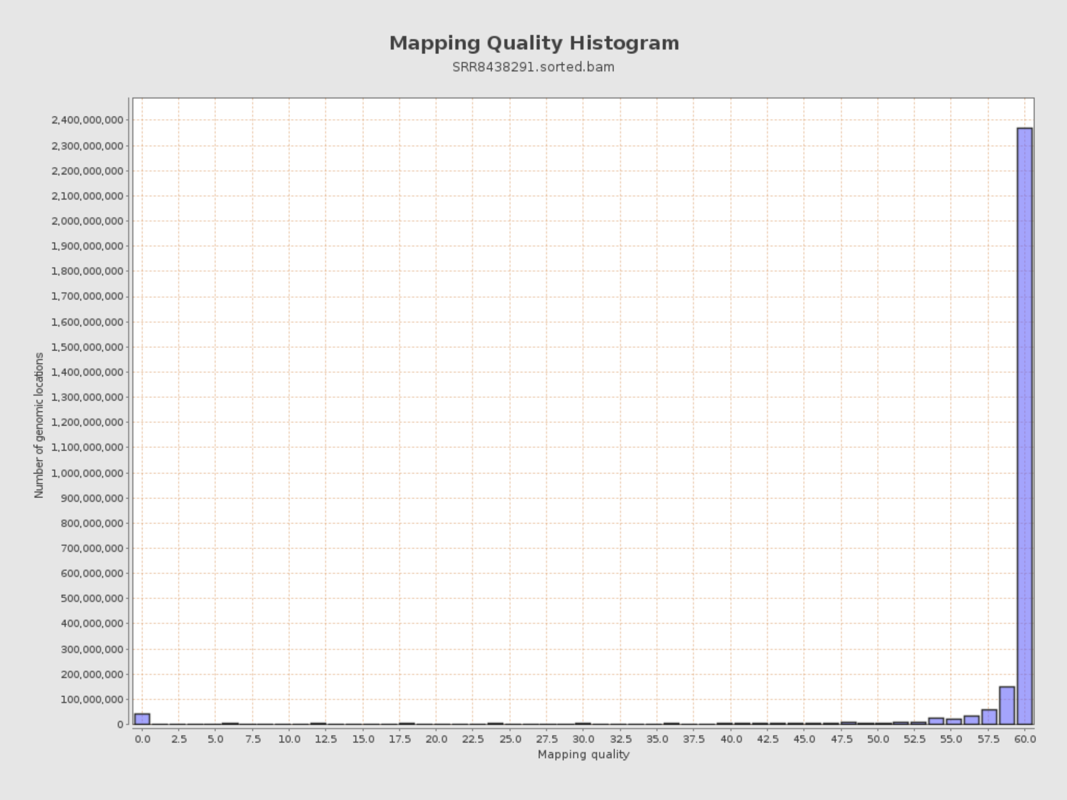
11. Results : Homopolymer Indels



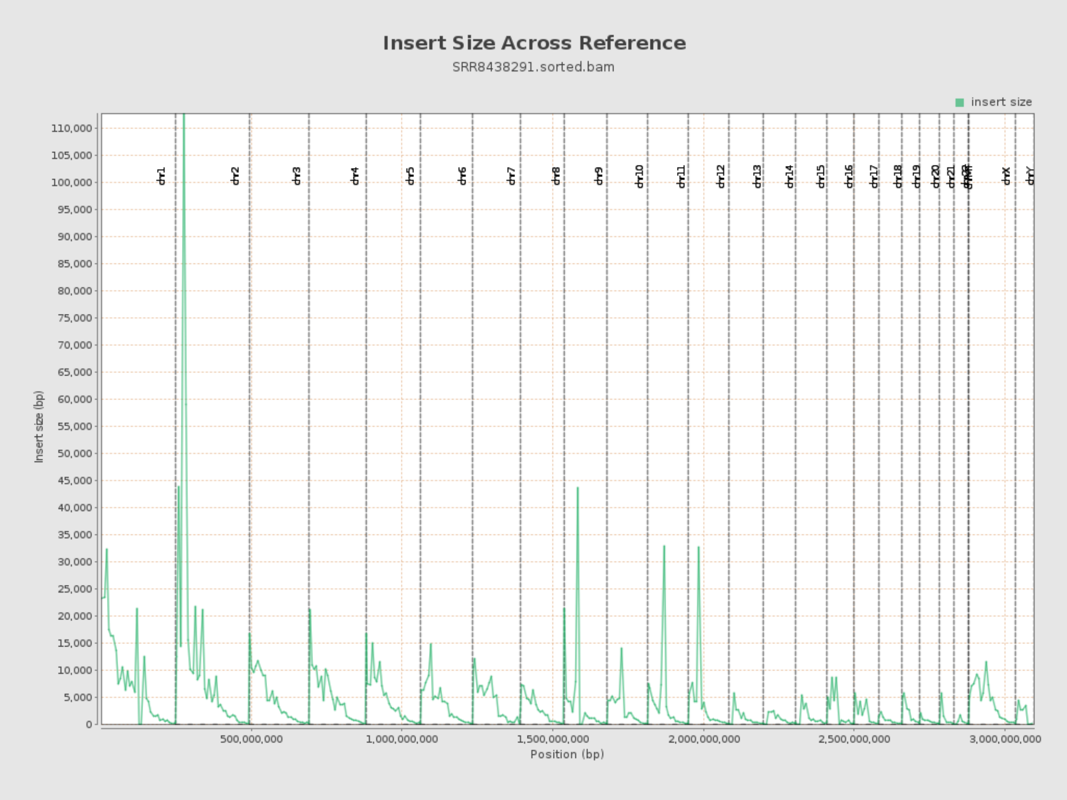
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram