Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/26 23:47:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438285.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_SRR8438285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438285_1.fastq.gz SRR8438285_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 26 23:47:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	811,866,872
Mapped reads	808,949,403 / 99.64%
Unmapped reads	2,917,469 / 0.36%
Mapped paired reads	808,949,403 / 99.64%
Mapped reads, first in pair	404,695,150 / 49.85%
Mapped reads, second in pair	404,254,253 / 49.79%
Mapped reads, both in pair	807,370,426 / 99.45%
Mapped reads, singletons	1,578,977 / 0.19%
Secondary alignments	0
Supplementary alignments	23,291,031 / 2.87%
Read min/max/mean length	30 / 149 / 121.65
Duplicated reads (estimated)	318,931,480 / 39.28%
Duplication rate	37.81%
Clipped reads	203,867,527 / 25.11%

2.2. ACGT Content

Number/percentage of A's	28,732,085,707 / 30.72%
Number/percentage of C's	18,165,577,597 / 19.42%
Number/percentage of T's	27,965,181,534 / 29.9%
Number/percentage of G's	18,662,260,163 / 19.95%
Number/percentage of N's	232,872 / 0%

GC Percentage	39.38%

2.3. Coverage

Mean	30.2187
Standard Deviation	389.0596

2.4. Mapping Quality

Mean Mapping Quality	53.05

2.5. Insert size

Mean	295,266.09
Standard Deviation	5,360,344.59
P25/Median/P75	83 / 146 / 220

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	265,807,274
Insertions	13,300,163
Mapped reads with at least one insertion	1.63%
Deletions	9,468,400
Mapped reads with at least one deletion	1.16%
Homopolymer indels	47.76%

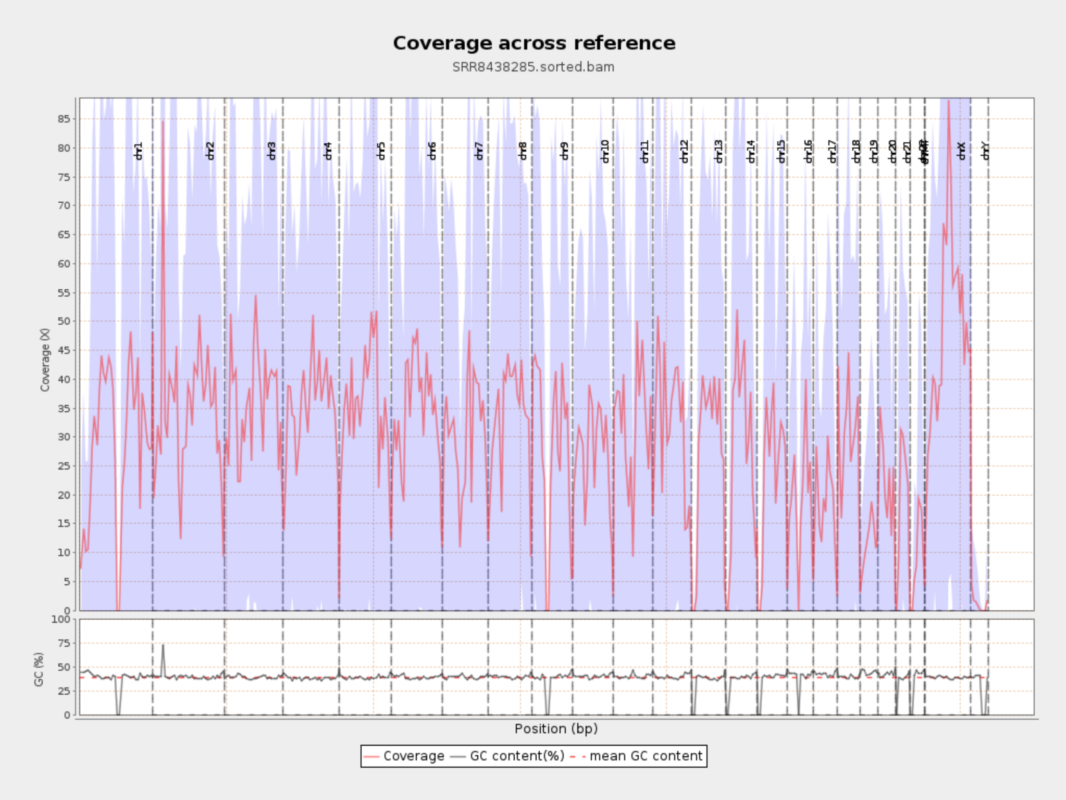
2.7. Chromosome stats

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

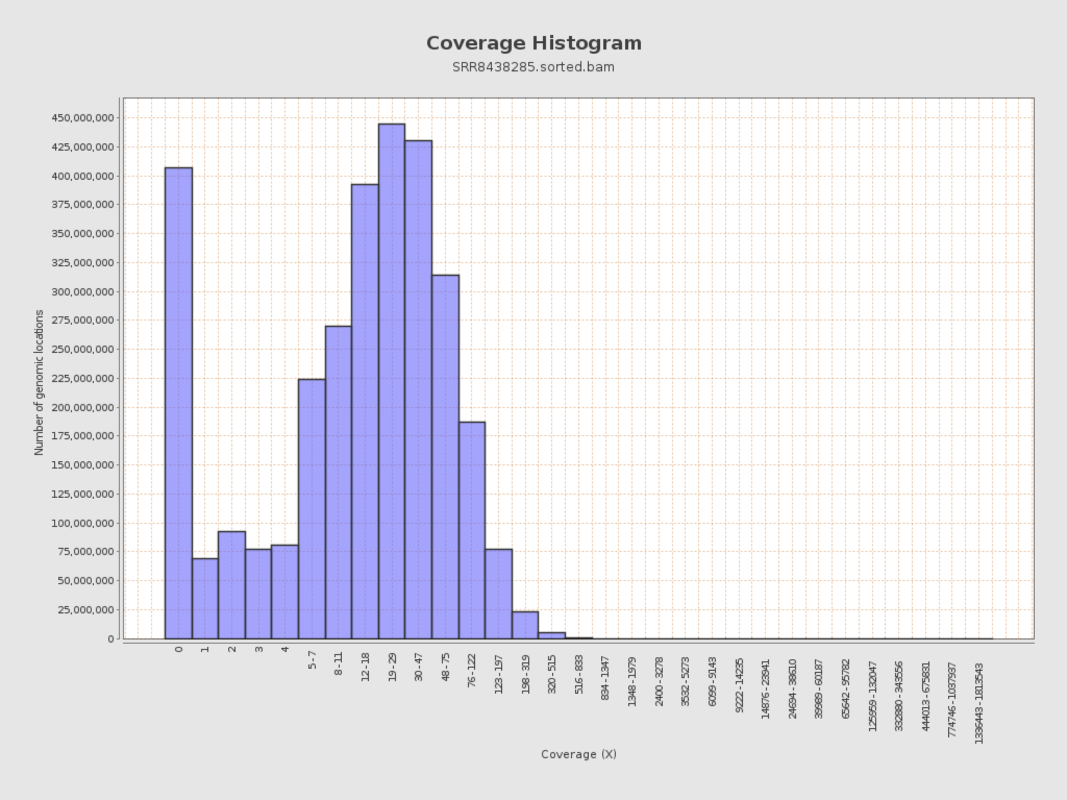
		bases	**coverage**	**deviation**
chr1	249250621	7249253048	29.0842	43.0351
chr2	243199373	8532497871	35.0844	1,380.9135
chr3	198022430	7131811037	36.0152	42.4675
chr4	191154276	6798281526	35.5644	39.7146
chr5	180915260	6328993427	34.9832	42.4924
chr6	171115067	5997096695	35.0472	42.6662
chr7	159138663	4824542372	30.3166	40.4364
chr8	146364022	5001467225	34.1714	41.0483
chr9	141213431	3946811420	27.9493	40.093
chr10	135534747	3713240401	27.397	36.2303
chr11	135006516	4314739741	31.9595	41.0198
chr12	133851895	4315287240	32.2393	42.2575
chr13	115169878	3234022211	28.0805	37.2794
chr14	107349540	3005538642	27.9977	41.0572
chr15	102531392	2425174999	23.653	37.6699
chr16	90354753	1656825198	18.3369	28.6653
chr17	81195210	1468931168	18.0914	29.3856
chr18	78077248	2383313886	30.5251	36.8962
chr19	59128983	700956221	11.8547	20.1398
chr20	63025520	1387427929	22.0137	33.7871
chr21	48129895	962057608	19.9888	32.3991
chr22	51304566	456296770	8.8939	22.0325
chrMT	16571	152723	9.2163	6.2681
chrX	155270560	7644368195	49.2326	59.8762

chrY	59373566	68790334	1.1586	7.2883

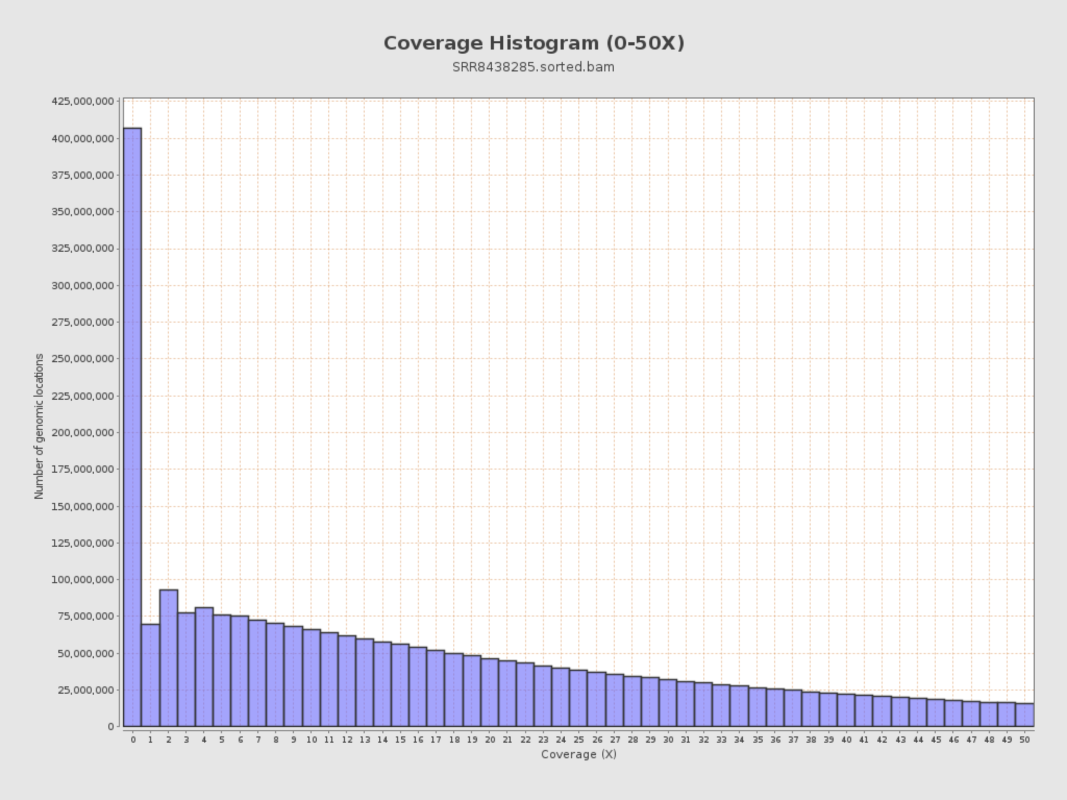
3. Results : Coverage across reference



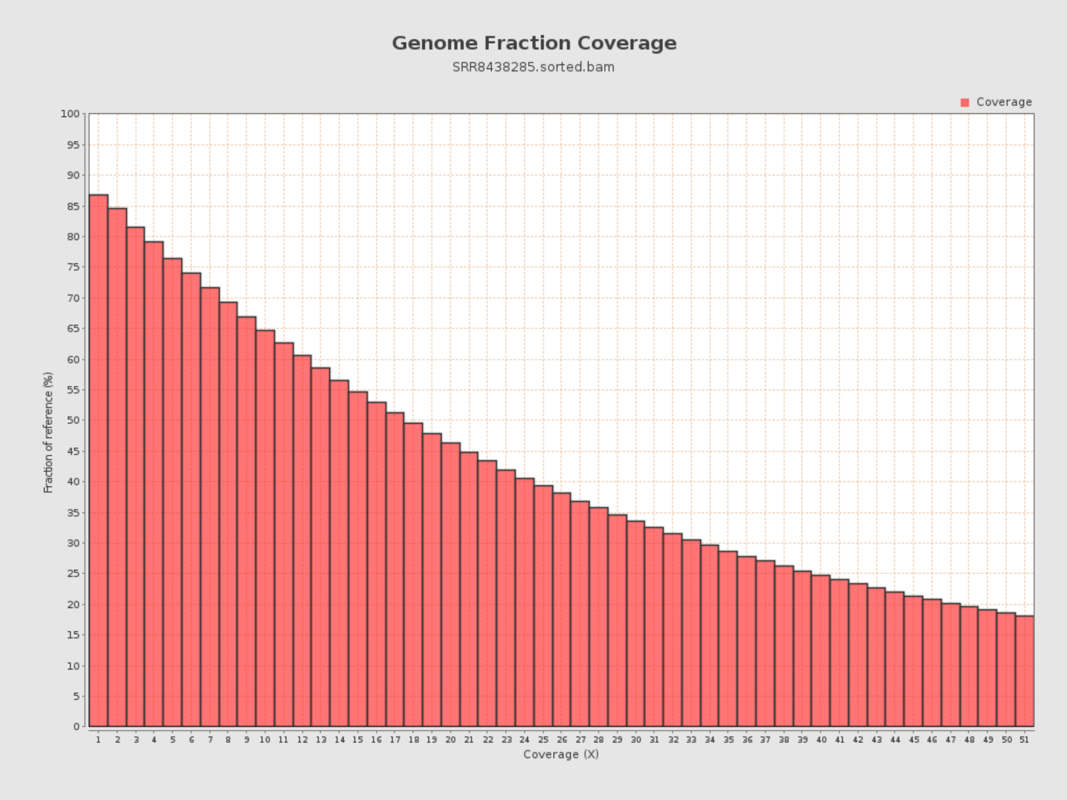
4. Results : Coverage Histogram



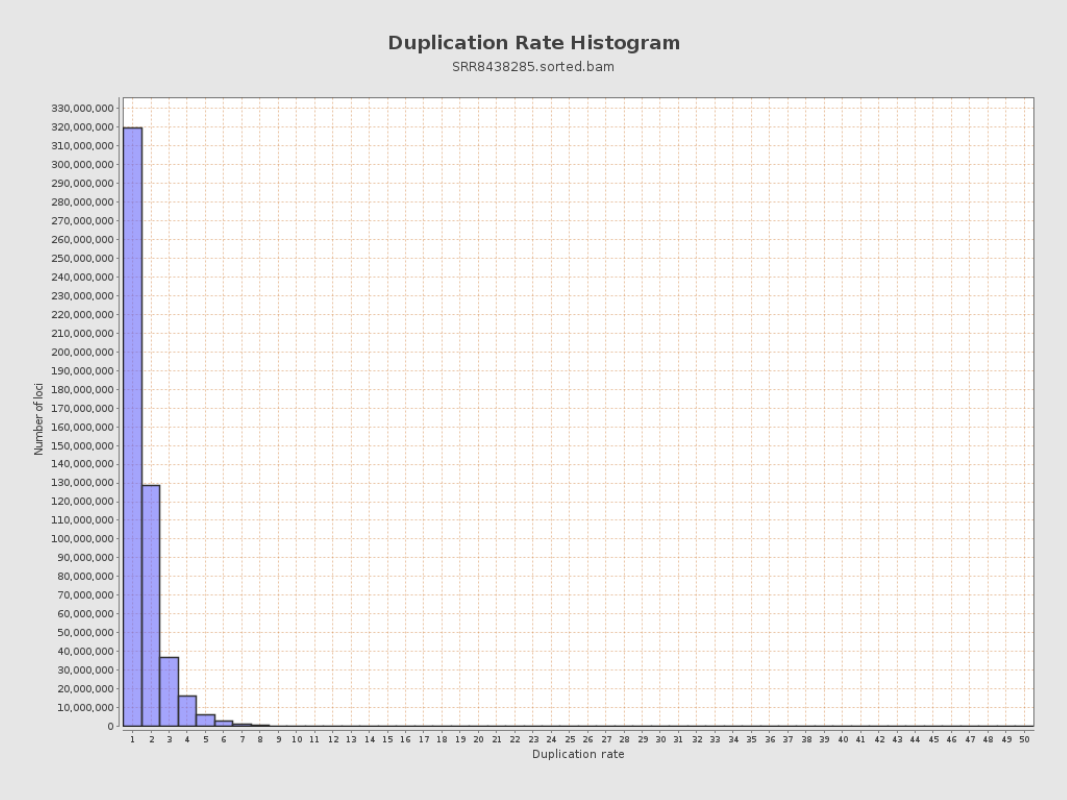
5. Results : Coverage Histogram (0-50X)



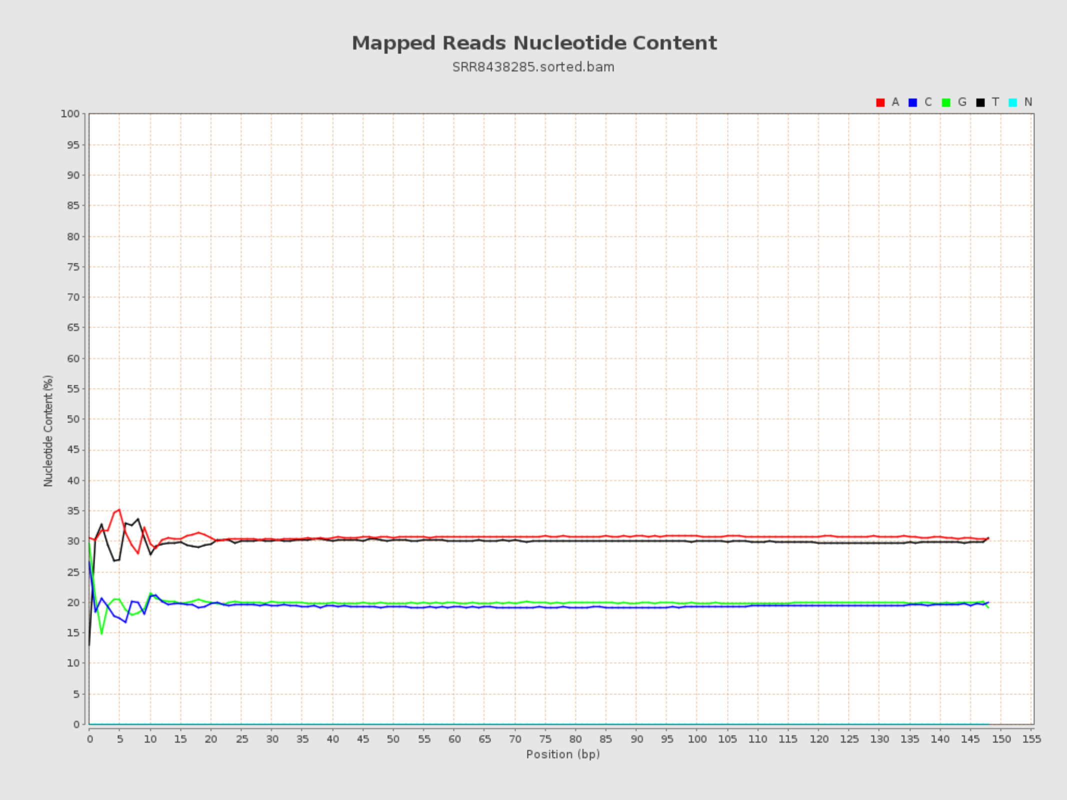
6. Results : Genome Fraction Coverage



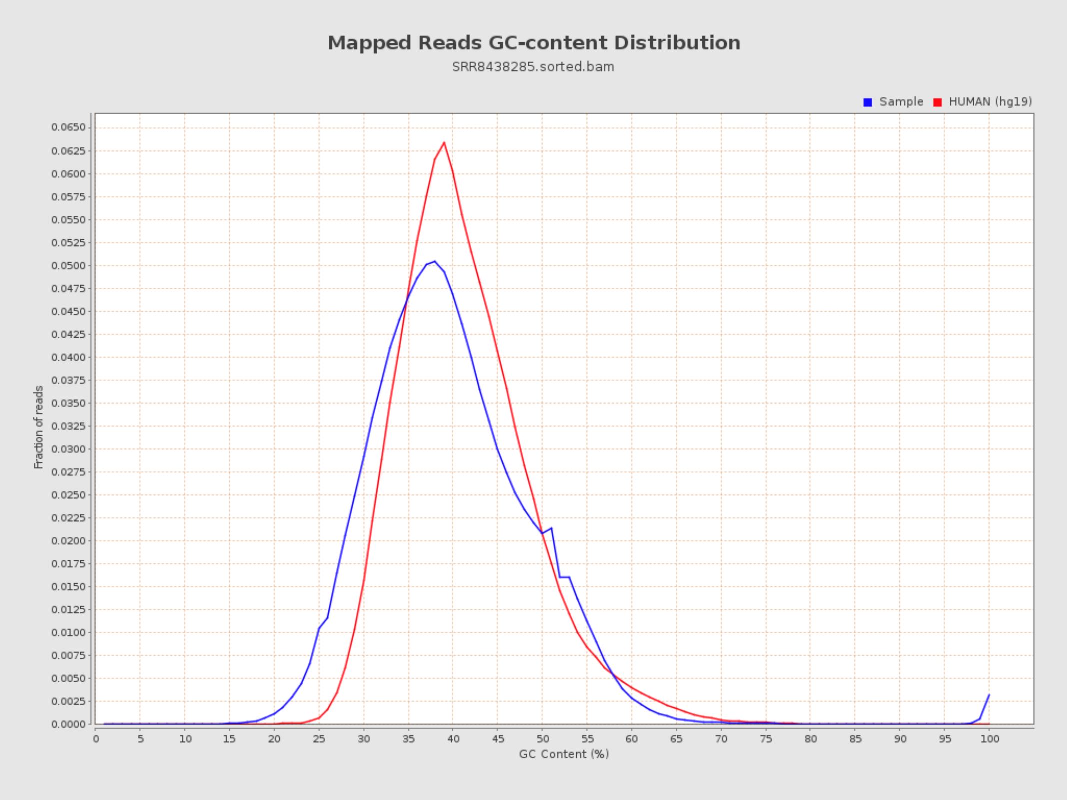
7. Results : Duplication Rate Histogram



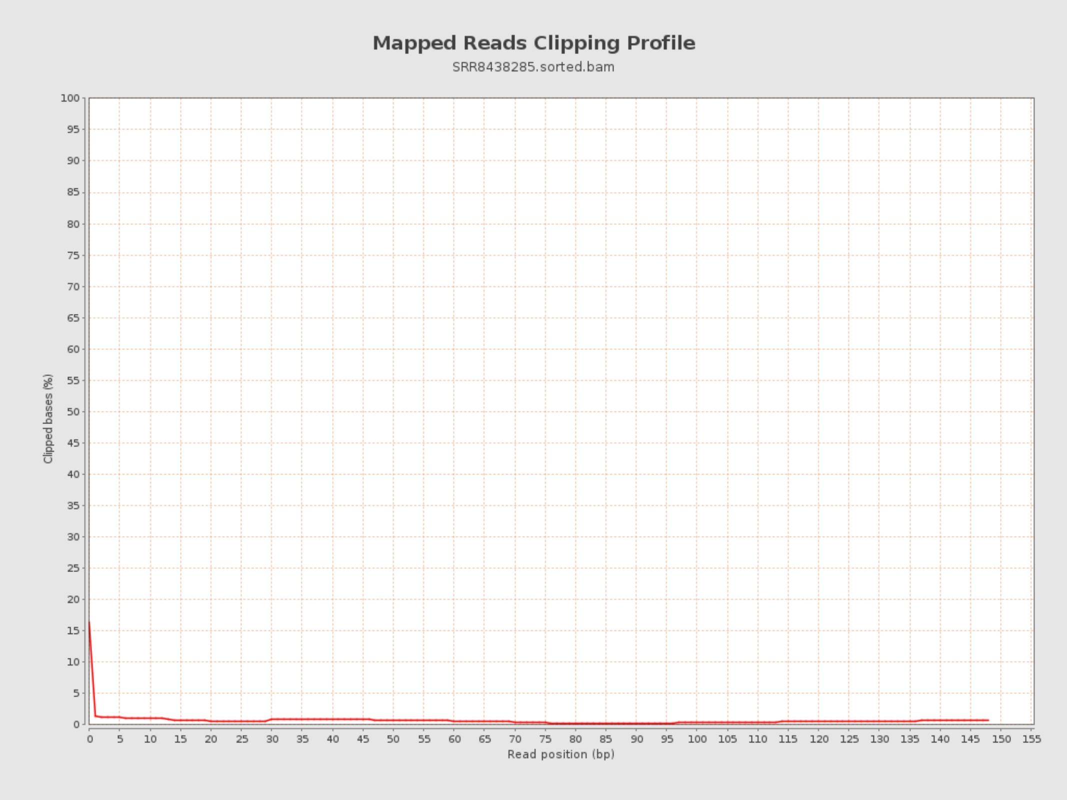
8. Results : Mapped Reads Nucleotide Content



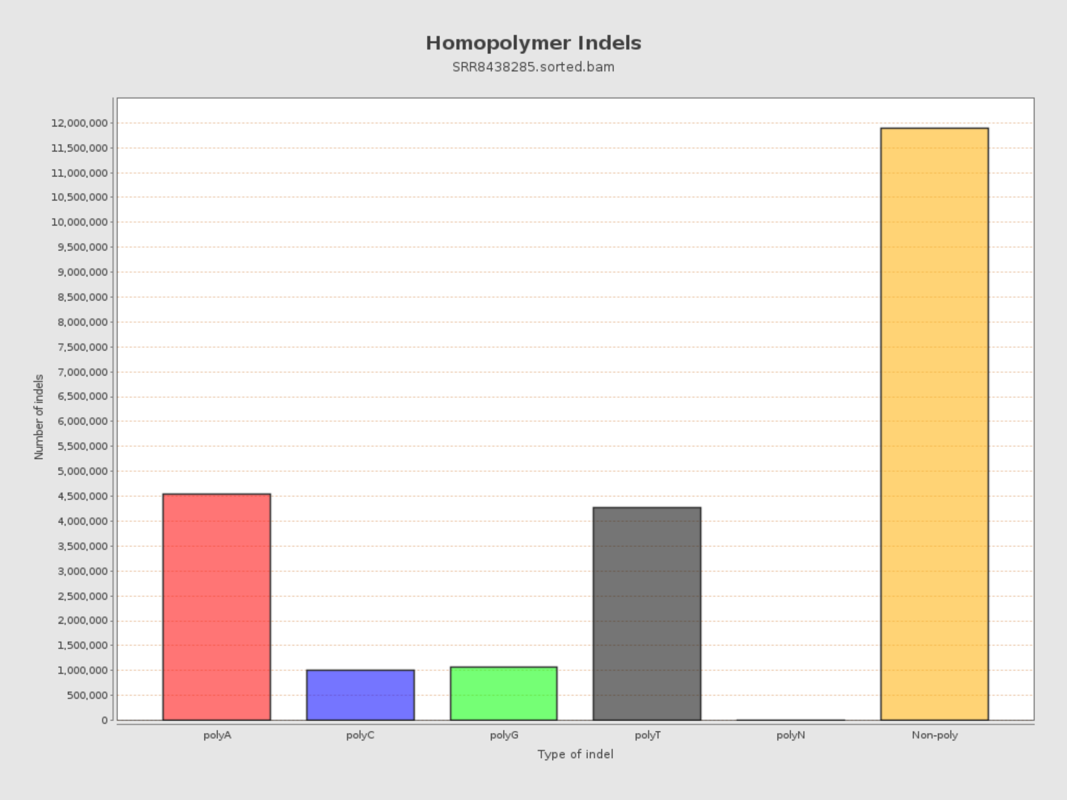
9. Results : Mapped Reads GC-content Distribution



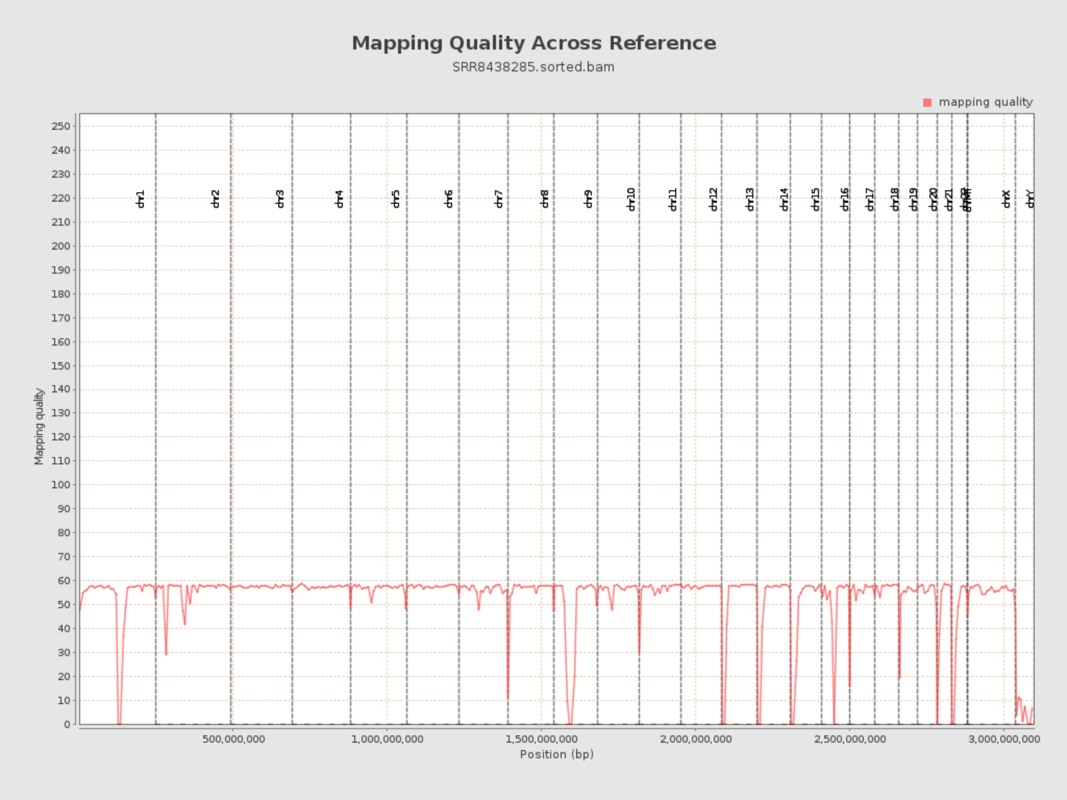
10. Results : Mapped Reads Clipping Profile



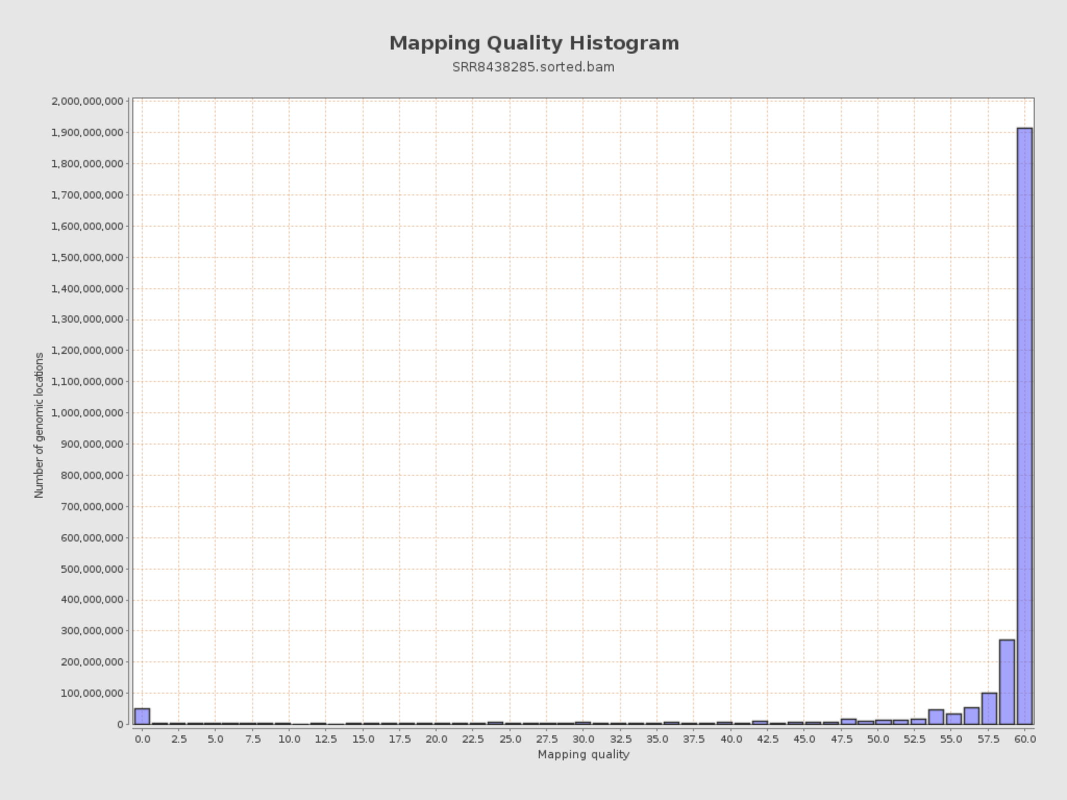
11. Results : Homopolymer Indels



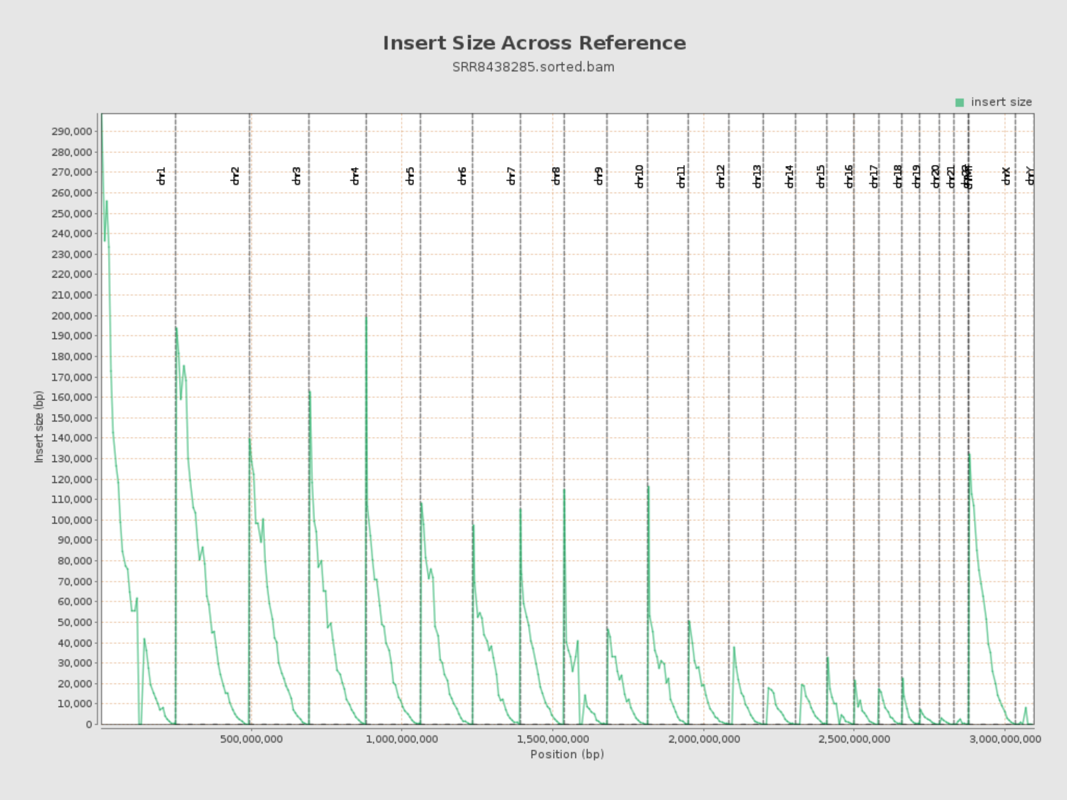
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram