Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/08 08:47:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124850.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_SRR3124850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124850_1.fastq.gz SRR3124850_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 08 08:47:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,782,492
Mapped reads	74,520,794 / 94.59%
Unmapped reads	4,261,698 / 5.41%
Mapped paired reads	74,520,794 / 94.59%
Mapped reads, first in pair	37,794,715 / 47.97%
Mapped reads, second in pair	36,726,079 / 46.62%
Mapped reads, both in pair	73,109,754 / 92.8%
Mapped reads, singletons	1,411,040 / 1.79%
Secondary alignments	0
Supplementary alignments	1,704,978 / 2.16%
Read min/max/mean length	30 / 150 / 151.05
Duplicated reads (estimated)	32,253,455 / 40.94%
Duplication rate	33.49%
Clipped reads	54,761,207 / 69.51%

2.2. ACGT Content

Number/percentage of A's	2,660,240,565 / 29.16%
Number/percentage of C's	1,806,977,609 / 19.81%
Number/percentage of T's	2,691,090,290 / 29.5%
Number/percentage of G's	1,963,569,862 / 21.53%
Number/percentage of N's	138,903 / 0%

GC Percentage	41.33%

2.3. Coverage

Mean	2.9488
Standard Deviation	43.4369

2.4. Mapping Quality

Mean Mapping Quality	52.96

2.5. Insert size

Mean	93,545.73
Standard Deviation	2,878,588.5
P25/Median/P75	118 / 158 / 214

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	107,809,977
Insertions	1,661,847
Mapped reads with at least one insertion	2.07%
Deletions	3,048,639
Mapped reads with at least one deletion	3.91%
Homopolymer indels	43.38%

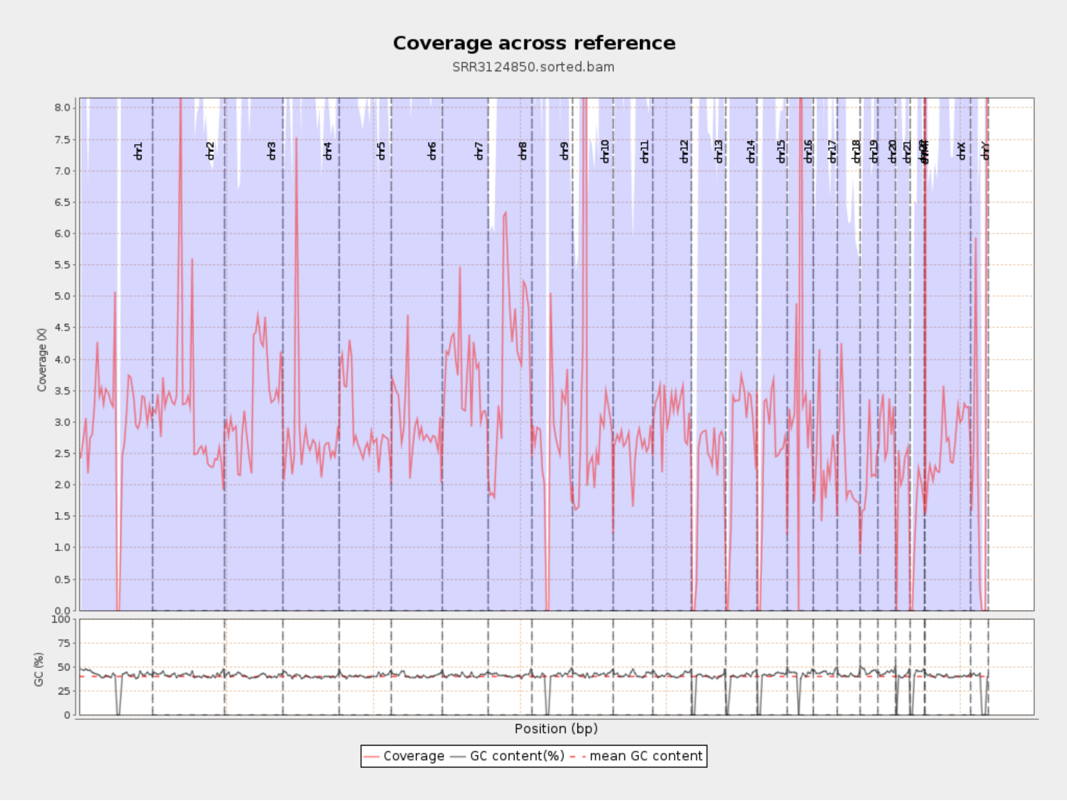
2.7. Chromosome stats

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

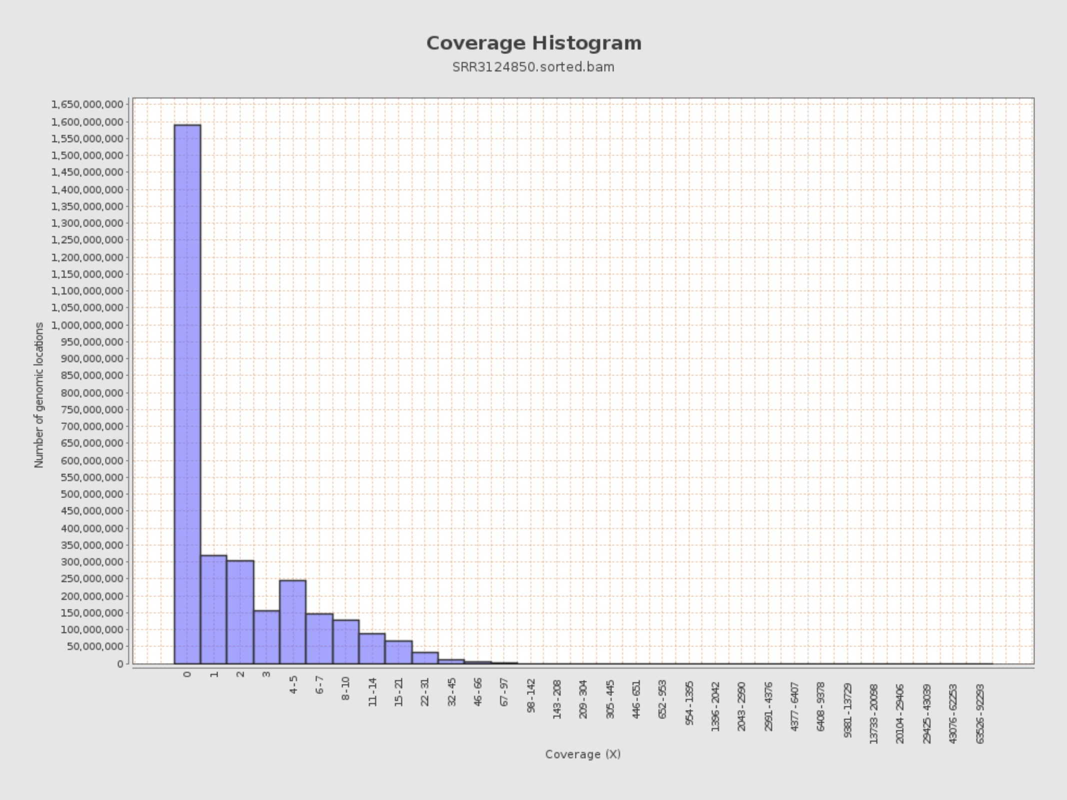
		bases	coverage	deviation
chr1	249250621	751174807	3.0137	34.7539
chr2	243199373	788464984	3.2421	49.6296
chr3	198022430	667554270	3.3711	8.1338
chr4	191154276	528891248	2.7668	31.4567
chr5	180915260	532992537	2.9461	7.0322
chr6	171115067	513679660	3.002	15.8492
chr7	159138663	595781297	3.7438	36.3393
chr8	146364022	589763646	4.0294	14.5471
chr9	141213431	362351535	2.566	48.5664
chr10	135534747	479395814	3.5371	146.523
chr11	135006516	348881350	2.5842	18.1803
chr12	133851895	422489907	3.1564	6.4619
chr13	115169878	252340203	2.191	4.8532
chr14	107349540	291854731	2.7187	7.7864
chr15	102531392	247686263	2.4157	6.1103
chr16	90354753	332721786	3.6824	72.0538
chr17	81195210	186459663	2.2964	36.2402
chr18	78077248	178051607	2.2805	46.9313
chr19	59128983	123186641	2.0834	19.979
chr20	63025520	181743596	2.8837	11.9129
chr21	48129895	98764308	2.052	17.1733
chr22	51304566	70101060	1.3664	6.6138
chrMT	16571	2403478	145.0412	82.9052
chrX	155270560	412401510	2.656	10.7472

chrY	59373566	169546849	2.8556	73.8006

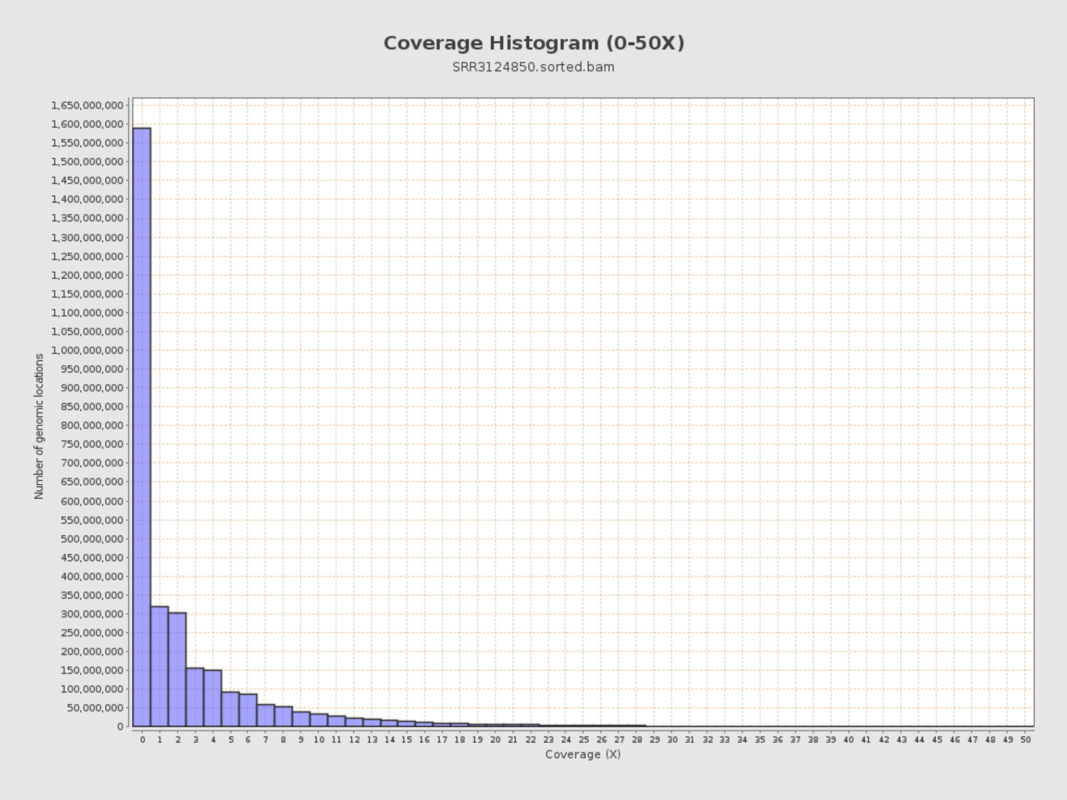
3. Results : Coverage across reference



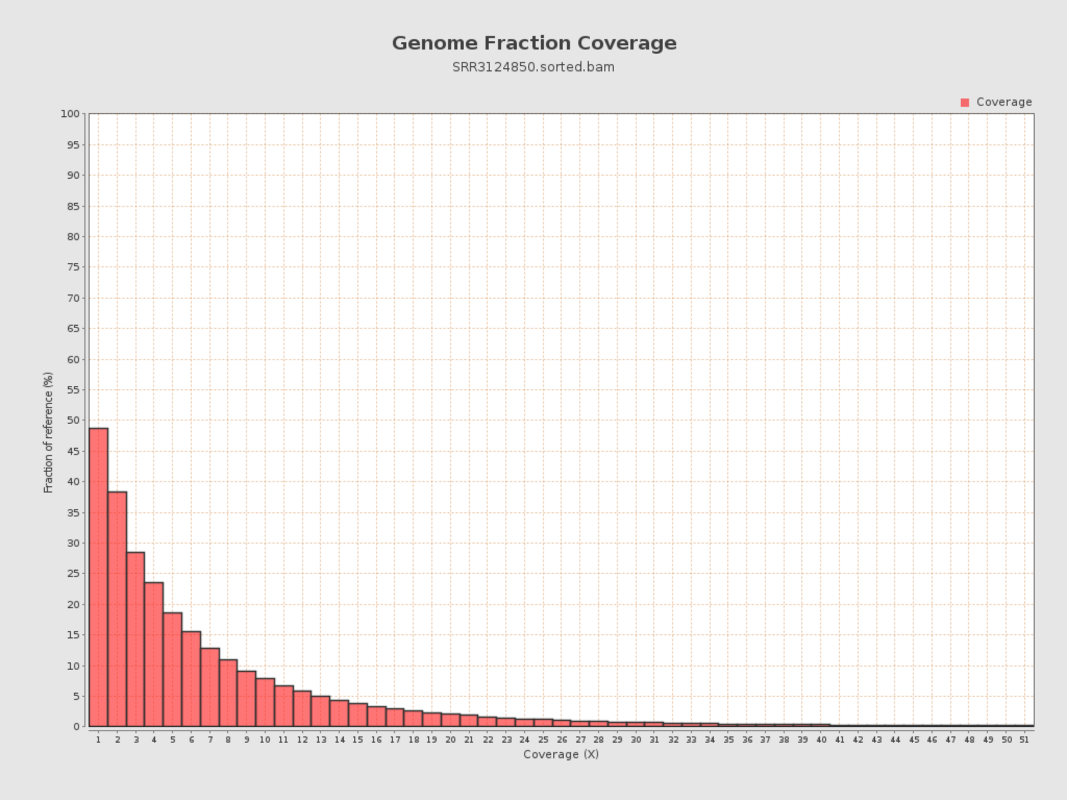
4. Results : Coverage Histogram



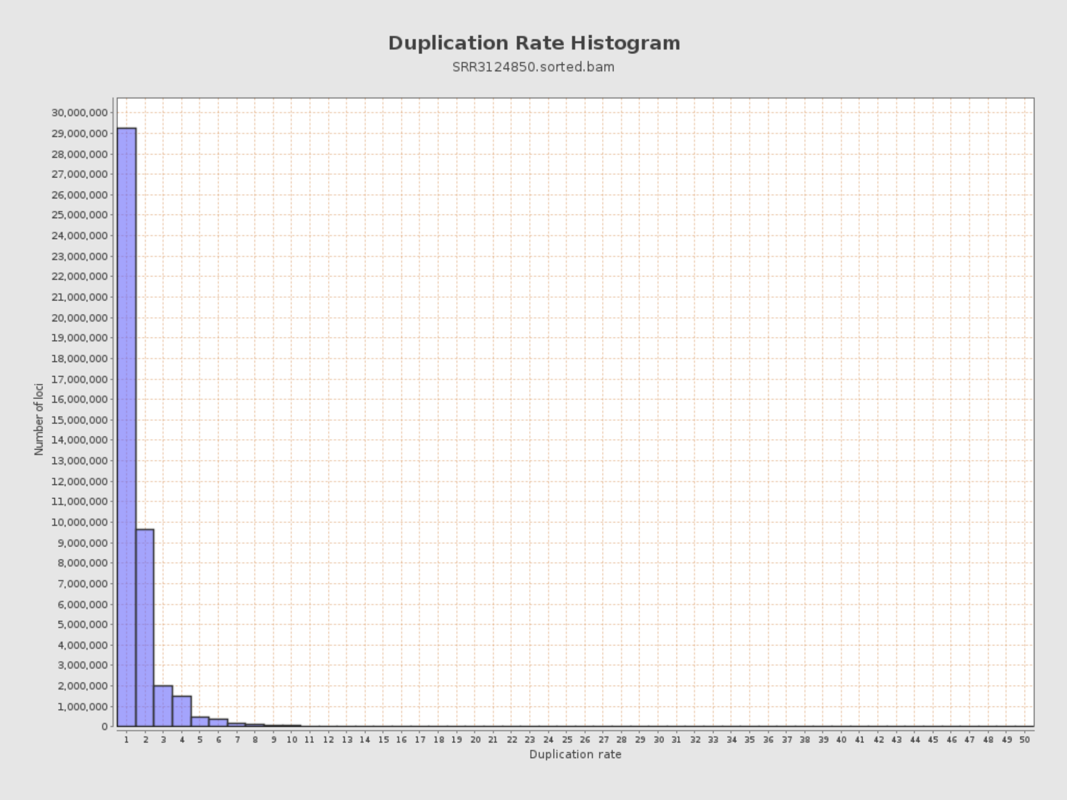
5. Results : Coverage Histogram (0-50X)



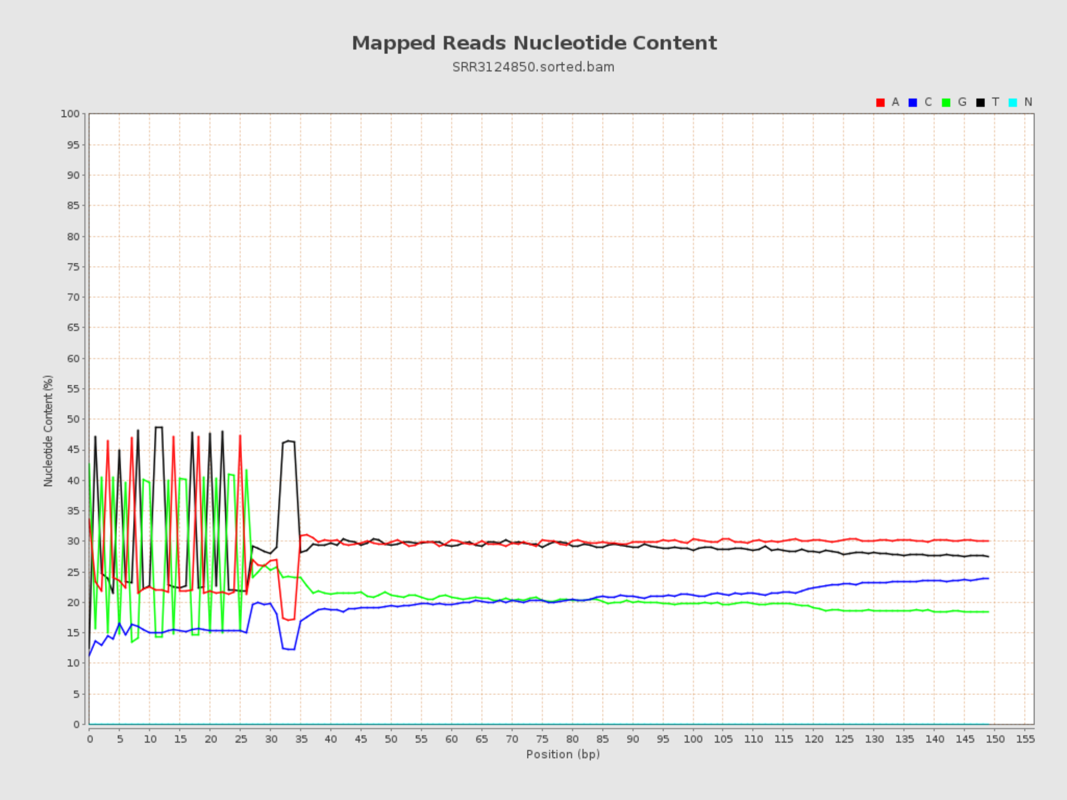
6. Results : Genome Fraction Coverage



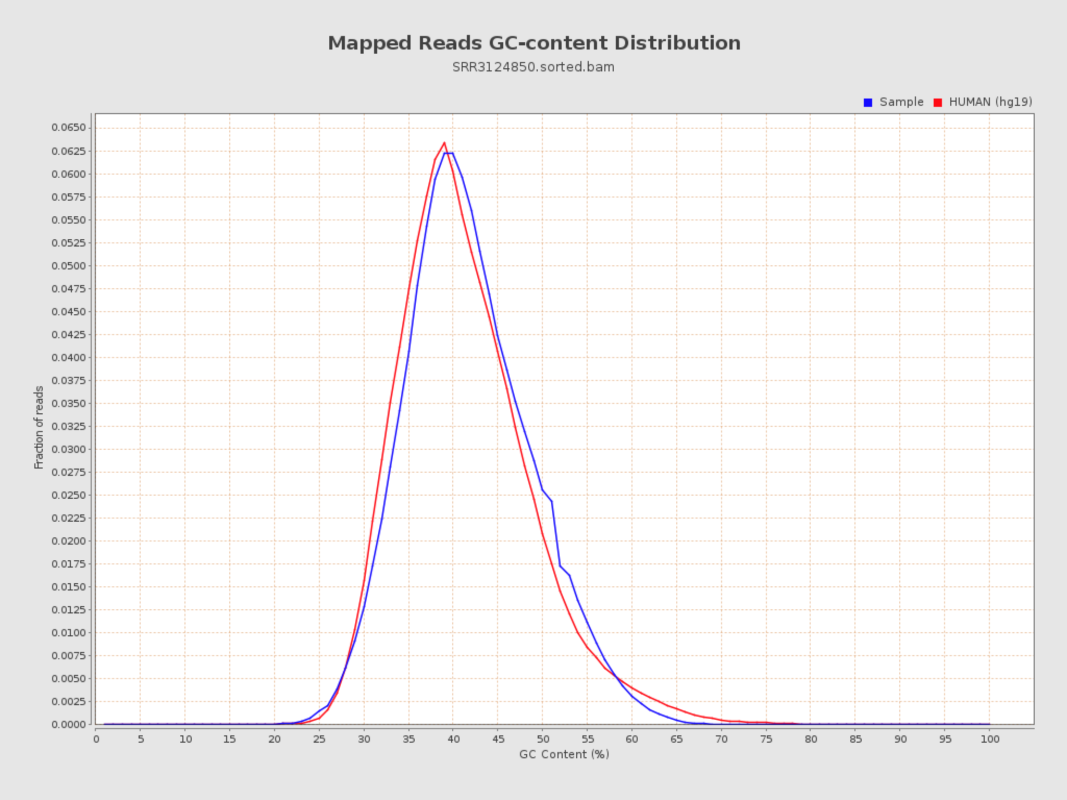
7. Results : Duplication Rate Histogram



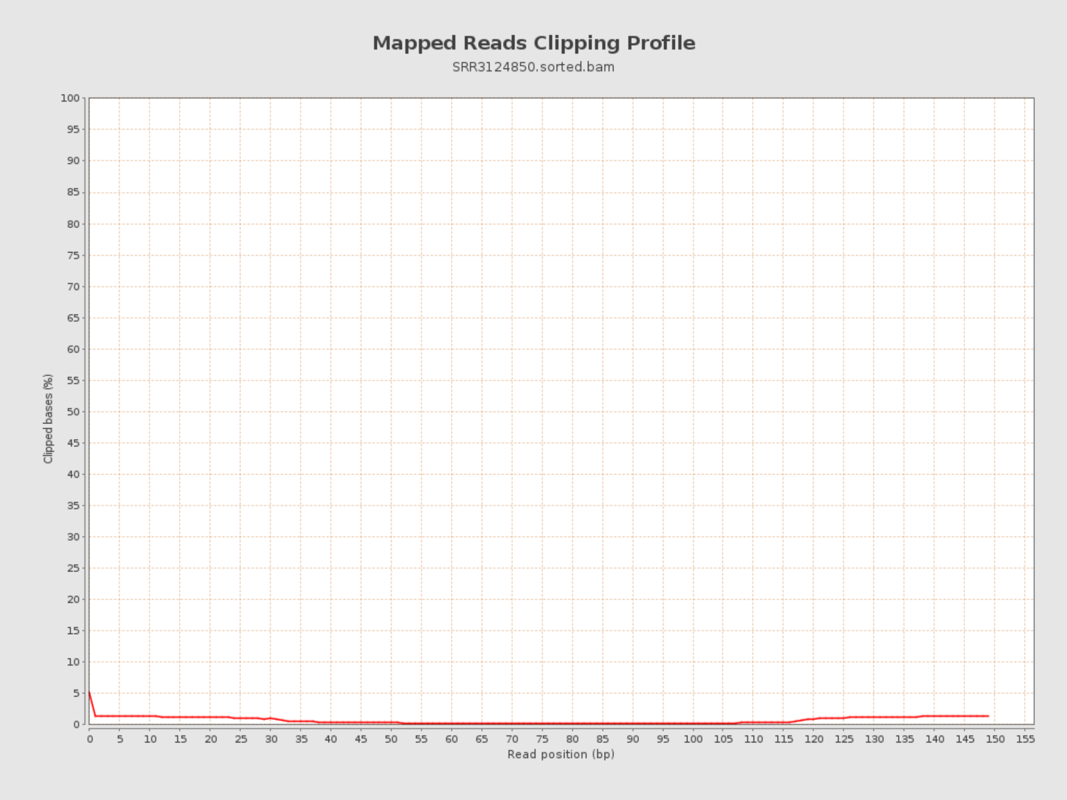
8. Results : Mapped Reads Nucleotide Content



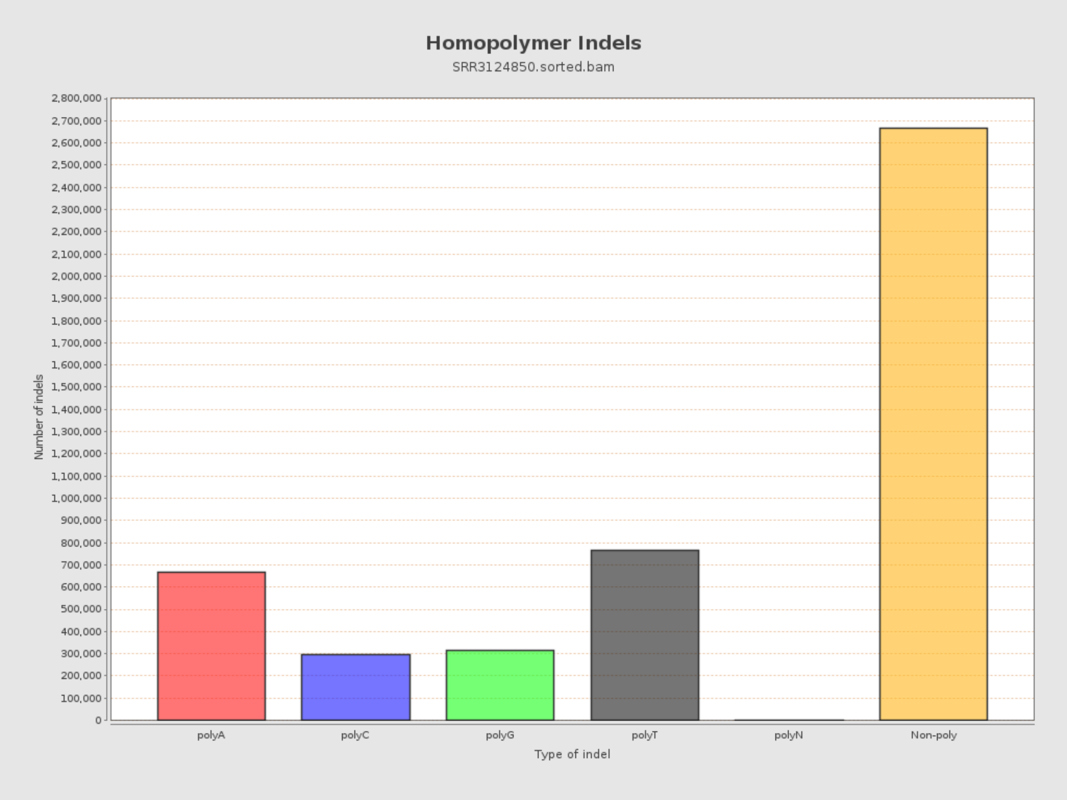
9. Results : Mapped Reads GC-content Distribution



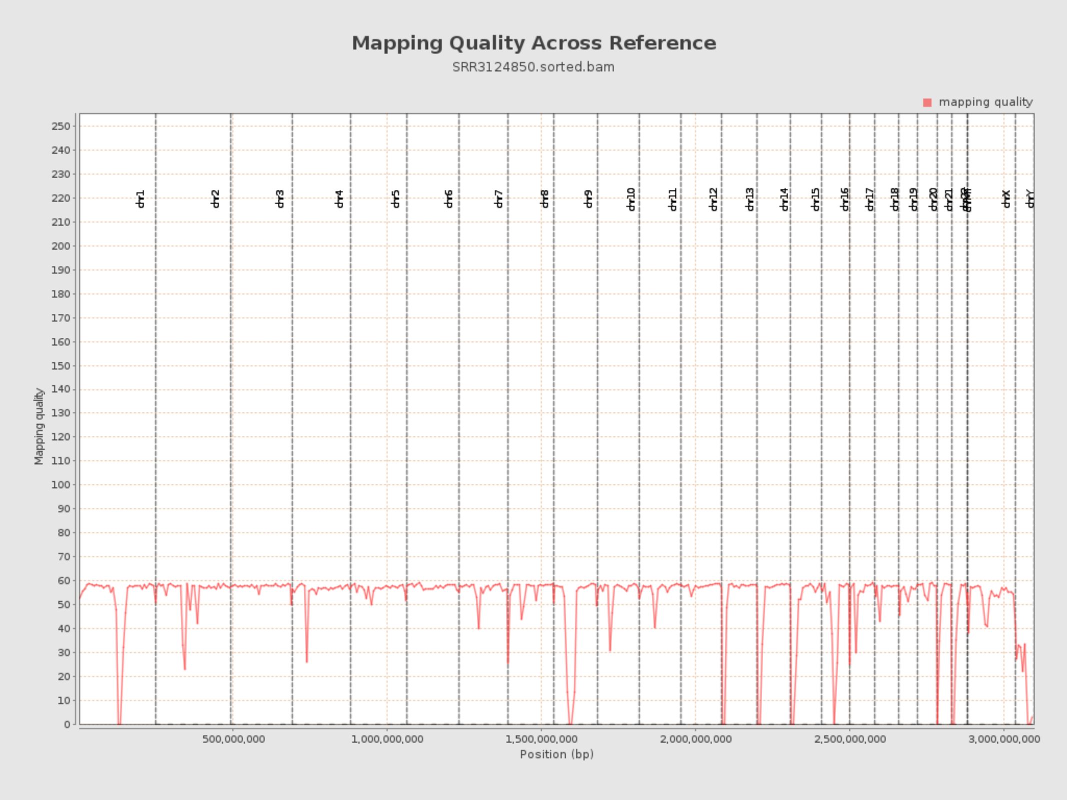
10. Results : Mapped Reads Clipping Profile



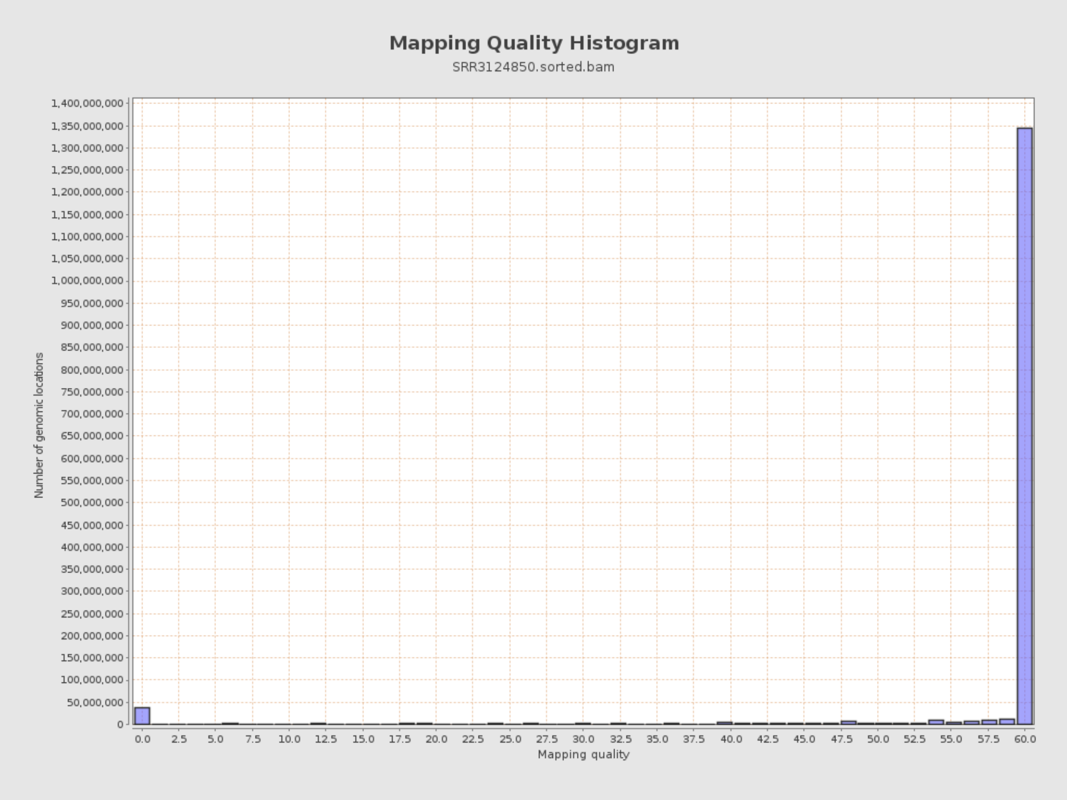
11. Results : Homopolymer Indels



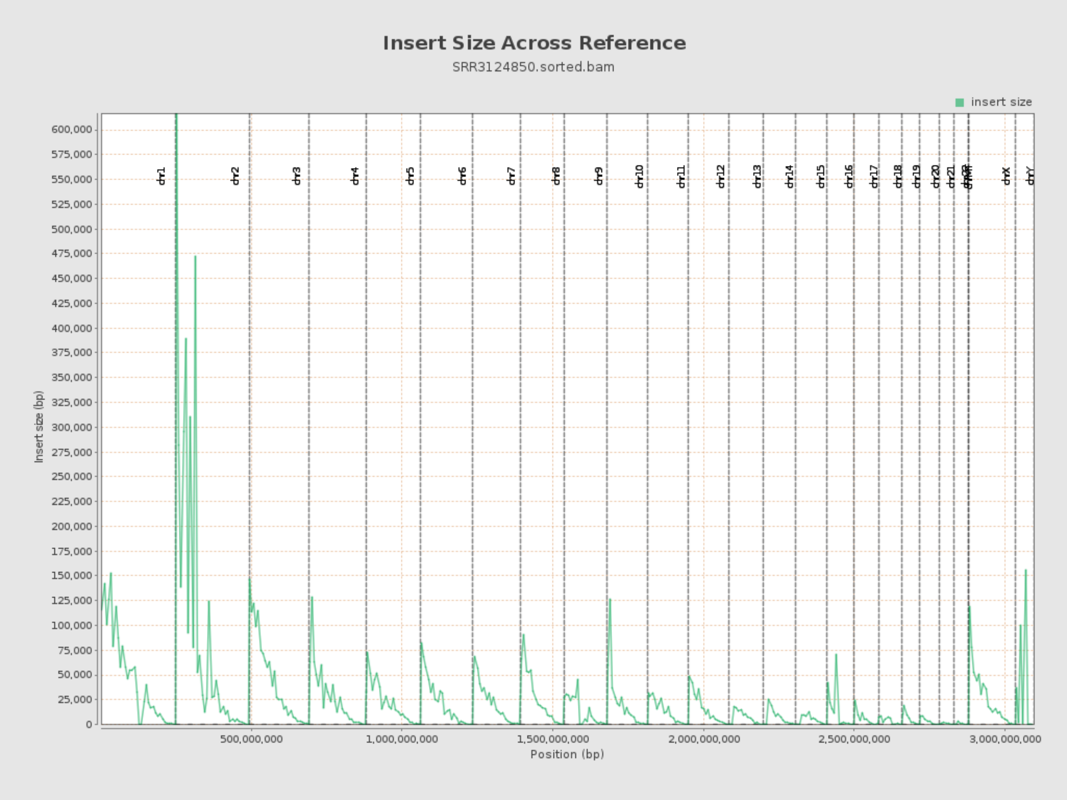
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram