Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:05:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124876.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_SRR3124876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124876_1.fastq.gz SRR3124876_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:05:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,832,820
Mapped reads	3,786,491 / 98.79%
Unmapped reads	46,329 / 1.21%
Mapped paired reads	3,786,491 / 98.79%
Mapped reads, first in pair	1,897,197 / 49.5%
Mapped reads, second in pair	1,889,294 / 49.29%
Mapped reads, both in pair	3,771,576 / 98.4%
Mapped reads, singletons	14,915 / 0.39%
Secondary alignments	0
Supplementary alignments	44,212 / 1.15%
Read min/max/mean length	30 / 151 / 151.56
Duplicated reads (estimated)	542,572 / 14.16%
Duplication rate	13.9%
Clipped reads	2,746,955 / 71.67%

2.2. ACGT Content

Number/percentage of A's	146,748,695 / 28.71%
Number/percentage of C's	105,666,323 / 20.67%
Number/percentage of T's	147,794,184 / 28.92%
Number/percentage of G's	110,888,144 / 21.7%
Number/percentage of N's	22,299 / 0%

GC Percentage	42.37%

2.3. Coverage

Mean	0.1652
Standard Deviation	1.5339

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	73,940.24
Standard Deviation	2,651,261.46
P25/Median/P75	137 / 168 / 211

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	6,810,300
Insertions	90,613
Mapped reads with at least one insertion	2.28%
Deletions	181,849
Mapped reads with at least one deletion	4.63%
Homopolymer indels	46.5%

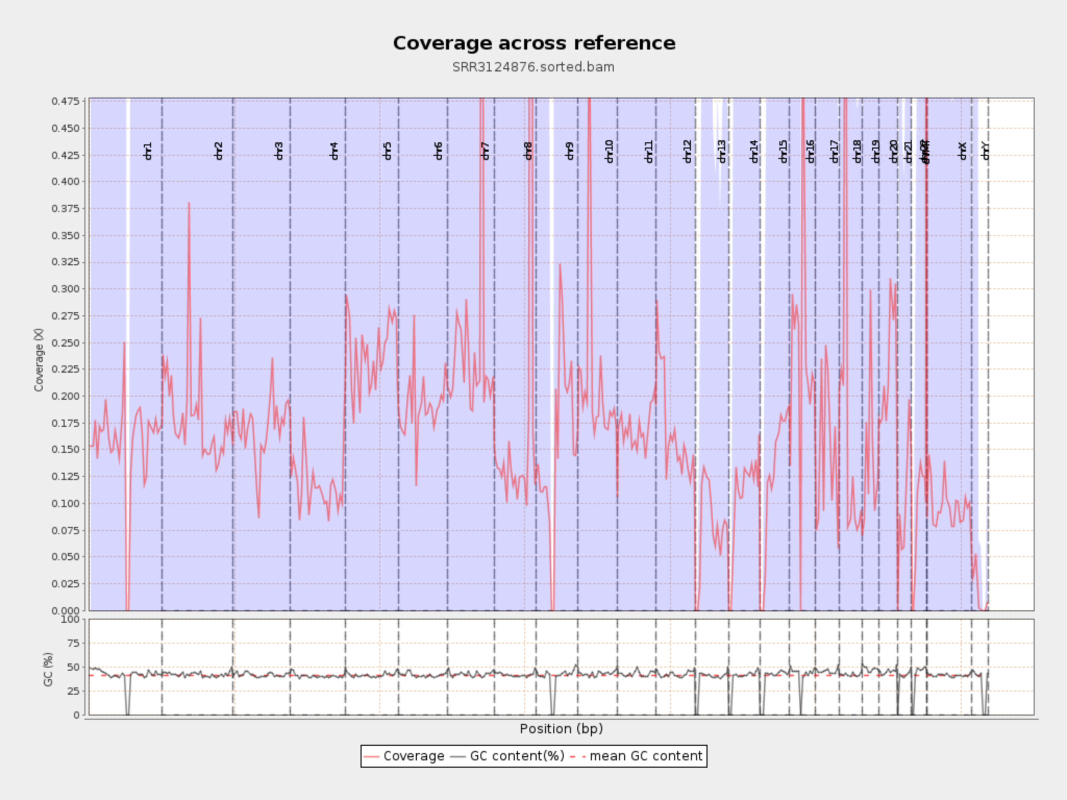
2.7. Chromosome stats

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

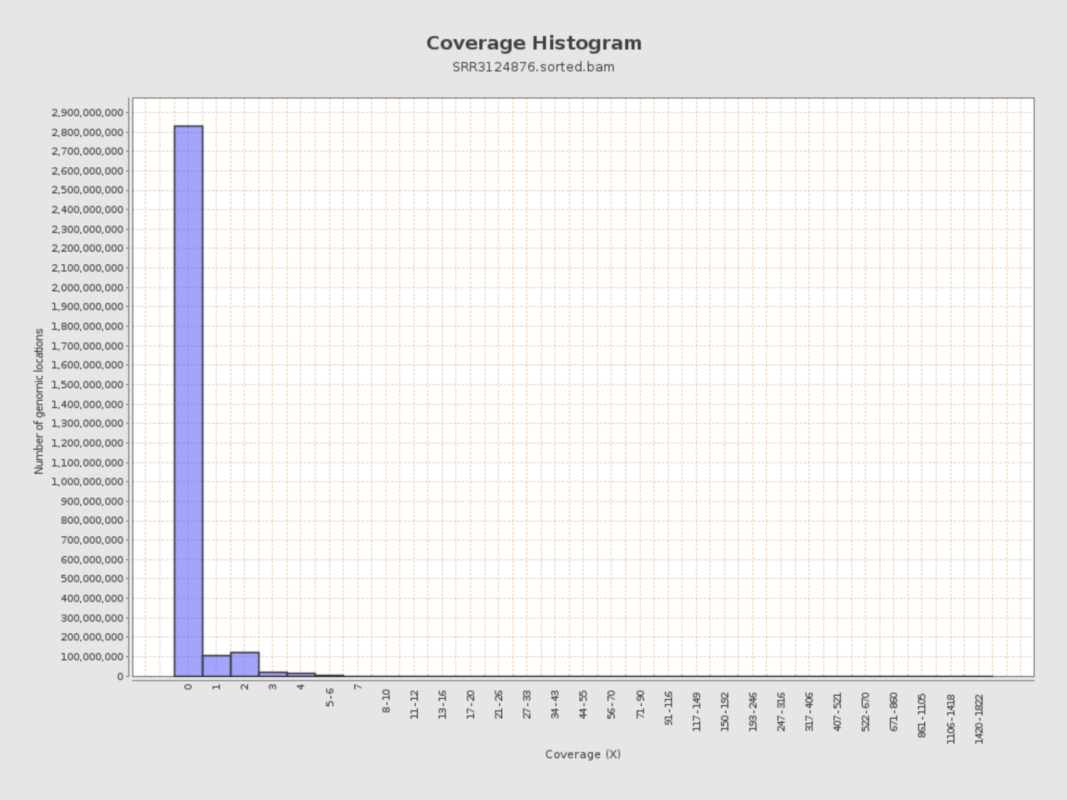
		bases	coverage	deviation
chr1	249250621	38739274	0.1554	1.8018
chr2	243199373	44549455	0.1832	1.6524
chr3	198022430	33690411	0.1701	0.617
chr4	191154276	22364507	0.117	0.7696
chr5	180915260	43446292	0.2401	0.7355
chr6	171115067	32718709	0.1912	1.2483
chr7	159138663	41272363	0.2593	2.2115
chr8	146364022	28777738	0.1966	1.291
chr9	141213431	21834708	0.1546	2.0699
chr10	135534747	29005663	0.214	3.757
chr11	135006516	22788117	0.1688	0.9764
chr12	133851895	22431059	0.1676	0.6044
chr13	115169878	8795058	0.0764	0.3931
chr14	107349540	11072582	0.1031	0.4914
chr15	102531392	12653259	0.1234	0.5148
chr16	90354753	22051904	0.2441	2.8014
chr17	81195210	11813619	0.1455	1.7687
chr18	78077248	14827803	0.1899	1.8662
chr19	59128983	8597111	0.1454	1.0679
chr20	63025520	14505508	0.2302	0.7465
chr21	48129895	4889353	0.1016	0.5669
chr22	51304566	4370428	0.0852	0.4369
chrMT	16571	48934	2.953	2.4815
chrX	155270560	15301822	0.0985	0.559

chrY	59373566	913723	0.0154	0.9046

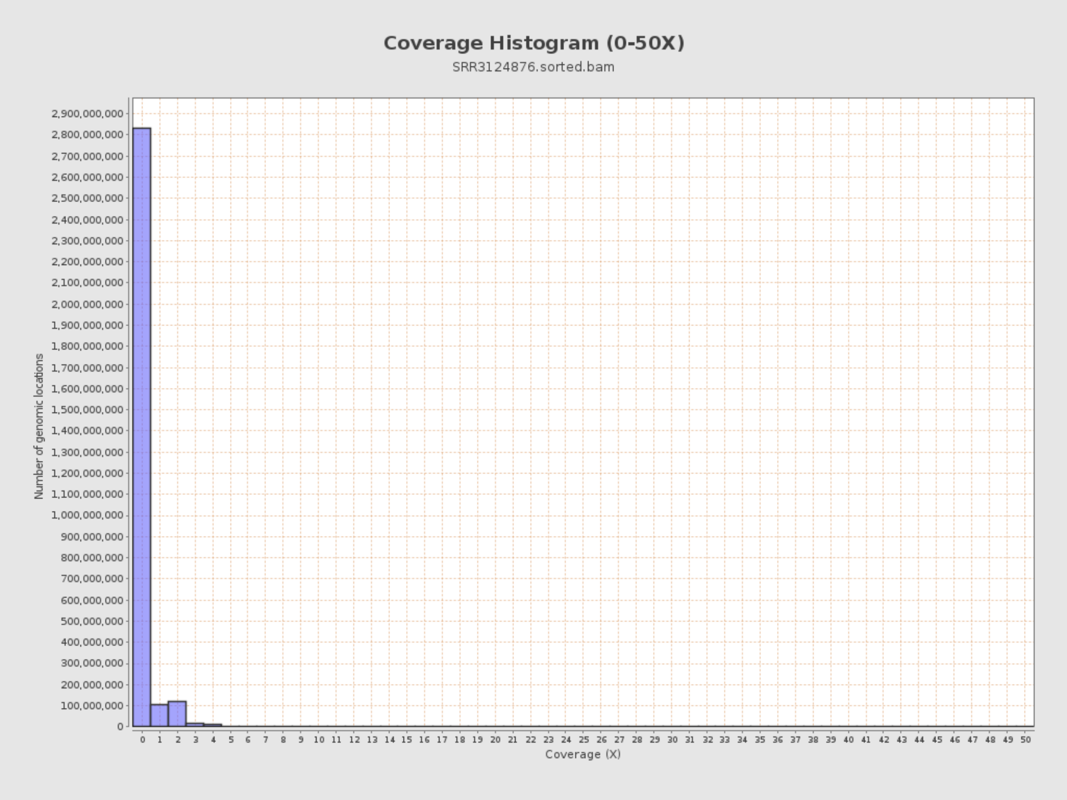
3. Results : Coverage across reference



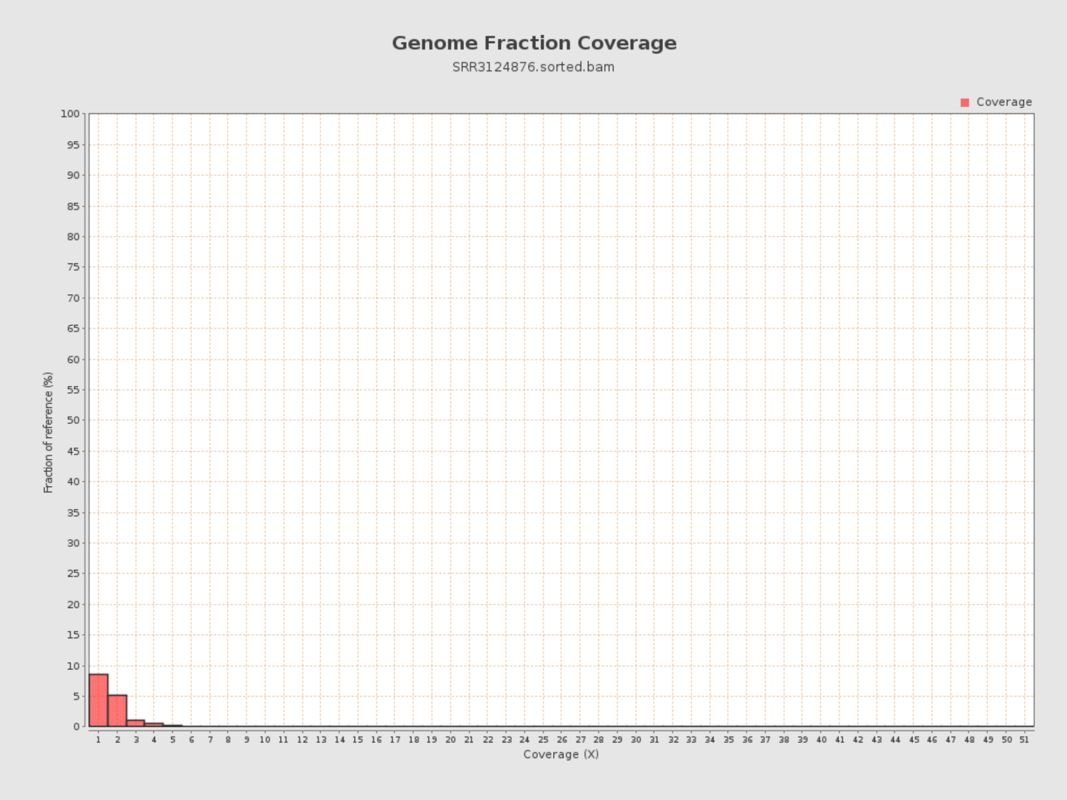
4. Results : Coverage Histogram



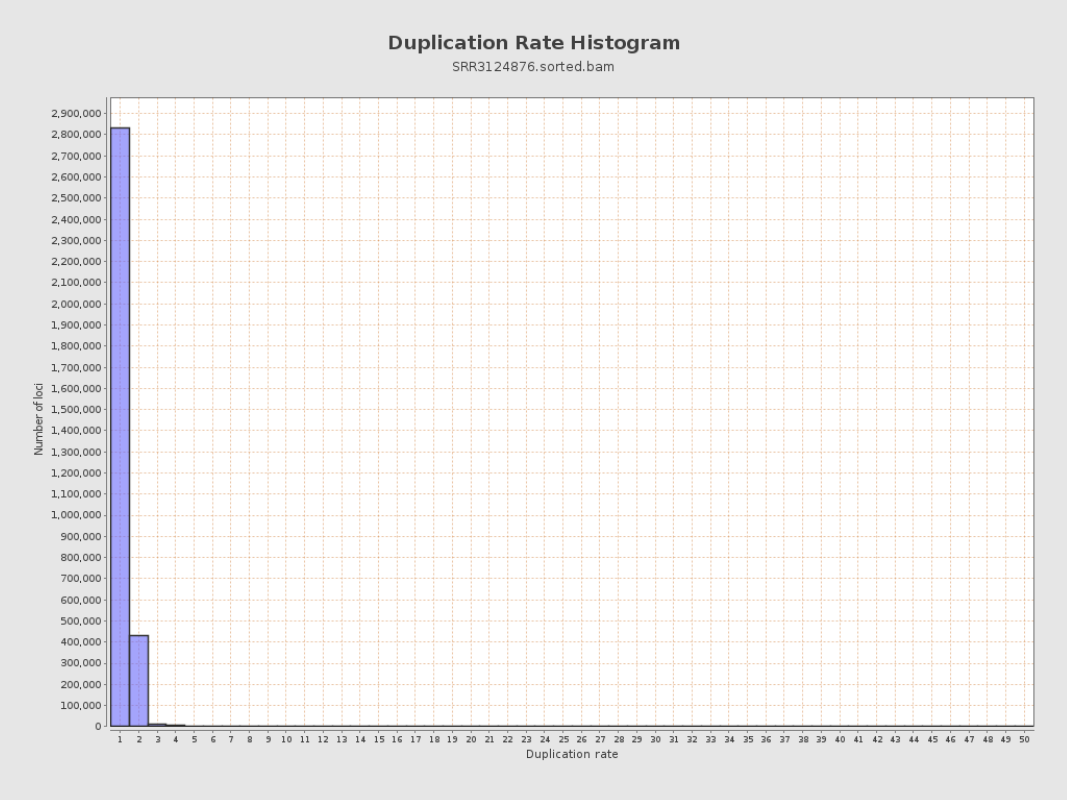
5. Results : Coverage Histogram (0-50X)



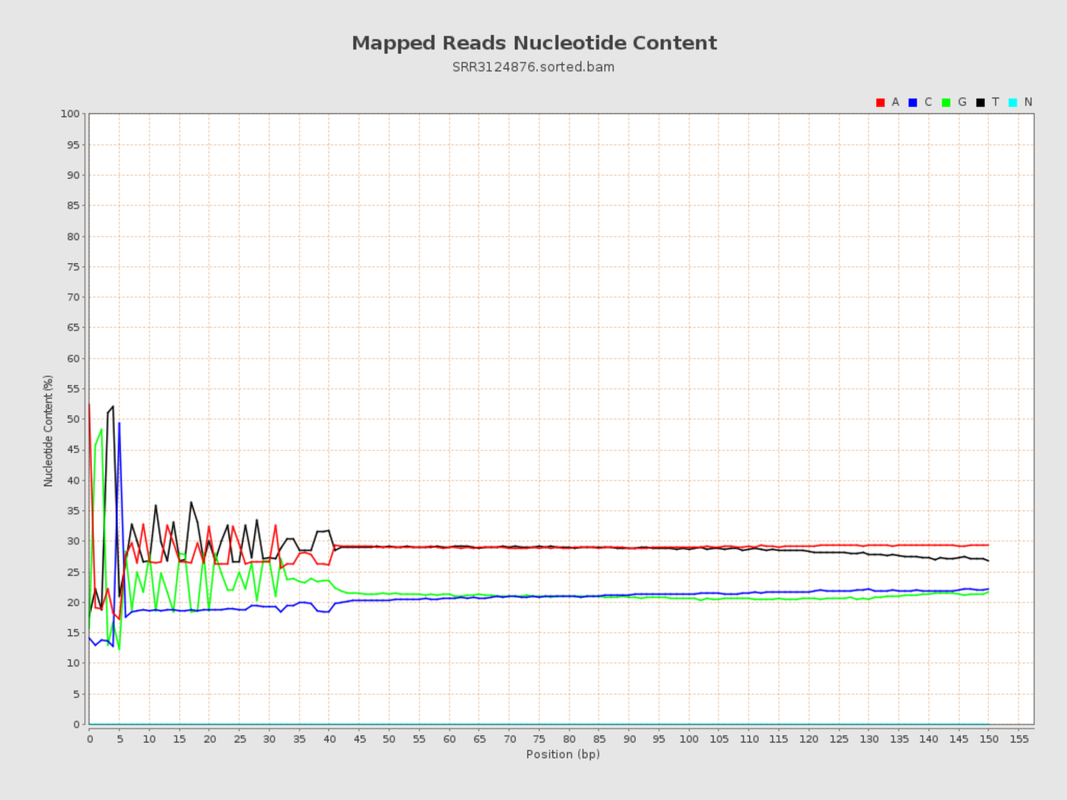
6. Results : Genome Fraction Coverage



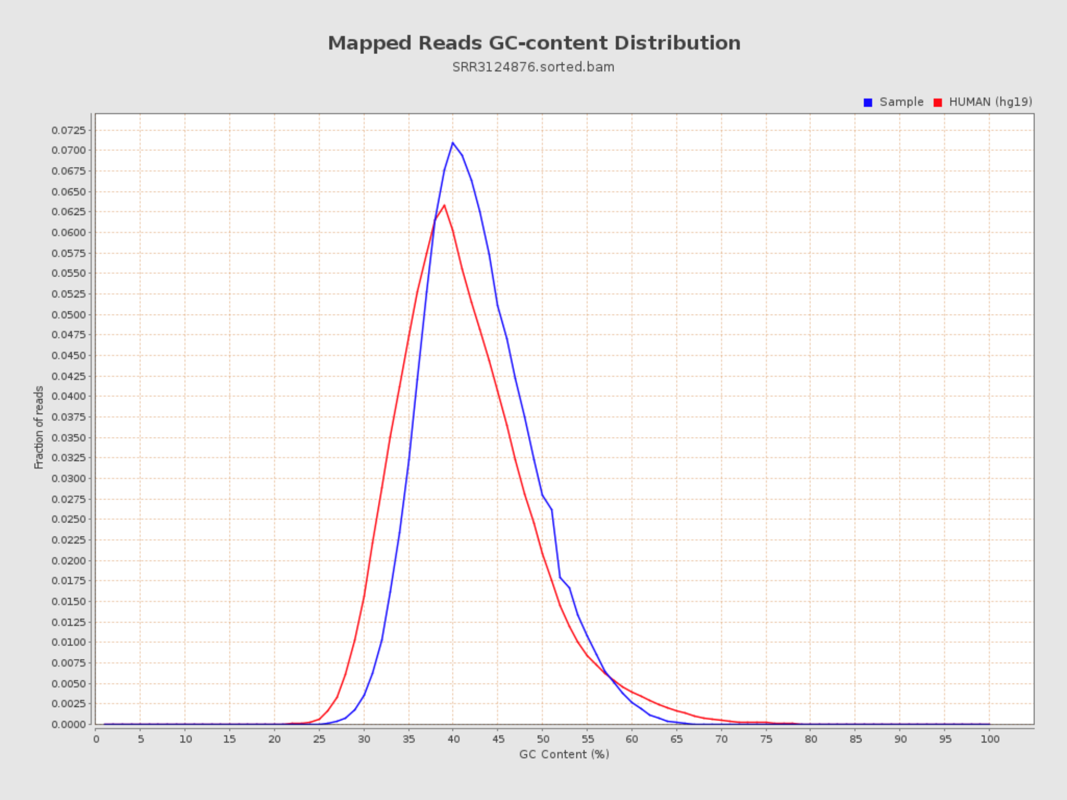
7. Results : Duplication Rate Histogram



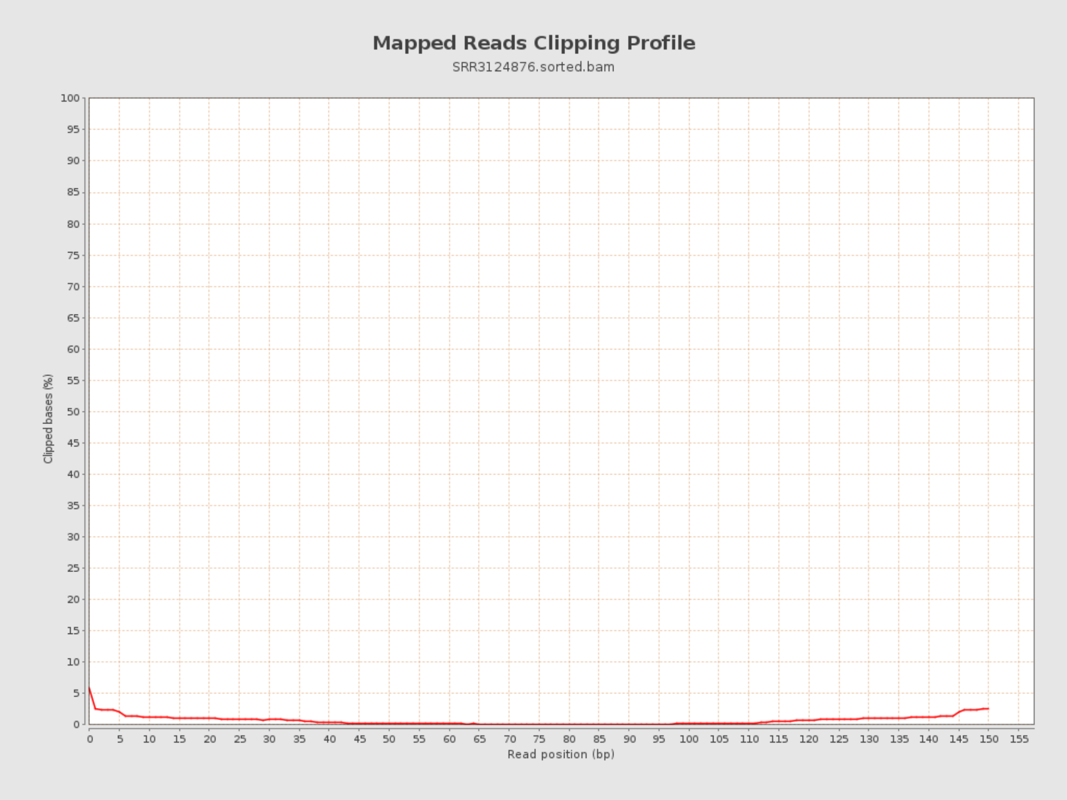
8. Results : Mapped Reads Nucleotide Content



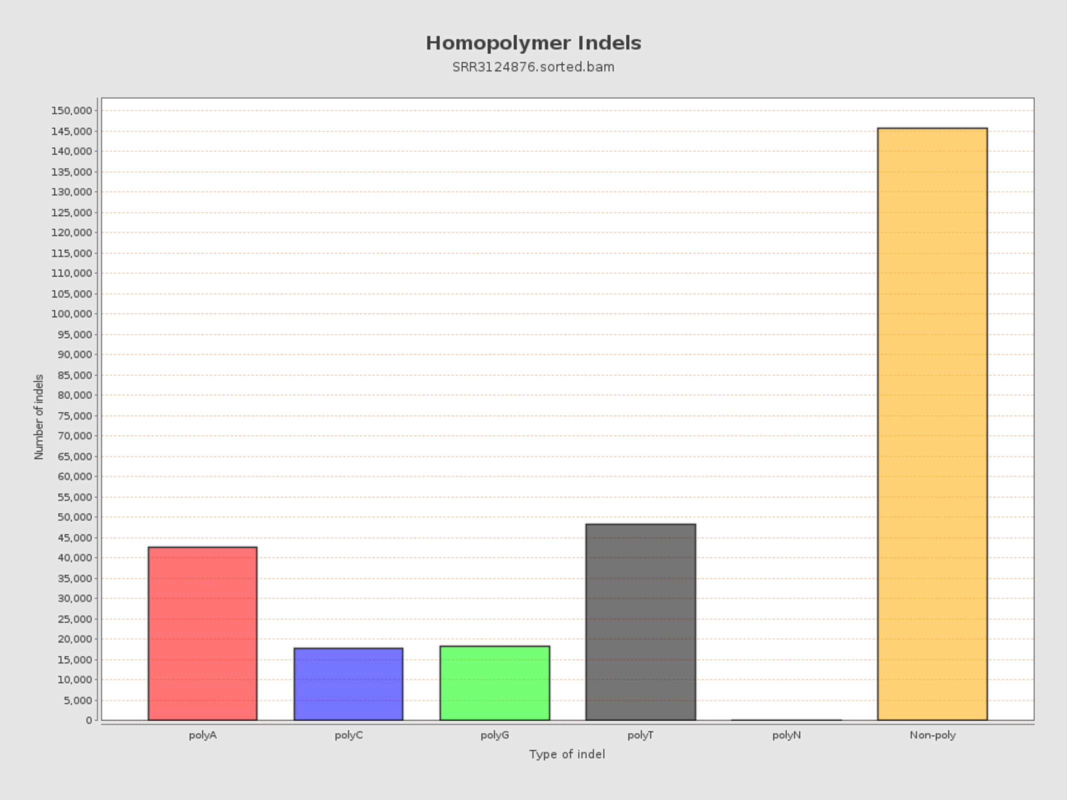
9. Results : Mapped Reads GC-content Distribution



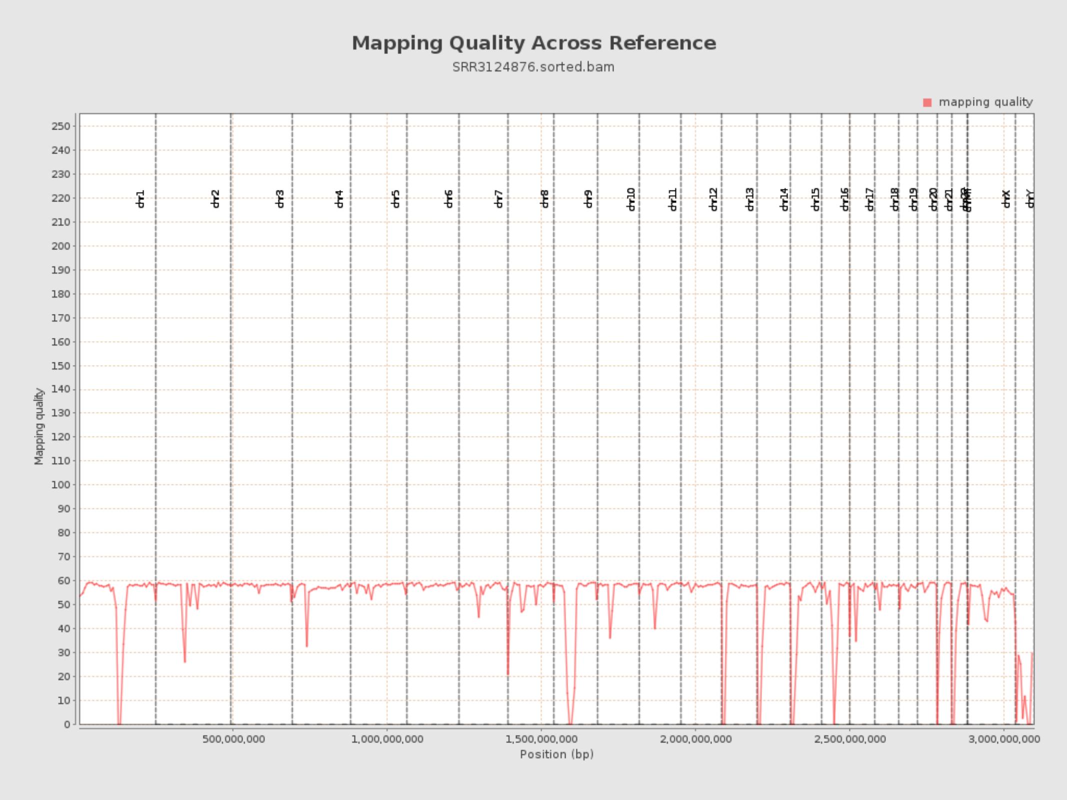
10. Results : Mapped Reads Clipping Profile



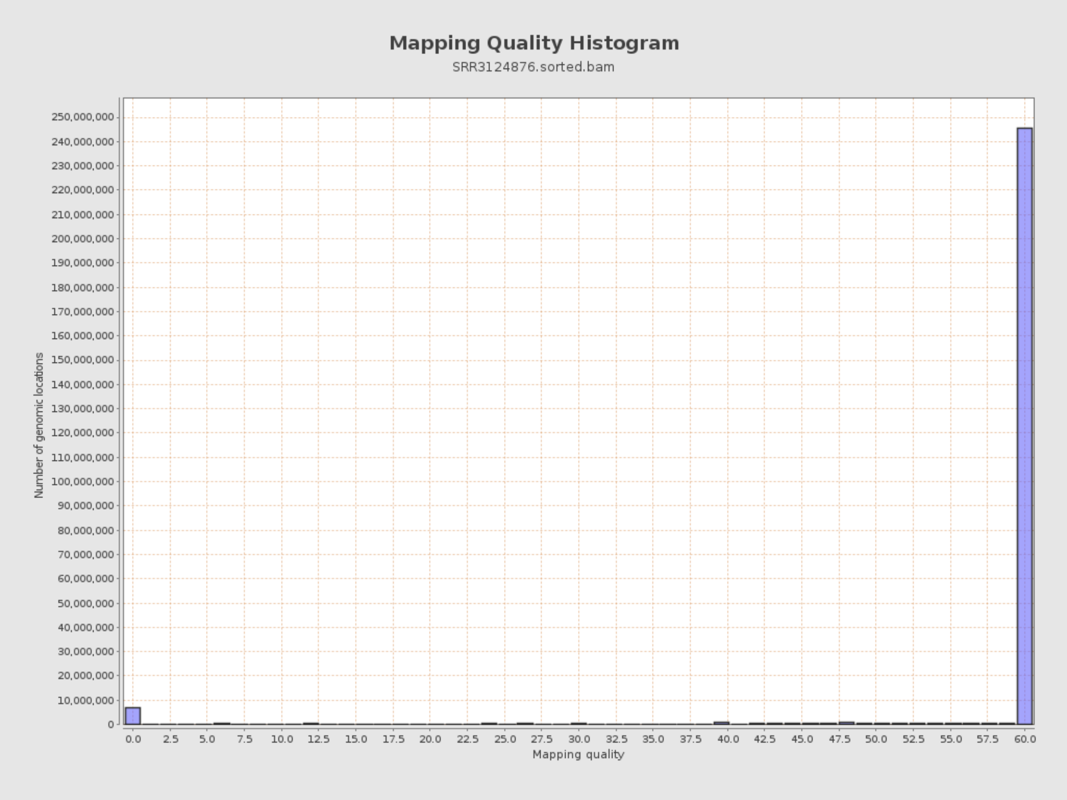
11. Results : Homopolymer Indels



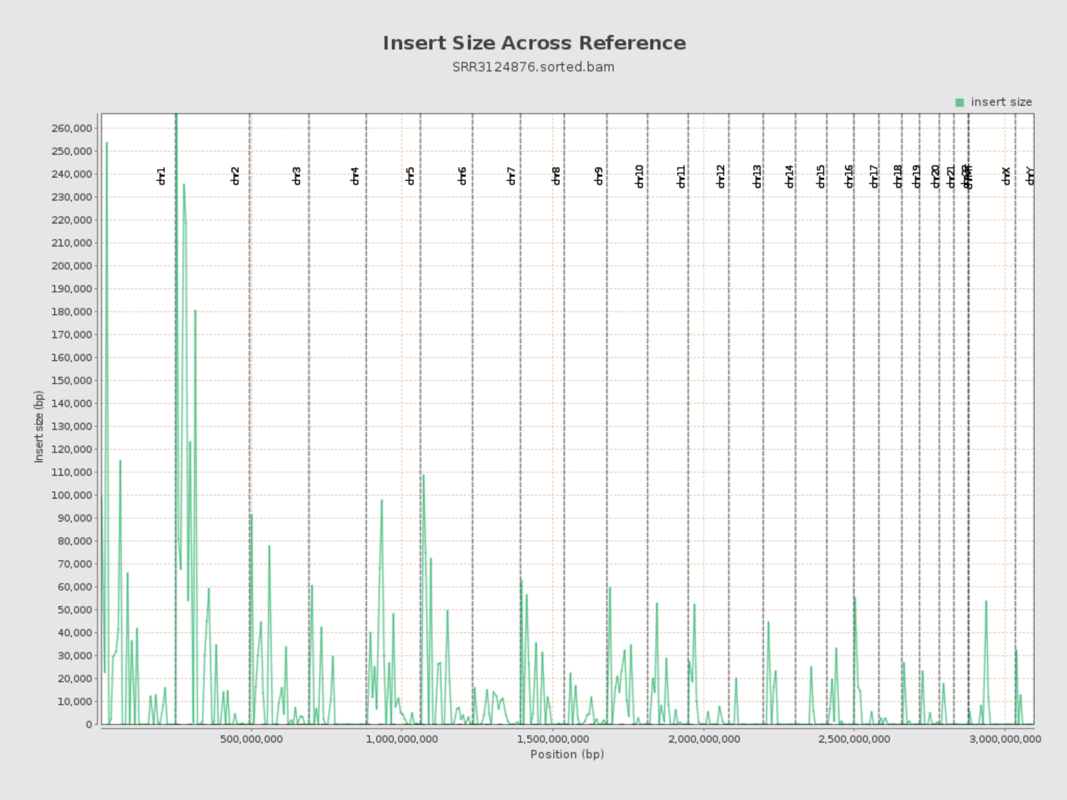
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram