Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 07:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124831.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_SRR3124831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124831_1.fastq.gz SRR3124831_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 07:16:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,432,478
Mapped reads	24,224,832 / 99.15%
Unmapped reads	207,646 / 0.85%
Mapped paired reads	24,224,832 / 99.15%
Mapped reads, first in pair	12,130,714 / 49.65%
Mapped reads, second in pair	12,094,118 / 49.5%
Mapped reads, both in pair	24,146,766 / 98.83%
Mapped reads, singletons	78,066 / 0.32%
Secondary alignments	0
Supplementary alignments	87,516 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	6,846,078 / 28.02%
Duplication rate	14.79%
Clipped reads	11,383,588 / 46.59%

2.2. ACGT Content

Number/percentage of A's	611,309,957 / 28.49%
Number/percentage of C's	396,377,043 / 18.47%
Number/percentage of T's	638,990,871 / 29.78%
Number/percentage of G's	499,031,040 / 23.26%
Number/percentage of N's	20,112 / 0%

GC Percentage	41.73%

2.3. Coverage

Mean	0.6935
Standard Deviation	11.675

2.4. Mapping Quality

Mean Mapping Quality	52.83

2.5. Insert size

Mean	30,282.19
Standard Deviation	1,616,103.83
P25/Median/P75	157 / 211 / 294

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	15,350,893
Insertions	244,053
Mapped reads with at least one insertion	0.98%
Deletions	571,912
Mapped reads with at least one deletion	2.32%
Homopolymer indels	48.27%

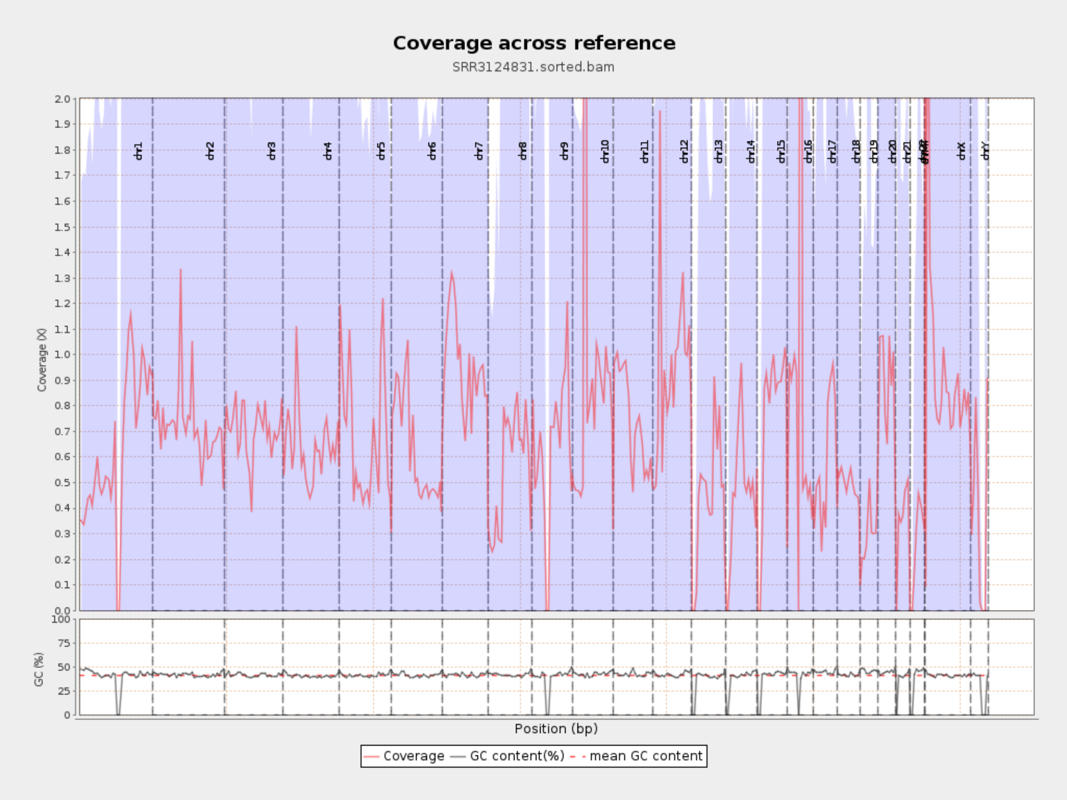
2.7. Chromosome stats

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

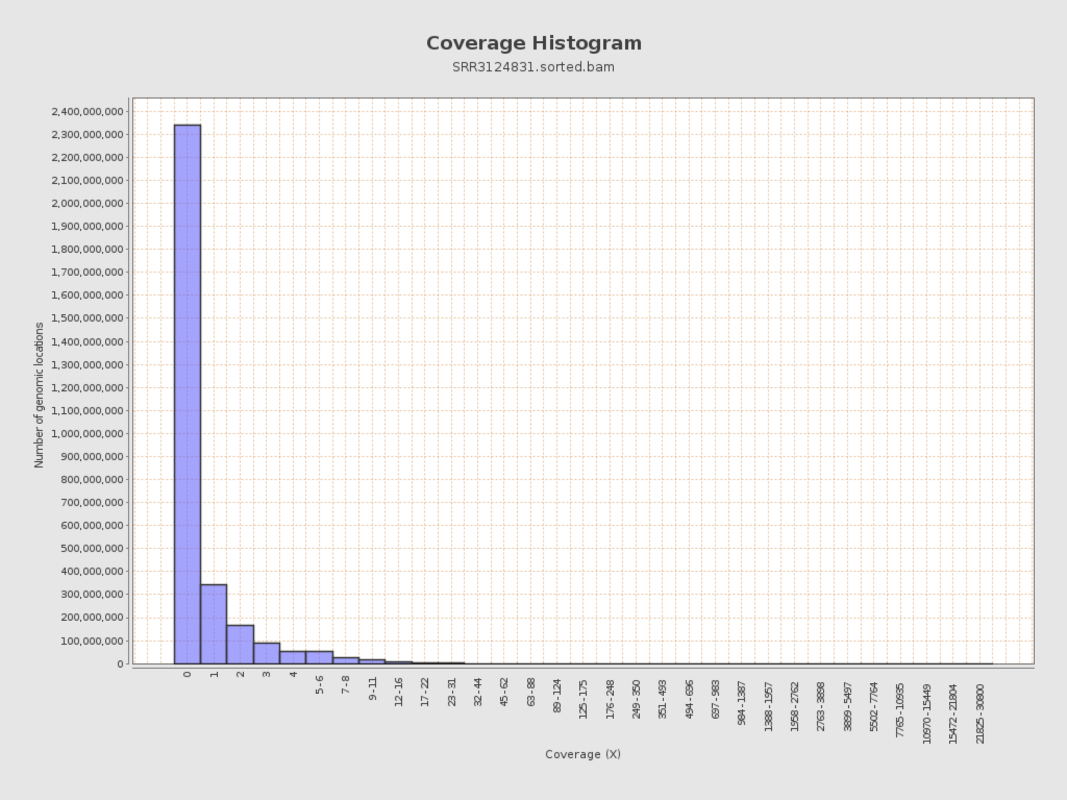
		bases	coverage	deviation
chr1	249250621	158894245	0.6375	3.9516
chr2	243199373	176859171	0.7272	5.879
chr3	198022430	139103135	0.7025	2.3353
chr4	191154276	122421117	0.6404	4.046
chr5	180915260	122781199	0.6787	1.8631
chr6	171115067	108079772	0.6316	2.6523
chr7	159138663	152805324	0.9602	6.7779
chr8	146364022	82217014	0.5617	1.9084
chr9	141213431	88700216	0.6281	5.0475
chr10	135534747	139519757	1.0294	45.691
chr11	135006516	99527415	0.7372	6.1719
chr12	133851895	126875586	0.9479	2.3557
chr13	115169878	51163891	0.4442	1.398
chr14	107349540	49255849	0.4588	1.7456
chr15	102531392	76085695	0.7421	1.9739
chr16	90354753	93355419	1.0332	32.0703
chr17	81195210	46534874	0.5731	3.1906
chr18	78077248	38991043	0.4994	5.4041
chr19	59128983	17194455	0.2908	2.729
chr20	63025520	56227758	0.8921	2.3568
chr21	48129895	17351906	0.3605	2.1692
chr22	51304566	13575276	0.2646	1.6006
chrMT	16571	1032174	62.288	36.8697
chrX	155270560	145271605	0.9356	3.8869

chrY	59373566	22901772	0.3857	6.6958

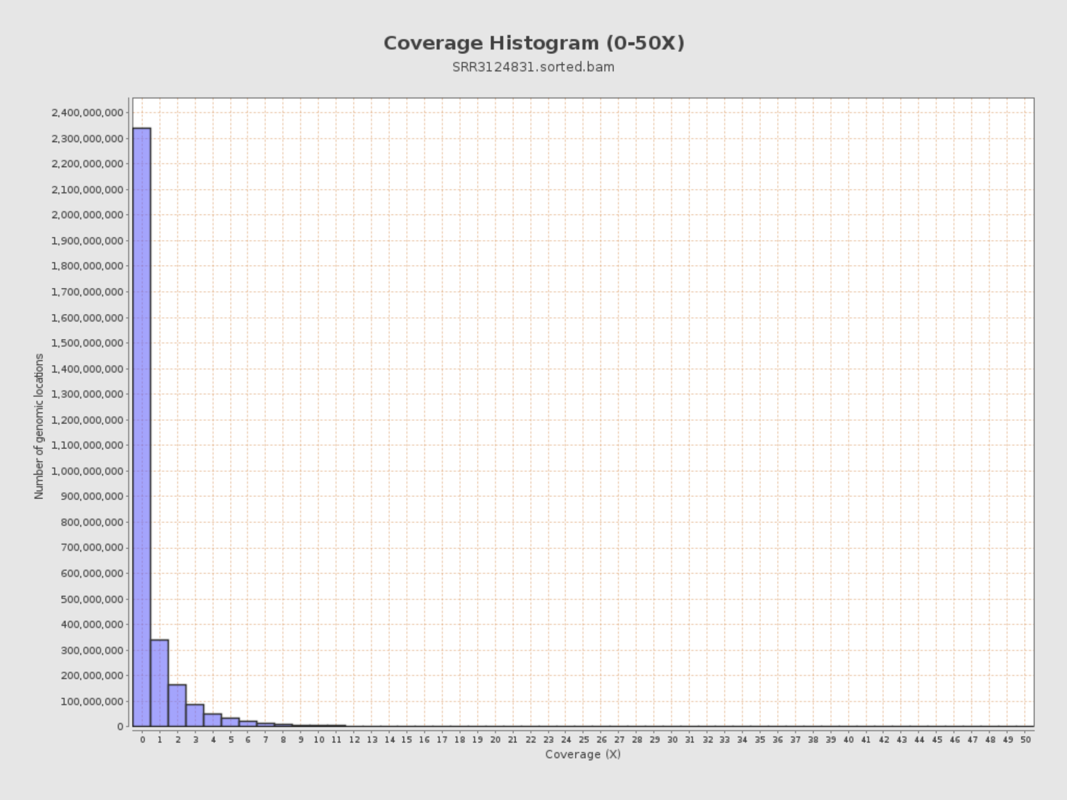
3. Results : Coverage across reference



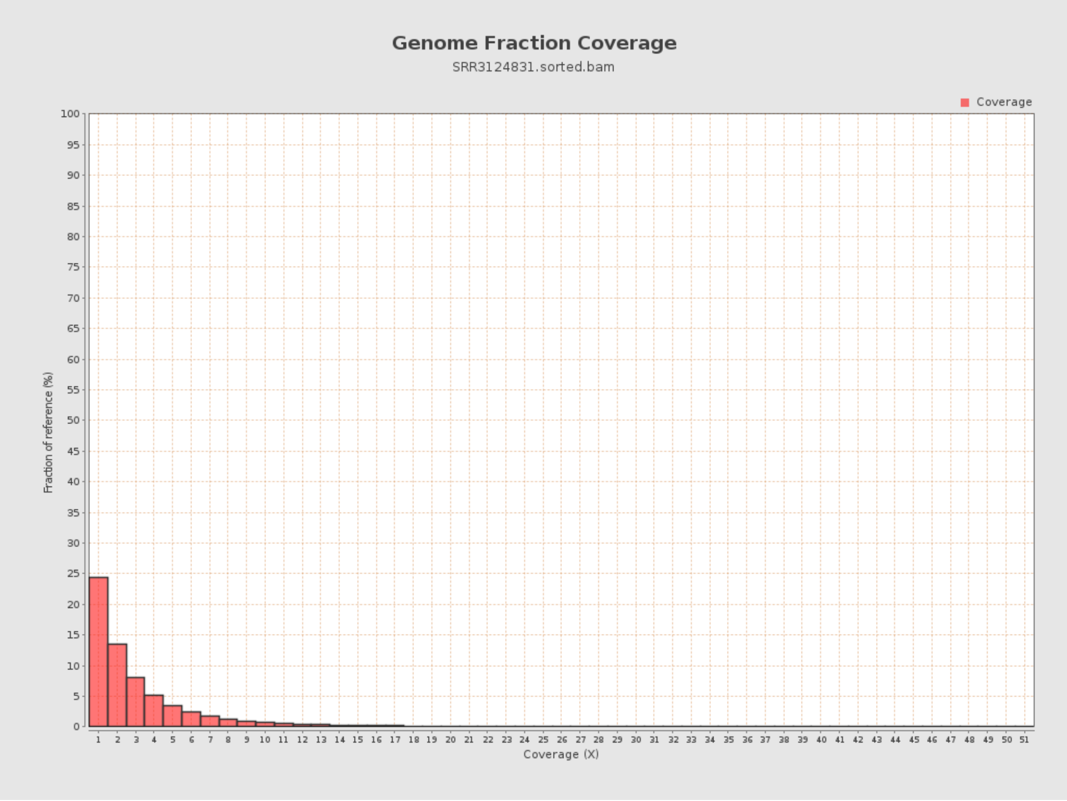
4. Results : Coverage Histogram



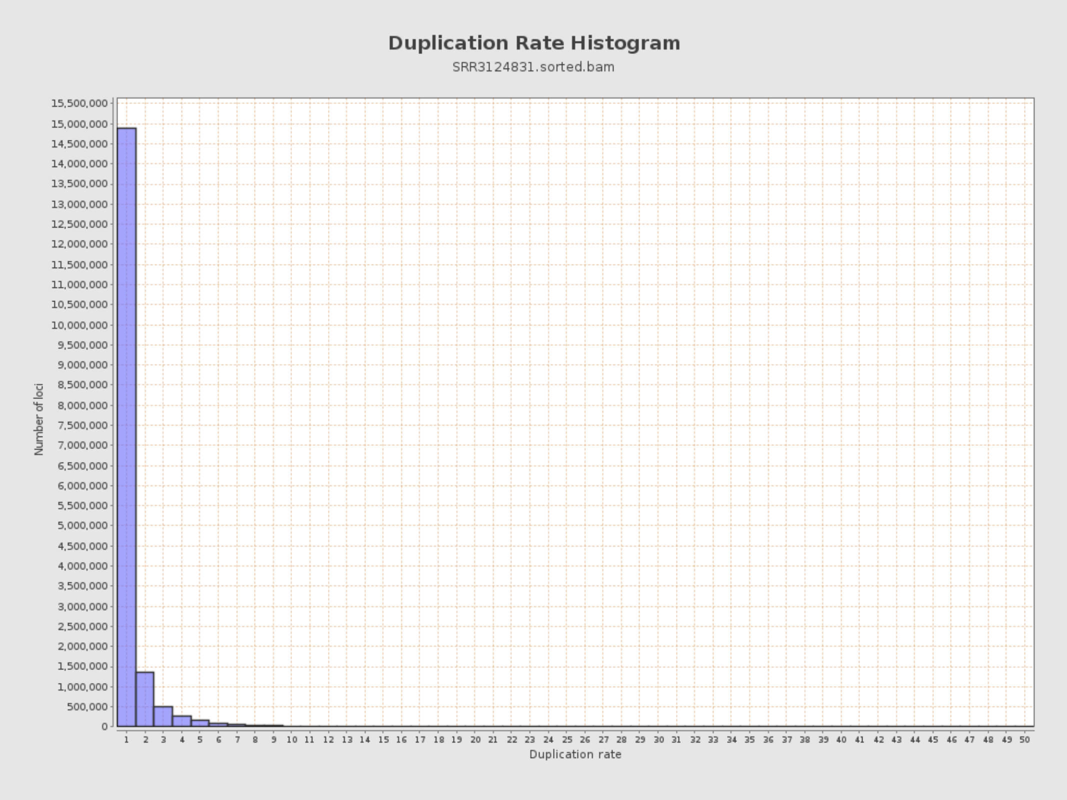
5. Results : Coverage Histogram (0-50X)



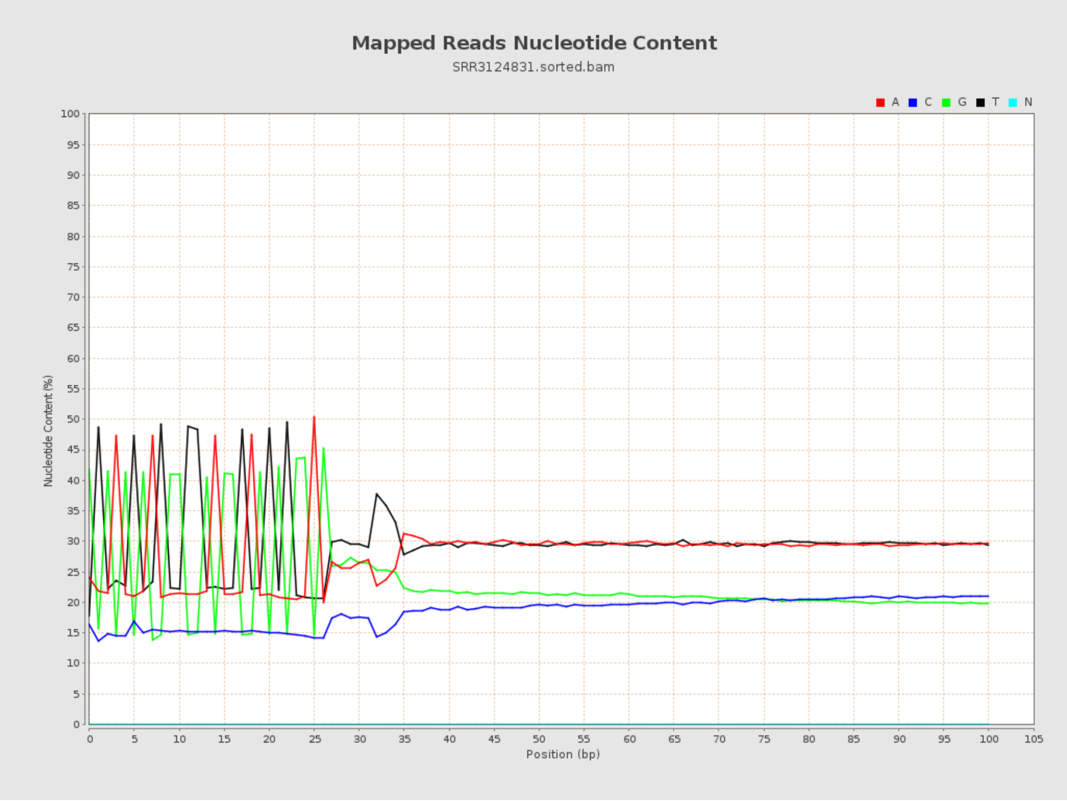
6. Results : Genome Fraction Coverage



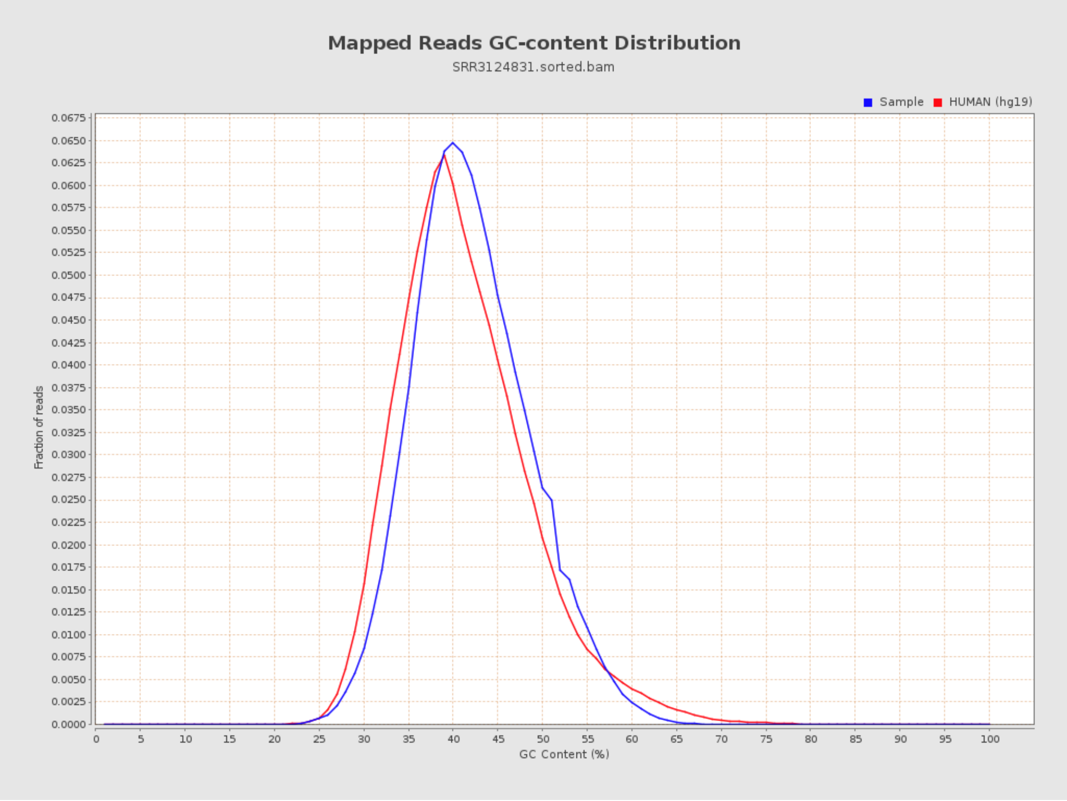
7. Results : Duplication Rate Histogram



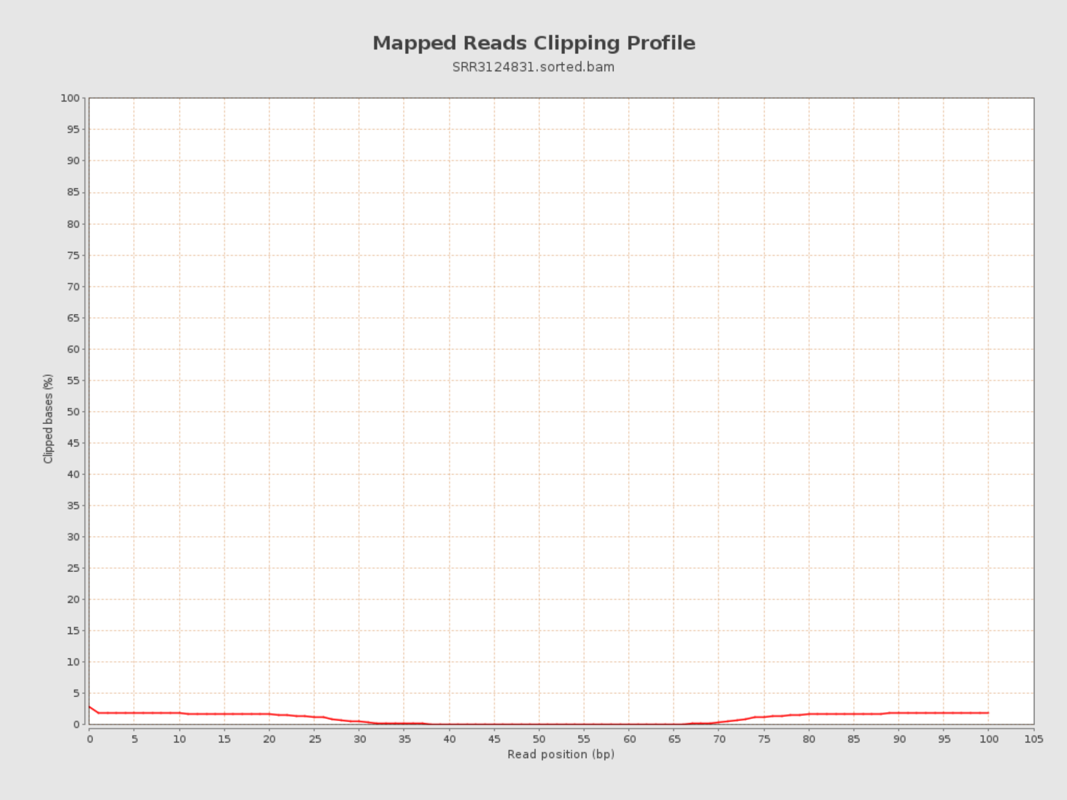
8. Results : Mapped Reads Nucleotide Content



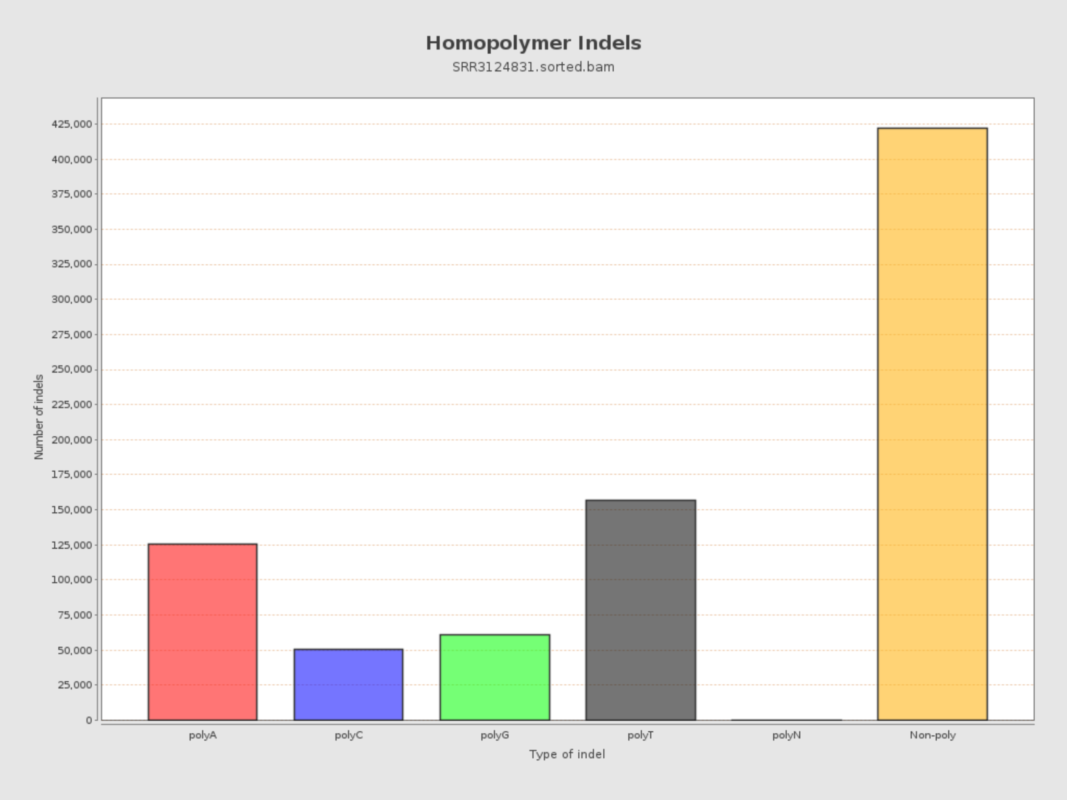
9. Results : Mapped Reads GC-content Distribution



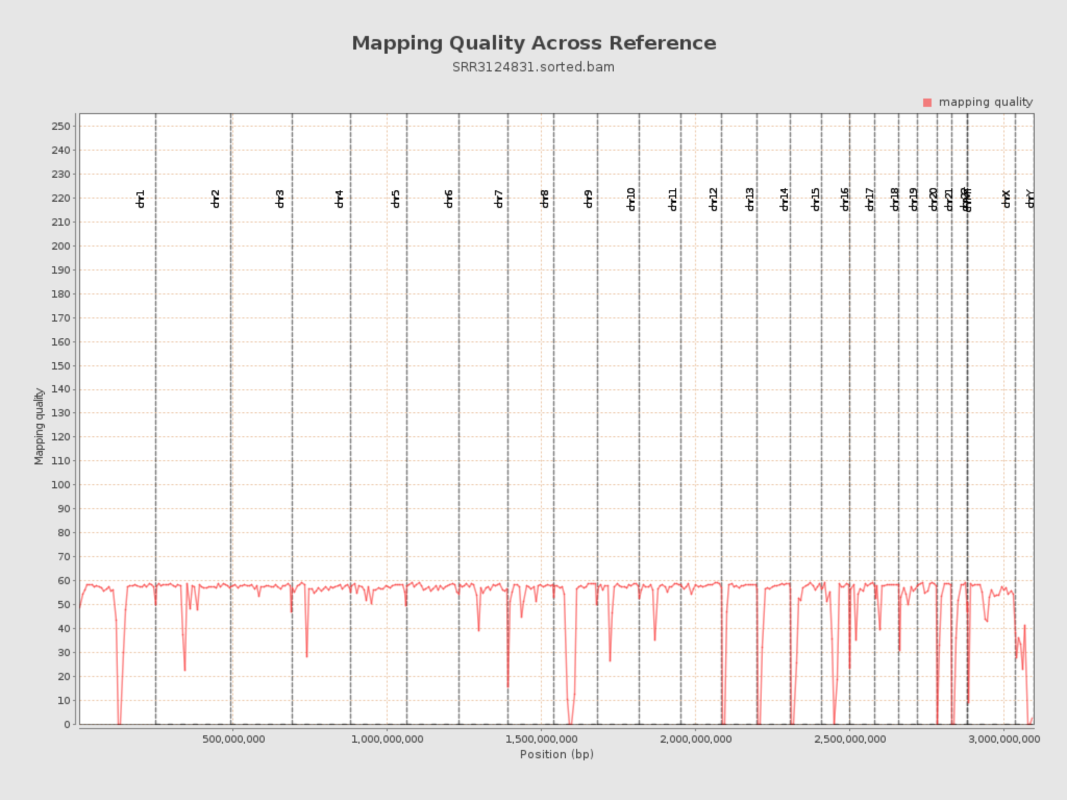
10. Results : Mapped Reads Clipping Profile



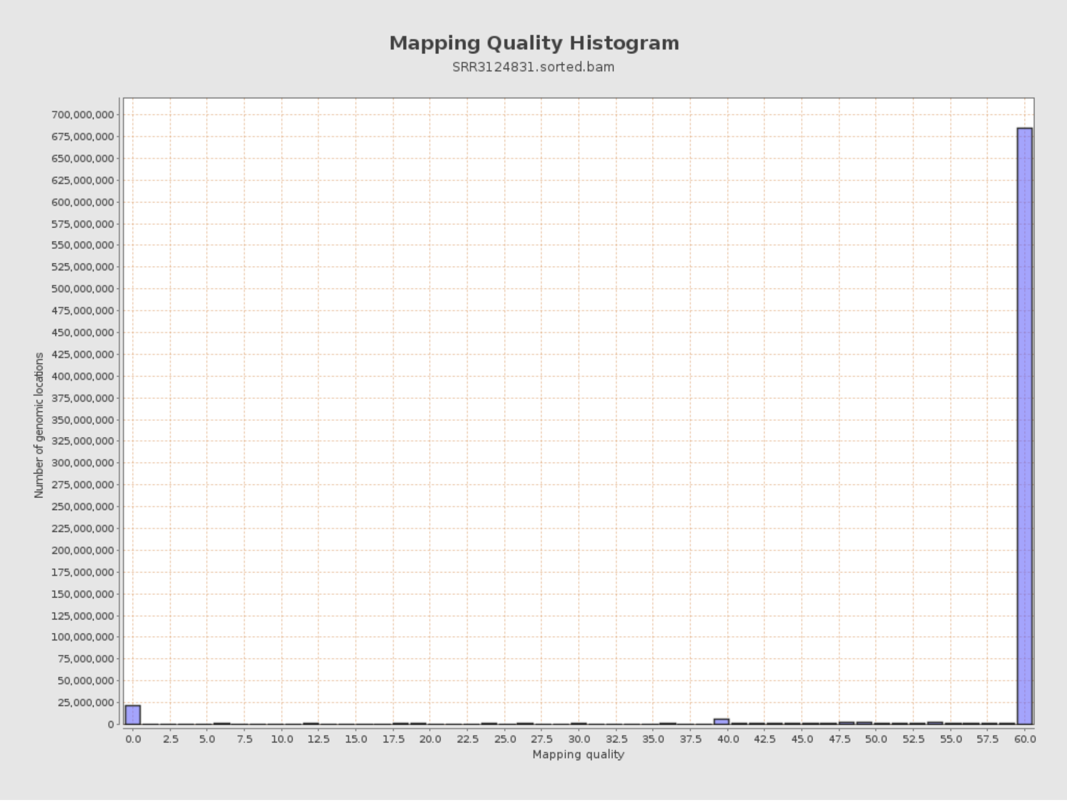
11. Results : Homopolymer Indels



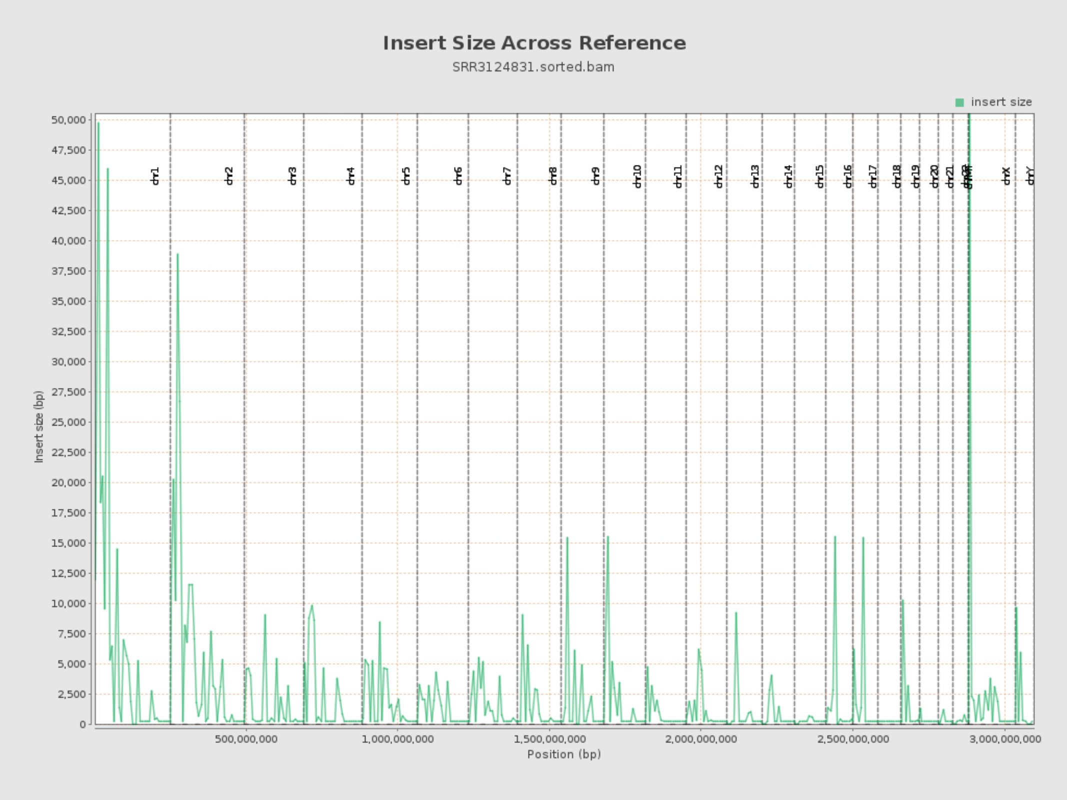
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram