Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:30:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472447.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_SRR3472447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472447_1.fastq.gz SRR3472447_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:30:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,028,752
Mapped reads	20,814,077 / 98.98%
Unmapped reads	214,675 / 1.02%
Mapped paired reads	20,814,077 / 98.98%
Mapped reads, first in pair	10,444,133 / 49.67%
Mapped reads, second in pair	10,369,944 / 49.31%
Mapped reads, both in pair	20,682,180 / 98.35%
Mapped reads, singletons	131,897 / 0.63%
Secondary alignments	0
Supplementary alignments	78,942 / 0.38%
Read min/max/mean length	30 / 100 / 99.49
Duplicated reads (estimated)	13,255,622 / 63.04%
Duplication rate	48.13%
Clipped reads	1,334,815 / 6.35%

2.2. ACGT Content

Number/percentage of A's	564,736,516 / 27.61%
Number/percentage of C's	459,015,030 / 22.44%
Number/percentage of T's	566,060,083 / 27.67%
Number/percentage of G's	455,451,395 / 22.27%
Number/percentage of N's	261,732 / 0.01%

GC Percentage	44.71%

2.3. Coverage

Mean	0.6608
Standard Deviation	19.9864

2.4. Mapping Quality

Mean Mapping Quality	54.68

2.5. Insert size

Mean	20,130.33
Standard Deviation	1,377,156.76
P25/Median/P75	167 / 233 / 312

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	11,776,341
Insertions	121,681
Mapped reads with at least one insertion	0.58%
Deletions	105,014
Mapped reads with at least one deletion	0.5%
Homopolymer indels	46.9%

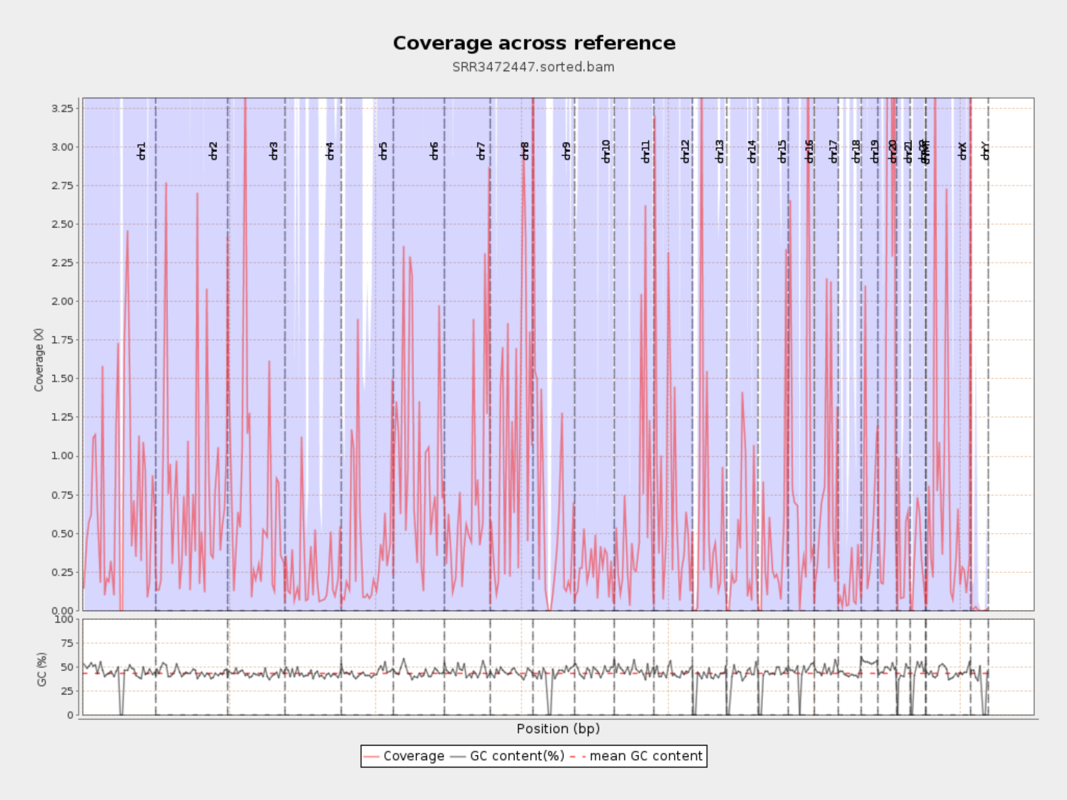
2.7. Chromosome stats

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

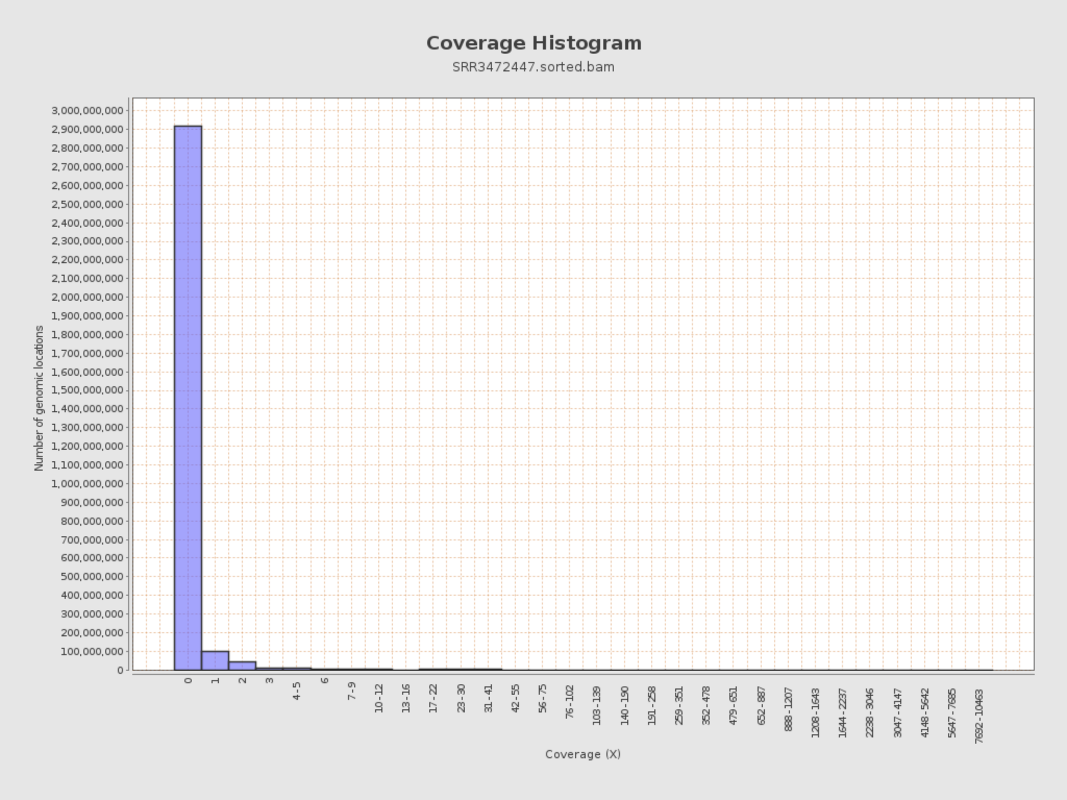
		bases	coverage	deviation
chr1	249250621	177219097	0.711	19.2816
chr2	243199373	178128459	0.7324	23.206
chr3	198022430	144570165	0.7301	15.7495
chr4	191154276	47886534	0.2505	8.2966
chr5	180915260	78102914	0.4317	13.7632
chr6	171115067	171778865	1.0039	24.1945
chr7	159138663	125298985	0.7874	21.3586
chr8	146364022	162664221	1.1114	27.2195
chr9	141213431	78032717	0.5526	12.7032
chr10	135534747	37328474	0.2754	7.8799
chr11	135006516	83348447	0.6174	21.4661
chr12	133851895	109424961	0.8175	18.8497
chr13	115169878	71622235	0.6219	22.1308
chr14	107349540	44766741	0.417	13.1653
chr15	102531392	44779220	0.4367	15.6459
chr16	90354753	85020285	0.941	22.9213
chr17	81195210	65449435	0.8061	16.5995
chr18	78077248	10919088	0.1398	5.5378
chr19	59128983	41619545	0.7039	14.5945
chr20	63025520	127395241	2.0213	52.6924
chr21	48129895	18973513	0.3942	19.3987
chr22	51304566	17120795	0.3337	9.6419
chrMT	16571	3878	0.234	0.6432
chrX	155270560	123888211	0.7979	26.7466

chrY	59373566	422888	0.0071	0.6843

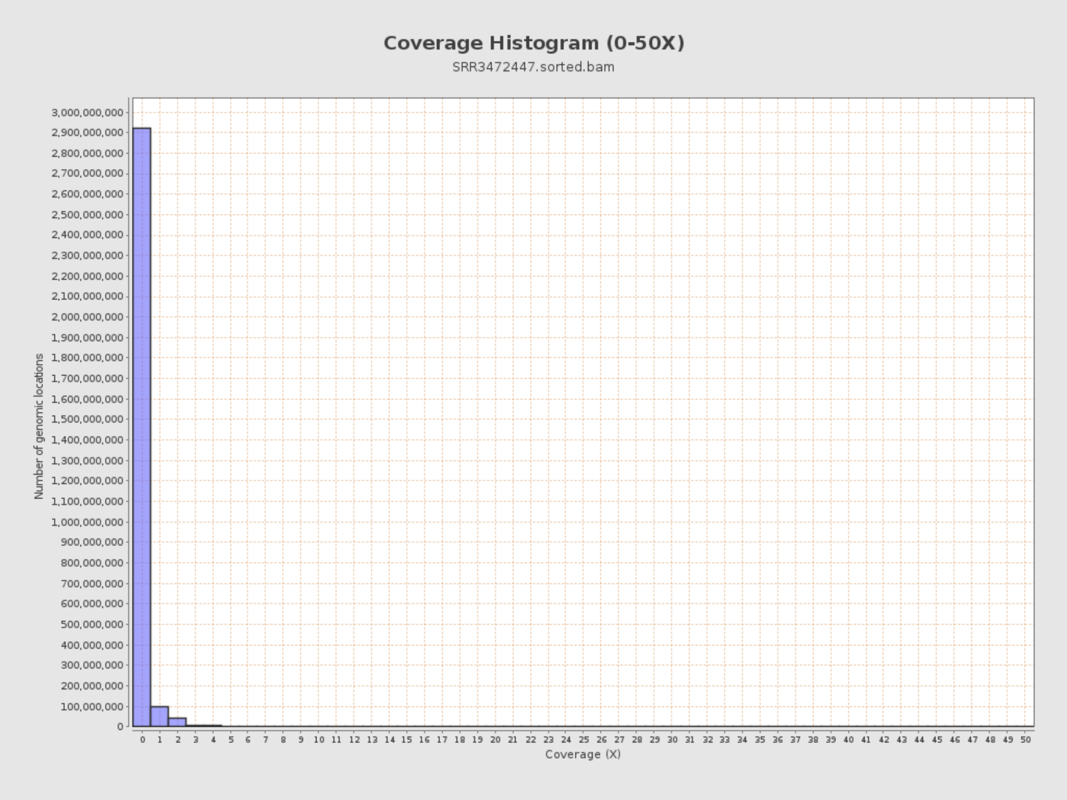
3. Results : Coverage across reference



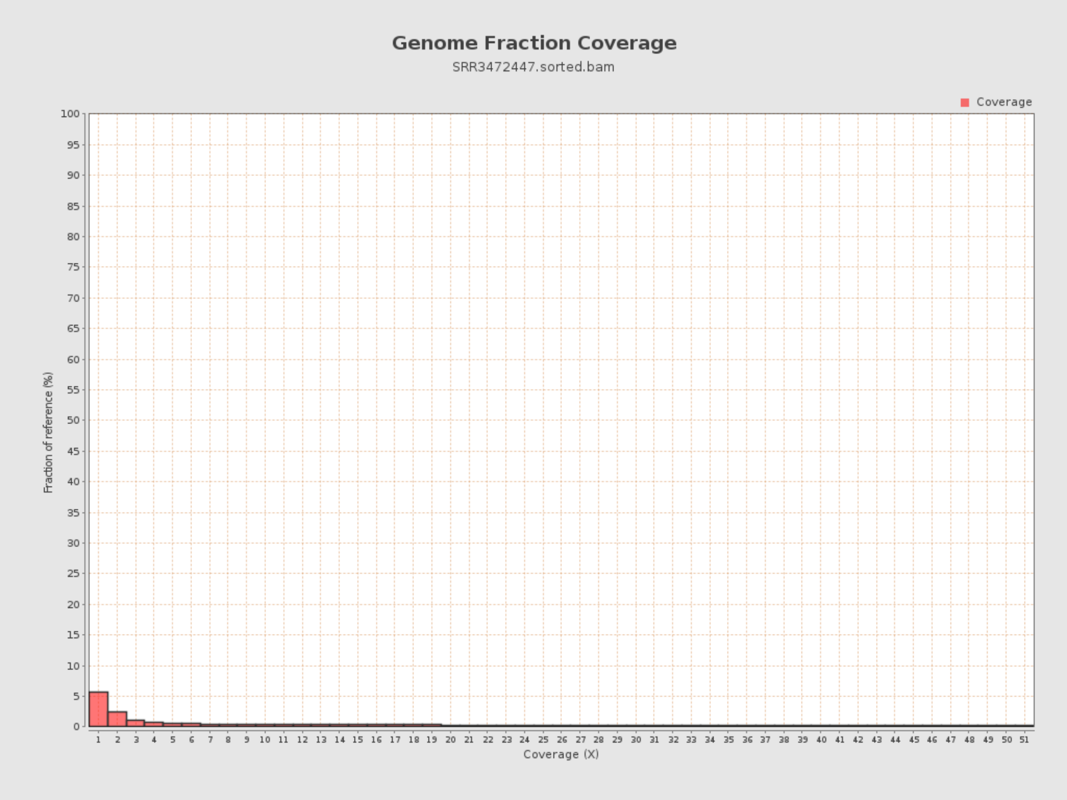
4. Results : Coverage Histogram



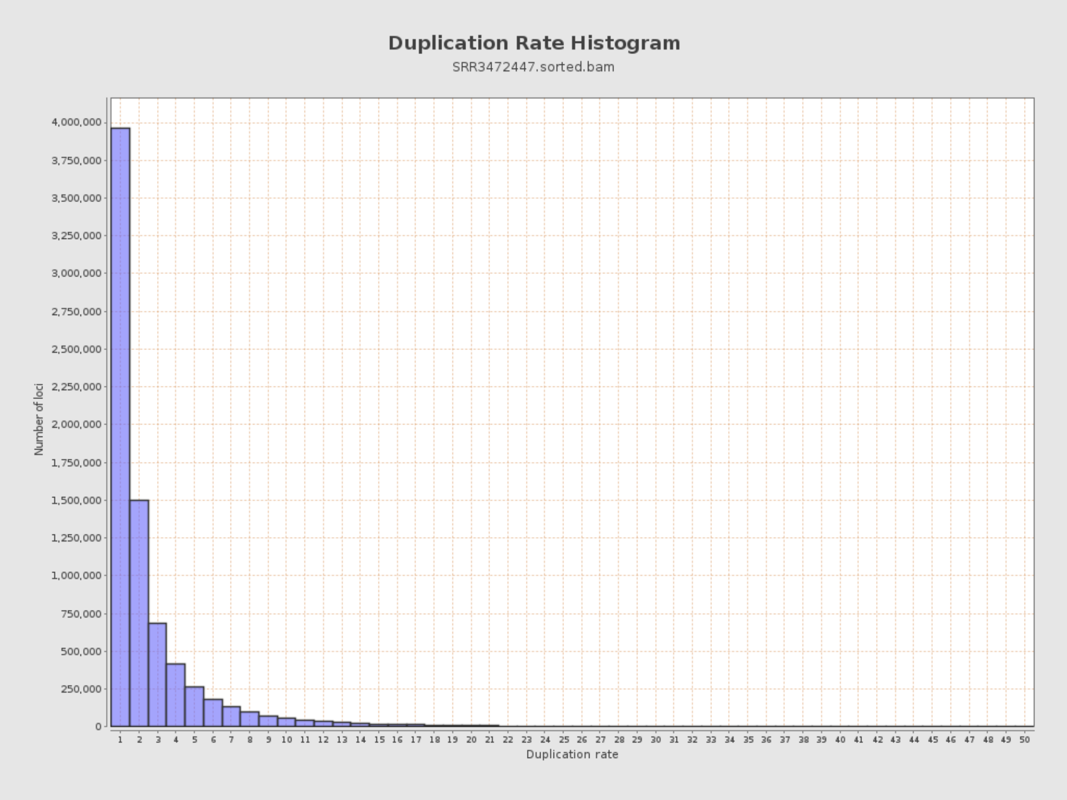
5. Results : Coverage Histogram (0-50X)



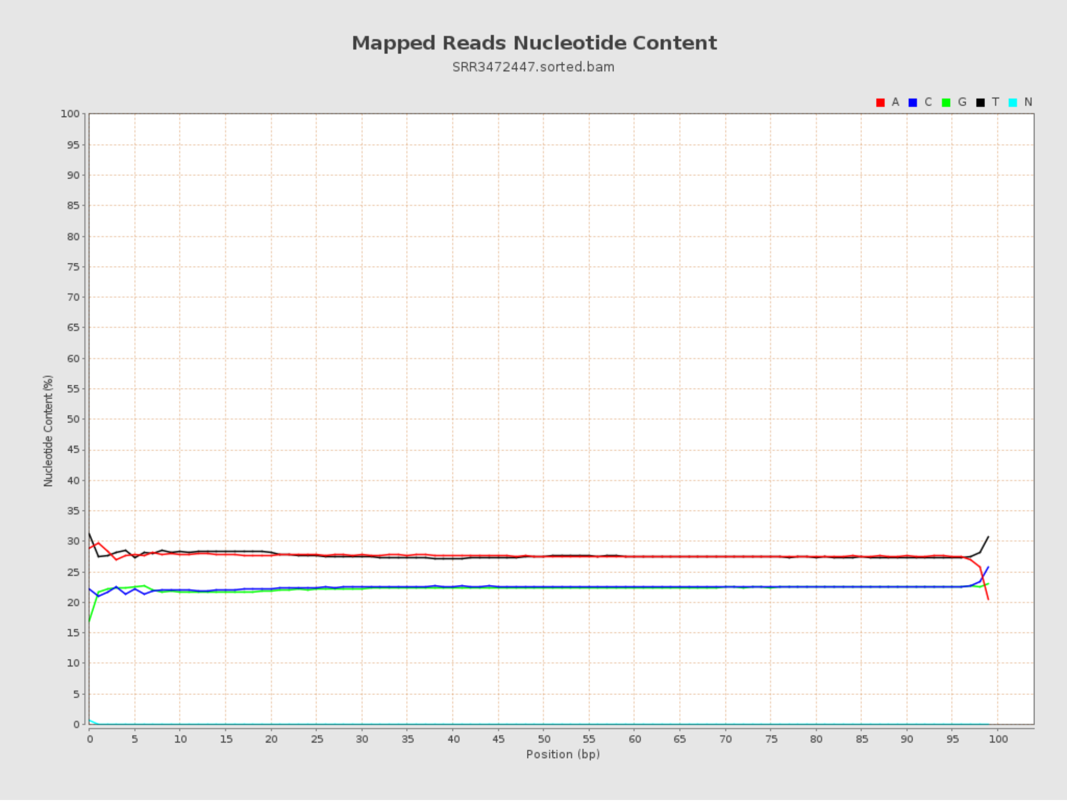
6. Results : Genome Fraction Coverage



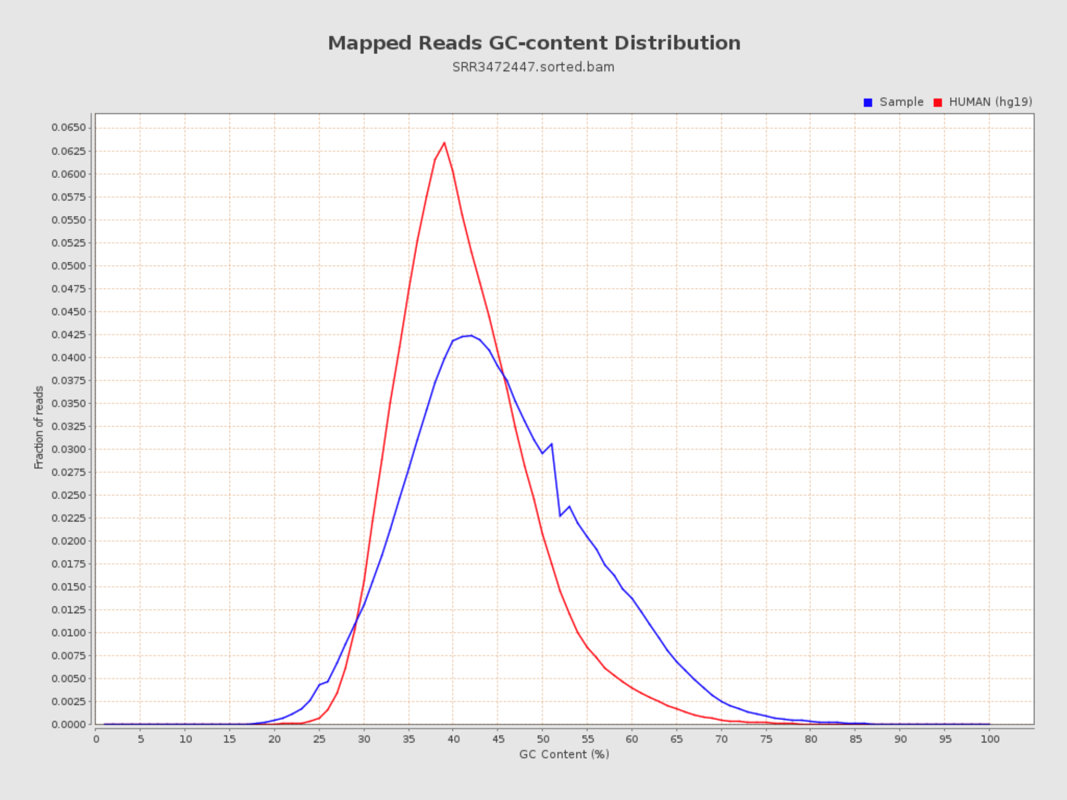
7. Results : Duplication Rate Histogram



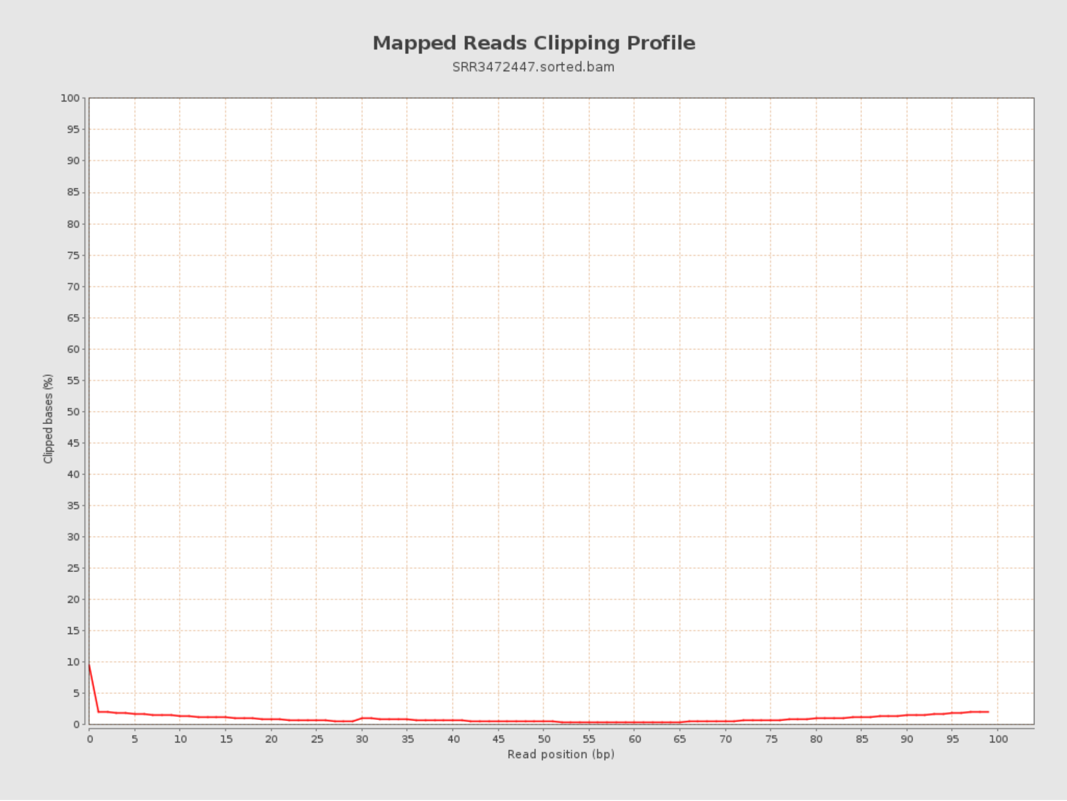
8. Results : Mapped Reads Nucleotide Content



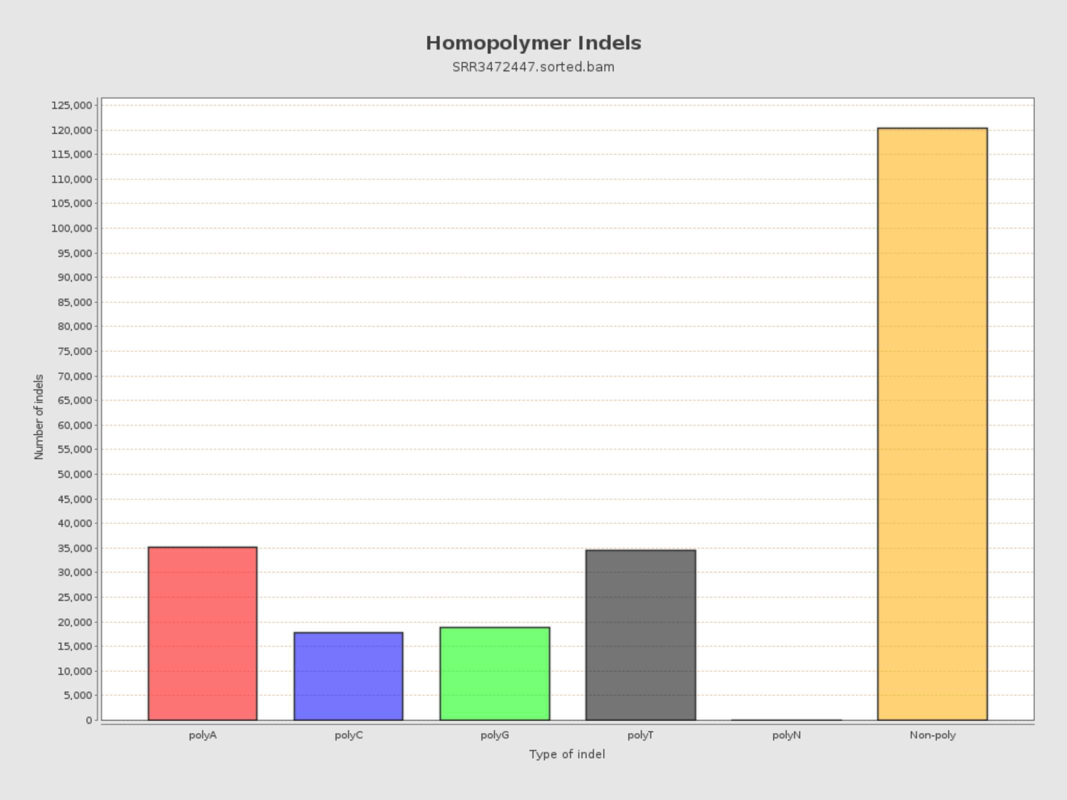
9. Results : Mapped Reads GC-content Distribution



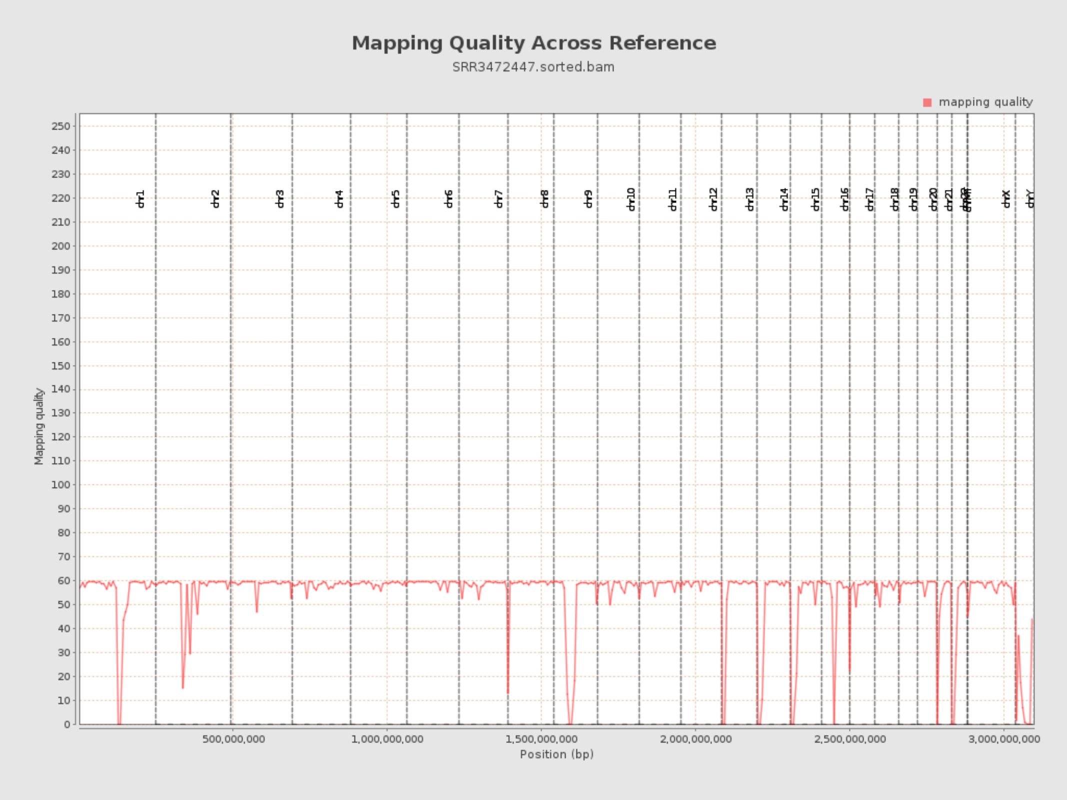
10. Results : Mapped Reads Clipping Profile



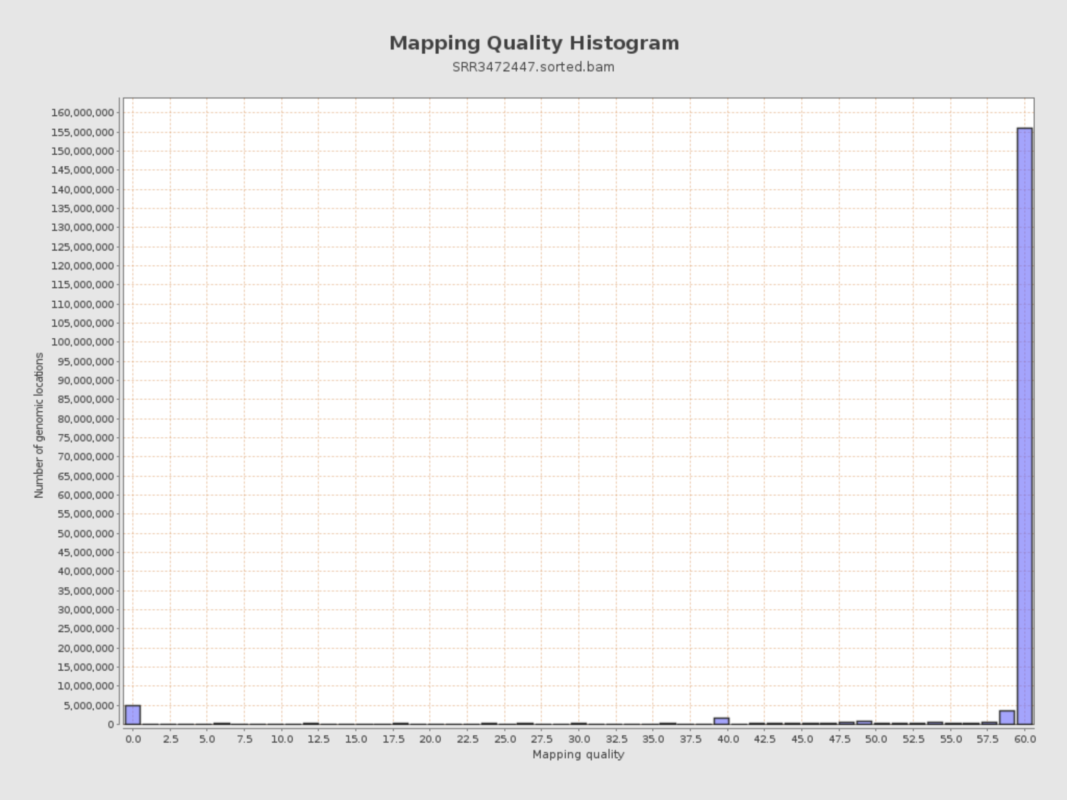
11. Results : Homopolymer Indels



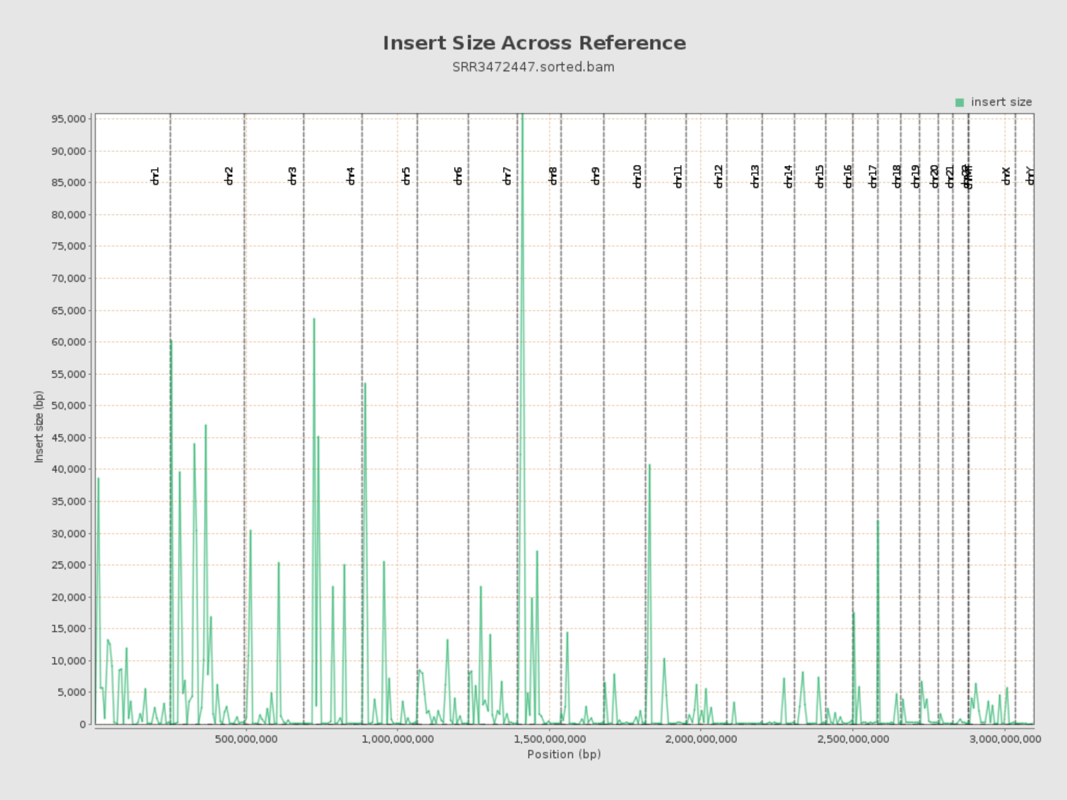
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram