Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:58:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472403.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_SRR3472403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472403_1.fastq.gz SRR3472403_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:58:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,409,886
Mapped reads	16,272,612 / 99.16%
Unmapped reads	137,274 / 0.84%
Mapped paired reads	16,272,612 / 99.16%
Mapped reads, first in pair	8,161,380 / 49.73%
Mapped reads, second in pair	8,111,232 / 49.43%
Mapped reads, both in pair	16,185,854 / 98.63%
Mapped reads, singletons	86,758 / 0.53%
Secondary alignments	0
Supplementary alignments	58,392 / 0.36%
Read min/max/mean length	30 / 100 / 99.4
Duplicated reads (estimated)	10,016,825 / 61.04%
Duplication rate	47.03%
Clipped reads	1,050,951 / 6.4%

2.2. ACGT Content

Number/percentage of A's	430,352,956 / 26.94%
Number/percentage of C's	369,426,077 / 23.12%
Number/percentage of T's	431,960,602 / 27.04%
Number/percentage of G's	365,776,368 / 22.89%
Number/percentage of N's	192,501 / 0.01%

GC Percentage	46.02%

2.3. Coverage

Mean	0.5162
Standard Deviation	15.982

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	18,326.4
Standard Deviation	1,337,869.73
P25/Median/P75	158 / 219 / 294

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	8,721,478
Insertions	96,139
Mapped reads with at least one insertion	0.58%
Deletions	78,014
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.79%

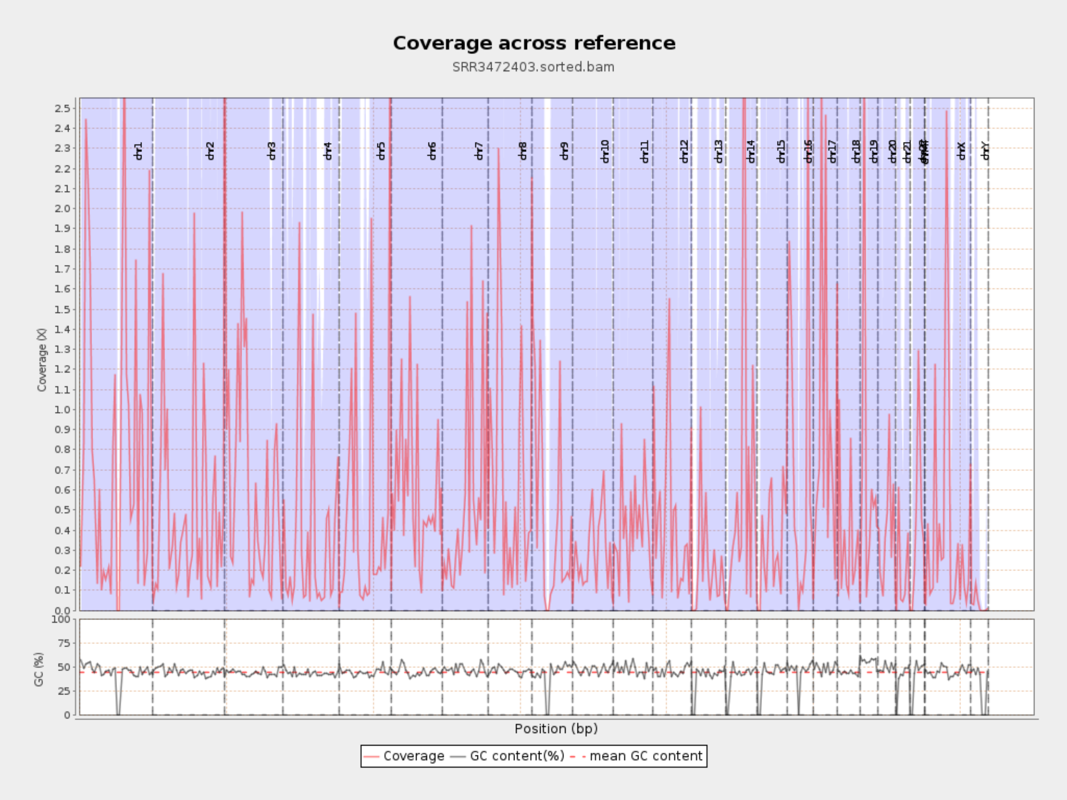
2.7. Chromosome stats

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

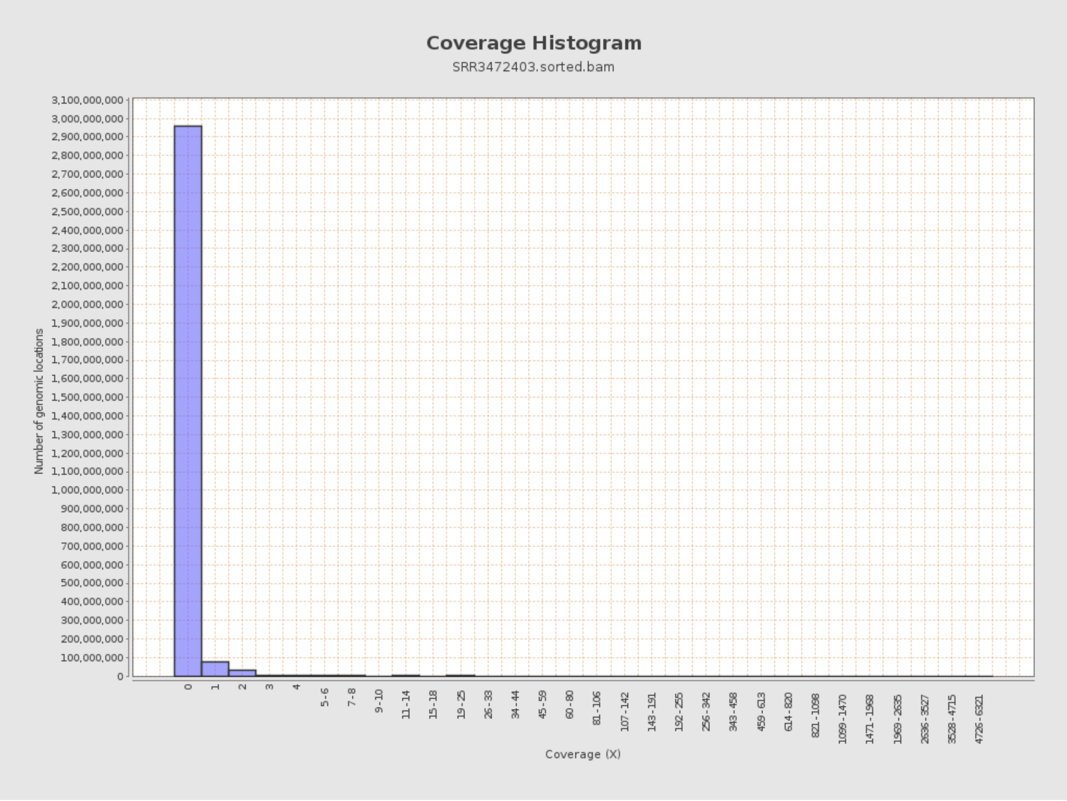
		bases	coverage	deviation
chr1	249250621	211145566	0.8471	23.8506
chr2	243199373	115558604	0.4752	16.3009
chr3	198022430	132187013	0.6675	15.2148
chr4	191154276	65877759	0.3446	13.0929
chr5	180915260	94732572	0.5236	20.09
chr6	171115067	102664789	0.6	13.2107
chr7	159138663	89875513	0.5648	17.0224
chr8	146364022	95483092	0.6524	18.6988
chr9	141213431	68692277	0.4864	13.8819
chr10	135534747	39072304	0.2883	8.9159
chr11	135006516	56475875	0.4183	13.3743
chr12	133851895	61659961	0.4607	10.4351
chr13	115169878	25934609	0.2252	6.464
chr14	107349540	65018911	0.6057	21.9367
chr15	102531392	32667466	0.3186	9.0542
chr16	90354753	67465650	0.7467	17.8477
chr17	81195210	78361821	0.9651	25.64
chr18	78077248	27355586	0.3504	11.1806
chr19	59128983	44786044	0.7574	15.1227
chr20	63025520	25612655	0.4064	12.1016
chr21	48129895	9545916	0.1983	10.5444
chr22	51304566	21680447	0.4226	13.5901
chrMT	16571	2887	0.1742	0.5452
chrX	155270560	64094888	0.4128	14.848

chrY	59373566	1938291	0.0326	1.271

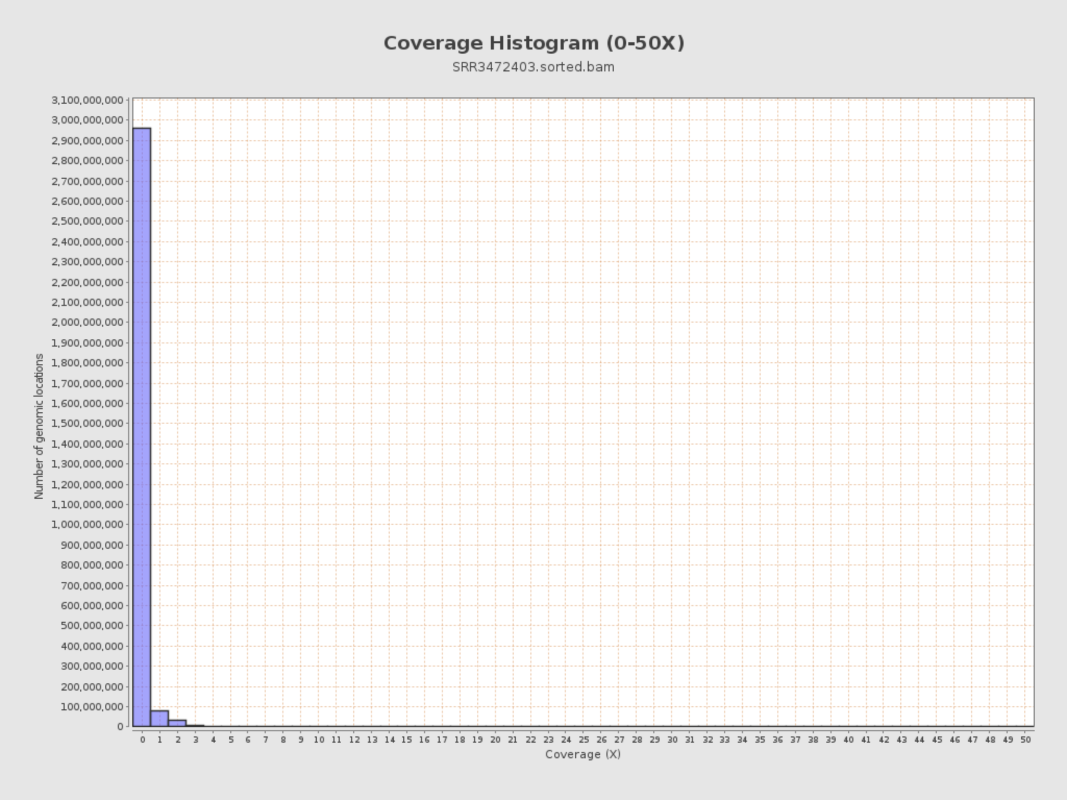
3. Results : Coverage across reference



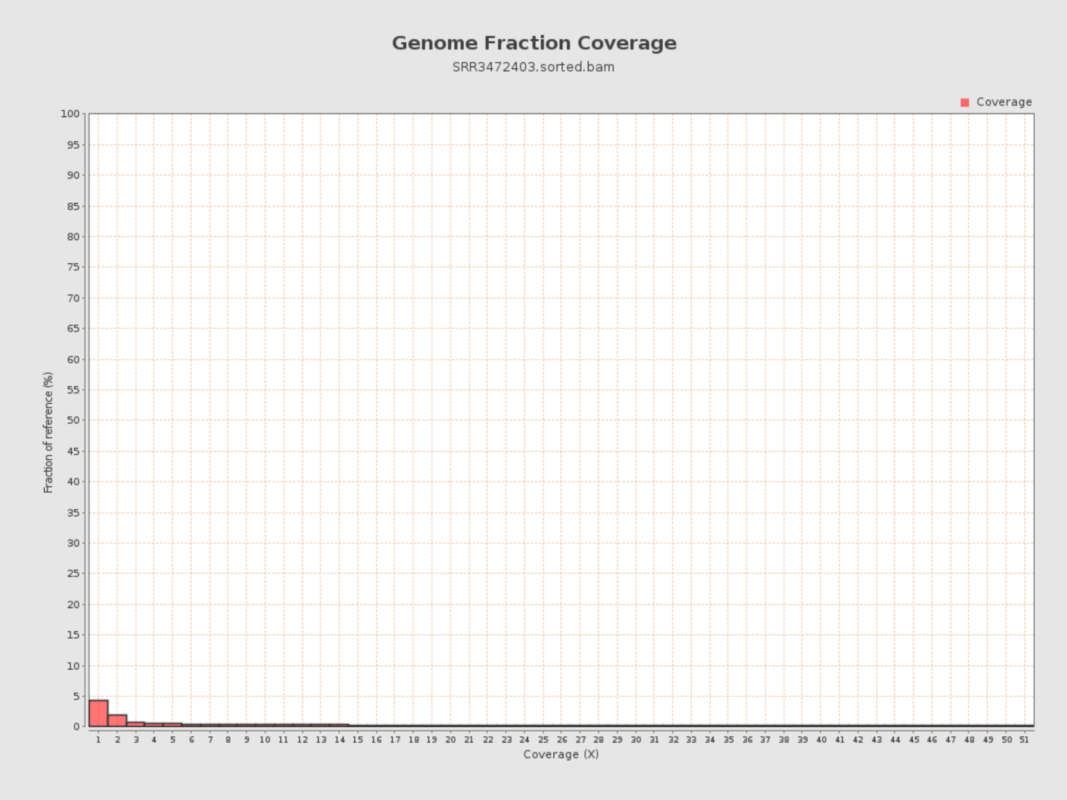
4. Results : Coverage Histogram



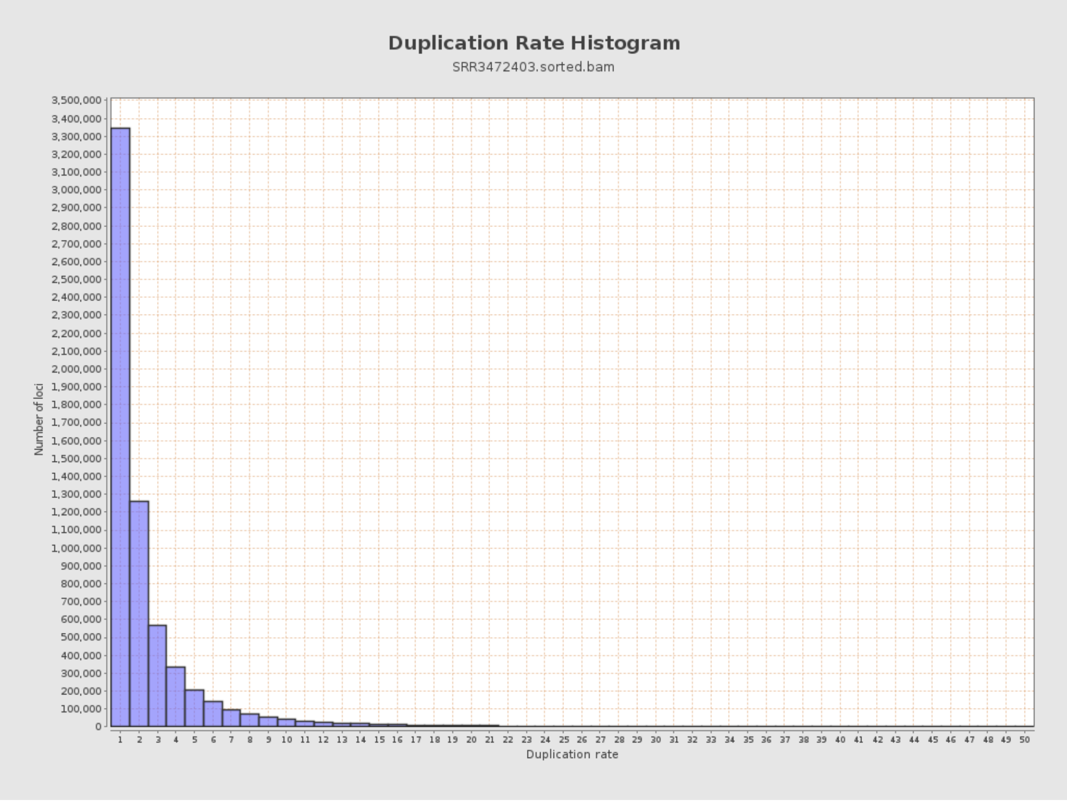
5. Results : Coverage Histogram (0-50X)



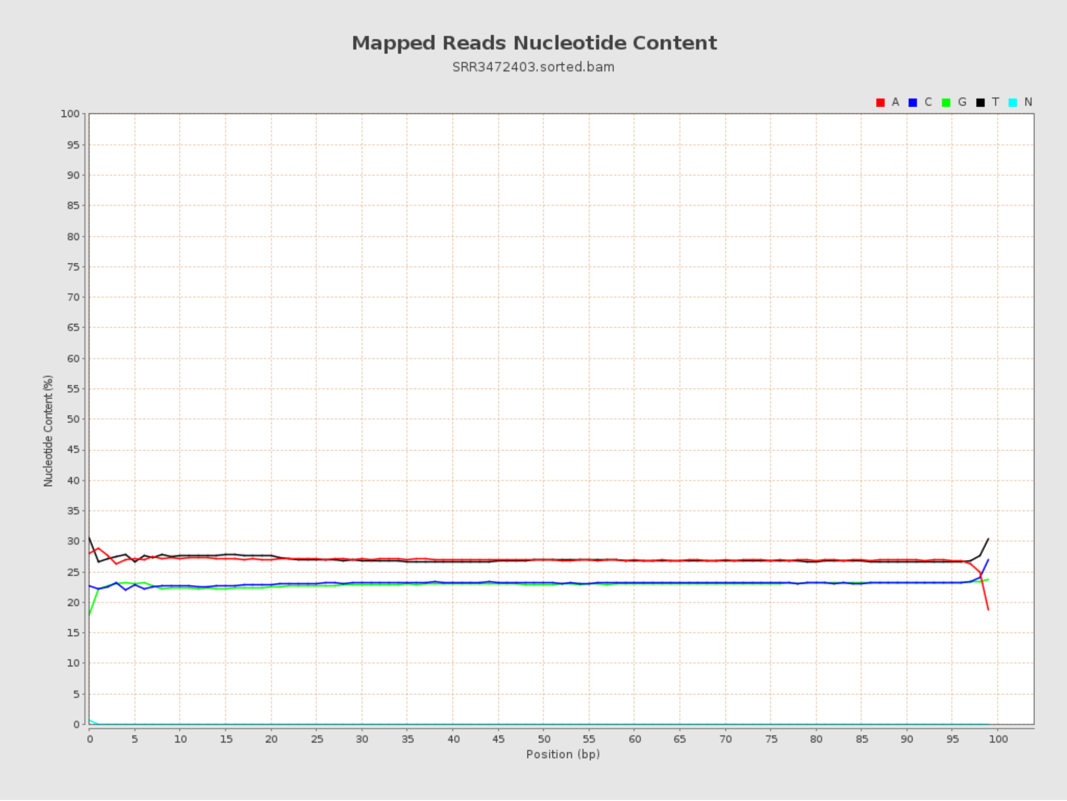
6. Results : Genome Fraction Coverage



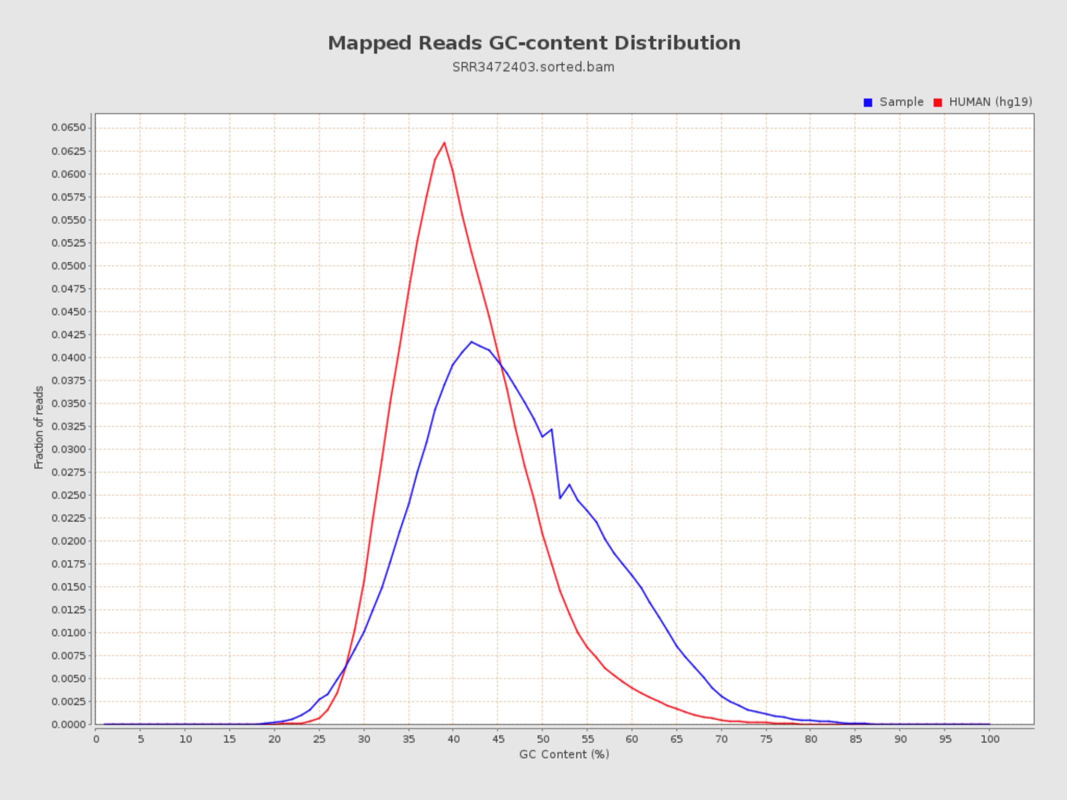
7. Results : Duplication Rate Histogram



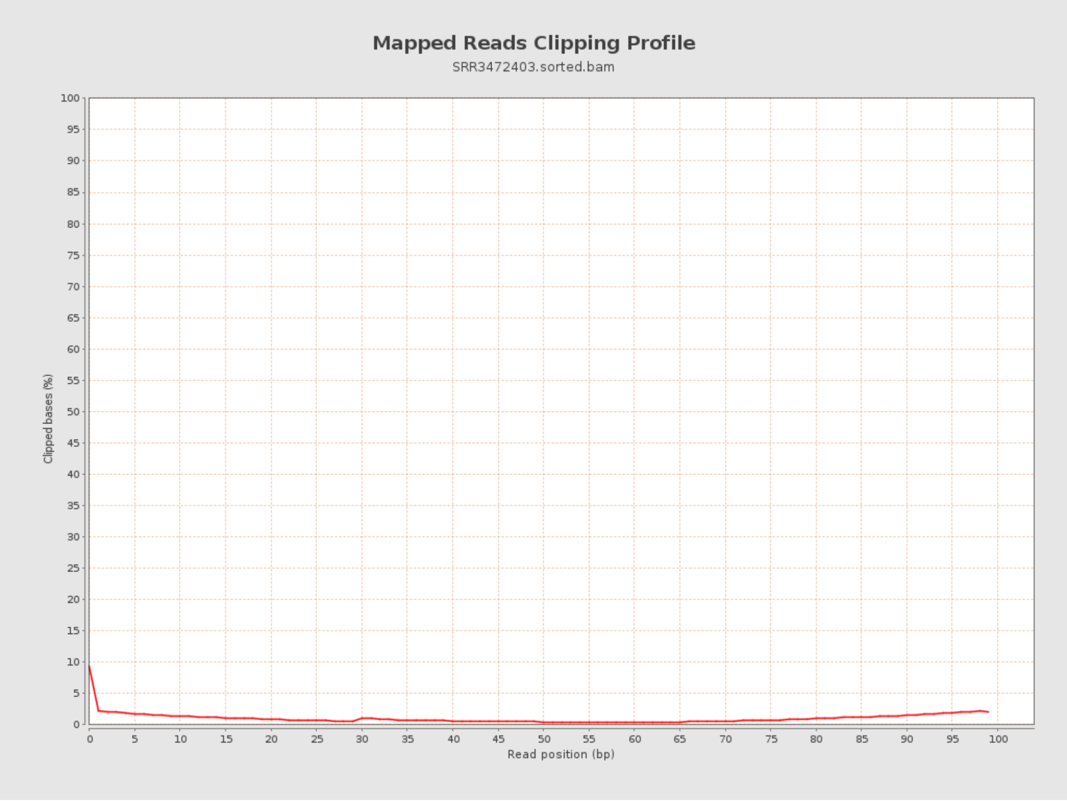
8. Results : Mapped Reads Nucleotide Content



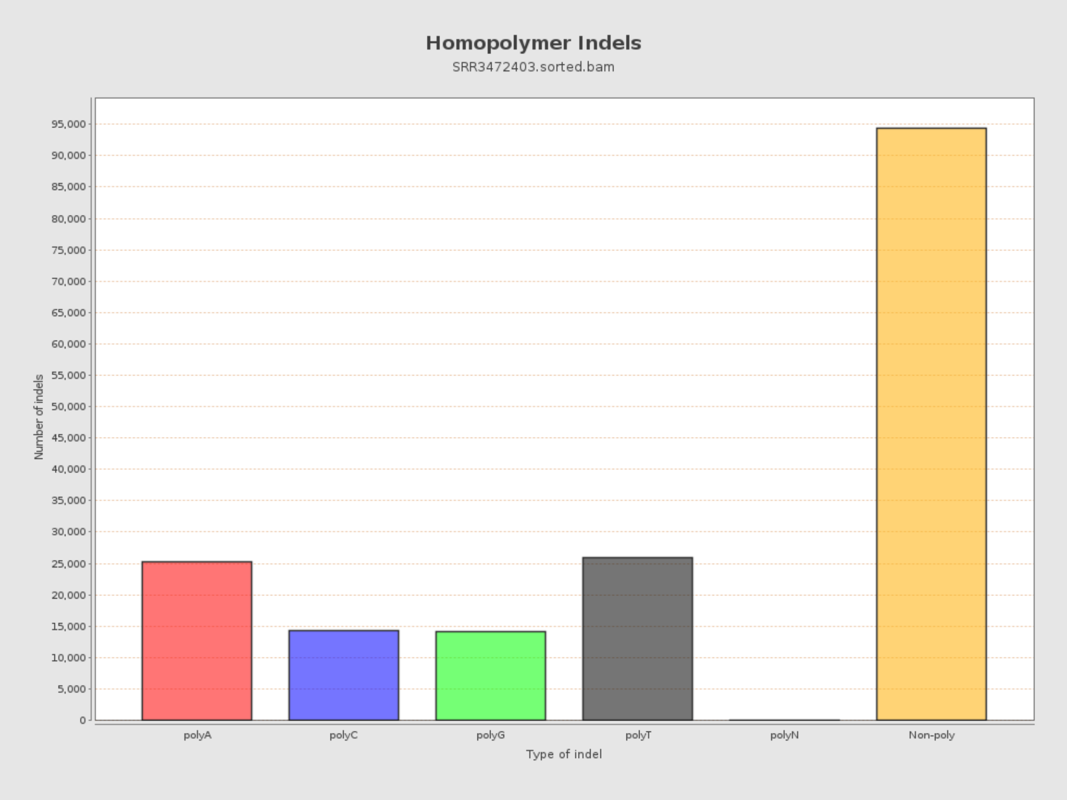
9. Results : Mapped Reads GC-content Distribution



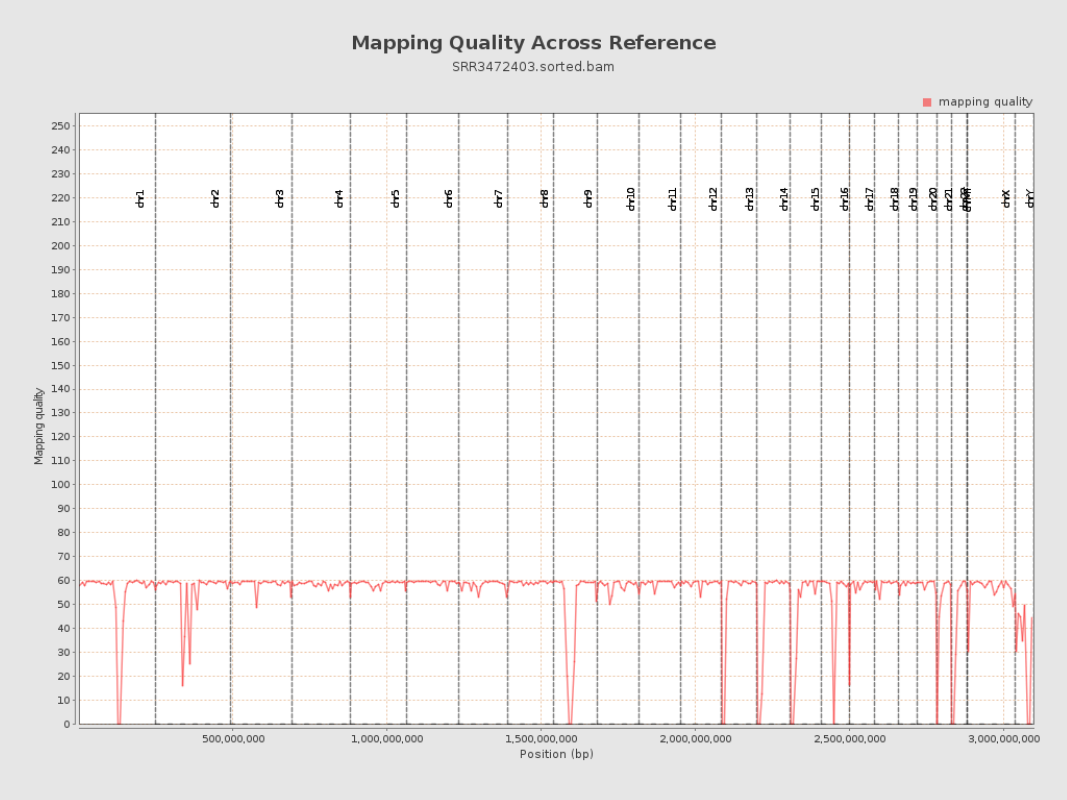
10. Results : Mapped Reads Clipping Profile



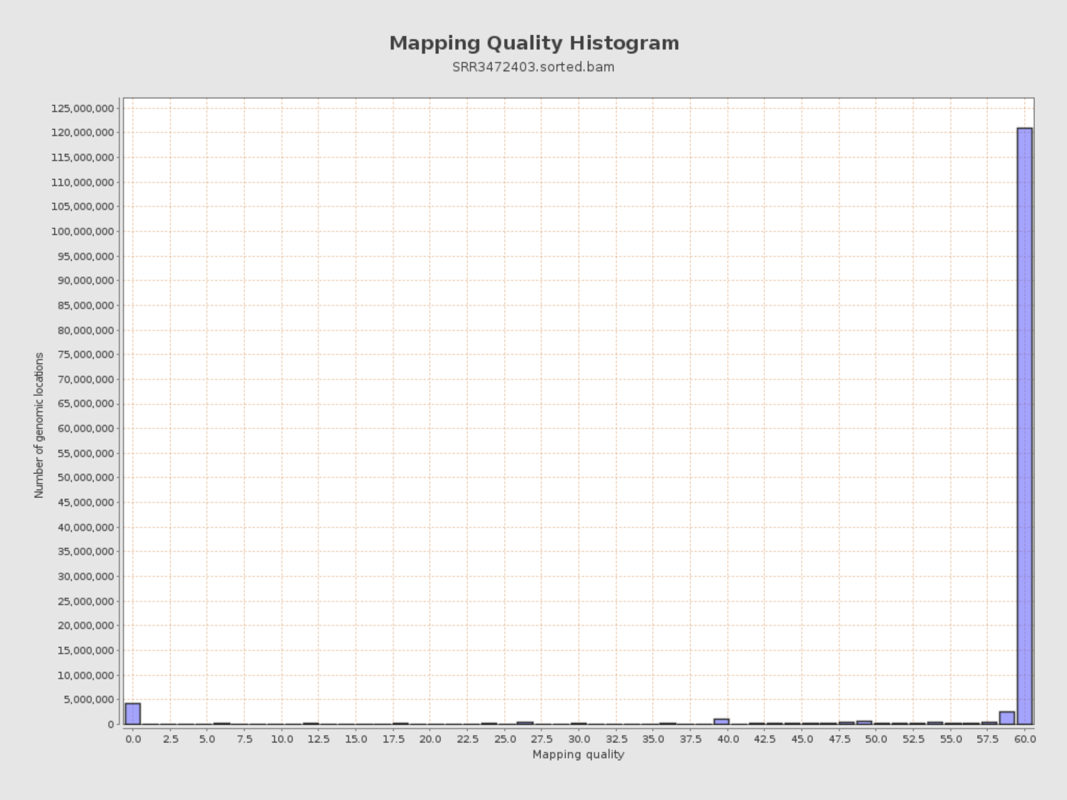
11. Results : Homopolymer Indels



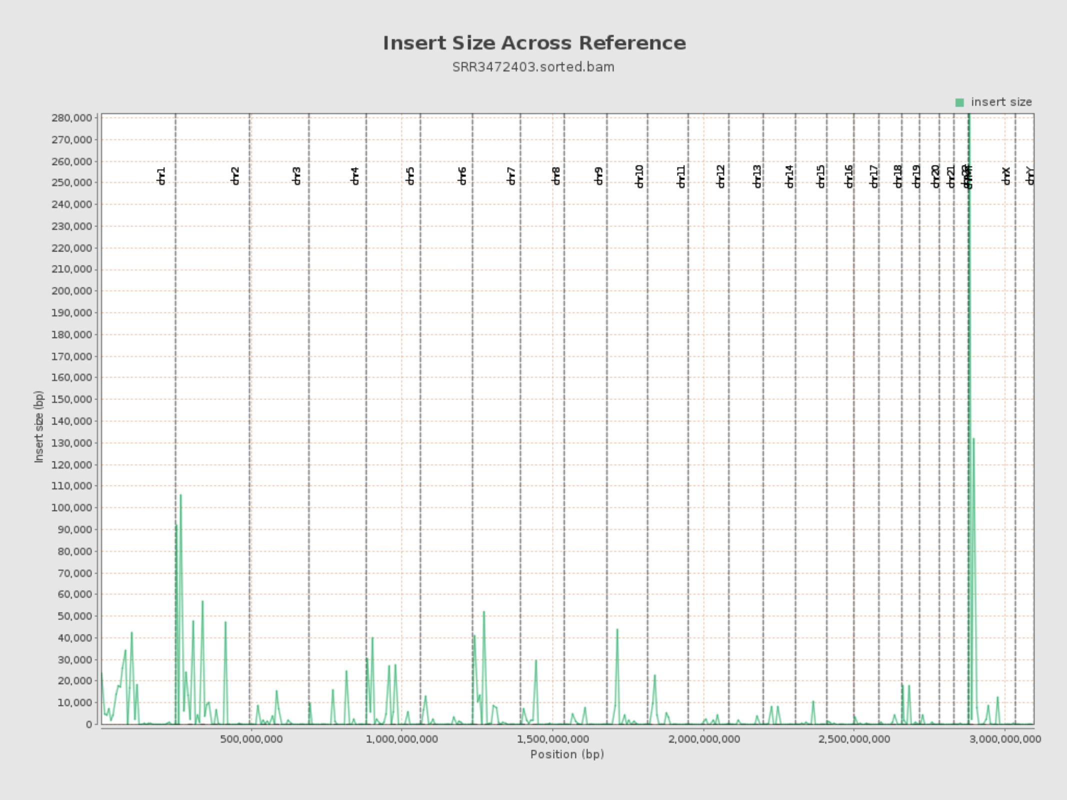
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram