Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:17:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472501.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_SRR3472501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472501_1.fastq.gz SRR3472501_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:17:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,758,460
Mapped reads	19,496,947 / 98.68%
Unmapped reads	261,513 / 1.32%
Mapped paired reads	19,496,947 / 98.68%
Mapped reads, first in pair	9,776,455 / 49.48%
Mapped reads, second in pair	9,720,492 / 49.2%
Mapped reads, both in pair	19,375,644 / 98.06%
Mapped reads, singletons	121,303 / 0.61%
Secondary alignments	0
Supplementary alignments	85,355 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	12,655,139 / 64.05%
Duplication rate	45.91%
Clipped reads	1,649,322 / 8.35%

2.2. ACGT Content

Number/percentage of A's	526,322,614 / 27.44%
Number/percentage of C's	435,407,414 / 22.7%
Number/percentage of T's	523,355,703 / 27.28%
Number/percentage of G's	432,856,433 / 22.57%
Number/percentage of N's	296,376 / 0.02%

GC Percentage	45.26%

2.3. Coverage

Mean	0.6197
Standard Deviation	22.6811

2.4. Mapping Quality

Mean Mapping Quality	54.94

2.5. Insert size

Mean	24,762.28
Standard Deviation	1,556,743.3
P25/Median/P75	167 / 232 / 313

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	11,644,792
Insertions	102,617
Mapped reads with at least one insertion	0.52%
Deletions	97,870
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.72%

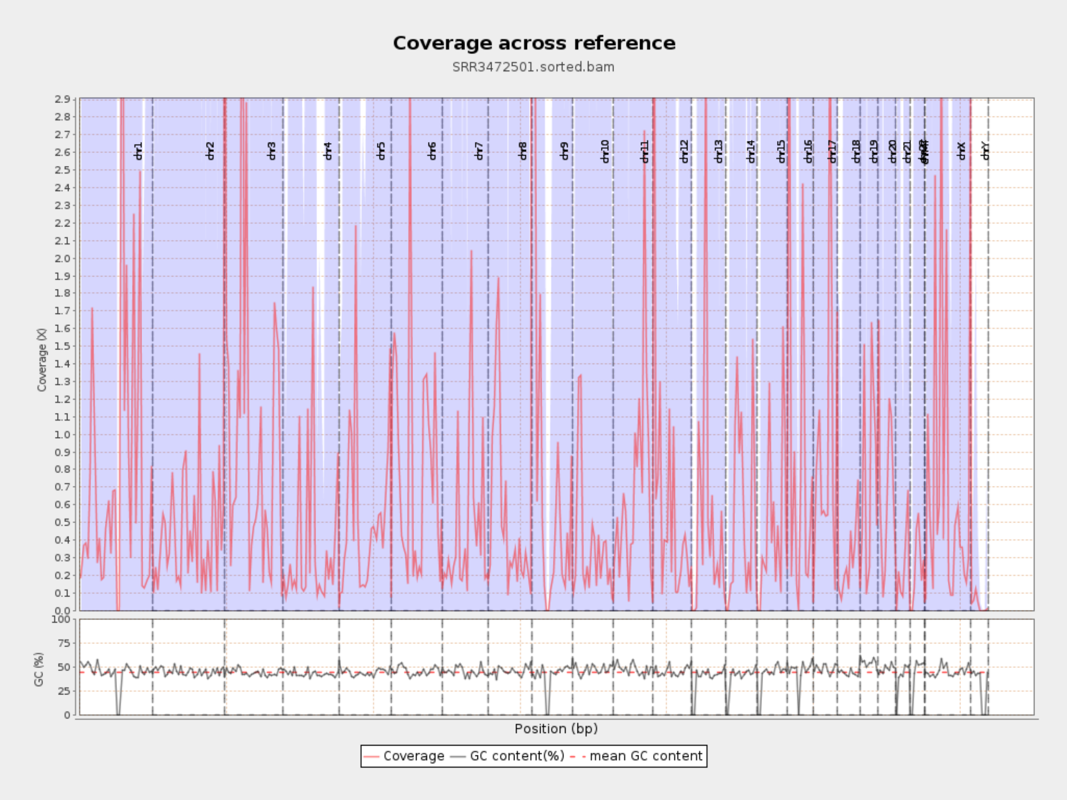
2.7. Chromosome stats

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

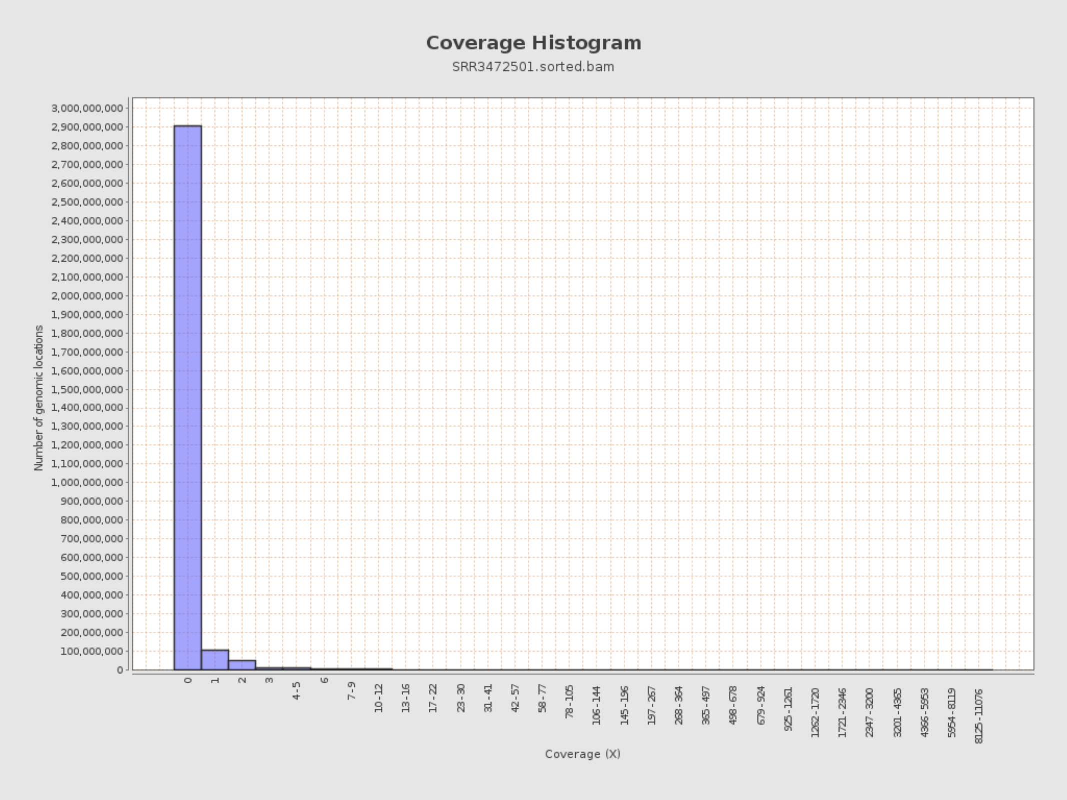
		bases	coverage	deviation
chr1	249250621	199161663	0.799	30.2648
chr2	243199373	103421420	0.4253	18.0797
chr3	198022430	214574999	1.0836	27.9136
chr4	191154276	66513896	0.348	15.9778
chr5	180915260	99162215	0.5481	15.9383
chr6	171115067	138797260	0.8111	28.0207
chr7	159138663	77989237	0.4901	15.5288
chr8	146364022	78254162	0.5347	20.282
chr9	141213431	115026806	0.8146	23.2595
chr10	135534747	50720488	0.3742	18.7634
chr11	135006516	96616409	0.7156	23.2347
chr12	133851895	95166686	0.711	21.2794
chr13	115169878	62391767	0.5417	26.9885
chr14	107349540	57730381	0.5378	18.4844
chr15	102531392	51065184	0.498	19.6609
chr16	90354753	77772914	0.8608	32.3719
chr17	81195210	74656797	0.9195	26.5279
chr18	78077248	21799861	0.2792	9.0484
chr19	59128983	48872905	0.8265	22.3481
chr20	63025520	45622085	0.7239	23.1401
chr21	48129895	11822361	0.2456	9.6245
chr22	51304566	12574514	0.2451	7.0203
chrMT	16571	3576	0.2158	0.7297
chrX	155270560	116659734	0.7513	31.7221

chrY	59373566	2092691	0.0352	0.8056

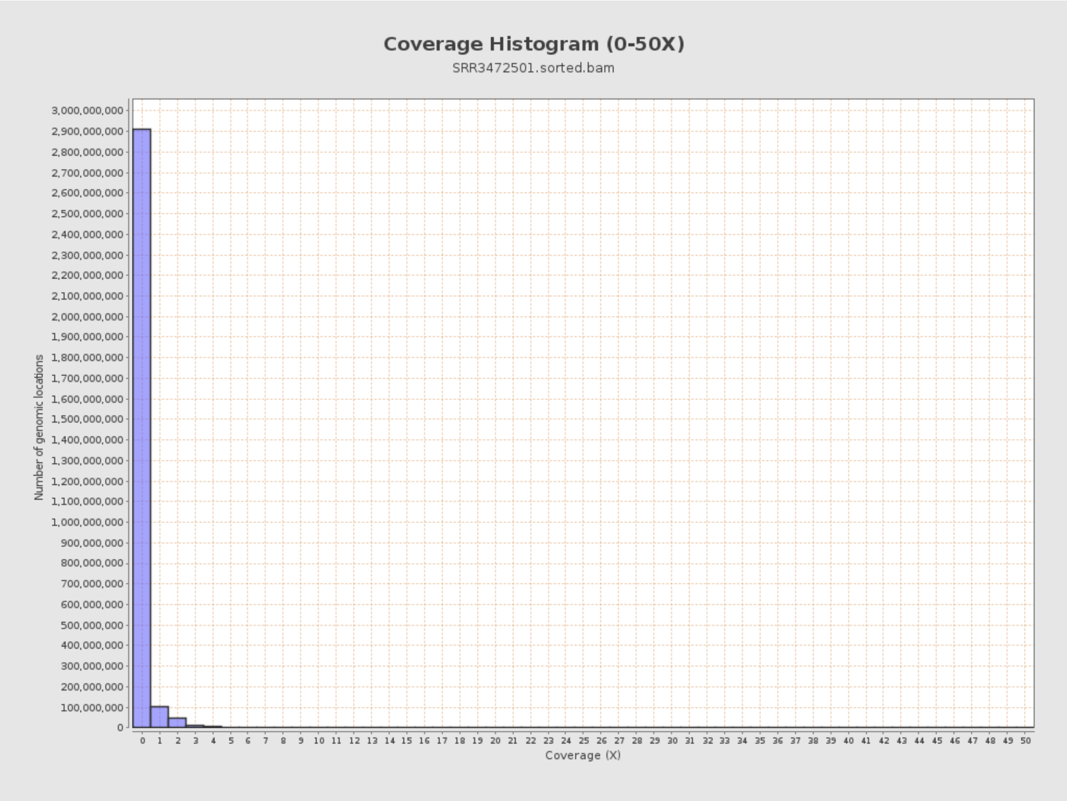
3. Results : Coverage across reference



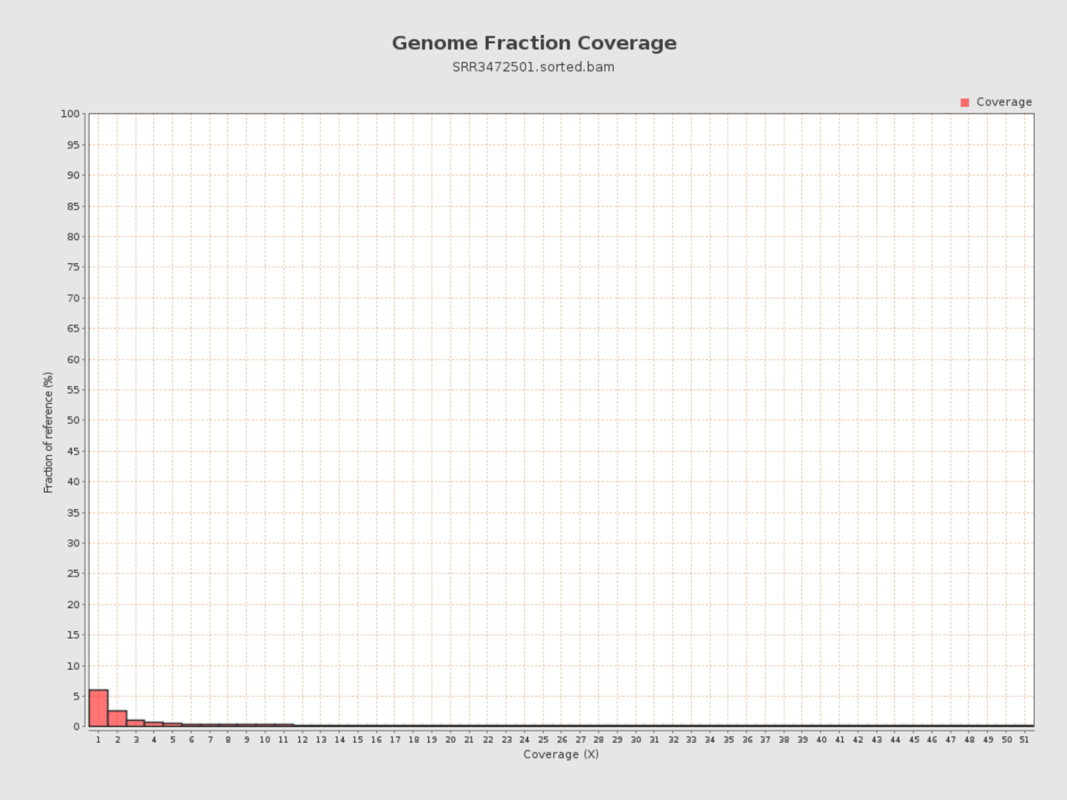
4. Results : Coverage Histogram



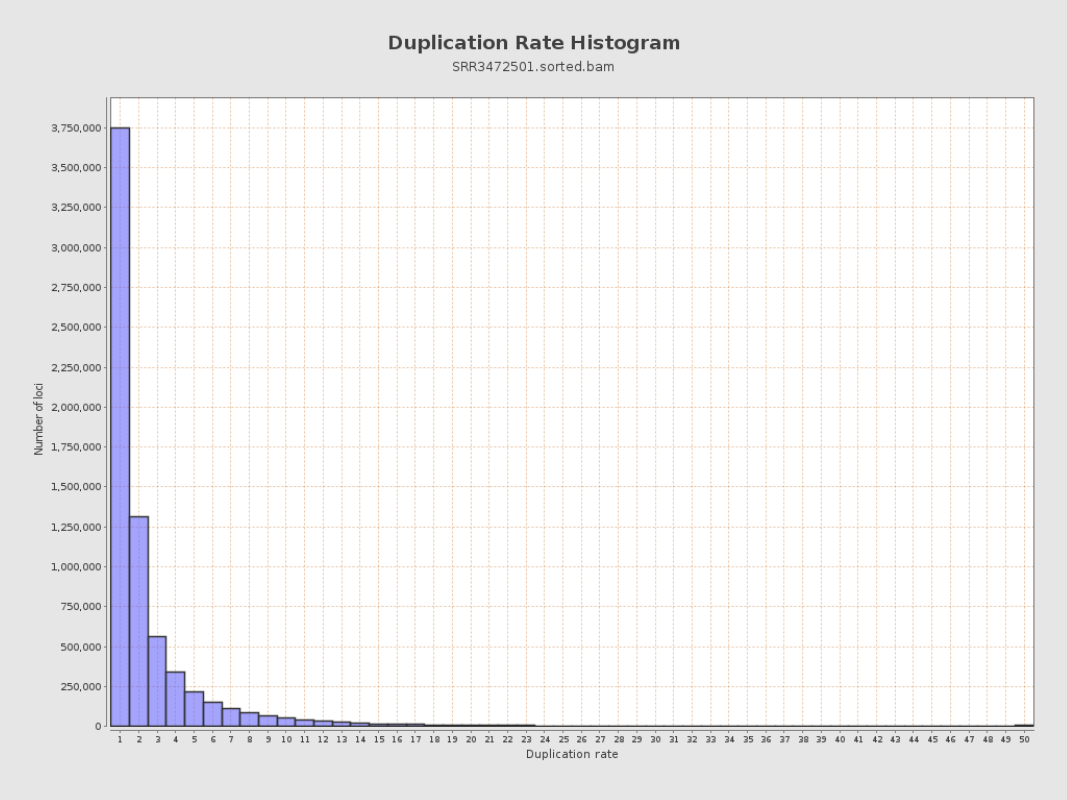
5. Results : Coverage Histogram (0-50X)



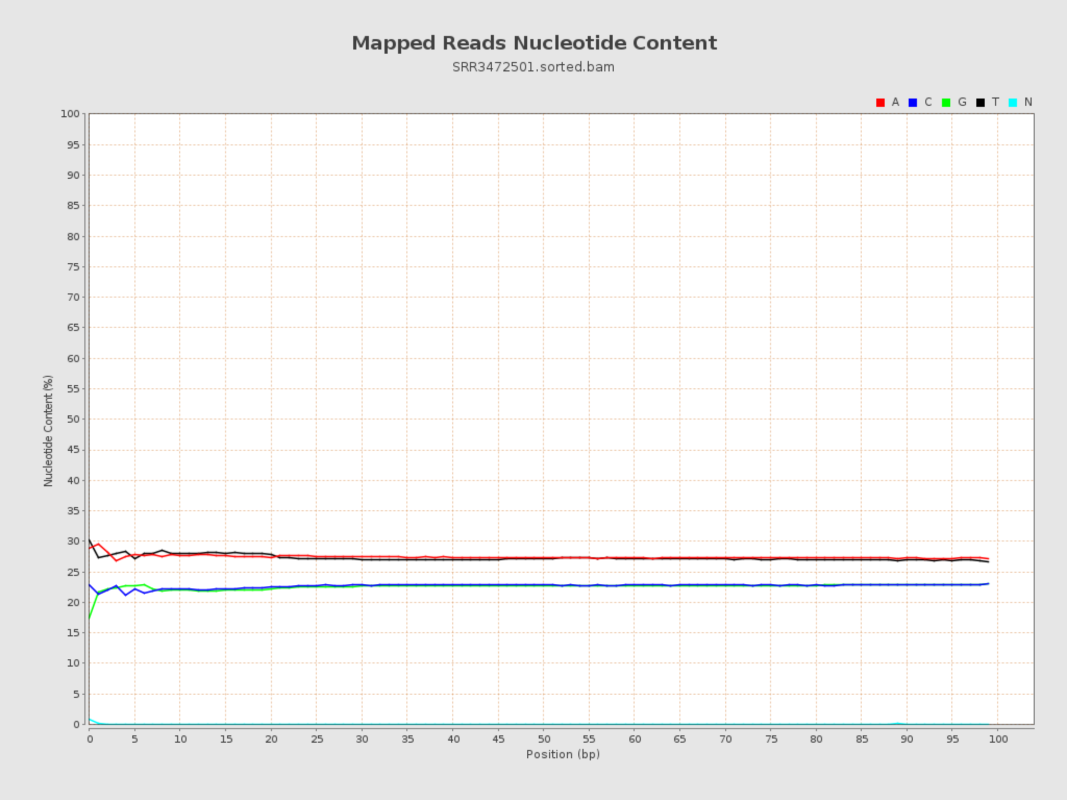
6. Results : Genome Fraction Coverage



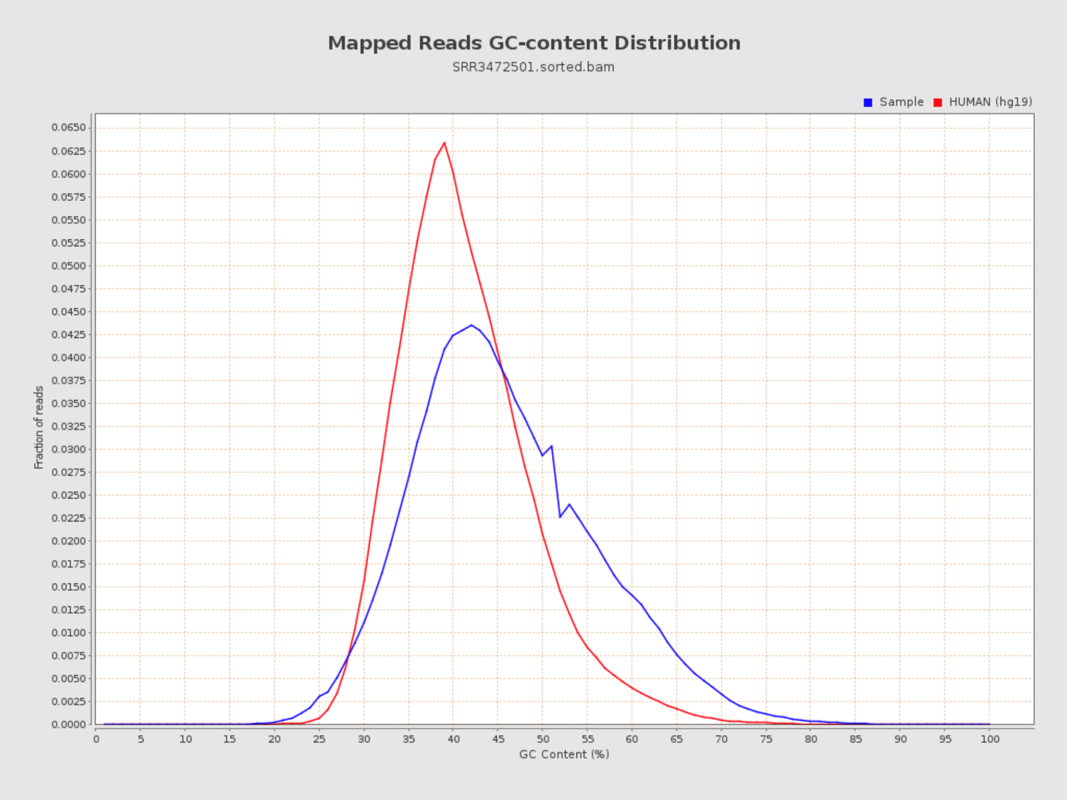
7. Results : Duplication Rate Histogram



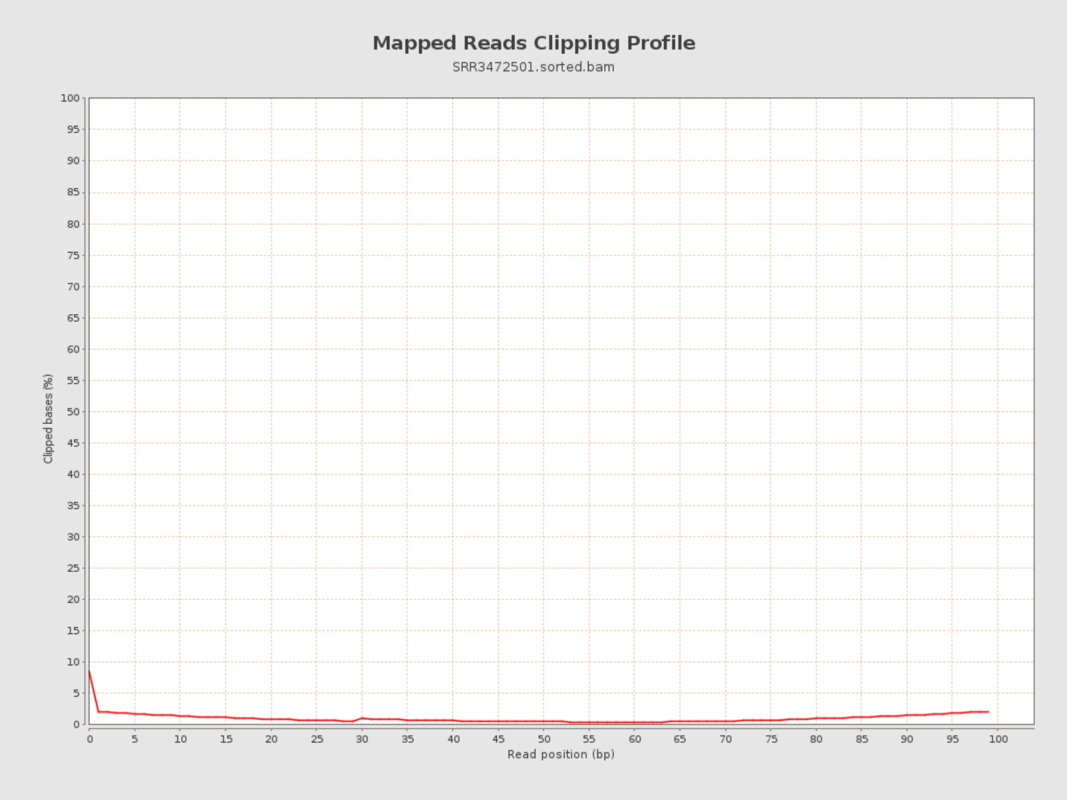
8. Results : Mapped Reads Nucleotide Content



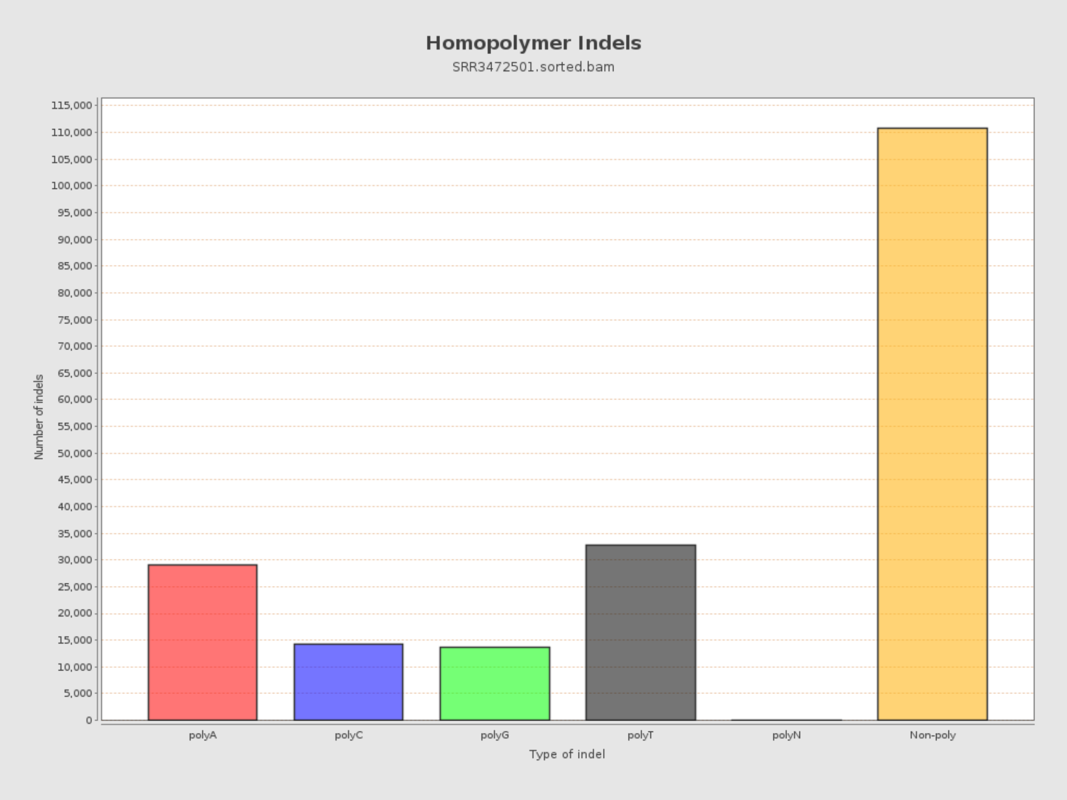
9. Results : Mapped Reads GC-content Distribution



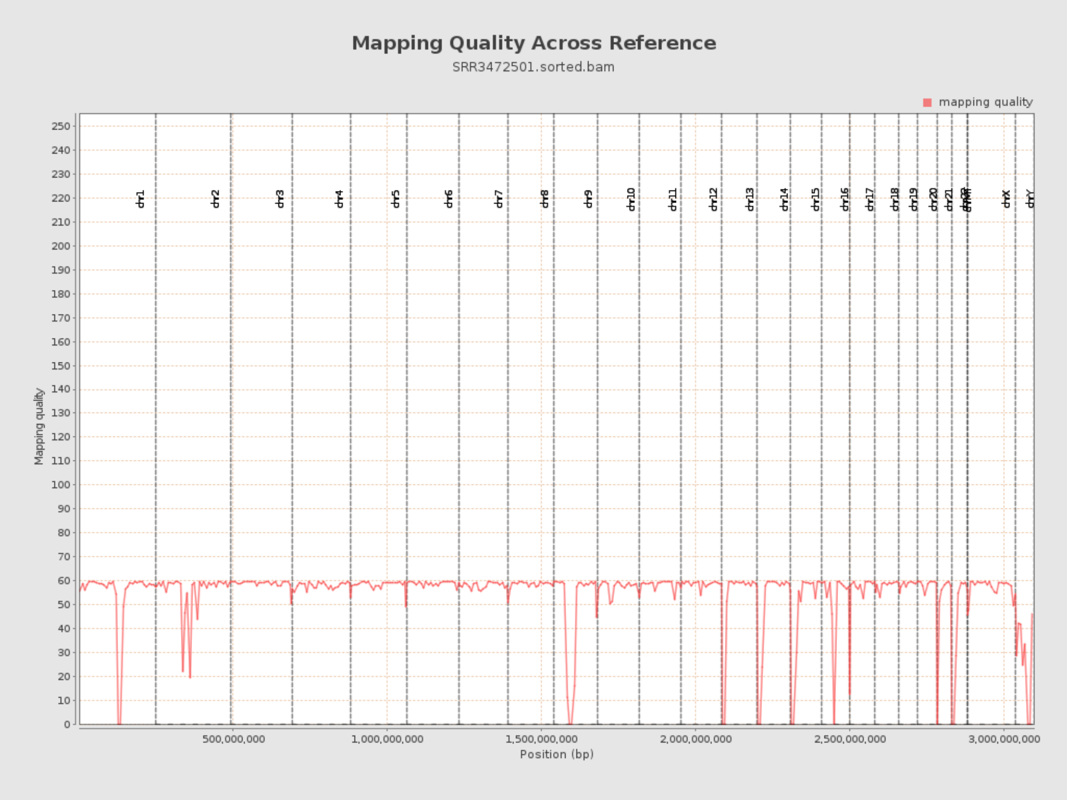
10. Results : Mapped Reads Clipping Profile



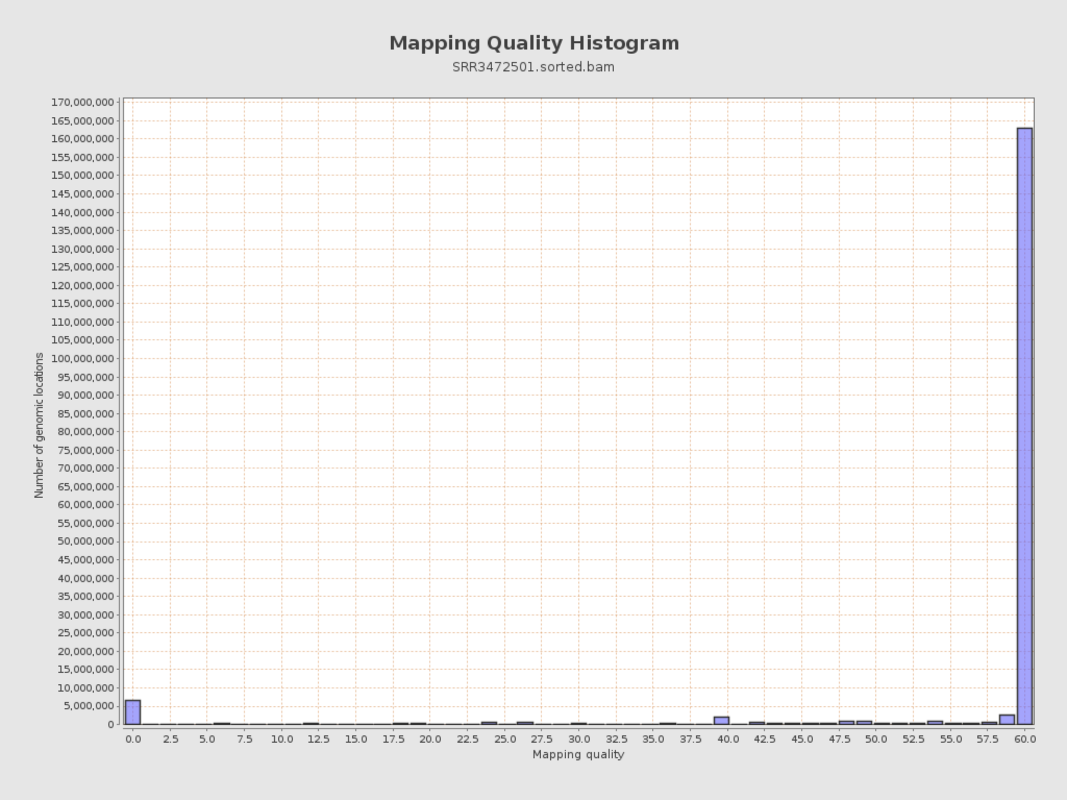
11. Results : Homopolymer Indels



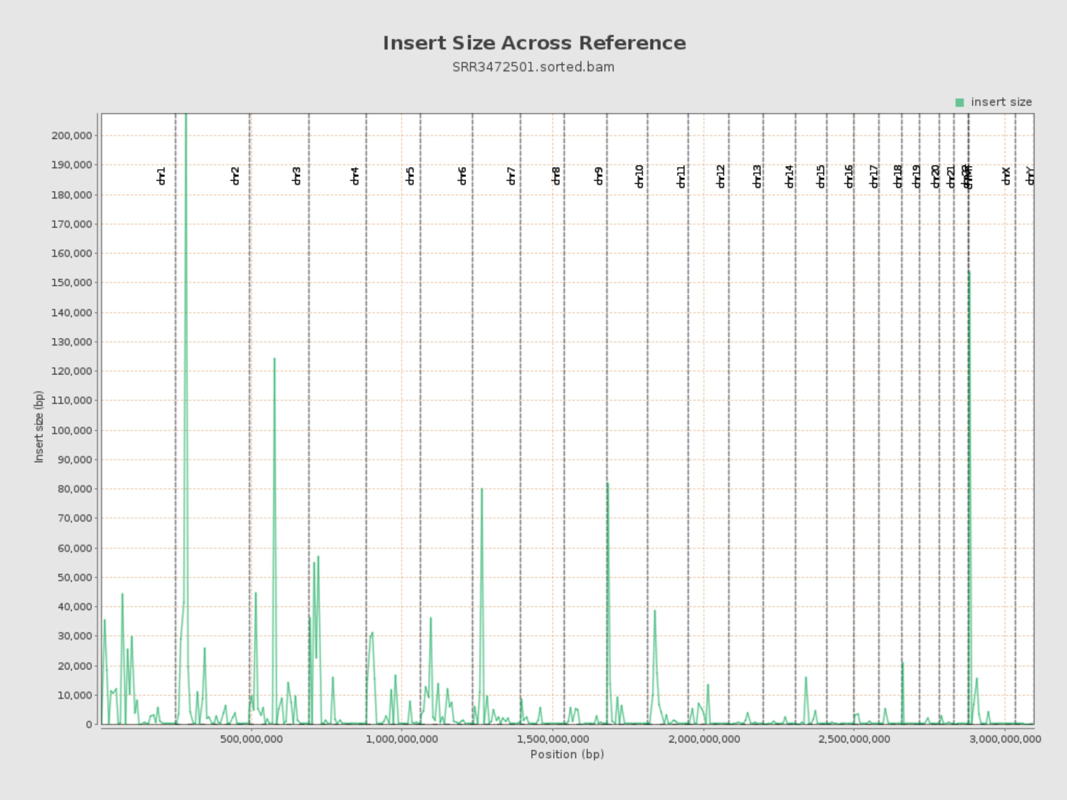
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram