Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 16:57:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472713.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_SRR3472713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472713_1.fastq.gz SRR3472713_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 16:57:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,551,680
Mapped reads	17,395,378 / 99.11%
Unmapped reads	156,302 / 0.89%
Mapped paired reads	17,395,378 / 99.11%
Mapped reads, first in pair	8,730,158 / 49.74%
Mapped reads, second in pair	8,665,220 / 49.37%
Mapped reads, both in pair	17,295,660 / 98.54%
Mapped reads, singletons	99,718 / 0.57%
Secondary alignments	0
Supplementary alignments	61,993 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,011,414 / 62.74%
Duplication rate	46.13%
Clipped reads	1,544,869 / 8.8%

2.2. ACGT Content

Number/percentage of A's	465,311,429 / 27.21%
Number/percentage of C's	392,578,377 / 22.95%
Number/percentage of T's	461,716,624 / 27%
Number/percentage of G's	390,349,846 / 22.82%
Number/percentage of N's	331,742 / 0.02%

GC Percentage	45.78%

2.3. Coverage

Mean	0.5526
Standard Deviation	19.3389

2.4. Mapping Quality

Mean Mapping Quality	55.16

2.5. Insert size

Mean	23,258.73
Standard Deviation	1,541,578.91
P25/Median/P75	161 / 225 / 305

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,006,711
Insertions	102,686
Mapped reads with at least one insertion	0.58%
Deletions	93,245
Mapped reads with at least one deletion	0.53%
Homopolymer indels	42.73%

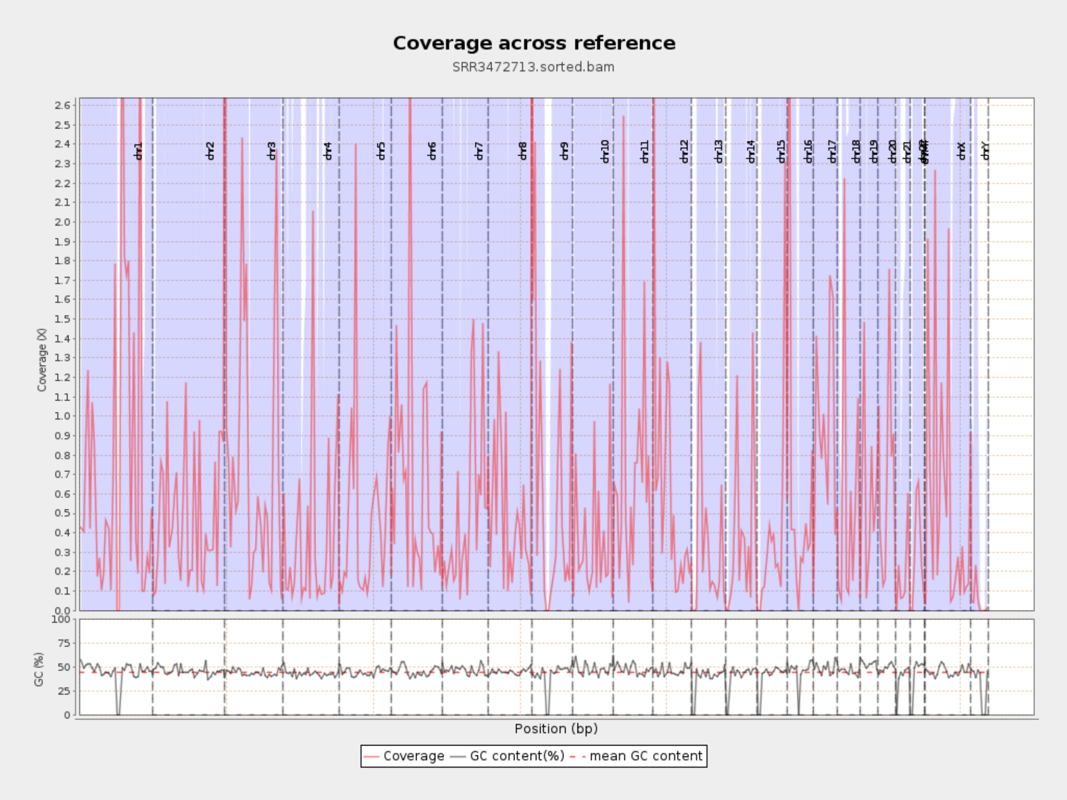
2.7. Chromosome stats

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

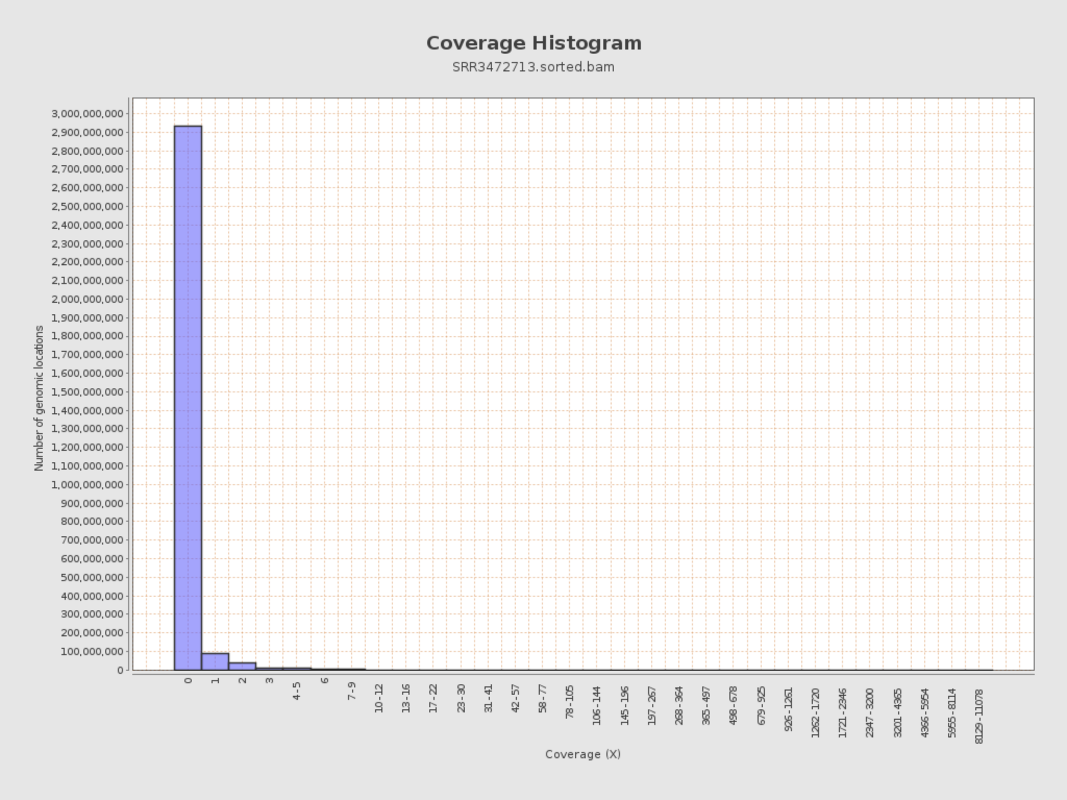
		bases	coverage	deviation
chr1	249250621	196740200	0.7893	27.5639
chr2	243199373	113791546	0.4679	15.0098
chr3	198022430	159169102	0.8038	19.1488
chr4	191154276	69075372	0.3614	13.4134
chr5	180915260	87773183	0.4852	14.9793
chr6	171115067	113460119	0.6631	16.9085
chr7	159138663	79488314	0.4995	17.8814
chr8	146364022	68834127	0.4703	16.8776
chr9	141213431	94417643	0.6686	16.3896
chr10	135534747	49550138	0.3656	18.068
chr11	135006516	94323965	0.6987	26.3998
chr12	133851895	84783551	0.6334	19.6659
chr13	115169878	39066549	0.3392	13.8998
chr14	107349540	40617946	0.3784	20.0052
chr15	102531392	45889484	0.4476	17.979
chr16	90354753	58874661	0.6516	18.4019
chr17	81195210	75618718	0.9313	25.2927
chr18	78077248	41177047	0.5274	26.8449
chr19	59128983	35814048	0.6057	16.0365
chr20	63025520	44605311	0.7077	22.8541
chr21	48129895	9306978	0.1934	9.6015
chr22	51304566	14476136	0.2822	8.292
chrMT	16571	1245	0.0751	0.3134
chrX	155270560	90665867	0.5839	25.7322

chrY	59373566	3035145	0.0511	2.2829

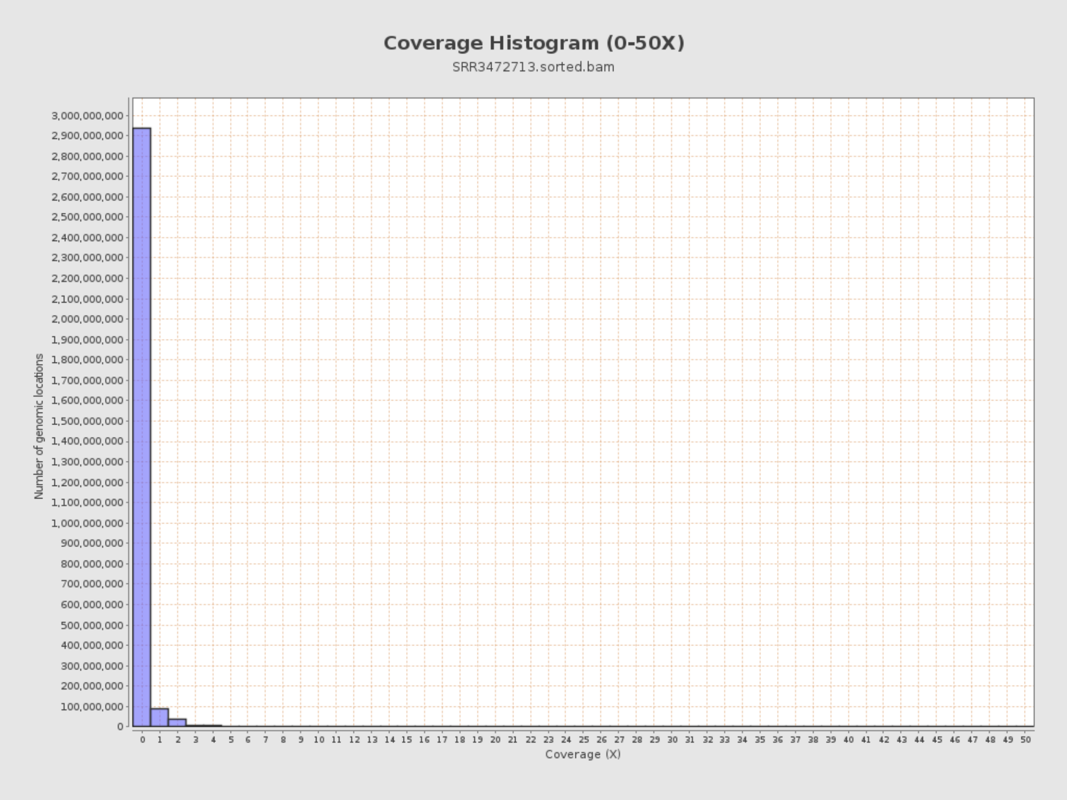
3. Results : Coverage across reference



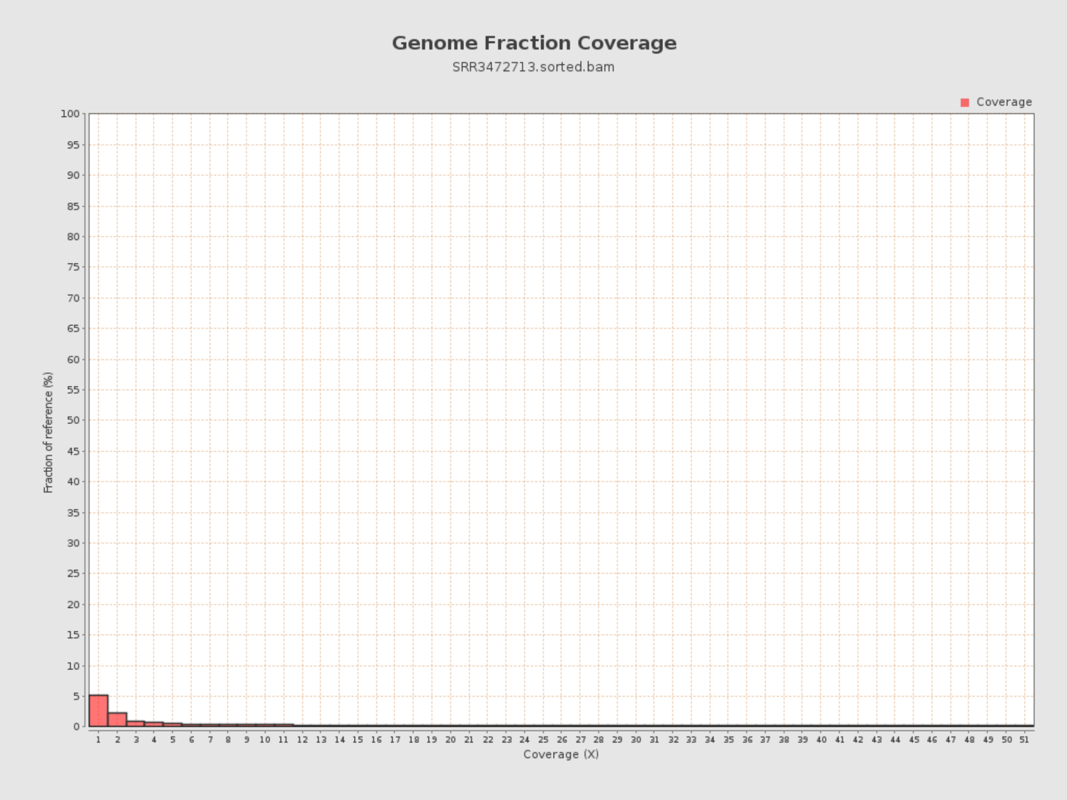
4. Results : Coverage Histogram



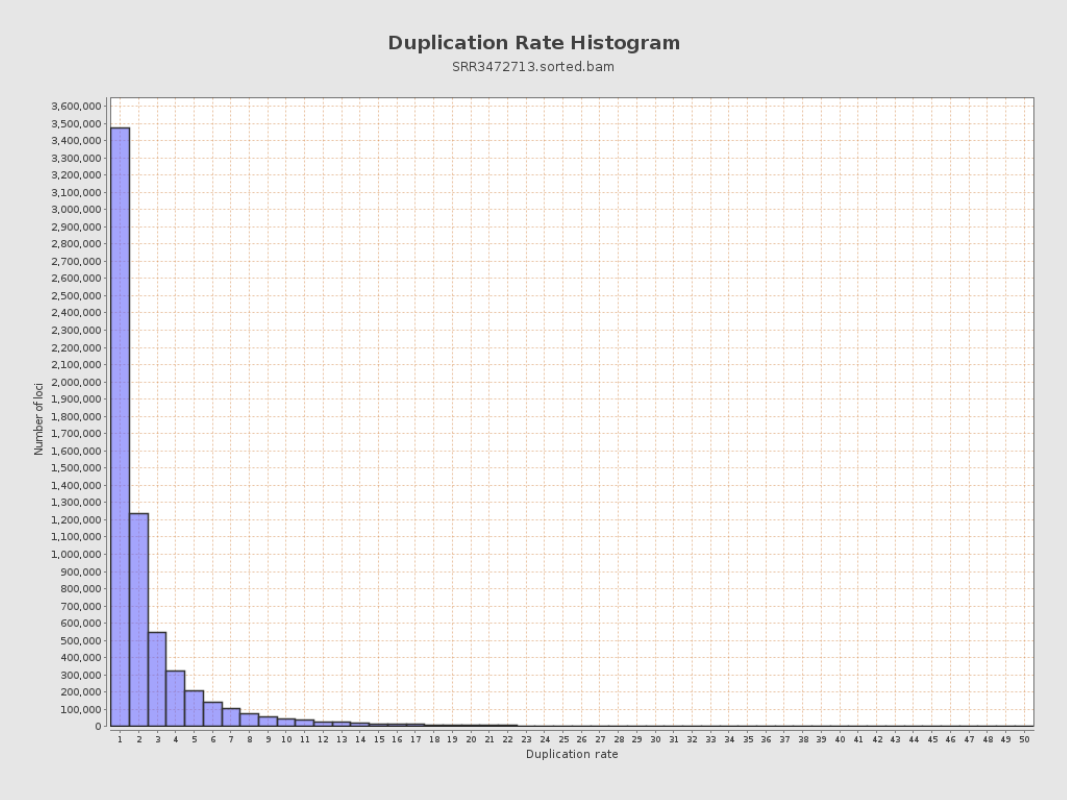
5. Results : Coverage Histogram (0-50X)



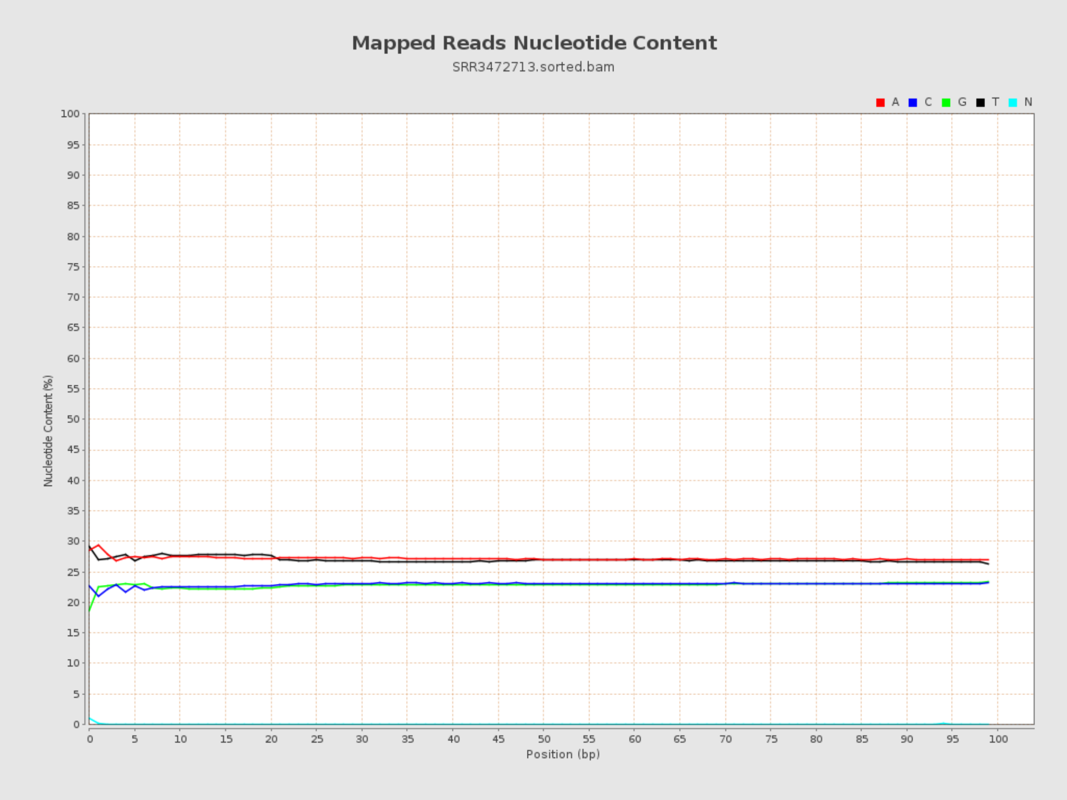
6. Results : Genome Fraction Coverage



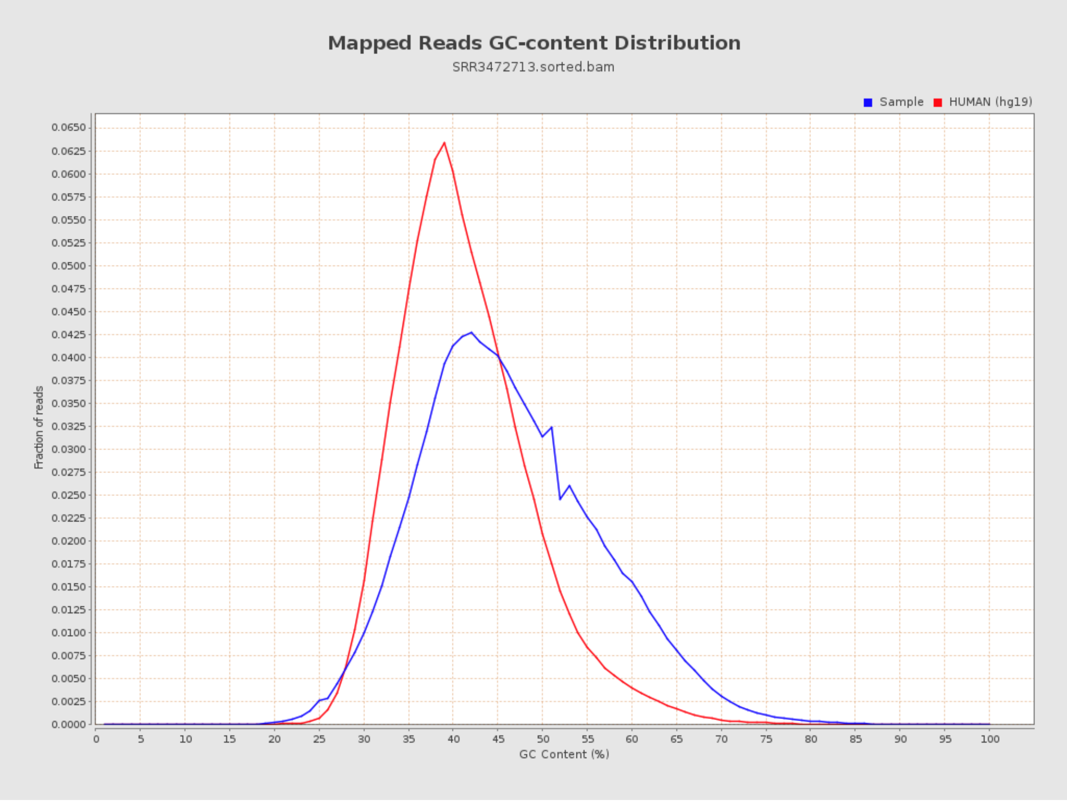
7. Results : Duplication Rate Histogram



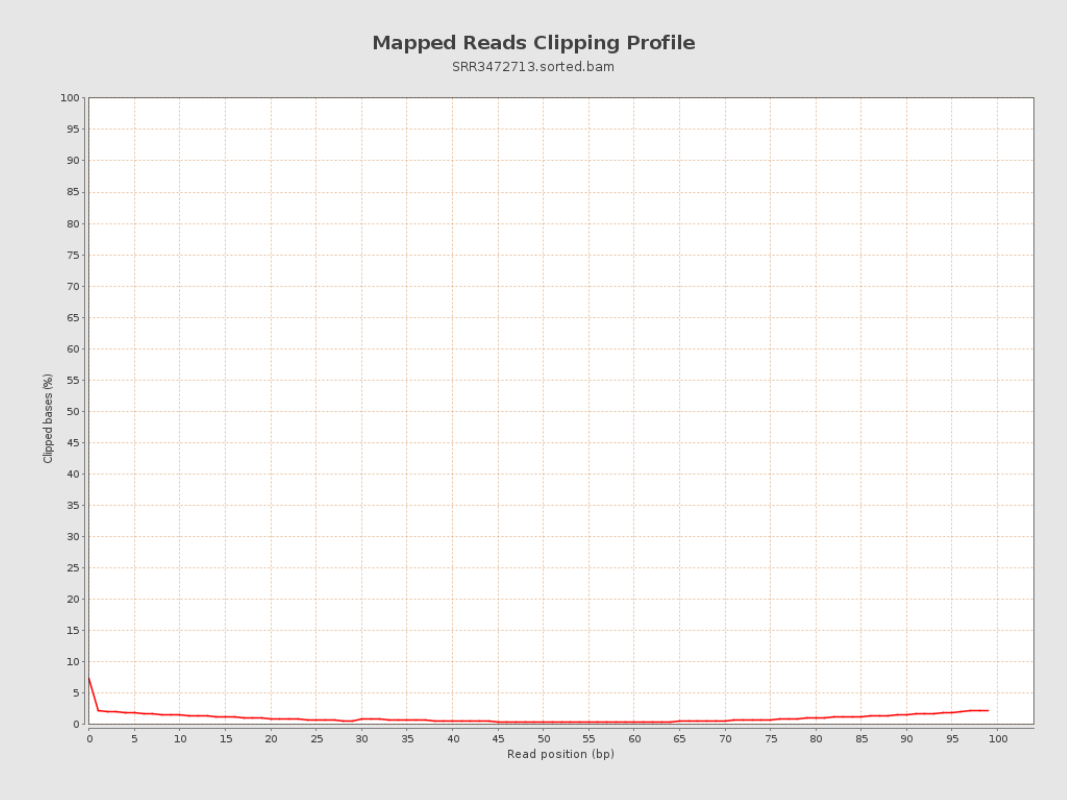
8. Results : Mapped Reads Nucleotide Content



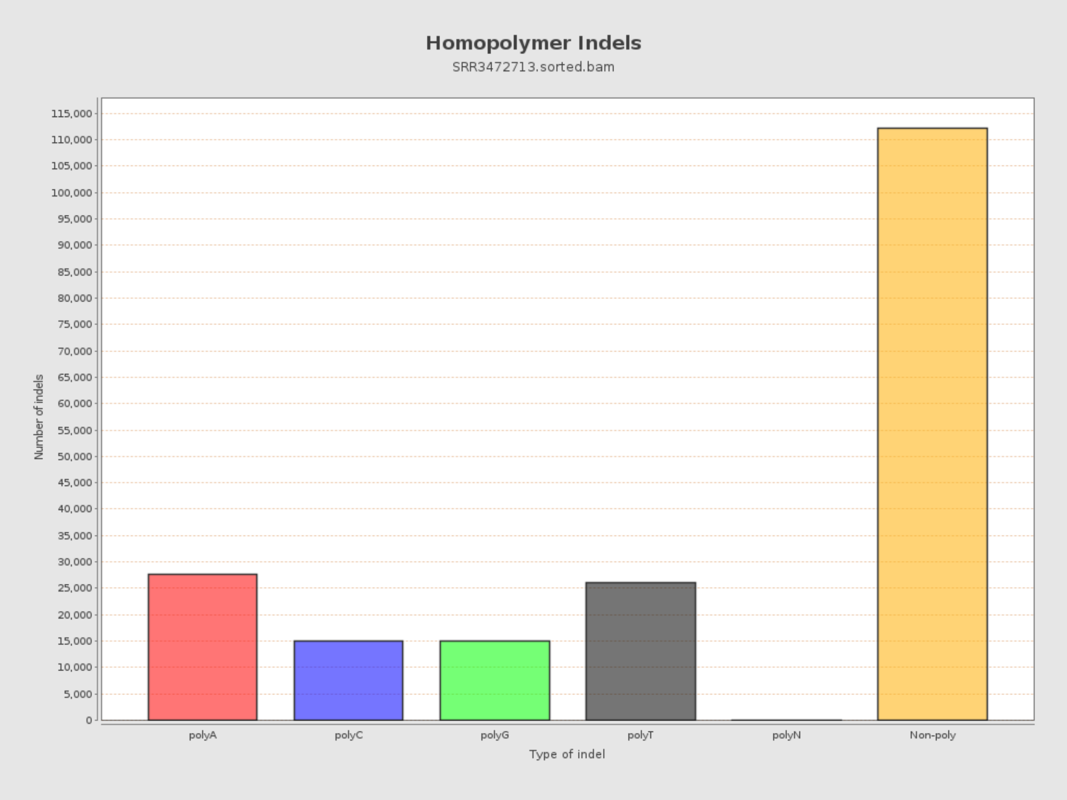
9. Results : Mapped Reads GC-content Distribution



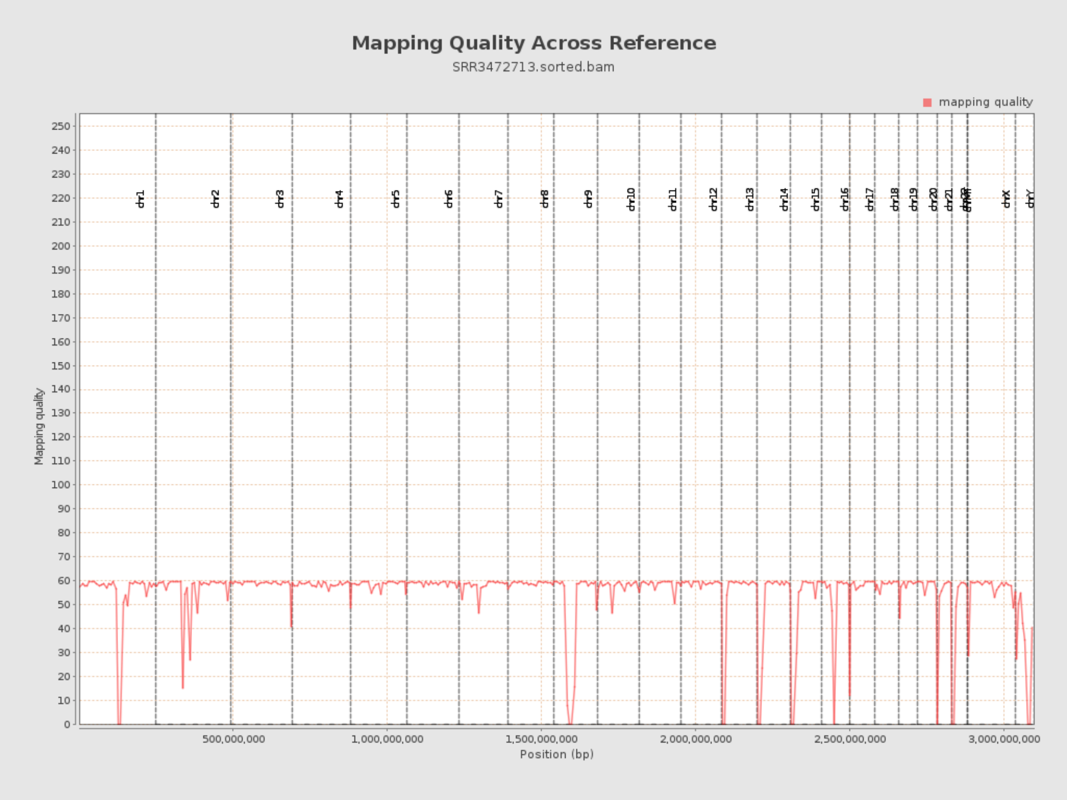
10. Results : Mapped Reads Clipping Profile



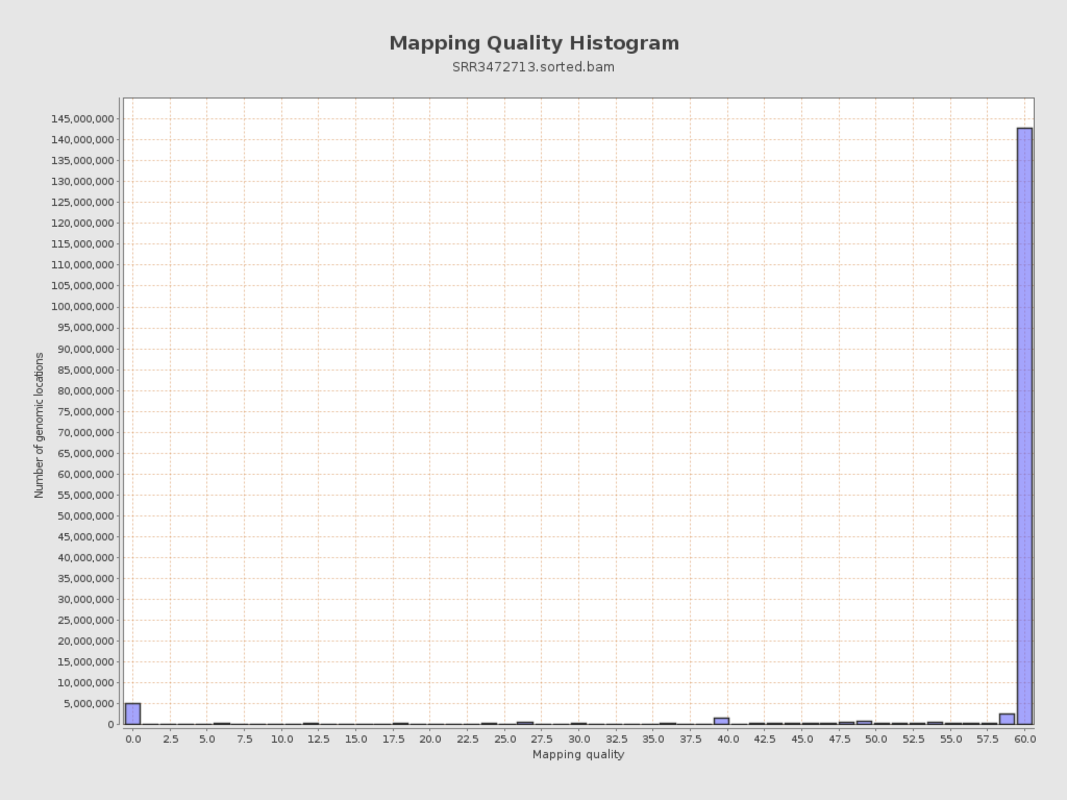
11. Results : Homopolymer Indels



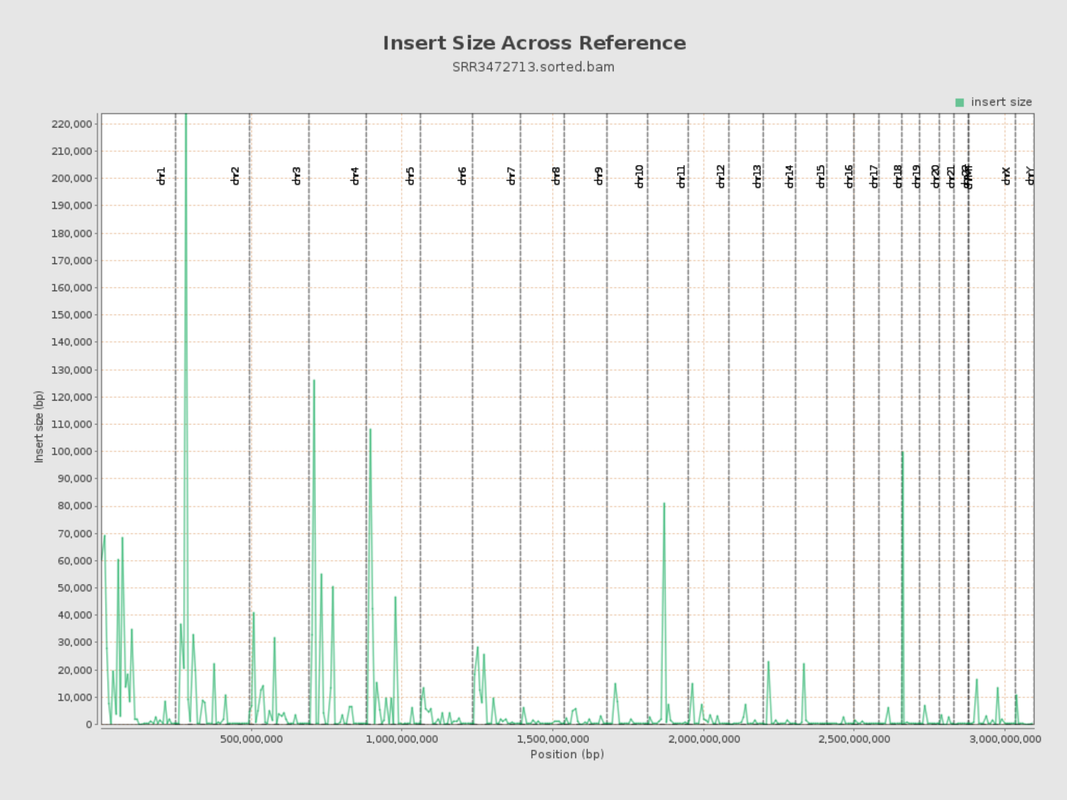
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram