Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:35:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472559.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_SRR3472559 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472559_1.fastq.gz SRR3472559_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:35:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472559.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,862,610
Mapped reads	12,592,838 / 97.9%
Unmapped reads	269,772 / 2.1%
Mapped paired reads	12,592,838 / 97.9%
Mapped reads, first in pair	6,322,322 / 49.15%
Mapped reads, second in pair	6,270,516 / 48.75%
Mapped reads, both in pair	12,474,656 / 96.98%
Mapped reads, singletons	118,182 / 0.92%
Secondary alignments	0
Supplementary alignments	59,741 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	7,695,276 / 59.83%
Duplication rate	46.72%
Clipped reads	1,249,726 / 9.72%

2.2. ACGT Content

Number/percentage of A's	335,360,886 / 27.2%
Number/percentage of C's	283,364,293 / 22.98%
Number/percentage of T's	332,013,574 / 26.93%
Number/percentage of G's	282,078,905 / 22.88%
Number/percentage of N's	189,411 / 0.02%

GC Percentage	45.86%

2.3. Coverage

Mean	0.3983
Standard Deviation	14.2124

2.4. Mapping Quality

Mean Mapping Quality	54.91

2.5. Insert size

Mean	32,235
Standard Deviation	1,775,532.64
P25/Median/P75	169 / 242 / 332

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	7,991,734
Insertions	75,290
Mapped reads with at least one insertion	0.59%
Deletions	61,428
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.84%

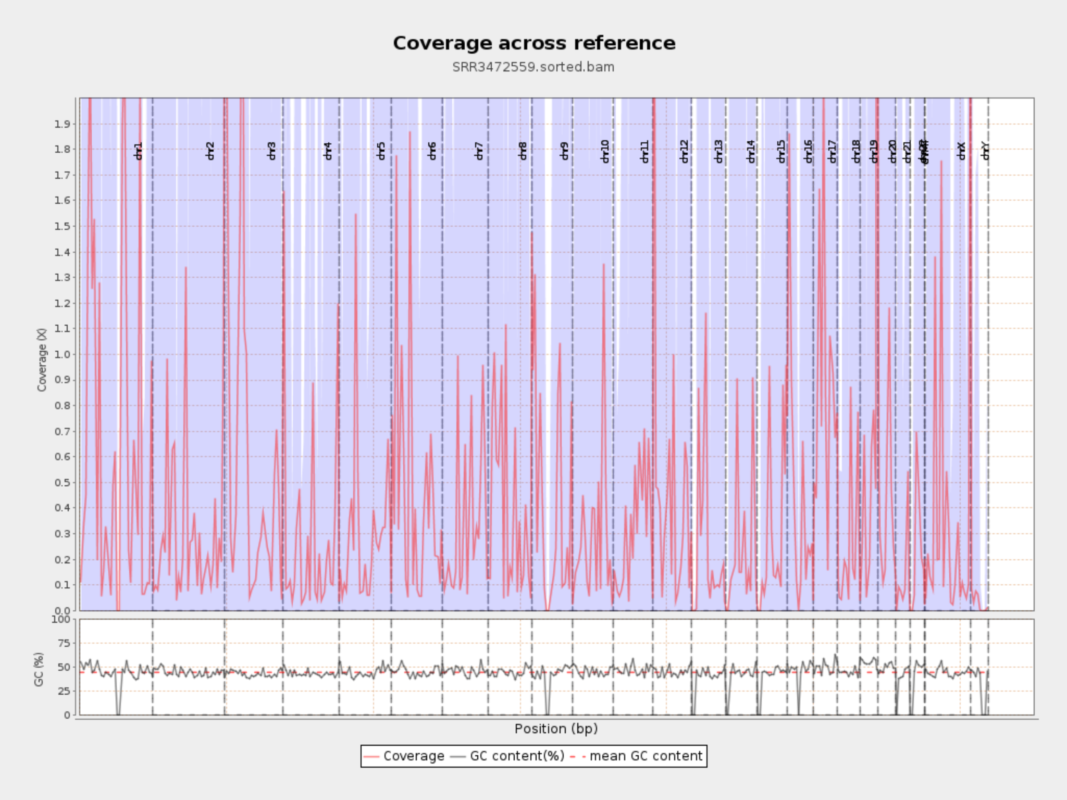
2.7. Chromosome stats

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

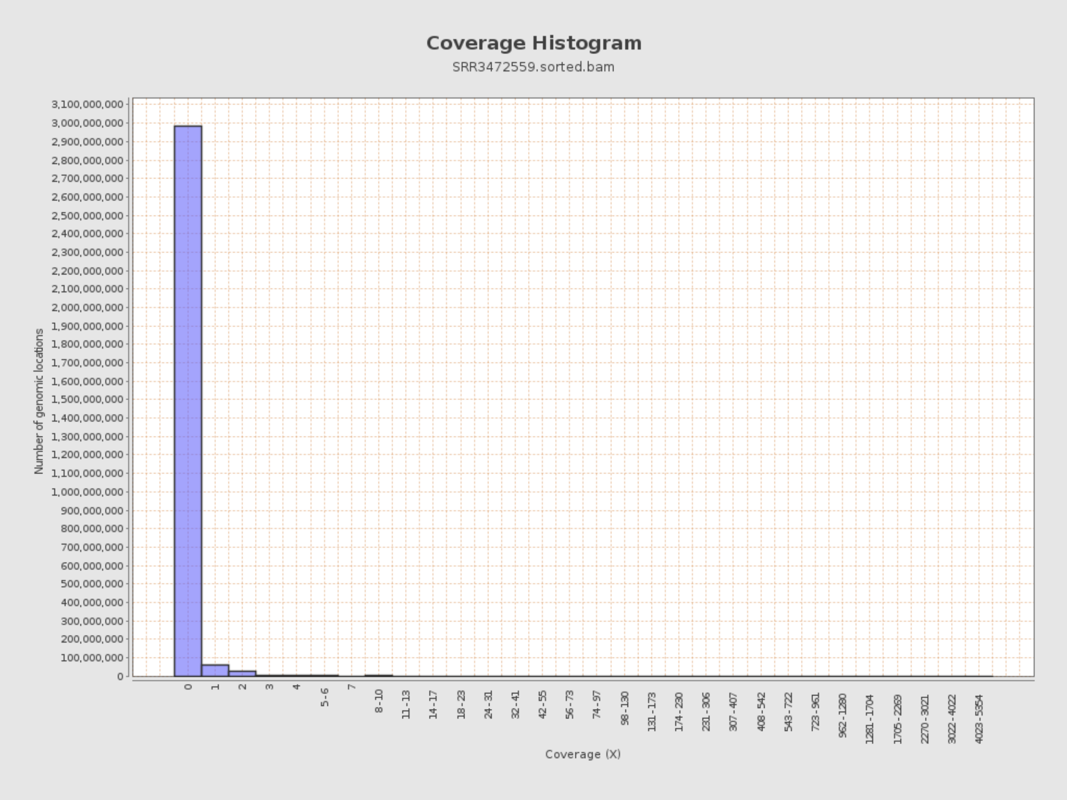
		bases	coverage	deviation
chr1	249250621	165388795	0.6635	23.5739
chr2	243199373	70445124	0.2897	9.4345
chr3	198022430	130968606	0.6614	16.4028
chr4	191154276	50068827	0.2619	10.2548
chr5	180915260	54360698	0.3005	9.1898
chr6	171115067	81240678	0.4748	15.4147
chr7	159138663	54817512	0.3445	10.953
chr8	146364022	58259122	0.398	13.9768
chr9	141213431	59580606	0.4219	10.2651
chr10	135534747	40135632	0.2961	12.0318
chr11	135006516	43286238	0.3206	9.9915
chr12	133851895	70279201	0.5251	20.3762
chr13	115169878	28644879	0.2487	11.7185
chr14	107349540	26084931	0.243	8.164
chr15	102531392	30015815	0.2927	9.8545
chr16	90354753	41647515	0.4609	13.5794
chr17	81195210	73007366	0.8992	25.3049
chr18	78077248	20673525	0.2648	10.0479
chr19	59128983	32560689	0.5507	20.0684
chr20	63025520	27823376	0.4415	12.3192
chr21	48129895	6819739	0.1417	6.0887
chr22	51304566	12690699	0.2474	13.9889
chrMT	16571	3319	0.2003	0.5802
chrX	155270560	52477311	0.338	13.8315

chrY	59373566	1875605	0.0316	1.4563

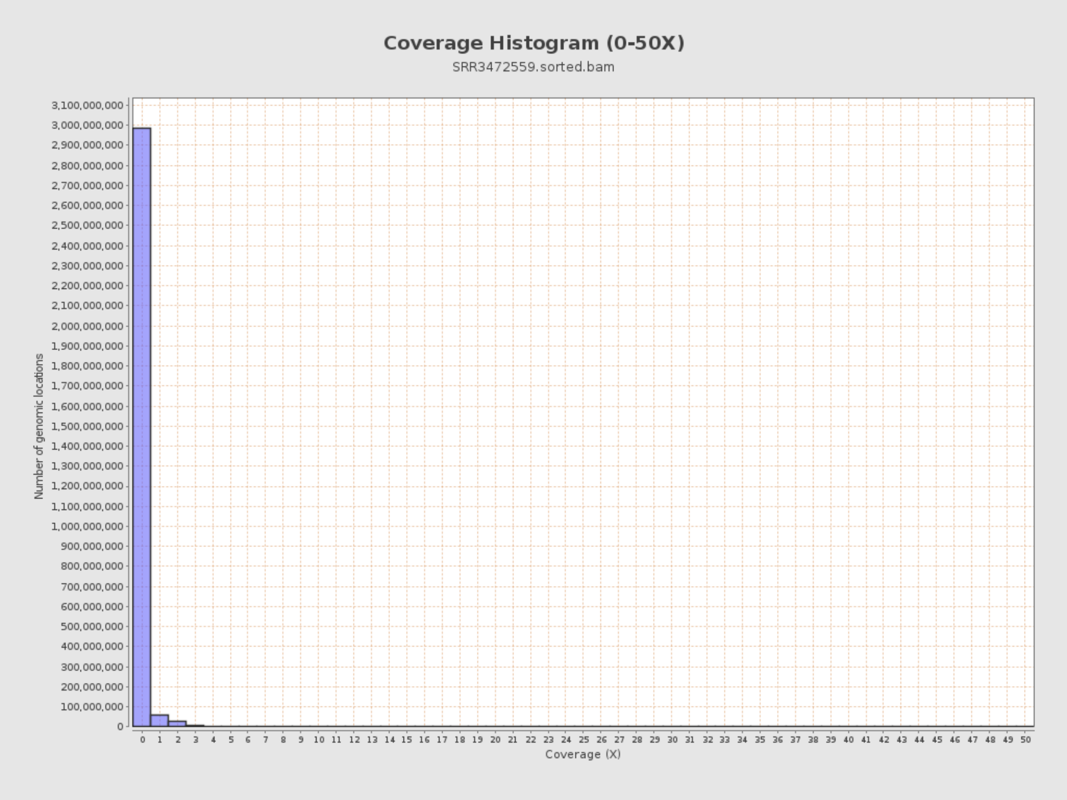
3. Results : Coverage across reference



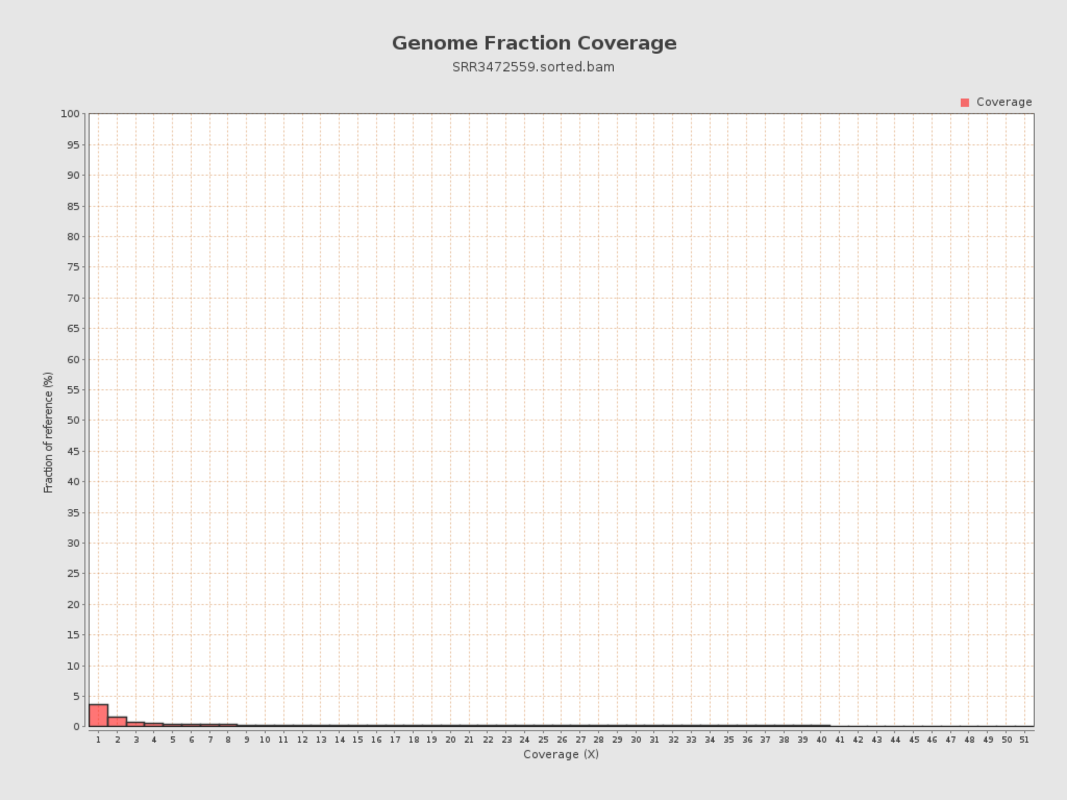
4. Results : Coverage Histogram



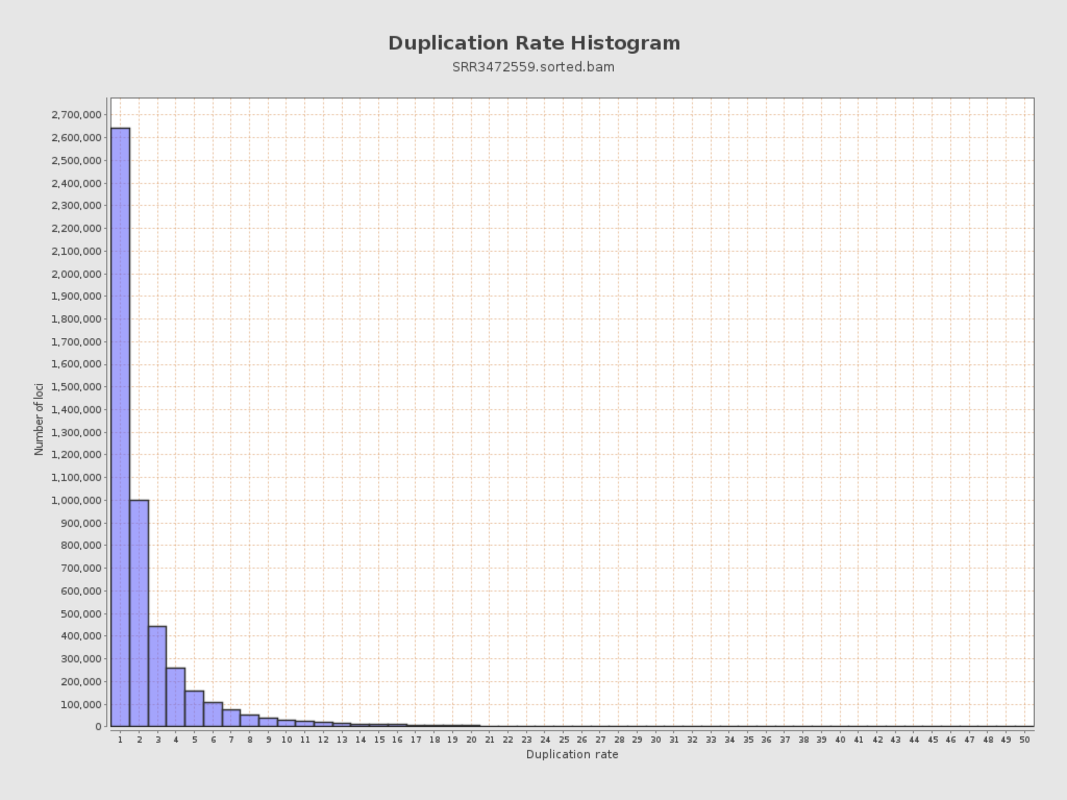
5. Results : Coverage Histogram (0-50X)



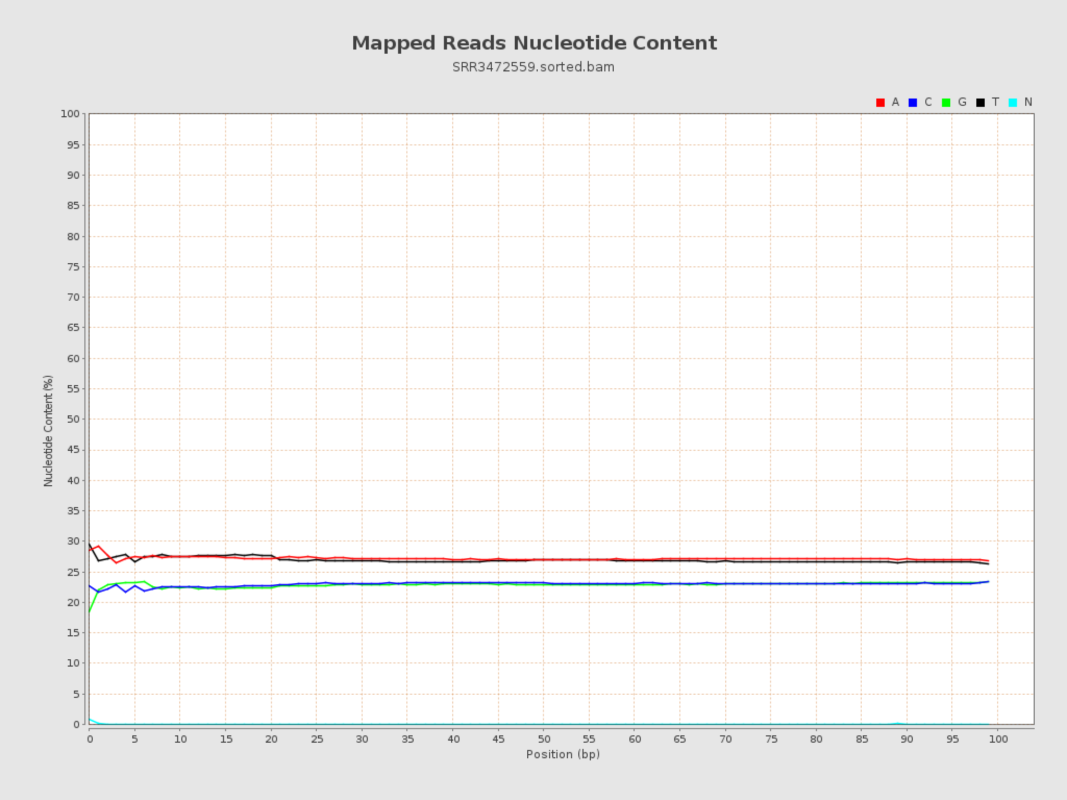
6. Results : Genome Fraction Coverage



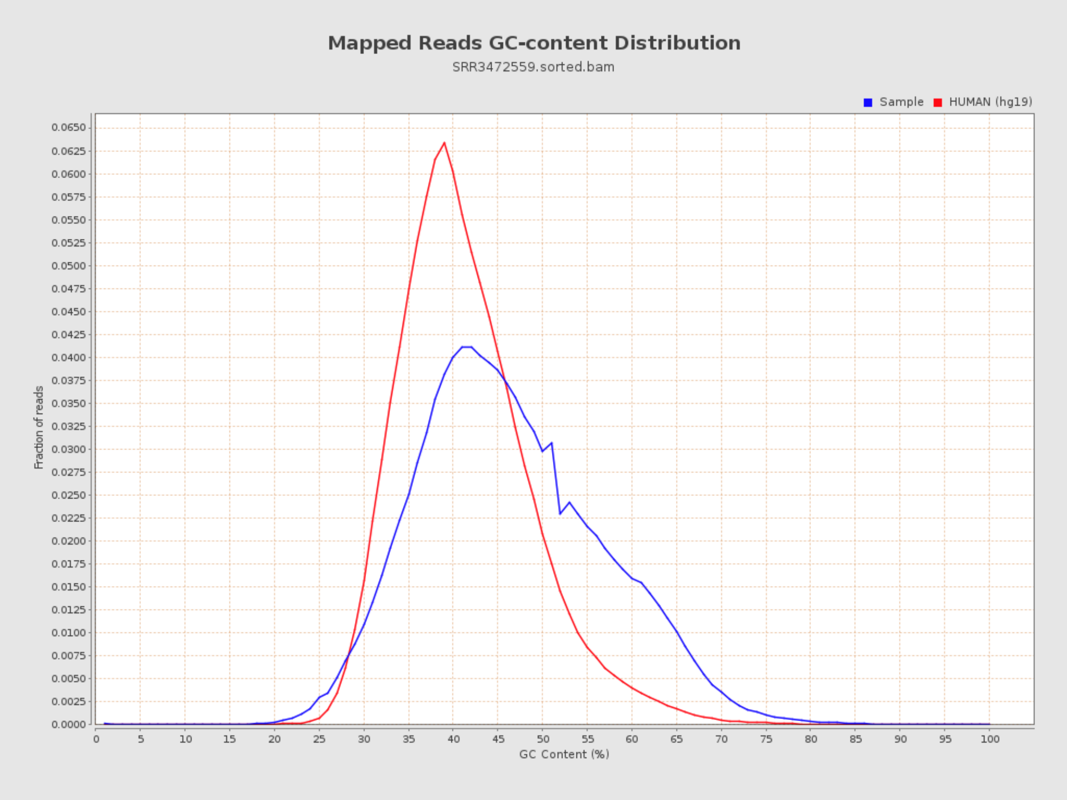
7. Results : Duplication Rate Histogram



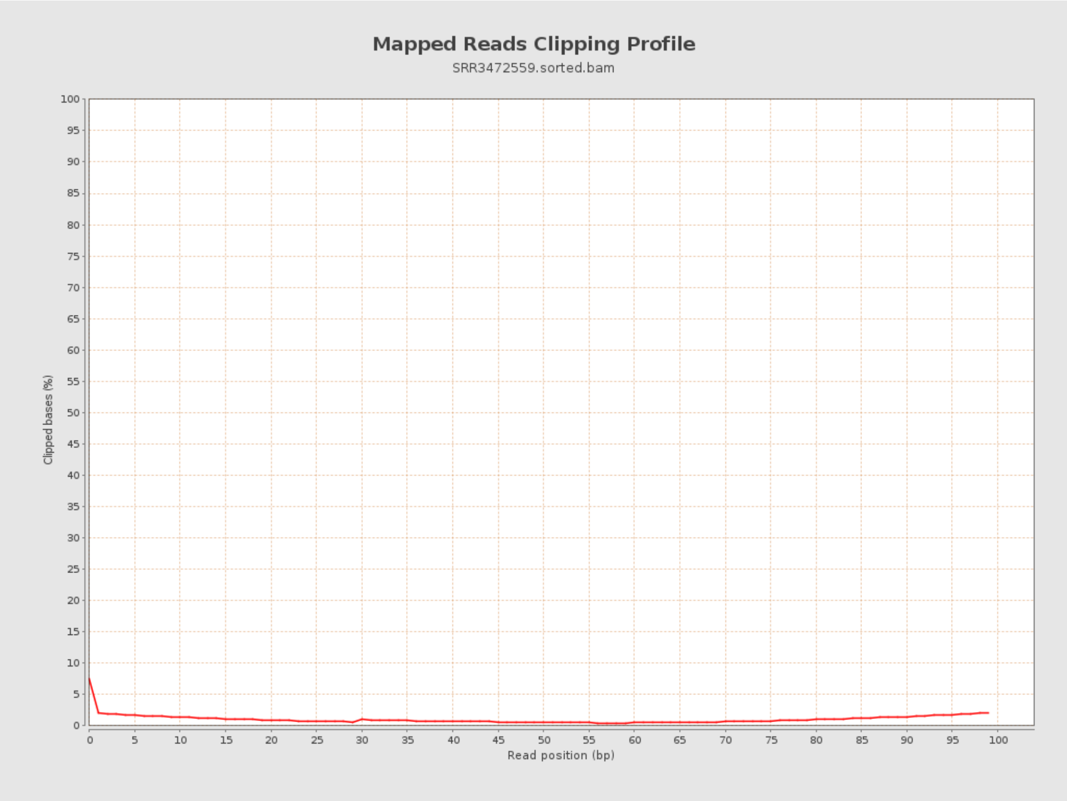
8. Results : Mapped Reads Nucleotide Content



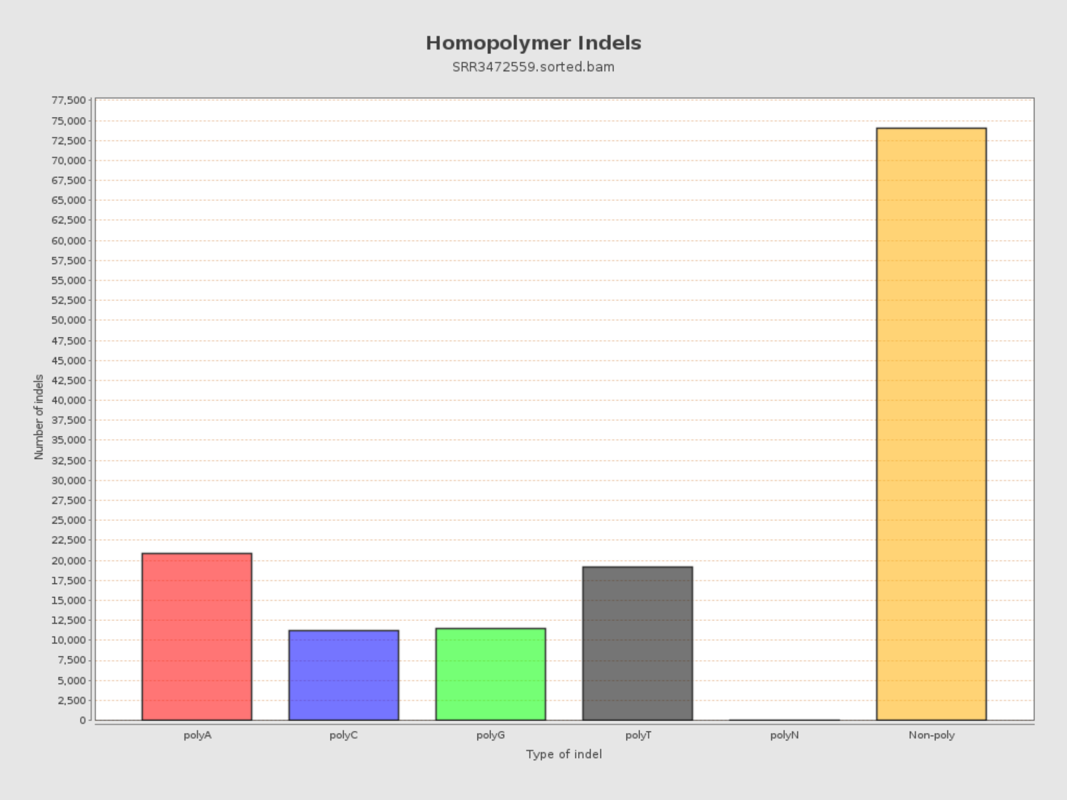
9. Results : Mapped Reads GC-content Distribution



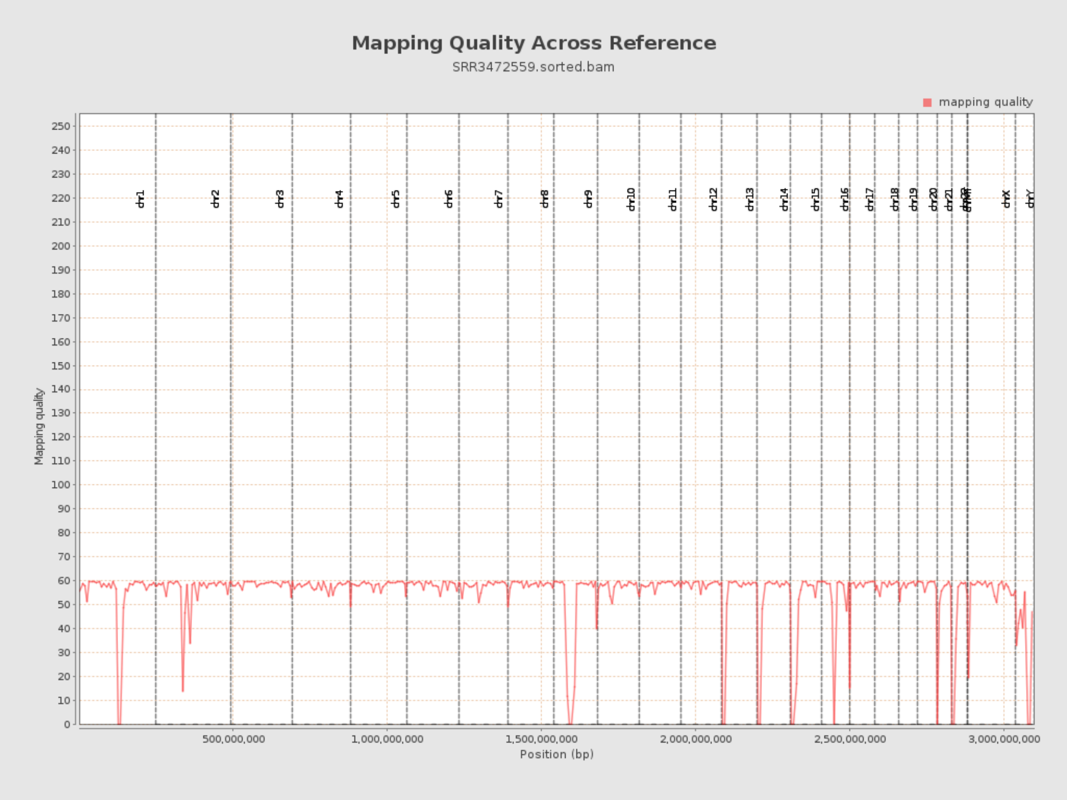
10. Results : Mapped Reads Clipping Profile



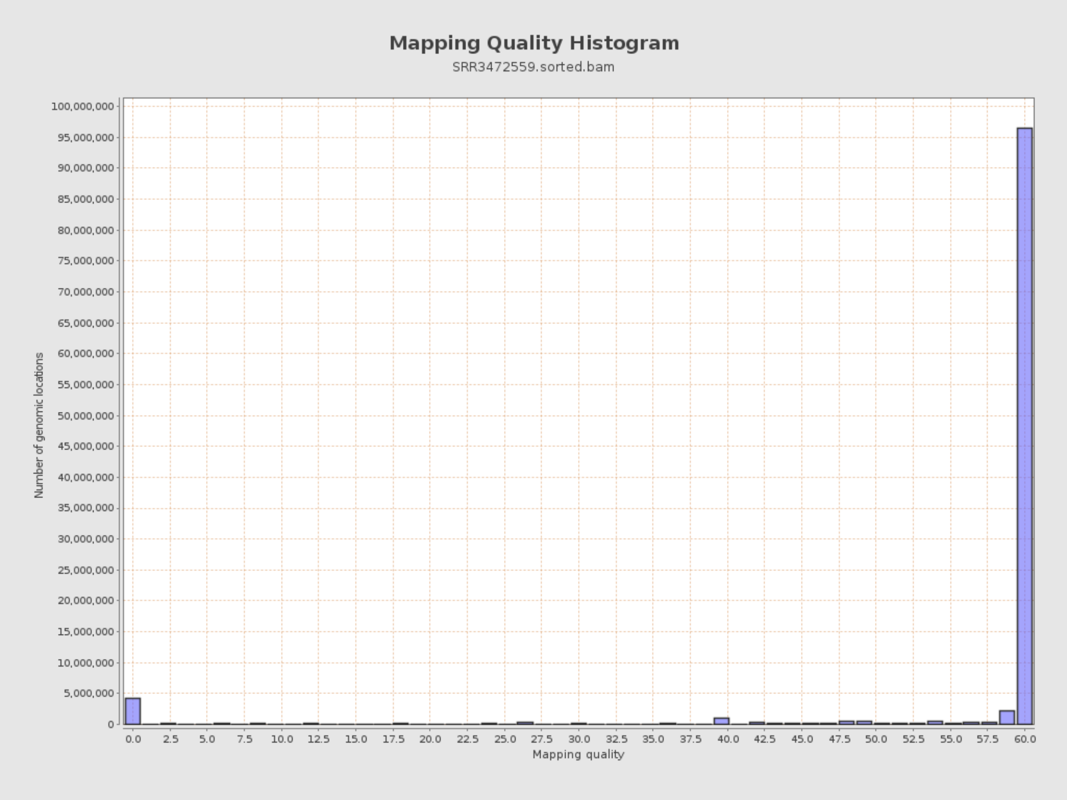
11. Results : Homopolymer Indels



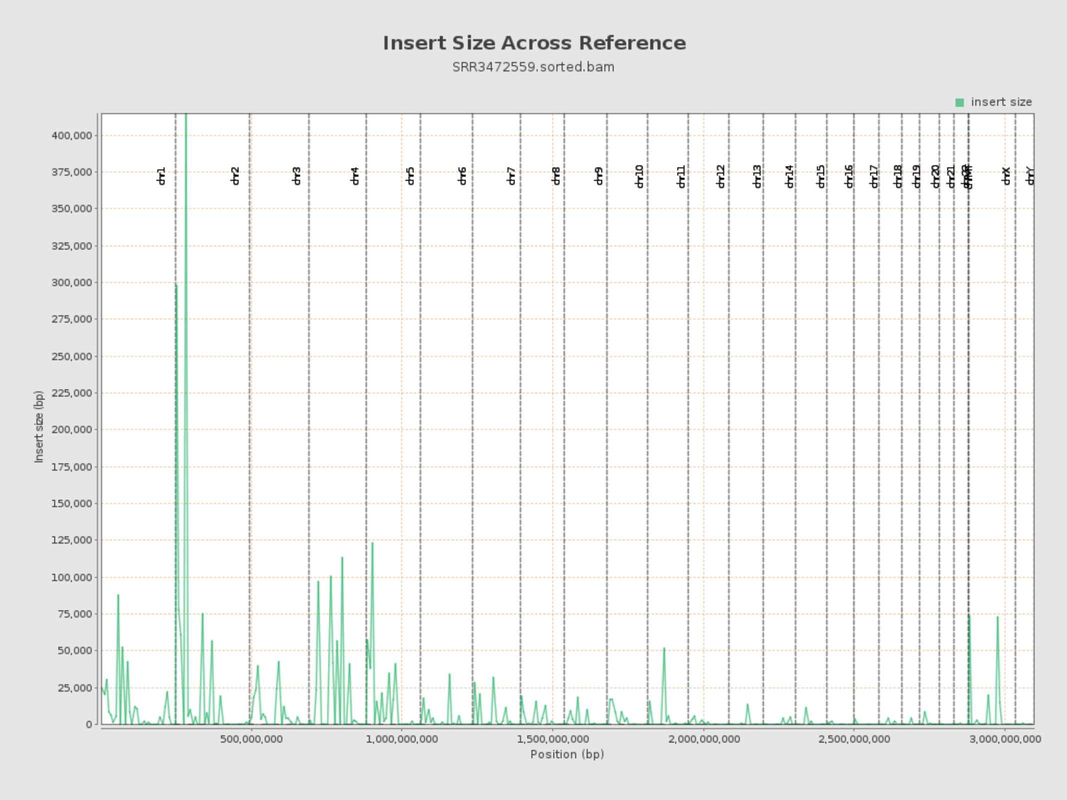
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram