Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 12:25:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472771.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_SRR3472771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472771_1.fastq.gz SRR3472771_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 12:25:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,551,826
Mapped reads	17,358,556 / 98.9%
Unmapped reads	193,270 / 1.1%
Mapped paired reads	17,358,556 / 98.9%
Mapped reads, first in pair	8,712,622 / 49.64%
Mapped reads, second in pair	8,645,934 / 49.26%
Mapped reads, both in pair	17,246,714 / 98.26%
Mapped reads, singletons	111,842 / 0.64%
Secondary alignments	0
Supplementary alignments	93,689 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	11,653,633 / 66.4%
Duplication rate	47.61%
Clipped reads	1,379,399 / 7.86%

2.2. ACGT Content

Number/percentage of A's	473,639,565 / 27.68%
Number/percentage of C's	384,817,176 / 22.49%
Number/percentage of T's	470,488,597 / 27.5%
Number/percentage of G's	381,746,632 / 22.31%
Number/percentage of N's	330,256 / 0.02%

GC Percentage	44.8%

2.3. Coverage

Mean	0.5528
Standard Deviation	21.7467

2.4. Mapping Quality

Mean Mapping Quality	55.03

2.5. Insert size

Mean	34,696.58
Standard Deviation	1,861,463.59
P25/Median/P75	178 / 248 / 333

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,545,480
Insertions	103,964
Mapped reads with at least one insertion	0.59%
Deletions	91,753
Mapped reads with at least one deletion	0.52%
Homopolymer indels	46.24%

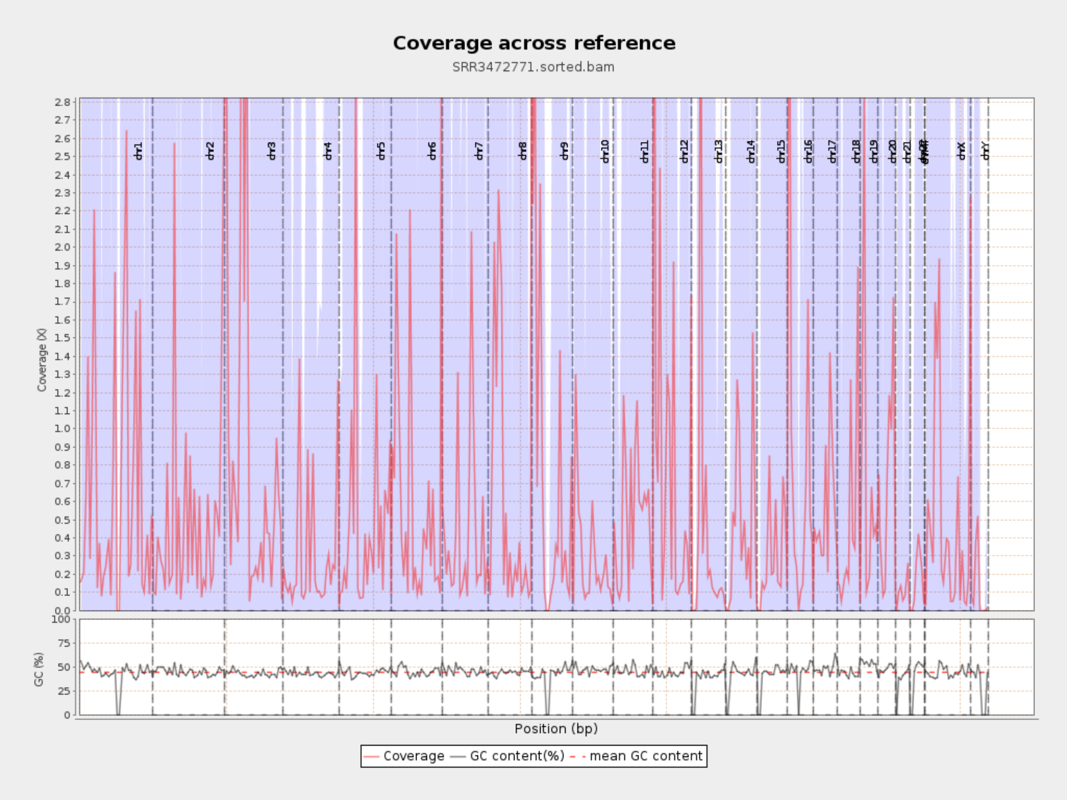
2.7. Chromosome stats

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

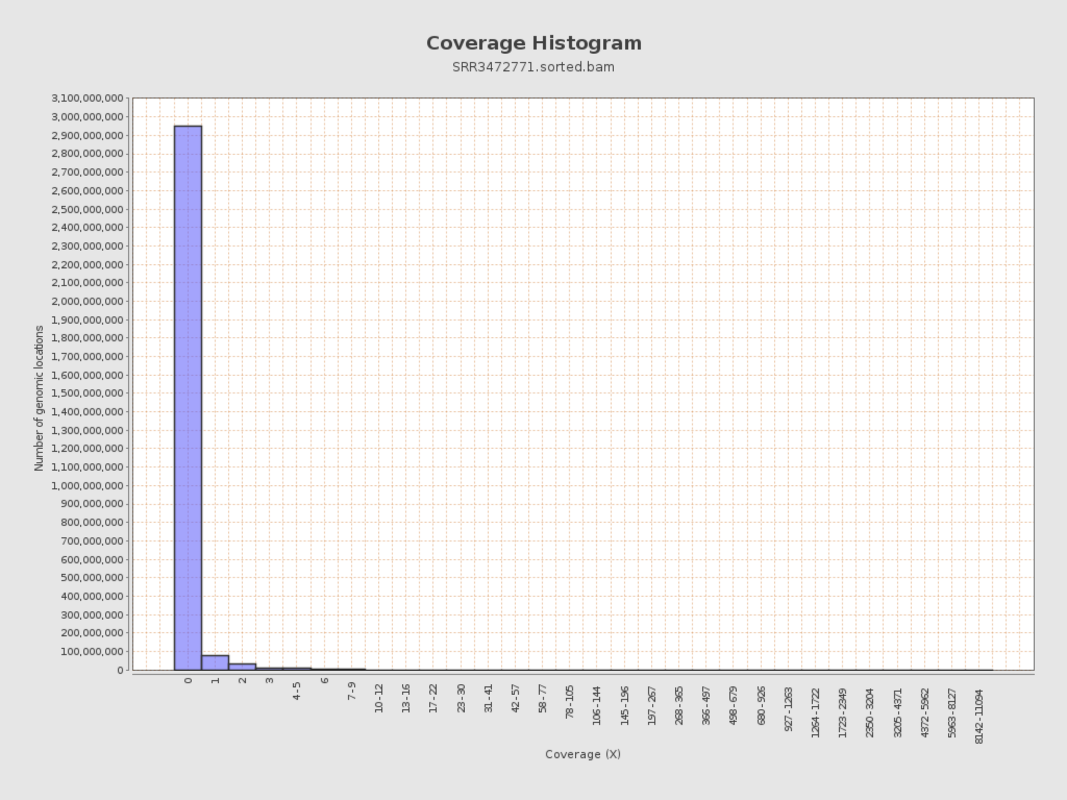
		bases	coverage	deviation
chr1	249250621	171221471	0.6869	23.5673
chr2	243199373	118458655	0.4871	18.593
chr3	198022430	193964825	0.9795	25.4062
chr4	191154276	56029519	0.2931	10.6194
chr5	180915260	91202908	0.5041	22.9831
chr6	171115067	98943713	0.5782	24.272
chr7	159138663	71951920	0.4521	16.6825
chr8	146364022	84770234	0.5792	25.1402
chr9	141213431	109033316	0.7721	22.6445
chr10	135534747	38494779	0.284	14.4209
chr11	135006516	72976541	0.5405	18.6451
chr12	133851895	122495241	0.9152	29.2484
chr13	115169878	52519386	0.456	31.1139
chr14	107349540	50380034	0.4693	16.3461
chr15	102531392	31307903	0.3053	12.4383
chr16	90354753	73018651	0.8081	30.3266
chr17	81195210	45382035	0.5589	16.6962
chr18	78077248	39258910	0.5028	22.2554
chr19	59128983	46839525	0.7922	26.676
chr20	63025520	45328032	0.7192	26.3888
chr21	48129895	5202261	0.1081	5.3962
chr22	51304566	8257827	0.161	6.8726
chrMT	16571	3547	0.214	0.5726
chrX	155270560	76493018	0.4926	25.7005

chrY	59373566	7722581	0.1301	8.1944

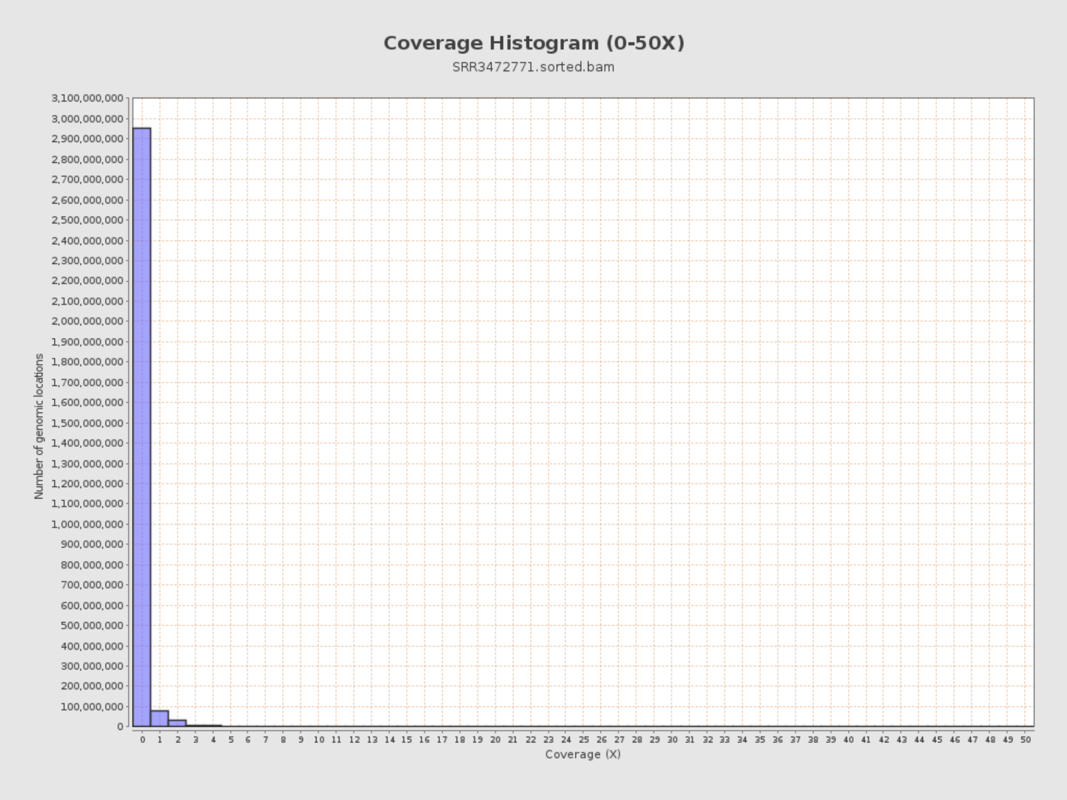
3. Results : Coverage across reference



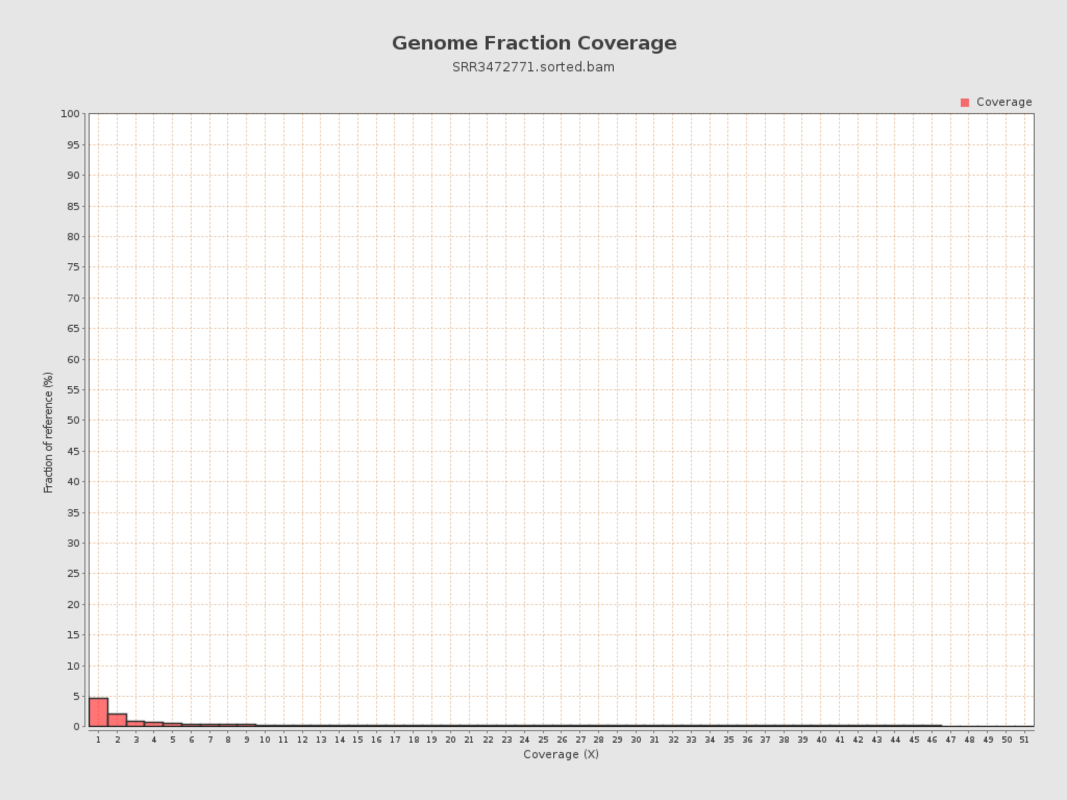
4. Results : Coverage Histogram



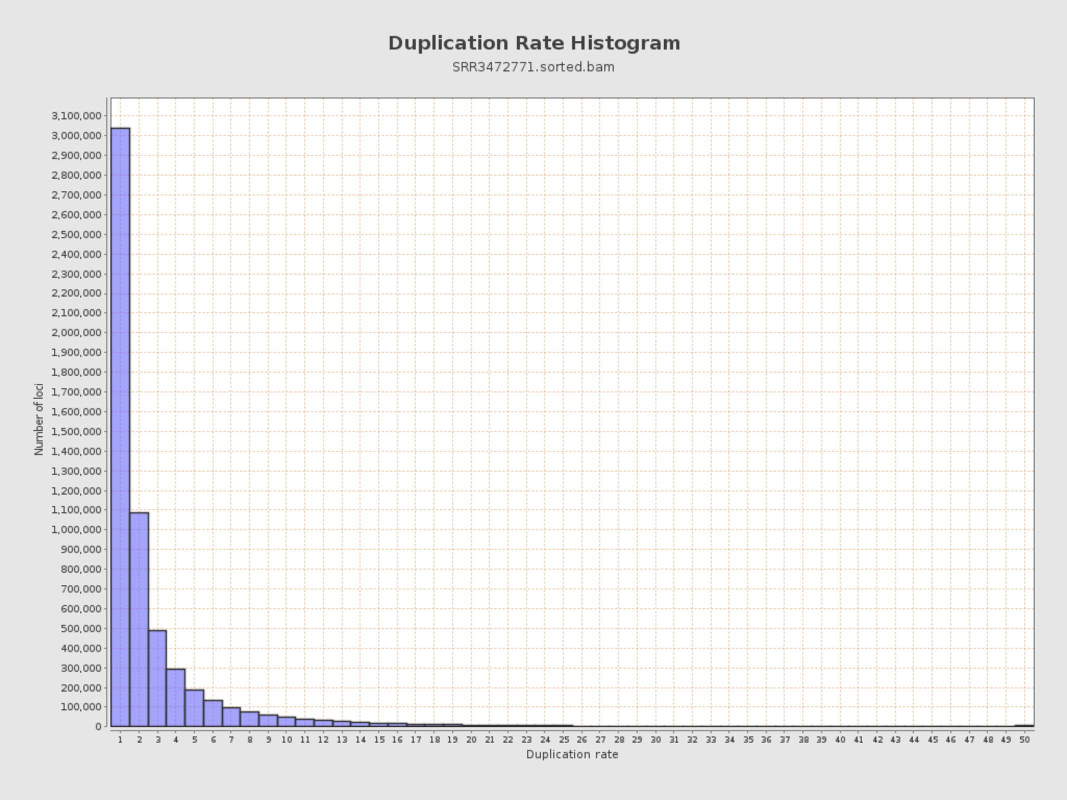
5. Results : Coverage Histogram (0-50X)



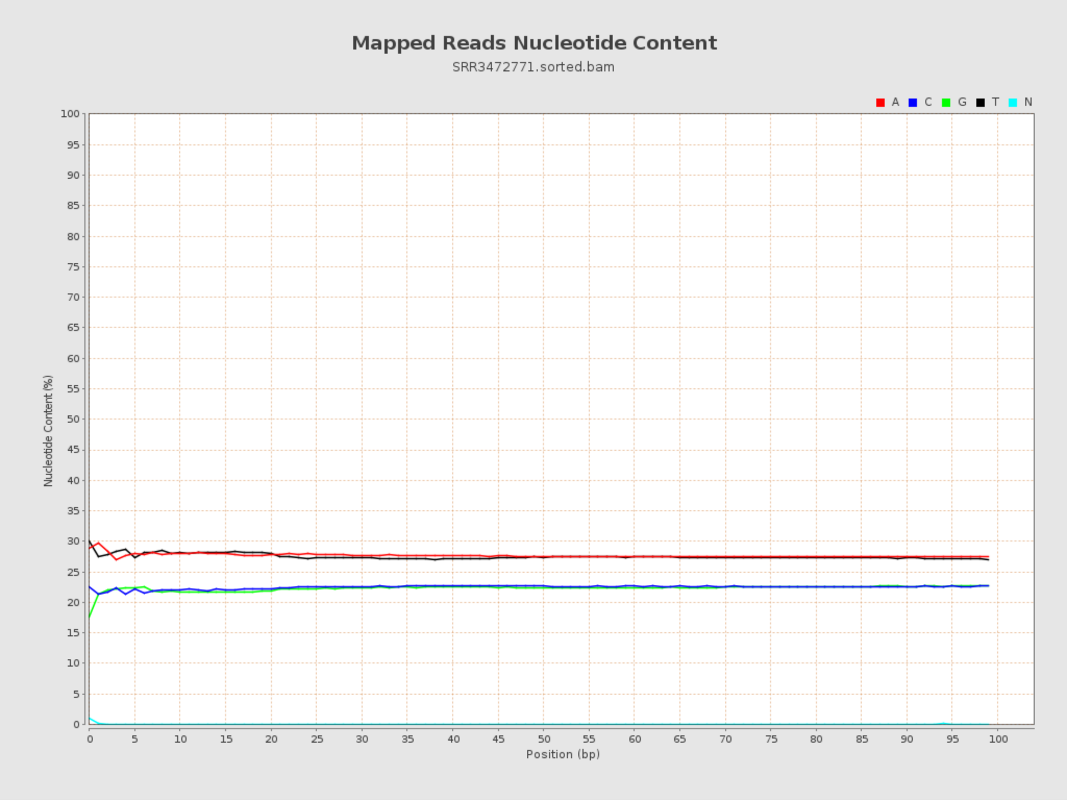
6. Results : Genome Fraction Coverage



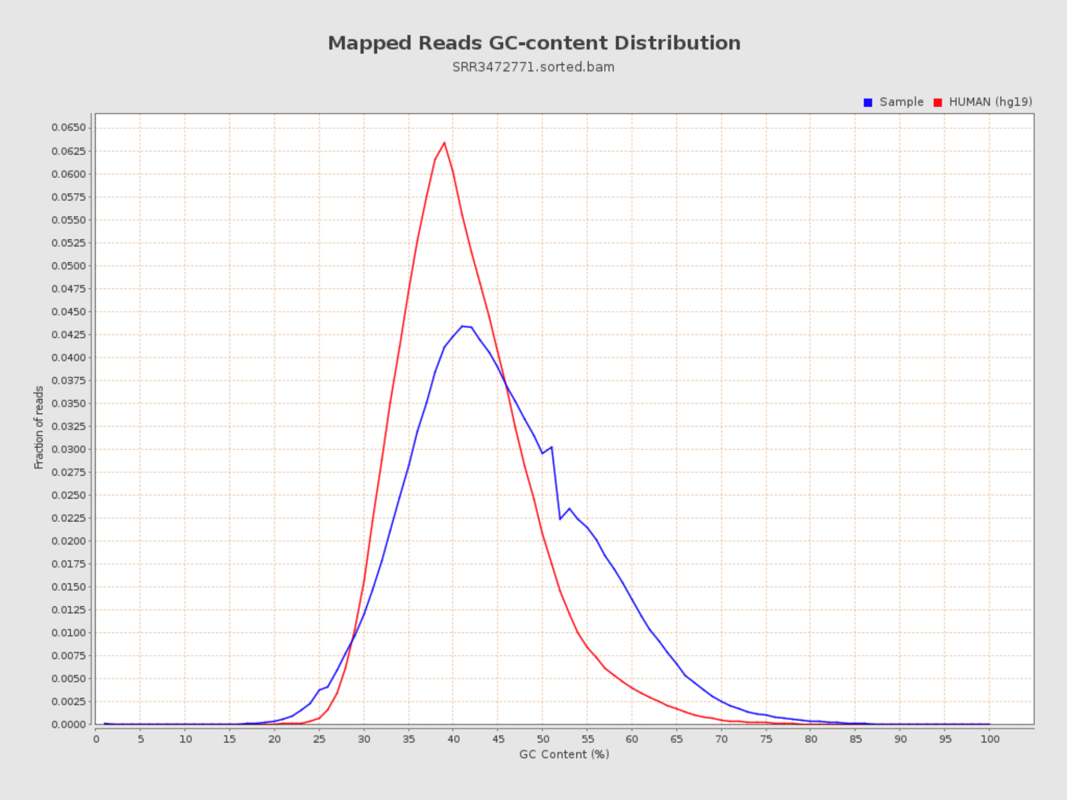
7. Results : Duplication Rate Histogram



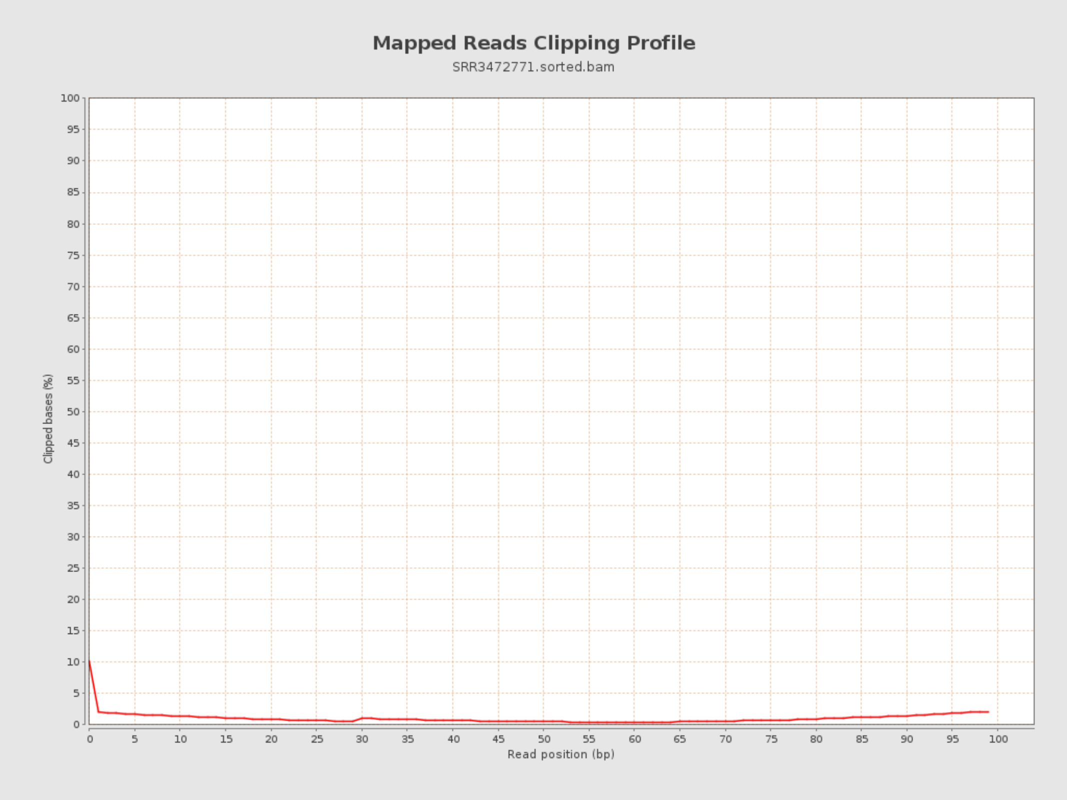
8. Results : Mapped Reads Nucleotide Content



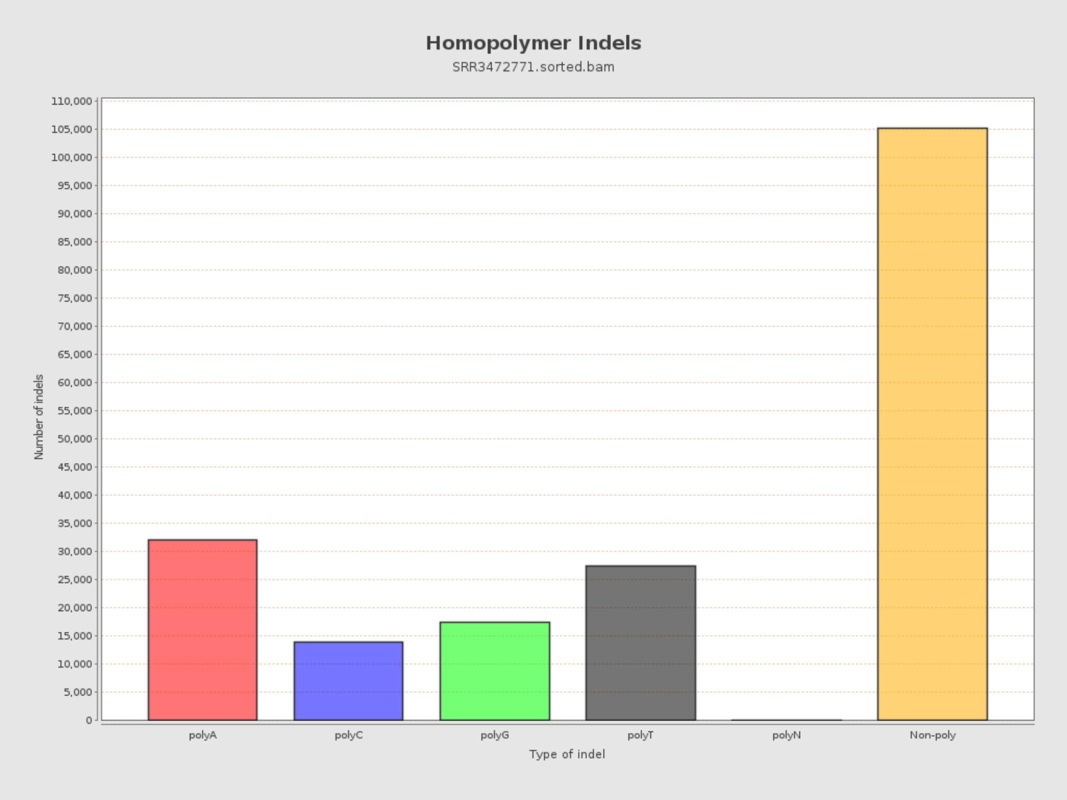
9. Results : Mapped Reads GC-content Distribution



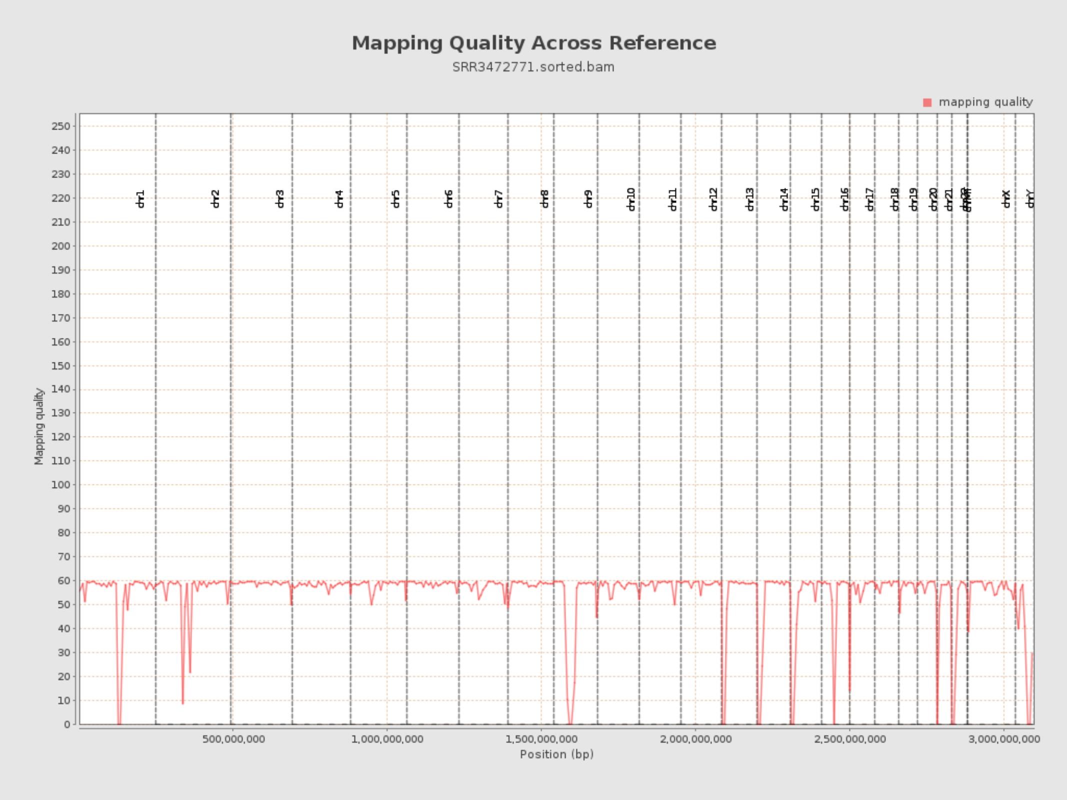
10. Results : Mapped Reads Clipping Profile



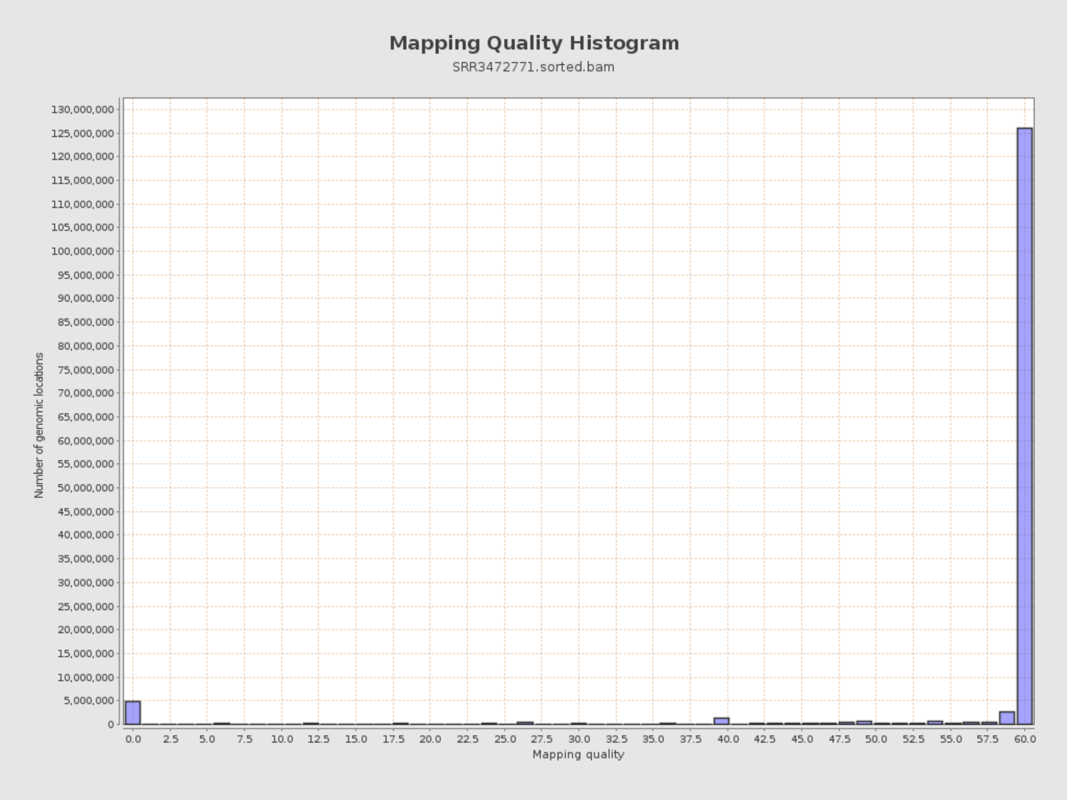
11. Results : Homopolymer Indels



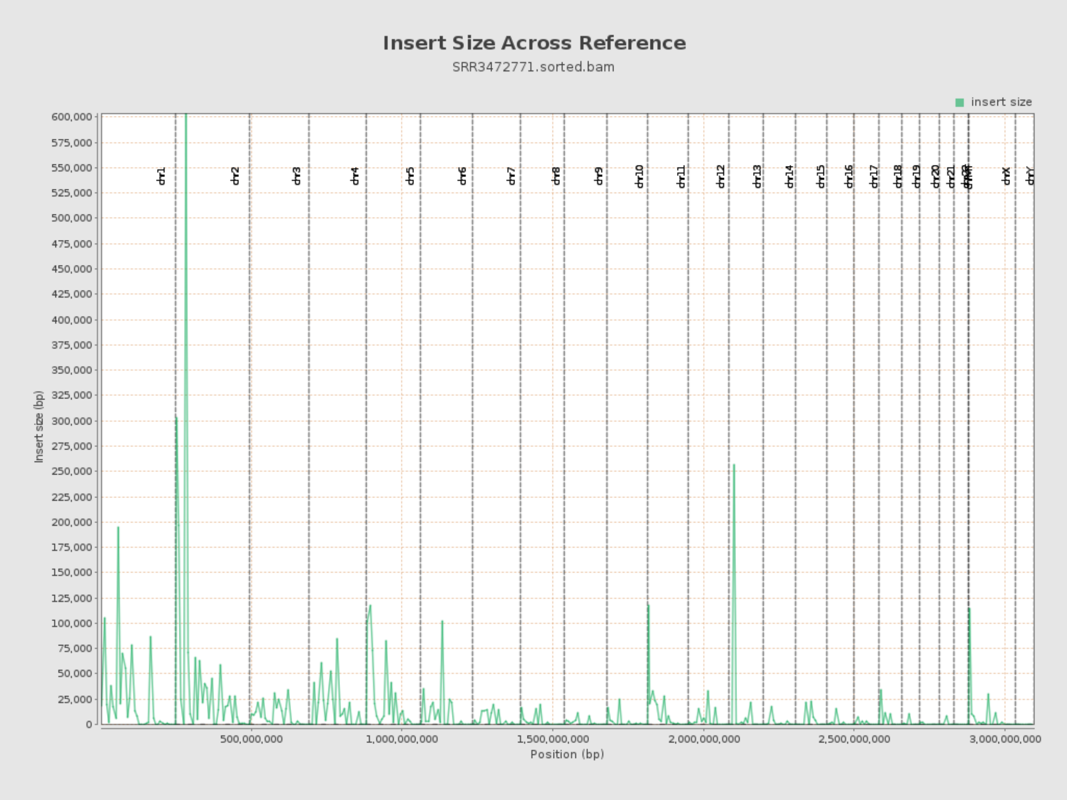
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram