Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 05:57:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472751.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_SRR3472751 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472751_1.fastq.gz SRR3472751_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 05:57:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472751.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,238,298
Mapped reads	13,098,342 / 98.94%
Unmapped reads	139,956 / 1.06%
Mapped paired reads	13,098,342 / 98.94%
Mapped reads, first in pair	6,580,382 / 49.71%
Mapped reads, second in pair	6,517,960 / 49.24%
Mapped reads, both in pair	13,008,598 / 98.26%
Mapped reads, singletons	89,744 / 0.68%
Secondary alignments	0
Supplementary alignments	48,287 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	7,877,129 / 59.5%
Duplication rate	46.12%
Clipped reads	1,018,626 / 7.69%

2.2. ACGT Content

Number/percentage of A's	361,583,954 / 28.01%
Number/percentage of C's	285,933,197 / 22.15%
Number/percentage of T's	359,735,654 / 27.87%
Number/percentage of G's	283,284,702 / 21.95%
Number/percentage of N's	249,054 / 0.02%

GC Percentage	44.1%

2.3. Coverage

Mean	0.417
Standard Deviation	15.8644

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	22,654.61
Standard Deviation	1,491,997.79
P25/Median/P75	182 / 257 / 348

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	8,586,904
Insertions	78,940
Mapped reads with at least one insertion	0.59%
Deletions	76,335
Mapped reads with at least one deletion	0.58%
Homopolymer indels	45.72%

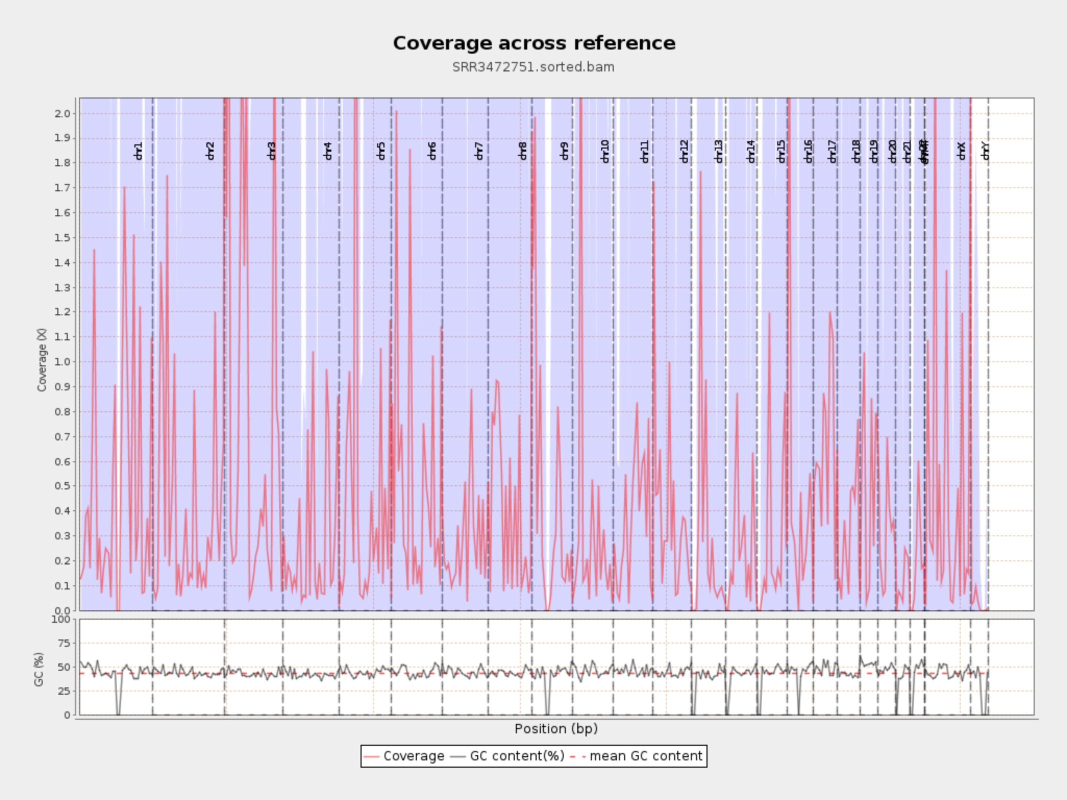
2.7. Chromosome stats

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

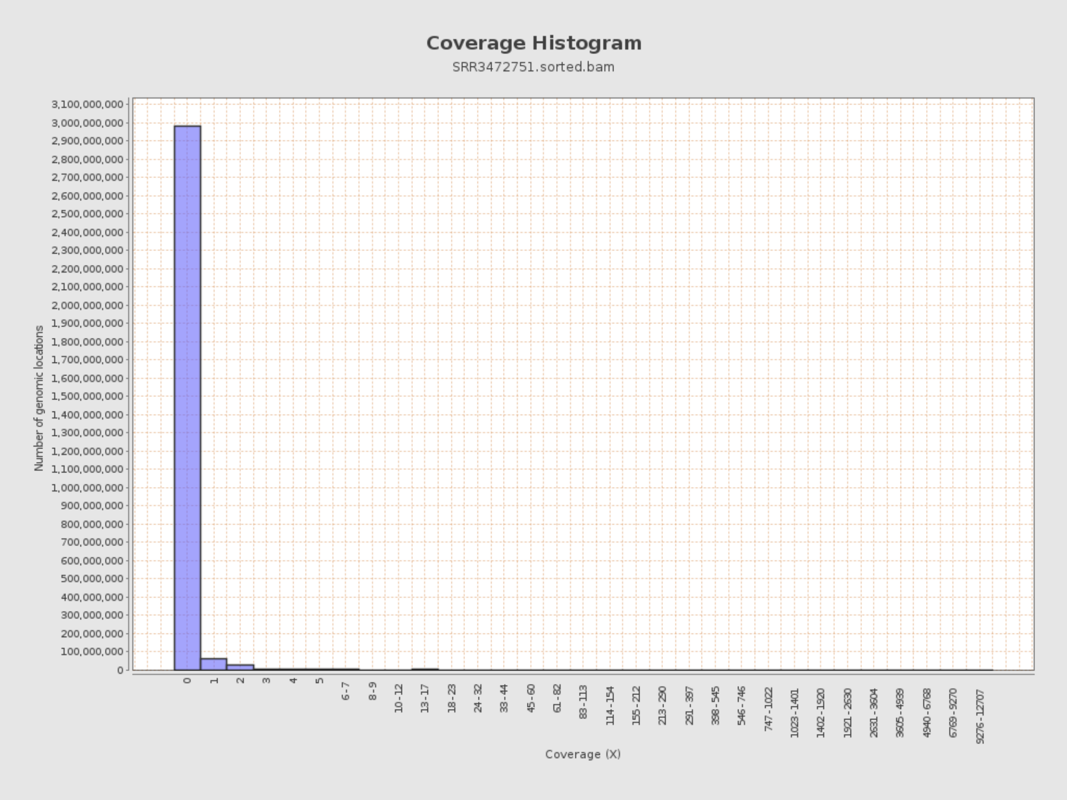
		bases	coverage	deviation
chr1	249250621	123409288	0.4951	16.7638
chr2	243199373	98903810	0.4067	17.0383
chr3	198022430	167571578	0.8462	23.986
chr4	191154276	53954076	0.2823	11.7132
chr5	180915260	89199014	0.493	20.1233
chr6	171115067	87474497	0.5112	13.2113
chr7	159138663	45061120	0.2832	8.1649
chr8	146364022	57748806	0.3946	18.9974
chr9	141213431	62465591	0.4423	10.0903
chr10	135534747	45627317	0.3366	32.4307
chr11	135006516	50627405	0.375	10.9012
chr12	133851895	55517466	0.4148	11.2138
chr13	115169878	33198771	0.2883	12.9658
chr14	107349540	27245008	0.2538	9.7478
chr15	102531392	28623616	0.2792	9.1585
chr16	90354753	42296143	0.4681	13.2381
chr17	81195210	52508278	0.6467	15.0653
chr18	78077248	24280340	0.311	11.5641
chr19	59128983	31085814	0.5257	15.3772
chr20	63025520	20520338	0.3256	12.6087
chr21	48129895	5697540	0.1184	5.6413
chr22	51304566	9837624	0.1917	4.8468
chrMT	16571	2327	0.1404	0.5837
chrX	155270560	76583263	0.4932	14.4064

chrY	59373566	1534722	0.0258	0.9144

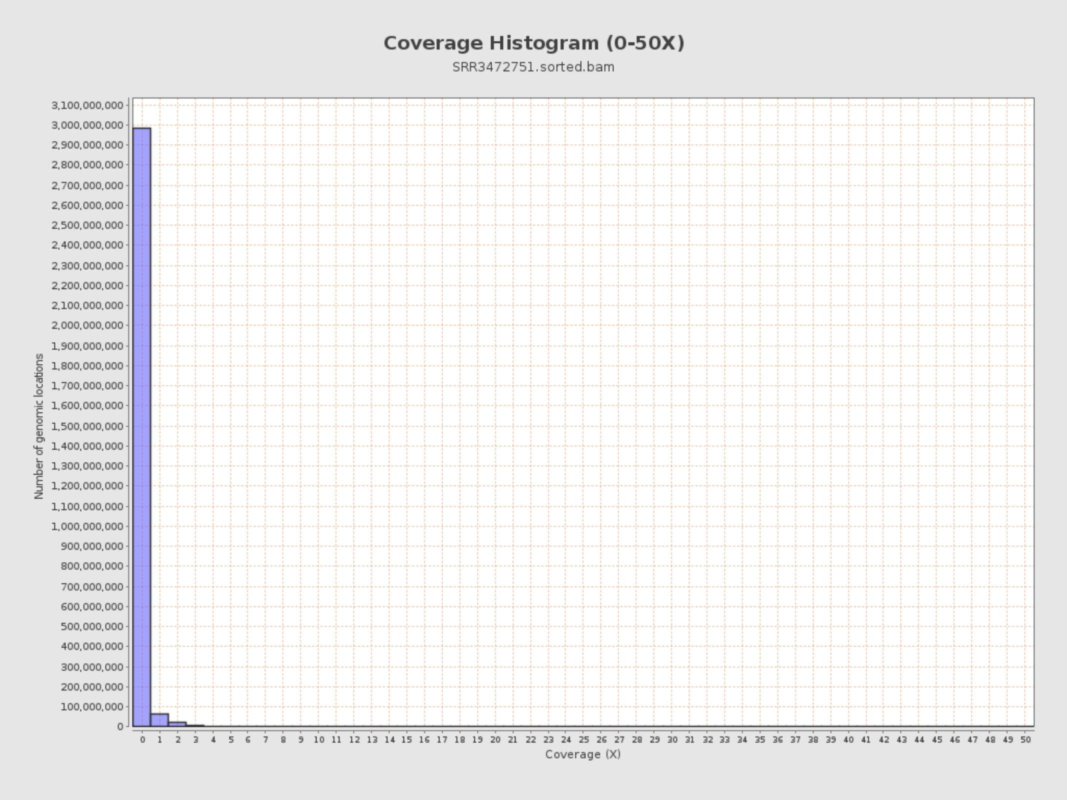
3. Results : Coverage across reference



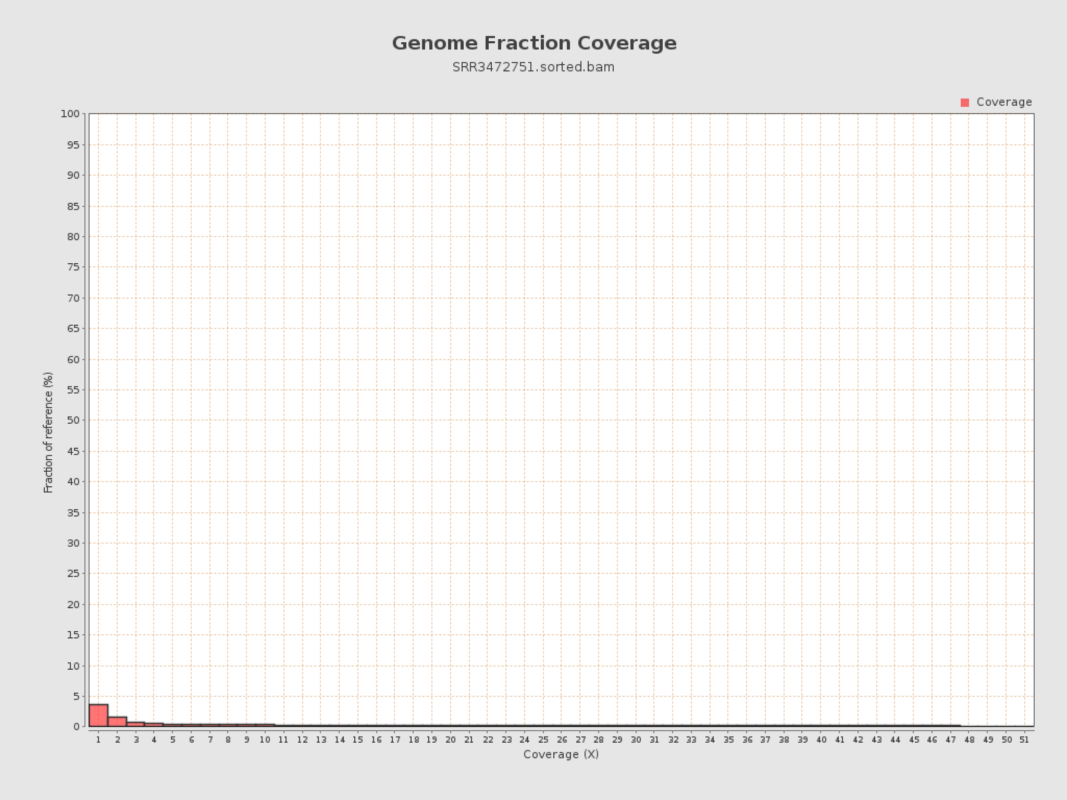
4. Results : Coverage Histogram



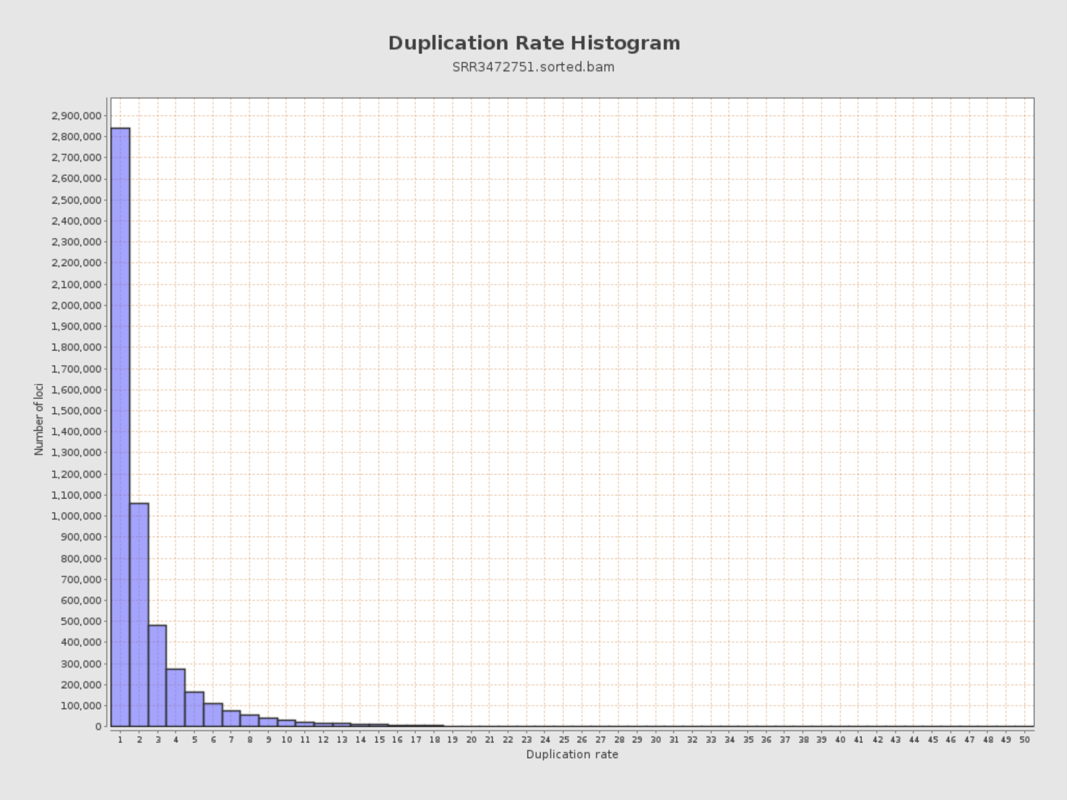
5. Results : Coverage Histogram (0-50X)



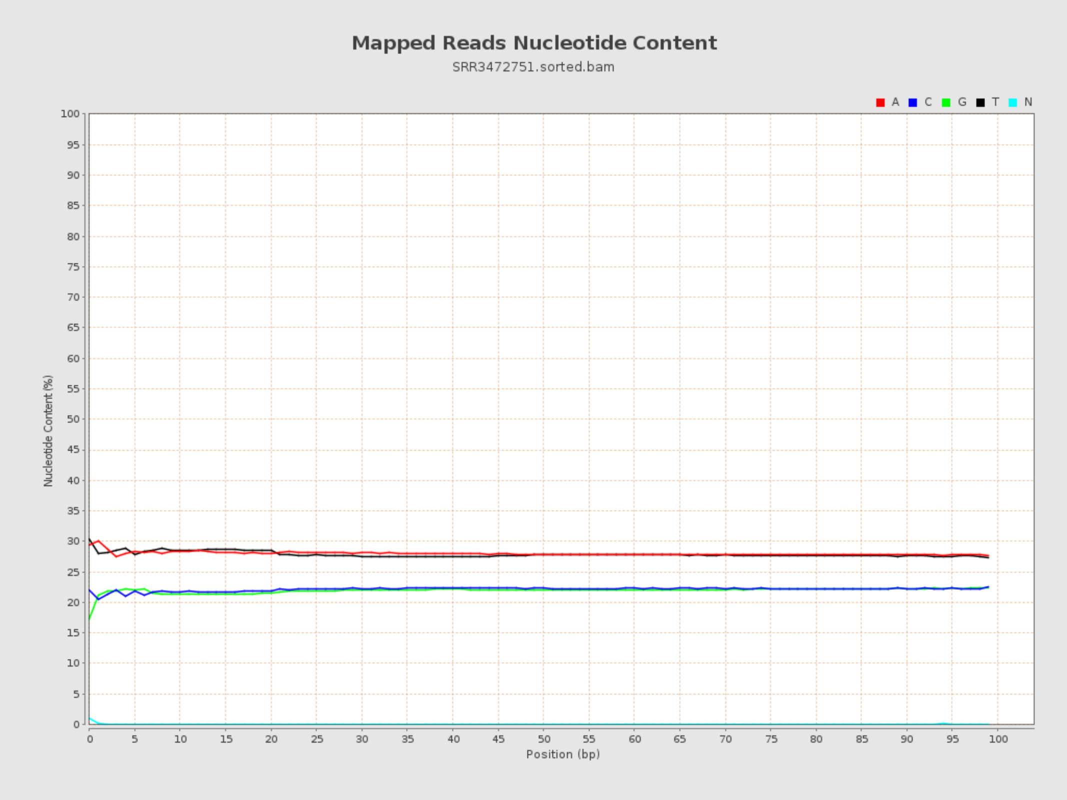
6. Results : Genome Fraction Coverage



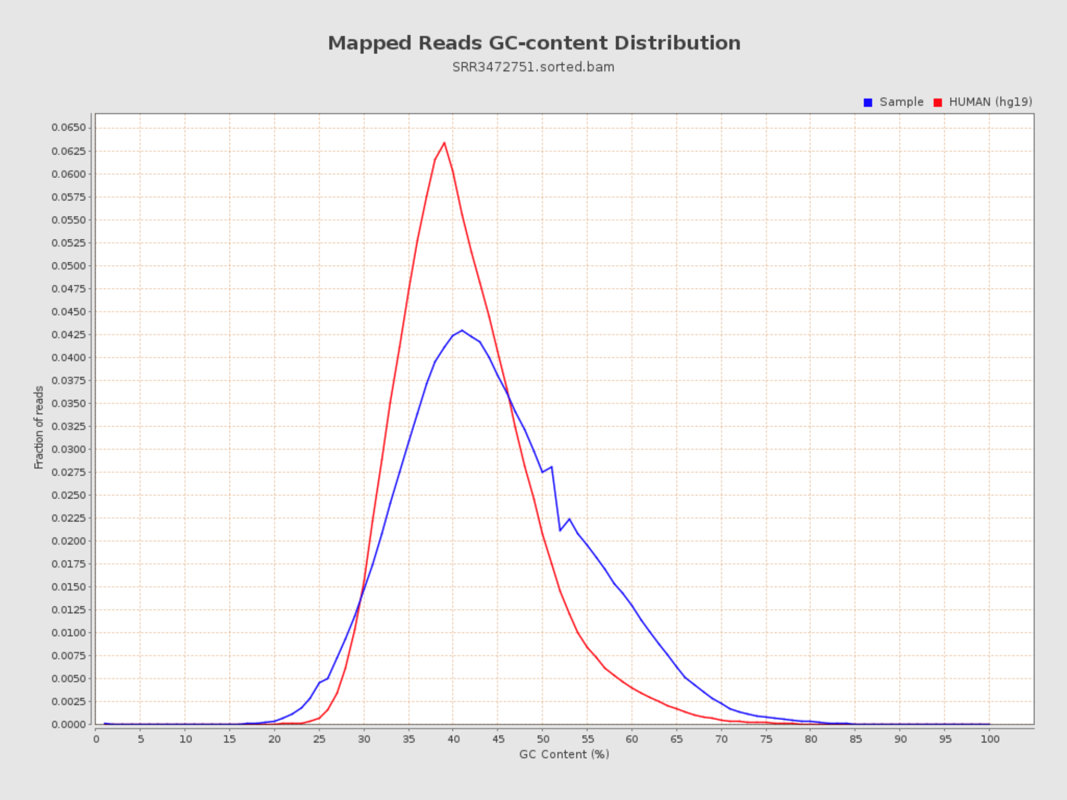
7. Results : Duplication Rate Histogram



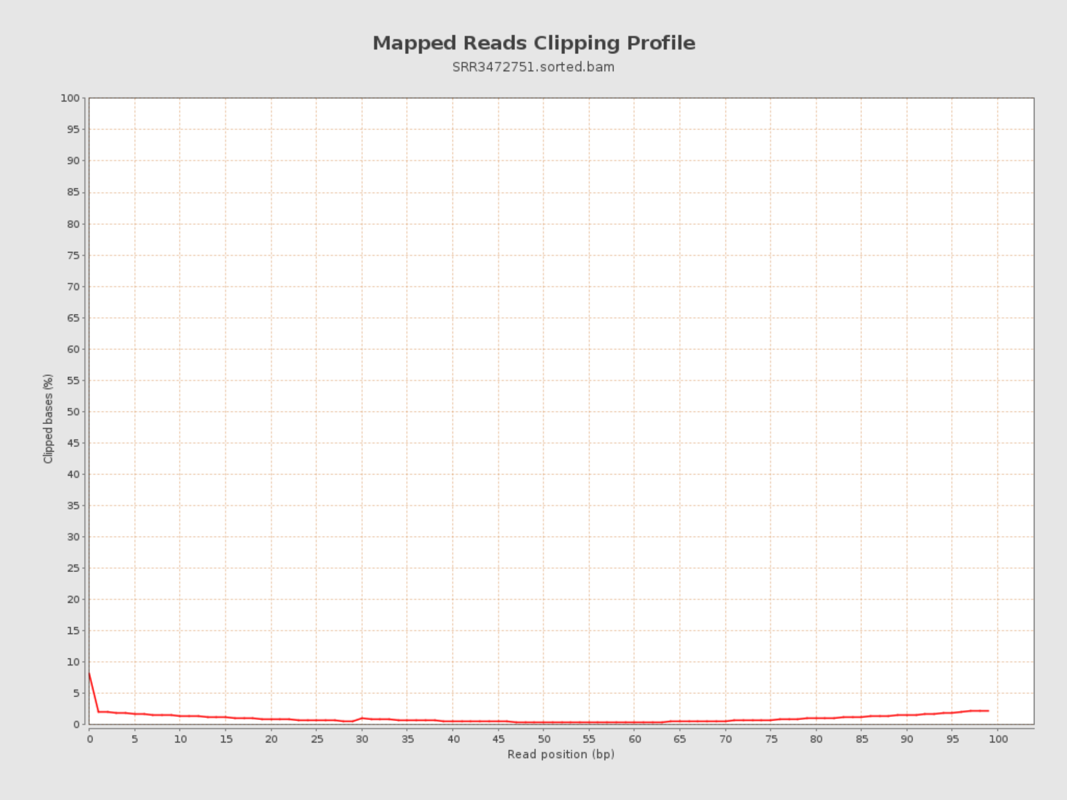
8. Results : Mapped Reads Nucleotide Content



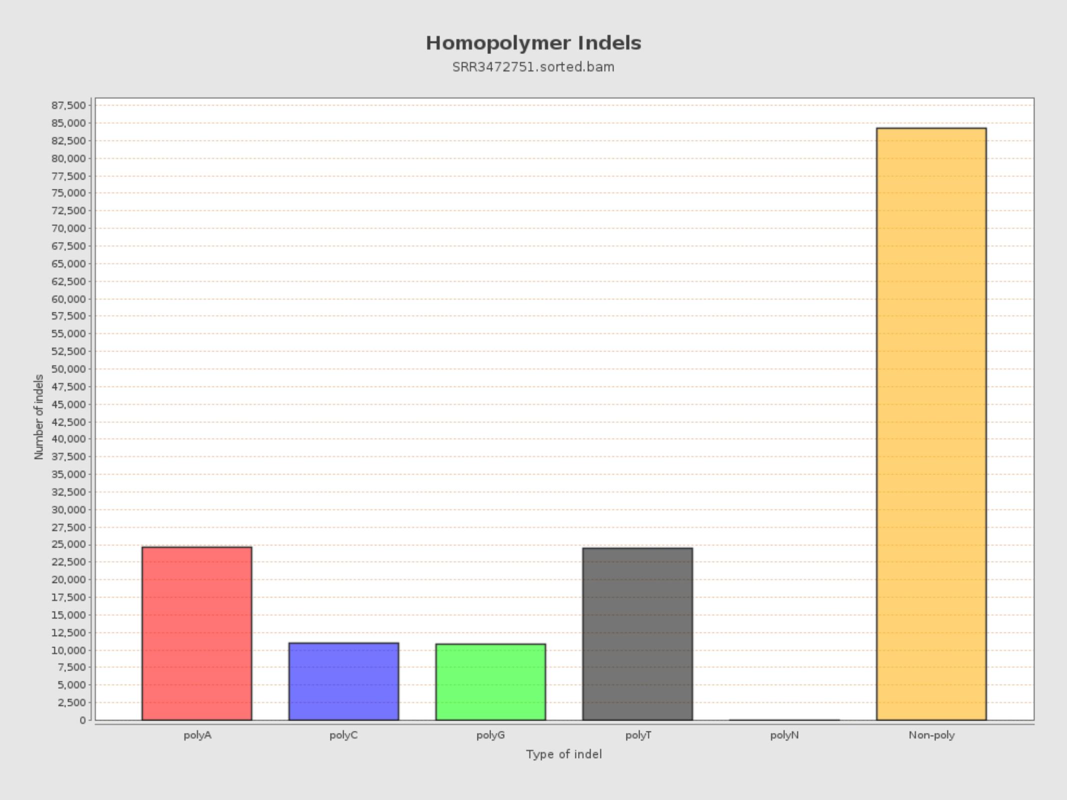
9. Results : Mapped Reads GC-content Distribution



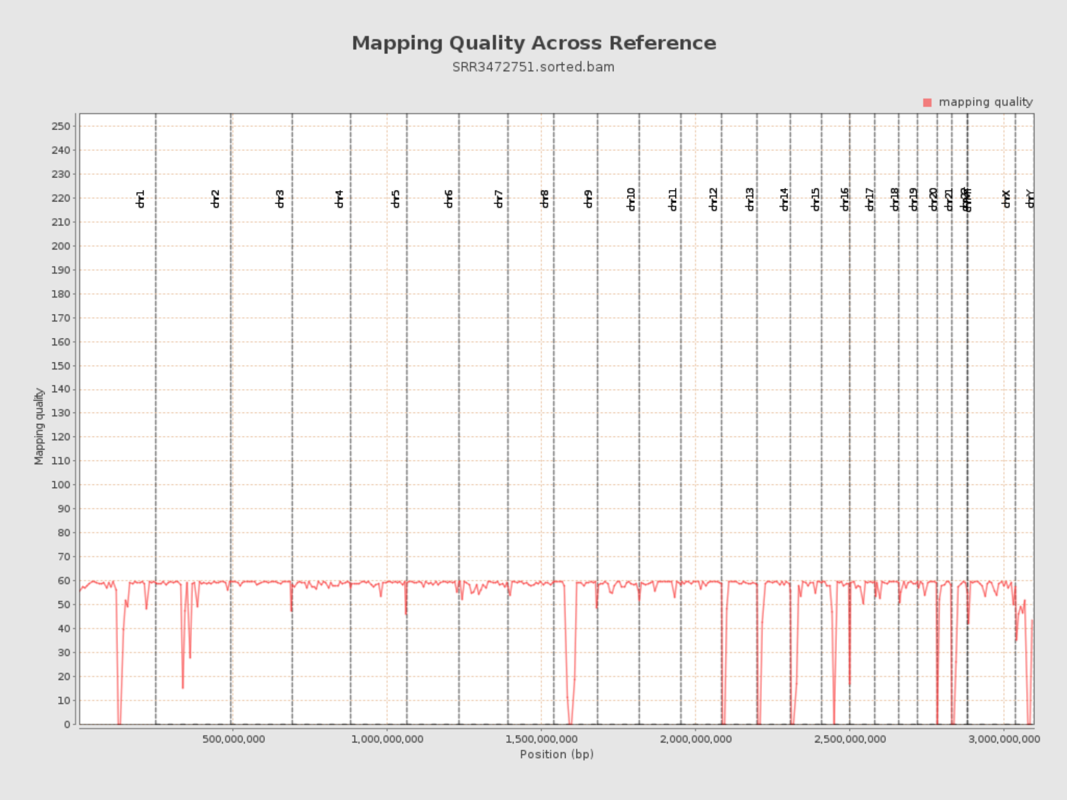
10. Results : Mapped Reads Clipping Profile



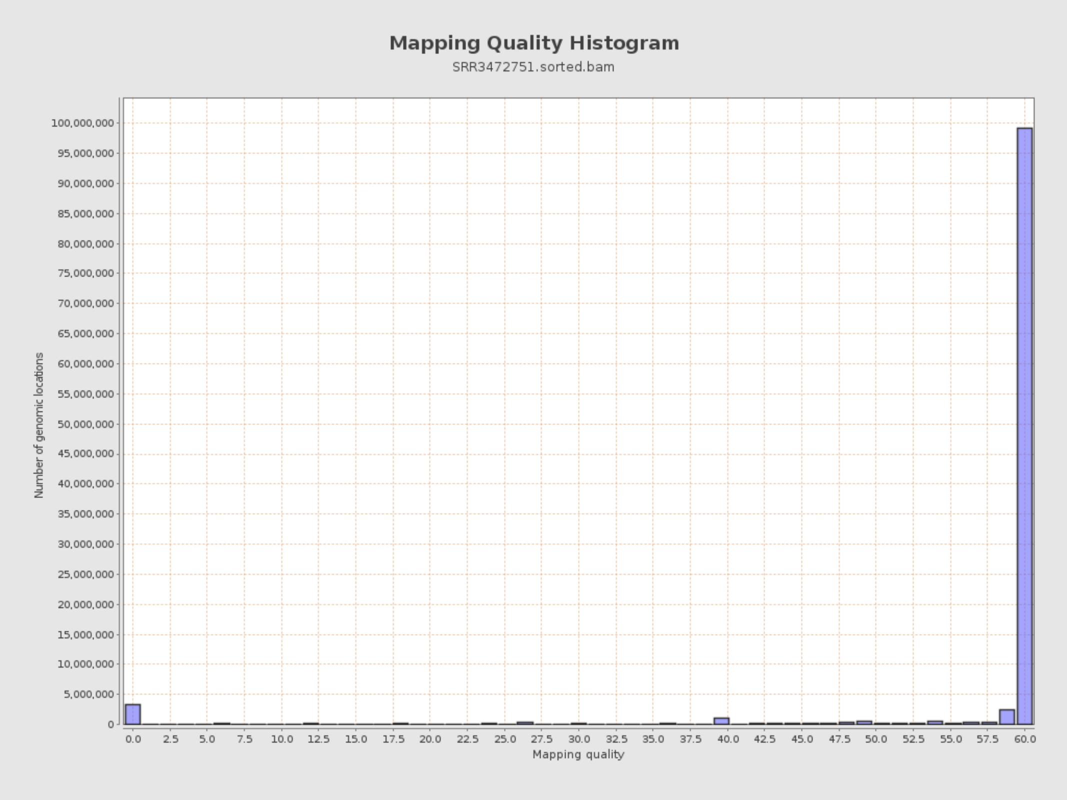
11. Results : Homopolymer Indels



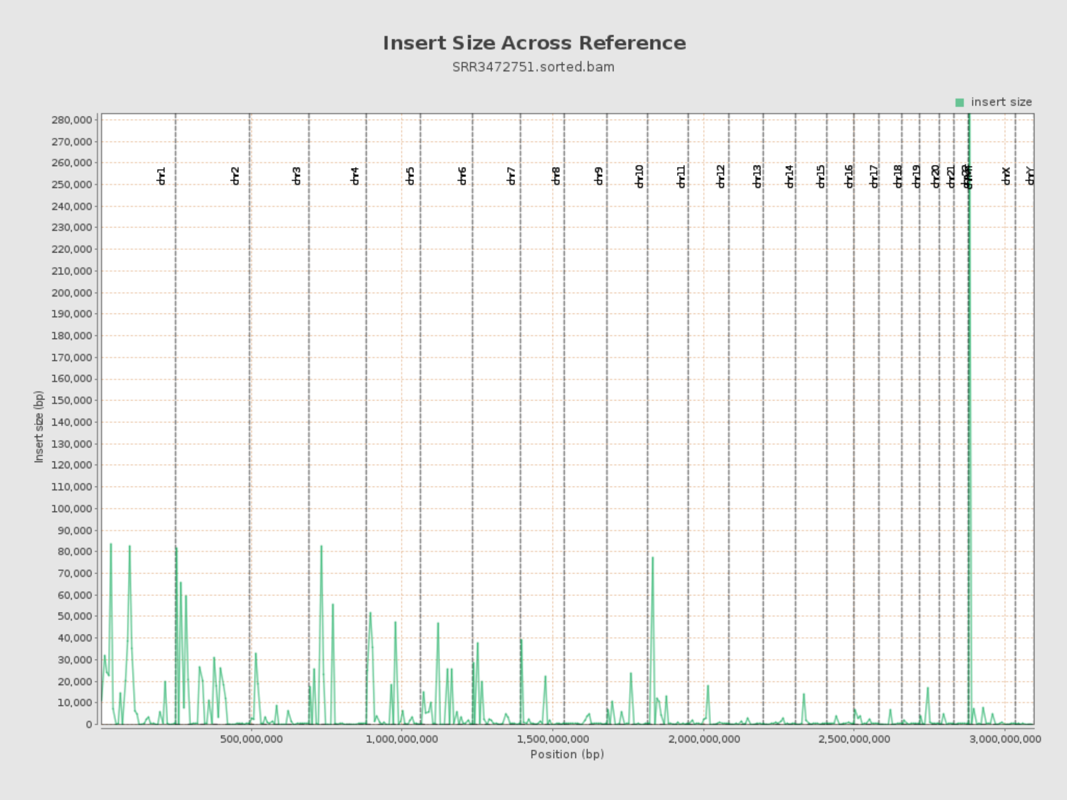
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram