Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 09:01:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472761.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_SRR3472761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472761_1.fastq.gz SRR3472761_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 09:01:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,063,472
Mapped reads	14,914,653 / 99.01%
Unmapped reads	148,819 / 0.99%
Mapped paired reads	14,914,653 / 99.01%
Mapped reads, first in pair	7,488,744 / 49.71%
Mapped reads, second in pair	7,425,909 / 49.3%
Mapped reads, both in pair	14,819,472 / 98.38%
Mapped reads, singletons	95,181 / 0.63%
Secondary alignments	0
Supplementary alignments	55,020 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	11,162,064 / 74.1%
Duplication rate	43.18%
Clipped reads	1,267,153 / 8.41%

2.2. ACGT Content

Number/percentage of A's	409,351,566 / 27.9%
Number/percentage of C's	325,731,489 / 22.2%
Number/percentage of T's	406,995,043 / 27.74%
Number/percentage of G's	324,938,248 / 22.15%
Number/percentage of N's	283,094 / 0.02%

GC Percentage	44.34%

2.3. Coverage

Mean	0.474
Standard Deviation	34.0417

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	28,948.49
Standard Deviation	1,729,919.5
P25/Median/P75	171 / 243 / 332

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,249,579
Insertions	94,006
Mapped reads with at least one insertion	0.61%
Deletions	74,848
Mapped reads with at least one deletion	0.5%
Homopolymer indels	48.05%

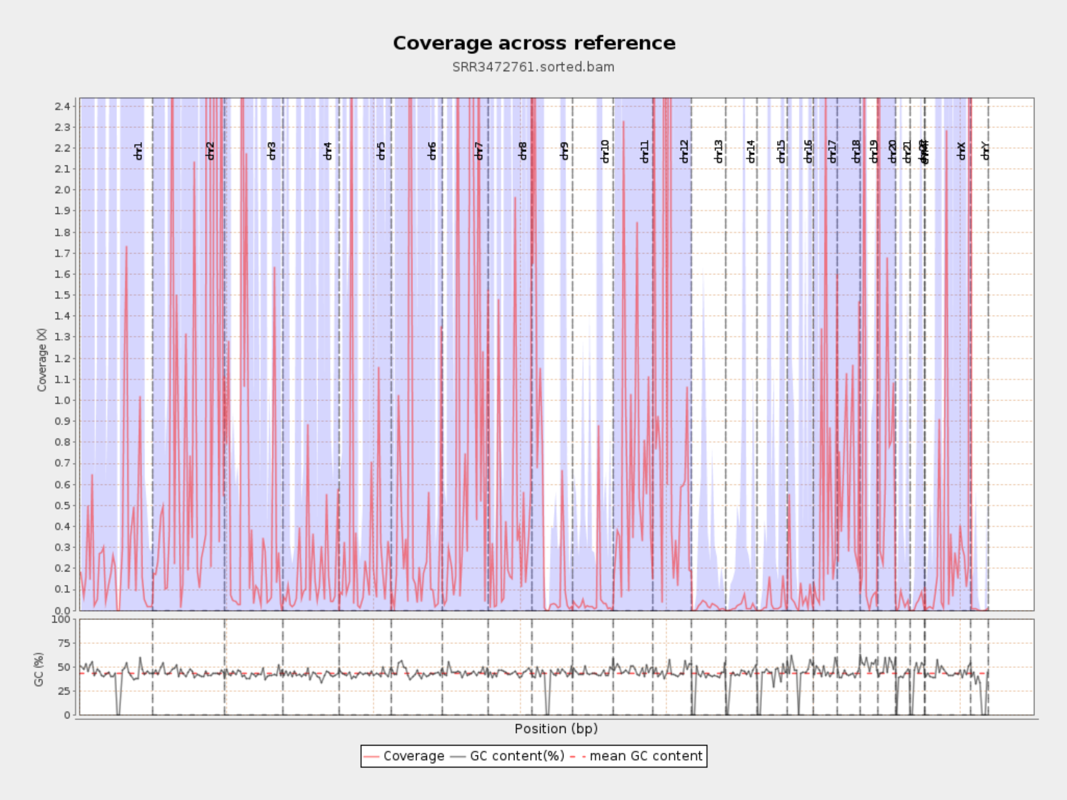
2.7. Chromosome stats

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

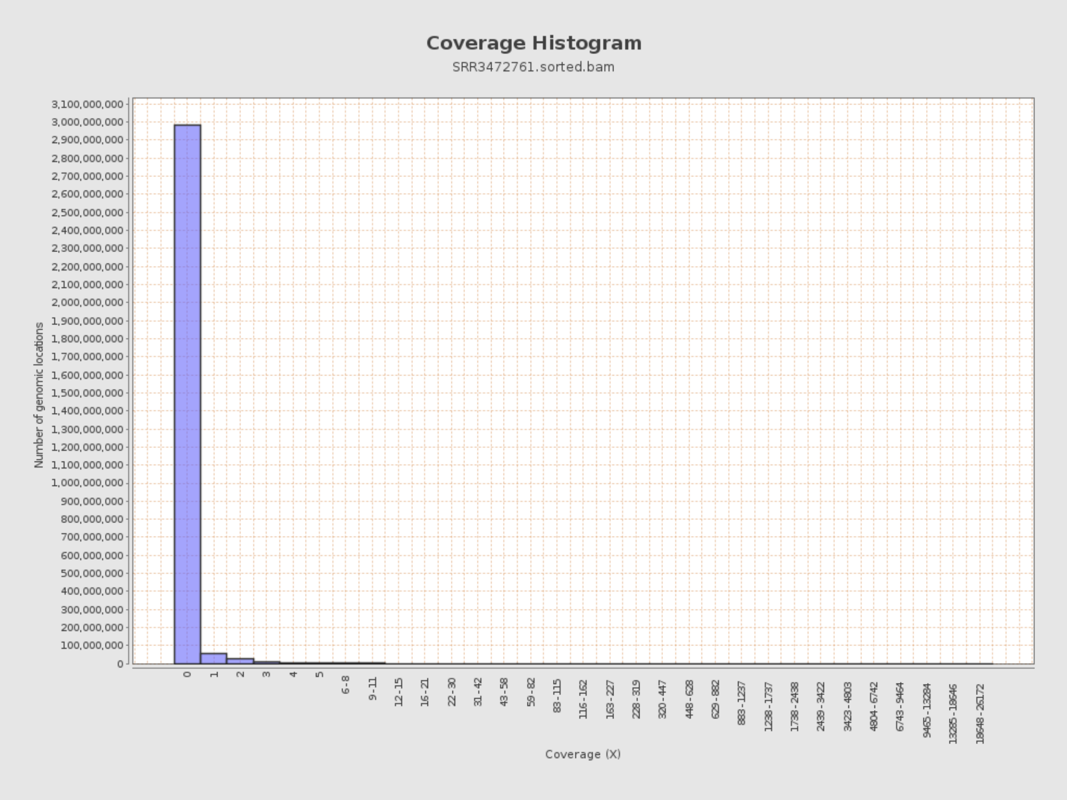
		bases	coverage	deviation
chr1	249250621	73931704	0.2966	20.8451
chr2	243199373	272049827	1.1186	65.1693
chr3	198022430	104010389	0.5252	25.8337
chr4	191154276	33686782	0.1762	14.8176
chr5	180915260	60710695	0.3356	25.8909
chr6	171115067	68952811	0.403	16.3744
chr7	159138663	175655792	1.1038	61.8463
chr8	146364022	56585947	0.3866	29.1211
chr9	141213431	64016104	0.4533	20.5603
chr10	135534747	9832105	0.0725	8.6841
chr11	135006516	94638000	0.701	33.9861
chr12	133851895	152476434	1.1391	53.1293
chr13	115169878	2138323	0.0186	0.5855
chr14	107349540	1925873	0.0179	1.047
chr15	102531392	3696491	0.0361	2.3545
chr16	90354753	8257401	0.0914	6.2238
chr17	81195210	49908516	0.6147	32.2095
chr18	78077248	53066086	0.6797	42.634
chr19	59128983	25368868	0.429	22.0116
chr20	63025520	76802493	1.2186	61.184
chr21	48129895	1739753	0.0361	1.5329
chr22	51304566	1510902	0.0294	1.2458
chrMT	16571	1844	0.1113	0.3891
chrX	155270560	76253369	0.4911	41.9185

chrY	59373566	265346	0.0045	0.2898

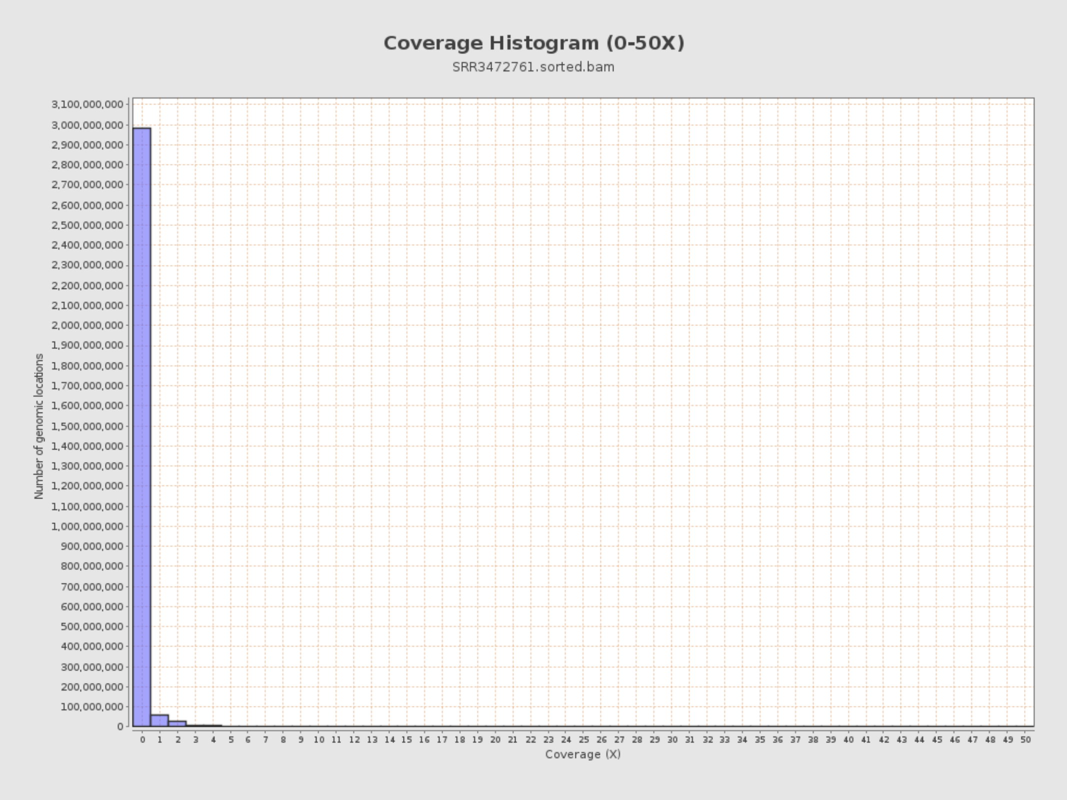
3. Results : Coverage across reference



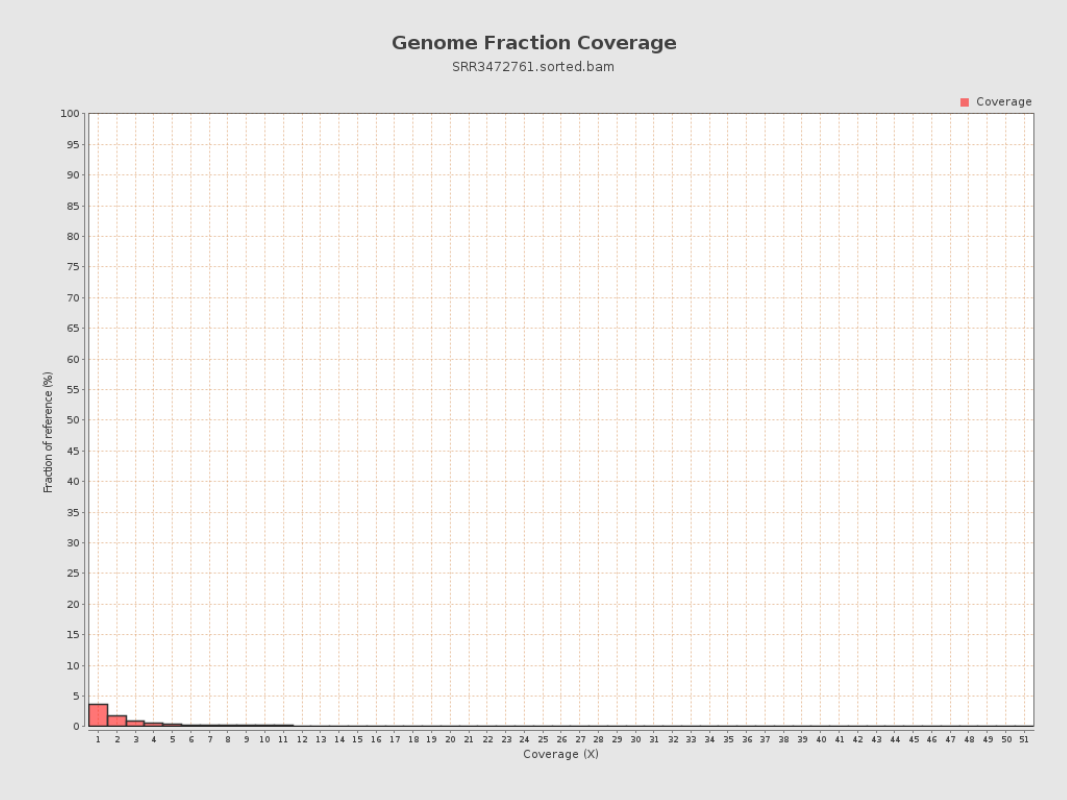
4. Results : Coverage Histogram



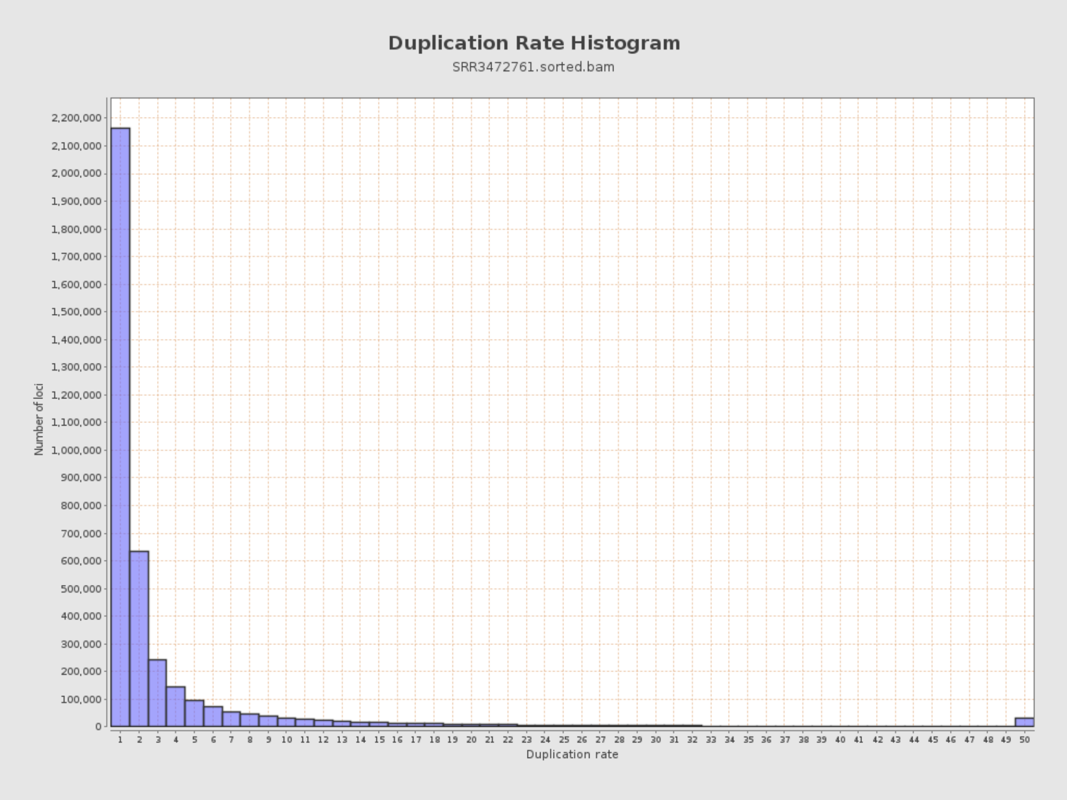
5. Results : Coverage Histogram (0-50X)



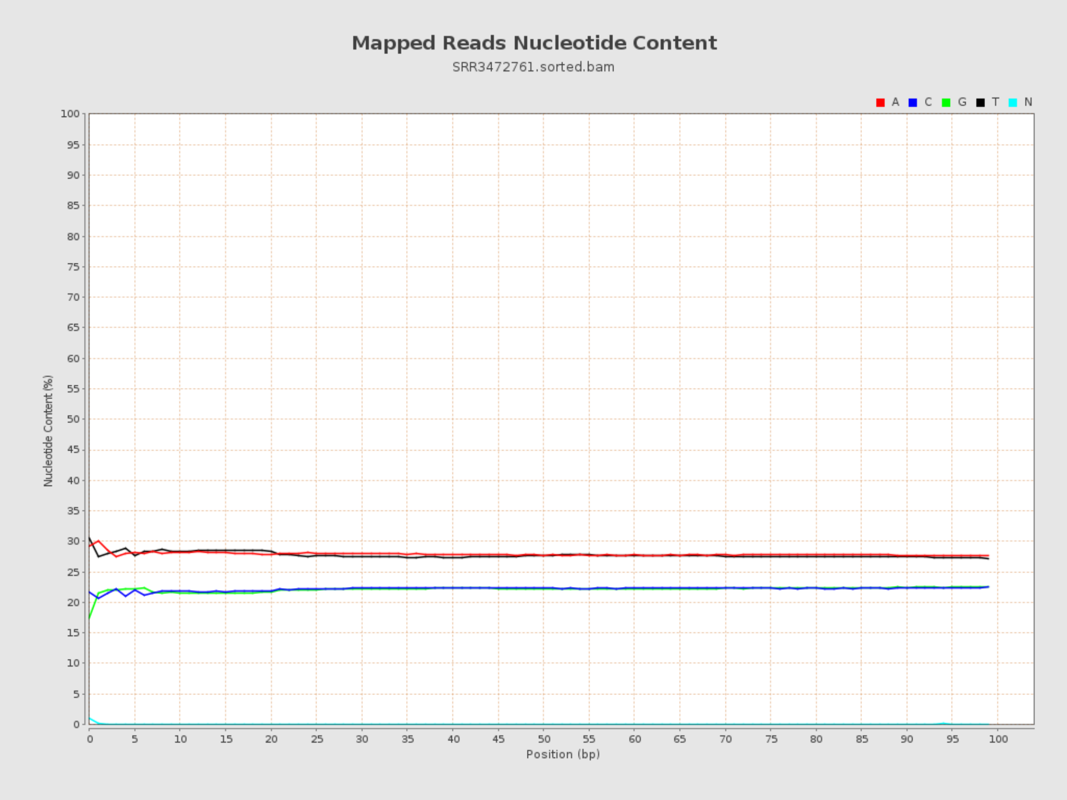
6. Results : Genome Fraction Coverage



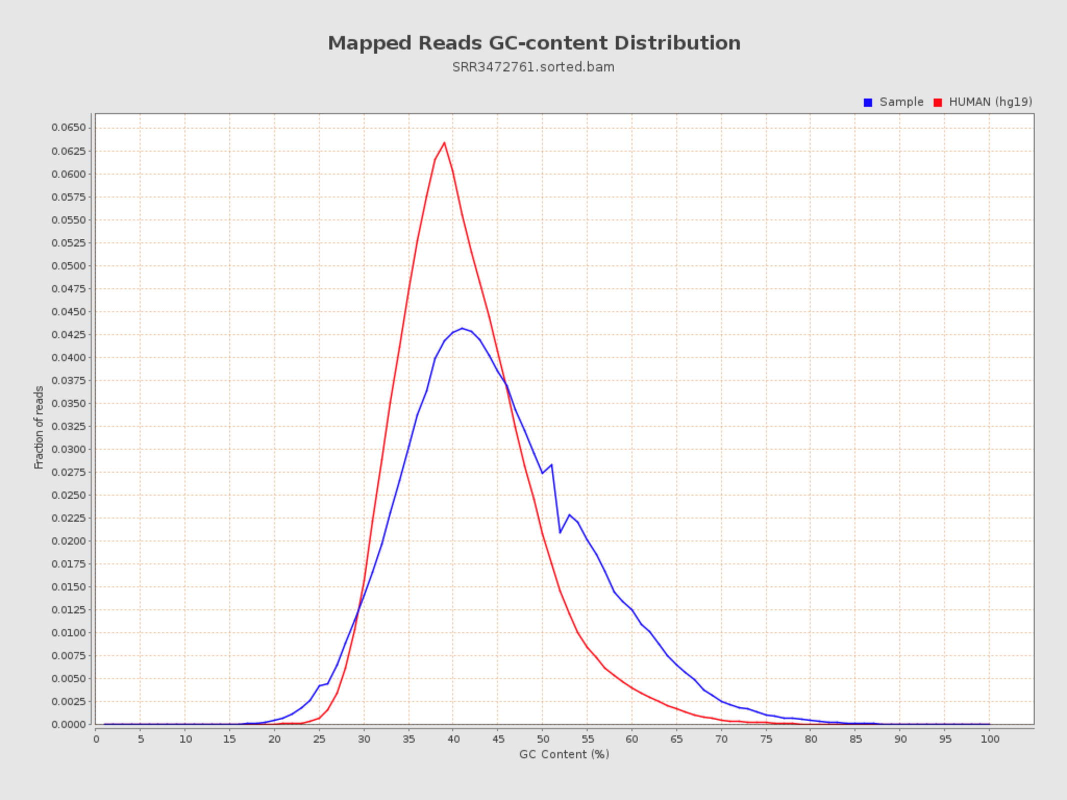
7. Results : Duplication Rate Histogram



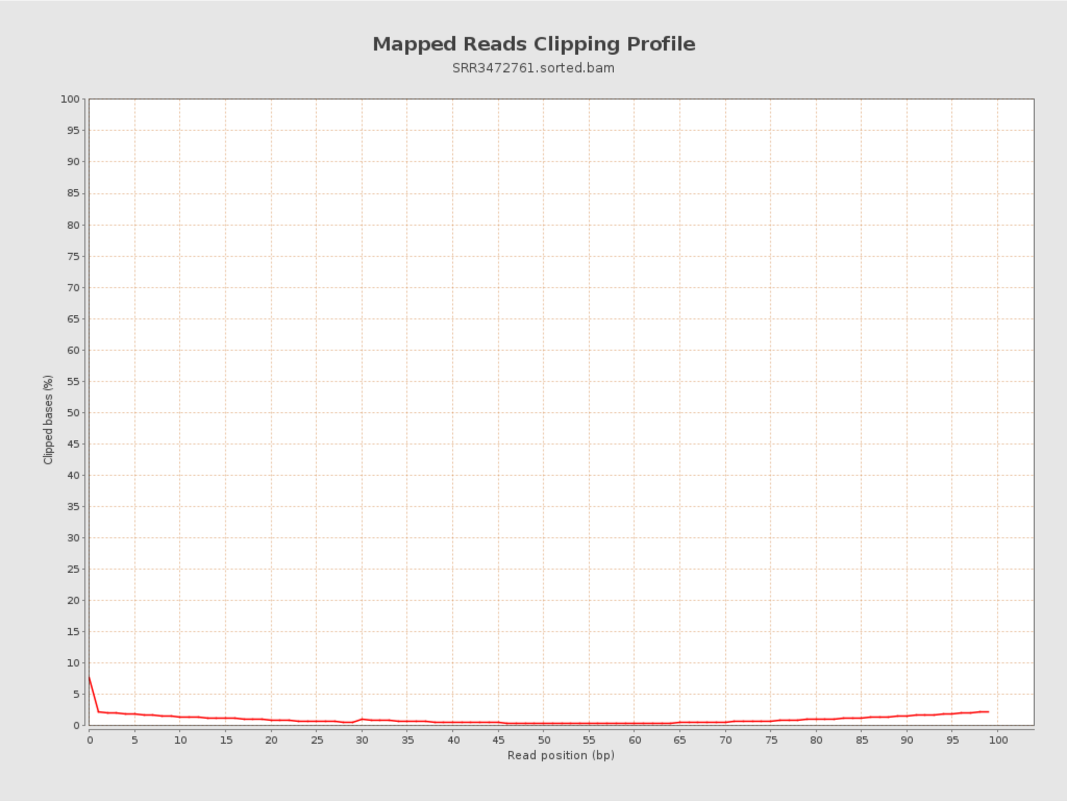
8. Results : Mapped Reads Nucleotide Content



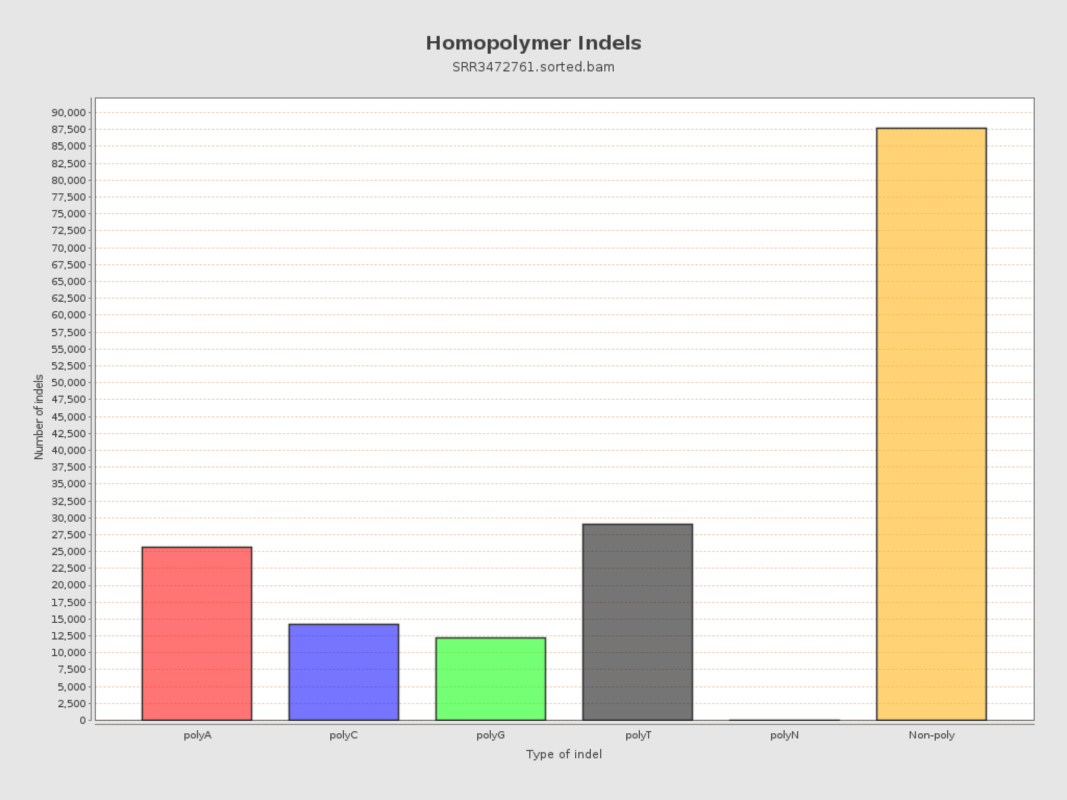
9. Results : Mapped Reads GC-content Distribution



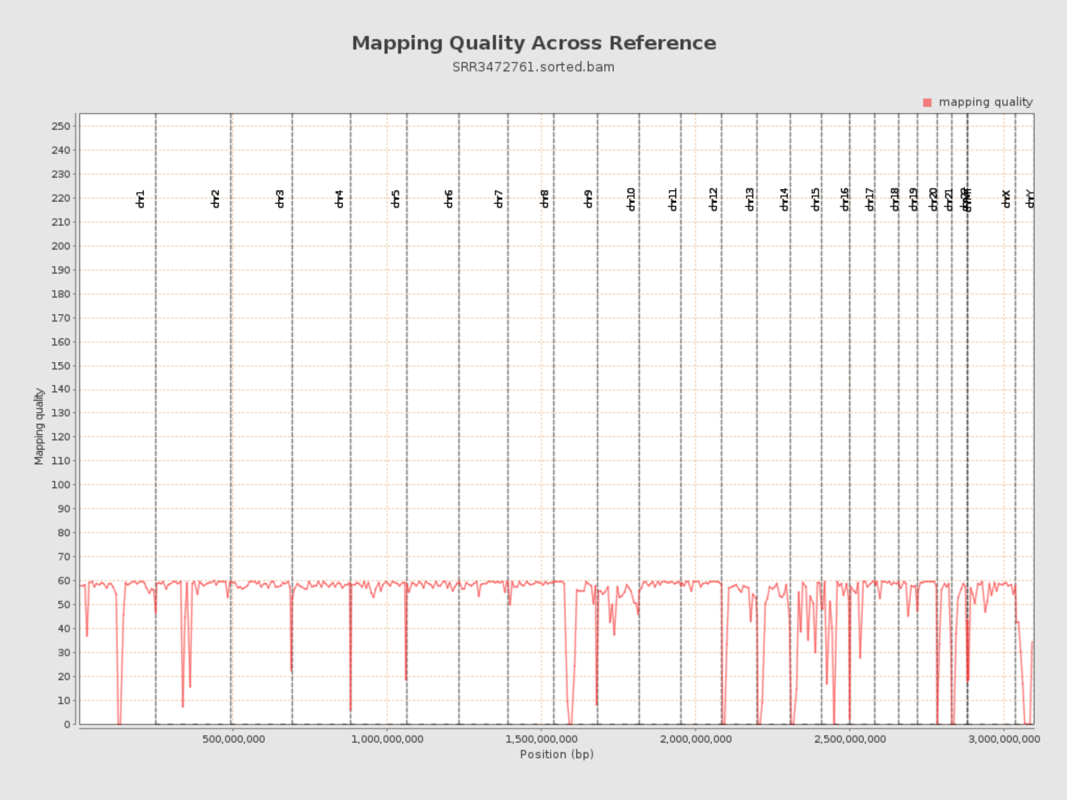
10. Results : Mapped Reads Clipping Profile



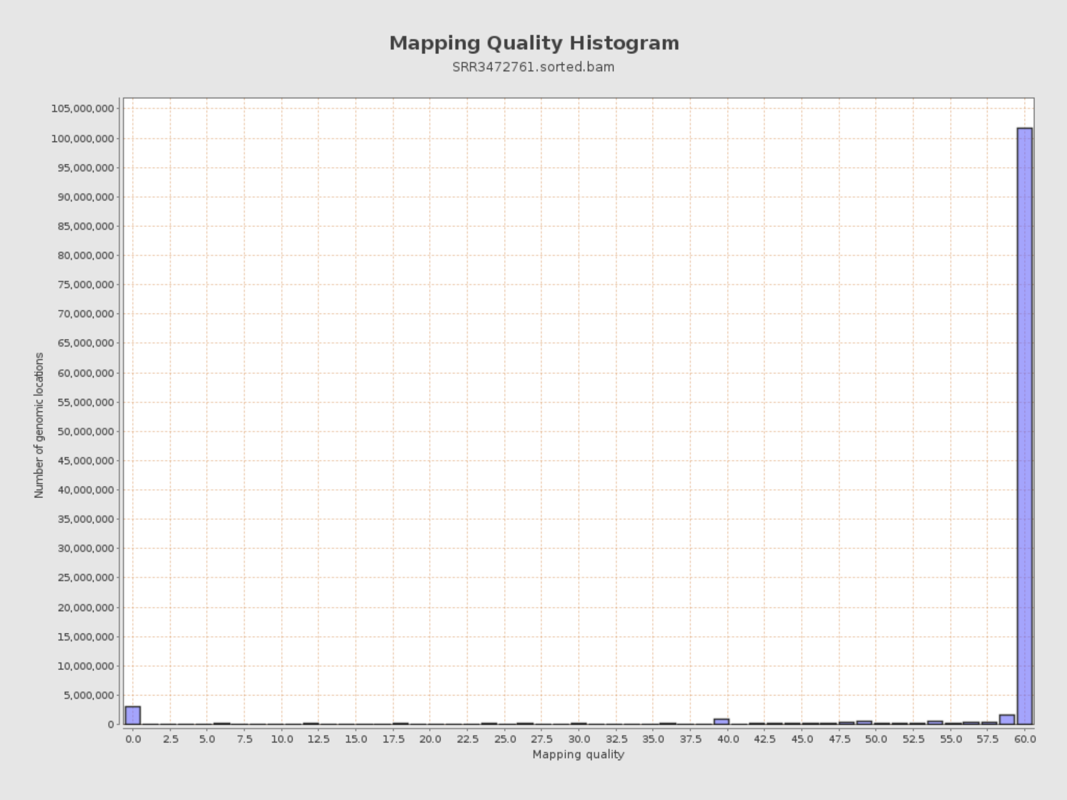
11. Results : Homopolymer Indels



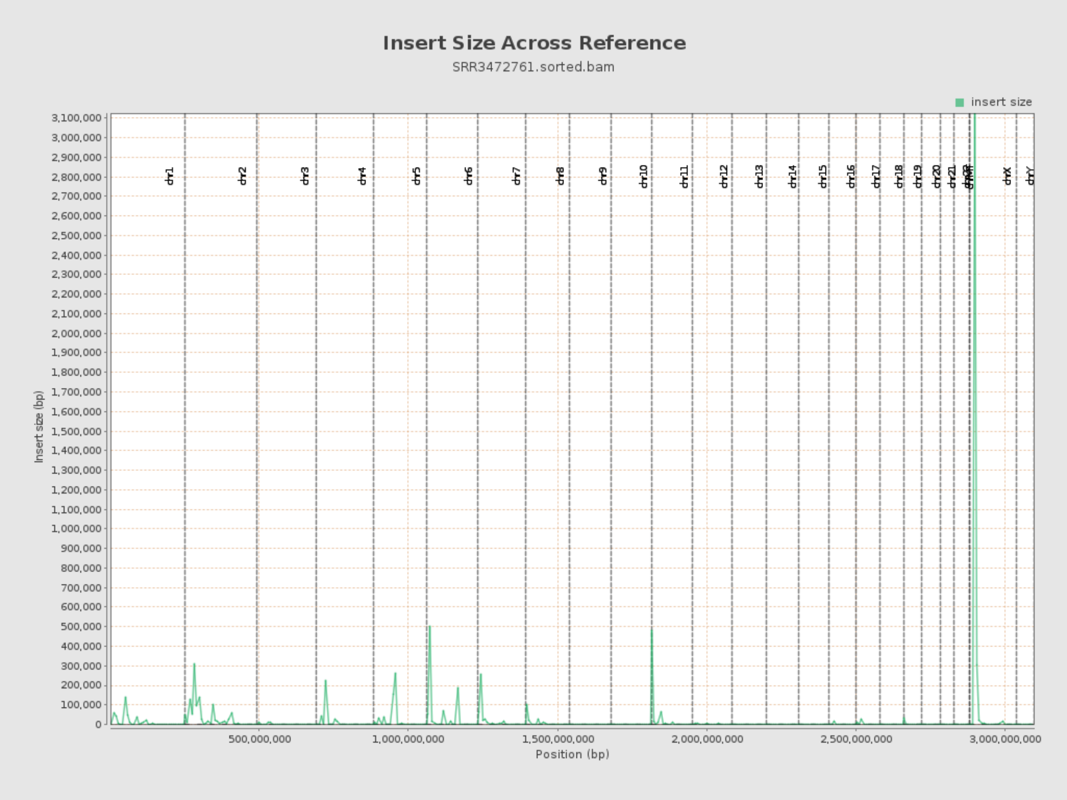
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram