Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 20:13:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472796.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_SRR3472796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472796_1.fastq.gz SRR3472796_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 20:13:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	108,394,740
Mapped reads	107,962,899 / 99.6%
Unmapped reads	431,841 / 0.4%
Mapped paired reads	107,962,899 / 99.6%
Mapped reads, first in pair	54,112,053 / 49.92%
Mapped reads, second in pair	53,850,846 / 49.68%
Mapped reads, both in pair	107,665,106 / 99.33%
Mapped reads, singletons	297,793 / 0.27%
Secondary alignments	0
Supplementary alignments	74,147 / 0.07%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	56,049,156 / 51.71%
Duplication rate	48.2%
Clipped reads	5,700,814 / 5.26%

2.2. ACGT Content

Number/percentage of A's	2,880,636,352 / 26.96%
Number/percentage of C's	2,459,965,719 / 23.02%
Number/percentage of T's	2,926,505,132 / 27.39%
Number/percentage of G's	2,417,784,866 / 22.63%
Number/percentage of N's	1,150,444 / 0.01%

GC Percentage	45.65%

2.3. Coverage

Mean	3.4523
Standard Deviation	25.2876

2.4. Mapping Quality

Mean Mapping Quality	53.53

2.5. Insert size

Mean	12,648.58
Standard Deviation	1,128,480.02
P25/Median/P75	169 / 223 / 289

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	41,925,193
Insertions	420,373
Mapped reads with at least one insertion	0.38%
Deletions	491,875
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.68%

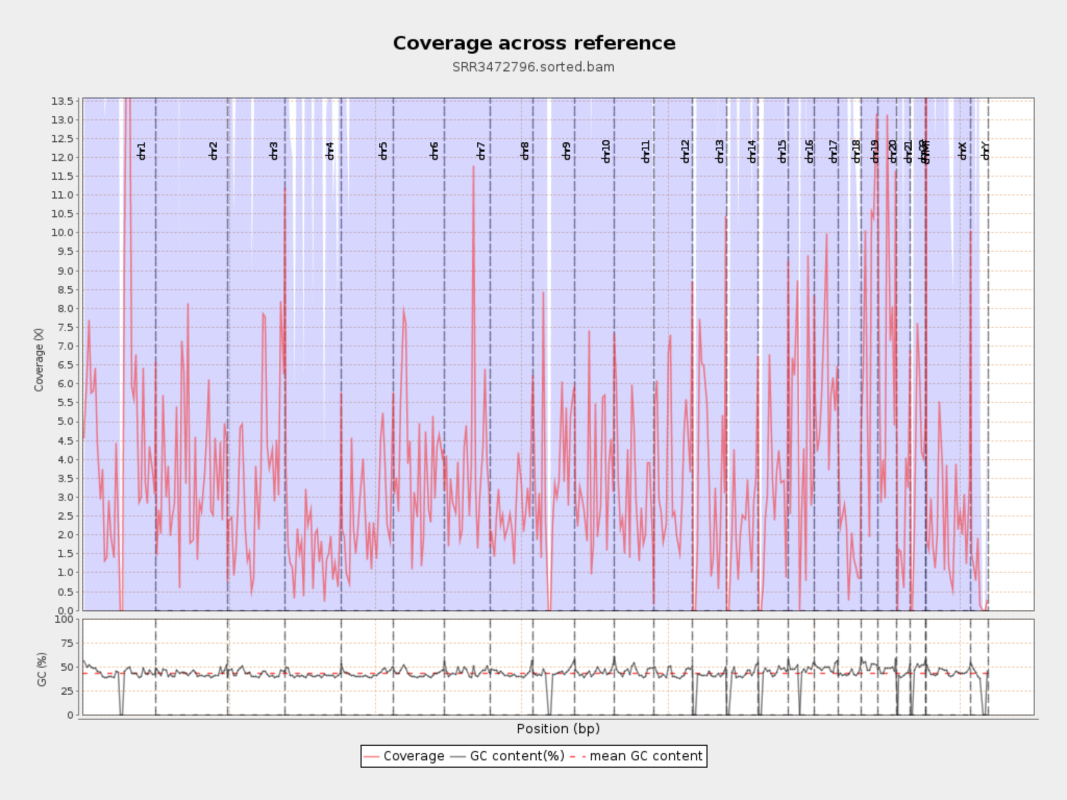
2.7. Chromosome stats

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

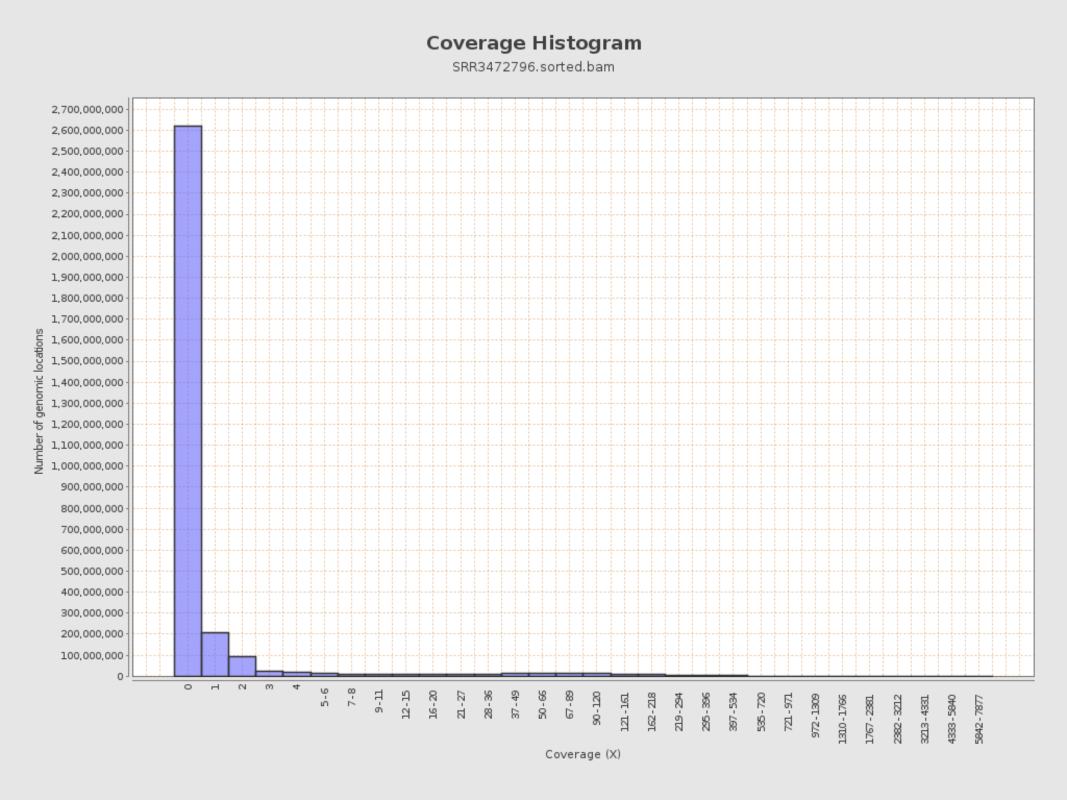
		bases	coverage	deviation
chr1	249250621	1203465659	4.8283	33.5822
chr2	243199373	878977071	3.6142	26.7837
chr3	198022430	708982744	3.5803	26.743
chr4	191154276	304303421	1.5919	13.1444
chr5	180915260	477496831	2.6393	19.7953
chr6	171115067	658774211	3.8499	27.6426
chr7	159138663	599264205	3.7657	29.7475
chr8	146364022	385020731	2.6306	20.7557
chr9	141213431	485601008	3.4388	25.4351
chr10	135534747	458985061	3.3865	24.3809
chr11	135006516	426458624	3.1588	19.481
chr12	133851895	527760251	3.9429	23.7913
chr13	115169878	393627504	3.4178	31.7613
chr14	107349540	229491946	2.1378	15.5274
chr15	102531392	275838577	2.6903	18.1164
chr16	90354753	416411789	4.6086	29.6468
chr17	81195210	481663815	5.9322	28.5216
chr18	78077248	139686896	1.7891	15.2742
chr19	59128983	483760291	8.1814	35.603
chr20	63025520	412958462	6.5522	39.8277
chr21	48129895	119697364	2.487	22.3817
chr22	51304566	196931278	3.8385	23.9019
chrMT	16571	458241	27.6532	80.5258
chrX	155270560	380684221	2.4517	20.3952

chrY	59373566	40941729	0.6896	11.1317

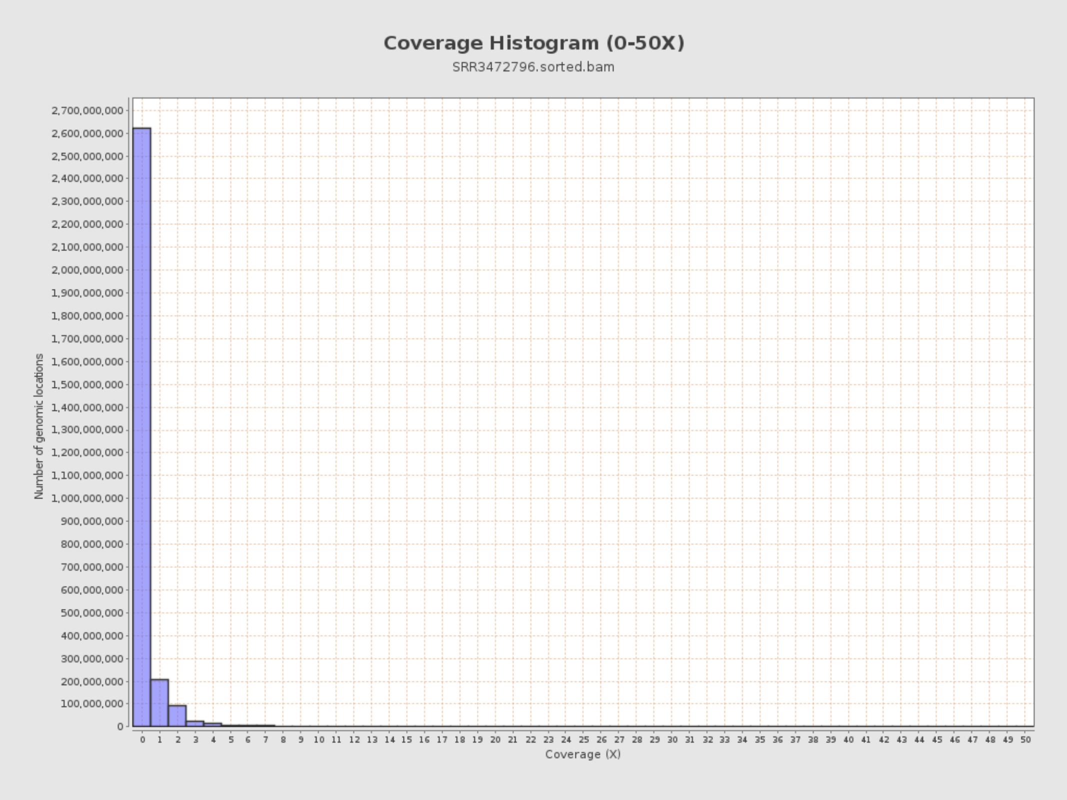
3. Results : Coverage across reference



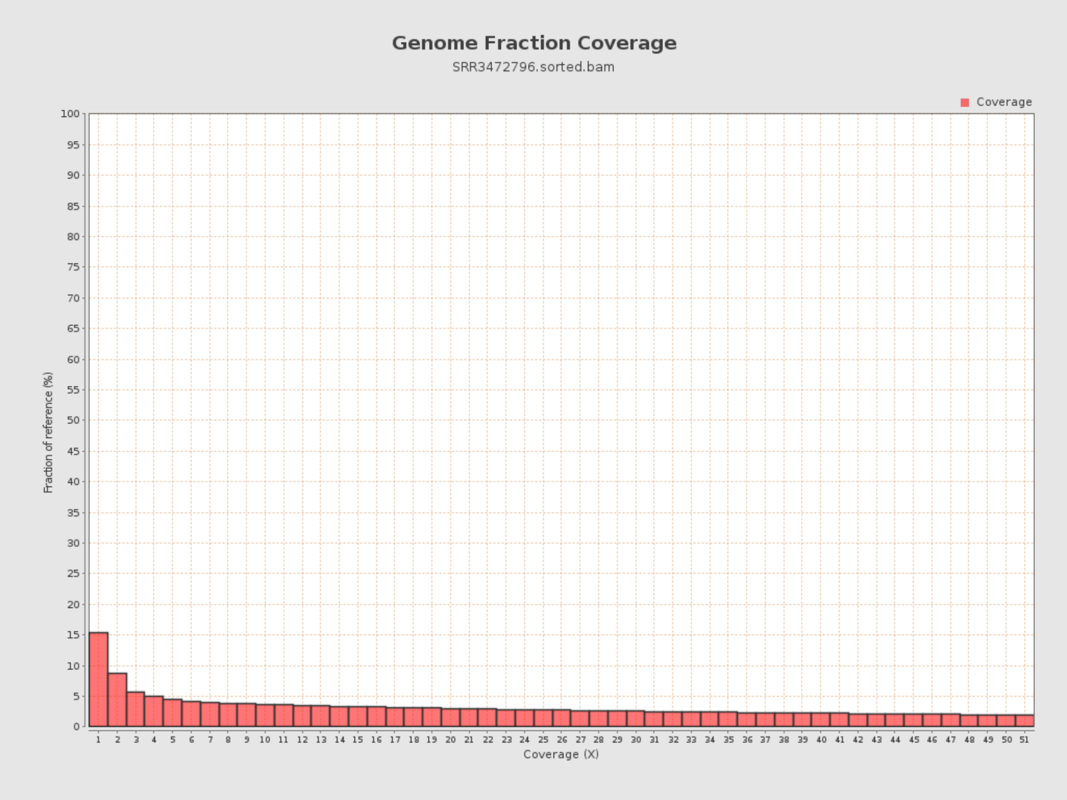
4. Results : Coverage Histogram



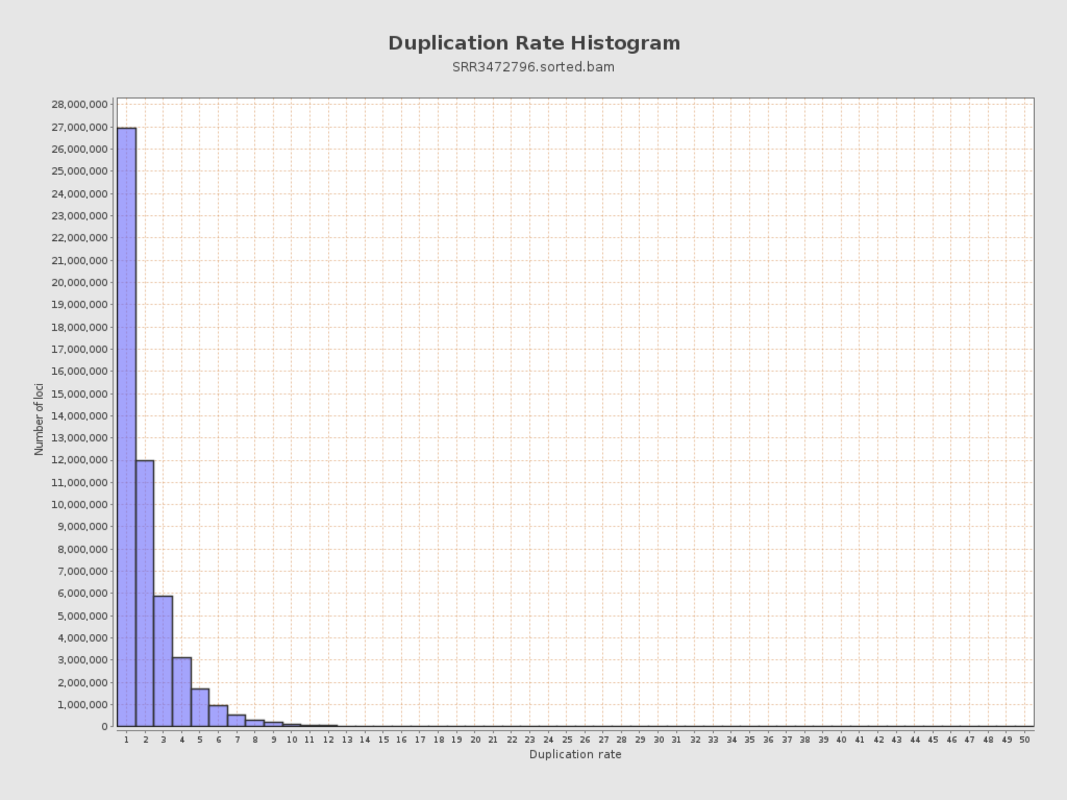
5. Results : Coverage Histogram (0-50X)



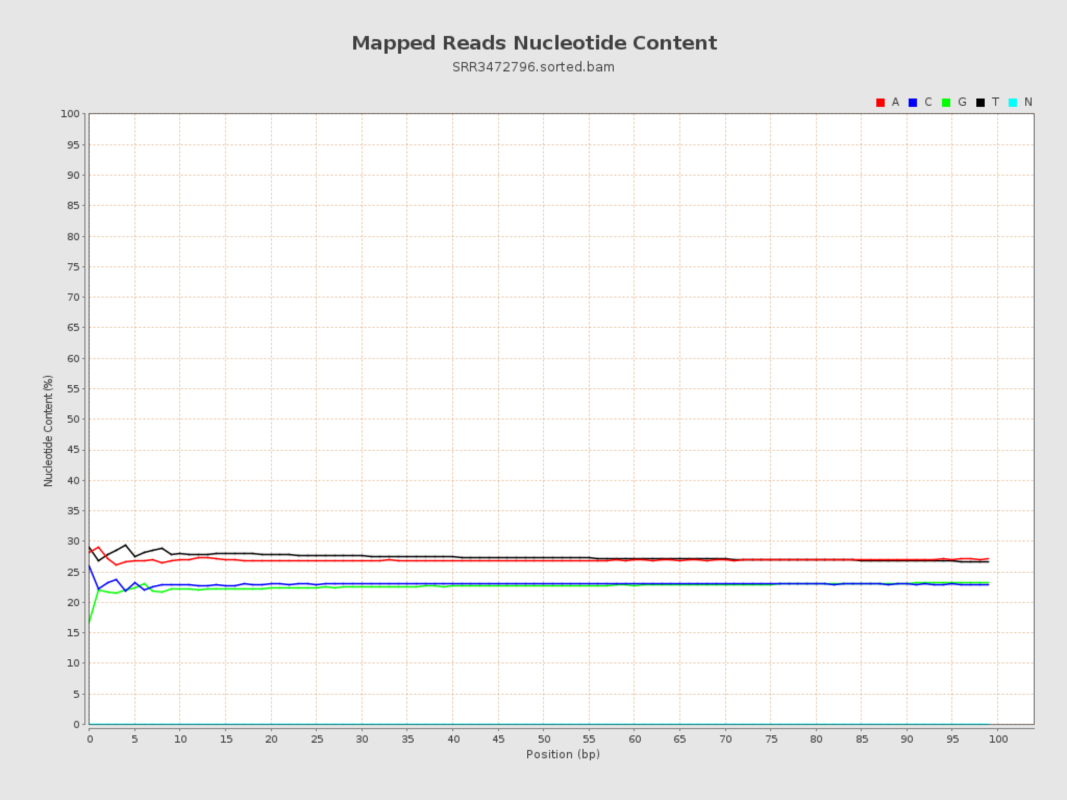
6. Results : Genome Fraction Coverage



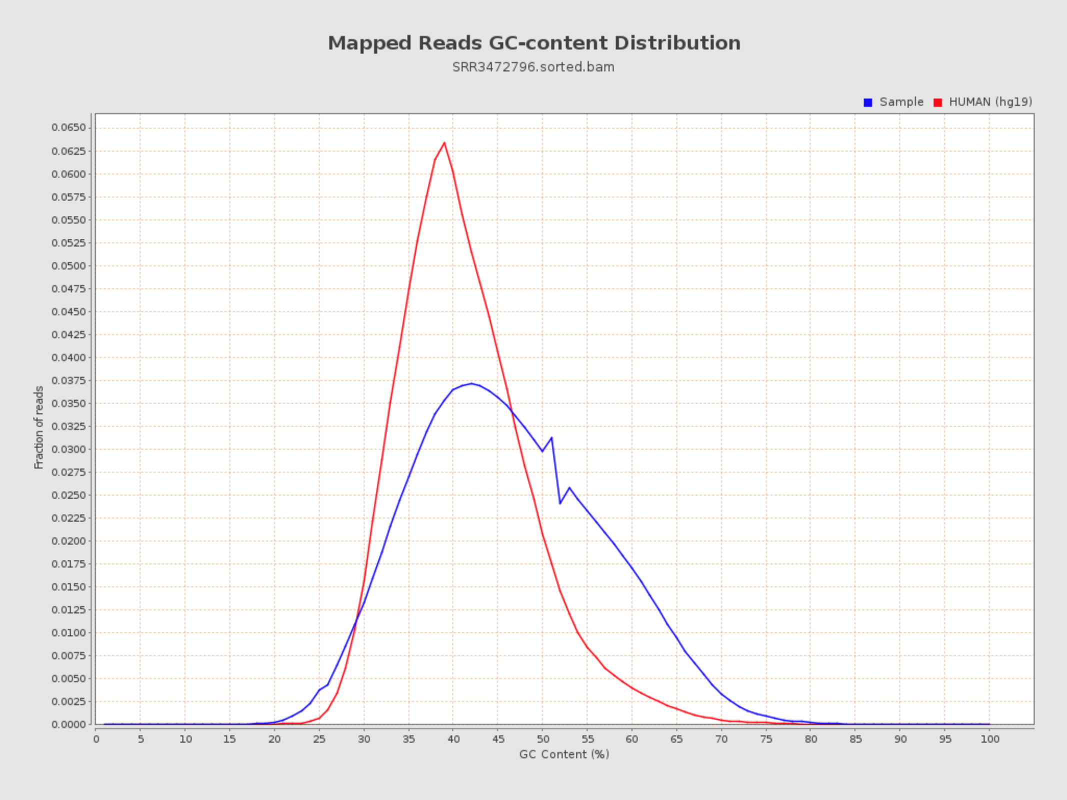
7. Results : Duplication Rate Histogram



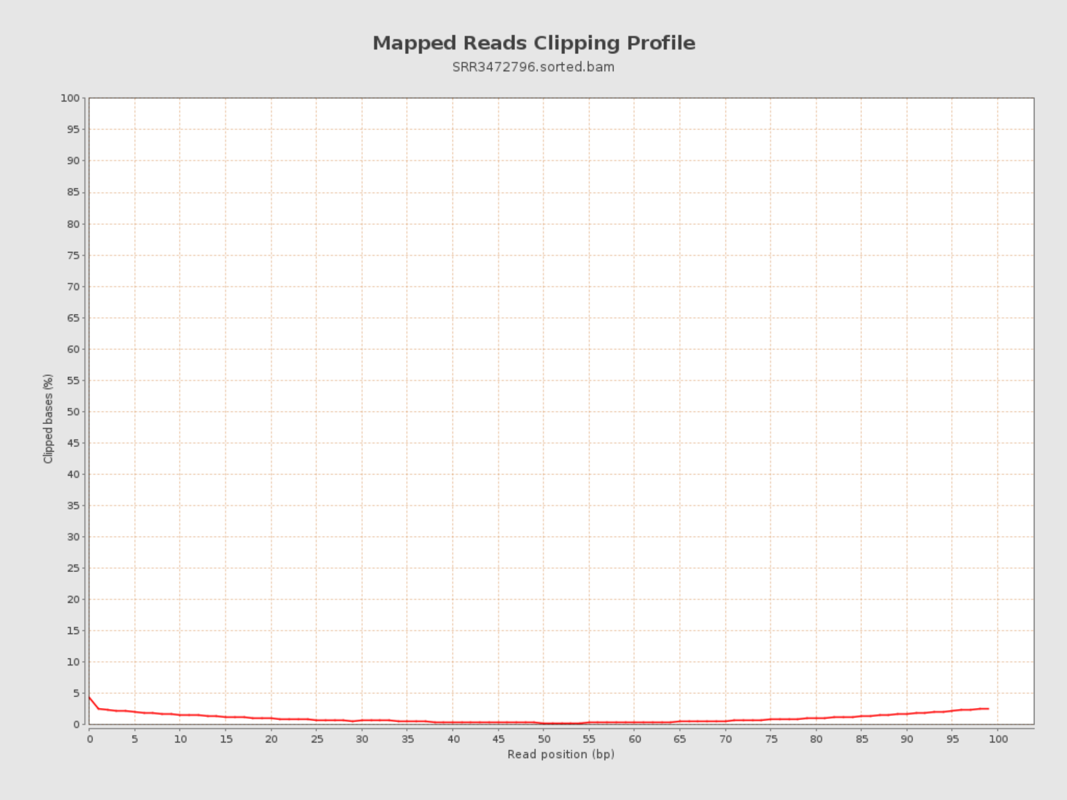
8. Results : Mapped Reads Nucleotide Content



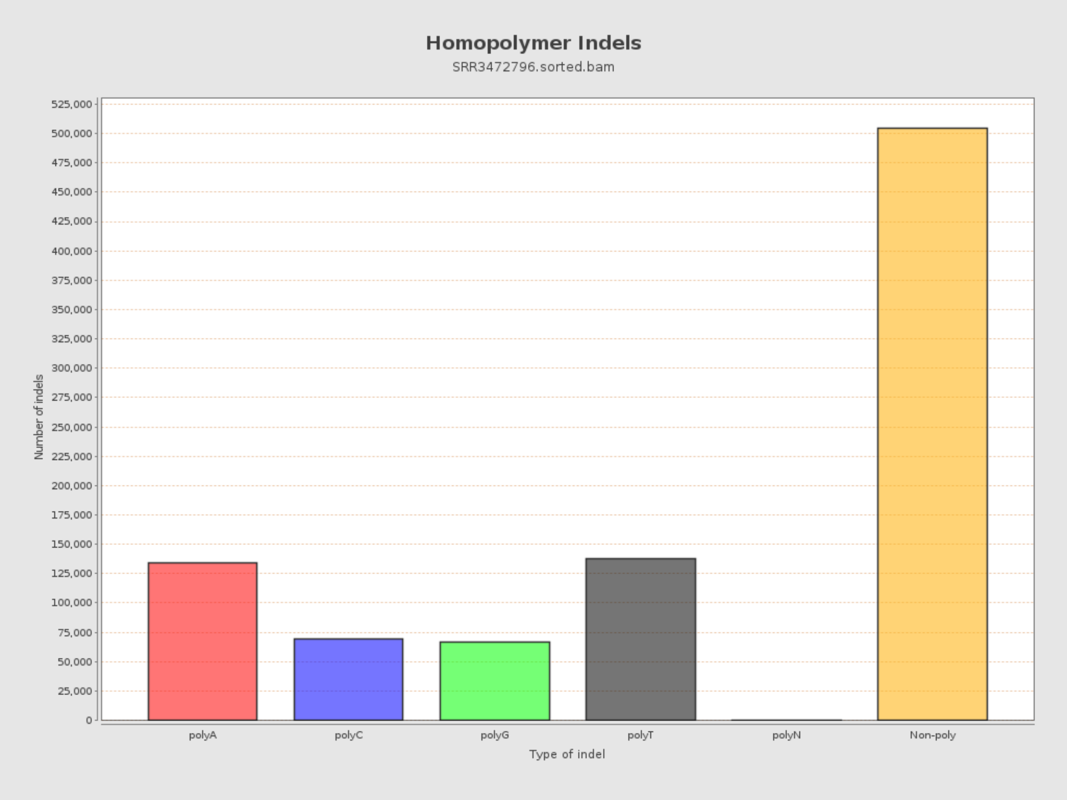
9. Results : Mapped Reads GC-content Distribution



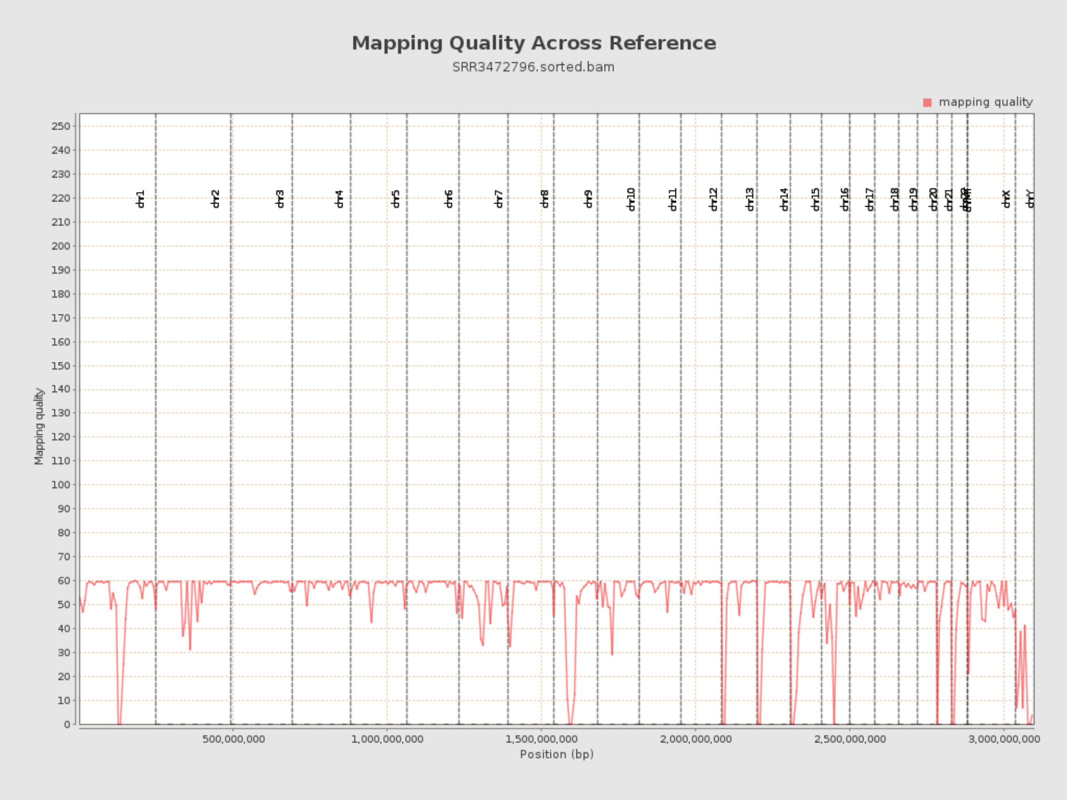
10. Results : Mapped Reads Clipping Profile



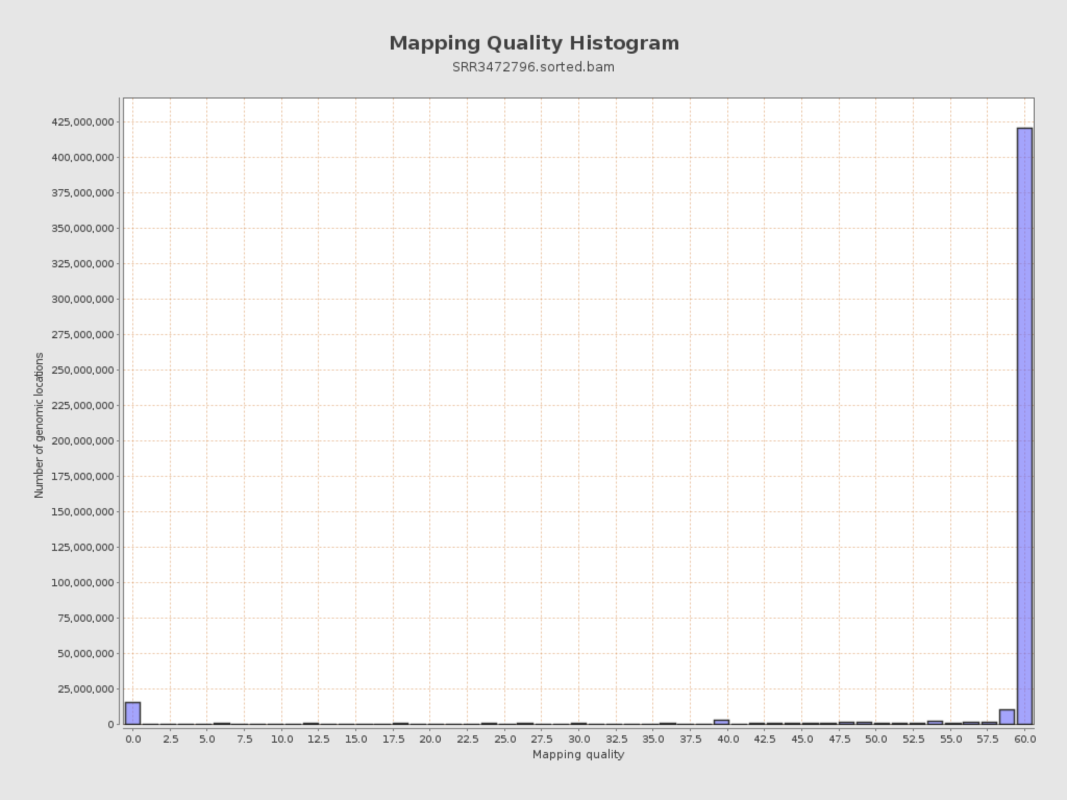
11. Results : Homopolymer Indels



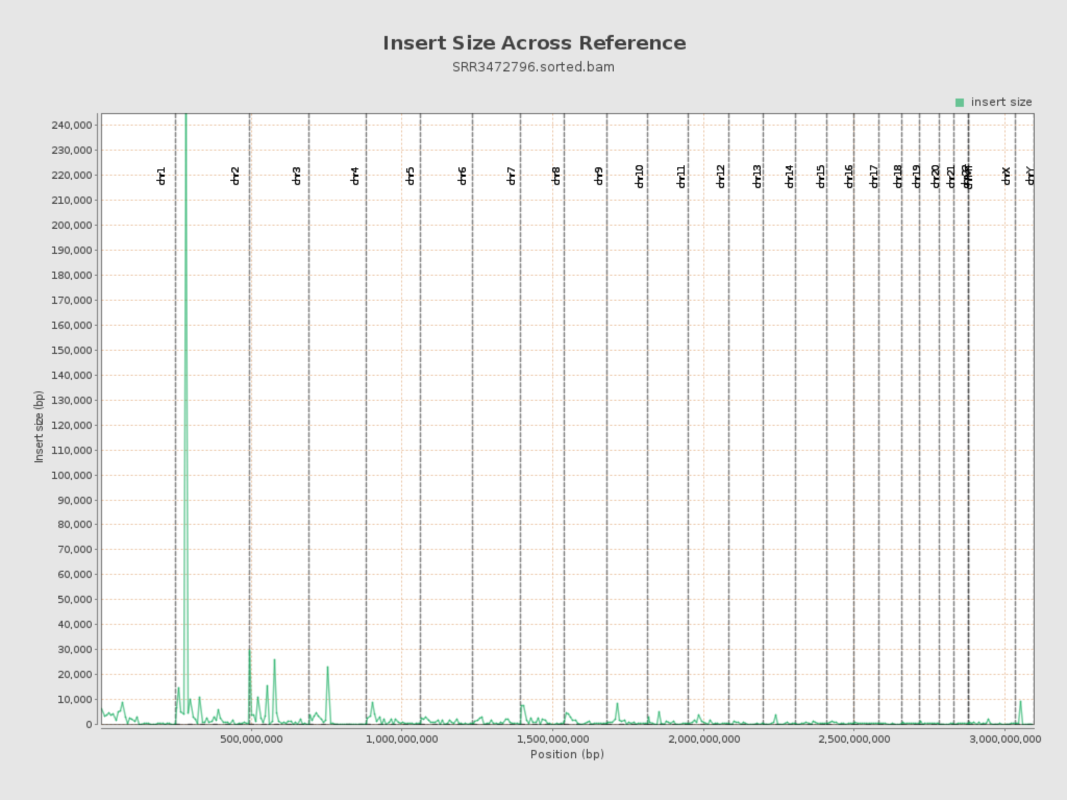
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram