Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 10:09:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472611.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_SRR3472611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472611_1.fastq.gz SRR3472611_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 10:09:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,197,354
Mapped reads	18,062,336 / 99.26%
Unmapped reads	135,018 / 0.74%
Mapped paired reads	18,062,336 / 99.26%
Mapped reads, first in pair	9,049,743 / 49.73%
Mapped reads, second in pair	9,012,593 / 49.53%
Mapped reads, both in pair	17,974,808 / 98.78%
Mapped reads, singletons	87,528 / 0.48%
Secondary alignments	0
Supplementary alignments	85,397 / 0.47%
Read min/max/mean length	30 / 101 / 99.72
Duplicated reads (estimated)	12,406,334 / 68.18%
Duplication rate	49.86%
Clipped reads	1,236,262 / 6.79%

2.2. ACGT Content

Number/percentage of A's	467,029,495 / 26.28%
Number/percentage of C's	423,799,567 / 23.84%
Number/percentage of T's	467,176,812 / 26.29%
Number/percentage of G's	418,987,200 / 23.57%
Number/percentage of N's	334,320 / 0.02%

GC Percentage	47.42%

2.3. Coverage

Mean	0.5742
Standard Deviation	22.8474

2.4. Mapping Quality

Mean Mapping Quality	54.68

2.5. Insert size

Mean	17,516.89
Standard Deviation	1,273,590.12
P25/Median/P75	155 / 214 / 284

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	10,775,207
Insertions	110,503
Mapped reads with at least one insertion	0.6%
Deletions	94,342
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.19%

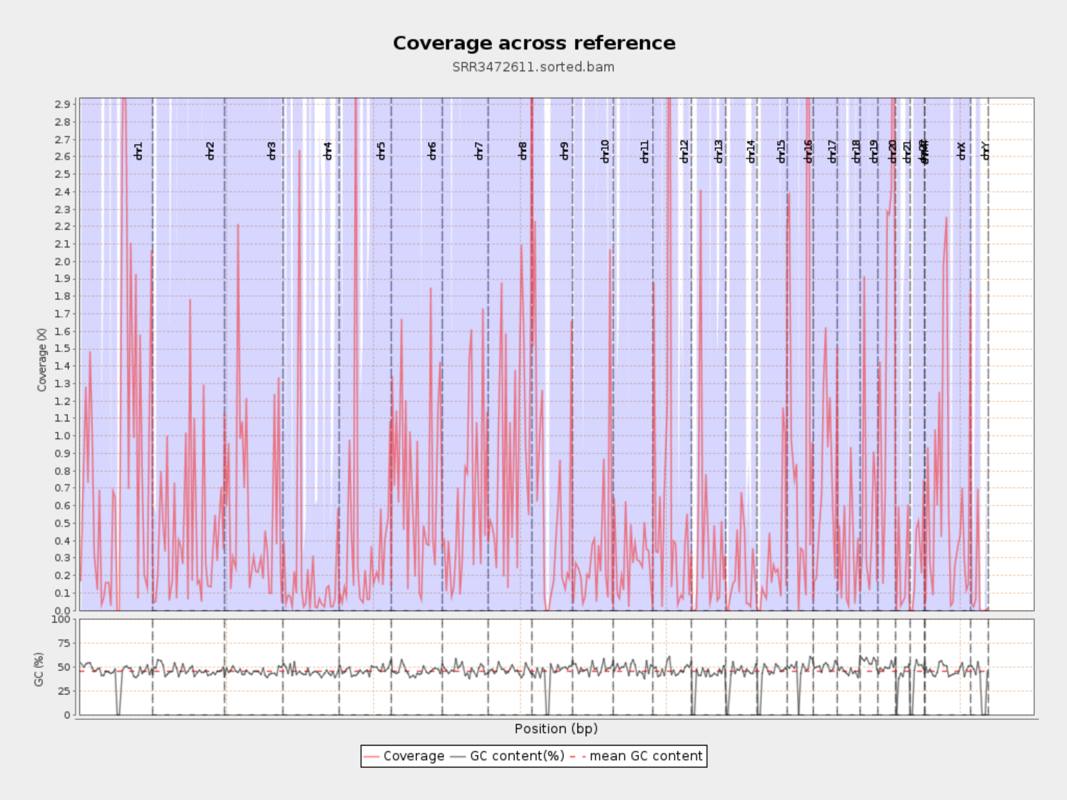
2.7. Chromosome stats

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

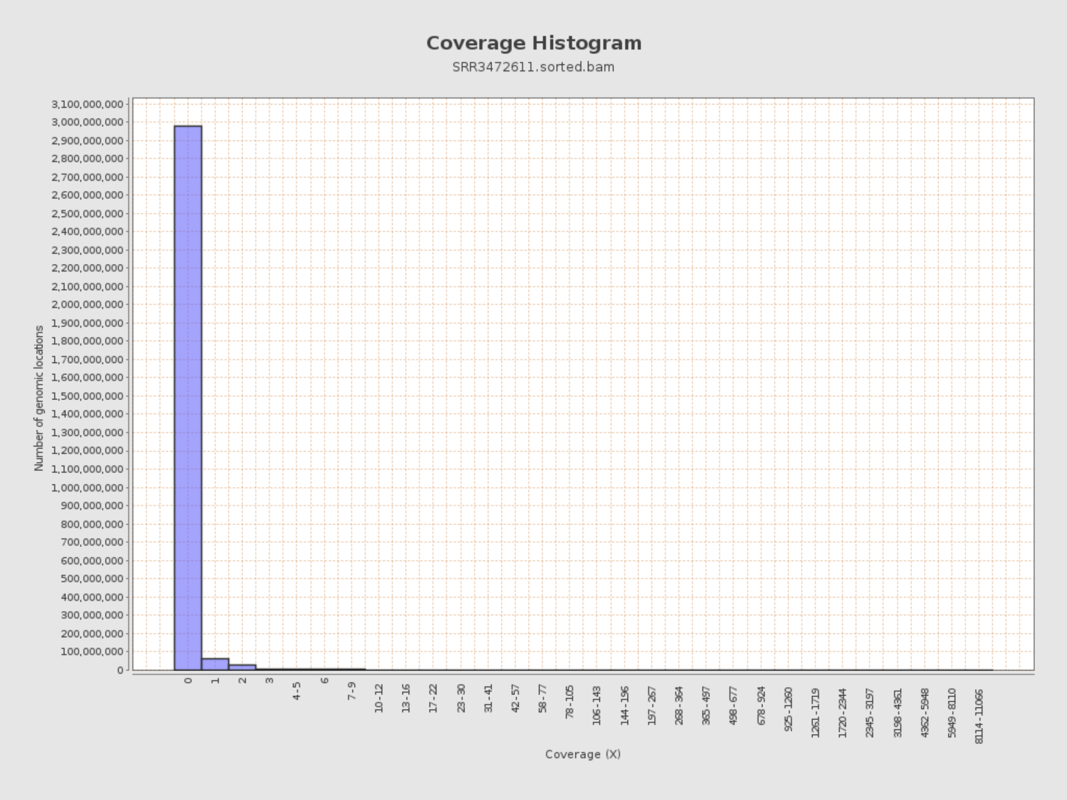
		bases	coverage	deviation
chr1	249250621	223285377	0.8958	27.9448
chr2	243199373	108361609	0.4456	20.1219
chr3	198022430	113173365	0.5715	20.6145
chr4	191154276	41257891	0.2158	19.1856
chr5	180915260	75725830	0.4186	17.2364
chr6	171115067	127819445	0.747	27.397
chr7	159138663	99804165	0.6272	21.8686
chr8	146364022	136366364	0.9317	26.7528
chr9	141213431	92321663	0.6538	18.6791
chr10	135534747	46140784	0.3404	22.8149
chr11	135006516	39697429	0.294	10.6757
chr12	133851895	93154602	0.696	25.8167
chr13	115169878	46583691	0.4045	16.8249
chr14	107349540	21186516	0.1974	11.0094
chr15	102531392	30403691	0.2965	10.4251
chr16	90354753	112571432	1.2459	38.3469
chr17	81195210	62977409	0.7756	19.6014
chr18	78077248	25994086	0.3329	16.9898
chr19	59128983	36489179	0.6171	15.4529
chr20	63025520	114508723	1.8169	55.7155
chr21	48129895	10899531	0.2265	12.3469
chr22	51304566	15983619	0.3115	11.2441
chrMT	16571	1596	0.0963	0.3731
chrX	155270560	96527613	0.6217	25.8425

chrY	59373566	6345329	0.1069	12.9385

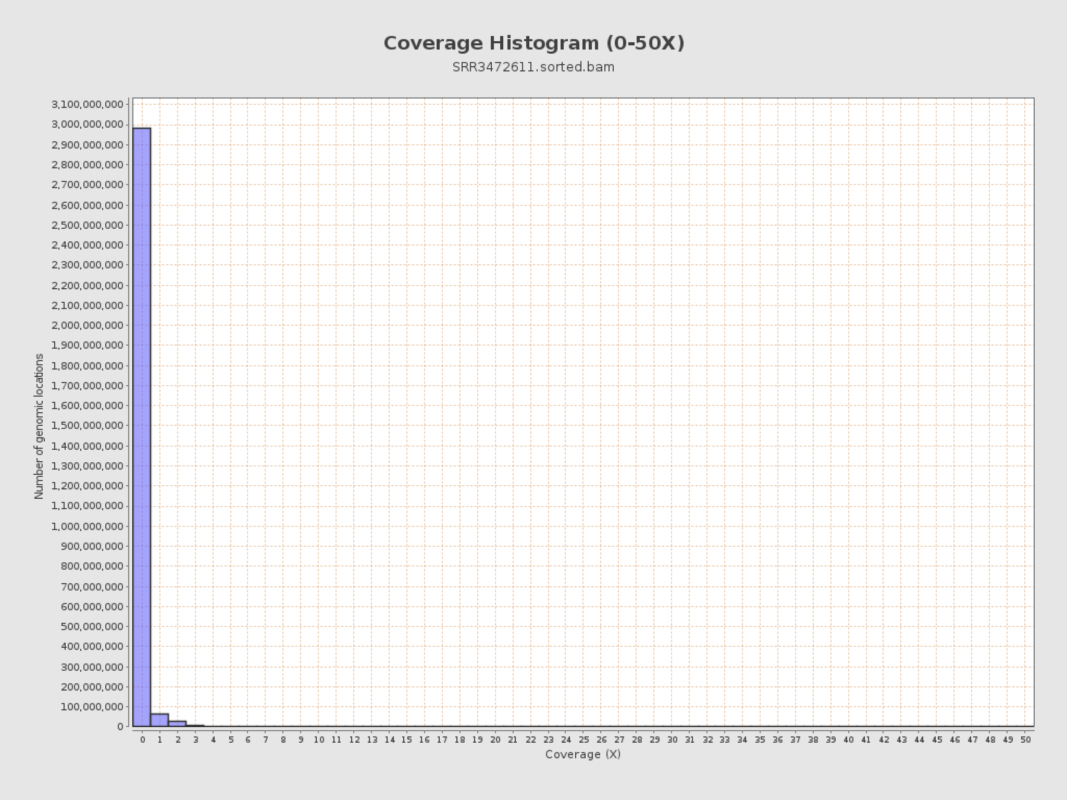
3. Results : Coverage across reference



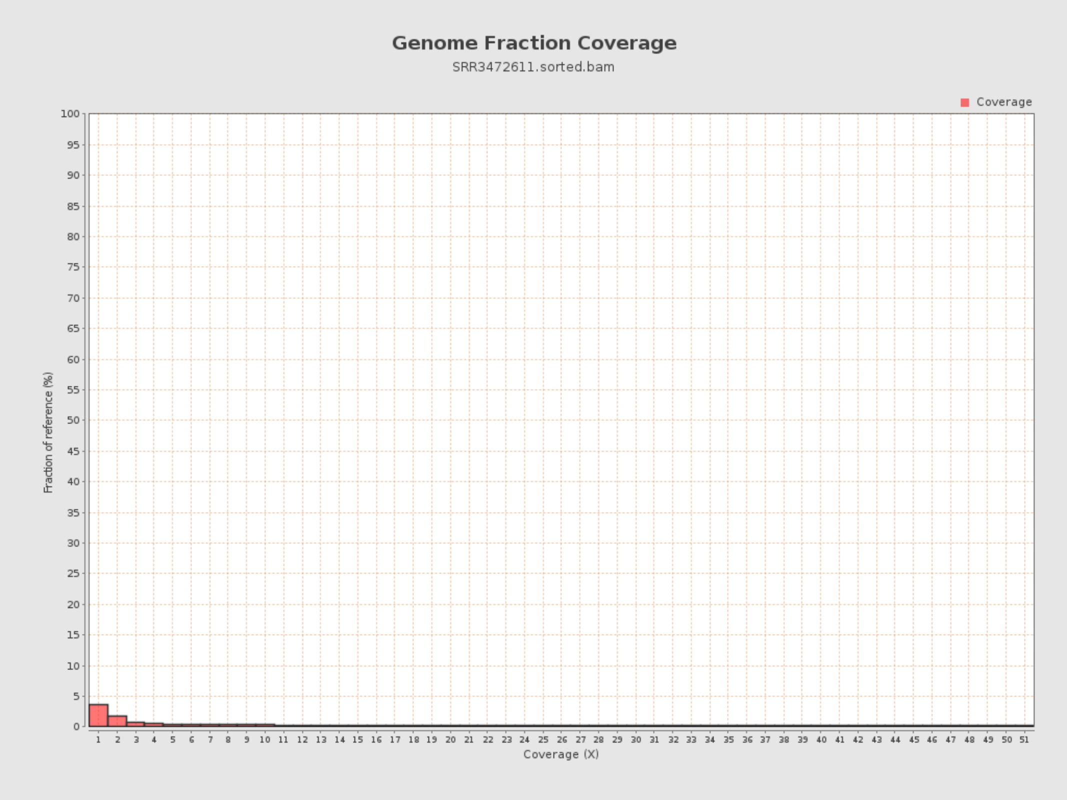
4. Results : Coverage Histogram



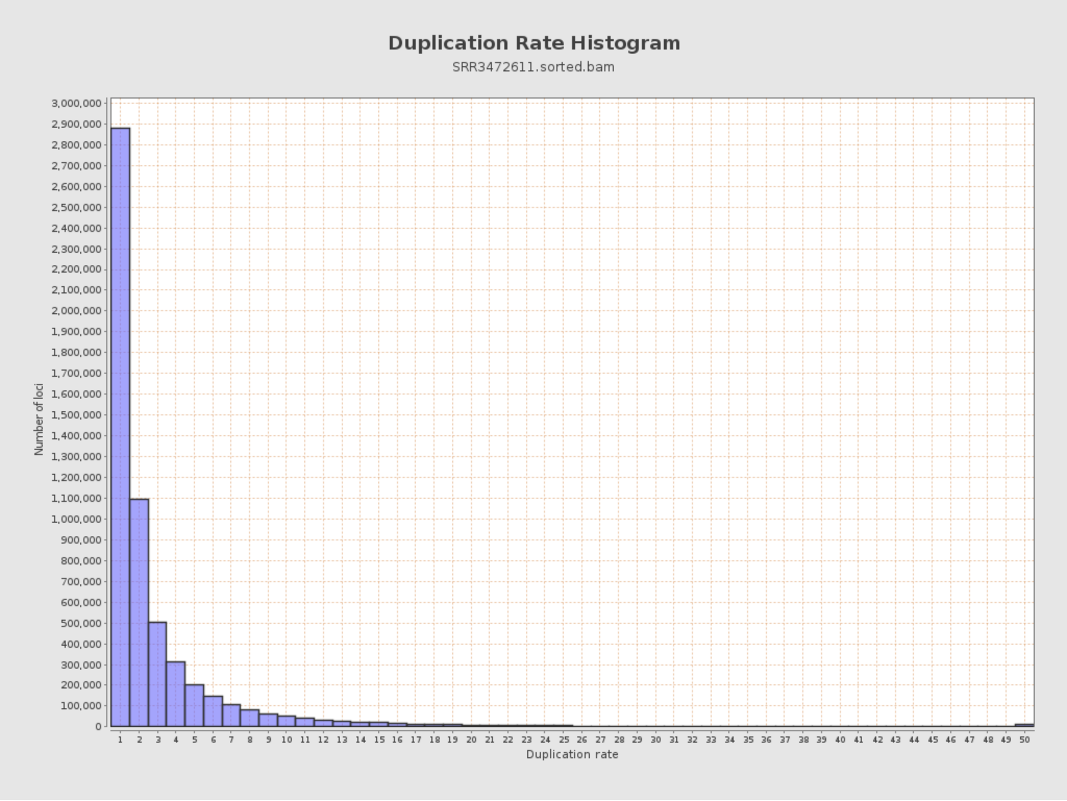
5. Results : Coverage Histogram (0-50X)



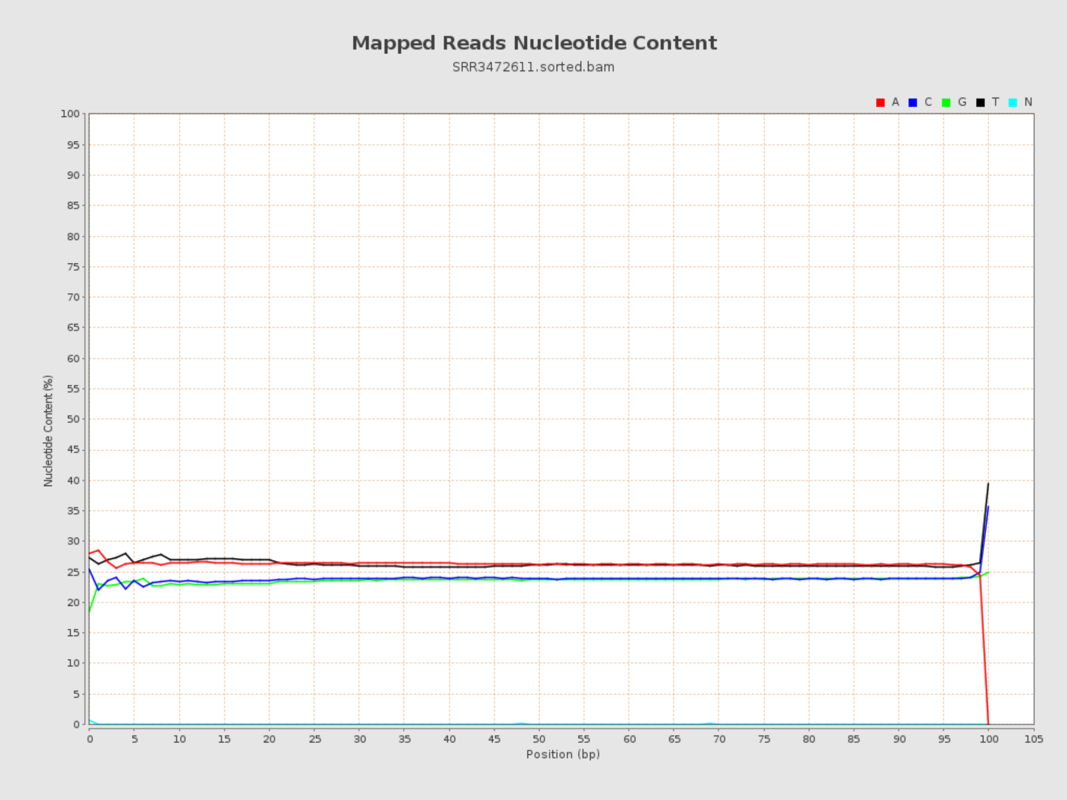
6. Results : Genome Fraction Coverage



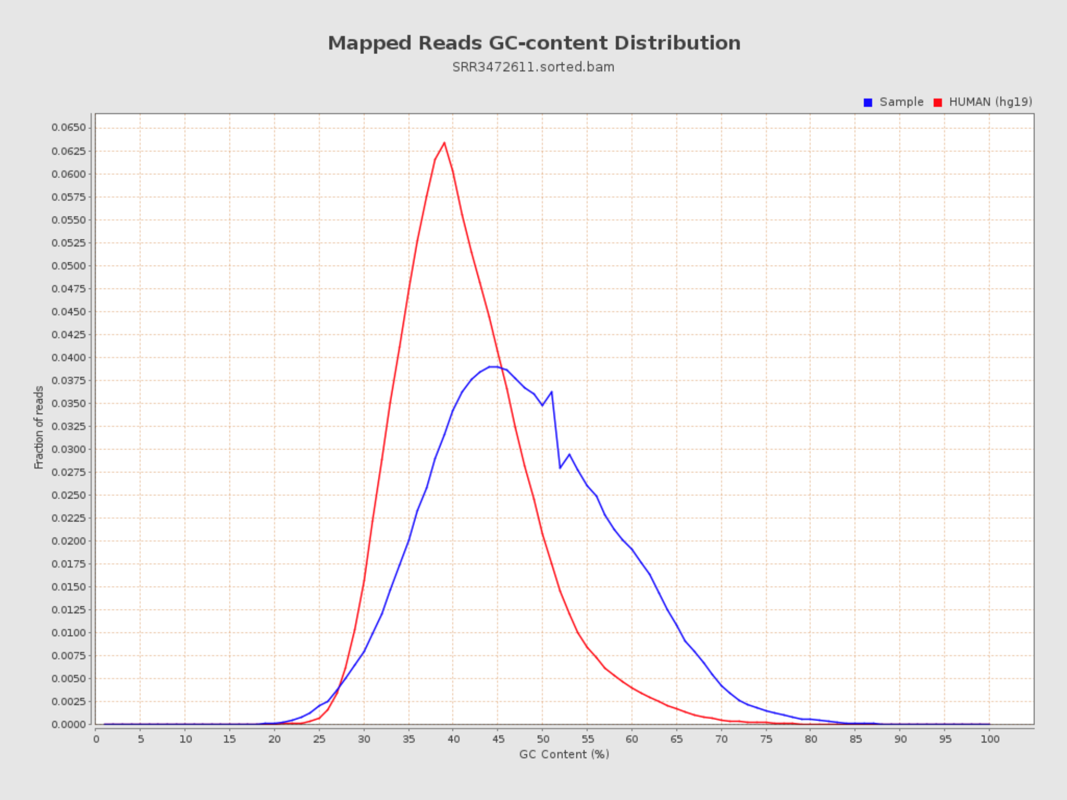
7. Results : Duplication Rate Histogram



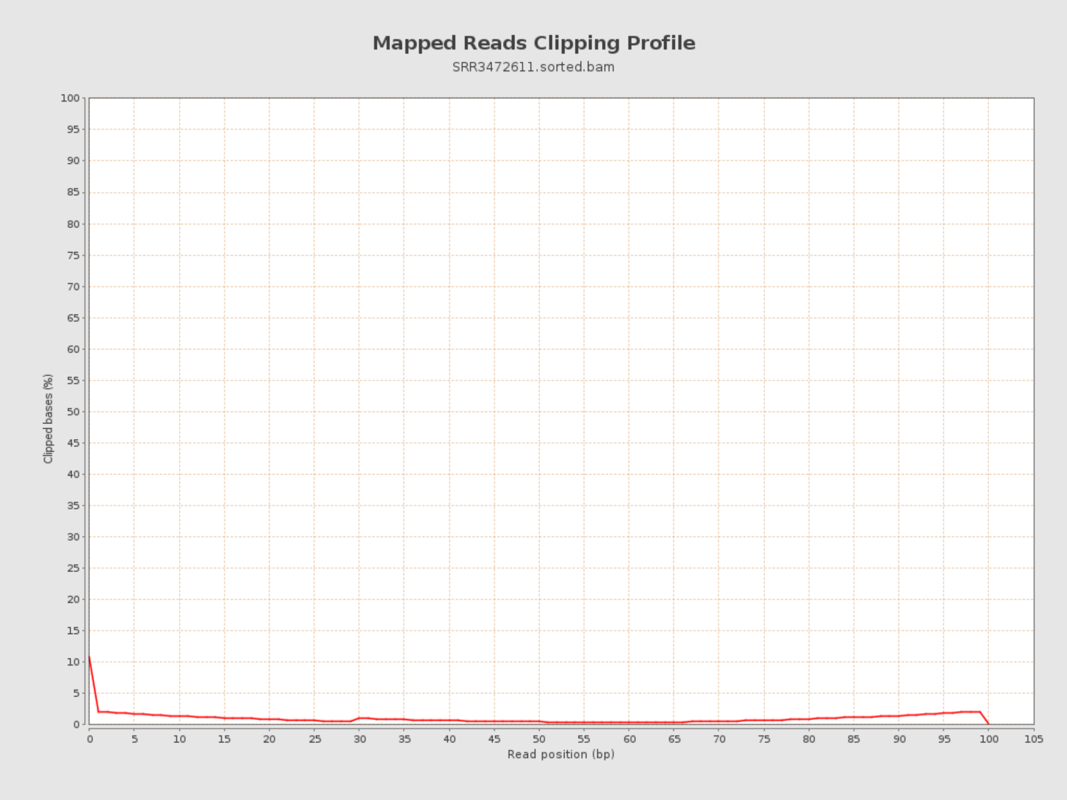
8. Results : Mapped Reads Nucleotide Content



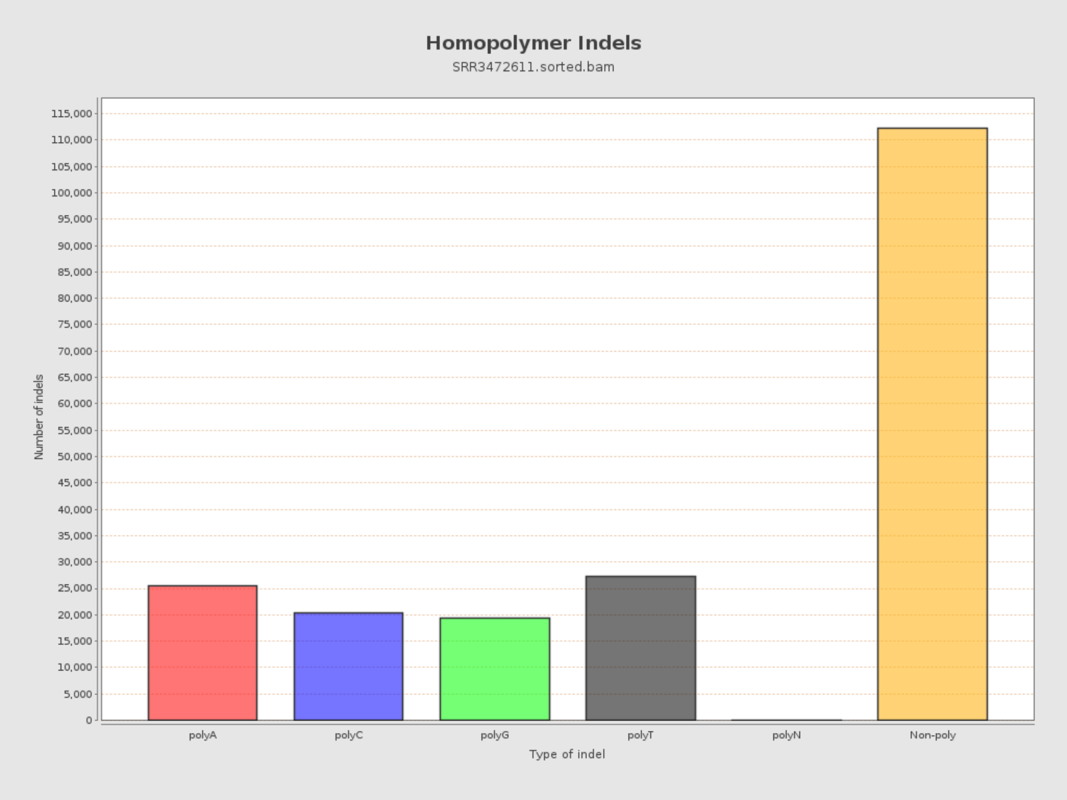
9. Results : Mapped Reads GC-content Distribution



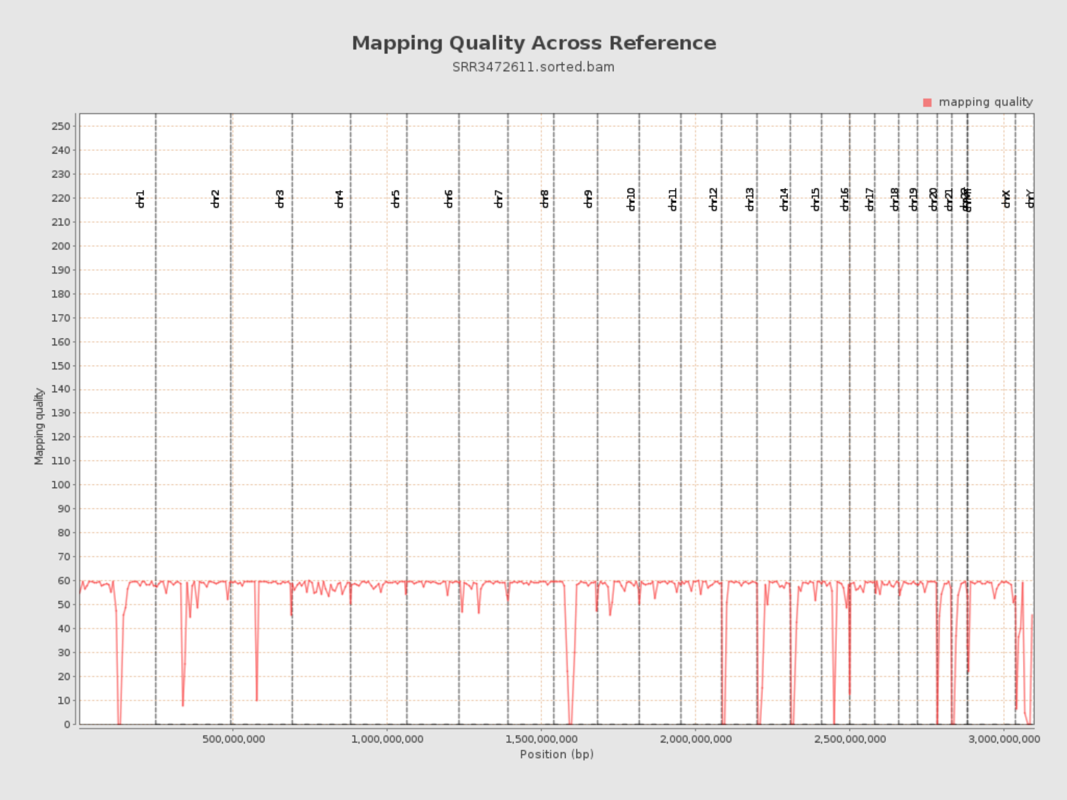
10. Results : Mapped Reads Clipping Profile



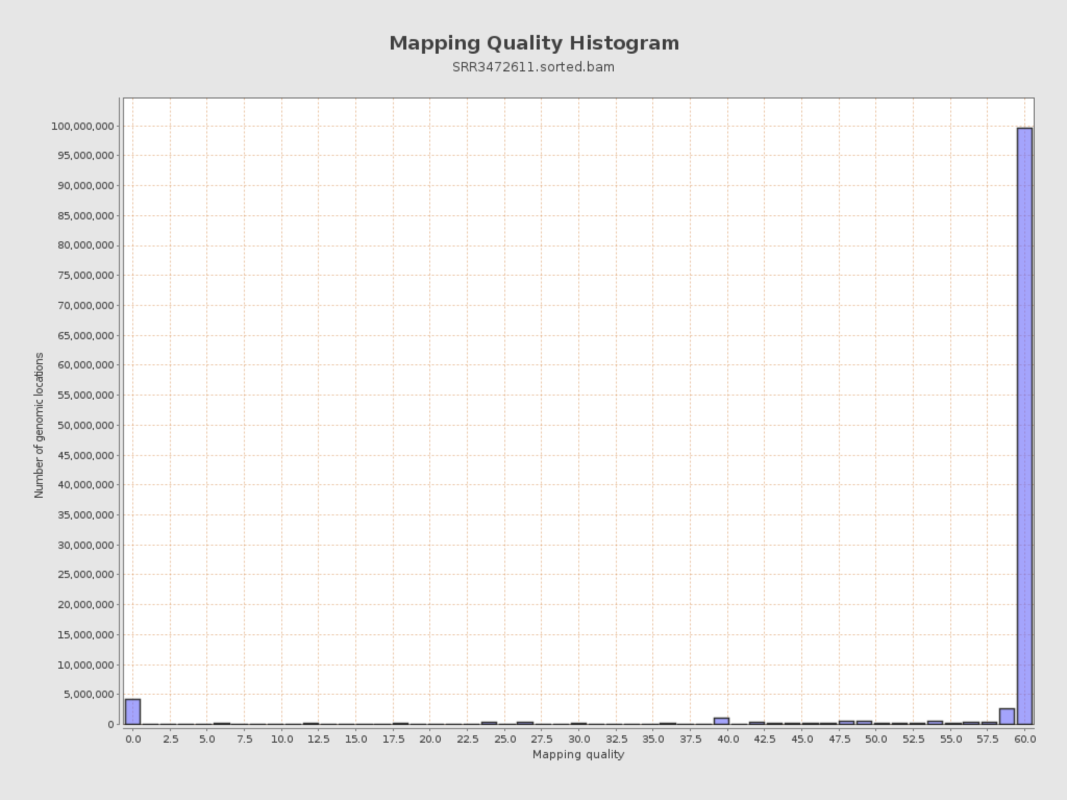
11. Results : Homopolymer Indels



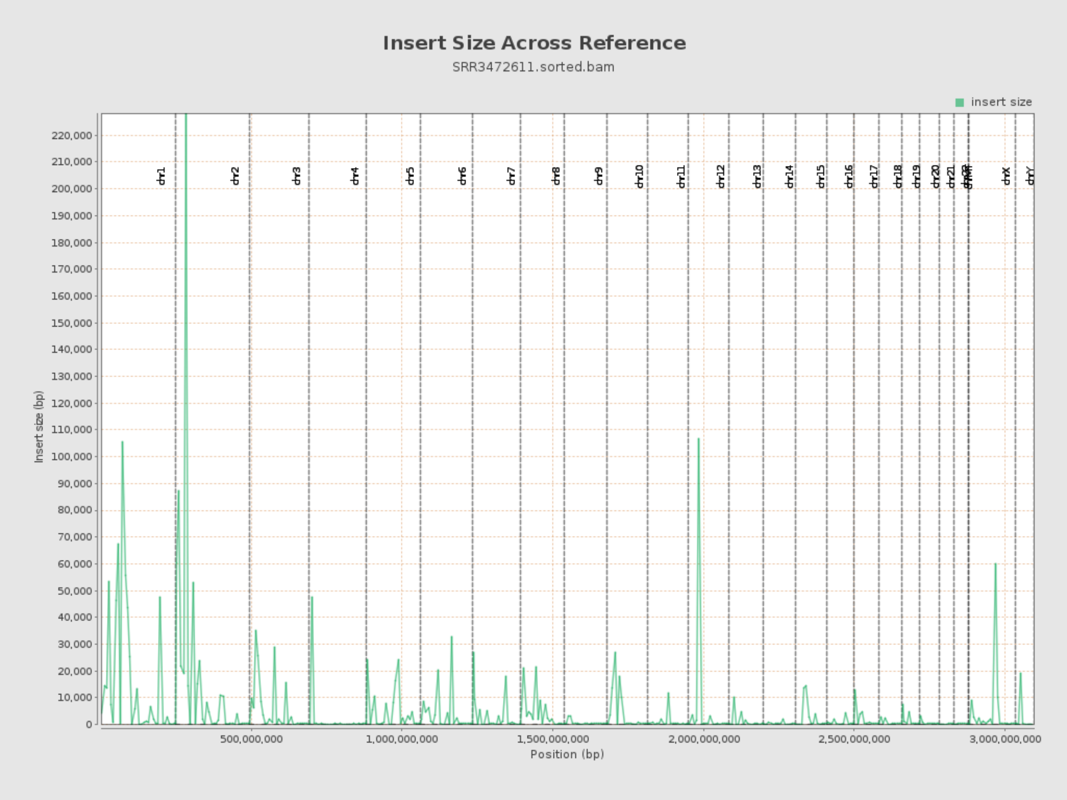
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram