Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:02:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472461.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_SRR3472461 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472461_1.fastq.gz SRR3472461_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:02:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472461.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,733,918
Mapped reads	16,618,749 / 99.31%
Unmapped reads	115,169 / 0.69%
Mapped paired reads	16,618,749 / 99.31%
Mapped reads, first in pair	8,328,593 / 49.77%
Mapped reads, second in pair	8,290,156 / 49.54%
Mapped reads, both in pair	16,556,028 / 98.94%
Mapped reads, singletons	62,721 / 0.37%
Secondary alignments	0
Supplementary alignments	59,030 / 0.35%
Read min/max/mean length	30 / 100 / 99.18
Duplicated reads (estimated)	10,950,656 / 65.44%
Duplication rate	48.15%
Clipped reads	1,244,614 / 7.44%

2.2. ACGT Content

Number/percentage of A's	432,346,799 / 26.61%
Number/percentage of C's	380,801,357 / 23.44%
Number/percentage of T's	433,891,679 / 26.7%
Number/percentage of G's	377,606,627 / 23.24%
Number/percentage of N's	202,505 / 0.01%

GC Percentage	46.68%

2.3. Coverage

Mean	0.5249
Standard Deviation	20.0151

2.4. Mapping Quality

Mean Mapping Quality	55.06

2.5. Insert size

Mean	15,542.96
Standard Deviation	1,242,821
P25/Median/P75	141 / 193 / 257

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	7,837,230
Insertions	99,074
Mapped reads with at least one insertion	0.59%
Deletions	73,239
Mapped reads with at least one deletion	0.43%
Homopolymer indels	46.26%

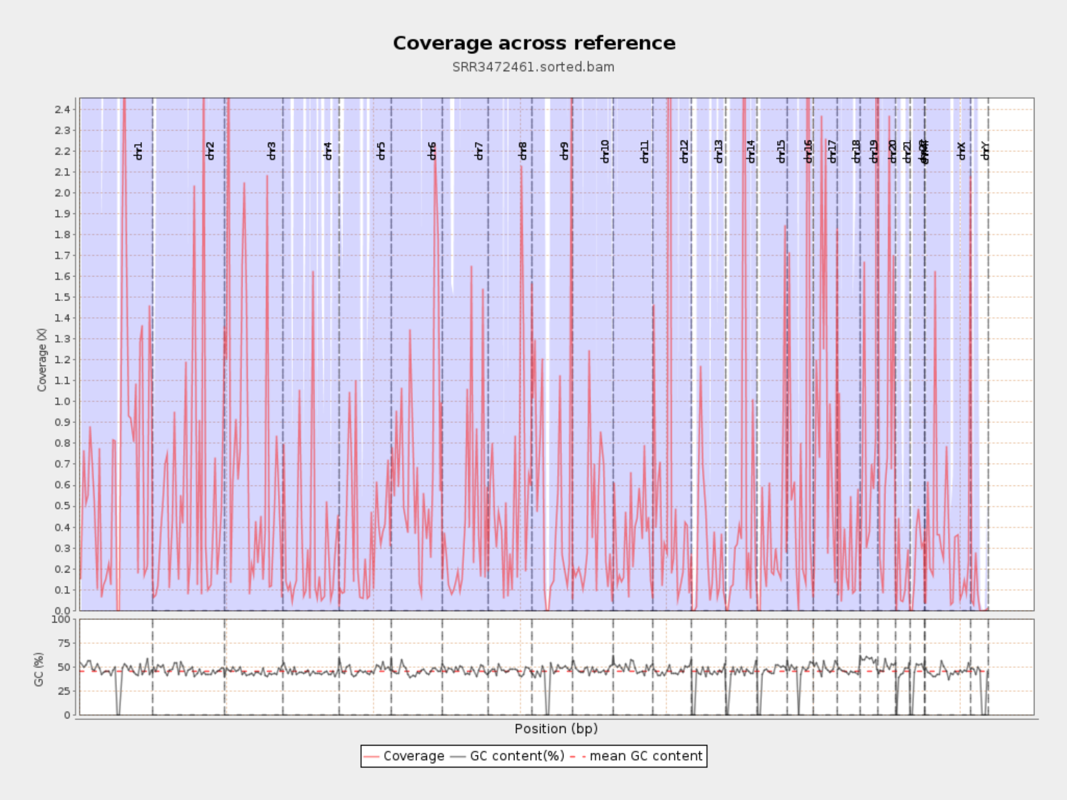
2.7. Chromosome stats

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

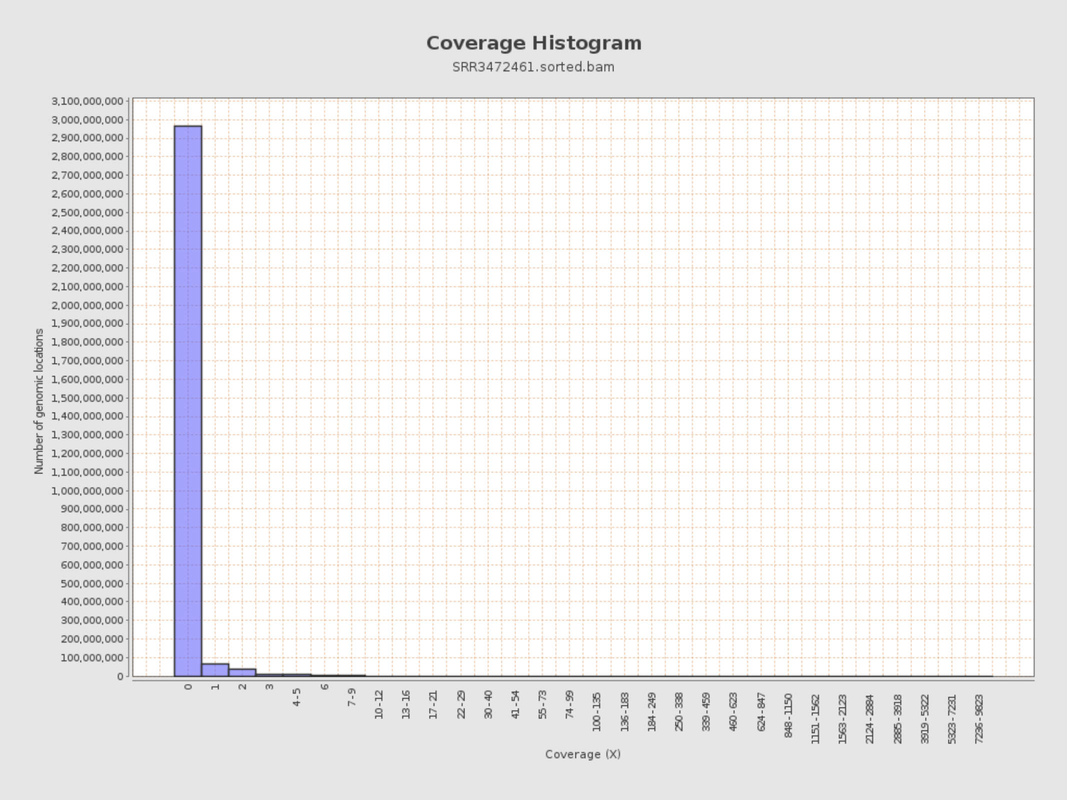
		bases	**coverage**	**deviation**
chr1	249250621	178901976	0.7178	20.0951
chr2	243199373	134828437	0.5544	22.0275
chr3	198022430	151145375	0.7633	24.7196
chr4	191154276	54224073	0.2837	11.8899
chr5	180915260	64494716	0.3565	12.0432
chr6	171115067	121499679	0.71	21.6533
chr7	159138663	69812272	0.4387	15.2896
chr8	146364022	81956969	0.56	18.0487
chr9	141213431	83608394	0.5921	18.7477
chr10	135534747	49734361	0.3669	19.4895
chr11	135006516	47993764	0.3555	12.3267
chr12	133851895	92160897	0.6885	36.9862
chr13	115169878	34187107	0.2968	14.4386
chr14	107349540	52820308	0.492	17.7636
chr15	102531392	41165514	0.4015	16.3573
chr16	90354753	70880519	0.7845	25.2274
chr17	81195210	83777860	1.0318	29.5238
chr18	78077248	25477659	0.3263	12.2782
chr19	59128983	52831924	0.8935	30.634
chr20	63025520	54332991	0.8621	32.2397
chr21	48129895	7493919	0.1557	8.1396
chr22	51304566	12828747	0.2501	7.1436
chrMT	16571	6492	0.3918	0.9307
chrX	155270560	55591714	0.358	12.4559

chrY	59373566	3294300	0.0555	4.0658

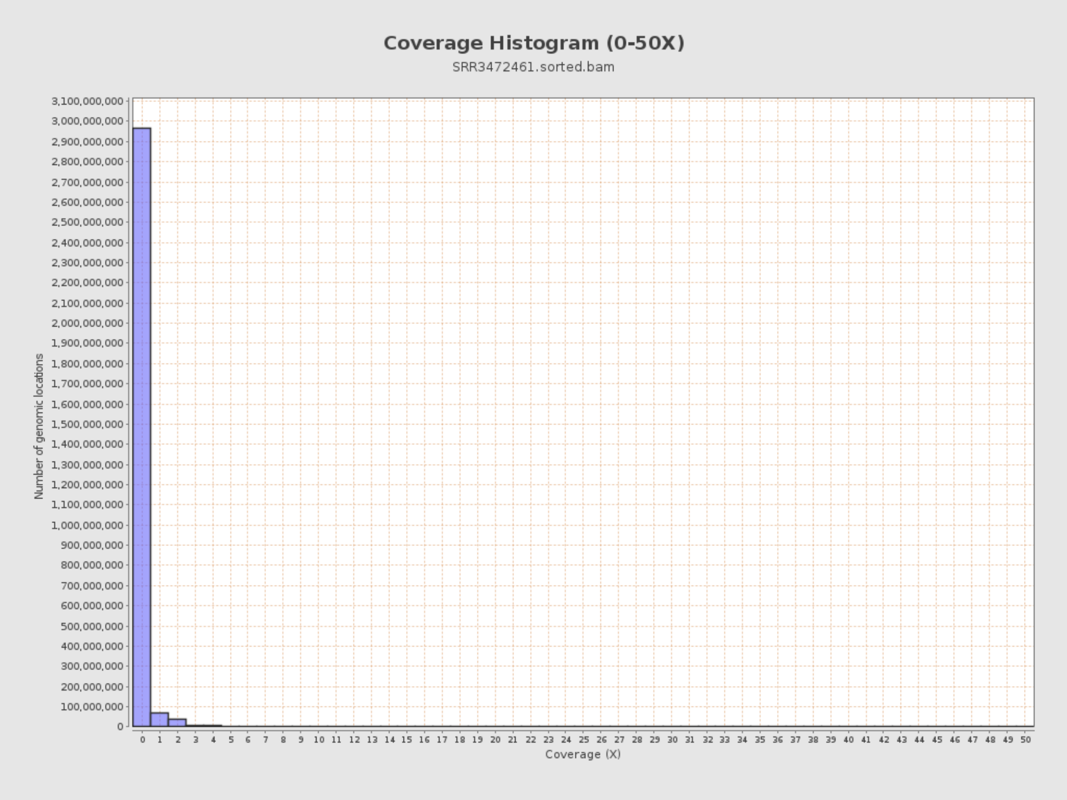
3. Results : Coverage across reference



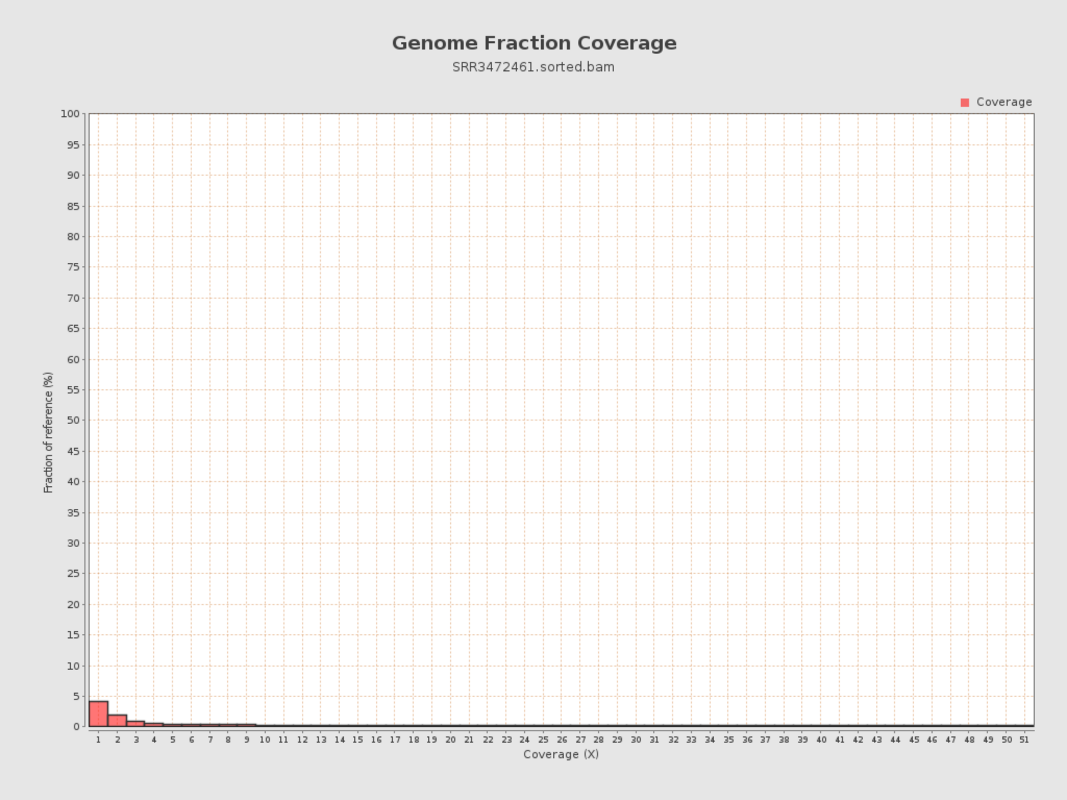
4. Results : Coverage Histogram



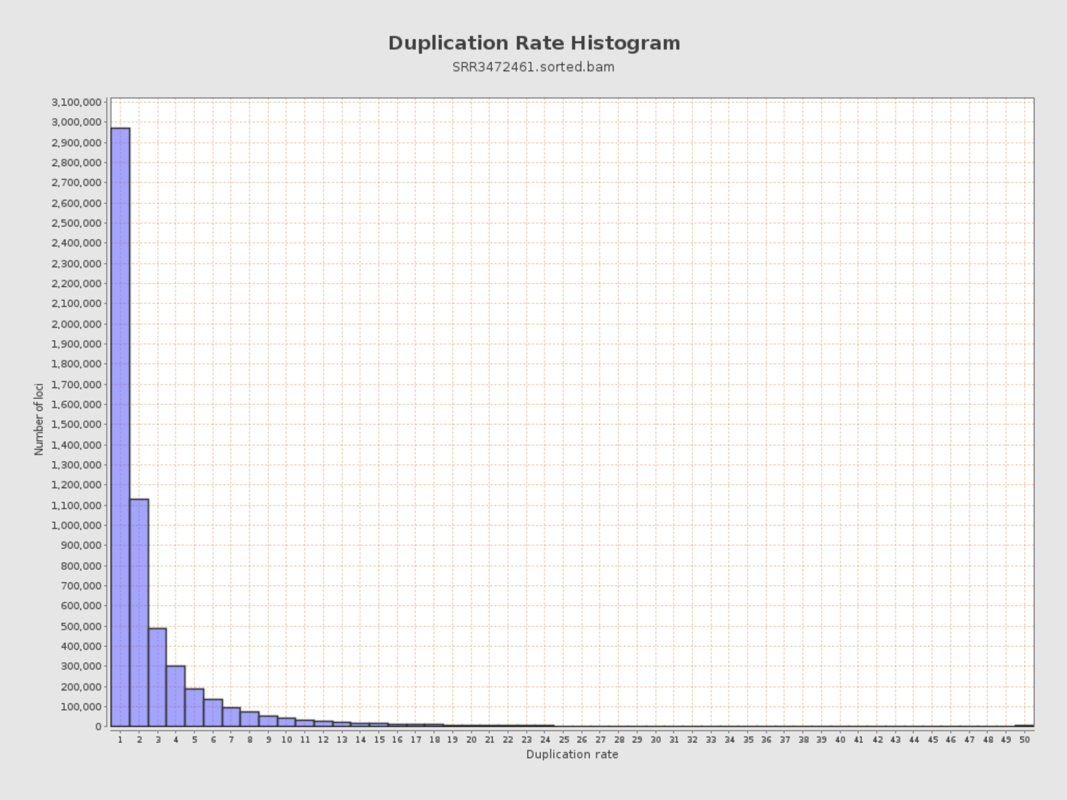
5. Results : Coverage Histogram (0-50X)



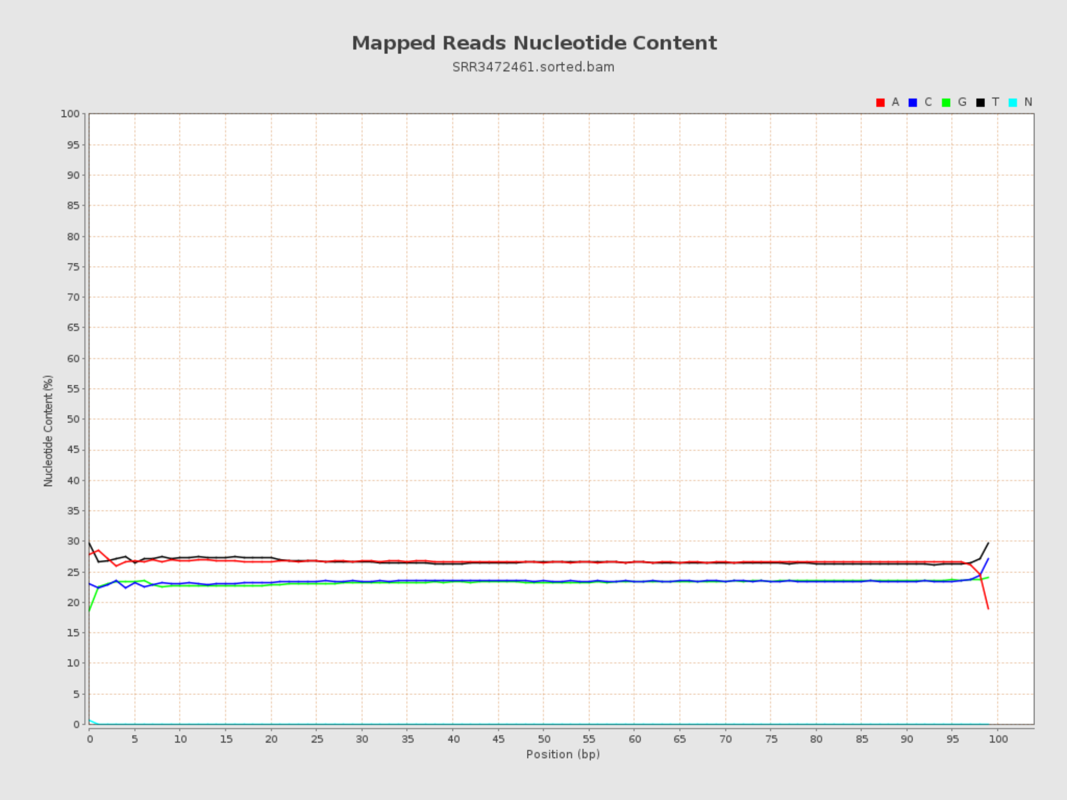
6. Results : Genome Fraction Coverage



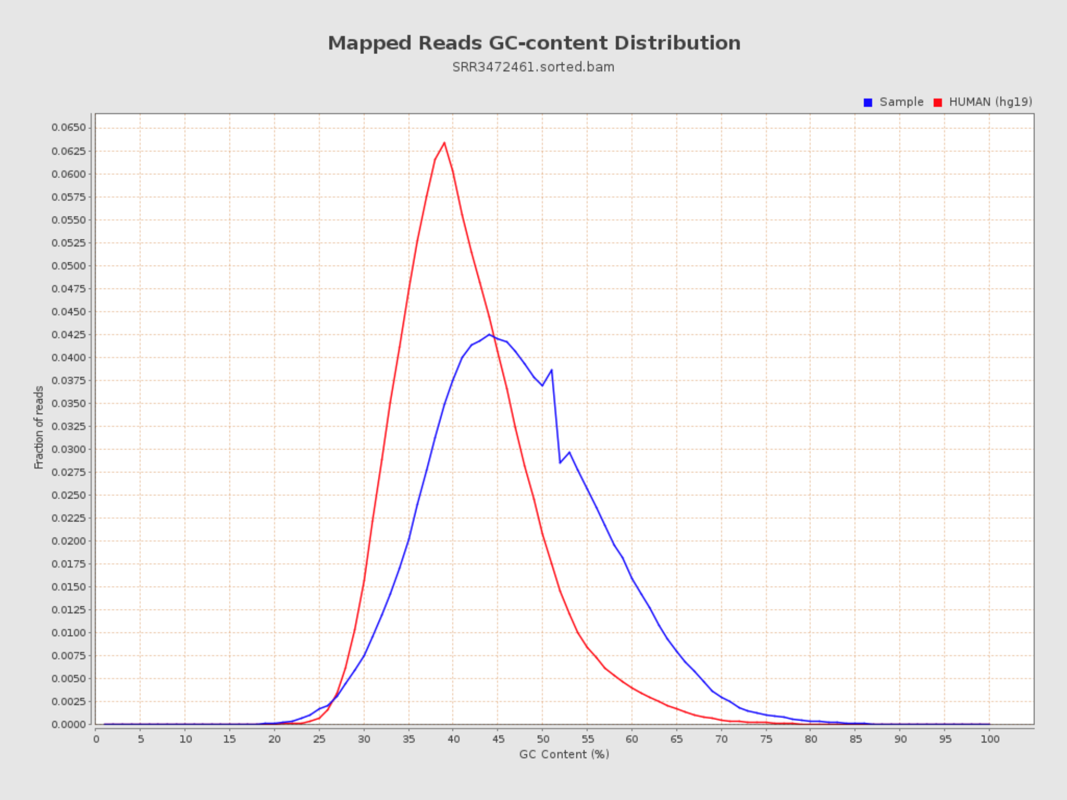
7. Results : Duplication Rate Histogram



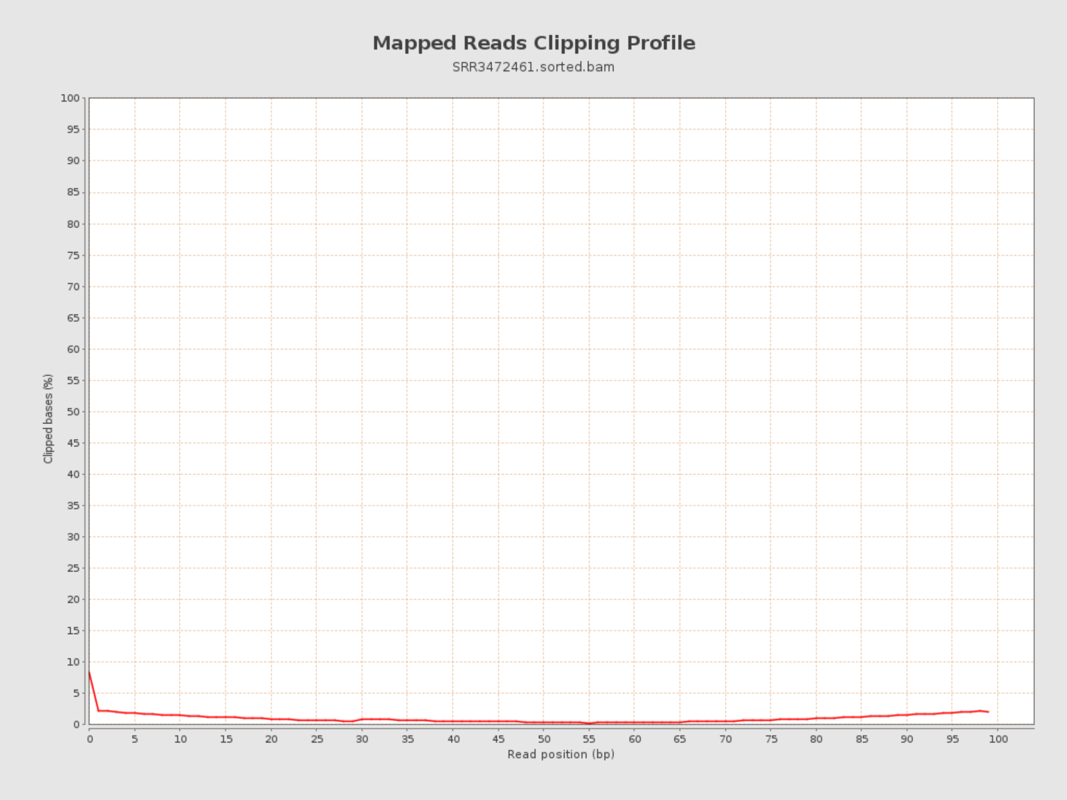
8. Results : Mapped Reads Nucleotide Content



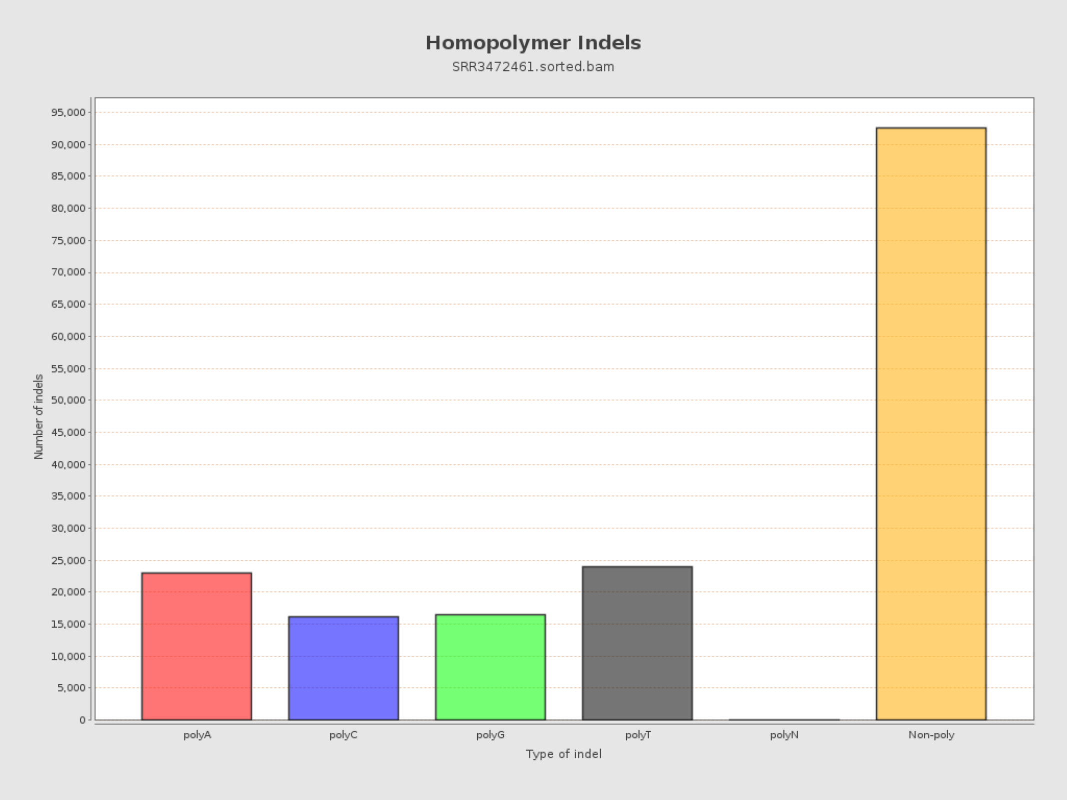
9. Results : Mapped Reads GC-content Distribution



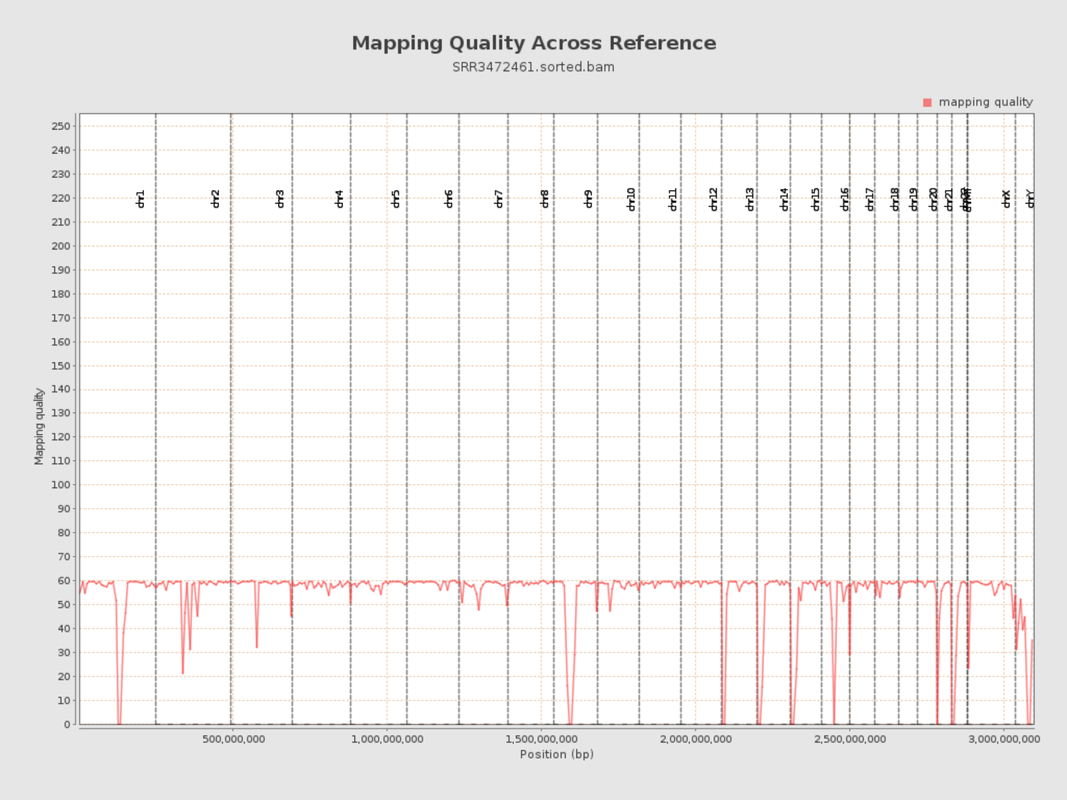
10. Results : Mapped Reads Clipping Profile



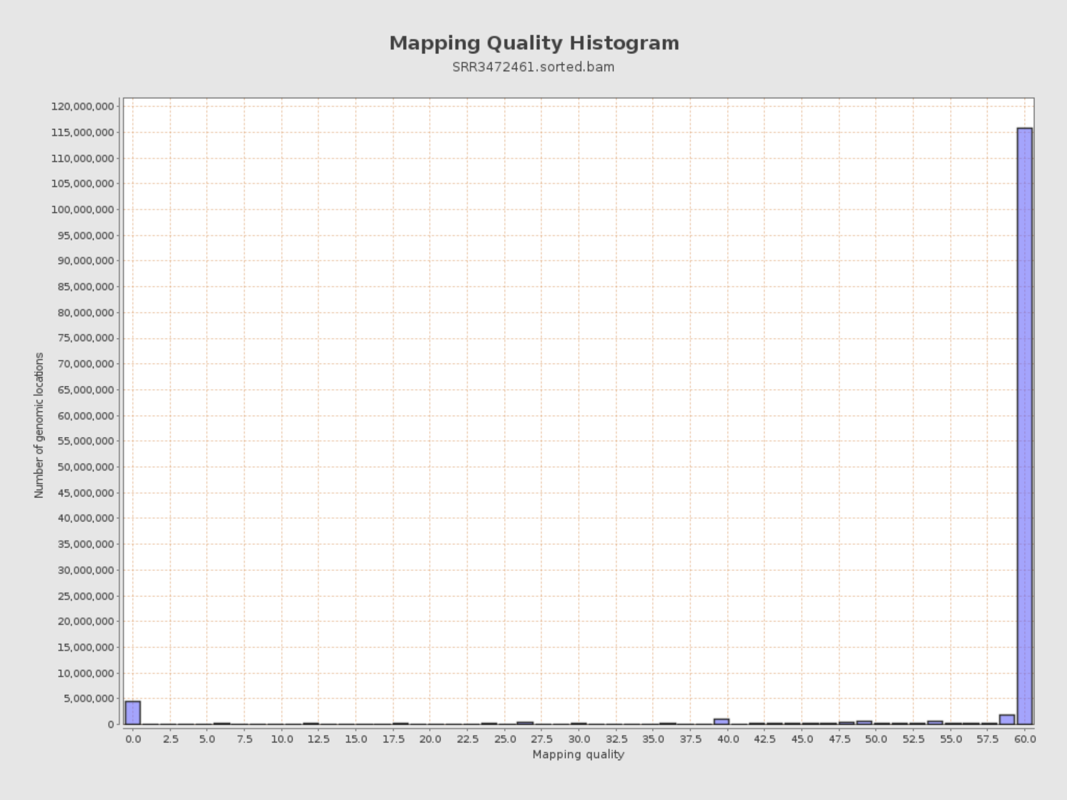
11. Results : Homopolymer Indels



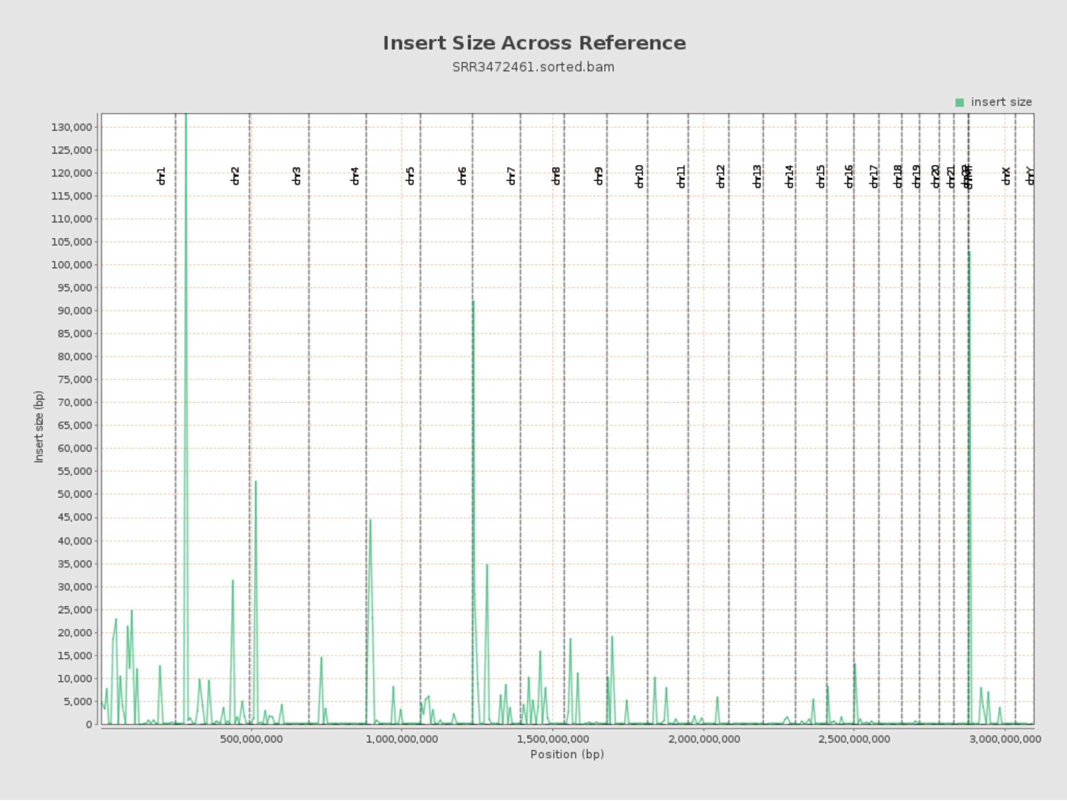
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram