Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:41:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472427.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_SRR3472427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472427_1.fastq.gz SRR3472427_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:41:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,964,632
Mapped reads	15,837,639 / 99.2%
Unmapped reads	126,993 / 0.8%
Mapped paired reads	15,837,639 / 99.2%
Mapped reads, first in pair	7,940,200 / 49.74%
Mapped reads, second in pair	7,897,439 / 49.47%
Mapped reads, both in pair	15,766,730 / 98.76%
Mapped reads, singletons	70,909 / 0.44%
Secondary alignments	0
Supplementary alignments	61,311 / 0.38%
Read min/max/mean length	30 / 100 / 99.4
Duplicated reads (estimated)	9,867,645 / 61.81%
Duplication rate	47.71%
Clipped reads	1,109,280 / 6.95%

2.2. ACGT Content

Number/percentage of A's	419,696,112 / 27.01%
Number/percentage of C's	357,843,568 / 23.03%
Number/percentage of T's	420,765,892 / 27.08%
Number/percentage of G's	355,175,784 / 22.86%
Number/percentage of N's	198,787 / 0.01%

GC Percentage	45.89%

2.3. Coverage

Mean	0.5019
Standard Deviation	16.5933

2.4. Mapping Quality

Mean Mapping Quality	54.87

2.5. Insert size

Mean	16,317.16
Standard Deviation	1,254,849.21
P25/Median/P75	151 / 208 / 279

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	8,101,235
Insertions	92,236
Mapped reads with at least one insertion	0.58%
Deletions	74,286
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.79%

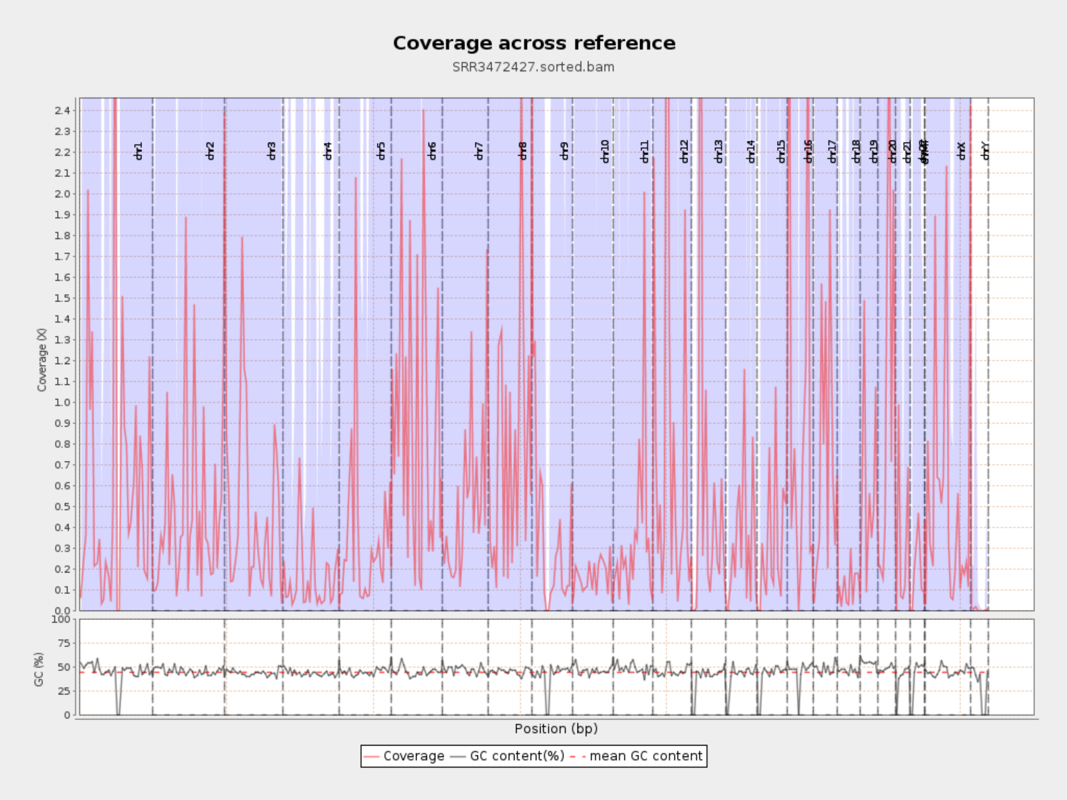
2.7. Chromosome stats

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

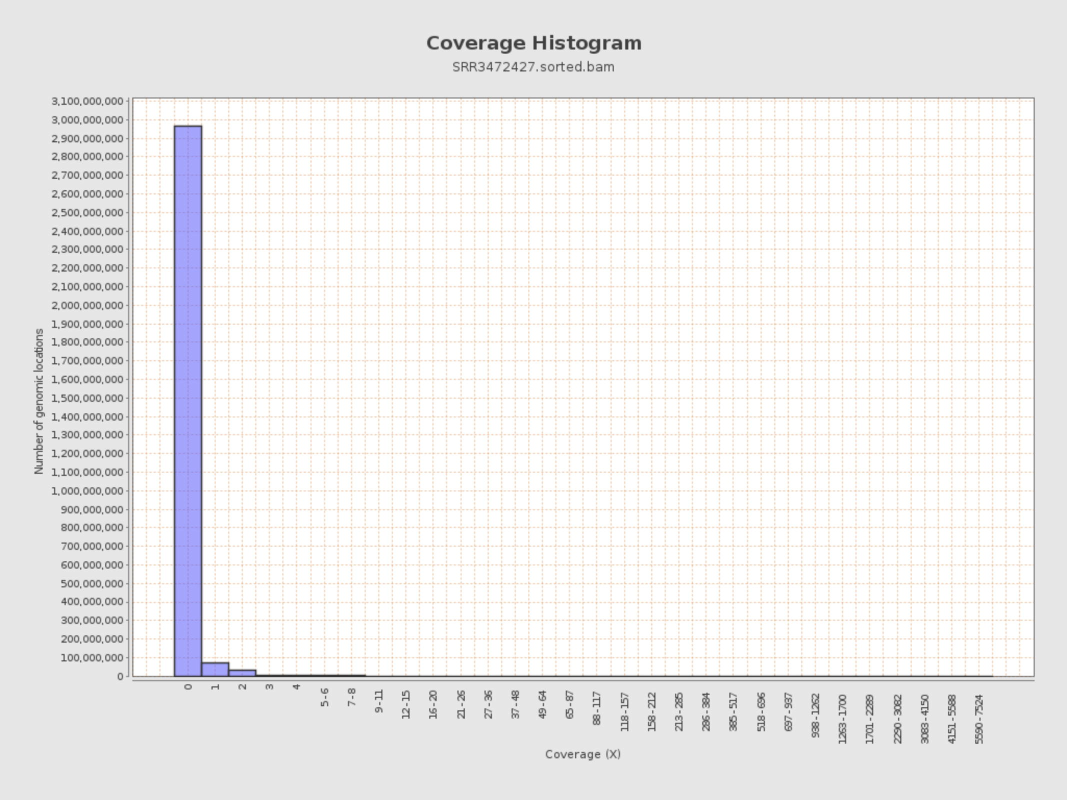
		bases	coverage	deviation
chr1	249250621	154971287	0.6217	22.6194
chr2	243199373	111271136	0.4575	13.0528
chr3	198022430	101615215	0.5132	12.1083
chr4	191154276	29749970	0.1556	5.675
chr5	180915260	63475258	0.3509	10.7075
chr6	171115067	149794354	0.8754	24.3583
chr7	159138663	84346638	0.53	13.2082
chr8	146364022	113630837	0.7764	18.7406
chr9	141213431	51139510	0.3621	9.0813
chr10	135534747	22318563	0.1647	5.1471
chr11	135006516	49789685	0.3688	13.2392
chr12	133851895	112885454	0.8434	27.0765
chr13	115169878	70265782	0.6101	25.7699
chr14	107349540	34566335	0.322	9.6047
chr15	102531392	33159850	0.3234	17.4705
chr16	90354753	88677924	0.9814	26.4732
chr17	81195210	60715742	0.7478	18.2008
chr18	78077248	9040368	0.1158	4.8413
chr19	59128983	37542588	0.6349	14.543
chr20	63025520	67416063	1.0697	27.0098
chr21	48129895	15608375	0.3243	16.5997
chr22	51304566	9173941	0.1788	5.0932
chrMT	16571	7198	0.4344	0.8581
chrX	155270560	82331409	0.5302	13.1192

chrY	59373566	364802	0.0061	0.6102

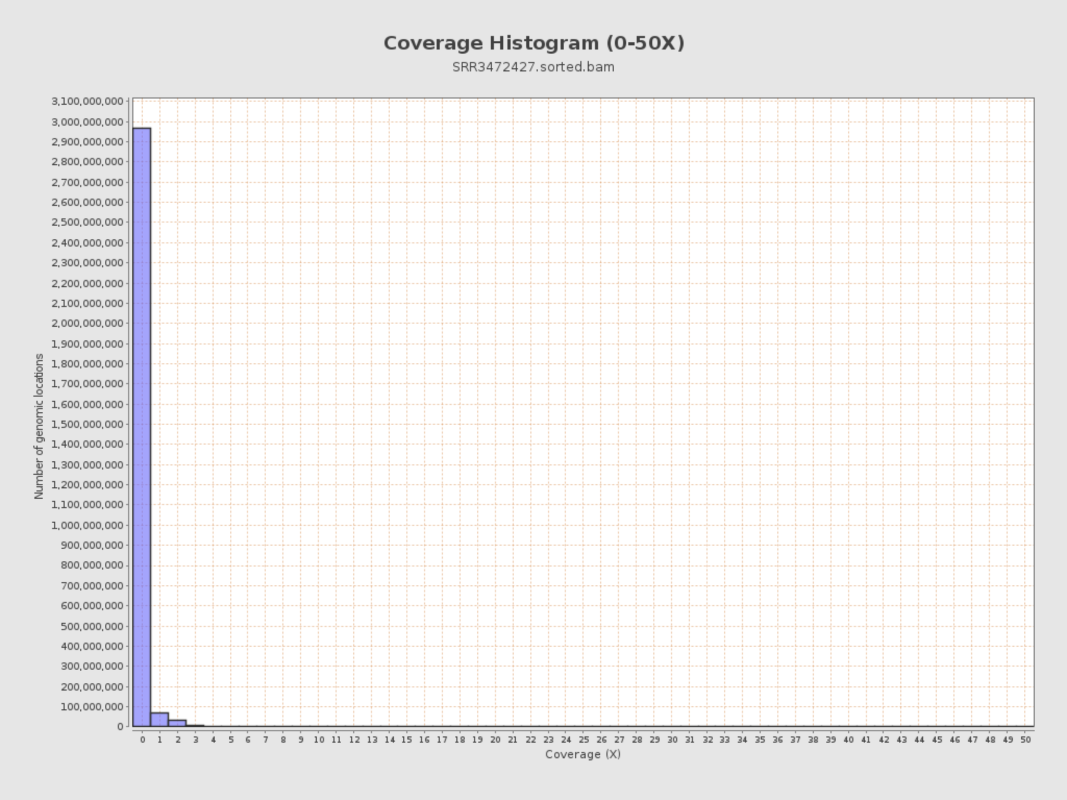
3. Results : Coverage across reference



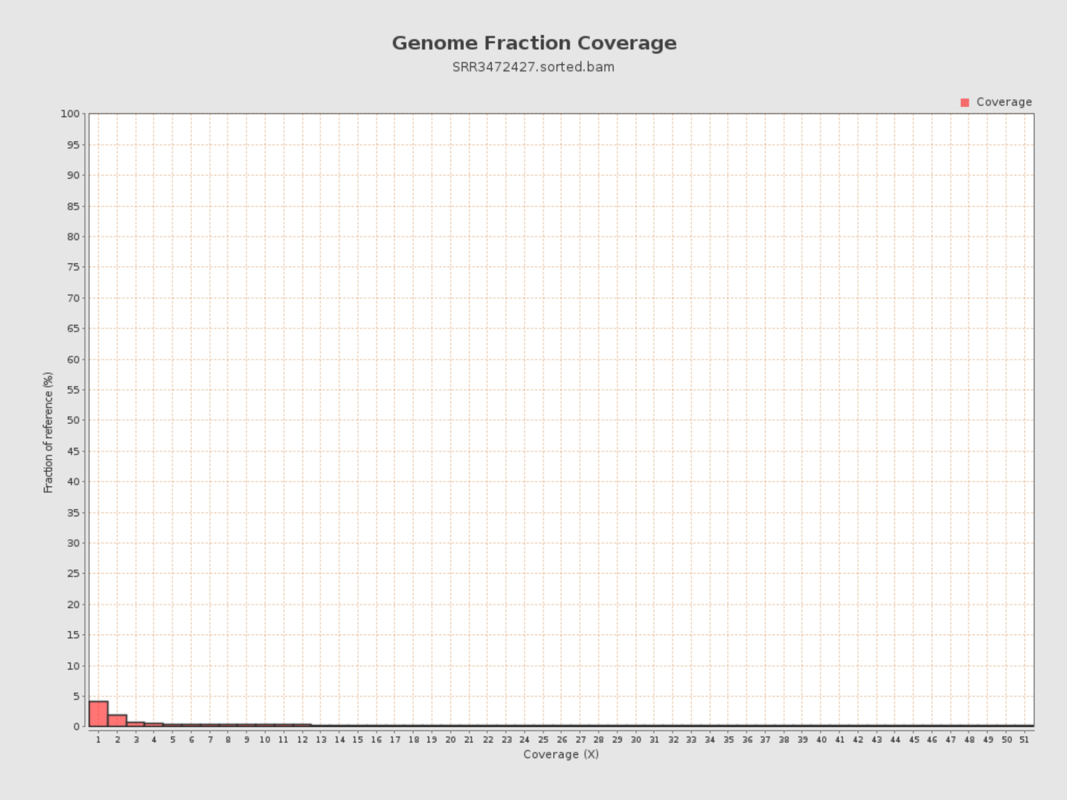
4. Results : Coverage Histogram



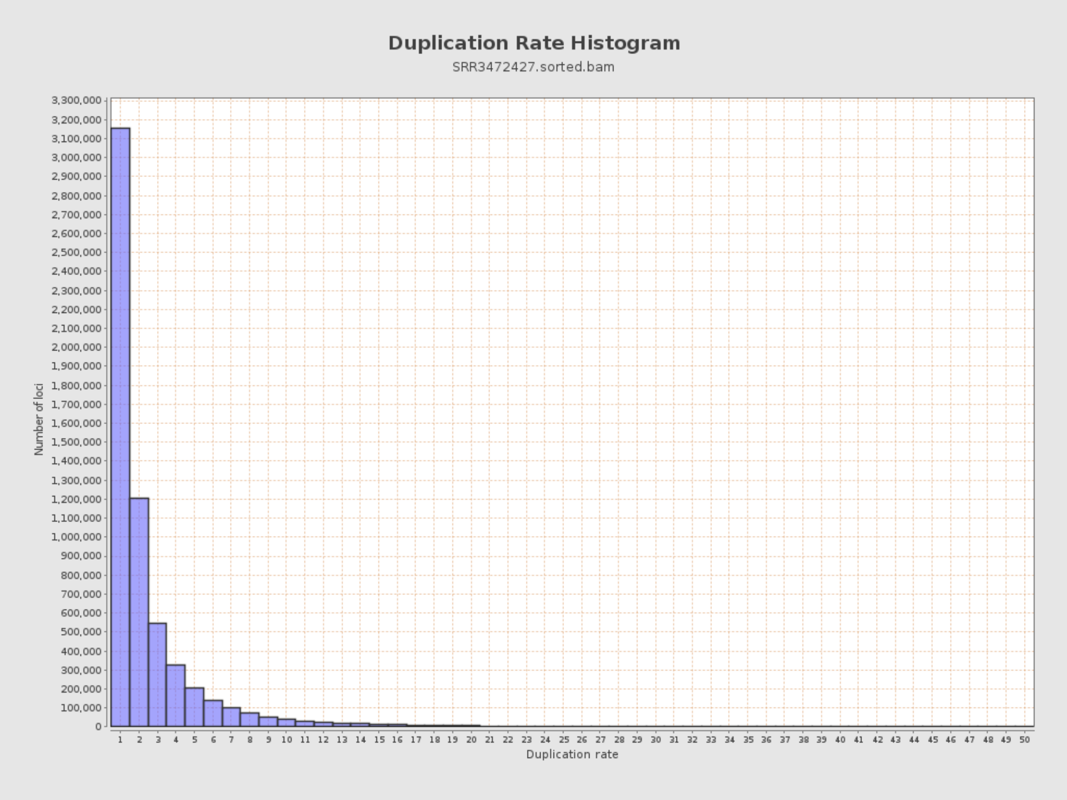
5. Results : Coverage Histogram (0-50X)



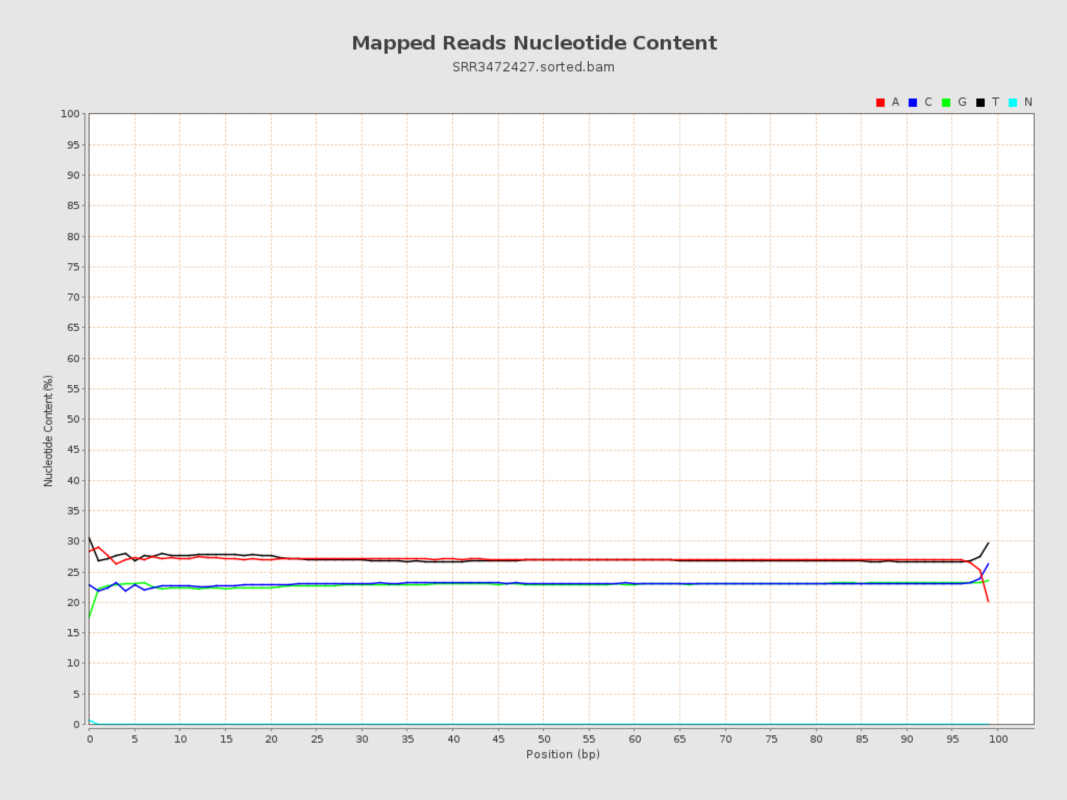
6. Results : Genome Fraction Coverage



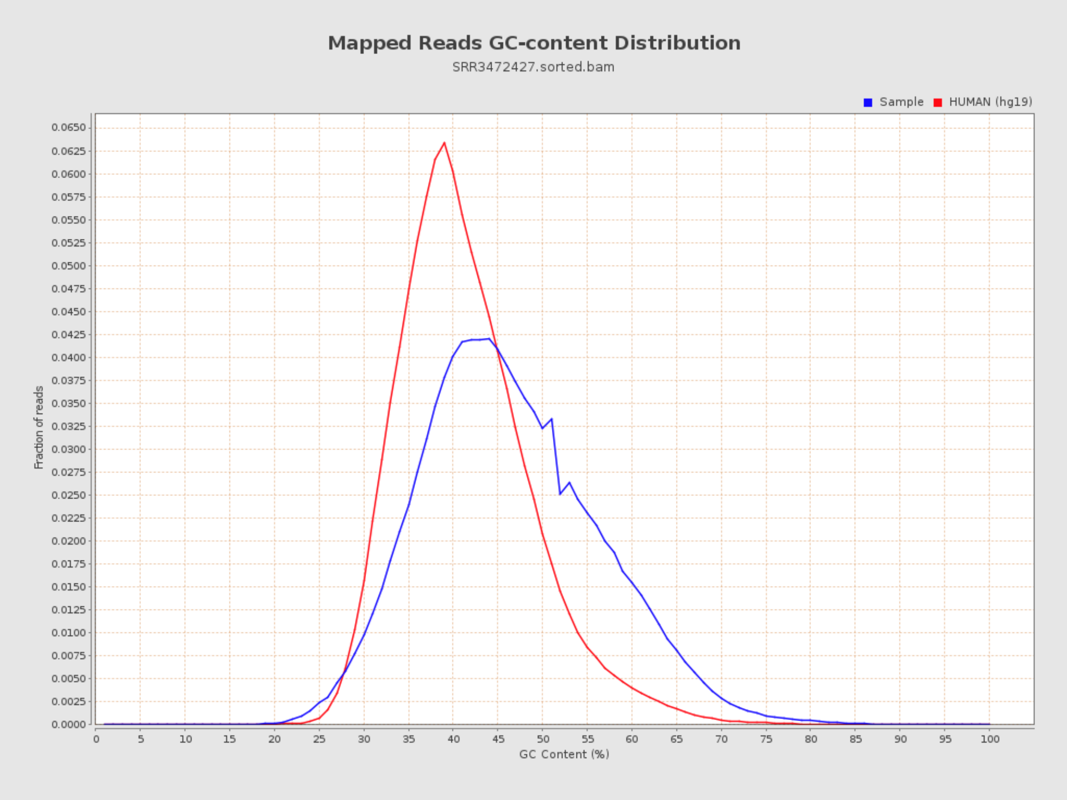
7. Results : Duplication Rate Histogram



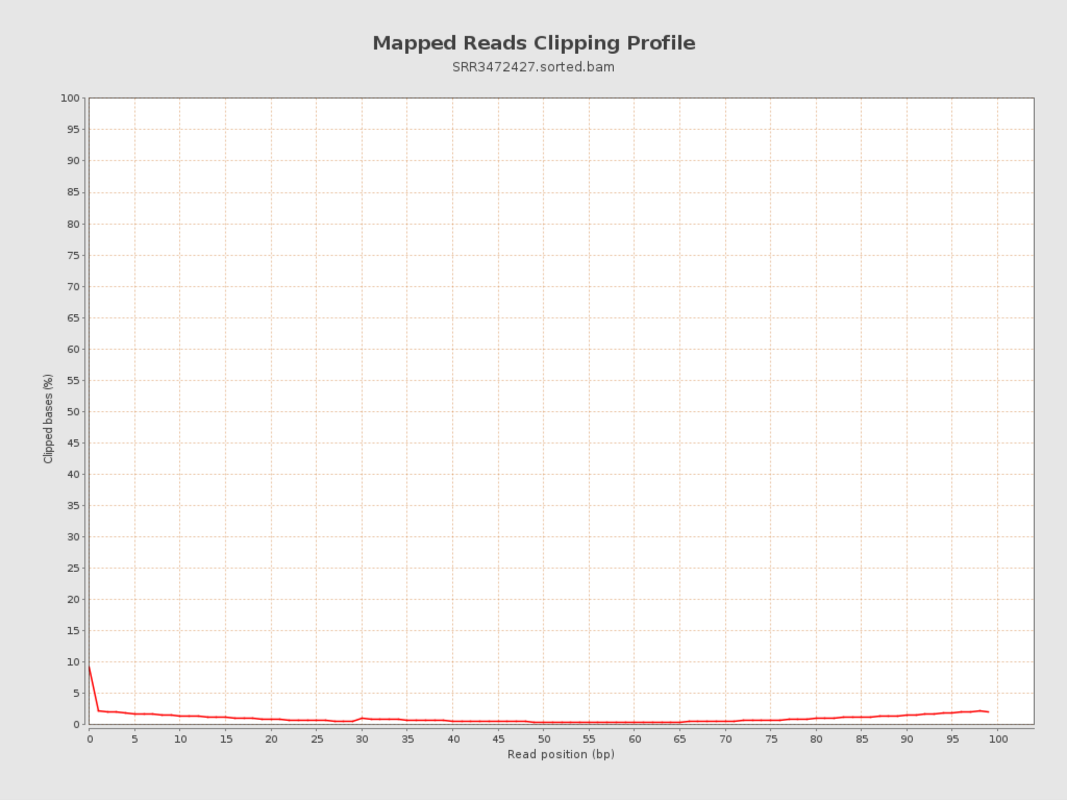
8. Results : Mapped Reads Nucleotide Content



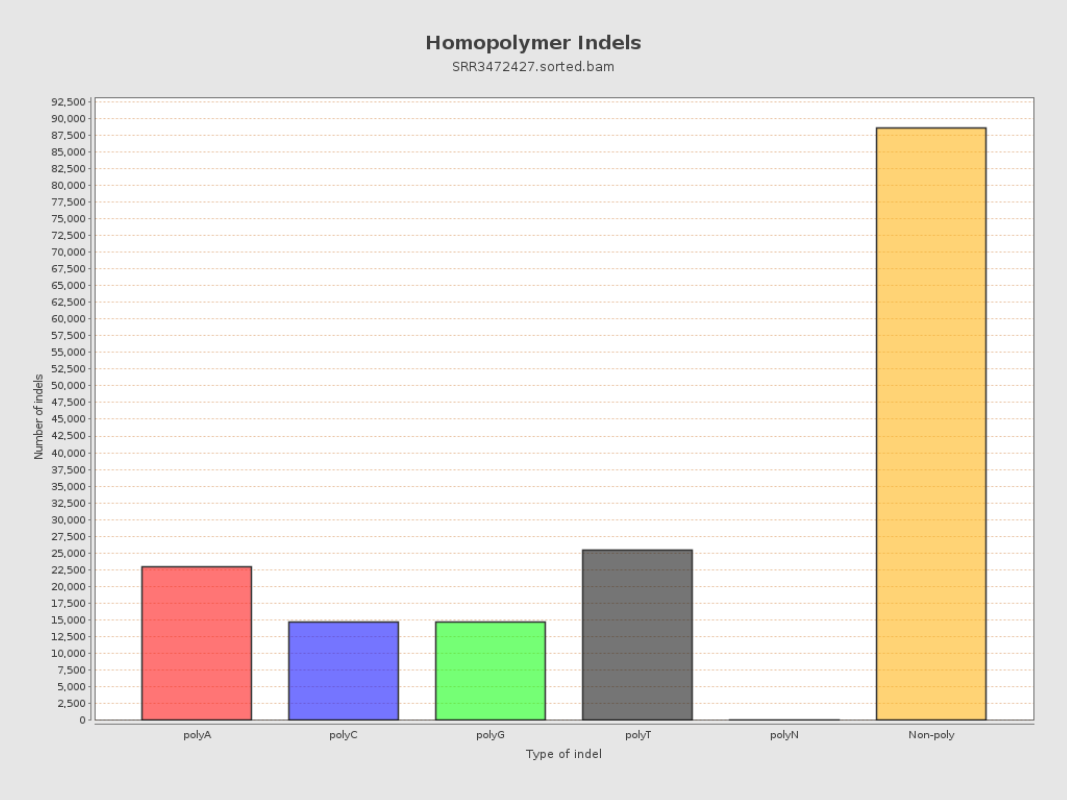
9. Results : Mapped Reads GC-content Distribution



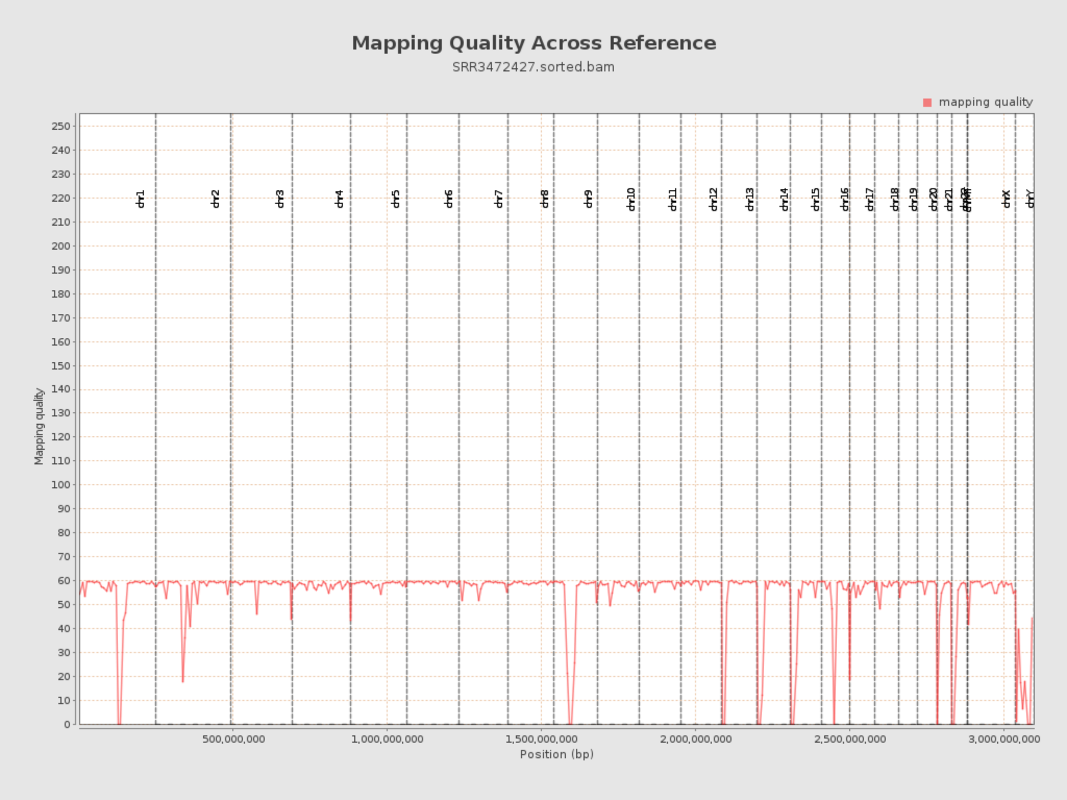
10. Results : Mapped Reads Clipping Profile



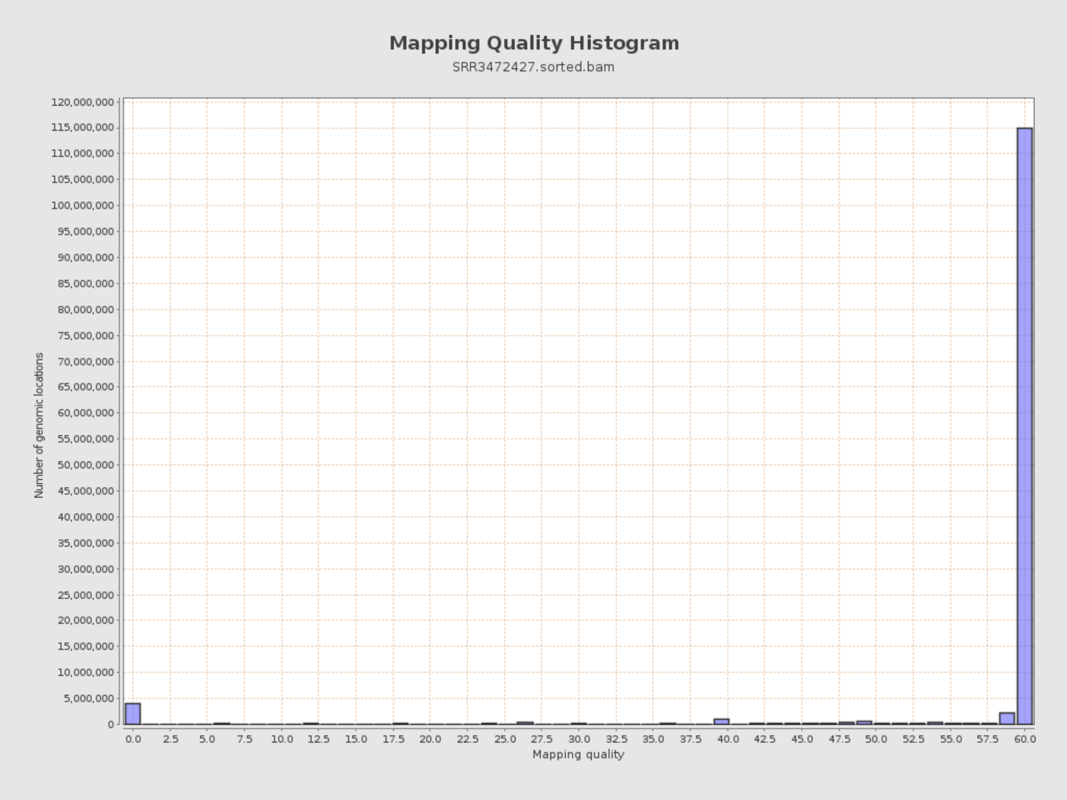
11. Results : Homopolymer Indels



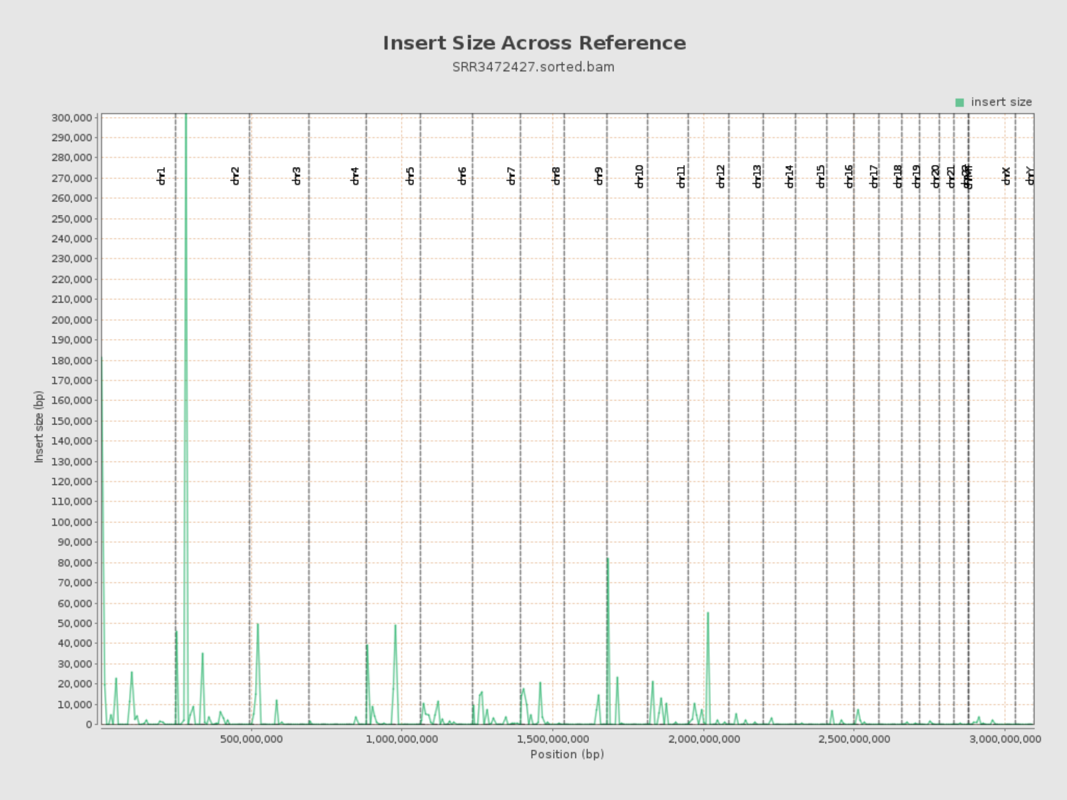
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram