Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:26:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472441.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_SRR3472441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472441_1.fastq.gz SRR3472441_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:26:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,277,274
Mapped reads	14,125,630 / 98.94%
Unmapped reads	151,644 / 1.06%
Mapped paired reads	14,125,630 / 98.94%
Mapped reads, first in pair	7,086,673 / 49.64%
Mapped reads, second in pair	7,038,957 / 49.3%
Mapped reads, both in pair	14,035,982 / 98.31%
Mapped reads, singletons	89,648 / 0.63%
Secondary alignments	0
Supplementary alignments	48,122 / 0.34%
Read min/max/mean length	30 / 100 / 99.37
Duplicated reads (estimated)	8,190,698 / 57.37%
Duplication rate	46.12%
Clipped reads	1,054,675 / 7.39%

2.2. ACGT Content

Number/percentage of A's	373,034,582 / 26.95%
Number/percentage of C's	321,298,410 / 23.21%
Number/percentage of T's	371,721,615 / 26.85%
Number/percentage of G's	318,118,860 / 22.98%
Number/percentage of N's	164,713 / 0.01%

GC Percentage	46.19%

2.3. Coverage

Mean	0.4472
Standard Deviation	12.8391

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	15,898.78
Standard Deviation	1,255,771.65
P25/Median/P75	154 / 213 / 288

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	9,047,775
Insertions	78,927
Mapped reads with at least one insertion	0.55%
Deletions	62,922
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.1%

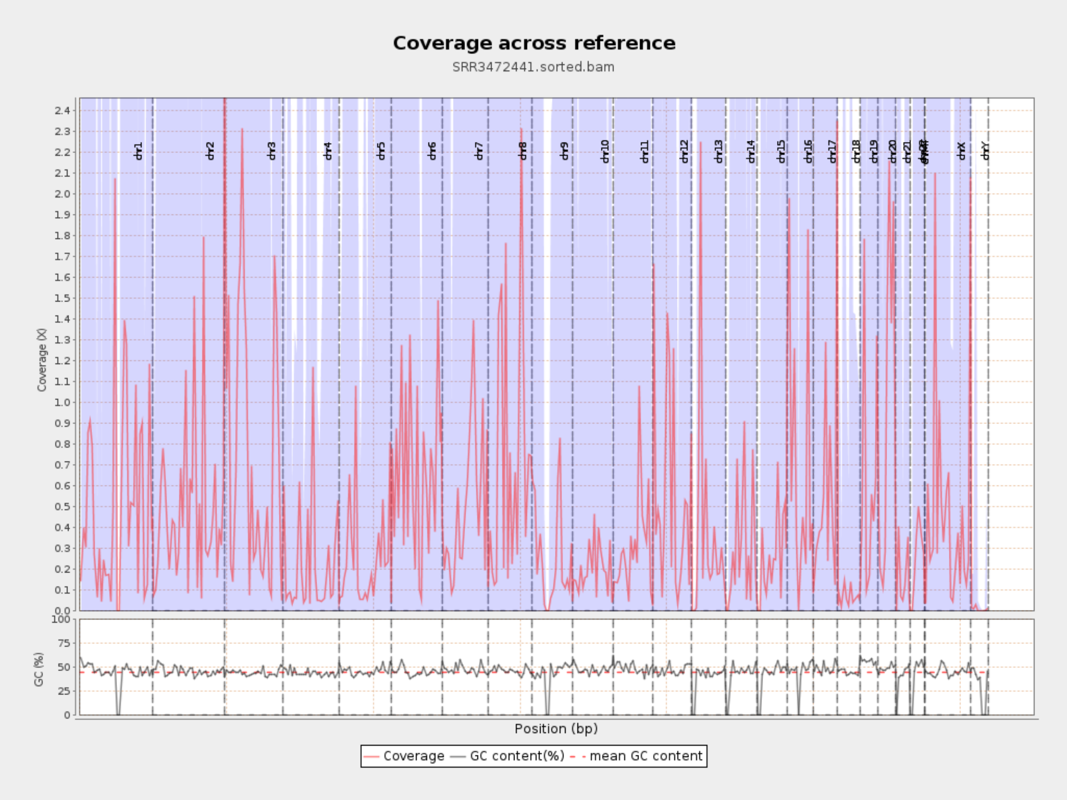
2.7. Chromosome stats

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

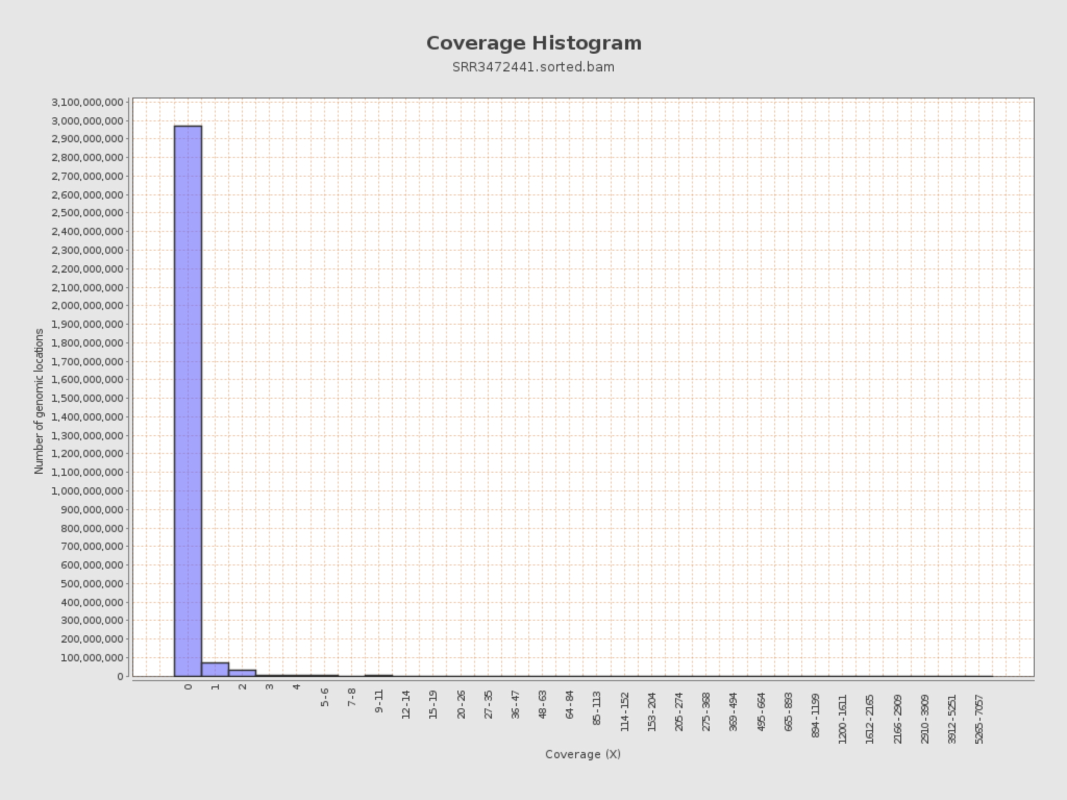
		bases	coverage	deviation
chr1	249250621	130547551	0.5238	15.8147
chr2	243199373	116459934	0.4789	13.2409
chr3	198022430	156679309	0.7912	17.878
chr4	191154276	40637730	0.2126	9.1968
chr5	180915260	47352478	0.2617	7.7366
chr6	171115067	113794079	0.665	15.1859
chr7	159138663	82599583	0.519	15.7308
chr8	146364022	111399693	0.7611	18.9764
chr9	141213431	36479812	0.2583	7.4282
chr10	135534747	27513502	0.203	6.5997
chr11	135006516	42009681	0.3112	9.2252
chr12	133851895	73795489	0.5513	13.2973
chr13	115169878	43568585	0.3783	11.6576
chr14	107349540	30507211	0.2842	8.8912
chr15	102531392	26120699	0.2548	8.38
chr16	90354753	64449750	0.7133	16.8403
chr17	81195210	45879055	0.565	11.8552
chr18	78077248	5177402	0.0663	2.0937
chr19	59128983	35079019	0.5933	12.8664
chr20	63025520	62473044	0.9912	23.45
chr21	48129895	8023361	0.1667	7.4577
chr22	51304566	12742768	0.2484	6.7638
chrMT	16571	3376	0.2037	0.5305
chrX	155270560	70790314	0.4559	10.232

chrY	59373566	402958	0.0068	0.9081

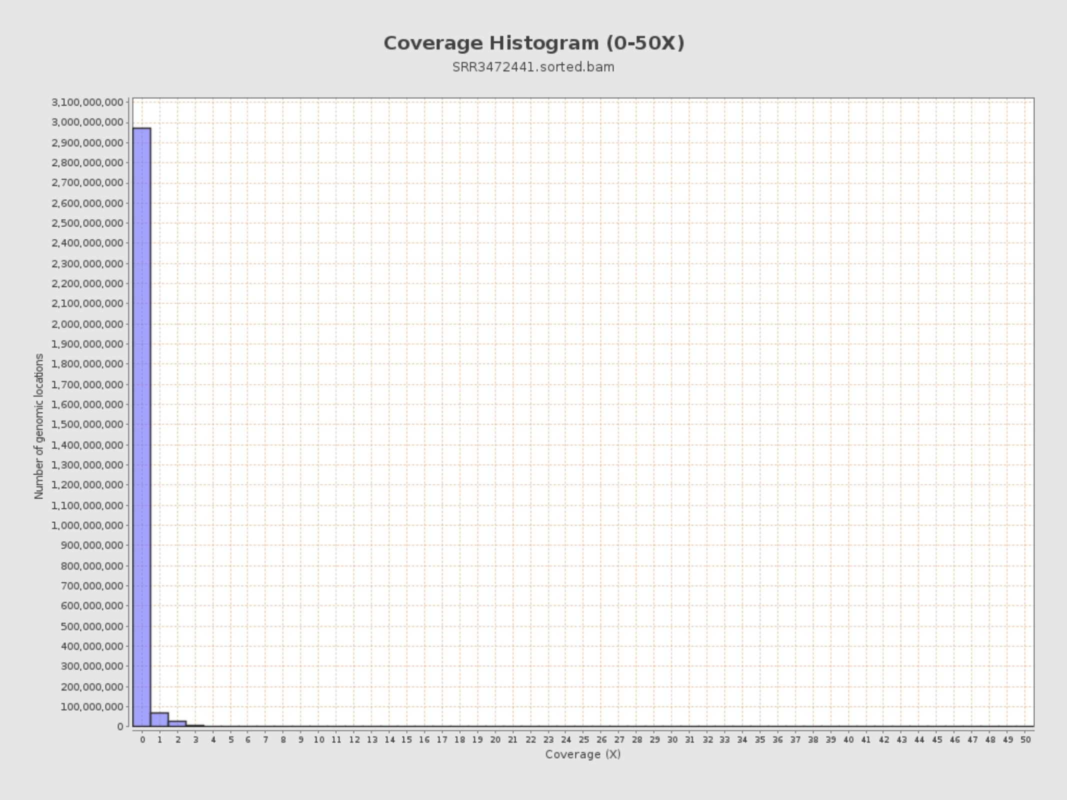
3. Results : Coverage across reference



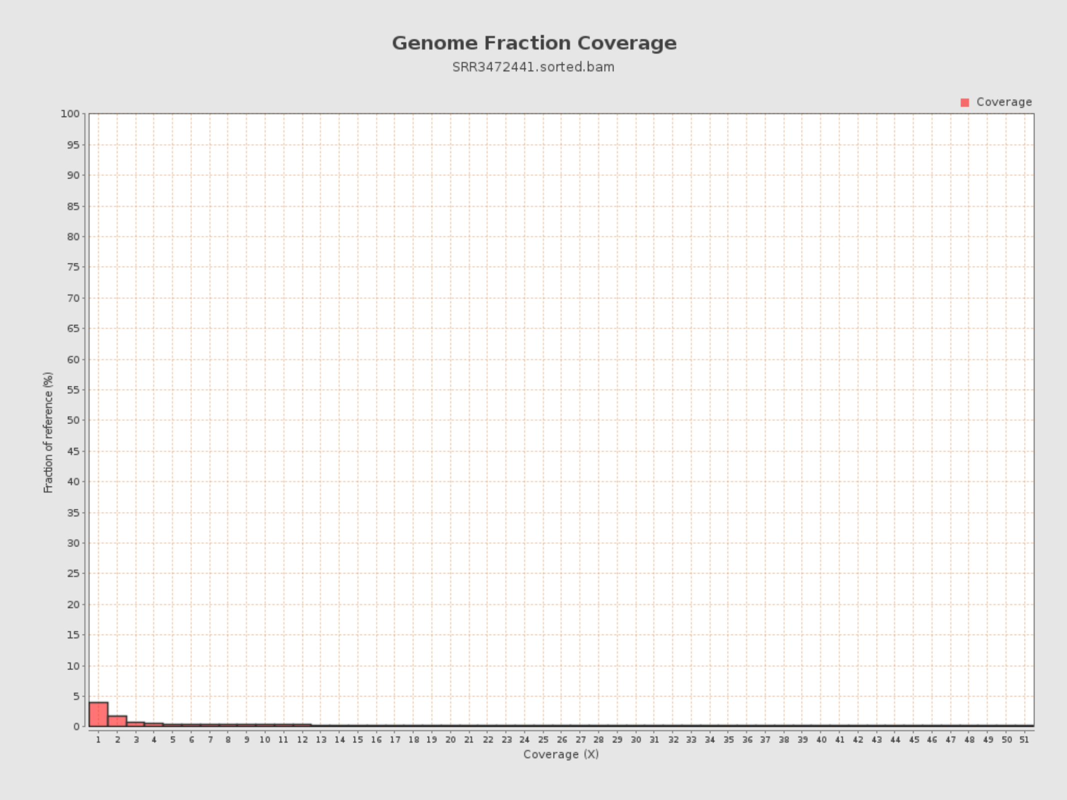
4. Results : Coverage Histogram



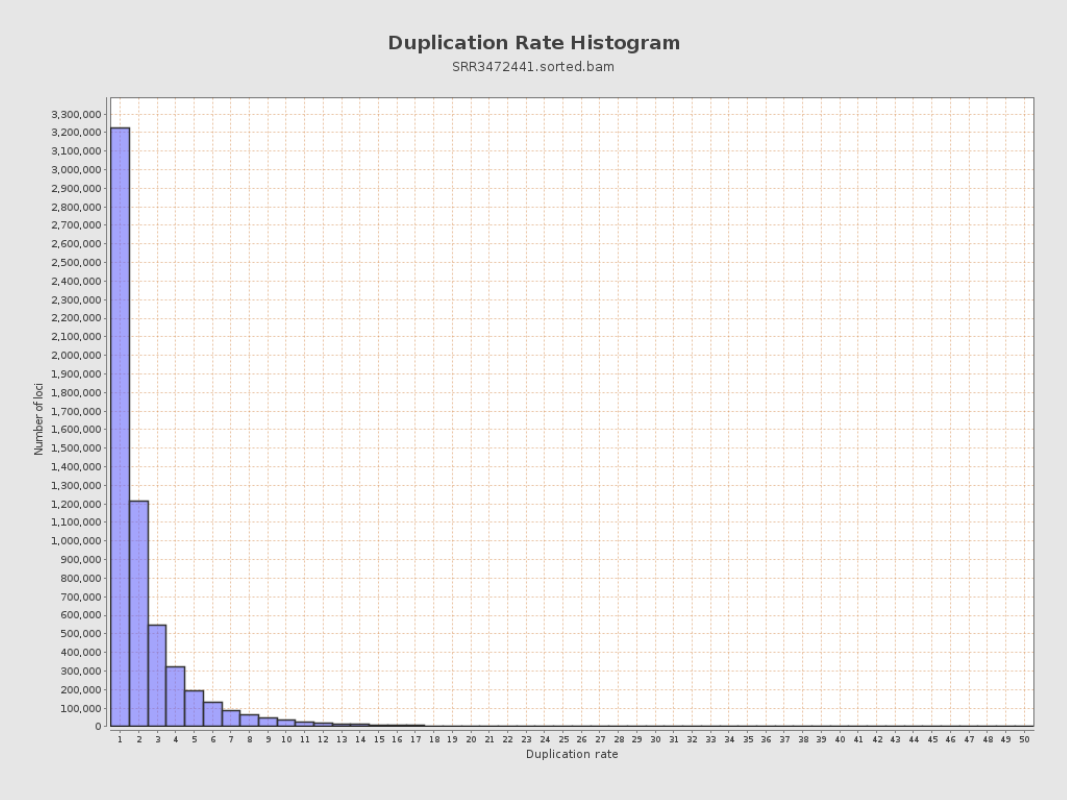
5. Results : Coverage Histogram (0-50X)



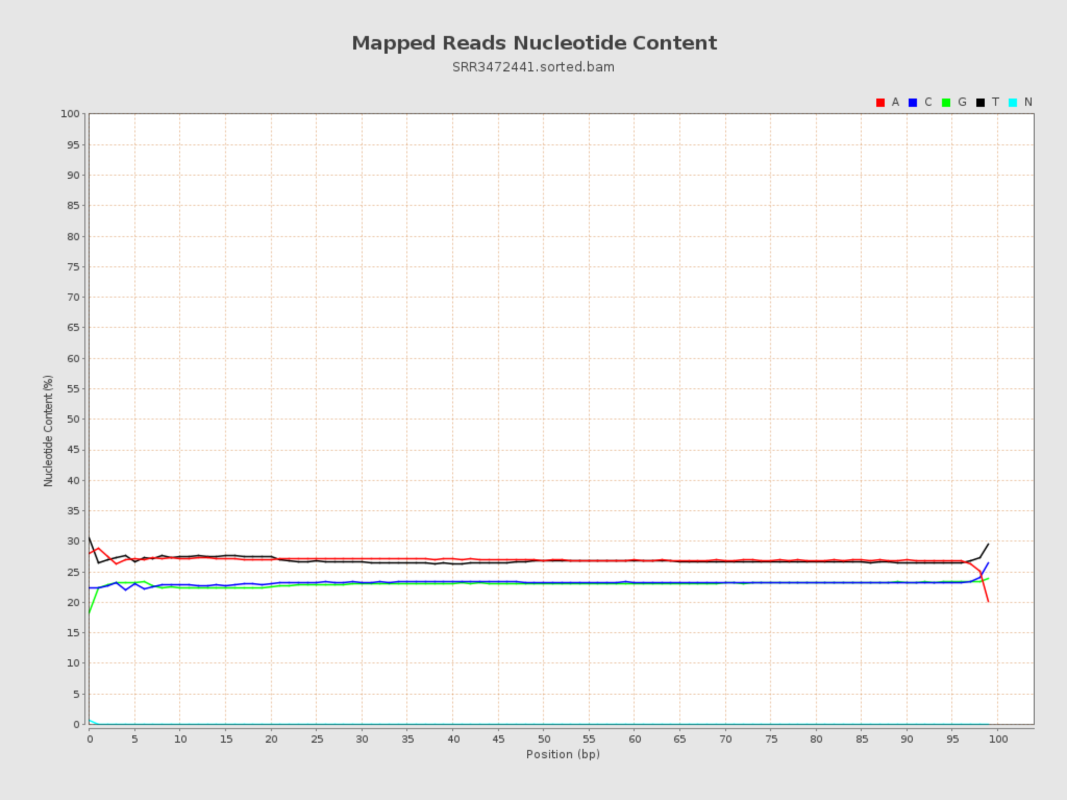
6. Results : Genome Fraction Coverage



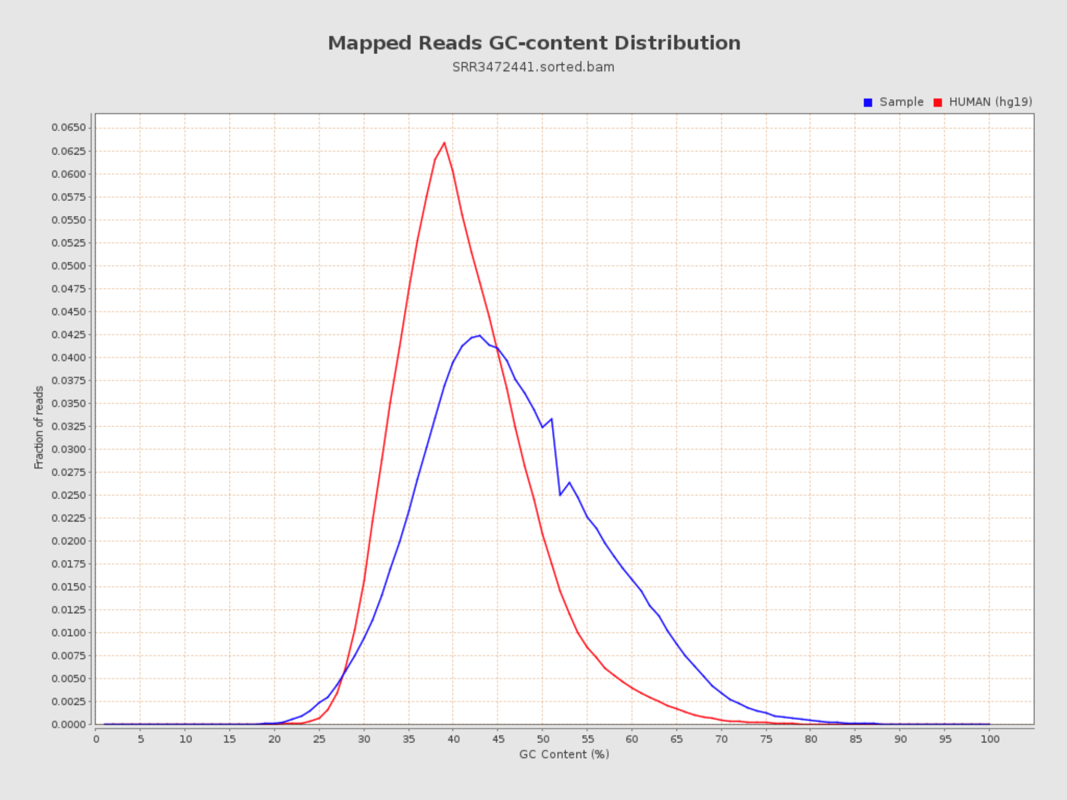
7. Results : Duplication Rate Histogram



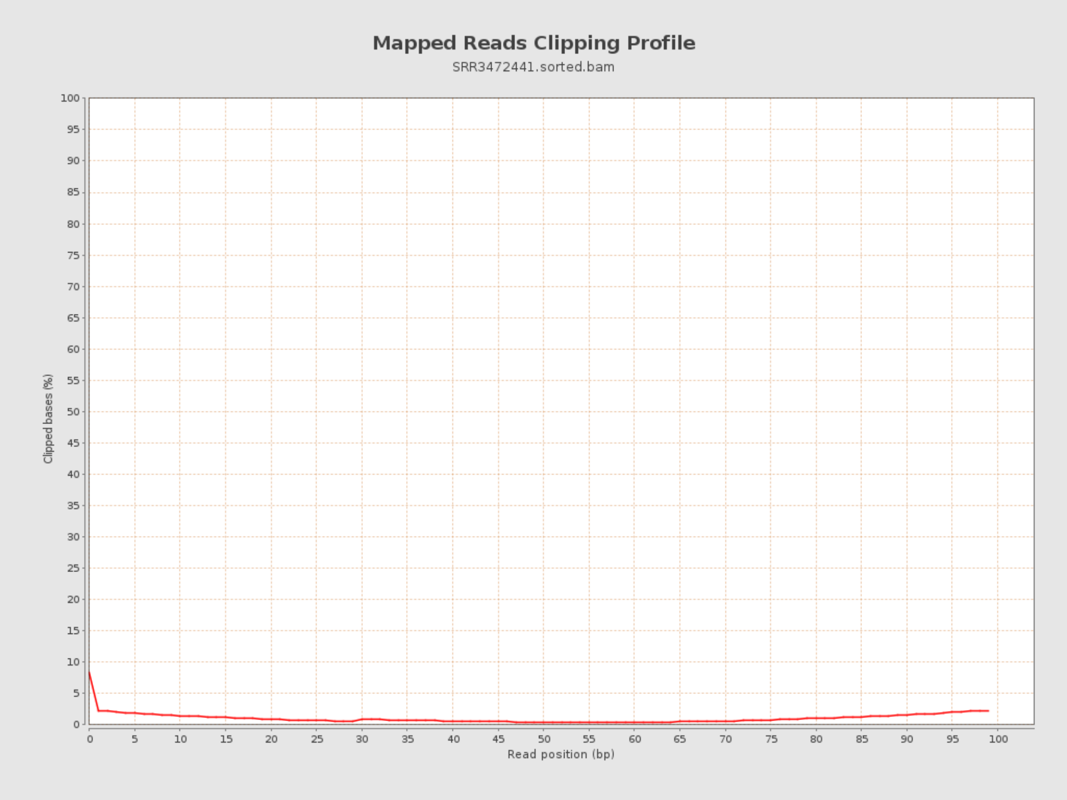
8. Results : Mapped Reads Nucleotide Content



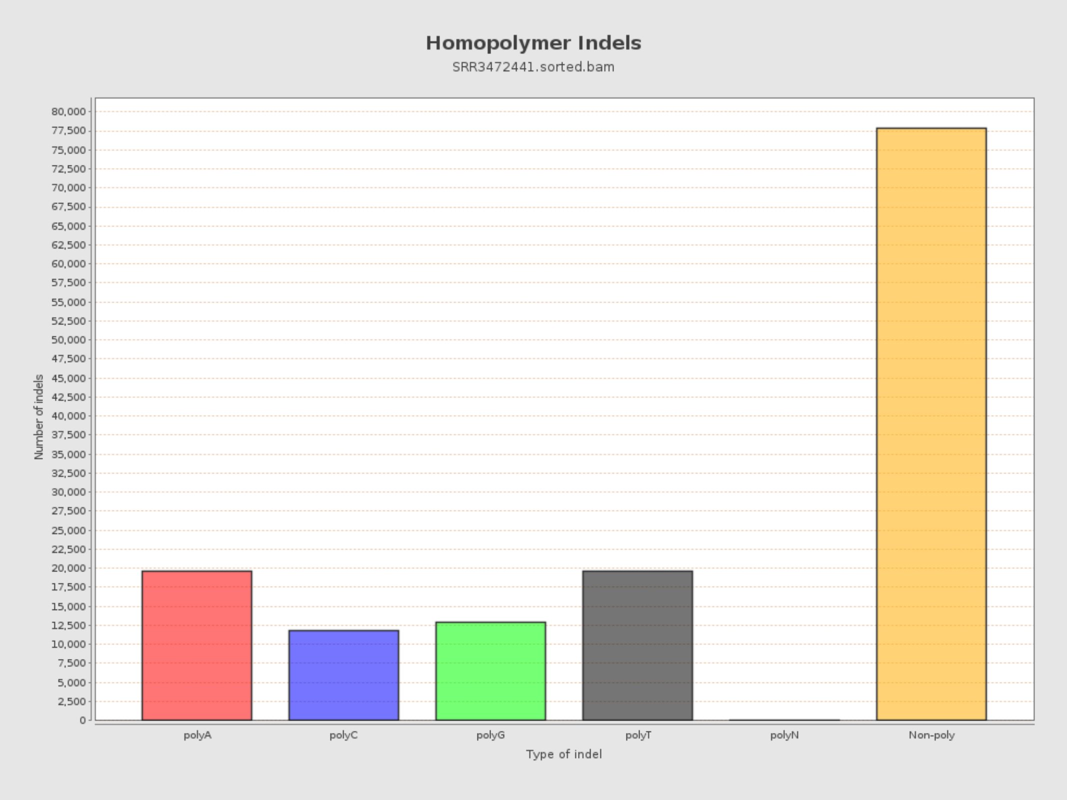
9. Results : Mapped Reads GC-content Distribution



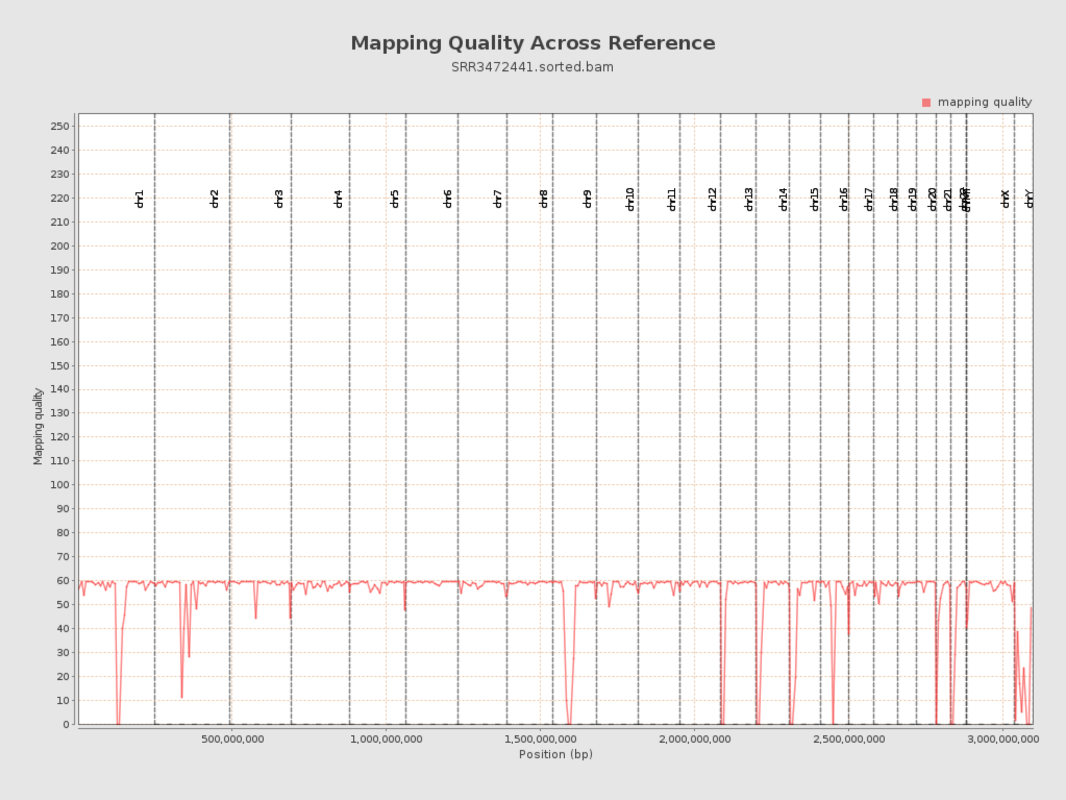
10. Results : Mapped Reads Clipping Profile



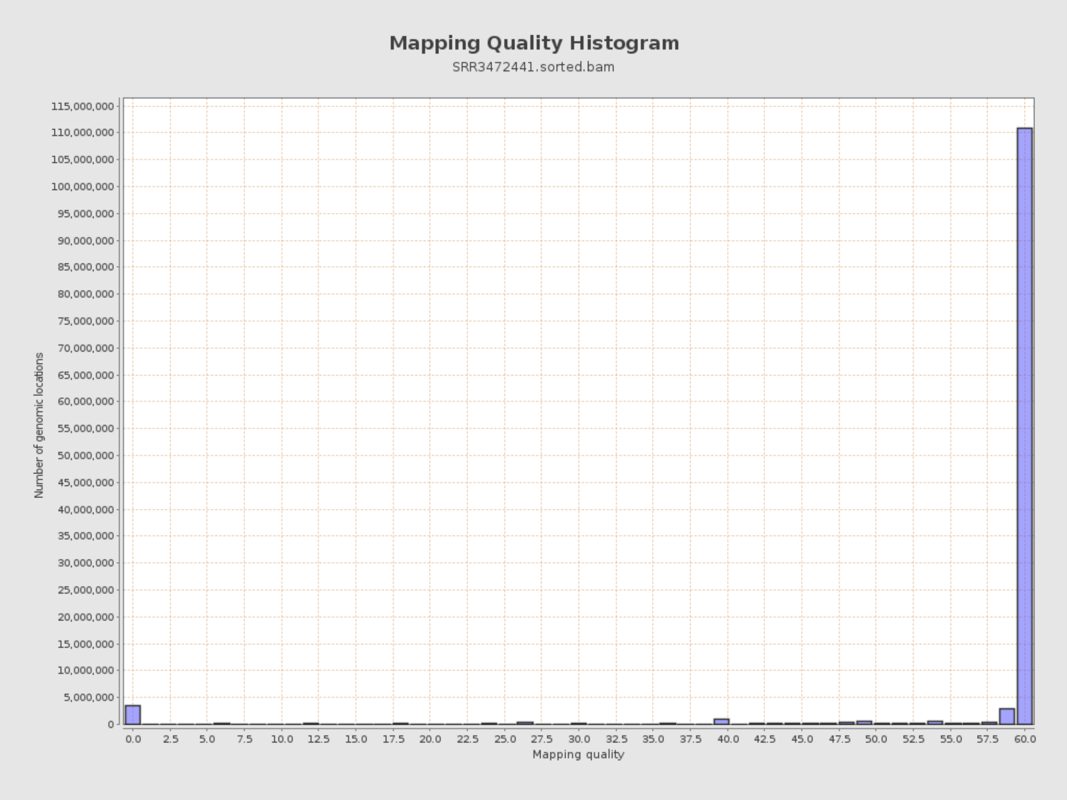
11. Results : Homopolymer Indels



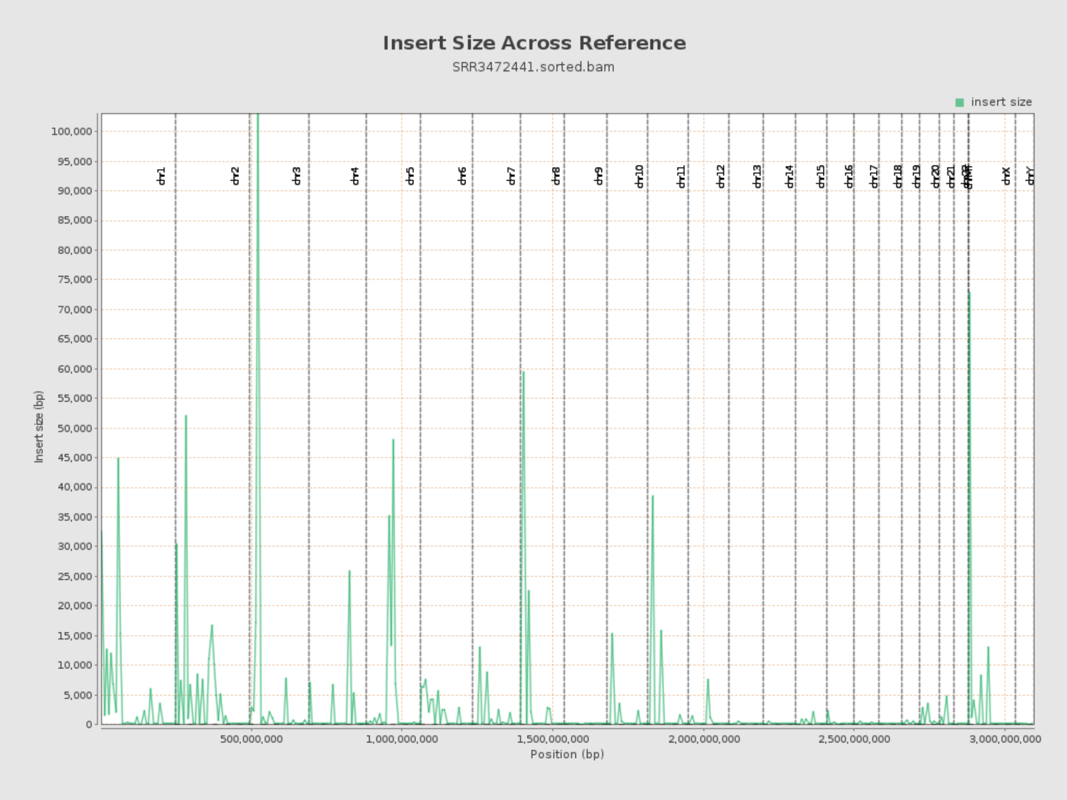
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram