Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:36:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472413.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_SRR3472413 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472413_1.fastq.gz SRR3472413_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:36:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472413.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,074,944
Mapped reads	17,909,856 / 99.09%
Unmapped reads	165,088 / 0.91%
Mapped paired reads	17,909,856 / 99.09%
Mapped reads, first in pair	8,979,863 / 49.68%
Mapped reads, second in pair	8,929,993 / 49.41%
Mapped reads, both in pair	17,810,048 / 98.53%
Mapped reads, singletons	99,808 / 0.55%
Secondary alignments	0
Supplementary alignments	73,506 / 0.41%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	11,256,860 / 62.28%
Duplication rate	46.81%
Clipped reads	1,198,299 / 6.63%

2.2. ACGT Content

Number/percentage of A's	482,073,088 / 27.42%
Number/percentage of C's	398,173,328 / 22.65%
Number/percentage of T's	482,933,154 / 27.47%
Number/percentage of G's	394,624,168 / 22.45%
Number/percentage of N's	209,764 / 0.01%

GC Percentage	45.1%

2.3. Coverage

Mean	0.568
Standard Deviation	18.1526

2.4. Mapping Quality

Mean Mapping Quality	55.05

2.5. Insert size

Mean	19,601.13
Standard Deviation	1,389,089.44
P25/Median/P75	157 / 217 / 292

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	9,602,571
Insertions	103,542
Mapped reads with at least one insertion	0.57%
Deletions	92,856
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.37%

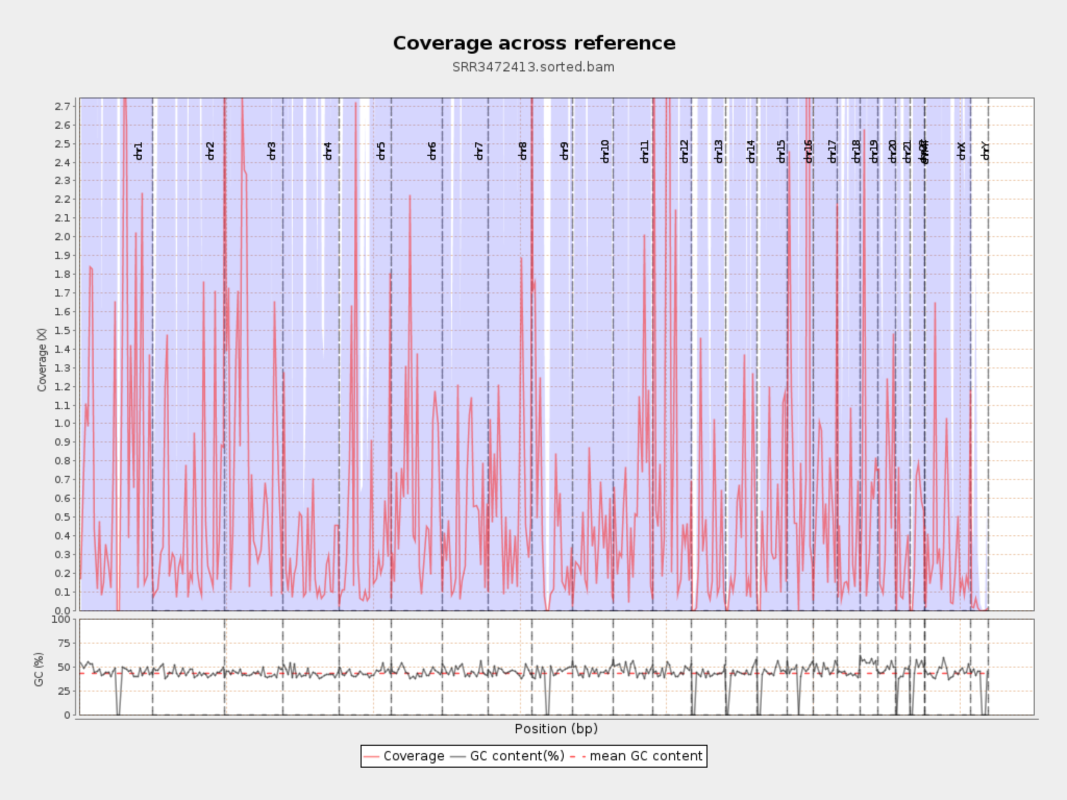
2.7. Chromosome stats

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

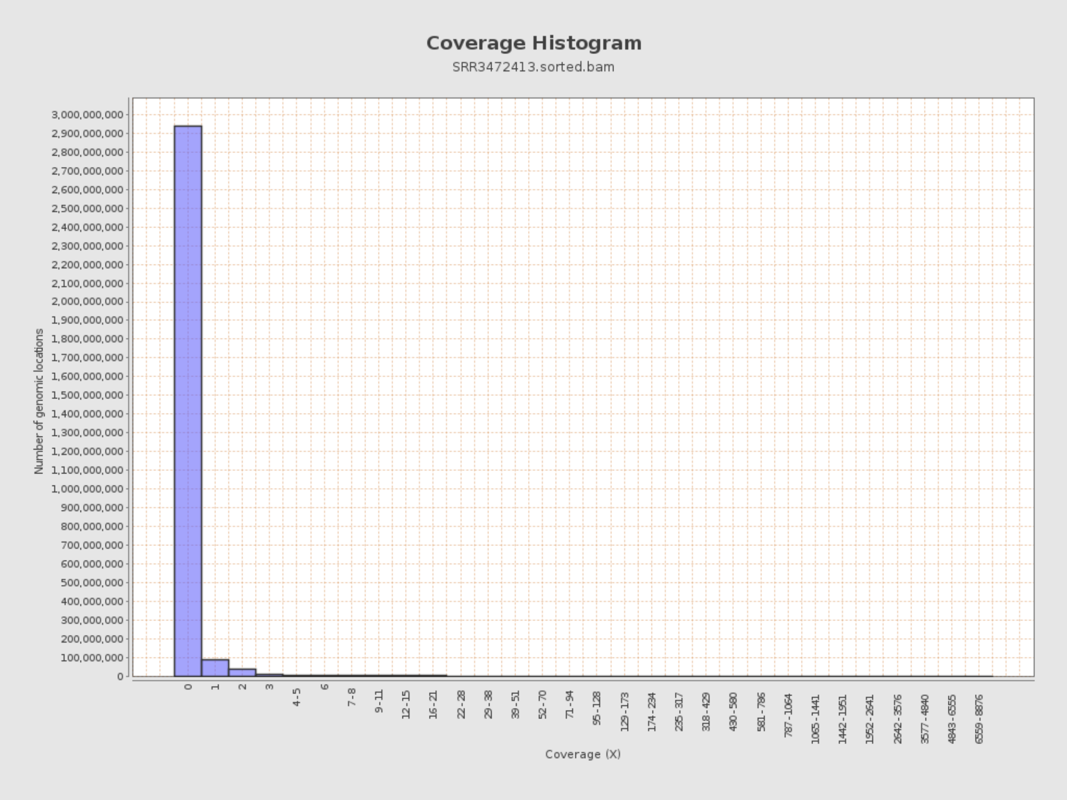
		bases	coverage	deviation
chr1	249250621	217773292	0.8737	23.1777
chr2	243199373	109892250	0.4519	14.4677
chr3	198022430	188056647	0.9497	22.3234
chr4	191154276	52760922	0.276	8.1169
chr5	180915260	85982956	0.4753	20.3624
chr6	171115067	112682565	0.6585	18.5195
chr7	159138663	74013488	0.4651	14.3249
chr8	146364022	87800121	0.5999	15.6301
chr9	141213431	70627971	0.5002	12.2341
chr10	135534747	47429261	0.3499	10.7143
chr11	135006516	81213298	0.6016	16.8489
chr12	133851895	136975230	1.0233	28.2293
chr13	115169878	37545746	0.326	12.7463
chr14	107349540	41452258	0.3861	19.7781
chr15	102531392	46754276	0.456	12.1241
chr16	90354753	117023217	1.2952	43.3006
chr17	81195210	50228057	0.6186	14.9702
chr18	78077248	25928898	0.3321	11.1378
chr19	59128983	45635301	0.7718	17.414
chr20	63025520	39892322	0.633	17.1348
chr21	48129895	12472451	0.2591	14.4717
chr22	51304566	22026283	0.4293	10.6619
chrMT	16571	7475	0.4511	0.7833
chrX	155270560	53137817	0.3422	9.6806

chrY	59373566	937515	0.0158	0.7169

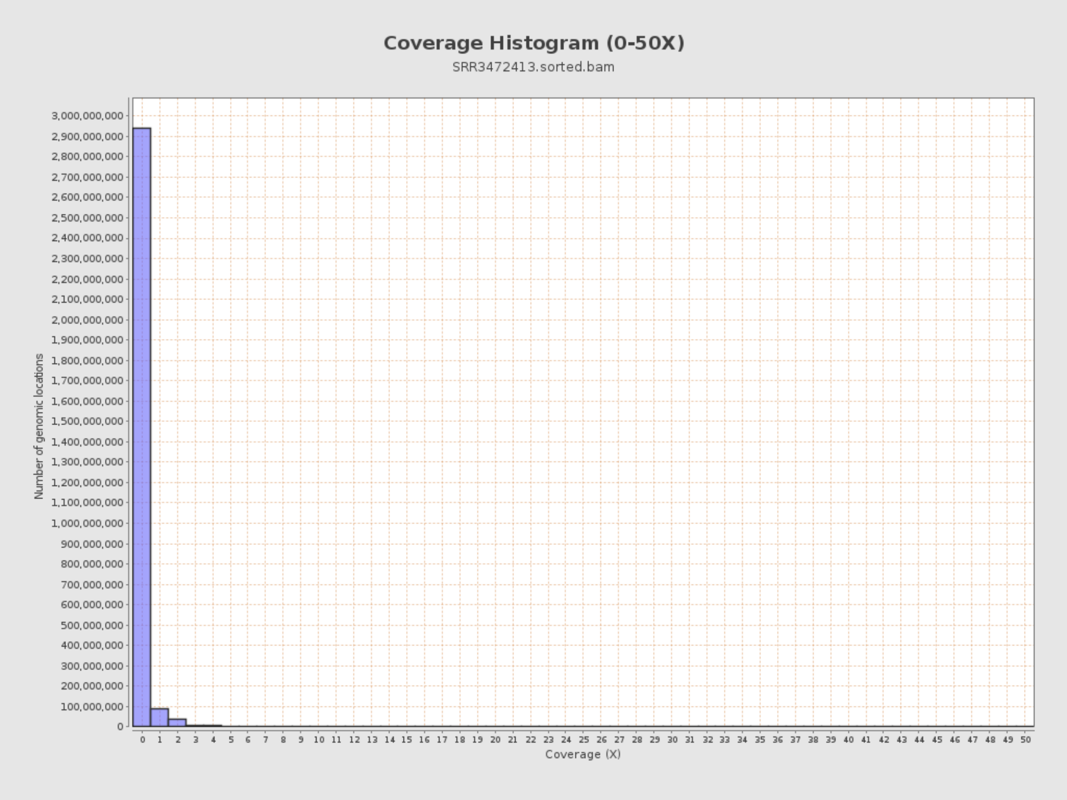
3. Results : Coverage across reference



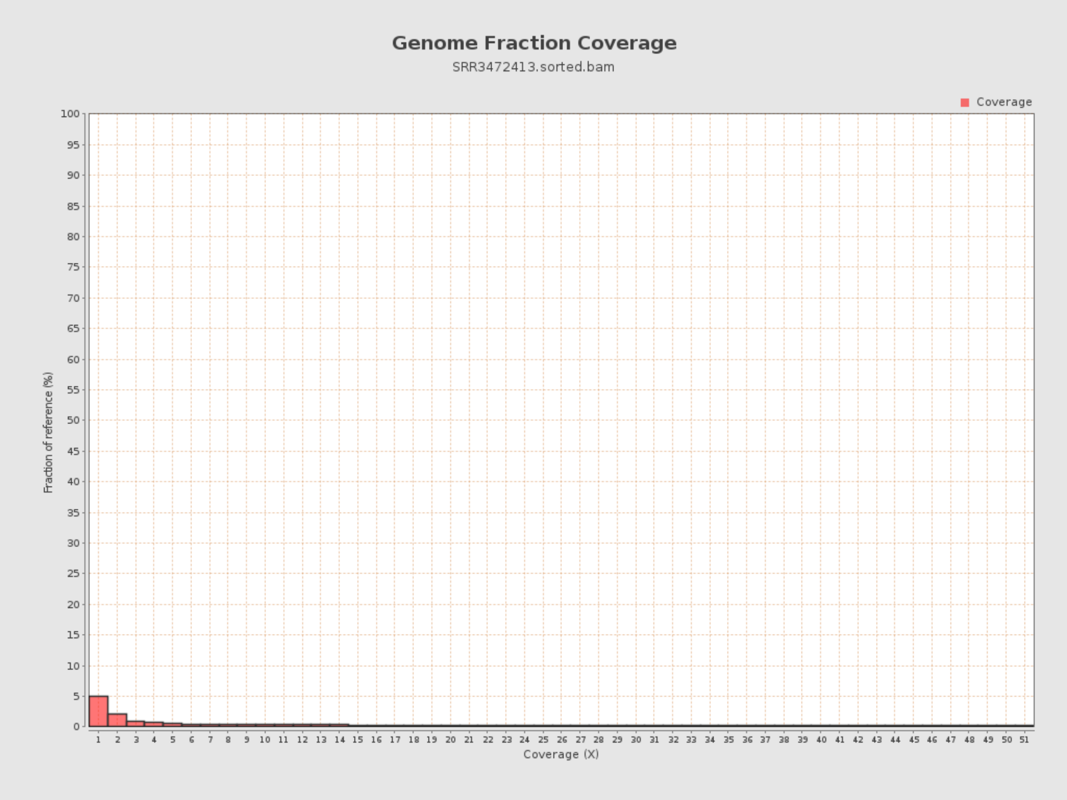
4. Results : Coverage Histogram



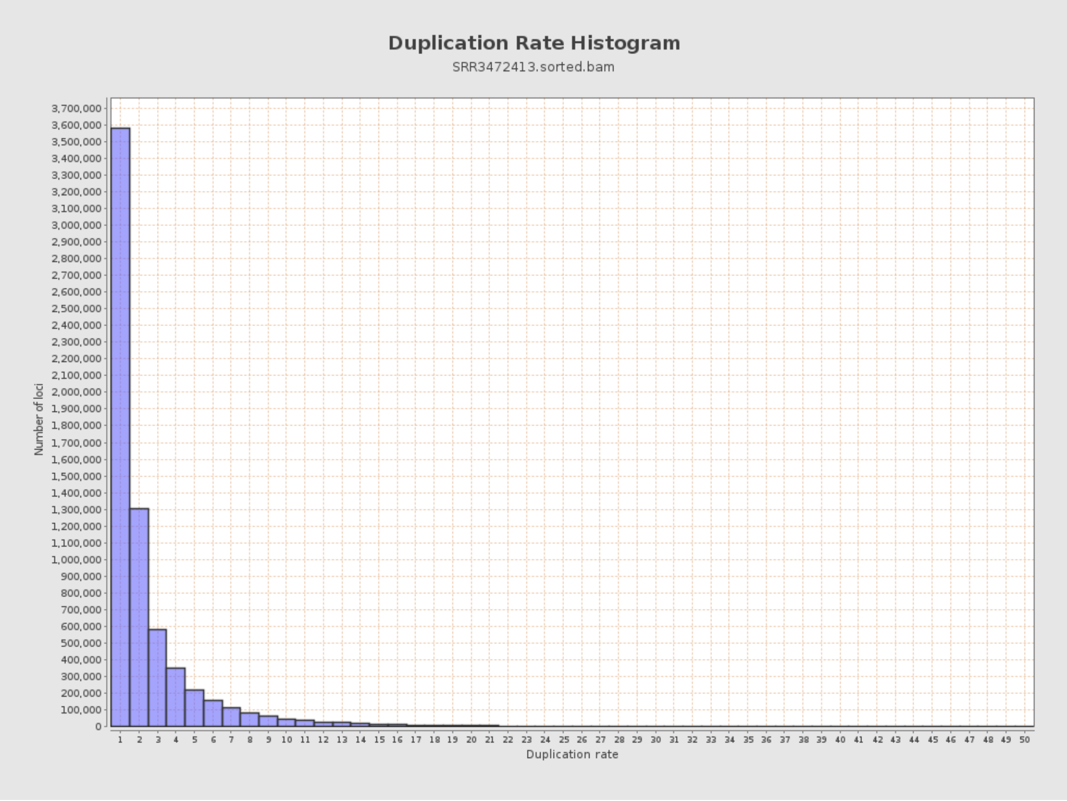
5. Results : Coverage Histogram (0-50X)



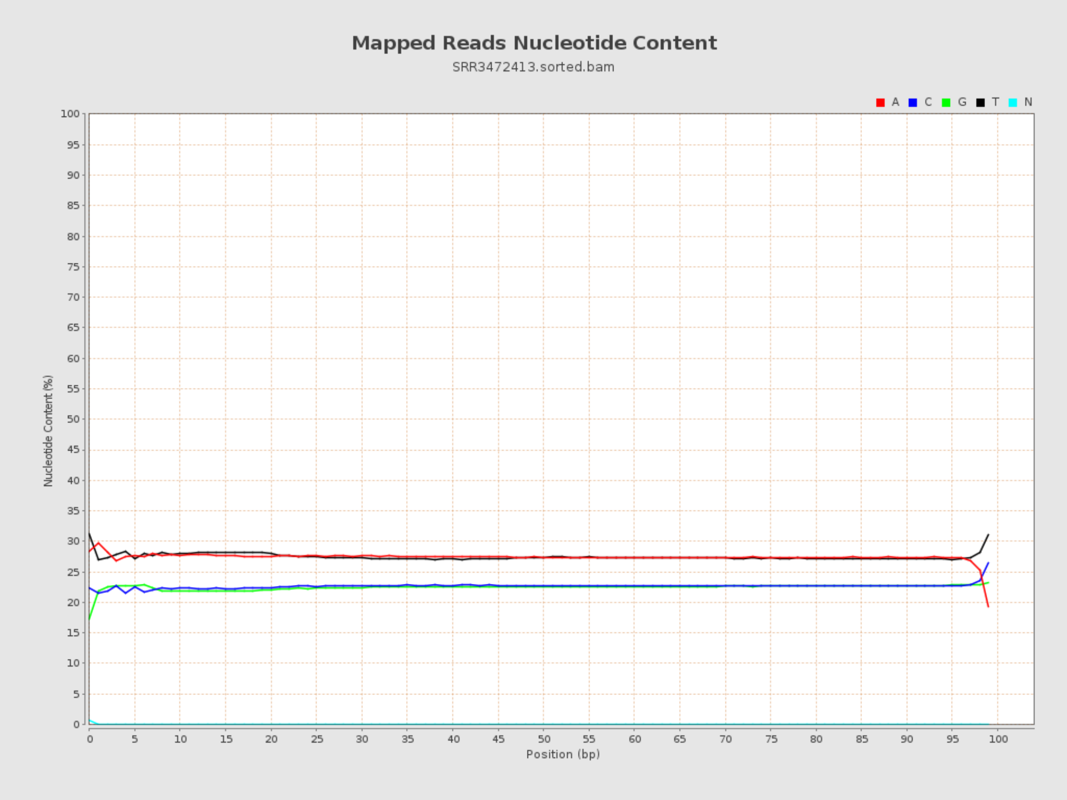
6. Results : Genome Fraction Coverage



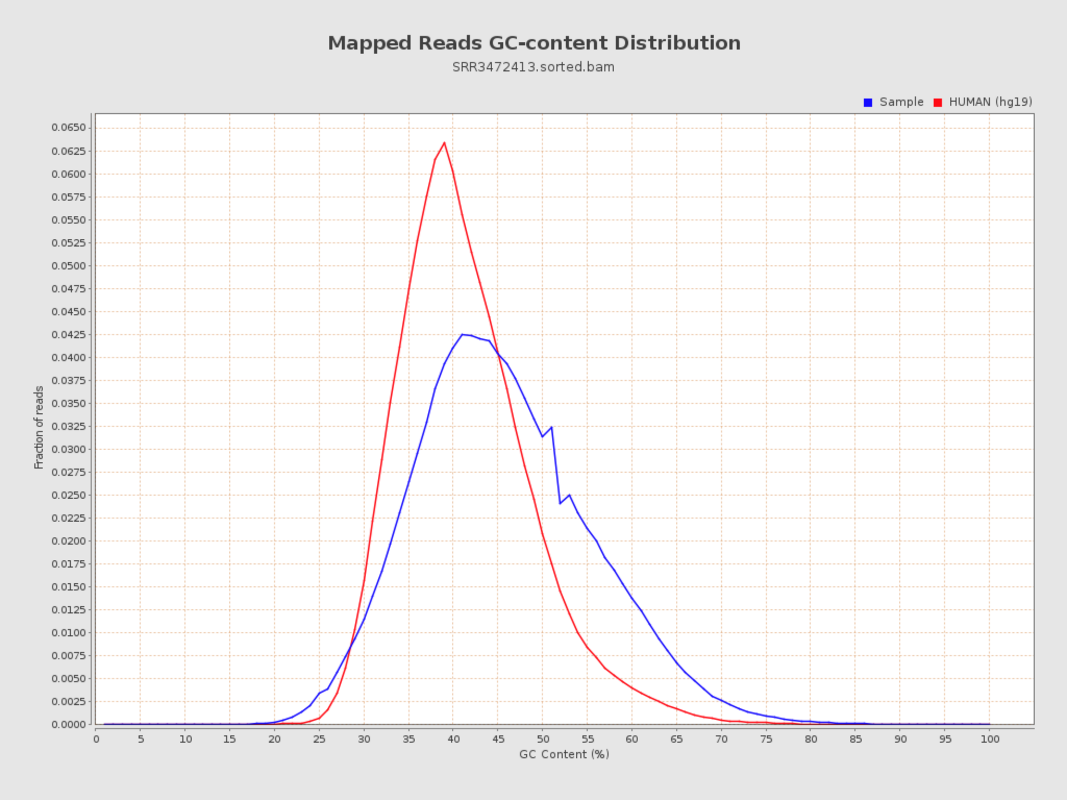
7. Results : Duplication Rate Histogram



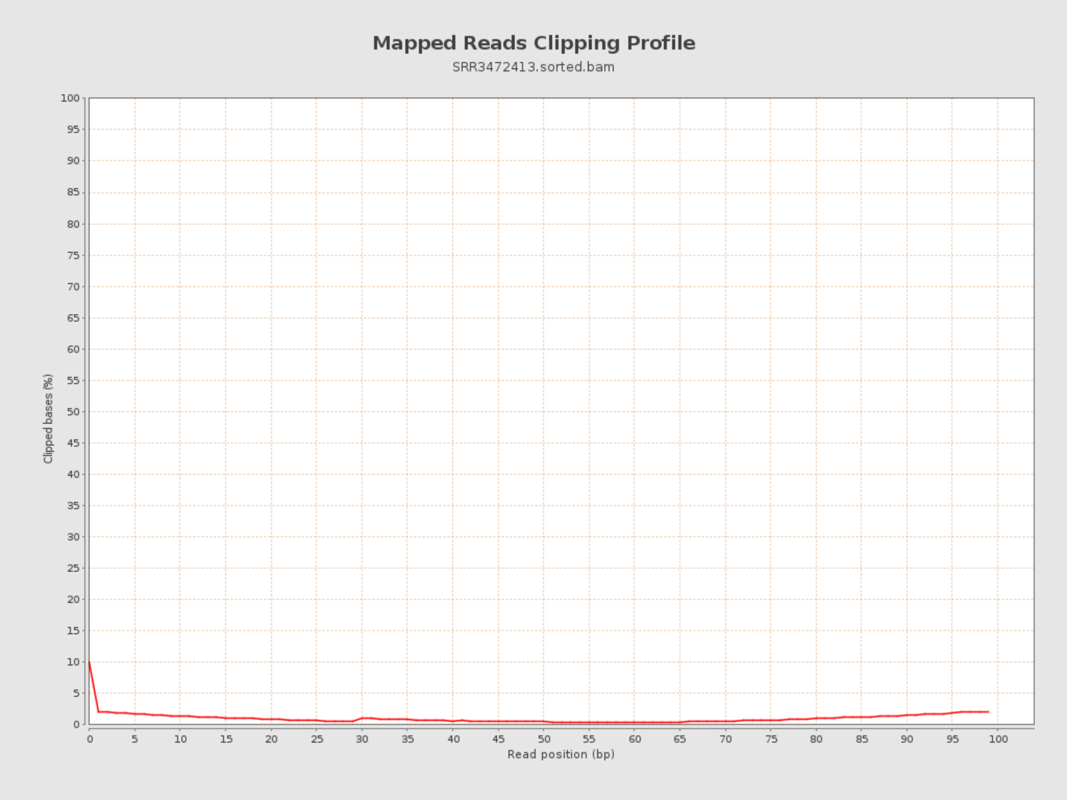
8. Results : Mapped Reads Nucleotide Content



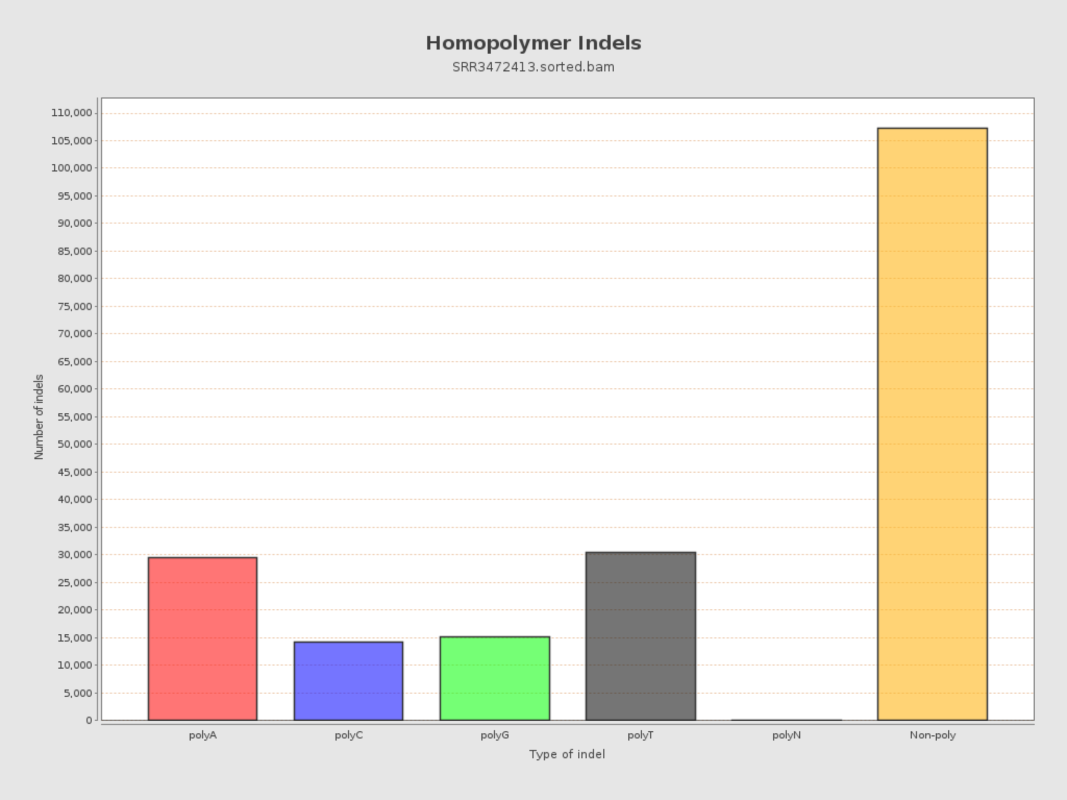
9. Results : Mapped Reads GC-content Distribution



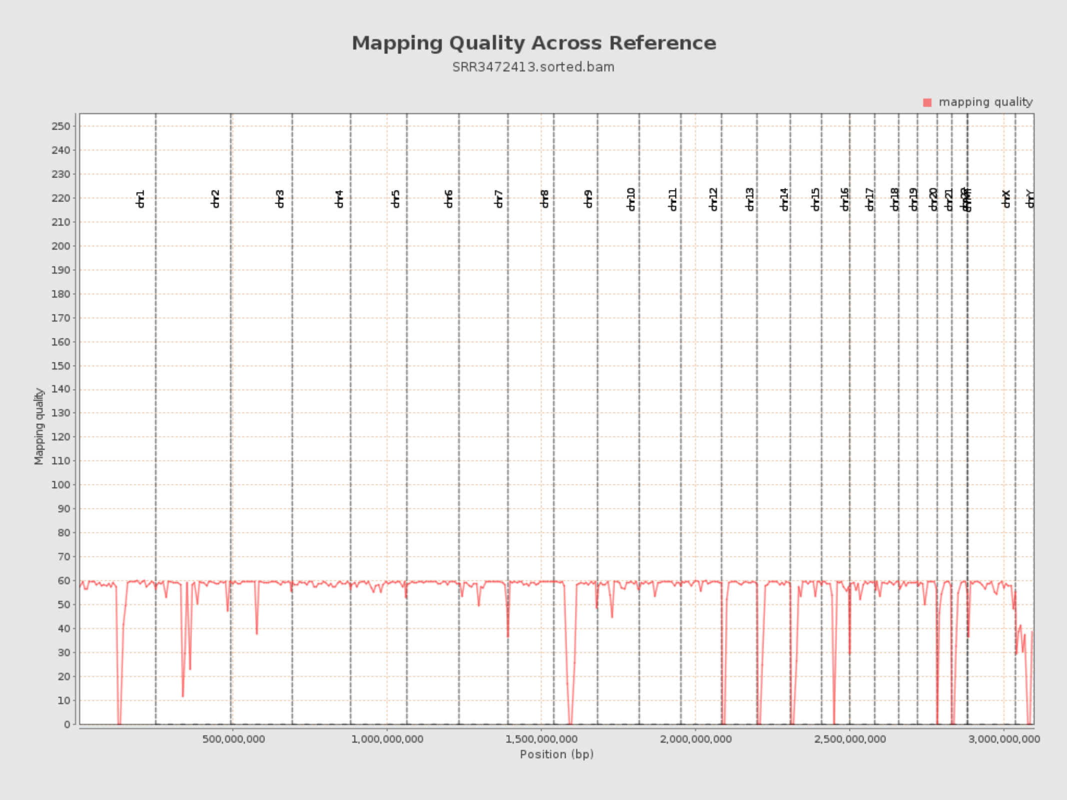
10. Results : Mapped Reads Clipping Profile



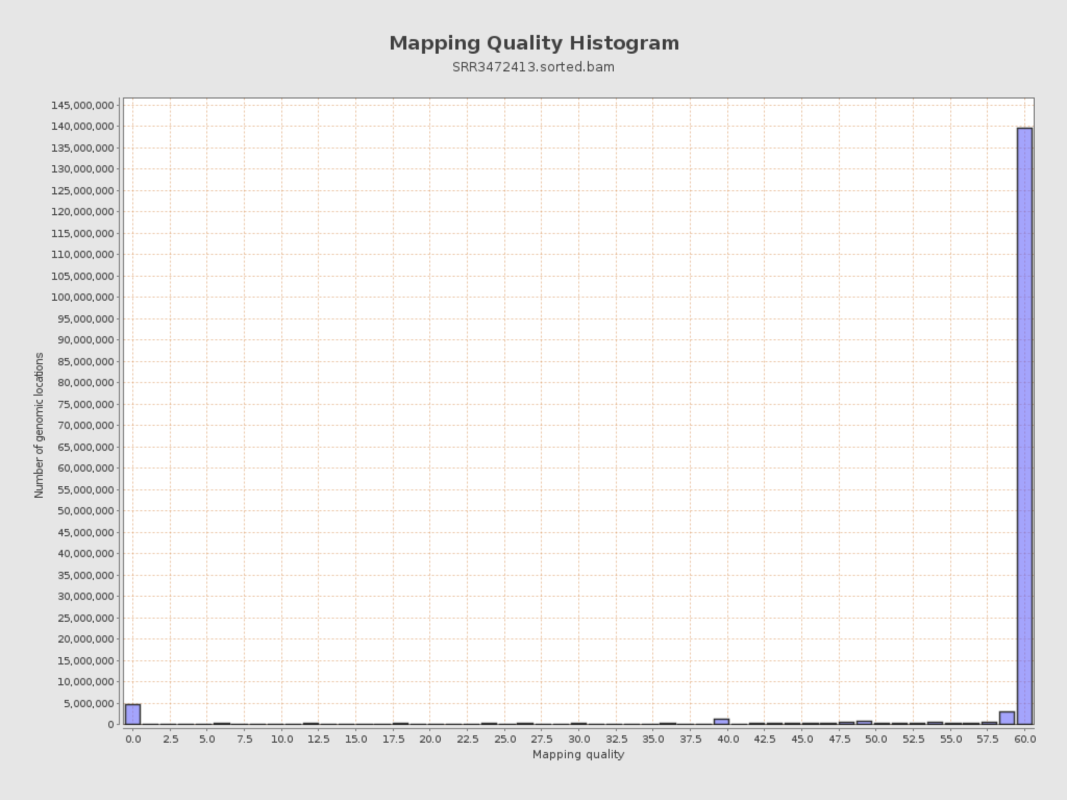
11. Results : Homopolymer Indels



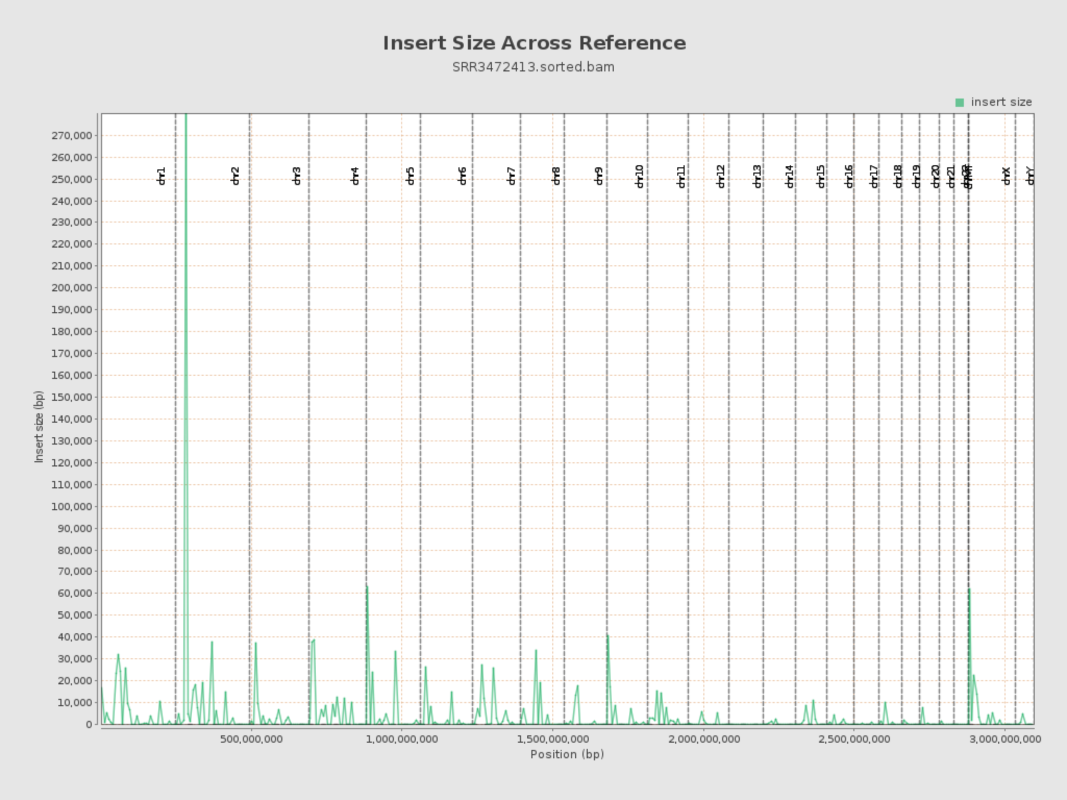
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram