Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:52:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472512.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_SRR3472512 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472512_1.fastq.gz SRR3472512_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:52:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472512.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,733,704
Mapped reads	16,549,486 / 98.9%
Unmapped reads	184,218 / 1.1%
Mapped paired reads	16,549,486 / 98.9%
Mapped reads, first in pair	8,300,108 / 49.6%
Mapped reads, second in pair	8,249,378 / 49.3%
Mapped reads, both in pair	16,451,872 / 98.32%
Mapped reads, singletons	97,614 / 0.58%
Secondary alignments	0
Supplementary alignments	76,244 / 0.46%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	10,130,773 / 60.54%
Duplication rate	44.51%
Clipped reads	1,505,345 / 9%

2.2. ACGT Content

Number/percentage of A's	449,593,055 / 27.64%
Number/percentage of C's	366,555,994 / 22.53%
Number/percentage of T's	446,450,973 / 27.44%
Number/percentage of G's	363,916,578 / 22.37%
Number/percentage of N's	252,684 / 0.02%

GC Percentage	44.9%

2.3. Coverage

Mean	0.5256
Standard Deviation	18.0644

2.4. Mapping Quality

Mean Mapping Quality	54.95

2.5. Insert size

Mean	34,932.86
Standard Deviation	1,830,426.46
P25/Median/P75	163 / 230 / 313

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	9,742,631
Insertions	92,697
Mapped reads with at least one insertion	0.56%
Deletions	80,696
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.73%

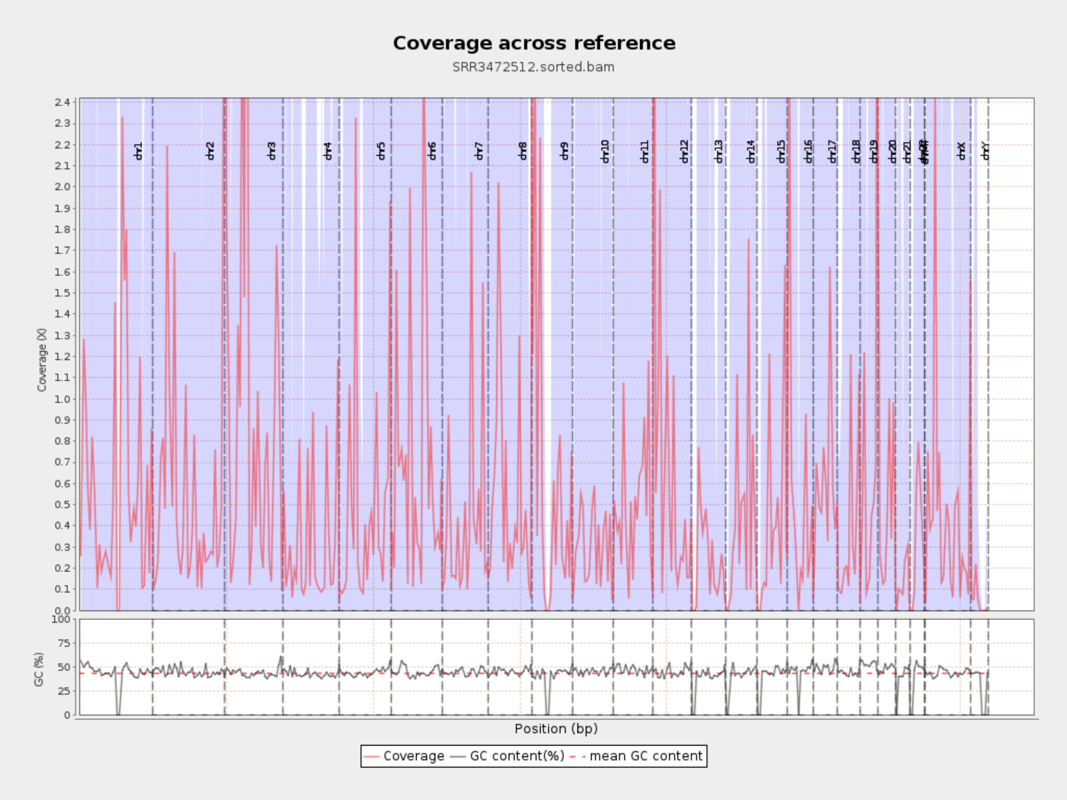
2.7. Chromosome stats

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

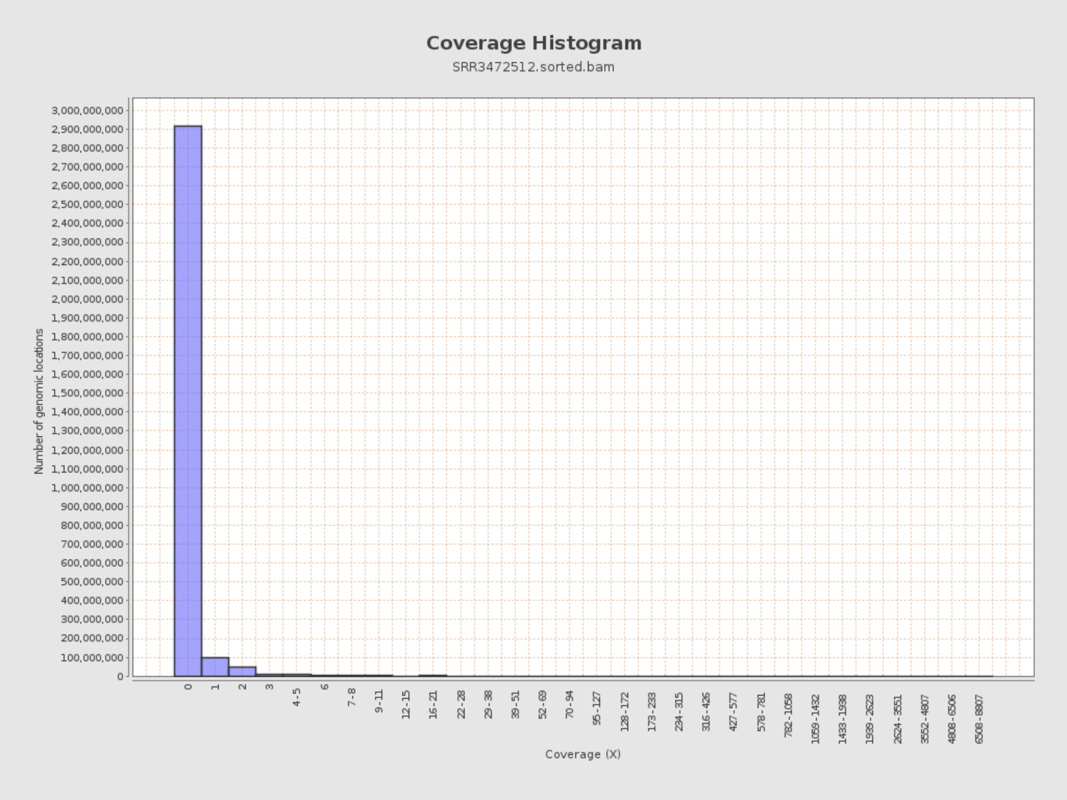
		bases	coverage	deviation
chr1	249250621	152053571	0.61	19.3405
chr2	243199373	130427478	0.5363	19.3274
chr3	198022430	207913897	1.05	26.6029
chr4	191154276	61036415	0.3193	11.1915
chr5	180915260	89617571	0.4954	19.6295
chr6	171115067	121574213	0.7105	20.0596
chr7	159138663	71289409	0.448	14.8309
chr8	146364022	78811097	0.5385	26.0161
chr9	141213431	88622022	0.6276	14.9831
chr10	135534747	42036953	0.3102	9.7891
chr11	135006516	68640959	0.5084	14.5696
chr12	133851895	99838026	0.7459	25.9607
chr13	115169878	28525827	0.2477	8.7046
chr14	107349540	47820426	0.4455	26.2681
chr15	102531392	46036844	0.449	16.0048
chr16	90354753	49084557	0.5432	17.3211
chr17	81195210	49260753	0.6067	13.3329
chr18	78077248	30295292	0.388	14.4062
chr19	59128983	34066344	0.5761	15.4049
chr20	63025520	33463872	0.531	14.8259
chr21	48129895	6621531	0.1376	4.6642
chr22	51304566	16858745	0.3286	11.0495
chrMT	16571	1909	0.1152	0.3773
chrX	155270560	70149247	0.4518	12.3115

chrY	59373566	2940815	0.0495	1.7265

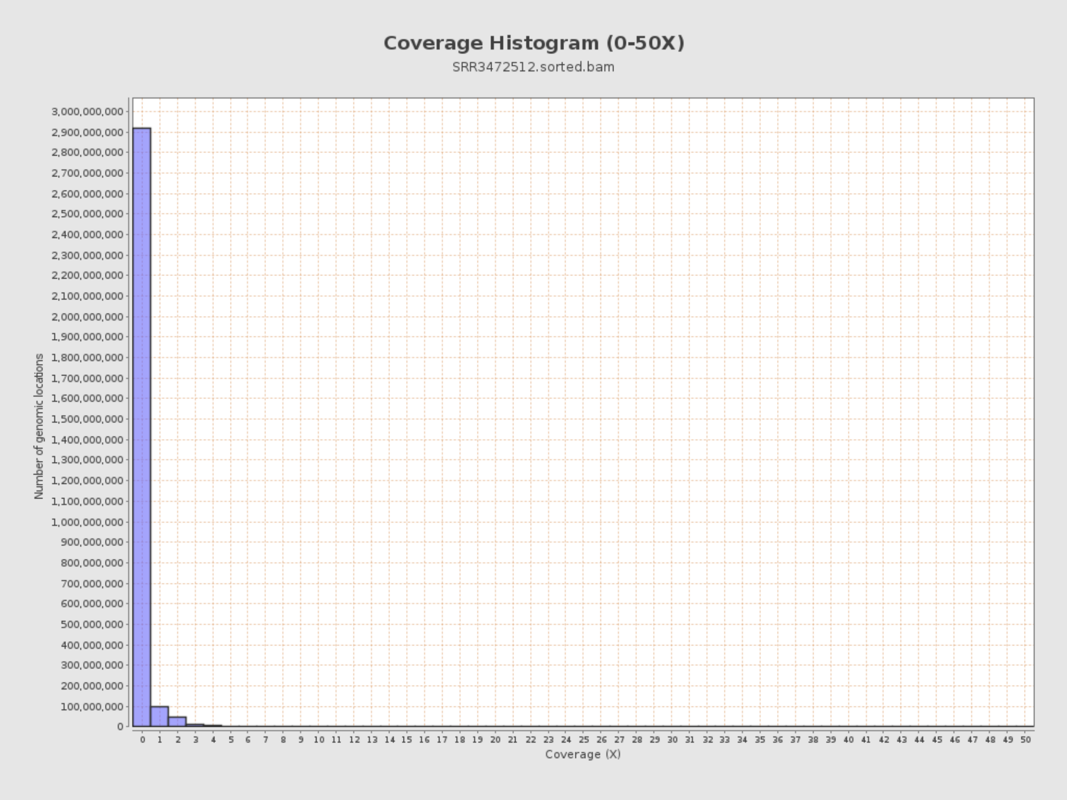
3. Results : Coverage across reference



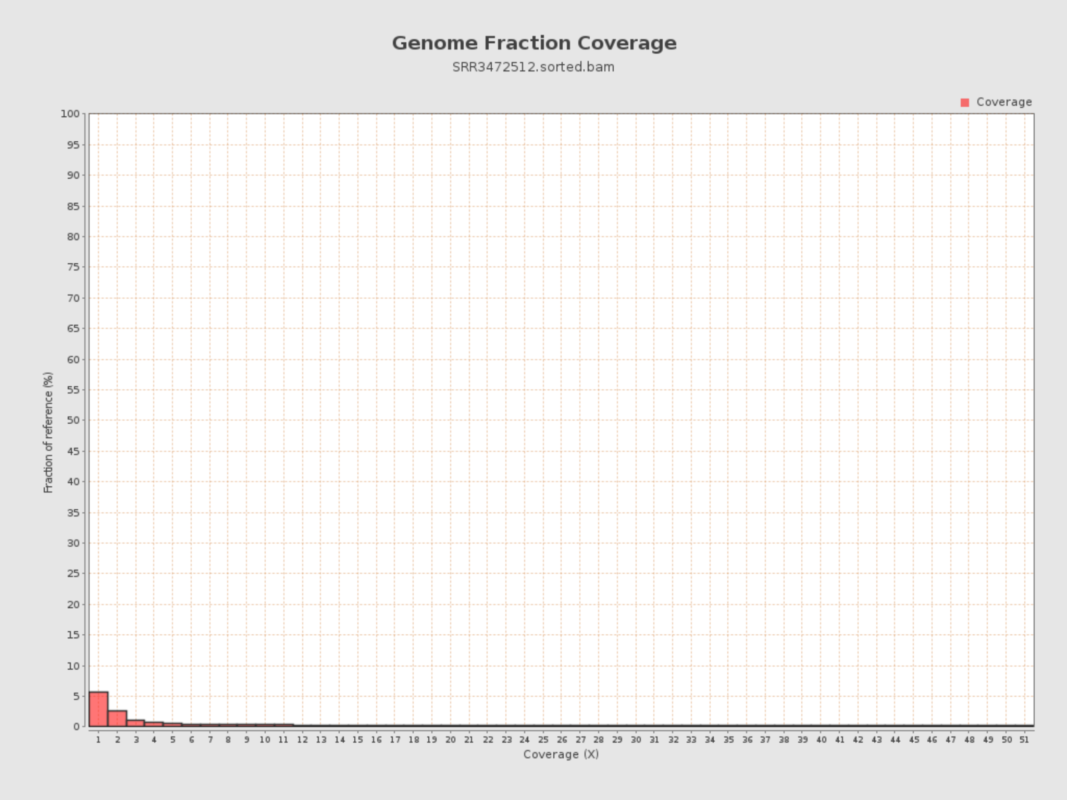
4. Results : Coverage Histogram



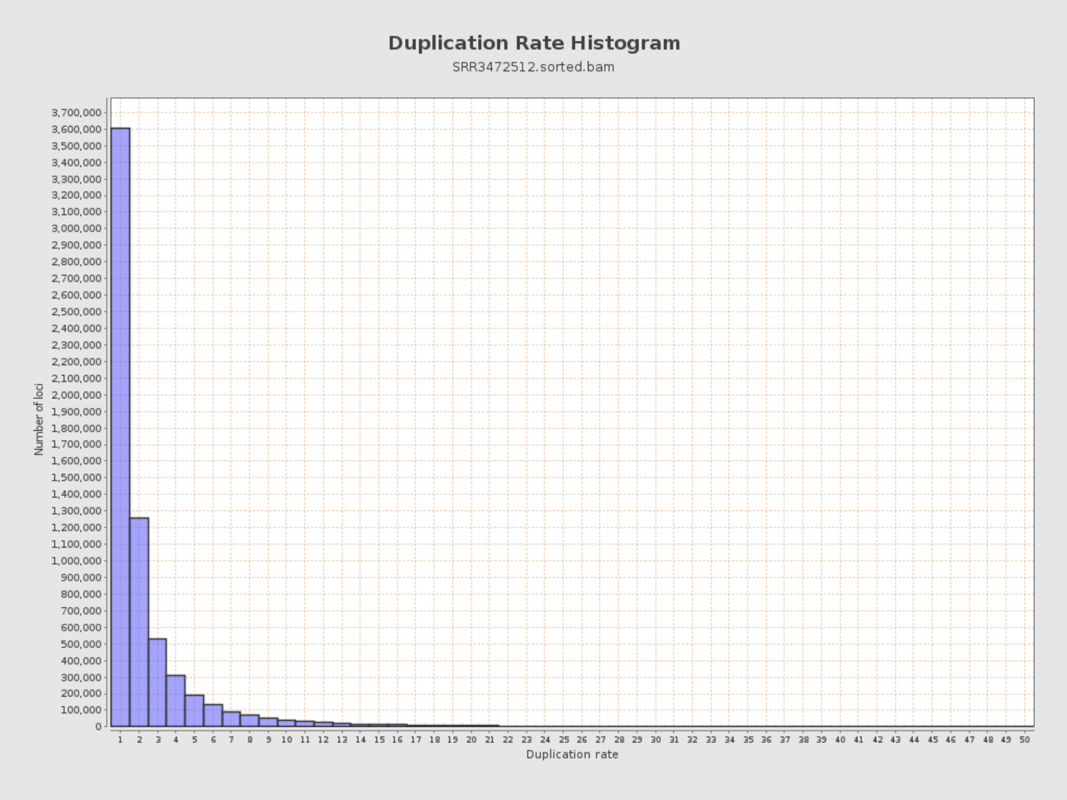
5. Results : Coverage Histogram (0-50X)



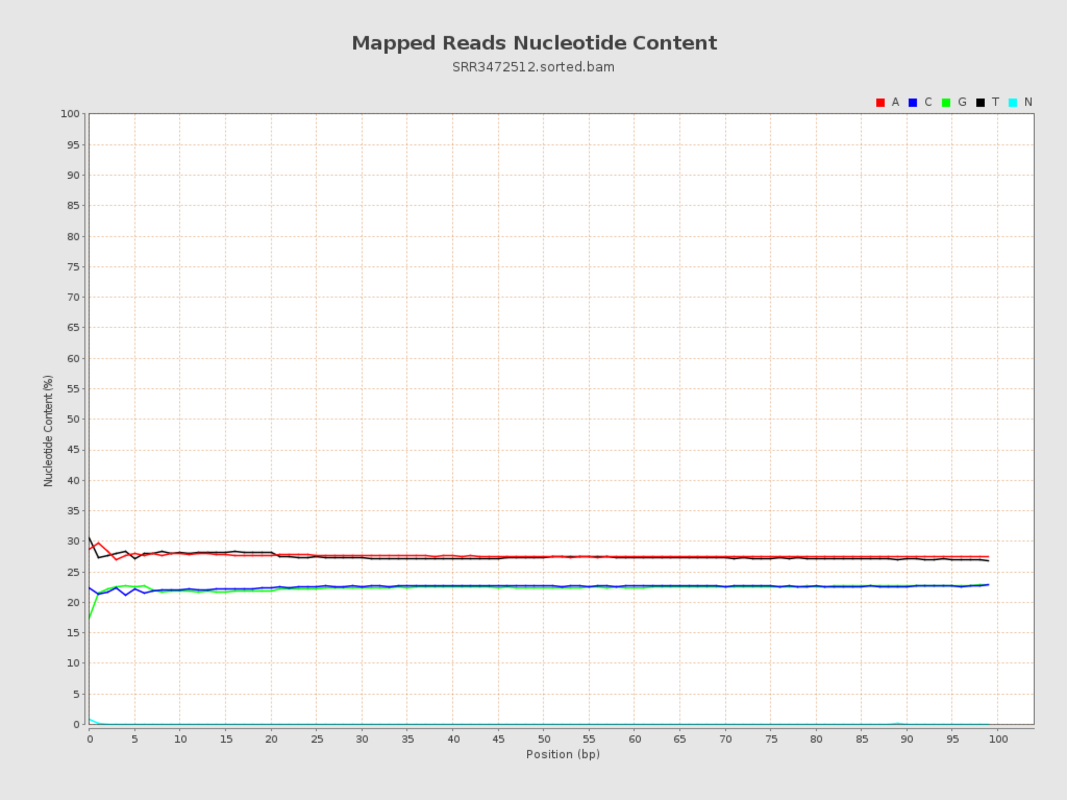
6. Results : Genome Fraction Coverage



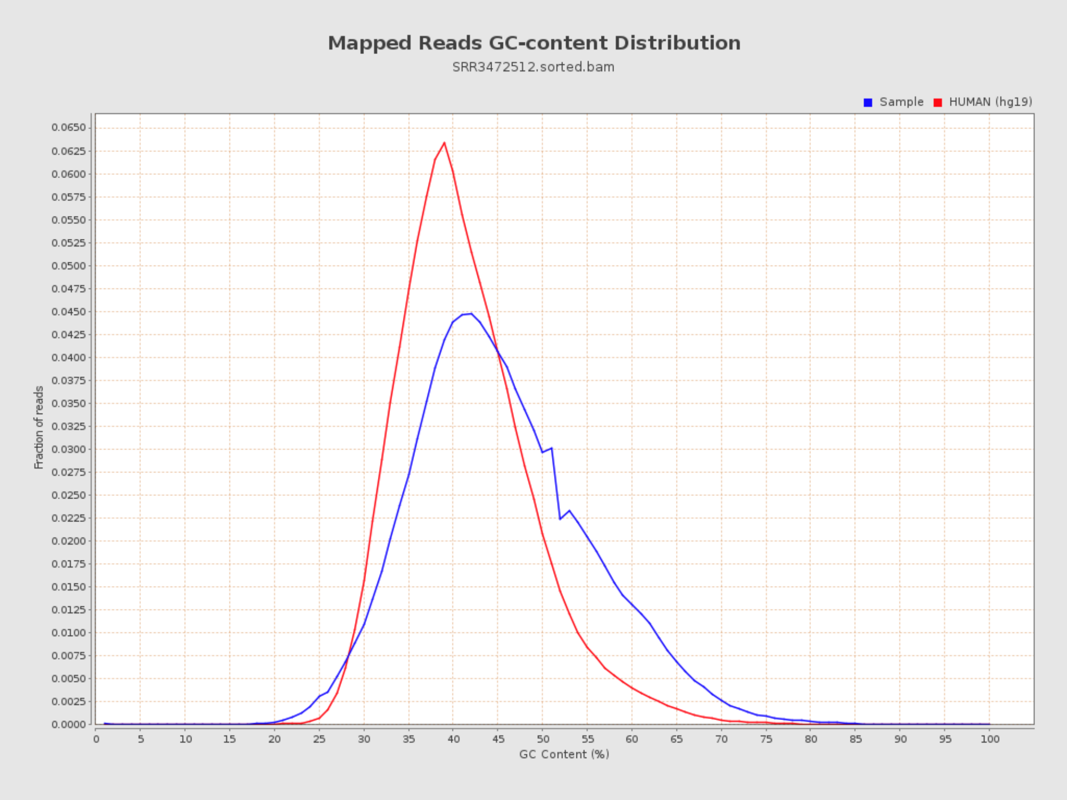
7. Results : Duplication Rate Histogram



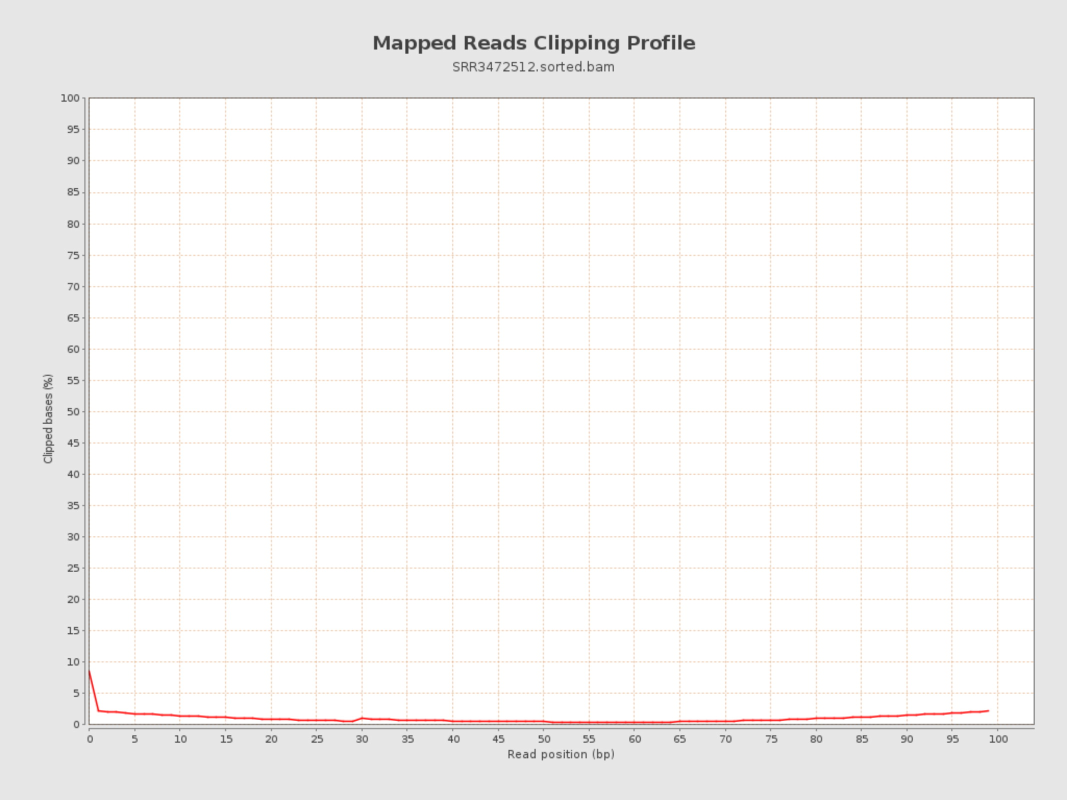
8. Results : Mapped Reads Nucleotide Content



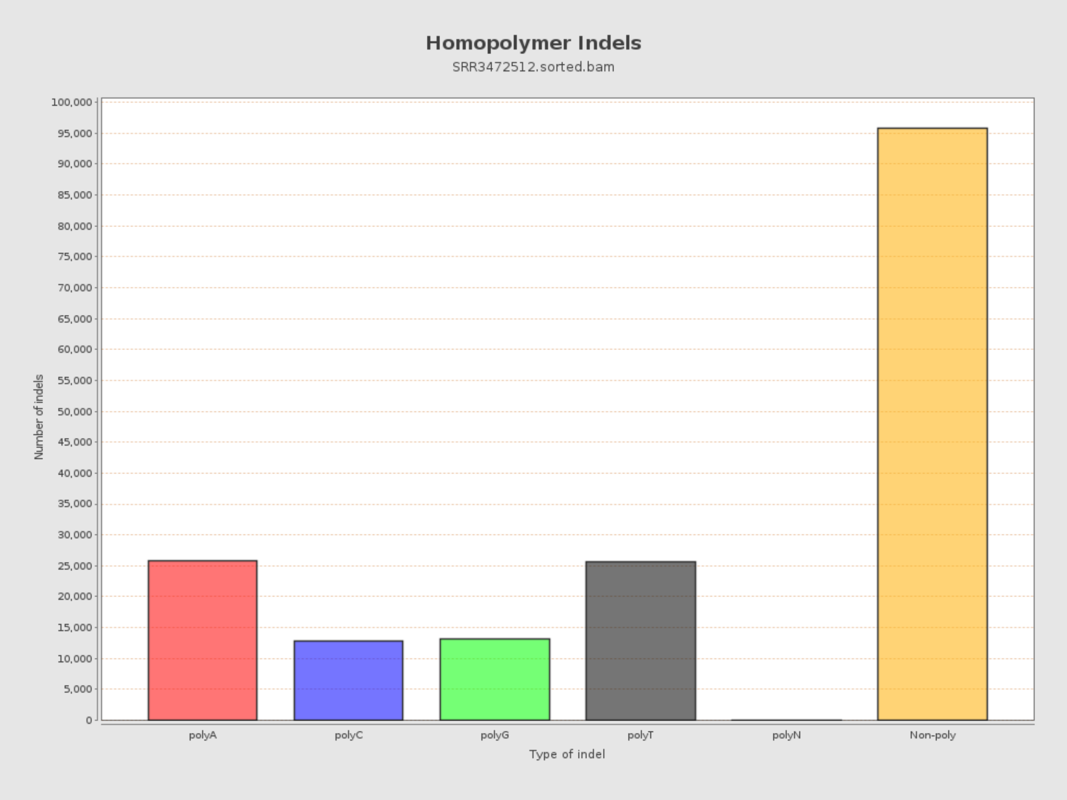
9. Results : Mapped Reads GC-content Distribution



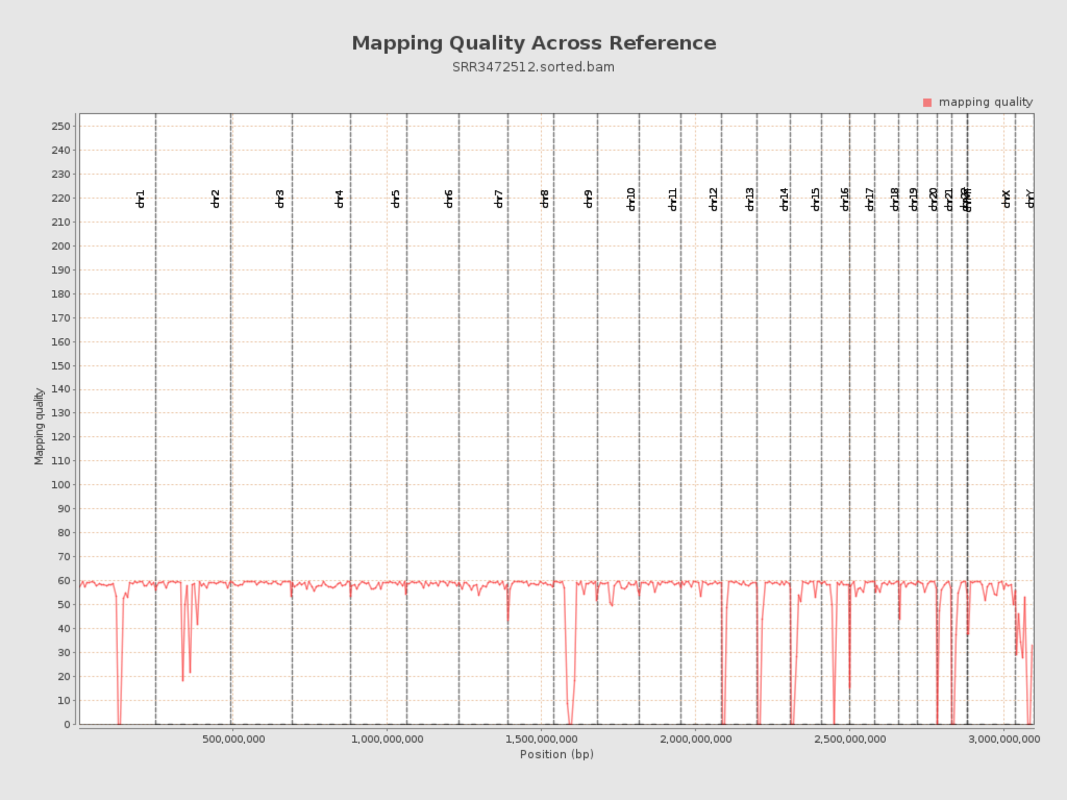
10. Results : Mapped Reads Clipping Profile



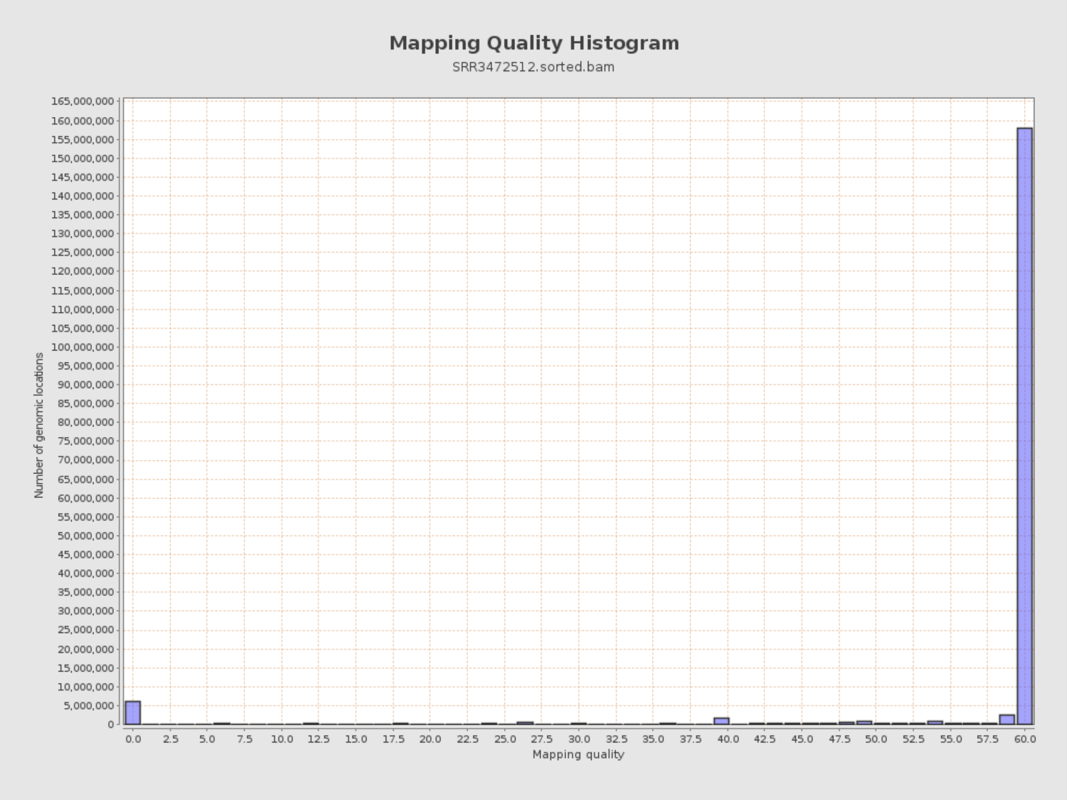
11. Results : Homopolymer Indels



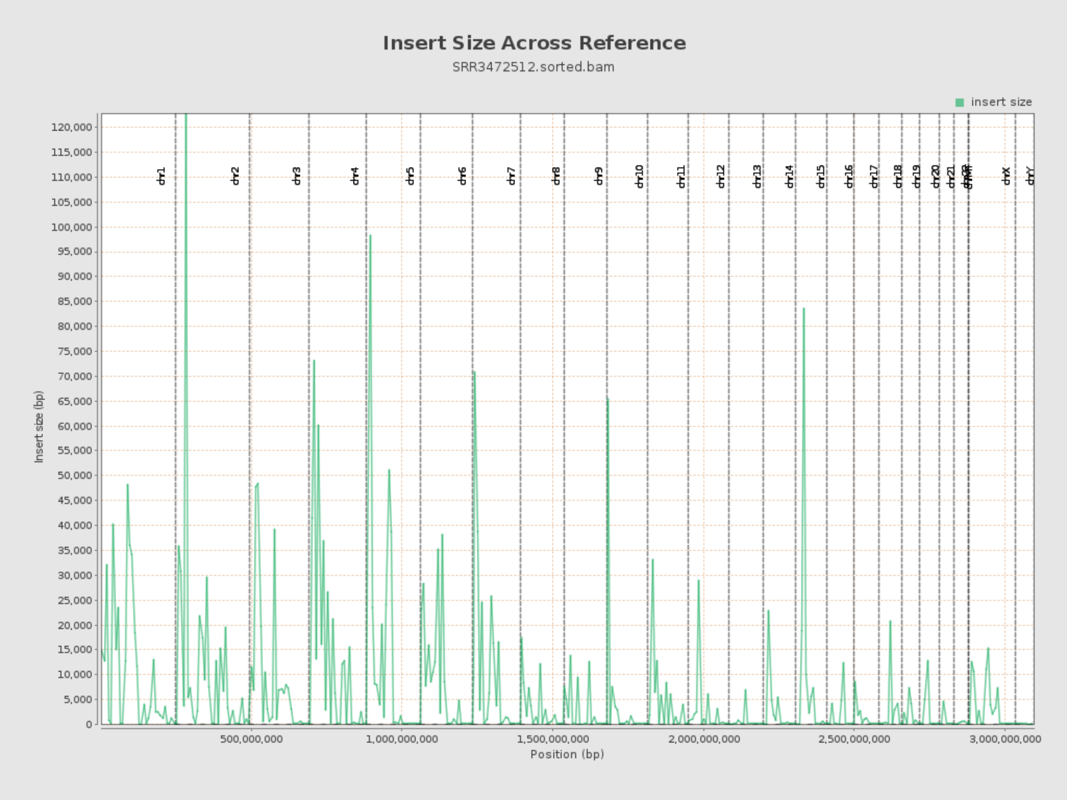
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram