Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:25:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472408.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_SRR3472408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472408_1.fastq.gz SRR3472408_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:25:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,514,242
Mapped reads	18,348,186 / 99.1%
Unmapped reads	166,056 / 0.9%
Mapped paired reads	18,348,186 / 99.1%
Mapped reads, first in pair	9,204,513 / 49.72%
Mapped reads, second in pair	9,143,673 / 49.39%
Mapped reads, both in pair	18,247,380 / 98.56%
Mapped reads, singletons	100,806 / 0.54%
Secondary alignments	0
Supplementary alignments	74,210 / 0.4%
Read min/max/mean length	30 / 100 / 99.32
Duplicated reads (estimated)	11,847,615 / 63.99%
Duplication rate	47.66%
Clipped reads	1,397,324 / 7.55%

2.2. ACGT Content

Number/percentage of A's	474,737,670 / 26.43%
Number/percentage of C's	424,418,909 / 23.63%
Number/percentage of T's	474,748,689 / 26.43%
Number/percentage of G's	421,823,504 / 23.49%
Number/percentage of N's	225,273 / 0.01%

GC Percentage	47.12%

2.3. Coverage

Mean	0.5802
Standard Deviation	20.056

2.4. Mapping Quality

Mean Mapping Quality	55.22

2.5. Insert size

Mean	18,656.46
Standard Deviation	1,351,202.51
P25/Median/P75	148 / 204 / 275

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	9,628,273
Insertions	103,600
Mapped reads with at least one insertion	0.56%
Deletions	84,269
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.56%

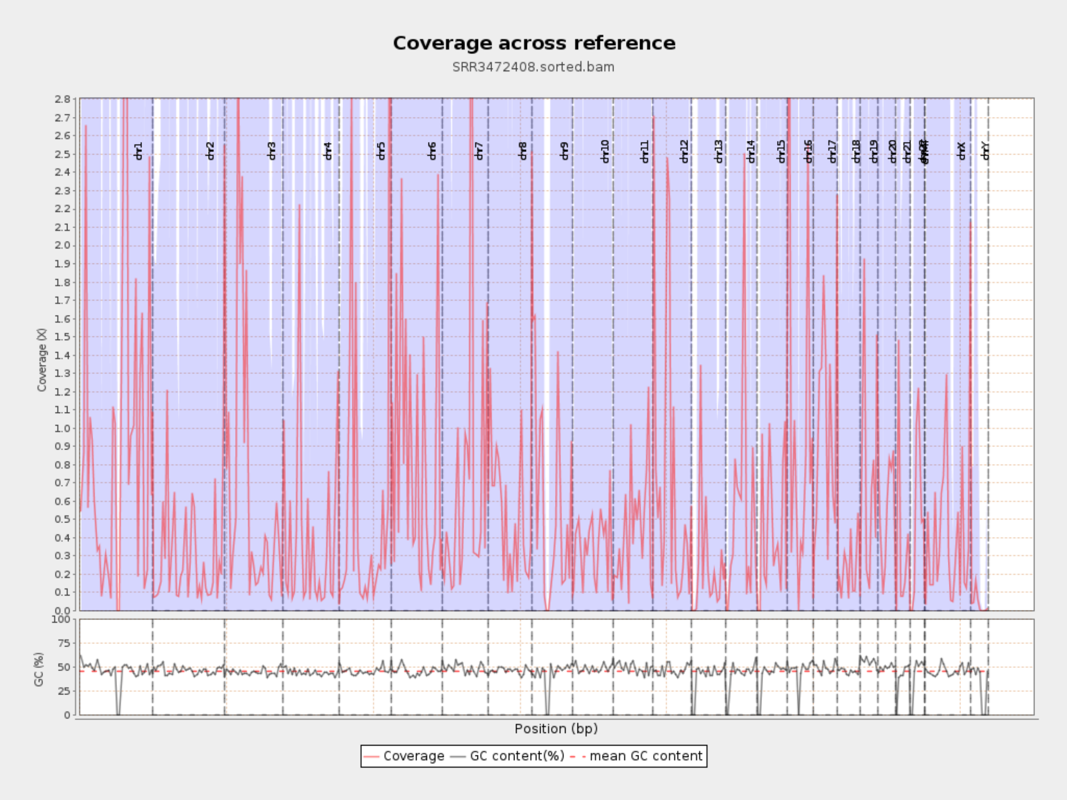
2.7. Chromosome stats

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

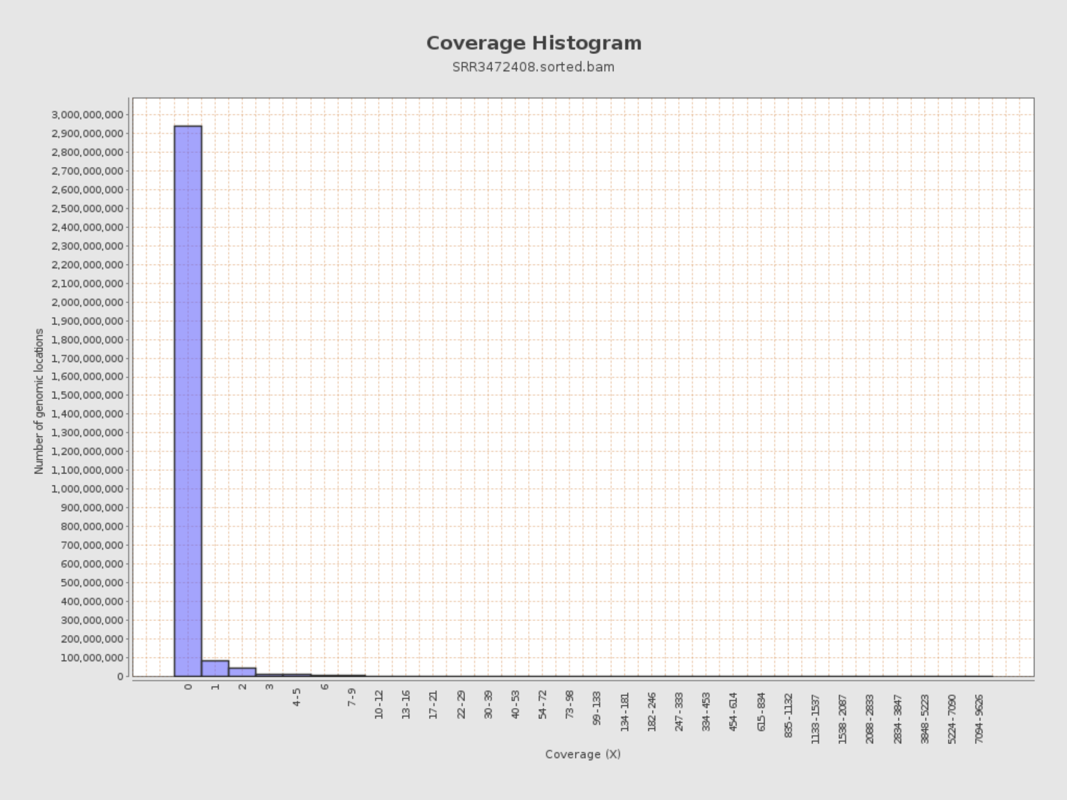
		bases	**coverage**	**deviation**
chr1	249250621	241568544	0.9692	26.8752
chr2	243199373	71297161	0.2932	10.1718
chr3	198022430	139046053	0.7022	23.859
chr4	191154276	75409932	0.3945	16.2061
chr5	180915260	120977683	0.6687	36.5207
chr6	171115067	140284010	0.8198	22.0273
chr7	159138663	122220637	0.768	23.9749
chr8	146364022	76323073	0.5215	13.7823
chr9	141213431	85340874	0.6043	16.0393
chr10	135534747	47356093	0.3494	12.14
chr11	135006516	62262705	0.4612	15.9552
chr12	133851895	98747804	0.7377	20.5999
chr13	115169878	28282980	0.2456	9.1352
chr14	107349540	57175745	0.5326	17.0336
chr15	102531392	45957595	0.4482	14.0613
chr16	90354753	94874753	1.05	25.9279
chr17	81195210	82455315	1.0155	22.8089
chr18	78077248	18912048	0.2422	6.6515
chr19	59128983	43312863	0.7325	15.0542
chr20	63025520	34765963	0.5516	15.2507
chr21	48129895	18646259	0.3874	22.6269
chr22	51304566	25900394	0.5048	14.3982
chrMT	16571	3811	0.23	0.6725
chrX	155270560	62699773	0.4038	18.8003

chrY	59373566	2343740	0.0395	1.6832

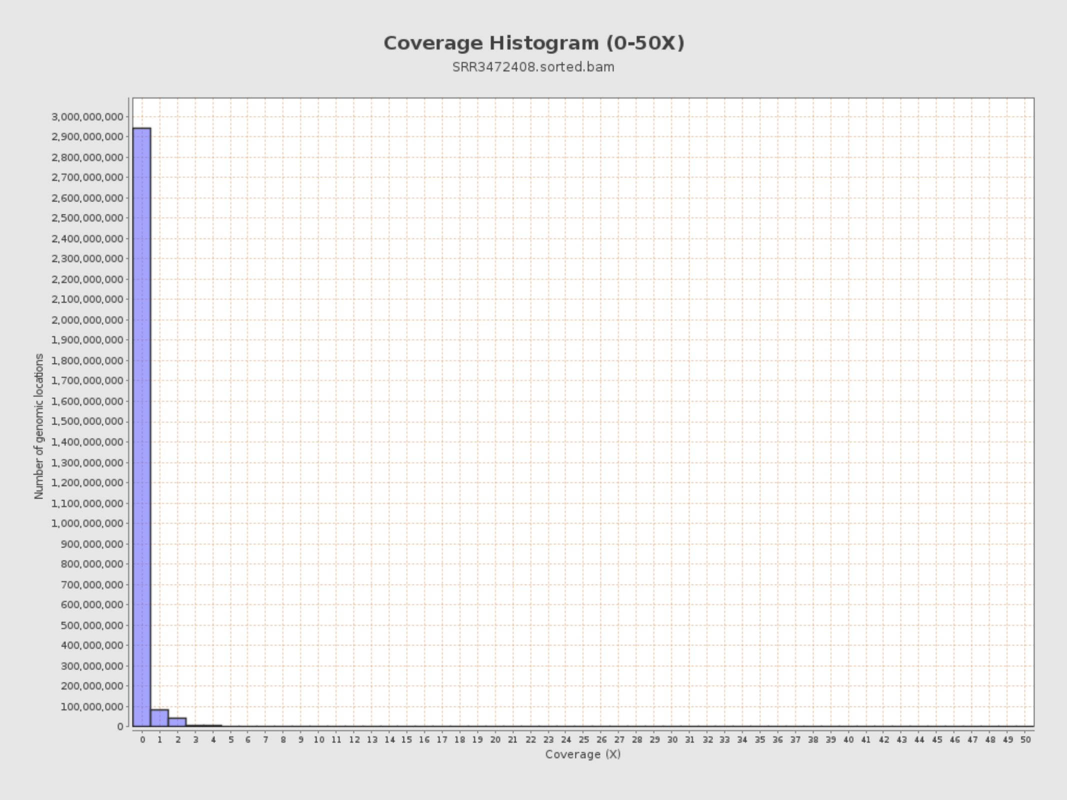
3. Results : Coverage across reference



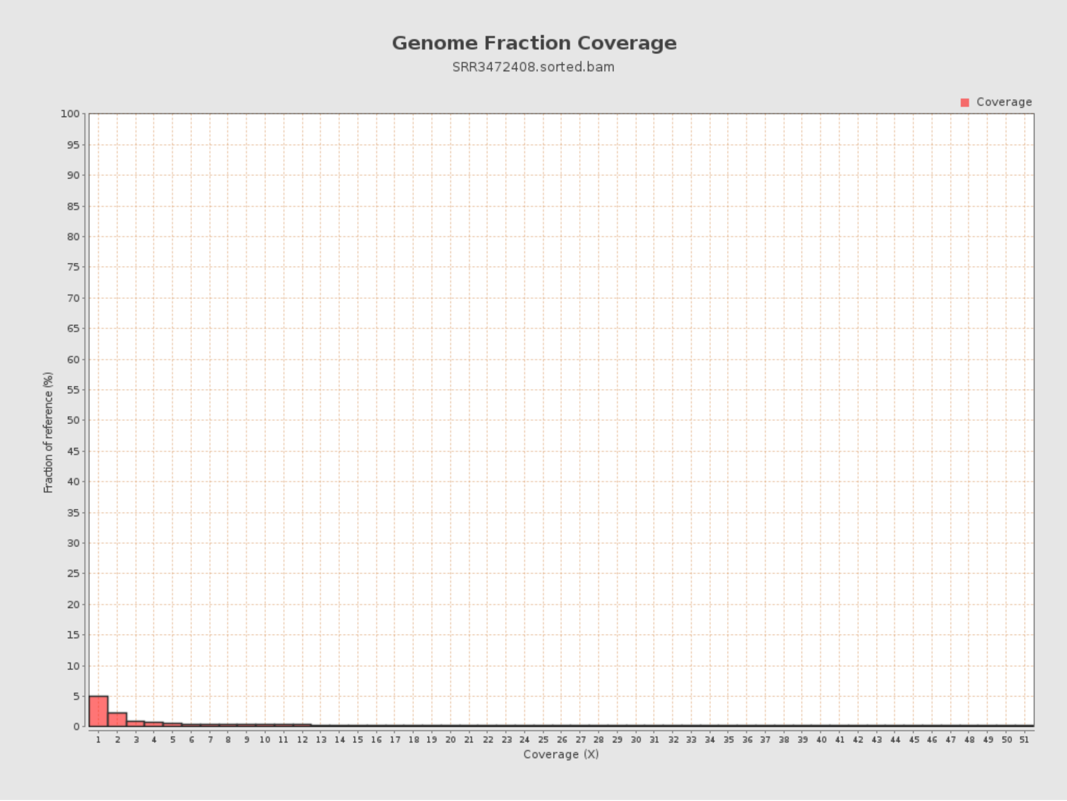
4. Results : Coverage Histogram



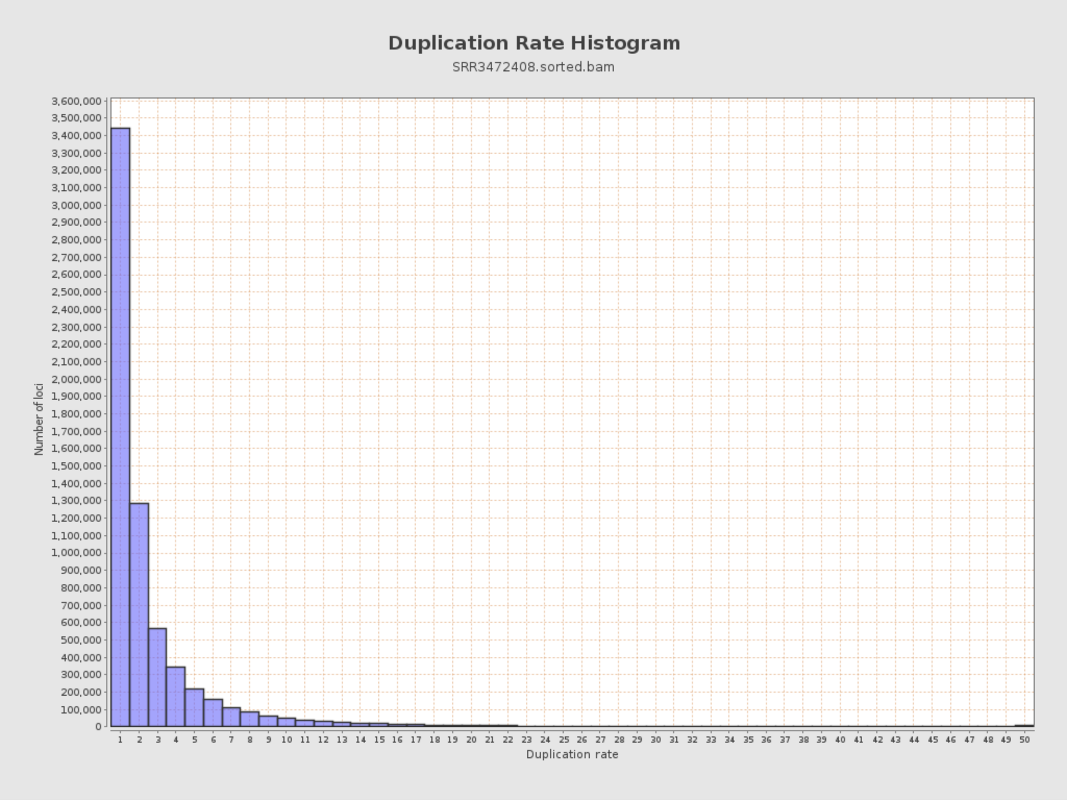
5. Results : Coverage Histogram (0-50X)



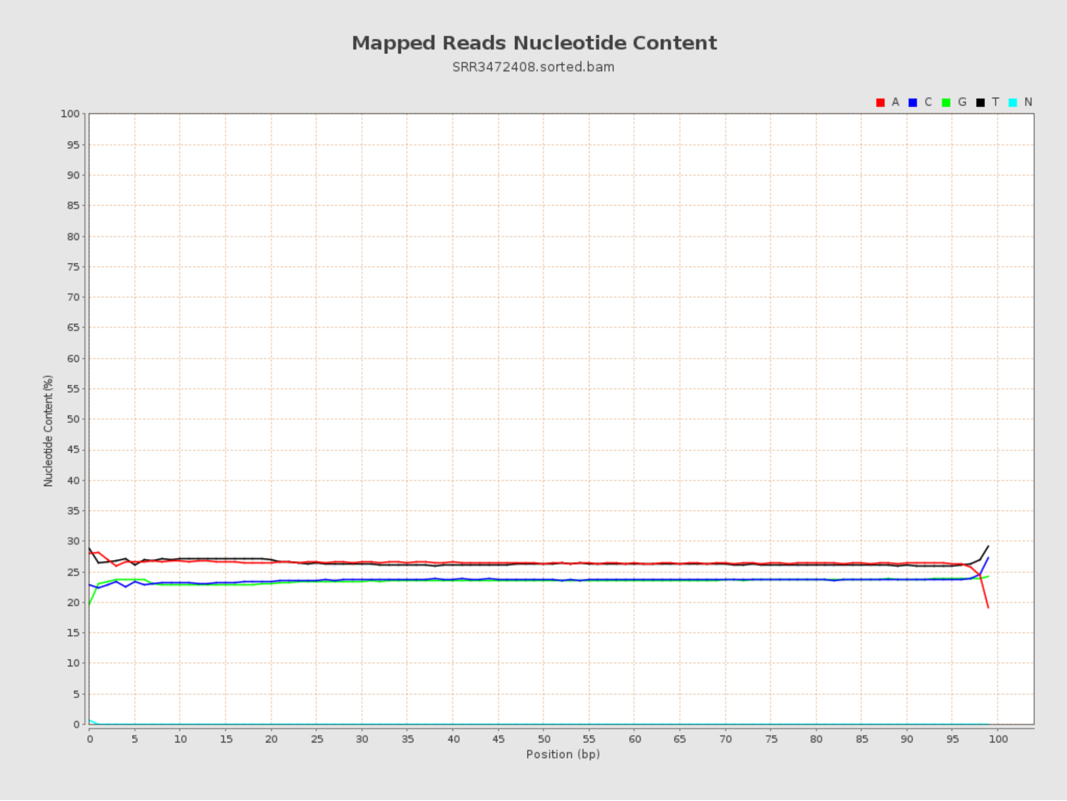
6. Results : Genome Fraction Coverage



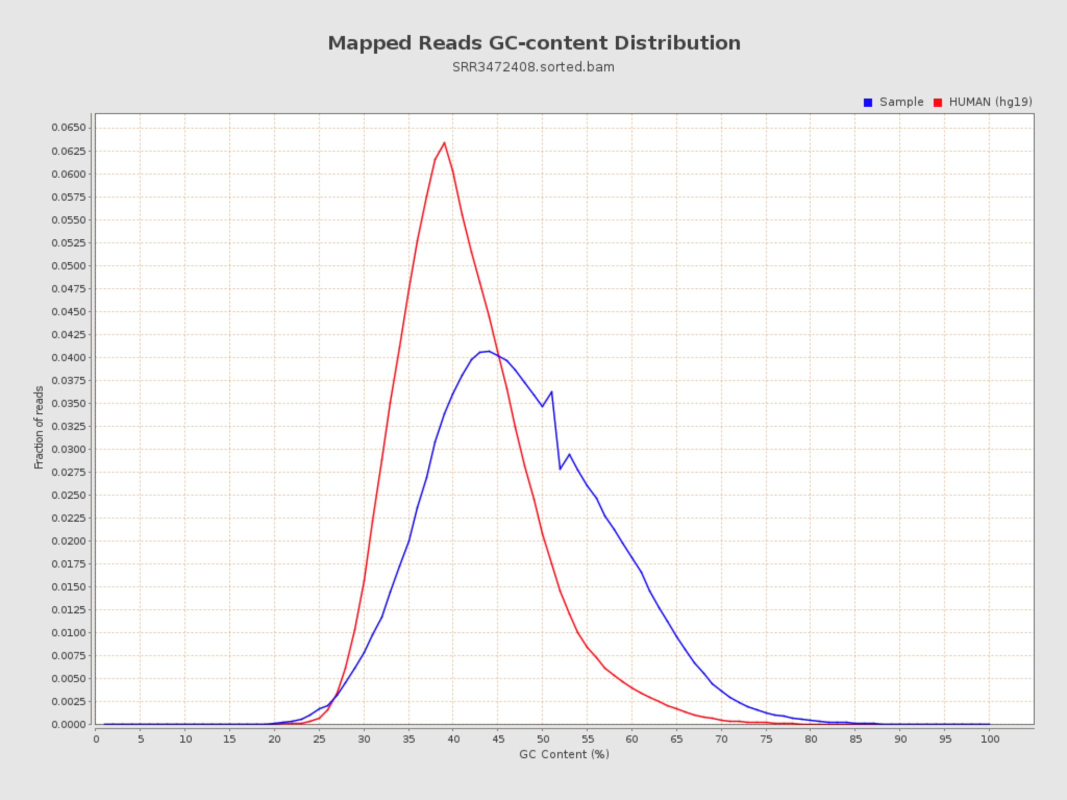
7. Results : Duplication Rate Histogram



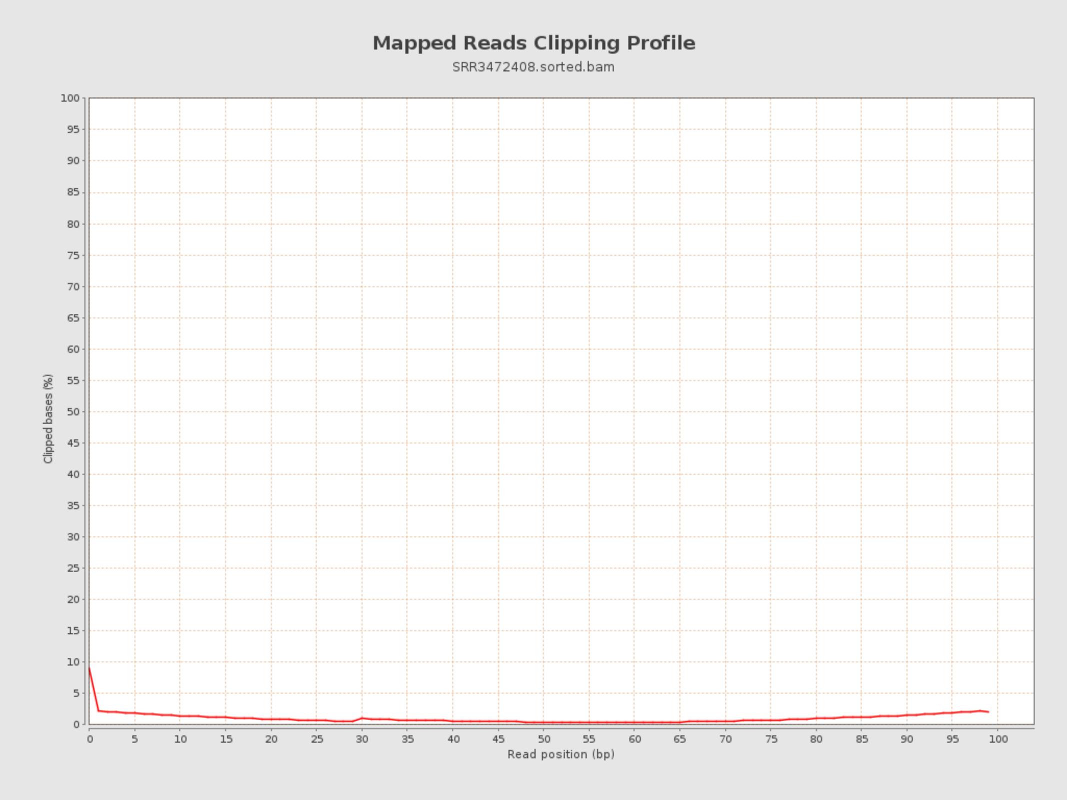
8. Results : Mapped Reads Nucleotide Content



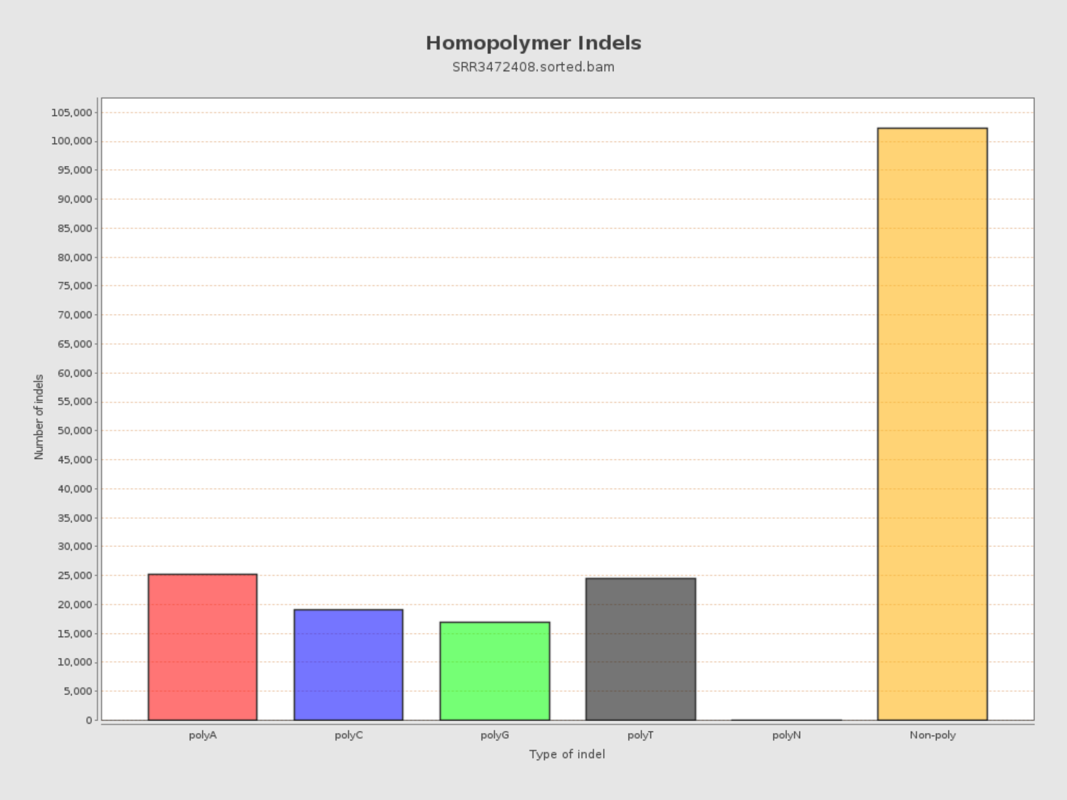
9. Results : Mapped Reads GC-content Distribution



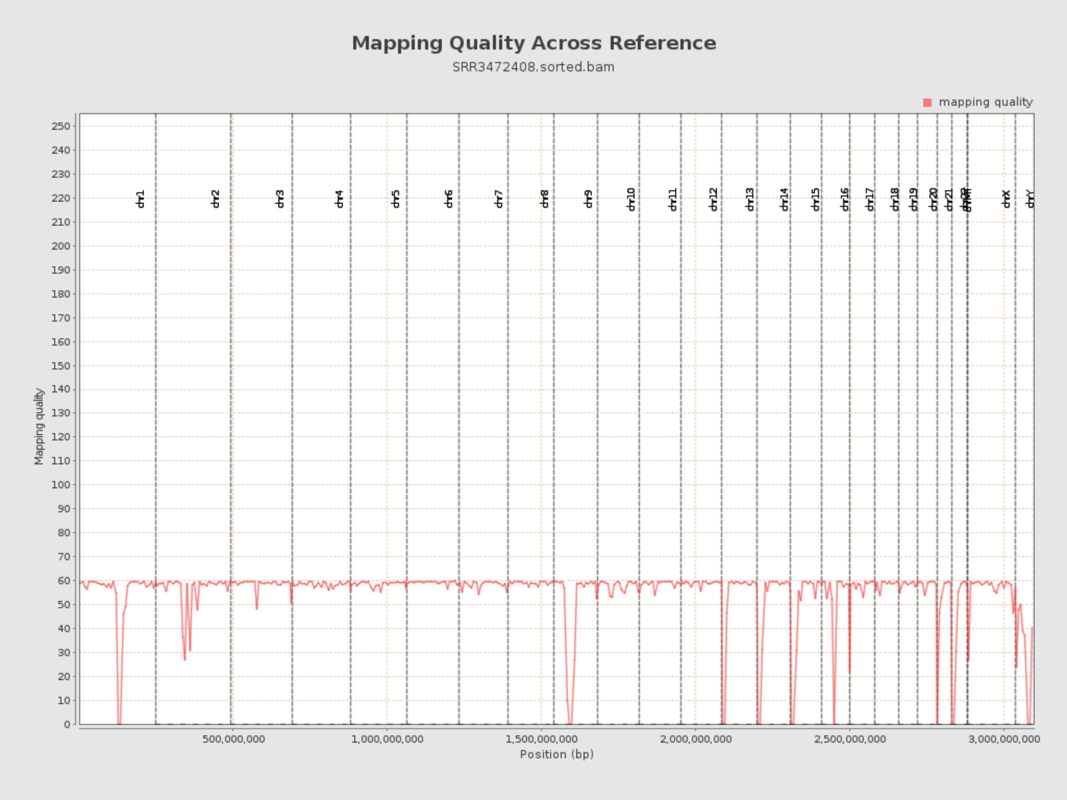
10. Results : Mapped Reads Clipping Profile



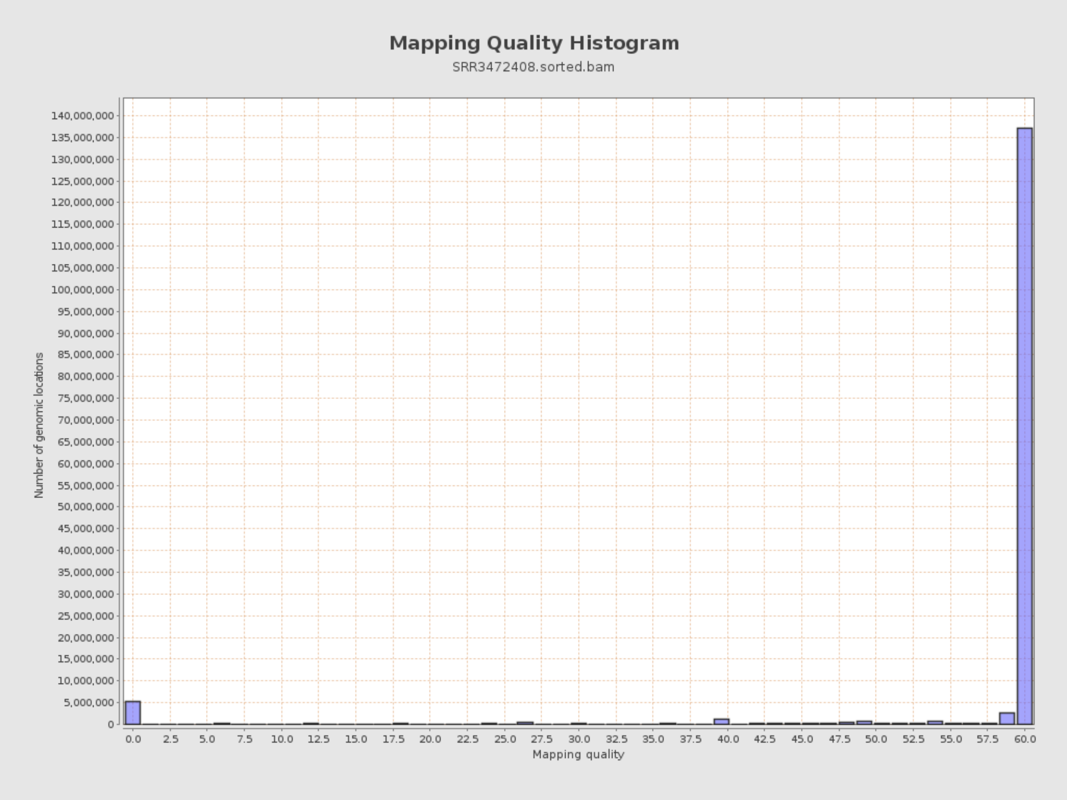
11. Results : Homopolymer Indels



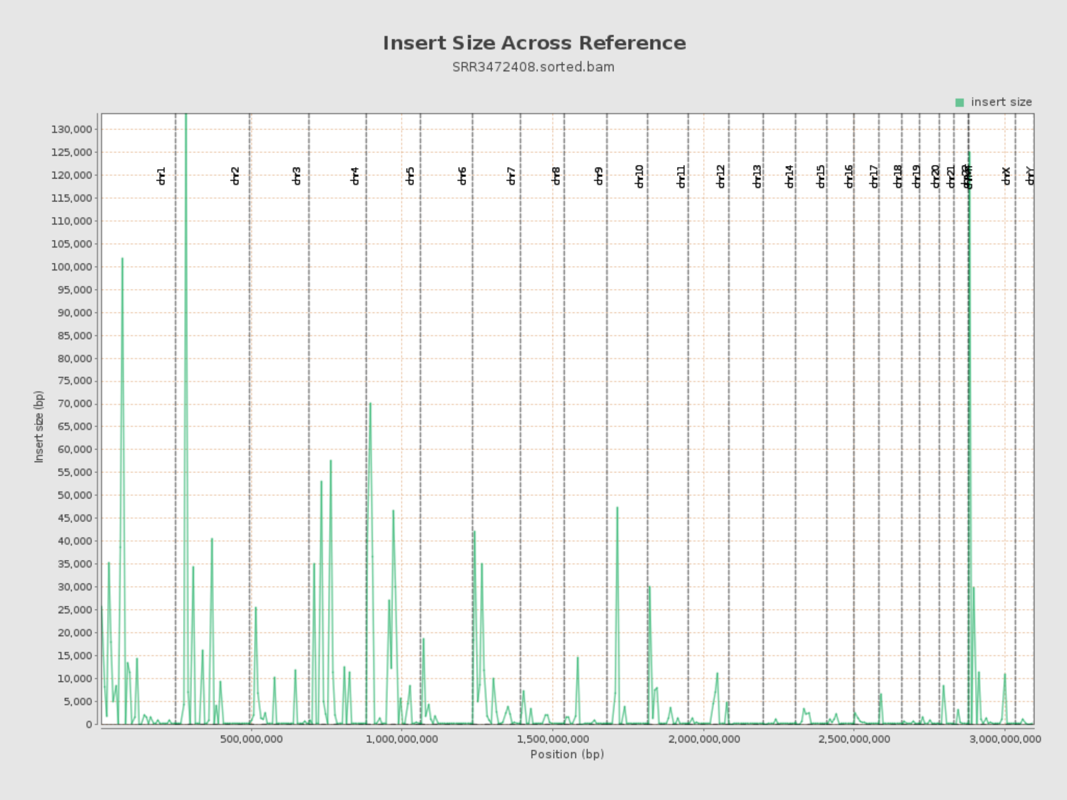
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram