Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:54:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472457.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_SRR3472457 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472457_1.fastq.gz SRR3472457_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:54:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472457.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,810,368
Mapped reads	14,679,037 / 99.11%
Unmapped reads	131,331 / 0.89%
Mapped paired reads	14,679,037 / 99.11%
Mapped reads, first in pair	7,364,430 / 49.72%
Mapped reads, second in pair	7,314,607 / 49.39%
Mapped reads, both in pair	14,607,100 / 98.63%
Mapped reads, singletons	71,937 / 0.49%
Secondary alignments	0
Supplementary alignments	56,976 / 0.38%
Read min/max/mean length	30 / 100 / 99.26
Duplicated reads (estimated)	9,007,383 / 60.82%
Duplication rate	46.21%
Clipped reads	942,829 / 6.37%

2.2. ACGT Content

Number/percentage of A's	392,084,274 / 27.23%
Number/percentage of C's	327,972,034 / 22.78%
Number/percentage of T's	394,033,967 / 27.37%
Number/percentage of G's	325,507,367 / 22.61%
Number/percentage of N's	195,364 / 0.01%

GC Percentage	45.39%

2.3. Coverage

Mean	0.4652
Standard Deviation	15.9167

2.4. Mapping Quality

Mean Mapping Quality	55.17

2.5. Insert size

Mean	19,604.46
Standard Deviation	1,379,719.81
P25/Median/P75	157 / 218 / 291

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	6,992,602
Insertions	89,797
Mapped reads with at least one insertion	0.61%
Deletions	76,678
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.57%

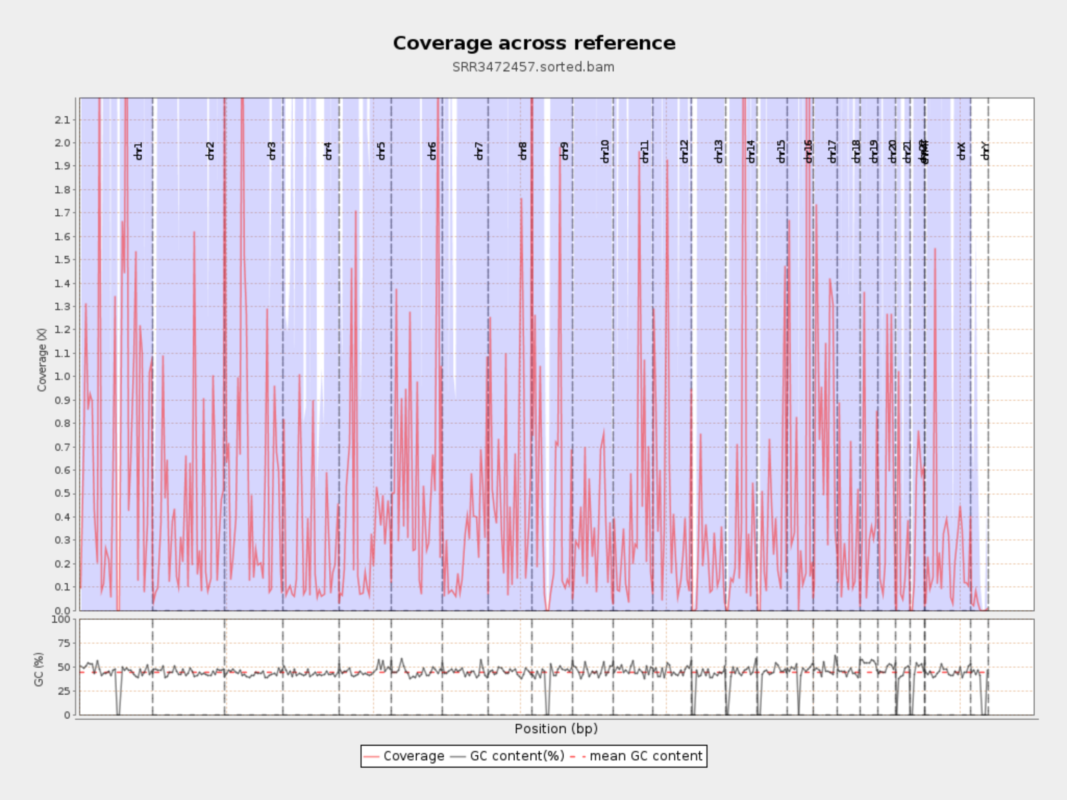
2.7. Chromosome stats

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

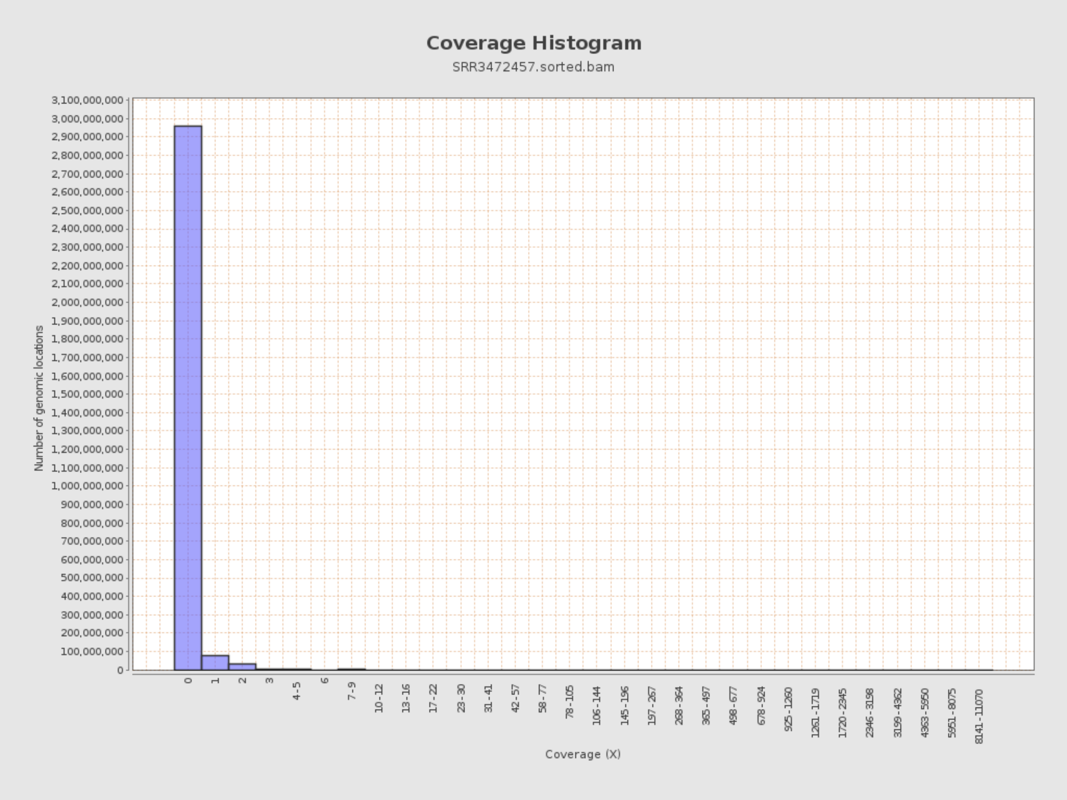
		bases	coverage	deviation
chr1	249250621	197405995	0.792	25.027
chr2	243199373	96316260	0.396	14.5264
chr3	198022430	125523186	0.6339	15.5016
chr4	191154276	50016416	0.2617	9.4577
chr5	180915260	69883951	0.3863	11.8961
chr6	171115067	106459920	0.6222	14.743
chr7	159138663	50552332	0.3177	10.5821
chr8	146364022	86925874	0.5939	17.0989
chr9	141213431	69796106	0.4943	15.2174
chr10	135534747	46367094	0.3421	11.5115
chr11	135006516	55696706	0.4125	14.7445
chr12	133851895	62797372	0.4692	12.7063
chr13	115169878	23996136	0.2084	6.6767
chr14	107349540	49578639	0.4618	21.3589
chr15	102531392	40817485	0.3981	12.4047
chr16	90354753	79508901	0.88	32.9892
chr17	81195210	66921808	0.8242	24.1869
chr18	78077248	23932352	0.3065	9.5066
chr19	59128983	25620412	0.4333	9.7185
chr20	63025520	34408938	0.546	21.3931
chr21	48129895	13689186	0.2844	17.3104
chr22	51304566	20498314	0.3995	11.3546
chrMT	16571	1565	0.0944	0.3633
chrX	155270560	42002757	0.2705	7.4998

chrY	59373566	1288565	0.0217	0.6894

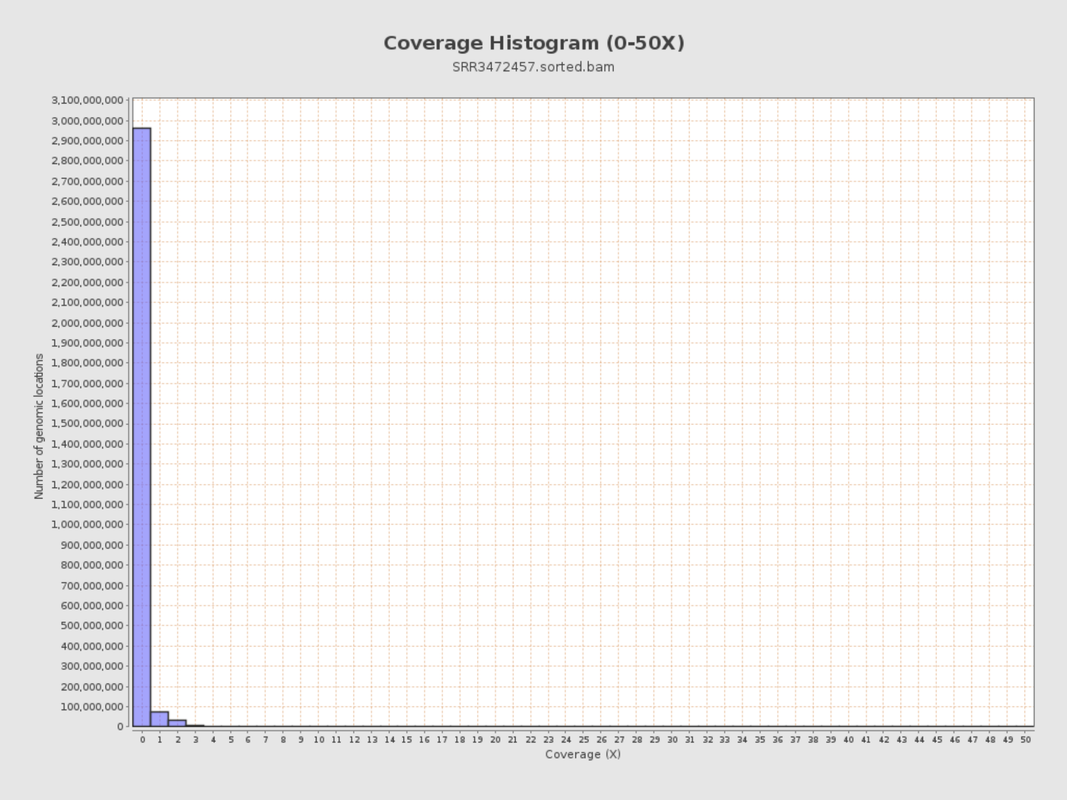
3. Results : Coverage across reference



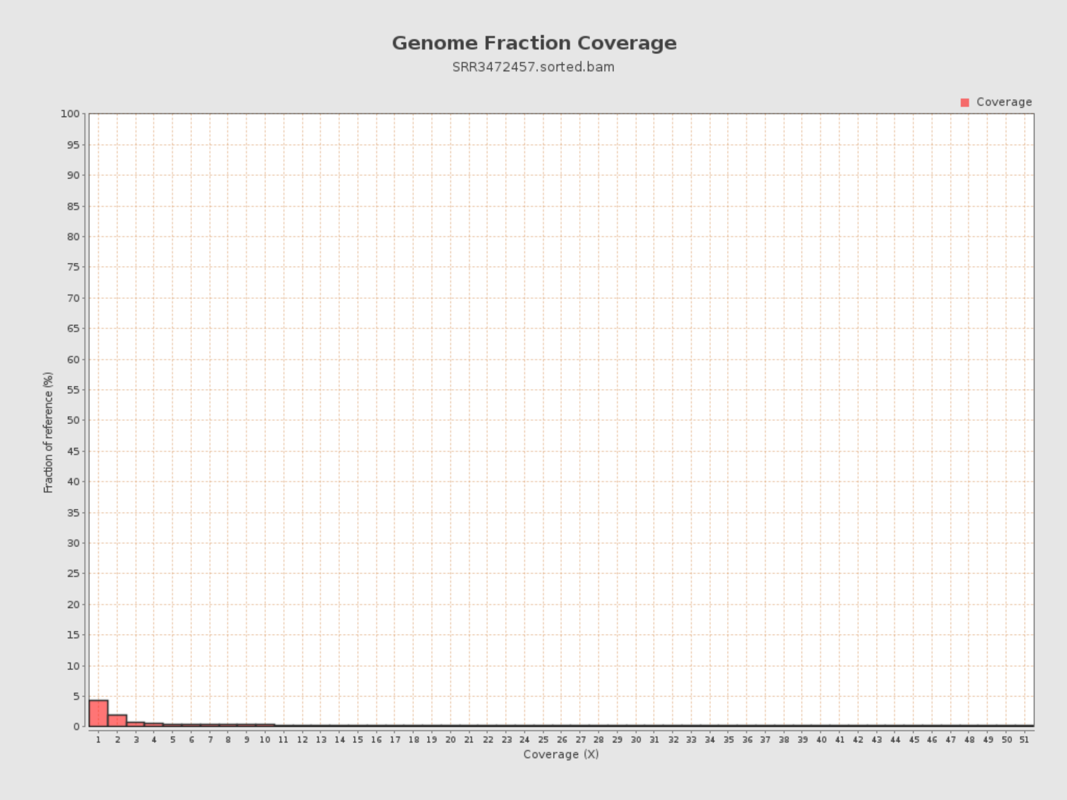
4. Results : Coverage Histogram



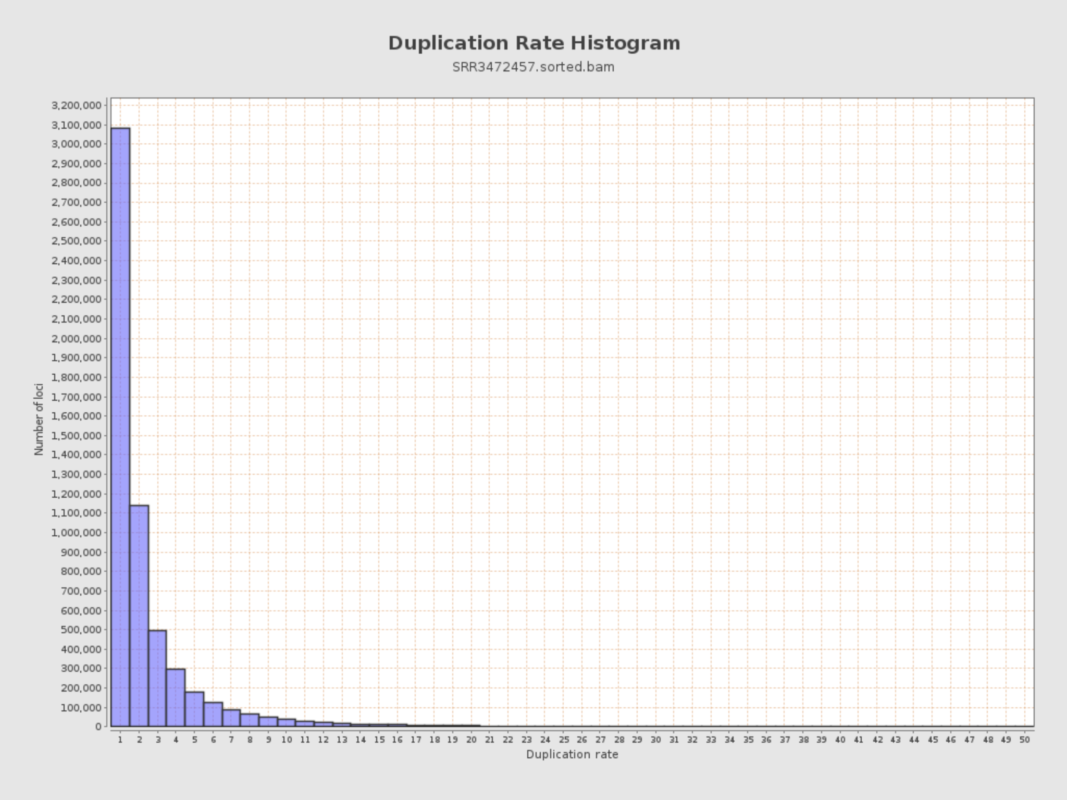
5. Results : Coverage Histogram (0-50X)



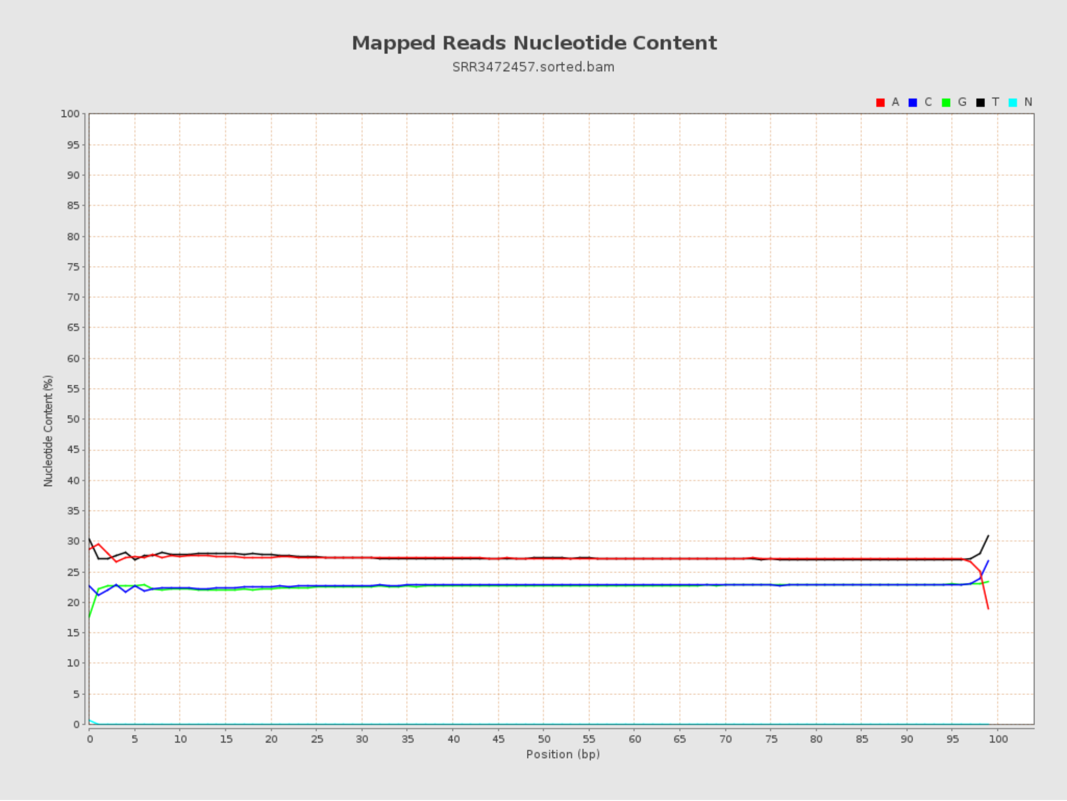
6. Results : Genome Fraction Coverage



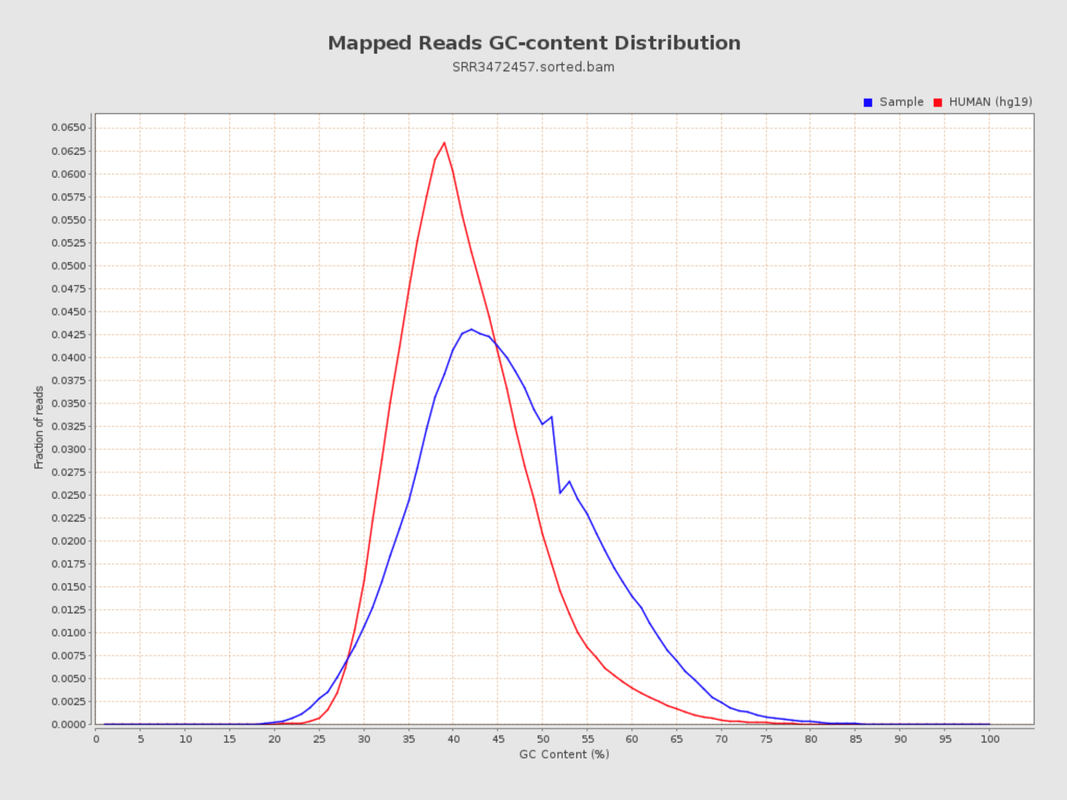
7. Results : Duplication Rate Histogram



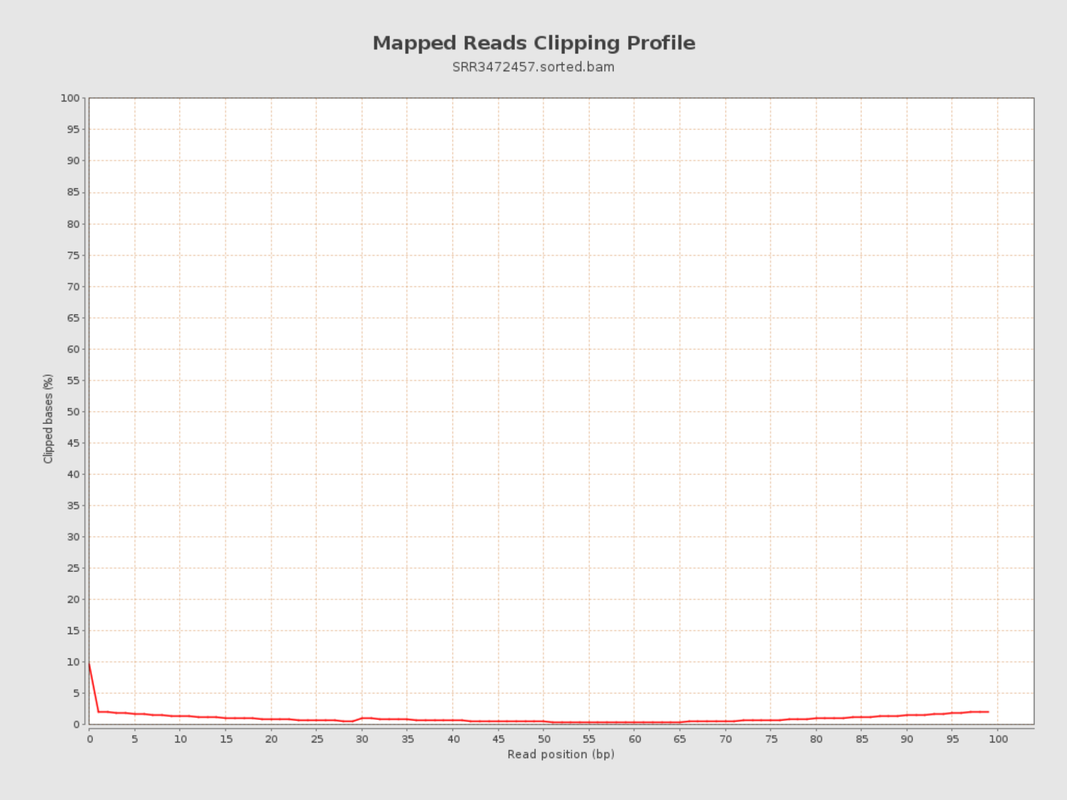
8. Results : Mapped Reads Nucleotide Content



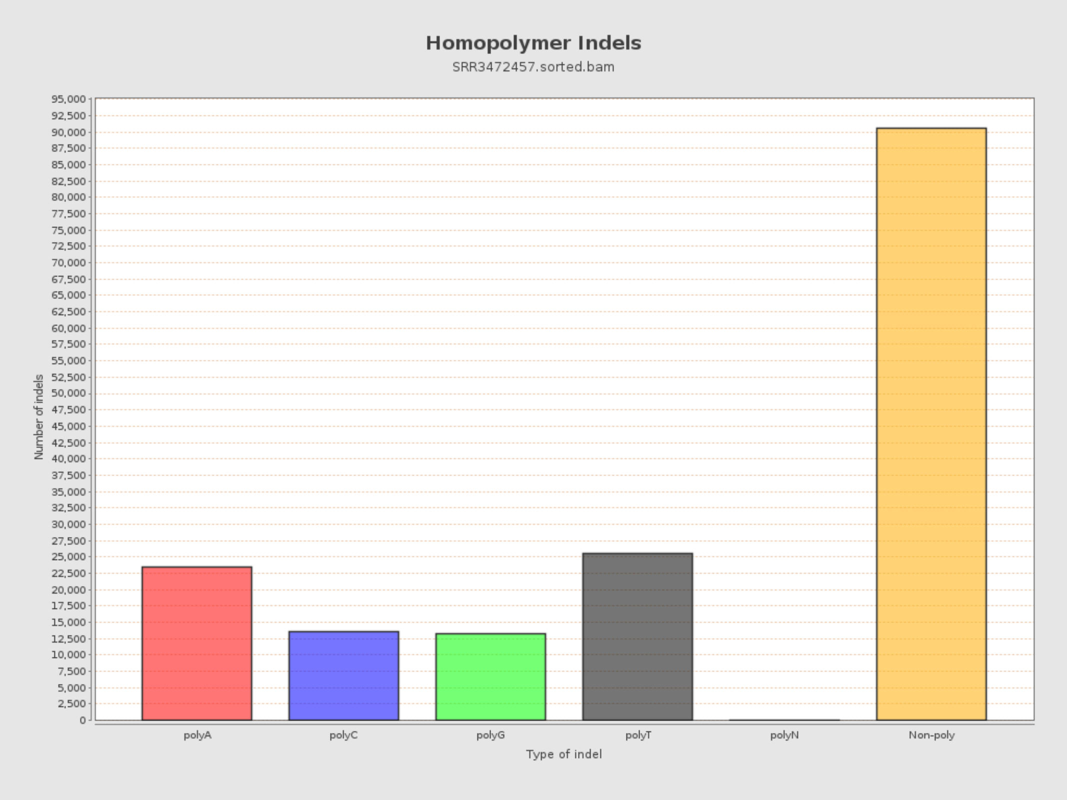
9. Results : Mapped Reads GC-content Distribution



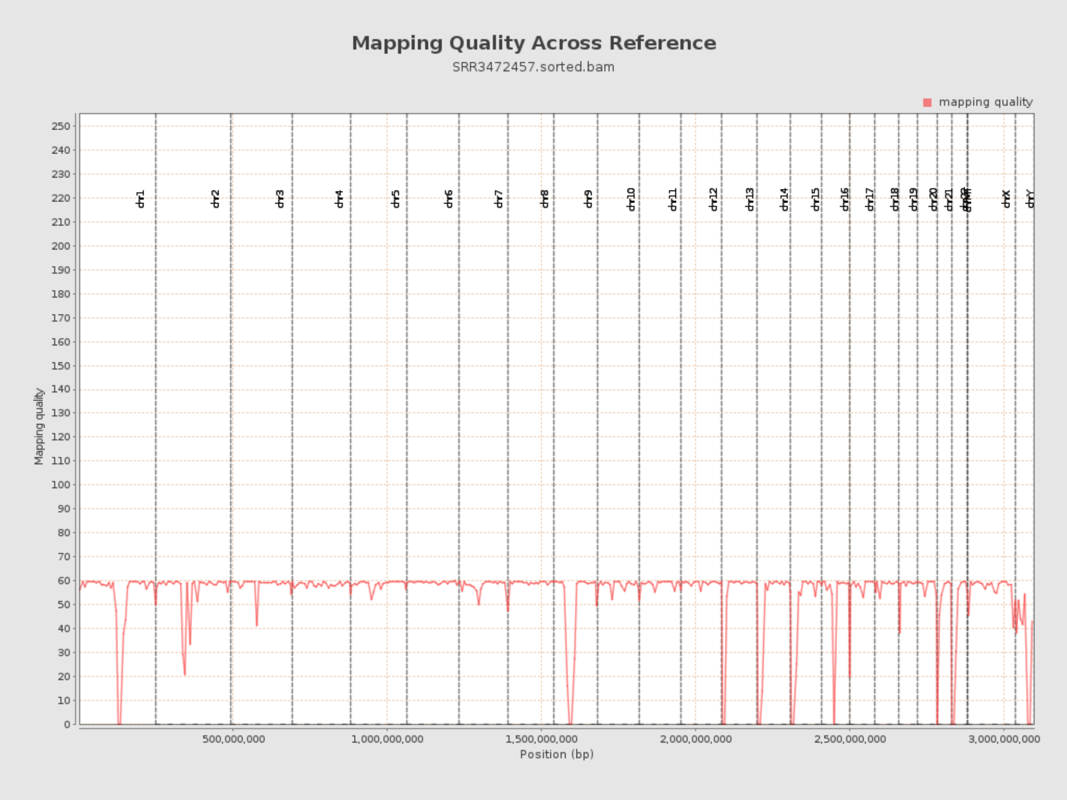
10. Results : Mapped Reads Clipping Profile



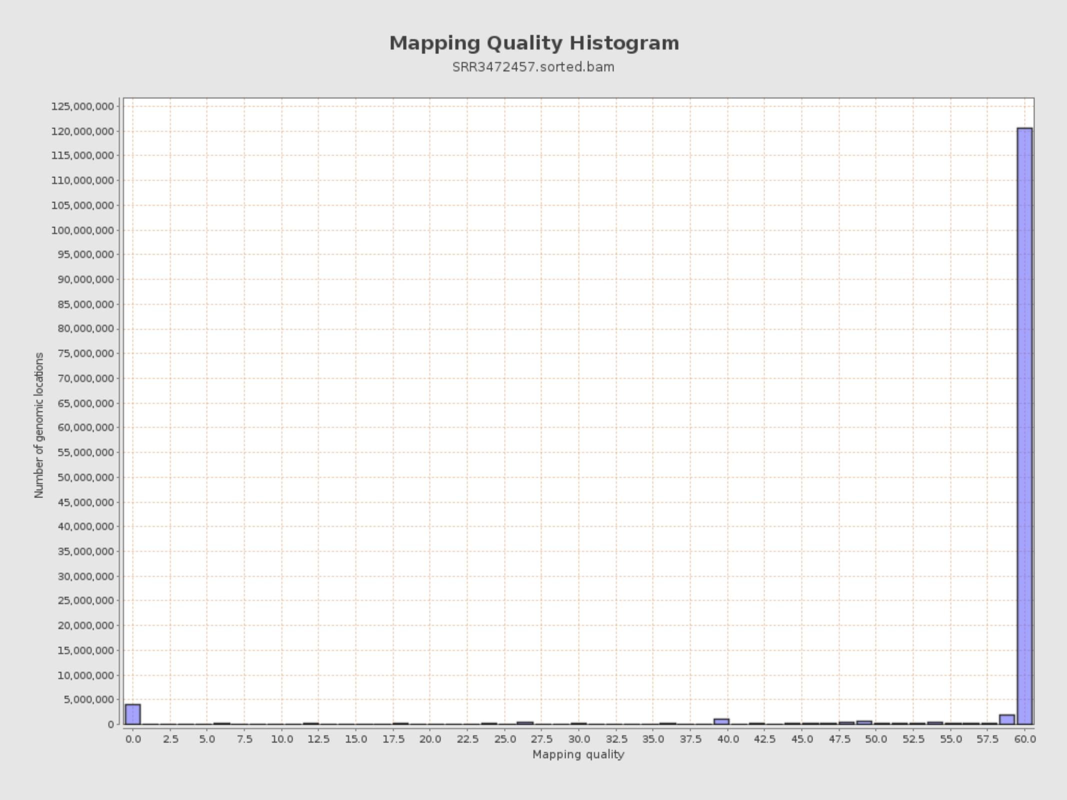
11. Results : Homopolymer Indels



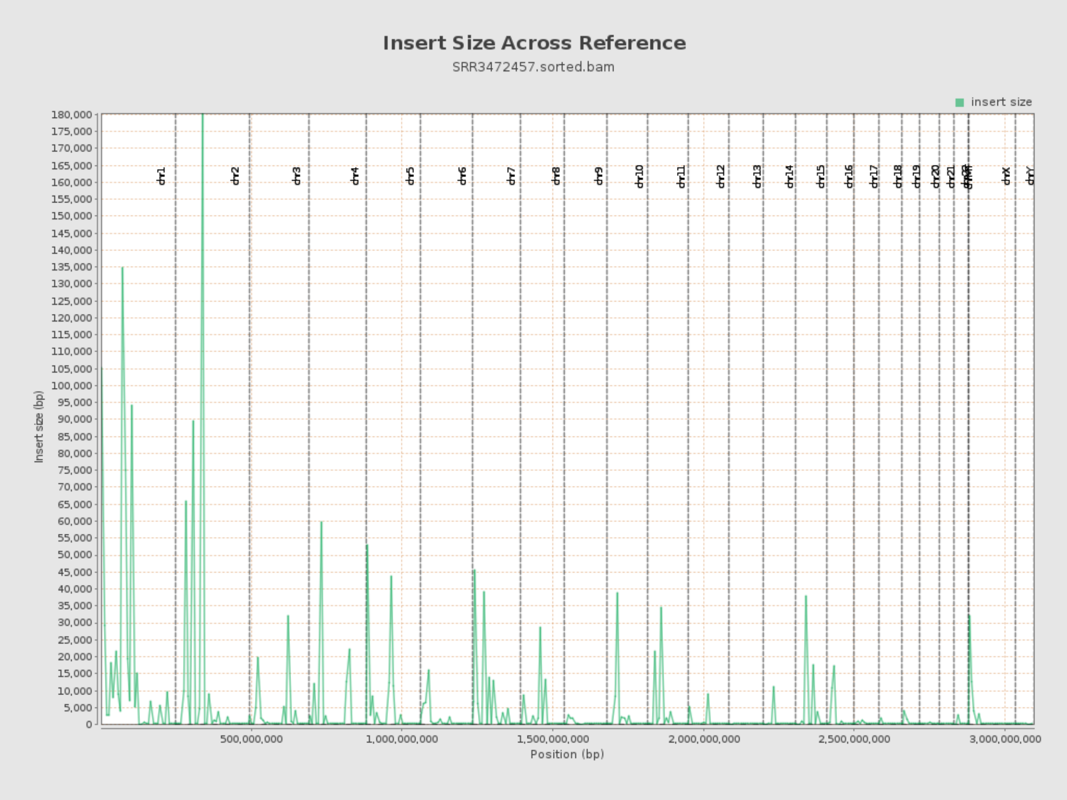
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram