Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 08:02:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472758.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_SRR3472758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472758_1.fastq.gz SRR3472758_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 08:02:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,931,792
Mapped reads	16,778,105 / 99.09%
Unmapped reads	153,687 / 0.91%
Mapped paired reads	16,778,105 / 99.09%
Mapped reads, first in pair	8,419,063 / 49.72%
Mapped reads, second in pair	8,359,042 / 49.37%
Mapped reads, both in pair	16,681,846 / 98.52%
Mapped reads, singletons	96,259 / 0.57%
Secondary alignments	0
Supplementary alignments	103,390 / 0.61%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	10,622,527 / 62.74%
Duplication rate	46.79%
Clipped reads	1,430,396 / 8.45%

2.2. ACGT Content

Number/percentage of A's	461,452,864 / 27.91%
Number/percentage of C's	367,080,240 / 22.2%
Number/percentage of T's	458,967,054 / 27.76%
Number/percentage of G's	365,474,352 / 22.11%
Number/percentage of N's	318,944 / 0.02%

GC Percentage	44.31%

2.3. Coverage

Mean	0.5341
Standard Deviation	17.629

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	44,307.36
Standard Deviation	2,040,879.09
P25/Median/P75	173 / 244 / 332

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,154,312
Insertions	94,014
Mapped reads with at least one insertion	0.56%
Deletions	95,063
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.56%

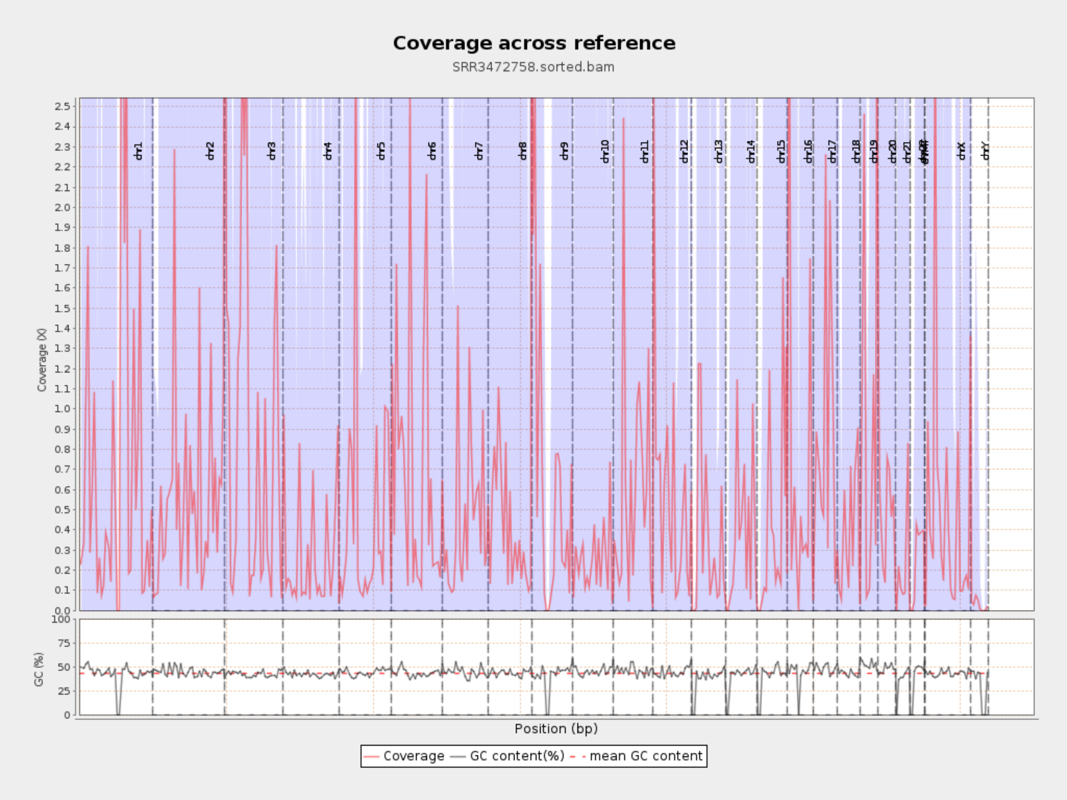
2.7. Chromosome stats

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

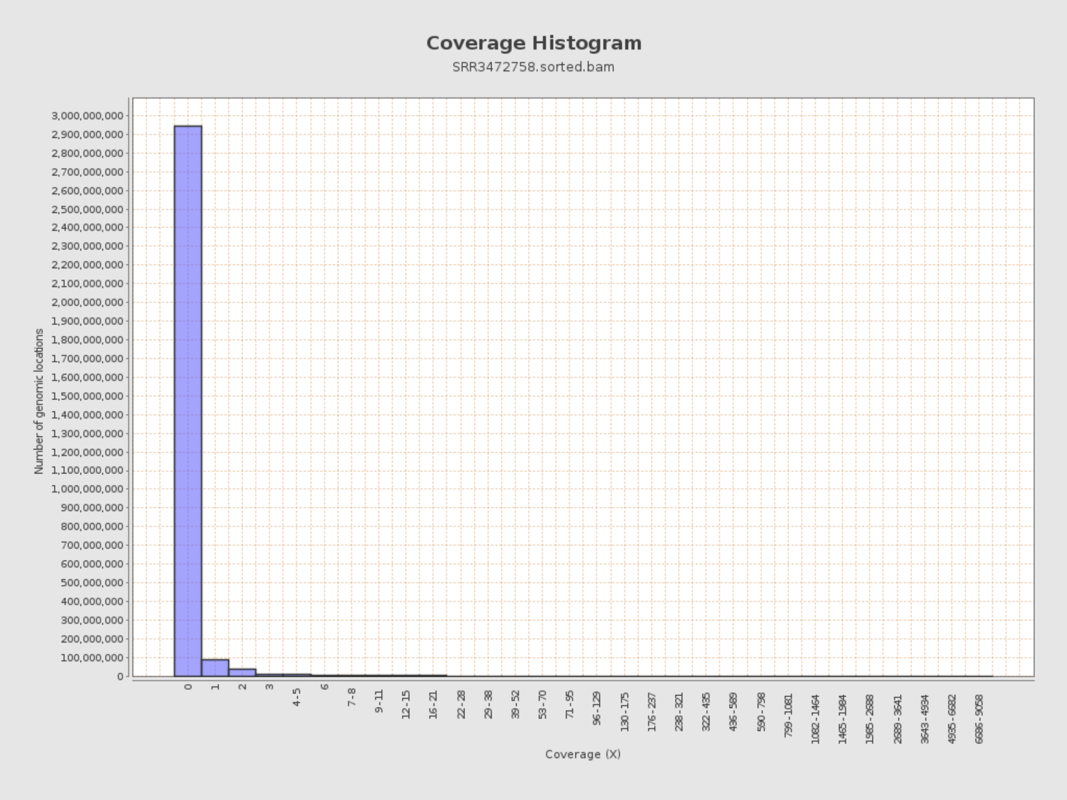
		bases	coverage	deviation
chr1	249250621	187083542	0.7506	27.3831
chr2	243199373	134963184	0.5549	19.4429
chr3	198022430	185487033	0.9367	24.153
chr4	191154276	50763044	0.2656	9.4249
chr5	180915260	84488112	0.467	14.9196
chr6	171115067	116734517	0.6822	18.7707
chr7	159138663	75392775	0.4738	15.6906
chr8	146364022	58725894	0.4012	12.3411
chr9	141213431	95800156	0.6784	17.1578
chr10	135534747	34420766	0.254	8.0115
chr11	135006516	83643313	0.6196	24.1854
chr12	133851895	78382511	0.5856	16.8645
chr13	115169878	40985424	0.3559	13.4744
chr14	107349540	39426813	0.3673	12.5754
chr15	102531392	42039381	0.41	13.4643
chr16	90354753	61445686	0.68	17.676
chr17	81195210	68439255	0.8429	19.5608
chr18	78077248	30147158	0.3861	13.0942
chr19	59128983	51656752	0.8736	24.1352
chr20	63025520	32505014	0.5157	13.3752
chr21	48129895	10825396	0.2249	11.4818
chr22	51304566	12756980	0.2487	7.9958
chrMT	16571	1833	0.1106	0.3989
chrX	155270560	75681492	0.4874	15.3753

chrY	59373566	1731414	0.0292	1.0828

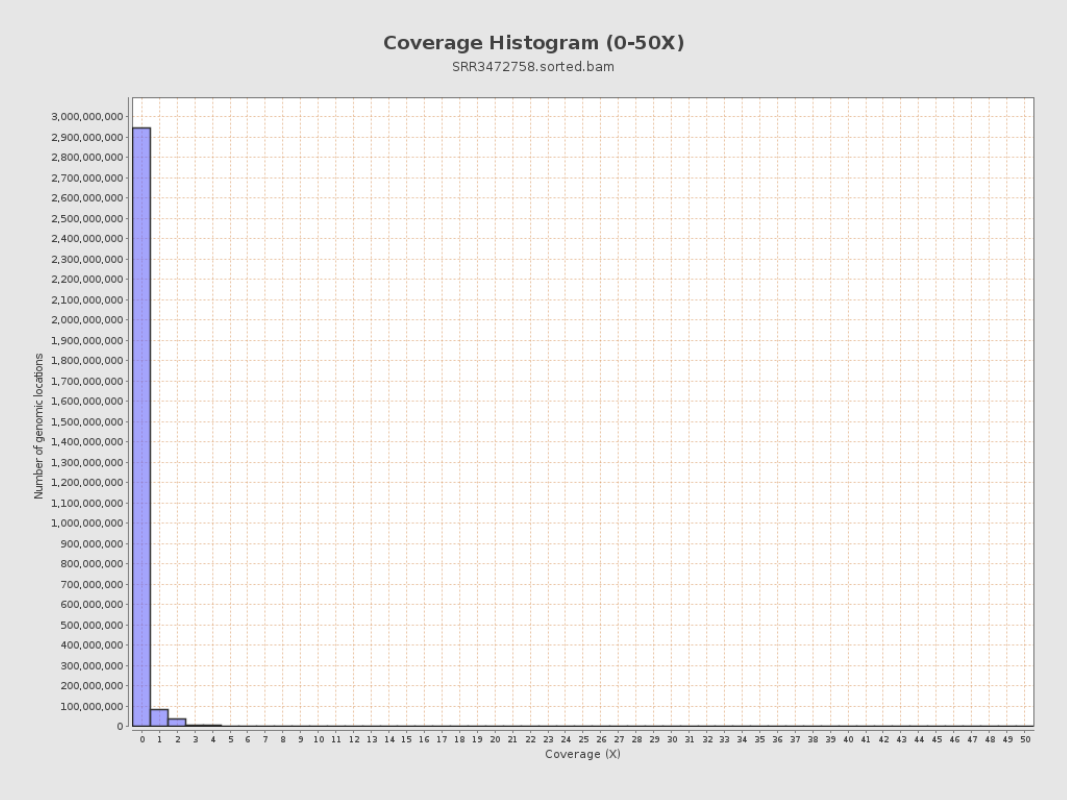
3. Results : Coverage across reference



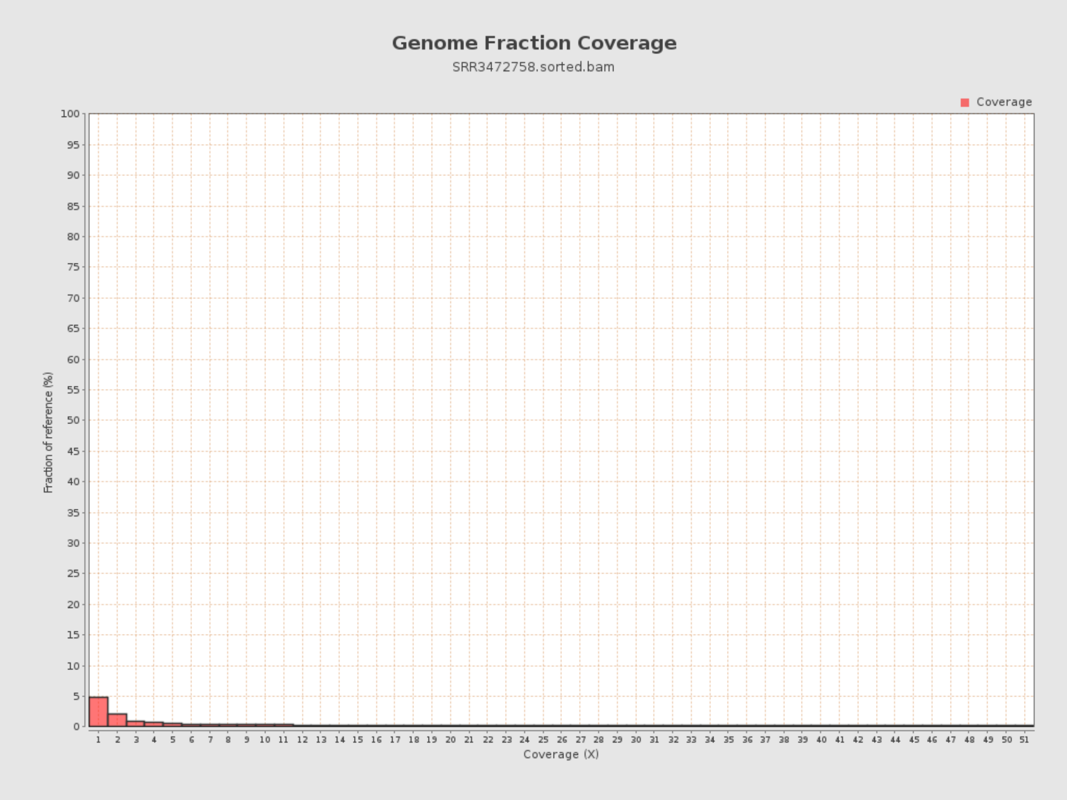
4. Results : Coverage Histogram



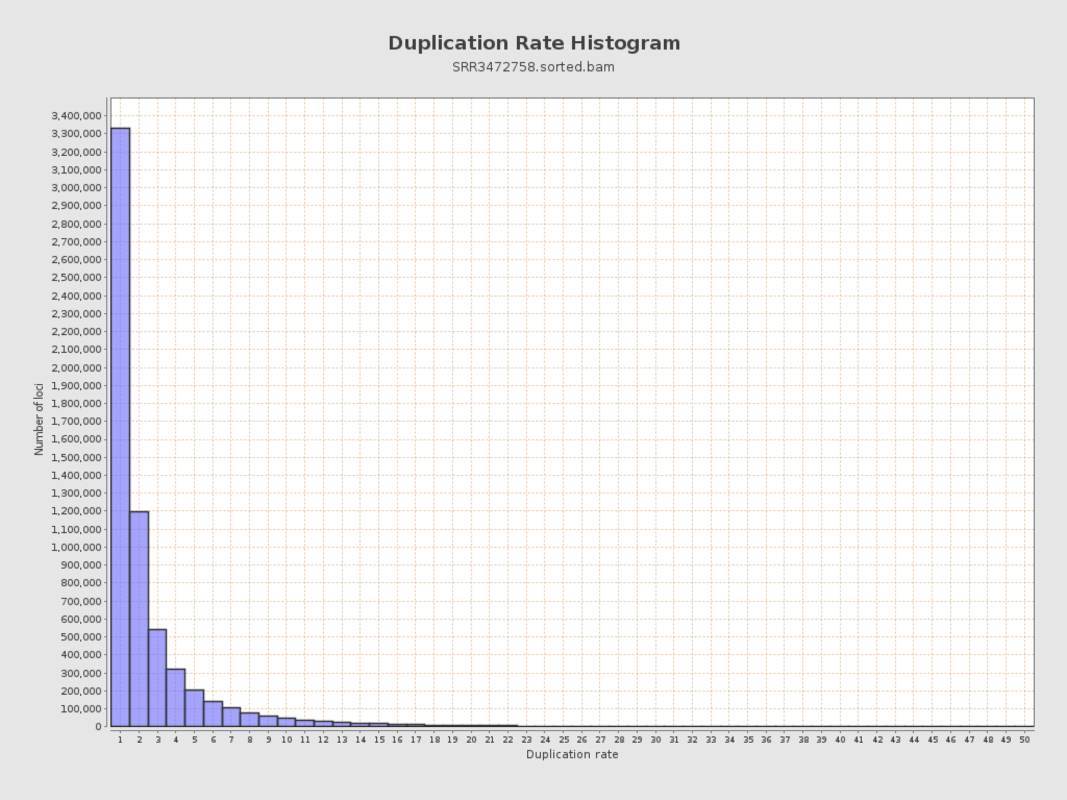
5. Results : Coverage Histogram (0-50X)



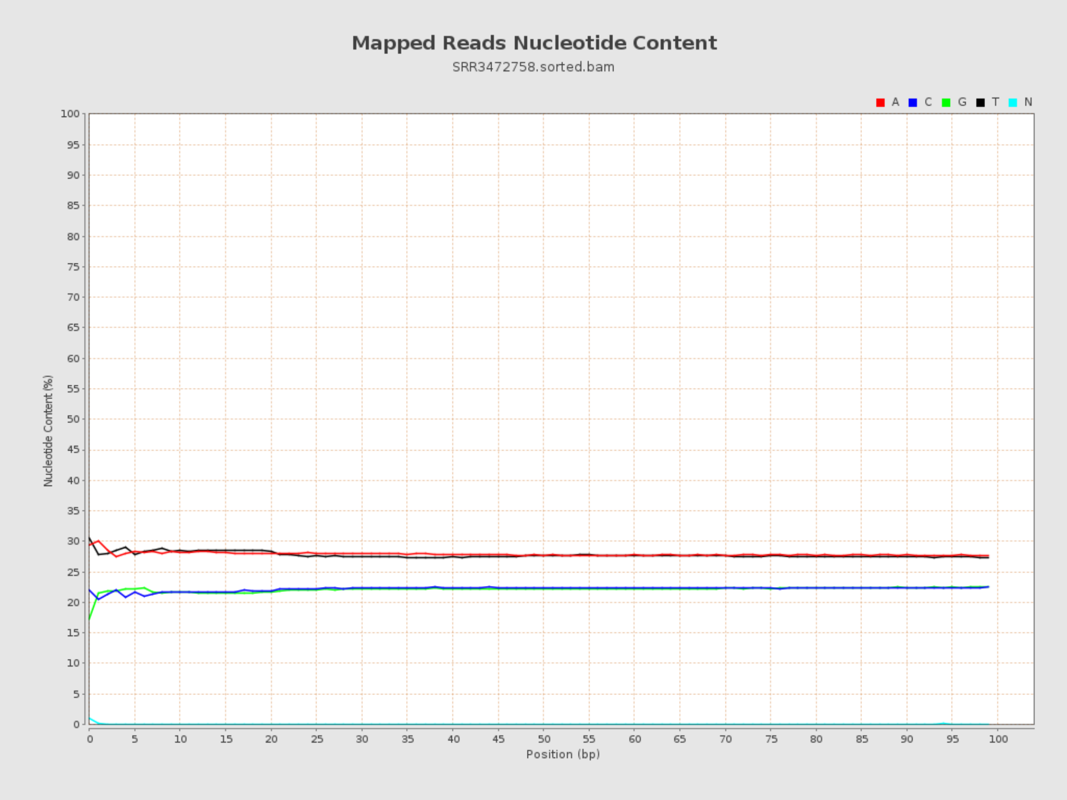
6. Results : Genome Fraction Coverage



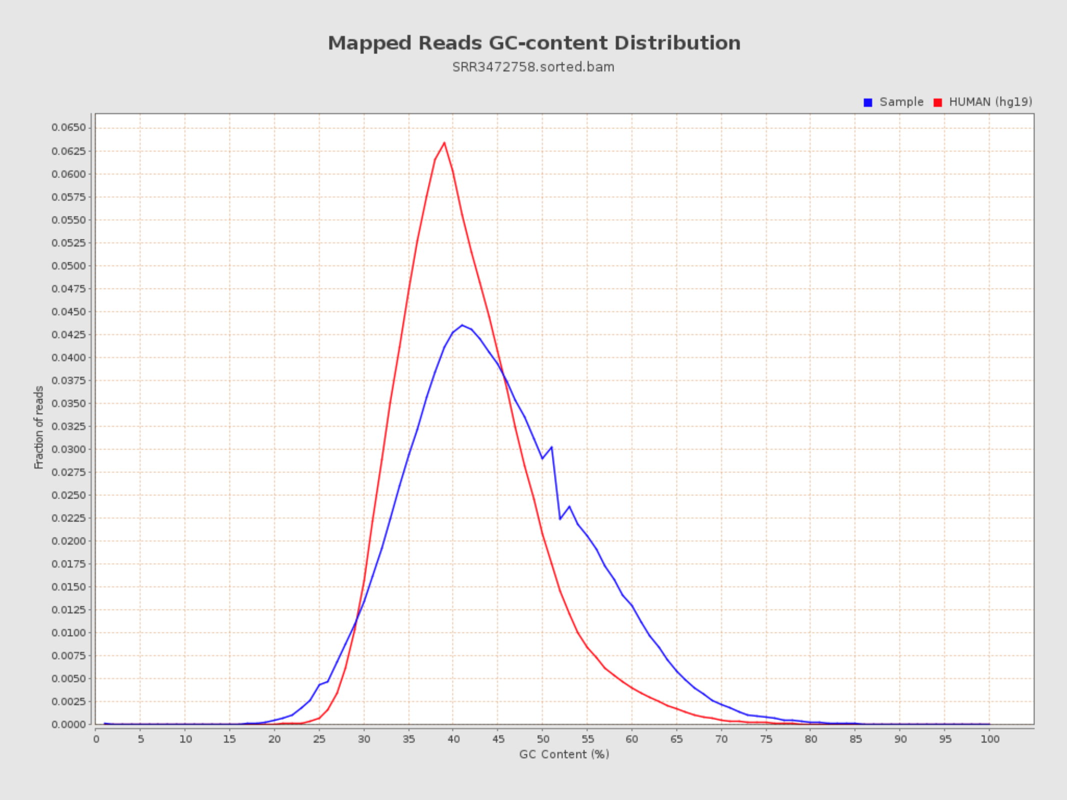
7. Results : Duplication Rate Histogram



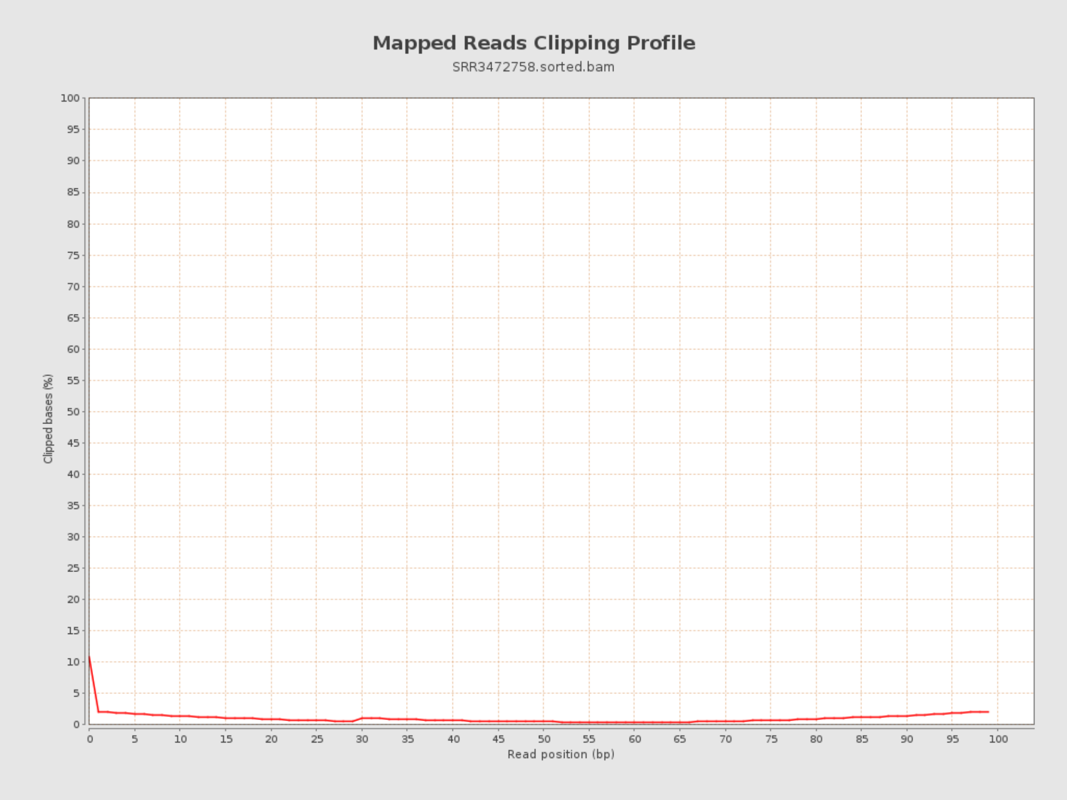
8. Results : Mapped Reads Nucleotide Content



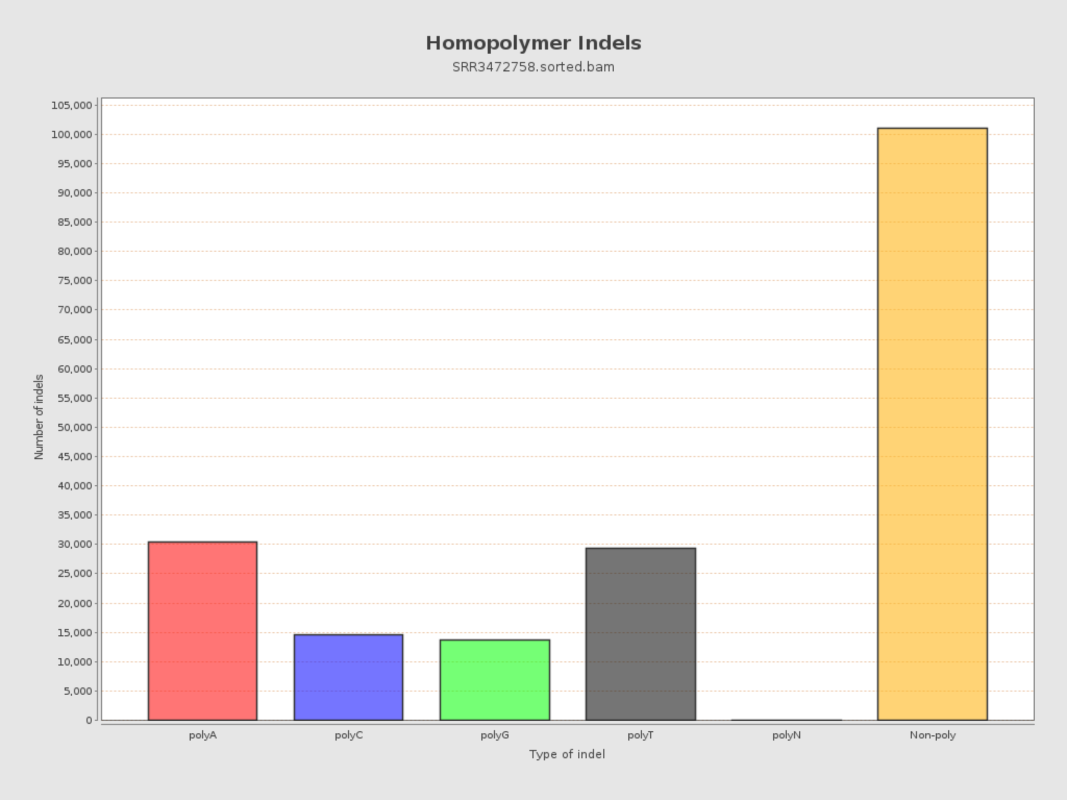
9. Results : Mapped Reads GC-content Distribution



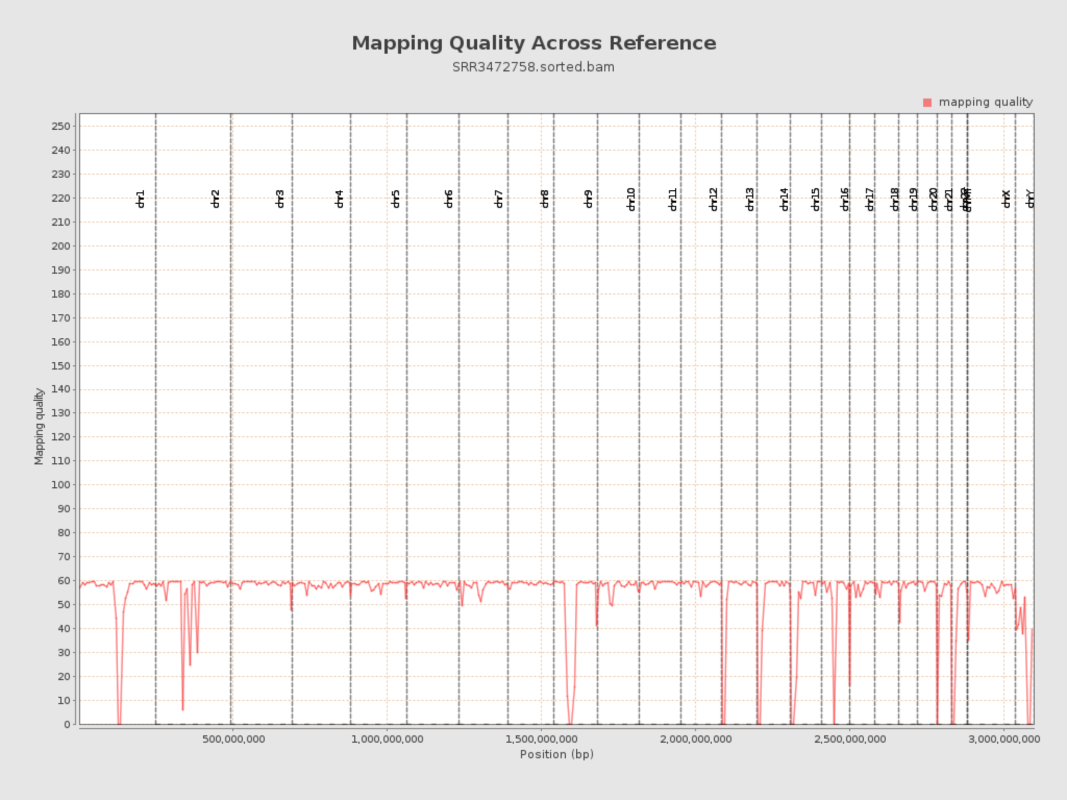
10. Results : Mapped Reads Clipping Profile



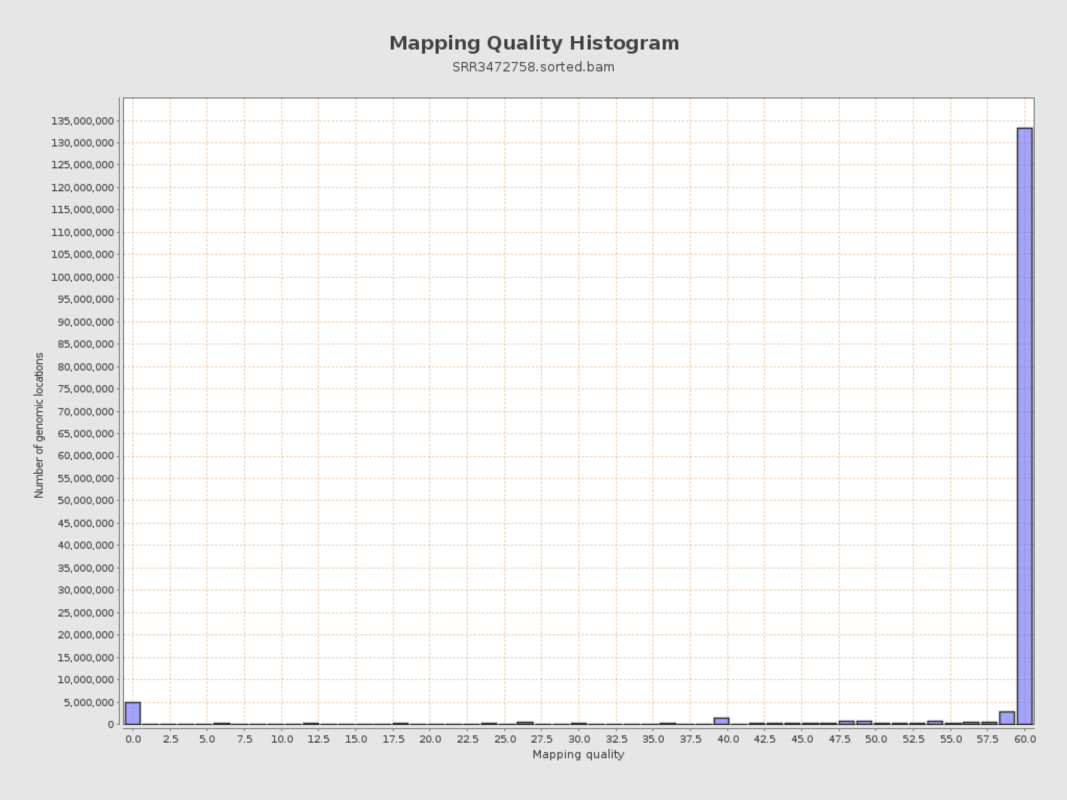
11. Results : Homopolymer Indels



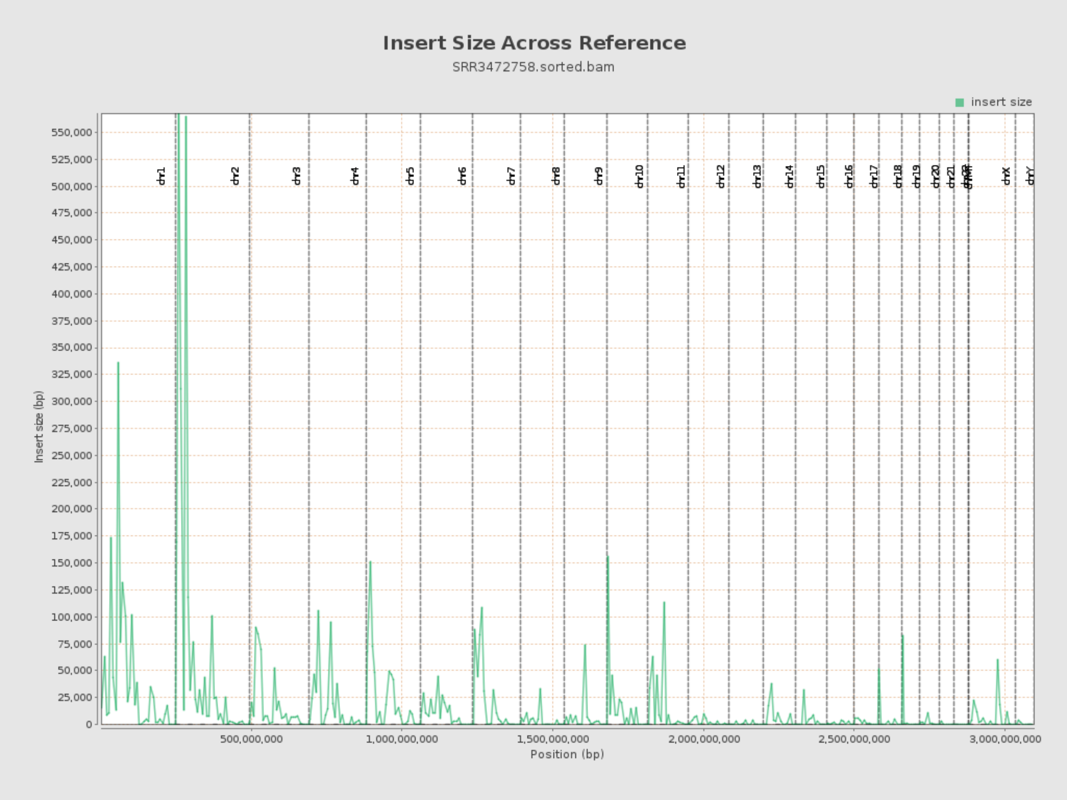
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram