Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 16:56:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472785.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_SRR3472785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472785_1.fastq.gz SRR3472785_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 16:56:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,170,014
Mapped reads	13,070,941 / 99.25%
Unmapped reads	99,073 / 0.75%
Mapped paired reads	13,070,941 / 99.25%
Mapped reads, first in pair	6,553,218 / 49.76%
Mapped reads, second in pair	6,517,723 / 49.49%
Mapped reads, both in pair	13,010,544 / 98.79%
Mapped reads, singletons	60,397 / 0.46%
Secondary alignments	0
Supplementary alignments	52,020 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	7,956,147 / 60.41%
Duplication rate	46.42%
Clipped reads	1,138,468 / 8.64%

2.2. ACGT Content

Number/percentage of A's	353,303,592 / 27.47%
Number/percentage of C's	291,336,784 / 22.65%
Number/percentage of T's	350,687,498 / 27.27%
Number/percentage of G's	290,441,617 / 22.58%
Number/percentage of N's	249,003 / 0.02%

GC Percentage	45.24%

2.3. Coverage

Mean	0.4155
Standard Deviation	14.9567

2.4. Mapping Quality

Mean Mapping Quality	55.18

2.5. Insert size

Mean	23,497.75
Standard Deviation	1,481,821.17
P25/Median/P75	166 / 236 / 321

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	7,675,182
Insertions	79,996
Mapped reads with at least one insertion	0.6%
Deletions	73,024
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.44%

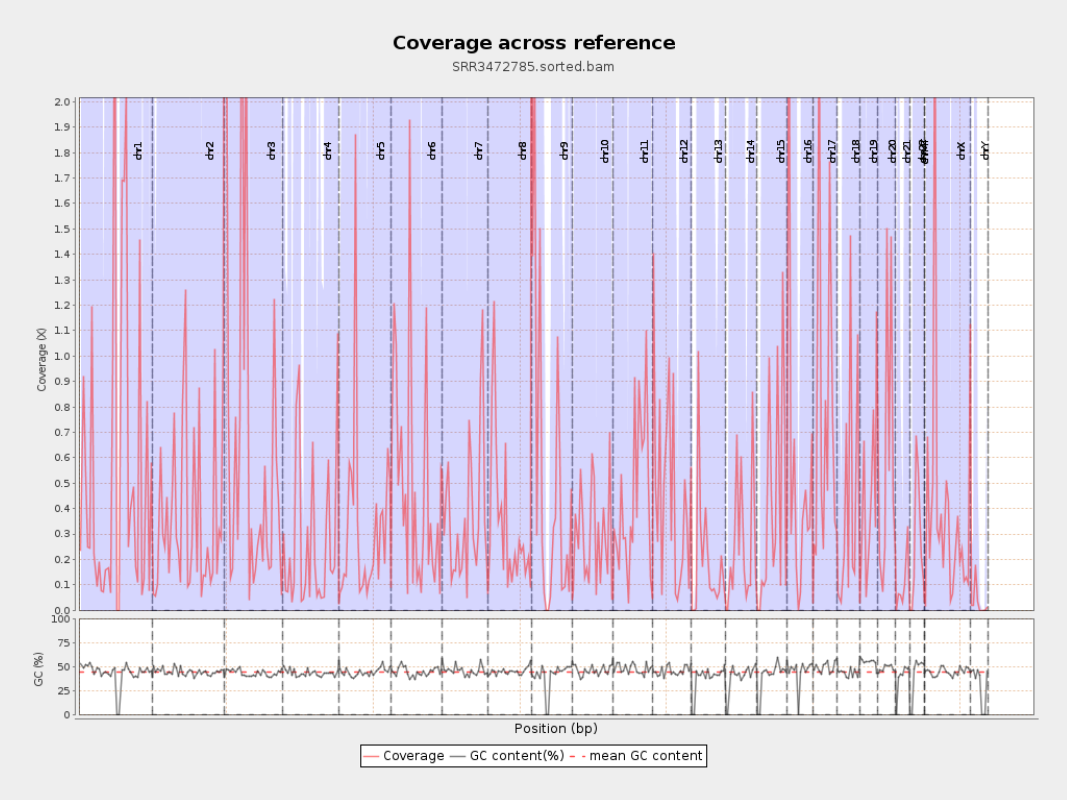
2.7. Chromosome stats

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

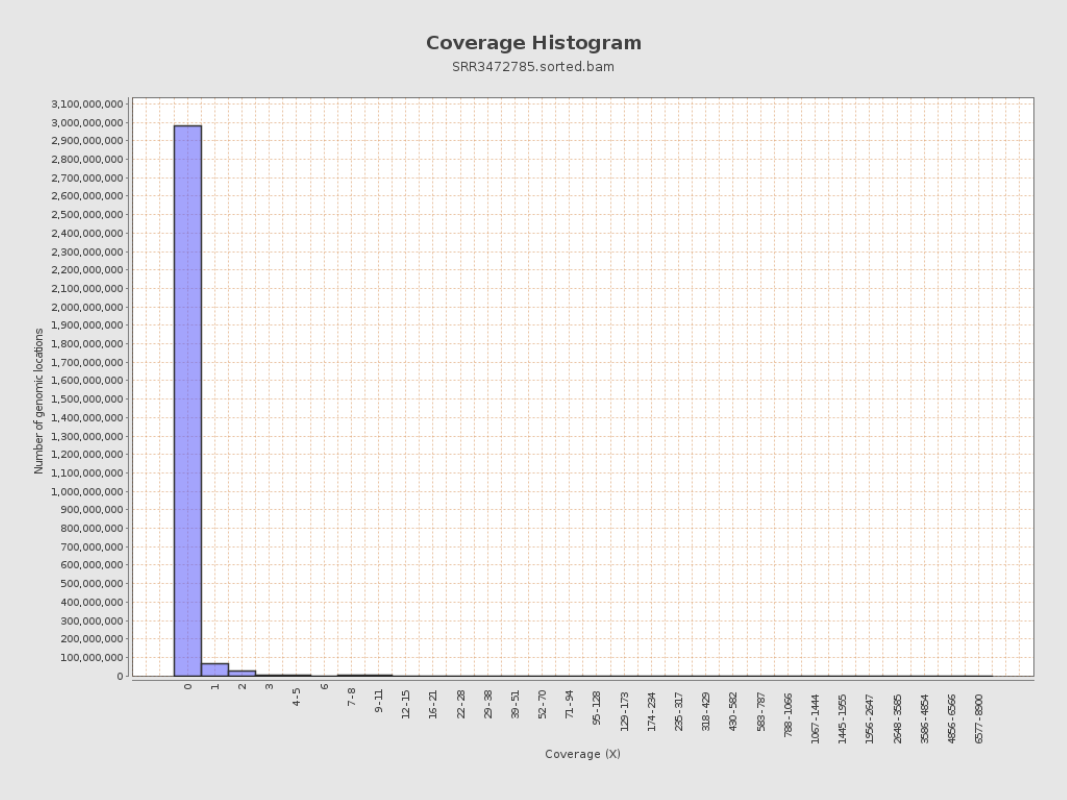
		bases	coverage	deviation
chr1	249250621	141137102	0.5662	20.8067
chr2	243199373	87950232	0.3616	15.9163
chr3	198022430	138799096	0.7009	16.5852
chr4	191154276	50928095	0.2664	11.6636
chr5	180915260	59572306	0.3293	10.3597
chr6	171115067	82194472	0.4803	14.3177
chr7	159138663	60667703	0.3812	15.7328
chr8	146364022	50545891	0.3453	10.5677
chr9	141213431	74971881	0.5309	14.8628
chr10	135534747	40336197	0.2976	11.2037
chr11	135006516	59760084	0.4426	17.7846
chr12	133851895	61868135	0.4622	13.0282
chr13	115169878	22577403	0.196	9.8886
chr14	107349540	26899324	0.2506	10.8703
chr15	102531392	42331633	0.4129	16.4119
chr16	90354753	47797909	0.529	15.1065
chr17	81195210	60682920	0.7474	23.0367
chr18	78077248	33552375	0.4297	18.3008
chr19	59128983	24700221	0.4177	10.7677
chr20	63025520	38147443	0.6053	24.8587
chr21	48129895	5088125	0.1057	4.4284
chr22	51304566	13211433	0.2575	9.0933
chrMT	16571	1053	0.0635	0.2871
chrX	155270560	60440686	0.3893	12.9467

chrY	59373566	2039186	0.0343	1.6421

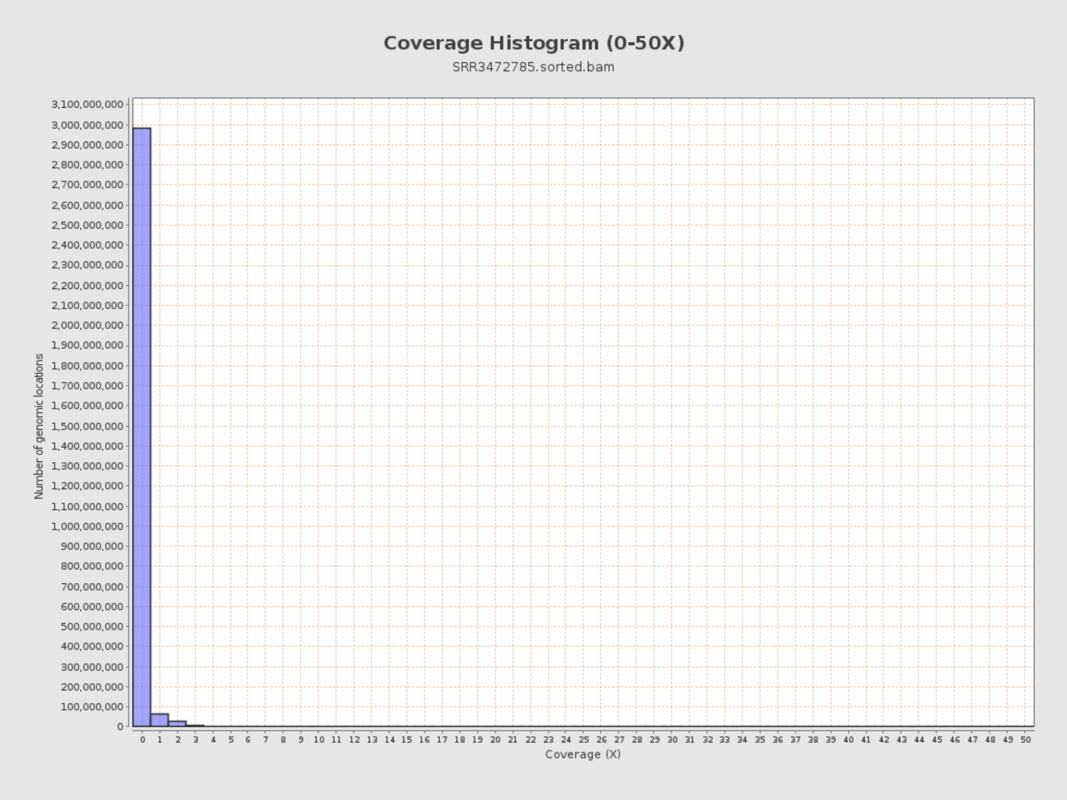
3. Results : Coverage across reference



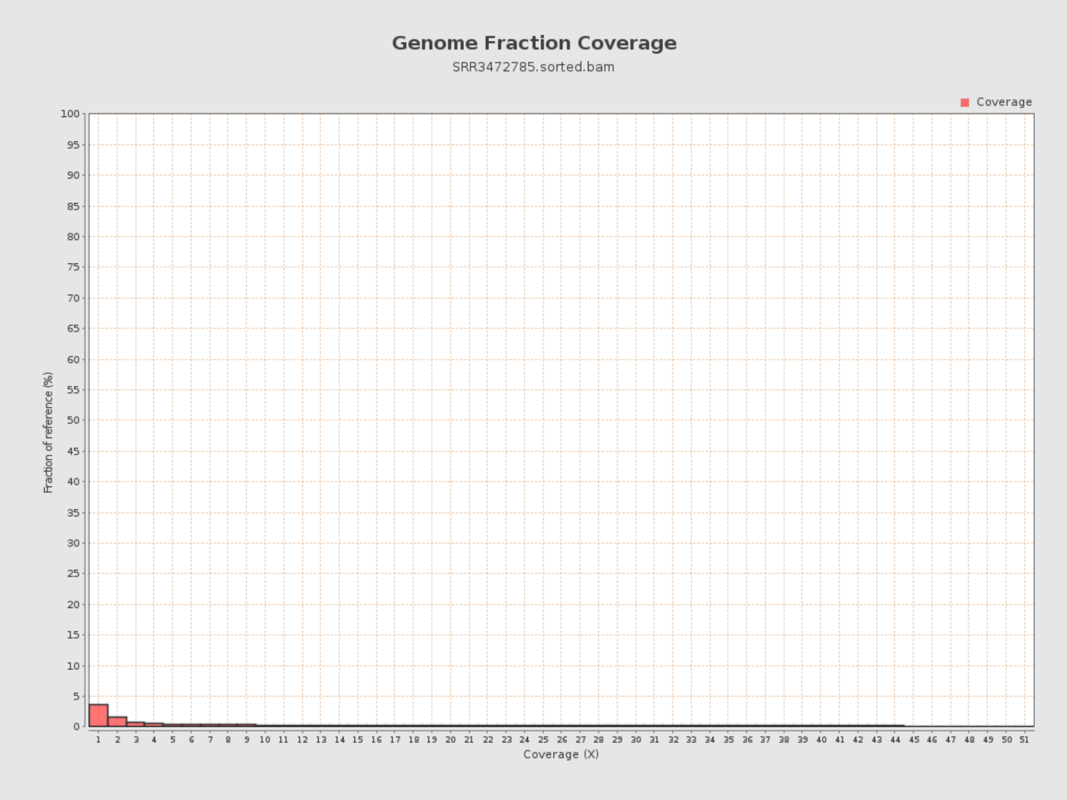
4. Results : Coverage Histogram



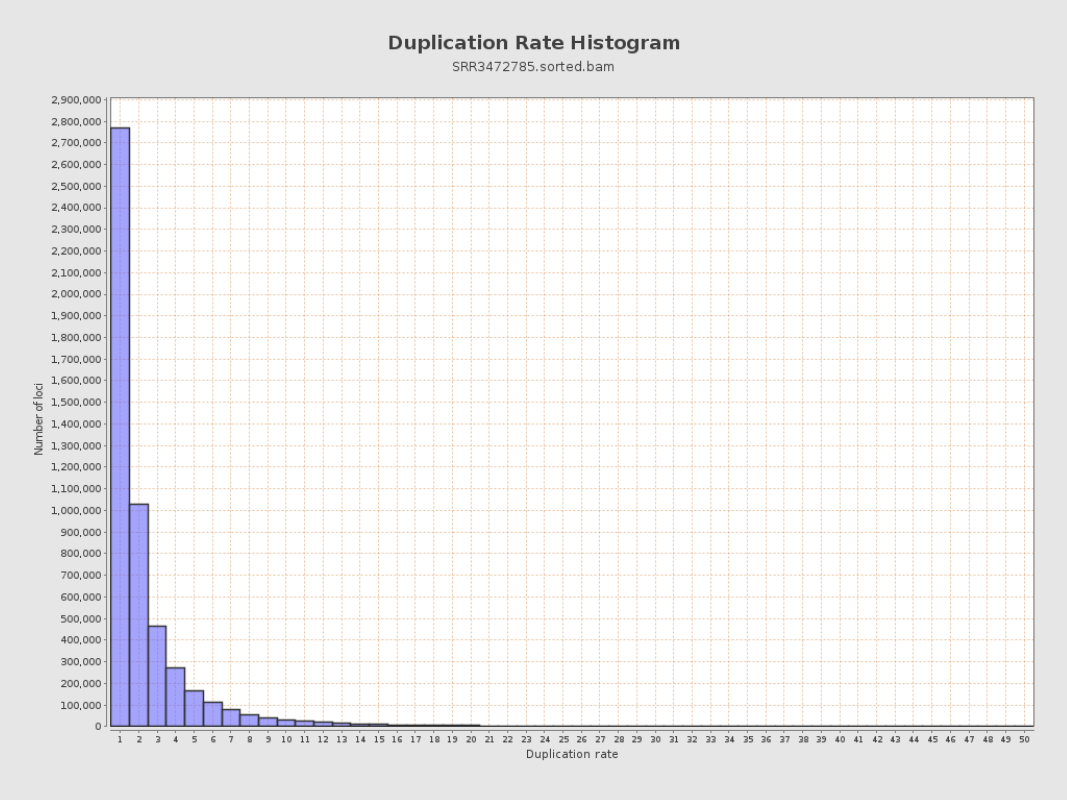
5. Results : Coverage Histogram (0-50X)



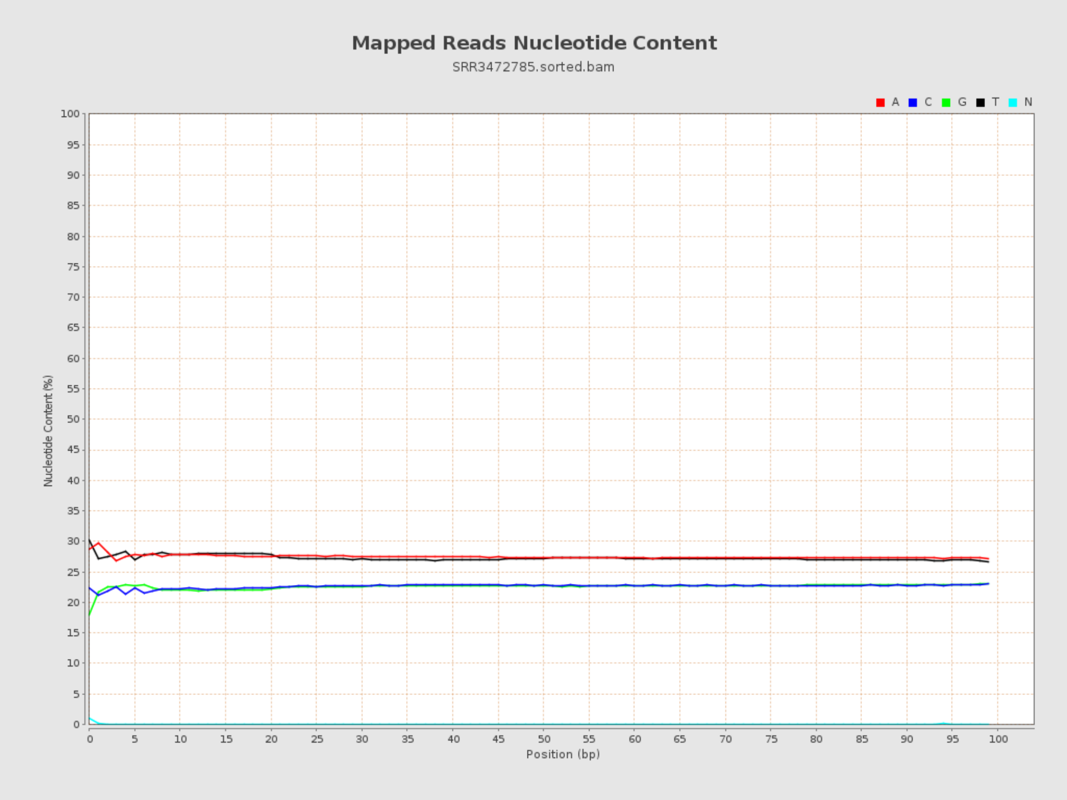
6. Results : Genome Fraction Coverage



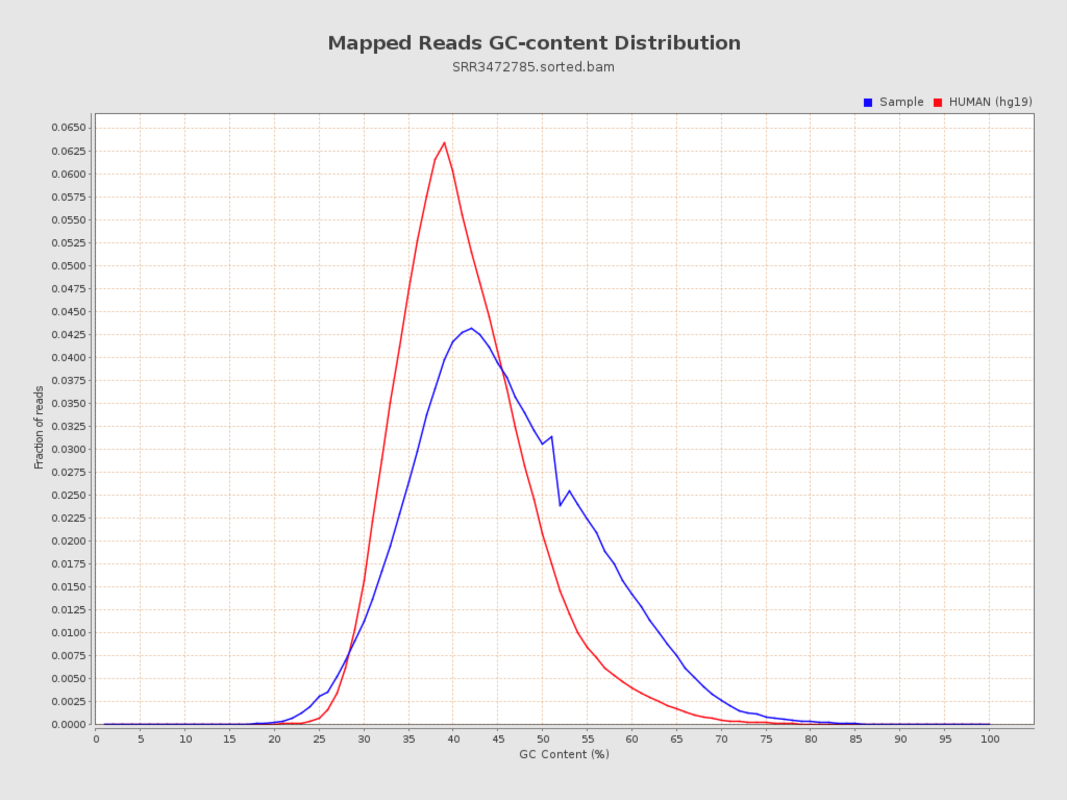
7. Results : Duplication Rate Histogram



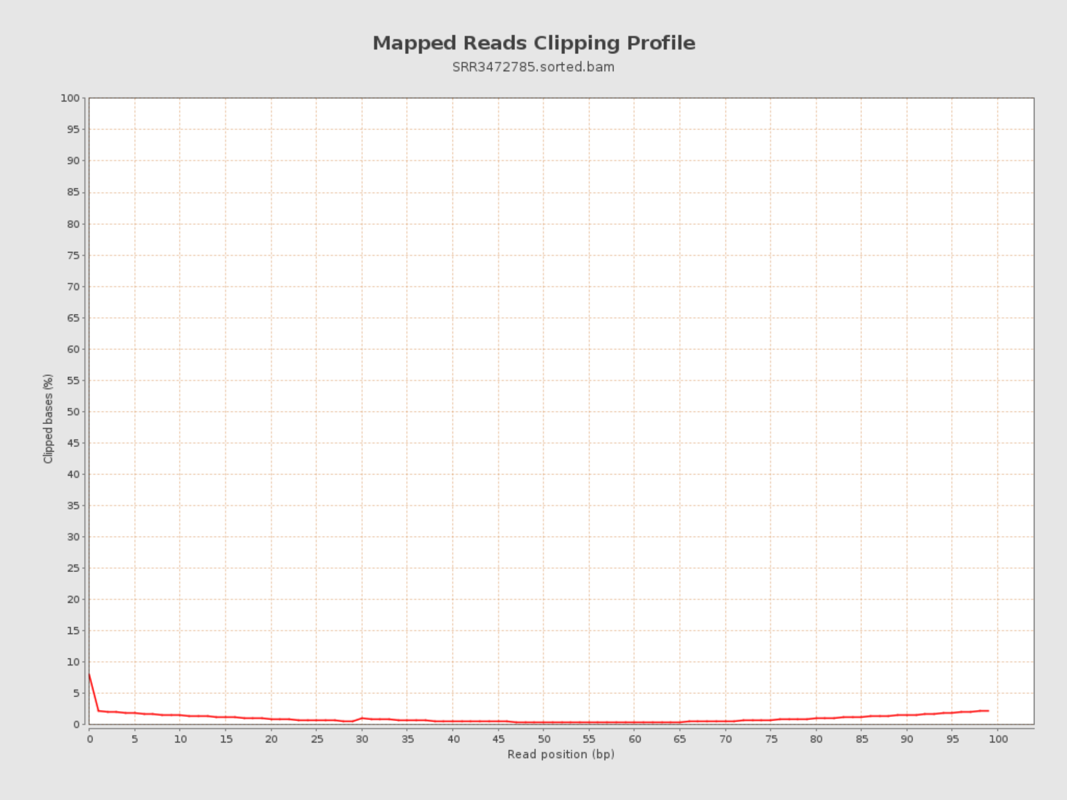
8. Results : Mapped Reads Nucleotide Content



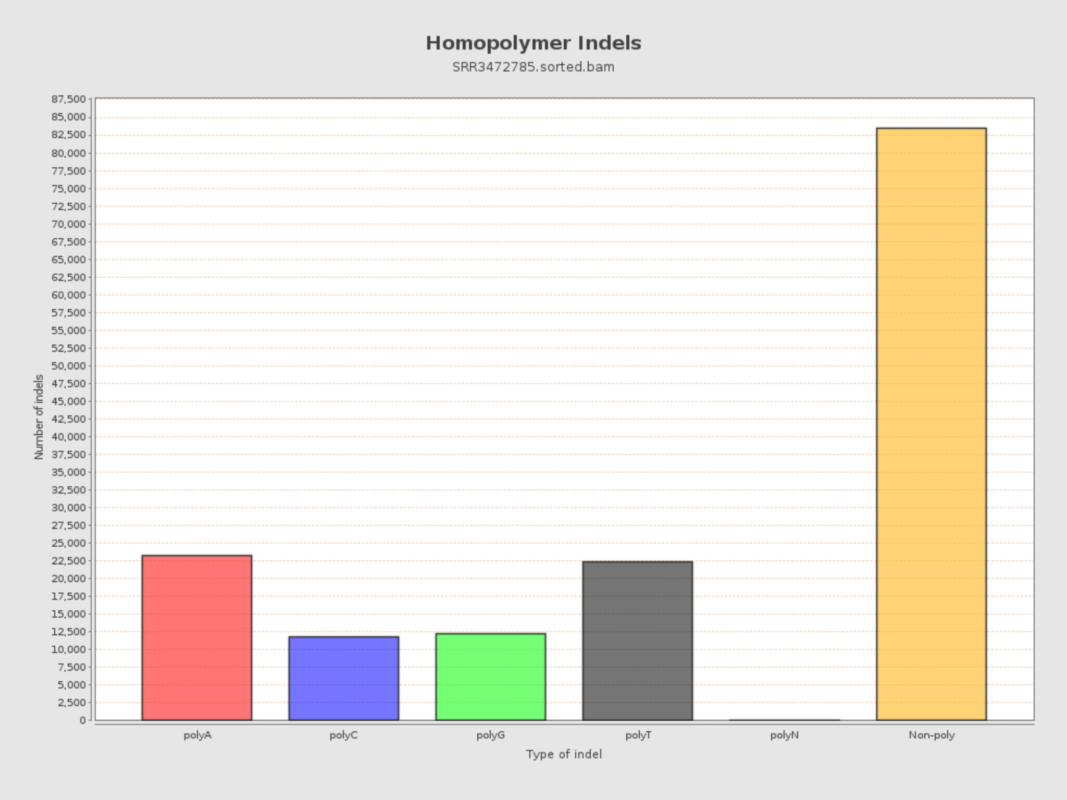
9. Results : Mapped Reads GC-content Distribution



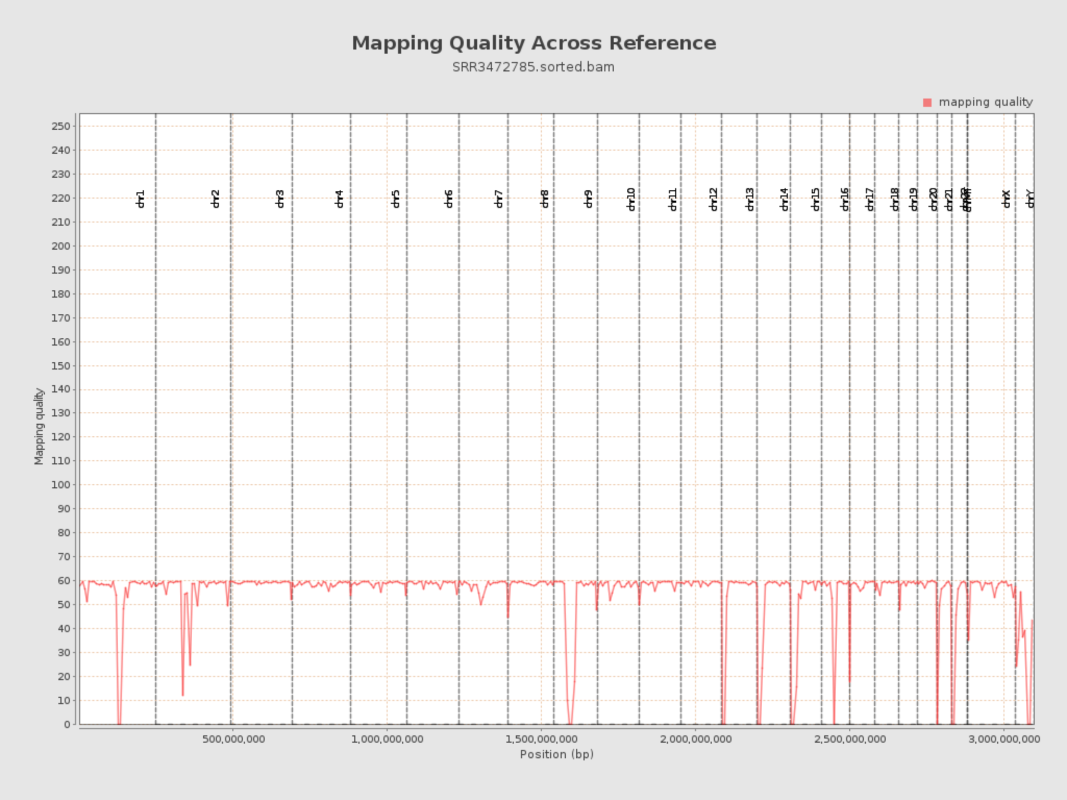
10. Results : Mapped Reads Clipping Profile



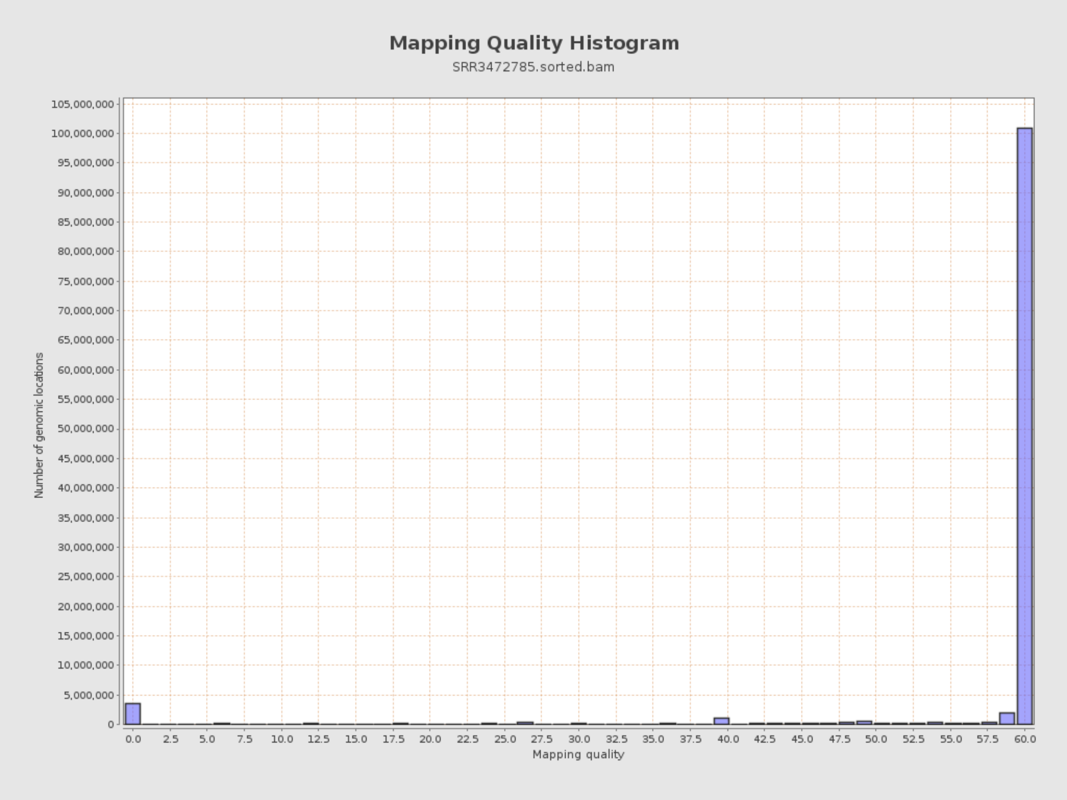
11. Results : Homopolymer Indels



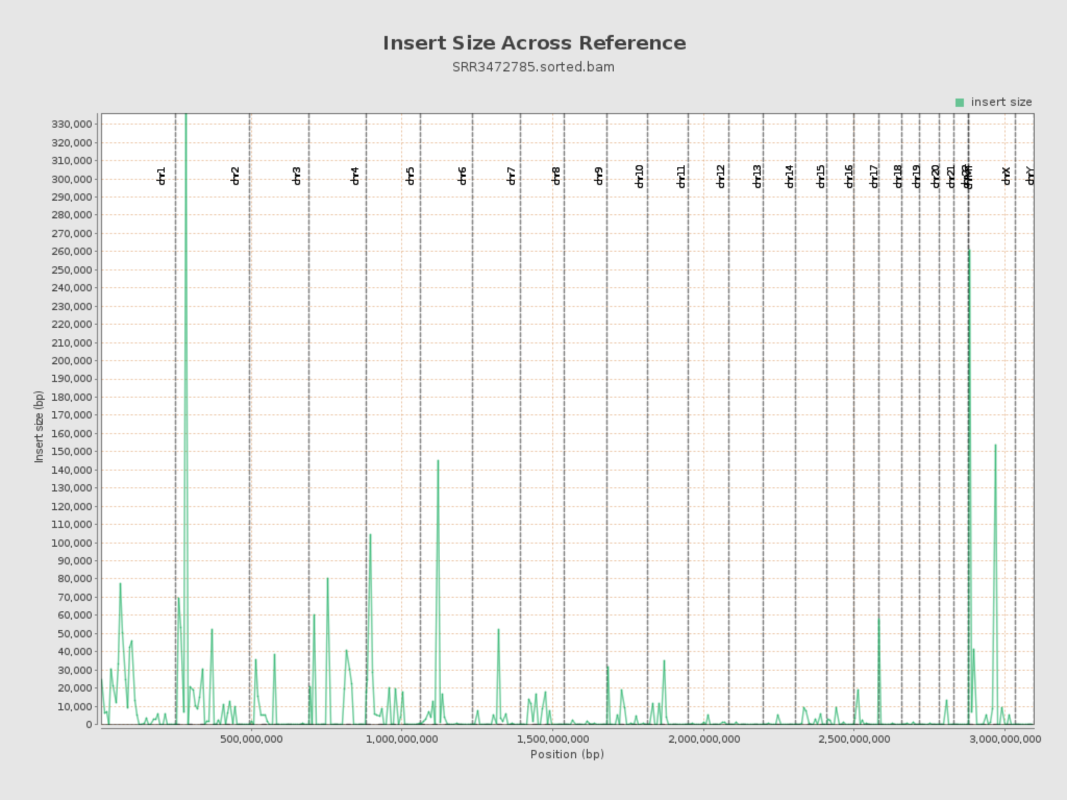
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram