Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 18:34:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472793.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_SRR3472793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472793_1.fastq.gz SRR3472793_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 18:34:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,484,308
Mapped reads	9,399,322 / 99.1%
Unmapped reads	84,986 / 0.9%
Mapped paired reads	9,399,322 / 99.1%
Mapped reads, first in pair	4,714,546 / 49.71%
Mapped reads, second in pair	4,684,776 / 49.4%
Mapped reads, both in pair	9,348,252 / 98.57%
Mapped reads, singletons	51,070 / 0.54%
Secondary alignments	0
Supplementary alignments	31,665 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	5,150,249 / 54.3%
Duplication rate	43.48%
Clipped reads	832,263 / 8.78%

2.2. ACGT Content

Number/percentage of A's	254,633,649 / 27.57%
Number/percentage of C's	208,772,027 / 22.6%
Number/percentage of T's	252,607,733 / 27.35%
Number/percentage of G's	207,555,843 / 22.47%
Number/percentage of N's	176,098 / 0.02%

GC Percentage	45.07%

2.3. Coverage

Mean	0.2984
Standard Deviation	10.1989

2.4. Mapping Quality

Mean Mapping Quality	55.17

2.5. Insert size

Mean	26,707.18
Standard Deviation	1,593,629.06
P25/Median/P75	166 / 237 / 324

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	5,527,822
Insertions	55,340
Mapped reads with at least one insertion	0.58%
Deletions	55,812
Mapped reads with at least one deletion	0.59%
Homopolymer indels	45.68%

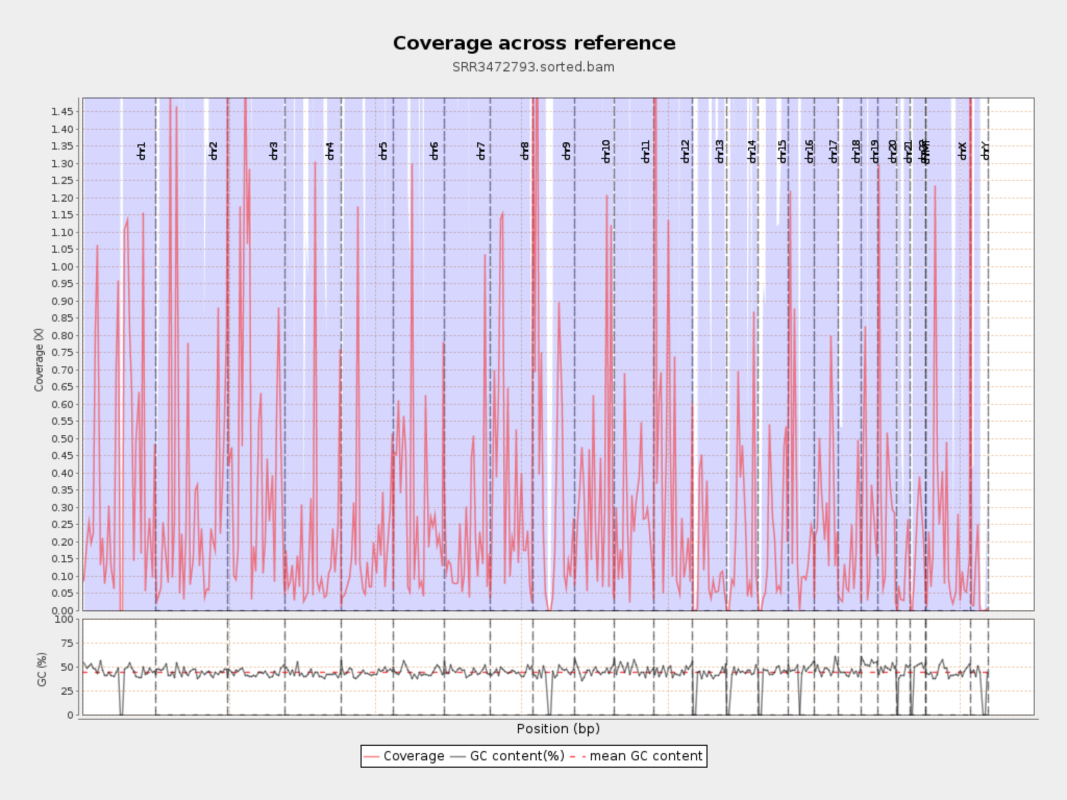
2.7. Chromosome stats

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

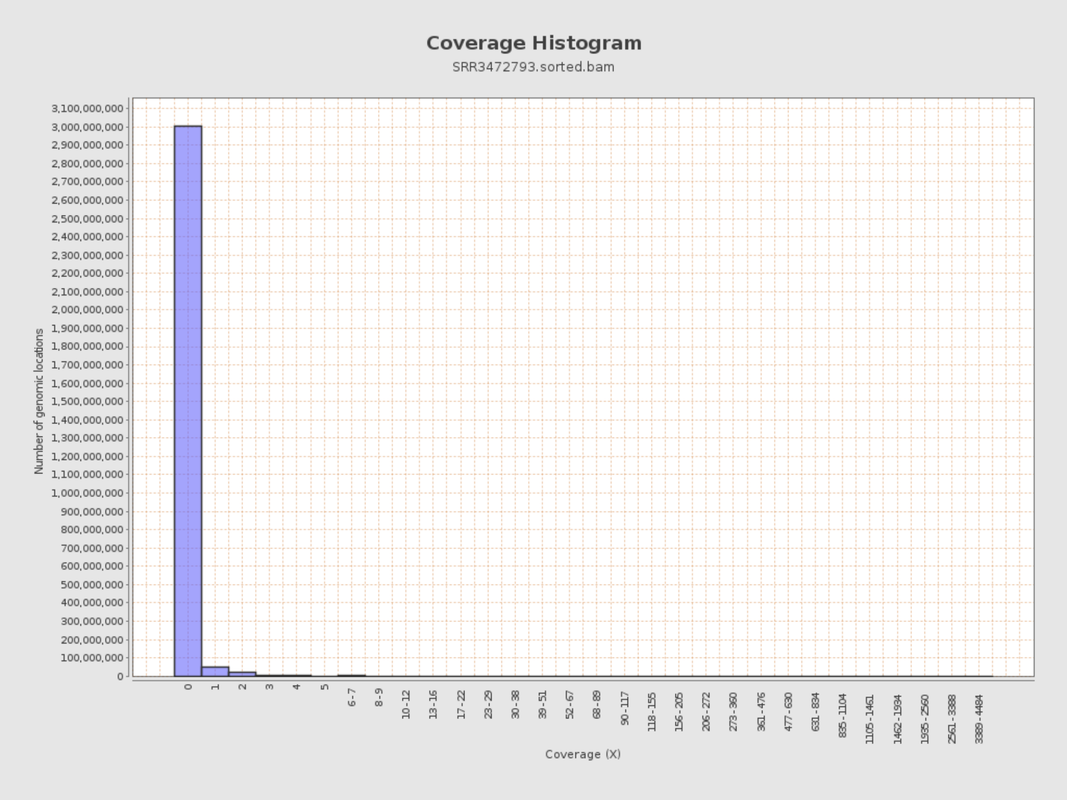
		bases	coverage	deviation
chr1	249250621	100187354	0.402	12.0761
chr2	243199373	76869581	0.3161	11.949
chr3	198022430	96677282	0.4882	13.7557
chr4	191154276	35777164	0.1872	8.4443
chr5	180915260	36081955	0.1994	5.6796
chr6	171115067	55657356	0.3253	7.7269
chr7	159138663	34687110	0.218	6.3748
chr8	146364022	54637695	0.3733	13.9344
chr9	141213431	55277787	0.3914	10.1264
chr10	135534747	49618179	0.3661	15.2457
chr11	135006516	35654839	0.2641	8.6209
chr12	133851895	67317837	0.5029	16.4172
chr13	115169878	14970142	0.13	5.1014
chr14	107349540	26234929	0.2444	8.3977
chr15	102531392	19345281	0.1887	6.0351
chr16	90354753	27623315	0.3057	10.5859
chr17	81195210	27284991	0.336	7.4342
chr18	78077248	11292204	0.1446	4.6407
chr19	59128983	17991406	0.3043	7.4966
chr20	63025520	22417104	0.3557	13.2018
chr21	48129895	4570238	0.095	3.8848
chr22	51304566	9921934	0.1934	5.1891
chrMT	16571	954	0.0576	0.2636
chrX	155270560	40510155	0.2609	7.6335

chrY	59373566	3276605	0.0552	3.4435

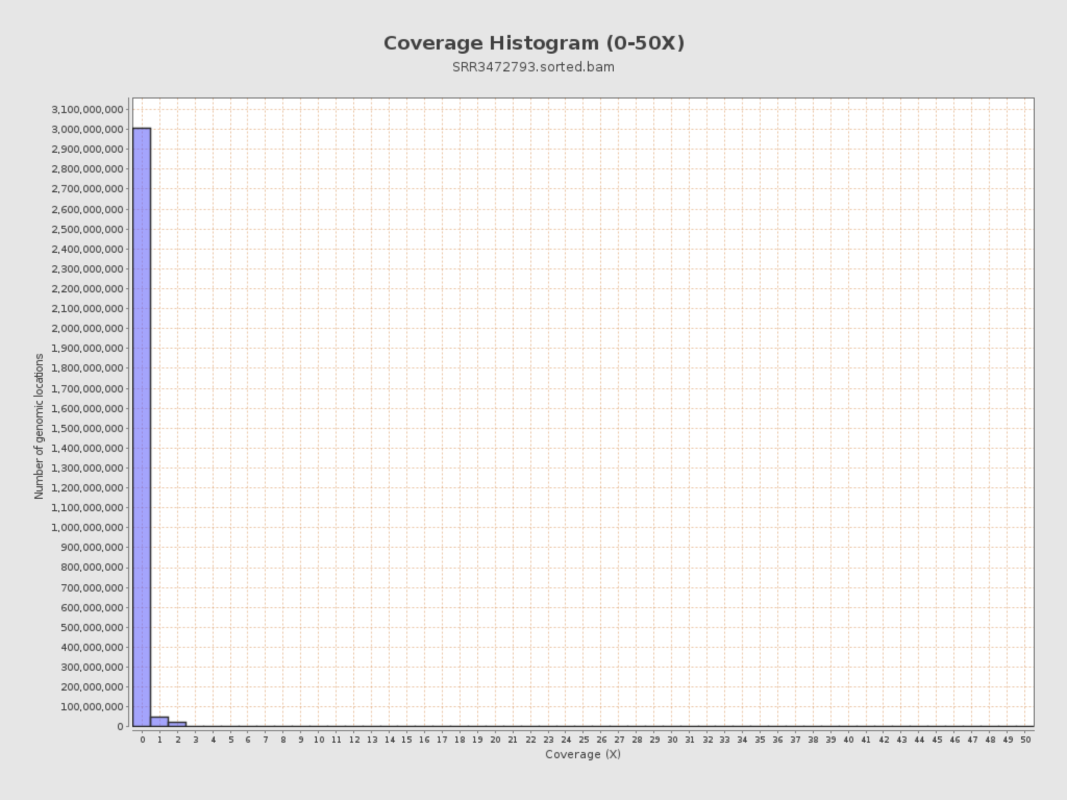
3. Results : Coverage across reference



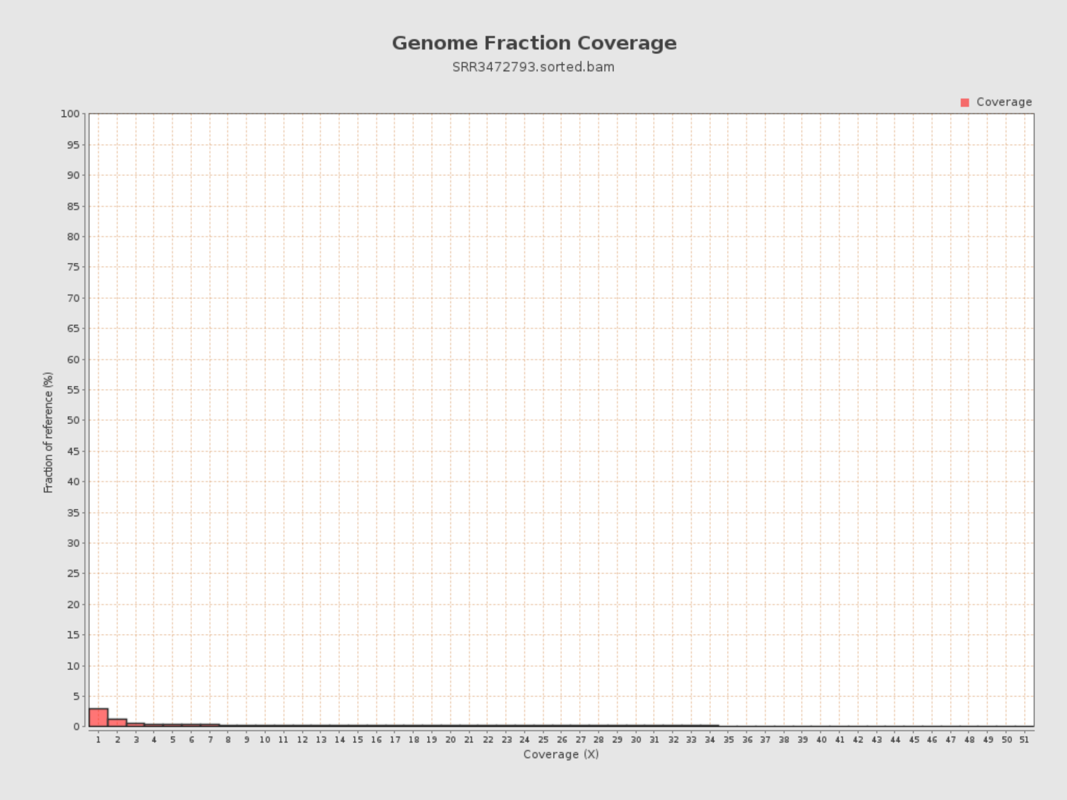
4. Results : Coverage Histogram



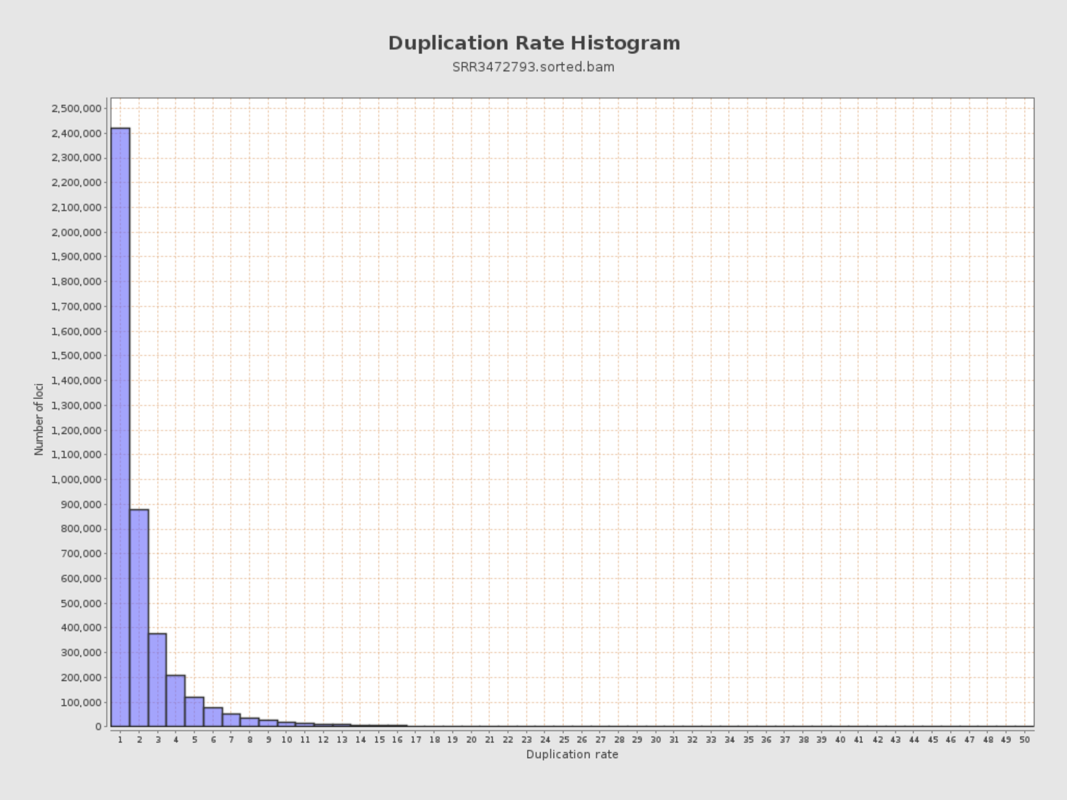
5. Results : Coverage Histogram (0-50X)



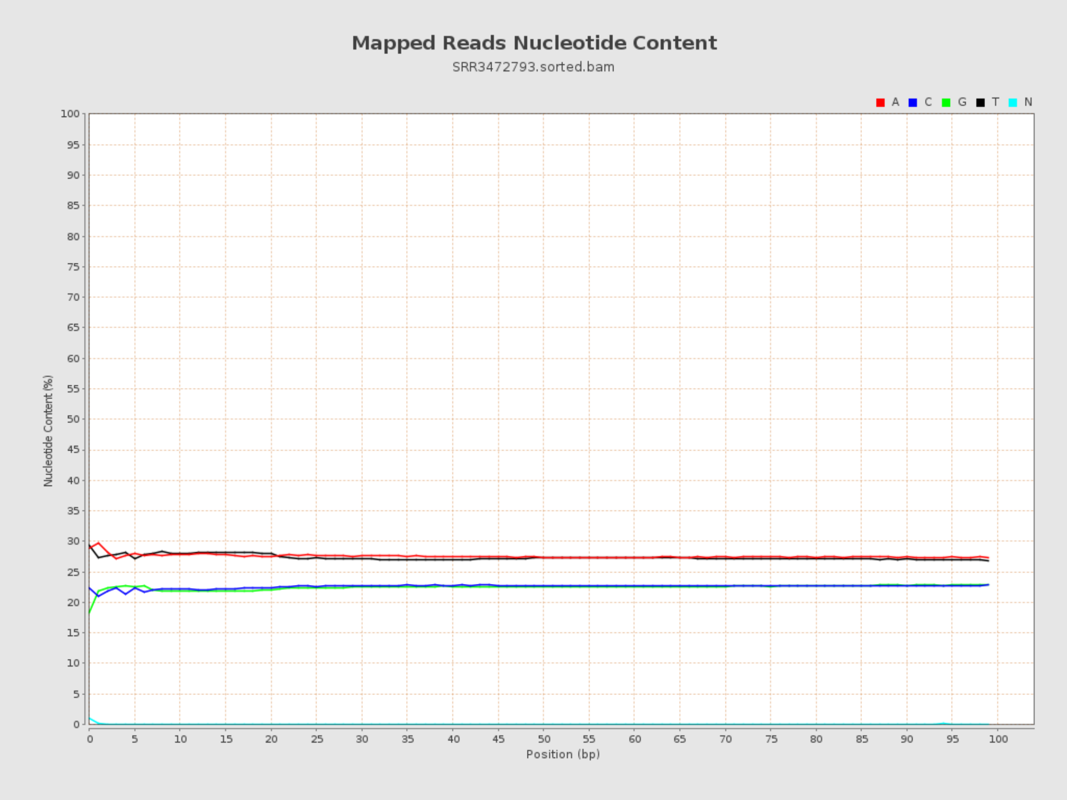
6. Results : Genome Fraction Coverage



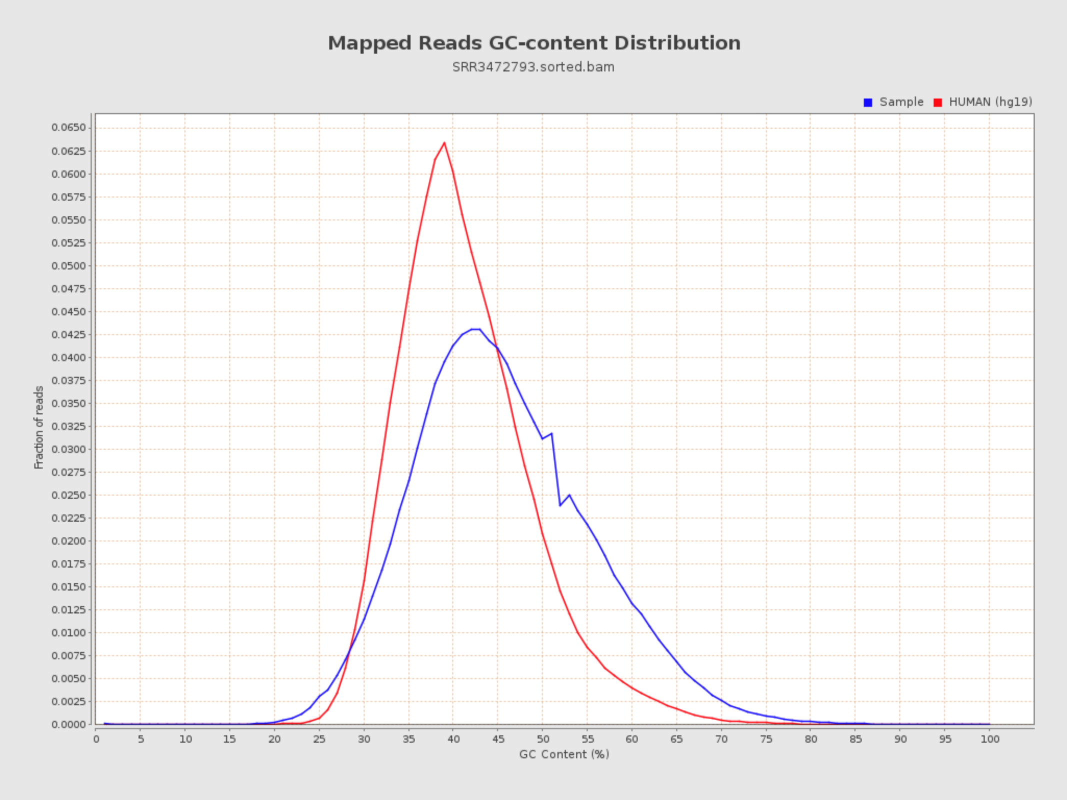
7. Results : Duplication Rate Histogram



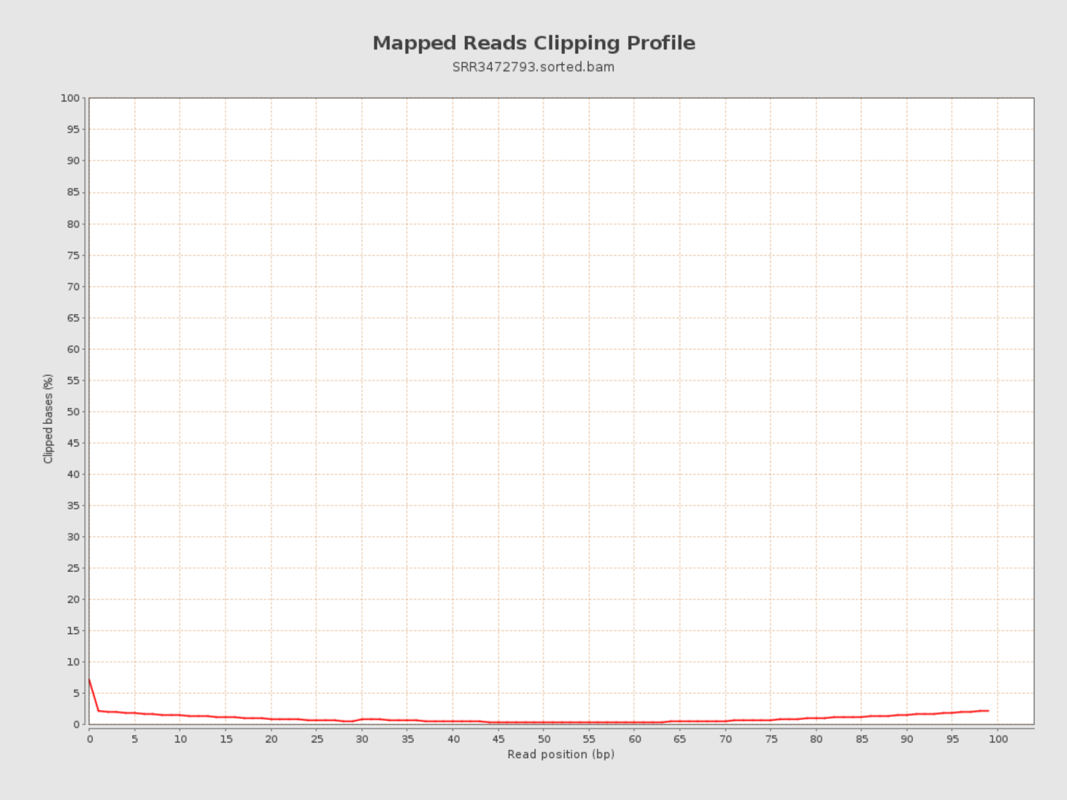
8. Results : Mapped Reads Nucleotide Content



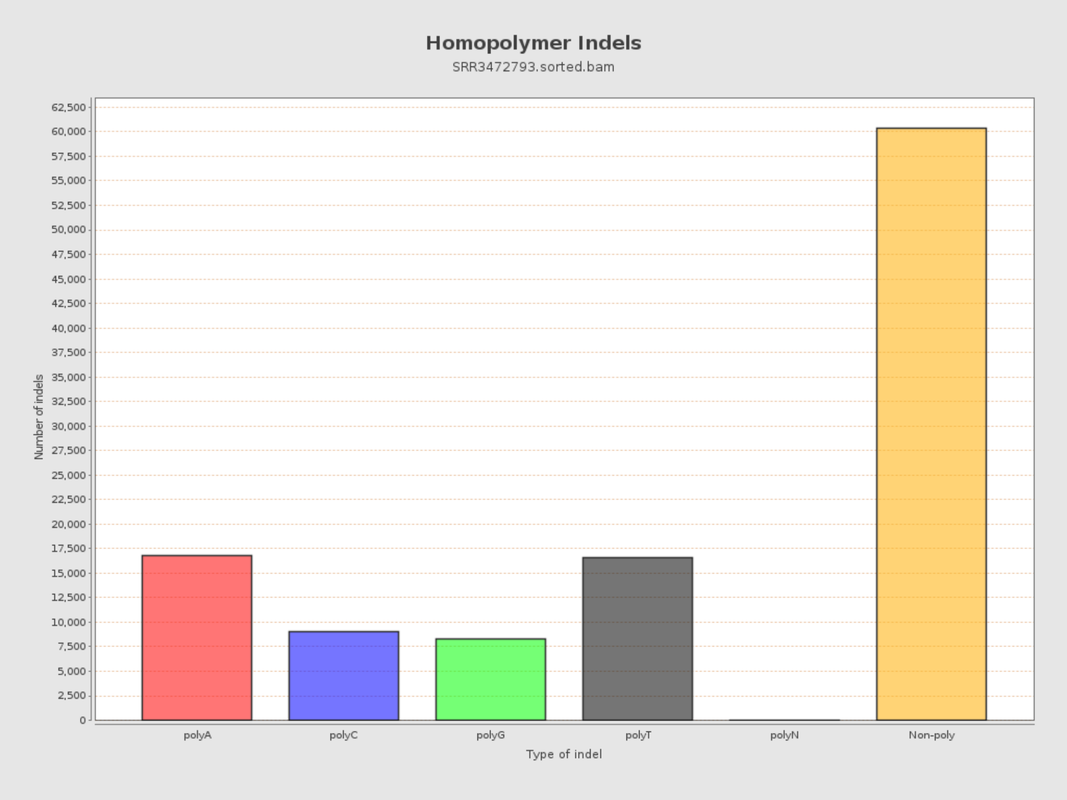
9. Results : Mapped Reads GC-content Distribution



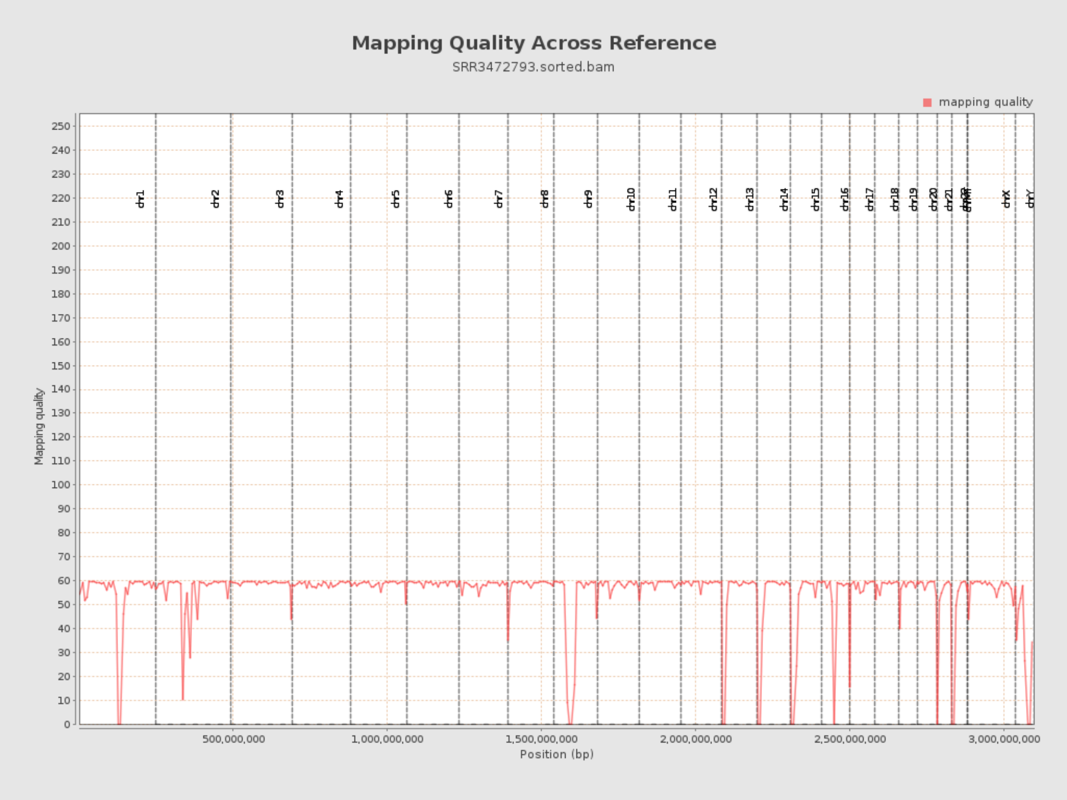
10. Results : Mapped Reads Clipping Profile



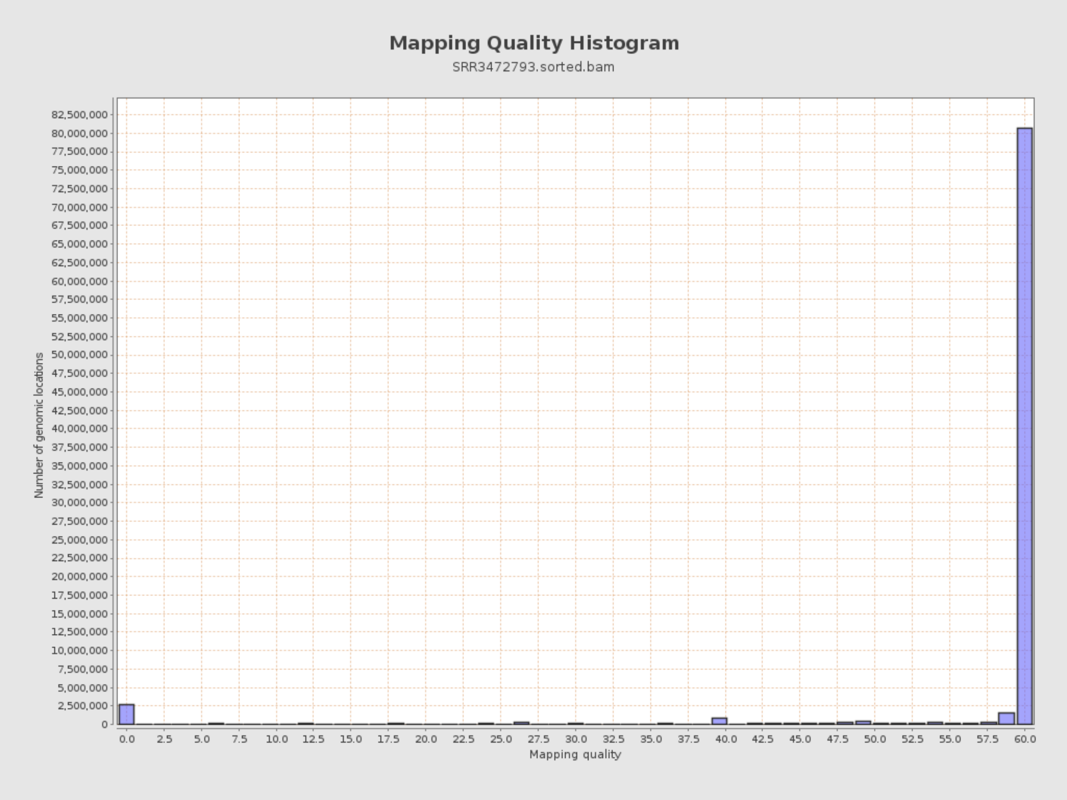
11. Results : Homopolymer Indels



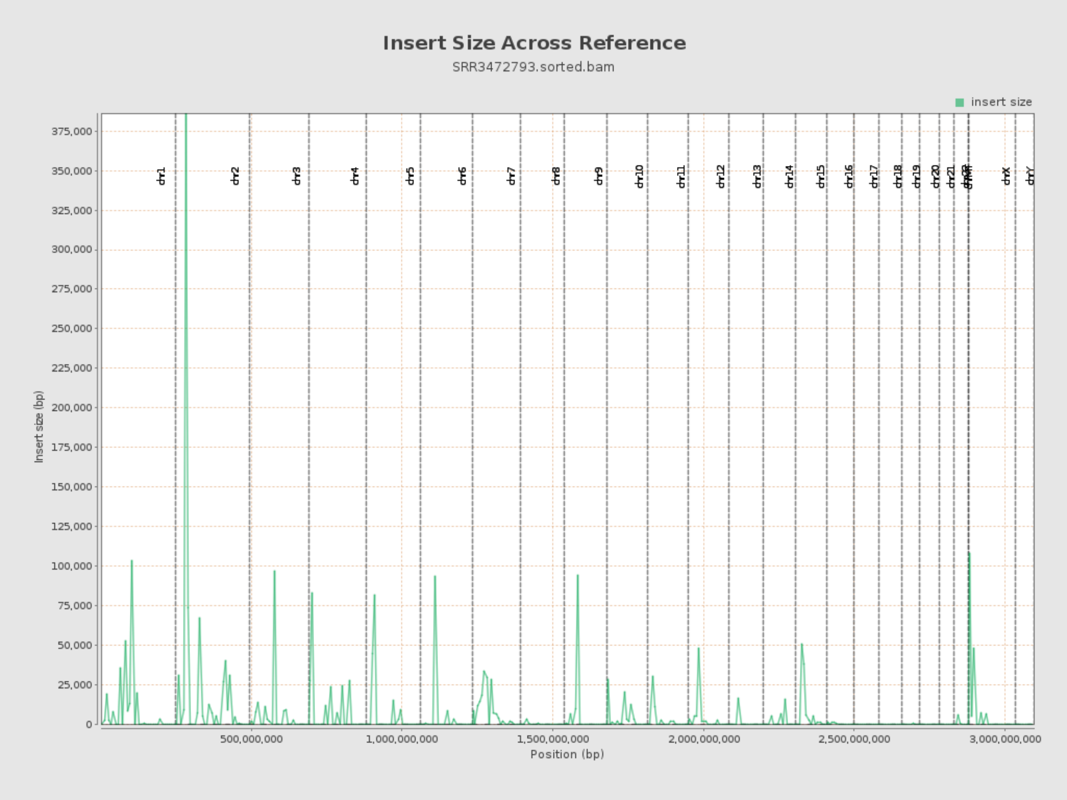
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram