Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 19:05:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472795.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_SRR3472795 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472795_1.fastq.gz SRR3472795_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 19:04:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472795.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,827,112
Mapped reads	16,699,881 / 99.24%
Unmapped reads	127,231 / 0.76%
Mapped paired reads	16,699,881 / 99.24%
Mapped reads, first in pair	8,372,149 / 49.75%
Mapped reads, second in pair	8,327,732 / 49.49%
Mapped reads, both in pair	16,623,010 / 98.79%
Mapped reads, singletons	76,871 / 0.46%
Secondary alignments	0
Supplementary alignments	55,164 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	10,579,687 / 62.87%
Duplication rate	46.65%
Clipped reads	1,513,254 / 8.99%

2.2. ACGT Content

Number/percentage of A's	441,722,846 / 26.91%
Number/percentage of C's	381,369,919 / 23.24%
Number/percentage of T's	439,049,002 / 26.75%
Number/percentage of G's	378,761,062 / 23.08%
Number/percentage of N's	319,241 / 0.02%

GC Percentage	46.31%

2.3. Coverage

Mean	0.5302
Standard Deviation	19.3251

2.4. Mapping Quality

Mean Mapping Quality	55.28

2.5. Insert size

Mean	22,769.32
Standard Deviation	1,466,283.75
P25/Median/P75	158 / 220 / 297

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	9,290,237
Insertions	92,030
Mapped reads with at least one insertion	0.55%
Deletions	87,307
Mapped reads with at least one deletion	0.51%
Homopolymer indels	43.72%

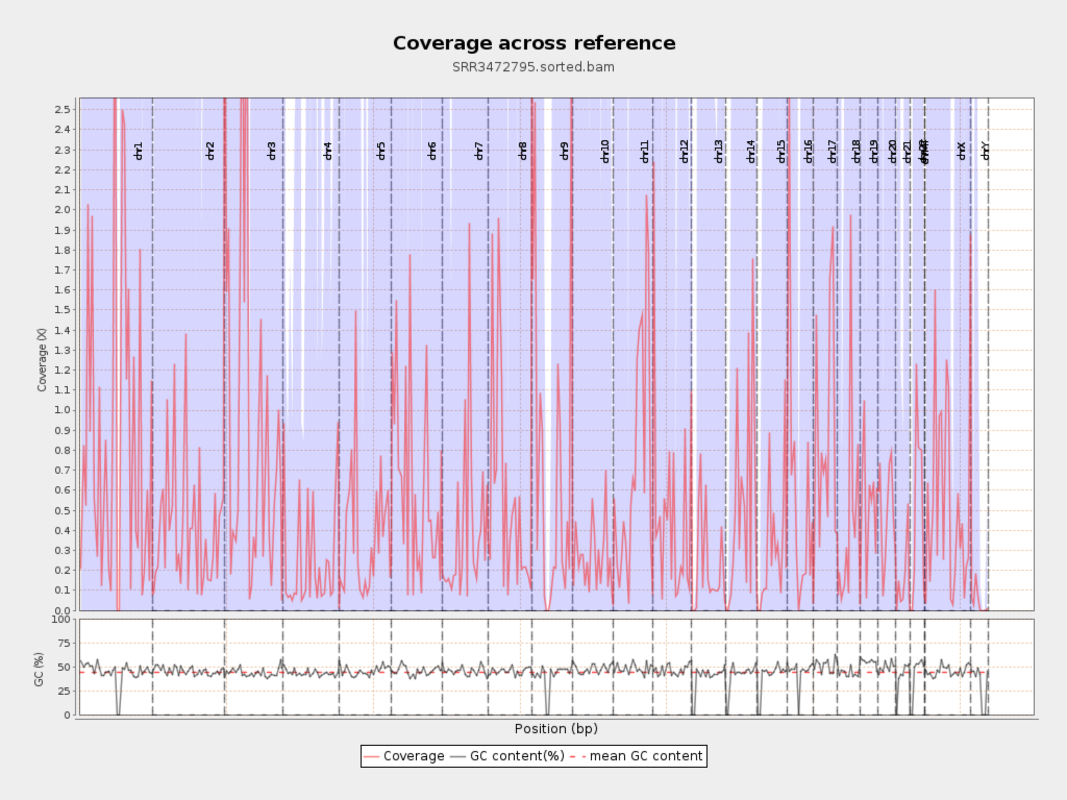
2.7. Chromosome stats

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

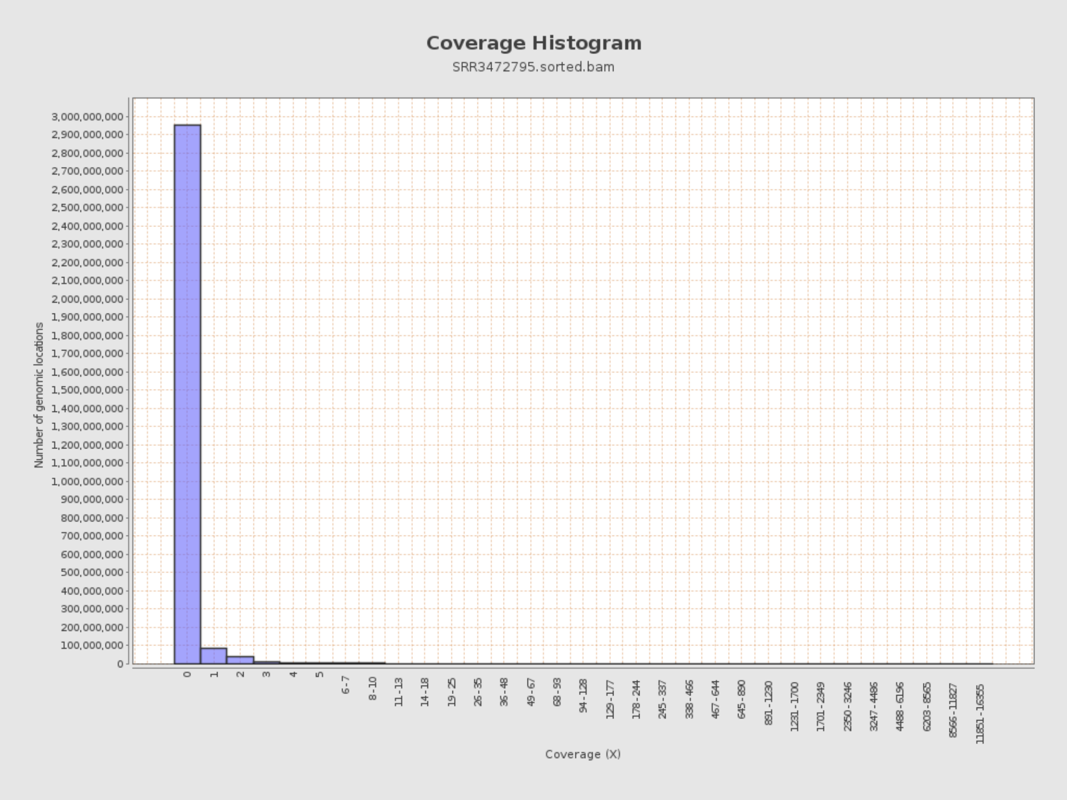
		bases	coverage	deviation
chr1	249250621	221907212	0.8903	34.3971
chr2	243199373	101852499	0.4188	13.7456
chr3	198022430	194939519	0.9844	23.2462
chr4	191154276	46410718	0.2428	7.9873
chr5	180915260	66832212	0.3694	11.807
chr6	171115067	105823165	0.6184	17.6993
chr7	159138663	65017127	0.4086	15.5797
chr8	146364022	81632781	0.5577	18.3484
chr9	141213431	105472753	0.7469	22.1894
chr10	135534747	36921621	0.2724	8.4897
chr11	135006516	98511658	0.7297	29.0197
chr12	133851895	64043626	0.4785	13.1045
chr13	115169878	26061919	0.2263	8.1459
chr14	107349540	55742865	0.5193	24.9265
chr15	102531392	32944121	0.3213	11.7325
chr16	90354753	52196520	0.5777	16.4732
chr17	81195210	68996508	0.8498	22.2825
chr18	78077248	36299761	0.4649	23.6327
chr19	59128983	31661798	0.5355	14.7971
chr20	63025520	31510786	0.5	25.0022
chr21	48129895	7758476	0.1612	8.3355
chr22	51304566	24556321	0.4786	13.1088
chrMT	16571	1143	0.069	0.3649
chrX	155270560	81665418	0.526	18.217

chrY	59373566	2691977	0.0453	2.0995

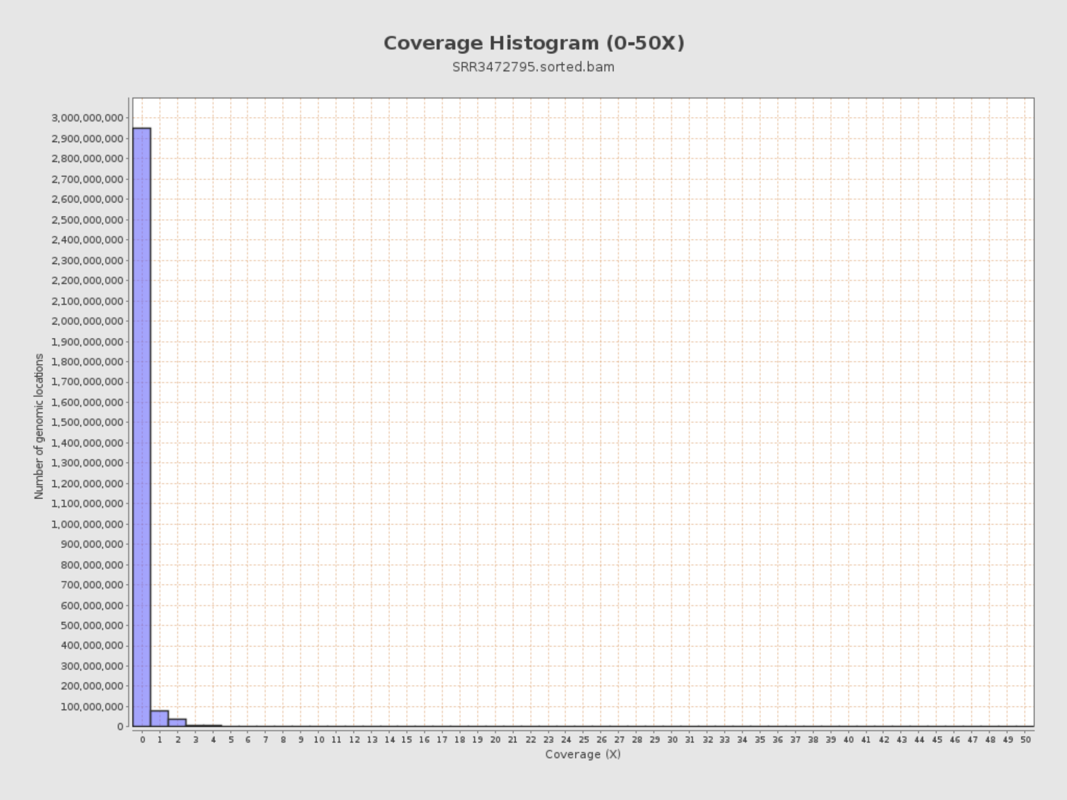
3. Results : Coverage across reference



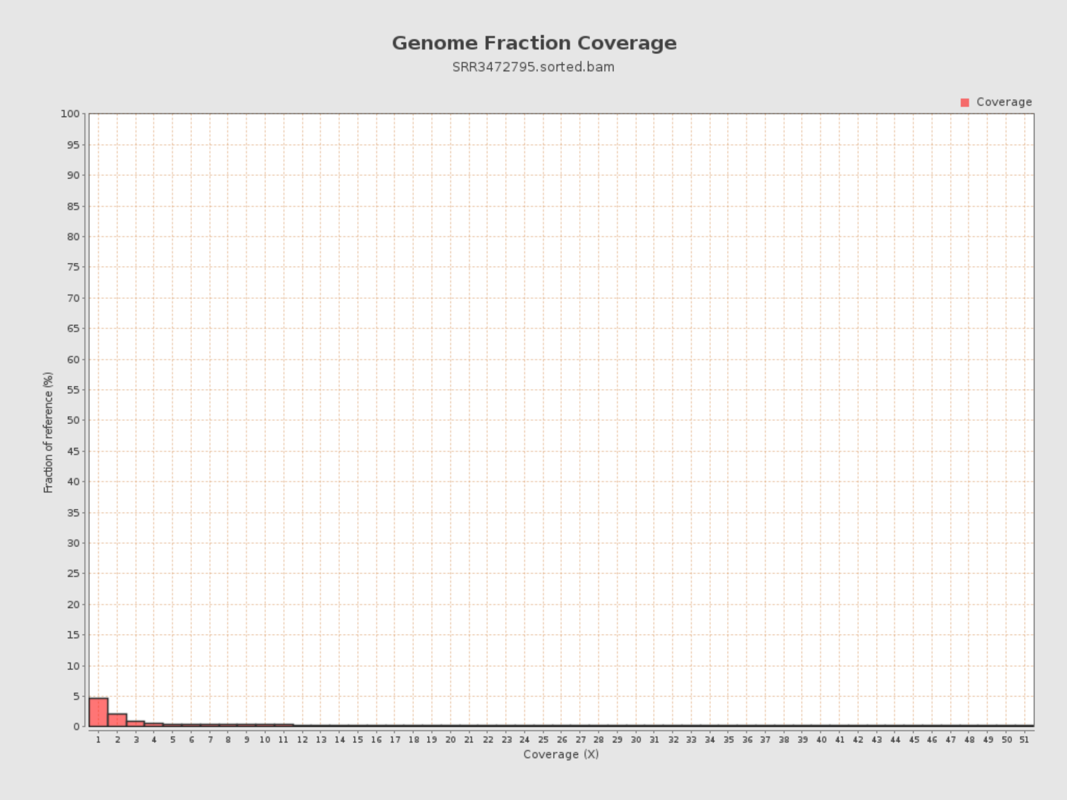
4. Results : Coverage Histogram



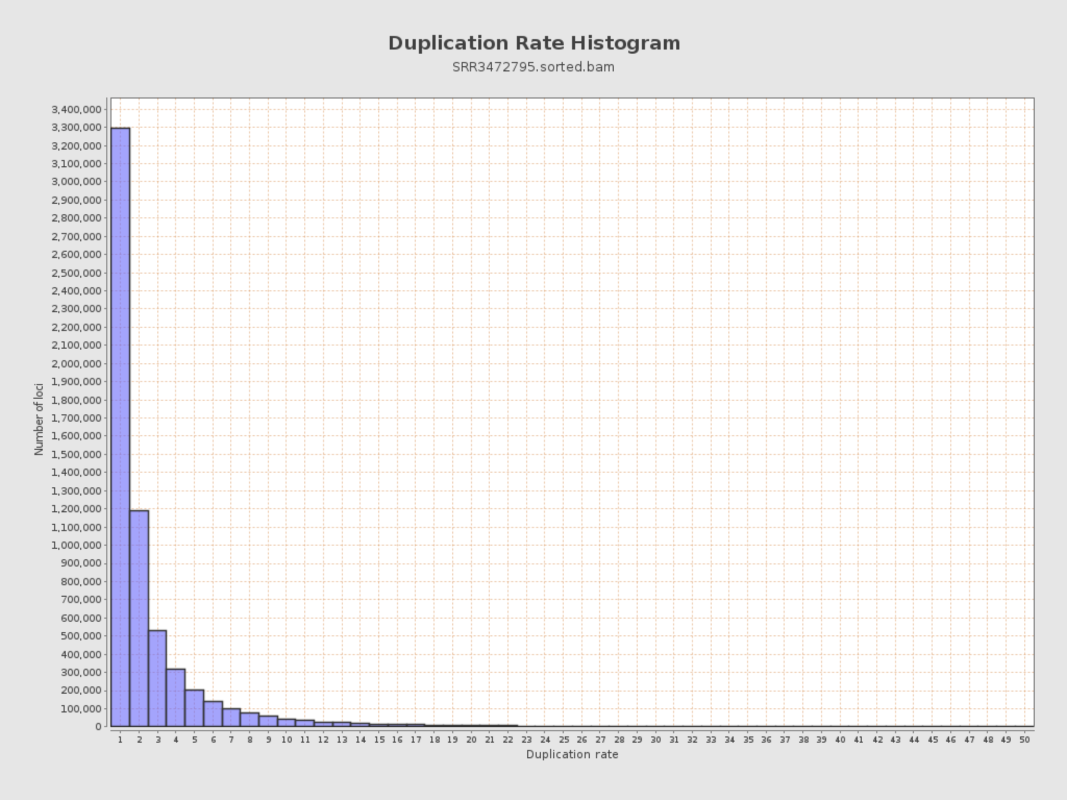
5. Results : Coverage Histogram (0-50X)



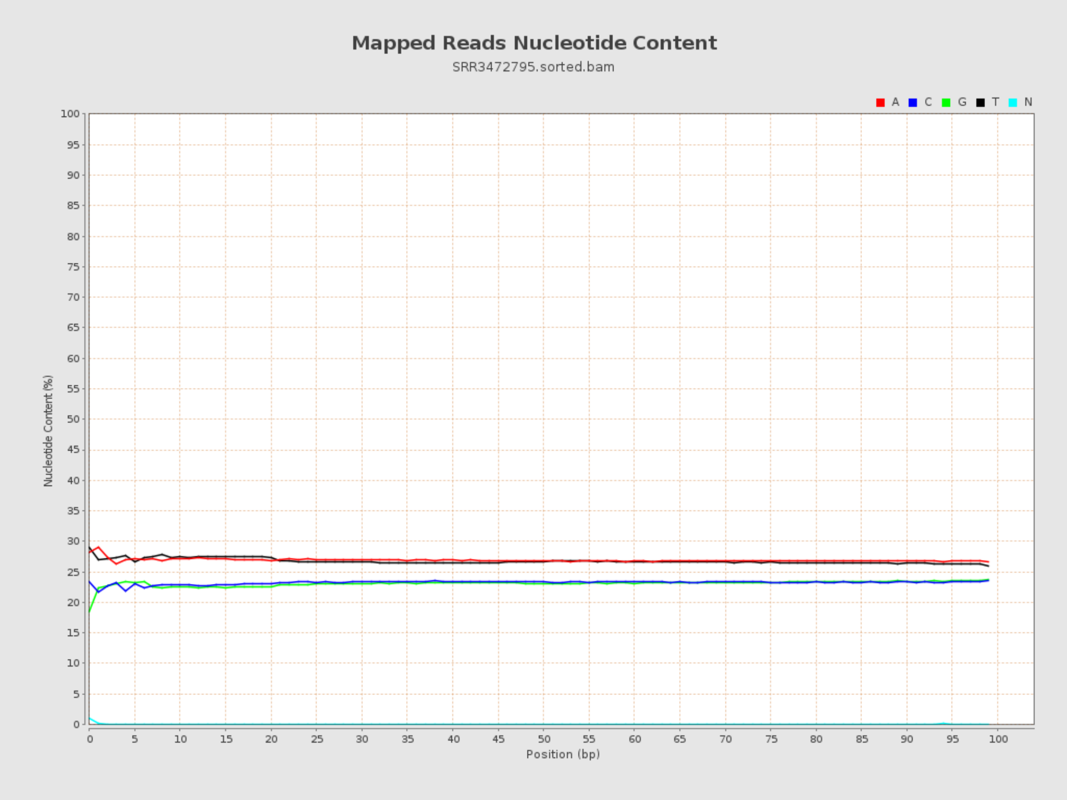
6. Results : Genome Fraction Coverage



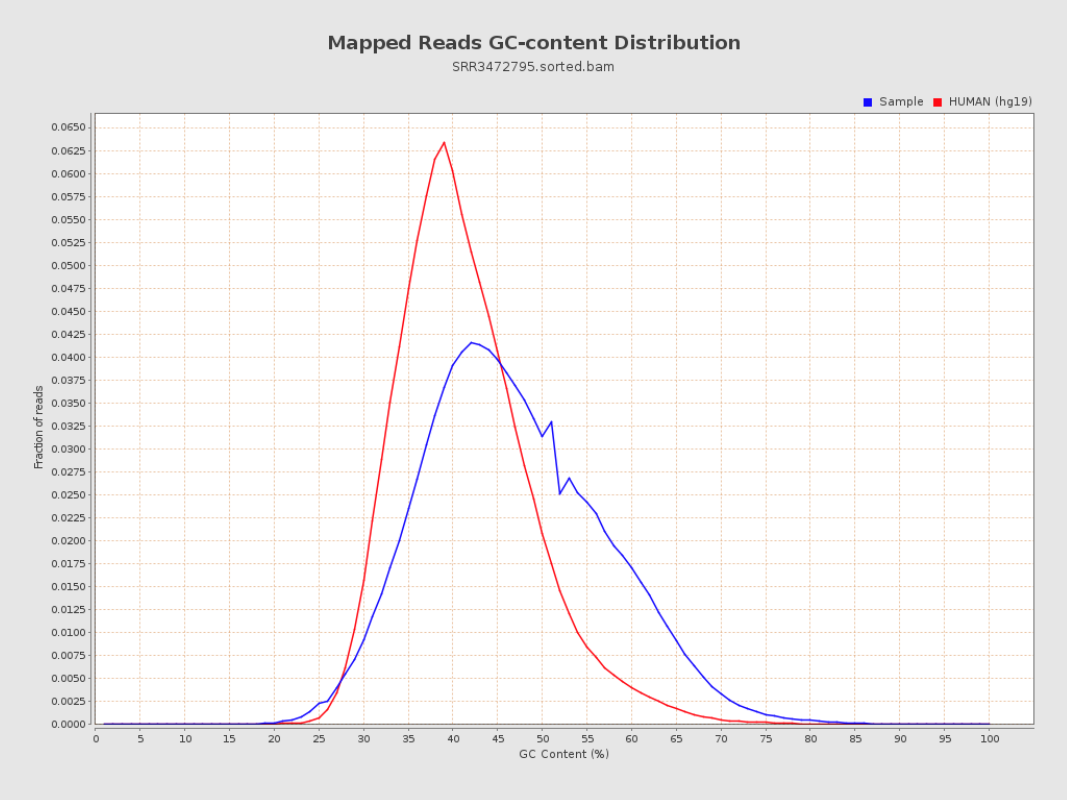
7. Results : Duplication Rate Histogram



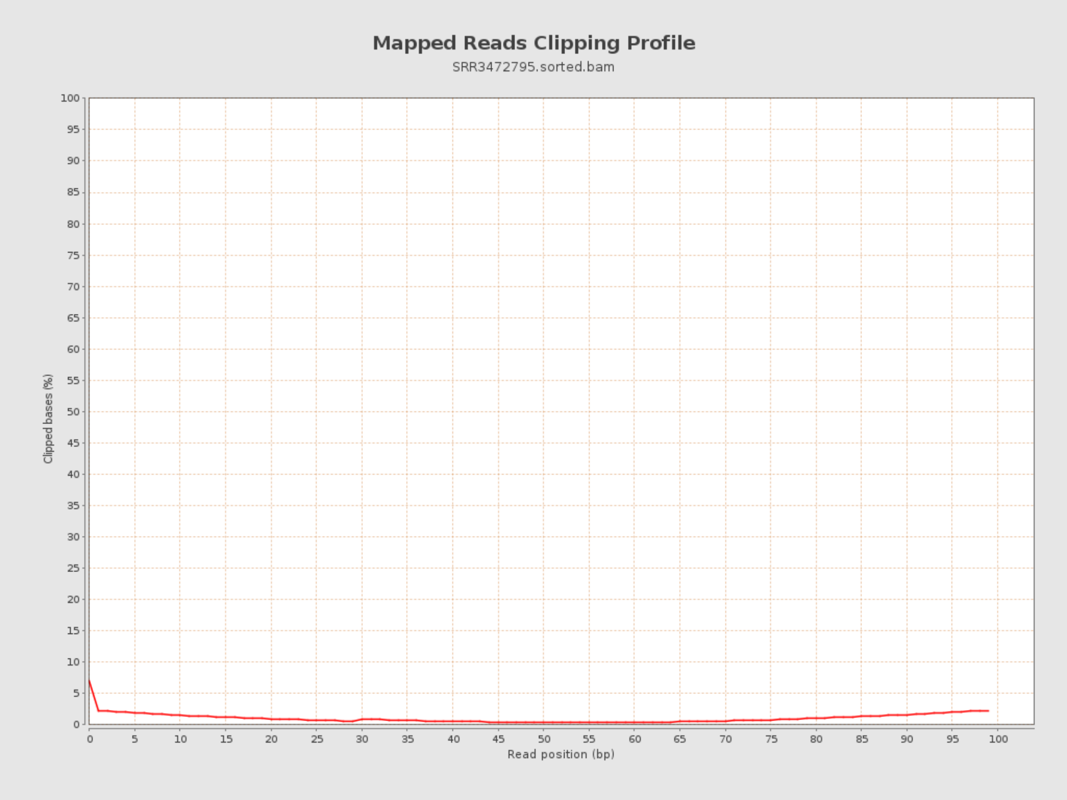
8. Results : Mapped Reads Nucleotide Content



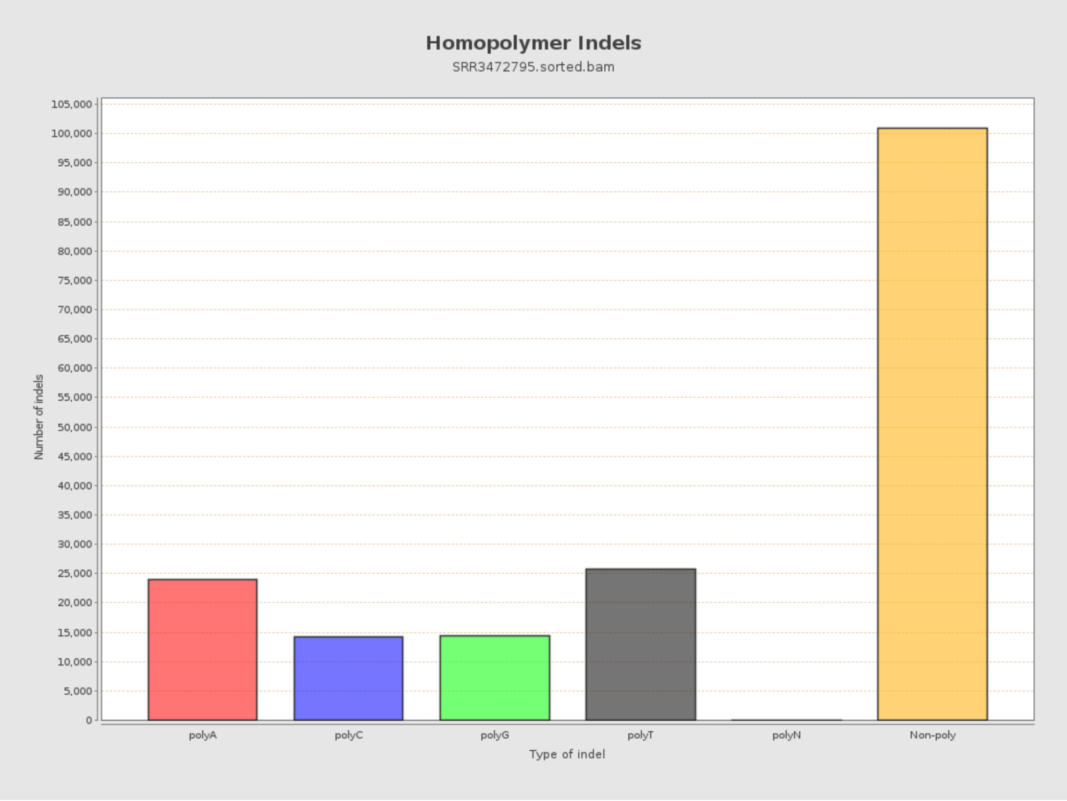
9. Results : Mapped Reads GC-content Distribution



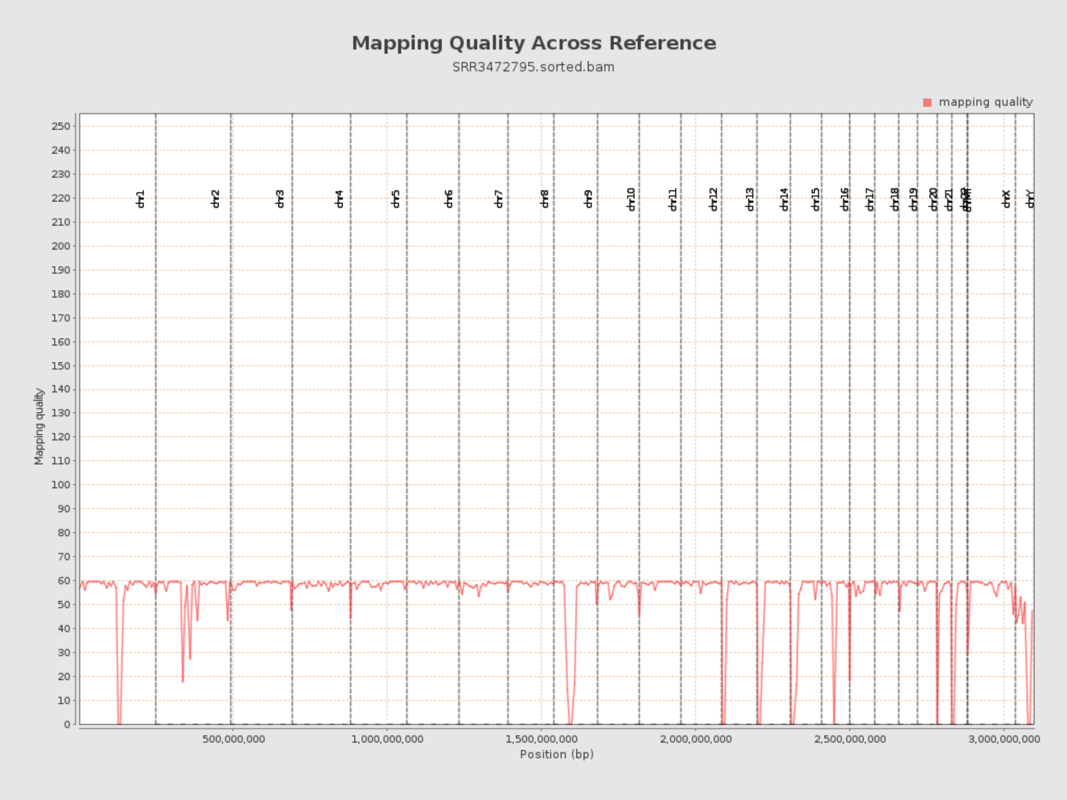
10. Results : Mapped Reads Clipping Profile



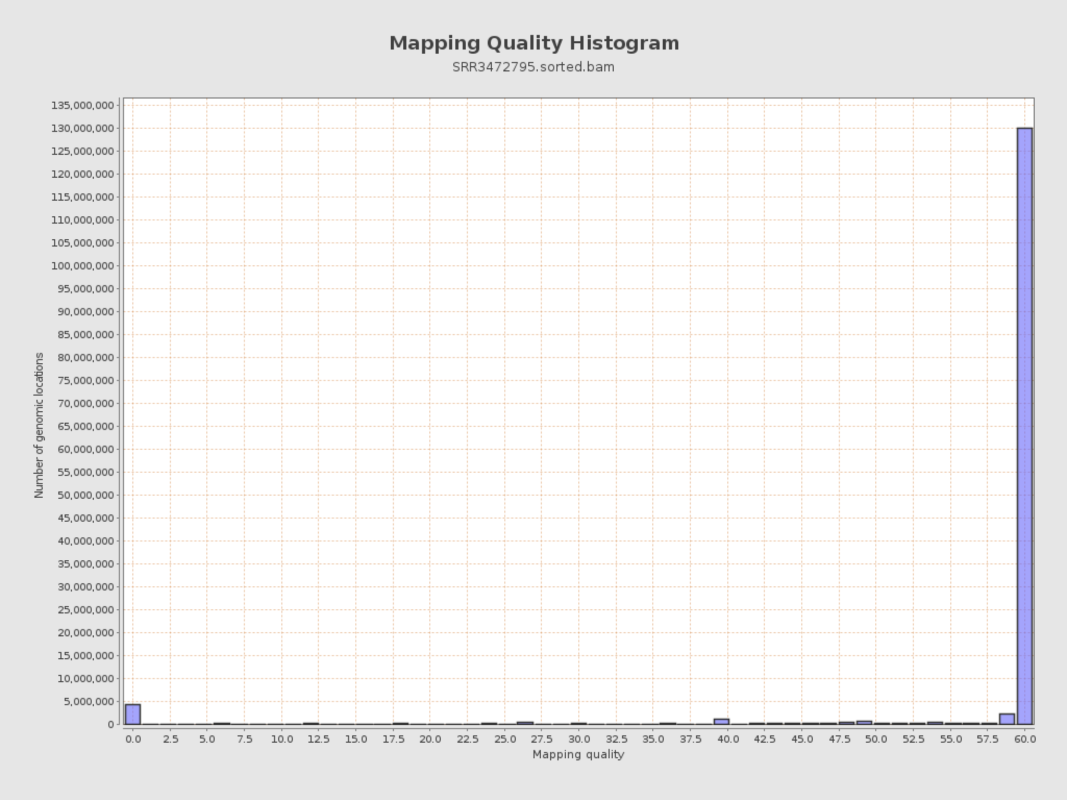
11. Results : Homopolymer Indels



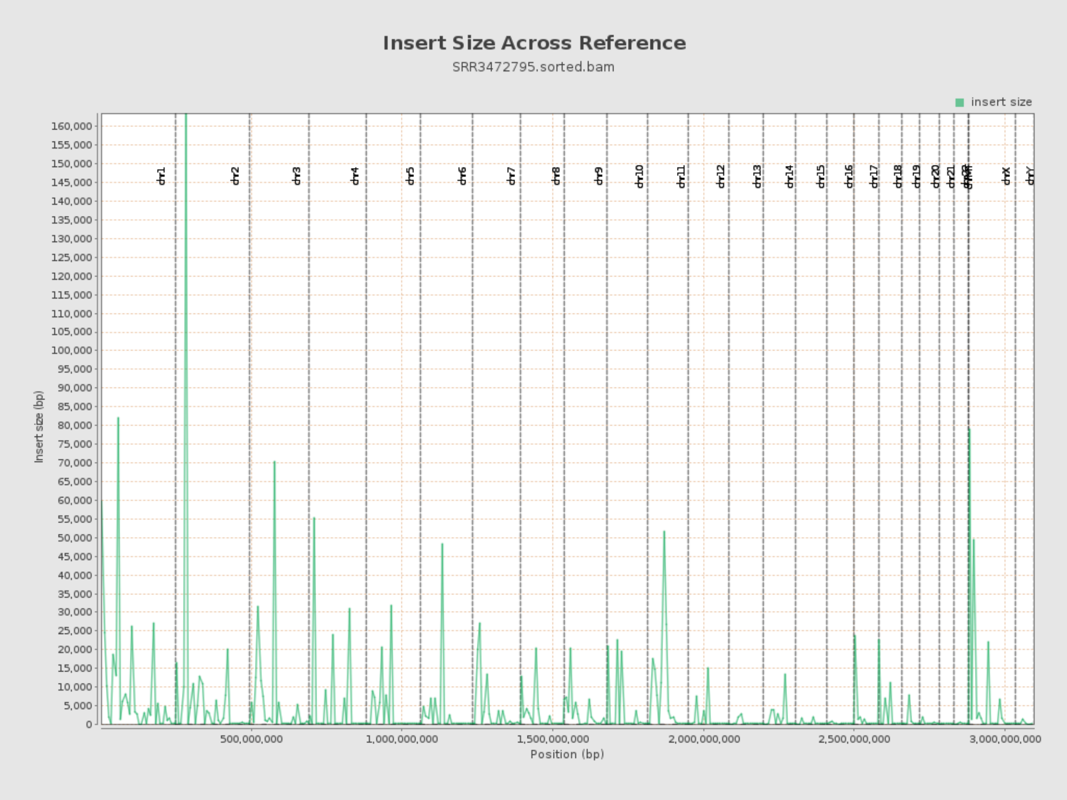
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram