Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 12:48:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472772.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_SRR3472772 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472772_1.fastq.gz SRR3472772_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 12:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472772.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,546,032
Mapped reads	15,370,975 / 98.87%
Unmapped reads	175,057 / 1.13%
Mapped paired reads	15,370,975 / 98.87%
Mapped reads, first in pair	7,728,103 / 49.71%
Mapped reads, second in pair	7,642,872 / 49.16%
Mapped reads, both in pair	15,254,398 / 98.12%
Mapped reads, singletons	116,577 / 0.75%
Secondary alignments	0
Supplementary alignments	57,469 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,646,264 / 62.05%
Duplication rate	47.22%
Clipped reads	1,164,293 / 7.49%

2.2. ACGT Content

Number/percentage of A's	418,654,636 / 27.63%
Number/percentage of C's	341,330,312 / 22.53%
Number/percentage of T's	415,518,673 / 27.42%
Number/percentage of G's	339,374,367 / 22.4%
Number/percentage of N's	292,611 / 0.02%

GC Percentage	44.93%

2.3. Coverage

Mean	0.4895
Standard Deviation	16.641

2.4. Mapping Quality

Mean Mapping Quality	55.05

2.5. Insert size

Mean	26,926.15
Standard Deviation	1,587,116.73
P25/Median/P75	186 / 260 / 349

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	9,951,421
Insertions	98,030
Mapped reads with at least one insertion	0.63%
Deletions	86,264
Mapped reads with at least one deletion	0.55%
Homopolymer indels	44.43%

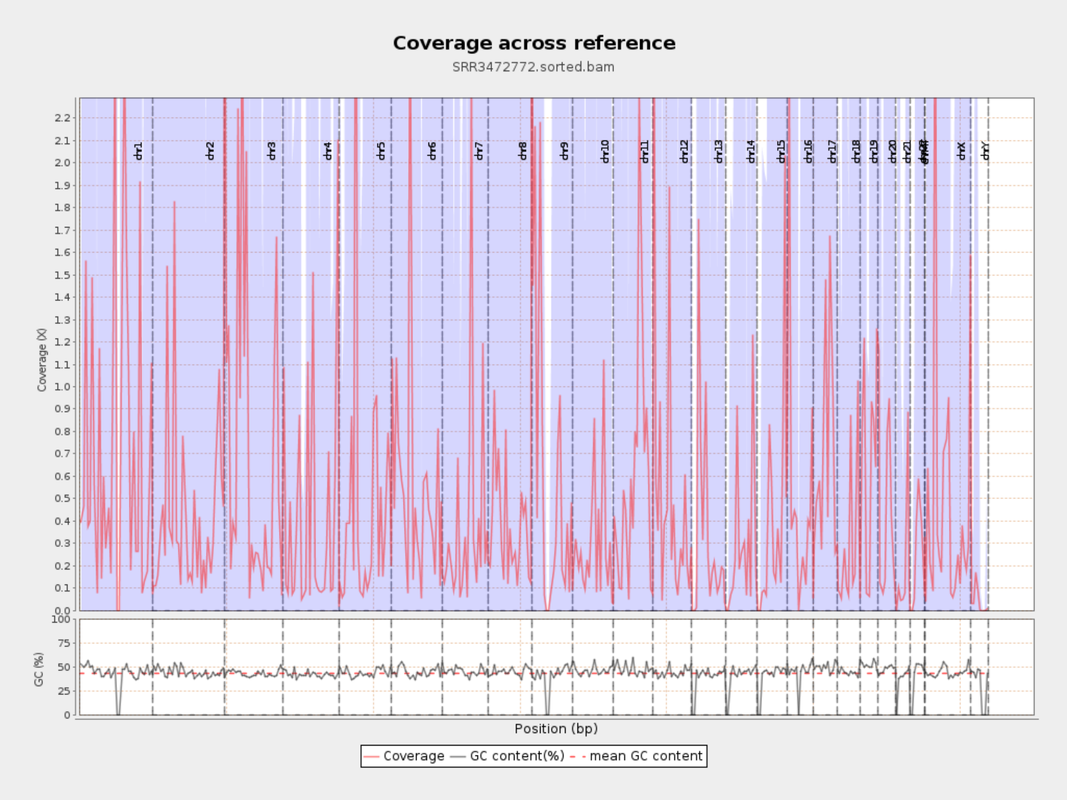
2.7. Chromosome stats

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

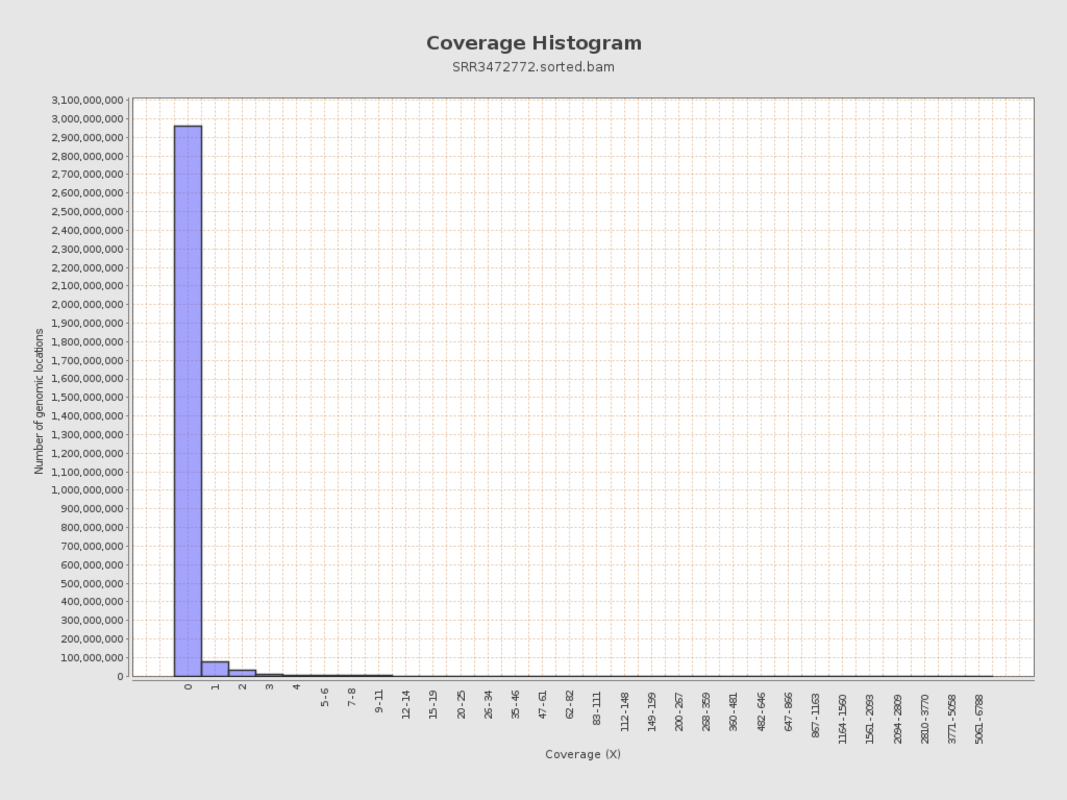
		bases	coverage	deviation
chr1	249250621	187788188	0.7534	23.1923
chr2	243199373	104671920	0.4304	15.1902
chr3	198022430	151408653	0.7646	21.3763
chr4	191154276	77527761	0.4056	19.0477
chr5	180915260	87189666	0.4819	16.0401
chr6	171115067	95458649	0.5579	15.2552
chr7	159138663	64013175	0.4022	15.3619
chr8	146364022	55220704	0.3773	11.9181
chr9	141213431	86524792	0.6127	14.5099
chr10	135534747	41215953	0.3041	13.8562
chr11	135006516	80822296	0.5987	22.111
chr12	133851895	75636451	0.5651	16.5673
chr13	115169878	39723544	0.3449	16.481
chr14	107349540	30956042	0.2884	12.7613
chr15	102531392	42457080	0.4141	14.9585
chr16	90354753	48134626	0.5327	15.7733
chr17	81195210	57646119	0.71	17.2626
chr18	78077248	23586490	0.3021	10.2885
chr19	59128983	38510328	0.6513	17.2173
chr20	63025520	27755248	0.4404	12.0677
chr21	48129895	9602431	0.1995	10.3223
chr22	51304566	12518757	0.244	6.8636
chrMT	16571	5430	0.3277	1.0924
chrX	155270560	74471669	0.4796	16.6235

chrY	59373566	2545392	0.0429	1.5737

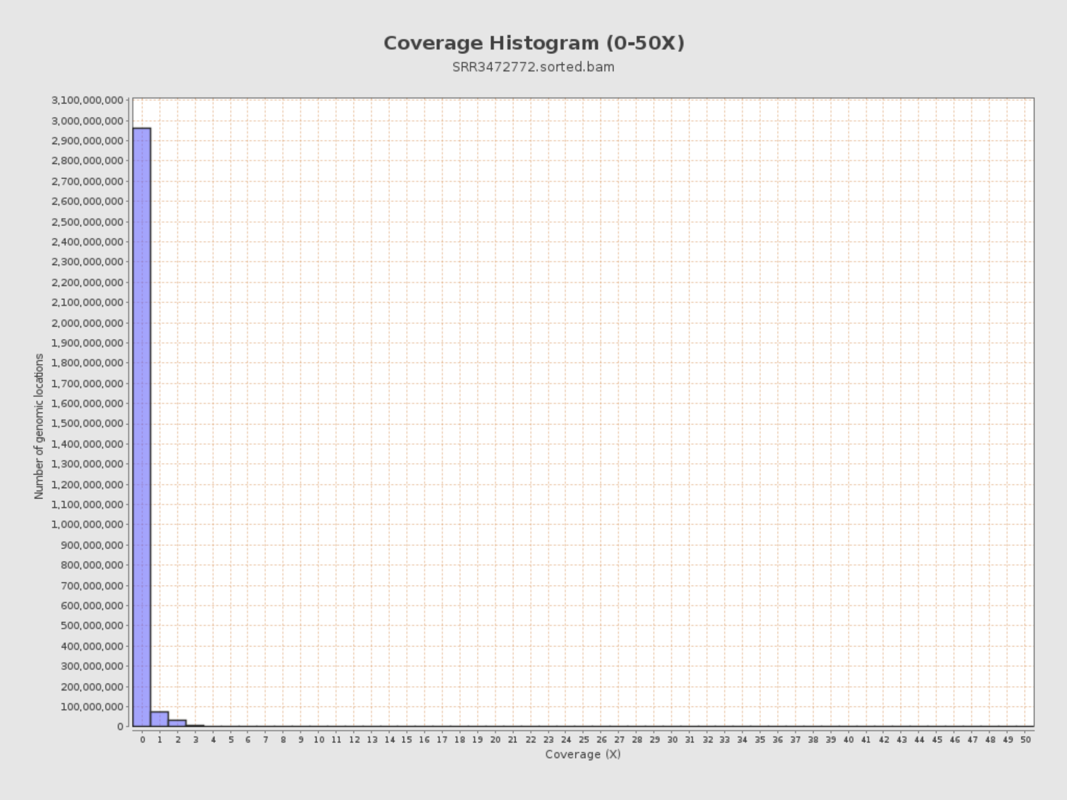
3. Results : Coverage across reference



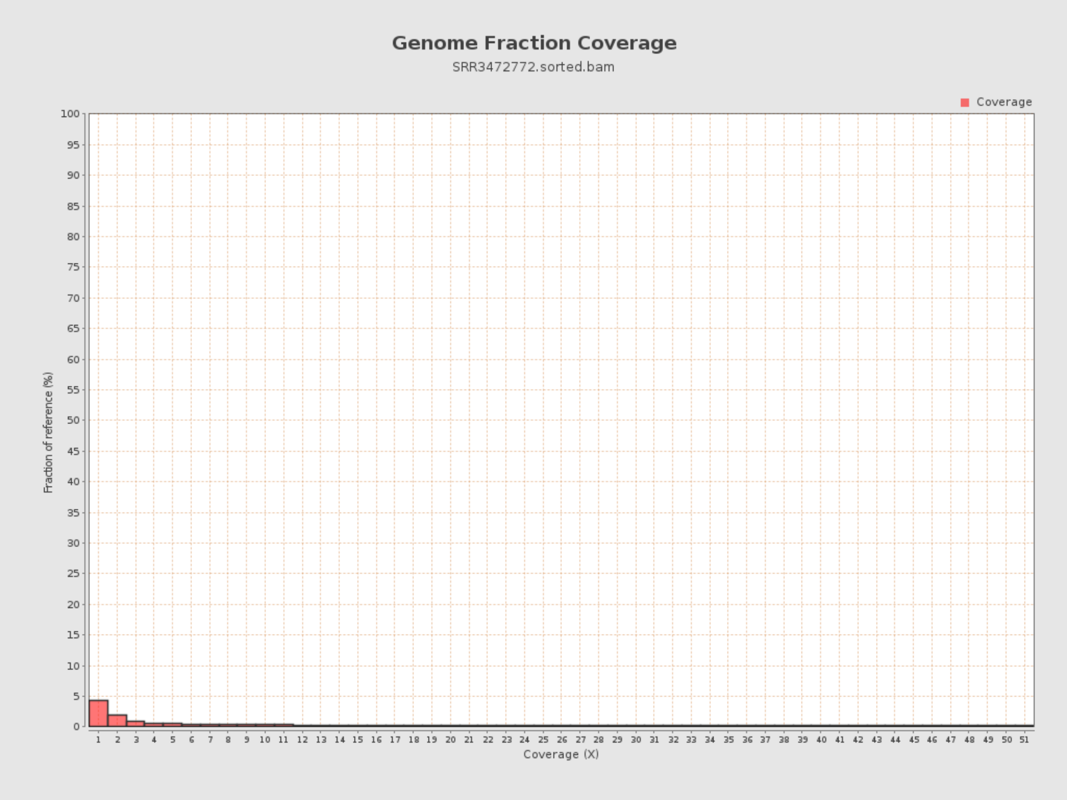
4. Results : Coverage Histogram



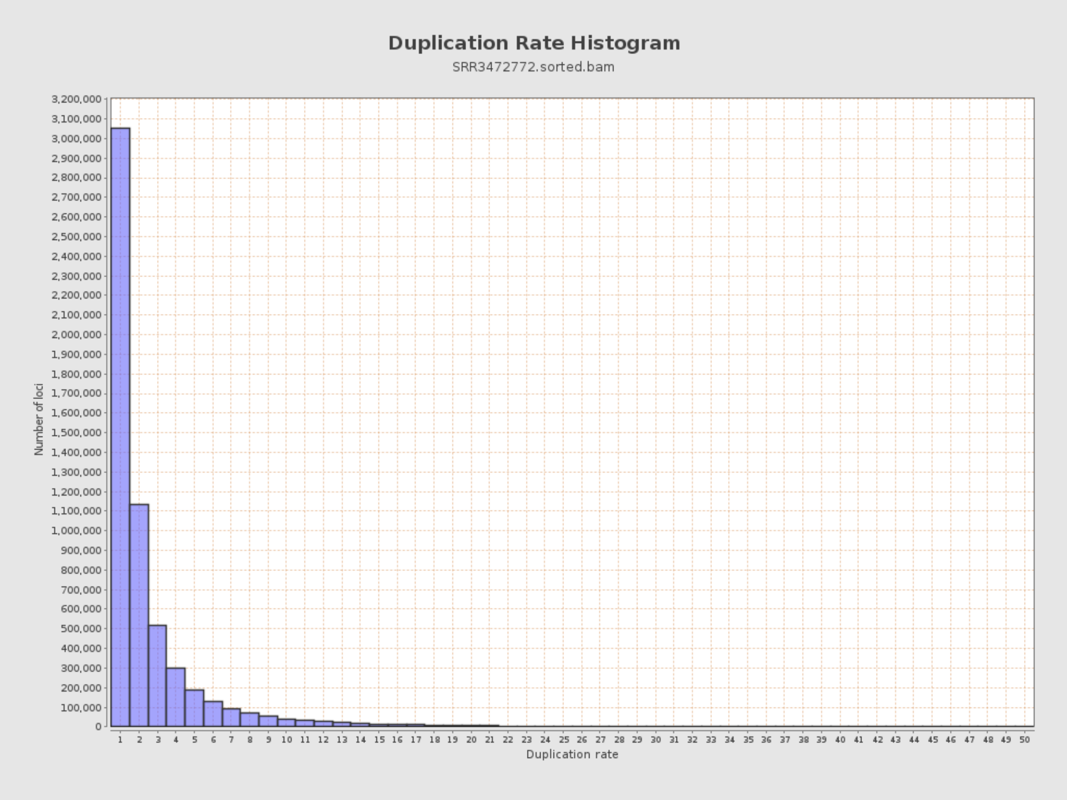
5. Results : Coverage Histogram (0-50X)



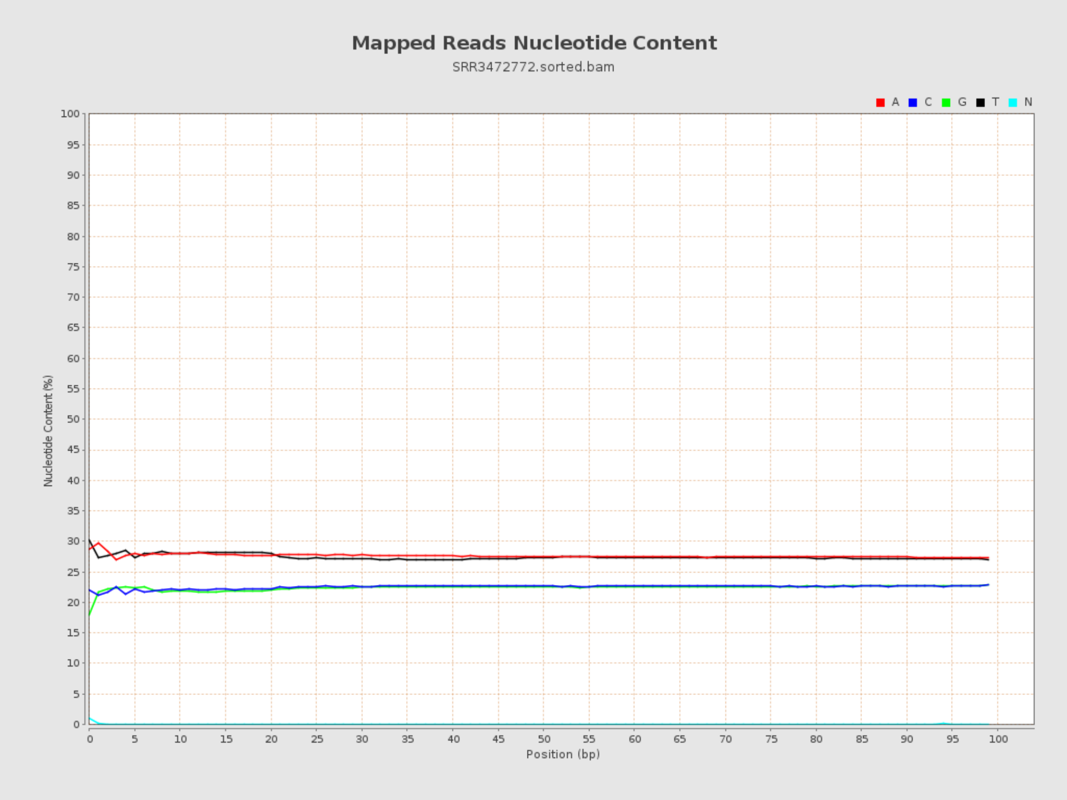
6. Results : Genome Fraction Coverage



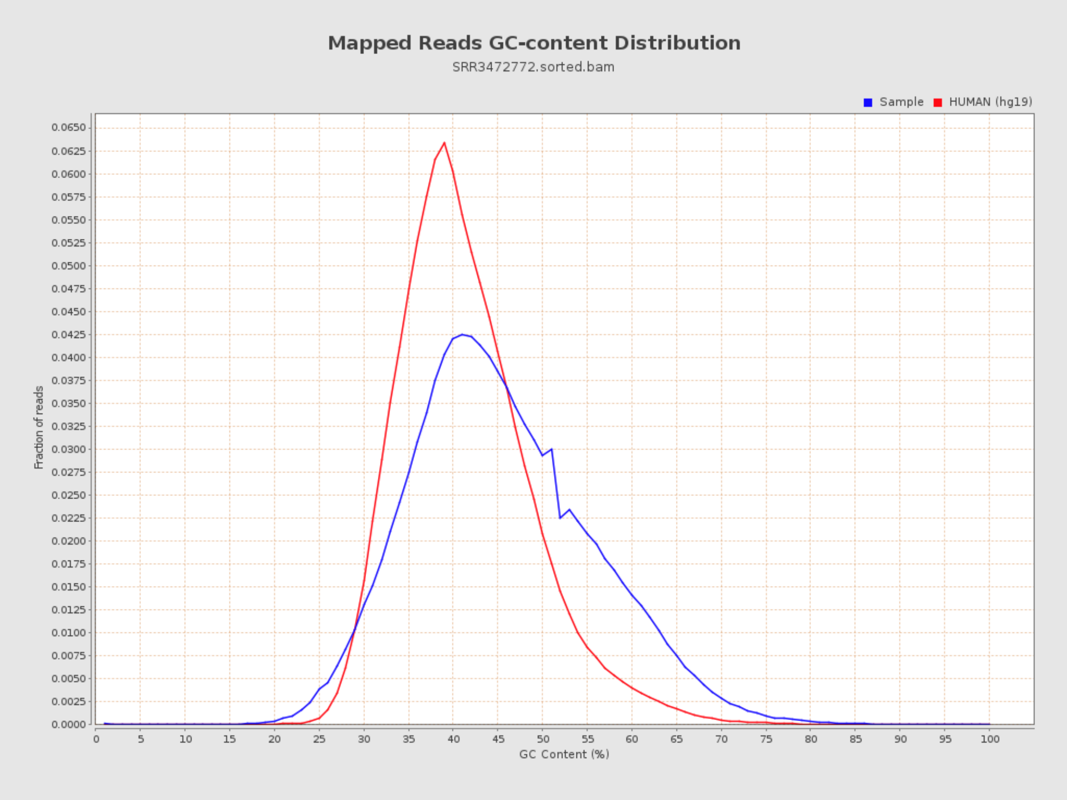
7. Results : Duplication Rate Histogram



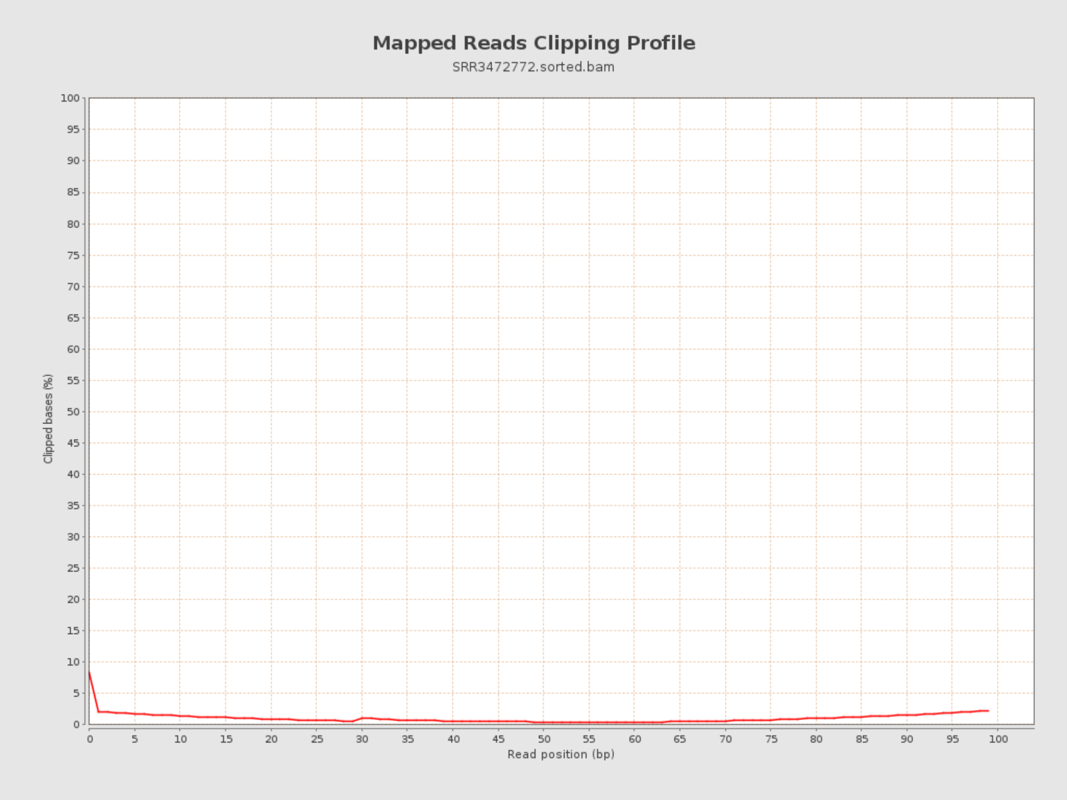
8. Results : Mapped Reads Nucleotide Content



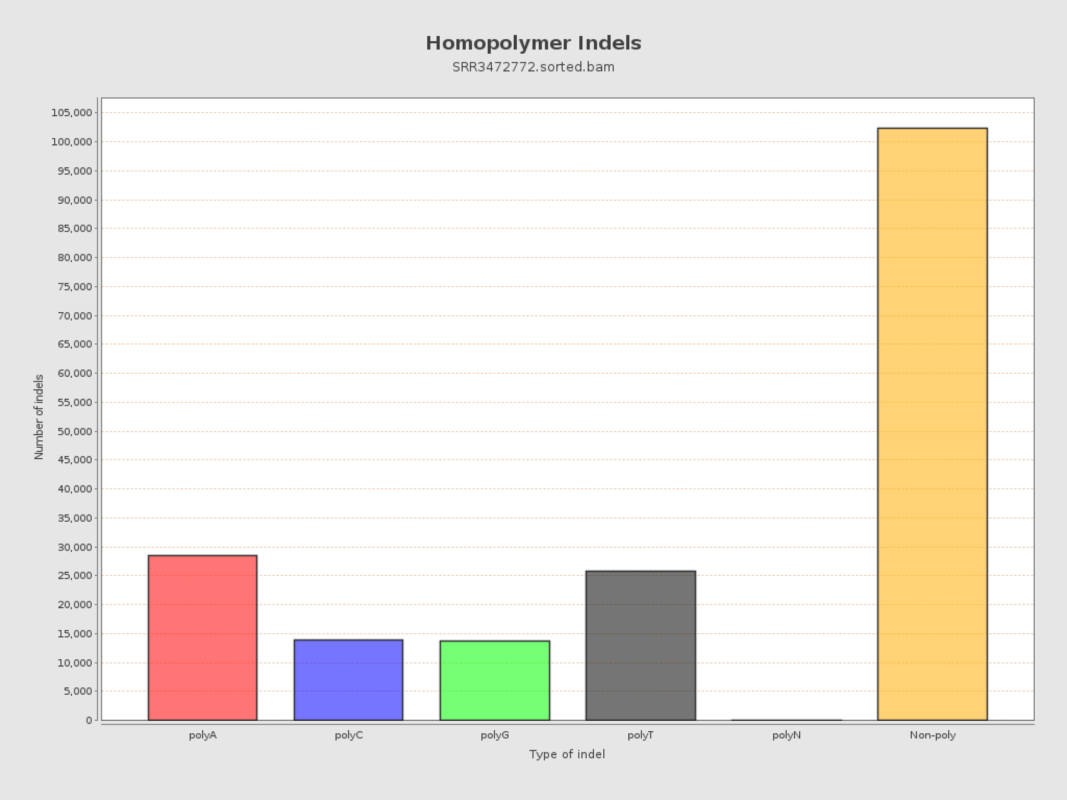
9. Results : Mapped Reads GC-content Distribution



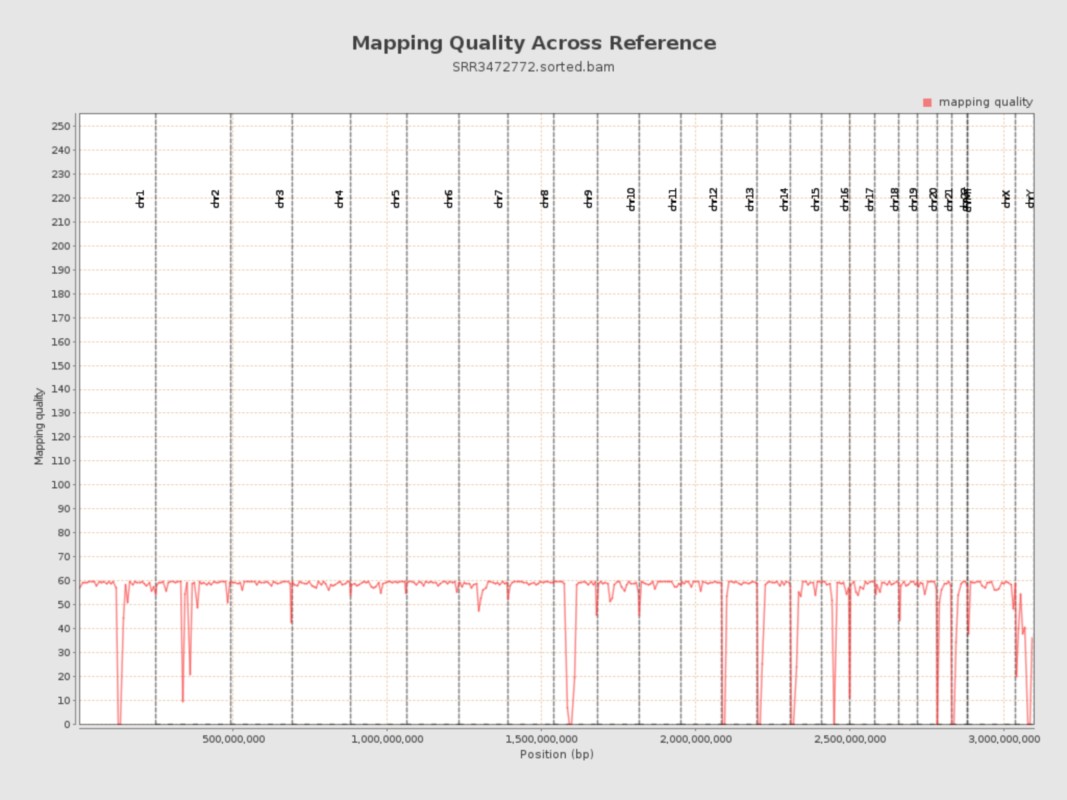
10. Results : Mapped Reads Clipping Profile



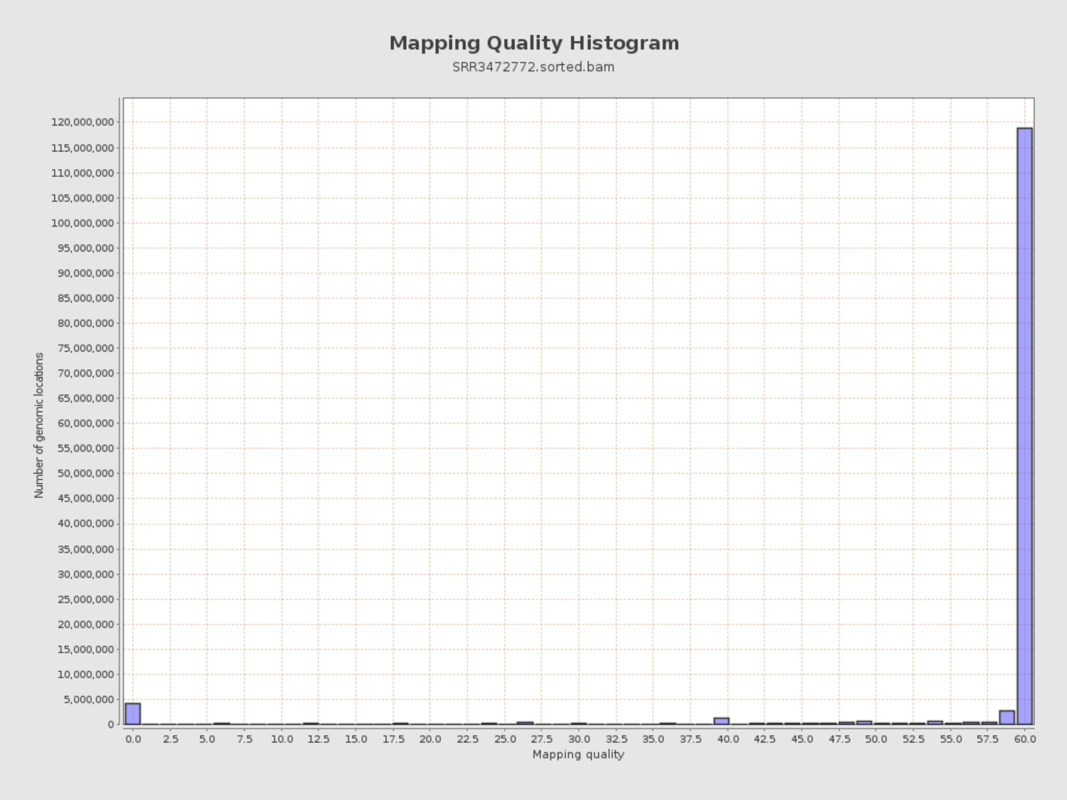
11. Results : Homopolymer Indels



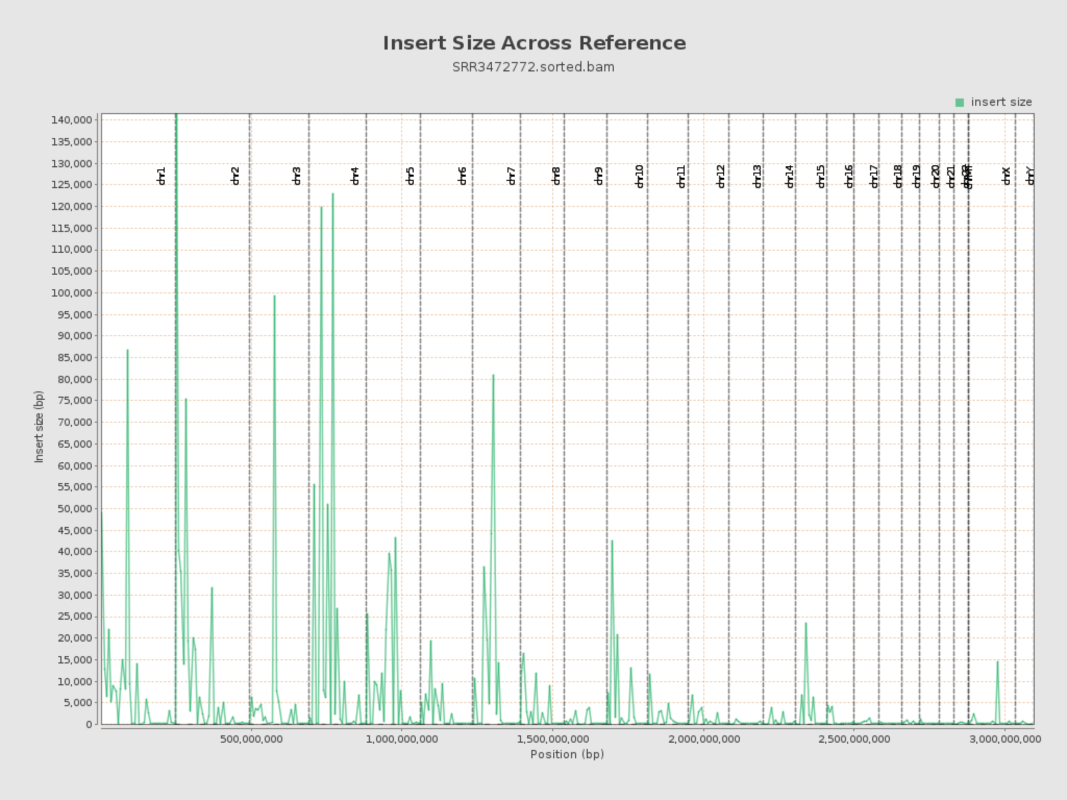
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram