Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:46:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472499.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_SRR3472499 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472499_1.fastq.gz SRR3472499_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:46:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,332,836
Mapped reads	15,115,908 / 98.59%
Unmapped reads	216,928 / 1.41%
Mapped paired reads	15,115,908 / 98.59%
Mapped reads, first in pair	7,581,736 / 49.45%
Mapped reads, second in pair	7,534,172 / 49.14%
Mapped reads, both in pair	15,014,850 / 97.93%
Mapped reads, singletons	101,058 / 0.66%
Secondary alignments	0
Supplementary alignments	62,262 / 0.41%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,620,495 / 62.74%
Duplication rate	45.53%
Clipped reads	1,259,637 / 8.22%

2.2. ACGT Content

Number/percentage of A's	402,898,840 / 27.09%
Number/percentage of C's	343,337,340 / 23.09%
Number/percentage of T's	400,726,683 / 26.94%
Number/percentage of G's	340,027,420 / 22.86%
Number/percentage of N's	229,030 / 0.02%

GC Percentage	45.95%

2.3. Coverage

Mean	0.4805
Standard Deviation	20.1017

2.4. Mapping Quality

Mean Mapping Quality	55.02

2.5. Insert size

Mean	30,620.36
Standard Deviation	1,715,464.83
P25/Median/P75	170 / 238 / 322

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	9,092,349
Insertions	72,991
Mapped reads with at least one insertion	0.48%
Deletions	70,145
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.86%

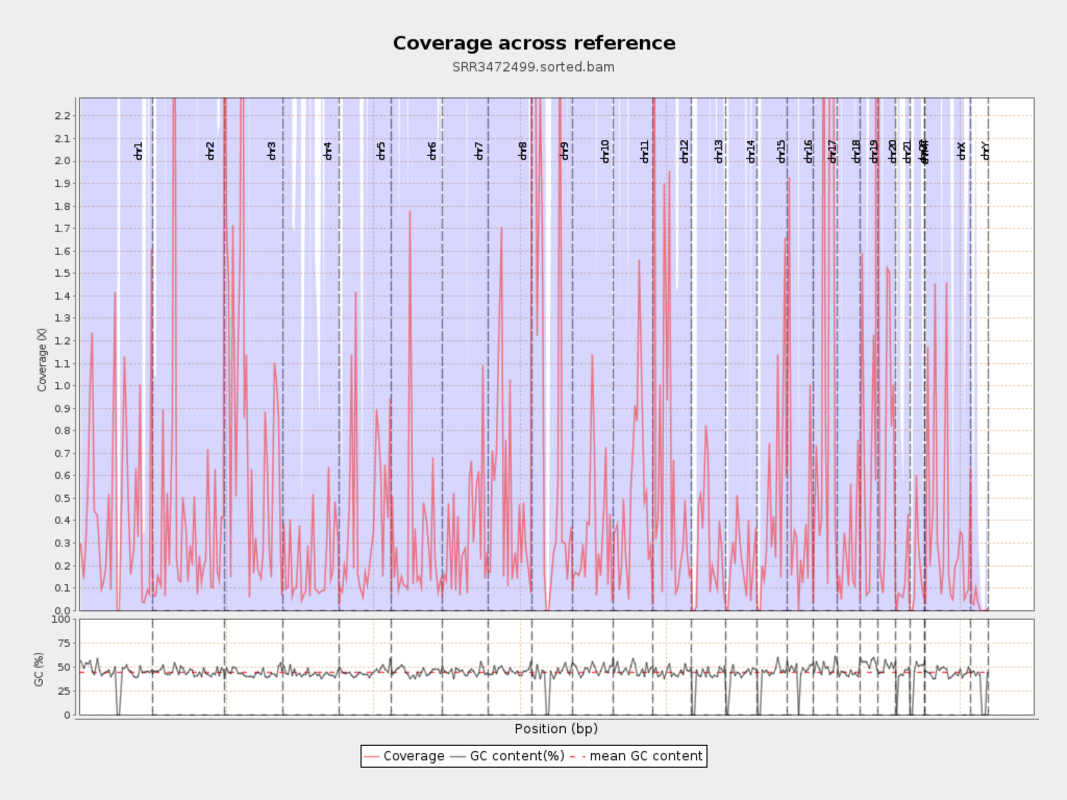
2.7. Chromosome stats

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

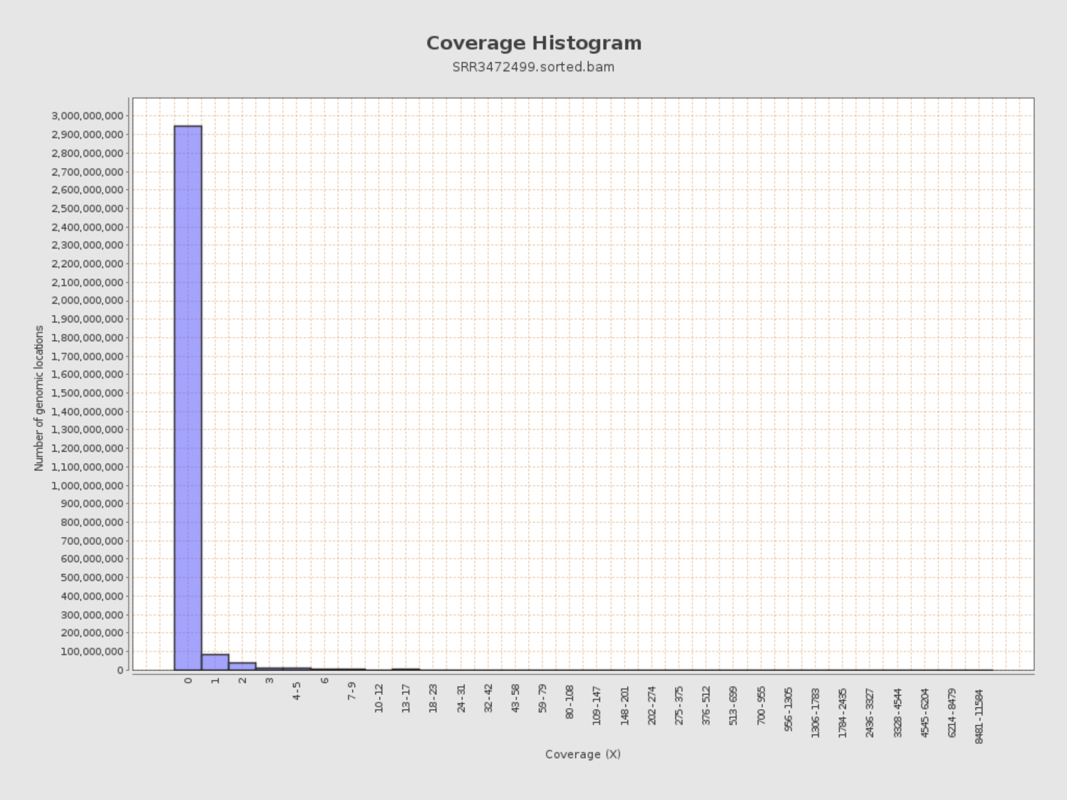
		bases	coverage	deviation
chr1	249250621	118087949	0.4738	16.9026
chr2	243199373	97229372	0.3998	18.0933
chr3	198022430	173881309	0.8781	26.7552
chr4	191154276	39299924	0.2056	7.8461
chr5	180915260	74778363	0.4133	17.0589
chr6	171115067	50145018	0.293	8.436
chr7	159138663	54653956	0.3434	12.8107
chr8	146364022	72051100	0.4923	18.5384
chr9	141213431	137895439	0.9765	30.2935
chr10	135534747	46043399	0.3397	15.6829
chr11	135006516	68051258	0.5041	17.0933
chr12	133851895	97737016	0.7302	21.7029
chr13	115169878	32733943	0.2842	9.6037
chr14	107349540	23227007	0.2164	7.799
chr15	102531392	49615744	0.4839	17.2307
chr16	90354753	41384209	0.458	17.0719
chr17	81195210	93114214	1.1468	32.2035
chr18	78077248	22446757	0.2875	8.9516
chr19	59128983	71872300	1.2155	71.5
chr20	63025520	49702402	0.7886	22.6115
chr21	48129895	5990496	0.1245	4.5802
chr22	51304566	8907978	0.1736	6.4274
chrMT	16571	1889	0.114	0.4294
chrX	155270560	57004071	0.3671	15.5608

chrY	59373566	1548094	0.0261	0.935

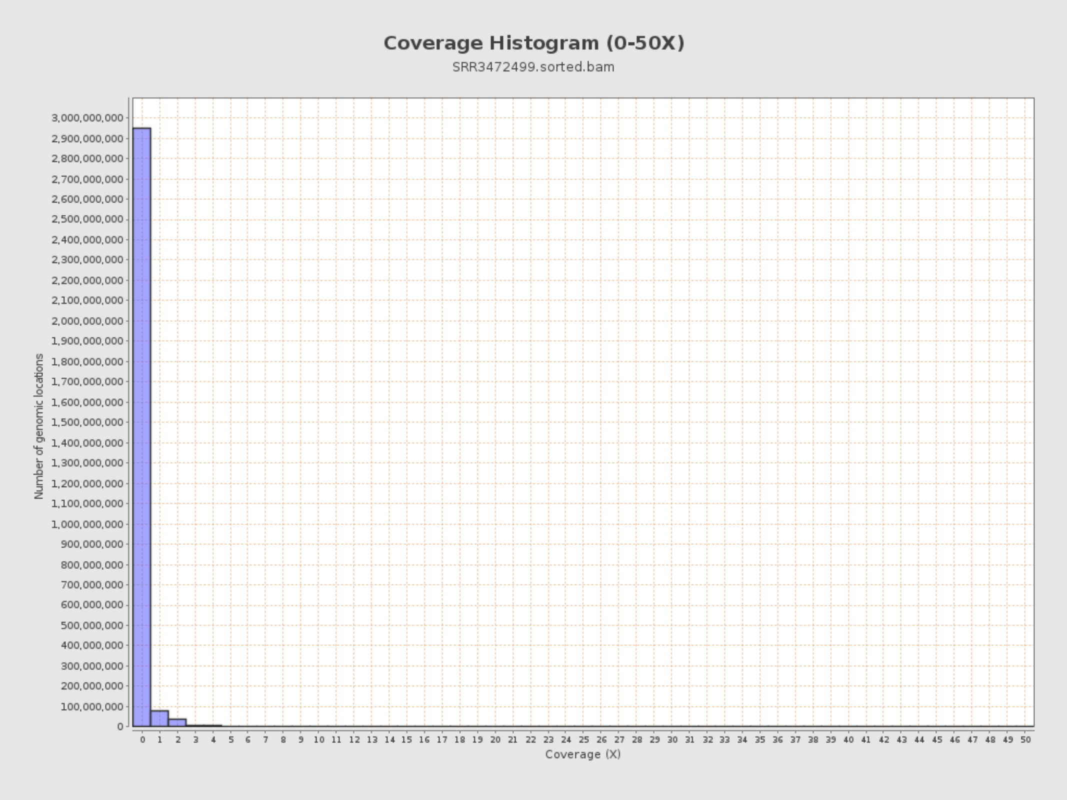
3. Results : Coverage across reference



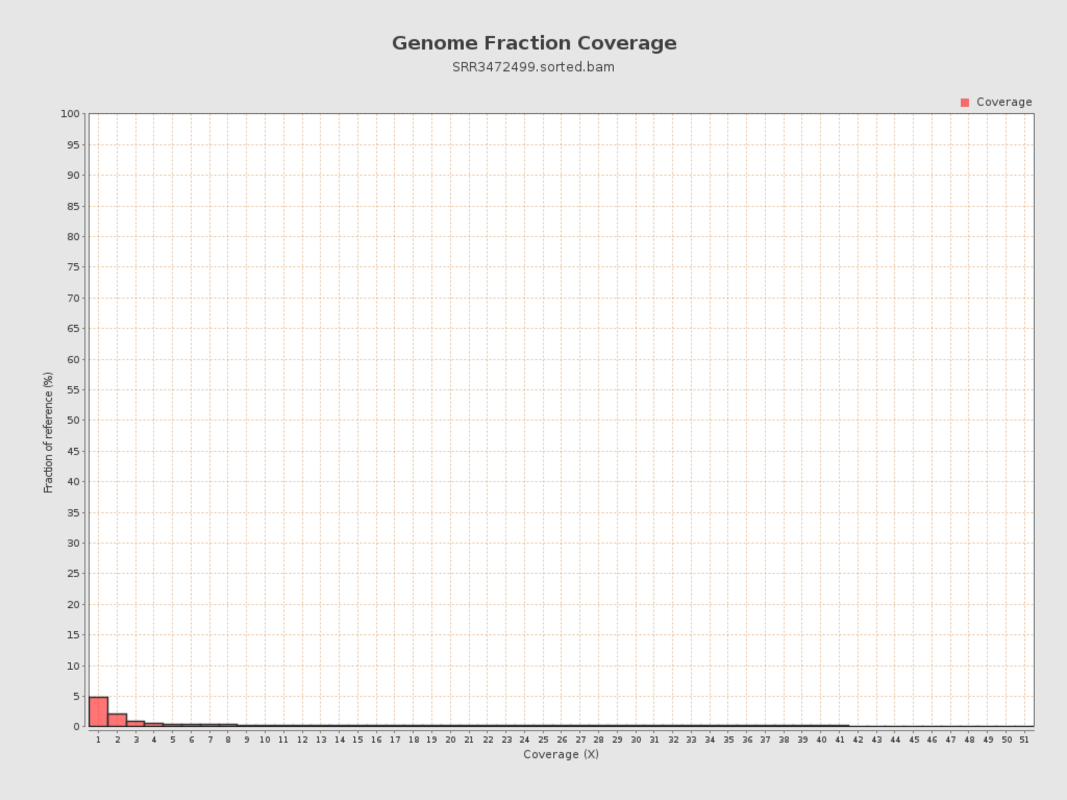
4. Results : Coverage Histogram



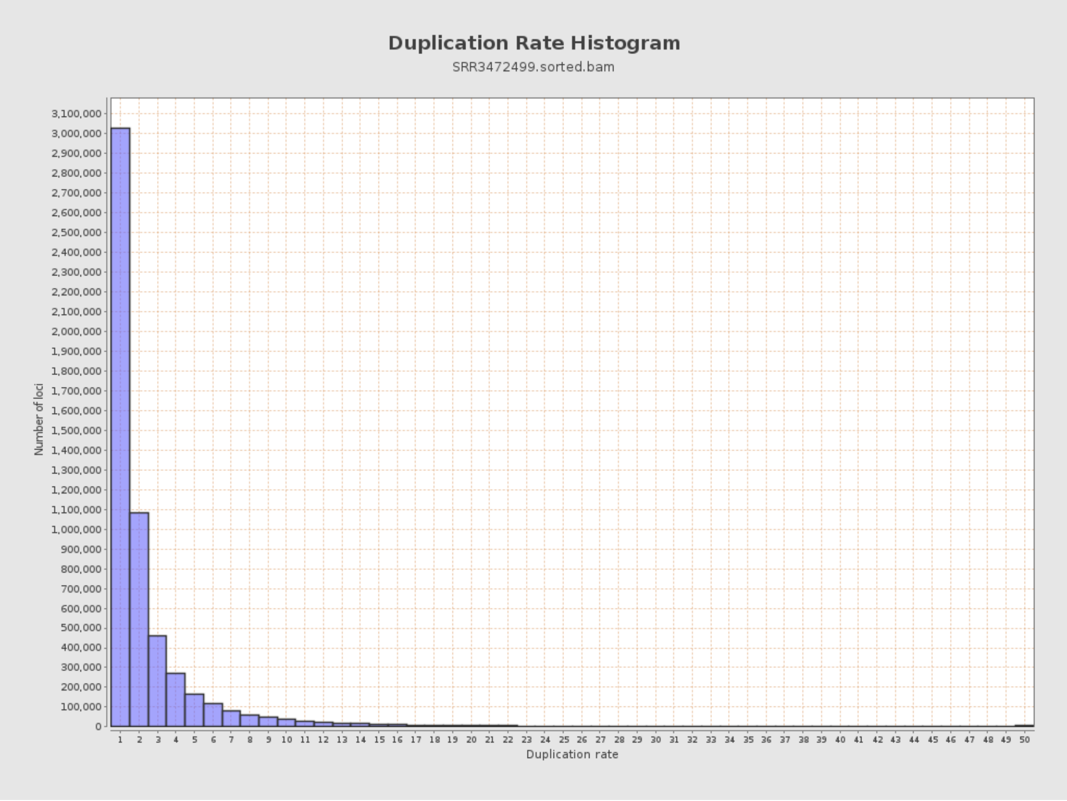
5. Results : Coverage Histogram (0-50X)



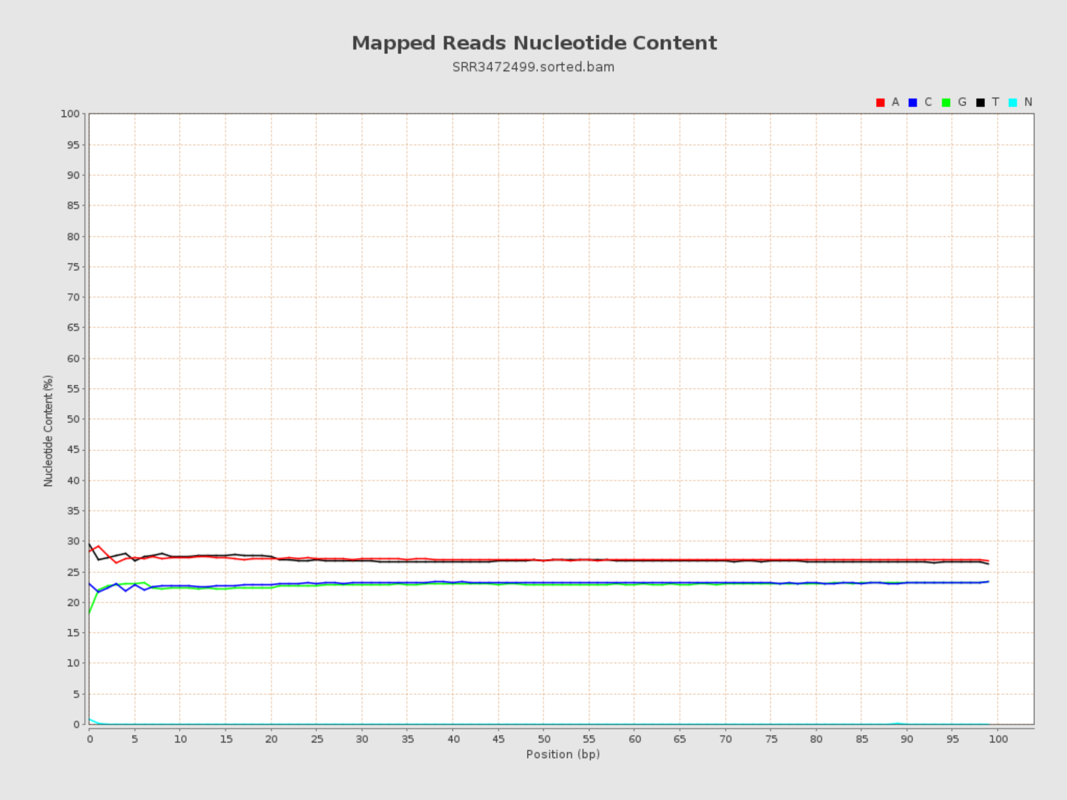
6. Results : Genome Fraction Coverage



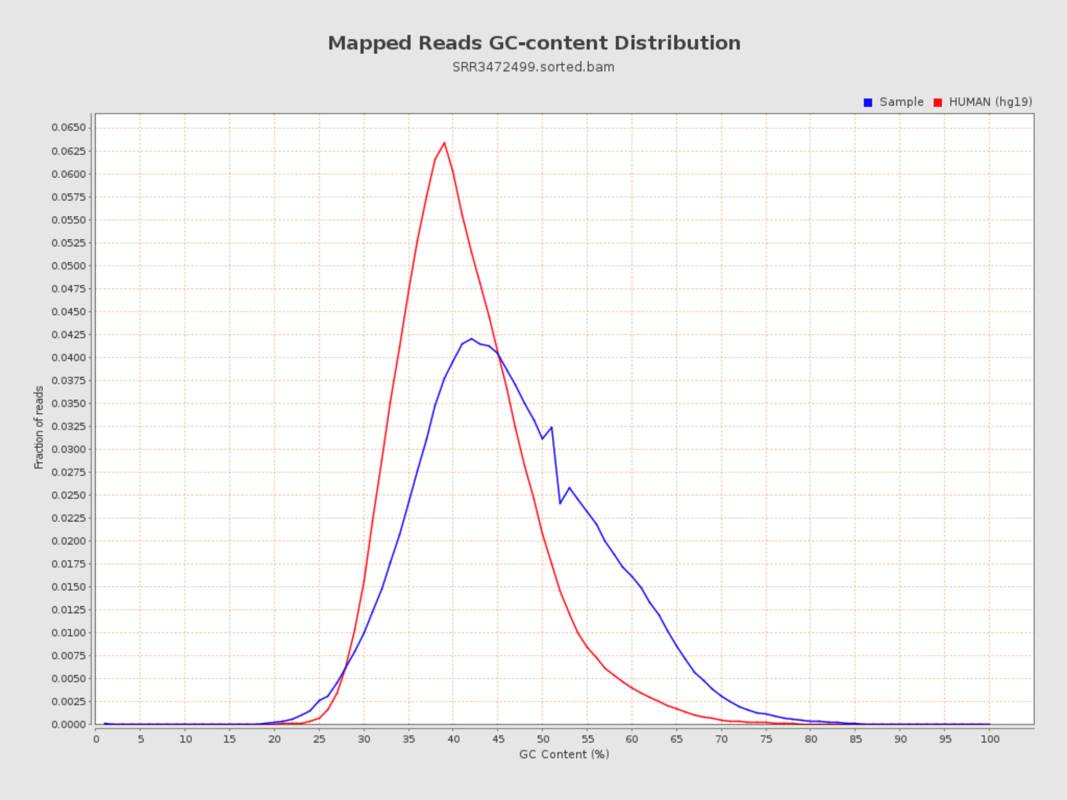
7. Results : Duplication Rate Histogram



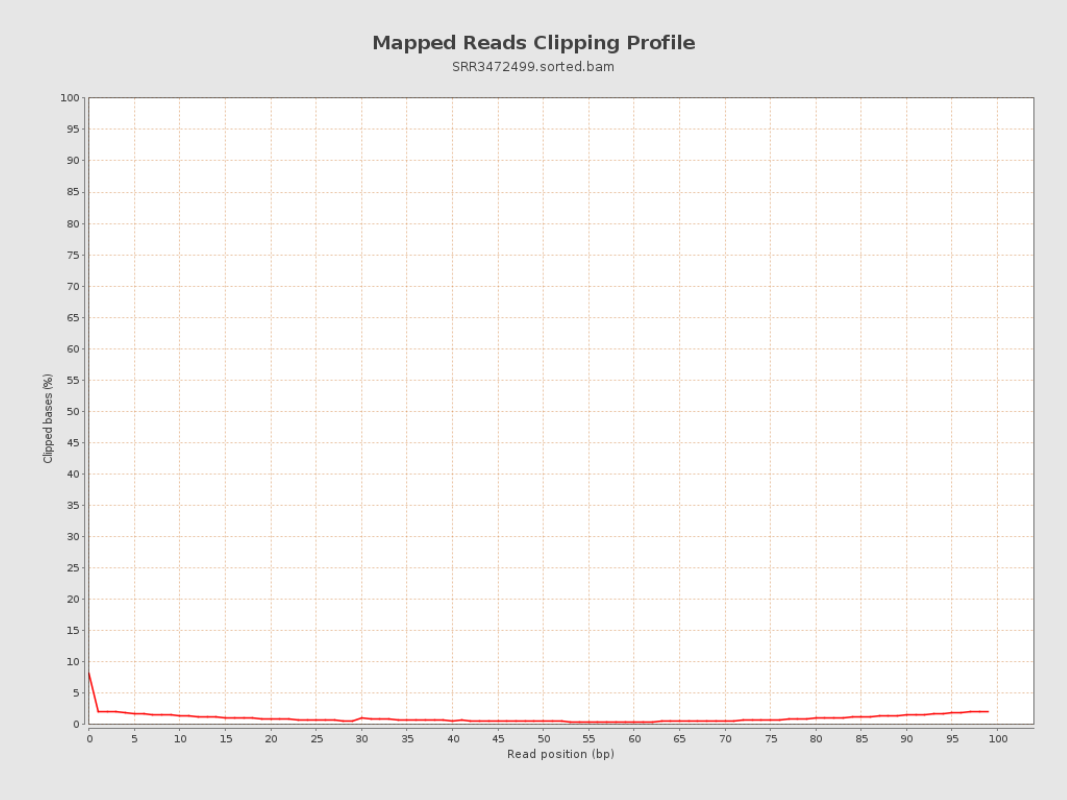
8. Results : Mapped Reads Nucleotide Content



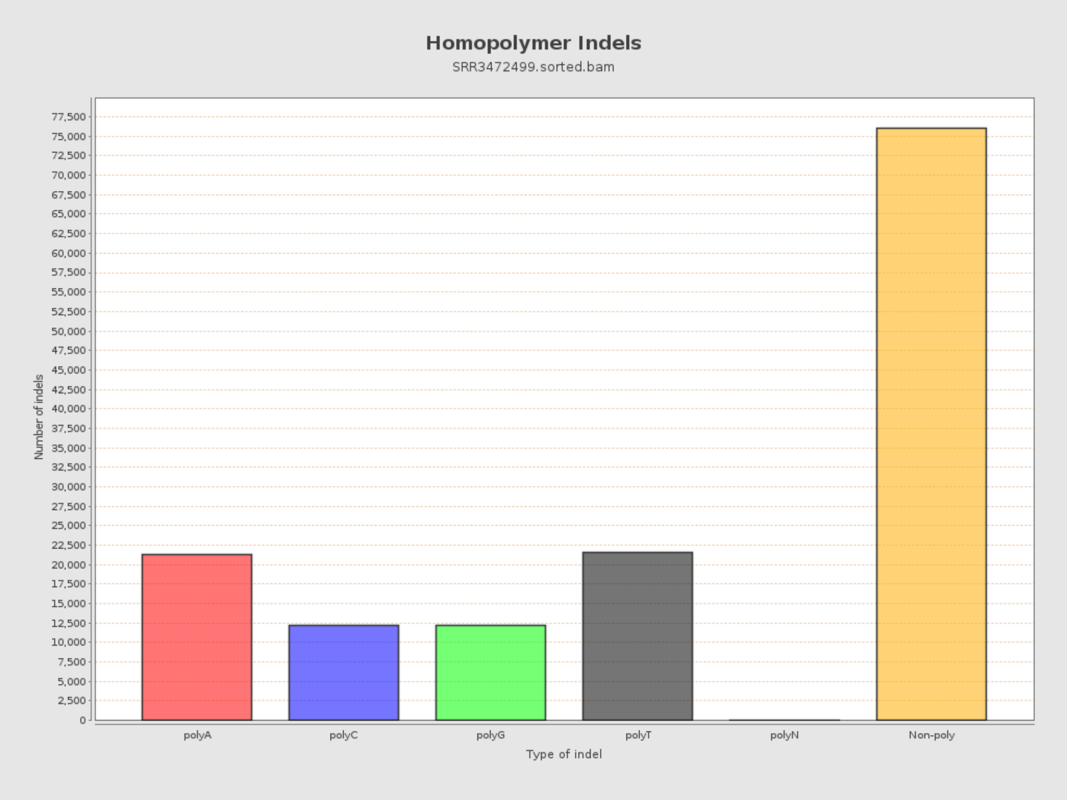
9. Results : Mapped Reads GC-content Distribution



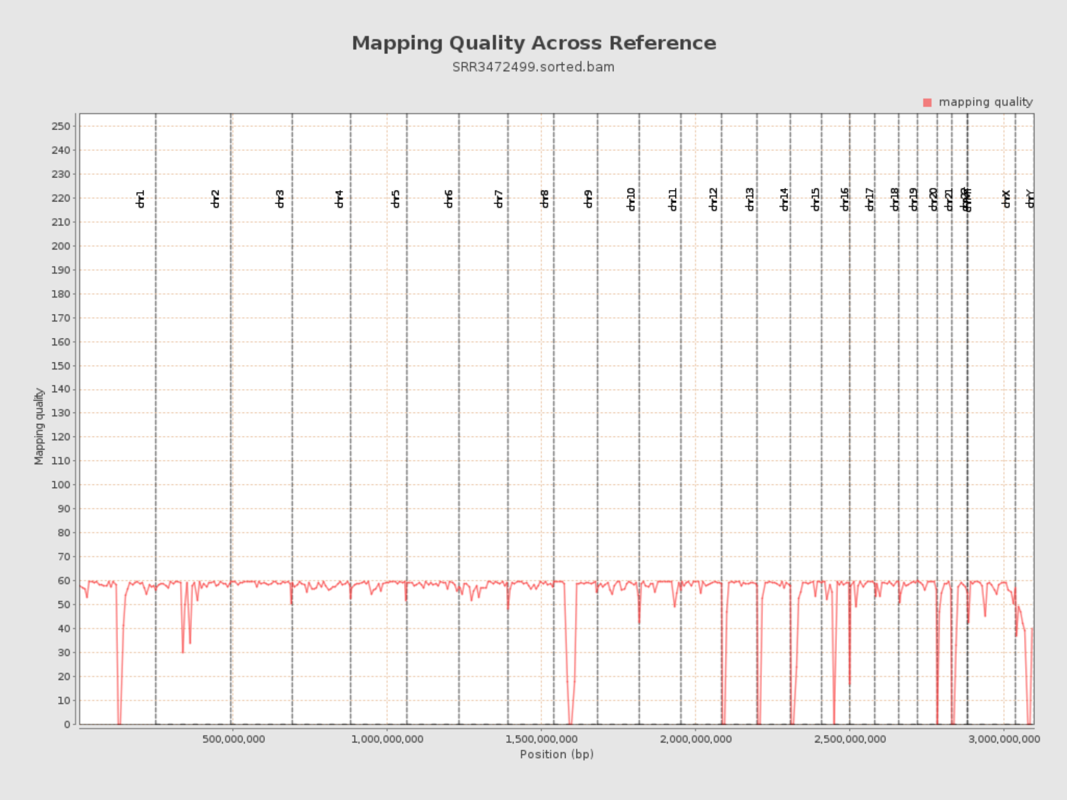
10. Results : Mapped Reads Clipping Profile



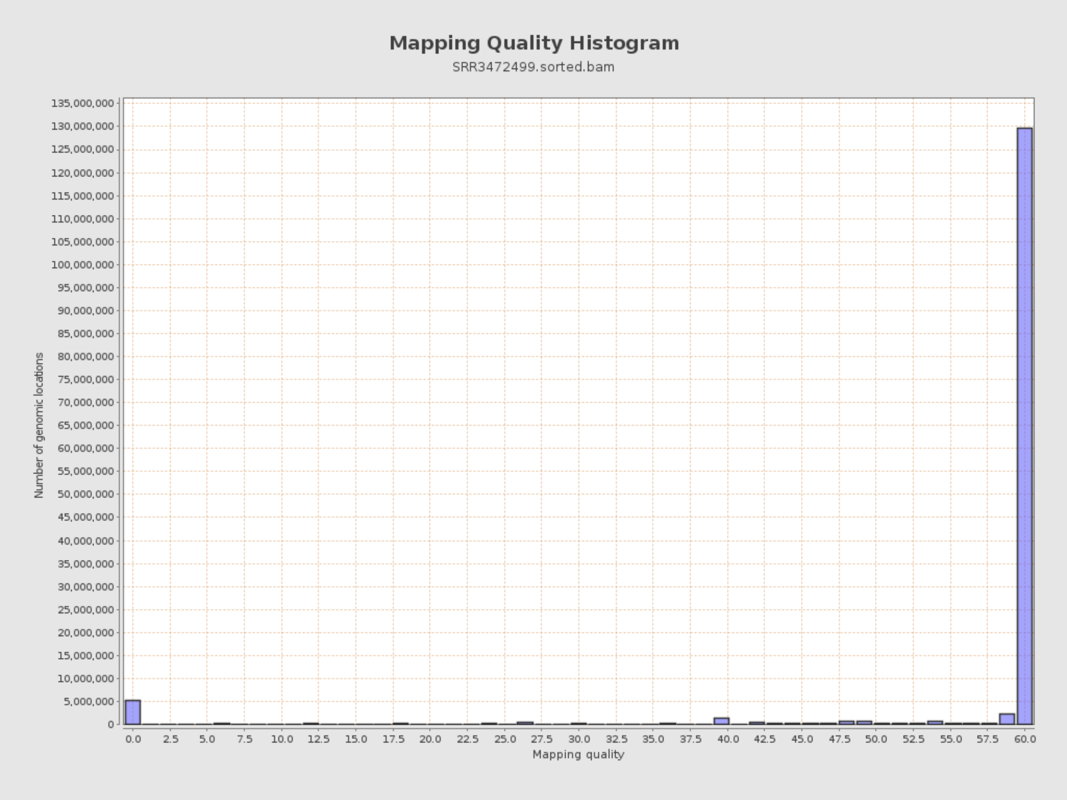
11. Results : Homopolymer Indels



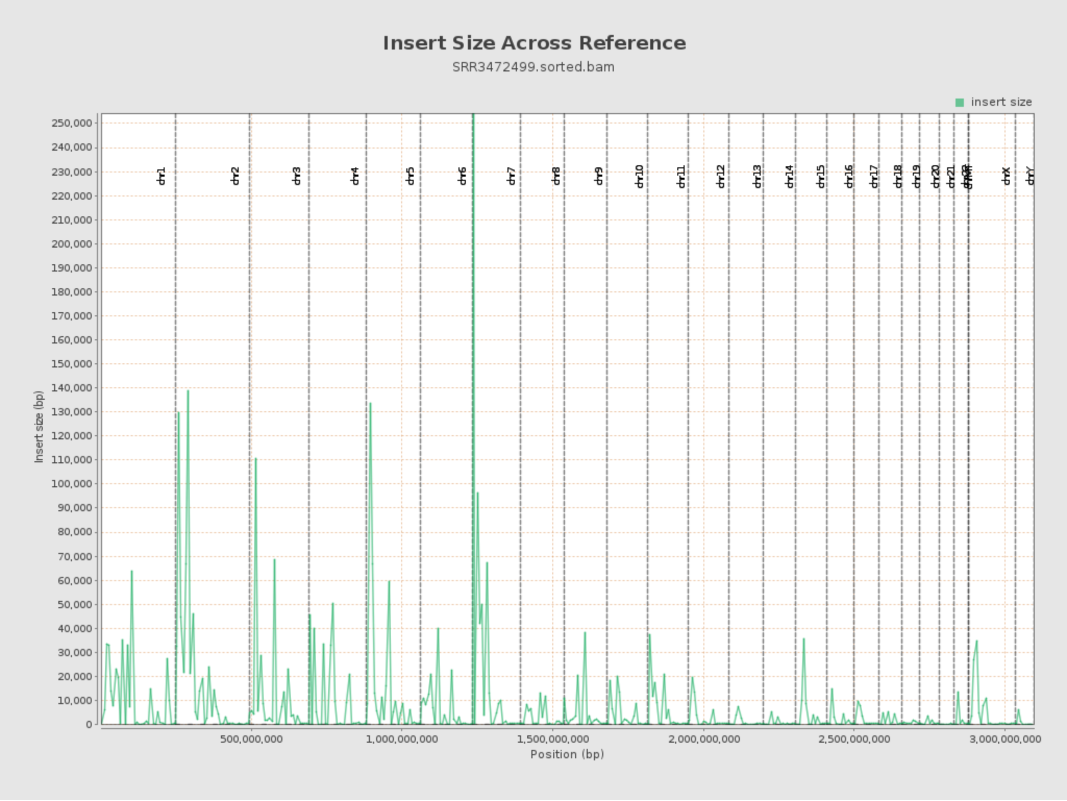
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram