Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 06:37:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472599.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_SRR3472599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472599_1.fastq.gz SRR3472599_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 06:37:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,715,172
Mapped reads	5,941,836 / 88.48%
Unmapped reads	773,336 / 11.52%
Mapped paired reads	5,941,836 / 88.48%
Mapped reads, first in pair	3,001,320 / 44.69%
Mapped reads, second in pair	2,940,516 / 43.79%
Mapped reads, both in pair	5,781,480 / 86.1%
Mapped reads, singletons	160,356 / 2.39%
Secondary alignments	0
Supplementary alignments	152,712 / 2.27%
Read min/max/mean length	30 / 100 / 100.88
Duplicated reads (estimated)	878,744 / 13.09%
Duplication rate	13.09%
Clipped reads	4,628,035 / 68.92%

2.2. ACGT Content

Number/percentage of A's	121,908,498 / 25.5%
Number/percentage of C's	95,148,422 / 19.9%
Number/percentage of T's	142,848,046 / 29.88%
Number/percentage of G's	117,824,761 / 24.65%
Number/percentage of N's	288,032 / 0.06%

GC Percentage	44.55%

2.3. Coverage

Mean	0.1545
Standard Deviation	1.5567

2.4. Mapping Quality

Mean Mapping Quality	50.6

2.5. Insert size

Mean	186,152.59
Standard Deviation	4,108,994.08
P25/Median/P75	91 / 130 / 181

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	5,711,371
Insertions	44,506
Mapped reads with at least one insertion	0.73%
Deletions	115,786
Mapped reads with at least one deletion	1.91%
Homopolymer indels	42.4%

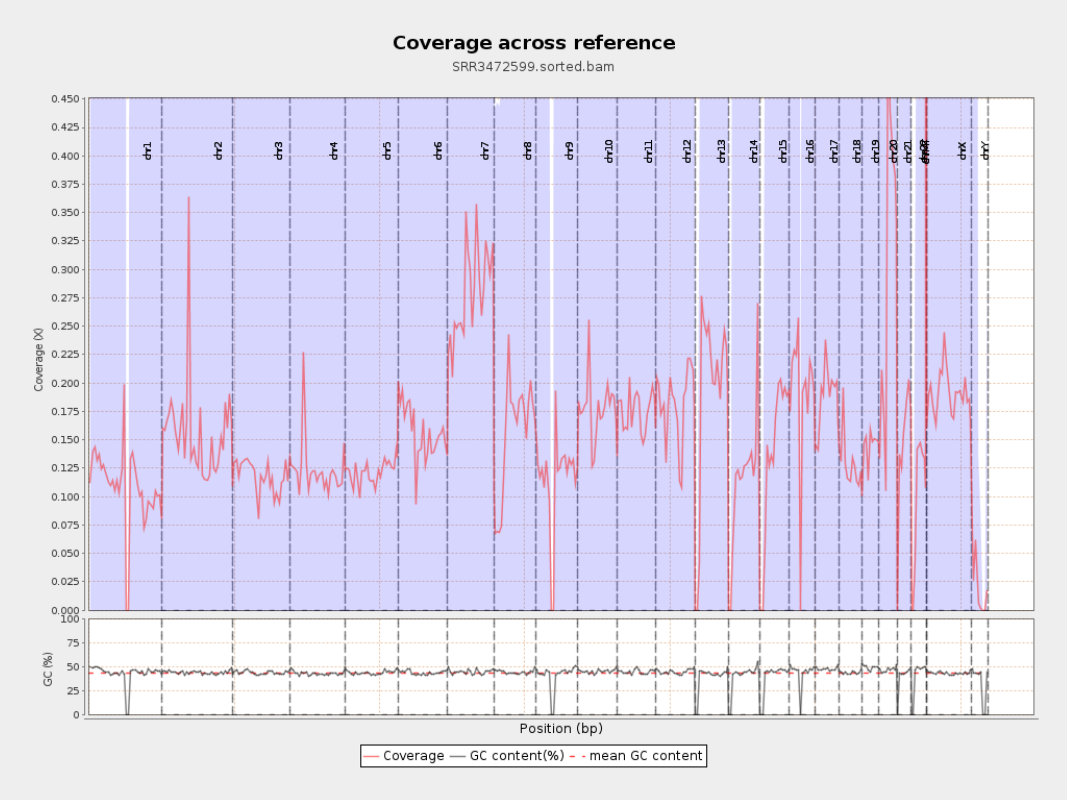
2.7. Chromosome stats

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

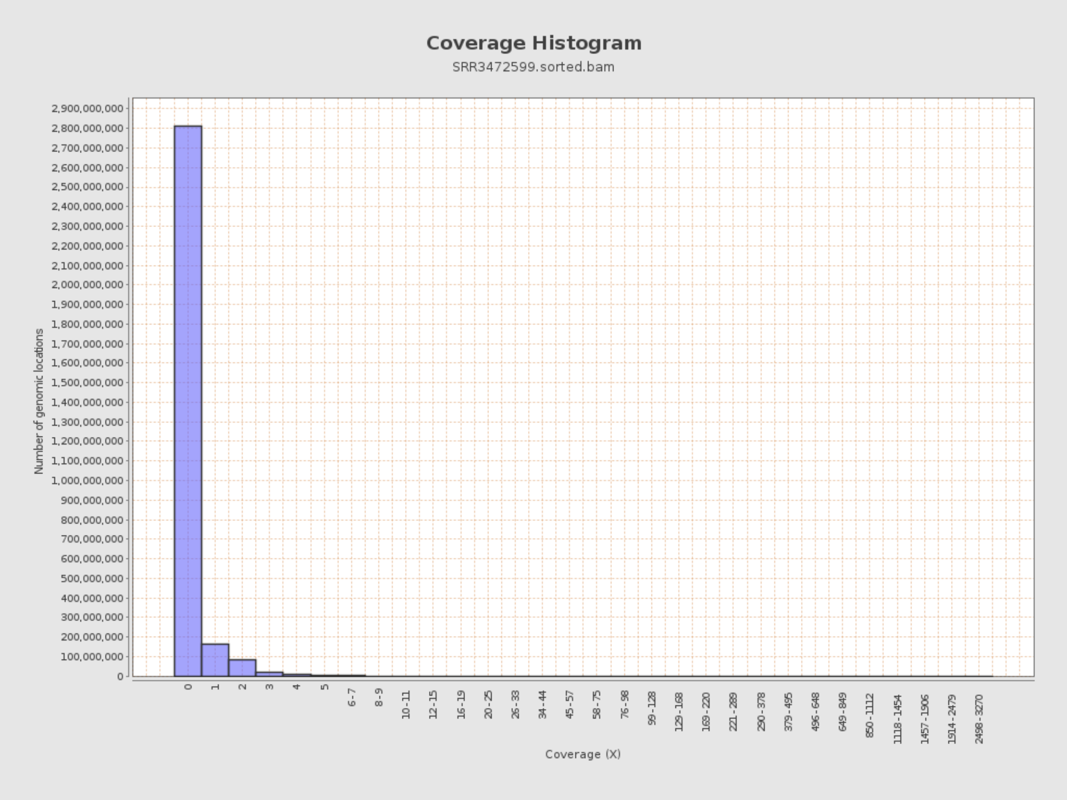
		bases	coverage	deviation
chr1	249250621	26992457	0.1083	1.553
chr2	243199373	38157312	0.1569	1.8577
chr3	198022430	23312842	0.1177	0.4901
chr4	191154276	23479193	0.1228	0.7544
chr5	180915260	21980275	0.1215	0.5139
chr6	171115067	26782463	0.1565	0.768
chr7	159138663	44631869	0.2805	2.4146
chr8	146364022	22791955	0.1557	1.2883
chr9	141213431	16097630	0.114	1.3668
chr10	135534747	24083318	0.1777	1.2948
chr11	135006516	23547401	0.1744	1.2462
chr12	133851895	24182635	0.1807	0.6296
chr13	115169878	22073507	0.1917	0.6547
chr14	107349540	12367421	0.1152	5.2043
chr15	102531392	14052074	0.1371	0.5458
chr16	90354753	17318375	0.1917	0.8915
chr17	81195210	15420408	0.1899	1.0978
chr18	78077248	10176777	0.1303	2.1259
chr19	59128983	8516843	0.144	1.1558
chr20	63025520	19198020	0.3046	1.1086
chr21	48129895	7124968	0.148	0.6642
chr22	51304566	4901189	0.0955	0.4557
chrMT	16571	74817	4.5149	4.5017
chrX	155270560	29731151	0.1915	0.8182

chrY	59373566	1239611	0.0209	0.5977

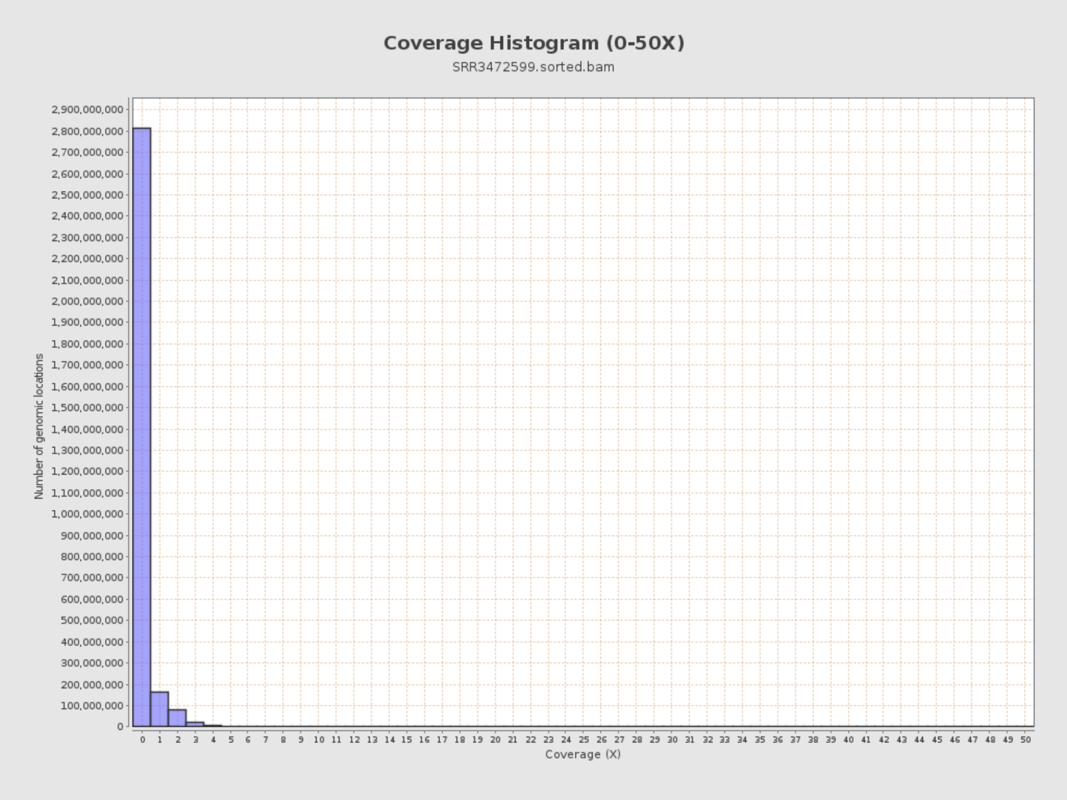
3. Results : Coverage across reference



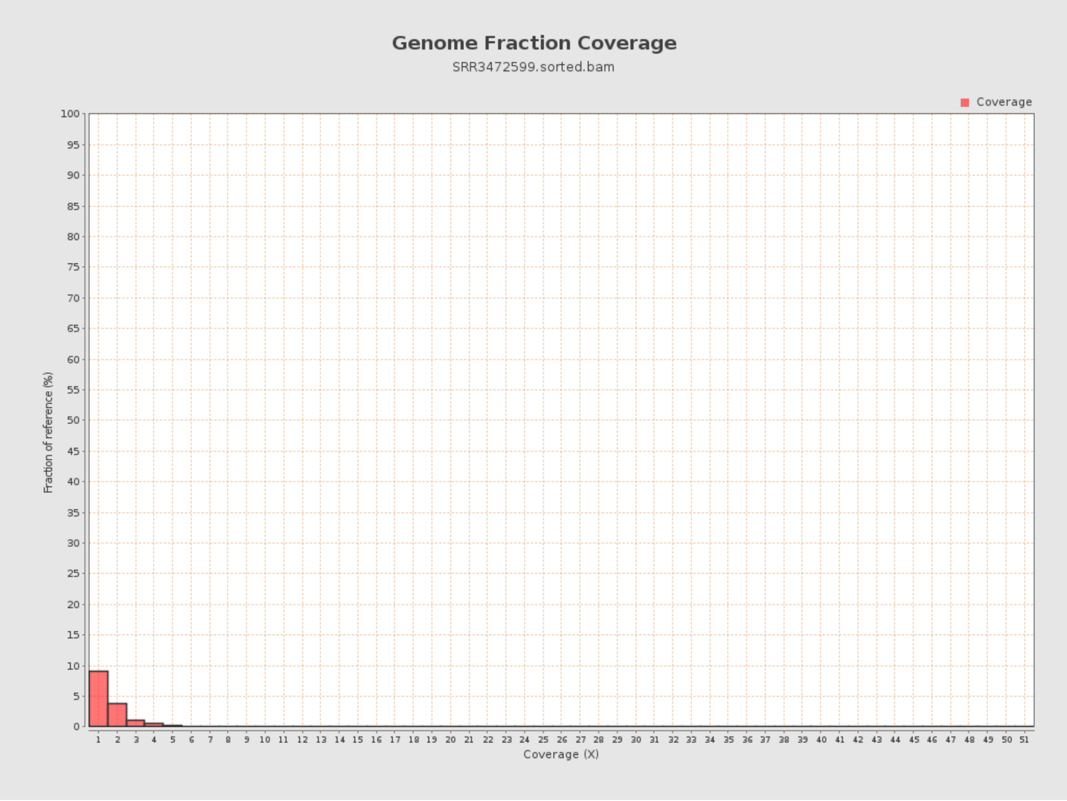
4. Results : Coverage Histogram



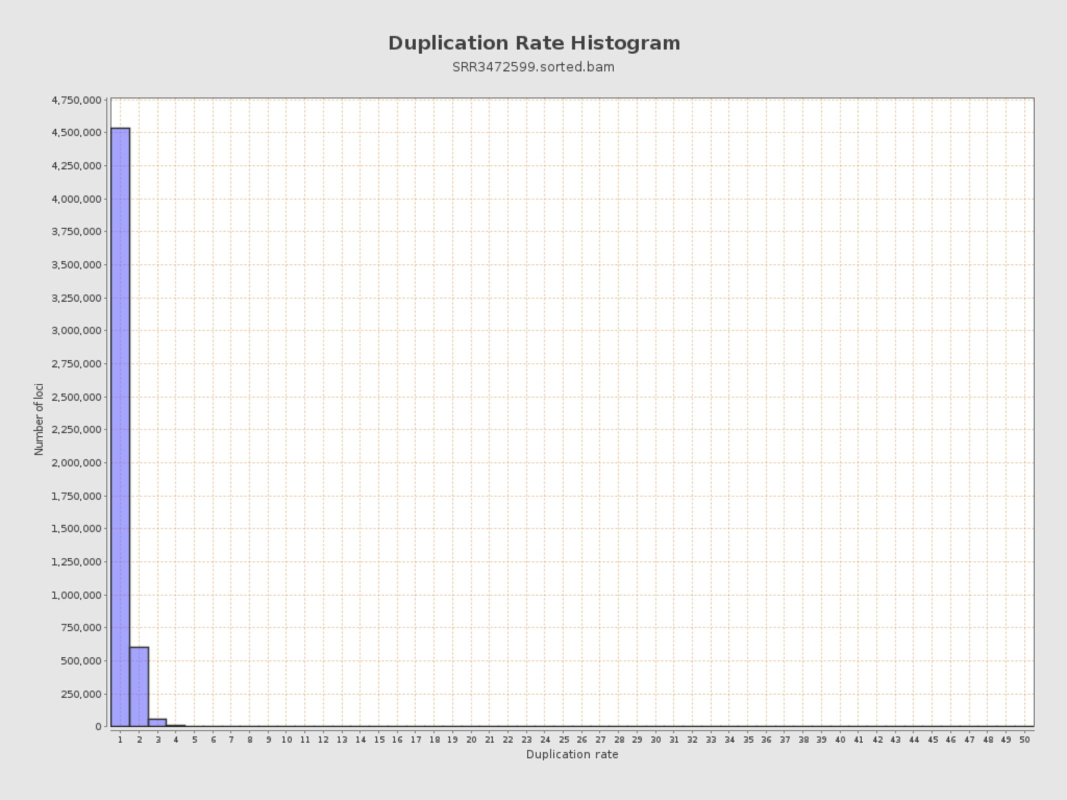
5. Results : Coverage Histogram (0-50X)



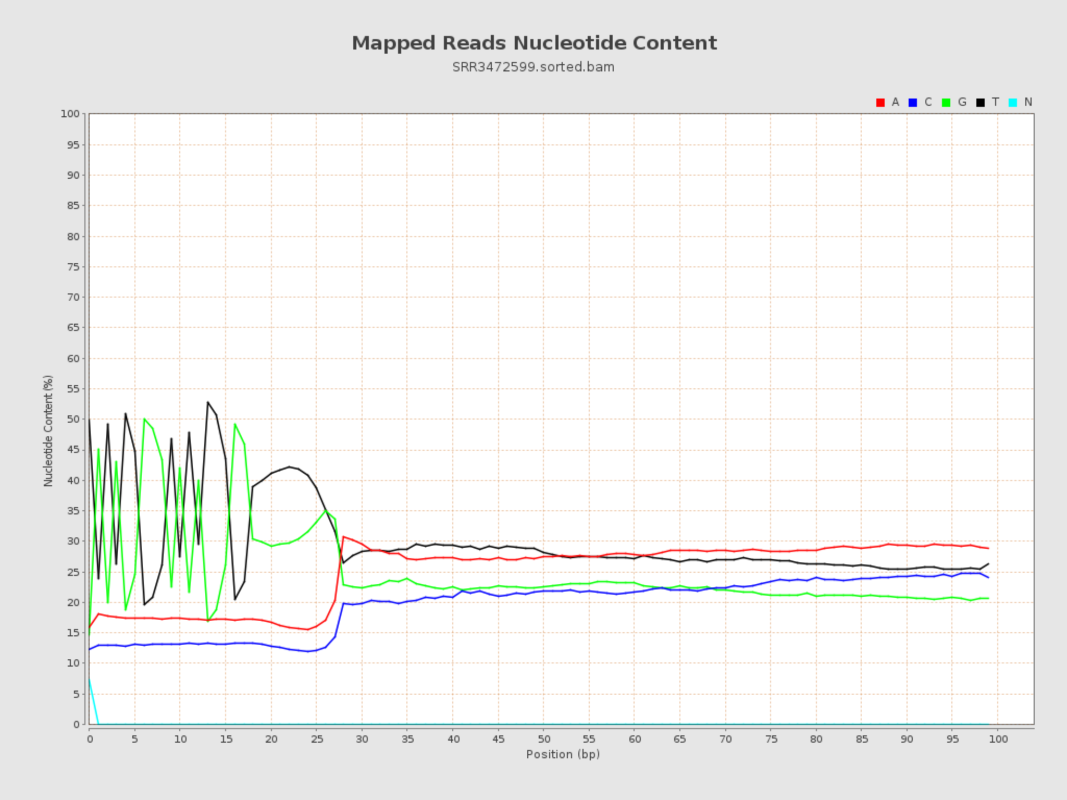
6. Results : Genome Fraction Coverage



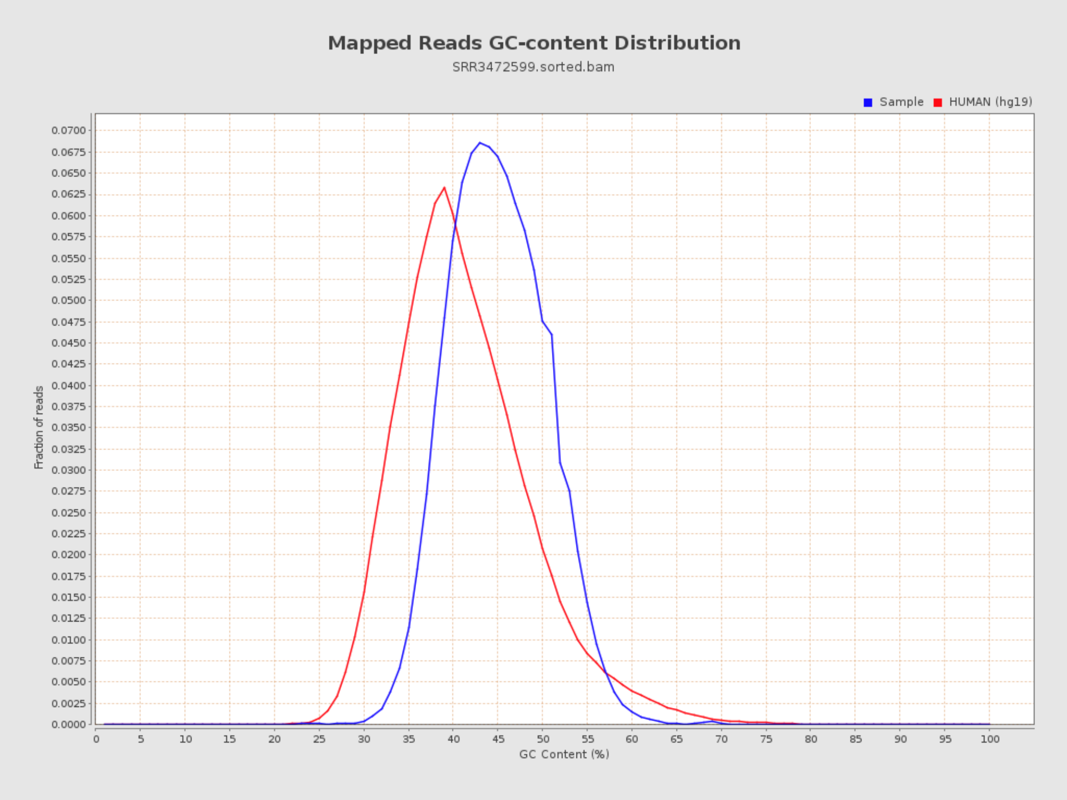
7. Results : Duplication Rate Histogram



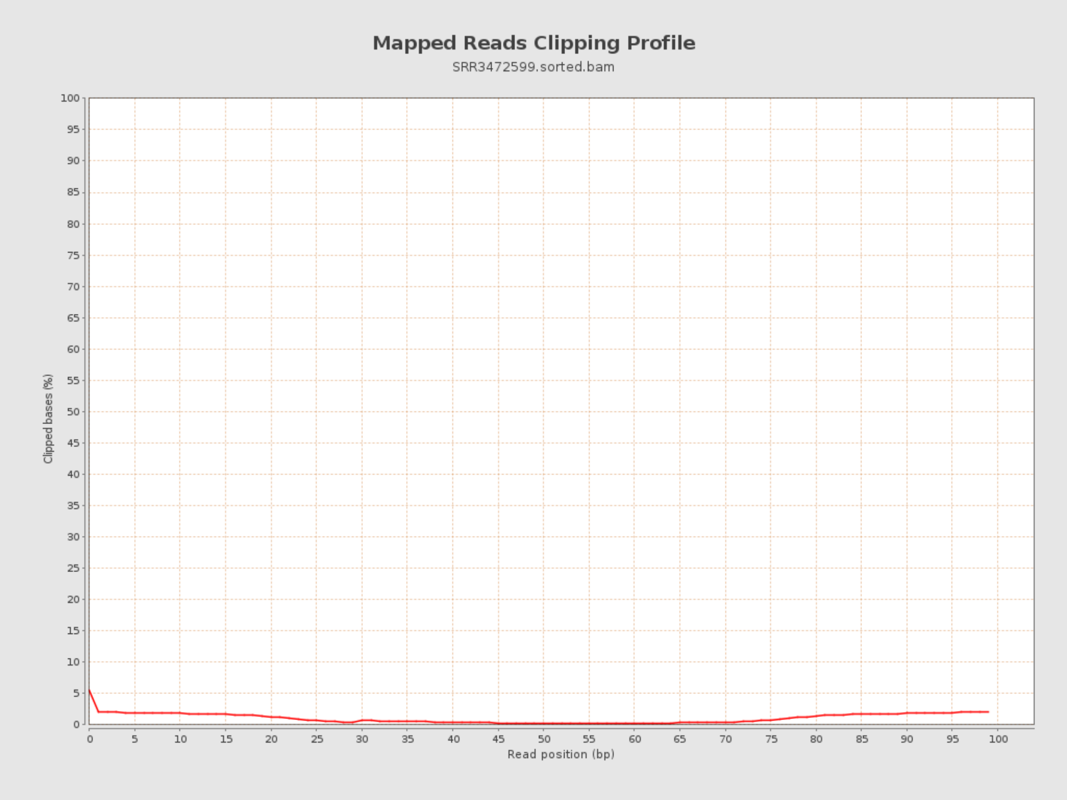
8. Results : Mapped Reads Nucleotide Content



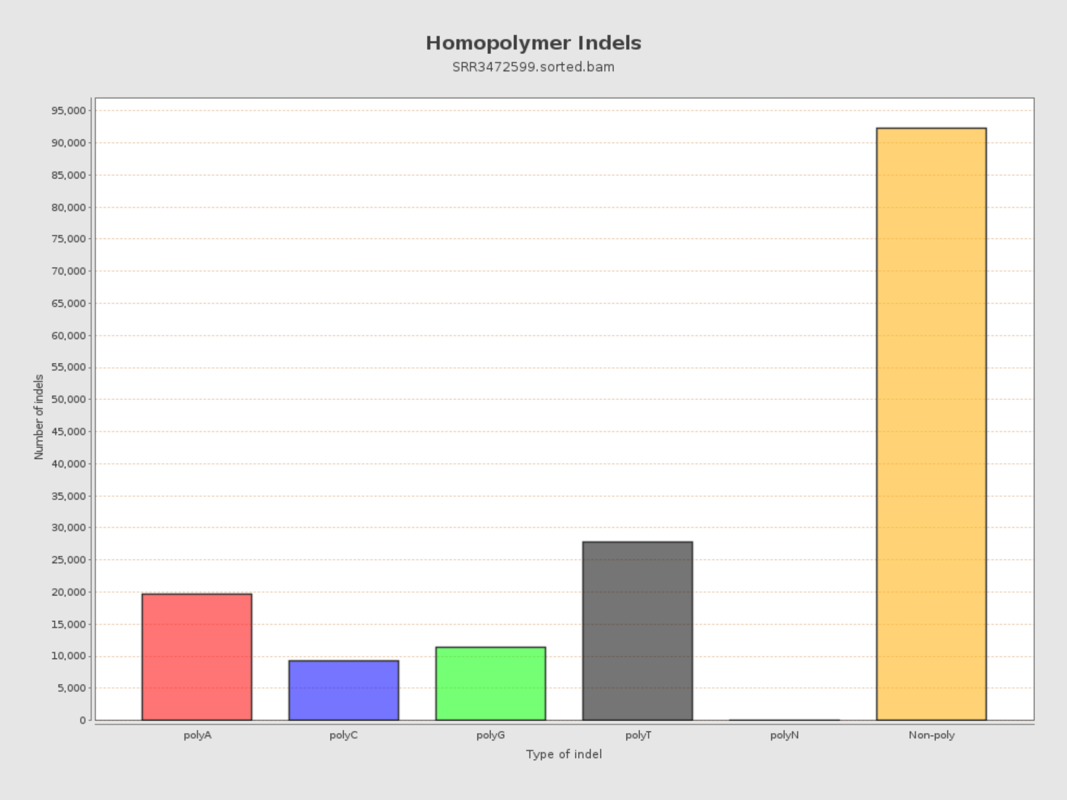
9. Results : Mapped Reads GC-content Distribution



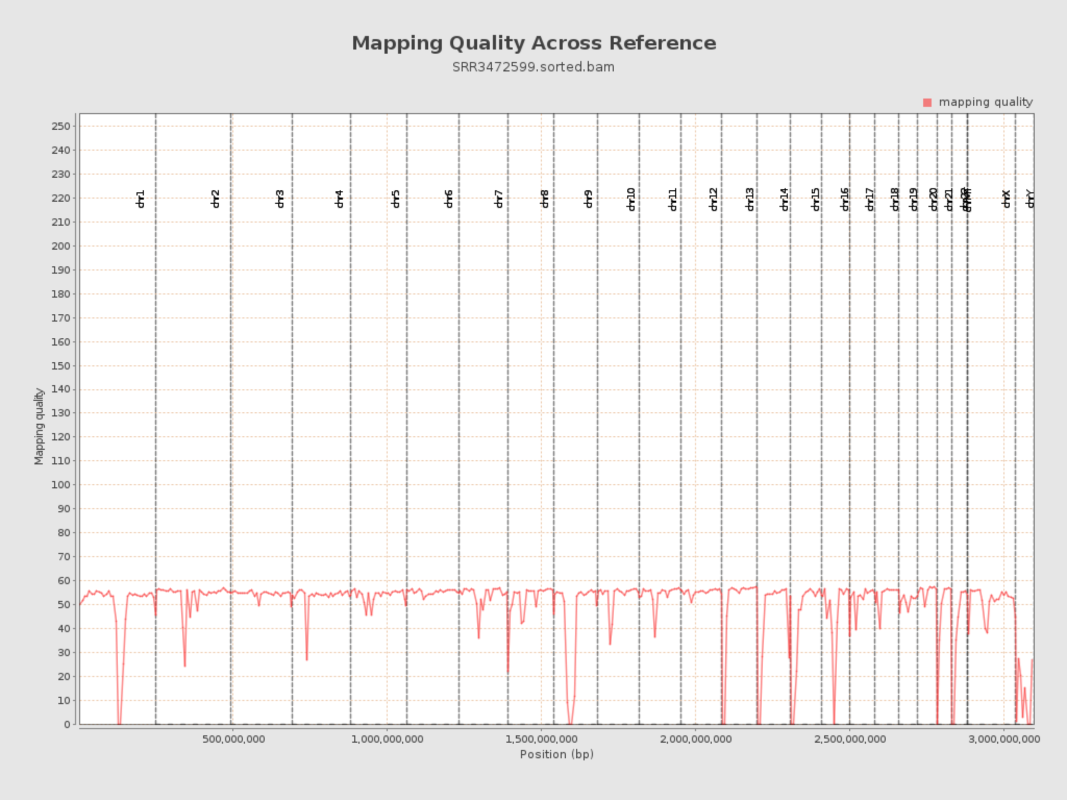
10. Results : Mapped Reads Clipping Profile



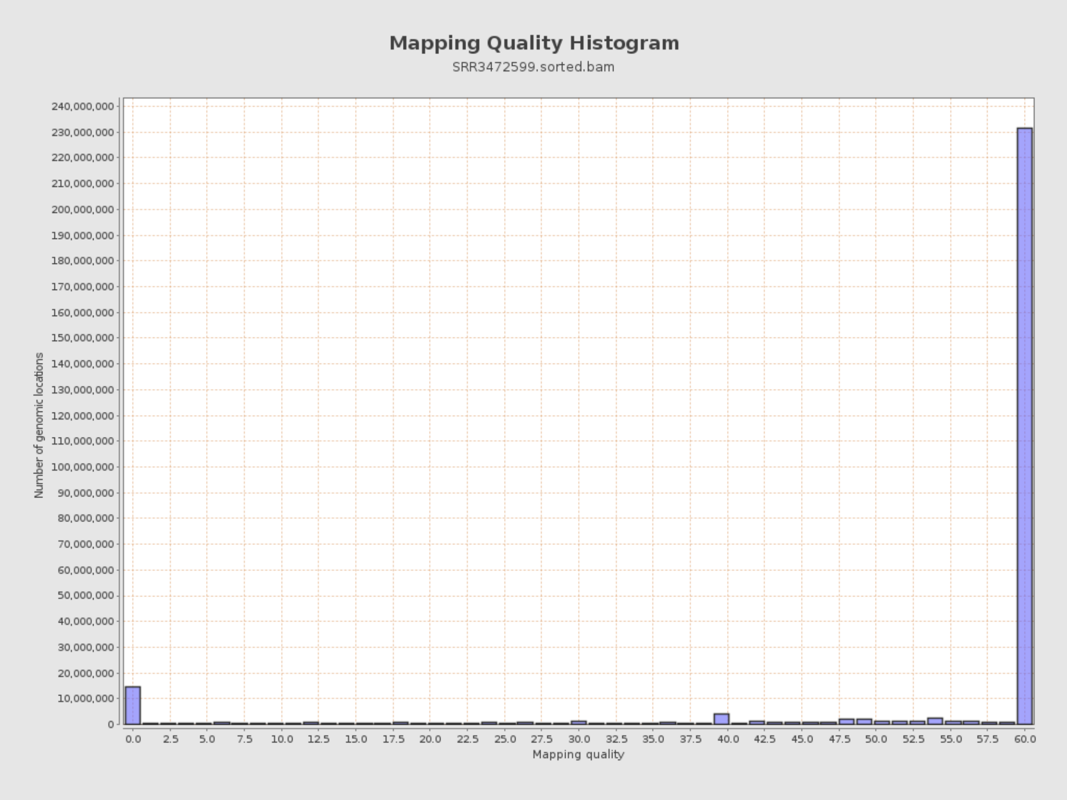
11. Results : Homopolymer Indels



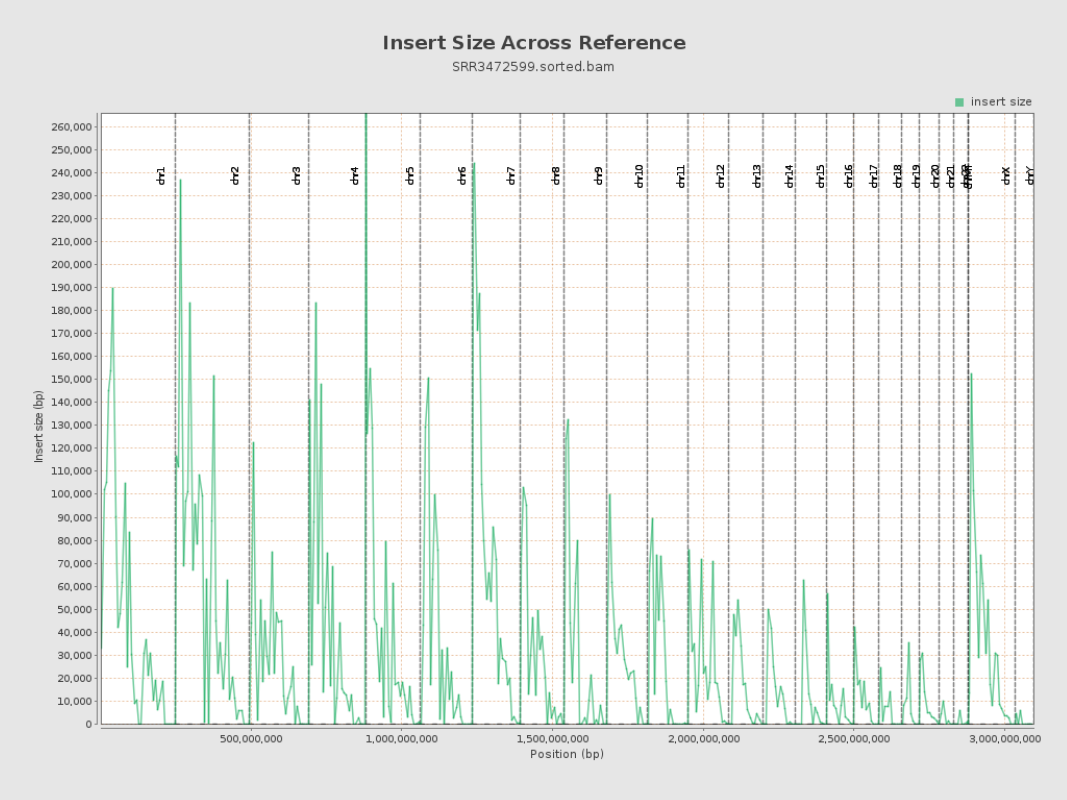
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram