Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:29:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472498.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_SRR3472498 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472498_1.fastq.gz SRR3472498_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:29:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472498.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,827,816
Mapped reads	17,592,135 / 98.68%
Unmapped reads	235,681 / 1.32%
Mapped paired reads	17,592,135 / 98.68%
Mapped reads, first in pair	8,821,961 / 49.48%
Mapped reads, second in pair	8,770,174 / 49.19%
Mapped reads, both in pair	17,481,254 / 98.06%
Mapped reads, singletons	110,881 / 0.62%
Secondary alignments	0
Supplementary alignments	63,184 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,310,260 / 63.44%
Duplication rate	46.08%
Clipped reads	1,347,591 / 7.56%

2.2. ACGT Content

Number/percentage of A's	477,688,826 / 27.57%
Number/percentage of C's	391,663,776 / 22.6%
Number/percentage of T's	474,451,672 / 27.38%
Number/percentage of G's	388,733,673 / 22.43%
Number/percentage of N's	269,051 / 0.02%

GC Percentage	45.04%

2.3. Coverage

Mean	0.5598
Standard Deviation	21.4152

2.4. Mapping Quality

Mean Mapping Quality	54.96

2.5. Insert size

Mean	22,990.96
Standard Deviation	1,495,317.64
P25/Median/P75	176 / 244 / 325

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	10,641,293
Insertions	92,336
Mapped reads with at least one insertion	0.52%
Deletions	89,511
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.13%

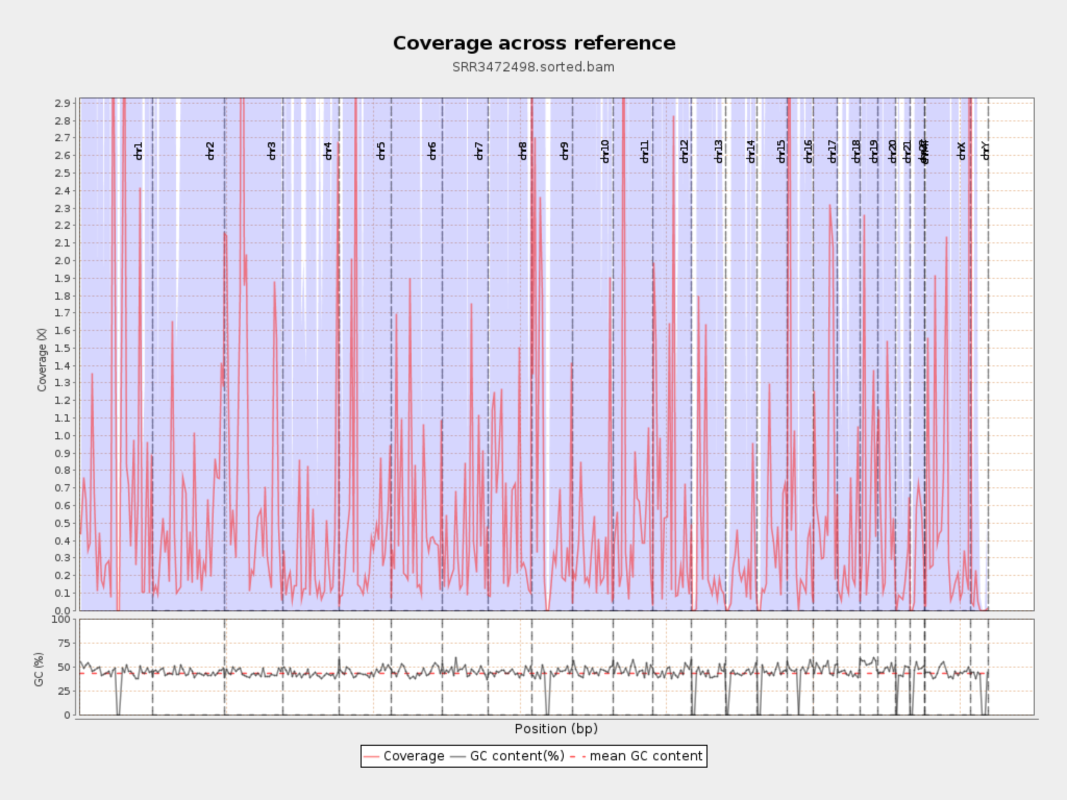
2.7. Chromosome stats

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

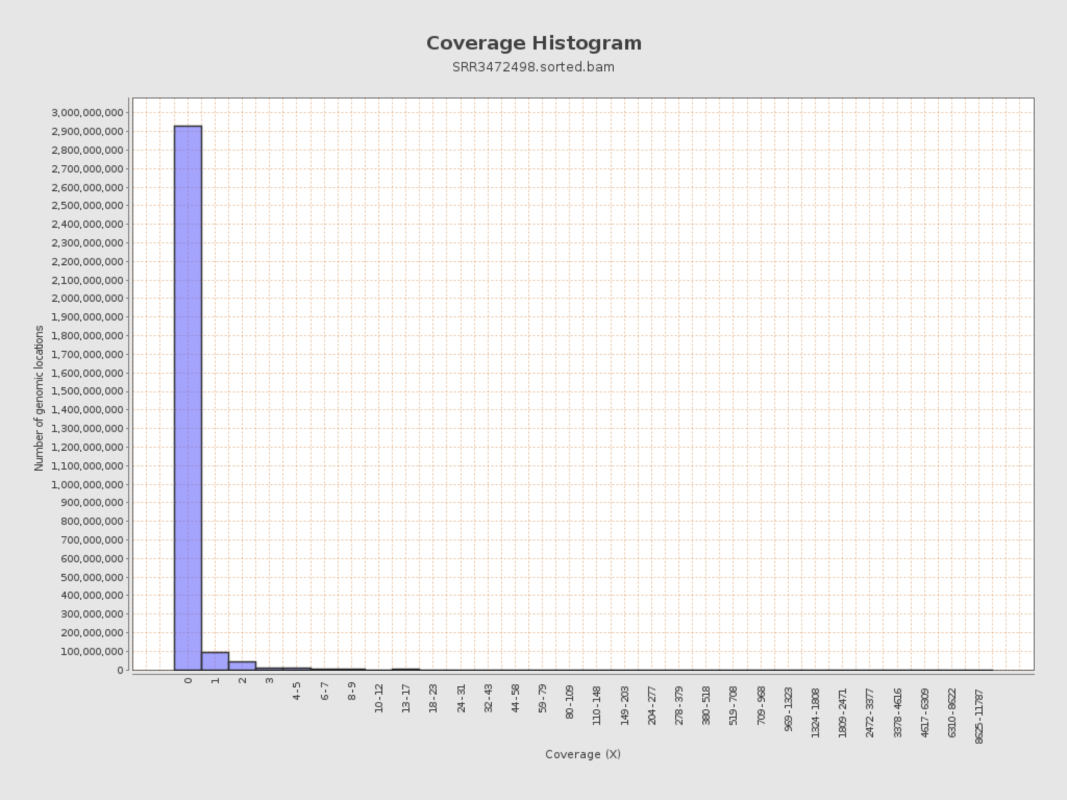
		bases	coverage	deviation
chr1	249250621	200218217	0.8033	34.3473
chr2	243199373	115992519	0.4769	18.8649
chr3	198022430	200614827	1.0131	23.1481
chr4	191154276	64160832	0.3356	12.7182
chr5	180915260	98001182	0.5417	20.846
chr6	171115067	89200684	0.5213	15.1809
chr7	159138663	72874923	0.4579	15.7637
chr8	146364022	81994409	0.5602	17.1262
chr9	141213431	103709368	0.7344	22.3916
chr10	135534747	52624339	0.3883	15.9331
chr11	135006516	87622479	0.649	37.1576
chr12	133851895	96113463	0.7181	25.1514
chr13	115169878	40812490	0.3544	17.8586
chr14	107349540	24890579	0.2319	7.7913
chr15	102531392	38649132	0.3769	14.537
chr16	90354753	59291570	0.6562	24.4671
chr17	81195210	67751503	0.8344	23.9055
chr18	78077248	24558660	0.3145	9.9356
chr19	59128983	46324277	0.7834	21.3295
chr20	63025520	39623537	0.6287	17.8511
chr21	48129895	8884570	0.1846	8.2158
chr22	51304566	17189520	0.335	13.3988
chrMT	16571	1575	0.095	0.3893
chrX	155270560	99191560	0.6388	24.3814

chrY	59373566	2742015	0.0462	2.1851

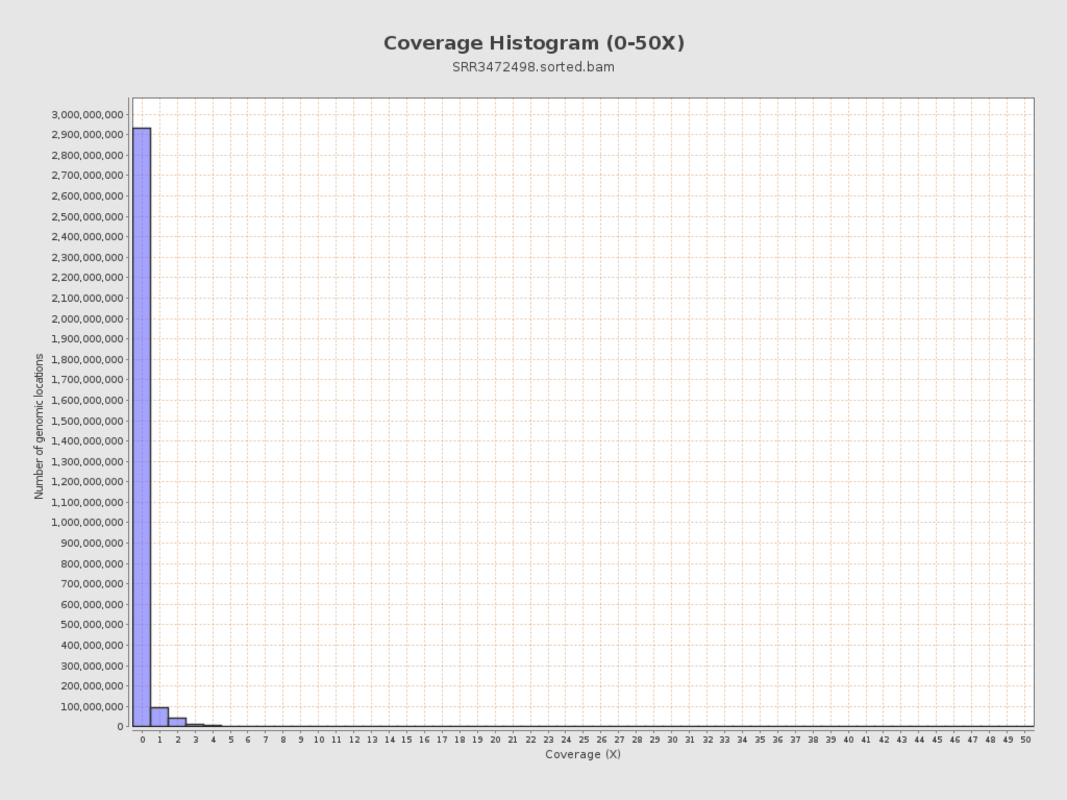
3. Results : Coverage across reference



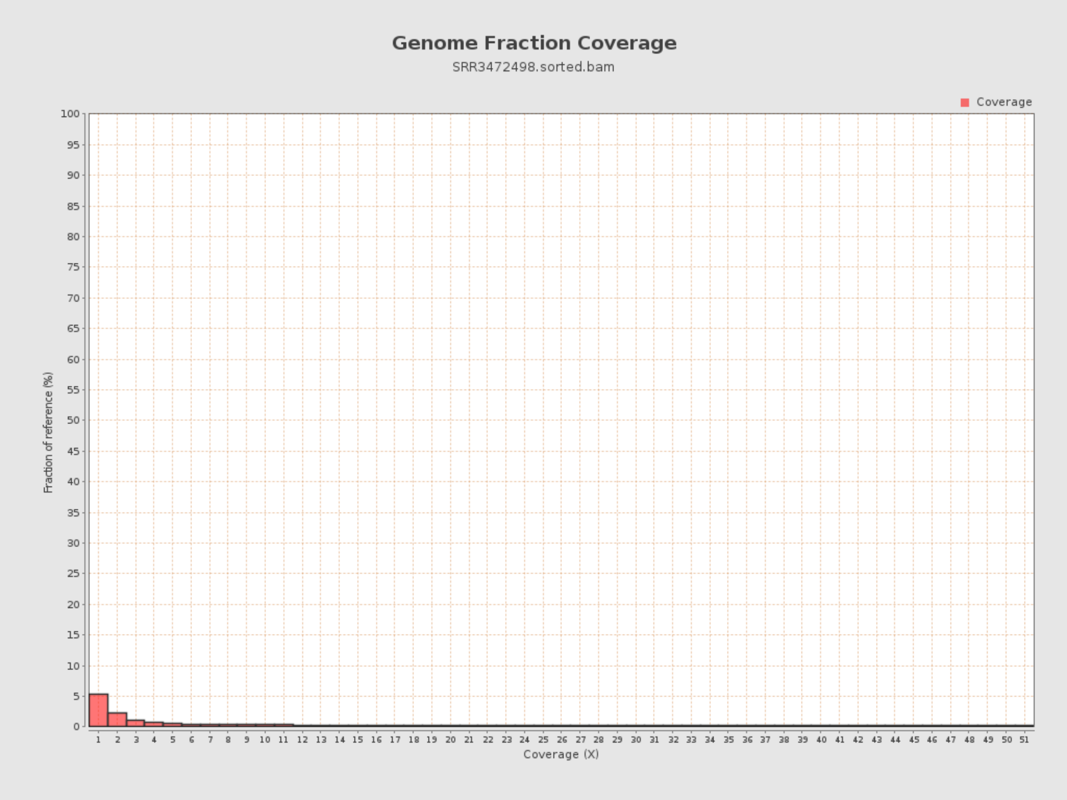
4. Results : Coverage Histogram



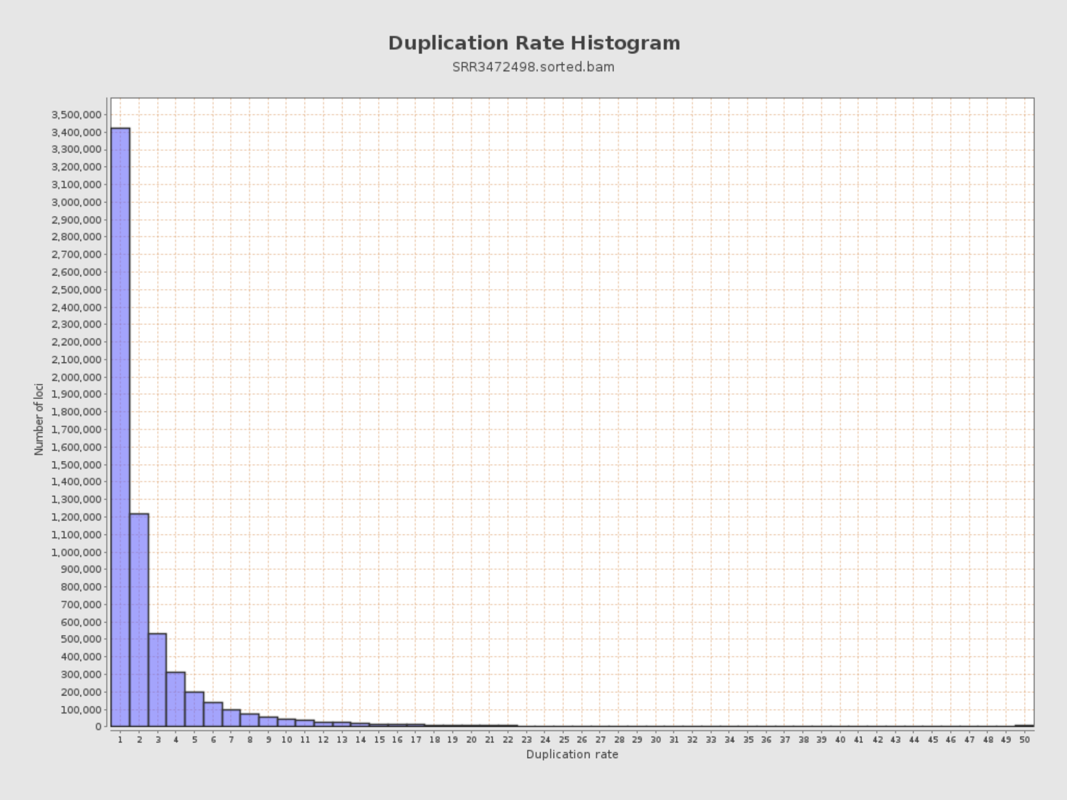
5. Results : Coverage Histogram (0-50X)



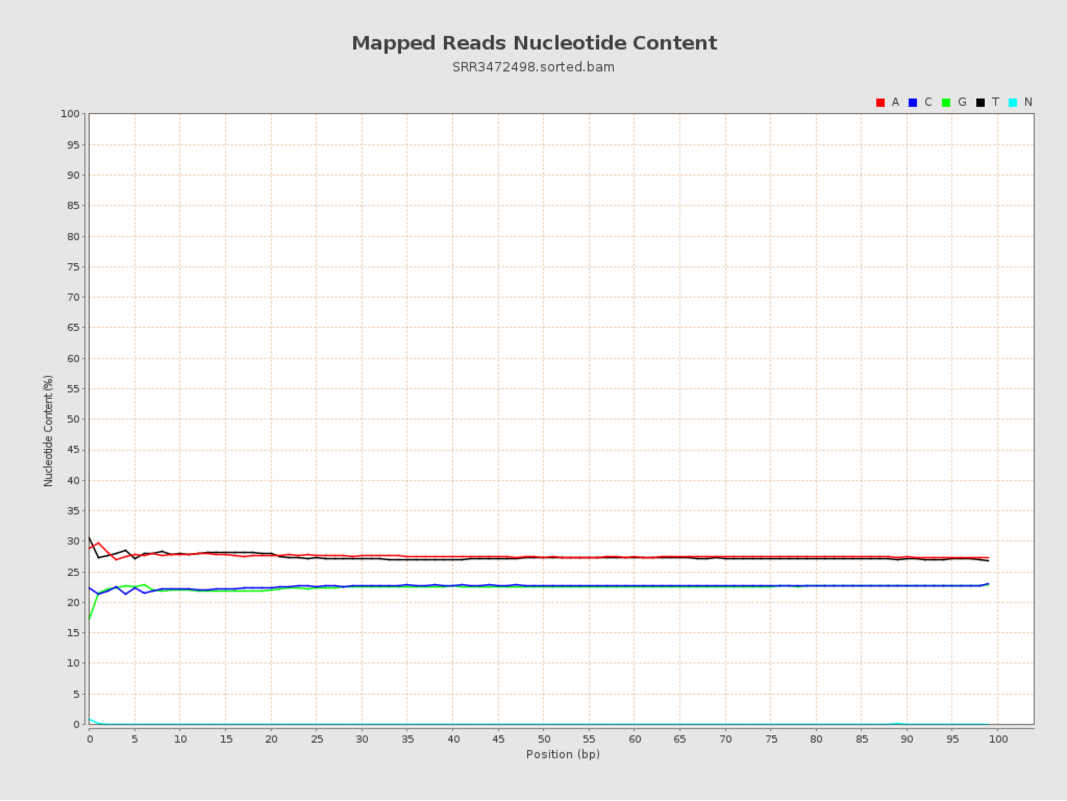
6. Results : Genome Fraction Coverage



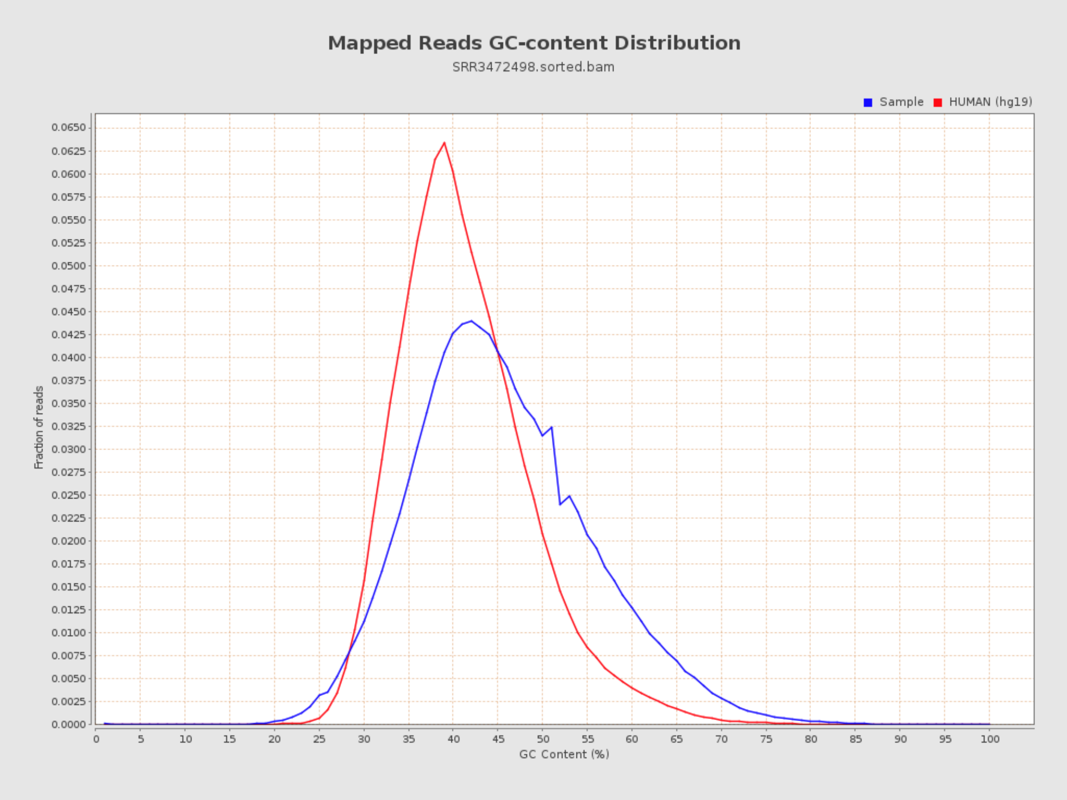
7. Results : Duplication Rate Histogram



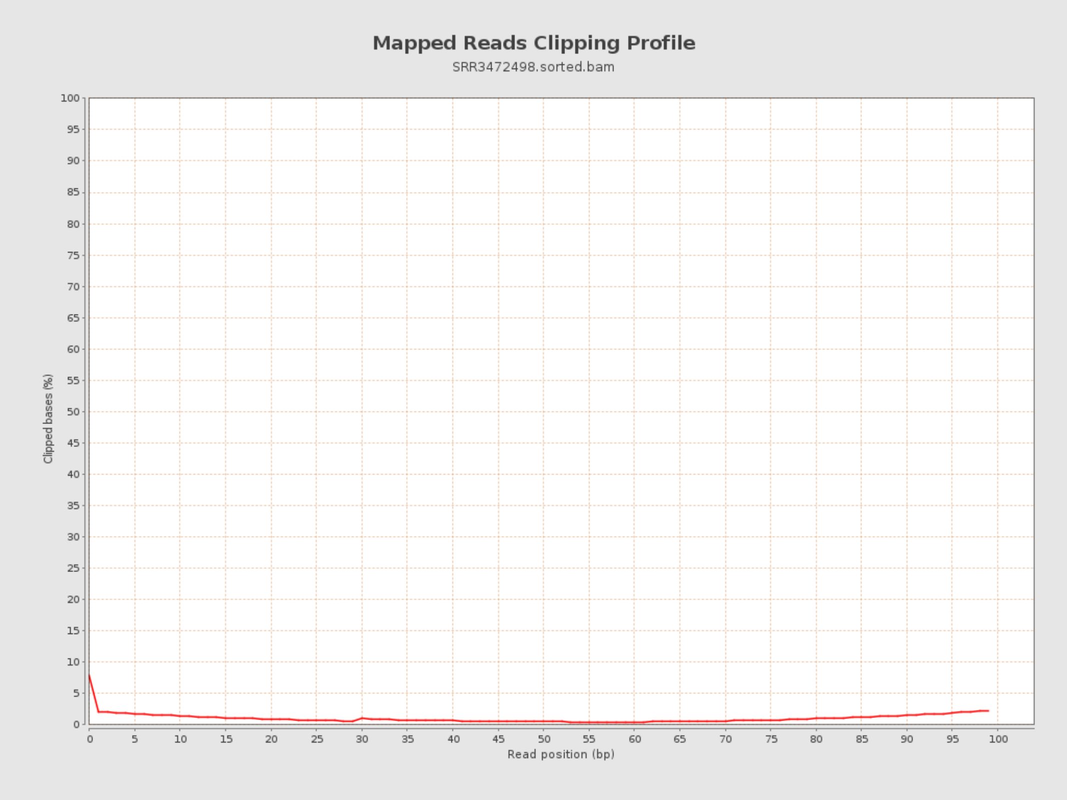
8. Results : Mapped Reads Nucleotide Content



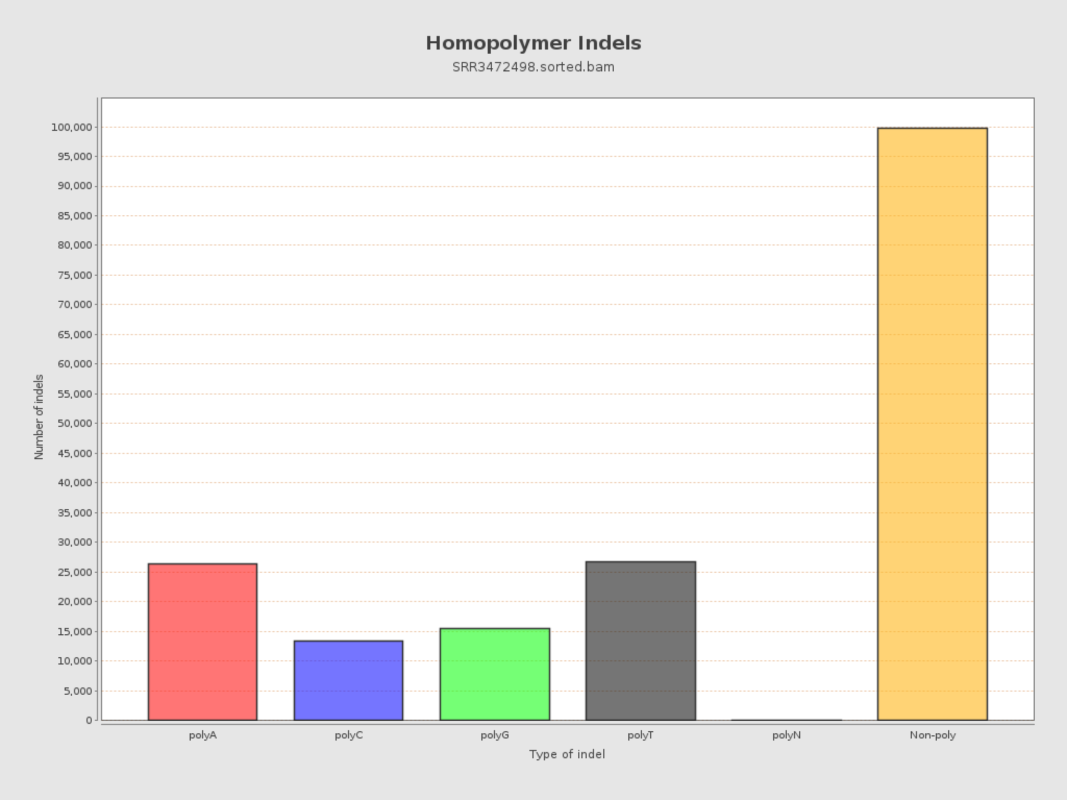
9. Results : Mapped Reads GC-content Distribution



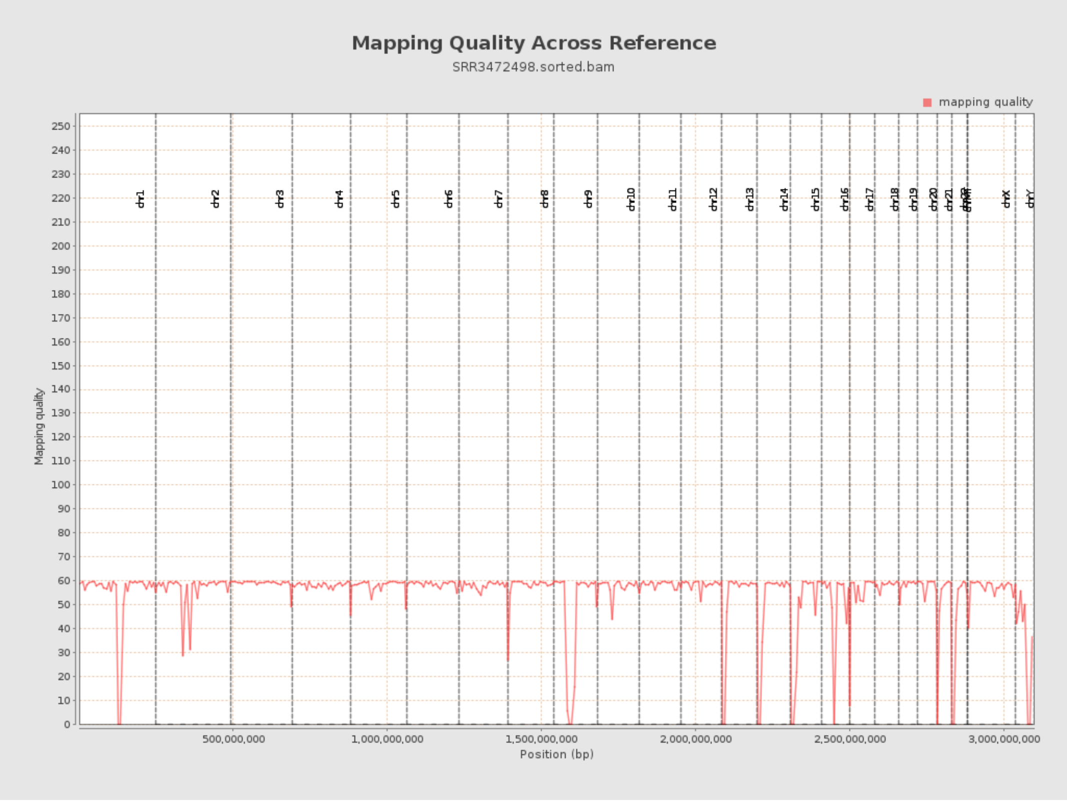
10. Results : Mapped Reads Clipping Profile



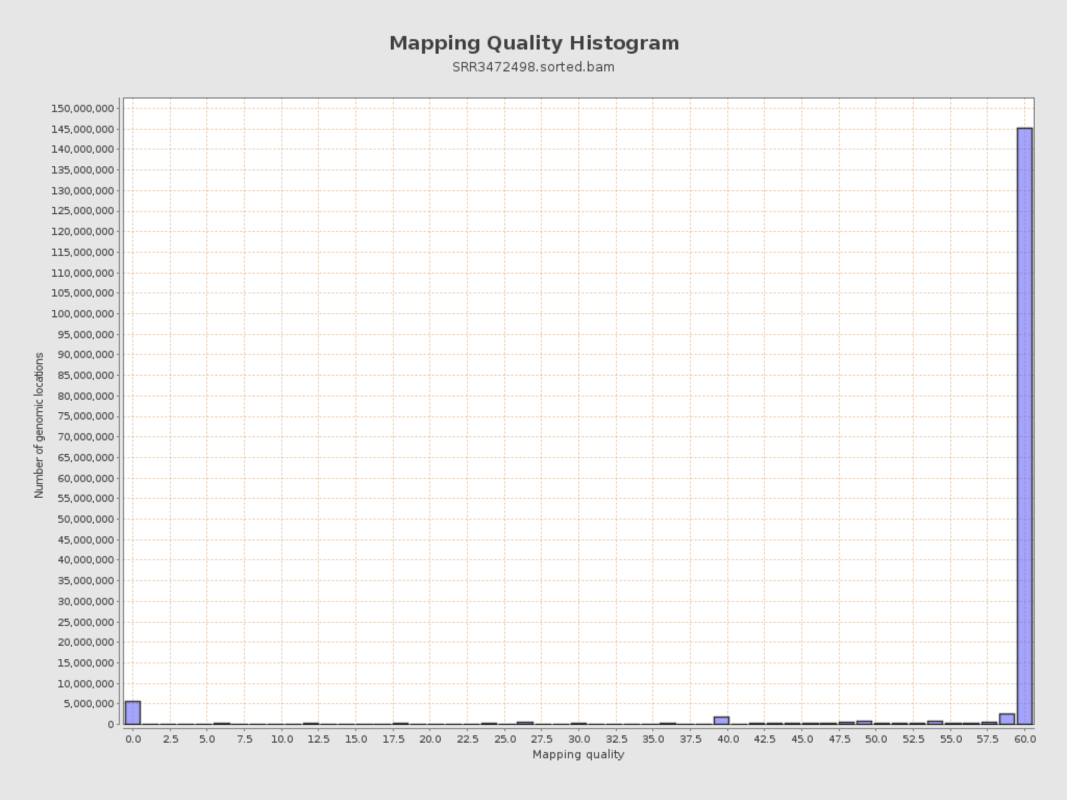
11. Results : Homopolymer Indels



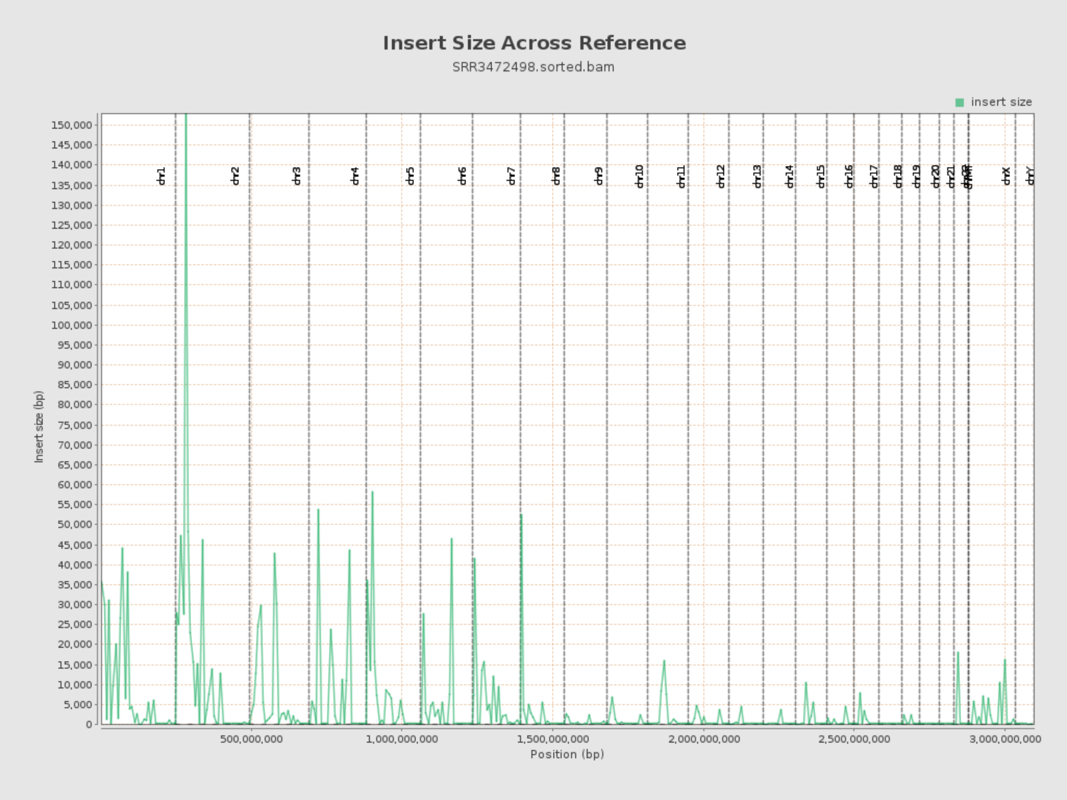
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram