Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 04:04:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472376.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_SRR3472376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472376_1.fastq.gz SRR3472376_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 04:04:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,327,972
Mapped reads	17,160,849 / 99.04%
Unmapped reads	167,123 / 0.96%
Mapped paired reads	17,160,849 / 99.04%
Mapped reads, first in pair	8,602,434 / 49.64%
Mapped reads, second in pair	8,558,415 / 49.39%
Mapped reads, both in pair	17,066,934 / 98.49%
Mapped reads, singletons	93,915 / 0.54%
Secondary alignments	0
Supplementary alignments	61,792 / 0.36%
Read min/max/mean length	30 / 100 / 99.43
Duplicated reads (estimated)	10,432,649 / 60.21%
Duplication rate	47.15%
Clipped reads	1,159,794 / 6.69%

2.2. ACGT Content

Number/percentage of A's	451,207,148 / 26.79%
Number/percentage of C's	392,424,073 / 23.3%
Number/percentage of T's	451,269,229 / 26.8%
Number/percentage of G's	388,998,254 / 23.1%
Number/percentage of N's	204,586 / 0.01%

GC Percentage	46.4%

2.3. Coverage

Mean	0.5441
Standard Deviation	15.5487

2.4. Mapping Quality

Mean Mapping Quality	54.87

2.5. Insert size

Mean	18,717.19
Standard Deviation	1,348,954.41
P25/Median/P75	158 / 217 / 291

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,435,718
Insertions	98,359
Mapped reads with at least one insertion	0.57%
Deletions	79,740
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.51%

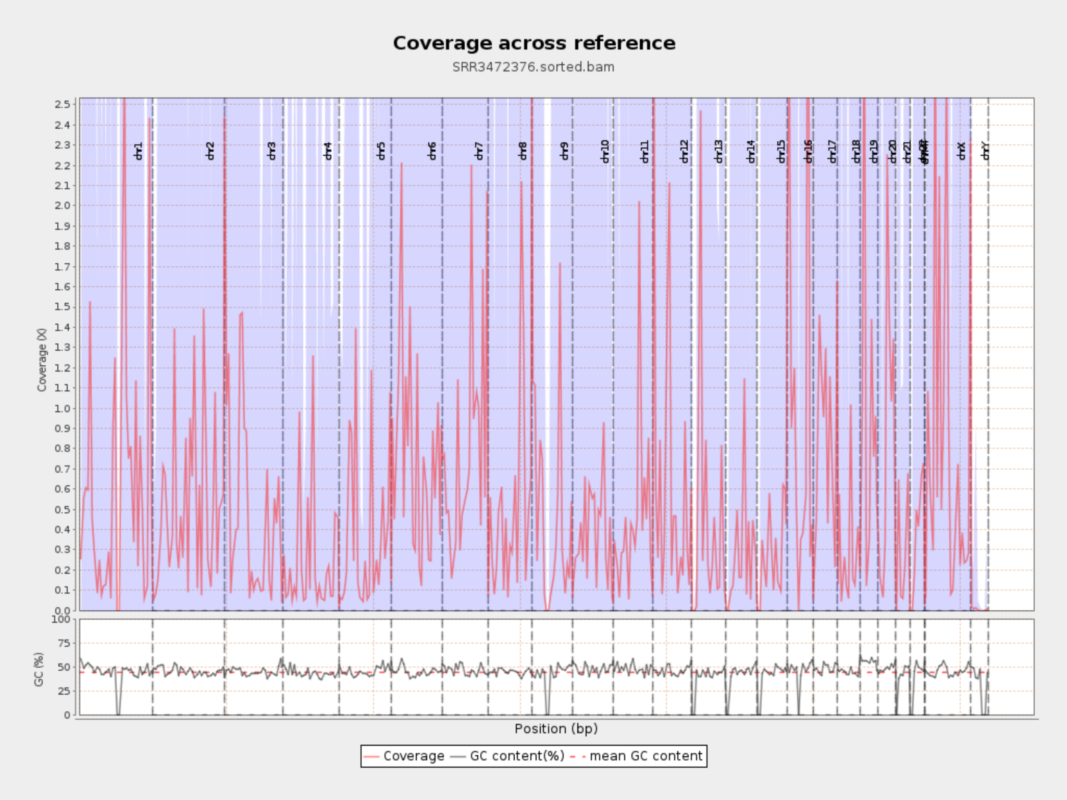
2.7. Chromosome stats

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

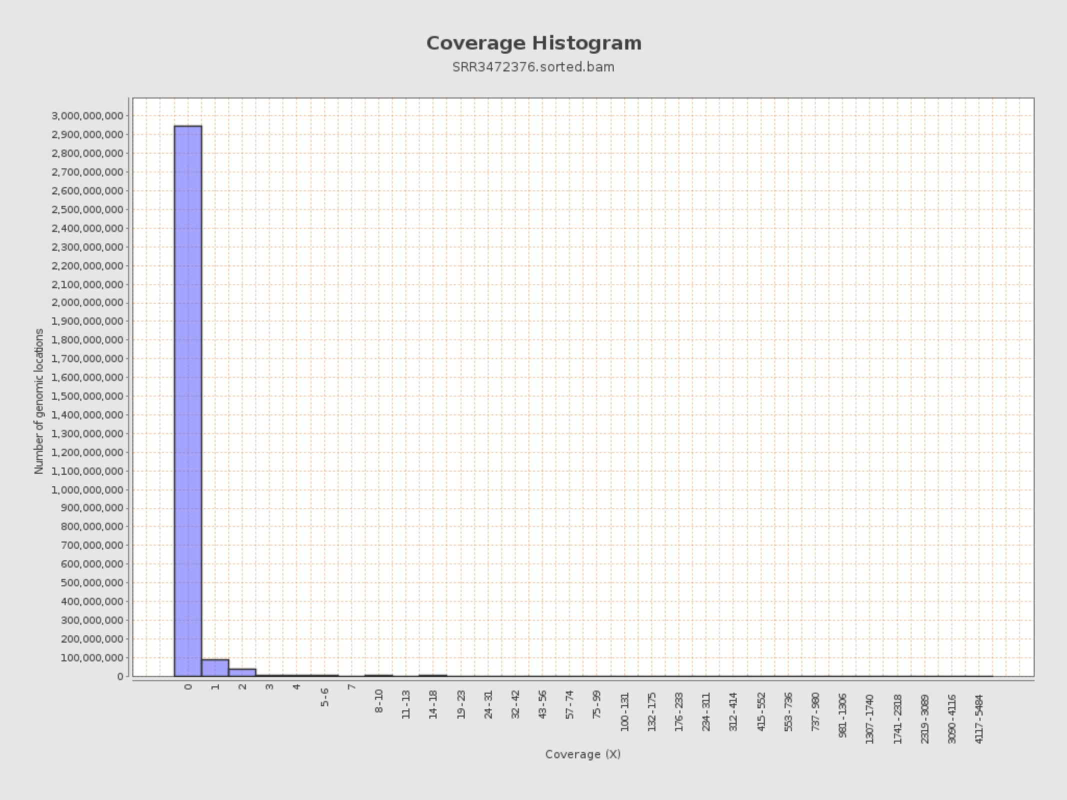
		bases	coverage	deviation
chr1	249250621	160292996	0.6431	18.2483
chr2	243199373	126928698	0.5219	14.7823
chr3	198022430	101904887	0.5146	12.1091
chr4	191154276	45676756	0.239	10.8972
chr5	180915260	68811611	0.3804	12.1251
chr6	171115067	127901063	0.7475	15.9309
chr7	159138663	128421232	0.807	20.1639
chr8	146364022	76892512	0.5254	13.5692
chr9	141213431	67178413	0.4757	13.5391
chr10	135534747	52624685	0.3883	10.8709
chr11	135006516	61809429	0.4578	15.0282
chr12	133851895	89854672	0.6713	15.2899
chr13	115169878	53959029	0.4685	15.344
chr14	107349540	29277386	0.2727	9.9963
chr15	102531392	28286596	0.2759	8.4389
chr16	90354753	96766766	1.071	26.4389
chr17	81195210	67683492	0.8336	17.2839
chr18	78077248	23526978	0.3013	12.0795
chr19	59128983	62376156	1.0549	23.3407
chr20	63025520	53620035	0.8508	22.1035
chr21	48129895	14101510	0.293	11.5657
chr22	51304566	19289313	0.376	15.3824
chrMT	16571	8027	0.4844	0.8472
chrX	155270560	126756047	0.8164	21.1538

chrY	59373566	339436	0.0057	0.3799

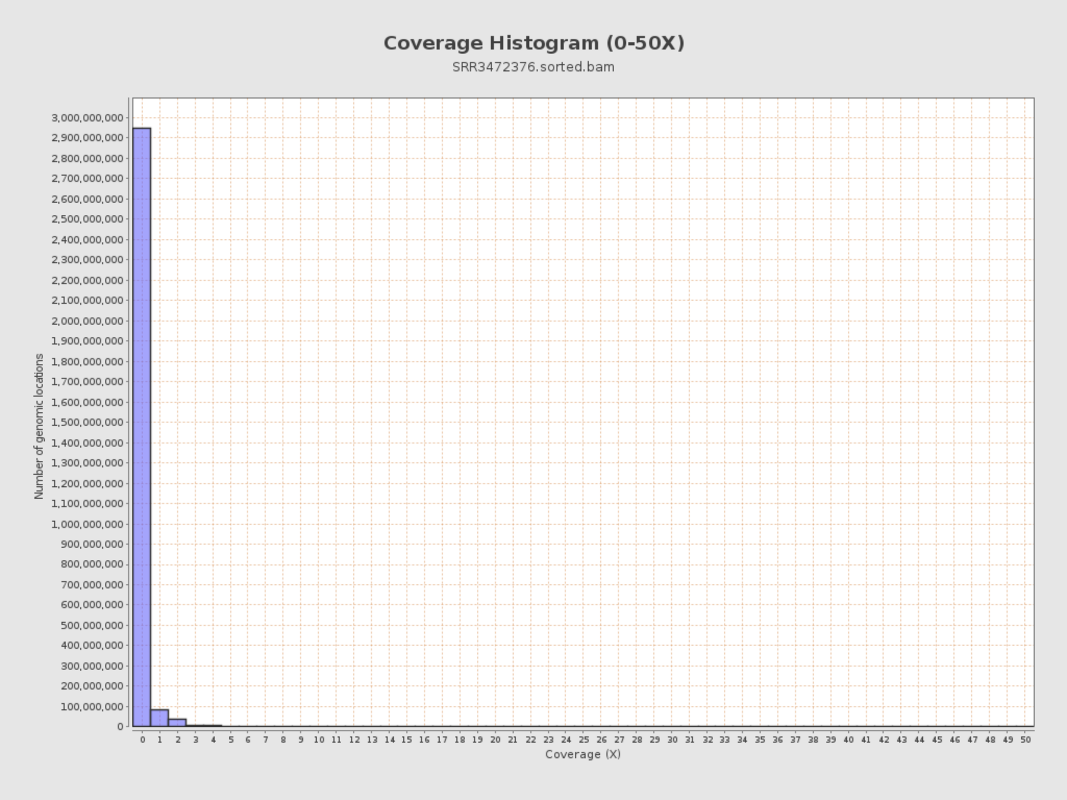
3. Results : Coverage across reference



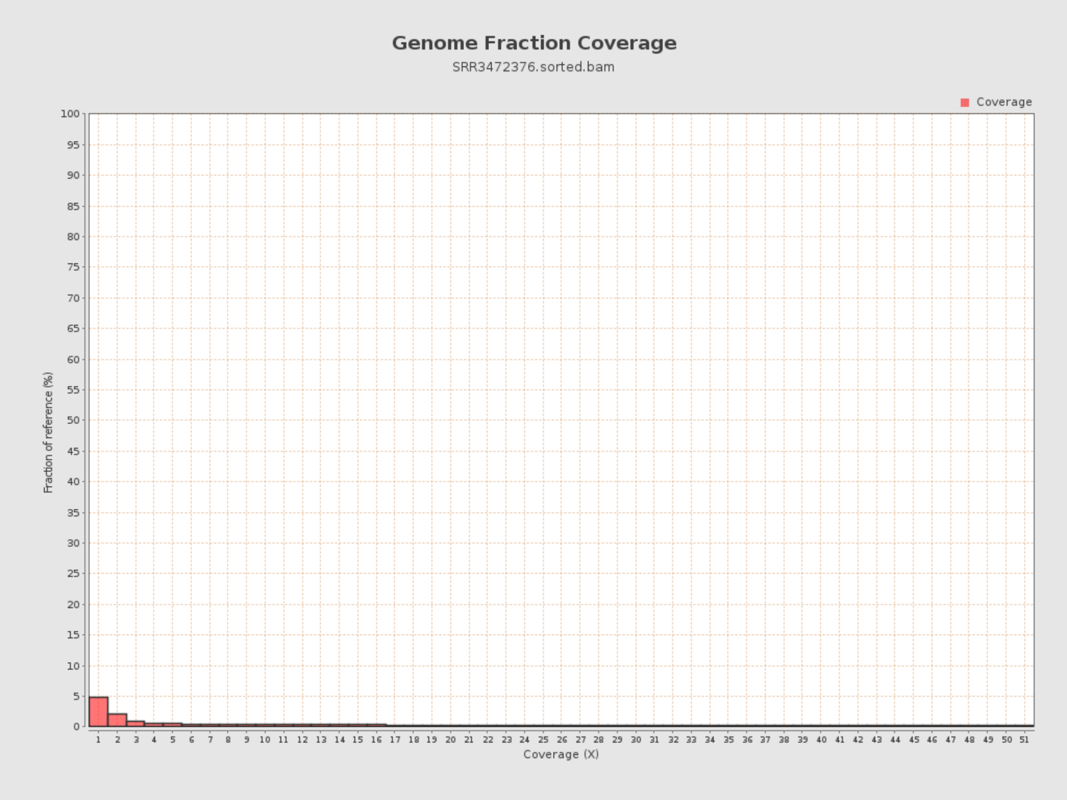
4. Results : Coverage Histogram



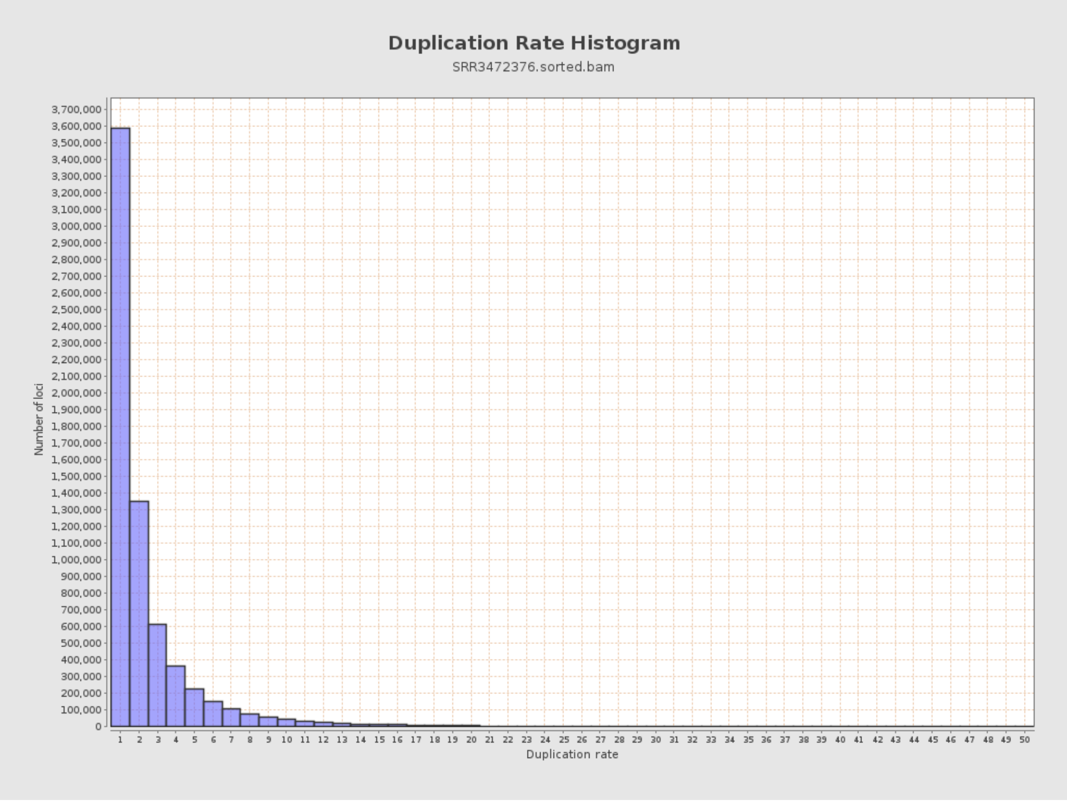
5. Results : Coverage Histogram (0-50X)



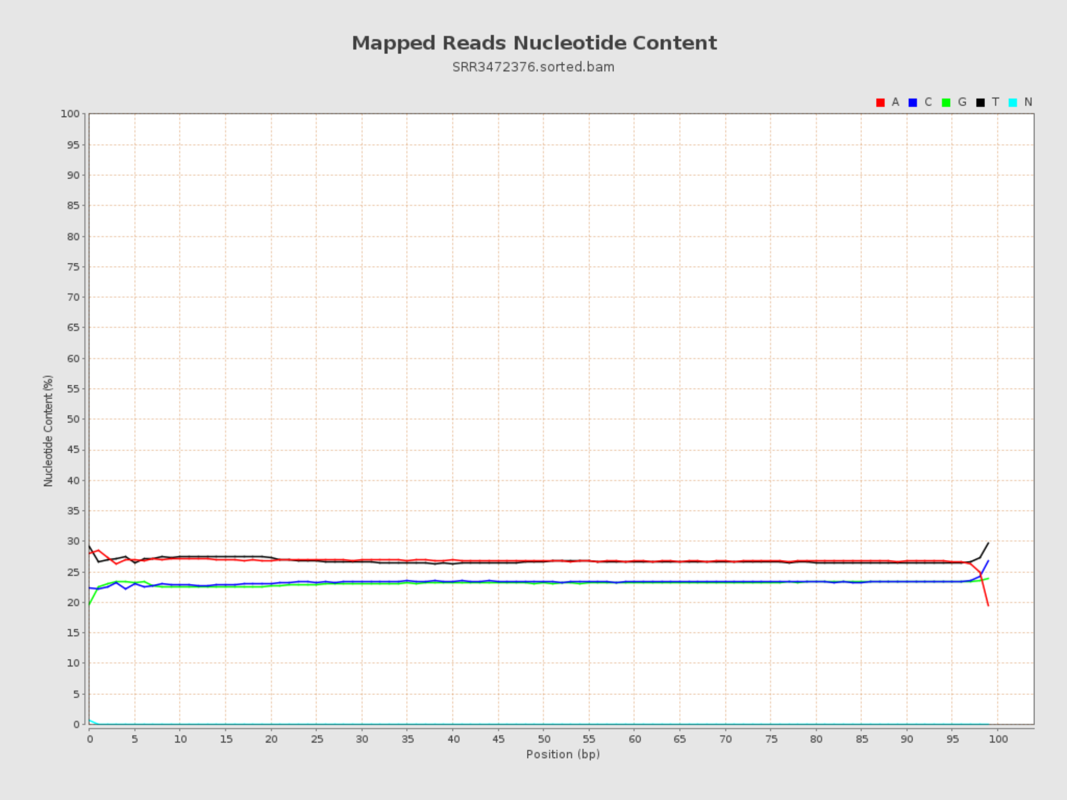
6. Results : Genome Fraction Coverage



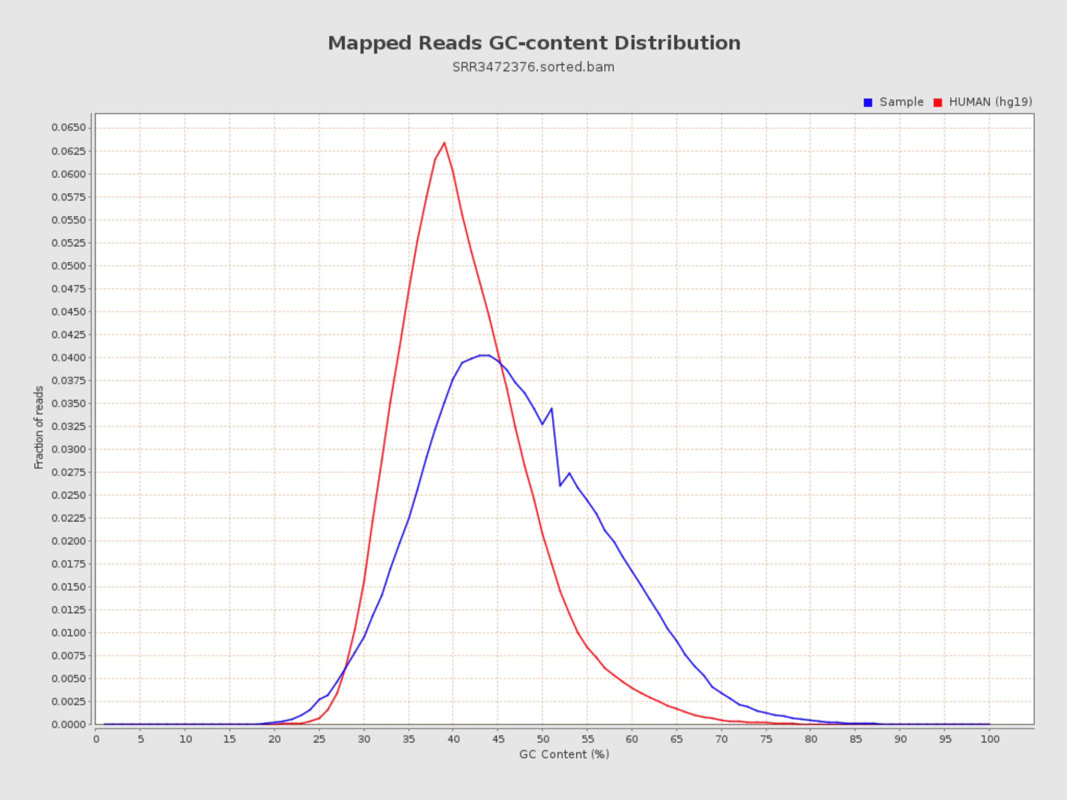
7. Results : Duplication Rate Histogram



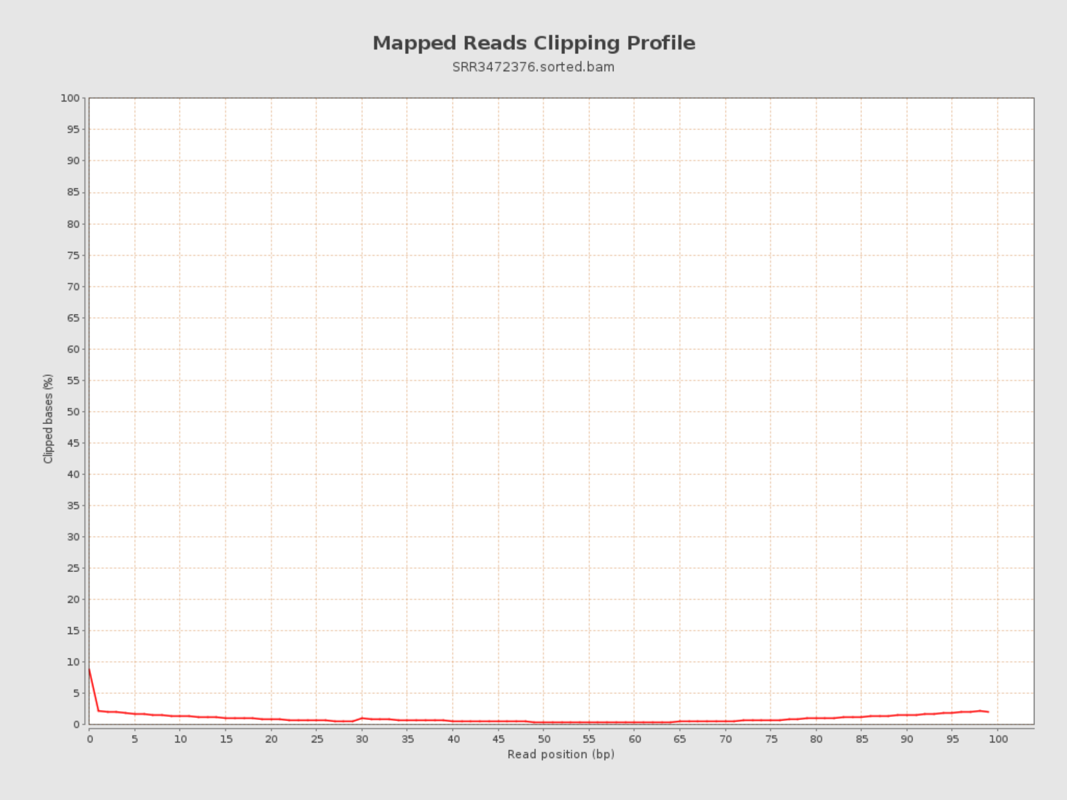
8. Results : Mapped Reads Nucleotide Content



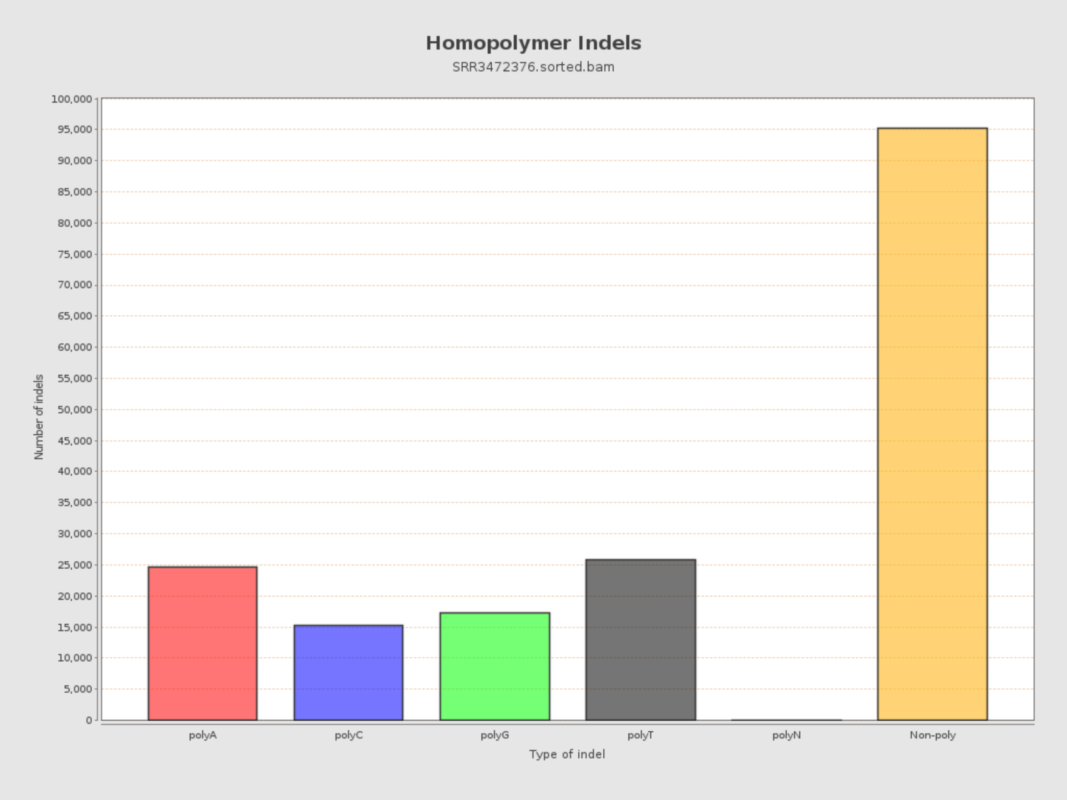
9. Results : Mapped Reads GC-content Distribution



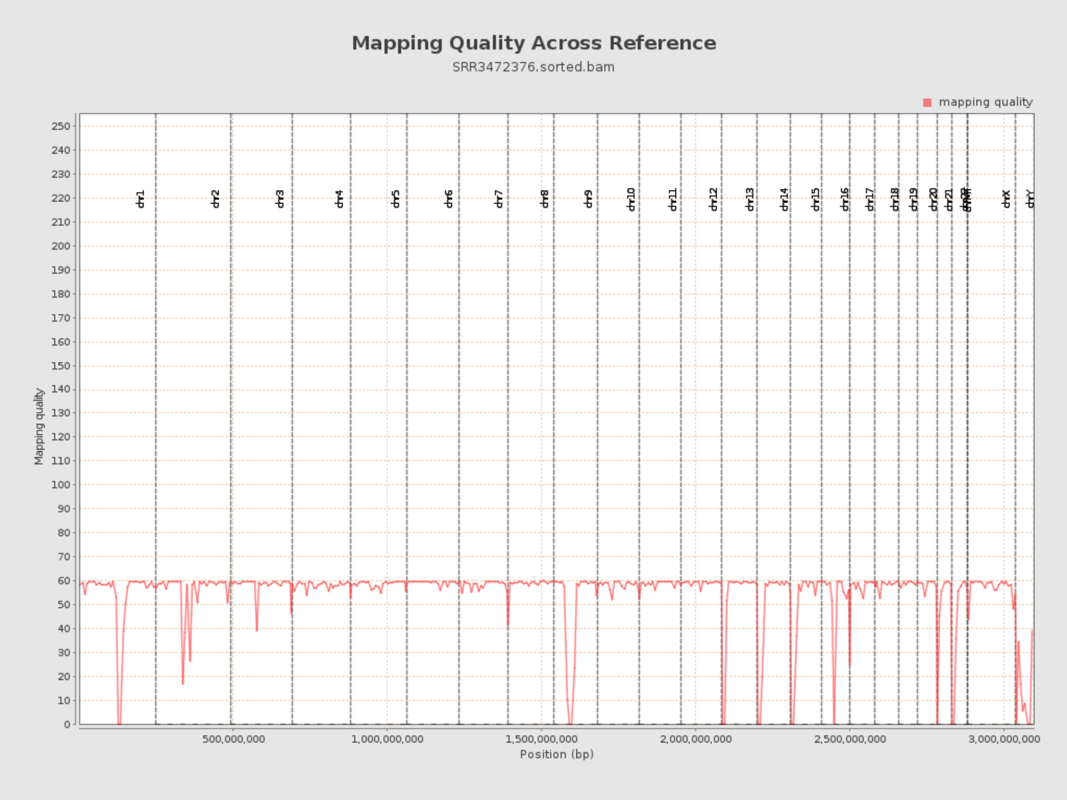
10. Results : Mapped Reads Clipping Profile



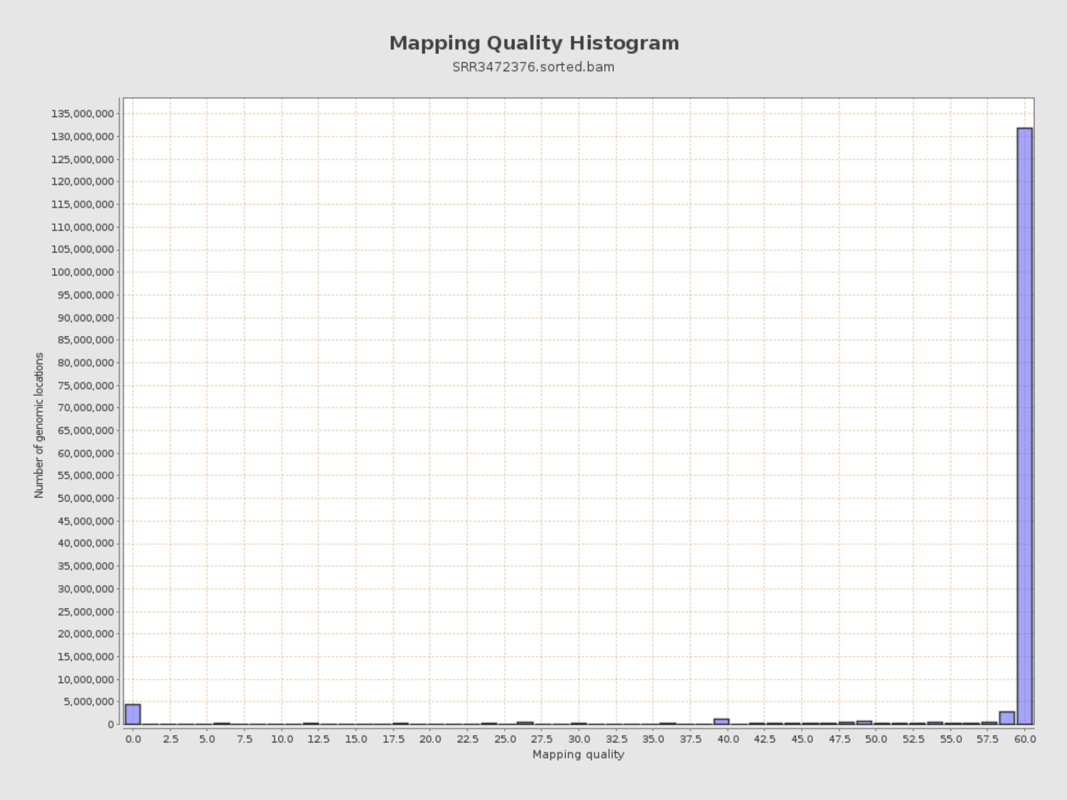
11. Results : Homopolymer Indels



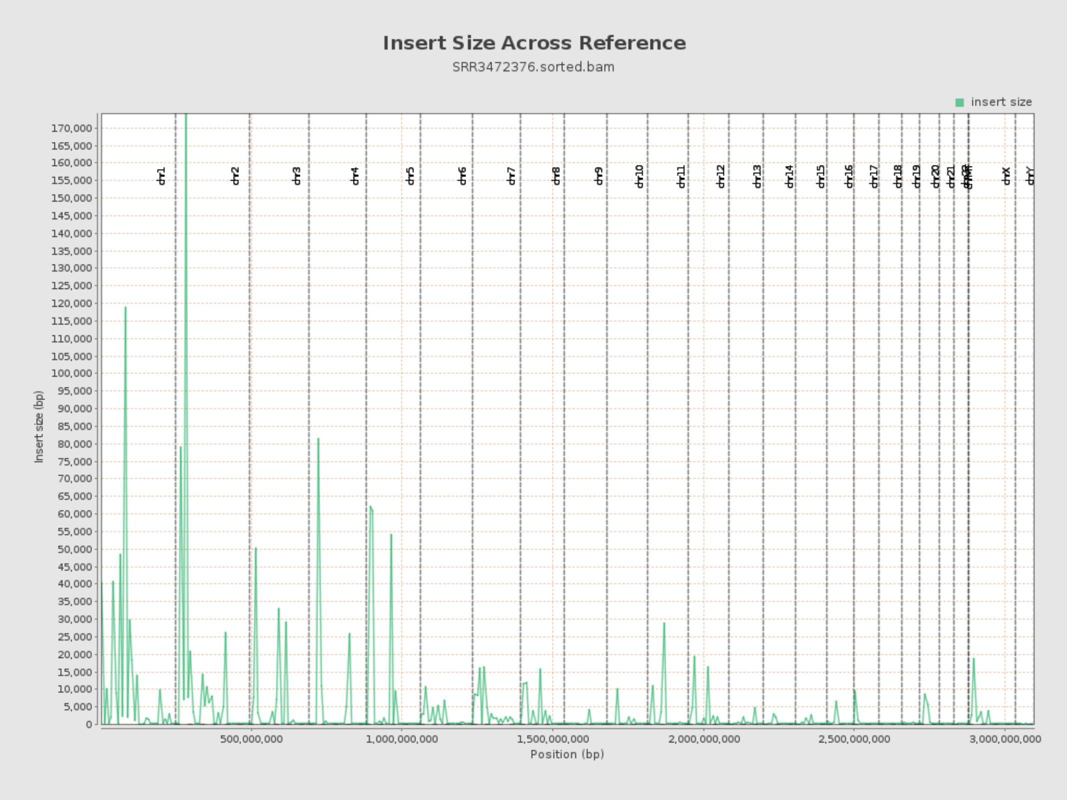
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram