Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 07:49:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472604.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_SRR3472604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472604_1.fastq.gz SRR3472604_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 07:49:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,833,956
Mapped reads	16,729,331 / 99.38%
Unmapped reads	104,625 / 0.62%
Mapped paired reads	16,729,331 / 99.38%
Mapped reads, first in pair	8,383,157 / 49.8%
Mapped reads, second in pair	8,346,174 / 49.58%
Mapped reads, both in pair	16,655,810 / 98.94%
Mapped reads, singletons	73,521 / 0.44%
Secondary alignments	0
Supplementary alignments	82,272 / 0.49%
Read min/max/mean length	30 / 101 / 99.69
Duplicated reads (estimated)	11,911,981 / 70.76%
Duplication rate	50.28%
Clipped reads	1,162,397 / 6.91%

2.2. ACGT Content

Number/percentage of A's	449,170,363 / 27.29%
Number/percentage of C's	375,081,497 / 22.79%
Number/percentage of T's	450,651,467 / 27.38%
Number/percentage of G's	370,421,527 / 22.51%
Number/percentage of N's	317,991 / 0.02%

GC Percentage	45.3%

2.3. Coverage

Mean	0.5317
Standard Deviation	29.603

2.4. Mapping Quality

Mean Mapping Quality	54.93

2.5. Insert size

Mean	17,531.45
Standard Deviation	1,304,320.93
P25/Median/P75	149 / 205 / 275

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	9,275,657
Insertions	102,779
Mapped reads with at least one insertion	0.6%
Deletions	79,246
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.49%

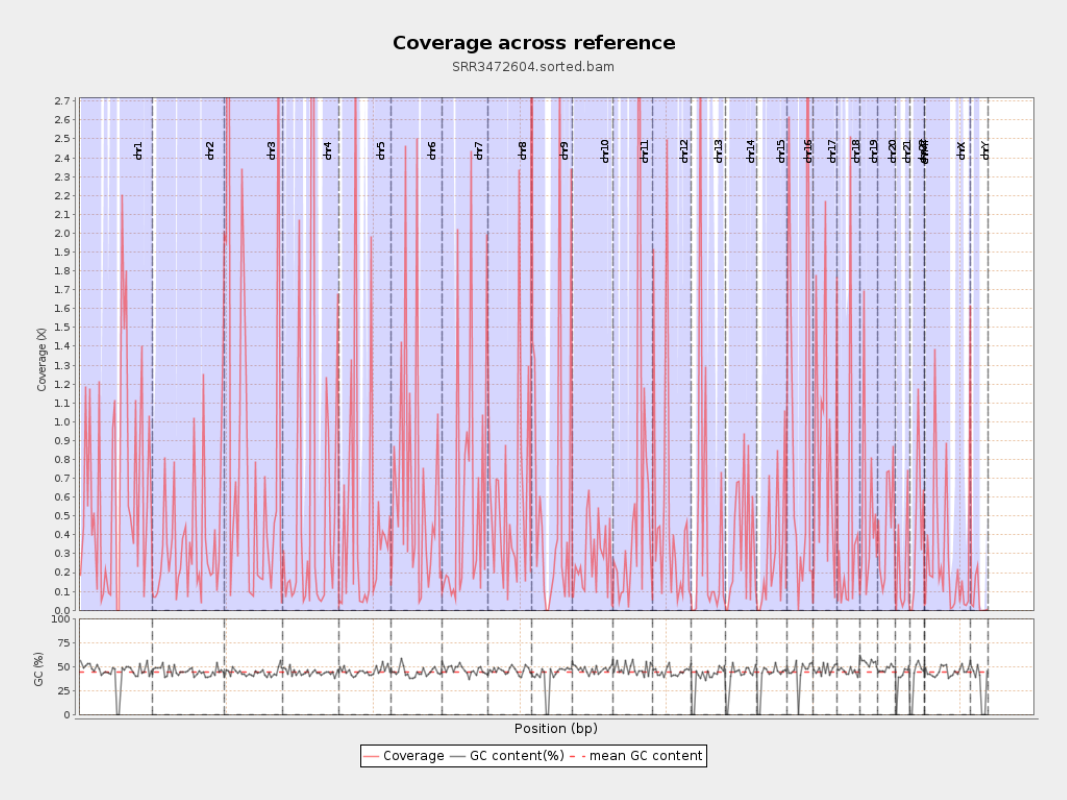
2.7. Chromosome stats

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

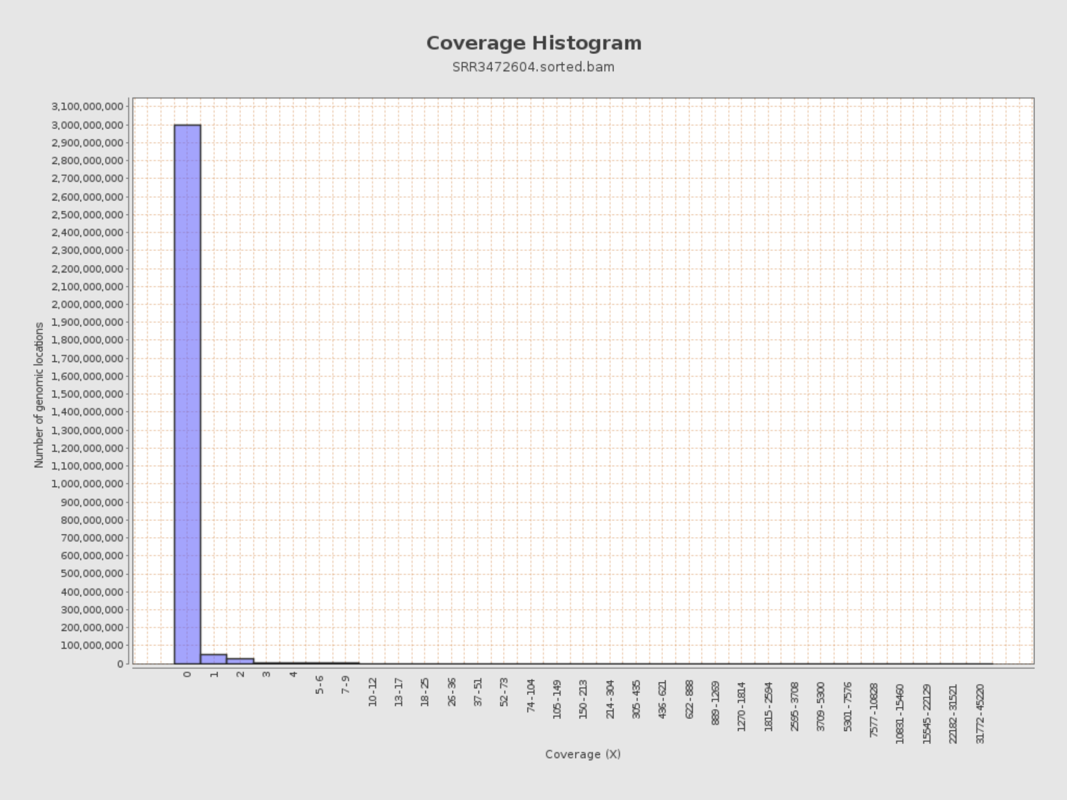
		bases	coverage	deviation
chr1	249250621	163118226	0.6544	20.6201
chr2	243199373	88926378	0.3657	13.8593
chr3	198022430	180323008	0.9106	41.7491
chr4	191154276	111566969	0.5836	39.9286
chr5	180915260	90944826	0.5027	23.0467
chr6	171115067	112544897	0.6577	29.6779
chr7	159138663	96974645	0.6094	24.145
chr8	146364022	82672632	0.5648	25.1731
chr9	141213431	92439354	0.6546	31.462
chr10	135534747	38393357	0.2833	12.4873
chr11	135006516	75761679	0.5612	74.299
chr12	133851895	65656797	0.4905	27.0325
chr13	115169878	50202933	0.4359	25.3028
chr14	107349540	38618803	0.3597	17.6864
chr15	102531392	30884948	0.3012	13.3765
chr16	90354753	83648098	0.9258	35.9112
chr17	81195210	72696332	0.8953	30.8062
chr18	78077248	31745807	0.4066	31.4703
chr19	59128983	31898421	0.5395	14.7551
chr20	63025520	28227601	0.4479	15.6507
chr21	48129895	10634778	0.221	15.2549
chr22	51304566	21460921	0.4183	17.3194
chrMT	16571	468	0.0282	0.1657
chrX	155270560	42850875	0.276	11.6493

chrY	59373566	3644762	0.0614	4.6488

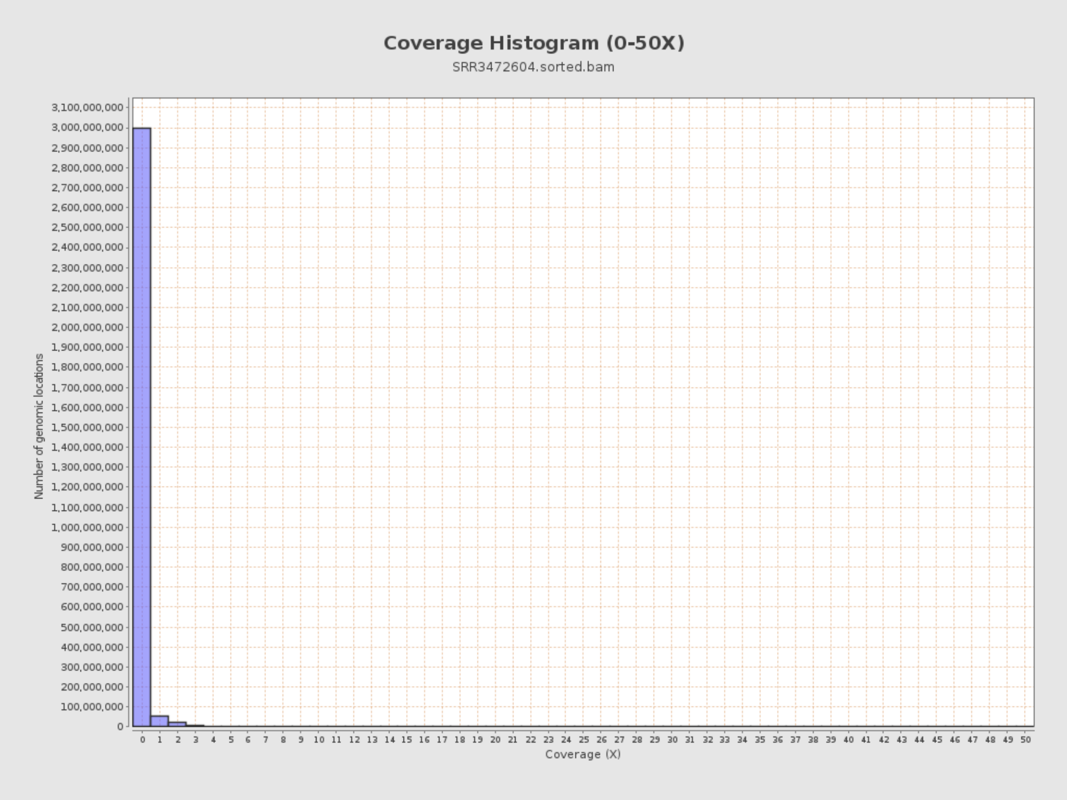
3. Results : Coverage across reference



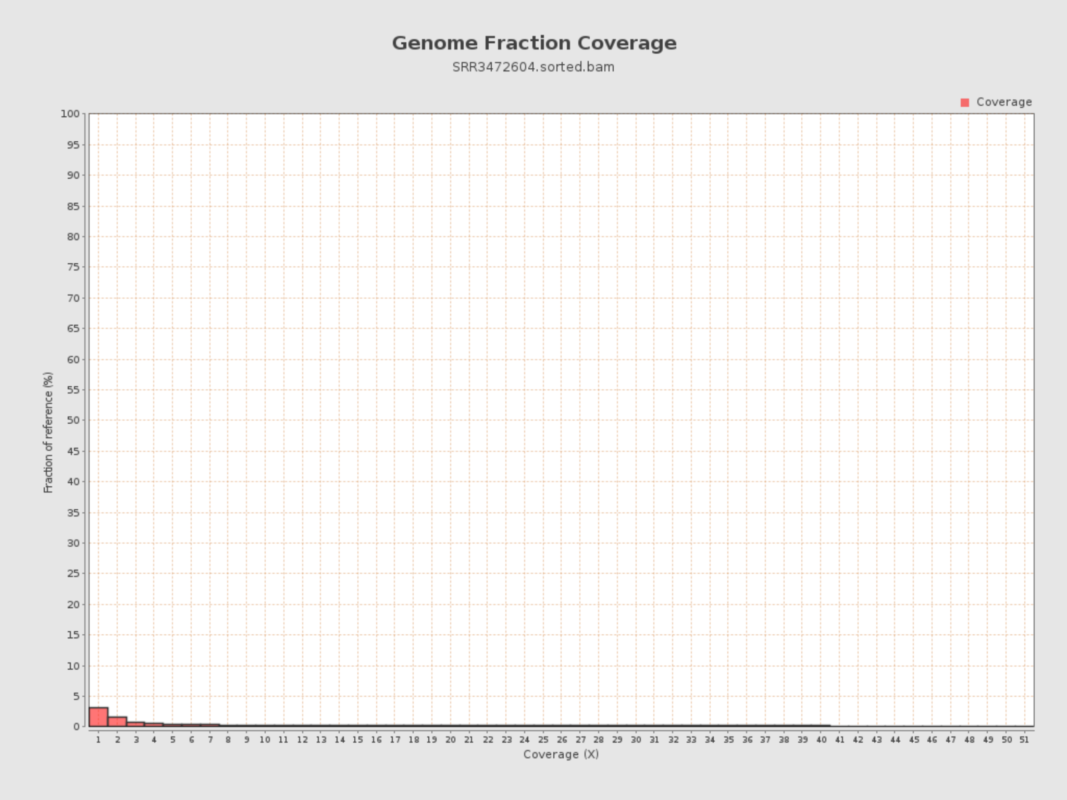
4. Results : Coverage Histogram



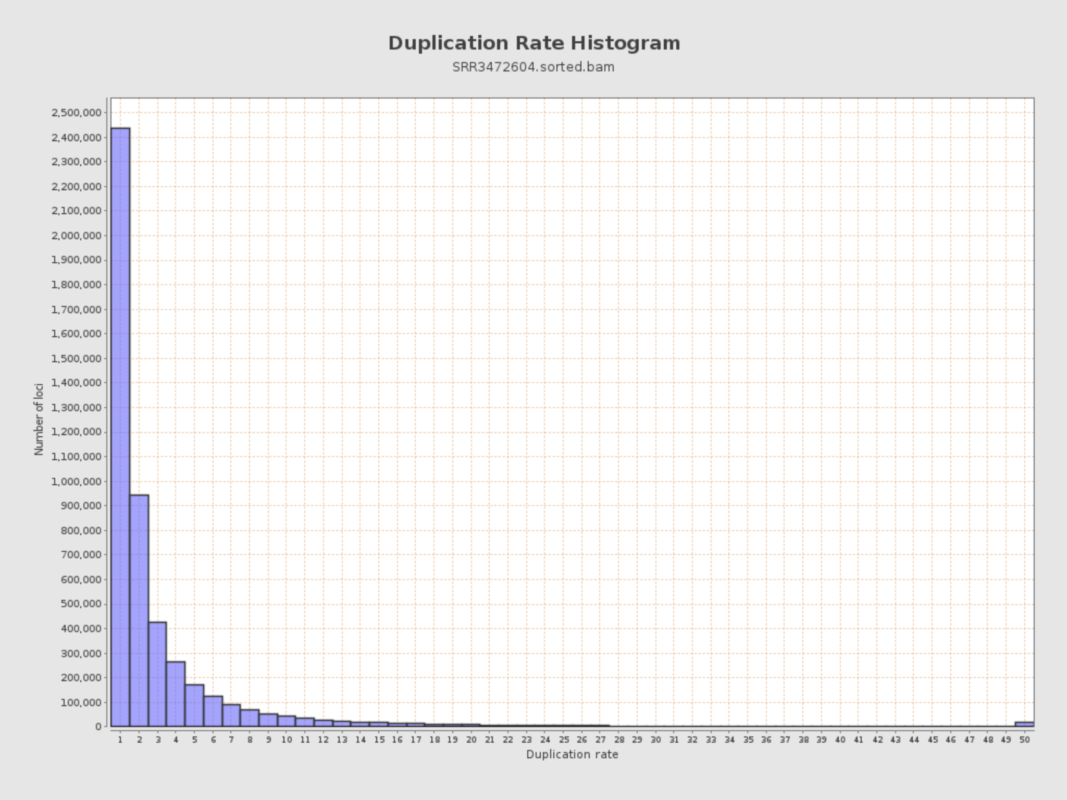
5. Results : Coverage Histogram (0-50X)



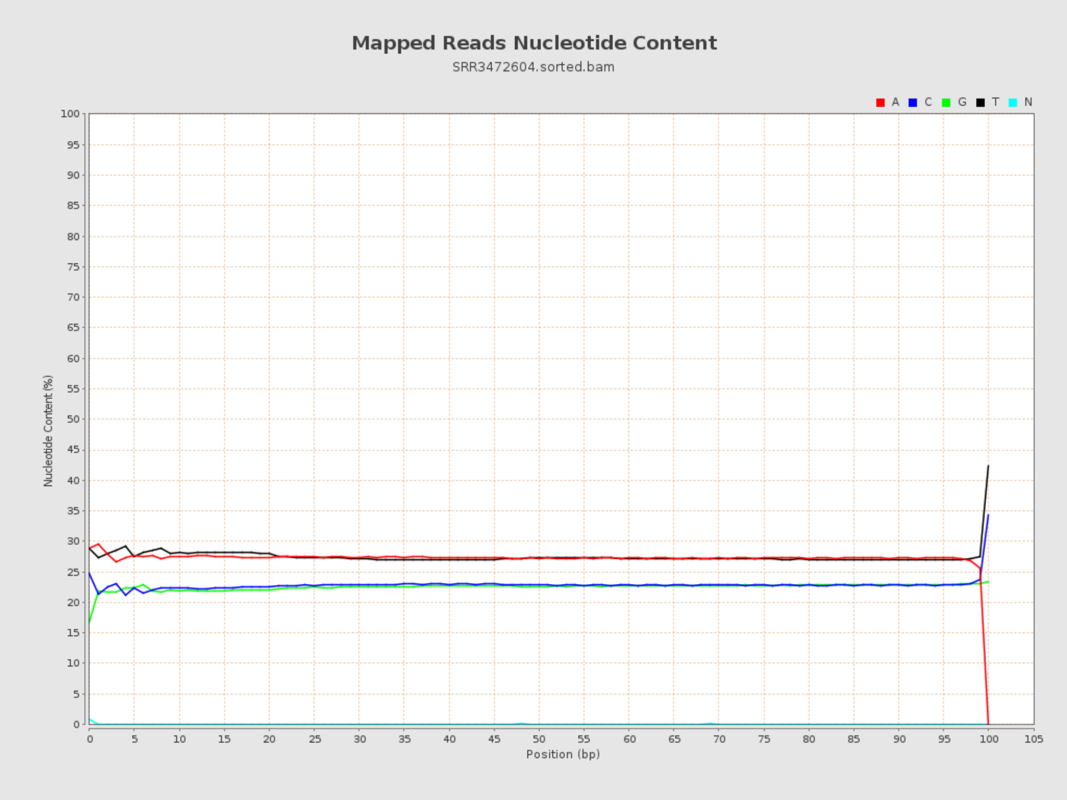
6. Results : Genome Fraction Coverage



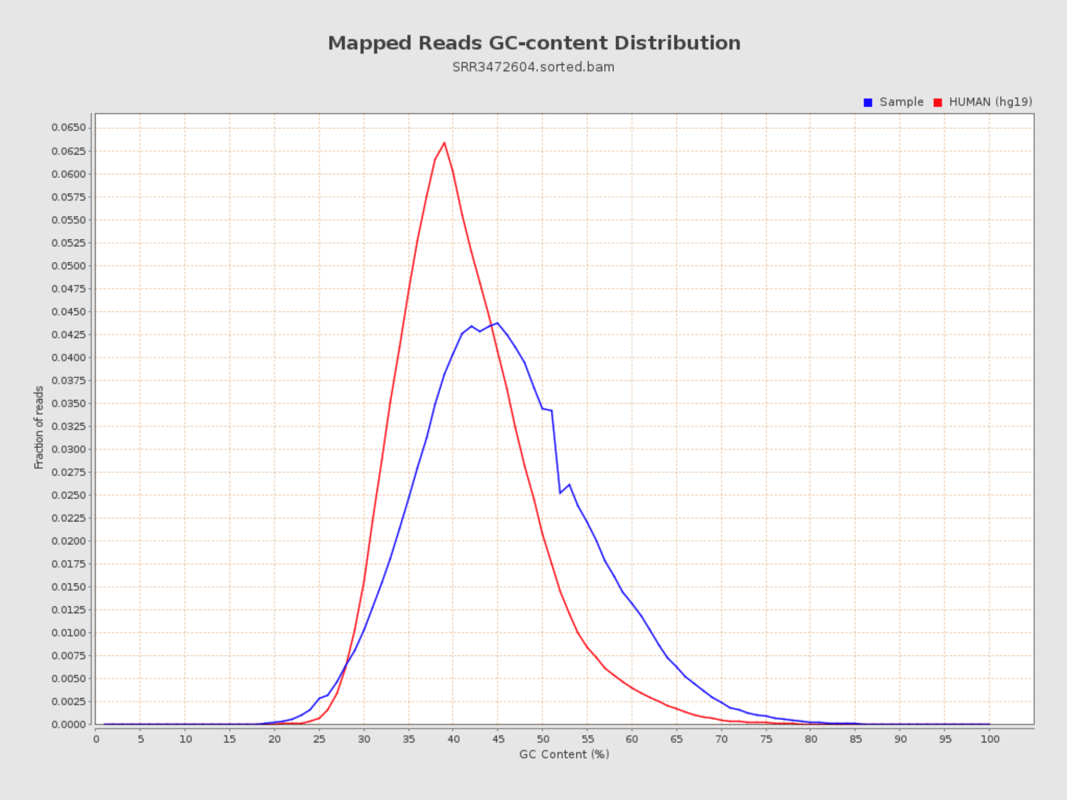
7. Results : Duplication Rate Histogram



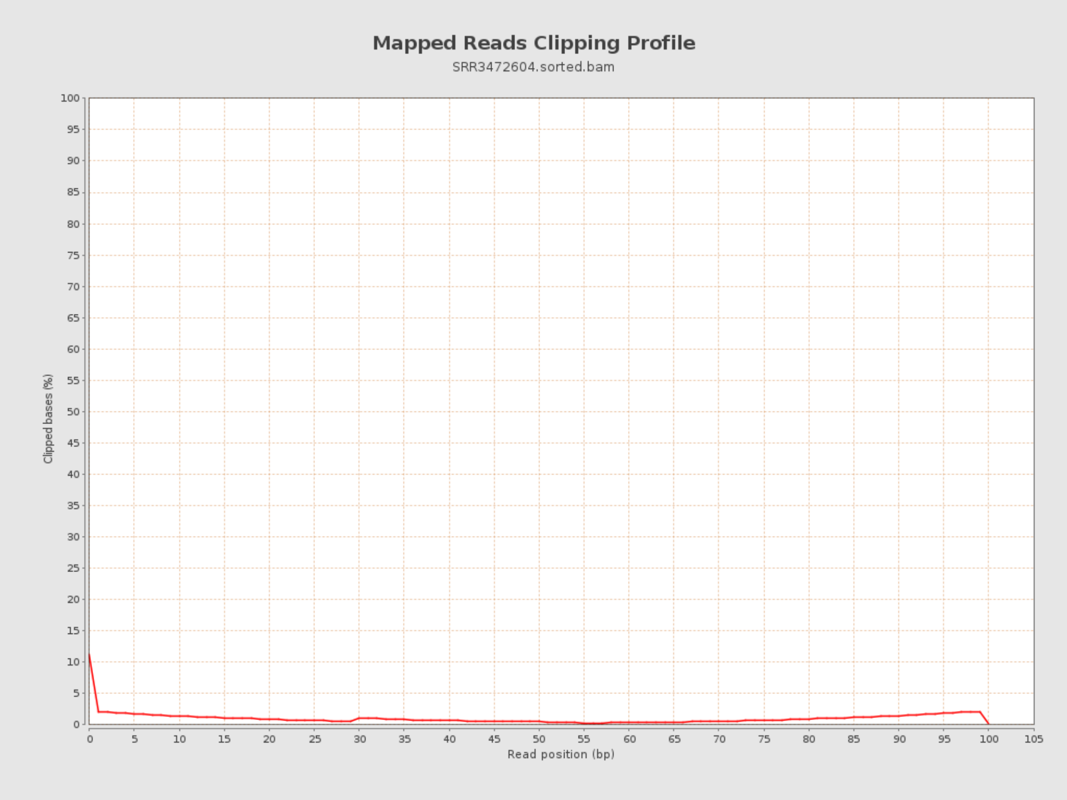
8. Results : Mapped Reads Nucleotide Content



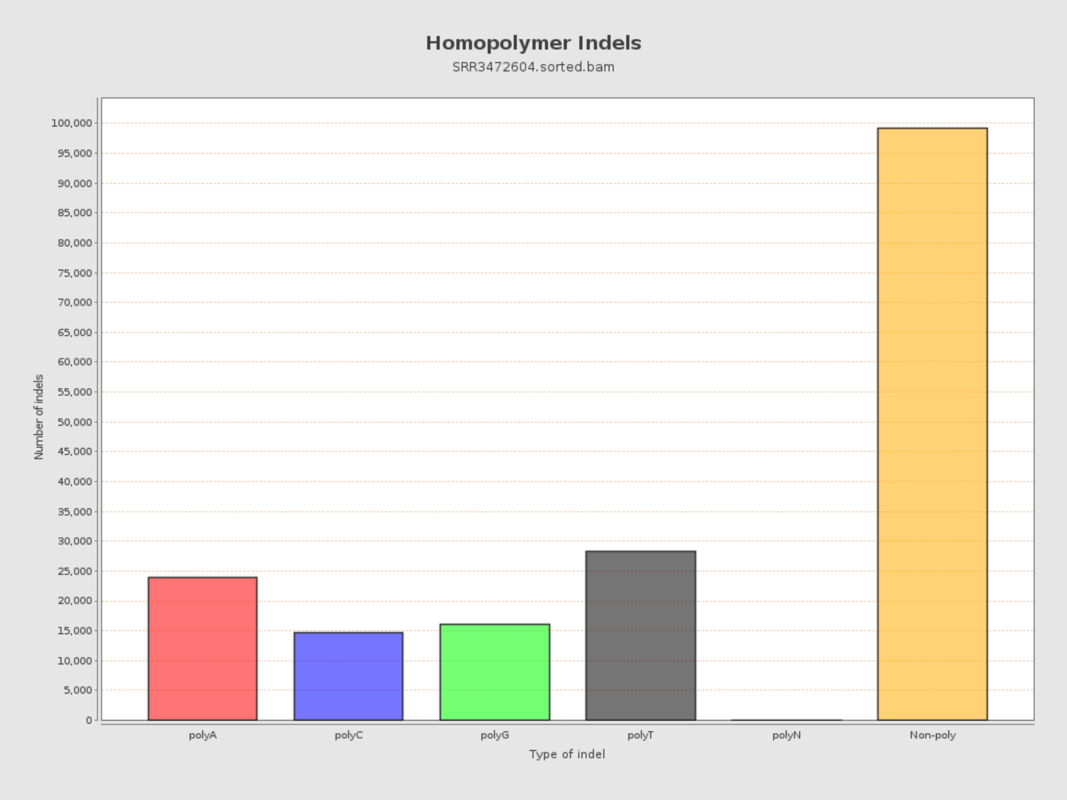
9. Results : Mapped Reads GC-content Distribution



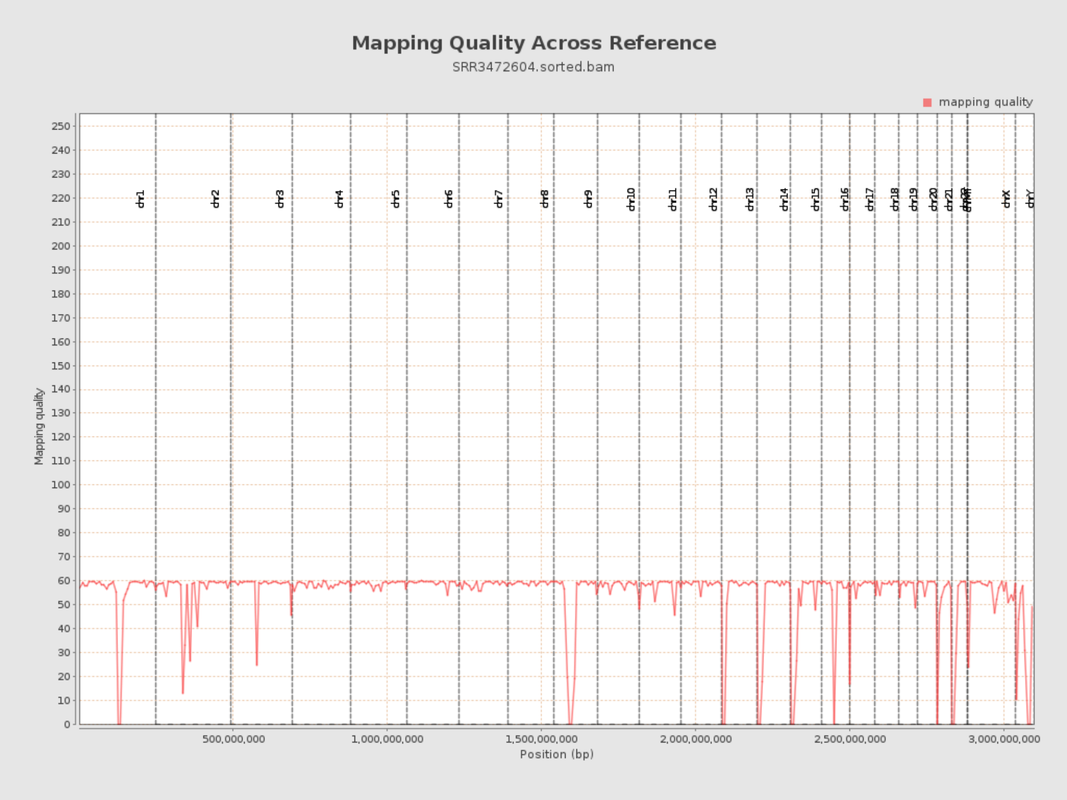
10. Results : Mapped Reads Clipping Profile



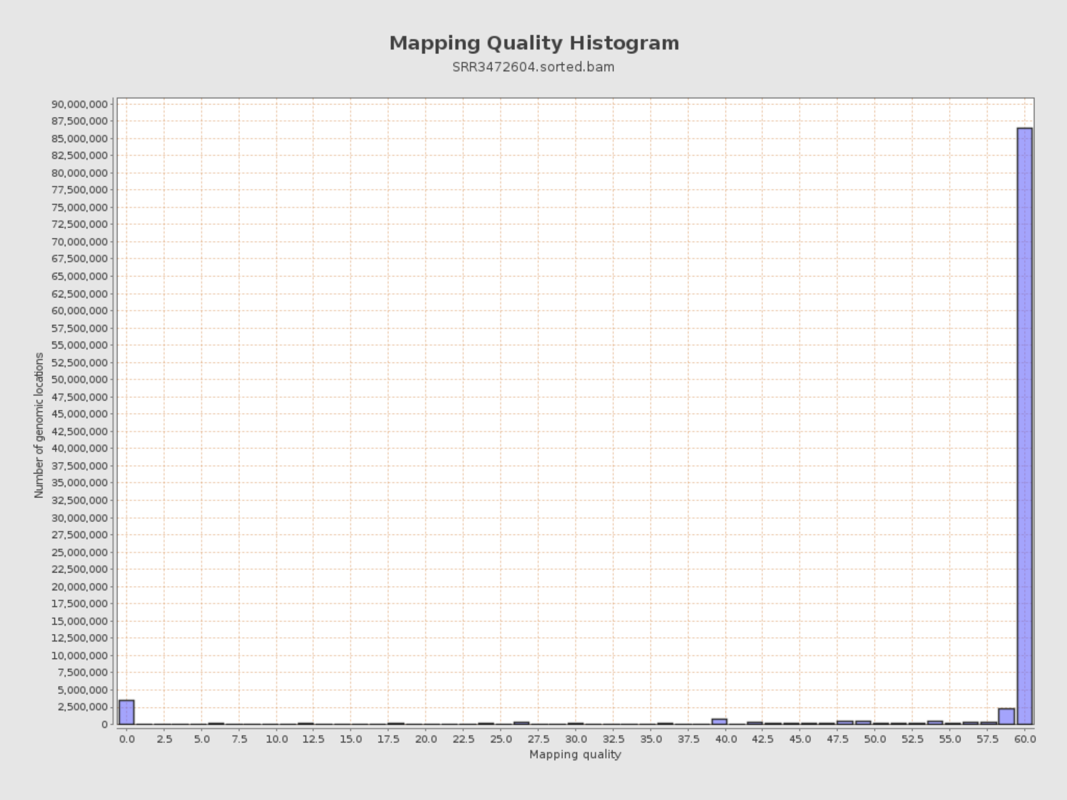
11. Results : Homopolymer Indels



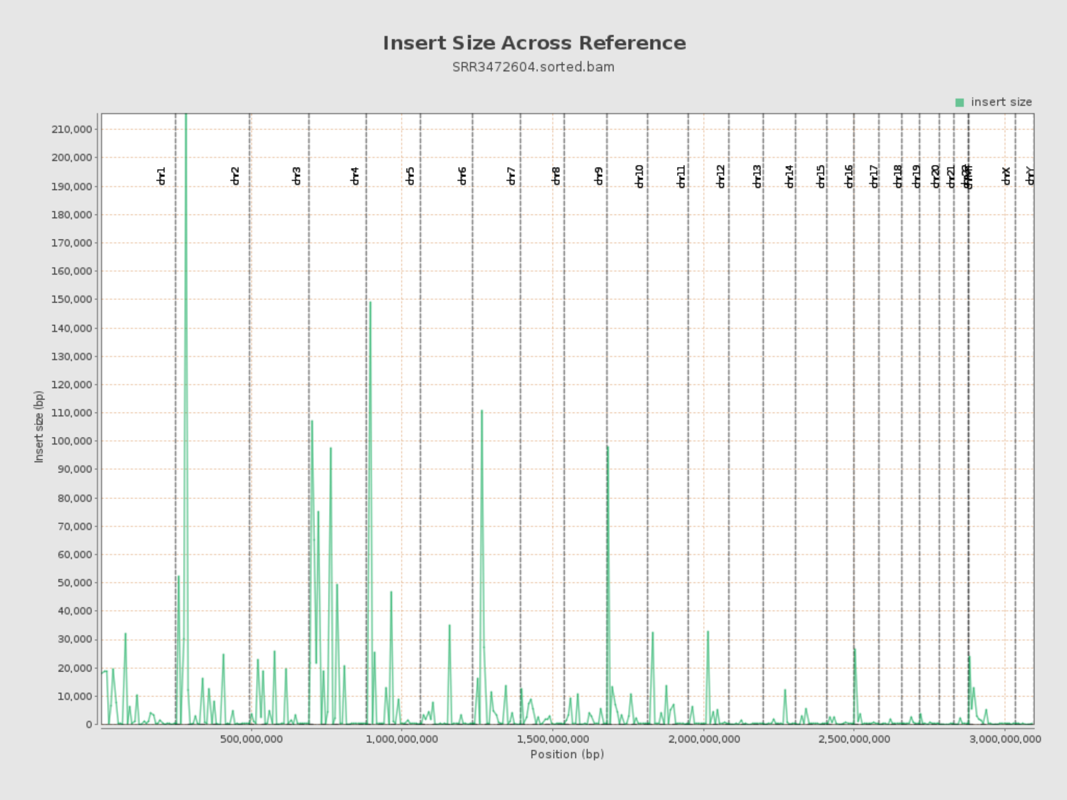
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram