Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 21:39:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472651.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_SRR3472651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472651_1.fastq.gz SRR3472651_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 21:39:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,123,666
Mapped reads	16,991,248 / 99.23%
Unmapped reads	132,418 / 0.77%
Mapped paired reads	16,991,248 / 99.23%
Mapped reads, first in pair	8,535,193 / 49.84%
Mapped reads, second in pair	8,456,055 / 49.38%
Mapped reads, both in pair	16,904,828 / 98.72%
Mapped reads, singletons	86,420 / 0.5%
Secondary alignments	0
Supplementary alignments	21,080 / 0.12%
Read min/max/mean length	30 / 101 / 99.55
Duplicated reads (estimated)	9,726,117 / 56.8%
Duplication rate	49.33%
Clipped reads	740,553 / 4.32%

2.2. ACGT Content

Number/percentage of A's	455,722,761 / 27.18%
Number/percentage of C's	382,139,972 / 22.79%
Number/percentage of T's	464,681,243 / 27.72%
Number/percentage of G's	373,671,695 / 22.29%
Number/percentage of N's	375,315 / 0.02%

GC Percentage	45.08%

2.3. Coverage

Mean	0.5417
Standard Deviation	11.6881

2.4. Mapping Quality

Mean Mapping Quality	54.8

2.5. Insert size

Mean	16,732.87
Standard Deviation	1,328,757.66
P25/Median/P75	158 / 218 / 293

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	7,036,319
Insertions	74,287
Mapped reads with at least one insertion	0.43%
Deletions	90,950
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.15%

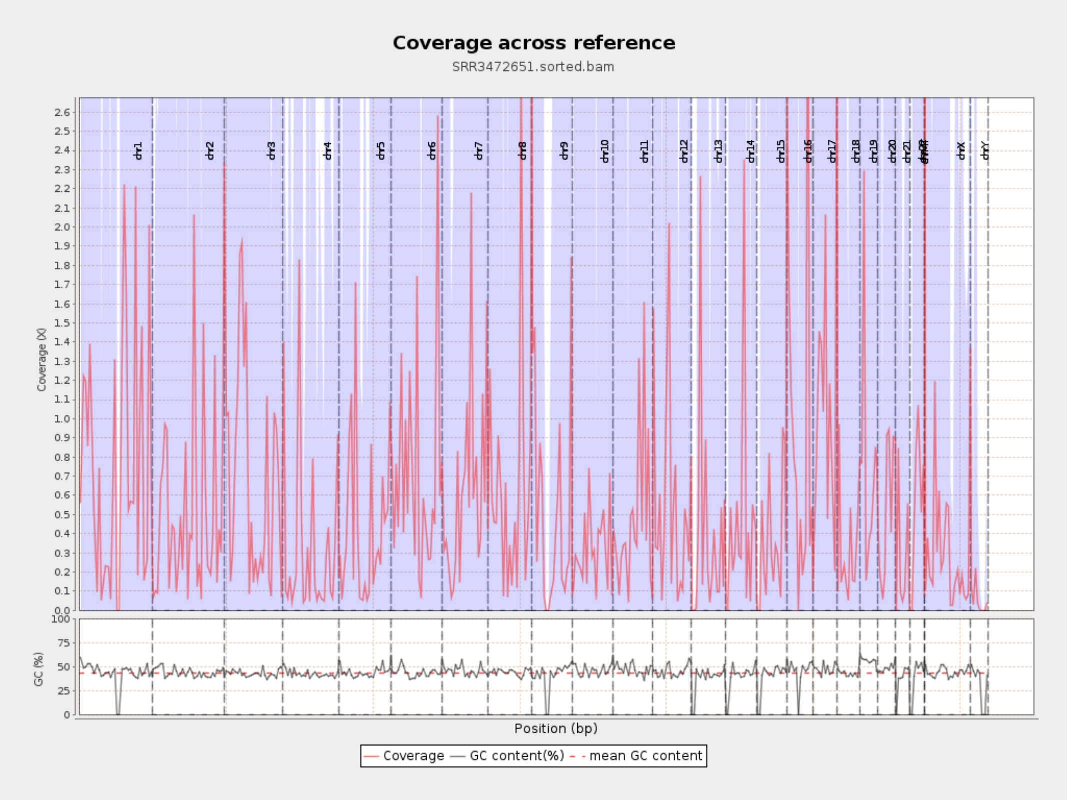
2.7. Chromosome stats

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

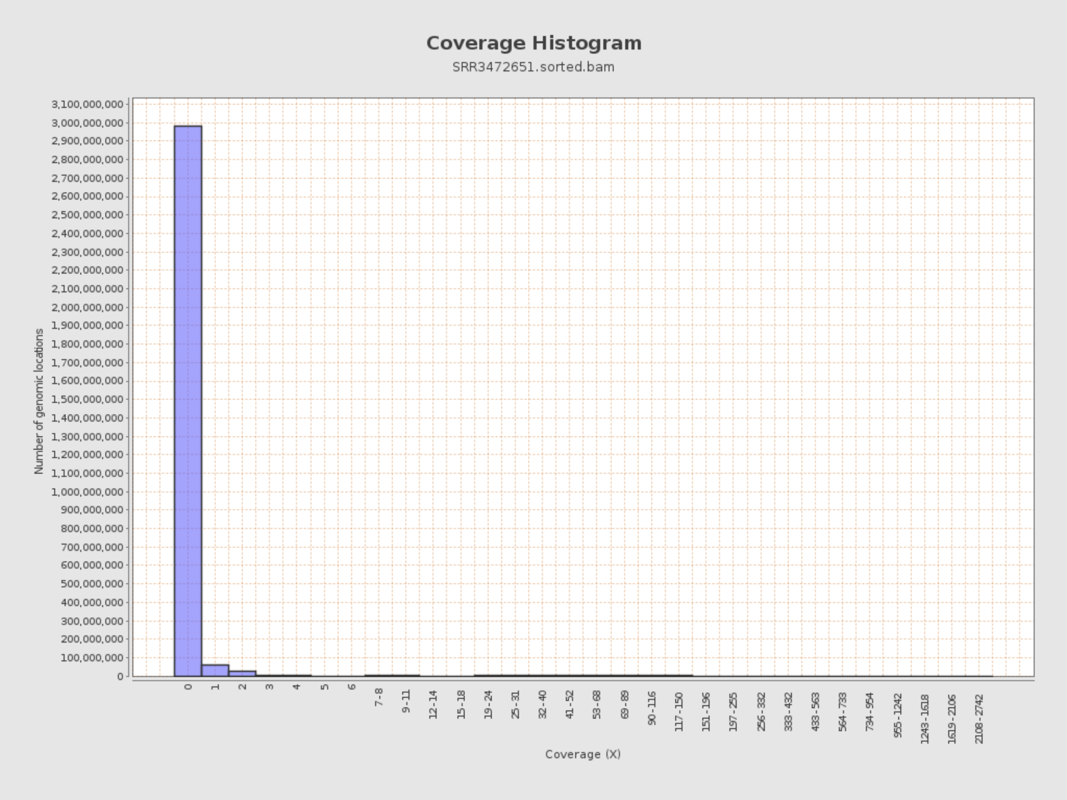
		bases	coverage	deviation
chr1	249250621	193922089	0.778	14.7113
chr2	243199373	121260549	0.4986	11.6876
chr3	198022430	142700311	0.7206	12.4184
chr4	191154276	60488717	0.3164	9.1063
chr5	180915260	81155638	0.4486	10.5366
chr6	171115067	119284018	0.6971	12.6486
chr7	159138663	102507086	0.6441	14.1228
chr8	146364022	94235514	0.6438	12.6955
chr9	141213431	76711207	0.5432	10.1831
chr10	135534747	43141172	0.3183	8.1922
chr11	135006516	65311069	0.4838	11.1037
chr12	133851895	75805340	0.5663	10.2247
chr13	115169878	43342577	0.3763	10.8551
chr14	107349540	46561388	0.4337	10.4287
chr15	102531392	37092398	0.3618	8.6258
chr16	90354753	90795982	1.0049	19.8903
chr17	81195210	87238584	1.0744	17.4506
chr18	78077248	25845267	0.331	7.8247
chr19	59128983	46496685	0.7864	11.1628
chr20	63025520	33000560	0.5236	10.8581
chr21	48129895	13431152	0.2791	12.5052
chr22	51304566	28208863	0.5498	12.0728
chrMT	16571	207861	12.5437	6.8135
chrX	155270560	44944183	0.2895	5.0278

chrY	59373566	3130501	0.0527	1.7931

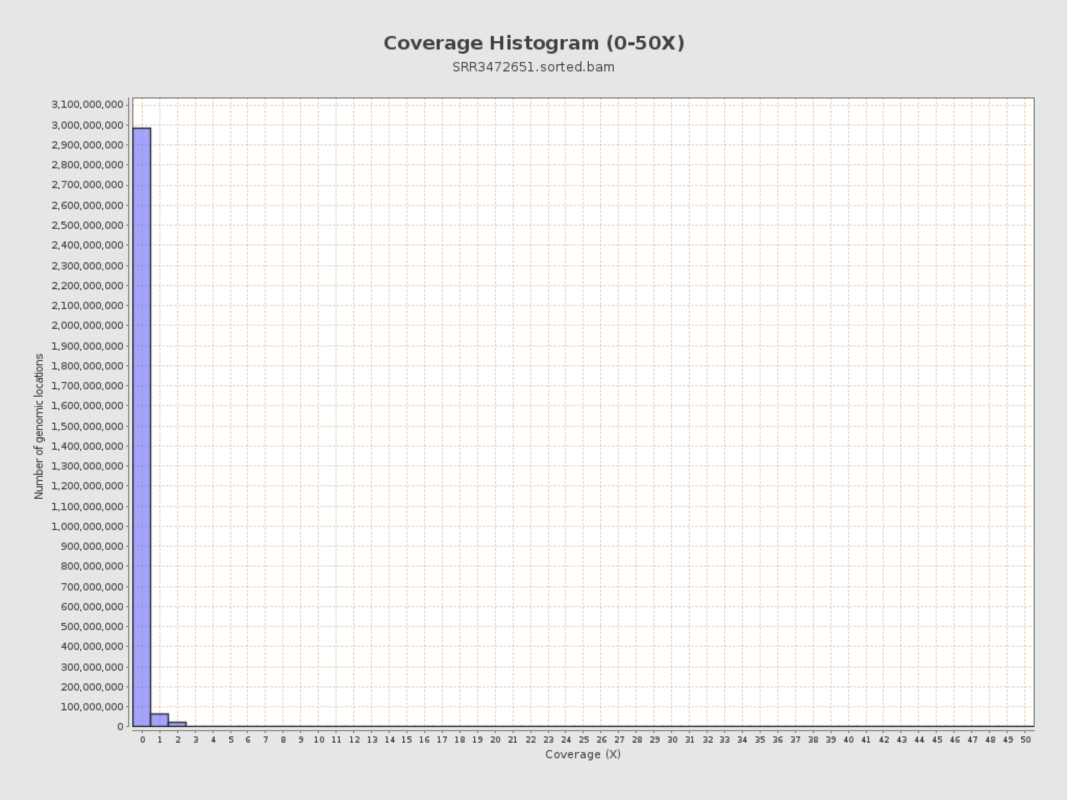
3. Results : Coverage across reference



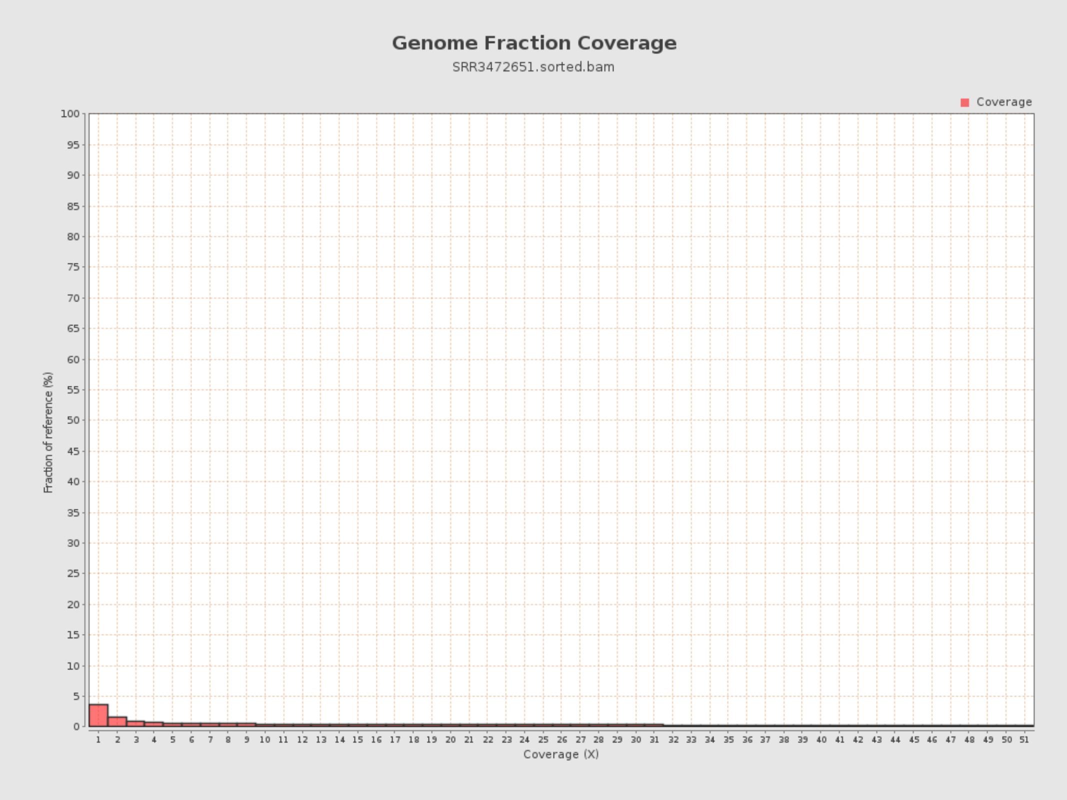
4. Results : Coverage Histogram



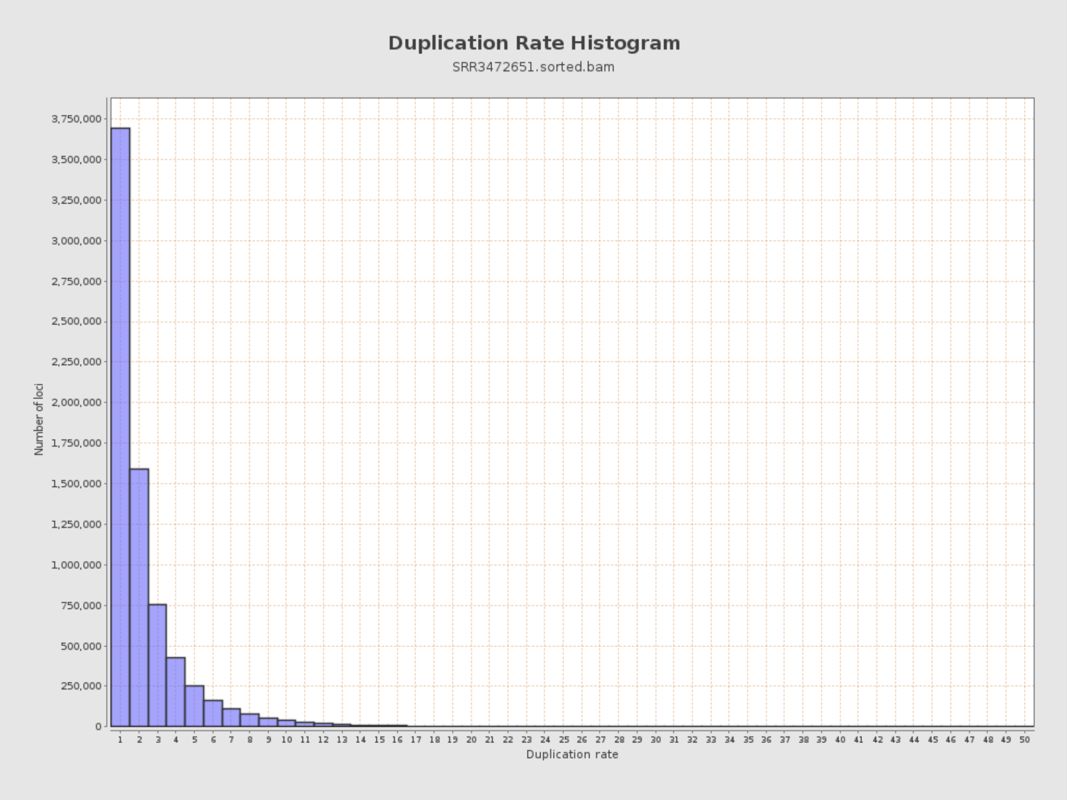
5. Results : Coverage Histogram (0-50X)



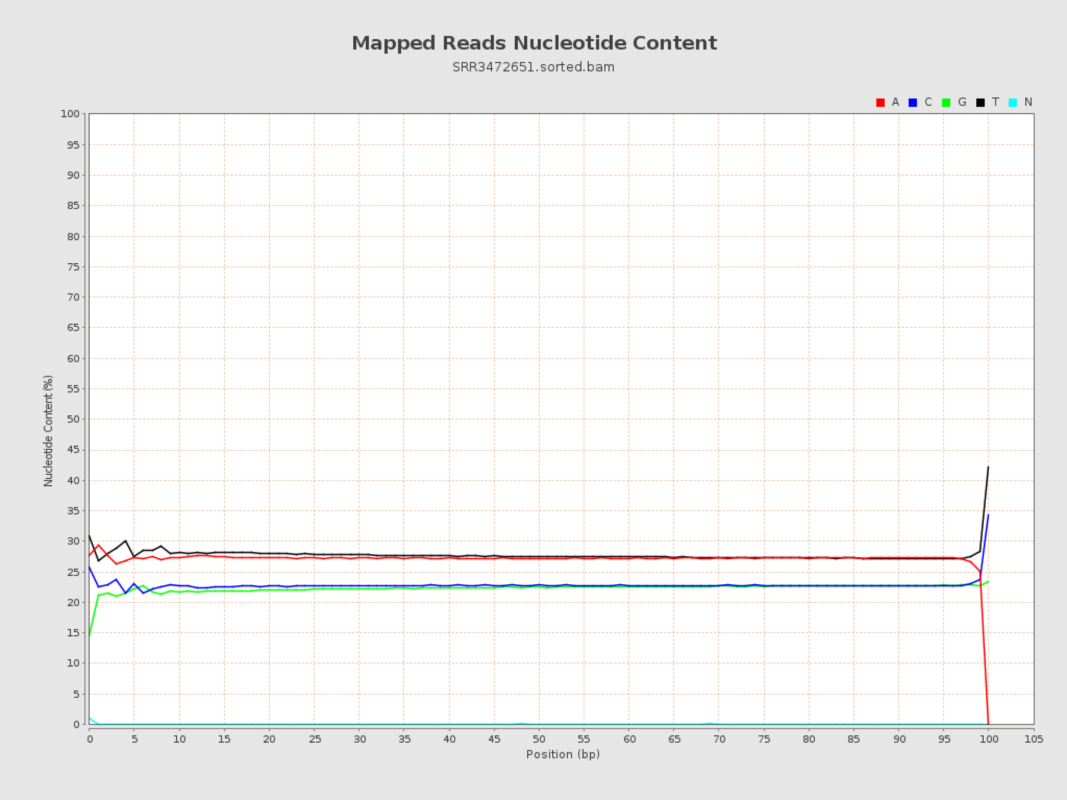
6. Results : Genome Fraction Coverage



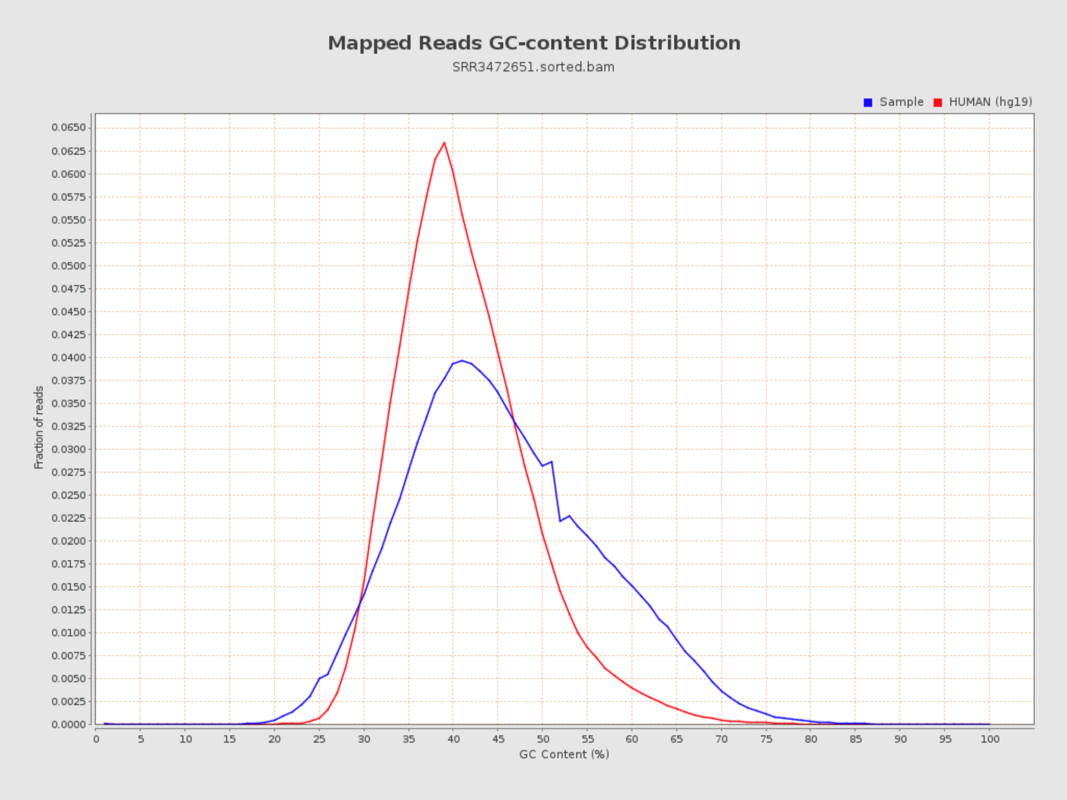
7. Results : Duplication Rate Histogram



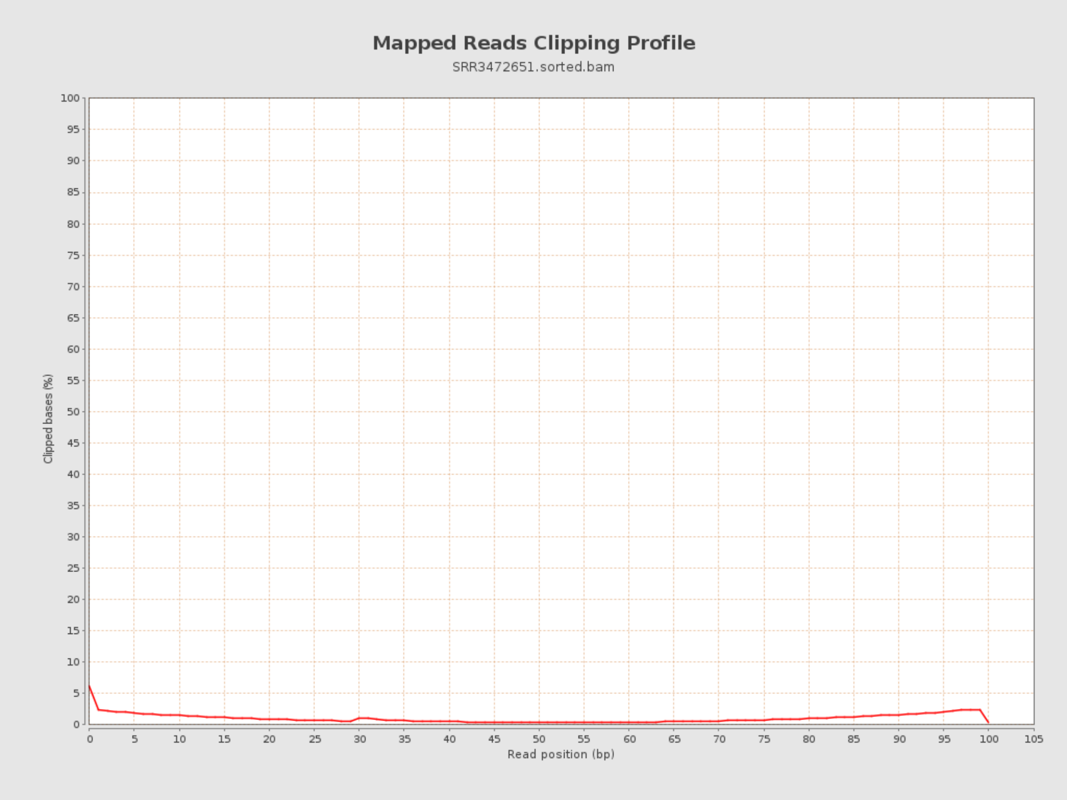
8. Results : Mapped Reads Nucleotide Content



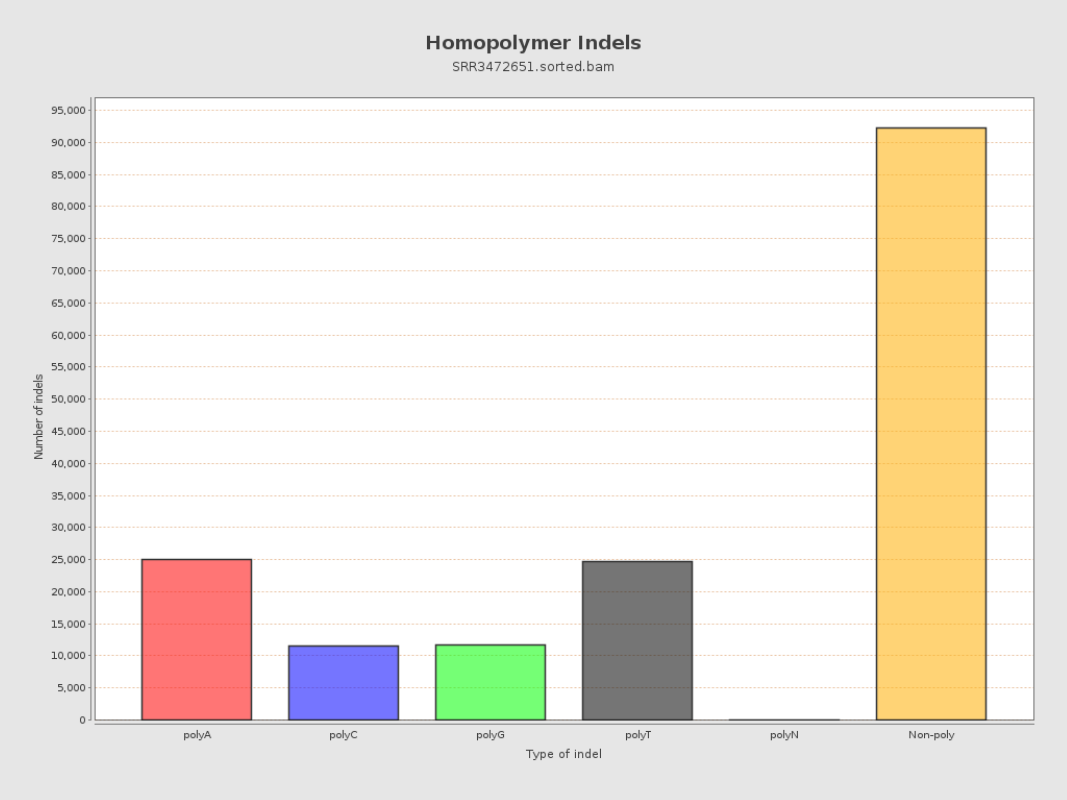
9. Results : Mapped Reads GC-content Distribution



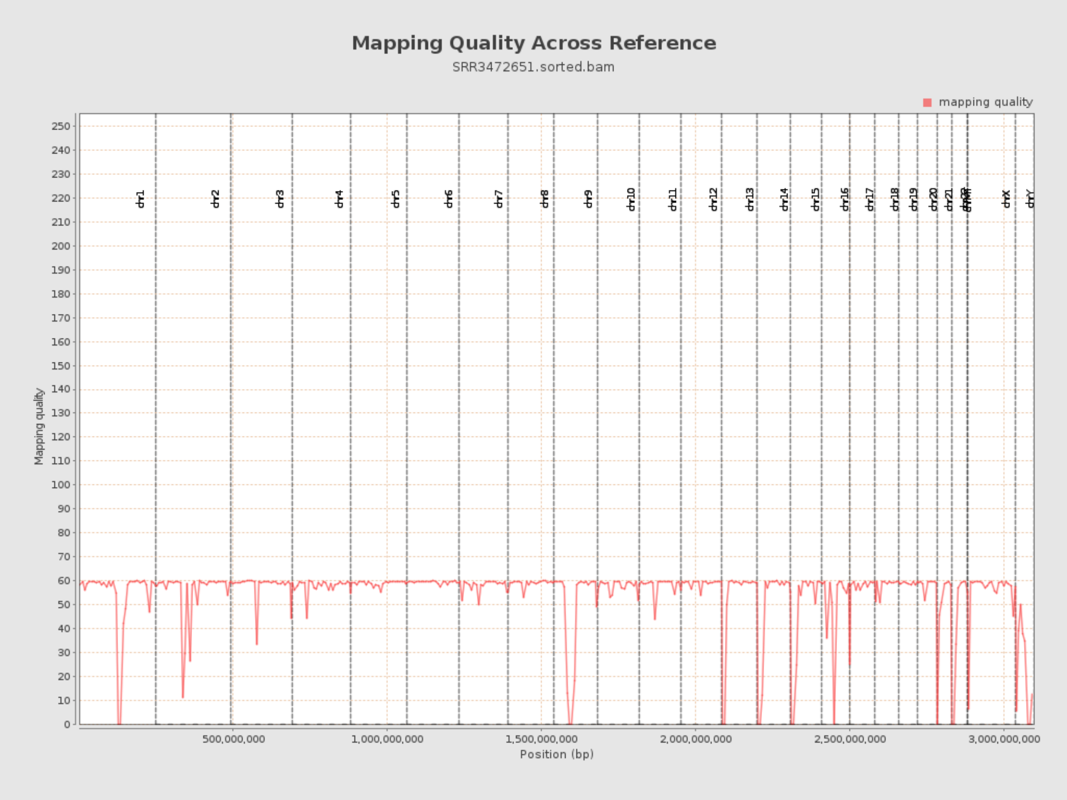
10. Results : Mapped Reads Clipping Profile



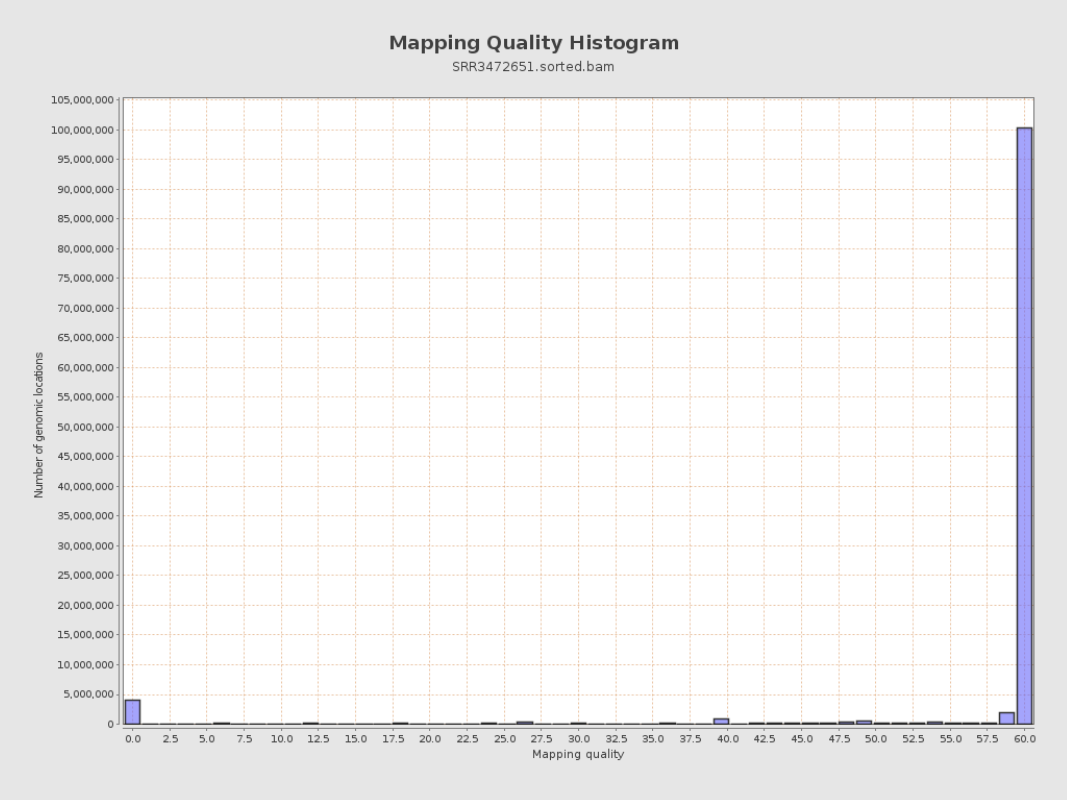
11. Results : Homopolymer Indels



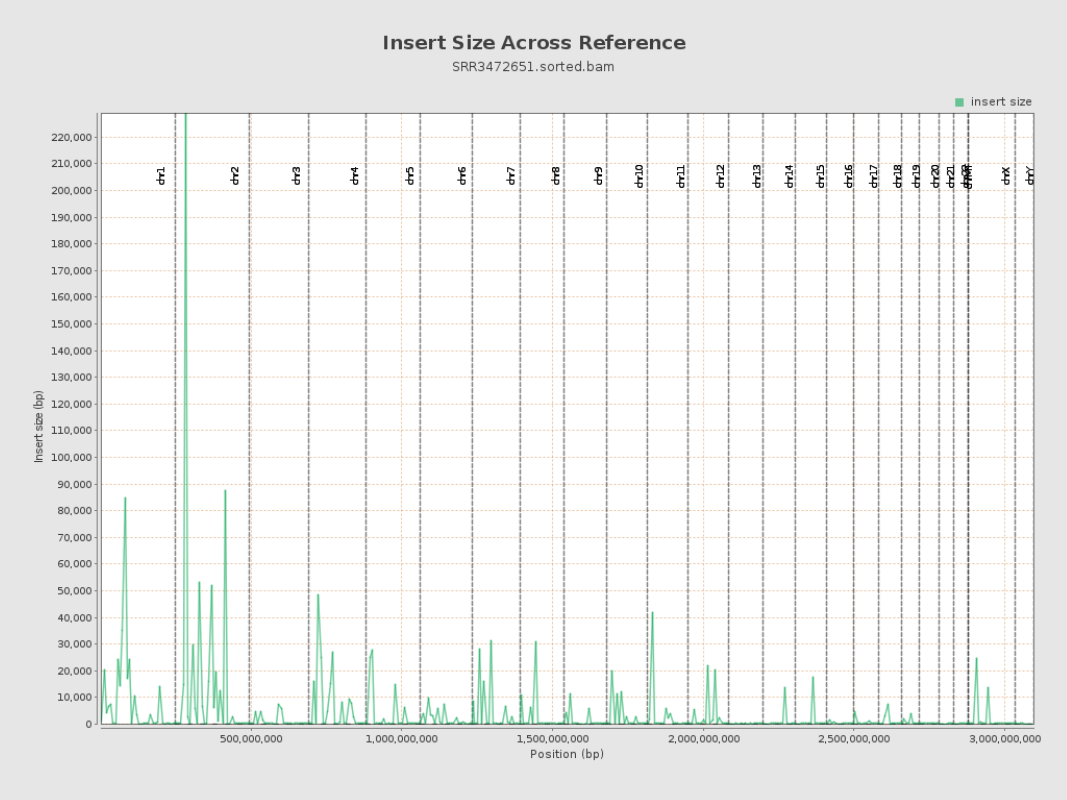
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram