Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:34:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472551.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_SRR3472551 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472551_1.fastq.gz SRR3472551_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:34:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472551.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,919,372
Mapped reads	18,665,651 / 98.66%
Unmapped reads	253,721 / 1.34%
Mapped paired reads	18,665,651 / 98.66%
Mapped reads, first in pair	9,379,066 / 49.57%
Mapped reads, second in pair	9,286,585 / 49.09%
Mapped reads, both in pair	18,520,232 / 97.89%
Mapped reads, singletons	145,419 / 0.77%
Secondary alignments	0
Supplementary alignments	62,254 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	11,885,756 / 62.82%
Duplication rate	46.97%
Clipped reads	1,502,780 / 7.94%

2.2. ACGT Content

Number/percentage of A's	505,644,358 / 27.53%
Number/percentage of C's	415,091,560 / 22.6%
Number/percentage of T's	503,279,084 / 27.4%
Number/percentage of G's	412,577,283 / 22.46%
Number/percentage of N's	287,154 / 0.02%

GC Percentage	45.06%

2.3. Coverage

Mean	0.5934
Standard Deviation	19.3345

2.4. Mapping Quality

Mean Mapping Quality	55.2

2.5. Insert size

Mean	24,668.1
Standard Deviation	1,573,879.9
P25/Median/P75	166 / 230 / 310

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,875,672
Insertions	99,516
Mapped reads with at least one insertion	0.53%
Deletions	90,412
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.61%

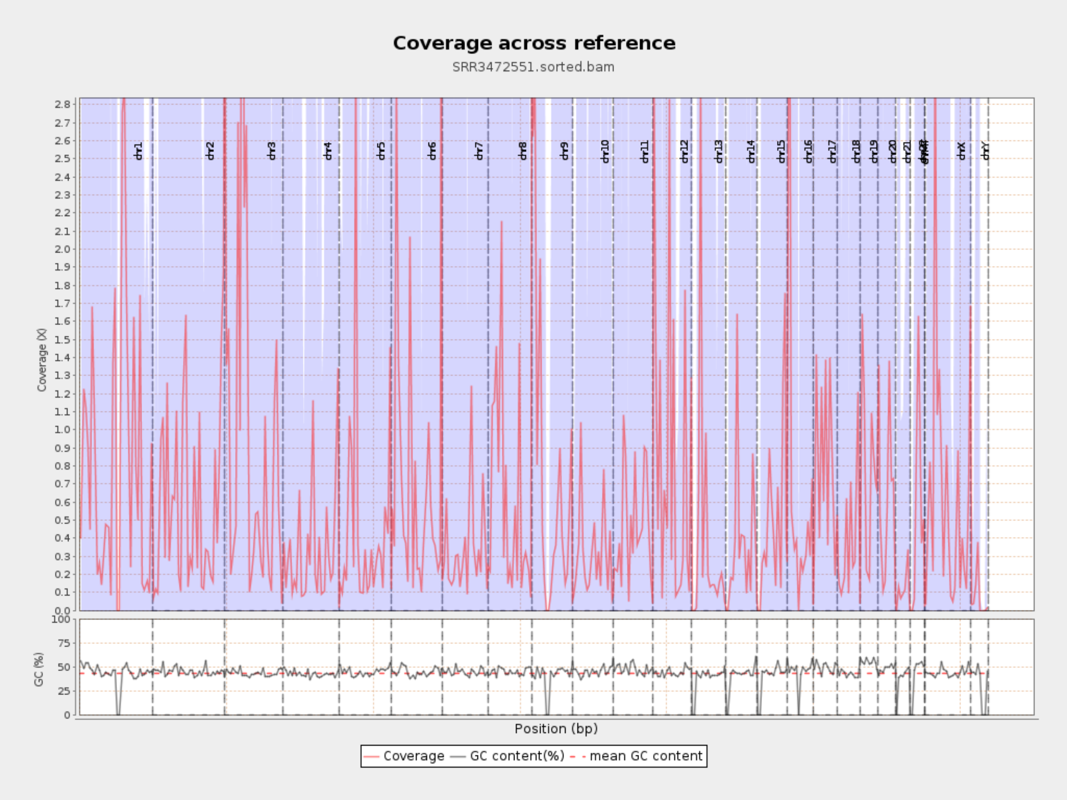
2.7. Chromosome stats

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

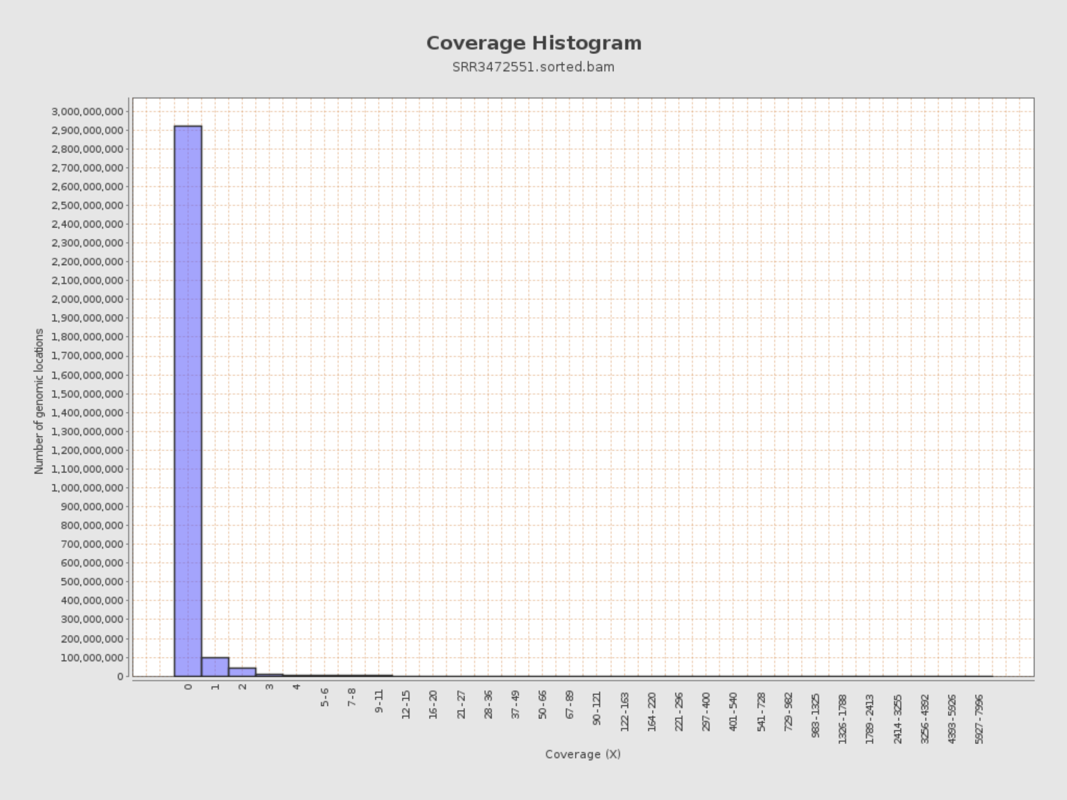
		bases	coverage	deviation
chr1	249250621	208438522	0.8363	24.4608
chr2	243199373	143250931	0.589	23.2357
chr3	198022430	207102966	1.0459	25.4753
chr4	191154276	63742141	0.3335	10.5477
chr5	180915260	85943784	0.475	14.9894
chr6	171115067	122799257	0.7176	23.1865
chr7	159138663	56119149	0.3526	9.3592
chr8	146364022	90963573	0.6215	19.584
chr9	141213431	107875443	0.7639	19.154
chr10	135534747	43519914	0.3211	12.7373
chr11	135006516	65099164	0.4822	14.9537
chr12	133851895	118550783	0.8857	27.9891
chr13	115169878	46368984	0.4026	18.8859
chr14	107349540	40651828	0.3787	12.7966
chr15	102531392	53331099	0.5201	17.1787
chr16	90354753	64584542	0.7148	23.5473
chr17	81195210	63878932	0.7867	20.6041
chr18	78077248	31365700	0.4017	13.6599
chr19	59128983	46915525	0.7934	22.0493
chr20	63025520	40437321	0.6416	17.7136
chr21	48129895	6157821	0.1279	3.9059
chr22	51304566	26615090	0.5188	16.1816
chrMT	16571	3526	0.2128	0.7051
chrX	155270560	98723914	0.6358	20.0256

chrY	59373566	4653122	0.0784	6.2118

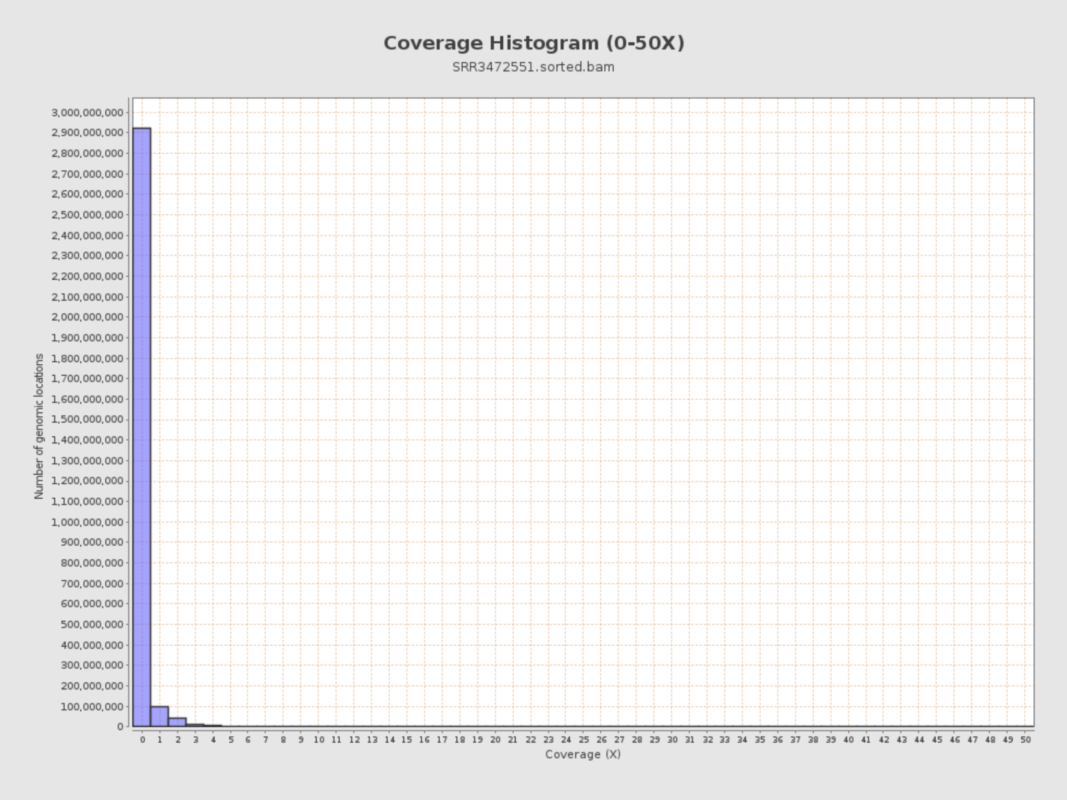
3. Results : Coverage across reference



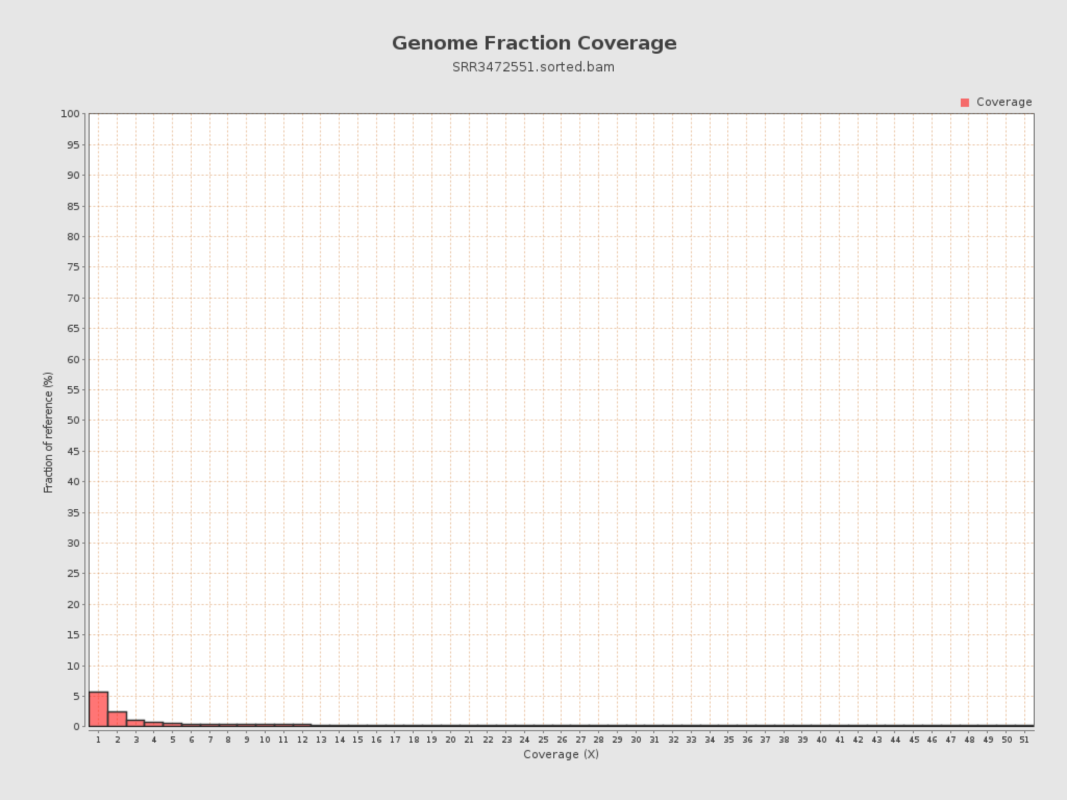
4. Results : Coverage Histogram



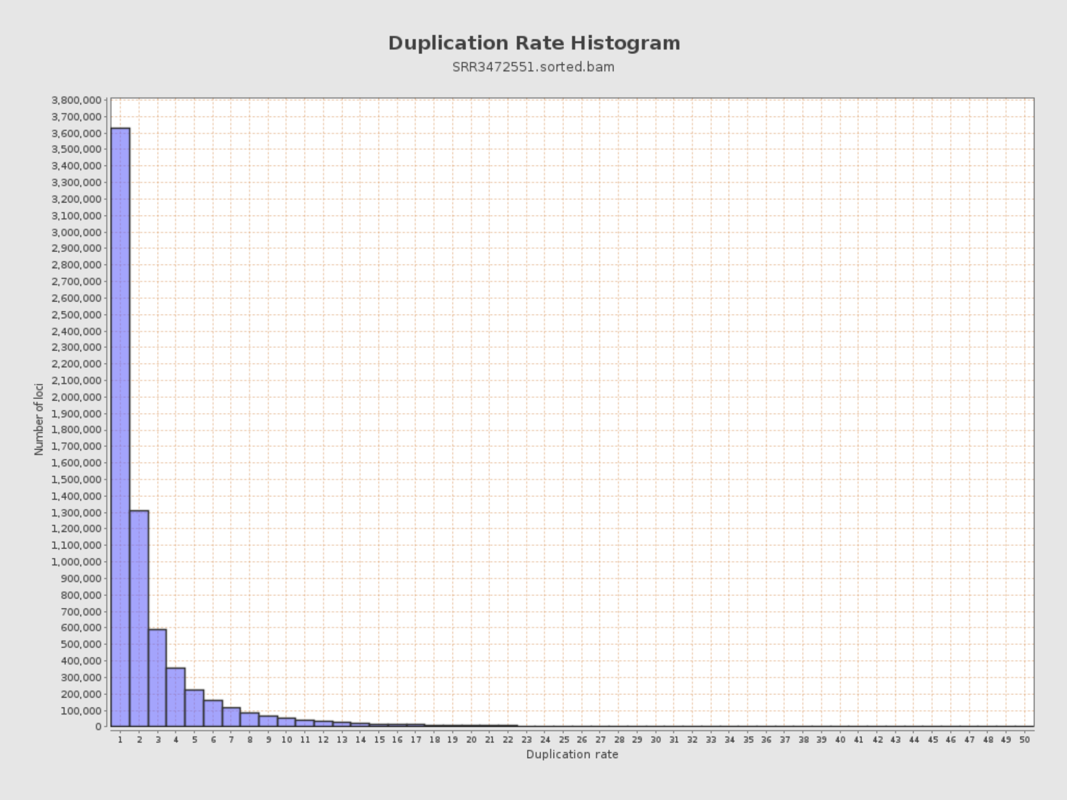
5. Results : Coverage Histogram (0-50X)



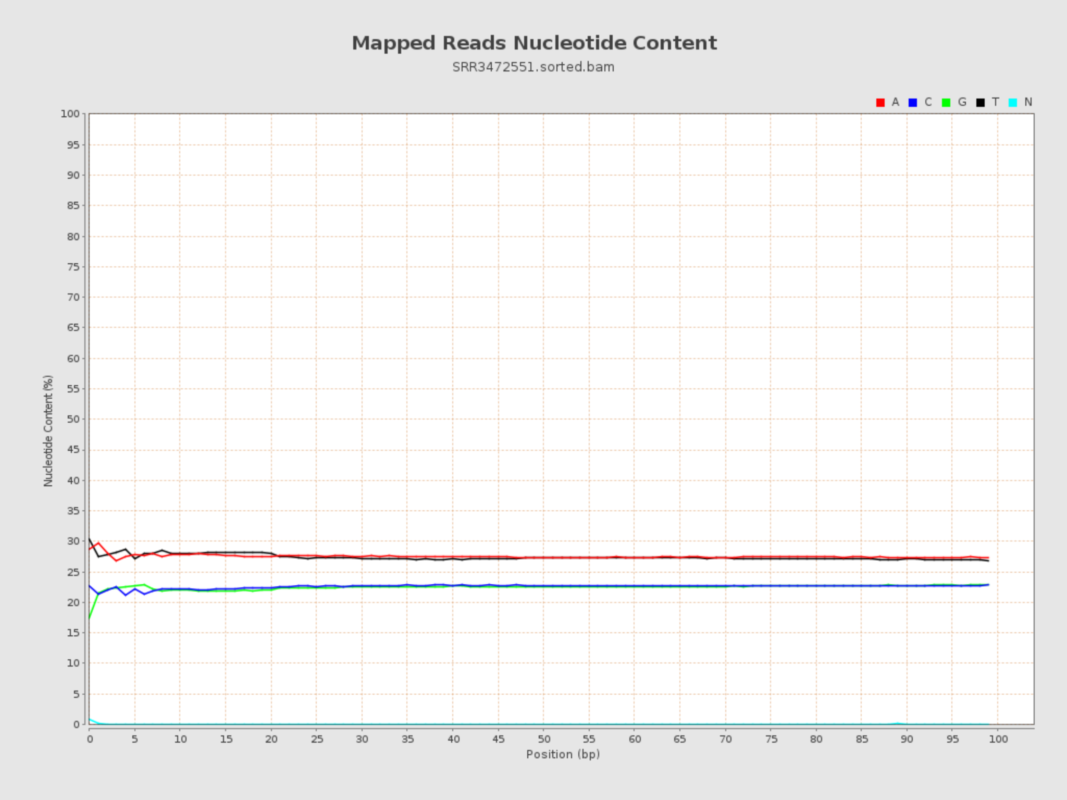
6. Results : Genome Fraction Coverage



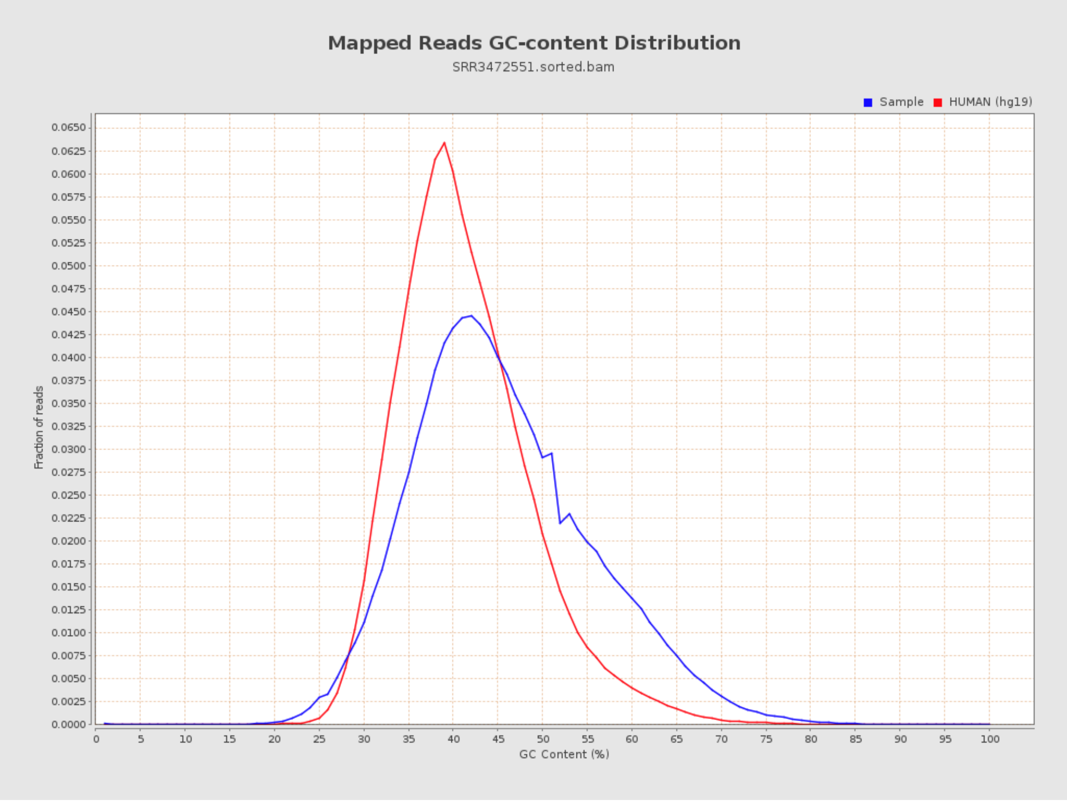
7. Results : Duplication Rate Histogram



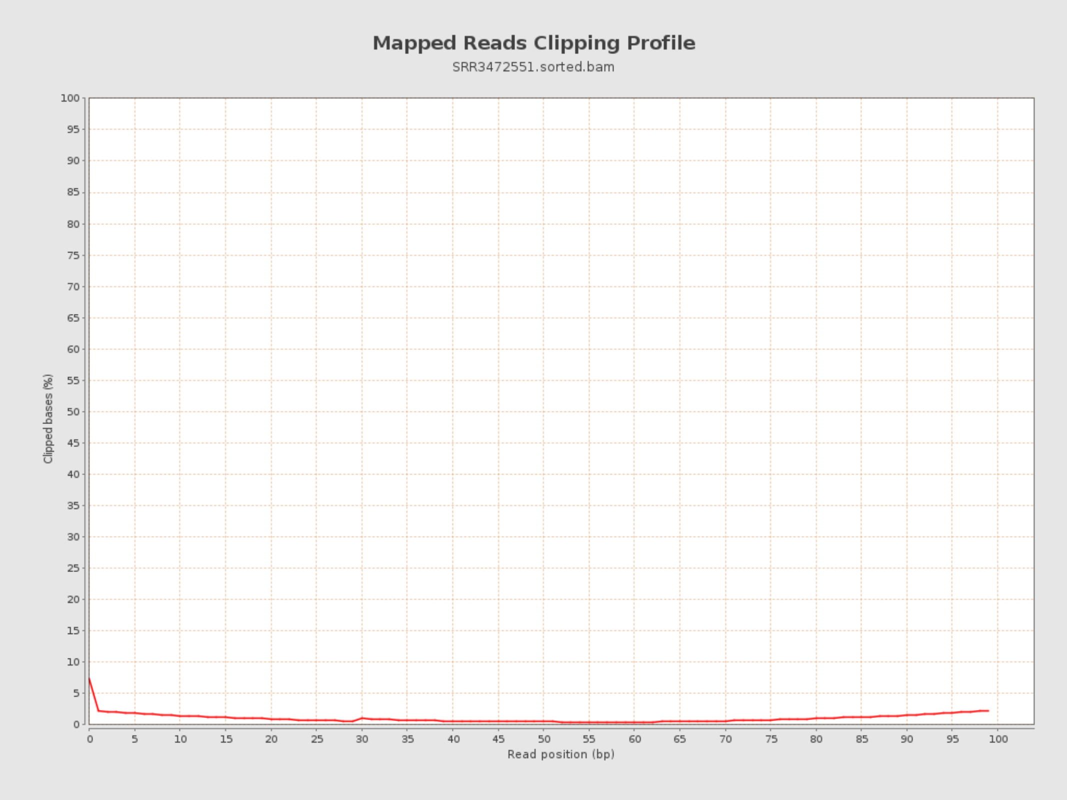
8. Results : Mapped Reads Nucleotide Content



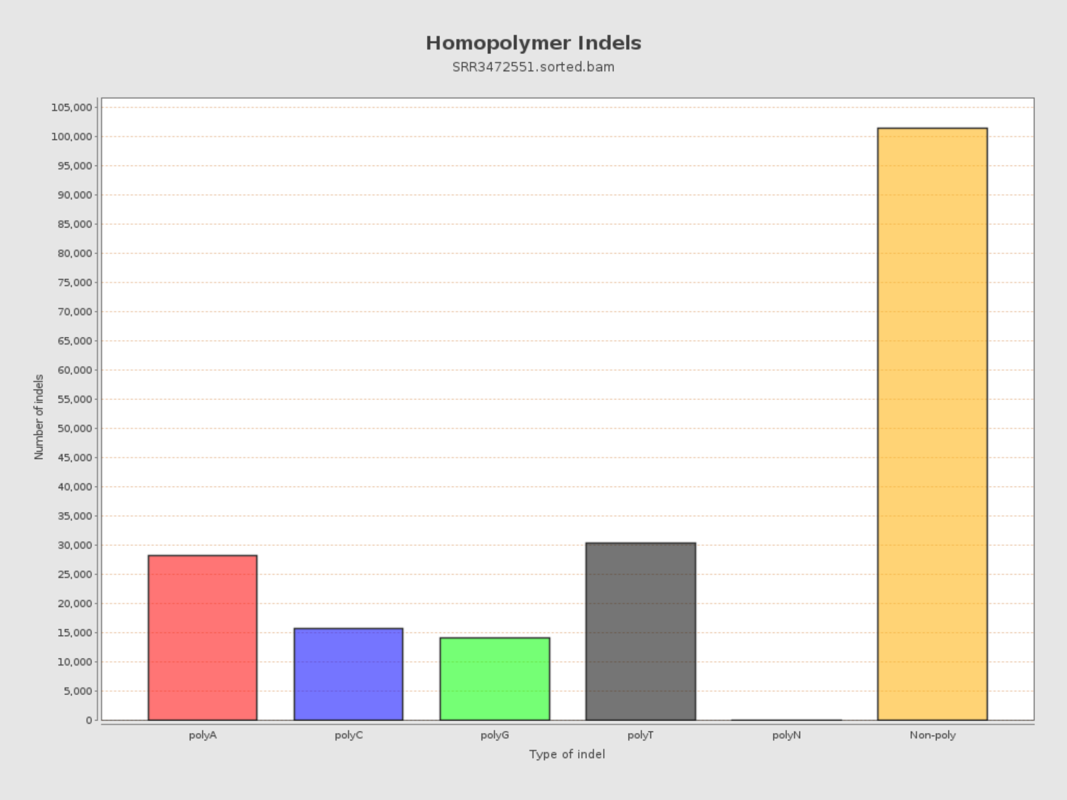
9. Results : Mapped Reads GC-content Distribution



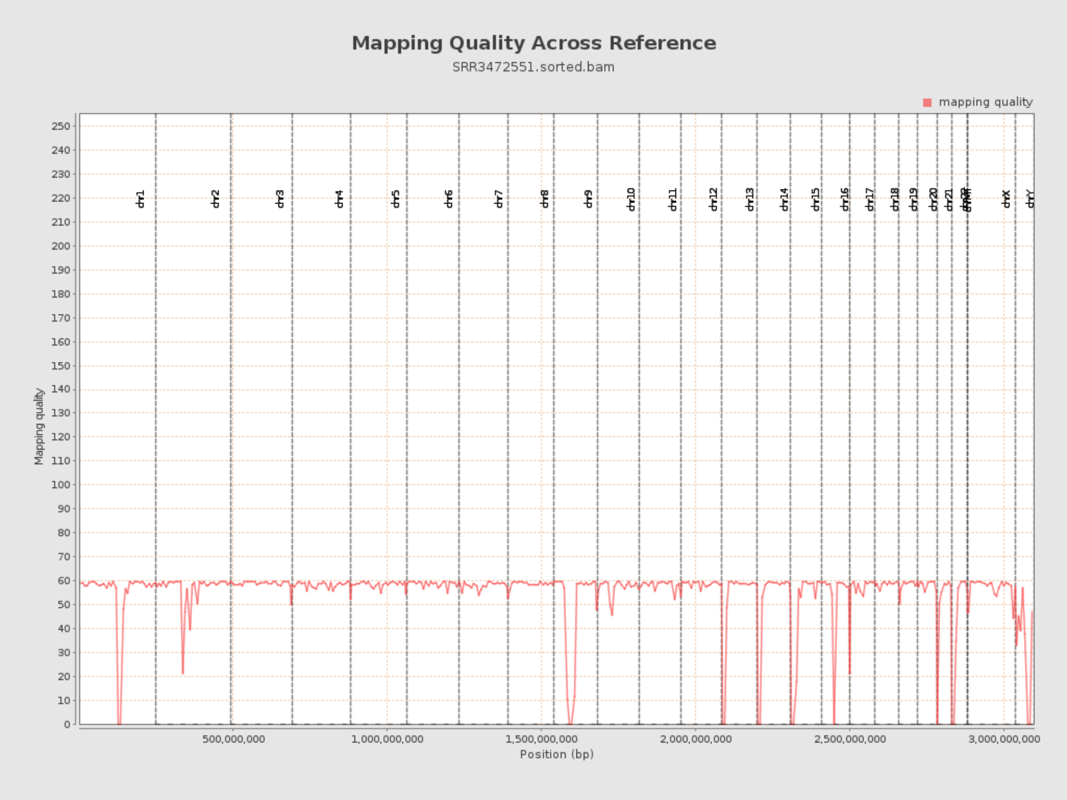
10. Results : Mapped Reads Clipping Profile



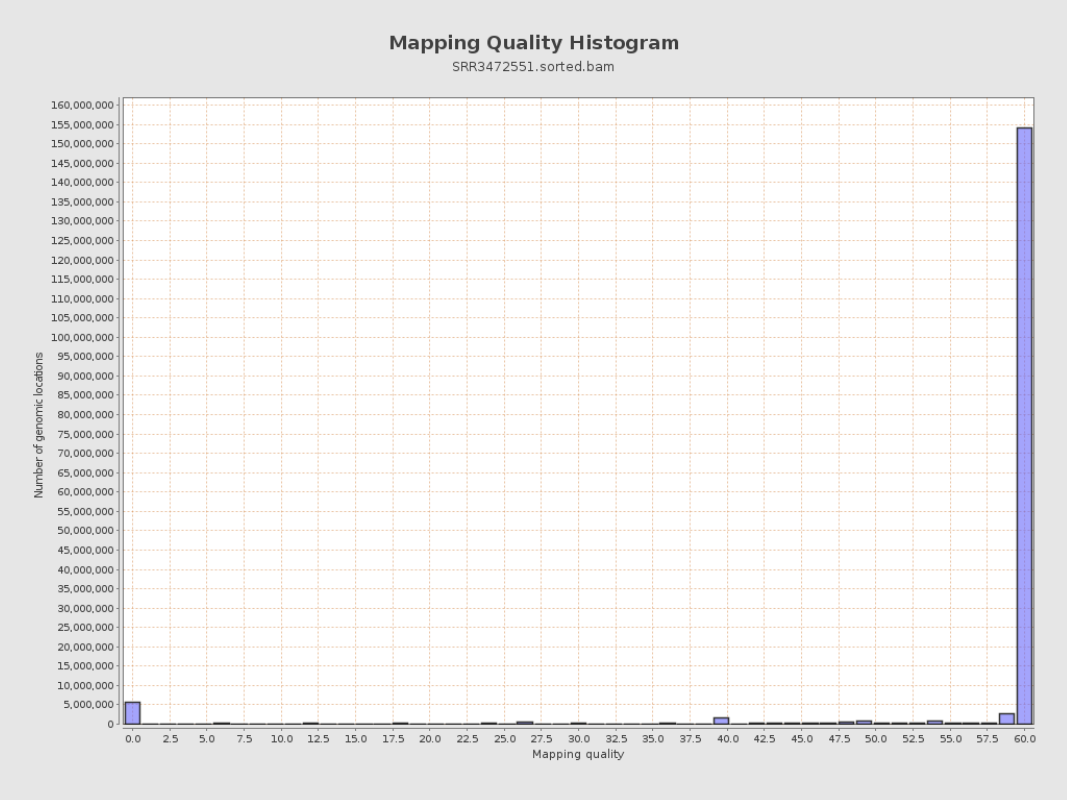
11. Results : Homopolymer Indels



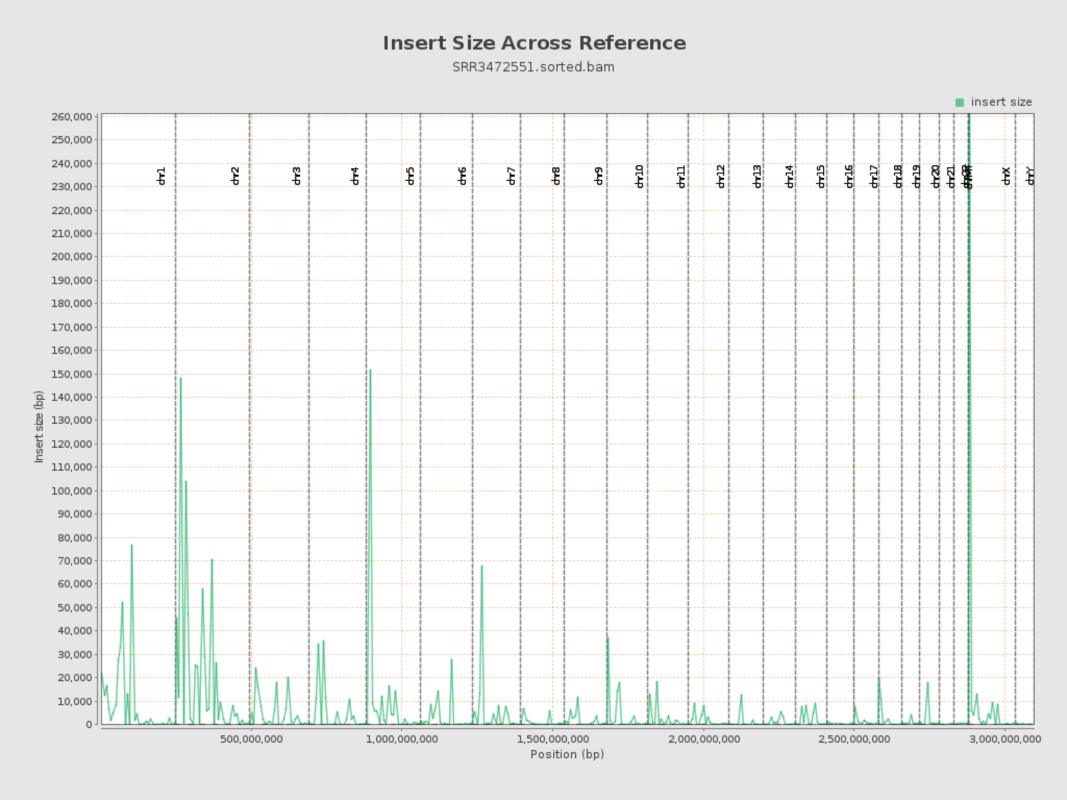
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram