Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 12:13:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472694.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_SRR3472694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472694_1.fastq.gz SRR3472694_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 12:13:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,844,280
Mapped reads	11,731,707 / 99.05%
Unmapped reads	112,573 / 0.95%
Mapped paired reads	11,731,707 / 99.05%
Mapped reads, first in pair	5,883,243 / 49.67%
Mapped reads, second in pair	5,848,464 / 49.38%
Mapped reads, both in pair	11,661,996 / 98.46%
Mapped reads, singletons	69,711 / 0.59%
Secondary alignments	0
Supplementary alignments	68,277 / 0.58%
Read min/max/mean length	30 / 101 / 99.35
Duplicated reads (estimated)	8,364,835 / 70.62%
Duplication rate	48.47%
Clipped reads	1,066,727 / 9.01%

2.2. ACGT Content

Number/percentage of A's	301,002,470 / 26.32%
Number/percentage of C's	271,945,309 / 23.78%
Number/percentage of T's	301,466,371 / 26.36%
Number/percentage of G's	269,169,832 / 23.53%
Number/percentage of N's	193,815 / 0.02%

GC Percentage	47.31%

2.3. Coverage

Mean	0.3695
Standard Deviation	22.9553

2.4. Mapping Quality

Mean Mapping Quality	54.6

2.5. Insert size

Mean	15,893.98
Standard Deviation	1,253,740.36
P25/Median/P75	139 / 193 / 259

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	7,210,166
Insertions	69,209
Mapped reads with at least one insertion	0.58%
Deletions	51,569
Mapped reads with at least one deletion	0.43%
Homopolymer indels	45.41%

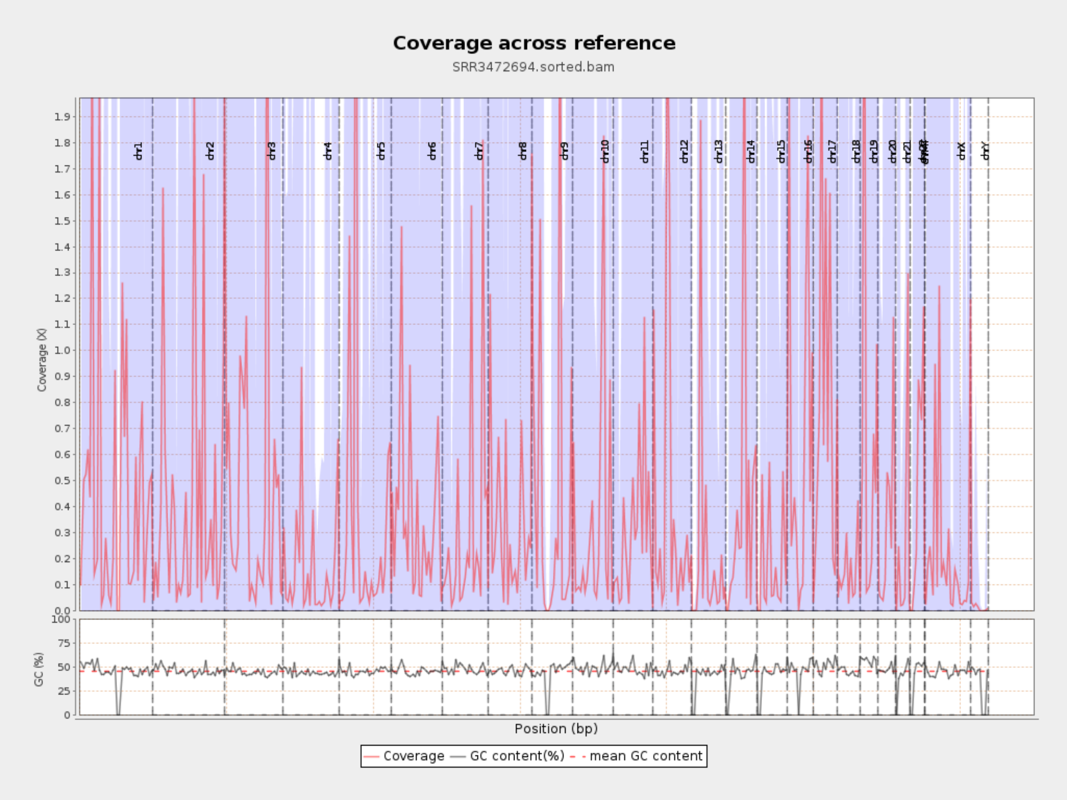
2.7. Chromosome stats

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

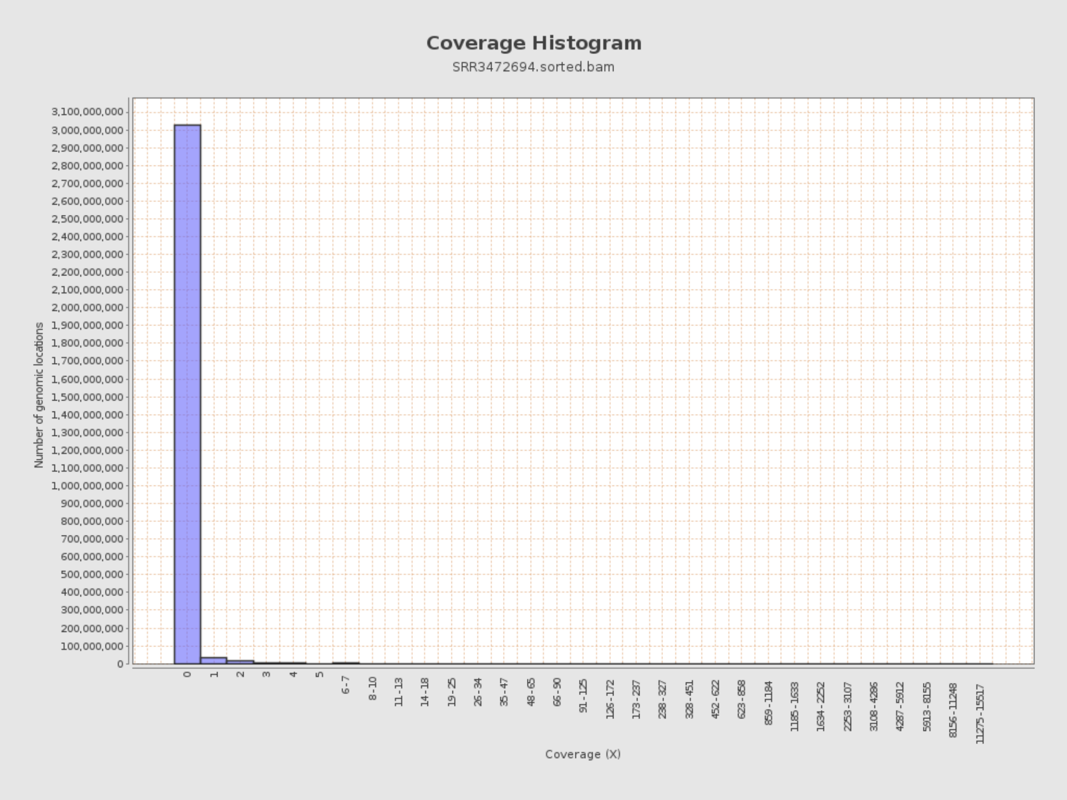
		bases	coverage	deviation
chr1	249250621	119638742	0.48	30.0078
chr2	243199373	97467610	0.4008	25.6335
chr3	198022430	99408240	0.502	21.7062
chr4	191154276	30303071	0.1585	17.7479
chr5	180915260	67117682	0.371	25.5017
chr6	171115067	60123352	0.3514	16.7894
chr7	159138663	51816262	0.3256	17.1419
chr8	146364022	47638595	0.3255	18.4464
chr9	141213431	62612042	0.4434	23.9955
chr10	135534747	44973397	0.3318	30.778
chr11	135006516	43182455	0.3199	13.4968
chr12	133851895	56117464	0.4193	24.674
chr13	115169878	24874383	0.216	16.5317
chr14	107349540	43619761	0.4063	20.7207
chr15	102531392	18028056	0.1758	12.1032
chr16	90354753	61882547	0.6849	36.0628
chr17	81195210	68860893	0.8481	35.4053
chr18	78077248	12094297	0.1549	8.7049
chr19	59128983	41307366	0.6986	33.4721
chr20	63025520	20704494	0.3285	22.5807
chr21	48129895	12865380	0.2673	30.7543
chr22	51304566	24188186	0.4715	22.4036
chrMT	16571	1830	0.1104	0.4011
chrX	155270560	34386504	0.2215	13.365

chrY	59373566	675309	0.0114	0.5119

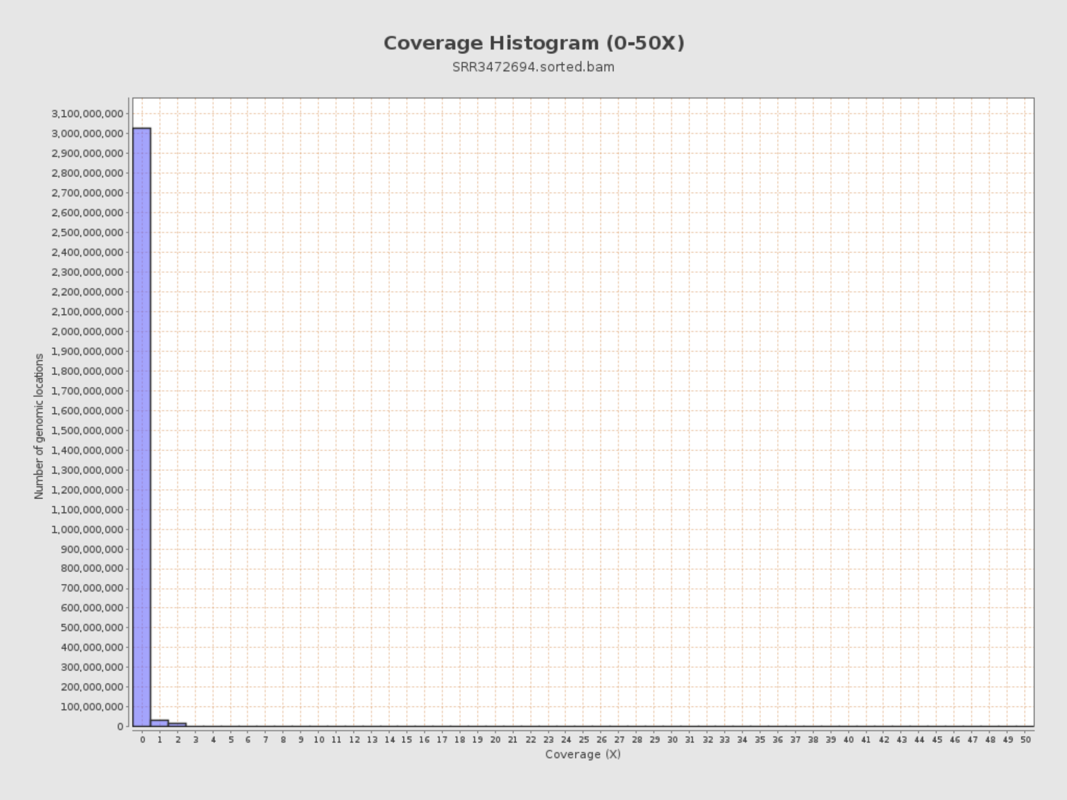
3. Results : Coverage across reference



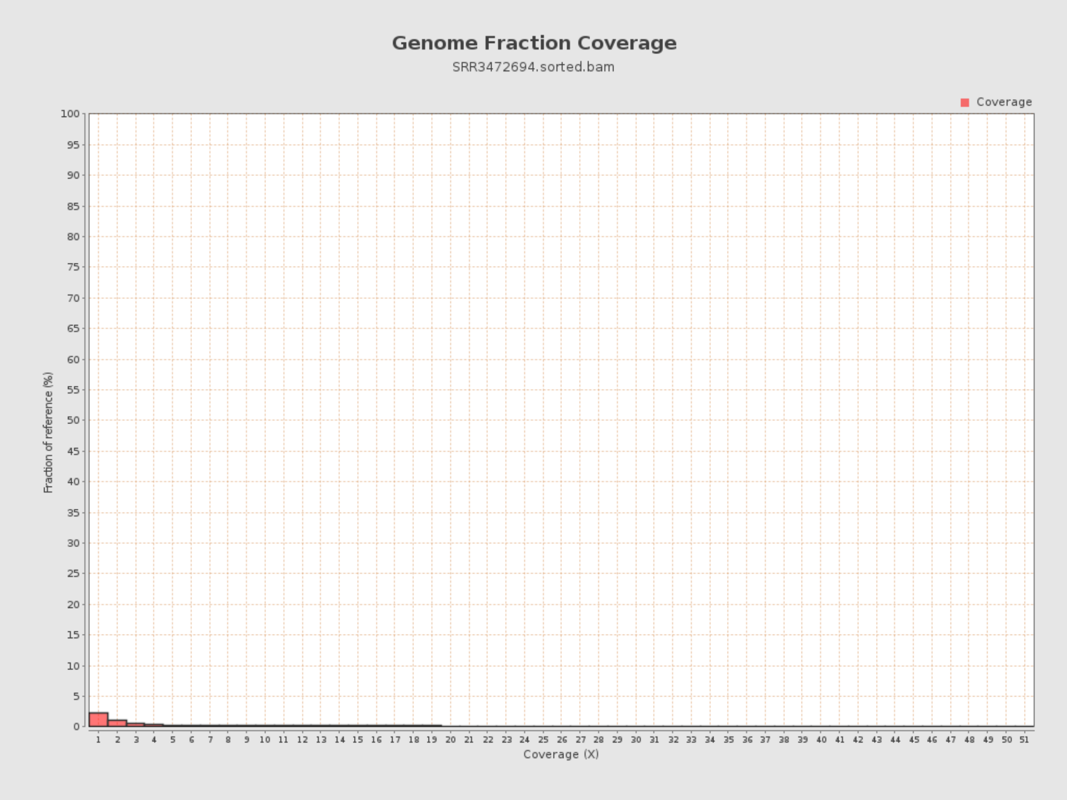
4. Results : Coverage Histogram



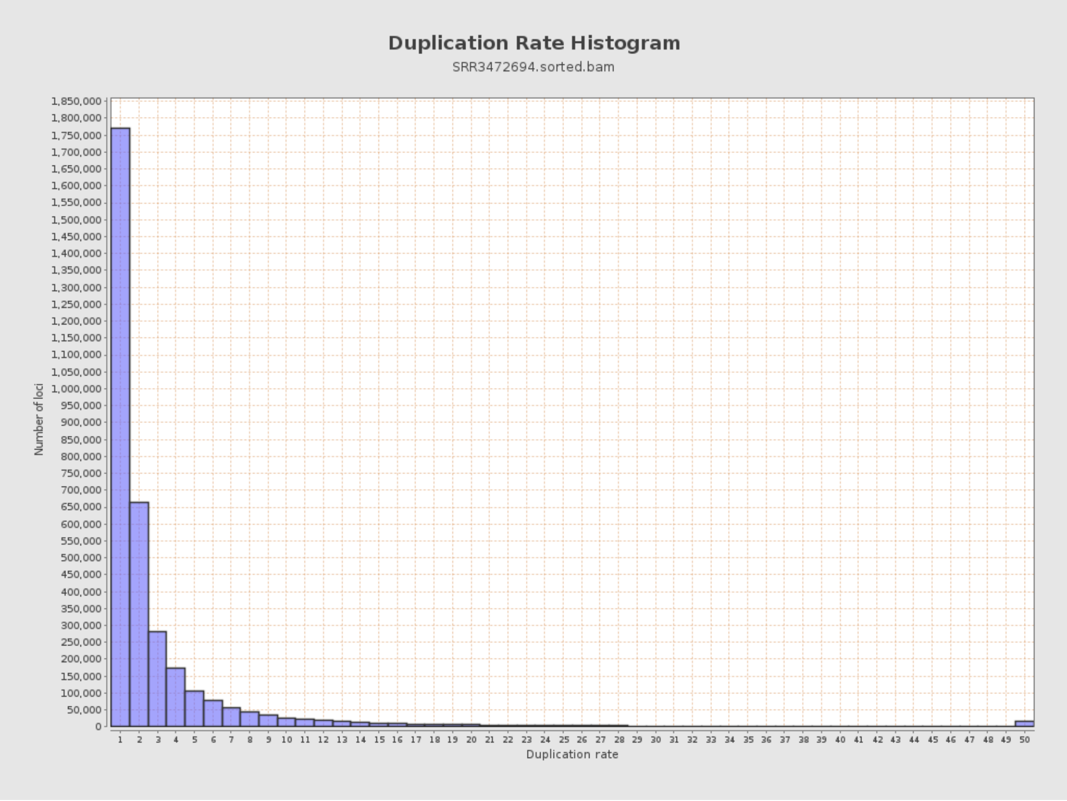
5. Results : Coverage Histogram (0-50X)



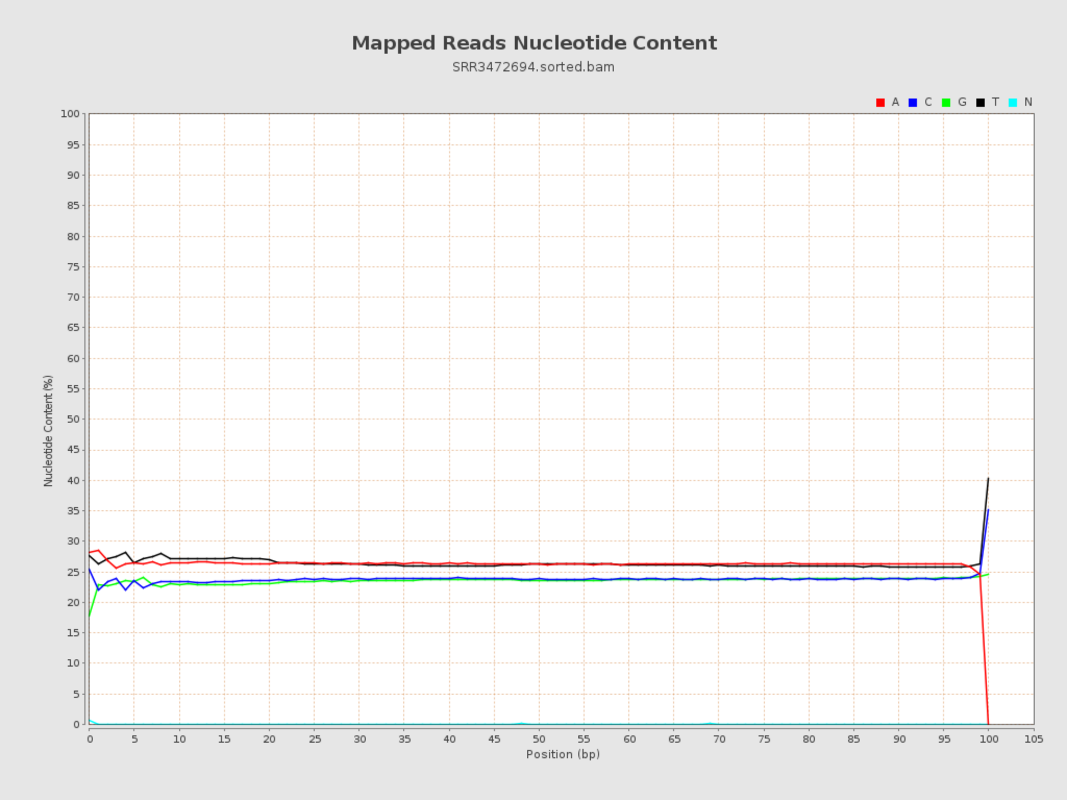
6. Results : Genome Fraction Coverage



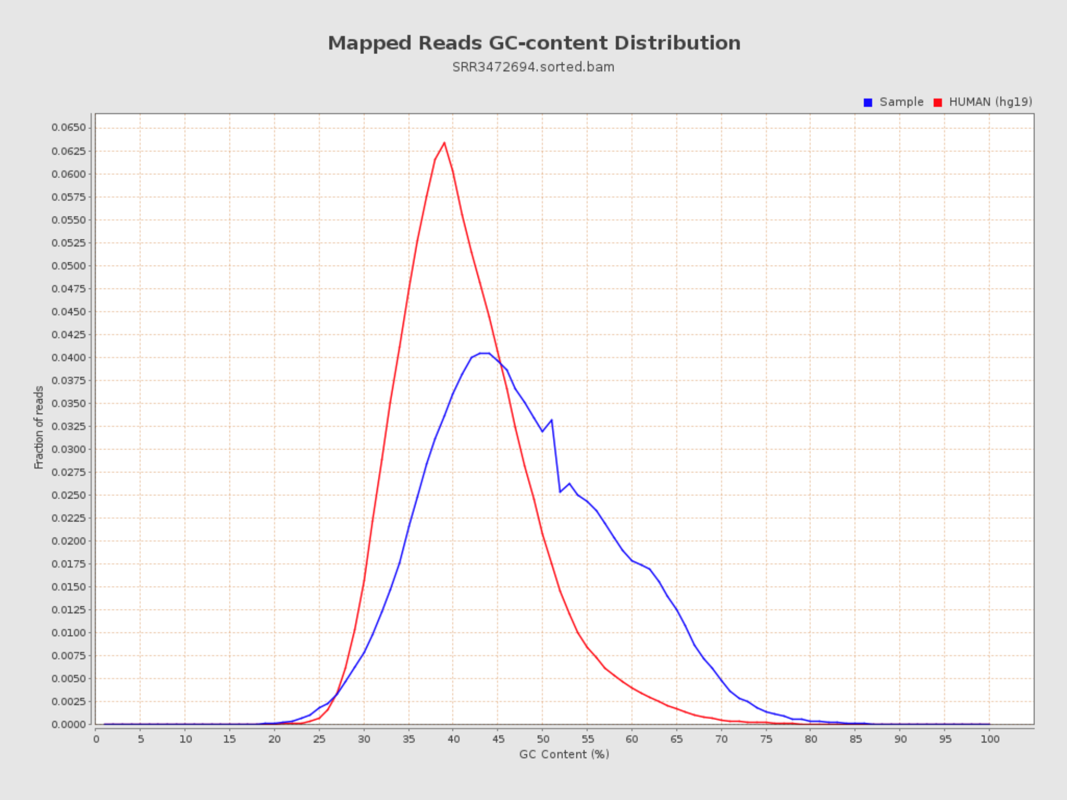
7. Results : Duplication Rate Histogram



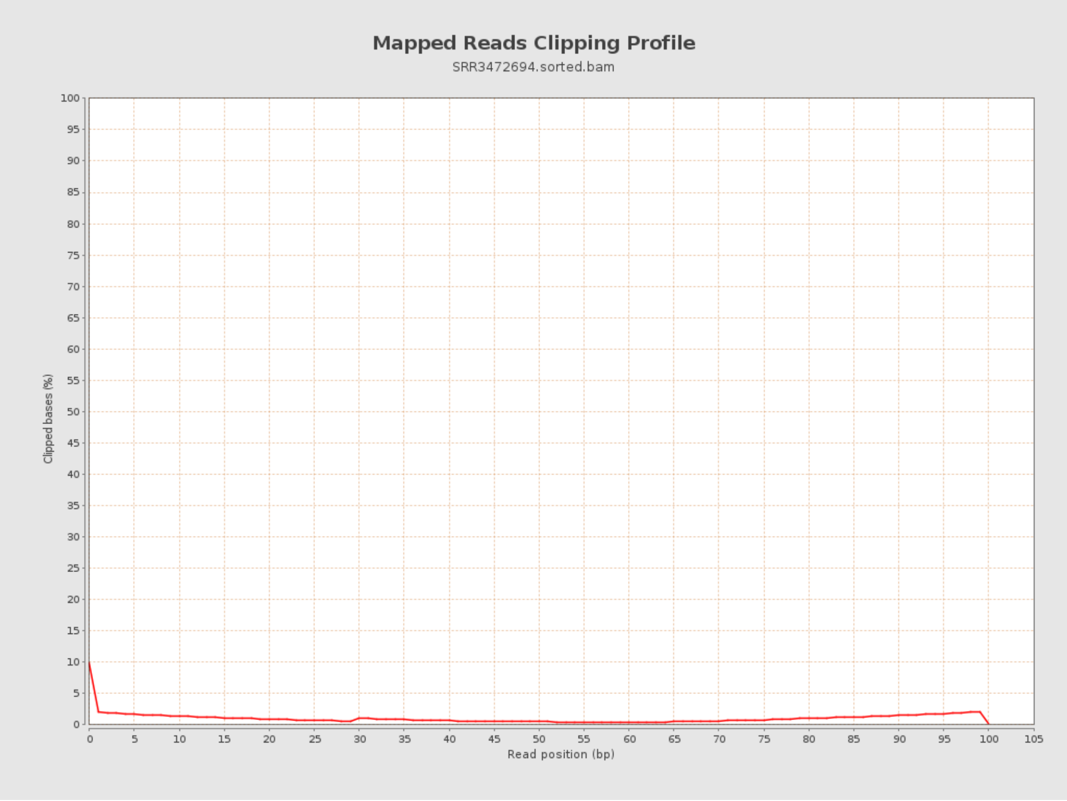
8. Results : Mapped Reads Nucleotide Content



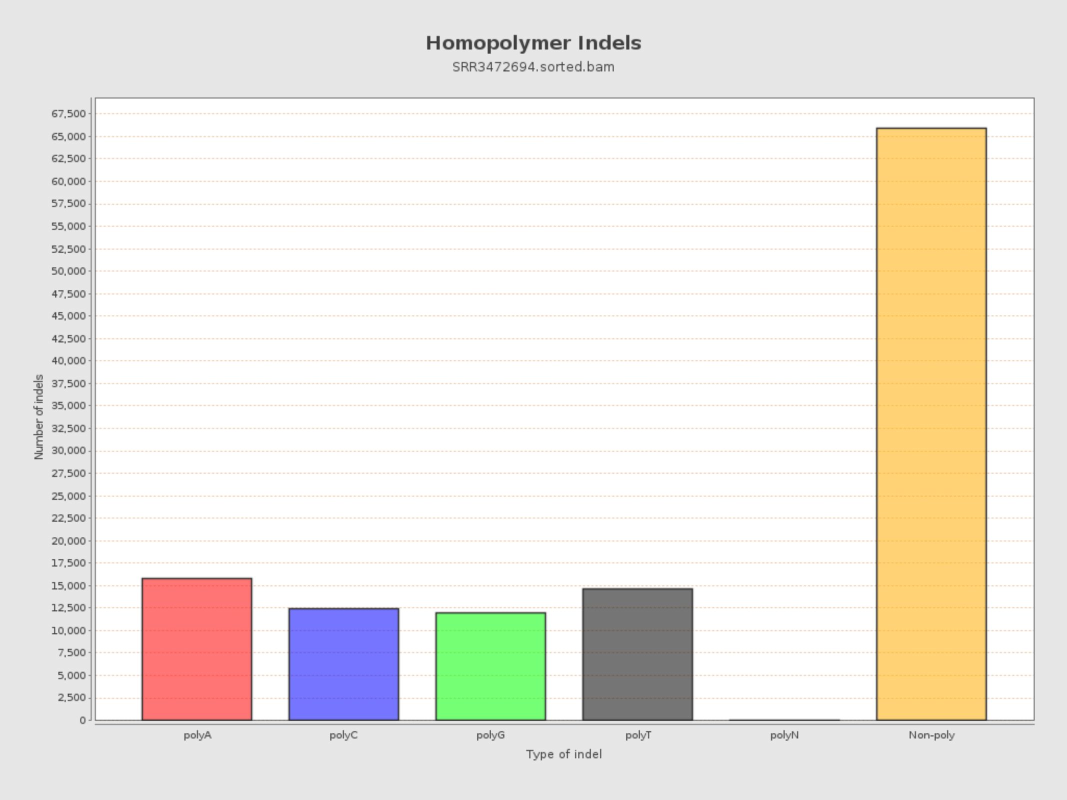
9. Results : Mapped Reads GC-content Distribution



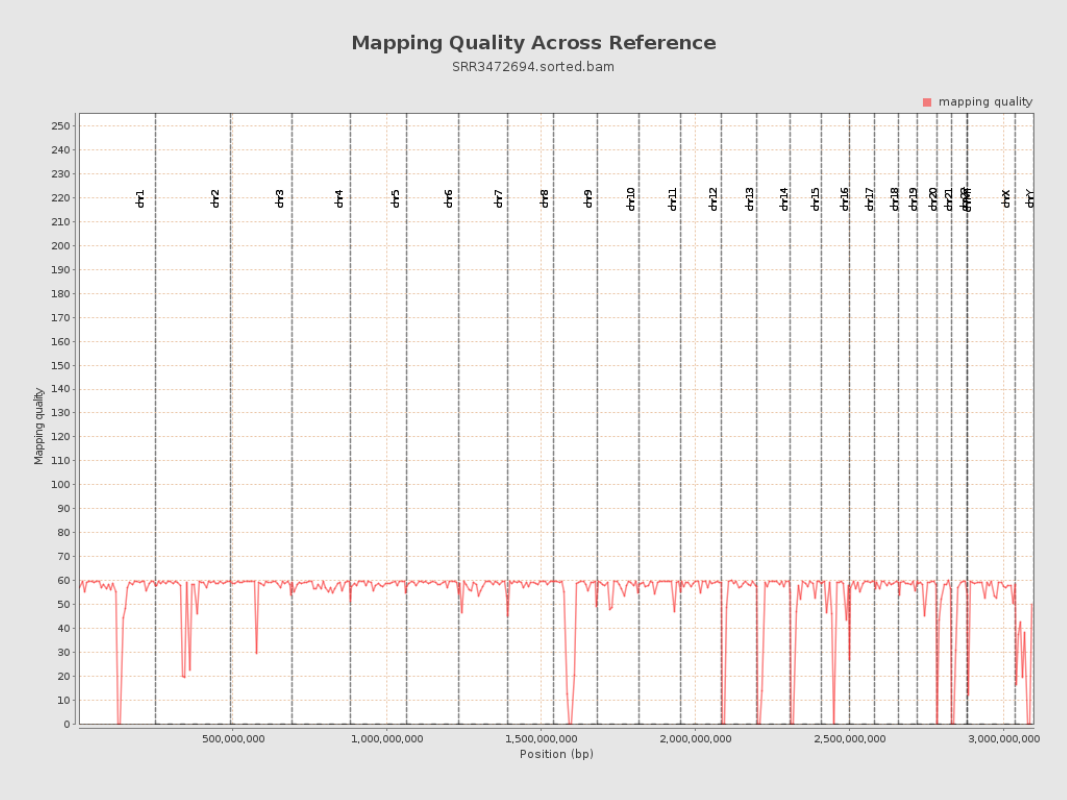
10. Results : Mapped Reads Clipping Profile



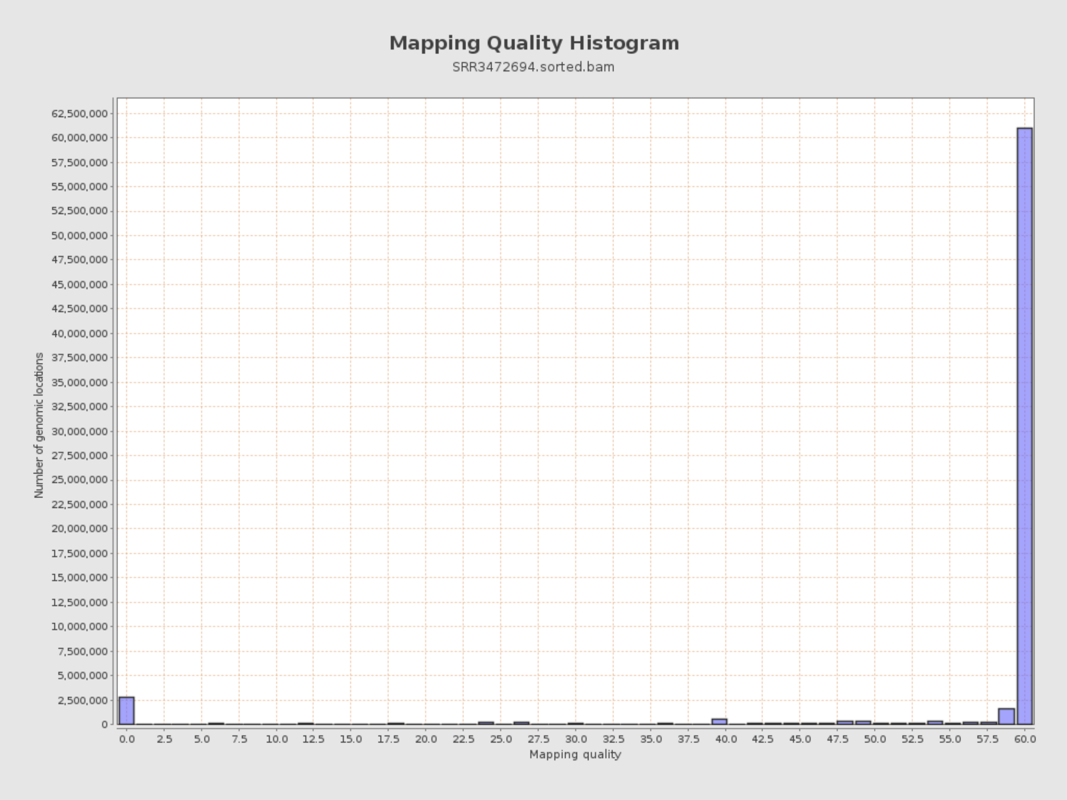
11. Results : Homopolymer Indels



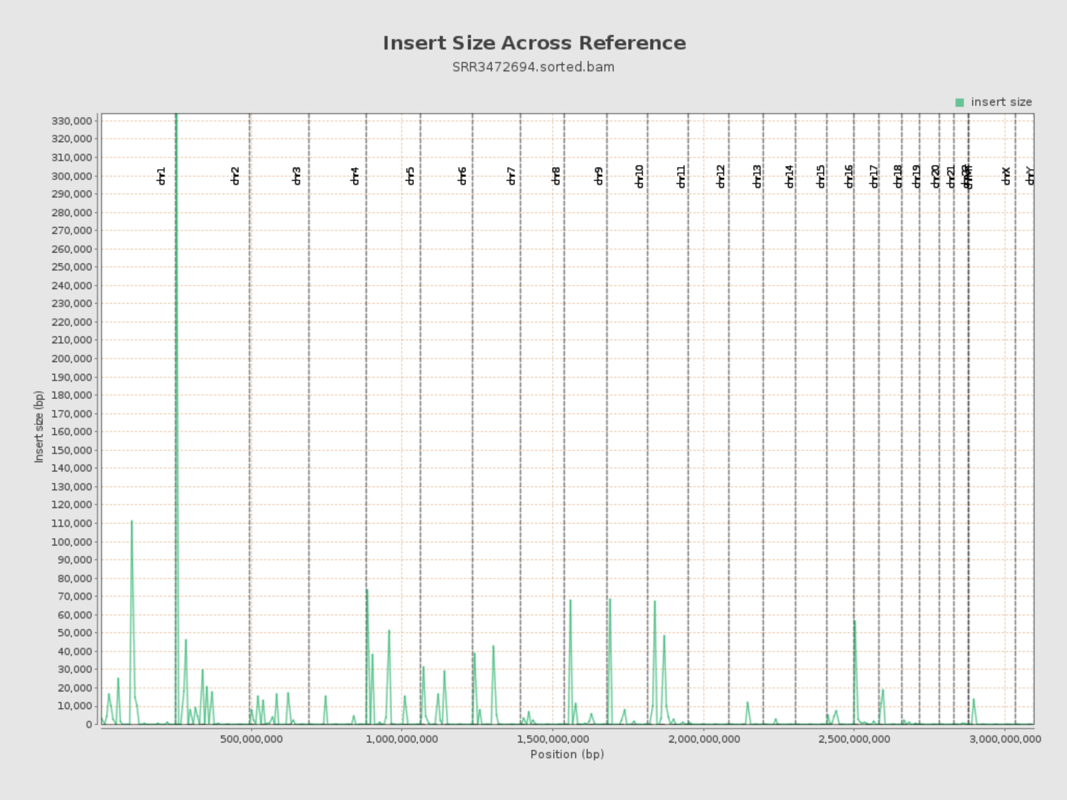
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram