Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 14:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472704.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_SRR3472704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472704_1.fastq.gz SRR3472704_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 14:26:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,885,402
Mapped reads	15,722,737 / 98.98%
Unmapped reads	162,665 / 1.02%
Mapped paired reads	15,722,737 / 98.98%
Mapped reads, first in pair	7,894,472 / 49.7%
Mapped reads, second in pair	7,828,265 / 49.28%
Mapped reads, both in pair	15,622,742 / 98.35%
Mapped reads, singletons	99,995 / 0.63%
Secondary alignments	0
Supplementary alignments	57,113 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,596,421 / 60.41%
Duplication rate	47.16%
Clipped reads	1,190,969 / 7.5%

2.2. ACGT Content

Number/percentage of A's	431,040,314 / 27.8%
Number/percentage of C's	346,886,757 / 22.37%
Number/percentage of T's	428,989,400 / 27.67%
Number/percentage of G's	343,158,482 / 22.13%
Number/percentage of N's	299,708 / 0.02%

GC Percentage	44.51%

2.3. Coverage

Mean	0.5009
Standard Deviation	15.5471

2.4. Mapping Quality

Mean Mapping Quality	55.08

2.5. Insert size

Mean	23,302.08
Standard Deviation	1,480,756.52
P25/Median/P75	176 / 244 / 329

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	9,803,656
Insertions	94,640
Mapped reads with at least one insertion	0.6%
Deletions	87,514
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.24%

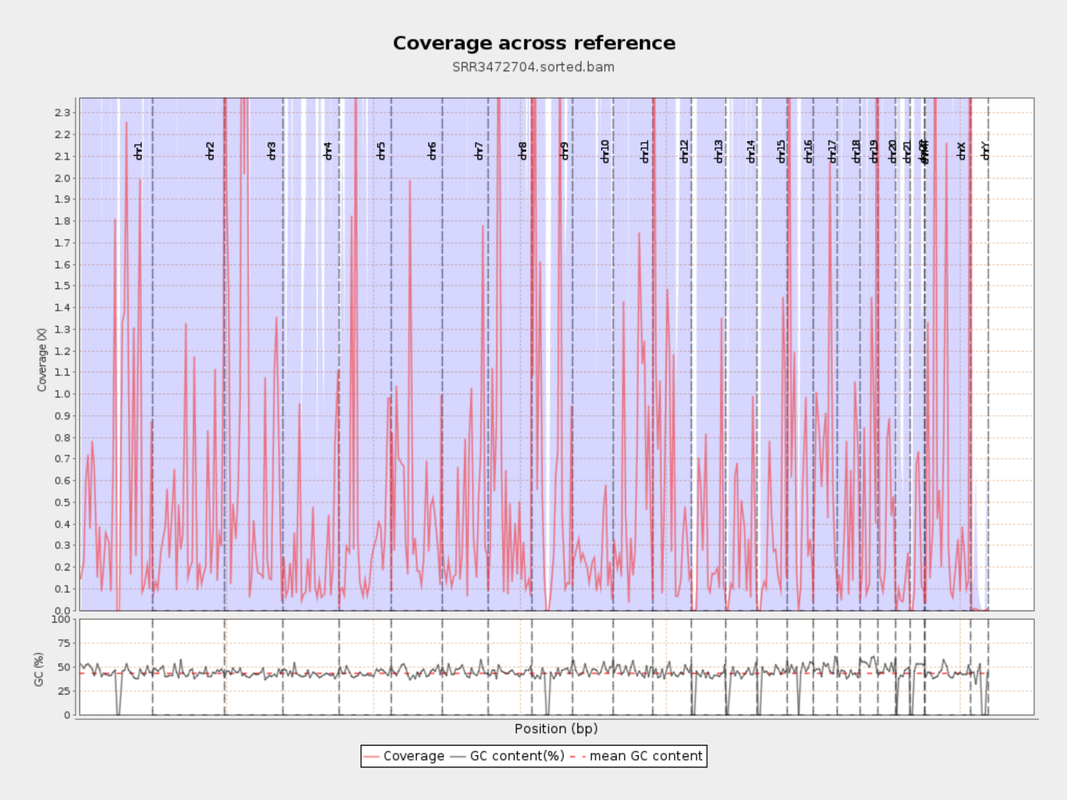
2.7. Chromosome stats

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

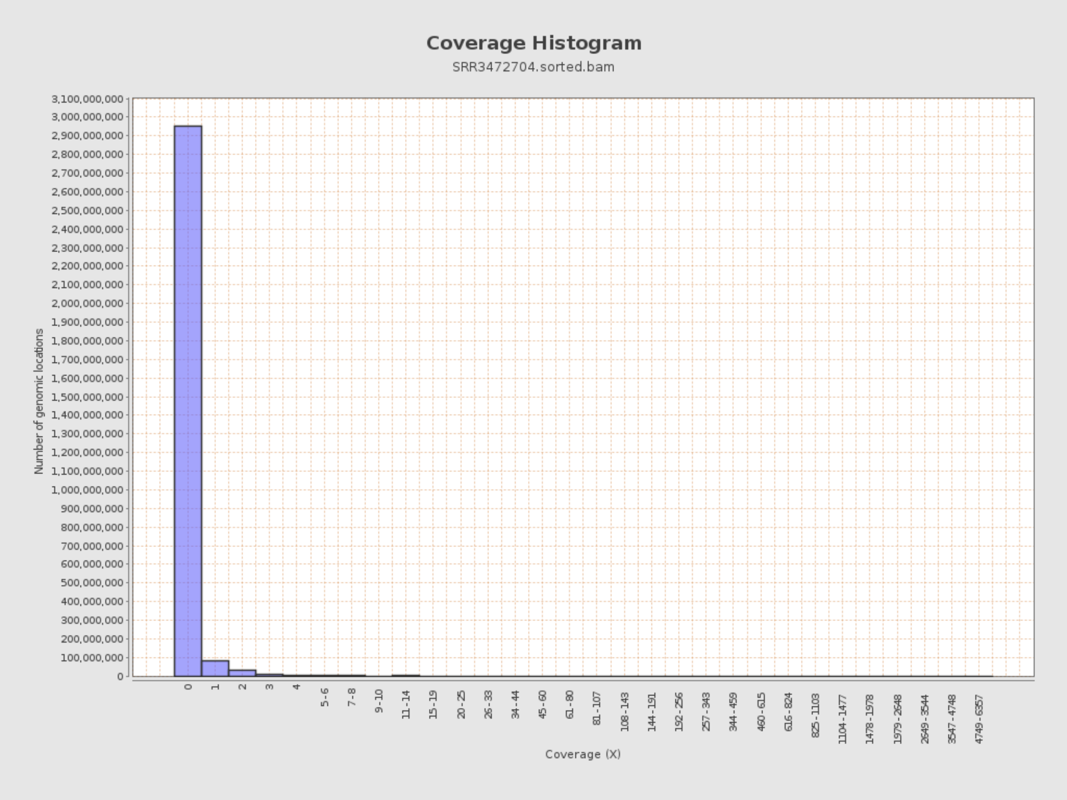
		bases	coverage	deviation
chr1	249250621	154331404	0.6192	17.2901
chr2	243199373	95625640	0.3932	11.115
chr3	198022430	179174203	0.9048	18.846
chr4	191154276	48513835	0.2538	8.8373
chr5	180915260	83299002	0.4604	14.8629
chr6	171115067	84474155	0.4937	12.9716
chr7	159138663	69727181	0.4382	12.2104
chr8	146364022	75915516	0.5187	21.1151
chr9	141213431	104289400	0.7385	21.7076
chr10	135534747	31936924	0.2356	7.2752
chr11	135006516	80561339	0.5967	20.6013
chr12	133851895	95980644	0.7171	19.6225
chr13	115169878	36529390	0.3172	13.4811
chr14	107349540	32545793	0.3032	8.9556
chr15	102531392	38650135	0.377	11.867
chr16	90354753	57808364	0.6398	18.7805
chr17	81195210	60691134	0.7475	16.9794
chr18	78077248	33766769	0.4325	16.7881
chr19	59128983	40803932	0.6901	22.2967
chr20	63025520	28677372	0.455	11.081
chr21	48129895	5071993	0.1054	3.6686
chr22	51304566	13306757	0.2594	8.9912
chrMT	16571	3621	0.2185	0.7795
chrX	155270560	98666633	0.6354	18.7915

chrY	59373566	247551	0.0042	0.3786

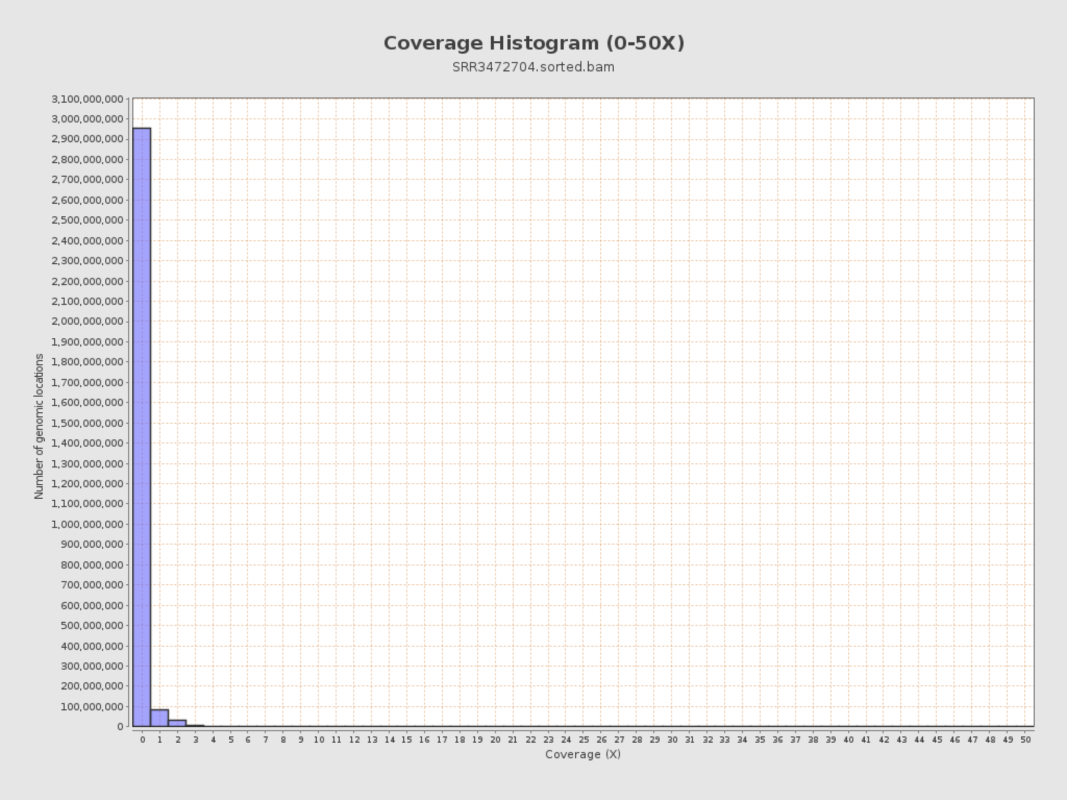
3. Results : Coverage across reference



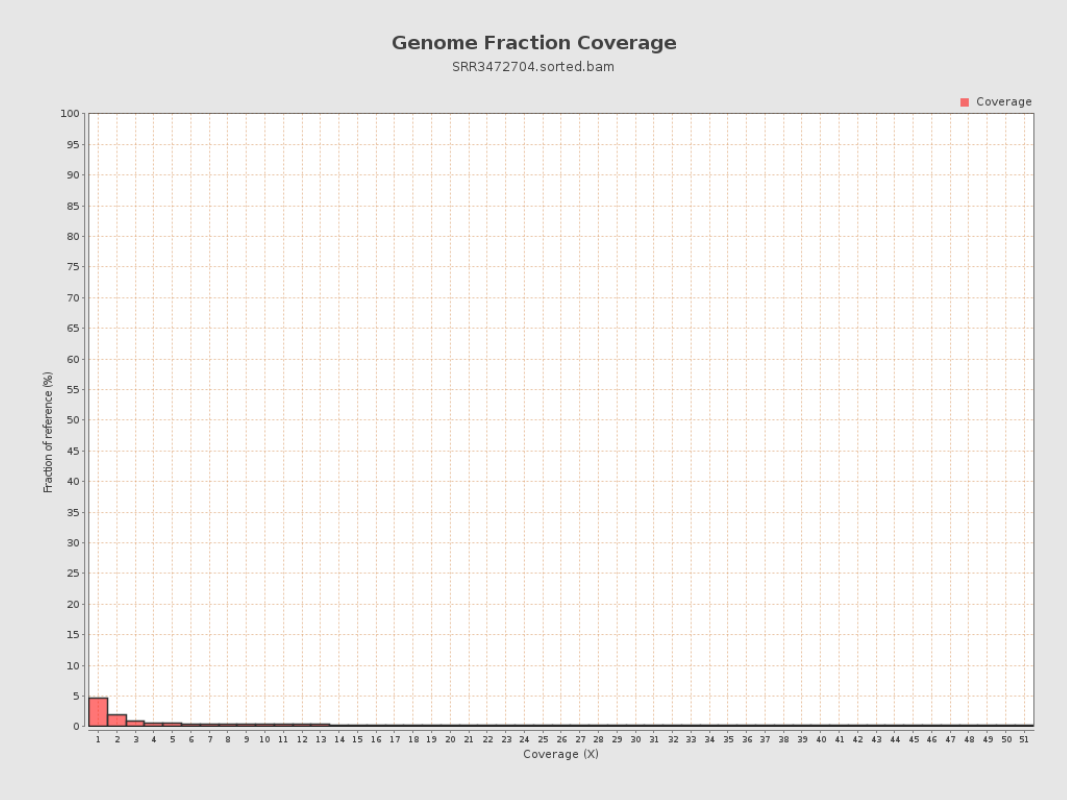
4. Results : Coverage Histogram



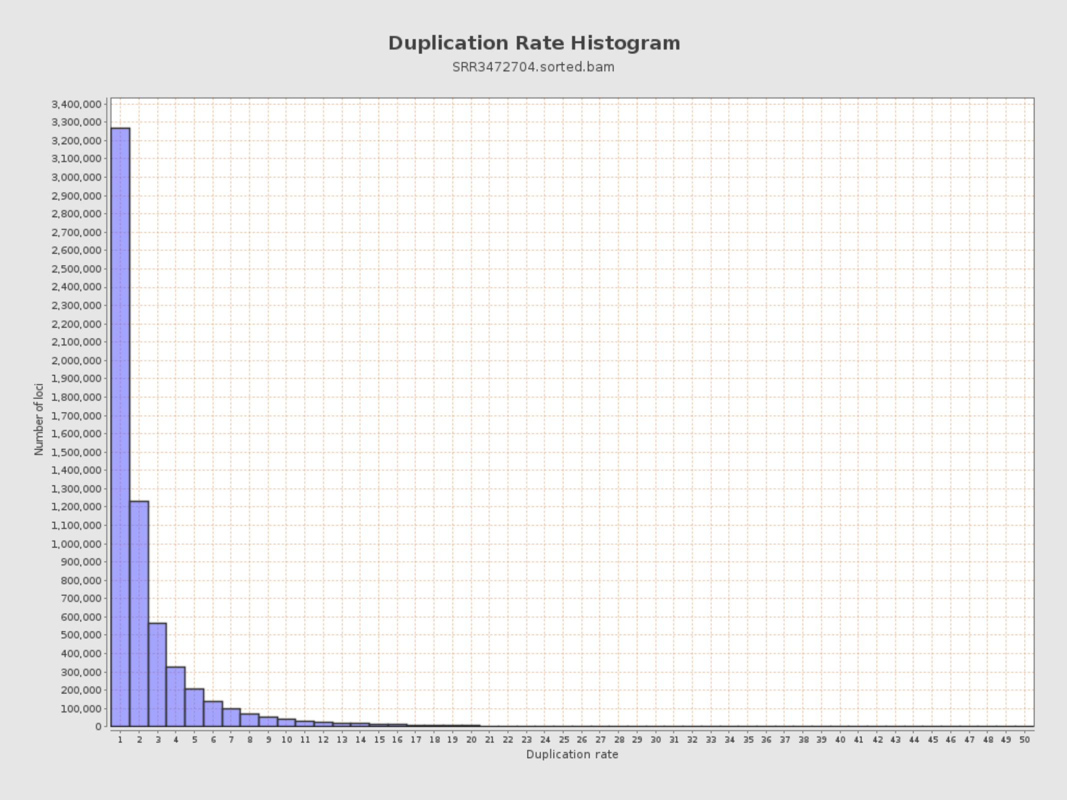
5. Results : Coverage Histogram (0-50X)



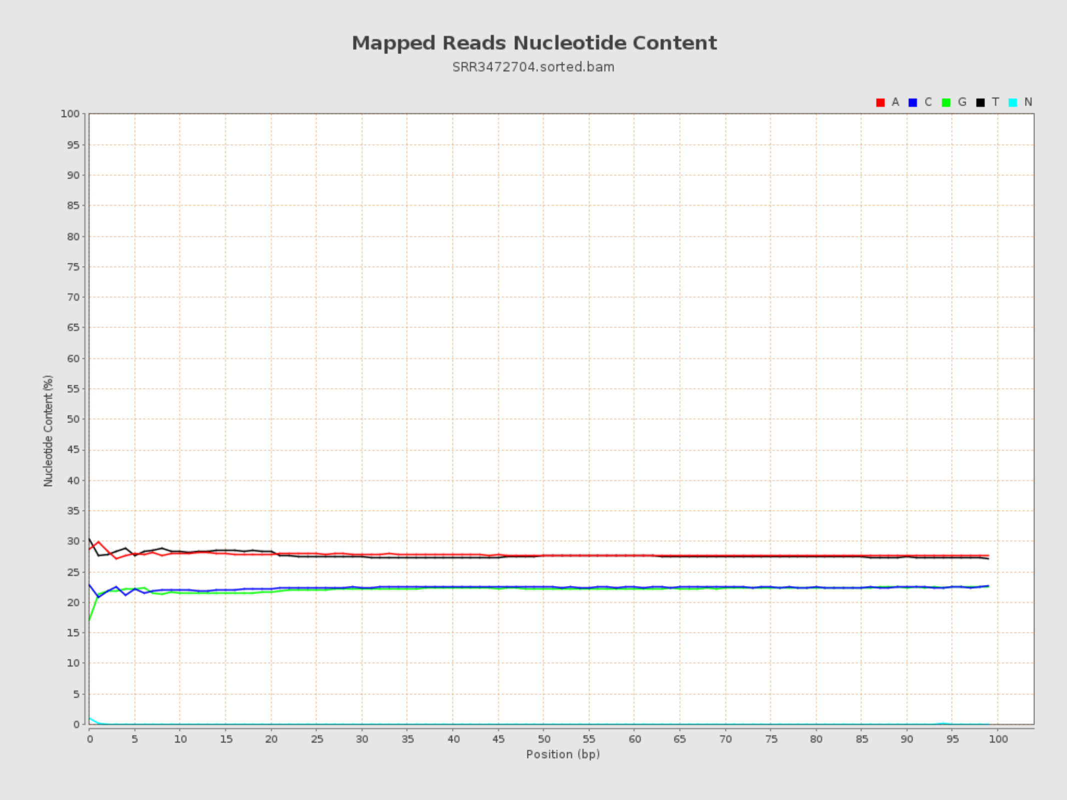
6. Results : Genome Fraction Coverage



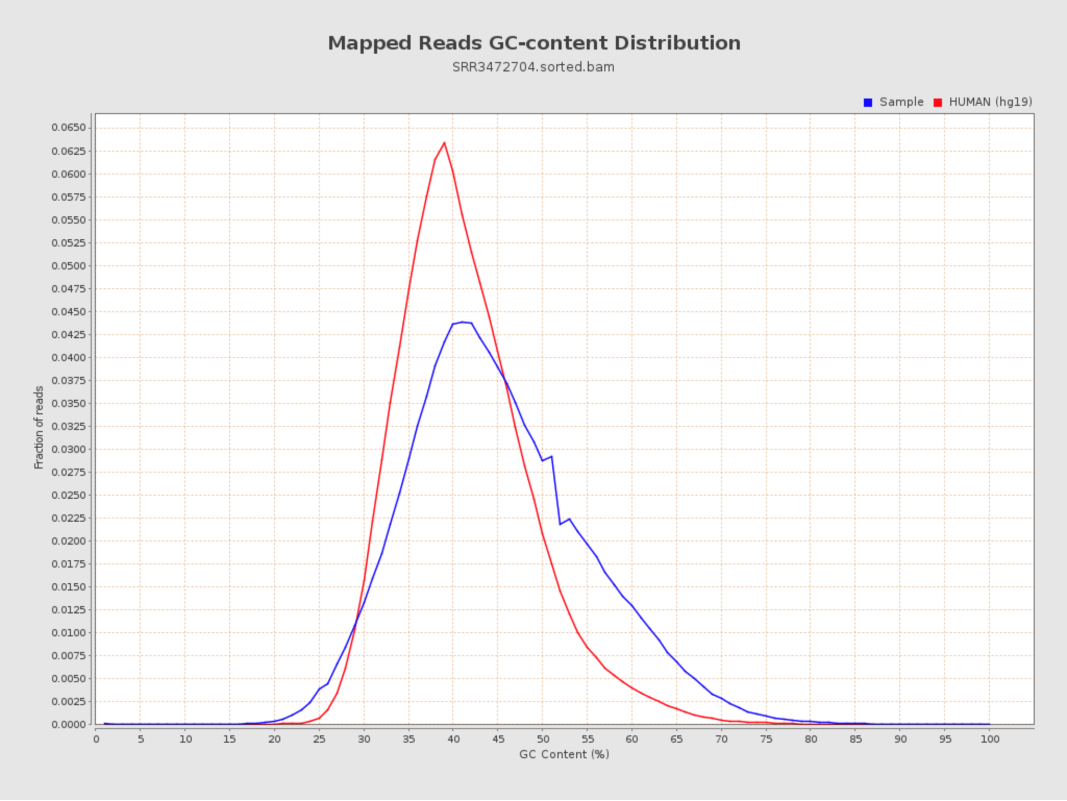
7. Results : Duplication Rate Histogram



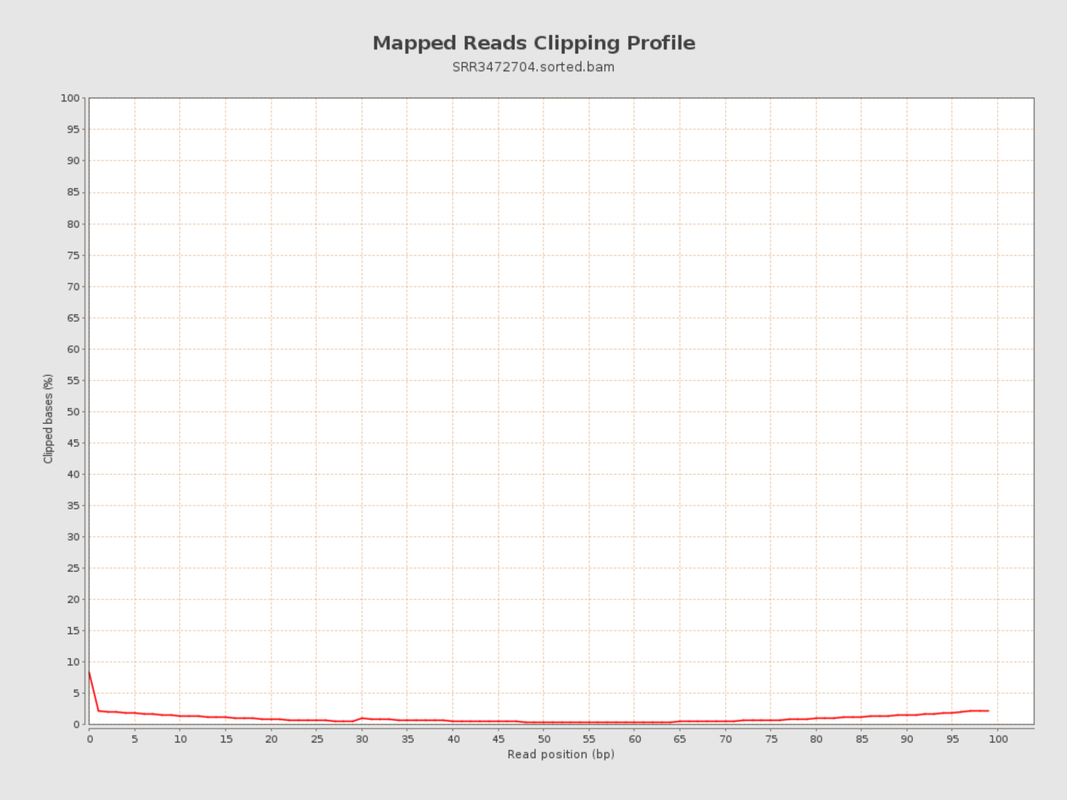
8. Results : Mapped Reads Nucleotide Content



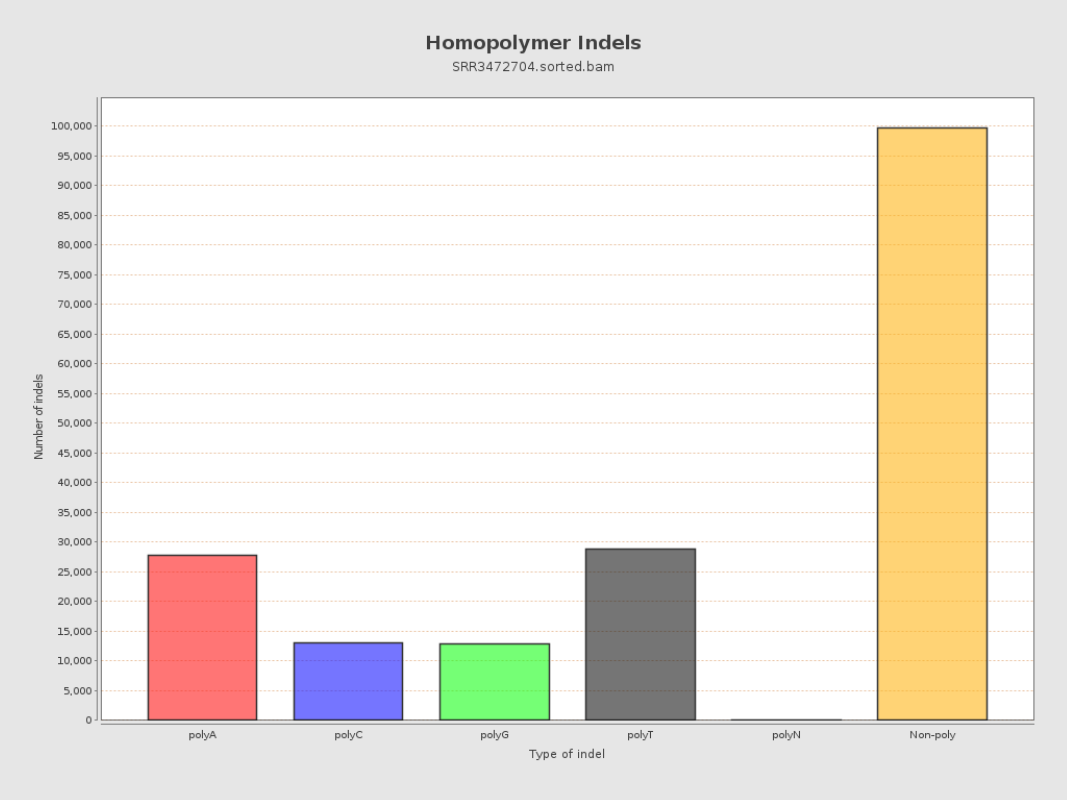
9. Results : Mapped Reads GC-content Distribution



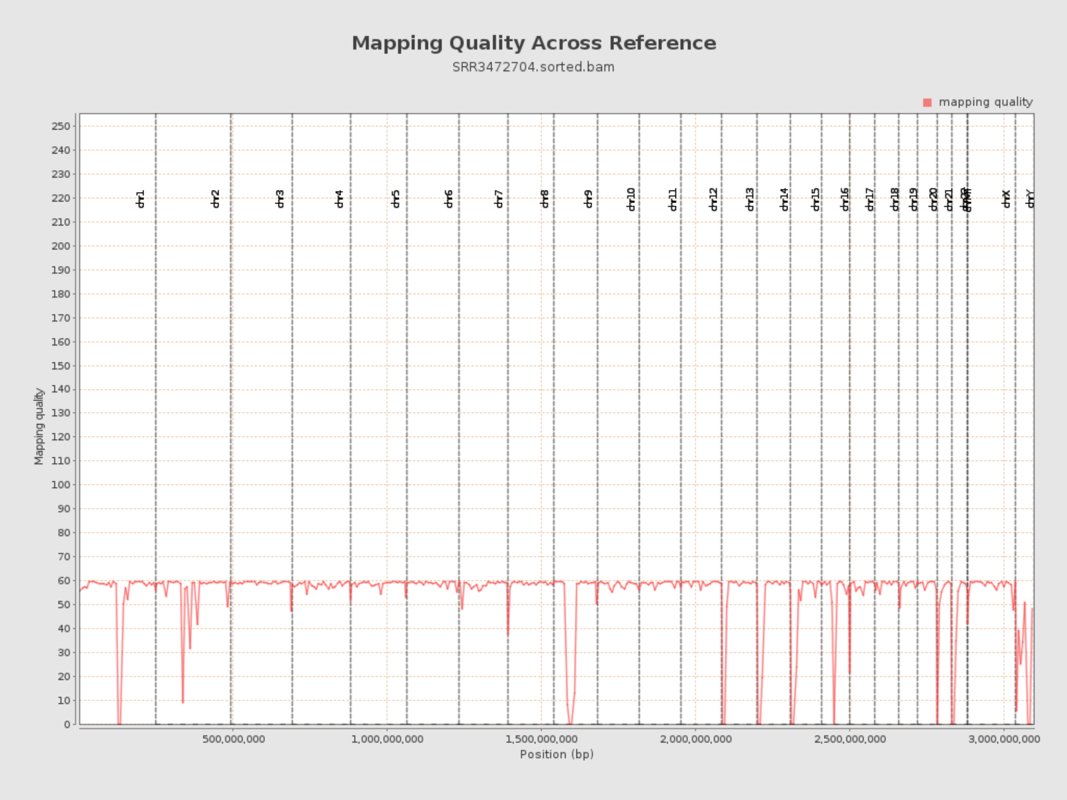
10. Results : Mapped Reads Clipping Profile



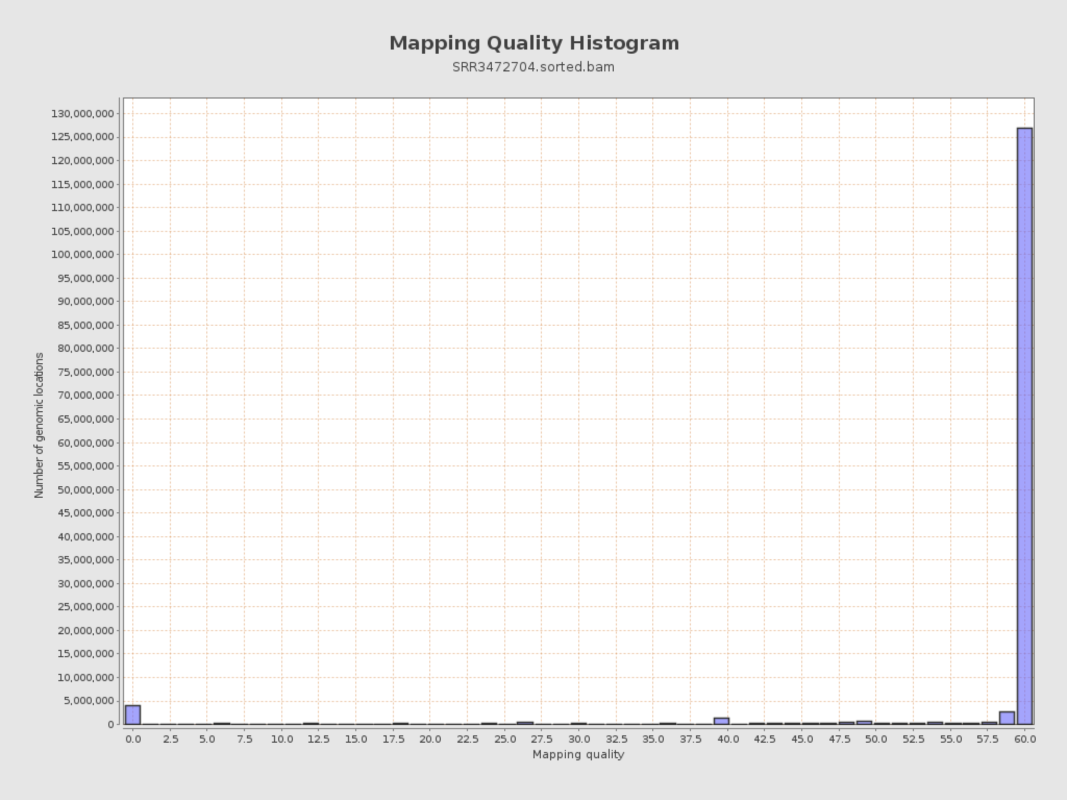
11. Results : Homopolymer Indels



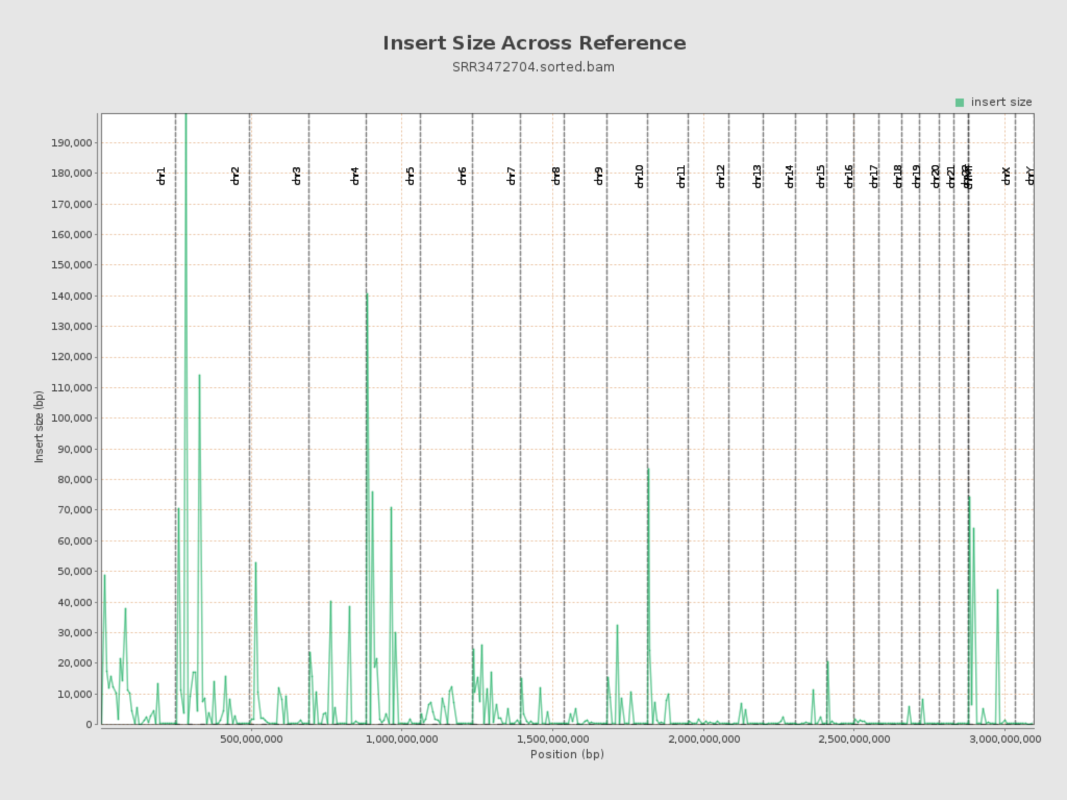
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram