Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 21:10:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472648.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_SRR3472648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472648_1.fastq.gz SRR3472648_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 21:10:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,606,592
Mapped reads	8,526,759 / 99.07%
Unmapped reads	79,833 / 0.93%
Mapped paired reads	8,526,759 / 99.07%
Mapped reads, first in pair	4,268,212 / 49.59%
Mapped reads, second in pair	4,258,547 / 49.48%
Mapped reads, both in pair	8,480,708 / 98.54%
Mapped reads, singletons	46,051 / 0.54%
Secondary alignments	0
Supplementary alignments	39,059 / 0.45%
Read min/max/mean length	30 / 101 / 99.32
Duplicated reads (estimated)	5,574,947 / 64.78%
Duplication rate	41.54%
Clipped reads	511,611 / 5.94%

2.2. ACGT Content

Number/percentage of A's	224,009,906 / 26.76%
Number/percentage of C's	196,181,852 / 23.43%
Number/percentage of T's	223,769,045 / 26.73%
Number/percentage of G's	193,118,881 / 23.07%
Number/percentage of N's	108,568 / 0.01%

GC Percentage	46.5%

2.3. Coverage

Mean	0.2705
Standard Deviation	18.1951

2.4. Mapping Quality

Mean Mapping Quality	54.55

2.5. Insert size

Mean	17,749.76
Standard Deviation	1,283,892.59
P25/Median/P75	145 / 198 / 263

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	6,335,217
Insertions	46,871
Mapped reads with at least one insertion	0.54%
Deletions	40,021
Mapped reads with at least one deletion	0.46%
Homopolymer indels	46.91%

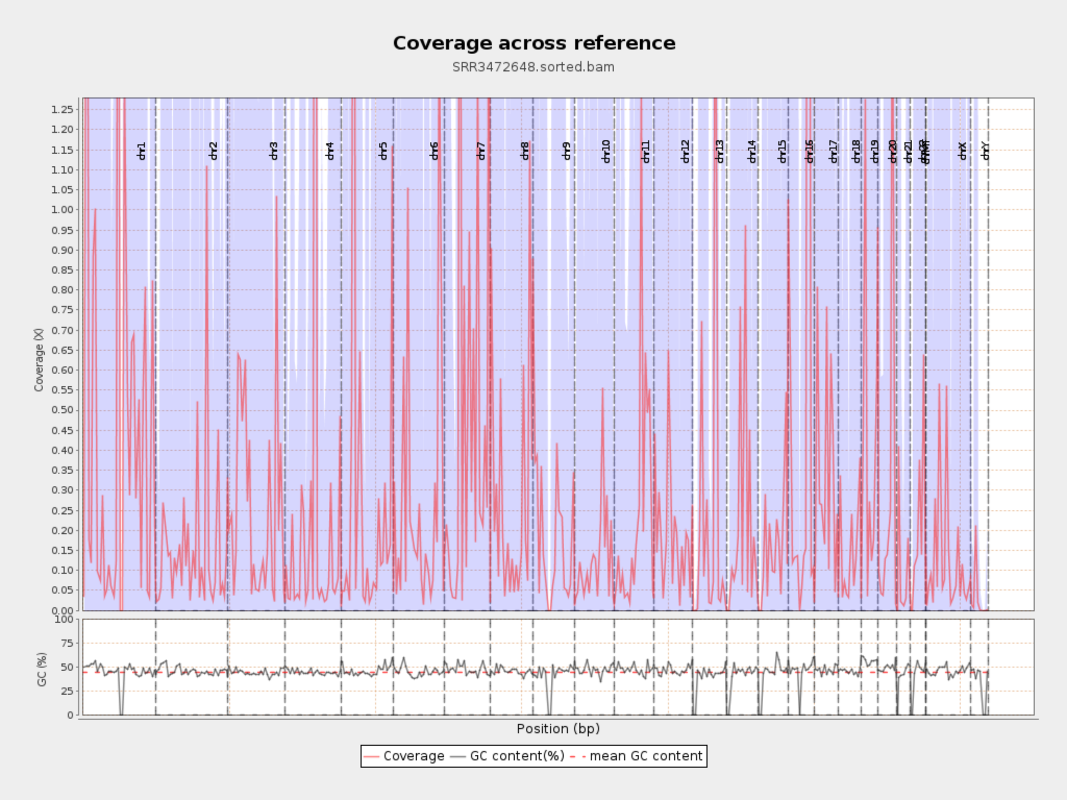
2.7. Chromosome stats

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

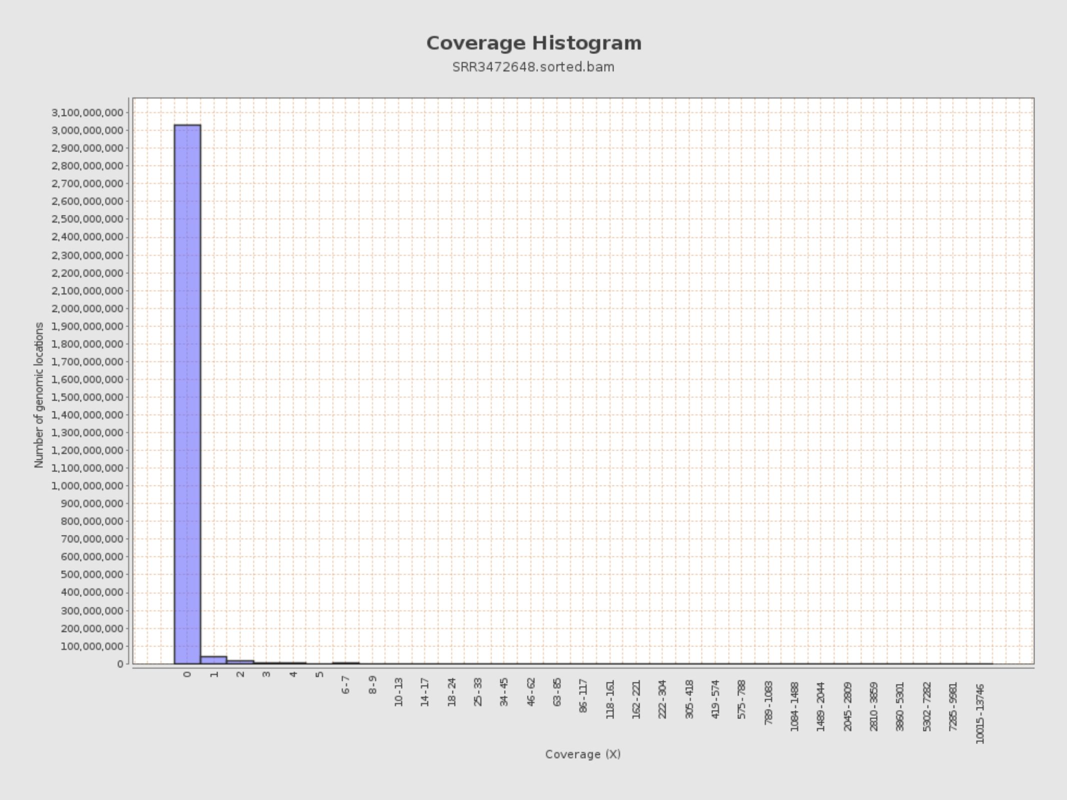
		bases	coverage	deviation
chr1	249250621	117849031	0.4728	22.6041
chr2	243199373	38137346	0.1568	7.1003
chr3	198022430	51679430	0.261	10.8271
chr4	191154276	56617790	0.2962	33.6558
chr5	180915260	56506918	0.3123	23.1672
chr6	171115067	47097778	0.2752	13.5647
chr7	159138663	83636226	0.5256	32.0342
chr8	146364022	41539873	0.2838	14.257
chr9	141213431	24059278	0.1704	9.5197
chr10	135534747	18409757	0.1358	7.6842
chr11	135006516	33402380	0.2474	22.8404
chr12	133851895	27044169	0.202	7.8118
chr13	115169878	26430834	0.2295	18.2555
chr14	107349540	23877529	0.2224	10.2174
chr15	102531392	16928379	0.1651	9.4069
chr16	90354753	49654902	0.5496	28.5638
chr17	81195210	28945337	0.3565	14.3102
chr18	78077248	11259413	0.1442	4.4986
chr19	59128983	24674407	0.4173	13.287
chr20	63025520	21515398	0.3414	27.451
chr21	48129895	5251652	0.1091	8.2353
chr22	51304566	10901250	0.2125	8.7799
chrMT	16571	2362	0.1425	0.425
chrX	155270560	19914271	0.1283	6.8667

chrY	59373566	1957288	0.033	4.7877

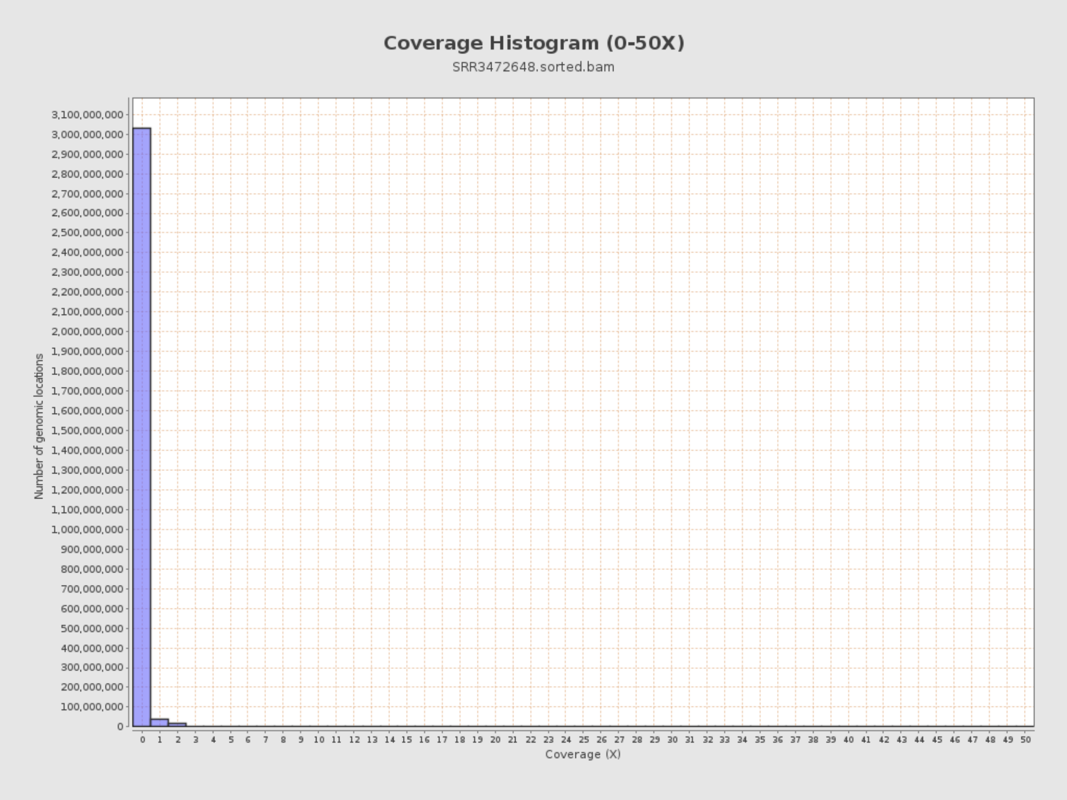
3. Results : Coverage across reference



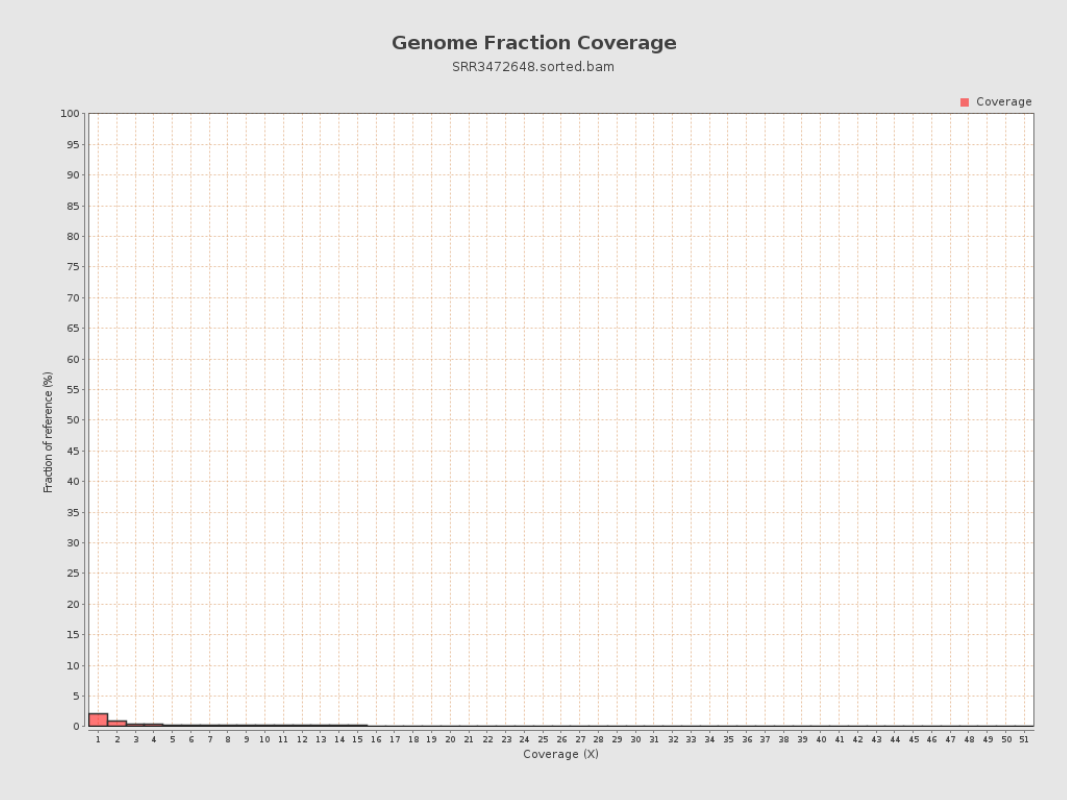
4. Results : Coverage Histogram



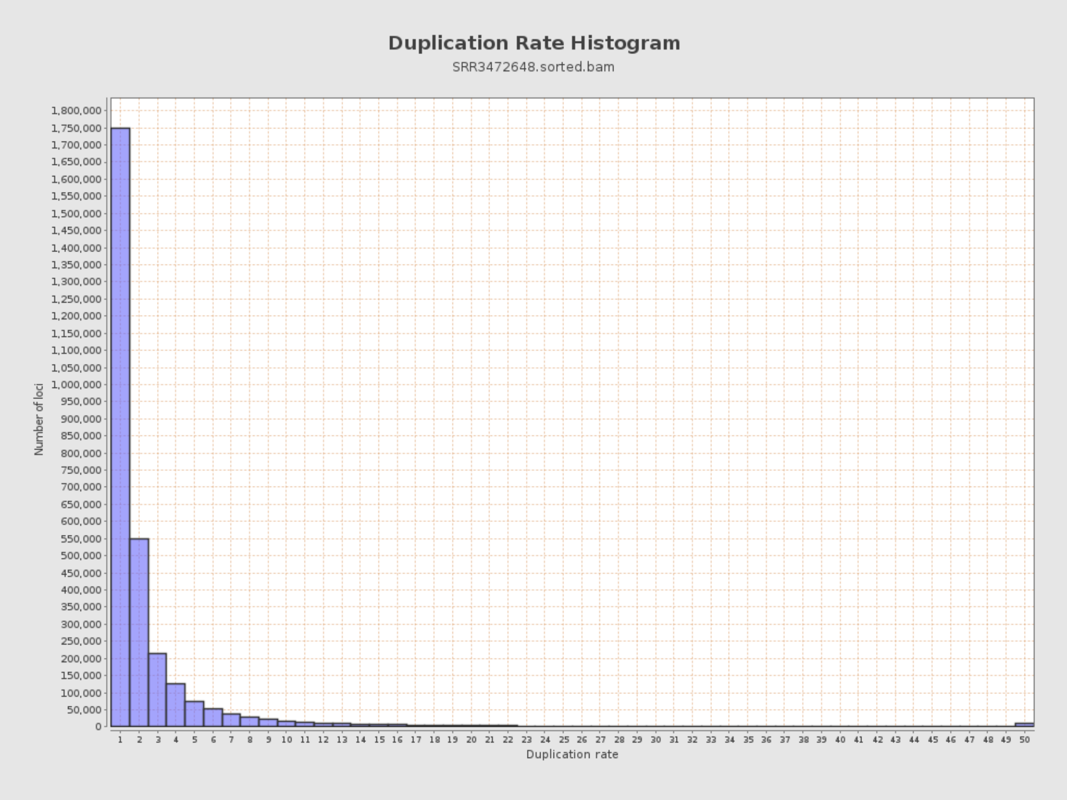
5. Results : Coverage Histogram (0-50X)



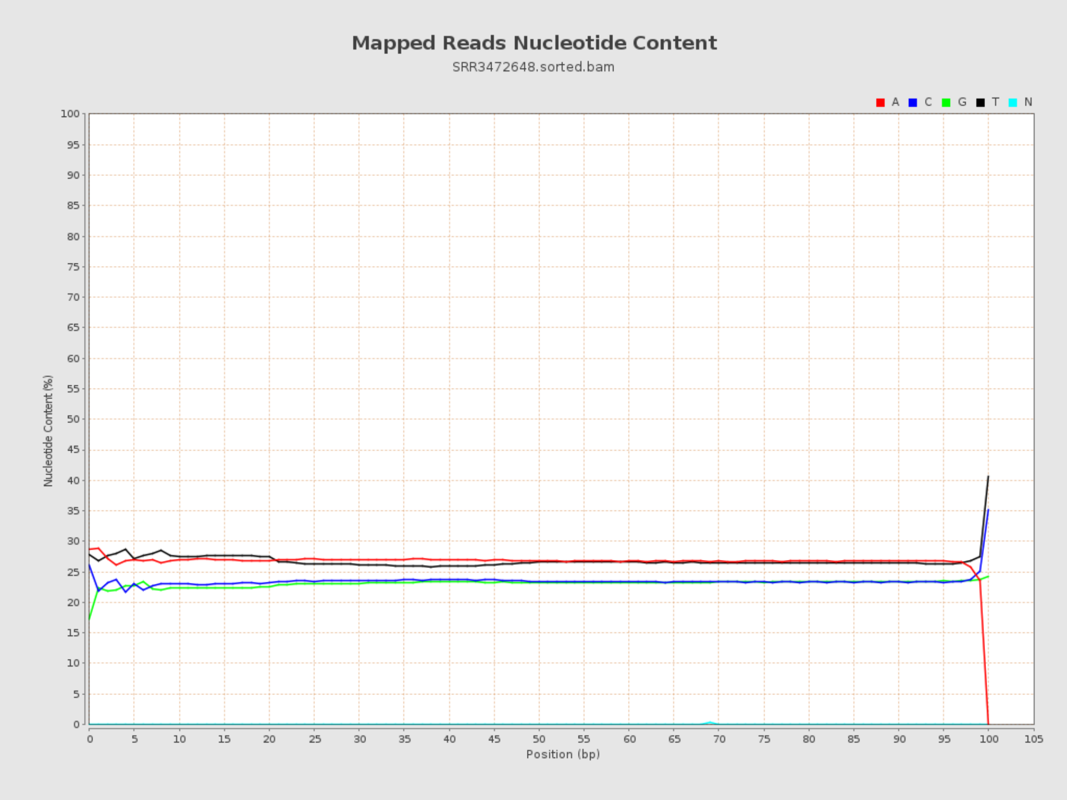
6. Results : Genome Fraction Coverage



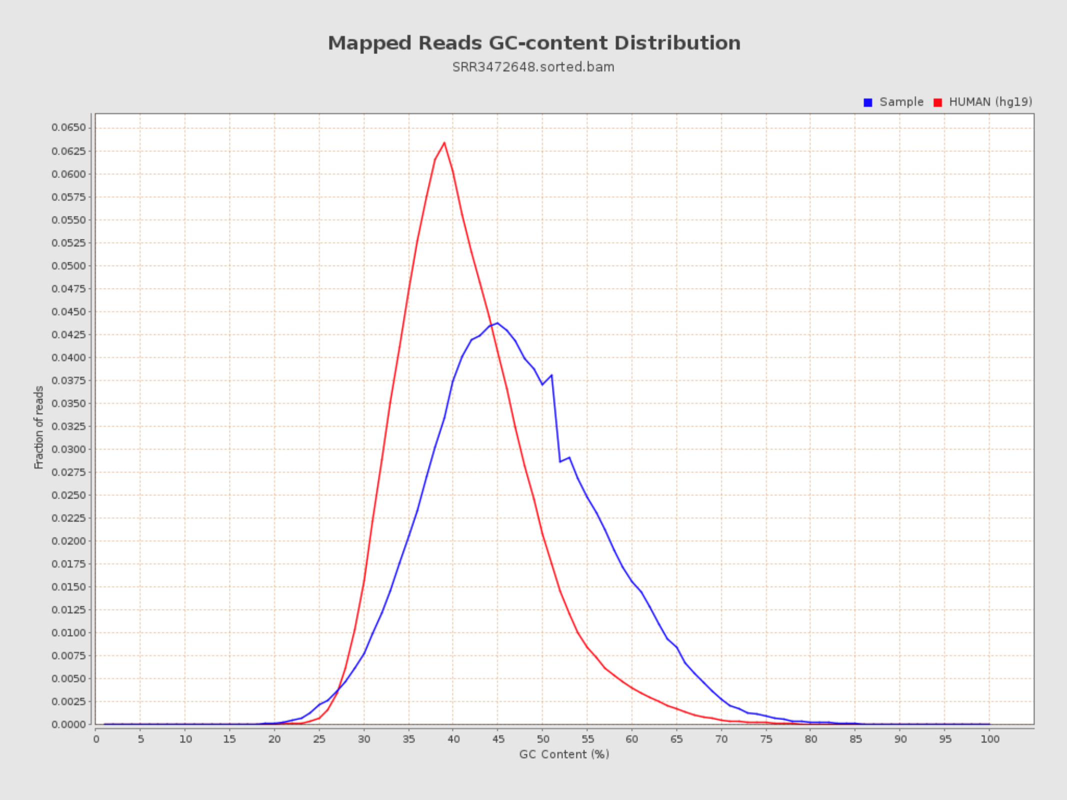
7. Results : Duplication Rate Histogram



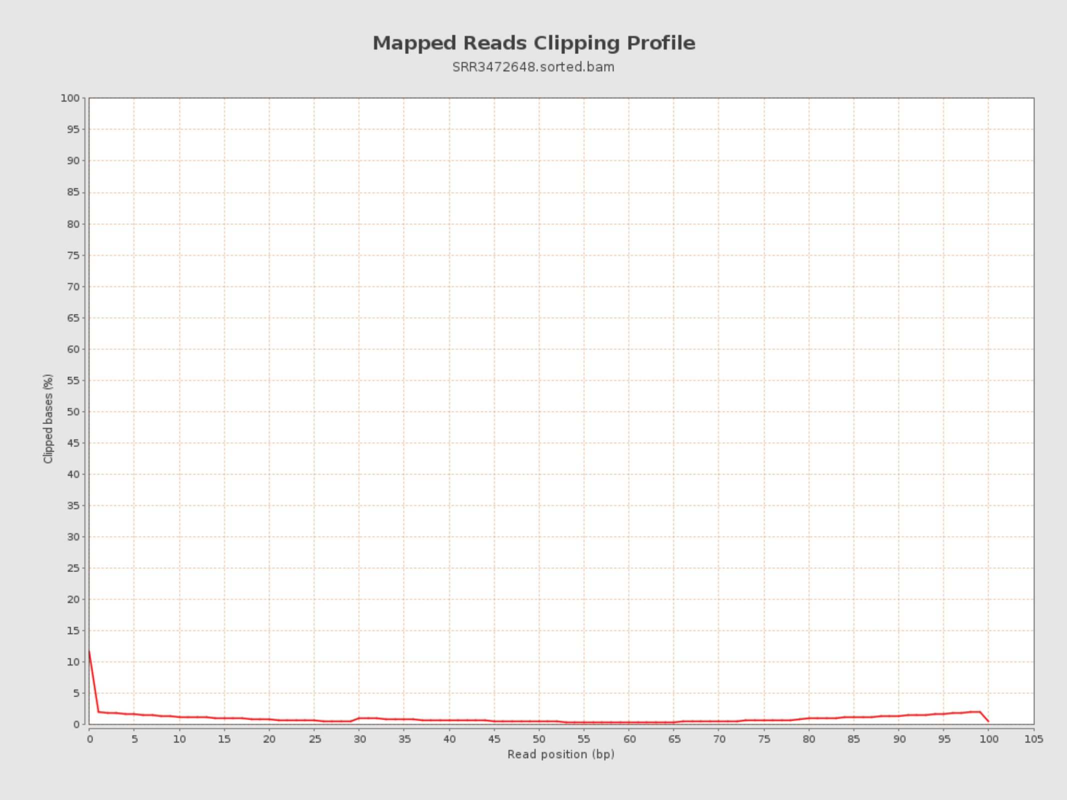
8. Results : Mapped Reads Nucleotide Content



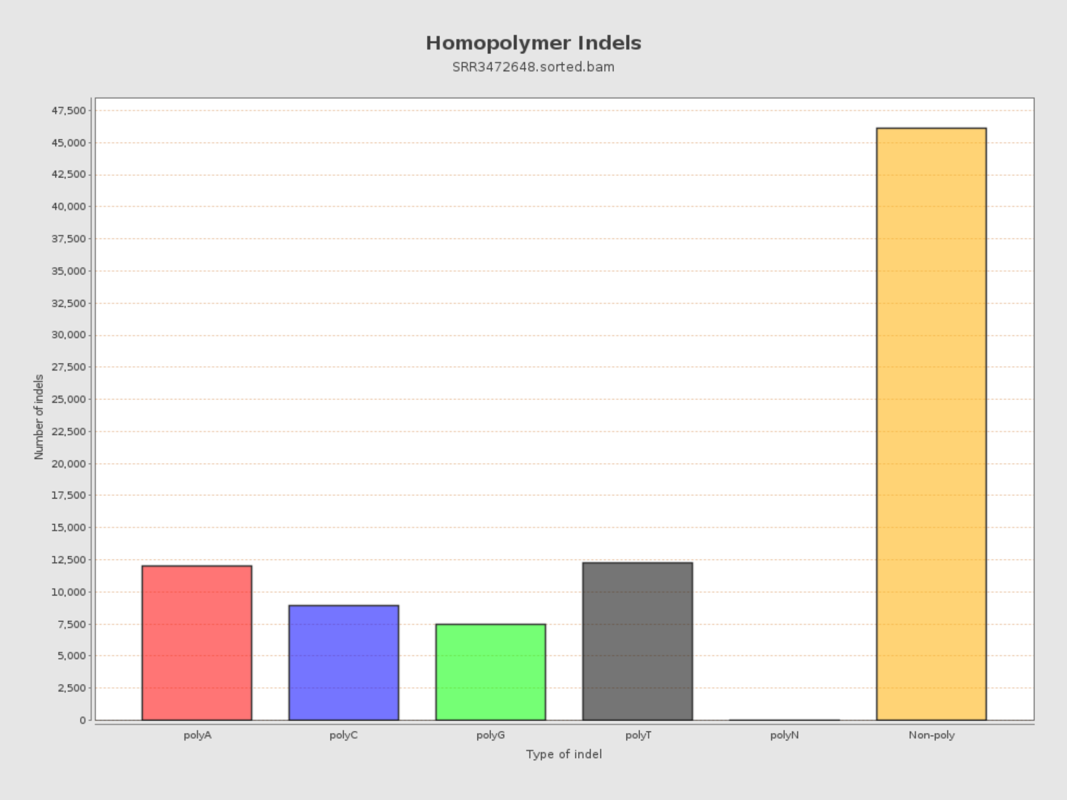
9. Results : Mapped Reads GC-content Distribution



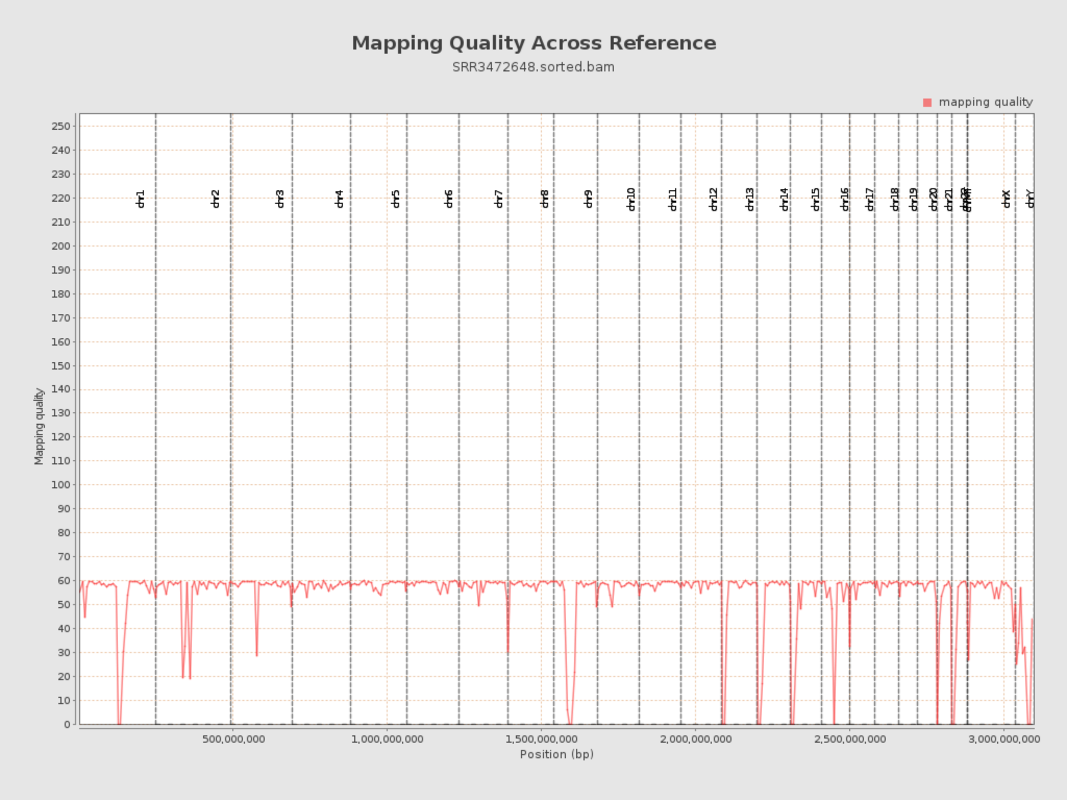
10. Results : Mapped Reads Clipping Profile



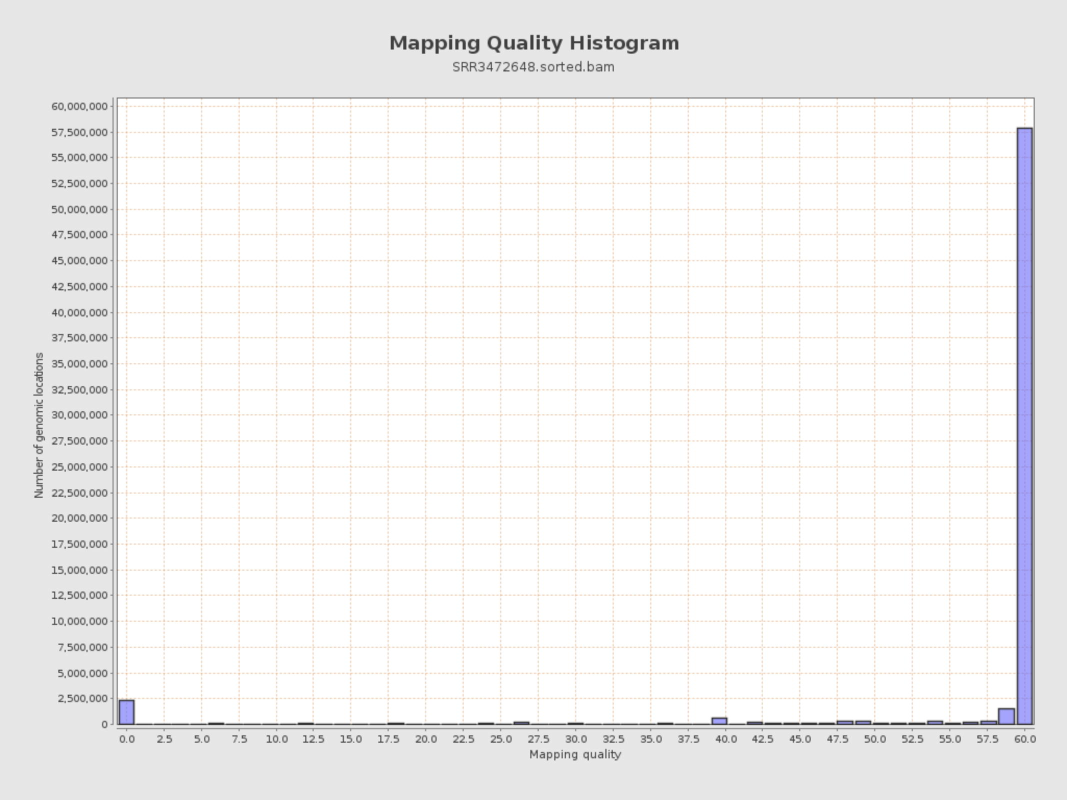
11. Results : Homopolymer Indels



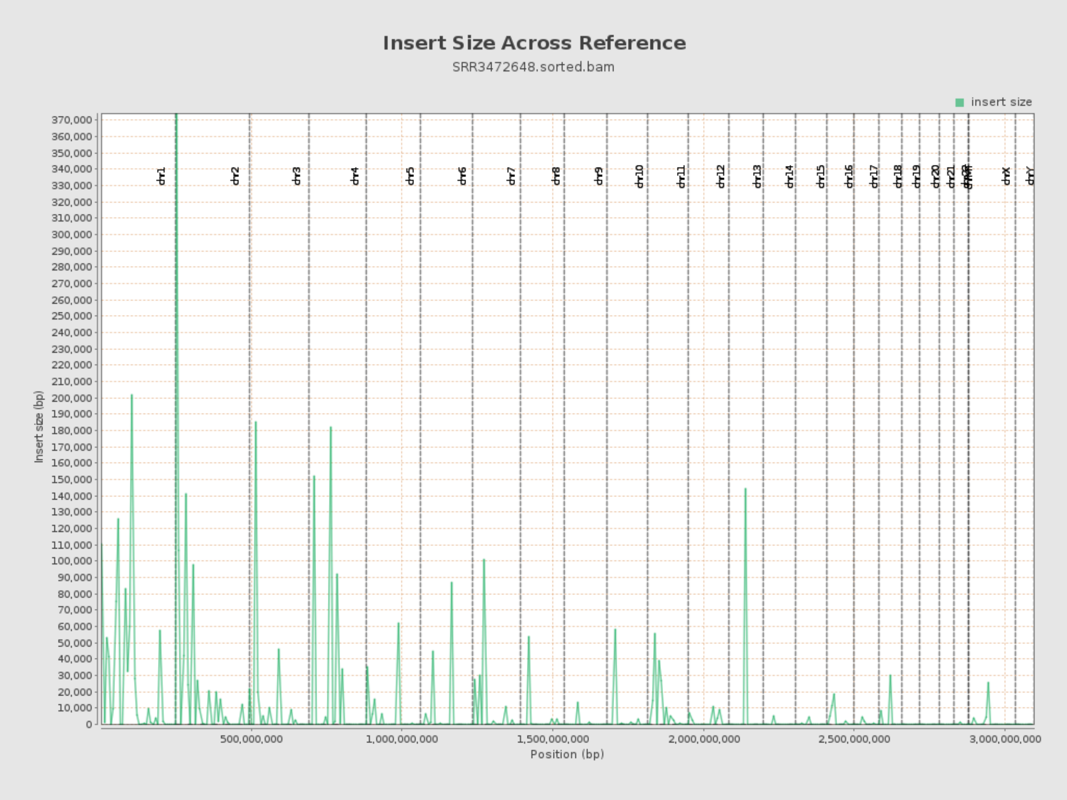
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram