Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 14:15:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472623.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_SRR3472623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472623_1.fastq.gz SRR3472623_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 14:15:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,832,568
Mapped reads	18,706,399 / 99.33%
Unmapped reads	126,169 / 0.67%
Mapped paired reads	18,706,399 / 99.33%
Mapped reads, first in pair	9,376,699 / 49.79%
Mapped reads, second in pair	9,329,700 / 49.54%
Mapped reads, both in pair	18,623,728 / 98.89%
Mapped reads, singletons	82,671 / 0.44%
Secondary alignments	0
Supplementary alignments	85,677 / 0.45%
Read min/max/mean length	30 / 101 / 99.63
Duplicated reads (estimated)	12,863,246 / 68.3%
Duplication rate	50.19%
Clipped reads	1,241,171 / 6.59%

2.2. ACGT Content

Number/percentage of A's	486,969,803 / 26.47%
Number/percentage of C's	434,936,954 / 23.64%
Number/percentage of T's	487,789,228 / 26.51%
Number/percentage of G's	429,983,545 / 23.37%
Number/percentage of N's	345,333 / 0.02%

GC Percentage	47.01%

2.3. Coverage

Mean	0.5945
Standard Deviation	23.7914

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	20,252.89
Standard Deviation	1,424,340.83
P25/Median/P75	157 / 217 / 288

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	11,039,222
Insertions	105,708
Mapped reads with at least one insertion	0.56%
Deletions	104,580
Mapped reads with at least one deletion	0.55%
Homopolymer indels	47.15%

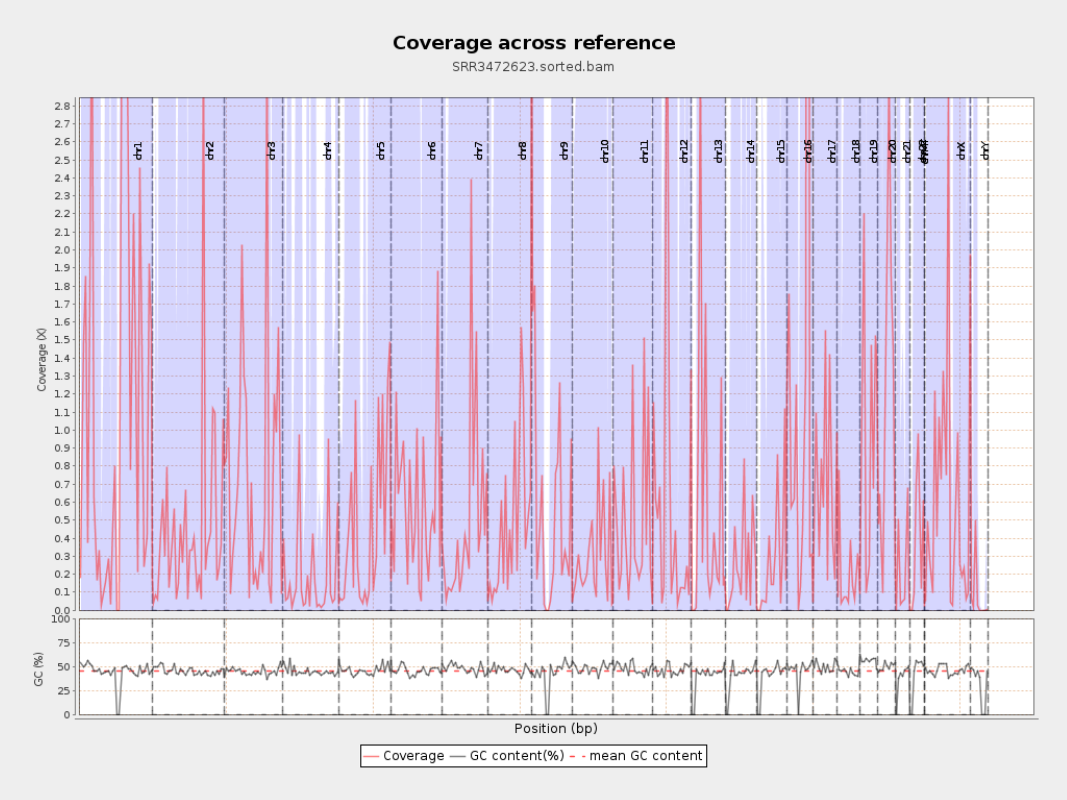
2.7. Chromosome stats

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

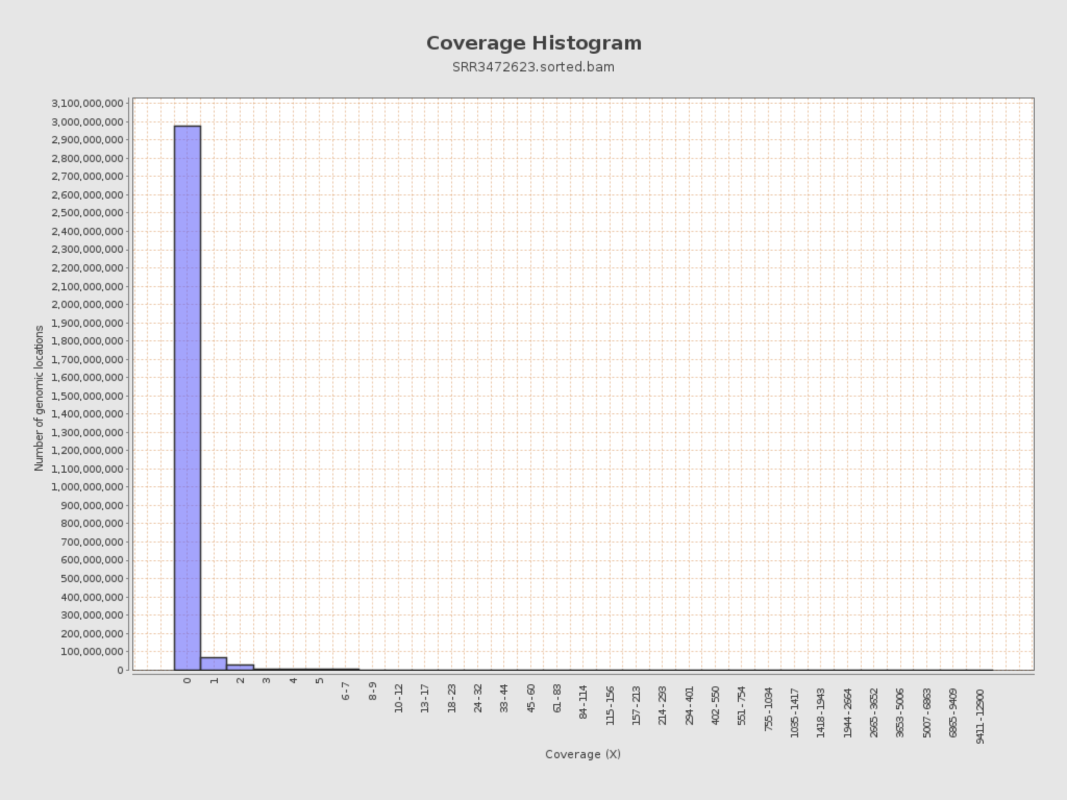
		bases	coverage	deviation
chr1	249250621	328477285	1.3179	38.9873
chr2	243199373	111457613	0.4583	20.613
chr3	198022430	152211750	0.7687	26.1541
chr4	191154276	36249774	0.1896	16.2771
chr5	180915260	84163021	0.4652	20.6235
chr6	171115067	100192915	0.5855	14.238
chr7	159138663	78795792	0.4951	16.9179
chr8	146364022	71638812	0.4895	17.3269
chr9	141213431	80547612	0.5704	16.7726
chr10	135534747	41873755	0.309	17.1318
chr11	135006516	68256831	0.5056	23.4335
chr12	133851895	77251014	0.5771	18.1165
chr13	115169878	69224090	0.6011	22.3847
chr14	107349540	26400696	0.2459	9.6676
chr15	102531392	28015575	0.2732	13.092
chr16	90354753	141748660	1.5688	60.8877
chr17	81195210	57314533	0.7059	19.0057
chr18	78077248	16303475	0.2088	8.2597
chr19	59128983	60078014	1.0161	23.3243
chr20	63025520	80307208	1.2742	34.211
chr21	48129895	10988861	0.2283	10.9805
chr22	51304566	19388350	0.3779	11.4365
chrMT	16571	2096	0.1265	0.5167
chrX	155270560	94813176	0.6106	26.2927

chrY	59373566	4603660	0.0775	8.3659

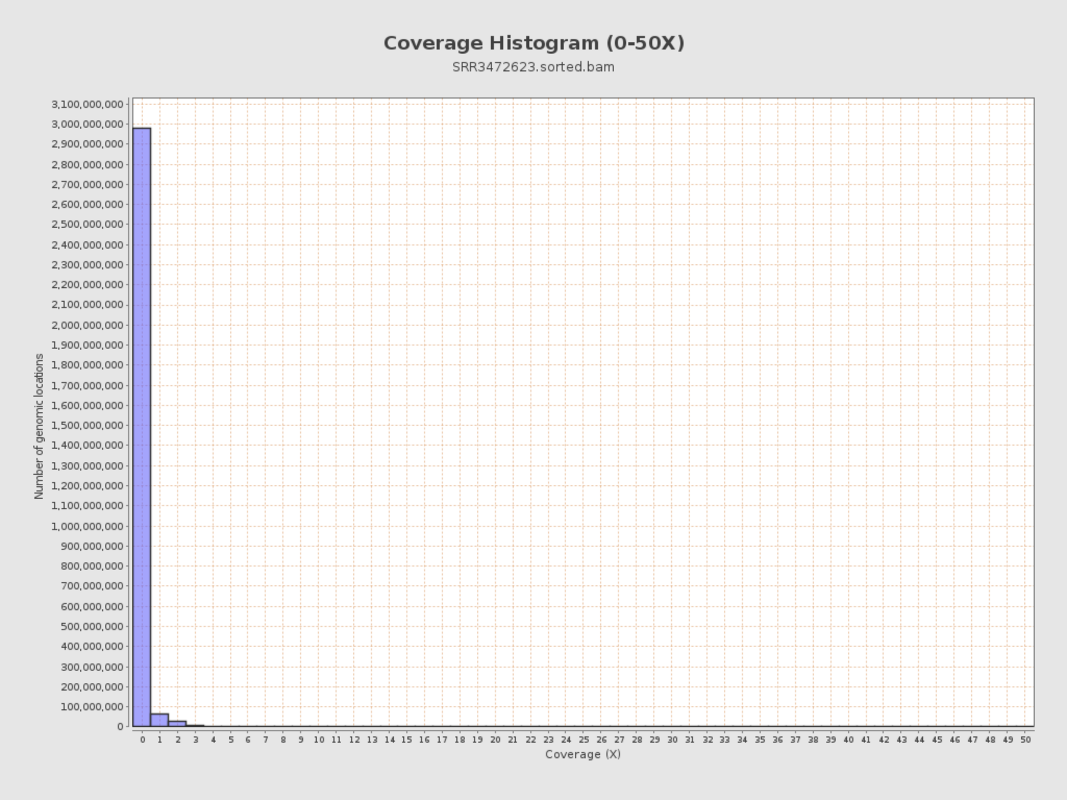
3. Results : Coverage across reference



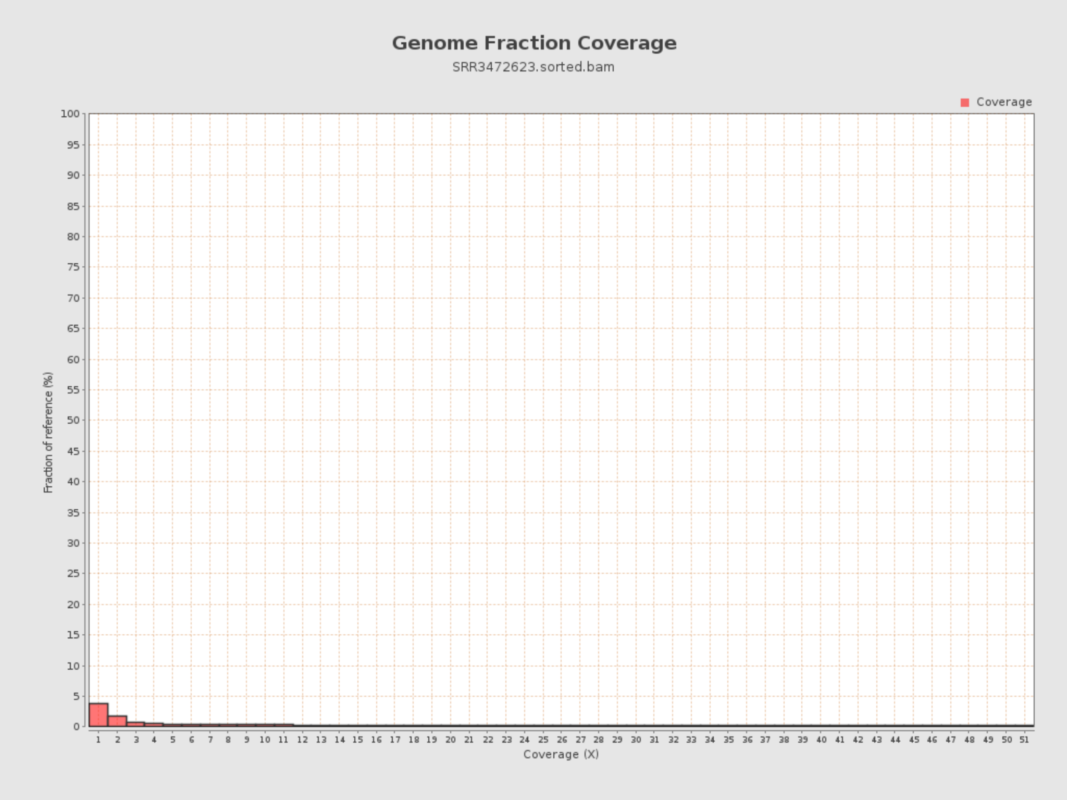
4. Results : Coverage Histogram



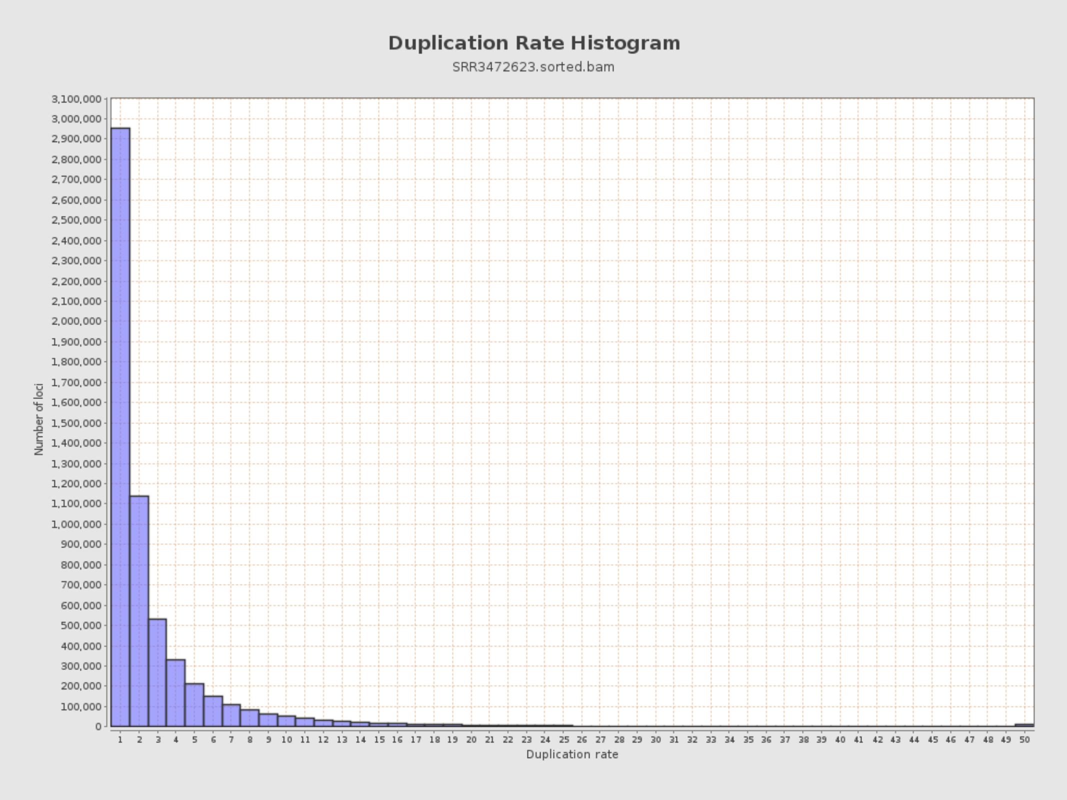
5. Results : Coverage Histogram (0-50X)



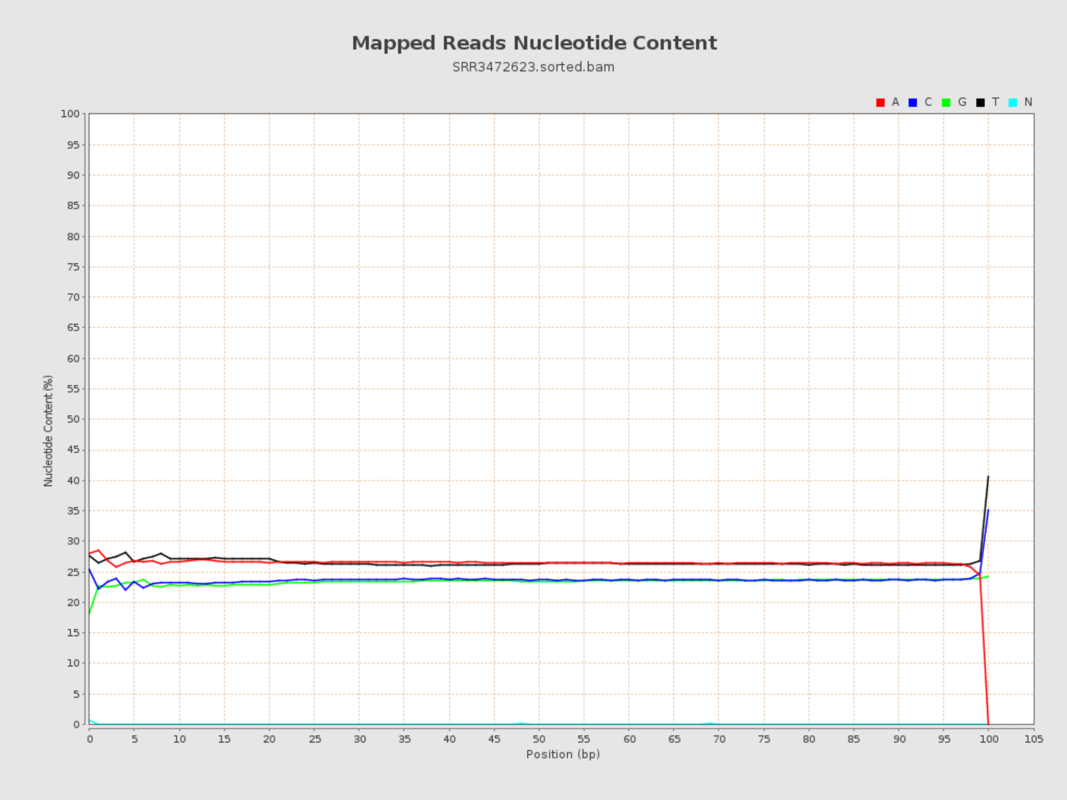
6. Results : Genome Fraction Coverage



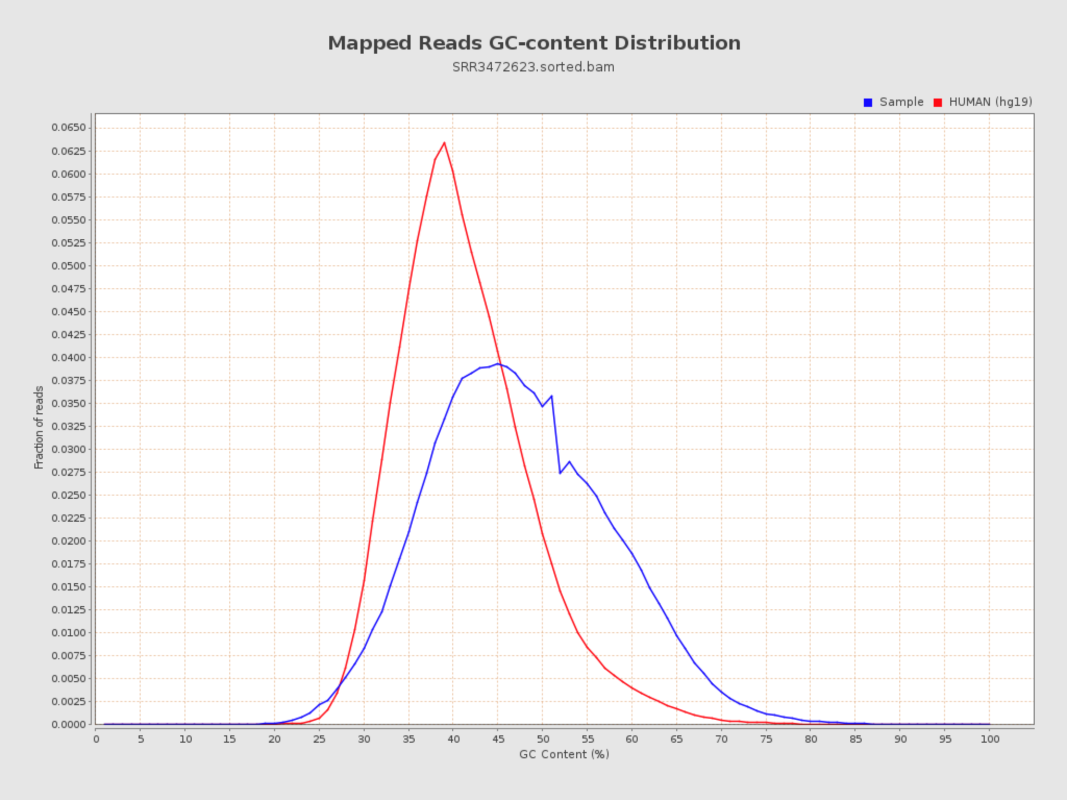
7. Results : Duplication Rate Histogram



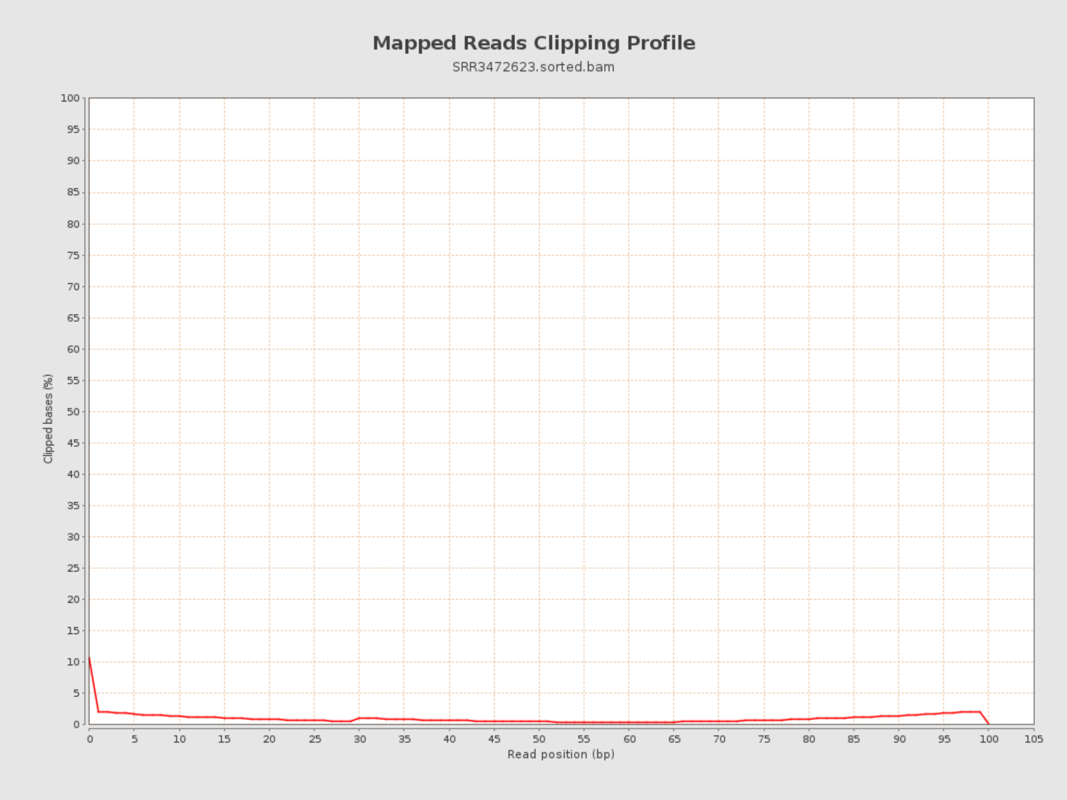
8. Results : Mapped Reads Nucleotide Content



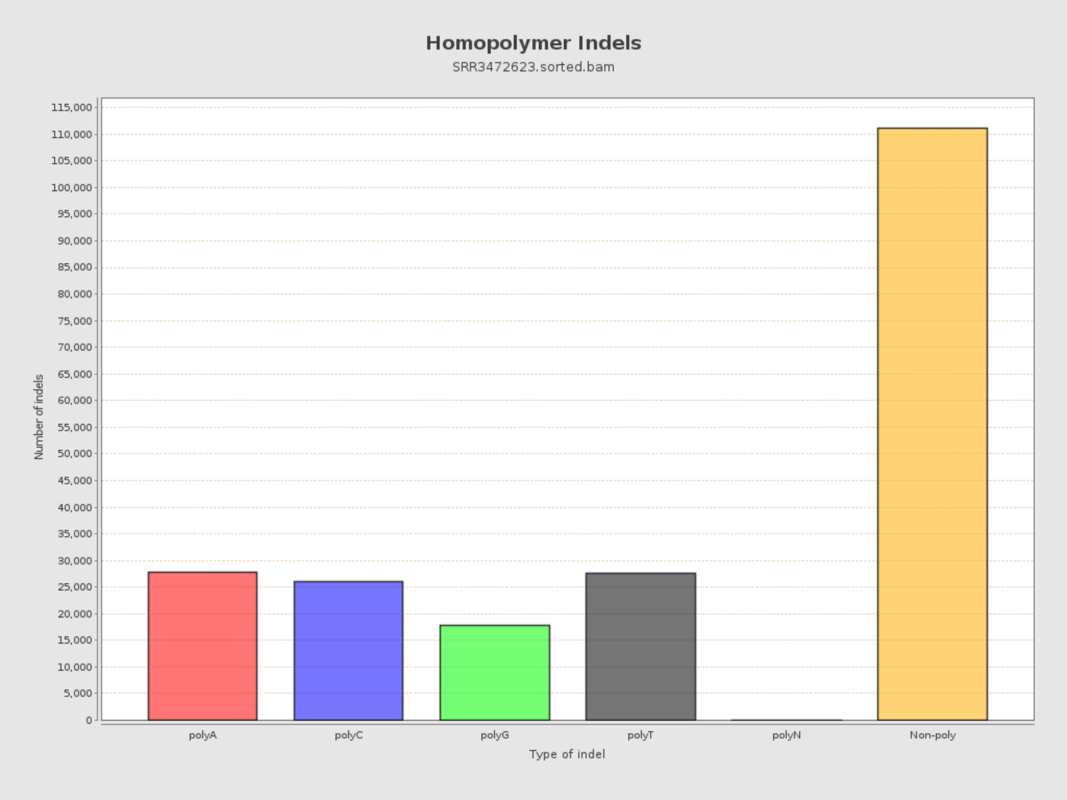
9. Results : Mapped Reads GC-content Distribution



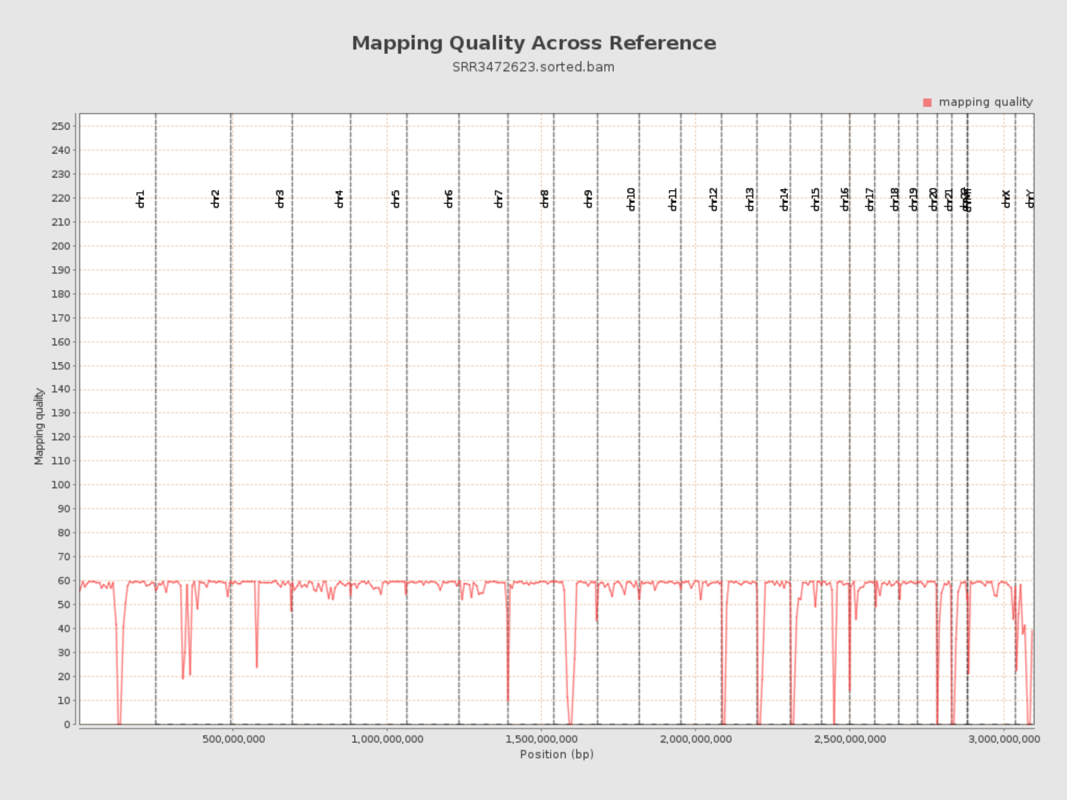
10. Results : Mapped Reads Clipping Profile



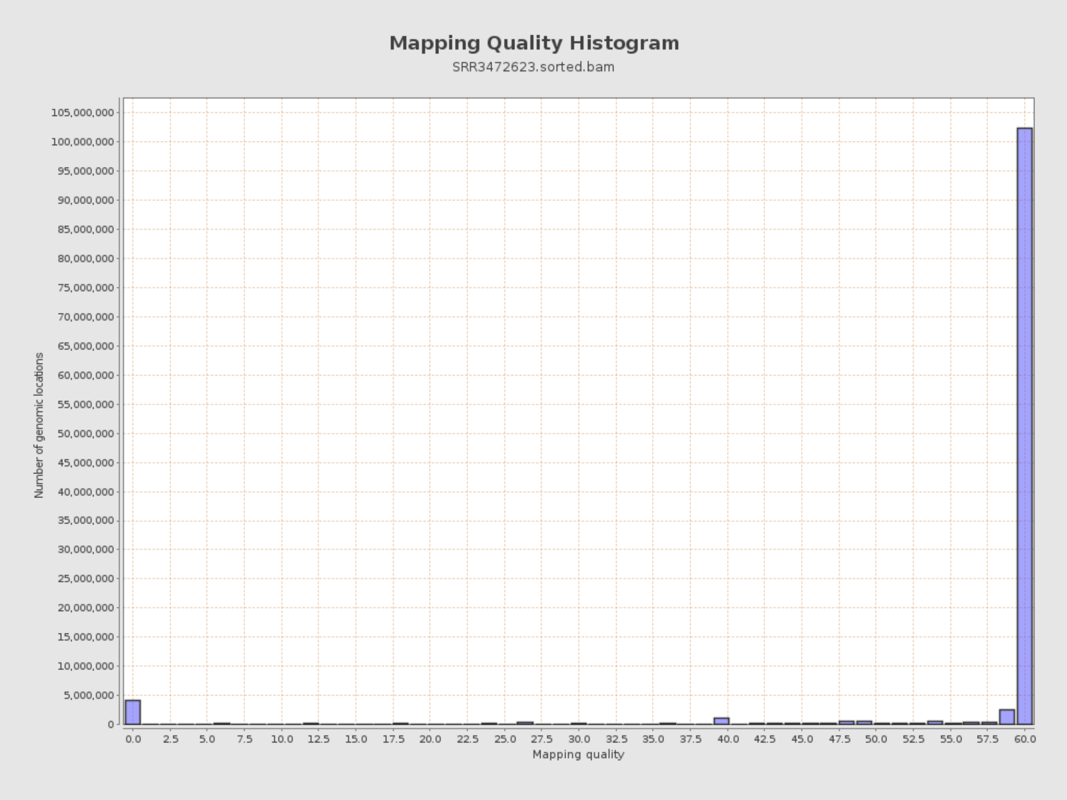
11. Results : Homopolymer Indels



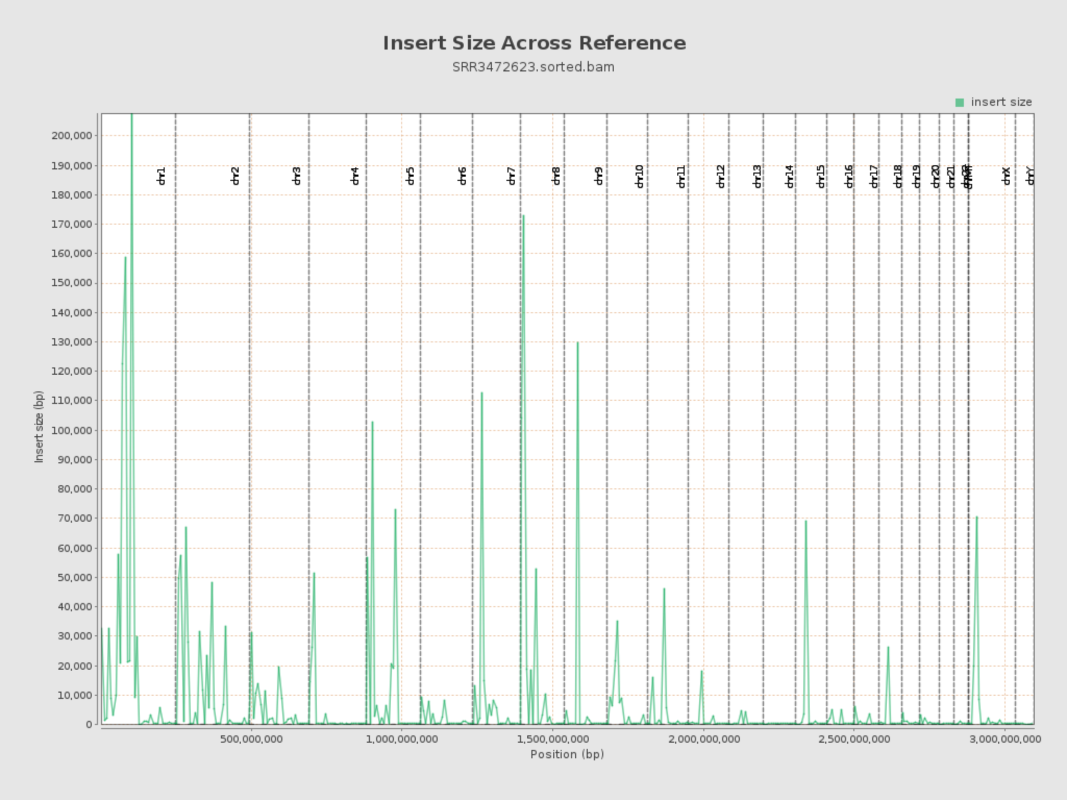
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram