Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 14:36:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472624.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_SRR3472624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472624_1.fastq.gz SRR3472624_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 14:36:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,216,502
Mapped reads	19,071,248 / 99.24%
Unmapped reads	145,254 / 0.76%
Mapped paired reads	19,071,248 / 99.24%
Mapped reads, first in pair	9,567,486 / 49.79%
Mapped reads, second in pair	9,503,762 / 49.46%
Mapped reads, both in pair	18,967,474 / 98.7%
Mapped reads, singletons	103,774 / 0.54%
Secondary alignments	0
Supplementary alignments	101,902 / 0.53%
Read min/max/mean length	30 / 101 / 99.78
Duplicated reads (estimated)	13,386,215 / 69.66%
Duplication rate	50.01%
Clipped reads	1,234,466 / 6.42%

2.2. ACGT Content

Number/percentage of A's	504,641,019 / 26.85%
Number/percentage of C's	437,500,740 / 23.28%
Number/percentage of T's	506,326,631 / 26.94%
Number/percentage of G's	430,602,943 / 22.91%
Number/percentage of N's	341,877 / 0.02%

GC Percentage	46.19%

2.3. Coverage

Mean	0.6072
Standard Deviation	26.6136

2.4. Mapping Quality

Mean Mapping Quality	54.68

2.5. Insert size

Mean	22,316.64
Standard Deviation	1,465,056.46
P25/Median/P75	166 / 228 / 301

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	11,656,309
Insertions	123,261
Mapped reads with at least one insertion	0.64%
Deletions	114,871
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.42%

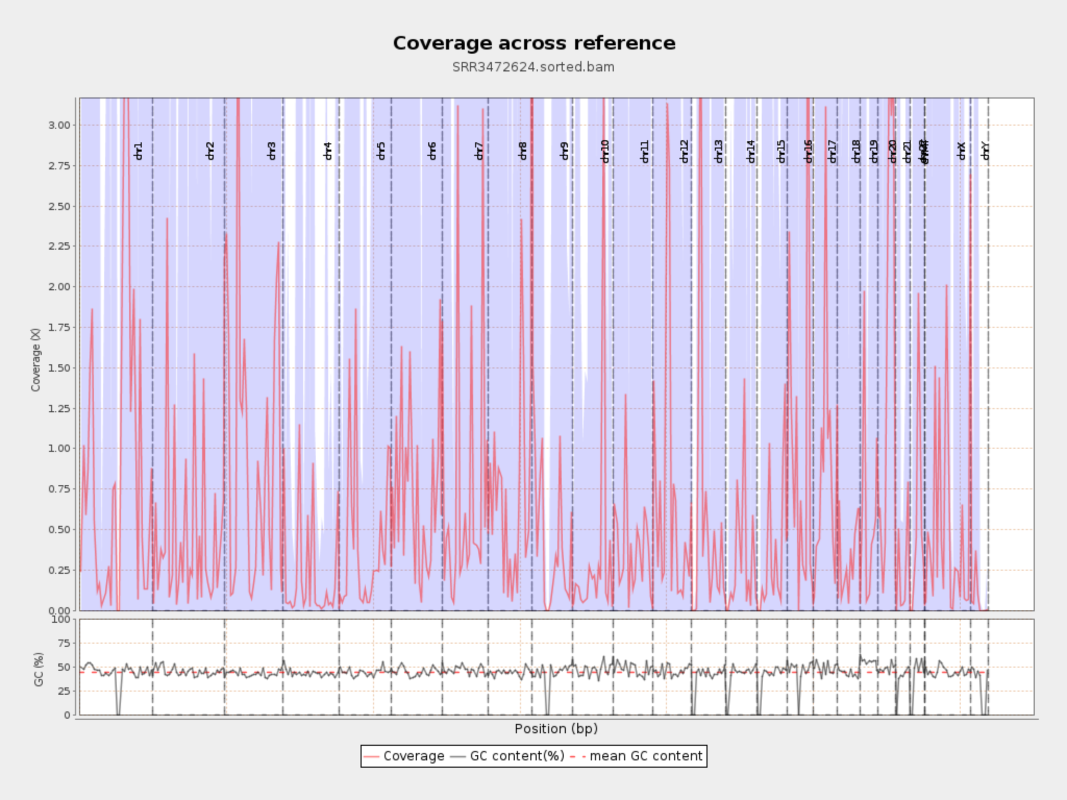
2.7. Chromosome stats

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

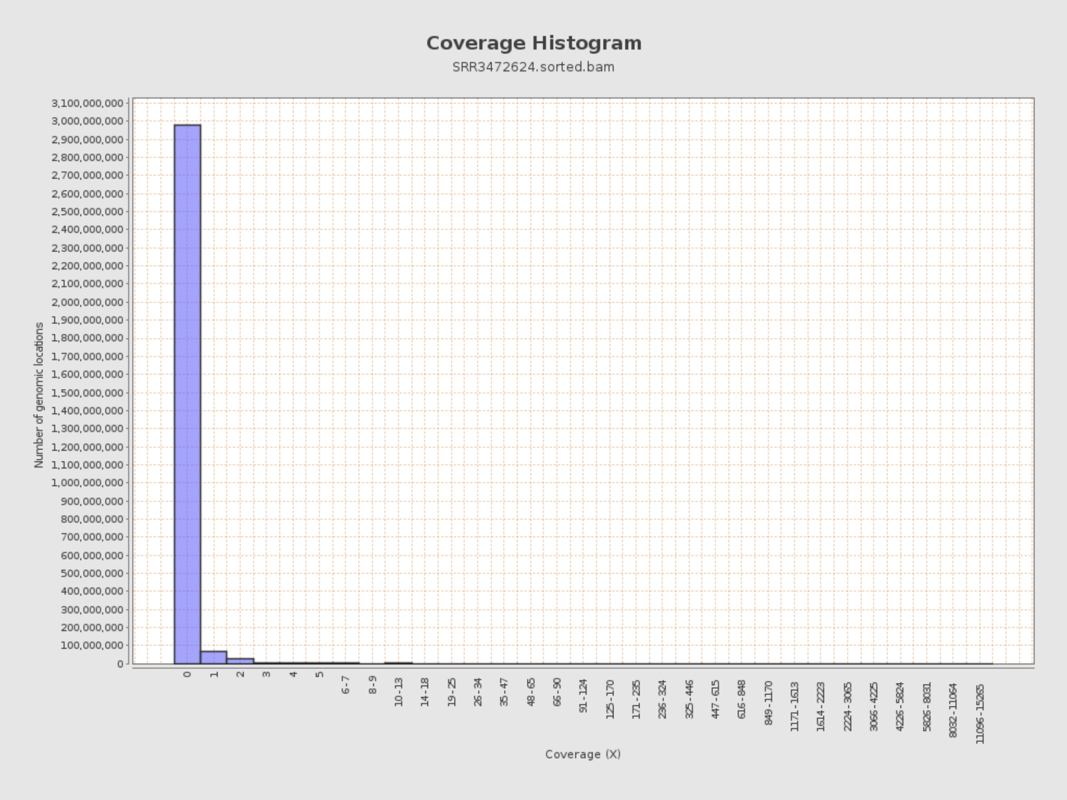
		bases	coverage	deviation
chr1	249250621	230374137	0.9243	30.2713
chr2	243199373	112261847	0.4616	22.2516
chr3	198022430	208494223	1.0529	39.4115
chr4	191154276	40672751	0.2128	10.6564
chr5	180915260	75223385	0.4158	15.7309
chr6	171115067	123112962	0.7195	23.0592
chr7	159138663	120188474	0.7552	35.7221
chr8	146364022	104249634	0.7123	24.1205
chr9	141213431	74058439	0.5244	20.7405
chr10	135534747	44640619	0.3294	30.4221
chr11	135006516	52265899	0.3871	15.7764
chr12	133851895	97183256	0.7261	28.006
chr13	115169878	70841972	0.6151	30.2984
chr14	107349540	32983174	0.3073	12.9343
chr15	102531392	37115550	0.362	16.9448
chr16	90354753	95440070	1.0563	39.2648
chr17	81195210	74366149	0.9159	26.7464
chr18	78077248	25882369	0.3315	12.4024
chr19	59128983	34796762	0.5885	13.4899
chr20	63025520	104602937	1.6597	63.4851
chr21	48129895	12443084	0.2585	12.0664
chr22	51304566	26386284	0.5143	24.8825
chrMT	16571	1425	0.086	0.4058
chrX	155270560	77776564	0.5009	24.9914

chrY	59373566	4329941	0.0729	6.4126

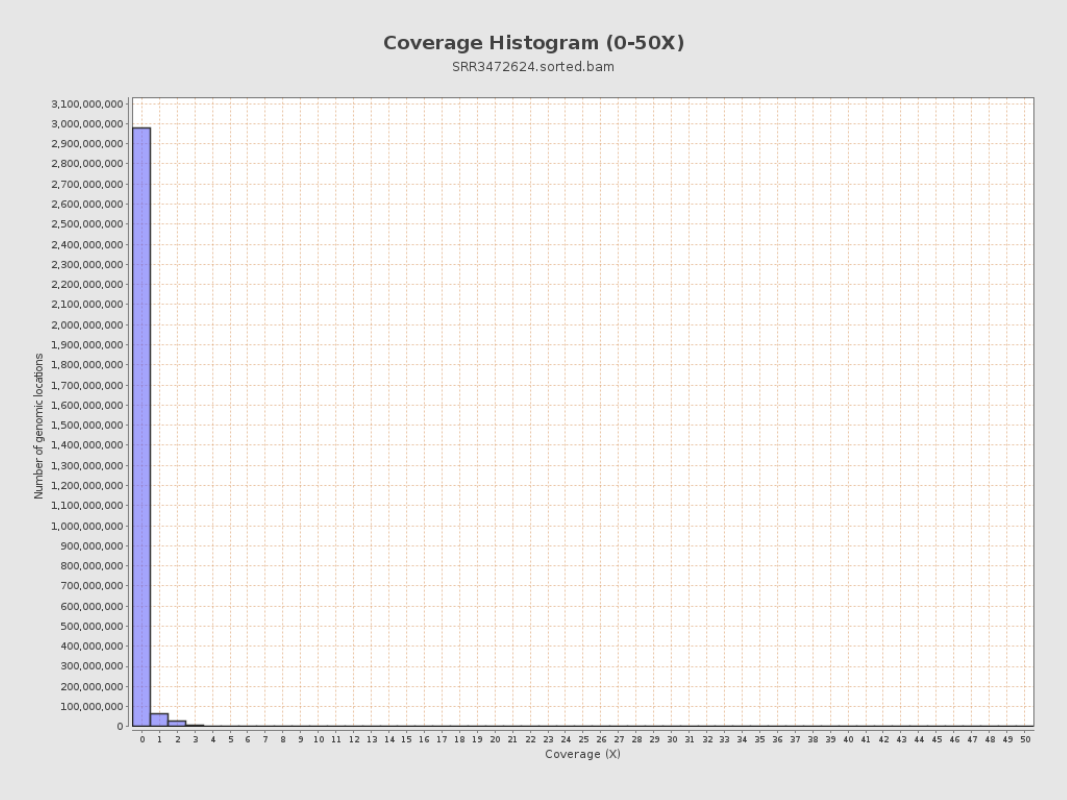
3. Results : Coverage across reference



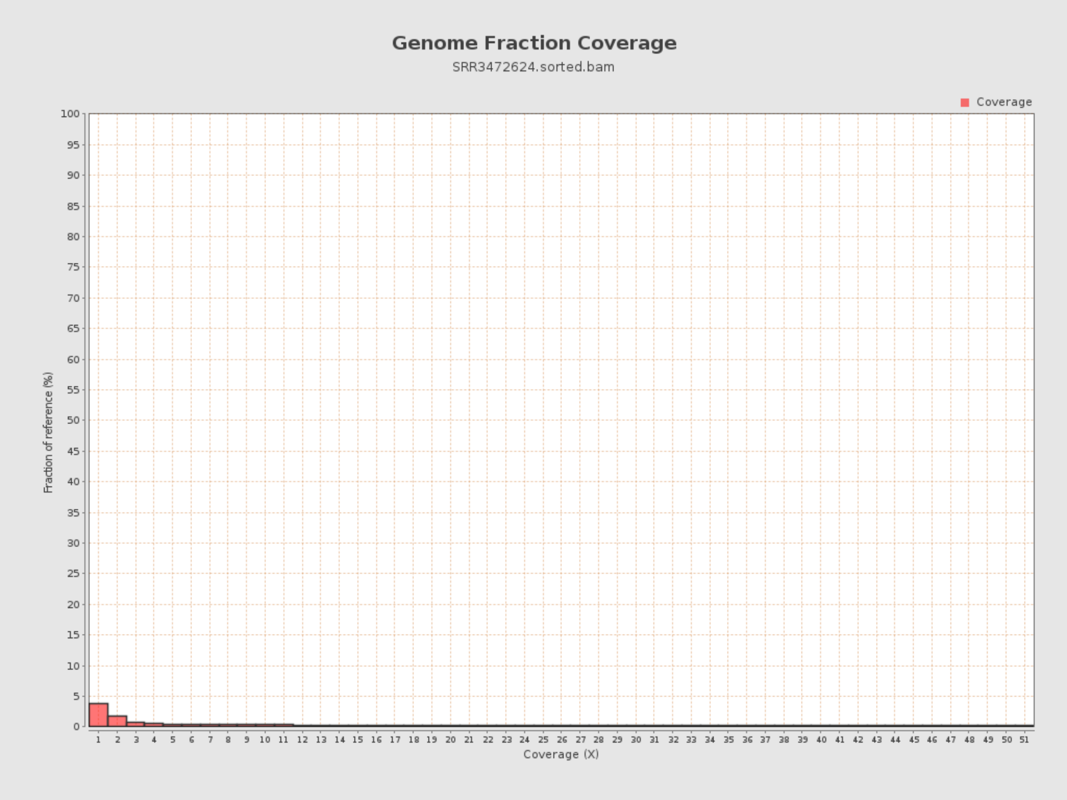
4. Results : Coverage Histogram



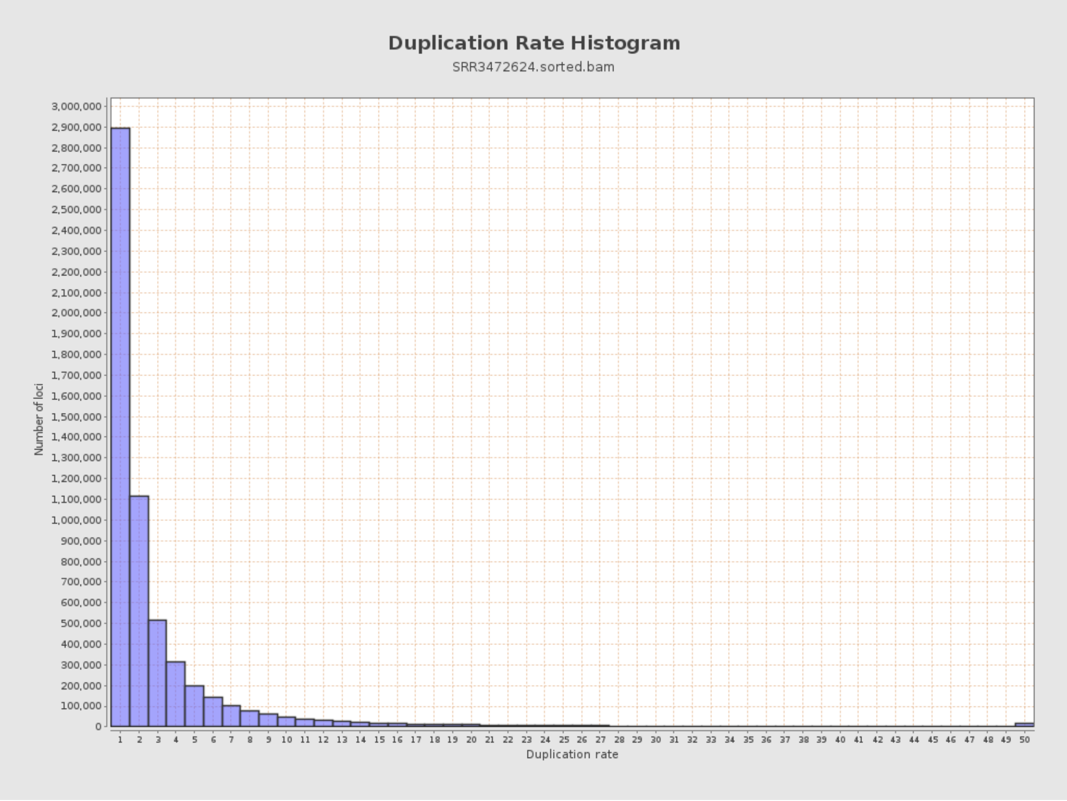
5. Results : Coverage Histogram (0-50X)



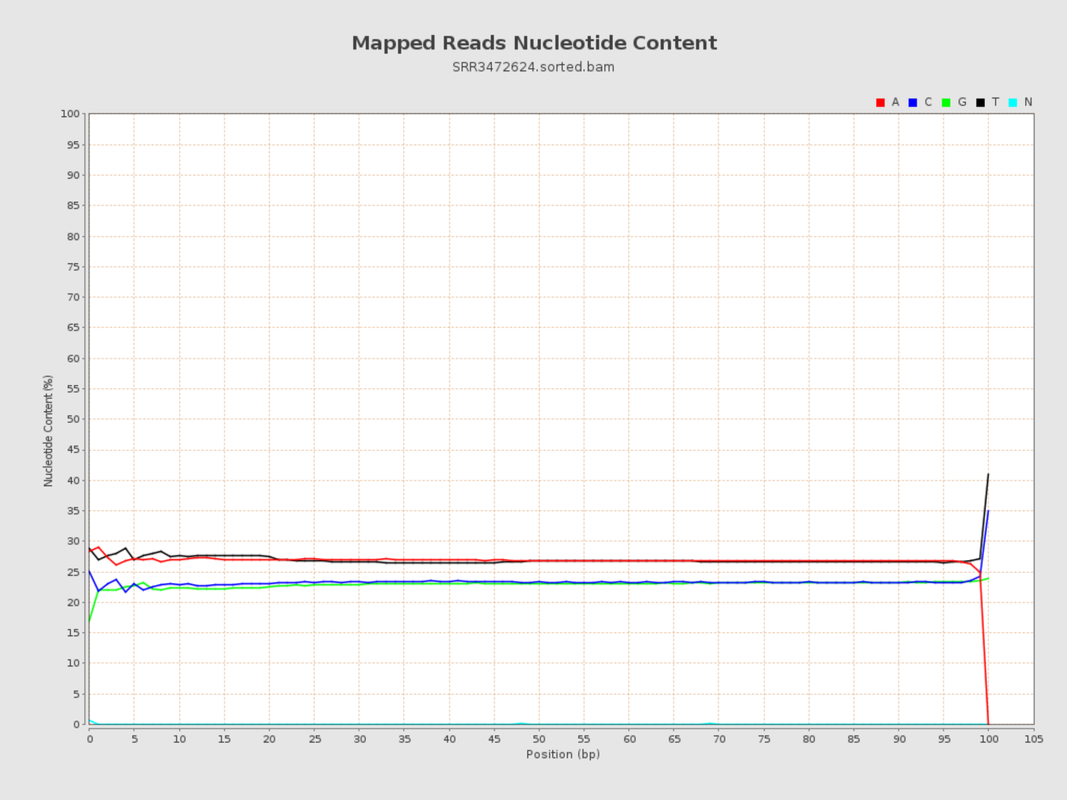
6. Results : Genome Fraction Coverage



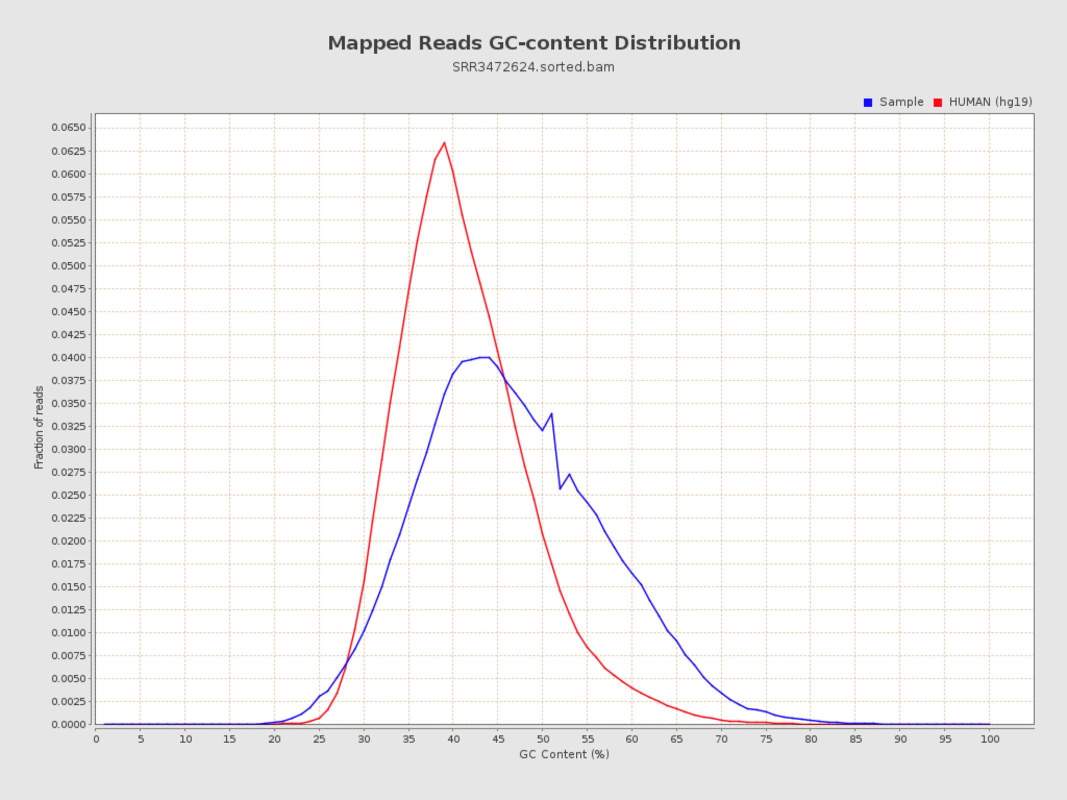
7. Results : Duplication Rate Histogram



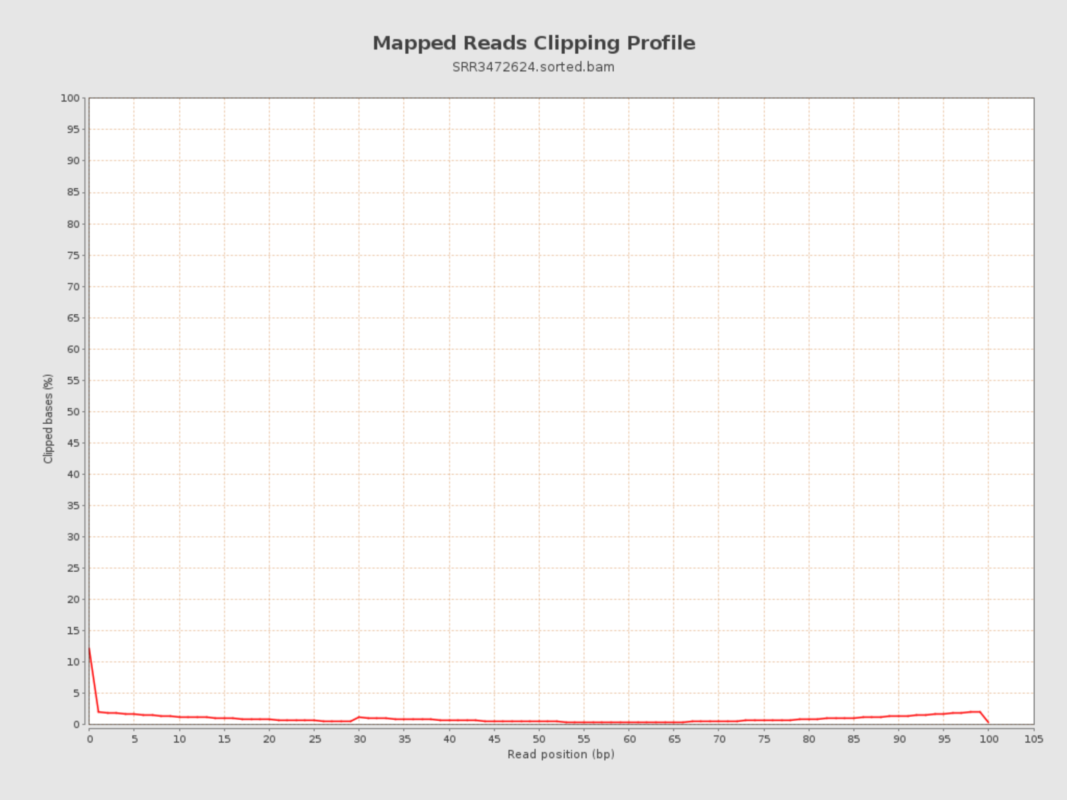
8. Results : Mapped Reads Nucleotide Content



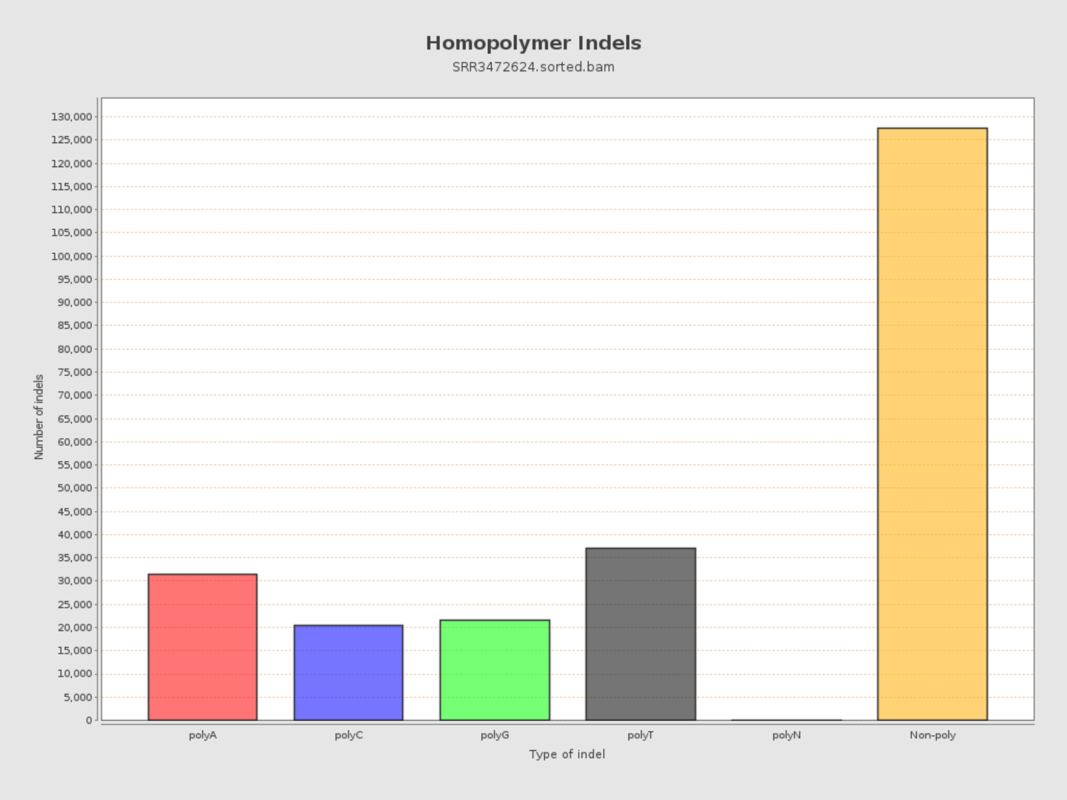
9. Results : Mapped Reads GC-content Distribution



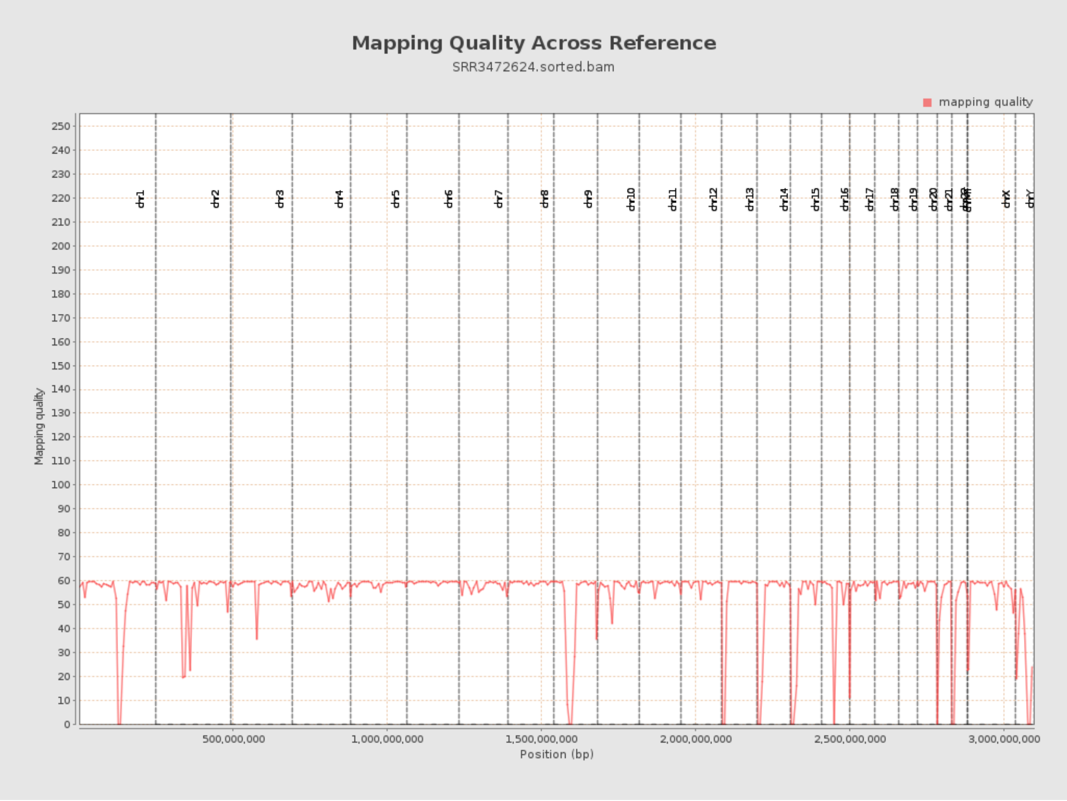
10. Results : Mapped Reads Clipping Profile



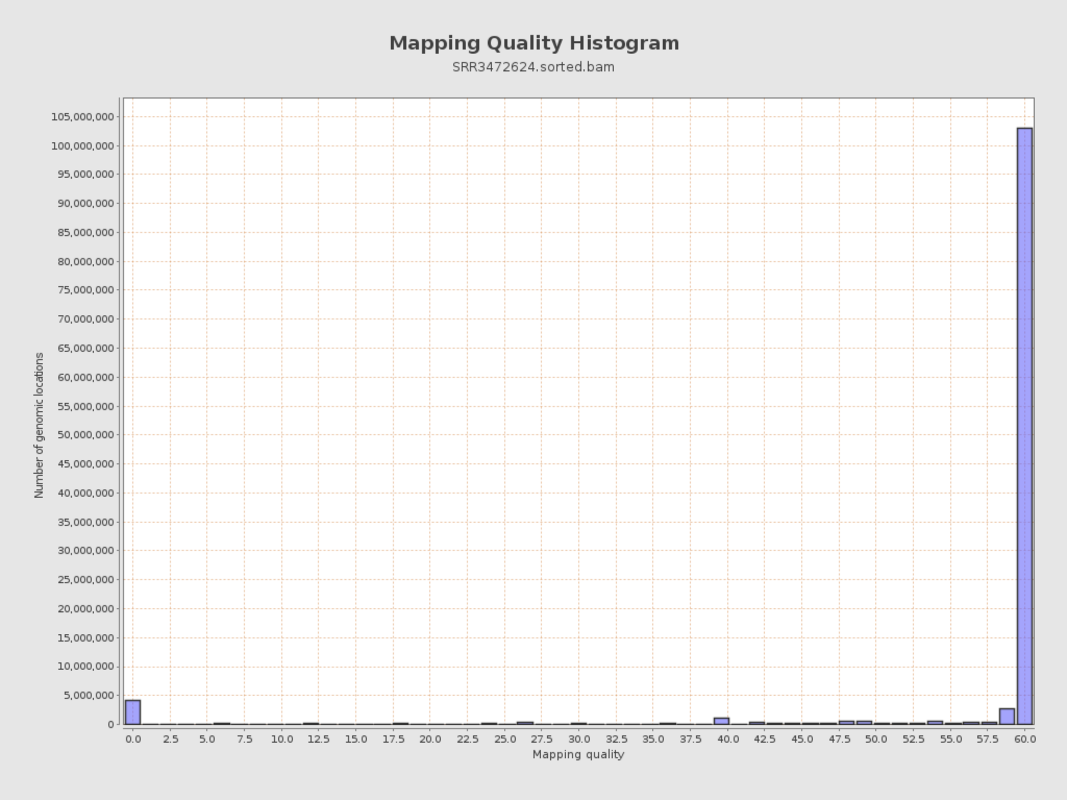
11. Results : Homopolymer Indels



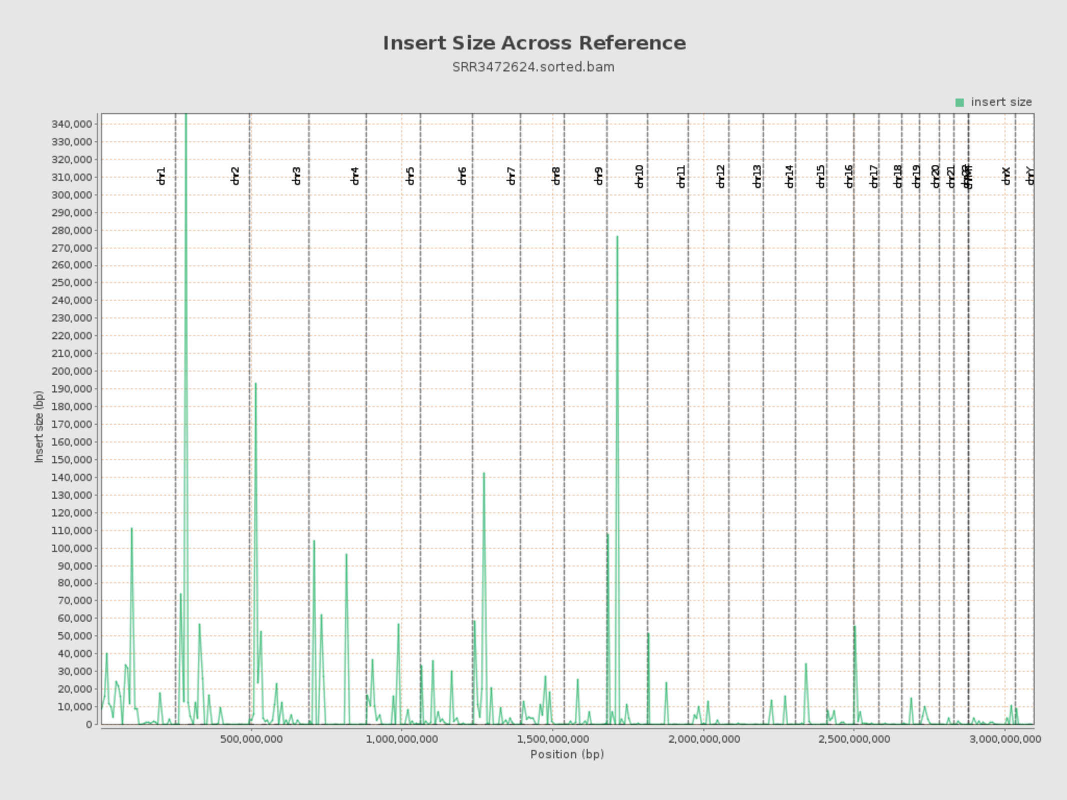
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram