Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:46:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472424.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_SRR3472424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472424_1.fastq.gz SRR3472424_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:46:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,163,910
Mapped reads	21,980,593 / 99.17%
Unmapped reads	183,317 / 0.83%
Mapped paired reads	21,980,593 / 99.17%
Mapped reads, first in pair	11,021,199 / 49.73%
Mapped reads, second in pair	10,959,394 / 49.45%
Mapped reads, both in pair	21,872,444 / 98.68%
Mapped reads, singletons	108,149 / 0.49%
Secondary alignments	0
Supplementary alignments	84,412 / 0.38%
Read min/max/mean length	30 / 100 / 99.38
Duplicated reads (estimated)	14,222,496 / 64.17%
Duplication rate	48.27%
Clipped reads	1,513,869 / 6.83%

2.2. ACGT Content

Number/percentage of A's	594,196,916 / 27.56%
Number/percentage of C's	485,193,050 / 22.51%
Number/percentage of T's	595,561,895 / 27.63%
Number/percentage of G's	480,472,010 / 22.29%
Number/percentage of N's	266,855 / 0.01%

GC Percentage	44.8%

2.3. Coverage

Mean	0.6964
Standard Deviation	20.4603

2.4. Mapping Quality

Mean Mapping Quality	54.81

2.5. Insert size

Mean	18,463.11
Standard Deviation	1,346,420.97
P25/Median/P75	156 / 218 / 294

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	11,751,388
Insertions	129,399
Mapped reads with at least one insertion	0.58%
Deletions	109,468
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.72%

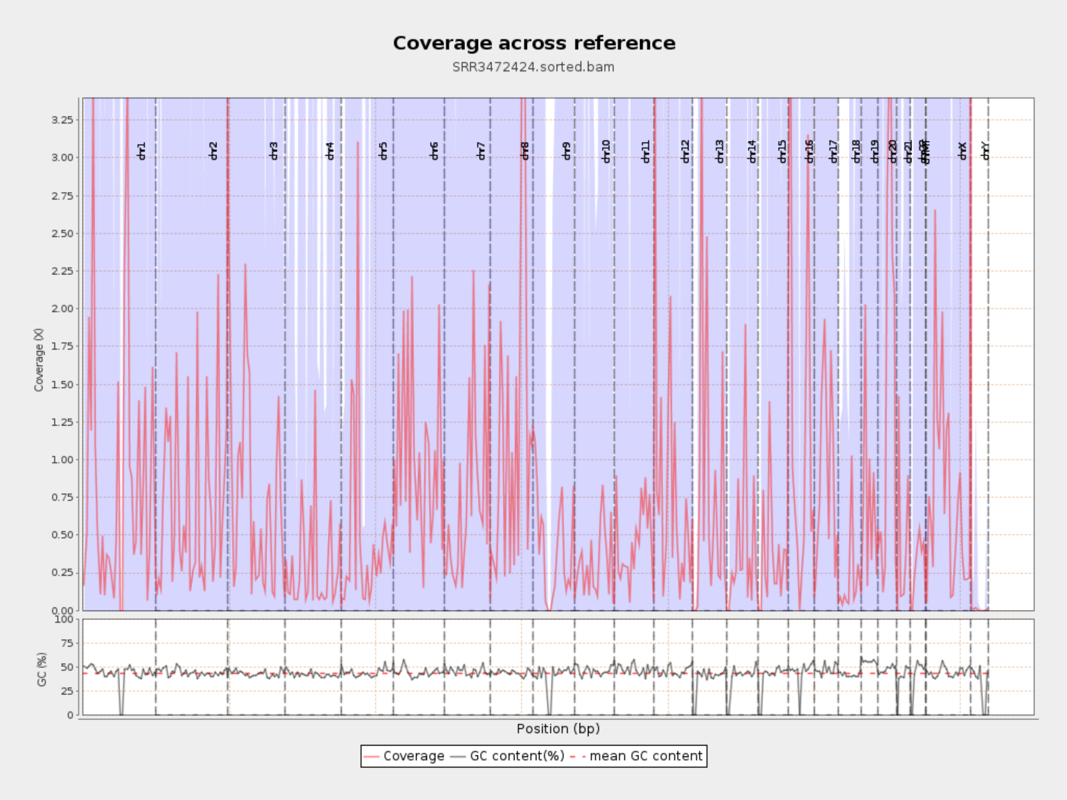
2.7. Chromosome stats

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

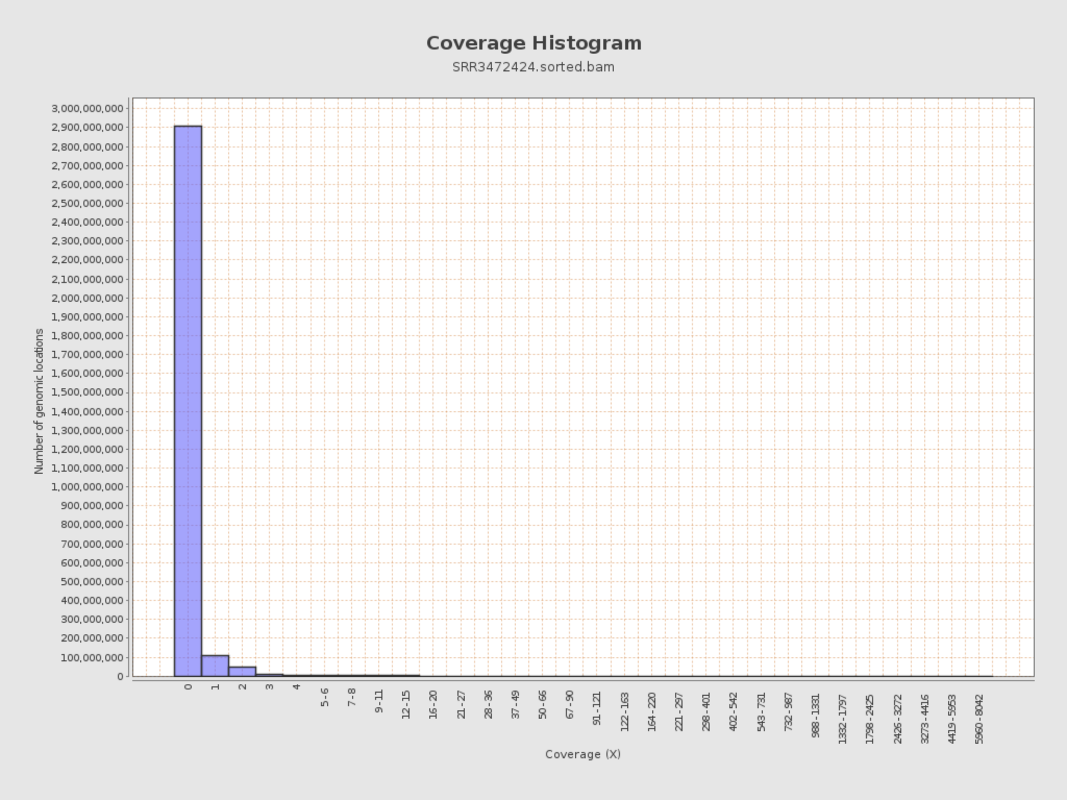
		bases	coverage	deviation
chr1	249250621	217397245	0.8722	25.5452
chr2	243199373	172122393	0.7077	19.3302
chr3	198022430	161350376	0.8148	18.4599
chr4	191154276	59103727	0.3092	11.1806
chr5	180915260	90777295	0.5018	15.0036
chr6	171115067	172947471	1.0107	22.1133
chr7	159138663	124300016	0.7811	20.0746
chr8	146364022	192422163	1.3147	35.6262
chr9	141213431	57259553	0.4055	10.5217
chr10	135534747	43715682	0.3225	11.063
chr11	135006516	61204554	0.4533	13.0898
chr12	133851895	114918794	0.8586	21.4279
chr13	115169878	94332299	0.8191	26.6859
chr14	107349540	43920594	0.4091	11.2178
chr15	102531392	35899710	0.3501	10.7014
chr16	90354753	112713587	1.2475	31.7204
chr17	81195210	75624241	0.9314	20.0009
chr18	78077248	15490252	0.1984	13.3033
chr19	59128983	43106234	0.729	17.5929
chr20	63025520	98354478	1.5606	38.297
chr21	48129895	23789989	0.4943	23.6982
chr22	51304566	15819008	0.3083	7.8657
chrMT	16571	7014	0.4233	0.8343
chrX	155270560	128983134	0.8307	21.8536

chrY	59373566	389830	0.0066	0.544

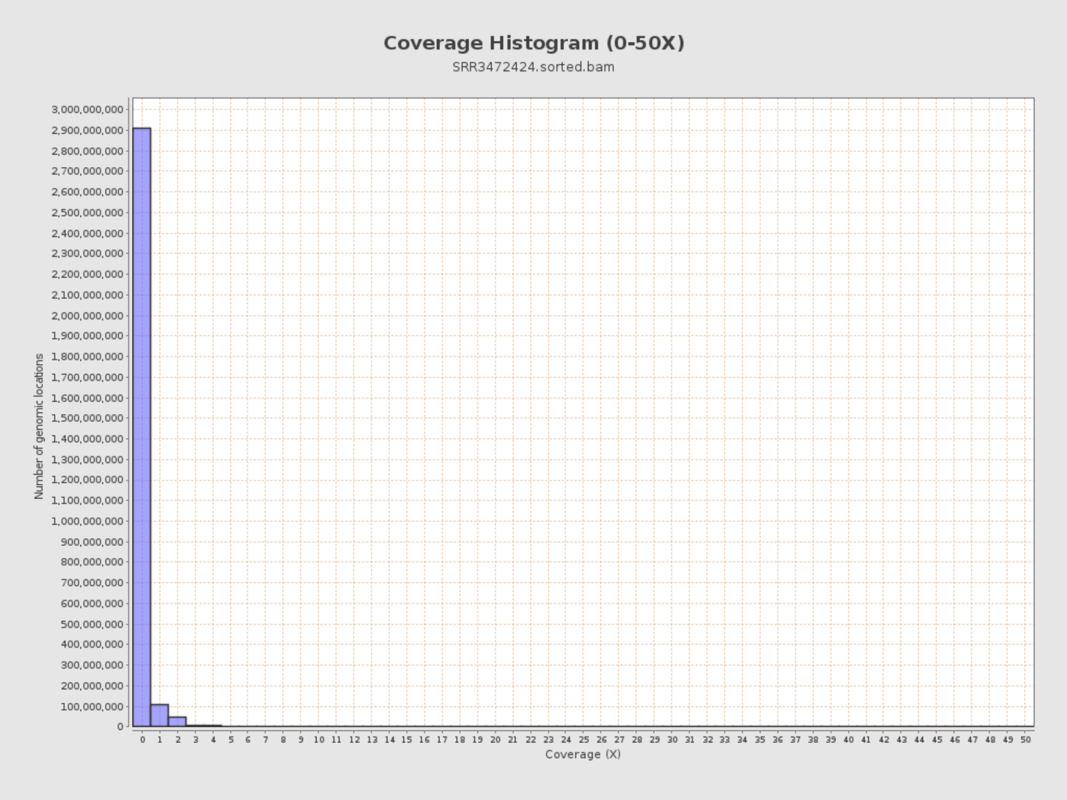
3. Results : Coverage across reference



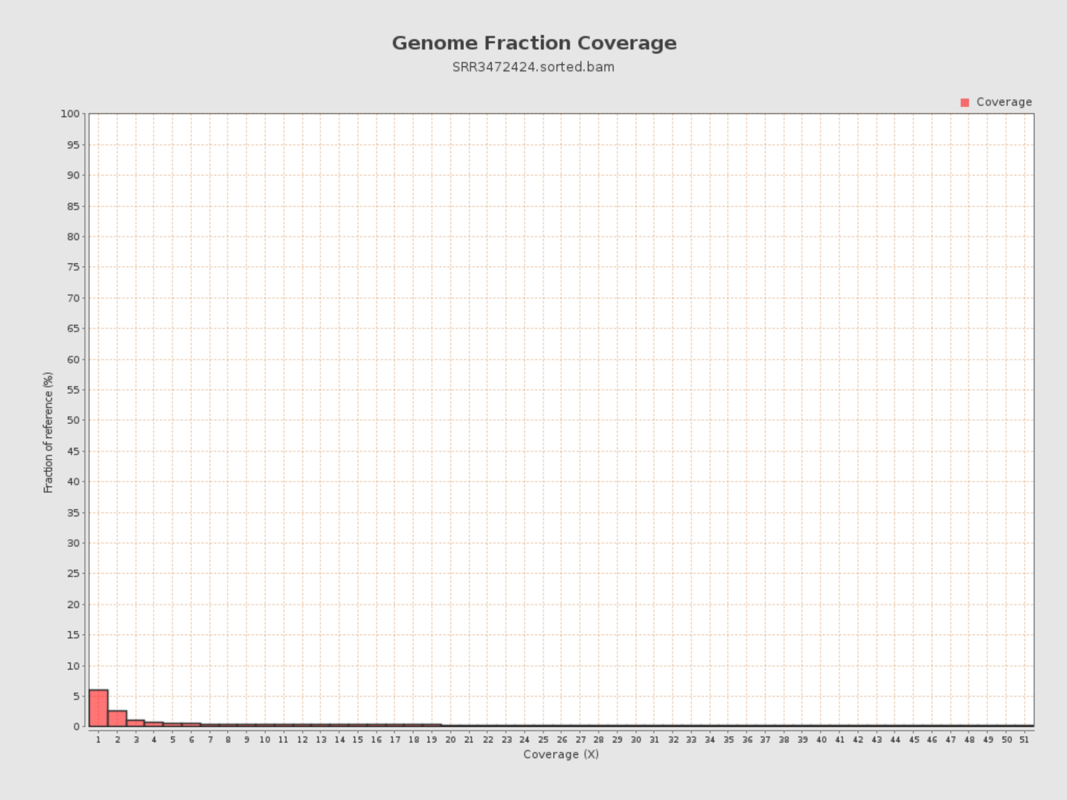
4. Results : Coverage Histogram



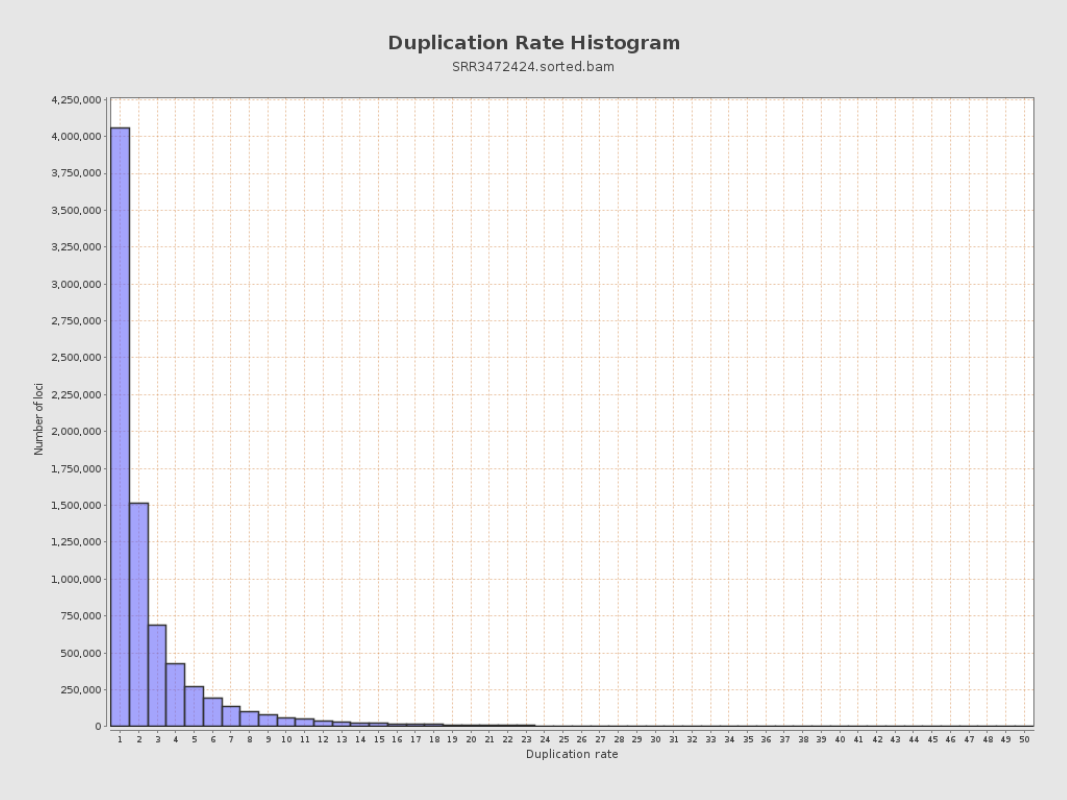
5. Results : Coverage Histogram (0-50X)



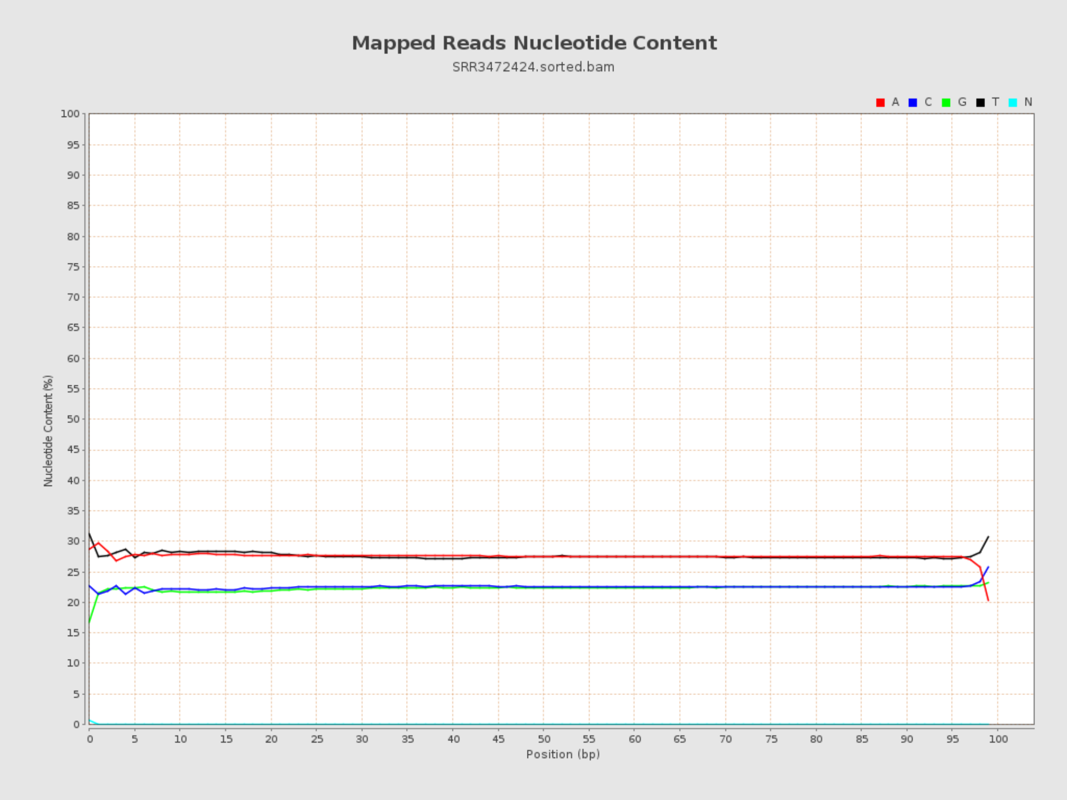
6. Results : Genome Fraction Coverage



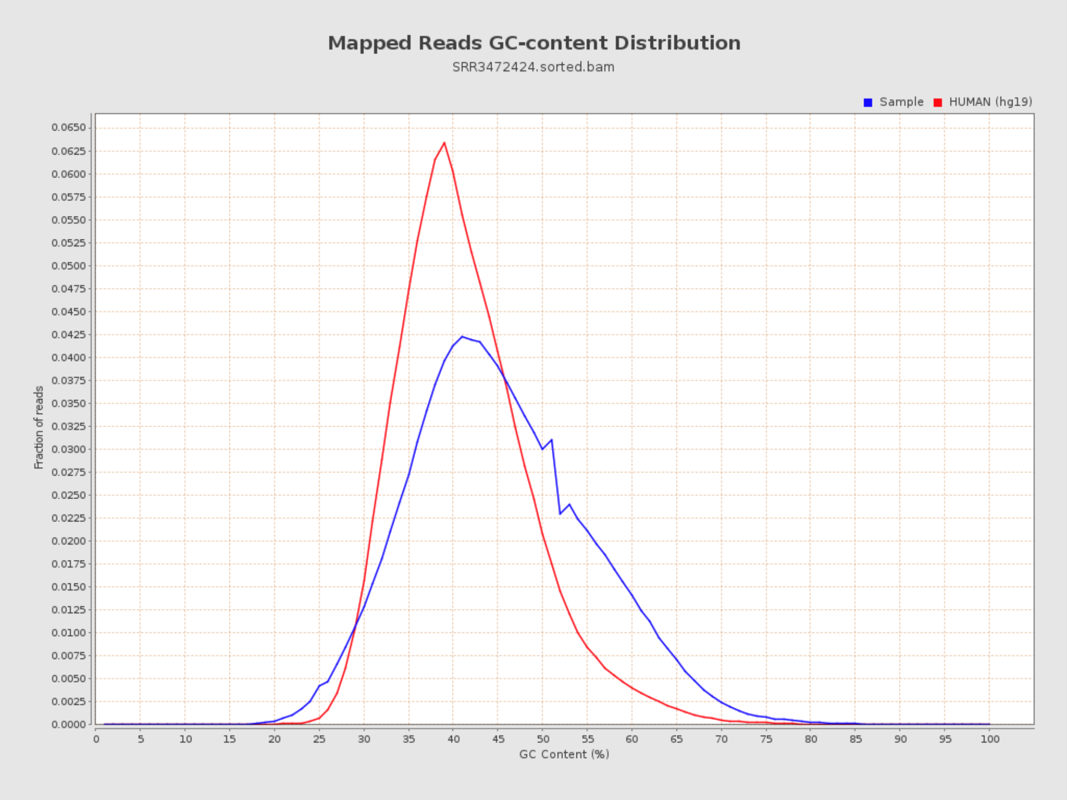
7. Results : Duplication Rate Histogram



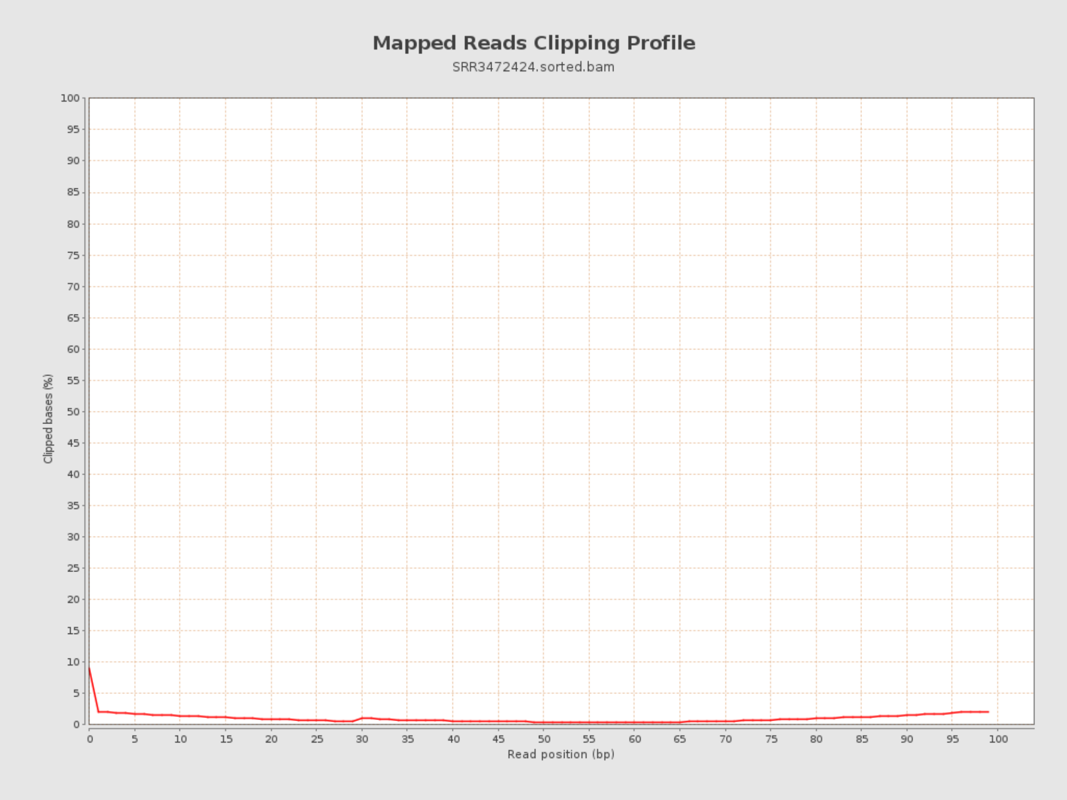
8. Results : Mapped Reads Nucleotide Content



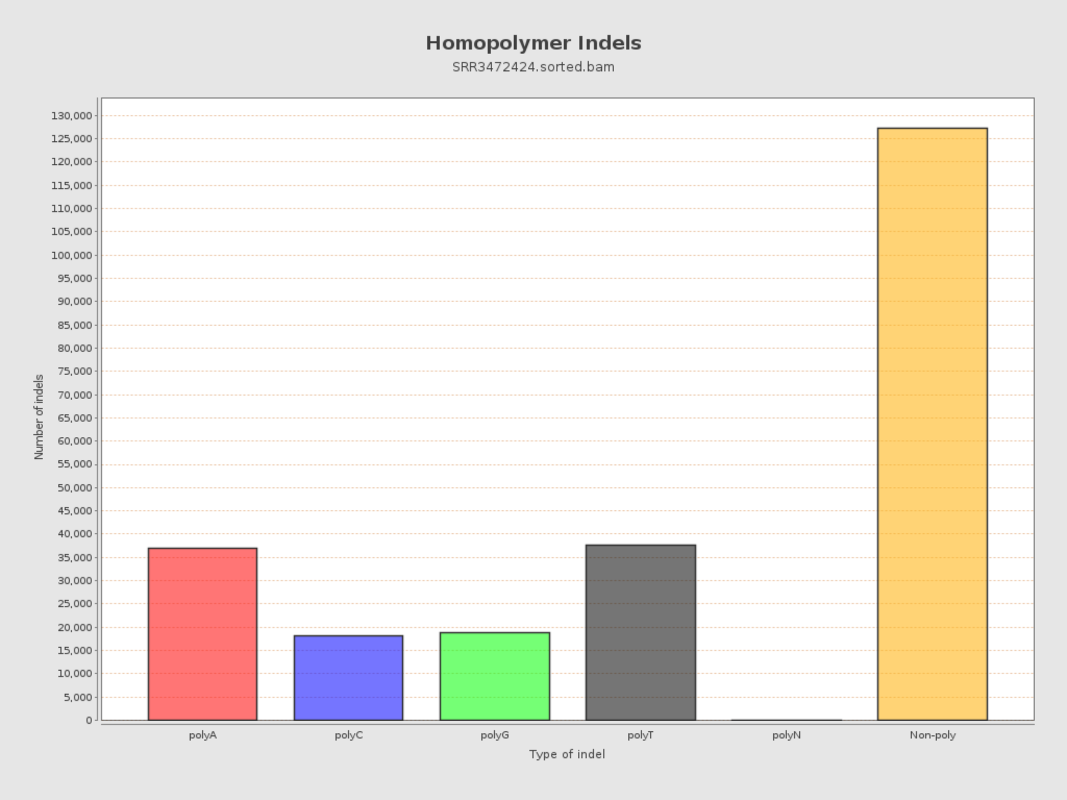
9. Results : Mapped Reads GC-content Distribution



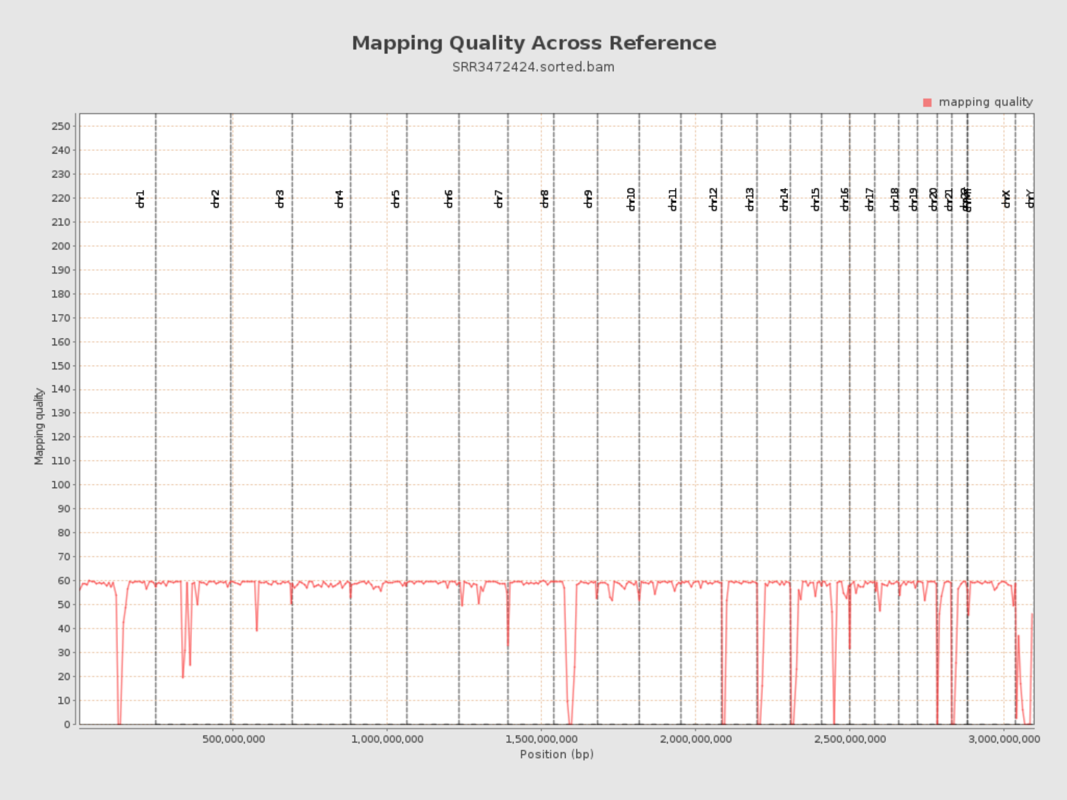
10. Results : Mapped Reads Clipping Profile



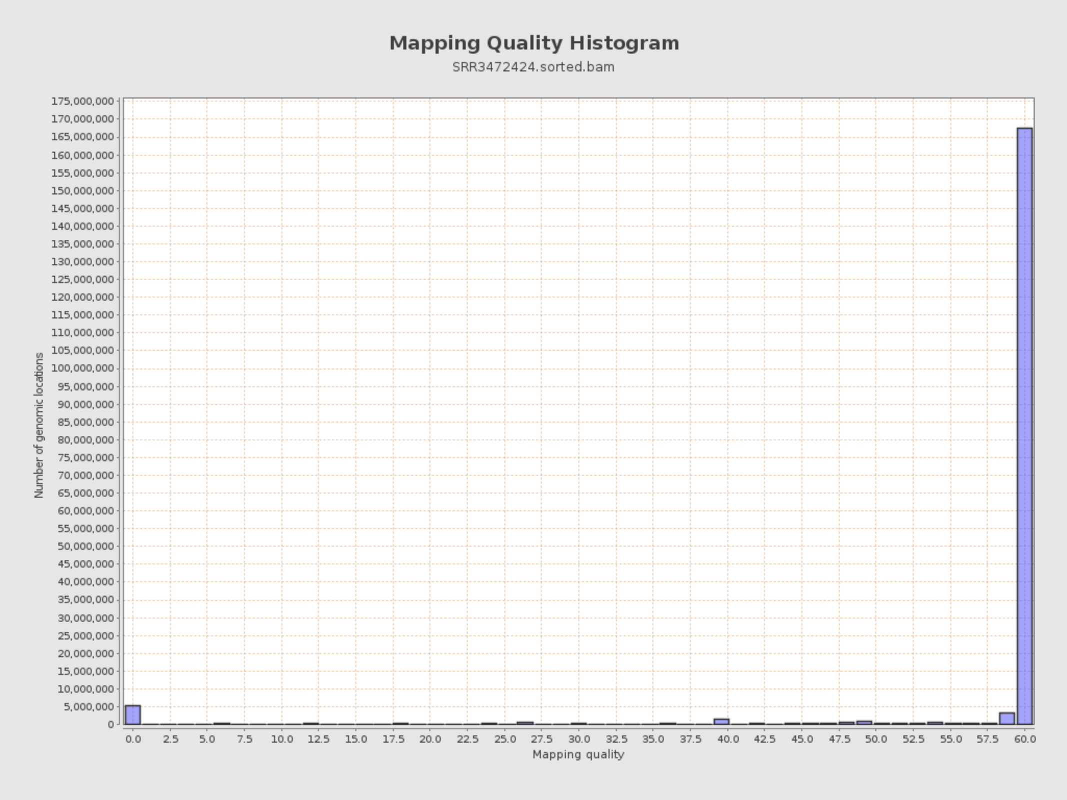
11. Results : Homopolymer Indels



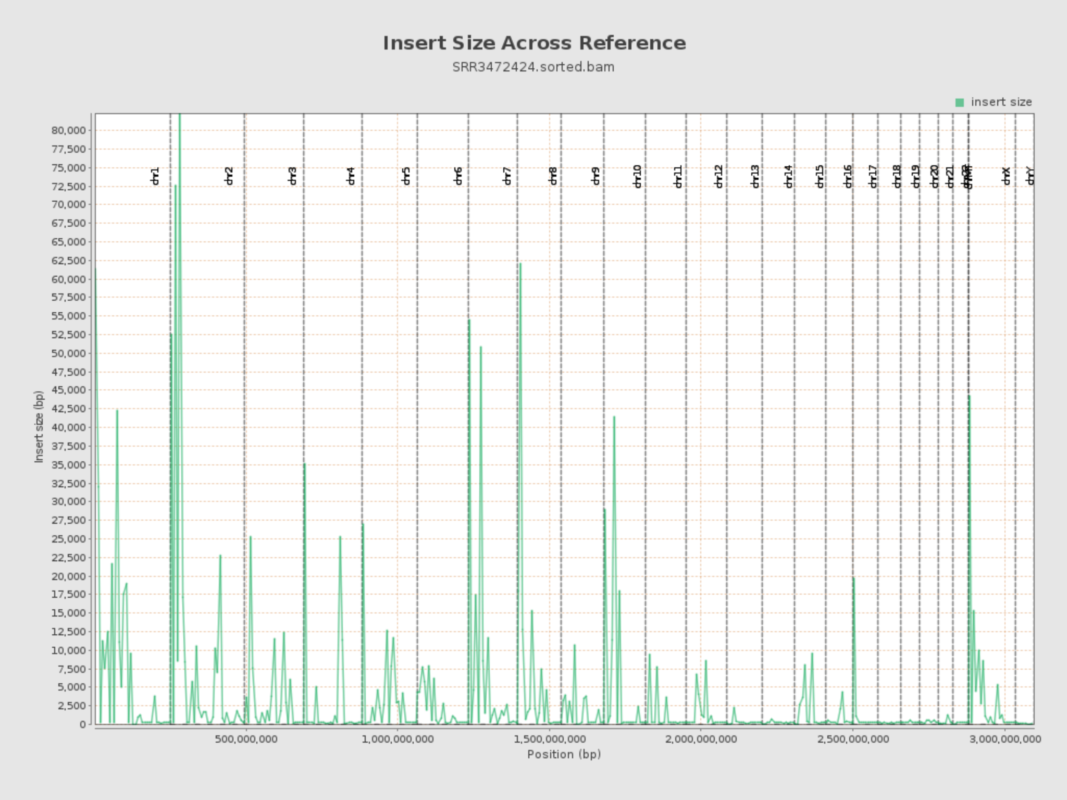
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram