Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 00:43:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472574.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_SRR3472574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472574_1.fastq.gz SRR3472574_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 00:43:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,975,908
Mapped reads	10,053,677 / 91.6%
Unmapped reads	922,231 / 8.4%
Mapped paired reads	10,053,677 / 91.6%
Mapped reads, first in pair	5,071,785 / 46.21%
Mapped reads, second in pair	4,981,892 / 45.39%
Mapped reads, both in pair	9,806,618 / 89.35%
Mapped reads, singletons	247,059 / 2.25%
Secondary alignments	0
Supplementary alignments	289,126 / 2.63%
Read min/max/mean length	30 / 100 / 101.03
Duplicated reads (estimated)	1,701,166 / 15.5%
Duplication rate	14.51%
Clipped reads	7,801,774 / 71.08%

2.2. ACGT Content

Number/percentage of A's	207,358,707 / 25.55%
Number/percentage of C's	163,833,634 / 20.19%
Number/percentage of T's	239,941,267 / 29.56%
Number/percentage of G's	199,915,792 / 24.63%
Number/percentage of N's	540,085 / 0.07%

GC Percentage	44.82%

2.3. Coverage

Mean	0.2623
Standard Deviation	2.5141

2.4. Mapping Quality

Mean Mapping Quality	50.17

2.5. Insert size

Mean	220,066.19
Standard Deviation	4,561,607.2
P25/Median/P75	89 / 126 / 174

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	9,951,745
Insertions	82,144
Mapped reads with at least one insertion	0.8%
Deletions	189,607
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.44%

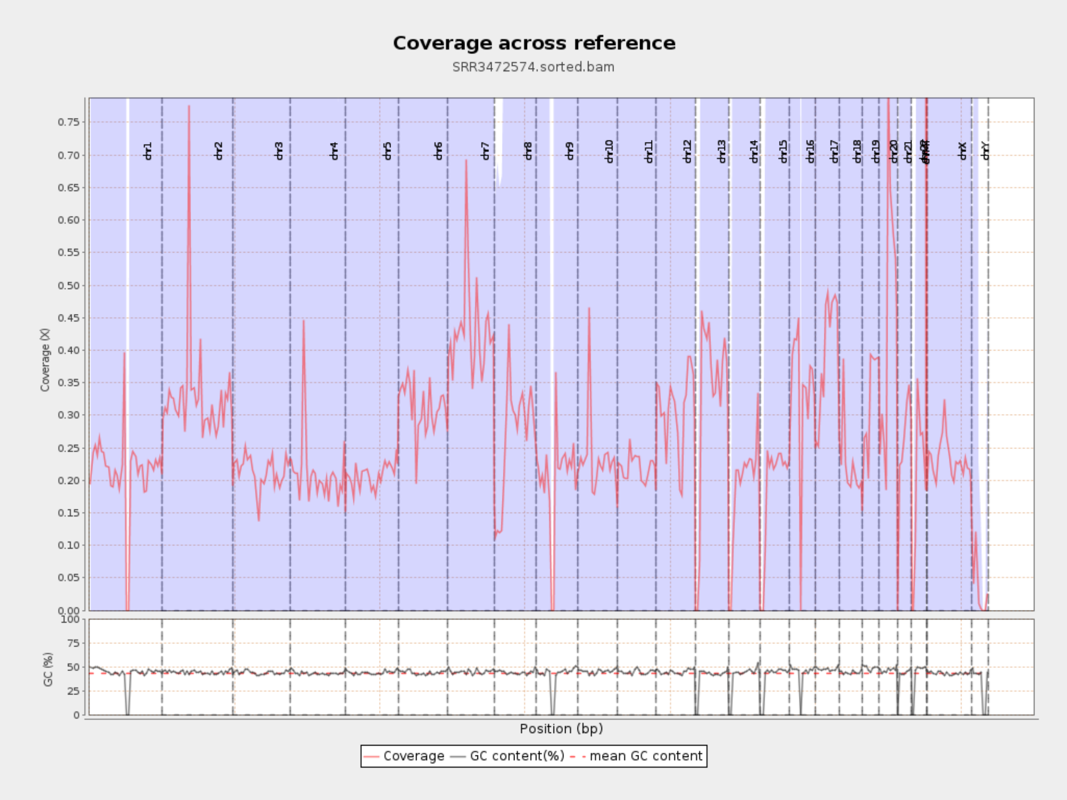
2.7. Chromosome stats

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

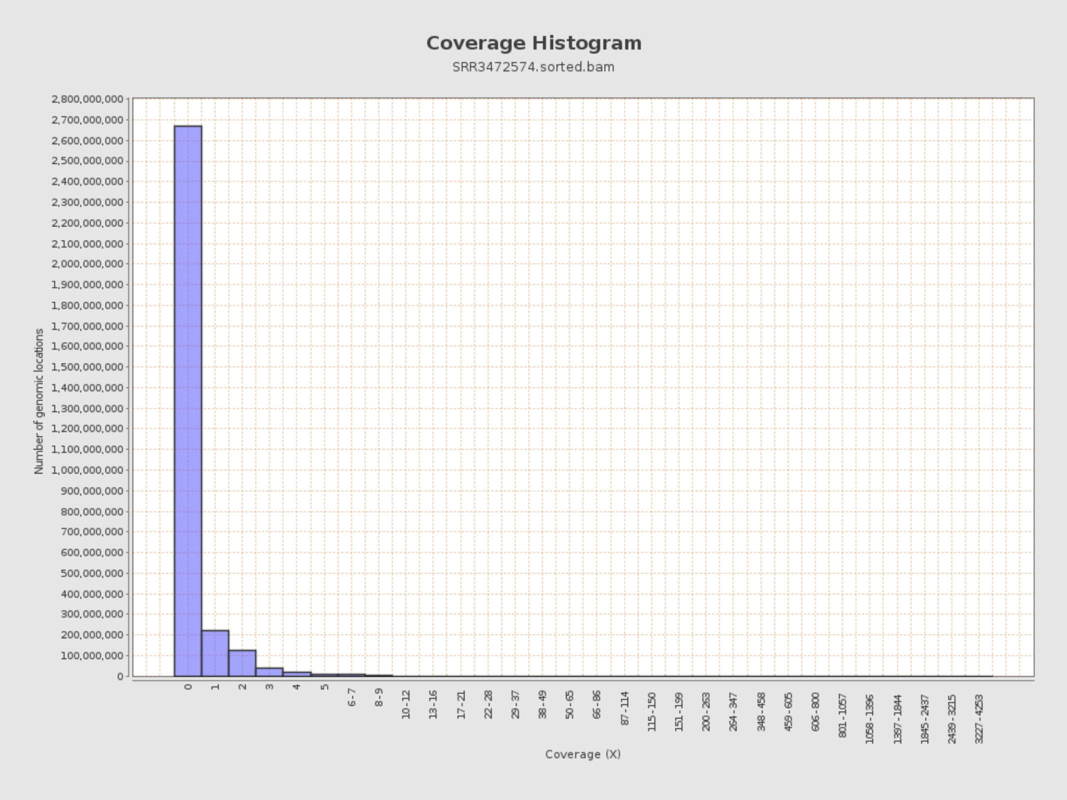
		bases	coverage	deviation
chr1	249250621	53178768	0.2134	3.4205
chr2	243199373	80448267	0.3308	3.5897
chr3	198022430	42107407	0.2126	0.7131
chr4	191154276	40269864	0.2107	1.4465
chr5	180915260	37600829	0.2078	0.7566
chr6	171115067	53645720	0.3135	1.4149
chr7	159138663	68761310	0.4321	4.842
chr8	146364022	39246813	0.2681	2.2058
chr9	141213431	28285951	0.2003	2.8221
chr10	135534747	31742327	0.2342	2.4587
chr11	135006516	29520346	0.2187	1.8332
chr12	133851895	41330820	0.3088	0.9131
chr13	115169878	37363542	0.3244	0.9399
chr14	107349540	20490229	0.1909	4.6739
chr15	102531392	19181816	0.1871	0.6831
chr16	90354753	30434856	0.3368	1.5393
chr17	81195210	32610495	0.4016	2.0648
chr18	78077248	17721804	0.227	4.6331
chr19	59128983	19029850	0.3218	2.4205
chr20	63025520	28609656	0.4539	1.4287
chr21	48129895	12146264	0.2524	1.0715
chr22	51304566	9828242	0.1916	0.7085
chrMT	16571	263784	15.9184	10.5205
chrX	155270560	36134667	0.2327	1.1597

chrY	59373566	1996511	0.0336	1.2774

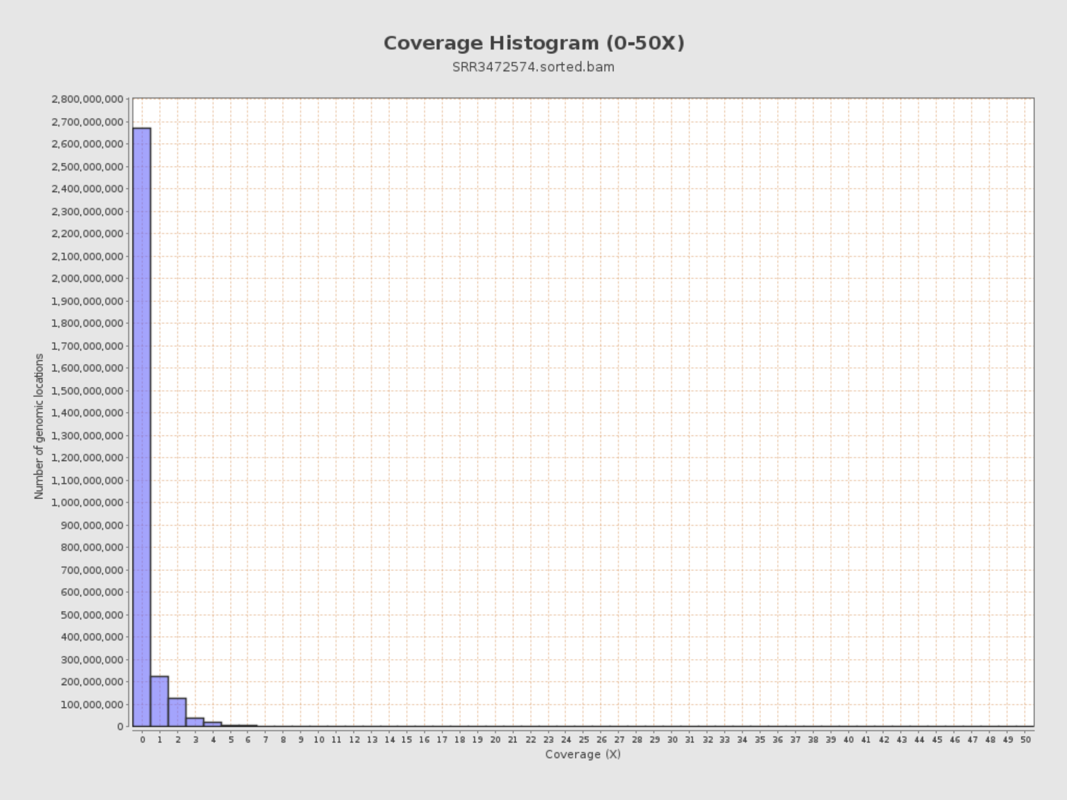
3. Results : Coverage across reference



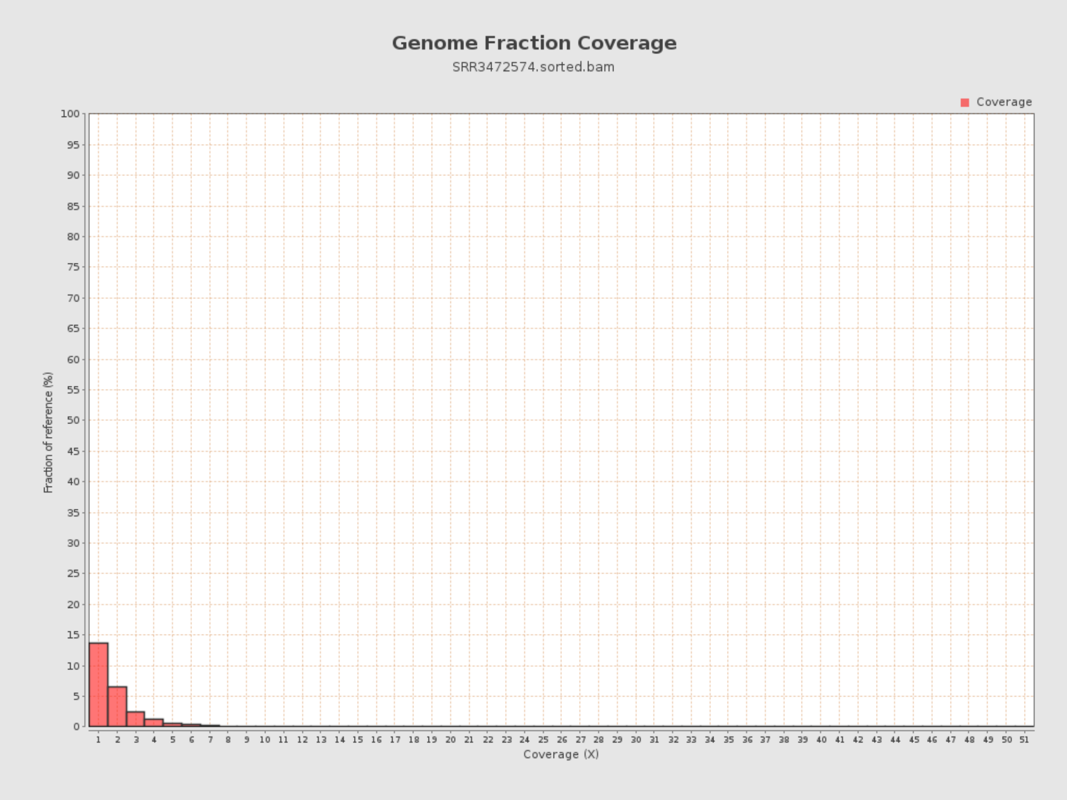
4. Results : Coverage Histogram



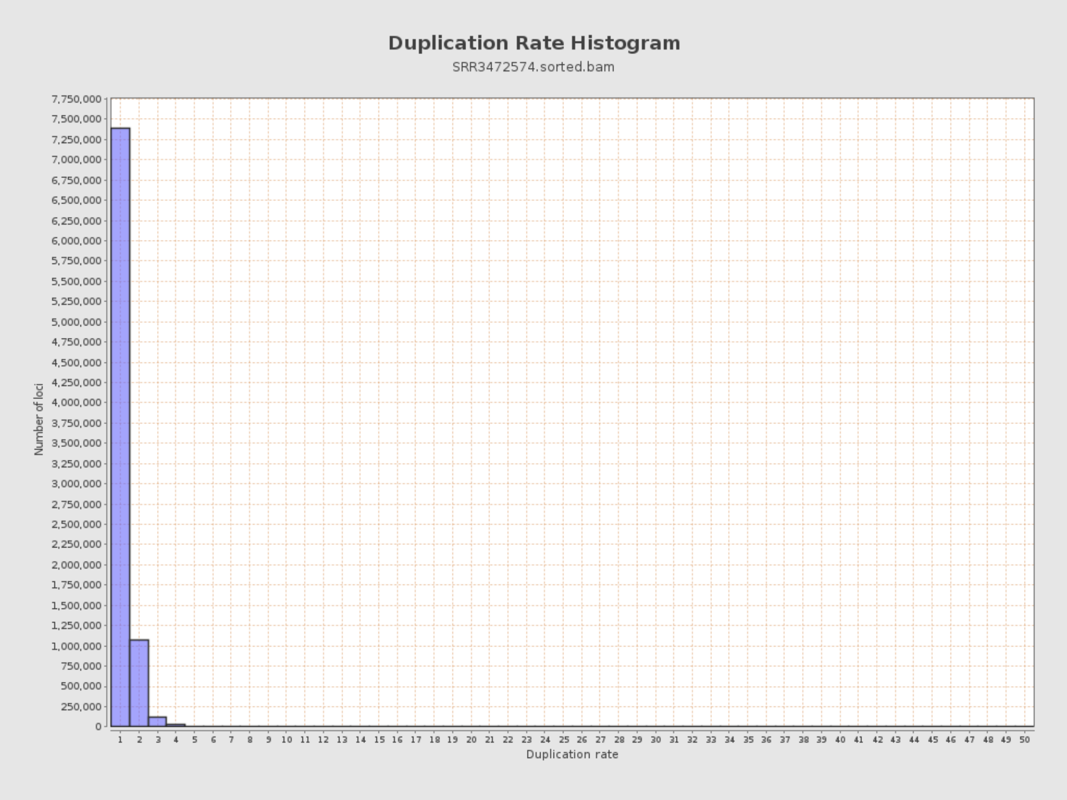
5. Results : Coverage Histogram (0-50X)



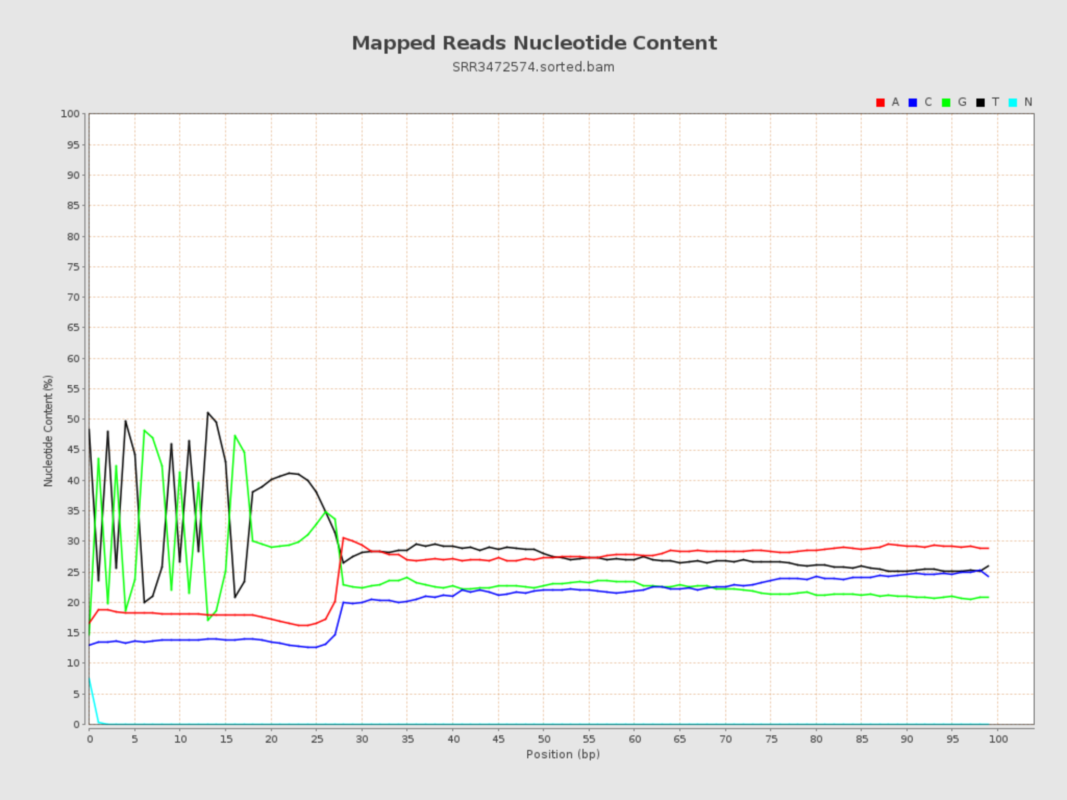
6. Results : Genome Fraction Coverage



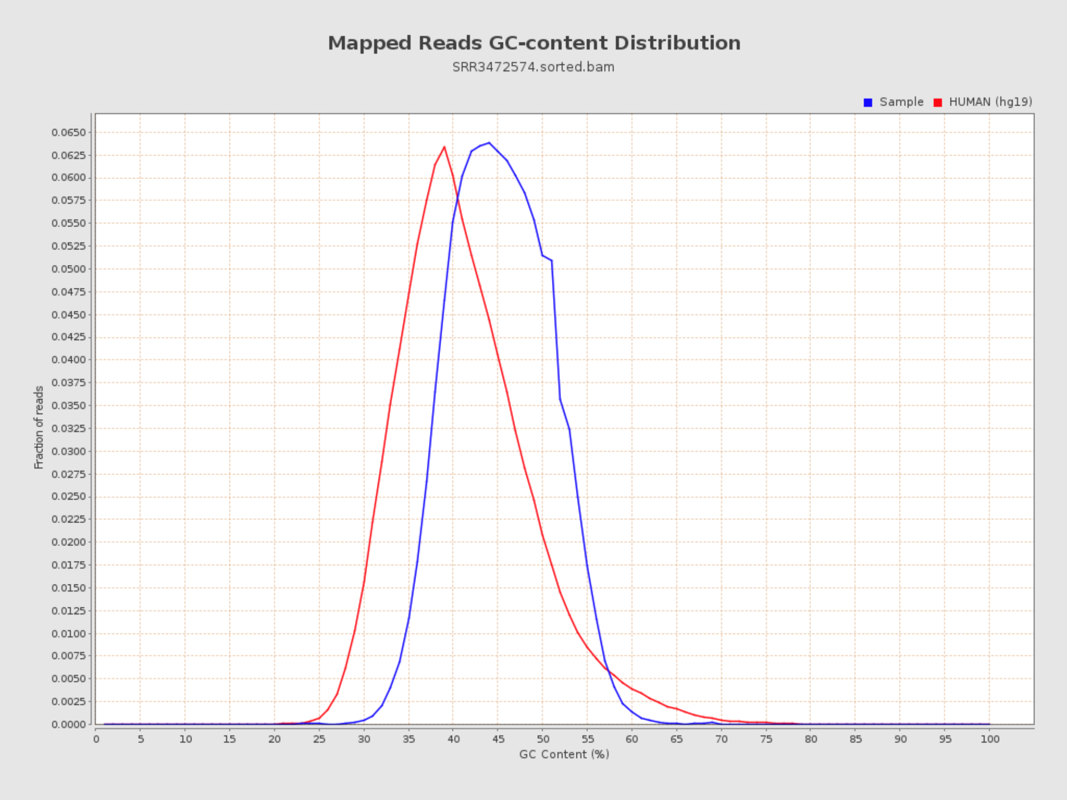
7. Results : Duplication Rate Histogram



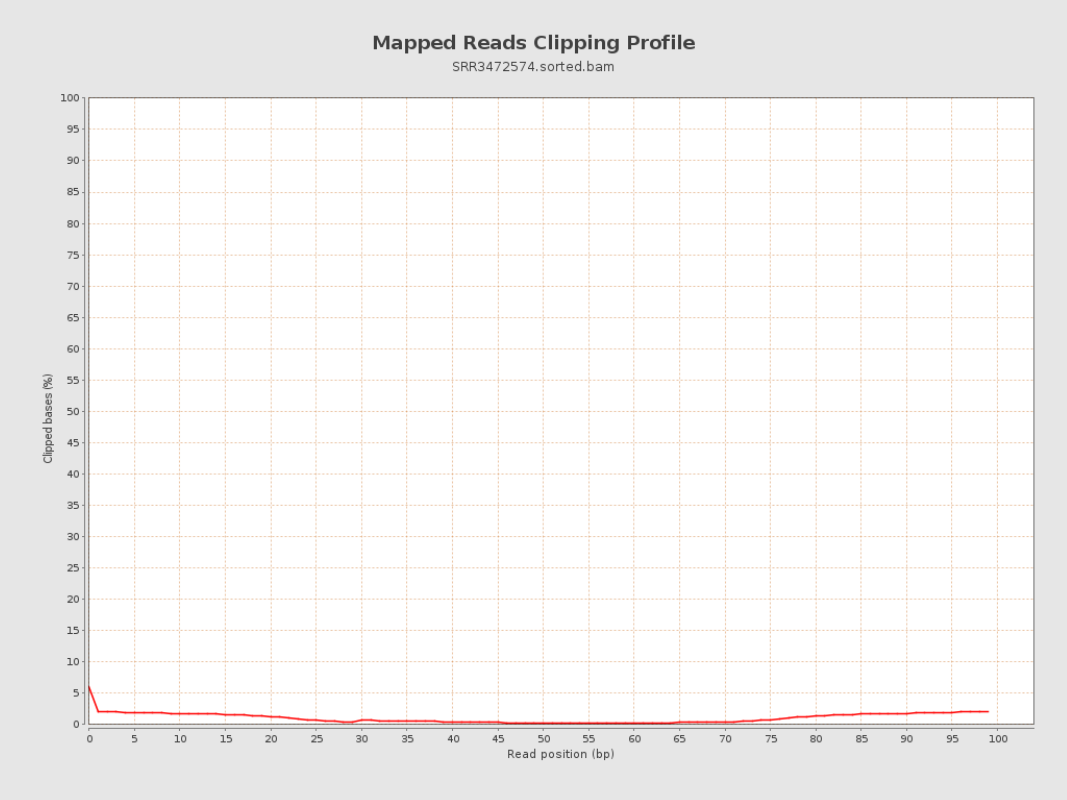
8. Results : Mapped Reads Nucleotide Content



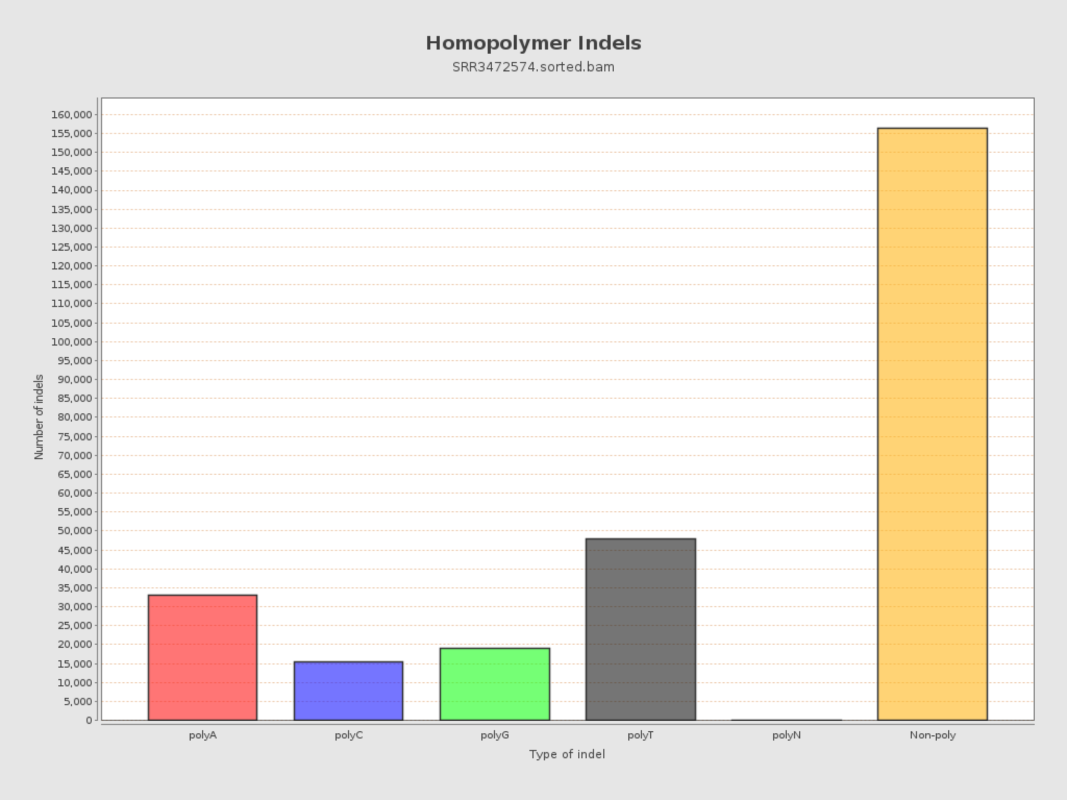
9. Results : Mapped Reads GC-content Distribution



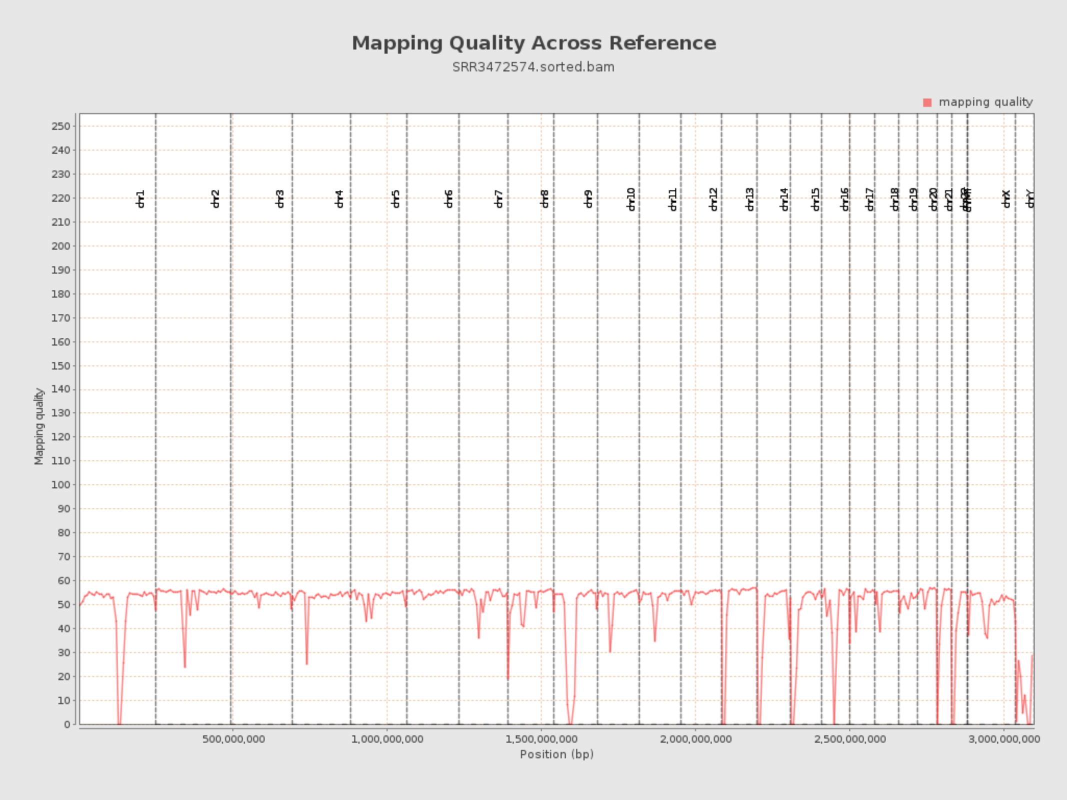
10. Results : Mapped Reads Clipping Profile



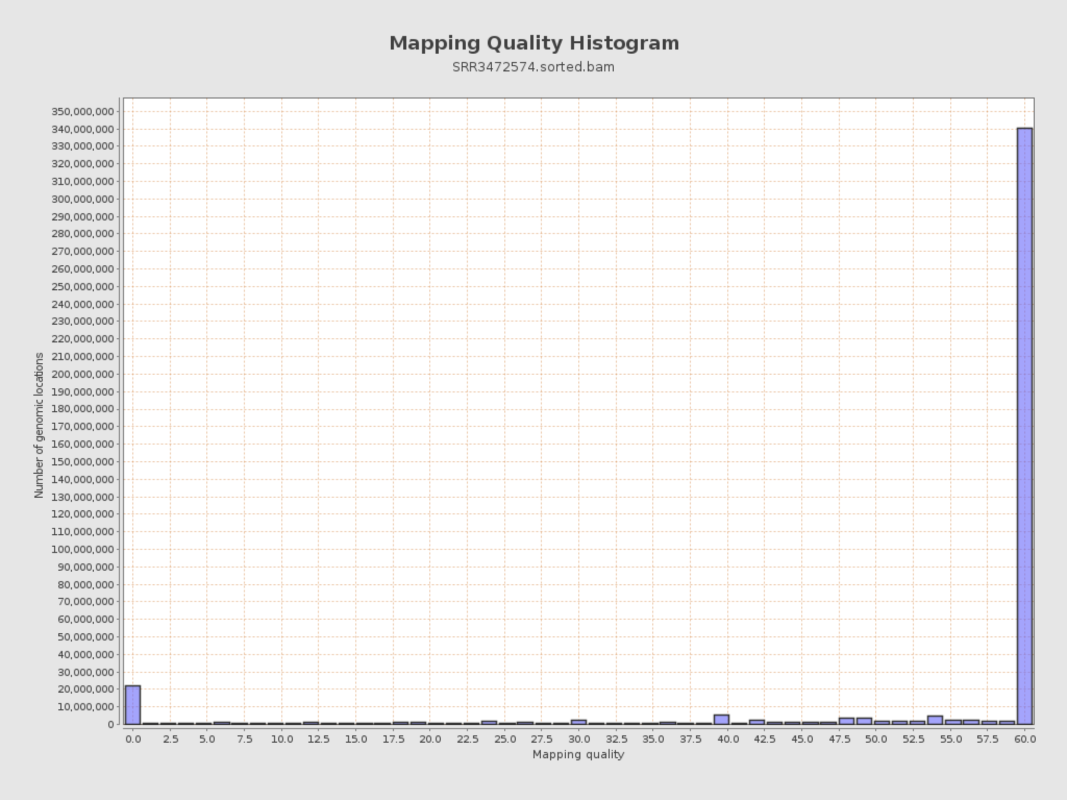
11. Results : Homopolymer Indels



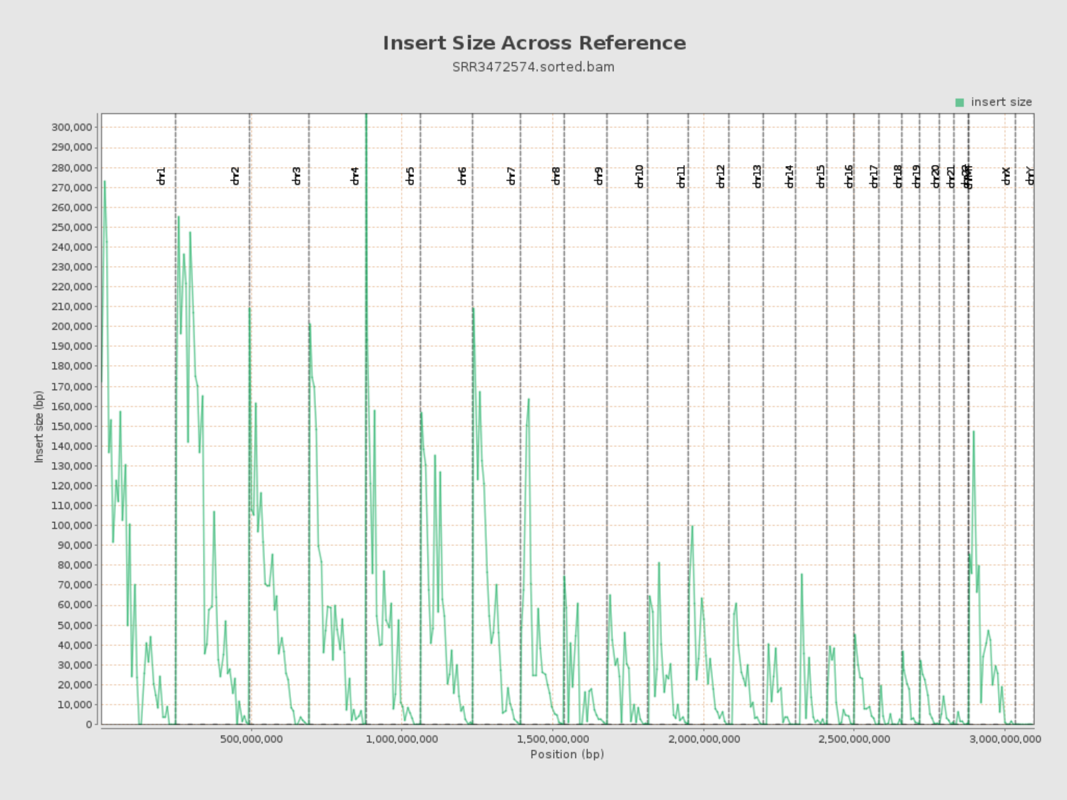
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram