Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:47:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472560.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_SRR3472560 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472560_1.fastq.gz SRR3472560_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:47:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472560.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,508,156
Mapped reads	11,326,217 / 98.42%
Unmapped reads	181,939 / 1.58%
Mapped paired reads	11,326,217 / 98.42%
Mapped reads, first in pair	5,691,466 / 49.46%
Mapped reads, second in pair	5,634,751 / 48.96%
Mapped reads, both in pair	11,231,830 / 97.6%
Mapped reads, singletons	94,387 / 0.82%
Secondary alignments	0
Supplementary alignments	44,733 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	6,725,815 / 58.44%
Duplication rate	44.15%
Clipped reads	1,049,987 / 9.12%

2.2. ACGT Content

Number/percentage of A's	308,530,375 / 27.76%
Number/percentage of C's	248,943,932 / 22.4%
Number/percentage of T's	305,908,045 / 27.53%
Number/percentage of G's	247,742,748 / 22.29%
Number/percentage of N's	168,649 / 0.02%

GC Percentage	44.69%

2.3. Coverage

Mean	0.359
Standard Deviation	14.5126

2.4. Mapping Quality

Mean Mapping Quality	54.91

2.5. Insert size

Mean	29,370.46
Standard Deviation	1,665,450.04
P25/Median/P75	172 / 247 / 338

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	7,490,857
Insertions	60,341
Mapped reads with at least one insertion	0.53%
Deletions	57,022
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.51%

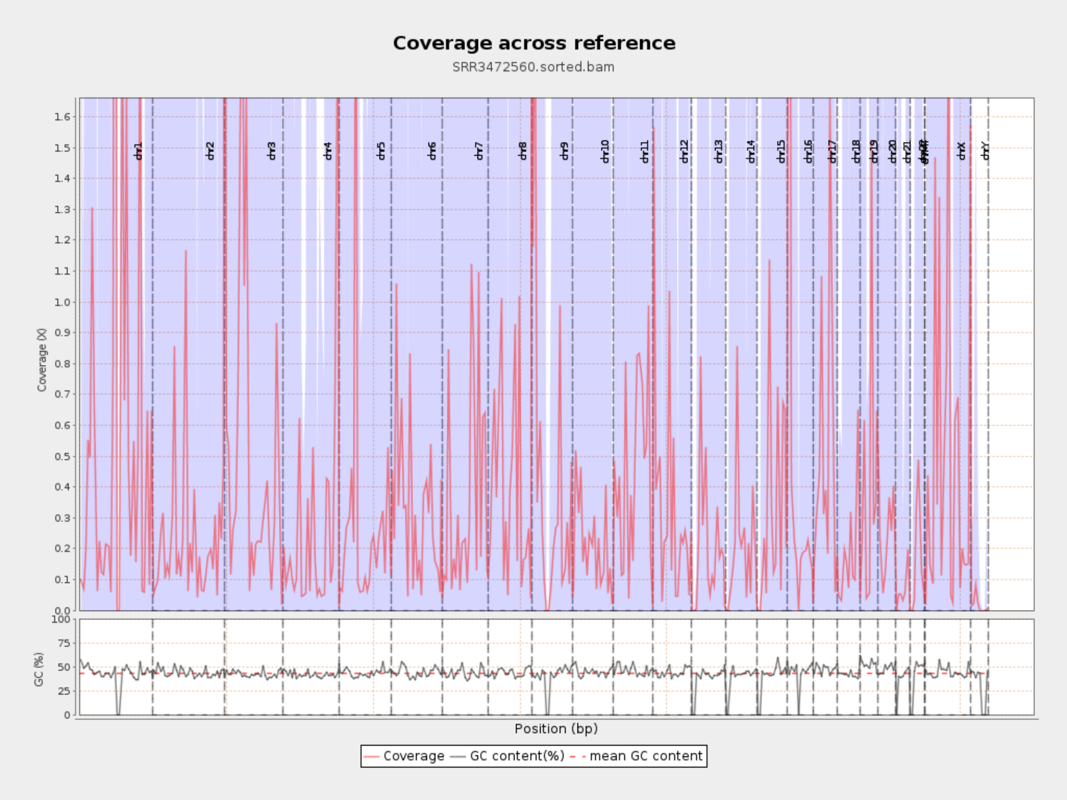
2.7. Chromosome stats

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

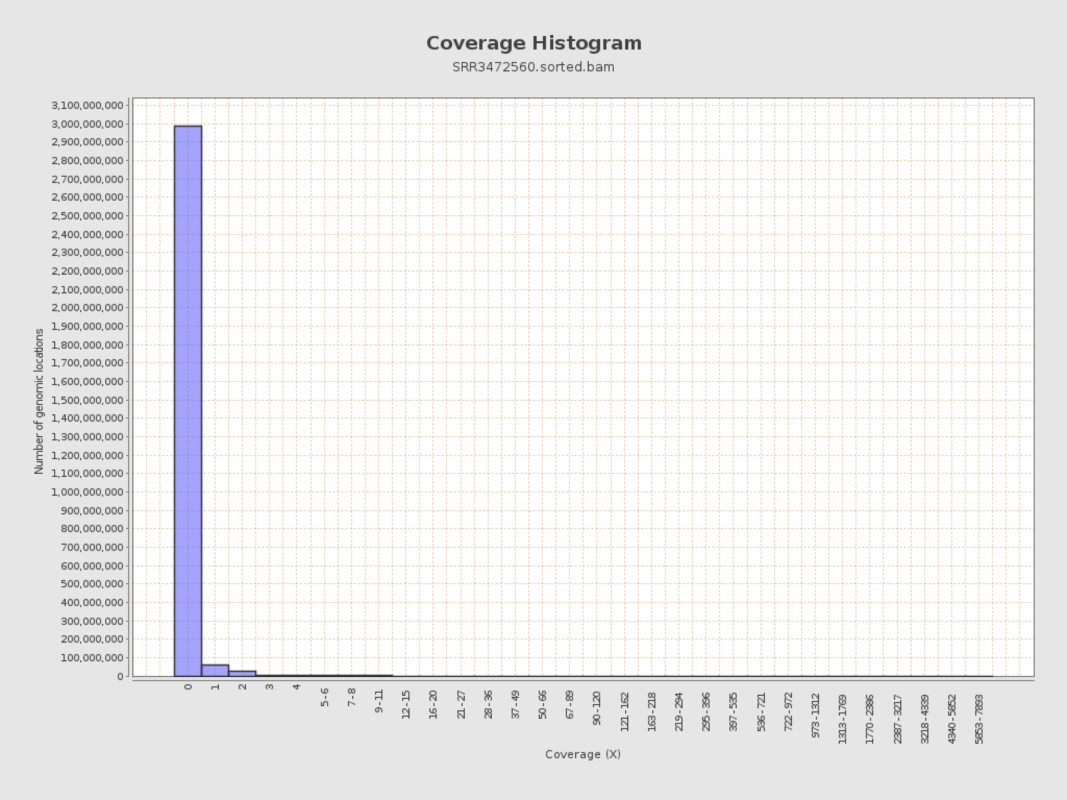
		bases	coverage	deviation
chr1	249250621	152369270	0.6113	24.4853
chr2	243199373	55082731	0.2265	6.9192
chr3	198022430	111998653	0.5656	14.249
chr4	191154276	51291775	0.2683	10.4576
chr5	180915260	53305303	0.2946	9.2294
chr6	171115067	56468418	0.33	10.2243
chr7	159138663	57461513	0.3611	13.9018
chr8	146364022	58763370	0.4015	15.66
chr9	141213431	61540069	0.4358	13.2524
chr10	135534747	29187497	0.2154	9.0343
chr11	135006516	61368521	0.4546	16.3108
chr12	133851895	47655628	0.356	13.659
chr13	115169878	23905975	0.2076	8.4894
chr14	107349540	22378521	0.2085	7.8582
chr15	102531392	33397154	0.3257	15.3603
chr16	90354753	47861076	0.5297	17.1667
chr17	81195210	41681781	0.5134	13.0333
chr18	78077248	15038436	0.1926	6.3307
chr19	59128983	25349096	0.4287	17.8933
chr20	63025520	15843600	0.2514	6.7934
chr21	48129895	3556092	0.0739	3.0404
chr22	51304566	8185610	0.1595	4.6219
chrMT	16571	2324	0.1402	0.4452
chrX	155270560	76574754	0.4932	28.5969

chrY	59373566	1160899	0.0196	0.6026

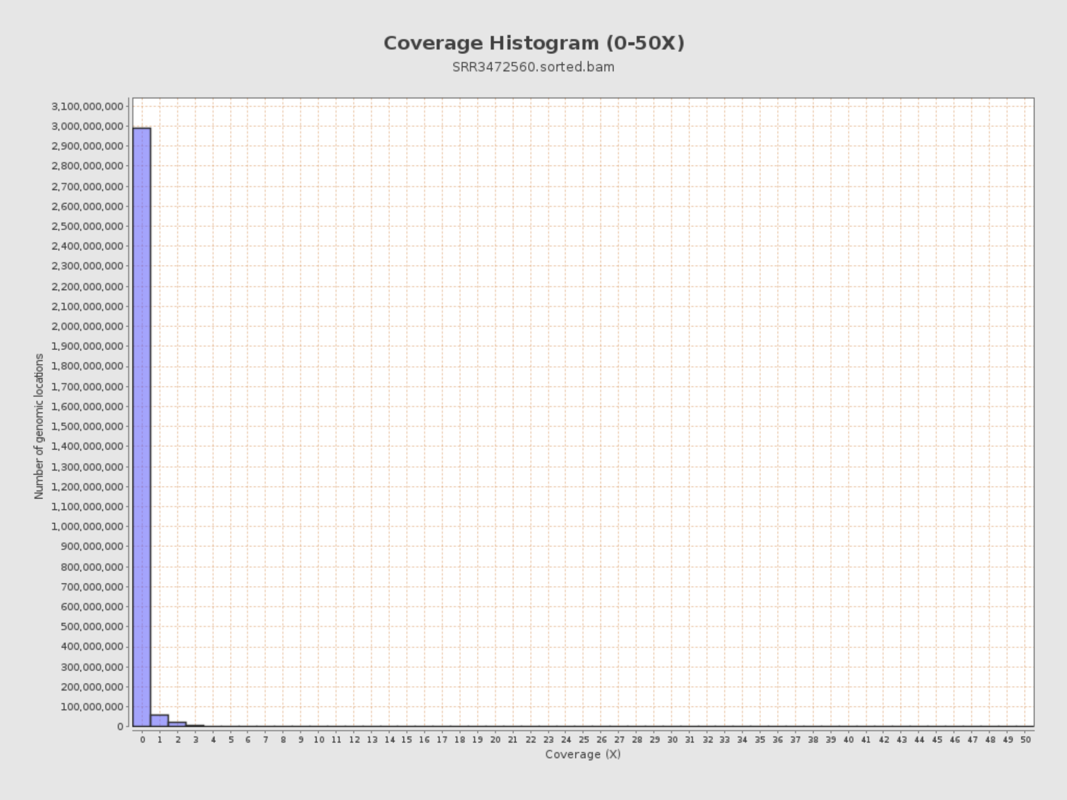
3. Results : Coverage across reference



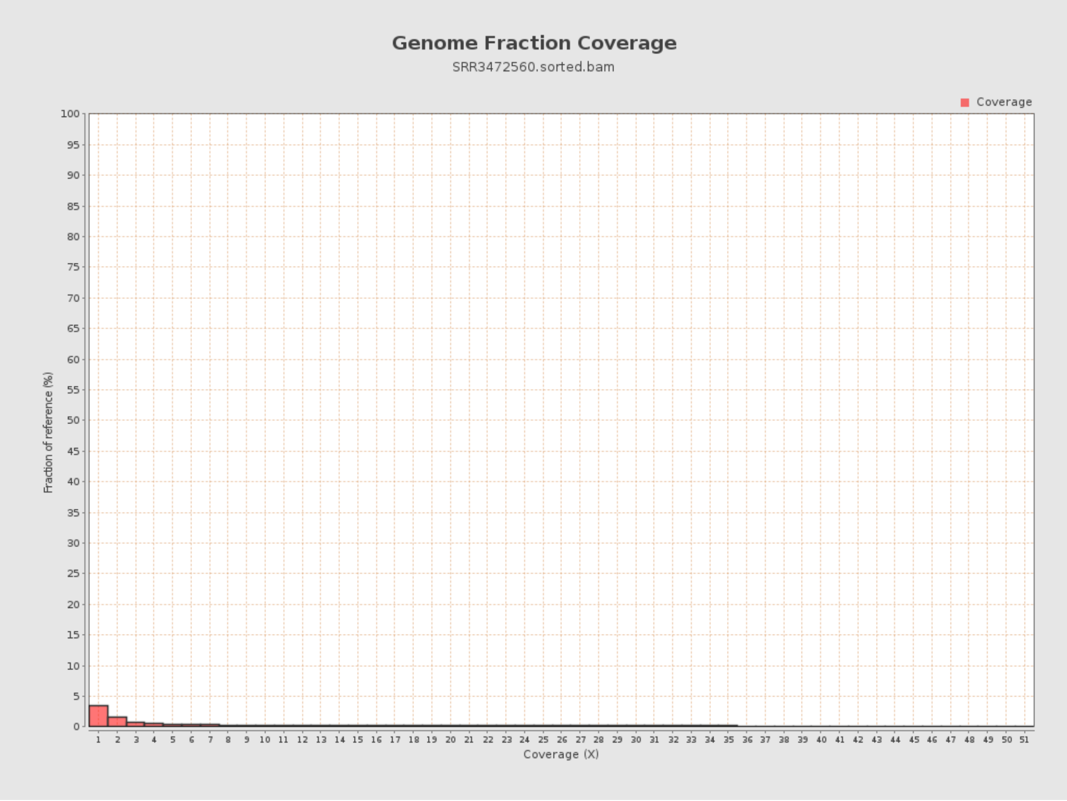
4. Results : Coverage Histogram



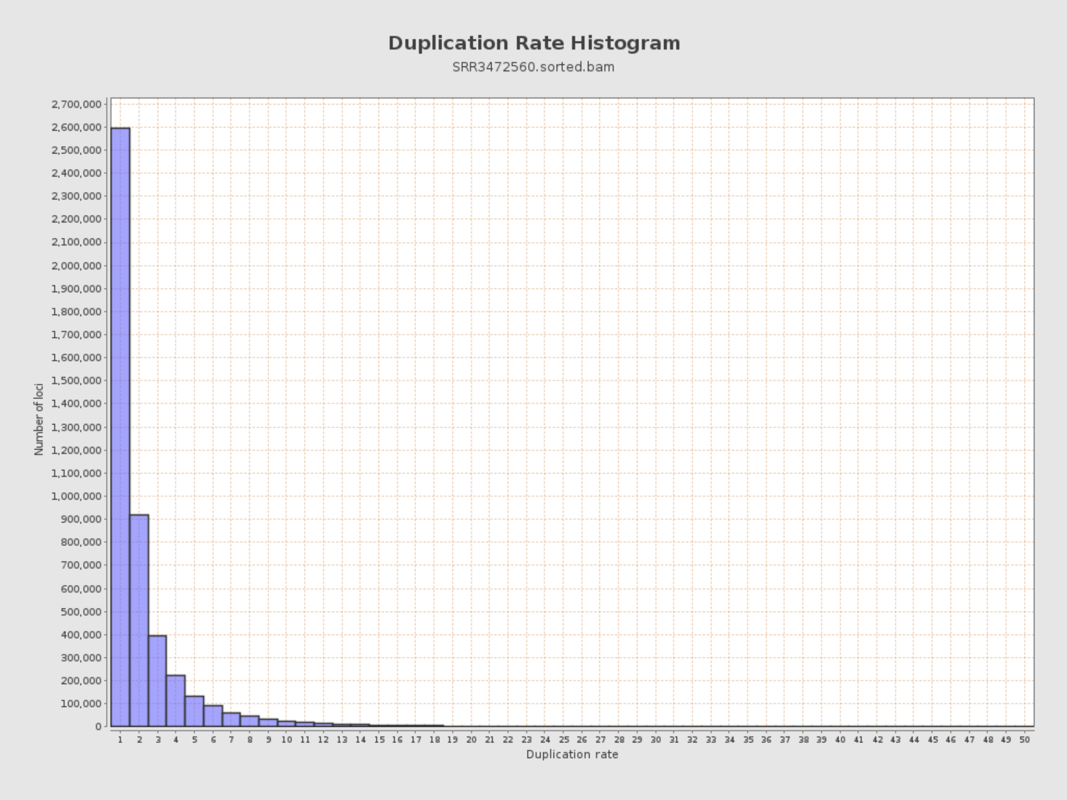
5. Results : Coverage Histogram (0-50X)



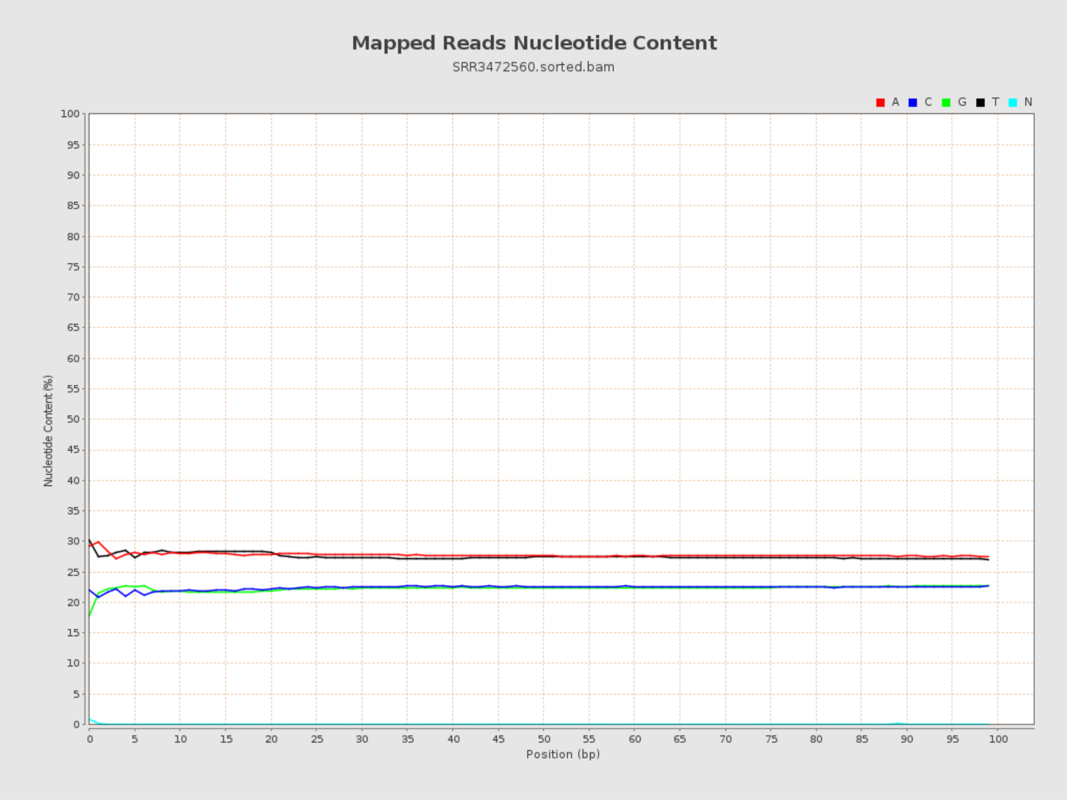
6. Results : Genome Fraction Coverage



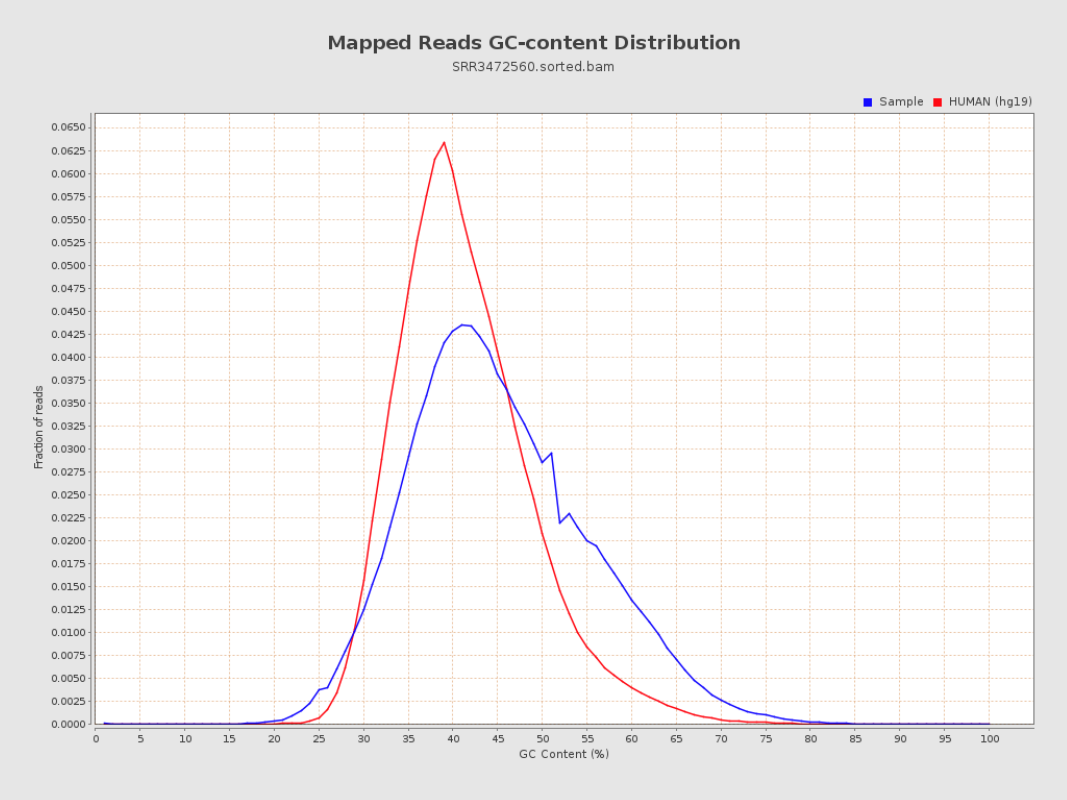
7. Results : Duplication Rate Histogram



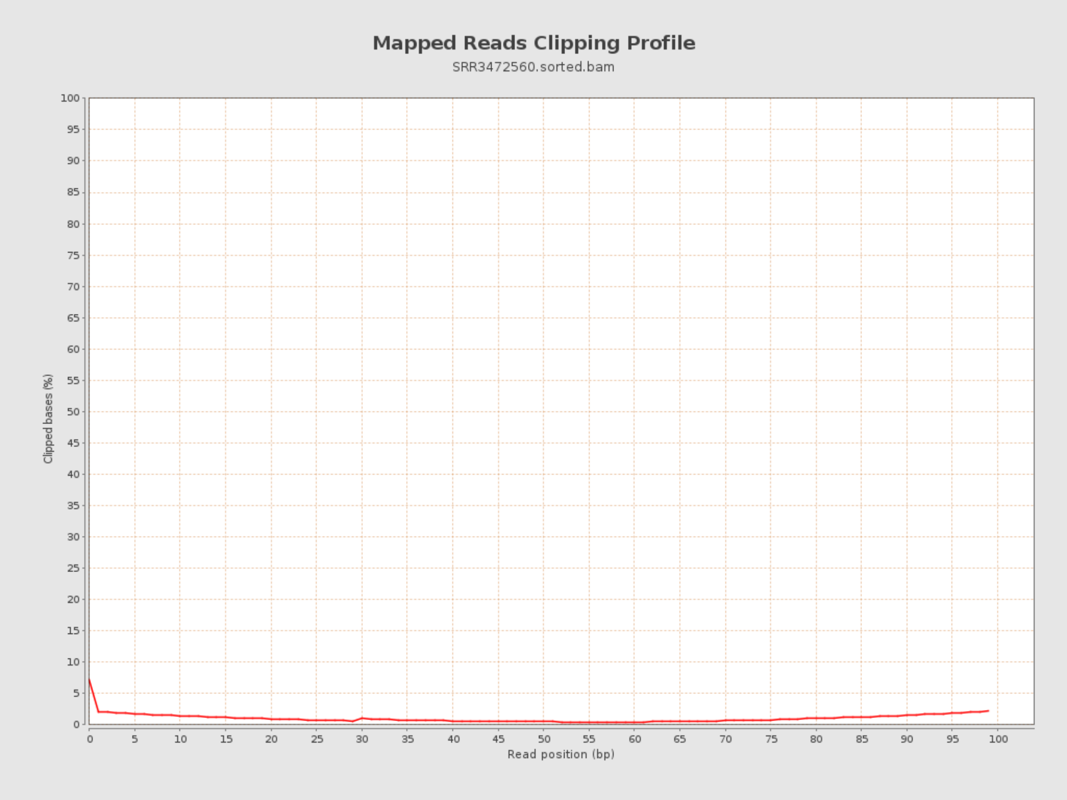
8. Results : Mapped Reads Nucleotide Content



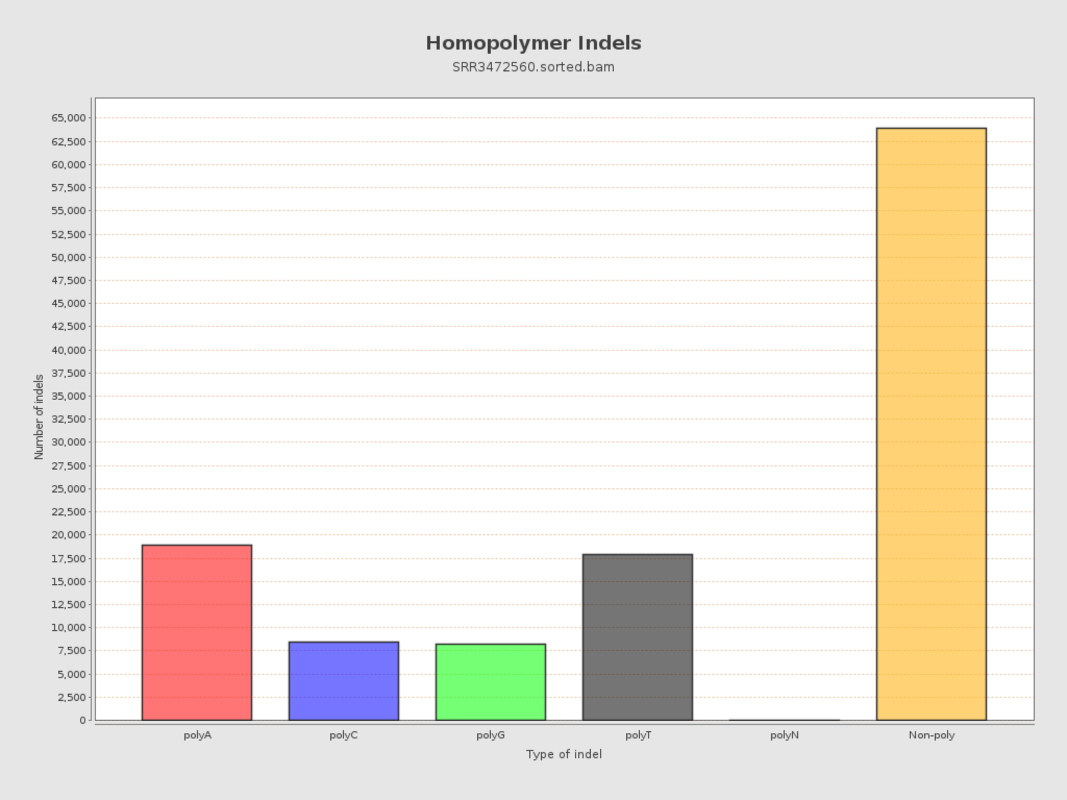
9. Results : Mapped Reads GC-content Distribution



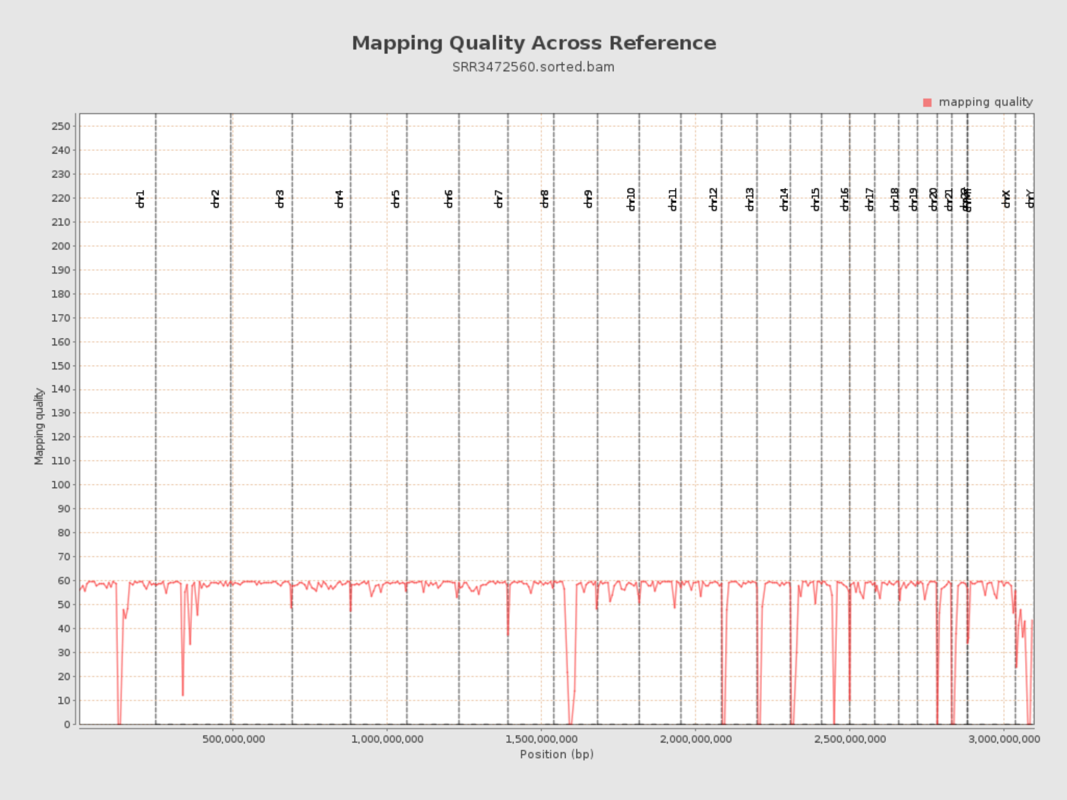
10. Results : Mapped Reads Clipping Profile



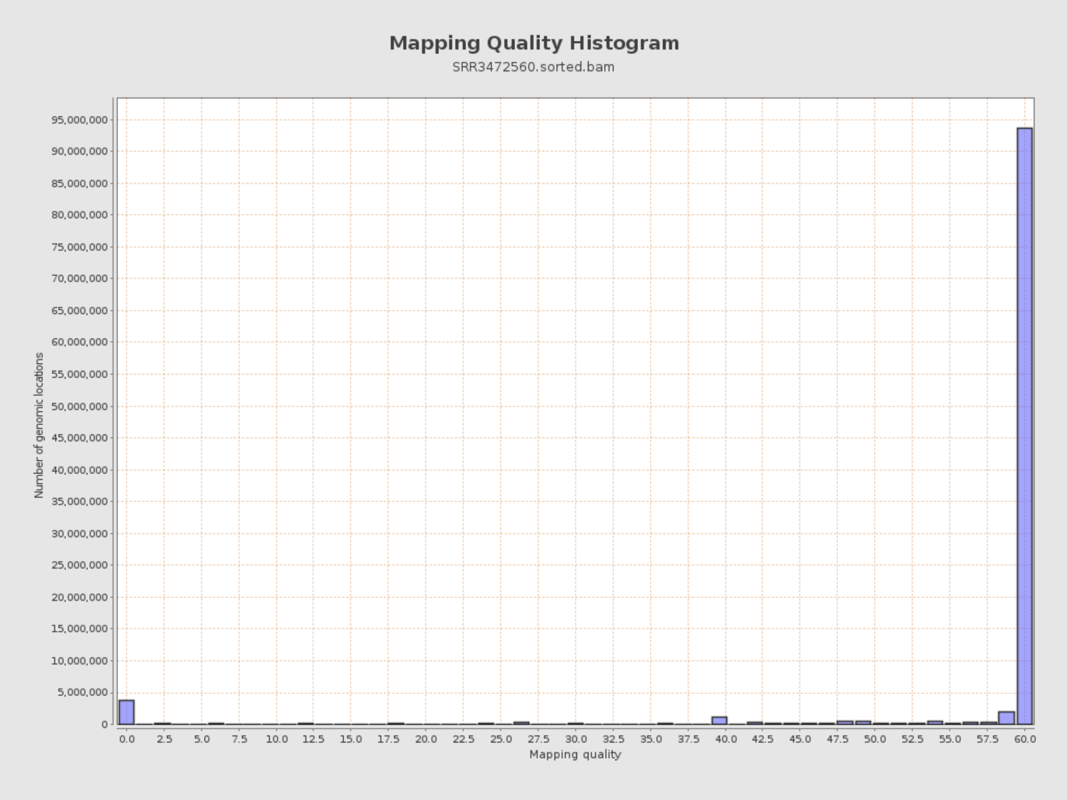
11. Results : Homopolymer Indels



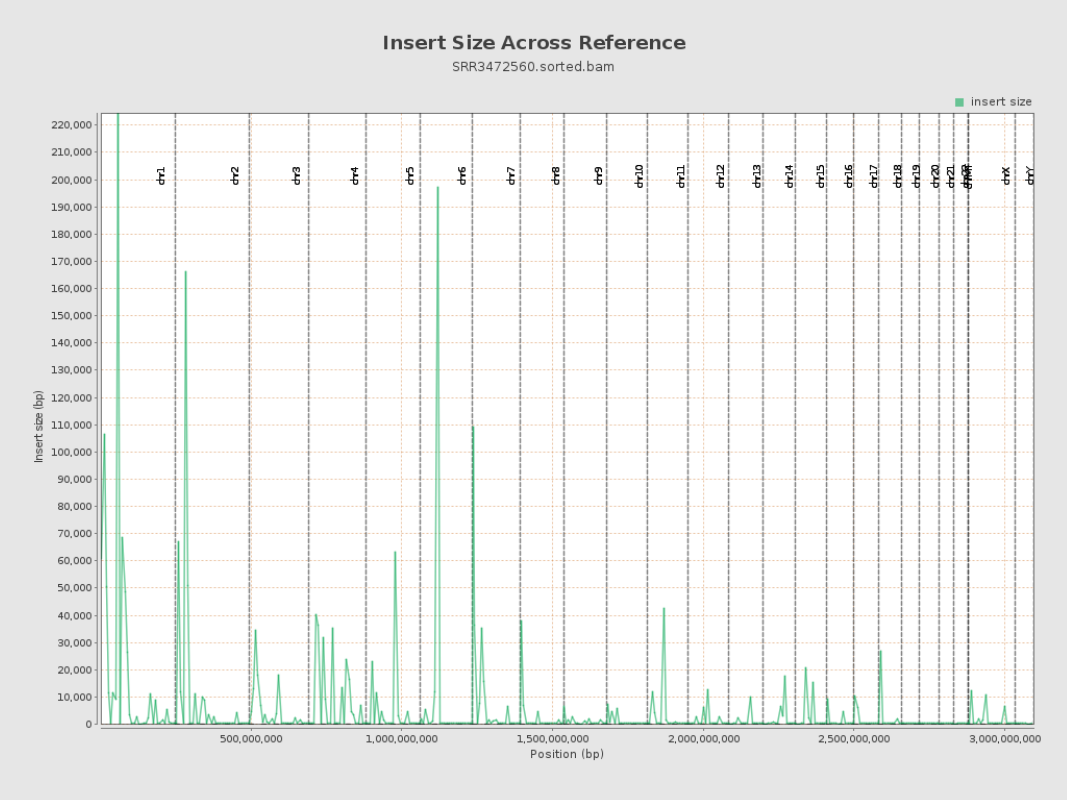
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram