Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 12:39:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472696.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_SRR3472696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472696_1.fastq.gz SRR3472696_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 12:39:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,759,980
Mapped reads	11,677,602 / 99.3%
Unmapped reads	82,378 / 0.7%
Mapped paired reads	11,677,602 / 99.3%
Mapped reads, first in pair	5,863,679 / 49.86%
Mapped reads, second in pair	5,813,923 / 49.44%
Mapped reads, both in pair	11,623,880 / 98.84%
Mapped reads, singletons	53,722 / 0.46%
Secondary alignments	0
Supplementary alignments	82,081 / 0.7%
Read min/max/mean length	30 / 101 / 99.47
Duplicated reads (estimated)	8,615,745 / 73.26%
Duplication rate	45.1%
Clipped reads	759,514 / 6.46%

2.2. ACGT Content

Number/percentage of A's	310,615,987 / 27.07%
Number/percentage of C's	261,939,137 / 22.83%
Number/percentage of T's	316,063,907 / 27.54%
Number/percentage of G's	258,680,632 / 22.54%
Number/percentage of N's	250,329 / 0.02%

GC Percentage	45.37%

2.3. Coverage

Mean	0.3707
Standard Deviation	32.5312

2.4. Mapping Quality

Mean Mapping Quality	54.55

2.5. Insert size

Mean	21,148.61
Standard Deviation	1,414,622.7
P25/Median/P75	151 / 207 / 274

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	4,636,035
Insertions	74,133
Mapped reads with at least one insertion	0.63%
Deletions	58,762
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.34%

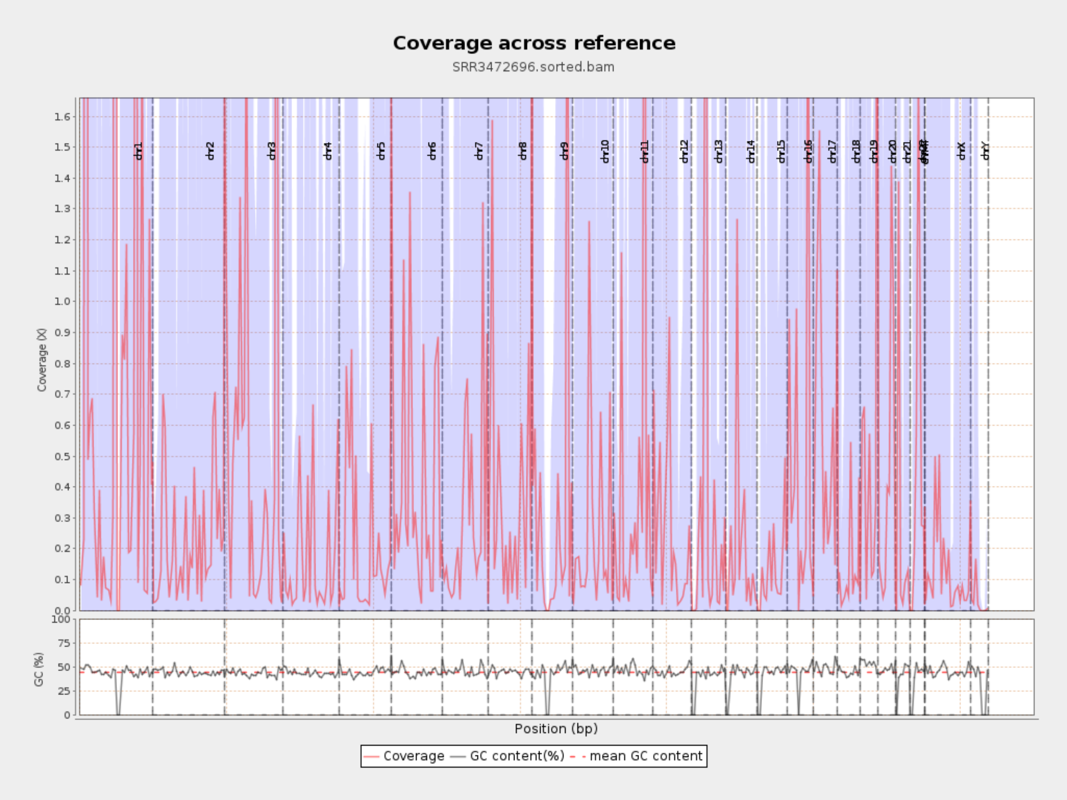
2.7. Chromosome stats

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

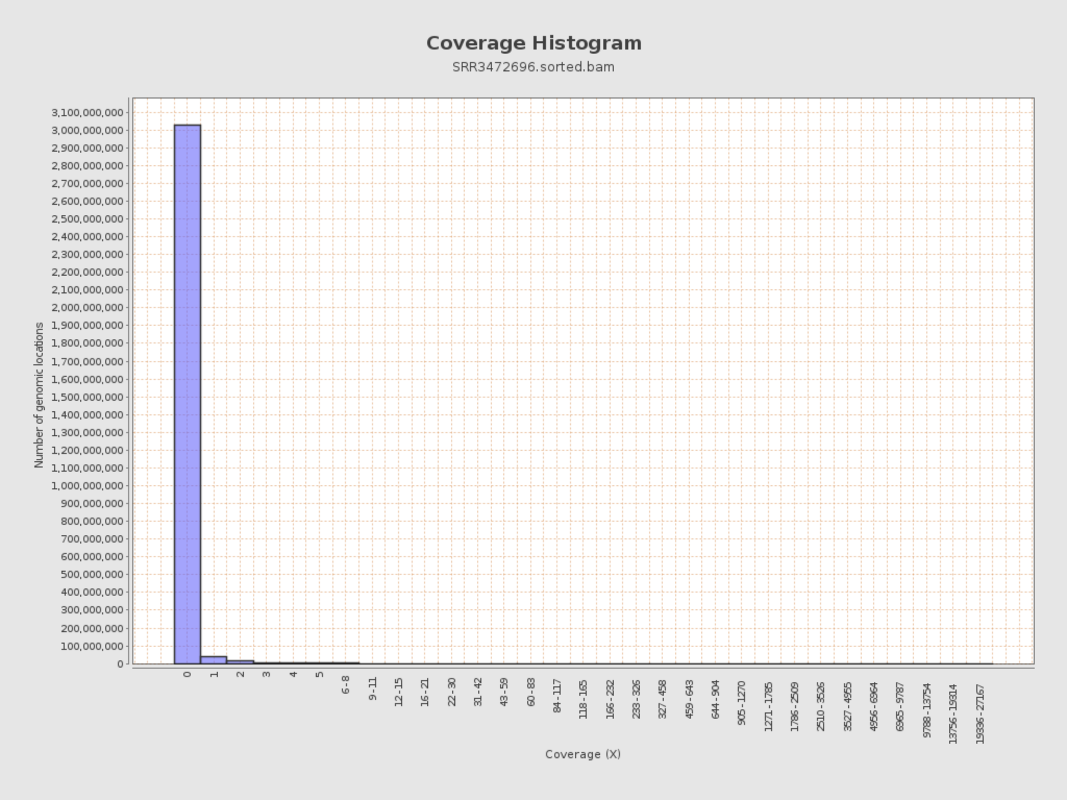
		bases	coverage	deviation
chr1	249250621	277791807	1.1145	85.6985
chr2	243199373	56217517	0.2312	12.3159
chr3	198022430	108854053	0.5497	34.8153
chr4	191154276	31912848	0.1669	11.4372
chr5	180915260	40114002	0.2217	12.5732
chr6	171115067	69014358	0.4033	24.5162
chr7	159138663	50196064	0.3154	15.5866
chr8	146364022	51626693	0.3527	23.1021
chr9	141213431	48561170	0.3439	31.8041
chr10	135534747	33568513	0.2477	18.3342
chr11	135006516	57493929	0.4259	35.284
chr12	133851895	34558125	0.2582	13.7941
chr13	115169878	36672170	0.3184	41.8588
chr14	107349540	21177764	0.1973	14.1675
chr15	102531392	14058655	0.1371	10.036
chr16	90354753	45798039	0.5069	27.6096
chr17	81195210	47632819	0.5866	25.6372
chr18	78077248	10835999	0.1388	7.5996
chr19	59128983	24850268	0.4203	17.622
chr20	63025520	27768225	0.4406	29.9467
chr21	48129895	13221349	0.2747	30.125
chr22	51304566	23843600	0.4647	23.5037
chrMT	16571	5562	0.3356	0.7862
chrX	155270560	20078055	0.1293	5.7381

chrY	59373566	1863529	0.0314	3.7267

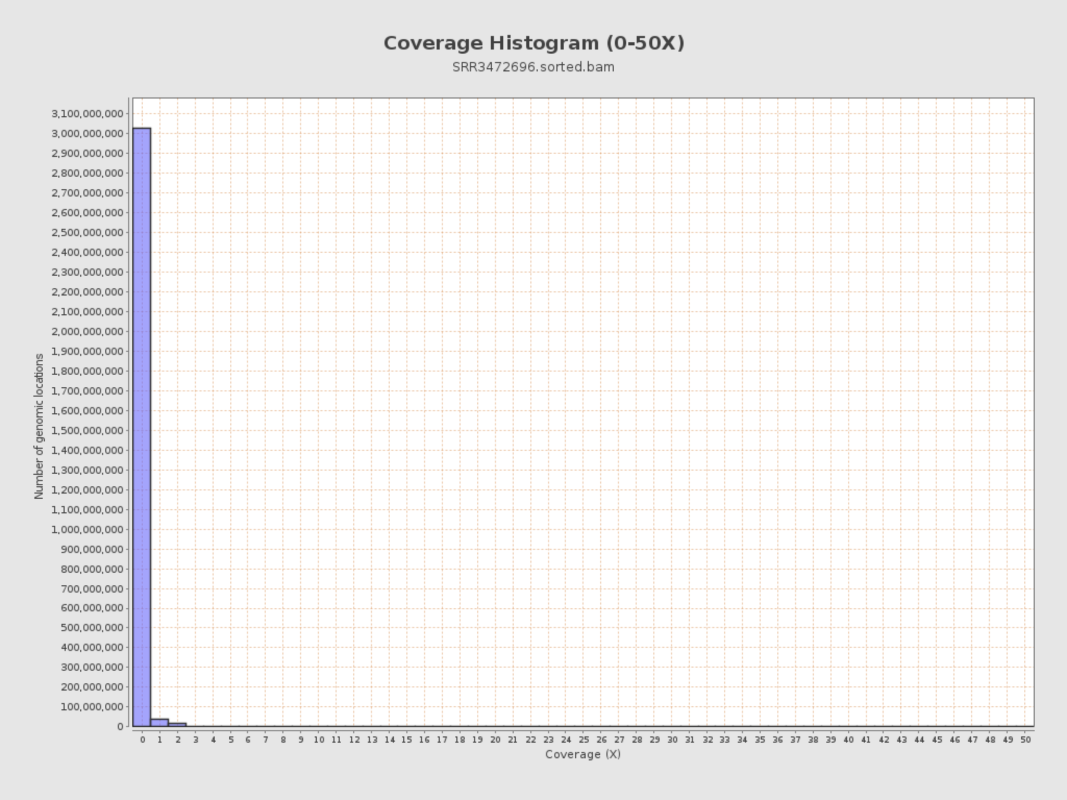
3. Results : Coverage across reference



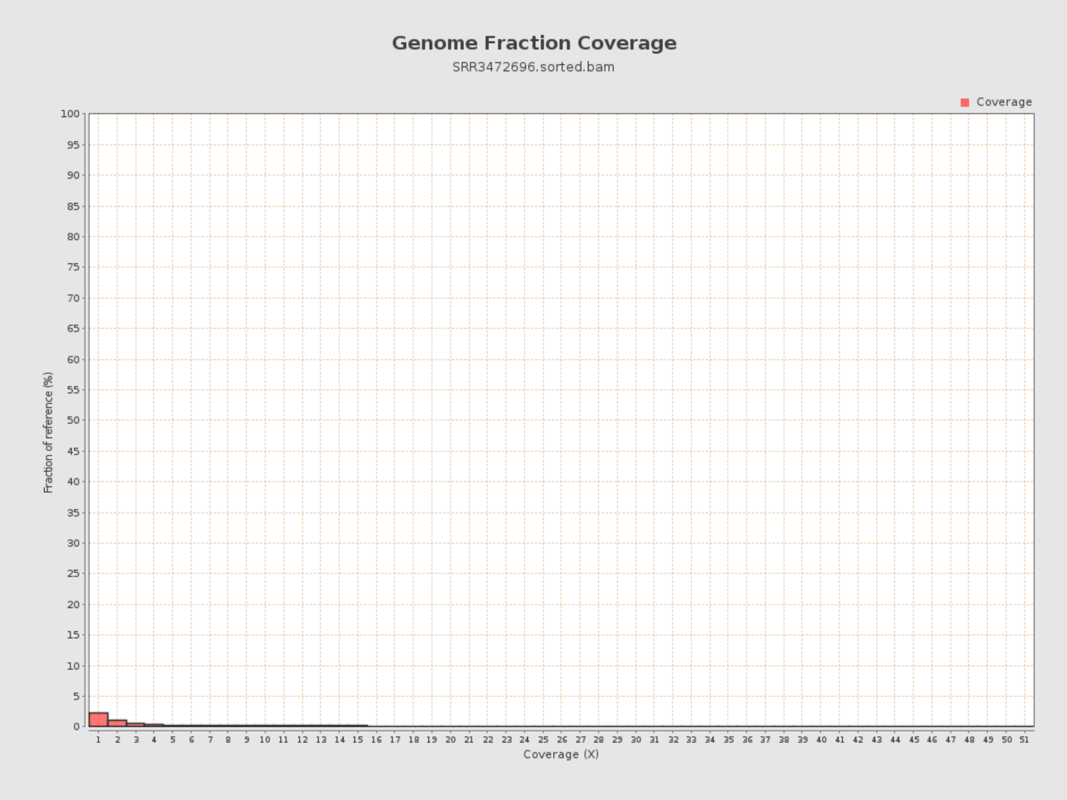
4. Results : Coverage Histogram



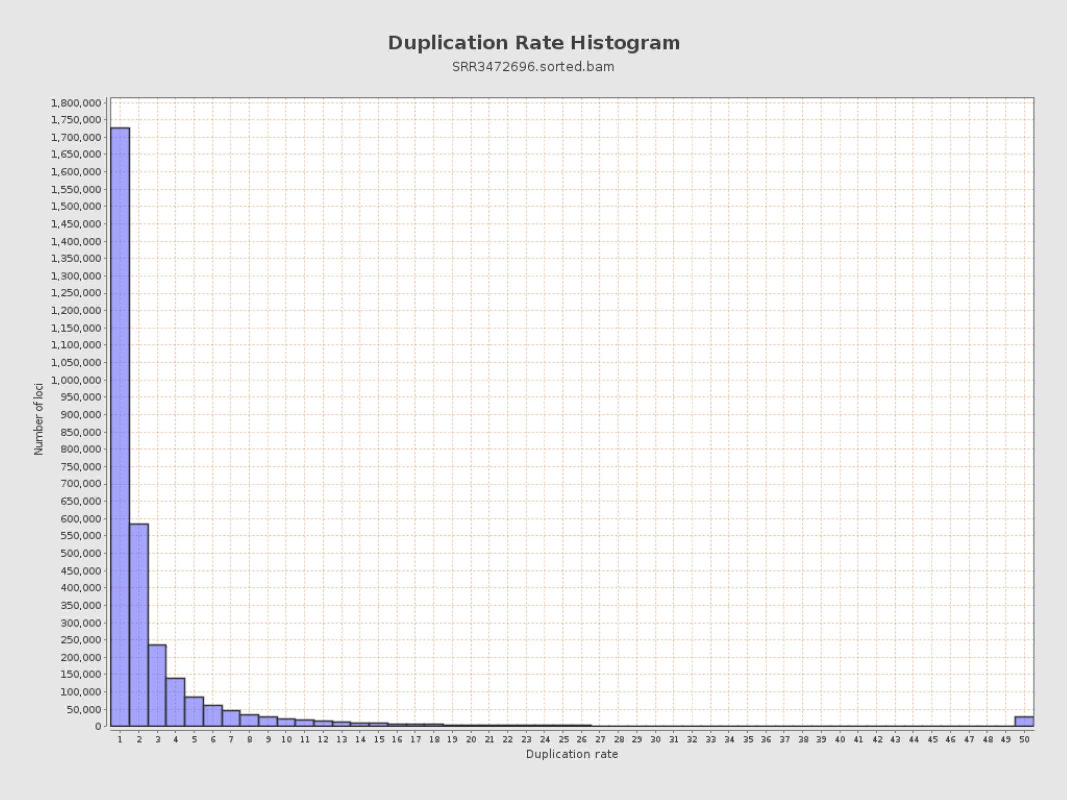
5. Results : Coverage Histogram (0-50X)



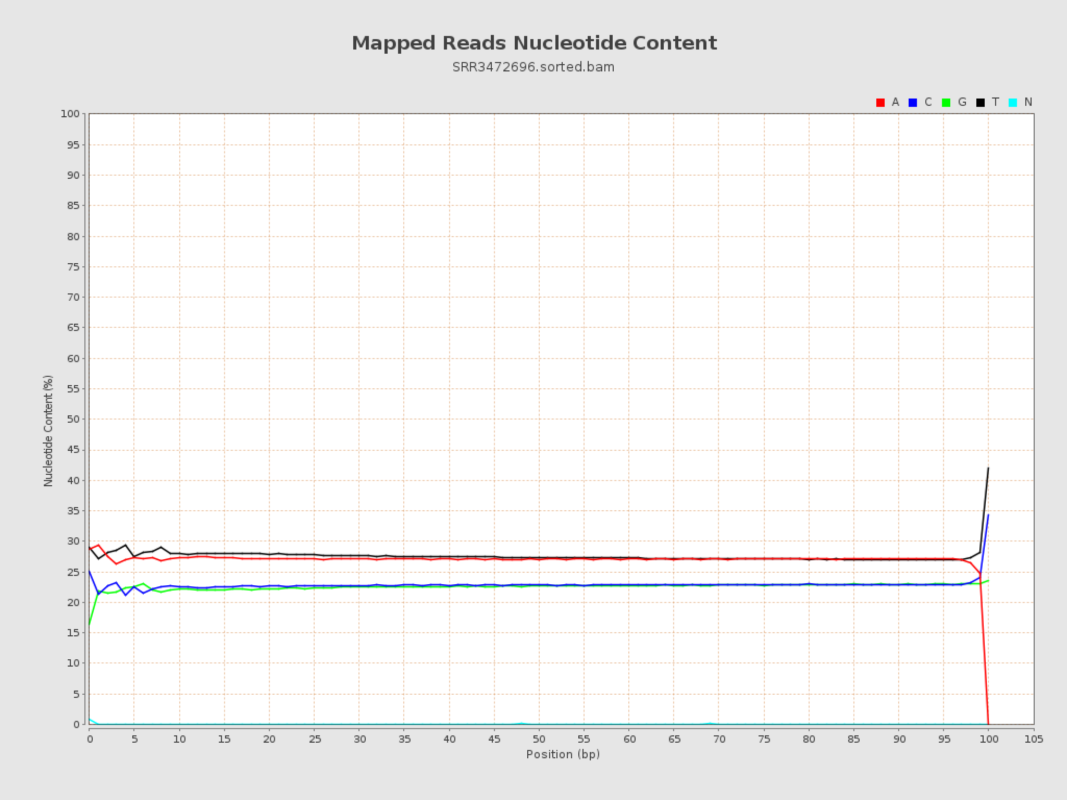
6. Results : Genome Fraction Coverage



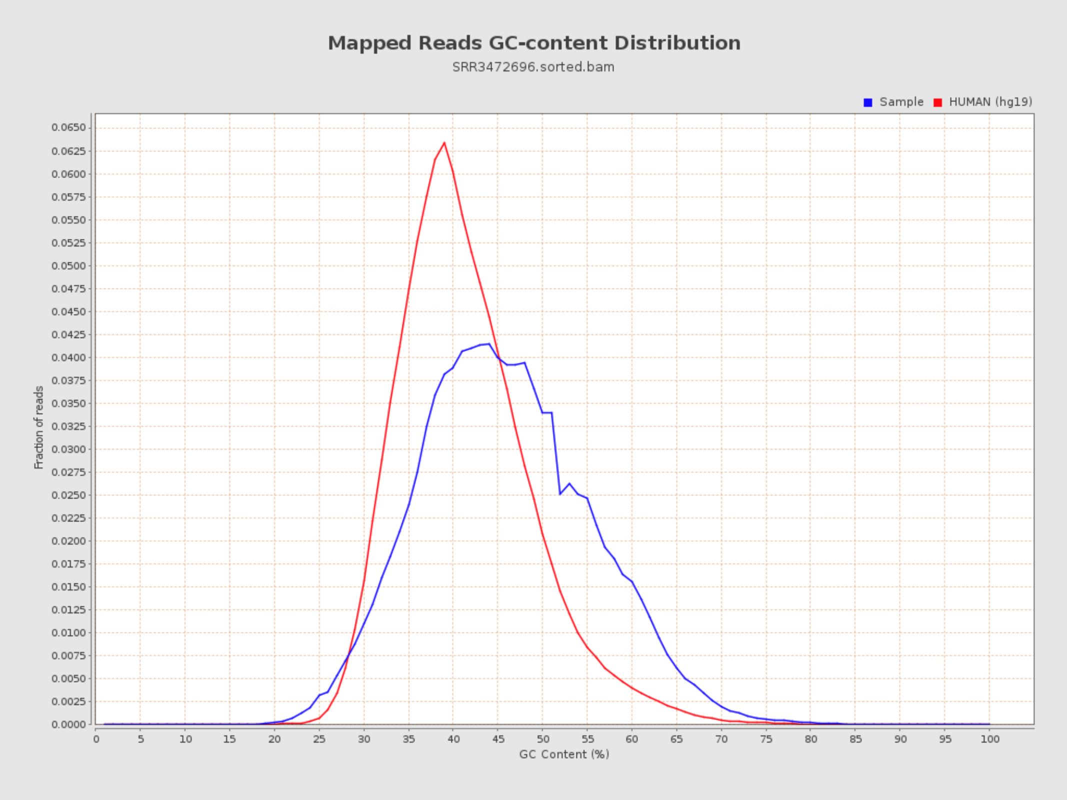
7. Results : Duplication Rate Histogram



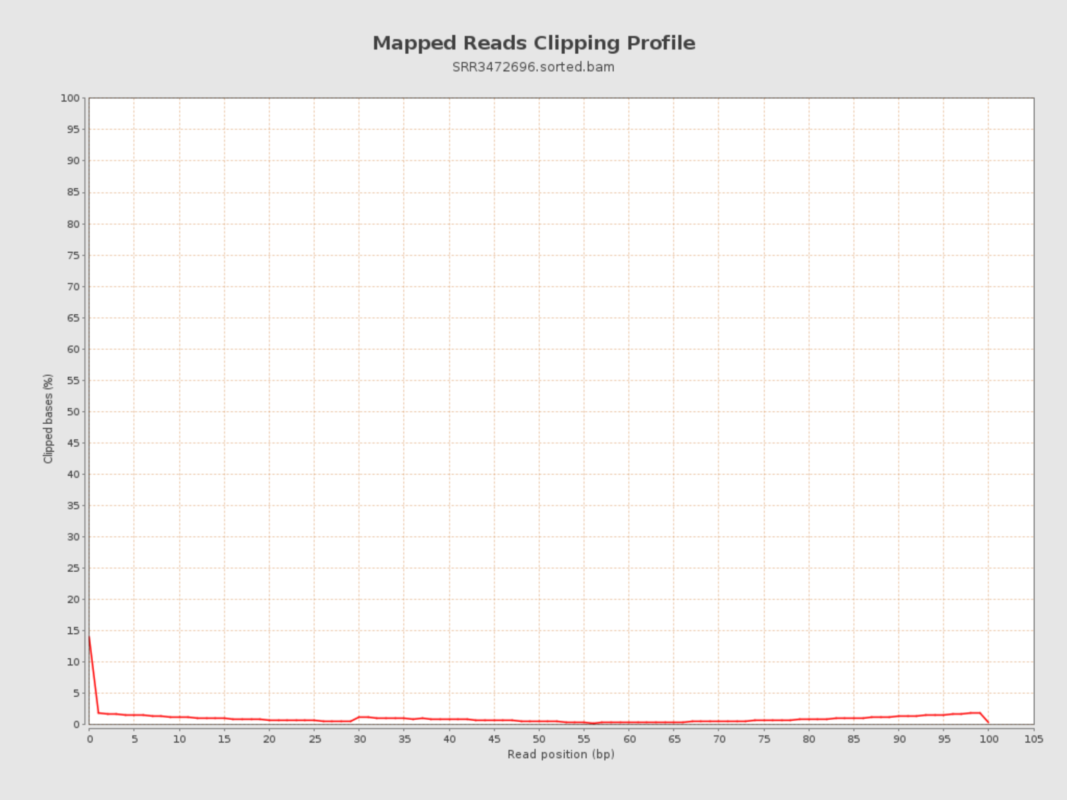
8. Results : Mapped Reads Nucleotide Content



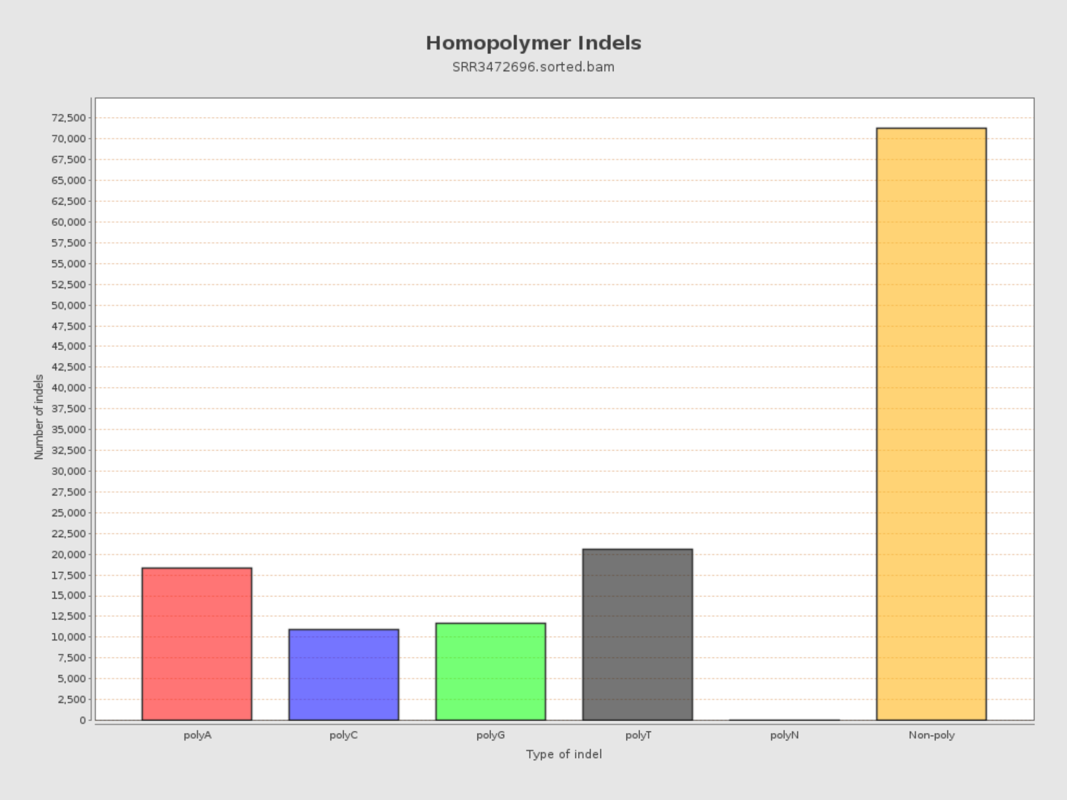
9. Results : Mapped Reads GC-content Distribution



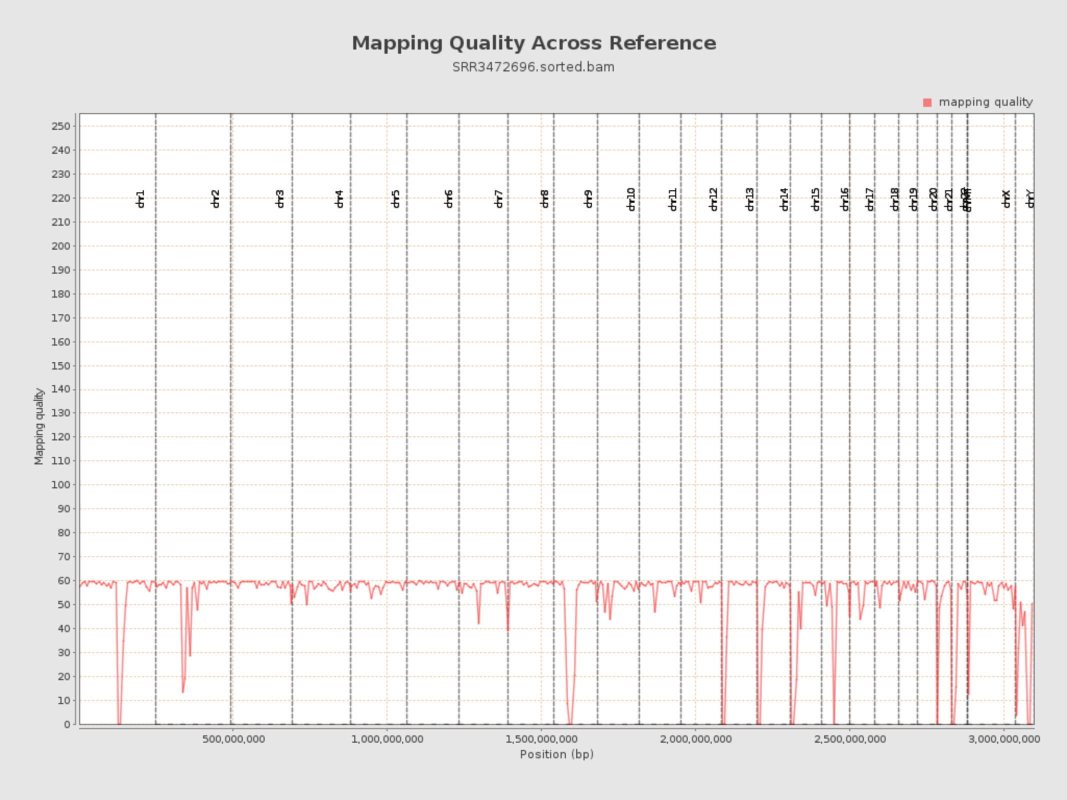
10. Results : Mapped Reads Clipping Profile



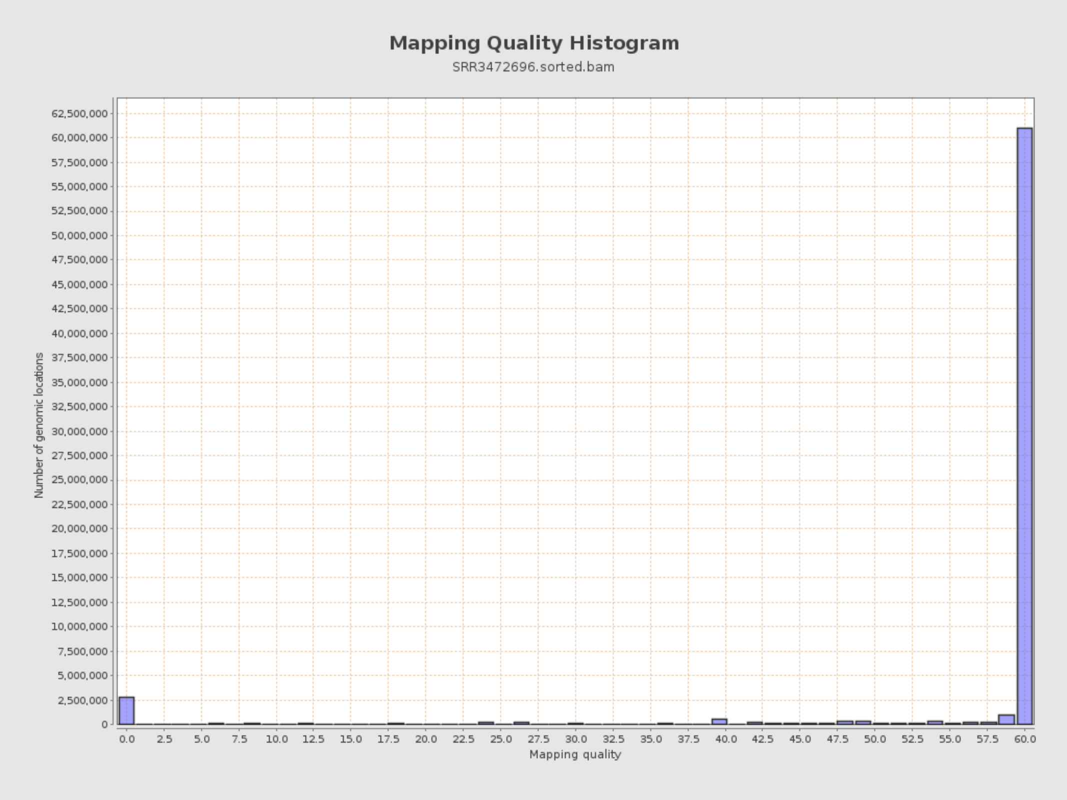
11. Results : Homopolymer Indels



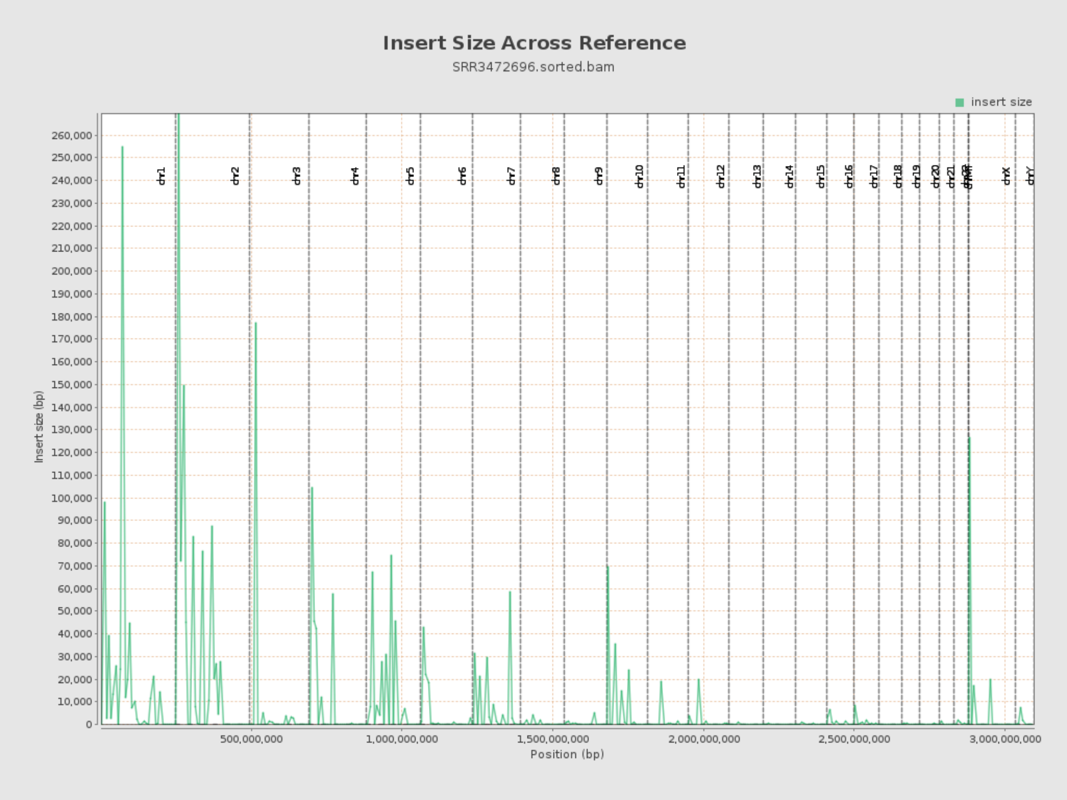
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram