Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:08:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472458.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_SRR3472458 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472458_1.fastq.gz SRR3472458_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:08:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472458.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,276,624
Mapped reads	13,128,689 / 98.89%
Unmapped reads	147,935 / 1.11%
Mapped paired reads	13,128,689 / 98.89%
Mapped reads, first in pair	6,589,179 / 49.63%
Mapped reads, second in pair	6,539,510 / 49.26%
Mapped reads, both in pair	13,057,202 / 98.35%
Mapped reads, singletons	71,487 / 0.54%
Secondary alignments	0
Supplementary alignments	57,298 / 0.43%
Read min/max/mean length	30 / 100 / 98.86
Duplicated reads (estimated)	8,386,142 / 63.16%
Duplication rate	45.54%
Clipped reads	1,050,270 / 7.91%

2.2. ACGT Content

Number/percentage of A's	341,219,981 / 26.72%
Number/percentage of C's	297,348,589 / 23.29%
Number/percentage of T's	343,587,150 / 26.91%
Number/percentage of G's	294,559,829 / 23.07%
Number/percentage of N's	167,759 / 0.01%

GC Percentage	46.36%

2.3. Coverage

Mean	0.4125
Standard Deviation	17.3068

2.4. Mapping Quality

Mean Mapping Quality	54.82

2.5. Insert size

Mean	20,955.28
Standard Deviation	1,458,256.43
P25/Median/P75	138 / 192 / 258

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	5,618,921
Insertions	74,582
Mapped reads with at least one insertion	0.56%
Deletions	63,975
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.65%

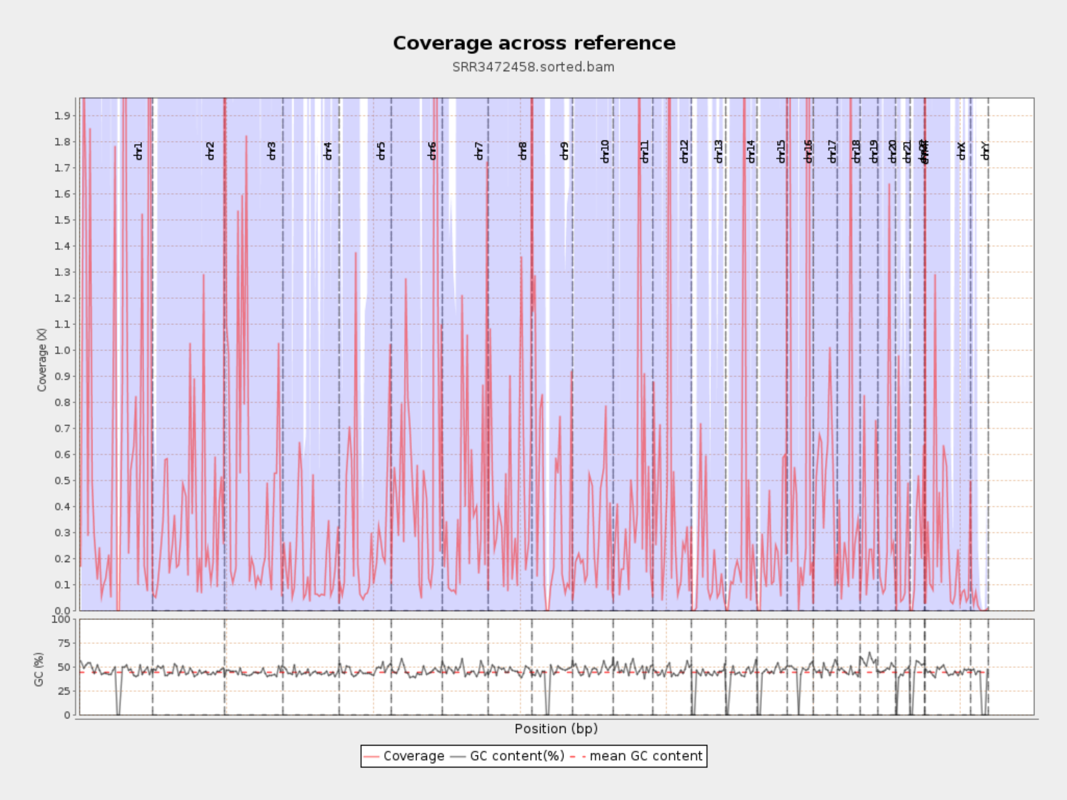
2.7. Chromosome stats

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

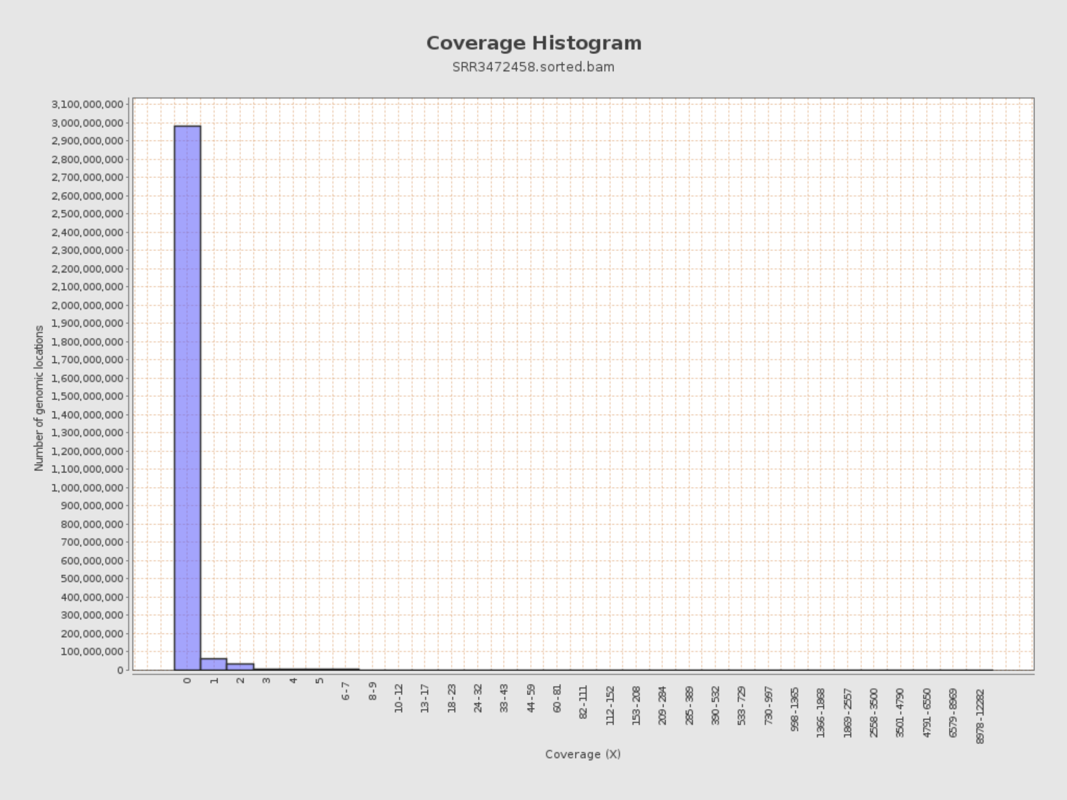
		bases	coverage	deviation
chr1	249250621	190157643	0.7629	24.494
chr2	243199373	83442135	0.3431	13.0494
chr3	198022430	108384240	0.5473	15.8705
chr4	191154276	35231302	0.1843	7.7155
chr5	180915260	57010249	0.3151	11.3539
chr6	171115067	103740776	0.6063	29.5501
chr7	159138663	69407868	0.4361	17.8573
chr8	146364022	67446284	0.4608	16.5127
chr9	141213431	62683182	0.4439	15.4252
chr10	135534747	38451443	0.2837	11.1714
chr11	135006516	56593319	0.4192	18.6736
chr12	133851895	61453039	0.4591	14.2742
chr13	115169878	19409355	0.1685	6.1592
chr14	107349540	32231797	0.3003	14.126
chr15	102531392	23307383	0.2273	8.4374
chr16	90354753	86178118	0.9538	35.1355
chr17	81195210	41308429	0.5088	15.0974
chr18	78077248	33032164	0.4231	29.5983
chr19	59128983	20032315	0.3388	11.2605
chr20	63025520	22022234	0.3494	13.9193
chr21	48129895	12951998	0.2691	16.1402
chr22	51304566	14086306	0.2746	10.7849
chrMT	16571	80319	4.847	9.5378
chrX	155270560	36975067	0.2381	10.3239

chrY	59373566	1413422	0.0238	2.4427

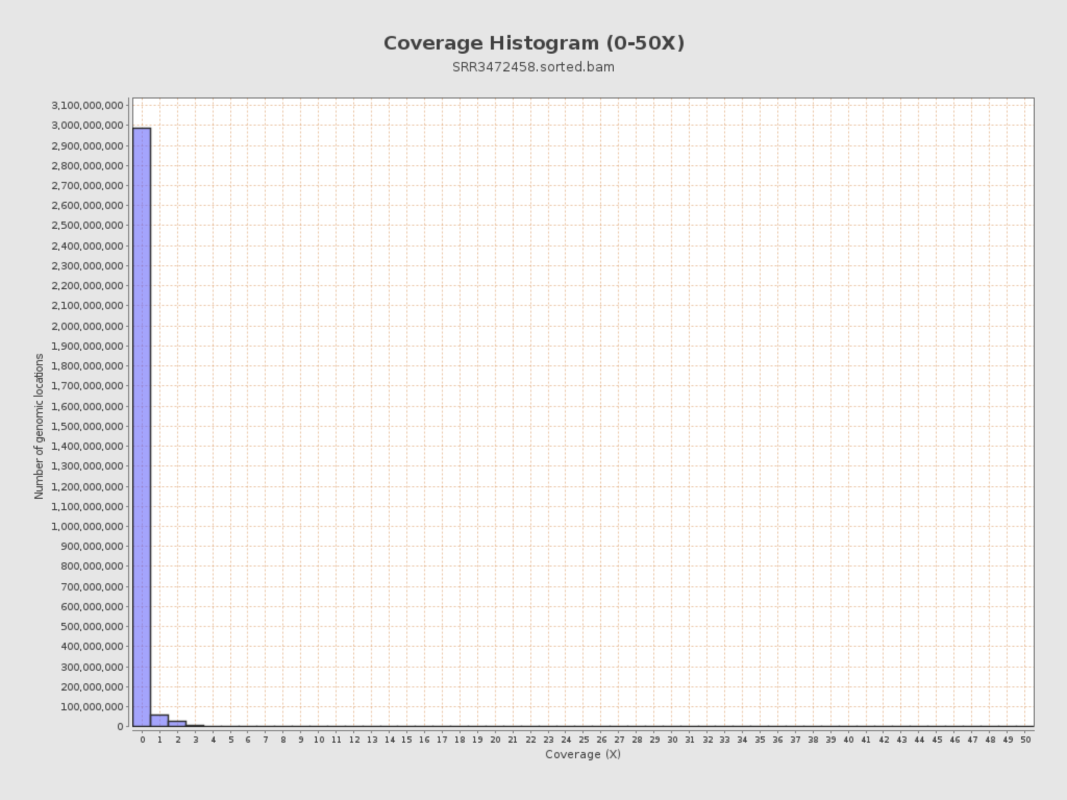
3. Results : Coverage across reference



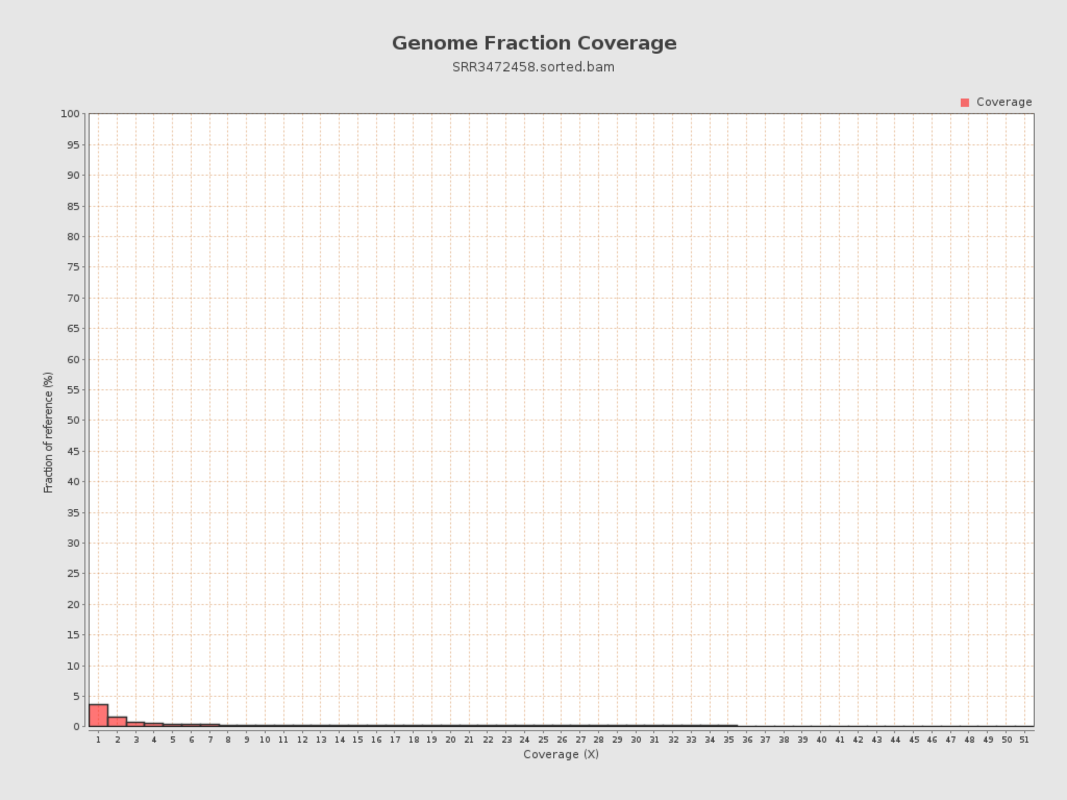
4. Results : Coverage Histogram



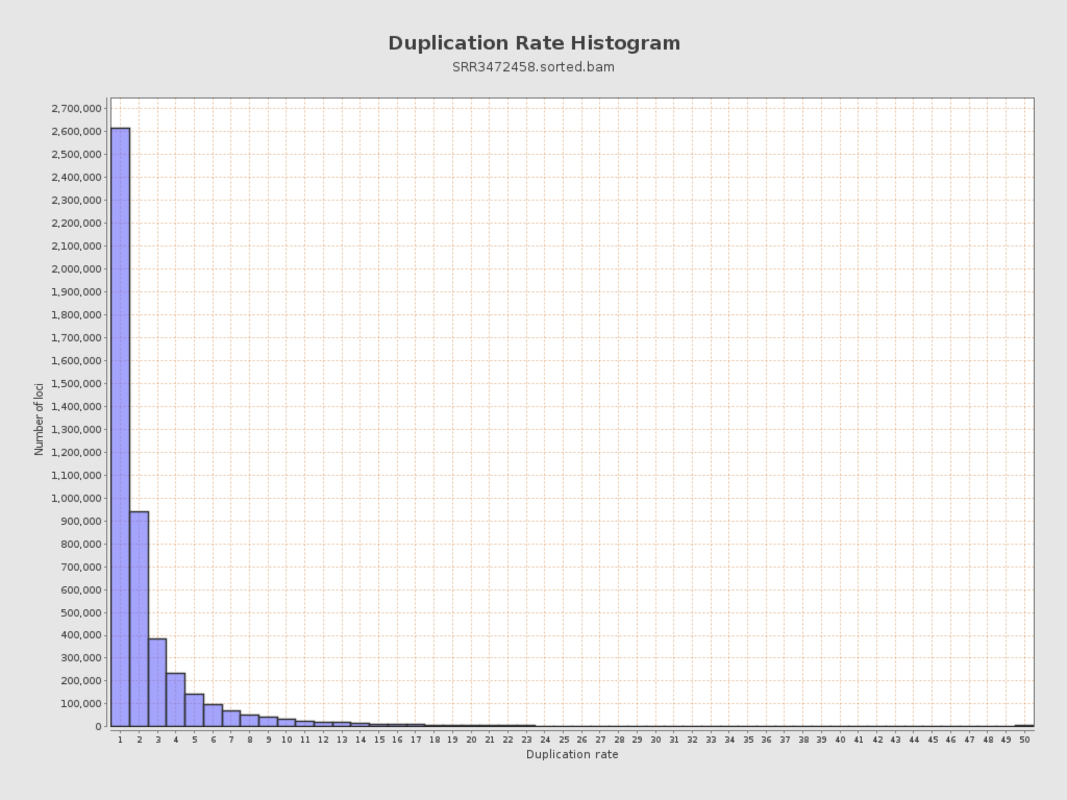
5. Results : Coverage Histogram (0-50X)



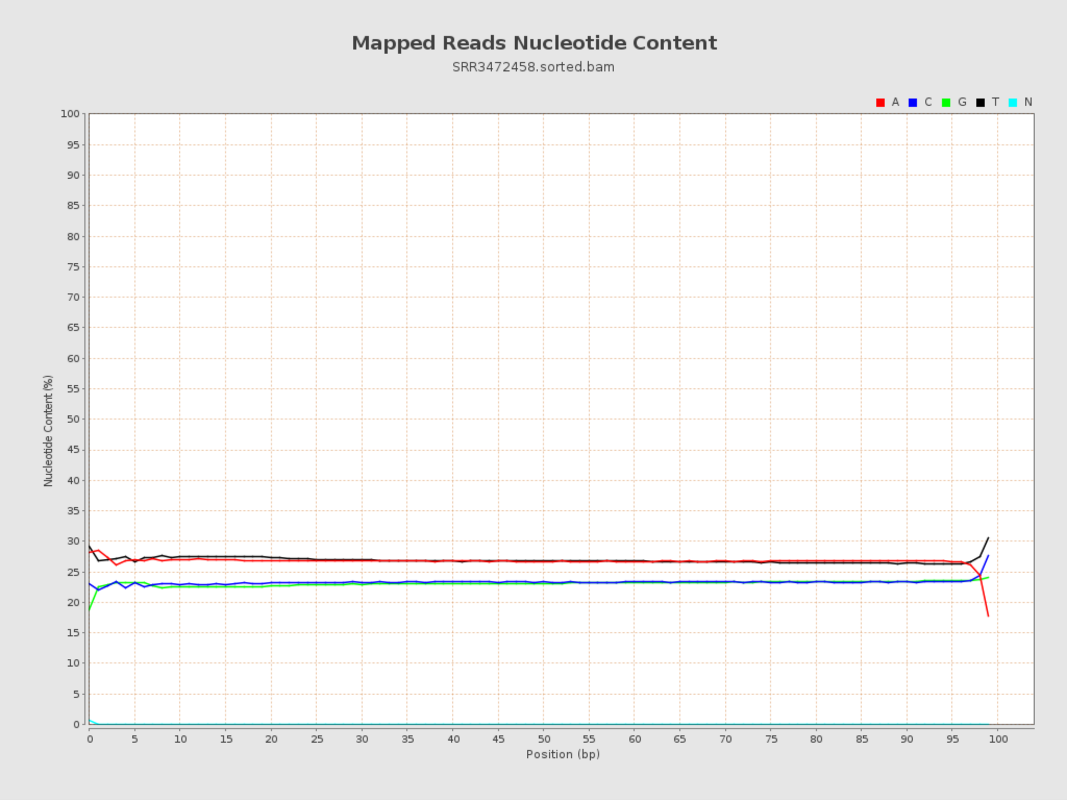
6. Results : Genome Fraction Coverage



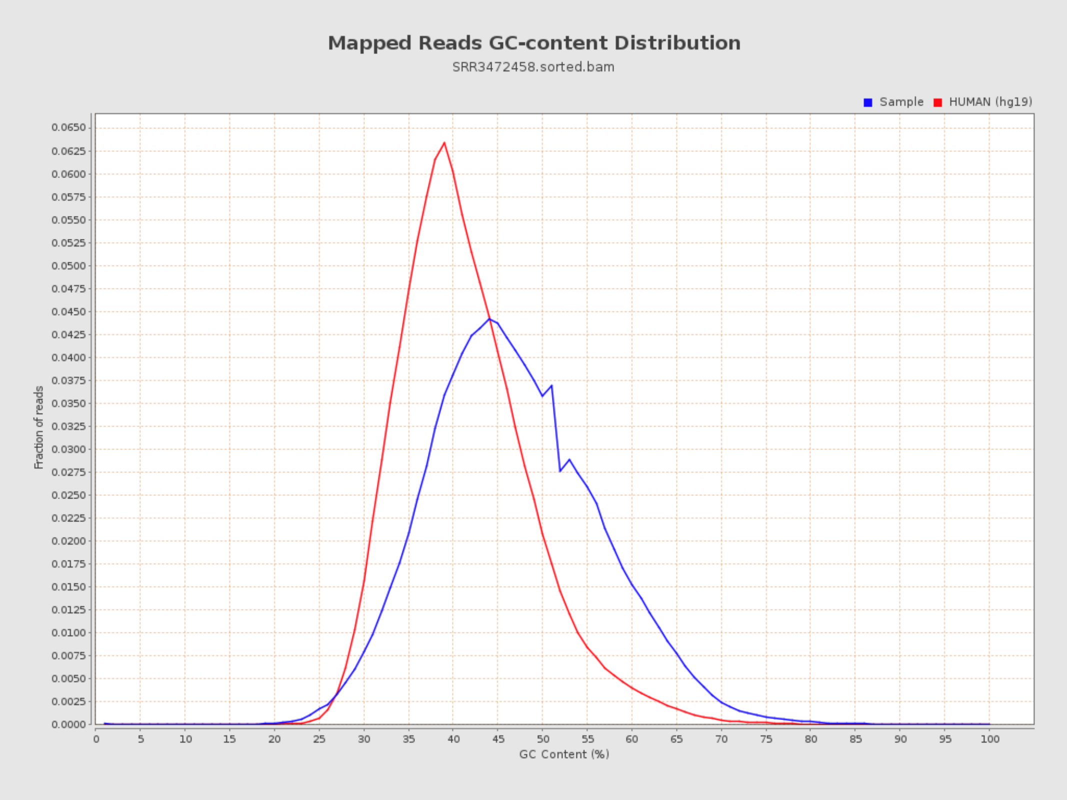
7. Results : Duplication Rate Histogram



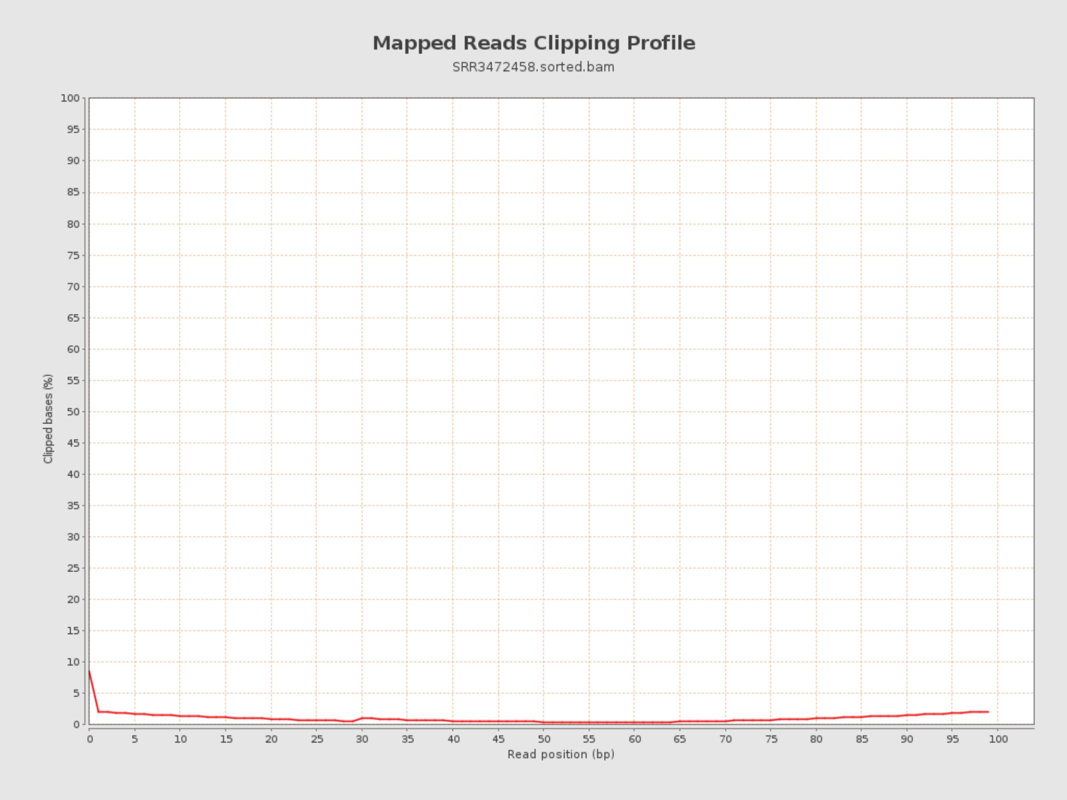
8. Results : Mapped Reads Nucleotide Content



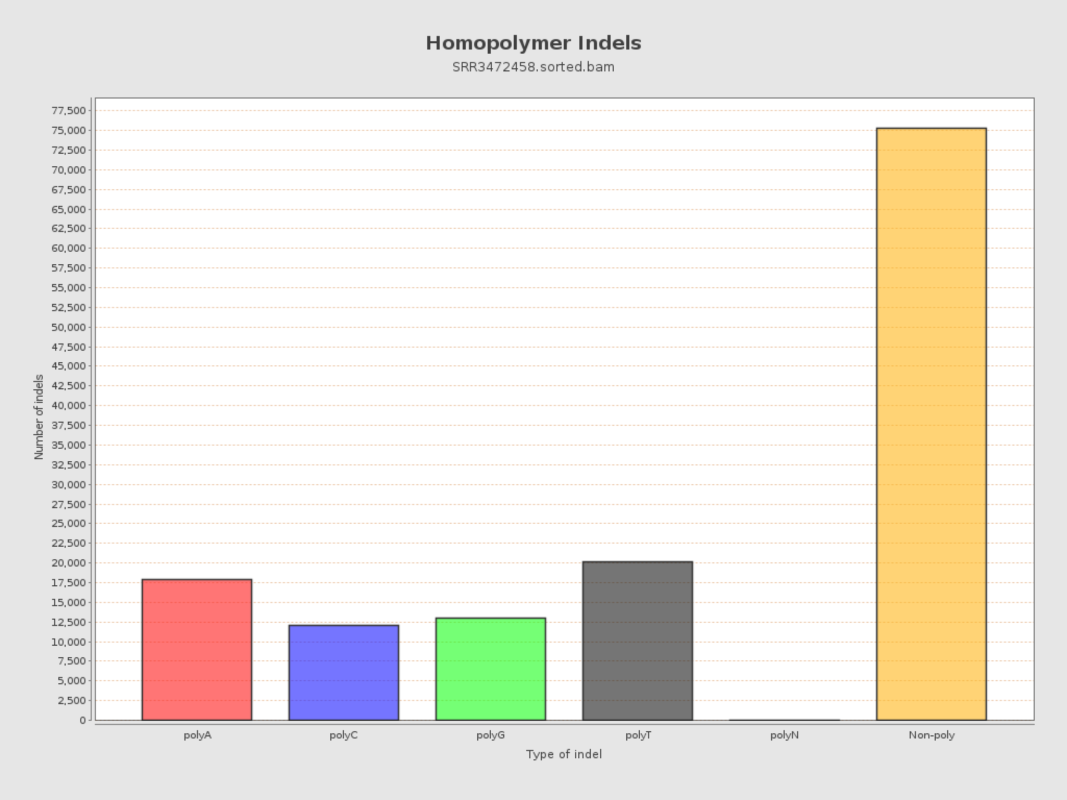
9. Results : Mapped Reads GC-content Distribution



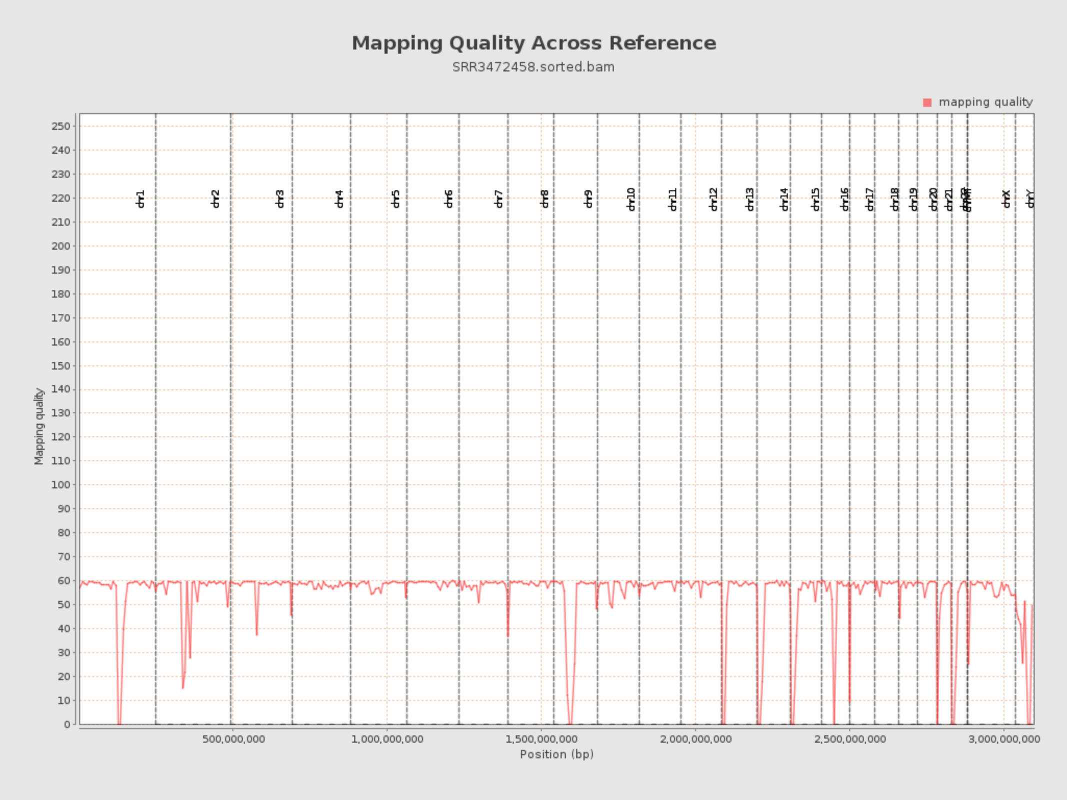
10. Results : Mapped Reads Clipping Profile



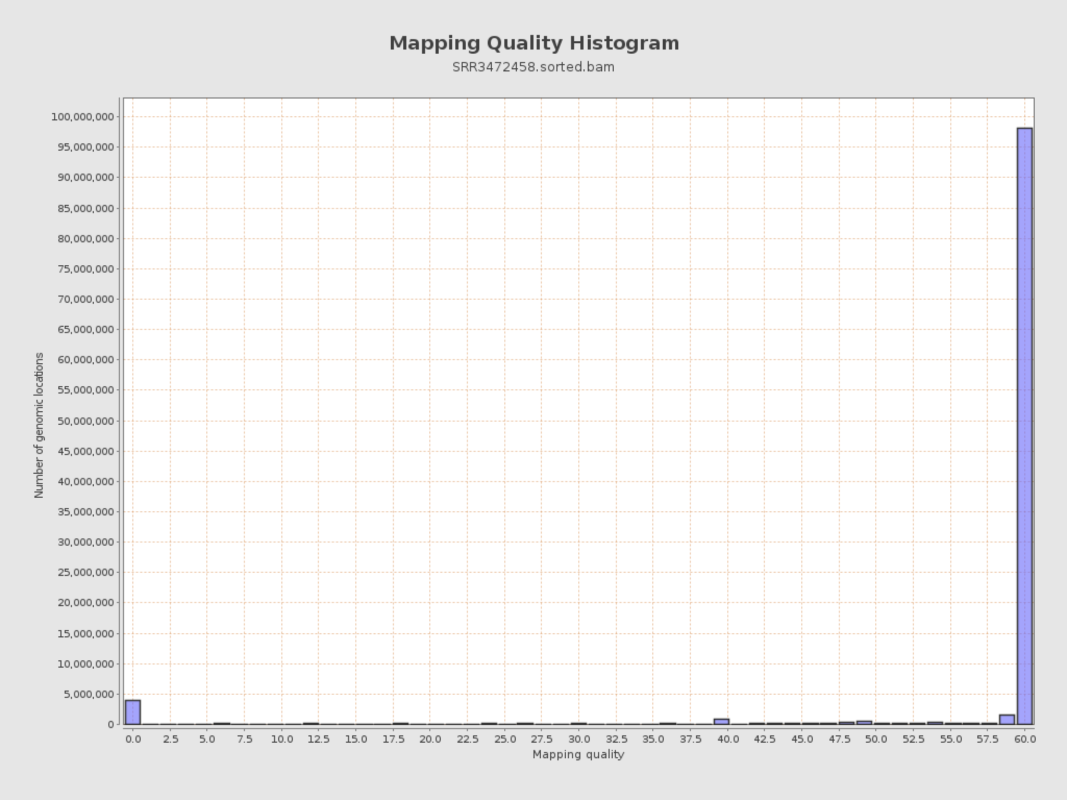
11. Results : Homopolymer Indels



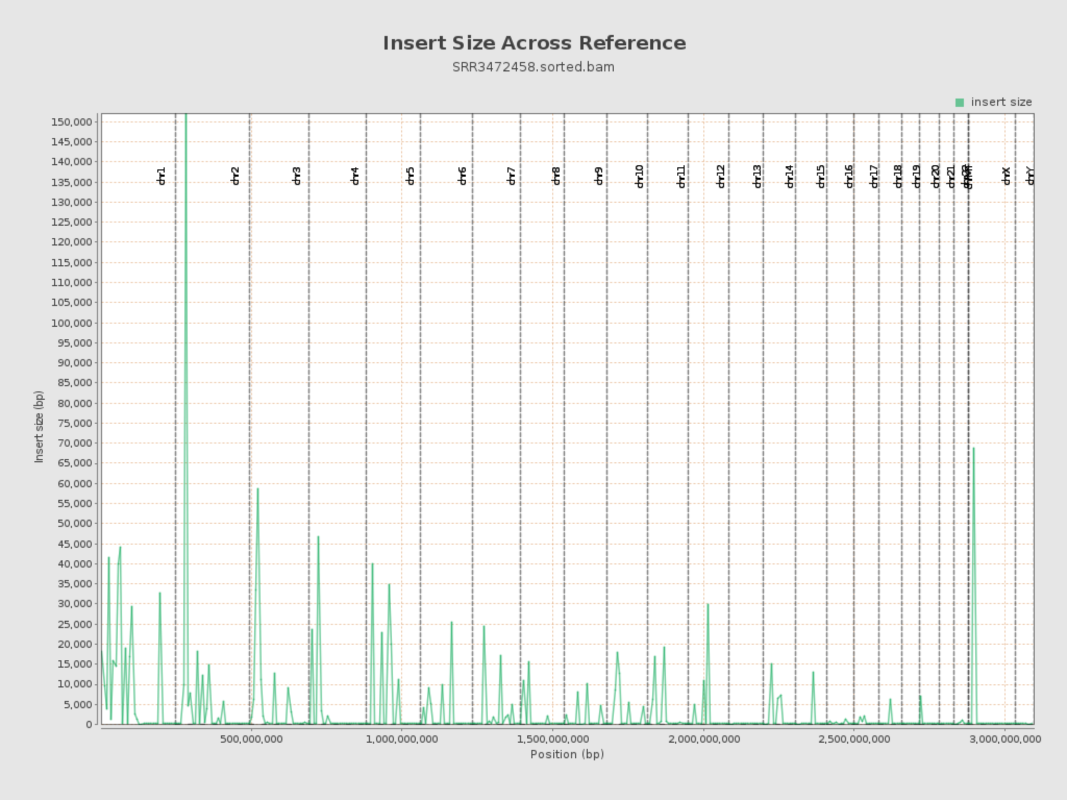
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram