Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 18:33:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472637.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_SRR3472637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472637_1.fastq.gz SRR3472637_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 18:33:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,676,068
Mapped reads	15,567,450 / 99.31%
Unmapped reads	108,618 / 0.69%
Mapped paired reads	15,567,450 / 99.31%
Mapped reads, first in pair	7,804,594 / 49.79%
Mapped reads, second in pair	7,762,856 / 49.52%
Mapped reads, both in pair	15,491,668 / 98.82%
Mapped reads, singletons	75,782 / 0.48%
Secondary alignments	0
Supplementary alignments	74,406 / 0.47%
Read min/max/mean length	30 / 101 / 99.7
Duplicated reads (estimated)	10,526,347 / 67.15%
Duplication rate	49.29%
Clipped reads	1,058,522 / 6.75%

2.2. ACGT Content

Number/percentage of A's	418,161,629 / 27.3%
Number/percentage of C's	349,620,945 / 22.82%
Number/percentage of T's	419,581,986 / 27.39%
Number/percentage of G's	344,296,013 / 22.47%
Number/percentage of N's	279,402 / 0.02%

GC Percentage	45.3%

2.3. Coverage

Mean	0.4949
Standard Deviation	20.0396

2.4. Mapping Quality

Mean Mapping Quality	54.82

2.5. Insert size

Mean	21,282.85
Standard Deviation	1,482,539.3
P25/Median/P75	152 / 212 / 288

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	9,040,383
Insertions	91,975
Mapped reads with at least one insertion	0.58%
Deletions	79,972
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.62%

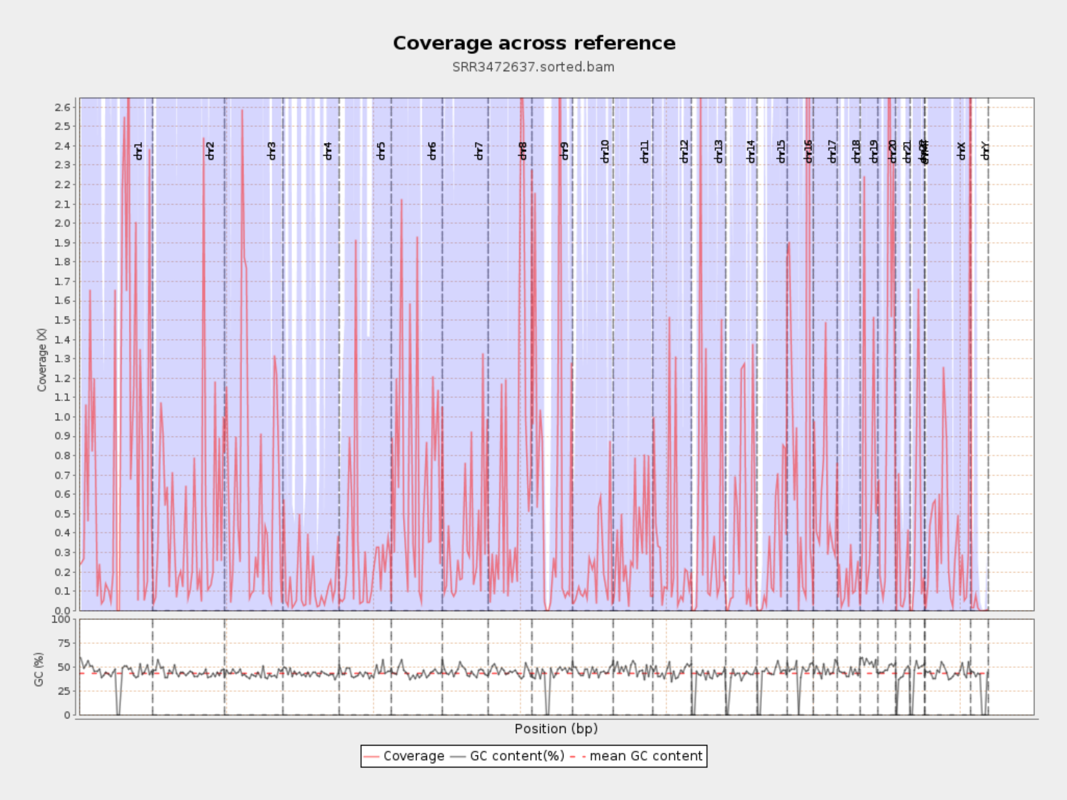
2.7. Chromosome stats

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

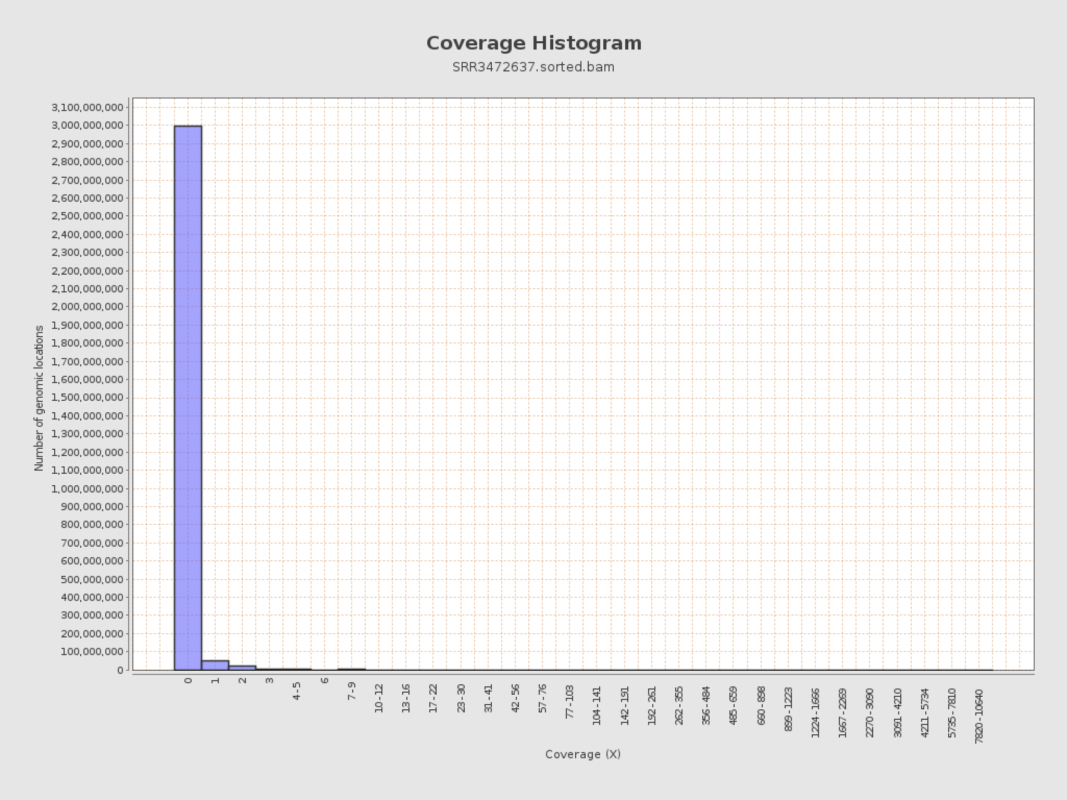
		bases	coverage	deviation
chr1	249250621	208501225	0.8365	27.9477
chr2	243199373	109249738	0.4492	17.4821
chr3	198022430	125316120	0.6328	20.1469
chr4	191154276	24889718	0.1302	5.6266
chr5	180915260	53592349	0.2962	13.6017
chr6	171115067	120457664	0.704	18.2656
chr7	159138663	61625375	0.3872	12.5516
chr8	146364022	104492578	0.7139	27.3955
chr9	141213431	96229016	0.6814	25.9215
chr10	135534747	28677896	0.2116	11.2996
chr11	135006516	44581674	0.3302	12.6229
chr12	133851895	47247279	0.353	15.4632
chr13	115169878	58882345	0.5113	23.511
chr14	107349540	44508025	0.4146	17.6028
chr15	102531392	30433929	0.2968	13.4992
chr16	90354753	101052765	1.1184	41.5176
chr17	81195210	49006755	0.6036	16.3838
chr18	78077248	11364101	0.1455	5.657
chr19	59128983	43441364	0.7347	28.7755
chr20	63025520	74605594	1.1837	35.5345
chr21	48129895	10190228	0.2117	15.9512
chr22	51304566	22732058	0.4431	21.8372
chrMT	16571	1779	0.1074	0.4156
chrX	155270560	60095665	0.387	15.0929

chrY	59373566	947150	0.016	1.1781

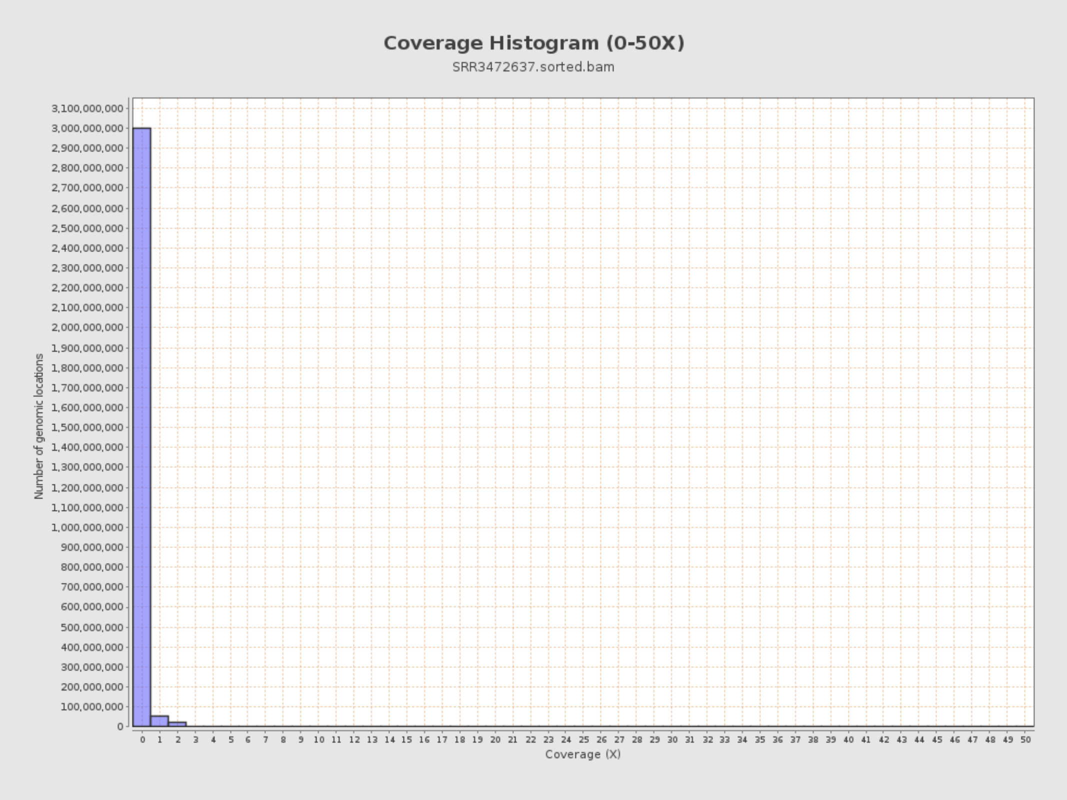
3. Results : Coverage across reference



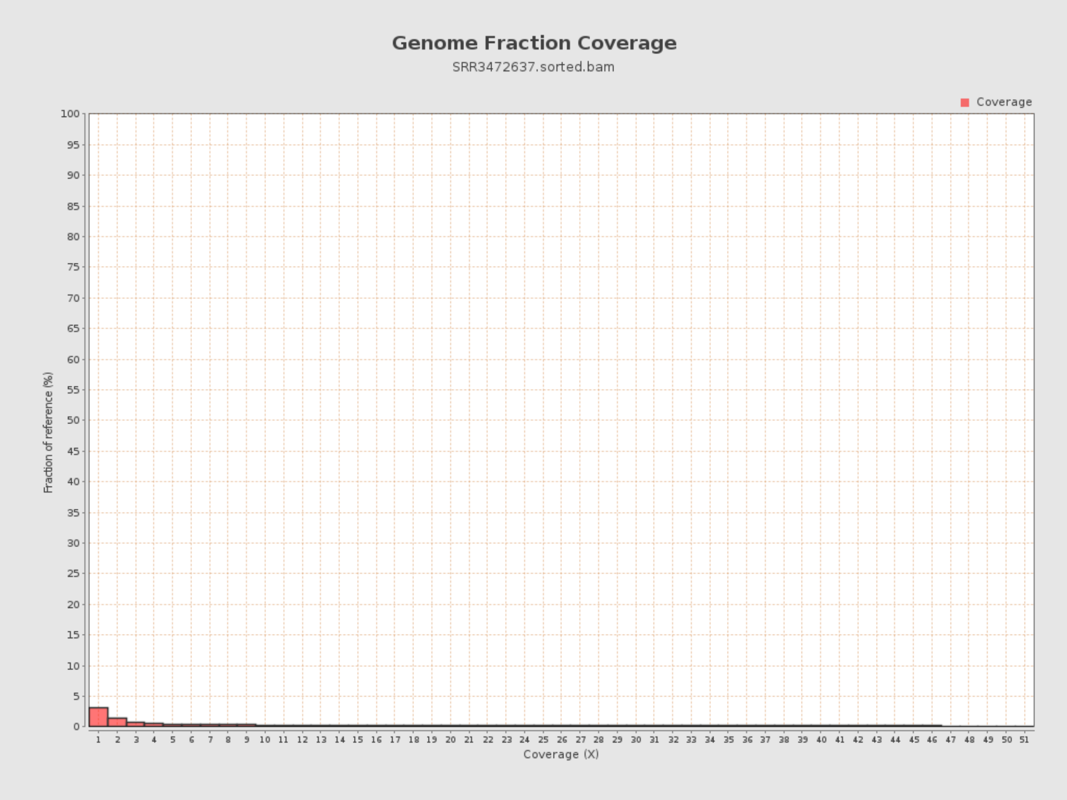
4. Results : Coverage Histogram



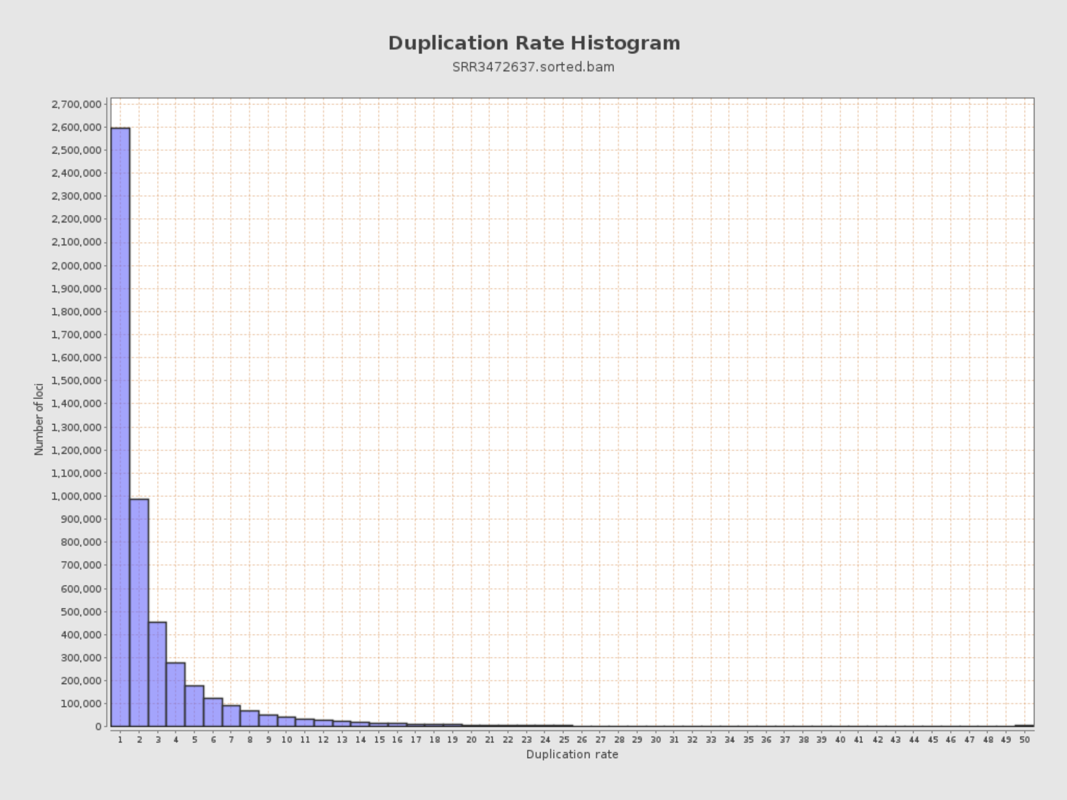
5. Results : Coverage Histogram (0-50X)



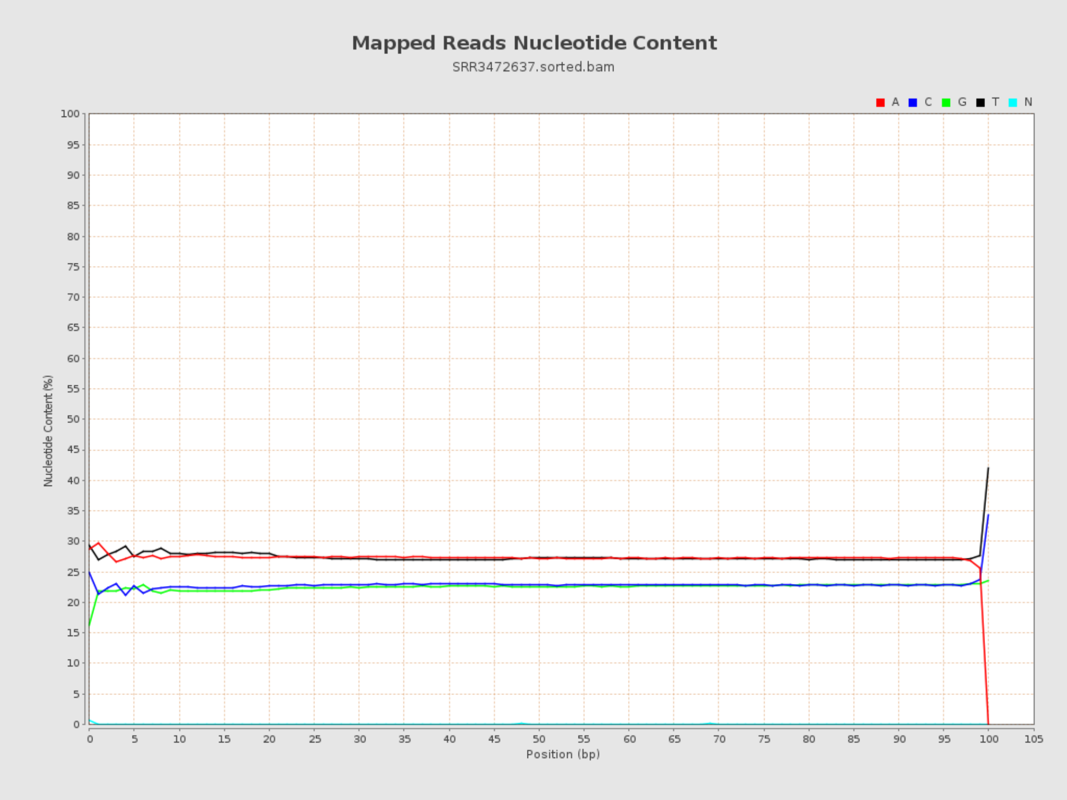
6. Results : Genome Fraction Coverage



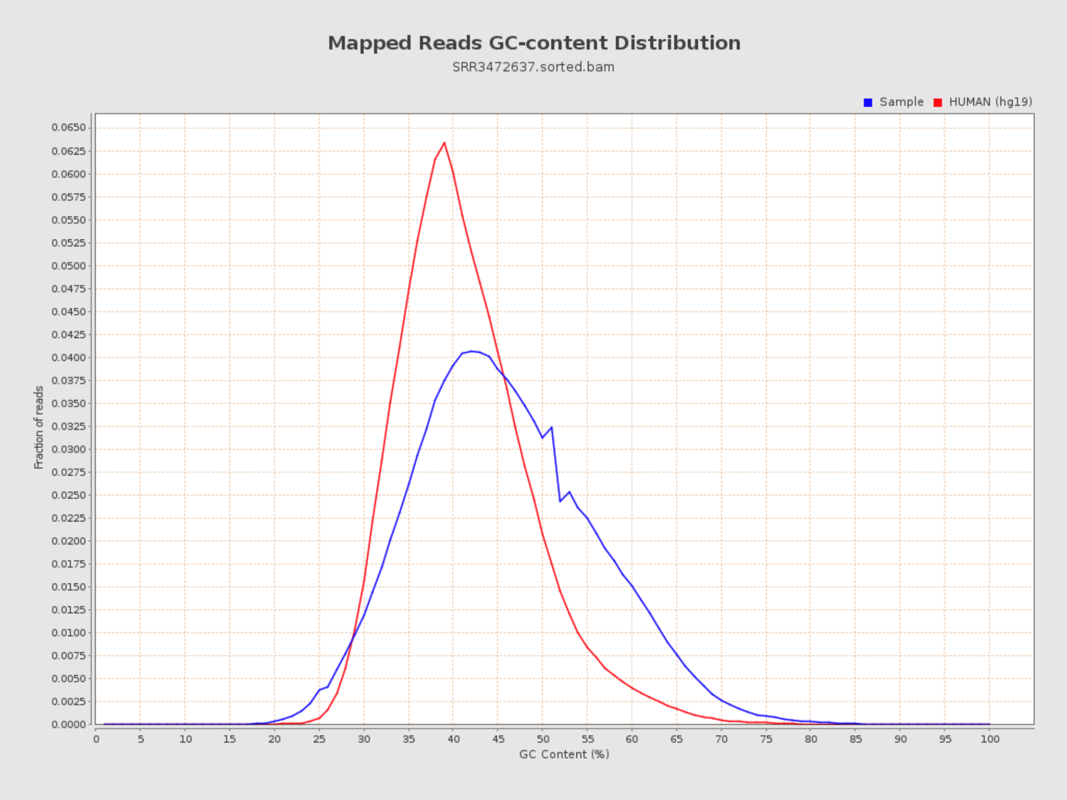
7. Results : Duplication Rate Histogram



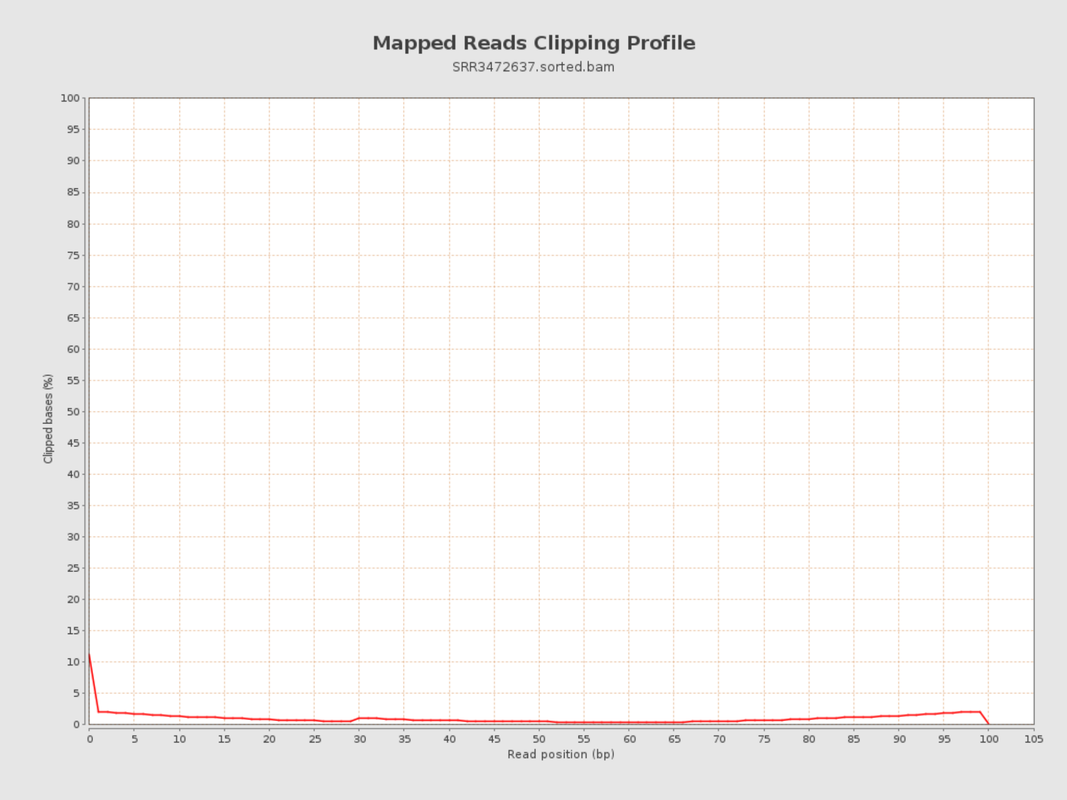
8. Results : Mapped Reads Nucleotide Content



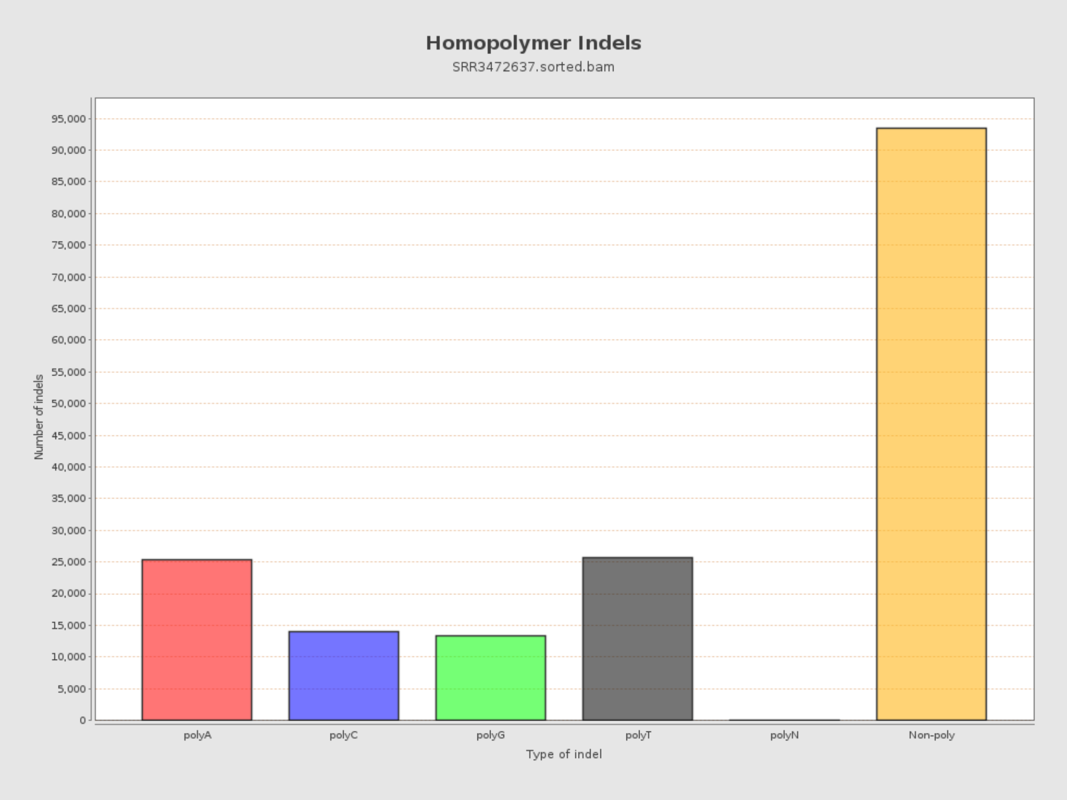
9. Results : Mapped Reads GC-content Distribution



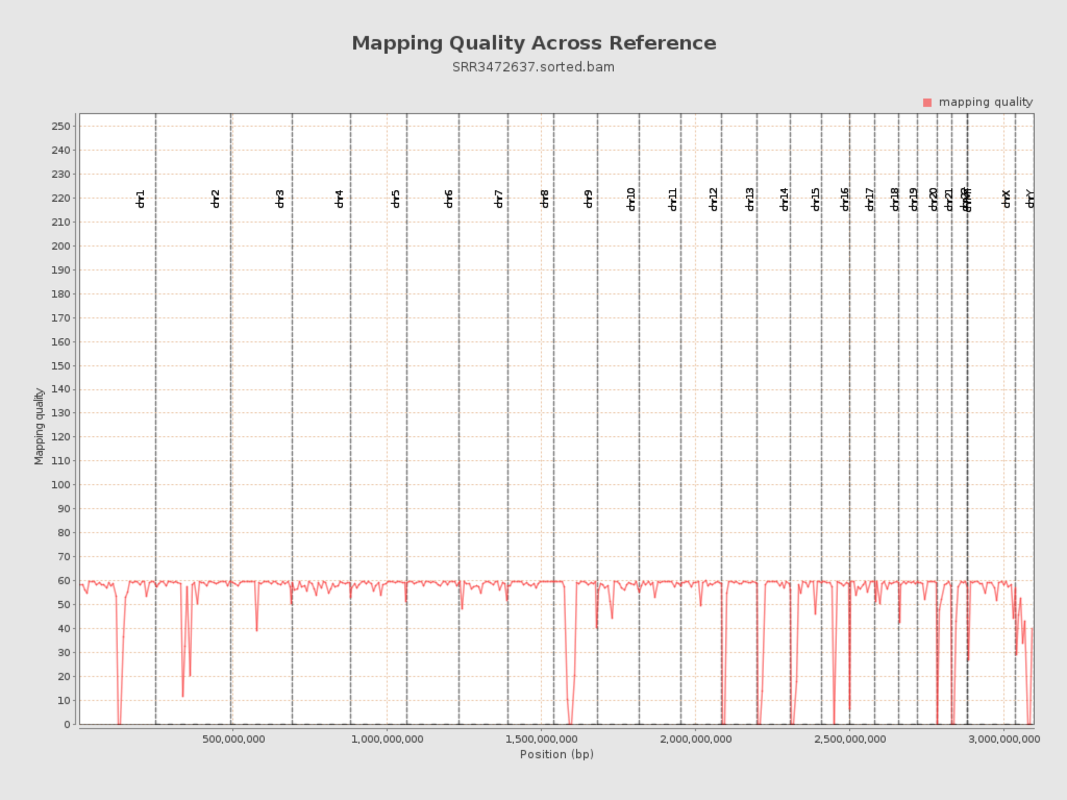
10. Results : Mapped Reads Clipping Profile



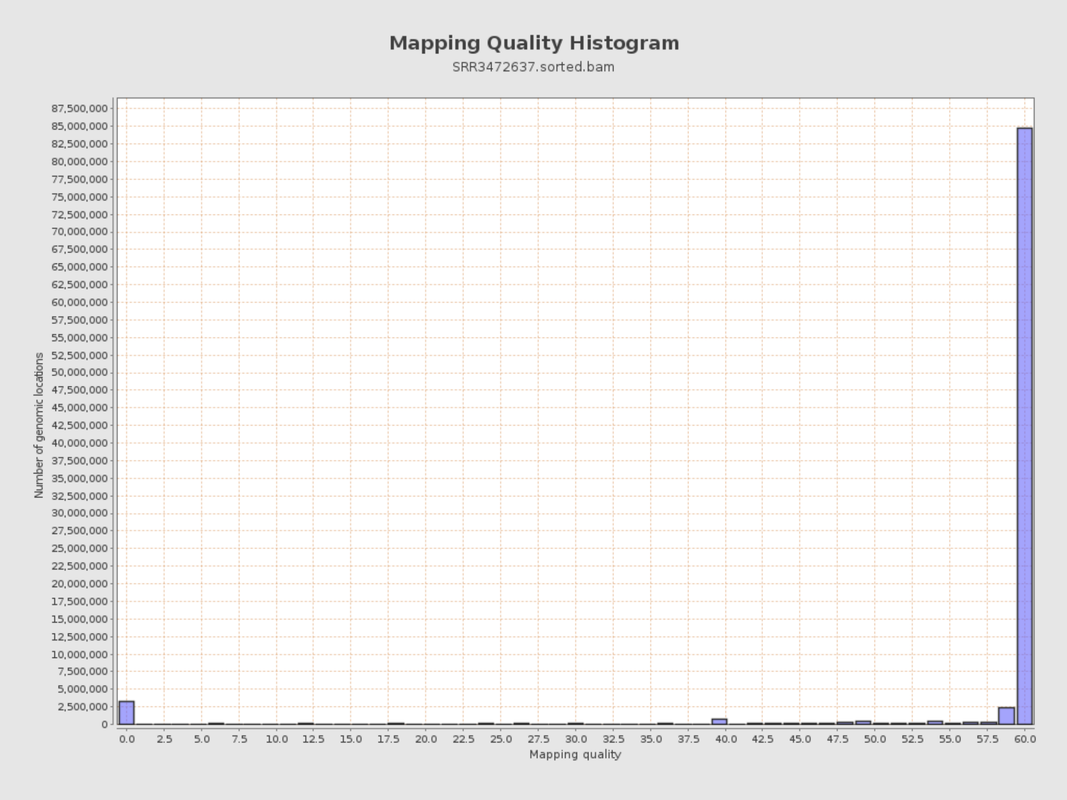
11. Results : Homopolymer Indels



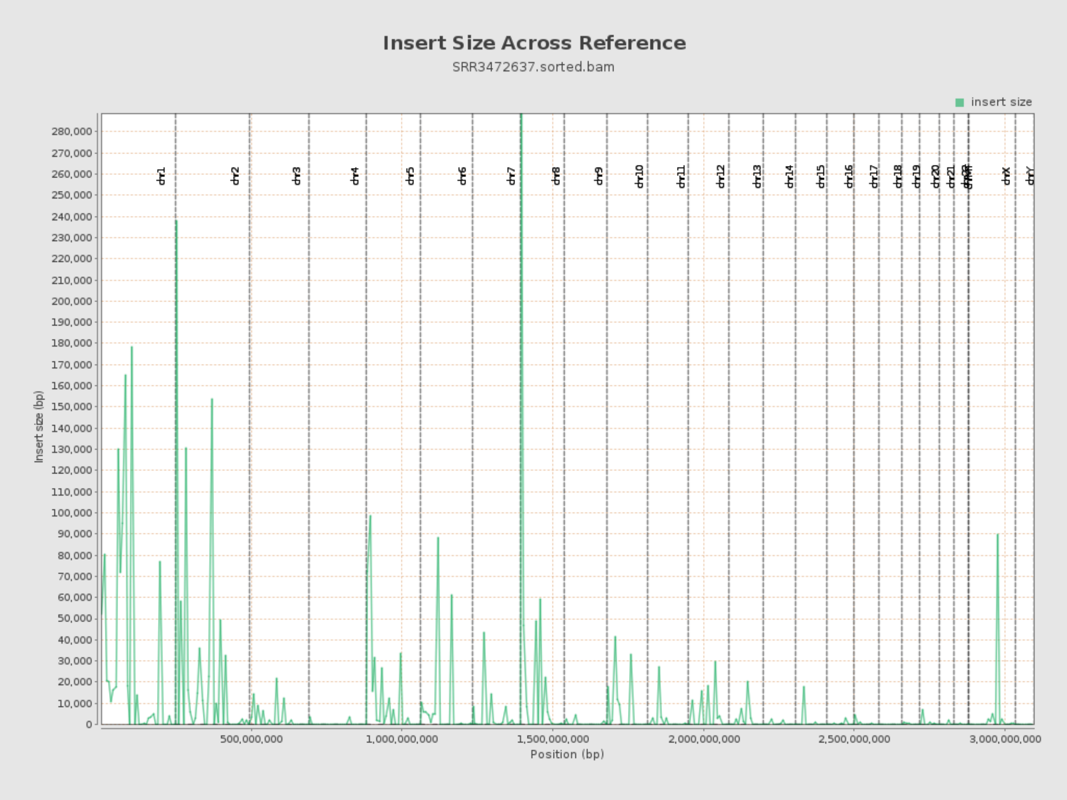
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram