Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 20:49:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472571.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_SRR3472571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472571_1.fastq.gz SRR3472571_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 20:49:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	379,444,244
Mapped reads	373,340,748 / 98.39%
Unmapped reads	6,103,496 / 1.61%
Mapped paired reads	373,340,748 / 98.39%
Mapped reads, first in pair	187,314,699 / 49.37%
Mapped reads, second in pair	186,026,049 / 49.03%
Mapped reads, both in pair	371,412,074 / 97.88%
Mapped reads, singletons	1,928,674 / 0.51%
Secondary alignments	0
Supplementary alignments	464,813 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	253,744,245 / 66.87%
Duplication rate	56.23%
Clipped reads	108,806,381 / 28.68%

2.2. ACGT Content

Number/percentage of A's	8,855,094,441 / 25.57%
Number/percentage of C's	8,488,161,056 / 24.51%
Number/percentage of T's	8,996,747,342 / 25.98%
Number/percentage of G's	8,286,770,050 / 23.93%
Number/percentage of N's	6,928,590 / 0.02%

GC Percentage	48.44%

2.3. Coverage

Mean	11.1898
Standard Deviation	118.5432

2.4. Mapping Quality

Mean Mapping Quality	51.81

2.5. Insert size

Mean	12,846.54
Standard Deviation	1,043,435.82
P25/Median/P75	96 / 140 / 210

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	329,730,002
Insertions	2,635,050
Mapped reads with at least one insertion	0.69%
Deletions	2,838,387
Mapped reads with at least one deletion	0.74%
Homopolymer indels	39.92%

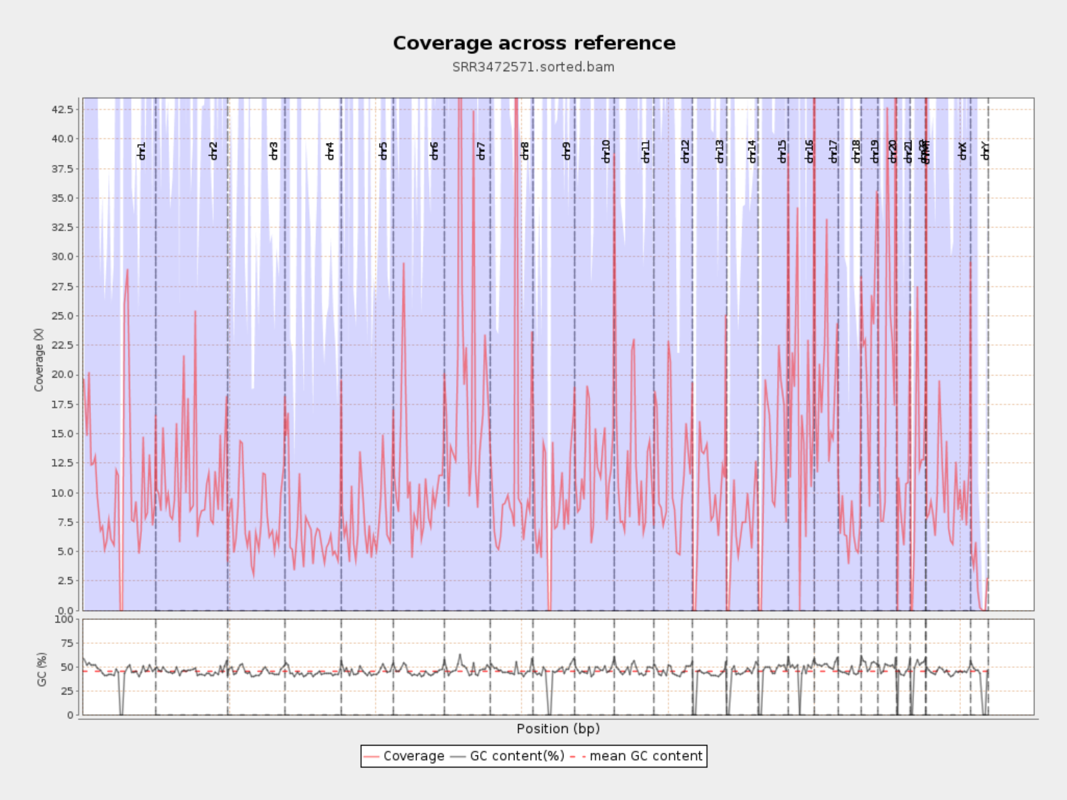
2.7. Chromosome stats

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

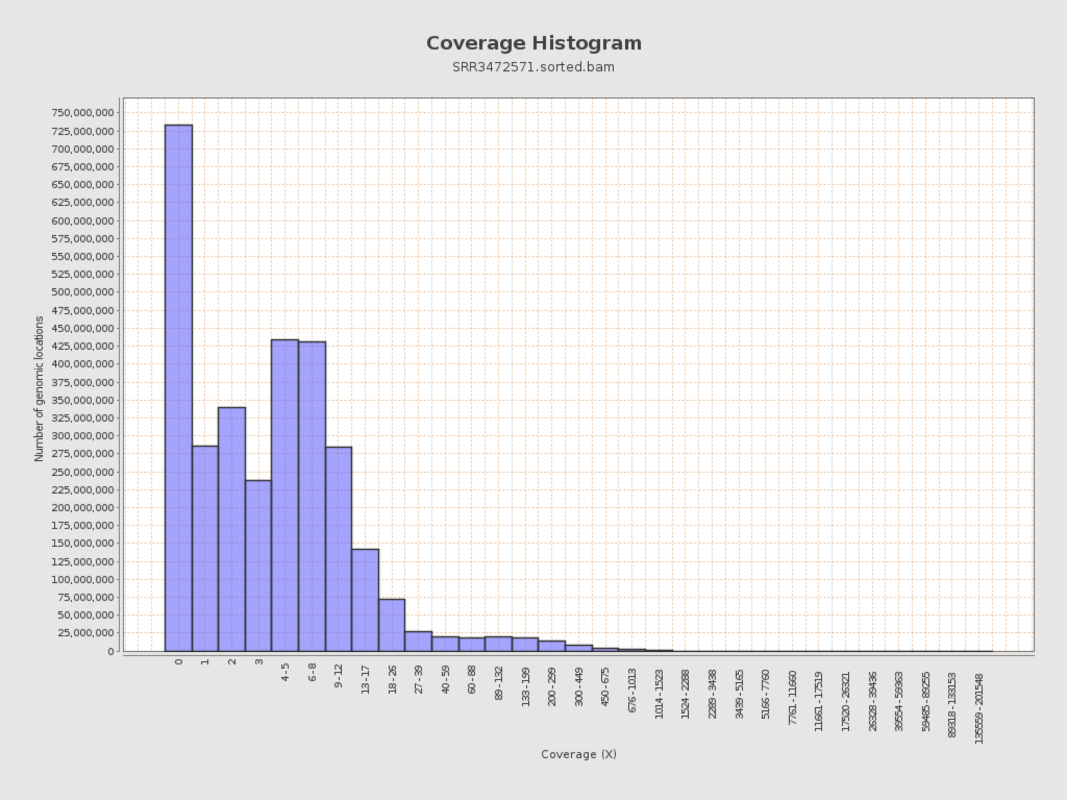
		bases	coverage	deviation
chr1	249250621	2651555171	10.6381	84.1742
chr2	243199373	2718648557	11.1787	84.016
chr3	198022430	1543359191	7.7939	38.1557
chr4	191154276	1286411411	6.7297	47.6609
chr5	180915260	1427415973	7.89	51.3079
chr6	171115067	1831055351	10.7007	47.47
chr7	159138663	3153678215	19.8172	416.2276
chr8	146364022	1750054492	11.9569	177.7338
chr9	141213431	1214967677	8.6038	47.2716
chr10	135534747	1592524731	11.7499	71.1575
chr11	135006516	1641702269	12.1602	51.2303
chr12	133851895	1614890610	12.0648	50.1176
chr13	115169878	1122985045	9.7507	41.5691
chr14	107349540	740838378	6.9012	31.0401
chr15	102531392	1306732923	12.7447	63.2462
chr16	90354753	1550309211	17.158	82.9328
chr17	81195210	1524126148	18.7711	103.5956
chr18	78077248	531510202	6.8075	52.4087
chr19	59128983	1382793327	23.386	90.0074
chr20	63025520	1278298588	20.2822	90.4557
chr21	48129895	487904682	10.1372	66.5934
chr22	51304566	586871224	11.439	57.9607
chrMT	16571	16441115	992.1619	236.8527
chrX	155270560	1550446046	9.9854	43.6652

chrY	59373566	134691801	2.2685	80.3976

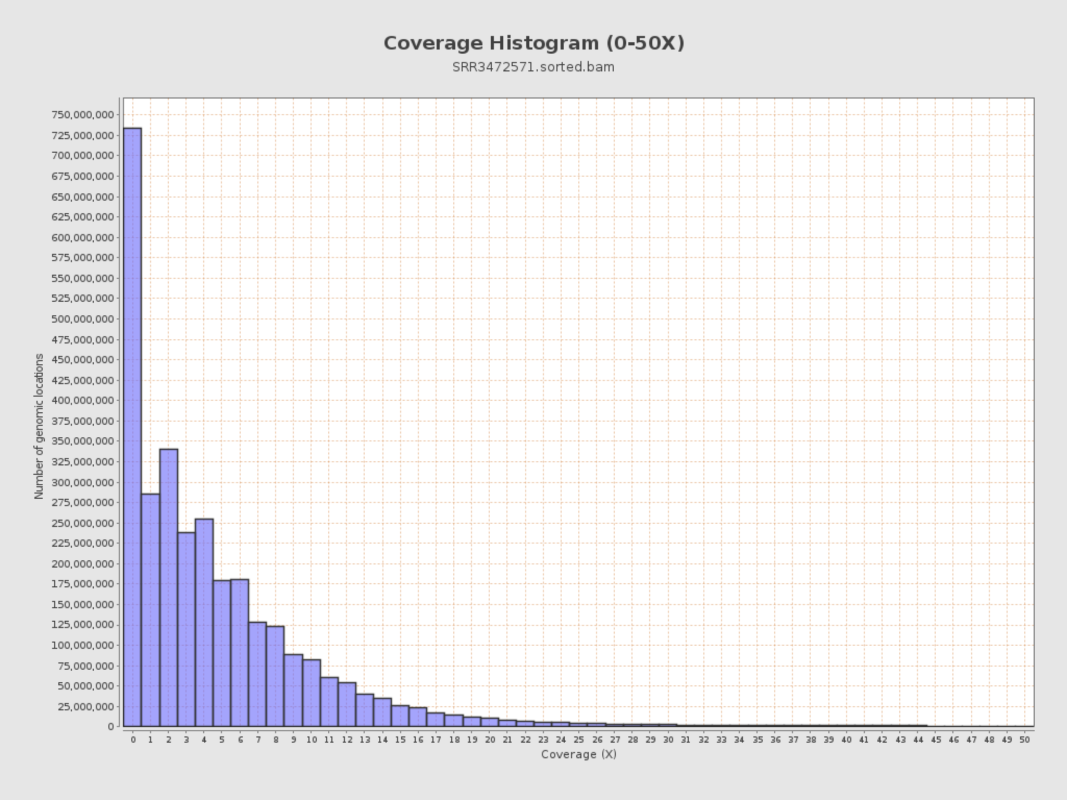
3. Results : Coverage across reference



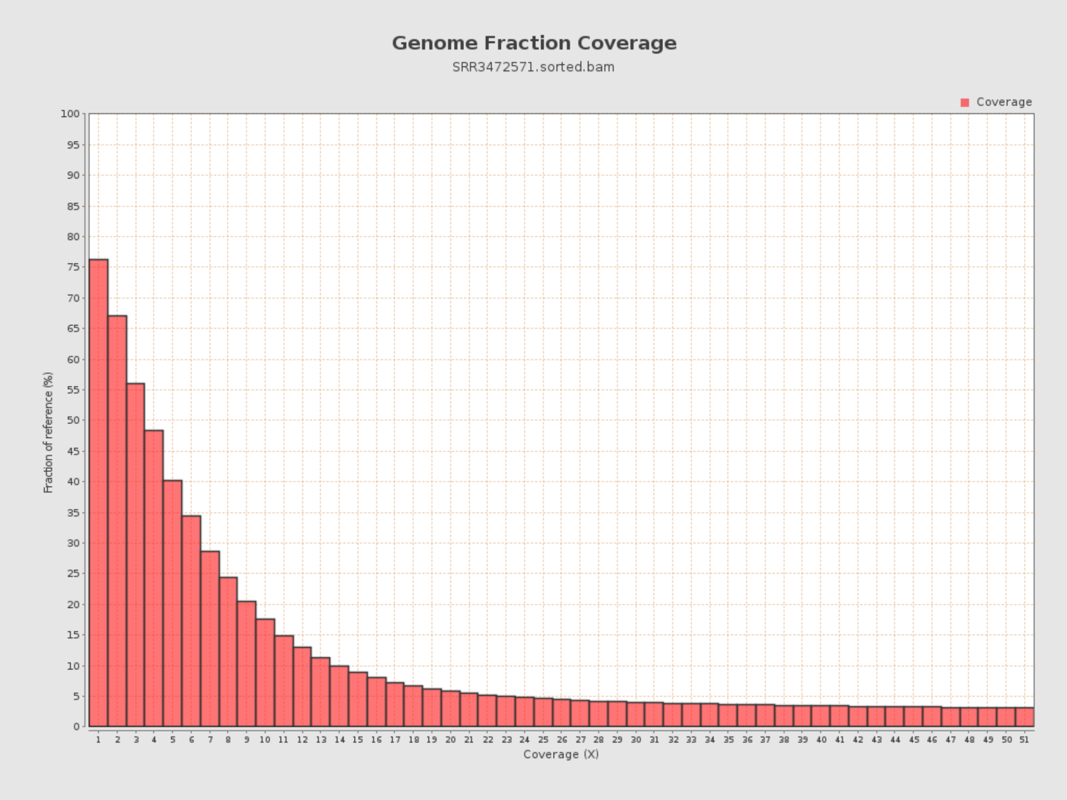
4. Results : Coverage Histogram



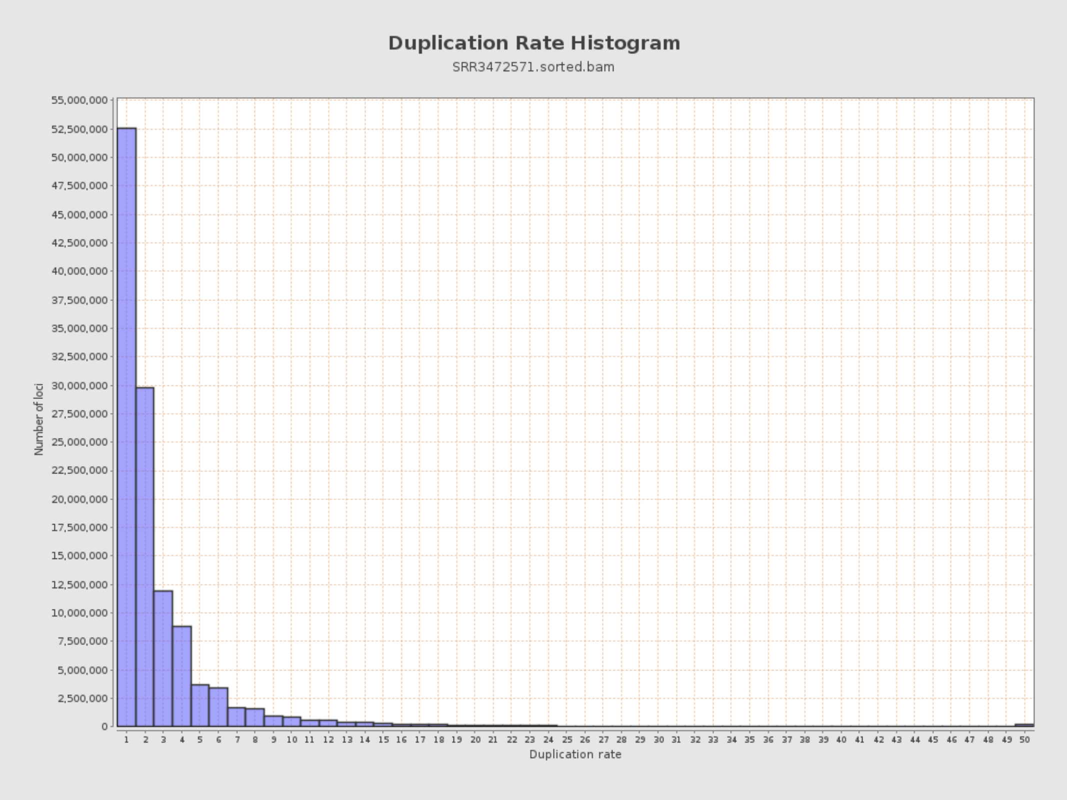
5. Results : Coverage Histogram (0-50X)



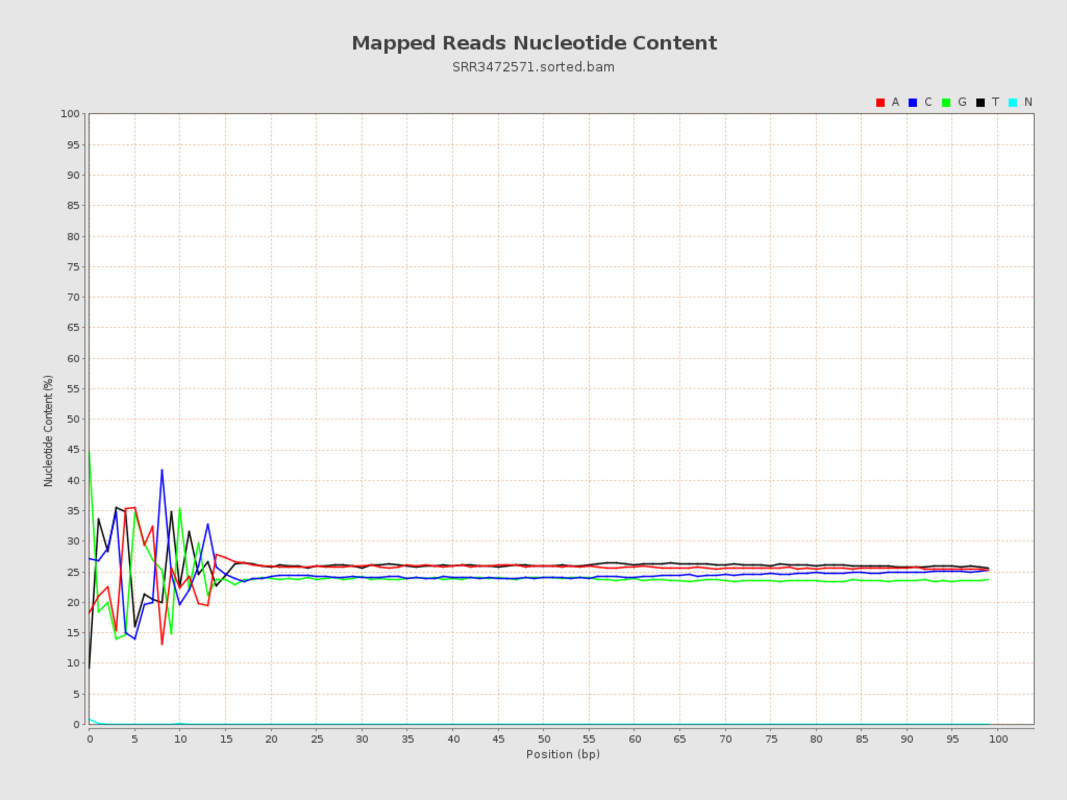
6. Results : Genome Fraction Coverage



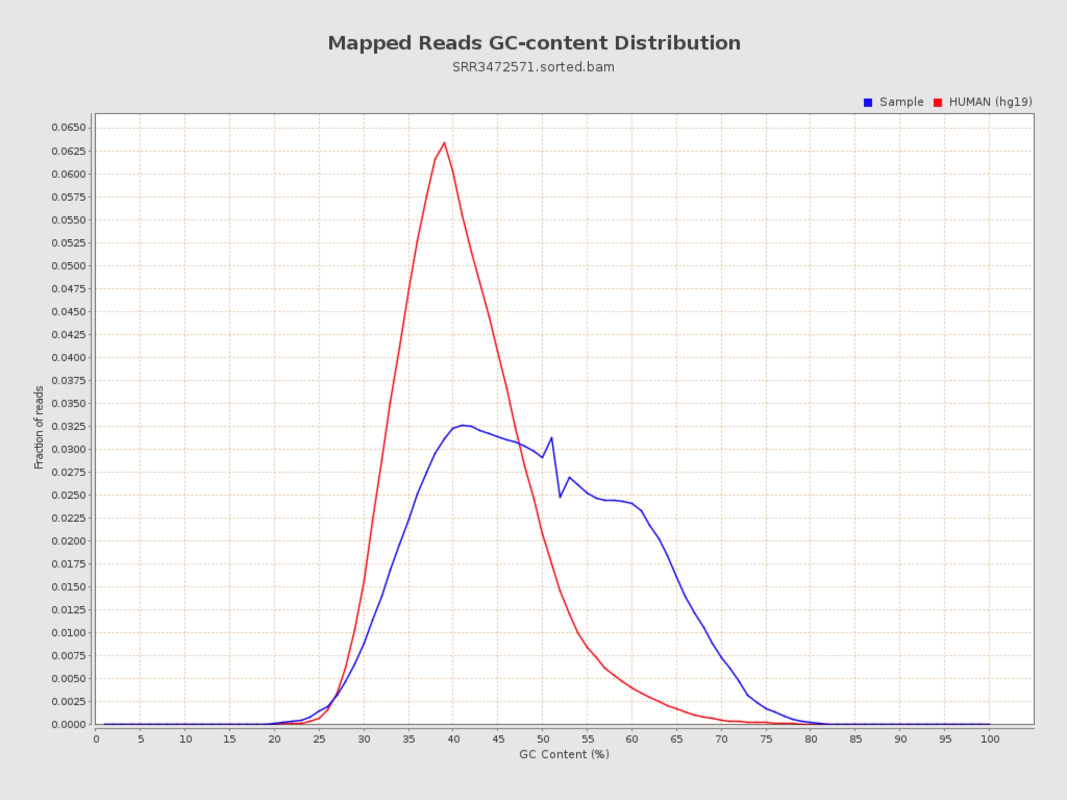
7. Results : Duplication Rate Histogram



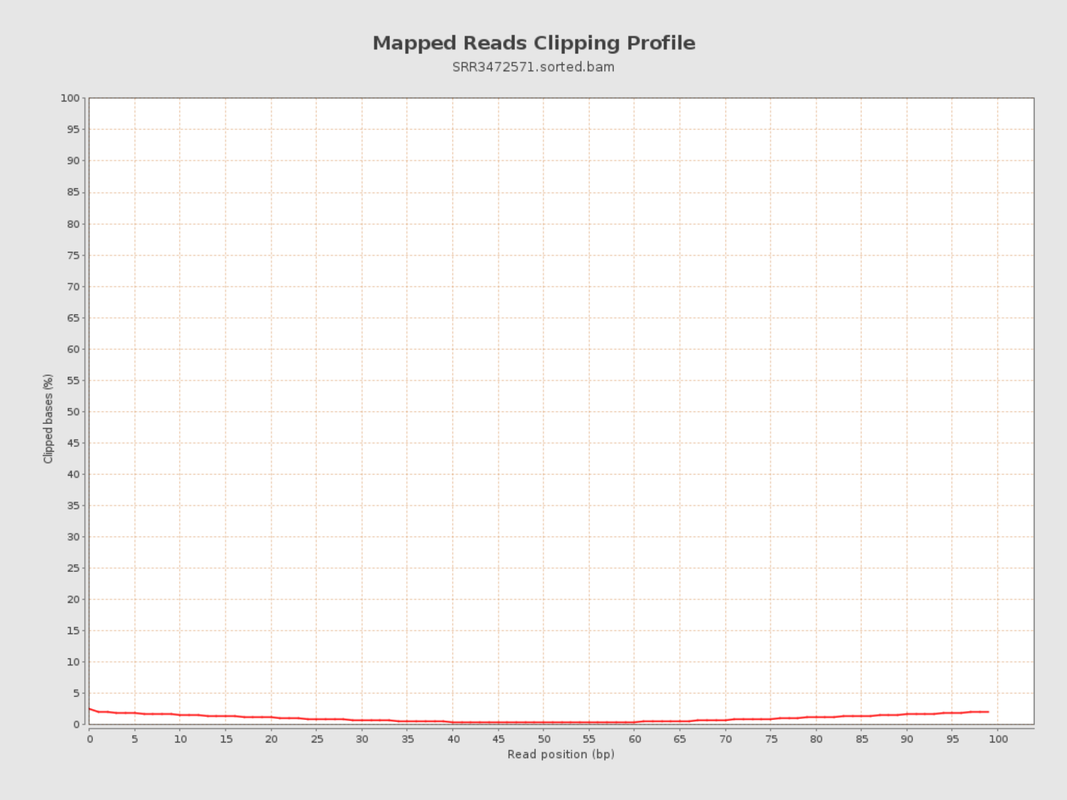
8. Results : Mapped Reads Nucleotide Content



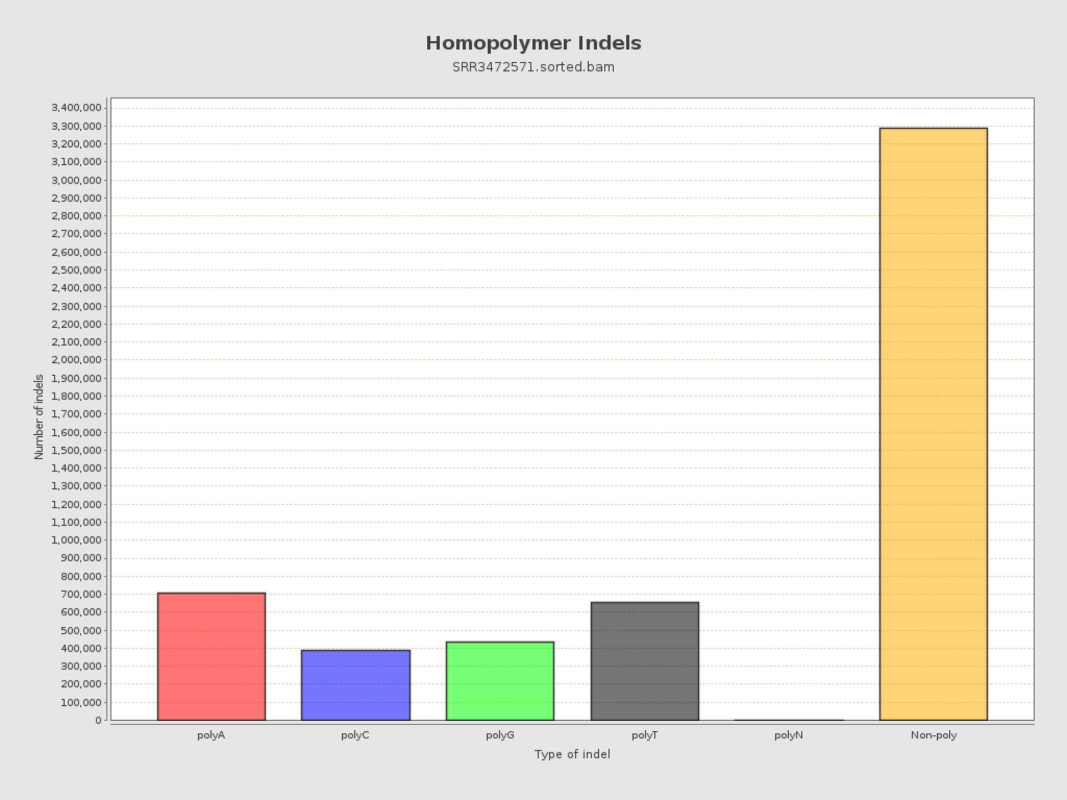
9. Results : Mapped Reads GC-content Distribution



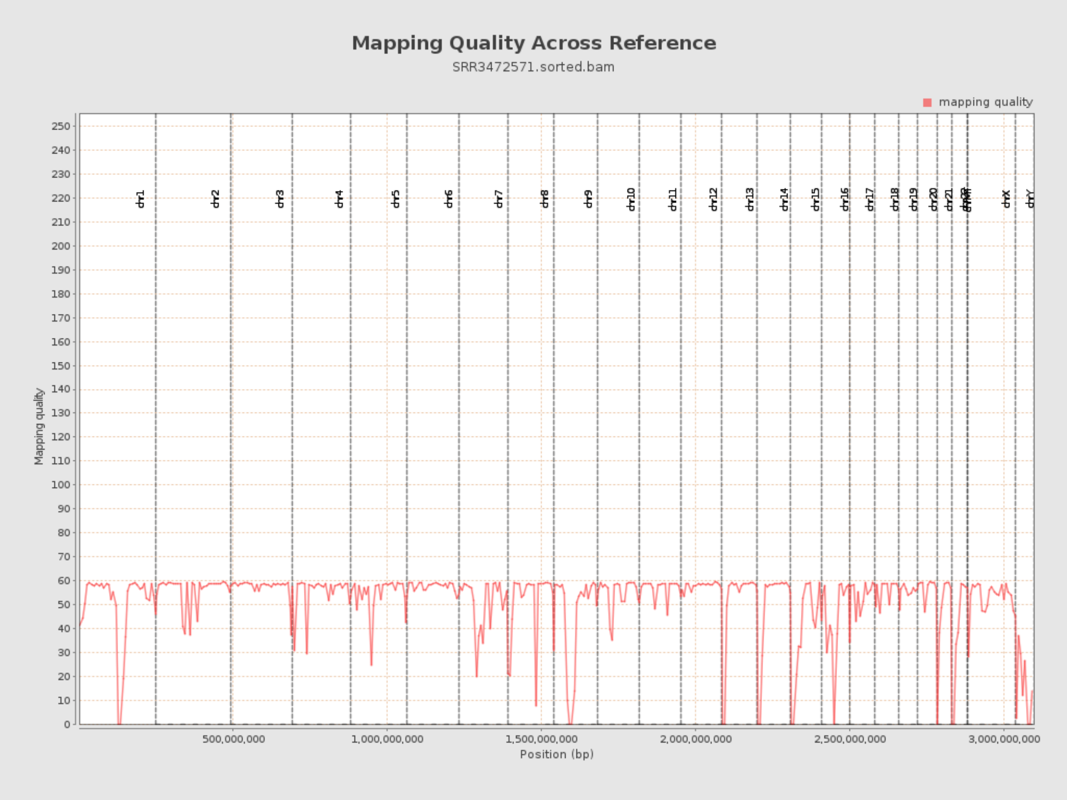
10. Results : Mapped Reads Clipping Profile



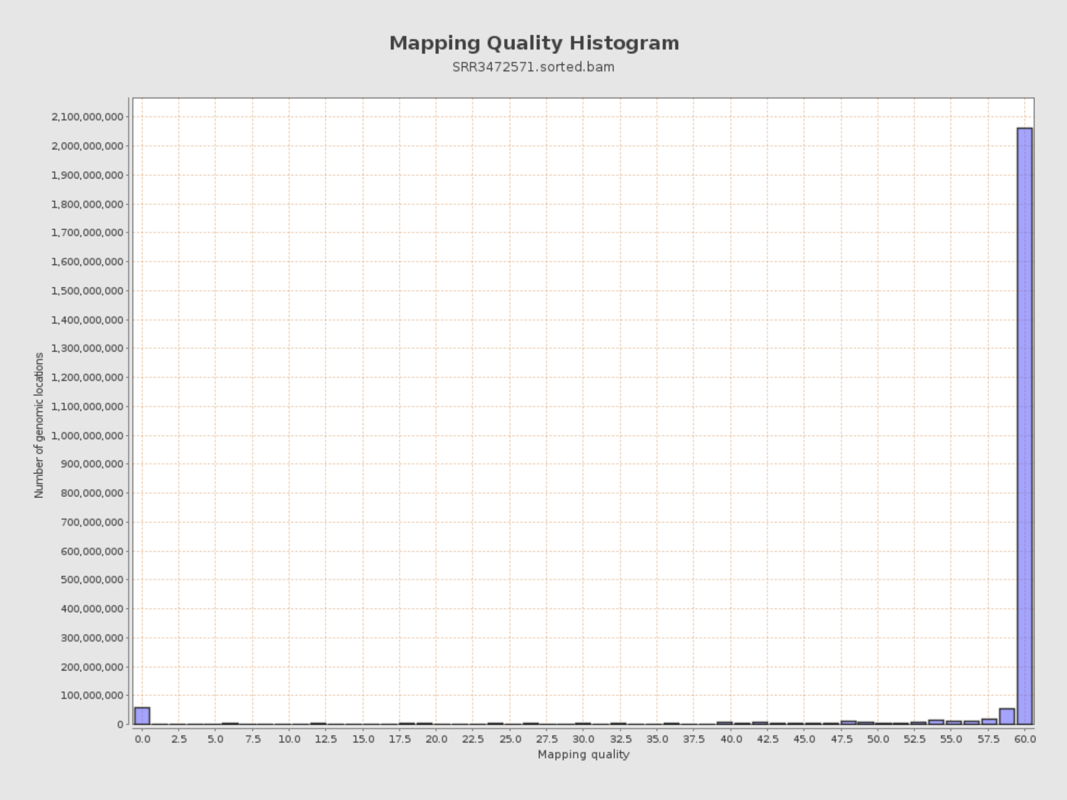
11. Results : Homopolymer Indels



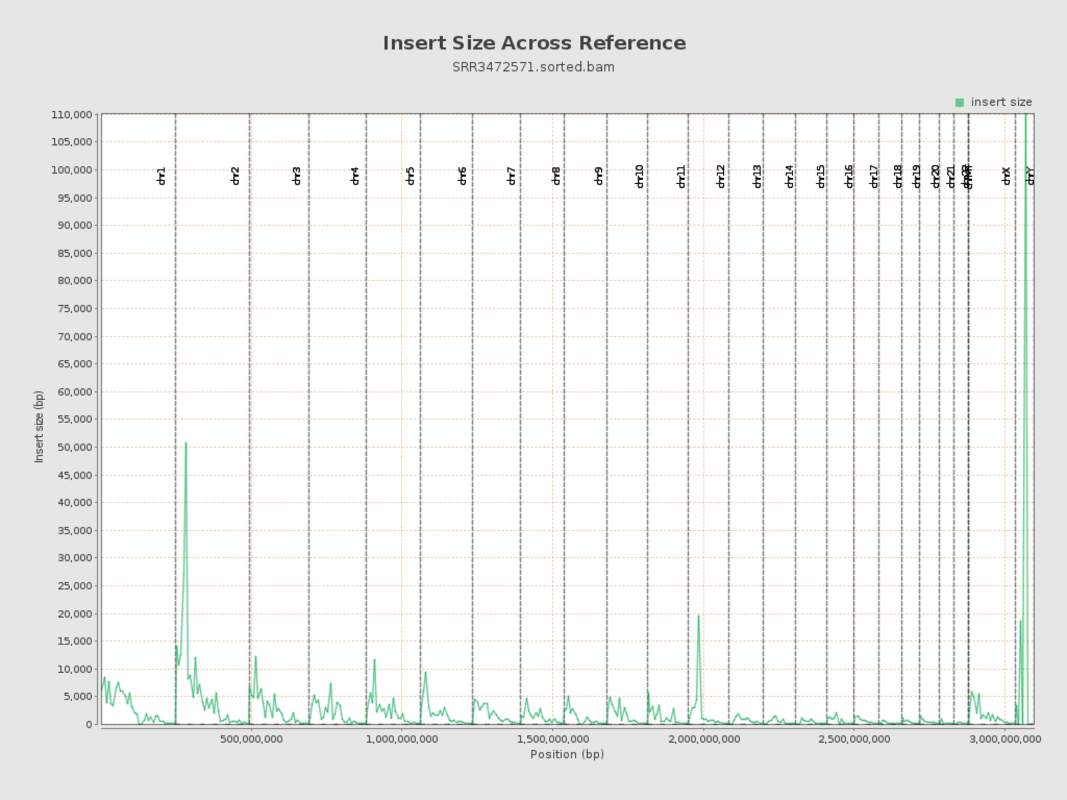
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram