Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 12:15:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472385.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_SRR3472385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472385_1.fastq.gz SRR3472385_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 12:14:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,879,184
Mapped reads	19,676,877 / 98.98%
Unmapped reads	202,307 / 1.02%
Mapped paired reads	19,676,877 / 98.98%
Mapped reads, first in pair	9,870,178 / 49.65%
Mapped reads, second in pair	9,806,699 / 49.33%
Mapped reads, both in pair	19,557,766 / 98.38%
Mapped reads, singletons	119,111 / 0.6%
Secondary alignments	0
Supplementary alignments	72,003 / 0.36%
Read min/max/mean length	30 / 100 / 99.29
Duplicated reads (estimated)	12,641,914 / 63.59%
Duplication rate	48.19%
Clipped reads	1,434,497 / 7.22%

2.2. ACGT Content

Number/percentage of A's	517,984,543 / 26.89%
Number/percentage of C's	447,122,107 / 23.21%
Number/percentage of T's	518,743,537 / 26.93%
Number/percentage of G's	442,330,915 / 22.96%
Number/percentage of N's	237,775 / 0.01%

GC Percentage	46.17%

2.3. Coverage

Mean	0.6224
Standard Deviation	19.5399

2.4. Mapping Quality

Mean Mapping Quality	54.97

2.5. Insert size

Mean	17,570.41
Standard Deviation	1,317,246.4
P25/Median/P75	153 / 216 / 292

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,817,044
Insertions	107,076
Mapped reads with at least one insertion	0.54%
Deletions	89,266
Mapped reads with at least one deletion	0.44%
Homopolymer indels	45.75%

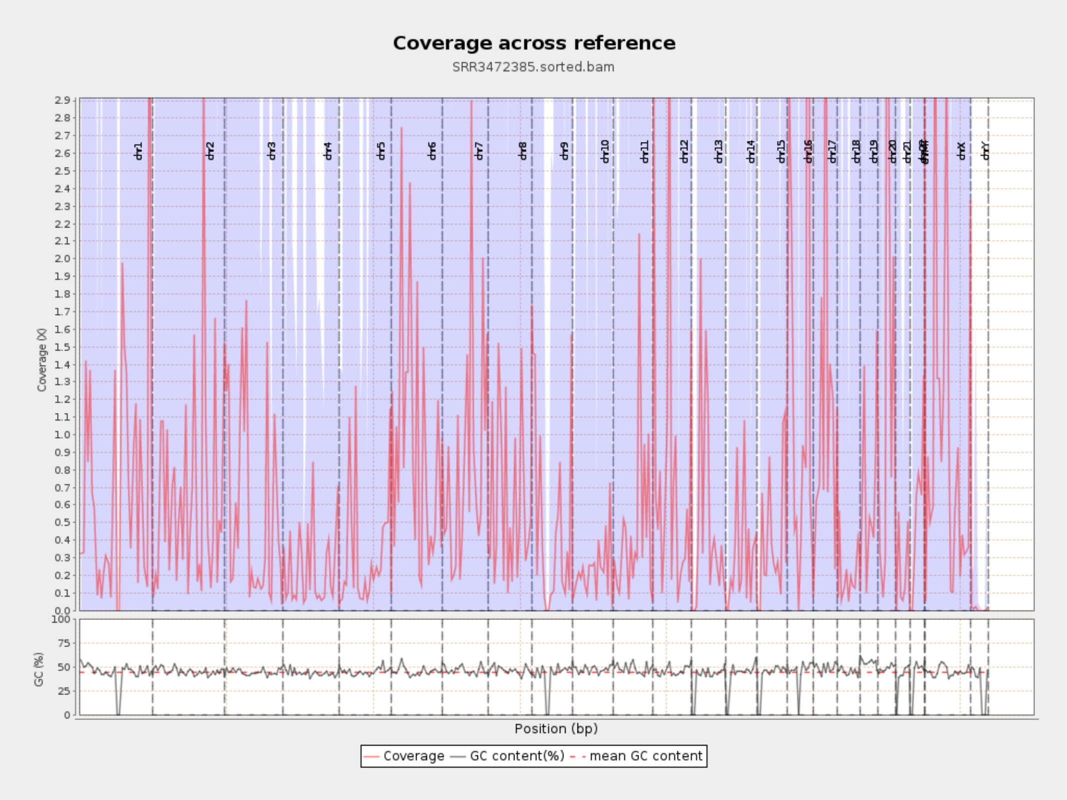
2.7. Chromosome stats

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

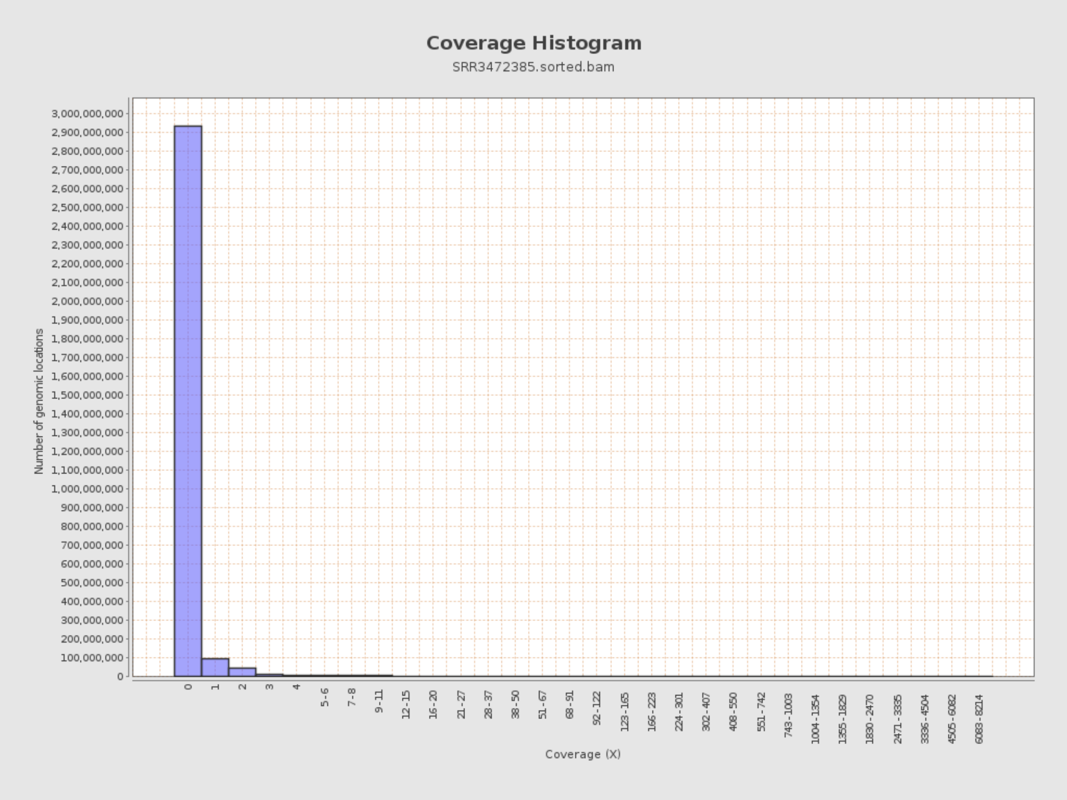
		bases	coverage	deviation
chr1	249250621	188419520	0.7559	24.6216
chr2	243199373	159356511	0.6553	19.4
chr3	198022430	120124161	0.6066	15.1528
chr4	191154276	45375813	0.2374	8.0229
chr5	180915260	60337942	0.3335	11.799
chr6	171115067	158917873	0.9287	22.7219
chr7	159138663	137248075	0.8624	22.7738
chr8	146364022	90938089	0.6213	19.7948
chr9	141213431	70337055	0.4981	13.8135
chr10	135534747	31839298	0.2349	7.1674
chr11	135006516	62502626	0.463	17.5001
chr12	133851895	108391725	0.8098	20.9725
chr13	115169878	58294188	0.5062	15.4424
chr14	107349540	33412039	0.3112	8.9973
chr15	102531392	42437619	0.4139	10.4384
chr16	90354753	129180191	1.4297	41.6151
chr17	81195210	98869057	1.2177	33.2599
chr18	78077248	16919329	0.2167	5.7999
chr19	59128983	38186298	0.6458	13.0944
chr20	63025520	87132117	1.3825	36.6765
chr21	48129895	10767800	0.2237	9.5378
chr22	51304566	28771003	0.5608	18.7942
chrMT	16571	53154	3.2077	2.3419
chrX	155270560	148342062	0.9554	22.6999

chrY	59373566	501739	0.0085	0.6806

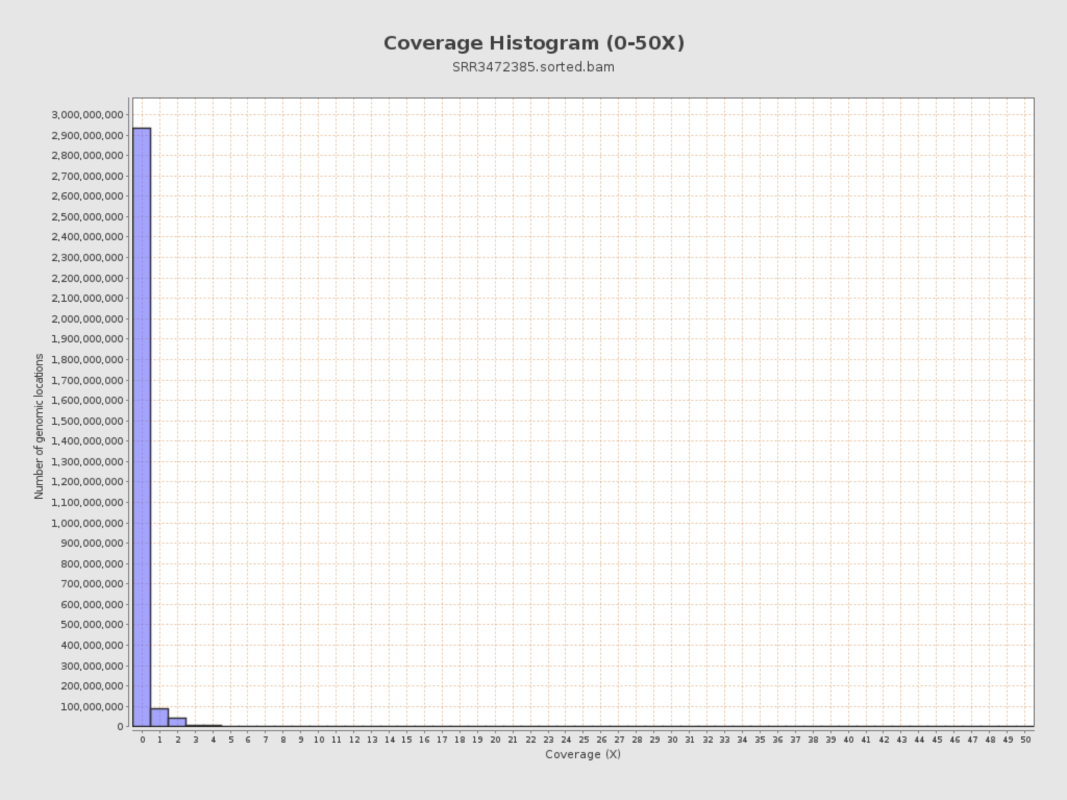
3. Results : Coverage across reference



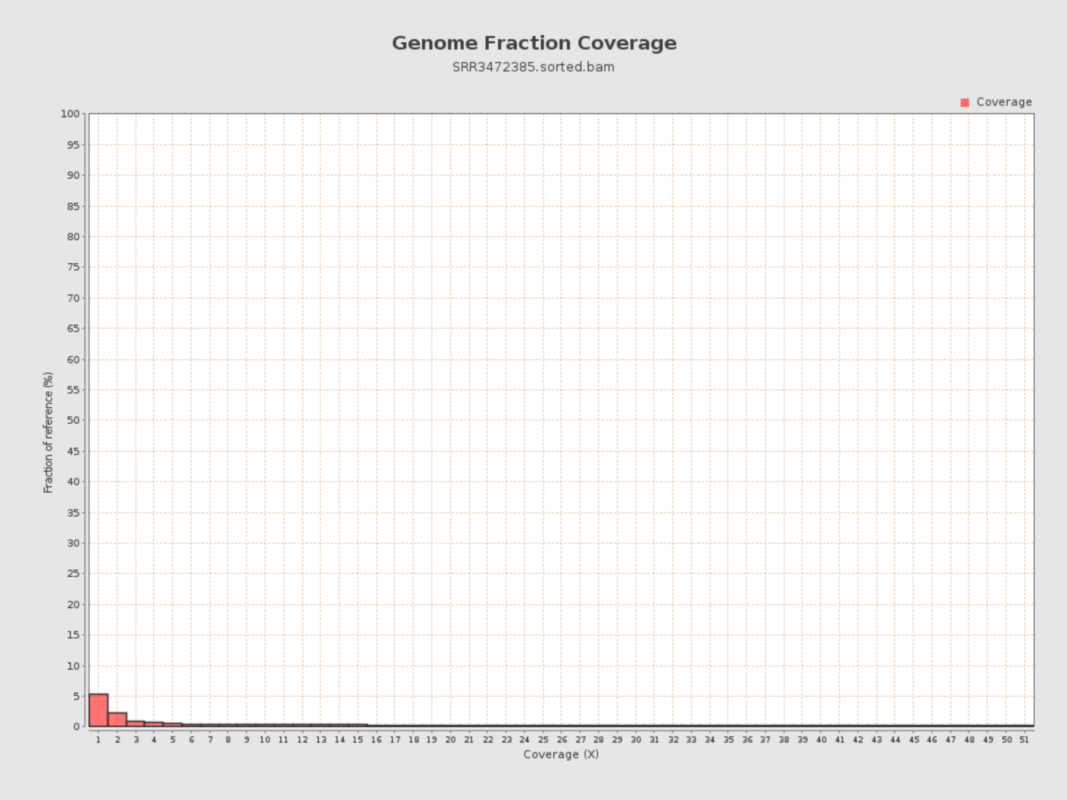
4. Results : Coverage Histogram



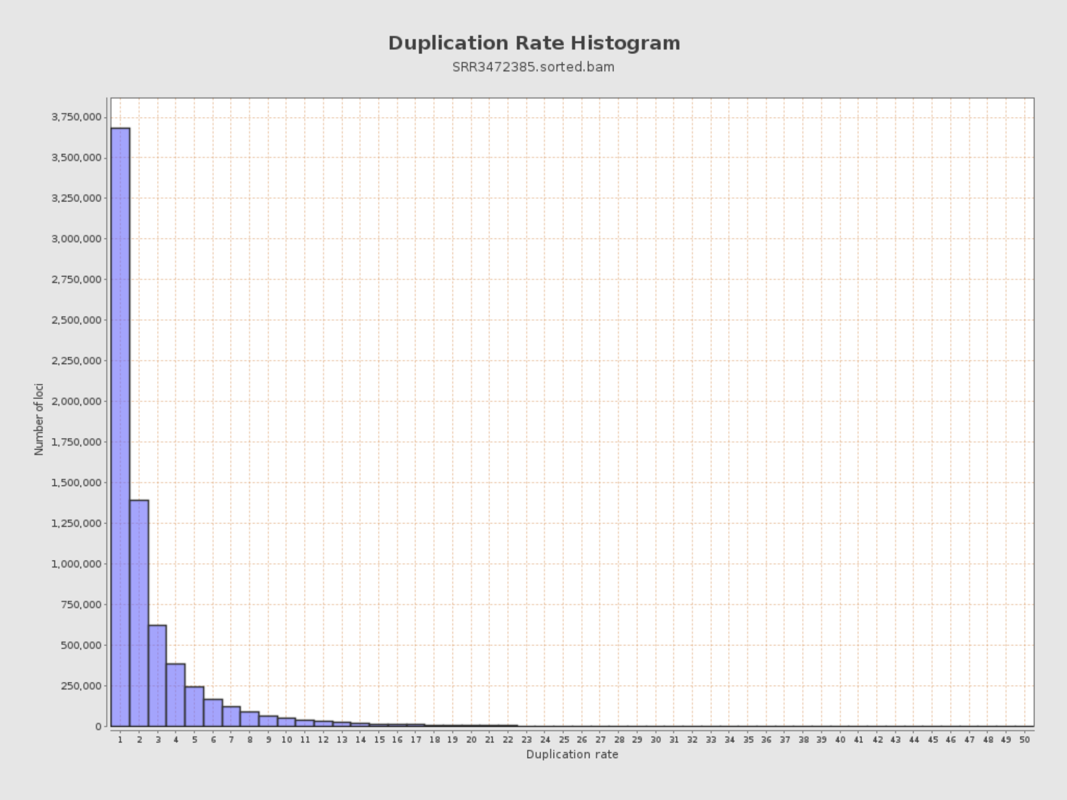
5. Results : Coverage Histogram (0-50X)



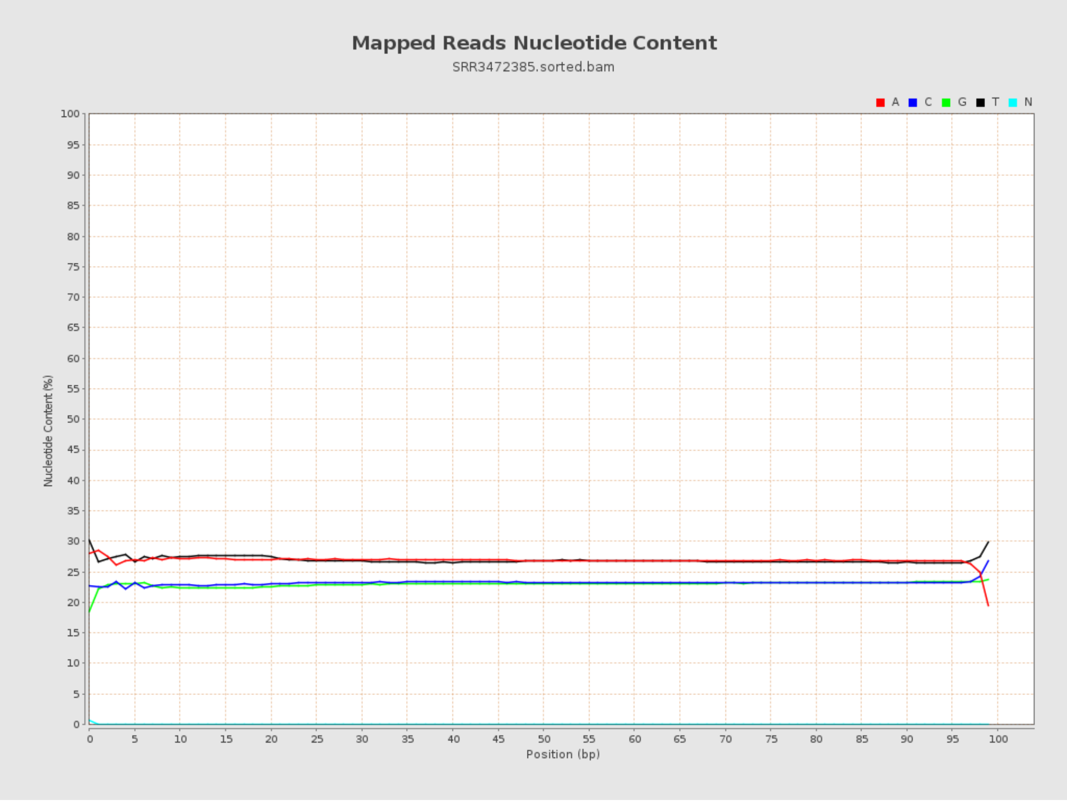
6. Results : Genome Fraction Coverage



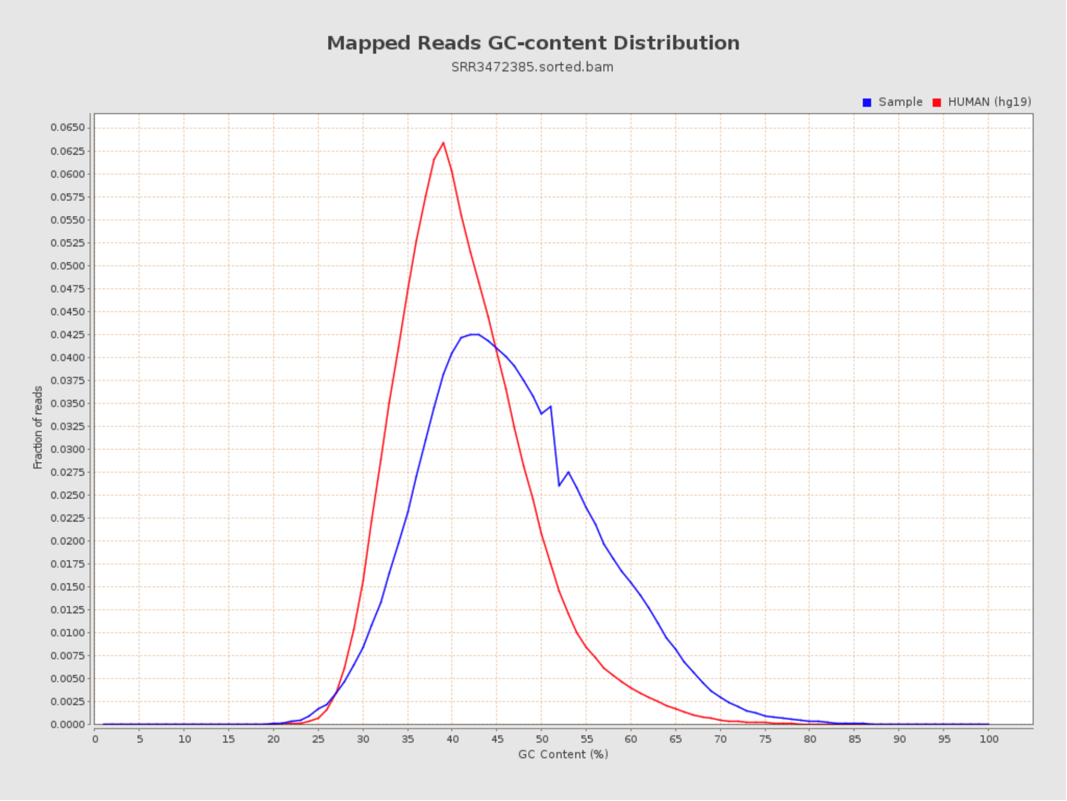
7. Results : Duplication Rate Histogram



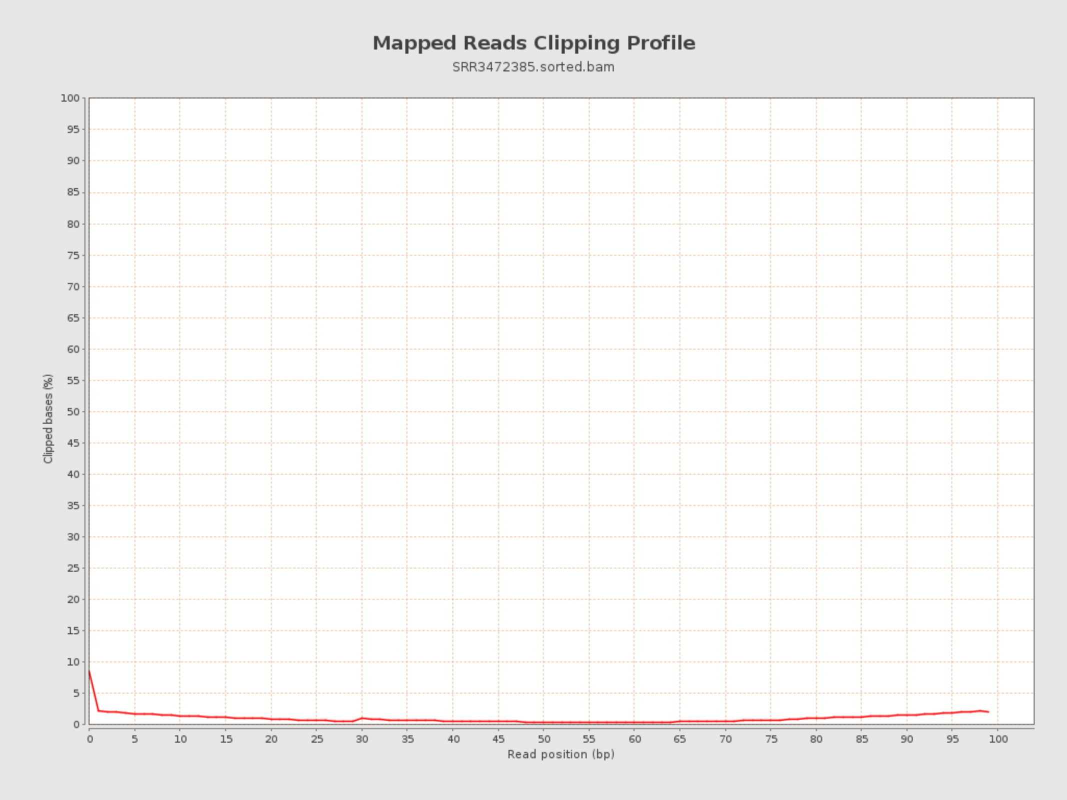
8. Results : Mapped Reads Nucleotide Content



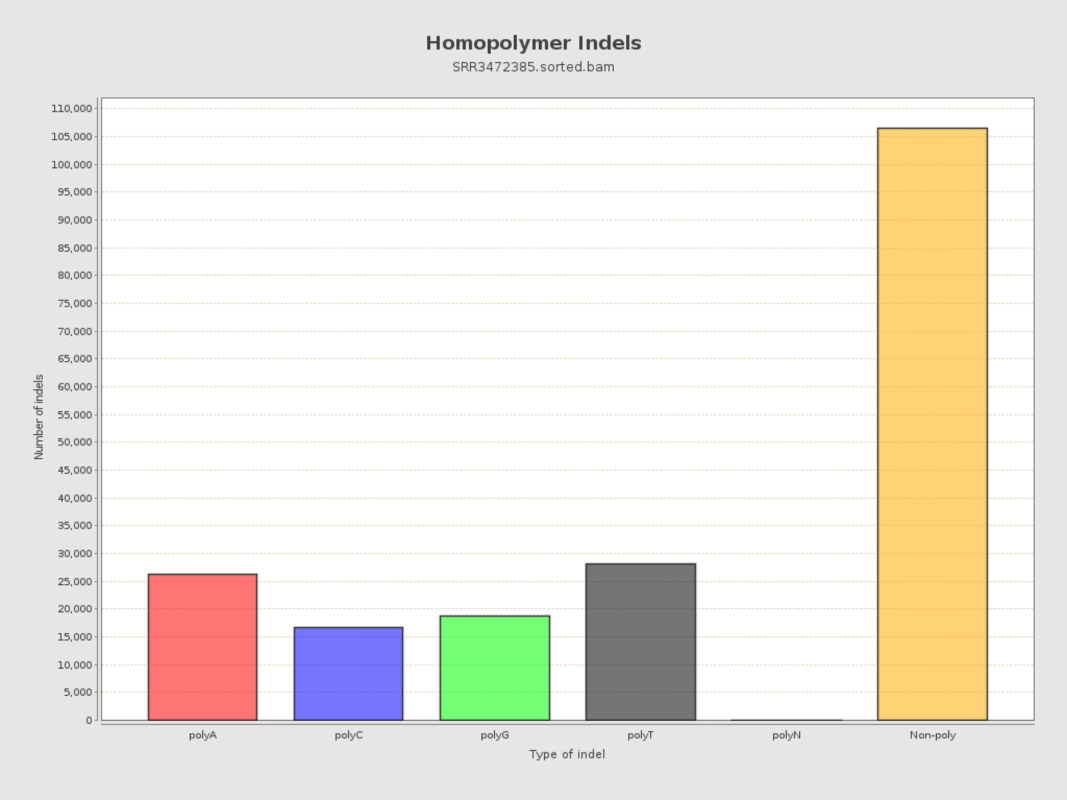
9. Results : Mapped Reads GC-content Distribution



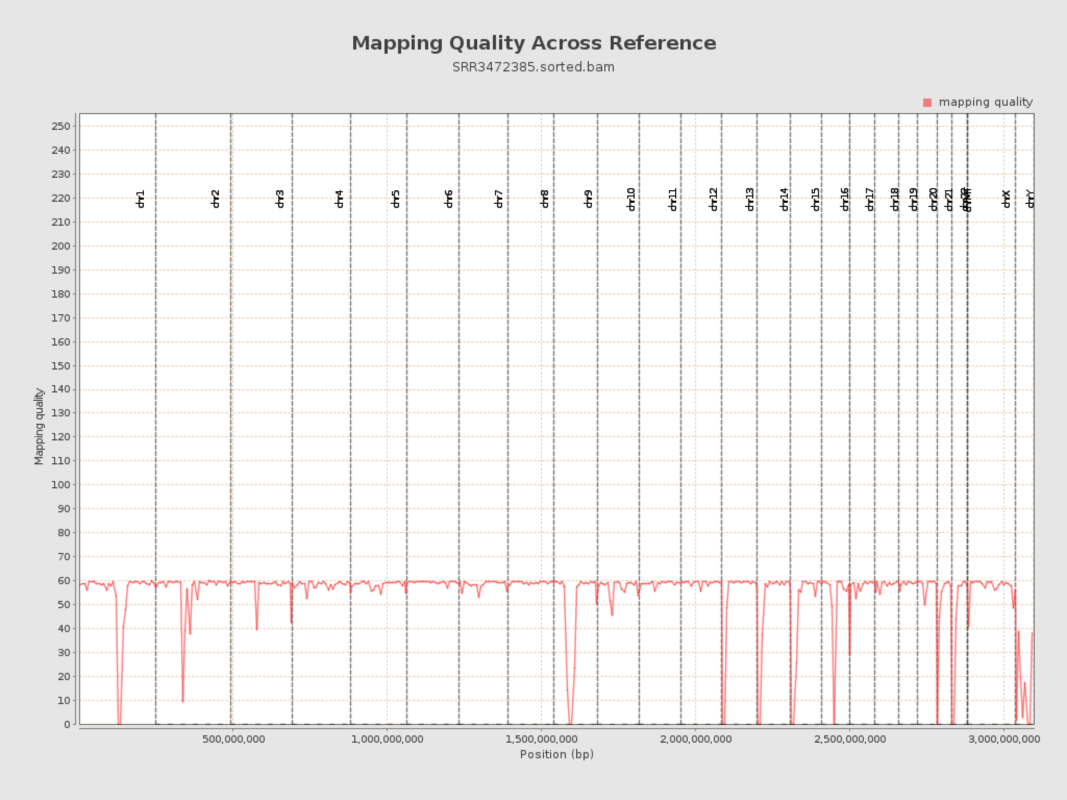
10. Results : Mapped Reads Clipping Profile



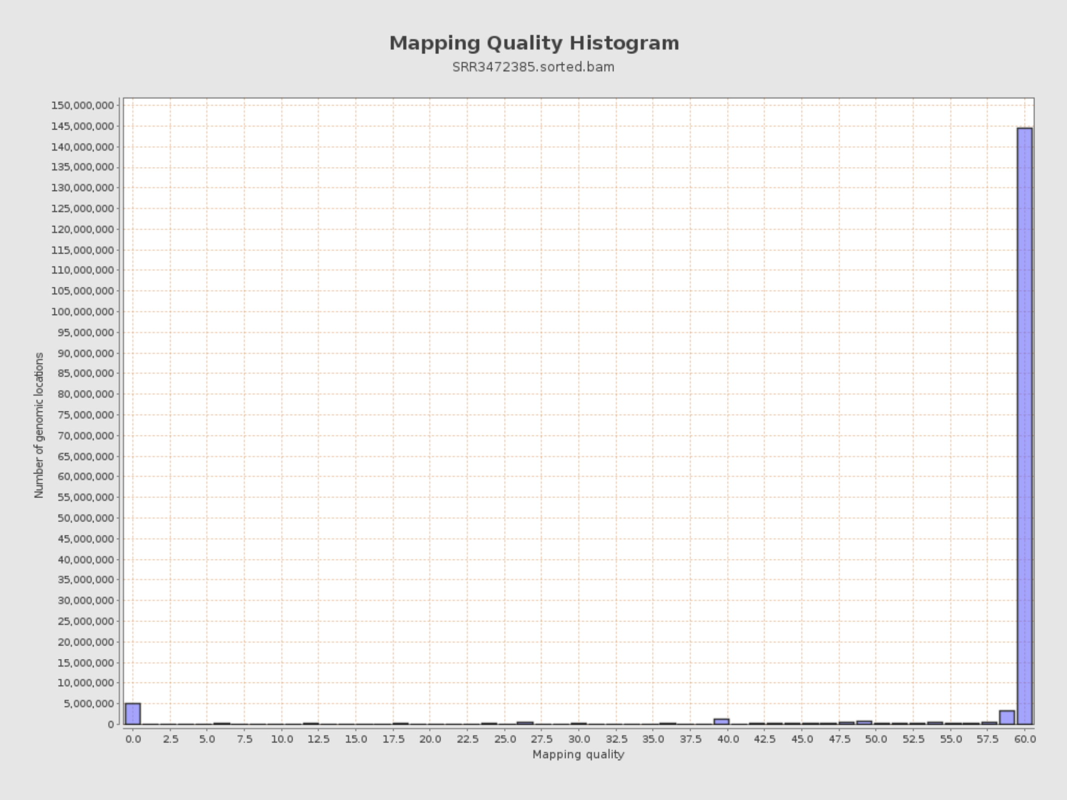
11. Results : Homopolymer Indels



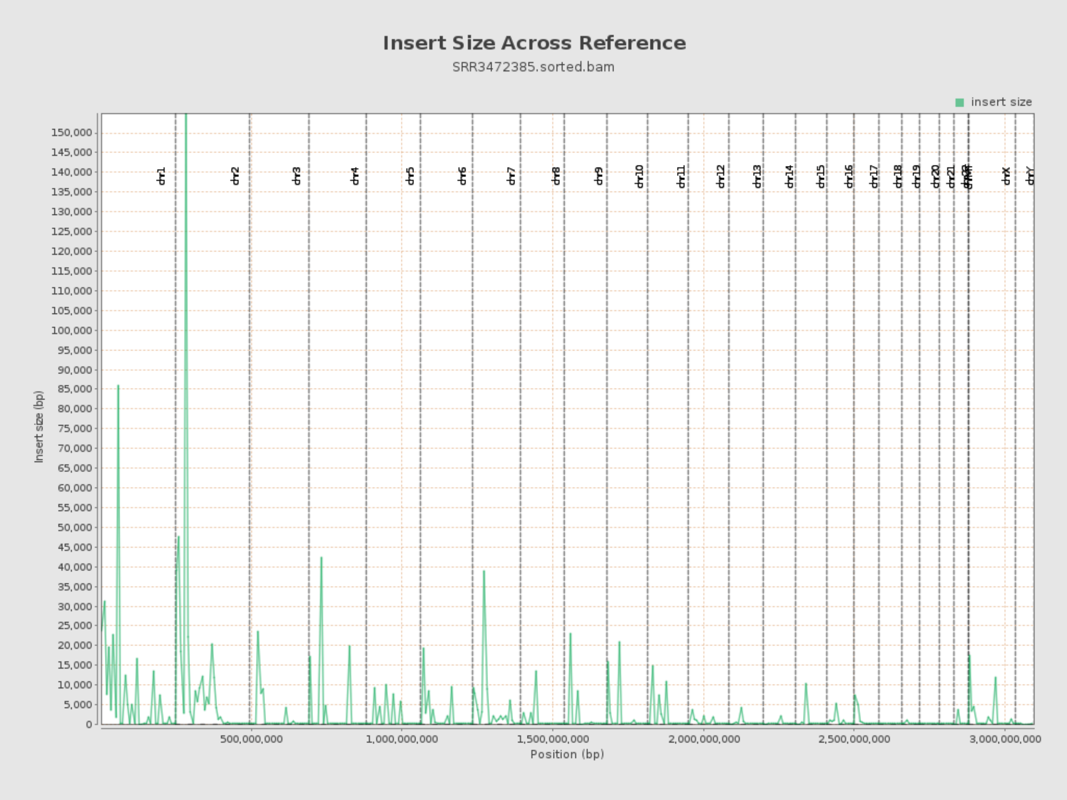
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram