Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 08:24:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472606.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_SRR3472606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472606_1.fastq.gz SRR3472606_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 08:24:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,087,434
Mapped reads	14,971,719 / 99.23%
Unmapped reads	115,715 / 0.77%
Mapped paired reads	14,971,719 / 99.23%
Mapped reads, first in pair	7,504,824 / 49.74%
Mapped reads, second in pair	7,466,895 / 49.49%
Mapped reads, both in pair	14,892,496 / 98.71%
Mapped reads, singletons	79,223 / 0.53%
Secondary alignments	0
Supplementary alignments	73,927 / 0.49%
Read min/max/mean length	30 / 101 / 99.68
Duplicated reads (estimated)	10,121,501 / 67.09%
Duplication rate	49.52%
Clipped reads	1,053,584 / 6.98%

2.2. ACGT Content

Number/percentage of A's	400,470,653 / 27.2%
Number/percentage of C's	337,396,020 / 22.92%
Number/percentage of T's	401,496,710 / 27.27%
Number/percentage of G's	332,626,876 / 22.59%
Number/percentage of N's	274,516 / 0.02%

GC Percentage	45.51%

2.3. Coverage

Mean	0.4757
Standard Deviation	19.6979

2.4. Mapping Quality

Mean Mapping Quality	54.72

2.5. Insert size

Mean	20,988.24
Standard Deviation	1,446,000.31
P25/Median/P75	149 / 206 / 279

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	8,795,838
Insertions	90,277
Mapped reads with at least one insertion	0.59%
Deletions	80,062
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.27%

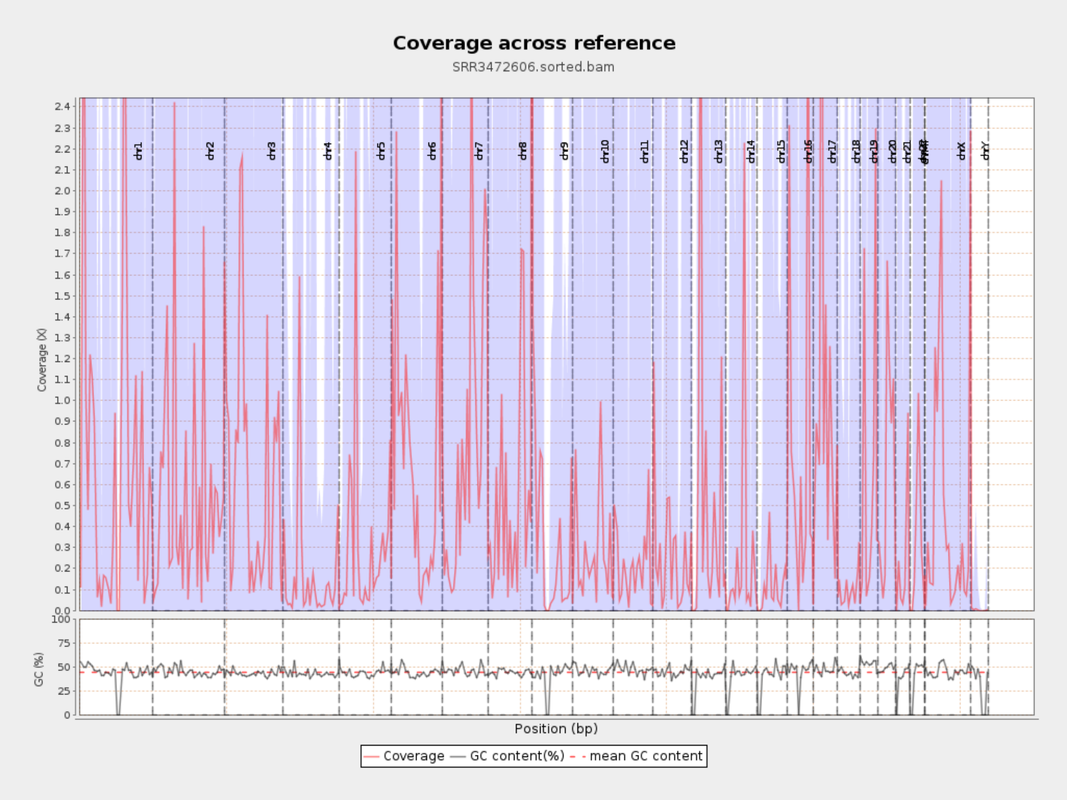
2.7. Chromosome stats

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

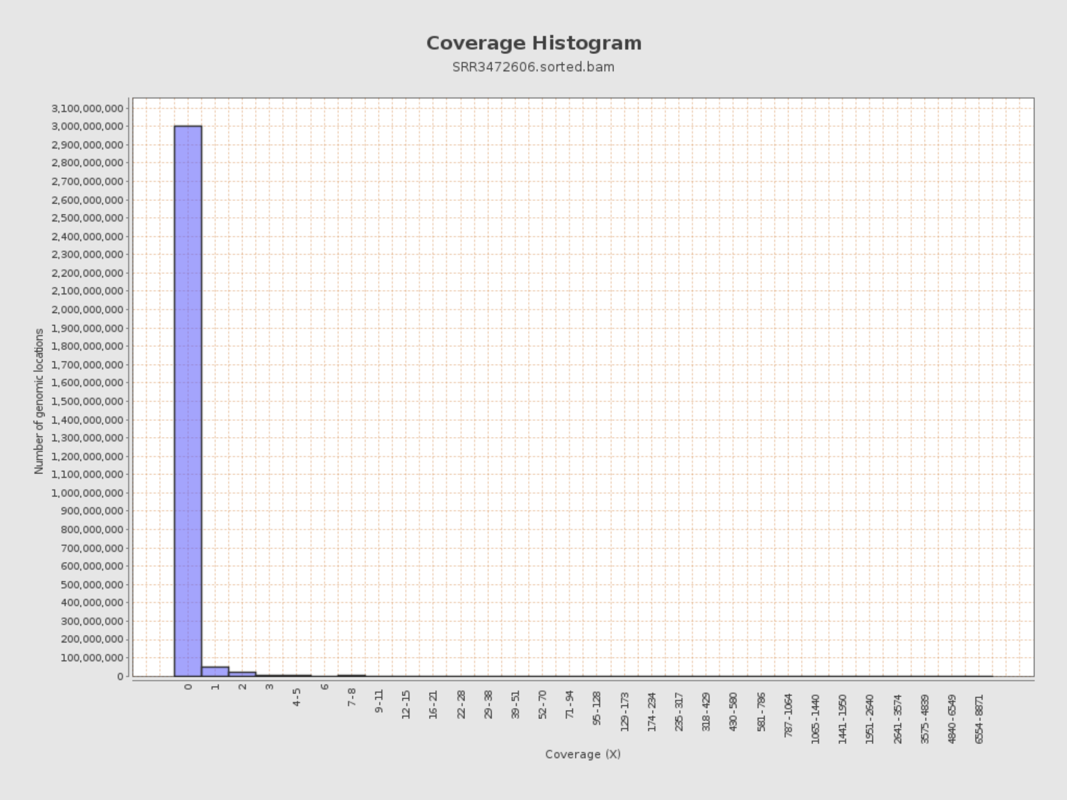
		bases	**coverage**	**deviation**
chr1	249250621	178589090	0.7165	25.235
chr2	243199373	133194774	0.5477	20.5859
chr3	198022430	129801977	0.6555	22.2398
chr4	191154276	31955049	0.1672	10.6078
chr5	180915260	57078341	0.3155	11.8019
chr6	171115067	121385226	0.7094	20.8656
chr7	159138663	131717263	0.8277	28.6216
chr8	146364022	76861405	0.5251	18.1221
chr9	141213431	53869708	0.3815	11.4783
chr10	135534747	39185216	0.2891	15.3986
chr11	135006516	29896665	0.2214	8.8025
chr12	133851895	35084965	0.2621	10.3301
chr13	115169878	62124823	0.5394	28.341
chr14	107349540	27782144	0.2588	11.0589
chr15	102531392	11368197	0.1109	6.0532
chr16	90354753	72109299	0.7981	24.6604
chr17	81195210	85036479	1.0473	42.0842
chr18	78077248	8213074	0.1052	3.5589
chr19	59128983	43262622	0.7317	31.0205
chr20	63025520	43756992	0.6943	20.4219
chr21	48129895	11038293	0.2293	9.0107
chr22	51304566	16030606	0.3125	10.3115
chrMT	16571	2749	0.1659	0.5307
chrX	155270560	72915151	0.4696	20.3695

chrY	59373566	226914	0.0038	0.2409

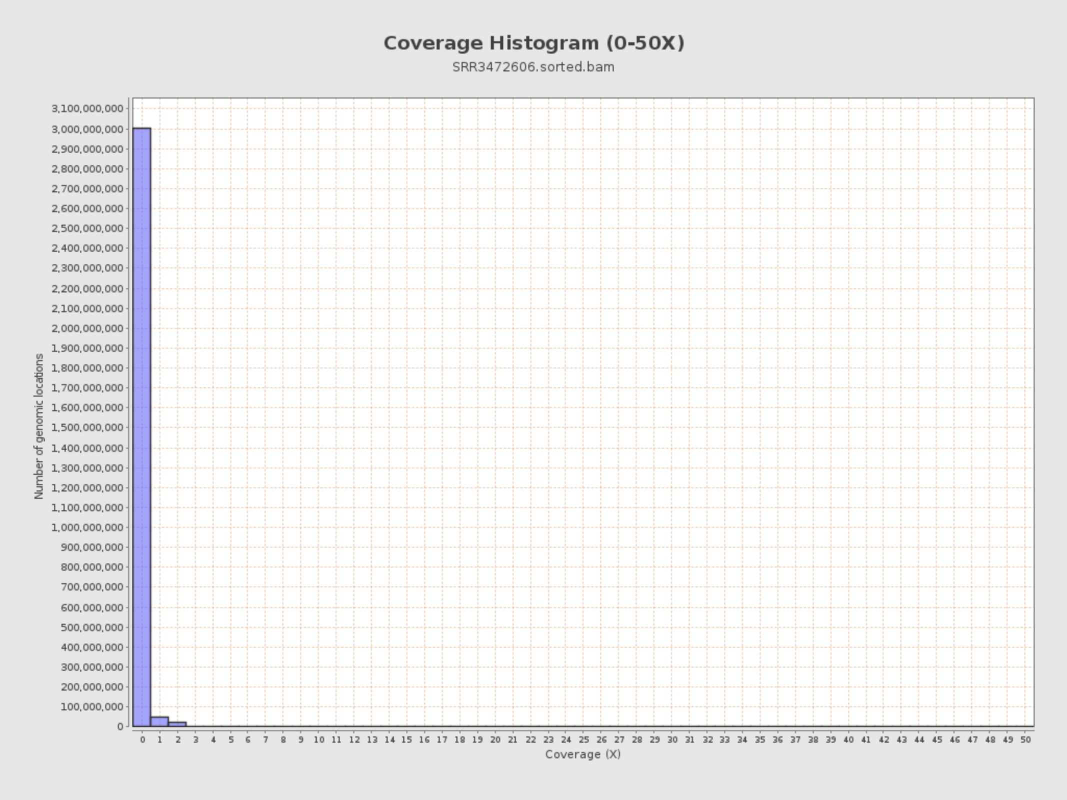
3. Results : Coverage across reference



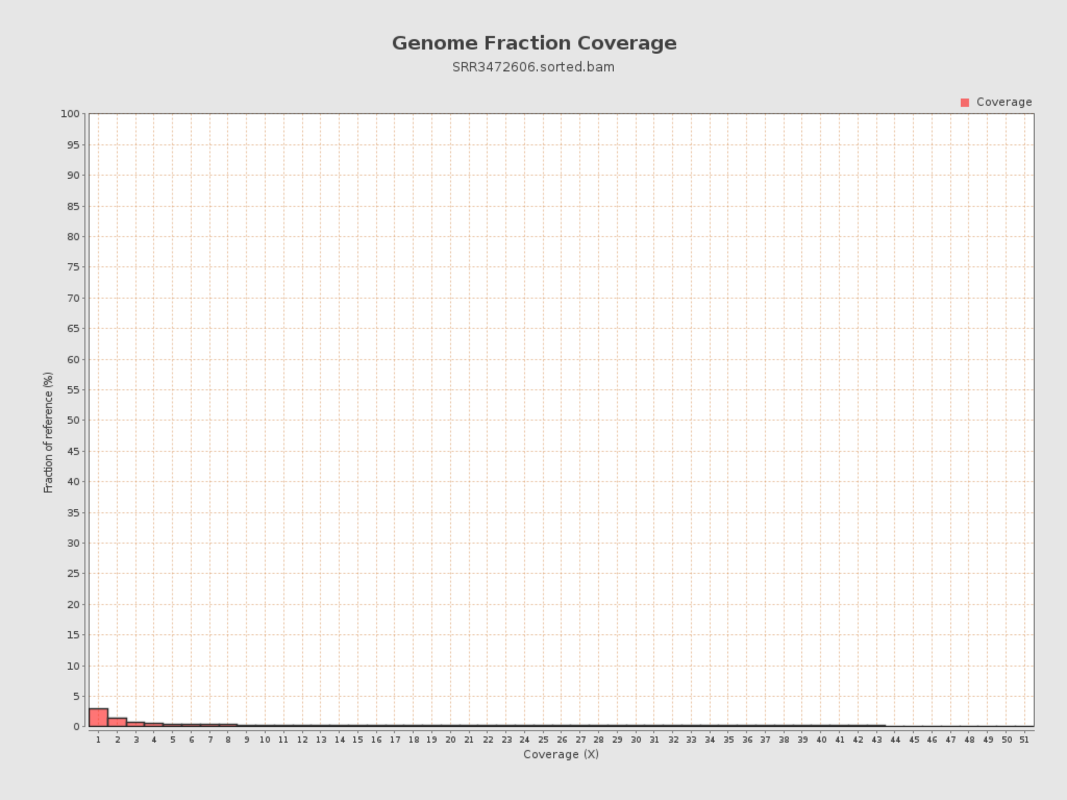
4. Results : Coverage Histogram



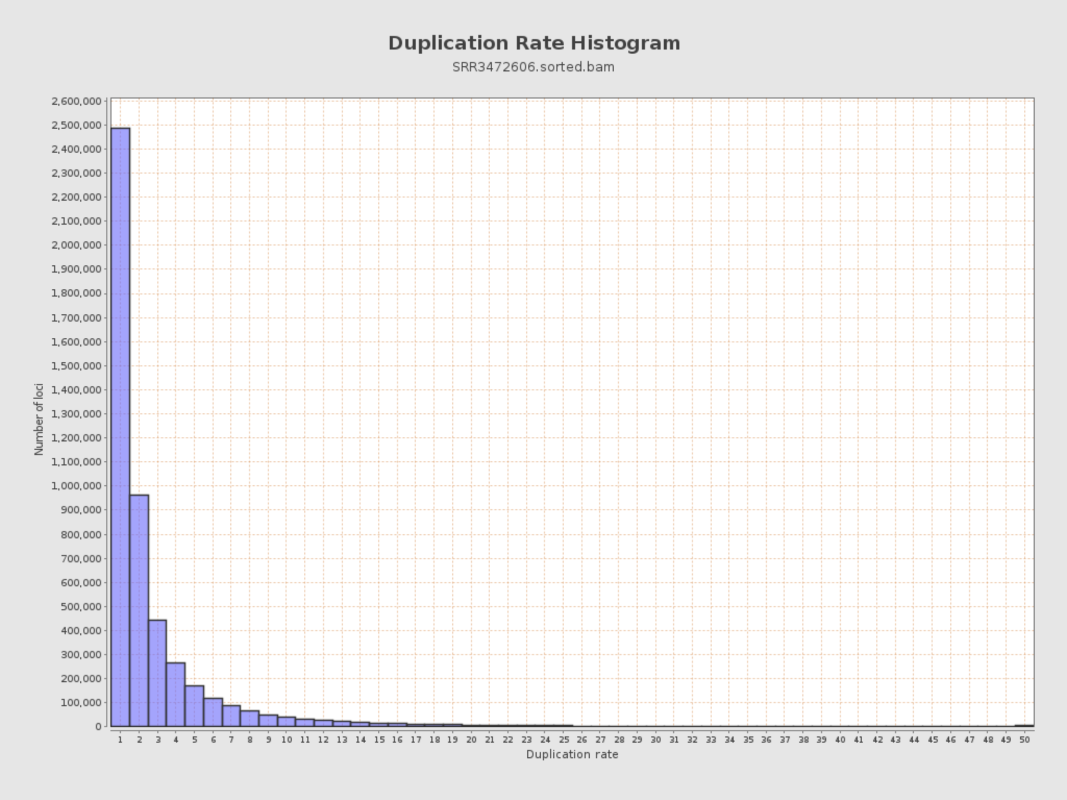
5. Results : Coverage Histogram (0-50X)



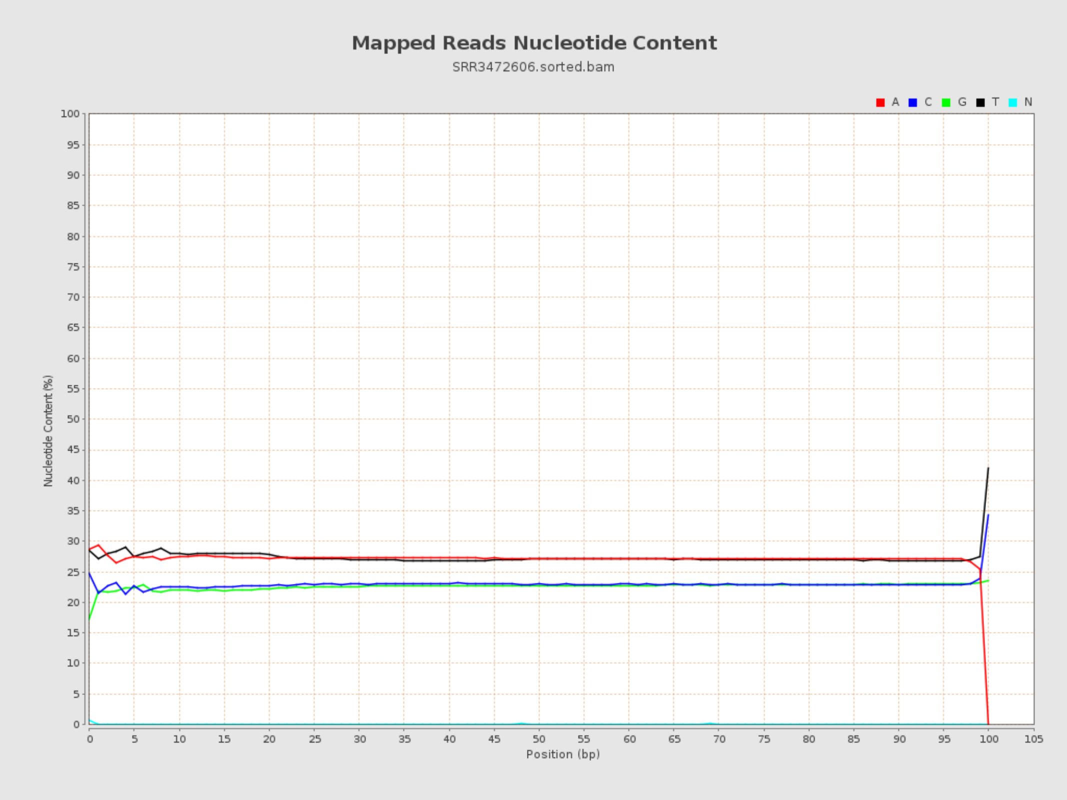
6. Results : Genome Fraction Coverage



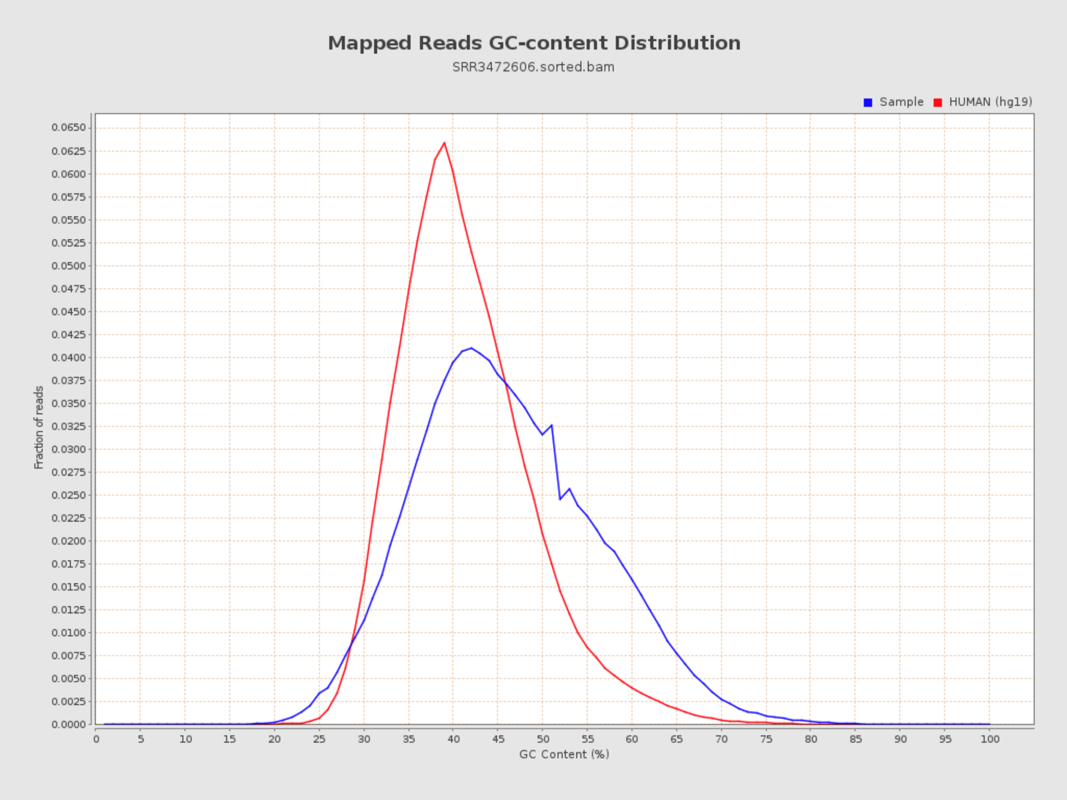
7. Results : Duplication Rate Histogram



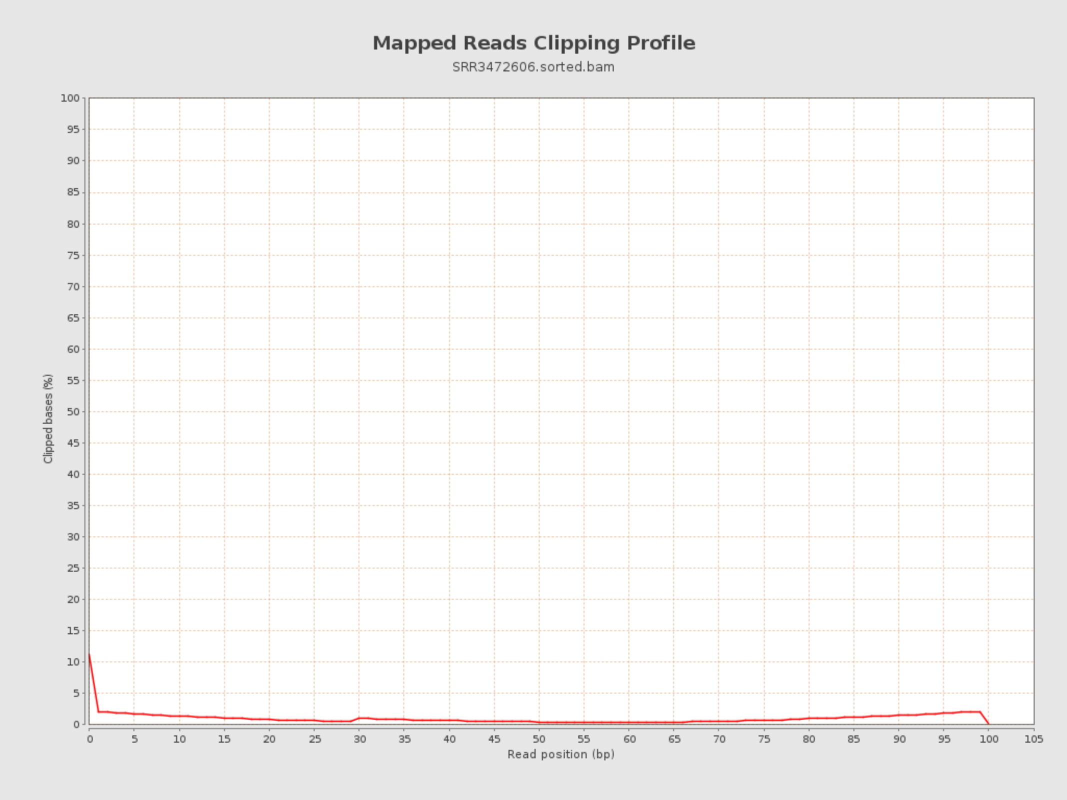
8. Results : Mapped Reads Nucleotide Content



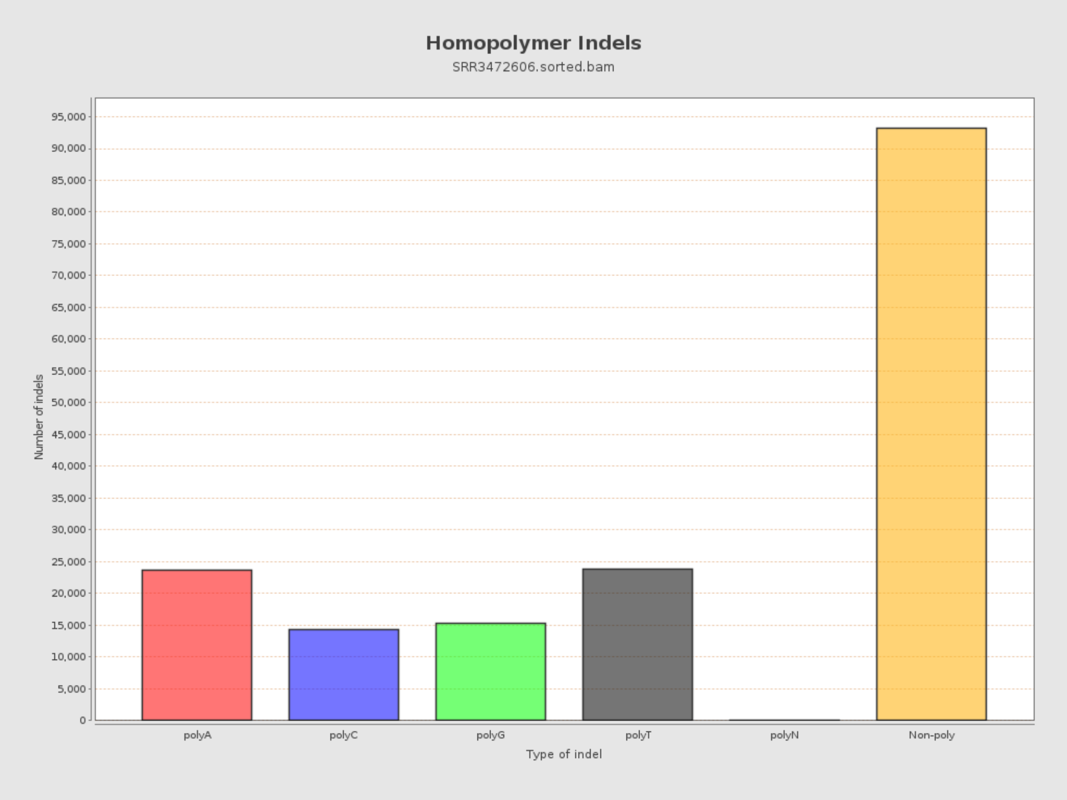
9. Results : Mapped Reads GC-content Distribution



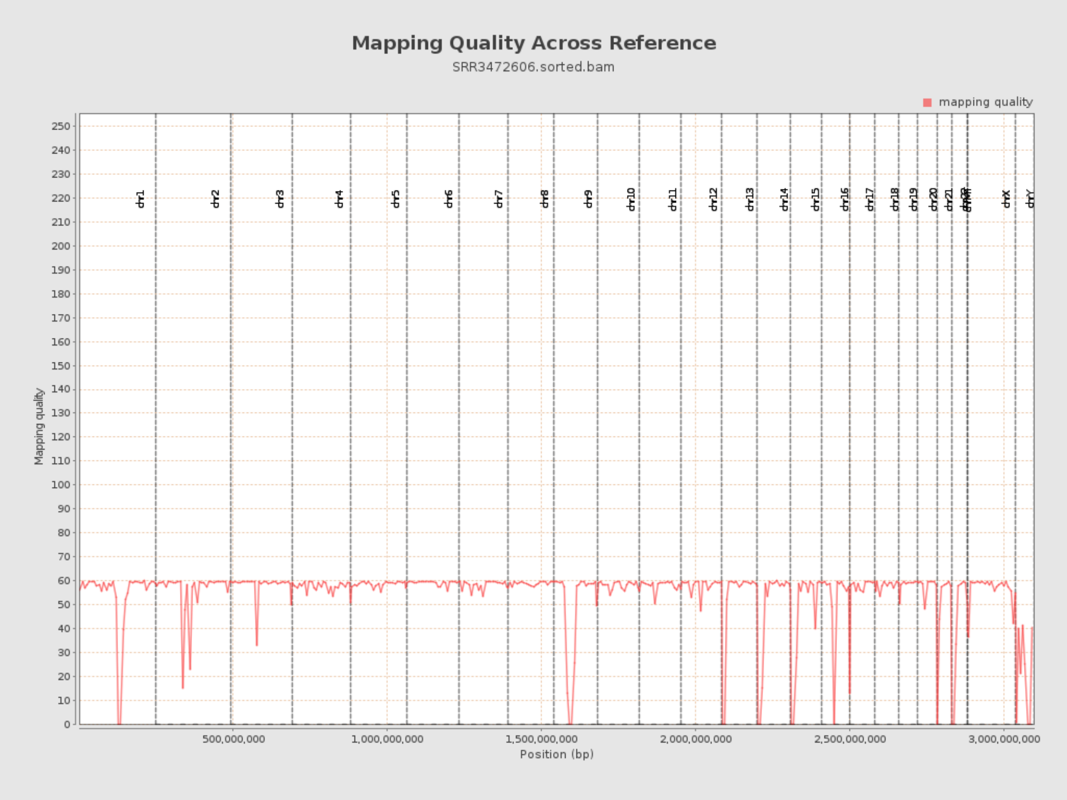
10. Results : Mapped Reads Clipping Profile



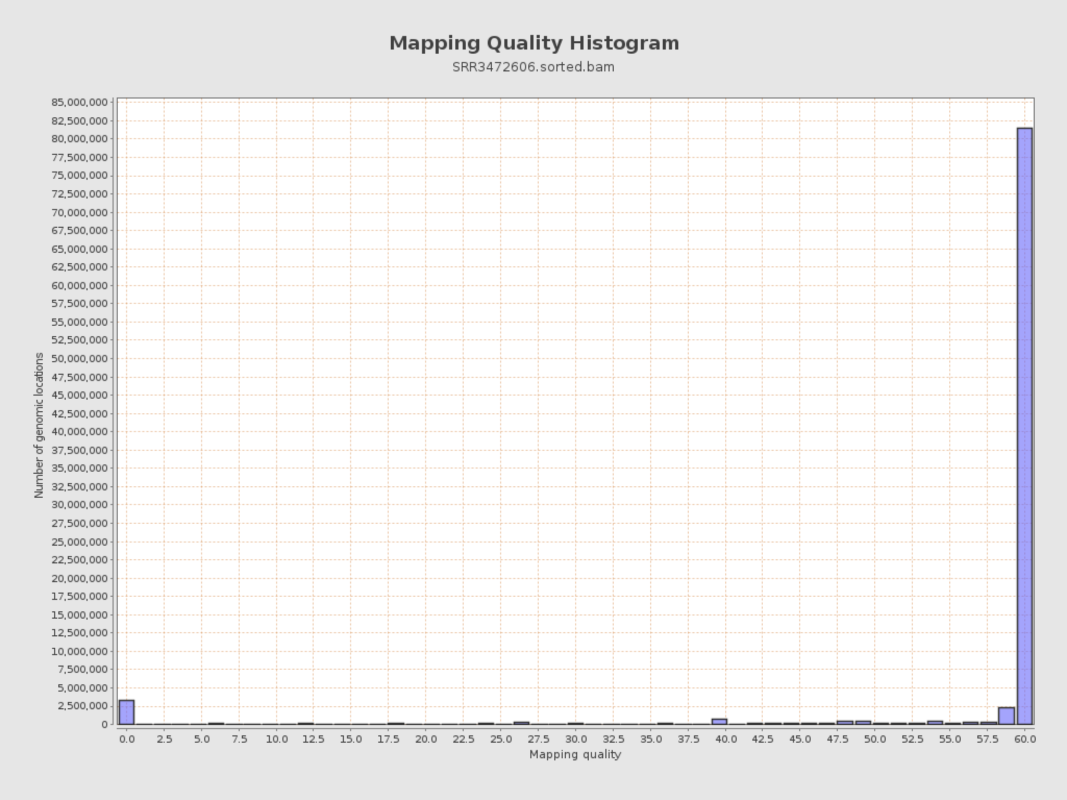
11. Results : Homopolymer Indels



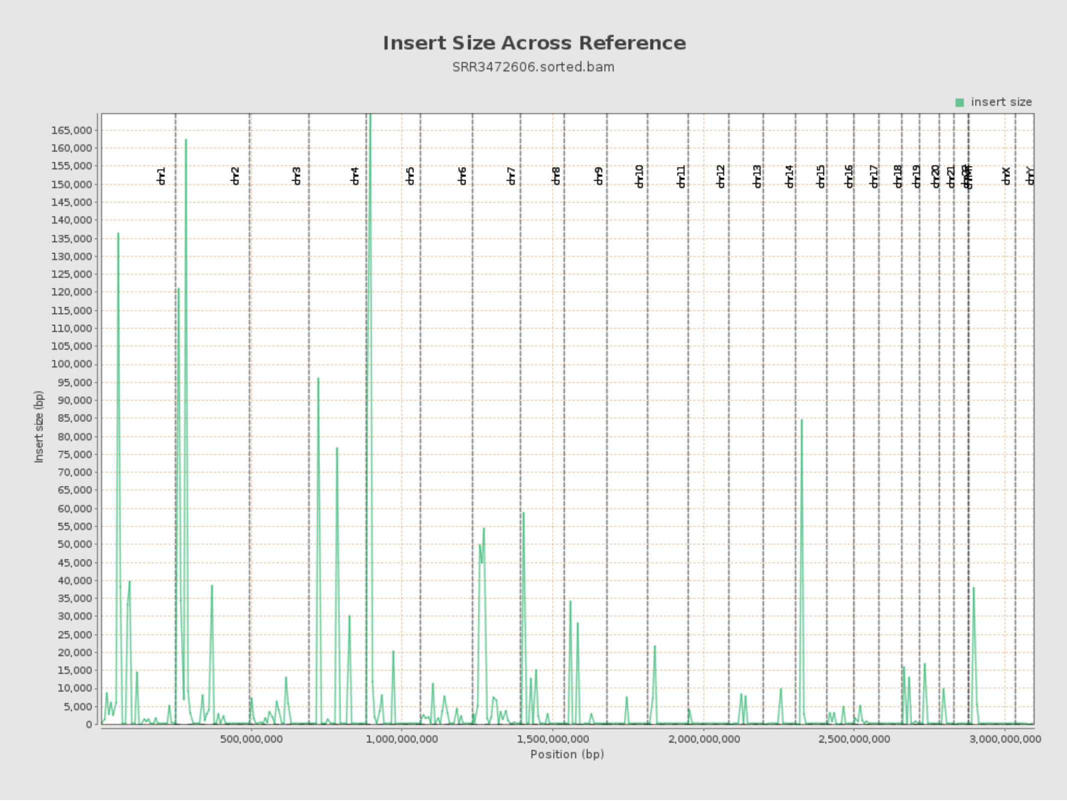
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram