Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 03:18:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR961017.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_SRR961017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961017_1.fastq.gz SRR961017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 03:18:53 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR961017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	305,517,976
Mapped reads	298,421,867 / 97.68%
Unmapped reads	7,096,109 / 2.32%
Mapped paired reads	298,421,867 / 97.68%
Mapped reads, first in pair	149,383,319 / 48.9%
Mapped reads, second in pair	149,038,548 / 48.78%
Mapped reads, both in pair	297,427,442 / 97.35%
Mapped reads, singletons	994,425 / 0.33%
Secondary alignments	0
Supplementary alignments	682,493 / 0.22%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	38,032,266 / 12.45%
Duplication rate	8.34%
Clipped reads	22,873,167 / 7.49%

2.2. ACGT Content

Number/percentage of A's	8,632,148,906 / 29.46%
Number/percentage of C's	5,994,375,814 / 20.46%
Number/percentage of T's	8,610,013,289 / 29.39%
Number/percentage of G's	6,044,847,037 / 20.63%
Number/percentage of N's	19,121,401 / 0.07%

GC Percentage	41.09%

2.3. Coverage

Mean	9.4679
Standard Deviation	104.1264

2.4. Mapping Quality

Mean Mapping Quality	53.66

2.5. Insert size

Mean	21,774.39
Standard Deviation	1,374,091.66
P25/Median/P75	137 / 148 / 158

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	144,203,771
Insertions	3,016,668
Mapped reads with at least one insertion	0.97%
Deletions	3,578,264
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.64%

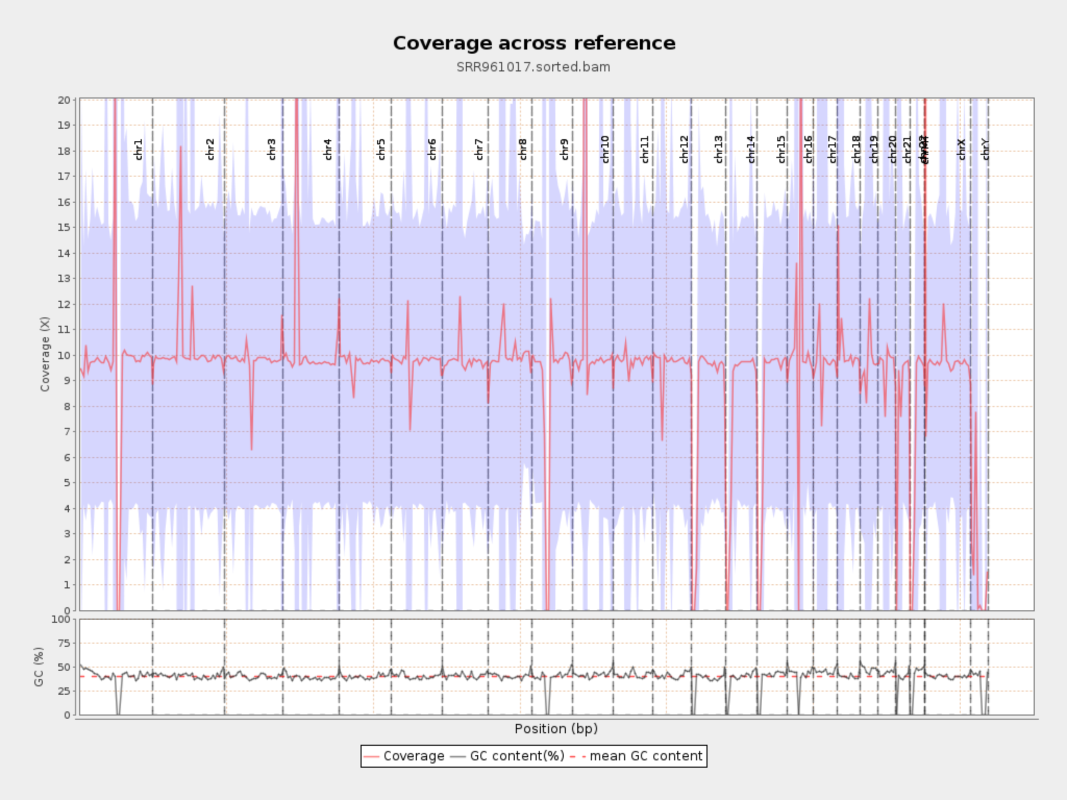
2.7. Chromosome stats

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

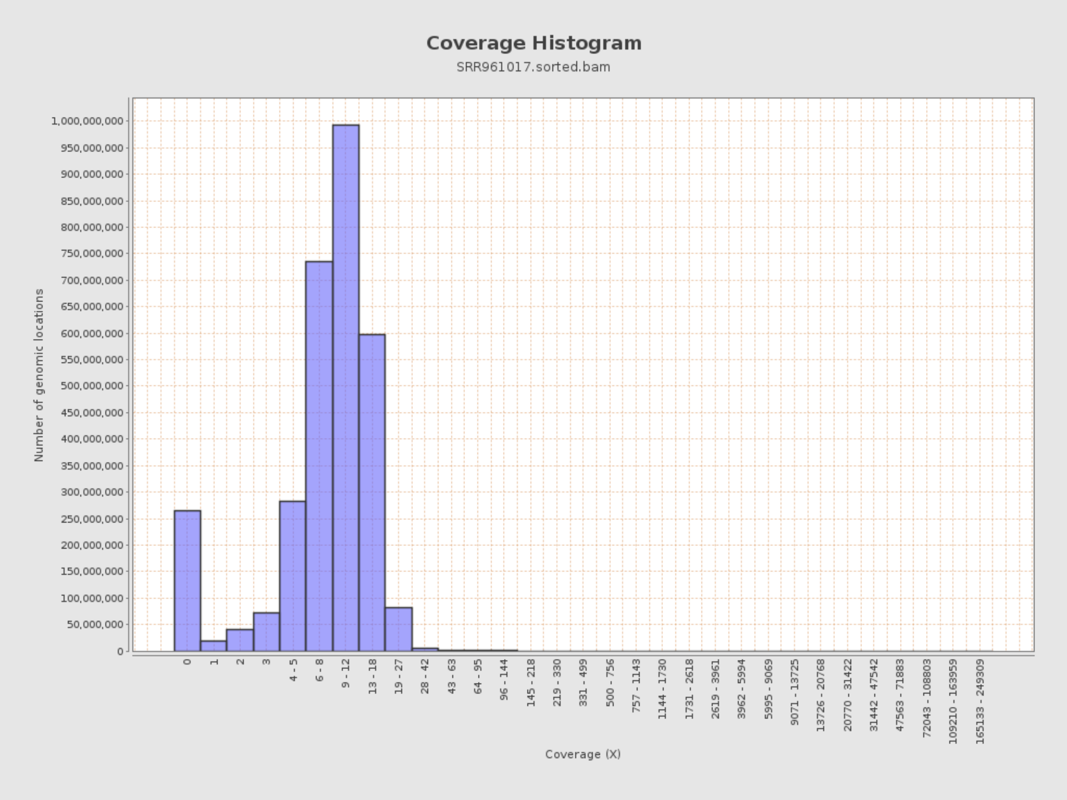
		bases	**coverage**	**deviation**
chr1	249250621	2384627503	9.5672	247.7018
chr2	243199373	2511148130	10.3255	64.9198
chr3	198022430	1927544646	9.734	21.2968
chr4	191154276	1972572776	10.3193	91.3935
chr5	180915260	1758371334	9.7193	10.1278
chr6	171115067	1676113314	9.7952	30.2794
chr7	159138663	1563878077	9.8271	63.5169
chr8	146364022	1471955507	10.0568	102.1147
chr9	141213431	1222769076	8.659	88.9724
chr10	135534747	1533940150	11.3177	245.416
chr11	135006516	1319828905	9.776	41.1161
chr12	133851895	1291187981	9.6464	7.9367
chr13	115169878	930754152	8.0816	5.8687
chr14	107349540	863028432	8.0394	9.2077
chr15	102531392	812287548	7.9223	5.9903
chr16	90354753	941748076	10.4228	100.5792
chr17	81195210	784509973	9.662	38.5619
chr18	78077248	797359494	10.2124	106.1427
chr19	59128983	571691295	9.6685	119.6383
chr20	63025520	604143817	9.5857	34.1364
chr21	48129895	402280721	8.3582	45.2255
chr22	51304566	344466809	6.7142	8.0463
chrMT	16571	22474936	1,356.2812	194.0478
chrX	155270560	1502355876	9.6757	31.4177

chrY	59373566	98535272	1.6596	96.7743

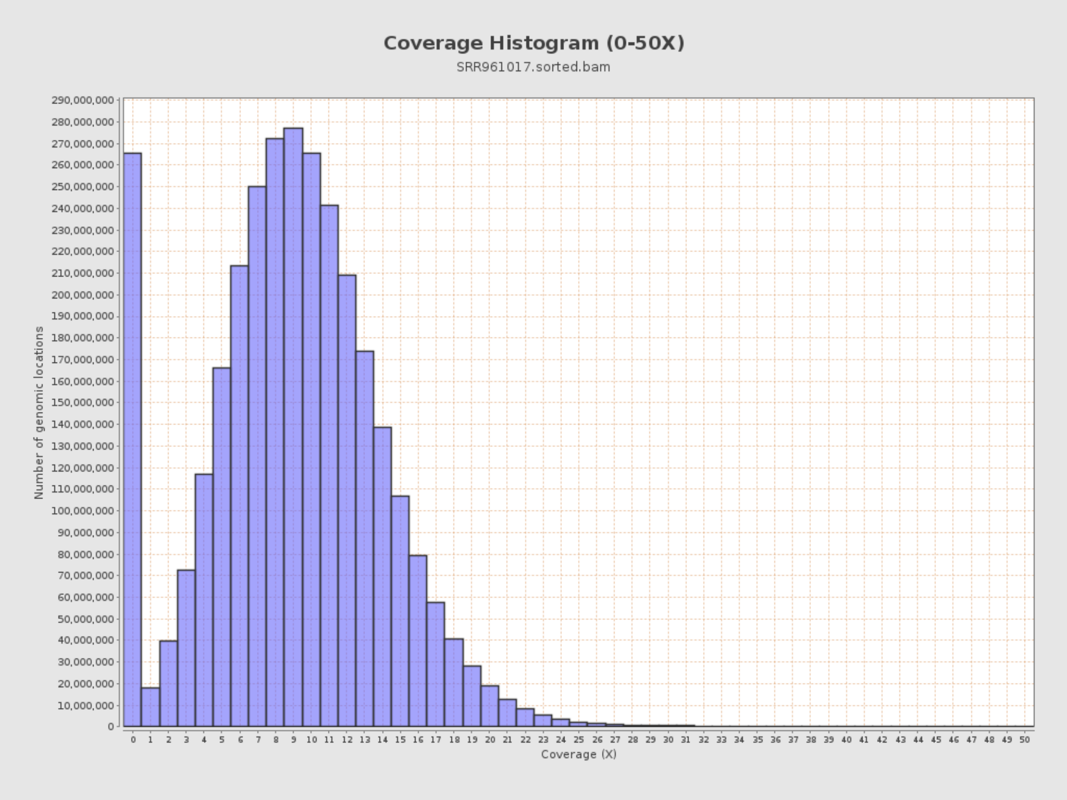
3. Results : Coverage across reference



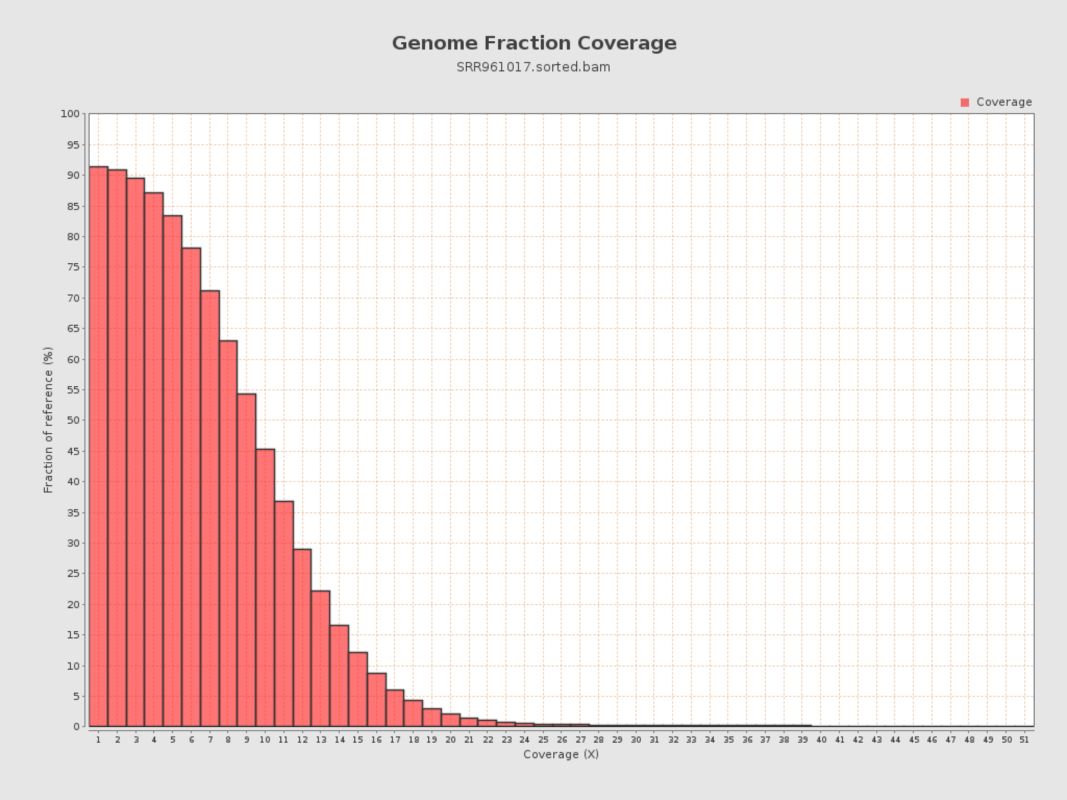
4. Results : Coverage Histogram



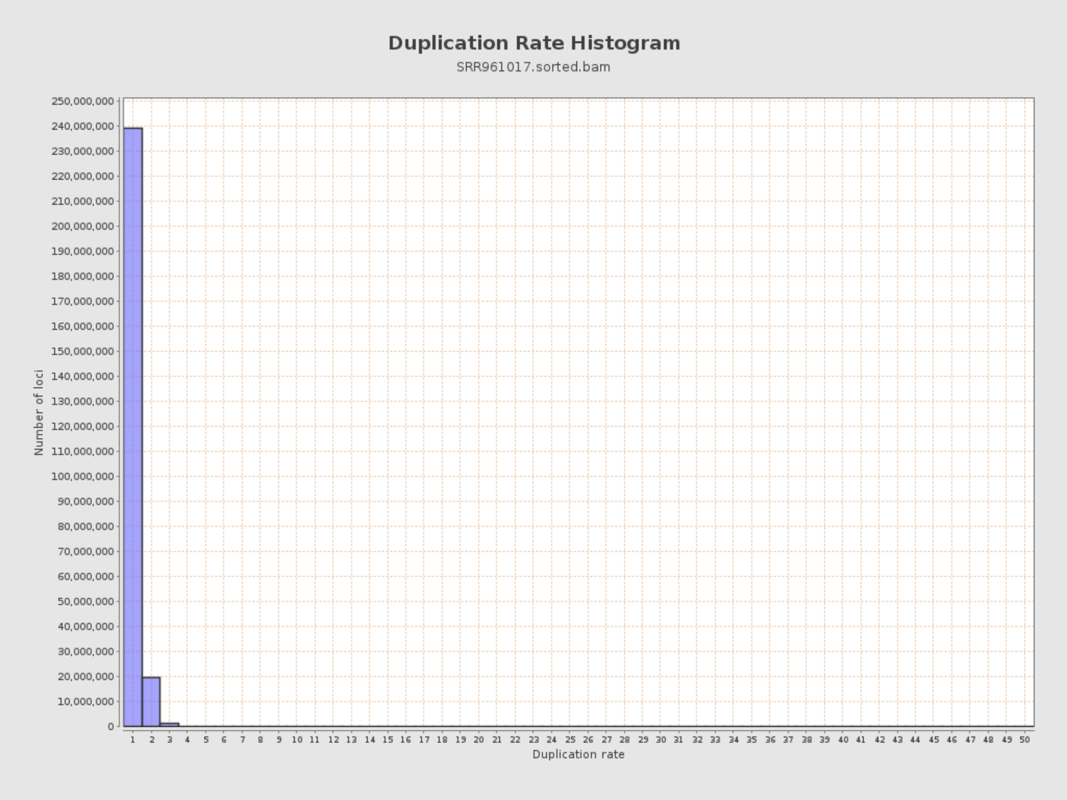
5. Results : Coverage Histogram (0-50X)



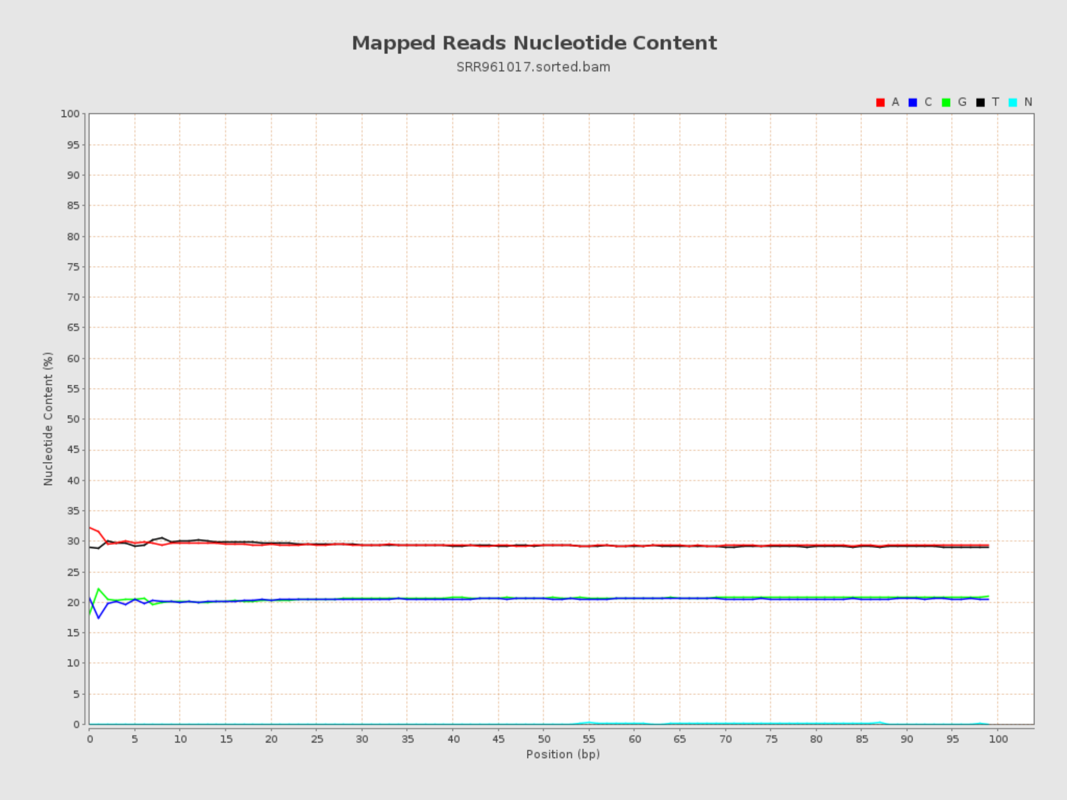
6. Results : Genome Fraction Coverage



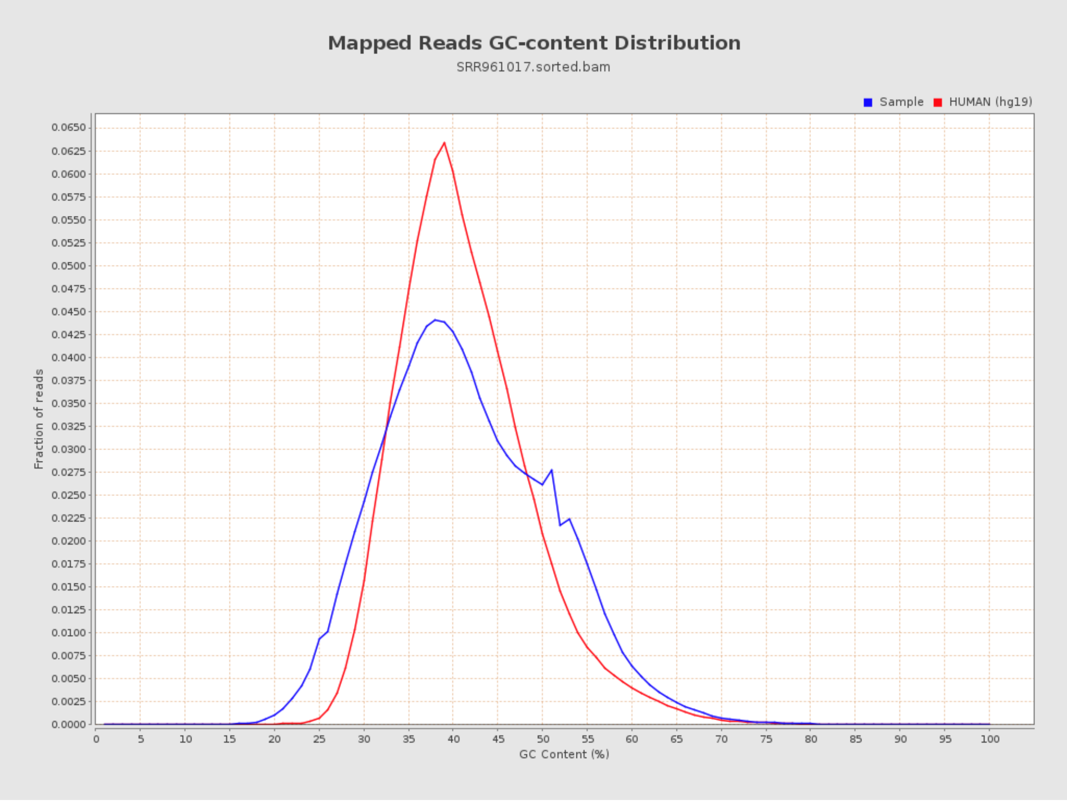
7. Results : Duplication Rate Histogram



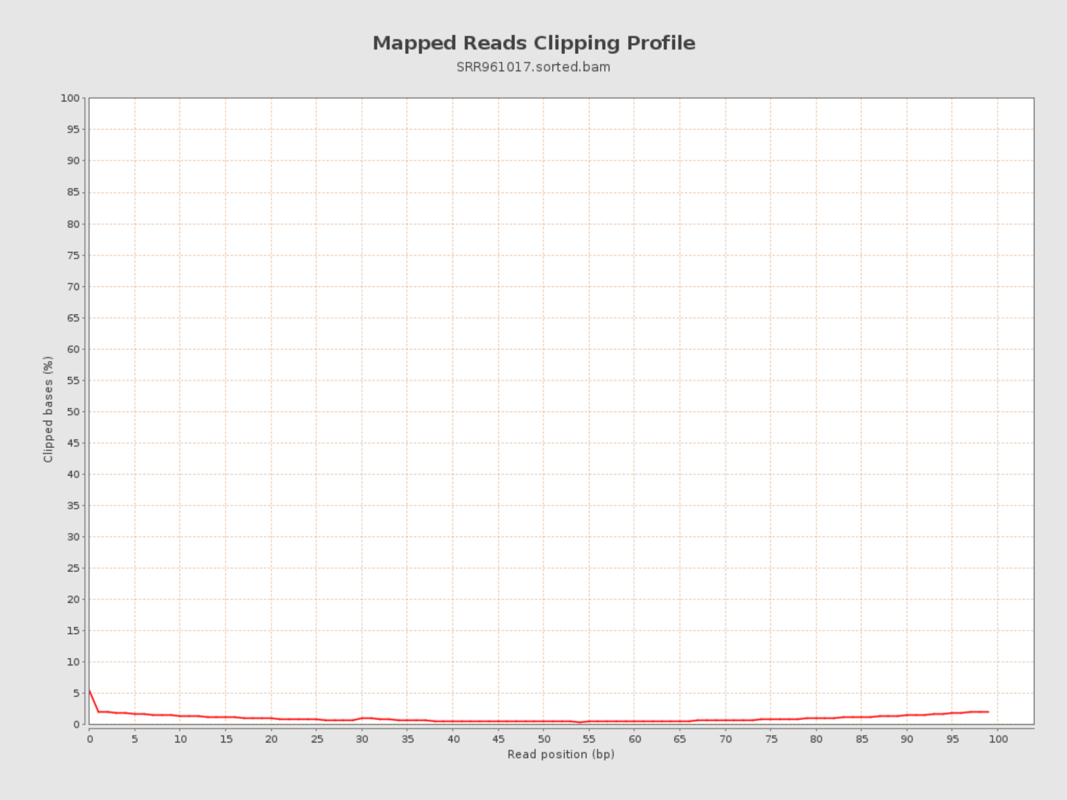
8. Results : Mapped Reads Nucleotide Content



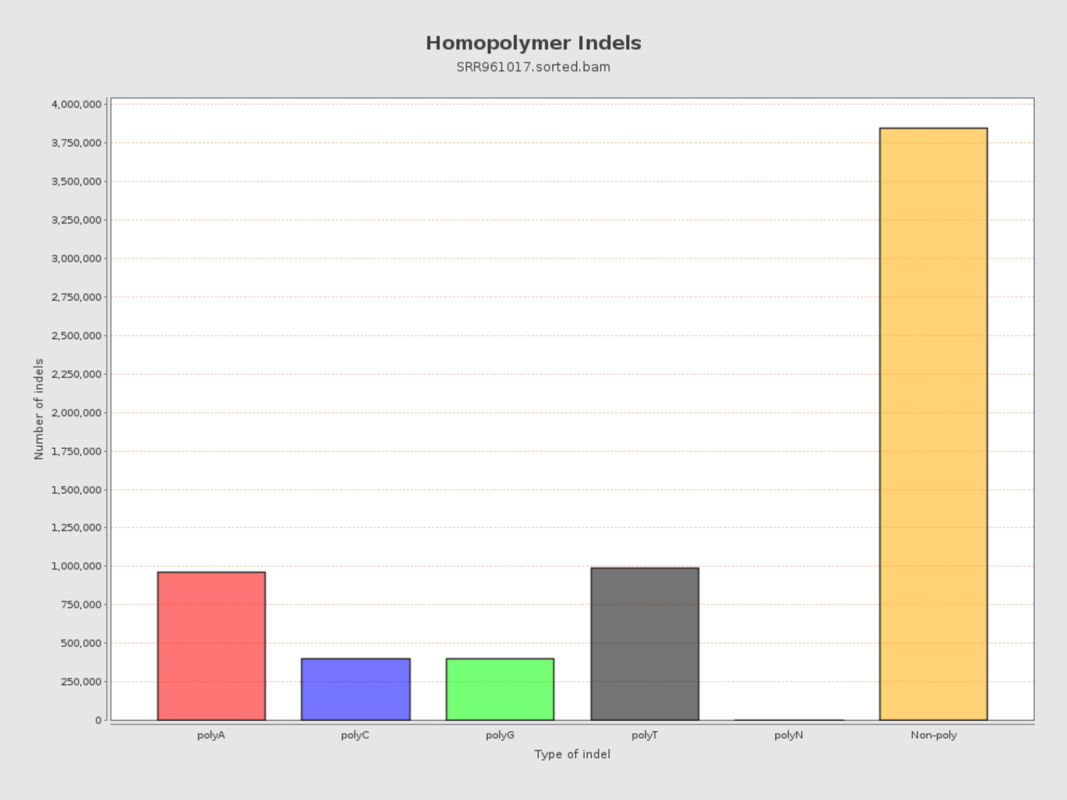
9. Results : Mapped Reads GC-content Distribution



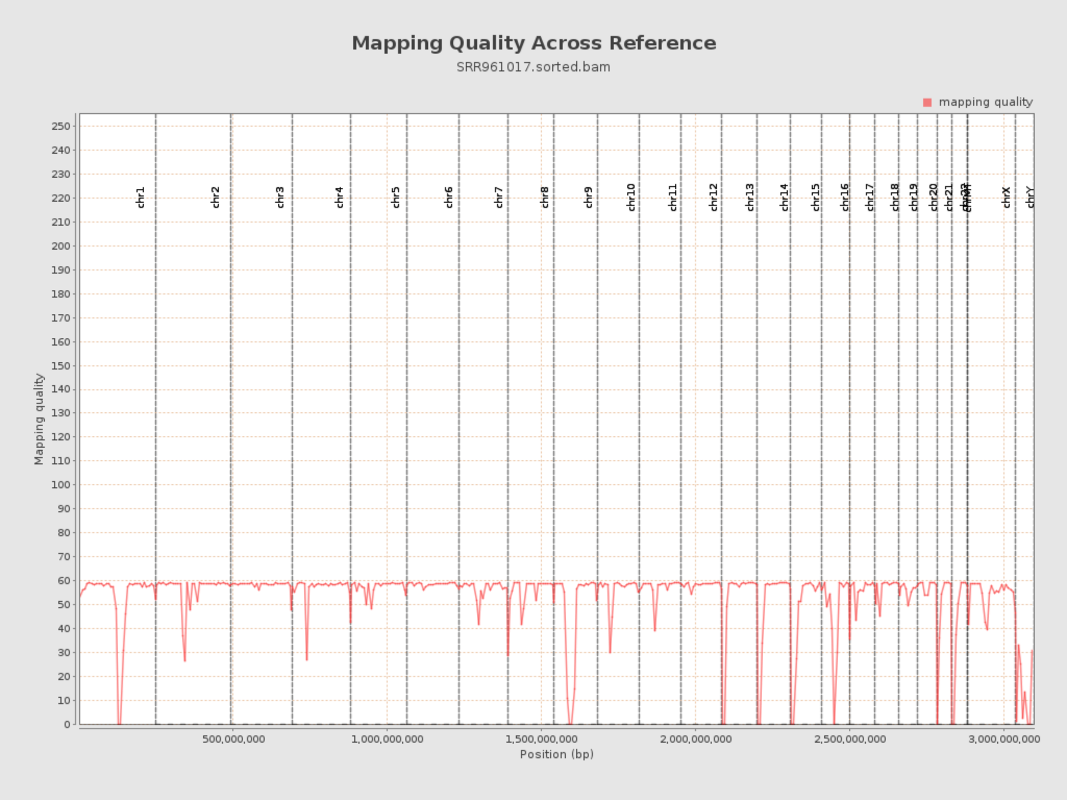
10. Results : Mapped Reads Clipping Profile



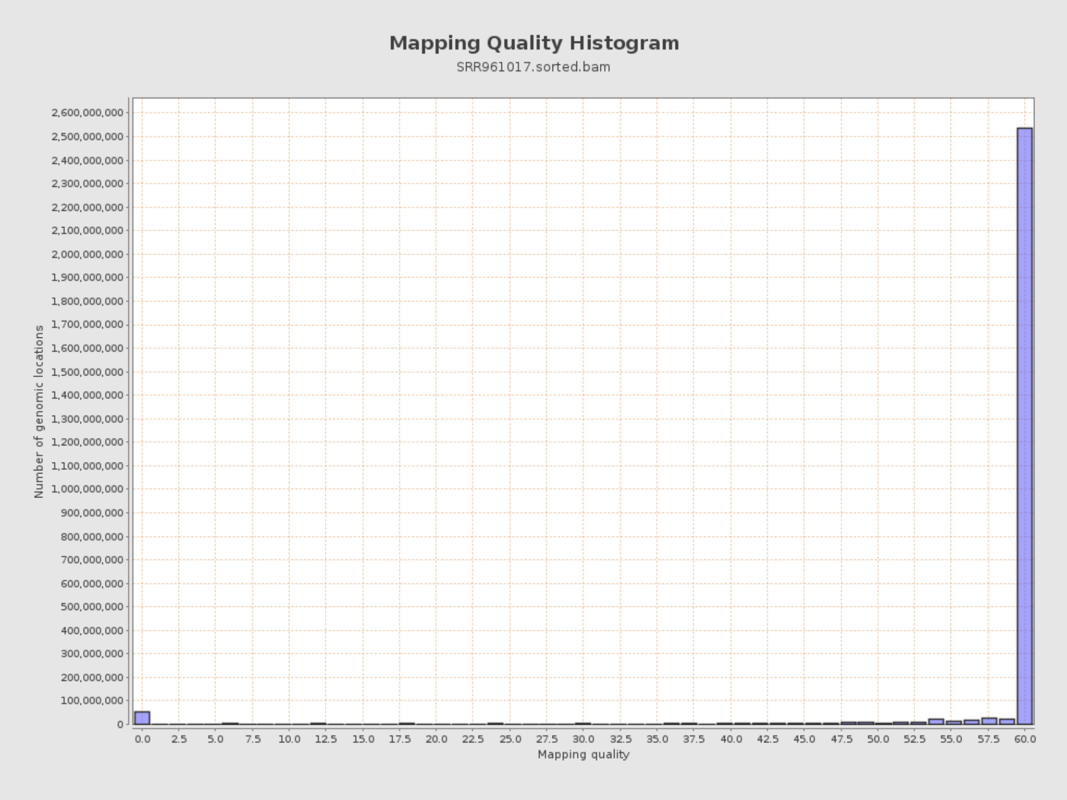
11. Results : Homopolymer Indels



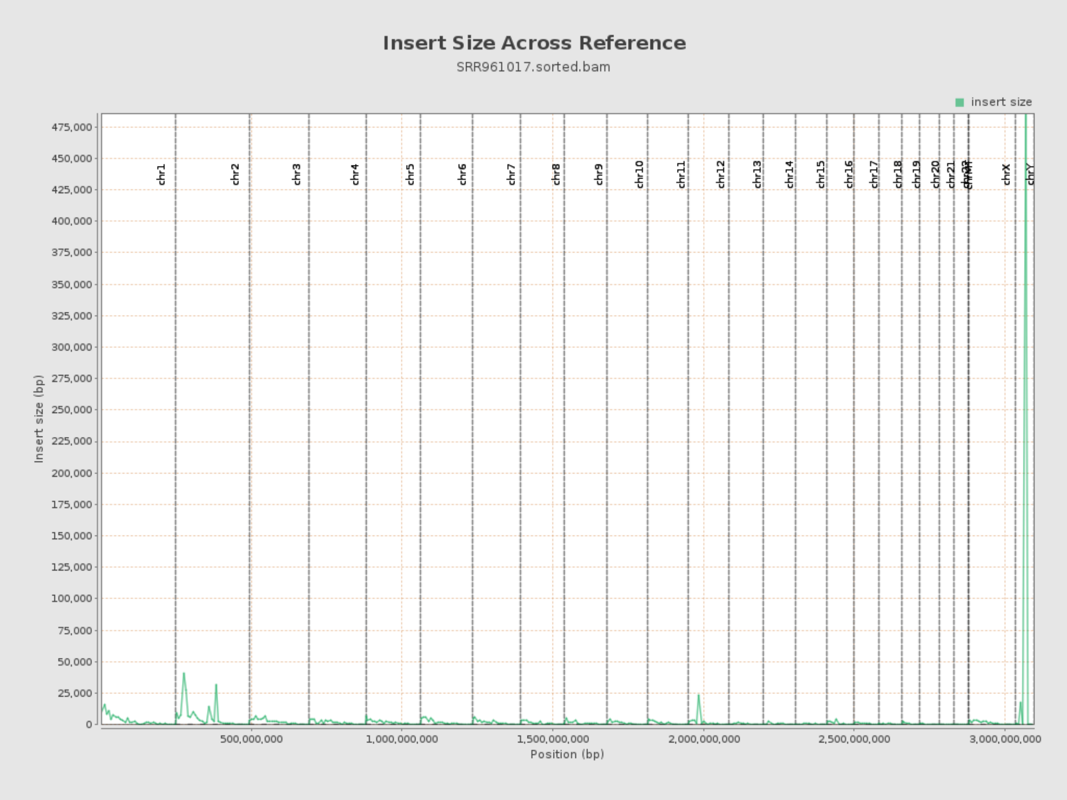
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram