Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 22:42:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174026.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_SRR10174026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174026_1.fastq.gz SRR10174026_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 22:42:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,610,454
Mapped reads	1,574,284 / 97.75%
Unmapped reads	36,170 / 2.25%
Mapped paired reads	1,574,284 / 97.75%
Mapped reads, first in pair	787,925 / 48.93%
Mapped reads, second in pair	786,359 / 48.83%
Mapped reads, both in pair	1,550,644 / 96.29%
Mapped reads, singletons	23,640 / 1.47%
Secondary alignments	0
Supplementary alignments	156,946 / 9.75%
Read min/max/mean length	30 / 133 / 128.19
Duplicated reads (estimated)	1,210,477 / 75.16%
Duplication rate	63.89%
Clipped reads	616,076 / 38.25%

2.2. ACGT Content

Number/percentage of A's	56,640,672 / 30.35%
Number/percentage of C's	36,077,201 / 19.33%
Number/percentage of T's	56,526,235 / 30.28%
Number/percentage of G's	37,402,550 / 20.04%
Number/percentage of N's	2,344 / 0%

GC Percentage	39.37%

2.3. Coverage

Mean	0.0603
Standard Deviation	1.0619

2.4. Mapping Quality

Mean Mapping Quality	53.02

2.5. Insert size

Mean	1,080,627.88
Standard Deviation	9,918,462.93
P25/Median/P75	144 / 197 / 280

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	1,823,856
Insertions	21,259
Mapped reads with at least one insertion	1.3%
Deletions	44,558
Mapped reads with at least one deletion	2.76%
Homopolymer indels	42.37%

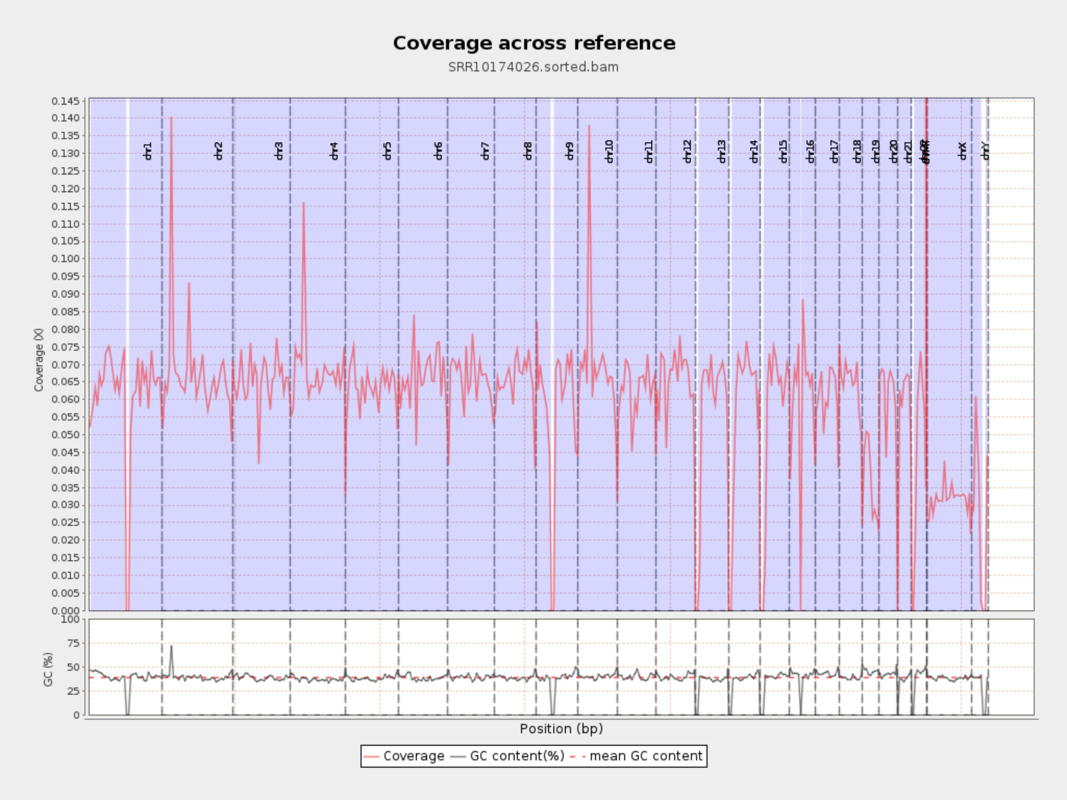
2.7. Chromosome stats

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

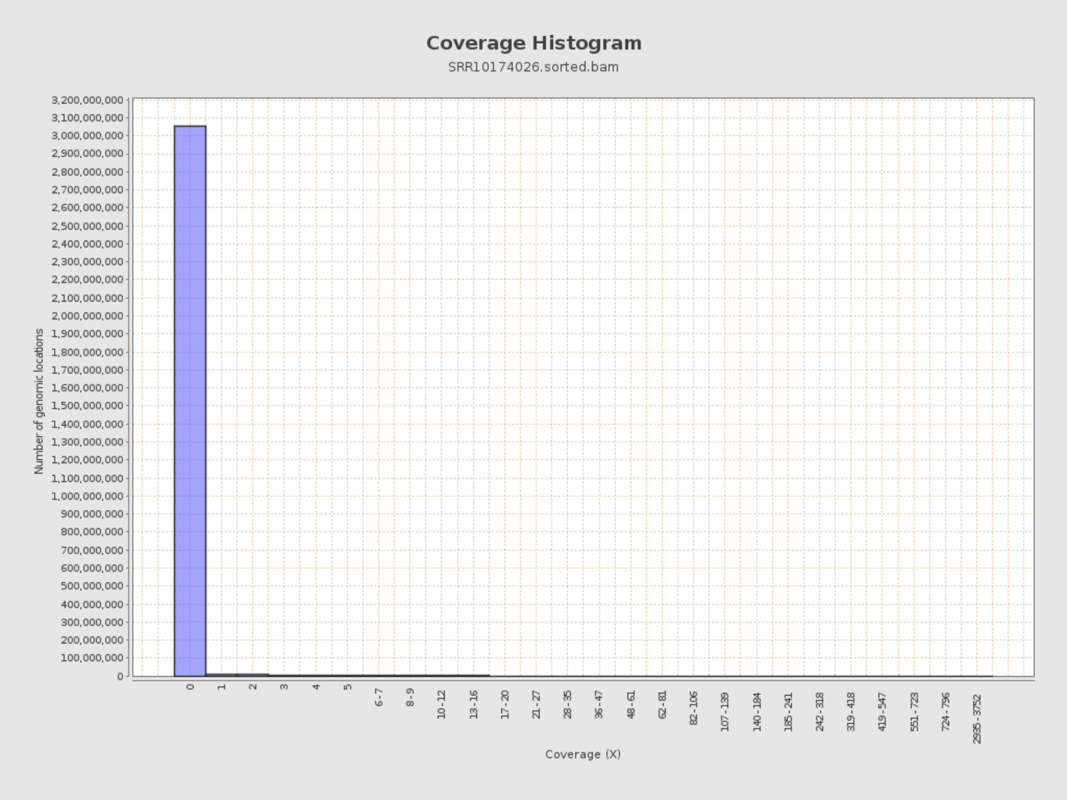
		bases	coverage	deviation
chr1	249250621	15233819	0.0611	0.8034
chr2	243199373	16505426	0.0679	2.7102
chr3	198022430	12964437	0.0655	0.7438
chr4	191154276	13130306	0.0687	0.8526
chr5	180915260	11547887	0.0638	0.7292
chr6	171115067	11413530	0.0667	0.7804
chr7	159138663	10531599	0.0662	0.843
chr8	146364022	9565024	0.0654	0.8623
chr9	141213431	7981341	0.0565	0.7593
chr10	135534747	9563048	0.0706	1.027
chr11	135006516	8478832	0.0628	0.7268
chr12	133851895	8815080	0.0659	0.7453
chr13	115169878	6310666	0.0548	0.6869
chr14	107349540	6008303	0.056	0.6945
chr15	102531392	5514576	0.0538	0.6625
chr16	90354753	5379978	0.0595	0.7681
chr17	81195210	4921463	0.0606	0.7467
chr18	78077248	5100156	0.0653	0.9377
chr19	59128983	2186970	0.037	0.612
chr20	63025520	3866424	0.0613	0.7043
chr21	48129895	2688879	0.0559	0.8122
chr22	51304566	2197281	0.0428	0.6116
chrMT	16571	414291	25.001	25.668
chrX	155270560	4928999	0.0317	0.5193

chrY	59373566	1508582	0.0254	0.533

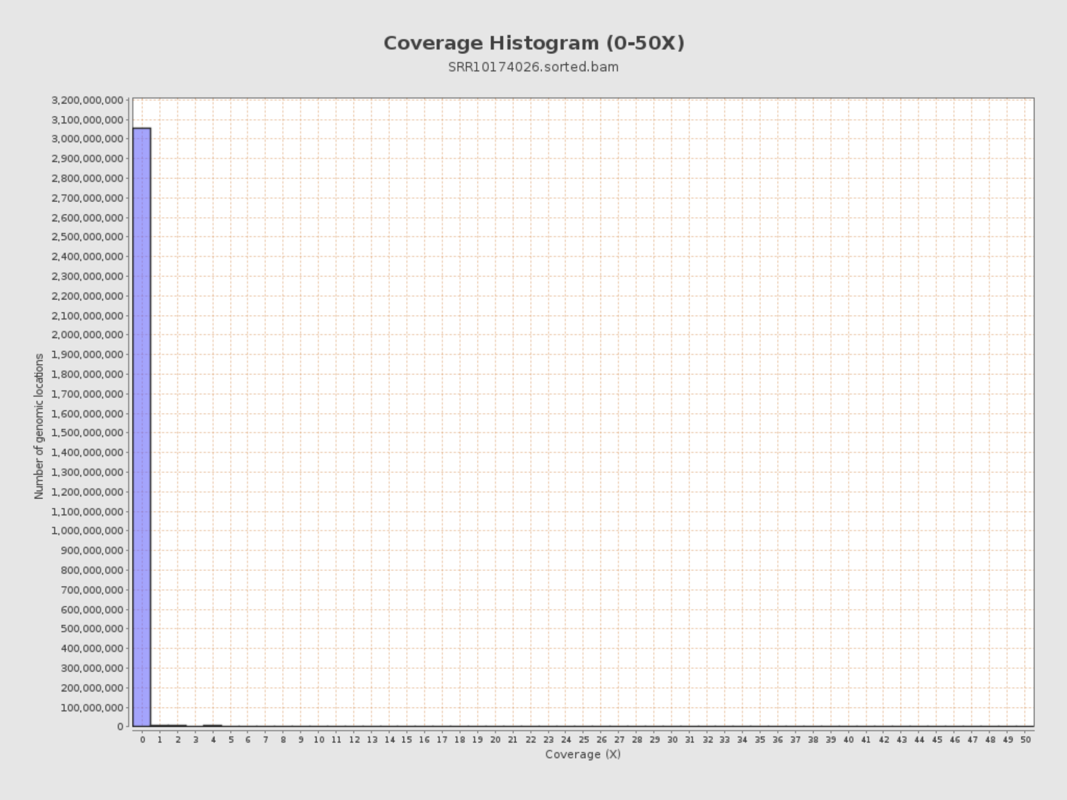
3. Results : Coverage across reference



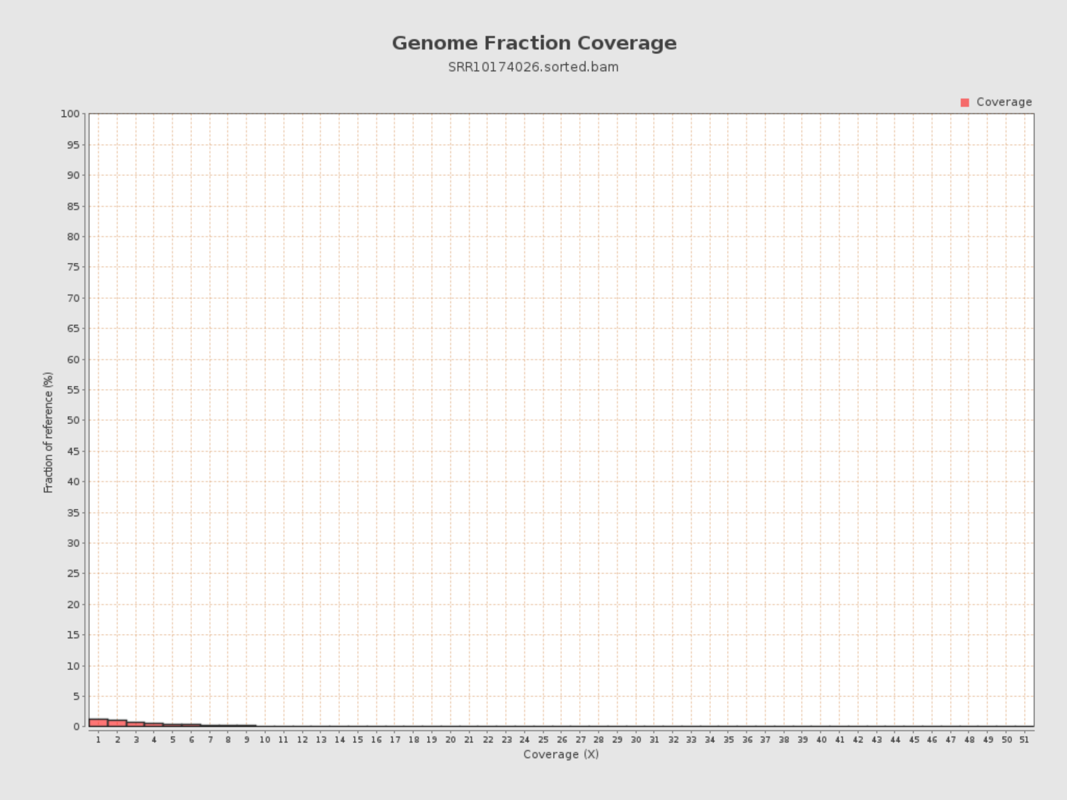
4. Results : Coverage Histogram



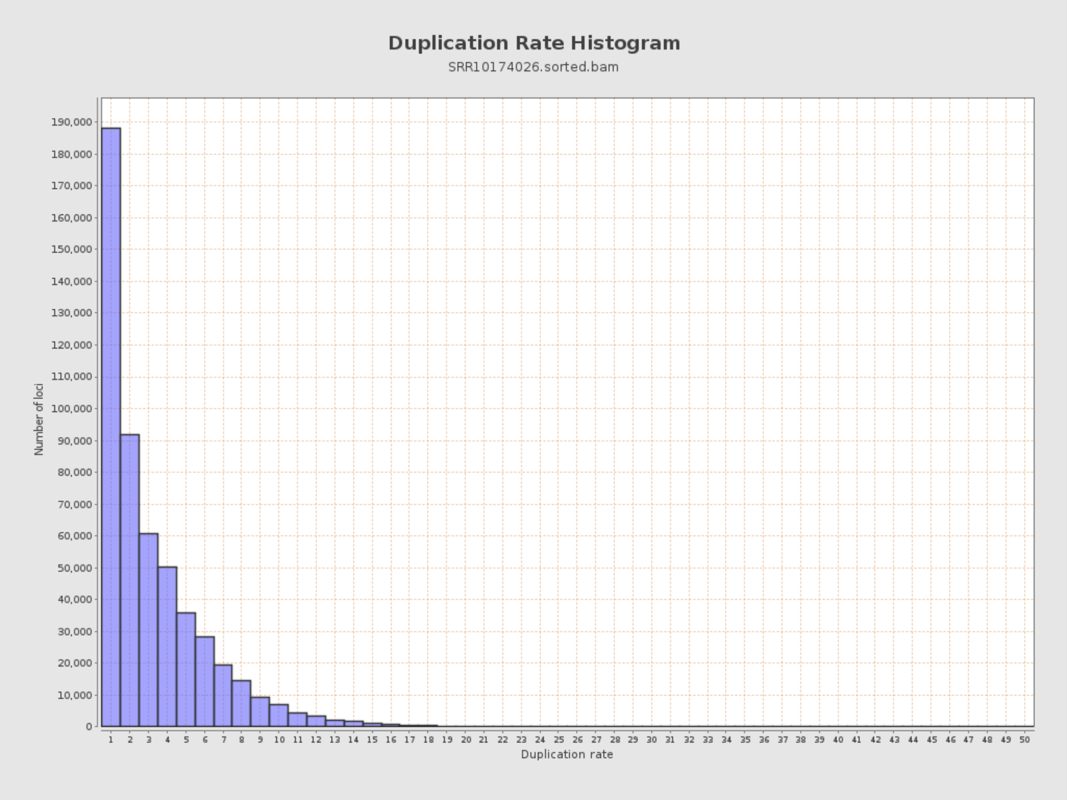
5. Results : Coverage Histogram (0-50X)



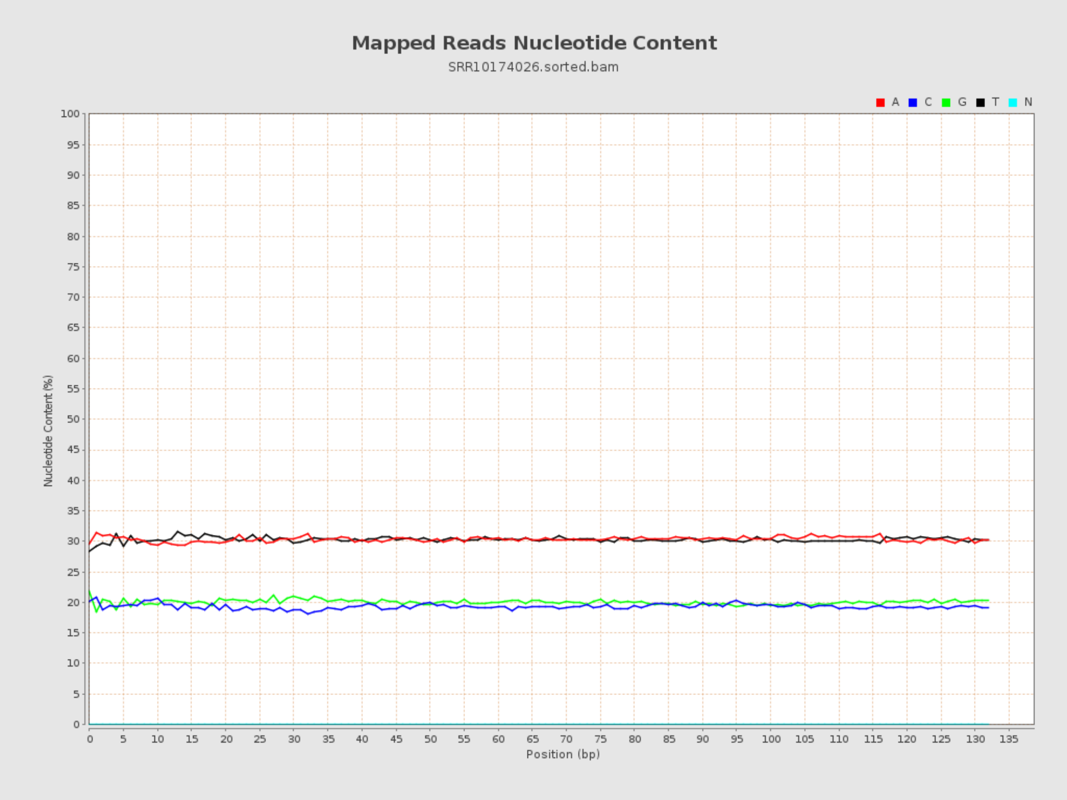
6. Results : Genome Fraction Coverage



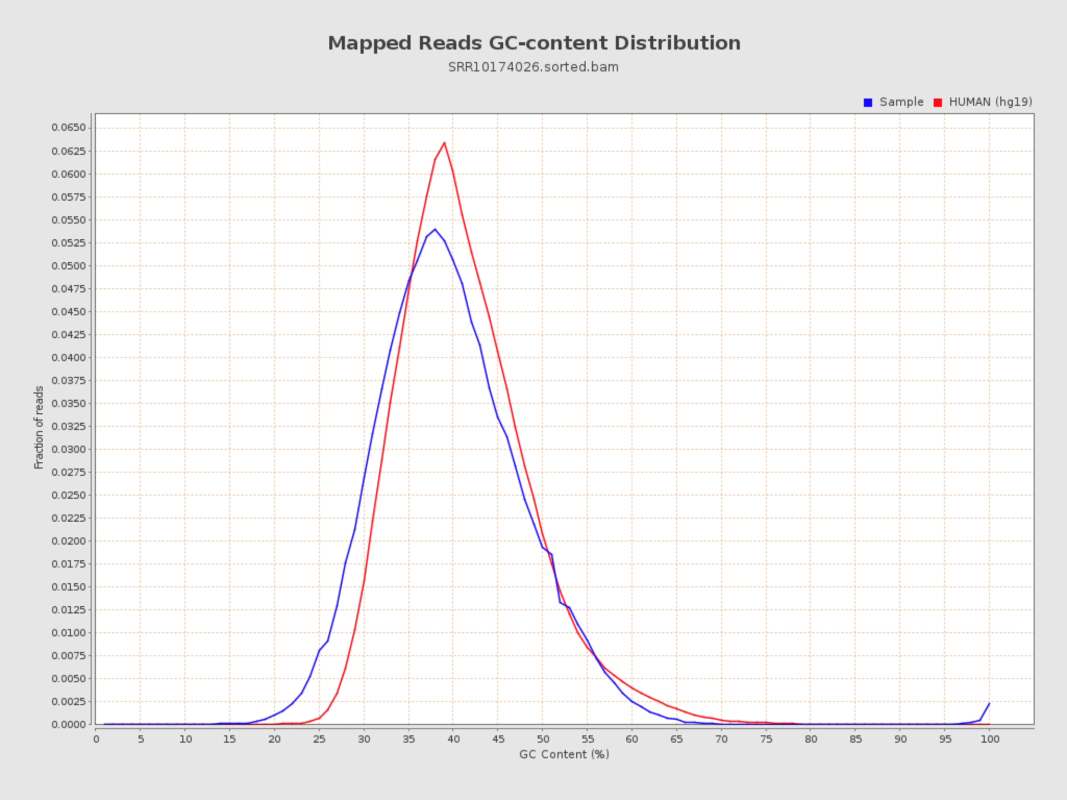
7. Results : Duplication Rate Histogram



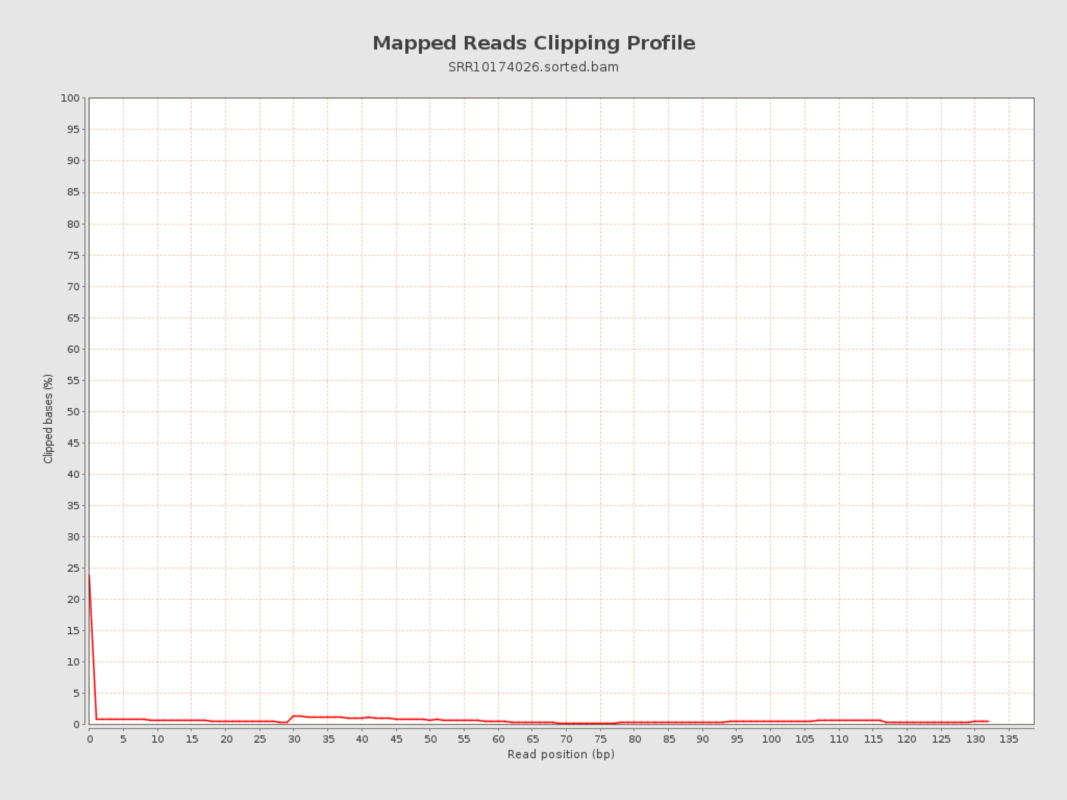
8. Results : Mapped Reads Nucleotide Content



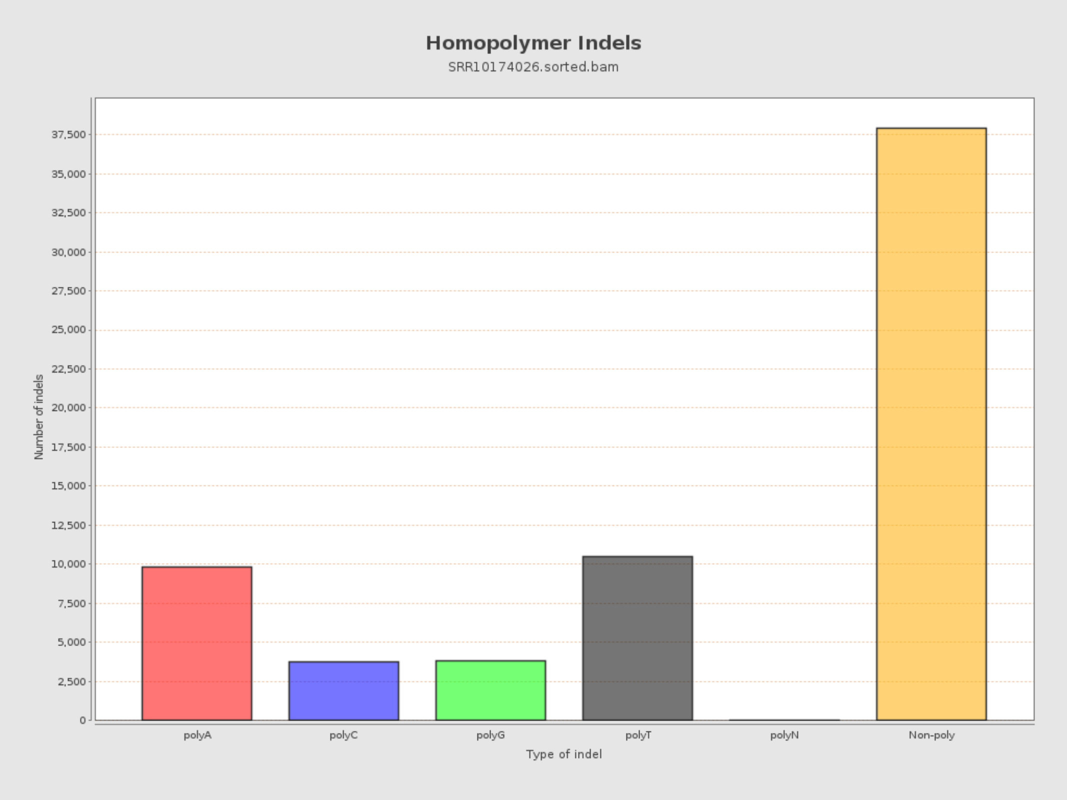
9. Results : Mapped Reads GC-content Distribution



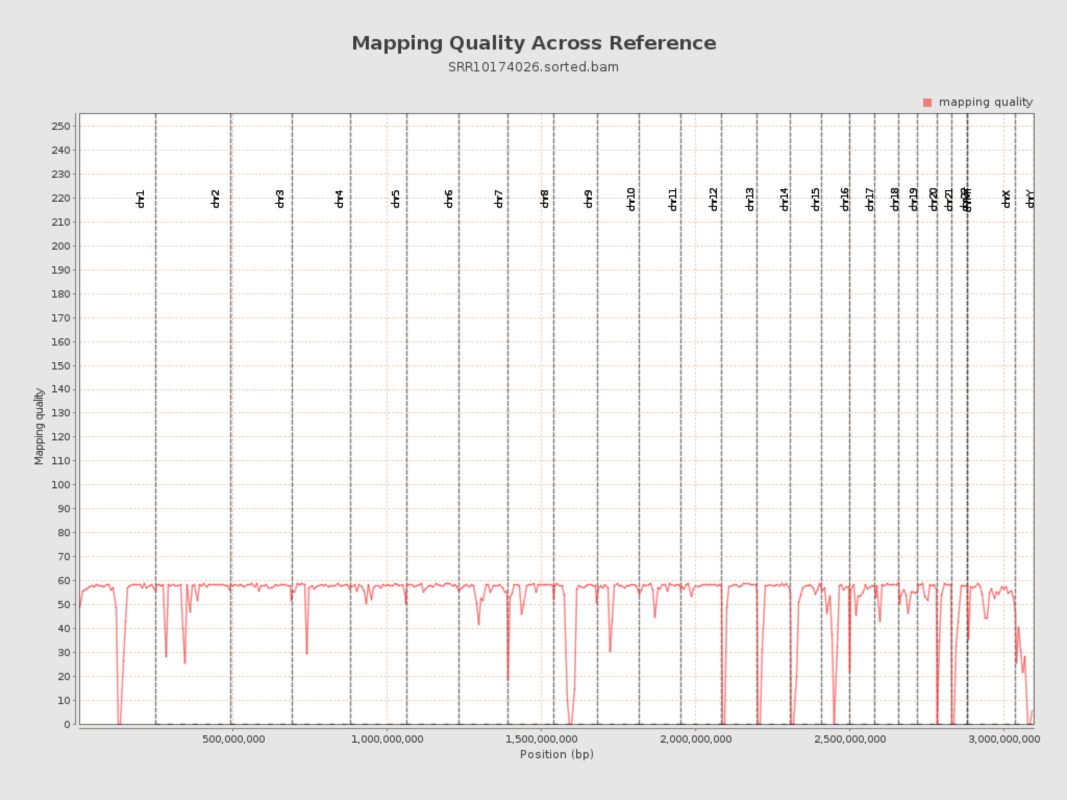
10. Results : Mapped Reads Clipping Profile



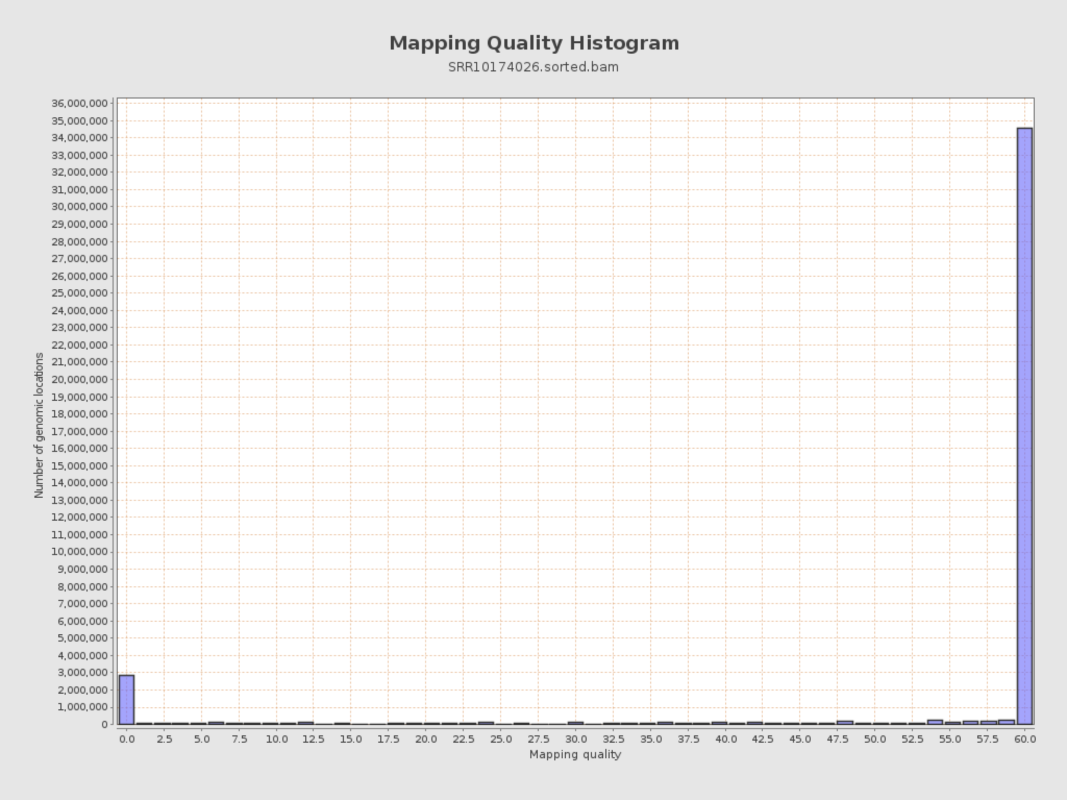
11. Results : Homopolymer Indels



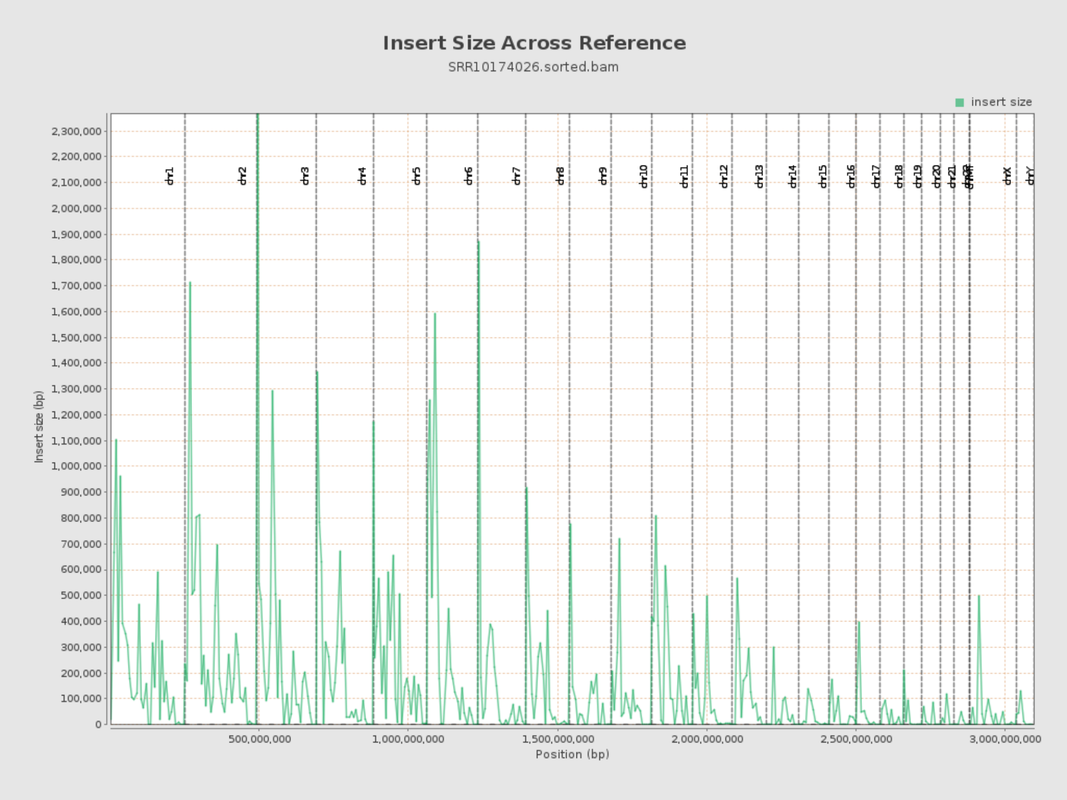
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram