

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:58:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173866.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_SRR10173866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173866_1.fastq.gz SRR10173866_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:58:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,549,252
Mapped reads	1,509,291 / 97.42%
Unmapped reads	39,961 / 2.58%
Mapped paired reads	1,509,291 / 97.42%
Mapped reads, first in pair	755,497 / 48.77%
Mapped reads, second in pair	753,794 / 48.66%
Mapped reads, both in pair	1,484,254 / 95.8%
Mapped reads, singletons	25,037 / 1.62%
Secondary alignments	0
Supplementary alignments	145,022 / 9.36%
Read min/max/mean length	30 / 133 / 127.83
Duplicated reads (estimated)	1,134,135 / 73.21%
Duplication rate	62.96%
Clipped reads	587,659 / 37.93%

2.2. ACGT Content

Number/percentage of A's	53,895,109 / 30.24%
Number/percentage of C's	34,735,100 / 19.49%
Number/percentage of T's	53,644,289 / 30.1%
Number/percentage of G's	35,968,026 / 20.18%
Number/percentage of N's	2,473 / 0%

GC Percentage	39.67%
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2.3. Coverage

Mean	0.0576
Standard Deviation	1.0053

2.4. Mapping Quality

Mean Mapping Quality	52.92
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2.5. Insert size

Mean	1,070,245.62
Standard Deviation	9,316,084.23
P25/Median/P75	144 / 202 / 288

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	1,864,741
Insertions	21,047
Mapped reads with at least one insertion	1.35%
Deletions	39,149
Mapped reads with at least one deletion	2.53%
Homopolymer indels	43.08%

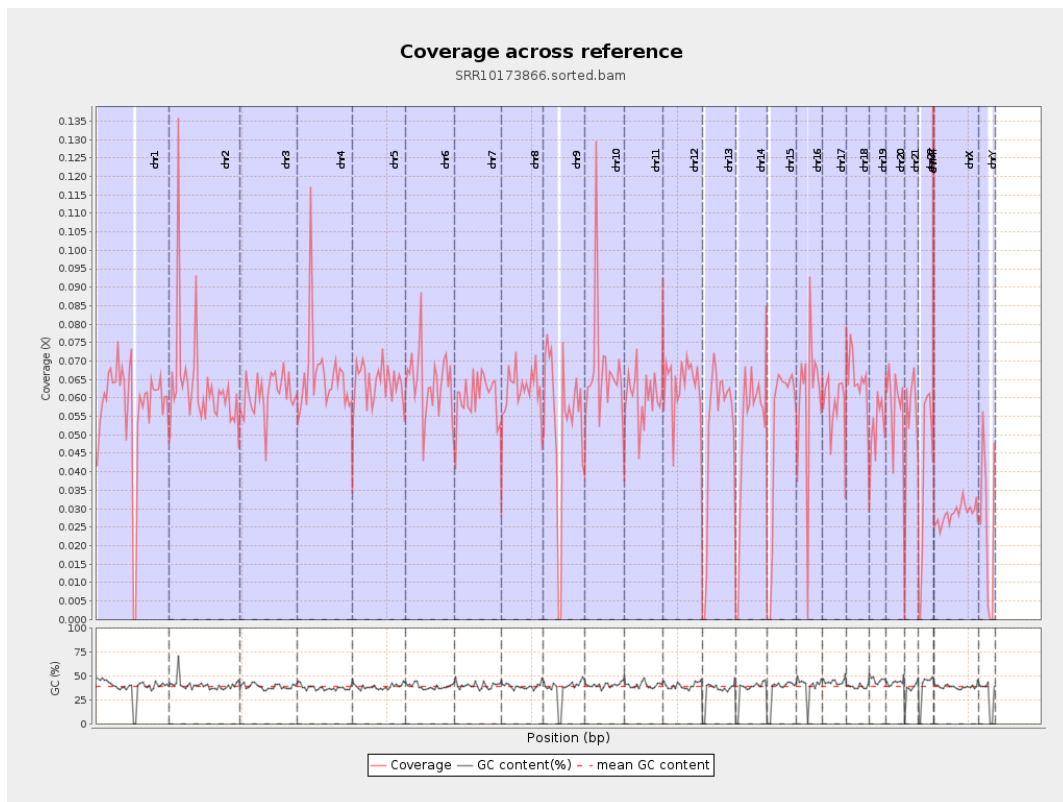
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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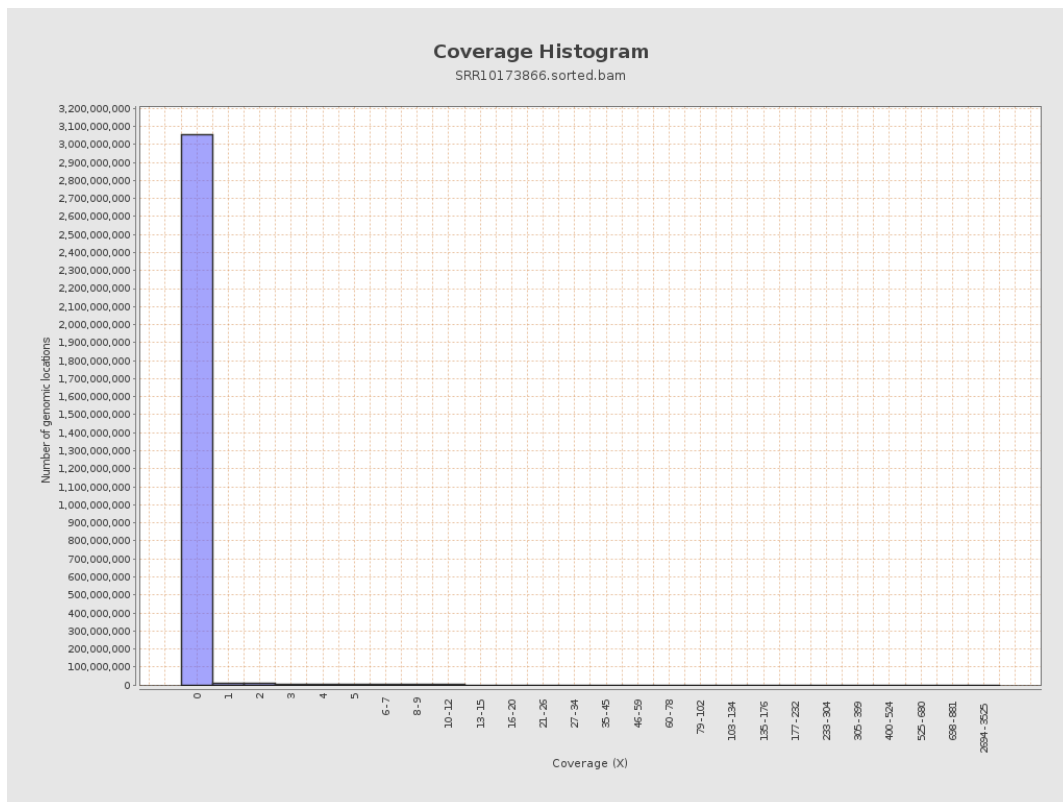
		bases	coverage	deviation
chr1	249250621	14322697	0.0575	0.7811
chr2	243199373	15404604	0.0633	2.5401
chr3	198022430	12080563	0.061	0.6842
chr4	191154276	12563898	0.0657	0.8276
chr5	180915260	11582324	0.064	0.7087
chr6	171115067	10964354	0.0641	0.7506
chr7	159138663	9635359	0.0605	0.7486
chr8	146364022	9133014	0.0624	0.8205
chr9	141213431	7688019	0.0544	0.836
chr10	135534747	9125155	0.0673	0.9351
chr11	135006516	8124440	0.0602	0.6868
chr12	133851895	8486020	0.0634	0.7067
chr13	115169878	5827511	0.0506	0.6267
chr14	107349540	5399991	0.0503	0.6239
chr15	102531392	5249463	0.0512	0.6233
chr16	90354753	5415388	0.0599	0.7462
chr17	81195210	4665873	0.0575	0.6895
chr18	78077248	5141908	0.0659	1.0558
chr19	59128983	3112265	0.0526	0.689
chr20	63025520	3682449	0.0584	0.6926
chr21	48129895	2536162	0.0527	0.7314
chr22	51304566	2027385	0.0395	0.5431
chrMT	16571	243676	14.705	14.2359
chrX	155270560	4462368	0.0287	0.4677

chrY	59373566	1465850	0.0247	0.5485
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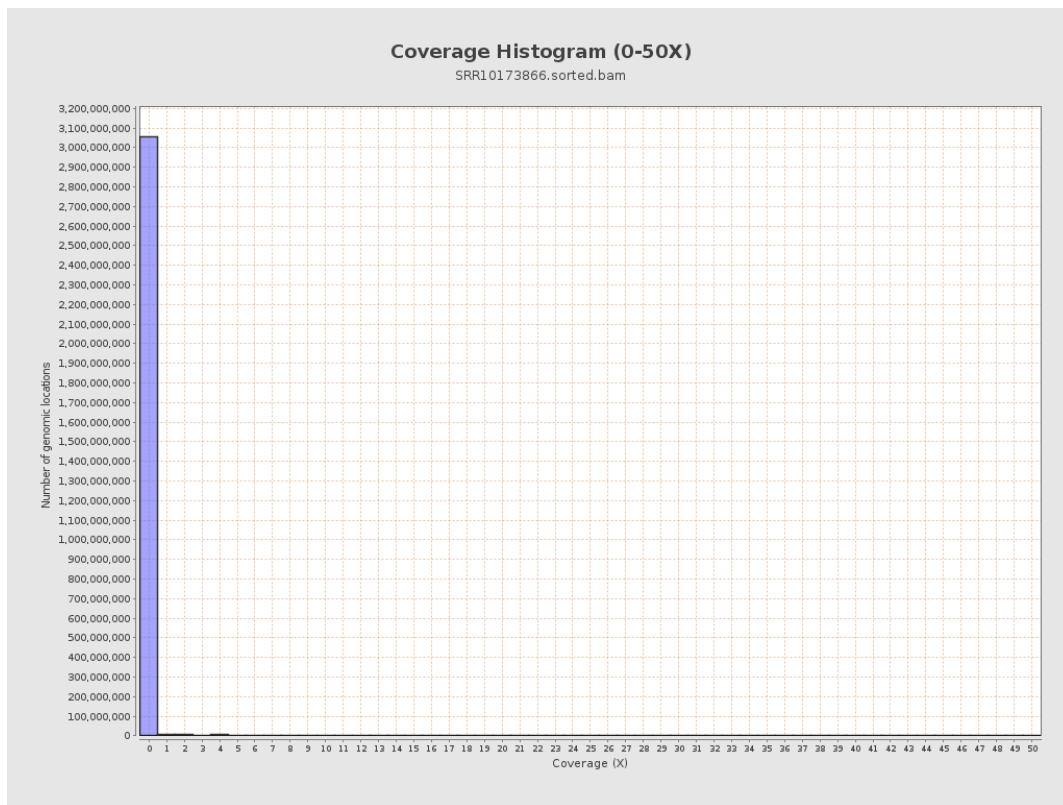
3. Results : Coverage across reference



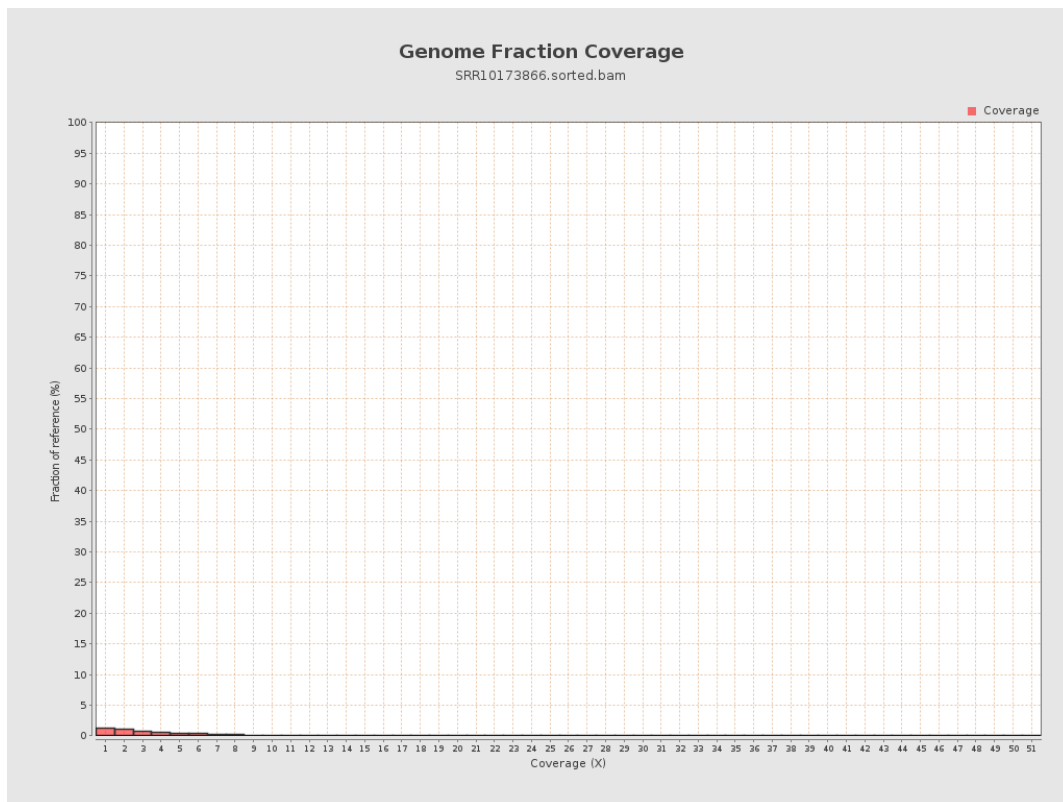
4. Results : Coverage Histogram



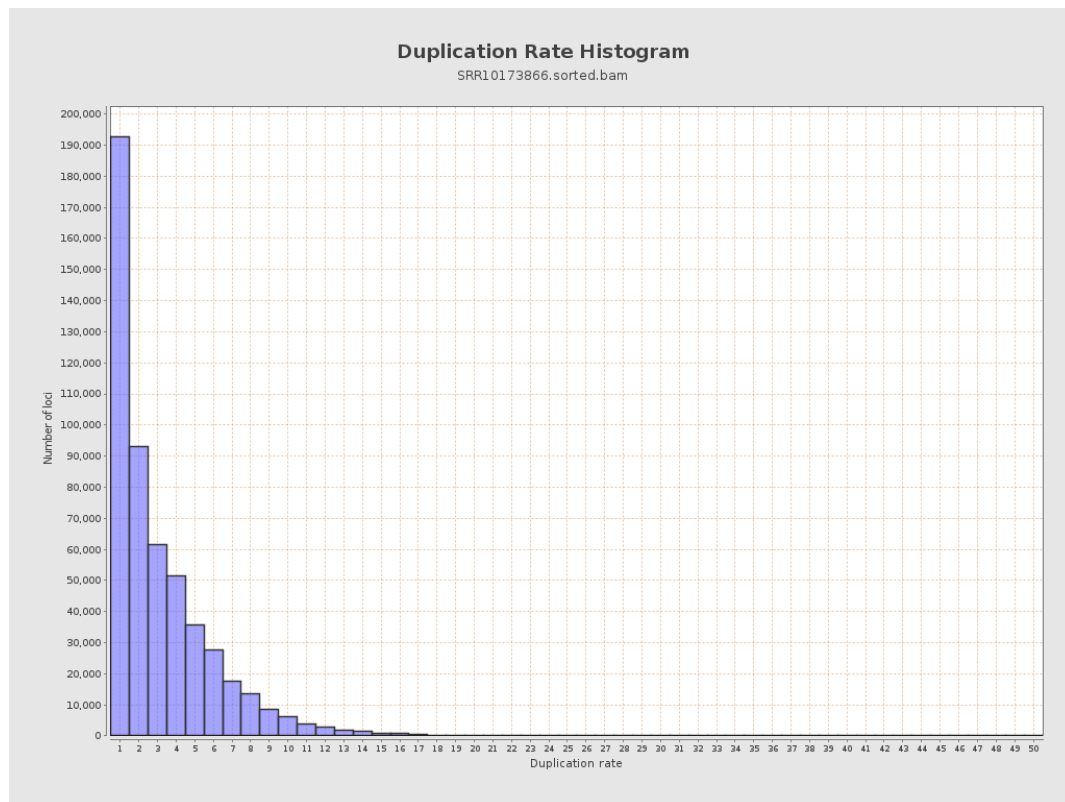
5. Results : Coverage Histogram (0-50X)



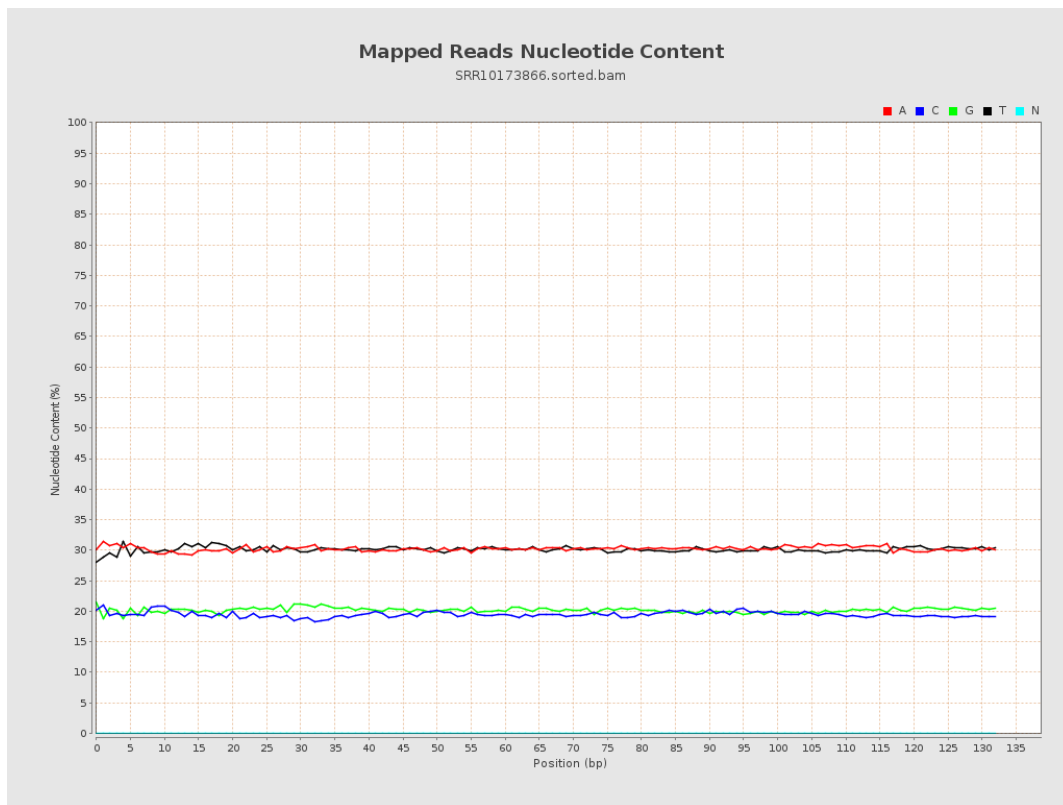
6. Results : Genome Fraction Coverage



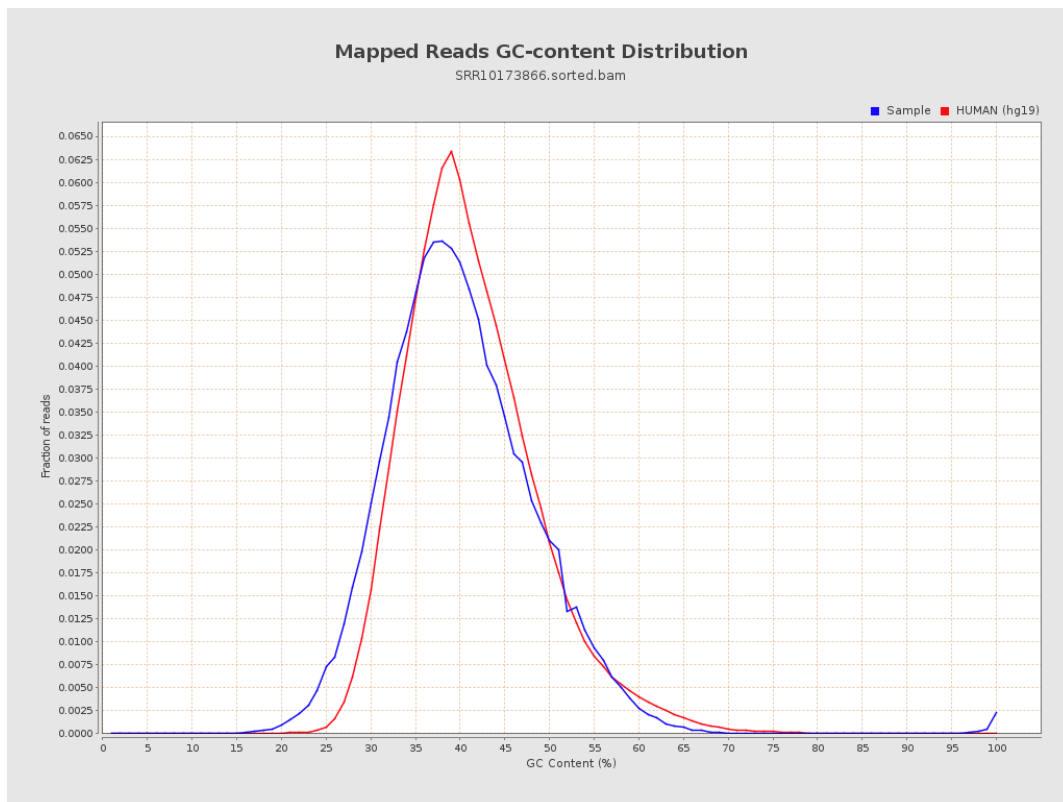
7. Results : Duplication Rate Histogram



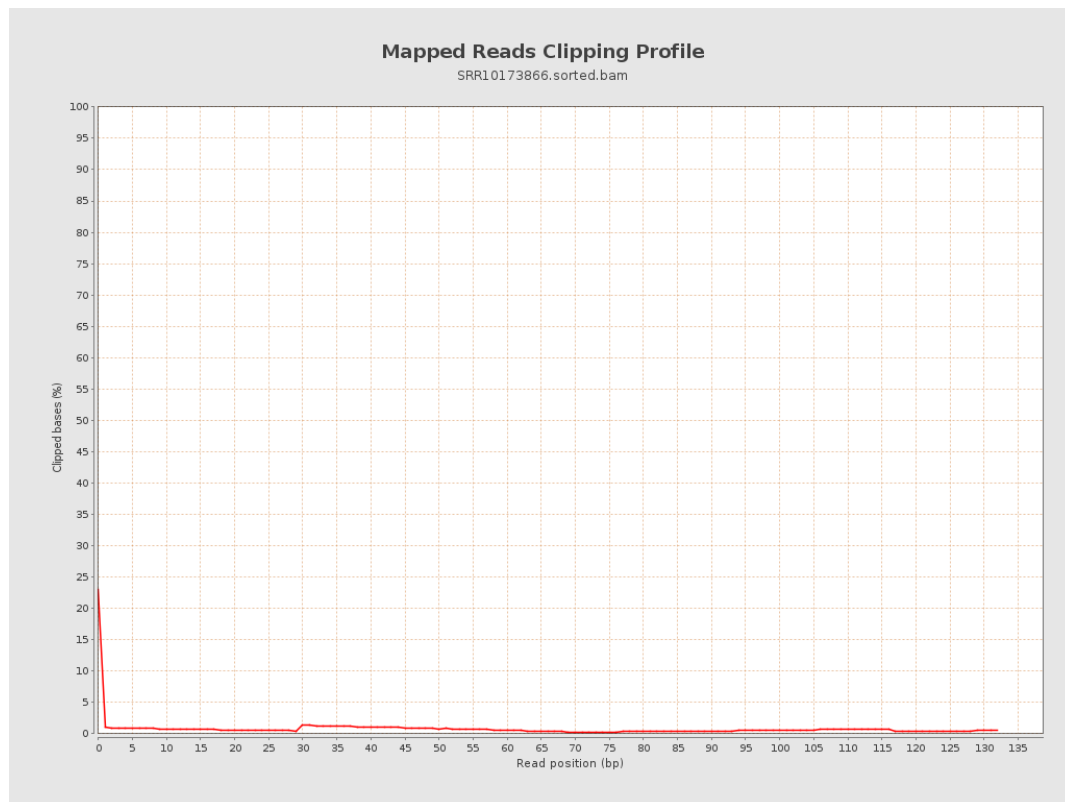
8. Results : Mapped Reads Nucleotide Content



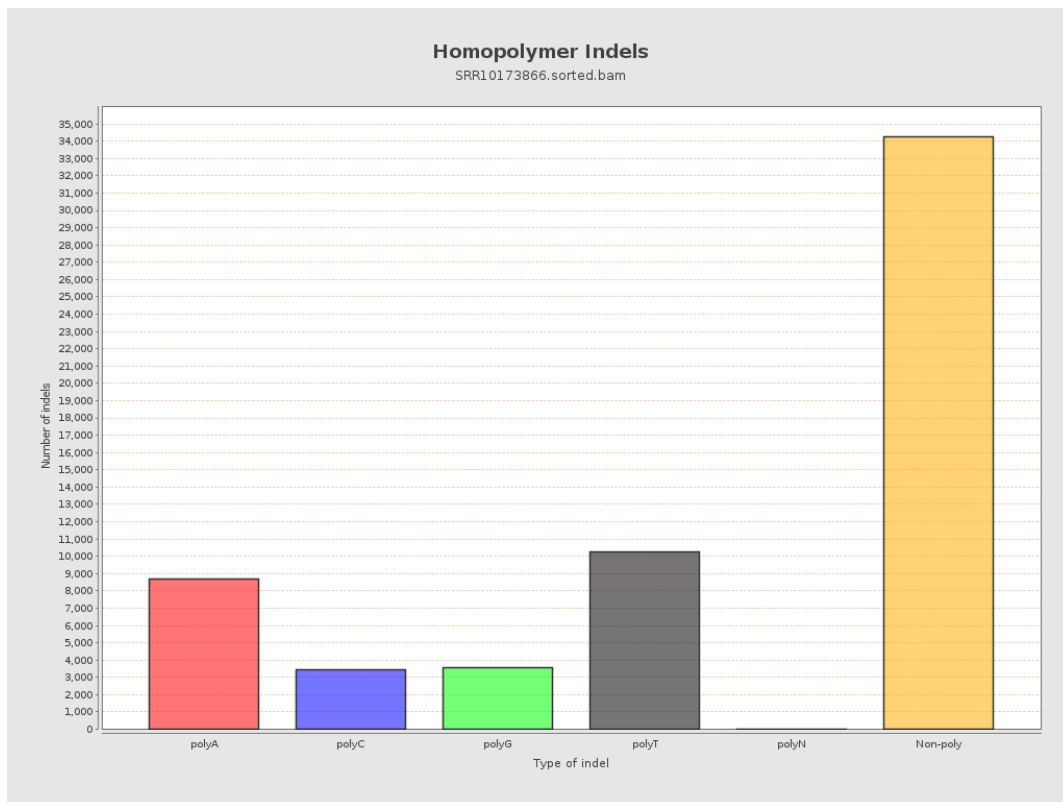
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



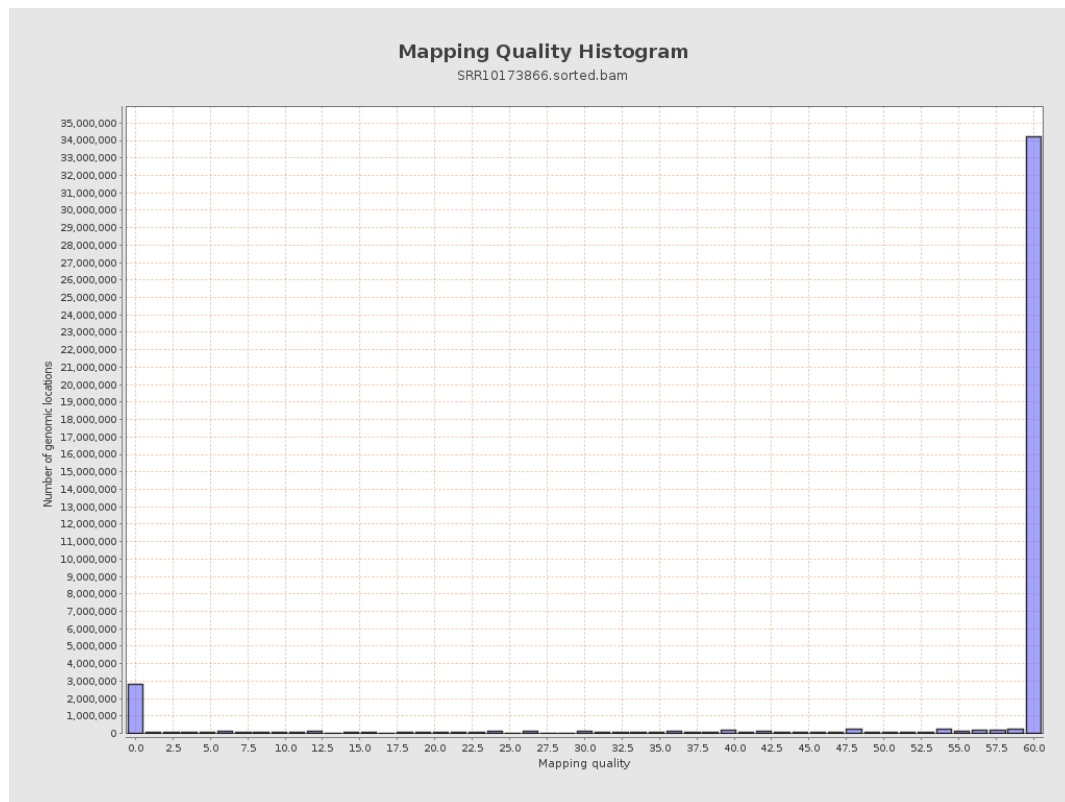
11. Results : Homopolymer Indels



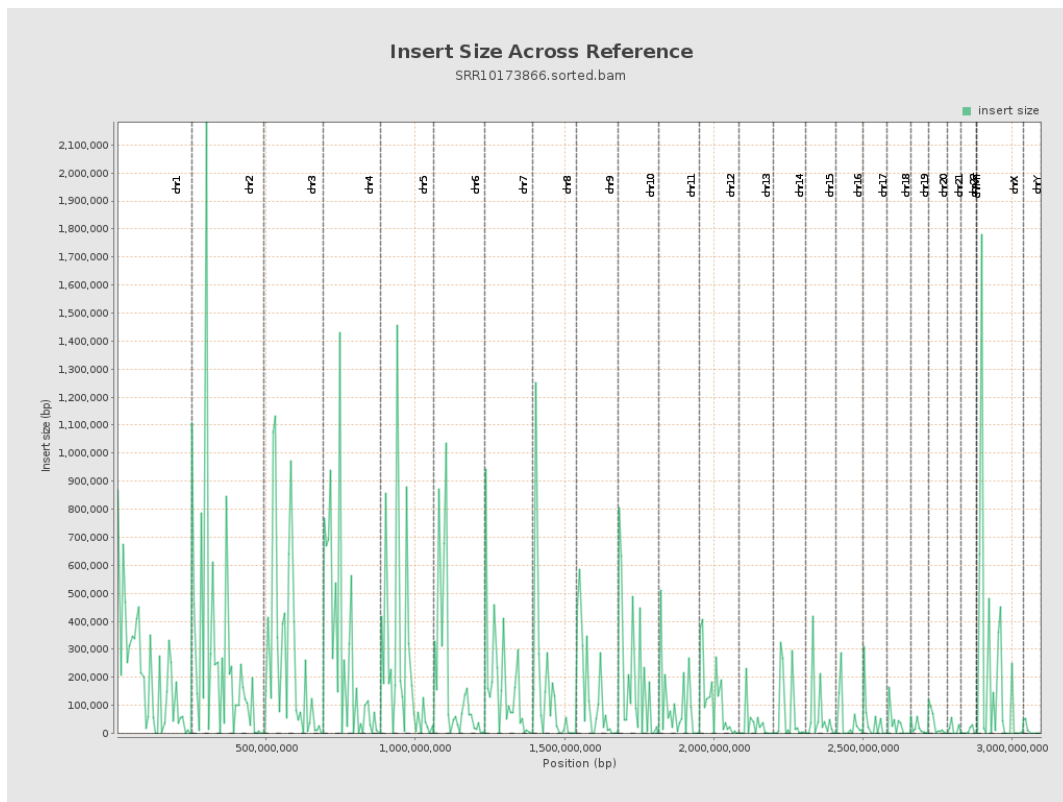
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

