

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:34:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173982.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_SRR10173982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173982_1.fastq.gz SRR10173982_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:34:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,231,920
Mapped reads	3,156,585 / 97.67%
Unmapped reads	75,335 / 2.33%
Mapped paired reads	3,156,585 / 97.67%
Mapped reads, first in pair	1,579,785 / 48.88%
Mapped reads, second in pair	1,576,800 / 48.79%
Mapped reads, both in pair	3,109,180 / 96.2%
Mapped reads, singletons	47,405 / 1.47%
Secondary alignments	0
Supplementary alignments	399,827 / 12.37%
Read min/max/mean length	30 / 133 / 125.61
Duplicated reads (estimated)	2,500,392 / 77.37%
Duplication rate	64.45%
Clipped reads	1,691,913 / 52.35%

2.2. ACGT Content

Number/percentage of A's	106,172,190 / 29.83%
Number/percentage of C's	70,837,447 / 19.9%
Number/percentage of T's	105,273,199 / 29.58%
Number/percentage of G's	73,610,898 / 20.68%
Number/percentage of N's	2,575 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.115
Standard Deviation	2.0802

2.4. Mapping Quality

Mean Mapping Quality	52.55
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2.5. Insert size

Mean	1,078,329.77
Standard Deviation	9,772,994.14
P25/Median/P75	107 / 158 / 243

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,086,449
Insertions	39,954
Mapped reads with at least one insertion	1.22%
Deletions	100,495
Mapped reads with at least one deletion	3.1%
Homopolymer indels	40.89%

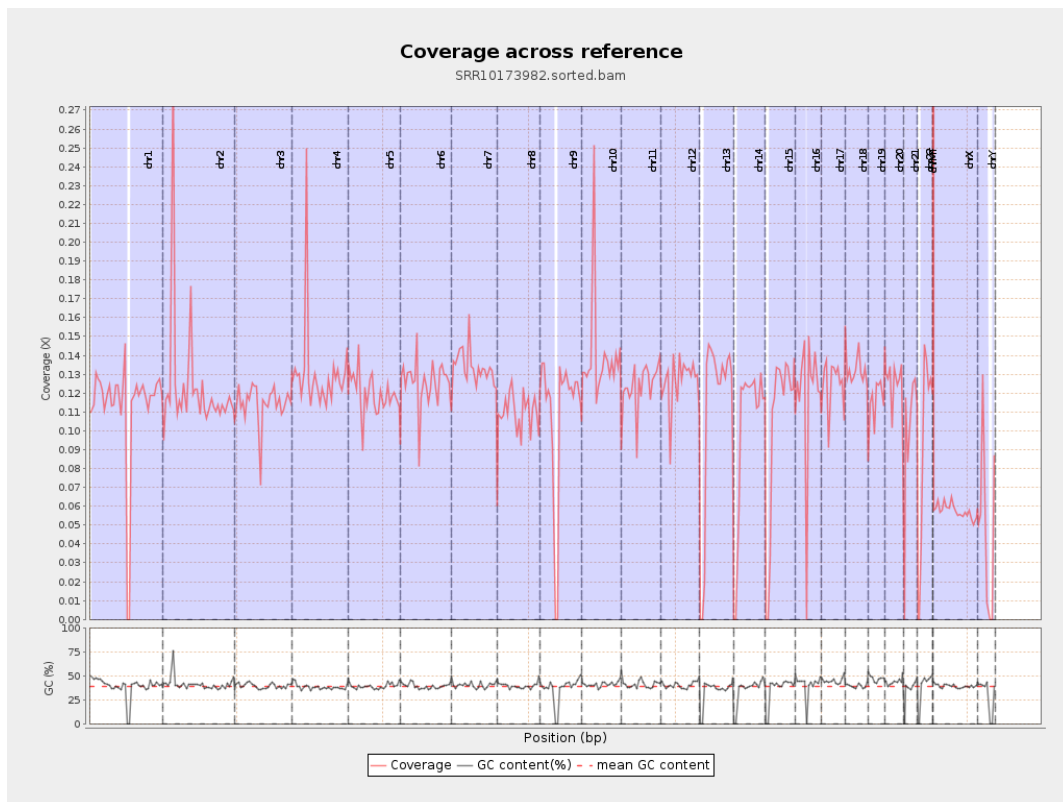
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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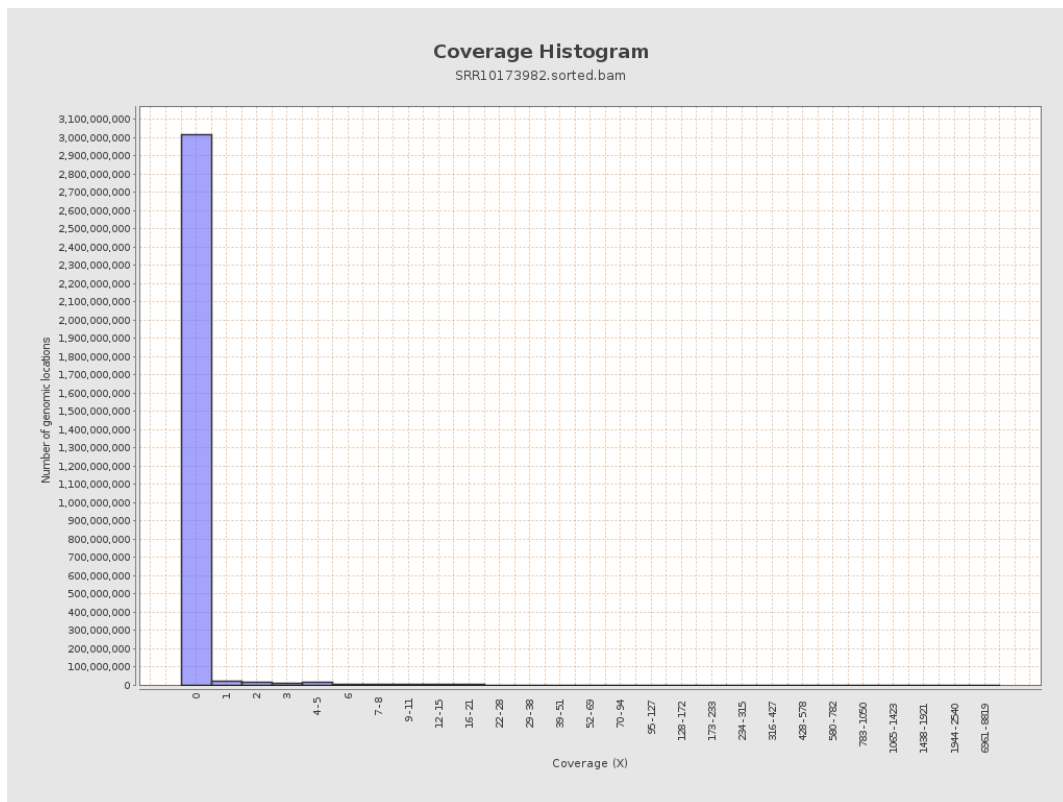
		bases	coverage	deviation
chr1	249250621	28203641	0.1132	1.2955
chr2	243199373	29904292	0.123	6.2215
chr3	198022430	22621493	0.1142	0.9984
chr4	191154276	24948648	0.1305	1.3756
chr5	180915260	21548350	0.1191	1.0186
chr6	171115067	21494337	0.1256	1.1596
chr7	159138663	21217260	0.1333	1.4178
chr8	146364022	16077308	0.1098	1.4569
chr9	141213431	15436222	0.1093	1.223
chr10	135534747	18794510	0.1387	1.5178
chr11	135006516	16677161	0.1235	1.0668
chr12	133851895	16945616	0.1266	1.0707
chr13	115169878	12844585	0.1115	1.0057
chr14	107349540	10956726	0.1021	0.9384
chr15	102531392	10379236	0.1012	0.9476
chr16	90354753	10714385	0.1186	1.1228
chr17	81195210	10182898	0.1254	1.0756
chr18	78077248	10316114	0.1321	1.58
chr19	59128983	6913500	0.1169	1.1053
chr20	63025520	7891292	0.1252	1.0842
chr21	48129895	4938074	0.1026	1.1131
chr22	51304566	4701088	0.0916	1.0224
chrMT	16571	530623	32.0212	25.9802
chrX	155270560	8951115	0.0576	0.696

chrY	59373566	2948621	0.0497	0.9701
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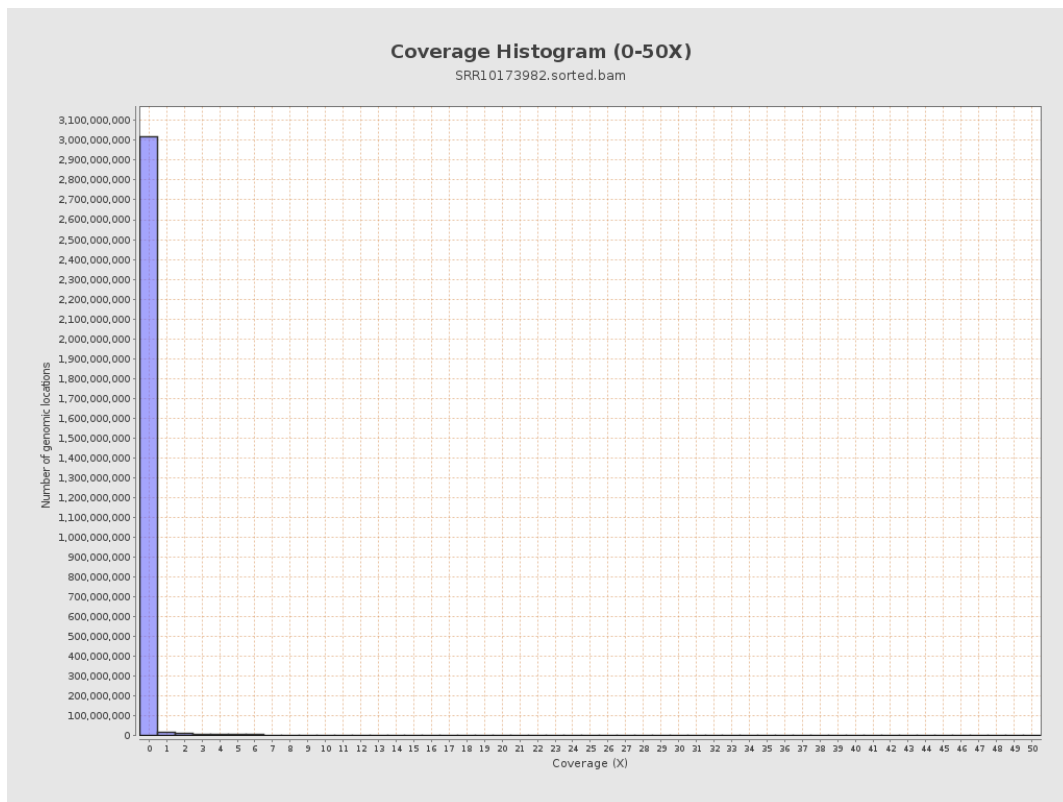
3. Results : Coverage across reference



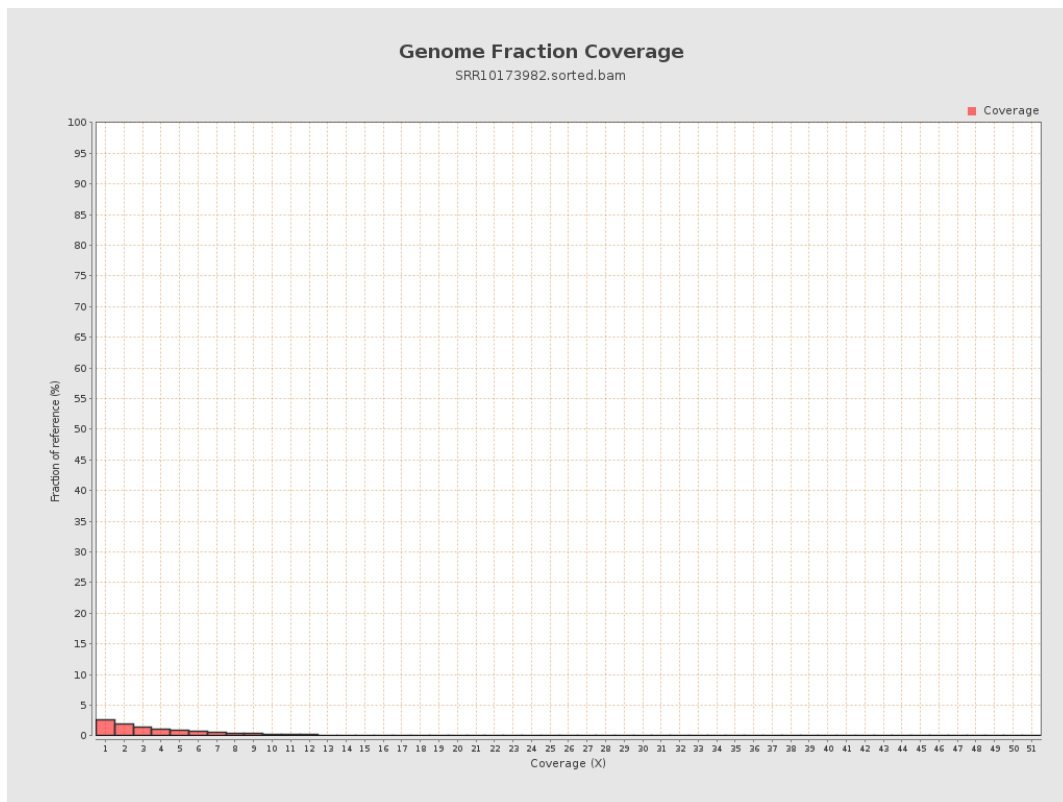
4. Results : Coverage Histogram



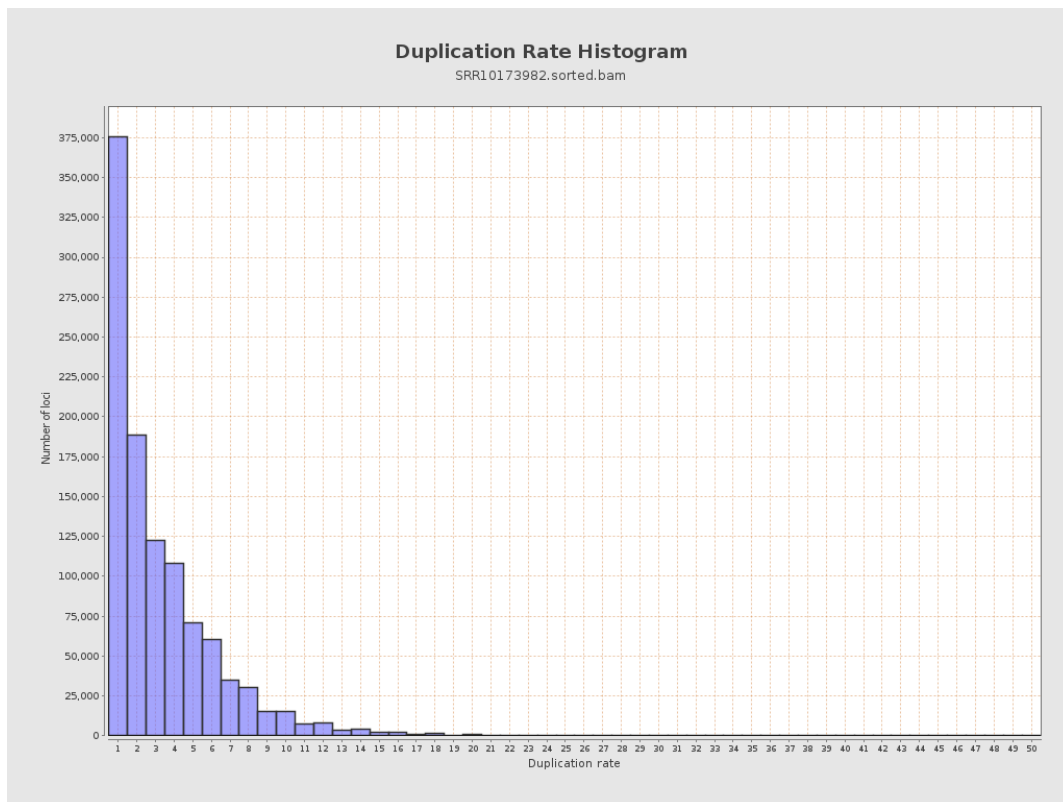
5. Results : Coverage Histogram (0-50X)



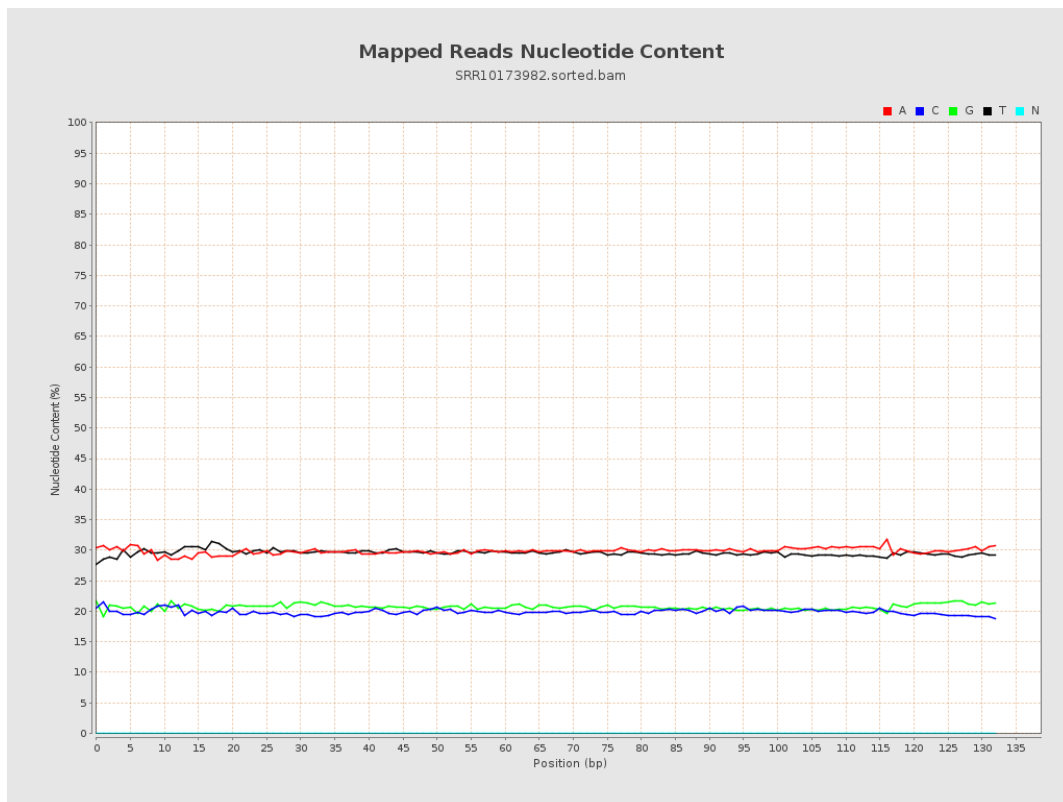
6. Results : Genome Fraction Coverage



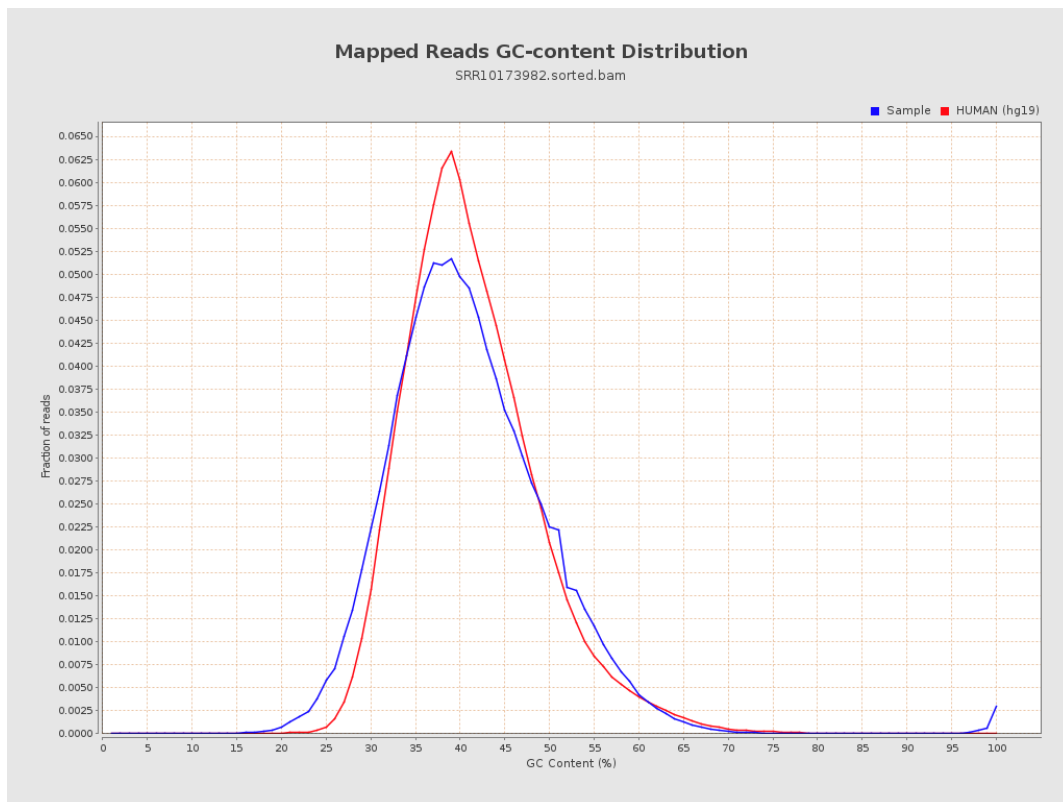
7. Results : Duplication Rate Histogram



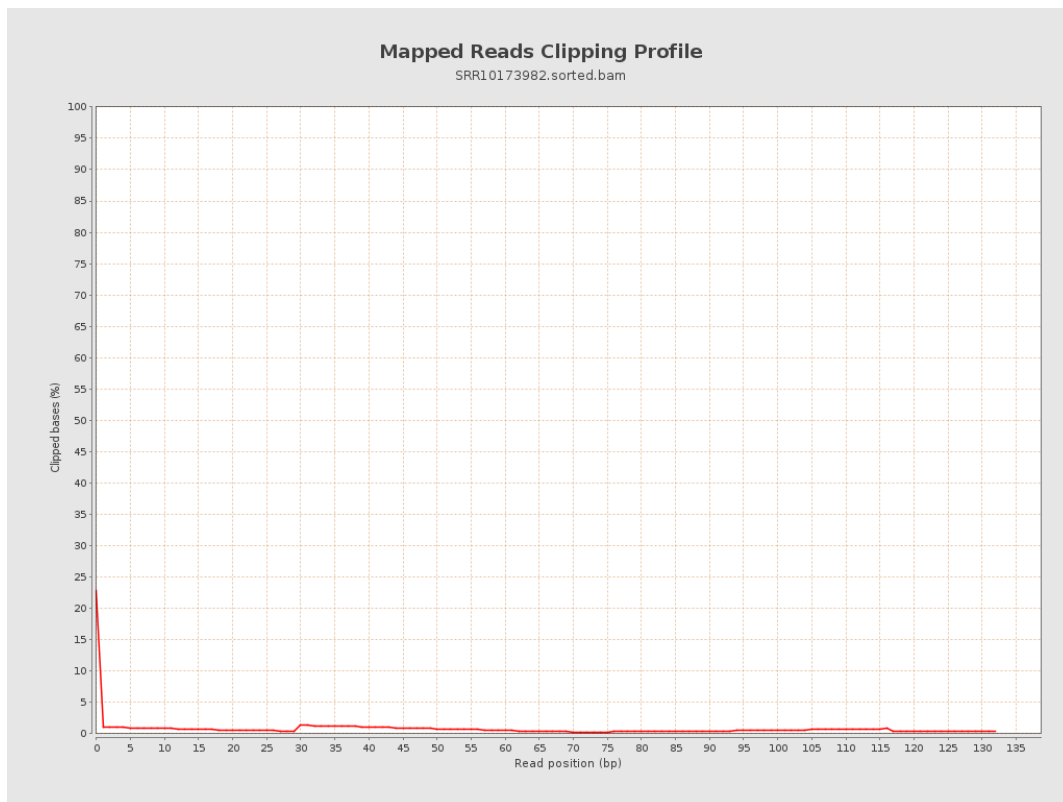
8. Results : Mapped Reads Nucleotide Content



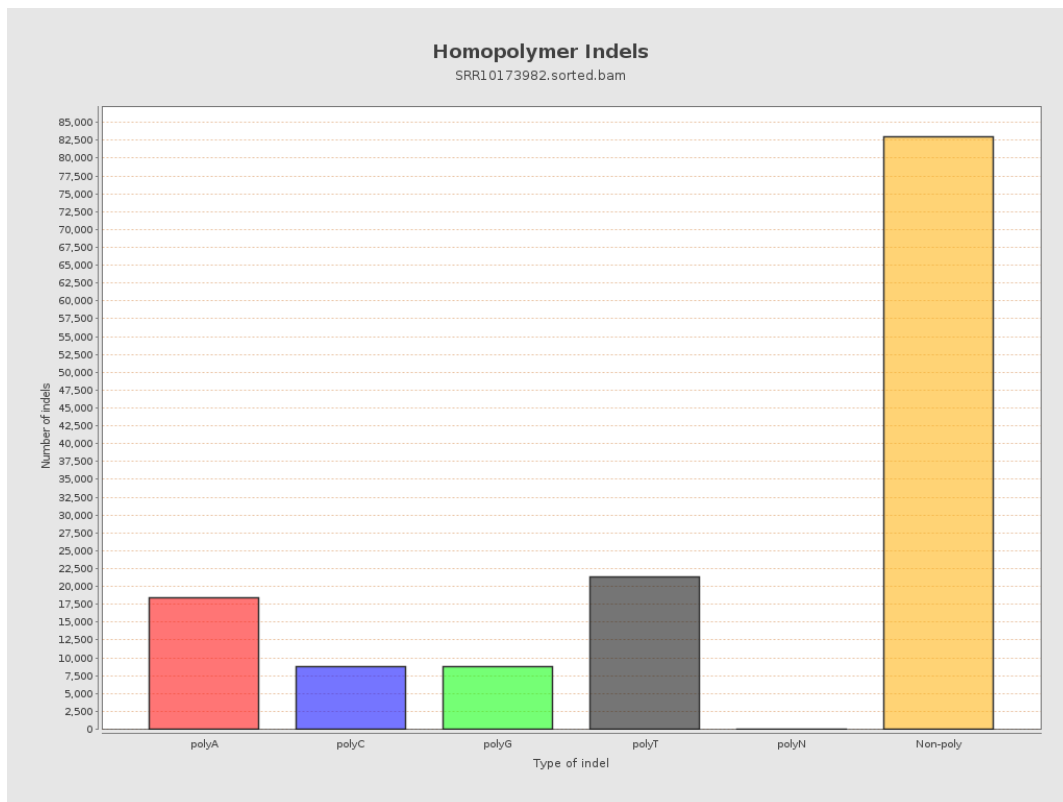
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



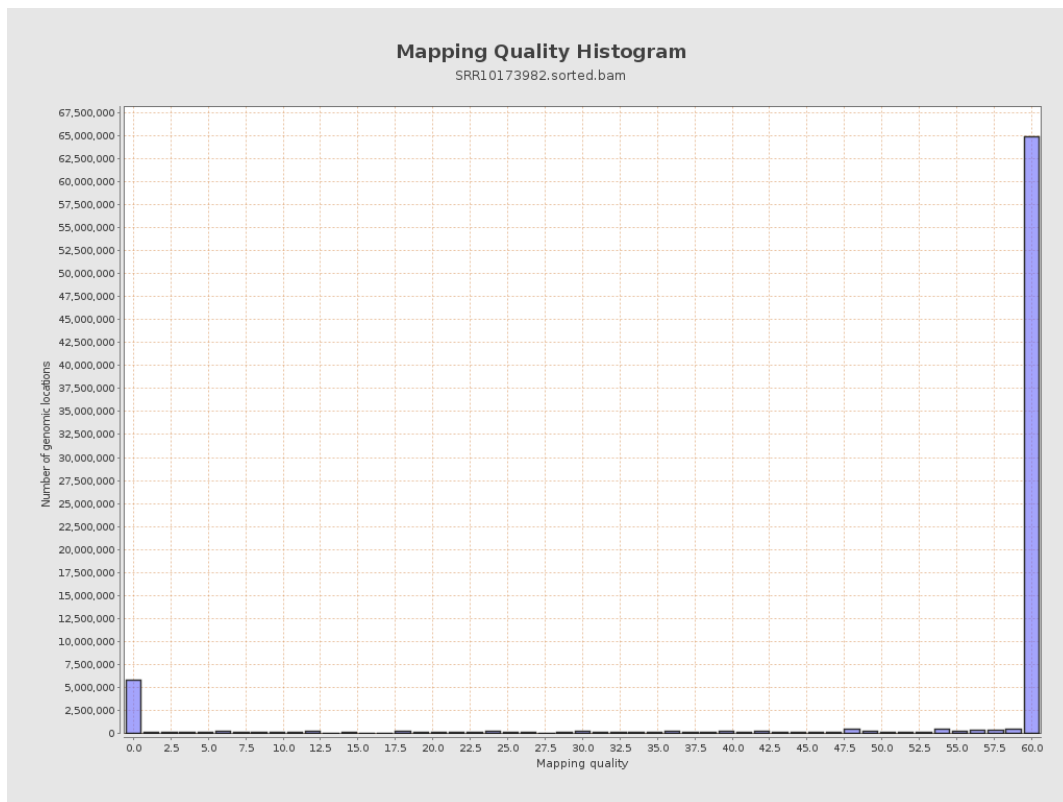
11. Results : Homopolymer Indels



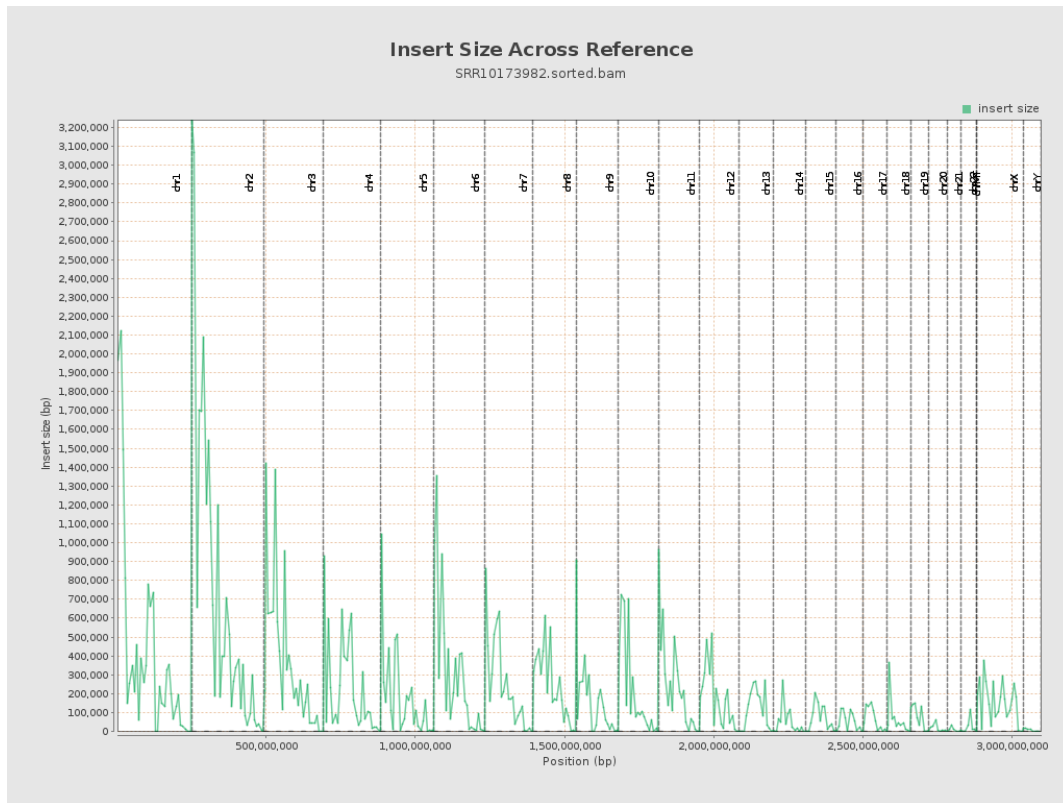
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

