

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:09:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173878.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_SRR10173878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173878_1.fastq.gz SRR10173878_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:09:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,857,730
Mapped reads	1,818,510 / 97.89%
Unmapped reads	39,220 / 2.11%
Mapped paired reads	1,818,510 / 97.89%
Mapped reads, first in pair	907,669 / 48.86%
Mapped reads, second in pair	910,841 / 49.03%
Mapped reads, both in pair	1,793,680 / 96.55%
Mapped reads, singletons	24,830 / 1.34%
Secondary alignments	0
Supplementary alignments	197,641 / 10.64%
Read min/max/mean length	30 / 133 / 128.42
Duplicated reads (estimated)	1,426,003 / 76.76%
Duplication rate	64.58%
Clipped reads	726,409 / 39.1%

2.2. ACGT Content

Number/percentage of A's	65,534,748 / 30.33%
Number/percentage of C's	41,929,385 / 19.41%
Number/percentage of T's	65,366,733 / 30.25%
Number/percentage of G's	43,231,466 / 20.01%
Number/percentage of N's	2,573 / 0%

GC Percentage	39.41%
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2.3. Coverage

Mean	0.0698
Standard Deviation	1.1772

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	848,737.53
Standard Deviation	8,507,841.69
P25/Median/P75	142 / 199 / 287

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	2,128,661
Insertions	23,567
Mapped reads with at least one insertion	1.25%
Deletions	40,618
Mapped reads with at least one deletion	2.16%
Homopolymer indels	45.17%

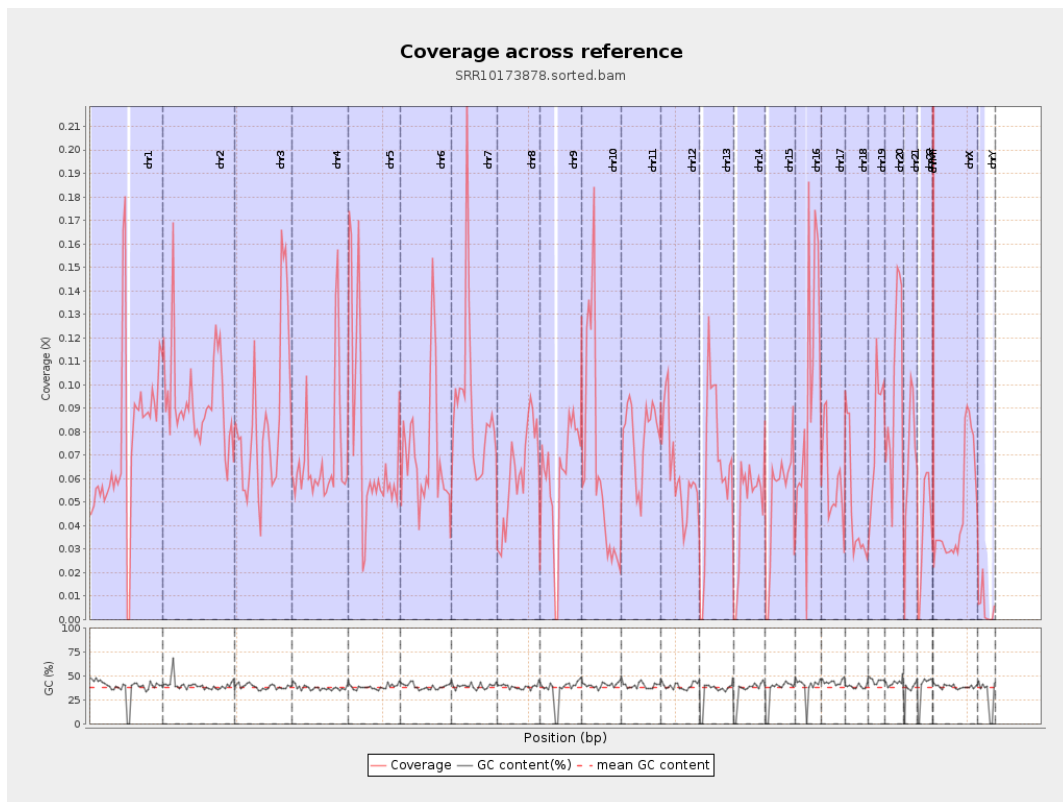
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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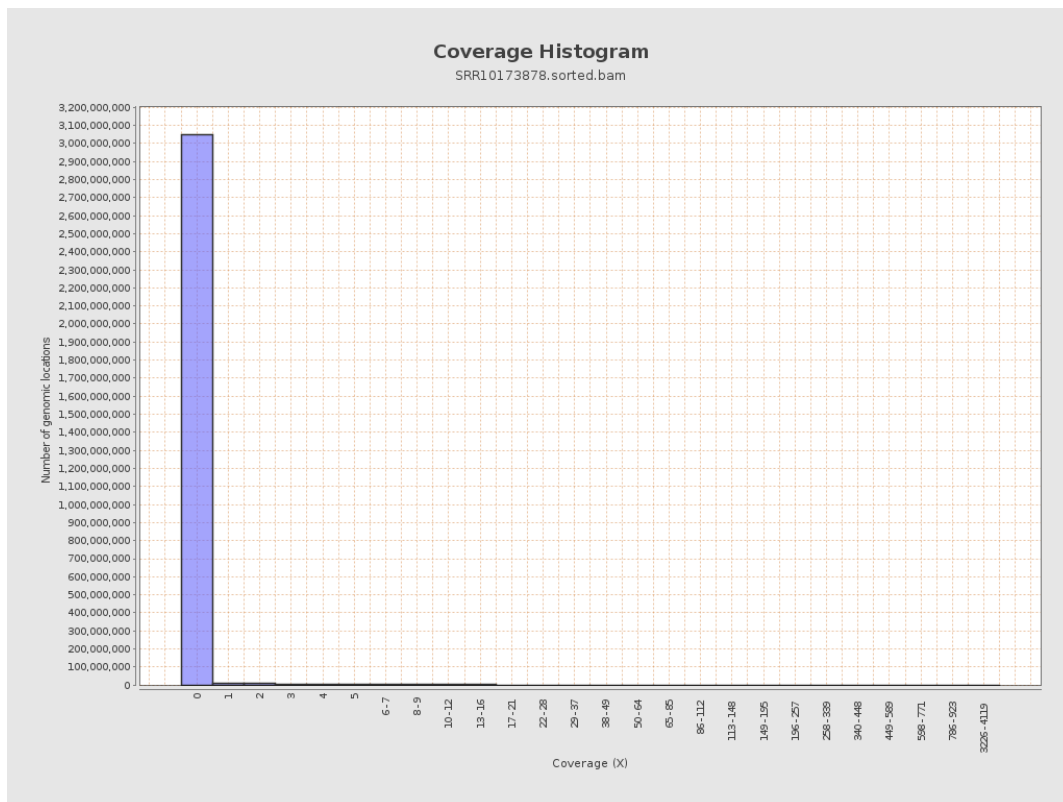
		bases	coverage	deviation
chr1	249250621	18858191	0.0757	0.9759
chr2	243199373	22617627	0.093	2.993
chr3	198022430	16656672	0.0841	0.8532
chr4	191154276	13298267	0.0696	0.8345
chr5	180915260	13670566	0.0756	0.8061
chr6	171115067	12086387	0.0706	0.7927
chr7	159138663	14256668	0.0896	1.2114
chr8	146364022	9120863	0.0623	0.8384
chr9	141213431	8855665	0.0627	0.8025
chr10	135534747	8679569	0.064	1.1579
chr11	135006516	10527237	0.078	0.8165
chr12	133851895	8472245	0.0633	0.7332
chr13	115169878	7589603	0.0659	0.7633
chr14	107349540	5143846	0.0479	0.6351
chr15	102531392	5274146	0.0514	0.6521
chr16	90354753	8417708	0.0932	1.0479
chr17	81195210	4864905	0.0599	0.7498
chr18	78077248	3628842	0.0465	0.8927
chr19	59128983	4713604	0.0797	0.993
chr20	63025520	6344092	0.1007	0.9133
chr21	48129895	3249729	0.0675	0.7763
chr22	51304566	2011183	0.0392	0.5434
chrMT	16571	376557	22.7239	21.9864
chrX	155270560	7154453	0.0461	0.6256

chrY	59373566	308037	0.0052	0.3193
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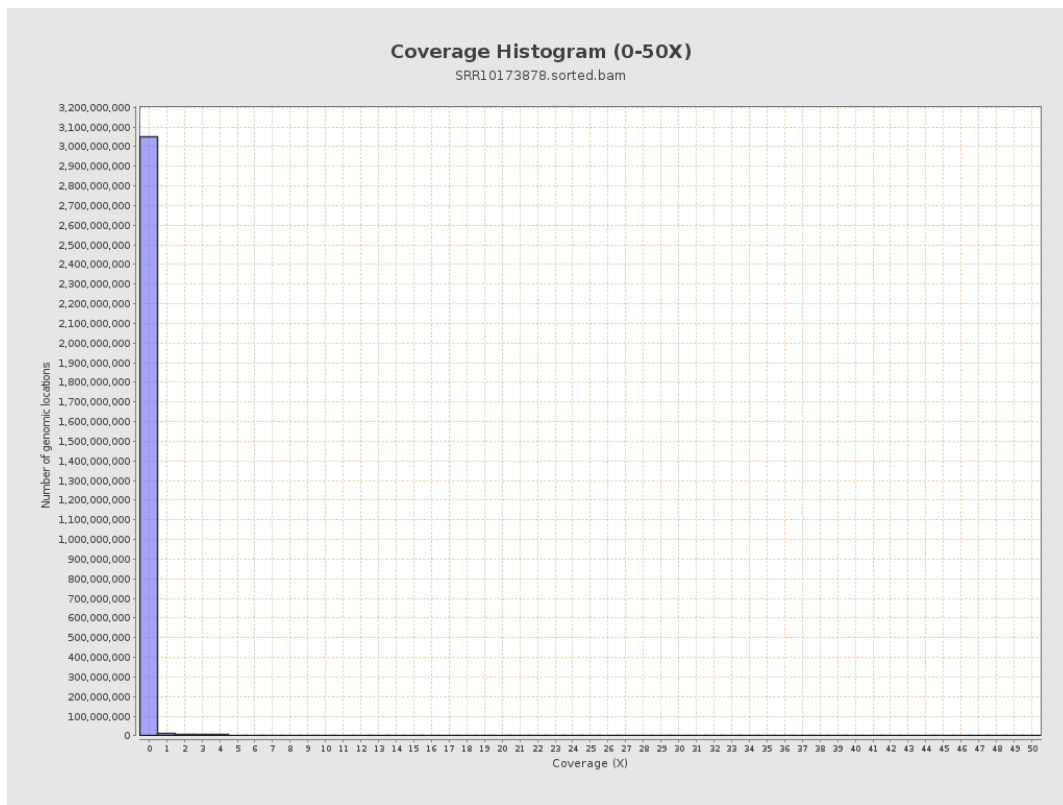
3. Results : Coverage across reference



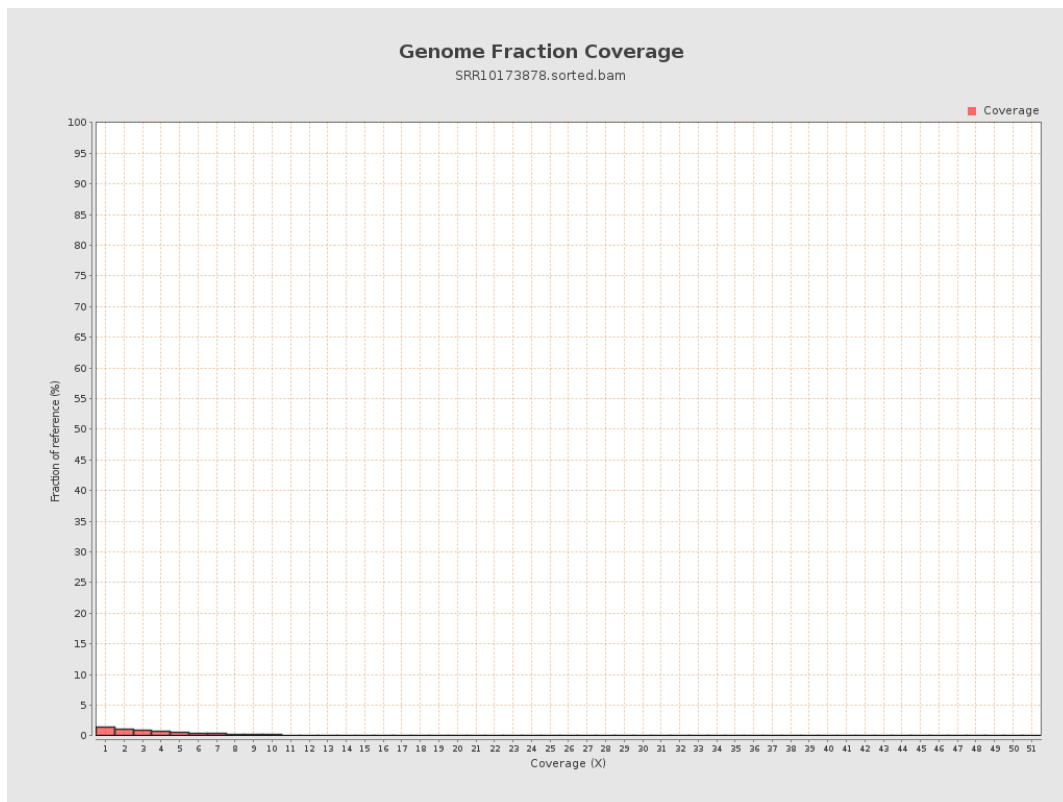
4. Results : Coverage Histogram



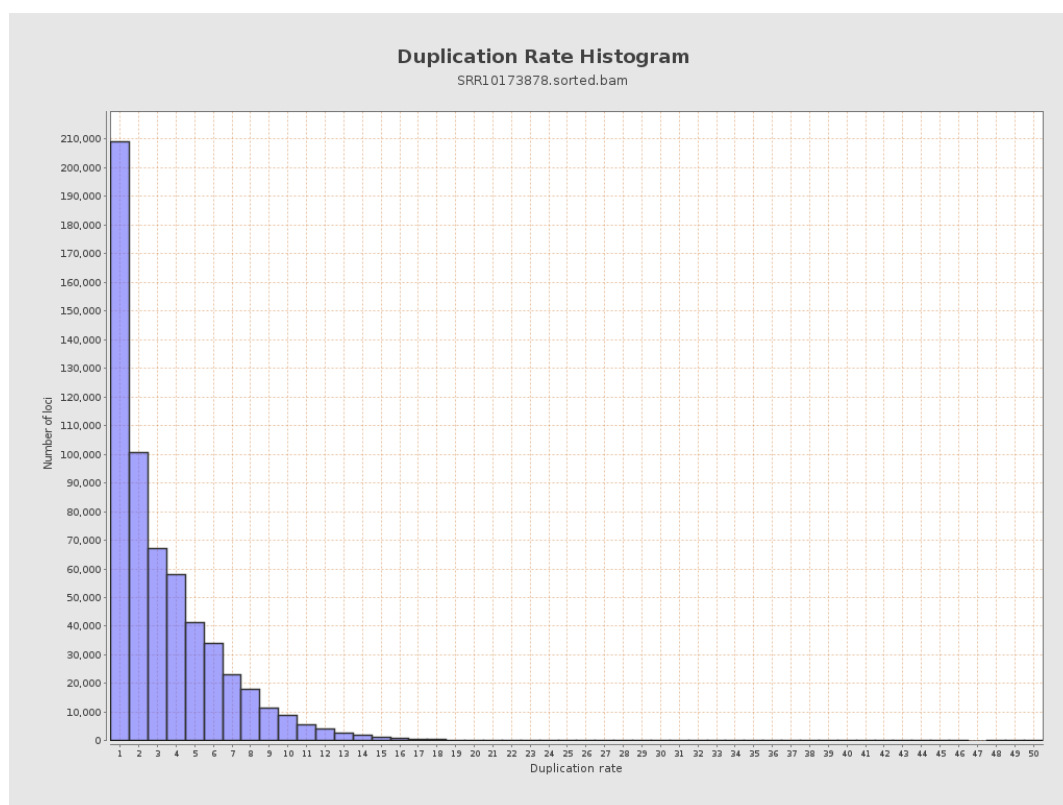
5. Results : Coverage Histogram (0-50X)



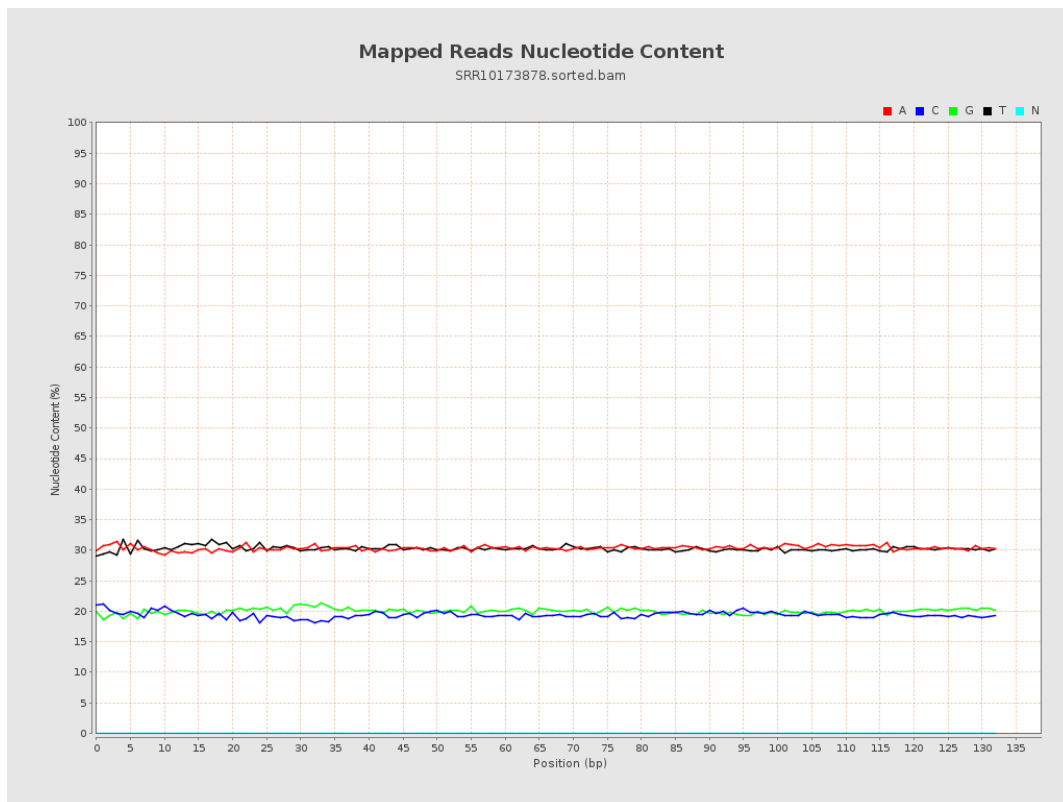
6. Results : Genome Fraction Coverage



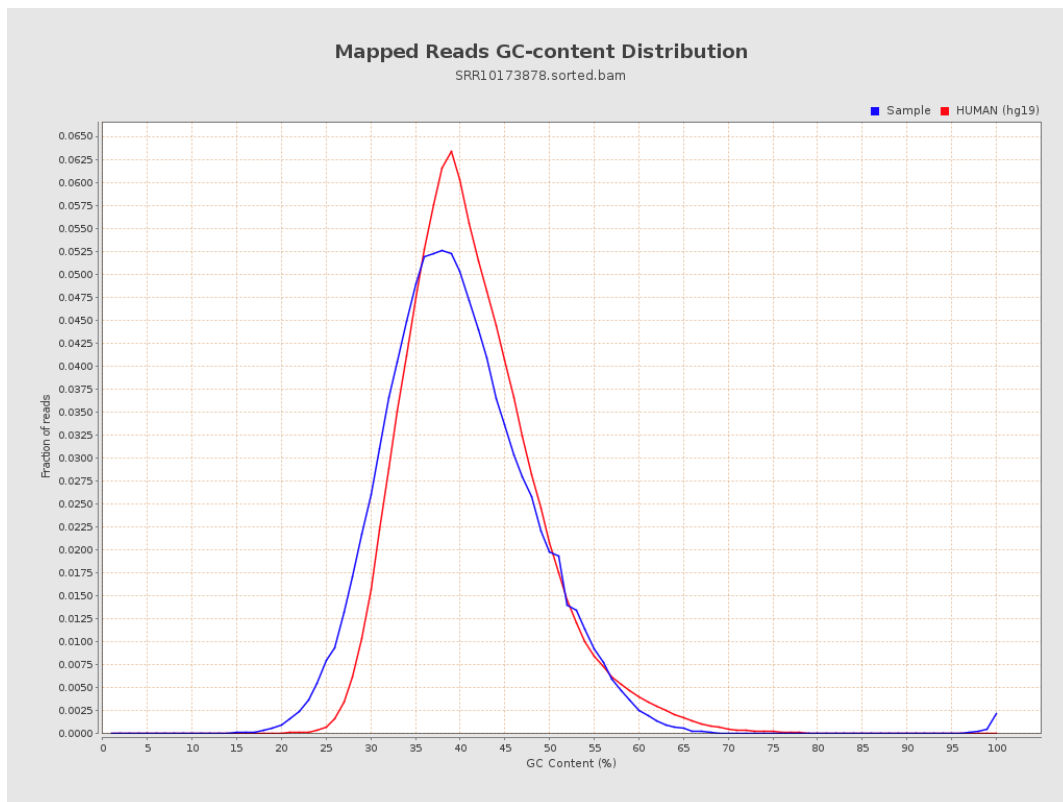
7. Results : Duplication Rate Histogram



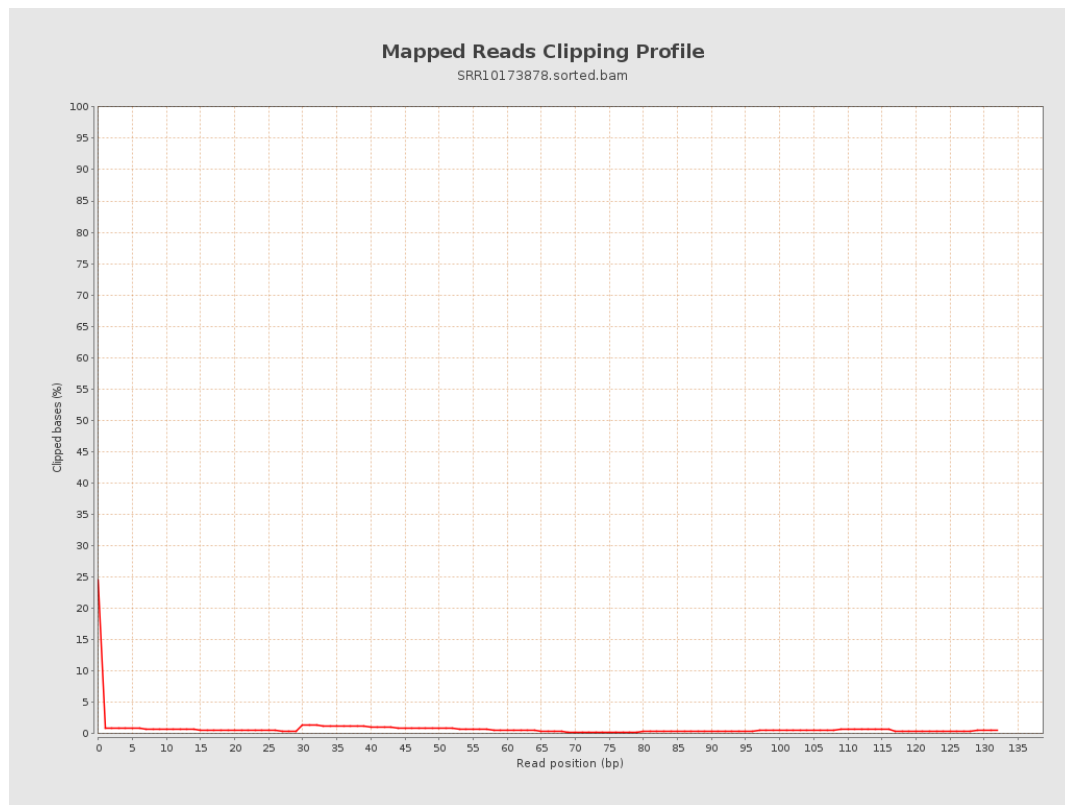
8. Results : Mapped Reads Nucleotide Content



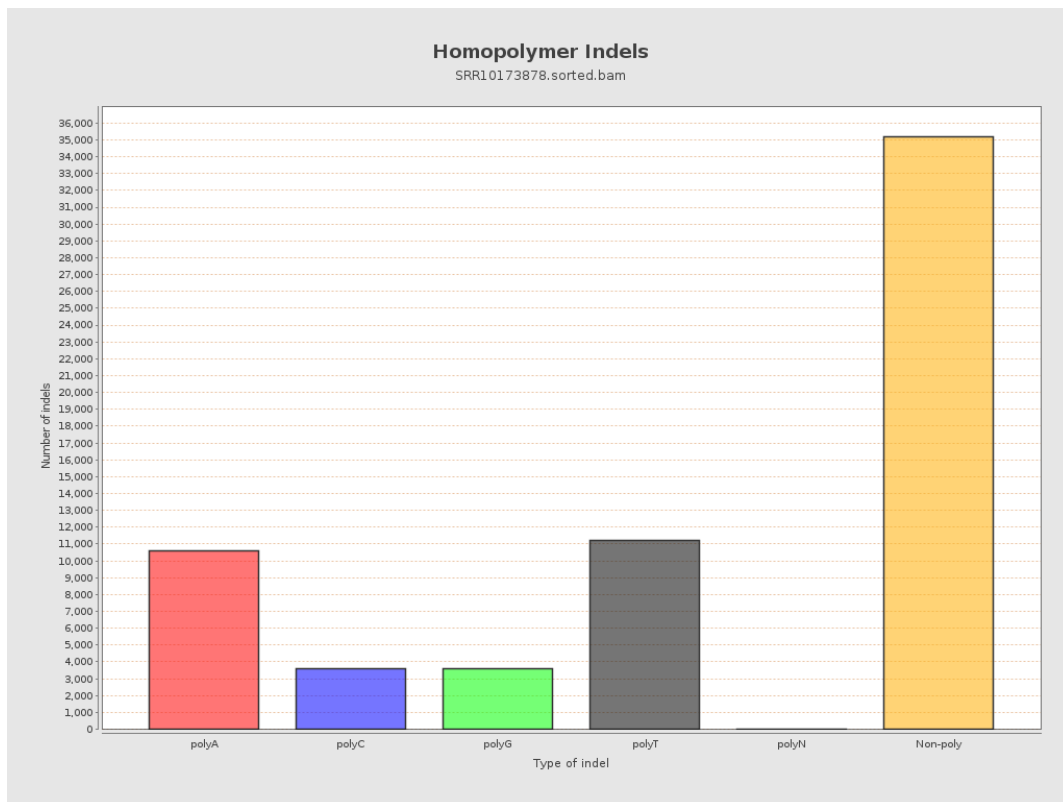
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



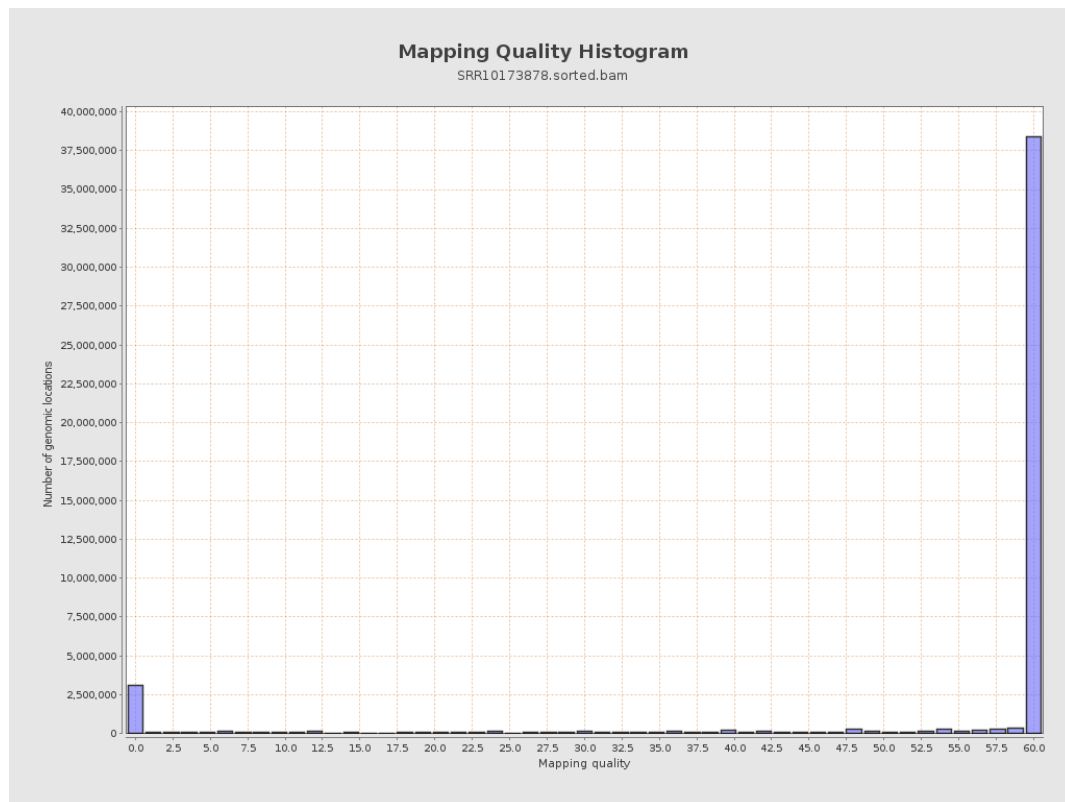
11. Results : Homopolymer Indels



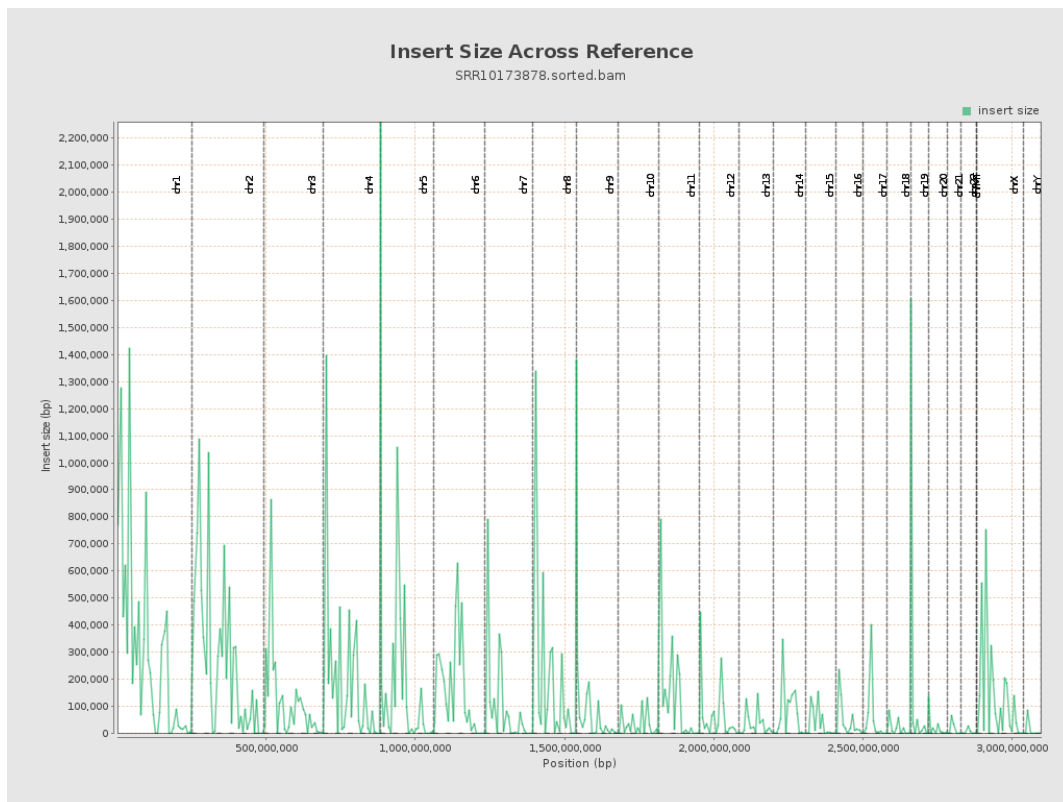
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

