

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:06:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173986.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_SRR10173986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173986_1.fastq.gz SRR10173986_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:06:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,473,178
Mapped reads	2,416,355 / 97.7%
Unmapped reads	56,823 / 2.3%
Mapped paired reads	2,416,355 / 97.7%
Mapped reads, first in pair	1,208,534 / 48.87%
Mapped reads, second in pair	1,207,821 / 48.84%
Mapped reads, both in pair	2,380,936 / 96.27%
Mapped reads, singletons	35,419 / 1.43%
Secondary alignments	0
Supplementary alignments	308,332 / 12.47%
Read min/max/mean length	30 / 133 / 125.62
Duplicated reads (estimated)	1,923,248 / 77.76%
Duplication rate	64.64%
Clipped reads	1,223,330 / 49.46%

2.2. ACGT Content

Number/percentage of A's	81,623,704 / 29.72%
Number/percentage of C's	54,890,936 / 19.99%
Number/percentage of T's	81,040,415 / 29.51%
Number/percentage of G's	57,068,974 / 20.78%
Number/percentage of N's	1,845 / 0%

GC Percentage	40.77%
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2.3. Coverage

Mean	0.0888
Standard Deviation	1.7471

2.4. Mapping Quality

Mean Mapping Quality	52.55
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2.5. Insert size

Mean	1,181,363.02
Standard Deviation	10,292,660.76
P25/Median/P75	108 / 157 / 244

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,316,636
Insertions	29,914
Mapped reads with at least one insertion	1.19%
Deletions	76,174
Mapped reads with at least one deletion	3.08%
Homopolymer indels	41.86%

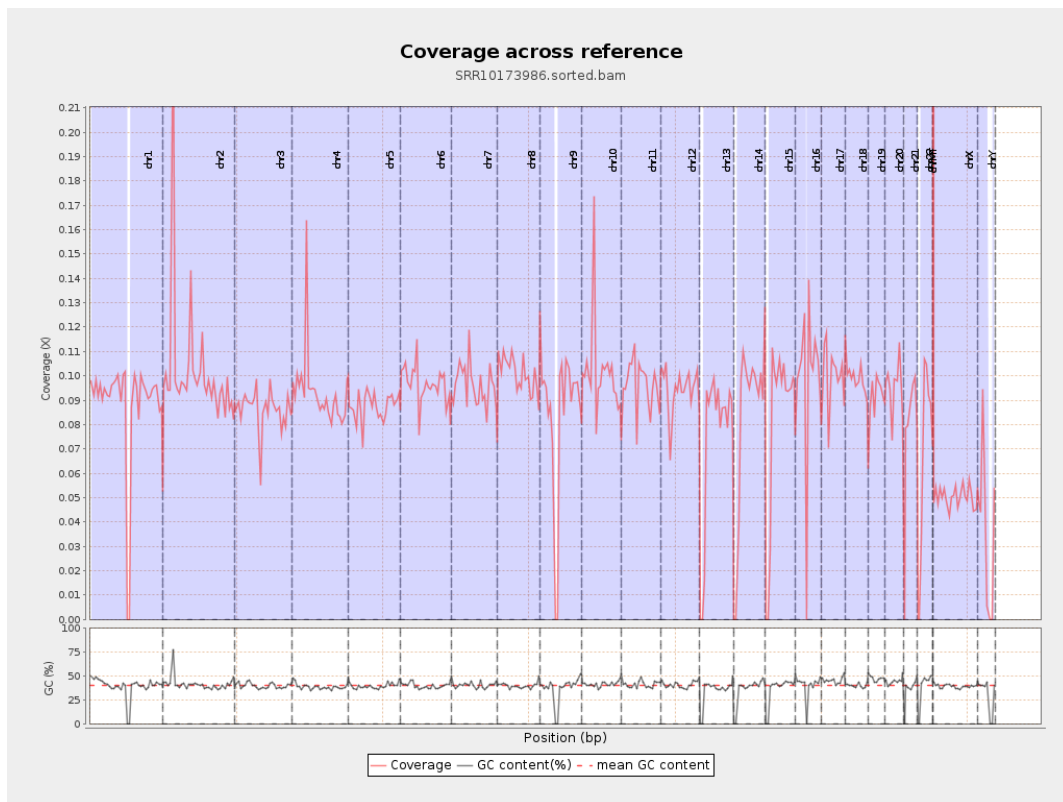
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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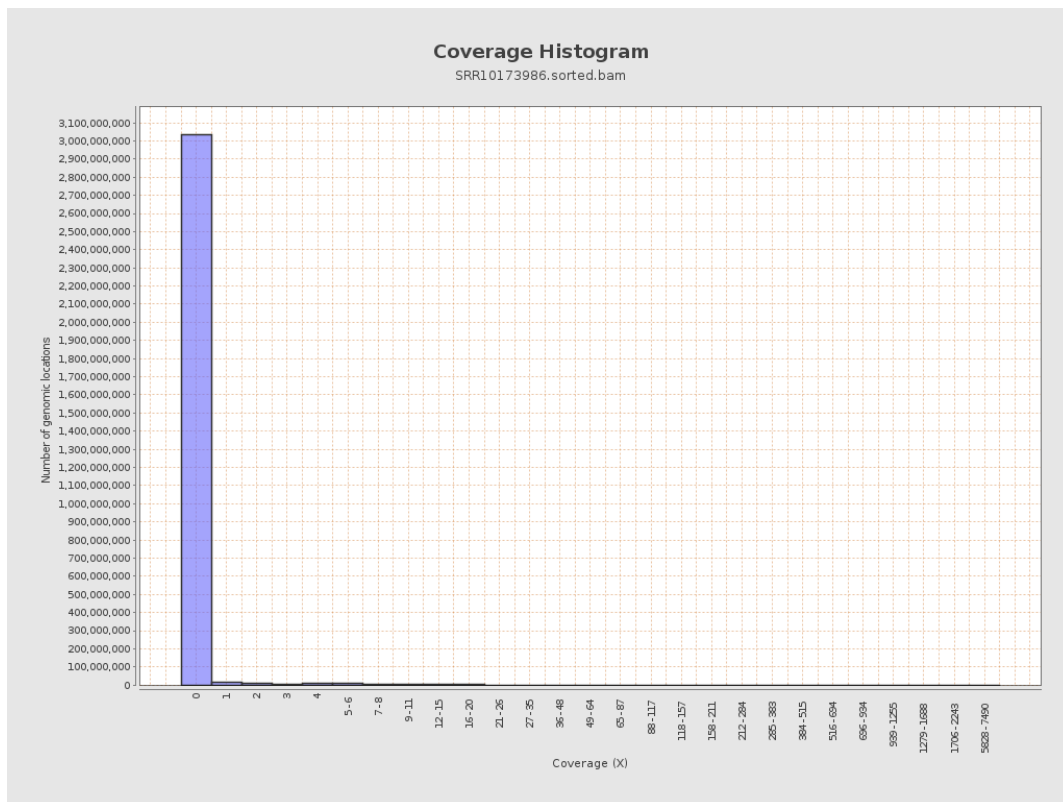
		bases	coverage	deviation
chr1	249250621	21974096	0.0882	1.0402
chr2	243199373	24769487	0.1018	5.2635
chr3	198022430	17040976	0.0861	0.8738
chr4	191154276	17849915	0.0934	1.0342
chr5	180915260	15852412	0.0876	0.8785
chr6	171115067	16551537	0.0967	0.9729
chr7	159138663	15304516	0.0962	1.0824
chr8	146364022	14744542	0.1007	1.2524
chr9	141213431	11804697	0.0836	0.938
chr10	135534747	13745621	0.1014	1.205
chr11	135006516	12946110	0.0959	0.9418
chr12	133851895	12668606	0.0946	0.9281
chr13	115169878	8563883	0.0744	0.8181
chr14	107349540	8880647	0.0827	0.8698
chr15	102531392	8253596	0.0805	0.844
chr16	90354753	8867985	0.0981	1.0041
chr17	81195210	8141846	0.1003	0.9596
chr18	78077248	7756340	0.0993	1.2052
chr19	59128983	5412775	0.0915	0.9351
chr20	63025520	6034134	0.0957	0.9321
chr21	48129895	3828237	0.0795	0.9865
chr22	51304566	3432793	0.0669	0.8514
chrMT	16571	354617	21.3999	19.1665
chrX	155270560	7826712	0.0504	0.6663

chrY	59373566	2202771	0.0371	0.6845
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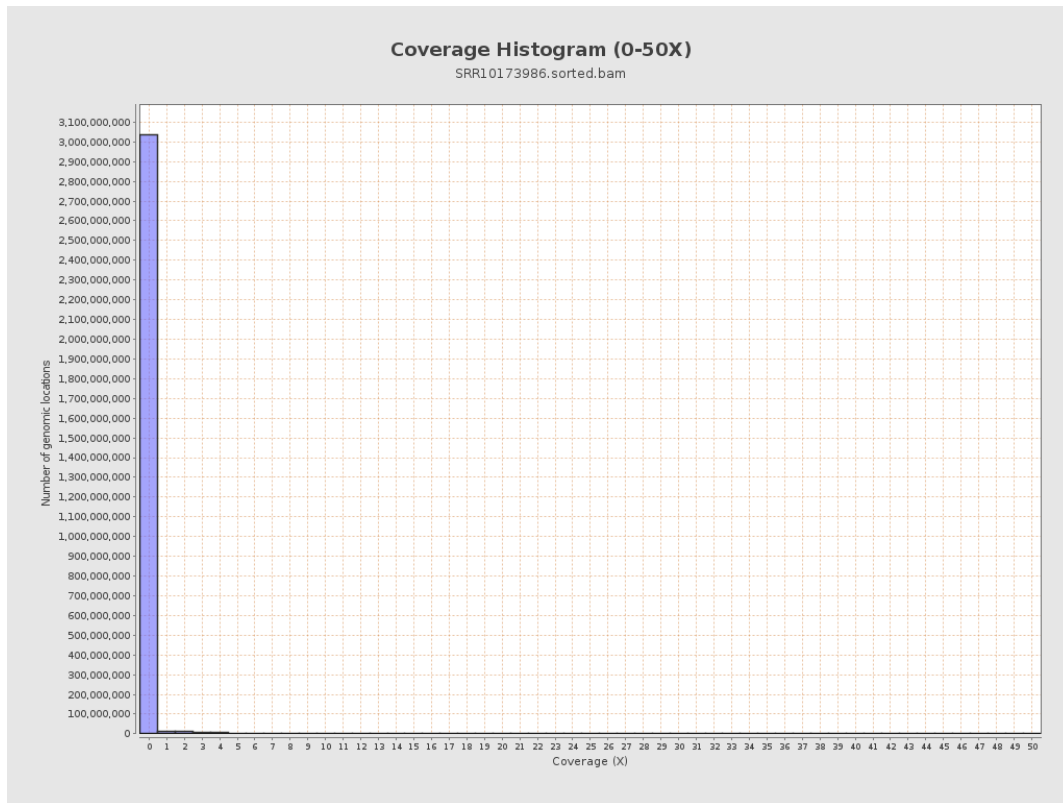
3. Results : Coverage across reference



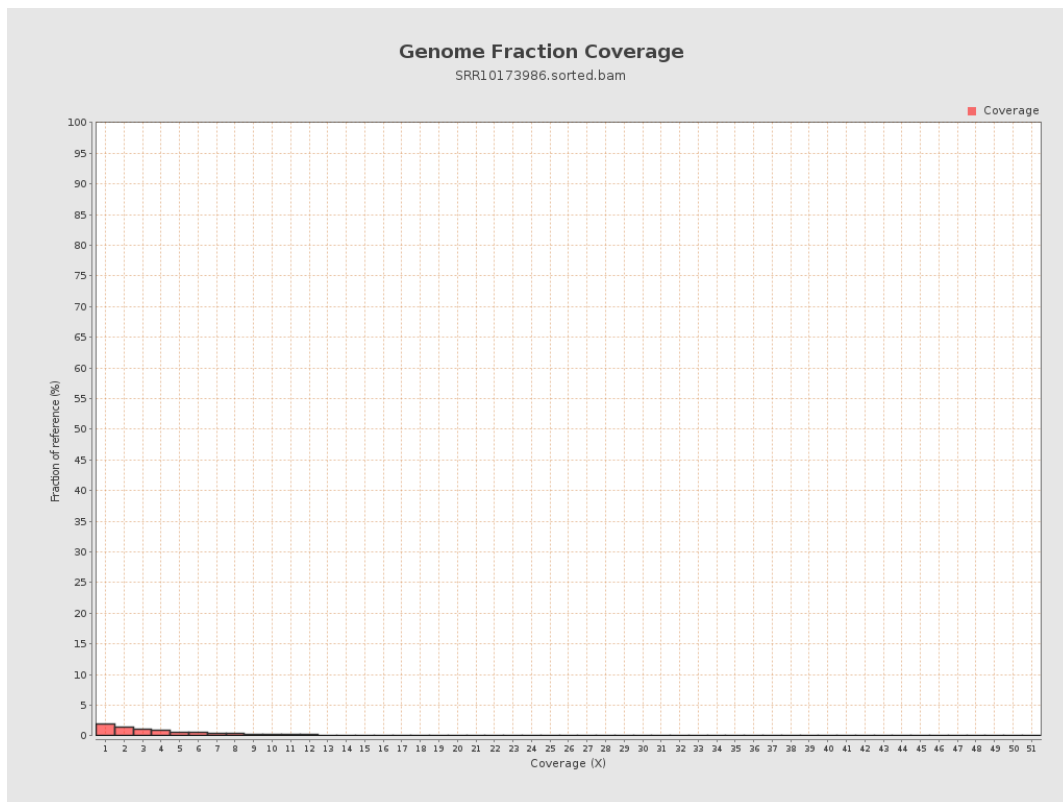
4. Results : Coverage Histogram



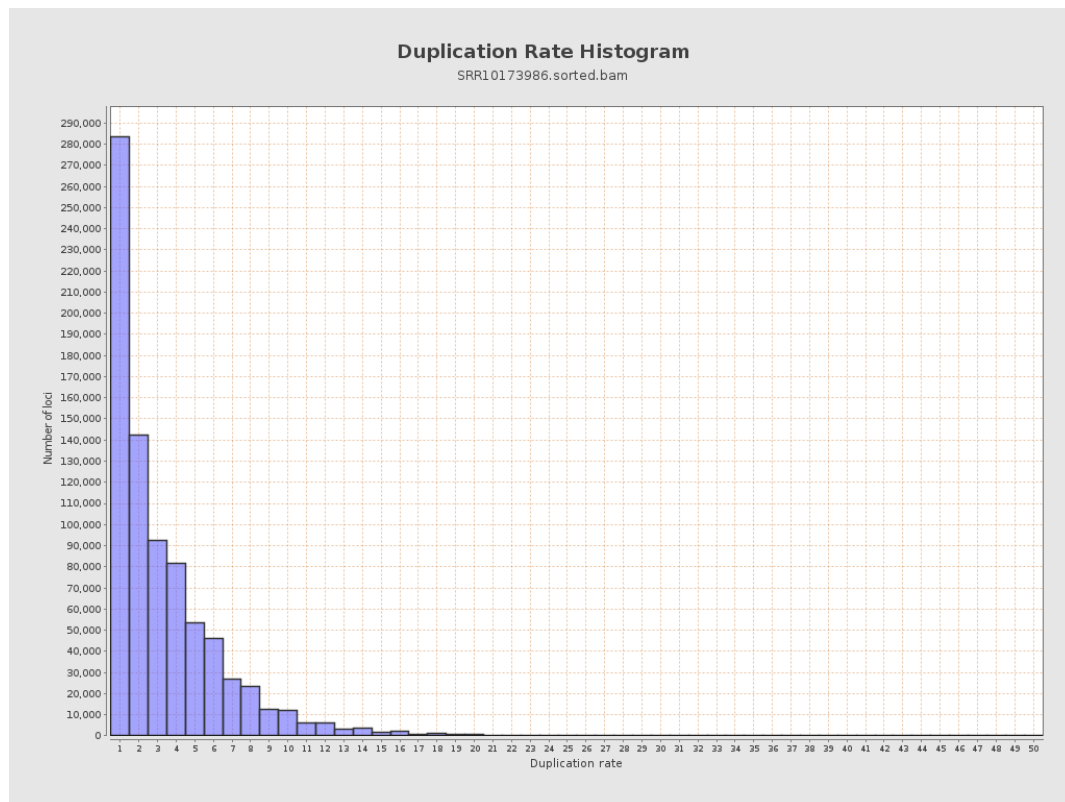
5. Results : Coverage Histogram (0-50X)



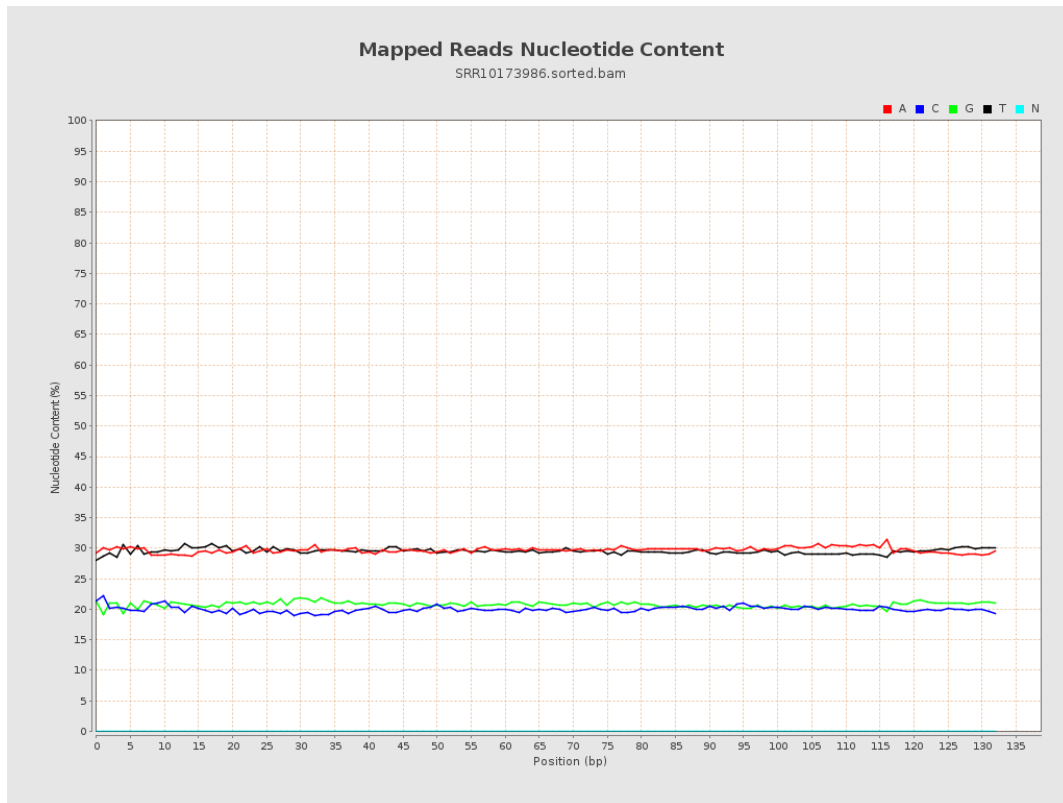
6. Results : Genome Fraction Coverage



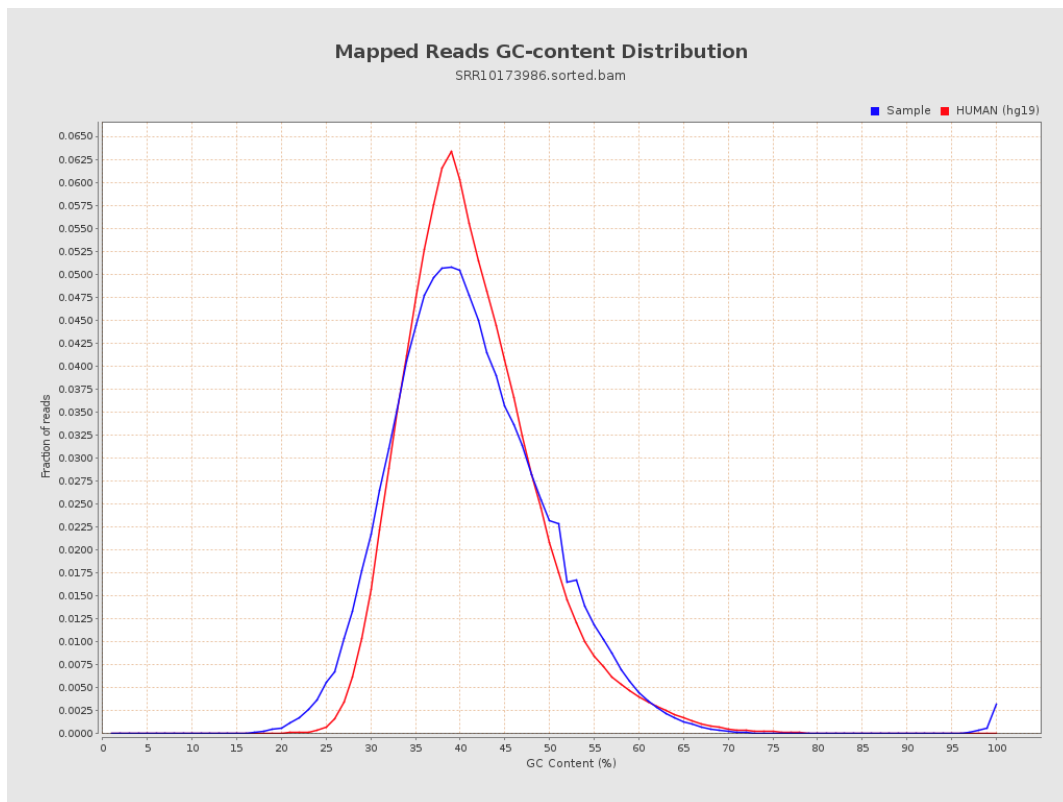
7. Results : Duplication Rate Histogram



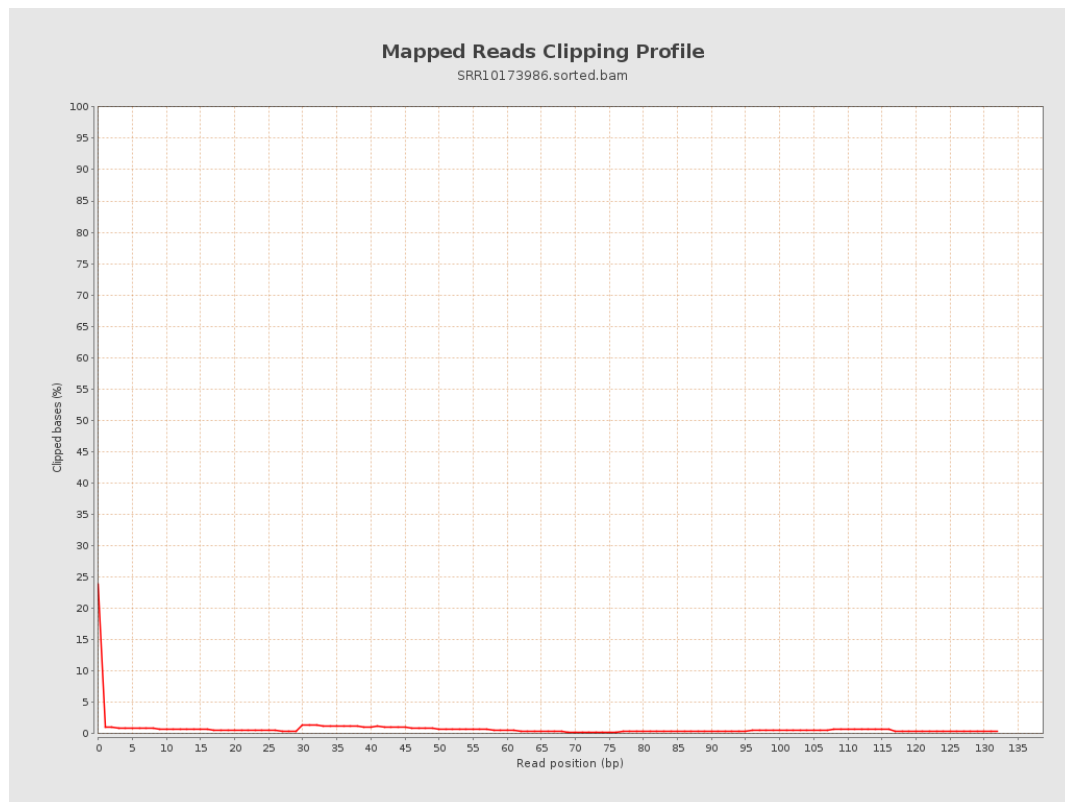
8. Results : Mapped Reads Nucleotide Content



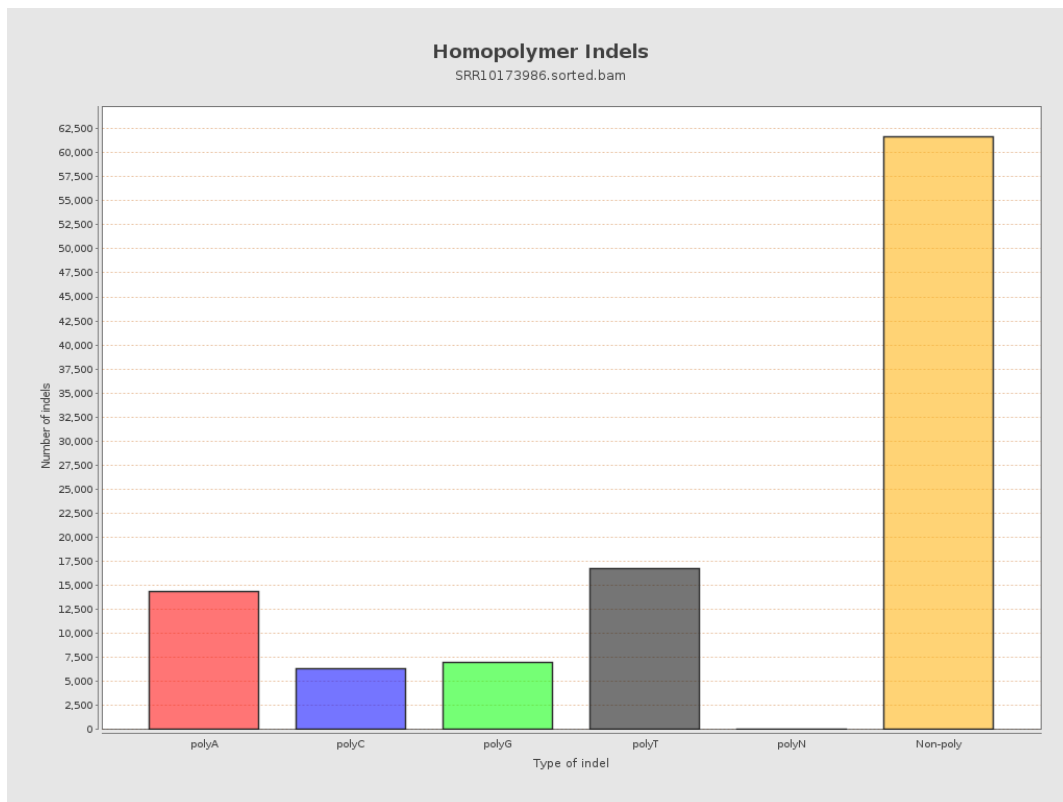
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



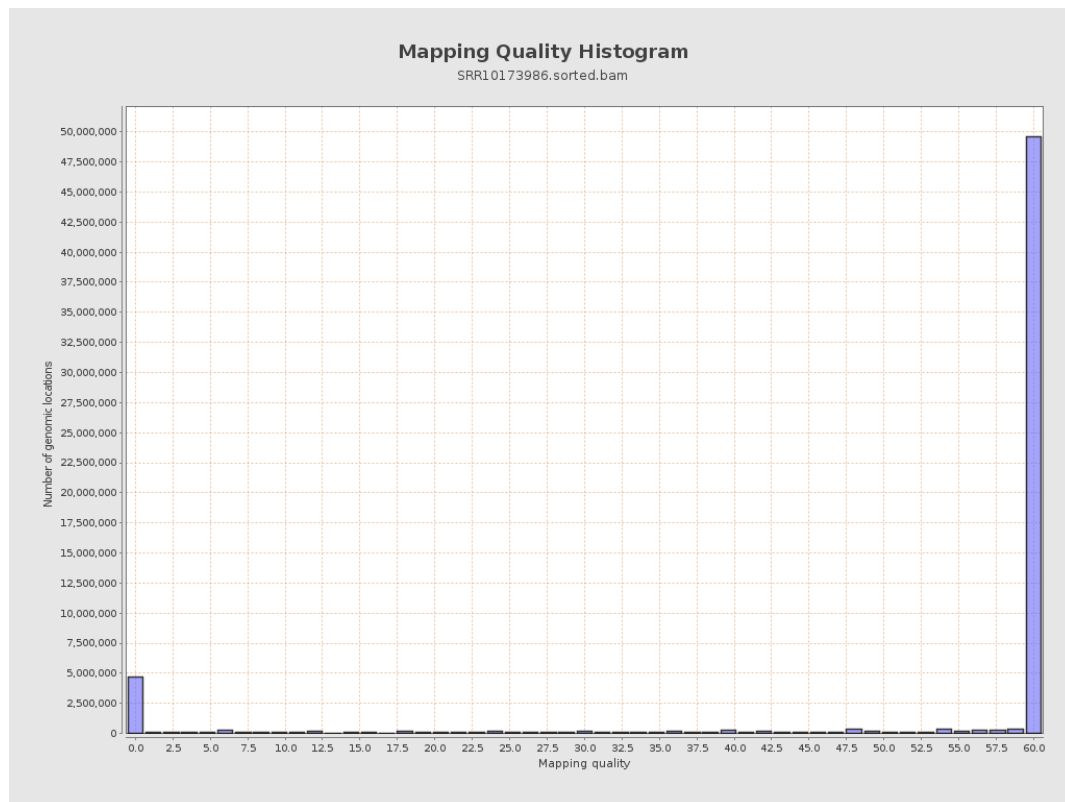
11. Results : Homopolymer Indels



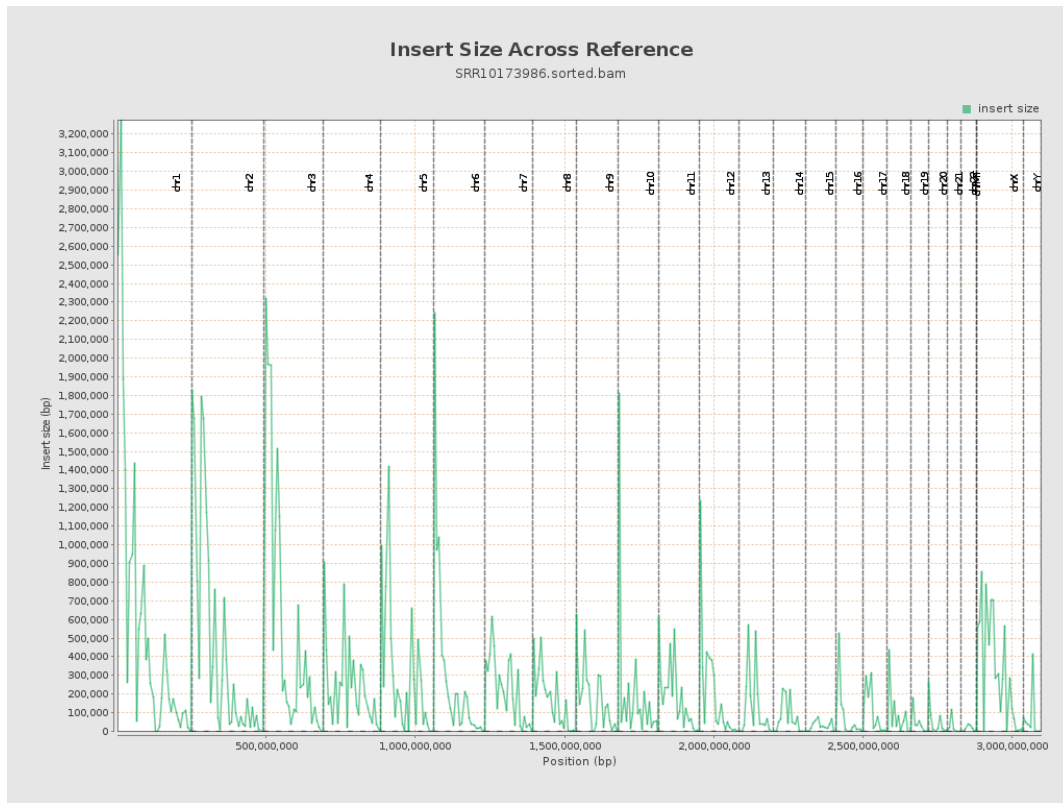
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

