

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 06:19:30

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR10174080.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_SRR10174080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174080_1.fastq.gz SRR10174080_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 06:19:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,346,286
Mapped reads	2,300,030 / 98.03%
Unmapped reads	46,256 / 1.97%
Mapped paired reads	2,300,030 / 98.03%
Mapped reads, first in pair	1,149,466 / 48.99%
Mapped reads, second in pair	1,150,564 / 49.04%
Mapped reads, both in pair	2,271,402 / 96.81%
Mapped reads, singletons	28,628 / 1.22%
Secondary alignments	0
Supplementary alignments	295,797 / 12.61%
Read min/max/mean length	30 / 133 / 125.1
Duplicated reads (estimated)	1,808,379 / 77.07%
Duplication rate	63.64%
Clipped reads	1,135,849 / 48.41%

2.2. ACGT Content

Number/percentage of A's	78,246,987 / 29.96%
Number/percentage of C's	51,711,920 / 19.8%
Number/percentage of T's	77,500,174 / 29.68%
Number/percentage of G's	53,695,482 / 20.56%
Number/percentage of N's	1,961 / 0%

GC Percentage	40.36%
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2.3. Coverage

Mean	0.0844
Standard Deviation	1.7465

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	1,124,496.81
Standard Deviation	9,939,012.39
P25/Median/P75	105 / 152 / 230

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	2,135,722
Insertions	28,176
Mapped reads with at least one insertion	1.18%
Deletions	68,463
Mapped reads with at least one deletion	2.91%
Homopolymer indels	41.81%

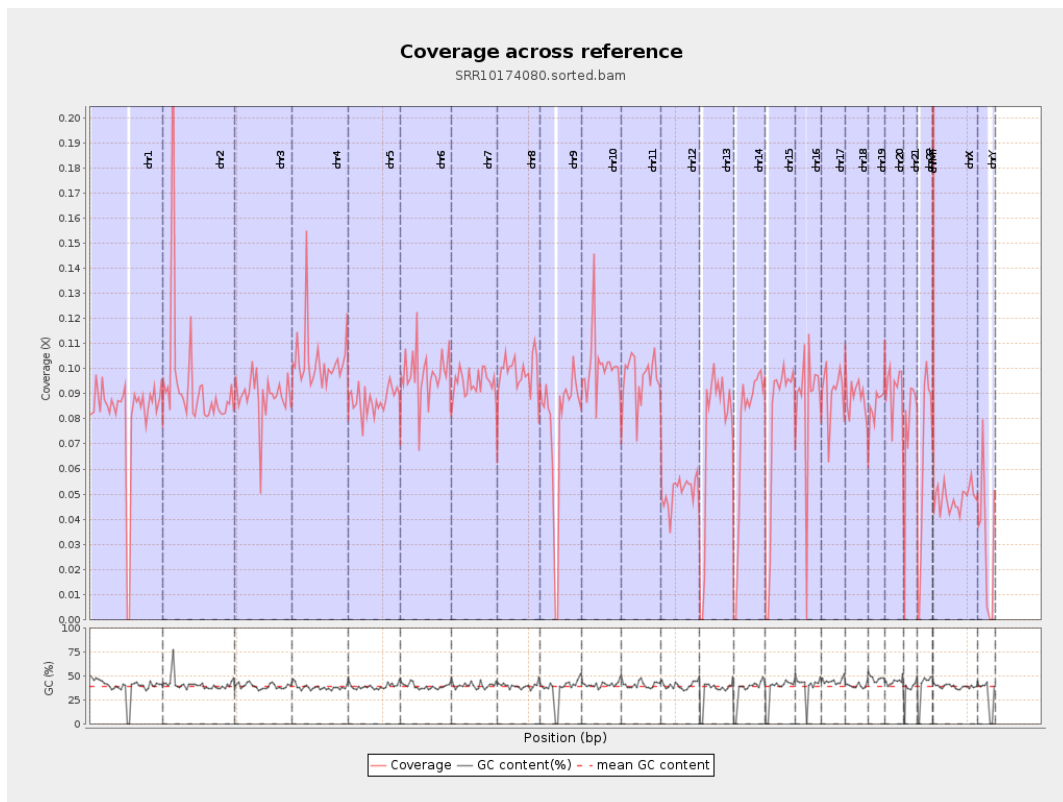
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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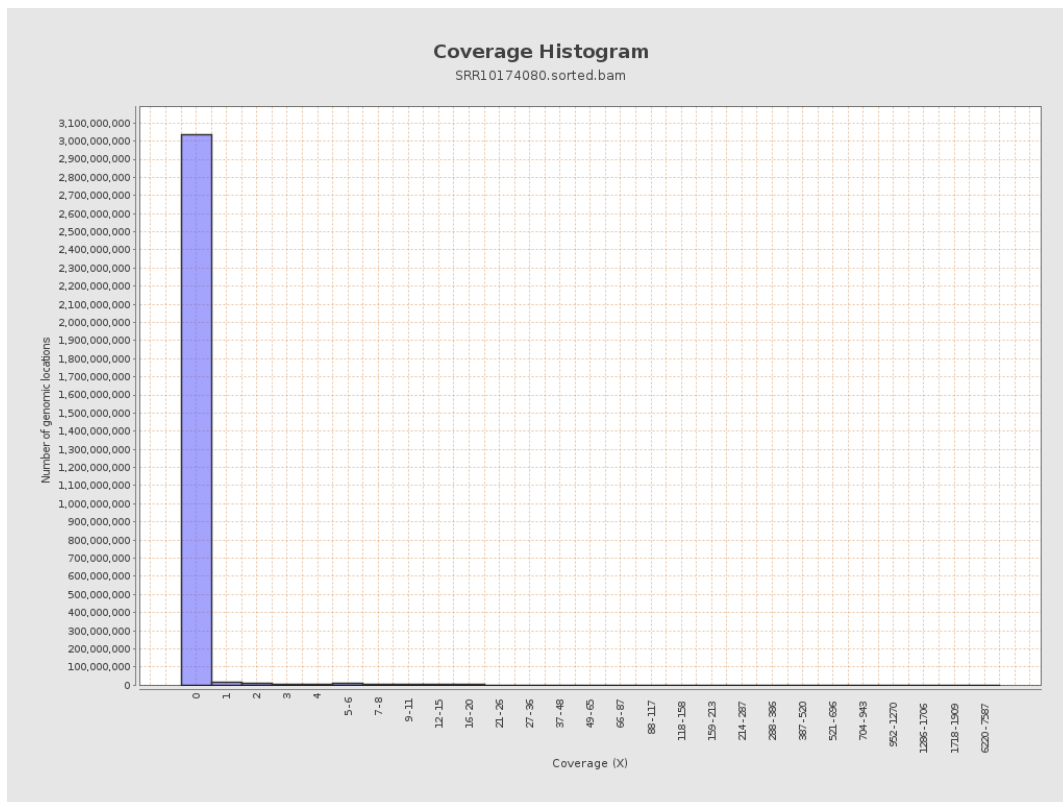
		bases	coverage	deviation
chr1	249250621	20370108	0.0817	0.9801
chr2	243199373	22732354	0.0935	5.3617
chr3	198022430	17612659	0.0889	0.8836
chr4	191154276	19754873	0.1033	1.0589
chr5	180915260	15800042	0.0873	0.8771
chr6	171115067	16737678	0.0978	1.001
chr7	159138663	14997576	0.0942	0.9955
chr8	146364022	14435683	0.0986	1.1771
chr9	141213431	11012305	0.078	0.8785
chr10	135534747	13647006	0.1007	1.0974
chr11	135006516	12994157	0.0962	0.9284
chr12	133851895	6812675	0.0509	0.6797
chr13	115169878	8590012	0.0746	0.8113
chr14	107349540	8169856	0.0761	0.8201
chr15	102531392	7802009	0.0761	0.8152
chr16	90354753	7779490	0.0861	0.9071
chr17	81195210	7414711	0.0913	0.9036
chr18	78077248	6951089	0.089	1.0711
chr19	59128983	5081330	0.0859	0.8856
chr20	63025520	5802616	0.0921	0.9066
chr21	48129895	3709927	0.0771	0.8985
chr22	51304566	3309616	0.0645	0.7837
chrMT	16571	398454	24.0453	21.1112
chrX	155270560	7506703	0.0483	0.651

chrY	59373566	1896031	0.0319	0.6127
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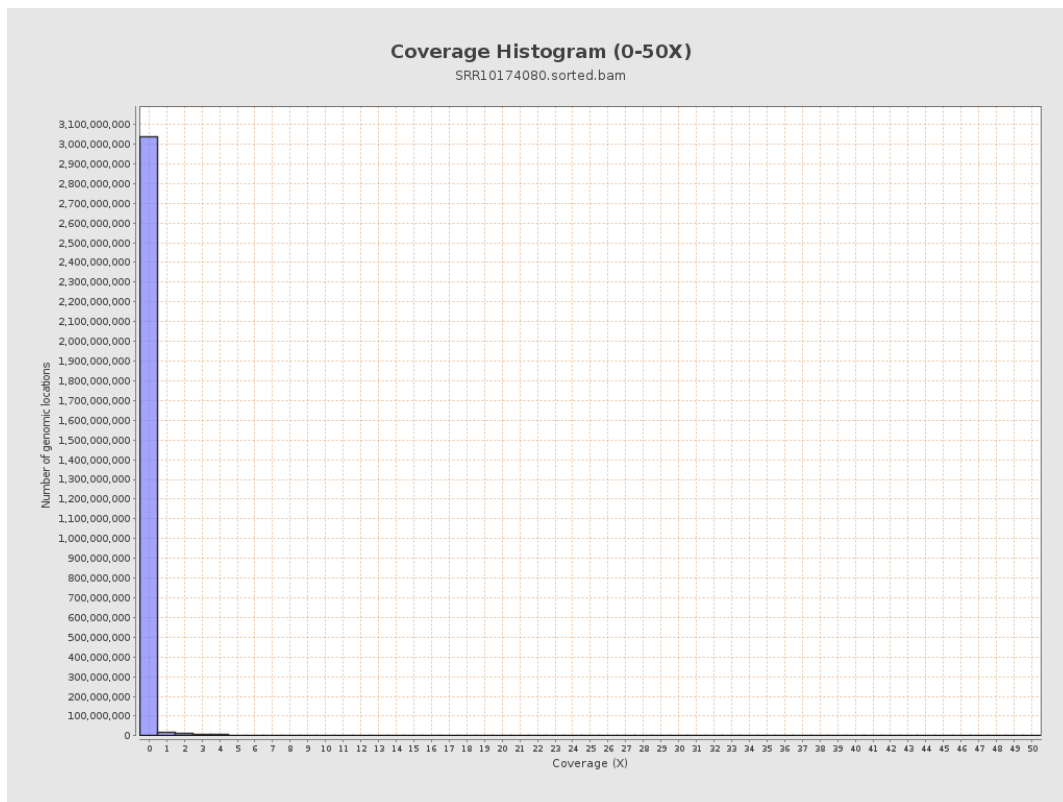
3. Results : Coverage across reference



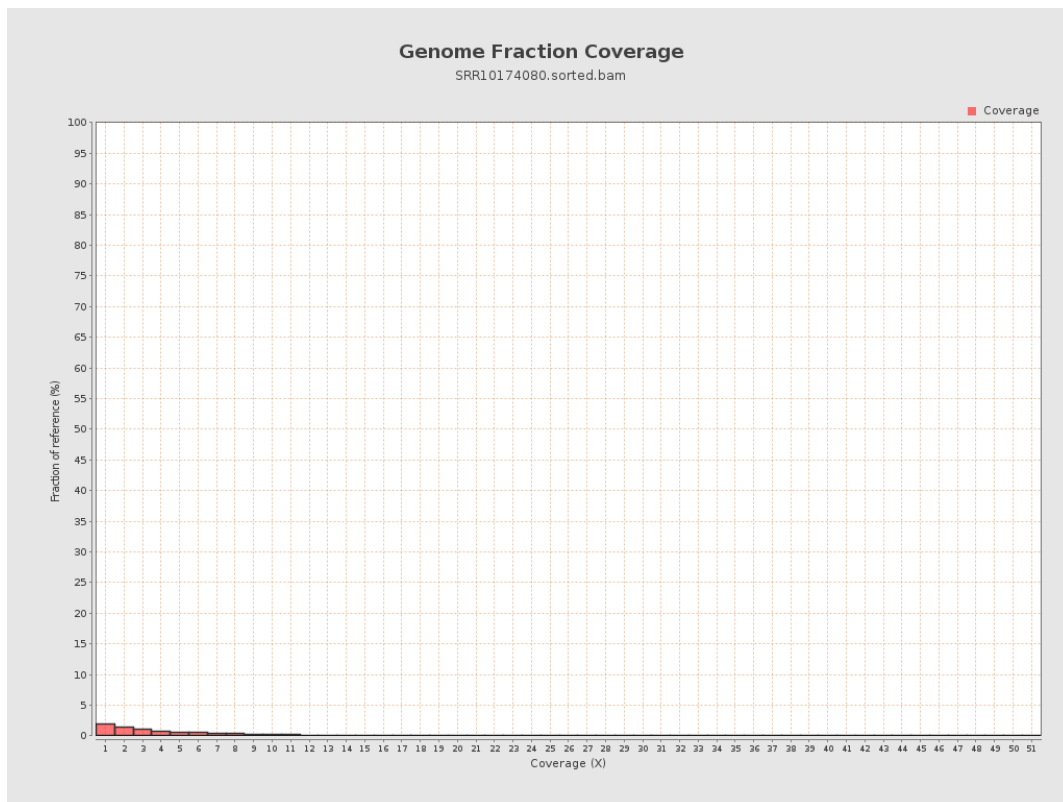
4. Results : Coverage Histogram



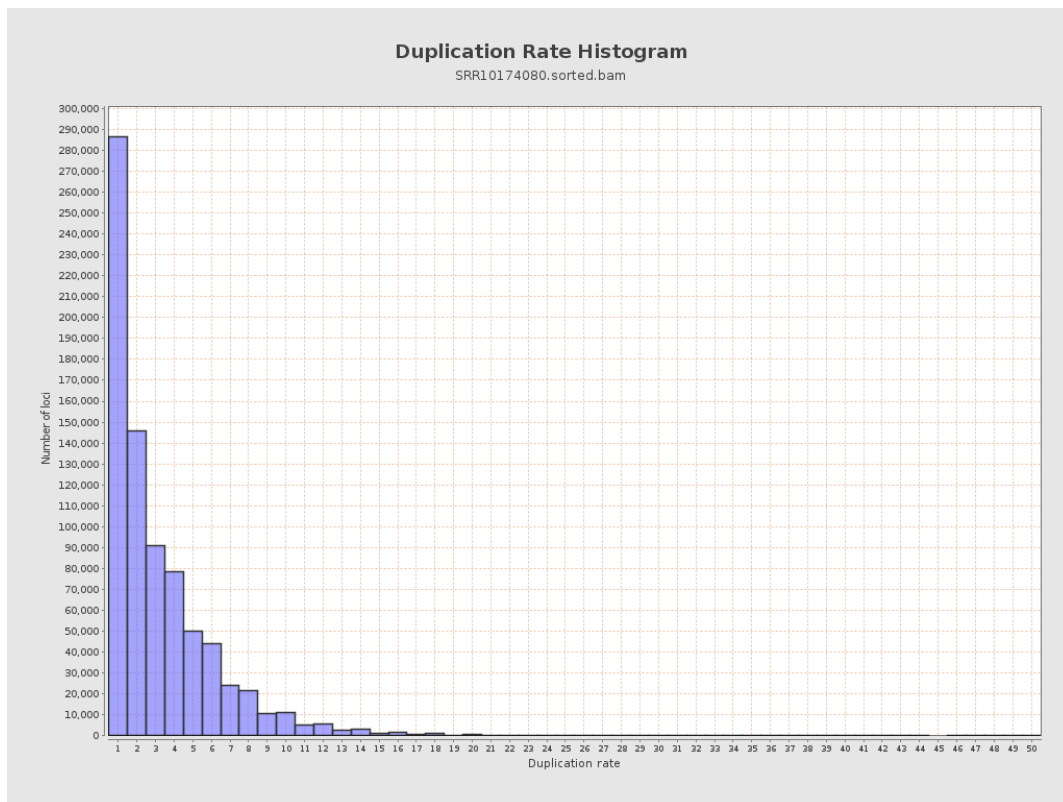
5. Results : Coverage Histogram (0-50X)



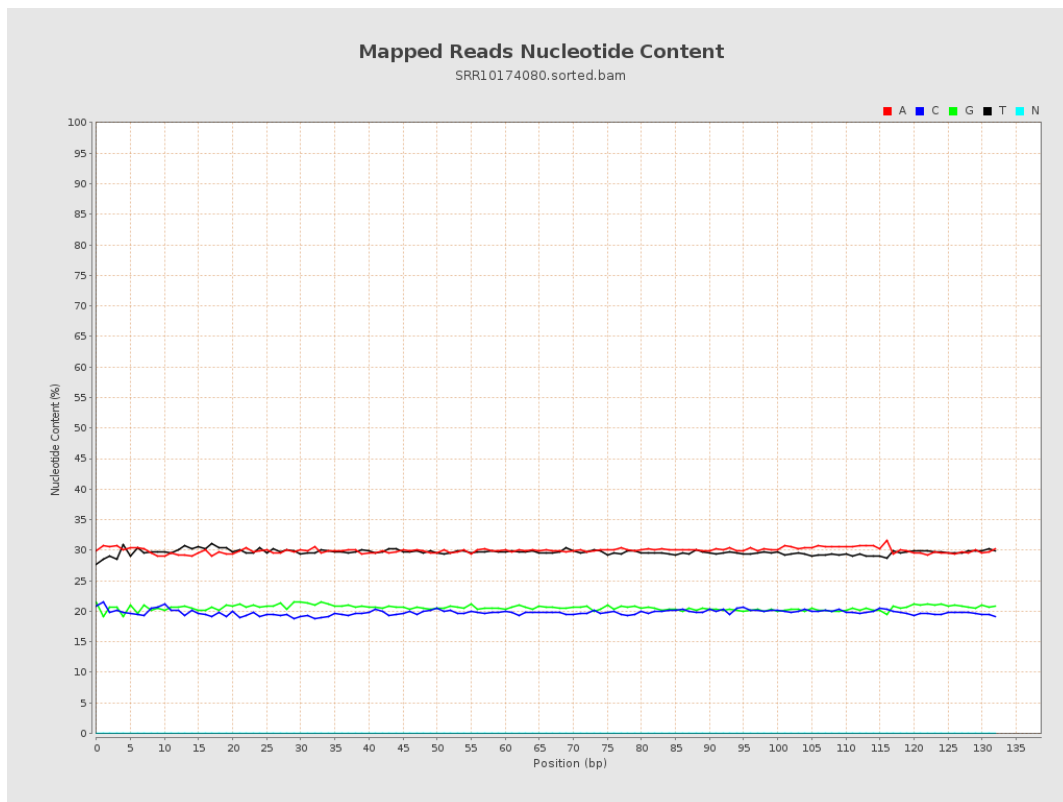
6. Results : Genome Fraction Coverage



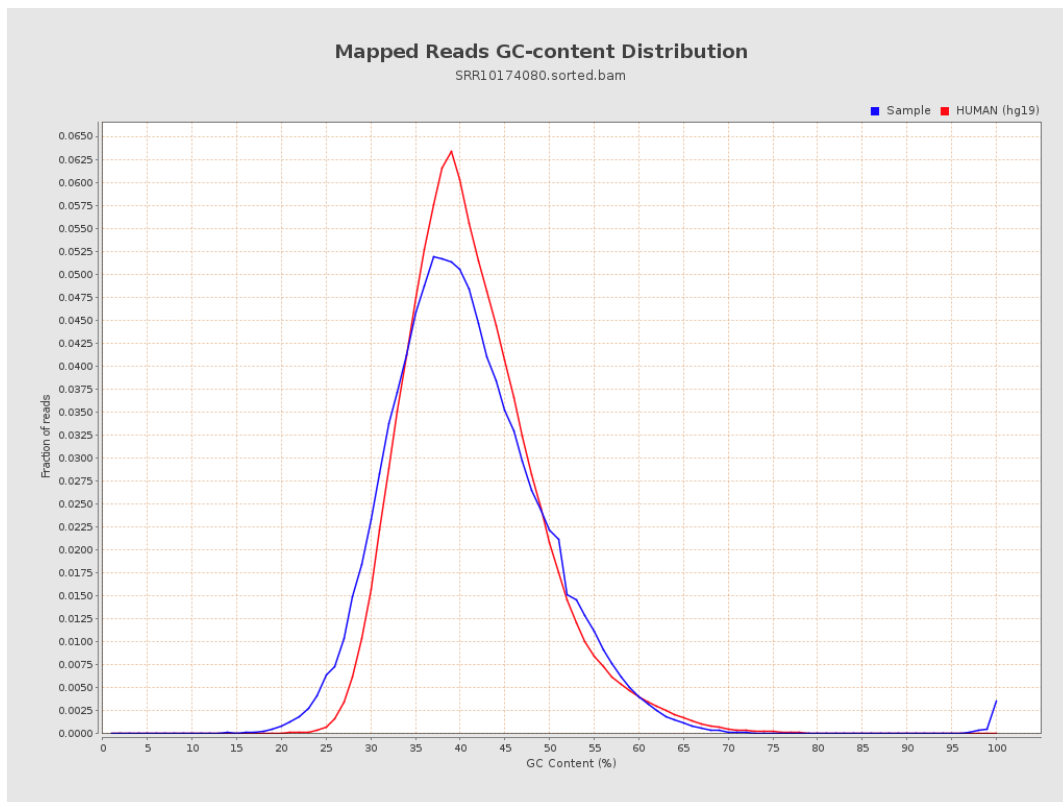
7. Results : Duplication Rate Histogram



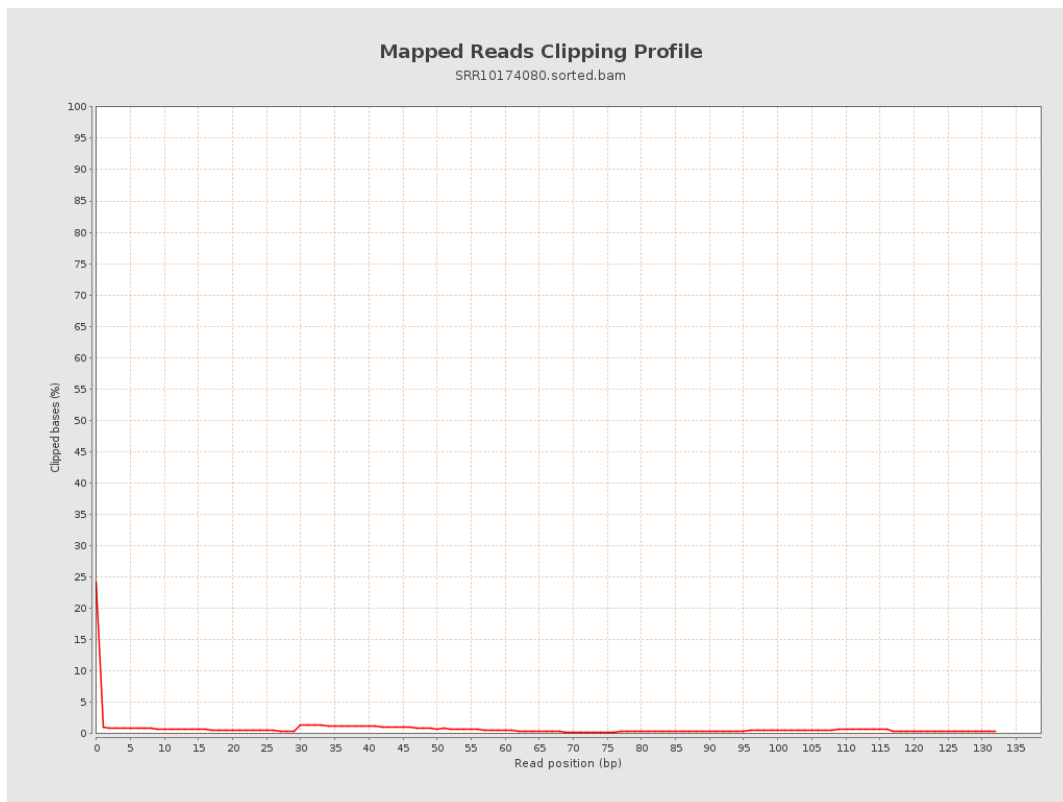
8. Results : Mapped Reads Nucleotide Content



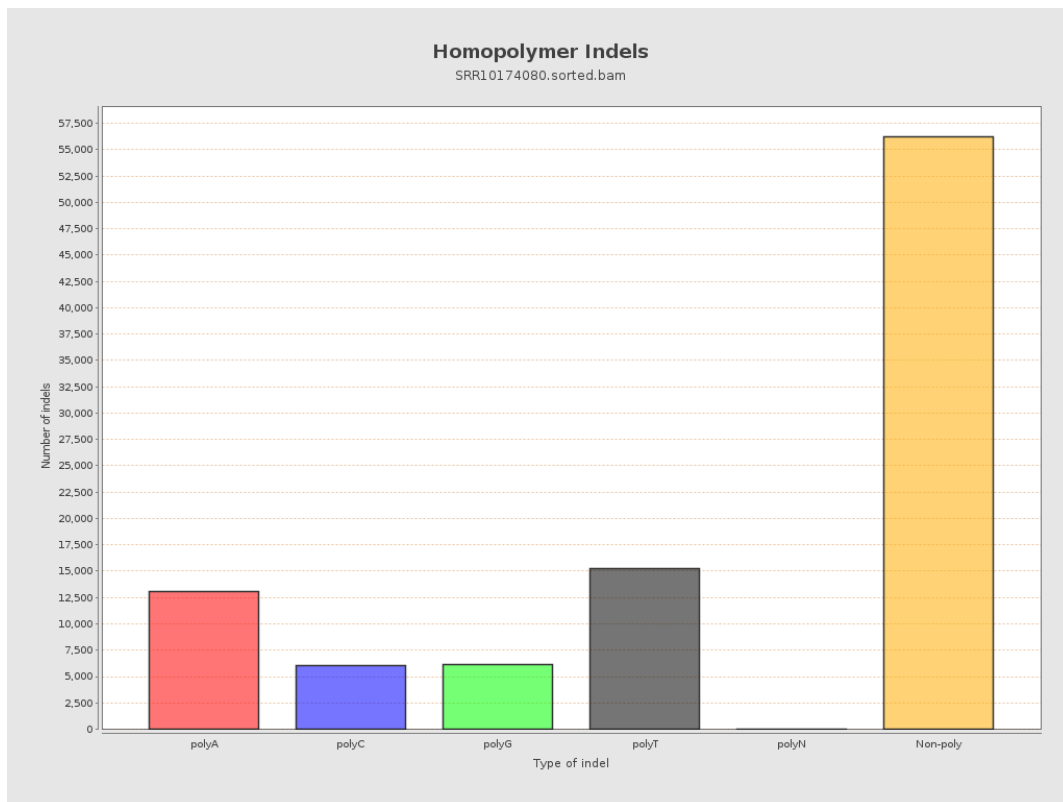
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



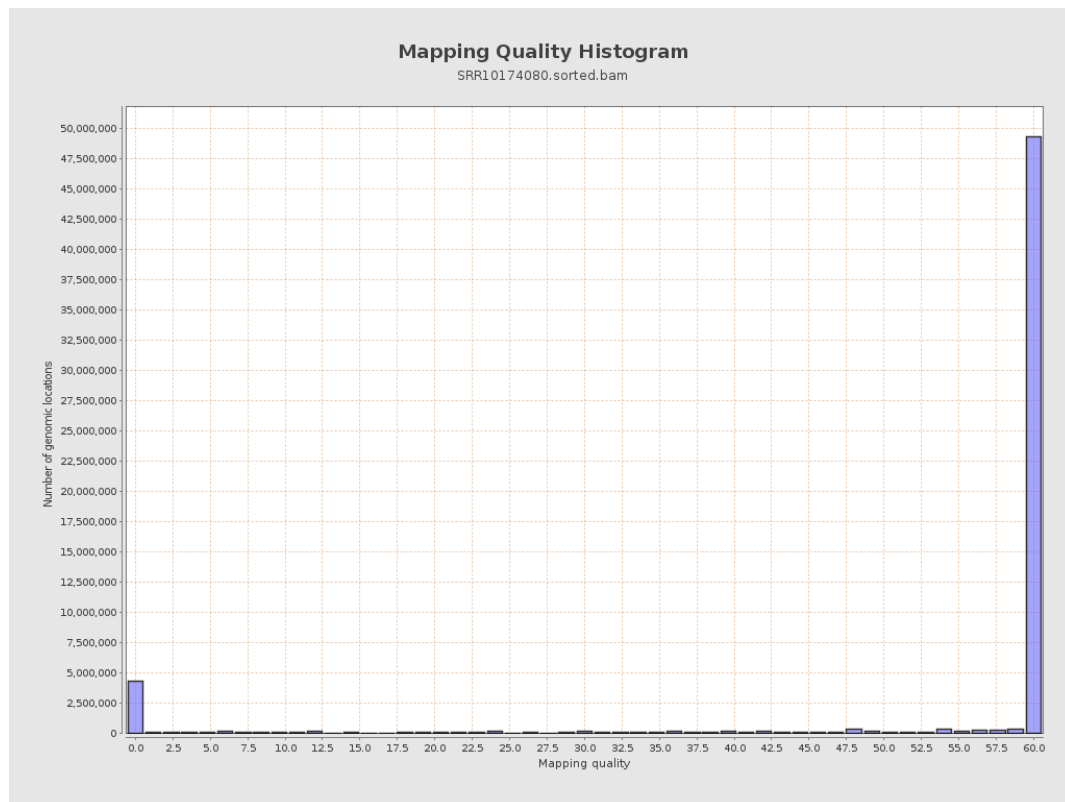
11. Results : Homopolymer Indels



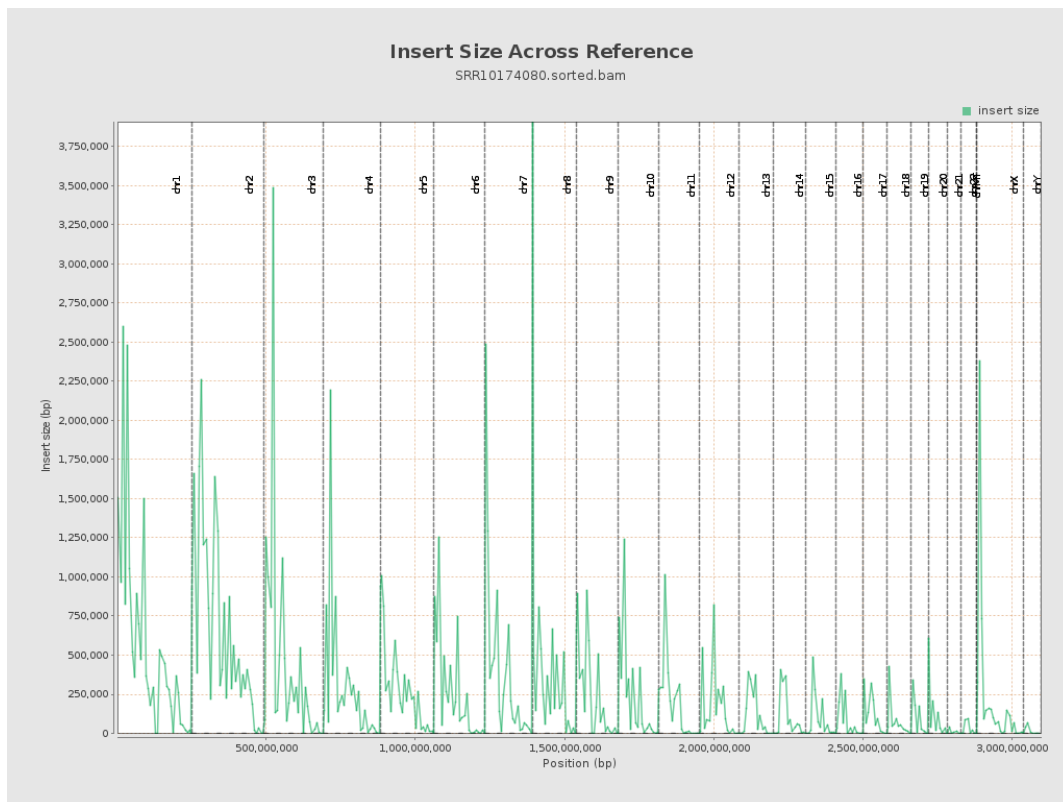
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

