

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 02:31:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174057.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_SRR10174057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174057_1.fastq.gz SRR10174057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 02:31:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,689,736
Mapped reads	11,368,805 / 97.25%
Unmapped reads	320,931 / 2.75%
Mapped paired reads	11,368,805 / 97.25%
Mapped reads, first in pair	5,689,660 / 48.67%
Mapped reads, second in pair	5,679,145 / 48.58%
Mapped reads, both in pair	11,149,698 / 95.38%
Mapped reads, singletons	219,107 / 1.87%
Secondary alignments	0
Supplementary alignments	1,168,731 / 10%
Read min/max/mean length	30 / 133 / 128.32
Duplicated reads (estimated)	9,219,258 / 78.87%
Duplication rate	66.76%
Clipped reads	4,668,582 / 39.94%

2.2. ACGT Content

Number/percentage of A's	404,855,639 / 30.19%
Number/percentage of C's	261,202,110 / 19.48%
Number/percentage of T's	404,156,801 / 30.14%
Number/percentage of G's	270,705,928 / 20.19%
Number/percentage of N's	16,419 / 0%

GC Percentage	39.67%
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2.3. Coverage

Mean	0.4334
Standard Deviation	6.3483

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	1,016,064.97
Standard Deviation	8,754,692.99
P25/Median/P75	145 / 203 / 291

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	13,663,631
Insertions	141,901
Mapped reads with at least one insertion	1.2%
Deletions	306,851
Mapped reads with at least one deletion	2.63%
Homopolymer indels	42.68%

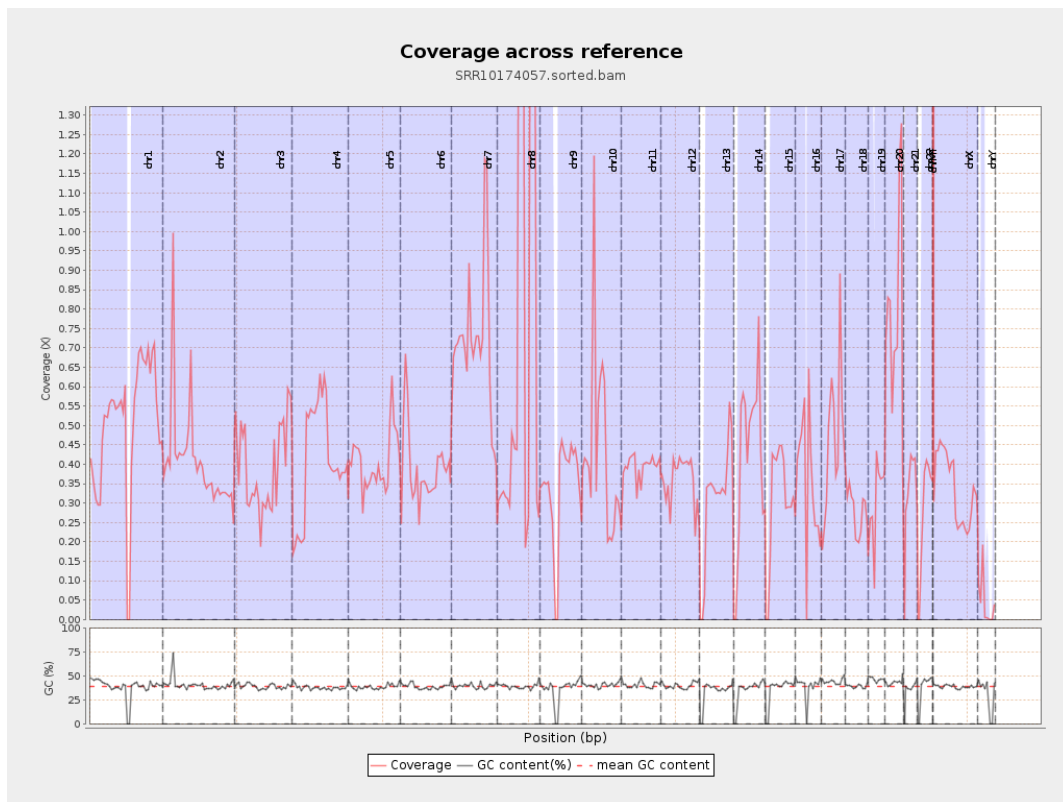
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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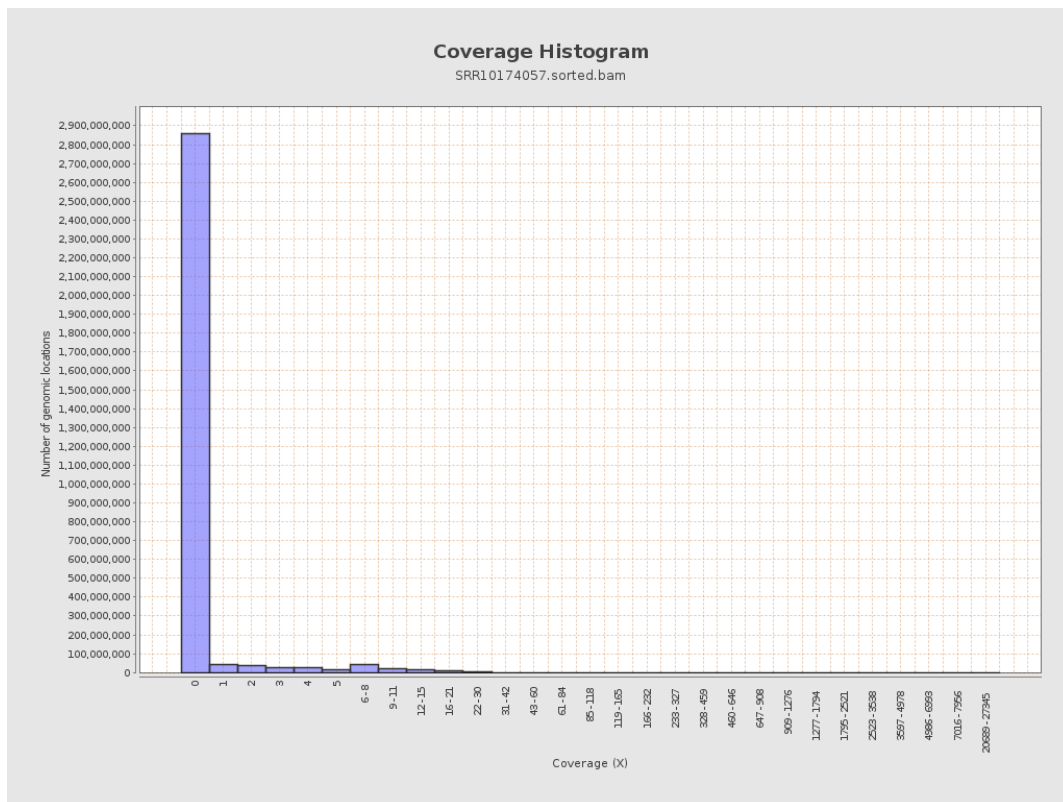
		bases	coverage	deviation
chr1	249250621	125820725	0.5048	3.3786
chr2	243199373	98509671	0.4051	19.1655
chr3	198022430	77862318	0.3932	1.9624
chr4	191154276	79104229	0.4138	3.0091
chr5	180915260	73299879	0.4052	1.9438
chr6	171115067	66501708	0.3886	2.1158
chr7	159138663	112986064	0.71	6.866
chr8	146364022	137213192	0.9375	4.1202
chr9	141213431	47961108	0.3396	2.911
chr10	135534747	58013540	0.428	8.2656
chr11	135006516	52688185	0.3903	2.0669
chr12	133851895	48066503	0.3591	1.854
chr13	115169878	36028692	0.3128	1.7184
chr14	107349540	46416655	0.4324	2.0654
chr15	102531392	31067497	0.303	1.6848
chr16	90354753	32081135	0.3551	3.1152
chr17	81195210	37319589	0.4596	2.6142
chr18	78077248	22230549	0.2847	4.0651
chr19	59128983	17907328	0.3029	2.4976
chr20	63025520	52115527	0.8269	2.9437
chr21	48129895	15671473	0.3256	2.108
chr22	51304566	13995000	0.2728	1.5477
chrMT	16571	3767608	227.3615	155.9892
chrX	155270560	52387774	0.3374	1.8215

chrY	59373566	2677015	0.0451	2.0306
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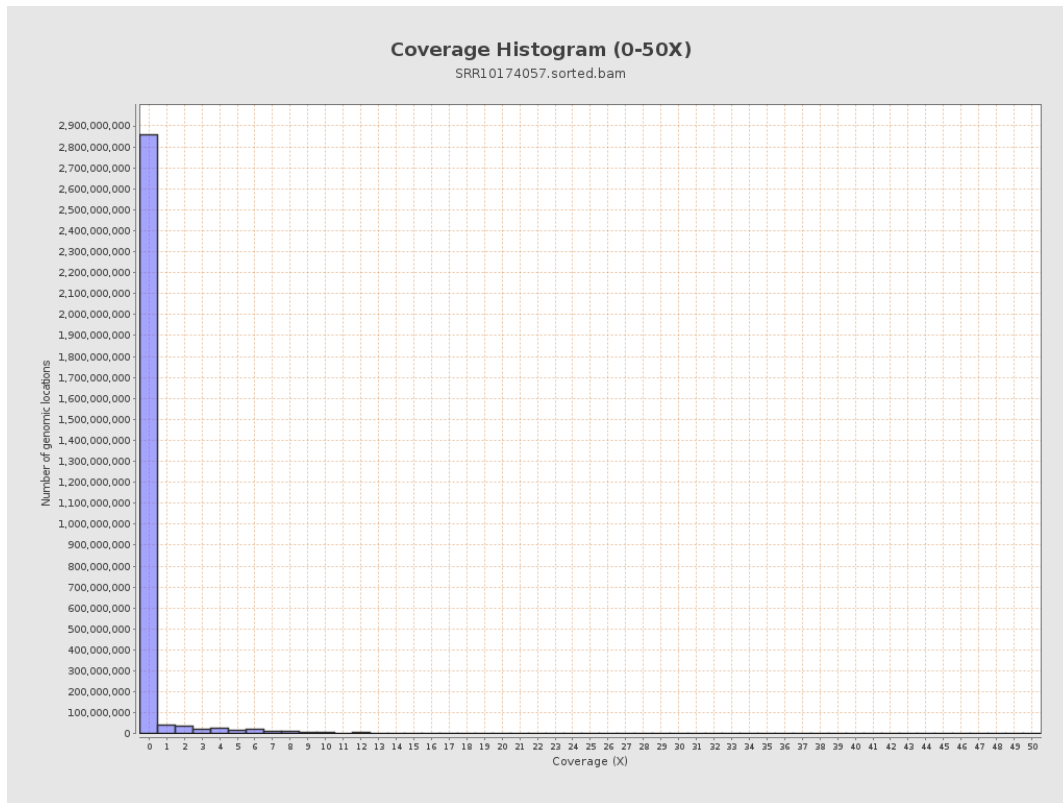
3. Results : Coverage across reference



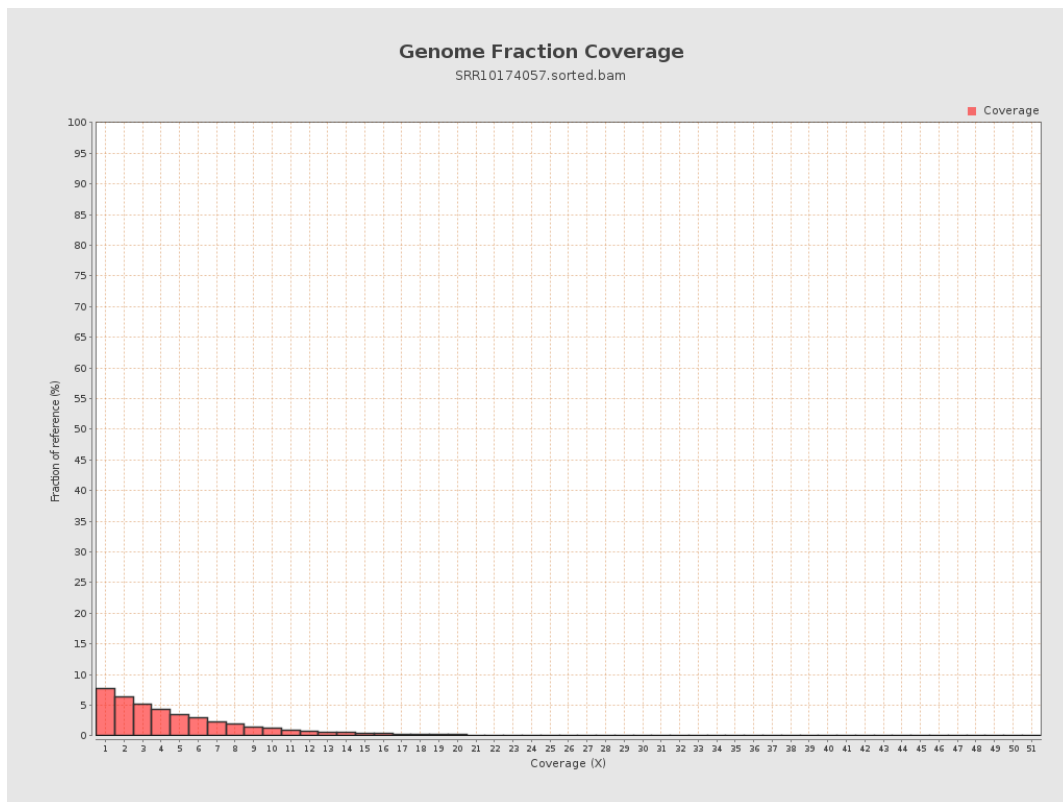
4. Results : Coverage Histogram



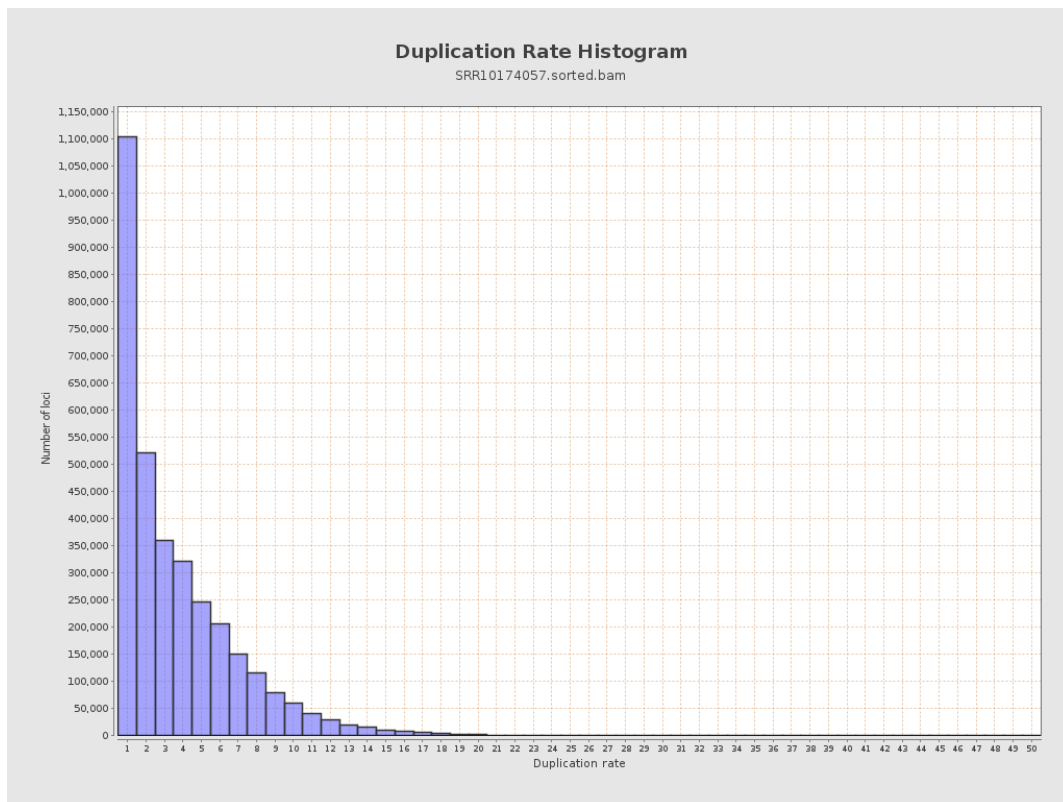
5. Results : Coverage Histogram (0-50X)



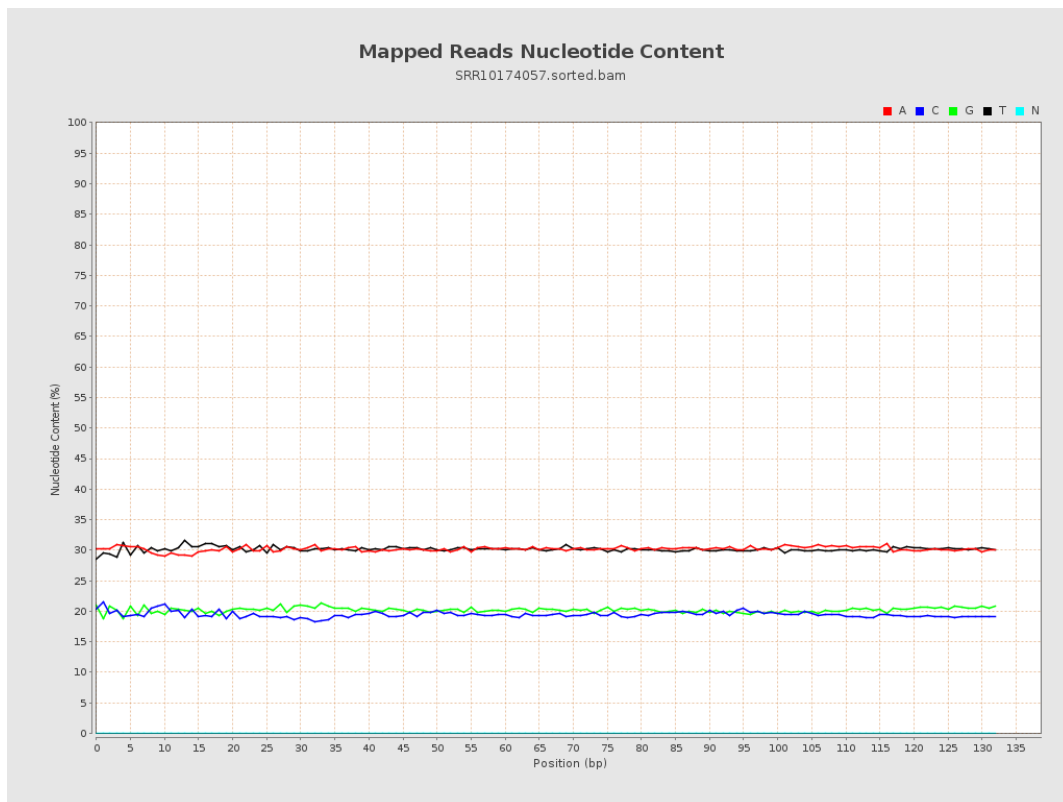
6. Results : Genome Fraction Coverage



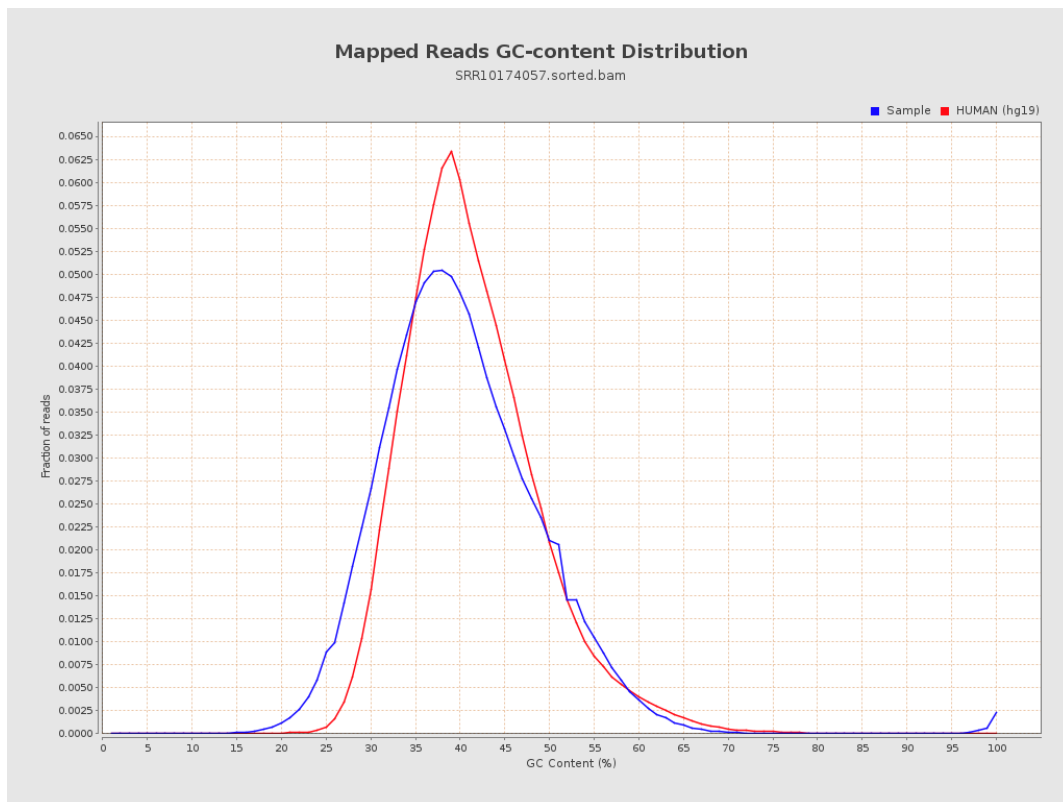
7. Results : Duplication Rate Histogram



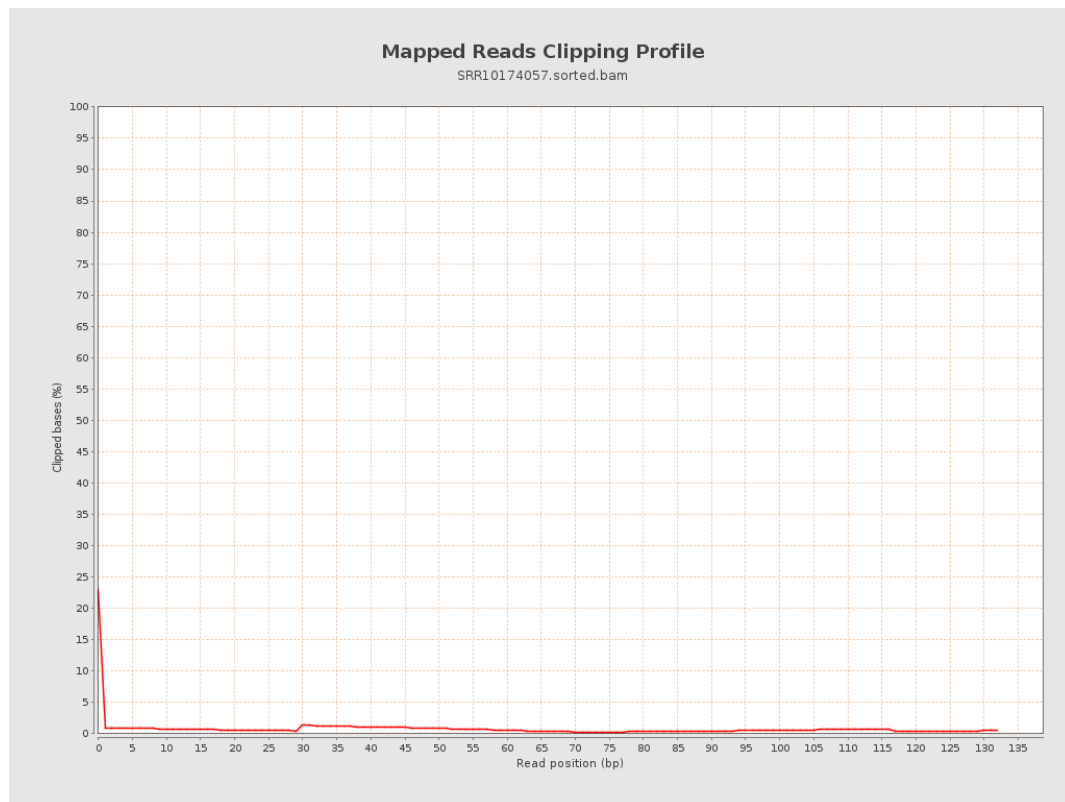
8. Results : Mapped Reads Nucleotide Content



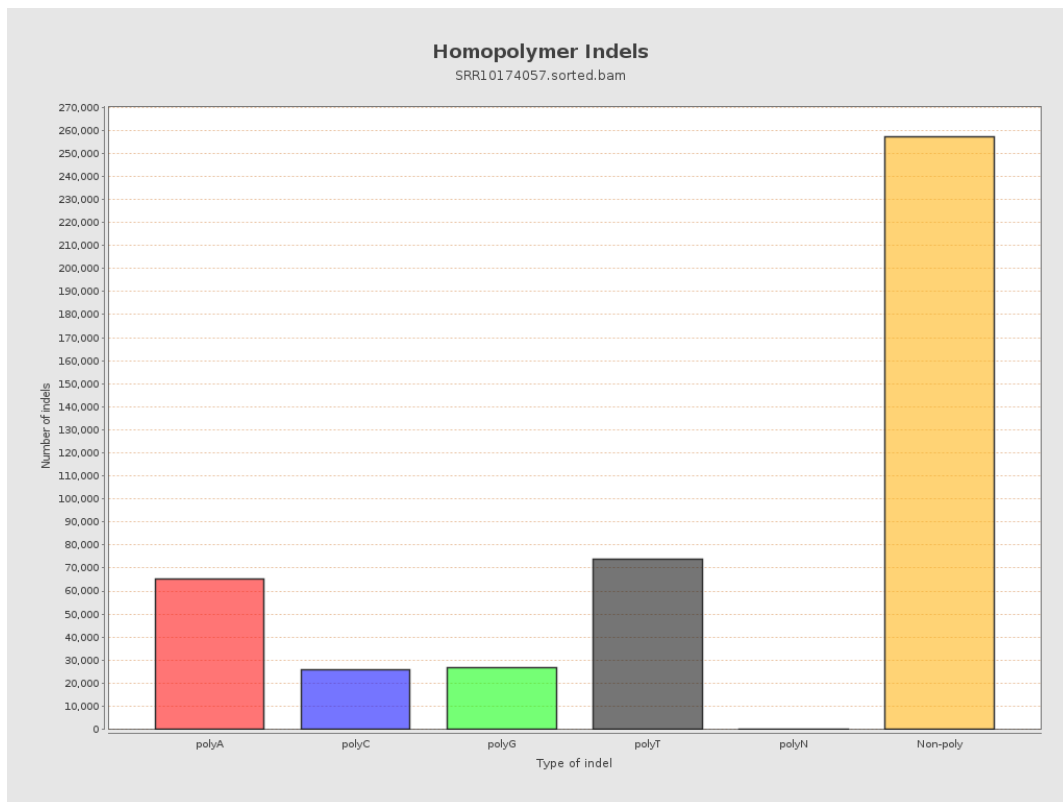
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



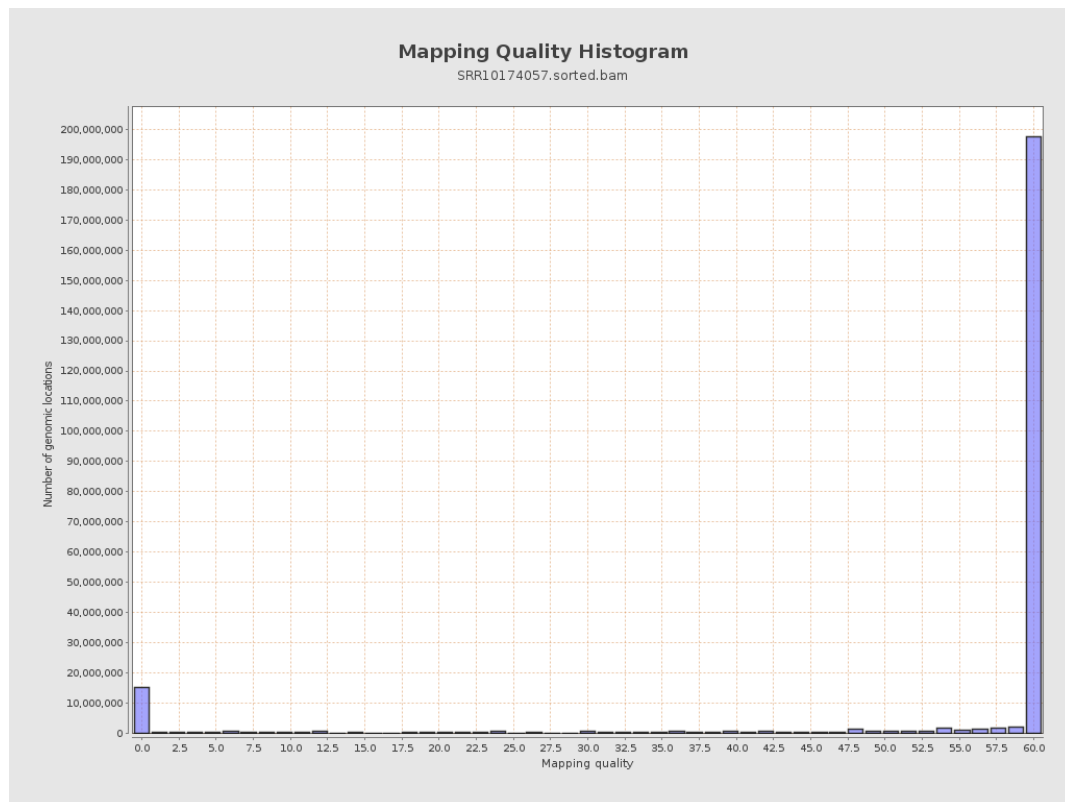
11. Results : Homopolymer Indels



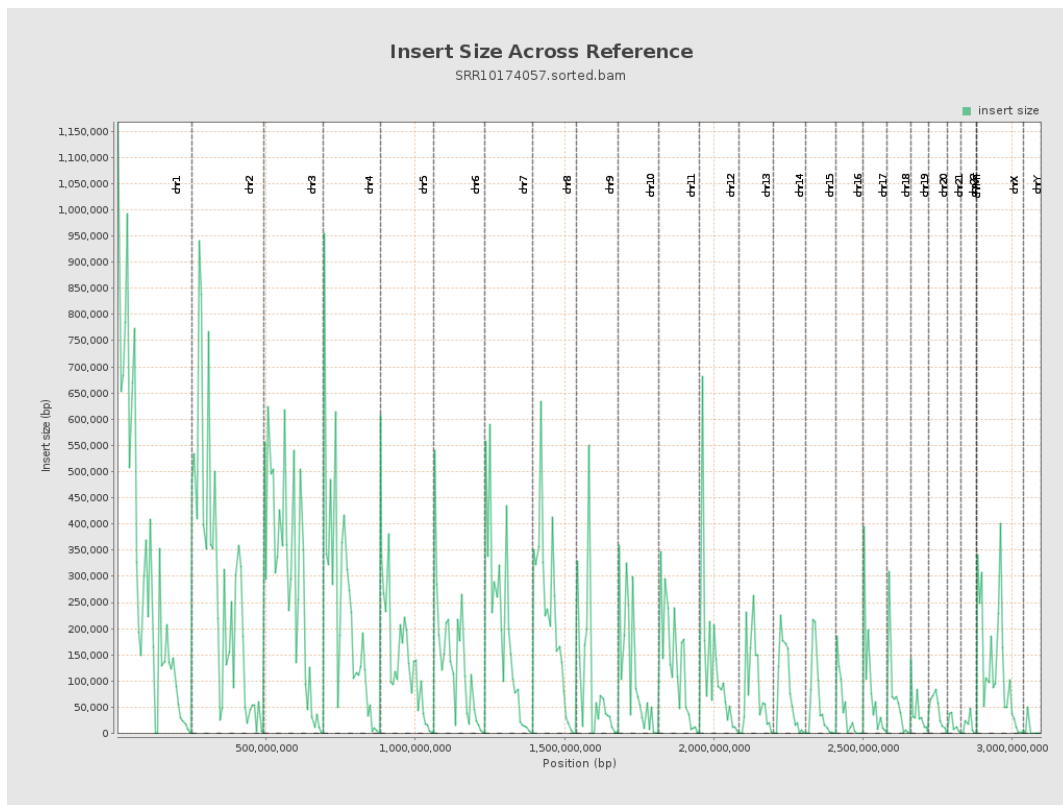
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

