

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:28:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174002.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_SRR10174002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174002_1.fastq.gz SRR10174002_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:28:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,096,982
Mapped reads	2,050,199 / 97.77%
Unmapped reads	46,783 / 2.23%
Mapped paired reads	2,050,199 / 97.77%
Mapped reads, first in pair	1,025,864 / 48.92%
Mapped reads, second in pair	1,024,335 / 48.85%
Mapped reads, both in pair	2,018,916 / 96.28%
Mapped reads, singletons	31,283 / 1.49%
Secondary alignments	0
Supplementary alignments	186,649 / 8.9%
Read min/max/mean length	30 / 133 / 127.58
Duplicated reads (estimated)	1,523,422 / 72.65%
Duplication rate	63.11%
Clipped reads	773,326 / 36.88%

2.2. ACGT Content

Number/percentage of A's	73,277,298 / 30.18%
Number/percentage of C's	47,361,501 / 19.51%
Number/percentage of T's	73,089,293 / 30.11%
Number/percentage of G's	49,038,385 / 20.2%
Number/percentage of N's	2,536 / 0%

GC Percentage	39.71%
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2.3. Coverage

Mean	0.0785
Standard Deviation	1.2642

2.4. Mapping Quality

Mean Mapping Quality	53.29
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2.5. Insert size

Mean	1,041,484.54
Standard Deviation	9,539,580.72
P25/Median/P75	143 / 195 / 270

2.6. Mismatches and indels

General error rate	1%
Mismatches	2,371,248
Insertions	26,066
Mapped reads with at least one insertion	1.23%
Deletions	58,998
Mapped reads with at least one deletion	2.81%
Homopolymer indels	42.35%

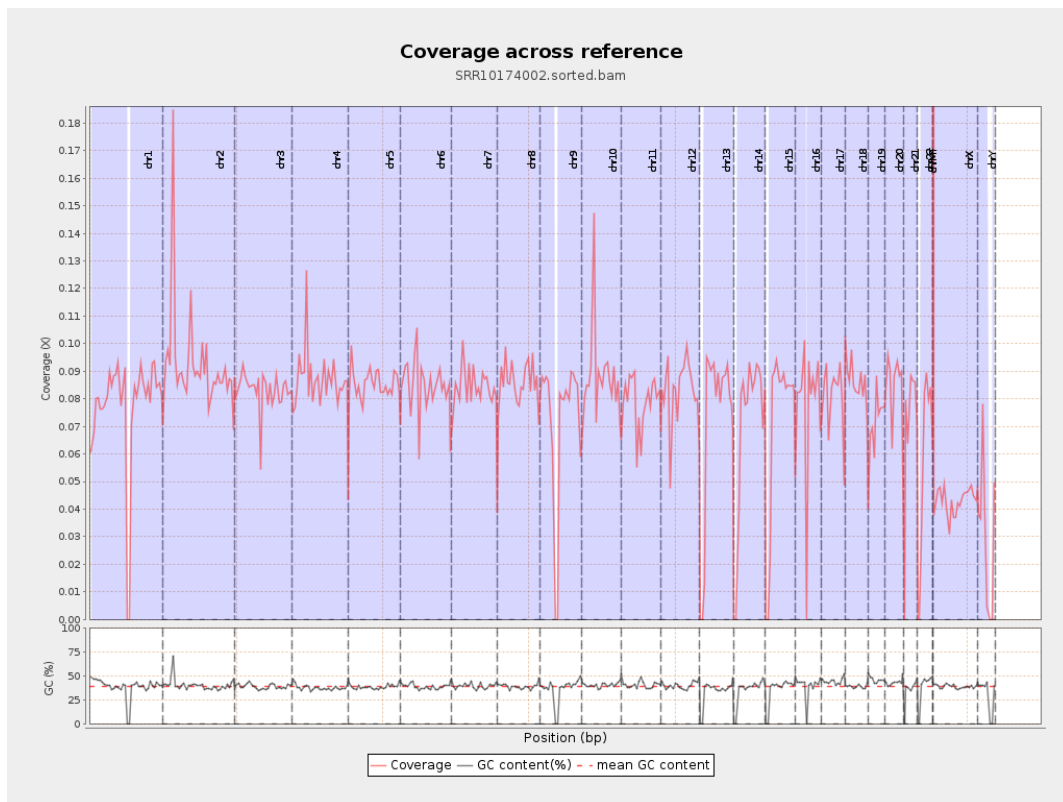
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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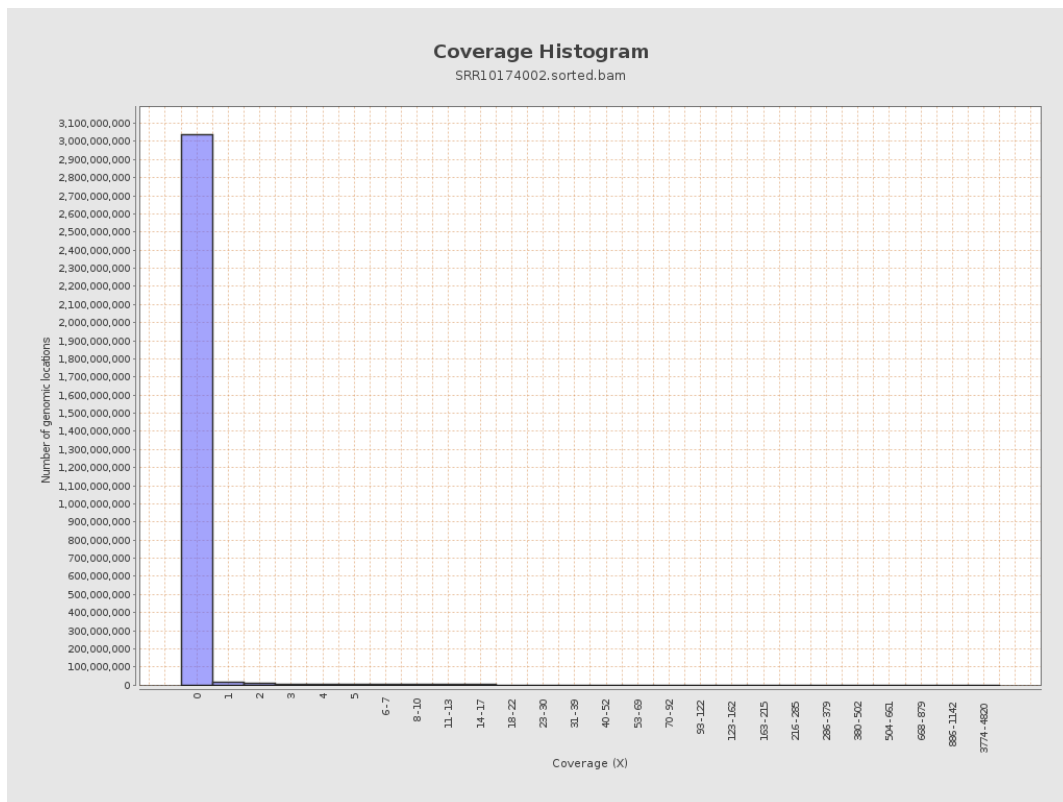
		bases	coverage	deviation
chr1	249250621	19321402	0.0775	0.8841
chr2	243199373	22491312	0.0925	3.4395
chr3	198022430	16461520	0.0831	0.7997
chr4	191154276	16672077	0.0872	0.9099
chr5	180915260	15412032	0.0852	0.806
chr6	171115067	14549226	0.085	0.849
chr7	159138663	13389970	0.0841	0.9686
chr8	146364022	12542254	0.0857	1.0609
chr9	141213431	10192376	0.0722	0.8495
chr10	135534747	11901033	0.0878	1.0605
chr11	135006516	10655311	0.0789	0.7914
chr12	133851895	11159295	0.0834	0.8055
chr13	115169878	8357301	0.0726	0.7566
chr14	107349540	7575511	0.0706	0.7382
chr15	102531392	7170718	0.0699	0.7244
chr16	90354753	6912216	0.0765	0.804
chr17	81195210	6650669	0.0819	0.8421
chr18	78077248	6777057	0.0868	1.131
chr19	59128983	4240329	0.0717	0.7832
chr20	63025520	5382996	0.0854	0.8226
chr21	48129895	3478092	0.0723	0.911
chr22	51304566	2940536	0.0573	0.6878
chrMT	16571	176649	10.6601	11.0827
chrX	155270560	6703665	0.0432	0.5656

chrY	59373566	1793490	0.0302	0.5611
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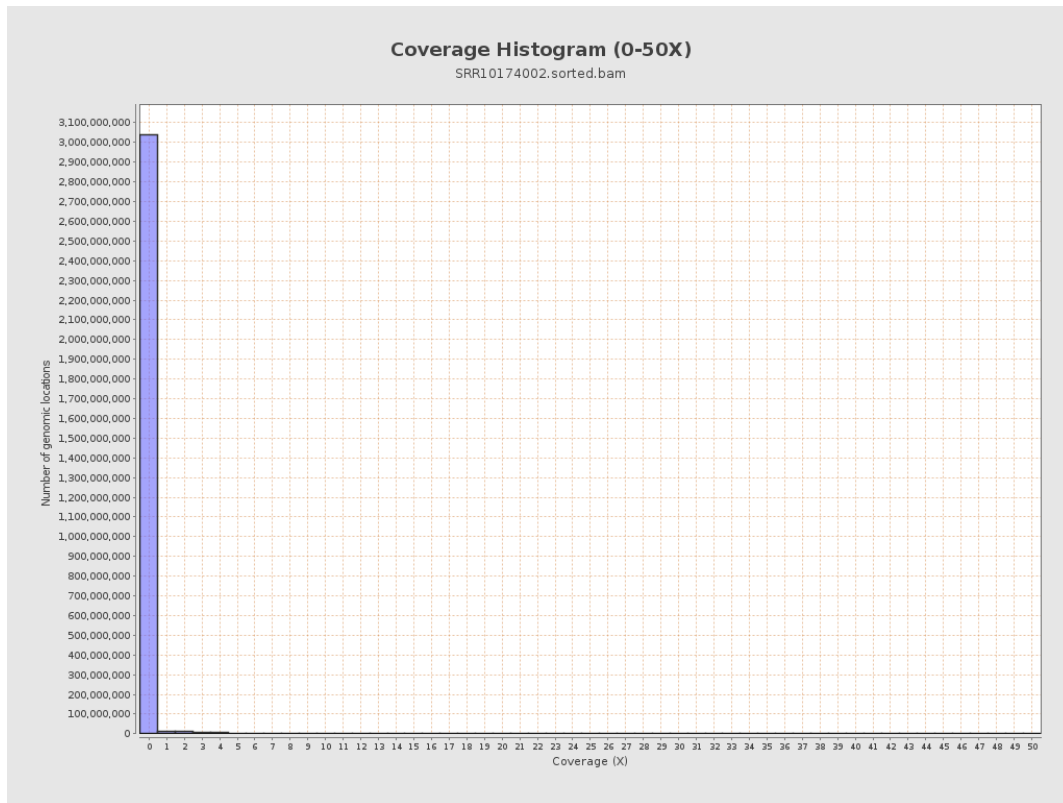
3. Results : Coverage across reference



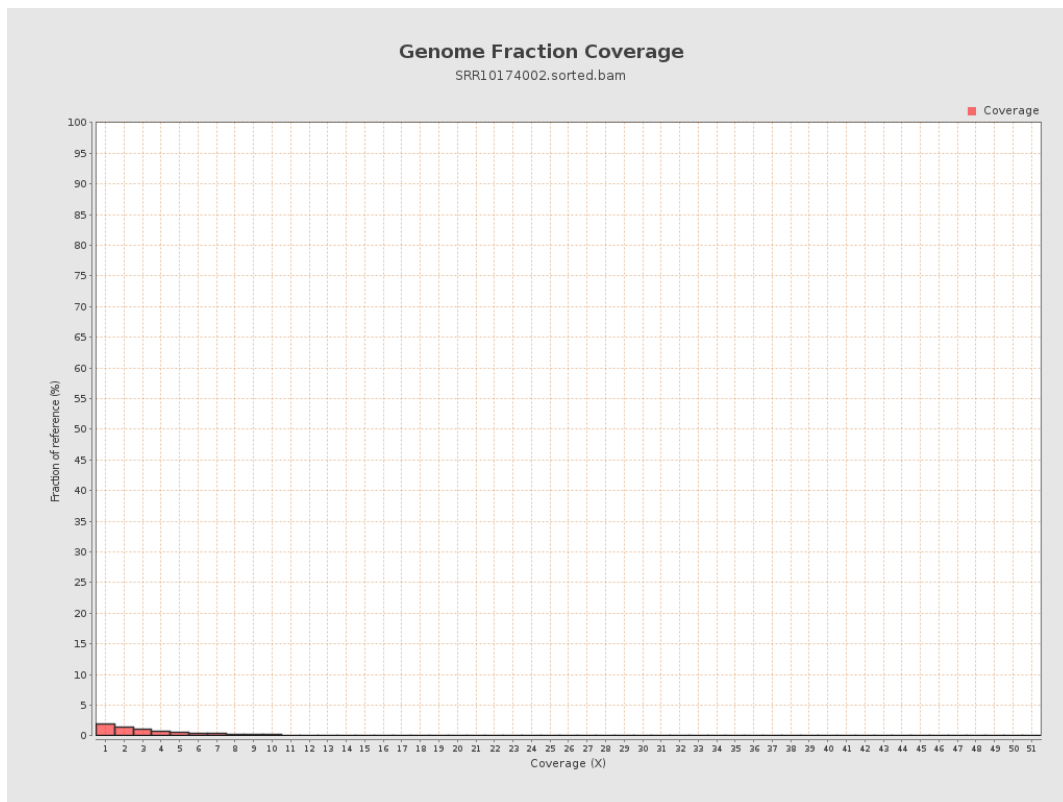
4. Results : Coverage Histogram



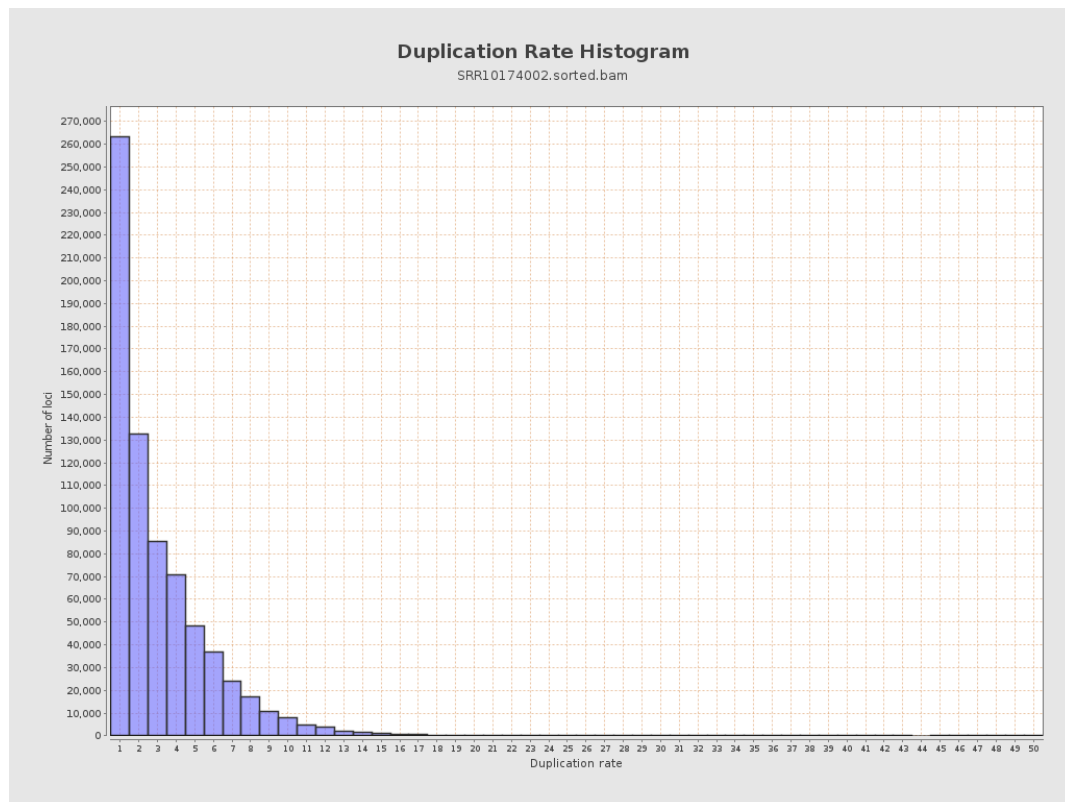
5. Results : Coverage Histogram (0-50X)



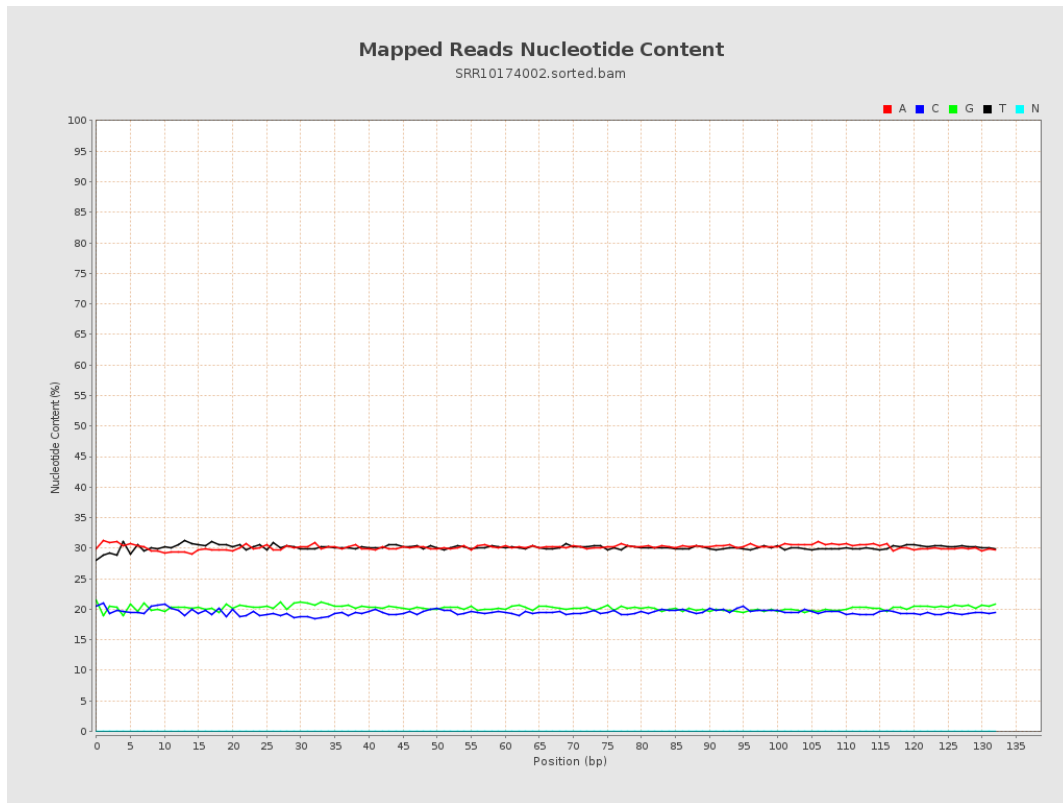
6. Results : Genome Fraction Coverage



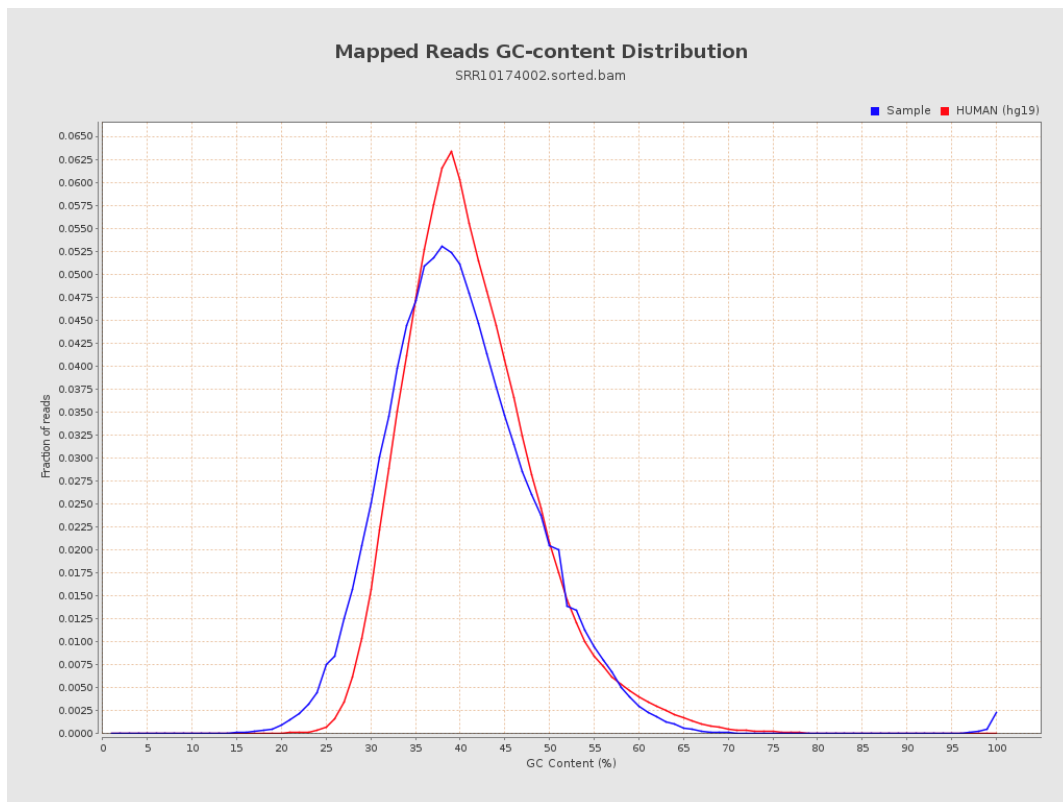
7. Results : Duplication Rate Histogram



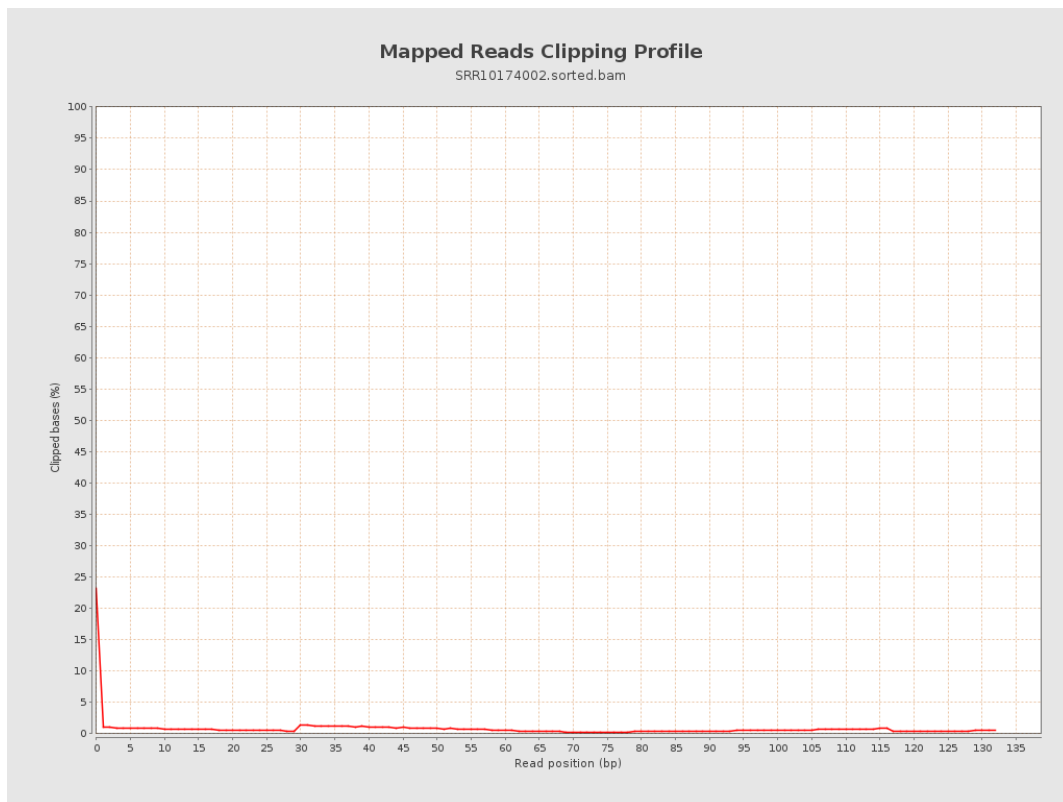
8. Results : Mapped Reads Nucleotide Content



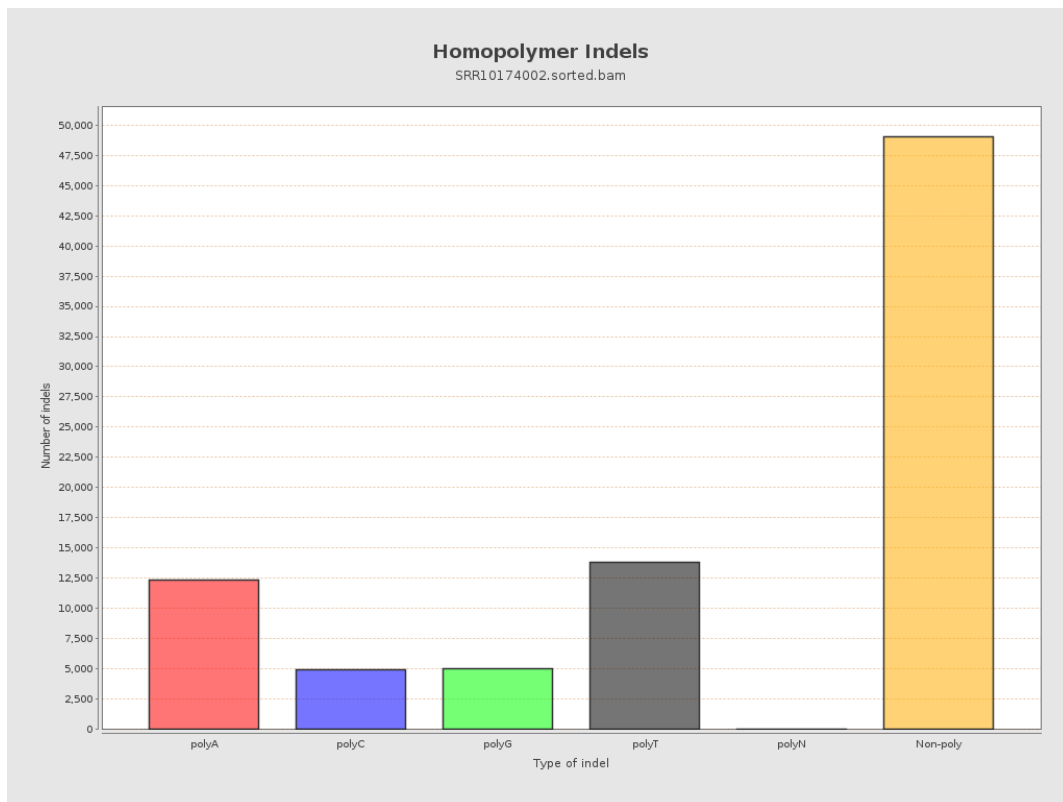
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



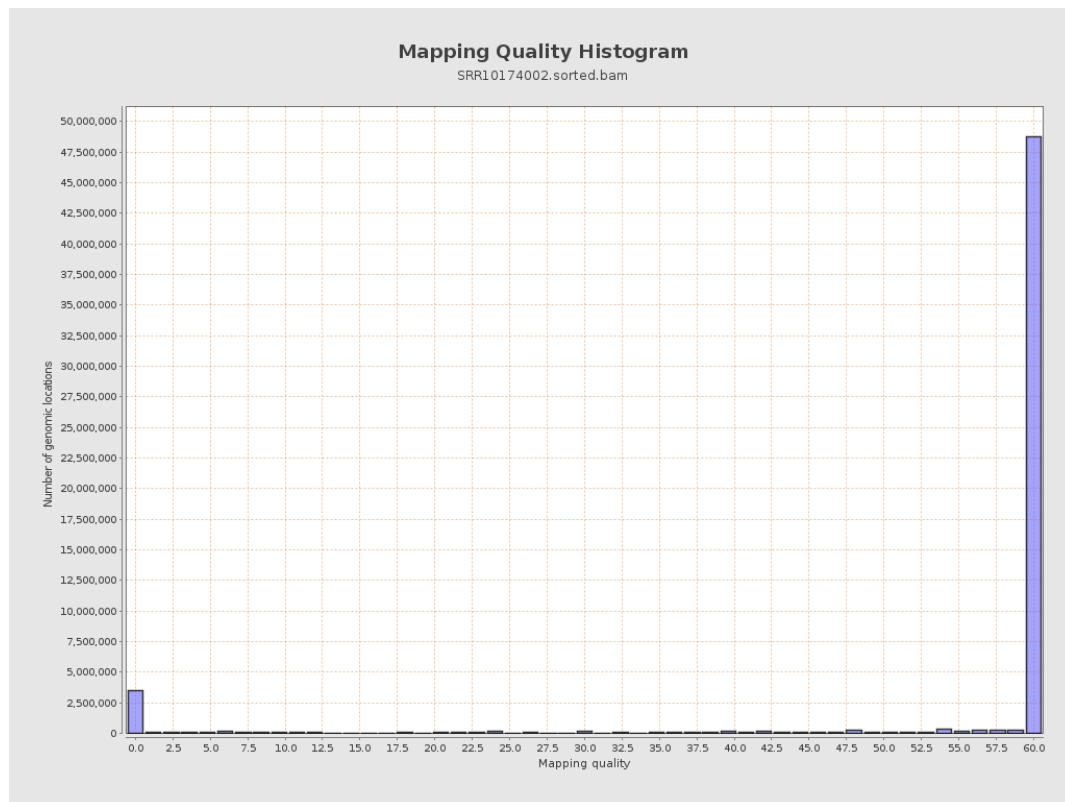
11. Results : Homopolymer Indels



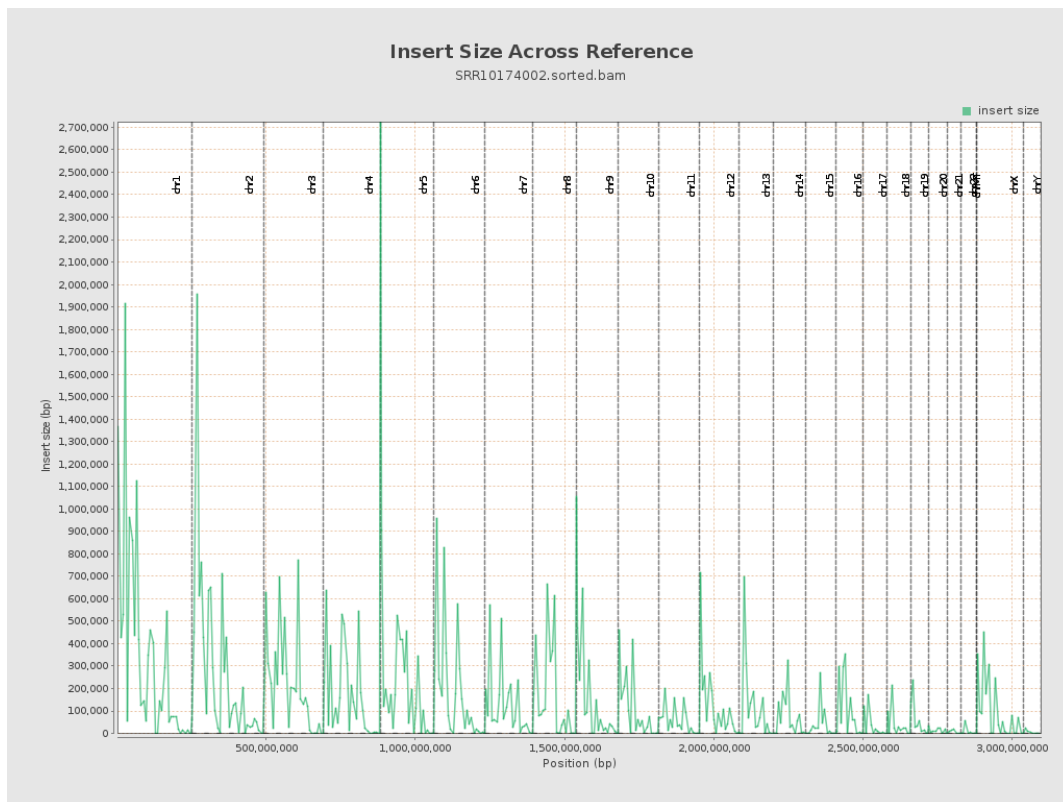
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

