

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:37:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174035.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_SRR10174035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174035_1.fastq.gz SRR10174035_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:37:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,575,230
Mapped reads	1,532,271 / 97.27%
Unmapped reads	42,959 / 2.73%
Mapped paired reads	1,532,271 / 97.27%
Mapped reads, first in pair	766,685 / 48.67%
Mapped reads, second in pair	765,586 / 48.6%
Mapped reads, both in pair	1,505,516 / 95.57%
Mapped reads, singletons	26,755 / 1.7%
Secondary alignments	0
Supplementary alignments	155,251 / 9.86%
Read min/max/mean length	30 / 133 / 128.44
Duplicated reads (estimated)	1,167,982 / 74.15%
Duplication rate	62.97%
Clipped reads	614,537 / 39.01%

2.2. ACGT Content

Number/percentage of A's	54,711,324 / 30.12%
Number/percentage of C's	35,595,091 / 19.59%
Number/percentage of T's	54,480,215 / 29.99%
Number/percentage of G's	36,867,820 / 20.3%
Number/percentage of N's	2,313 / 0%

GC Percentage	39.89%
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2.3. Coverage

Mean	0.0587
Standard Deviation	1.0017

2.4. Mapping Quality

Mean Mapping Quality	52.98
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2.5. Insert size

Mean	1,177,237.22
Standard Deviation	10,206,355.79
P25/Median/P75	148 / 204 / 286

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	1,959,245
Insertions	20,027
Mapped reads with at least one insertion	1.25%
Deletions	43,836
Mapped reads with at least one deletion	2.79%
Homopolymer indels	43.04%

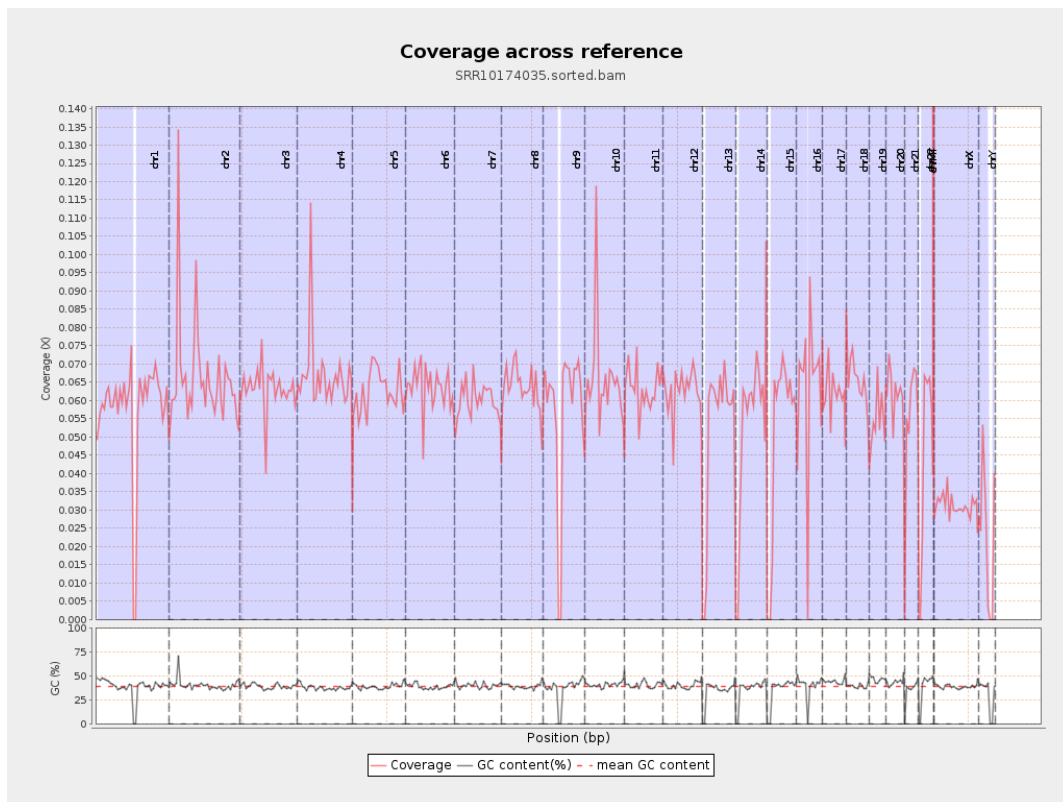
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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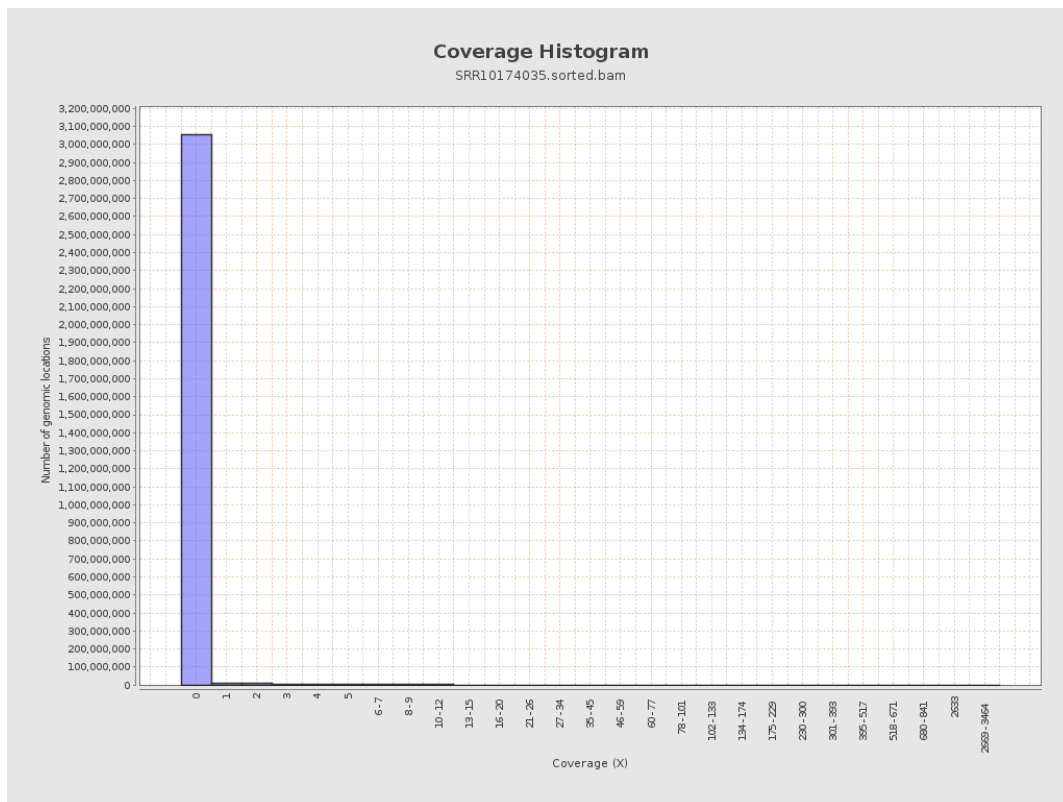
		bases	coverage	deviation
chr1	249250621	14384811	0.0577	0.8175
chr2	243199373	16117792	0.0663	2.5007
chr3	198022430	12498266	0.0631	0.7075
chr4	191154276	12791875	0.0669	0.8415
chr5	180915260	11305527	0.0625	0.7046
chr6	171115067	10852018	0.0634	0.7544
chr7	159138663	9608028	0.0604	0.7795
chr8	146364022	9292754	0.0635	0.8606
chr9	141213431	8080057	0.0572	0.7617
chr10	135534747	8929328	0.0659	0.8939
chr11	135006516	8517271	0.0631	0.711
chr12	133851895	8392715	0.0627	0.7013
chr13	115169878	5916765	0.0514	0.6463
chr14	107349540	5583358	0.052	0.6429
chr15	102531392	5264362	0.0513	0.6328
chr16	90354753	5707115	0.0632	0.792
chr17	81195210	4986490	0.0614	0.737
chr18	78077248	5159409	0.0661	0.948
chr19	59128983	3240401	0.0548	0.7311
chr20	63025520	3904084	0.0619	0.7006
chr21	48129895	2630965	0.0547	0.7273
chr22	51304566	2234331	0.0436	0.5779
chrMT	16571	210752	12.7181	11.9032
chrX	155270560	4849849	0.0312	0.4865

chrY	59373566	1304744	0.022	0.5222
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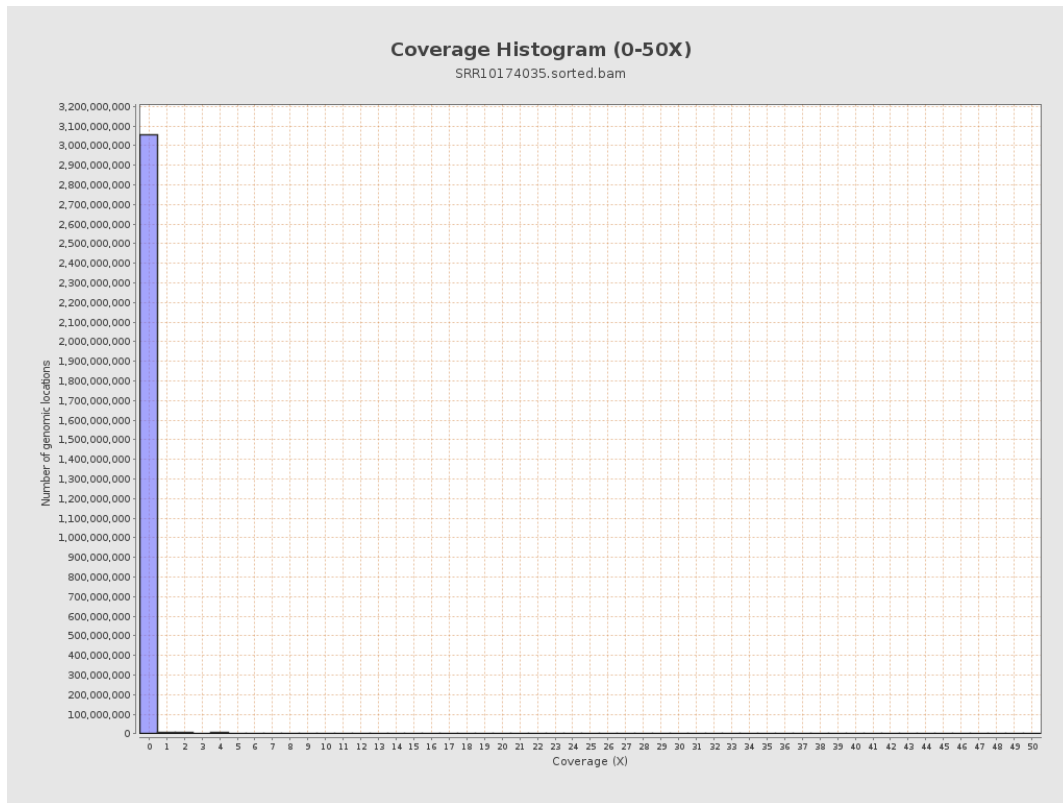
3. Results : Coverage across reference



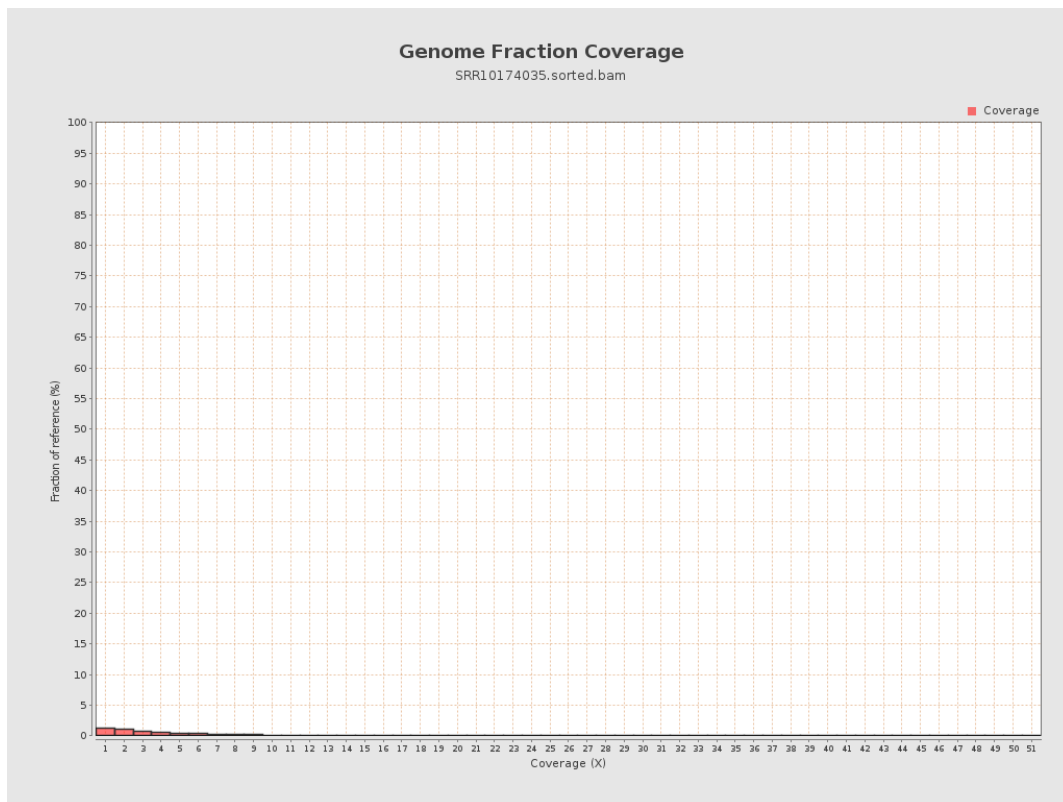
4. Results : Coverage Histogram



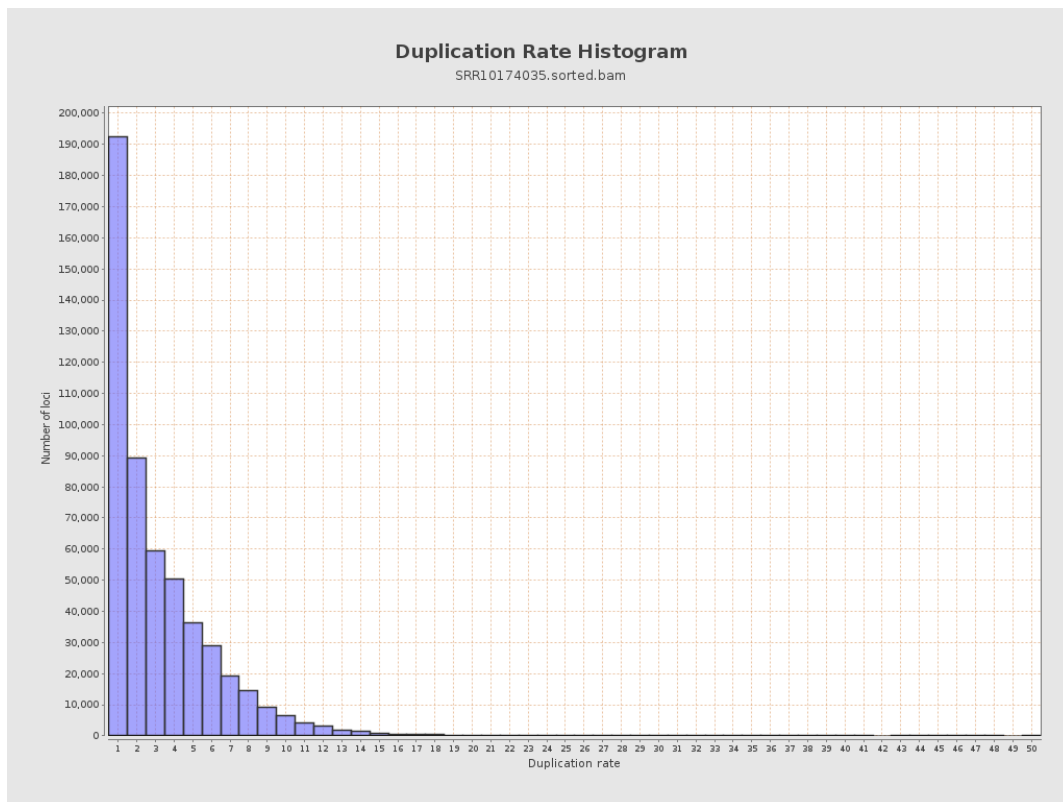
5. Results : Coverage Histogram (0-50X)



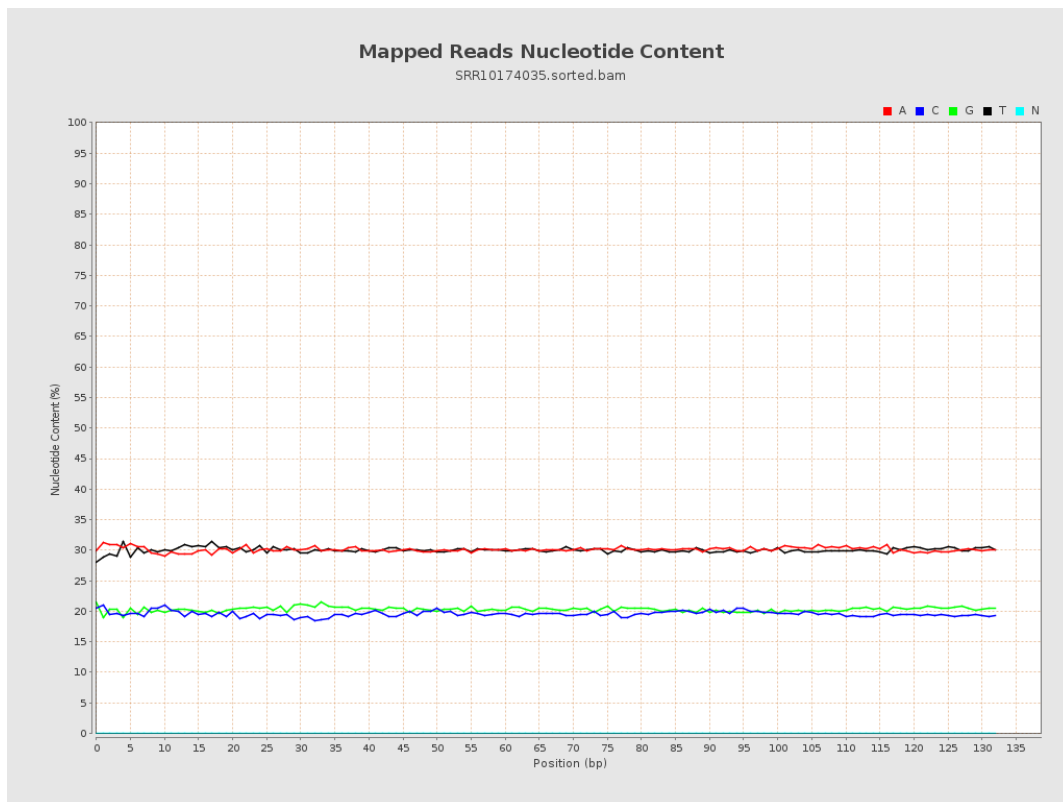
6. Results : Genome Fraction Coverage



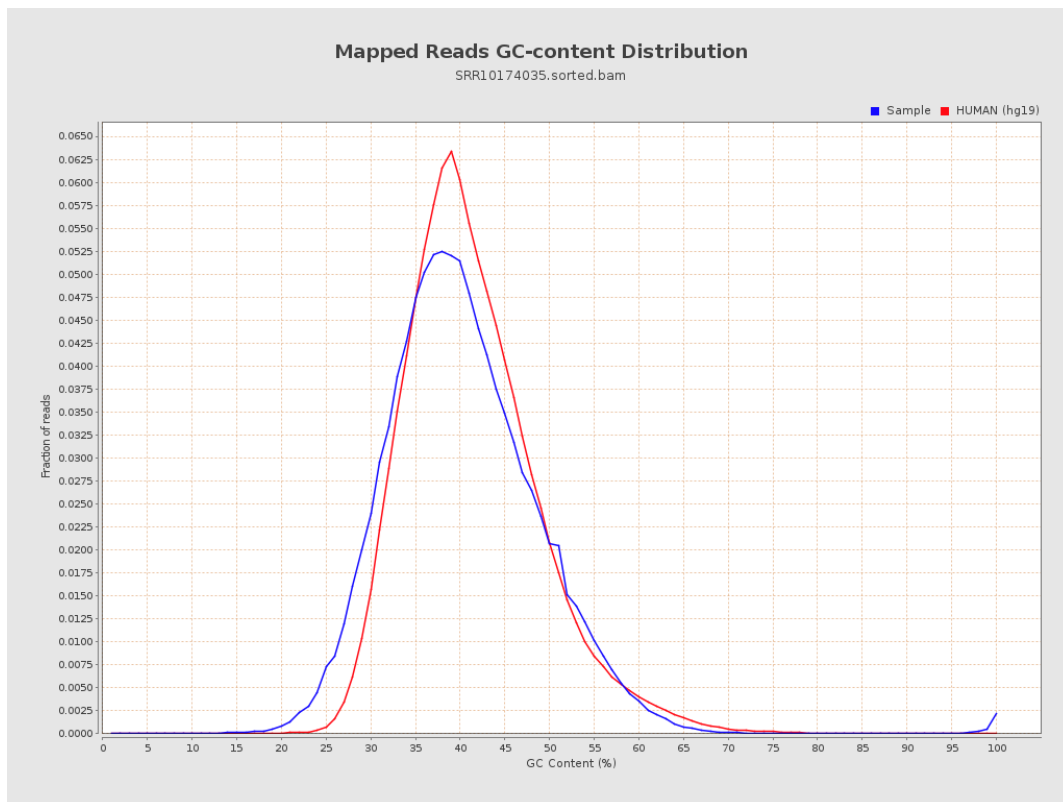
7. Results : Duplication Rate Histogram



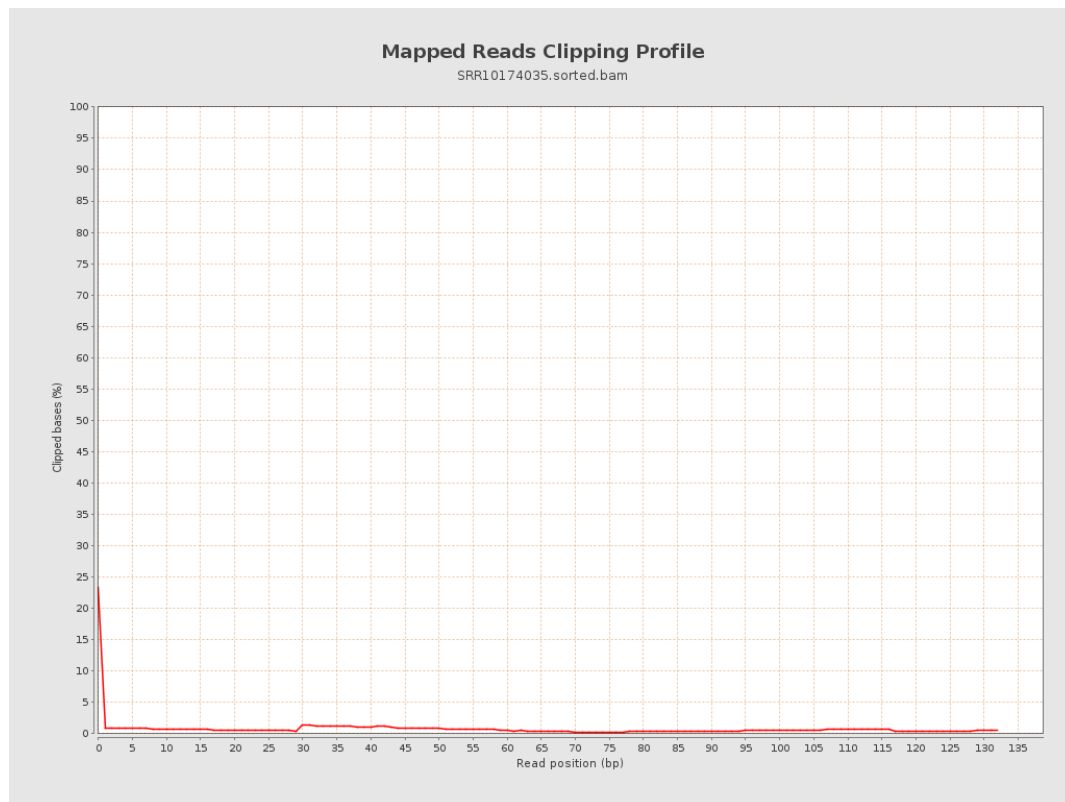
8. Results : Mapped Reads Nucleotide Content



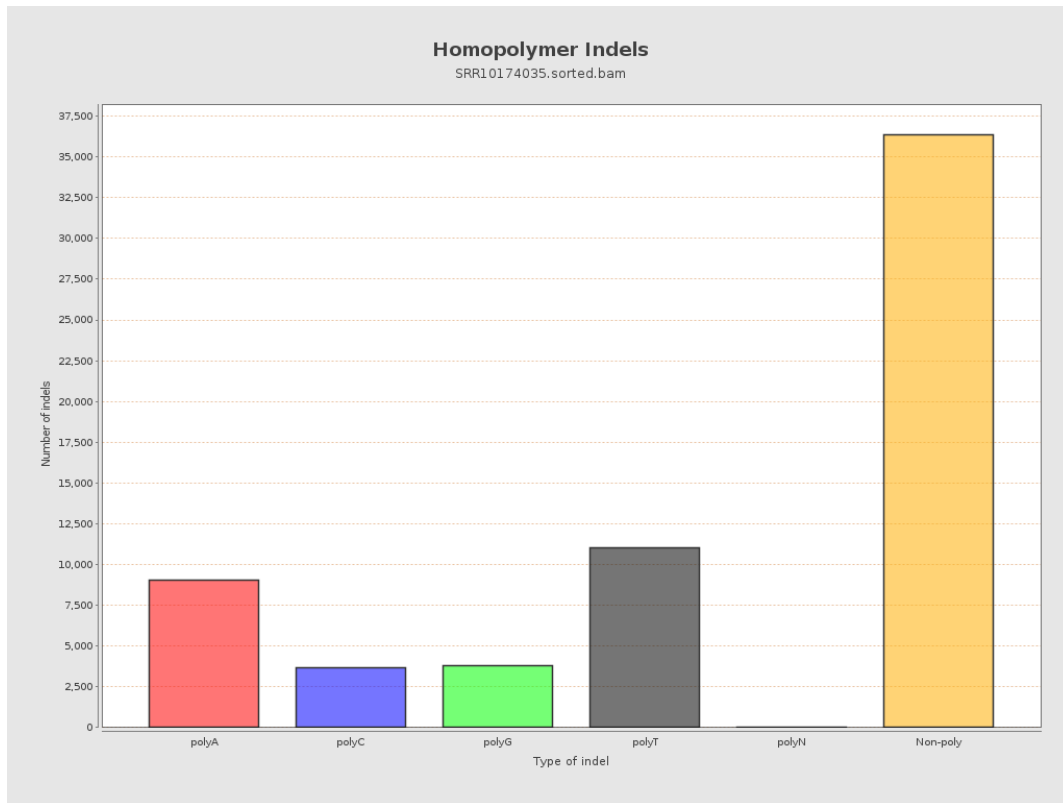
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



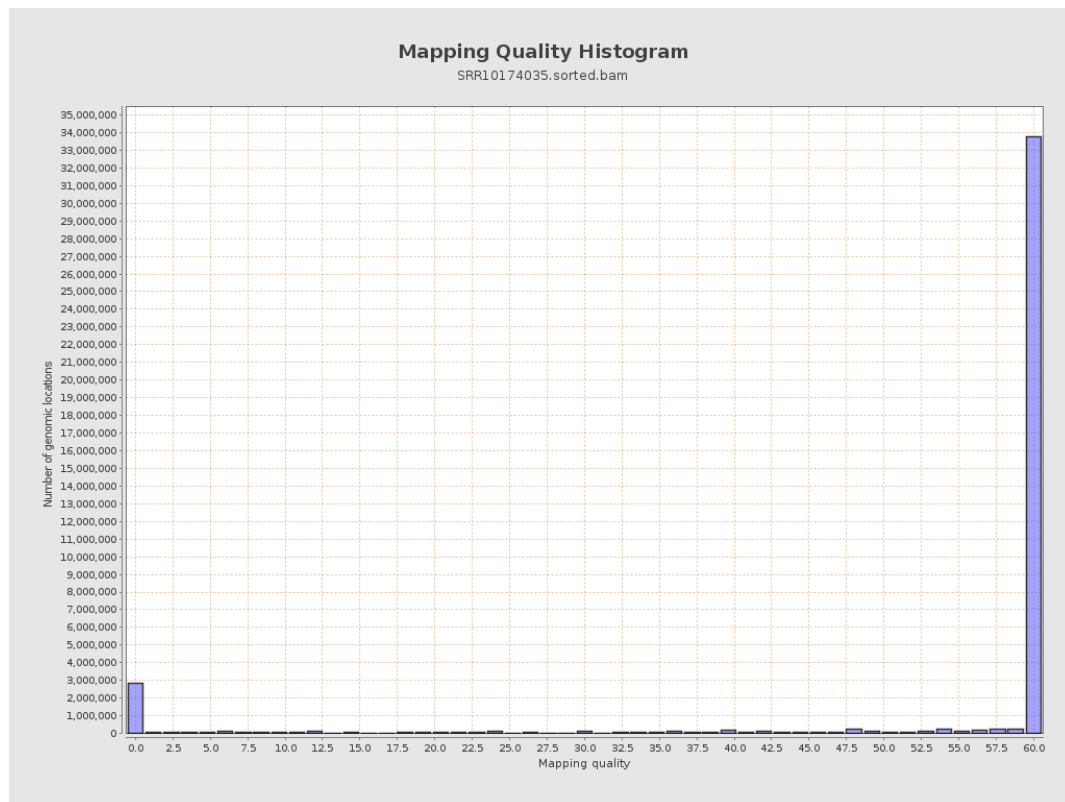
11. Results : Homopolymer Indels



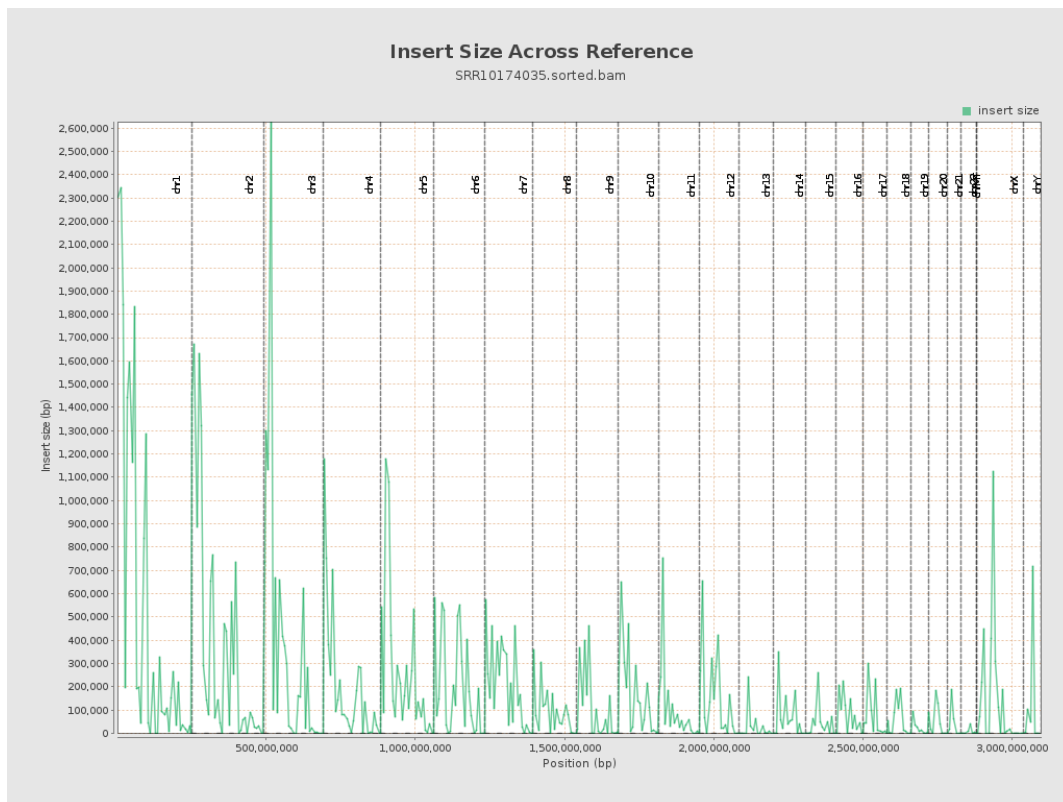
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

