

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 06:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174083.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_SRR10174083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174083_1.fastq.gz SRR10174083_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 06:34:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,202,508
Mapped reads	2,157,994 / 97.98%
Unmapped reads	44,514 / 2.02%
Mapped paired reads	2,157,994 / 97.98%
Mapped reads, first in pair	1,079,006 / 48.99%
Mapped reads, second in pair	1,078,988 / 48.99%
Mapped reads, both in pair	2,130,808 / 96.74%
Mapped reads, singletons	27,186 / 1.23%
Secondary alignments	0
Supplementary alignments	296,039 / 13.44%
Read min/max/mean length	30 / 133 / 124.77
Duplicated reads (estimated)	1,634,301 / 74.2%
Duplication rate	60.21%
Clipped reads	1,152,209 / 52.31%

2.2. ACGT Content

Number/percentage of A's	72,464,674 / 29.89%
Number/percentage of C's	48,121,406 / 19.85%
Number/percentage of T's	71,915,416 / 29.67%
Number/percentage of G's	49,901,127 / 20.59%
Number/percentage of N's	1,945 / 0%

GC Percentage	40.44%
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2.3. Coverage

Mean	0.0784
Standard Deviation	1.5981

2.4. Mapping Quality

Mean Mapping Quality	52.51
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2.5. Insert size

Mean	960,049.68
Standard Deviation	8,979,869.79
P25/Median/P75	101 / 144 / 217

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,047,738
Insertions	26,851
Mapped reads with at least one insertion	1.2%
Deletions	72,041
Mapped reads with at least one deletion	3.26%
Homopolymer indels	41.19%

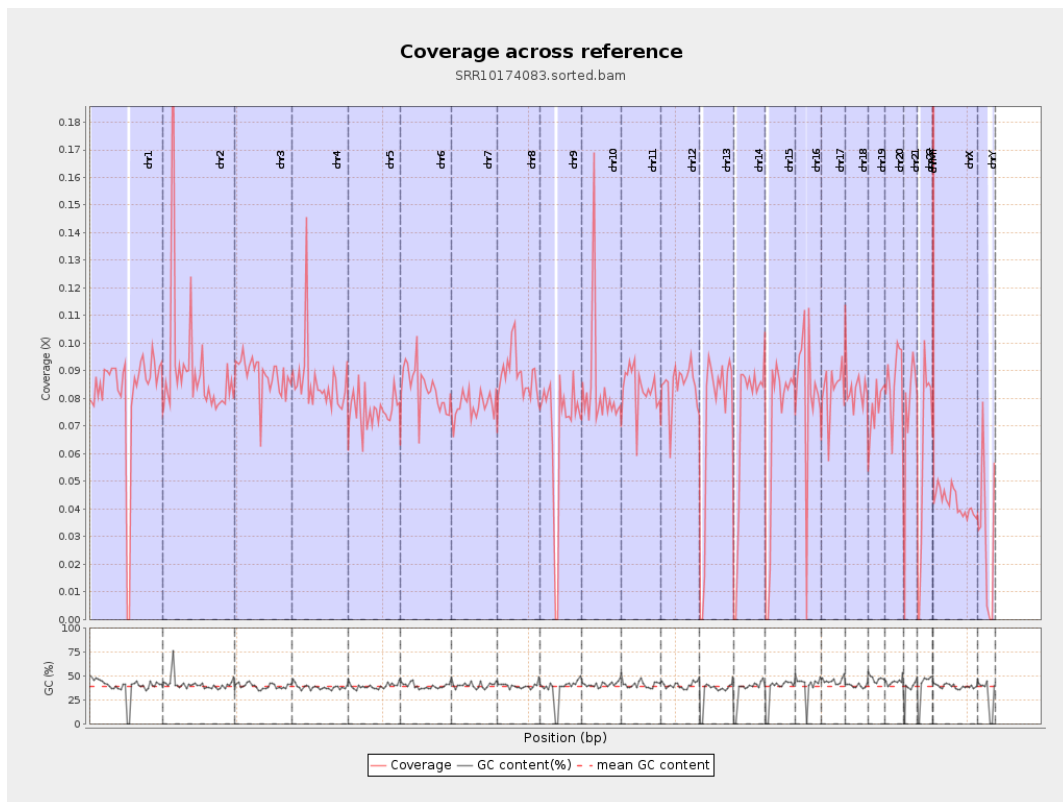
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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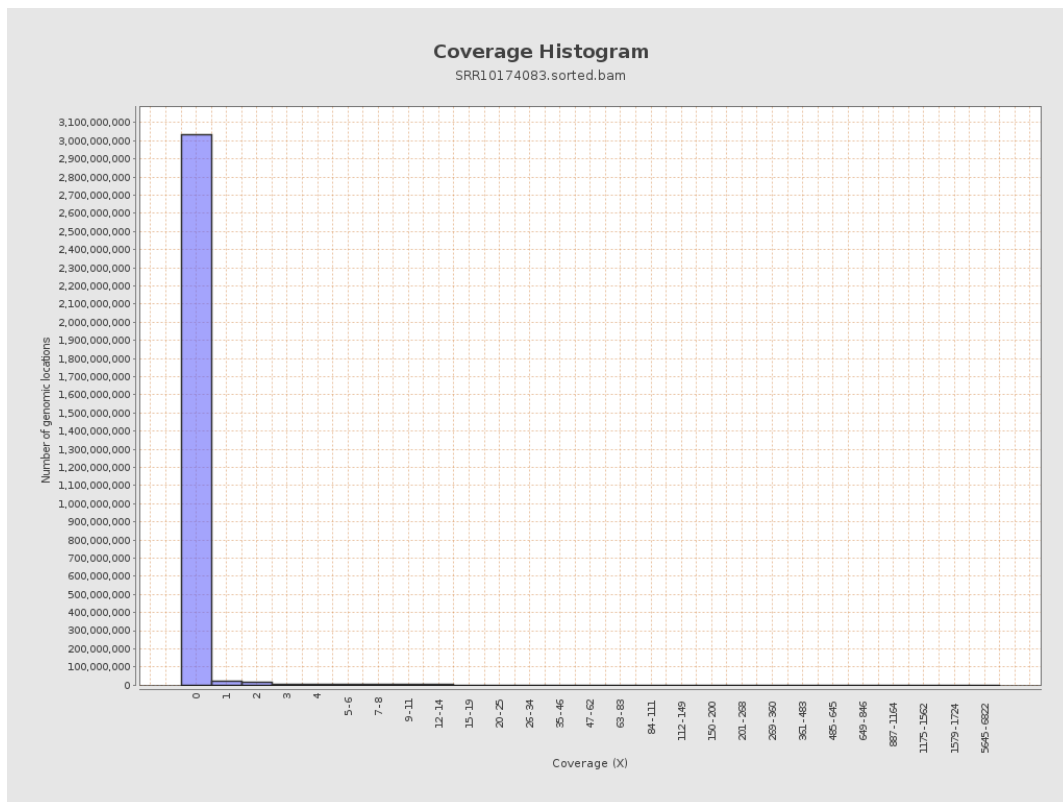
		bases	coverage	deviation
chr1	249250621	20447708	0.082	0.9392
chr2	243199373	21871754	0.0899	4.8536
chr3	198022430	17490318	0.0883	0.8494
chr4	191154276	16436549	0.086	0.9619
chr5	180915260	13676416	0.0756	0.7751
chr6	171115067	14316910	0.0837	0.869
chr7	159138663	12332405	0.0775	0.8686
chr8	146364022	12957475	0.0885	1.0905
chr9	141213431	9827545	0.0696	0.8295
chr10	135534747	11247099	0.083	1.1493
chr11	135006516	11296657	0.0837	0.8257
chr12	133851895	11381040	0.085	0.834
chr13	115169878	8367166	0.0727	0.7703
chr14	107349540	7727856	0.072	0.7621
chr15	102531392	6999779	0.0683	0.7405
chr16	90354753	7383795	0.0817	0.8777
chr17	81195210	6790877	0.0836	0.833
chr18	78077248	6509076	0.0834	1.0628
chr19	59128983	4538299	0.0768	0.8185
chr20	63025520	5448376	0.0864	0.8351
chr21	48129895	3674611	0.0763	0.8764
chr22	51304566	3096946	0.0604	0.8159
chrMT	16571	327088	19.7386	19.4436
chrX	155270560	6575684	0.0423	0.5786

chrY	59373566	1854466	0.0312	0.621
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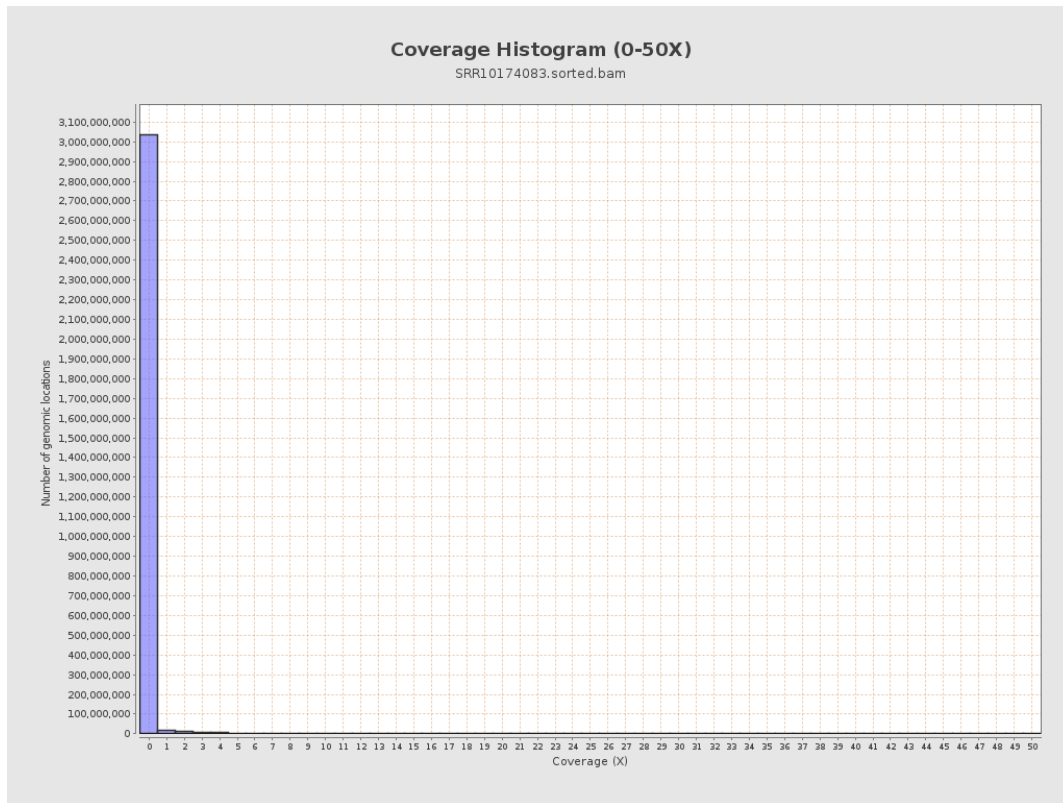
3. Results : Coverage across reference



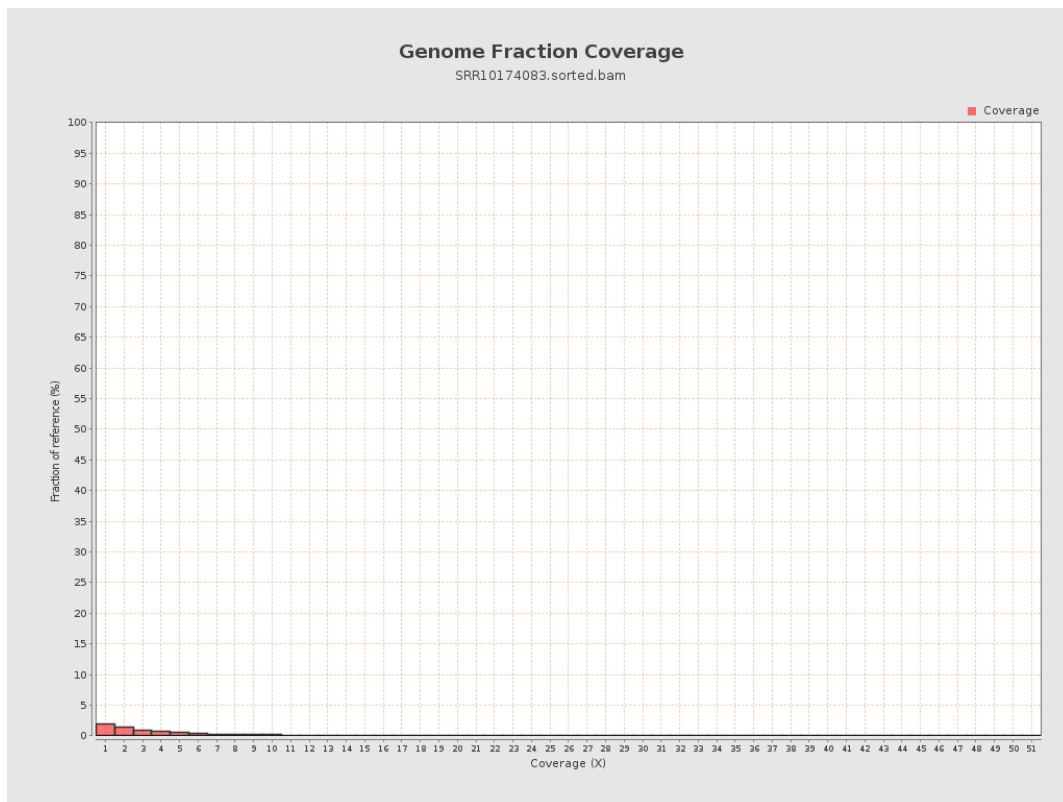
4. Results : Coverage Histogram



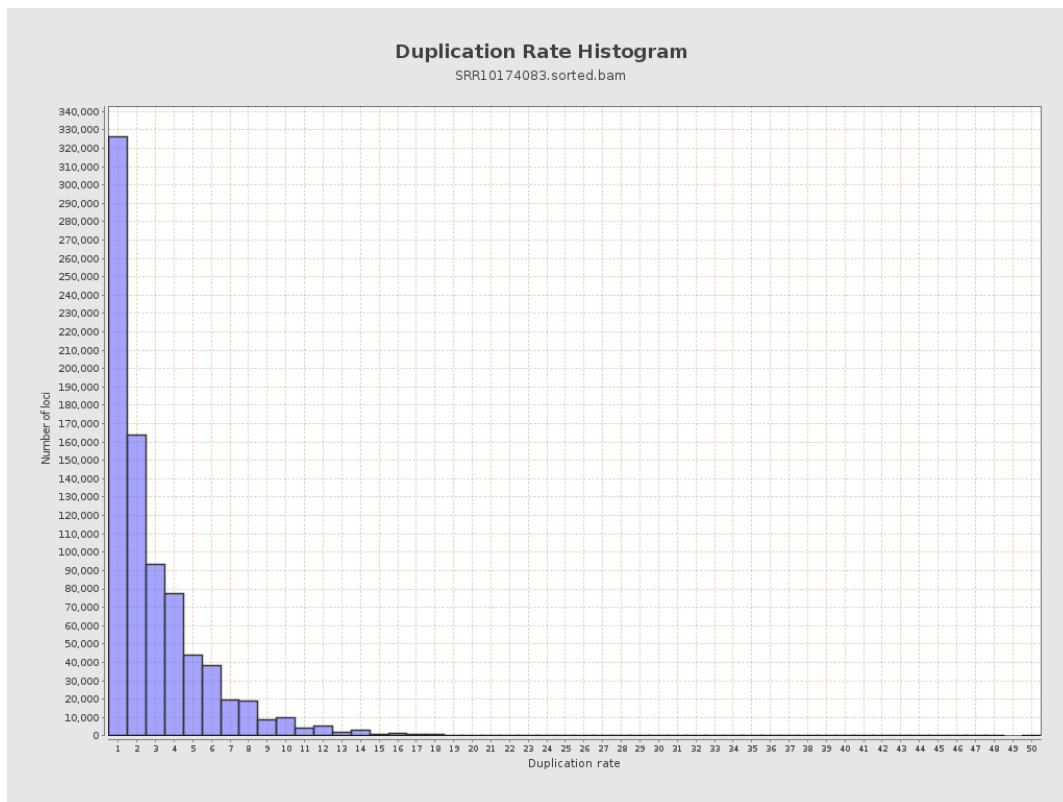
5. Results : Coverage Histogram (0-50X)



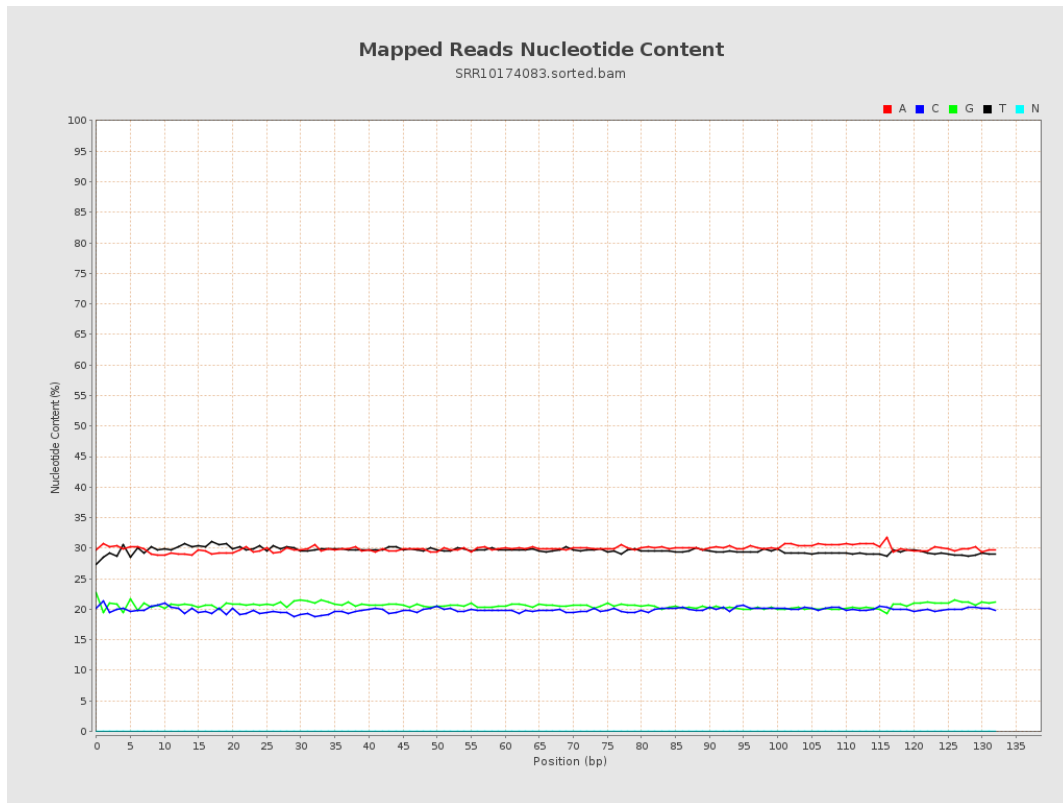
6. Results : Genome Fraction Coverage



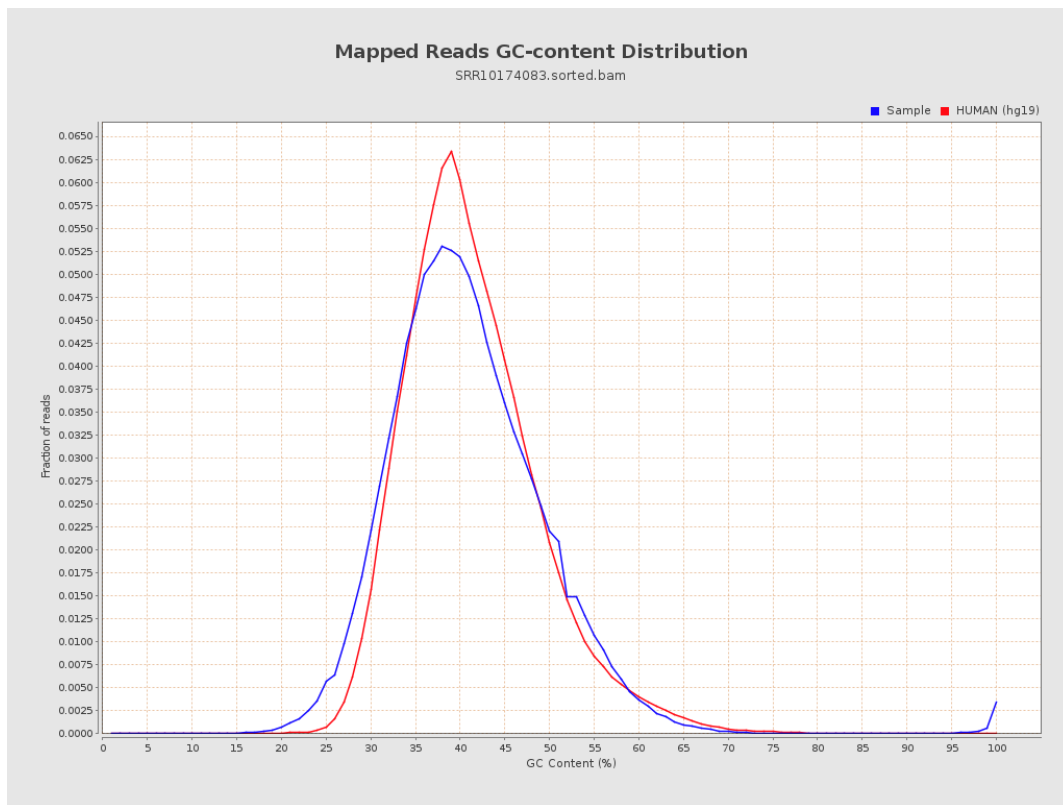
7. Results : Duplication Rate Histogram



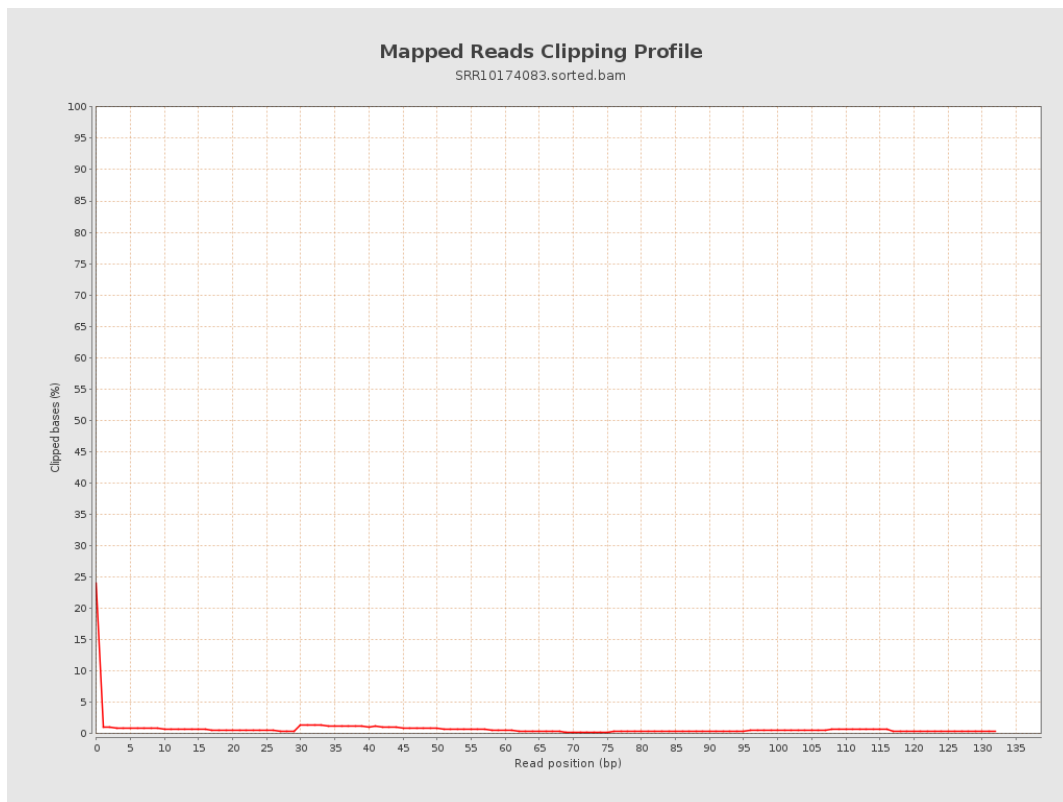
8. Results : Mapped Reads Nucleotide Content



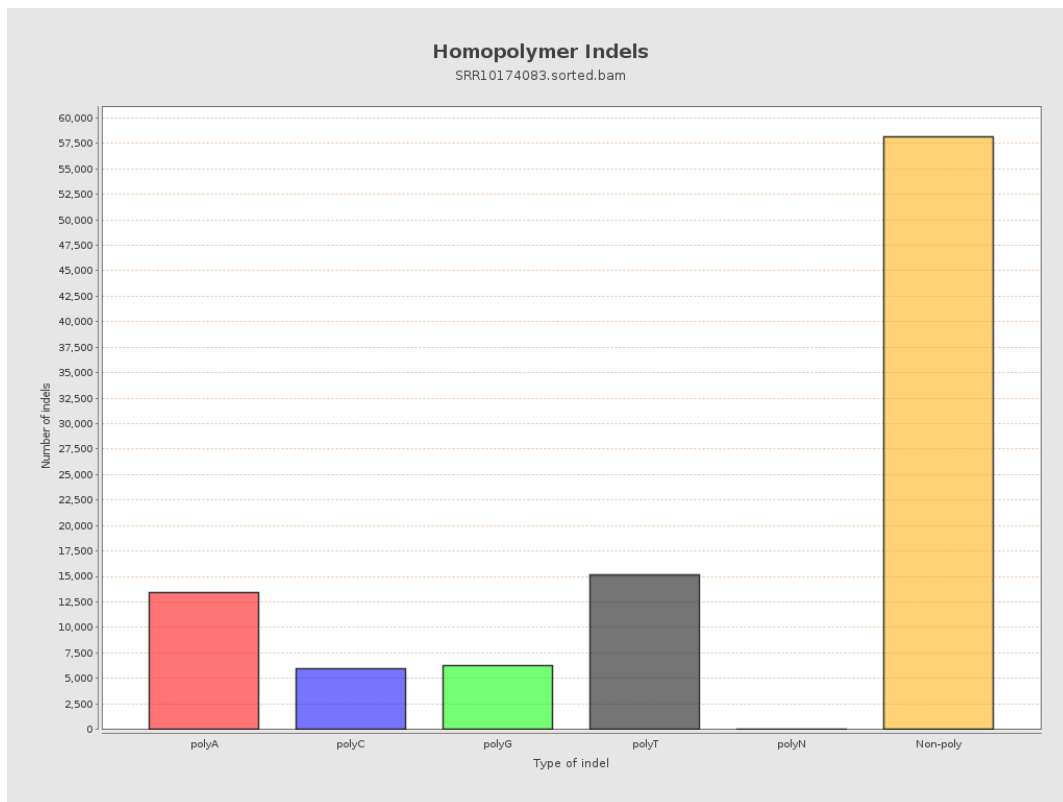
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



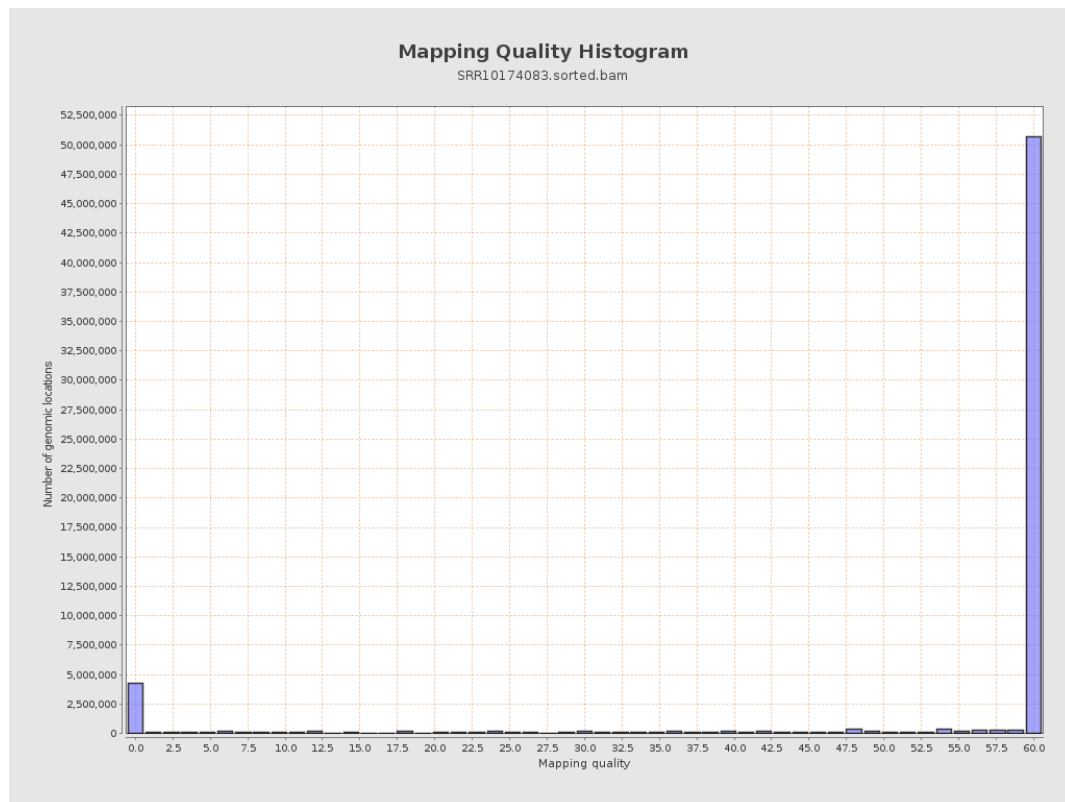
11. Results : Homopolymer Indels



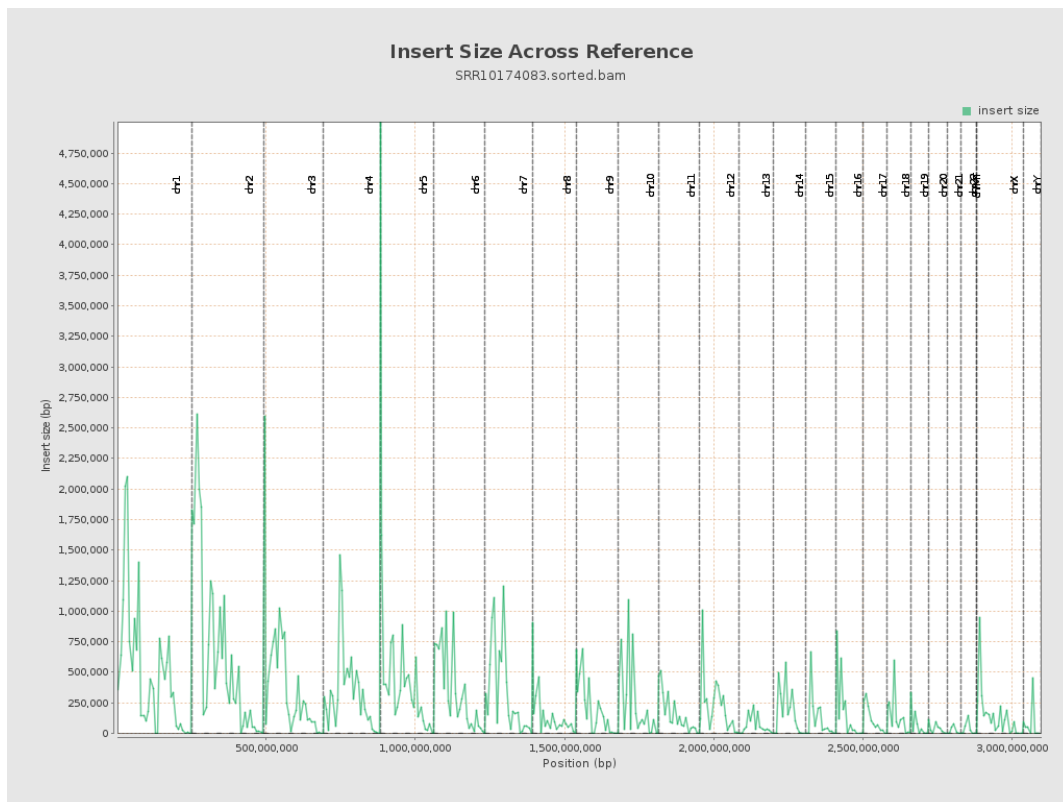
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

