

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 01:43:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174052.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_SRR10174052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174052_1.fastq.gz SRR10174052_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 01:43:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,318,974
Mapped reads	8,089,736 / 97.24%
Unmapped reads	229,238 / 2.76%
Mapped paired reads	8,089,736 / 97.24%
Mapped reads, first in pair	4,052,206 / 48.71%
Mapped reads, second in pair	4,037,530 / 48.53%
Mapped reads, both in pair	7,943,168 / 95.48%
Mapped reads, singletons	146,568 / 1.76%
Secondary alignments	0
Supplementary alignments	852,318 / 10.25%
Read min/max/mean length	30 / 133 / 128.45
Duplicated reads (estimated)	6,331,886 / 76.11%
Duplication rate	64.45%
Clipped reads	3,311,183 / 39.8%

2.2. ACGT Content

Number/percentage of A's	289,522,754 / 30.25%
Number/percentage of C's	186,128,178 / 19.45%
Number/percentage of T's	288,834,576 / 30.18%
Number/percentage of G's	192,617,567 / 20.12%
Number/percentage of N's	11,716 / 0%

GC Percentage	39.57%
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2.3. Coverage

Mean	0.3093
Standard Deviation	4.3372

2.4. Mapping Quality

Mean Mapping Quality	52.62
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2.5. Insert size

Mean	917,835.62
Standard Deviation	8,772,941.47
P25/Median/P75	145 / 202 / 290

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	9,971,323
Insertions	98,700
Mapped reads with at least one insertion	1.18%
Deletions	211,856
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.27%

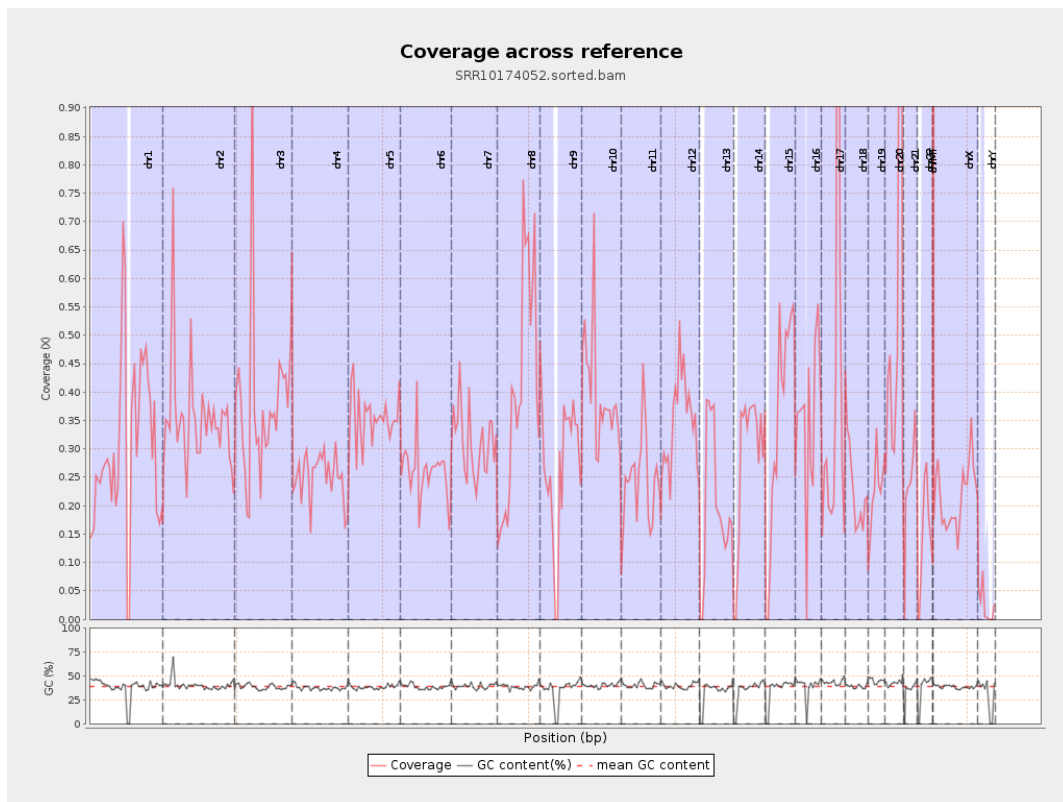
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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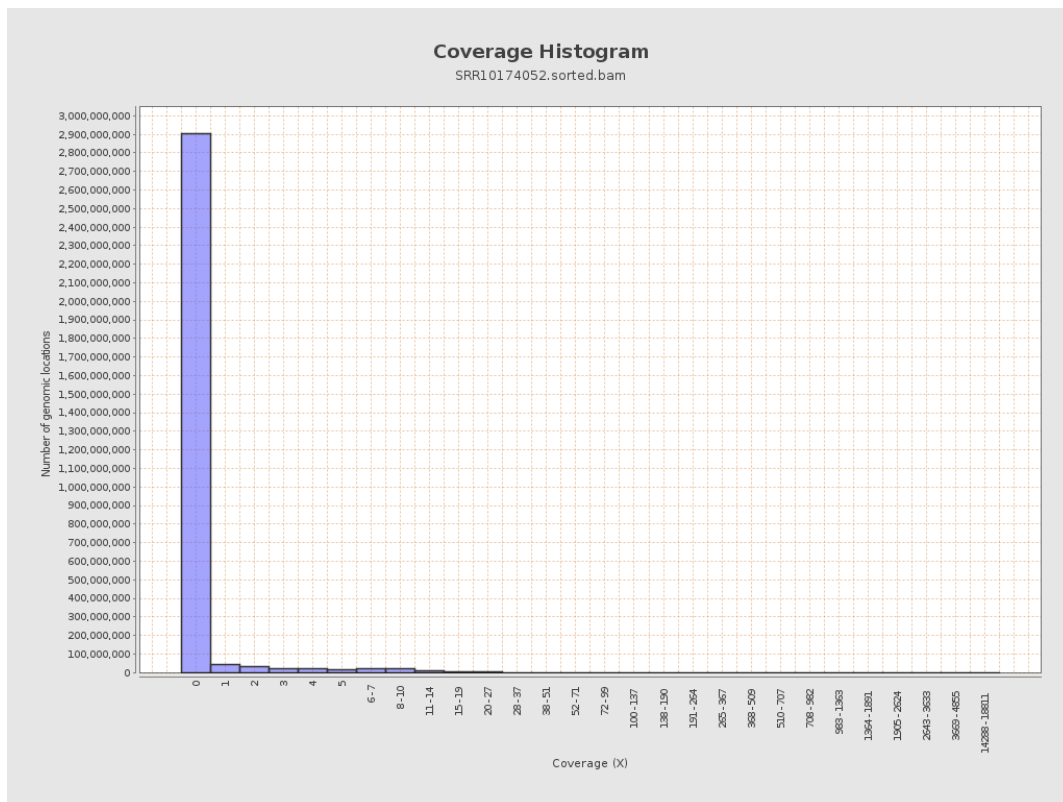
		bases	coverage	deviation
chr1	249250621	75575352	0.3032	3.3282
chr2	243199373	85863243	0.3531	13.1674
chr3	198022430	74581561	0.3766	1.858
chr4	191154276	48184526	0.2521	1.6503
chr5	180915260	63950695	0.3535	1.7345
chr6	171115067	44546612	0.2603	2.0738
chr7	159138663	49538348	0.3113	2.6156
chr8	146364022	58370400	0.3988	2.8927
chr9	141213431	37415047	0.265	2.3105
chr10	135534747	53729245	0.3964	4.3636
chr11	135006516	32744299	0.2425	1.5143
chr12	133851895	46887688	0.3503	1.7459
chr13	115169878	22871286	0.1986	1.3077
chr14	107349540	31039075	0.2891	1.592
chr15	102531392	35019455	0.3415	1.7086
chr16	90354753	31398377	0.3475	2.617
chr17	81195210	36532165	0.4499	2.296
chr18	78077248	18206518	0.2332	3.485
chr19	59128983	13532868	0.2289	2.3657
chr20	63025520	41560672	0.6594	2.7389
chr21	48129895	11592458	0.2409	1.5205
chr22	51304566	7512798	0.1464	1.0772
chrMT	16571	1979602	119.4618	89.6698
chrX	155270560	33557114	0.2161	1.3621

chrY	59373566	1450307	0.0244	0.7875
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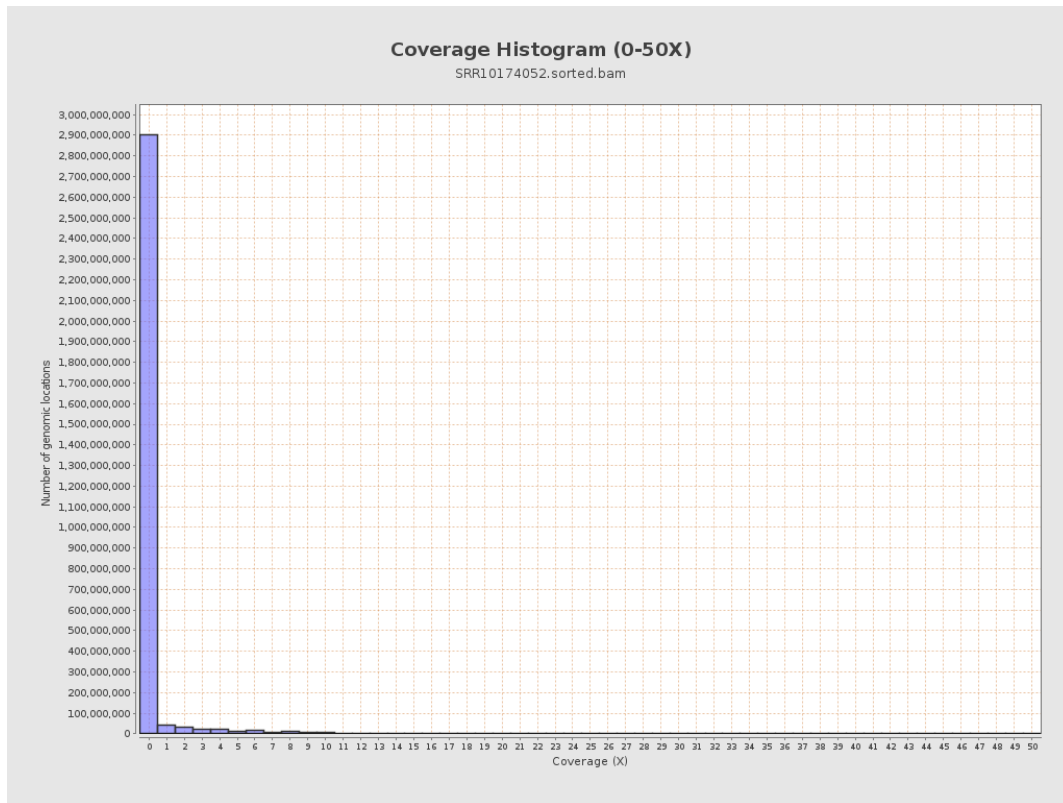
3. Results : Coverage across reference



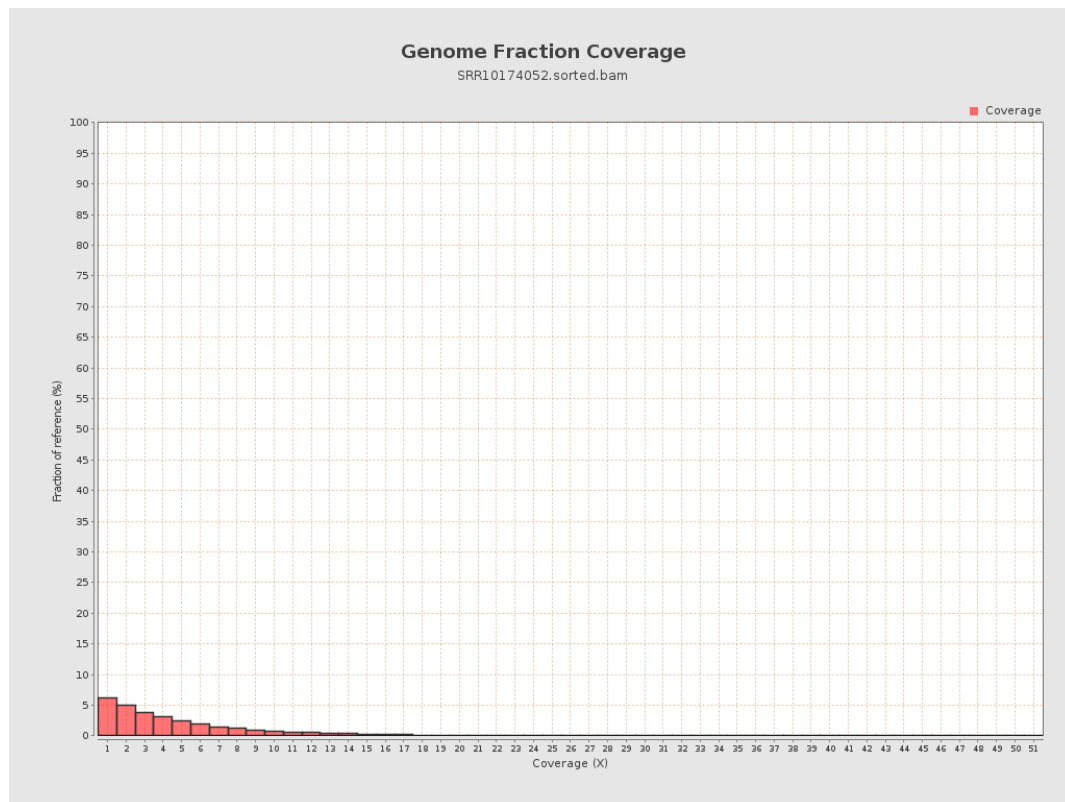
4. Results : Coverage Histogram



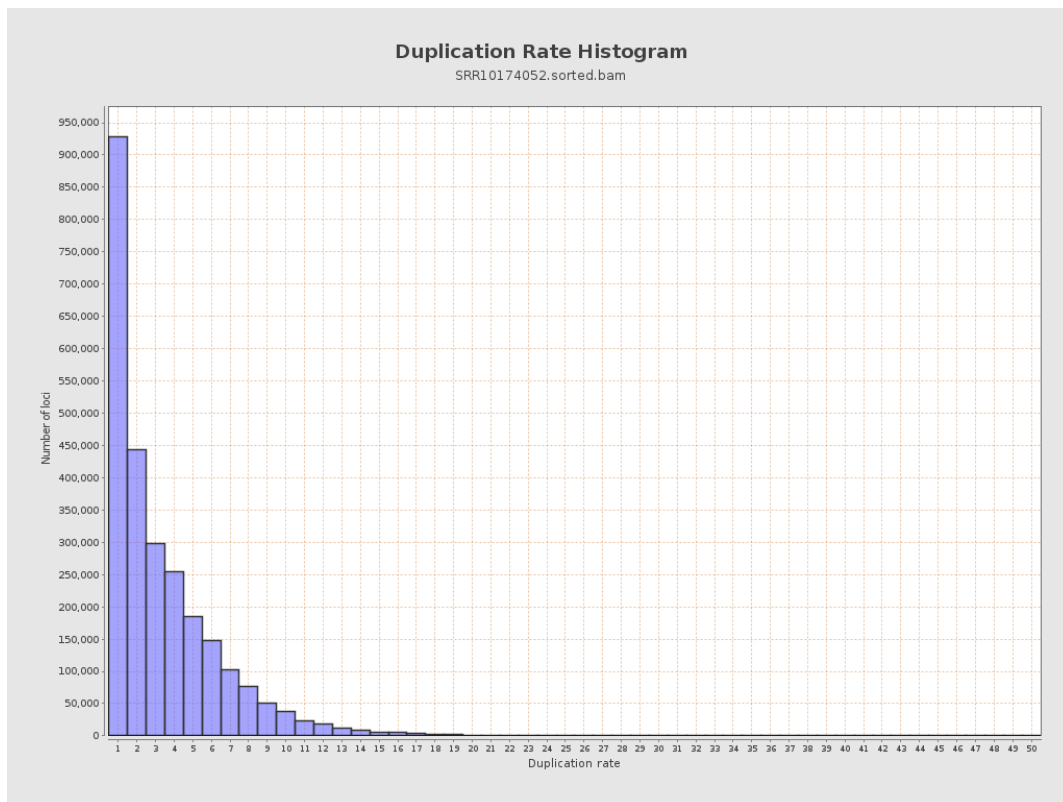
5. Results : Coverage Histogram (0-50X)



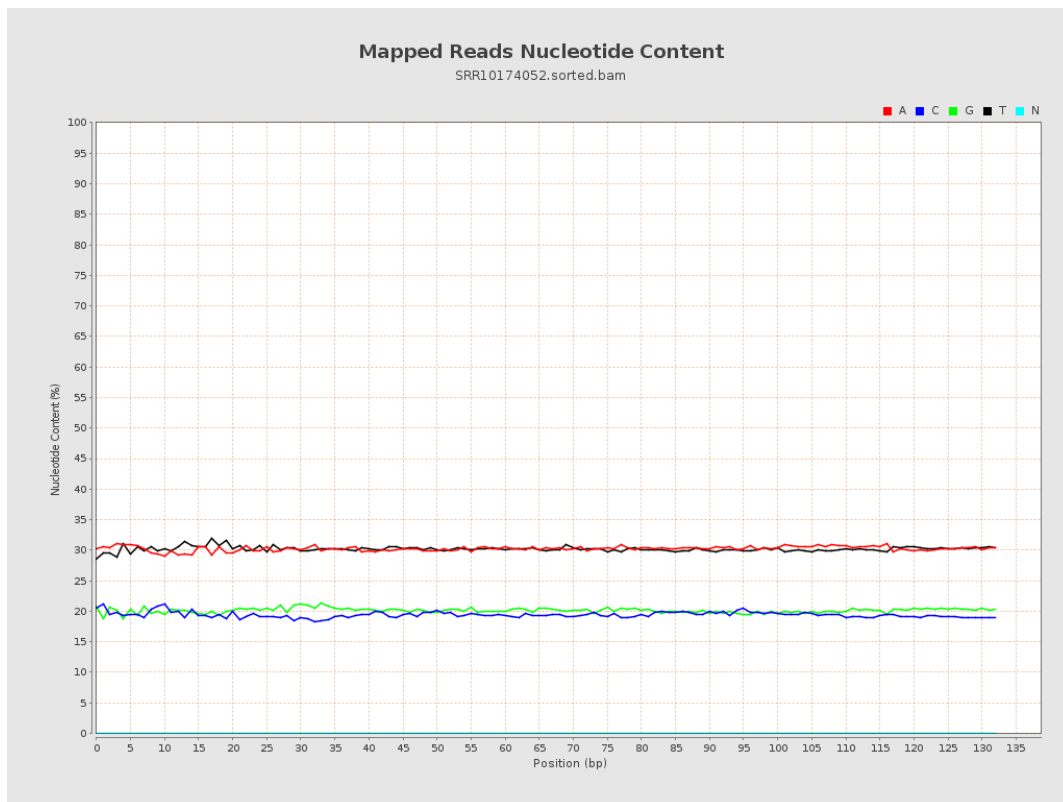
6. Results : Genome Fraction Coverage



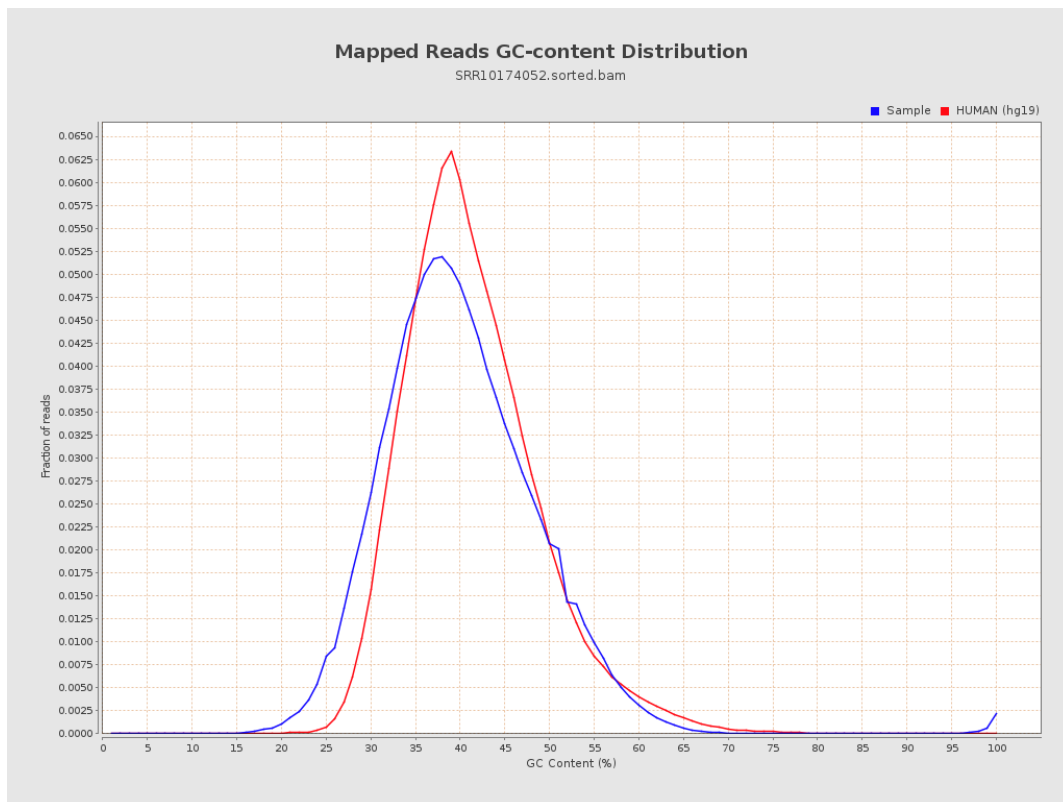
7. Results : Duplication Rate Histogram



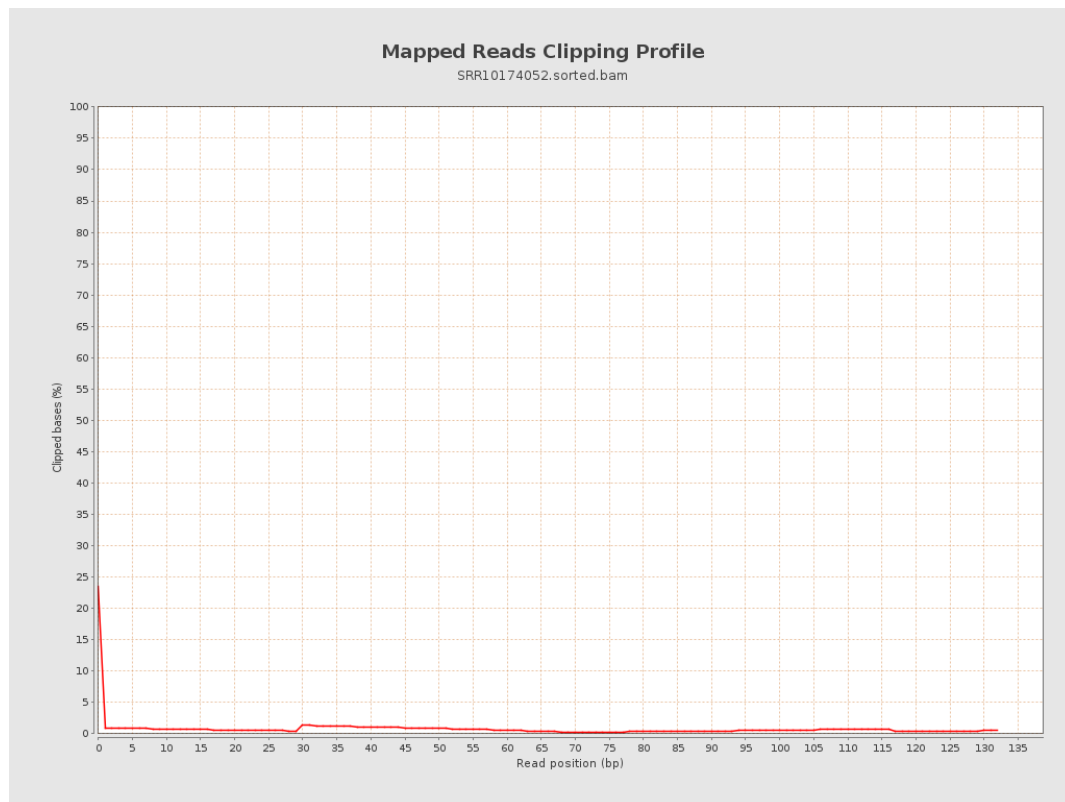
8. Results : Mapped Reads Nucleotide Content



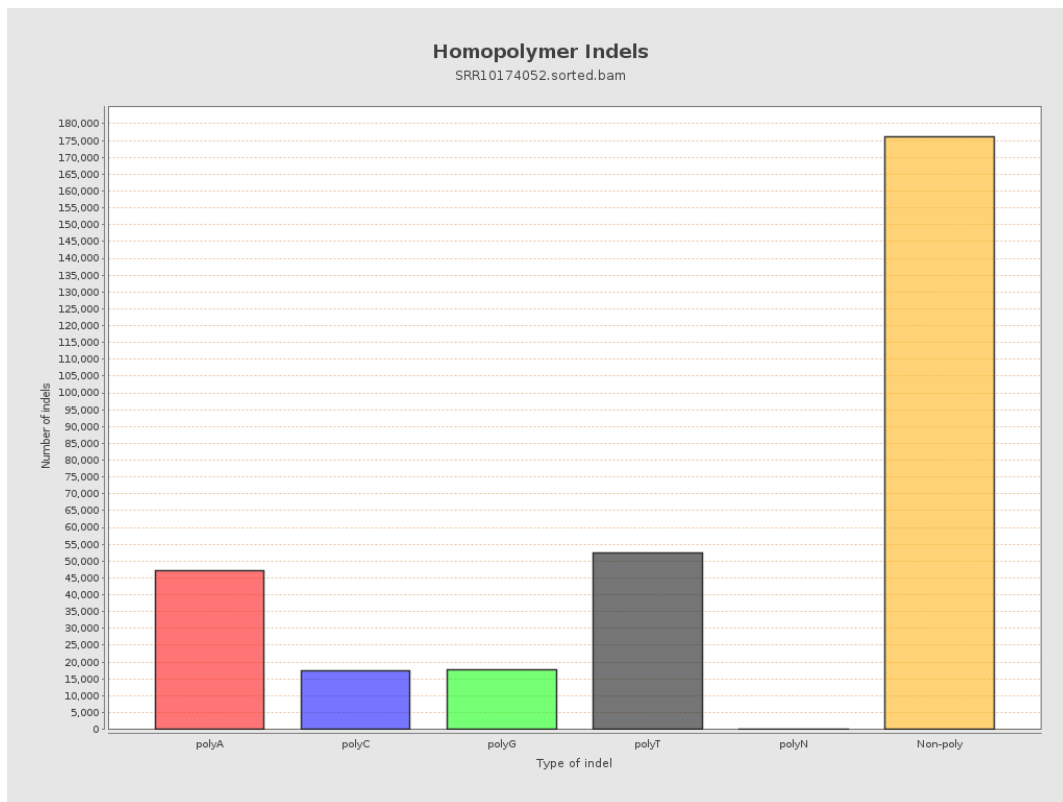
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



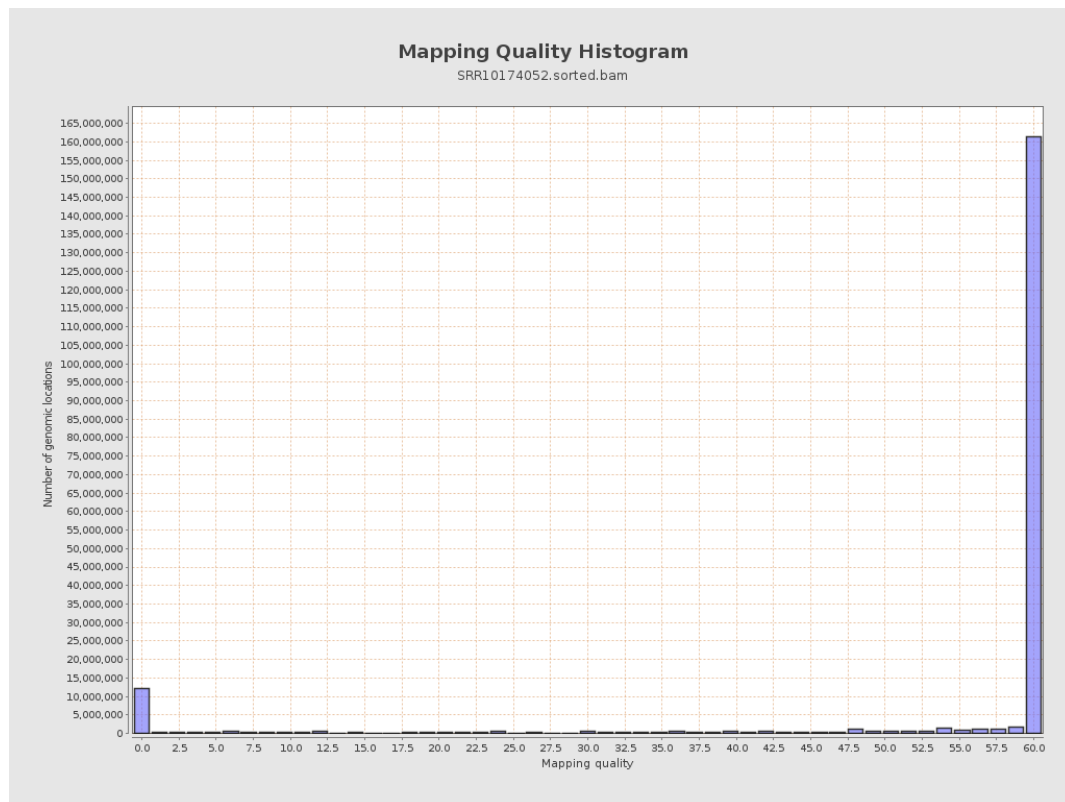
11. Results : Homopolymer Indels



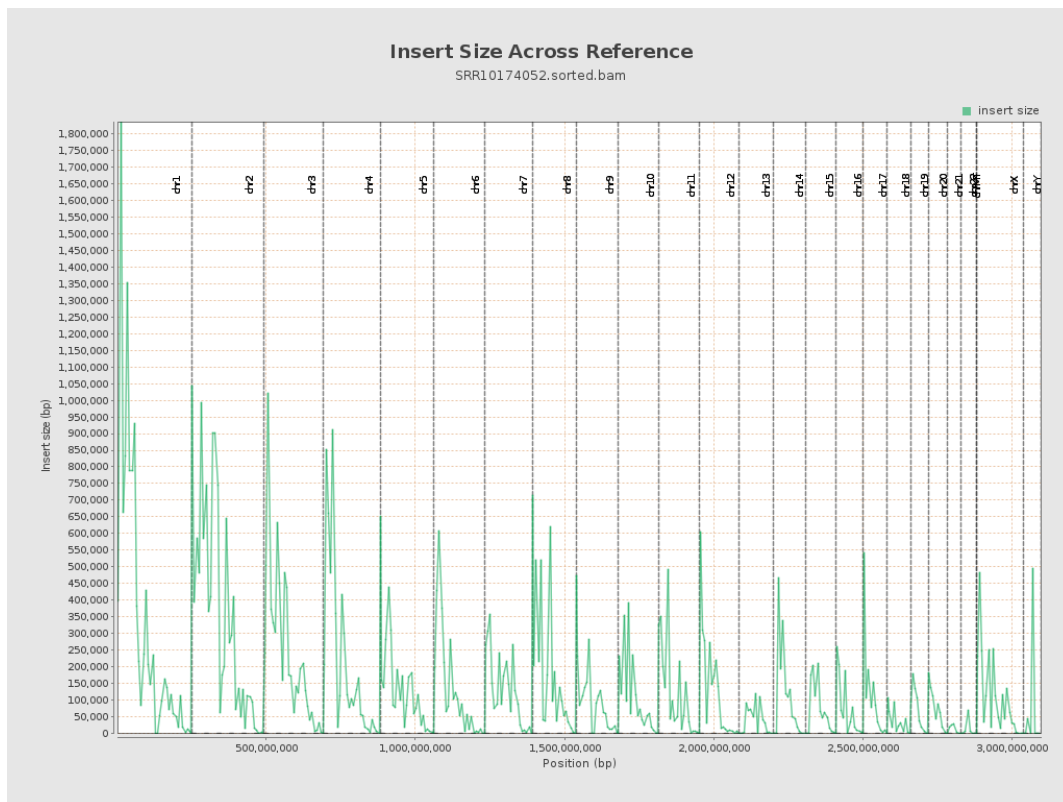
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

