

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:32:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124871.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_SRR3124871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124871_1.fastq.gz SRR3124871_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:32:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,947,098
Mapped reads	7,730,582 / 97.28%
Unmapped reads	216,516 / 2.72%
Mapped paired reads	7,730,582 / 97.28%
Mapped reads, first in pair	3,919,217 / 49.32%
Mapped reads, second in pair	3,811,365 / 47.96%
Mapped reads, both in pair	7,594,374 / 95.56%
Mapped reads, singletons	136,208 / 1.71%
Secondary alignments	0
Supplementary alignments	8,880 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	507,294 / 6.38%
Duplication rate	4.23%
Clipped reads	3,524,190 / 44.35%

2.2. ACGT Content

Number/percentage of A's	133,093,796 / 27.66%
Number/percentage of C's	85,417,274 / 17.75%
Number/percentage of T's	145,015,832 / 30.14%
Number/percentage of G's	117,685,295 / 24.46%
Number/percentage of N's	3,627 / 0%

GC Percentage	42.21%
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2.3. Coverage

Mean	0.1555
Standard Deviation	1.3331

2.4. Mapping Quality

Mean Mapping Quality	51.79
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2.5. Insert size

Mean	30,216.2
Standard Deviation	1,617,400.15
P25/Median/P75	155 / 208 / 282

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	3,189,008
Insertions	49,935
Mapped reads with at least one insertion	0.64%
Deletions	134,151
Mapped reads with at least one deletion	1.72%
Homopolymer indels	48.44%

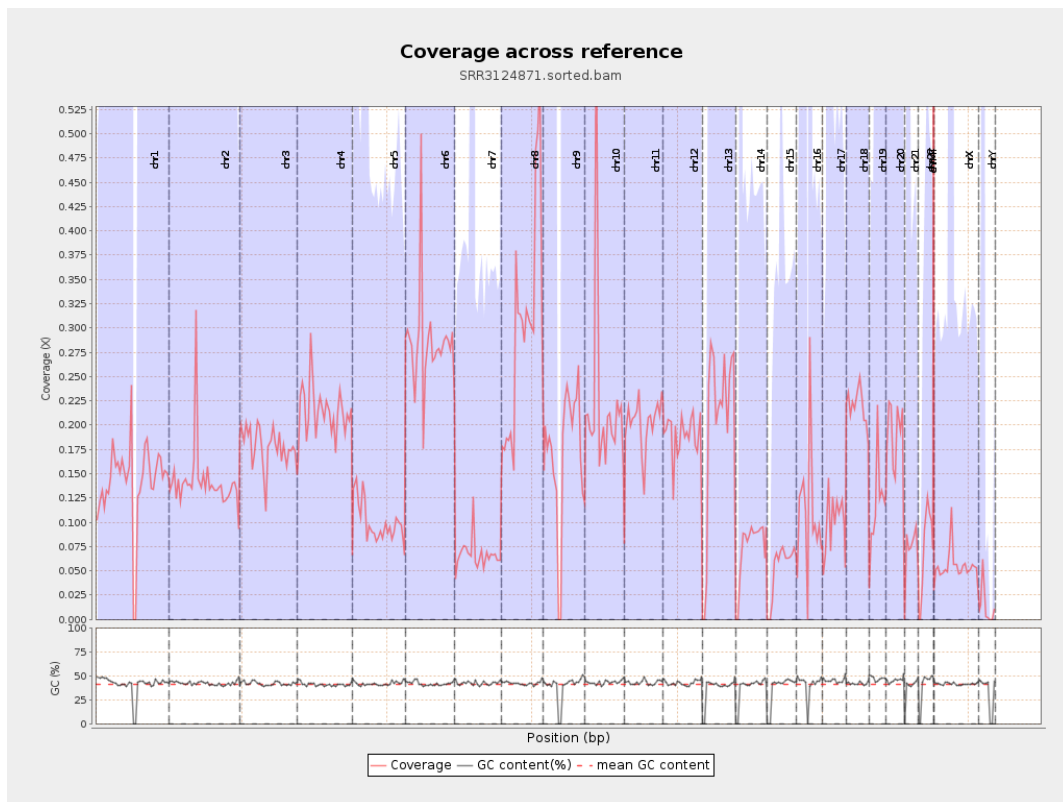
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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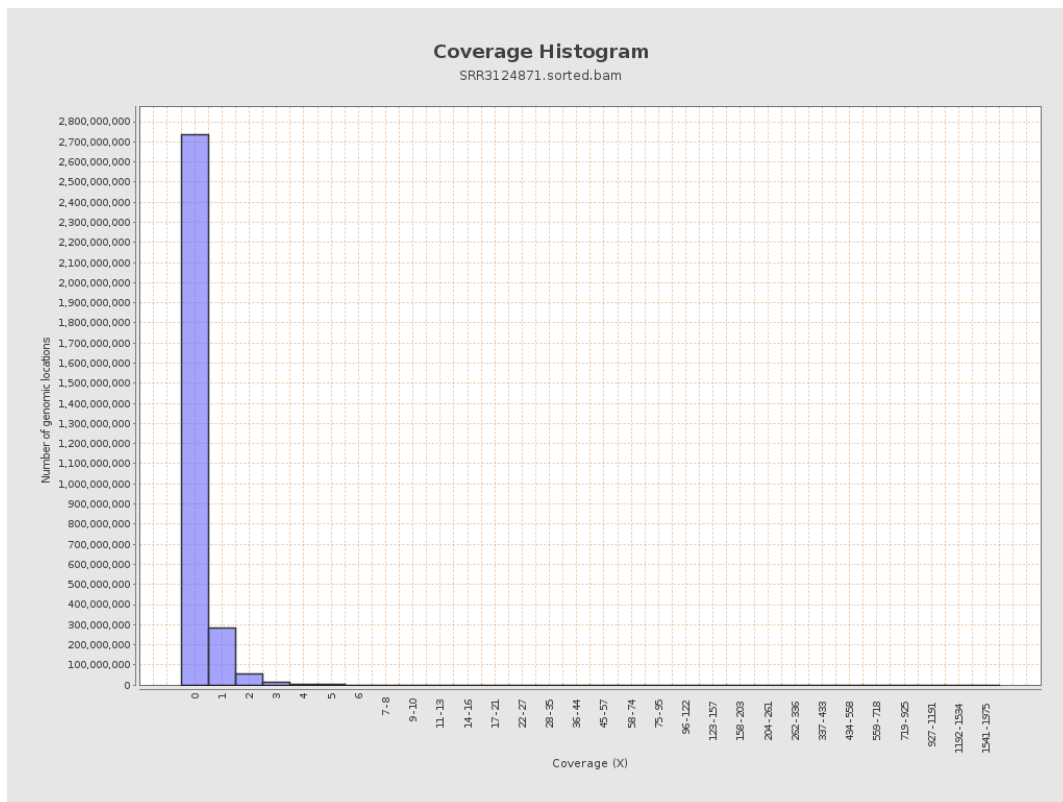
		bases	coverage	deviation
chr1	249250621	35382790	0.142	1.4029
chr2	243199373	34638599	0.1424	1.2431
chr3	198022430	35217762	0.1778	0.5318
chr4	191154276	40862790	0.2138	0.8126
chr5	180915260	18032275	0.0997	0.3819
chr6	171115067	48748734	0.2849	2.4935
chr7	159138663	10696866	0.0672	0.9012
chr8	146364022	44203425	0.302	0.9776
chr9	141213431	24367969	0.1726	1.2354
chr10	135534747	29803550	0.2199	3.3856
chr11	135006516	27005369	0.2	1.6417
chr12	133851895	25198705	0.1883	0.5494
chr13	115169878	23141251	0.2009	0.5572
chr14	107349540	7875472	0.0734	0.4888
chr15	102531392	5493559	0.0536	0.2961
chr16	90354753	9864540	0.1092	1.4483
chr17	81195210	7983620	0.0983	1.3048
chr18	78077248	17236947	0.2208	1.8002
chr19	59128983	7181292	0.1215	1.29
chr20	63025520	11916836	0.1891	0.5605
chr21	48129895	3461670	0.0719	0.474
chr22	51304566	3748441	0.0731	0.321
chrMT	16571	16573	1.0001	1.3607
chrX	155270560	8567220	0.0552	0.7935

chrY	59373566	764871	0.0129	0.5938
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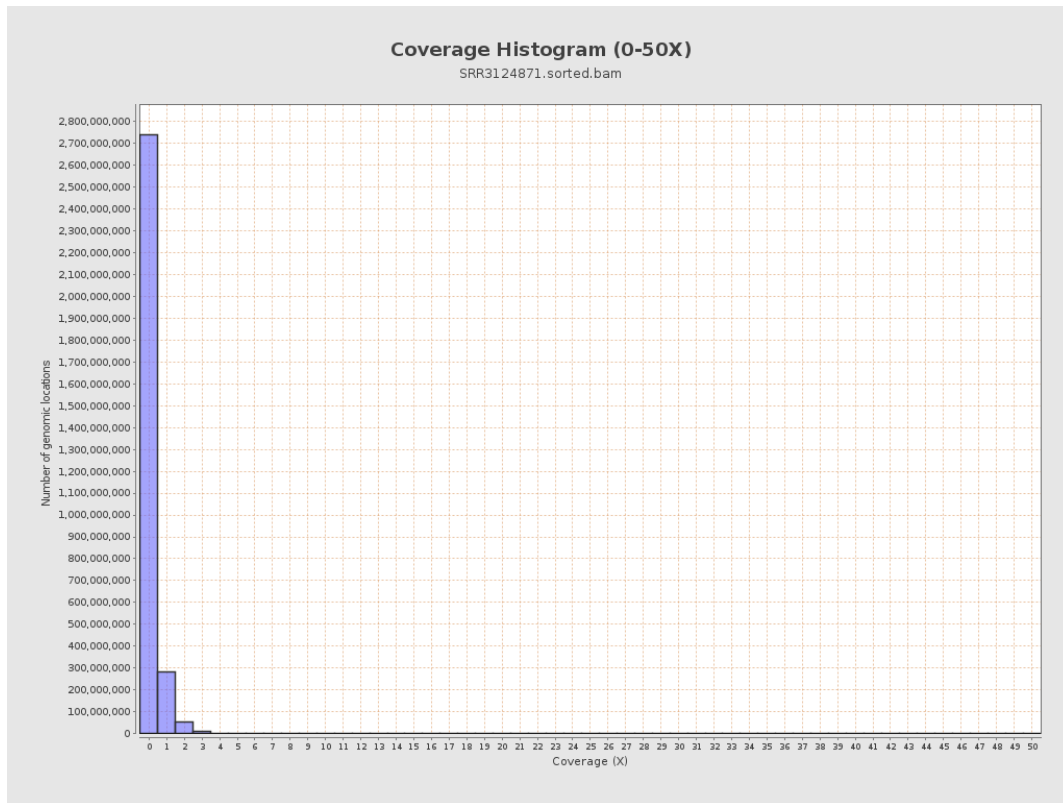
3. Results : Coverage across reference



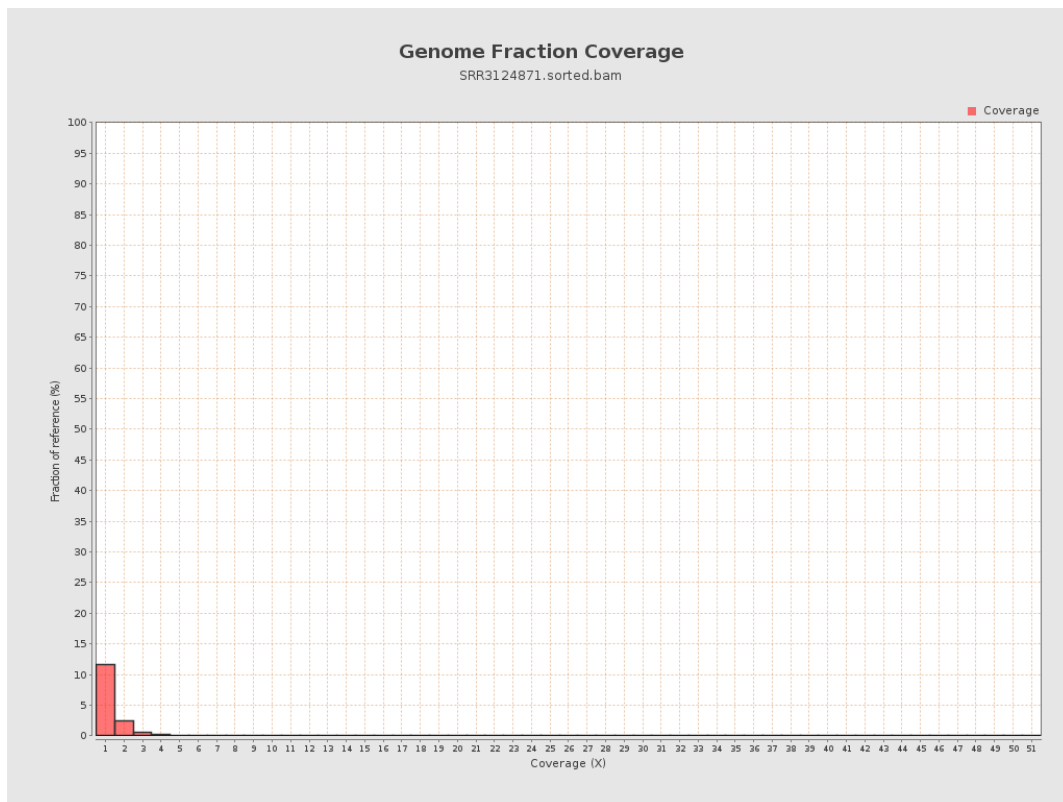
4. Results : Coverage Histogram



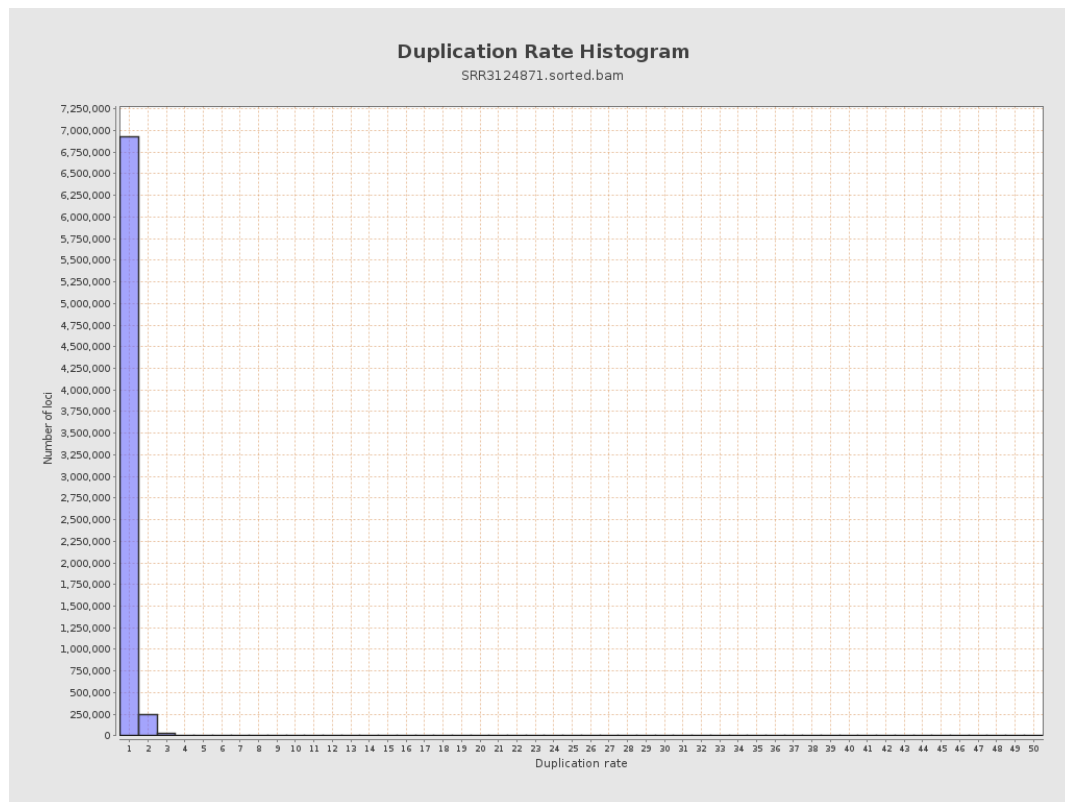
5. Results : Coverage Histogram (0-50X)



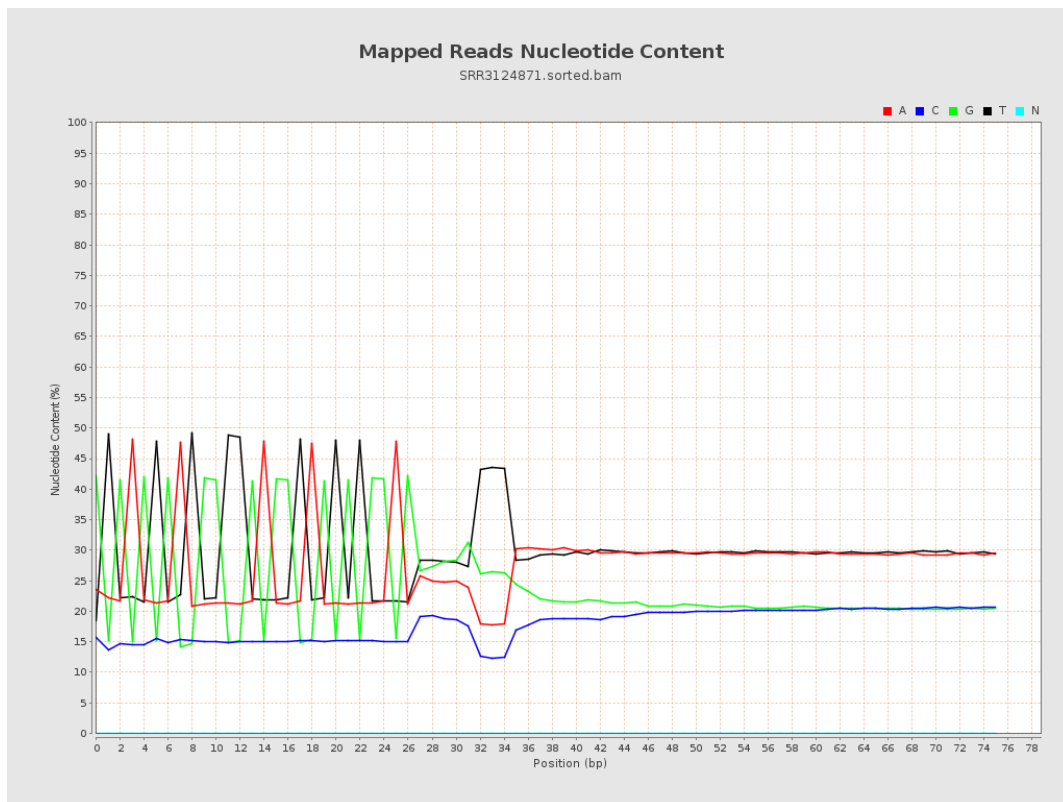
6. Results : Genome Fraction Coverage



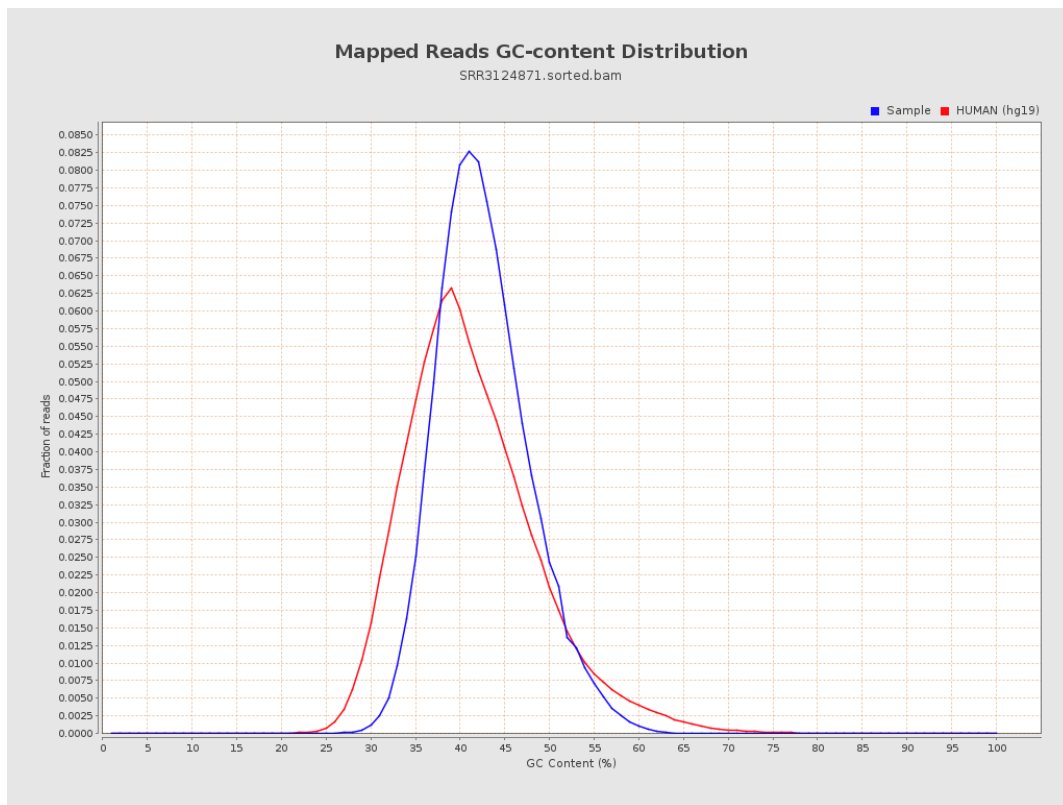
7. Results : Duplication Rate Histogram



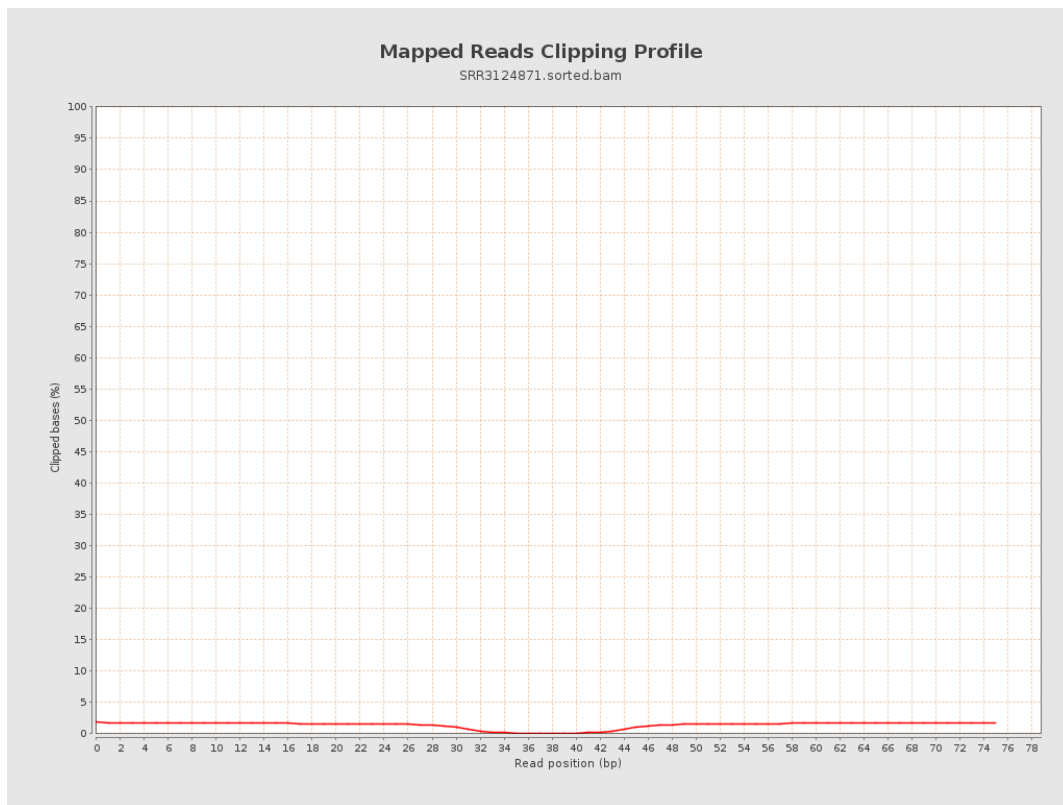
8. Results : Mapped Reads Nucleotide Content



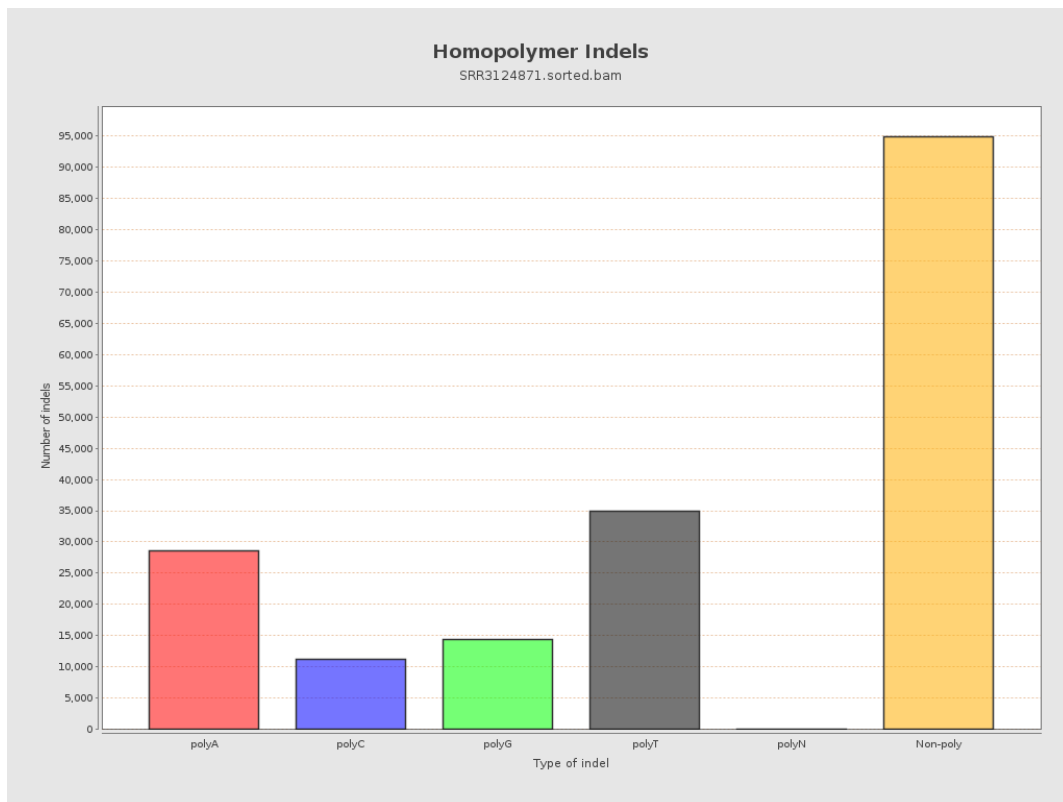
9. Results : Mapped Reads GC-content Distribution



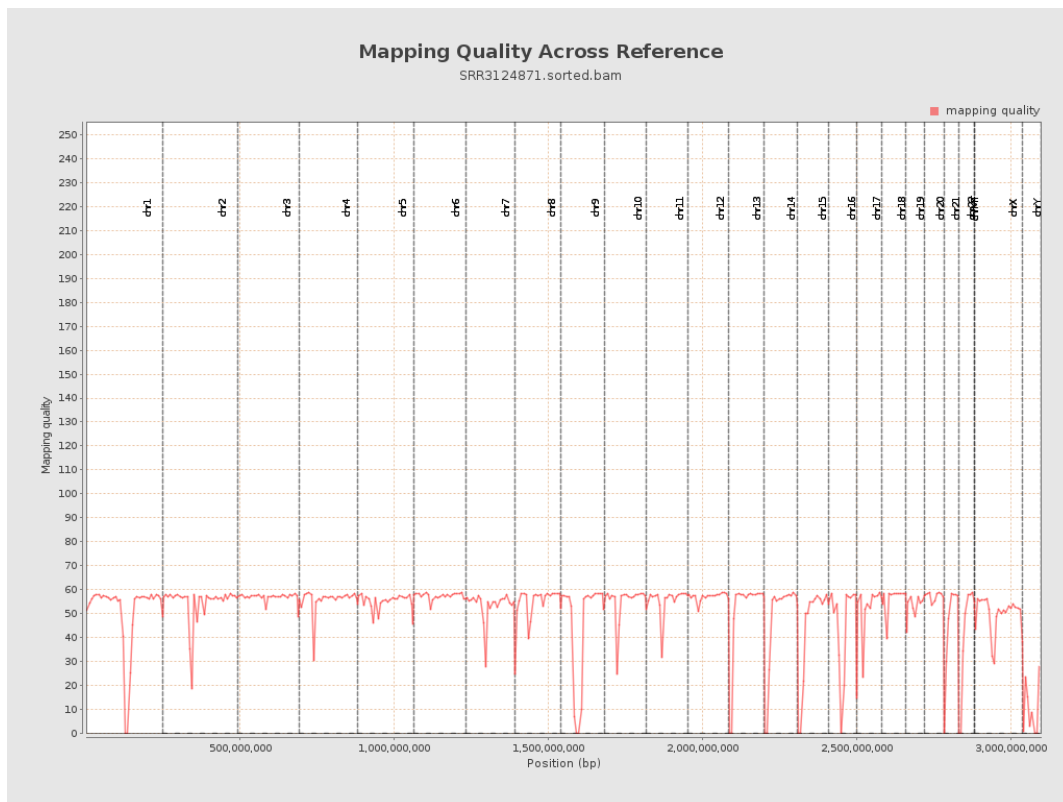
10. Results : Mapped Reads Clipping Profile



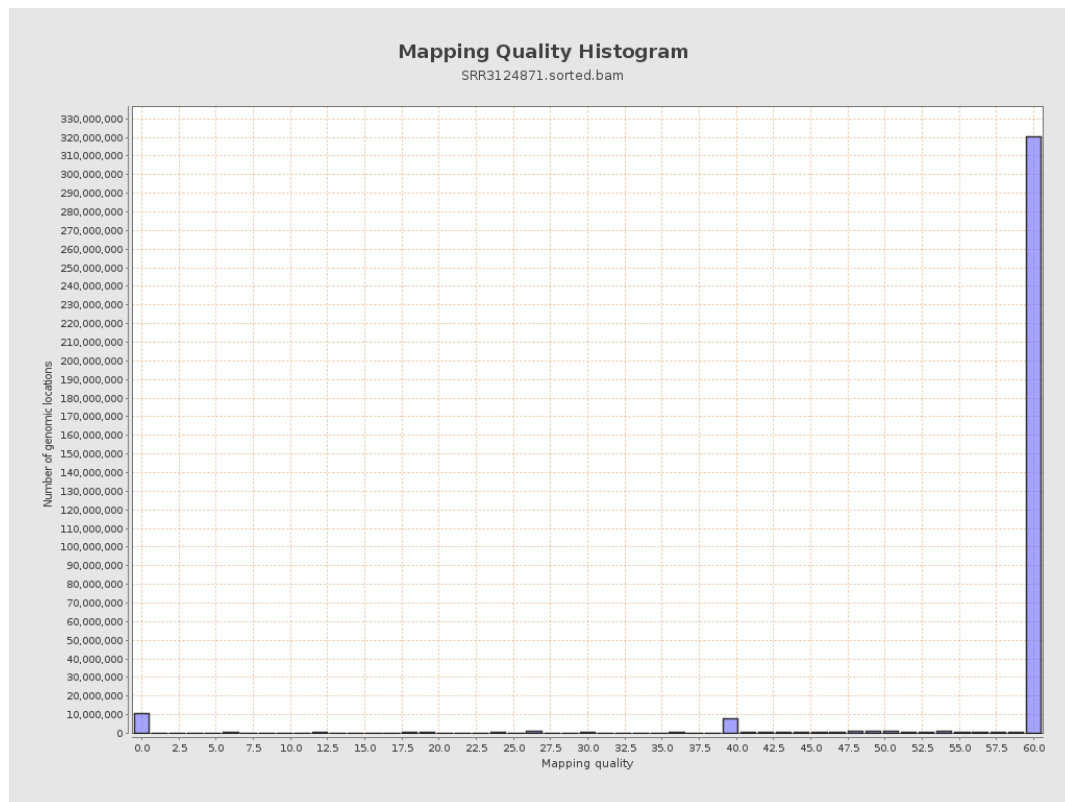
11. Results : Homopolymer Indels



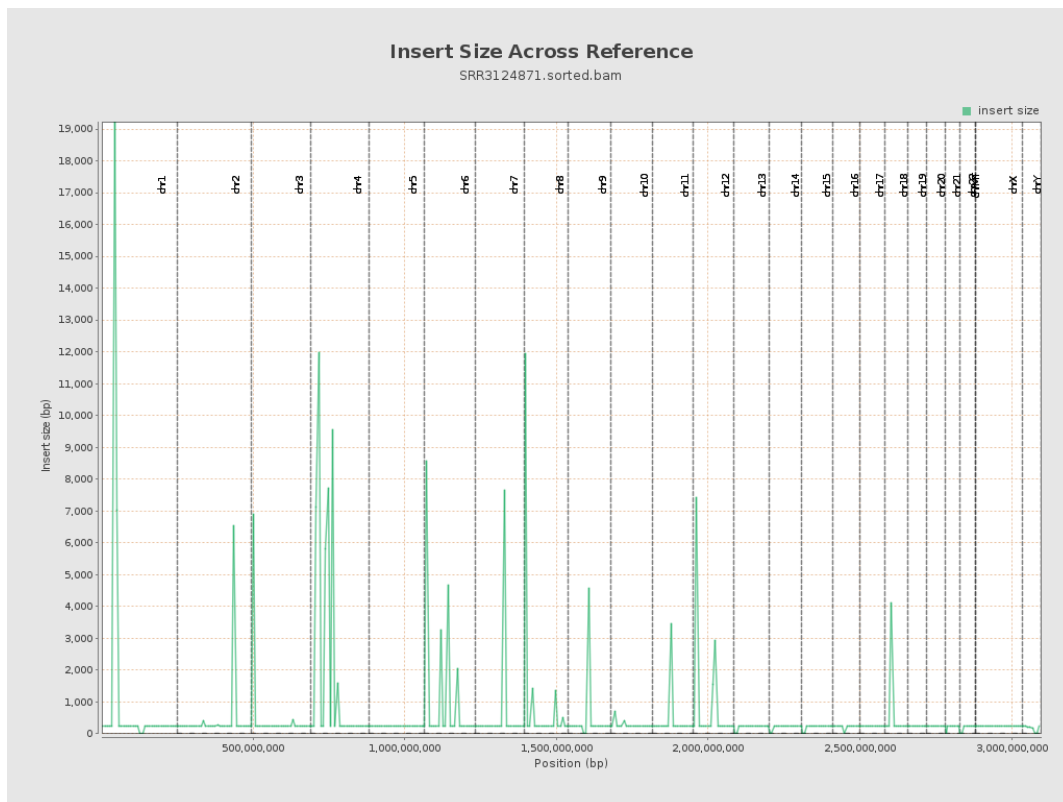
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

