

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 01:11:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124886.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_SRR3124886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124886_1.fastq.gz SRR3124886_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 01:11:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,208,350
Mapped reads	5,053,546 / 97.03%
Unmapped reads	154,804 / 2.97%
Mapped paired reads	5,053,546 / 97.03%
Mapped reads, first in pair	2,540,013 / 48.77%
Mapped reads, second in pair	2,513,533 / 48.26%
Mapped reads, both in pair	4,979,772 / 95.61%
Mapped reads, singletons	73,774 / 1.42%
Secondary alignments	0
Supplementary alignments	5,680 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	240,136 / 4.61%
Duplication rate	2.93%
Clipped reads	1,593,307 / 30.59%

2.2. ACGT Content

Number/percentage of A's	95,823,449 / 28.43%
Number/percentage of C's	63,099,533 / 18.72%
Number/percentage of T's	99,958,256 / 29.66%
Number/percentage of G's	78,163,481 / 23.19%
Number/percentage of N's	2,899 / 0%

GC Percentage	41.91%
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2.3. Coverage

Mean	0.1089
Standard Deviation	0.9634

2.4. Mapping Quality

Mean Mapping Quality	51.86
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2.5. Insert size

Mean	36,887.74
Standard Deviation	1,760,010.18
P25/Median/P75	152 / 197 / 263

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	2,300,648
Insertions	36,389
Mapped reads with at least one insertion	0.71%
Deletions	93,989
Mapped reads with at least one deletion	1.84%
Homopolymer indels	49.54%

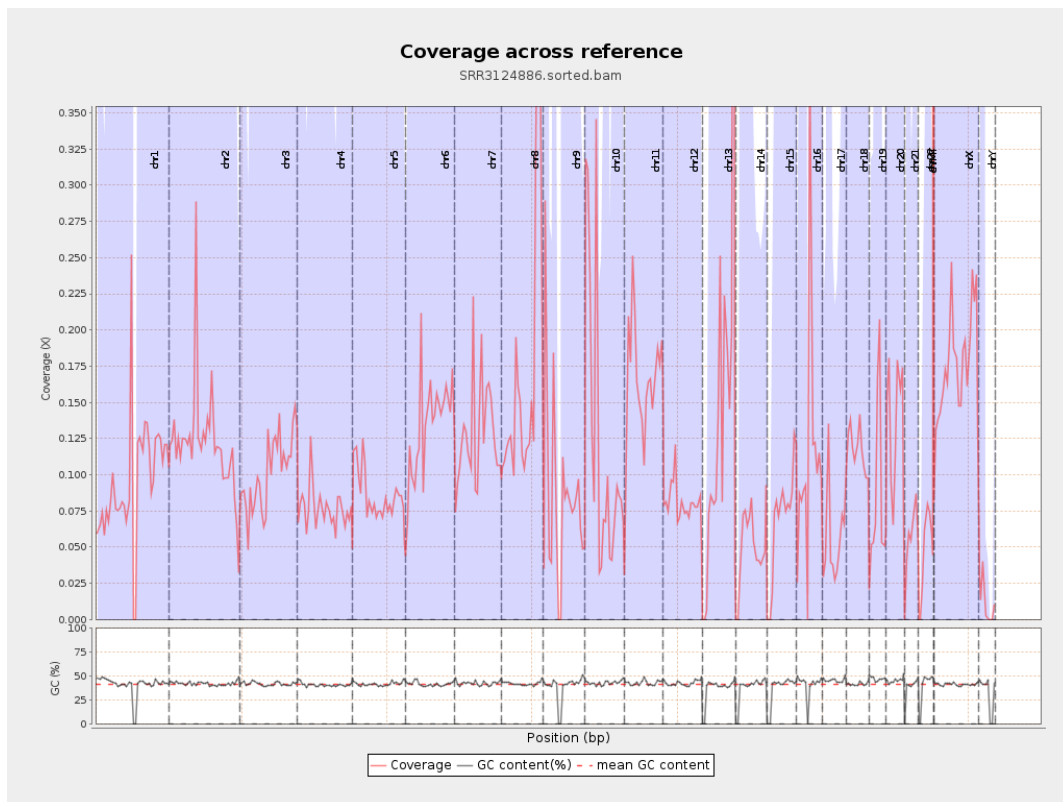
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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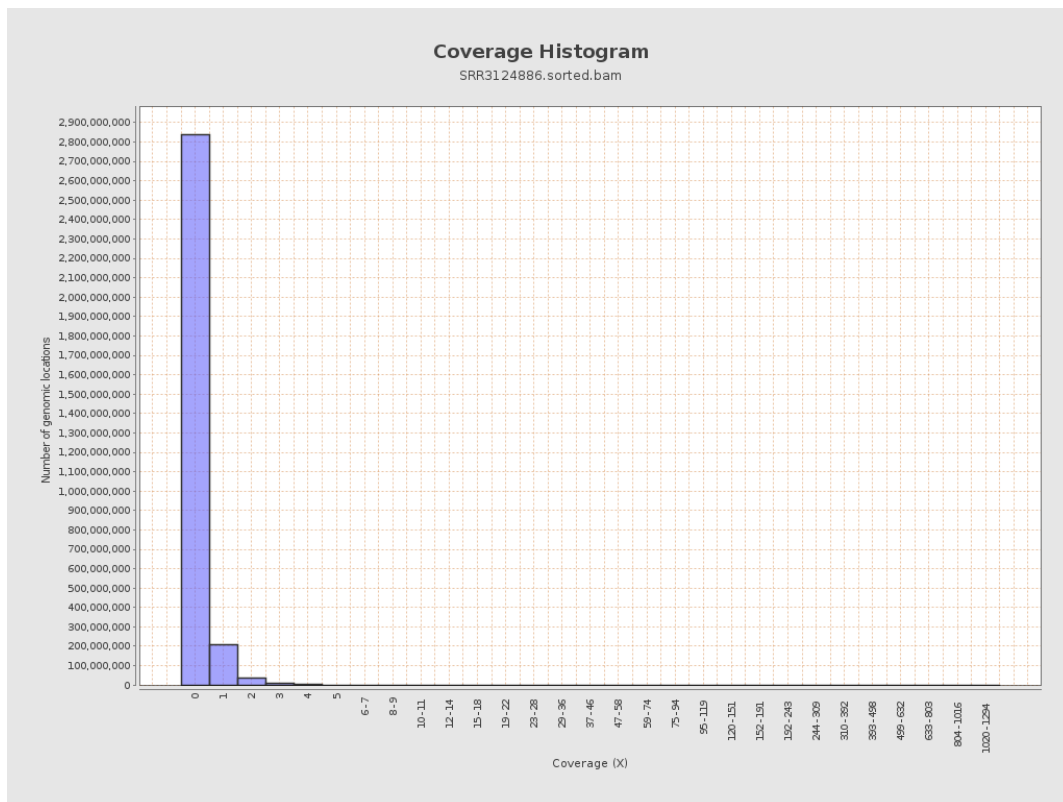
		bases	coverage	deviation
chr1	249250621	23698376	0.0951	1.3609
chr2	243199373	29748928	0.1223	1.0525
chr3	198022430	19916739	0.1006	0.3779
chr4	191154276	14575051	0.0762	0.4553
chr5	180915260	15523051	0.0858	0.341
chr6	171115067	22805015	0.1333	0.9403
chr7	159138663	20517997	0.1289	1.3476
chr8	146364022	25883785	0.1768	0.6357
chr9	141213431	12320019	0.0872	0.8615
chr10	135534747	16605482	0.1225	2.1758
chr11	135006516	22155052	0.1641	0.8225
chr12	133851895	10834782	0.0809	0.336
chr13	115169878	19250050	0.1671	0.7289
chr14	107349540	5214243	0.0486	0.3063
chr15	102531392	7029693	0.0686	0.3115
chr16	90354753	10176871	0.1126	1.6936
chr17	81195210	4441356	0.0547	0.7692
chr18	78077248	9190552	0.1177	1.359
chr19	59128983	5212864	0.0882	0.87
chr20	63025520	8555705	0.1357	0.4549
chr21	48129895	2715427	0.0564	0.3316
chr22	51304566	2399083	0.0468	0.2474
chrMT	16571	268645	16.2118	10.0037
chrX	155270560	27480517	0.177	0.7015

chrY	59373566	667315	0.0112	0.4983
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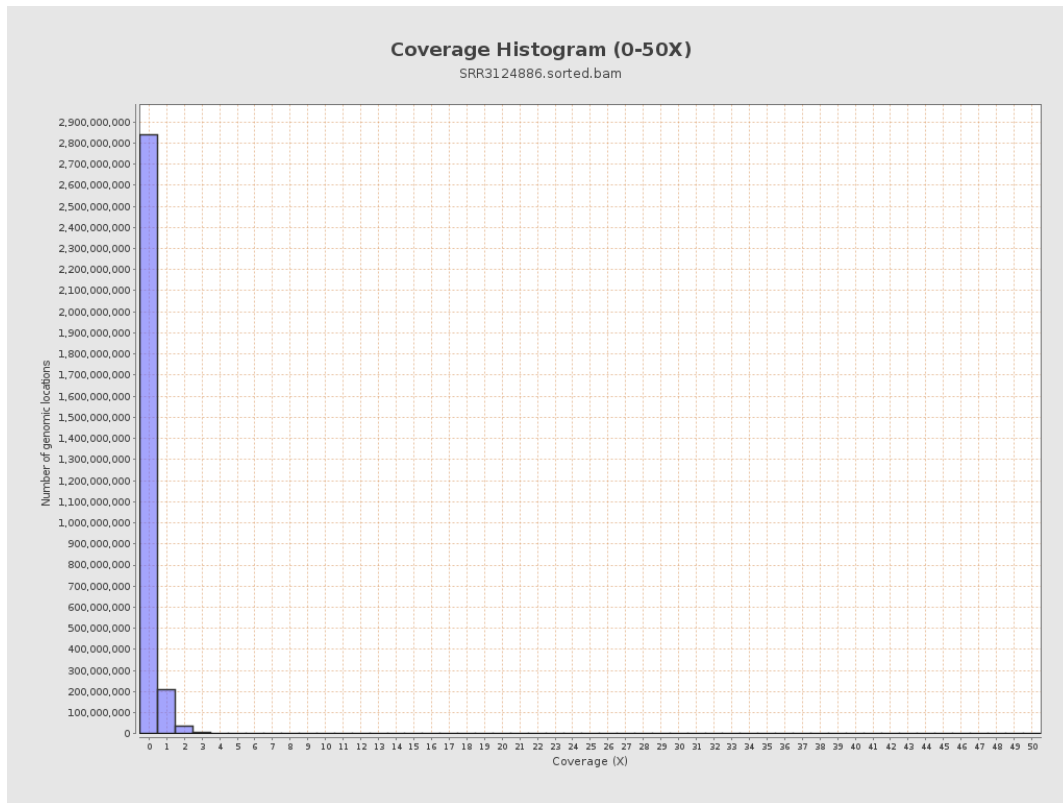
3. Results : Coverage across reference



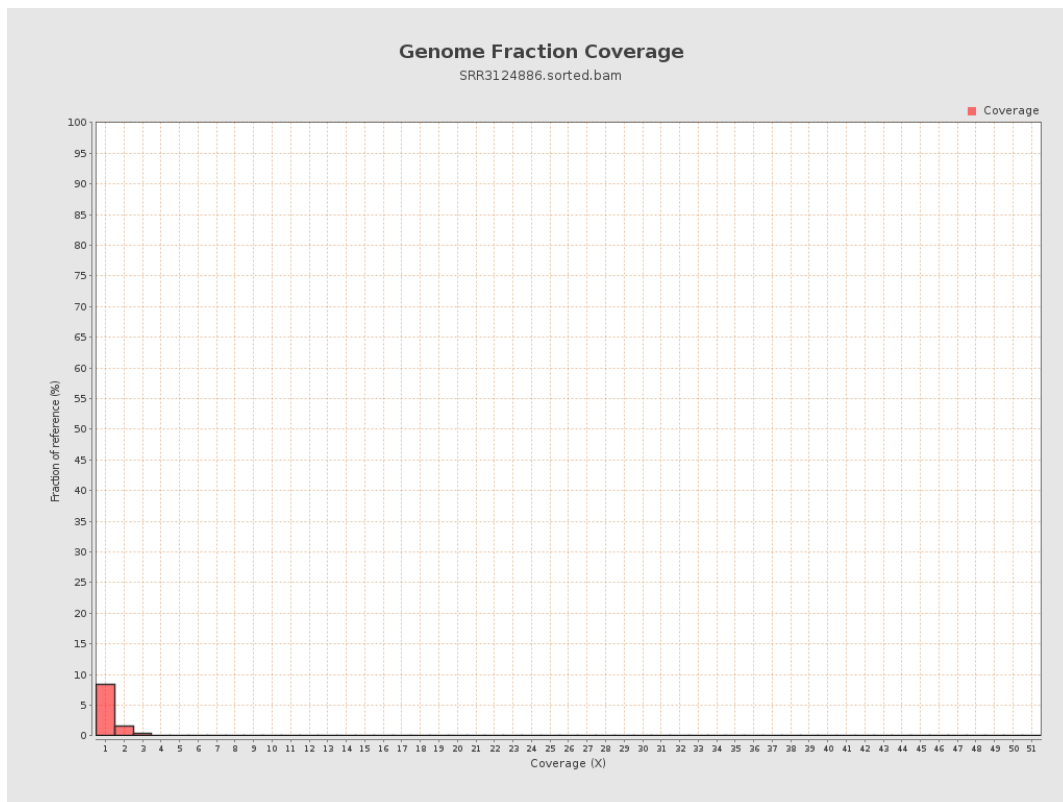
4. Results : Coverage Histogram



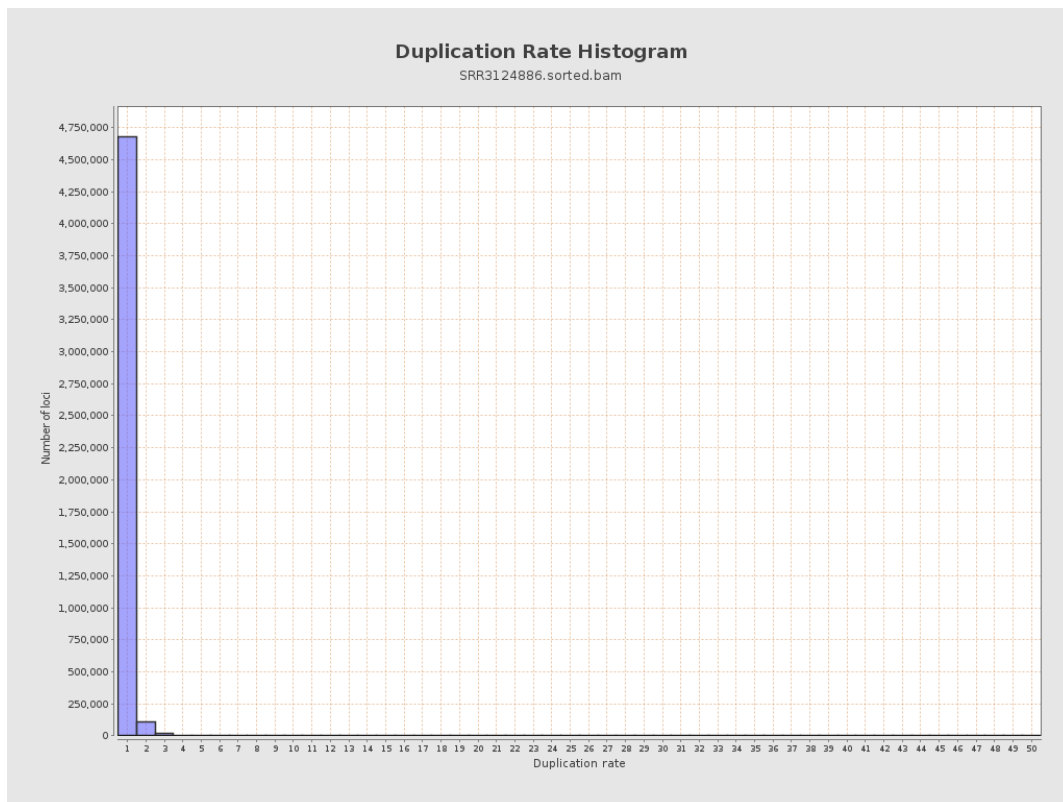
5. Results : Coverage Histogram (0-50X)



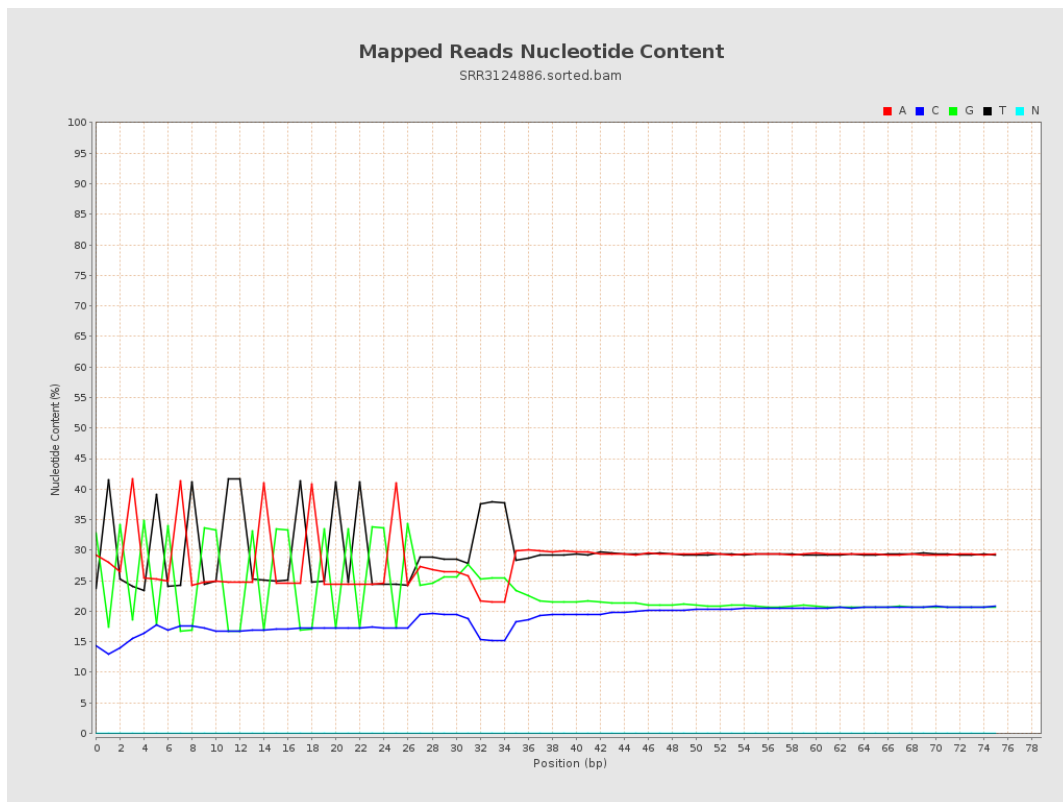
6. Results : Genome Fraction Coverage



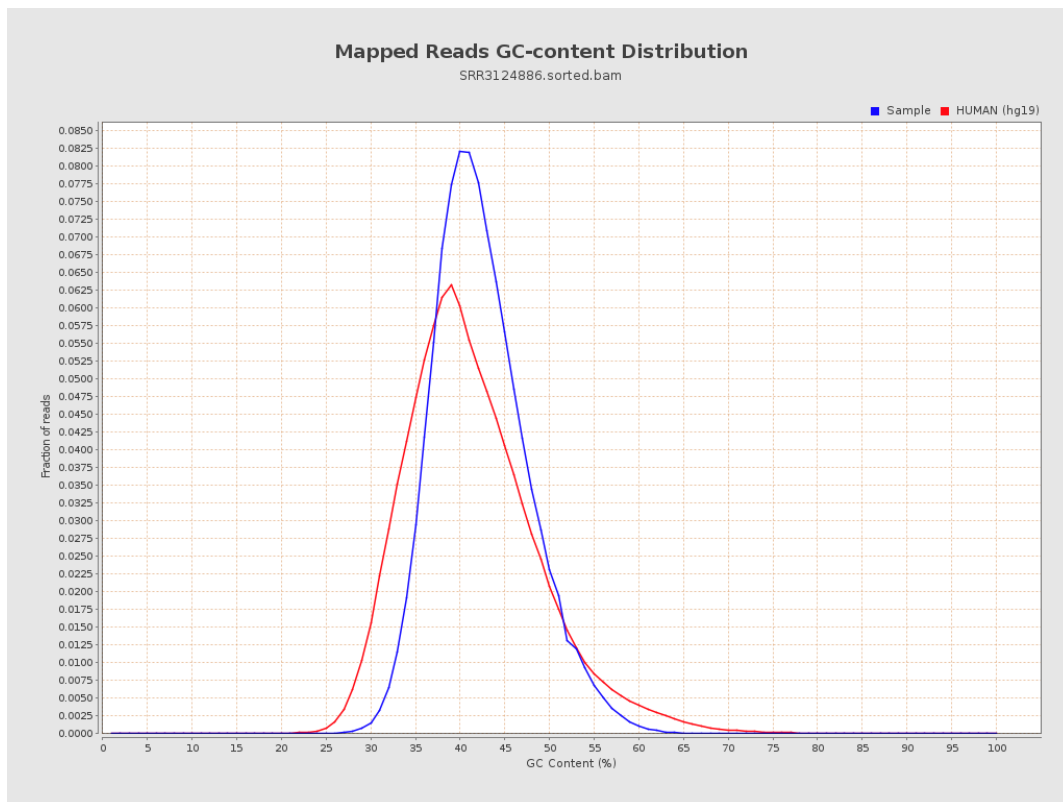
7. Results : Duplication Rate Histogram



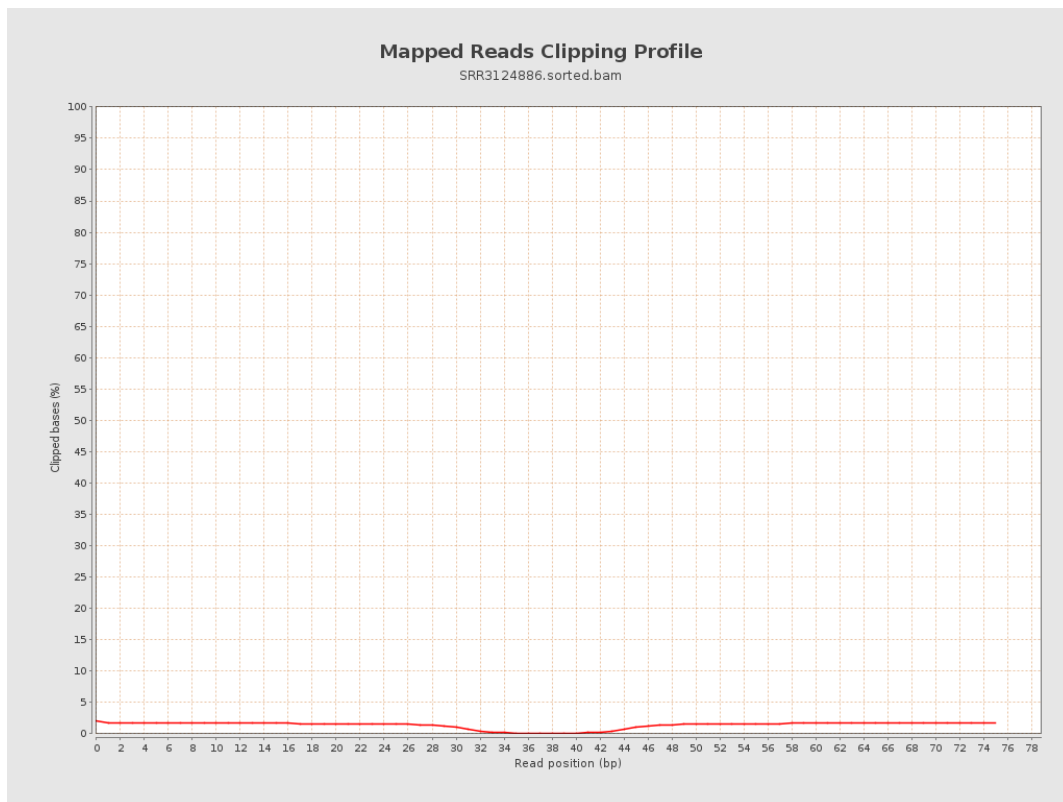
8. Results : Mapped Reads Nucleotide Content



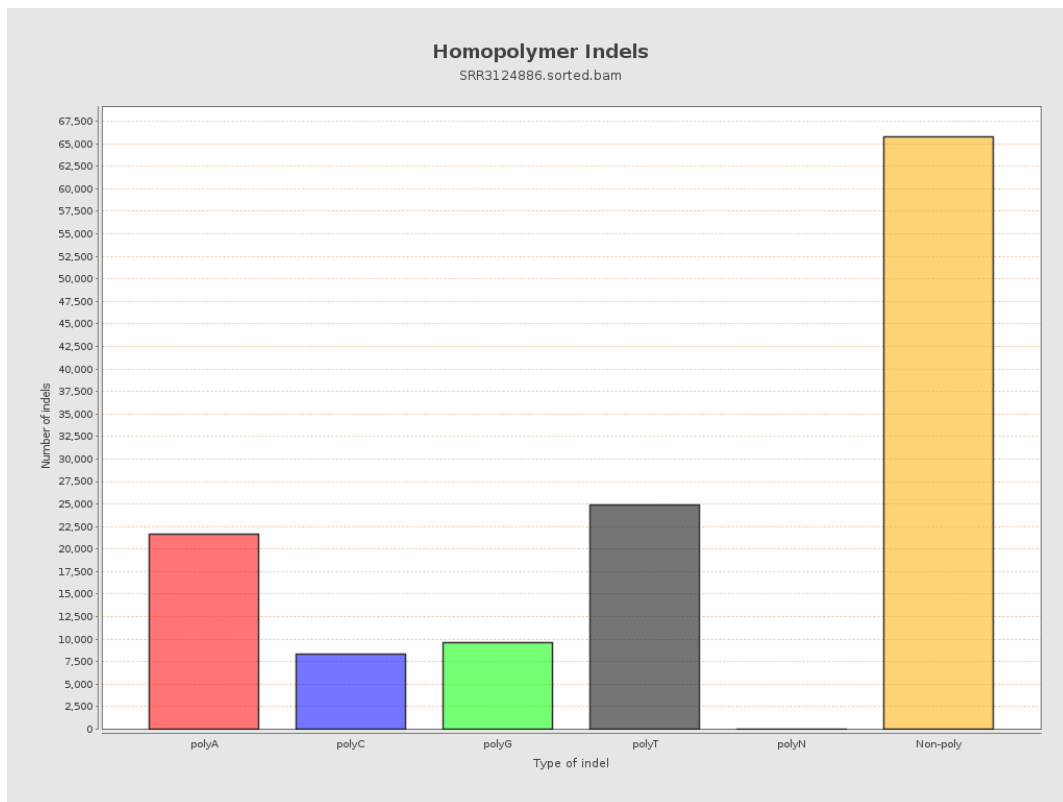
9. Results : Mapped Reads GC-content Distribution



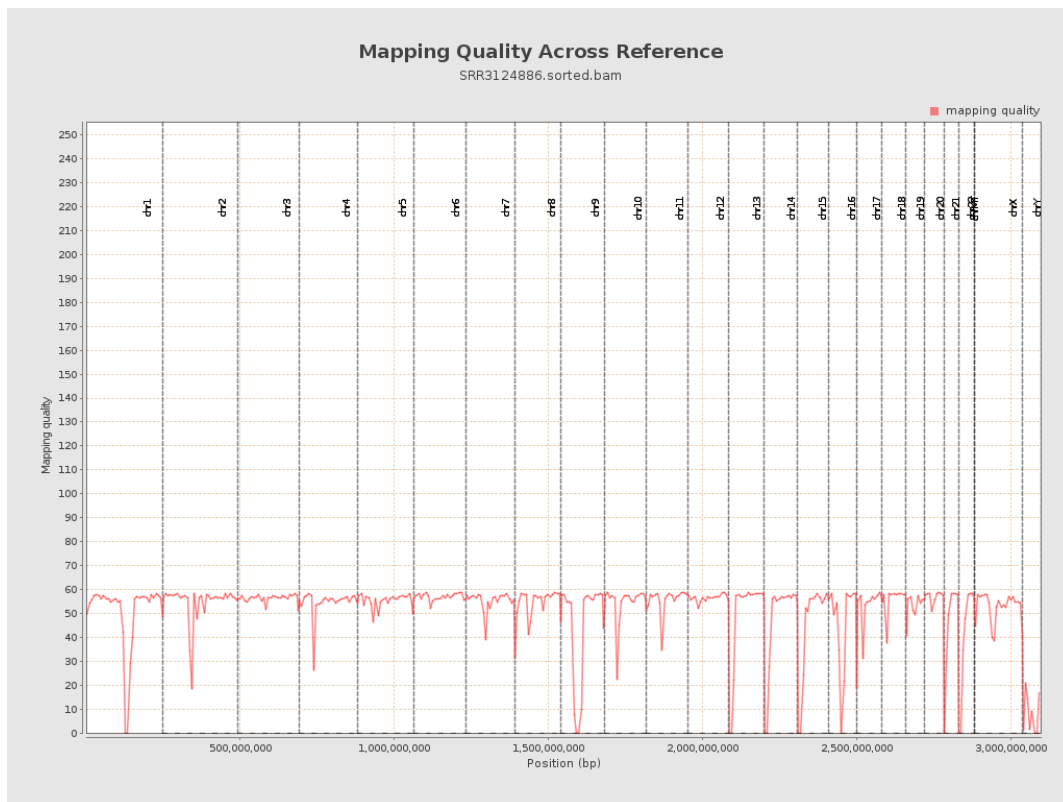
10. Results : Mapped Reads Clipping Profile



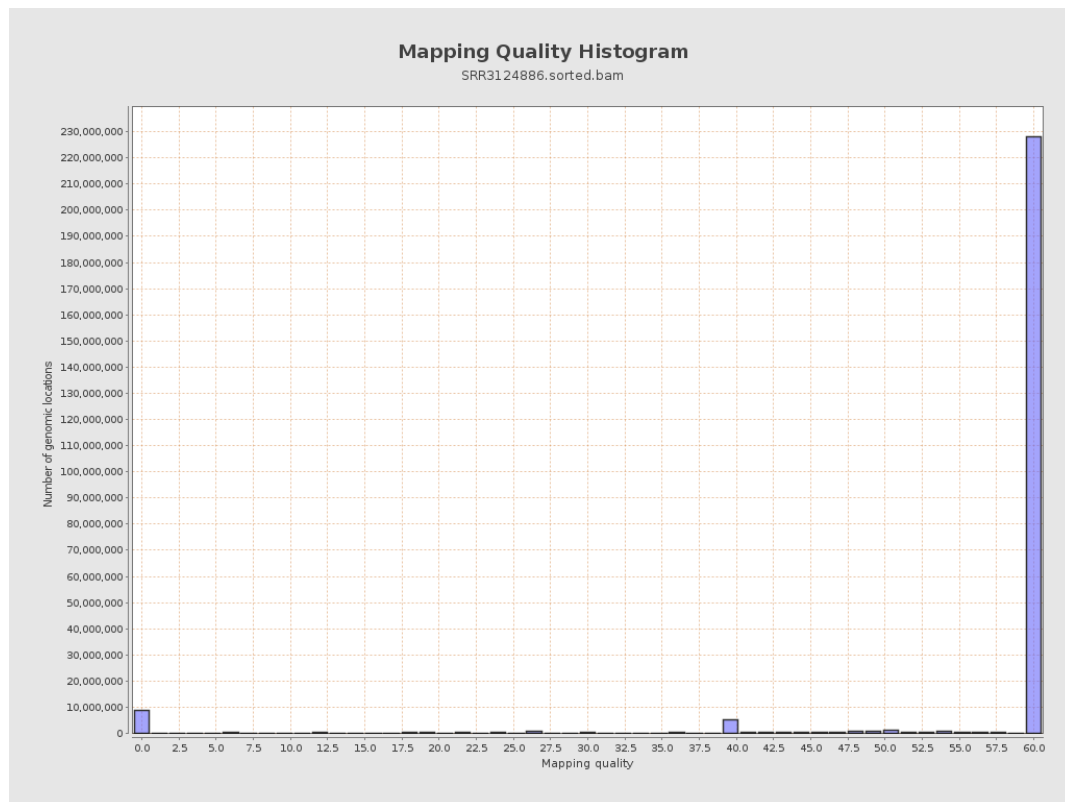
11. Results : Homopolymer Indels



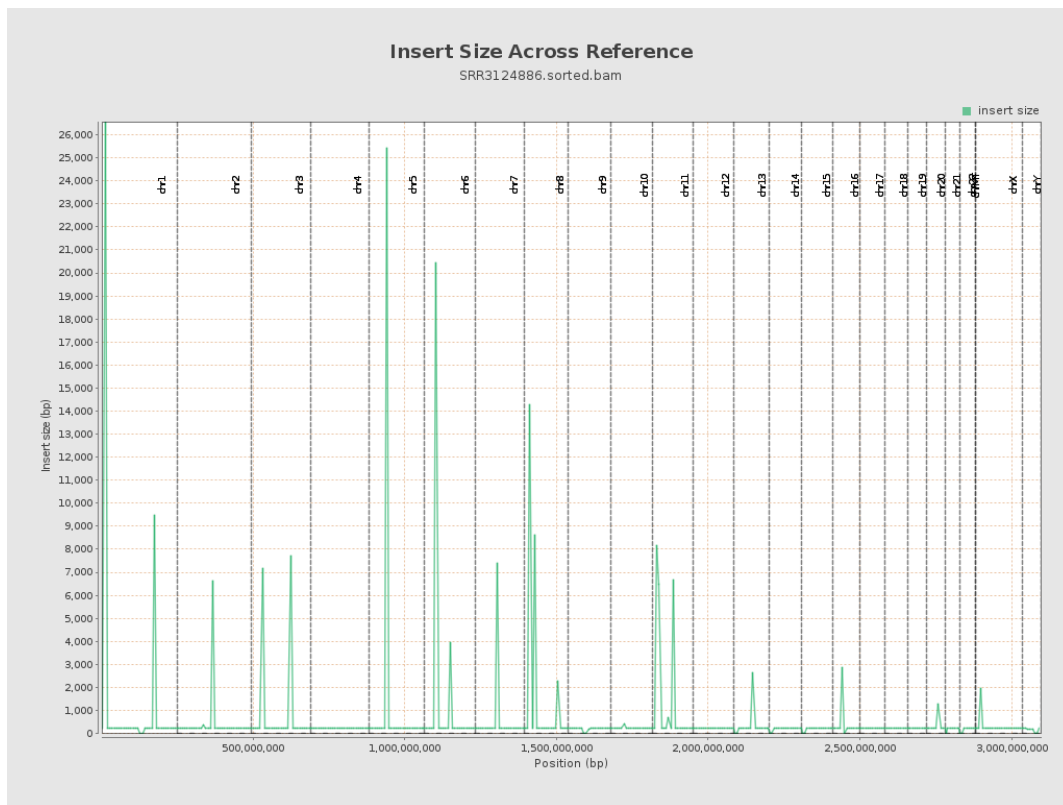
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

