

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:48:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124930.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_SRR3124930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124930_1.fastq.gz SRR3124930_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,790,414
Mapped reads	4,734,132 / 98.83%
Unmapped reads	56,282 / 1.17%
Mapped paired reads	4,734,132 / 98.83%
Mapped reads, first in pair	2,369,813 / 49.47%
Mapped reads, second in pair	2,364,319 / 49.36%
Mapped reads, both in pair	4,713,806 / 98.4%
Mapped reads, singletons	20,326 / 0.42%
Secondary alignments	0
Supplementary alignments	20,534 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	332,599 / 6.94%
Duplication rate	3.27%
Clipped reads	2,840,488 / 59.3%

2.2. ACGT Content

Number/percentage of A's	123,736,834 / 28.71%
Number/percentage of C's	83,956,666 / 19.48%
Number/percentage of T's	128,664,570 / 29.85%
Number/percentage of G's	94,379,082 / 21.9%
Number/percentage of N's	282,964 / 0.07%

GC Percentage	41.38%
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2.3. Coverage

Mean	0.1393
Standard Deviation	2.2287

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	72,596.09
Standard Deviation	2,562,455.89
P25/Median/P75	133 / 165 / 210

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	4,048,029
Insertions	64,134
Mapped reads with at least one insertion	1.32%
Deletions	135,488
Mapped reads with at least one deletion	2.81%
Homopolymer indels	46.84%

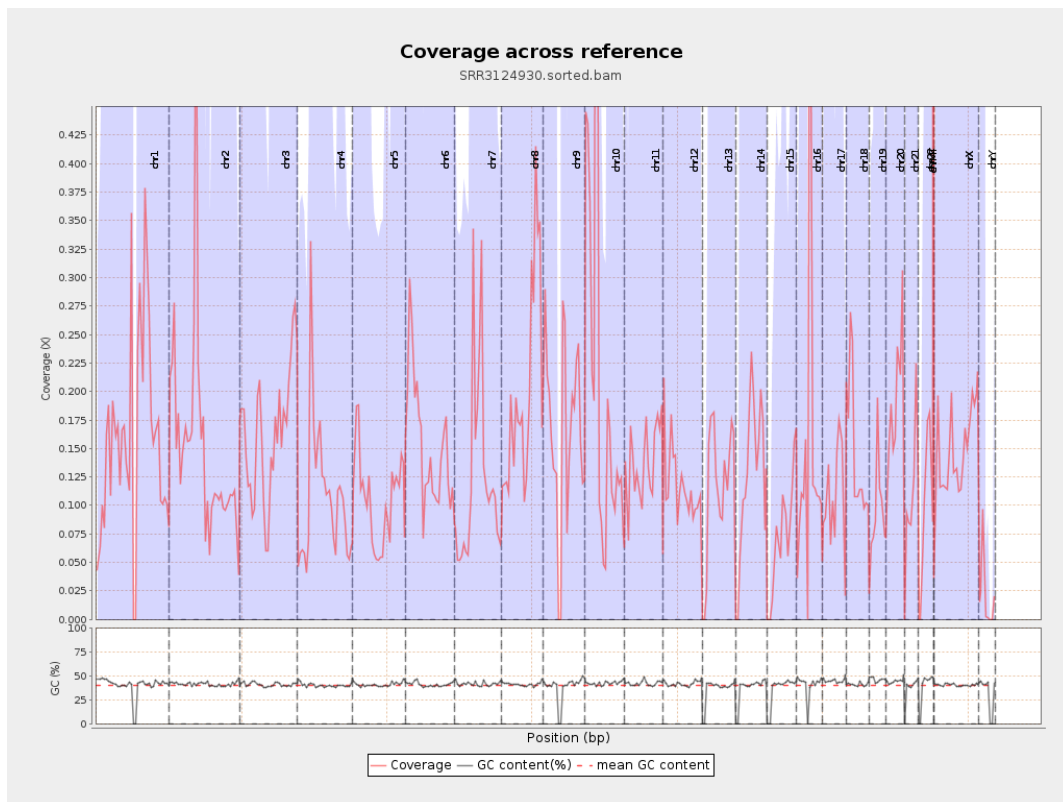
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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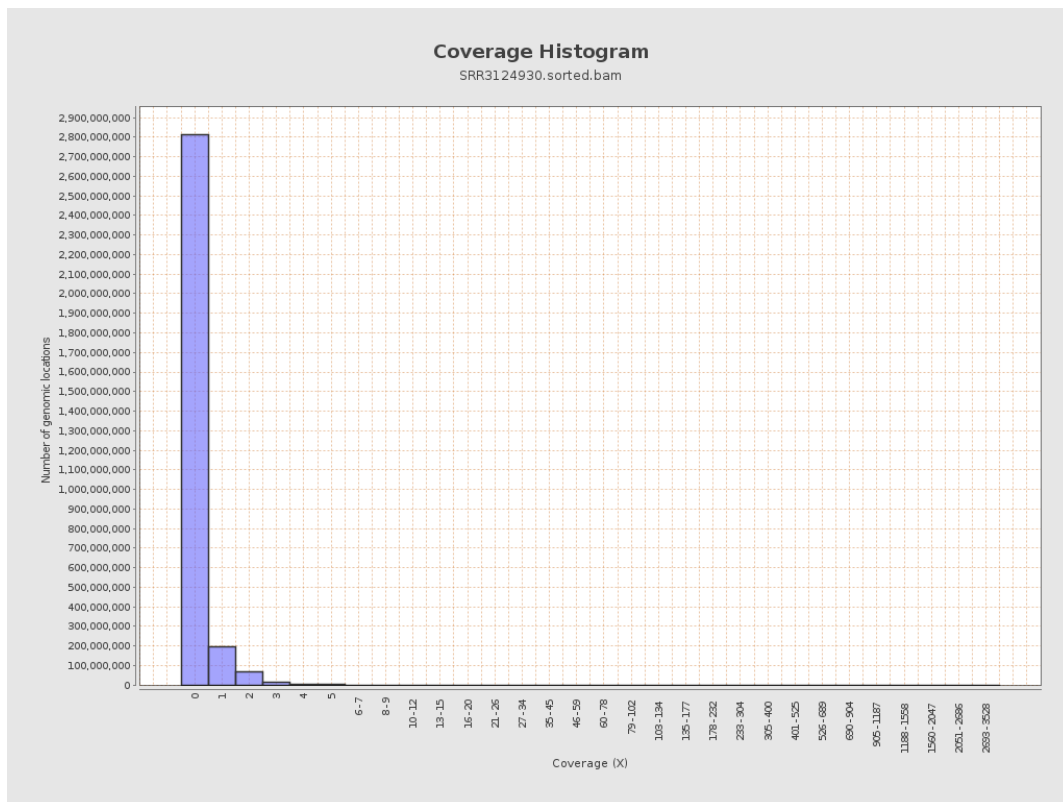
		bases	coverage	deviation
chr1	249250621	39796341	0.1597	2.112
chr2	243199373	37412093	0.1538	2.3537
chr3	198022430	32024174	0.1617	0.6774
chr4	191154276	20004923	0.1047	1.6616
chr5	180915260	18971428	0.1049	0.4291
chr6	171115067	26018829	0.1521	0.9423
chr7	159138663	19982242	0.1256	3.2102
chr8	146364022	29314078	0.2003	0.877
chr9	141213431	23604351	0.1672	2.6279
chr10	135534747	29918620	0.2207	7.2478
chr11	135006516	18492672	0.137	0.7845
chr12	133851895	15703758	0.1173	0.4534
chr13	115169878	13222842	0.1148	0.4351
chr14	107349540	13757367	0.1282	0.5492
chr15	102531392	7316202	0.0714	0.3441
chr16	90354753	13585464	0.1504	3.5362
chr17	81195210	8568575	0.1055	0.9662
chr18	78077248	11563503	0.1481	2.5438
chr19	59128983	5735584	0.097	1.1789
chr20	63025520	11948870	0.1896	0.7118
chr21	48129895	5340732	0.111	0.8373
chr22	51304566	5075123	0.0989	0.4209
chrMT	16571	50676	3.0581	2.2289
chrX	155270560	22643023	0.1458	0.6985

chrY	59373566	1198326	0.0202	1.5413
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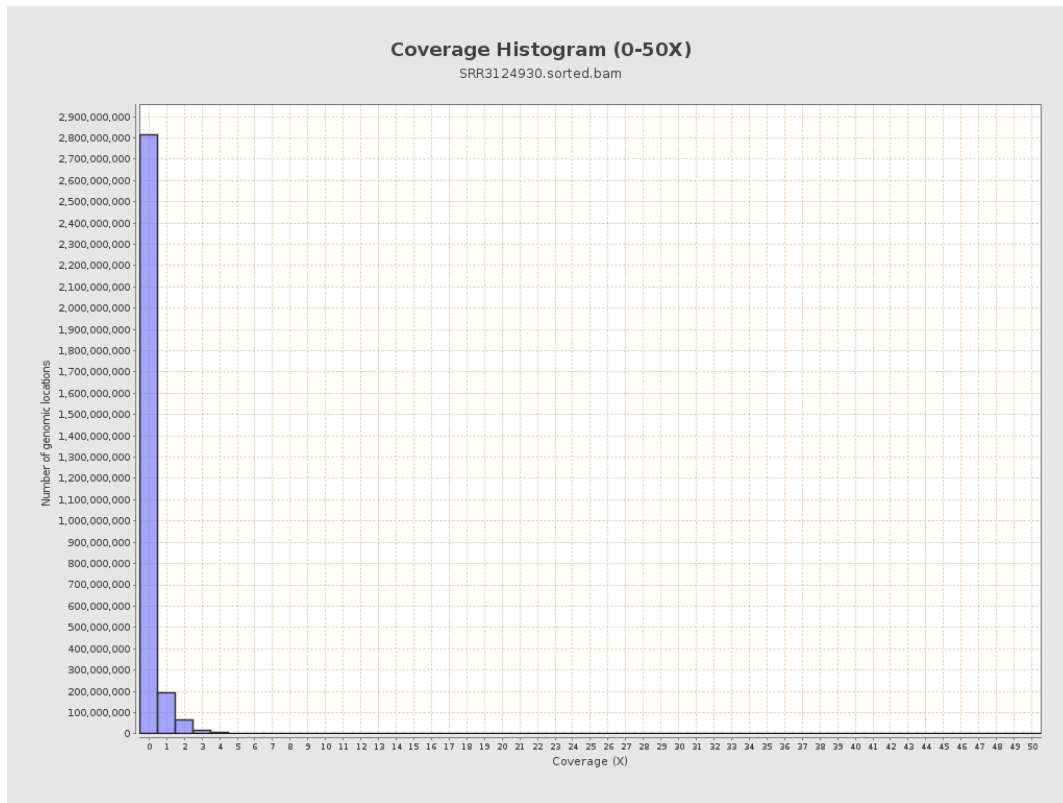
3. Results : Coverage across reference



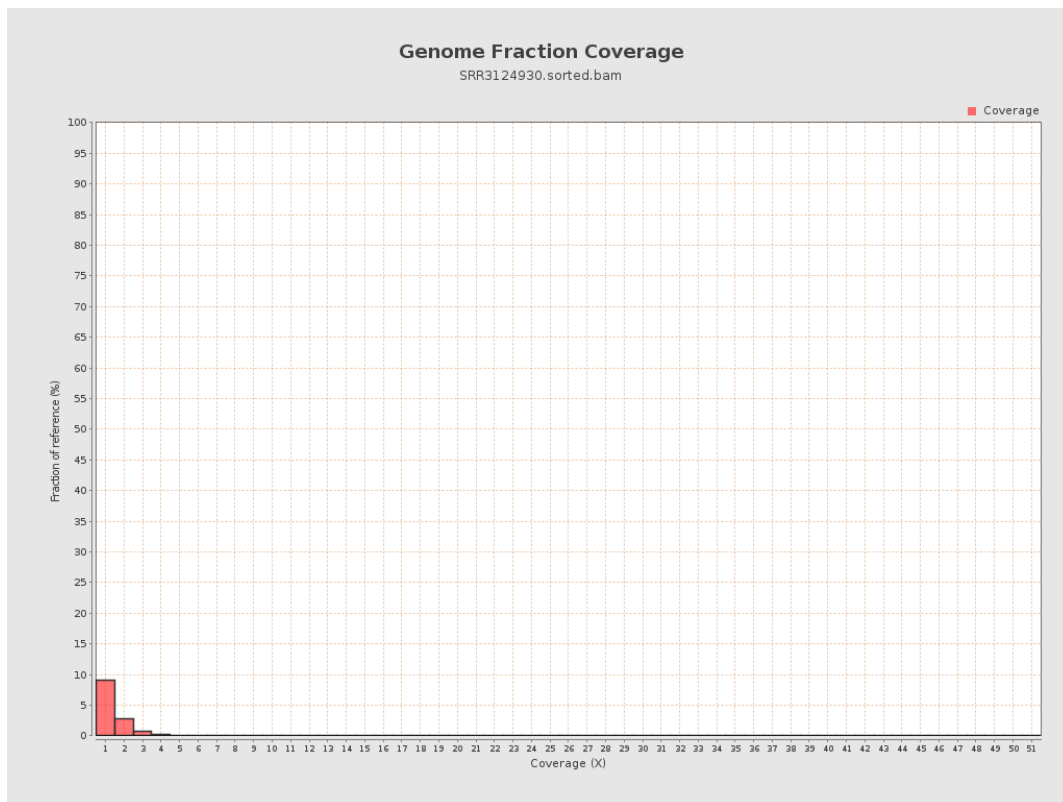
4. Results : Coverage Histogram



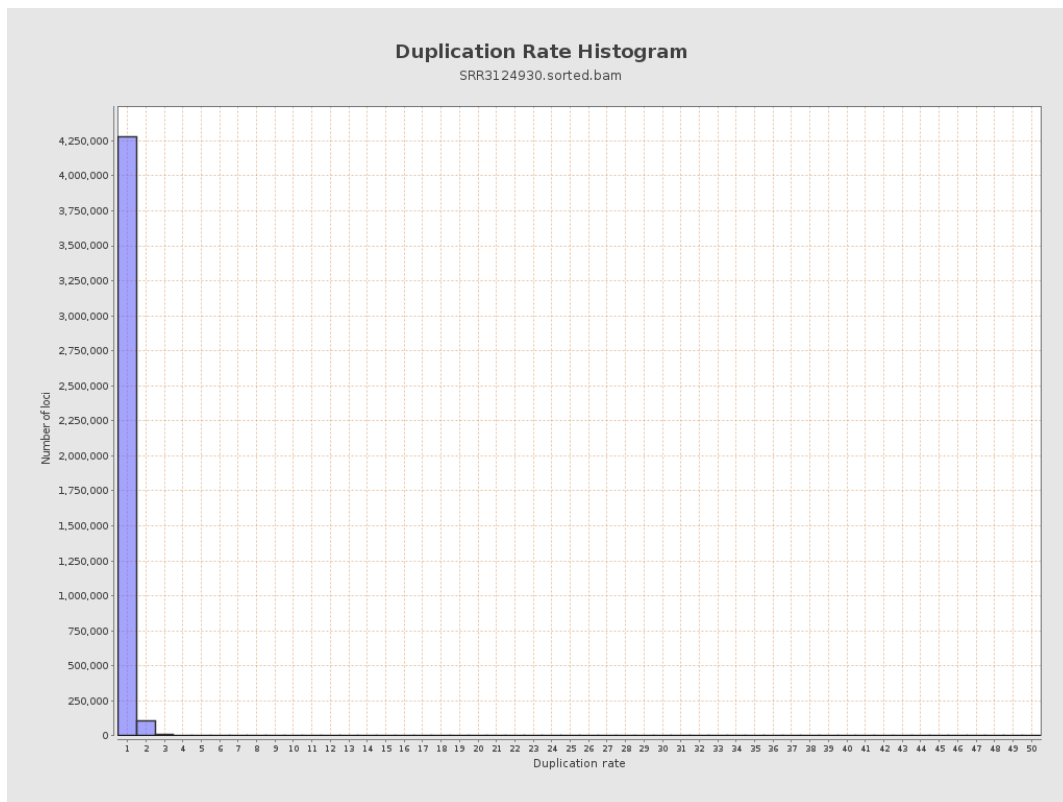
5. Results : Coverage Histogram (0-50X)



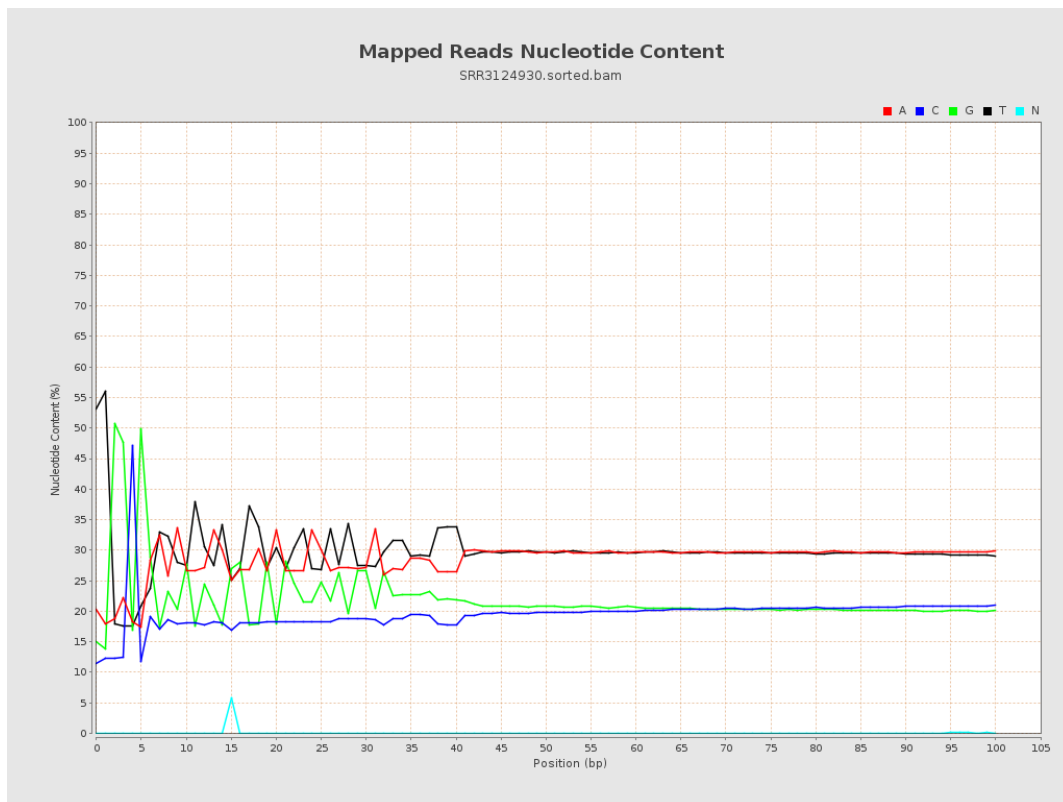
6. Results : Genome Fraction Coverage



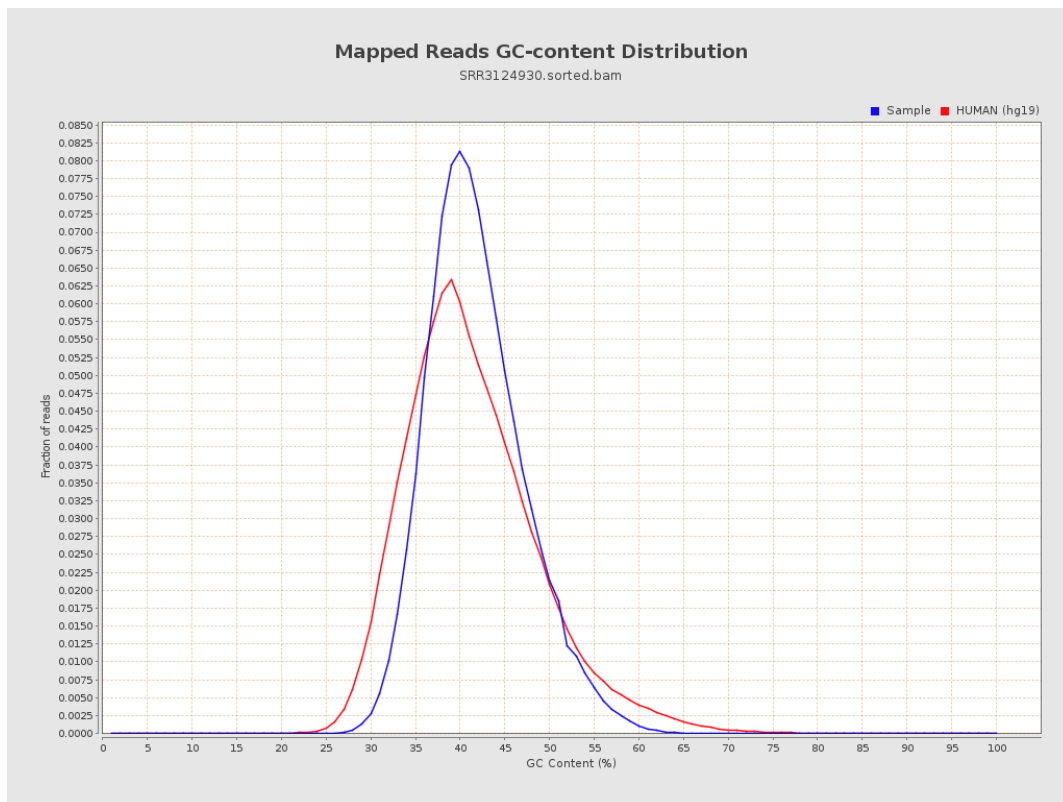
7. Results : Duplication Rate Histogram



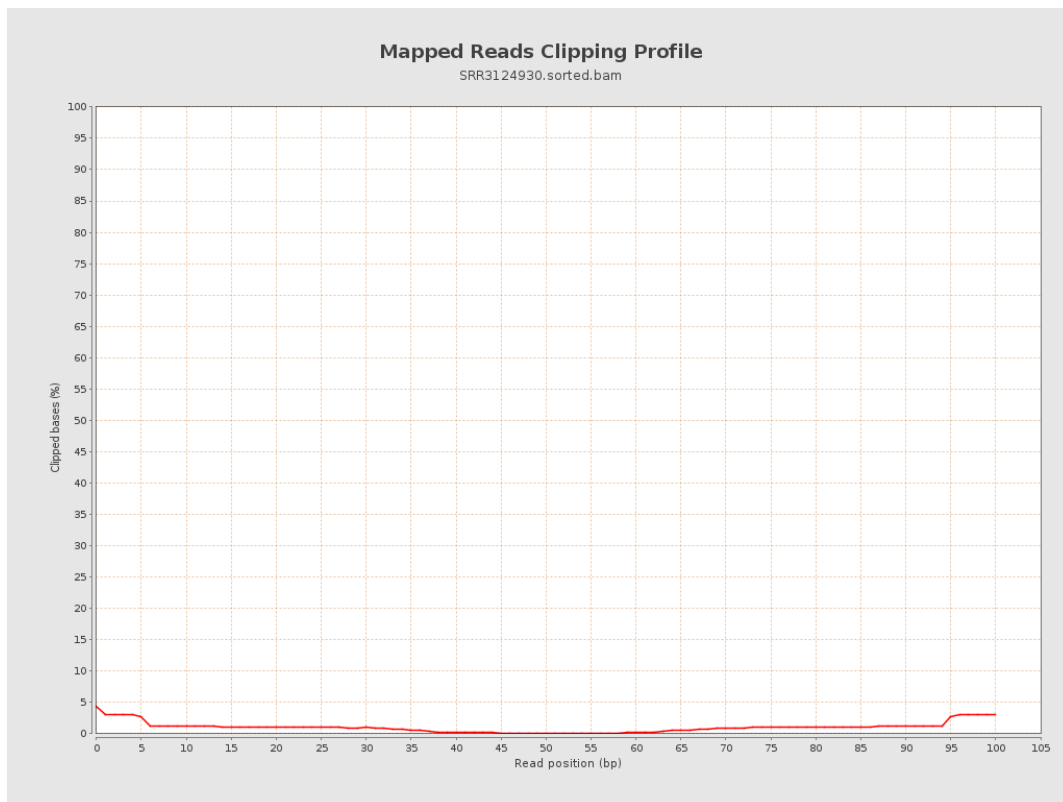
8. Results : Mapped Reads Nucleotide Content



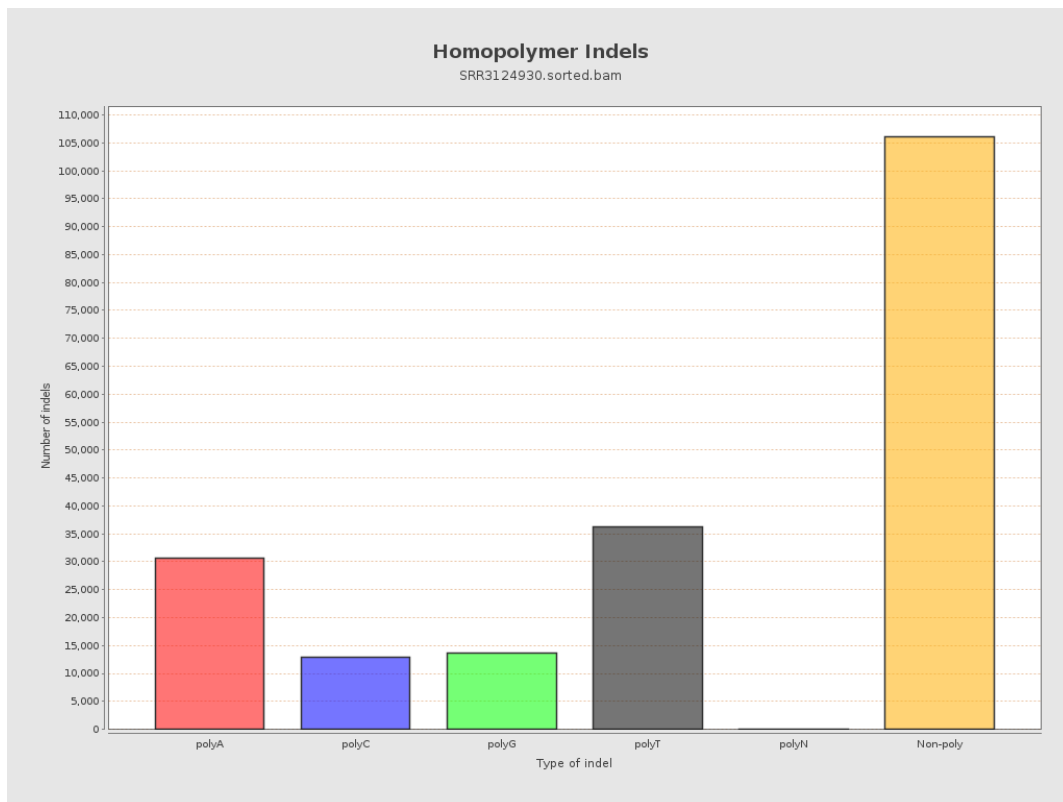
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



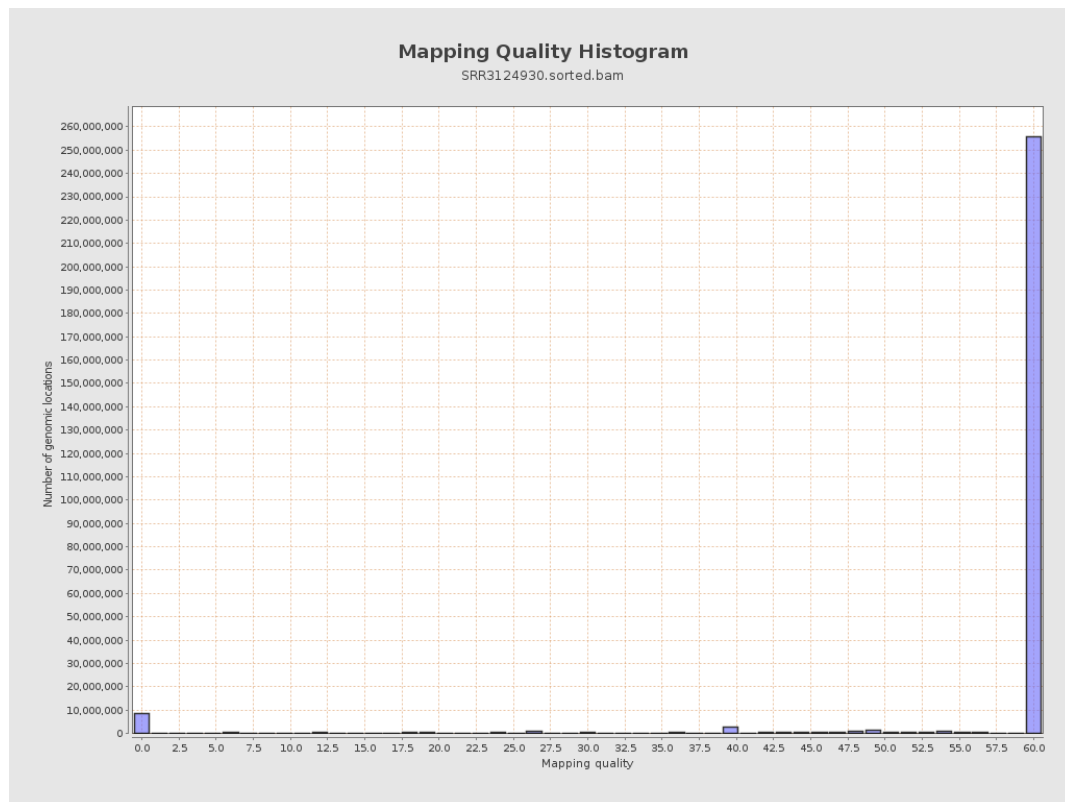
11. Results : Homopolymer Indels



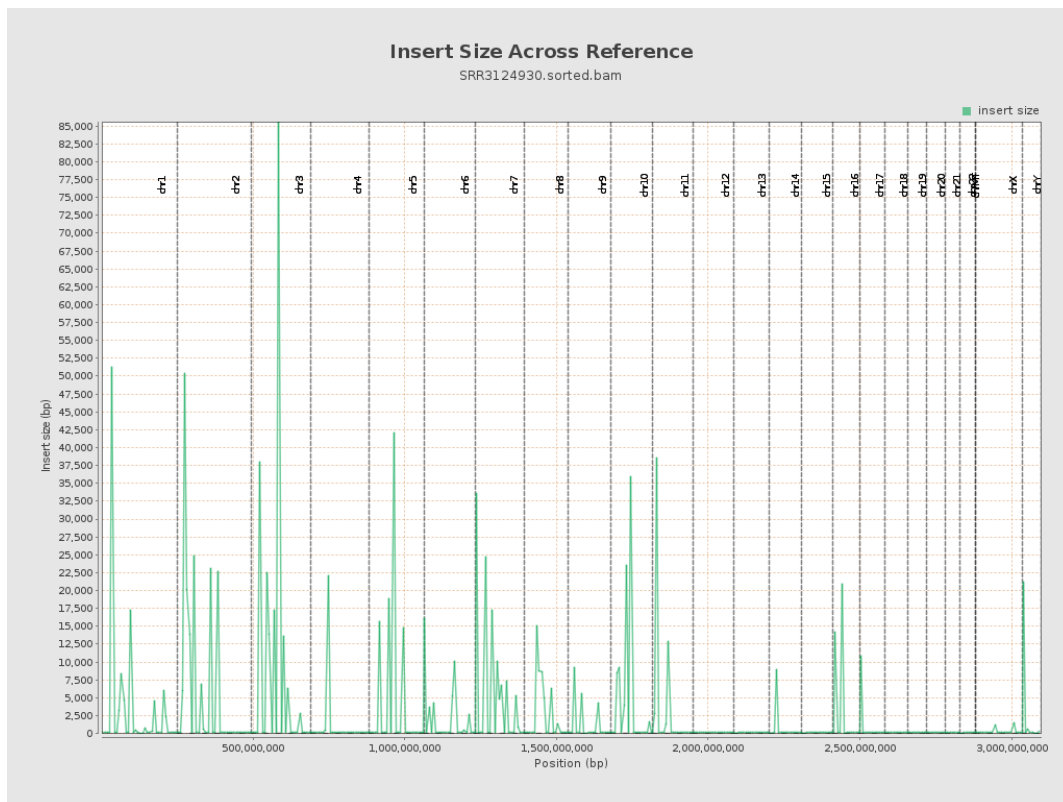
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

