

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 03:34:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124906.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_SRR3124906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124906_1.fastq.gz SRR3124906_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 03:34:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,470,756
Mapped reads	4,409,247 / 98.62%
Unmapped reads	61,509 / 1.38%
Mapped paired reads	4,409,247 / 98.62%
Mapped reads, first in pair	2,206,354 / 49.35%
Mapped reads, second in pair	2,202,893 / 49.27%
Mapped reads, both in pair	4,393,106 / 98.26%
Mapped reads, singletons	16,141 / 0.36%
Secondary alignments	0
Supplementary alignments	22,511 / 0.5%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	216,964 / 4.85%
Duplication rate	2.9%
Clipped reads	2,628,148 / 58.79%

2.2. ACGT Content

Number/percentage of A's	115,522,551 / 28.75%
Number/percentage of C's	81,066,818 / 20.18%
Number/percentage of T's	117,988,179 / 29.37%
Number/percentage of G's	86,927,111 / 21.64%
Number/percentage of N's	262,566 / 0.07%

GC Percentage	41.81%
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2.3. Coverage

Mean	0.1299
Standard Deviation	1.1738

2.4. Mapping Quality

Mean Mapping Quality	52.97
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2.5. Insert size

Mean	78,859.99
Standard Deviation	2,658,117.8
P25/Median/P75	137 / 169 / 214

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	3,499,213
Insertions	69,249
Mapped reads with at least one insertion	1.53%
Deletions	144,206
Mapped reads with at least one deletion	3.2%
Homopolymer indels	44.96%

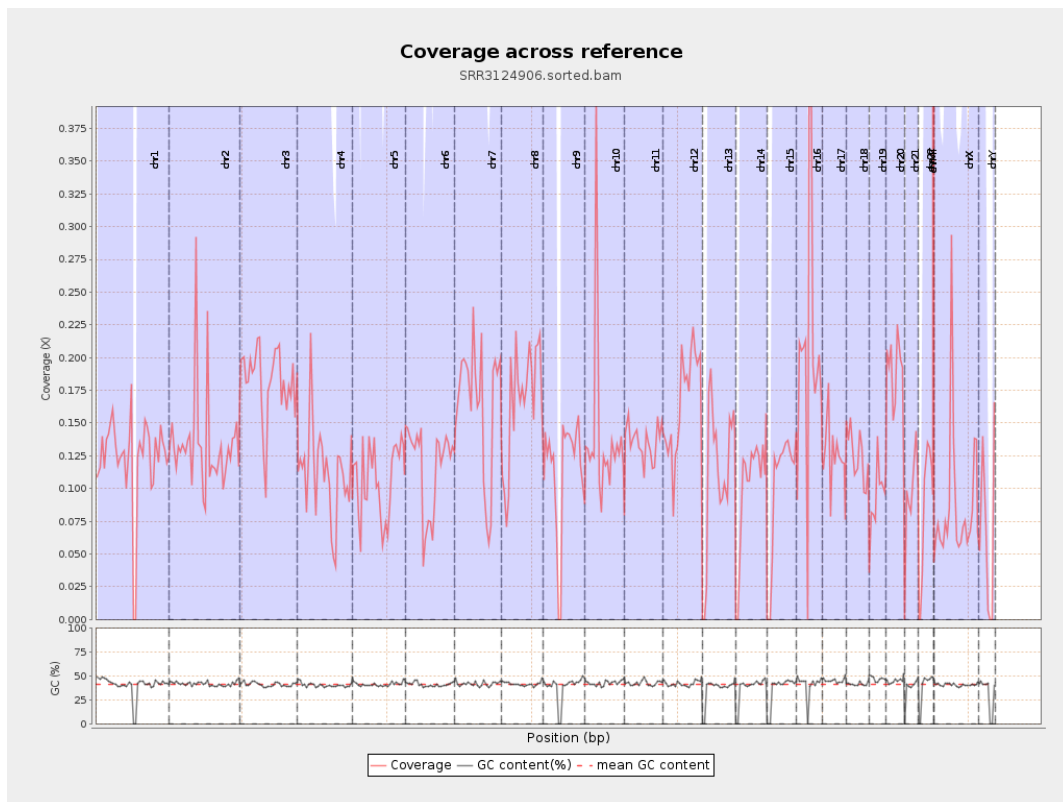
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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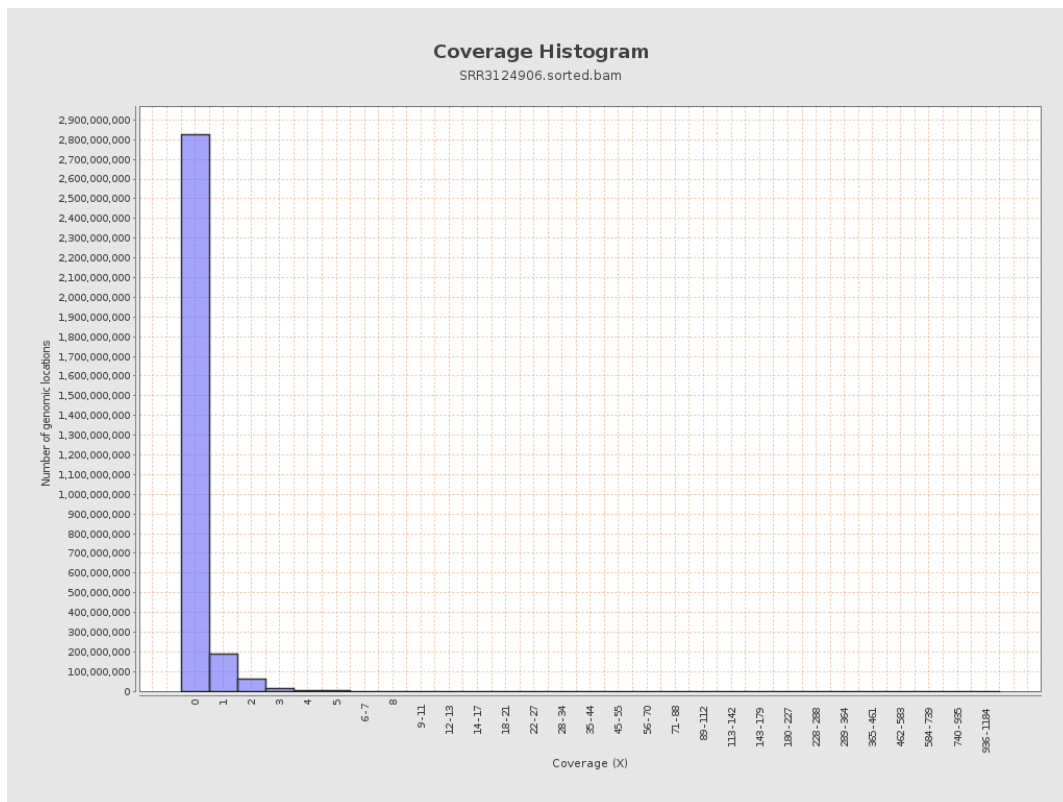
		bases	coverage	deviation
chr1	249250621	30664053	0.123	1.0514
chr2	243199373	32452583	0.1334	1.5657
chr3	198022430	35862189	0.1811	0.5693
chr4	191154276	21209402	0.111	0.875
chr5	180915260	19188253	0.1061	0.4415
chr6	171115067	20004436	0.1169	0.7433
chr7	159138663	26467618	0.1663	1.8112
chr8	146364022	24280348	0.1659	0.6572
chr9	141213431	16239325	0.115	1.2575
chr10	135534747	18641962	0.1375	2.3617
chr11	135006516	18165476	0.1346	0.9055
chr12	133851895	22039655	0.1647	0.5372
chr13	115169878	12803428	0.1112	0.4354
chr14	107349540	10699995	0.0997	0.4635
chr15	102531392	10482310	0.1022	0.4167
chr16	90354753	18916443	0.2094	2.9867
chr17	81195210	10072394	0.1241	1.0199
chr18	78077248	9781734	0.1253	1.3766
chr19	59128983	5628920	0.0952	0.7105
chr20	63025520	11886233	0.1886	0.6127
chr21	48129895	4619412	0.096	0.5495
chr22	51304566	4262381	0.0831	0.418
chrMT	16571	110448	6.6651	4.818
chrX	155270560	13677126	0.0881	0.5806

chrY	59373566	3857935	0.065	1.3291
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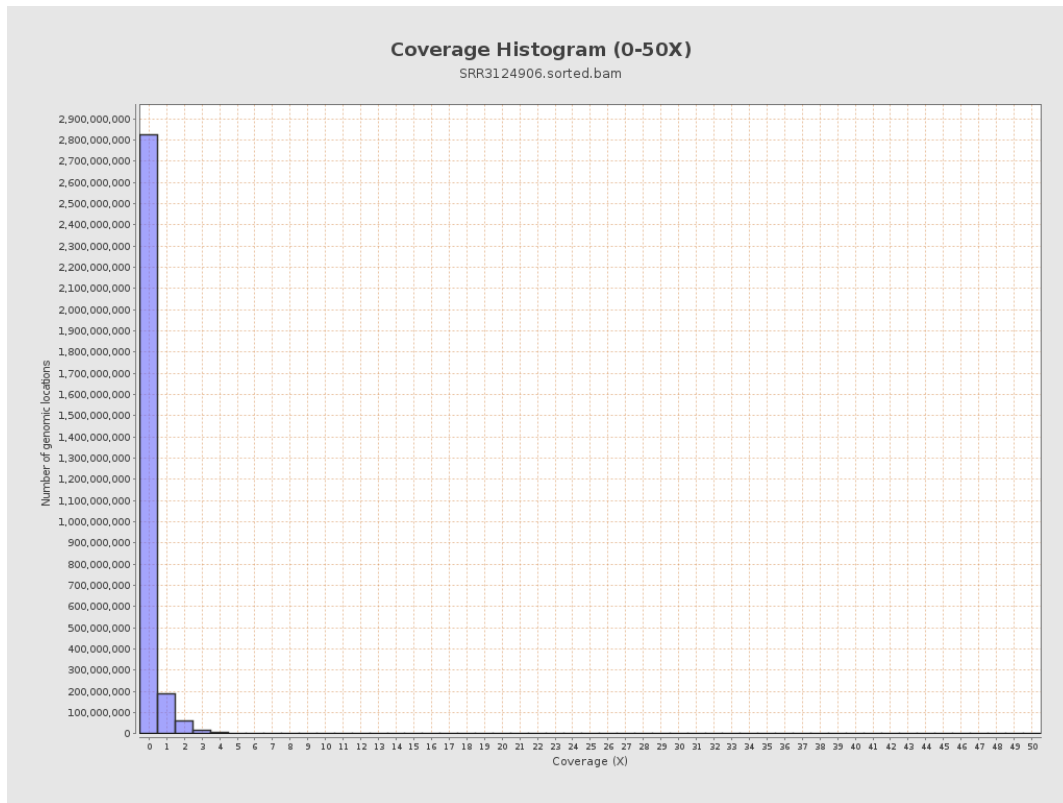
3. Results : Coverage across reference



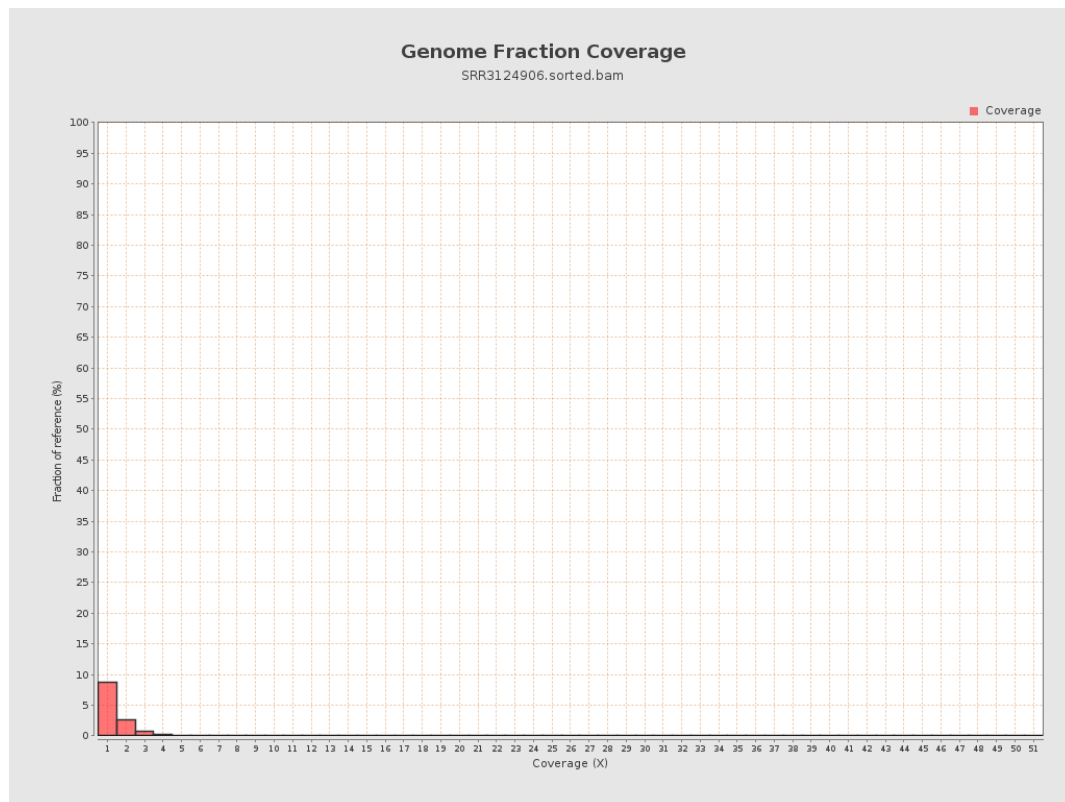
4. Results : Coverage Histogram



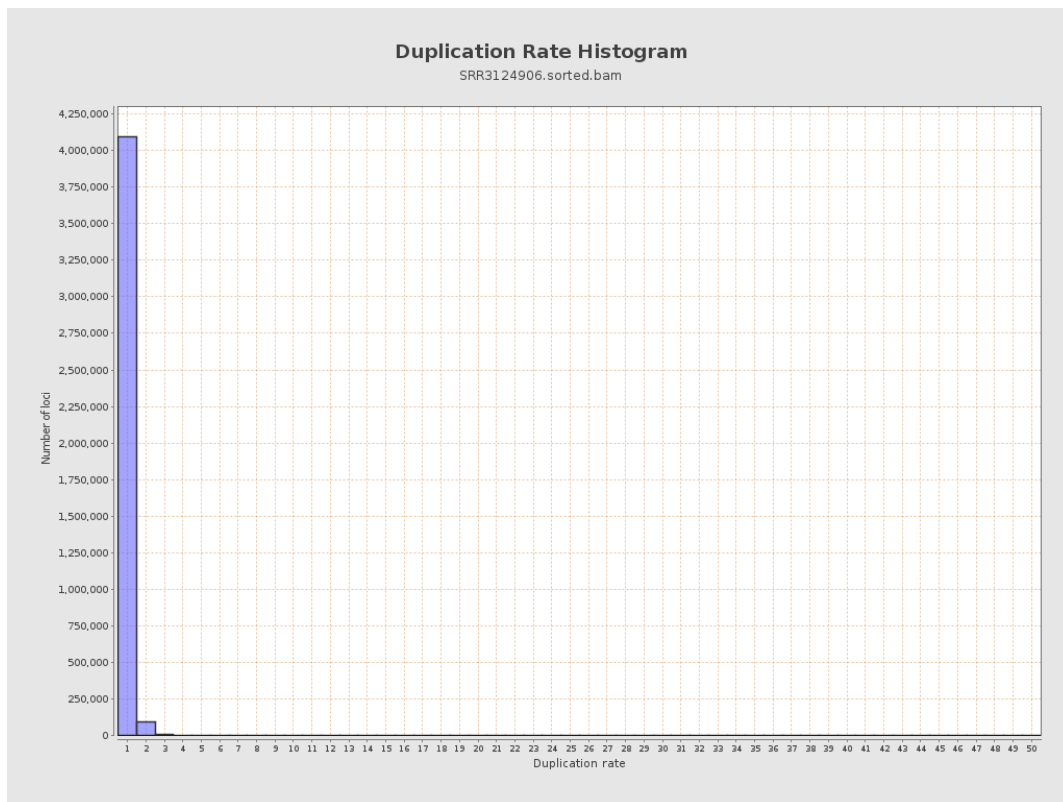
5. Results : Coverage Histogram (0-50X)



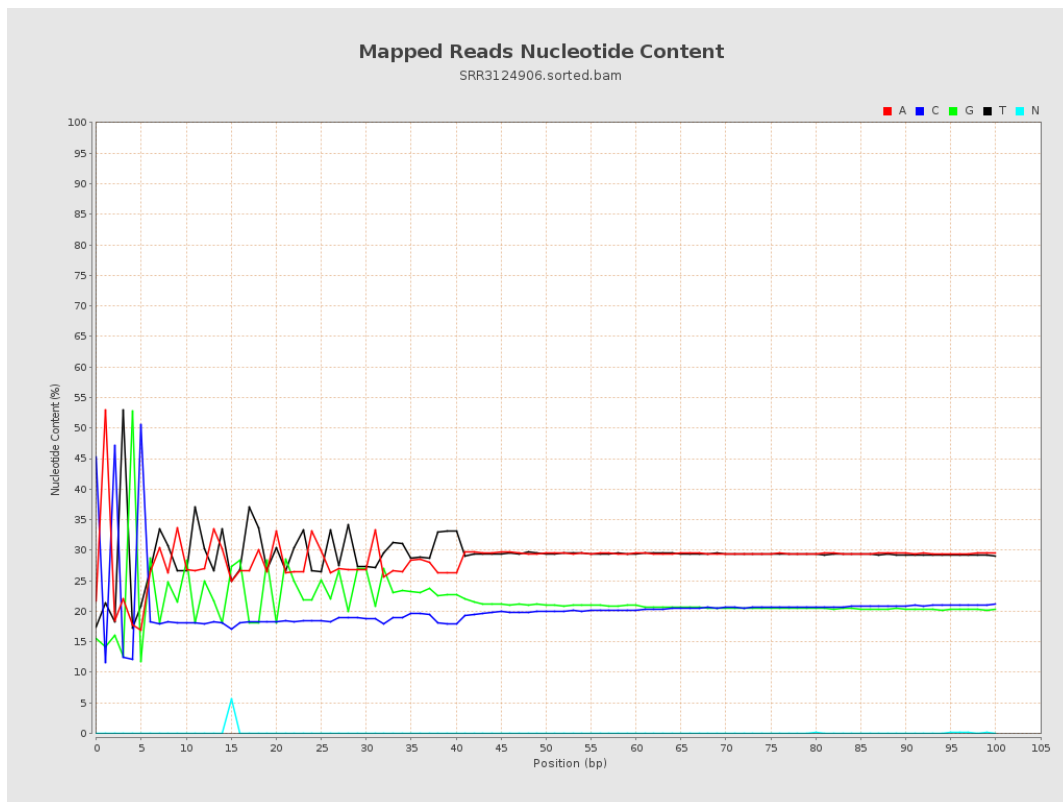
6. Results : Genome Fraction Coverage



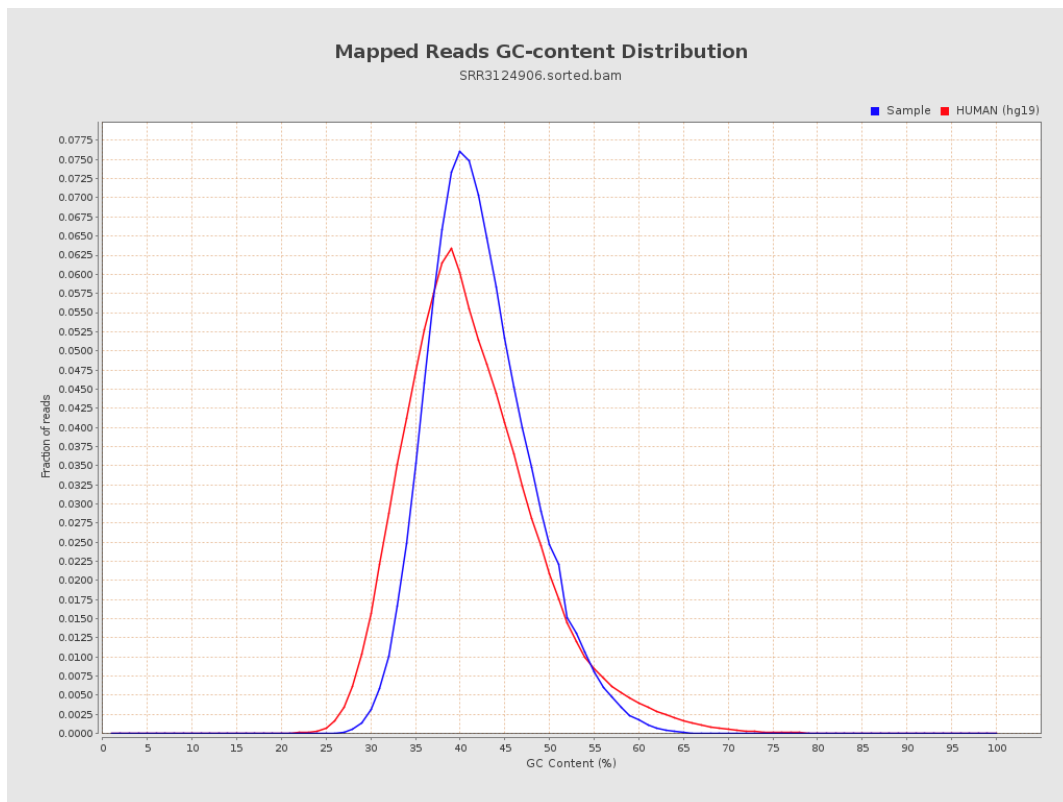
7. Results : Duplication Rate Histogram



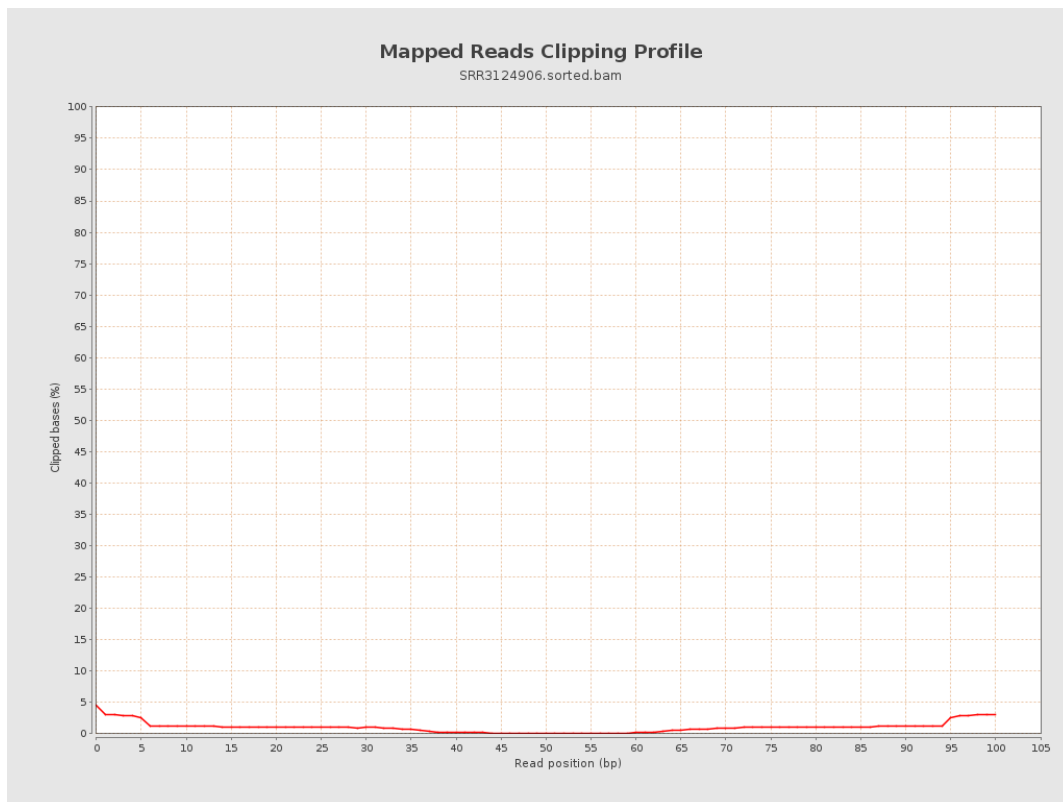
8. Results : Mapped Reads Nucleotide Content



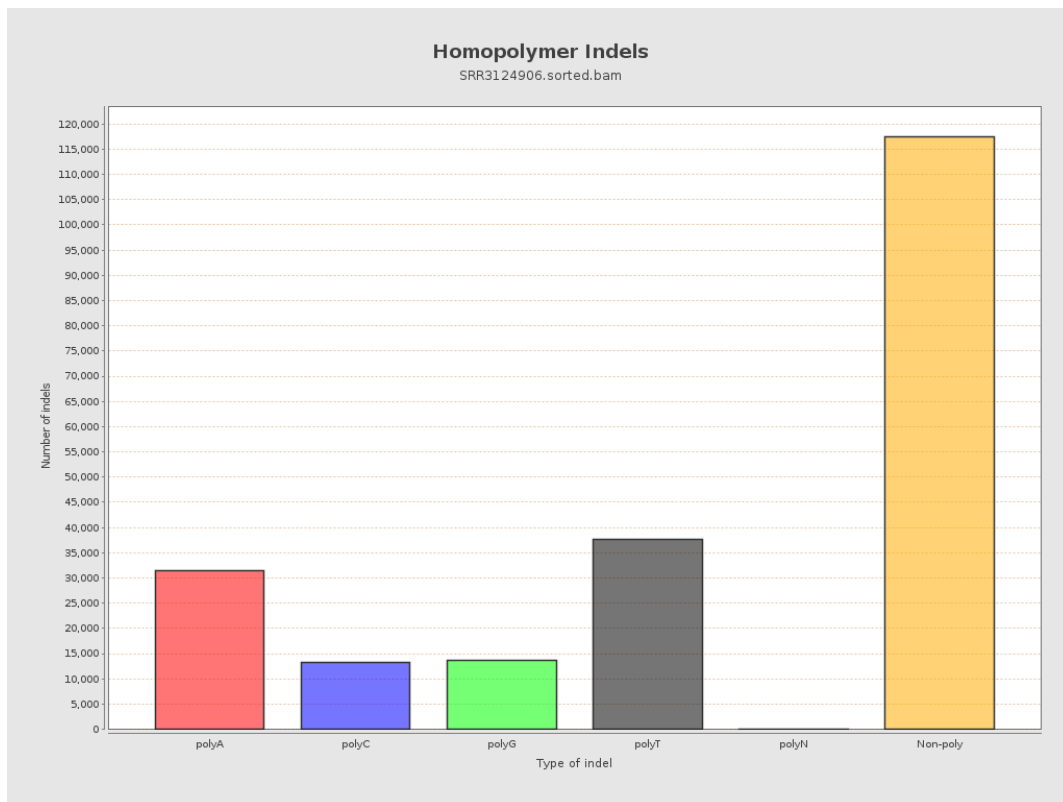
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



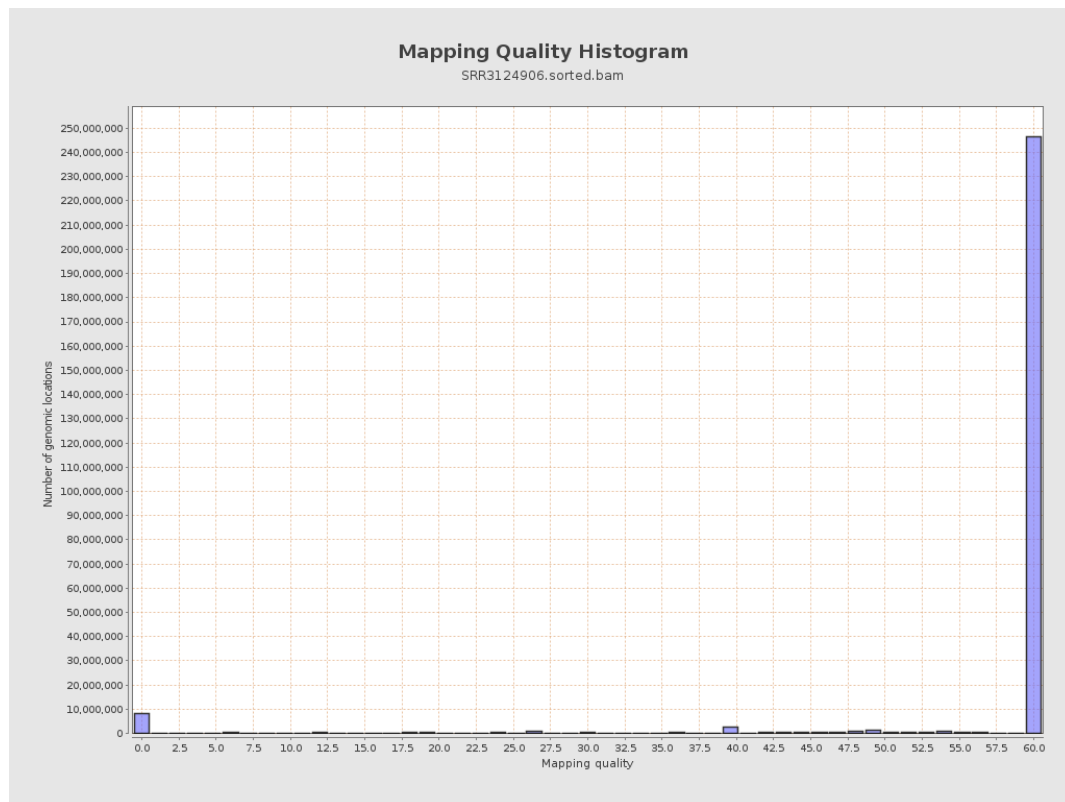
11. Results : Homopolymer Indels



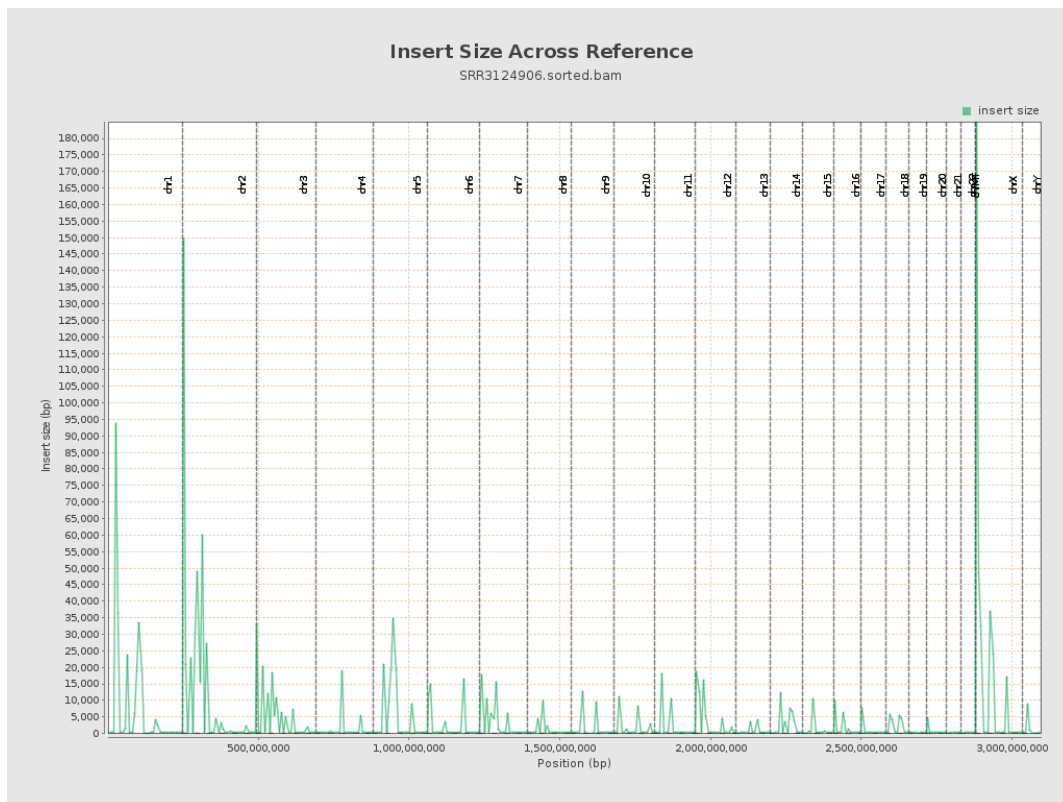
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

