

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:45:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124946.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_SRR3124946 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124946_1.fastq.gz SRR3124946_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:45:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,124,364
Mapped reads	4,020,115 / 97.47%
Unmapped reads	104,249 / 2.53%
Mapped paired reads	4,020,115 / 97.47%
Mapped reads, first in pair	2,013,048 / 48.81%
Mapped reads, second in pair	2,007,067 / 48.66%
Mapped reads, both in pair	4,003,408 / 97.07%
Mapped reads, singletons	16,707 / 0.41%
Secondary alignments	0
Supplementary alignments	20,118 / 0.49%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	290,902 / 7.05%
Duplication rate	5%
Clipped reads	1,752,124 / 42.48%

2.2. ACGT Content

Number/percentage of A's	100,915,559 / 28.5%
Number/percentage of C's	65,584,476 / 18.52%
Number/percentage of T's	106,311,265 / 30.02%
Number/percentage of G's	81,322,075 / 22.96%
Number/percentage of N's	5,048 / 0%

GC Percentage	41.48%
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2.3. Coverage

Mean	0.1145
Standard Deviation	1.1326

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	51,959.52
Standard Deviation	2,119,936.08
P25/Median/P75	159 / 214 / 291

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	2,589,100
Insertions	48,360
Mapped reads with at least one insertion	1.17%
Deletions	114,414
Mapped reads with at least one deletion	2.79%
Homopolymer indels	48.48%

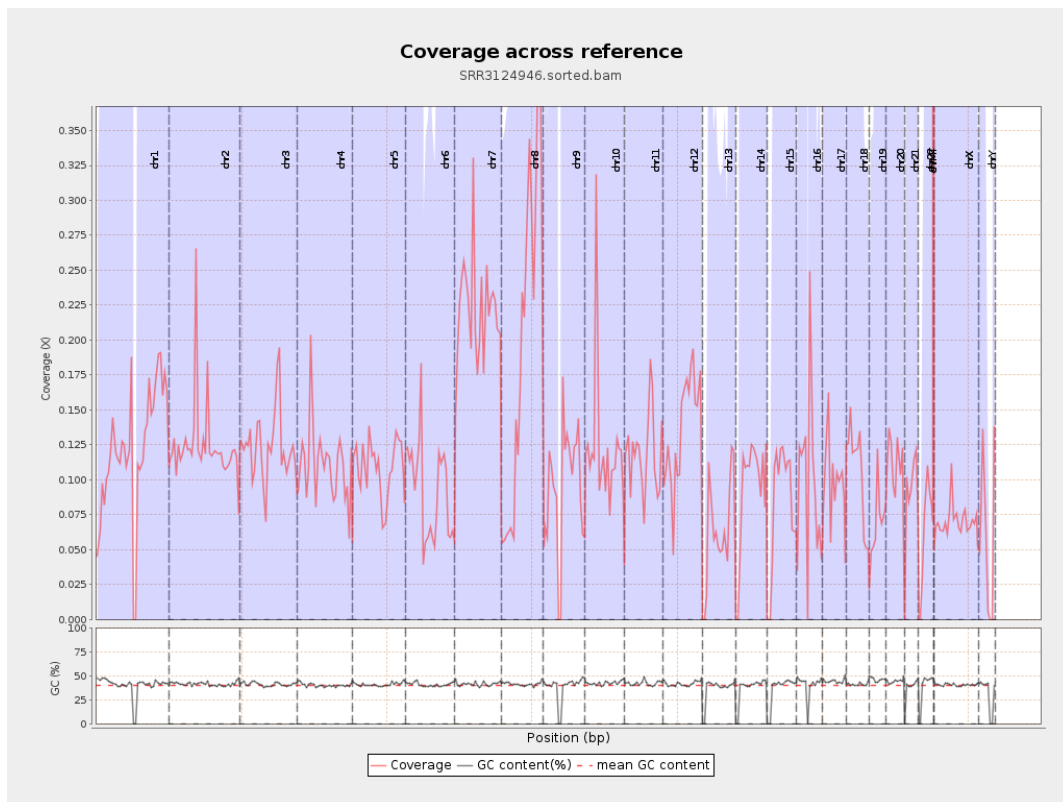
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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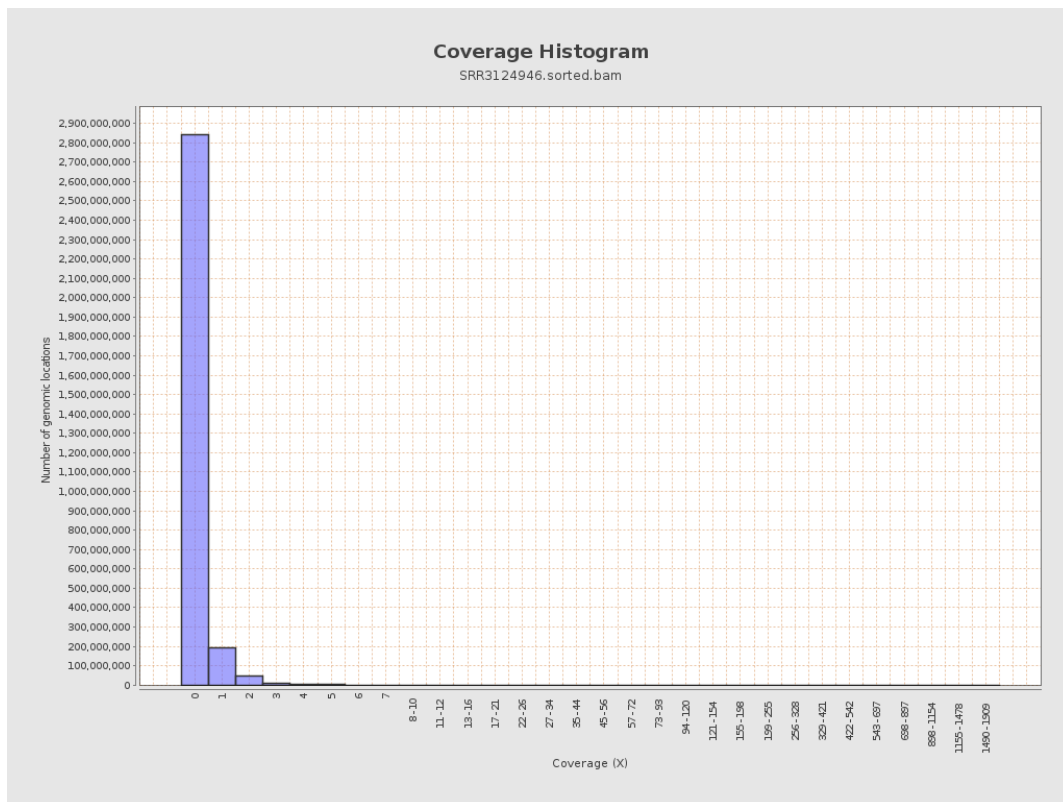
		bases	coverage	deviation
chr1	249250621	30386035	0.1219	1.2195
chr2	243199373	30350902	0.1248	1.1799
chr3	198022430	24592948	0.1242	0.444
chr4	191154276	21024092	0.11	0.6842
chr5	180915260	19629939	0.1085	0.4235
chr6	171115067	15677008	0.0916	0.8664
chr7	159138663	35442159	0.2227	2.9753
chr8	146364022	28972174	0.1979	0.6818
chr9	141213431	13526819	0.0958	1.5596
chr10	135534747	16537117	0.122	1.6195
chr11	135006516	15961104	0.1182	0.8506
chr12	133851895	18151384	0.1356	0.4728
chr13	115169878	7332892	0.0637	0.3118
chr14	107349540	9780011	0.0911	0.4639
chr15	102531392	8545409	0.0833	0.3667
chr16	90354753	8826451	0.0977	1.2475
chr17	81195210	7917318	0.0975	1.1217
chr18	78077248	8324032	0.1066	1.5548
chr19	59128983	4126534	0.0698	0.6929
chr20	63025520	6990305	0.1109	0.4571
chr21	48129895	4322748	0.0898	0.485
chr22	51304566	3167685	0.0617	0.3294
chrMT	16571	372331	22.4688	15.9816
chrX	155270560	10913256	0.0703	0.4829

chrY	59373566	3459284	0.0583	1.1459
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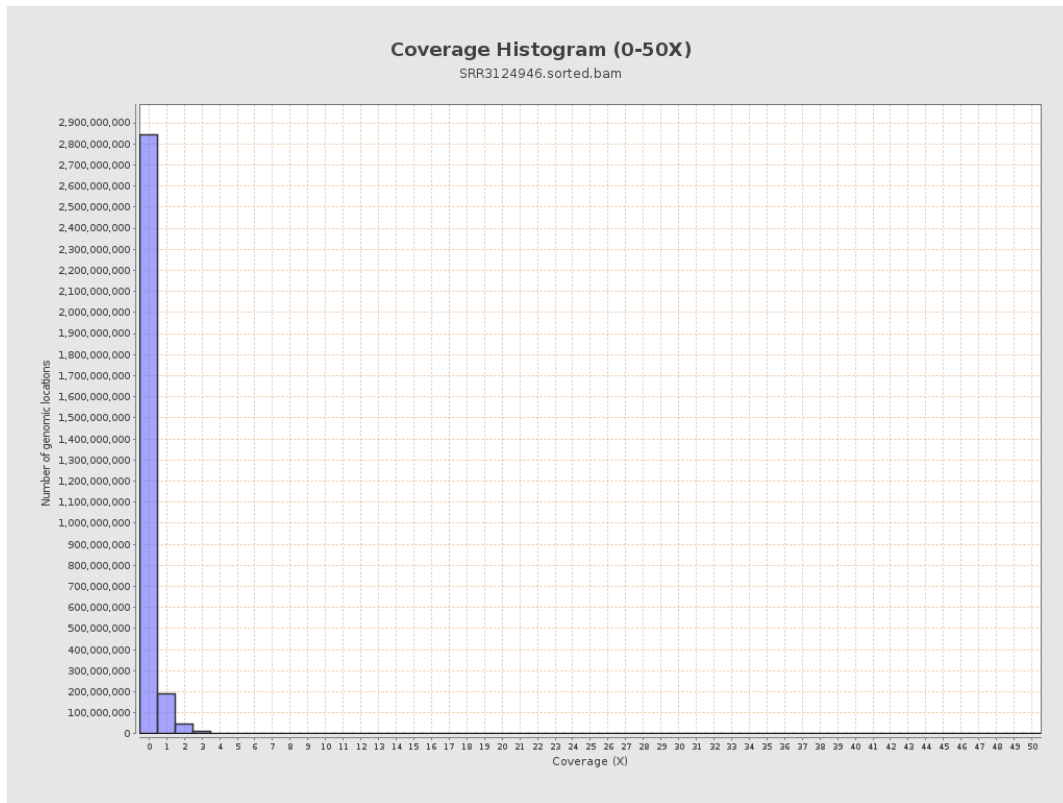
3. Results : Coverage across reference



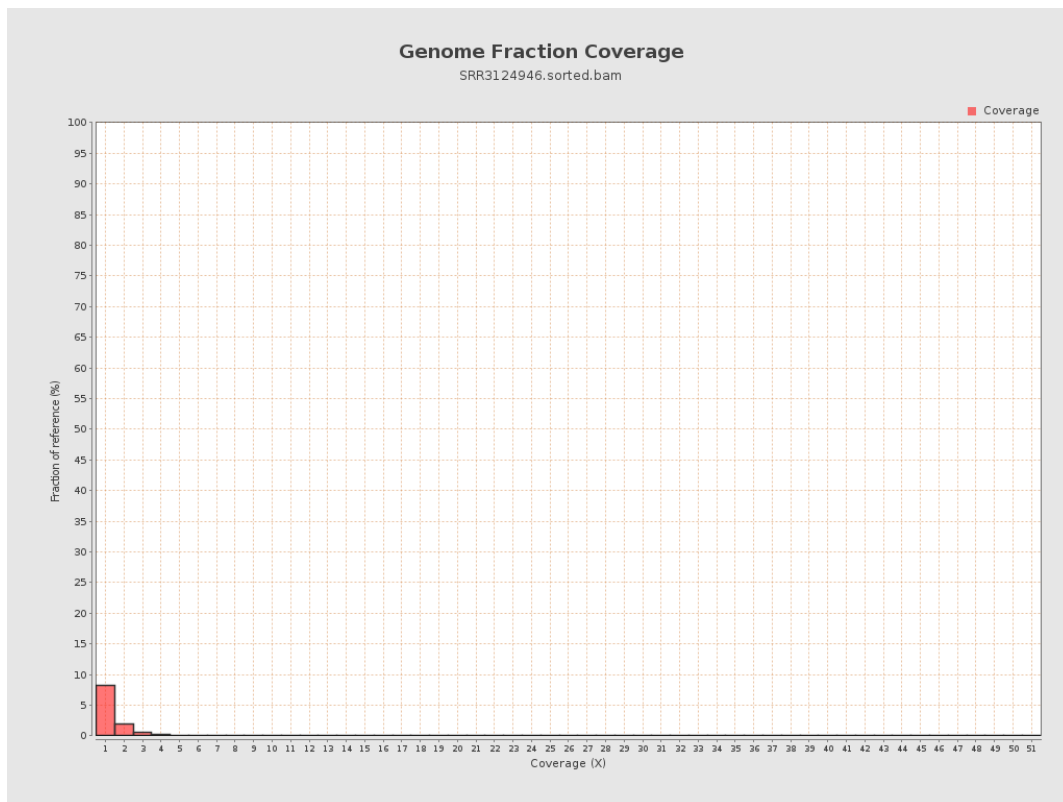
4. Results : Coverage Histogram



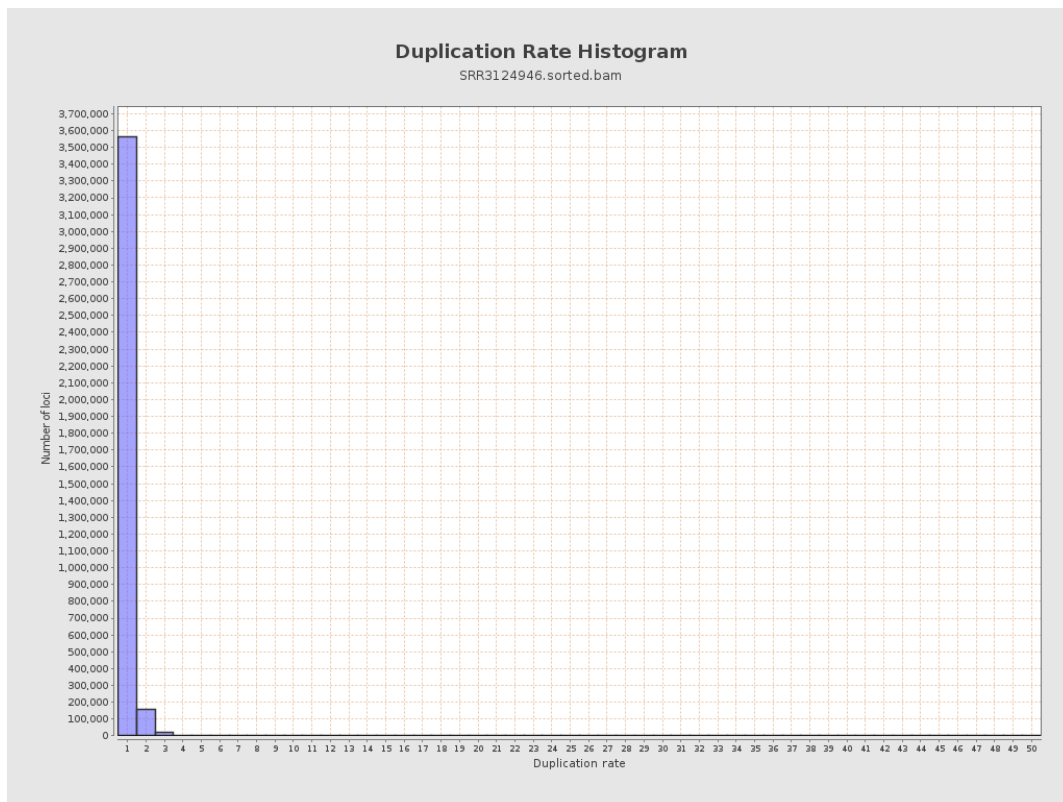
5. Results : Coverage Histogram (0-50X)



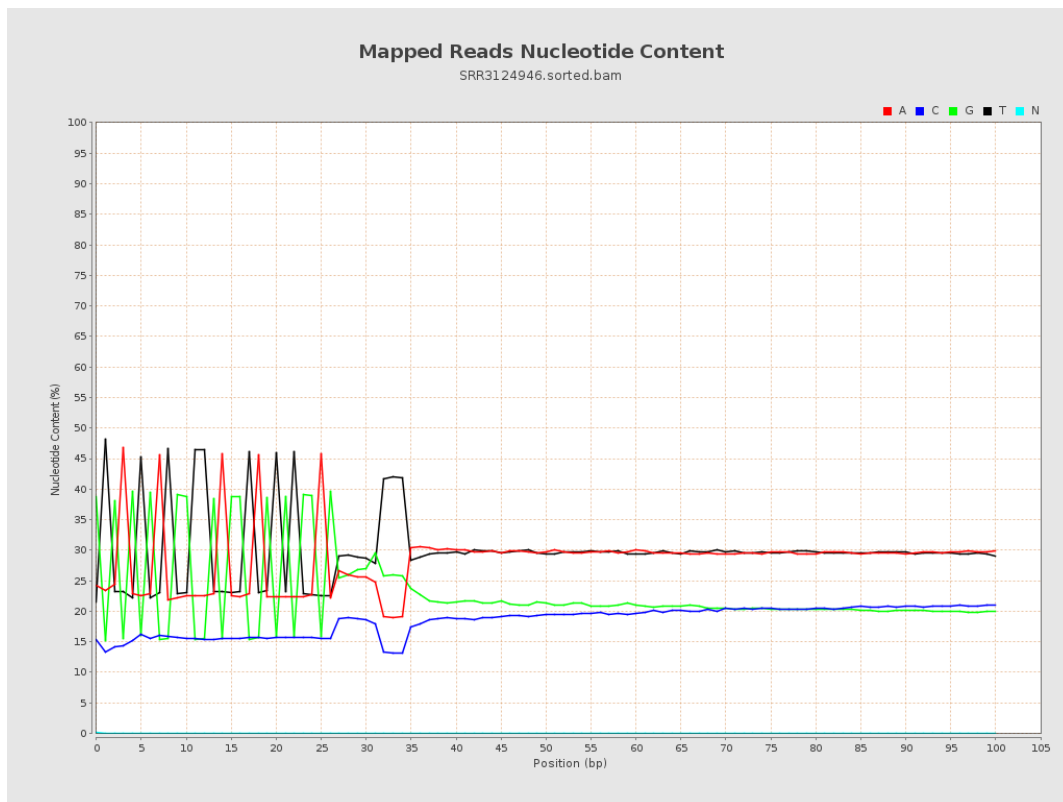
6. Results : Genome Fraction Coverage



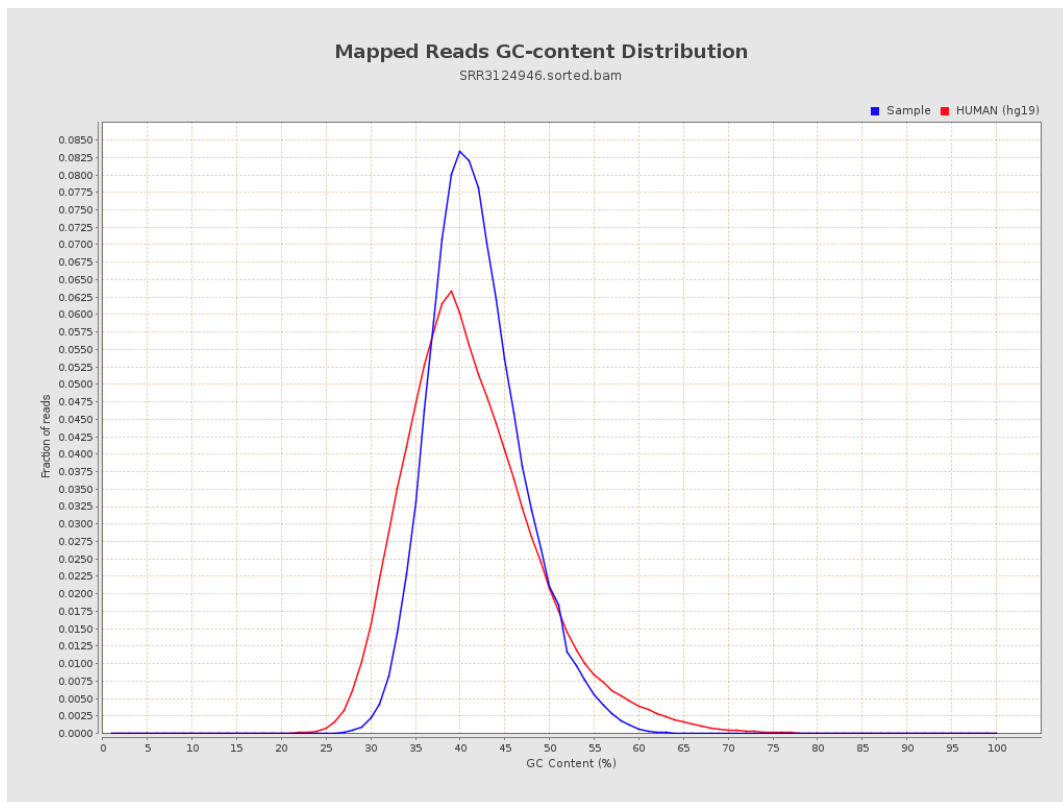
7. Results : Duplication Rate Histogram



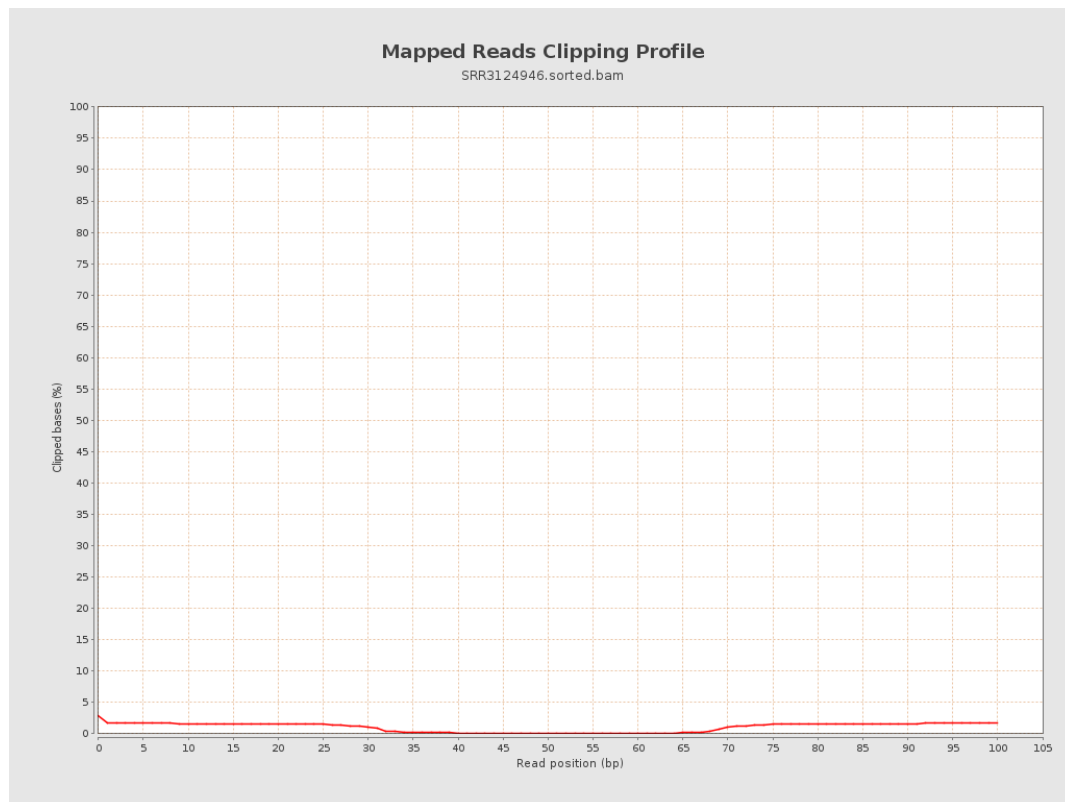
8. Results : Mapped Reads Nucleotide Content



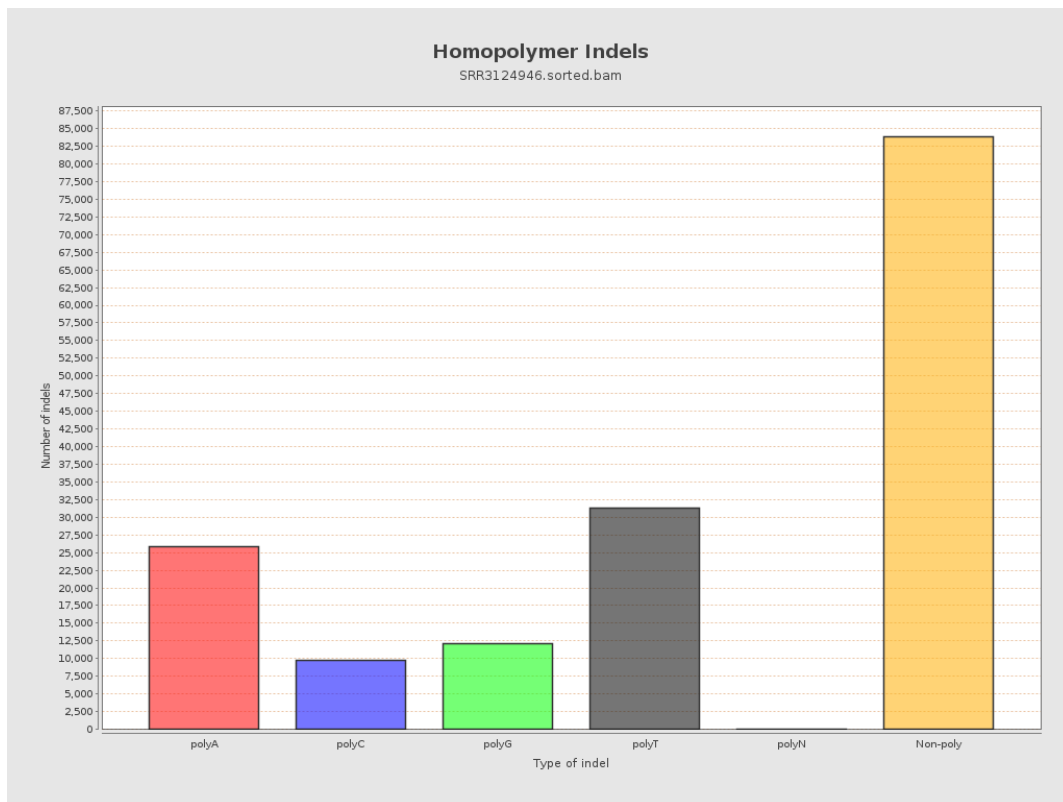
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



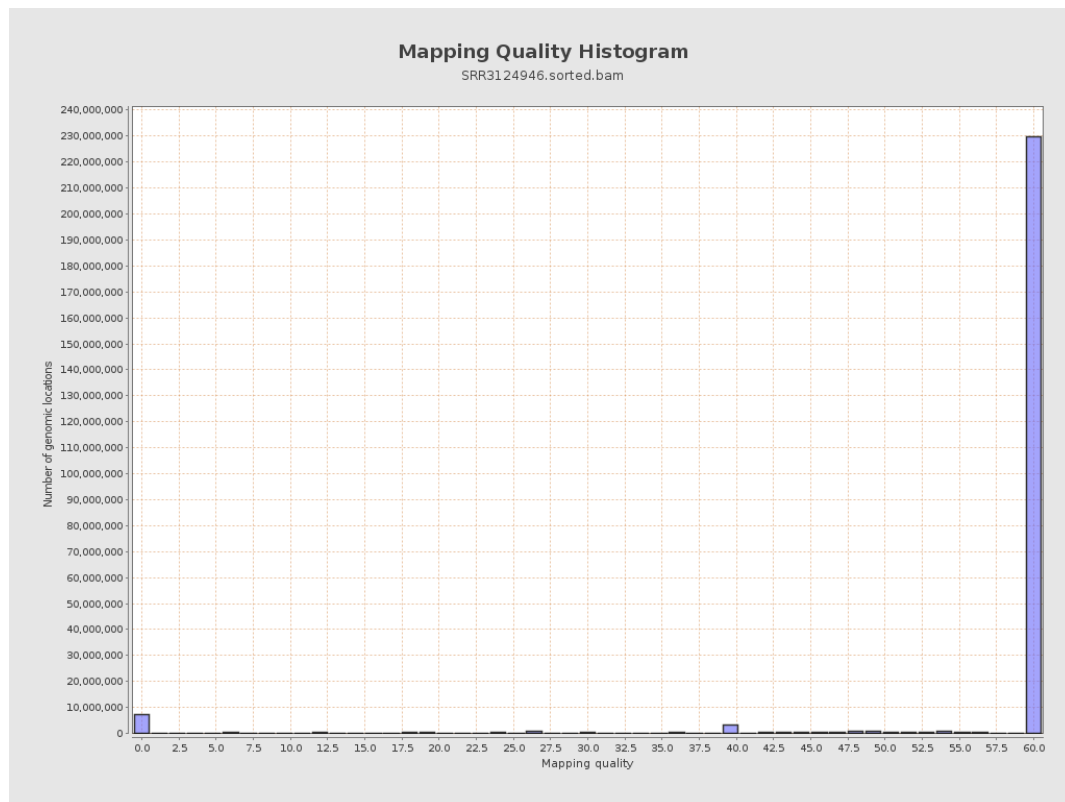
11. Results : Homopolymer Indels



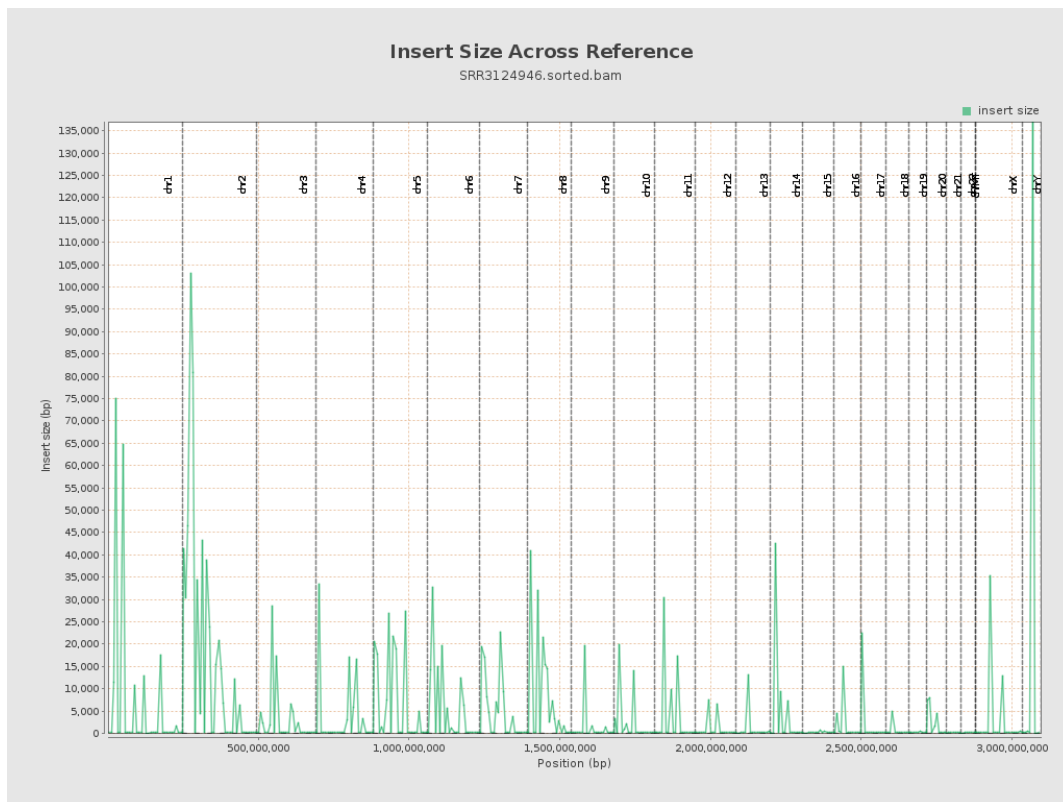
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

