

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 08:52:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124947.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_SRR3124947 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124947_1.fastq.gz SRR3124947_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 08:52:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124947.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,990,142
Mapped reads	3,901,918 / 97.79%
Unmapped reads	88,224 / 2.21%
Mapped paired reads	3,901,918 / 97.79%
Mapped reads, first in pair	1,953,957 / 48.97%
Mapped reads, second in pair	1,947,961 / 48.82%
Mapped reads, both in pair	3,886,562 / 97.4%
Mapped reads, singletons	15,356 / 0.38%
Secondary alignments	0
Supplementary alignments	18,009 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	280,321 / 7.03%
Duplication rate	4.99%
Clipped reads	1,692,067 / 42.41%

2.2. ACGT Content

Number/percentage of A's	97,649,854 / 28.38%
Number/percentage of C's	64,246,120 / 18.67%
Number/percentage of T's	102,707,140 / 29.85%
Number/percentage of G's	79,453,204 / 23.09%
Number/percentage of N's	4,964 / 0%

GC Percentage	41.77%
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2.3. Coverage

Mean	0.1112
Standard Deviation	1.0436

2.4. Mapping Quality

Mean Mapping Quality	52.68
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2.5. Insert size

Mean	43,649.9
Standard Deviation	1,981,164.98
P25/Median/P75	151 / 203 / 282

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	2,541,213
Insertions	45,227
Mapped reads with at least one insertion	1.13%
Deletions	111,631
Mapped reads with at least one deletion	2.8%
Homopolymer indels	48.07%

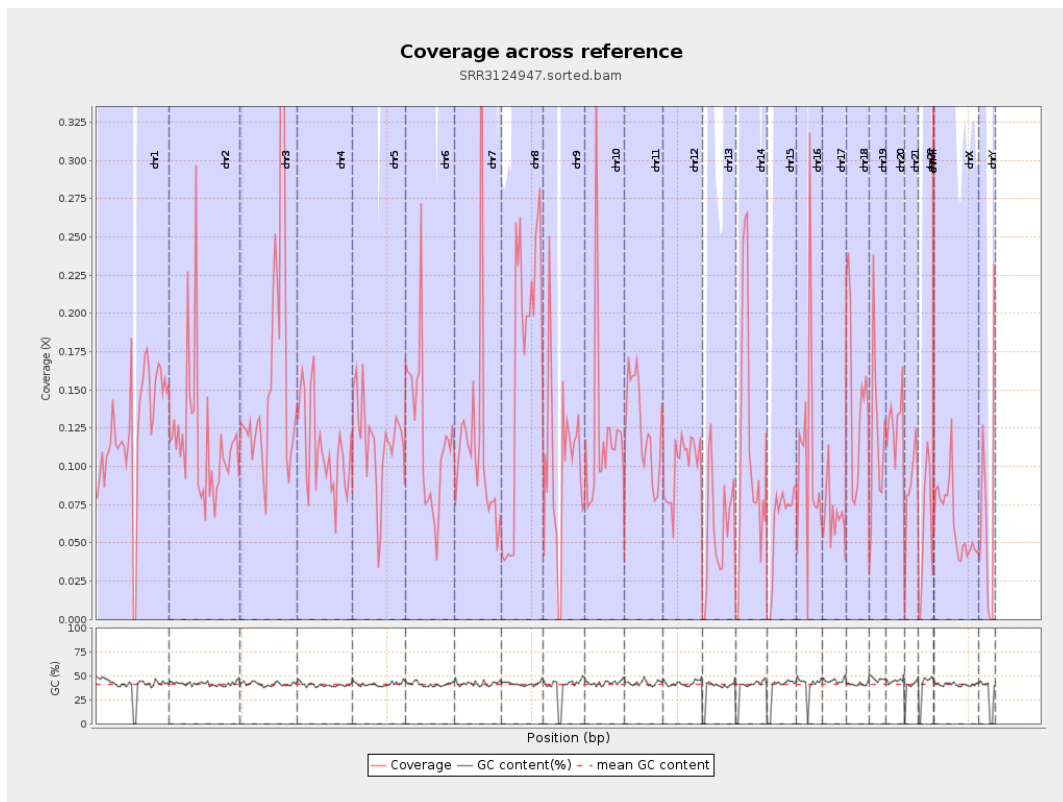
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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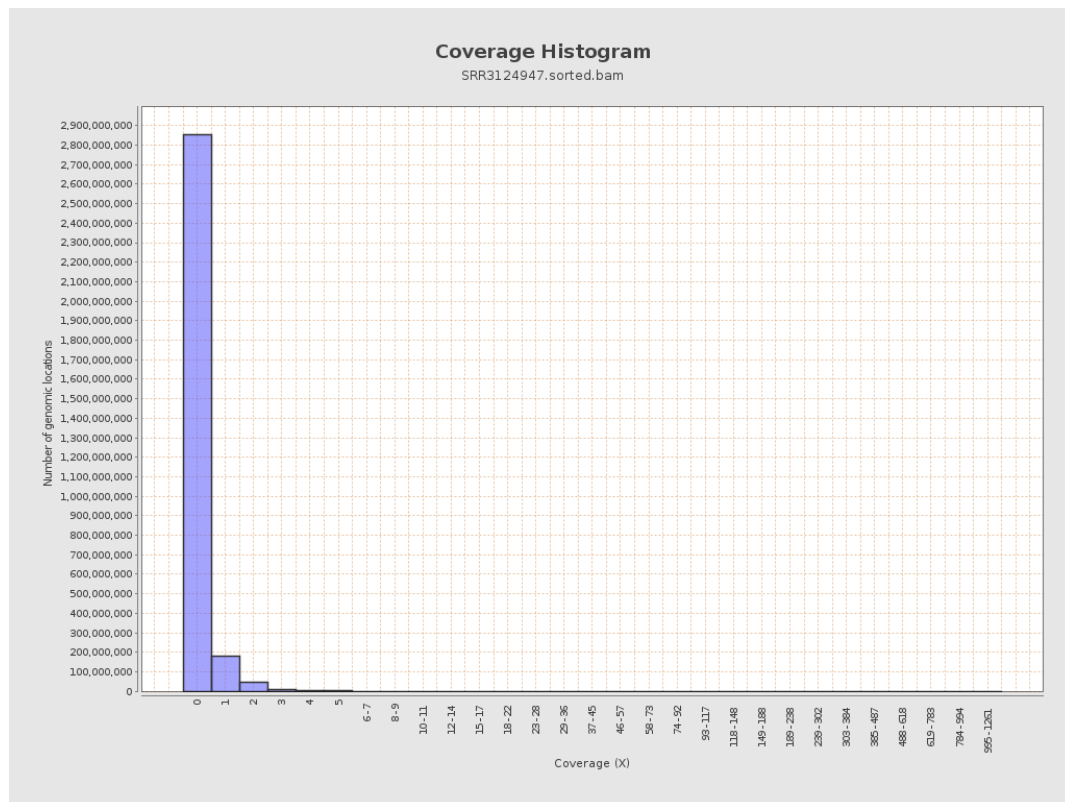
		bases	coverage	deviation
chr1	249250621	30795201	0.1236	1.2225
chr2	243199373	28404304	0.1168	1.2951
chr3	198022430	31880721	0.161	0.5589
chr4	191154276	21132394	0.1106	0.6421
chr5	180915260	20907492	0.1156	0.4363
chr6	171115067	20311324	0.1187	1.418
chr7	159138663	18449472	0.1159	1.1972
chr8	146364022	24331314	0.1662	0.6426
chr9	141213431	14673144	0.1039	1.4936
chr10	135534747	16197048	0.1195	2.0712
chr11	135006516	16760105	0.1241	0.924
chr12	133851895	13375278	0.0999	0.4005
chr13	115169878	6637399	0.0576	0.298
chr14	107349540	11508174	0.1072	0.4914
chr15	102531392	6317881	0.0616	0.3138
chr16	90354753	9372411	0.1037	1.6239
chr17	81195210	5468706	0.0674	0.7949
chr18	78077248	11330387	0.1451	1.6465
chr19	59128983	7128973	0.1206	0.8372
chr20	63025520	8088317	0.1283	0.4752
chr21	48129895	4133655	0.0859	0.4463
chr22	51304566	2999218	0.0585	0.3162
chrMT	16571	73855	4.4569	3.6223
chrX	155270560	9924410	0.0639	0.4699

chrY	59373566	4045721	0.0681	1.2647
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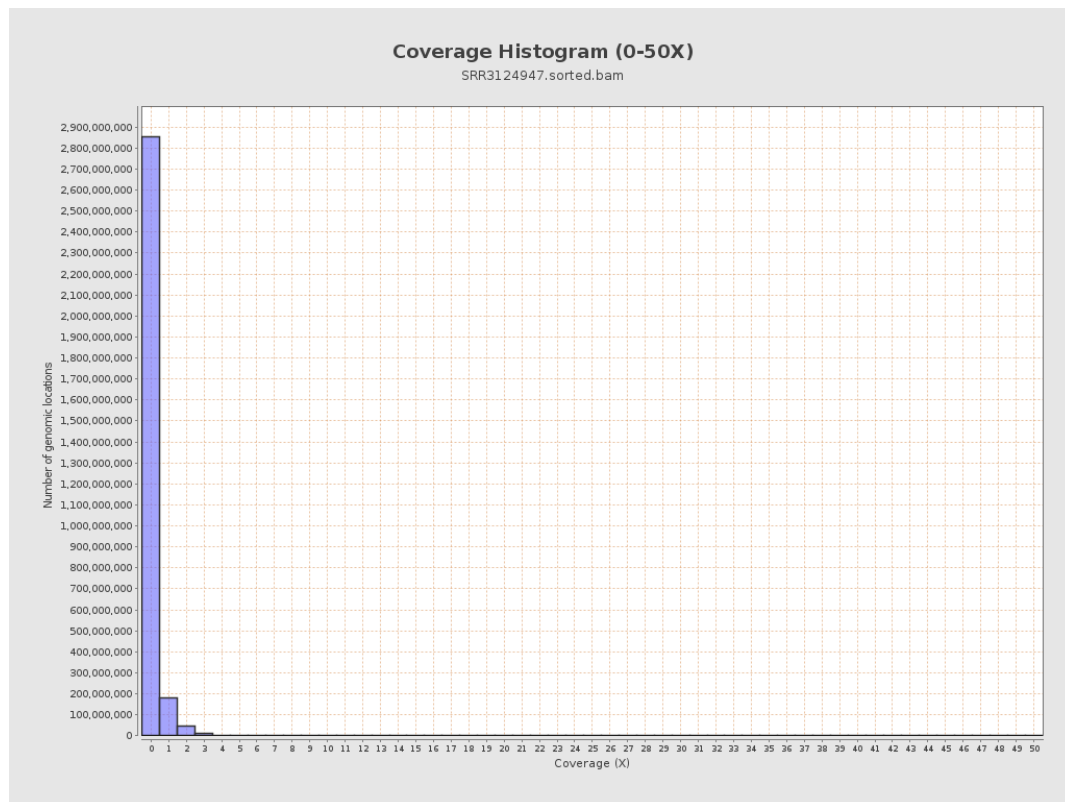
3. Results : Coverage across reference



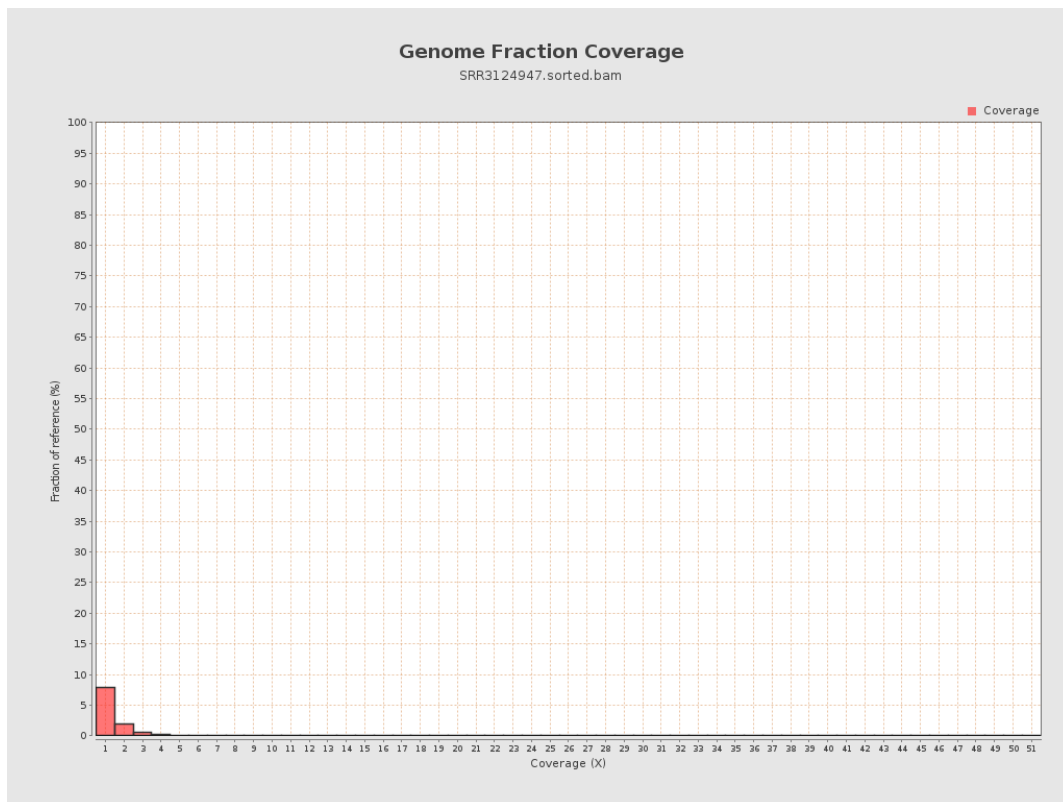
4. Results : Coverage Histogram



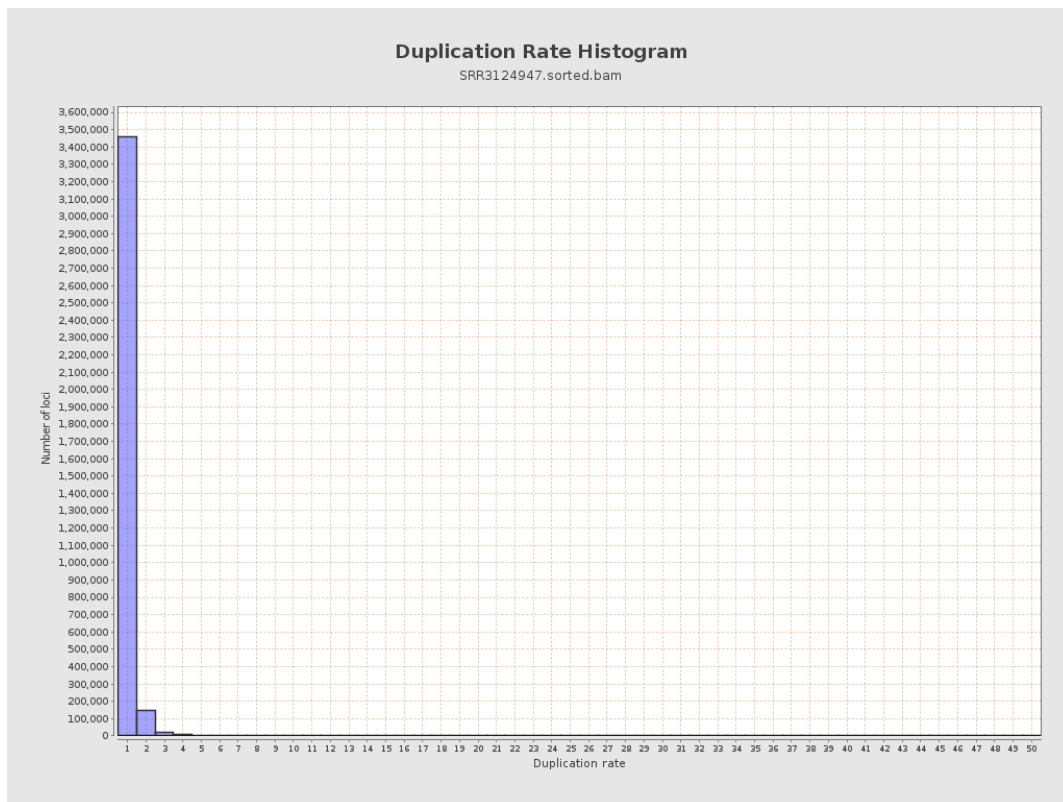
5. Results : Coverage Histogram (0-50X)



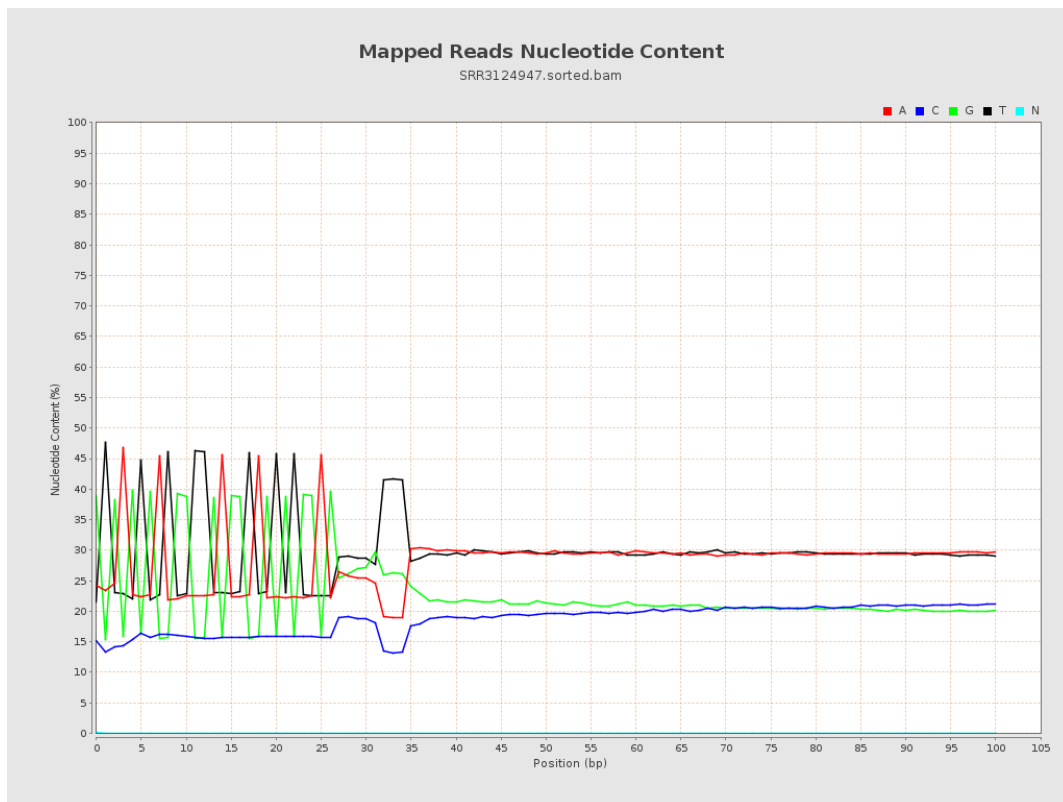
6. Results : Genome Fraction Coverage



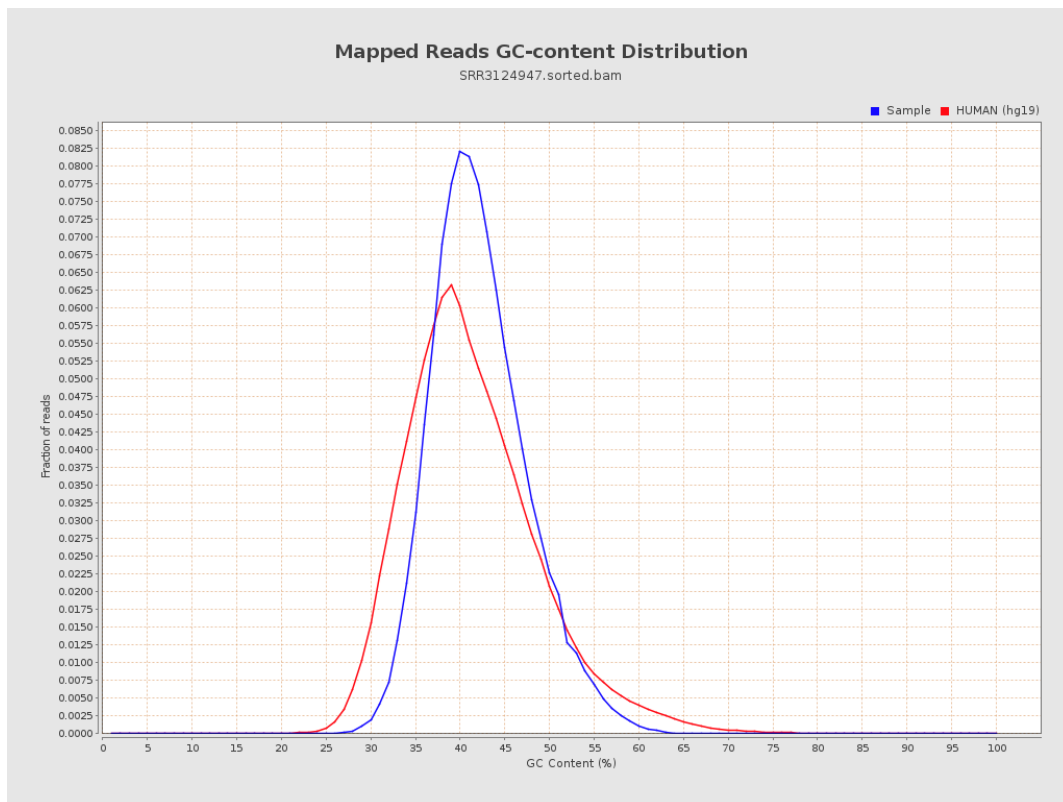
7. Results : Duplication Rate Histogram



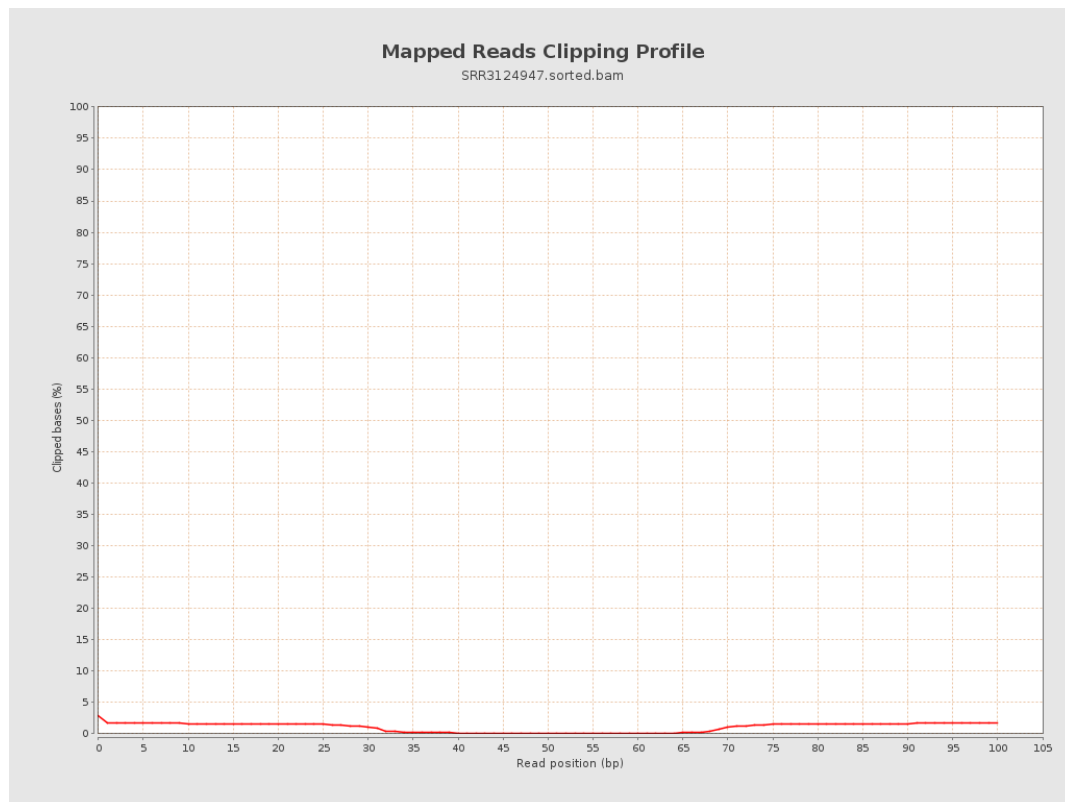
8. Results : Mapped Reads Nucleotide Content



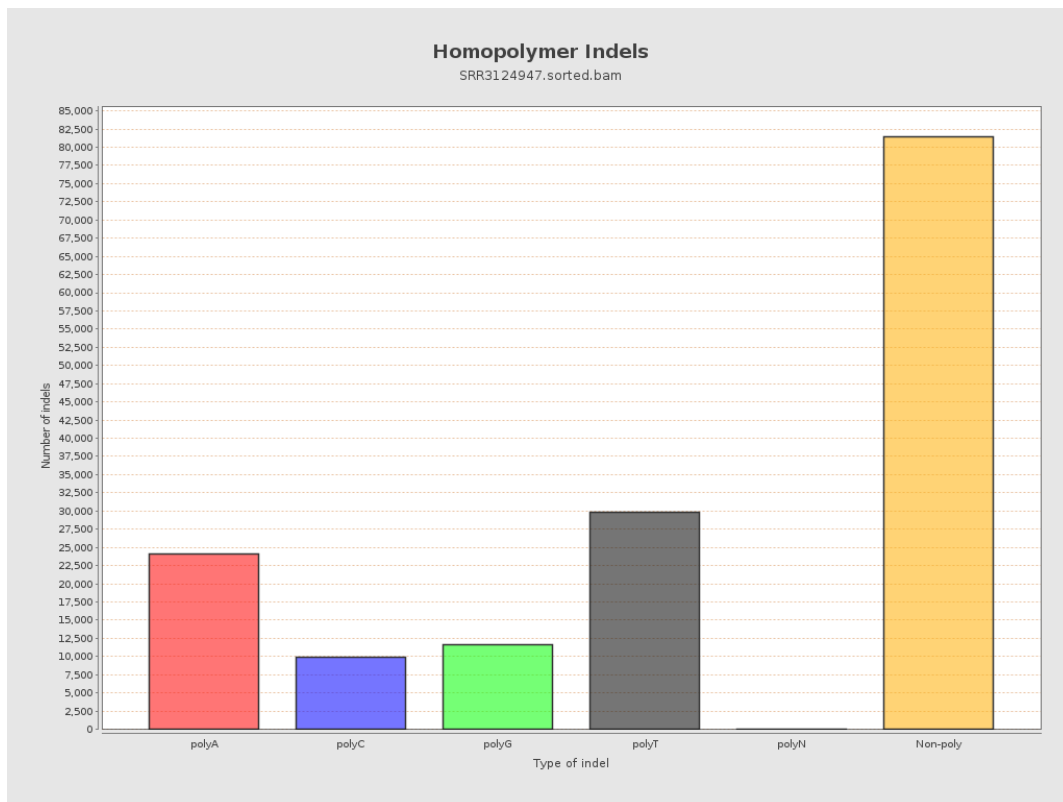
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



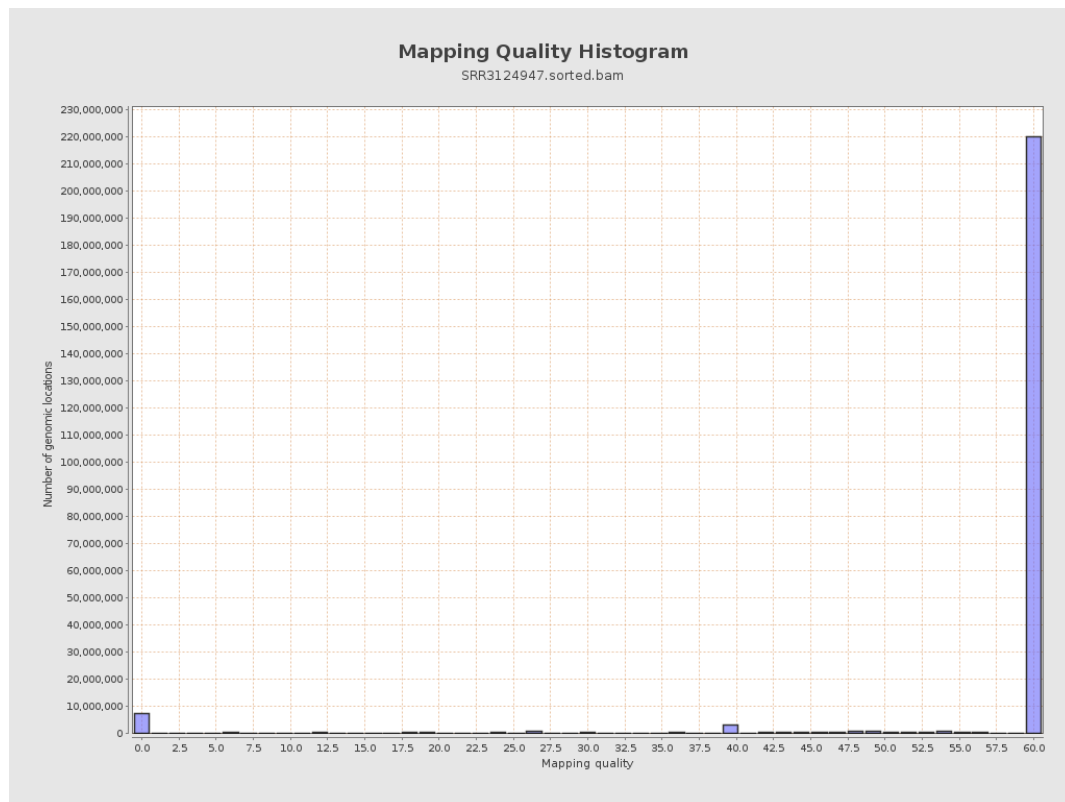
11. Results : Homopolymer Indels



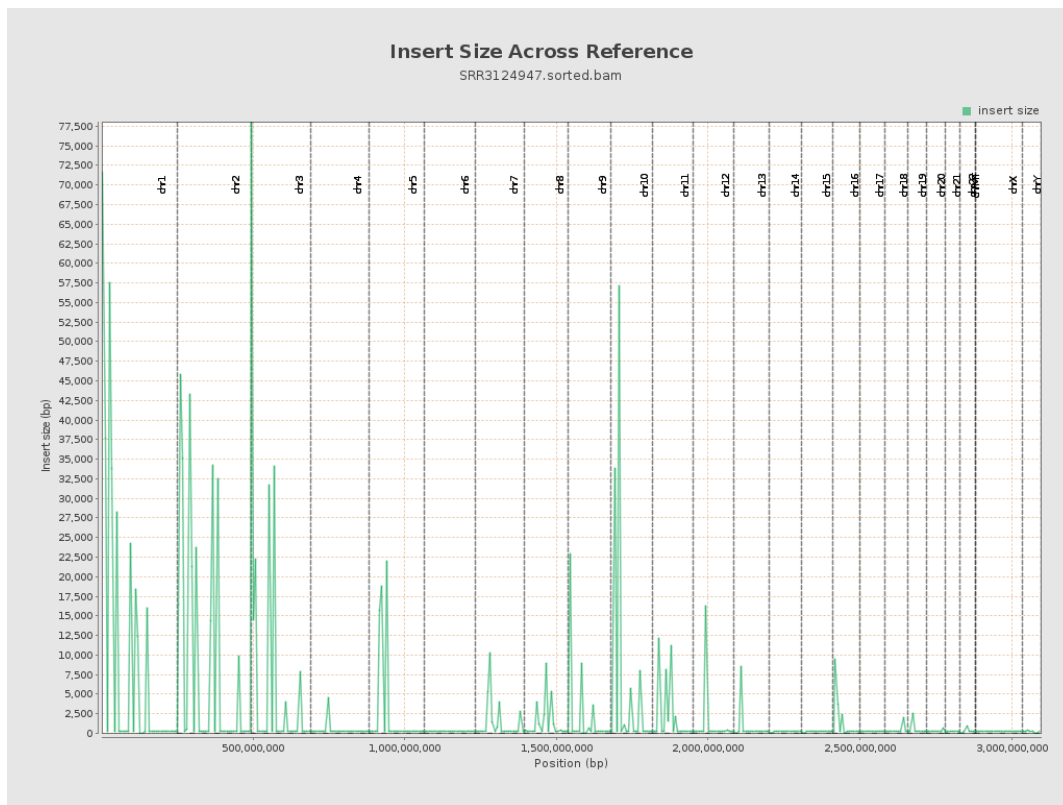
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

