

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:10:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124975.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_SRR3124975 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124975_1.fastq.gz SRR3124975_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:10:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,355,138
Mapped reads	3,293,912 / 98.18%
Unmapped reads	61,226 / 1.82%
Mapped paired reads	3,293,912 / 98.18%
Mapped reads, first in pair	1,660,466 / 49.49%
Mapped reads, second in pair	1,633,446 / 48.68%
Mapped reads, both in pair	3,264,196 / 97.29%
Mapped reads, singletons	29,716 / 0.89%
Secondary alignments	0
Supplementary alignments	75,627 / 2.25%
Read min/max/mean length	30 / 151 / 152.1
Duplicated reads (estimated)	651,493 / 19.42%
Duplication rate	16.82%
Clipped reads	2,305,568 / 68.72%

2.2. ACGT Content

Number/percentage of A's	120,731,298 / 28.98%
Number/percentage of C's	82,598,433 / 19.83%
Number/percentage of T's	122,588,228 / 29.42%
Number/percentage of G's	90,715,376 / 21.77%
Number/percentage of N's	3,202 / 0%

GC Percentage	41.6%
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2.3. Coverage

Mean	0.1347
Standard Deviation	2.0852

2.4. Mapping Quality

Mean Mapping Quality	53.25
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2.5. Insert size

Mean	86,499.61
Standard Deviation	2,757,748.89
P25/Median/P75	126 / 170 / 238

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	4,645,514
Insertions	89,647
Mapped reads with at least one insertion	2.53%
Deletions	163,779
Mapped reads with at least one deletion	4.75%
Homopolymer indels	45.47%

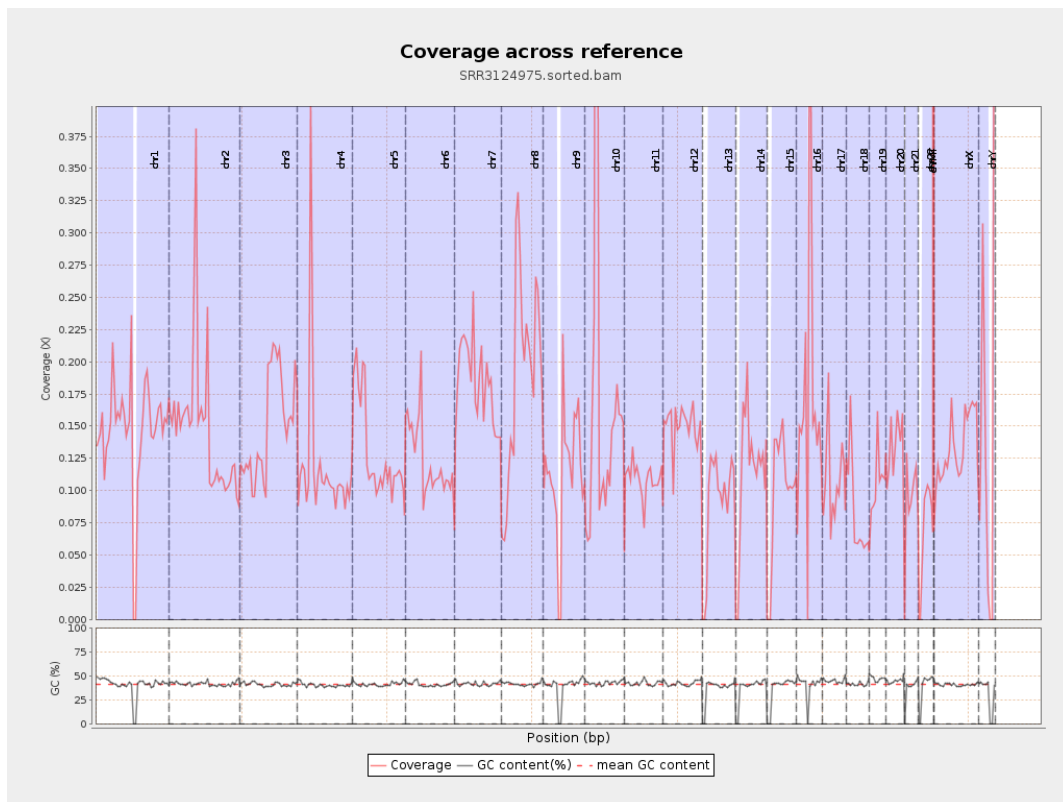
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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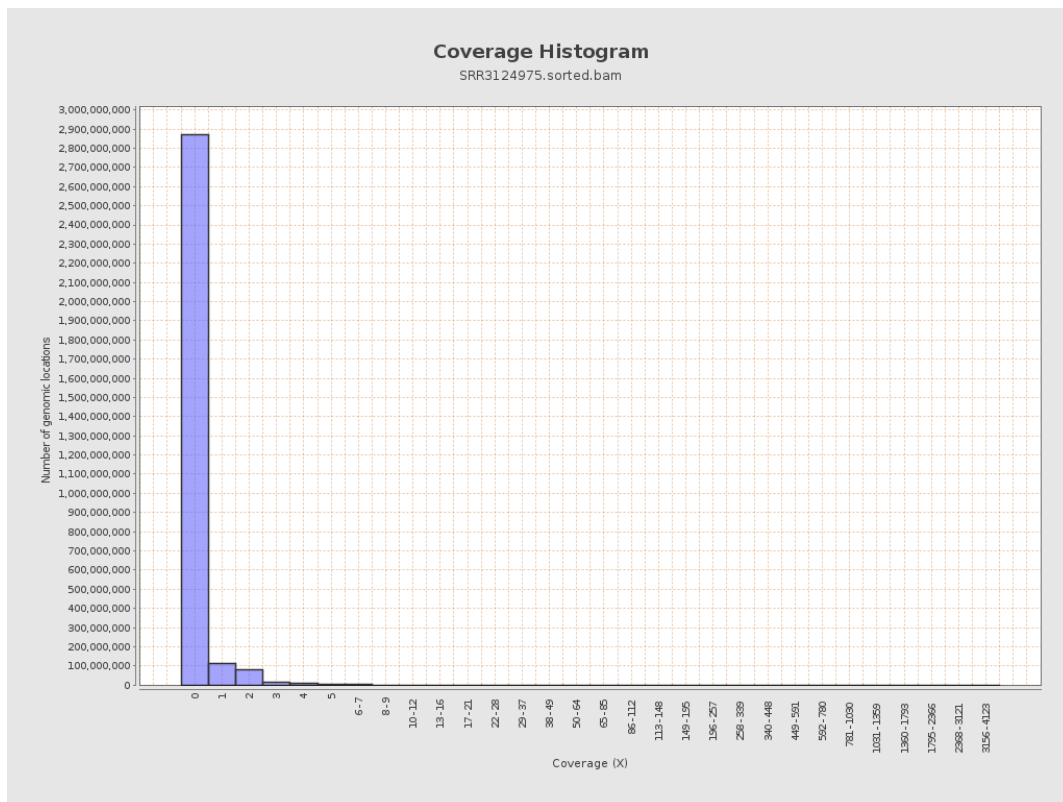
		bases	coverage	deviation
chr1	249250621	36476576	0.1463	1.8132
chr2	243199373	36158537	0.1487	2.2286
chr3	198022430	29682698	0.1499	0.6151
chr4	191154276	22234275	0.1163	2.0264
chr5	180915260	23462062	0.1297	0.5624
chr6	171115067	21154374	0.1236	0.8388
chr7	159138663	29488922	0.1853	1.7966
chr8	146364022	28119134	0.1921	0.8567
chr9	141213431	16232134	0.1149	2.0906
chr10	135534747	22992786	0.1696	6.8311
chr11	135006516	14613807	0.1082	0.7937
chr12	133851895	20056348	0.1498	0.5824
chr13	115169878	10383067	0.0902	0.4427
chr14	107349540	12228107	0.1139	0.5477
chr15	102531392	10236432	0.0998	0.4741
chr16	90354753	15542006	0.172	3.1166
chr17	81195210	8588737	0.1058	1.6566
chr18	78077248	6617341	0.0848	2.0332
chr19	59128983	6273029	0.1061	1.0784
chr20	63025520	8446770	0.134	0.8711
chr21	48129895	4486718	0.0932	1.136
chr22	51304566	3483373	0.0679	0.4433
chrMT	16571	343358	20.7204	12.4311
chrX	155270560	20676531	0.1332	0.6977

chrY	59373566	9013737	0.1518	3.9457
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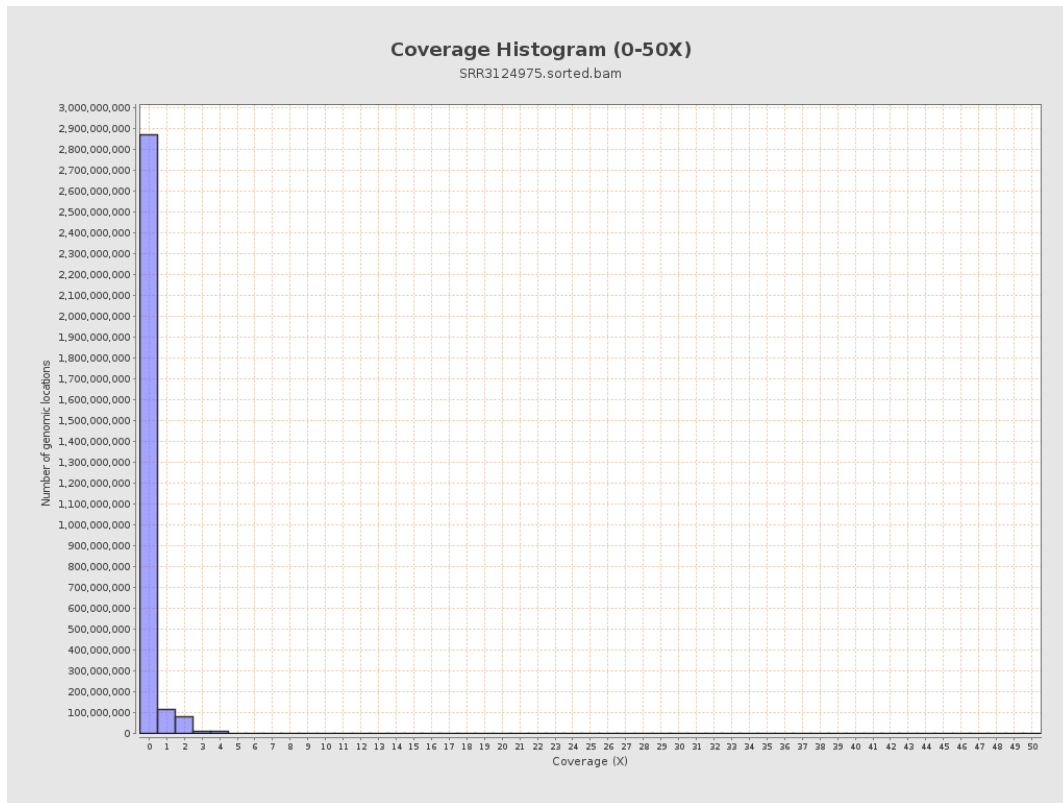
3. Results : Coverage across reference



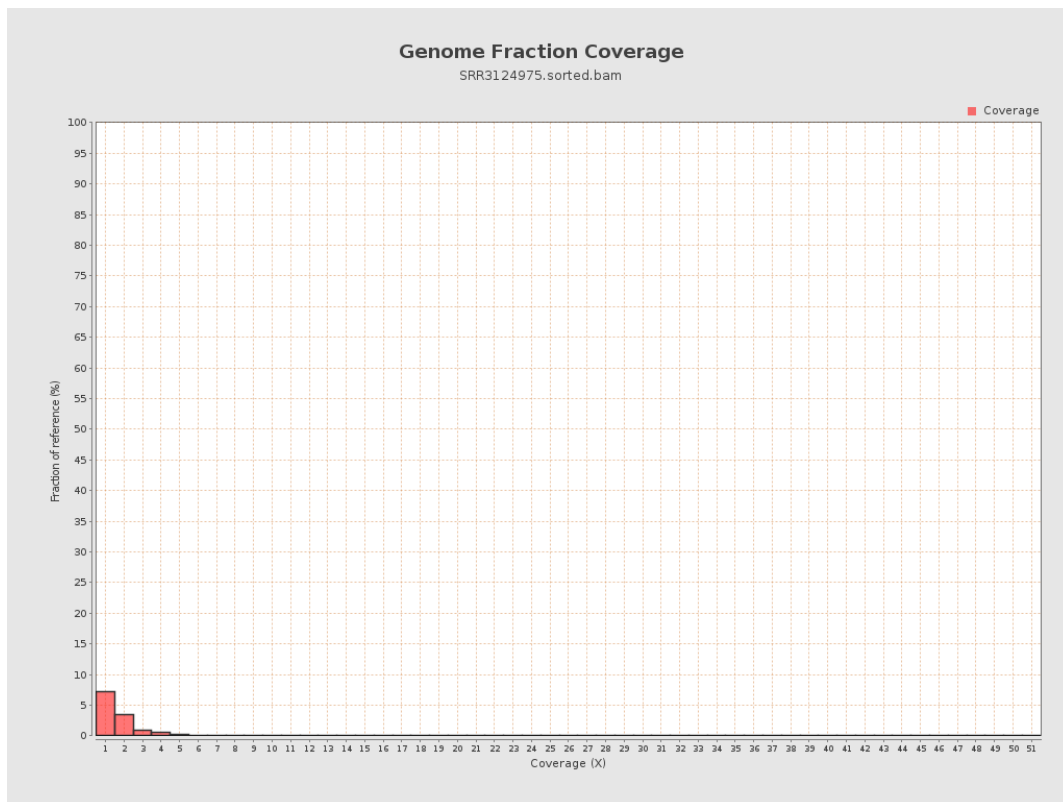
4. Results : Coverage Histogram



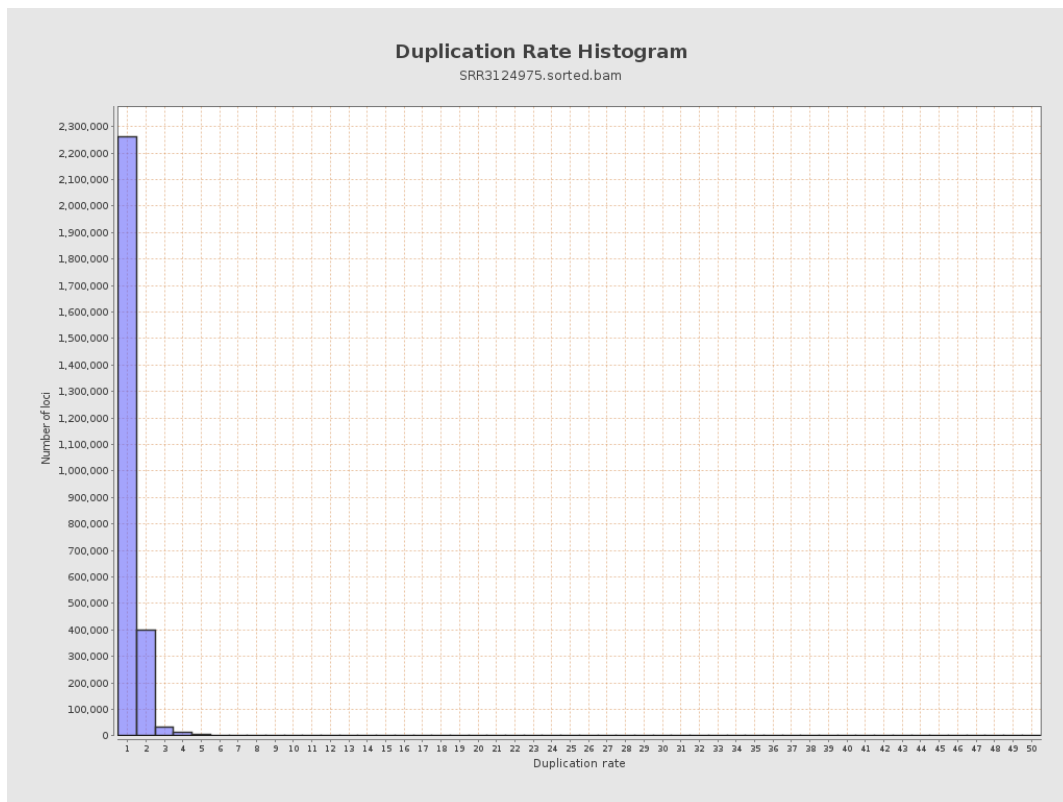
5. Results : Coverage Histogram (0-50X)



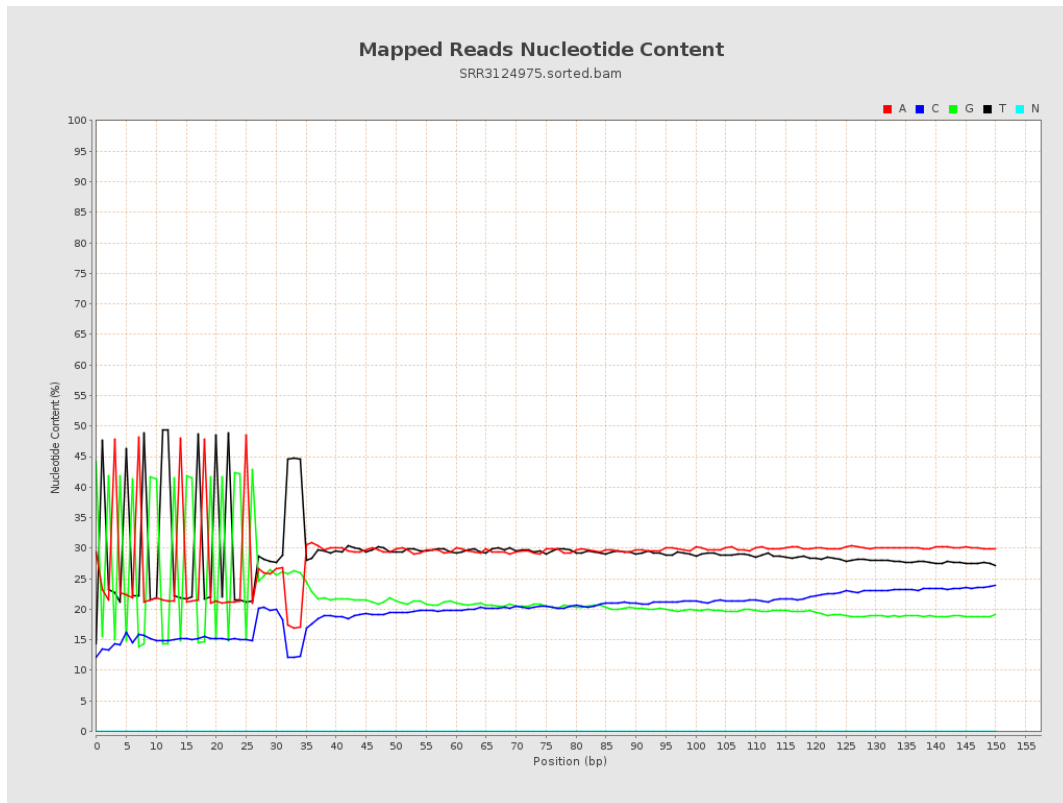
6. Results : Genome Fraction Coverage



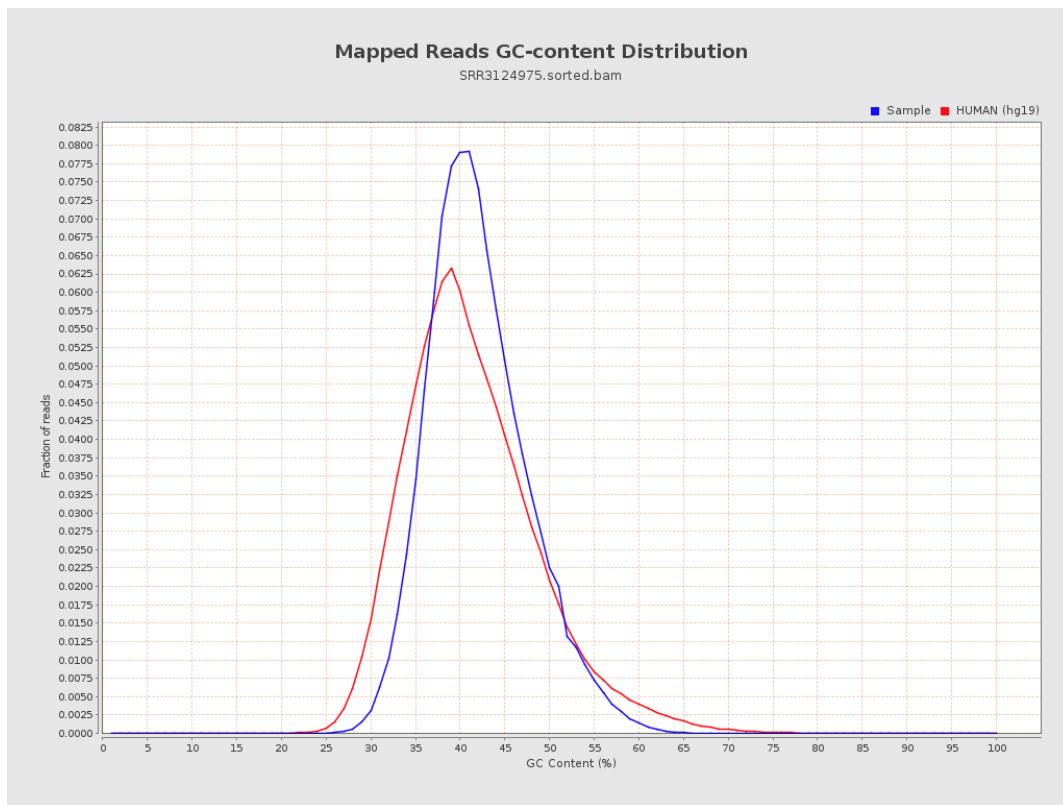
7. Results : Duplication Rate Histogram



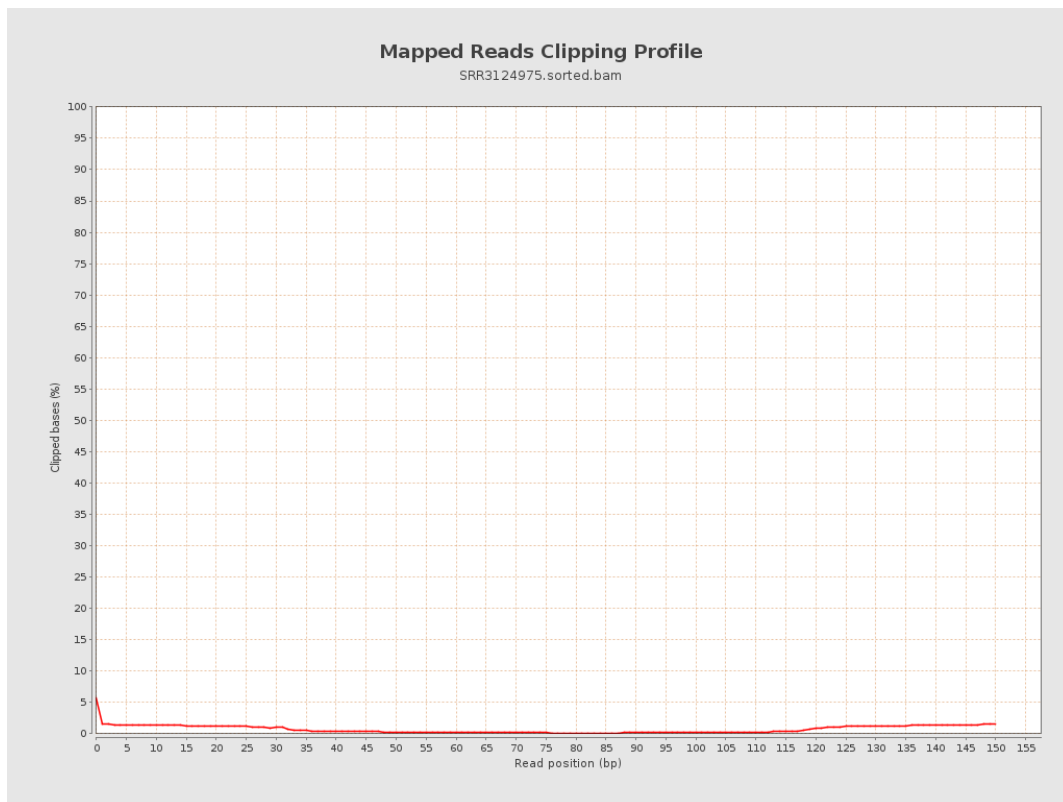
8. Results : Mapped Reads Nucleotide Content



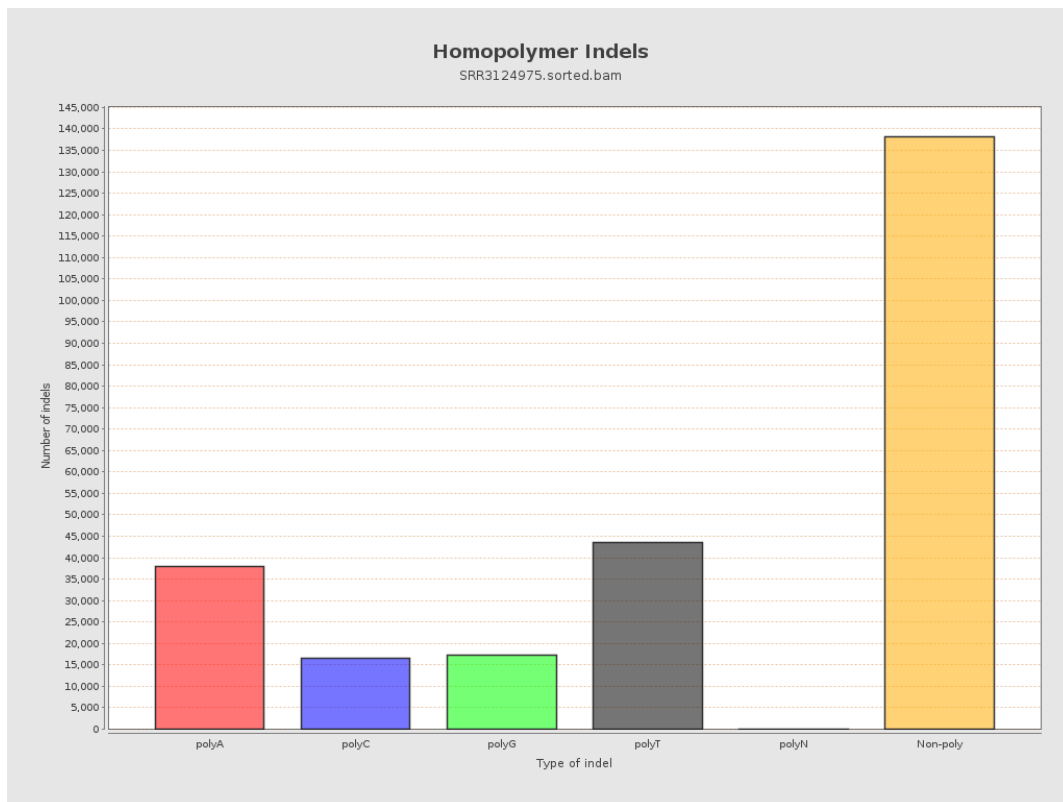
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



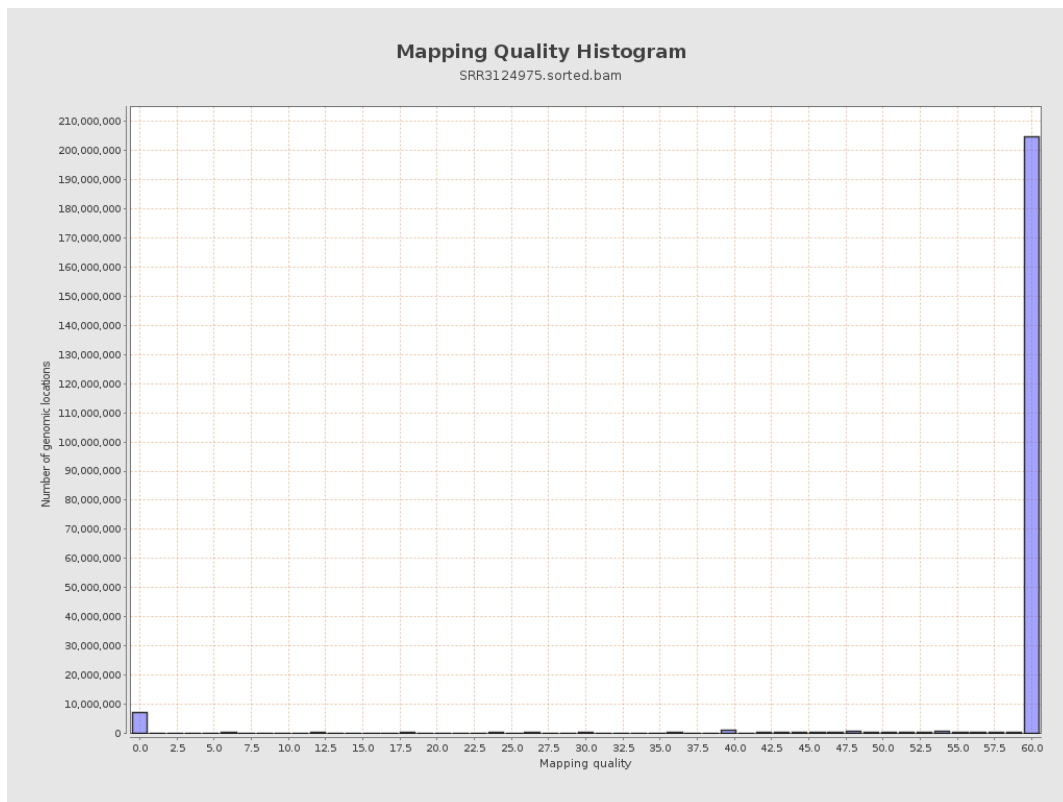
11. Results : Homopolymer Indels



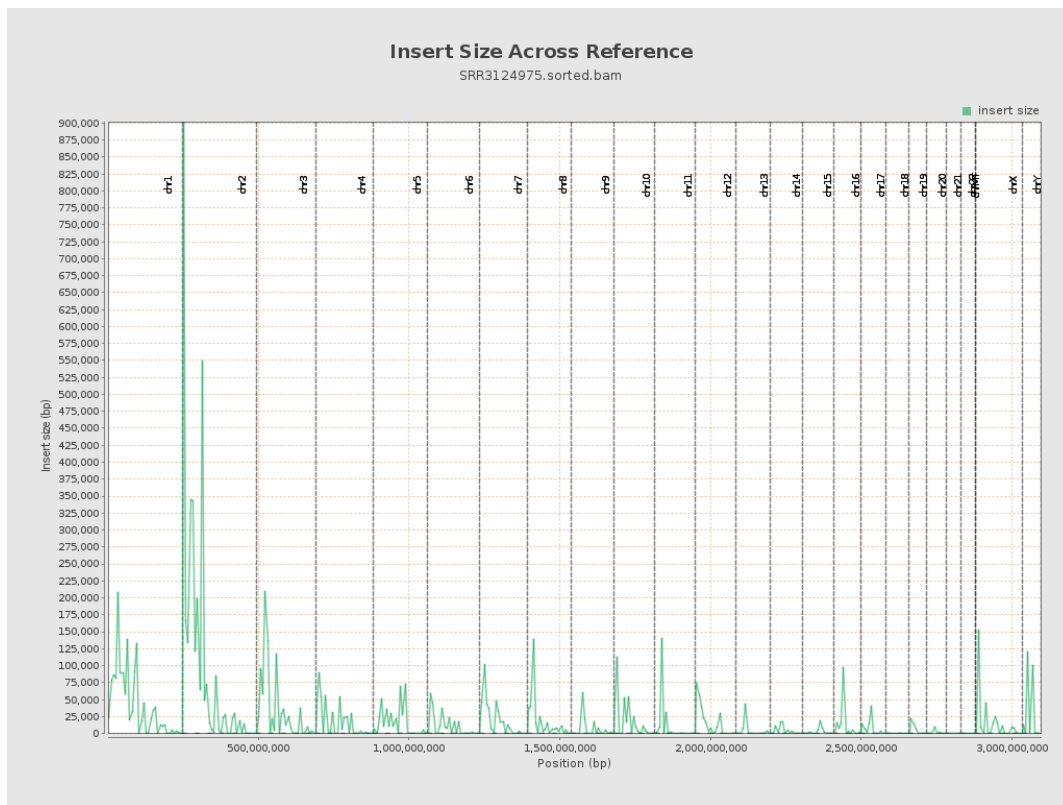
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

