

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:23:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124977.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_SRR3124977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124977_1.fastq.gz SRR3124977_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:23:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124977.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,851,354
Mapped reads	2,794,345 / 98%
Unmapped reads	57,009 / 2%
Mapped paired reads	2,794,345 / 98%
Mapped reads, first in pair	1,412,245 / 49.53%
Mapped reads, second in pair	1,382,100 / 48.47%
Mapped reads, both in pair	2,761,624 / 96.85%
Mapped reads, singletons	32,721 / 1.15%
Secondary alignments	0
Supplementary alignments	58,175 / 2.04%
Read min/max/mean length	30 / 151 / 151.98
Duplicated reads (estimated)	497,964 / 17.46%
Duplication rate	15.06%
Clipped reads	1,918,807 / 67.29%

2.2. ACGT Content

Number/percentage of A's	101,988,074 / 28.67%
Number/percentage of C's	70,933,001 / 19.94%
Number/percentage of T's	104,156,067 / 29.28%
Number/percentage of G's	78,607,491 / 22.1%
Number/percentage of N's	2,621 / 0%

GC Percentage	42.04%
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2.3. Coverage

Mean	0.115
Standard Deviation	1.5452

2.4. Mapping Quality

Mean Mapping Quality	53.21
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2.5. Insert size

Mean	74,786.53
Standard Deviation	2,535,659.99
P25/Median/P75	131 / 178 / 248

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	3,998,925
Insertions	79,278
Mapped reads with at least one insertion	2.63%
Deletions	139,781
Mapped reads with at least one deletion	4.77%
Homopolymer indels	45.49%

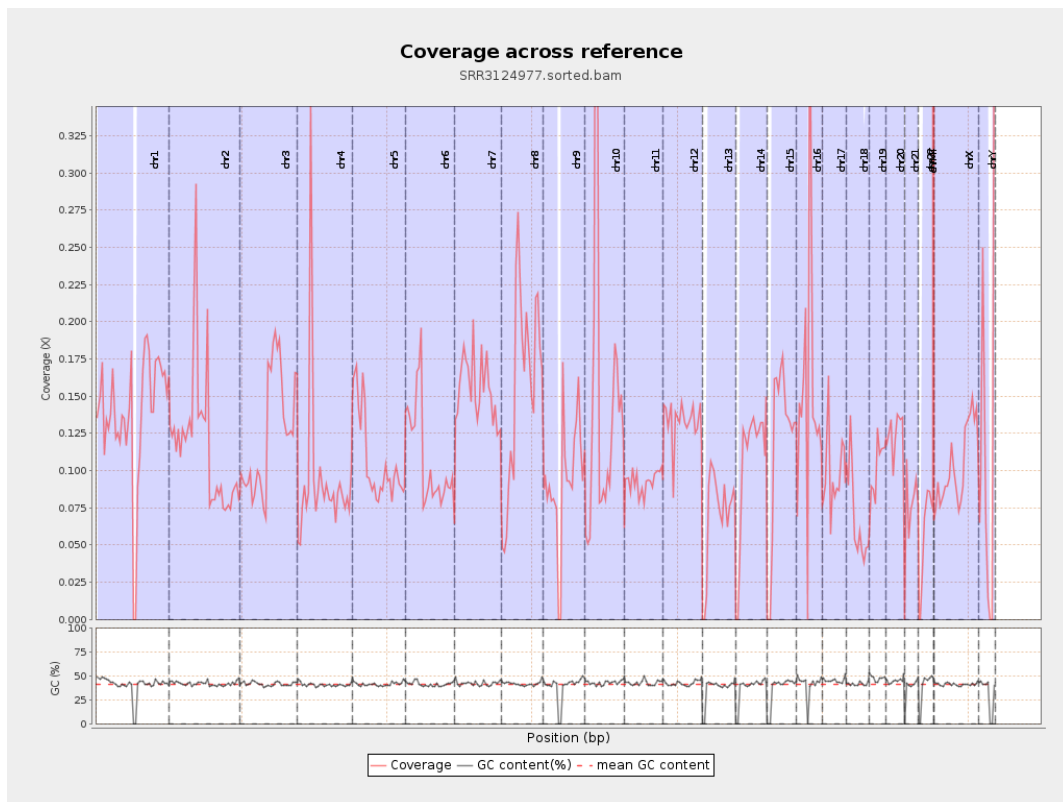
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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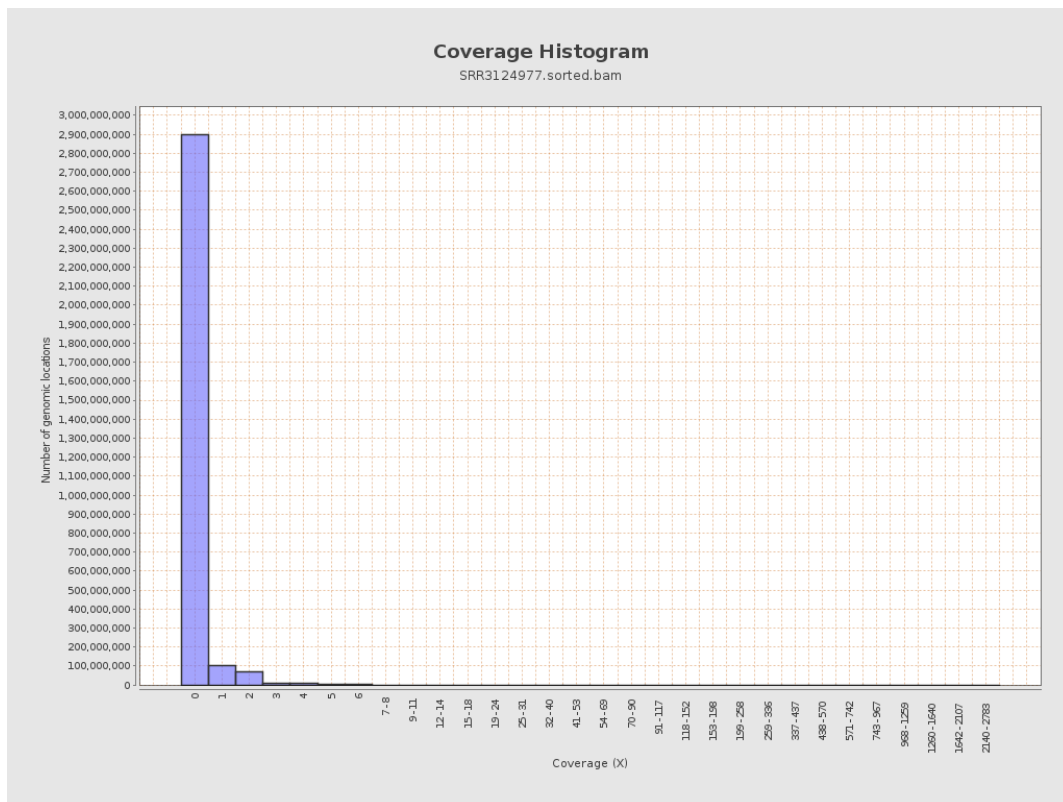
		bases	coverage	deviation
chr1	249250621	34523662	0.1385	1.1562
chr2	243199373	28745780	0.1182	1.8521
chr3	198022430	24572257	0.1241	0.5398
chr4	191154276	17601521	0.0921	1.8507
chr5	180915260	19305171	0.1067	0.5015
chr6	171115067	18654727	0.109	0.6787
chr7	159138663	24736862	0.1554	1.2937
chr8	146364022	23039751	0.1574	0.7166
chr9	141213431	13274012	0.094	1.5978
chr10	135534747	19294945	0.1424	4.5404
chr11	135006516	12438073	0.0921	0.6126
chr12	133851895	17800083	0.133	0.5483
chr13	115169878	8006125	0.0695	0.3813
chr14	107349540	11224199	0.1046	0.4987
chr15	102531392	12303293	0.12	0.5241
chr16	90354753	13711936	0.1518	2.432
chr17	81195210	7920717	0.0976	1.3003
chr18	78077248	5386197	0.069	1.4722
chr19	59128983	6026204	0.1019	0.7803
chr20	63025520	7791951	0.1236	0.8156
chr21	48129895	3579423	0.0744	1.1221
chr22	51304566	2860514	0.0558	0.3901
chrMT	16571	324811	19.6012	12.2754
chrX	155270560	15957689	0.1028	0.5493

chrY	59373566	6915653	0.1165	3.3923
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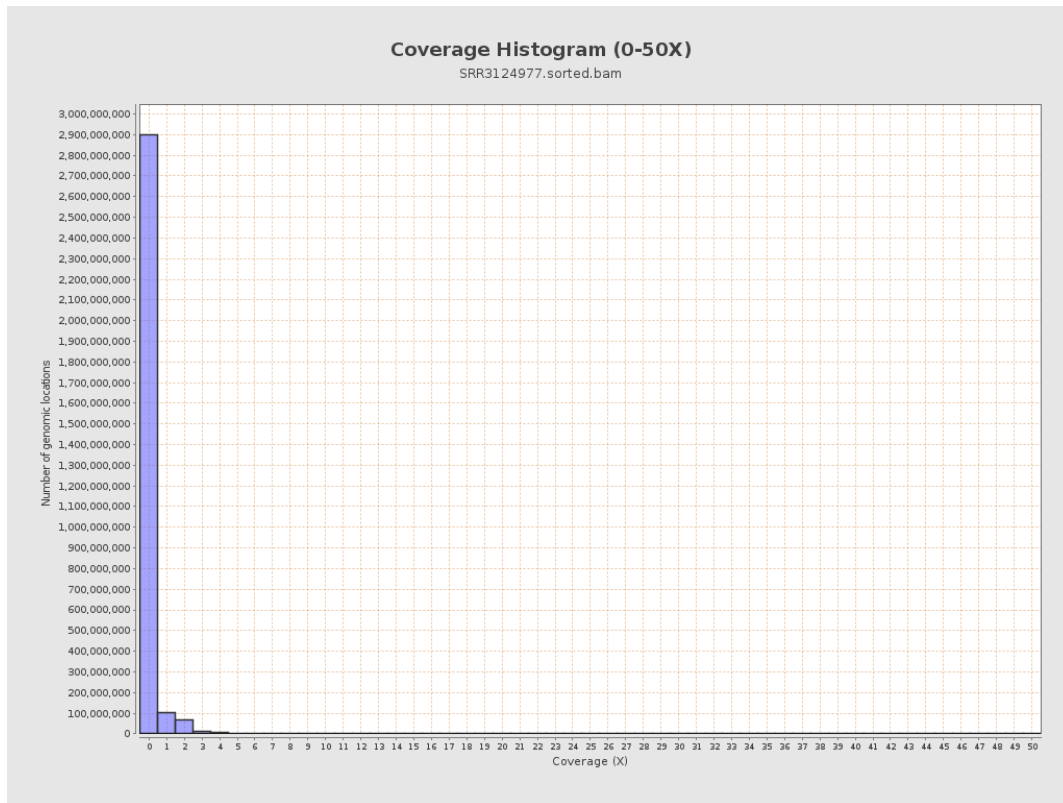
3. Results : Coverage across reference



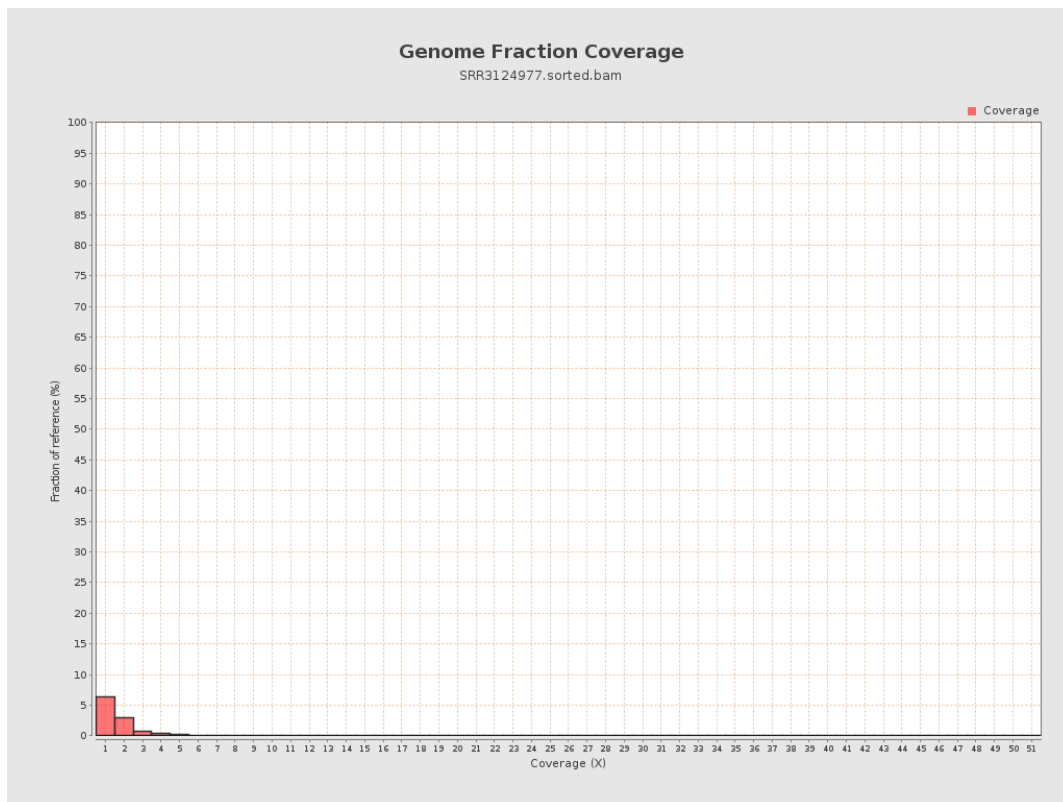
4. Results : Coverage Histogram



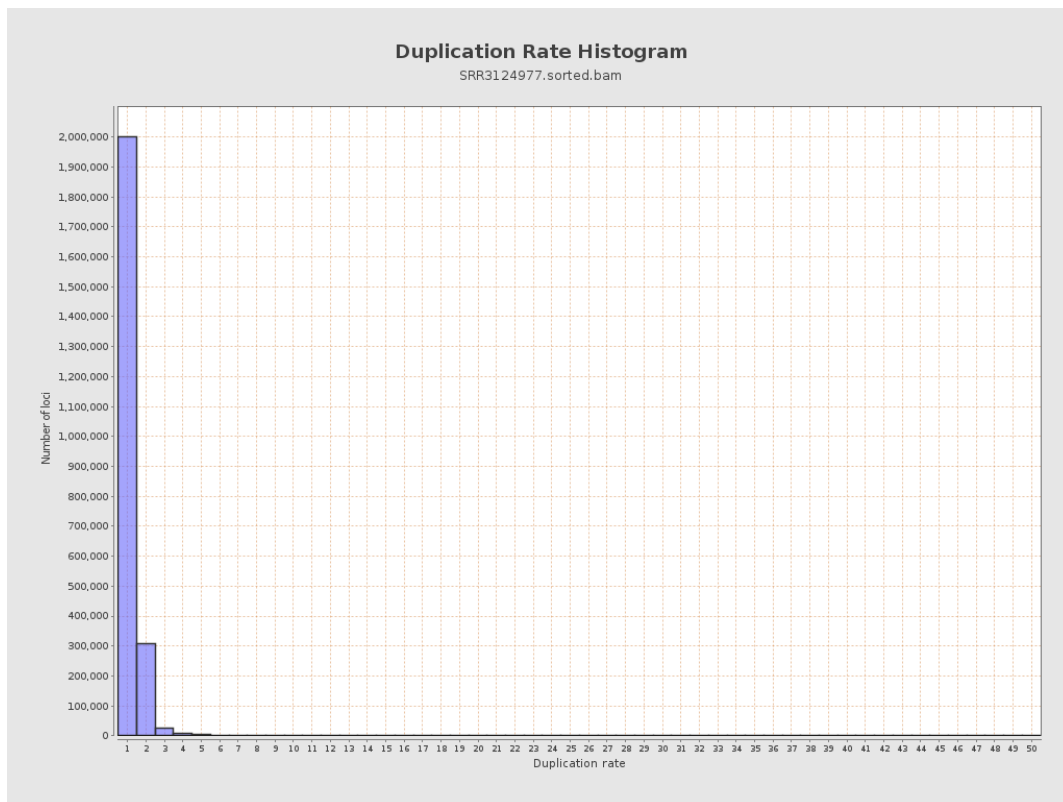
5. Results : Coverage Histogram (0-50X)



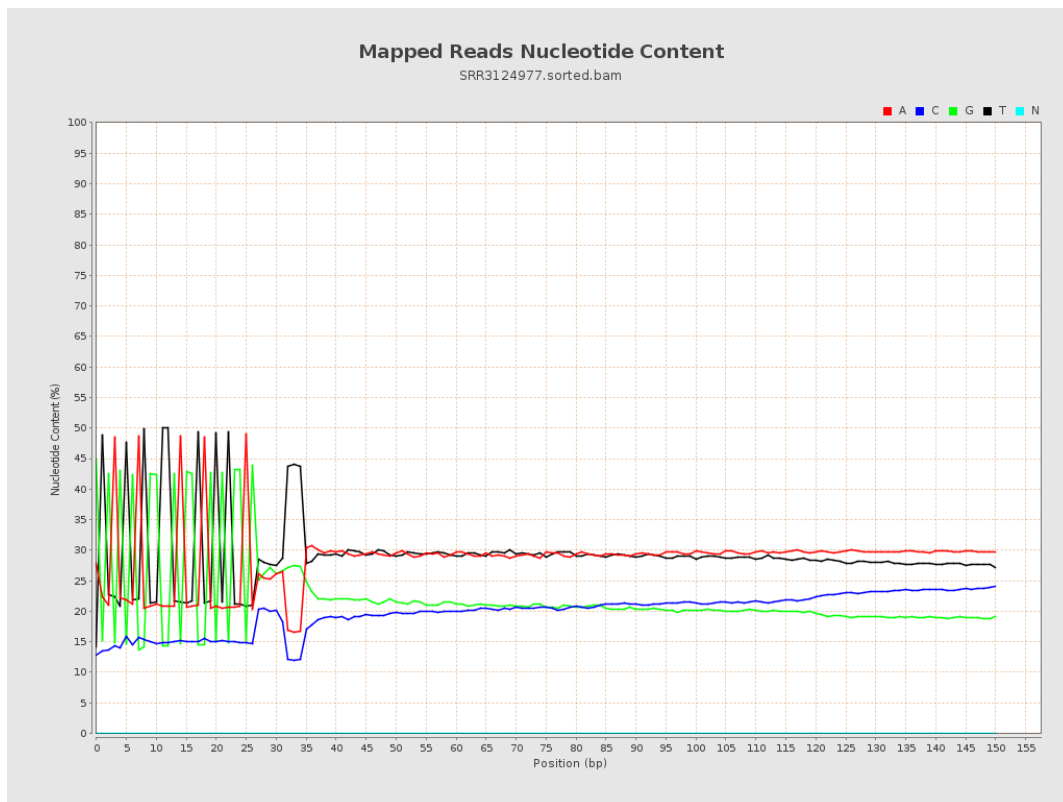
6. Results : Genome Fraction Coverage



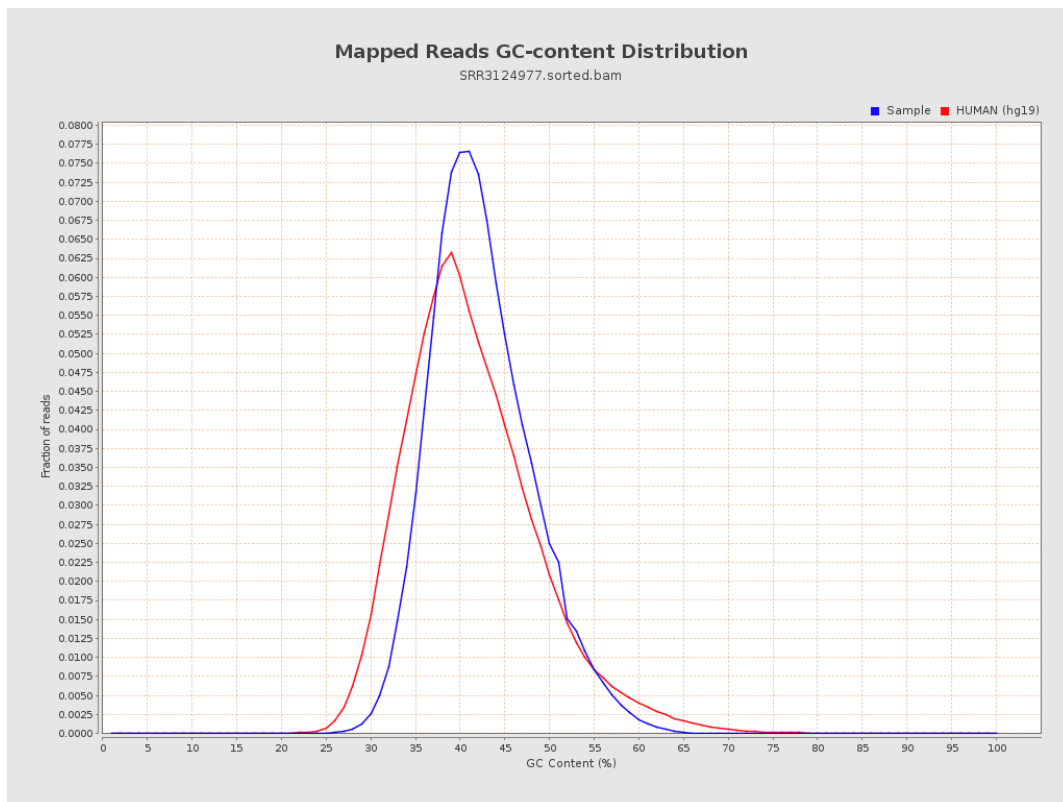
7. Results : Duplication Rate Histogram



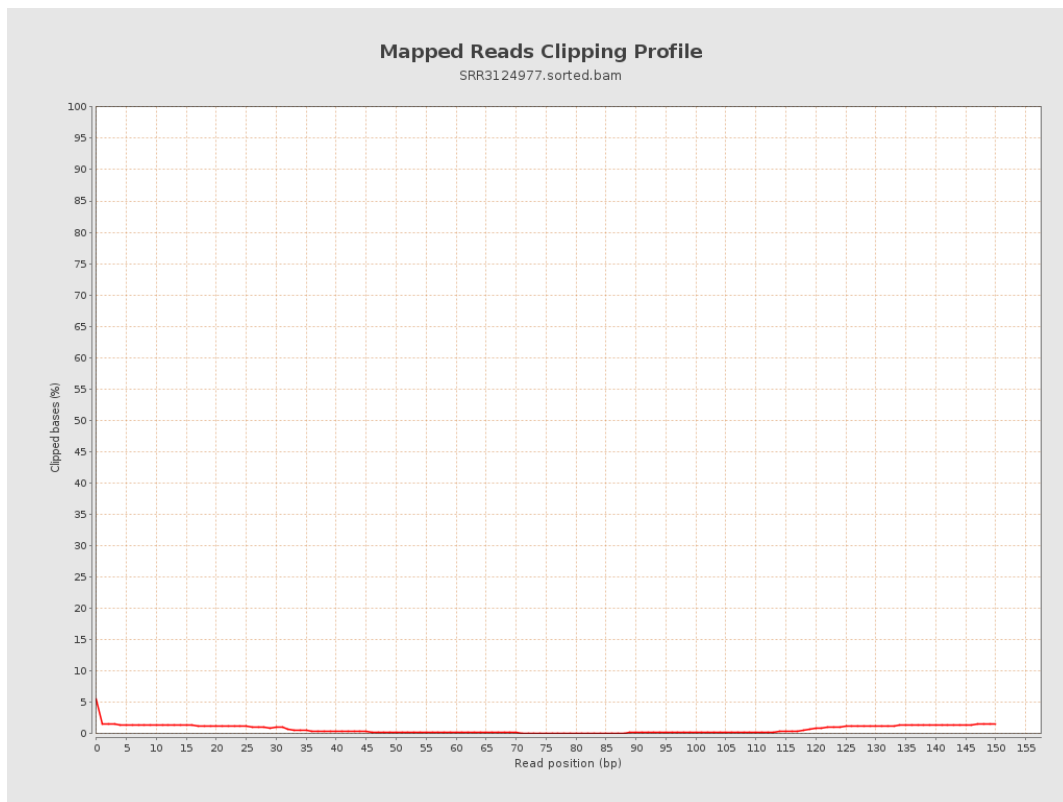
8. Results : Mapped Reads Nucleotide Content



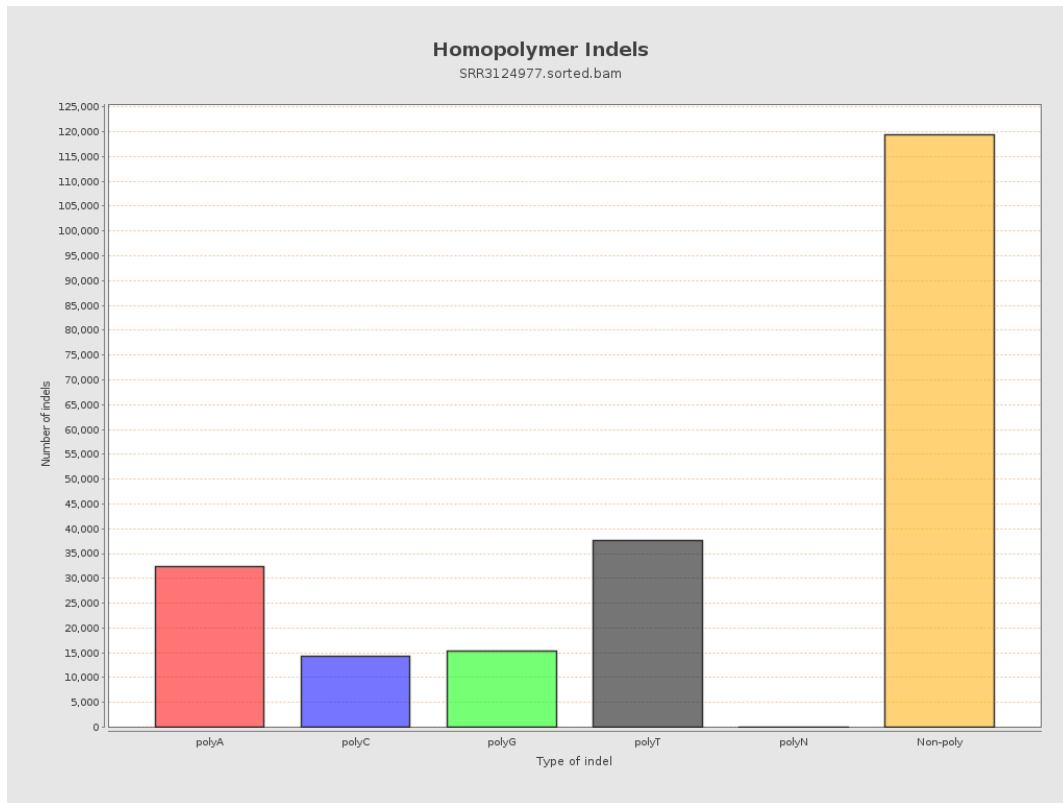
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



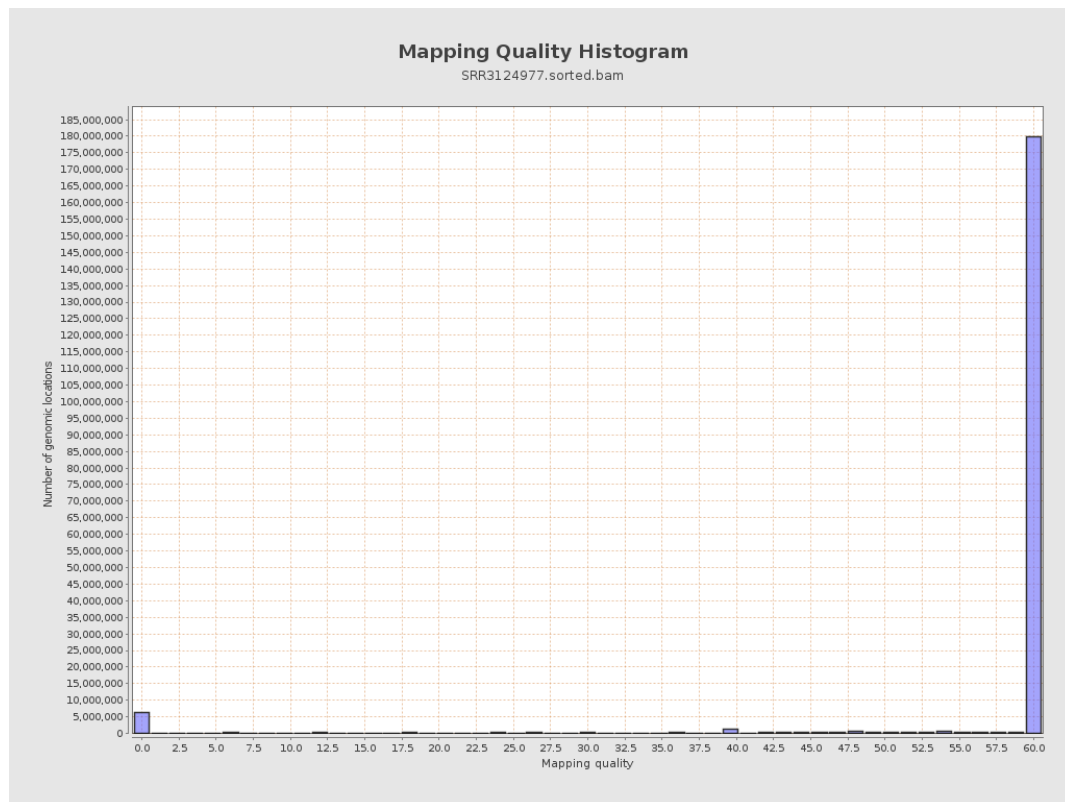
11. Results : Homopolymer Indels



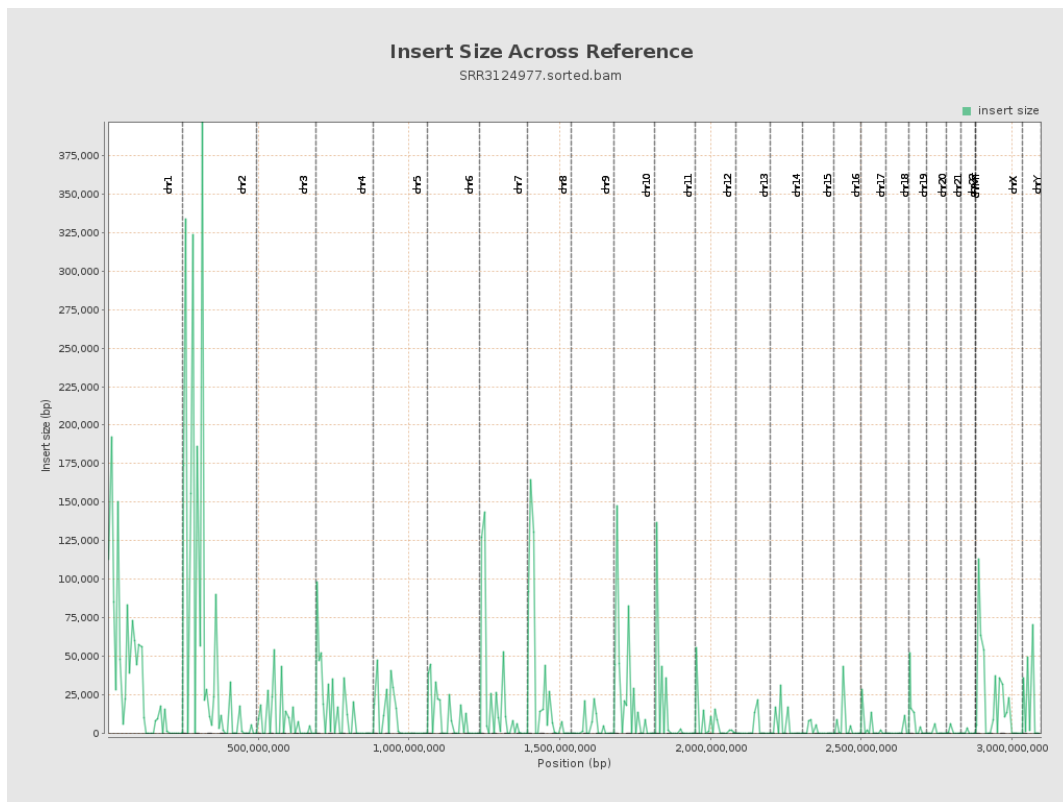
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

