

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 07:44:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124937.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_SRR3124937 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124937_1.fastq.gz SRR3124937_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 07:44:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124937.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,907,760
Mapped reads	4,840,359 / 98.63%
Unmapped reads	67,401 / 1.37%
Mapped paired reads	4,840,359 / 98.63%
Mapped reads, first in pair	2,421,834 / 49.35%
Mapped reads, second in pair	2,418,525 / 49.28%
Mapped reads, both in pair	4,824,348 / 98.3%
Mapped reads, singletons	16,011 / 0.33%
Secondary alignments	0
Supplementary alignments	22,306 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	237,321 / 4.84%
Duplication rate	2.86%
Clipped reads	2,844,921 / 57.97%

2.2. ACGT Content

Number/percentage of A's	131,247,528 / 29.47%
Number/percentage of C's	87,677,905 / 19.69%
Number/percentage of T's	131,077,374 / 29.43%
Number/percentage of G's	95,086,516 / 21.35%
Number/percentage of N's	291,948 / 0.07%

GC Percentage	41.04%
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2.3. Coverage

Mean	0.144
Standard Deviation	1.3523

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	72,067.06
Standard Deviation	2,588,530.65
P25/Median/P75	138 / 170 / 215

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,884,940
Insertions	71,937
Mapped reads with at least one insertion	1.45%
Deletions	148,962
Mapped reads with at least one deletion	3.02%
Homopolymer indels	46.69%

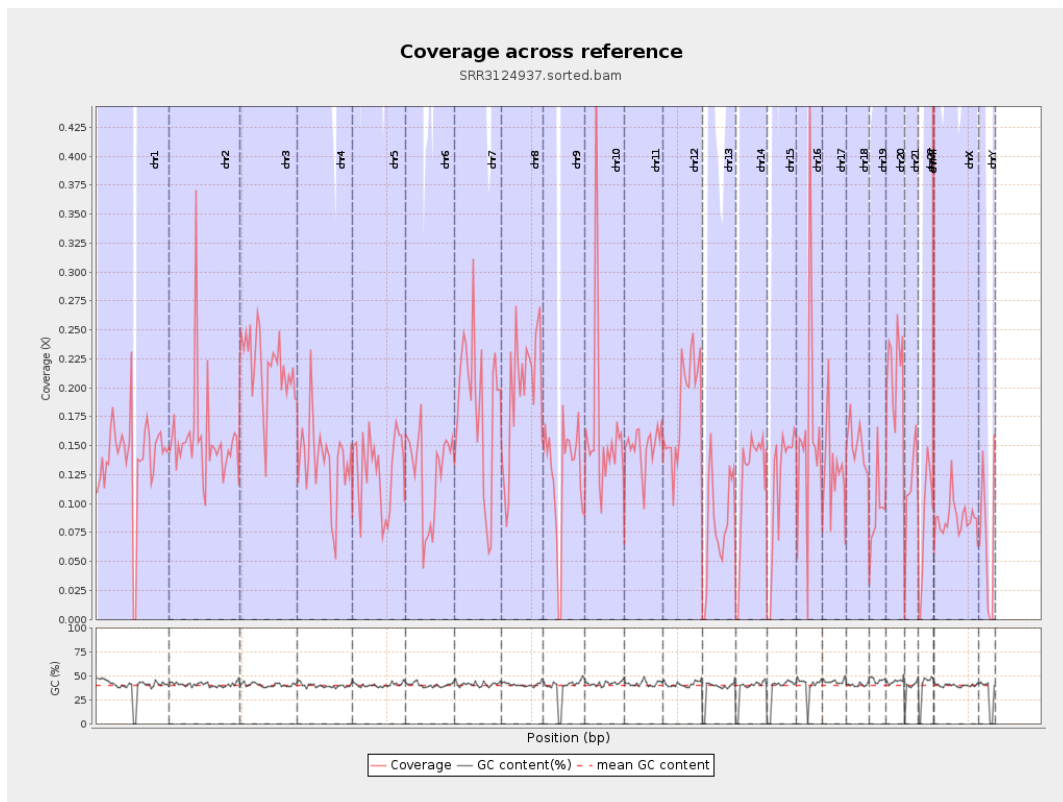
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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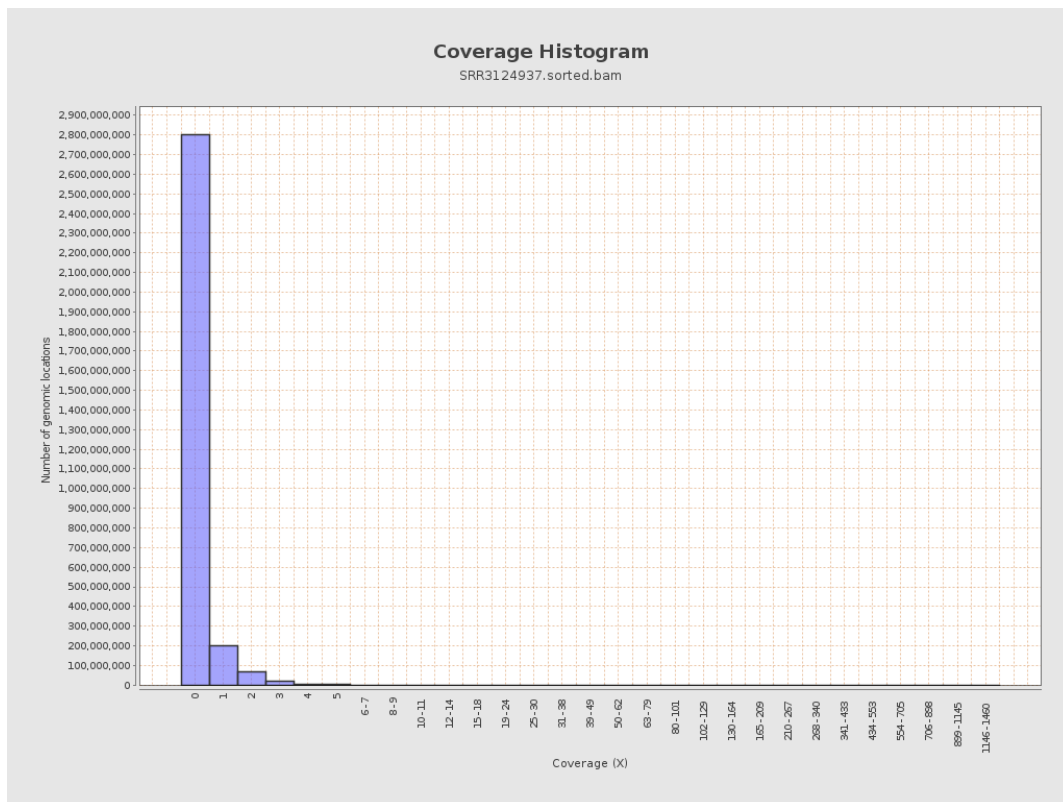
		bases	coverage	deviation
chr1	249250621	34655411	0.139	1.3751
chr2	243199373	37726814	0.1551	1.5828
chr3	198022430	43134238	0.2178	0.648
chr4	191154276	25786728	0.1349	0.8093
chr5	180915260	23366138	0.1292	0.4822
chr6	171115067	21877487	0.1279	0.9318
chr7	159138663	29485619	0.1853	2.6741
chr8	146364022	28678734	0.1959	0.8074
chr9	141213431	17628238	0.1248	1.6902
chr10	135534747	22036909	0.1626	2.9263
chr11	135006516	19917780	0.1475	1.0674
chr12	133851895	24447968	0.1826	0.5768
chr13	115169878	9309198	0.0808	0.3708
chr14	107349540	12762165	0.1189	0.4877
chr15	102531392	11741962	0.1145	0.4539
chr16	90354753	14217132	0.1573	2.2258
chr17	81195210	10397252	0.1281	1.5222
chr18	78077248	11794832	0.1511	1.7776
chr19	59128983	5589365	0.0945	0.8632
chr20	63025520	13455956	0.2135	0.6513
chr21	48129895	5443880	0.1131	0.5787
chr22	51304566	4340796	0.0846	0.3982
chrMT	16571	273854	16.5261	8.9523
chrX	155270560	13568667	0.0874	0.5951

chrY	59373566	3988990	0.0672	1.1634
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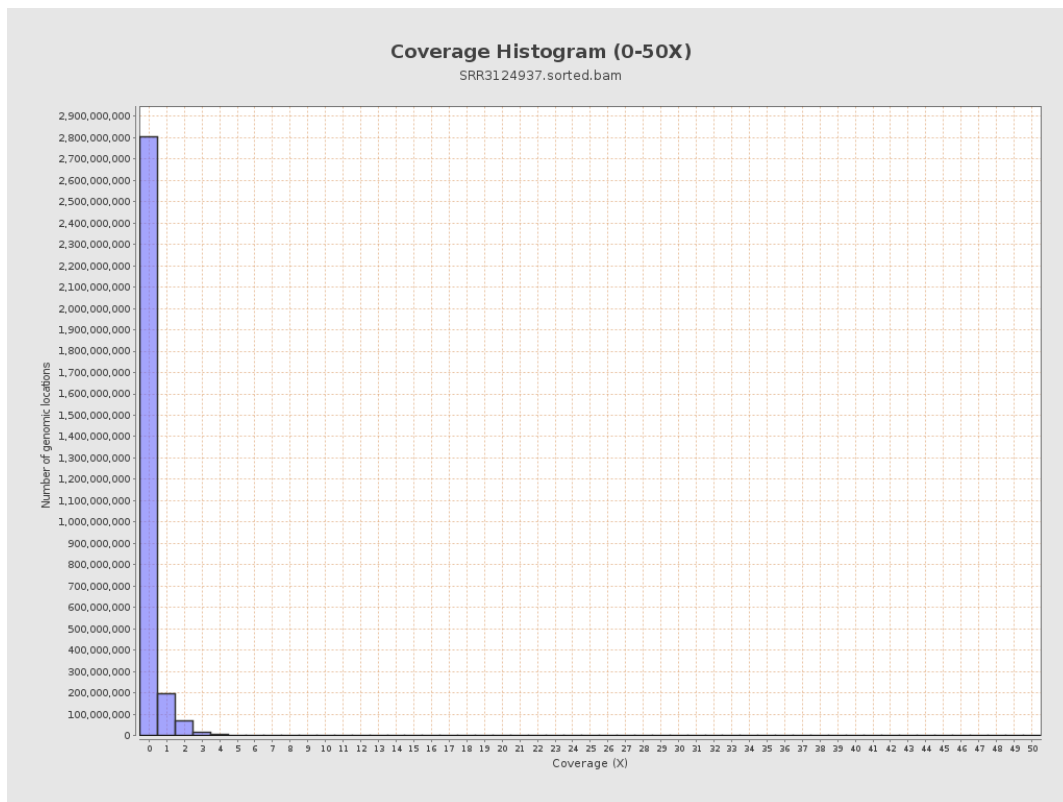
3. Results : Coverage across reference



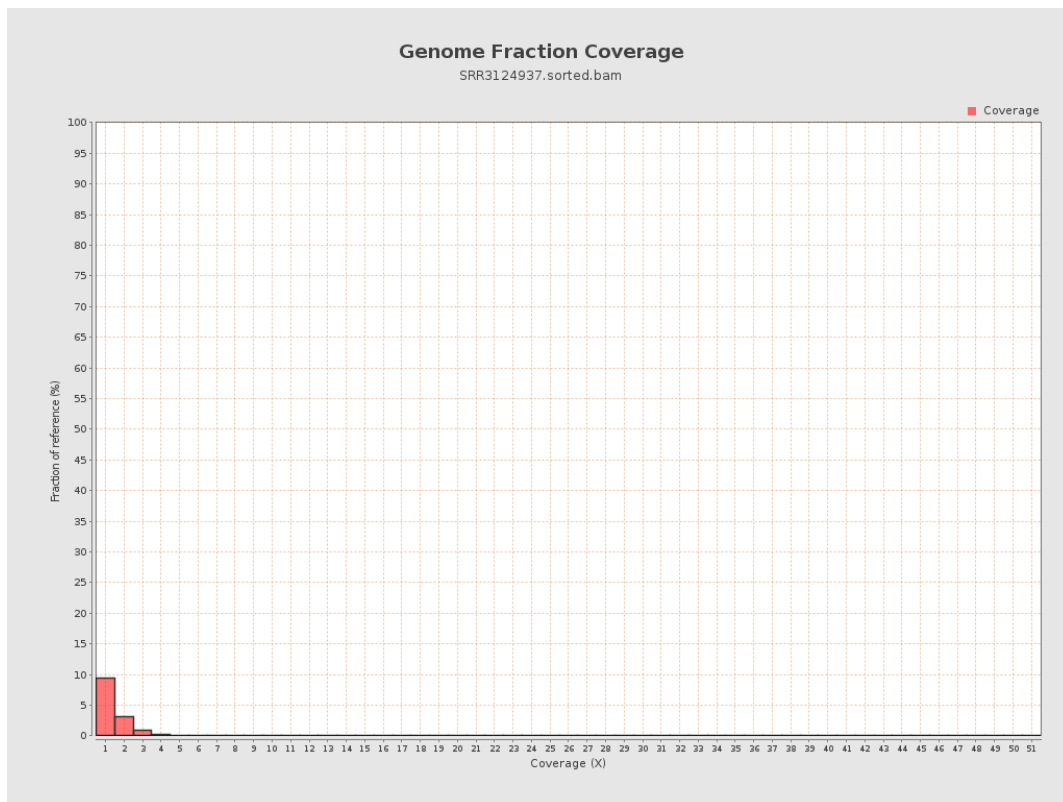
4. Results : Coverage Histogram



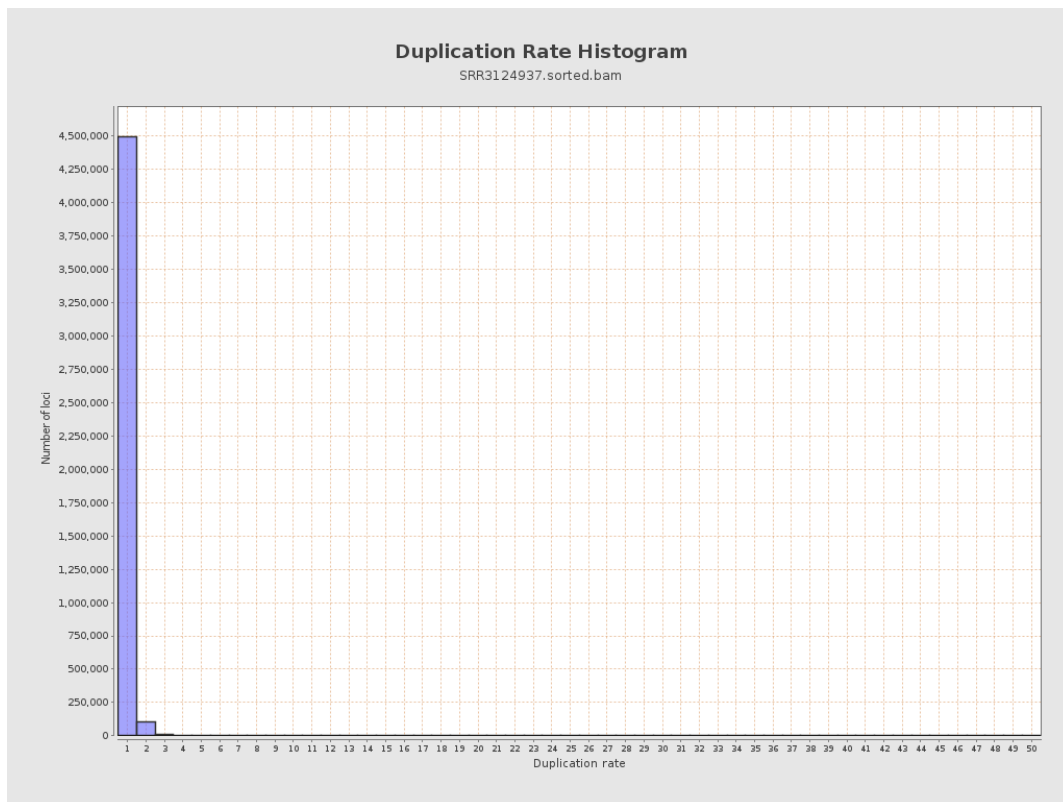
5. Results : Coverage Histogram (0-50X)



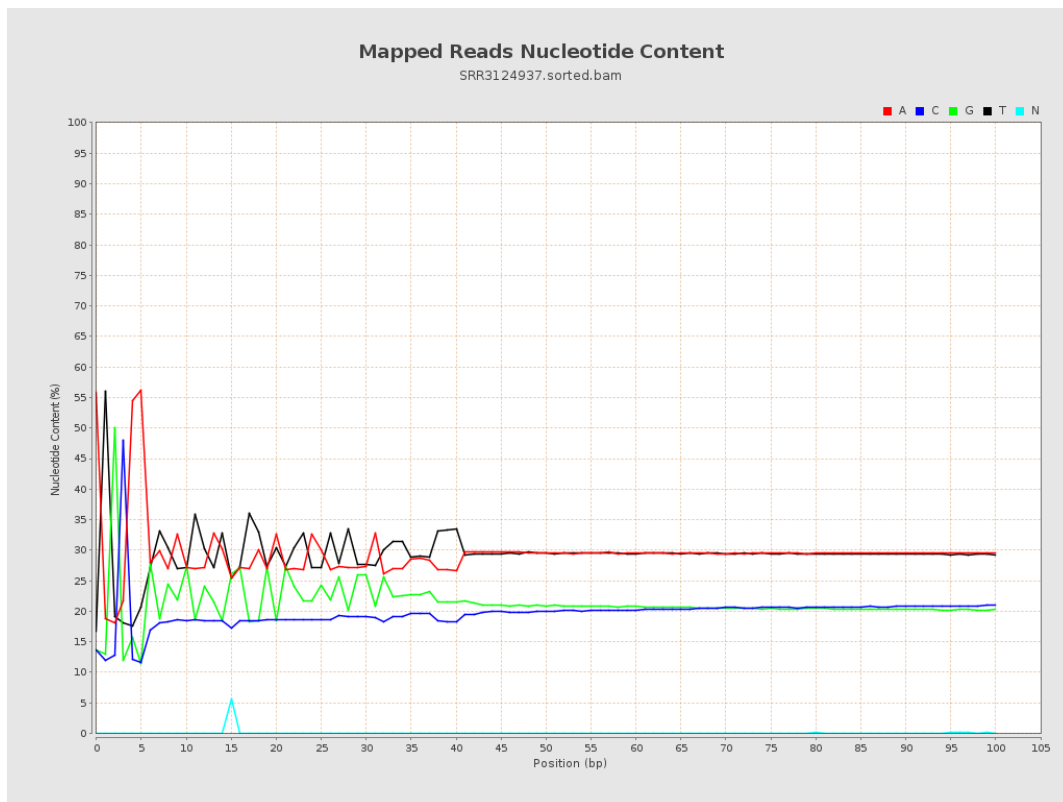
6. Results : Genome Fraction Coverage



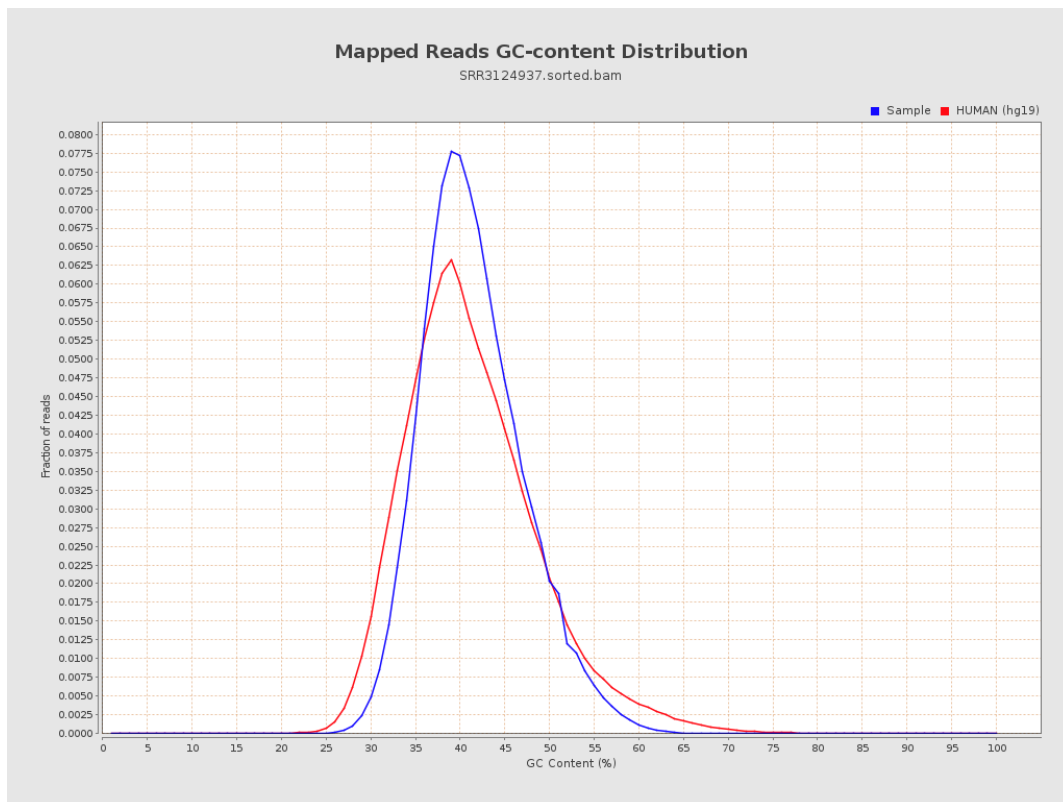
7. Results : Duplication Rate Histogram



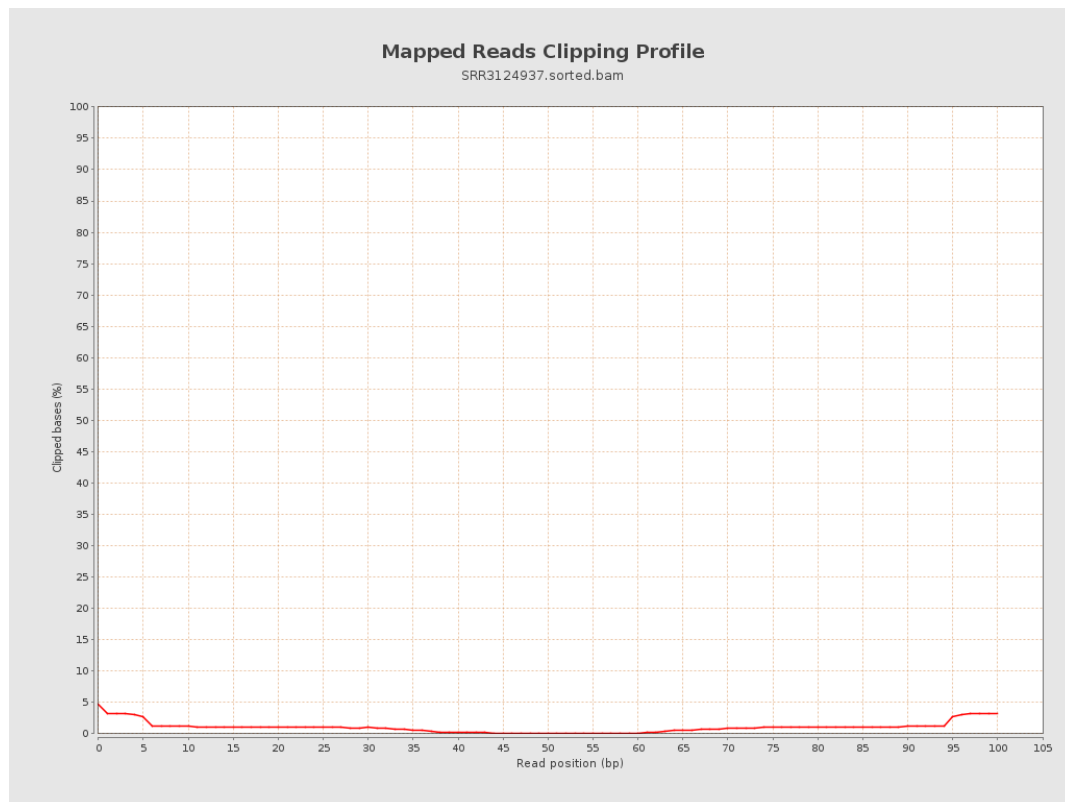
8. Results : Mapped Reads Nucleotide Content



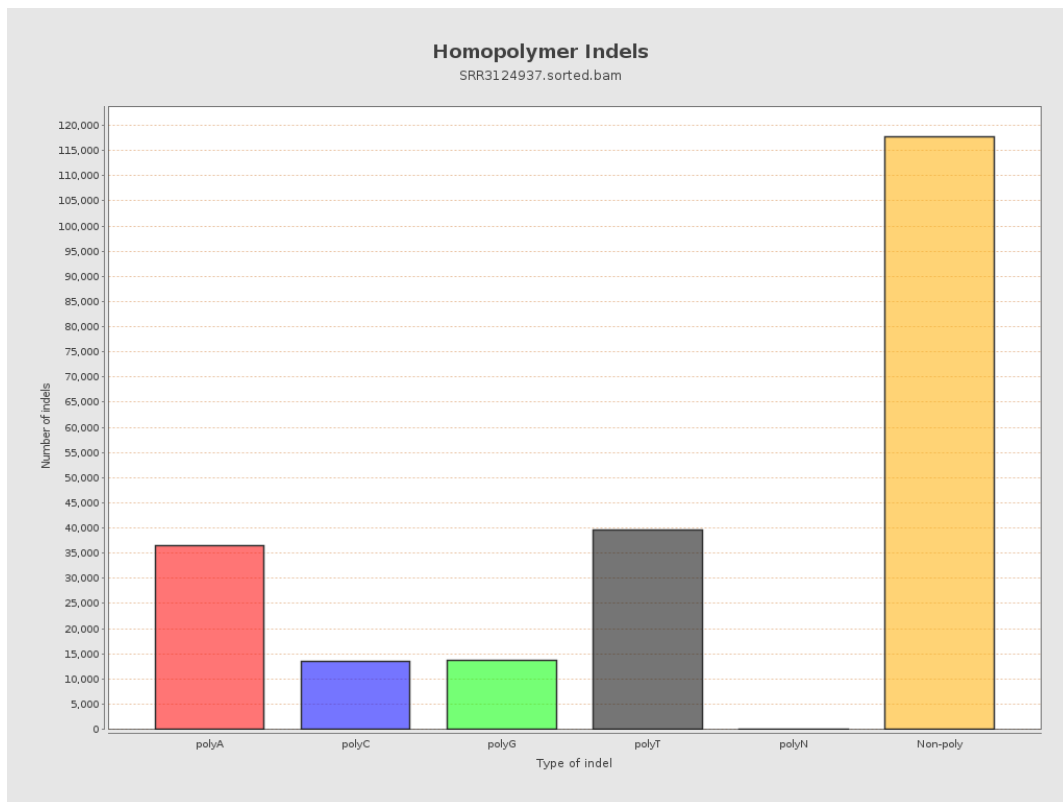
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



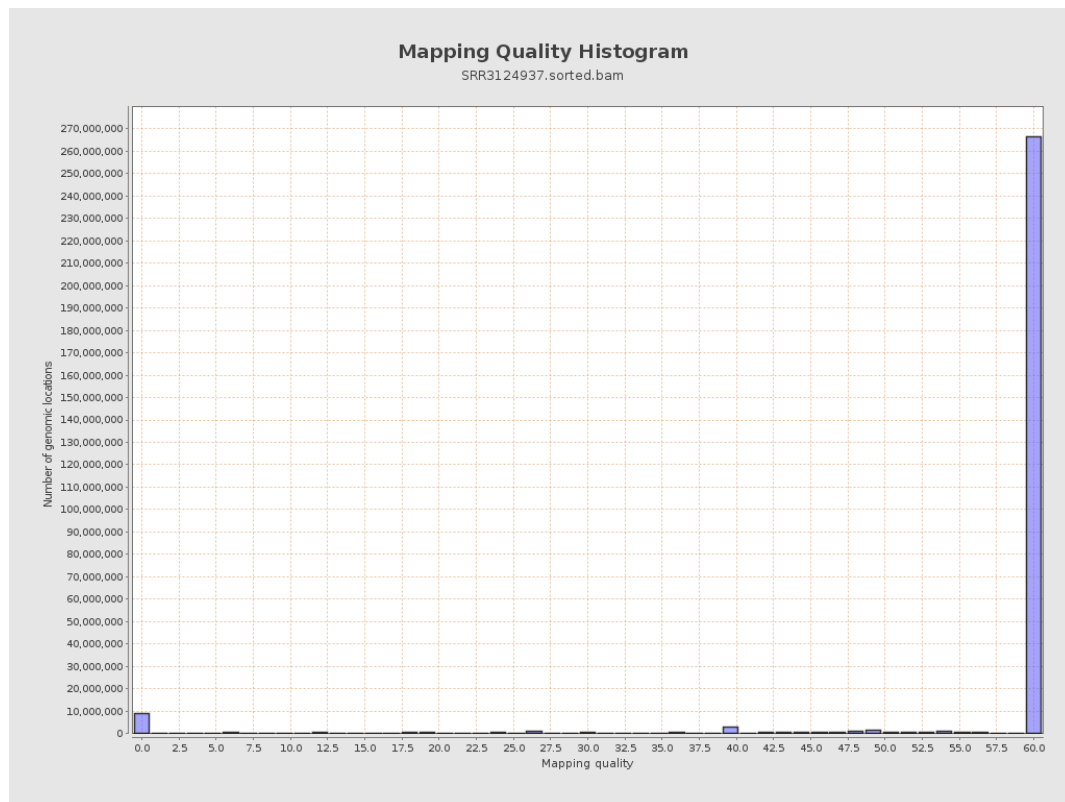
11. Results : Homopolymer Indels



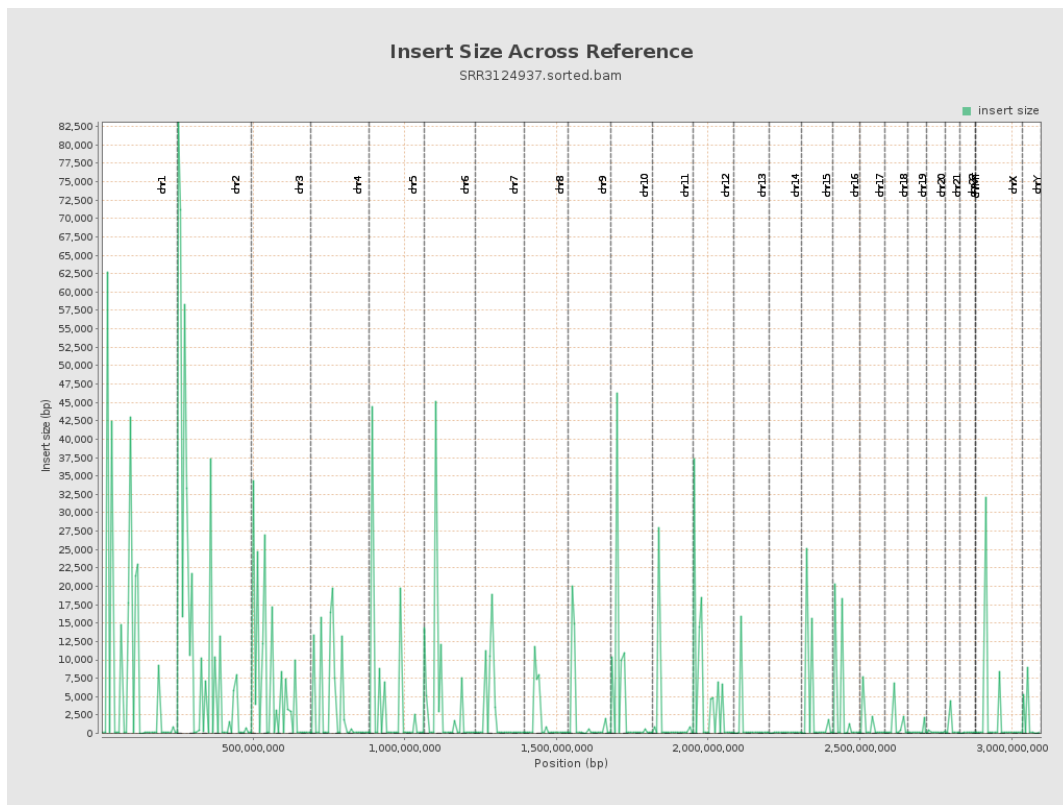
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

