

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 03:26:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124839.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_SRR3124839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124839_1.fastq.gz SRR3124839_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 03:26:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	97,500,404
Mapped reads	94,079,843 / 96.49%
Unmapped reads	3,420,561 / 3.51%
Mapped paired reads	94,079,843 / 96.49%
Mapped reads, first in pair	48,367,044 / 49.61%
Mapped reads, second in pair	45,712,799 / 46.88%
Mapped reads, both in pair	91,267,338 / 93.61%
Mapped reads, singletons	2,812,505 / 2.88%
Secondary alignments	0
Supplementary alignments	1,734,341 / 1.78%
Read min/max/mean length	30 / 150 / 150.81
Duplicated reads (estimated)	30,856,546 / 31.65%
Duplication rate	19.2%
Clipped reads	45,407,522 / 46.57%

2.2. ACGT Content

Number/percentage of A's	3,692,566,295 / 29.19%
Number/percentage of C's	2,448,303,240 / 19.36%
Number/percentage of T's	3,733,979,412 / 29.52%
Number/percentage of G's	2,773,369,443 / 21.93%
Number/percentage of N's	226,120 / 0%

GC Percentage	41.28%
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2.3. Coverage

Mean	4.0885
Standard Deviation	37.4067

2.4. Mapping Quality

Mean Mapping Quality	53.47
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2.5. Insert size

Mean	117,713.83
Standard Deviation	3,309,130.15
P25/Median/P75	208 / 263 / 330

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	165,147,072
Insertions	1,968,651
Mapped reads with at least one insertion	1.98%
Deletions	4,427,753
Mapped reads with at least one deletion	4.53%
Homopolymer indels	46.38%

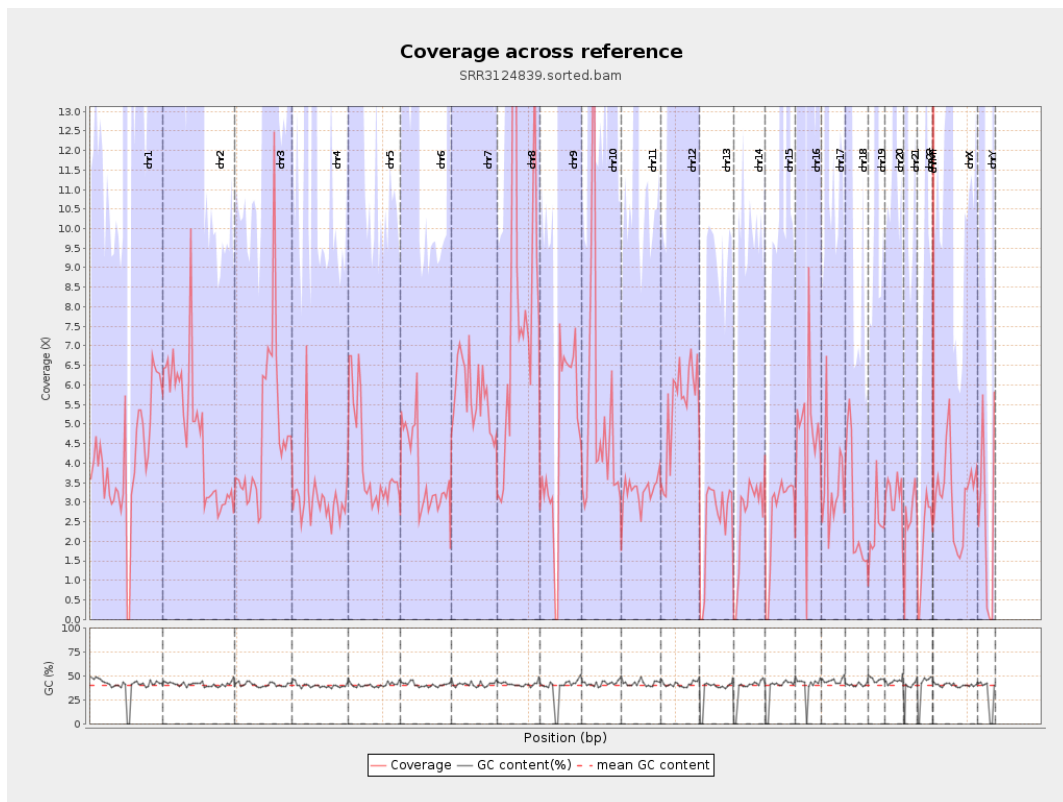
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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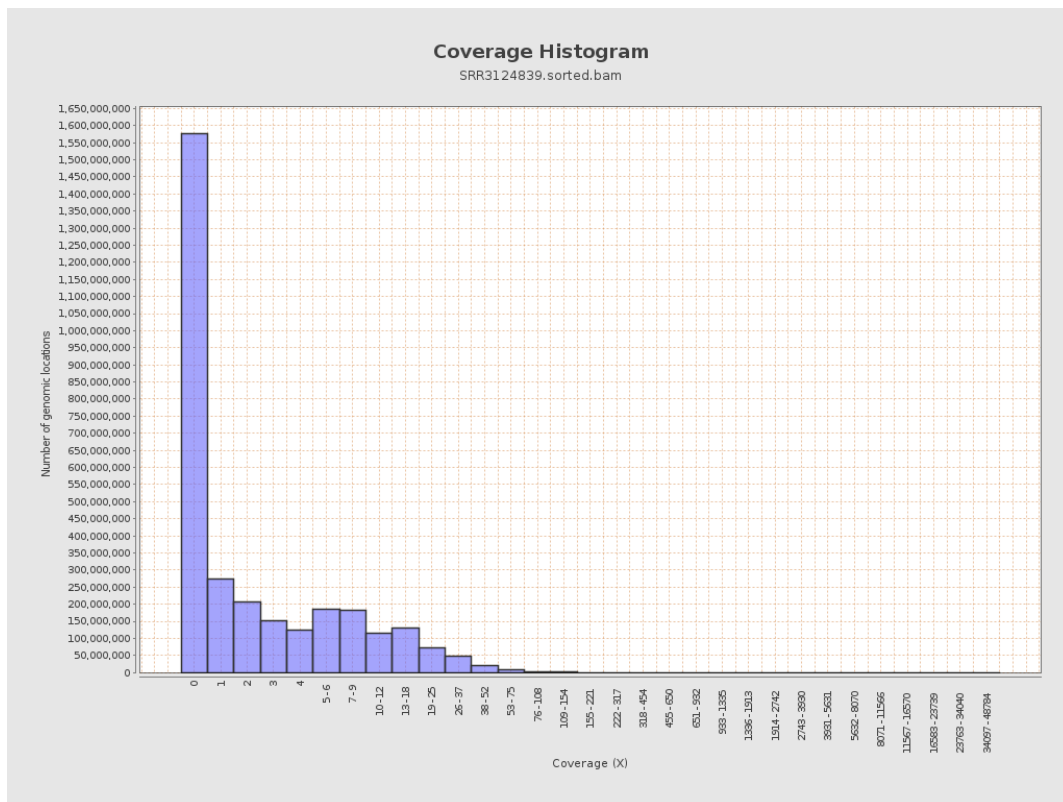
		bases	coverage	deviation
chr1	249250621	1027947426	4.1242	41.3481
chr2	243199373	1147278345	4.7174	40.5117
chr3	198022430	930400671	4.6985	9.2505
chr4	191154276	597509044	3.1258	30.8696
chr5	180915260	724488390	4.0046	8.4759
chr6	171115067	638609002	3.732	21.1233
chr7	159138663	910130839	5.7191	51.7944
chr8	146364022	1172921816	8.0137	23.4292
chr9	141213431	654851130	4.6373	69.1457
chr10	135534747	692217481	5.1073	89.0791
chr11	135006516	444650640	3.2935	21.1758
chr12	133851895	729501560	5.4501	19.8357
chr13	115169878	287918415	2.4999	5.7271
chr14	107349540	280574095	2.6136	6.5953
chr15	102531392	272937032	2.662	11.6426
chr16	90354753	425340711	4.7075	39.3831
chr17	81195210	279680040	3.4445	60.3708
chr18	78077248	219873385	2.8161	46.6302
chr19	59128983	138899707	2.3491	26.6695
chr20	63025520	203699560	3.232	11.6578
chr21	48129895	124860143	2.5942	15.6886
chr22	51304566	102164849	1.9913	6.7771
chrMT	16571	5236724	316.0174	185.32
chrX	155270560	491091119	3.1628	14.3569

chrY	59373566	154019925	2.5941	43.8844
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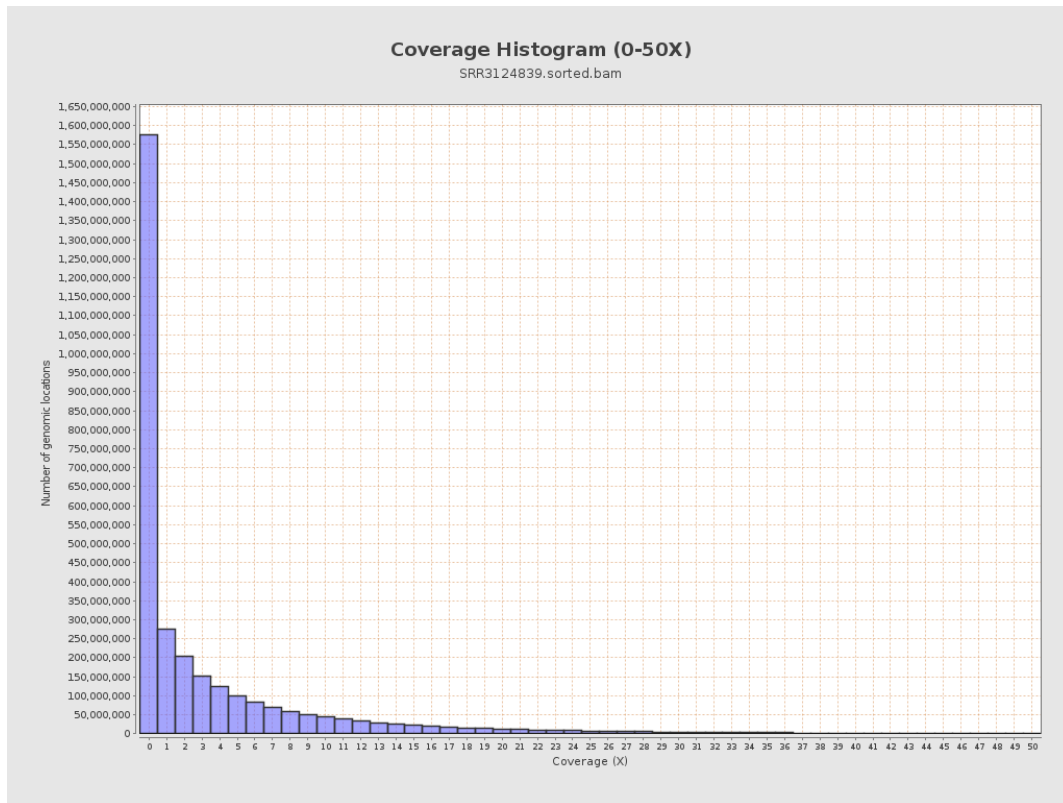
3. Results : Coverage across reference



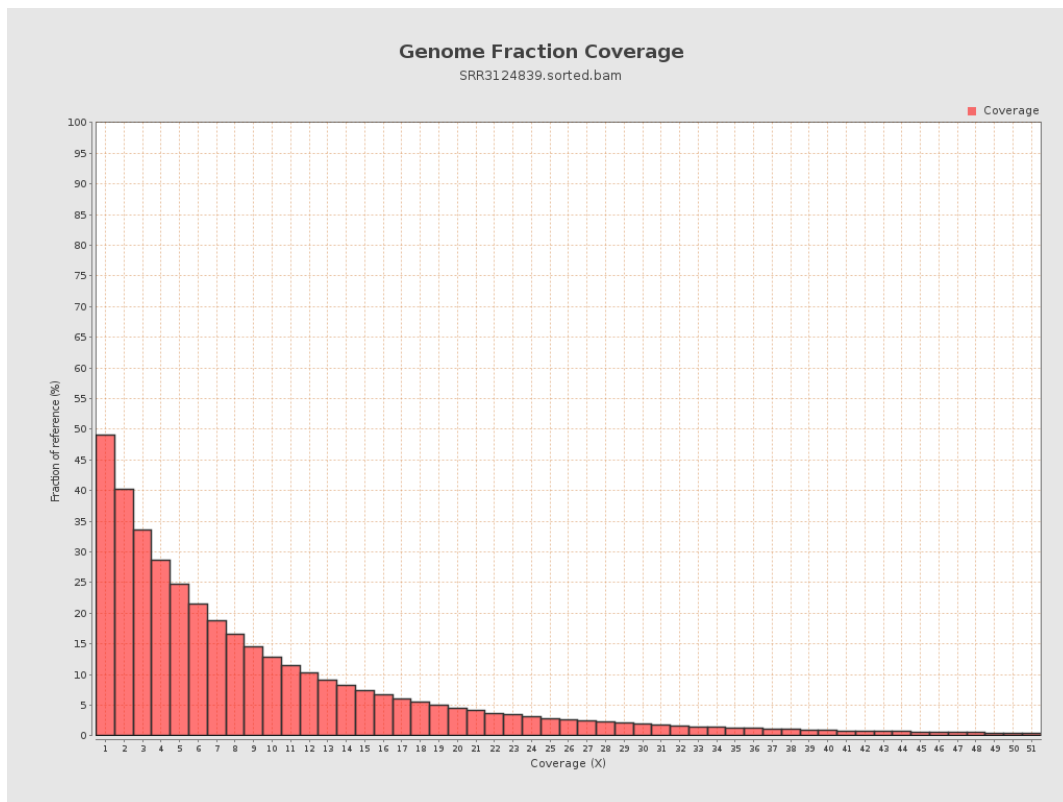
4. Results : Coverage Histogram



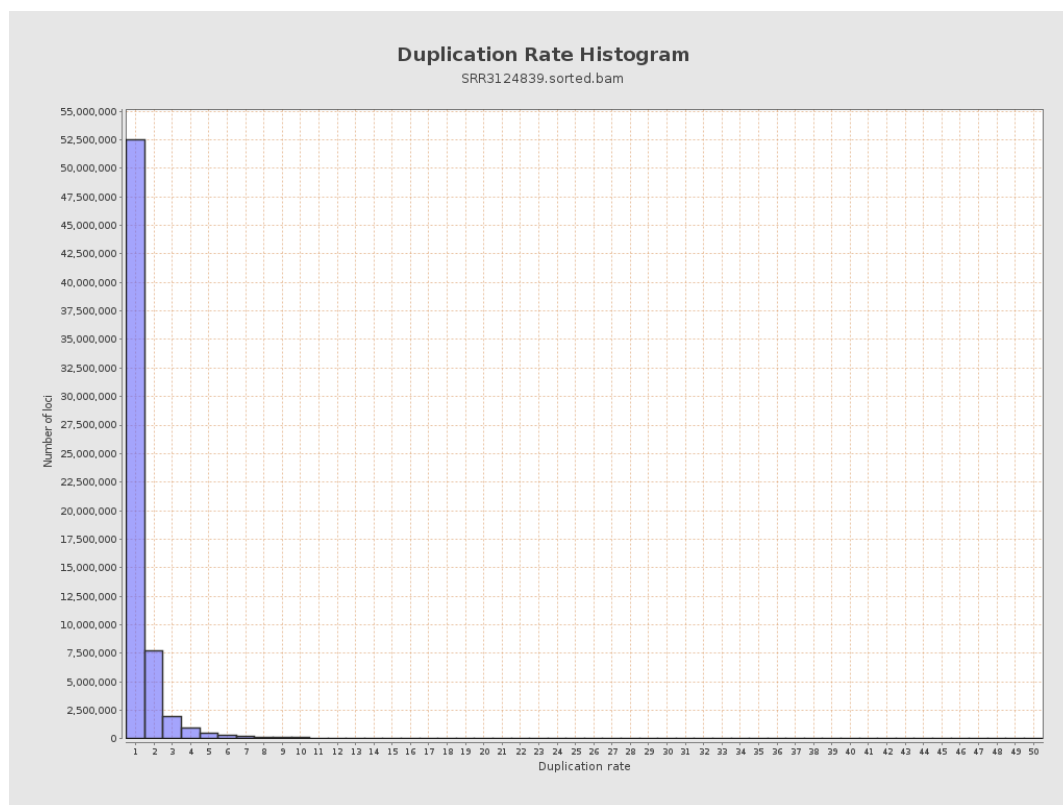
5. Results : Coverage Histogram (0-50X)



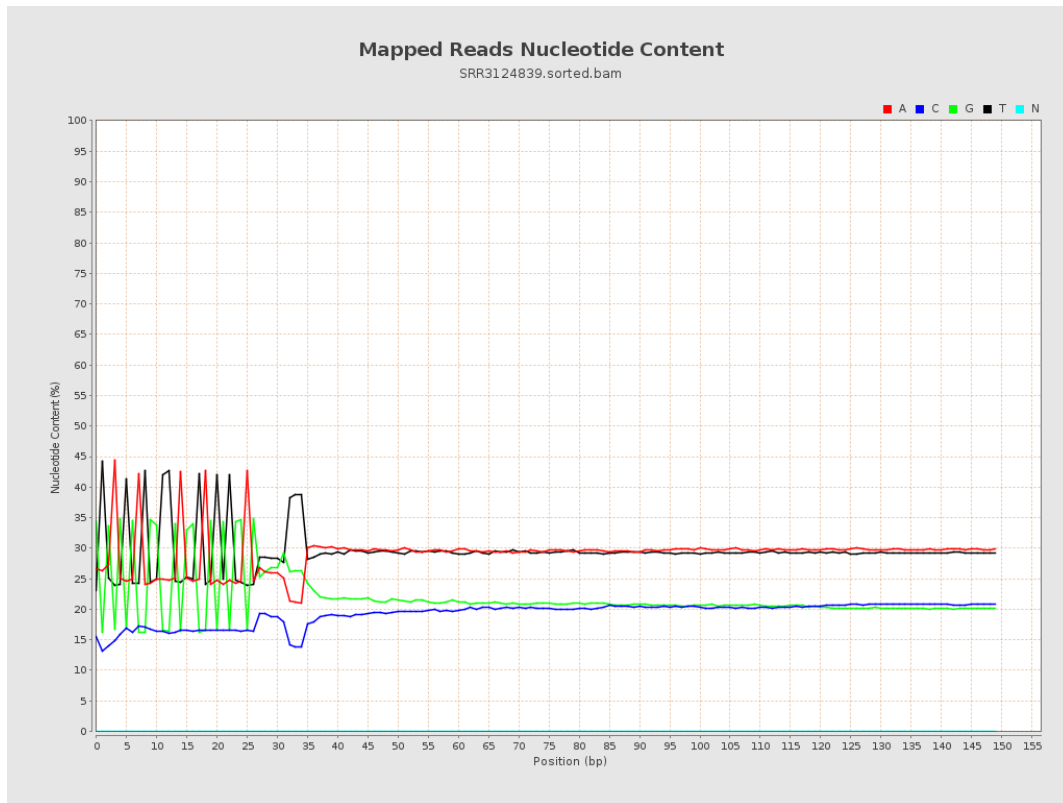
6. Results : Genome Fraction Coverage



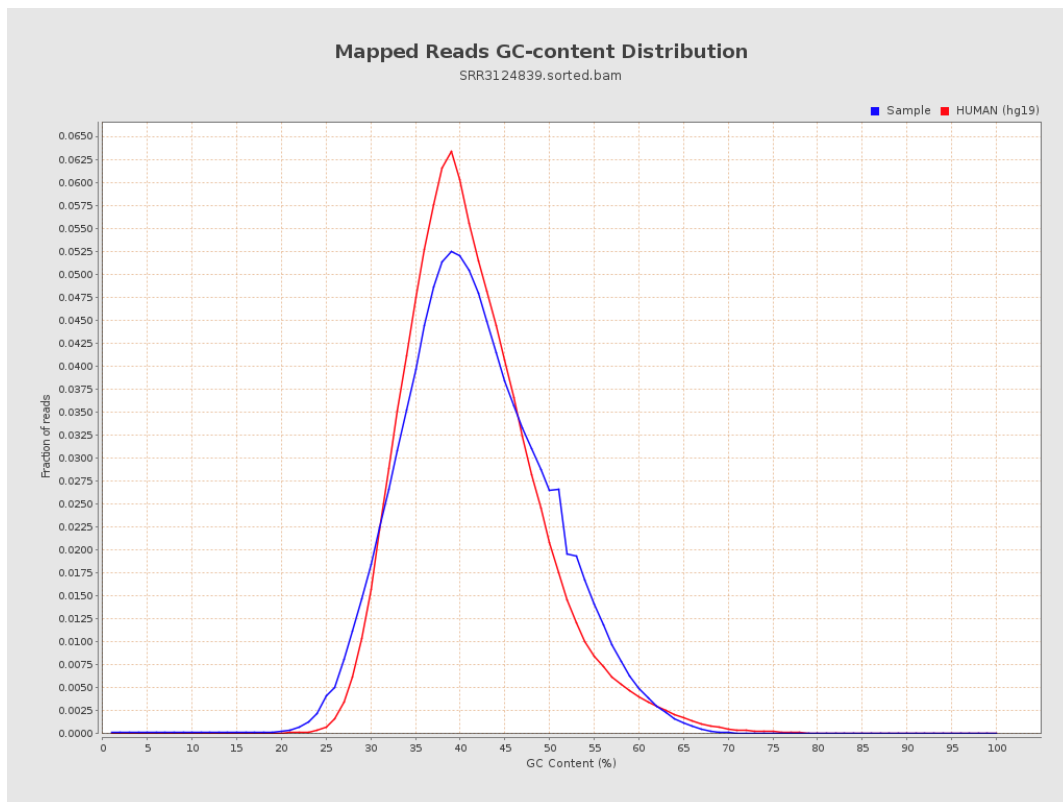
7. Results : Duplication Rate Histogram



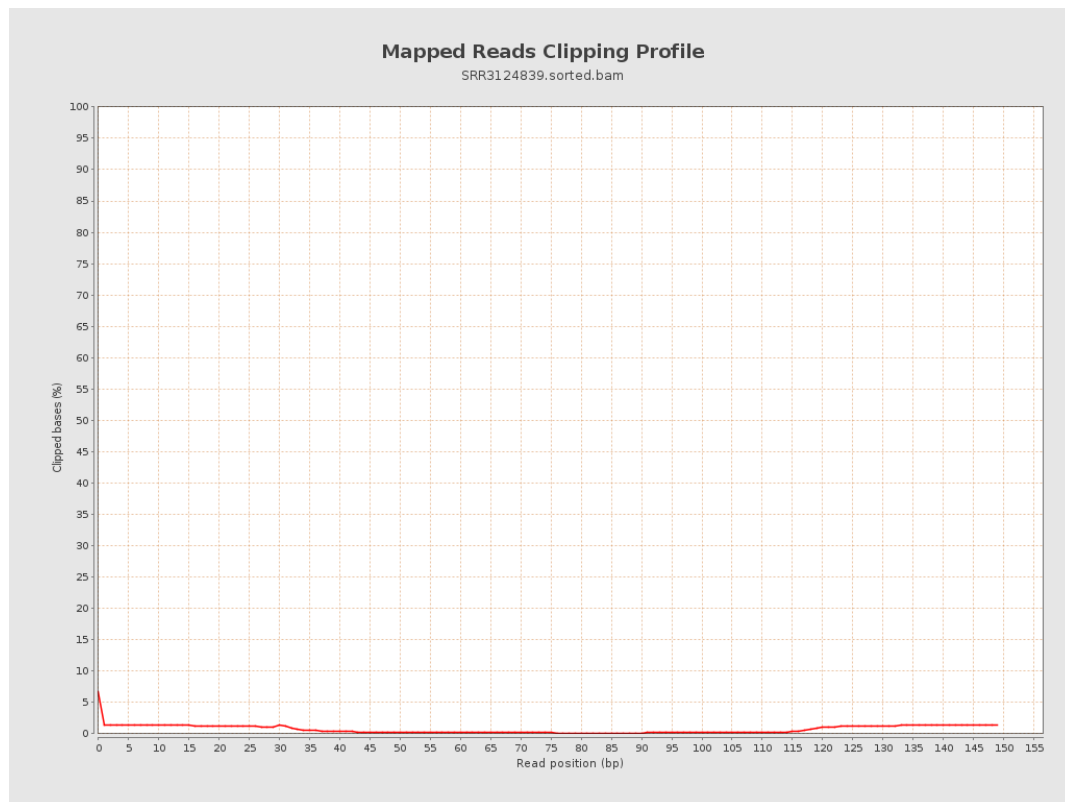
8. Results : Mapped Reads Nucleotide Content



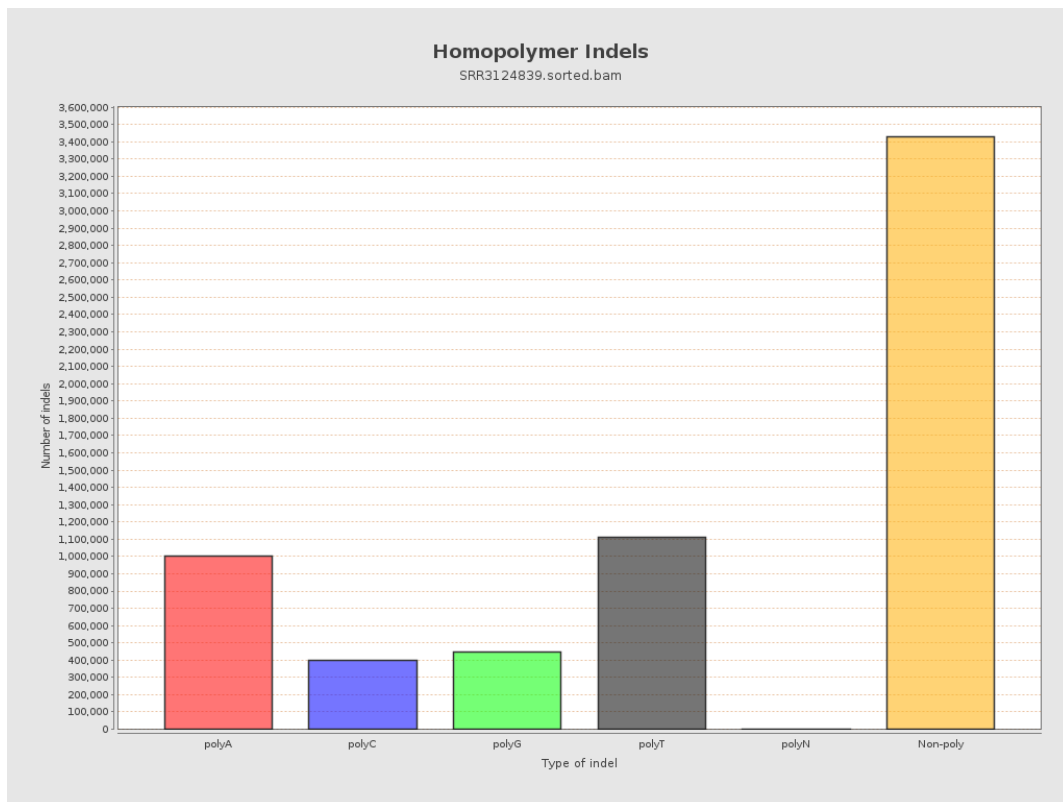
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



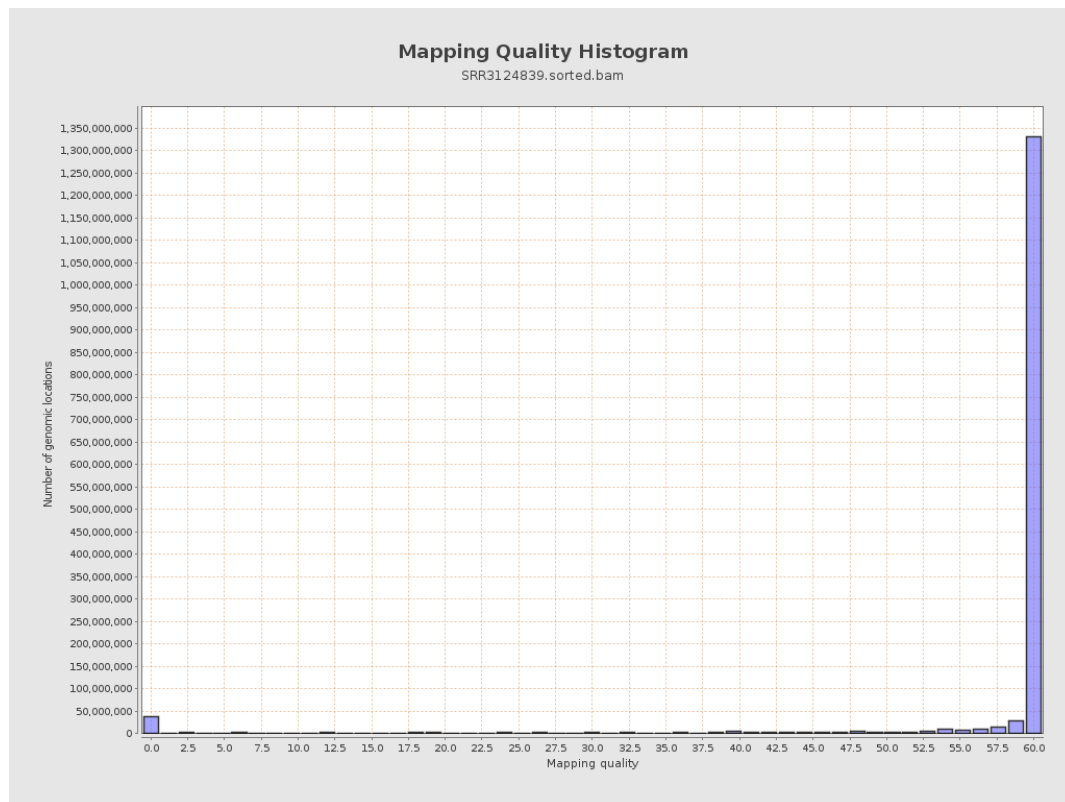
11. Results : Homopolymer Indels



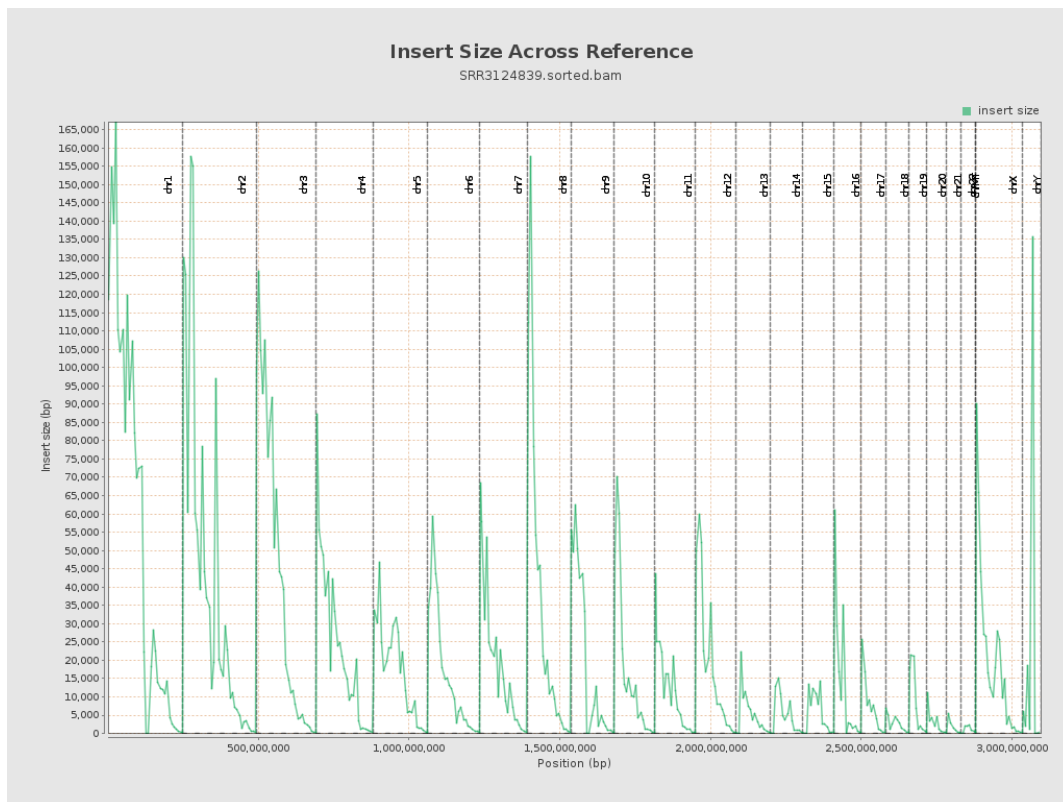
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

