

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 23:17:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124869.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_SRR3124869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124869_1.fastq.gz SRR3124869_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 23:17:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,147,290
Mapped reads	6,083,844 / 98.97%
Unmapped reads	63,446 / 1.03%
Mapped paired reads	6,083,844 / 98.97%
Mapped reads, first in pair	3,043,920 / 49.52%
Mapped reads, second in pair	3,039,924 / 49.45%
Mapped reads, both in pair	6,062,546 / 98.62%
Mapped reads, singletons	21,298 / 0.35%
Secondary alignments	0
Supplementary alignments	28,357 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	365,718 / 5.95%
Duplication rate	3.14%
Clipped reads	3,613,623 / 58.78%

2.2. ACGT Content

Number/percentage of A's	160,264,009 / 28.78%
Number/percentage of C's	109,646,614 / 19.69%
Number/percentage of T's	165,663,595 / 29.75%
Number/percentage of G's	121,307,852 / 21.78%
Number/percentage of N's	9,341 / 0%

GC Percentage	41.47%
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2.3. Coverage

Mean	0.18
Standard Deviation	2.0063

2.4. Mapping Quality

Mean Mapping Quality	52.78
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2.5. Insert size

Mean	63,620.7
Standard Deviation	2,404,176.32
P25/Median/P75	140 / 173 / 219

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	4,188,016
Insertions	89,918
Mapped reads with at least one insertion	1.44%
Deletions	178,990
Mapped reads with at least one deletion	2.88%
Homopolymer indels	46.21%

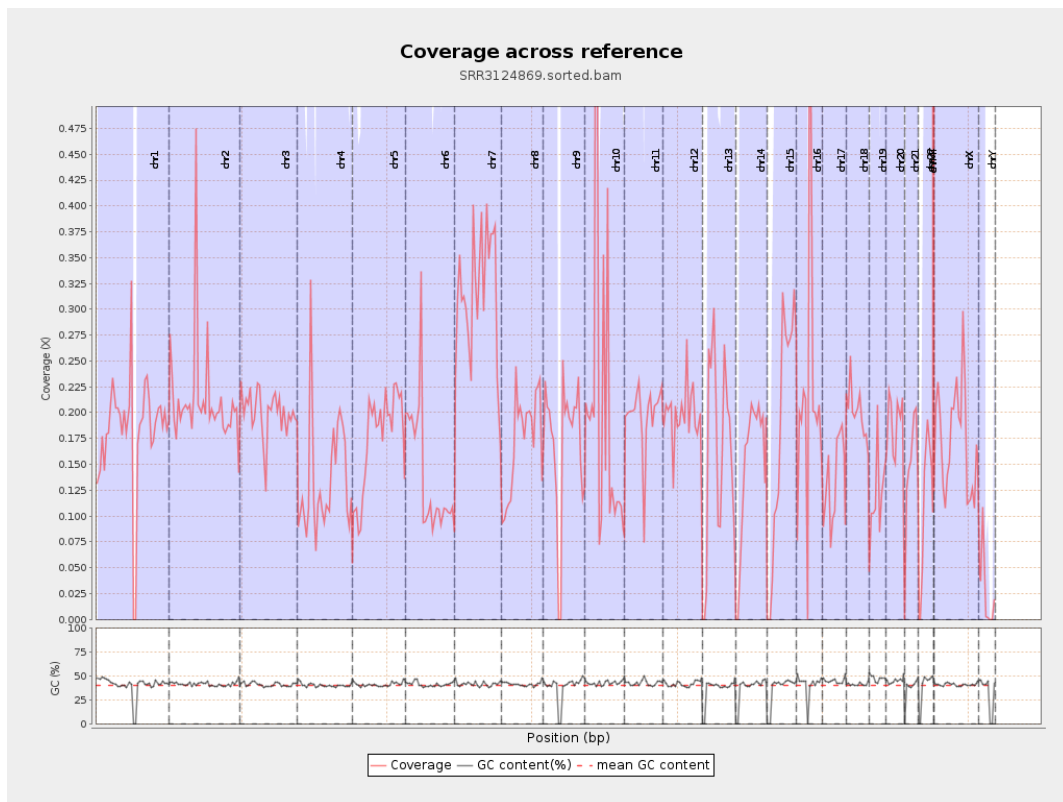
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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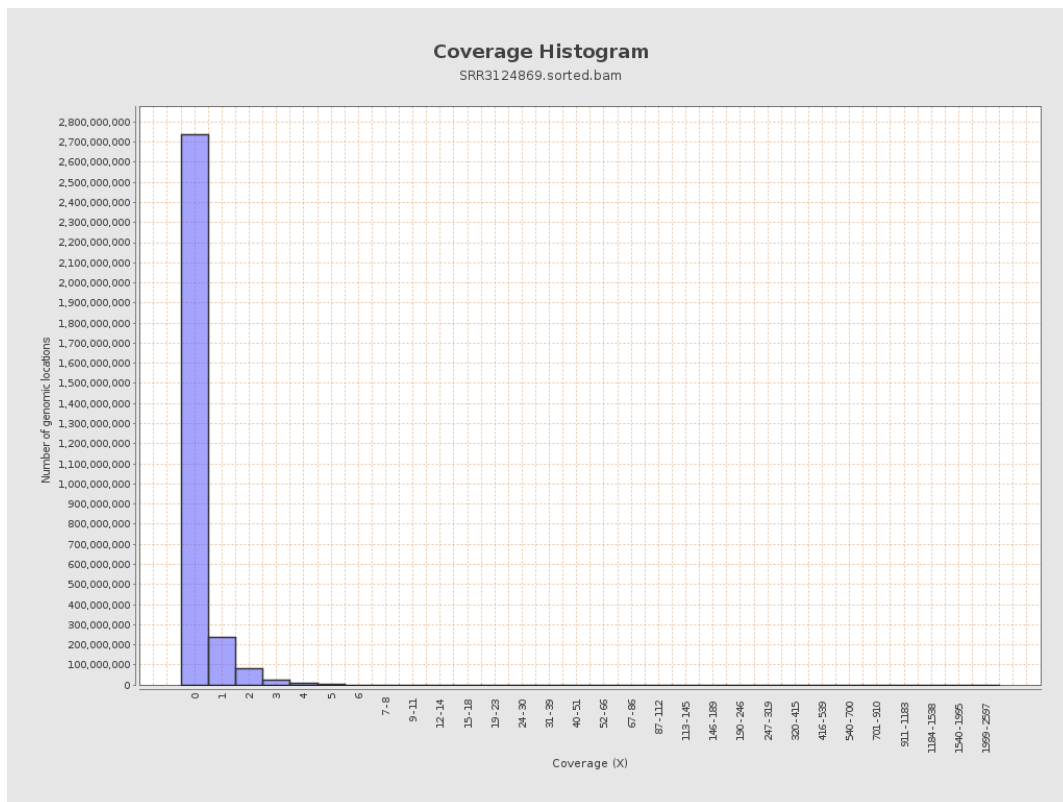
		bases	coverage	deviation
chr1	249250621	45560902	0.1828	2.5806
chr2	243199373	51755450	0.2128	2.0678
chr3	198022430	39544564	0.1997	0.6543
chr4	191154276	25377149	0.1328	1.3947
chr5	180915260	31606626	0.1747	0.5734
chr6	171115067	23980690	0.1401	1.6942
chr7	159138663	50832892	0.3194	3.016
chr8	146364022	25206508	0.1722	0.8035
chr9	141213431	24076634	0.1705	2.534
chr10	135534747	27786873	0.205	5.2588
chr11	135006516	26359013	0.1952	1.4451
chr12	133851895	26389897	0.1972	0.5994
chr13	115169878	17958853	0.1559	0.5335
chr14	107349540	15838739	0.1475	0.5922
chr15	102531392	18536649	0.1808	0.5857
chr16	90354753	19641651	0.2174	3.351
chr17	81195210	10682851	0.1316	1.1151
chr18	78077248	15688990	0.2009	2.6713
chr19	59128983	7219170	0.1221	1.3836
chr20	63025520	11772186	0.1868	0.6694
chr21	48129895	7018181	0.1458	0.7309
chr22	51304566	5652868	0.1102	0.4729
chrMT	16571	153082	9.2379	6.5204
chrX	155270560	27021157	0.174	0.8696

chrY	59373566	1533891	0.0258	1.553
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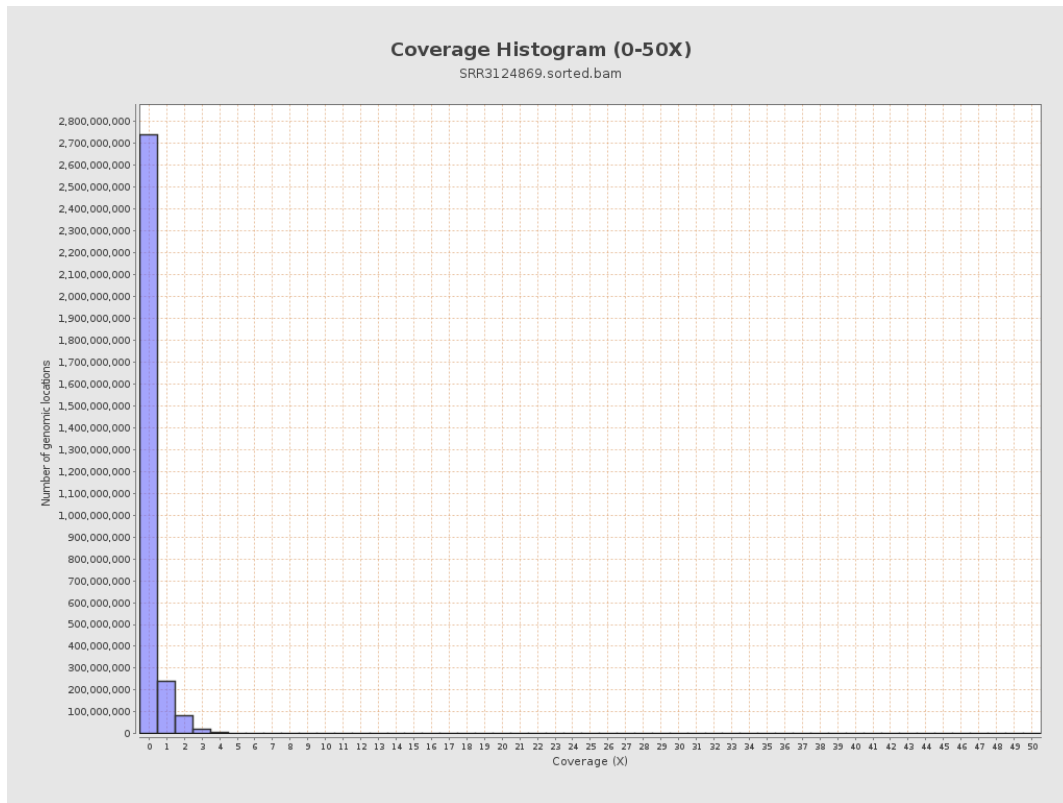
3. Results : Coverage across reference



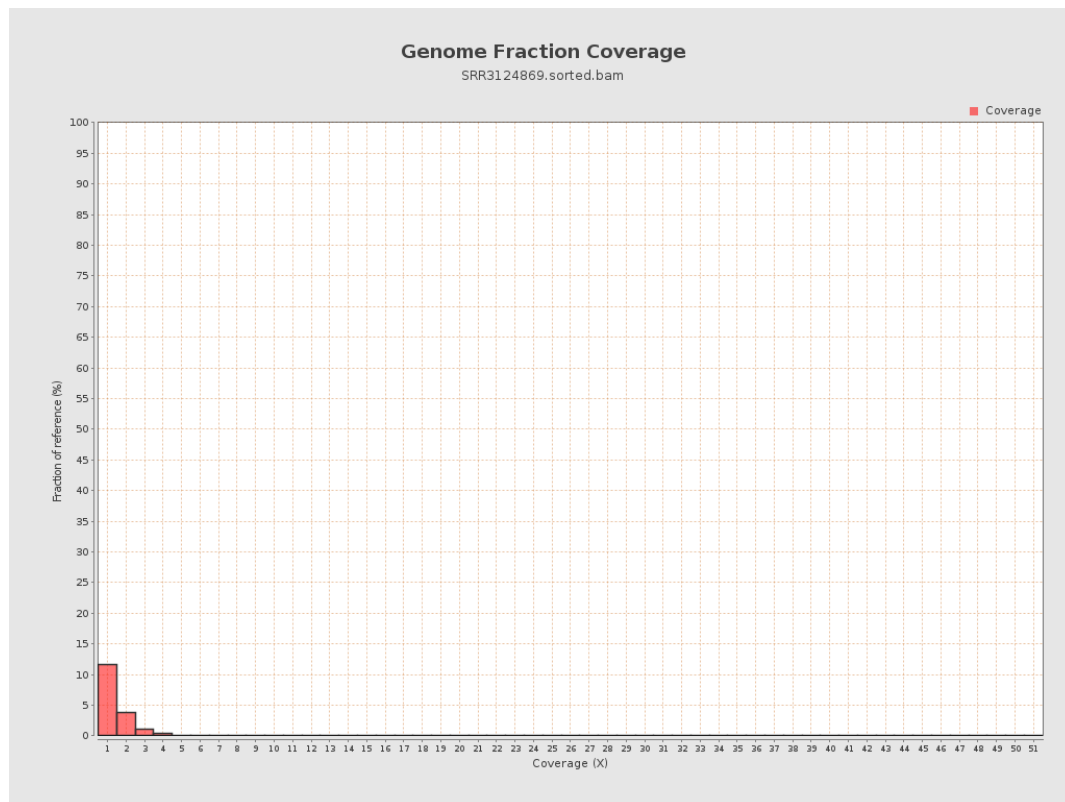
4. Results : Coverage Histogram



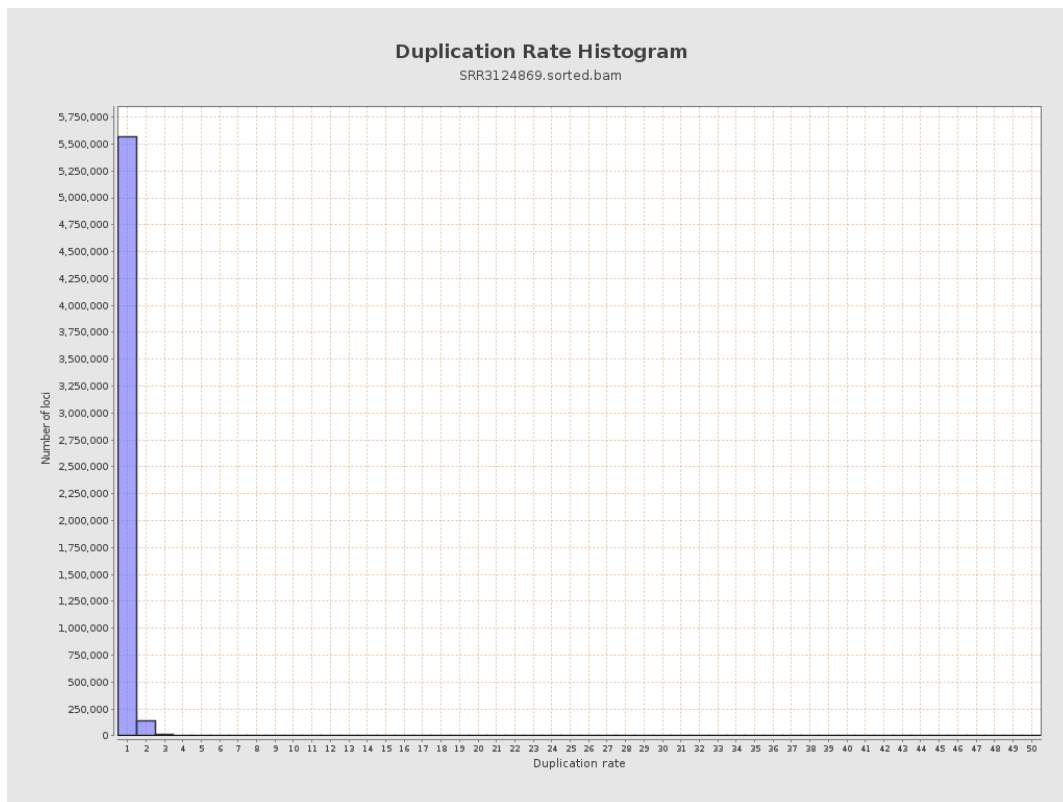
5. Results : Coverage Histogram (0-50X)



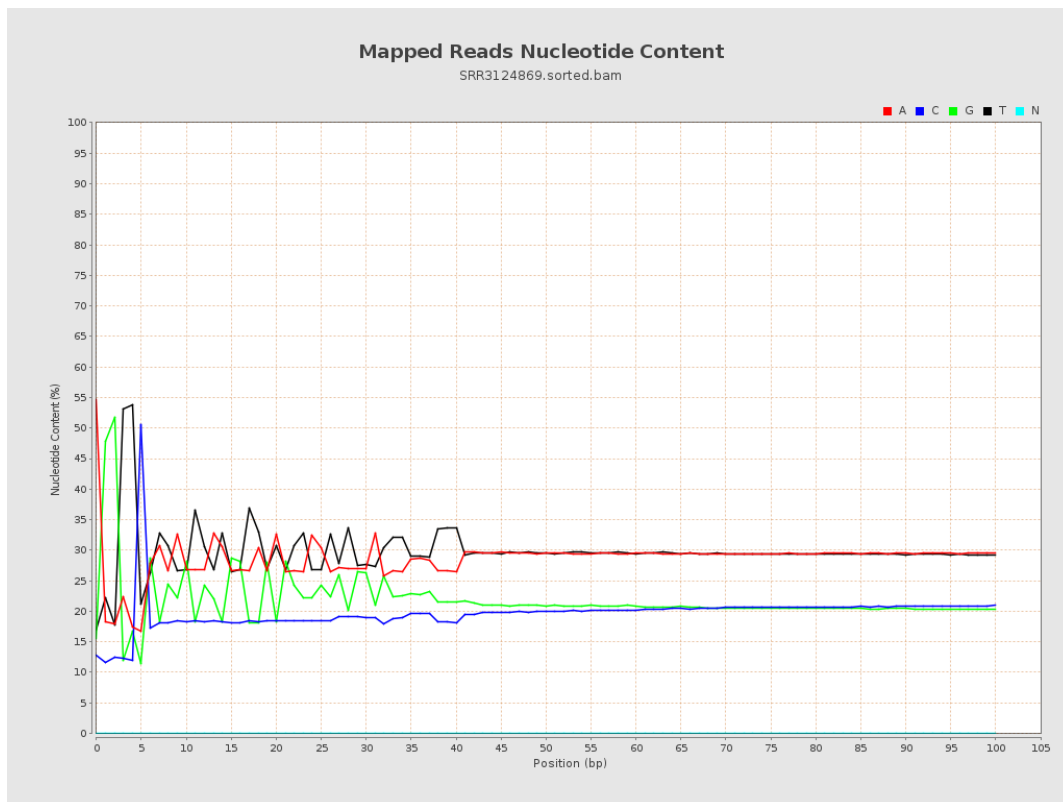
6. Results : Genome Fraction Coverage



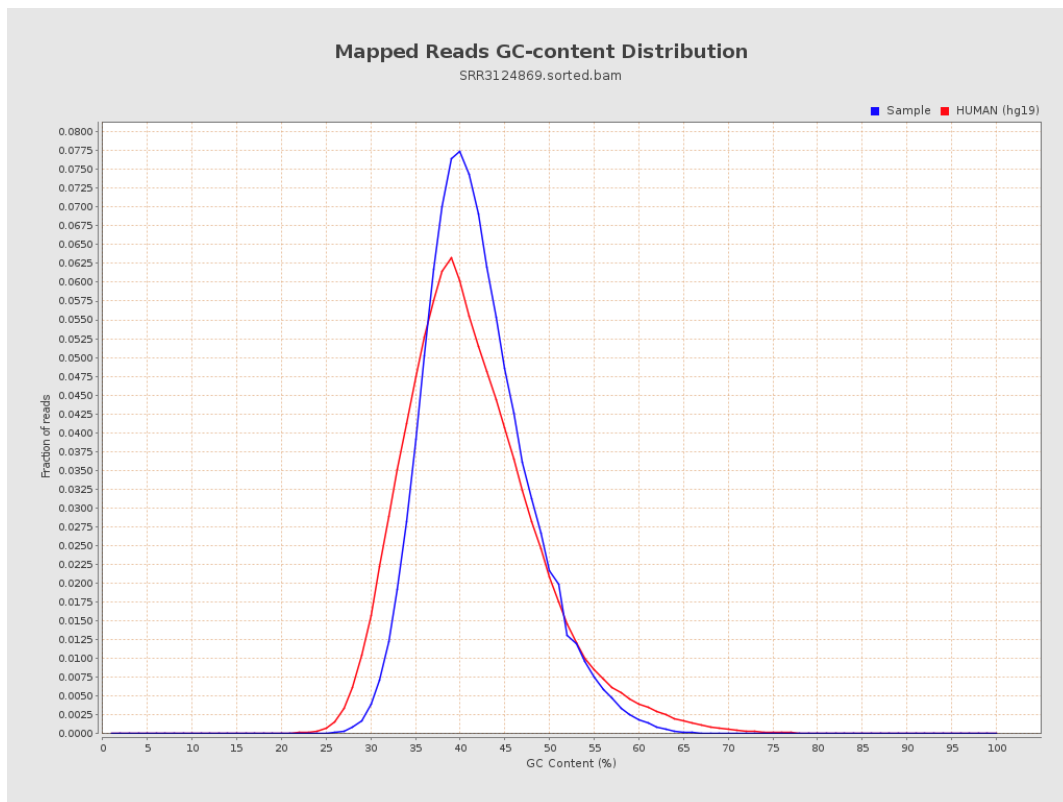
7. Results : Duplication Rate Histogram



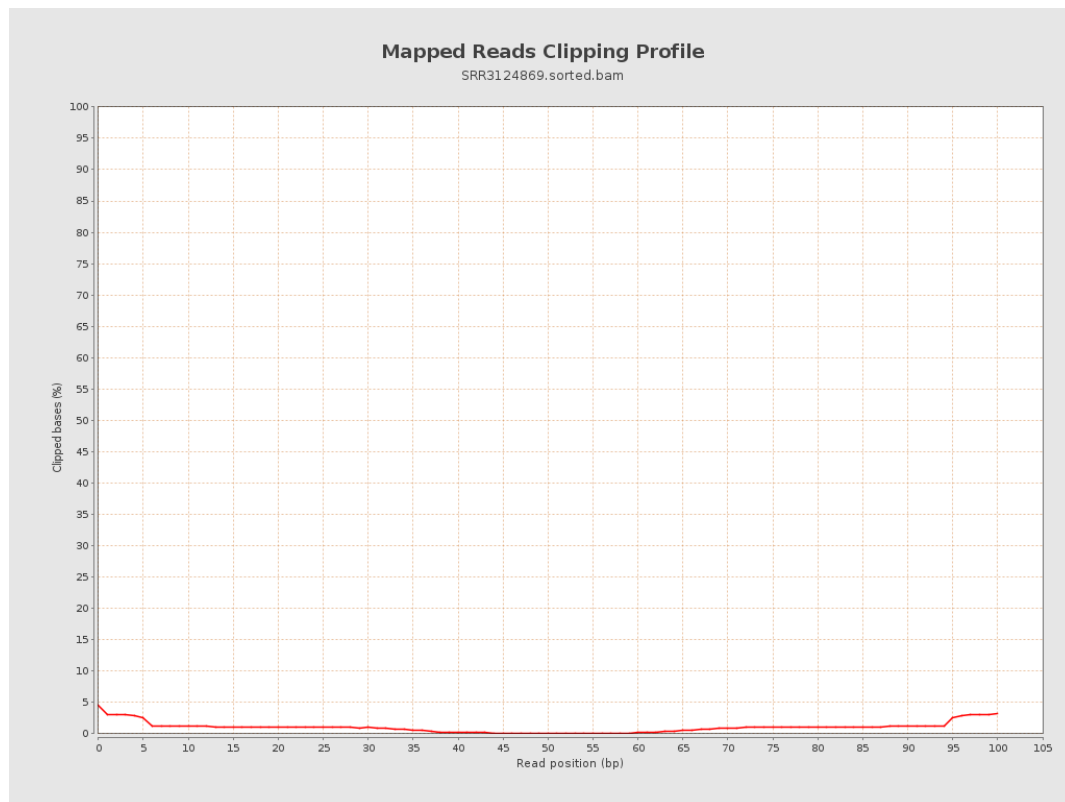
8. Results : Mapped Reads Nucleotide Content



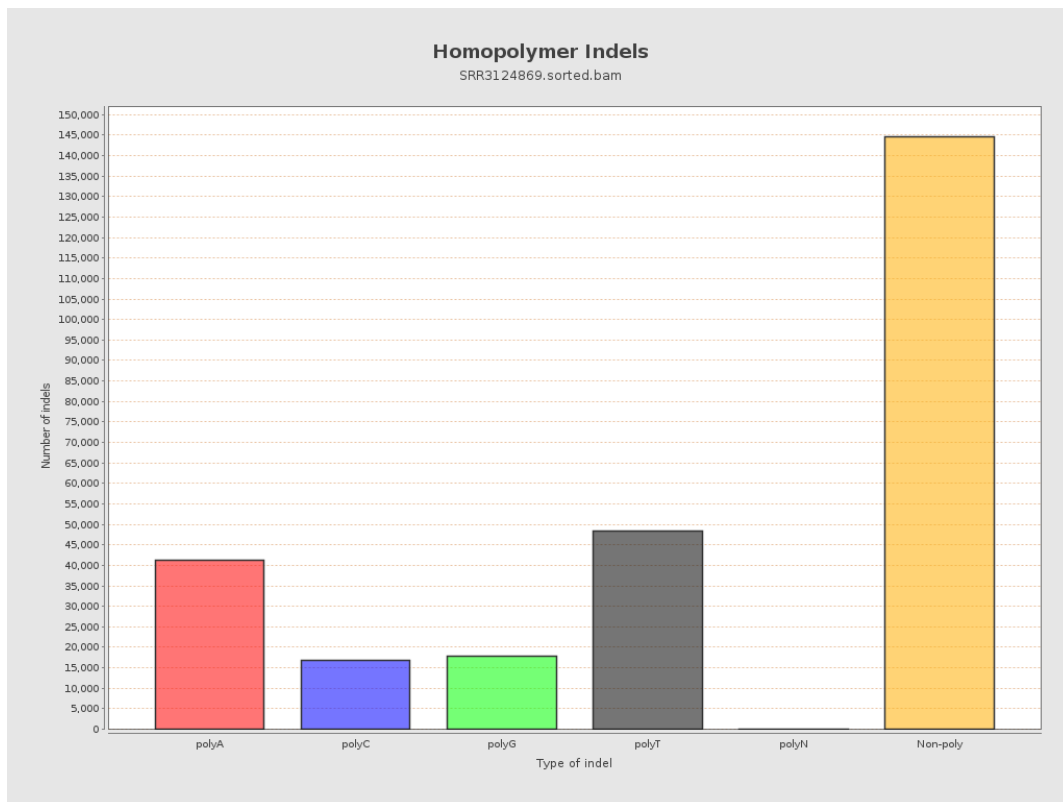
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



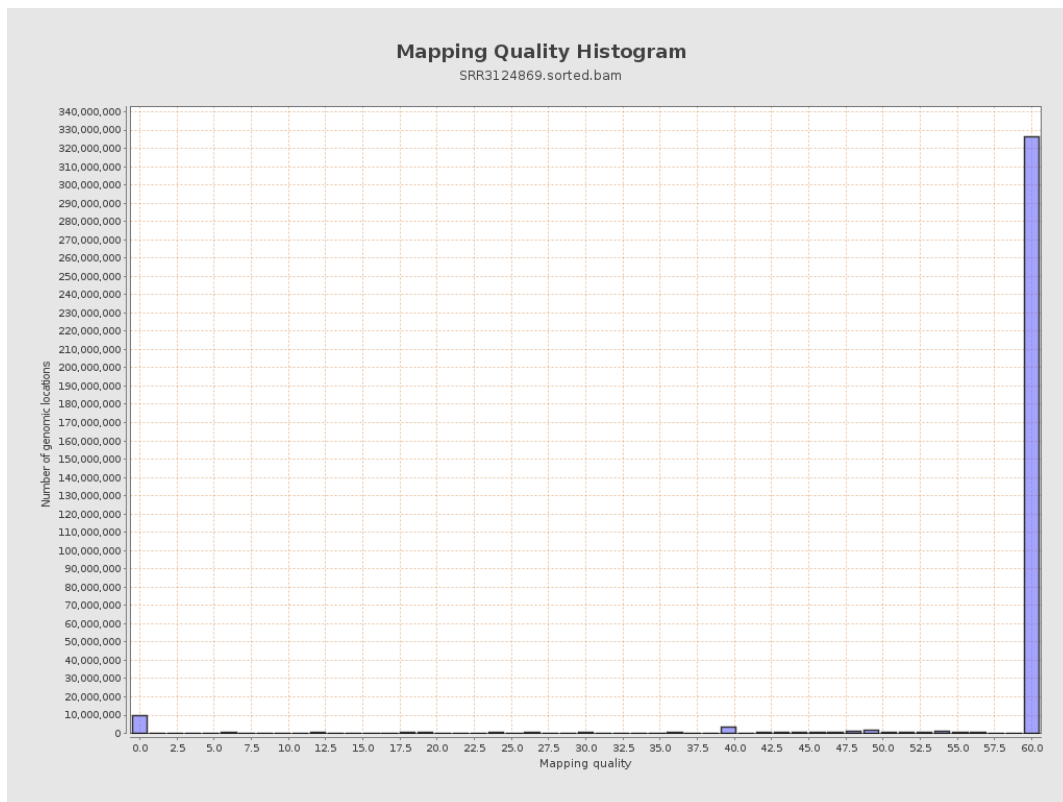
11. Results : Homopolymer Indels



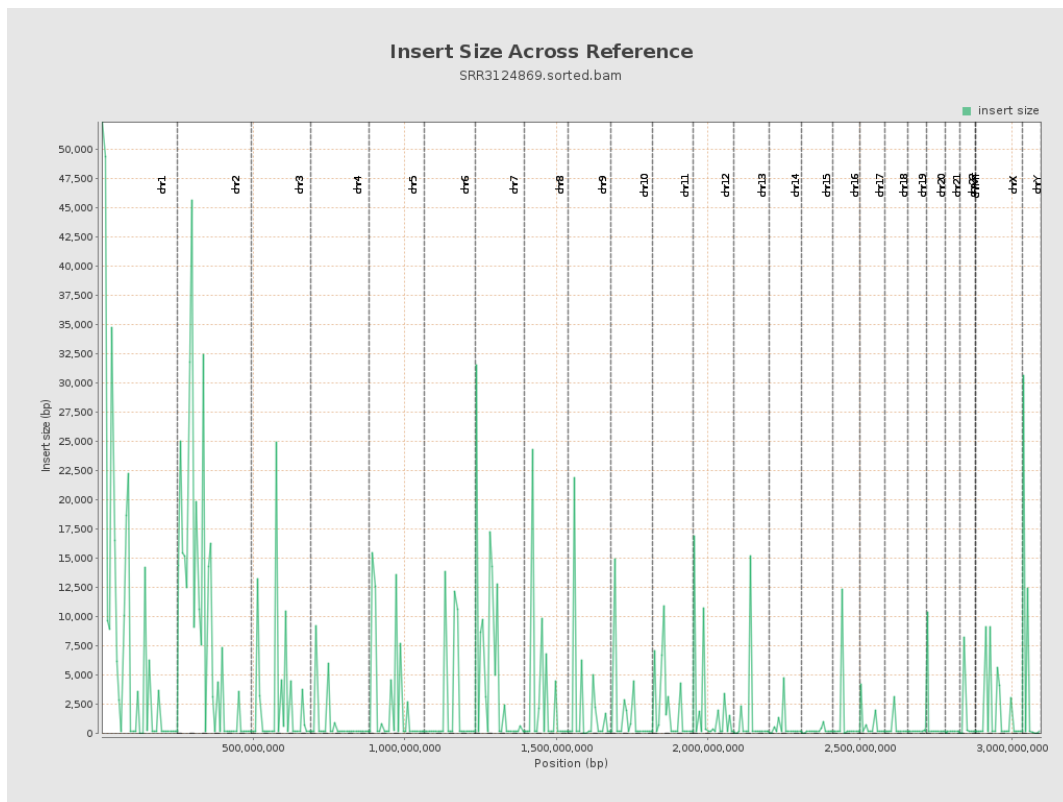
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

