

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:00:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124893.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_SRR3124893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124893_1.fastq.gz SRR3124893_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:00:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,462,718
Mapped reads	4,404,432 / 98.69%
Unmapped reads	58,286 / 1.31%
Mapped paired reads	4,404,432 / 98.69%
Mapped reads, first in pair	2,206,575 / 49.44%
Mapped reads, second in pair	2,197,857 / 49.25%
Mapped reads, both in pair	4,385,268 / 98.26%
Mapped reads, singletons	19,164 / 0.43%
Secondary alignments	0
Supplementary alignments	15,909 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	363,723 / 8.15%
Duplication rate	5.7%
Clipped reads	2,133,382 / 47.8%

2.2. ACGT Content

Number/percentage of A's	107,659,742 / 28.28%
Number/percentage of C's	70,270,543 / 18.46%
Number/percentage of T's	113,499,581 / 29.81%
Number/percentage of G's	89,123,238 / 23.41%
Number/percentage of N's	141,281 / 0.04%

GC Percentage	41.87%
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2.3. Coverage

Mean	0.123
Standard Deviation	1.2066

2.4. Mapping Quality

Mean Mapping Quality	52.69
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2.5. Insert size

Mean	32,031.09
Standard Deviation	1,669,259.91
P25/Median/P75	148 / 199 / 272

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	2,946,584
Insertions	51,614
Mapped reads with at least one insertion	1.14%
Deletions	120,335
Mapped reads with at least one deletion	2.68%
Homopolymer indels	48.02%

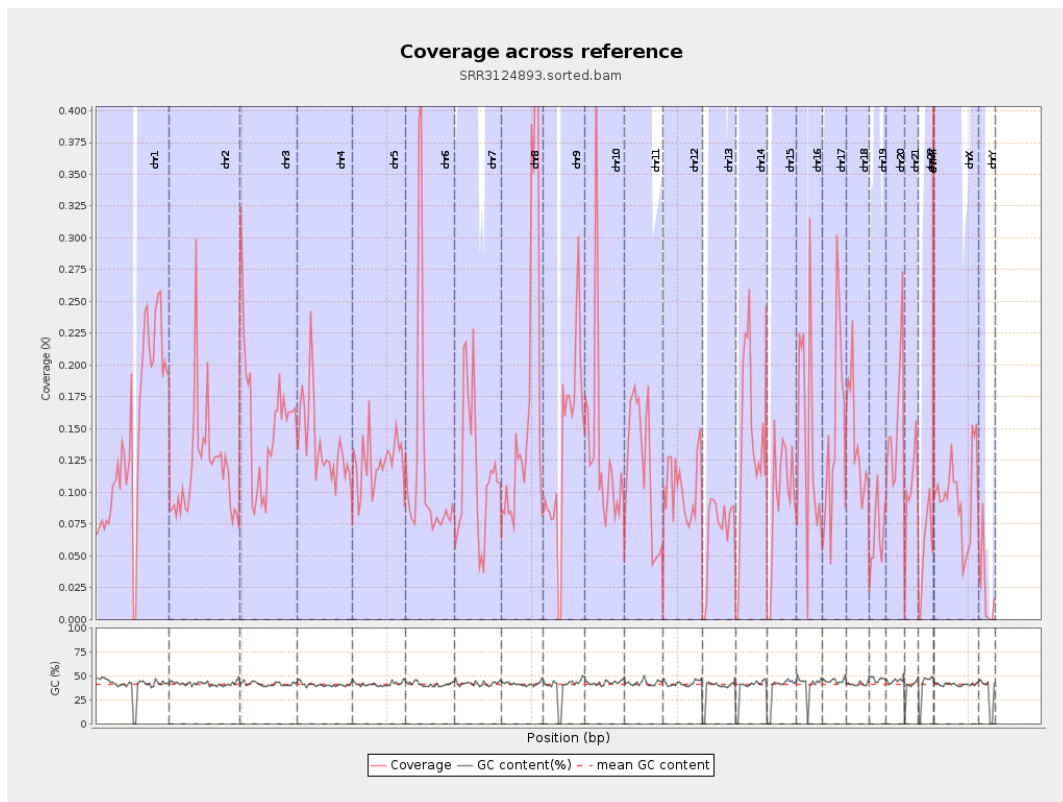
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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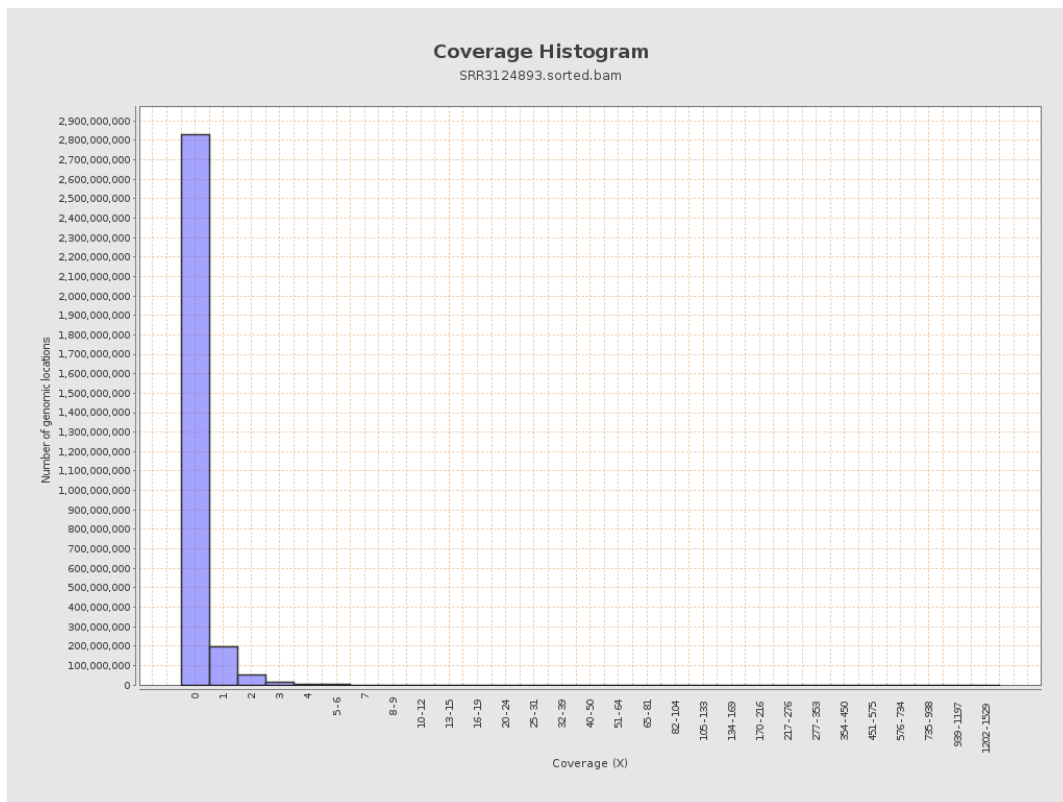
		bases	coverage	deviation
chr1	249250621	35982405	0.1444	1.2131
chr2	243199373	28663663	0.1179	1.3514
chr3	198022430	30751387	0.1553	0.5158
chr4	191154276	26130474	0.1367	0.8566
chr5	180915260	22283572	0.1232	0.4573
chr6	171115067	20316476	0.1187	1.6201
chr7	159138663	18523478	0.1164	1.9219
chr8	146364022	25641685	0.1752	0.6817
chr9	141213431	19294670	0.1366	1.6357
chr10	135534747	17647994	0.1302	2.6015
chr11	135006516	15891150	0.1177	1.1484
chr12	133851895	13749868	0.1027	0.4144
chr13	115169878	7934467	0.0689	0.325
chr14	107349540	14822184	0.1381	0.5703
chr15	102531392	9691440	0.0945	0.4056
chr16	90354753	12327703	0.1364	1.5544
chr17	81195210	11980870	0.1476	1.2854
chr18	78077248	11066866	0.1417	1.627
chr19	59128983	4062158	0.0687	0.7102
chr20	63025520	9918591	0.1574	0.5629
chr21	48129895	4847112	0.1007	0.7282
chr22	51304566	2795799	0.0545	0.3152
chrMT	16571	81929	4.9441	3.9715
chrX	155270560	15255173	0.0982	0.5894

chrY	59373566	1233927	0.0208	1.319
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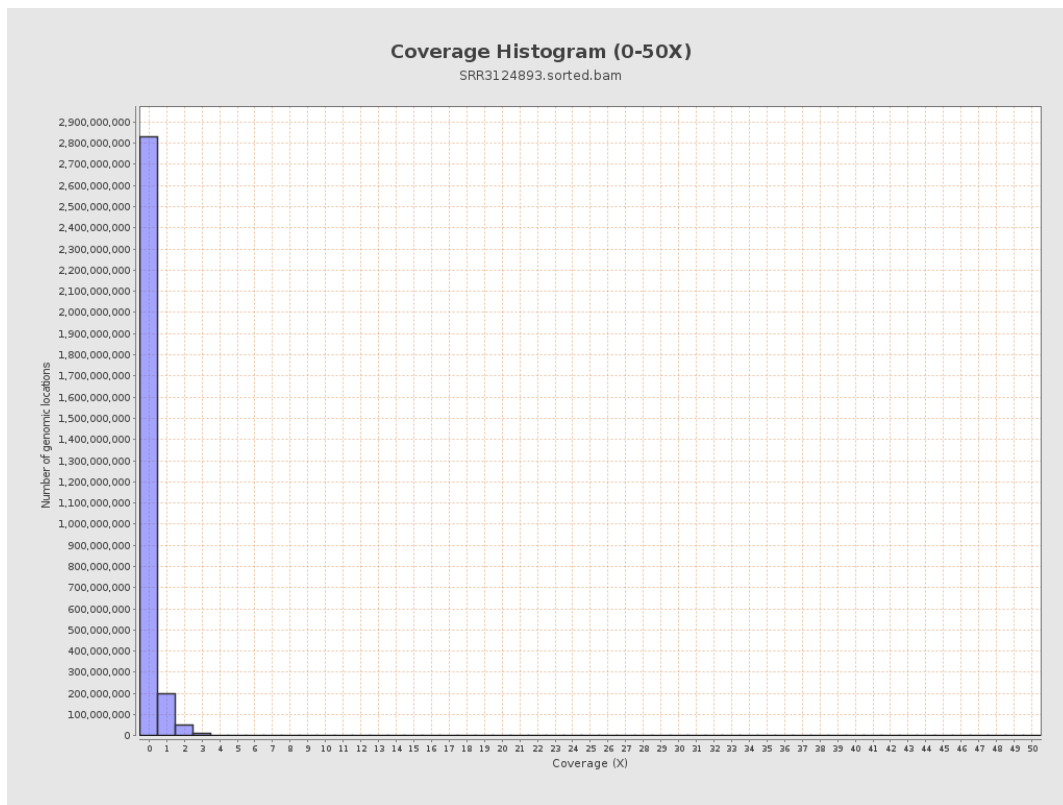
3. Results : Coverage across reference



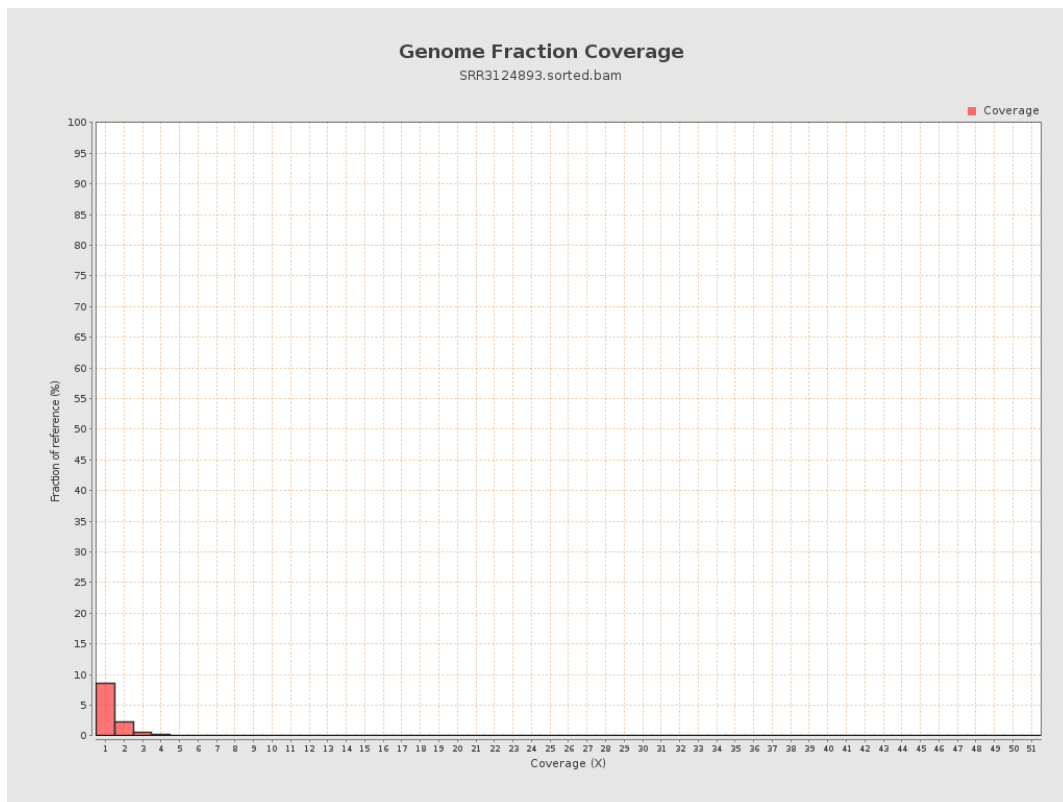
4. Results : Coverage Histogram



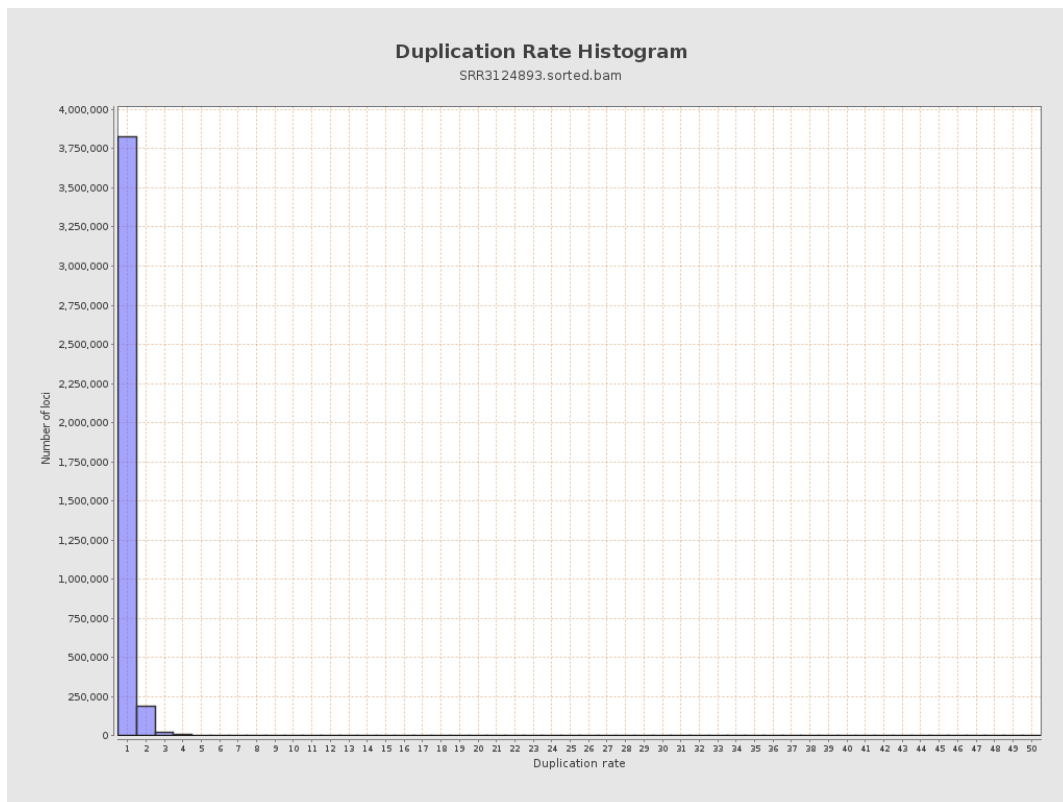
5. Results : Coverage Histogram (0-50X)



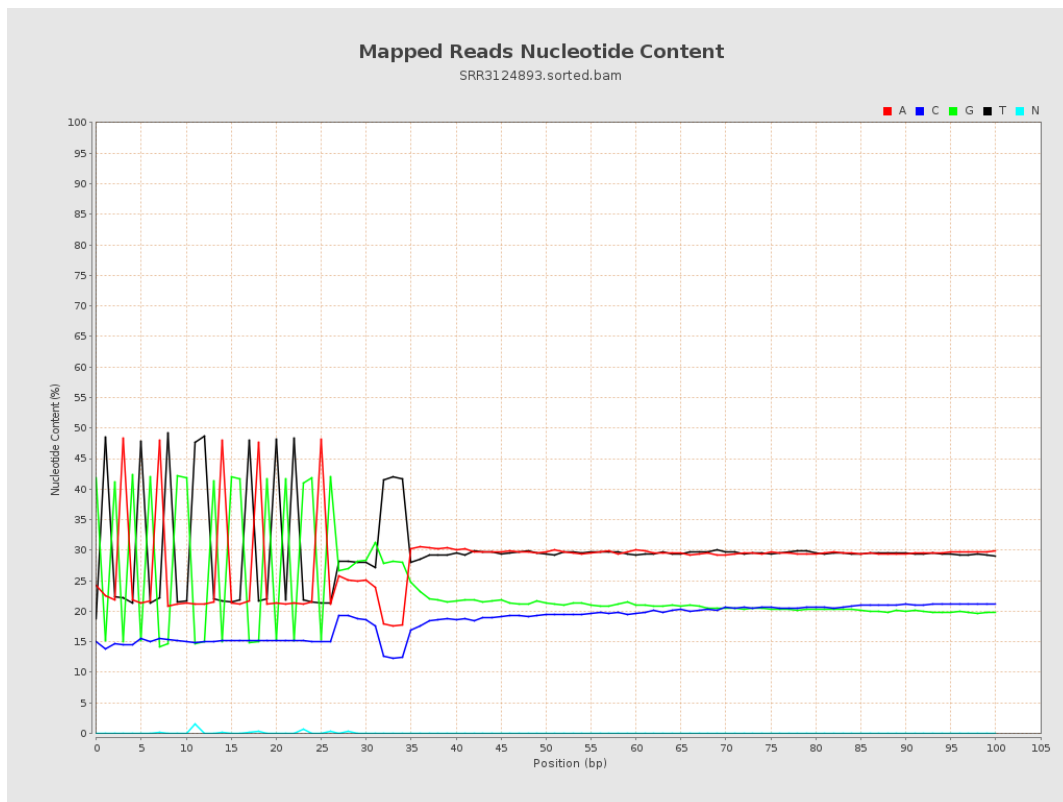
6. Results : Genome Fraction Coverage



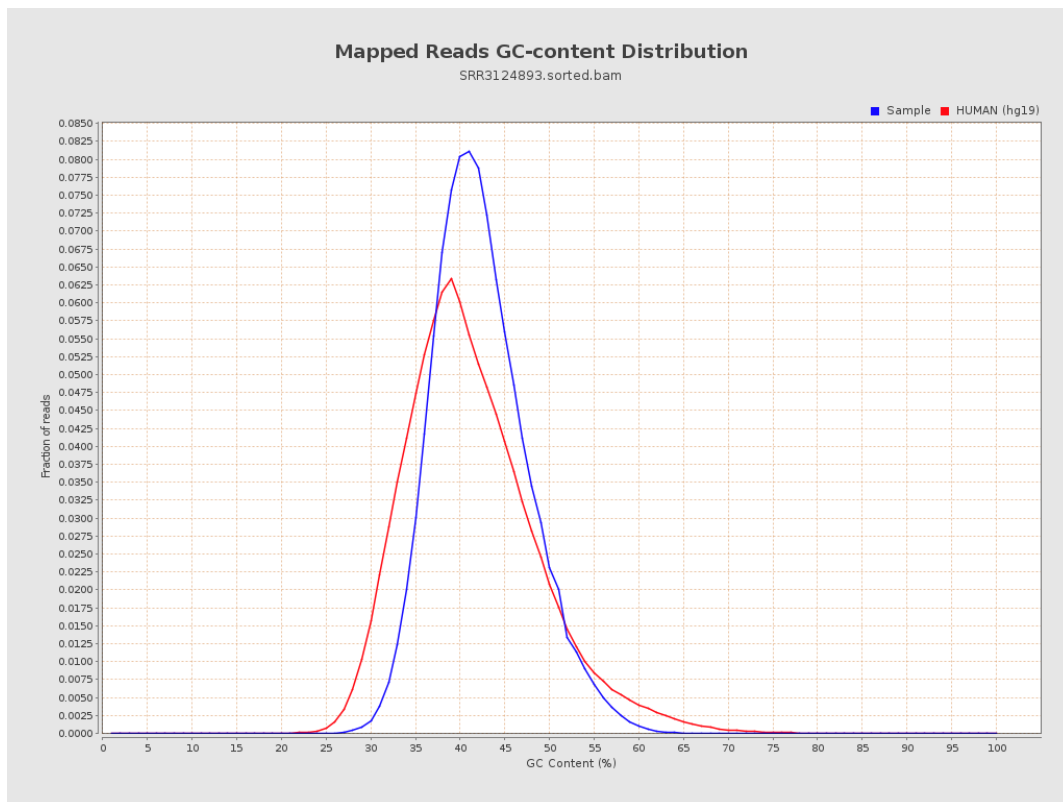
7. Results : Duplication Rate Histogram



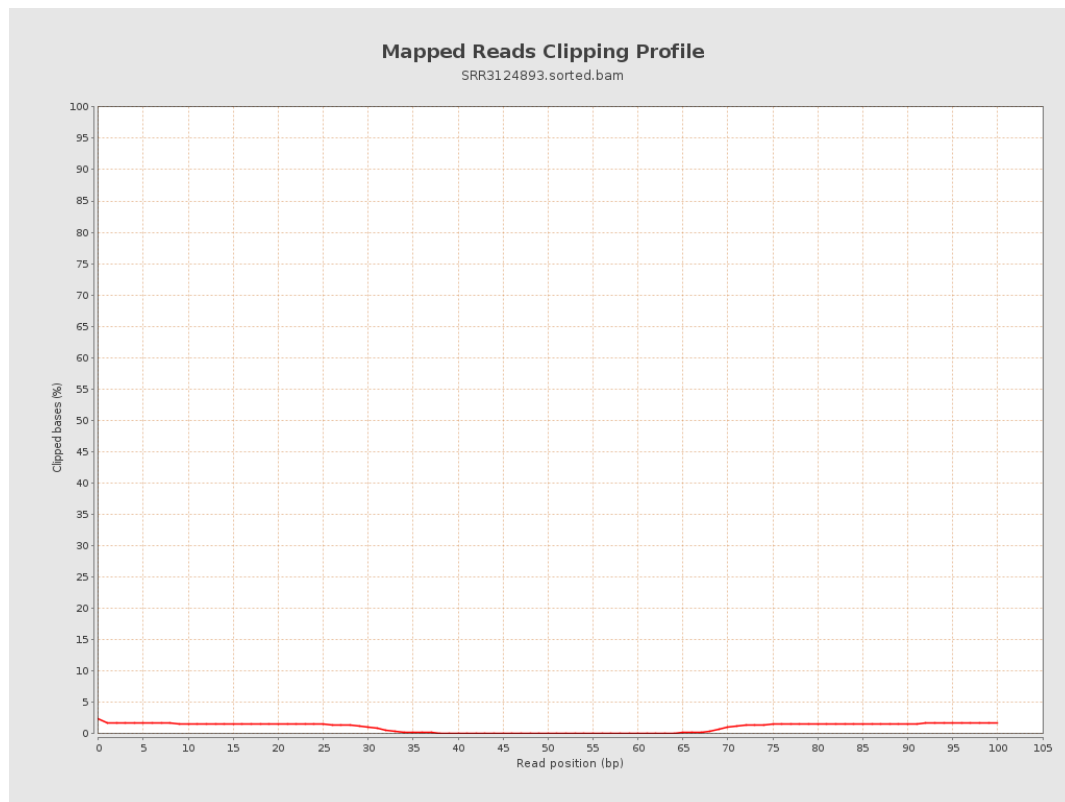
8. Results : Mapped Reads Nucleotide Content



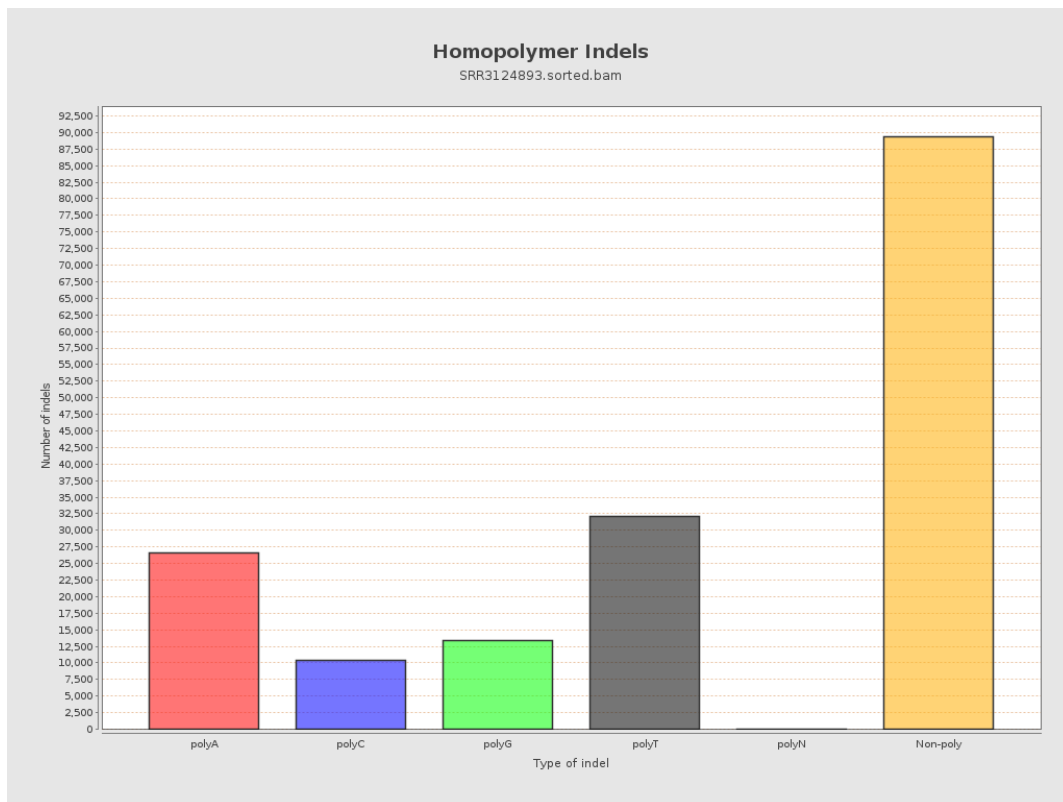
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



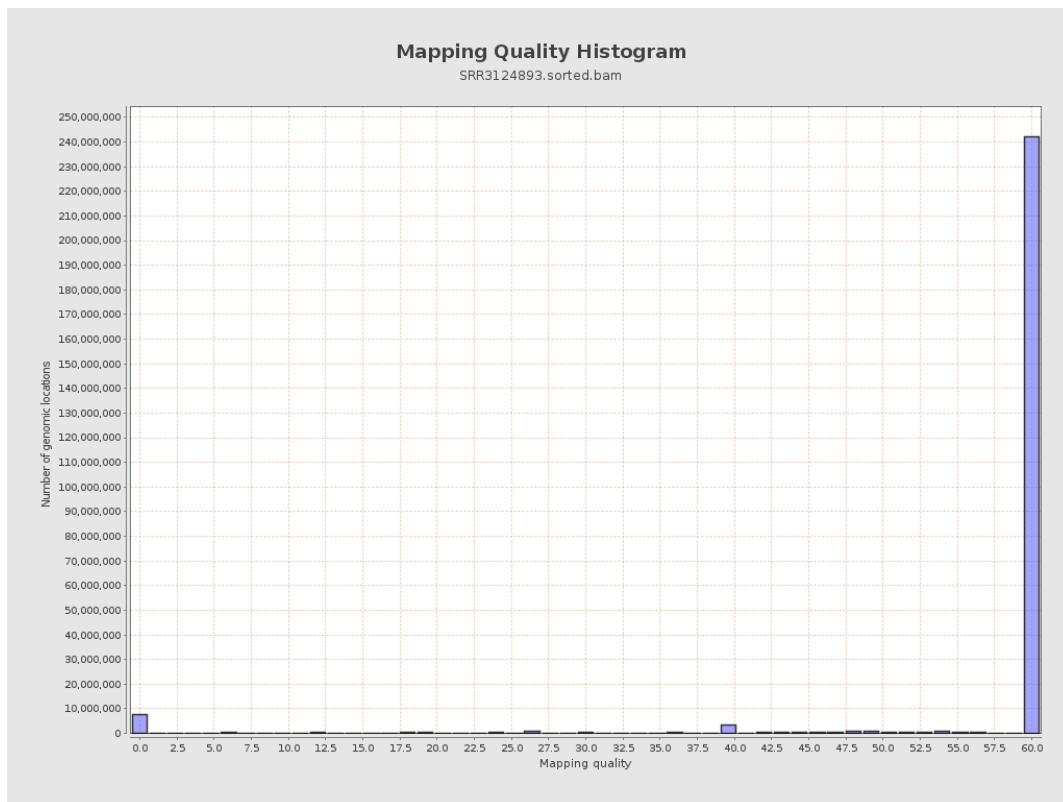
11. Results : Homopolymer Indels



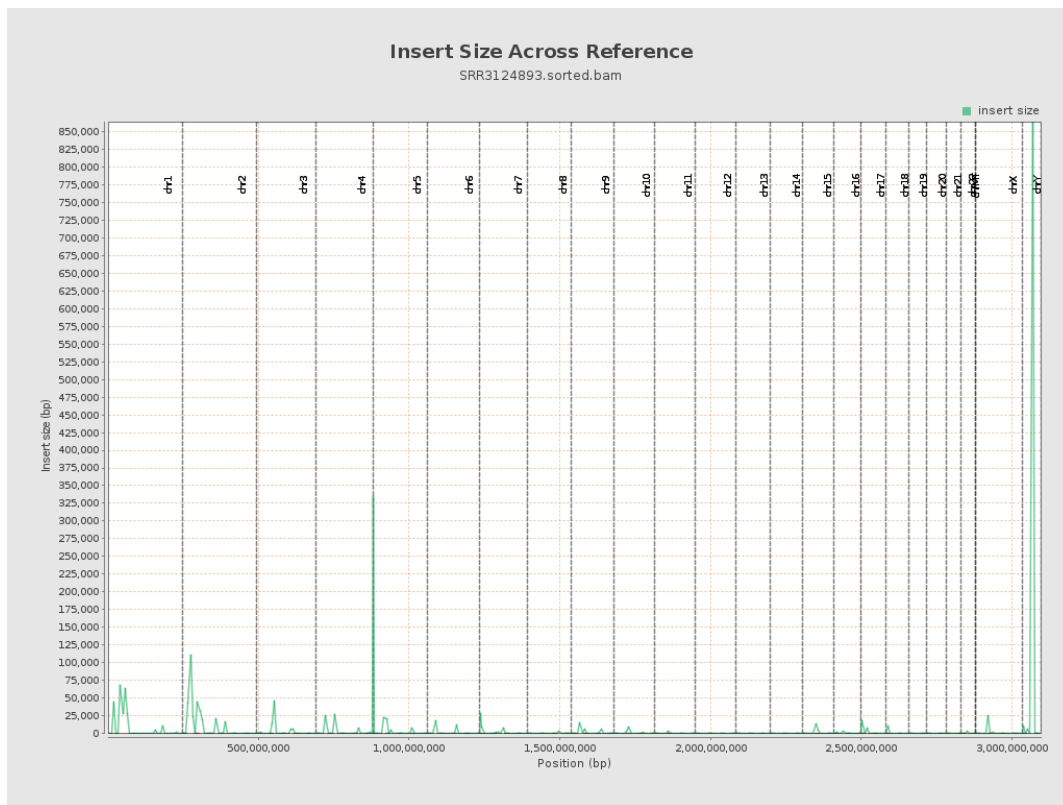
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

