

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:54:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124931.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_SRR3124931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124931_1.fastq.gz SRR3124931_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:54:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,290,218
Mapped reads	4,227,130 / 98.53%
Unmapped reads	63,088 / 1.47%
Mapped paired reads	4,227,130 / 98.53%
Mapped reads, first in pair	2,117,969 / 49.37%
Mapped reads, second in pair	2,109,161 / 49.16%
Mapped reads, both in pair	4,207,008 / 98.06%
Mapped reads, singletons	20,122 / 0.47%
Secondary alignments	0
Supplementary alignments	19,669 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	342,524 / 7.98%
Duplication rate	5.05%
Clipped reads	2,109,499 / 49.17%

2.2. ACGT Content

Number/percentage of A's	103,966,115 / 28.28%
Number/percentage of C's	68,284,172 / 18.58%
Number/percentage of T's	110,021,661 / 29.93%
Number/percentage of G's	85,284,488 / 23.2%
Number/percentage of N's	11,869 / 0%

GC Percentage	41.78%
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2.3. Coverage

Mean	0.1188
Standard Deviation	1.4087

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	36,454.78
Standard Deviation	1,777,525.58
P25/Median/P75	142 / 189 / 262

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	2,696,410
Insertions	52,206
Mapped reads with at least one insertion	1.2%
Deletions	115,582
Mapped reads with at least one deletion	2.68%
Homopolymer indels	46.63%

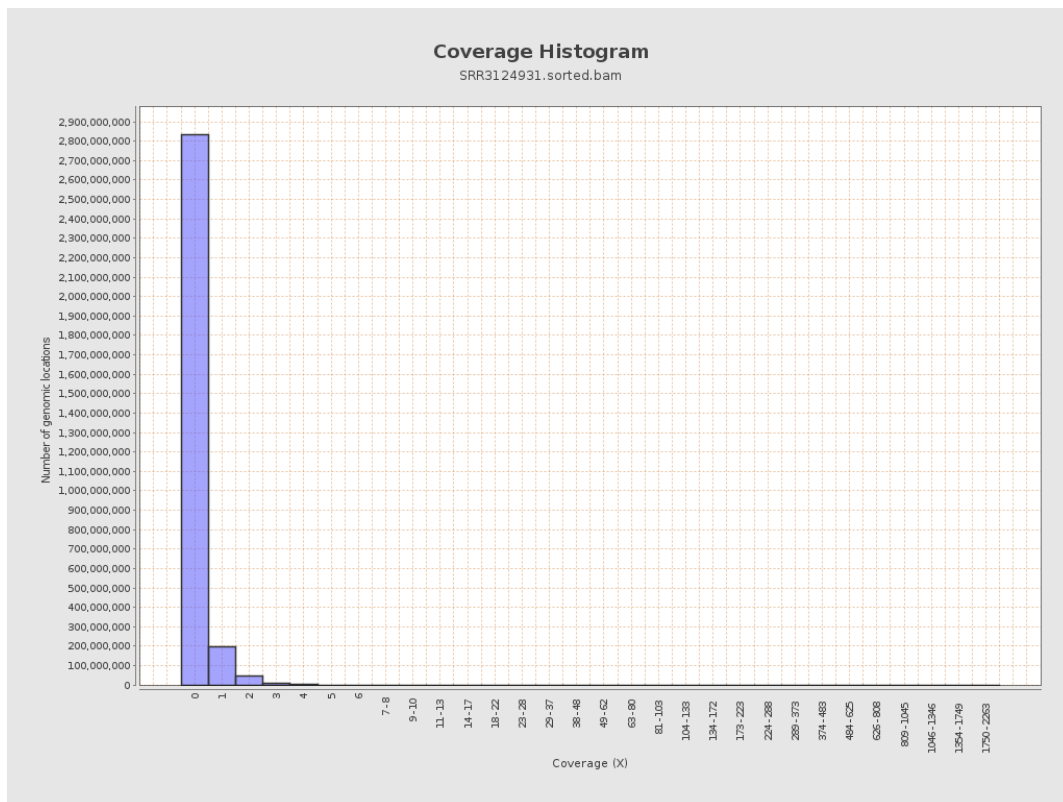
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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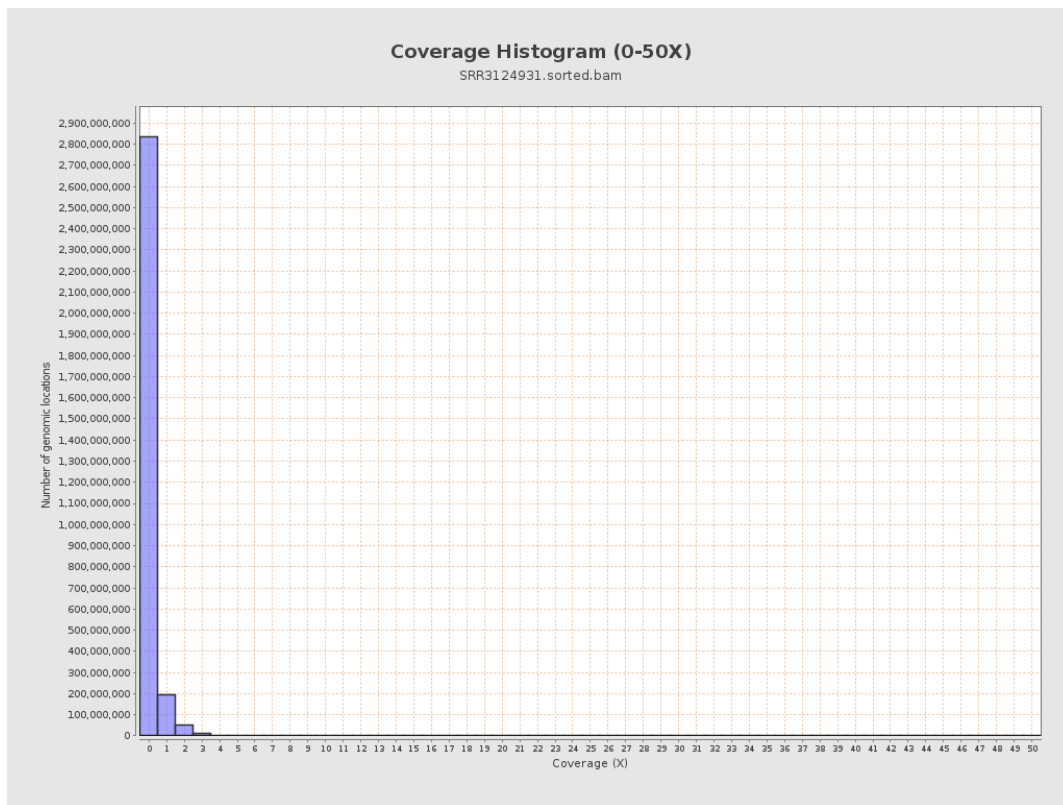
		bases	coverage	deviation
chr1	249250621	29461631	0.1182	1.2533
chr2	243199373	33682540	0.1385	1.4703
chr3	198022430	31434872	0.1587	0.5204
chr4	191154276	23221041	0.1215	0.7279
chr5	180915260	16560177	0.0915	0.4504
chr6	171115067	23422843	0.1369	3.6339
chr7	159138663	19668236	0.1236	1.1507
chr8	146364022	24148703	0.165	0.651
chr9	141213431	20784929	0.1472	1.5794
chr10	135534747	17459380	0.1288	2.4735
chr11	135006516	14175097	0.105	1.3449
chr12	133851895	16555012	0.1237	0.5111
chr13	115169878	8250269	0.0716	0.3285
chr14	107349540	8031285	0.0748	0.4164
chr15	102531392	13433112	0.131	0.4772
chr16	90354753	12441280	0.1377	2.1882
chr17	81195210	7151622	0.0881	0.9774
chr18	78077248	7488232	0.0959	1.5069
chr19	59128983	3805222	0.0644	0.9061
chr20	63025520	9928776	0.1575	0.547
chr21	48129895	4904380	0.1019	0.6132
chr22	51304566	5113784	0.0997	0.4263
chrMT	16571	87800	5.2984	3.5319
chrX	155270560	15087726	0.0972	0.6445

chrY	59373566	1470410	0.0248	1.5206
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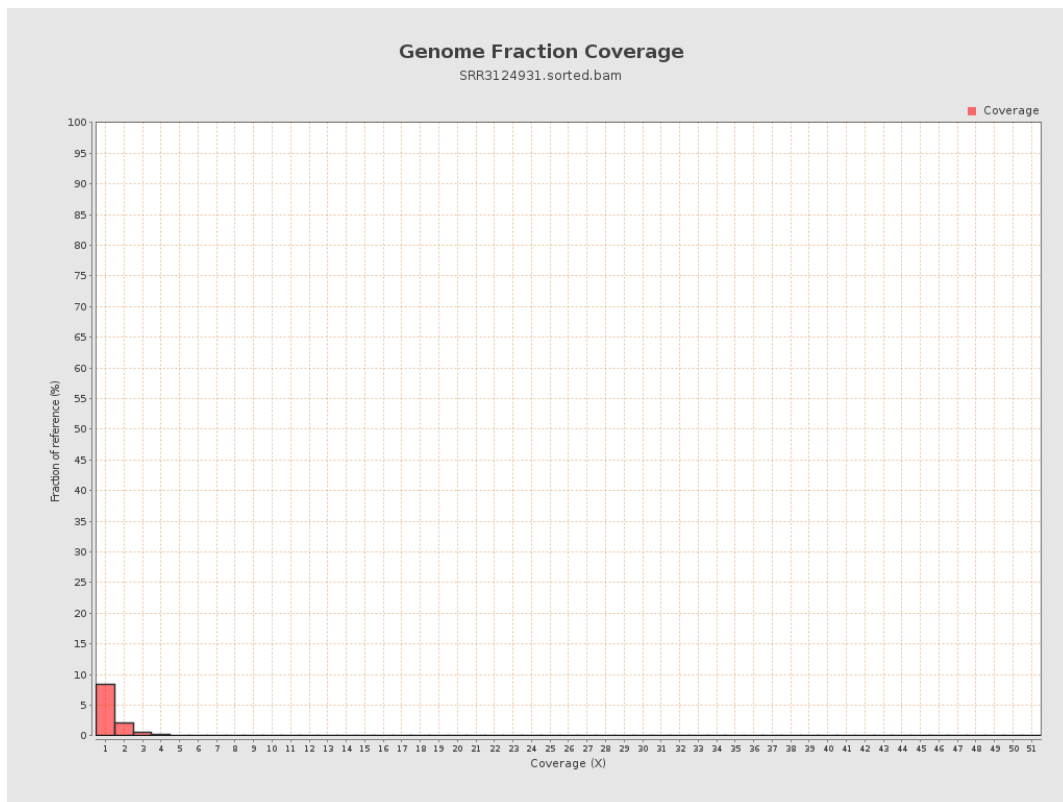
4. Results : Coverage Histogram



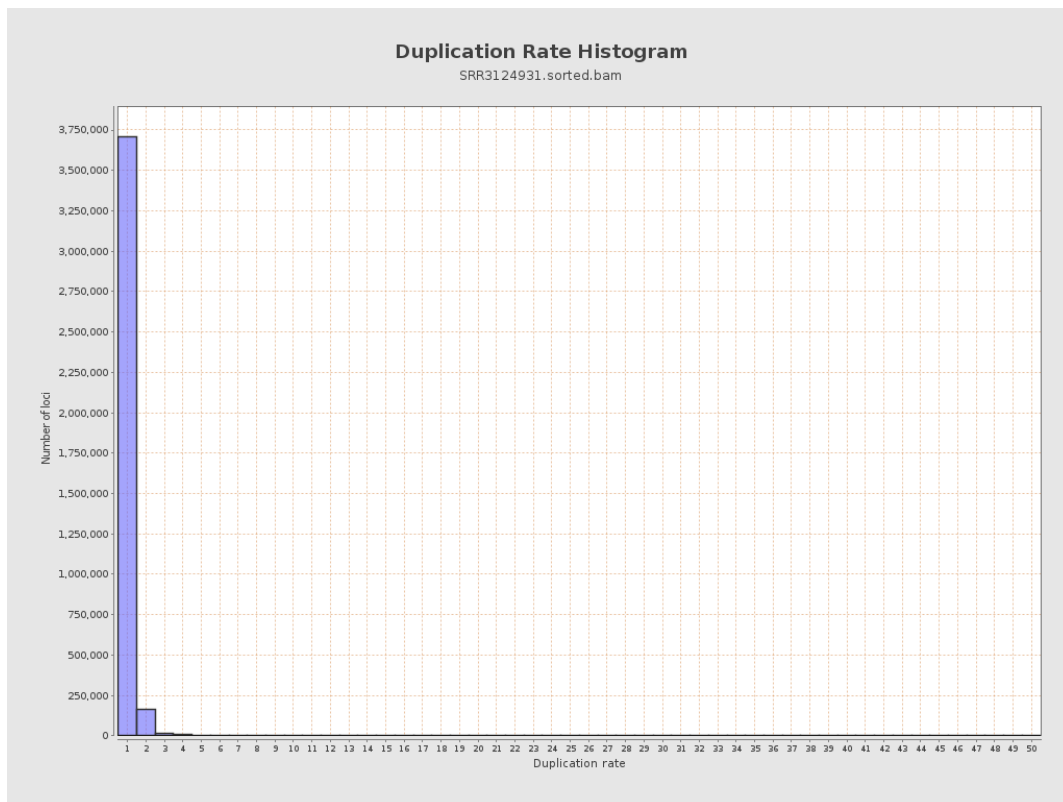
5. Results : Coverage Histogram (0-50X)



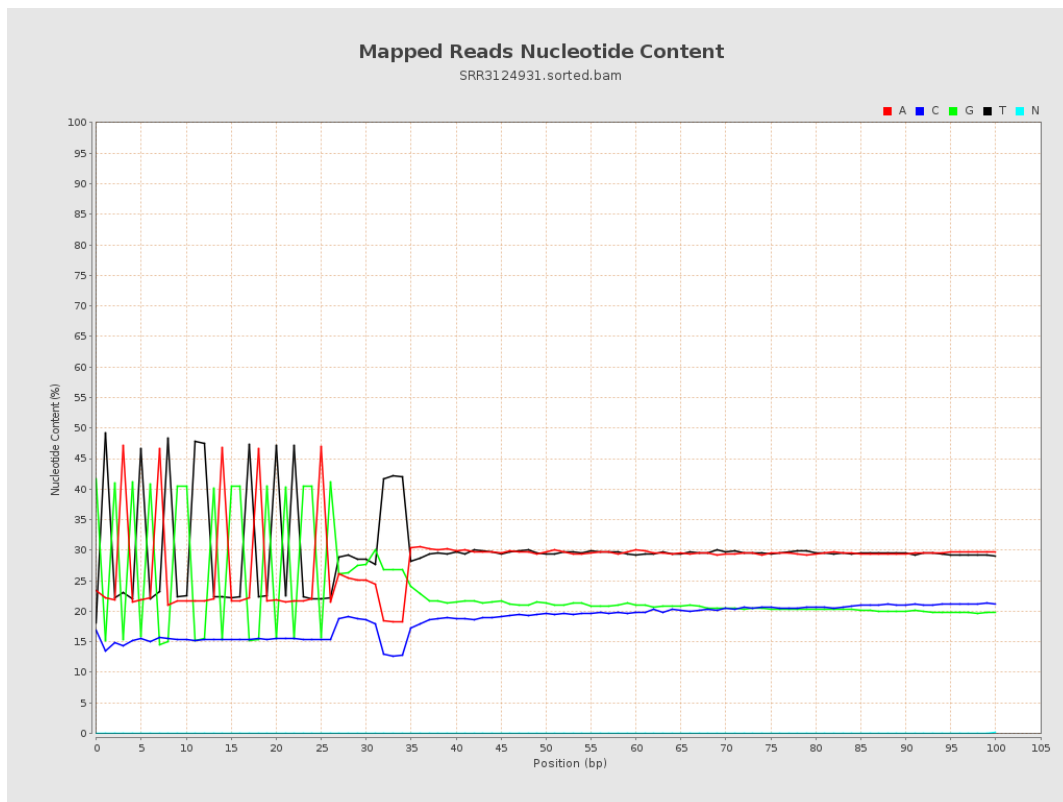
6. Results : Genome Fraction Coverage



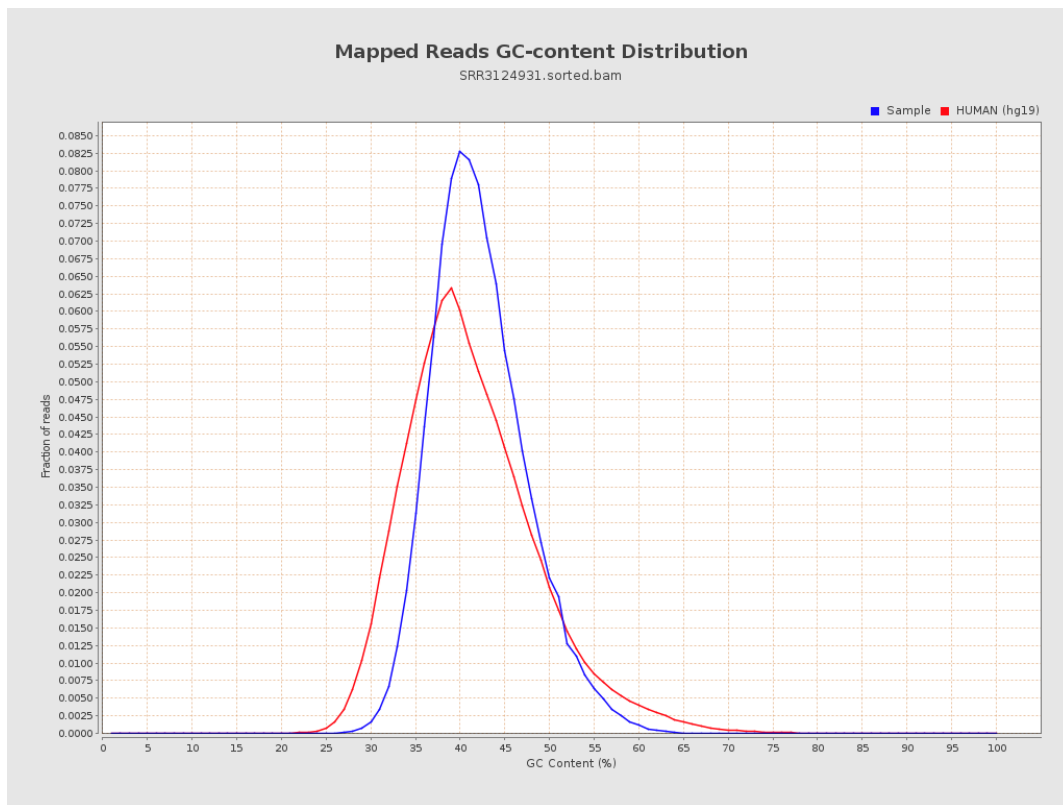
7. Results : Duplication Rate Histogram



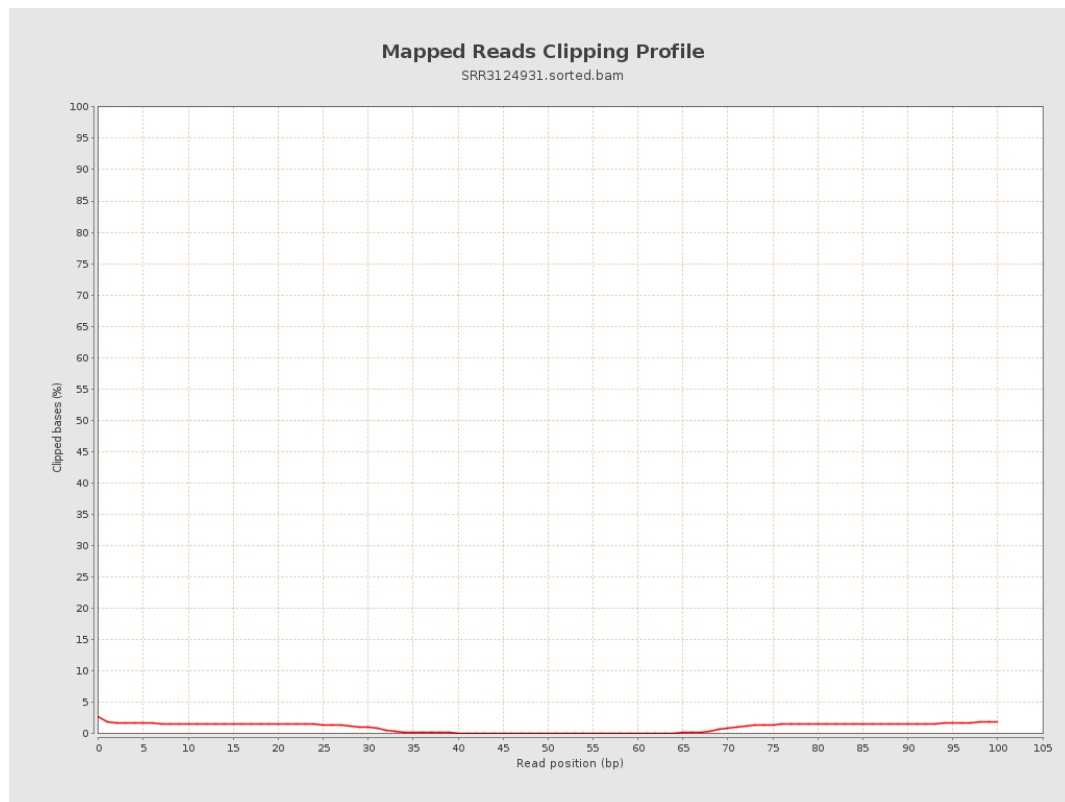
8. Results : Mapped Reads Nucleotide Content



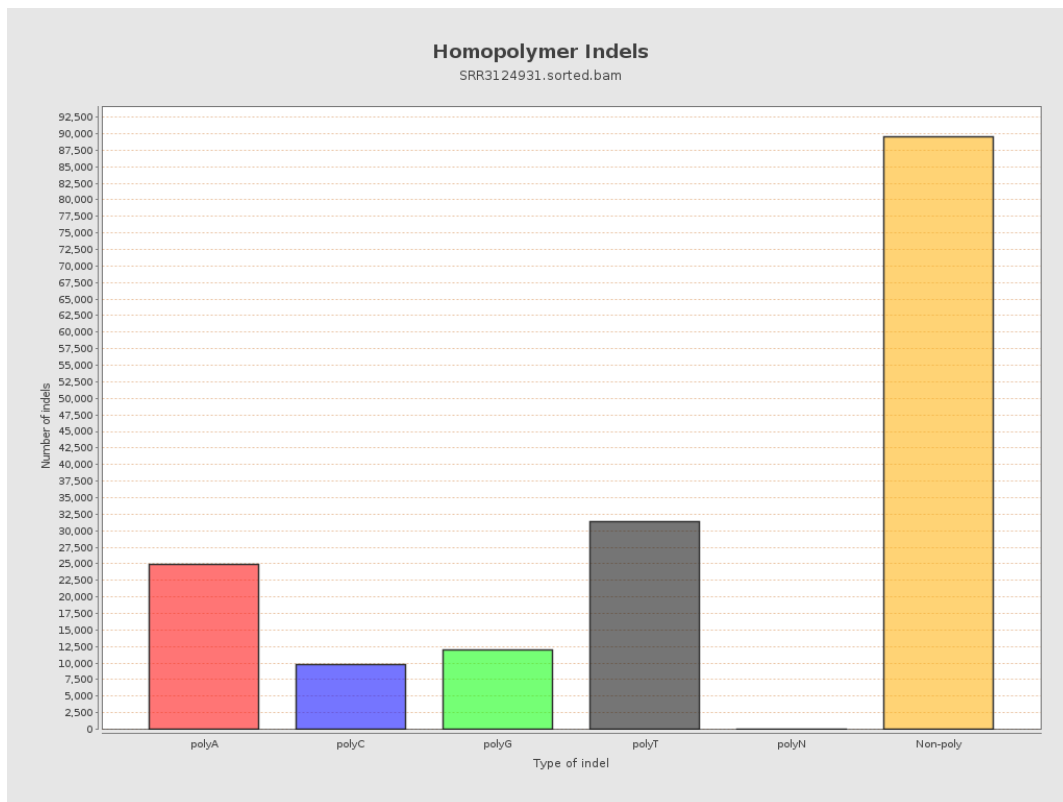
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



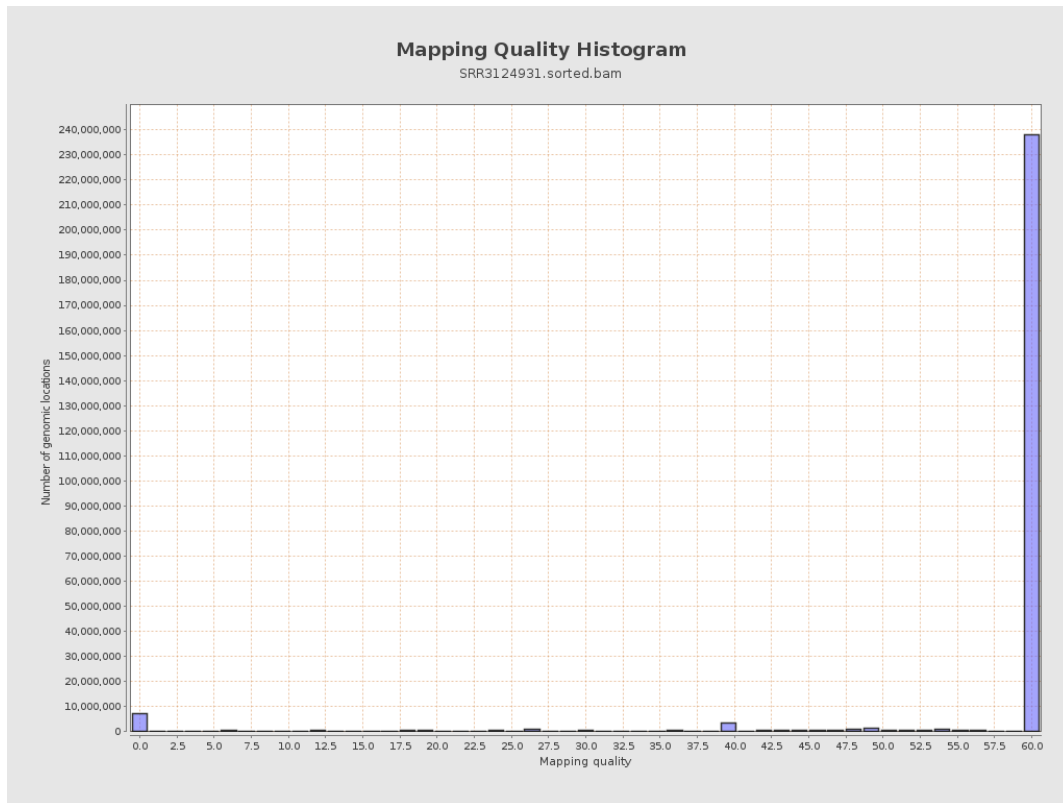
11. Results : Homopolymer Indels



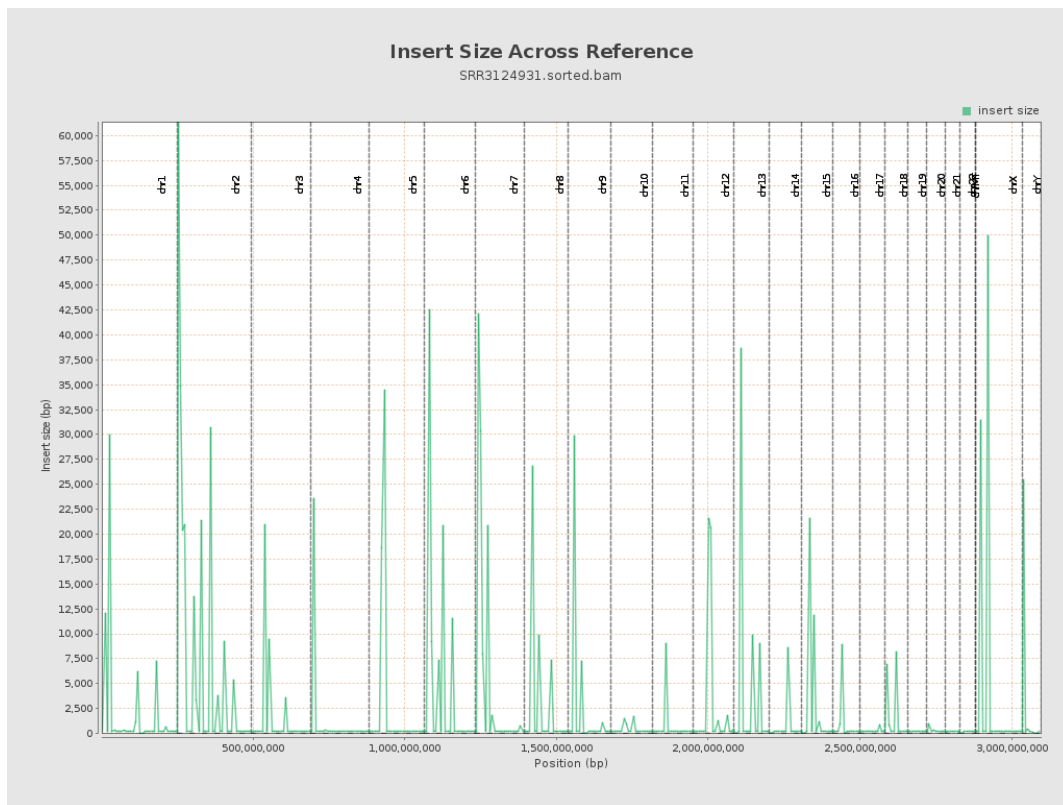
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

