

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 16:43:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124811.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_SRR3124811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124811_1.fastq.gz SRR3124811_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 16:43:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	71,946,268
Mapped reads	71,904,414 / 99.94%
Unmapped reads	41,854 / 0.06%
Mapped paired reads	71,904,414 / 99.94%
Mapped reads, first in pair	35,953,238 / 49.97%
Mapped reads, second in pair	35,951,176 / 49.97%
Mapped reads, both in pair	71,886,856 / 99.92%
Mapped reads, singletons	17,558 / 0.02%
Secondary alignments	0
Supplementary alignments	25,751 / 0.04%
Read min/max/mean length	30 / 101 / 101.01
Duplicated reads (estimated)	28,923,149 / 40.2%
Duplication rate	37.83%
Clipped reads	35,619,101 / 49.51%

2.2. ACGT Content

Number/percentage of A's	1,844,582,462 / 26.16%
Number/percentage of C's	1,659,186,933 / 23.53%
Number/percentage of T's	1,907,113,779 / 27.05%
Number/percentage of G's	1,640,505,229 / 23.26%
Number/percentage of N's	79,282 / 0%

GC Percentage	46.79%
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2.3. Coverage

Mean	2.2781
Standard Deviation	15.9521

2.4. Mapping Quality

Mean Mapping Quality	55.78
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2.5. Insert size

Mean	84,747.29
Standard Deviation	2,904,062.84
P25/Median/P75	156 / 193 / 243

2.6. Mismatches and indels

General error rate	0.18%
Mismatches	11,716,881
Insertions	393,258
Mapped reads with at least one insertion	0.54%
Deletions	335,044
Mapped reads with at least one deletion	0.46%
Homopolymer indels	39.35%

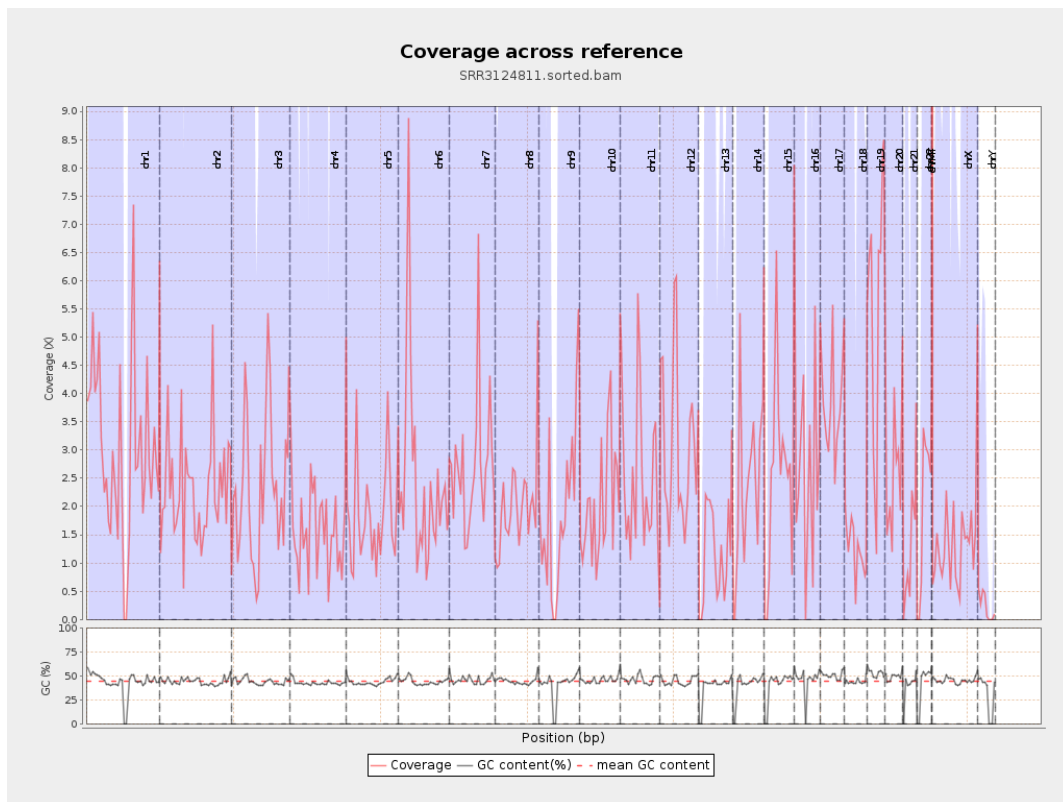
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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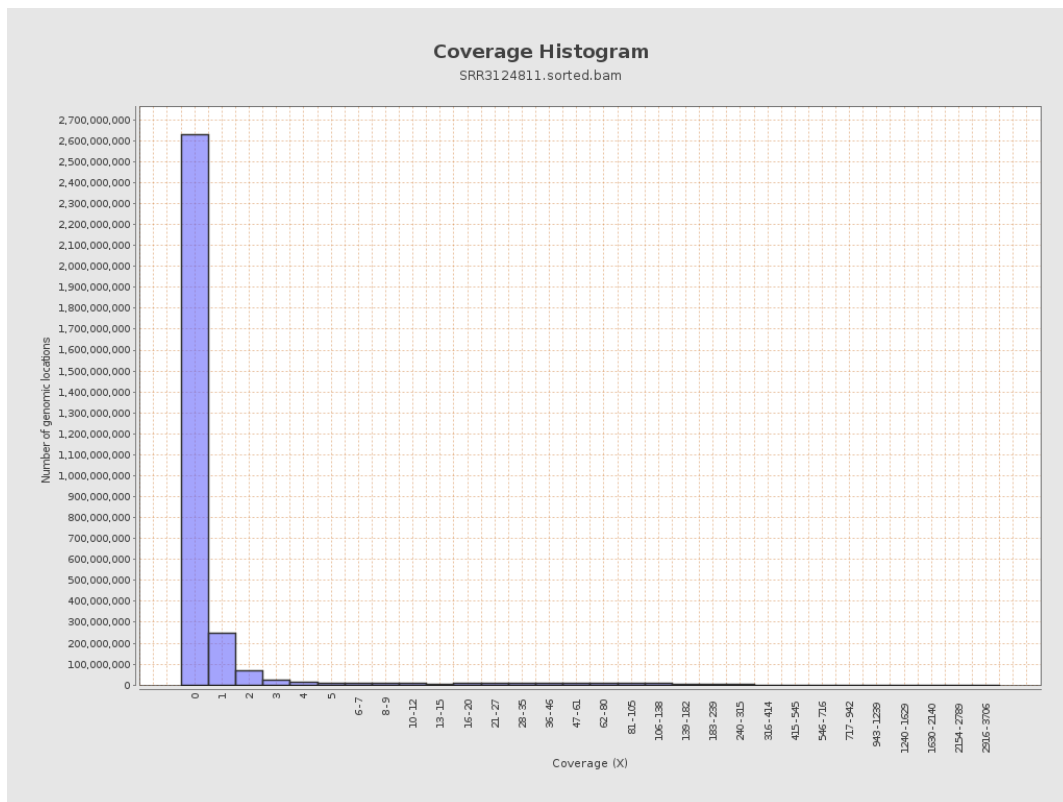
		bases	coverage	deviation
chr1	249250621	755811845	3.0323	19.1056
chr2	243199373	563039834	2.3151	16.4404
chr3	198022430	461025828	2.3281	17.0002
chr4	191154276	297721906	1.5575	13.1555
chr5	180915260	339754910	1.878	14.6915
chr6	171115067	407603088	2.382	17.1513
chr7	159138663	434136255	2.728	19.6761
chr8	146364022	299213492	2.0443	16.6336
chr9	141213431	271623752	1.9235	14.049
chr10	135534747	275038182	2.0293	14.6162
chr11	135006516	354237503	2.6239	16.065
chr12	133851895	409959241	3.0628	18.6546
chr13	115169878	132973506	1.1546	10.894
chr14	107349540	252478944	2.3519	16.4306
chr15	102531392	248683939	2.4254	16.4379
chr16	90354753	256588847	2.8398	16.4799
chr17	81195210	311598596	3.8376	18.2369
chr18	78077248	96834509	1.2402	10.3948
chr19	59128983	333649574	5.6427	22.2593
chr20	63025520	164627936	2.6121	16.7869
chr21	48129895	63276903	1.3147	11.3005
chr22	51304566	106243337	2.0708	12.3225
chrMT	16571	1318206	79.549	19.6016
chrX	155270560	200809407	1.2933	10.3812

chrY	59373566	13958070	0.2351	3.6972
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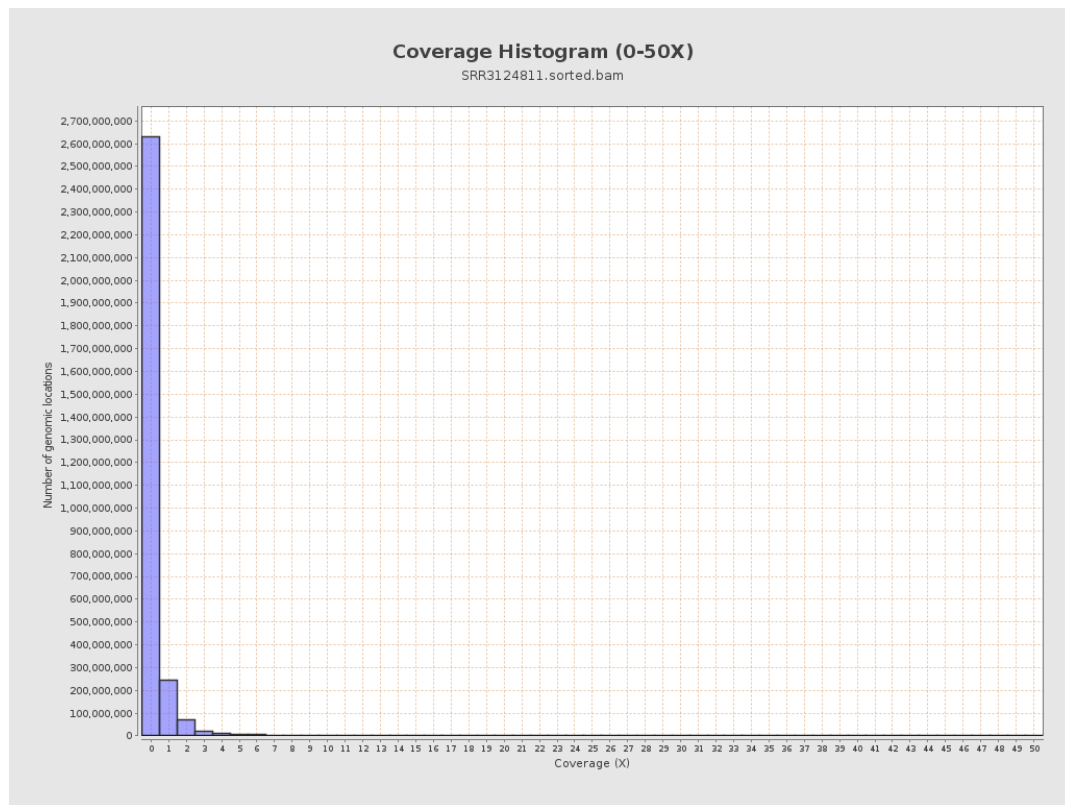
3. Results : Coverage across reference



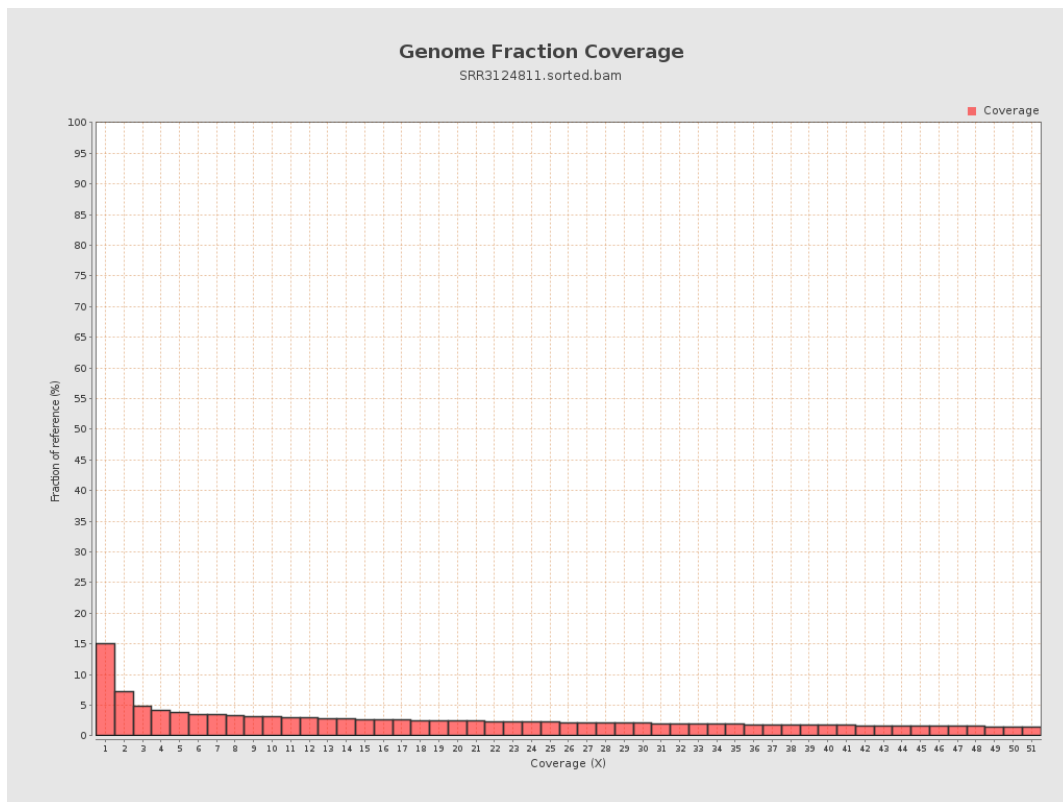
4. Results : Coverage Histogram



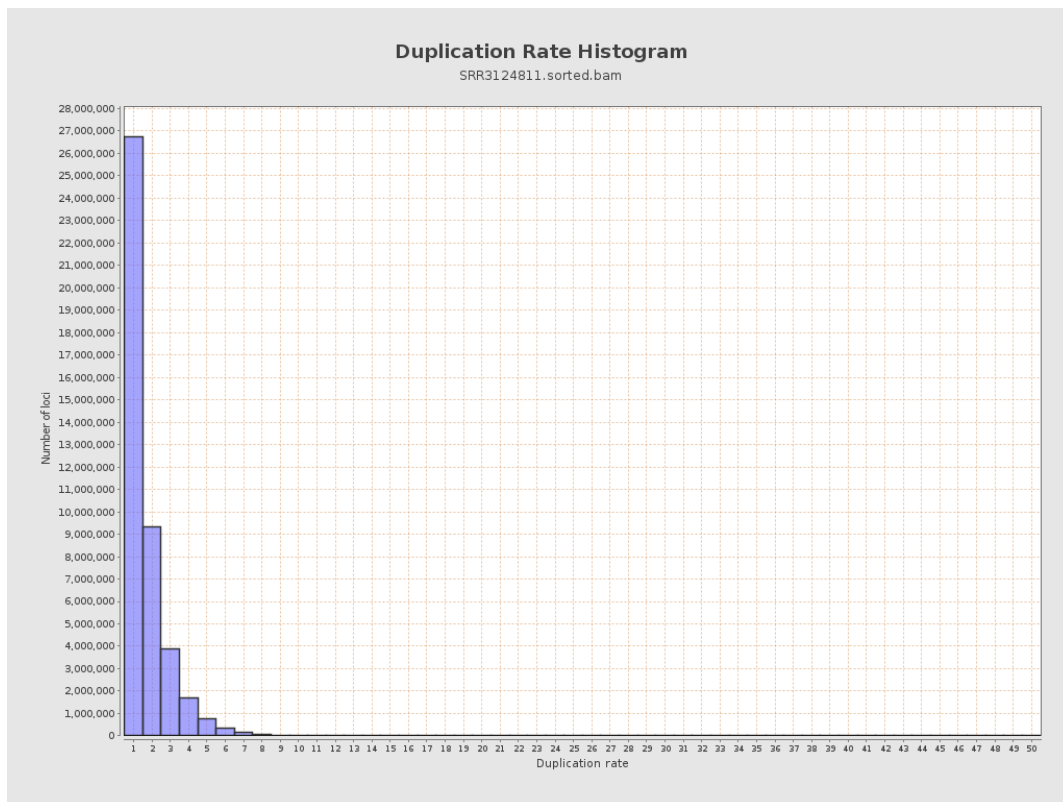
5. Results : Coverage Histogram (0-50X)



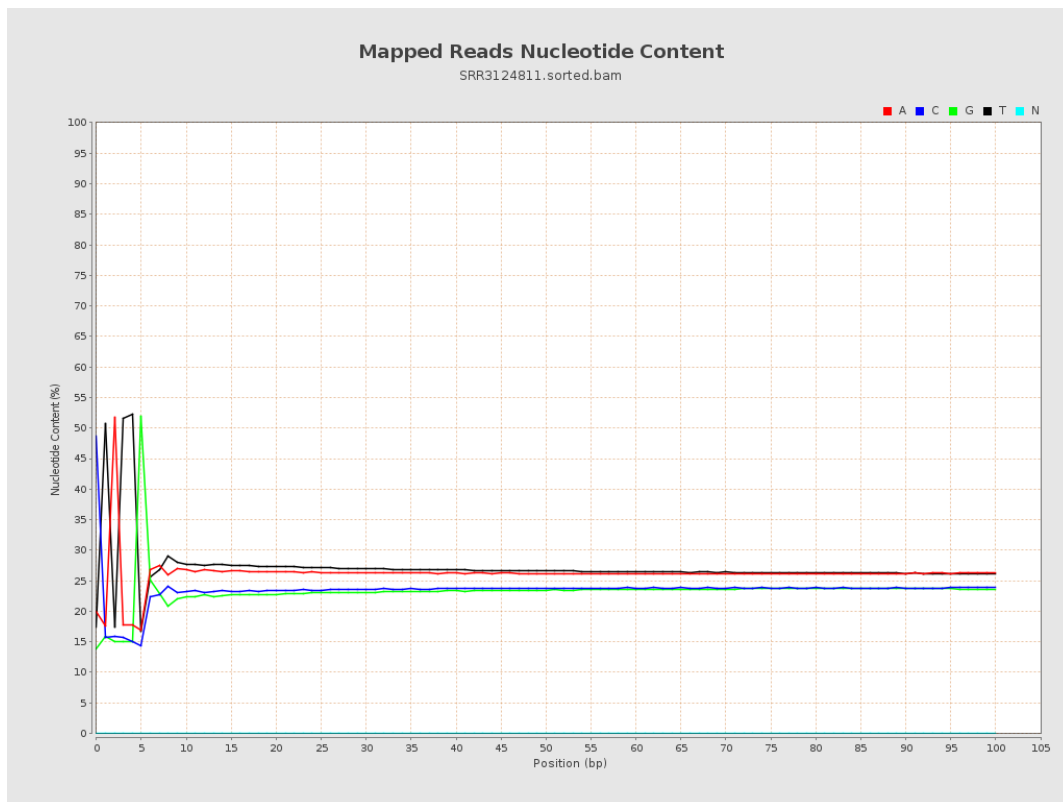
6. Results : Genome Fraction Coverage



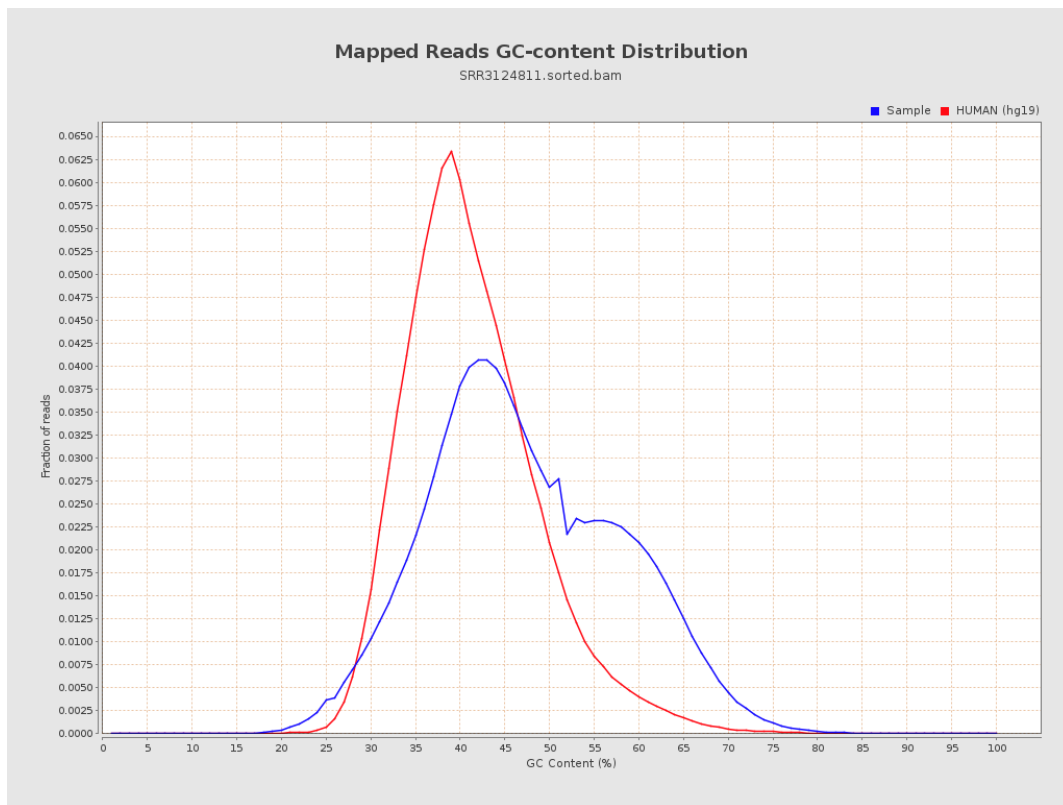
7. Results : Duplication Rate Histogram



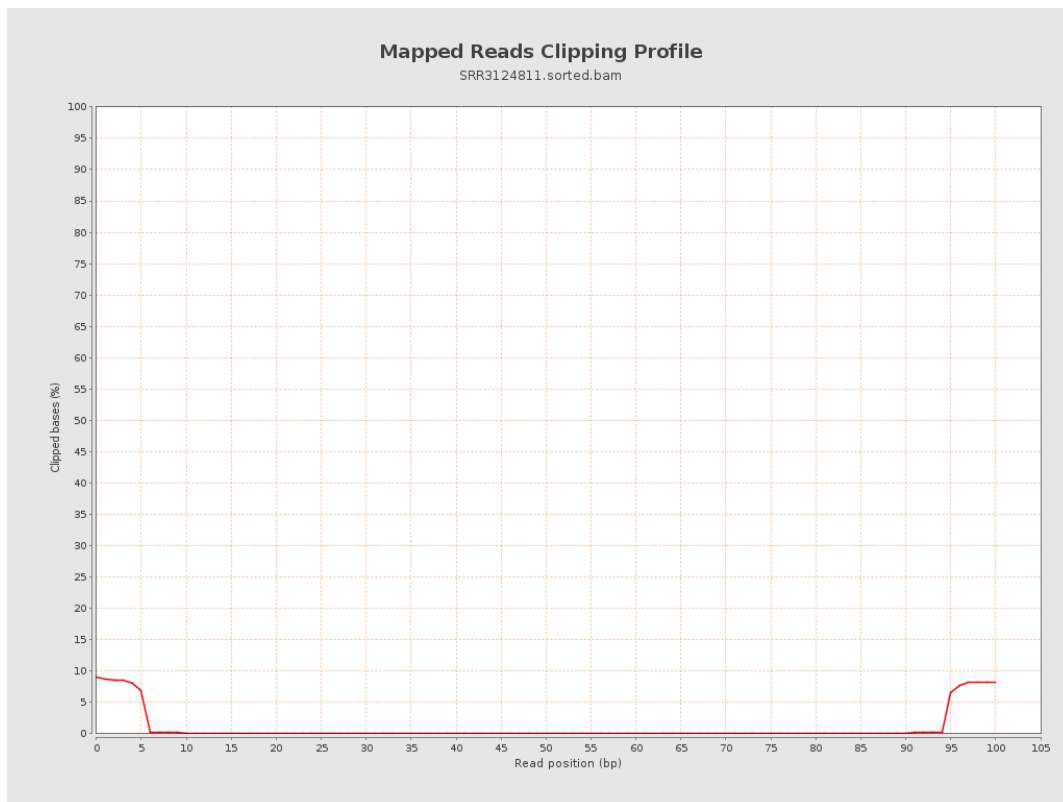
8. Results : Mapped Reads Nucleotide Content



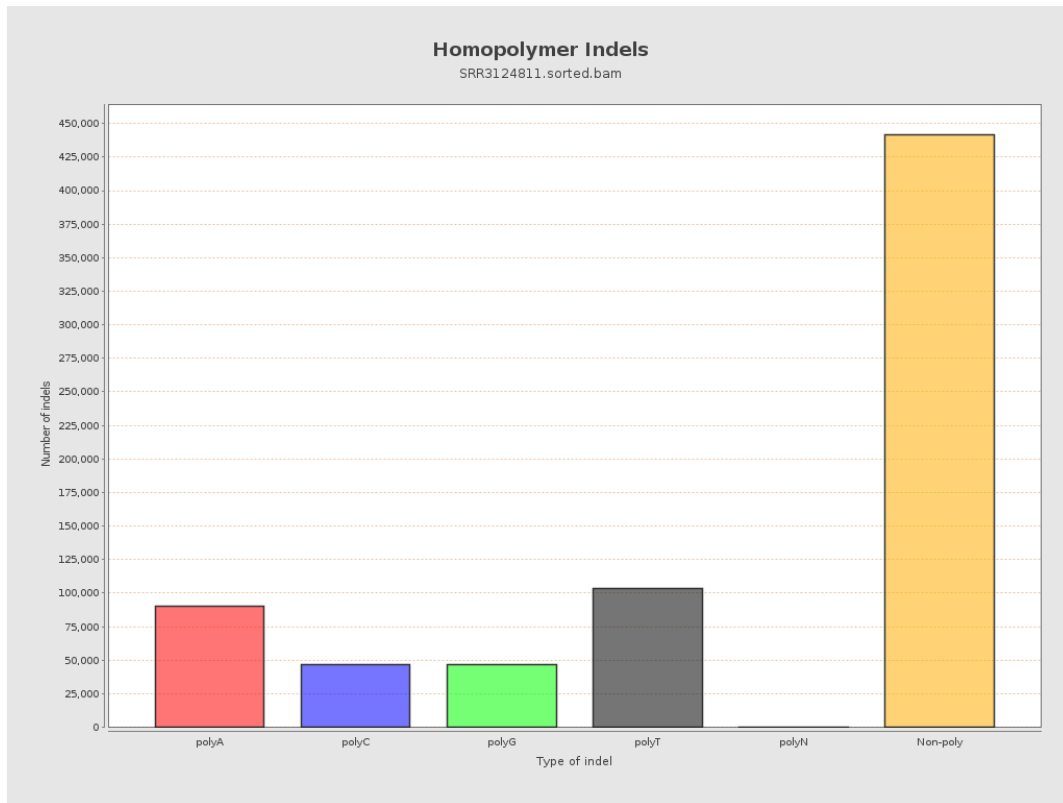
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



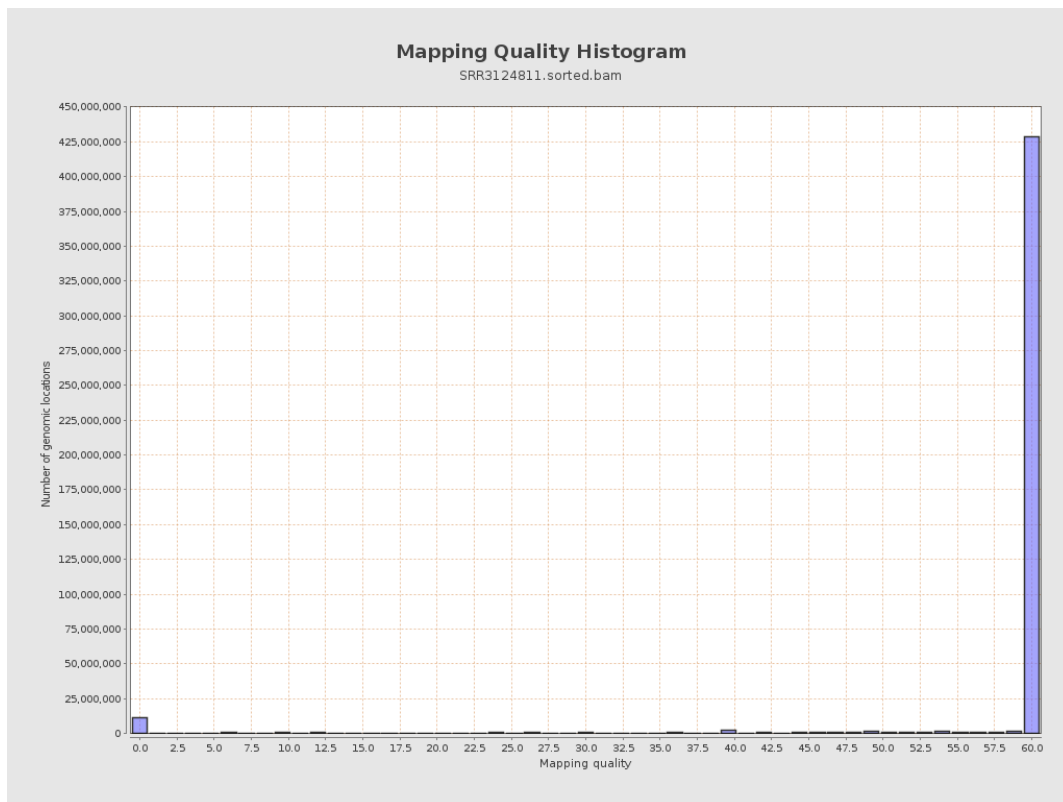
11. Results : Homopolymer Indels



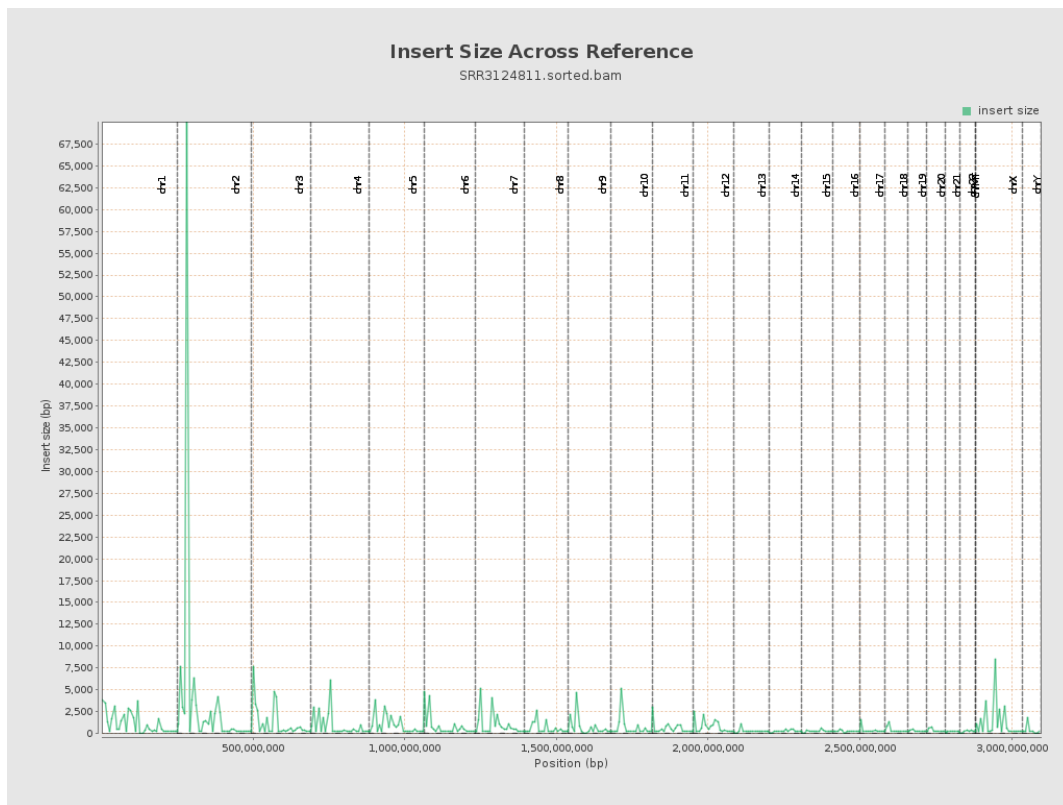
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

