

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:22:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124959.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_SRR3124959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124959_1.fastq.gz SRR3124959_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:22:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,564,644
Mapped reads	4,353,489 / 95.37%
Unmapped reads	211,155 / 4.63%
Mapped paired reads	4,353,489 / 95.37%
Mapped reads, first in pair	2,210,902 / 48.44%
Mapped reads, second in pair	2,142,587 / 46.94%
Mapped reads, both in pair	4,260,880 / 93.35%
Mapped reads, singletons	92,609 / 2.03%
Secondary alignments	0
Supplementary alignments	20,467 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	268,707 / 5.89%
Duplication rate	3.45%
Clipped reads	2,276,664 / 49.88%

2.2. ACGT Content

Number/percentage of A's	74,015,566 / 27.79%
Number/percentage of C's	47,169,225 / 17.71%
Number/percentage of T's	80,558,200 / 30.24%
Number/percentage of G's	64,629,717 / 24.26%
Number/percentage of N's	0 / 0%

GC Percentage	41.97%
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2.3. Coverage

Mean	0.0861
Standard Deviation	1.0767

2.4. Mapping Quality

Mean Mapping Quality	51.28
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2.5. Insert size

Mean	99,687.14
Standard Deviation	3,046,553.9
P25/Median/P75	121 / 165 / 229

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	1,881,365
Insertions	32,478
Mapped reads with at least one insertion	0.73%
Deletions	69,583
Mapped reads with at least one deletion	1.58%
Homopolymer indels	45.2%

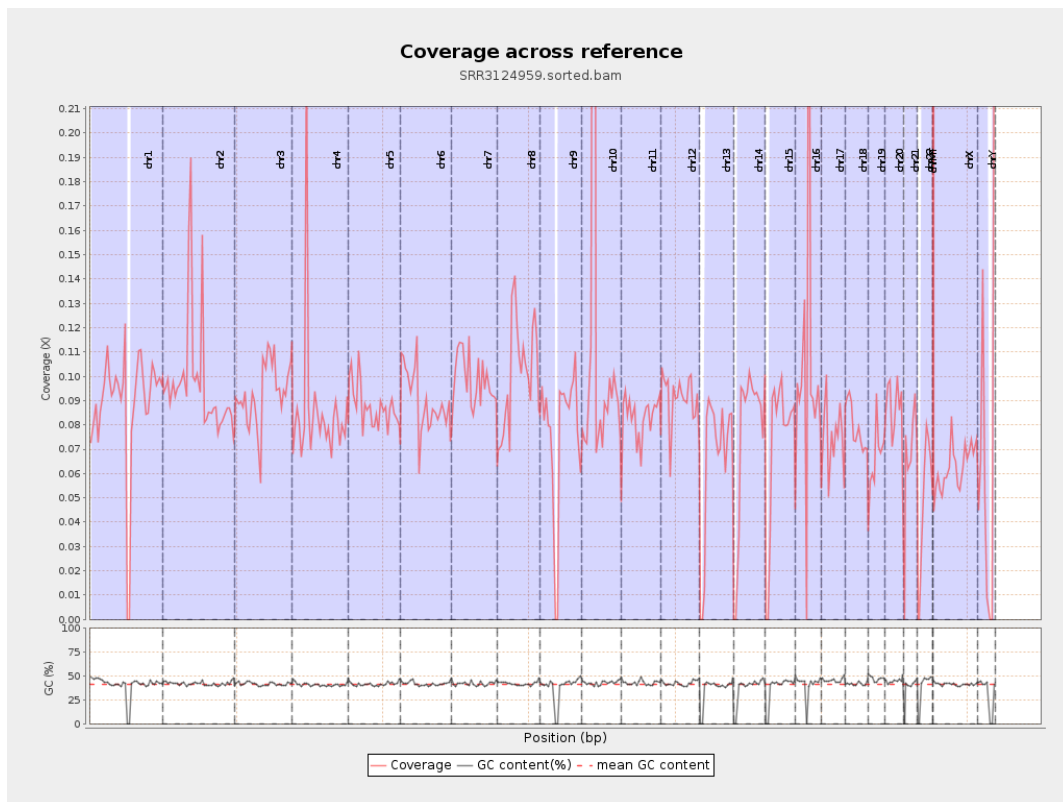
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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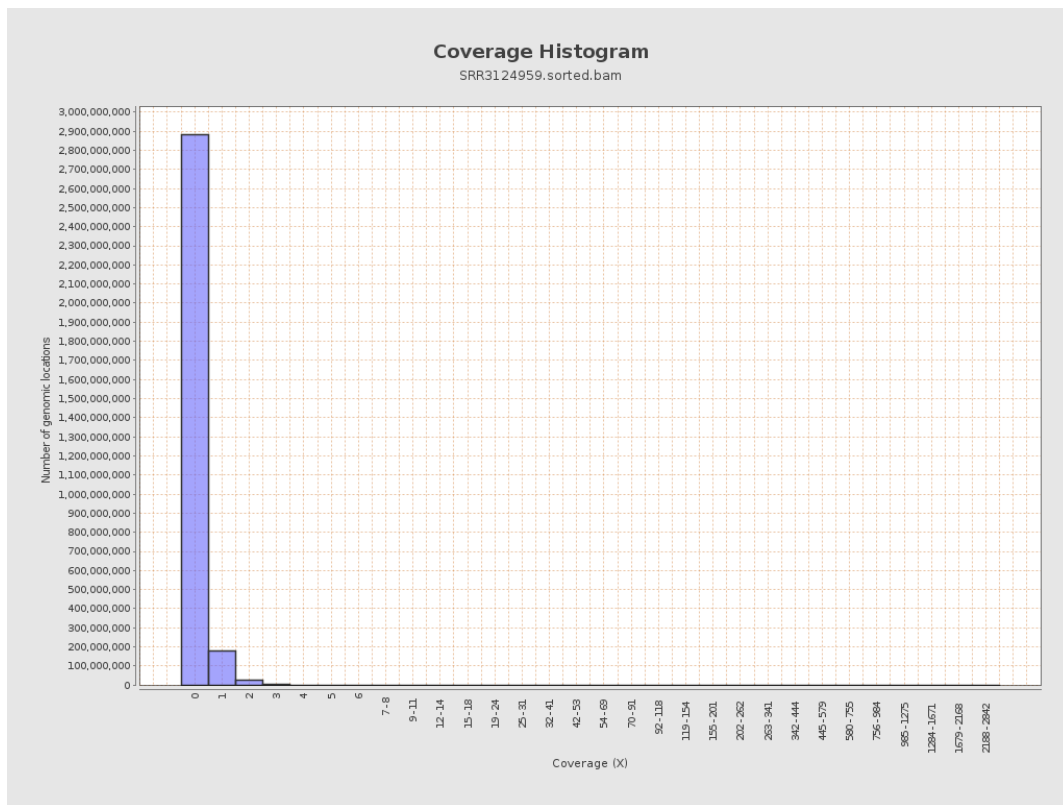
		bases	coverage	deviation
chr1	249250621	22185545	0.089	0.6624
chr2	243199373	23728287	0.0976	1.1423
chr3	198022430	18377081	0.0928	0.4343
chr4	191154276	16474675	0.0862	0.7859
chr5	180915260	15834951	0.0875	0.3618
chr6	171115067	15374392	0.0898	0.4397
chr7	159138663	15639240	0.0983	0.6462
chr8	146364022	14842085	0.1014	0.4202
chr9	141213431	10862341	0.0769	0.6216
chr10	135534747	15361545	0.1133	3.941
chr11	135006516	11201907	0.083	0.4416
chr12	133851895	12249248	0.0915	0.356
chr13	115169878	7589255	0.0659	0.2923
chr14	107349540	8167997	0.0761	0.3806
chr15	102531392	7330787	0.0715	0.3241
chr16	90354753	9538126	0.1056	1.7913
chr17	81195210	6144604	0.0757	0.5912
chr18	78077248	6179857	0.0792	0.8995
chr19	59128983	3972404	0.0672	0.5593
chr20	63025520	5502286	0.0873	0.5013
chr21	48129895	3267171	0.0679	0.4861
chr22	51304566	2506739	0.0489	0.3101
chrMT	16571	71185	4.2958	3.2988
chrX	155270560	9748396	0.0628	0.3725

chrY	59373566	4338266	0.0731	1.6623
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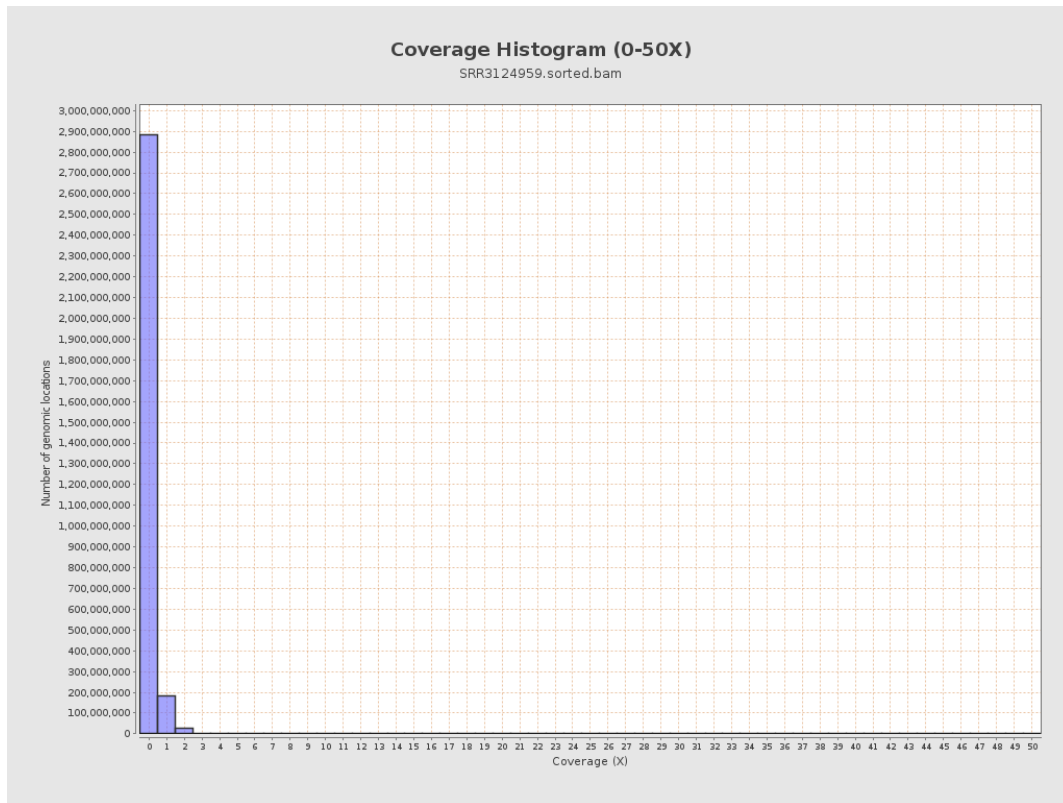
3. Results : Coverage across reference



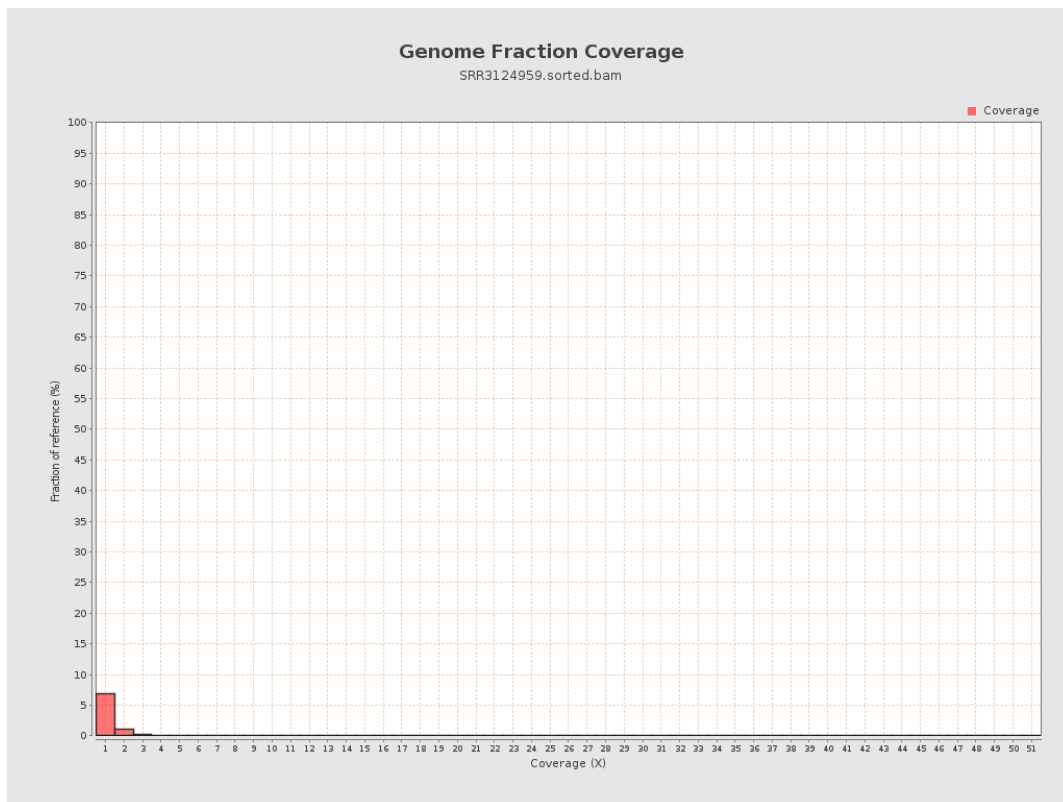
4. Results : Coverage Histogram



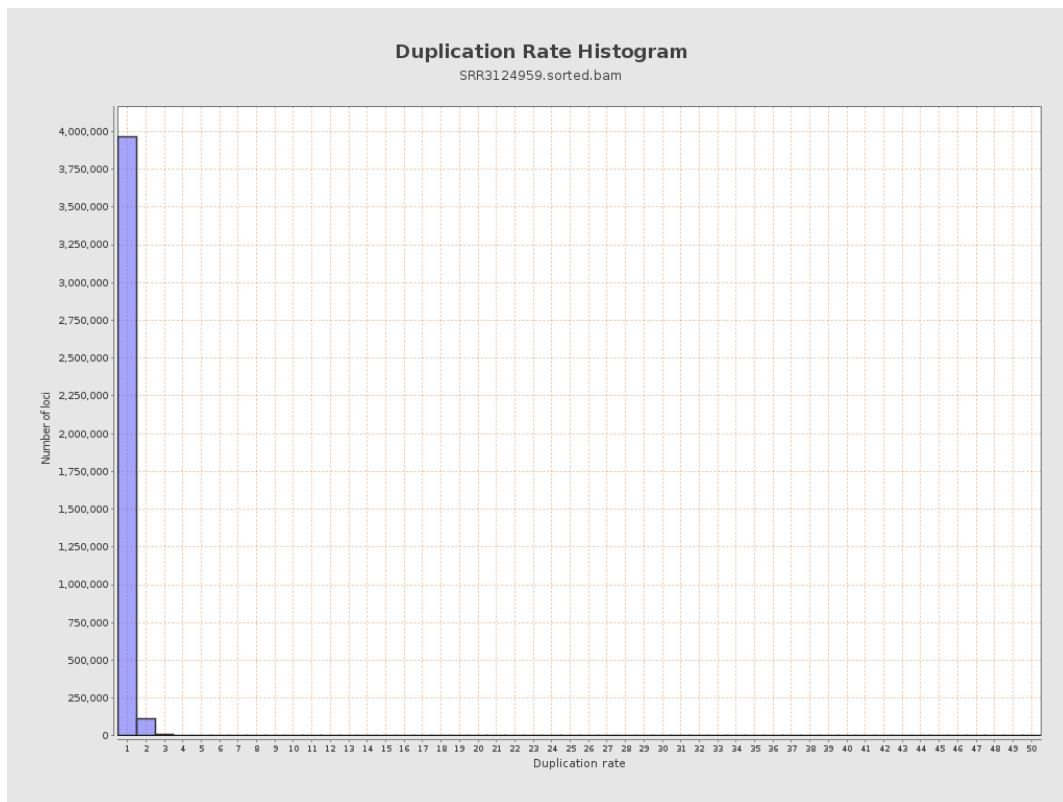
5. Results : Coverage Histogram (0-50X)



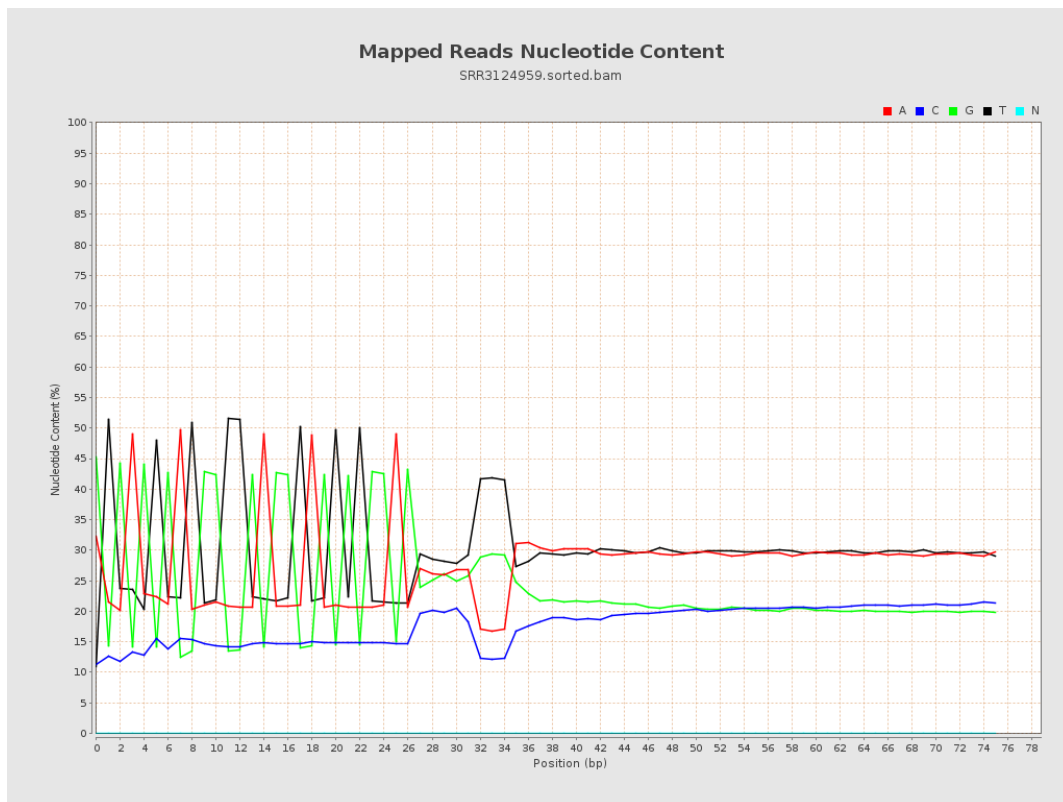
6. Results : Genome Fraction Coverage



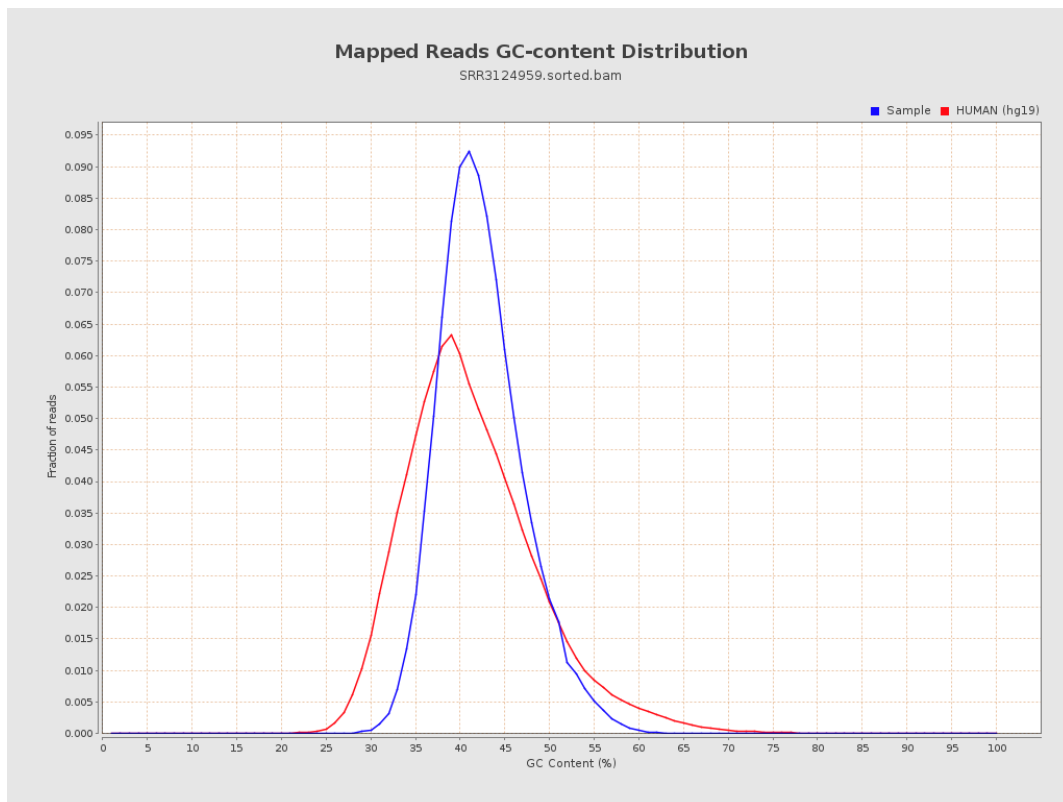
7. Results : Duplication Rate Histogram



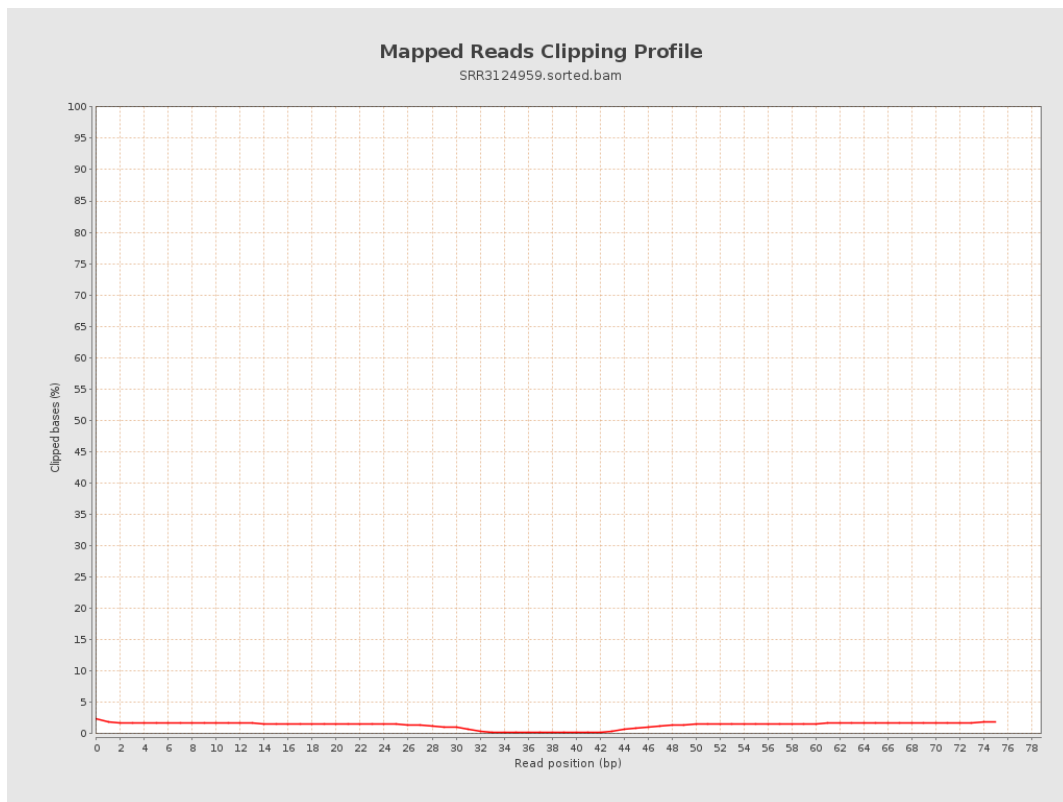
8. Results : Mapped Reads Nucleotide Content



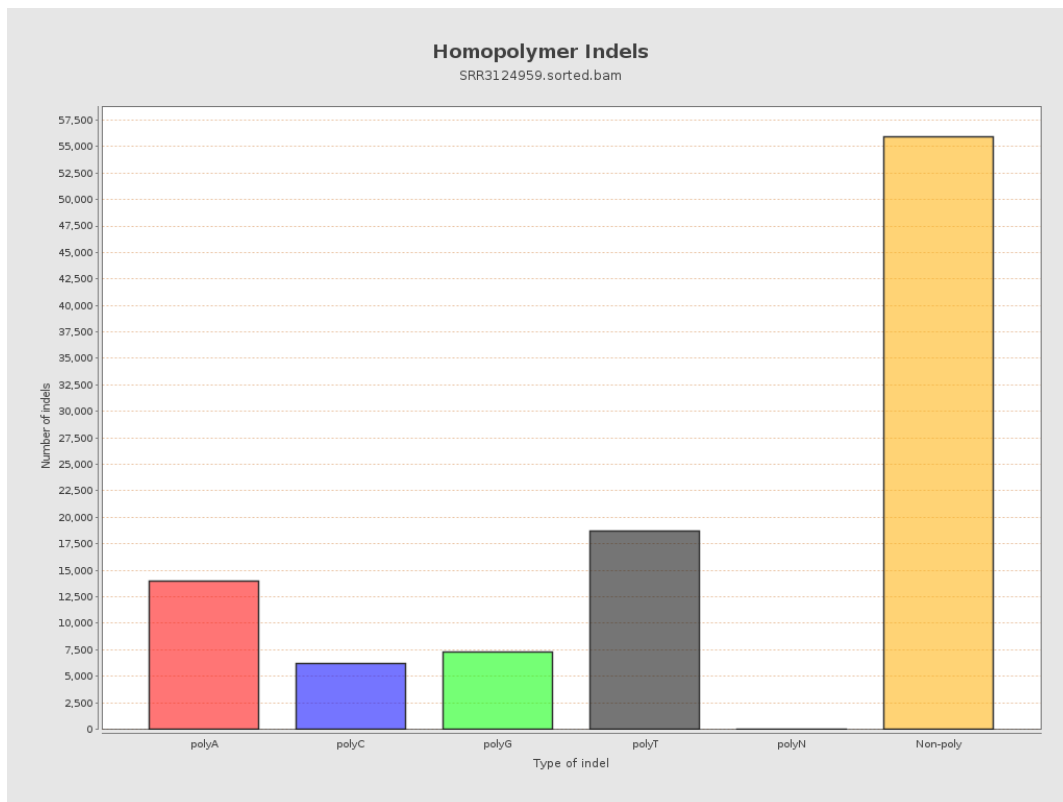
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



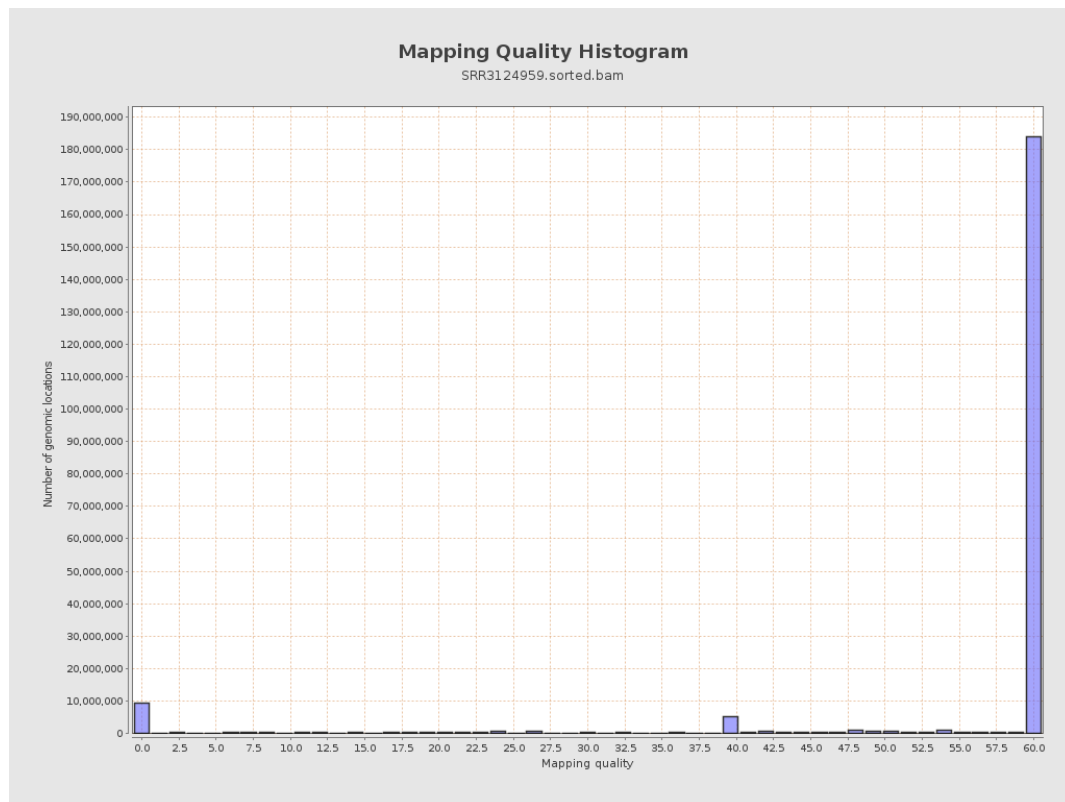
11. Results : Homopolymer Indels



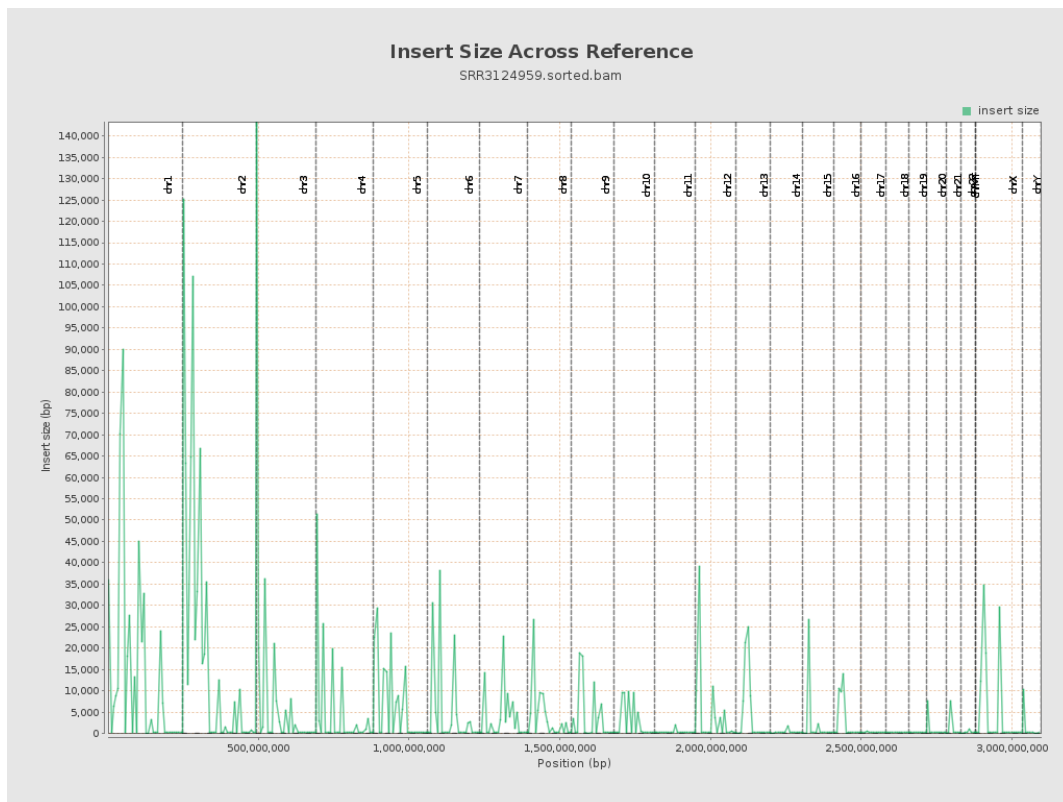
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

