

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:23:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173859.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_SRR10173859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173859_1.fastq.gz SRR10173859_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:22:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,074,964
Mapped reads	2,022,808 / 97.49%
Unmapped reads	52,156 / 2.51%
Mapped paired reads	2,022,808 / 97.49%
Mapped reads, first in pair	1,011,151 / 48.73%
Mapped reads, second in pair	1,011,657 / 48.76%
Mapped reads, both in pair	1,988,906 / 95.85%
Mapped reads, singletons	33,902 / 1.63%
Secondary alignments	0
Supplementary alignments	194,179 / 9.36%
Read min/max/mean length	30 / 133 / 127.54
Duplicated reads (estimated)	1,548,968 / 74.65%
Duplication rate	64.68%
Clipped reads	805,663 / 38.83%

2.2. ACGT Content

Number/percentage of A's	71,957,263 / 30.19%
Number/percentage of C's	46,606,129 / 19.56%
Number/percentage of T's	71,604,961 / 30.05%
Number/percentage of G's	48,154,077 / 20.21%
Number/percentage of N's	2,926 / 0%

GC Percentage	39.76%
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2.3. Coverage

Mean	0.077
Standard Deviation	1.2929

2.4. Mapping Quality

Mean Mapping Quality	53.06
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2.5. Insert size

Mean	1,082,296.08
Standard Deviation	9,833,279
P25/Median/P75	136 / 188 / 267

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	2,393,904
Insertions	26,553
Mapped reads with at least one insertion	1.27%
Deletions	52,717
Mapped reads with at least one deletion	2.53%
Homopolymer indels	43.4%

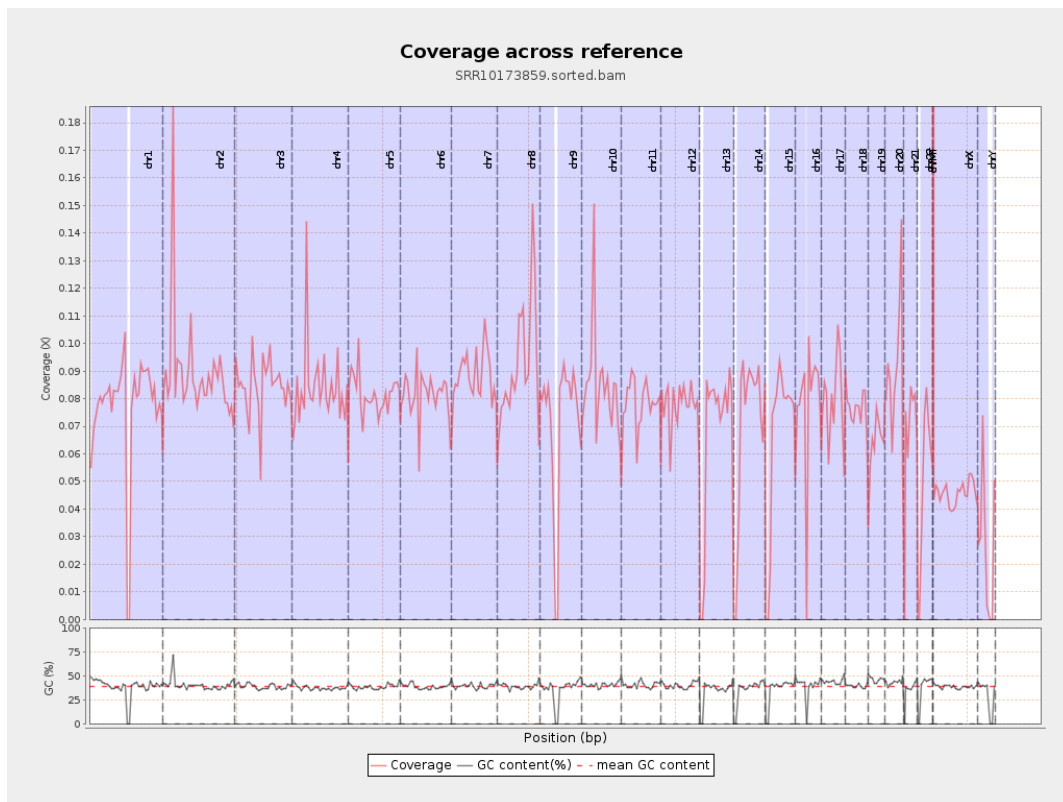
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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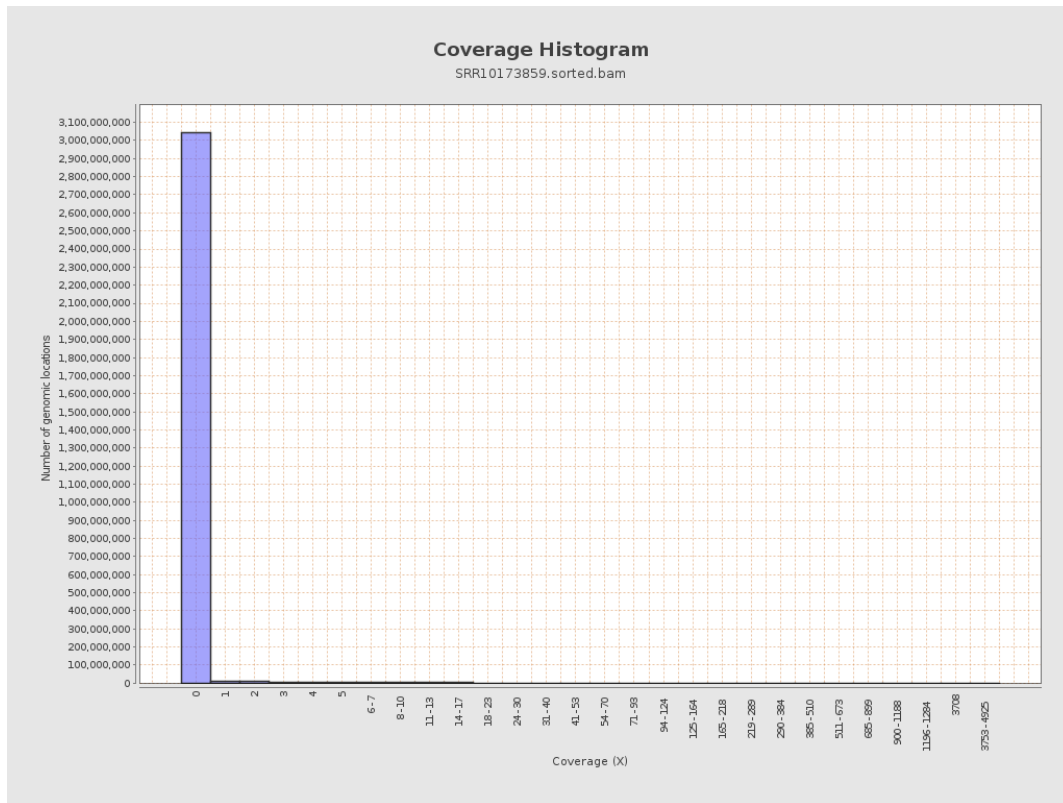
		bases	coverage	deviation
chr1	249250621	19161292	0.0769	0.9697
chr2	243199373	21651768	0.089	3.5024
chr3	198022430	16698378	0.0843	0.836
chr4	191154276	16045697	0.0839	0.9971
chr5	180915260	14743258	0.0815	0.8198
chr6	171115067	13936812	0.0814	0.8531
chr7	159138663	14027321	0.0881	0.9494
chr8	146364022	13720907	0.0937	1.1322
chr9	141213431	10118685	0.0717	0.8839
chr10	135534747	11429666	0.0843	1.0863
chr11	135006516	10529272	0.078	0.8
chr12	133851895	10408269	0.0778	0.7968
chr13	115169878	7712889	0.067	0.7414
chr14	107349540	7529129	0.0701	0.758
chr15	102531392	6670721	0.0651	0.7305
chr16	90354753	6909940	0.0765	0.8251
chr17	81195210	6537362	0.0805	0.8113
chr18	78077248	5987248	0.0767	1.0201
chr19	59128983	3847066	0.0651	0.7666
chr20	63025520	5839320	0.0927	0.8698
chr21	48129895	3256105	0.0677	0.8406
chr22	51304566	2581074	0.0503	0.6391
chrMT	16571	351535	21.2139	20.2693
chrX	155270560	7110842	0.0458	0.617

chrY	59373566	1651762	0.0278	0.6169
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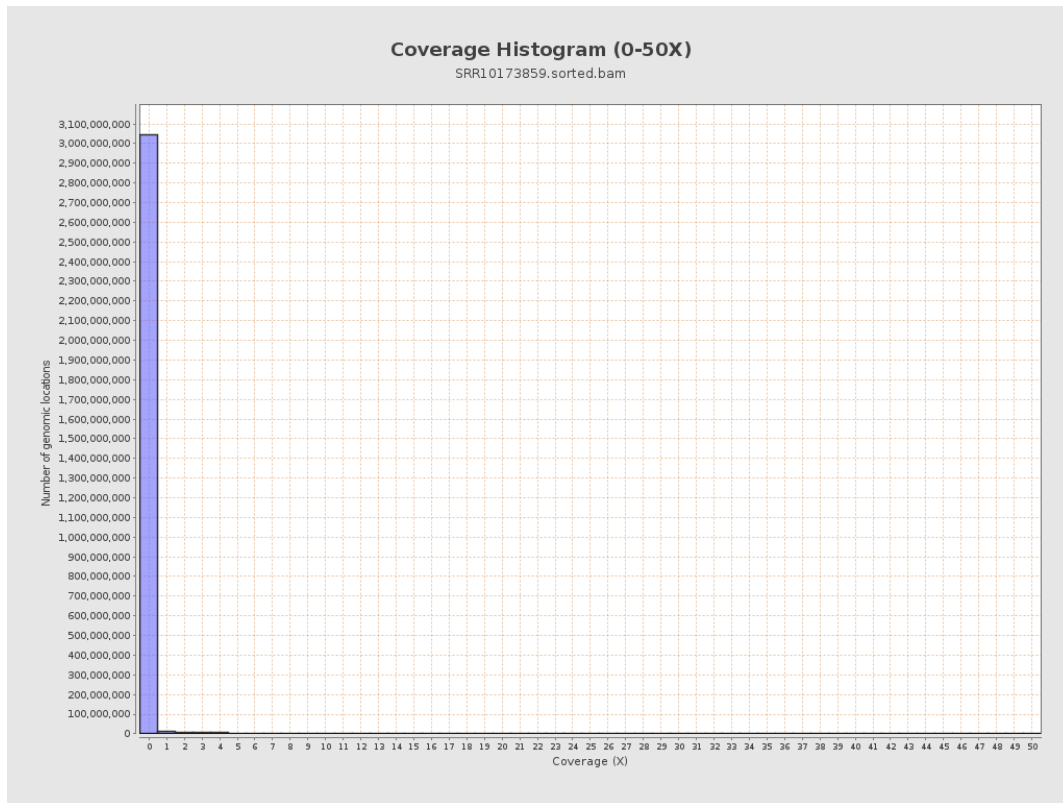
3. Results : Coverage across reference



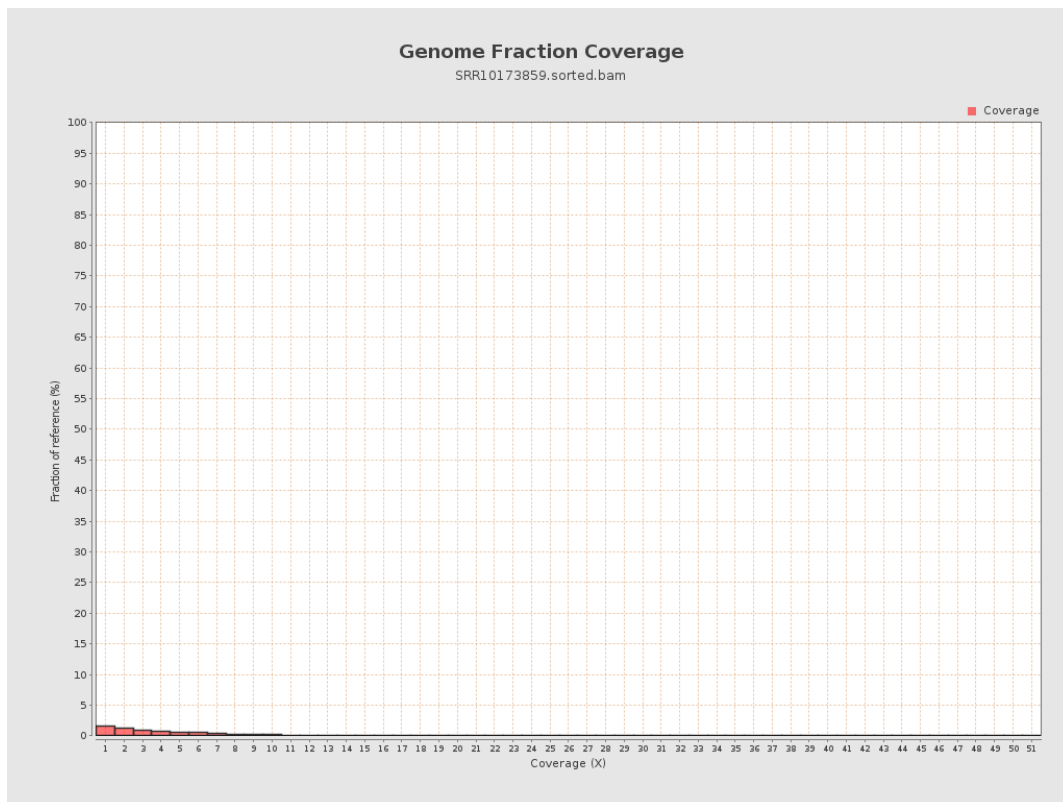
4. Results : Coverage Histogram



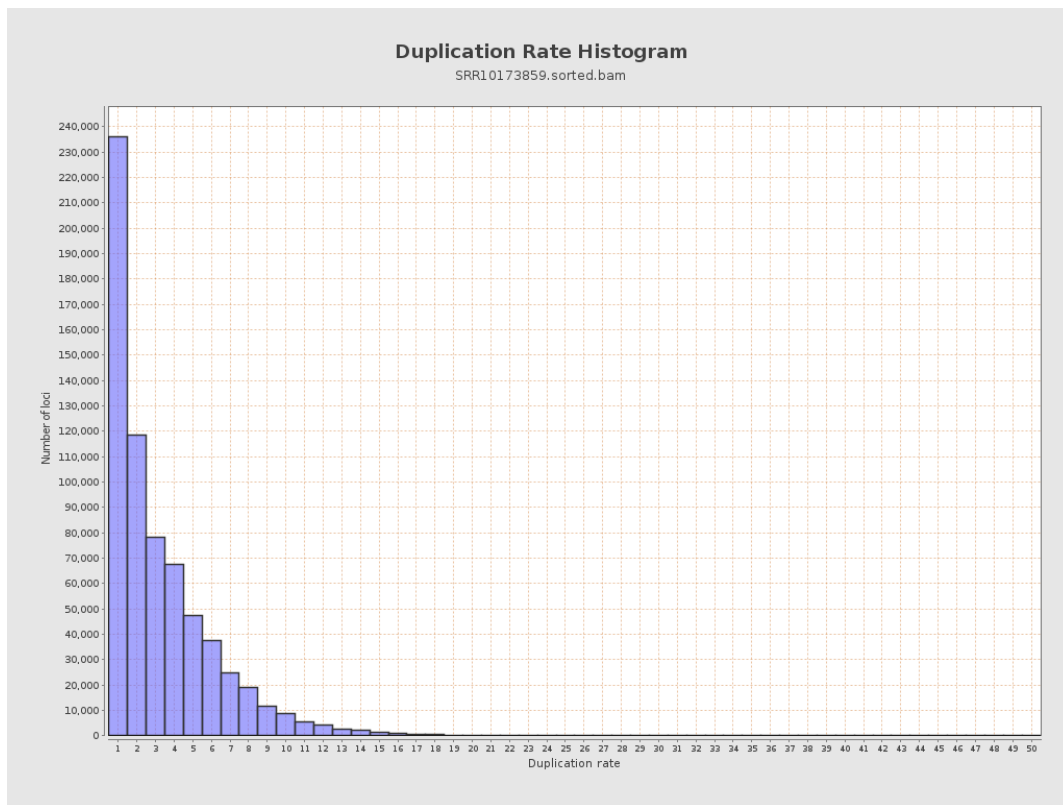
5. Results : Coverage Histogram (0-50X)



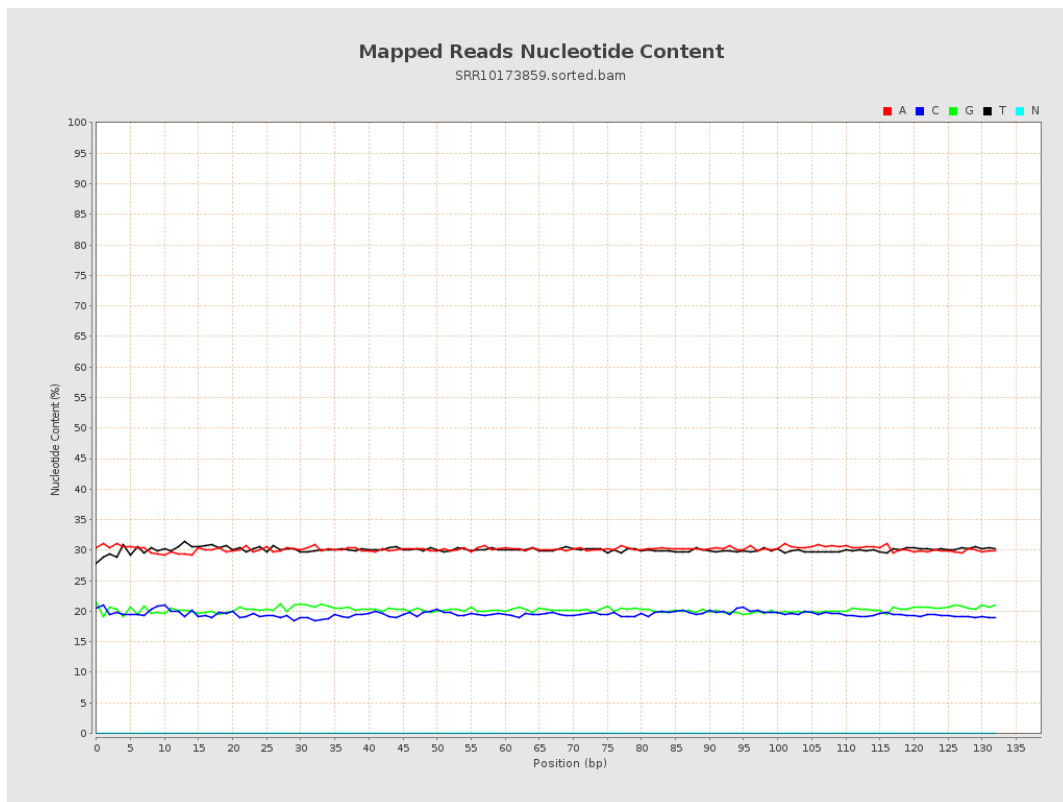
6. Results : Genome Fraction Coverage



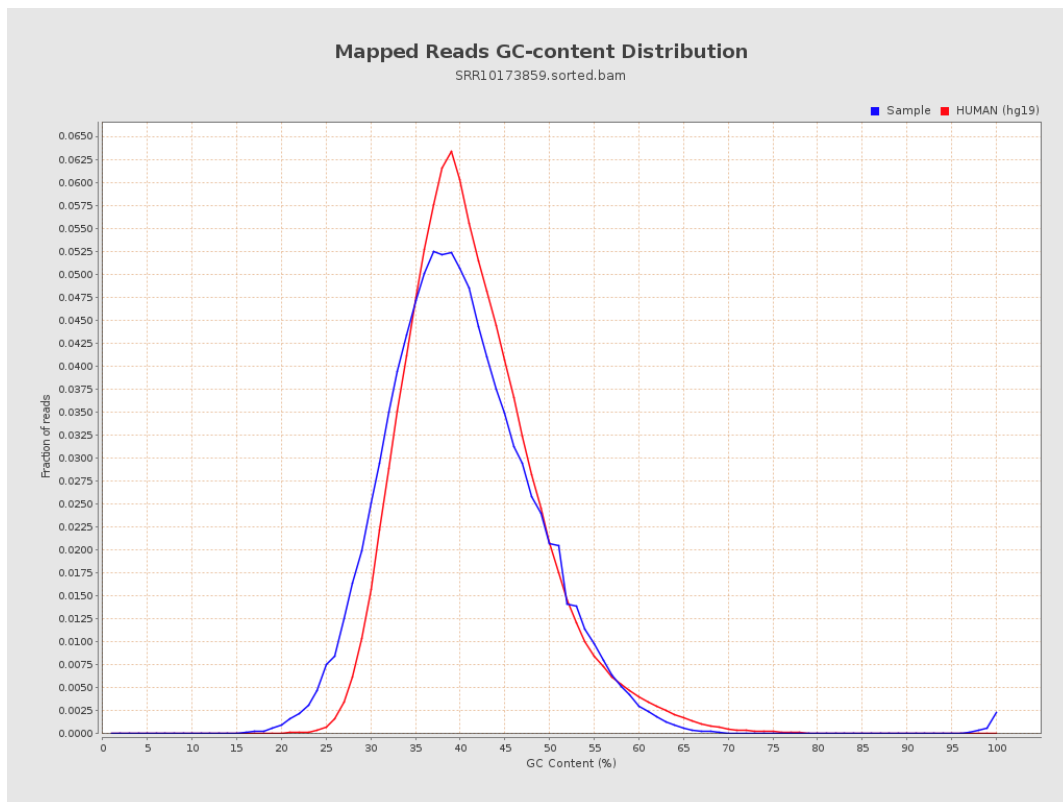
7. Results : Duplication Rate Histogram



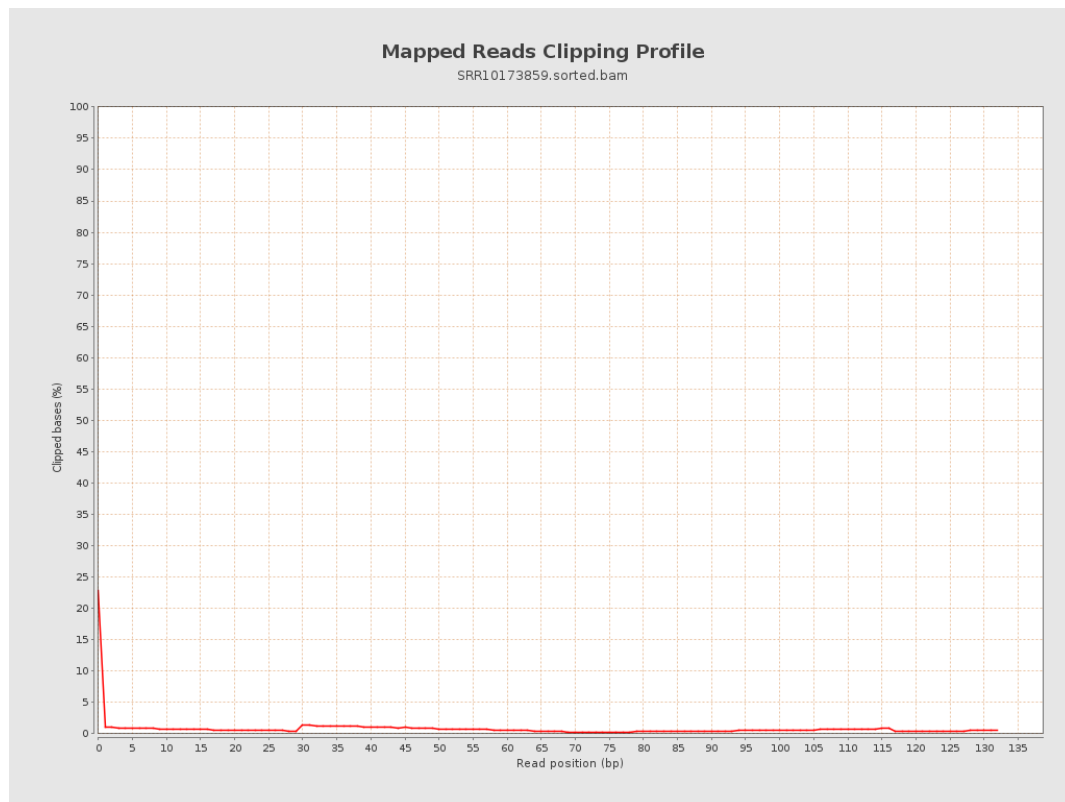
8. Results : Mapped Reads Nucleotide Content



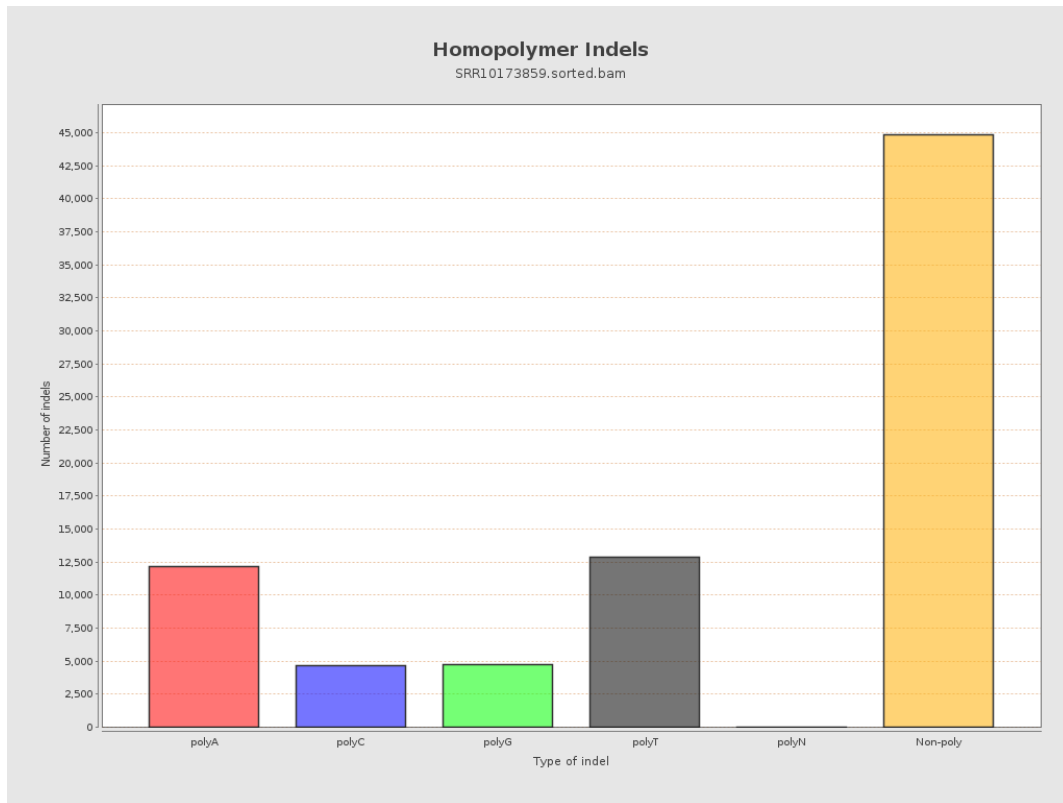
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



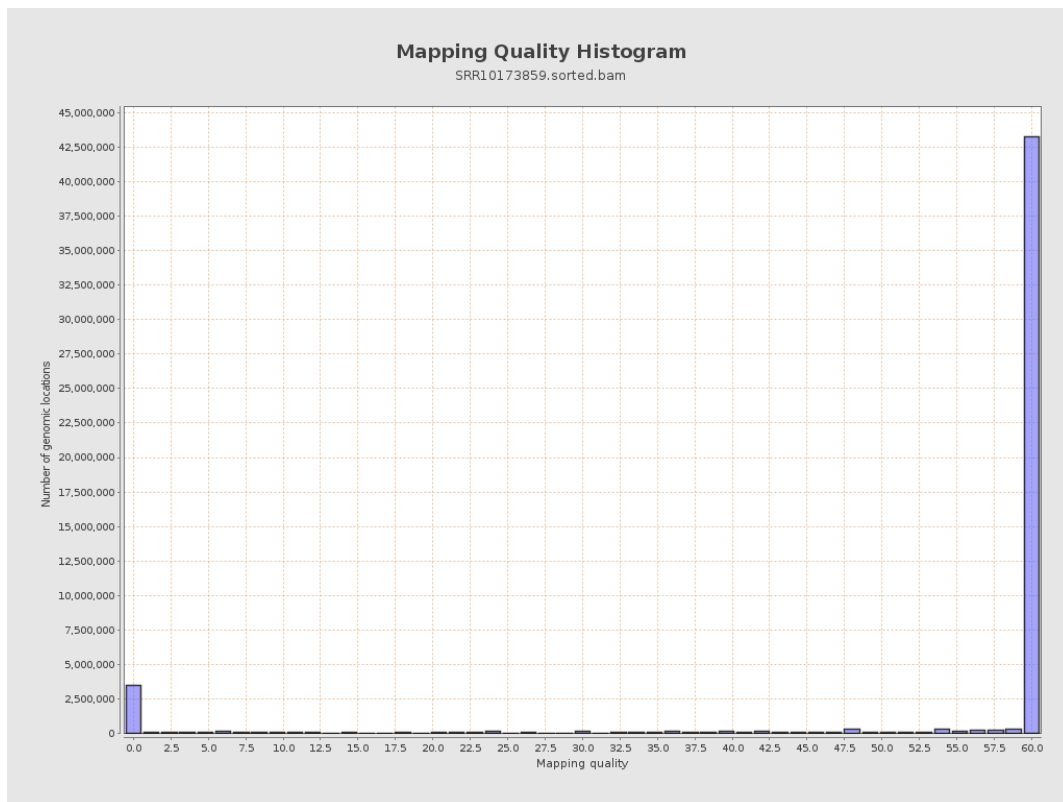
11. Results : Homopolymer Indels



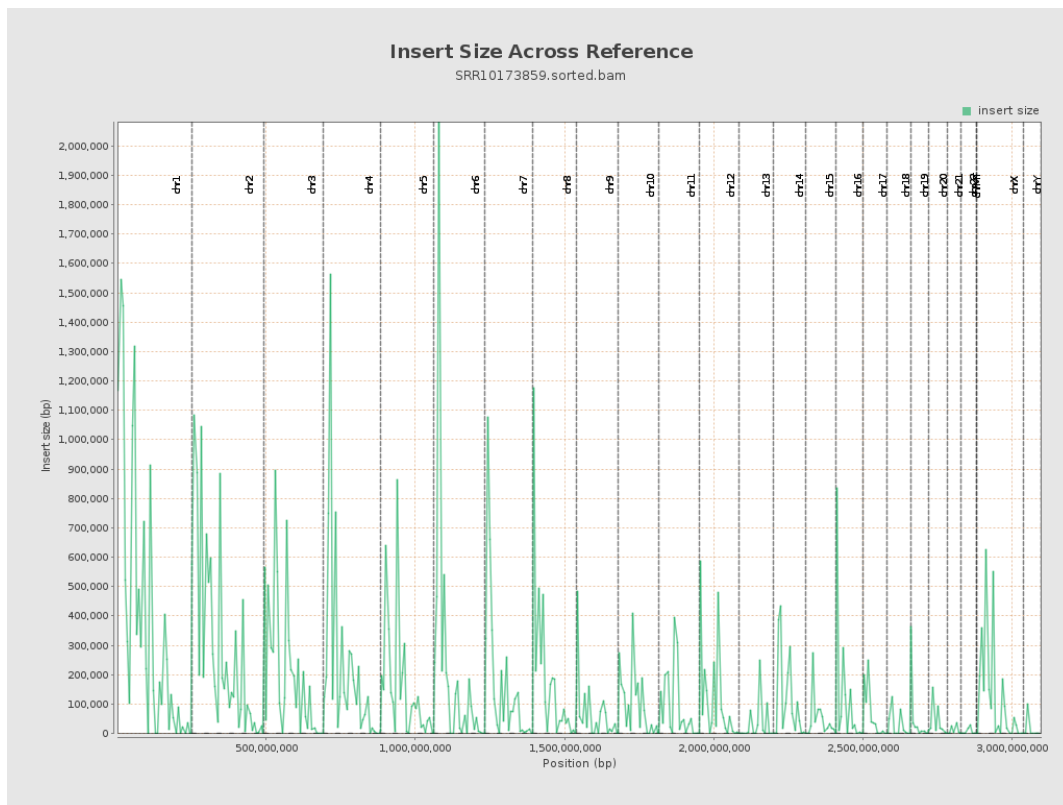
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

