

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:02:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173897.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_SRR10173897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173897_1.fastq.gz SRR10173897_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:02:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,841,664
Mapped reads	1,790,072 / 97.2%
Unmapped reads	51,592 / 2.8%
Mapped paired reads	1,790,072 / 97.2%
Mapped reads, first in pair	895,985 / 48.65%
Mapped reads, second in pair	894,087 / 48.55%
Mapped reads, both in pair	1,758,274 / 95.47%
Mapped reads, singletons	31,798 / 1.73%
Secondary alignments	0
Supplementary alignments	170,563 / 9.26%
Read min/max/mean length	30 / 133 / 128.19
Duplicated reads (estimated)	1,414,577 / 76.81%
Duplication rate	64.96%
Clipped reads	688,104 / 37.36%

2.2. ACGT Content

Number/percentage of A's	63,998,160 / 30.14%
Number/percentage of C's	41,566,711 / 19.58%
Number/percentage of T's	63,732,119 / 30.02%
Number/percentage of G's	43,022,473 / 20.26%
Number/percentage of N's	2,118 / 0%

GC Percentage	39.84%
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2.3. Coverage

Mean	0.0686
Standard Deviation	1.1833

2.4. Mapping Quality

Mean Mapping Quality	52.98
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2.5. Insert size

Mean	1,004,055.45
Standard Deviation	9,285,821.06
P25/Median/P75	150 / 208 / 294

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	2,265,315
Insertions	24,500
Mapped reads with at least one insertion	1.31%
Deletions	46,952
Mapped reads with at least one deletion	2.55%
Homopolymer indels	43.06%

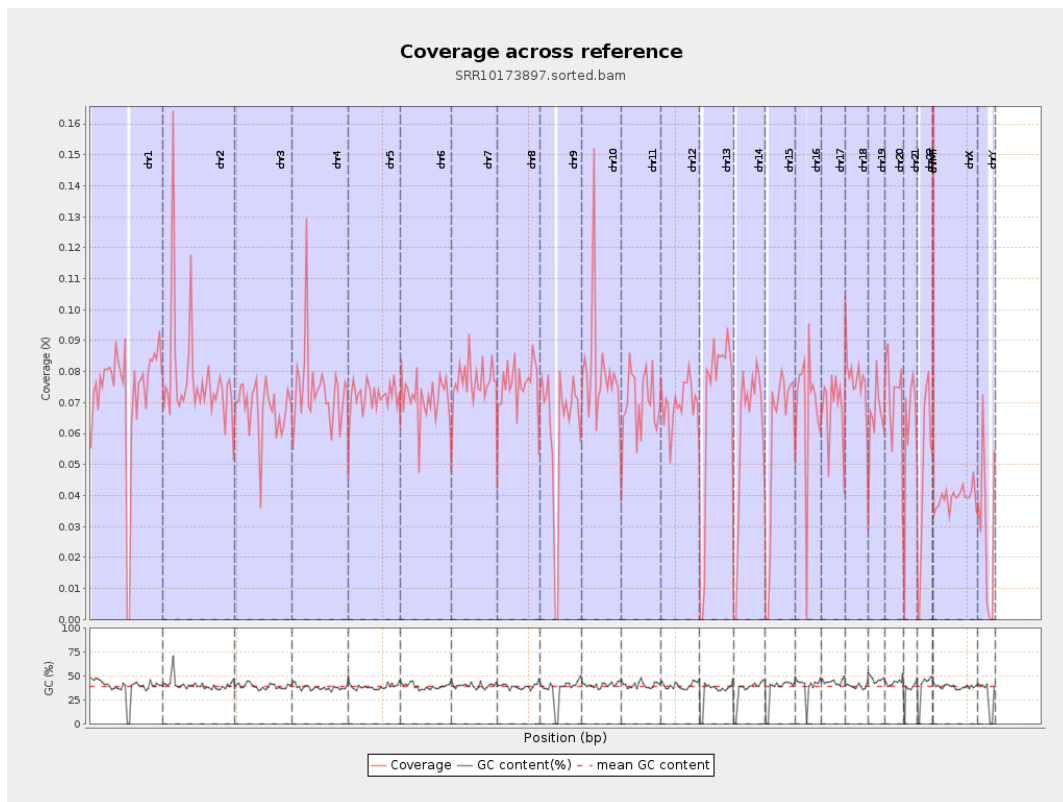
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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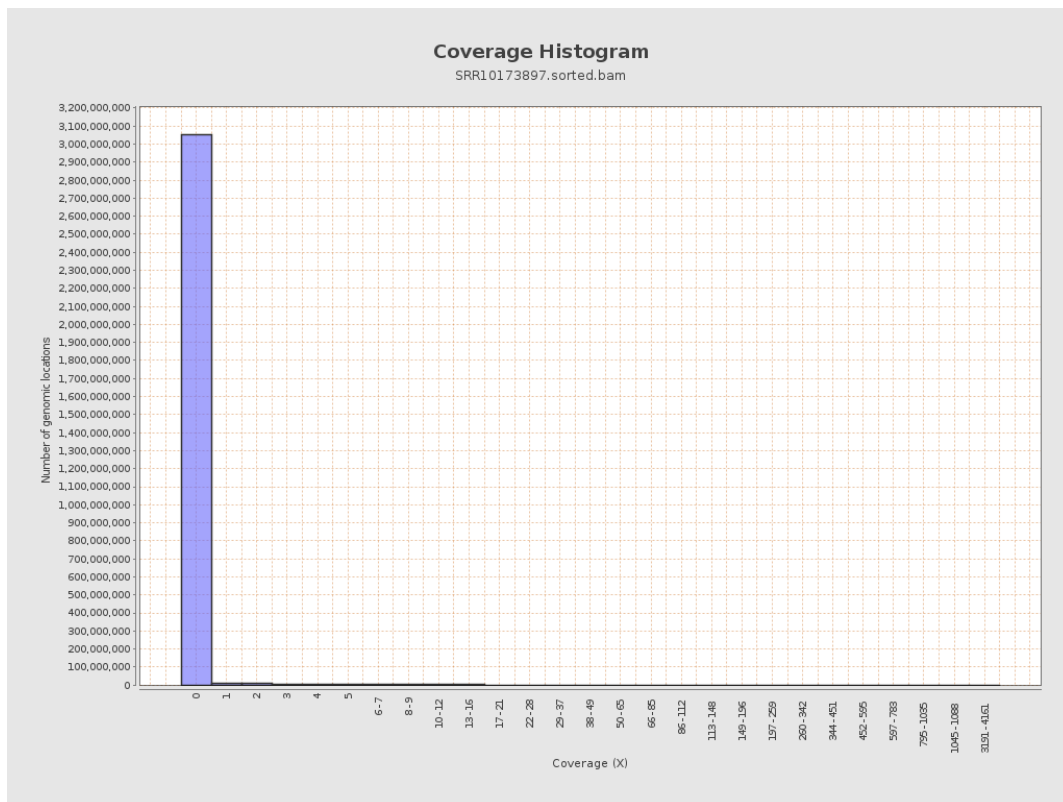
		bases	coverage	deviation
chr1	249250621	18259132	0.0733	0.9936
chr2	243199373	18836917	0.0775	3.0013
chr3	198022430	13444208	0.0679	0.7745
chr4	191154276	14182893	0.0742	0.9384
chr5	180915260	12987606	0.0718	0.7932
chr6	171115067	12213347	0.0714	0.8403
chr7	159138663	12217344	0.0768	0.9354
chr8	146364022	11126924	0.076	1.0385
chr9	141213431	8769942	0.0621	0.8622
chr10	135534747	10831363	0.0799	1.0983
chr11	135006516	9464270	0.0701	0.784
chr12	133851895	9330836	0.0697	0.7792
chr13	115169878	7964675	0.0692	0.7961
chr14	107349540	6569208	0.0612	0.7349
chr15	102531392	6023375	0.0587	0.7076
chr16	90354753	6121449	0.0677	0.831
chr17	81195210	5574981	0.0687	0.7807
chr18	78077248	6080896	0.0779	1.0921
chr19	59128983	3930784	0.0665	0.8173
chr20	63025520	4575100	0.0726	0.802
chr21	48129895	2978715	0.0619	0.8608
chr22	51304566	2469184	0.0481	0.6829
chrMT	16571	624869	37.7086	31.9274
chrX	155270560	6079168	0.0392	0.5844

chrY	59373566	1783299	0.03	0.6578
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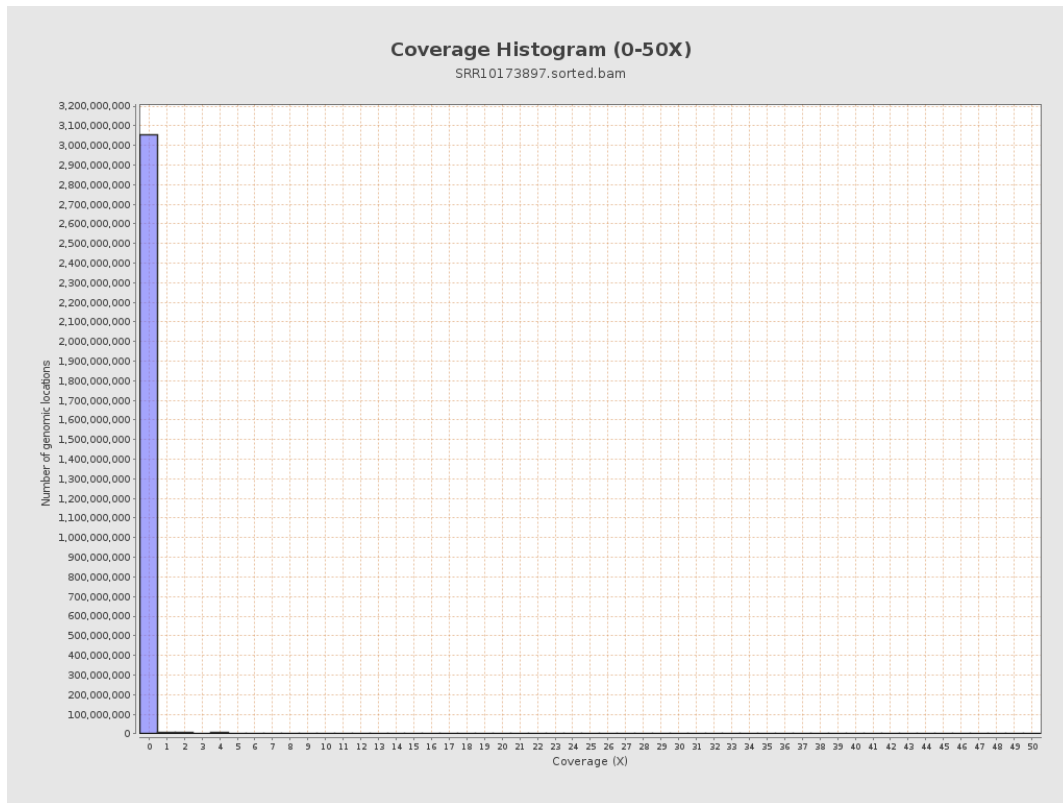
3. Results : Coverage across reference



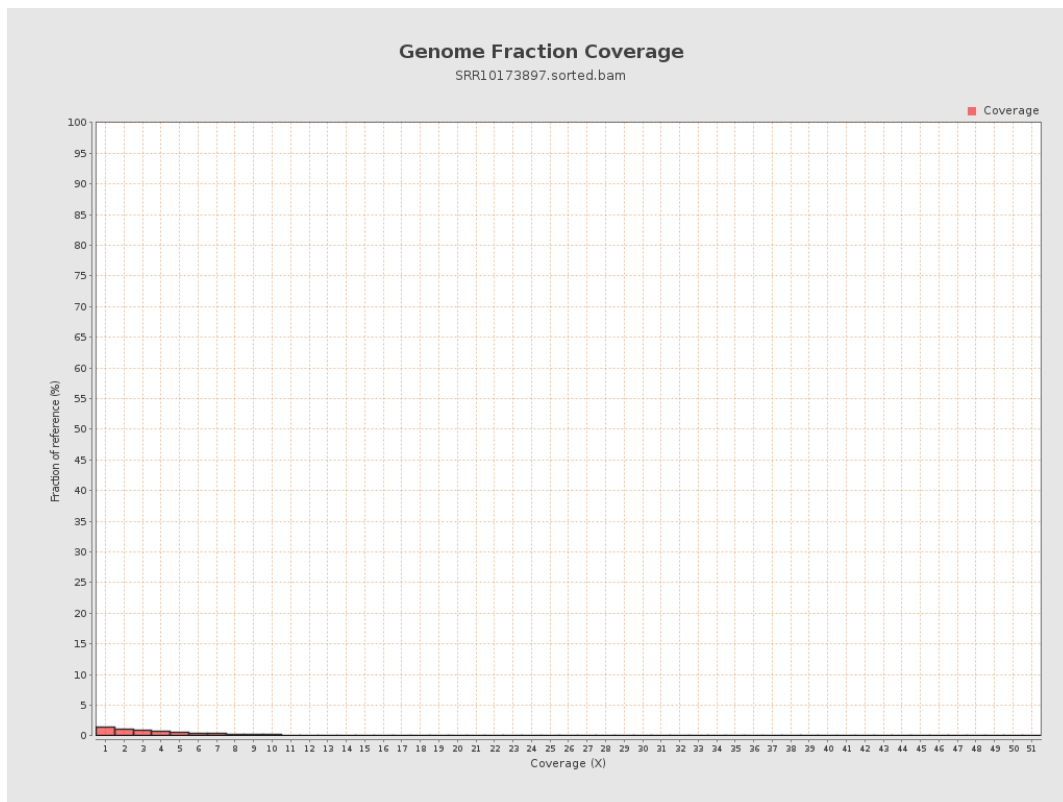
4. Results : Coverage Histogram



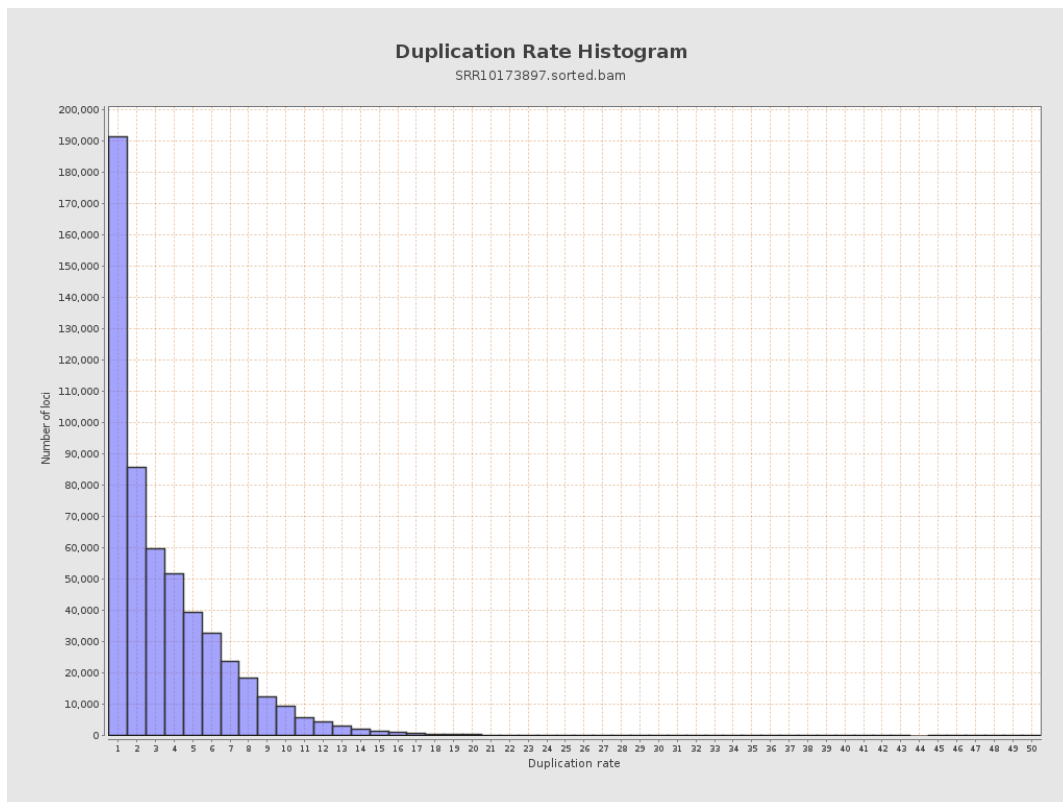
5. Results : Coverage Histogram (0-50X)



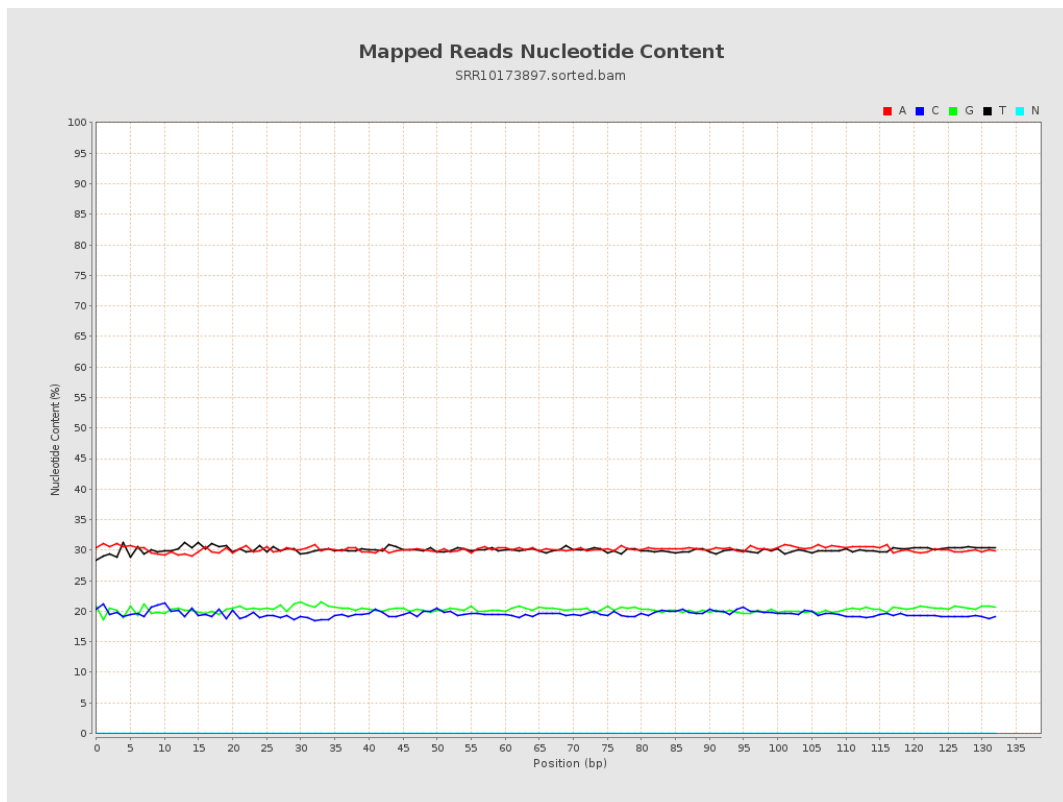
6. Results : Genome Fraction Coverage



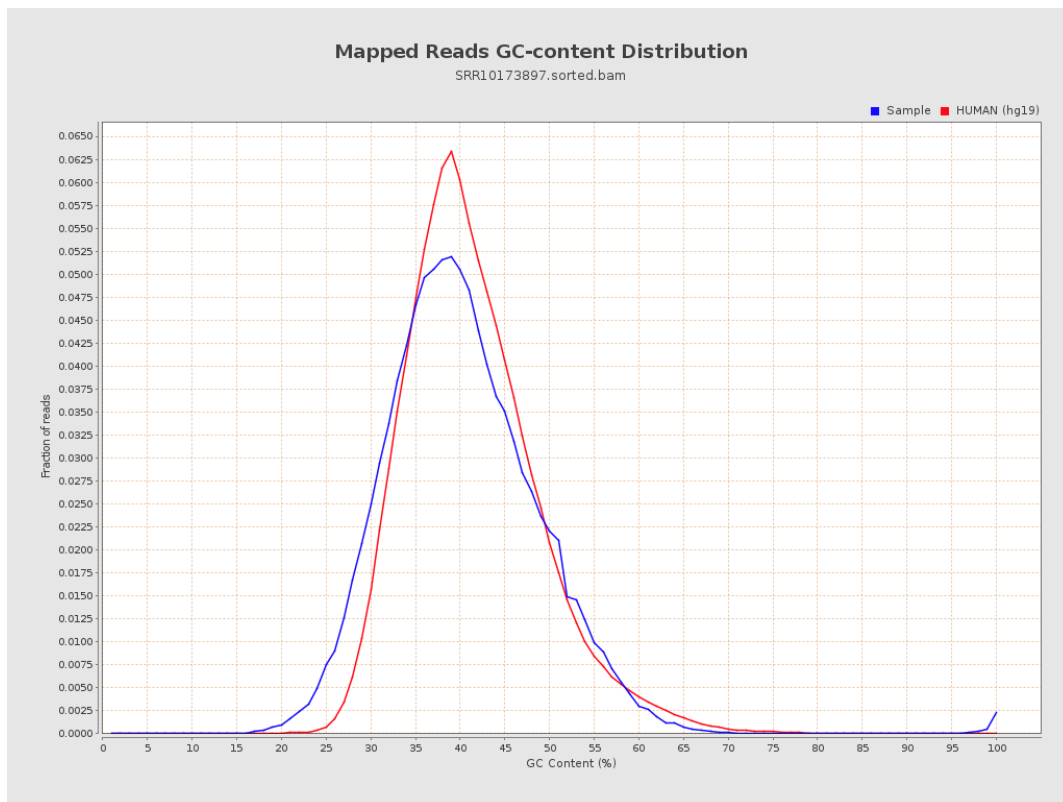
7. Results : Duplication Rate Histogram



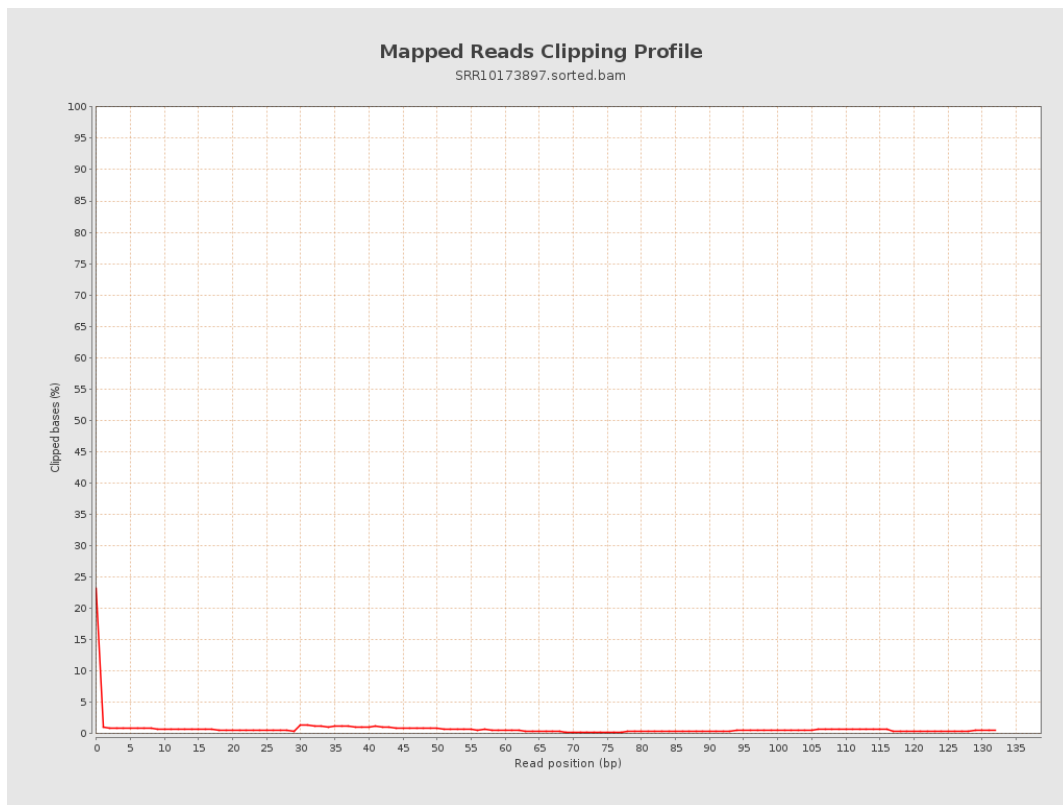
8. Results : Mapped Reads Nucleotide Content



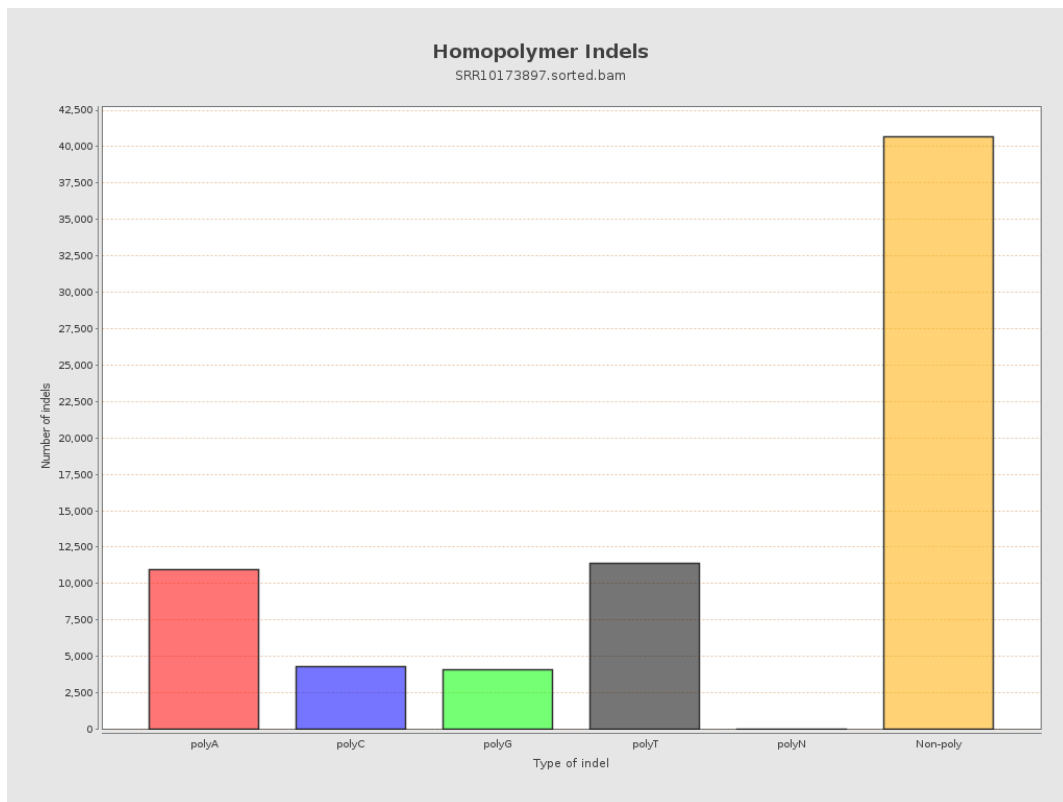
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



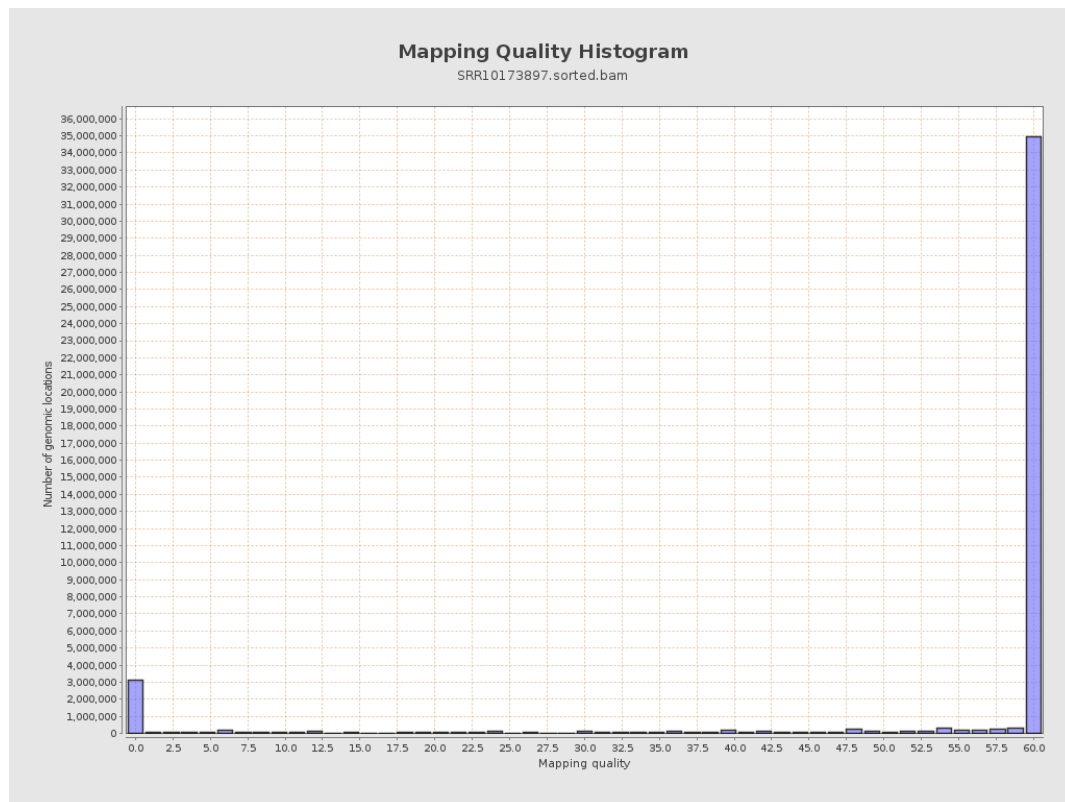
11. Results : Homopolymer Indels



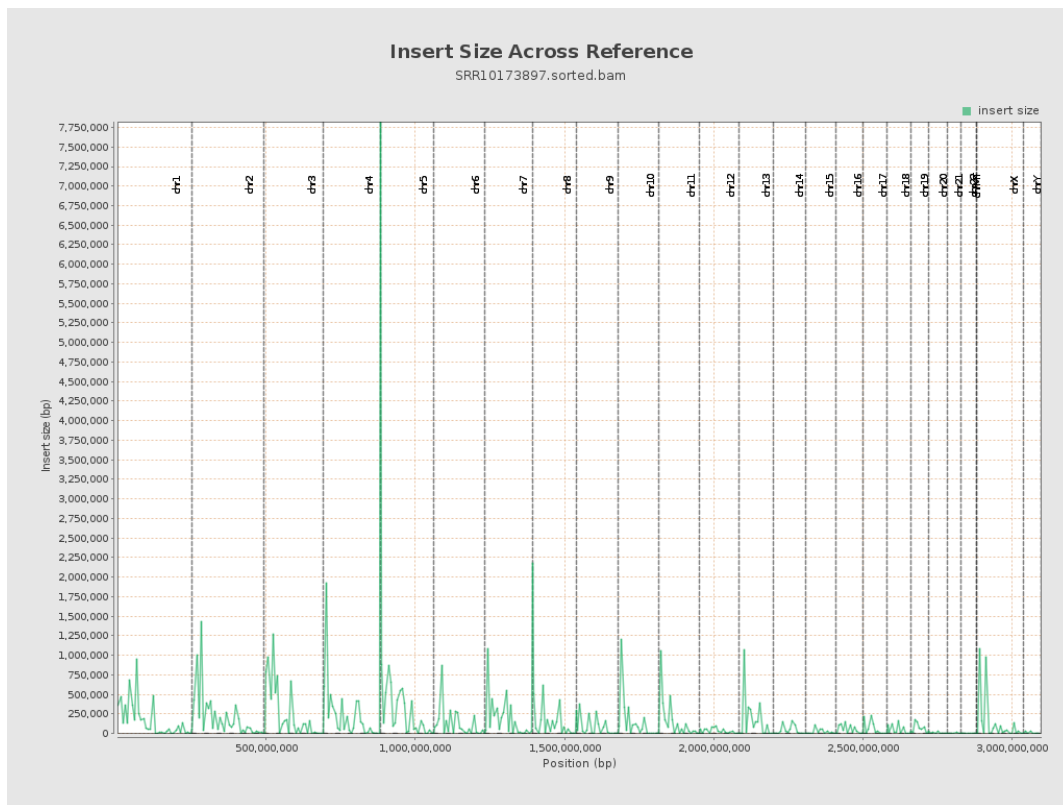
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

