

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:46:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173997.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_SRR10173997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173997_1.fastq.gz SRR10173997_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:46:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,075,872
Mapped reads	6,932,709 / 97.98%
Unmapped reads	143,163 / 2.02%
Mapped paired reads	6,932,709 / 97.98%
Mapped reads, first in pair	3,466,550 / 48.99%
Mapped reads, second in pair	3,466,159 / 48.99%
Mapped reads, both in pair	6,840,190 / 96.67%
Mapped reads, singletons	92,519 / 1.31%
Secondary alignments	0
Supplementary alignments	877,837 / 12.41%
Read min/max/mean length	30 / 133 / 125.04
Duplicated reads (estimated)	5,602,165 / 79.17%
Duplication rate	65.56%
Clipped reads	3,354,238 / 47.4%

2.2. ACGT Content

Number/percentage of A's	235,661,360 / 29.92%
Number/percentage of C's	156,331,527 / 19.85%
Number/percentage of T's	233,612,444 / 29.66%
Number/percentage of G's	162,014,239 / 20.57%
Number/percentage of N's	5,844 / 0%

GC Percentage	40.42%
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2.3. Coverage

Mean	0.2546
Standard Deviation	4.2069

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	1,069,017.31
Standard Deviation	9,515,054.66
P25/Median/P75	106 / 156 / 242

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	6,566,402
Insertions	86,403
Mapped reads with at least one insertion	1.2%
Deletions	219,884
Mapped reads with at least one deletion	3.1%
Homopolymer indels	41.71%

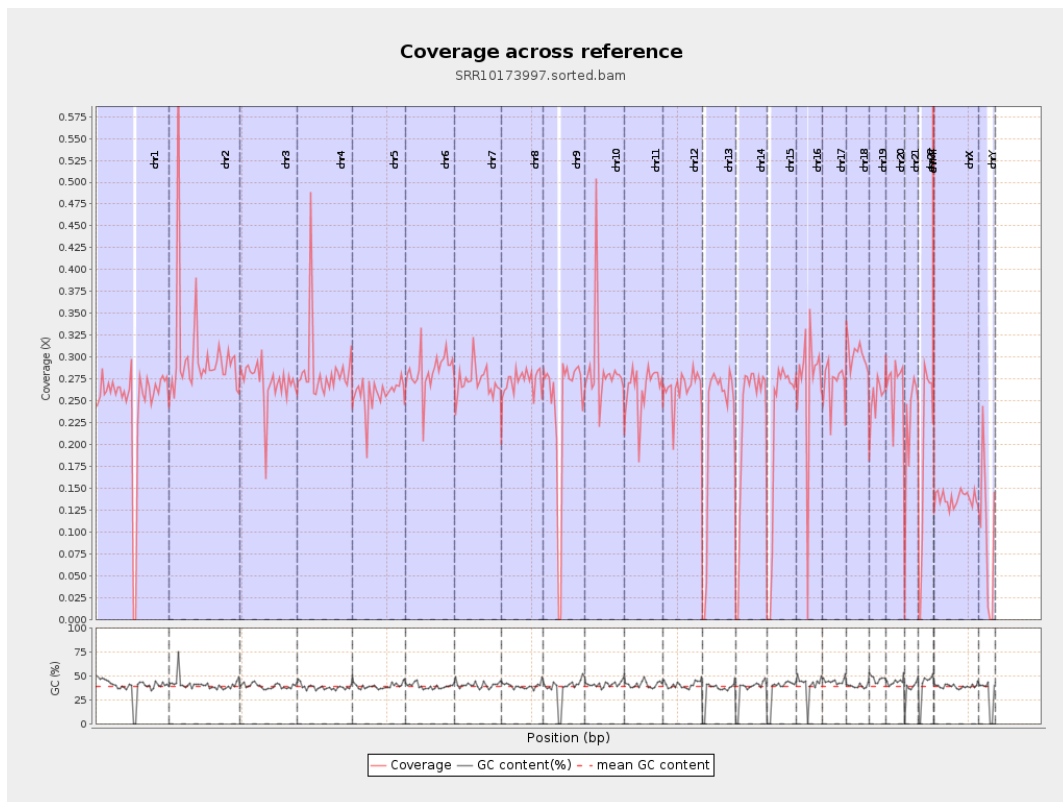
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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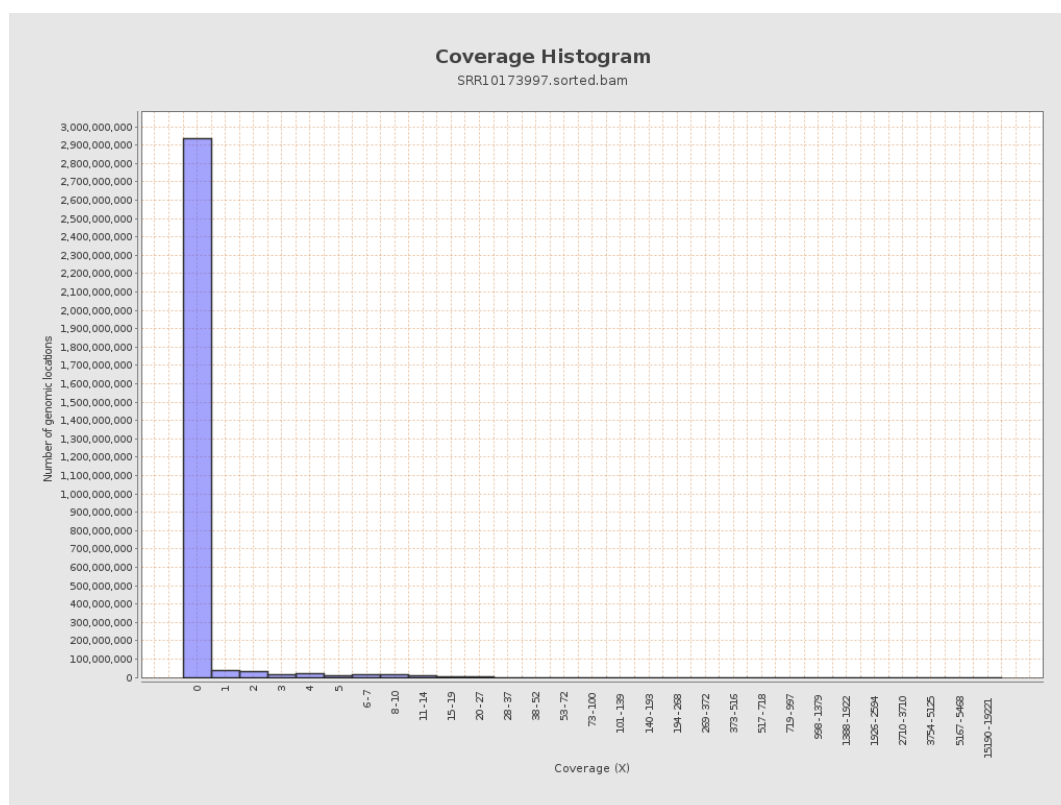
		bases	coverage	deviation
chr1	249250621	61559379	0.247	2.1776
chr2	243199373	73513446	0.3023	13.46
chr3	198022430	53683550	0.2711	1.601
chr4	191154276	54258833	0.2838	2.3139
chr5	180915260	46718840	0.2582	1.5469
chr6	171115067	48501644	0.2834	1.8837
chr7	159138663	43345453	0.2724	2.2124
chr8	146364022	39889939	0.2725	2.4947
chr9	141213431	34163799	0.2419	2.0306
chr10	135534747	38714534	0.2856	2.6545
chr11	135006516	35803581	0.2652	1.6317
chr12	133851895	35409809	0.2645	1.625
chr13	115169878	25558767	0.2219	1.4486
chr14	107349540	24383552	0.2271	1.4729
chr15	102531392	22531190	0.2197	1.4579
chr16	90354753	24226317	0.2681	1.9728
chr17	81195210	21782219	0.2683	1.7333
chr18	78077248	23683075	0.3033	2.7797
chr19	59128983	15124981	0.2558	1.828
chr20	63025520	16899336	0.2681	1.6757
chr21	48129895	10638994	0.221	1.8585
chr22	51304566	9783767	0.1907	1.574
chrMT	16571	1029047	62.0993	57.4947
chrX	155270560	21390662	0.1378	1.1453

chrY	59373566	5546559	0.0934	1.5749
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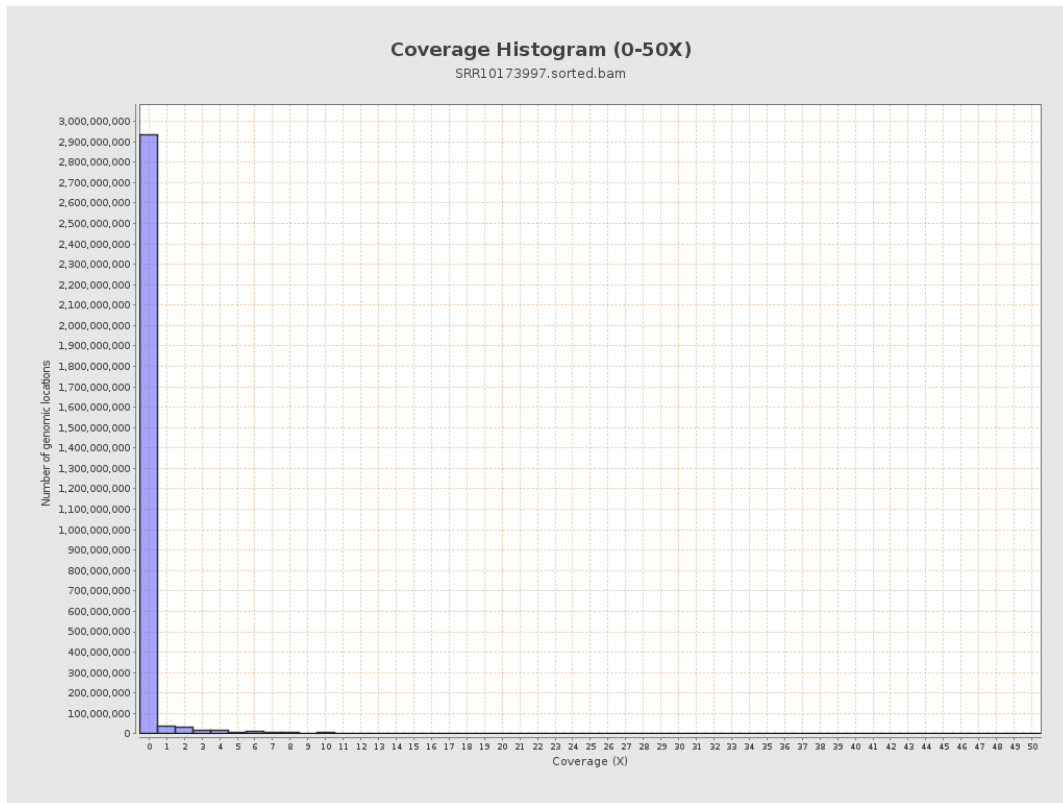
3. Results : Coverage across reference



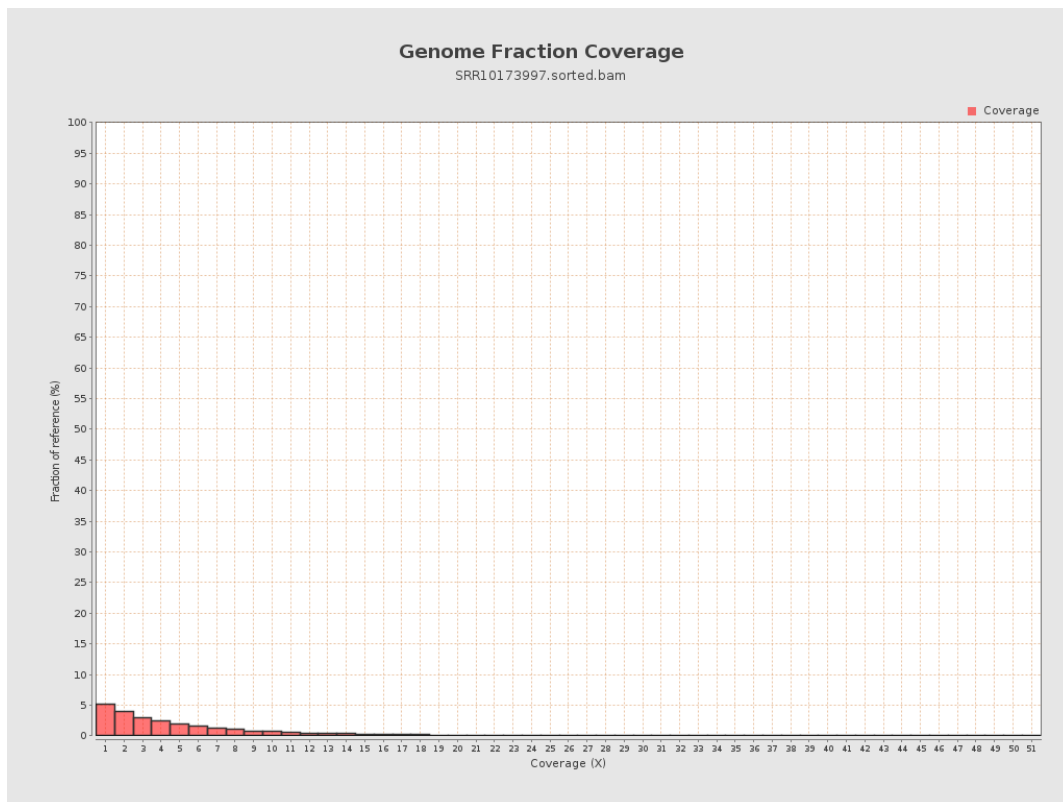
4. Results : Coverage Histogram



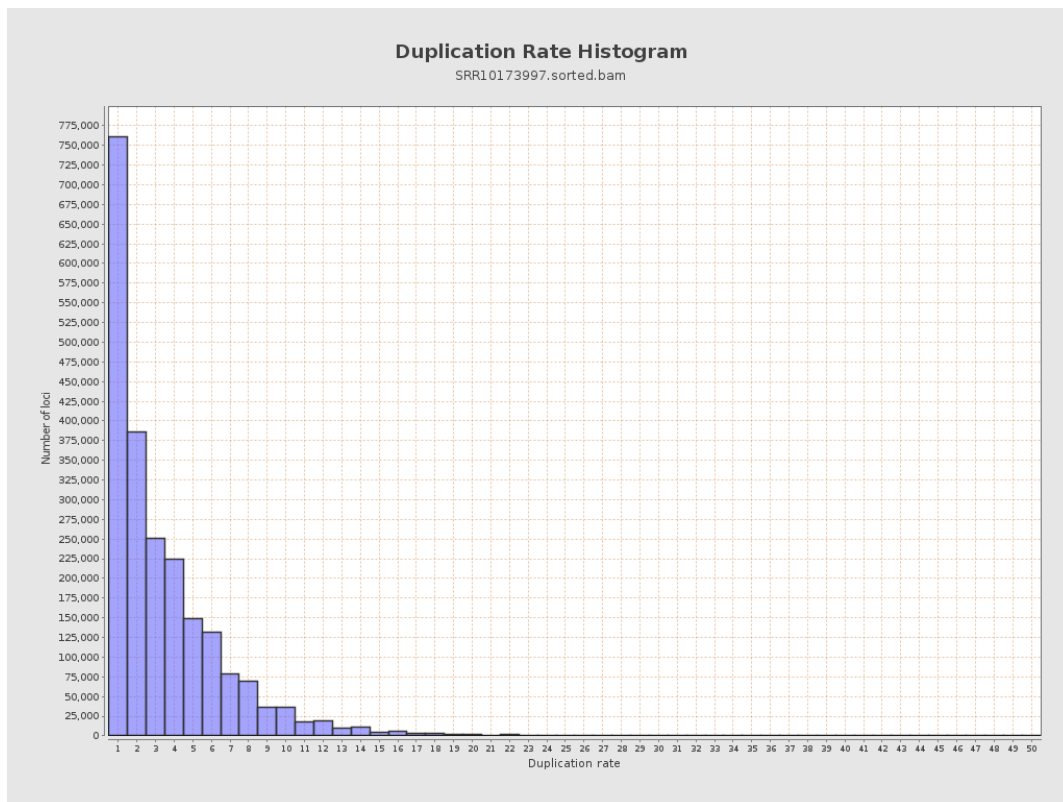
5. Results : Coverage Histogram (0-50X)



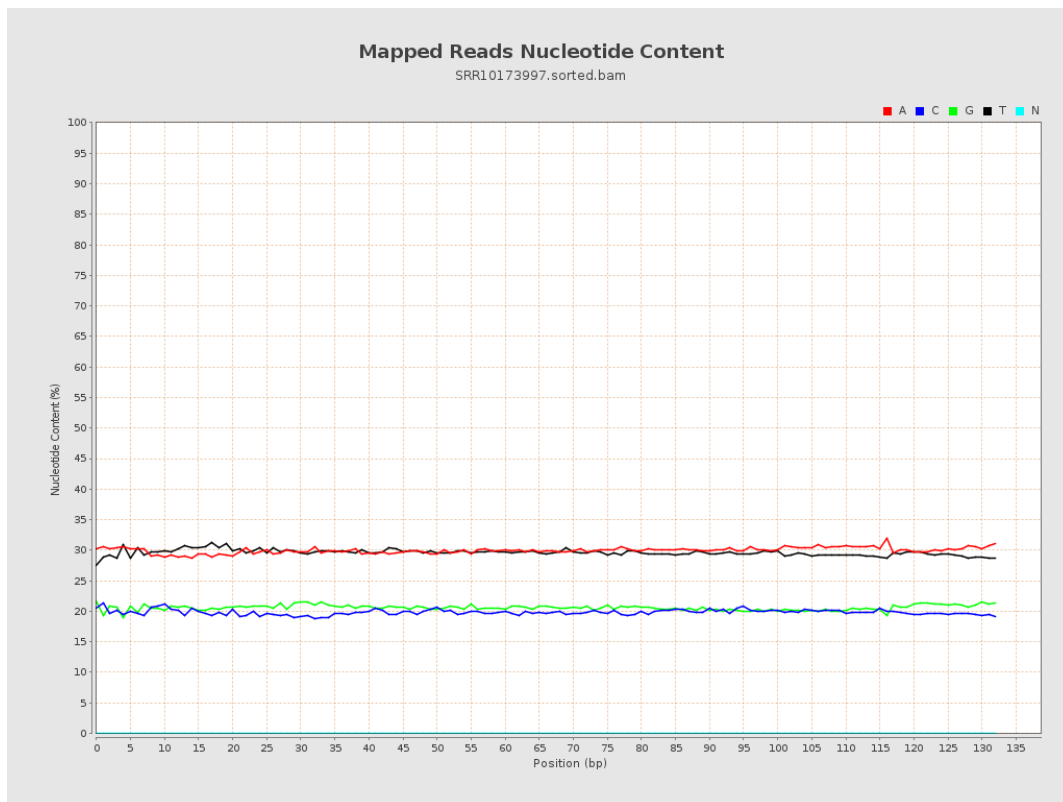
6. Results : Genome Fraction Coverage



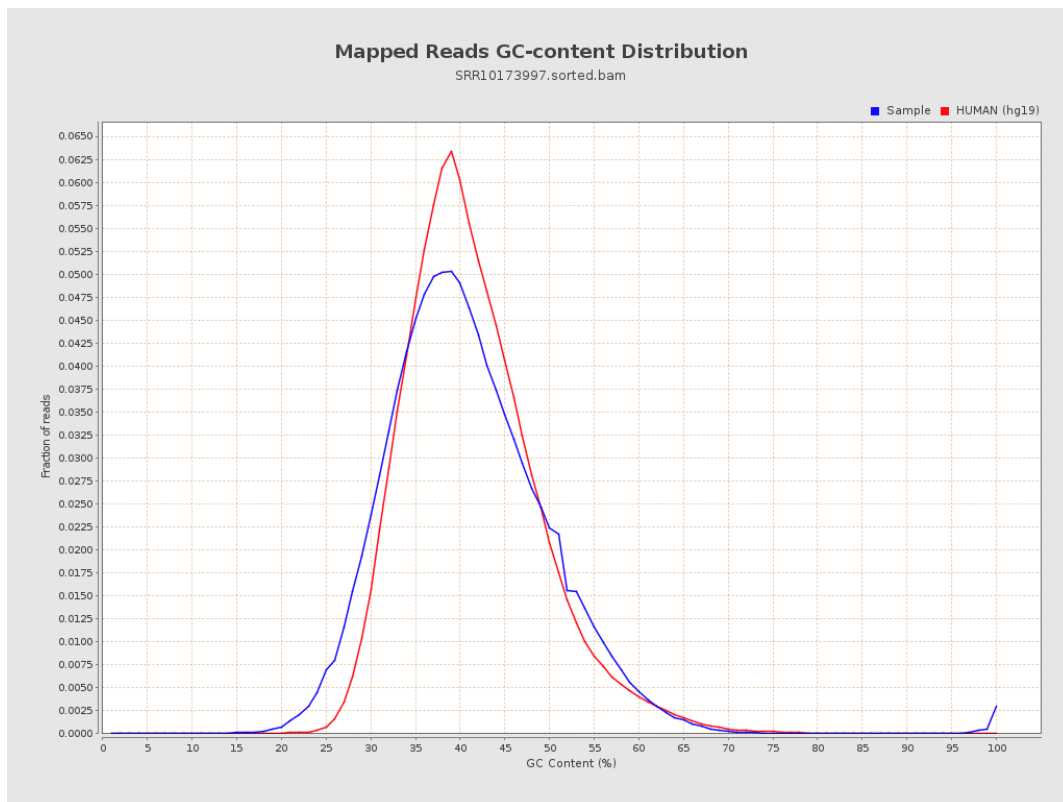
7. Results : Duplication Rate Histogram



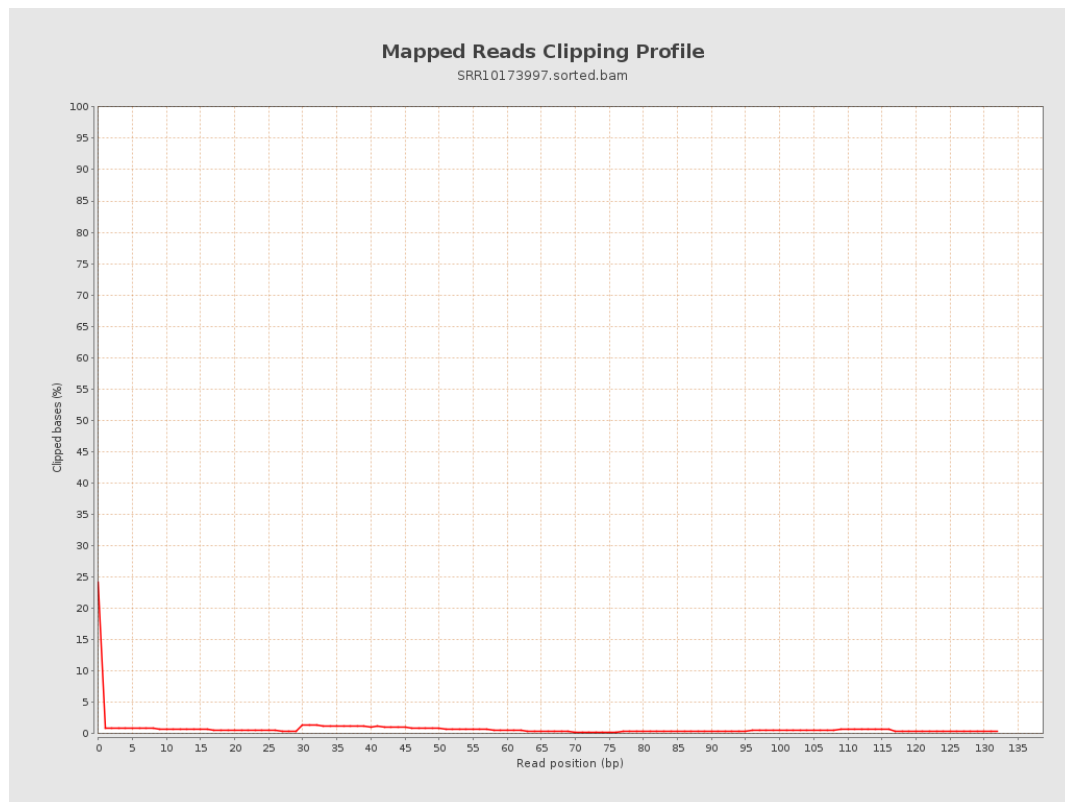
8. Results : Mapped Reads Nucleotide Content



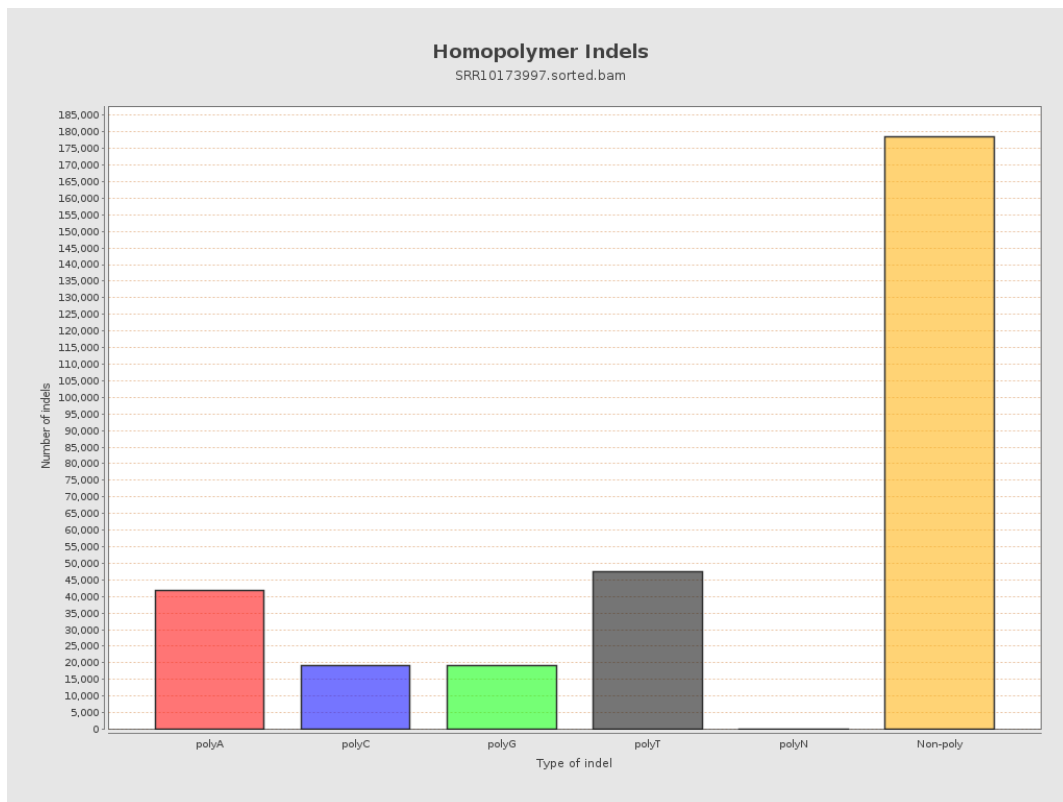
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



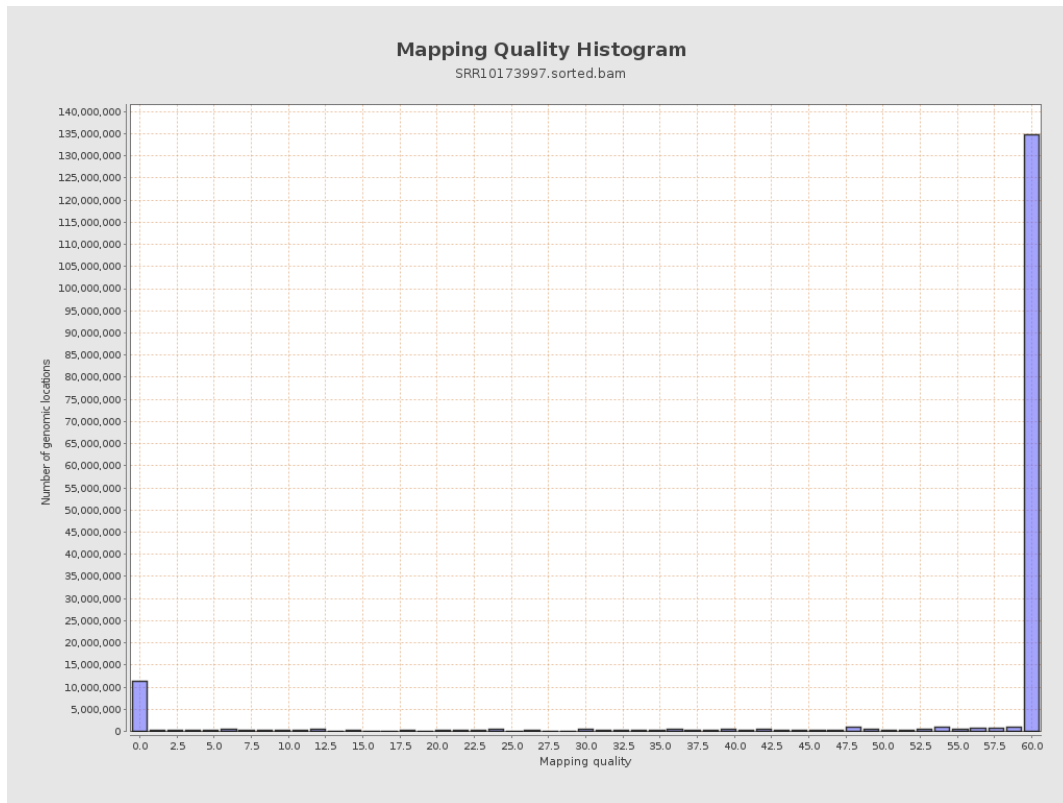
11. Results : Homopolymer Indels



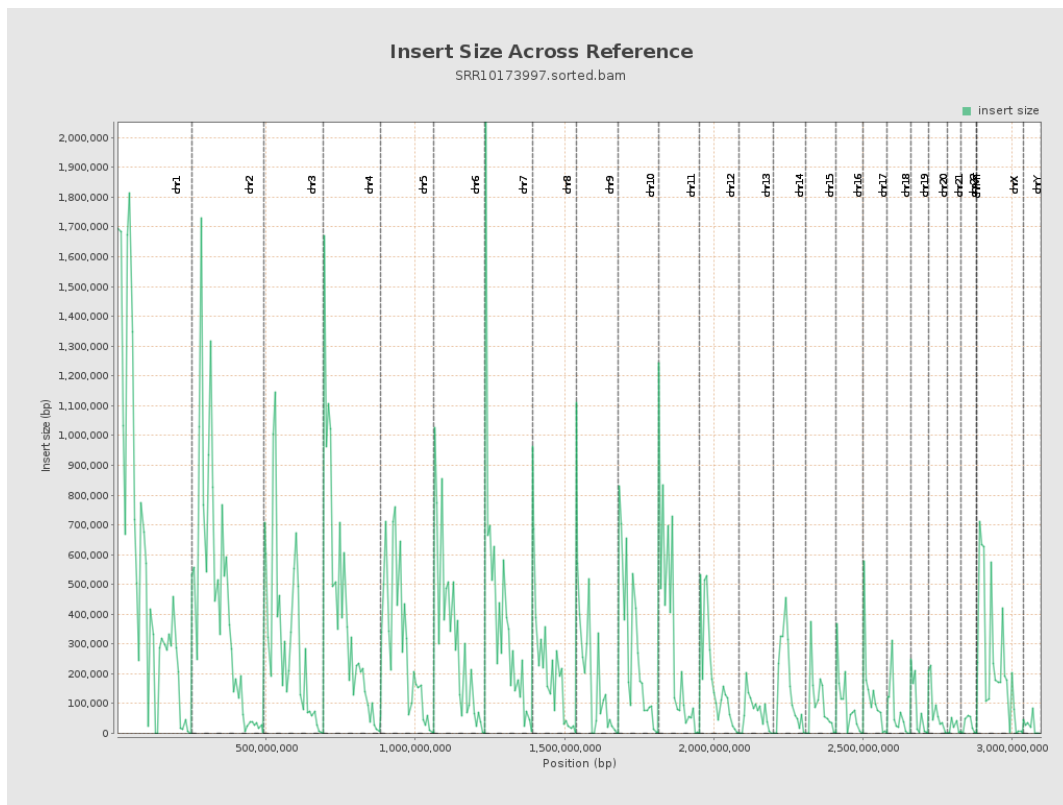
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

