

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:54:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173998.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_SRR10173998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173998_1.fastq.gz SRR10173998_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:54:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,981,828
Mapped reads	4,888,536 / 98.13%
Unmapped reads	93,292 / 1.87%
Mapped paired reads	4,888,536 / 98.13%
Mapped reads, first in pair	2,445,197 / 49.08%
Mapped reads, second in pair	2,443,339 / 49.05%
Mapped reads, both in pair	4,833,134 / 97.02%
Mapped reads, singletons	55,402 / 1.11%
Secondary alignments	0
Supplementary alignments	568,755 / 11.42%
Read min/max/mean length	30 / 133 / 123.29
Duplicated reads (estimated)	3,967,453 / 79.64%
Duplication rate	65.91%
Clipped reads	2,268,783 / 45.54%

2.2. ACGT Content

Number/percentage of A's	165,346,056 / 30.06%
Number/percentage of C's	108,578,701 / 19.74%
Number/percentage of T's	163,820,378 / 29.78%
Number/percentage of G's	112,303,238 / 20.42%
Number/percentage of N's	4,316 / 0%

GC Percentage	40.16%
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2.3. Coverage

Mean	0.1778
Standard Deviation	3.2111

2.4. Mapping Quality

Mean Mapping Quality	52.95
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2.5. Insert size

Mean	881,946.12
Standard Deviation	8,931,334.64
P25/Median/P75	101 / 143 / 209

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	4,473,629
Insertions	57,344
Mapped reads with at least one insertion	1.13%
Deletions	170,947
Mapped reads with at least one deletion	3.42%
Homopolymer indels	40.45%

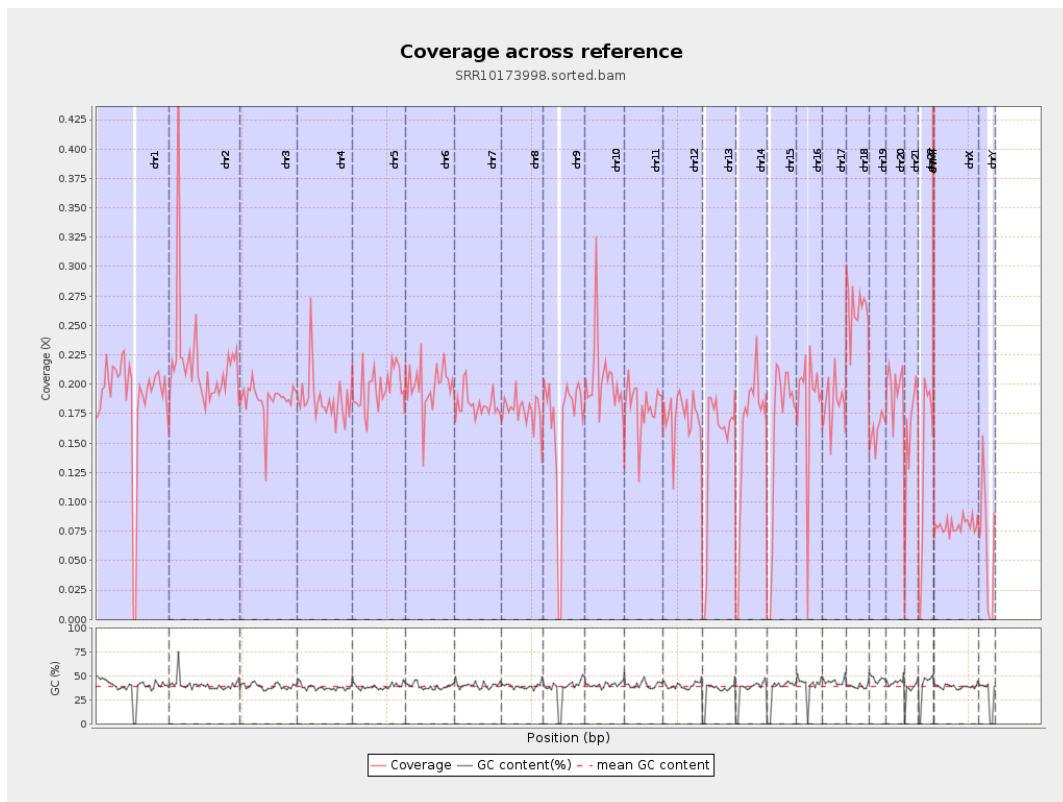
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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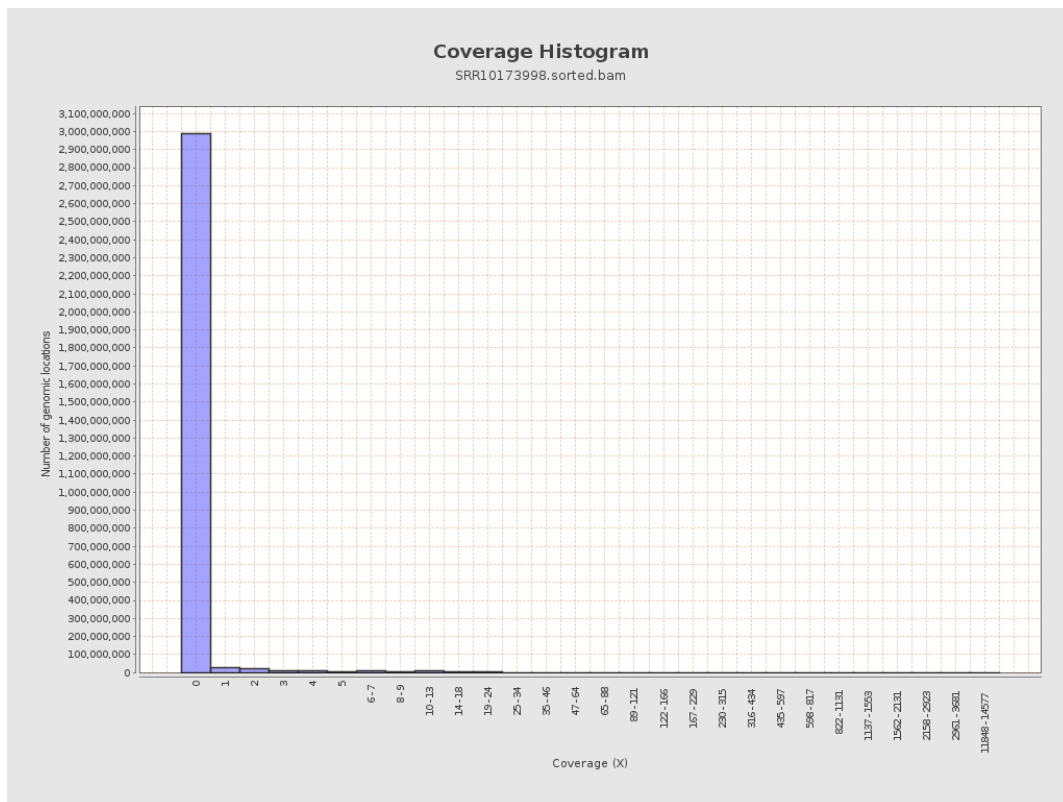
		bases	coverage	deviation
chr1	249250621	46686503	0.1873	1.6374
chr2	243199373	53199891	0.2188	10.2512
chr3	198022430	37097788	0.1873	1.3897
chr4	191154276	35662502	0.1866	1.5705
chr5	180915260	35590599	0.1967	1.4362
chr6	171115067	33997987	0.1987	1.507
chr7	159138663	29149615	0.1832	1.5564
chr8	146364022	25913312	0.177	1.9105
chr9	141213431	23053101	0.1633	1.4684
chr10	135534747	27742958	0.2047	1.9528
chr11	135006516	24413408	0.1808	1.3796
chr12	133851895	23122903	0.1727	1.3526
chr13	115169878	16561249	0.1438	1.2126
chr14	107349540	16885862	0.1573	1.2809
chr15	102531392	16141203	0.1574	1.2685
chr16	90354753	16702933	0.1849	1.5117
chr17	81195210	14836490	0.1827	1.3995
chr18	78077248	20713346	0.2653	1.9881
chr19	59128983	9518166	0.161	1.3366
chr20	63025520	12457733	0.1977	1.4219
chr21	48129895	7597130	0.1578	1.4266
chr22	51304566	6772916	0.132	1.29
chrMT	16571	669669	40.4121	36.0789
chrX	155270560	12339221	0.0795	0.8939

chrY	59373566	3625406	0.0611	0.9985
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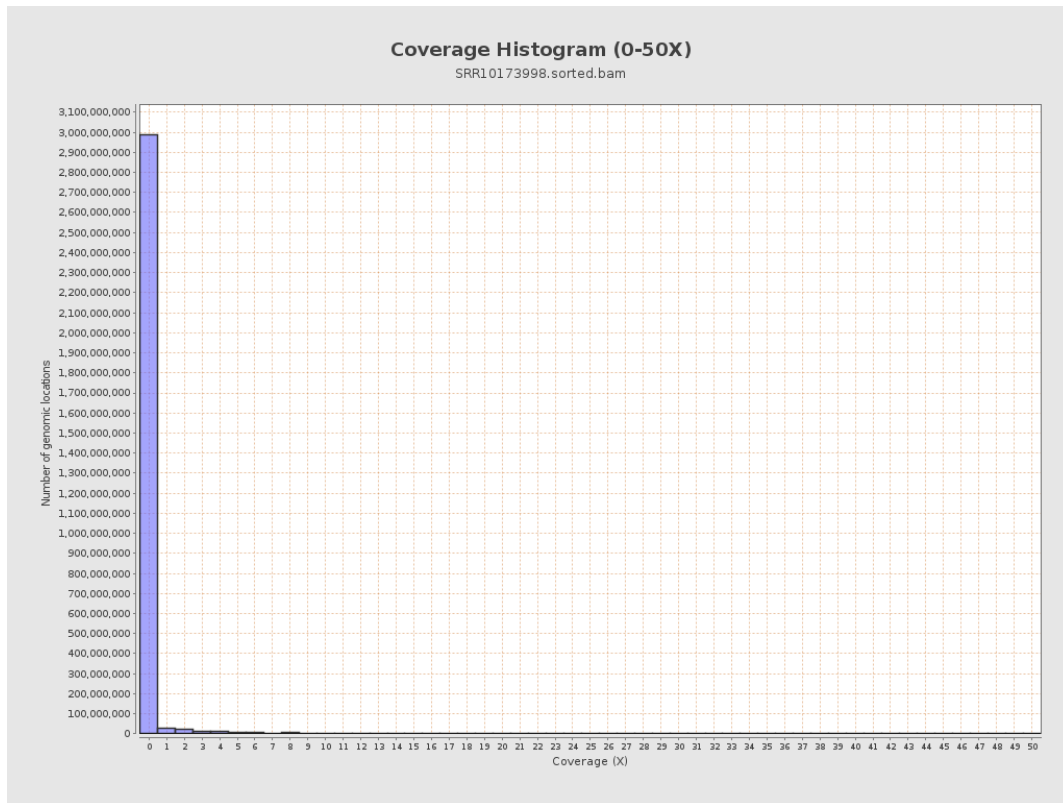
3. Results : Coverage across reference



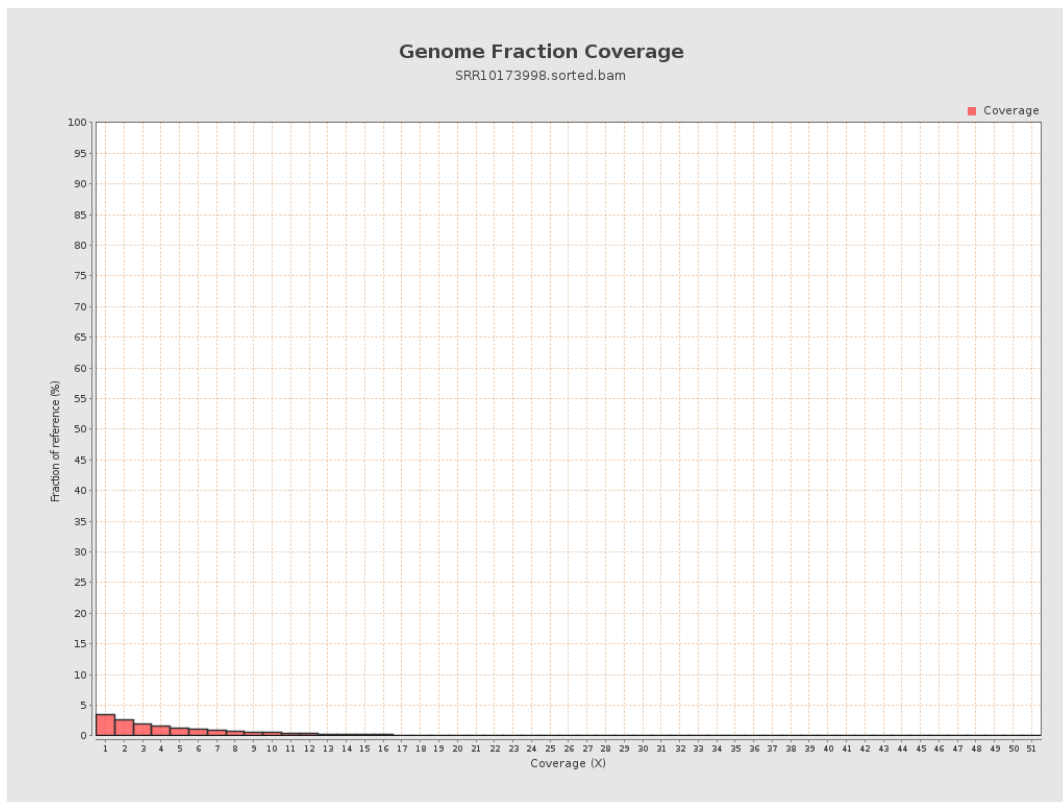
4. Results : Coverage Histogram



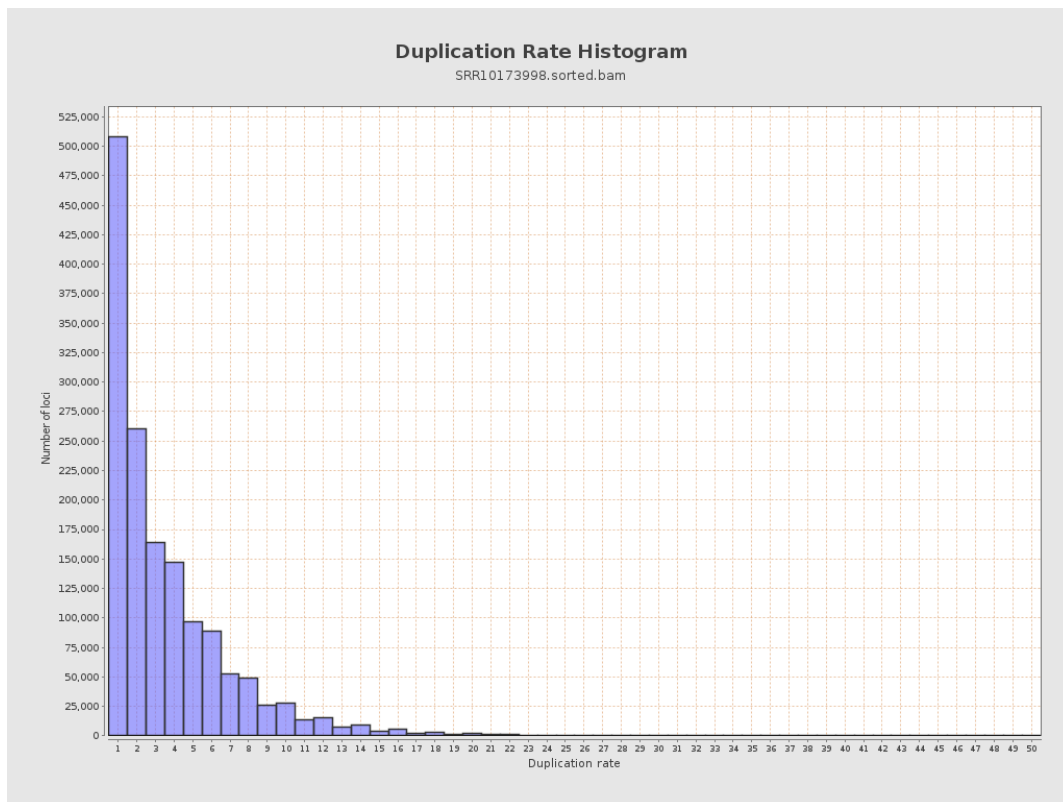
5. Results : Coverage Histogram (0-50X)



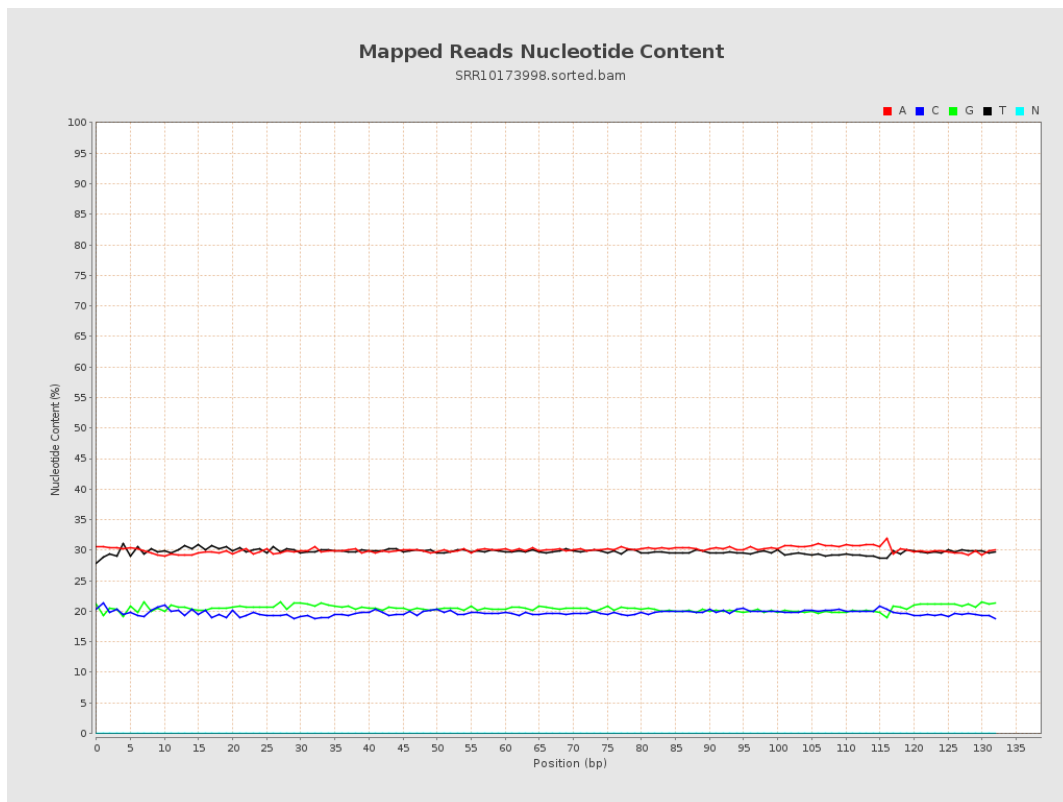
6. Results : Genome Fraction Coverage



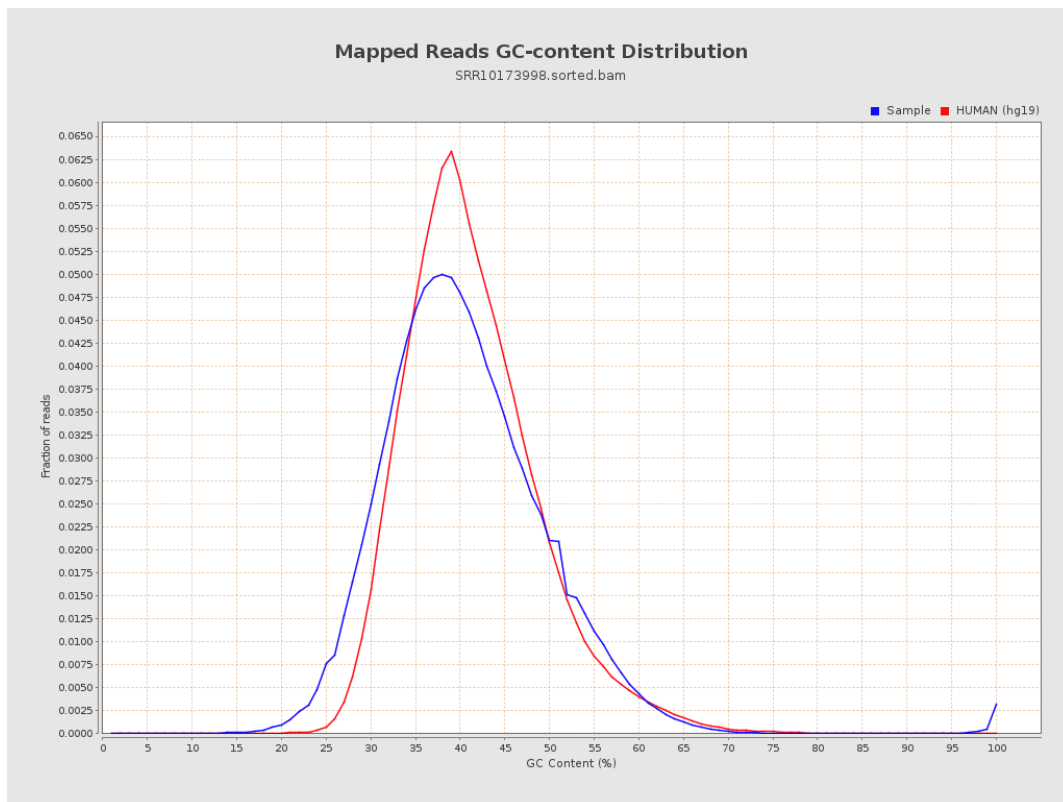
7. Results : Duplication Rate Histogram



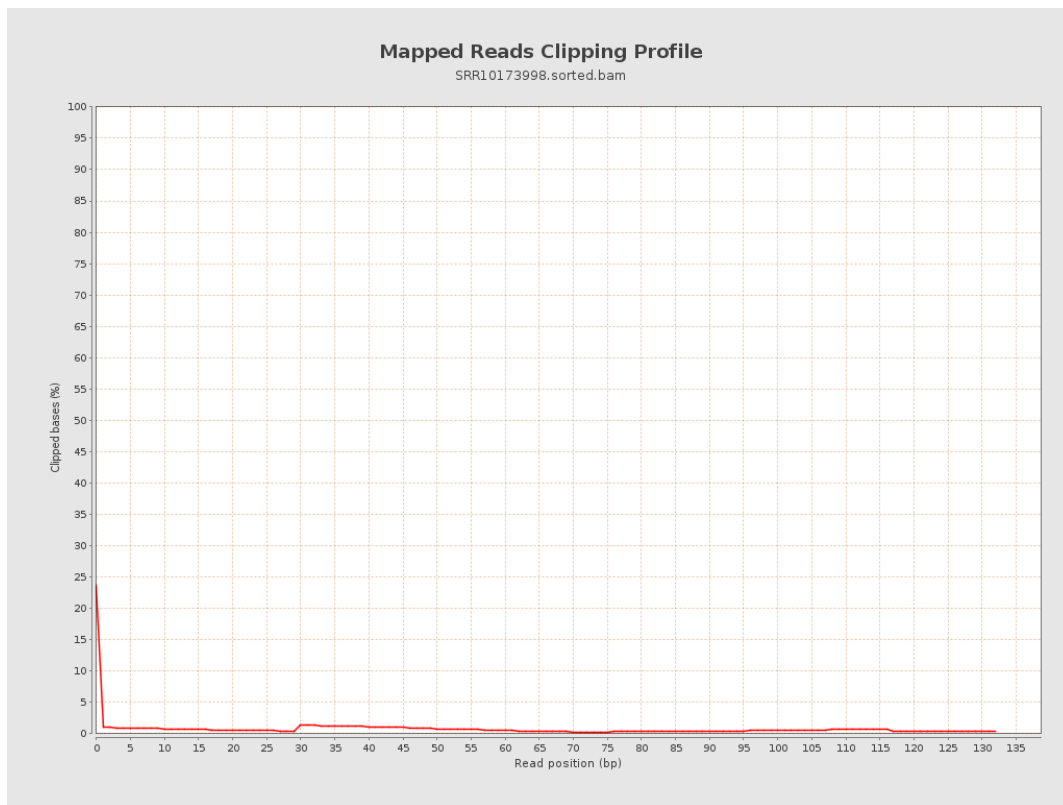
8. Results : Mapped Reads Nucleotide Content



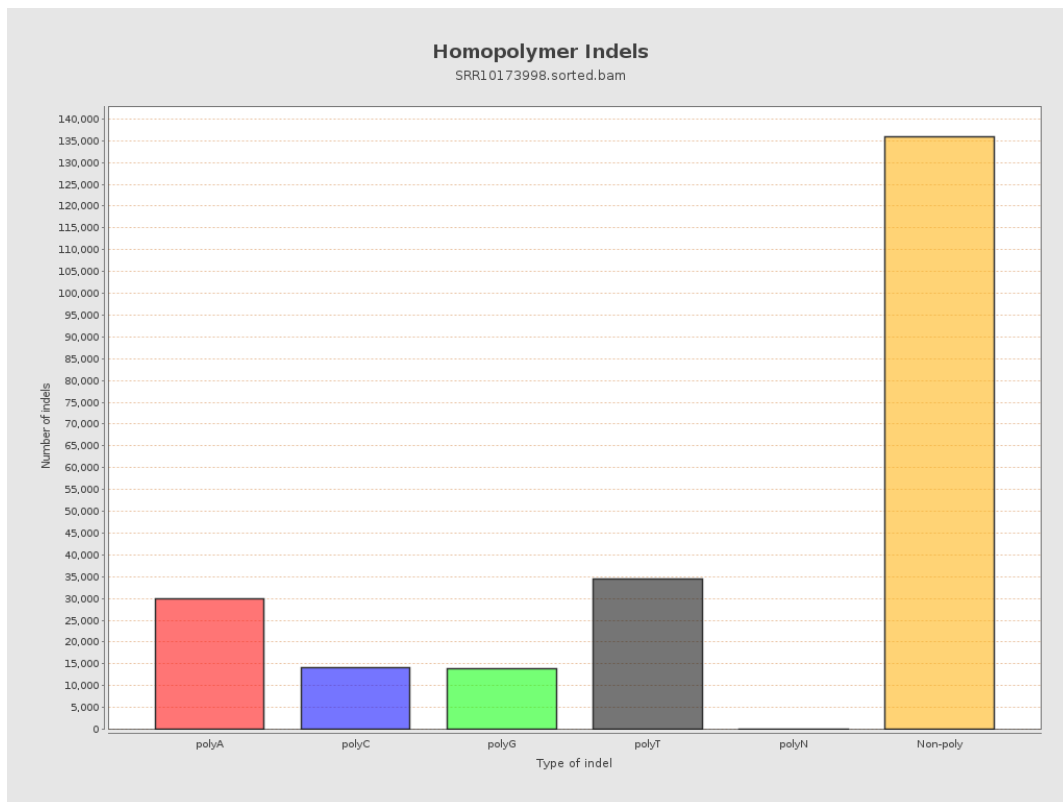
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



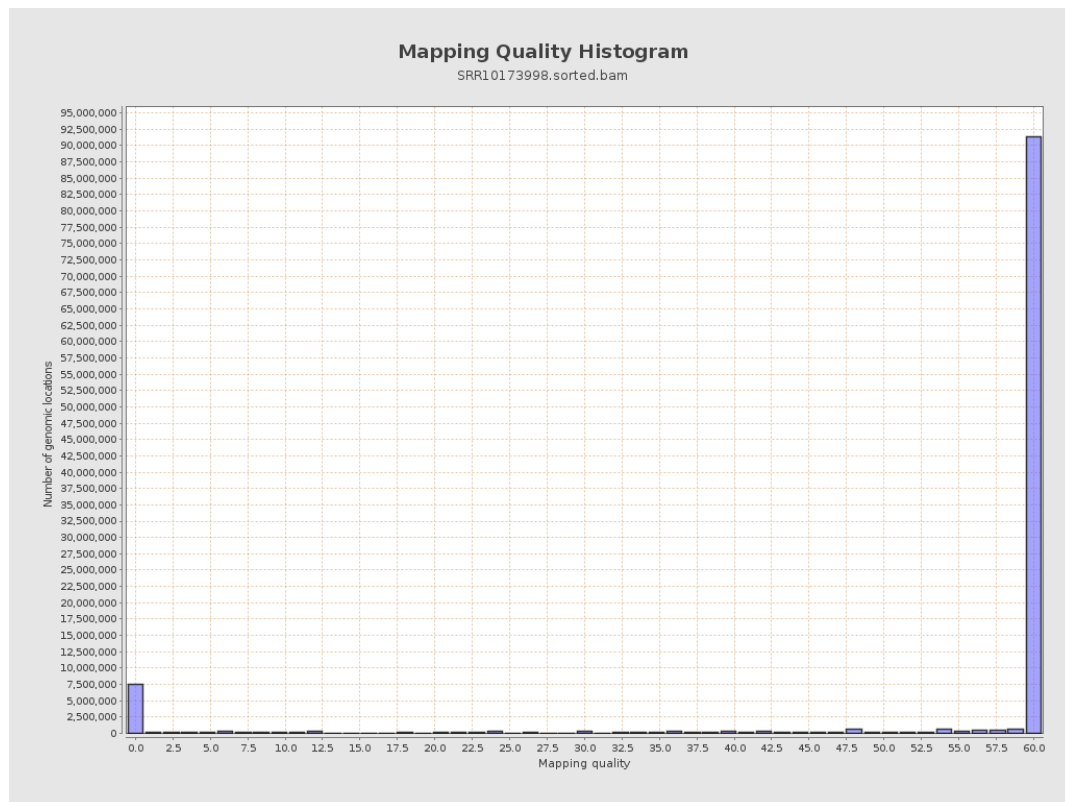
11. Results : Homopolymer Indels



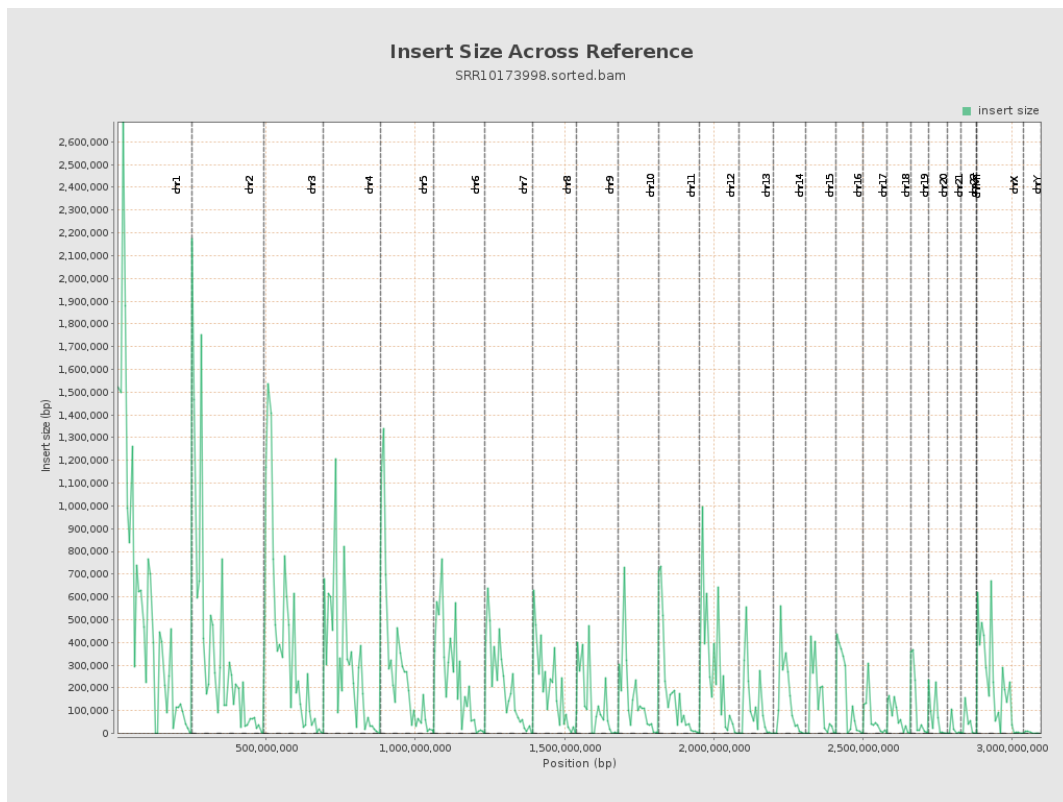
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

