

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 18:05:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173992.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_SRR10173992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173992_1.fastq.gz SRR10173992_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 18:05:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,896,774
Mapped reads	4,787,355 / 97.77%
Unmapped reads	109,419 / 2.23%
Mapped paired reads	4,787,355 / 97.77%
Mapped reads, first in pair	2,394,221 / 48.89%
Mapped reads, second in pair	2,393,134 / 48.87%
Mapped reads, both in pair	4,718,462 / 96.36%
Mapped reads, singletons	68,893 / 1.41%
Secondary alignments	0
Supplementary alignments	606,228 / 12.38%
Read min/max/mean length	30 / 133 / 125.51
Duplicated reads (estimated)	3,800,193 / 77.61%
Duplication rate	64.5%
Clipped reads	2,401,986 / 49.05%

2.2. ACGT Content

Number/percentage of A's	161,695,132 / 29.72%
Number/percentage of C's	108,919,177 / 20.02%
Number/percentage of T's	160,344,270 / 29.47%
Number/percentage of G's	113,059,949 / 20.78%
Number/percentage of N's	4,456 / 0%

GC Percentage	40.8%
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2.3. Coverage

Mean	0.1759
Standard Deviation	3.1011

2.4. Mapping Quality

Mean Mapping Quality	52.58
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2.5. Insert size

Mean	846,752.46
Standard Deviation	8,840,813.42
P25/Median/P75	108 / 157 / 240

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	4,643,853
Insertions	60,288
Mapped reads with at least one insertion	1.21%
Deletions	147,508
Mapped reads with at least one deletion	3.01%
Homopolymer indels	41.49%

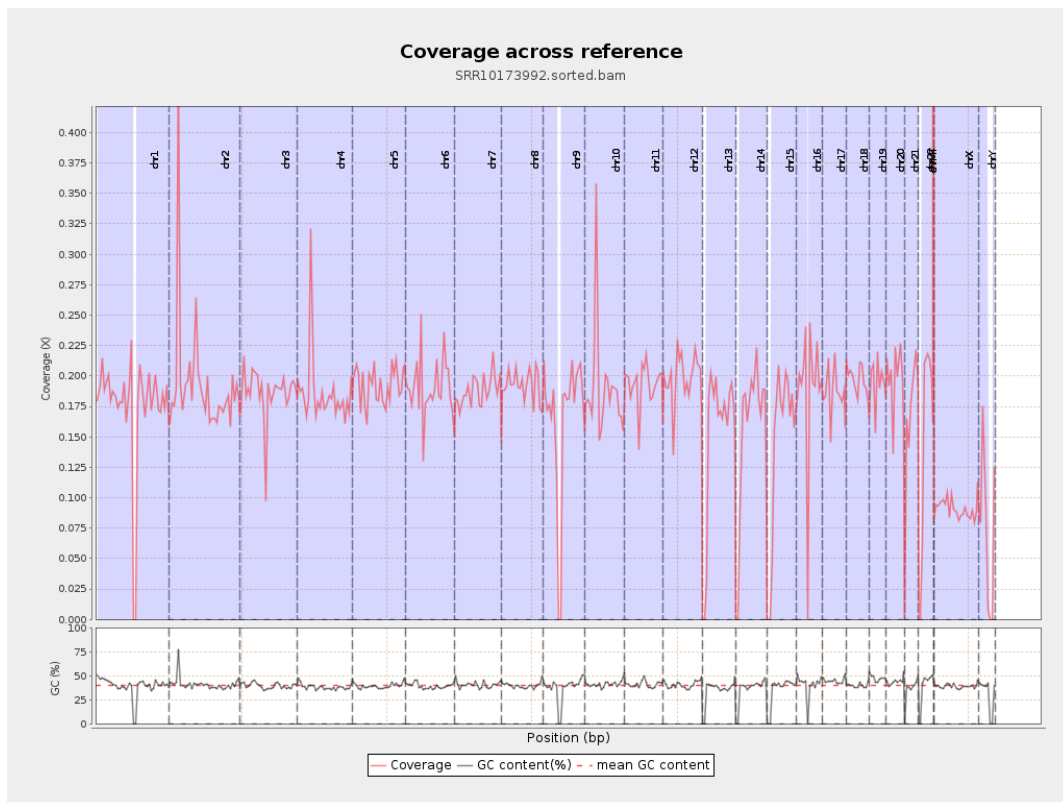
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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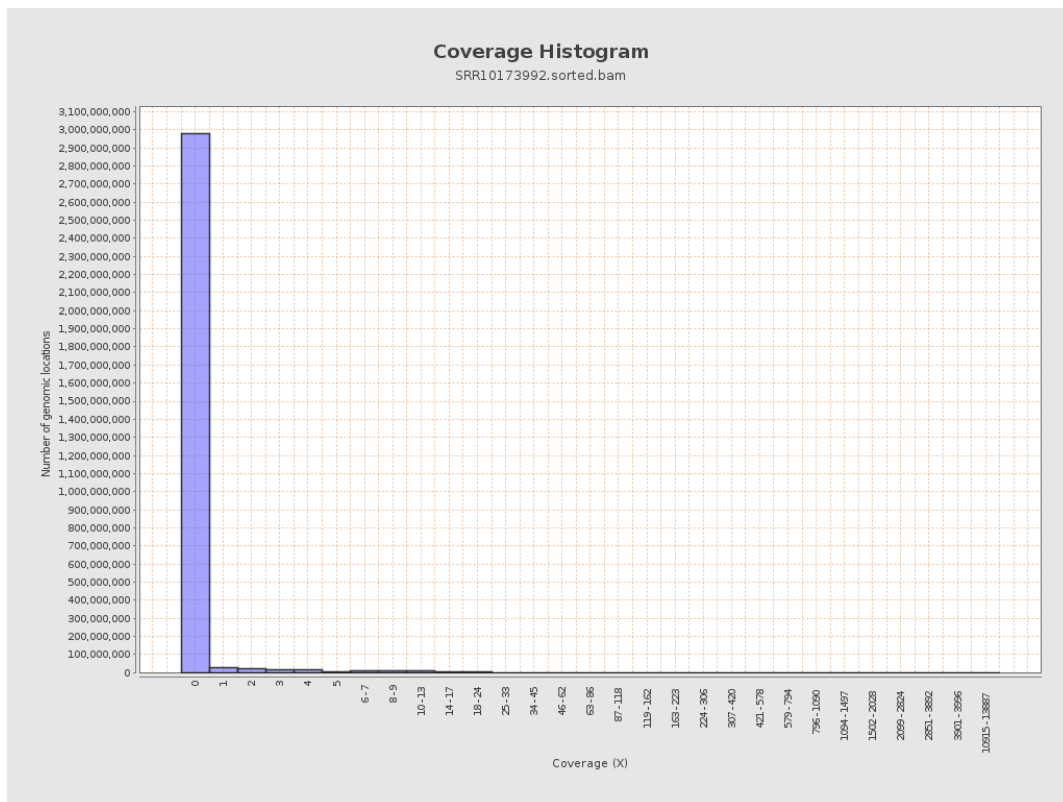
		bases	coverage	deviation
chr1	249250621	43660563	0.1752	1.9137
chr2	243199373	47009185	0.1933	9.7196
chr3	198022430	36820167	0.1859	1.2893
chr4	191154276	35455761	0.1855	1.651
chr5	180915260	34735778	0.192	1.3145
chr6	171115067	32611708	0.1906	1.5146
chr7	159138663	30006413	0.1886	1.6086
chr8	146364022	28145551	0.1923	1.8872
chr9	141213431	23079378	0.1634	1.6193
chr10	135534747	25601711	0.1889	2.0085
chr11	135006516	26113145	0.1934	1.3626
chr12	133851895	26545617	0.1983	1.3694
chr13	115169878	17309174	0.1503	1.1614
chr14	107349540	16640792	0.155	1.1899
chr15	102531392	14838373	0.1447	1.1462
chr16	90354753	17063108	0.1888	1.5489
chr17	81195210	15084067	0.1858	1.3902
chr18	78077248	15446958	0.1978	2.3359
chr19	59128983	11470931	0.194	1.6018
chr20	63025520	12411812	0.1969	1.3993
chr21	48129895	7990979	0.166	1.46
chr22	51304566	7322310	0.1427	1.2399
chrMT	16571	819956	49.4814	43.355
chrX	155270560	14049008	0.0905	0.8957

chrY	59373566	4146308	0.0698	1.1485
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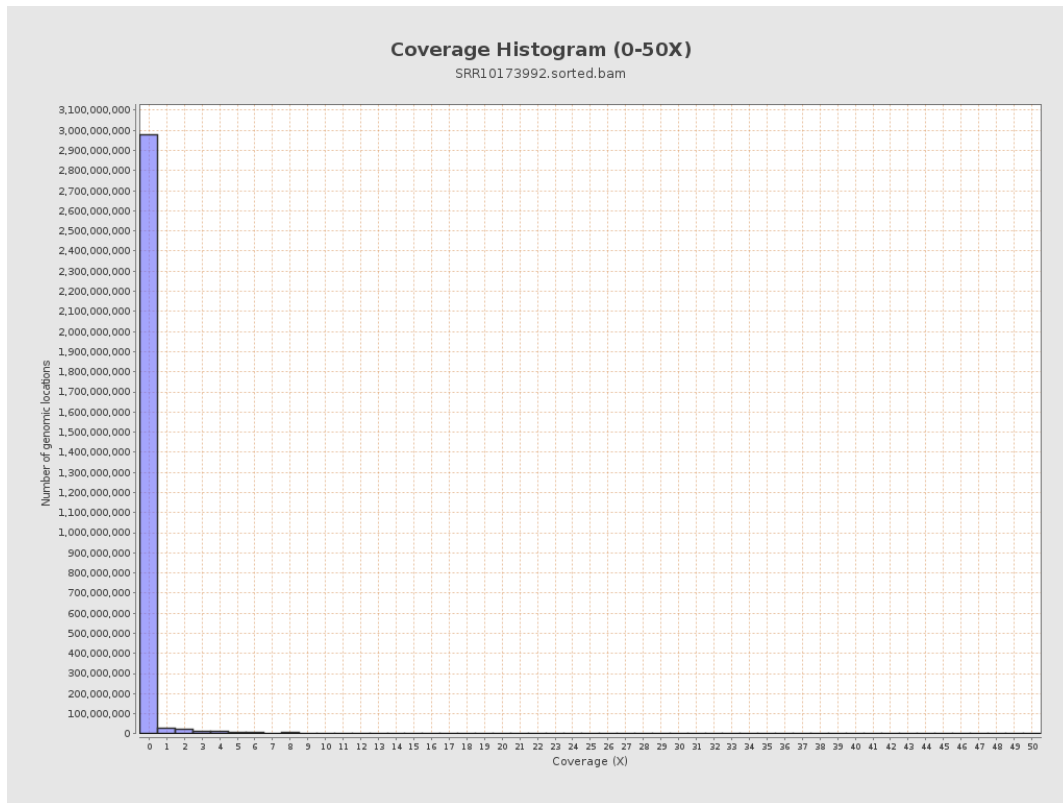
3. Results : Coverage across reference



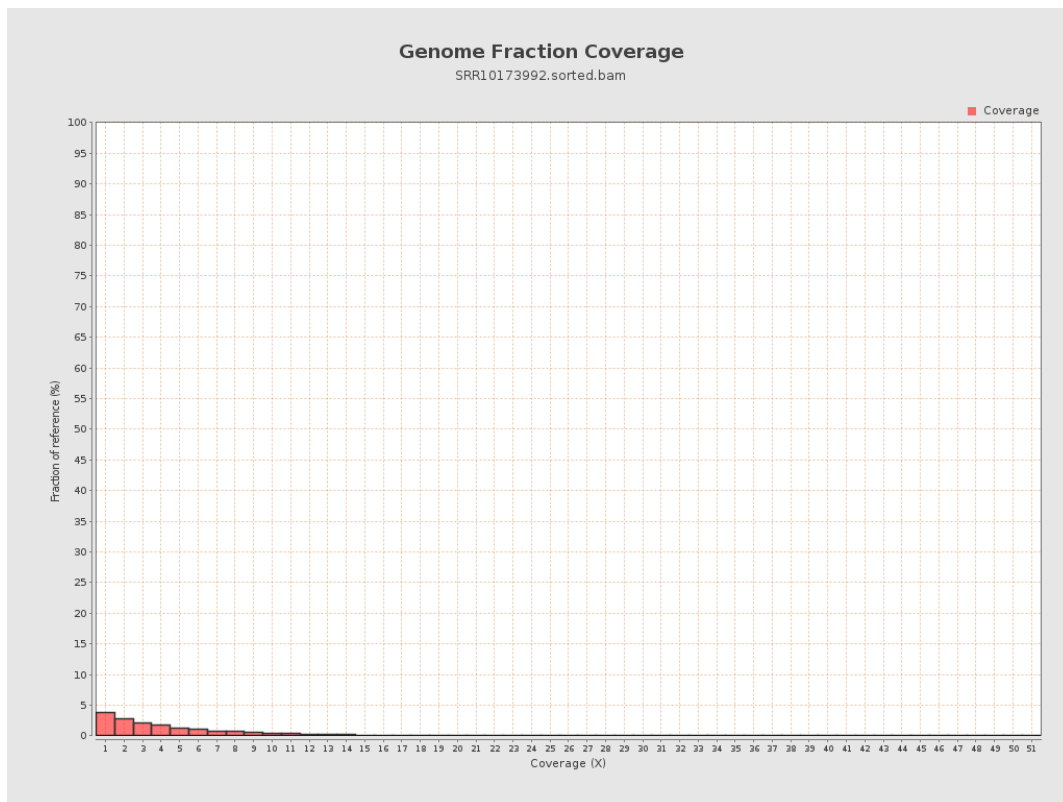
4. Results : Coverage Histogram



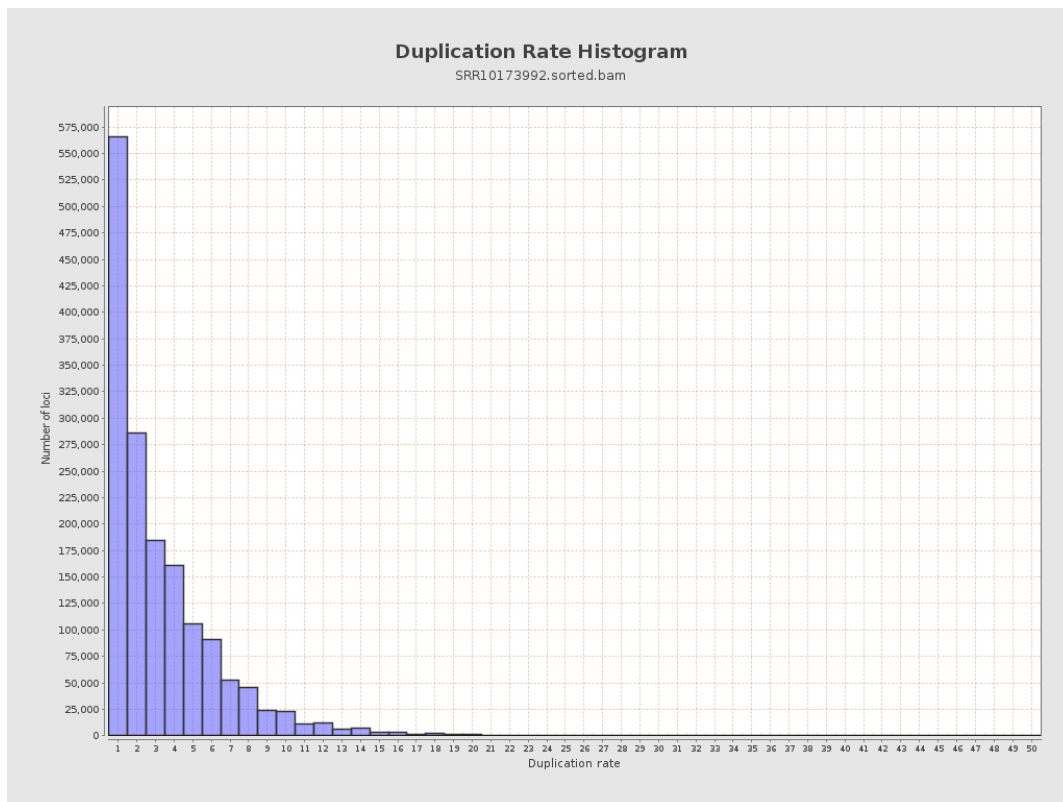
5. Results : Coverage Histogram (0-50X)



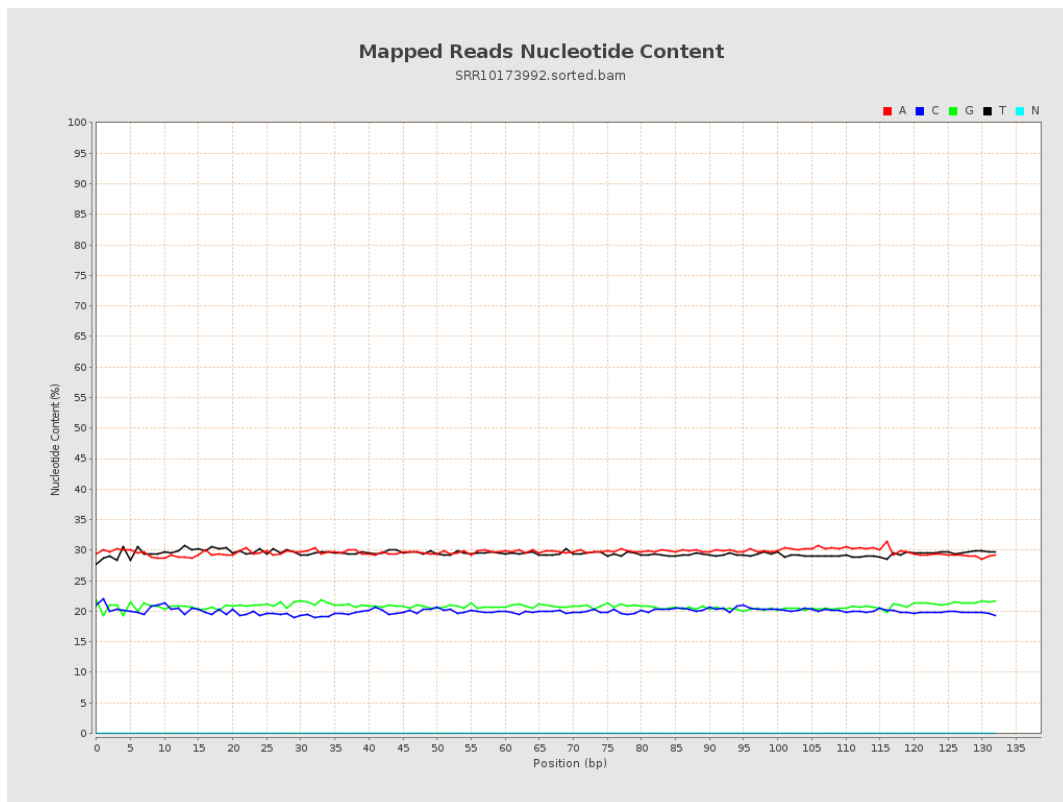
6. Results : Genome Fraction Coverage



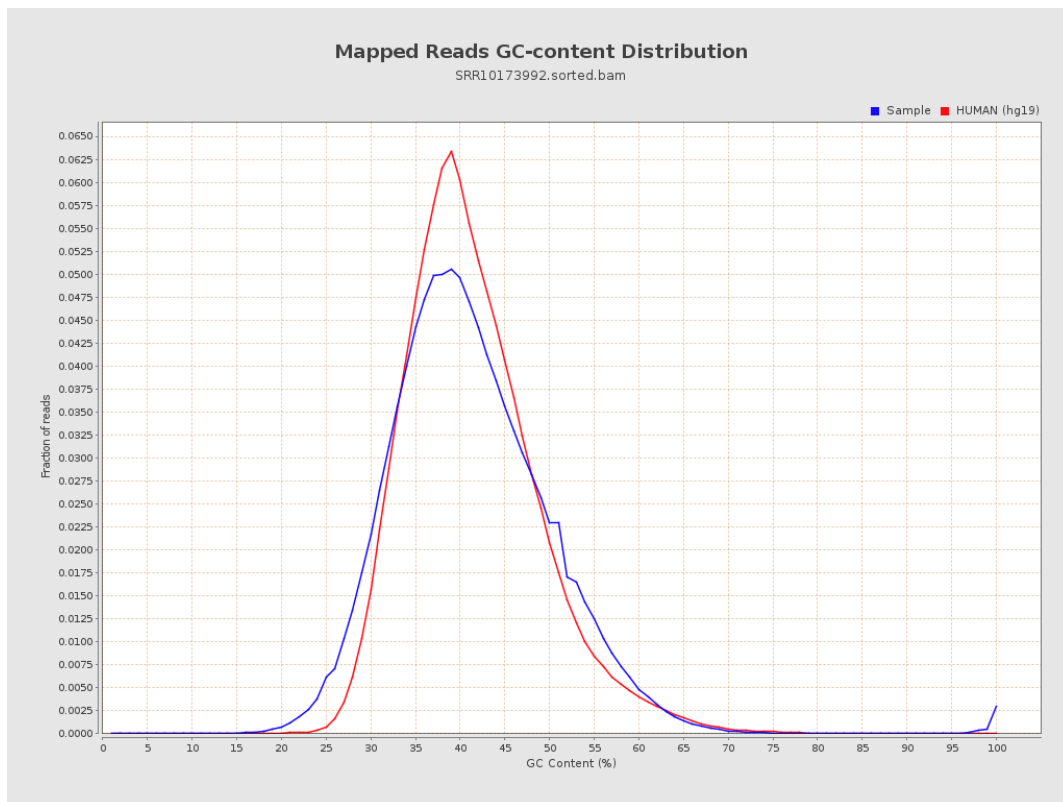
7. Results : Duplication Rate Histogram



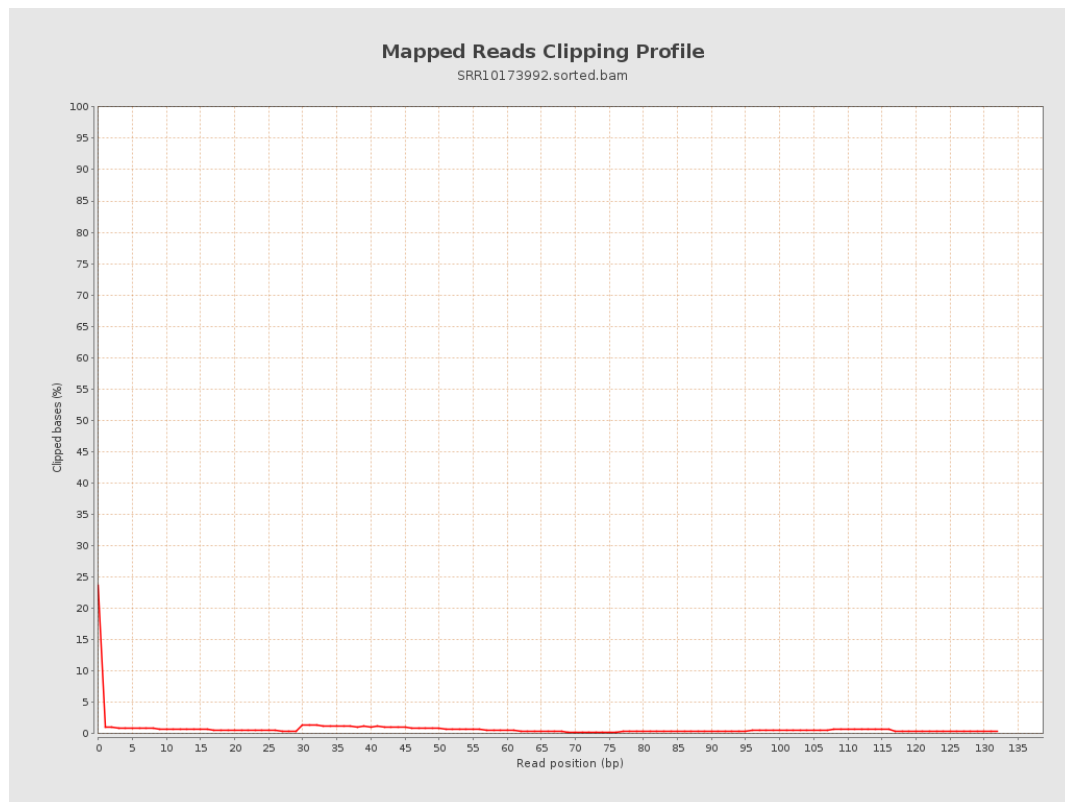
8. Results : Mapped Reads Nucleotide Content



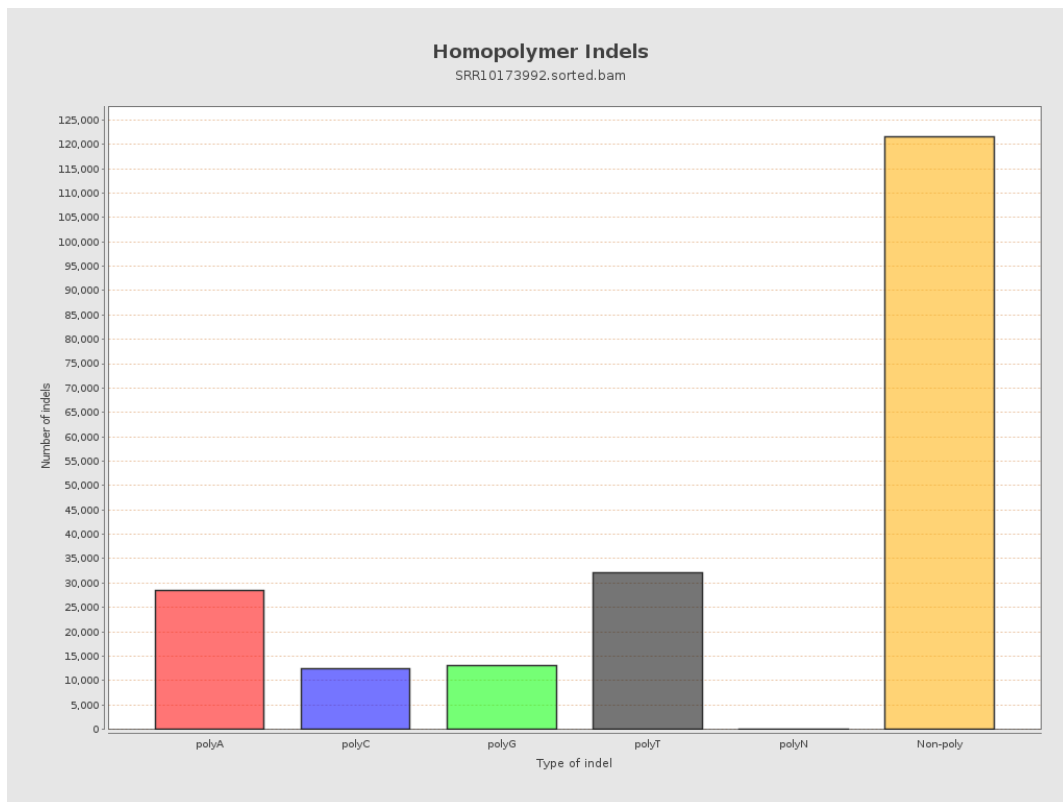
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



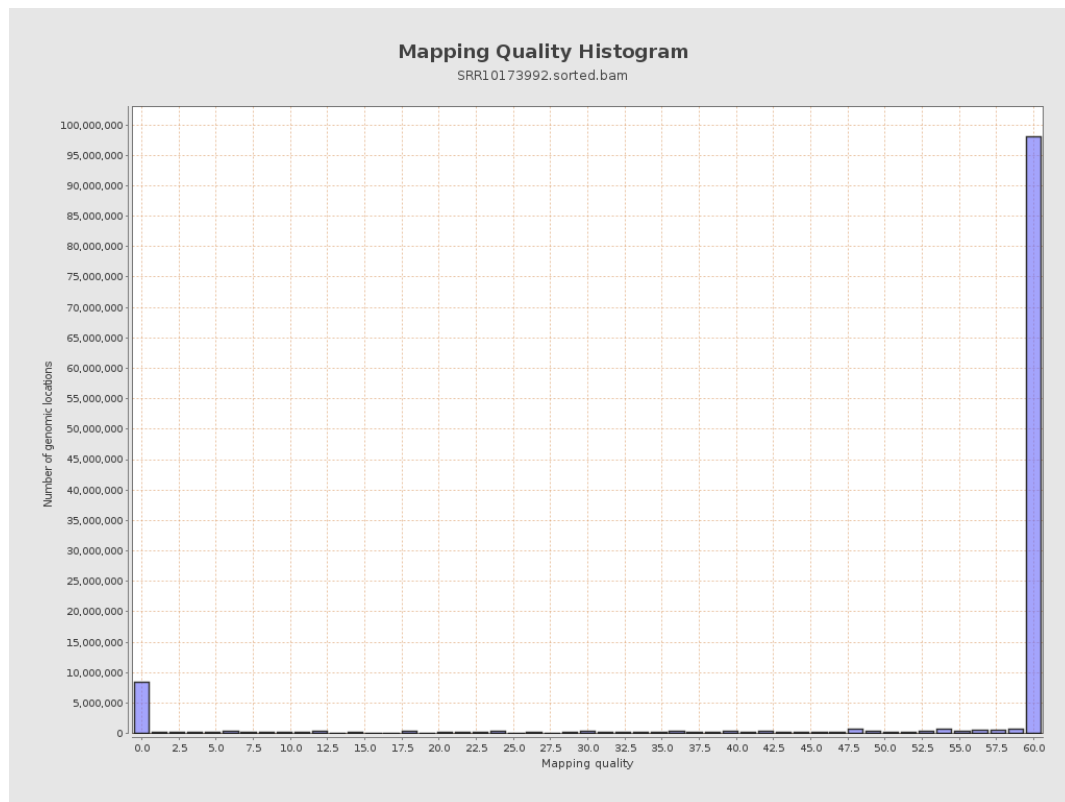
11. Results : Homopolymer Indels



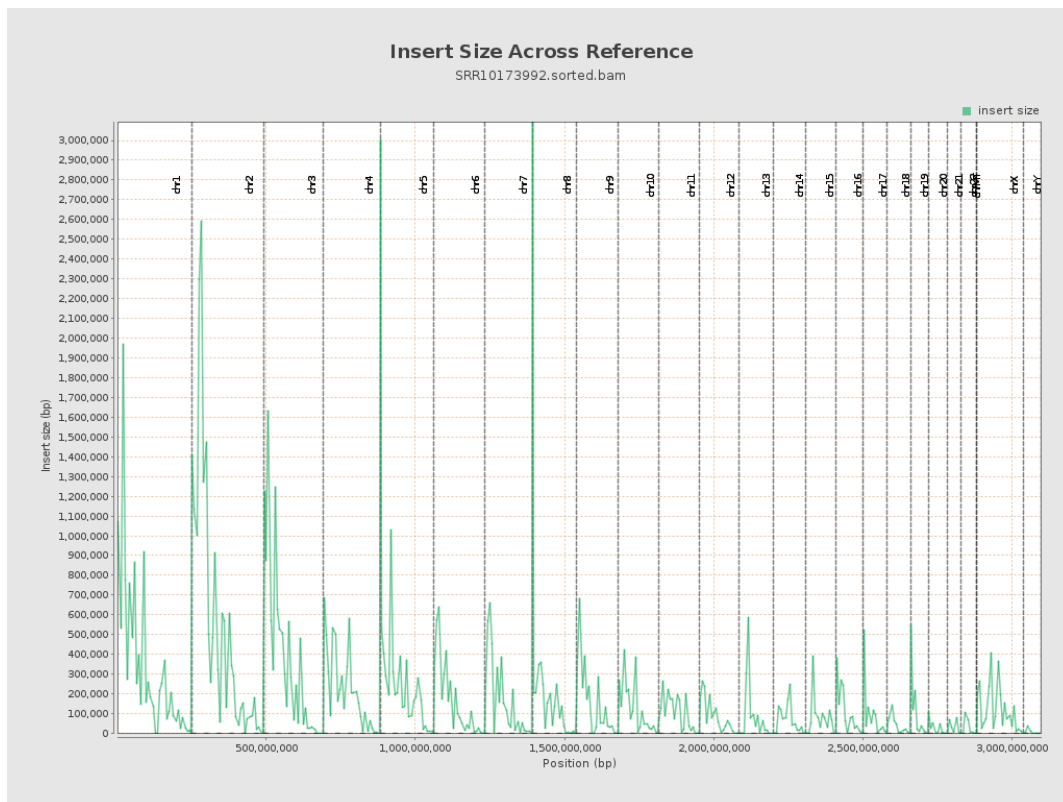
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

