

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 16:40:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173983.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_SRR10173983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173983_1.fastq.gz SRR10173983_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 16:40:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,908,282
Mapped reads	3,824,216 / 97.85%
Unmapped reads	84,066 / 2.15%
Mapped paired reads	3,824,216 / 97.85%
Mapped reads, first in pair	1,912,008 / 48.92%
Mapped reads, second in pair	1,912,208 / 48.93%
Mapped reads, both in pair	3,769,222 / 96.44%
Mapped reads, singletons	54,994 / 1.41%
Secondary alignments	0
Supplementary alignments	518,308 / 13.26%
Read min/max/mean length	30 / 133 / 126.15
Duplicated reads (estimated)	3,059,009 / 78.27%
Duplication rate	64.59%
Clipped reads	1,962,426 / 50.21%

2.2. ACGT Content

Number/percentage of A's	129,437,460 / 29.71%
Number/percentage of C's	86,971,782 / 19.97%
Number/percentage of T's	128,683,422 / 29.54%
Number/percentage of G's	90,512,407 / 20.78%
Number/percentage of N's	3,629 / 0%

GC Percentage	40.74%
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2.3. Coverage

Mean	0.1408
Standard Deviation	2.4962

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	1,218,754.19
Standard Deviation	10,472,267.37
P25/Median/P75	108 / 159 / 245

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	3,692,277
Insertions	48,009
Mapped reads with at least one insertion	1.21%
Deletions	134,886
Mapped reads with at least one deletion	3.44%
Homopolymer indels	40.68%

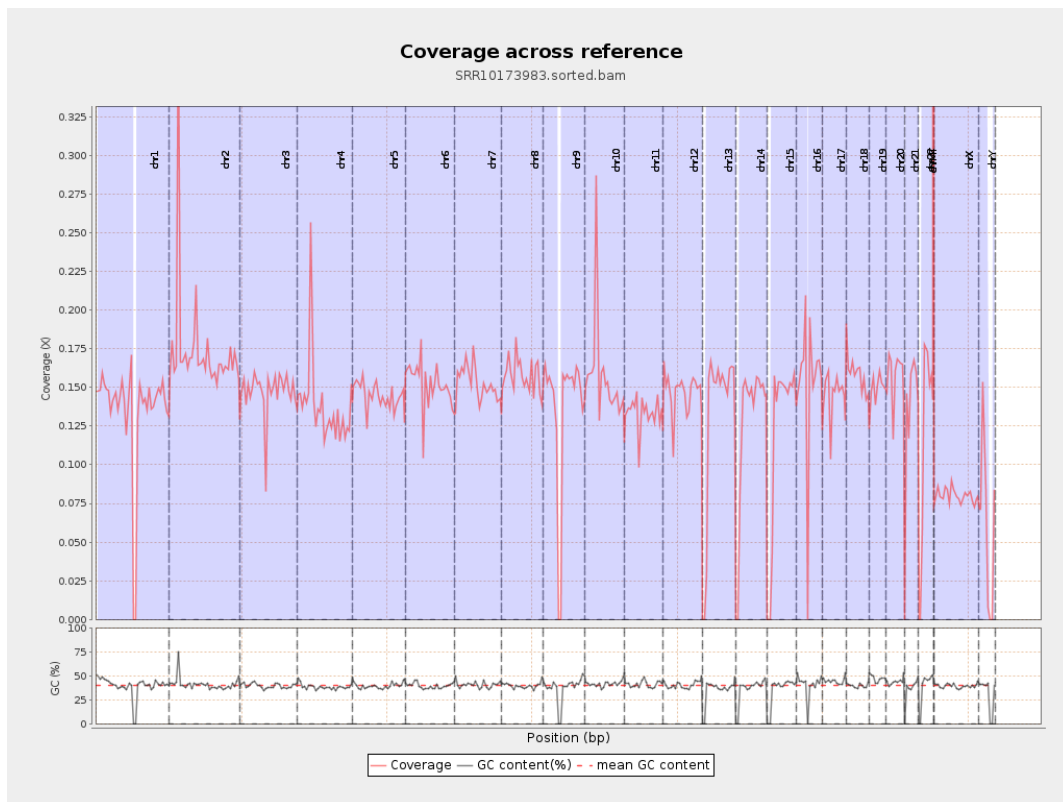
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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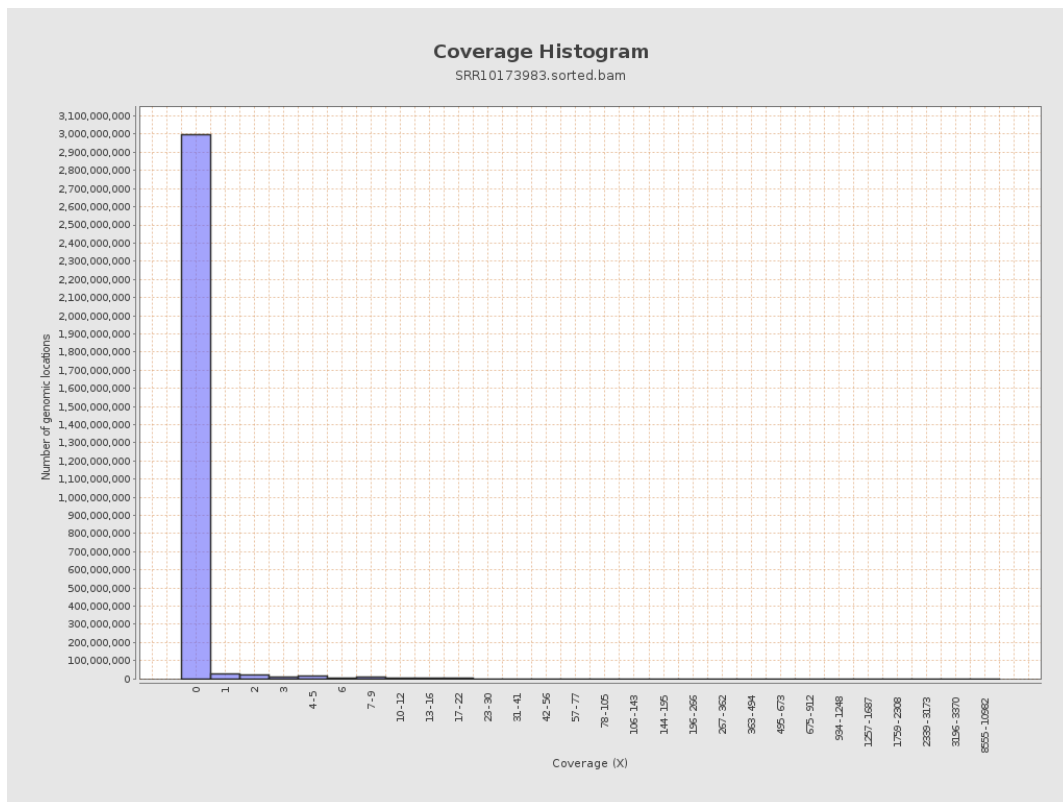
		bases	coverage	deviation
chr1	249250621	33764535	0.1355	1.4046
chr2	243199373	42452722	0.1746	7.7173
chr3	198022430	29108247	0.147	1.1395
chr4	191154276	26241520	0.1373	1.3962
chr5	180915260	26198221	0.1448	1.133
chr6	171115067	26035503	0.1522	1.2435
chr7	159138663	24370873	0.1531	1.553
chr8	146364022	23135204	0.1581	1.6539
chr9	141213431	19182122	0.1358	1.3326
chr10	135534747	21294007	0.1571	1.7258
chr11	135006516	18014066	0.1334	1.0912
chr12	133851895	19637954	0.1467	1.1648
chr13	115169878	15100197	0.1311	1.0792
chr14	107349540	13507163	0.1258	1.05
chr15	102531392	12493140	0.1218	1.04
chr16	90354753	13830425	0.1531	1.334
chr17	81195210	11729703	0.1445	1.1466
chr18	78077248	12340424	0.1581	1.7113
chr19	59128983	8859518	0.1498	1.3365
chr20	63025520	9931657	0.1576	1.2328
chr21	48129895	6494137	0.1349	1.3429
chr22	51304566	5848967	0.114	1.1288
chrMT	16571	481568	29.0609	26.0206
chrX	155270560	12401253	0.0799	0.8405

chrY	59373566	3469316	0.0584	0.9696
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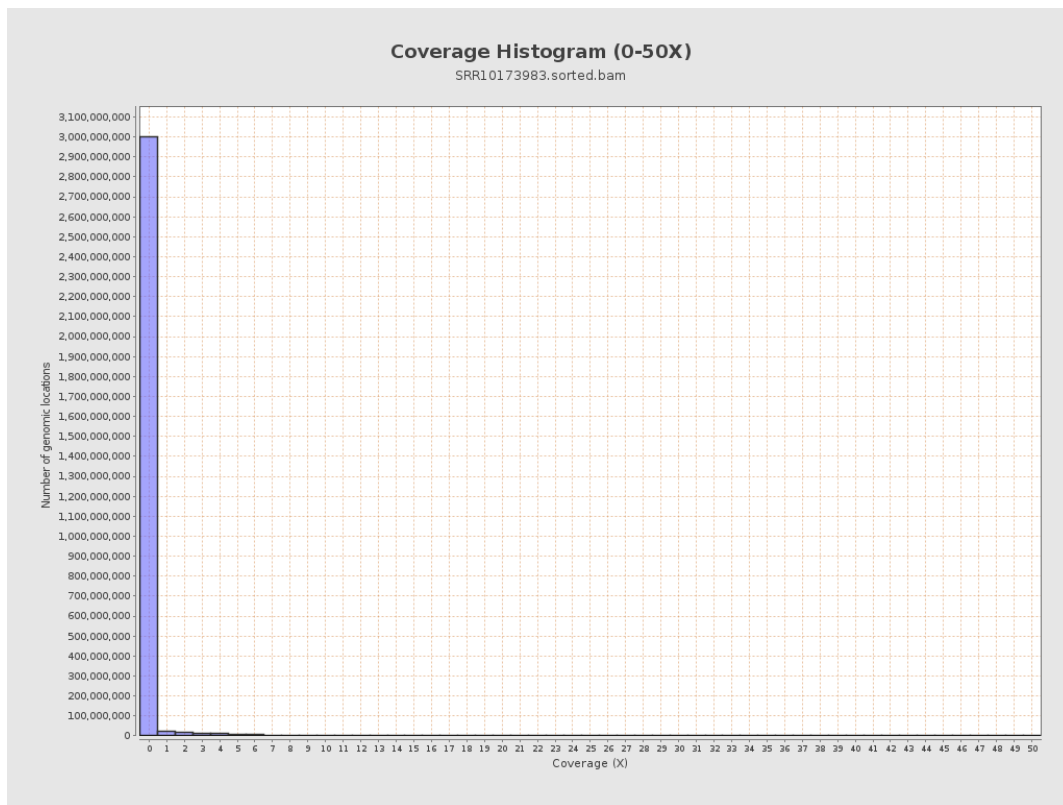
3. Results : Coverage across reference



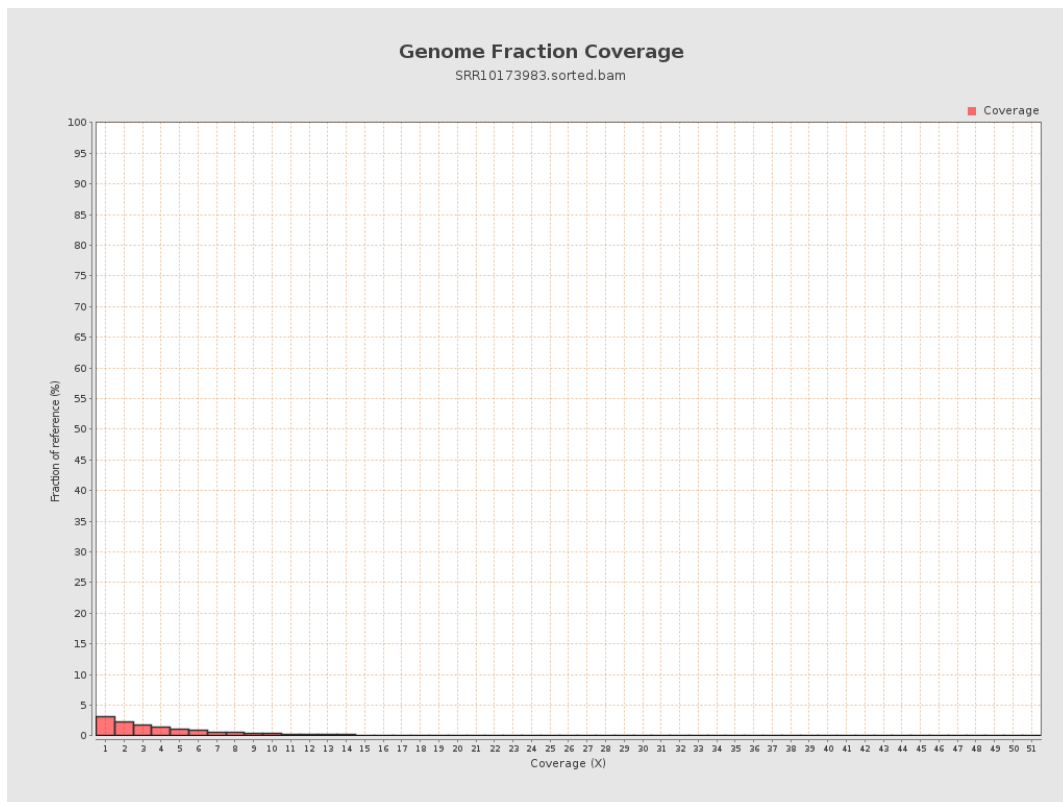
4. Results : Coverage Histogram



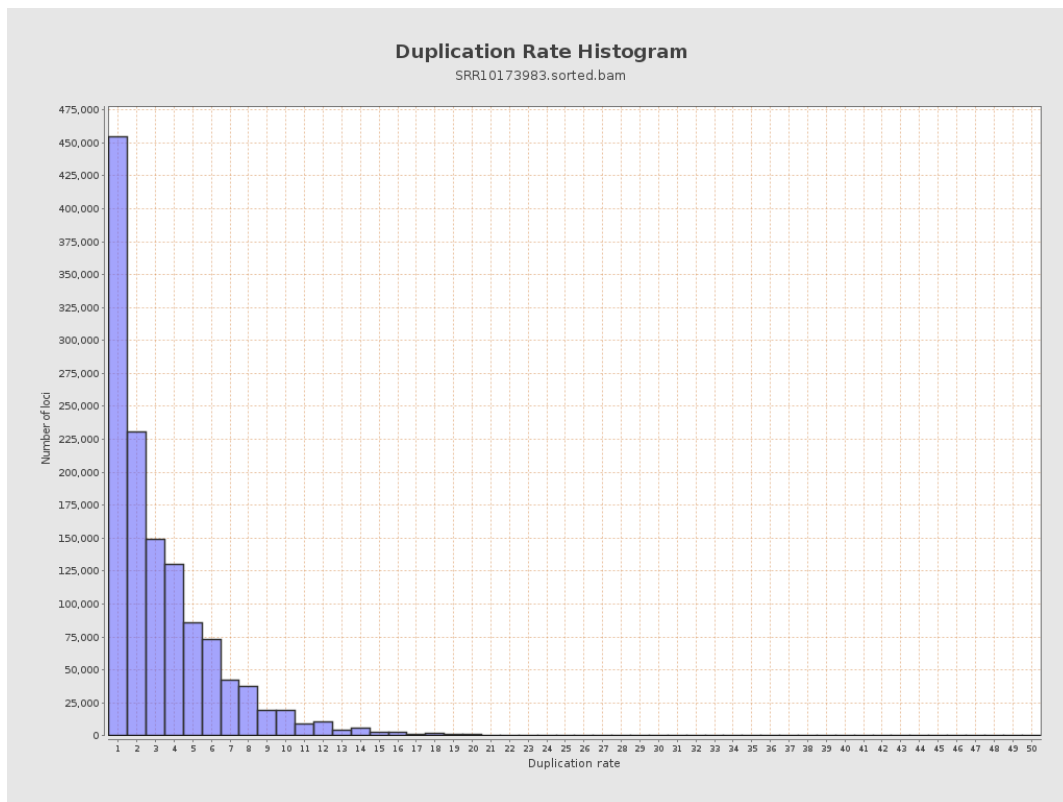
5. Results : Coverage Histogram (0-50X)



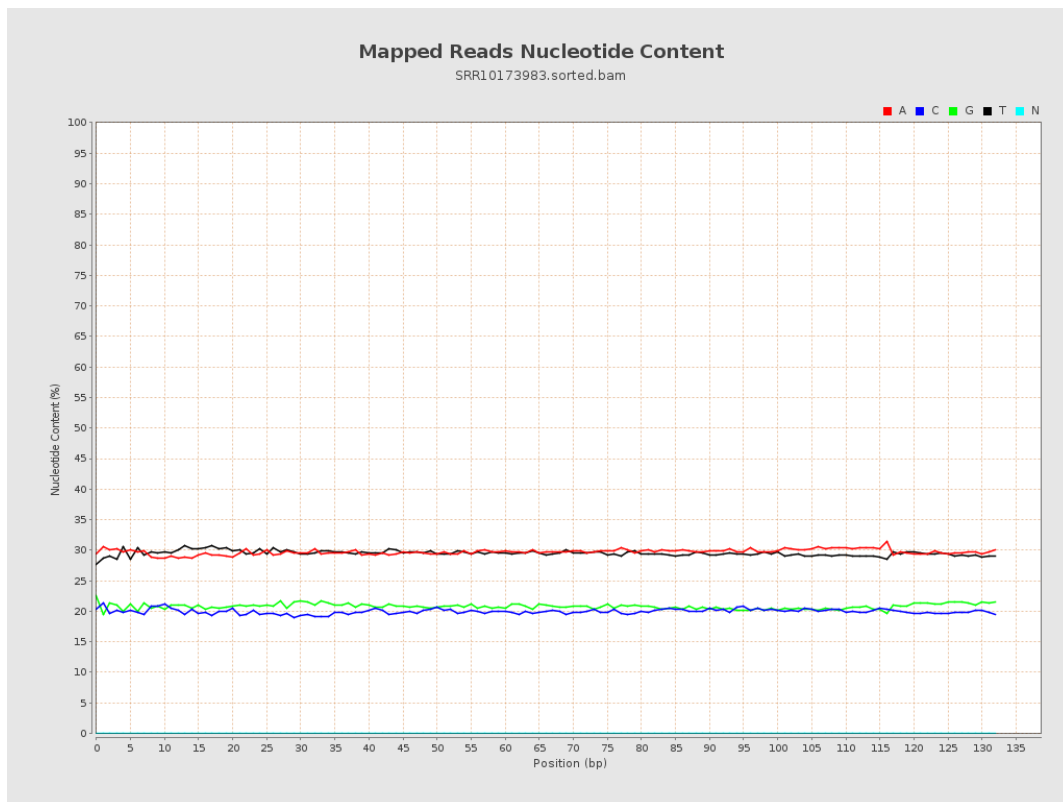
6. Results : Genome Fraction Coverage



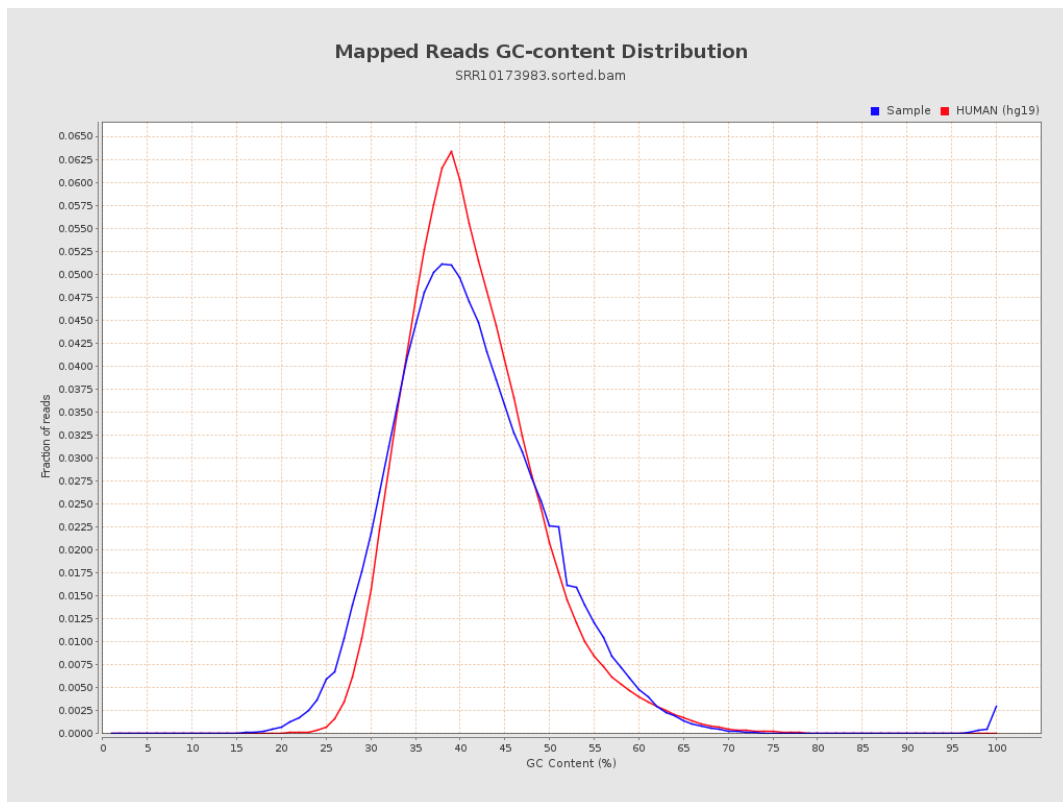
7. Results : Duplication Rate Histogram



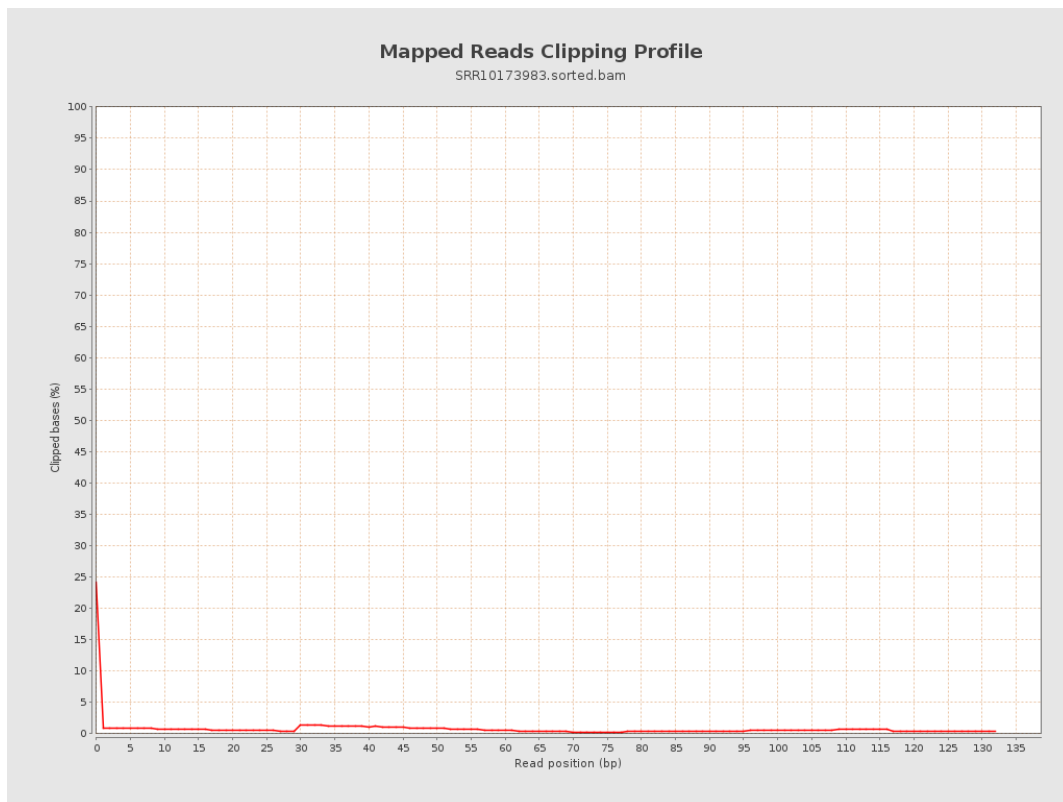
8. Results : Mapped Reads Nucleotide Content



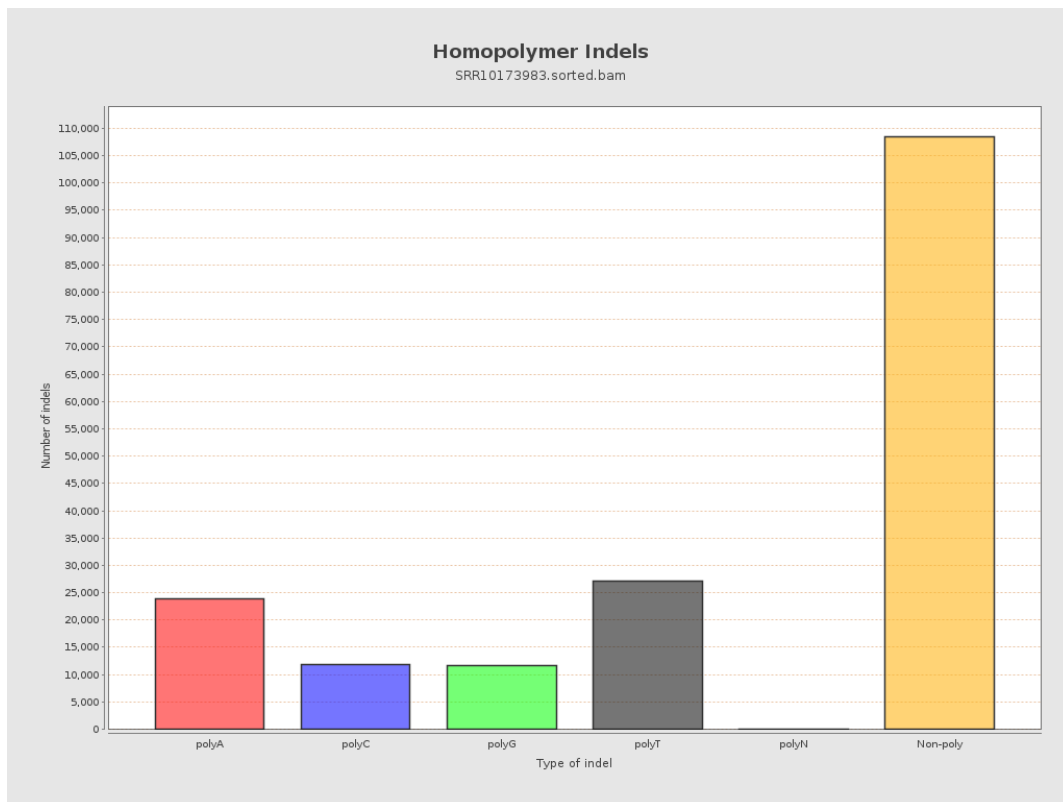
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



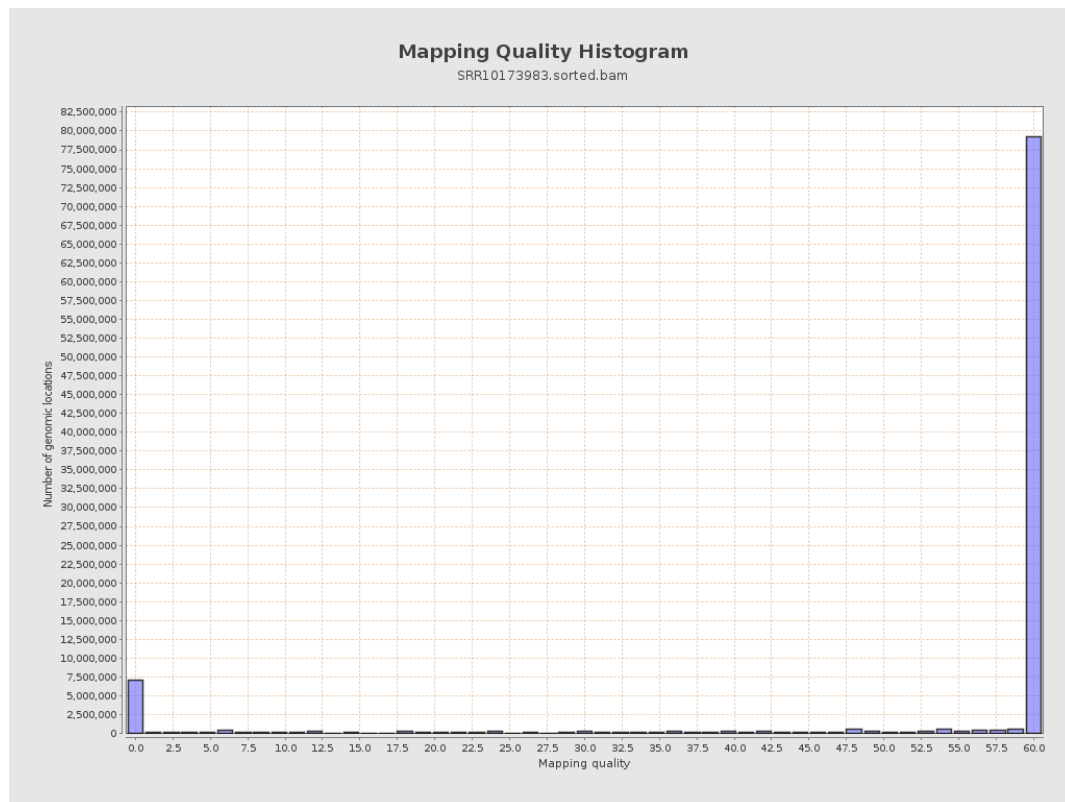
11. Results : Homopolymer Indels



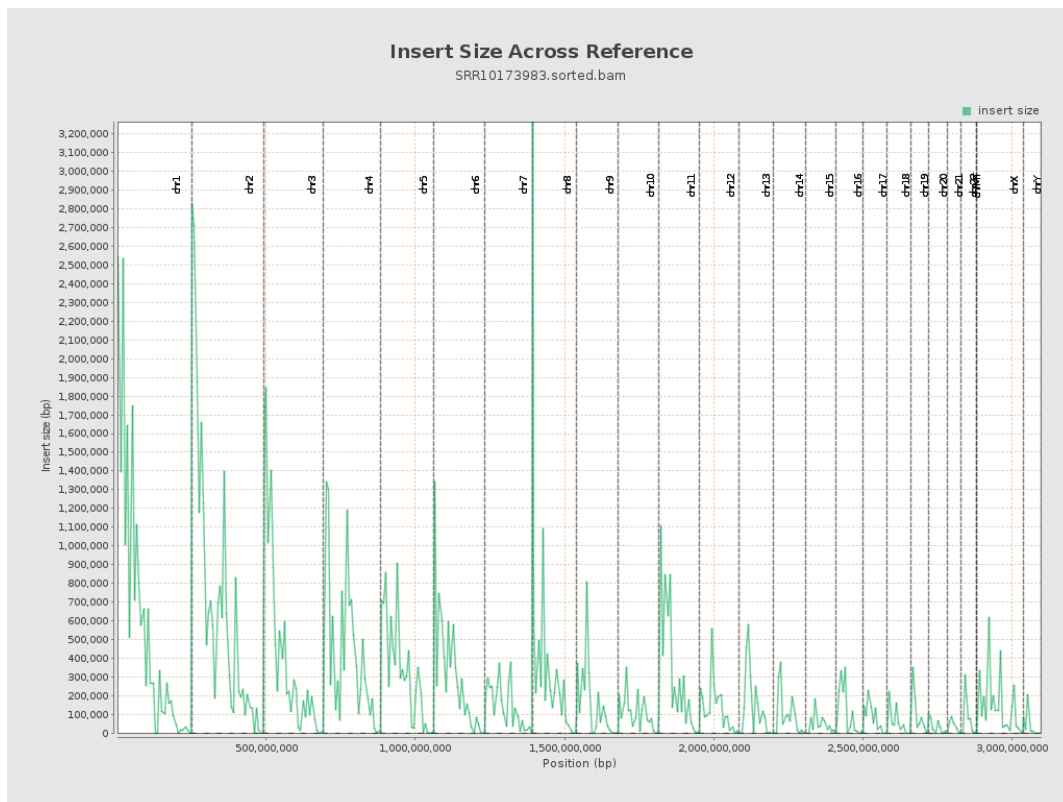
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

