

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:18:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173930.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_SRR10173930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173930_1.fastq.gz SRR10173930_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:18:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,546,356
Mapped reads	3,472,213 / 97.91%
Unmapped reads	74,143 / 2.09%
Mapped paired reads	3,472,213 / 97.91%
Mapped reads, first in pair	1,737,190 / 48.99%
Mapped reads, second in pair	1,735,023 / 48.92%
Mapped reads, both in pair	3,430,022 / 96.72%
Mapped reads, singletons	42,191 / 1.19%
Secondary alignments	0
Supplementary alignments	397,336 / 11.2%
Read min/max/mean length	30 / 133 / 123.27
Duplicated reads (estimated)	2,739,801 / 77.26%
Duplication rate	63.65%
Clipped reads	1,624,950 / 45.82%

2.2. ACGT Content

Number/percentage of A's	117,366,368 / 30.1%
Number/percentage of C's	76,982,380 / 19.74%
Number/percentage of T's	116,038,872 / 29.76%
Number/percentage of G's	79,553,253 / 20.4%
Number/percentage of N's	2,907 / 0%

GC Percentage	40.14%
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2.3. Coverage

Mean	0.126
Standard Deviation	2.3774

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	815,579.81
Standard Deviation	8,356,596.7
P25/Median/P75	101 / 145 / 216

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	3,284,842
Insertions	43,492
Mapped reads with at least one insertion	1.21%
Deletions	108,081
Mapped reads with at least one deletion	3.03%
Homopolymer indels	41.67%

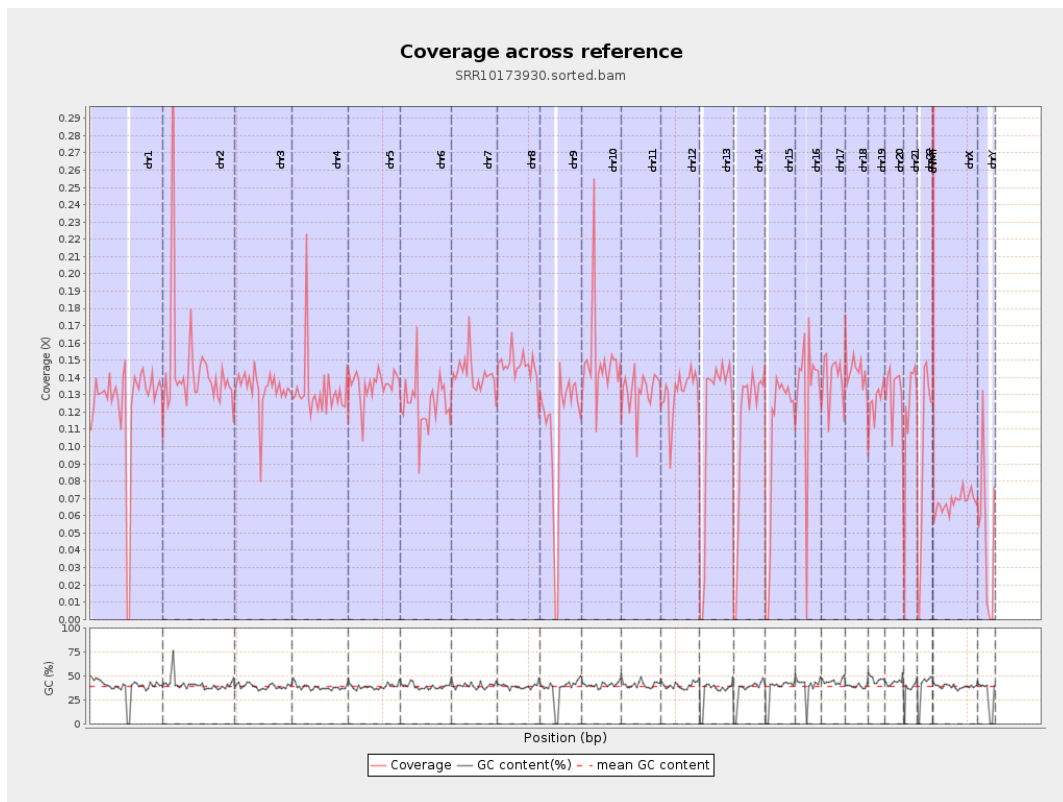
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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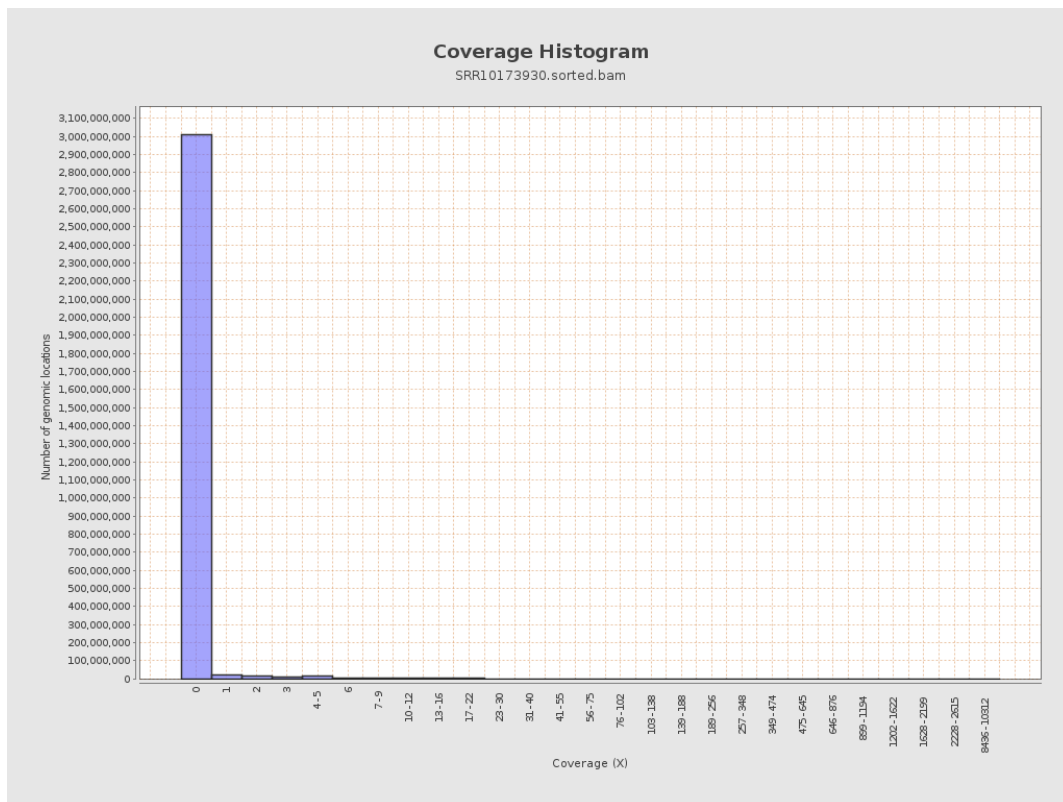
		bases	coverage	deviation
chr1	249250621	30973269	0.1243	1.384
chr2	243199373	35106748	0.1444	7.2964
chr3	198022430	26421424	0.1334	1.1339
chr4	191154276	25330054	0.1325	1.2979
chr5	180915260	24534994	0.1356	1.1358
chr6	171115067	21432909	0.1253	1.1978
chr7	159138663	22549913	0.1417	1.4406
chr8	146364022	21398945	0.1462	1.7632
chr9	141213431	15691969	0.1111	1.3085
chr10	135534747	20223197	0.1492	1.6734
chr11	135006516	17803705	0.1319	1.1428
chr12	133851895	17629180	0.1317	1.1685
chr13	115169878	13475972	0.117	1.0768
chr14	107349540	11984976	0.1116	1.0279
chr15	102531392	10700282	0.1044	0.9974
chr16	90354753	11883505	0.1315	1.2357
chr17	81195210	11353694	0.1398	1.1811
chr18	78077248	11243140	0.144	1.5365
chr19	59128983	7466733	0.1263	1.21
chr20	63025520	8296129	0.1316	1.1245
chr21	48129895	5753355	0.1195	1.2153
chr22	51304566	4923317	0.096	1.06
chrMT	16571	502231	30.3078	31.1338
chrX	155270560	10534068	0.0678	0.7886

chrY	59373566	2993692	0.0504	0.8448
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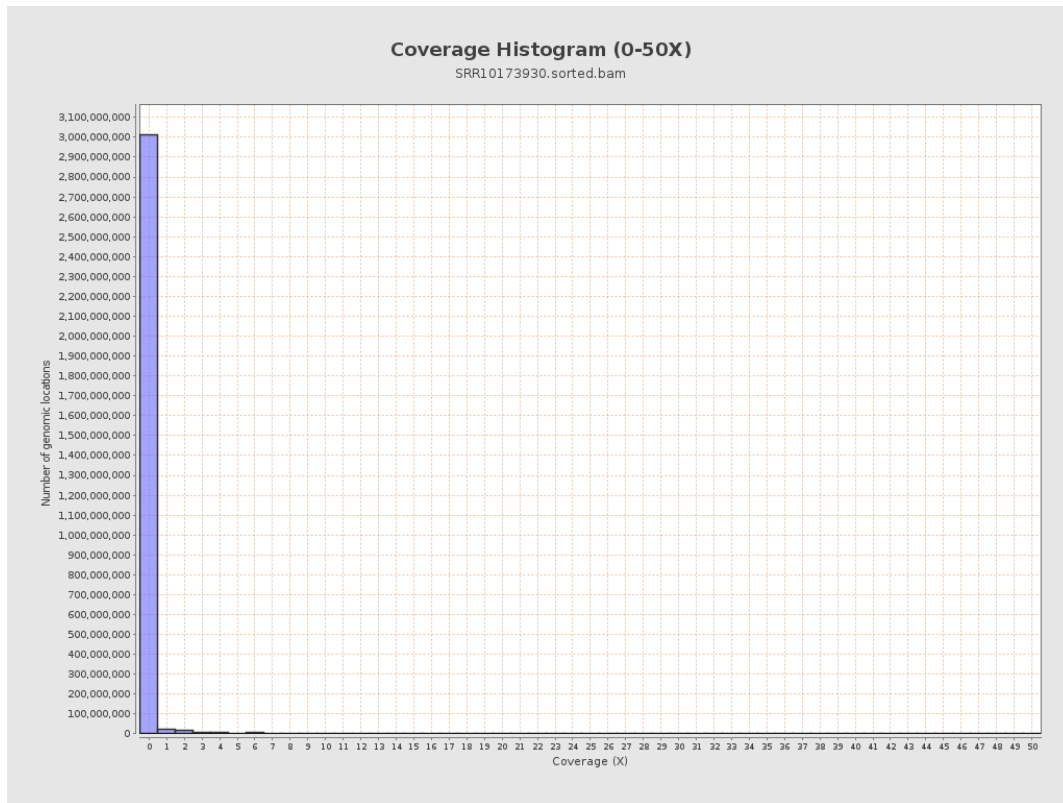
3. Results : Coverage across reference



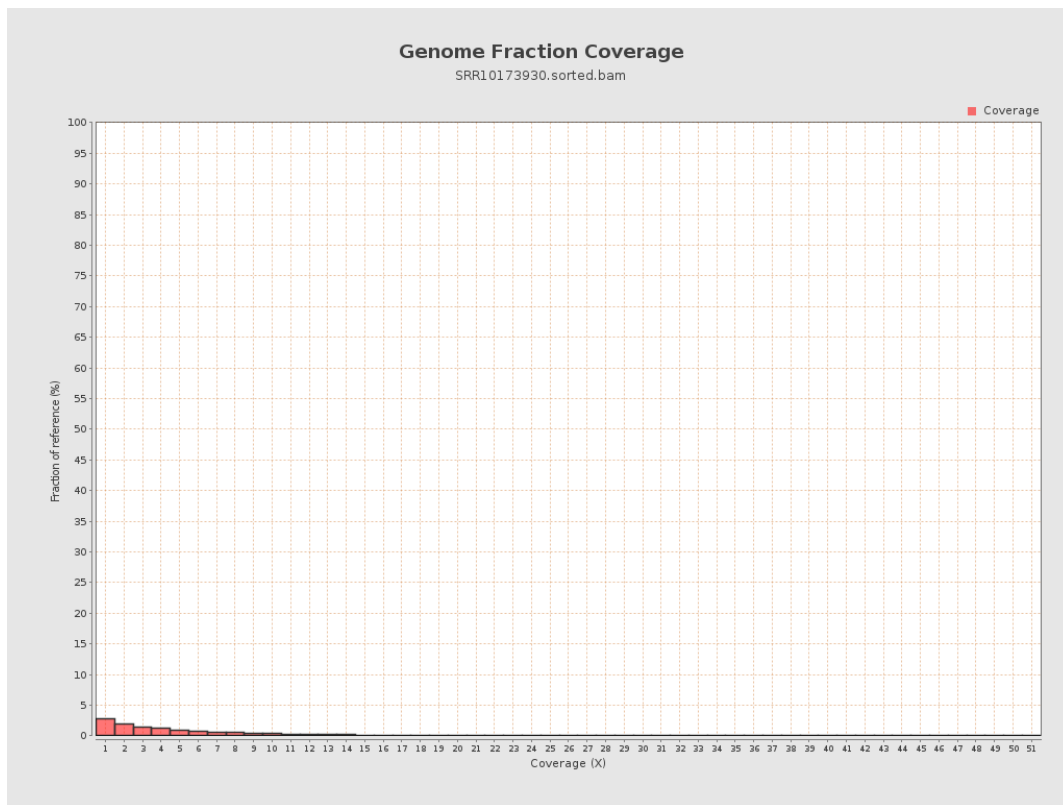
4. Results : Coverage Histogram



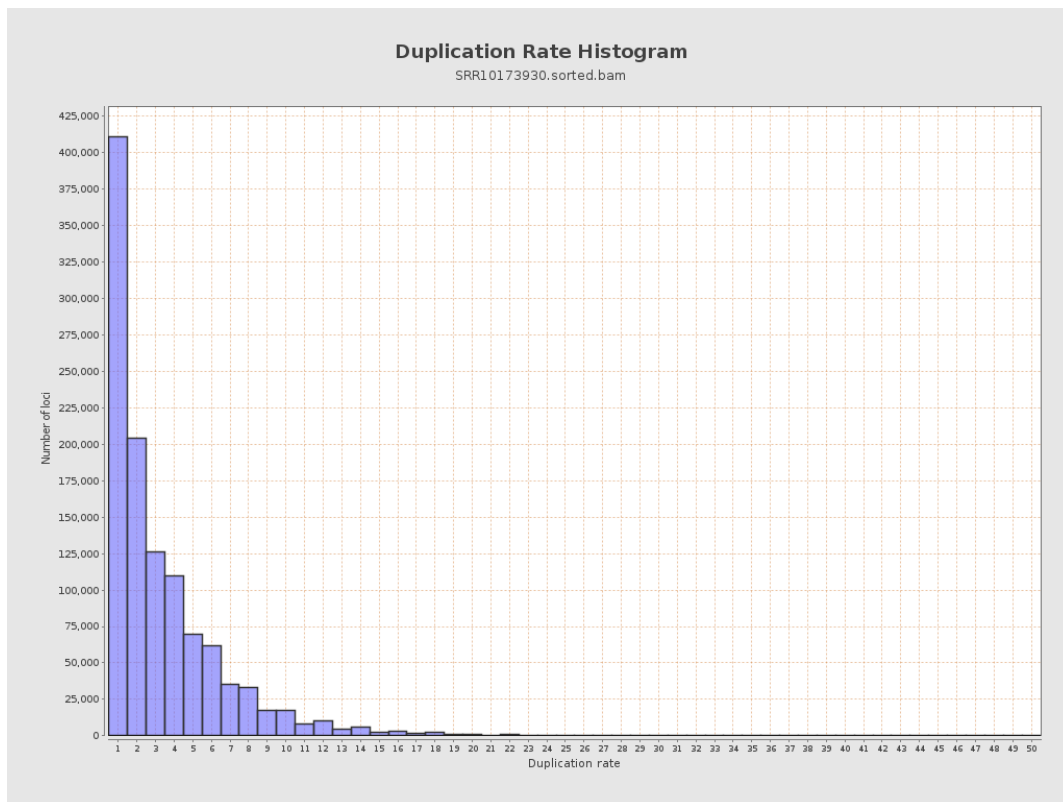
5. Results : Coverage Histogram (0-50X)



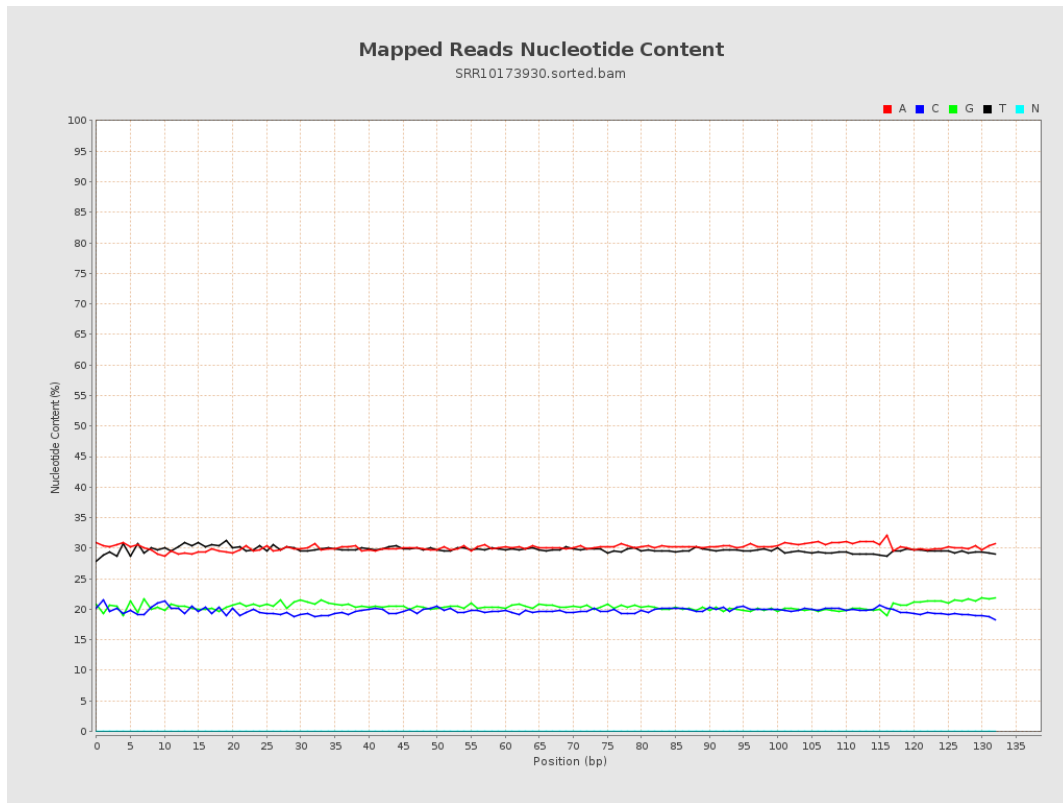
6. Results : Genome Fraction Coverage



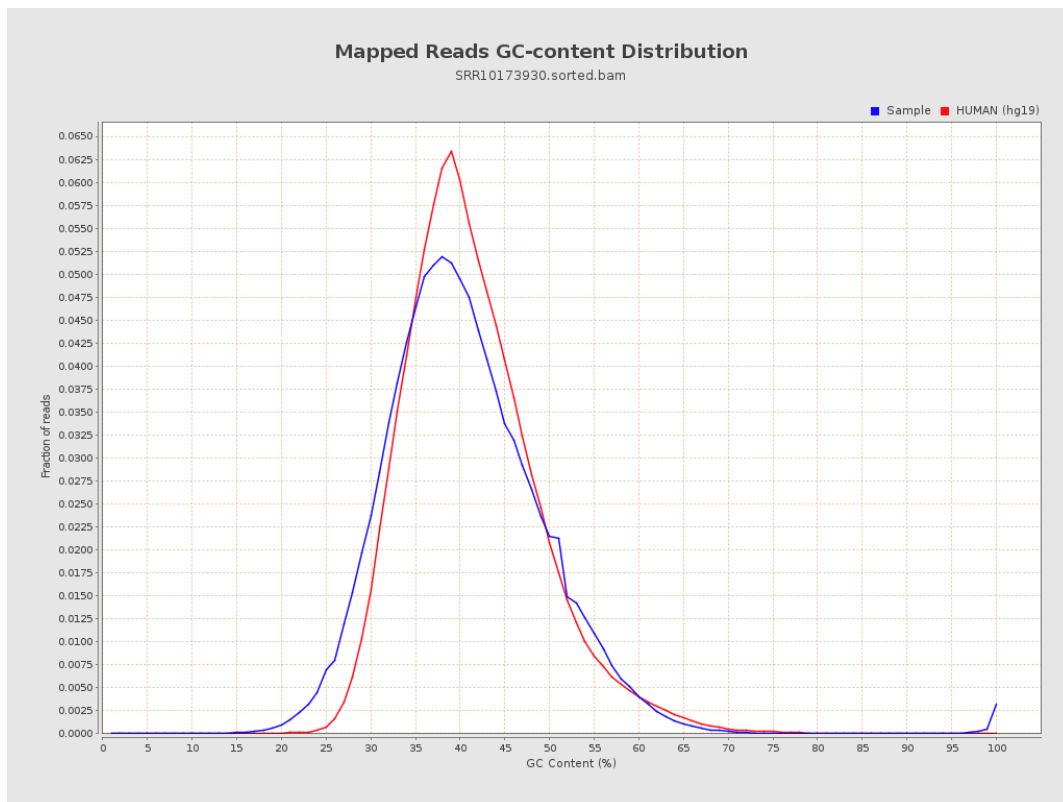
7. Results : Duplication Rate Histogram



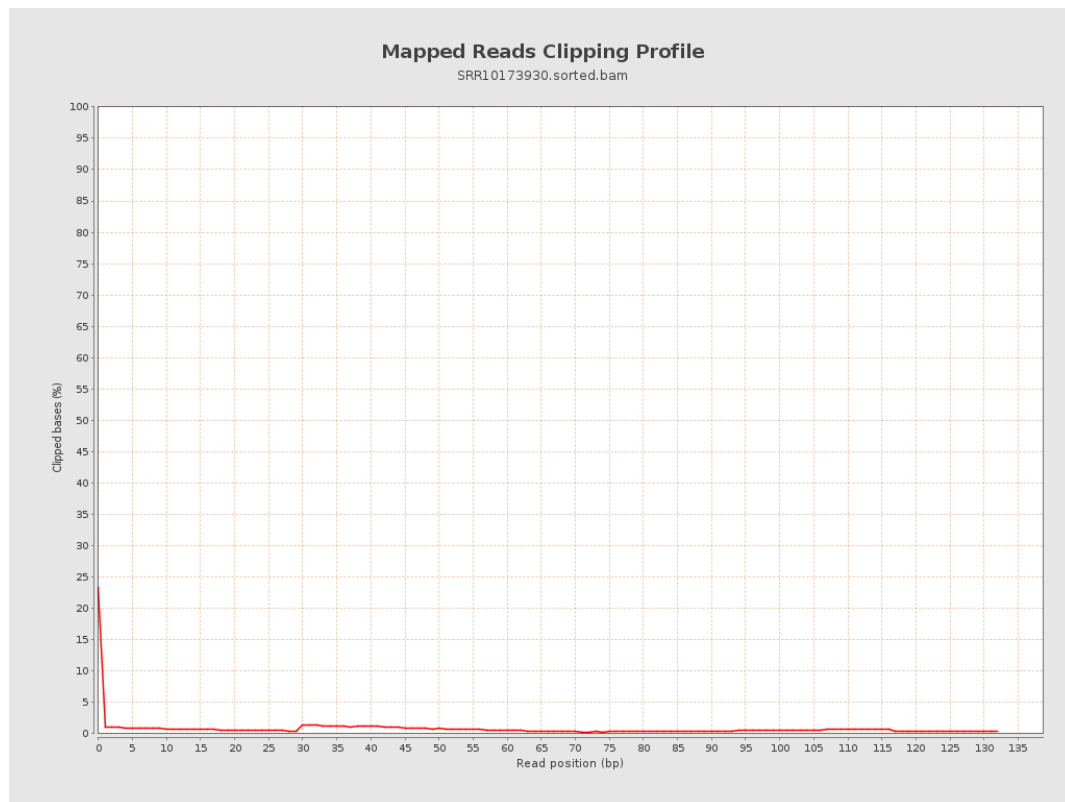
8. Results : Mapped Reads Nucleotide Content



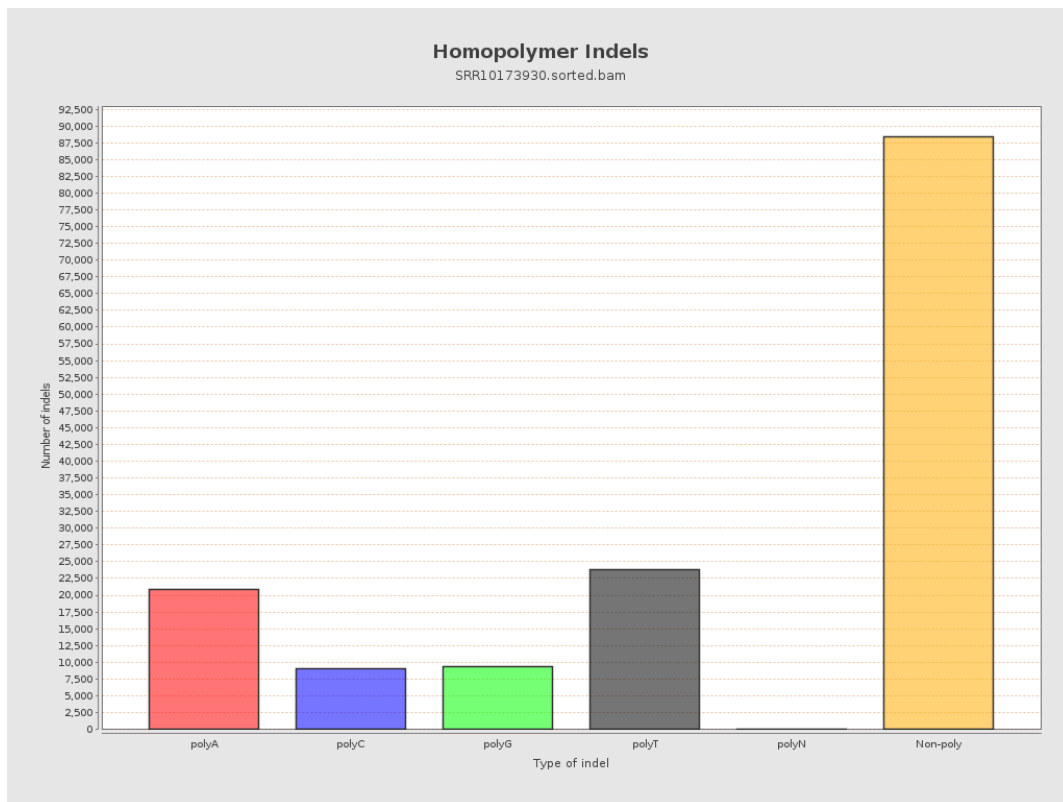
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



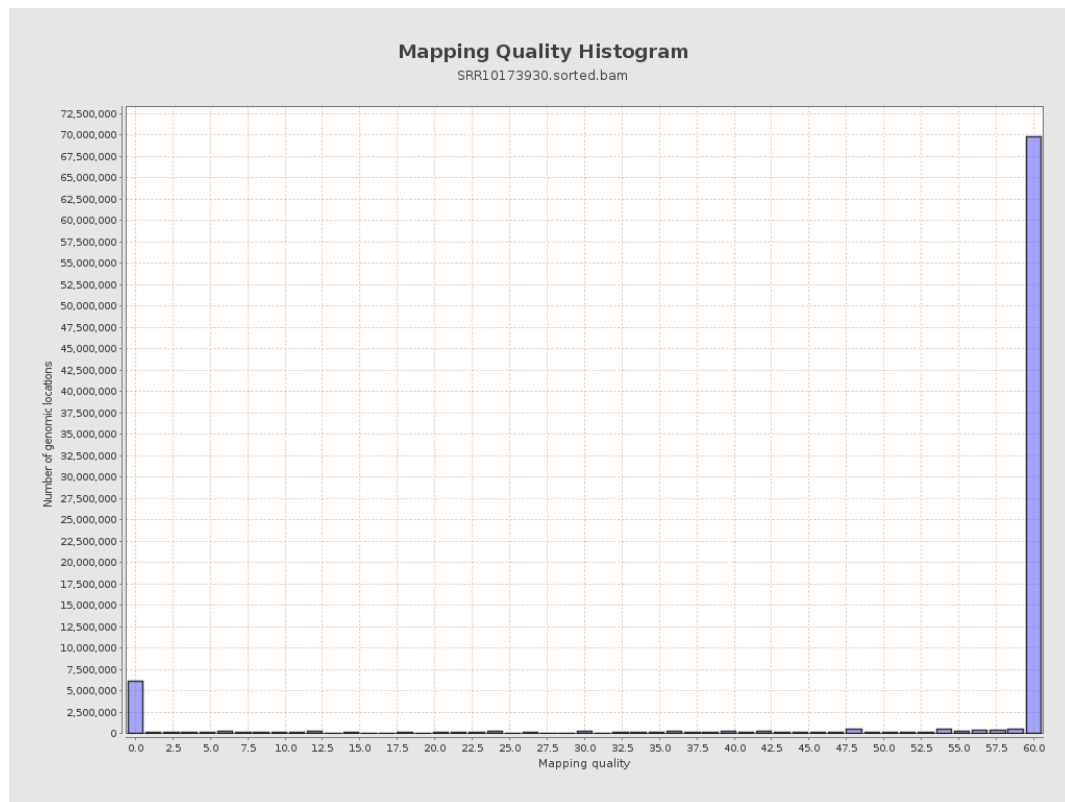
11. Results : Homopolymer Indels



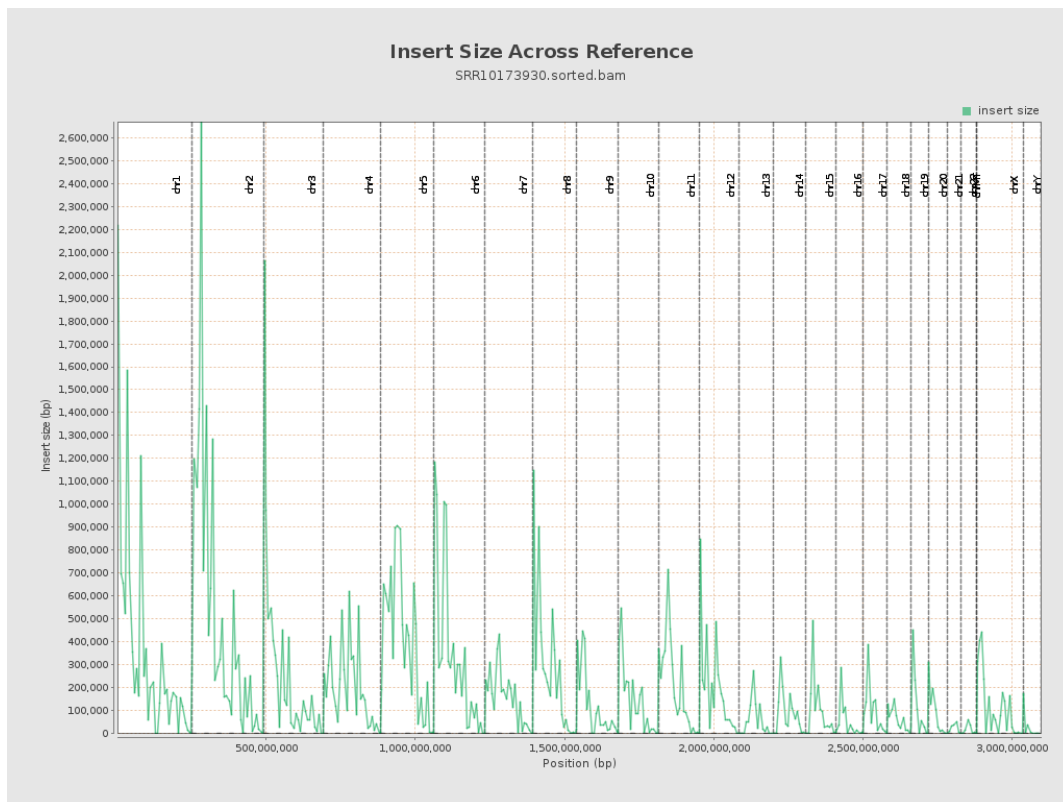
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

