

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:00:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173876.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_SRR10173876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173876_1.fastq.gz SRR10173876_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:00:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,148,502
Mapped reads	3,076,185 / 97.7%
Unmapped reads	72,317 / 2.3%
Mapped paired reads	3,076,185 / 97.7%
Mapped reads, first in pair	1,540,026 / 48.91%
Mapped reads, second in pair	1,536,159 / 48.79%
Mapped reads, both in pair	3,028,742 / 96.2%
Mapped reads, singletons	47,443 / 1.51%
Secondary alignments	0
Supplementary alignments	309,072 / 9.82%
Read min/max/mean length	30 / 133 / 127.66
Duplicated reads (estimated)	2,307,532 / 73.29%
Duplication rate	63.03%
Clipped reads	1,286,951 / 40.88%

2.2. ACGT Content

Number/percentage of A's	109,541,786 / 30.26%
Number/percentage of C's	70,342,414 / 19.43%
Number/percentage of T's	109,265,195 / 30.18%
Number/percentage of G's	72,892,237 / 20.13%
Number/percentage of N's	3,923 / 0%

GC Percentage	39.56%
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2.3. Coverage

Mean	0.117
Standard Deviation	1.8747

2.4. Mapping Quality

Mean Mapping Quality	52.82
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2.5. Insert size

Mean	792,528.54
Standard Deviation	8,484,253.82
P25/Median/P75	136 / 189 / 269

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	3,637,944
Insertions	36,916
Mapped reads with at least one insertion	1.16%
Deletions	95,203
Mapped reads with at least one deletion	3.02%
Homopolymer indels	42.7%

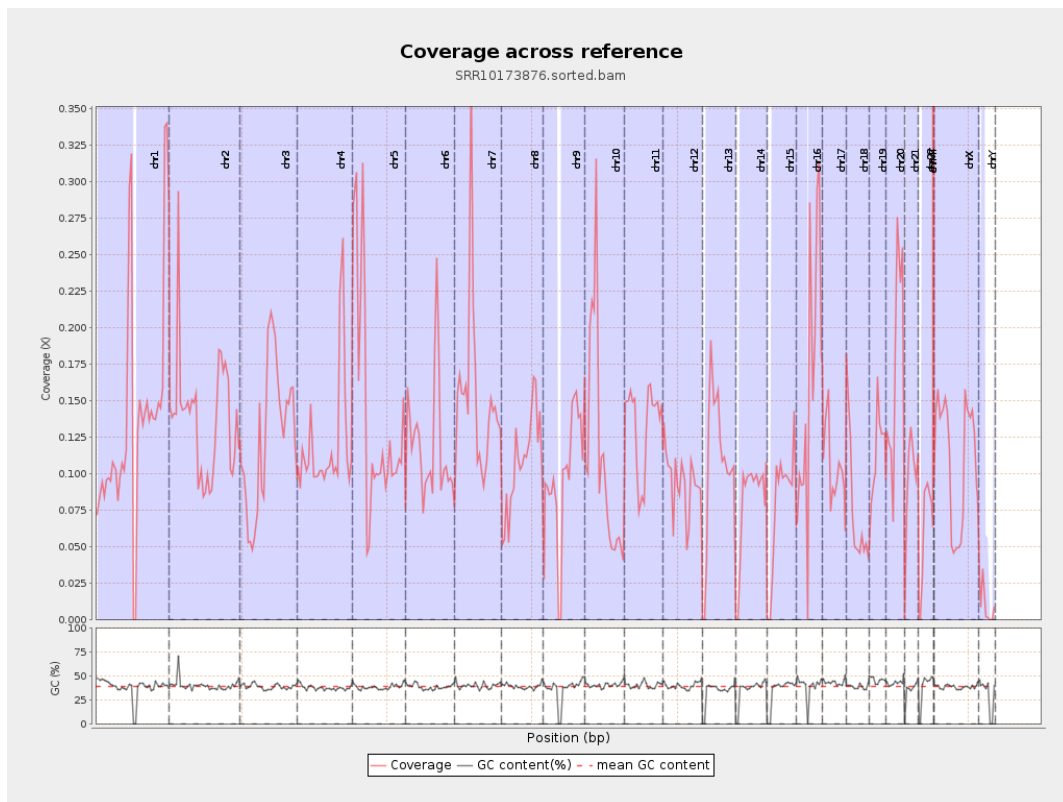
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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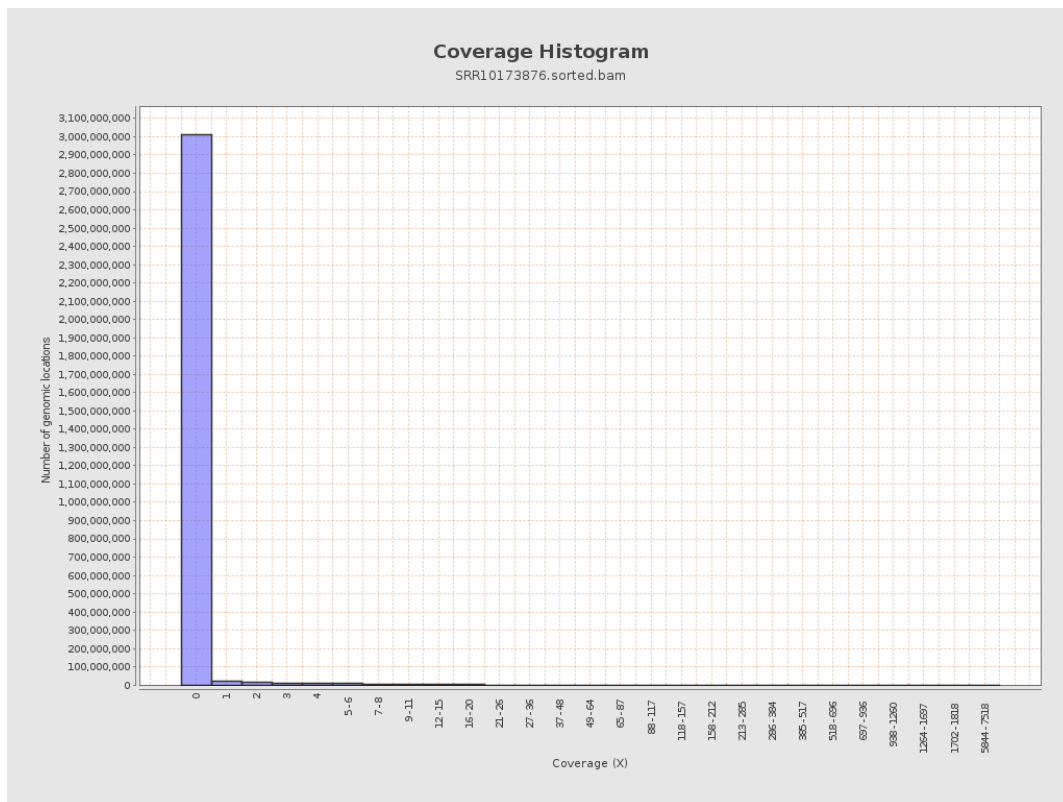
		bases	coverage	deviation
chr1	249250621	34097088	0.1368	1.5338
chr2	243199373	33479099	0.1377	5.3142
chr3	198022430	24937630	0.1259	1.0081
chr4	191154276	22584949	0.1182	1.0701
chr5	180915260	25287568	0.1398	1.0554
chr6	171115067	20511698	0.1199	0.9876
chr7	159138663	24167559	0.1519	1.624
chr8	146364022	15852012	0.1083	1.0353
chr9	141213431	14008775	0.0992	0.9652
chr10	135534747	15089855	0.1113	1.916
chr11	135006516	17972457	0.1331	1.0354
chr12	133851895	12481368	0.0932	0.8553
chr13	115169878	12300492	0.1068	0.9318
chr14	107349540	8483806	0.079	0.7865
chr15	102531392	8068804	0.0787	0.7769
chr16	90354753	14622429	0.1618	1.4789
chr17	81195210	8327962	0.1026	0.9744
chr18	78077248	5878239	0.0753	1.3236
chr19	59128983	6762388	0.1144	1.4583
chr20	63025520	10865205	0.1724	1.1601
chr21	48129895	4618578	0.096	0.8842
chr22	51304566	3038555	0.0592	0.637
chrMT	16571	1142790	68.9632	59.2089
chrX	155270560	17130938	0.1103	0.9259

chrY	59373566	567721	0.0096	0.3526
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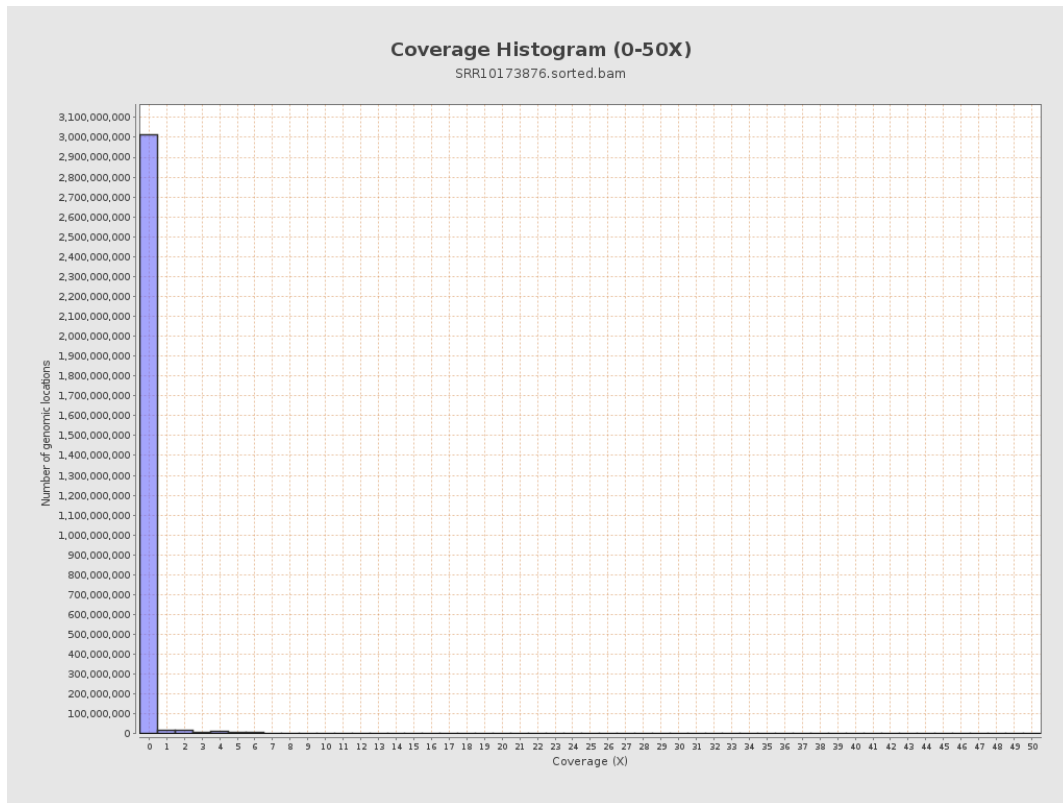
3. Results : Coverage across reference



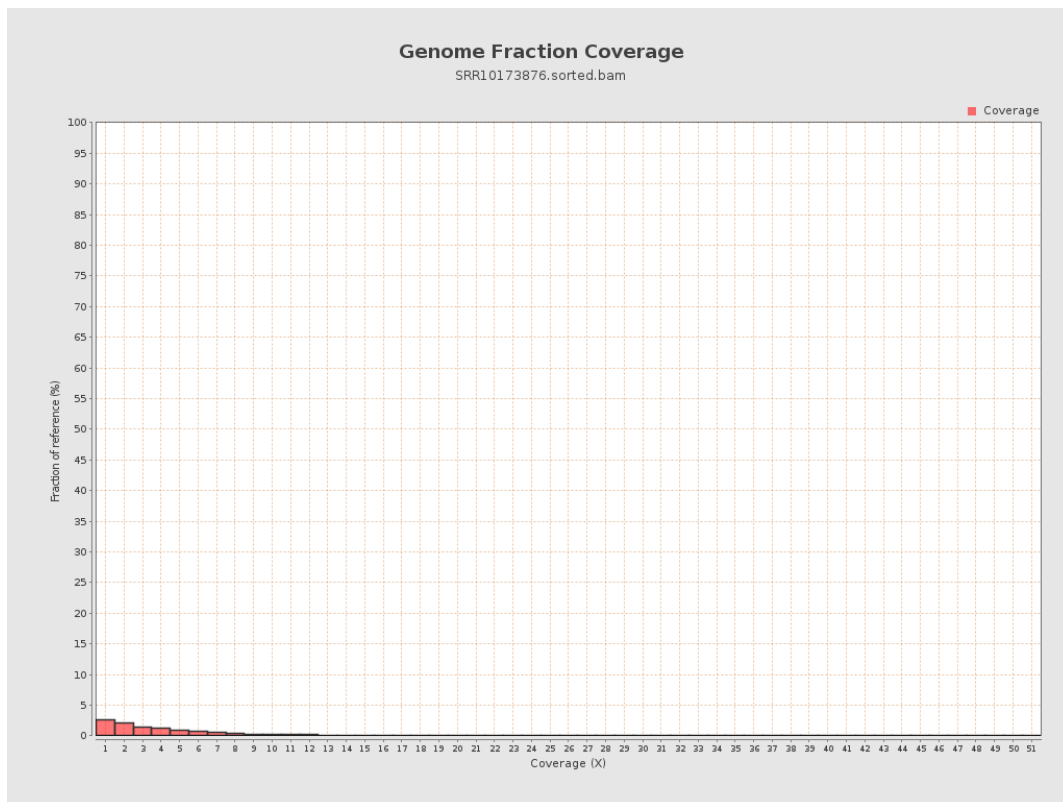
4. Results : Coverage Histogram



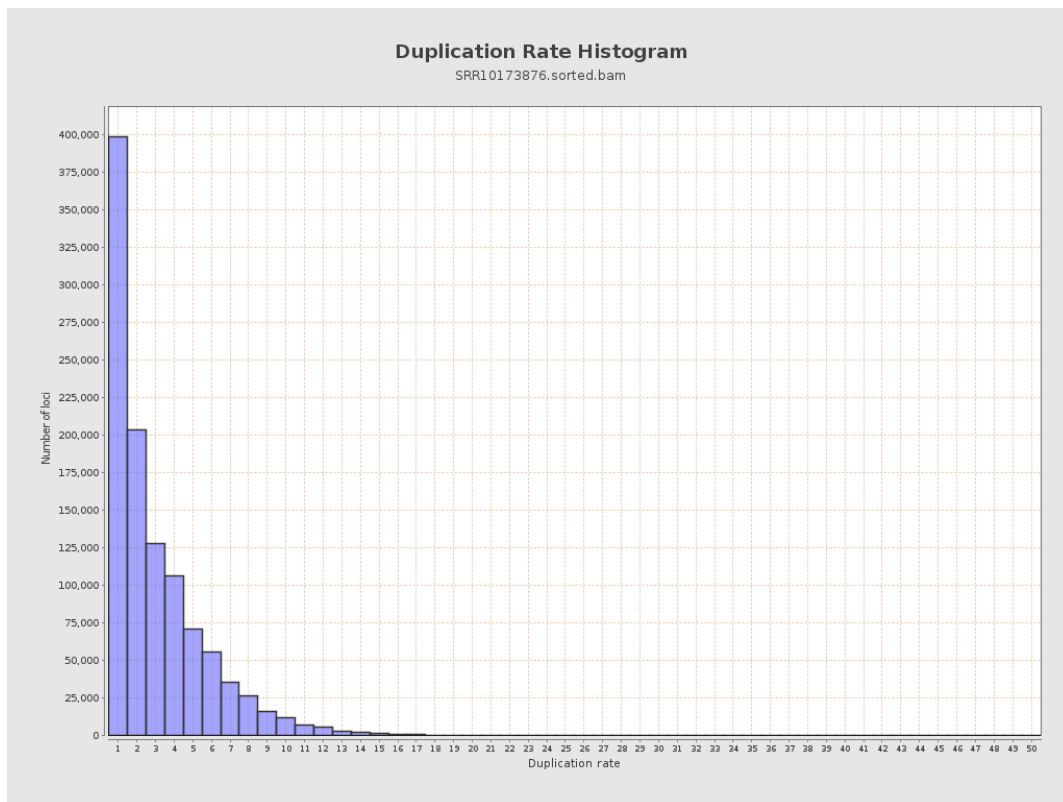
5. Results : Coverage Histogram (0-50X)



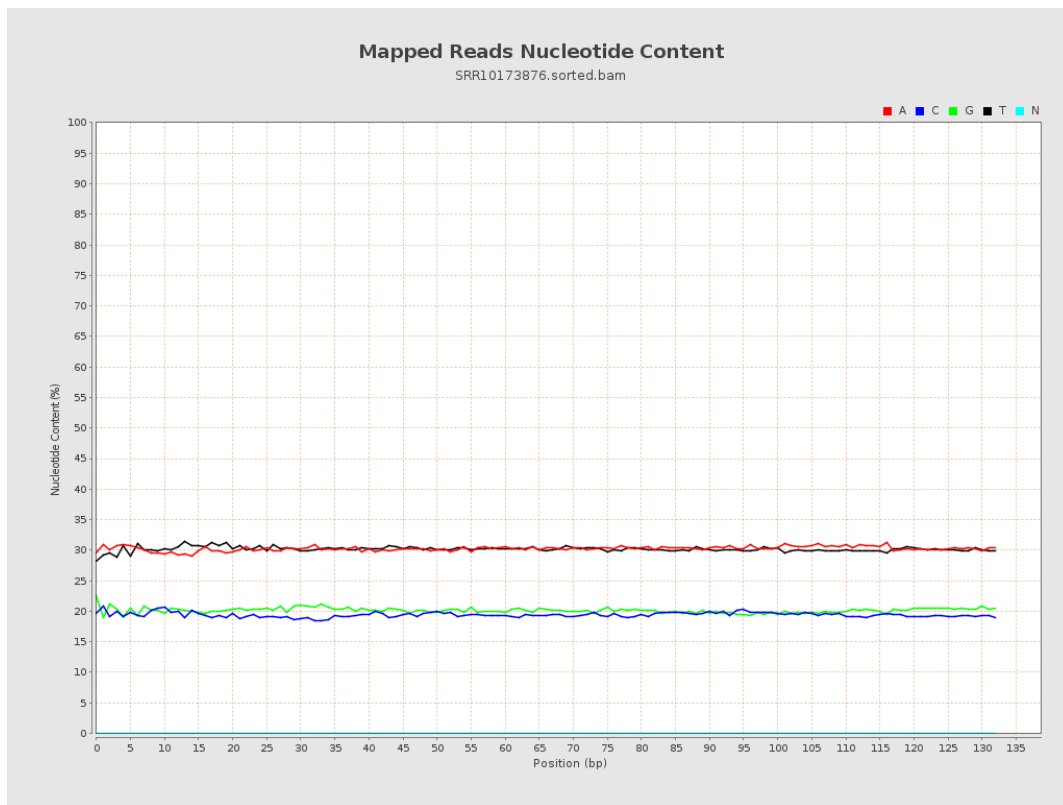
6. Results : Genome Fraction Coverage



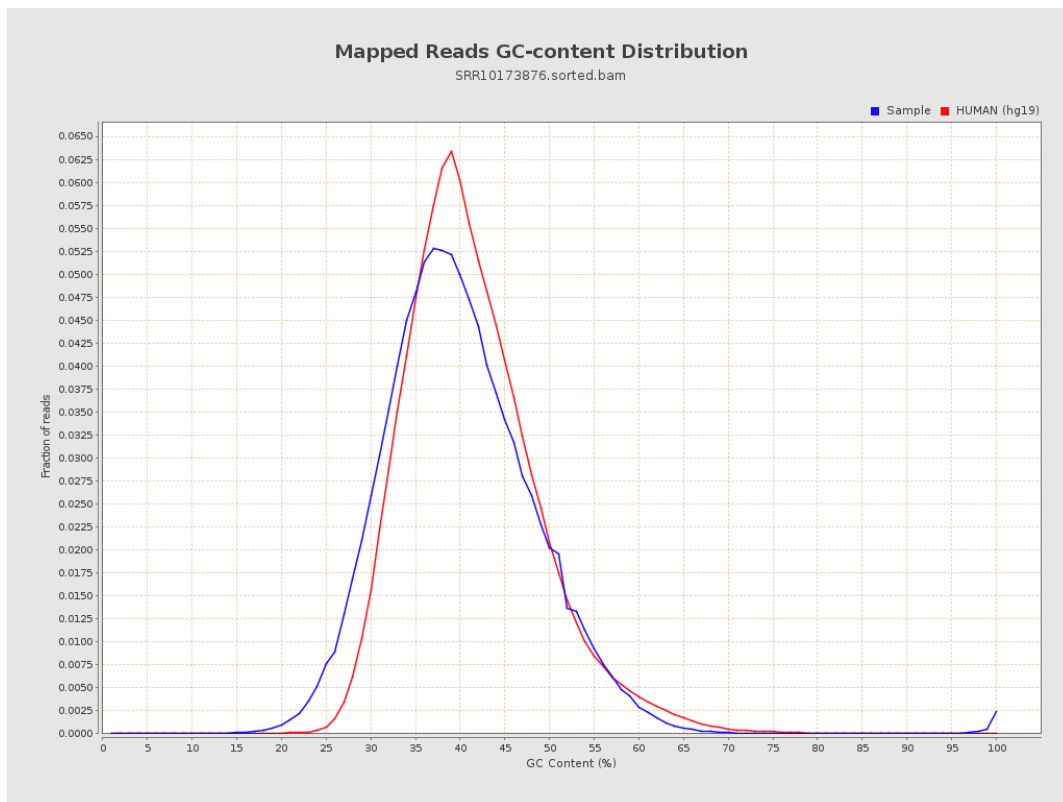
7. Results : Duplication Rate Histogram



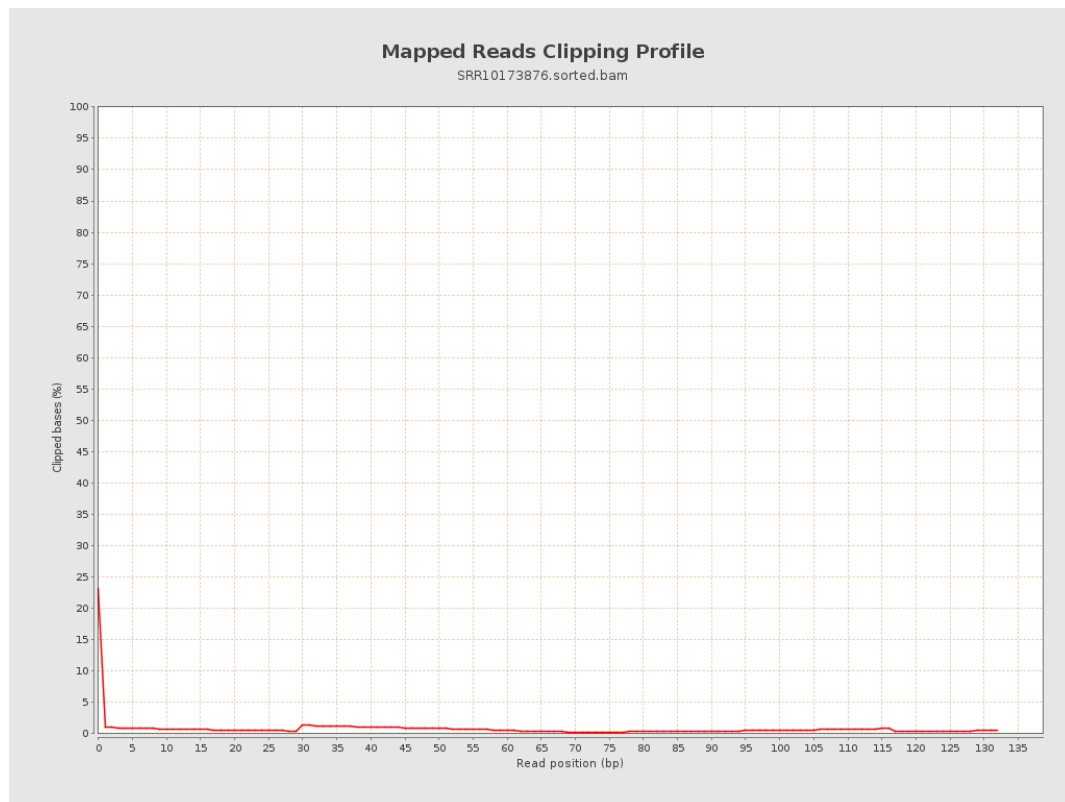
8. Results : Mapped Reads Nucleotide Content



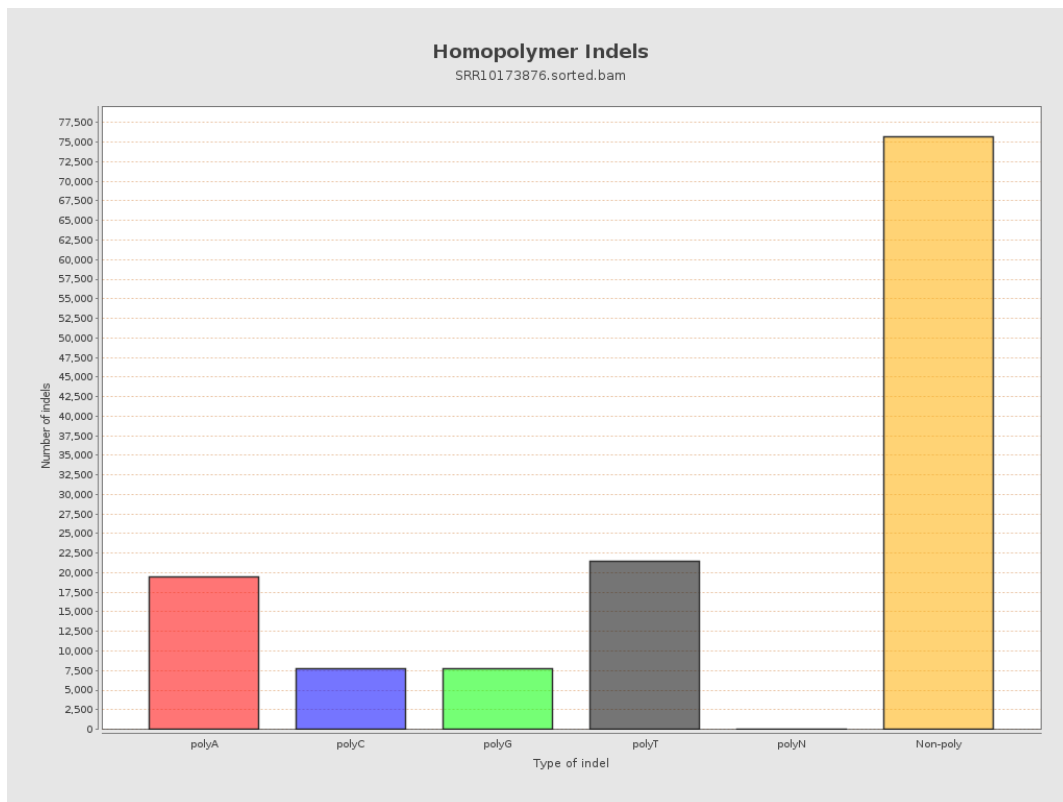
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



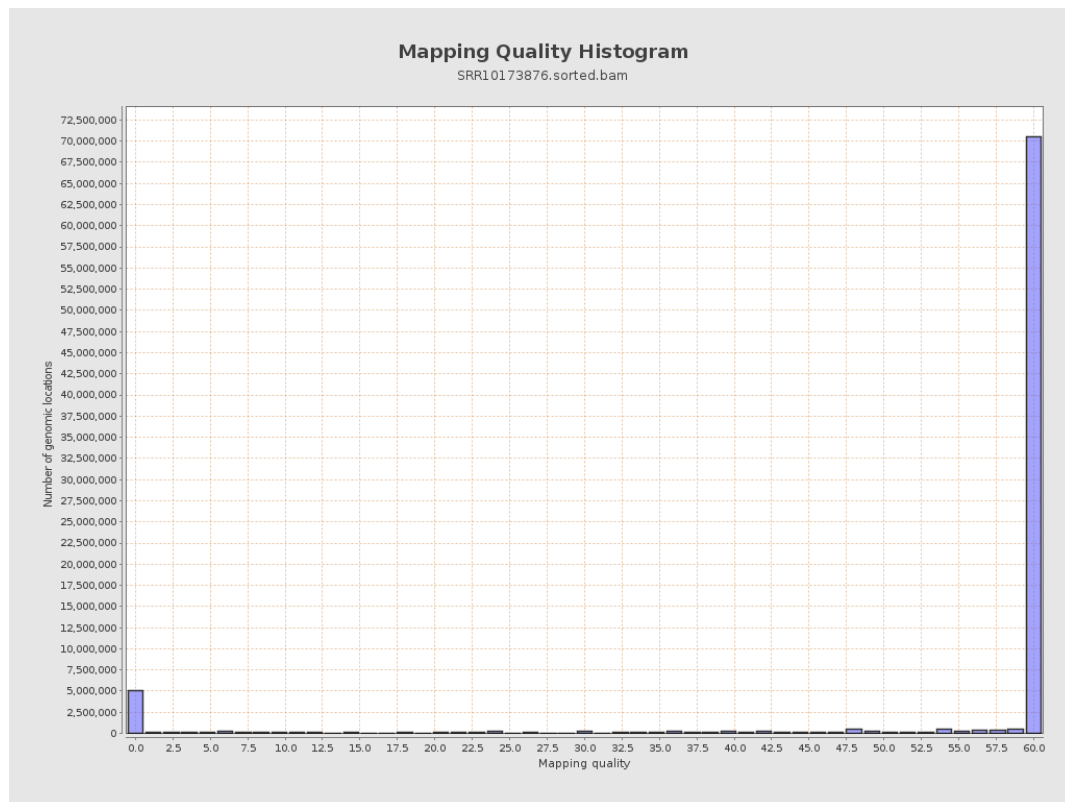
11. Results : Homopolymer Indels



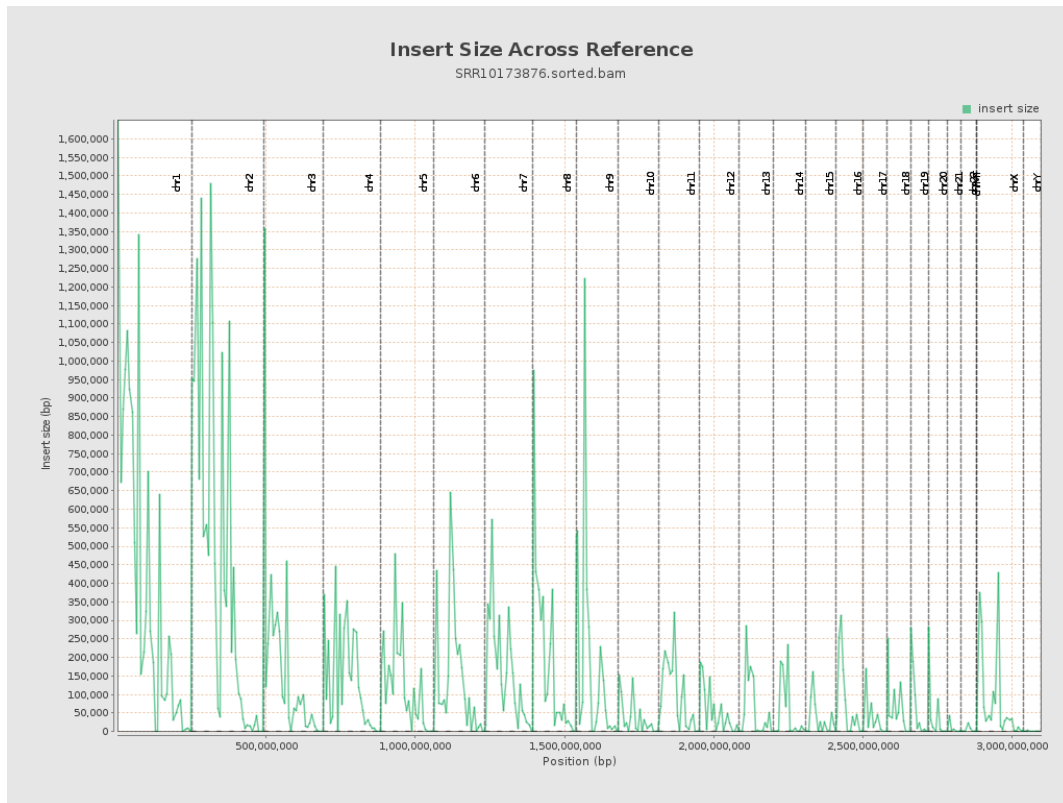
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

