

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 15:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173976.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_SRR10173976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173976_1.fastq.gz SRR10173976_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 15:55:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,569,914
Mapped reads	11,331,737 / 97.94%
Unmapped reads	238,177 / 2.06%
Mapped paired reads	11,331,737 / 97.94%
Mapped reads, first in pair	5,663,282 / 48.95%
Mapped reads, second in pair	5,668,455 / 48.99%
Mapped reads, both in pair	11,177,950 / 96.61%
Mapped reads, singletons	153,787 / 1.33%
Secondary alignments	0
Supplementary alignments	1,568,120 / 13.55%
Read min/max/mean length	30 / 133 / 125.49
Duplicated reads (estimated)	9,229,743 / 79.77%
Duplication rate	65.12%
Clipped reads	5,828,500 / 50.38%

2.2. ACGT Content

Number/percentage of A's	384,593,367 / 29.94%
Number/percentage of C's	254,387,753 / 19.81%
Number/percentage of T's	381,433,924 / 29.7%
Number/percentage of G's	264,036,090 / 20.56%
Number/percentage of N's	9,677 / 0%

GC Percentage	40.36%
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2.3. Coverage

Mean	0.4152
Standard Deviation	6.9799

2.4. Mapping Quality

Mean Mapping Quality	52.45
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2.5. Insert size

Mean	923,571.39
Standard Deviation	9,092,079.46
P25/Median/P75	104 / 152 / 233

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	10,714,634
Insertions	142,797
Mapped reads with at least one insertion	1.21%
Deletions	352,202
Mapped reads with at least one deletion	3.03%
Homopolymer indels	41.51%

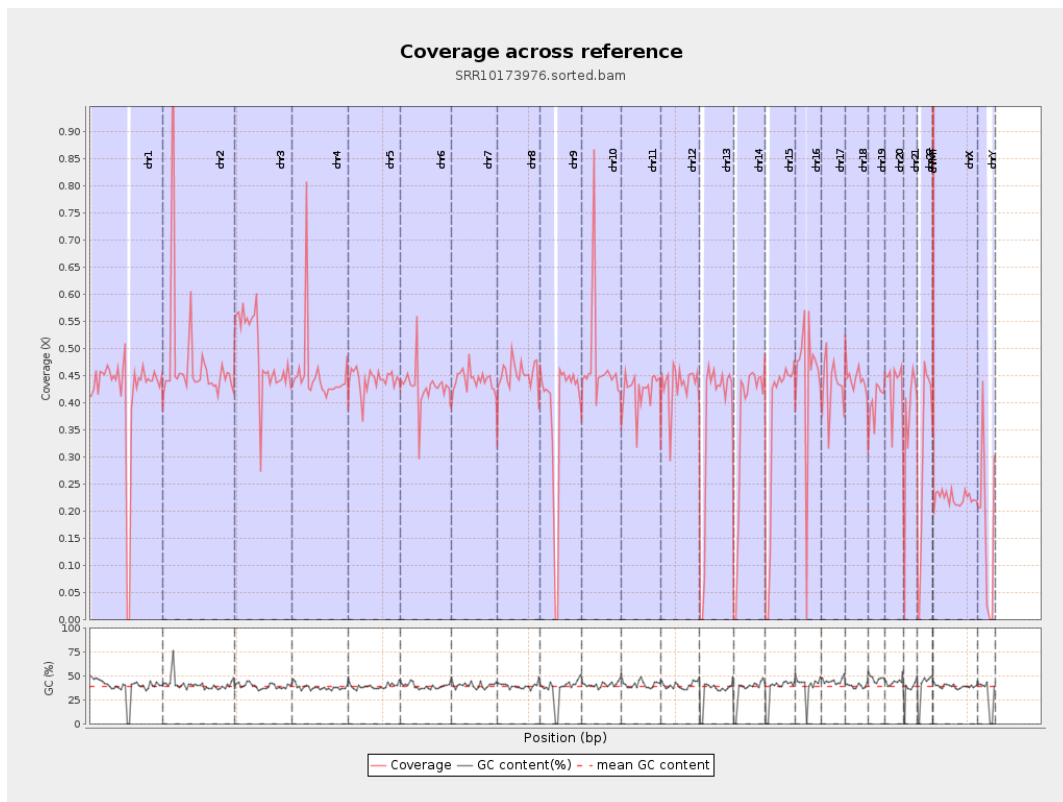
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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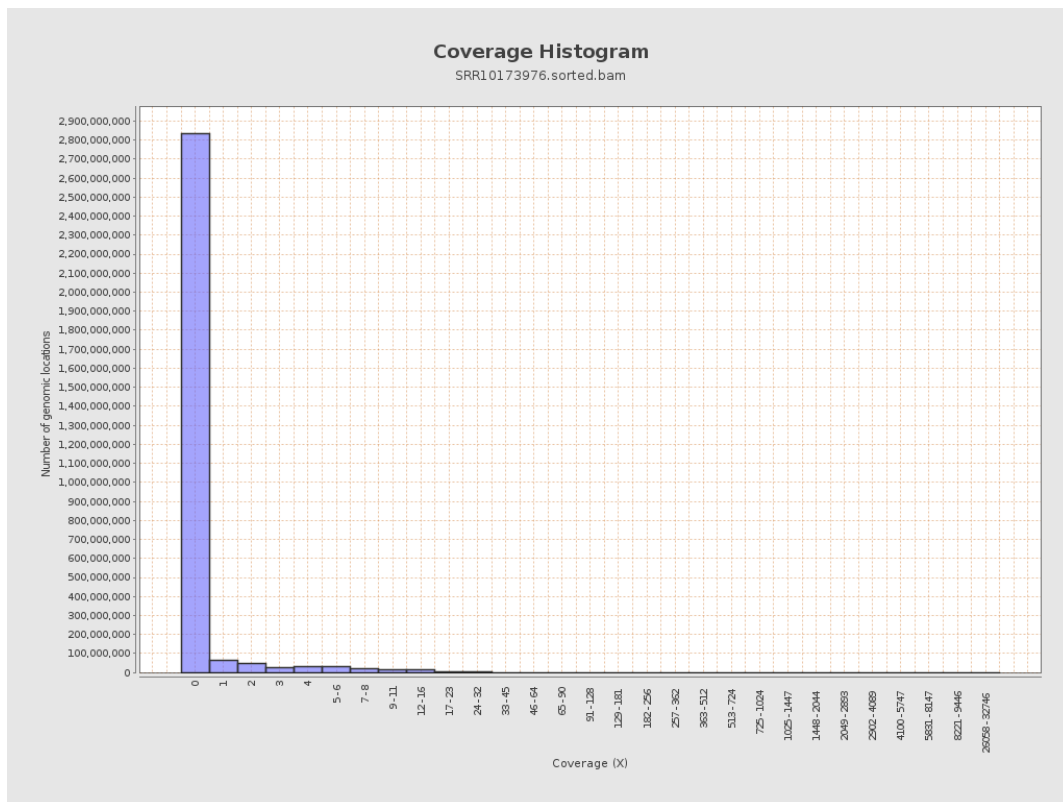
		bases	coverage	deviation
chr1	249250621	103996526	0.4172	3.2772
chr2	243199373	114916343	0.4725	22.892
chr3	198022430	96664319	0.4881	2.1523
chr4	191154276	86344682	0.4517	3.4145
chr5	180915260	79918878	0.4417	2.0532
chr6	171115067	73445242	0.4292	2.5515
chr7	159138663	70058270	0.4402	2.9605
chr8	146364022	66211893	0.4524	3.6736
chr9	141213431	53961956	0.3821	3.0148
chr10	135534747	63320645	0.4672	4.3327
chr11	135006516	57004002	0.4222	2.1222
chr12	133851895	58170890	0.4346	2.1325
chr13	115169878	42182909	0.3663	1.879
chr14	107349540	39156519	0.3648	1.9029
chr15	102531392	36683992	0.3578	1.9141
chr16	90354753	39974996	0.4424	2.9251
chr17	81195210	35149787	0.4329	2.4215
chr18	78077248	34717699	0.4447	4.1087
chr19	59128983	23820752	0.4029	2.6888
chr20	63025520	27232905	0.4321	2.1614
chr21	48129895	17892395	0.3718	2.9356
chr22	51304566	15813692	0.3082	2.2353
chrMT	16571	3573579	215.6526	175.9199
chrX	155270560	34711644	0.2236	1.4709

chrY	59373566	10387525	0.175	2.8959
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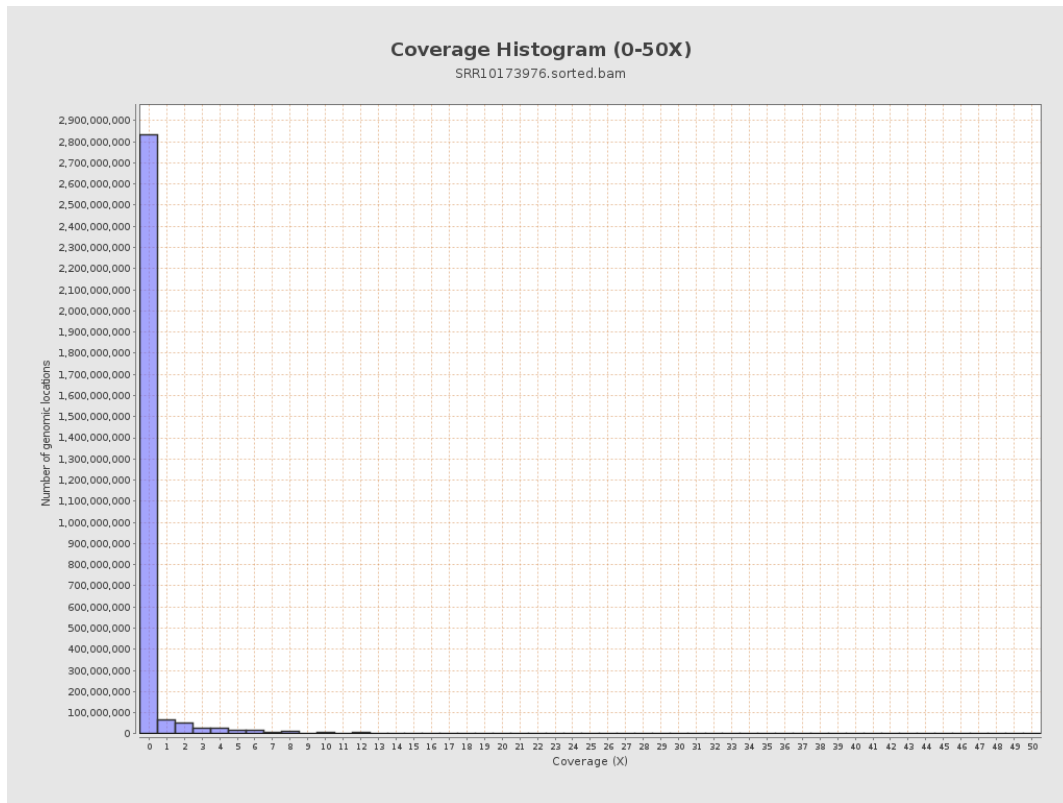
3. Results : Coverage across reference



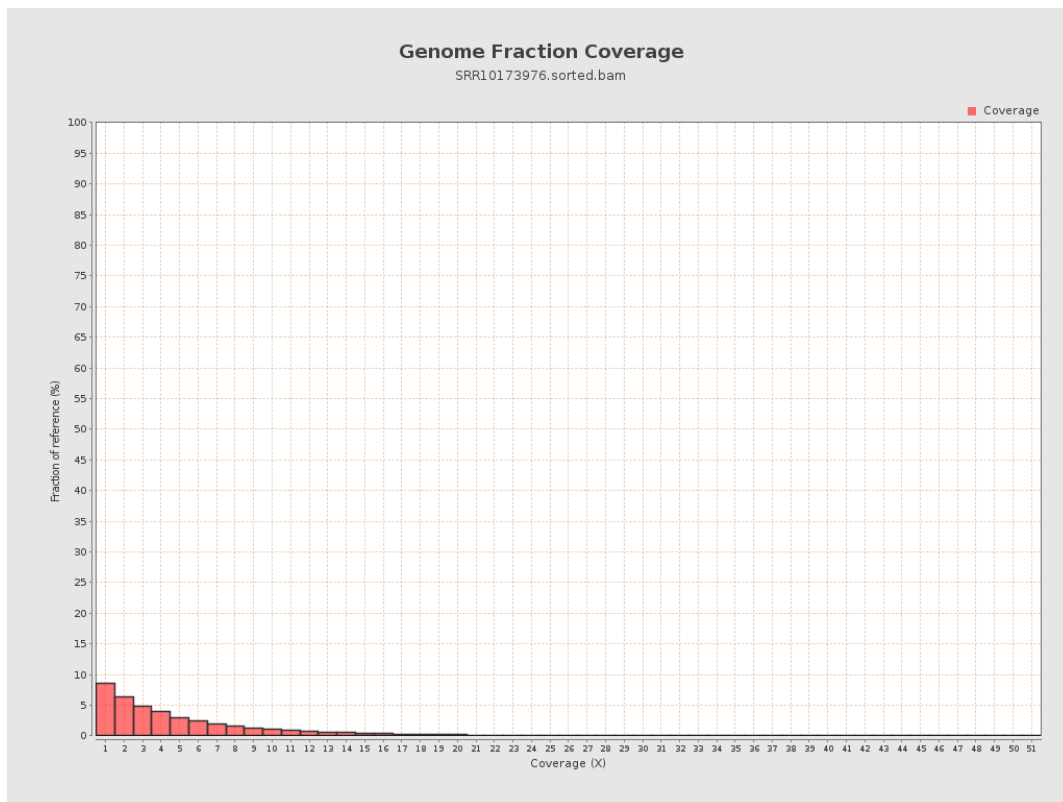
4. Results : Coverage Histogram



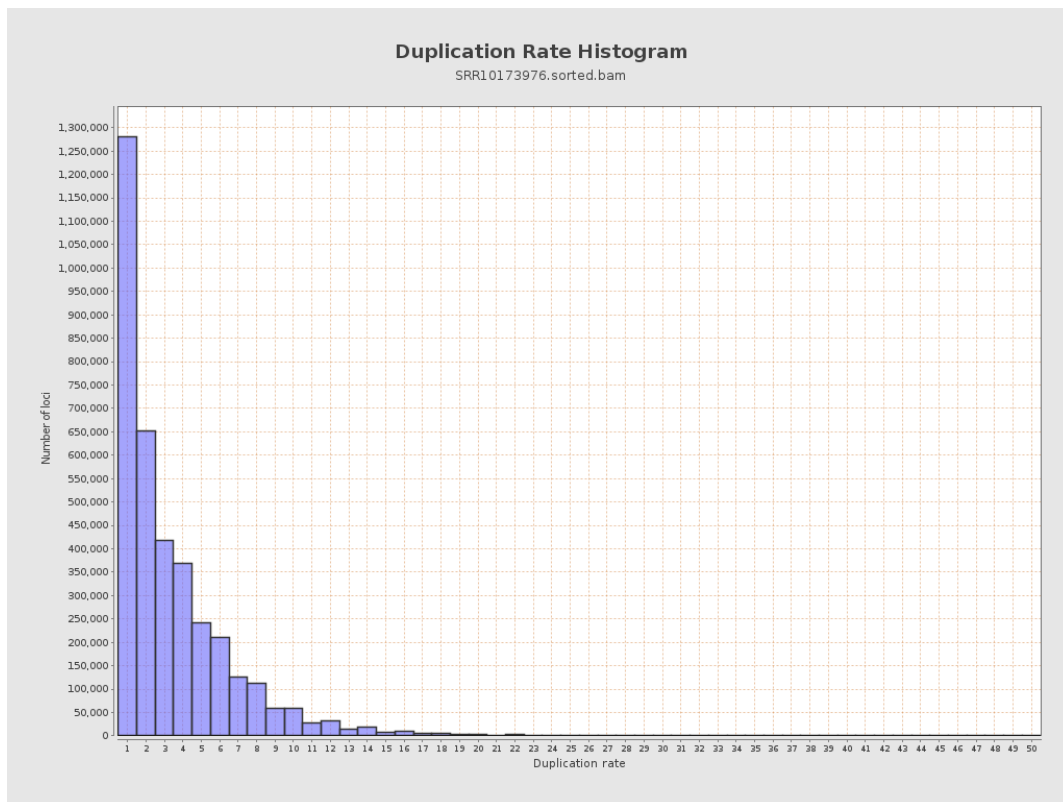
5. Results : Coverage Histogram (0-50X)



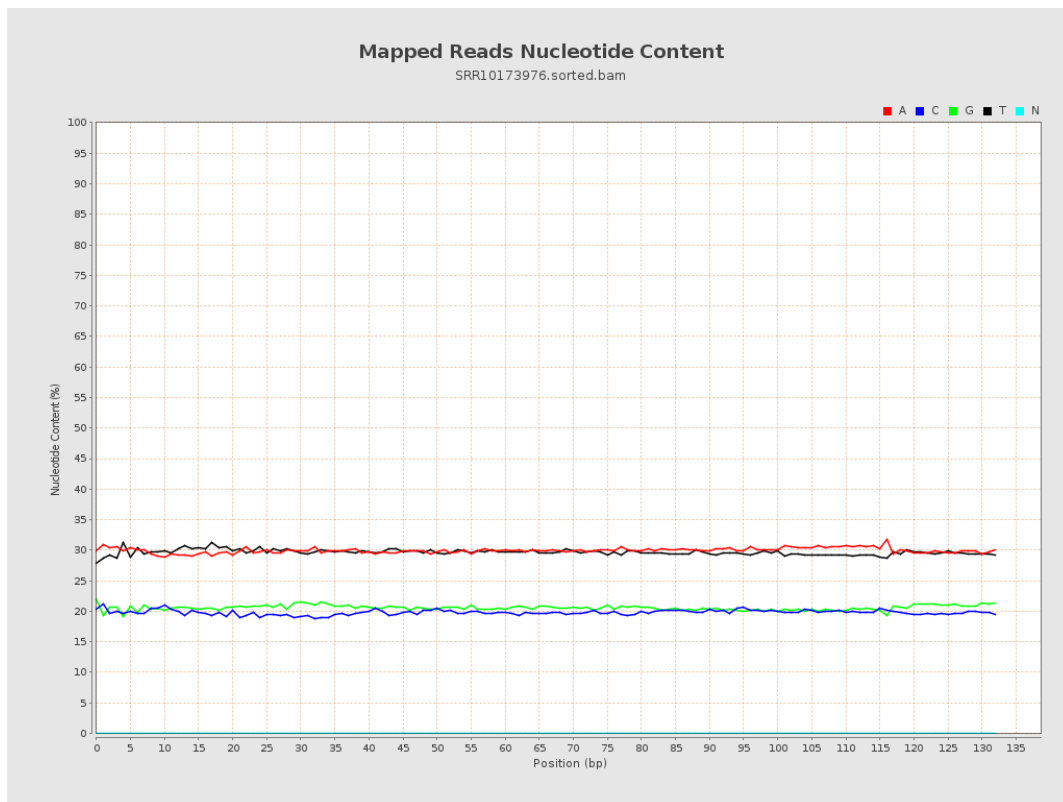
6. Results : Genome Fraction Coverage



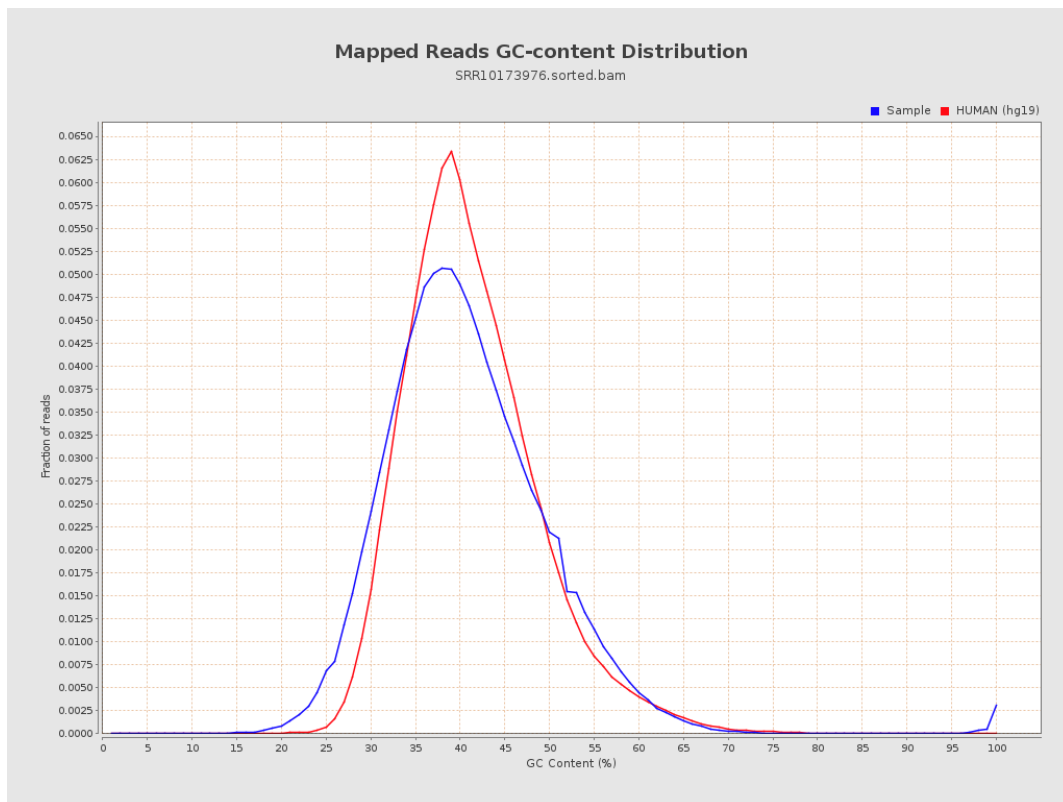
7. Results : Duplication Rate Histogram



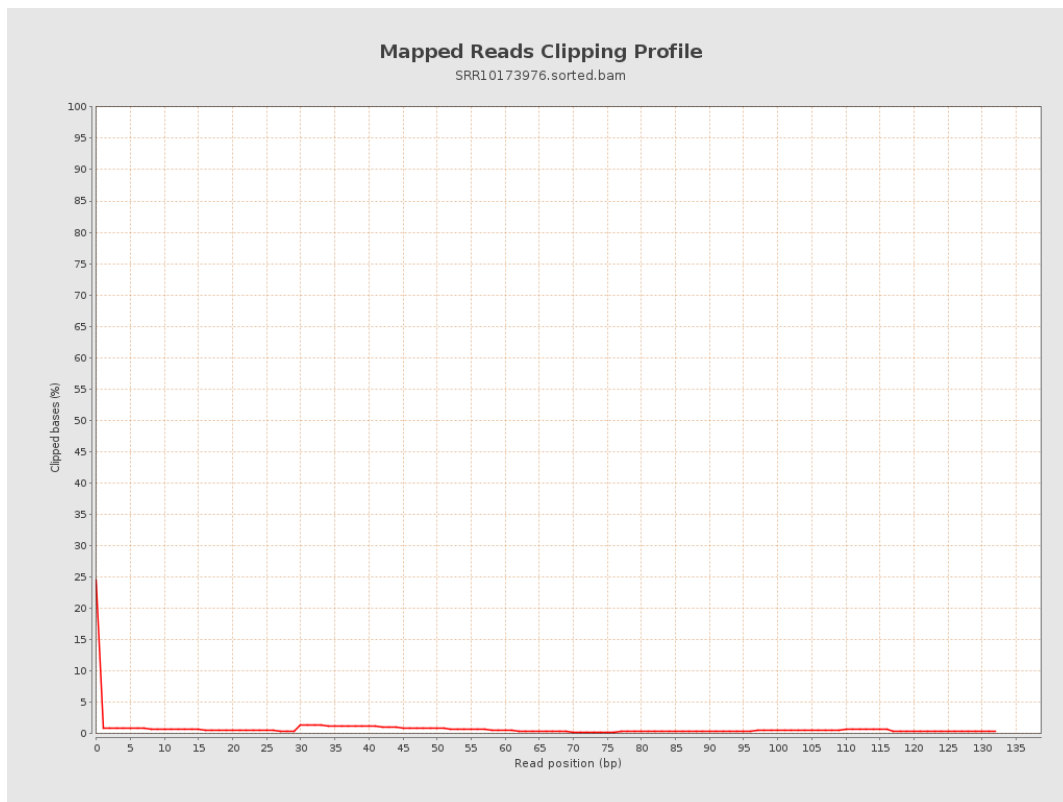
8. Results : Mapped Reads Nucleotide Content



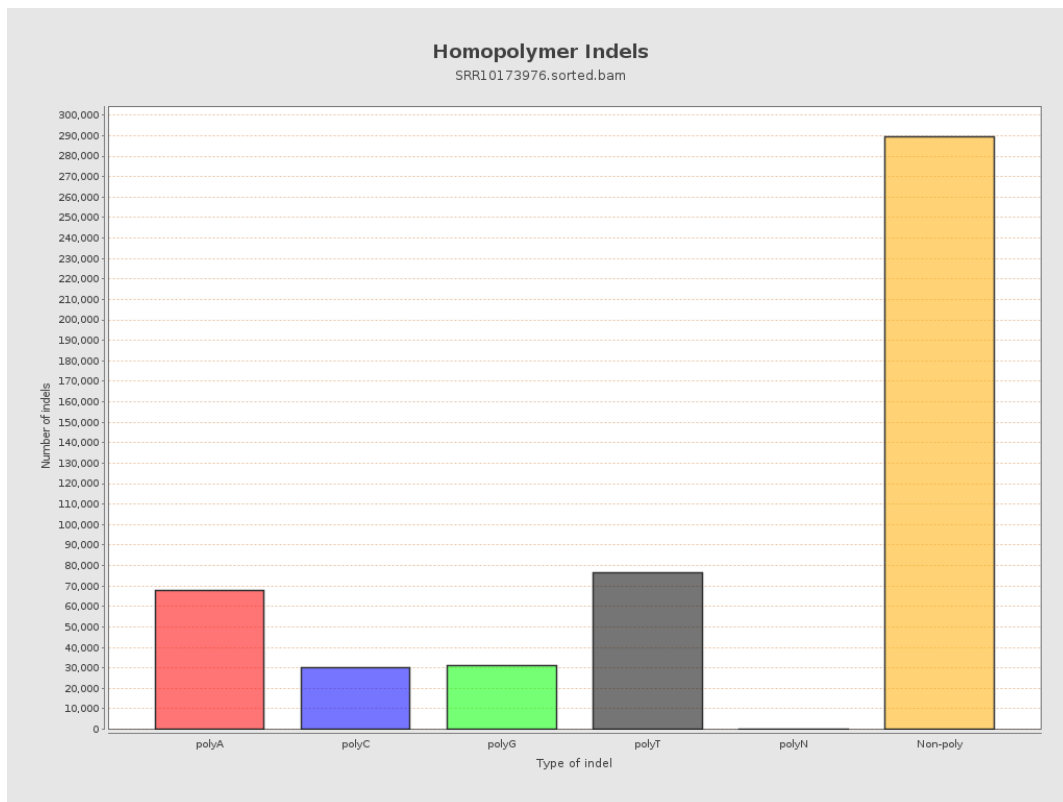
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



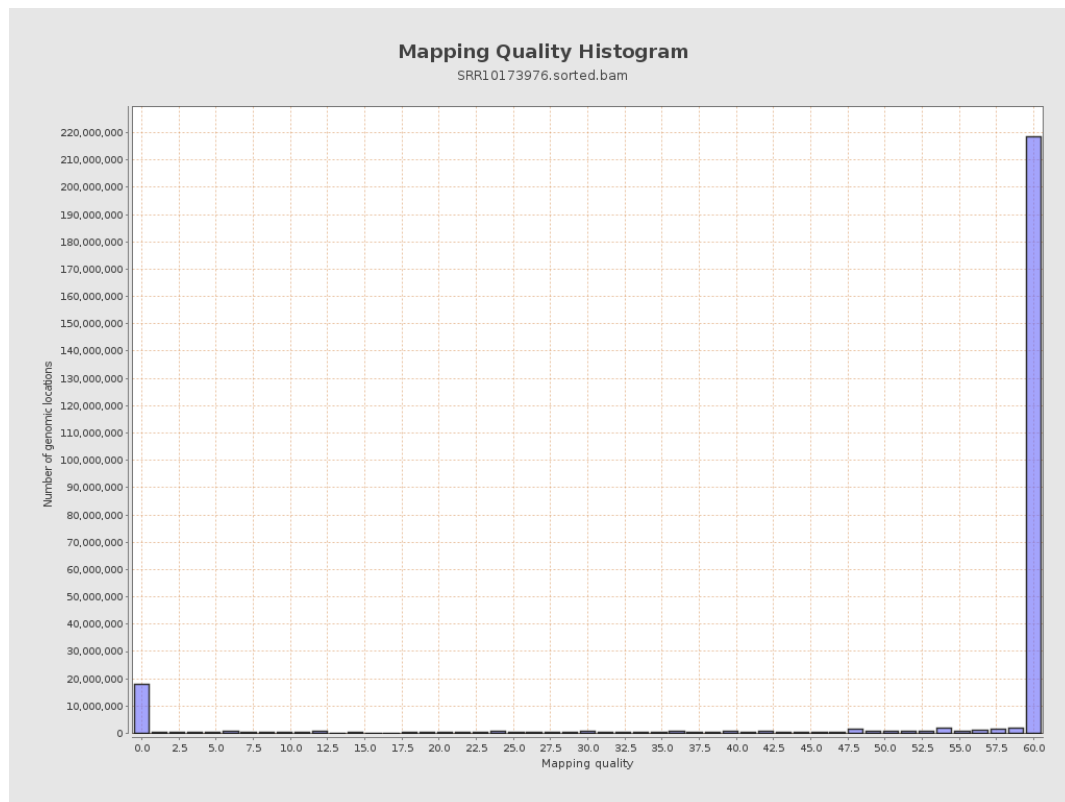
11. Results : Homopolymer Indels



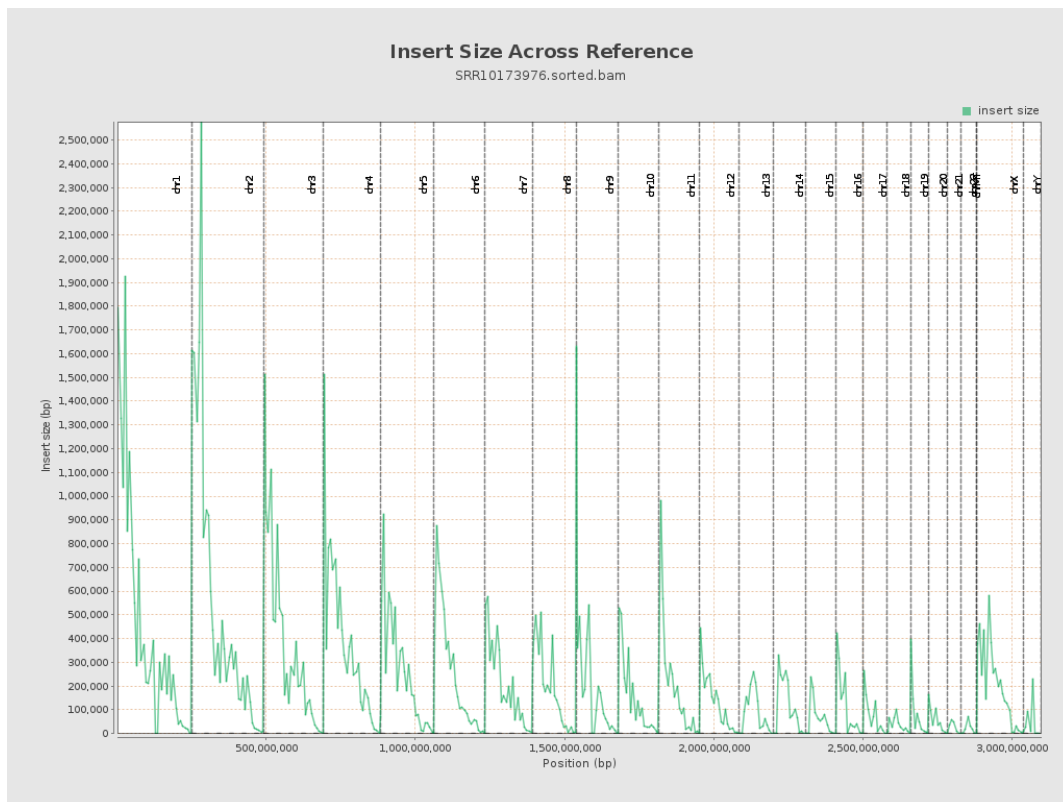
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

