

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 11:33:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173950.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_SRR10173950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173950_1.fastq.gz SRR10173950_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 11:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,472,608
Mapped reads	3,395,673 / 97.78%
Unmapped reads	76,935 / 2.22%
Mapped paired reads	3,395,673 / 97.78%
Mapped reads, first in pair	1,698,594 / 48.91%
Mapped reads, second in pair	1,697,079 / 48.87%
Mapped reads, both in pair	3,345,754 / 96.35%
Mapped reads, singletons	49,919 / 1.44%
Secondary alignments	0
Supplementary alignments	459,164 / 13.22%
Read min/max/mean length	30 / 133 / 125.85
Duplicated reads (estimated)	2,760,695 / 79.5%
Duplication rate	65.65%
Clipped reads	1,724,281 / 49.65%

2.2. ACGT Content

Number/percentage of A's	114,947,375 / 29.76%
Number/percentage of C's	77,018,944 / 19.94%
Number/percentage of T's	113,941,227 / 29.5%
Number/percentage of G's	80,341,661 / 20.8%
Number/percentage of N's	2,908 / 0%

GC Percentage	40.74%
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2.3. Coverage

Mean	0.1249
Standard Deviation	2.4052

2.4. Mapping Quality

Mean Mapping Quality	52.58
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2.5. Insert size

Mean	1,210,052.55
Standard Deviation	10,156,263.92
P25/Median/P75	107 / 156 / 240

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,369,916
Insertions	42,263
Mapped reads with at least one insertion	1.19%
Deletions	126,327
Mapped reads with at least one deletion	3.63%
Homopolymer indels	40.19%

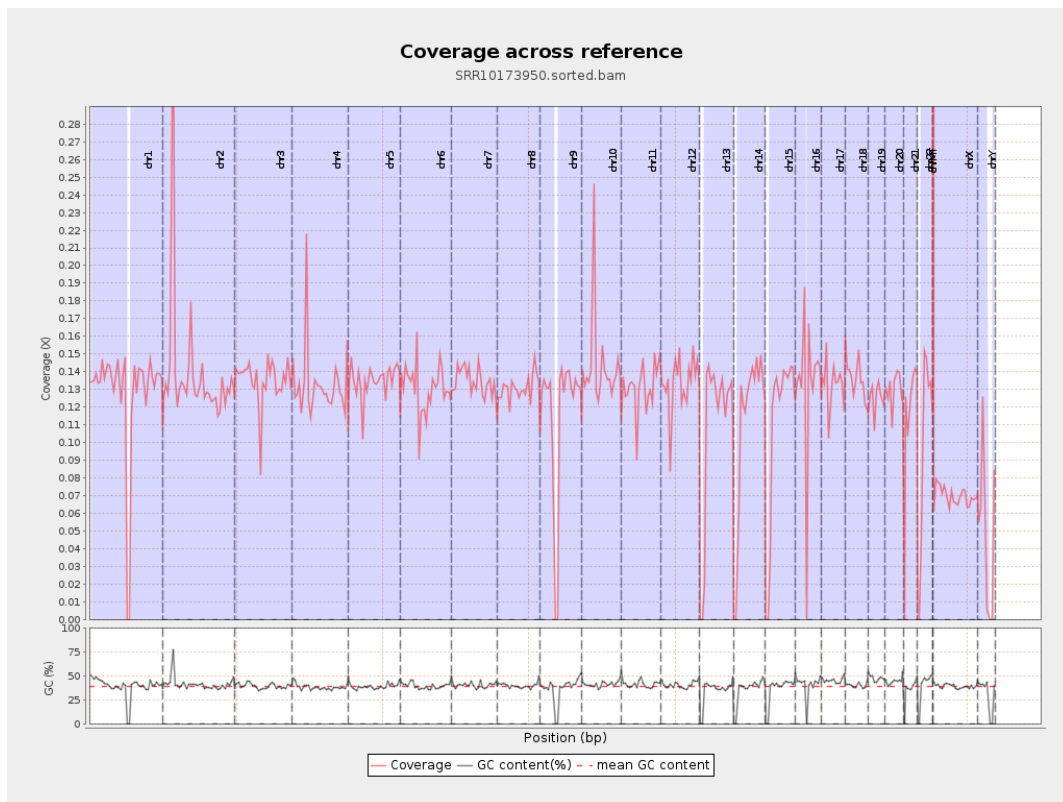
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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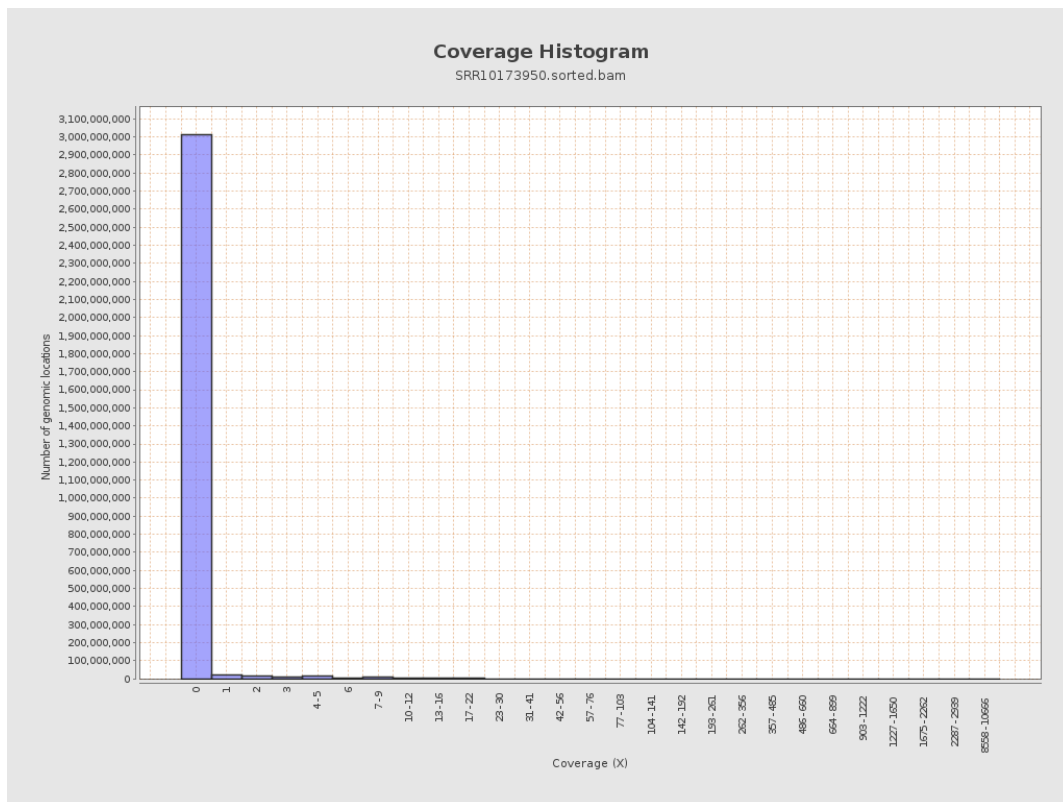
		bases	coverage	deviation
chr1	249250621	31938462	0.1281	1.2954
chr2	243199373	33674067	0.1385	7.5061
chr3	198022430	26708380	0.1349	1.1306
chr4	191154276	25435214	0.1331	1.3281
chr5	180915260	24368283	0.1347	1.1328
chr6	171115067	22349960	0.1306	1.1718
chr7	159138663	21394800	0.1344	1.3014
chr8	146364022	19177366	0.131	1.354
chr9	141213431	16464437	0.1166	1.1813
chr10	135534747	19344227	0.1427	1.5866
chr11	135006516	17653845	0.1308	1.1187
chr12	133851895	17938968	0.134	1.1338
chr13	115169878	12581334	0.1092	1.0146
chr14	107349540	12038712	0.1121	1.0231
chr15	102531392	11065848	0.1079	0.995
chr16	90354753	11930102	0.132	1.232
chr17	81195210	10841530	0.1335	1.1301
chr18	78077248	10611424	0.1359	1.5213
chr19	59128983	7398224	0.1251	1.1319
chr20	63025520	8197564	0.1301	1.1088
chr21	48129895	5610858	0.1166	1.2045
chr22	51304566	4966775	0.0968	1.0607
chrMT	16571	1069363	64.5322	57.7282
chrX	155270560	10826560	0.0697	0.815

chrY	59373566	2958126	0.0498	0.9296
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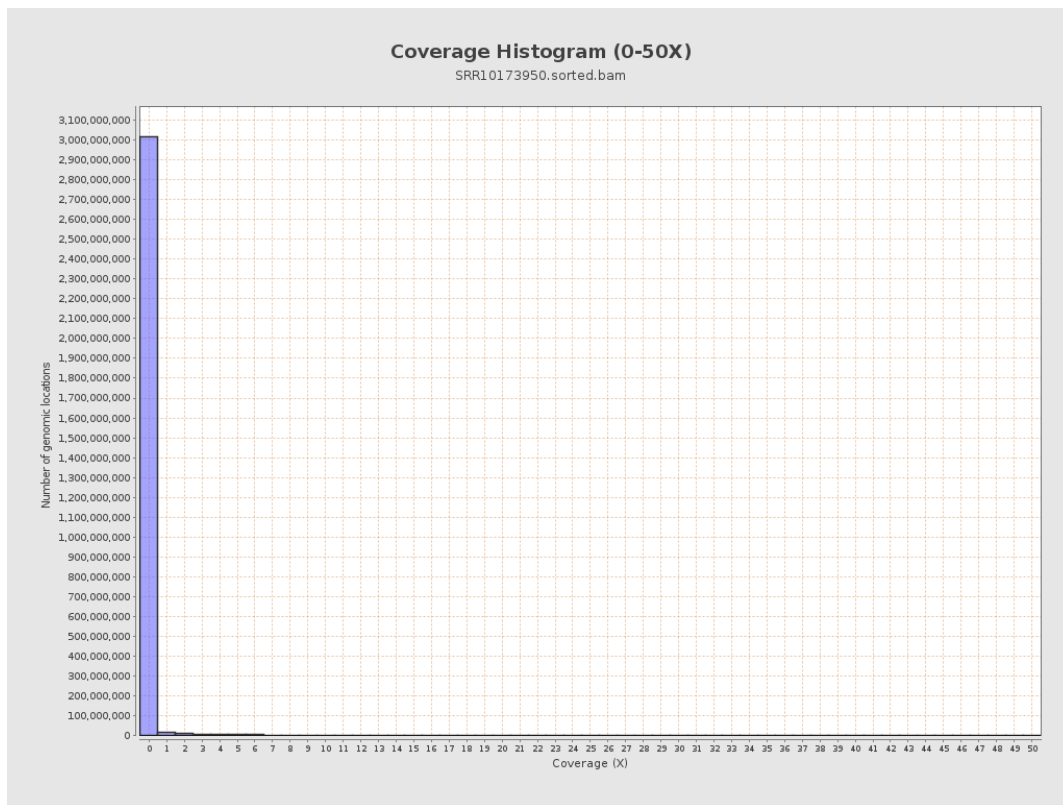
3. Results : Coverage across reference



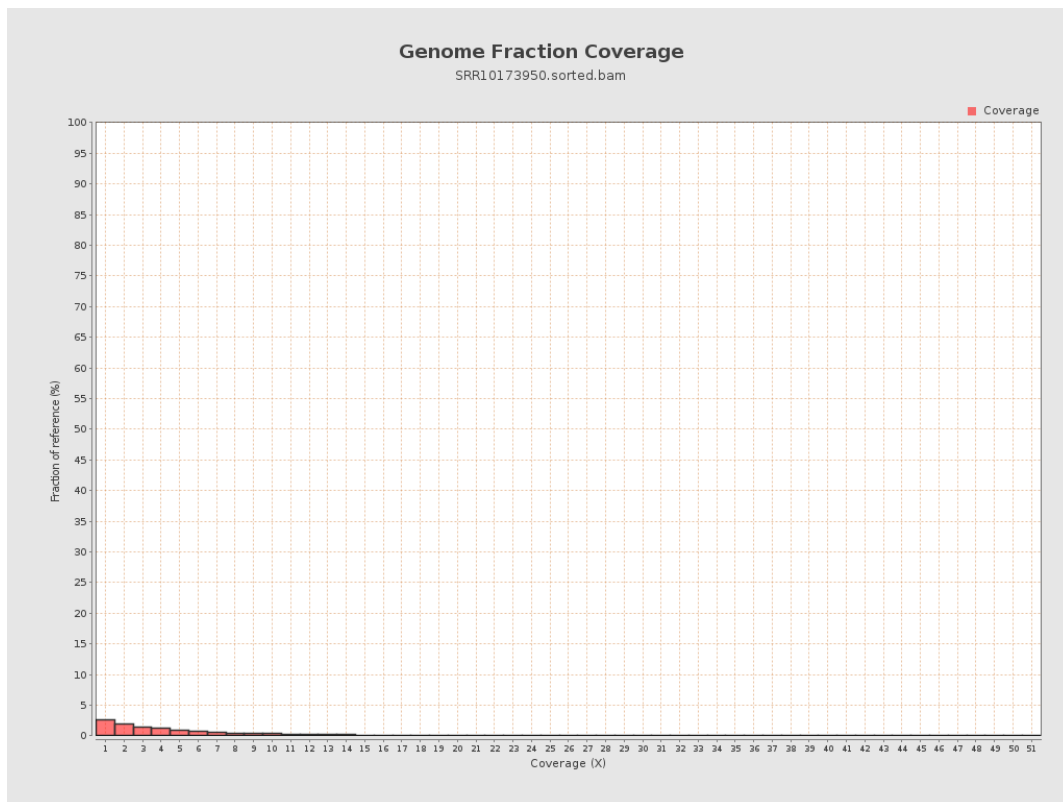
4. Results : Coverage Histogram



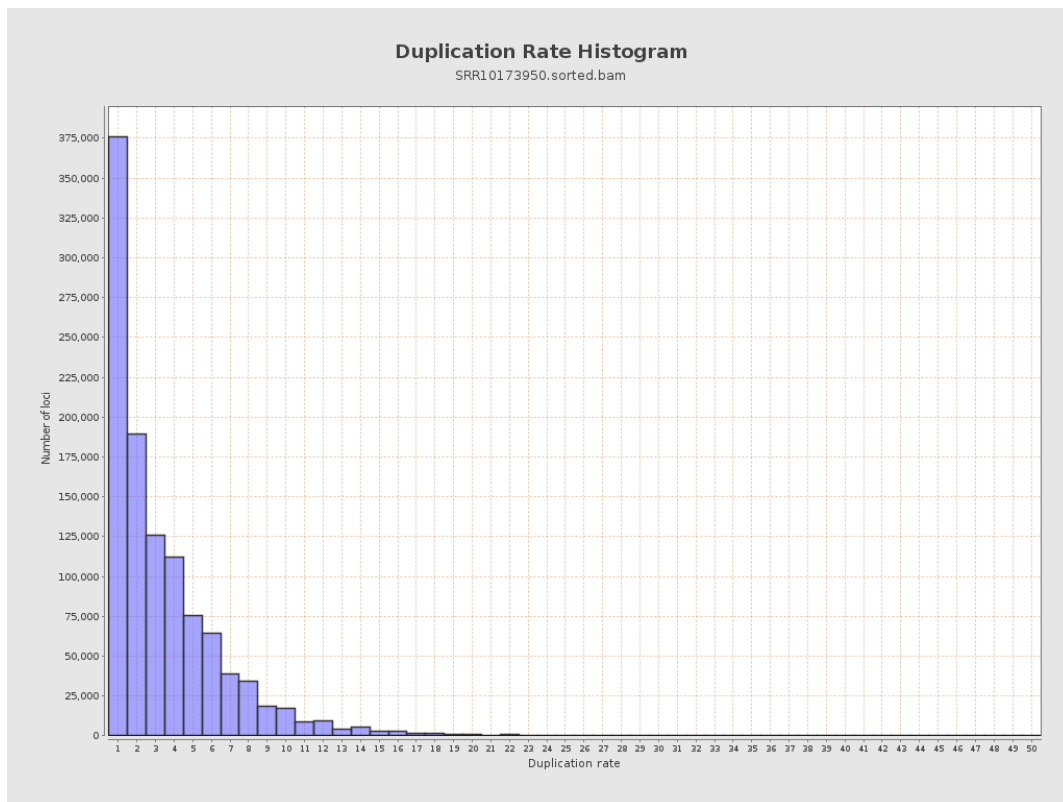
5. Results : Coverage Histogram (0-50X)



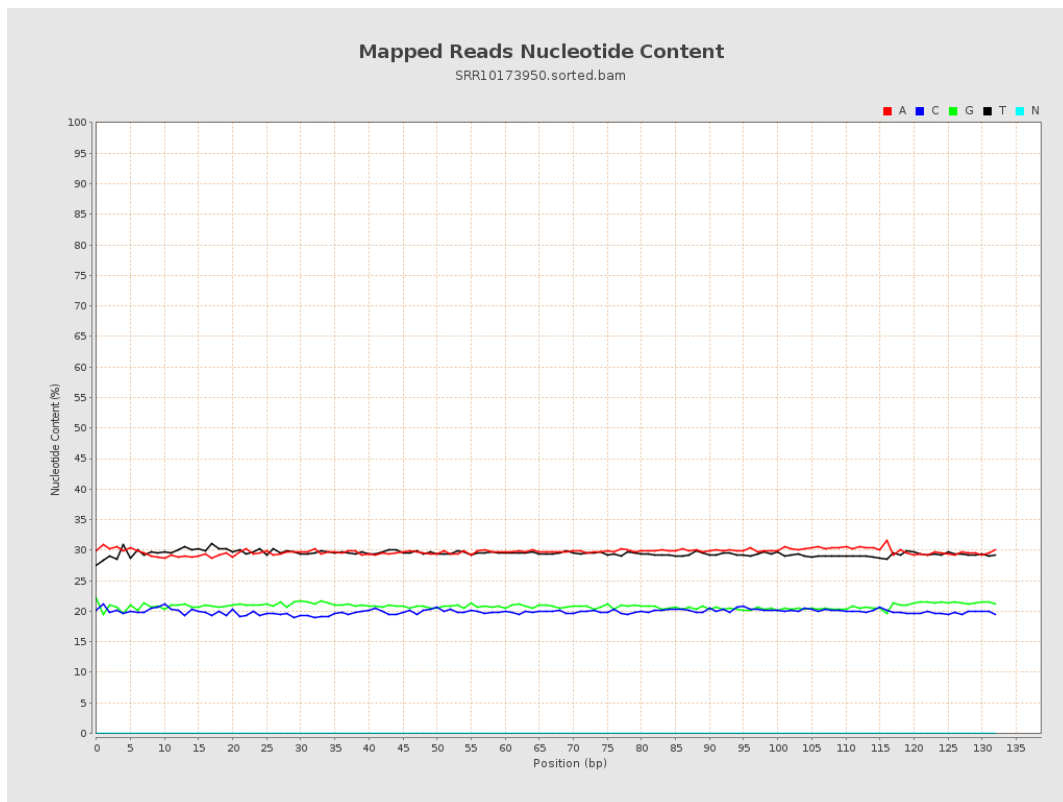
6. Results : Genome Fraction Coverage



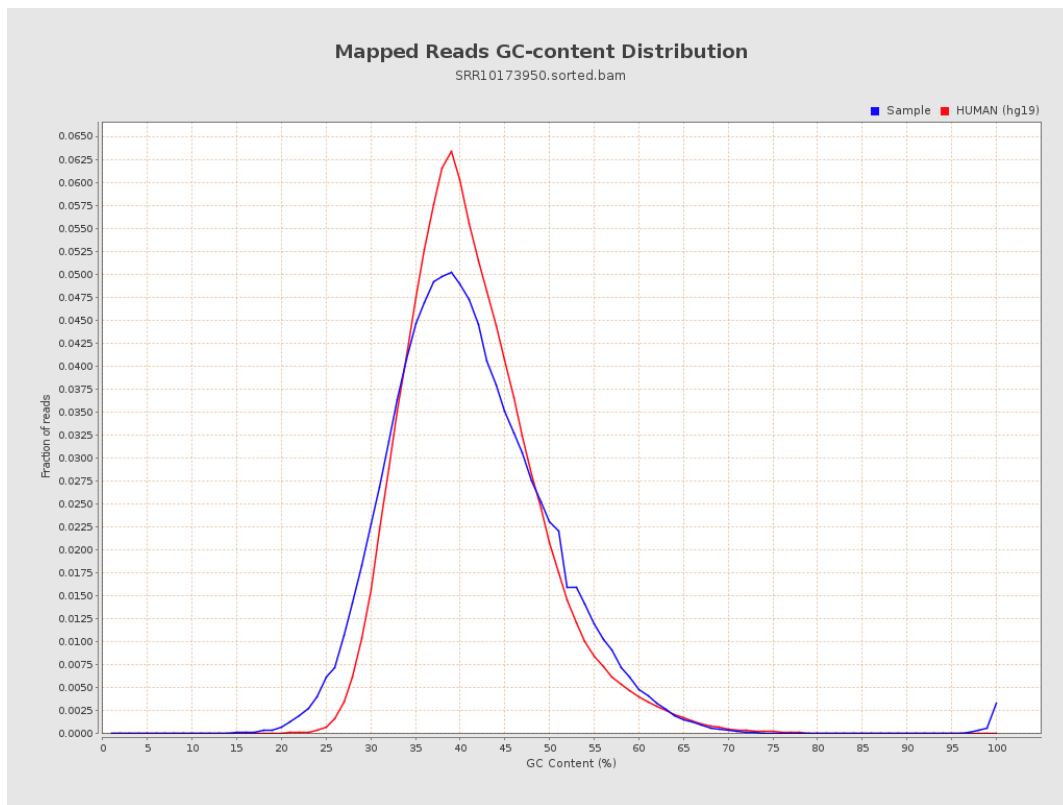
7. Results : Duplication Rate Histogram



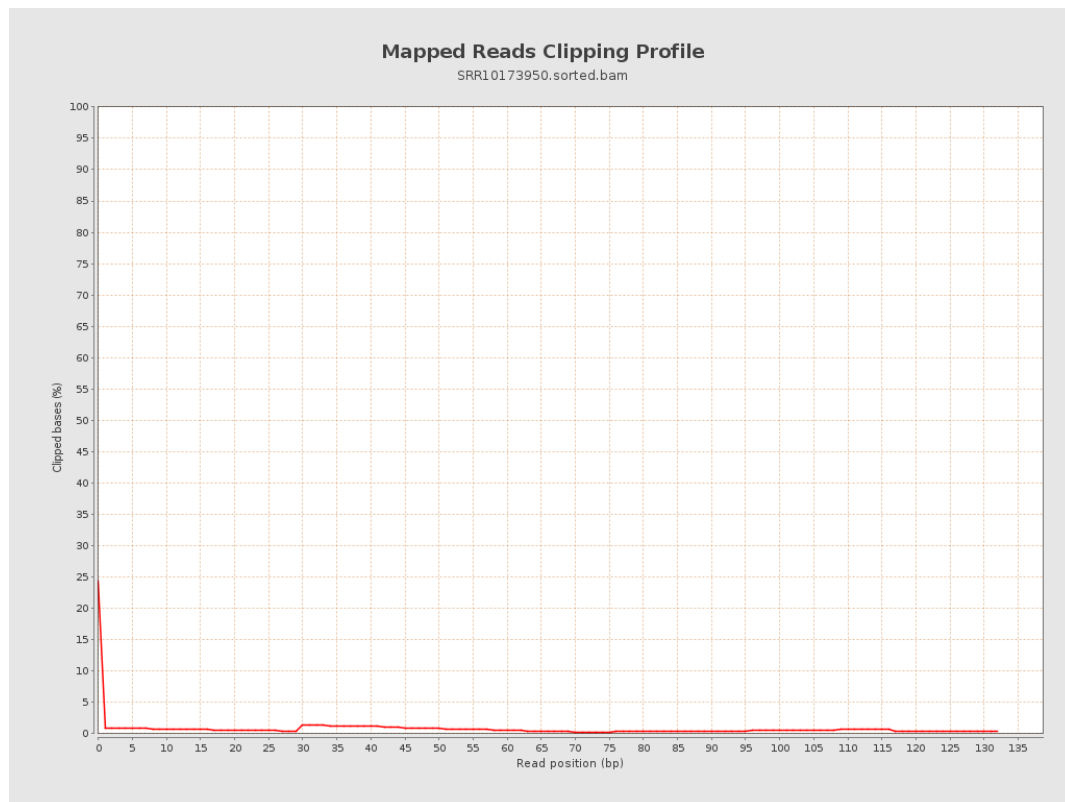
8. Results : Mapped Reads Nucleotide Content



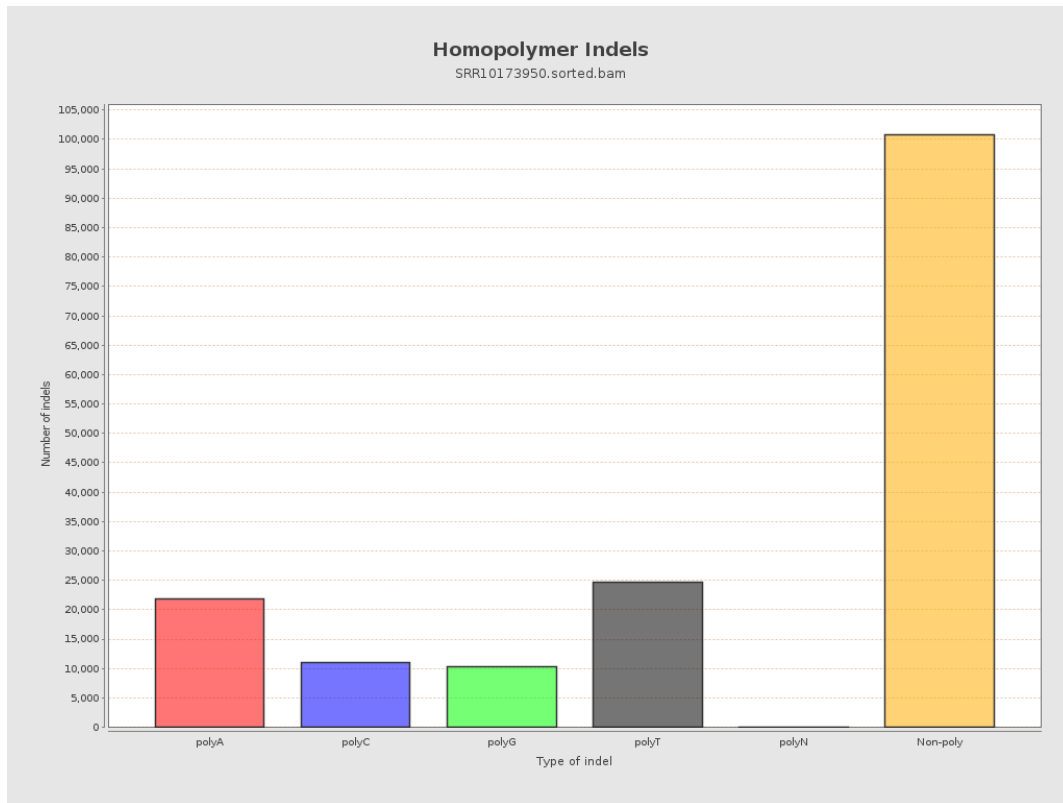
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



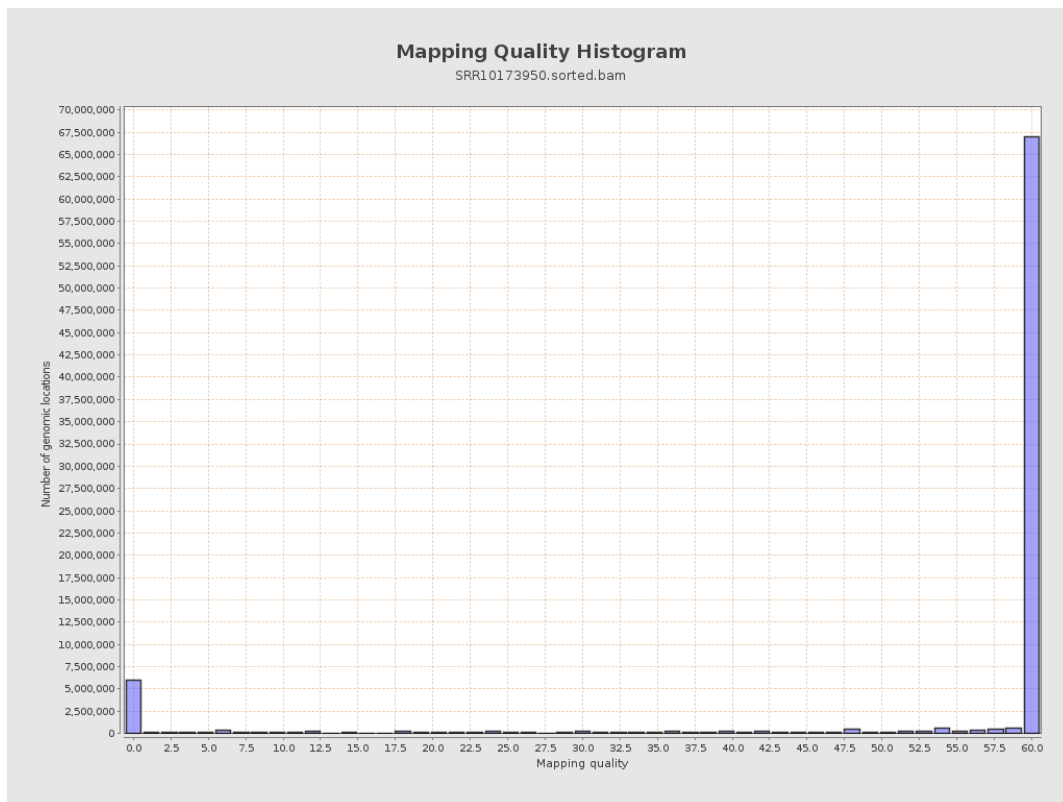
11. Results : Homopolymer Indels



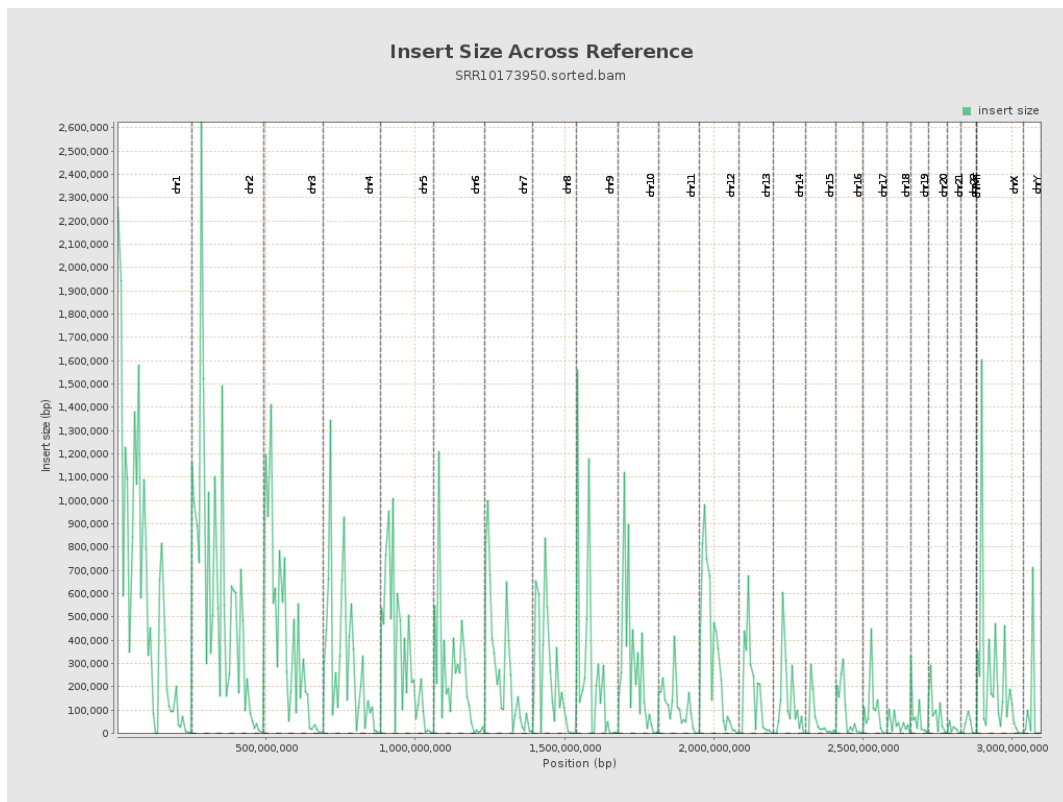
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

