

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:48:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173933.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_SRR10173933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173933_1.fastq.gz SRR10173933_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:48:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,356,954
Mapped reads	5,240,156 / 97.82%
Unmapped reads	116,798 / 2.18%
Mapped paired reads	5,240,156 / 97.82%
Mapped reads, first in pair	2,619,184 / 48.89%
Mapped reads, second in pair	2,620,972 / 48.93%
Mapped reads, both in pair	5,168,240 / 96.48%
Mapped reads, singletons	71,916 / 1.34%
Secondary alignments	0
Supplementary alignments	712,143 / 13.29%
Read min/max/mean length	30 / 133 / 125.68
Duplicated reads (estimated)	4,154,758 / 77.56%
Duplication rate	64.04%
Clipped reads	2,693,070 / 50.27%

2.2. ACGT Content

Number/percentage of A's	177,689,523 / 29.87%
Number/percentage of C's	118,066,489 / 19.85%
Number/percentage of T's	176,165,921 / 29.62%
Number/percentage of G's	122,872,637 / 20.66%
Number/percentage of N's	4,956 / 0%

GC Percentage	40.51%
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2.3. Coverage

Mean	0.1923
Standard Deviation	3.5773

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	1,084,160.79
Standard Deviation	9,596,798.72
P25/Median/P75	106 / 155 / 237

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	5,164,058
Insertions	66,696
Mapped reads with at least one insertion	1.22%
Deletions	181,731
Mapped reads with at least one deletion	3.38%
Homopolymer indels	40.73%

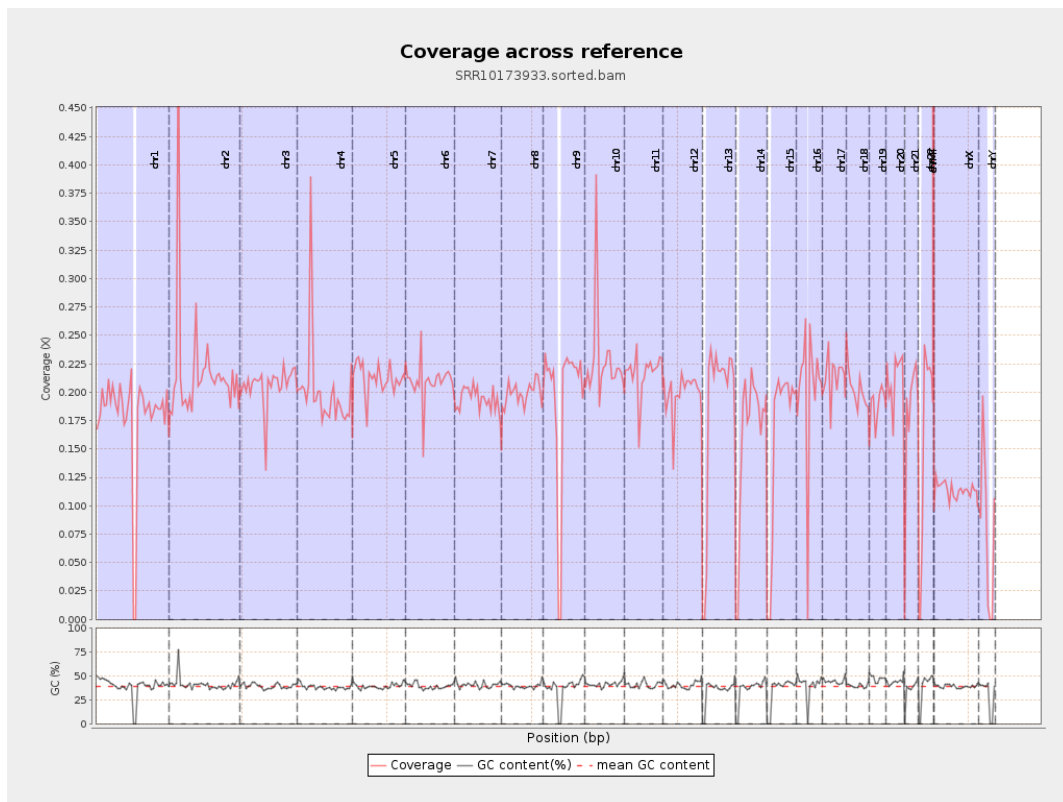
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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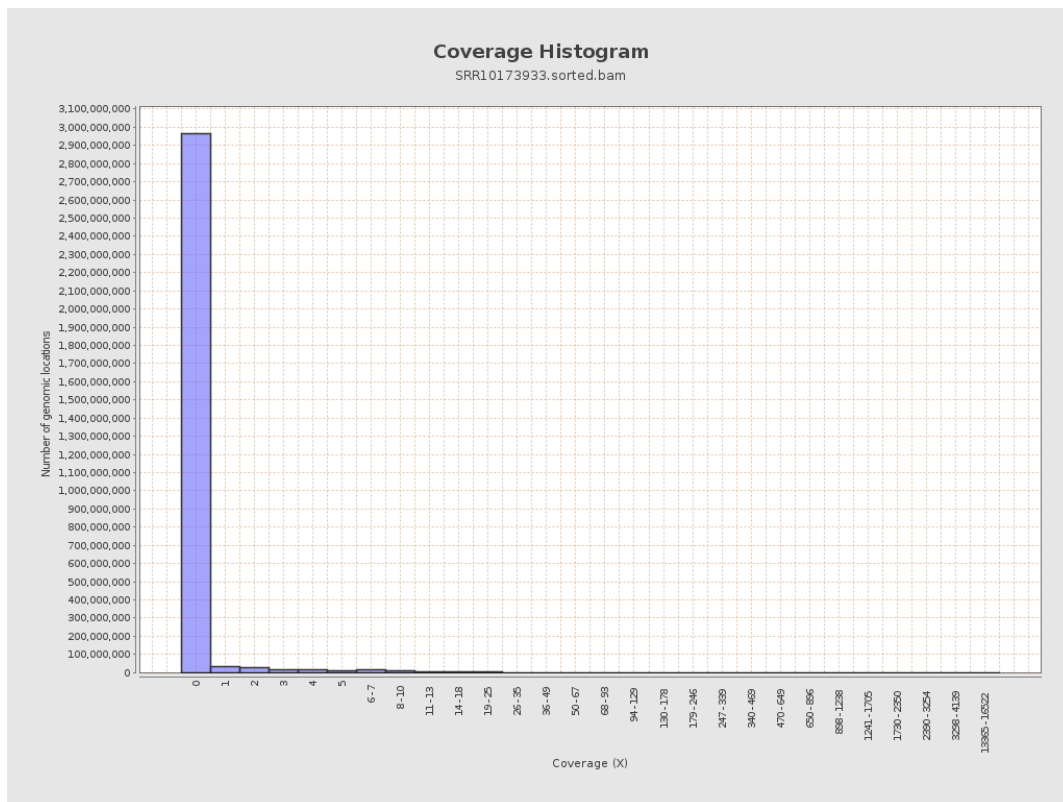
		bases	coverage	deviation
chr1	249250621	44394943	0.1781	1.7675
chr2	243199373	53199830	0.2187	11.5592
chr3	198022430	40773544	0.2059	1.3447
chr4	191154276	38252889	0.2001	1.8517
chr5	180915260	38380208	0.2121	1.3653
chr6	171115067	35854457	0.2095	1.5139
chr7	159138663	30911949	0.1942	1.5797
chr8	146364022	29113197	0.1989	2.0056
chr9	141213431	27312430	0.1934	1.65
chr10	135534747	30782284	0.2271	2.1436
chr11	135006516	29359183	0.2175	1.4209
chr12	133851895	26620364	0.1989	1.3504
chr13	115169878	21266993	0.1847	1.2874
chr14	107349540	17236200	0.1606	1.1863
chr15	102531392	16669757	0.1626	1.2045
chr16	90354753	18259665	0.2021	1.6045
chr17	81195210	17233438	0.2122	1.4368
chr18	78077248	15826192	0.2027	2.3007
chr19	59128983	11145802	0.1885	1.4838
chr20	63025520	13228491	0.2099	1.4273
chr21	48129895	8707985	0.1809	1.6073
chr22	51304566	7935549	0.1547	1.4319
chrMT	16571	607491	36.6599	37.4384
chrX	155270560	17656832	0.1137	1.0021

chrY	59373566	4502883	0.0758	1.2572
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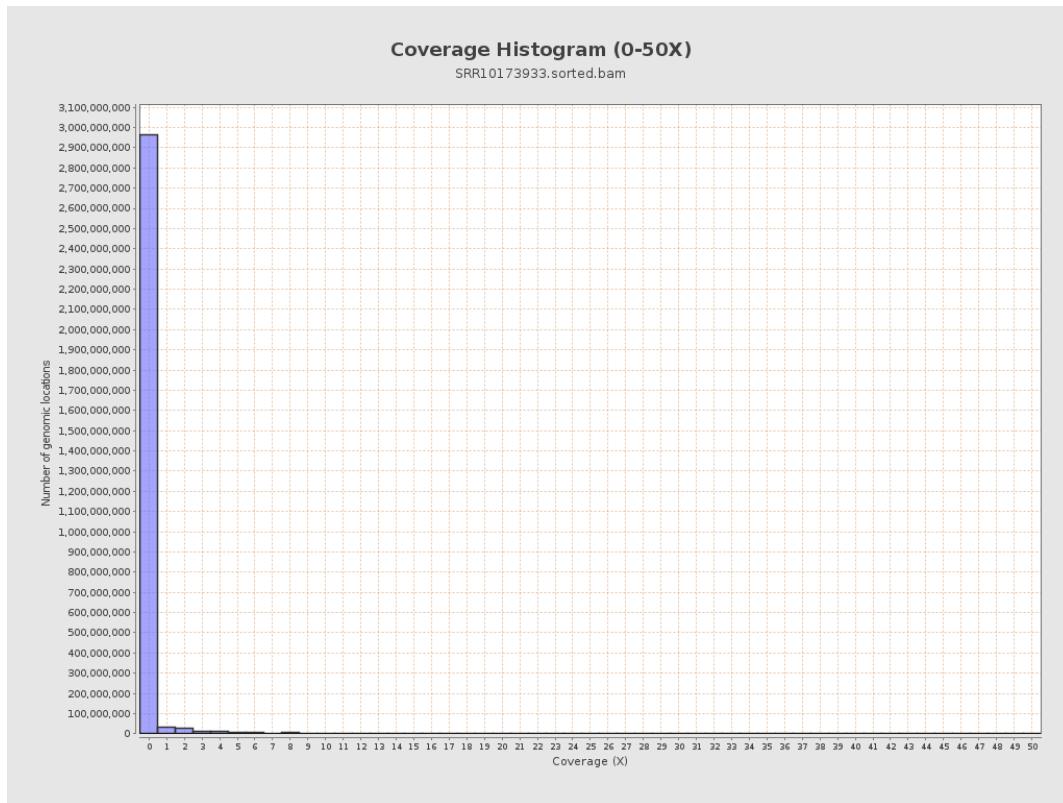
3. Results : Coverage across reference



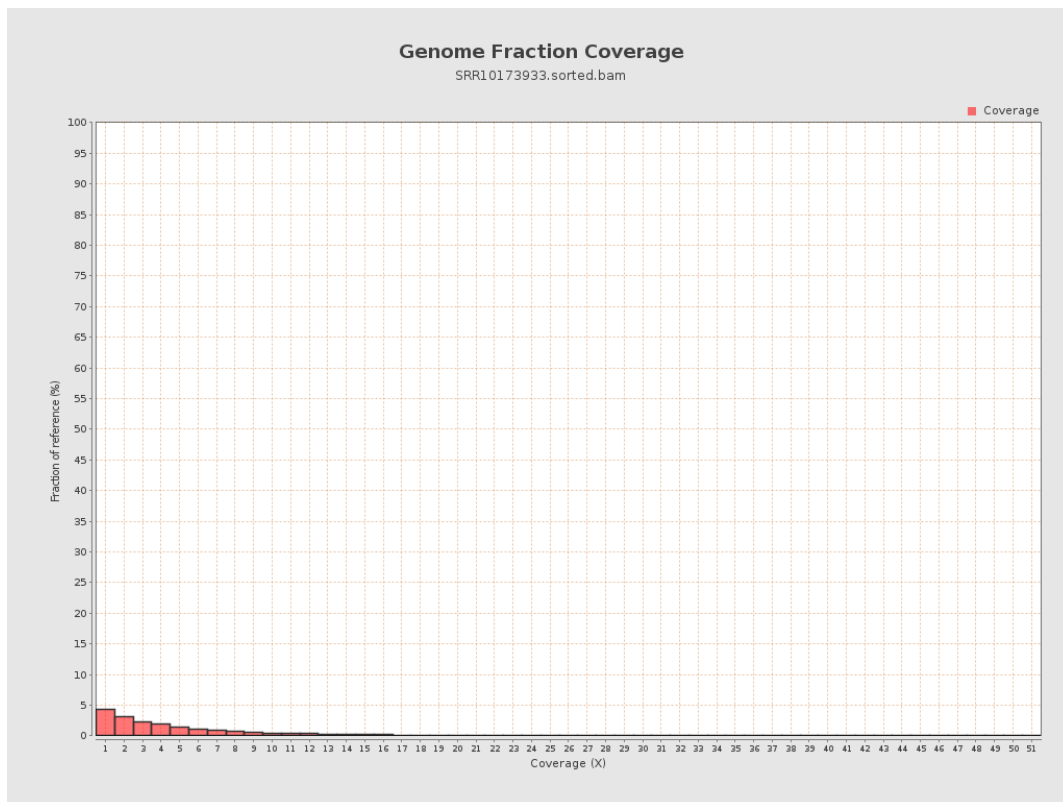
4. Results : Coverage Histogram



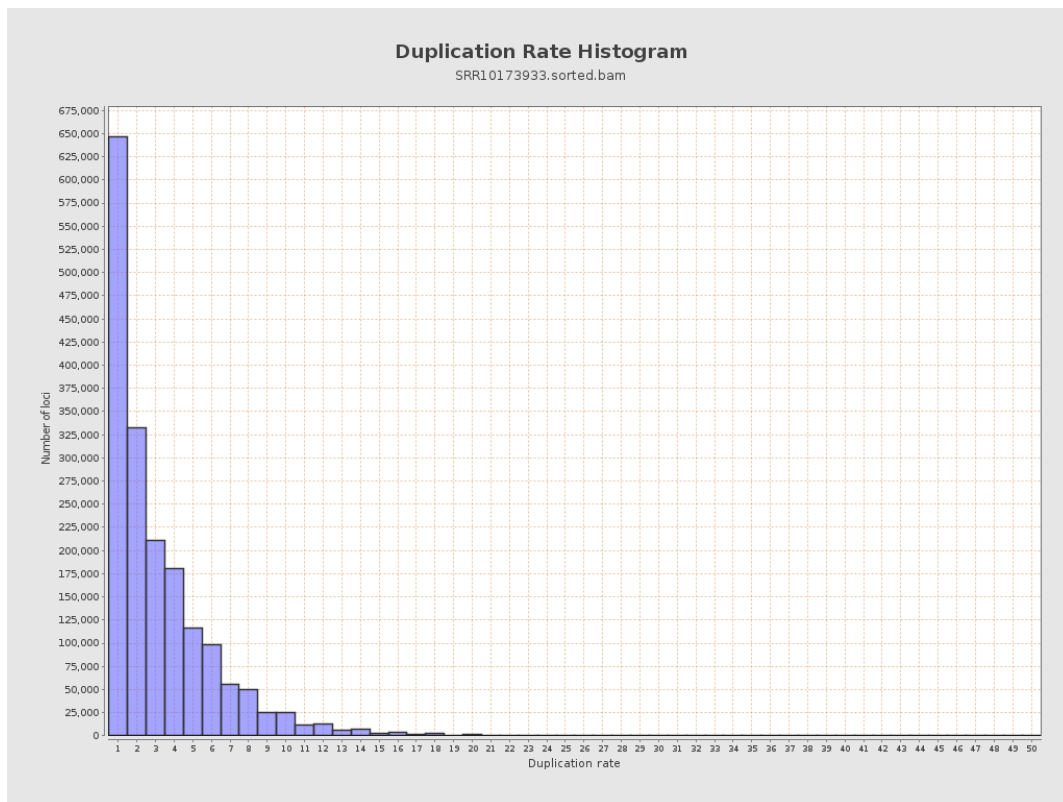
5. Results : Coverage Histogram (0-50X)



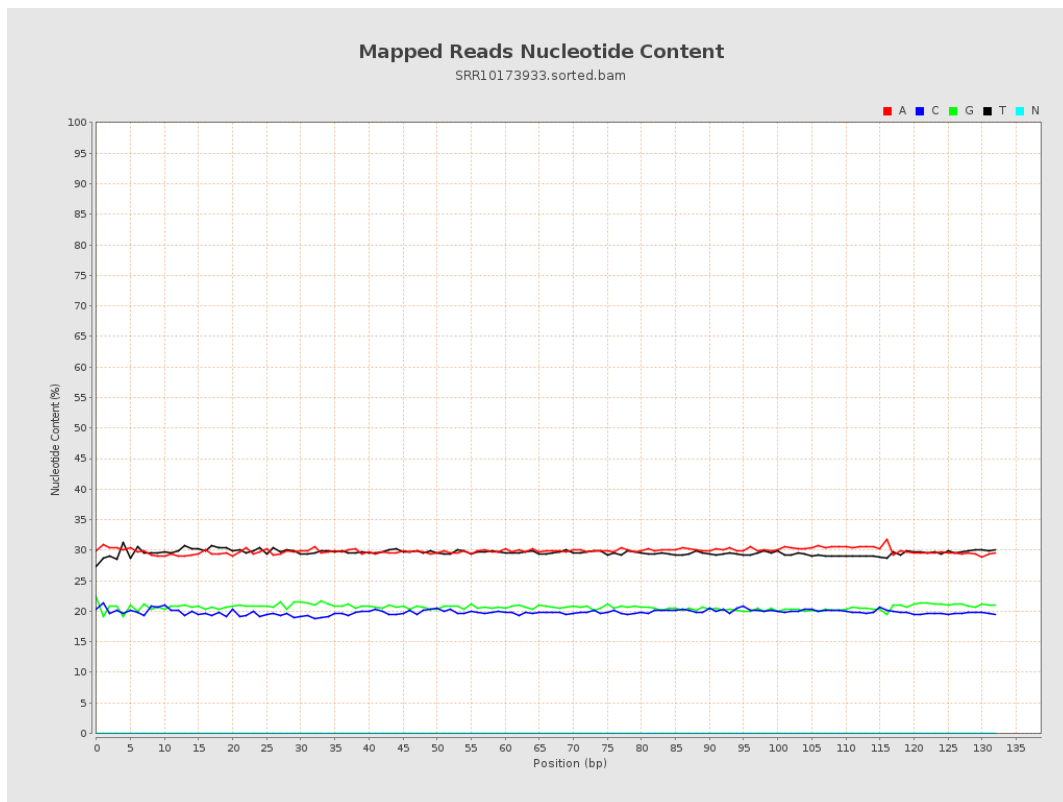
6. Results : Genome Fraction Coverage



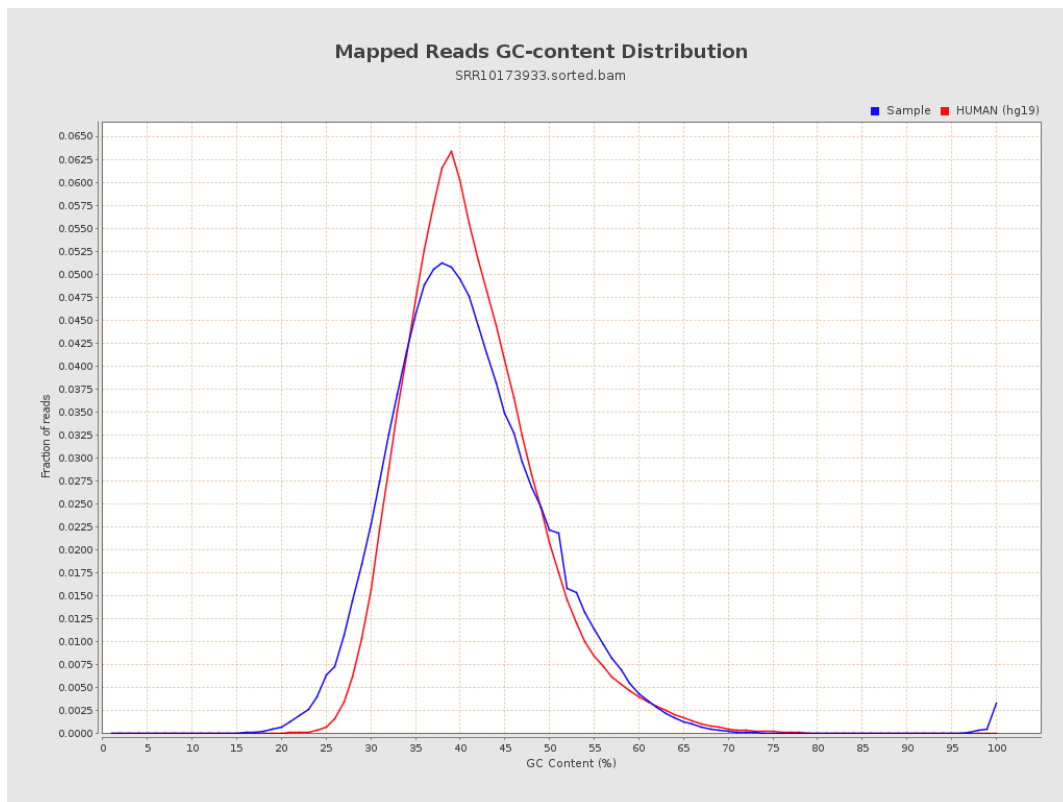
7. Results : Duplication Rate Histogram



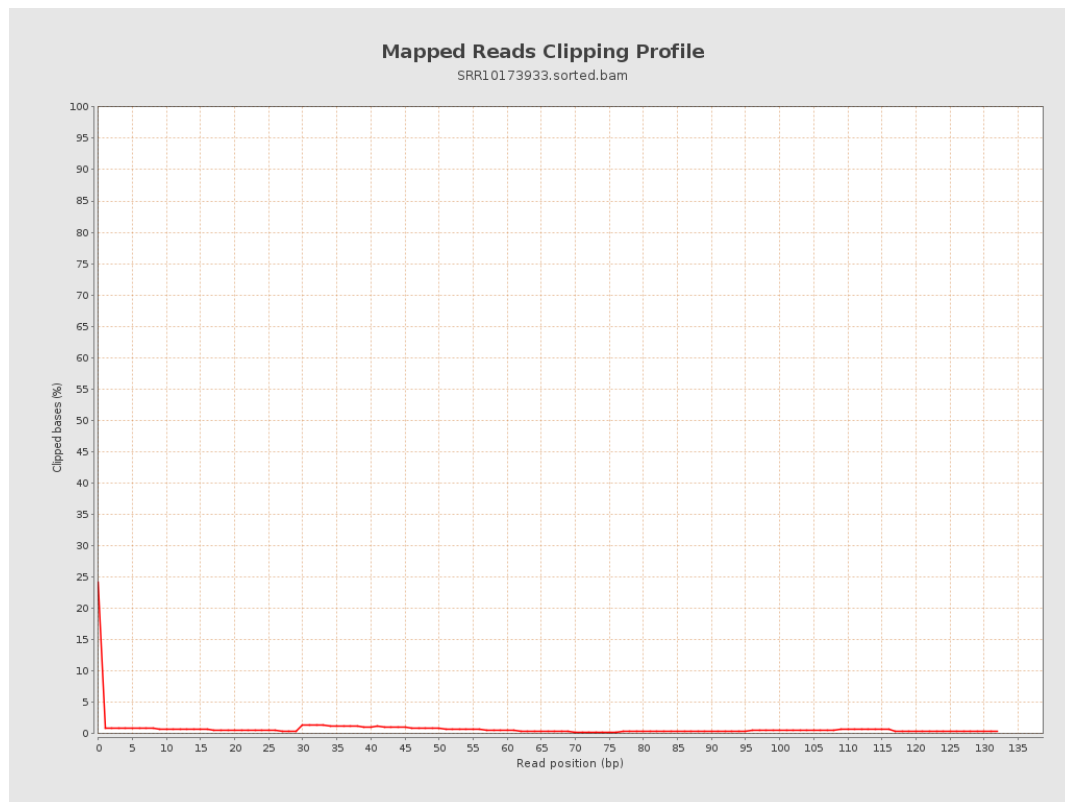
8. Results : Mapped Reads Nucleotide Content



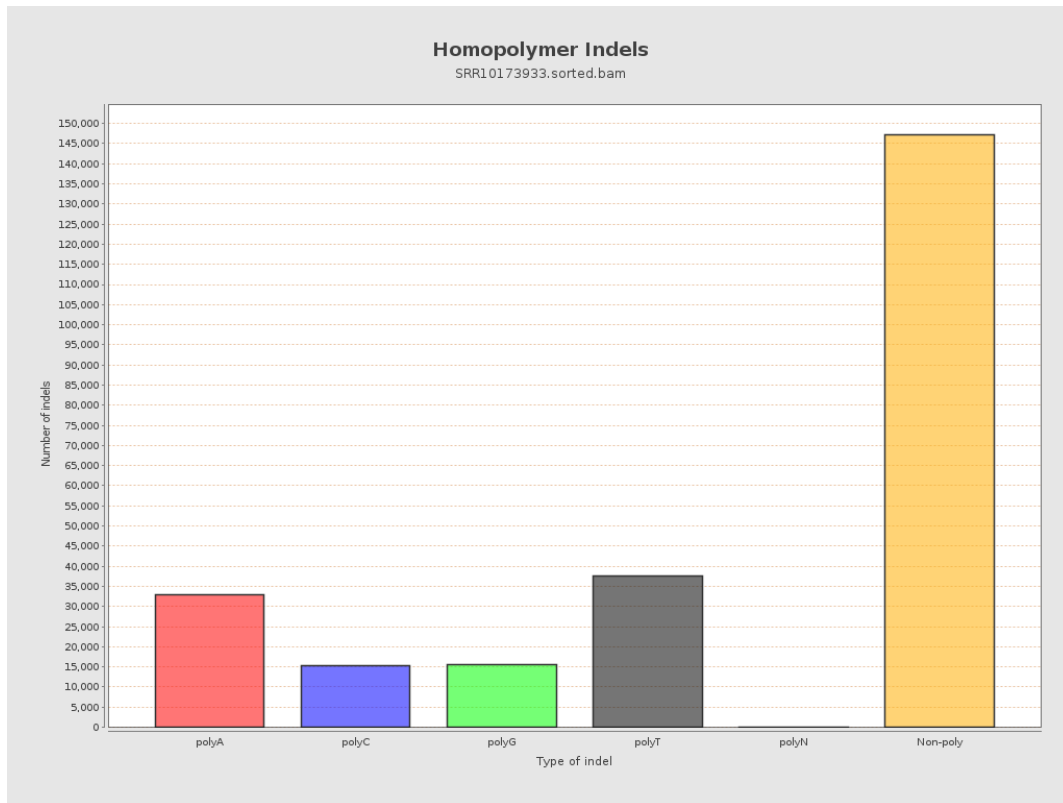
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



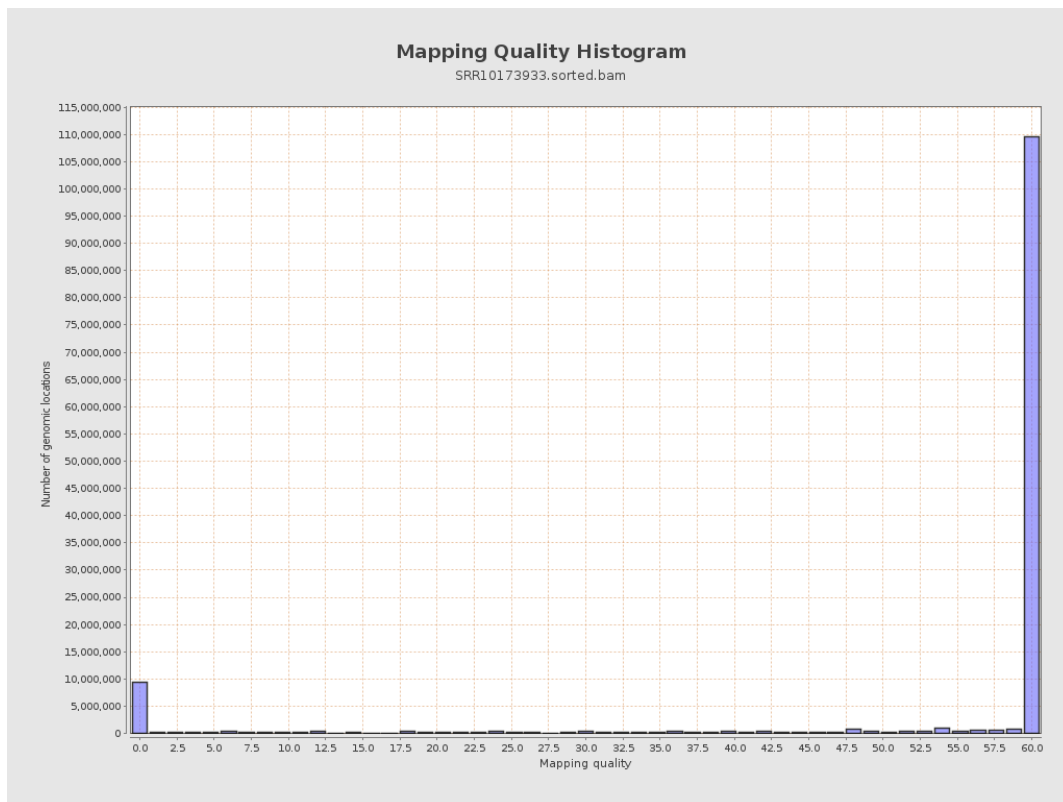
11. Results : Homopolymer Indels



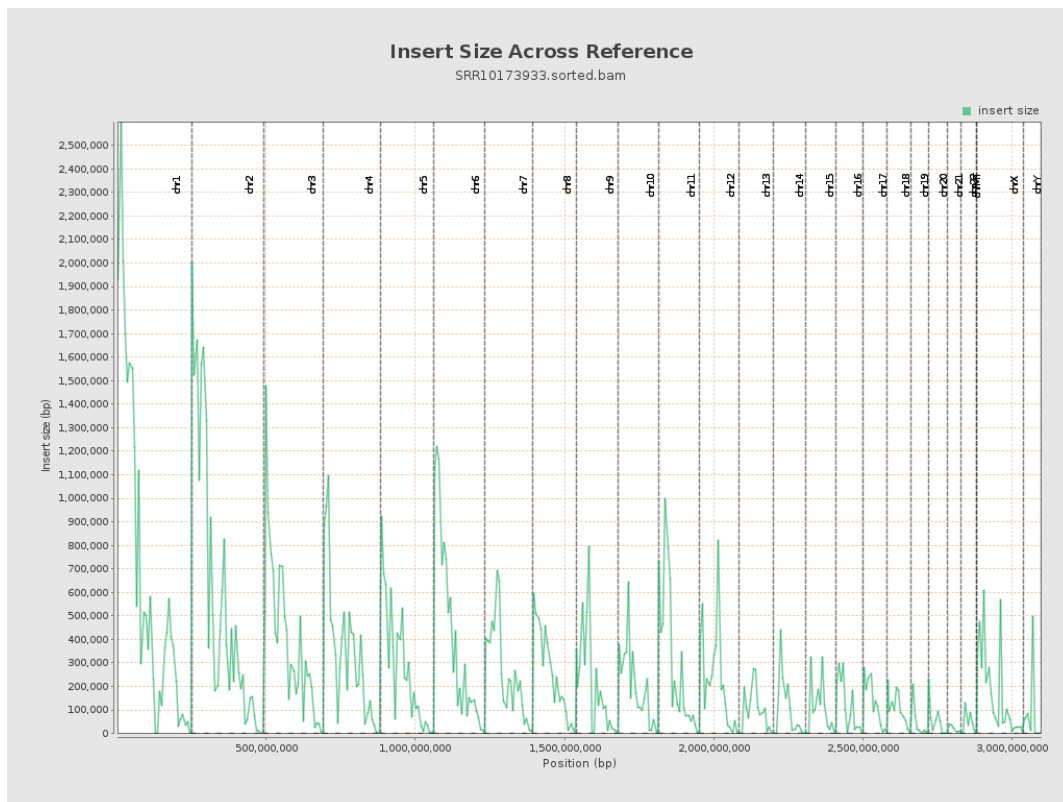
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

