Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:06:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173919.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_SRR10173919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173919_1.fastq.gz SRR10173919_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:06:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,388,568
Mapped reads	7,148,282 / 96.75%
Unmapped reads	240,286 / 3.25%
Mapped paired reads	7,148,282 / 96.75%
Mapped reads, first in pair	3,586,109 / 48.54%
Mapped reads, second in pair	3,562,173 / 48.21%
Mapped reads, both in pair	6,990,998 / 94.62%
Mapped reads, singletons	157,284 / 2.13%
Secondary alignments	0
Supplementary alignments	772,190 / 10.45%
Read min/max/mean length	30 / 133 / 128.57
Duplicated reads (estimated)	5,614,270 / 75.99%
Duplication rate	64.3%
Clipped reads	3,127,439 / 42.33%

2.2. ACGT Content

Number/percentage of A's	251,780,974 / 29.97%
Number/percentage of C's	165,216,125 / 19.66%
Number/percentage of T's	251,684,981 / 29.95%
Number/percentage of G's	171,545,914 / 20.42%
Number/percentage of N's	10,515 / 0%

GC Percentage	40.08%

2.3. Coverage

Mean	0.2716
Standard Deviation	3.8799

2.4. Mapping Quality

Mean Mapping Quality	52.59

2.5. Insert size

Mean	974,483.64
Standard Deviation	9,193,099.44
P25/Median/P75	144 / 203 / 294

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	9,152,209
Insertions	88,897
Mapped reads with at least one insertion	1.2%
Deletions	215,172
Mapped reads with at least one deletion	2.94%
Homopolymer indels	42.37%

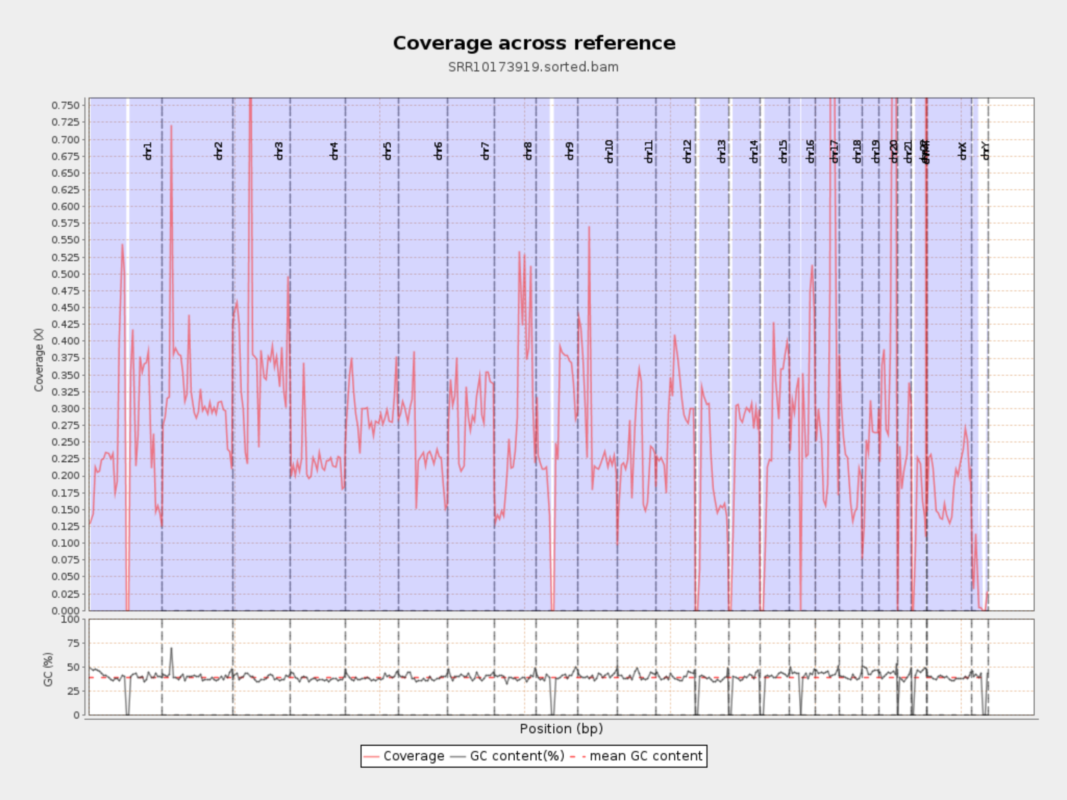
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

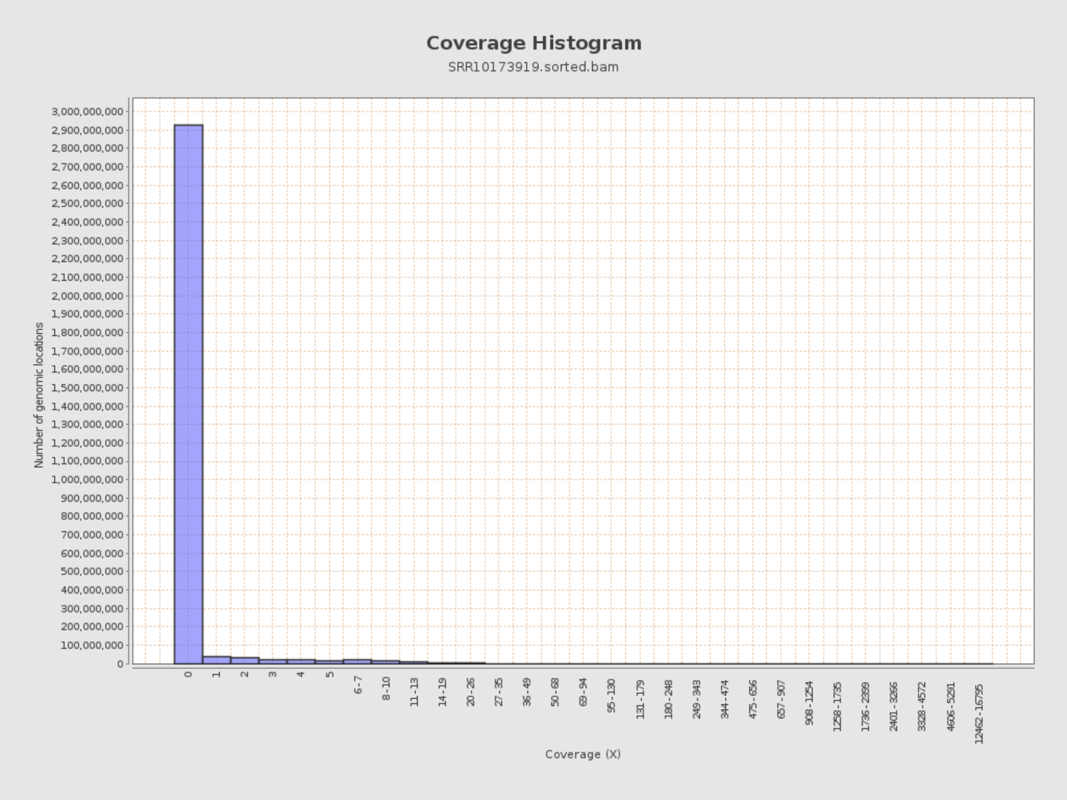
		bases	coverage	deviation
chr1	249250621	62988490	0.2527	2.8644
chr2	243199373	79392906	0.3265	11.7774
chr3	198022430	75437911	0.381	1.8346
chr4	191154276	41877959	0.2191	1.7932
chr5	180915260	53537001	0.2959	1.581
chr6	171115067	42173385	0.2465	1.8742
chr7	159138663	48094188	0.3022	2.352
chr8	146364022	41521225	0.2837	2.778
chr9	141213431	36123904	0.2558	1.9915
chr10	135534747	37154134	0.2741	3.6104
chr11	135006516	30991805	0.2296	1.4638
chr12	133851895	38622404	0.2885	1.5866
chr13	115169878	20666688	0.1794	1.2406
chr14	107349540	25985159	0.2421	1.4628
chr15	102531392	26655401	0.26	1.4907
chr16	90354753	28582807	0.3163	2.1555
chr17	81195210	34478311	0.4246	2.1091
chr18	78077248	16440653	0.2106	3.1764
chr19	59128983	14184212	0.2399	2.1582
chr20	63025520	36273339	0.5755	2.448
chr21	48129895	10815540	0.2247	1.5212
chr22	51304566	6674743	0.1301	1.0215
chrMT	16571	1342759	81.0307	56.157
chrX	155270560	29085020	0.1873	1.2676

chrY	59373566	1660952	0.028	1.1174

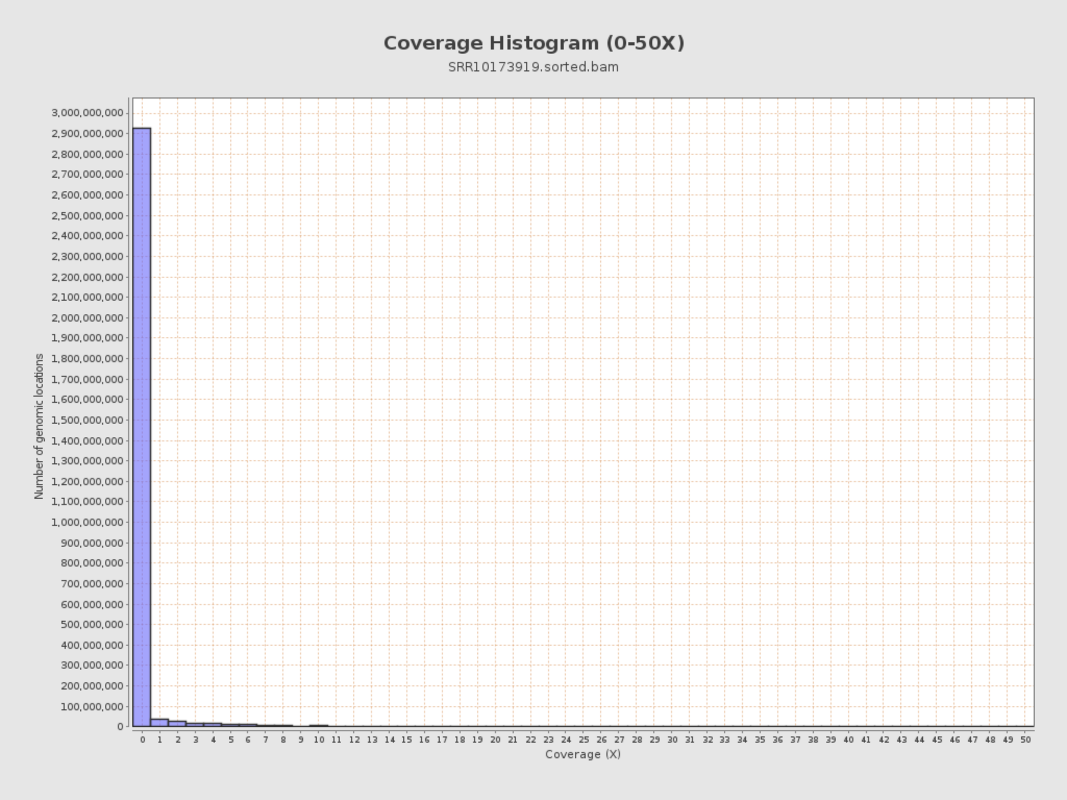
3. Results : Coverage across reference



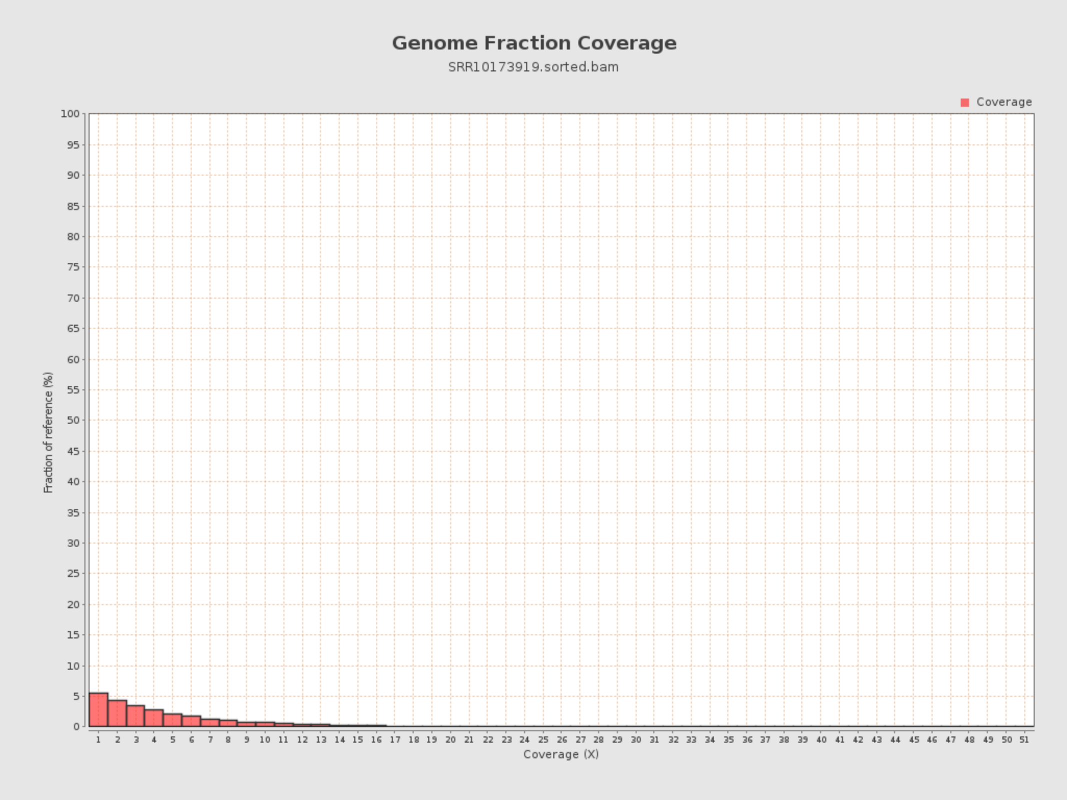
4. Results : Coverage Histogram



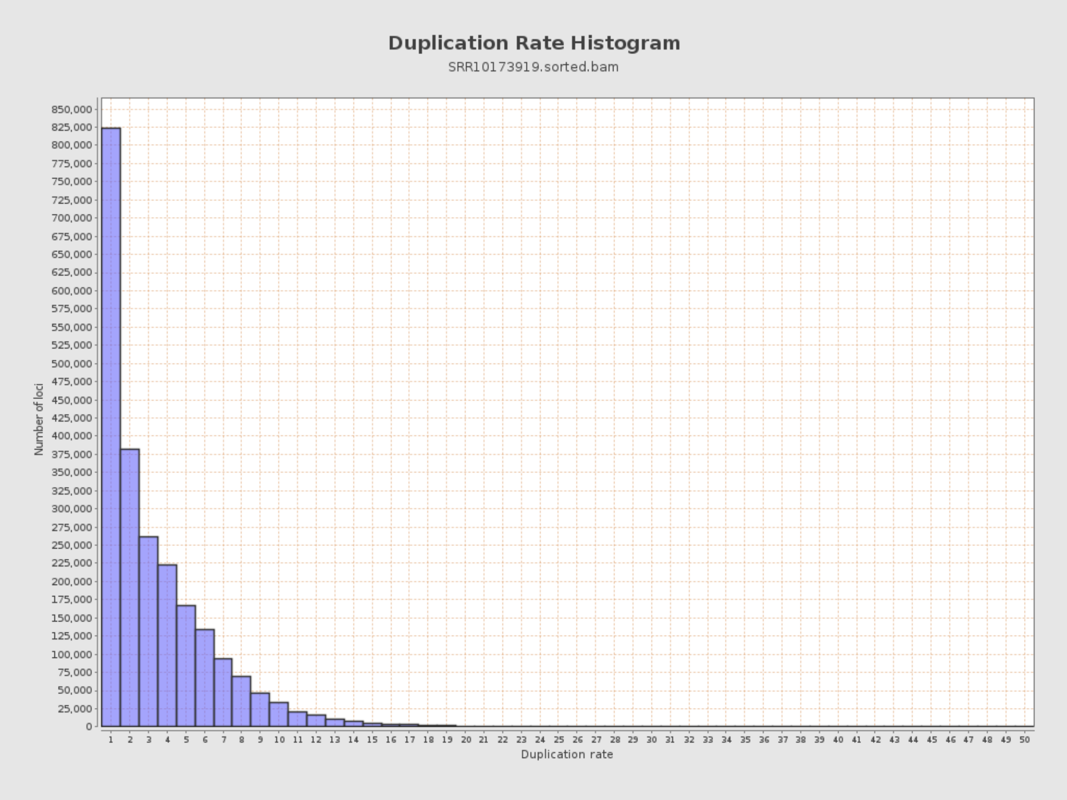
5. Results : Coverage Histogram (0-50X)



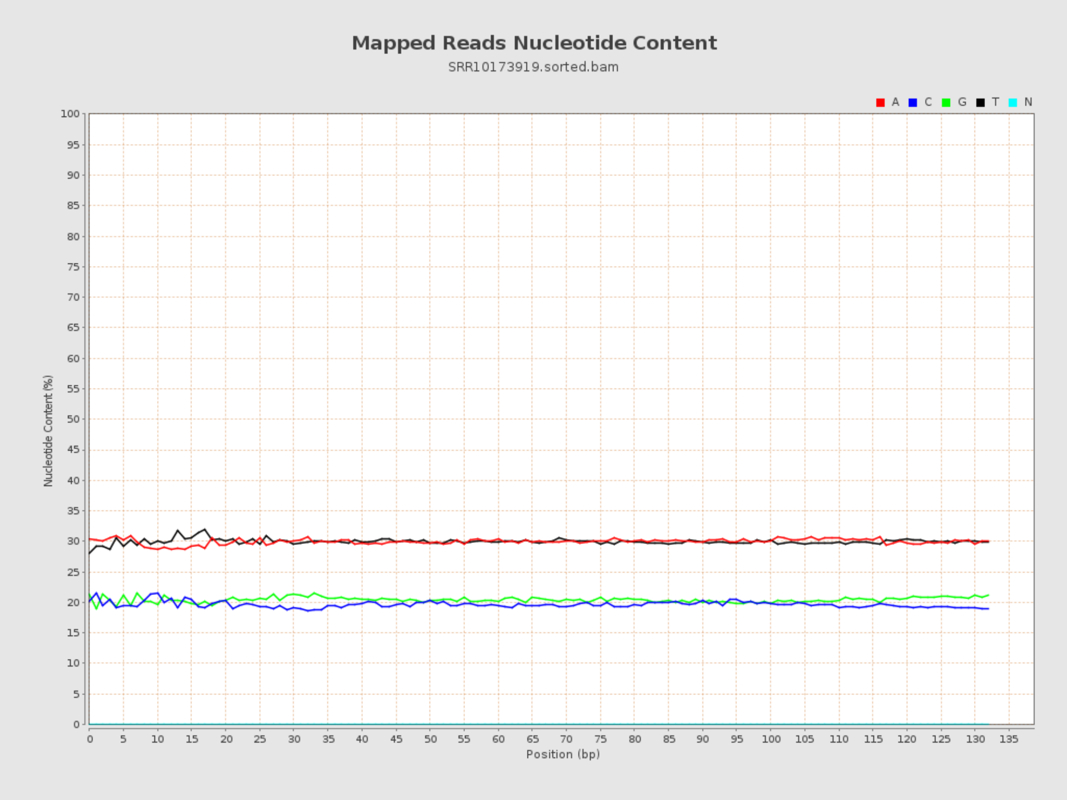
6. Results : Genome Fraction Coverage



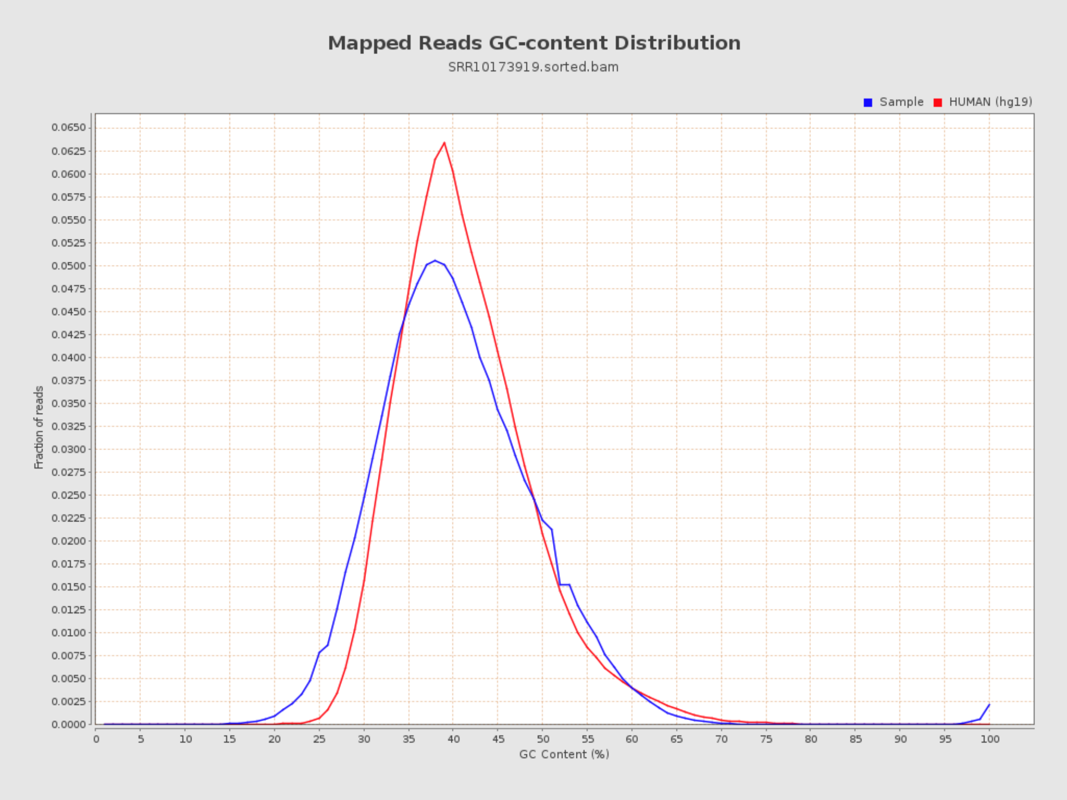
7. Results : Duplication Rate Histogram



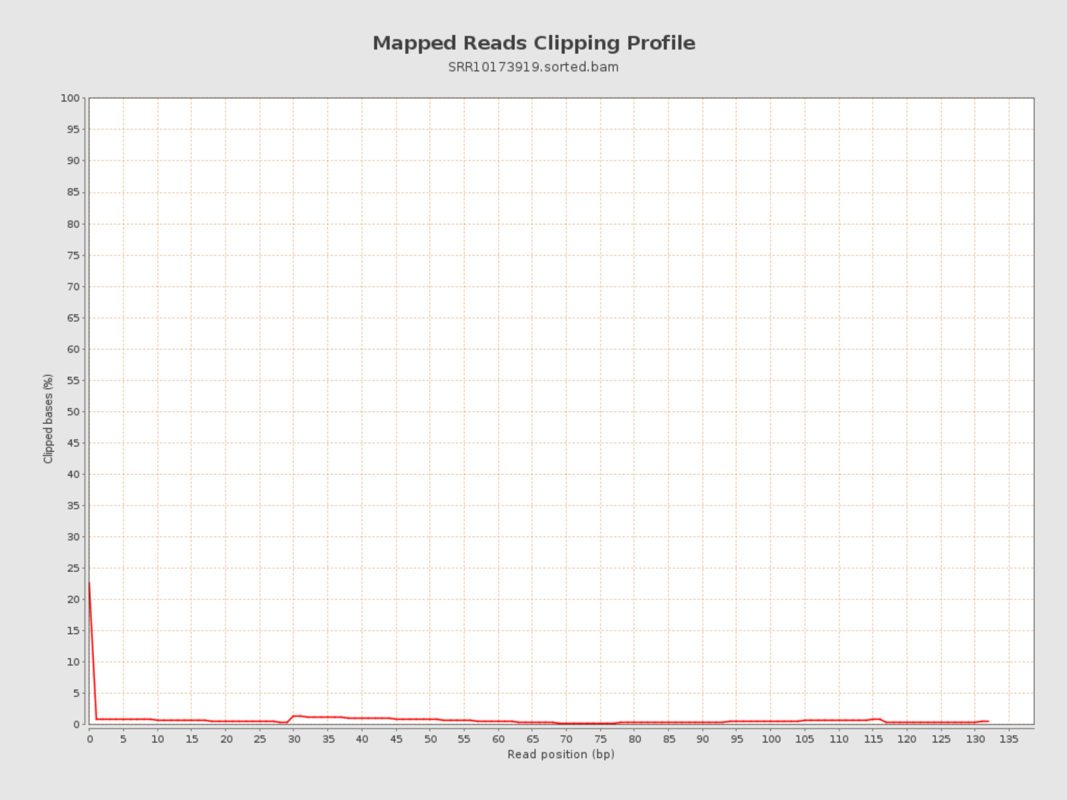
8. Results : Mapped Reads Nucleotide Content



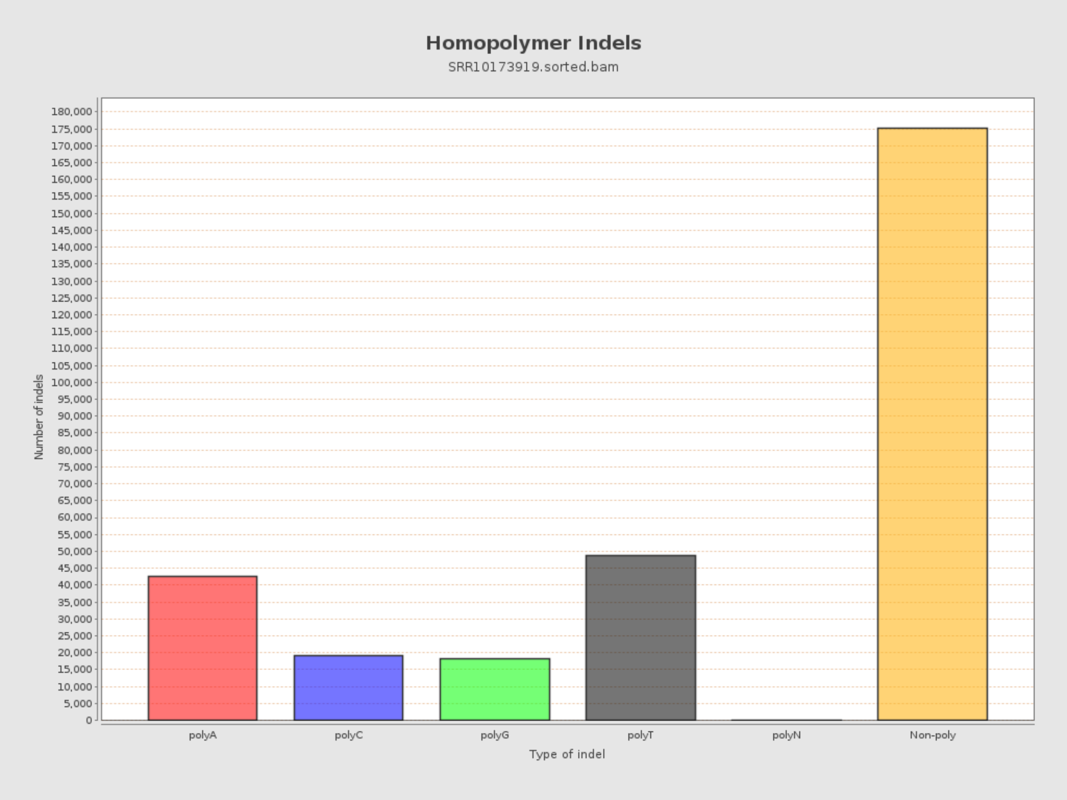
9. Results : Mapped Reads GC-content Distribution



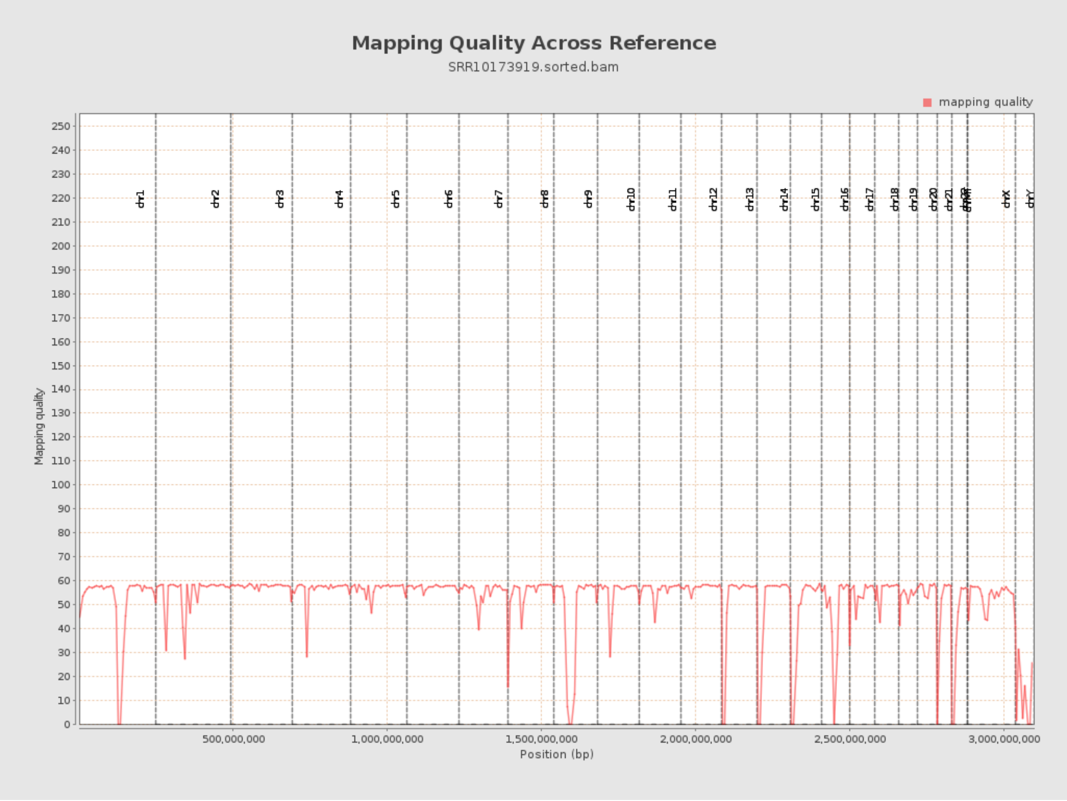
10. Results : Mapped Reads Clipping Profile



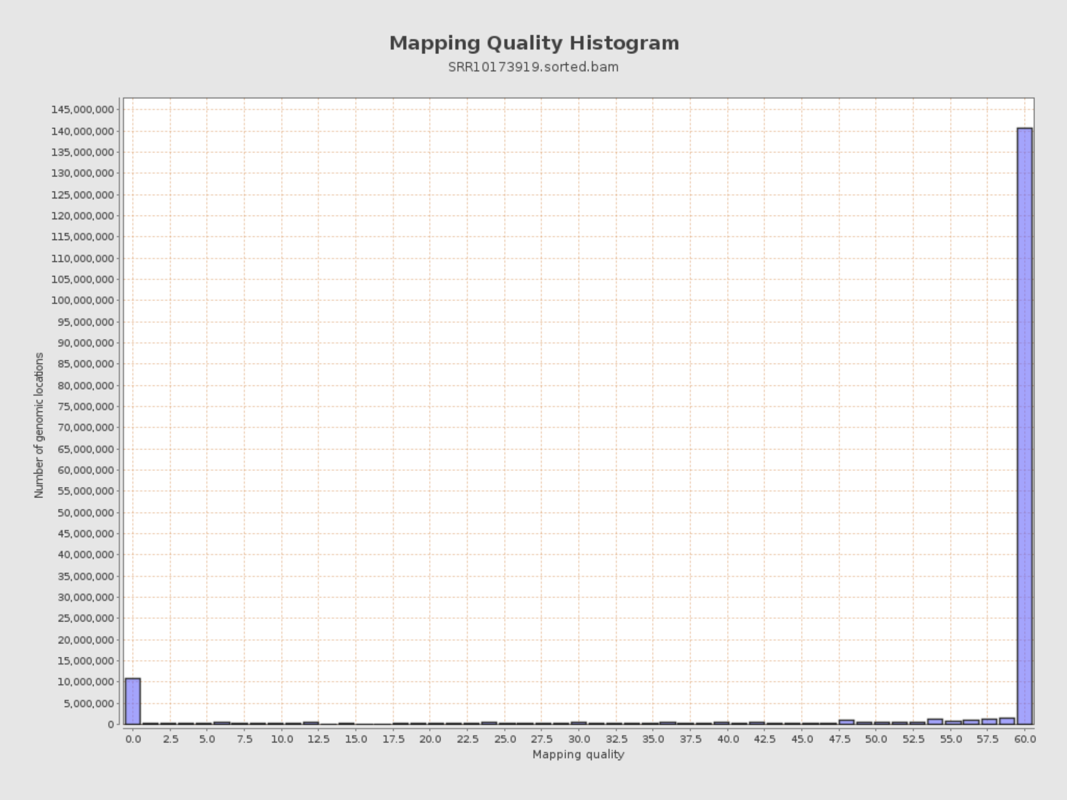
11. Results : Homopolymer Indels



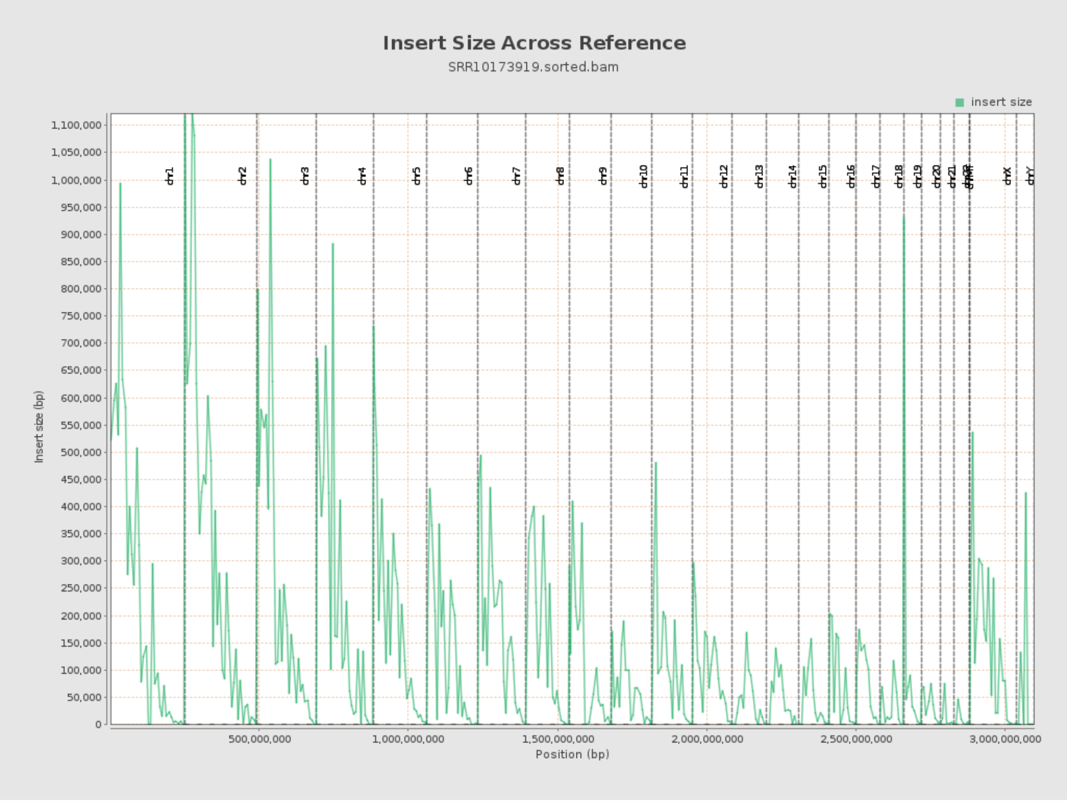
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram