Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:10:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173857.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_SRR10173857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173857_1.fastq.gz SRR10173857_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:10:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,428,122
Mapped reads	4,311,550 / 97.37%
Unmapped reads	116,572 / 2.63%
Mapped paired reads	4,311,550 / 97.37%
Mapped reads, first in pair	2,161,509 / 48.81%
Mapped reads, second in pair	2,150,041 / 48.55%
Mapped reads, both in pair	4,235,372 / 95.65%
Mapped reads, singletons	76,178 / 1.72%
Secondary alignments	0
Supplementary alignments	428,709 / 9.68%
Read min/max/mean length	30 / 133 / 127.77
Duplicated reads (estimated)	3,153,908 / 71.22%
Duplication rate	62.02%
Clipped reads	1,869,382 / 42.22%

2.2. ACGT Content

Number/percentage of A's	152,210,585 / 30.16%
Number/percentage of C's	98,571,654 / 19.53%
Number/percentage of T's	151,745,352 / 30.07%
Number/percentage of G's	102,091,597 / 20.23%
Number/percentage of N's	6,150 / 0%

GC Percentage	39.76%

2.3. Coverage

Mean	0.1631
Standard Deviation	2.5279

2.4. Mapping Quality

Mean Mapping Quality	52.81

2.5. Insert size

Mean	828,318.13
Standard Deviation	8,411,656.97
P25/Median/P75	138 / 195 / 280

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	5,262,998
Insertions	66,413
Mapped reads with at least one insertion	1.47%
Deletions	119,200
Mapped reads with at least one deletion	2.68%
Homopolymer indels	42.34%

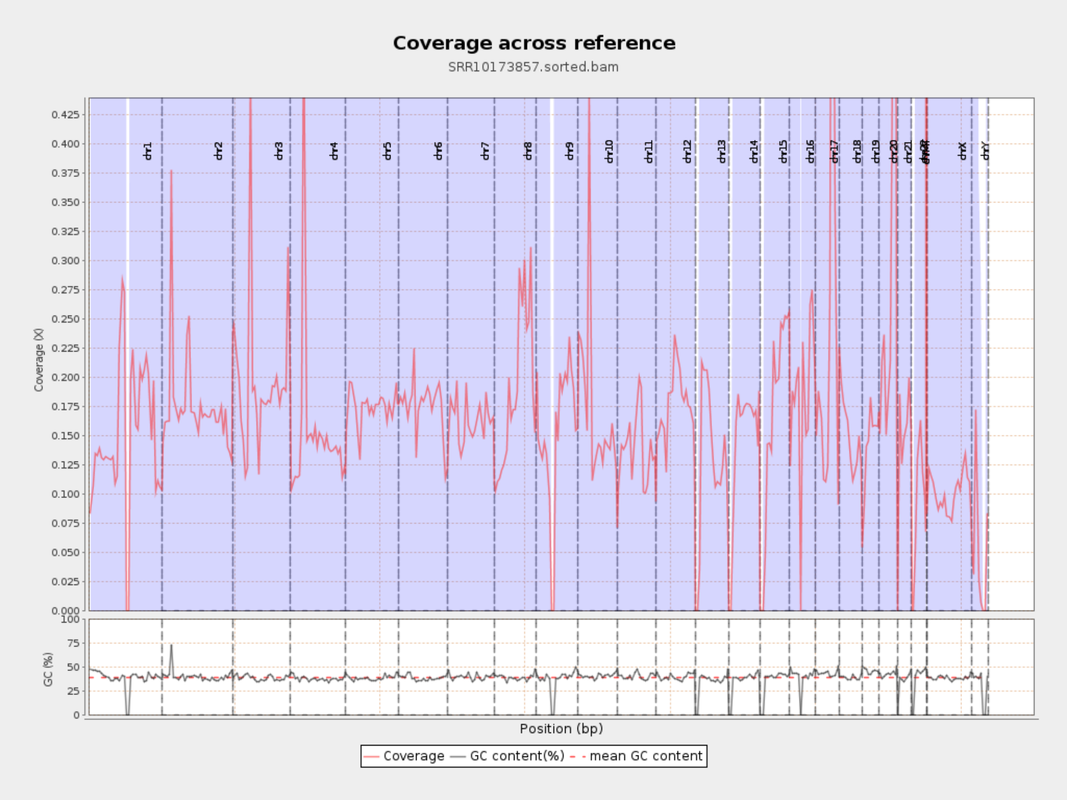
2.7. Chromosome stats

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

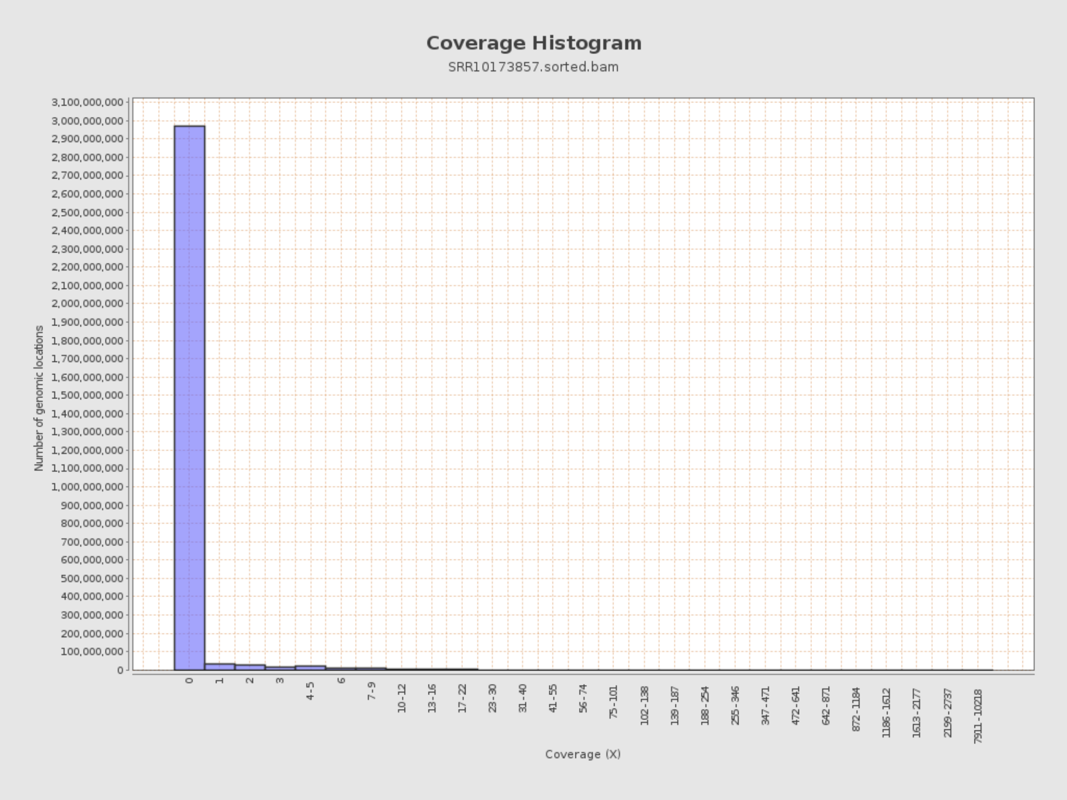
		bases	**coverage**	**deviation**
chr1	249250621	37481461	0.1504	1.5946
chr2	243199373	42708647	0.1756	7.2243
chr3	198022430	38739755	0.1956	1.195
chr4	191154276	29019451	0.1518	2.7152
chr5	180915260	31510122	0.1742	1.1184
chr6	171115067	30005467	0.1754	1.2804
chr7	159138663	26045015	0.1637	1.522
chr8	146364022	27736246	0.1895	1.7604
chr9	141213431	21113615	0.1495	1.4081
chr10	135534747	23480766	0.1732	2.5
chr11	135006516	18743706	0.1388	1.0293
chr12	133851895	23663392	0.1768	1.132
chr13	115169878	14473113	0.1257	0.951
chr14	107349540	15166651	0.1413	1.0002
chr15	102531392	16896918	0.1648	1.0716
chr16	90354753	16673003	0.1845	1.444
chr17	81195210	19798189	0.2438	1.4411
chr18	78077248	11813871	0.1513	2.1315
chr19	59128983	8516686	0.144	1.2674
chr20	63025520	20283983	0.3218	1.8569
chr21	48129895	7105454	0.1476	1.6928
chr22	51304566	4487674	0.0875	0.7694
chrMT	16571	993439	59.9505	42.5694
chrX	155270560	15787895	0.1017	0.8492

chrY	59373566	2686916	0.0453	2.1123

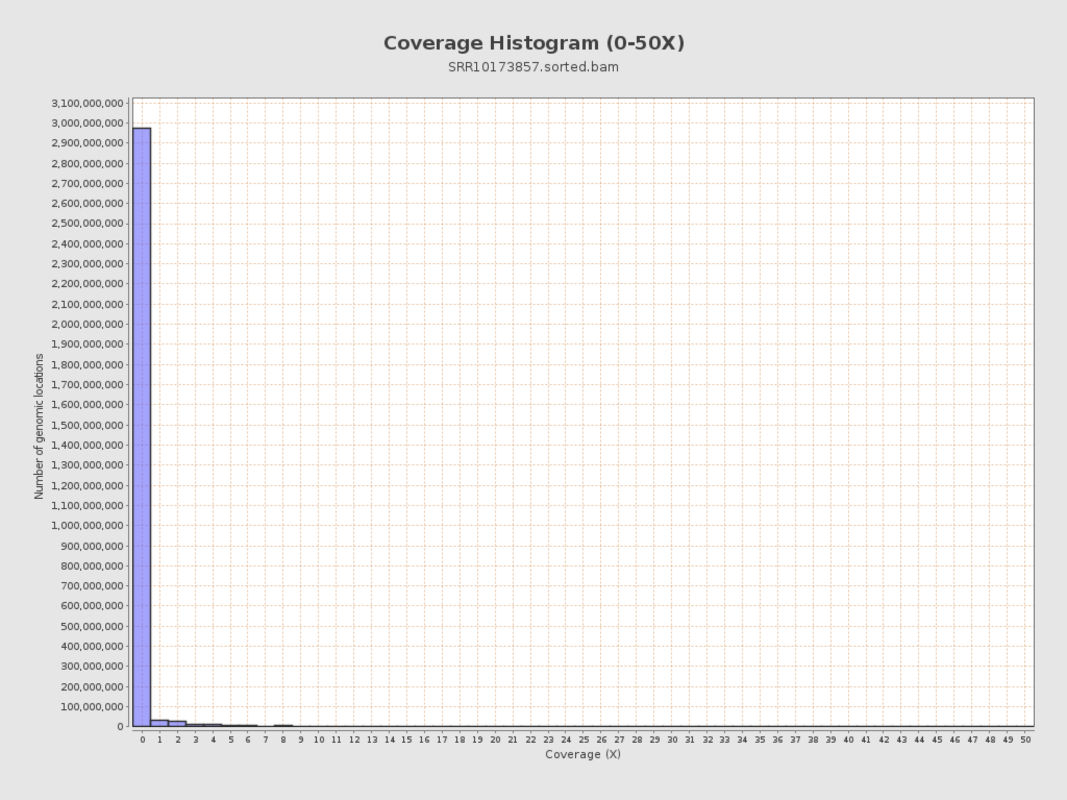
3. Results : Coverage across reference



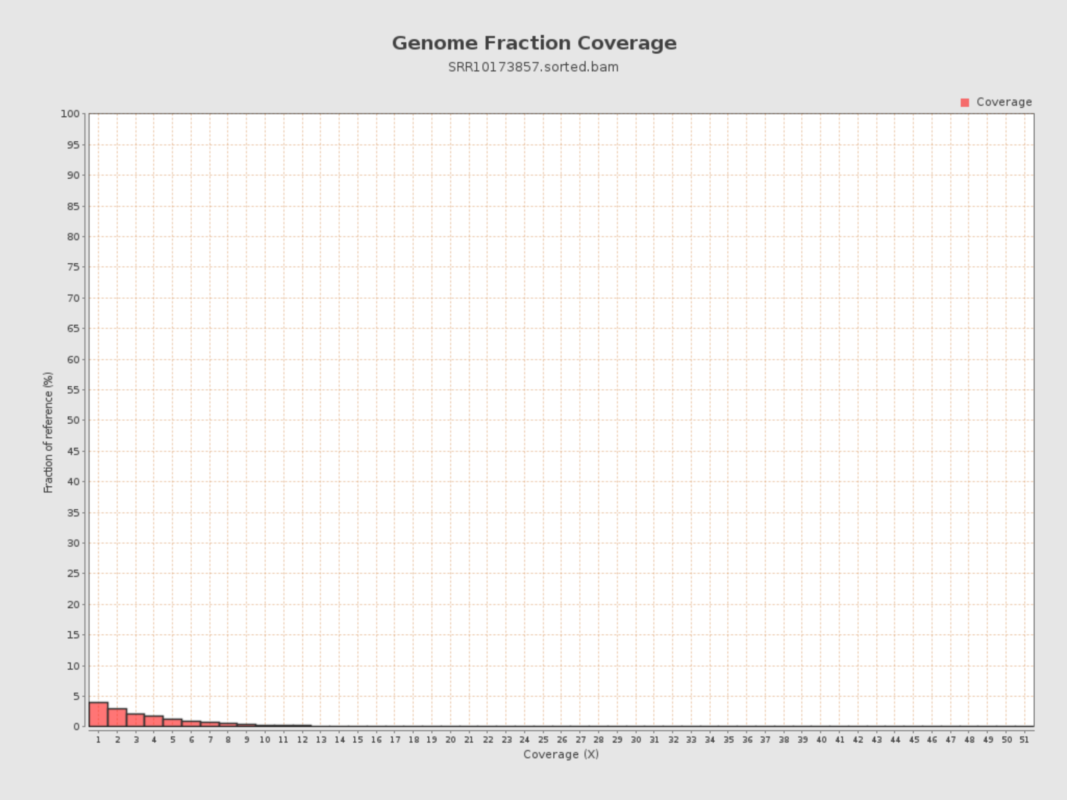
4. Results : Coverage Histogram



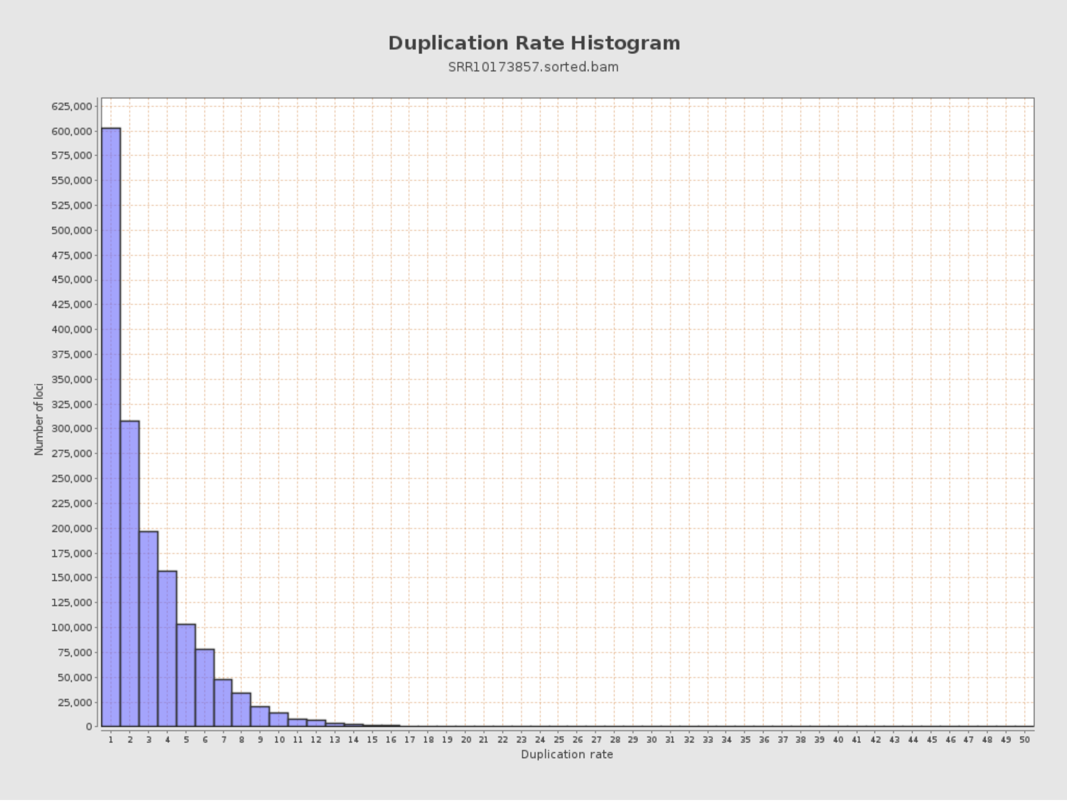
5. Results : Coverage Histogram (0-50X)



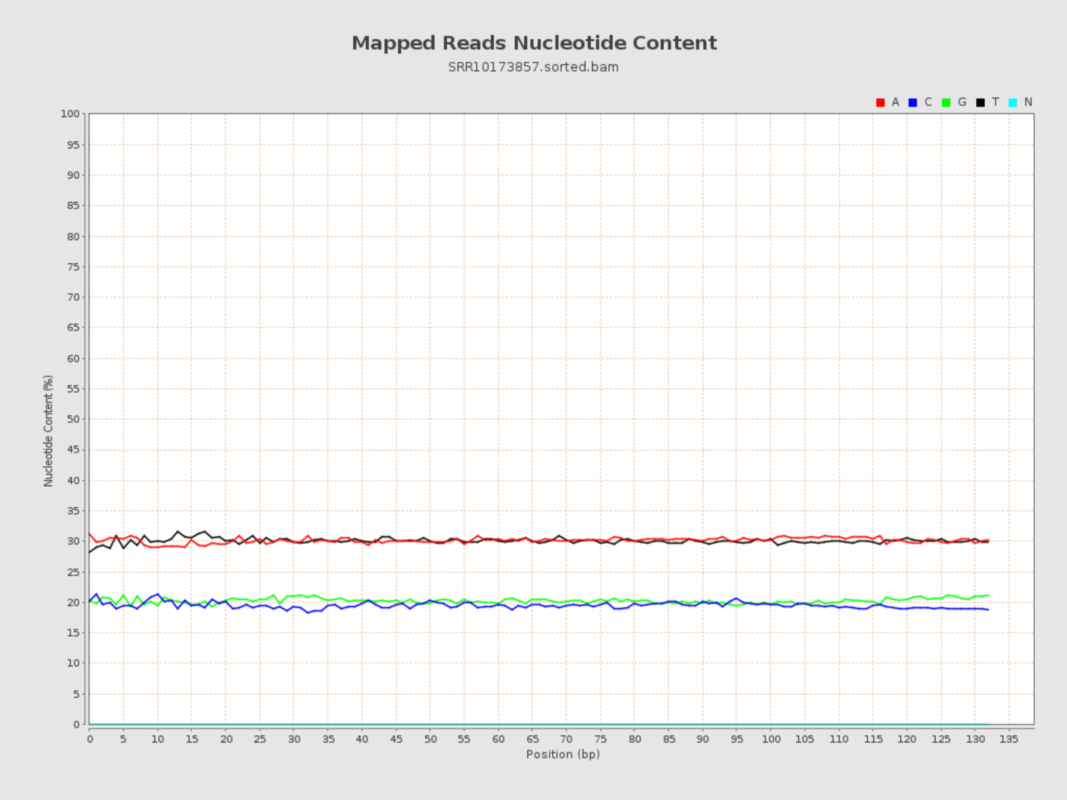
6. Results : Genome Fraction Coverage



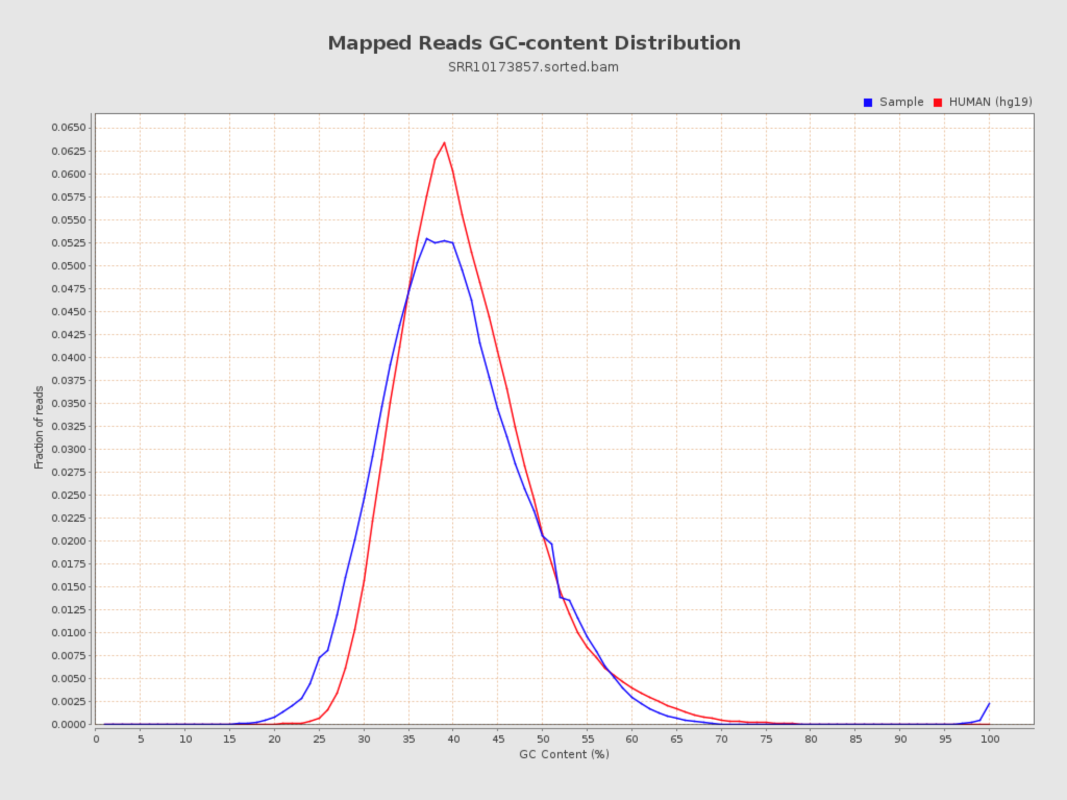
7. Results : Duplication Rate Histogram



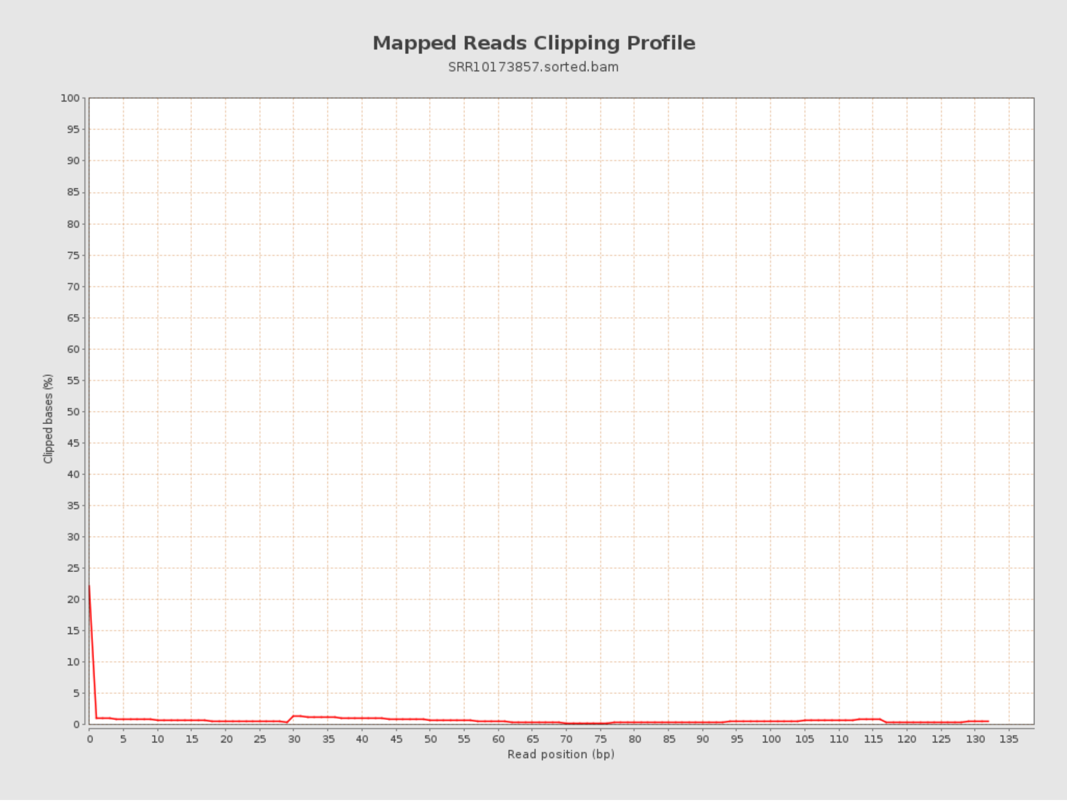
8. Results : Mapped Reads Nucleotide Content



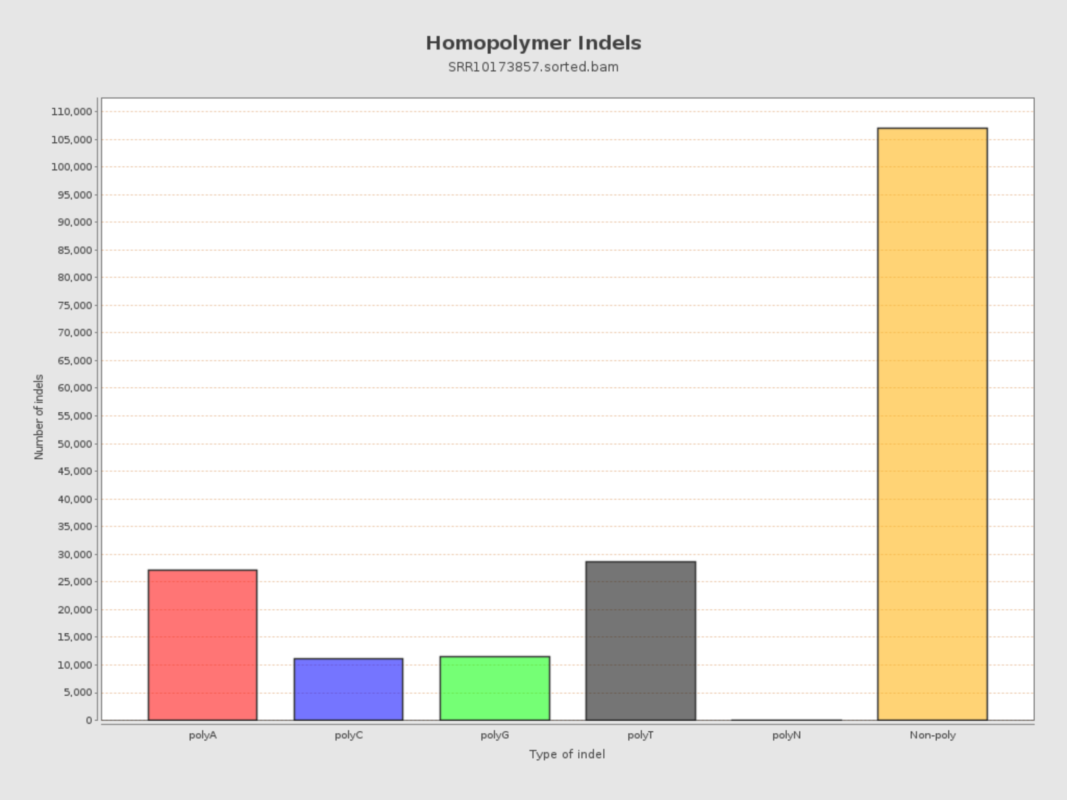
9. Results : Mapped Reads GC-content Distribution



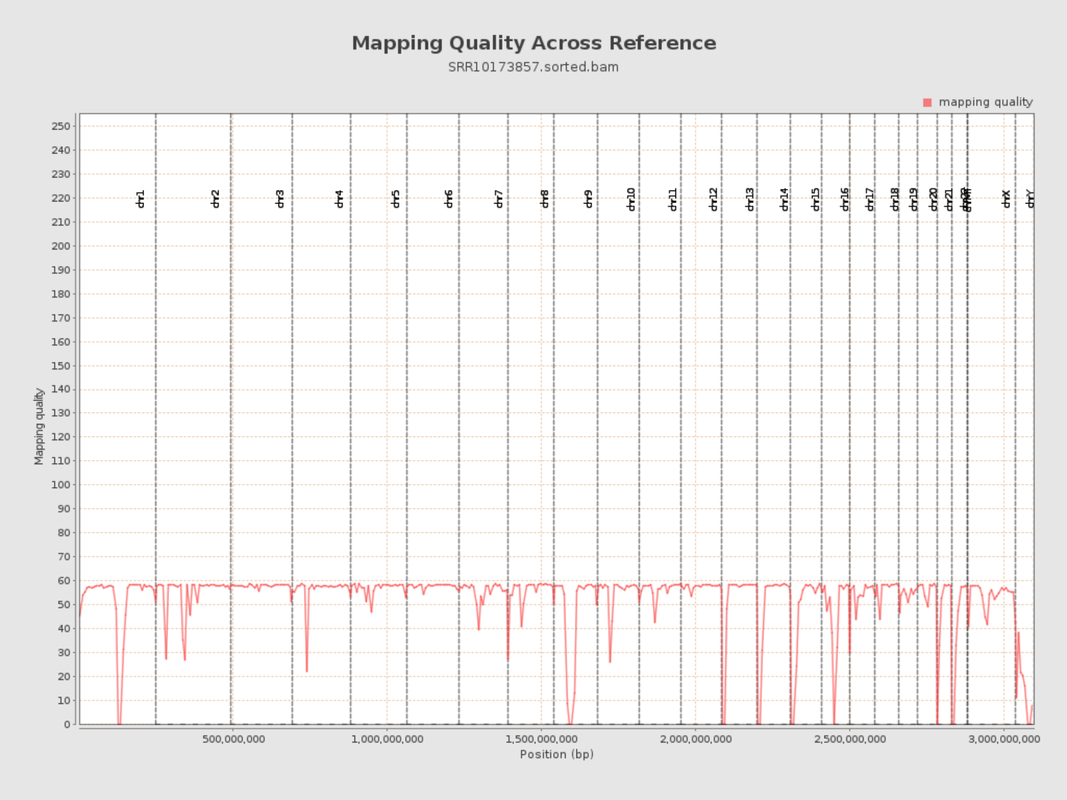
10. Results : Mapped Reads Clipping Profile



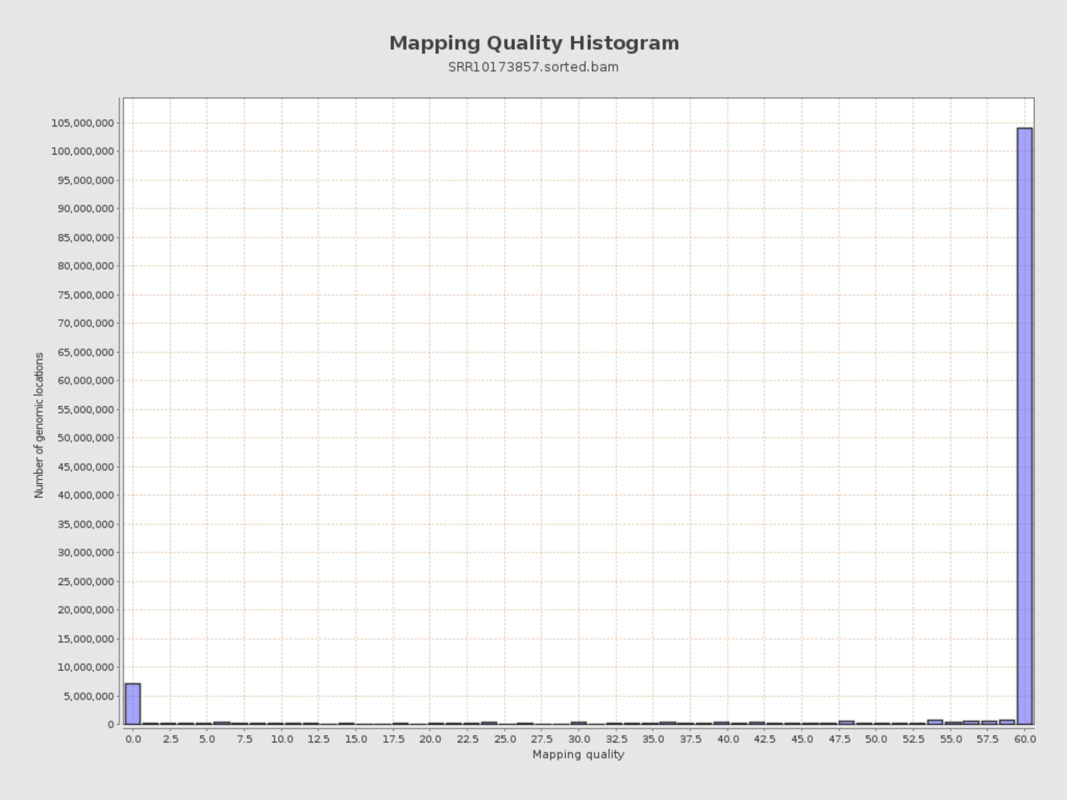
11. Results : Homopolymer Indels



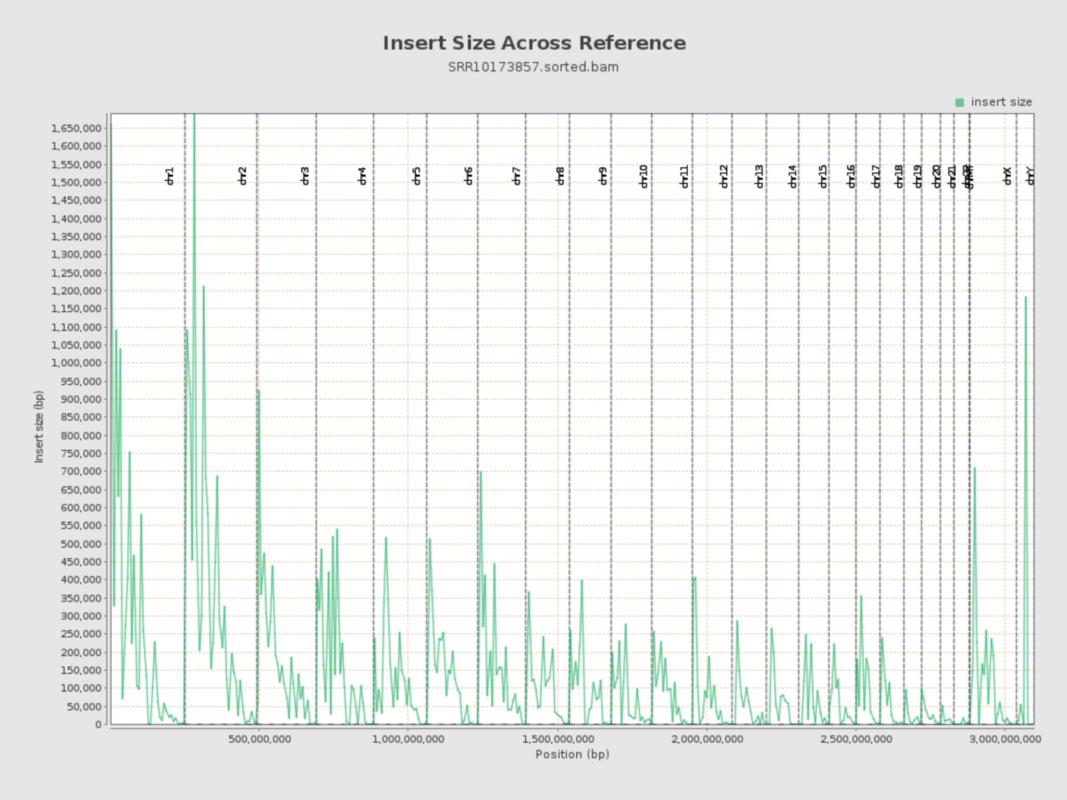
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram