Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:10:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173849.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_SRR10173849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173849_1.fastq.gz SRR10173849_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:10:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,292,424
Mapped reads	2,226,731 / 97.13%
Unmapped reads	65,693 / 2.87%
Mapped paired reads	2,226,731 / 97.13%
Mapped reads, first in pair	1,115,710 / 48.67%
Mapped reads, second in pair	1,111,021 / 48.46%
Mapped reads, both in pair	2,184,610 / 95.3%
Mapped reads, singletons	42,121 / 1.84%
Secondary alignments	0
Supplementary alignments	219,574 / 9.58%
Read min/max/mean length	30 / 133 / 127.71
Duplicated reads (estimated)	1,667,758 / 72.75%
Duplication rate	63.13%
Clipped reads	927,798 / 40.47%

2.2. ACGT Content

Number/percentage of A's	78,659,587 / 30.16%
Number/percentage of C's	51,018,045 / 19.56%
Number/percentage of T's	78,418,685 / 30.06%
Number/percentage of G's	52,732,316 / 20.22%
Number/percentage of N's	3,517 / 0%

GC Percentage	39.78%

2.3. Coverage

Mean	0.0843
Standard Deviation	1.4039

2.4. Mapping Quality

Mean Mapping Quality	52.81

2.5. Insert size

Mean	1,032,009.03
Standard Deviation	9,272,371.48
P25/Median/P75	140 / 197 / 286

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	2,746,367
Insertions	31,283
Mapped reads with at least one insertion	1.35%
Deletions	61,611
Mapped reads with at least one deletion	2.69%
Homopolymer indels	42.93%

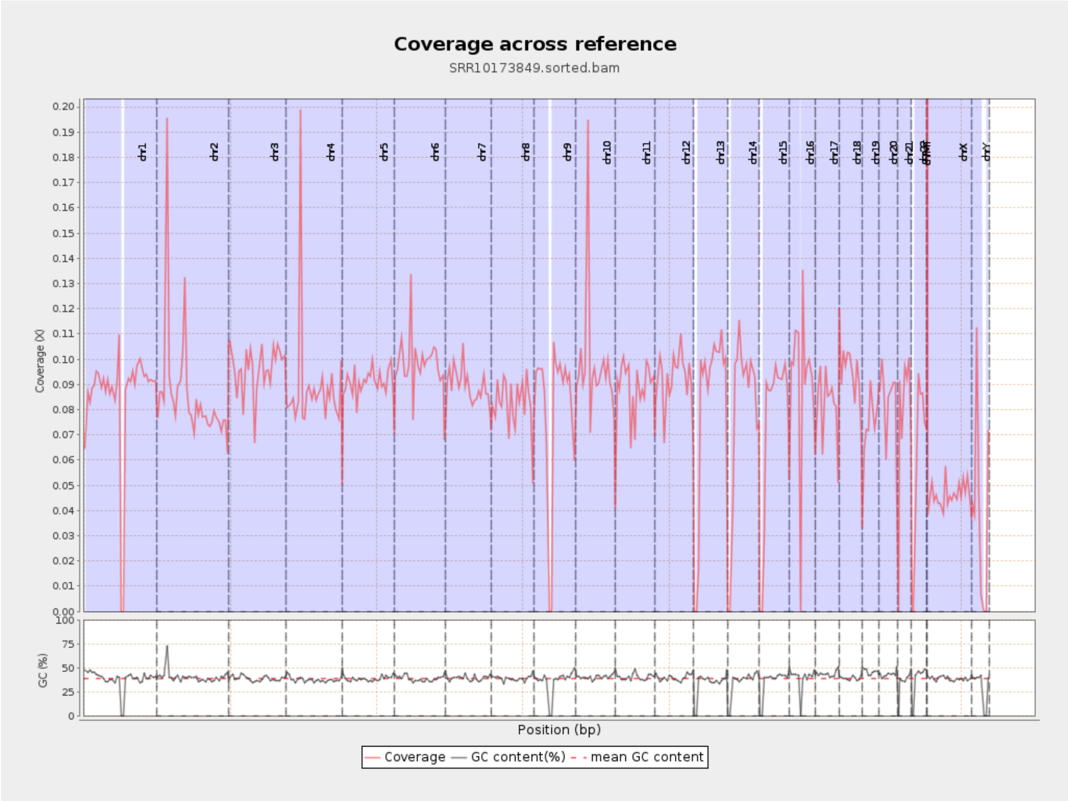
2.7. Chromosome stats

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

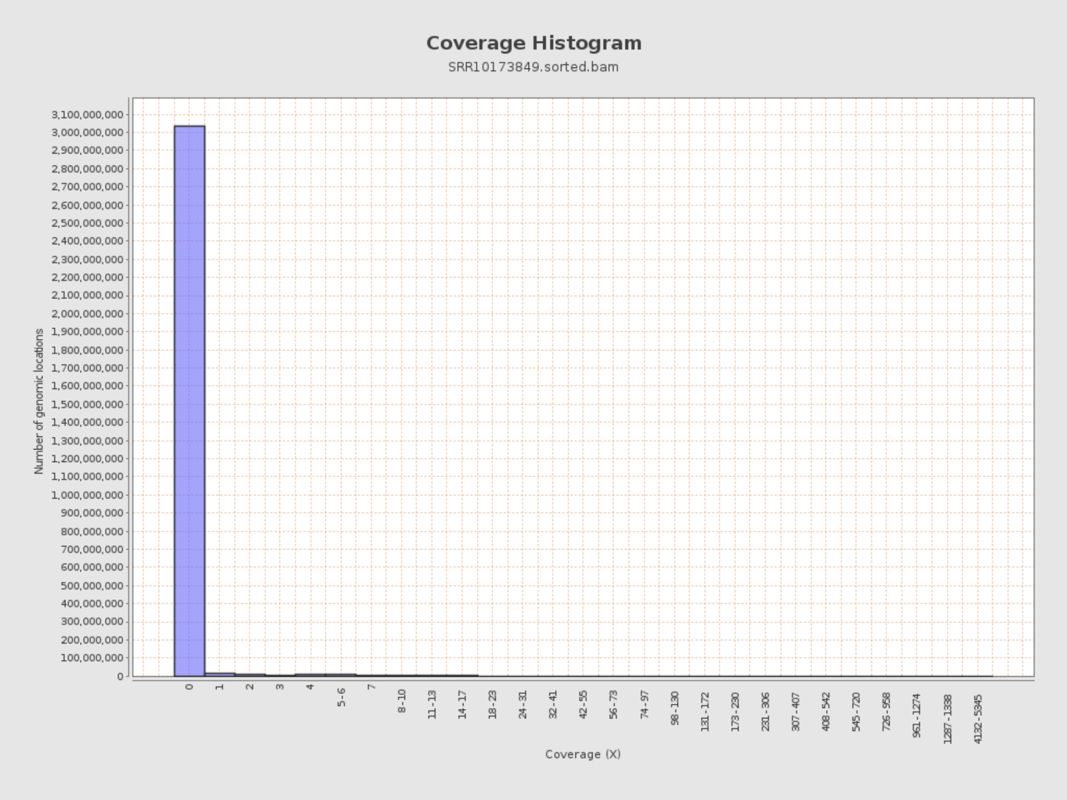
		bases	coverage	deviation
chr1	249250621	21236921	0.0852	1.031
chr2	243199373	20913751	0.086	3.7954
chr3	198022430	19077368	0.0963	0.8586
chr4	191154276	17012862	0.089	1.1783
chr5	180915260	16380336	0.0905	0.8306
chr6	171115067	16871507	0.0986	0.957
chr7	159138663	14173483	0.0891	0.9946
chr8	146364022	12070650	0.0825	1.1819
chr9	141213431	11362790	0.0805	1.0334
chr10	135534747	13233856	0.0976	1.2549
chr11	135006516	11937396	0.0884	0.8396
chr12	133851895	12392879	0.0926	0.8422
chr13	115169878	9533439	0.0828	0.808
chr14	107349540	8574007	0.0799	0.7793
chr15	102531392	7559768	0.0737	0.7385
chr16	90354753	8099527	0.0896	0.9596
chr17	81195210	6704324	0.0826	0.8116
chr18	78077248	7453596	0.0955	1.2905
chr19	59128983	4428521	0.0749	0.8358
chr20	63025520	5321081	0.0844	0.813
chr21	48129895	3821093	0.0794	0.946
chr22	51304566	3051722	0.0595	0.7034
chrMT	16571	271957	16.4116	16.1057
chrX	155270560	7154286	0.0461	0.5946

chrY	59373566	2350748	0.0396	0.8739

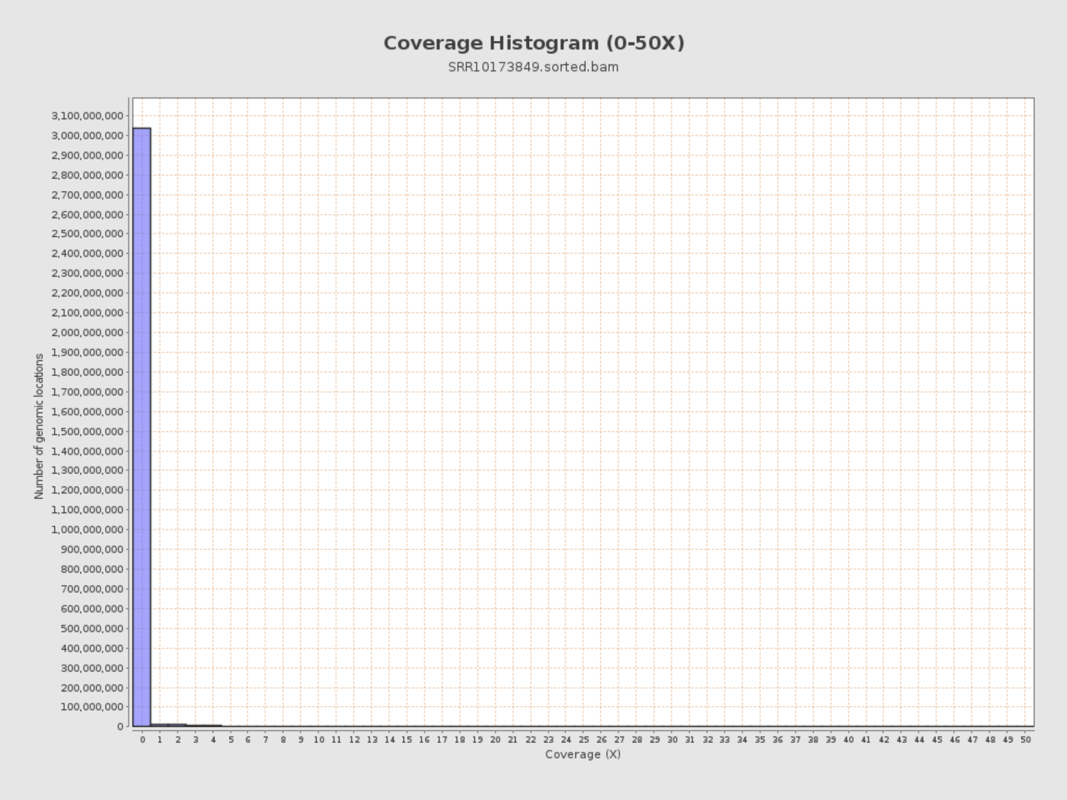
3. Results : Coverage across reference



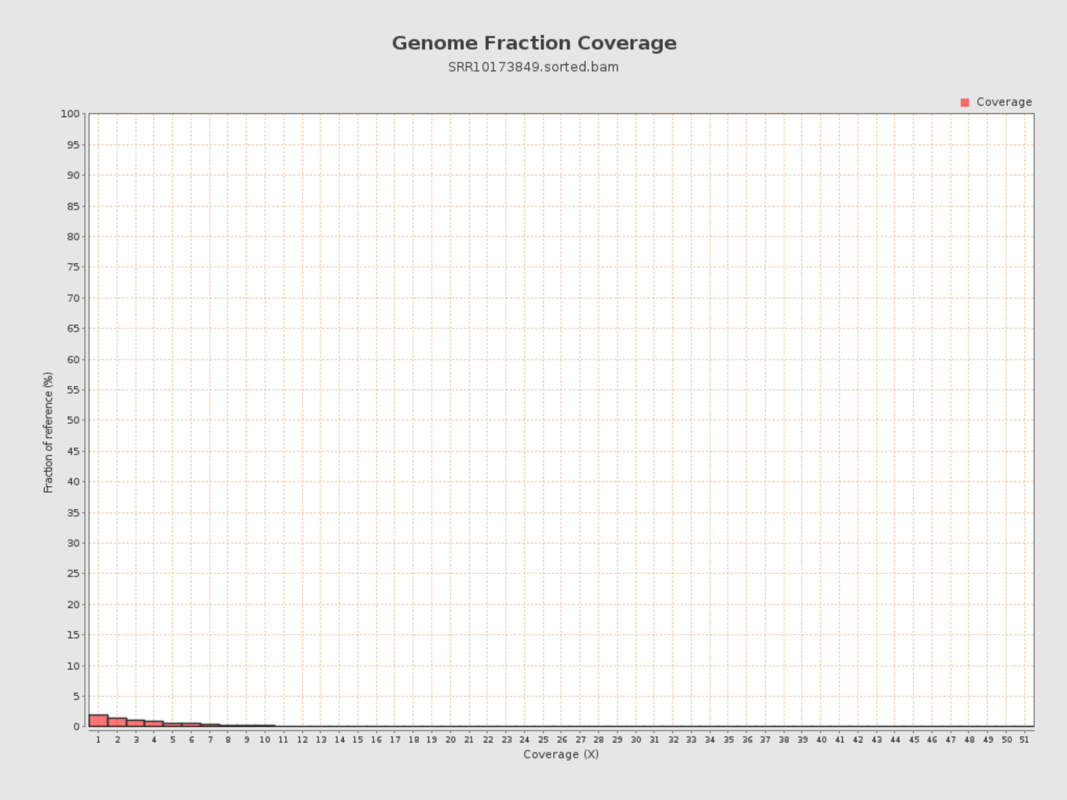
4. Results : Coverage Histogram



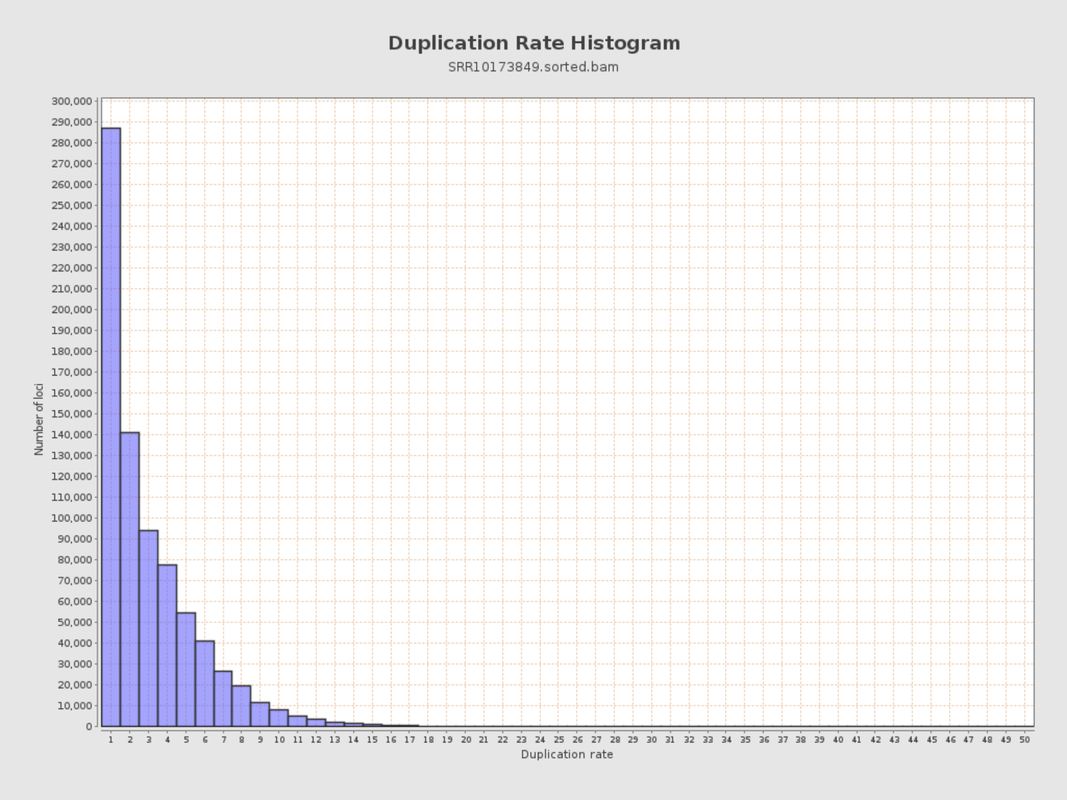
5. Results : Coverage Histogram (0-50X)



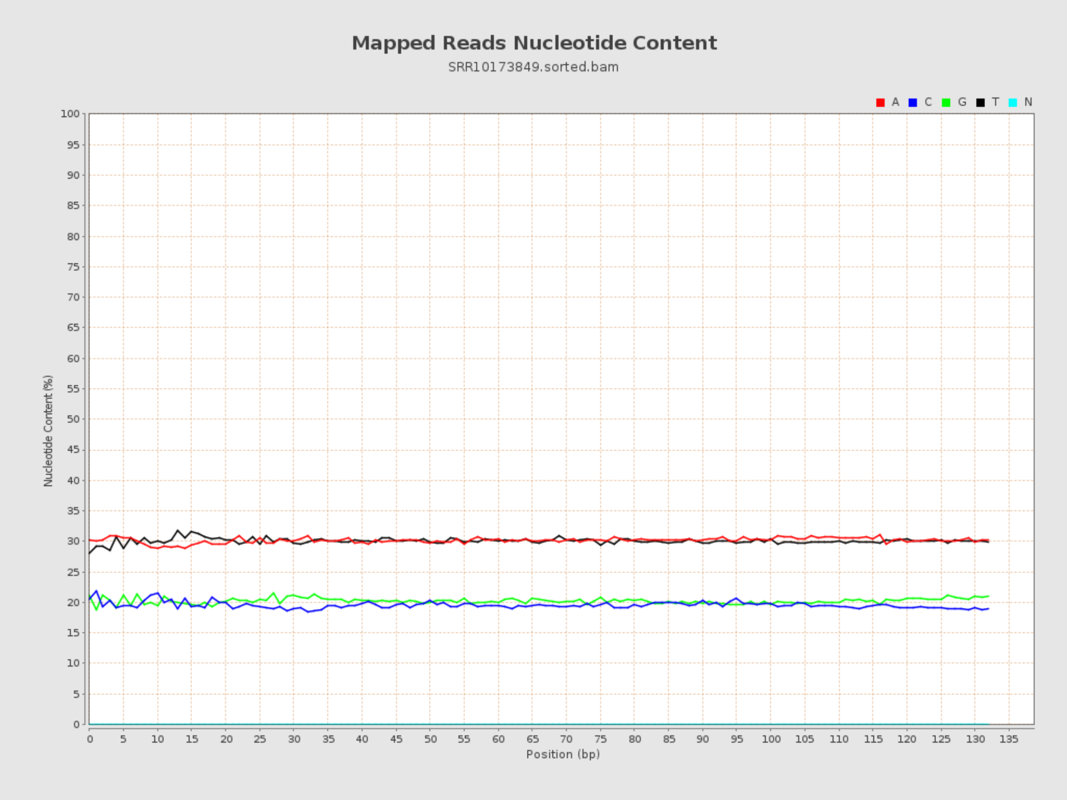
6. Results : Genome Fraction Coverage



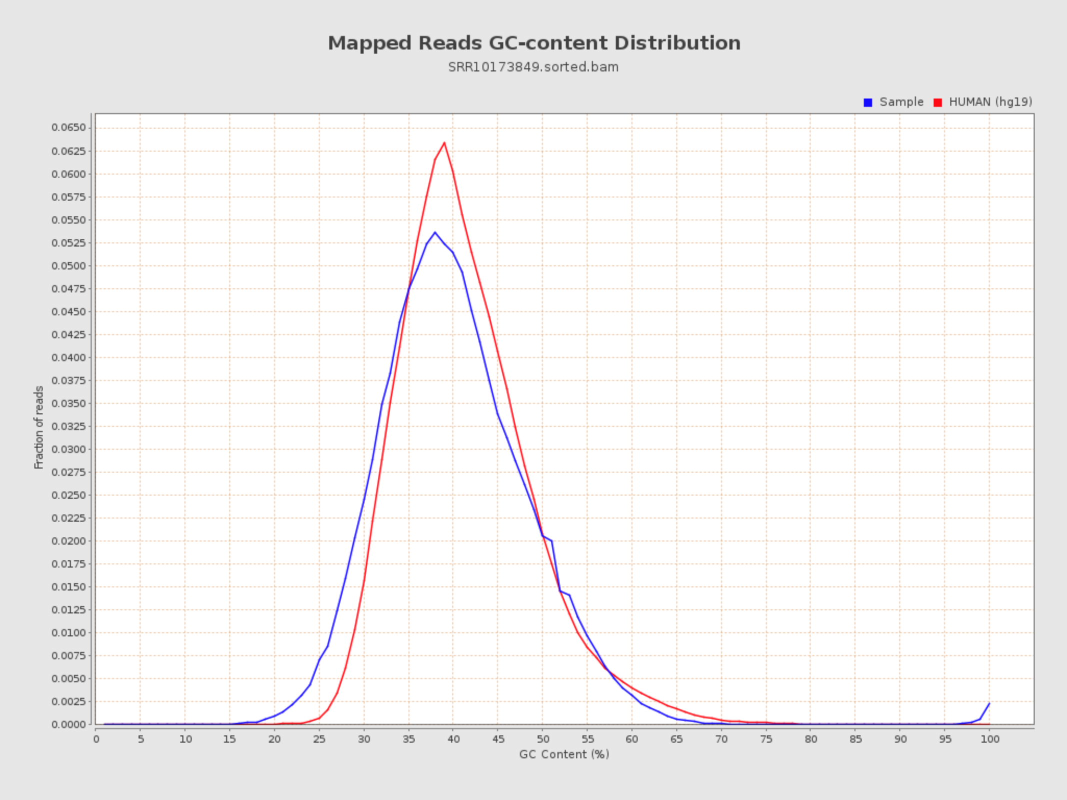
7. Results : Duplication Rate Histogram



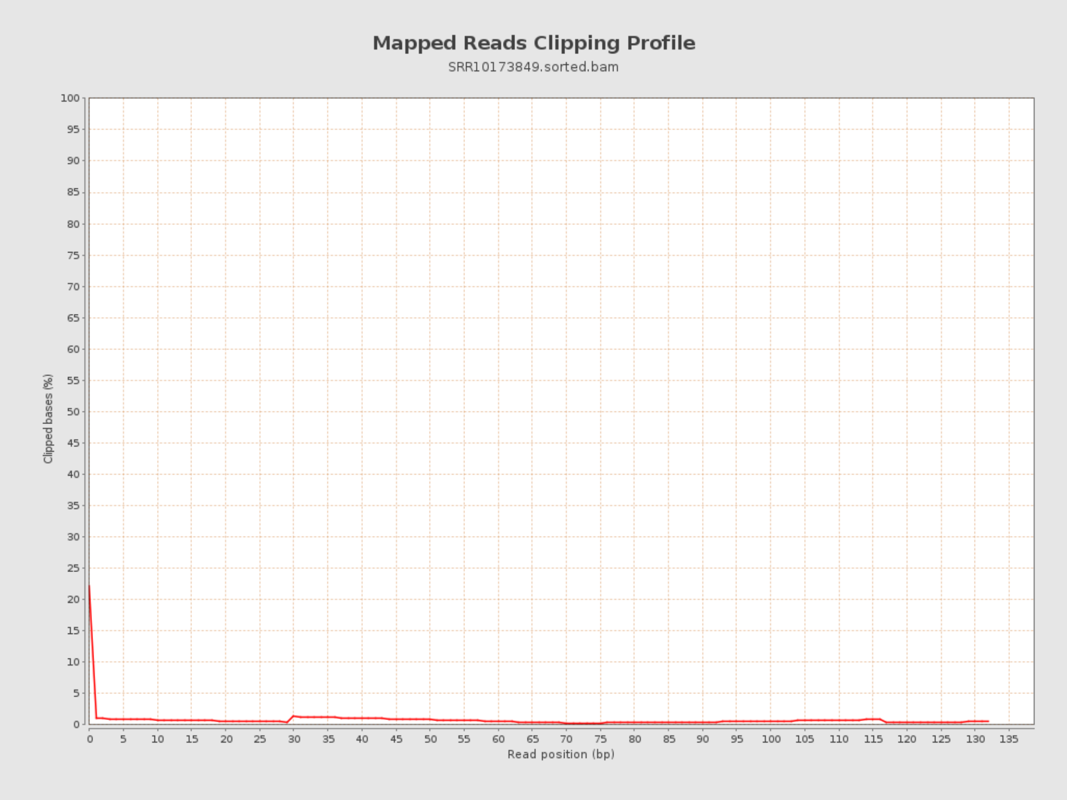
8. Results : Mapped Reads Nucleotide Content



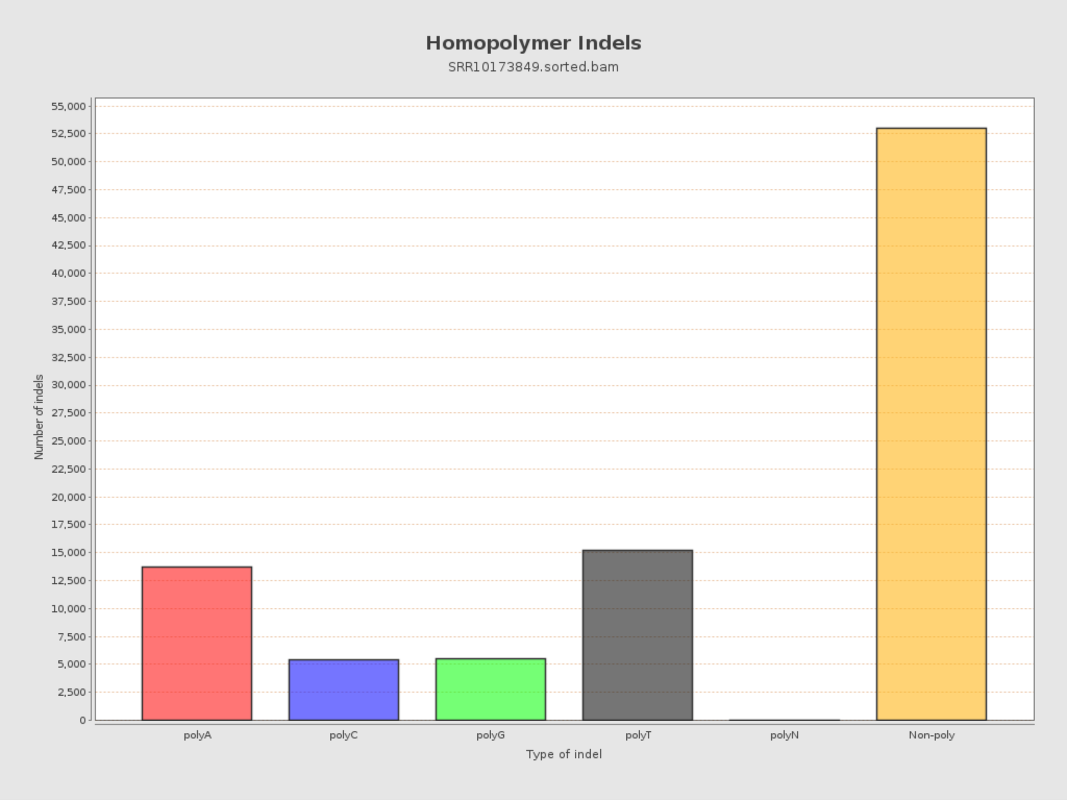
9. Results : Mapped Reads GC-content Distribution



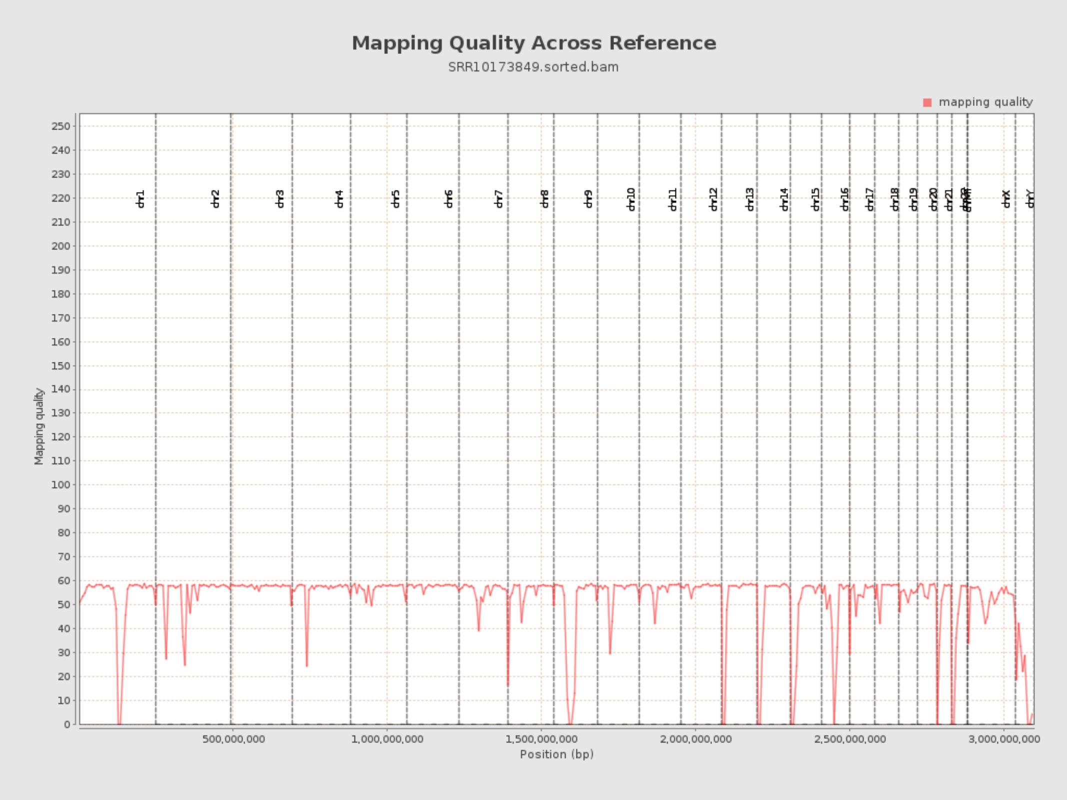
10. Results : Mapped Reads Clipping Profile



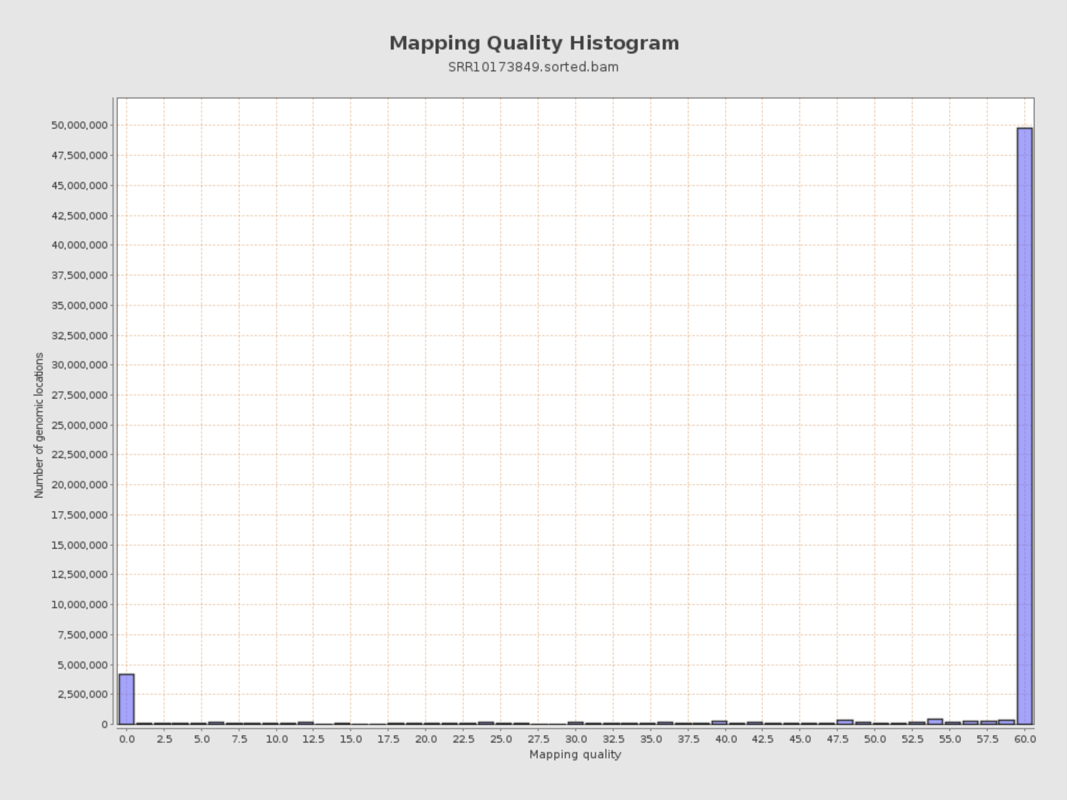
11. Results : Homopolymer Indels



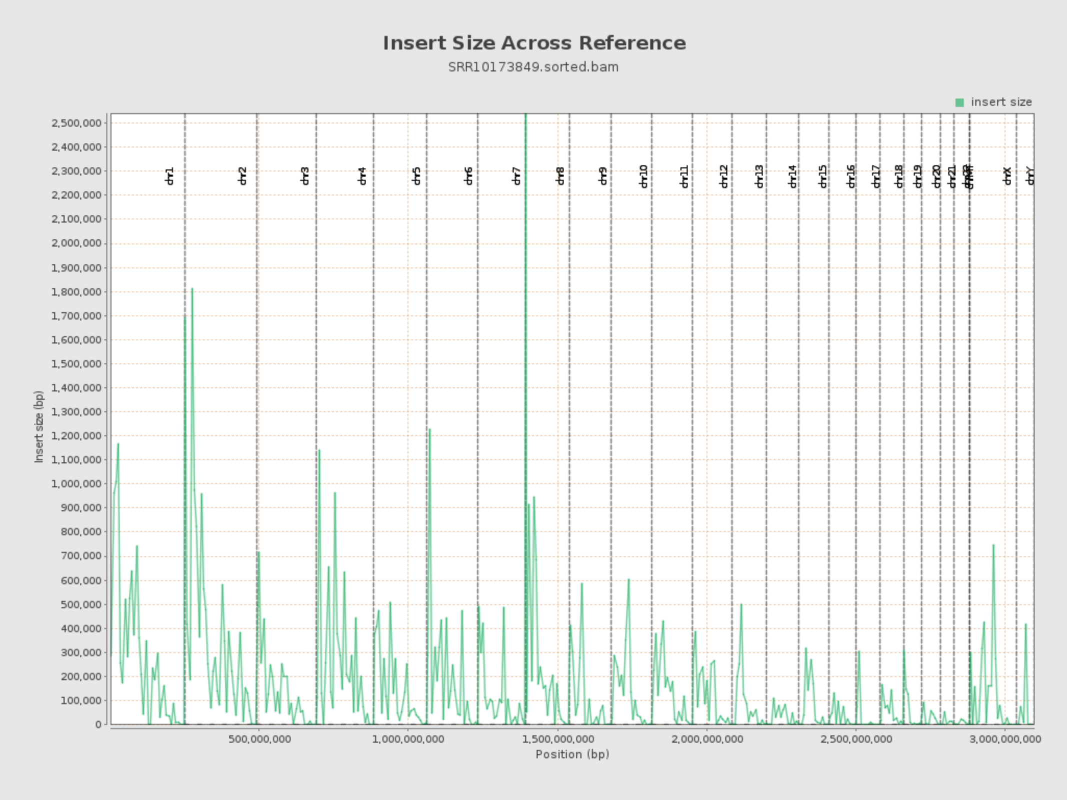
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram