Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:25:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124879.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_SRR3124879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124879_1.fastq.gz SRR3124879_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:25:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,650,468
Mapped reads	3,572,809 / 97.87%
Unmapped reads	77,659 / 2.13%
Mapped paired reads	3,572,809 / 97.87%
Mapped reads, first in pair	1,789,563 / 49.02%
Mapped reads, second in pair	1,783,246 / 48.85%
Mapped reads, both in pair	3,558,962 / 97.49%
Mapped reads, singletons	13,847 / 0.38%
Secondary alignments	0
Supplementary alignments	16,389 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	265,205 / 7.26%
Duplication rate	5.45%
Clipped reads	1,671,567 / 45.79%

2.2. ACGT Content

Number/percentage of A's	87,835,182 / 28.23%
Number/percentage of C's	57,812,350 / 18.58%
Number/percentage of T's	93,233,107 / 29.96%
Number/percentage of G's	72,270,153 / 23.23%
Number/percentage of N's	4,539 / 0%

GC Percentage	41.81%

2.3. Coverage

Mean	0.1006
Standard Deviation	0.896

2.4. Mapping Quality

Mean Mapping Quality	52.94

2.5. Insert size

Mean	39,205.41
Standard Deviation	1,893,631.77
P25/Median/P75	148 / 204 / 287

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	2,289,622
Insertions	41,232
Mapped reads with at least one insertion	1.13%
Deletions	103,727
Mapped reads with at least one deletion	2.85%
Homopolymer indels	48.49%

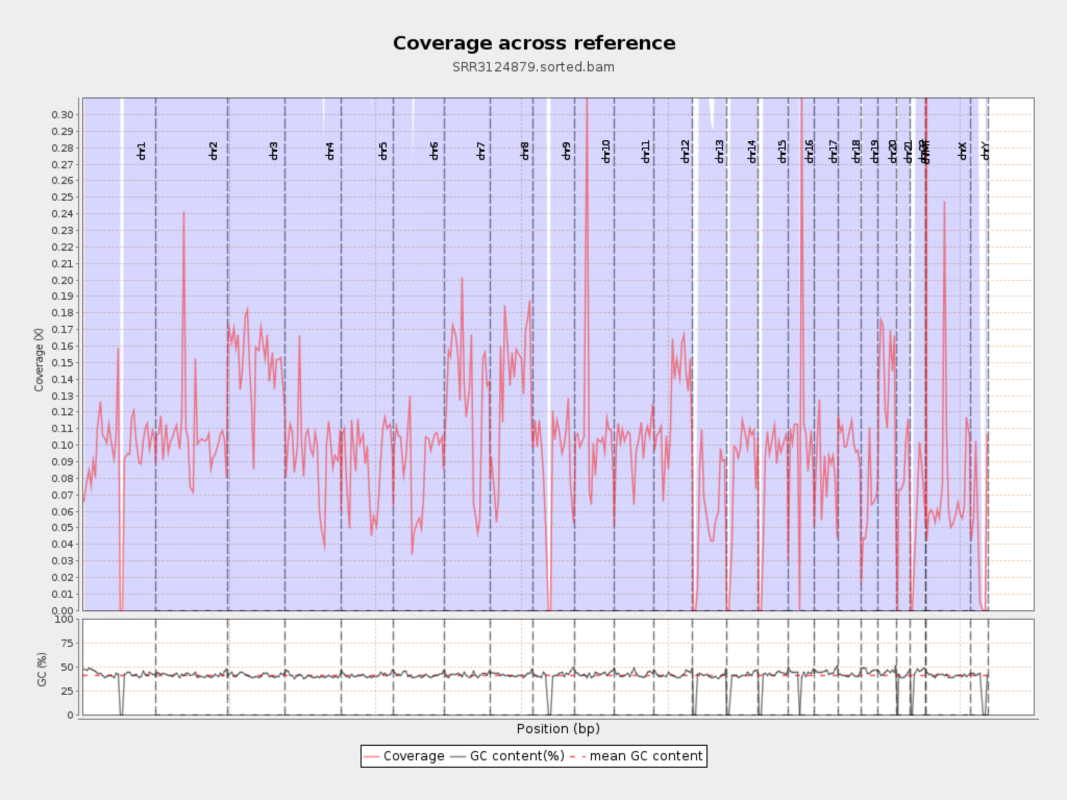
2.7. Chromosome stats

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

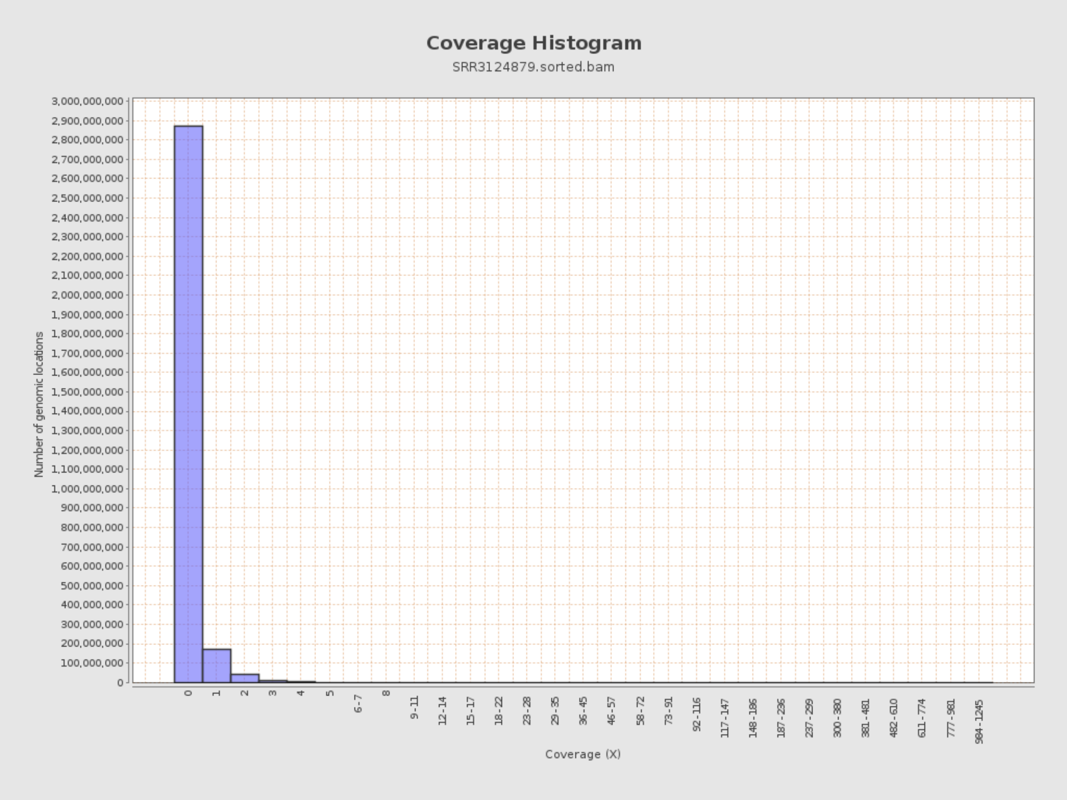
		bases	coverage	deviation
chr1	249250621	23645079	0.0949	0.9386
chr2	243199373	26070892	0.1072	1.0899
chr3	198022430	30129667	0.1522	0.5035
chr4	191154276	18353774	0.096	0.5771
chr5	180915260	16311459	0.0902	0.383
chr6	171115067	15315526	0.0895	0.6803
chr7	159138663	20686266	0.13	1.653
chr8	146364022	19843397	0.1356	0.6009
chr9	141213431	12386399	0.0877	1.0258
chr10	135534747	14977946	0.1105	1.8758
chr11	135006516	13733728	0.1017	0.7021
chr12	133851895	16795094	0.1255	0.4542
chr13	115169878	6743017	0.0585	0.2998
chr14	107349540	8974027	0.0836	0.3979
chr15	102531392	8406655	0.082	0.3665
chr16	90354753	9802267	0.1085	1.6059
chr17	81195210	6981450	0.086	0.8444
chr18	78077248	8059145	0.1032	1.0665
chr19	59128983	3714298	0.0628	0.6264
chr20	63025520	9215785	0.1462	0.5086
chr21	48129895	3716691	0.0772	0.4386
chr22	51304566	2903631	0.0566	0.3078
chrMT	16571	99641	6.013	4.0708
chrX	155270560	11721568	0.0755	0.4931

chrY	59373566	2736726	0.0461	0.7691

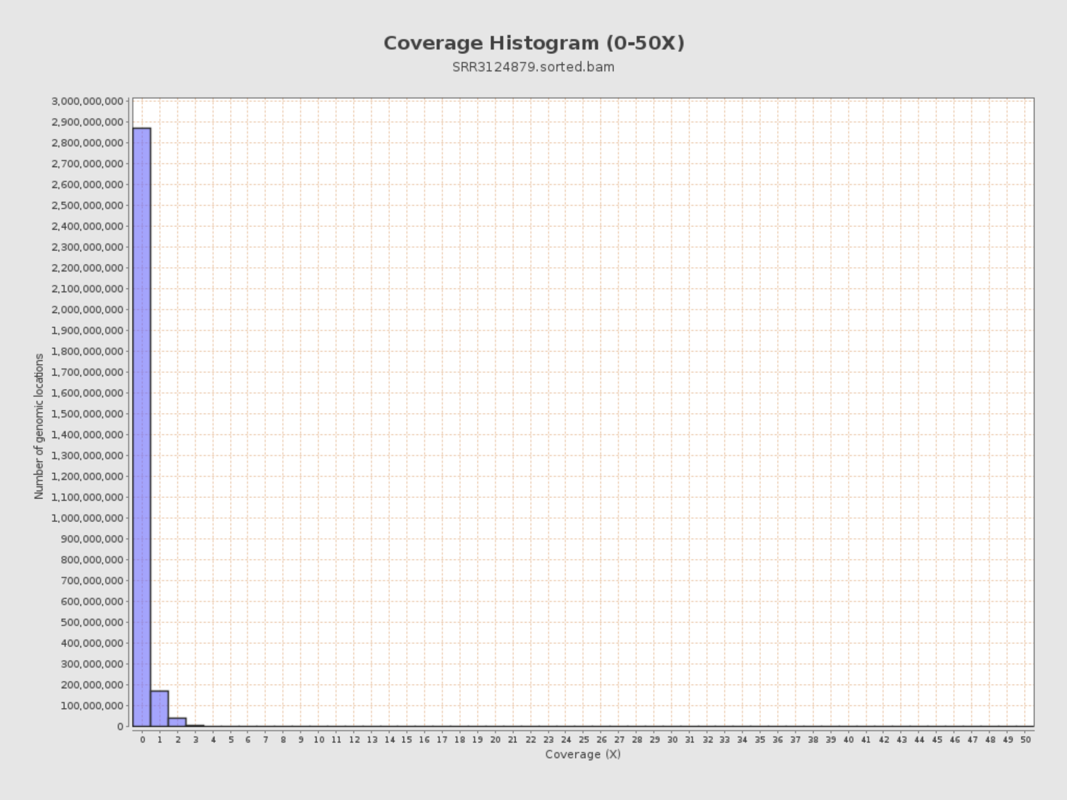
3. Results : Coverage across reference



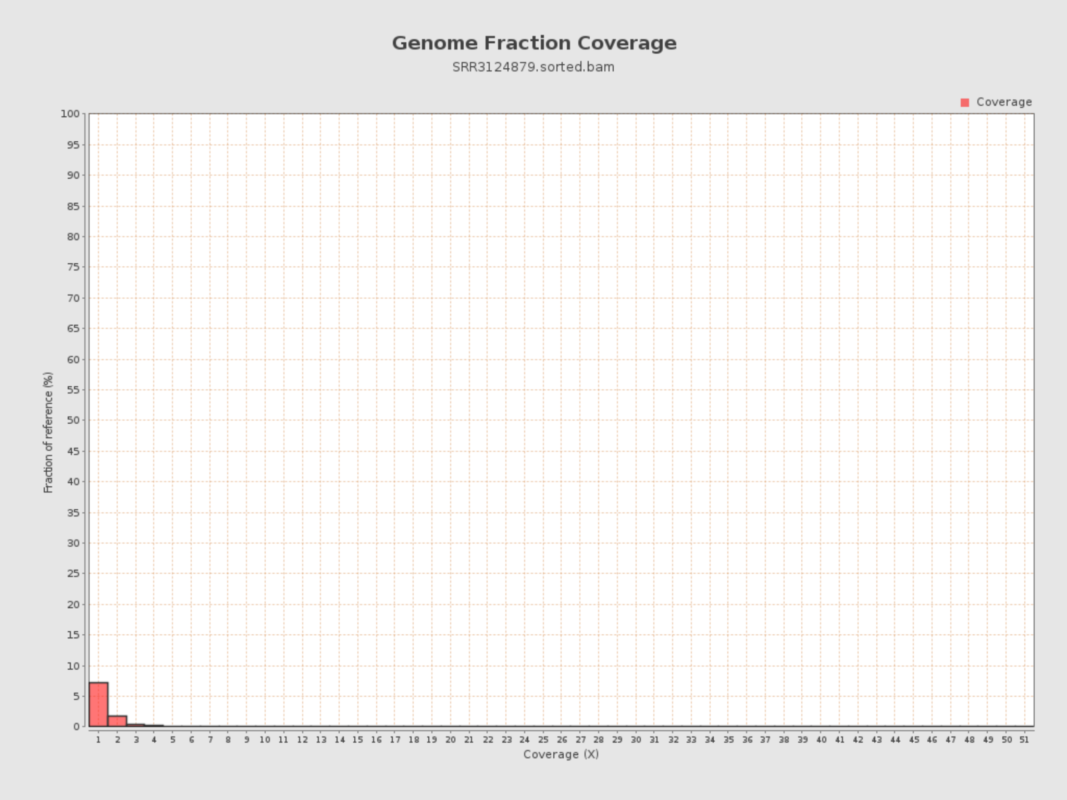
4. Results : Coverage Histogram



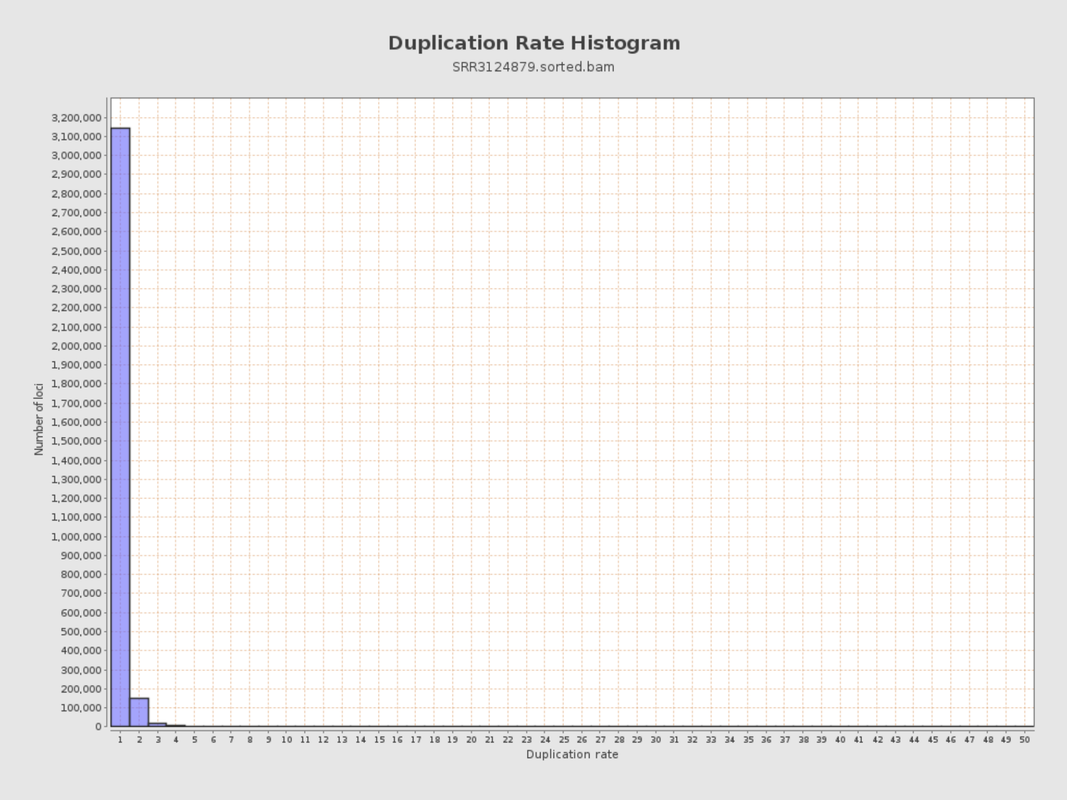
5. Results : Coverage Histogram (0-50X)



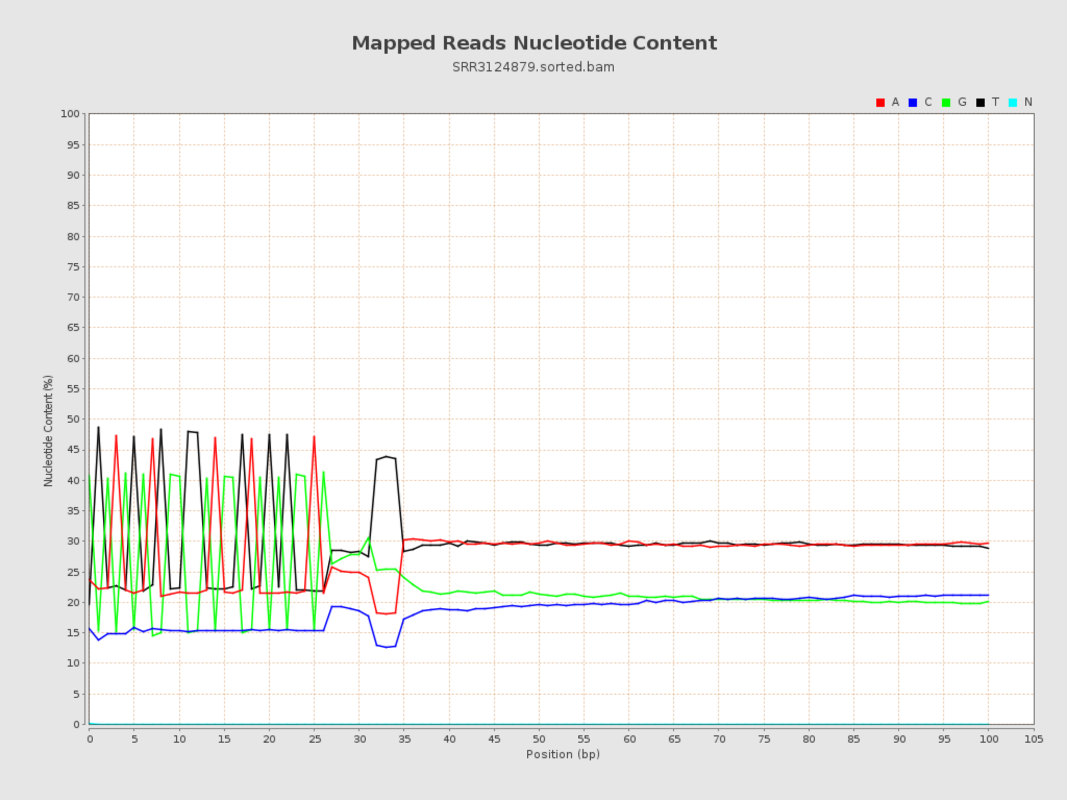
6. Results : Genome Fraction Coverage



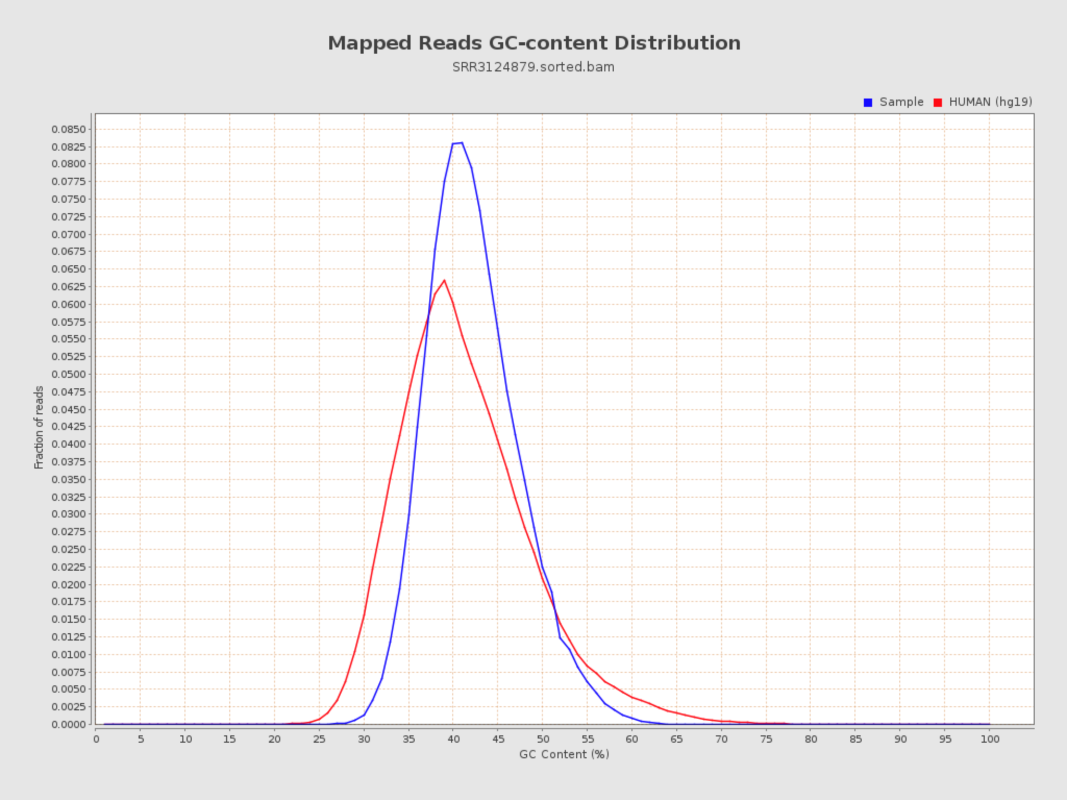
7. Results : Duplication Rate Histogram



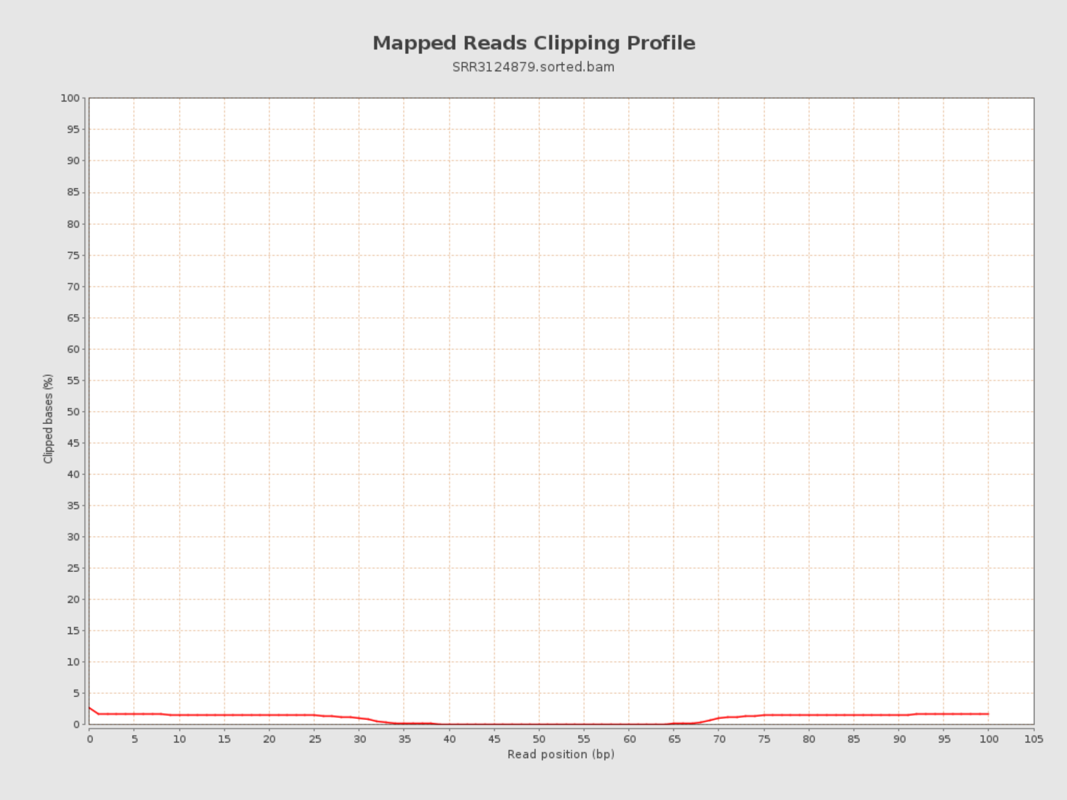
8. Results : Mapped Reads Nucleotide Content



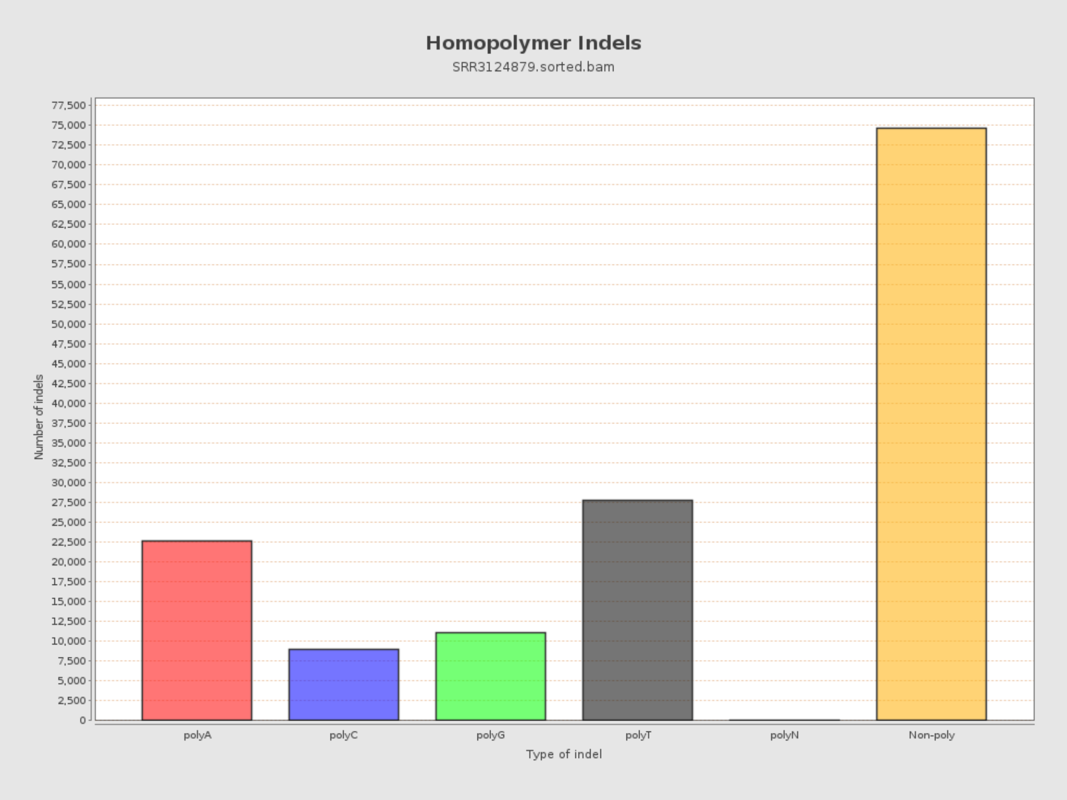
9. Results : Mapped Reads GC-content Distribution



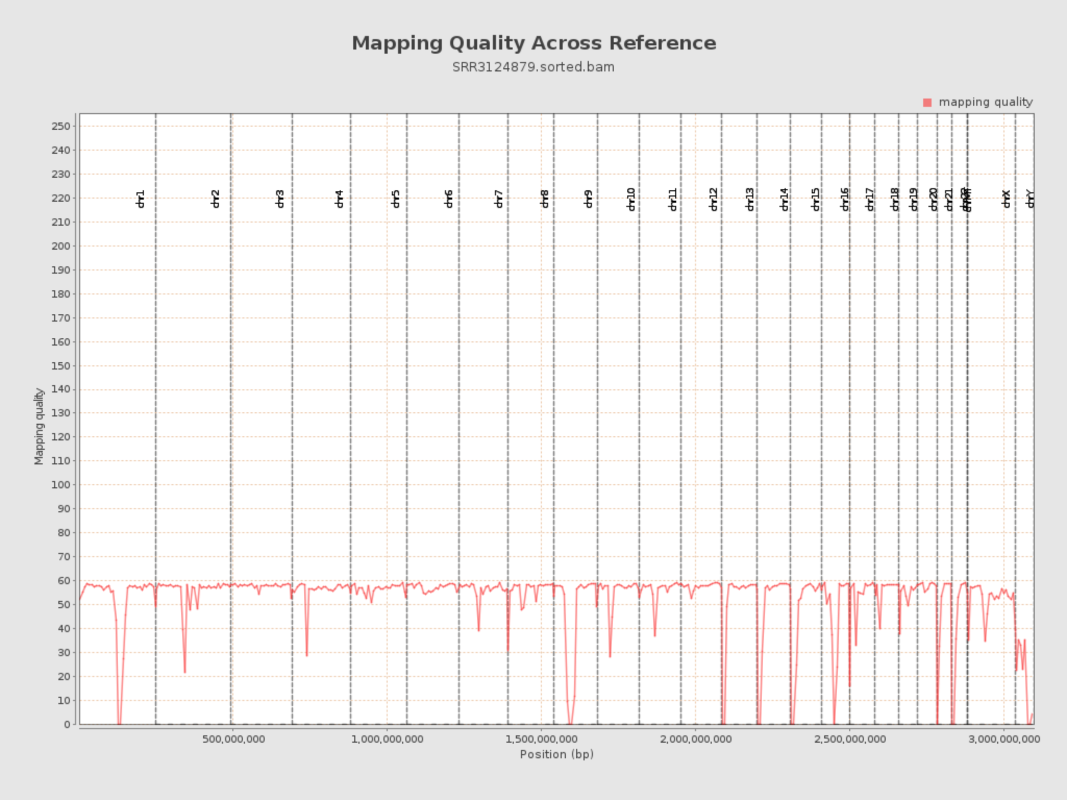
10. Results : Mapped Reads Clipping Profile



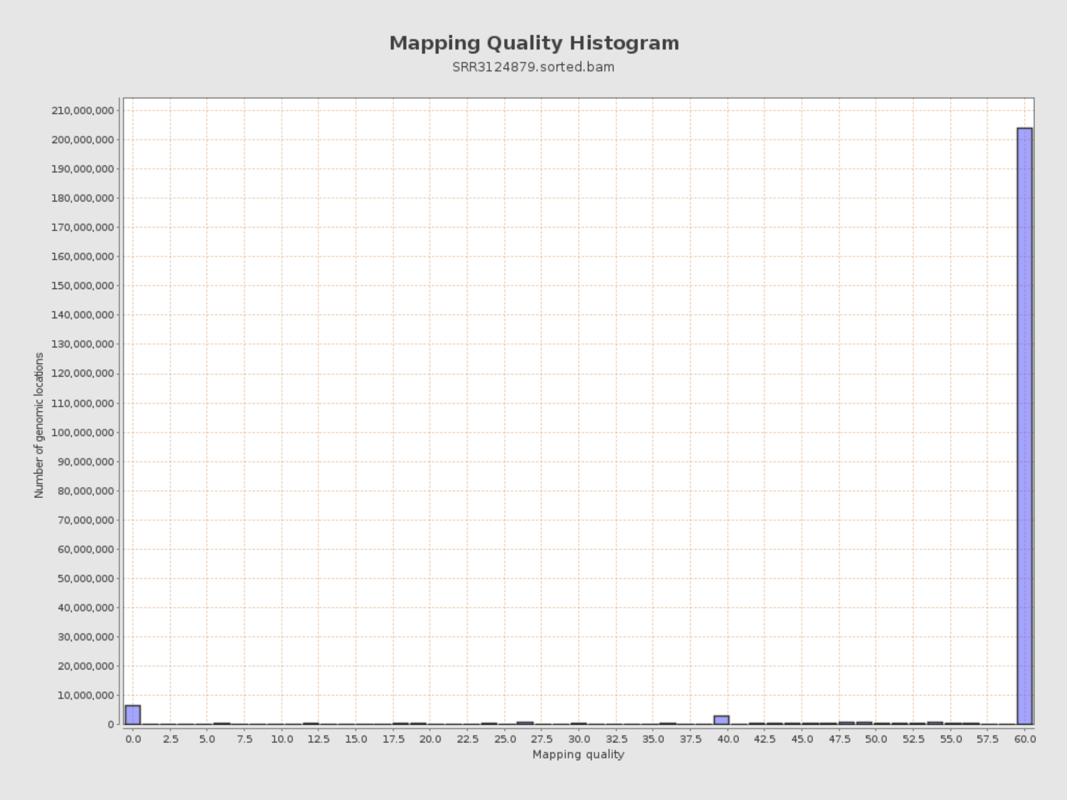
11. Results : Homopolymer Indels



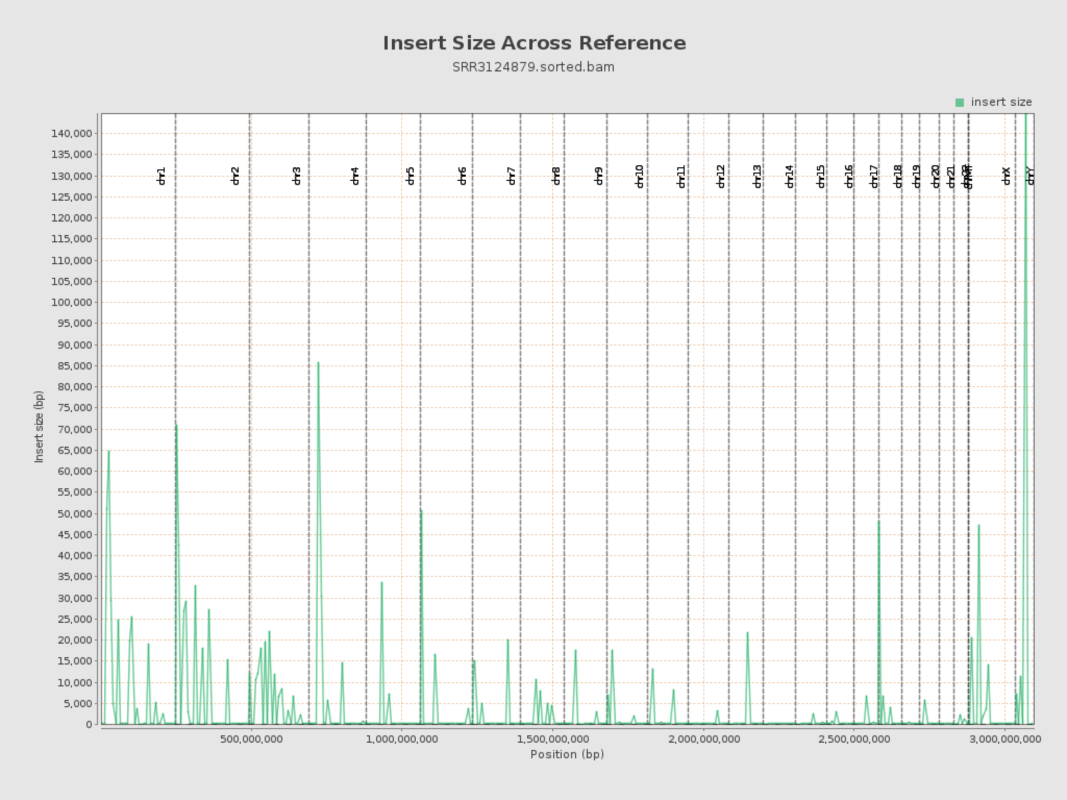
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram