Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 02:36:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124856.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_SRR3124856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124856_1.fastq.gz SRR3124856_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 02:36:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	123,936,082
Mapped reads	119,454,487 / 96.38%
Unmapped reads	4,481,595 / 3.62%
Mapped paired reads	119,454,487 / 96.38%
Mapped reads, first in pair	60,451,926 / 48.78%
Mapped reads, second in pair	59,002,561 / 47.61%
Mapped reads, both in pair	117,369,660 / 94.7%
Mapped reads, singletons	2,084,827 / 1.68%
Secondary alignments	0
Supplementary alignments	2,247,753 / 1.81%
Read min/max/mean length	30 / 150 / 150.87
Duplicated reads (estimated)	52,050,896 / 42%
Duplication rate	27.97%
Clipped reads	56,309,628 / 45.43%

2.2. ACGT Content

Number/percentage of A's	4,606,124,274 / 28.59%
Number/percentage of C's	3,208,749,316 / 19.92%
Number/percentage of T's	4,686,399,821 / 29.09%
Number/percentage of G's	3,609,604,285 / 22.4%
Number/percentage of N's	35,568 / 0%

GC Percentage	42.32%

2.3. Coverage

Mean	5.209
Standard Deviation	70.2959

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	71,079.04
Standard Deviation	2,521,835.85
P25/Median/P75	203 / 260 / 328

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	226,896,388
Insertions	3,708,181
Mapped reads with at least one insertion	2.81%
Deletions	6,242,036
Mapped reads with at least one deletion	4.93%
Homopolymer indels	43.43%

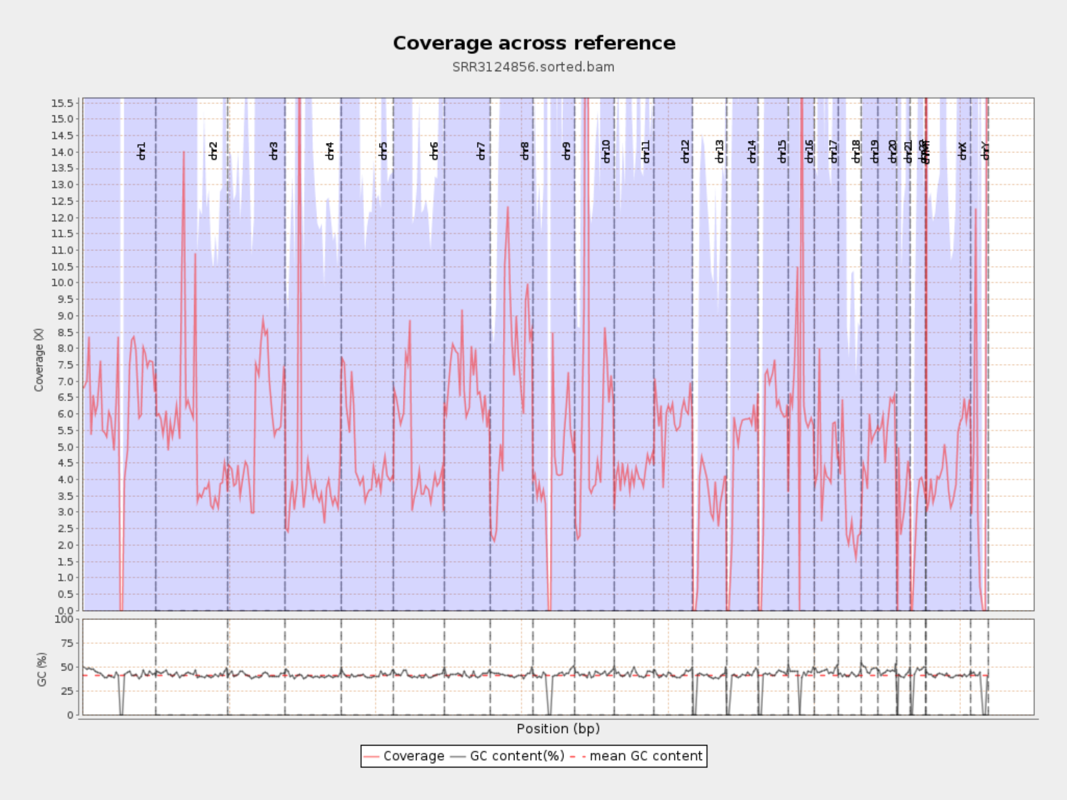
2.7. Chromosome stats

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

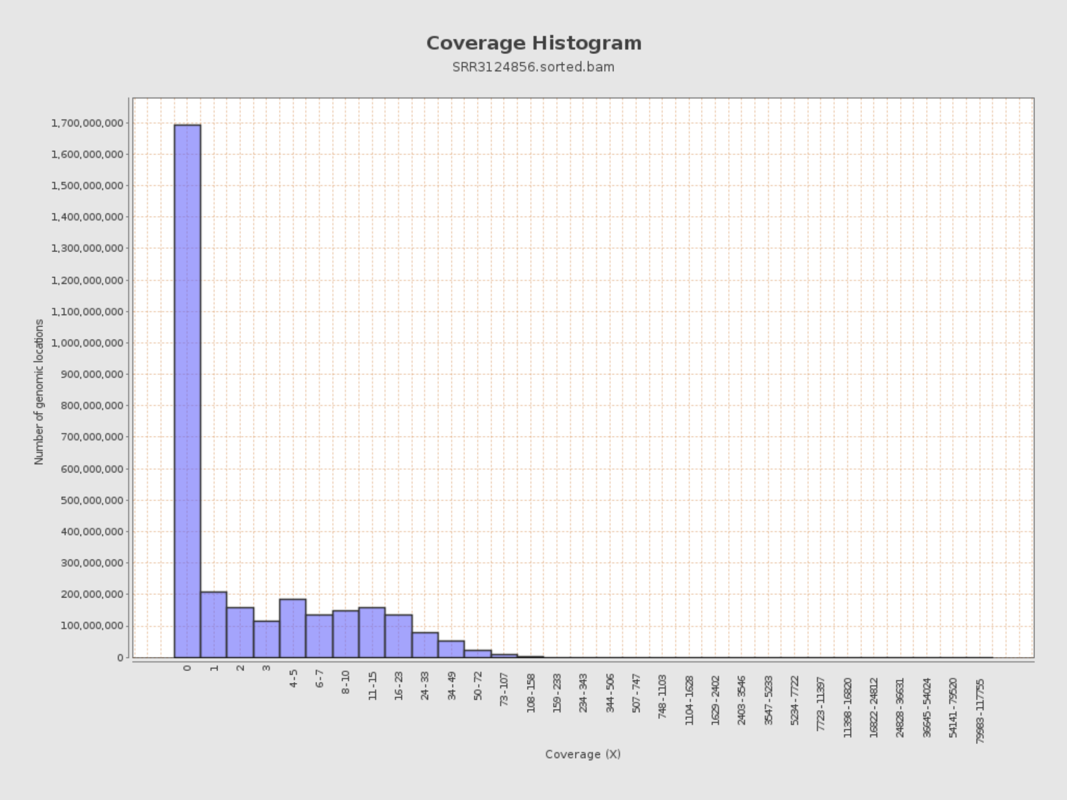
		bases	coverage	deviation
chr1	249250621	1558599955	6.2531	51.149
chr2	243199373	1319883089	5.4272	95.0618
chr3	198022430	1091375755	5.5114	11.8329
chr4	191154276	795102415	4.1595	107.8387
chr5	180915260	850931139	4.7035	12.945
chr6	171115067	828630542	4.8425	24.3187
chr7	159138663	1108099648	6.9631	53.4243
chr8	146364022	1030860564	7.0431	21.7493
chr9	141213431	603166249	4.2713	83.9913
chr10	135534747	893446174	6.592	188.1889
chr11	135006516	563030531	4.1704	19.5636
chr12	133851895	803982856	6.0065	13.3175
chr13	115169878	354645212	3.0793	8.0368
chr14	107349540	508620286	4.738	13.8605
chr15	102531392	554761541	5.4107	11.7634
chr16	90354753	634441406	7.0217	102.847
chr17	81195210	379449358	4.6733	60.8786
chr18	78077248	245220612	3.1407	64.7862
chr19	59128983	286350978	4.8428	29.5195
chr20	63025520	363454626	5.7668	33.9959
chr21	48129895	162656306	3.3795	49.178
chr22	51304566	135859727	2.6481	11.455
chrMT	16571	12589944	759.7576	364.2641
chrX	155270560	697898055	4.4947	15.2306

chrY	59373566	342481676	5.7683	171.4159

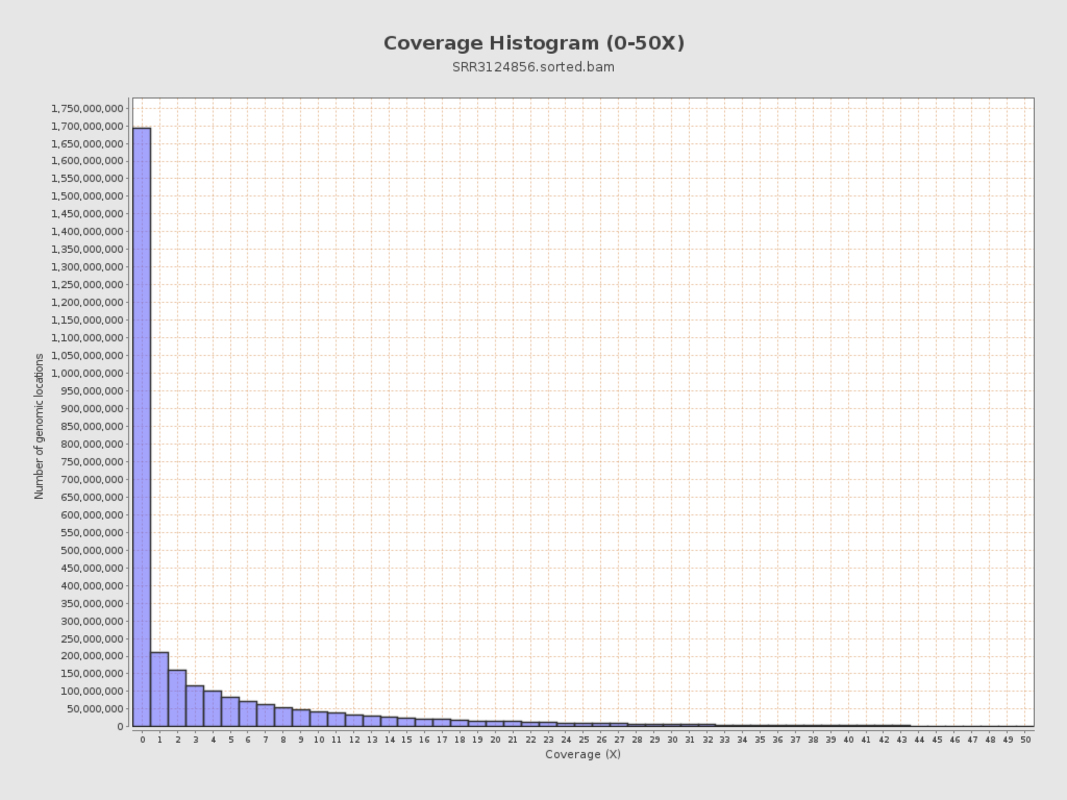
3. Results : Coverage across reference



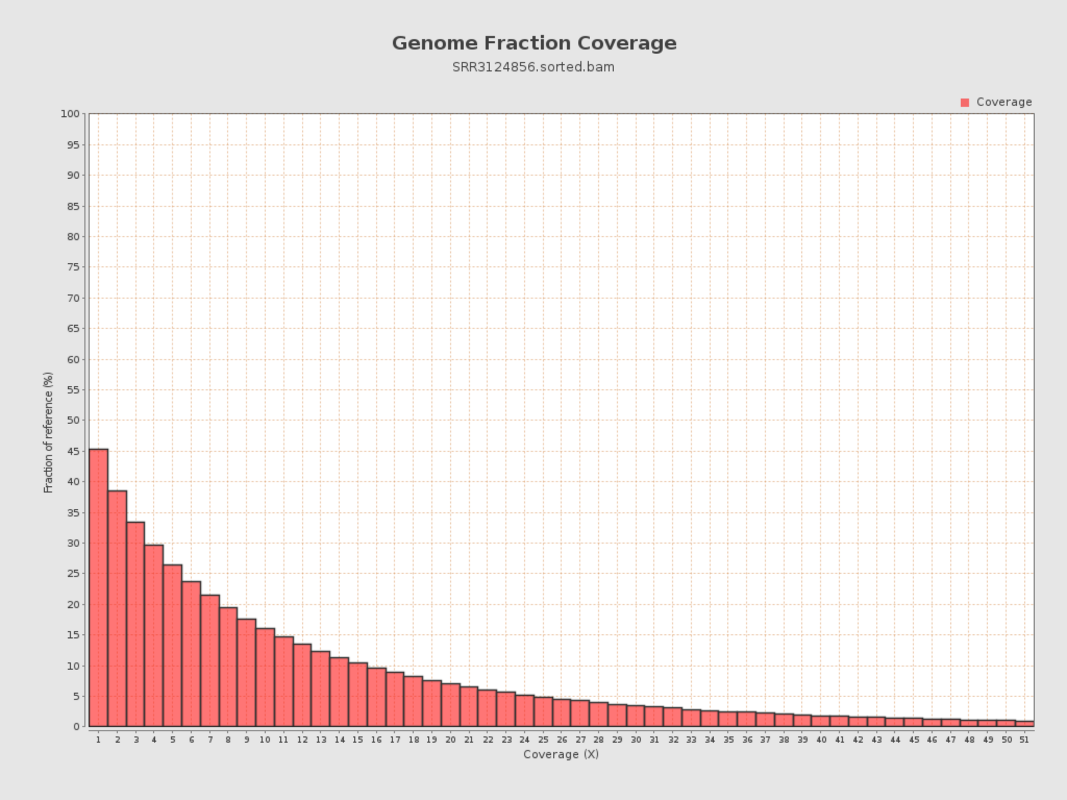
4. Results : Coverage Histogram



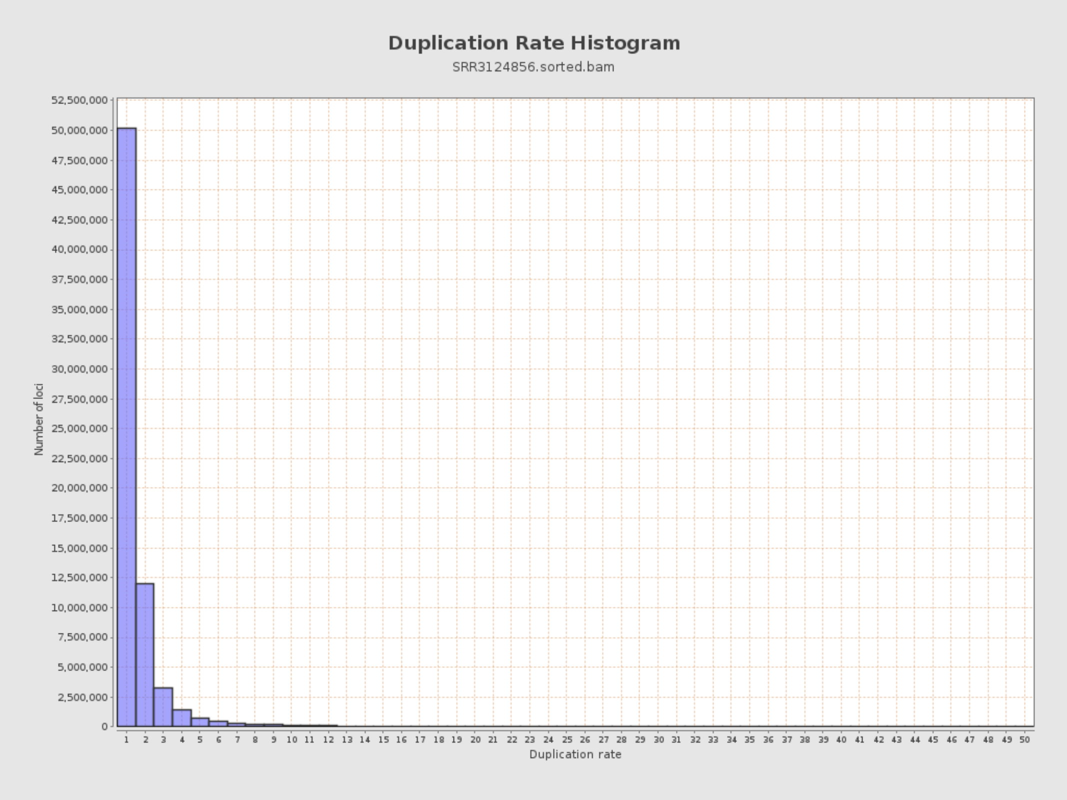
5. Results : Coverage Histogram (0-50X)



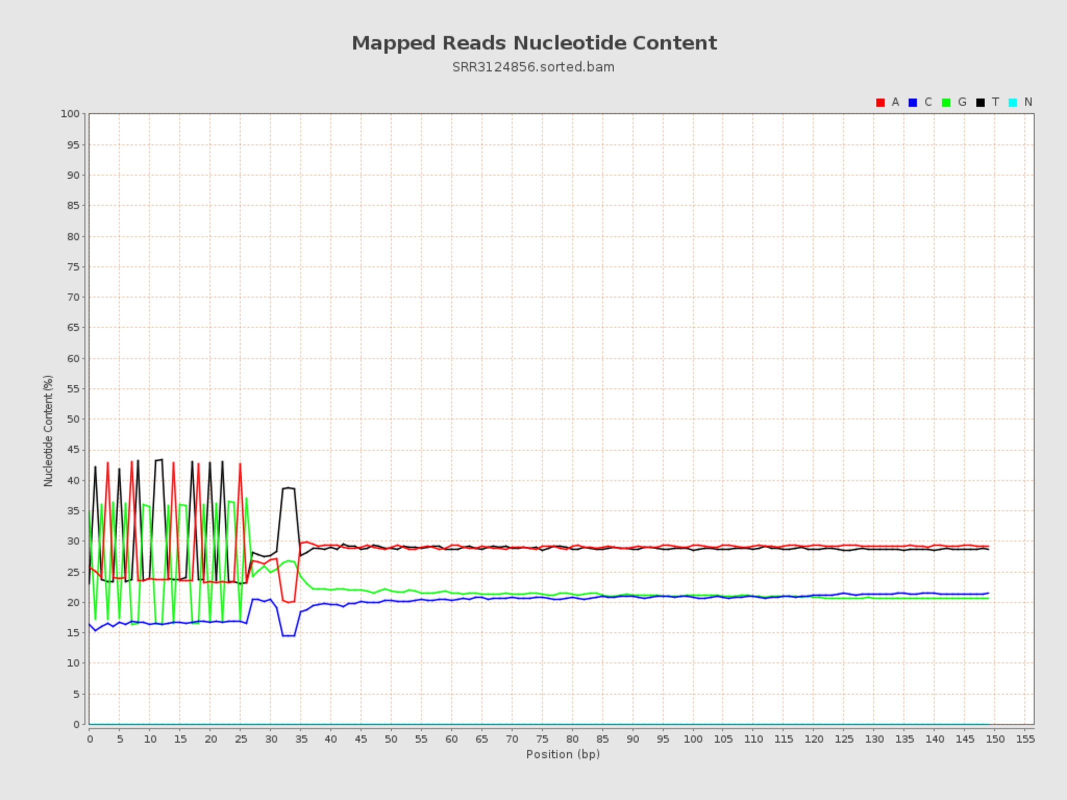
6. Results : Genome Fraction Coverage



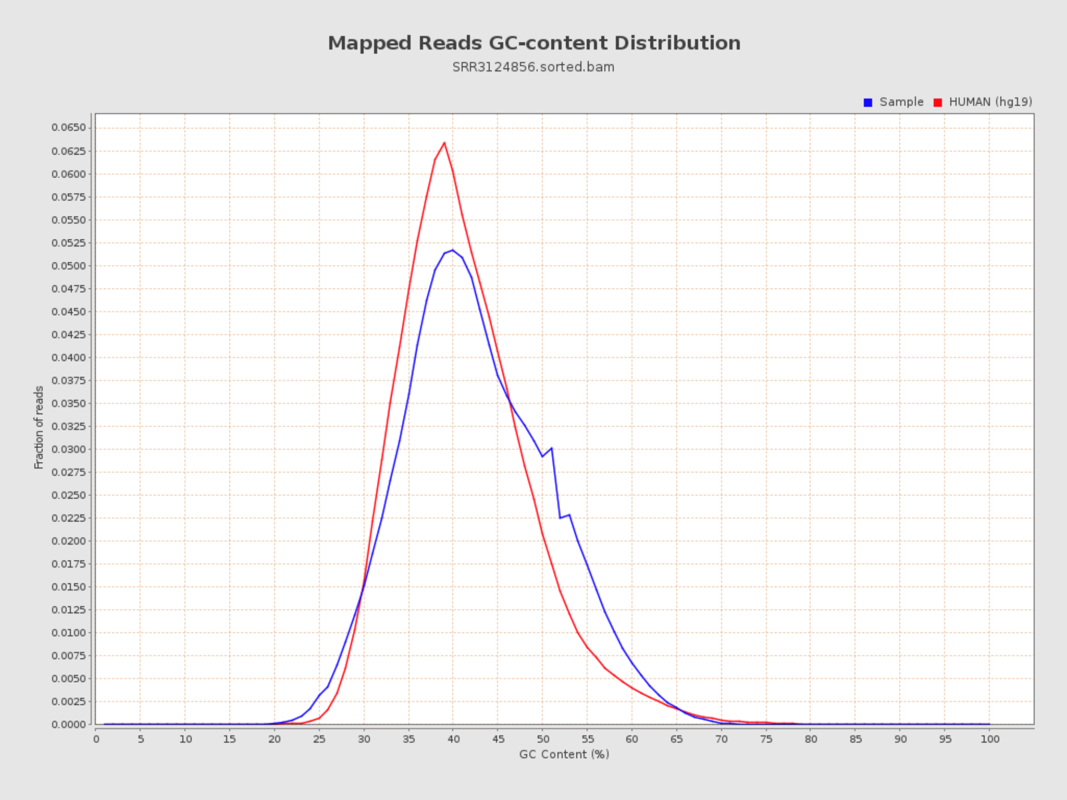
7. Results : Duplication Rate Histogram



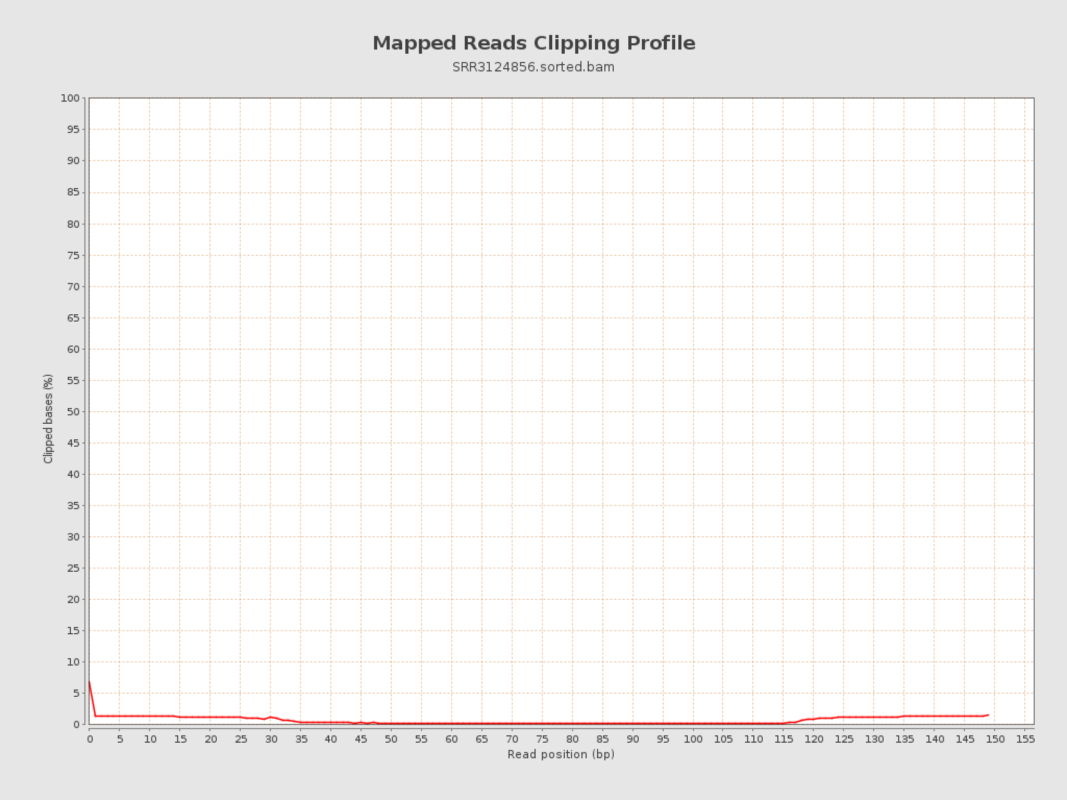
8. Results : Mapped Reads Nucleotide Content



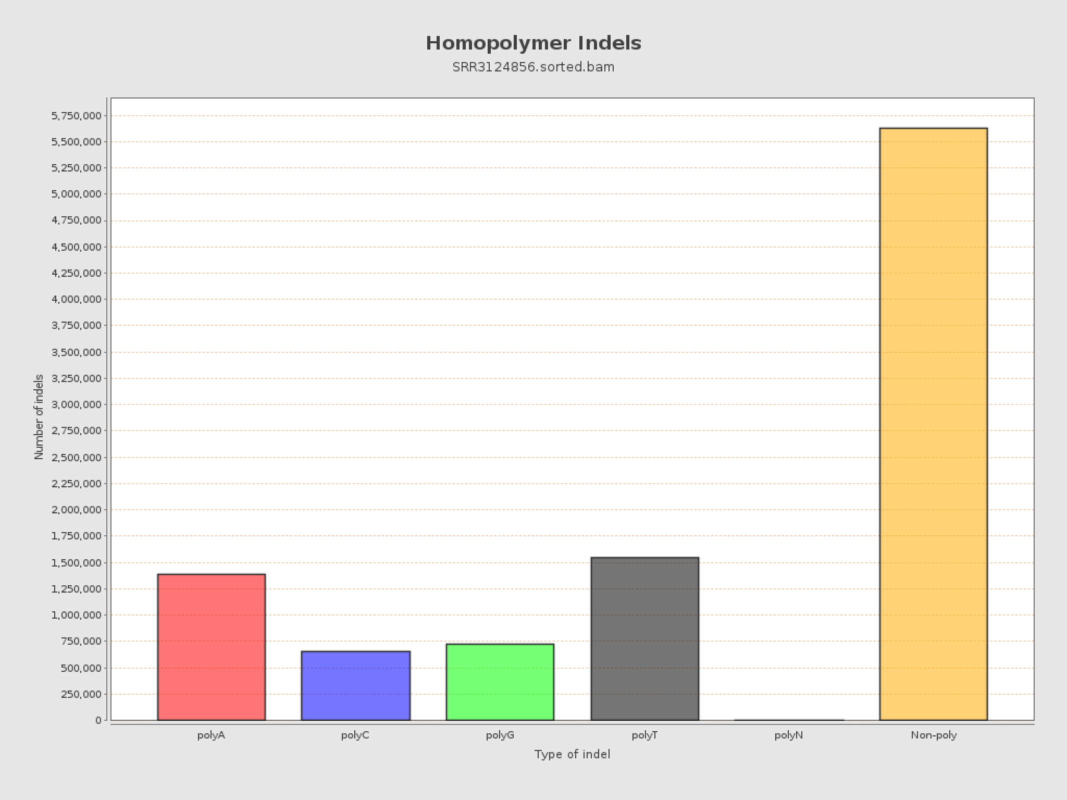
9. Results : Mapped Reads GC-content Distribution



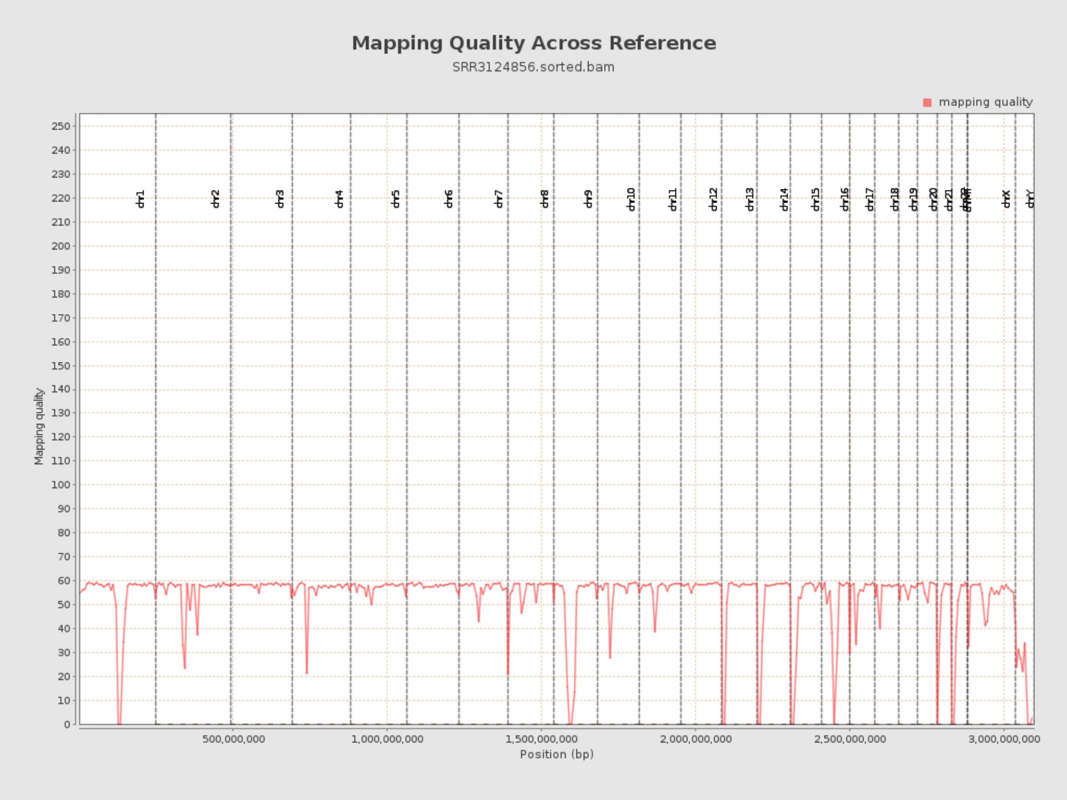
10. Results : Mapped Reads Clipping Profile



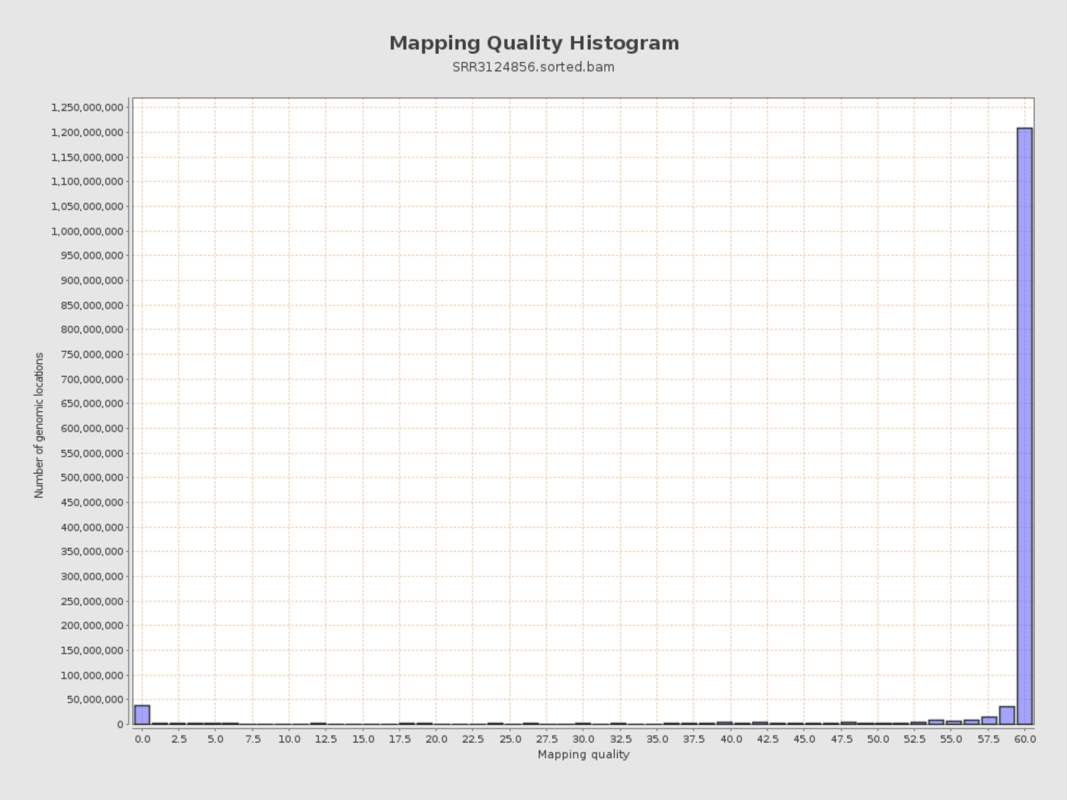
11. Results : Homopolymer Indels



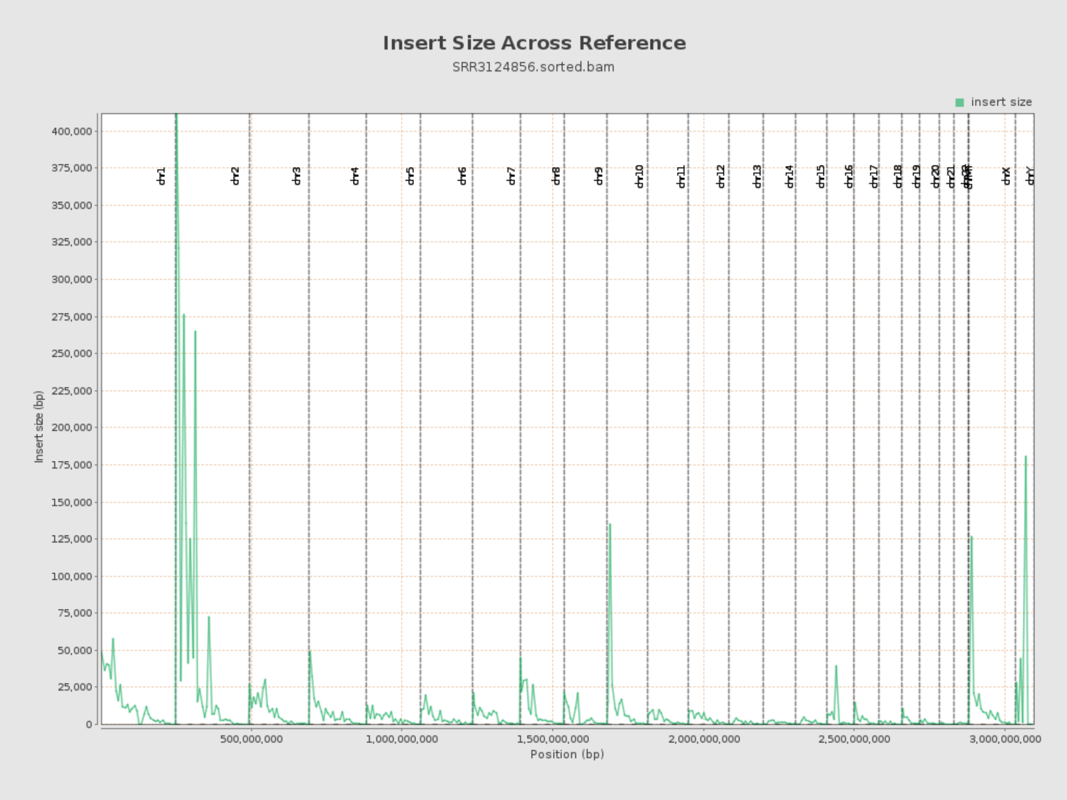
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram