Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/09 22:44:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124864.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_SRR3124864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124864_1.fastq.gz SRR3124864_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 09 22:44:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,052,750
Mapped reads	4,982,342 / 98.61%
Unmapped reads	70,408 / 1.39%
Mapped paired reads	4,982,342 / 98.61%
Mapped reads, first in pair	2,497,689 / 49.43%
Mapped reads, second in pair	2,484,653 / 49.17%
Mapped reads, both in pair	4,954,170 / 98.05%
Mapped reads, singletons	28,172 / 0.56%
Secondary alignments	0
Supplementary alignments	23,353 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	470,507 / 9.31%
Duplication rate	5.7%
Clipped reads	2,440,342 / 48.3%

2.2. ACGT Content

Number/percentage of A's	122,752,007 / 28.56%
Number/percentage of C's	78,350,569 / 18.23%
Number/percentage of T's	130,013,287 / 30.25%
Number/percentage of G's	98,524,096 / 22.92%
Number/percentage of N's	165,406 / 0.04%

GC Percentage	41.15%

2.3. Coverage

Mean	0.1389
Standard Deviation	1.842

2.4. Mapping Quality

Mean Mapping Quality	52.56

2.5. Insert size

Mean	28,491.57
Standard Deviation	1,516,979.66
P25/Median/P75	143 / 192 / 267

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	3,563,376
Insertions	62,051
Mapped reads with at least one insertion	1.21%
Deletions	137,773
Mapped reads with at least one deletion	2.71%
Homopolymer indels	47.58%

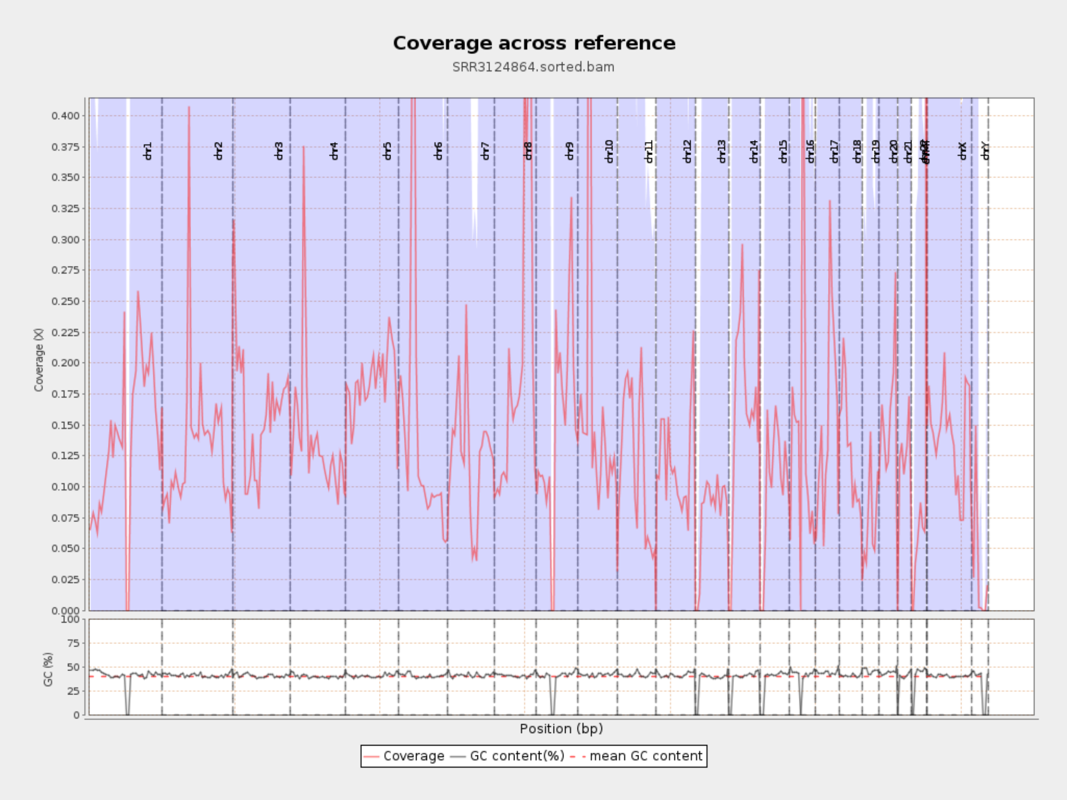
2.7. Chromosome stats

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

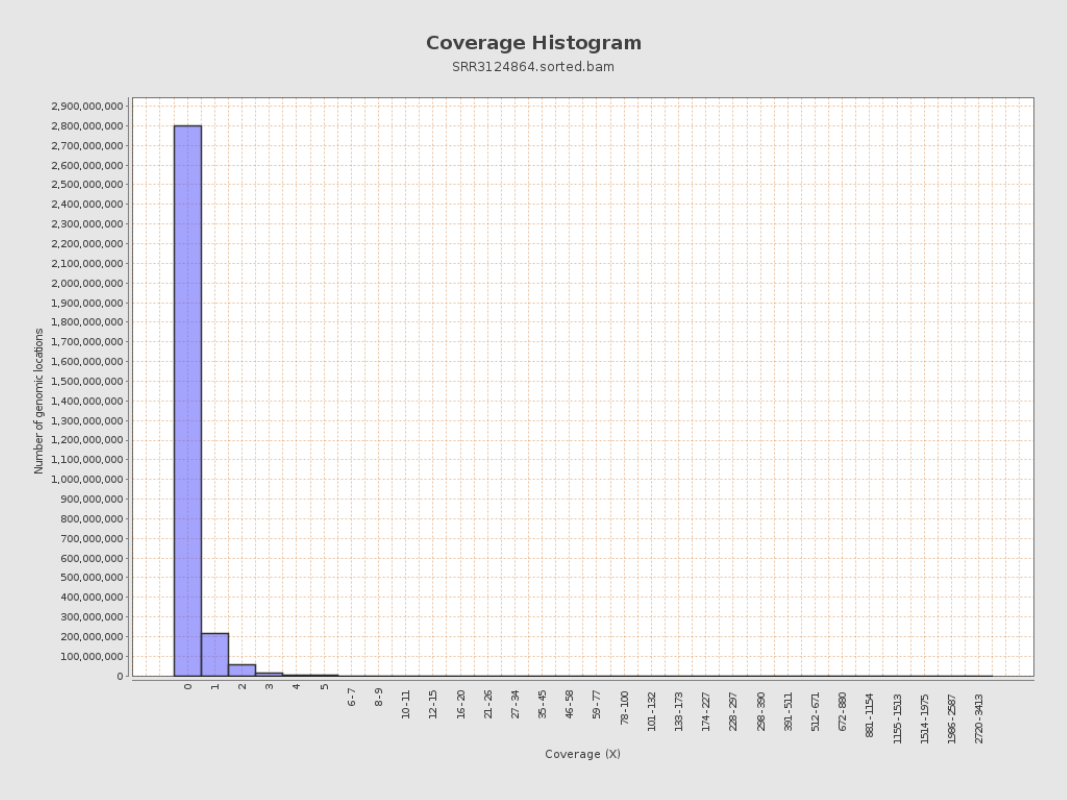
		bases	coverage	deviation
chr1	249250621	34785004	0.1396	1.773
chr2	243199373	32070631	0.1319	1.7891
chr3	198022430	32232615	0.1628	0.5383
chr4	191154276	26224134	0.1372	1.3847
chr5	180915260	33520769	0.1853	0.5686
chr6	171115067	25505968	0.1491	2.3586
chr7	159138663	20456358	0.1285	1.8961
chr8	146364022	30085564	0.2056	0.8613
chr9	141213431	21539734	0.1525	2.3366
chr10	135534747	22660003	0.1672	5.2355
chr11	135006516	16012223	0.1186	1.3551
chr12	133851895	15903326	0.1188	0.4529
chr13	115169878	8868472	0.077	0.3412
chr14	107349540	17364280	0.1618	0.688
chr15	102531392	10441381	0.1018	0.4153
chr16	90354753	12732078	0.1409	3.0243
chr17	81195210	12414881	0.1529	1.333
chr18	78077248	10287341	0.1318	2.5006
chr19	59128983	4386491	0.0742	1.2399
chr20	63025520	10050366	0.1595	0.6285
chr21	48129895	5599206	0.1163	1.01
chr22	51304566	2563647	0.05	0.2928
chrMT	16571	121575	7.3366	5.04
chrX	155270560	22415120	0.1444	0.7693

chrY	59373566	1800930	0.0303	2.0849

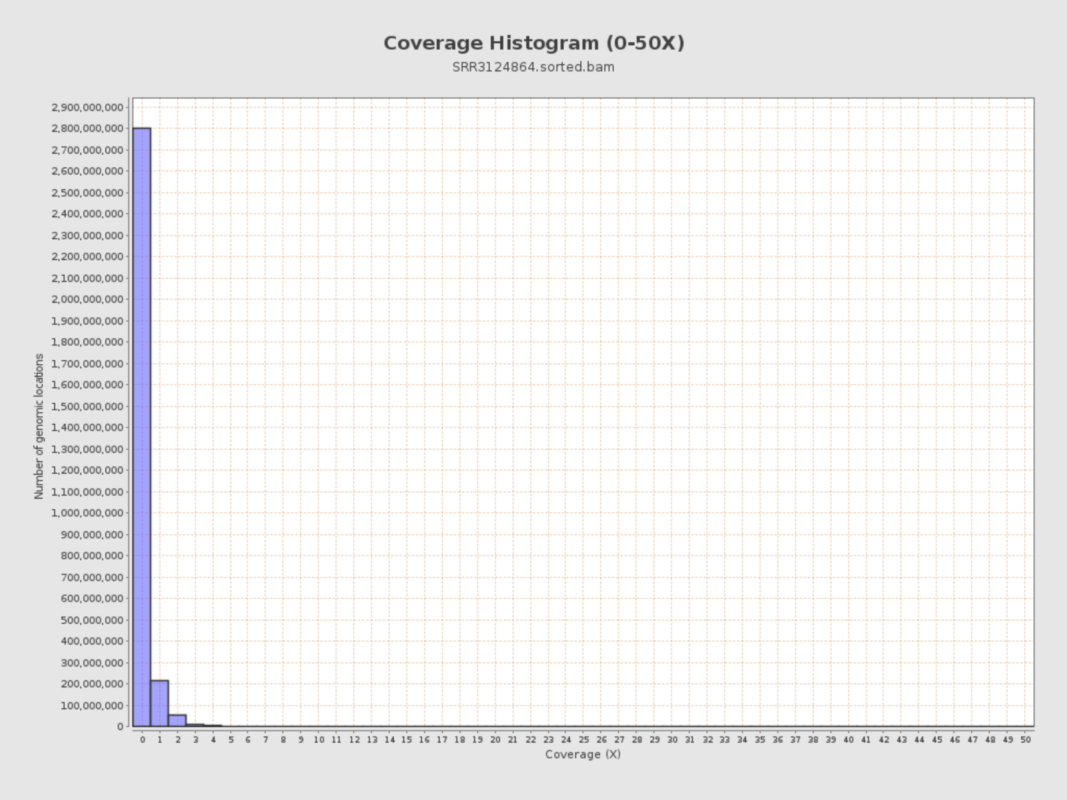
3. Results : Coverage across reference



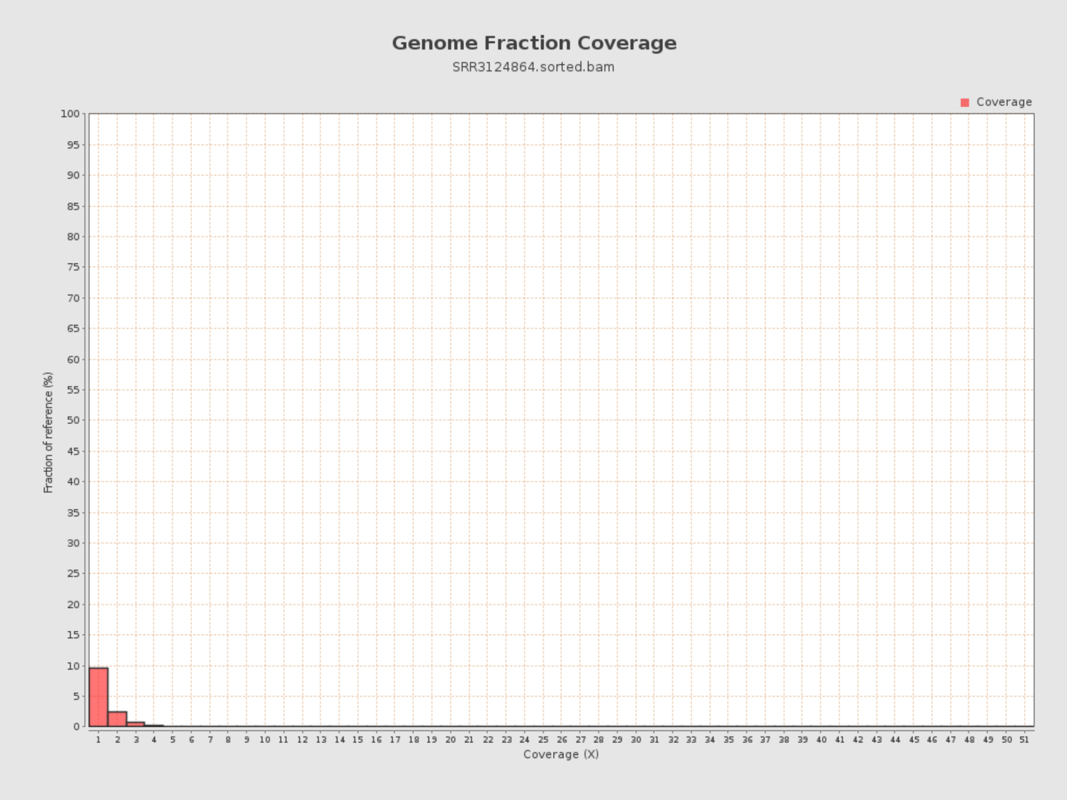
4. Results : Coverage Histogram



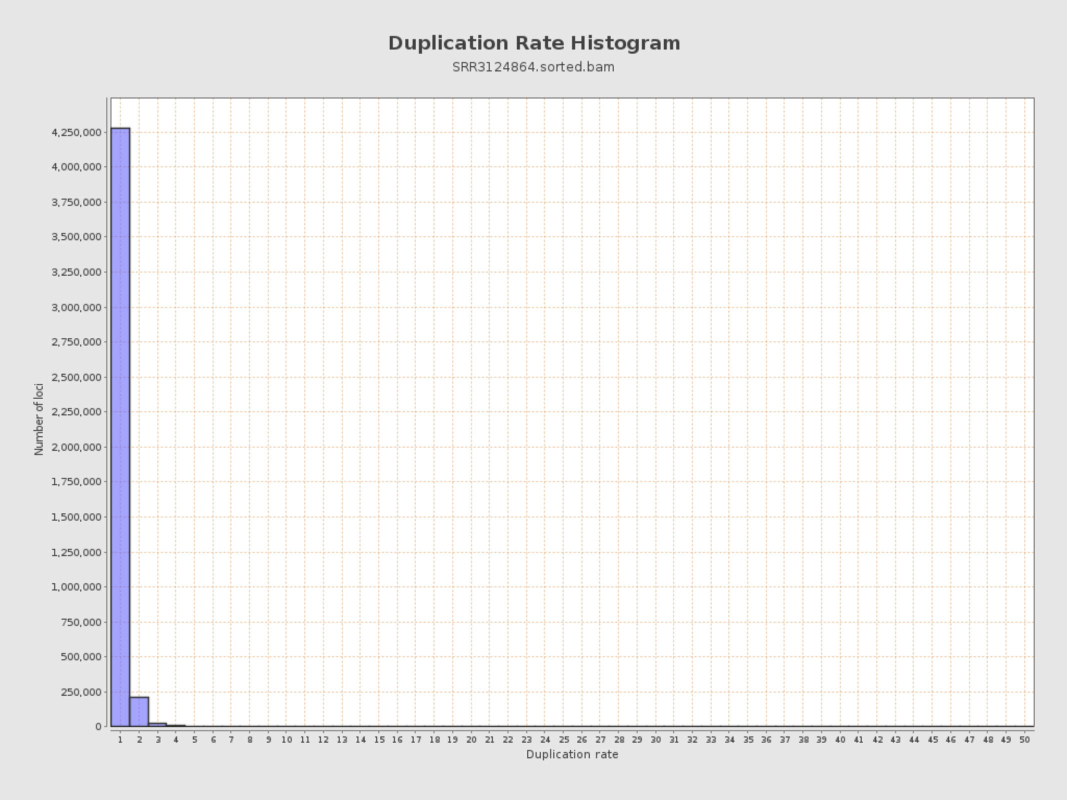
5. Results : Coverage Histogram (0-50X)



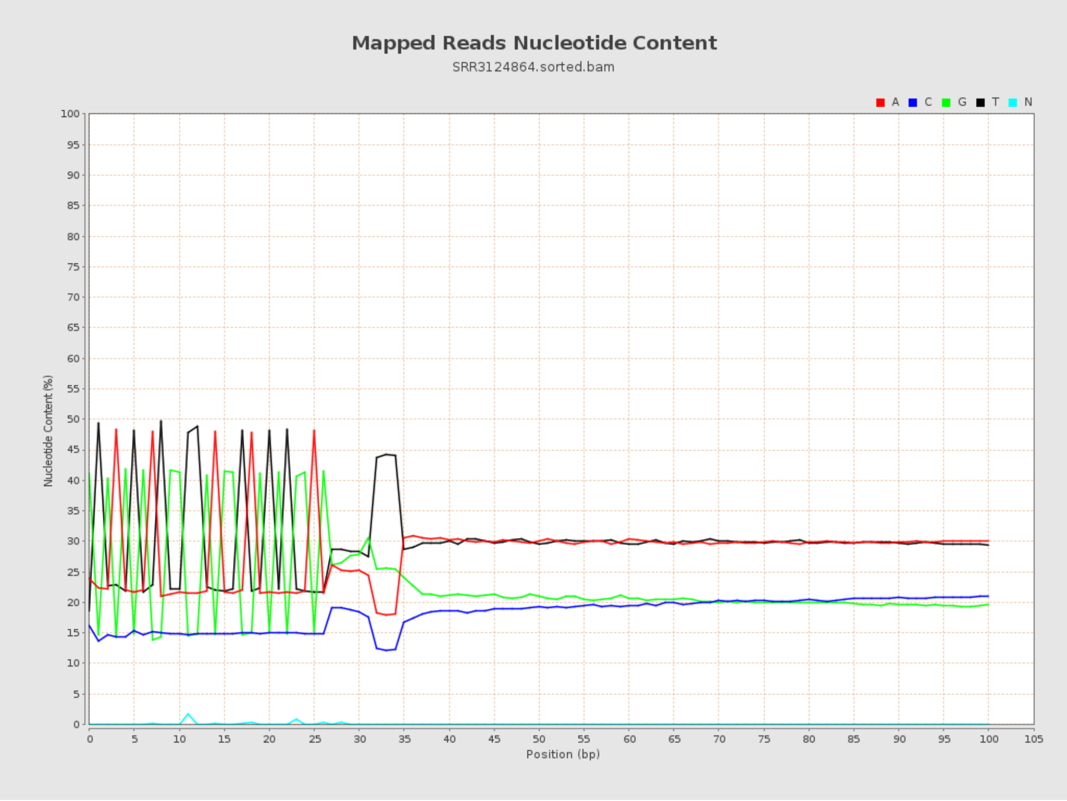
6. Results : Genome Fraction Coverage



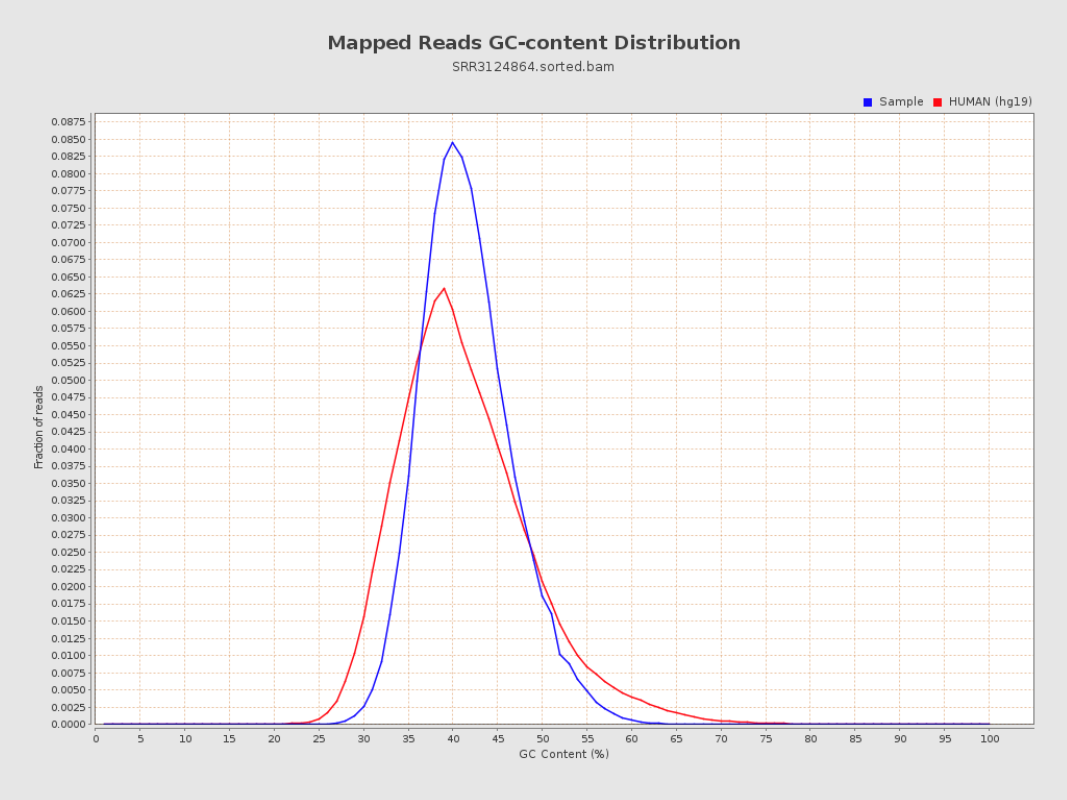
7. Results : Duplication Rate Histogram



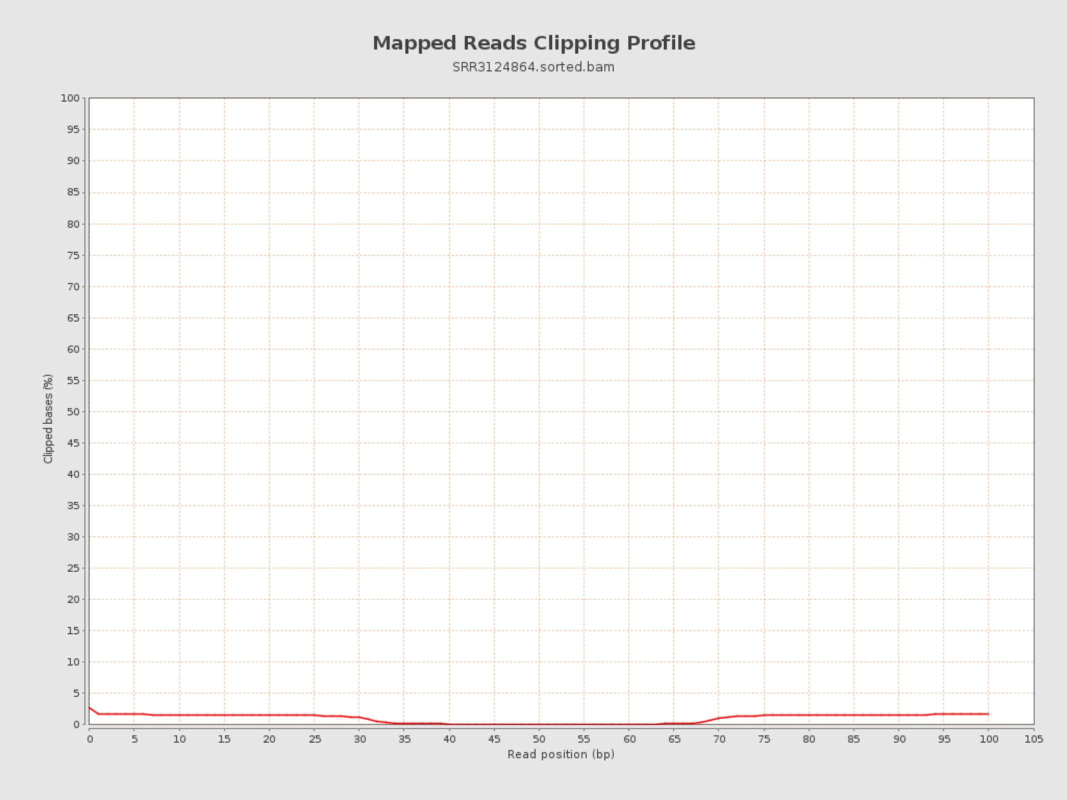
8. Results : Mapped Reads Nucleotide Content



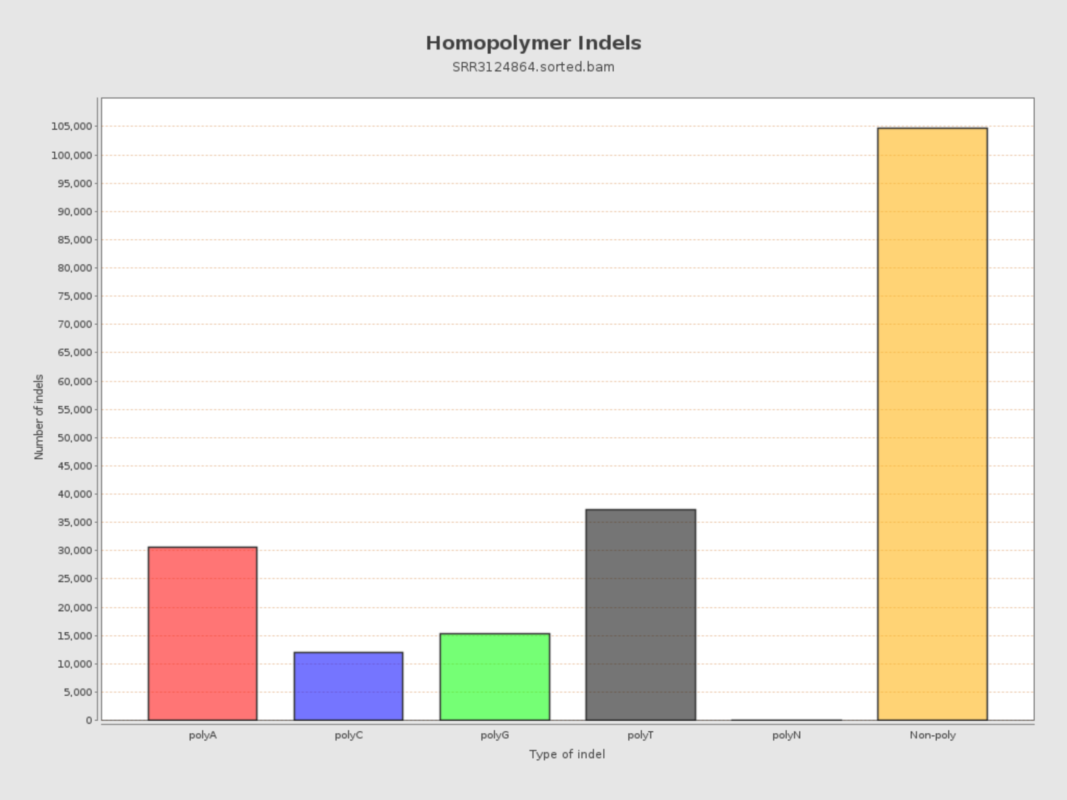
9. Results : Mapped Reads GC-content Distribution



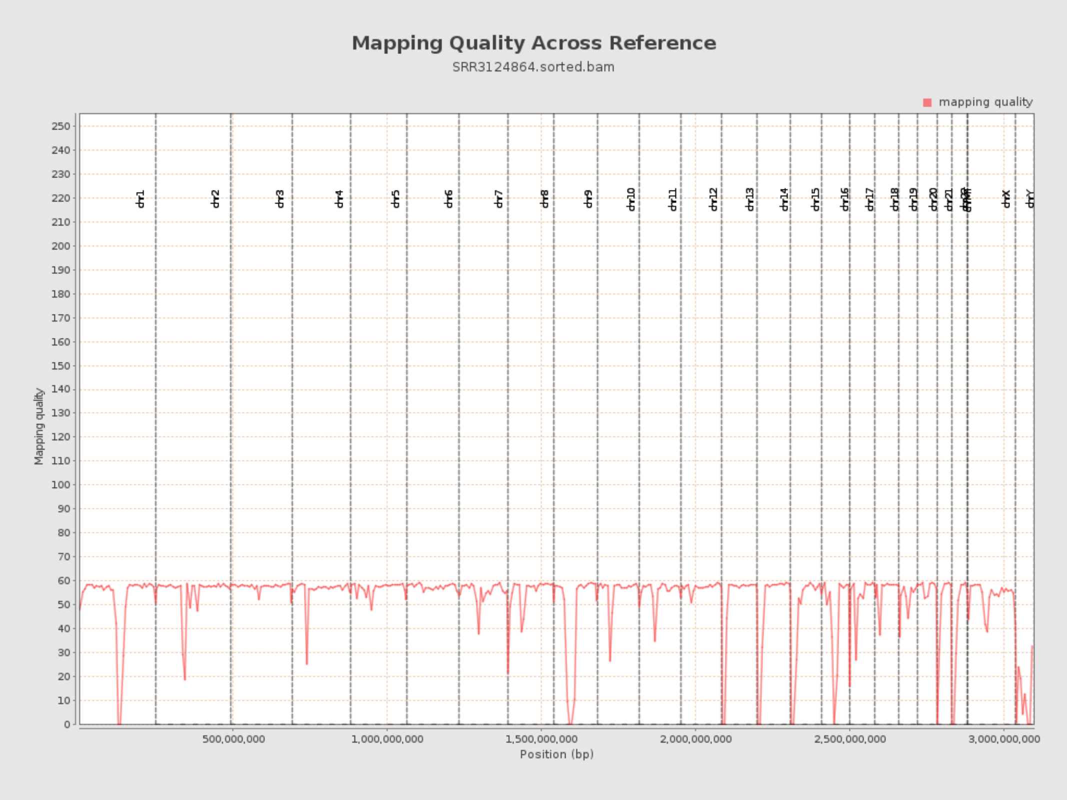
10. Results : Mapped Reads Clipping Profile



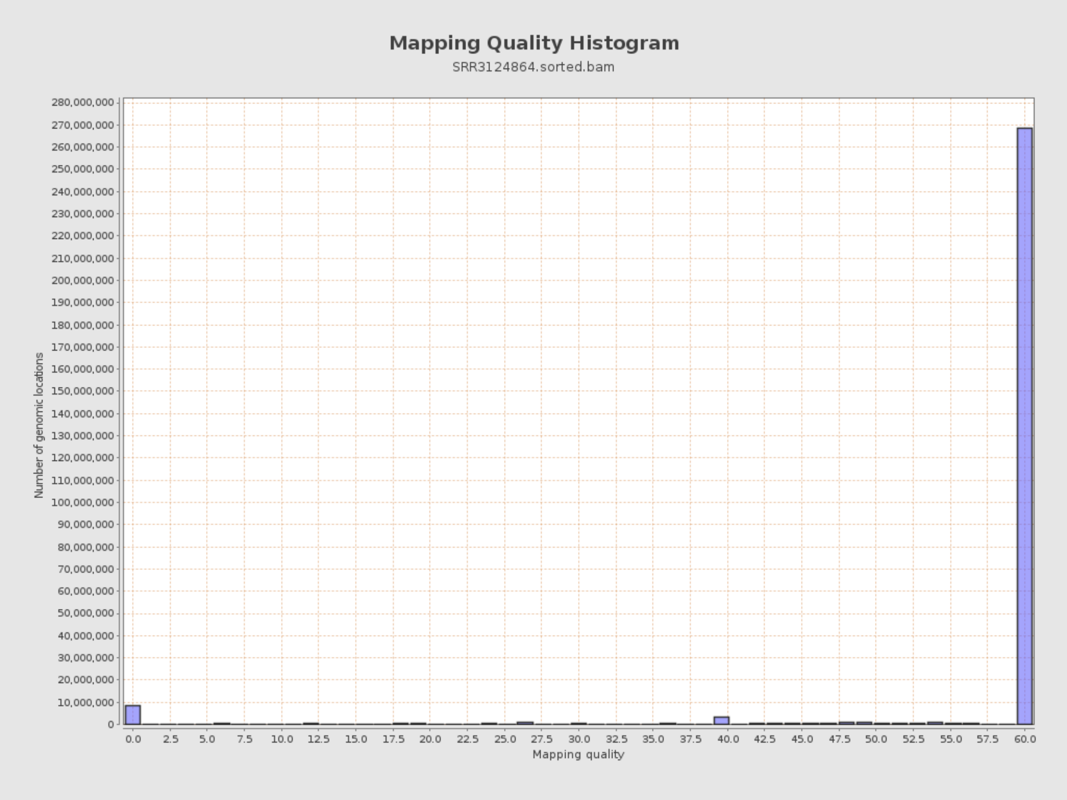
11. Results : Homopolymer Indels



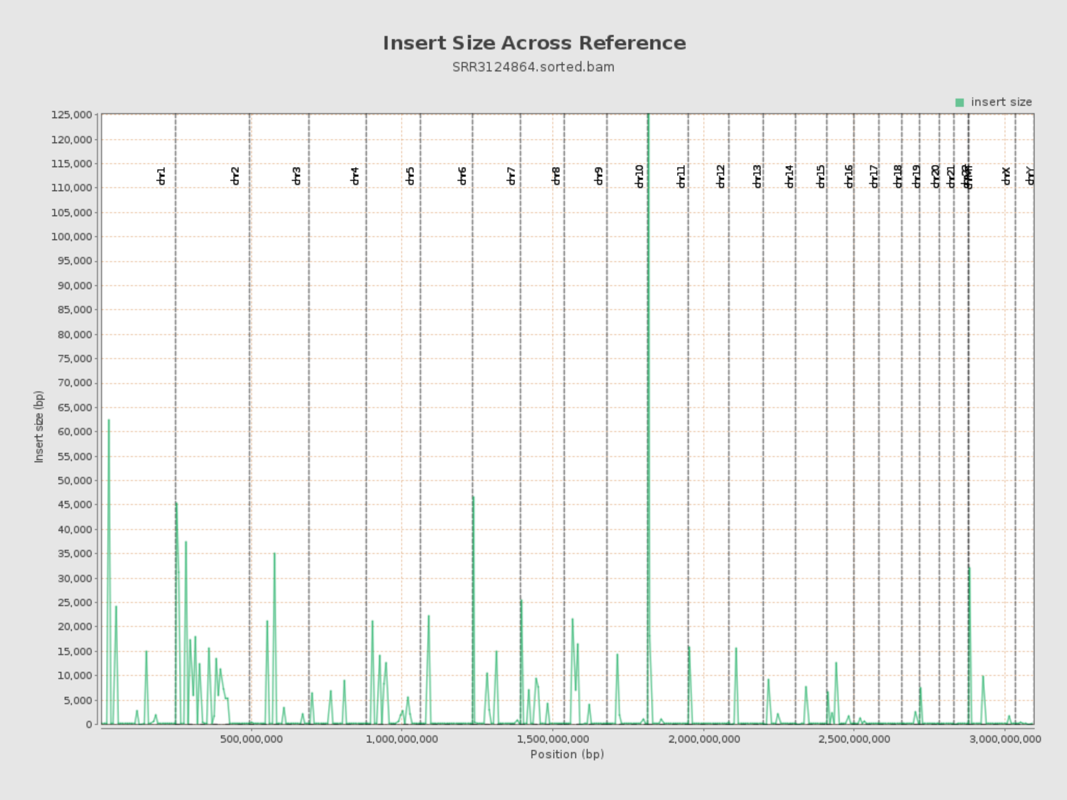
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram