Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 19:47:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124814.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_SRR3124814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124814_1.fastq.gz SRR3124814_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 19:47:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,141,418
Mapped reads	26,751,296 / 98.56%
Unmapped reads	390,122 / 1.44%
Mapped paired reads	26,751,296 / 98.56%
Mapped reads, first in pair	13,416,682 / 49.43%
Mapped reads, second in pair	13,334,614 / 49.13%
Mapped reads, both in pair	26,579,542 / 97.93%
Mapped reads, singletons	171,754 / 0.63%
Secondary alignments	0
Supplementary alignments	126,120 / 0.46%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	5,426,683 / 19.99%
Duplication rate	12.16%
Clipped reads	12,971,347 / 47.79%

2.2. ACGT Content

Number/percentage of A's	654,544,762 / 28.25%
Number/percentage of C's	427,276,536 / 18.44%
Number/percentage of T's	698,926,215 / 30.17%
Number/percentage of G's	536,162,753 / 23.14%
Number/percentage of N's	21,713 / 0%

GC Percentage	41.58%

2.3. Coverage

Mean	0.7489
Standard Deviation	9.1181

2.4. Mapping Quality

Mean Mapping Quality	52.47

2.5. Insert size

Mean	33,875.59
Standard Deviation	1,723,665.18
P25/Median/P75	150 / 203 / 285

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	18,909,676
Insertions	333,935
Mapped reads with at least one insertion	1.21%
Deletions	773,411
Mapped reads with at least one deletion	2.83%
Homopolymer indels	46.91%

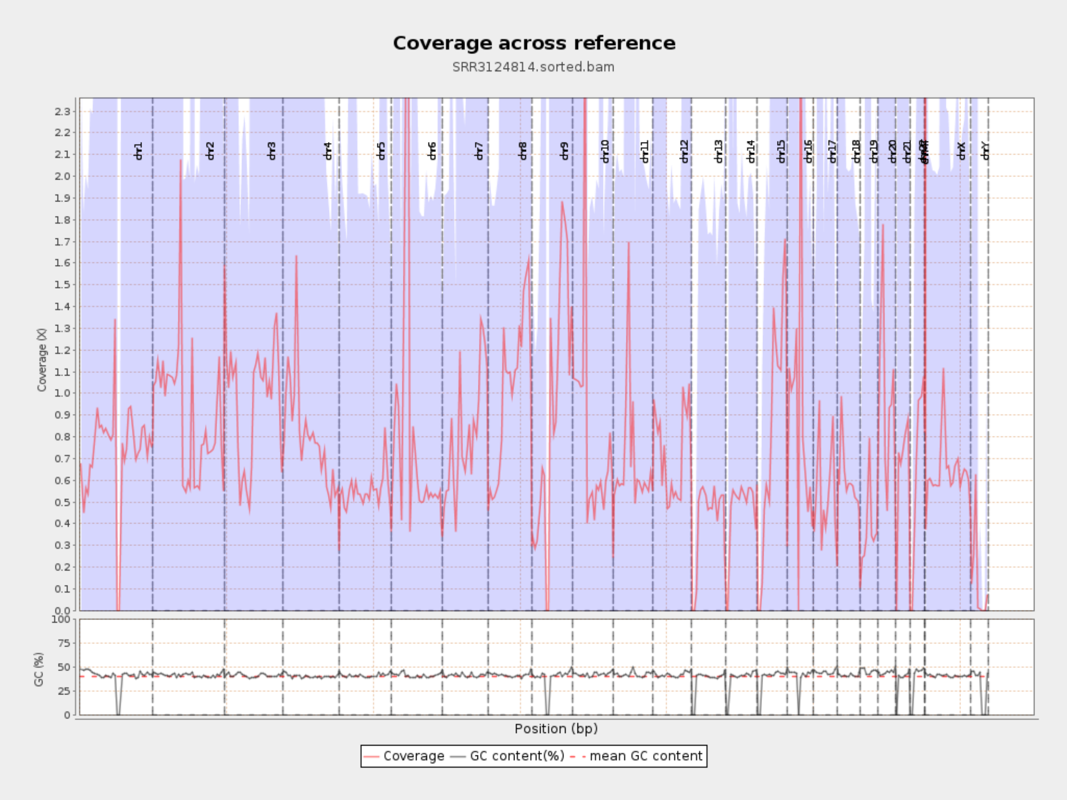
2.7. Chromosome stats

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

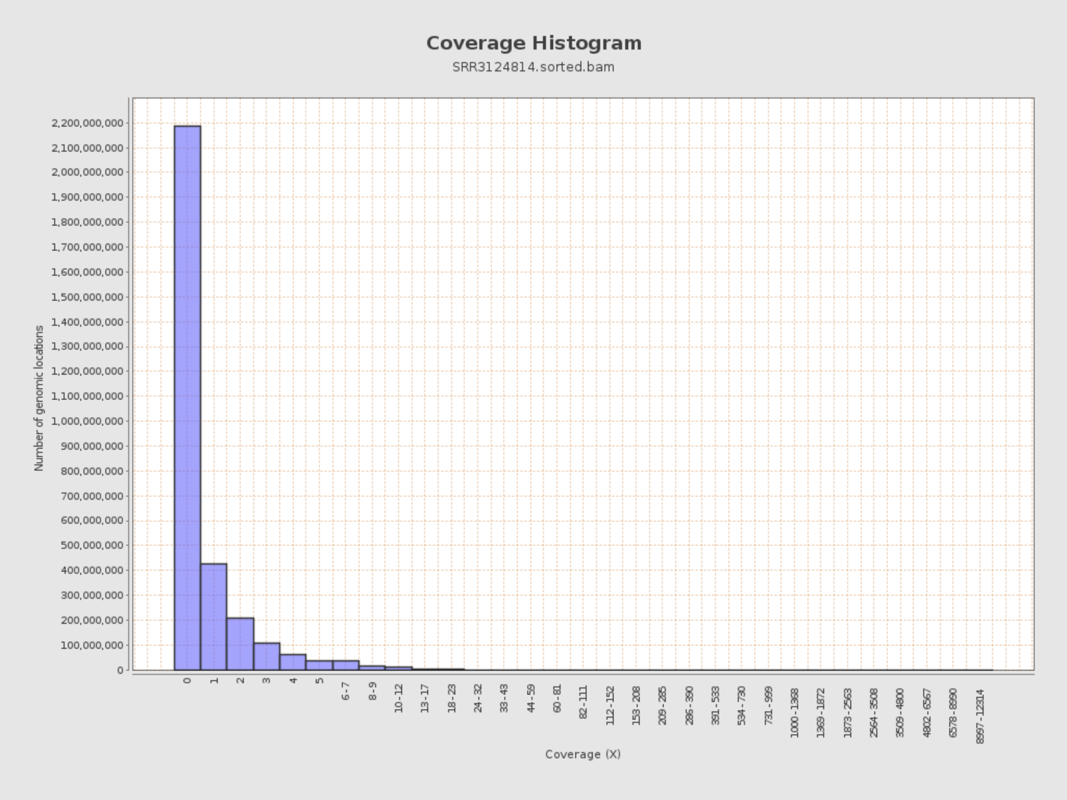
		bases	coverage	deviation
chr1	249250621	182003375	0.7302	8.1602
chr2	243199373	222006277	0.9129	9.5348
chr3	198022430	191529937	0.9672	2.1206
chr4	191154276	154151774	0.8064	4.8142
chr5	180915260	99605779	0.5506	2.4297
chr6	171115067	147345803	0.8611	20.4697
chr7	159138663	129184884	0.8118	8.7565
chr8	146364022	150348009	1.0272	3.435
chr9	141213431	127909859	0.9058	12.1441
chr10	135534747	112788049	0.8322	16.5038
chr11	135006516	91417268	0.6771	10.277
chr12	133851895	97330679	0.7272	2.6436
chr13	115169878	48632625	0.4223	1.1691
chr14	107349540	49021078	0.4566	2.3444
chr15	102531392	86921637	0.8478	2.0398
chr16	90354753	81259079	0.8993	16.1297
chr17	81195210	42656476	0.5254	7.2022
chr18	78077248	47309740	0.6059	11.9763
chr19	59128983	21482813	0.3633	6.169
chr20	63025520	61628590	0.9778	2.4701
chr21	48129895	32473048	0.6747	4.0319
chr22	51304566	33134191	0.6458	1.824
chrMT	16571	624193	37.6678	24.2104
chrX	155270560	99270657	0.6393	4.417

chrY	59373566	8200318	0.1381	10.752

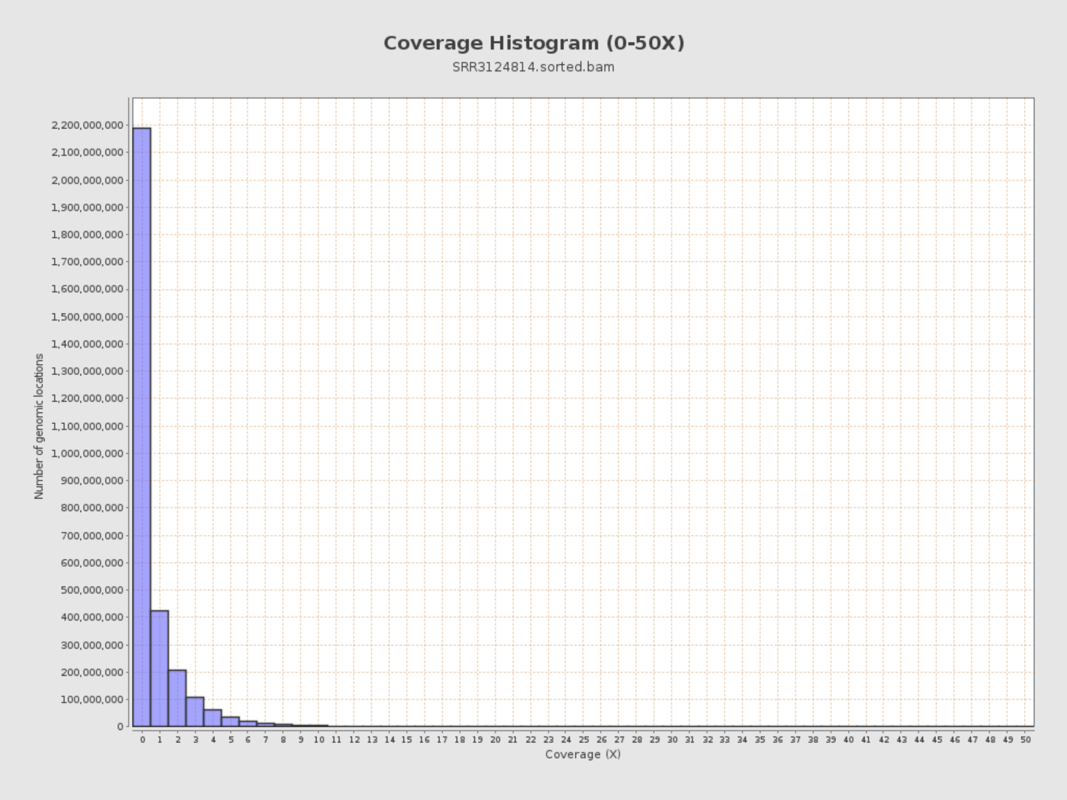
3. Results : Coverage across reference



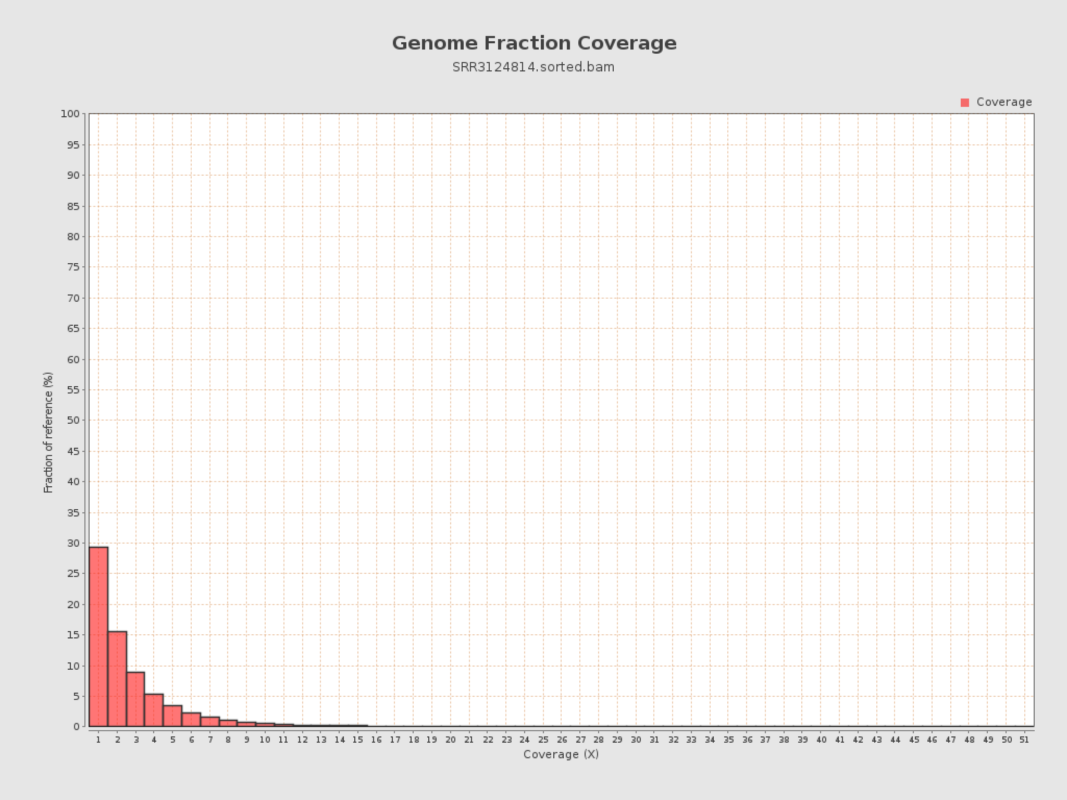
4. Results : Coverage Histogram



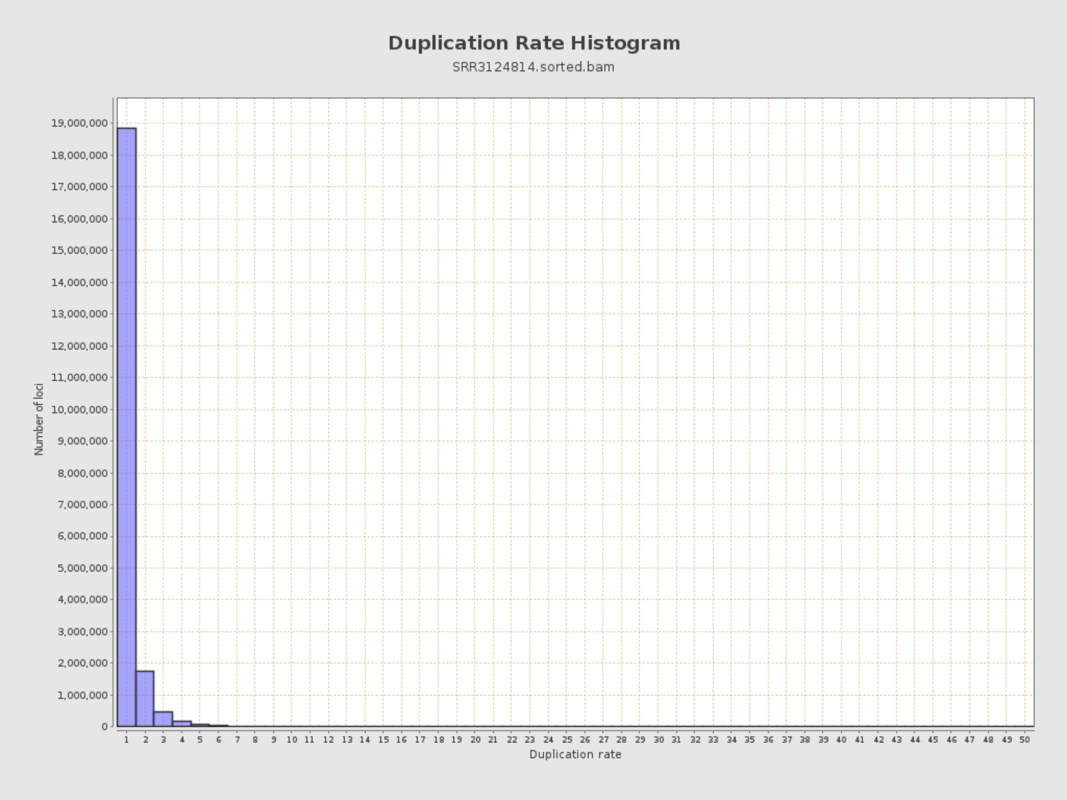
5. Results : Coverage Histogram (0-50X)



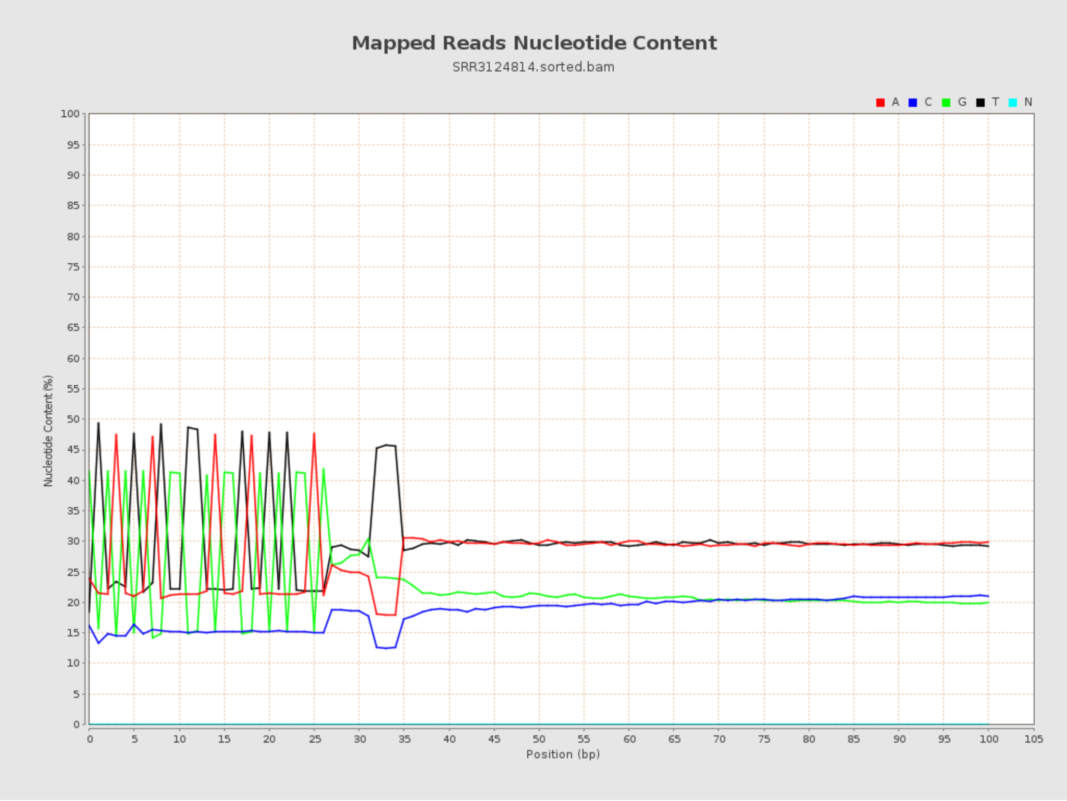
6. Results : Genome Fraction Coverage



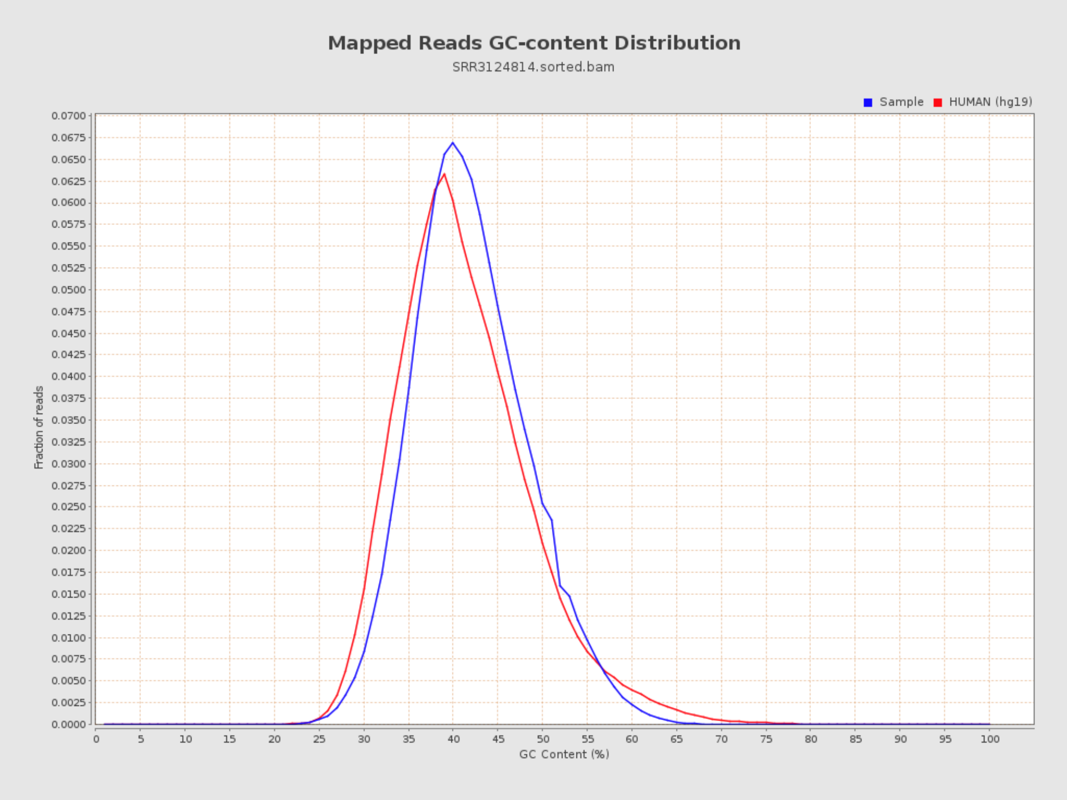
7. Results : Duplication Rate Histogram



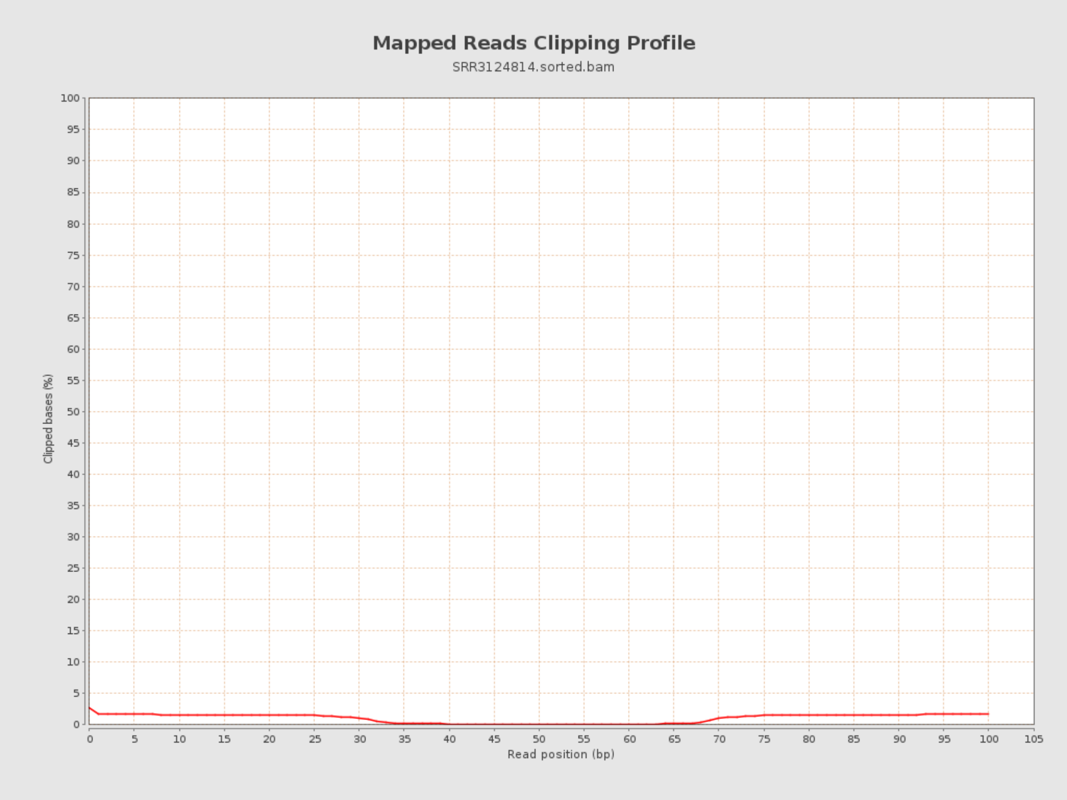
8. Results : Mapped Reads Nucleotide Content



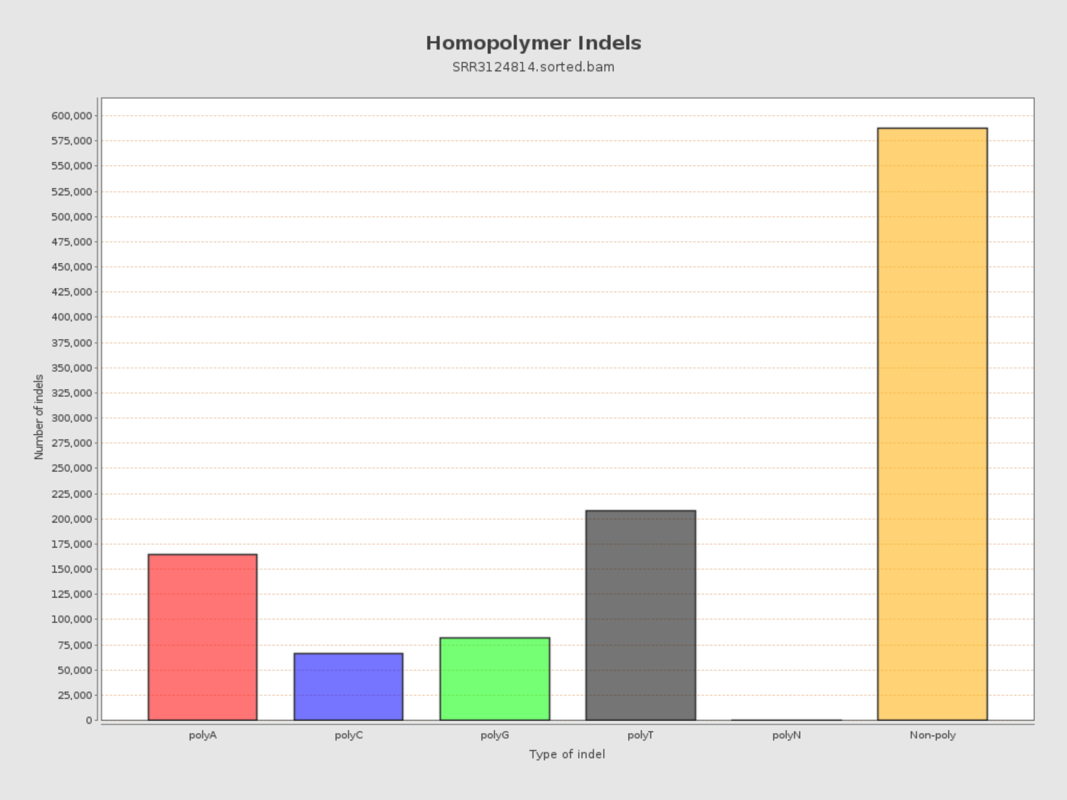
9. Results : Mapped Reads GC-content Distribution



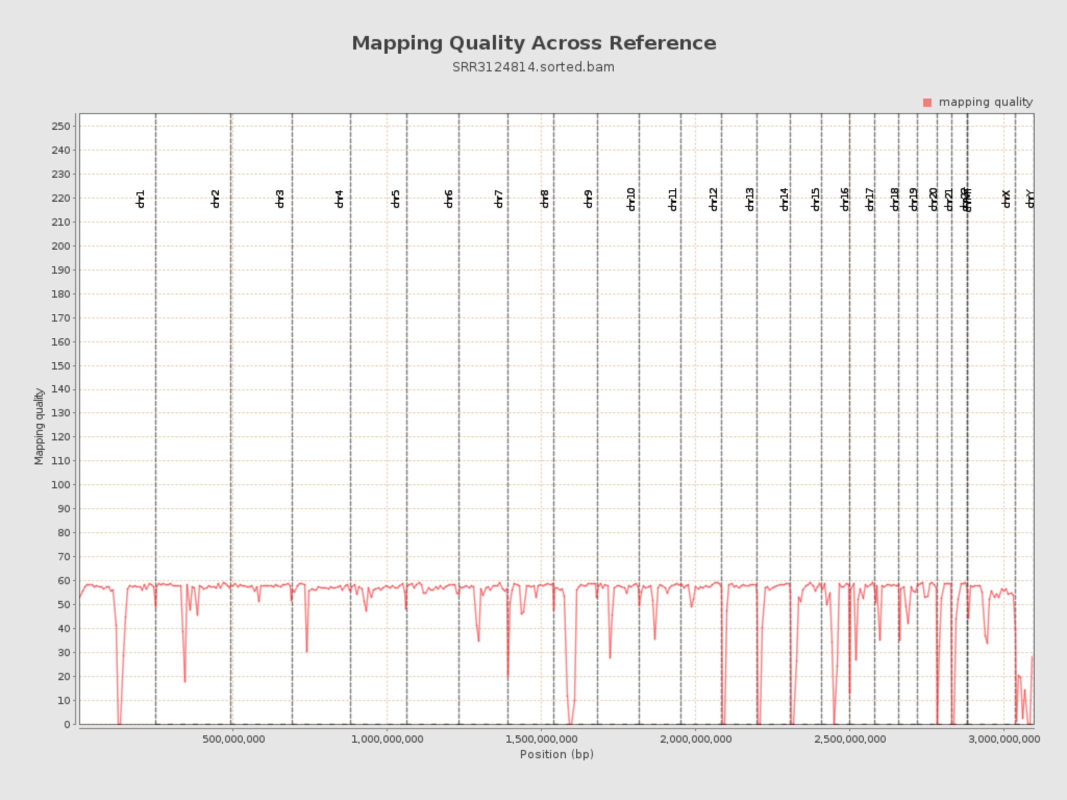
10. Results : Mapped Reads Clipping Profile



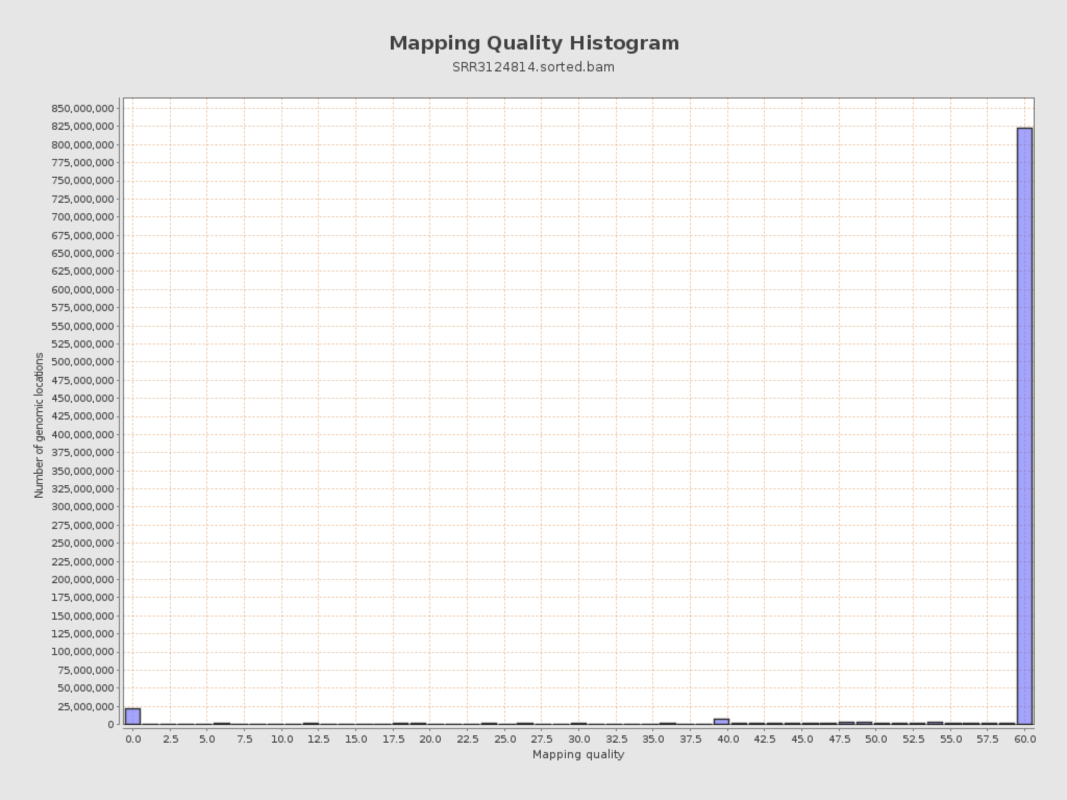
11. Results : Homopolymer Indels



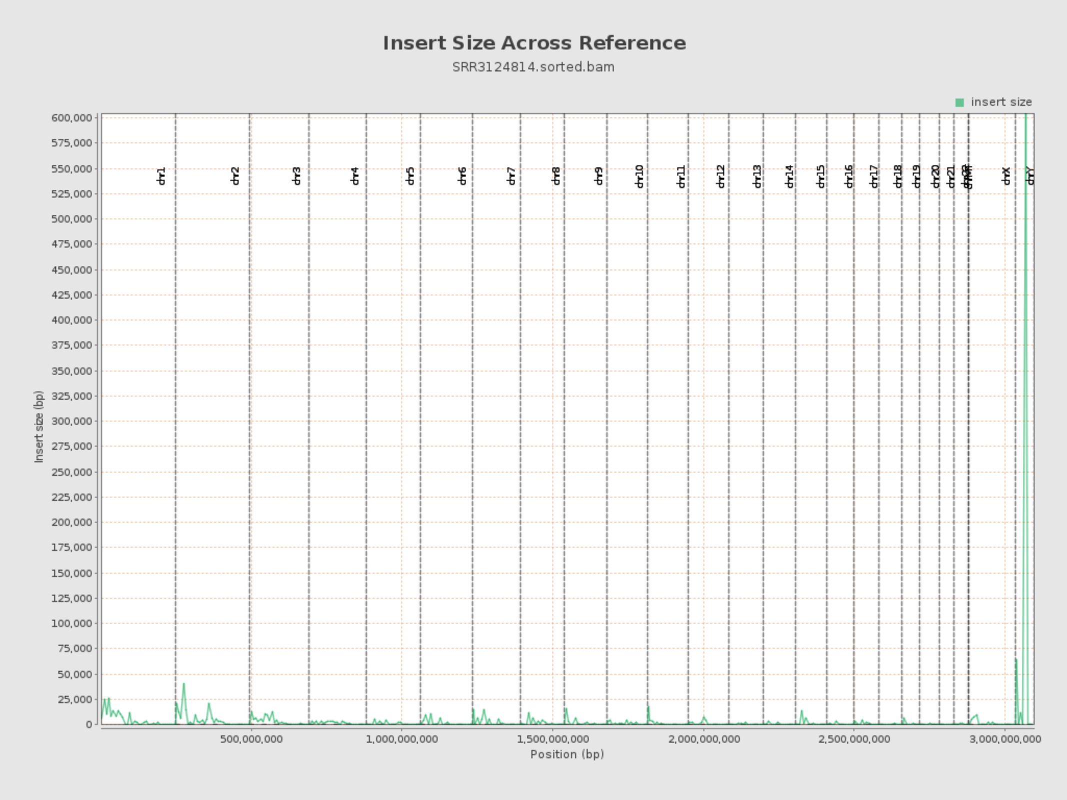
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram