Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/02 03:03:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1264614.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_SRR1264614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1264614_1.fastq.gz SRR1264614_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 02 03:03:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1264614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,055,213,826
Mapped reads	1,051,084,156 / 99.61%
Unmapped reads	4,129,670 / 0.39%
Mapped paired reads	1,051,084,156 / 99.61%
Mapped reads, first in pair	526,574,725 / 49.9%
Mapped reads, second in pair	524,509,431 / 49.71%
Mapped reads, both in pair	1,048,059,698 / 99.32%
Mapped reads, singletons	3,024,458 / 0.29%
Secondary alignments	0
Supplementary alignments	12,747,785 / 1.21%
Read min/max/mean length	30 / 100 / 100.5
Duplicated reads (estimated)	306,536,503 / 29.05%
Duplication rate	29.19%
Clipped reads	69,278,184 / 6.57%

2.2. ACGT Content

Number/percentage of A's	32,311,004,820 / 30.96%
Number/percentage of C's	19,770,528,431 / 18.94%
Number/percentage of T's	32,226,809,803 / 30.88%
Number/percentage of G's	20,014,307,106 / 19.18%
Number/percentage of N's	50,900,808 / 0.05%

GC Percentage	38.12%

2.3. Coverage

Mean	33.7234
Standard Deviation	27.5108

2.4. Mapping Quality

Mean Mapping Quality	54.52

2.5. Insert size

Mean	181,822.87
Standard Deviation	4,077,857.8
P25/Median/P75	270 / 304 / 341

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	380,678,203
Insertions	10,704,197
Mapped reads with at least one insertion	1%
Deletions	10,521,501
Mapped reads with at least one deletion	0.98%
Homopolymer indels	47.05%

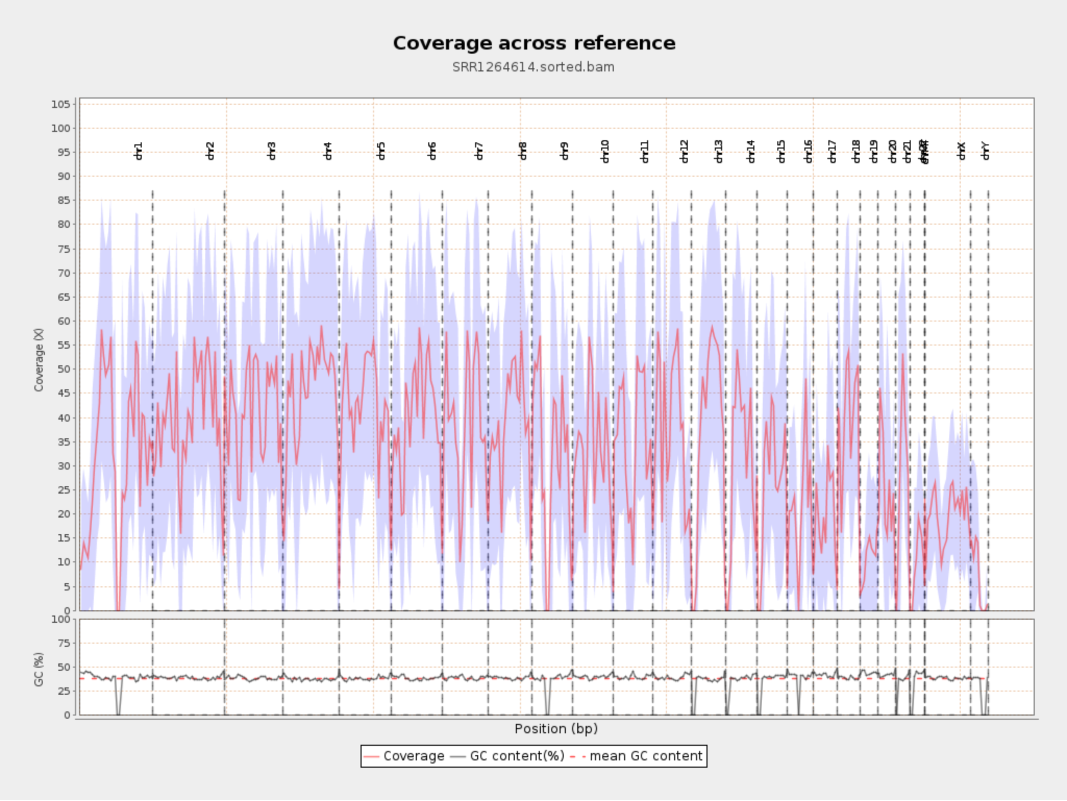
2.7. Chromosome stats

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

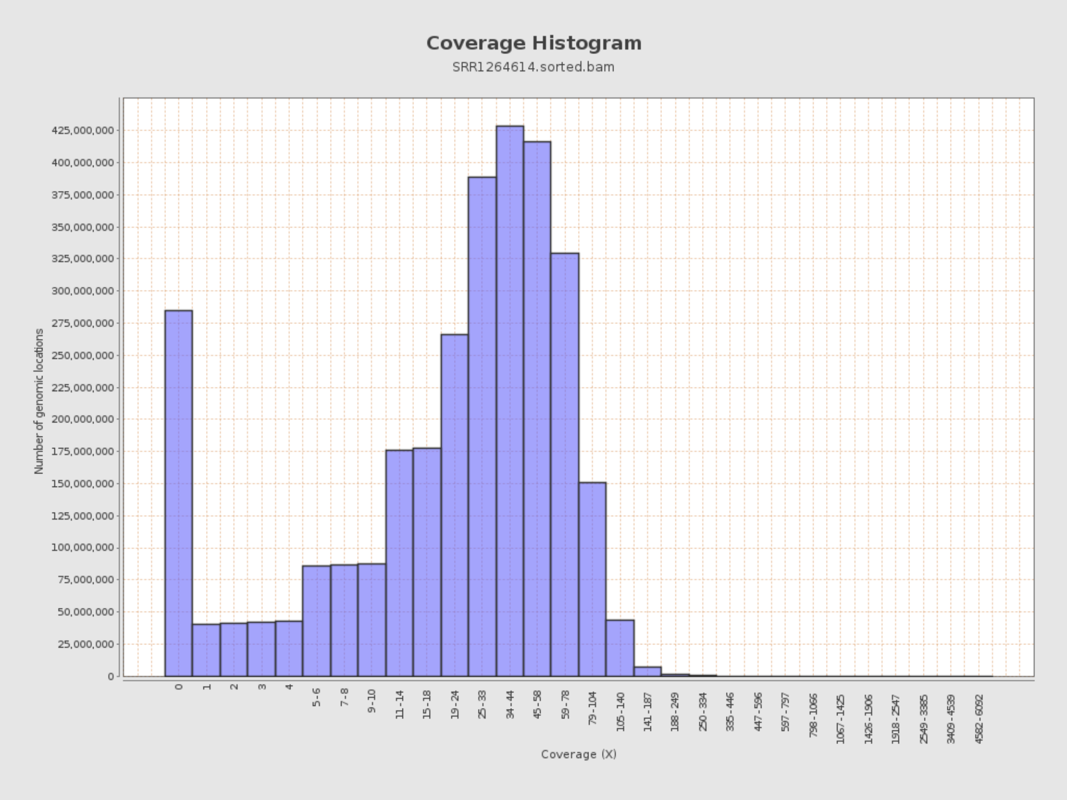
		bases	coverage	deviation
chr1	249250621	8008950338	32.1321	28.1802
chr2	243199373	9611977340	39.523	26.4498
chr3	198022430	8217032781	41.4955	25.9823
chr4	191154276	8776156716	45.9114	26.8802
chr5	180915260	7604976648	42.0361	26.3238
chr6	171115067	6989501783	40.8468	26.7927
chr7	159138663	6084296518	38.2327	28.8165
chr8	146364022	5778891529	39.483	26.1052
chr9	141213431	4364954645	30.9103	29.0256
chr10	135534747	4528203363	33.4099	24.6888
chr11	135006516	4786580938	35.4544	27.3224
chr12	133851895	4998417711	37.3429	28.1751
chr13	115169878	4477805436	38.88	29.8046
chr14	107349540	3327720072	30.9989	27.8855
chr15	102531392	2751112611	26.8319	26.4988
chr16	90354753	1847226102	20.4441	21.7221
chr17	81195210	1565194150	19.2769	20.7038
chr18	78077248	3124603416	40.0194	26.4041
chr19	59128983	623210498	10.5398	13.6125
chr20	63025520	1546247213	24.5337	26.1749
chr21	48129895	1397944644	29.0452	32.6387
chr22	51304566	495780655	9.6635	15.1667
chrMT	16571	384819	23.2224	7.0835
chrX	155270560	3083600631	19.8595	13.9818

chrY	59373566	406417306	6.8451	13.1254

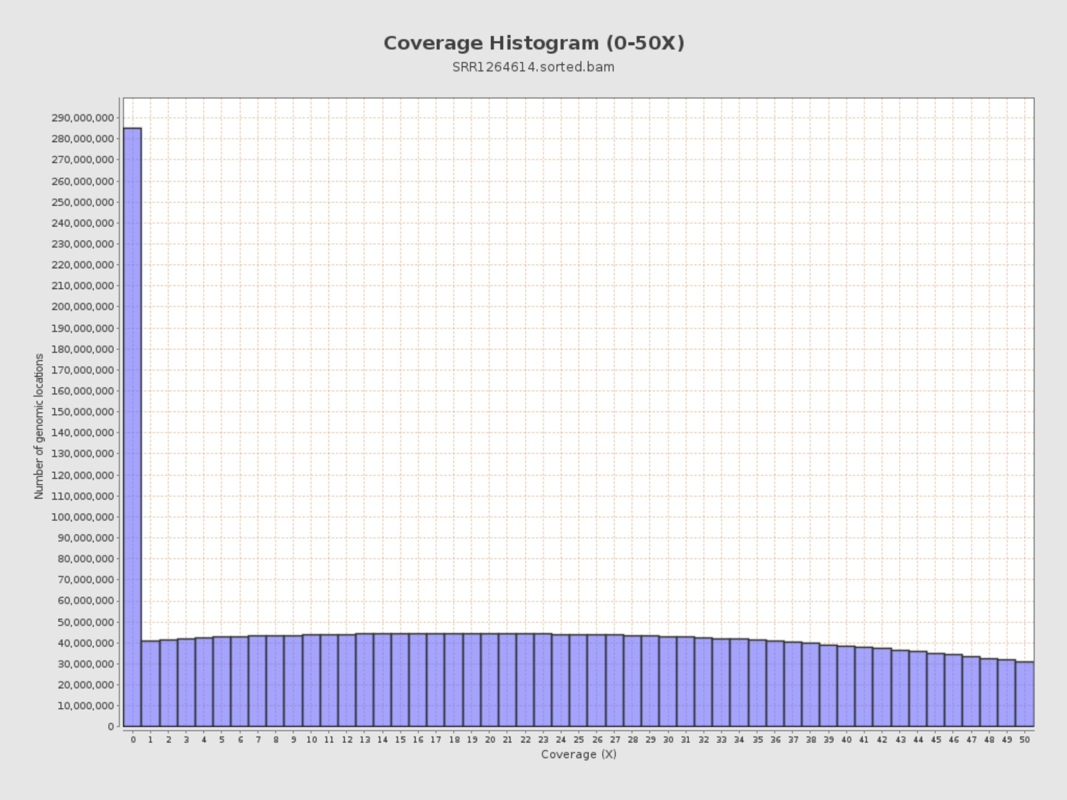
3. Results : Coverage across reference



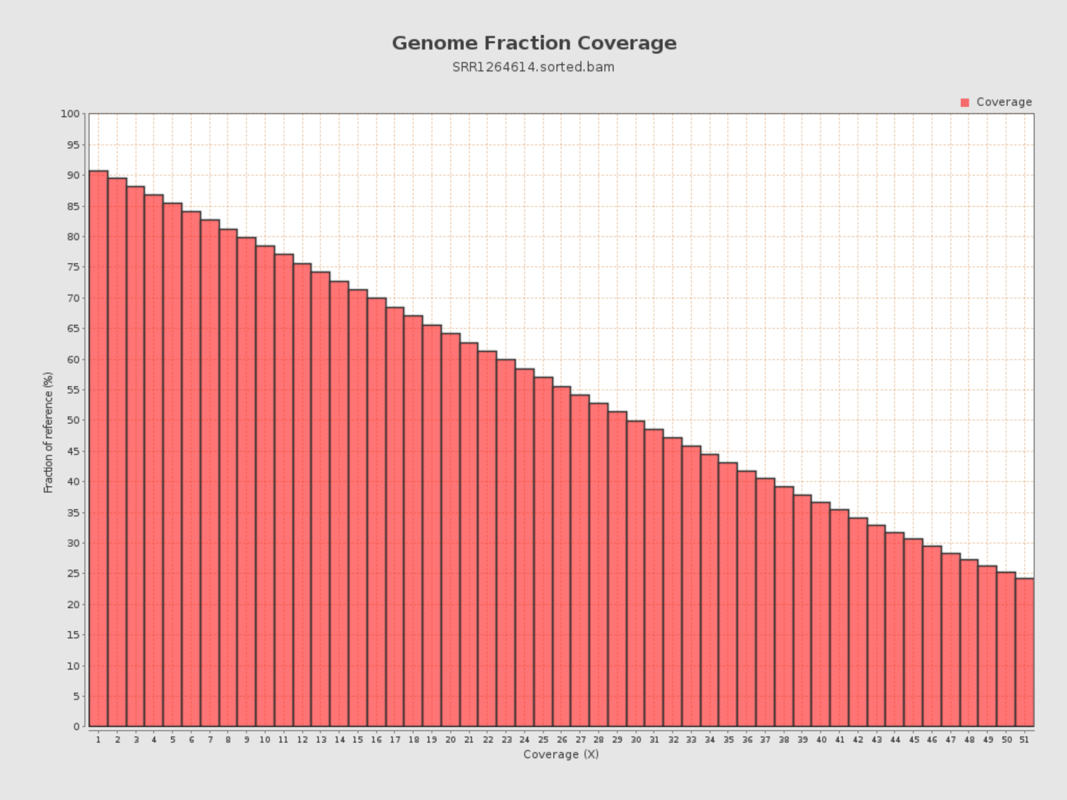
4. Results : Coverage Histogram



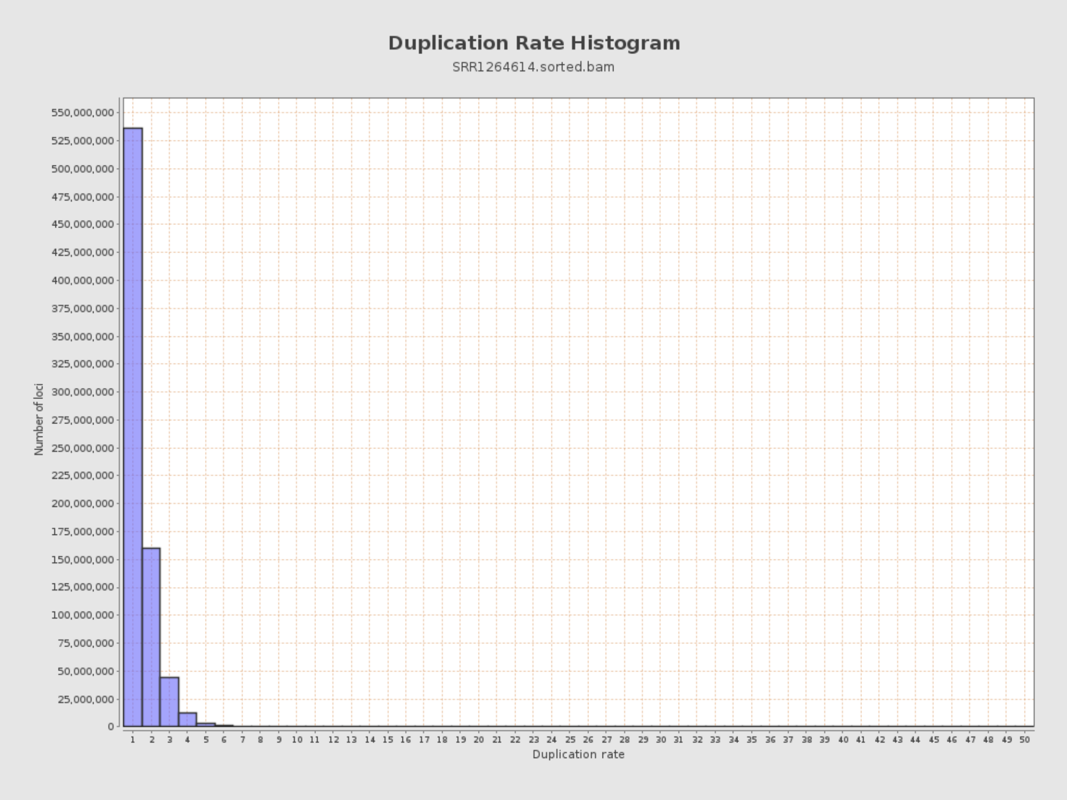
5. Results : Coverage Histogram (0-50X)



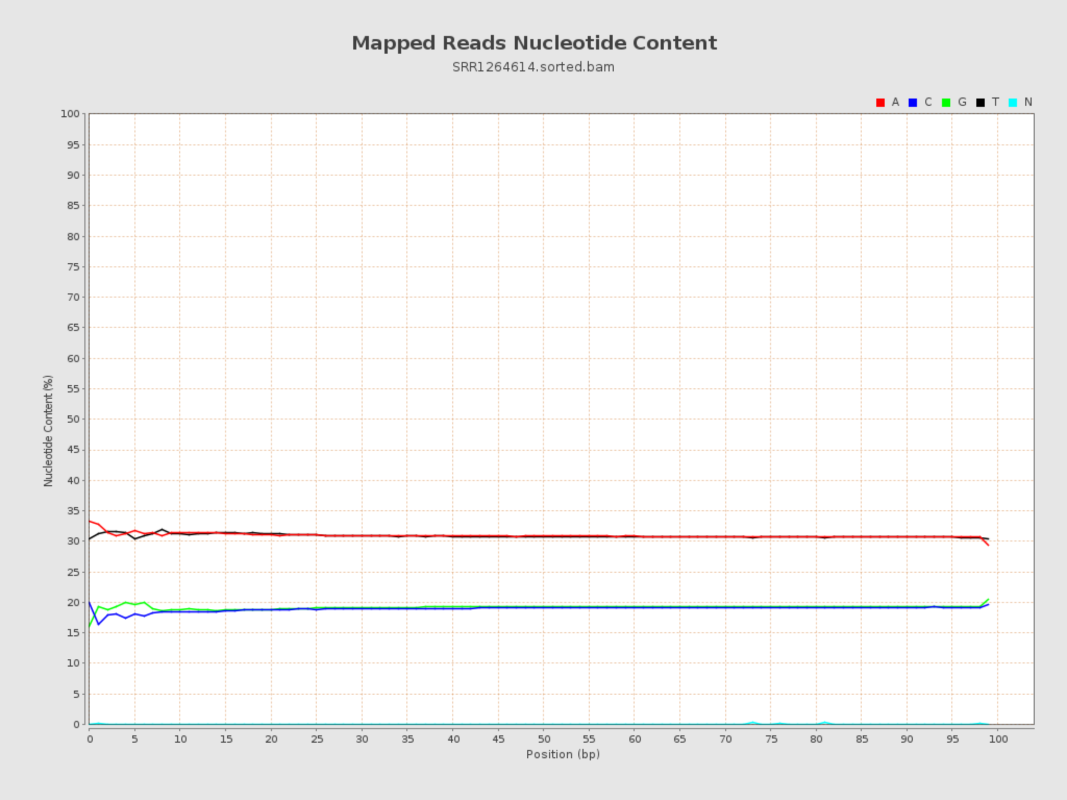
6. Results : Genome Fraction Coverage



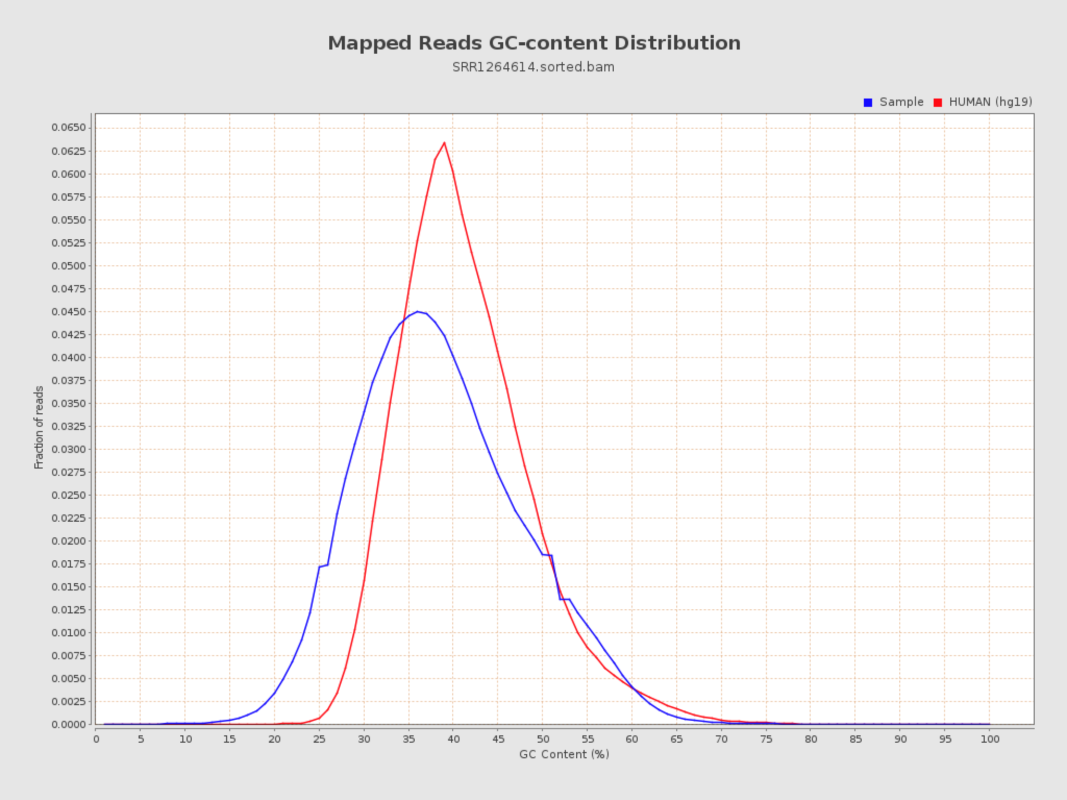
7. Results : Duplication Rate Histogram



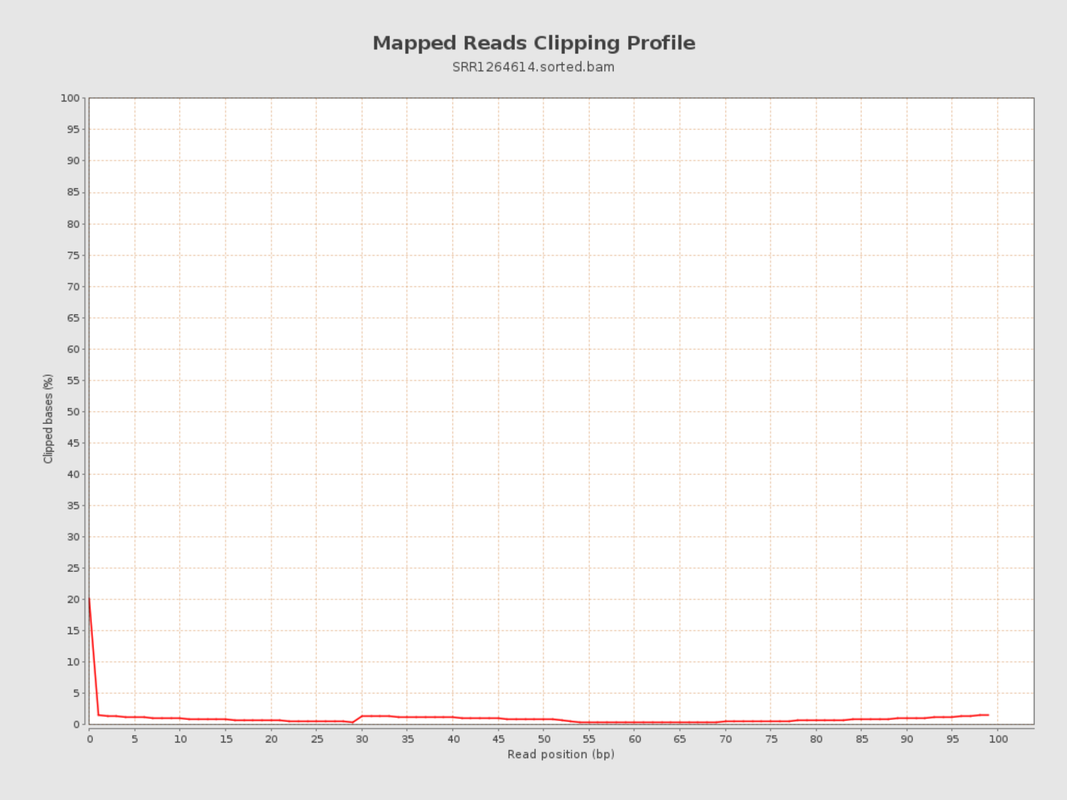
8. Results : Mapped Reads Nucleotide Content



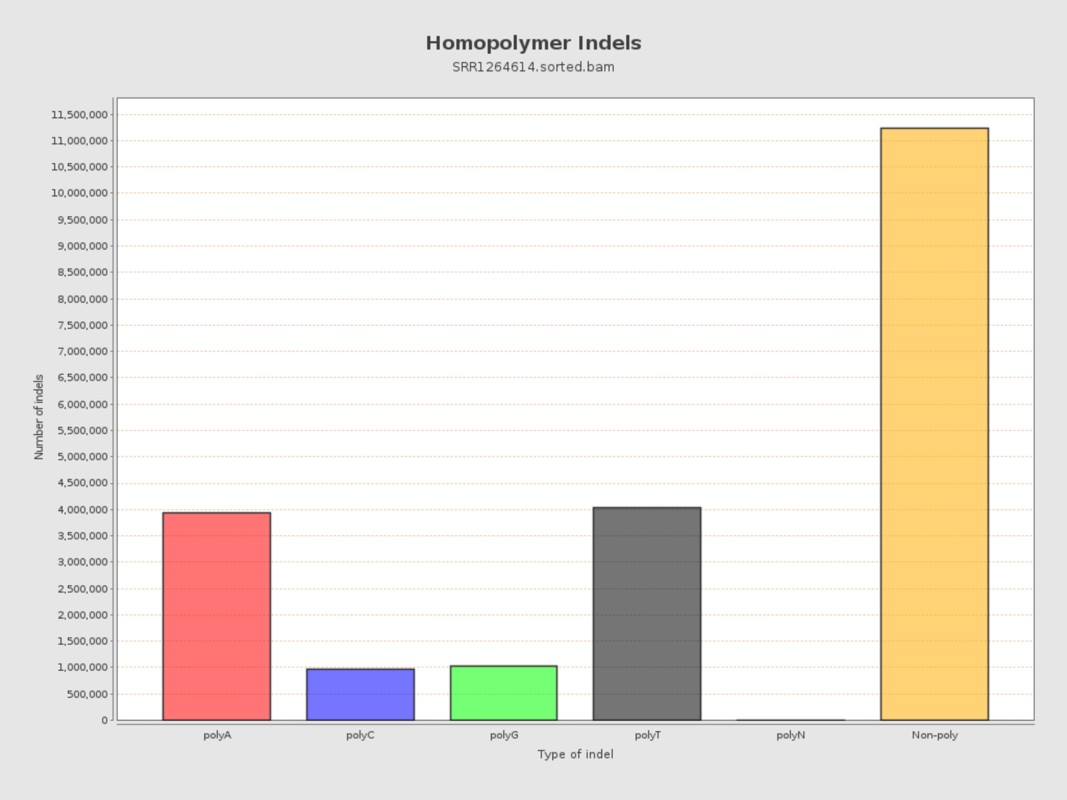
9. Results : Mapped Reads GC-content Distribution



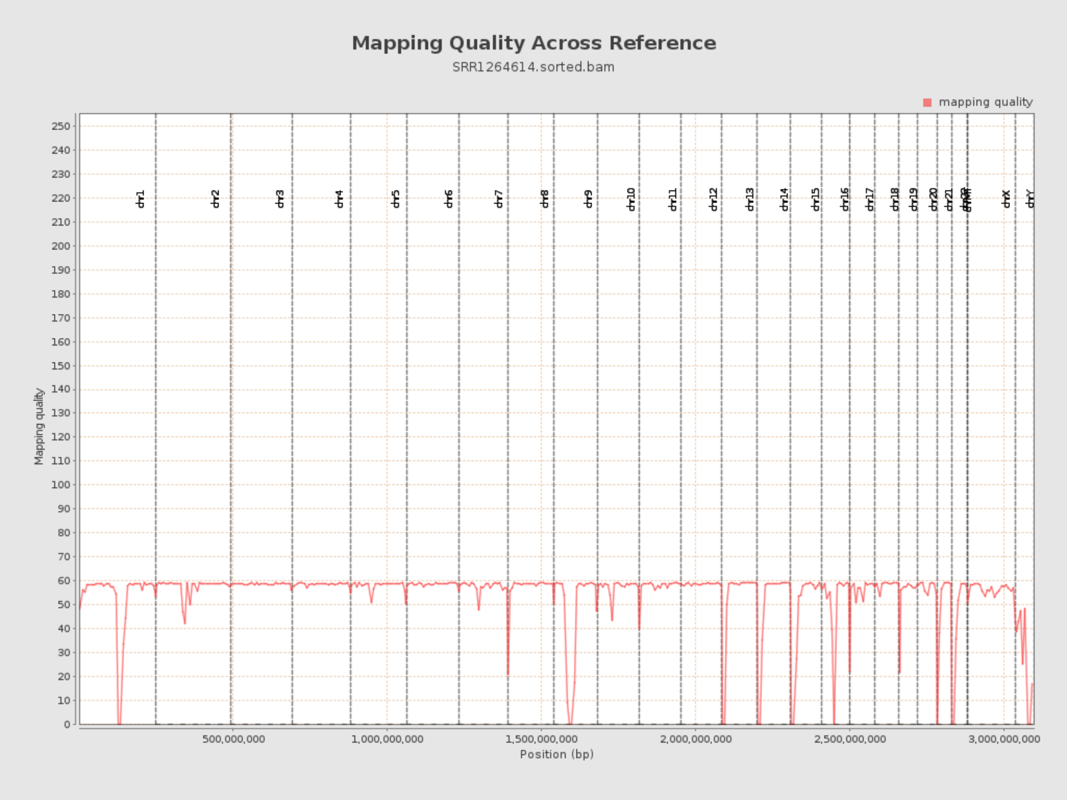
10. Results : Mapped Reads Clipping Profile



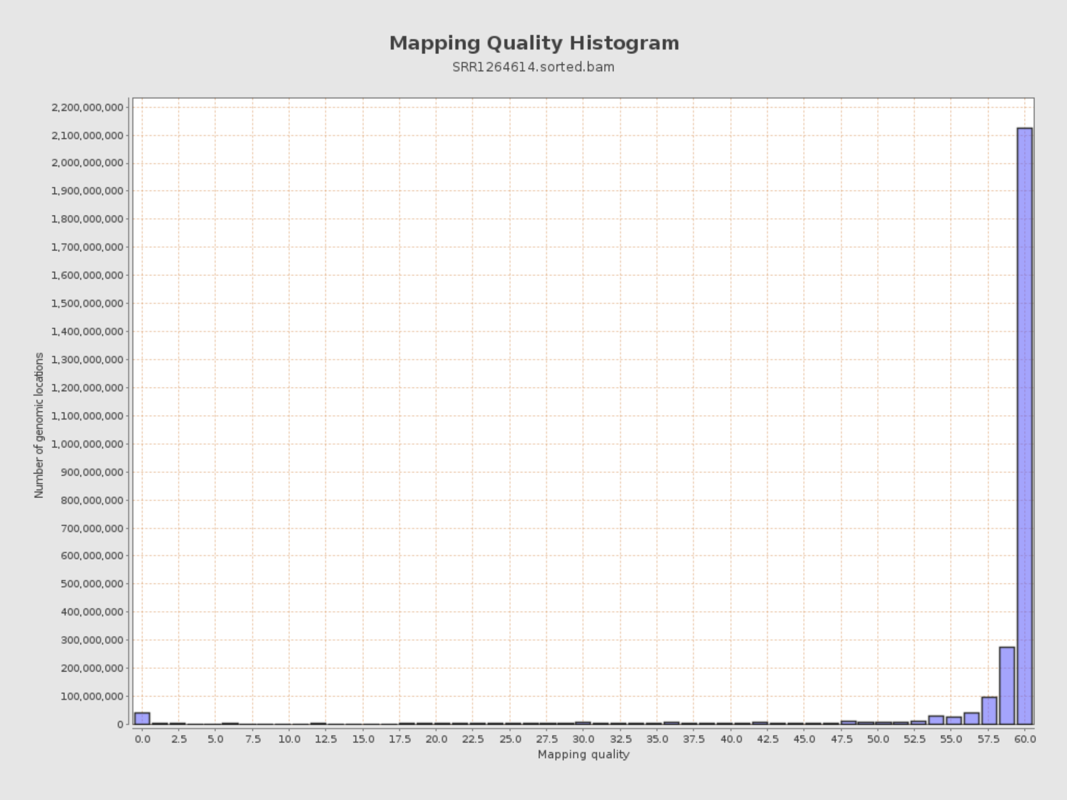
11. Results : Homopolymer Indels



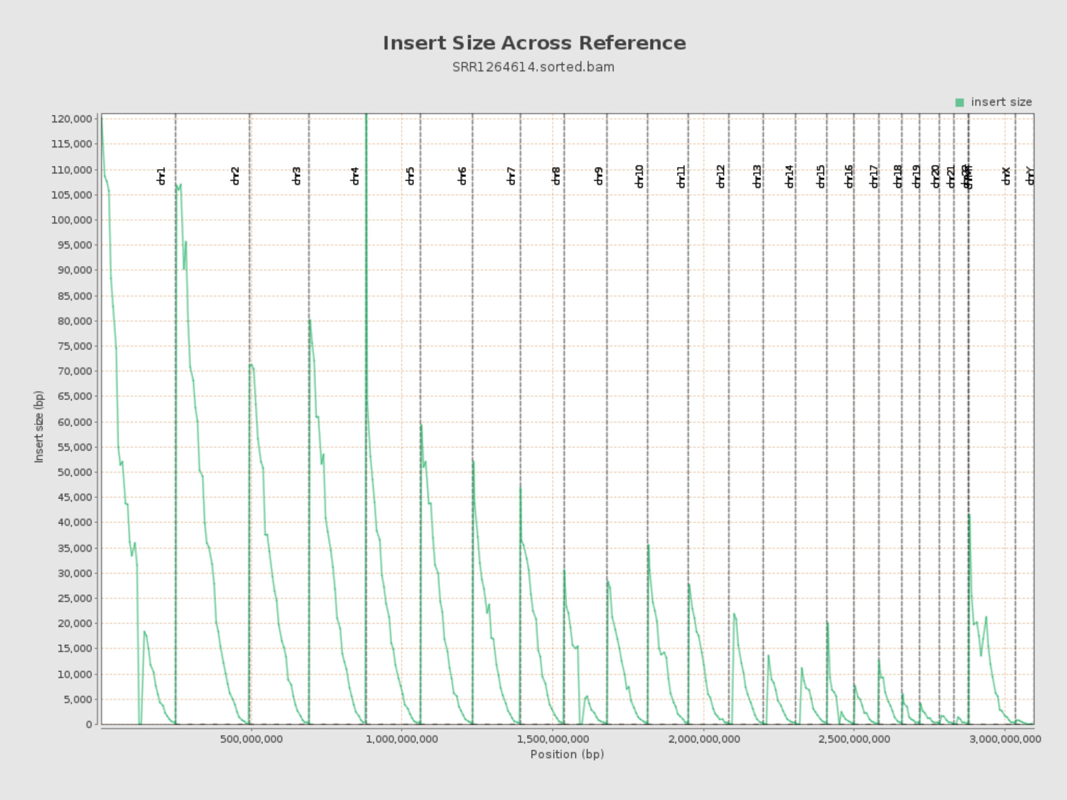
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram