Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 04:06:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124910.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_SRR3124910 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124910_1.fastq.gz SRR3124910_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 04:06:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124910.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,075,232
Mapped reads	5,013,313 / 98.78%
Unmapped reads	61,919 / 1.22%
Mapped paired reads	5,013,313 / 98.78%
Mapped reads, first in pair	2,522,249 / 49.7%
Mapped reads, second in pair	2,491,064 / 49.08%
Mapped reads, both in pair	4,979,142 / 98.11%
Mapped reads, singletons	34,171 / 0.67%
Secondary alignments	0
Supplementary alignments	49,422 / 0.97%
Read min/max/mean length	30 / 151 / 151.47
Duplicated reads (estimated)	955,444 / 18.83%
Duplication rate	13.65%
Clipped reads	2,897,566 / 57.09%

2.2. ACGT Content

Number/percentage of A's	194,375,193 / 28.92%
Number/percentage of C's	131,229,862 / 19.52%
Number/percentage of T's	197,895,613 / 29.44%
Number/percentage of G's	148,704,253 / 22.12%
Number/percentage of N's	303 / 0%

GC Percentage	41.64%

2.3. Coverage

Mean	0.2173
Standard Deviation	4.1791

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	40,145.05
Standard Deviation	1,905,813.06
P25/Median/P75	154 / 206 / 286

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	5,533,128
Insertions	100,899
Mapped reads with at least one insertion	1.9%
Deletions	204,937
Mapped reads with at least one deletion	3.94%
Homopolymer indels	48.19%

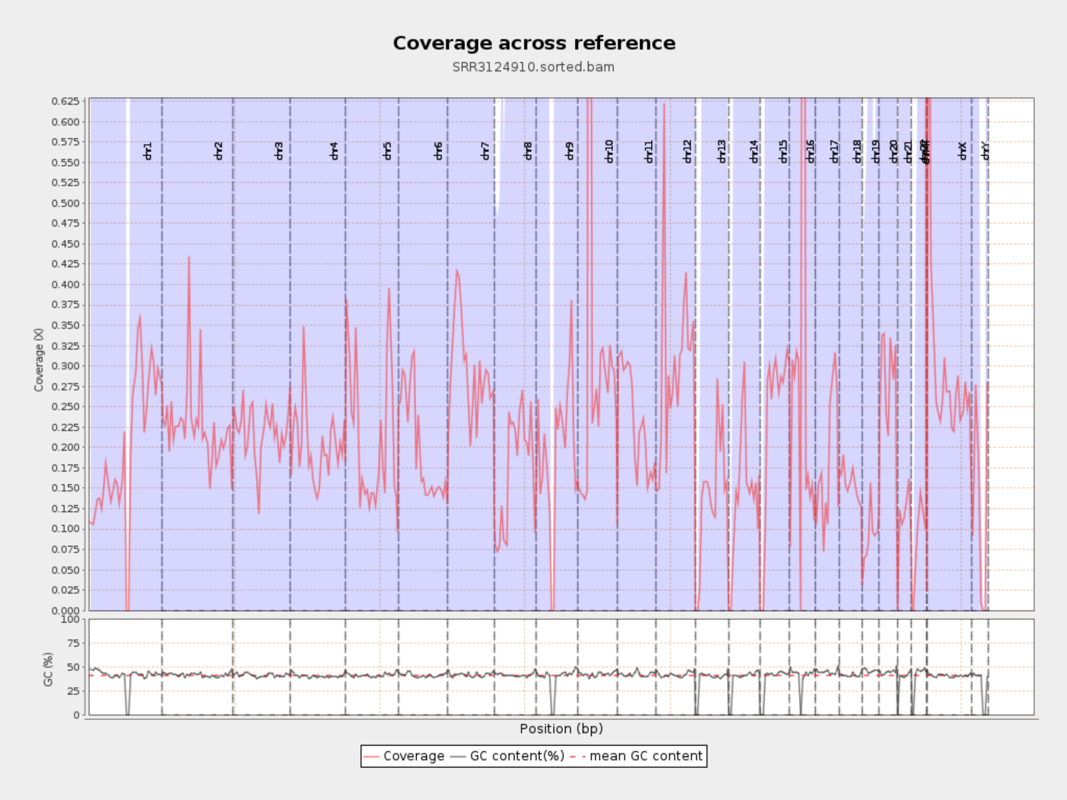
2.7. Chromosome stats

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

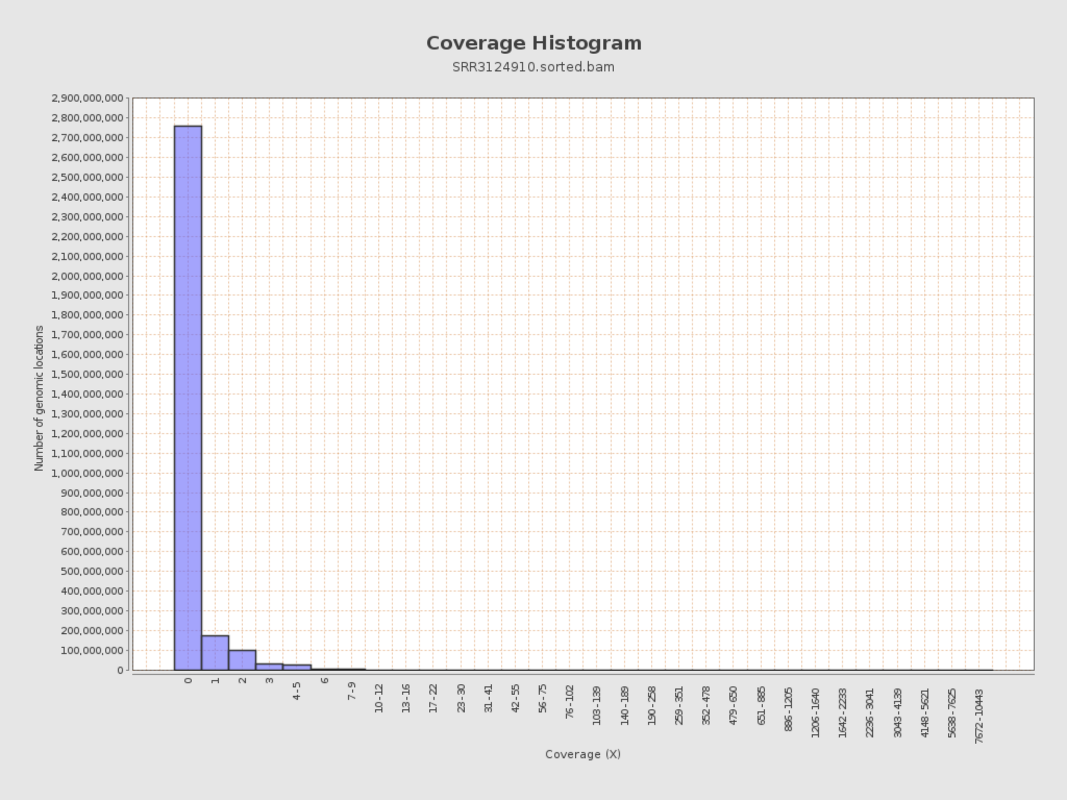
		bases	coverage	deviation
chr1	249250621	49202092	0.1974	1.2812
chr2	243199373	55247627	0.2272	2.1703
chr3	198022430	43180024	0.2181	0.8722
chr4	191154276	38558632	0.2017	1.5767
chr5	180915260	38432755	0.2124	0.769
chr6	171115067	34176557	0.1997	0.9054
chr7	159138663	47280718	0.2971	2.1861
chr8	146364022	25477881	0.1741	0.7389
chr9	141213431	27922936	0.1977	2.0763
chr10	135534747	43756115	0.3228	16.6543
chr11	135006516	31321216	0.232	2.6304
chr12	133851895	39955276	0.2985	0.9453
chr13	115169878	15810137	0.1373	0.5883
chr14	107349540	15342267	0.1429	0.632
chr15	102531392	24056651	0.2346	0.8149
chr16	90354753	29396891	0.3253	10.5723
chr17	81195210	14862298	0.183	1.1601
chr18	78077248	12244851	0.1568	2.0376
chr19	59128983	5426547	0.0918	0.9192
chr20	63025520	17881045	0.2837	0.9978
chr21	48129895	5404941	0.1123	0.9312
chr22	51304566	4273374	0.0833	0.6123
chrMT	16571	316288	19.0868	12.0419
chrX	155270560	45788543	0.2949	1.3543

chrY	59373566	7311489	0.1231	2.5354

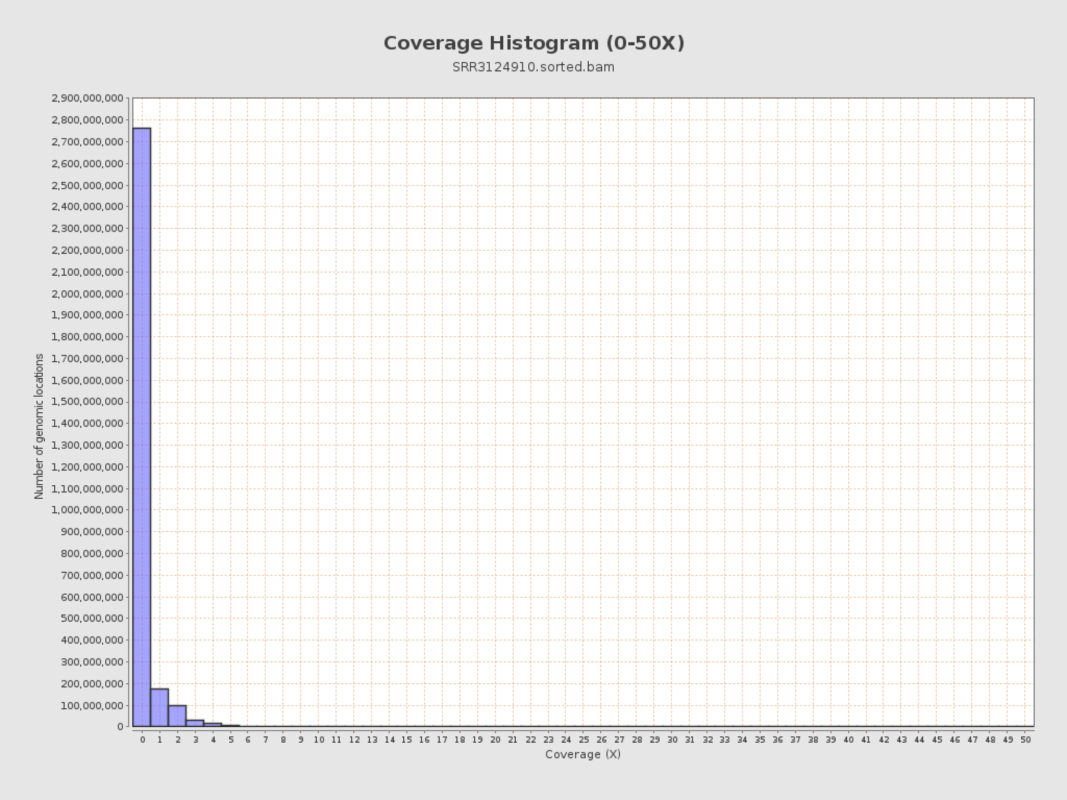
3. Results : Coverage across reference



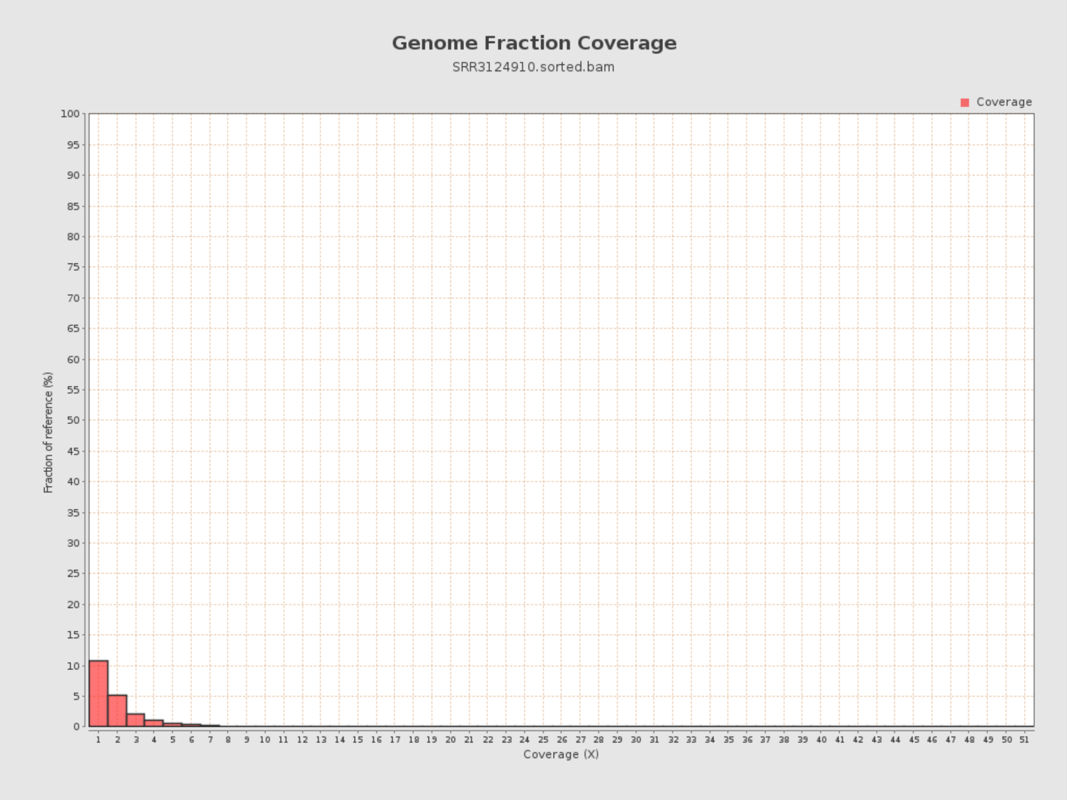
4. Results : Coverage Histogram



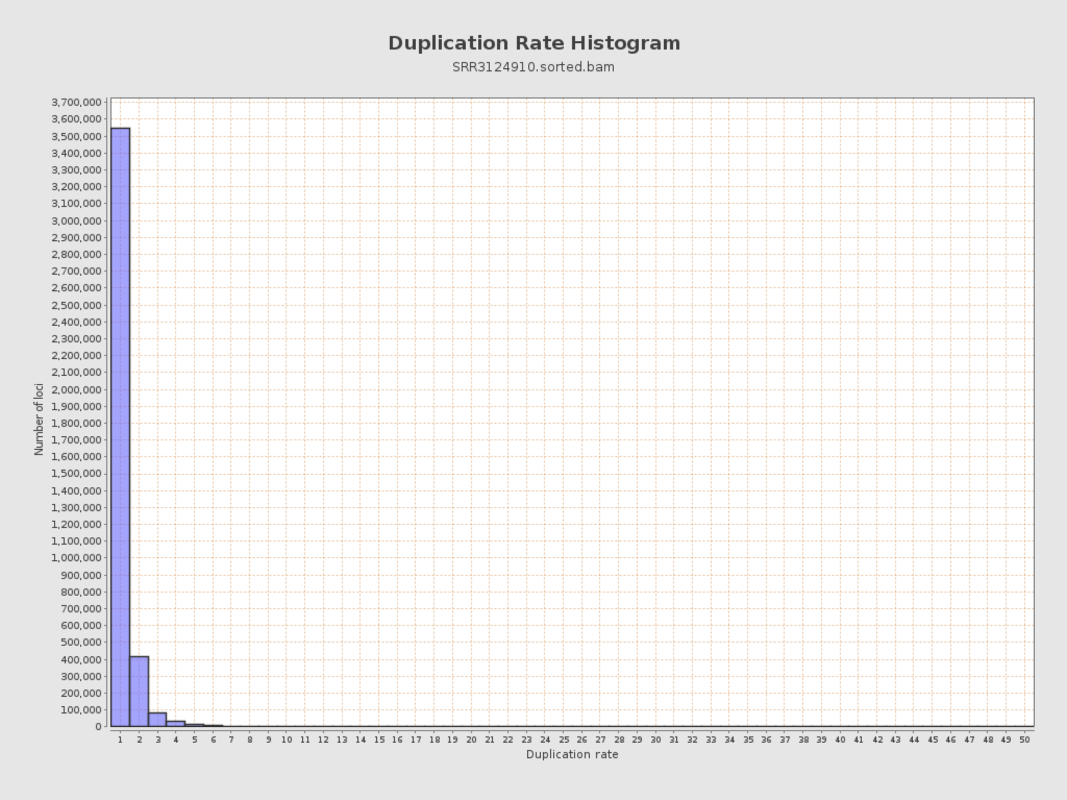
5. Results : Coverage Histogram (0-50X)



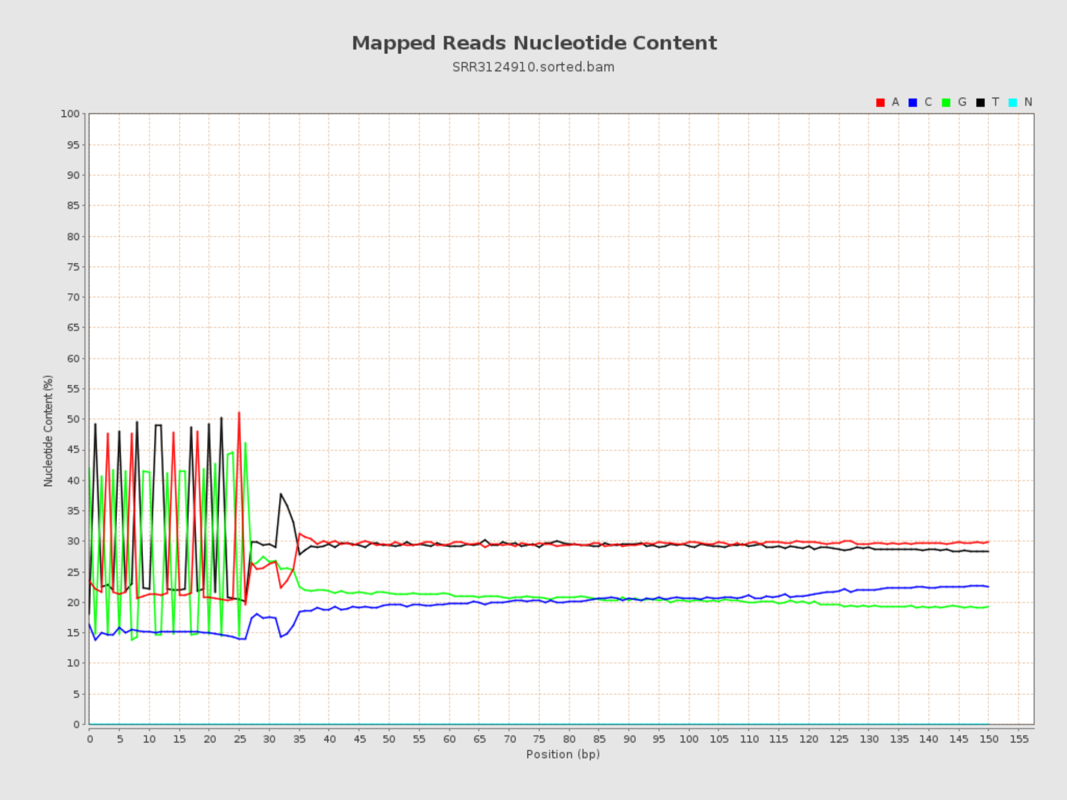
6. Results : Genome Fraction Coverage



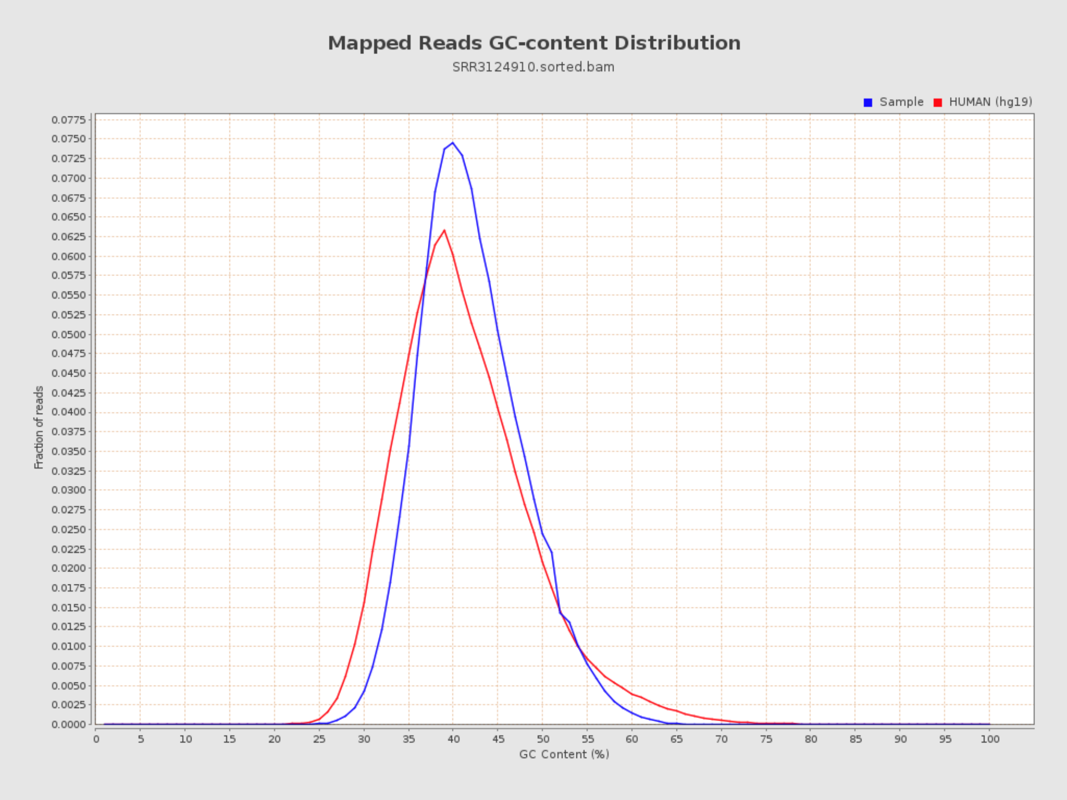
7. Results : Duplication Rate Histogram



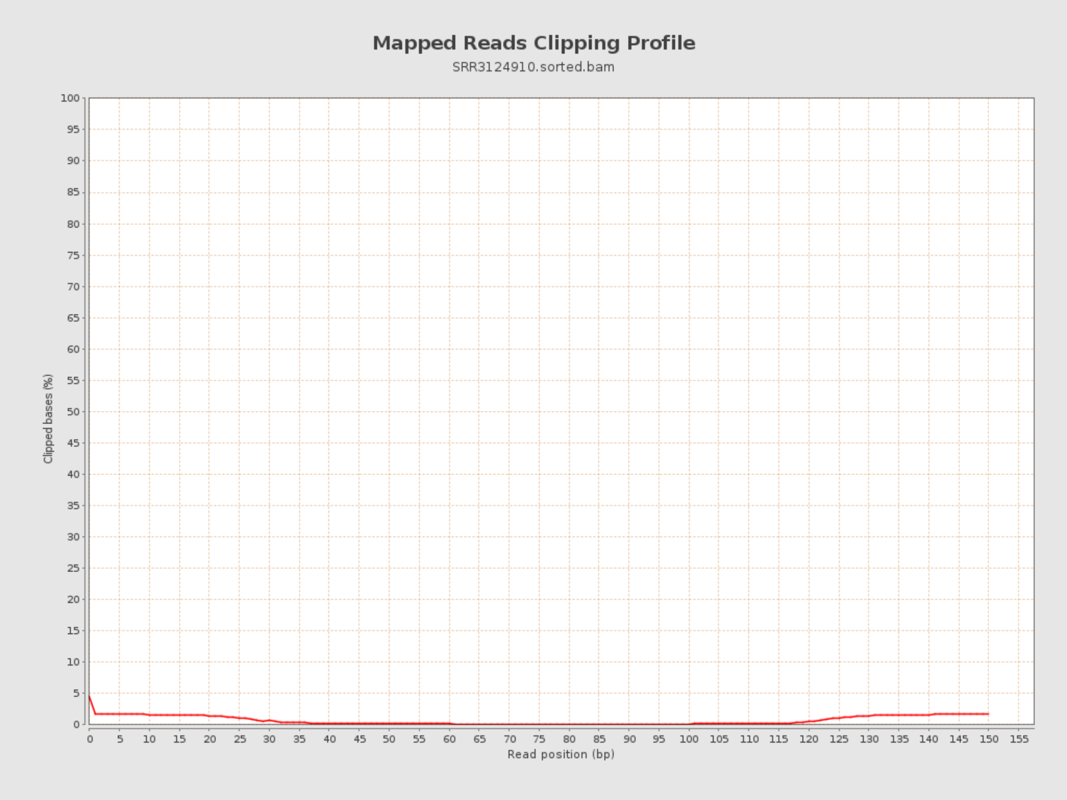
8. Results : Mapped Reads Nucleotide Content



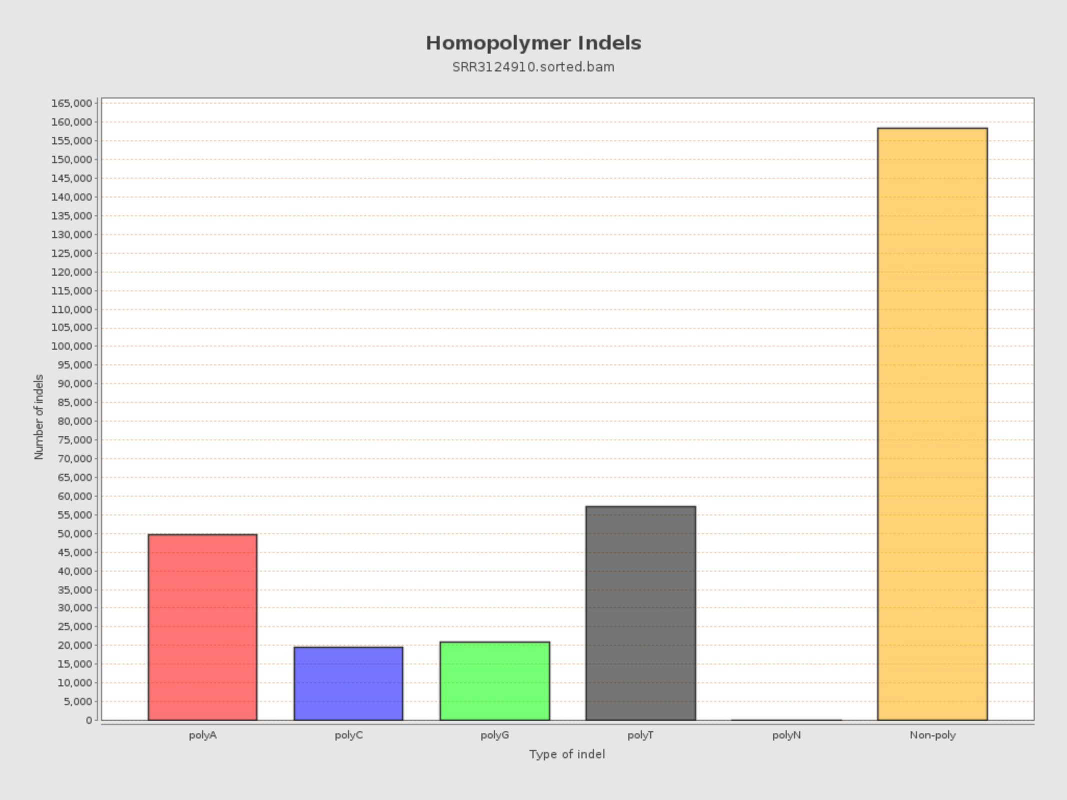
9. Results : Mapped Reads GC-content Distribution



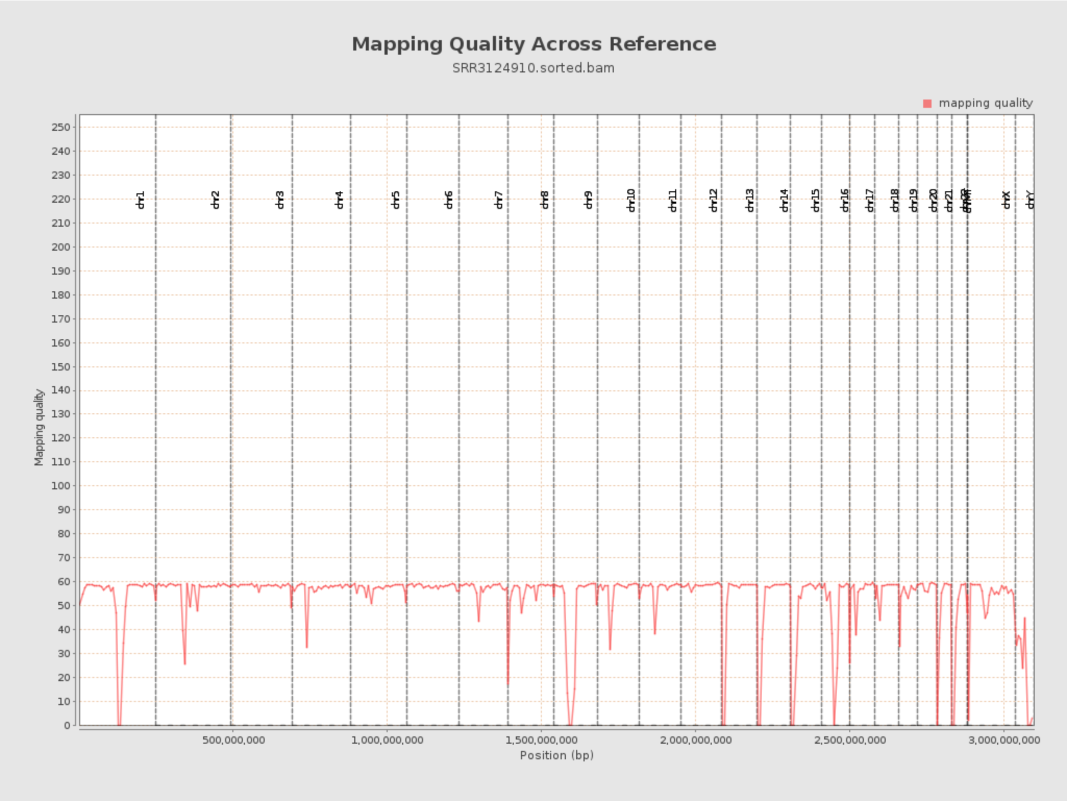
10. Results : Mapped Reads Clipping Profile



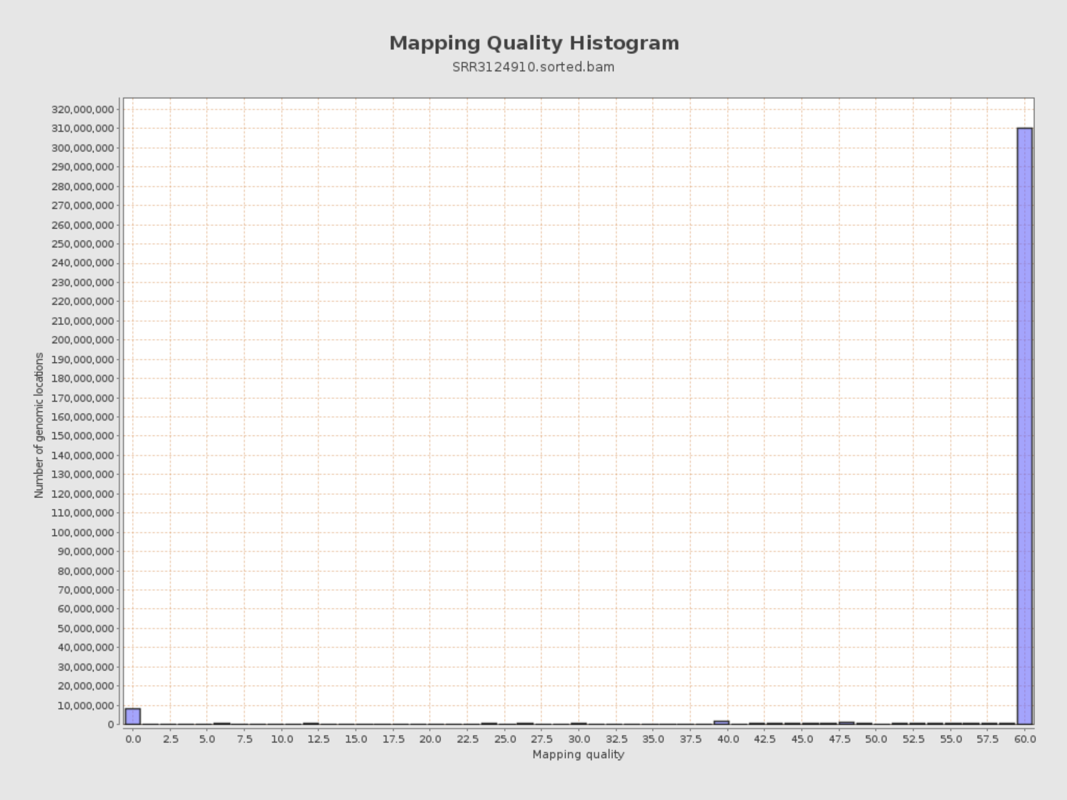
11. Results : Homopolymer Indels



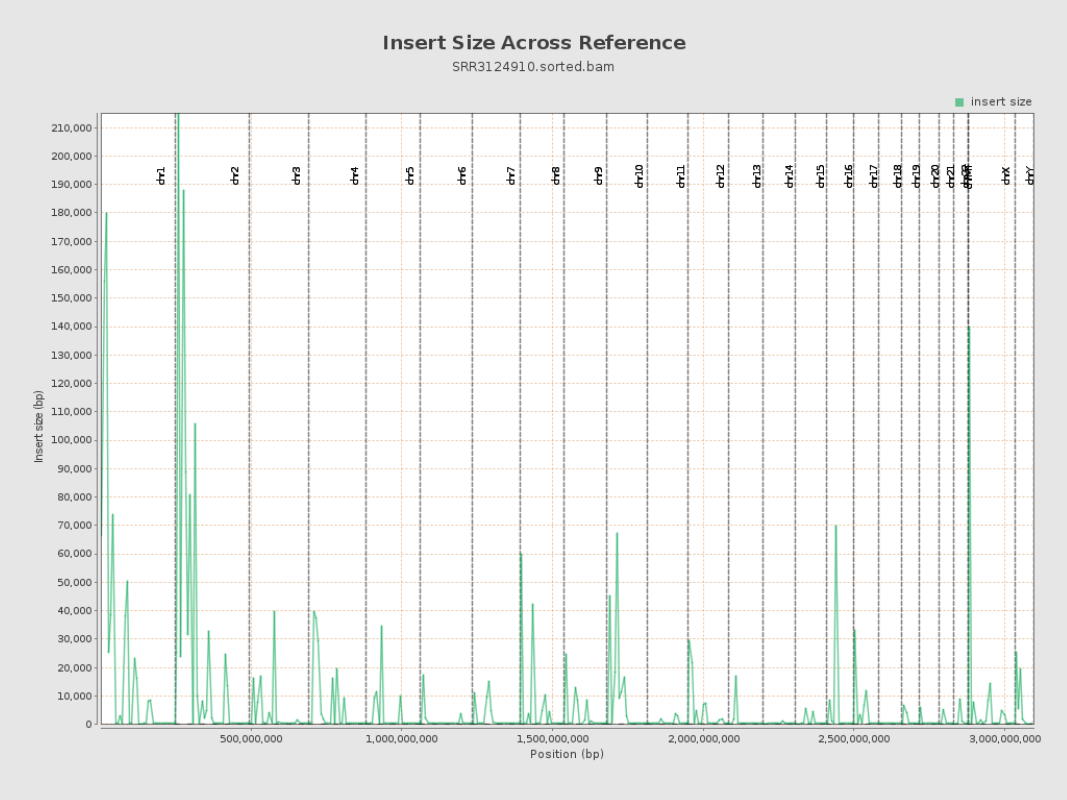
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram