Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 22:31:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504614.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_SRR504614 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504614_1.fastq.gz SRR504614_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 22:31:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504614.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	481,467,640
Mapped reads	320,458,430 / 66.56%
Unmapped reads	161,009,210 / 33.44%
Mapped paired reads	320,458,430 / 66.56%
Mapped reads, first in pair	160,535,647 / 33.34%
Mapped reads, second in pair	159,922,783 / 33.22%
Mapped reads, both in pair	318,362,214 / 66.12%
Mapped reads, singletons	2,096,216 / 0.44%
Secondary alignments	0
Supplementary alignments	2,066,647 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	88,491,680 / 18.38%
Duplication rate	23.99%
Clipped reads	15,587,661 / 3.24%

2.2. ACGT Content

Number/percentage of A's	8,228,898,595 / 25.86%
Number/percentage of C's	7,612,749,633 / 23.92%
Number/percentage of T's	8,266,730,350 / 25.98%
Number/percentage of G's	7,709,726,776 / 24.23%
Number/percentage of N's	1,767,210 / 0.01%

GC Percentage	48.15%

2.3. Coverage

Mean	10.2814
Standard Deviation	26.522

2.4. Mapping Quality

Mean Mapping Quality	53.76

2.5. Insert size

Mean	25,519.38
Standard Deviation	1,546,446.53
P25/Median/P75	173 / 207 / 264

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	156,726,517
Insertions	2,368,802
Mapped reads with at least one insertion	0.72%
Deletions	3,125,972
Mapped reads with at least one deletion	0.95%
Homopolymer indels	40.1%

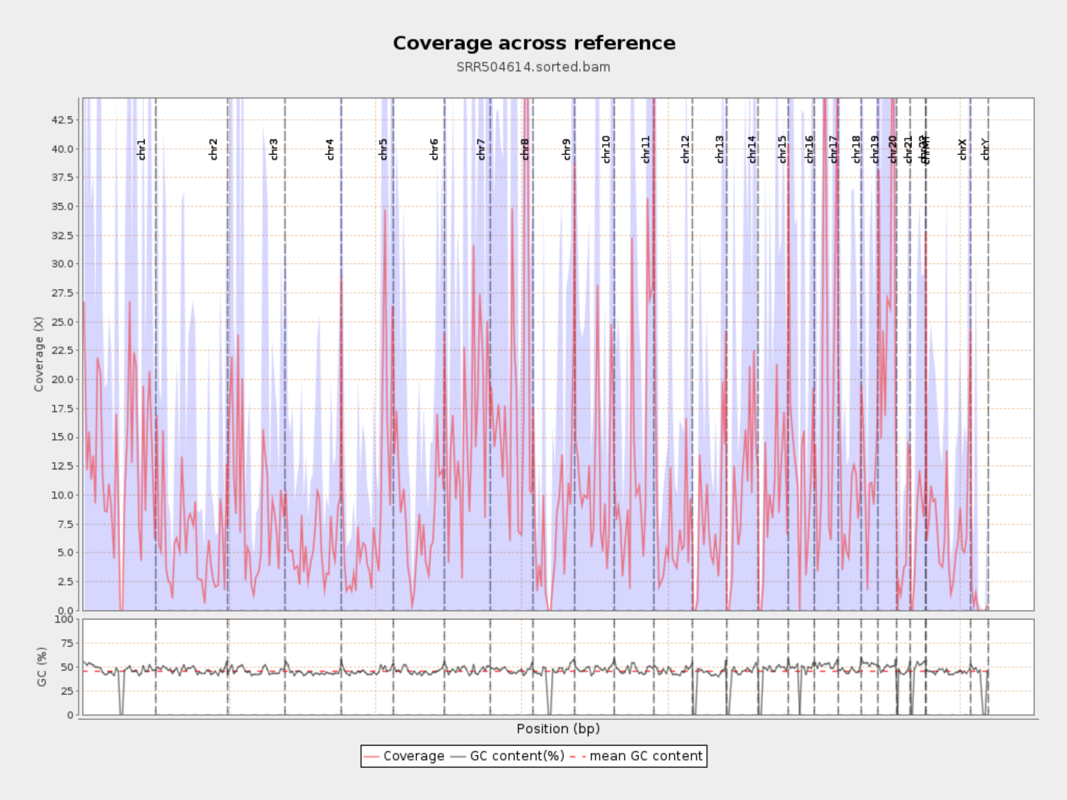
2.7. Chromosome stats

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

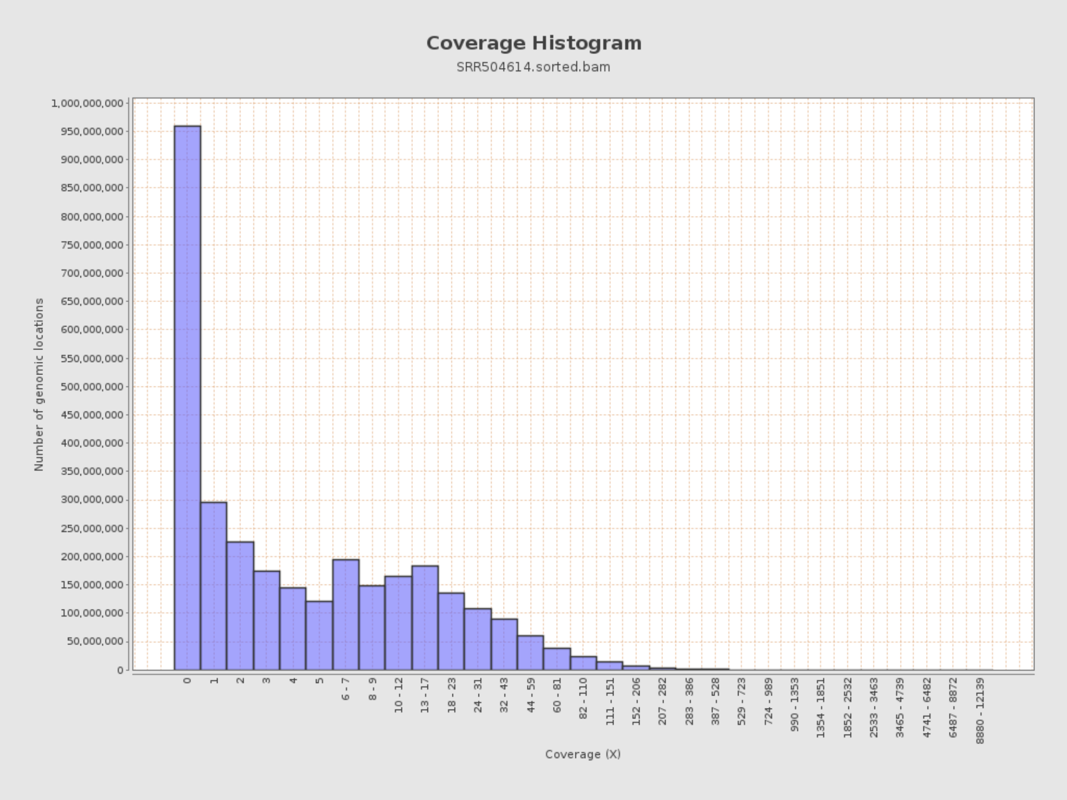
		bases	coverage	deviation
chr1	249250621	3227768870	12.9499	25.864
chr2	243199373	1421382596	5.8445	15.5323
chr3	198022430	1797907105	9.0793	24.7037
chr4	191154276	1073289942	5.6148	10.6529
chr5	180915260	1551884064	8.578	24.6309
chr6	171115067	1348824059	7.8826	15.3262
chr7	159138663	2545680138	15.9966	29.6349
chr8	146364022	2867541690	19.5918	46.9728
chr9	141213431	970729557	6.8742	19.1638
chr10	135534747	1563960979	11.5392	23.9221
chr11	135006516	1794396150	13.2912	30.6007
chr12	133851895	959345532	7.1672	17.8437
chr13	115169878	870115992	7.5551	16.8689
chr14	107349540	1127610154	10.5041	21.0205
chr15	102531392	970628586	9.4666	19.7659
chr16	90354753	1187933912	13.1474	29.7064
chr17	81195210	1546319873	19.0445	61.4703
chr18	78077248	726926994	9.3104	26.5604
chr19	59128983	670133896	11.3334	24.2844
chr20	63025520	1807367607	28.6768	51.1898
chr21	48129895	265178961	5.5097	14.1869
chr22	51304566	350137159	6.8247	17.5911
chrMT	16571	543455	32.7955	16.3181
chrX	155270560	1151824527	7.4182	13.9145

chrY	59373566	30573953	0.5149	11.7377

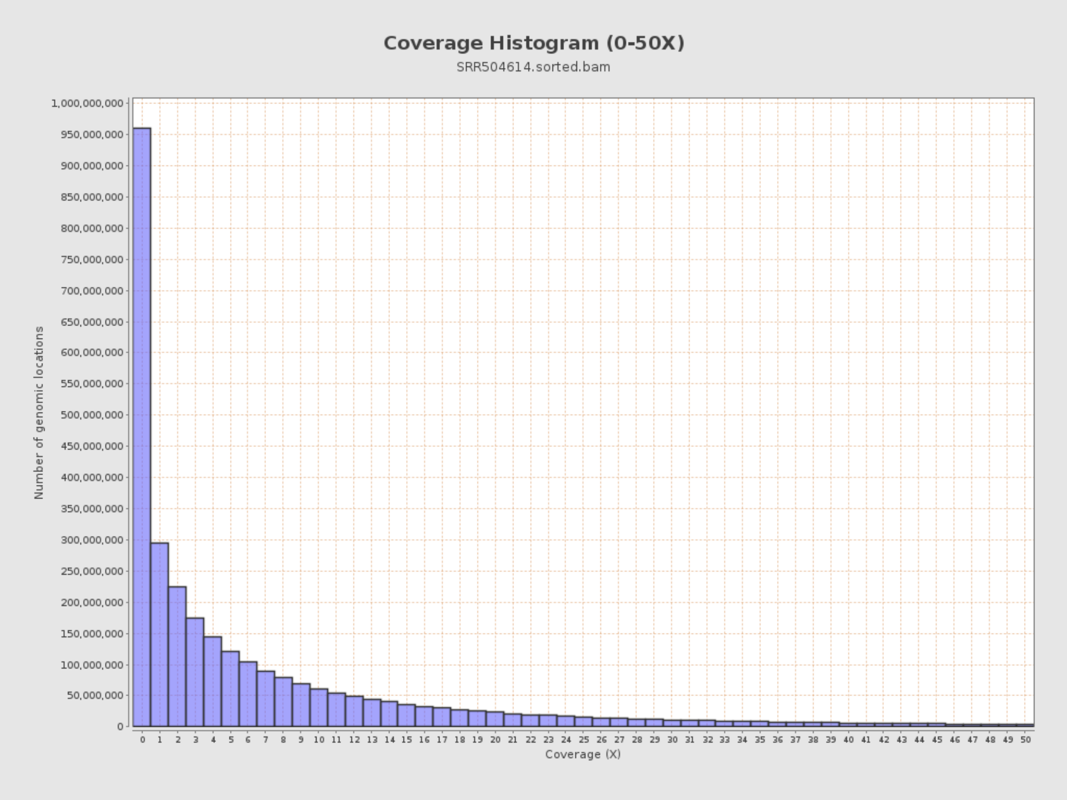
3. Results : Coverage across reference



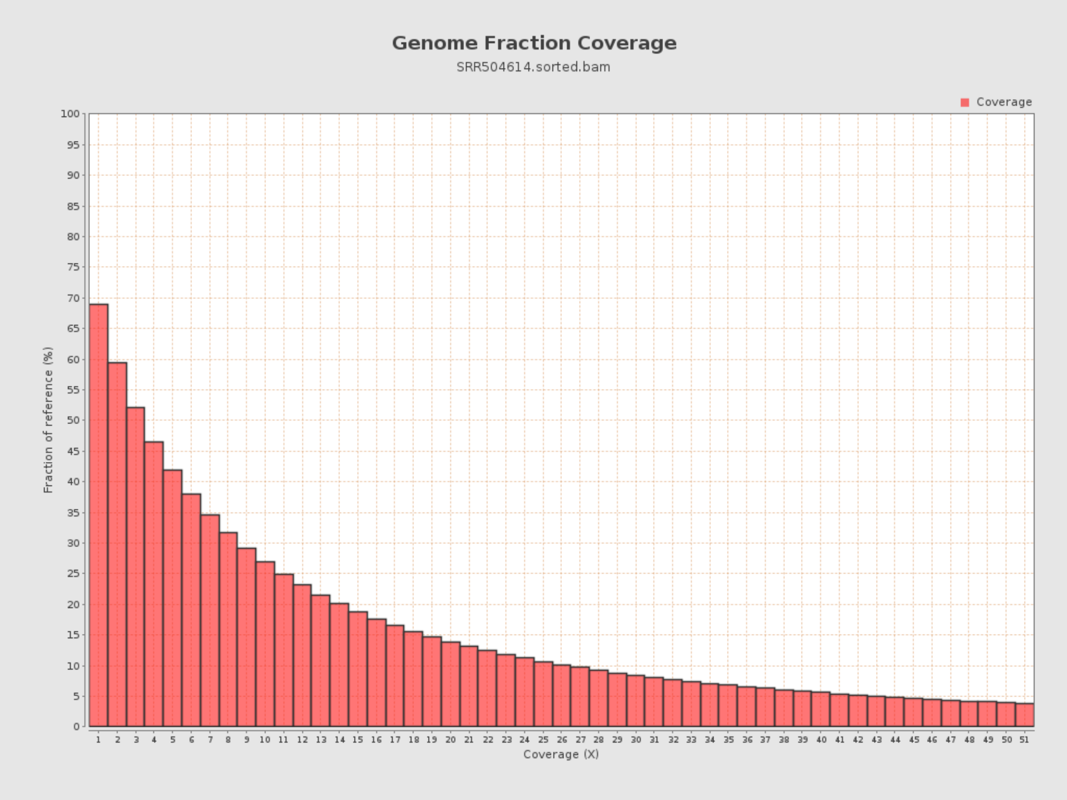
4. Results : Coverage Histogram



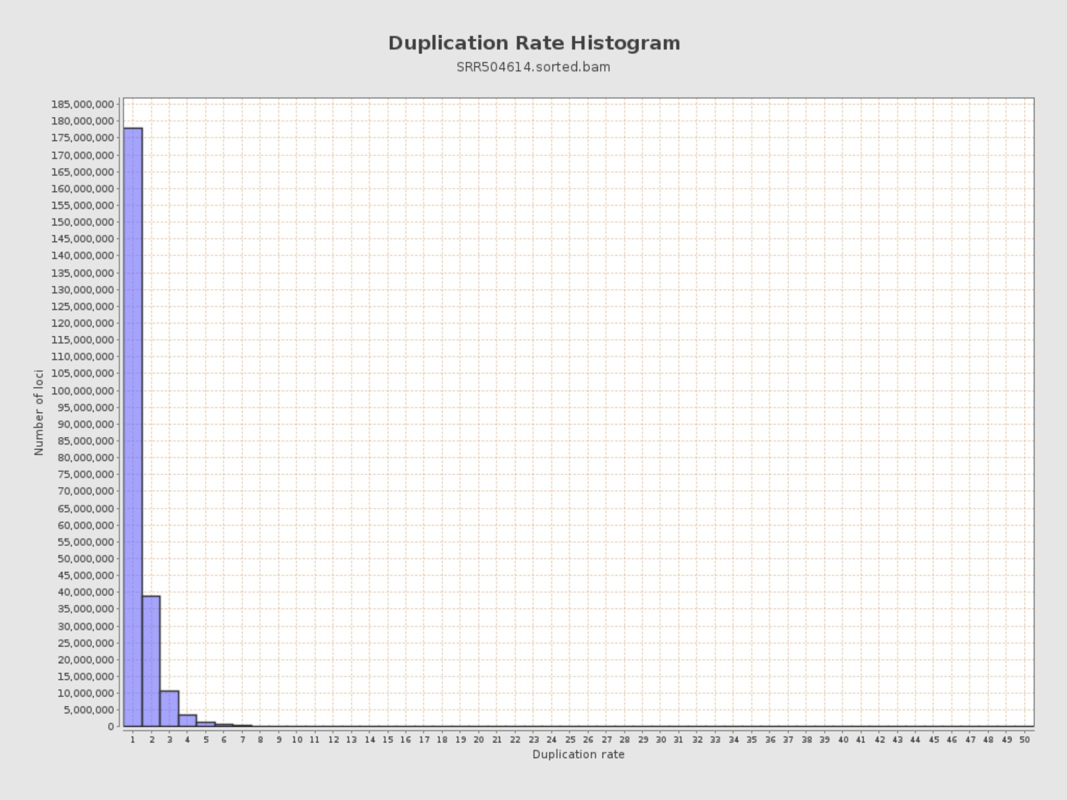
5. Results : Coverage Histogram (0-50X)



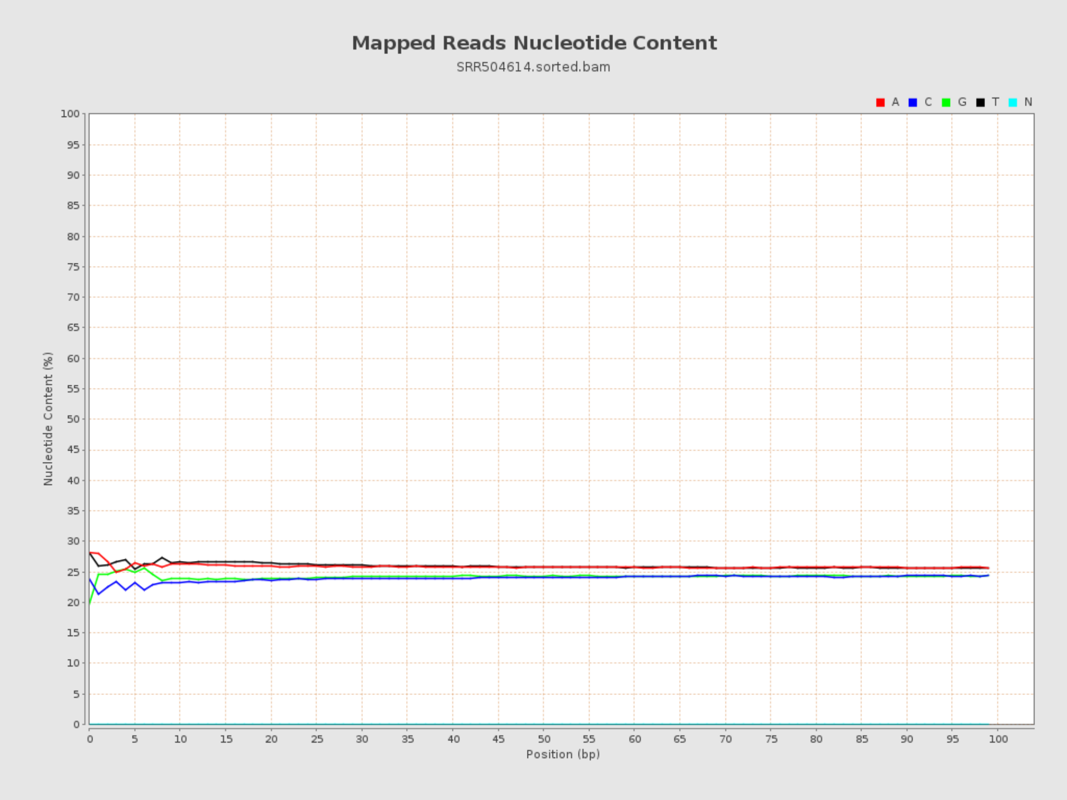
6. Results : Genome Fraction Coverage



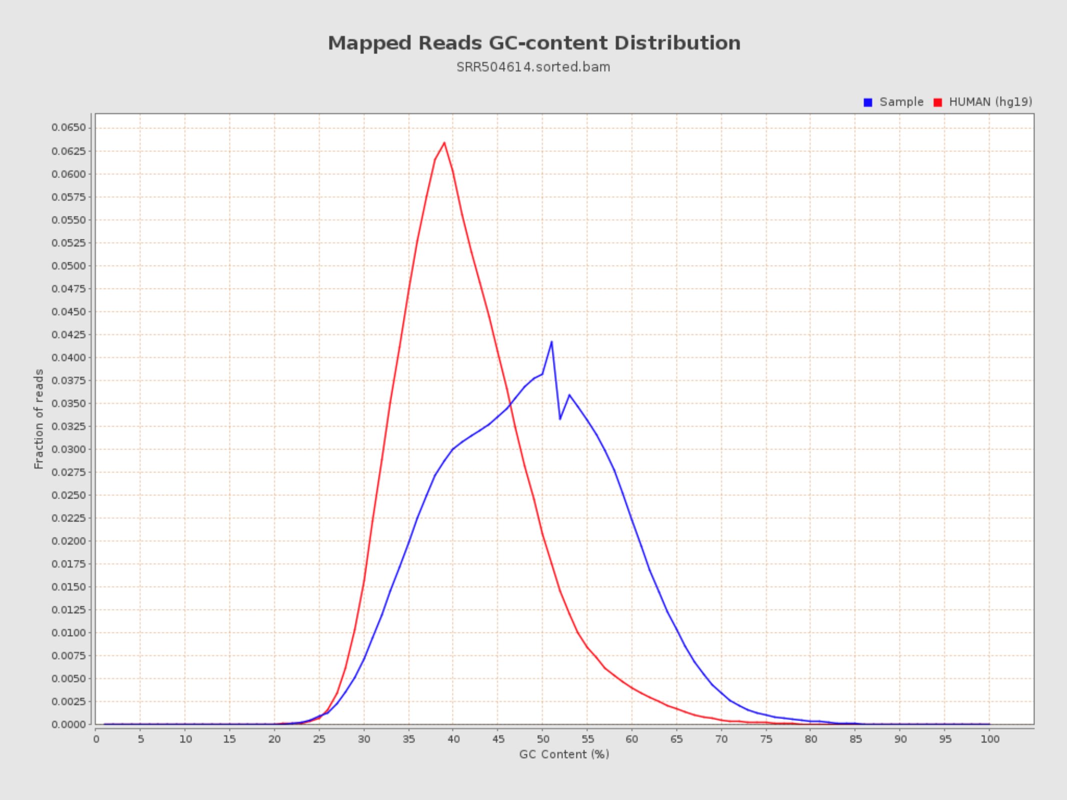
7. Results : Duplication Rate Histogram



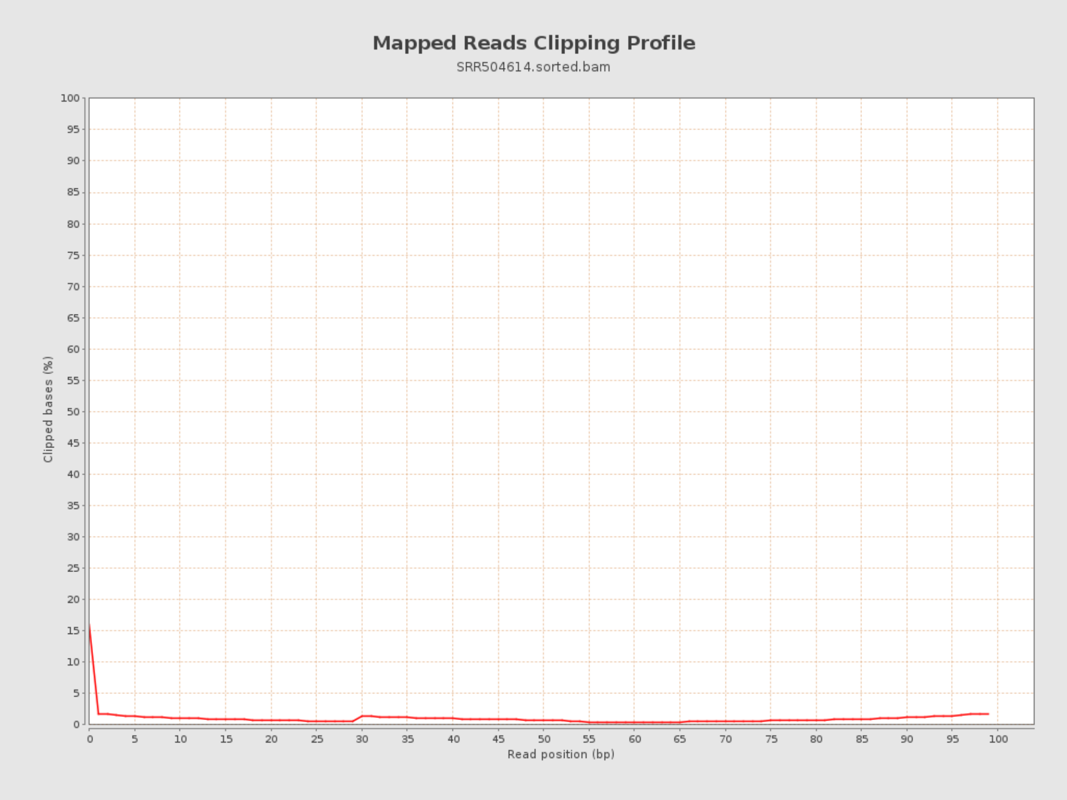
8. Results : Mapped Reads Nucleotide Content



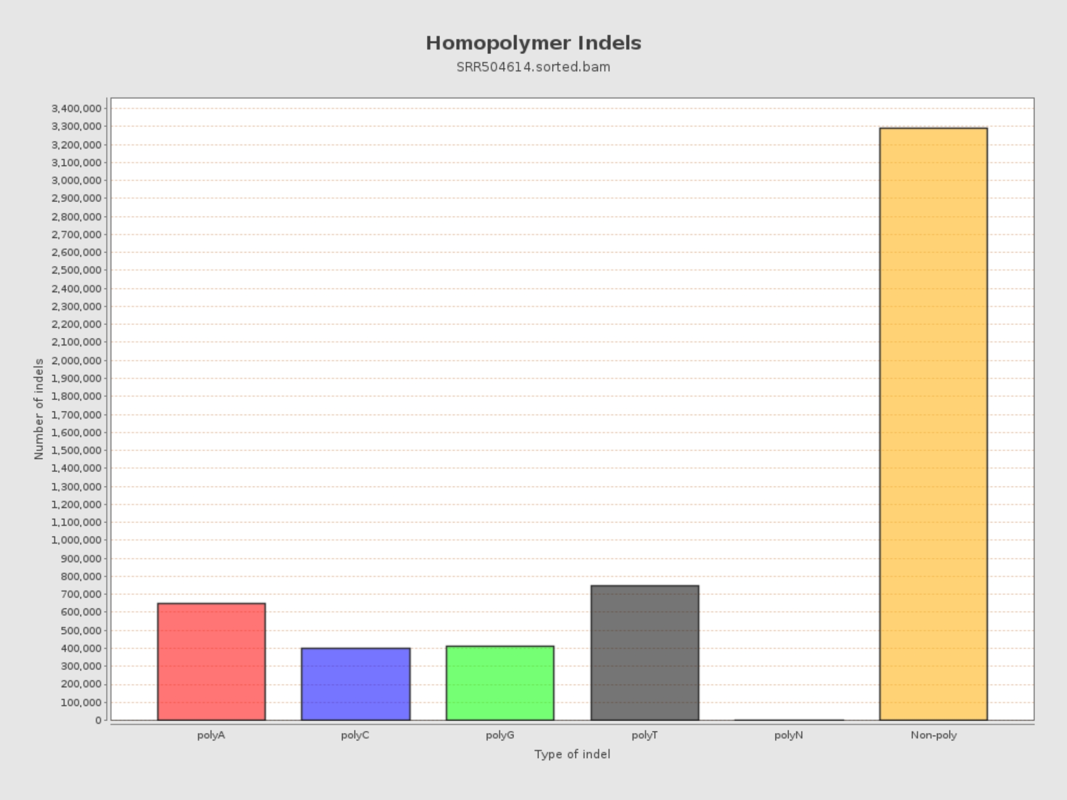
9. Results : Mapped Reads GC-content Distribution



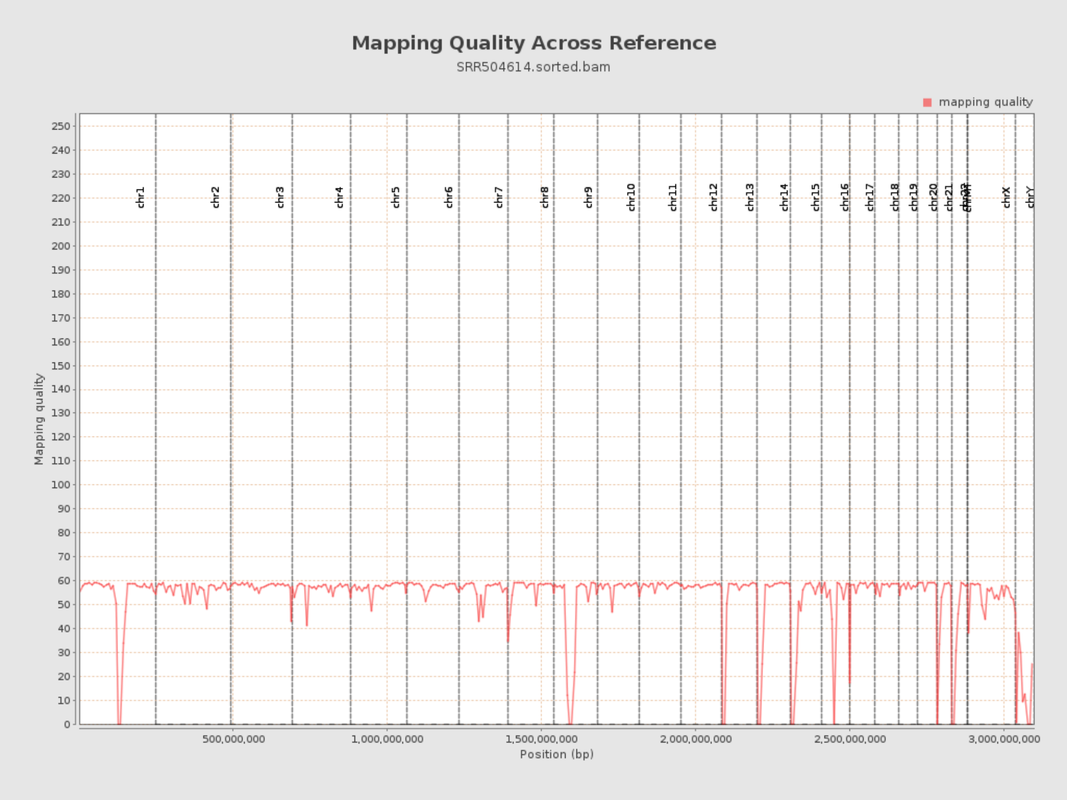
10. Results : Mapped Reads Clipping Profile



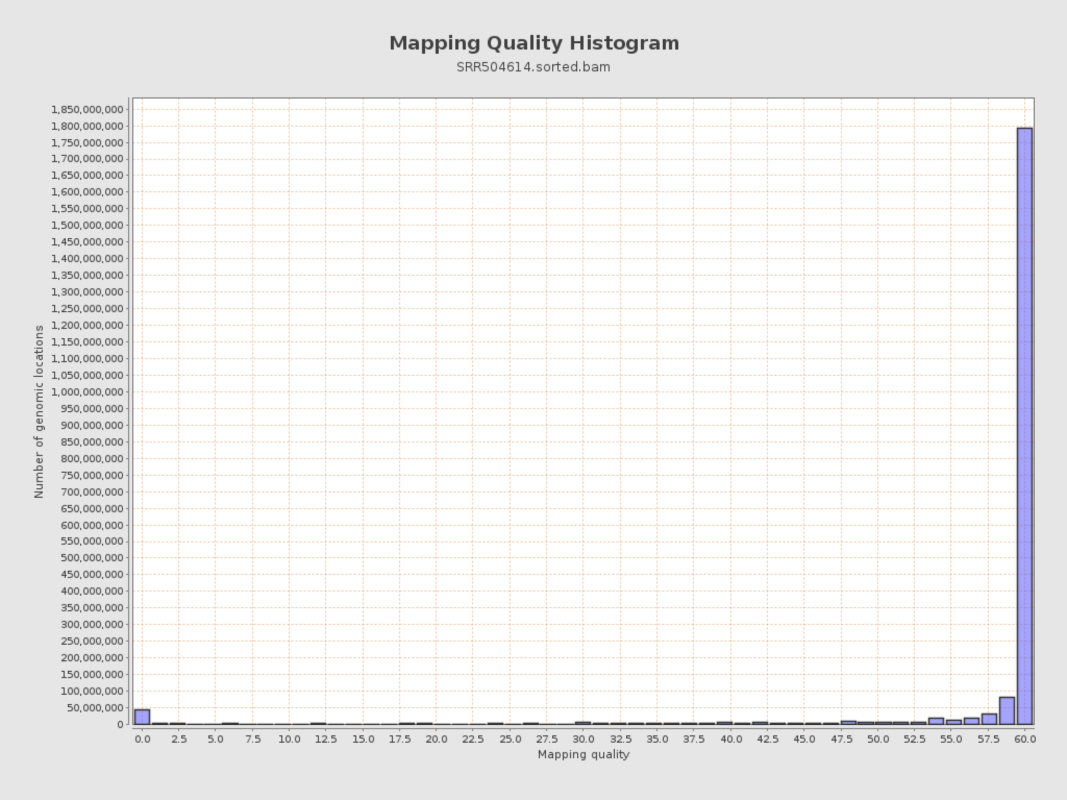
11. Results : Homopolymer Indels



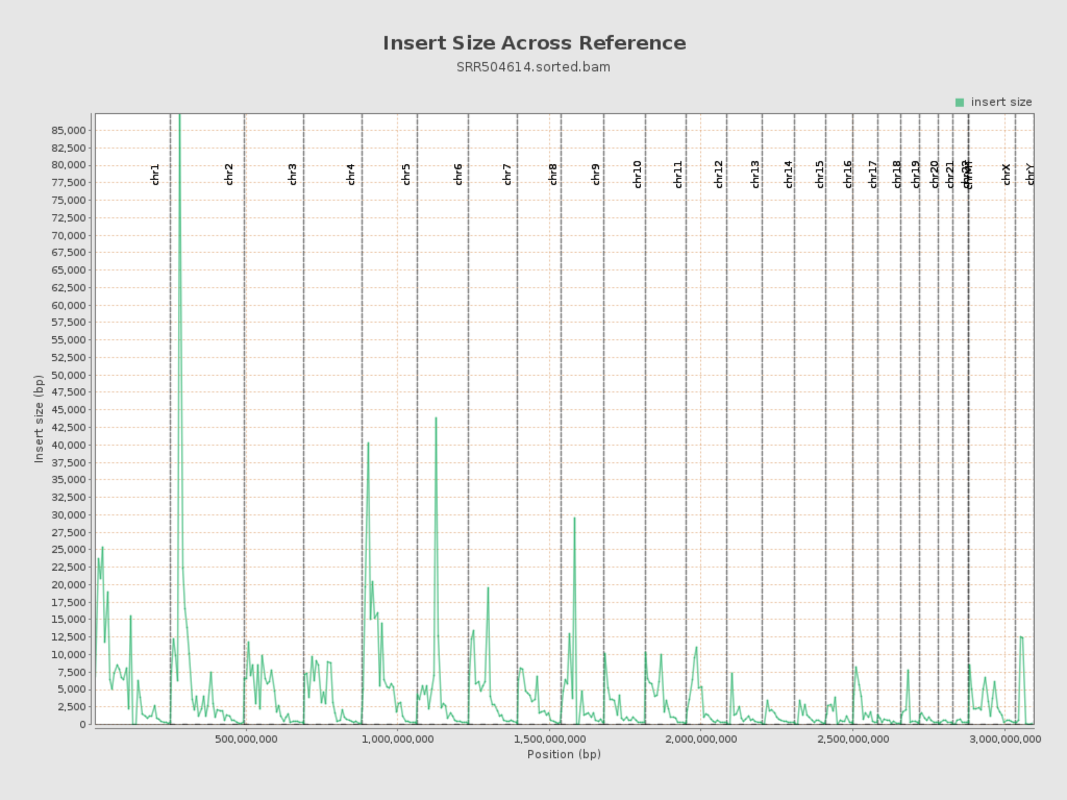
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram