Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 09:21:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504594.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_SRR504594 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504594_1.fastq.gz SRR504594_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 09:21:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504594.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	365,590,394
Mapped reads	349,912,673 / 95.71%
Unmapped reads	15,677,721 / 4.29%
Mapped paired reads	349,912,673 / 95.71%
Mapped reads, first in pair	175,162,923 / 47.91%
Mapped reads, second in pair	174,749,750 / 47.8%
Mapped reads, both in pair	347,098,772 / 94.94%
Mapped reads, singletons	2,813,901 / 0.77%
Secondary alignments	0
Supplementary alignments	1,011,548 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	77,056,110 / 21.08%
Duplication rate	18.05%
Clipped reads	54,674,057 / 14.96%

2.2. ACGT Content

Number/percentage of A's	9,549,933,489 / 28.41%
Number/percentage of C's	7,210,339,592 / 21.45%
Number/percentage of T's	9,454,979,467 / 28.13%
Number/percentage of G's	7,387,499,526 / 21.98%
Number/percentage of N's	10,249,757 / 0.03%

GC Percentage	43.43%

2.3. Coverage

Mean	10.8615
Standard Deviation	95.7155

2.4. Mapping Quality

Mean Mapping Quality	53.37

2.5. Insert size

Mean	33,970.96
Standard Deviation	1,747,548.58
P25/Median/P75	133 / 189 / 246

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	186,362,042
Insertions	3,394,592
Mapped reads with at least one insertion	0.93%
Deletions	4,175,293
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.38%

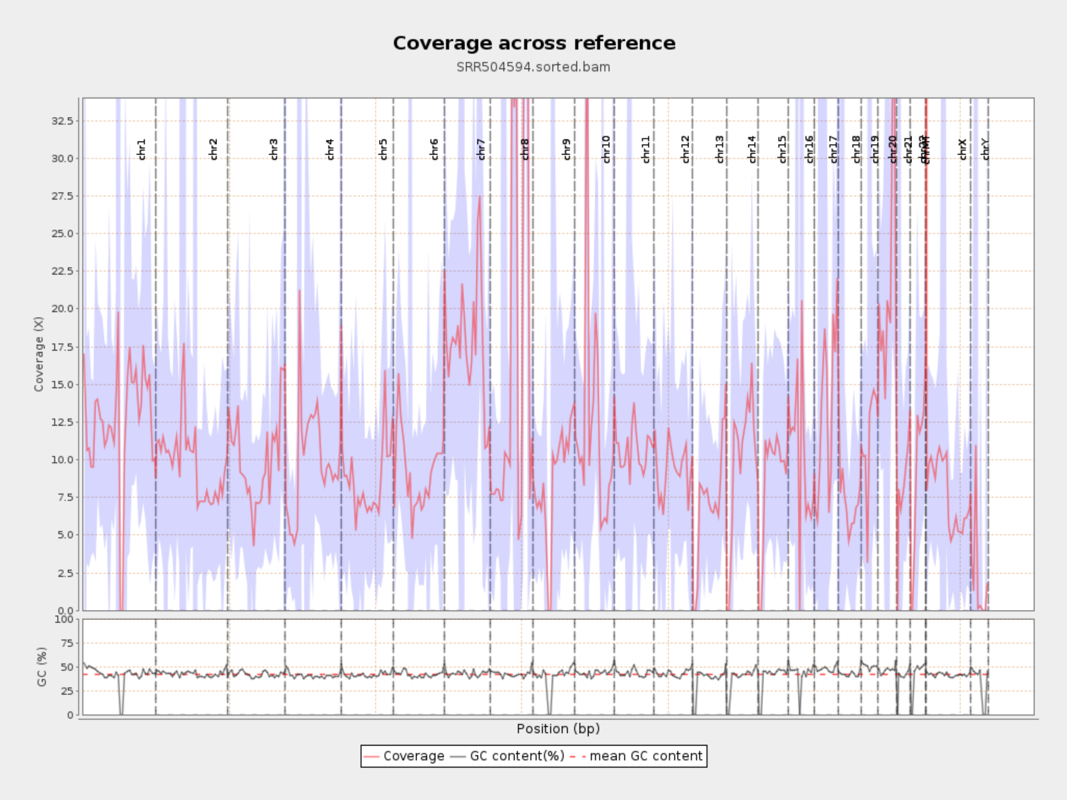
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

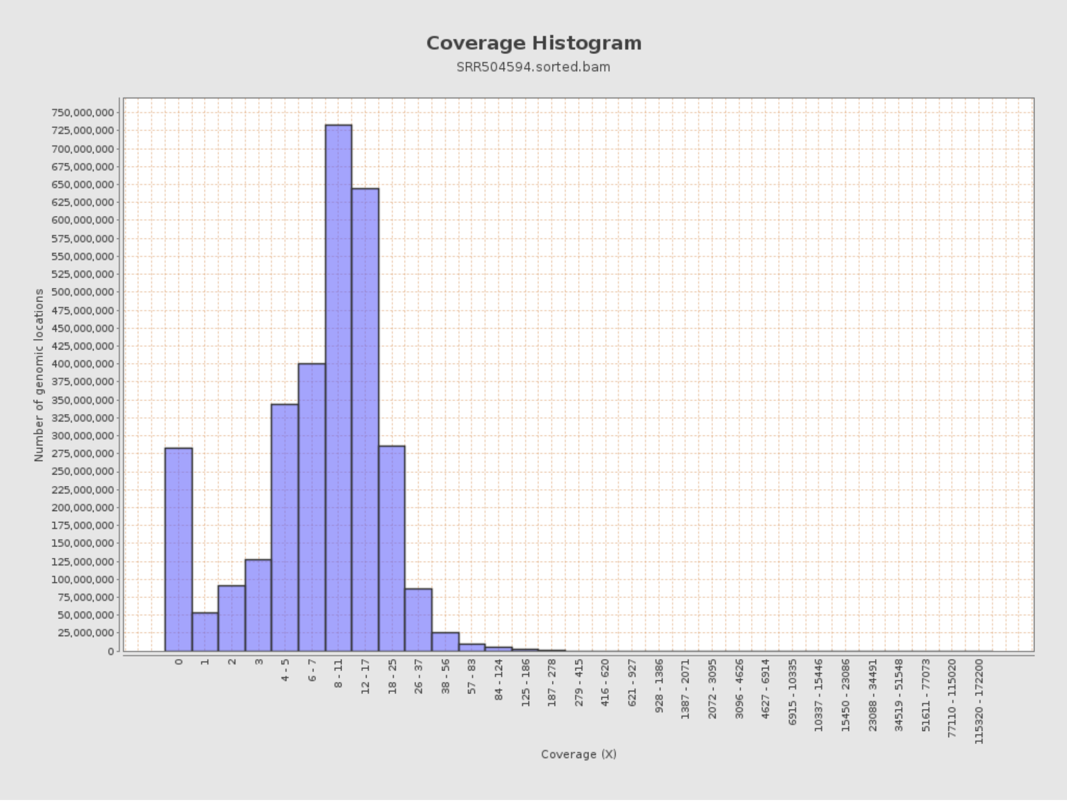
		bases	coverage	deviation
chr1	249250621	3127165353	12.5463	173.4209
chr2	243199373	2374796169	9.7648	57.6369
chr3	198022430	1990032383	10.0495	16.5544
chr4	191154276	1905118866	9.9664	115.0697
chr5	180915260	1586703001	8.7704	10.4026
chr6	171115067	1575819766	9.2091	22.6555
chr7	159138663	2836619043	17.8248	138.2804
chr8	146364022	2955934421	20.1958	67.022
chr9	141213431	1212058986	8.5832	60.7292
chr10	135534747	1636715833	12.076	259.2411
chr11	135006516	1443232512	10.6901	39.0018
chr12	133851895	1257473052	9.3945	8.8307
chr13	115169878	815577784	7.0815	6.4825
chr14	107349540	1091129750	10.1643	9.5719
chr15	102531392	878336477	8.5665	7.3097
chr16	90354753	933780674	10.3346	73.4816
chr17	81195210	1042845693	12.8437	45.1492
chr18	78077248	573480270	7.345	95.0029
chr19	59128983	672685931	11.3766	90.1693
chr20	63025520	1413742994	22.4313	29.1066
chr21	48129895	403442037	8.3824	40.5865
chr22	51304566	454033065	8.8498	9.4963
chrMT	16571	120263461	7,257.4655	1,548.8584
chrX	155270560	1193551485	7.6869	18.8173

chrY	59373566	129261117	2.1771	117.136

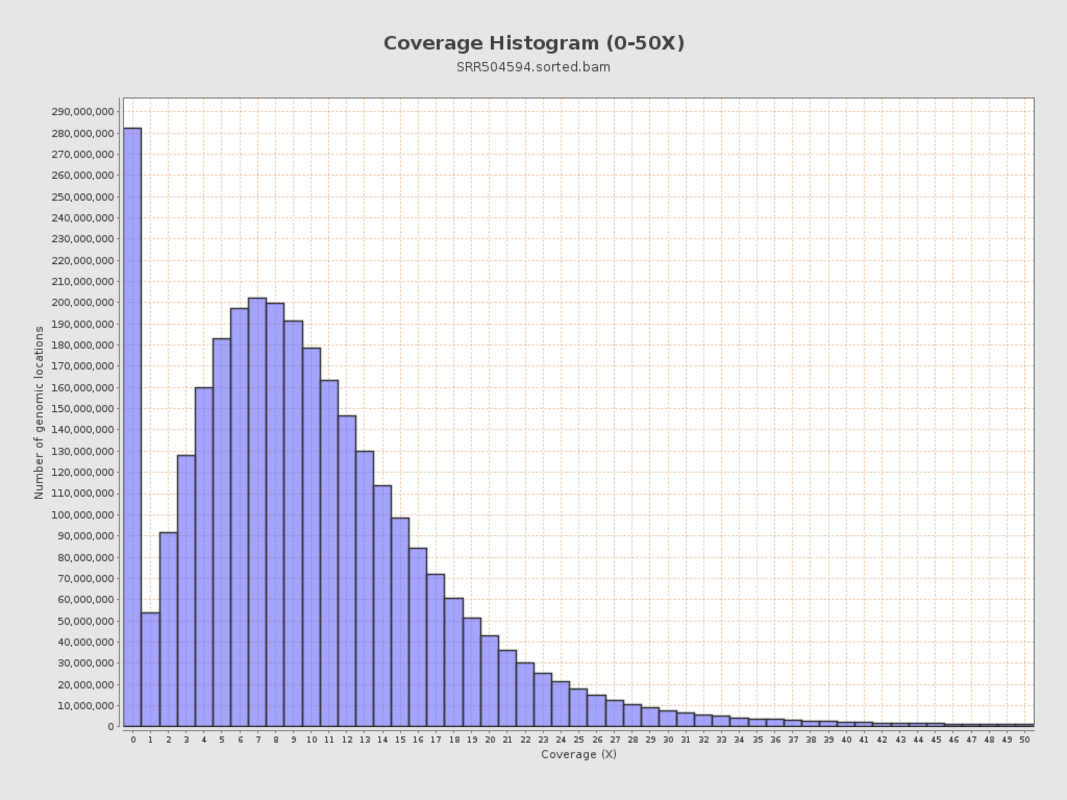
3. Results : Coverage across reference



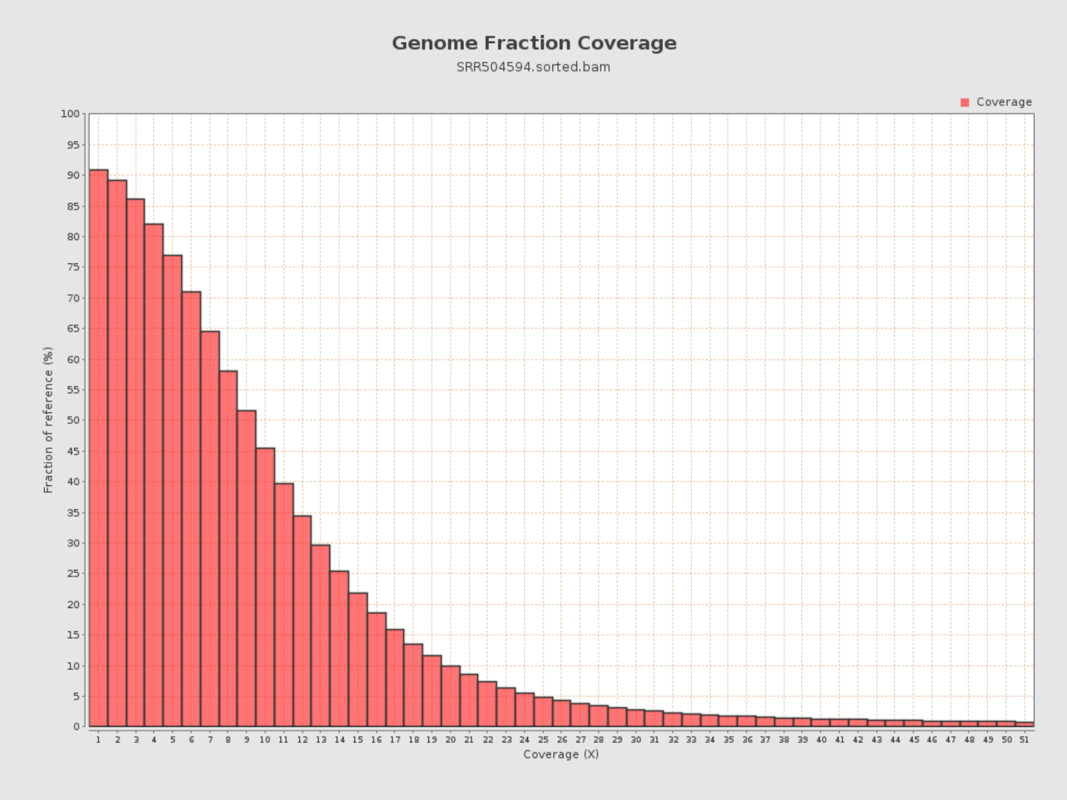
4. Results : Coverage Histogram



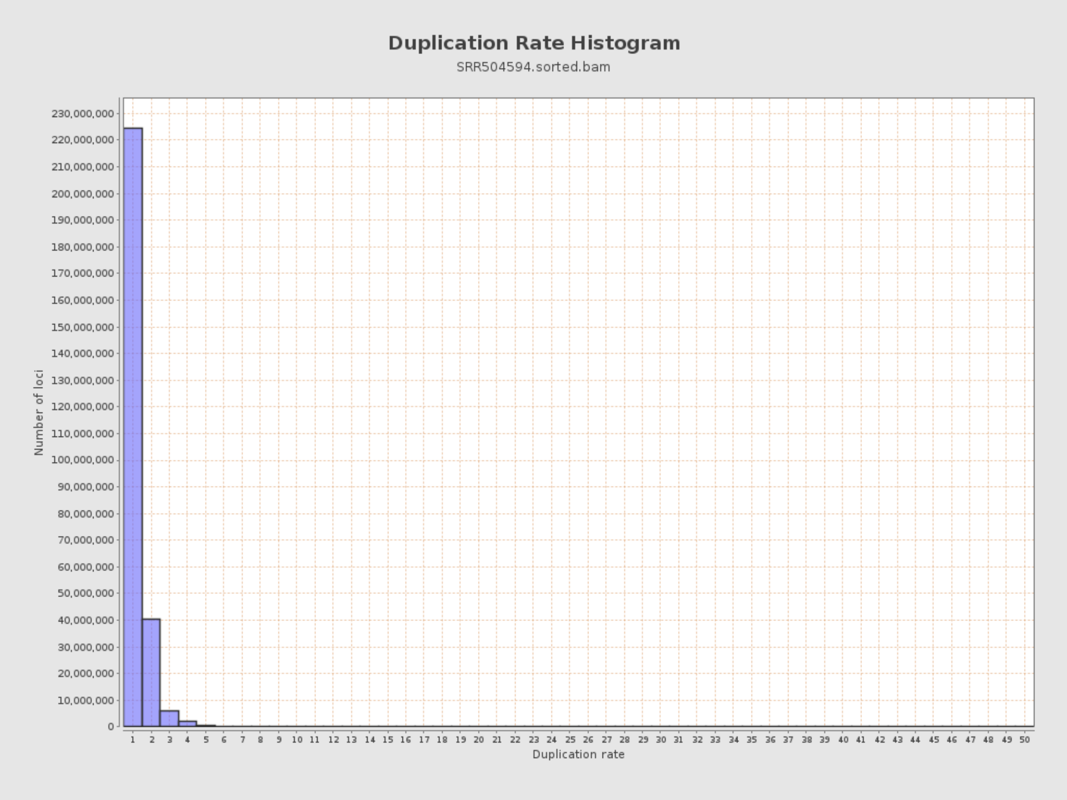
5. Results : Coverage Histogram (0-50X)



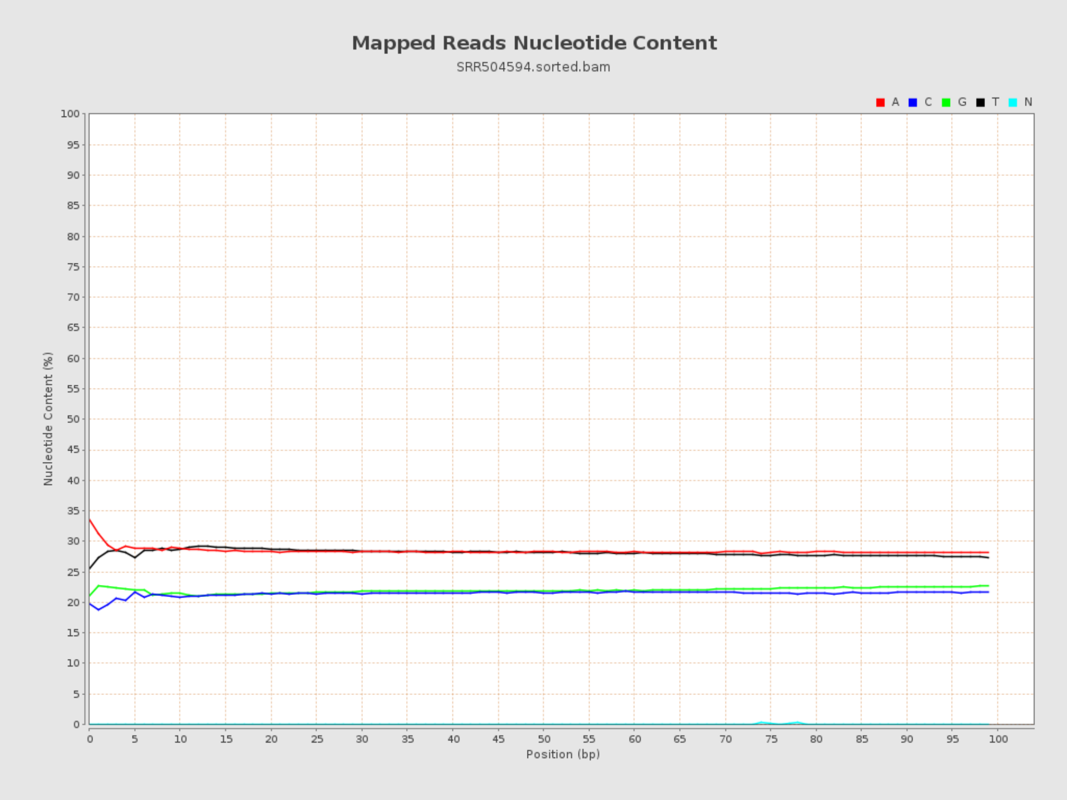
6. Results : Genome Fraction Coverage



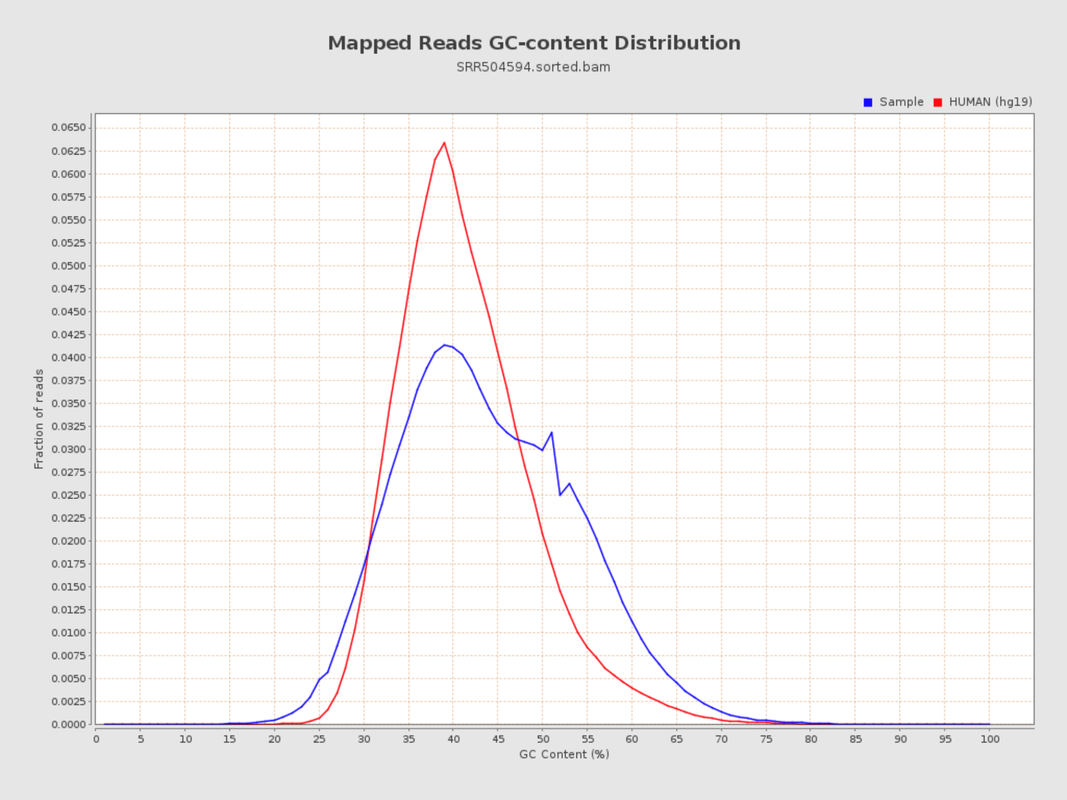
7. Results : Duplication Rate Histogram



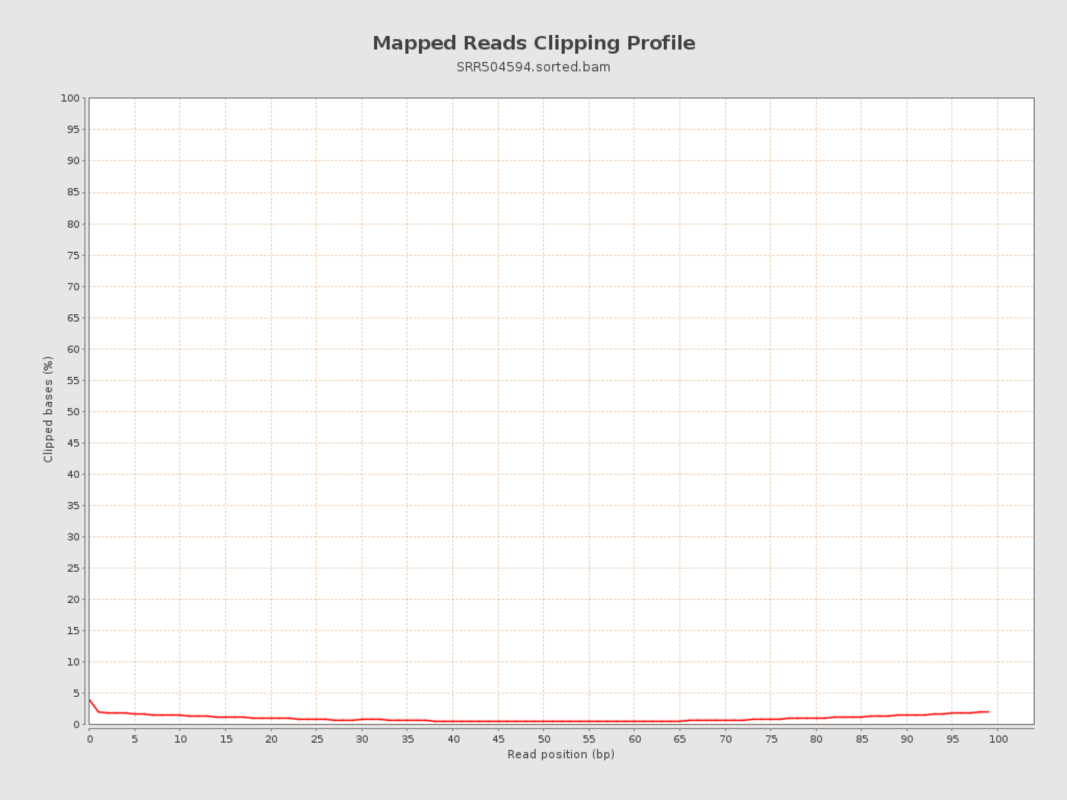
8. Results : Mapped Reads Nucleotide Content



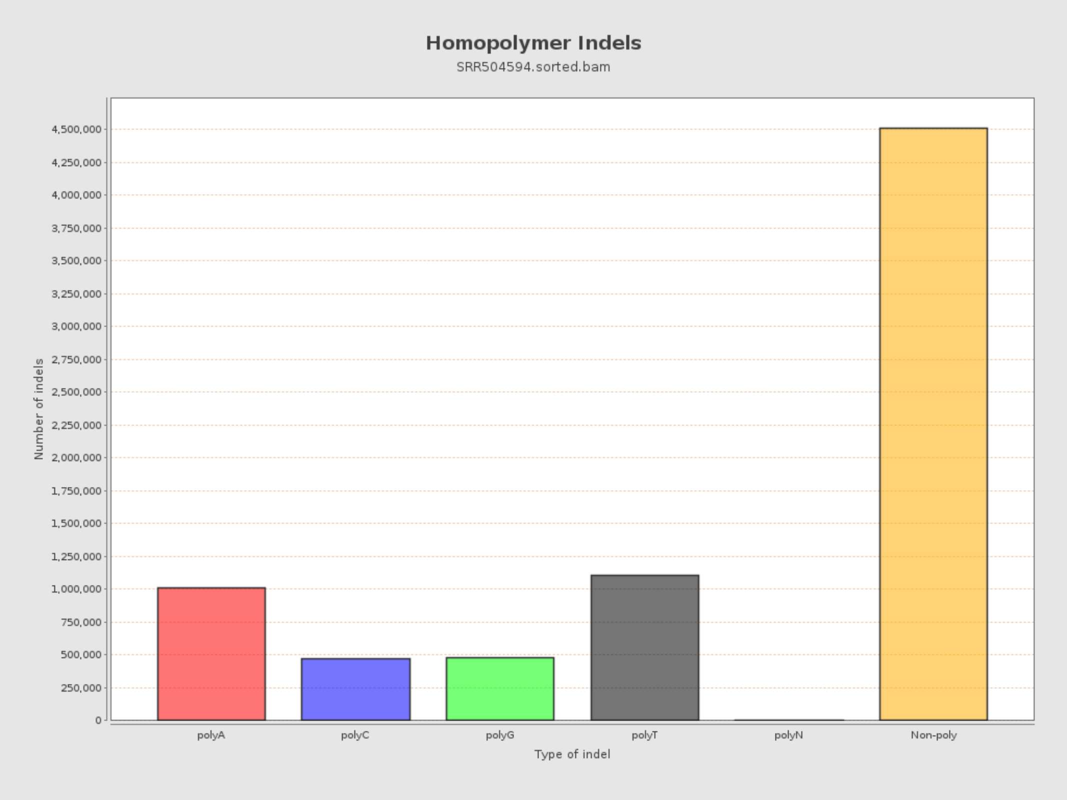
9. Results : Mapped Reads GC-content Distribution



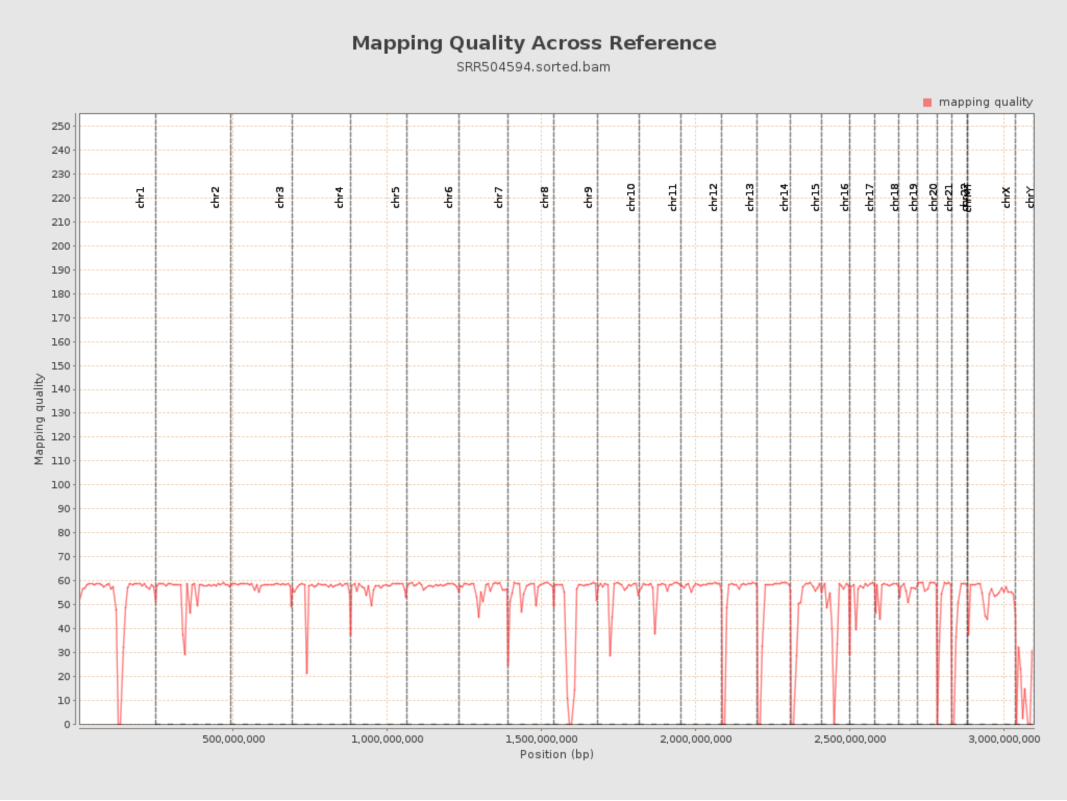
10. Results : Mapped Reads Clipping Profile



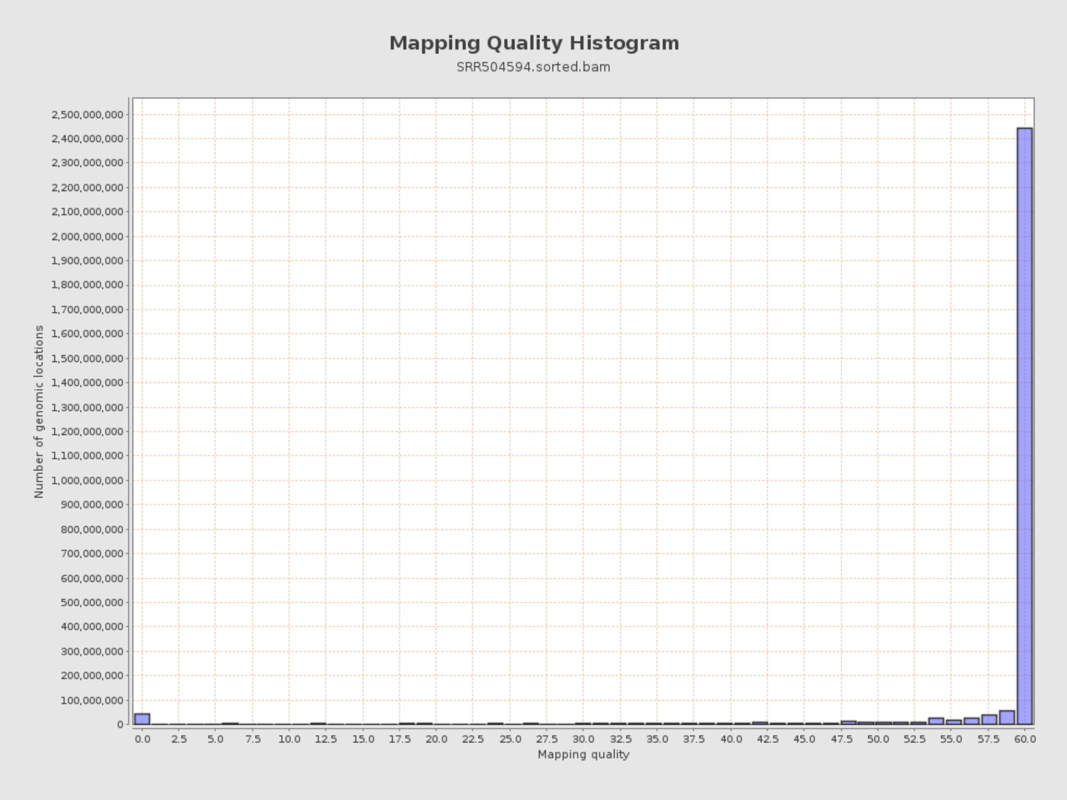
11. Results : Homopolymer Indels



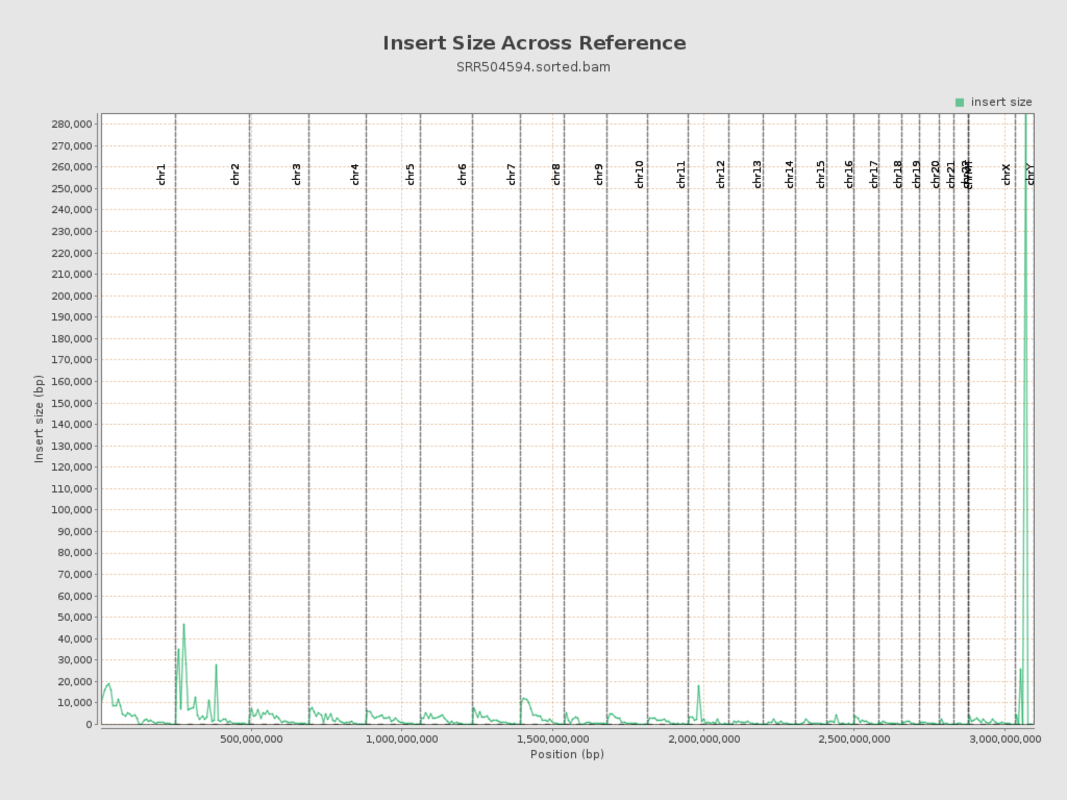
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram