Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 21:47:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504591.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_SRR504591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504591_1.fastq.gz SRR504591_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 21:47:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	365,804,720
Mapped reads	349,347,015 / 95.5%
Unmapped reads	16,457,705 / 4.5%
Mapped paired reads	349,347,015 / 95.5%
Mapped reads, first in pair	174,900,303 / 47.81%
Mapped reads, second in pair	174,446,712 / 47.69%
Mapped reads, both in pair	346,621,222 / 94.76%
Mapped reads, singletons	2,725,793 / 0.75%
Secondary alignments	0
Supplementary alignments	987,043 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	76,802,999 / 21%
Duplication rate	18.03%
Clipped reads	54,500,132 / 14.9%

2.2. ACGT Content

Number/percentage of A's	9,536,407,848 / 28.41%
Number/percentage of C's	7,200,189,290 / 21.45%
Number/percentage of T's	9,441,201,727 / 28.13%
Number/percentage of G's	7,377,920,625 / 21.98%
Number/percentage of N's	7,805,801 / 0.02%

GC Percentage	43.43%

2.3. Coverage

Mean	10.8455
Standard Deviation	95.4733

2.4. Mapping Quality

Mean Mapping Quality	53.38

2.5. Insert size

Mean	33,349.34
Standard Deviation	1,733,353.94
P25/Median/P75	133 / 189 / 246

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	189,242,246
Insertions	3,393,146
Mapped reads with at least one insertion	0.93%
Deletions	4,168,671
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.39%

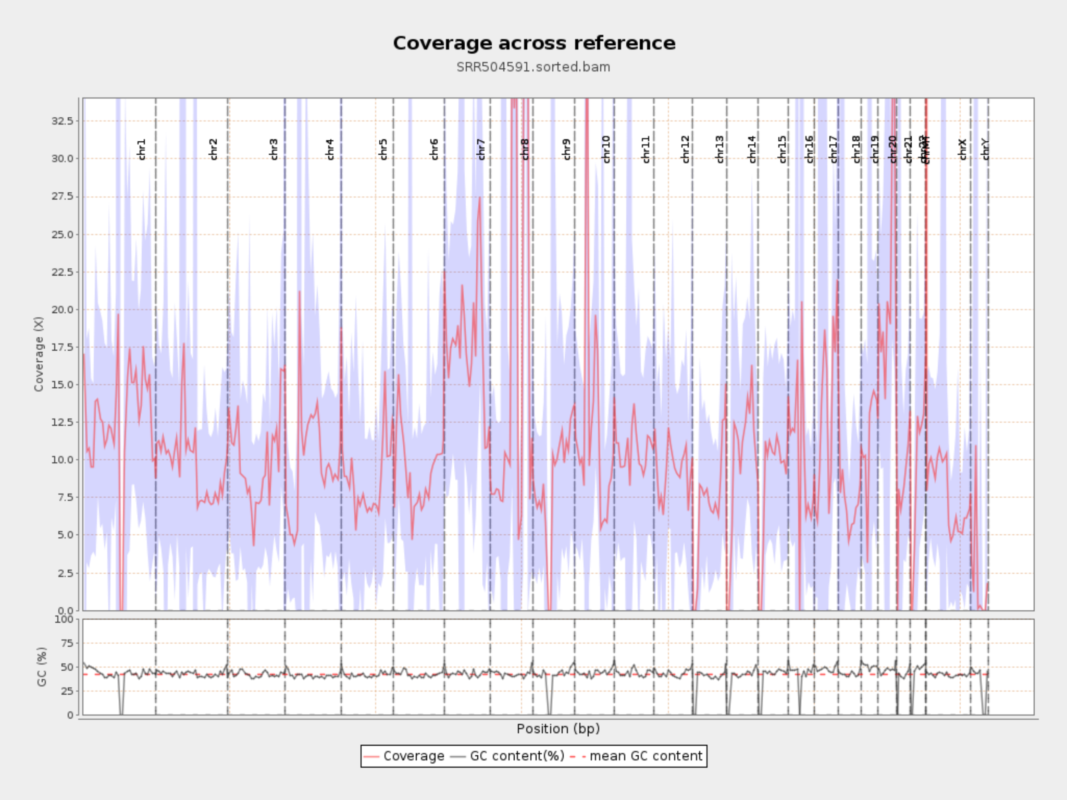
2.7. Chromosome stats

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

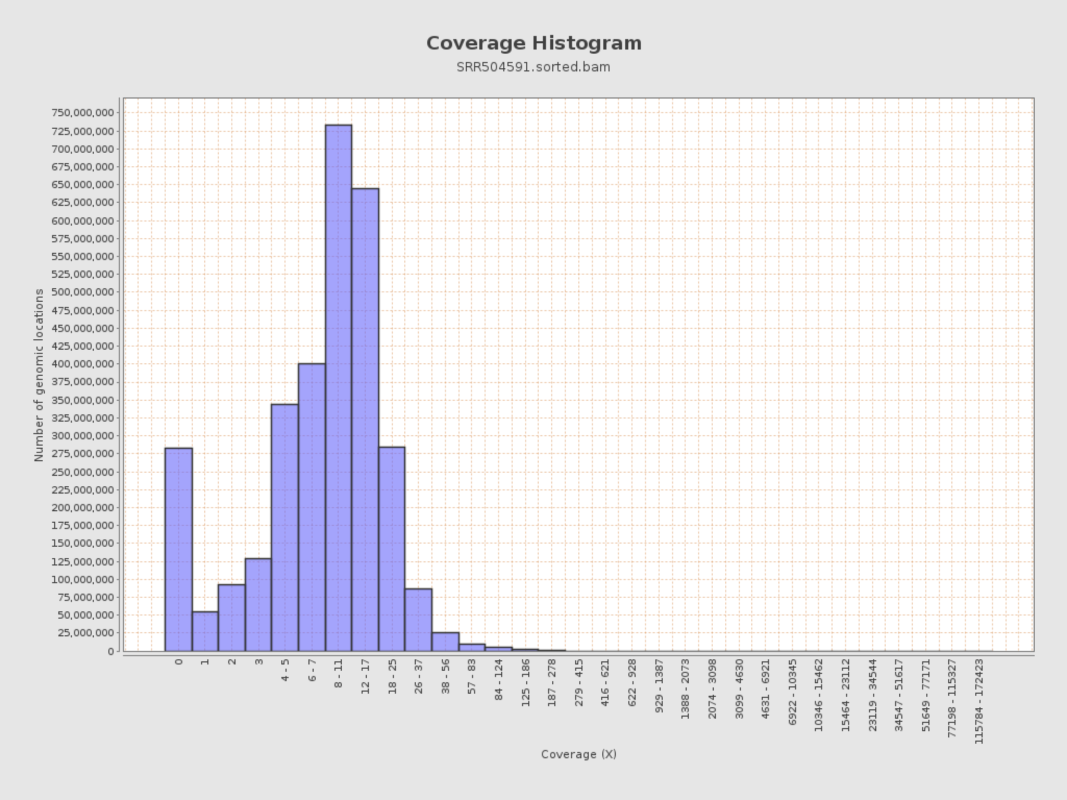
		bases	coverage	deviation
chr1	249250621	3122278716	12.5267	172.9487
chr2	243199373	2372060075	9.7536	57.4655
chr3	198022430	1986844394	10.0334	16.7108
chr4	191154276	1903182744	9.9563	114.7949
chr5	180915260	1585309682	8.7627	10.3673
chr6	171115067	1572861632	9.1918	22.6125
chr7	159138663	2833546091	17.8055	137.5243
chr8	146364022	2952517737	20.1724	67.3686
chr9	141213431	1210085101	8.5692	60.9746
chr10	135534747	1634744388	12.0614	258.8746
chr11	135006516	1441668847	10.6785	38.7006
chr12	133851895	1254518112	9.3724	8.6232
chr13	115169878	814890143	7.0755	6.3985
chr14	107349540	1088456648	10.1394	9.4773
chr15	102531392	877597442	8.5593	7.1801
chr16	90354753	932263314	10.3178	73.4786
chr17	81195210	1040714224	12.8174	45.1758
chr18	78077248	571984970	7.3259	94.2847
chr19	59128983	671218366	11.3518	89.1503
chr20	63025520	1411146793	22.3901	29.0846
chr21	48129895	402354264	8.3598	40.0168
chr22	51304566	453155482	8.8327	9.4257
chrMT	16571	120129485	7,249.3805	1,533.851
chrX	155270560	1191795981	7.6756	18.7225

chrY	59373566	128972988	2.1722	116.6118

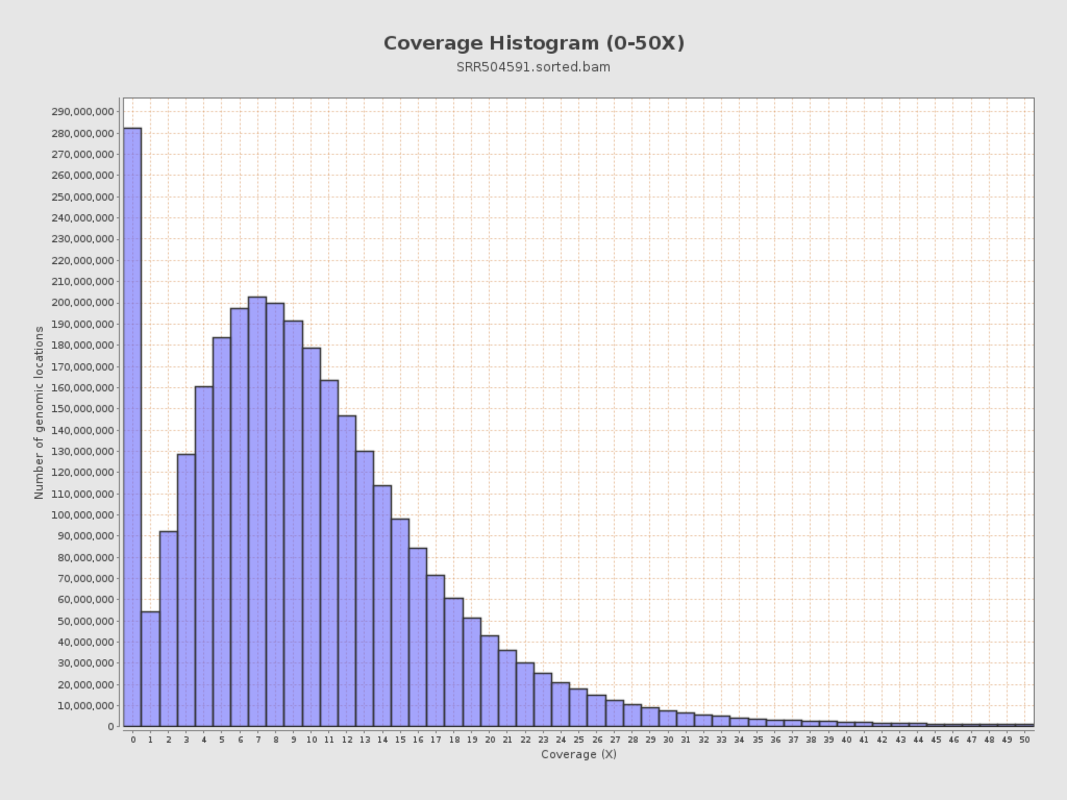
3. Results : Coverage across reference



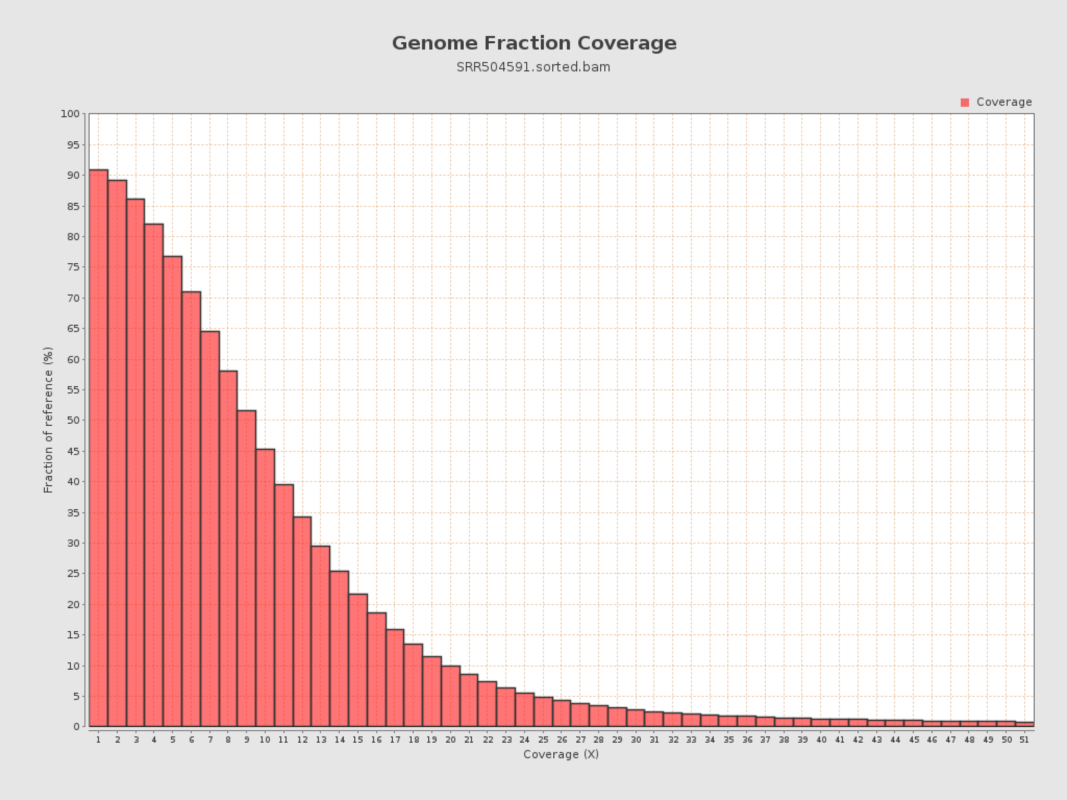
4. Results : Coverage Histogram



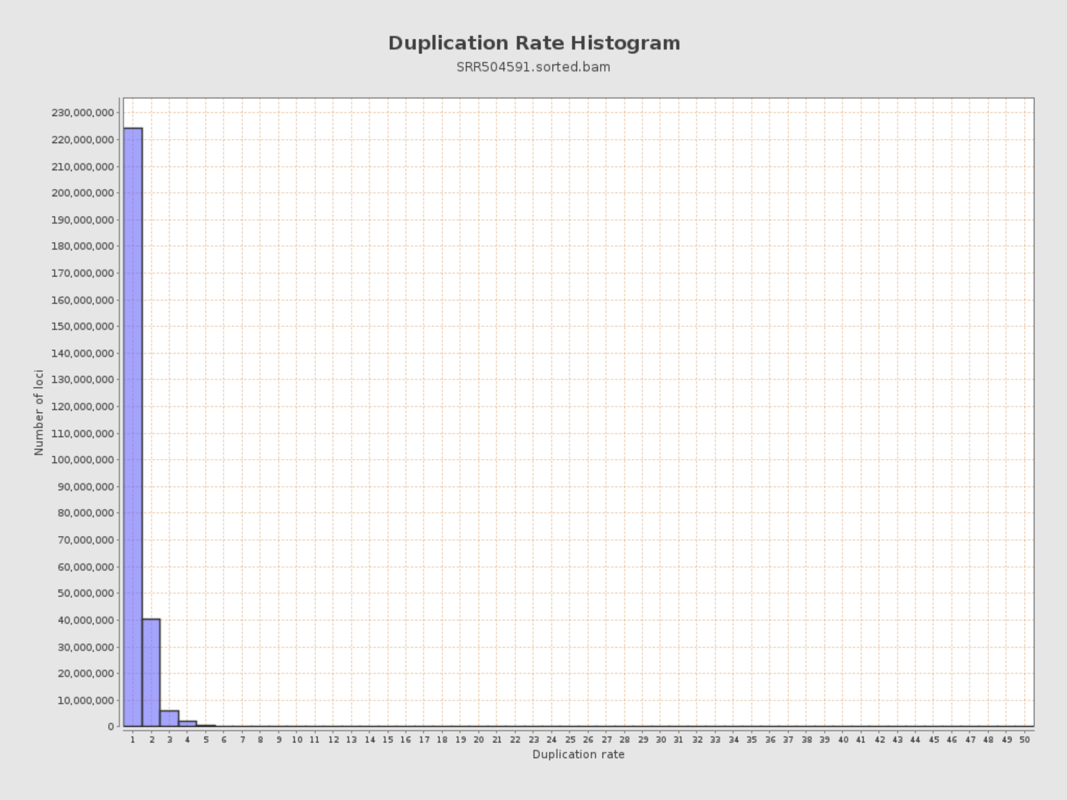
5. Results : Coverage Histogram (0-50X)



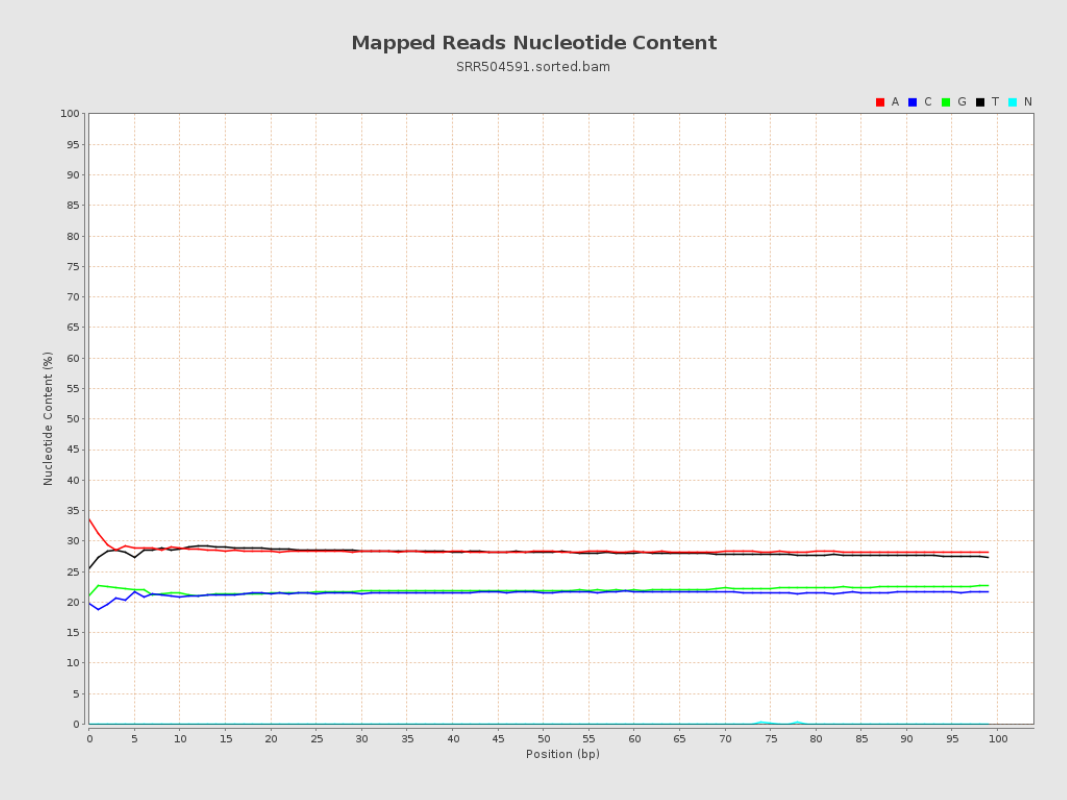
6. Results : Genome Fraction Coverage



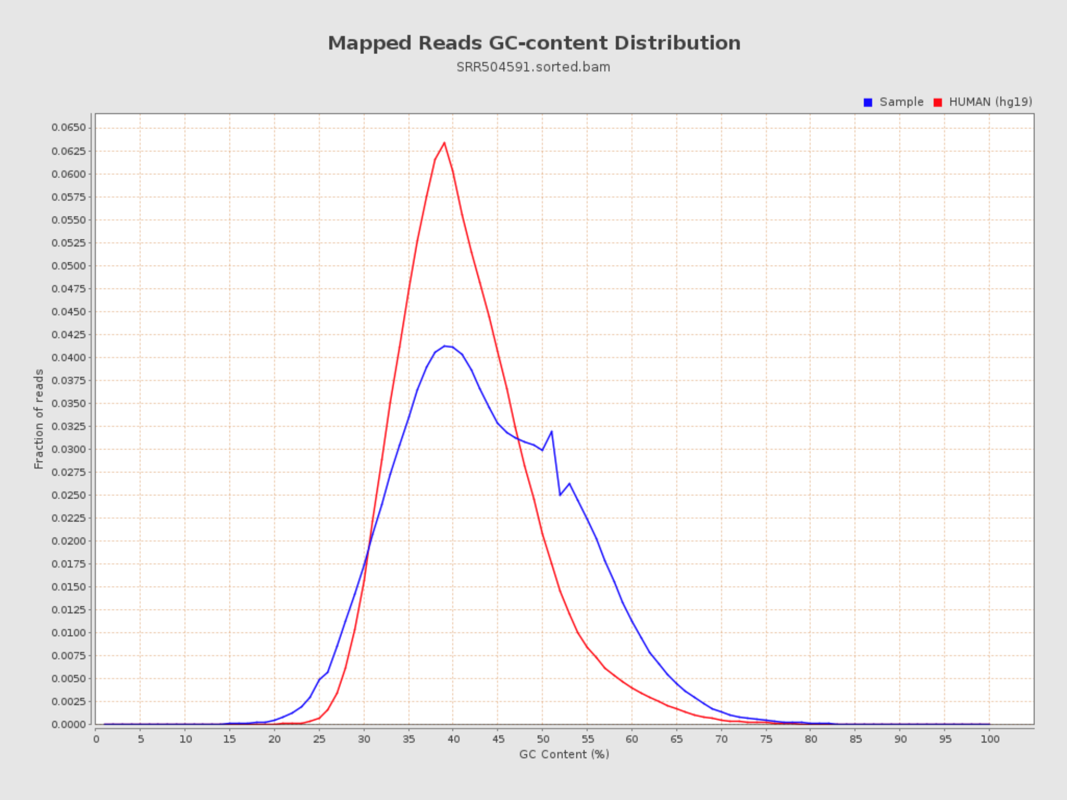
7. Results : Duplication Rate Histogram



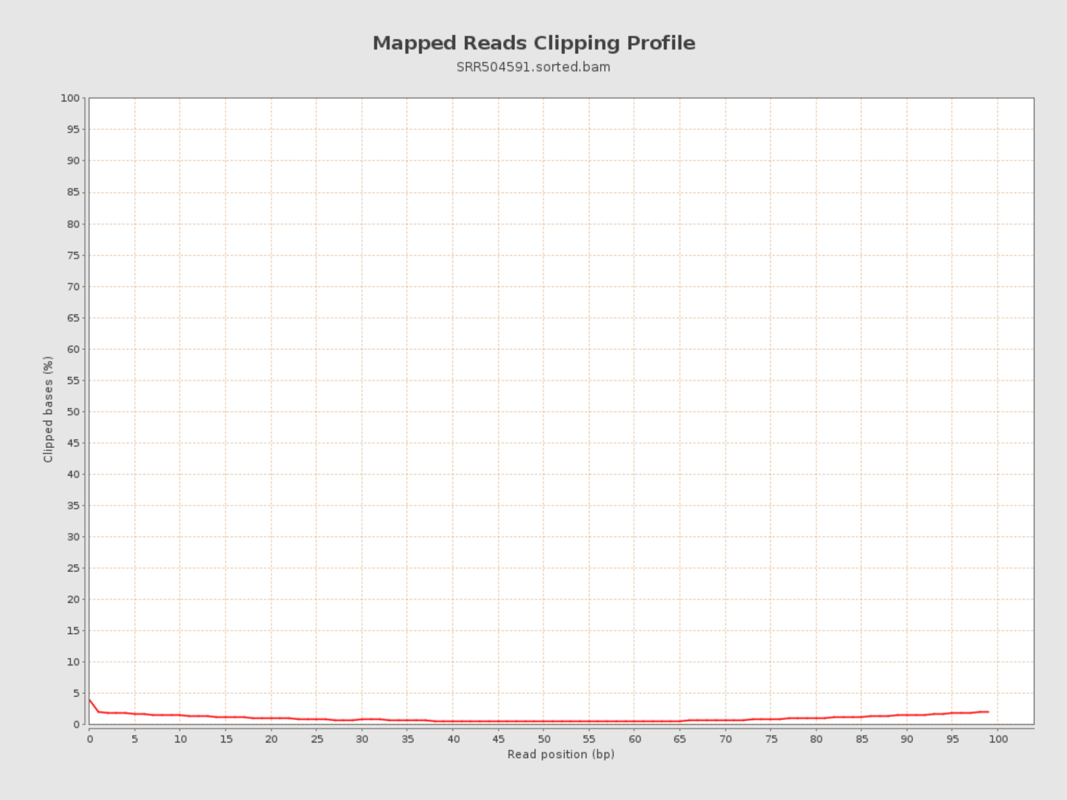
8. Results : Mapped Reads Nucleotide Content



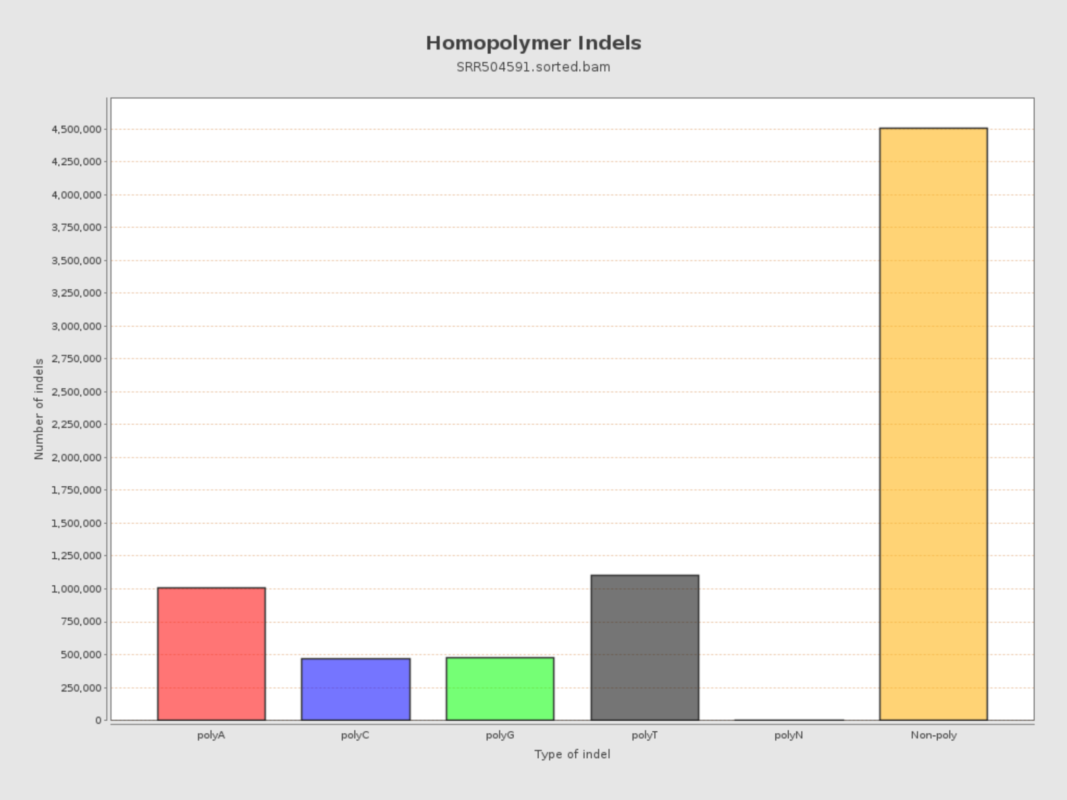
9. Results : Mapped Reads GC-content Distribution



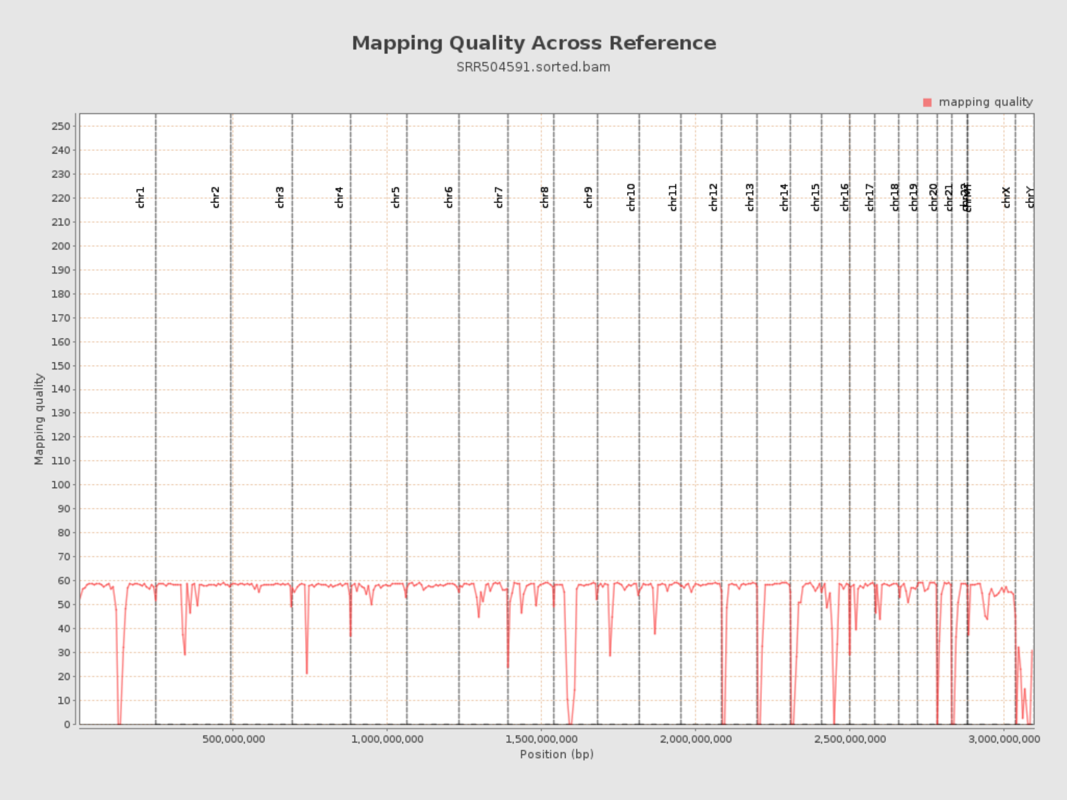
10. Results : Mapped Reads Clipping Profile



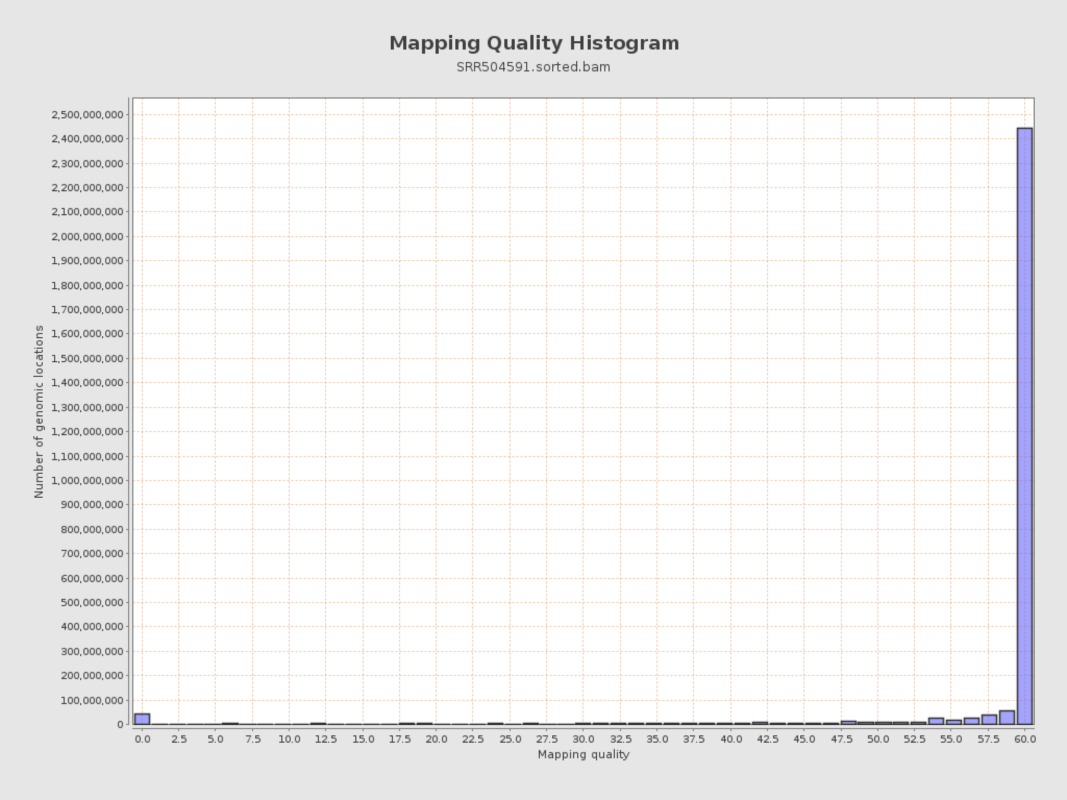
11. Results : Homopolymer Indels



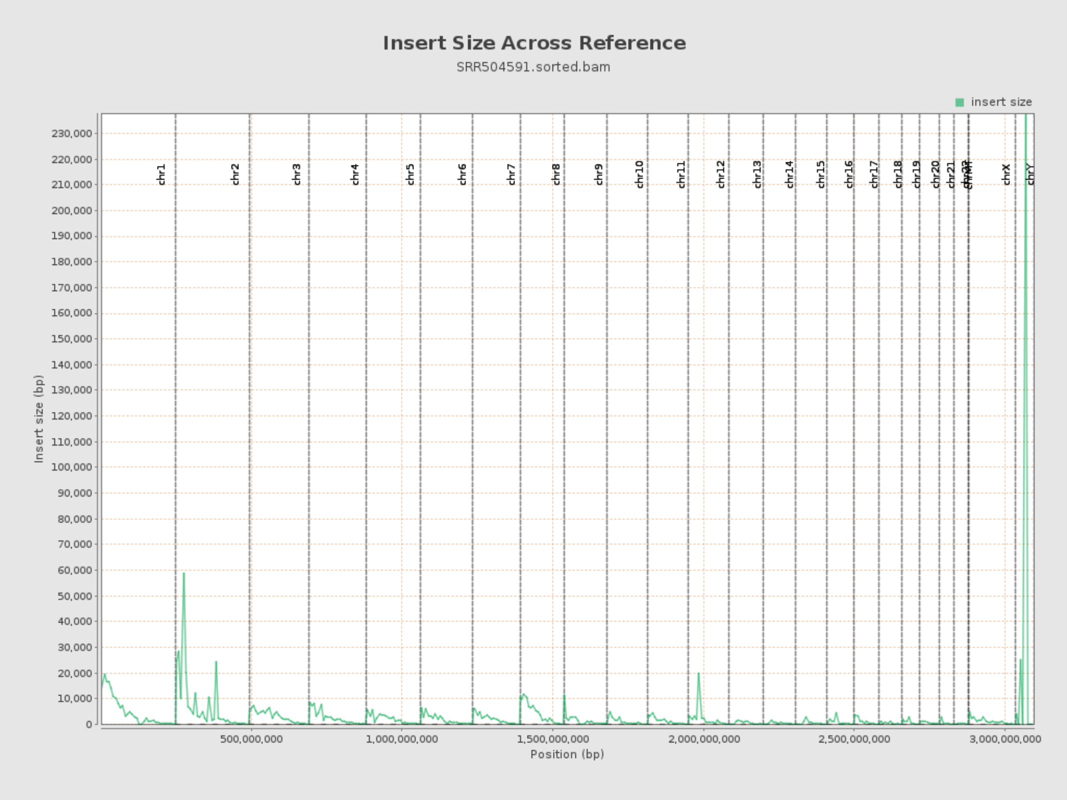
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram