Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 02:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779424.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_SRR1779424 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779424_1.fastq.gz SRR1779424_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 02:25:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779424.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,431,558
Mapped reads	3,508,021 / 21.35%
Unmapped reads	12,923,537 / 78.65%
Mapped paired reads	3,508,021 / 21.35%
Mapped reads, first in pair	1,719,193 / 10.46%
Mapped reads, second in pair	1,788,828 / 10.89%
Mapped reads, both in pair	3,355,720 / 20.42%
Mapped reads, singletons	152,301 / 0.93%
Secondary alignments	0
Supplementary alignments	83,272 / 0.51%
Read min/max/mean length	30 / 80 / 80.18
Duplicated reads (estimated)	2,368,962 / 14.42%
Duplication rate	11.2%
Clipped reads	543,899 / 3.31%

2.2. ACGT Content

Number/percentage of A's	81,821,783 / 29.98%
Number/percentage of C's	53,996,477 / 19.78%
Number/percentage of T's	80,209,694 / 29.39%
Number/percentage of G's	56,847,686 / 20.83%
Number/percentage of N's	56,687 / 0.02%

GC Percentage	40.61%

2.3. Coverage

Mean	0.0882
Standard Deviation	32.6791

2.4. Mapping Quality

Mean Mapping Quality	50.22

2.5. Insert size

Mean	48,972.26
Standard Deviation	2,049,027.96
P25/Median/P75	133 / 174 / 234

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	1,097,599
Insertions	30,778
Mapped reads with at least one insertion	0.87%
Deletions	19,445
Mapped reads with at least one deletion	0.55%
Homopolymer indels	36.4%

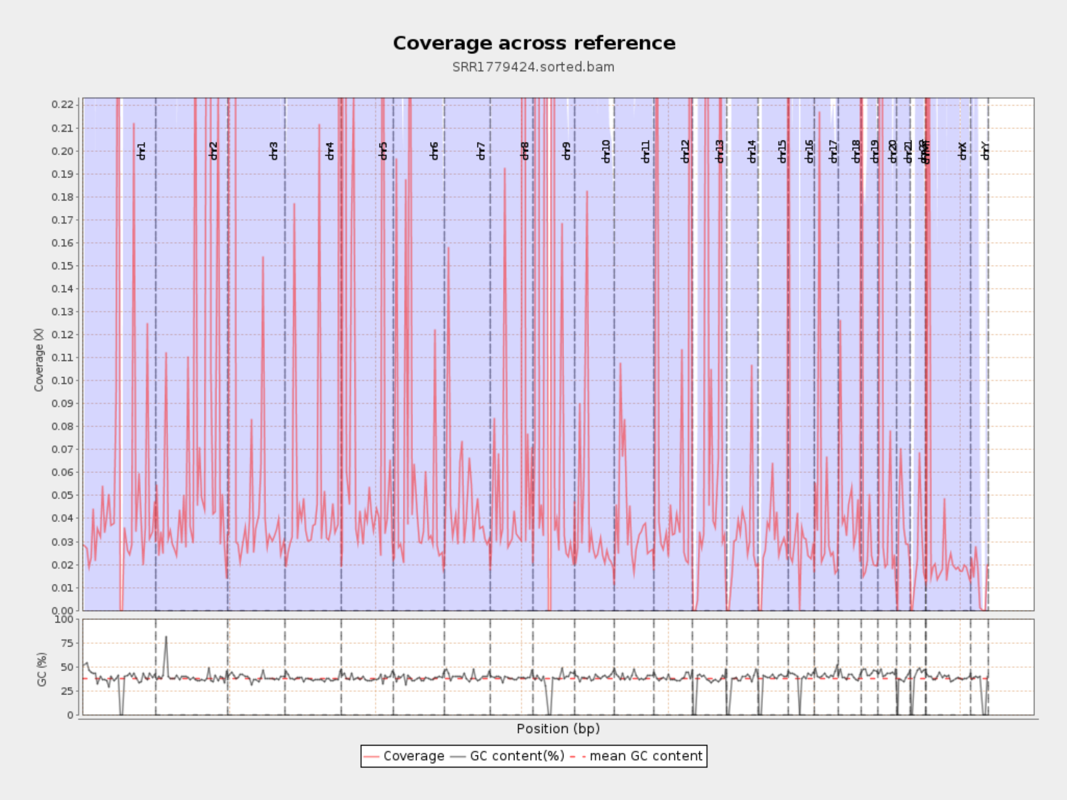
2.7. Chromosome stats

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

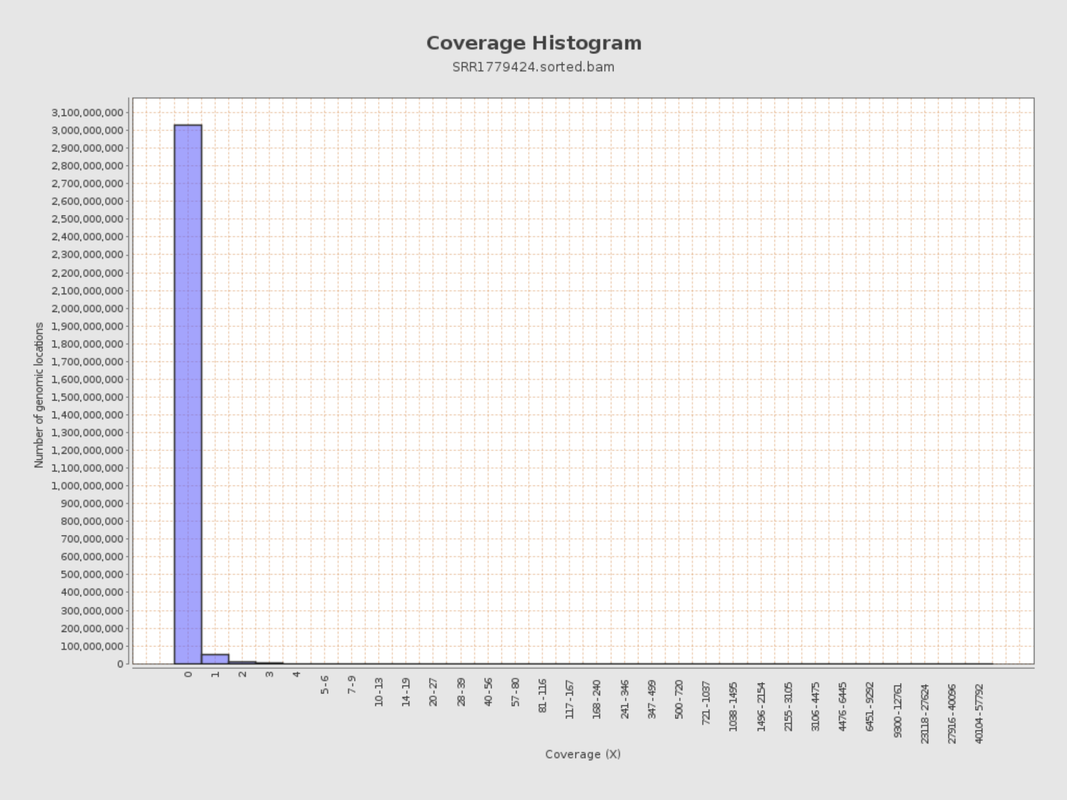
		bases	coverage	deviation
chr1	249250621	13326688	0.0535	9.5407
chr2	243199373	25144667	0.1034	21.6928
chr3	198022430	59310557	0.2995	101.577
chr4	191154276	13784590	0.0721	12.9805
chr5	180915260	18790286	0.1039	17.3635
chr6	171115067	11422605	0.0668	8.8271
chr7	159138663	7664367	0.0482	3.6188
chr8	146364022	17604751	0.1203	27.6318
chr9	141213431	37754605	0.2674	76.2983
chr10	135534747	5400561	0.0398	2.0765
chr11	135006516	5379515	0.0398	2.6916
chr12	133851895	10392604	0.0776	9.4149
chr13	115169878	9389088	0.0815	12.5786
chr14	107349540	3381045	0.0315	1.8011
chr15	102531392	2947078	0.0287	1.3815
chr16	90354753	4092419	0.0453	5.2777
chr17	81195210	4028894	0.0496	3.5764
chr18	78077248	3693395	0.0473	6.222
chr19	59128983	2705053	0.0457	6.2915
chr20	63025520	7303587	0.1159	26.2536
chr21	48129895	1656139	0.0344	0.8445
chr22	51304566	1218334	0.0237	1.626
chrMT	16571	730990	44.1126	15.7745
chrX	155270560	5091446	0.0328	5.6143

chrY	59373566	753017	0.0127	0.3848

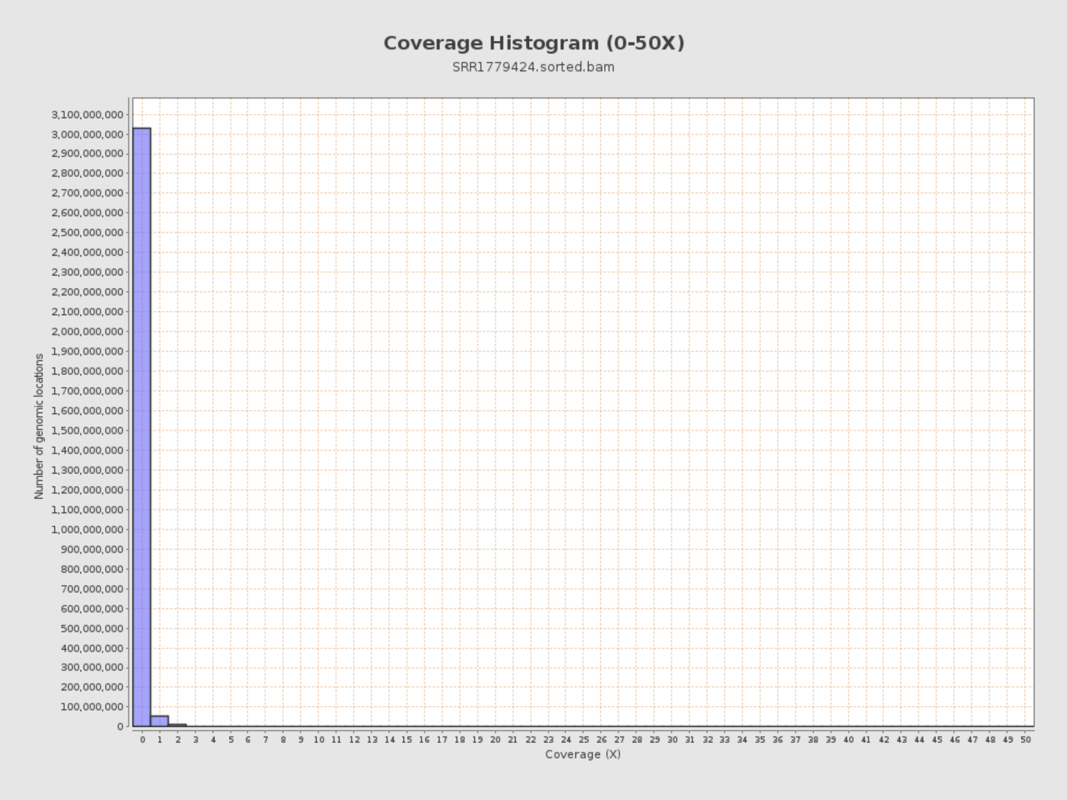
3. Results : Coverage across reference



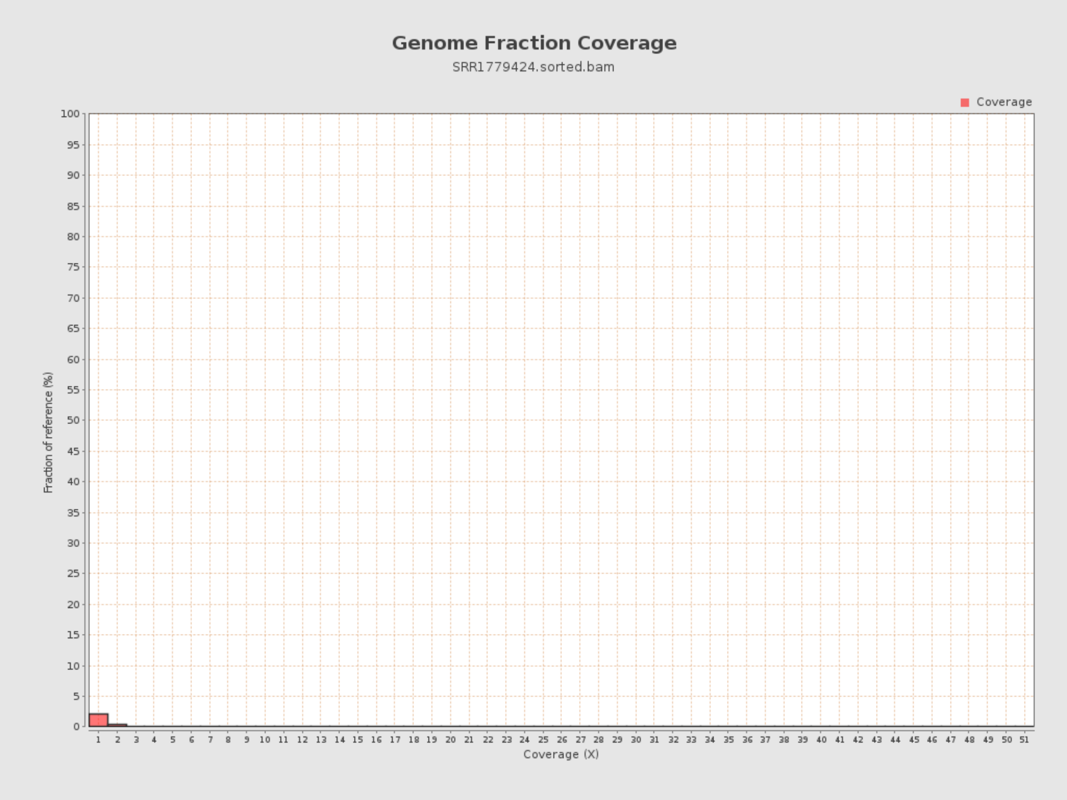
4. Results : Coverage Histogram



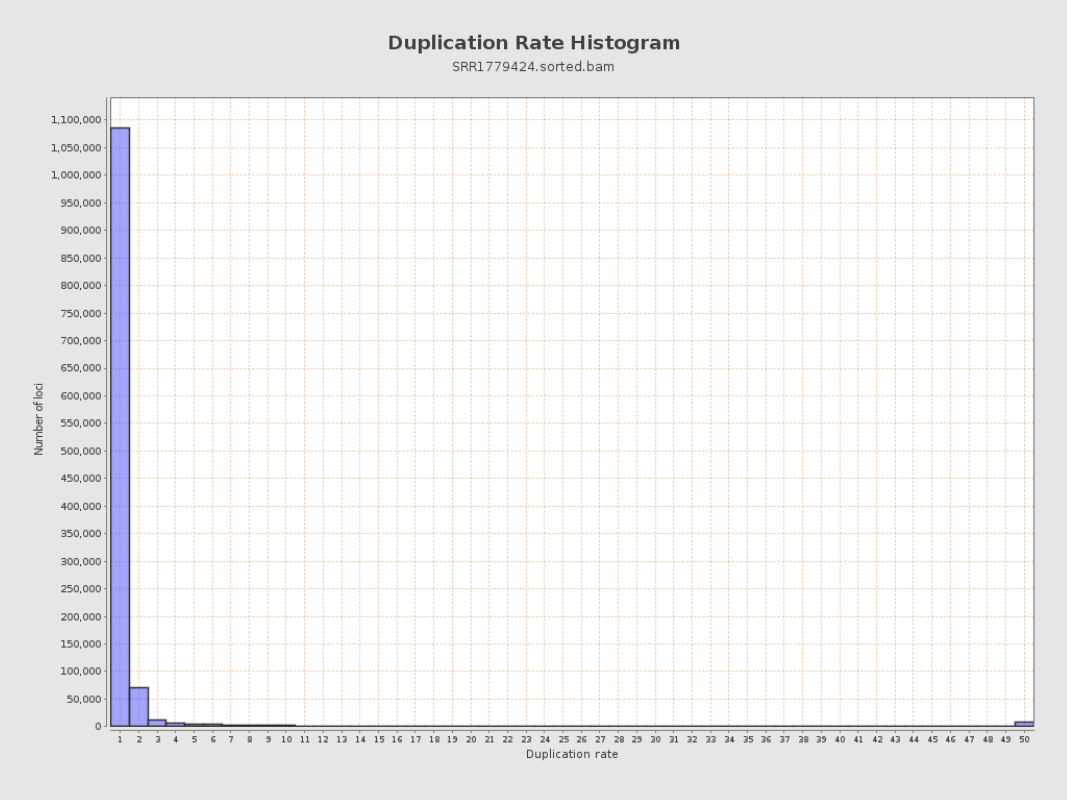
5. Results : Coverage Histogram (0-50X)



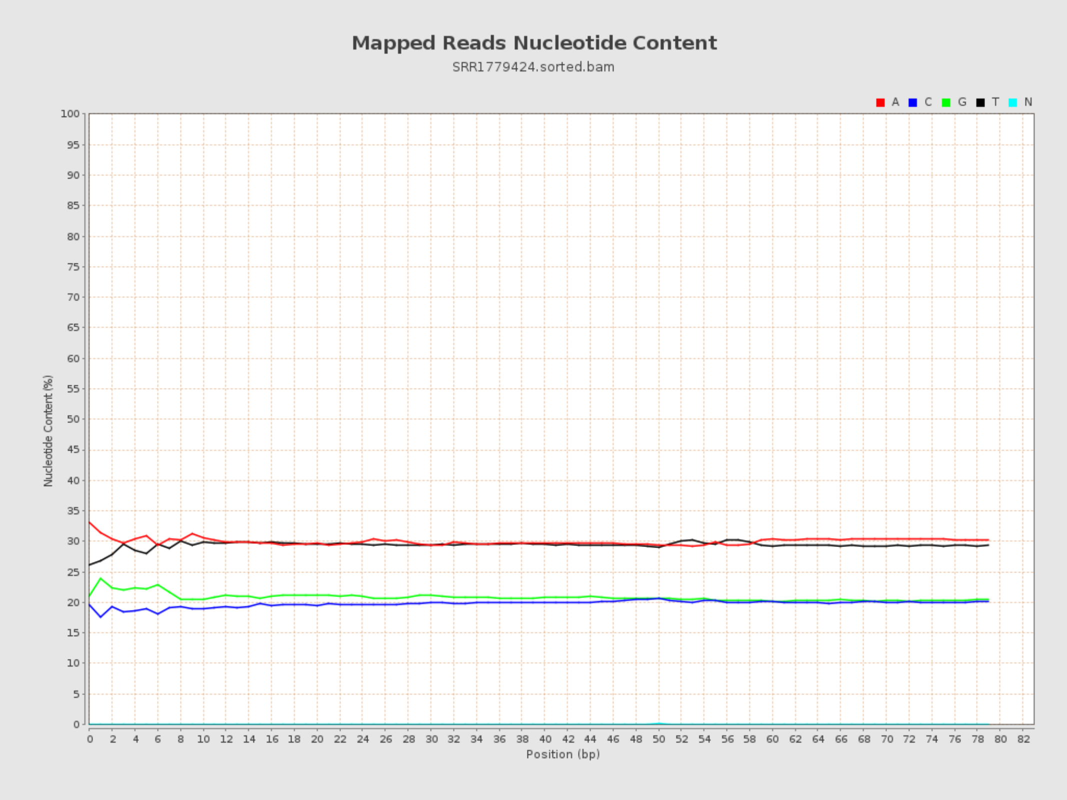
6. Results : Genome Fraction Coverage



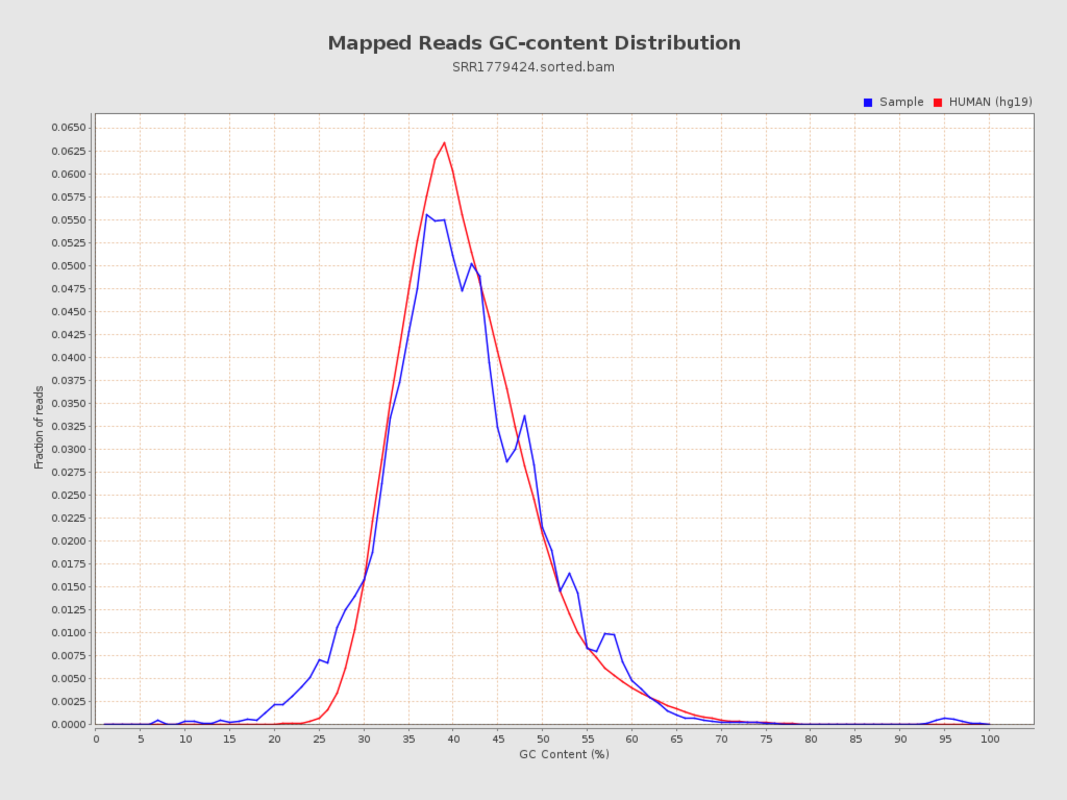
7. Results : Duplication Rate Histogram



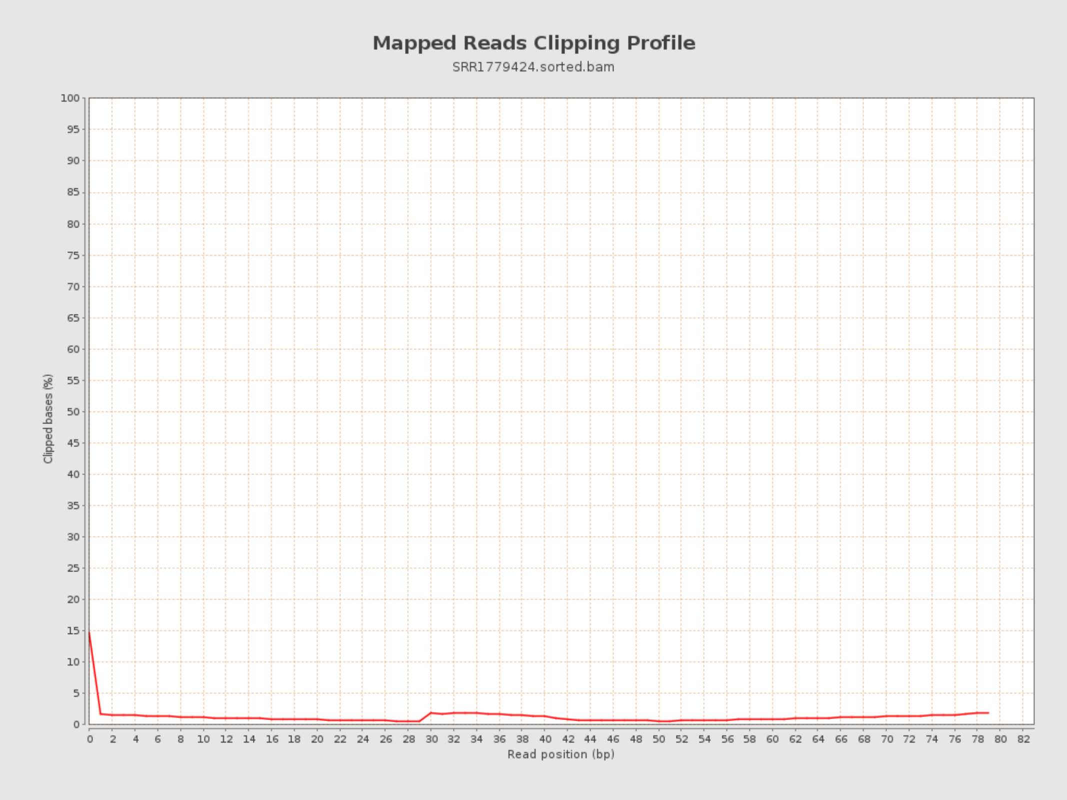
8. Results : Mapped Reads Nucleotide Content



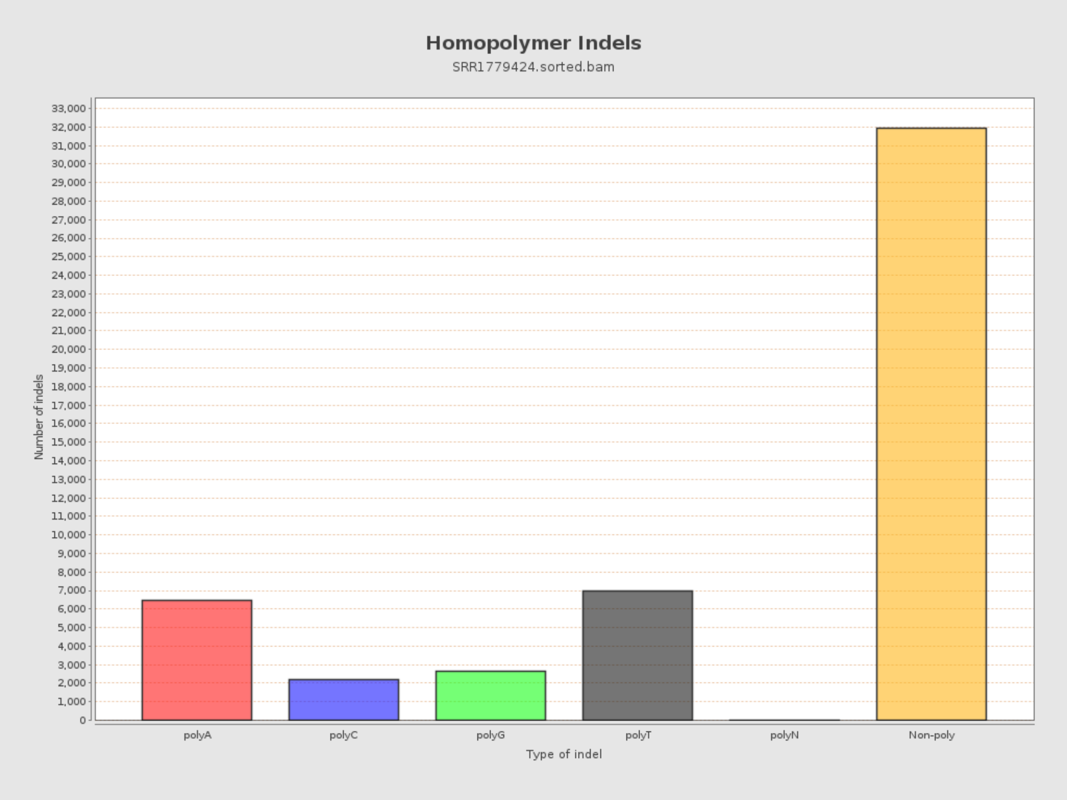
9. Results : Mapped Reads GC-content Distribution



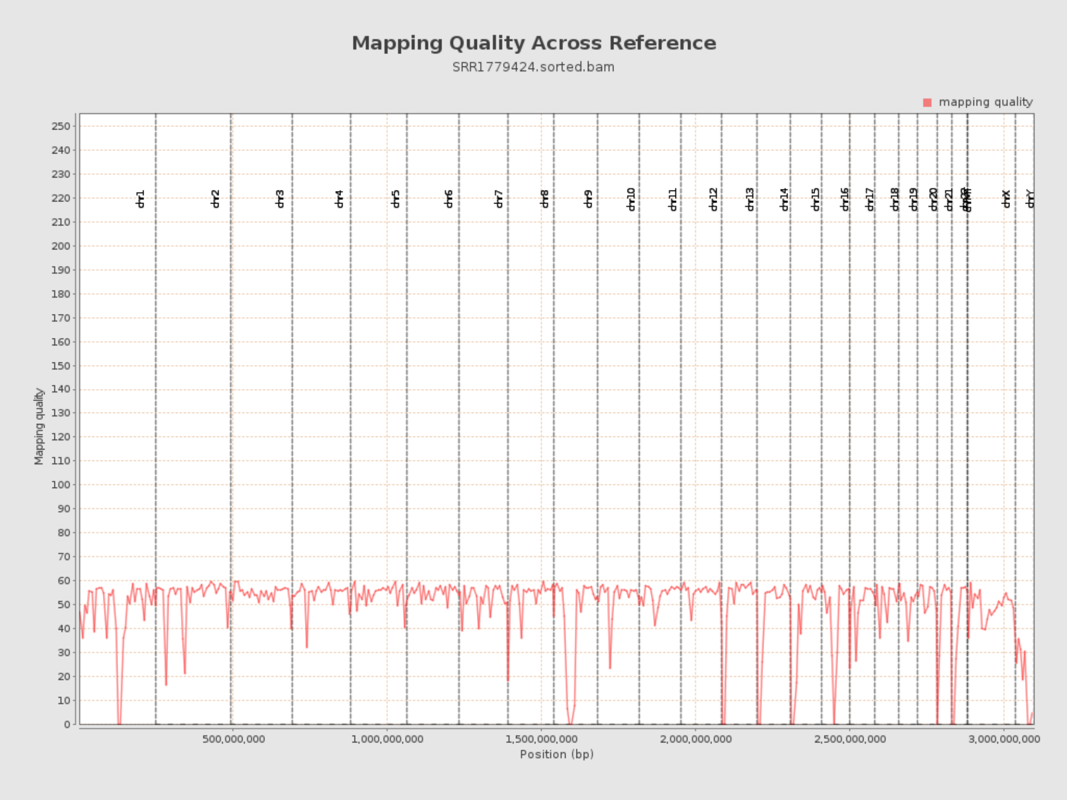
10. Results : Mapped Reads Clipping Profile



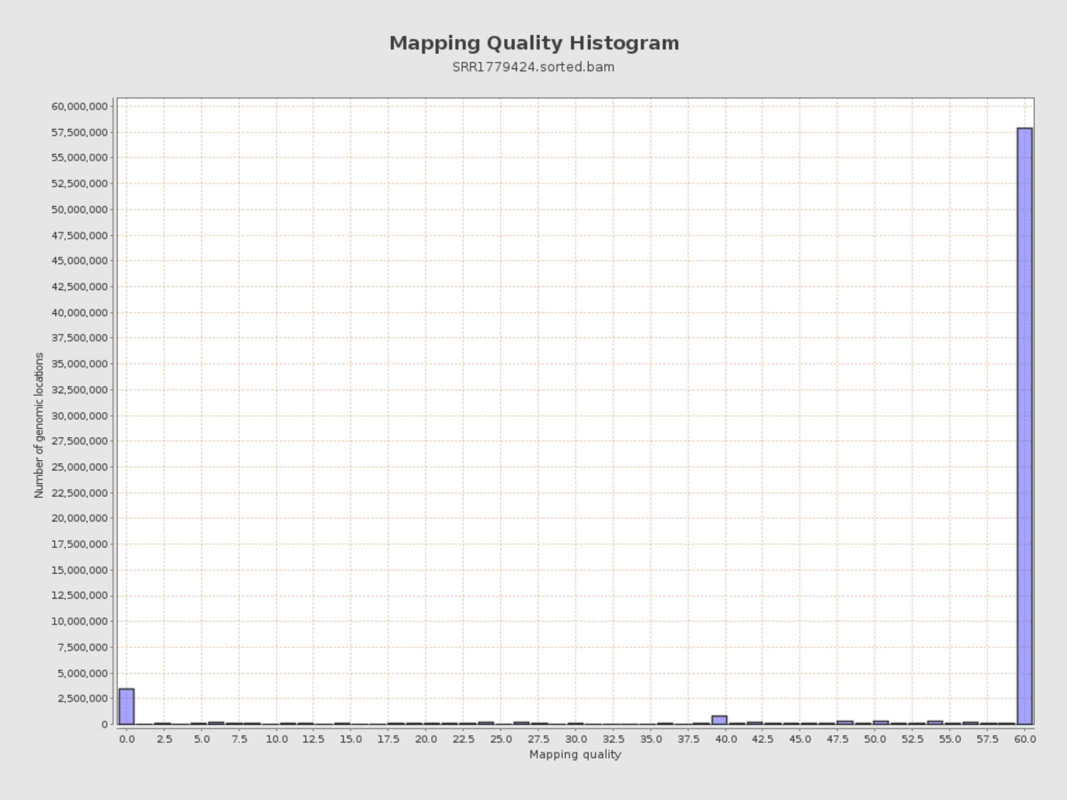
11. Results : Homopolymer Indels



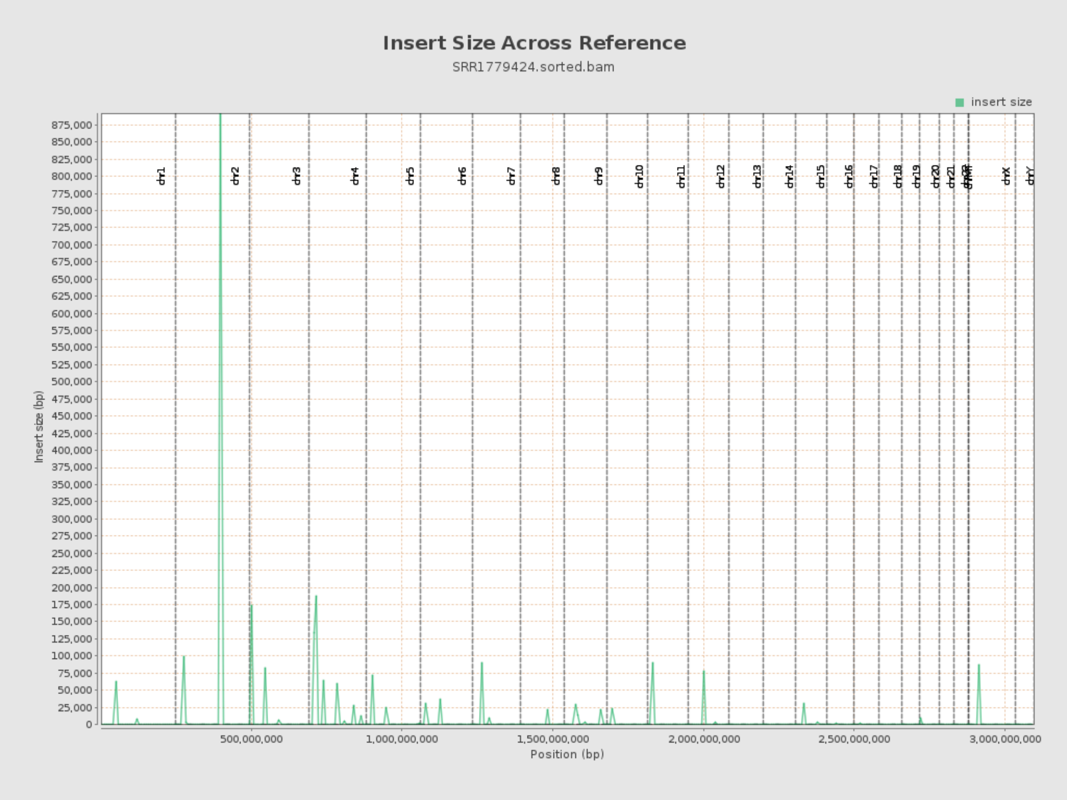
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram