Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:41:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124979.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_SRR3124979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124979_1.fastq.gz SRR3124979_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:41:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,042,770
Mapped reads	5,934,798 / 98.21%
Unmapped reads	107,972 / 1.79%
Mapped paired reads	5,934,798 / 98.21%
Mapped reads, first in pair	2,975,106 / 49.23%
Mapped reads, second in pair	2,959,692 / 48.98%
Mapped reads, both in pair	5,899,682 / 97.63%
Mapped reads, singletons	35,116 / 0.58%
Secondary alignments	0
Supplementary alignments	50,732 / 0.84%
Read min/max/mean length	30 / 101 / 101.33
Duplicated reads (estimated)	1,055,898 / 17.47%
Duplication rate	12.22%
Clipped reads	3,286,505 / 54.39%

2.2. ACGT Content

Number/percentage of A's	145,152,458 / 28.79%
Number/percentage of C's	92,241,261 / 18.3%
Number/percentage of T's	152,236,841 / 30.2%
Number/percentage of G's	114,466,497 / 22.71%
Number/percentage of N's	5,260 / 0%

GC Percentage	41.01%

2.3. Coverage

Mean	0.1629
Standard Deviation	2.5307

2.4. Mapping Quality

Mean Mapping Quality	52.28

2.5. Insert size

Mean	75,029.89
Standard Deviation	2,522,114.95
P25/Median/P75	124 / 169 / 234

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	4,144,133
Insertions	85,826
Mapped reads with at least one insertion	1.39%
Deletions	176,714
Mapped reads with at least one deletion	2.91%
Homopolymer indels	45.58%

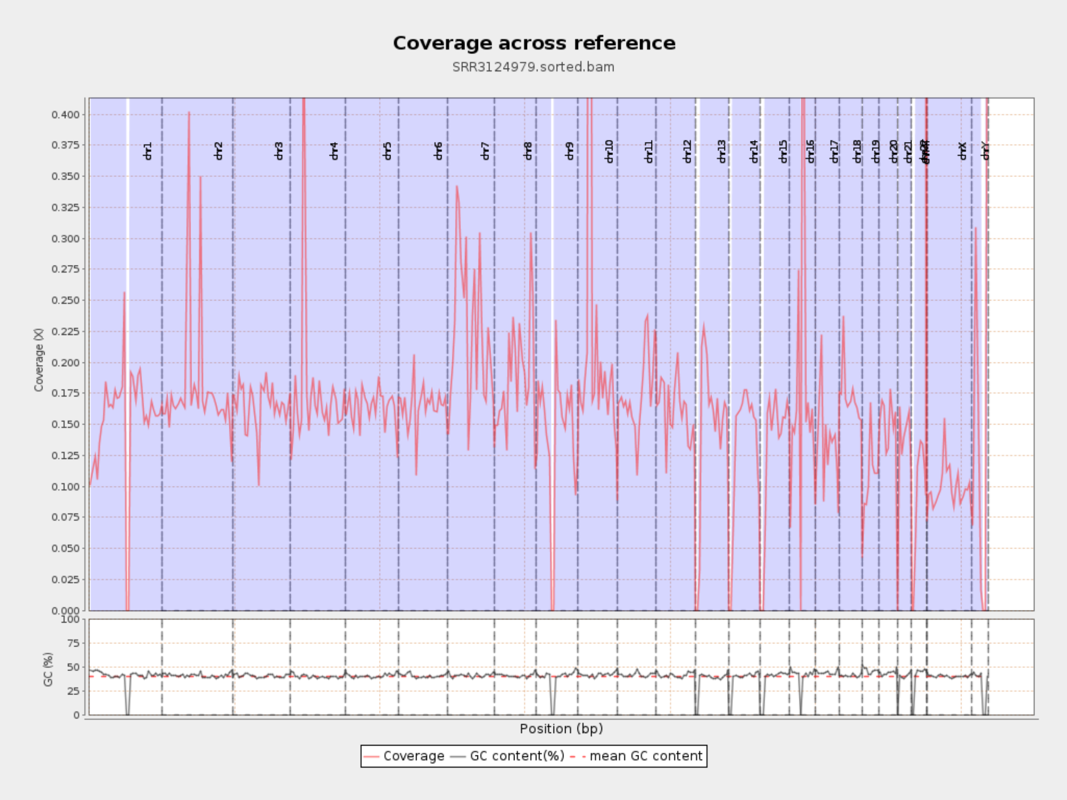
2.7. Chromosome stats

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

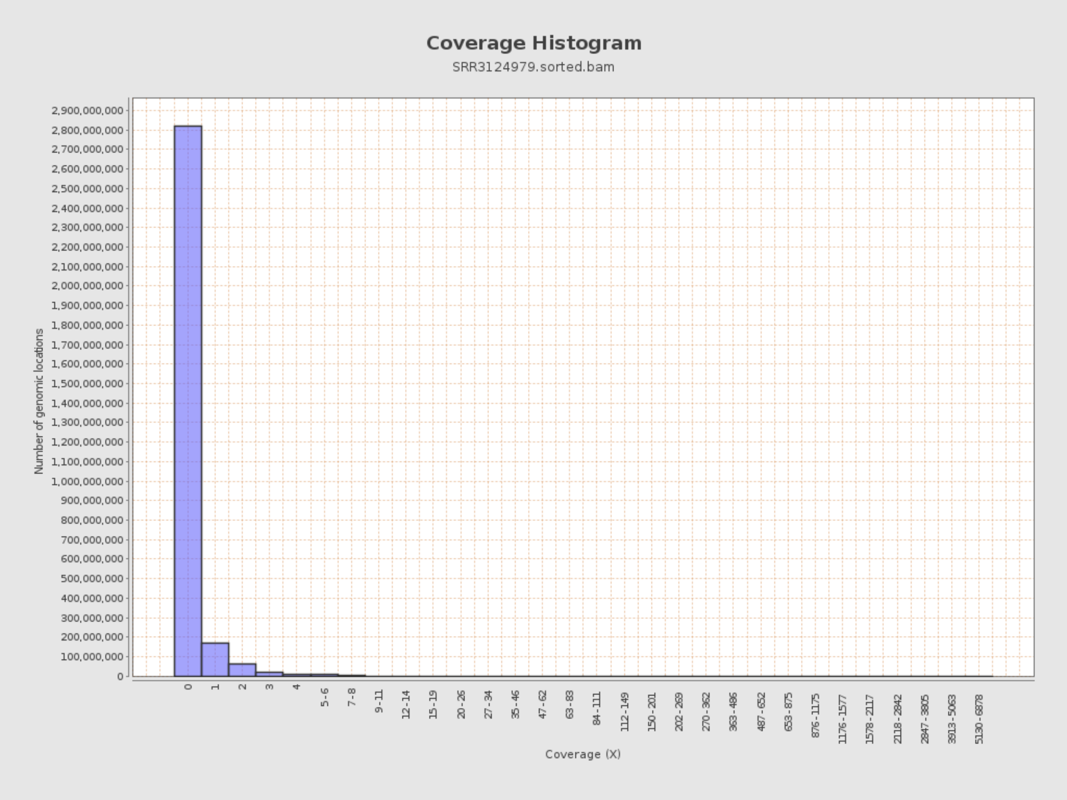
		bases	coverage	deviation
chr1	249250621	38134149	0.153	1.5697
chr2	243199373	44341469	0.1823	2.8066
chr3	198022430	32762706	0.1654	0.7358
chr4	191154276	33526578	0.1754	1.9826
chr5	180915260	29695729	0.1641	0.6959
chr6	171115067	28292778	0.1653	0.9221
chr7	159138663	36041356	0.2265	1.8698
chr8	146364022	27715251	0.1894	0.8628
chr9	141213431	20259876	0.1435	2.1617
chr10	135534747	32365603	0.2388	9.2065
chr11	135006516	23406130	0.1734	1.0857
chr12	133851895	21579928	0.1612	0.6532
chr13	115169878	16549126	0.1437	0.6114
chr14	107349540	14059274	0.131	0.6983
chr15	102531392	13195241	0.1287	0.6009
chr16	90354753	16705725	0.1849	3.6948
chr17	81195210	10941220	0.1348	1.6086
chr18	78077248	13606623	0.1743	2.4681
chr19	59128983	6438245	0.1089	0.9896
chr20	63025520	9446989	0.1499	0.844
chr21	48129895	6296794	0.1308	1.0733
chr22	51304566	4444370	0.0866	0.5696
chrMT	16571	170504	10.2893	7.7172
chrX	155270560	15426236	0.0994	0.7419

chrY	59373566	9031266	0.1521	3.8016

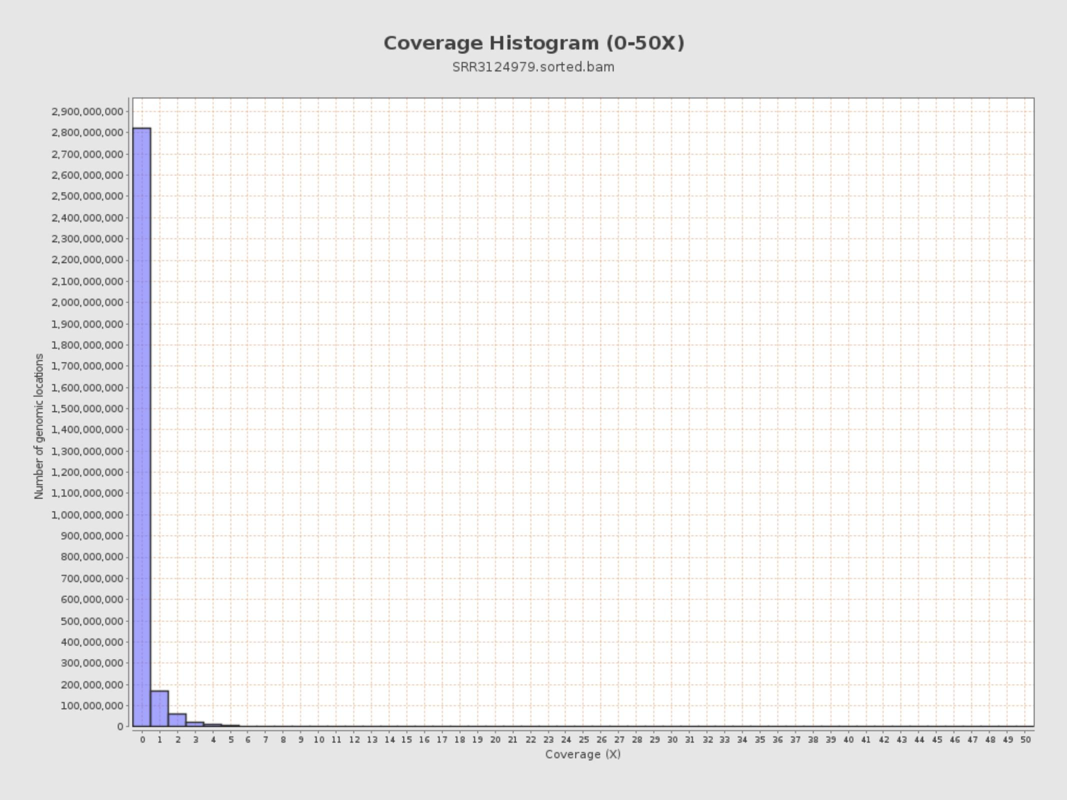
3. Results : Coverage across reference



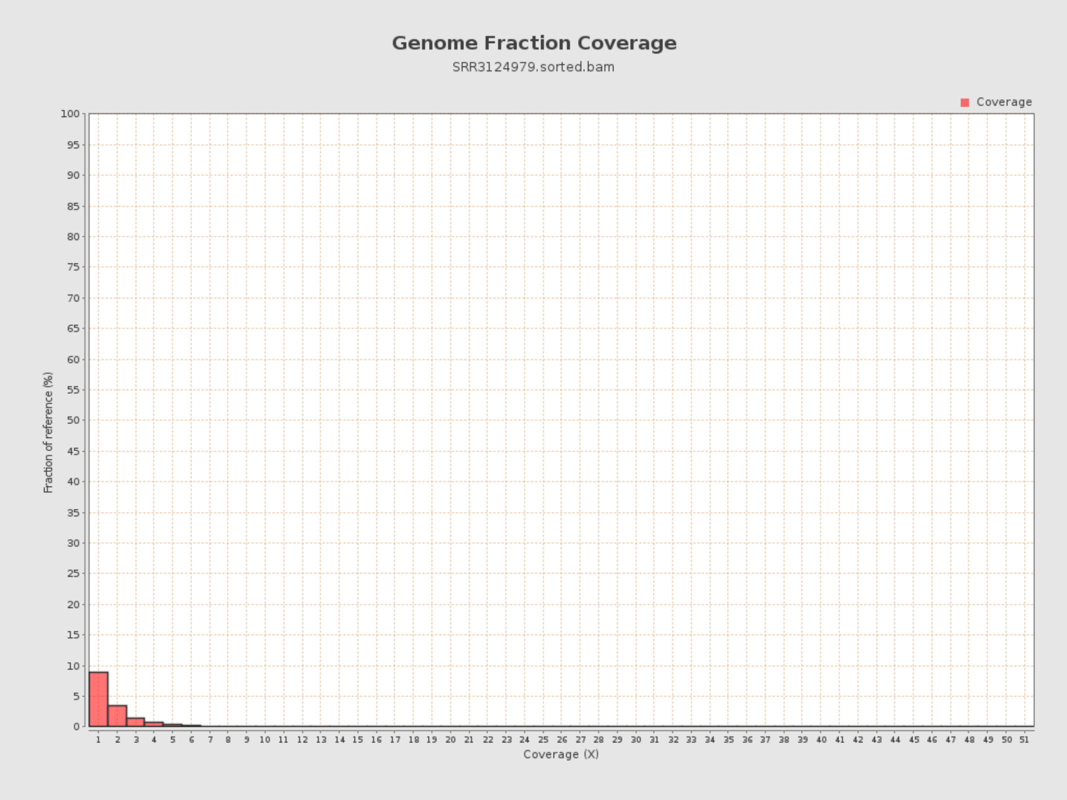
4. Results : Coverage Histogram



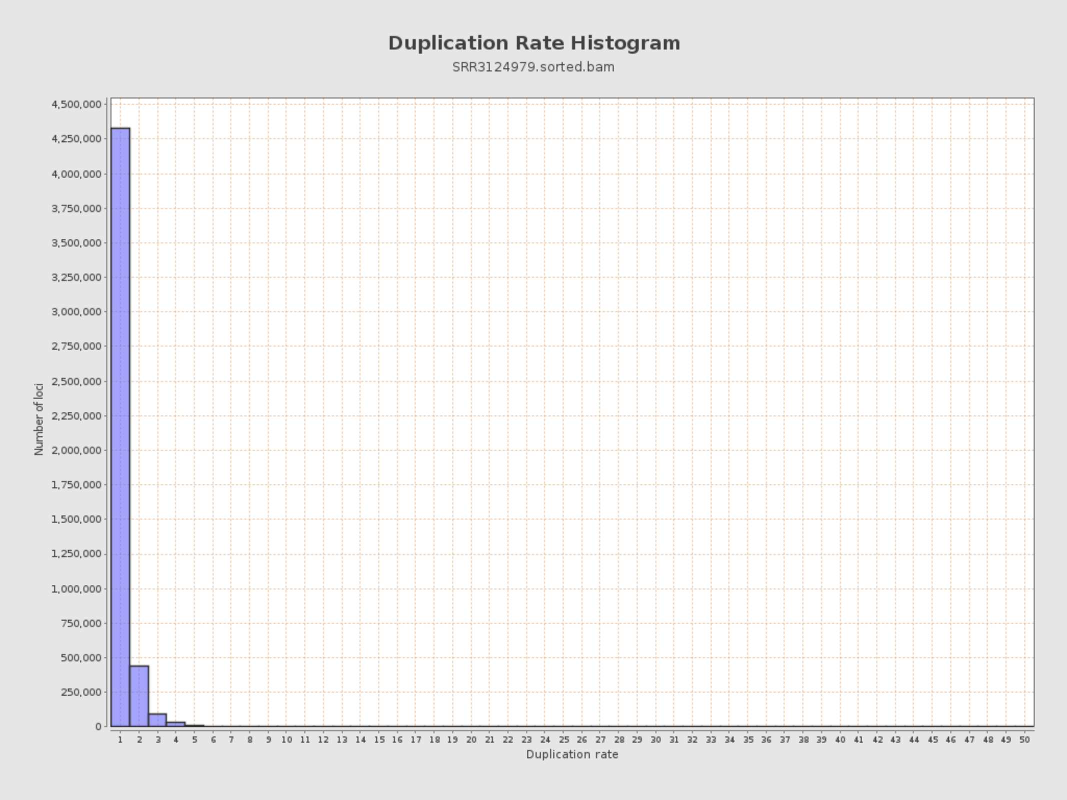
5. Results : Coverage Histogram (0-50X)



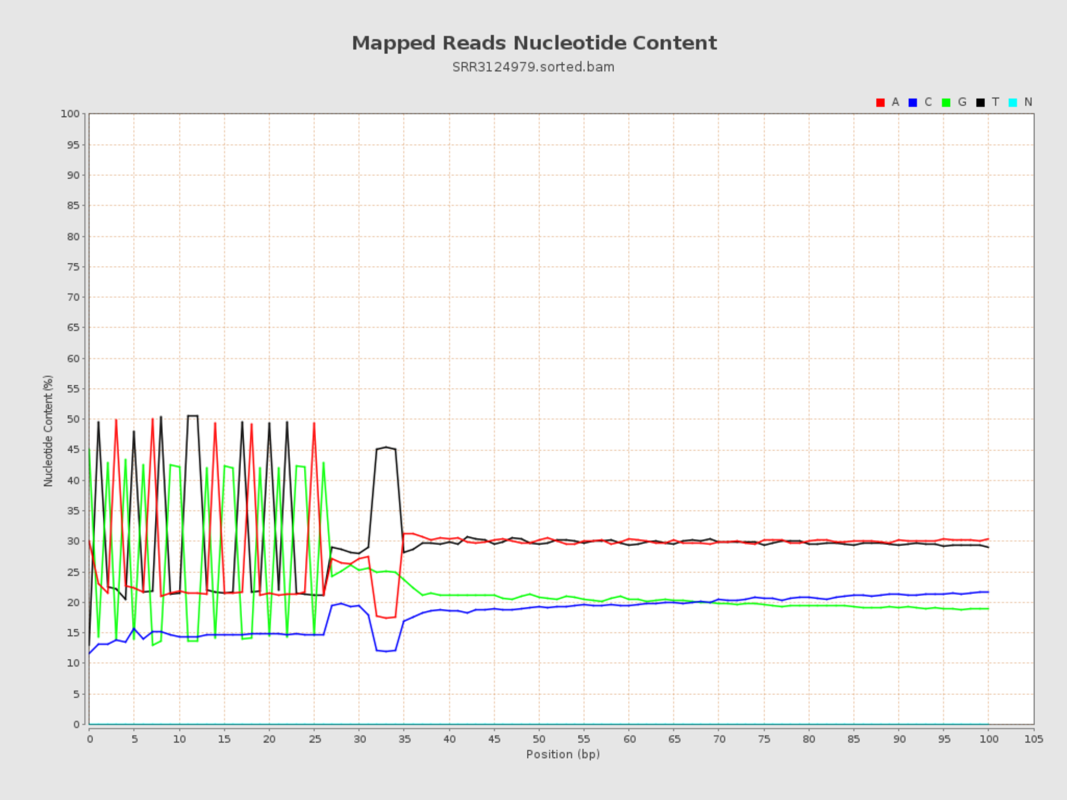
6. Results : Genome Fraction Coverage



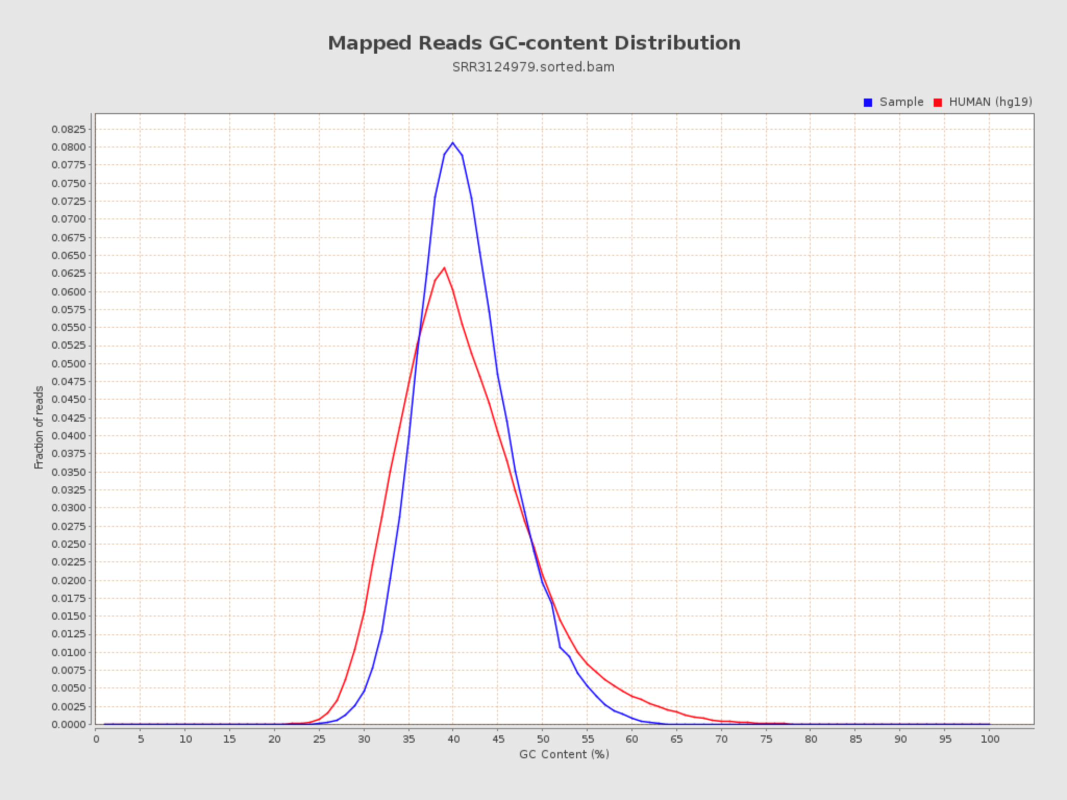
7. Results : Duplication Rate Histogram



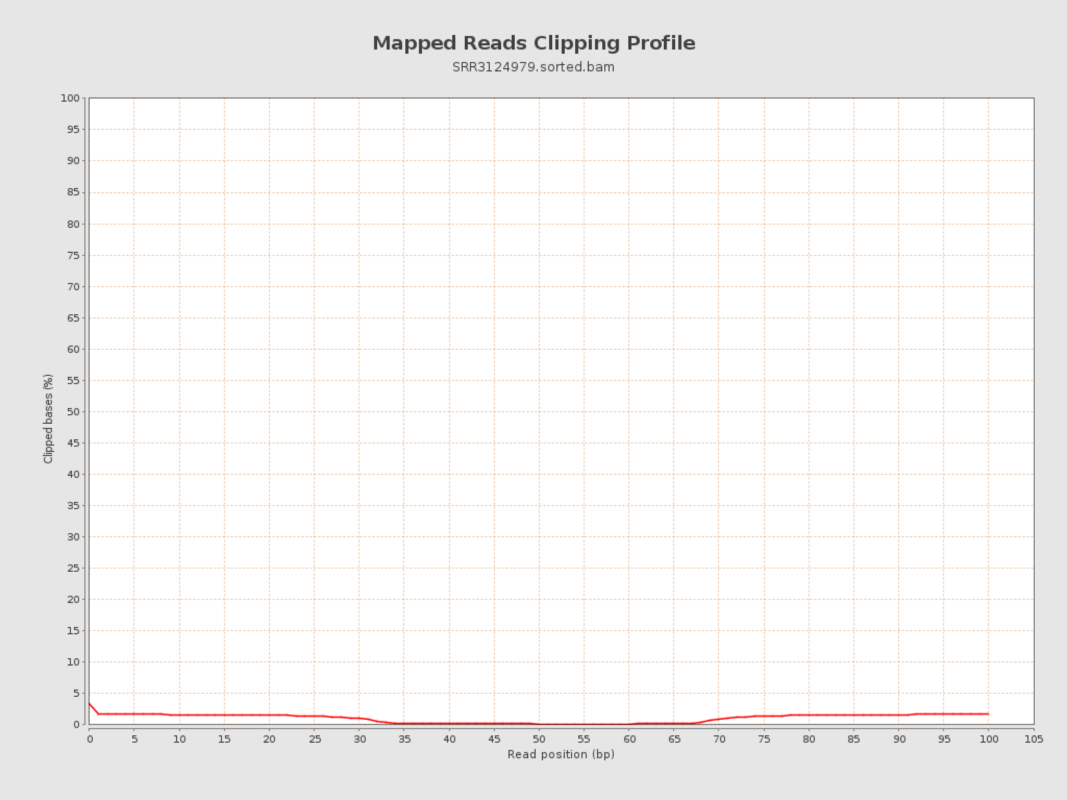
8. Results : Mapped Reads Nucleotide Content



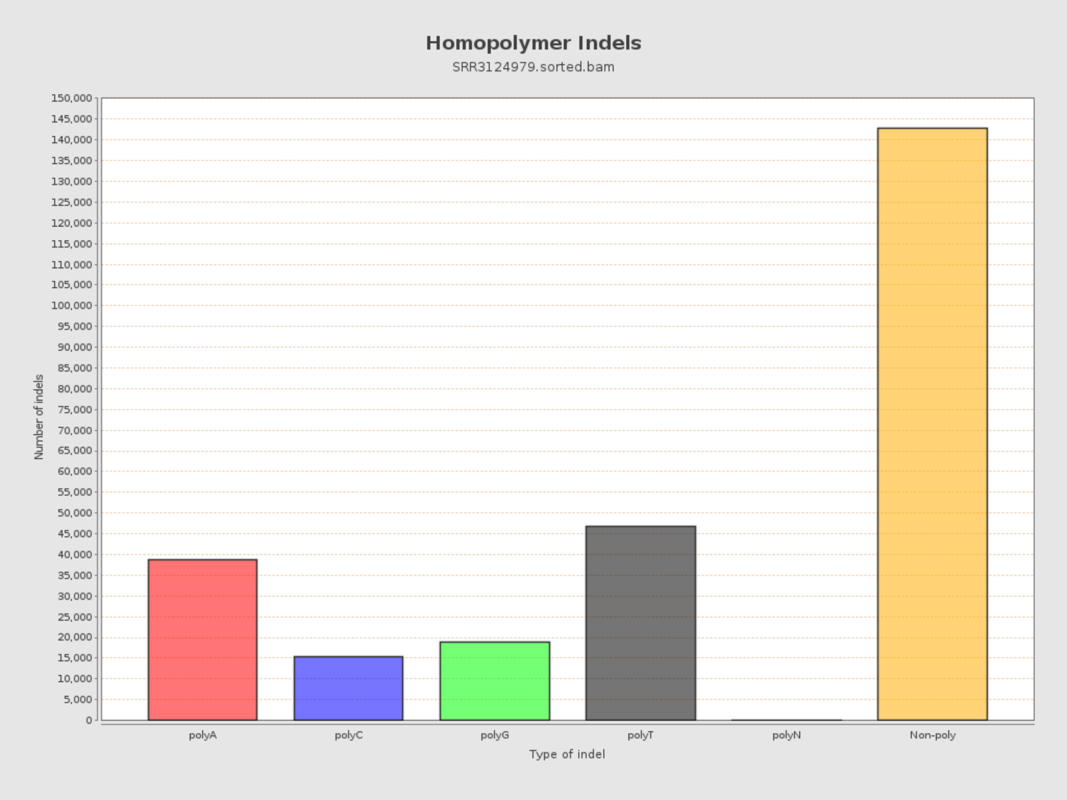
9. Results : Mapped Reads GC-content Distribution



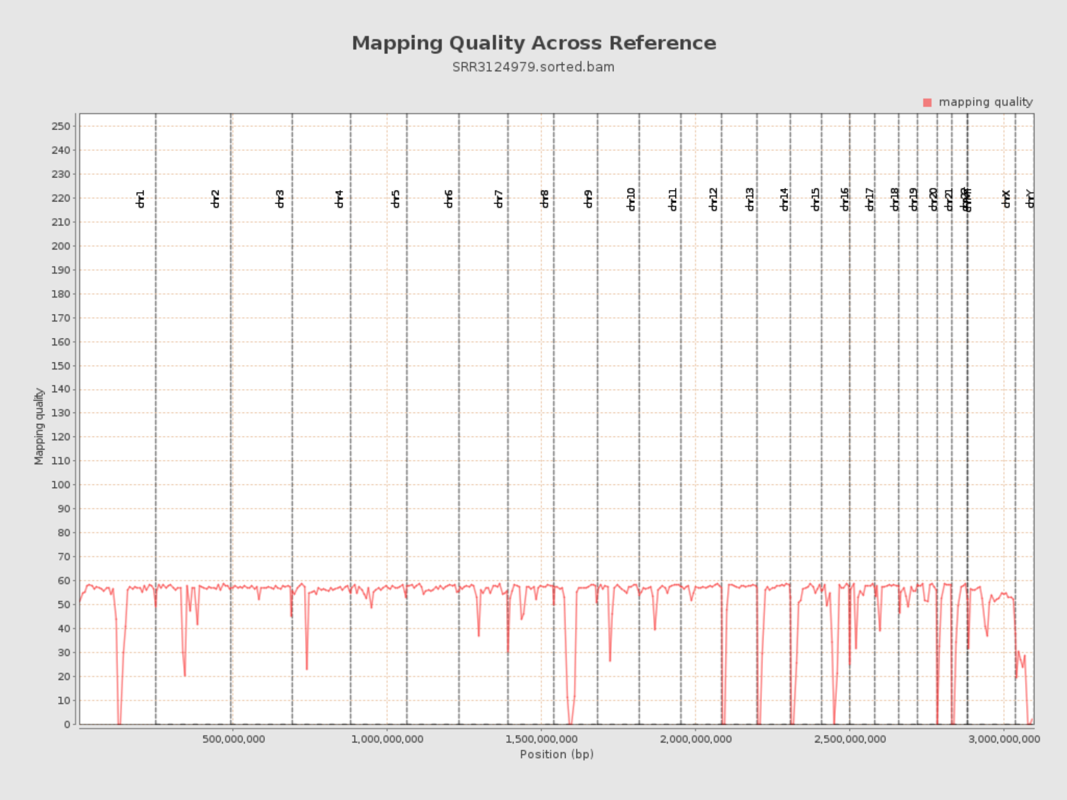
10. Results : Mapped Reads Clipping Profile



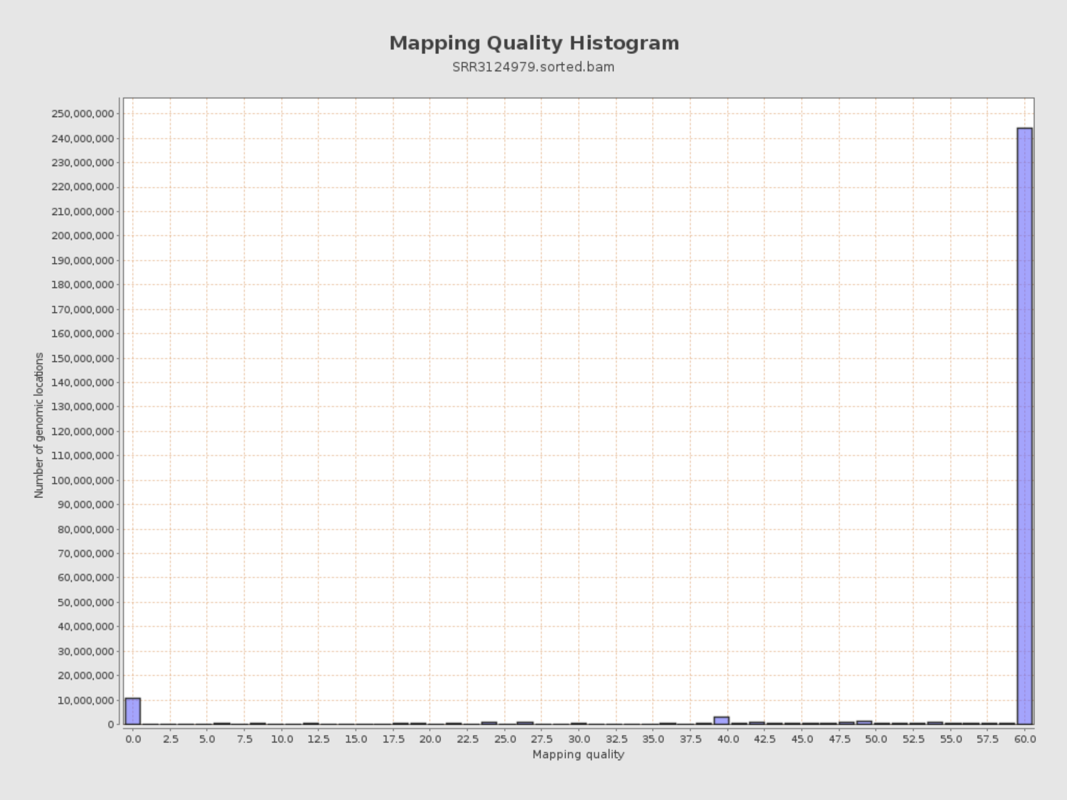
11. Results : Homopolymer Indels



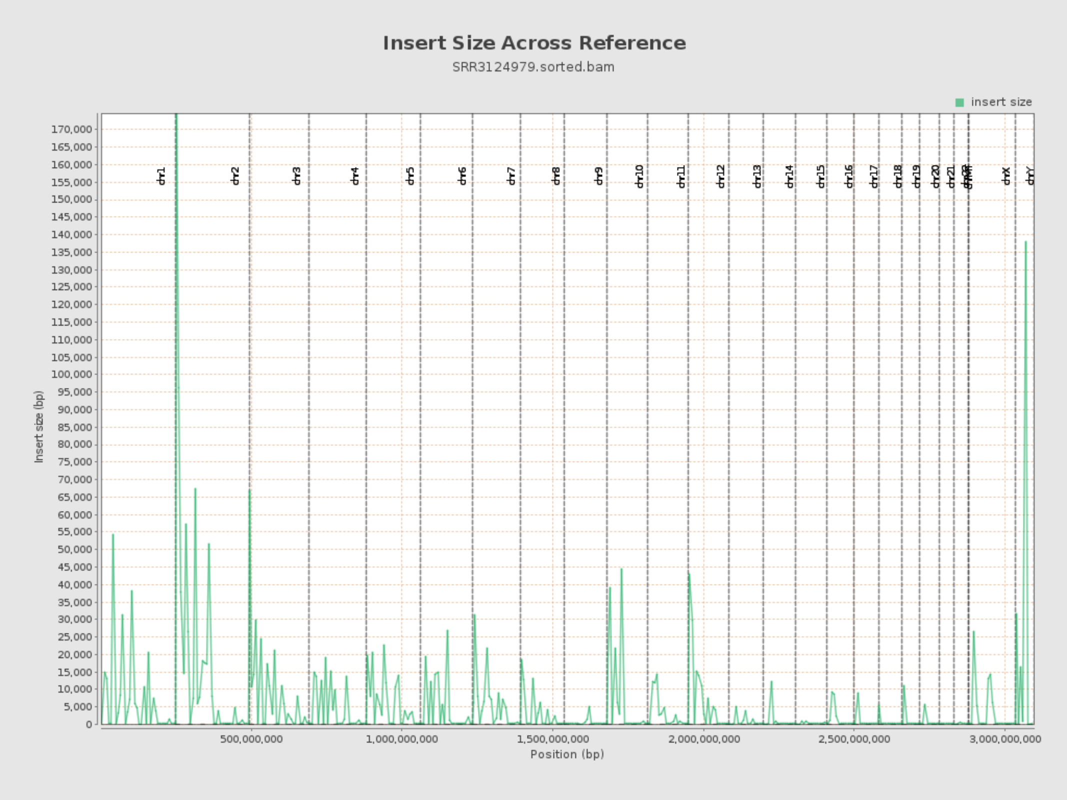
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram