Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:47:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975217.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_SRR975217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975217_1.fastq.gz SRR975217_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:47:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,594,582
Mapped reads	3,557,576 / 98.97%
Unmapped reads	37,006 / 1.03%
Mapped paired reads	3,557,576 / 98.97%
Mapped reads, first in pair	1,785,882 / 49.68%
Mapped reads, second in pair	1,771,694 / 49.29%
Mapped reads, both in pair	3,540,418 / 98.49%
Mapped reads, singletons	17,158 / 0.48%
Secondary alignments	0
Supplementary alignments	51,453 / 1.43%
Read min/max/mean length	30 / 151 / 151.72
Duplicated reads (estimated)	517,490 / 14.4%
Duplication rate	12.08%
Clipped reads	1,402,057 / 39%

2.2. ACGT Content

Number/percentage of A's	149,169,644 / 29.41%
Number/percentage of C's	103,614,133 / 20.43%
Number/percentage of T's	147,768,780 / 29.13%
Number/percentage of G's	106,610,969 / 21.02%
Number/percentage of N's	45,738 / 0.01%

GC Percentage	41.45%

2.3. Coverage

Mean	0.164
Standard Deviation	2.3125

2.4. Mapping Quality

Mean Mapping Quality	53.76

2.5. Insert size

Mean	113,196.15
Standard Deviation	3,337,071.05
P25/Median/P75	147 / 177 / 221

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	4,660,326
Insertions	95,385
Mapped reads with at least one insertion	2.52%
Deletions	192,566
Mapped reads with at least one deletion	5.19%
Homopolymer indels	47.13%

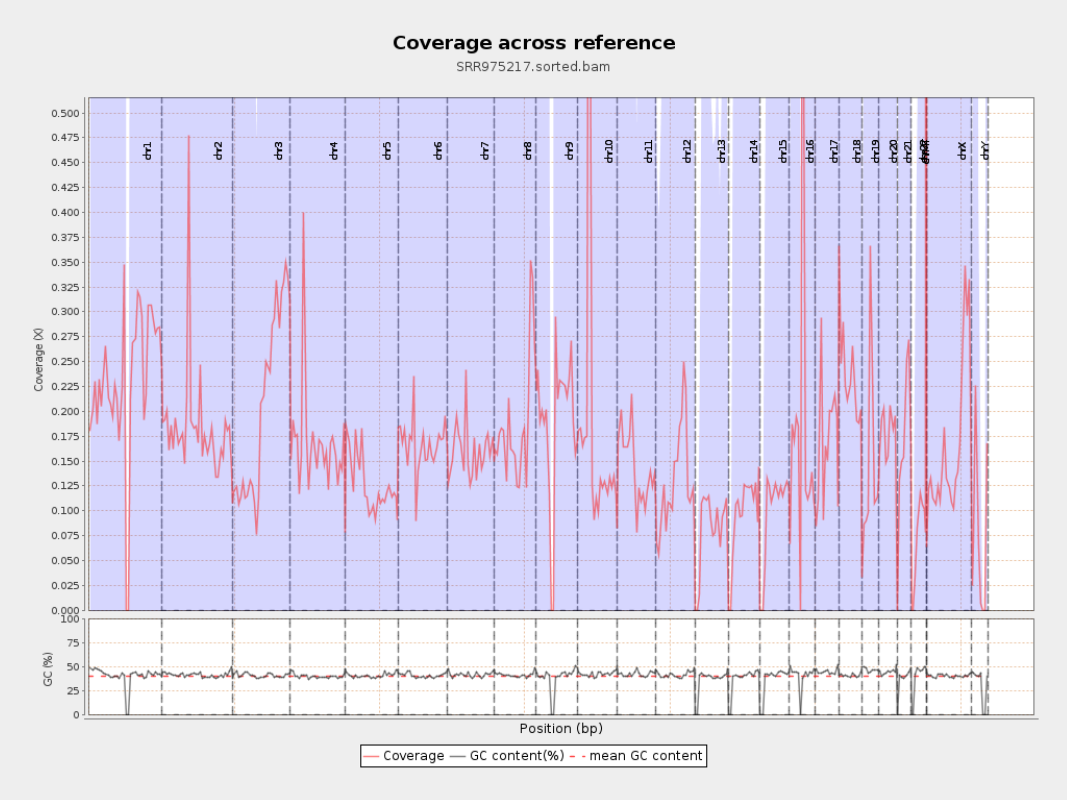
2.7. Chromosome stats

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

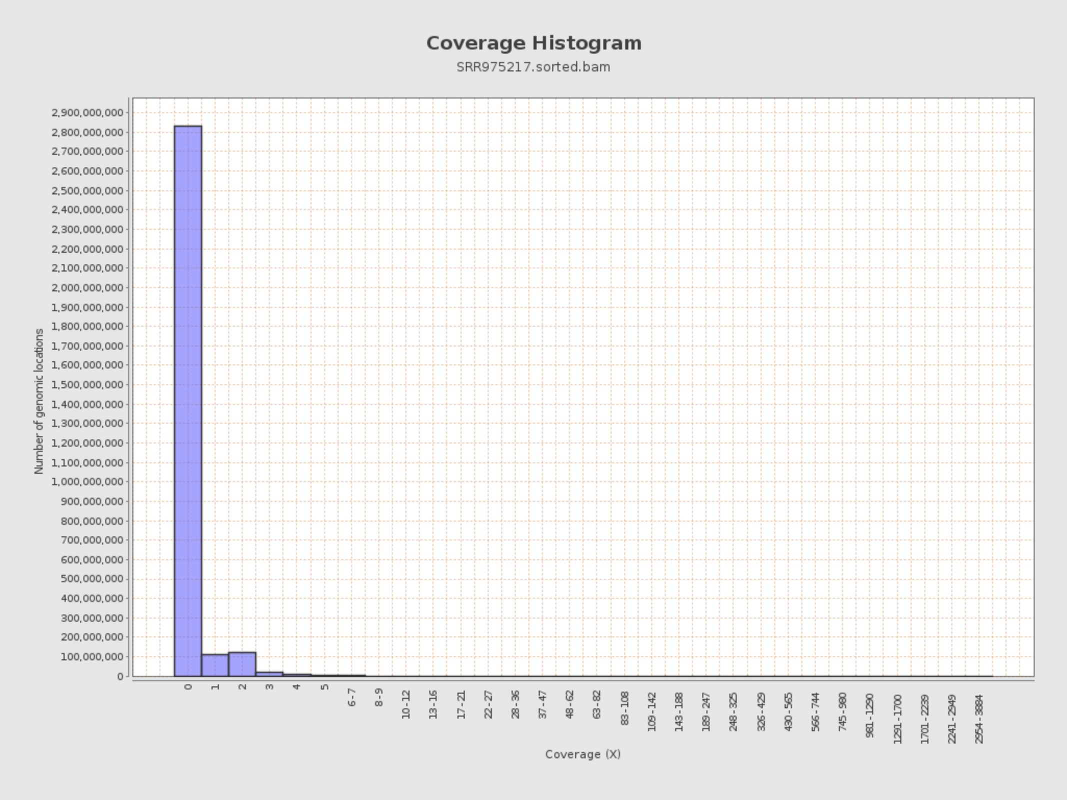
		bases	coverage	deviation
chr1	249250621	57556927	0.2309	2.2528
chr2	243199373	44958938	0.1849	2.0981
chr3	198022430	40024775	0.2021	0.7337
chr4	191154276	31871464	0.1667	1.8744
chr5	180915260	22971119	0.127	0.5253
chr6	171115067	28566245	0.1669	0.9269
chr7	159138663	25591999	0.1608	1.9837
chr8	146364022	27439880	0.1875	0.8052
chr9	141213431	26660304	0.1888	2.9242
chr10	135534747	25010615	0.1845	7.336
chr11	135006516	19179658	0.1421	1.7259
chr12	133851895	17469949	0.1305	0.5304
chr13	115169878	9253242	0.0803	0.4023
chr14	107349540	10117862	0.0943	0.4574
chr15	102531392	10130332	0.0988	0.4525
chr16	90354753	16903561	0.1871	4.1866
chr17	81195210	13630755	0.1679	2.599
chr18	78077248	18347782	0.235	2.8141
chr19	59128983	8942602	0.1512	1.3617
chr20	63025520	11136359	0.1767	0.9022
chr21	48129895	8249155	0.1714	1.1761
chr22	51304566	3596974	0.0701	0.394
chrMT	16571	60783	3.668	3.1283
chrX	155270560	25661894	0.1653	0.835

chrY	59373566	4265666	0.0718	2.6583

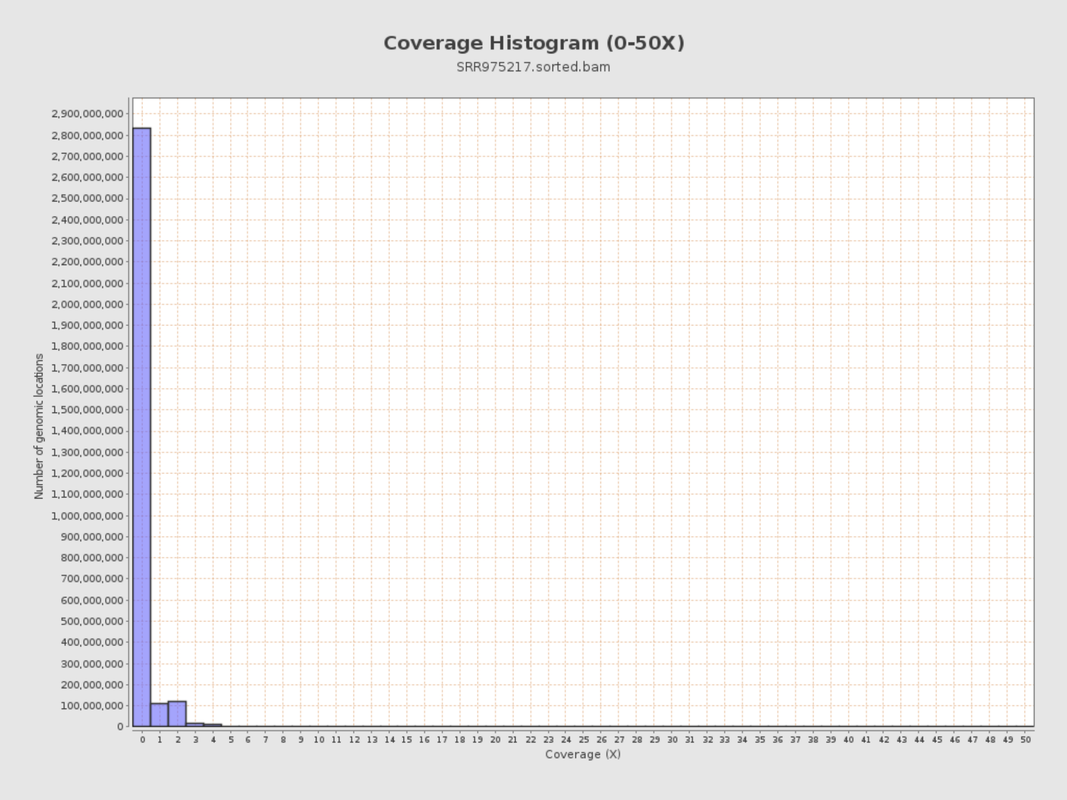
3. Results : Coverage across reference



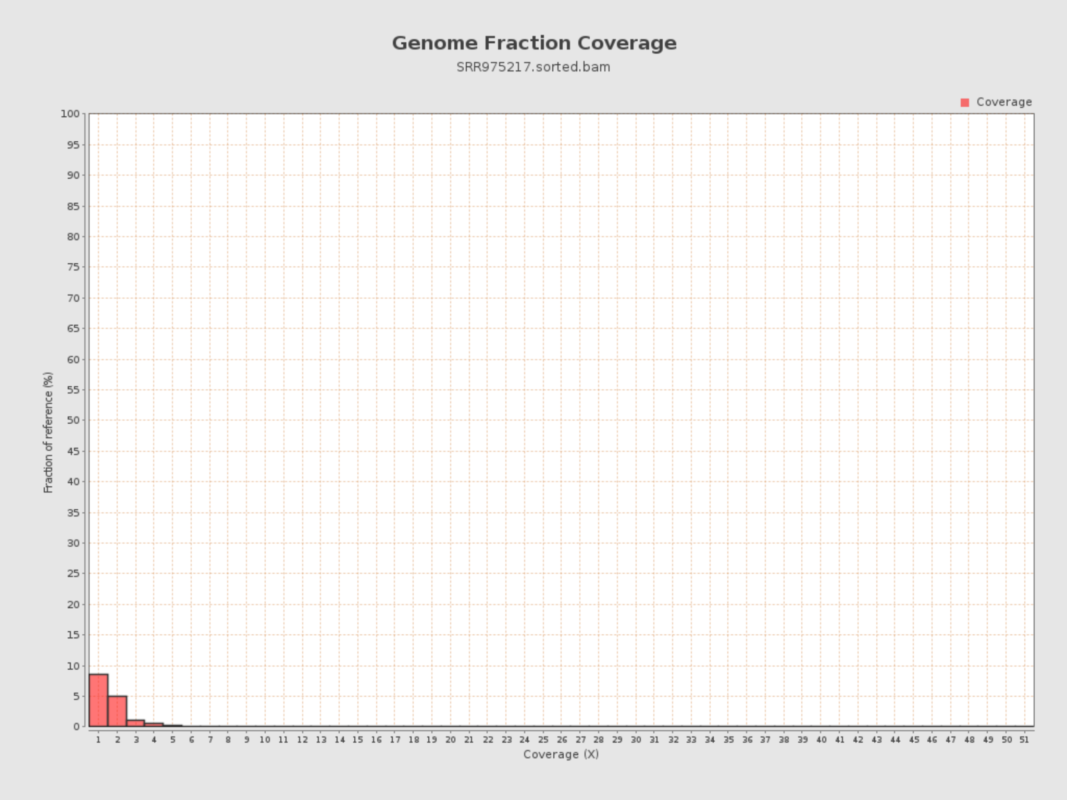
4. Results : Coverage Histogram



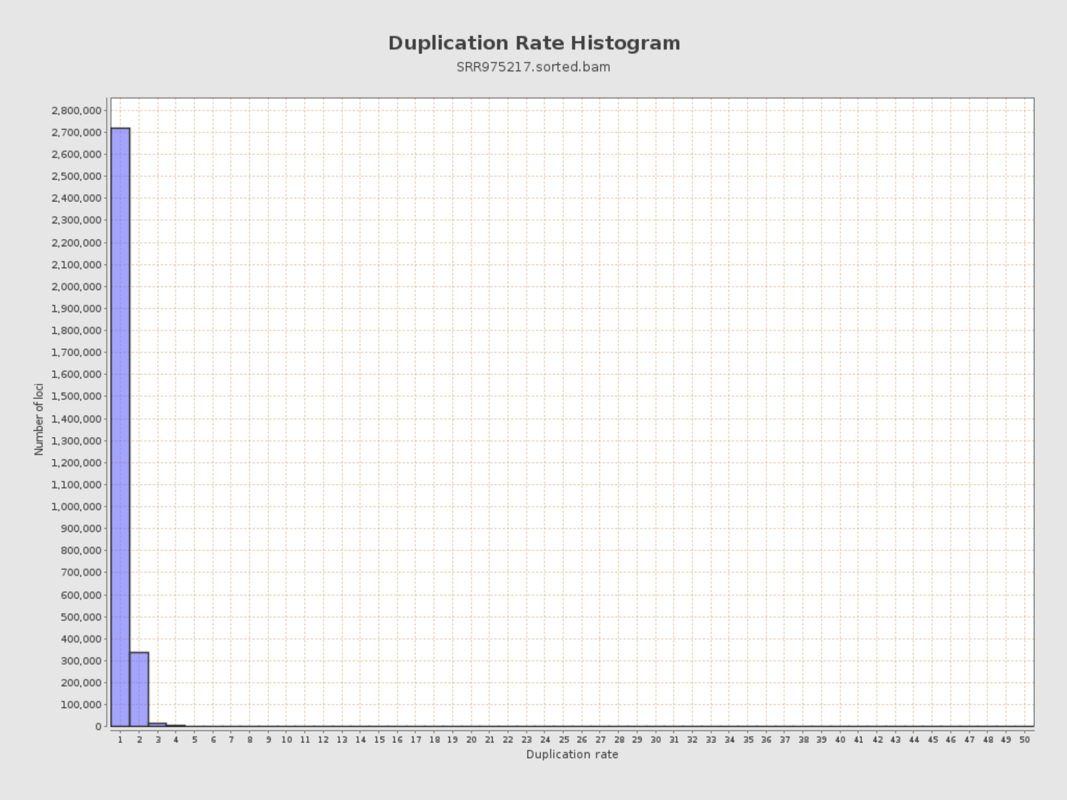
5. Results : Coverage Histogram (0-50X)



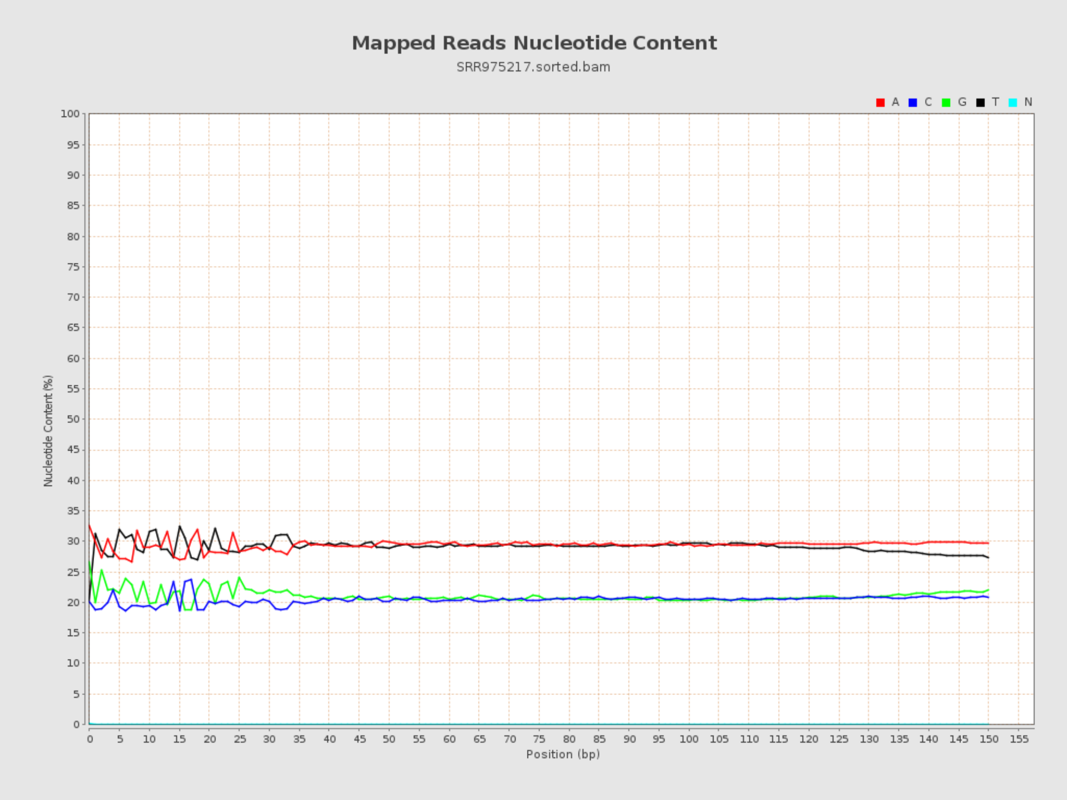
6. Results : Genome Fraction Coverage



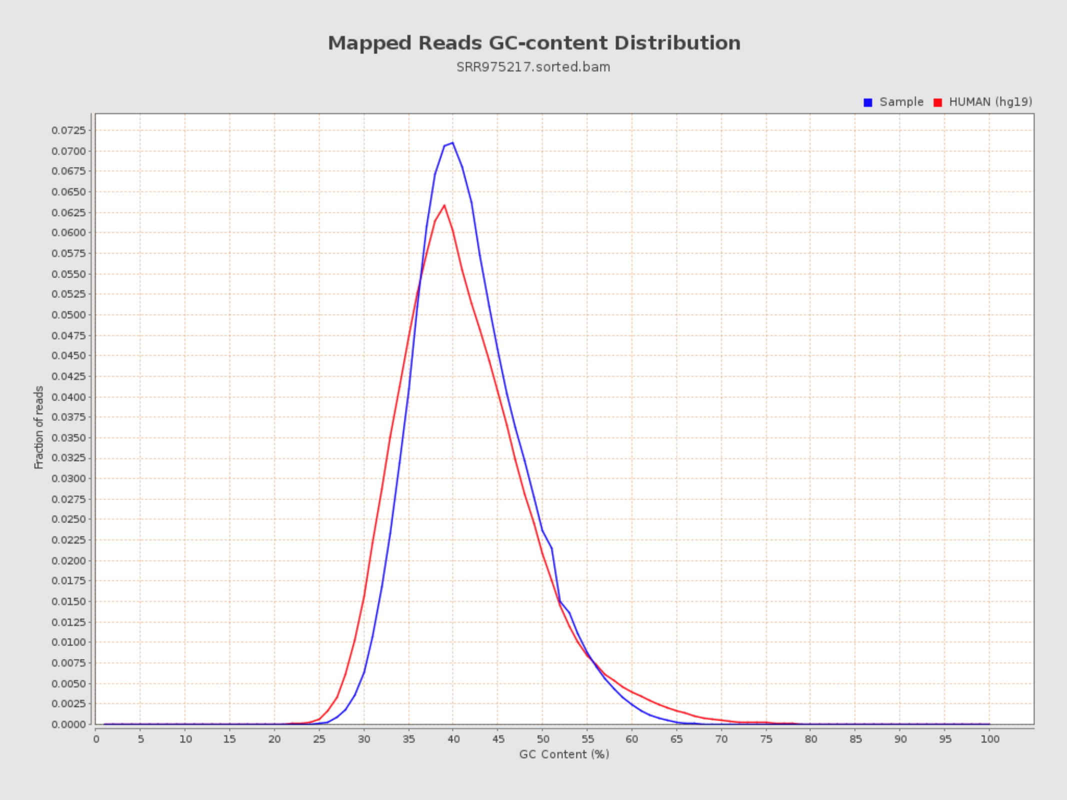
7. Results : Duplication Rate Histogram



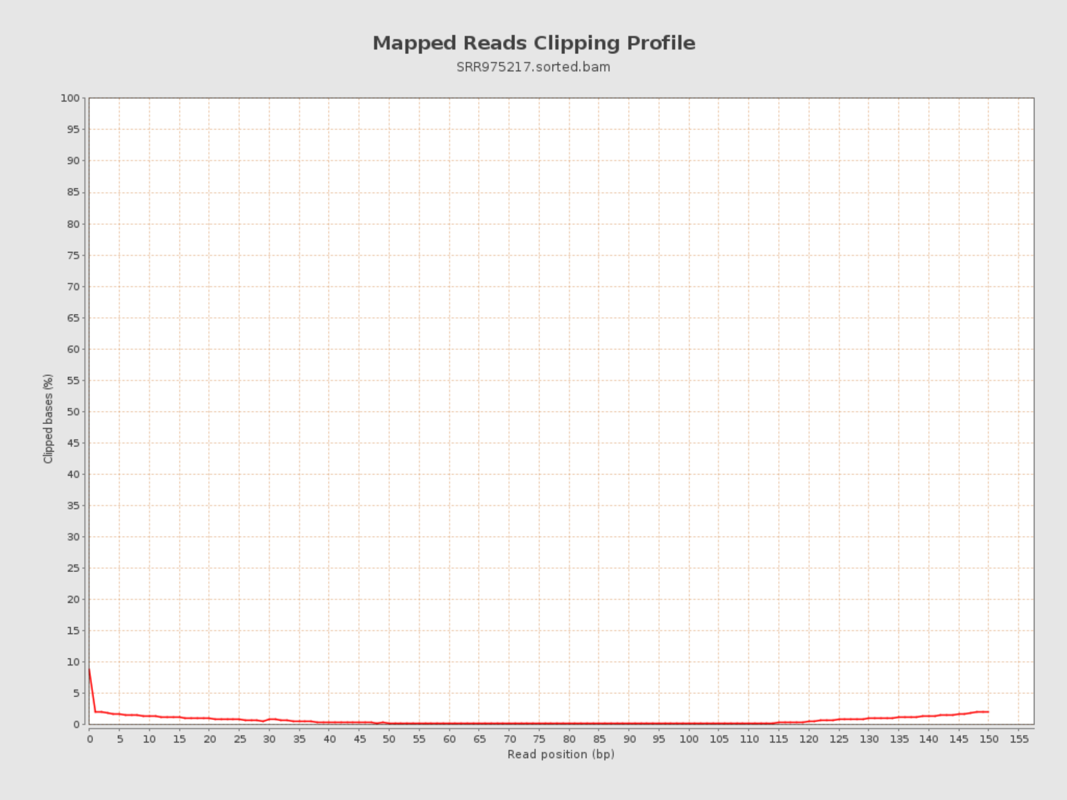
8. Results : Mapped Reads Nucleotide Content



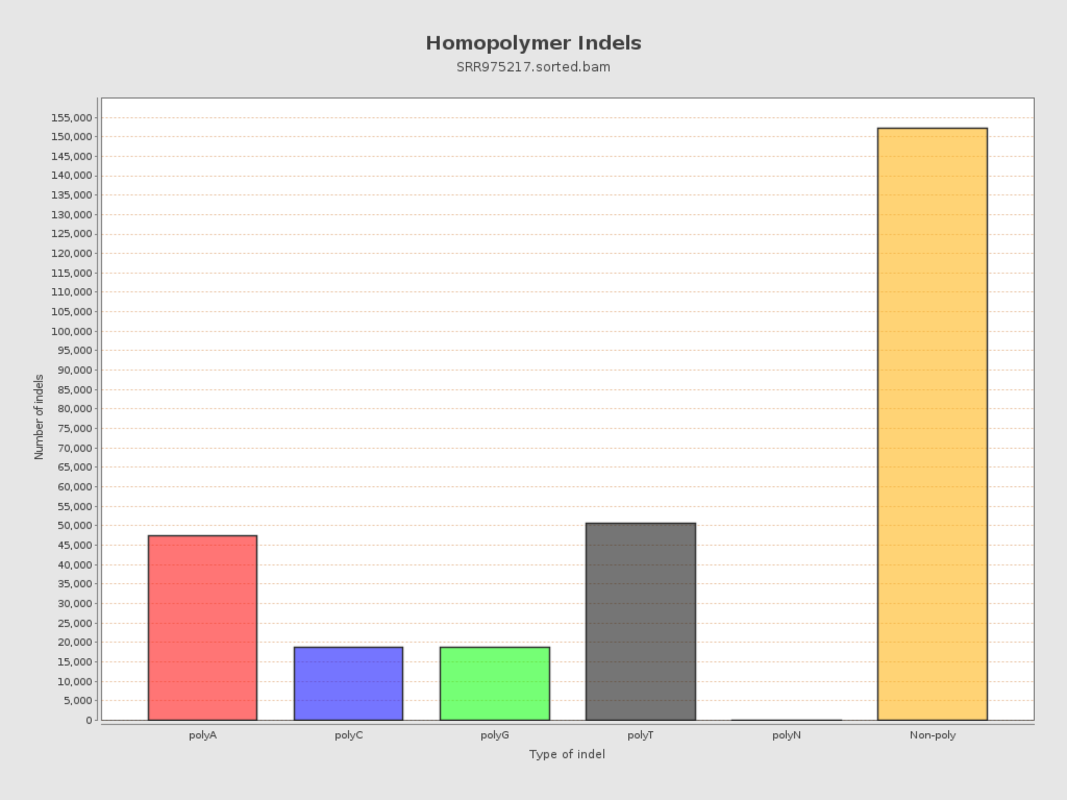
9. Results : Mapped Reads GC-content Distribution



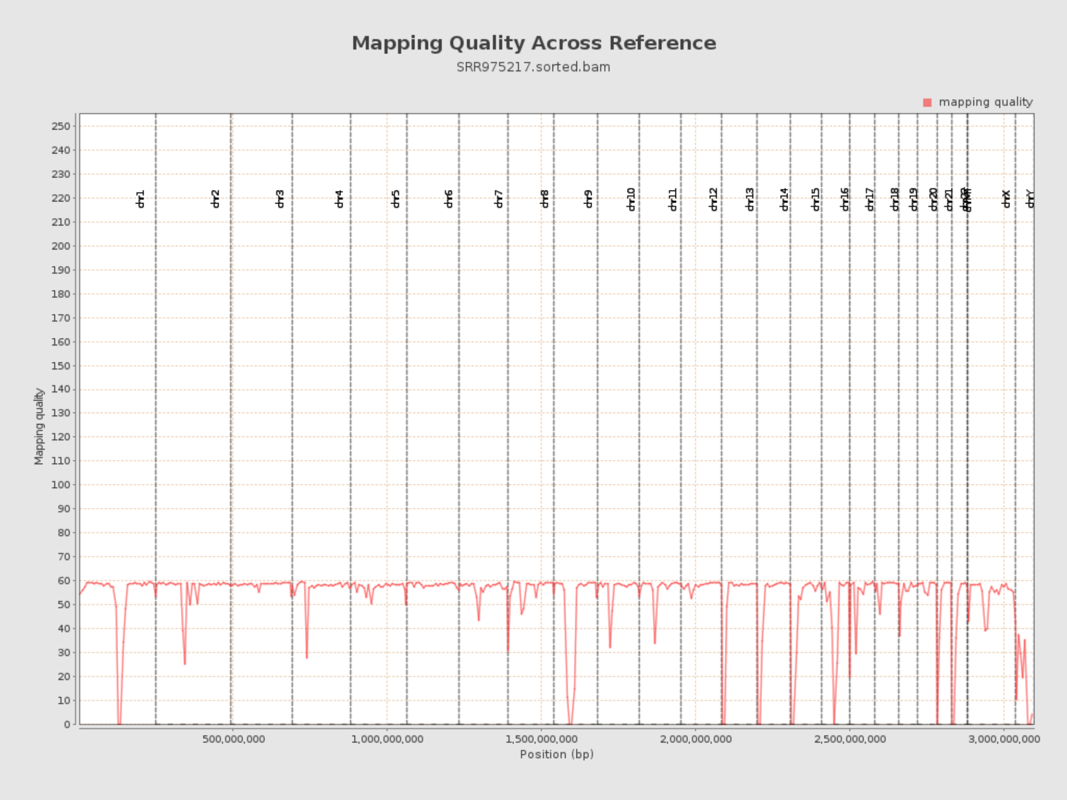
10. Results : Mapped Reads Clipping Profile



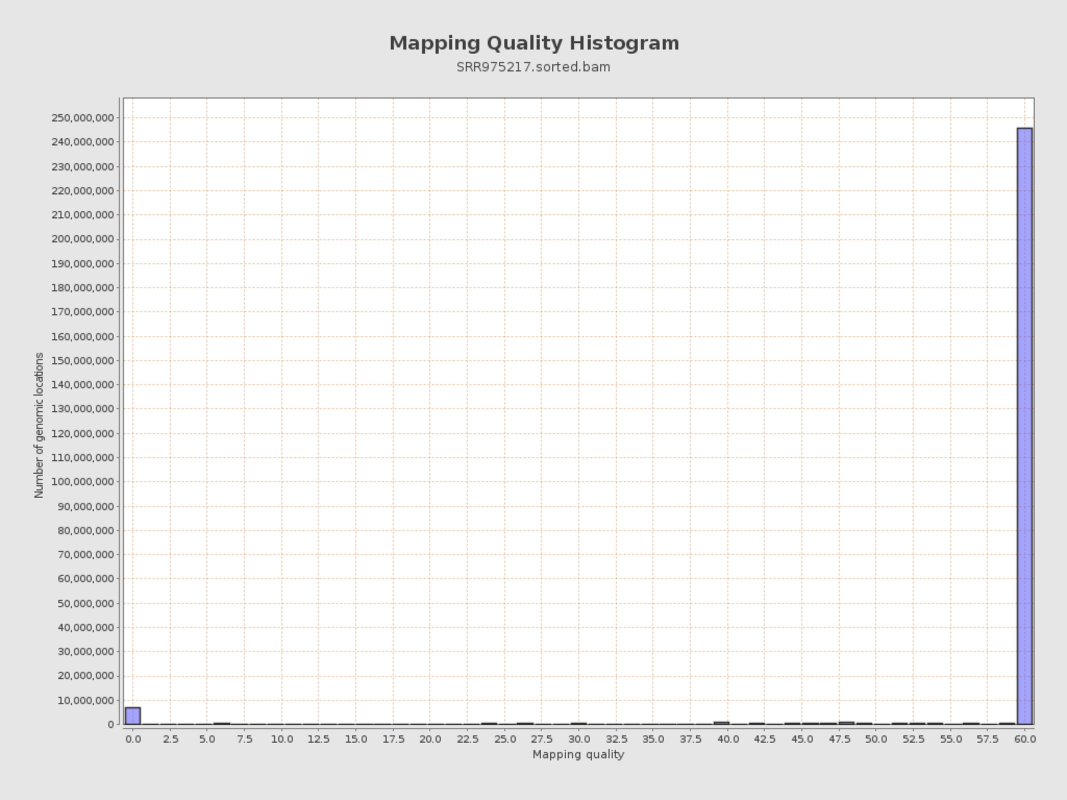
11. Results : Homopolymer Indels



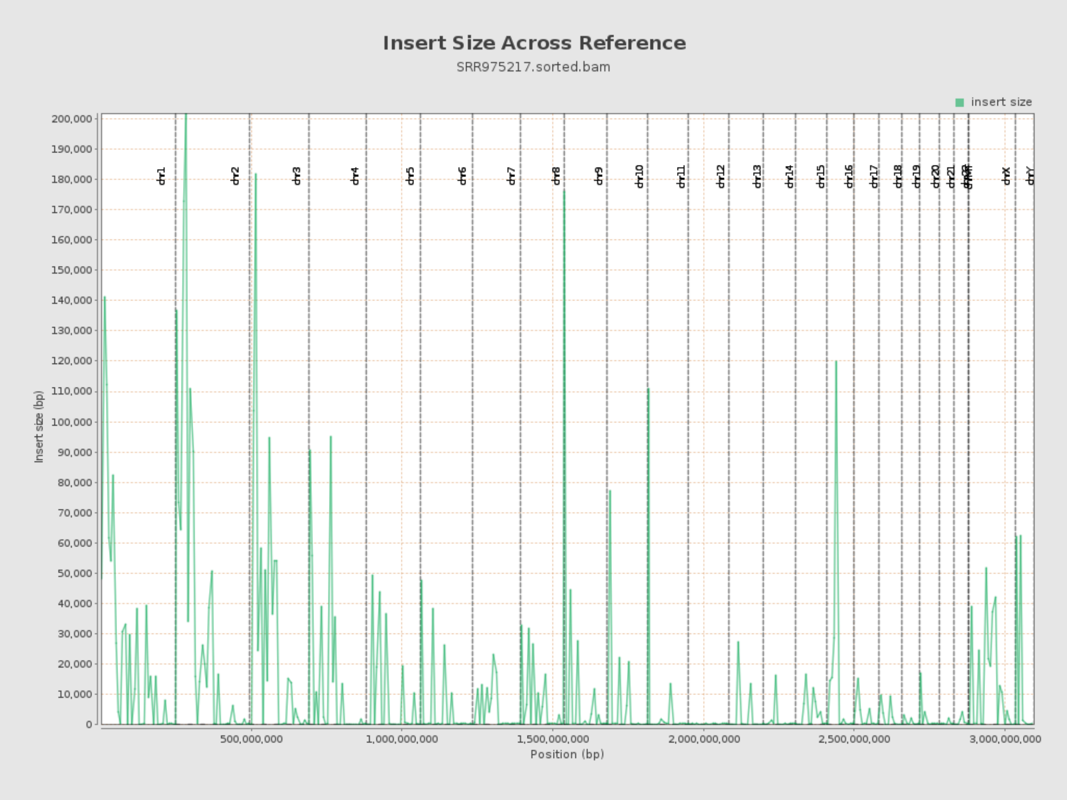
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram