Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:12:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975214.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_SRR975214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975214_1.fastq.gz SRR975214_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:12:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975214.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,339,192
Mapped reads	48,206,116 / 99.72%
Unmapped reads	133,076 / 0.28%
Mapped paired reads	48,206,116 / 99.72%
Mapped reads, first in pair	24,128,241 / 49.91%
Mapped reads, second in pair	24,077,875 / 49.81%
Mapped reads, both in pair	48,126,850 / 99.56%
Mapped reads, singletons	79,266 / 0.16%
Secondary alignments	0
Supplementary alignments	127,197 / 0.26%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	28,326,591 / 58.6%
Duplication rate	36.93%
Clipped reads	7,408,339 / 15.33%

2.2. ACGT Content

Number/percentage of A's	1,287,686,161 / 27.13%
Number/percentage of C's	1,057,884,349 / 22.29%
Number/percentage of T's	1,305,891,868 / 27.51%
Number/percentage of G's	1,094,364,160 / 23.06%
Number/percentage of N's	360,071 / 0.01%

GC Percentage	45.35%

2.3. Coverage

Mean	1.5337
Standard Deviation	23.5702

2.4. Mapping Quality

Mean Mapping Quality	55.7

2.5. Insert size

Mean	75,523.75
Standard Deviation	2,737,694.17
P25/Median/P75	167 / 203 / 250

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	27,943,897
Insertions	406,960
Mapped reads with at least one insertion	0.83%
Deletions	1,137,744
Mapped reads with at least one deletion	2.32%
Homopolymer indels	48.9%

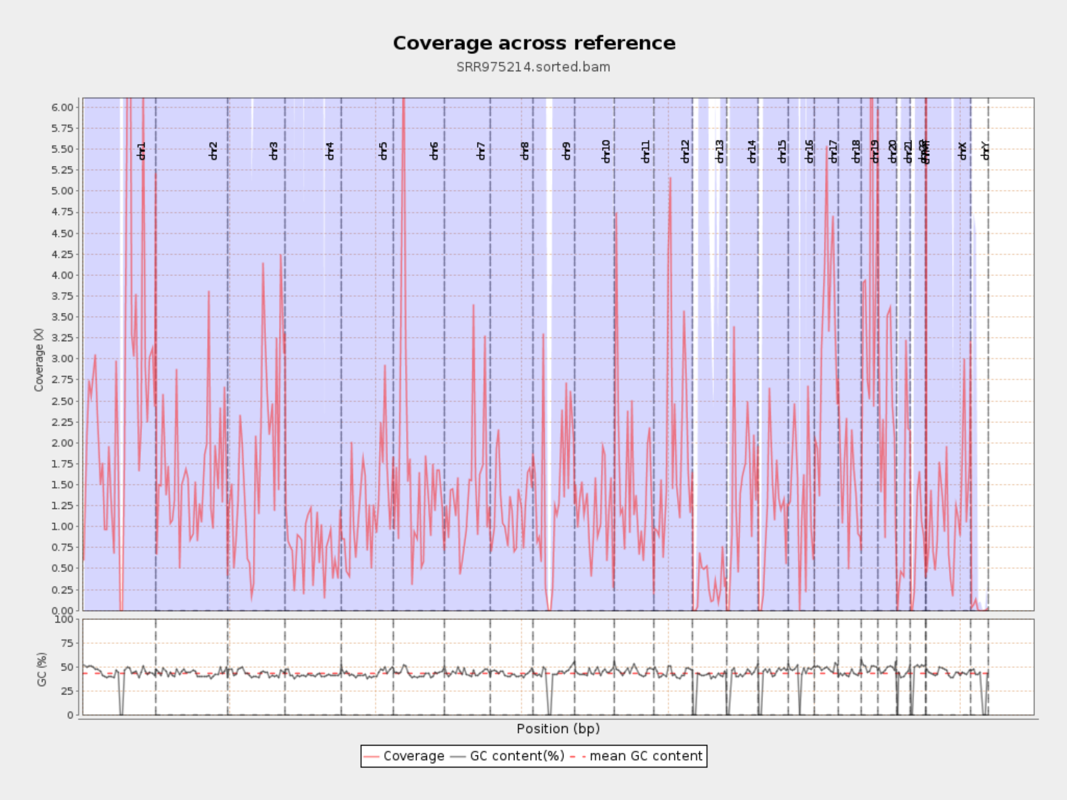
2.7. Chromosome stats

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

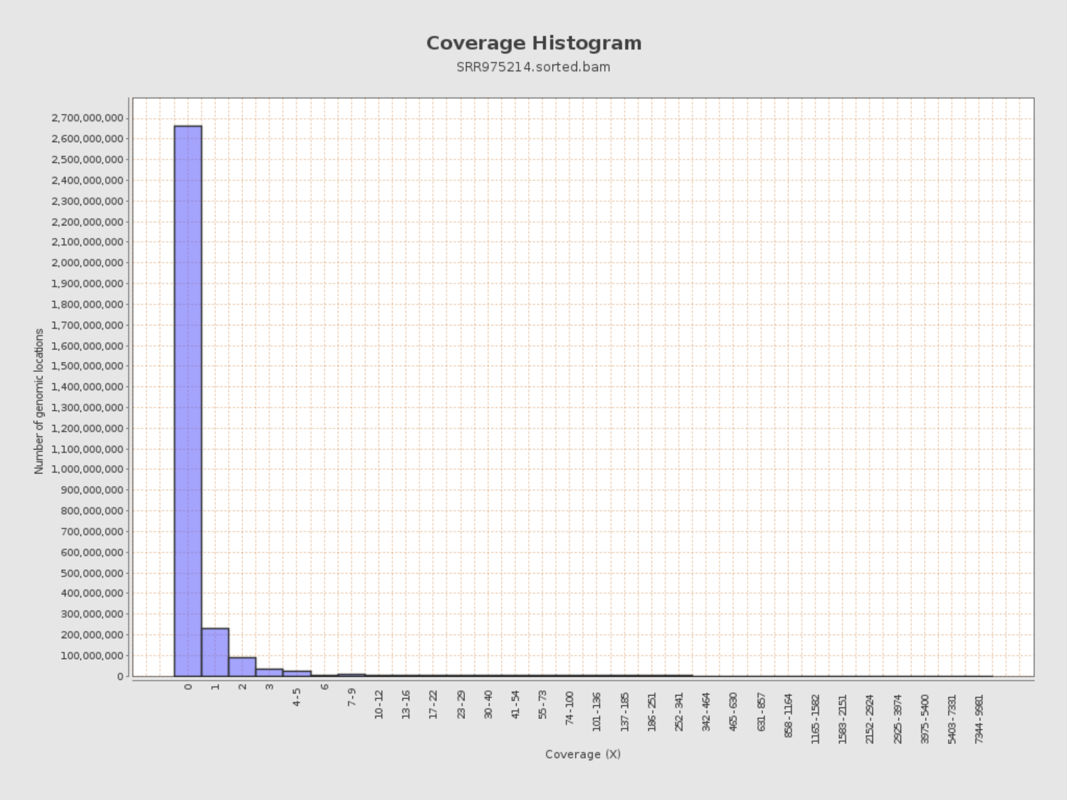
		bases	coverage	deviation
chr1	249250621	642172532	2.5764	32.8901
chr2	243199373	382540532	1.573	21.8847
chr3	198022430	360080072	1.8184	25.6651
chr4	191154276	145229590	0.7598	13.0637
chr5	180915260	230205443	1.2724	18.8627
chr6	171115067	281731855	1.6464	25.8685
chr7	159138663	224359788	1.4098	22.7484
chr8	146364022	180837818	1.2355	17.8792
chr9	141213431	188812043	1.3371	20.8882
chr10	135534747	159977290	1.1803	18.2496
chr11	135006516	208421496	1.5438	21.3197
chr12	133851895	265837072	1.9861	28.4891
chr13	115169878	35632451	0.3094	6.748
chr14	107349540	152035654	1.4163	20.6731
chr15	102531392	109094024	1.064	15.5484
chr16	90354753	118130417	1.3074	18.7848
chr17	81195210	270557557	3.3322	40.2776
chr18	78077248	119801761	1.5344	23.3921
chr19	59128983	238857949	4.0396	47.9498
chr20	63025520	145690458	2.3116	33.3503
chr21	48129895	60725164	1.2617	22.5204
chr22	51304566	41550636	0.8099	12.1133
chrMT	16571	200510	12.1001	20.7383
chrX	155270560	183528286	1.182	20.2705

chrY	59373566	1975407	0.0333	2.3223

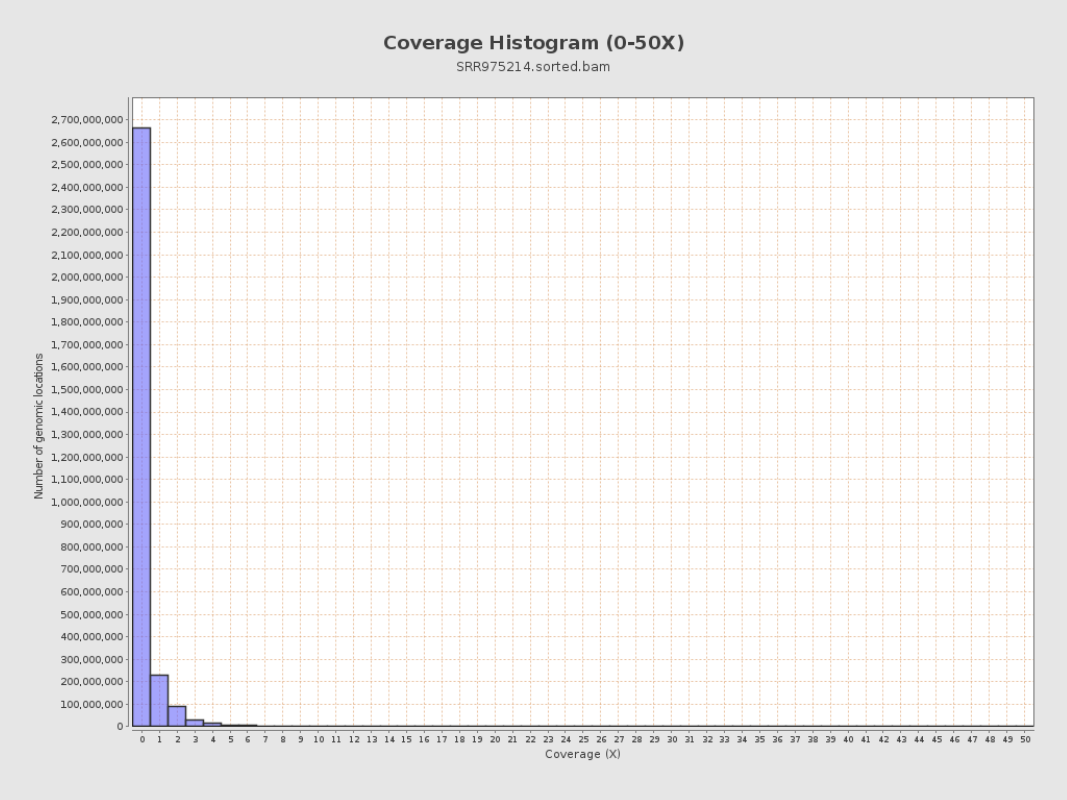
3. Results : Coverage across reference



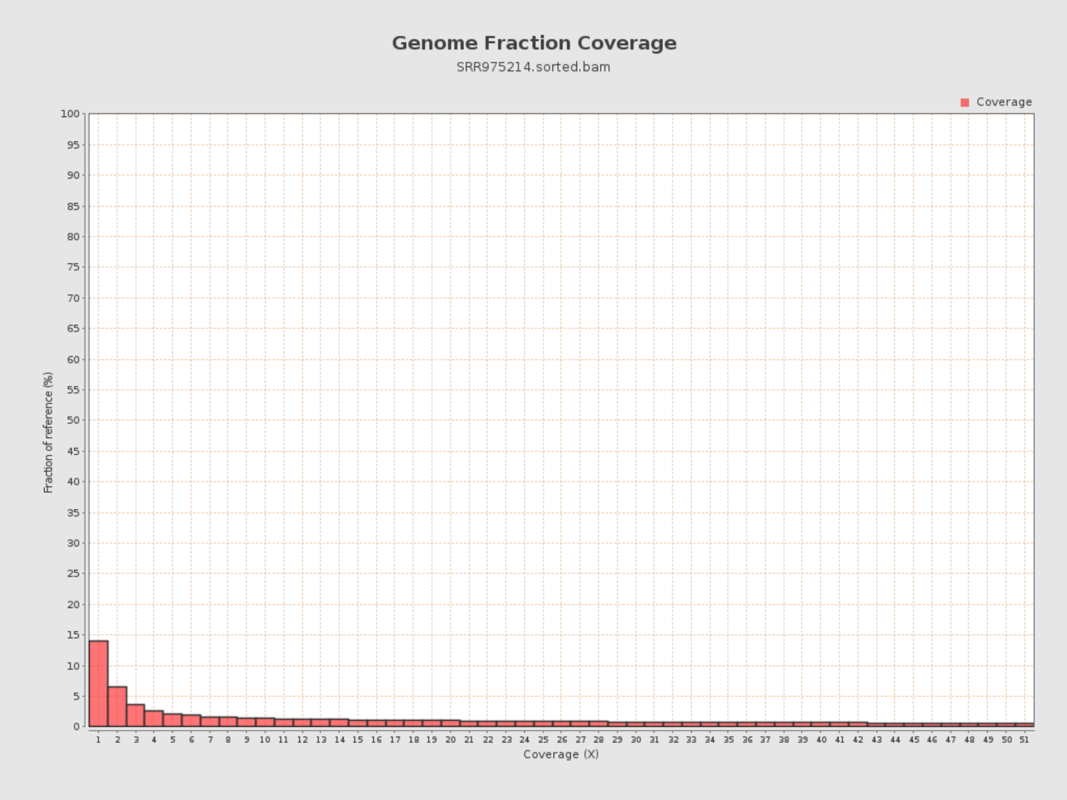
4. Results : Coverage Histogram



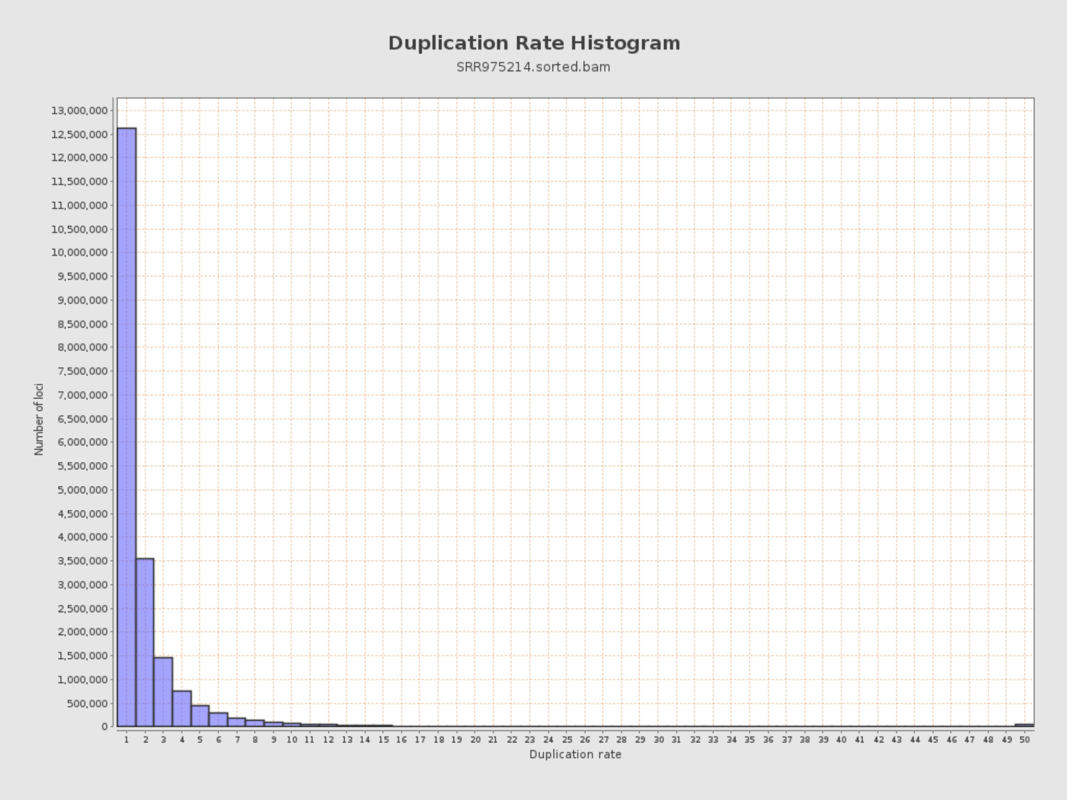
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



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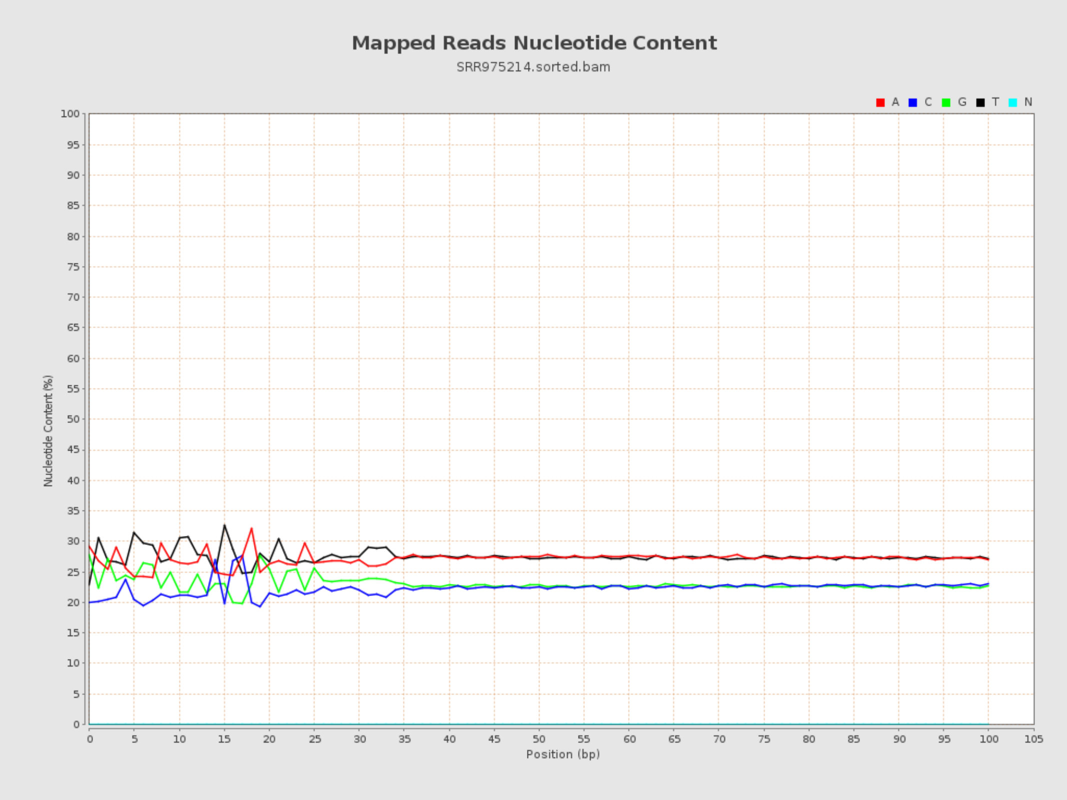
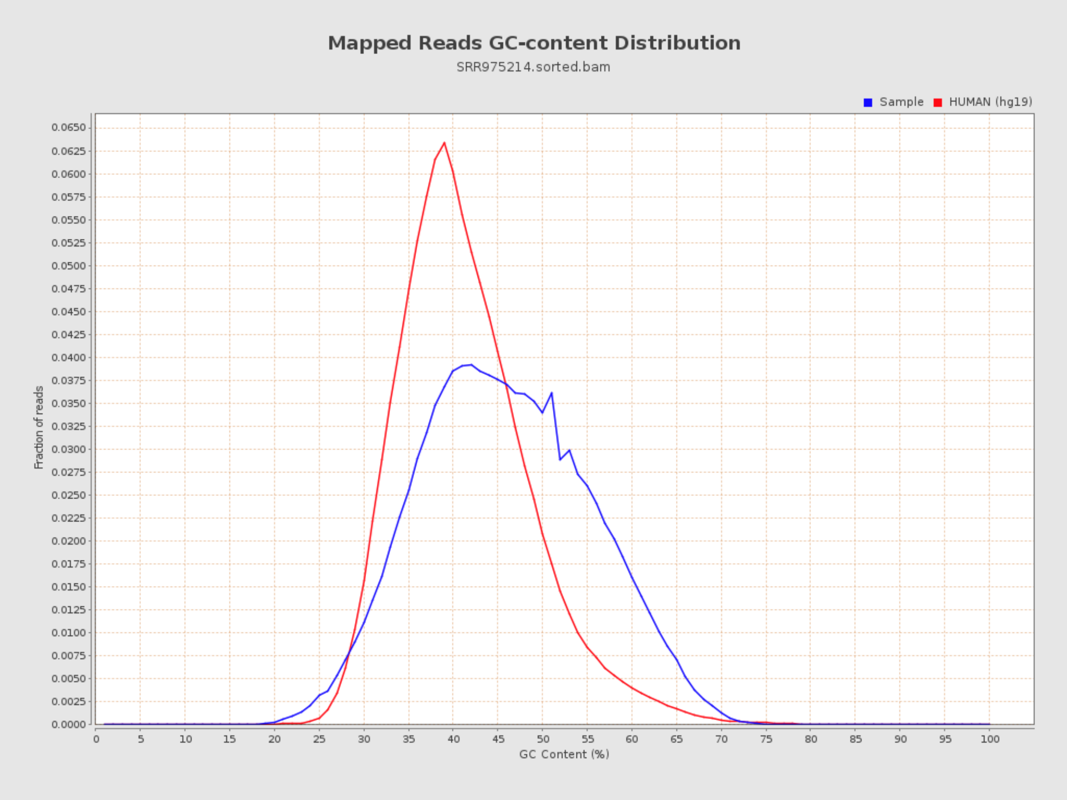
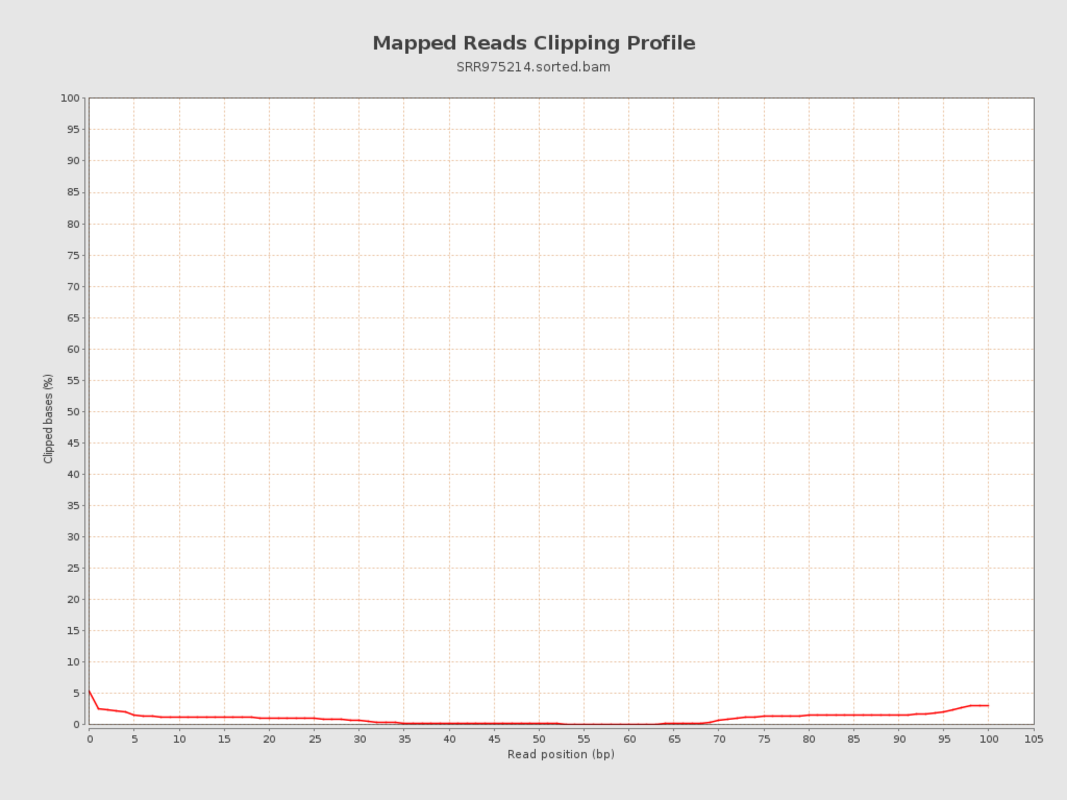
8. Results : Mapped Reads Nucleotide Content



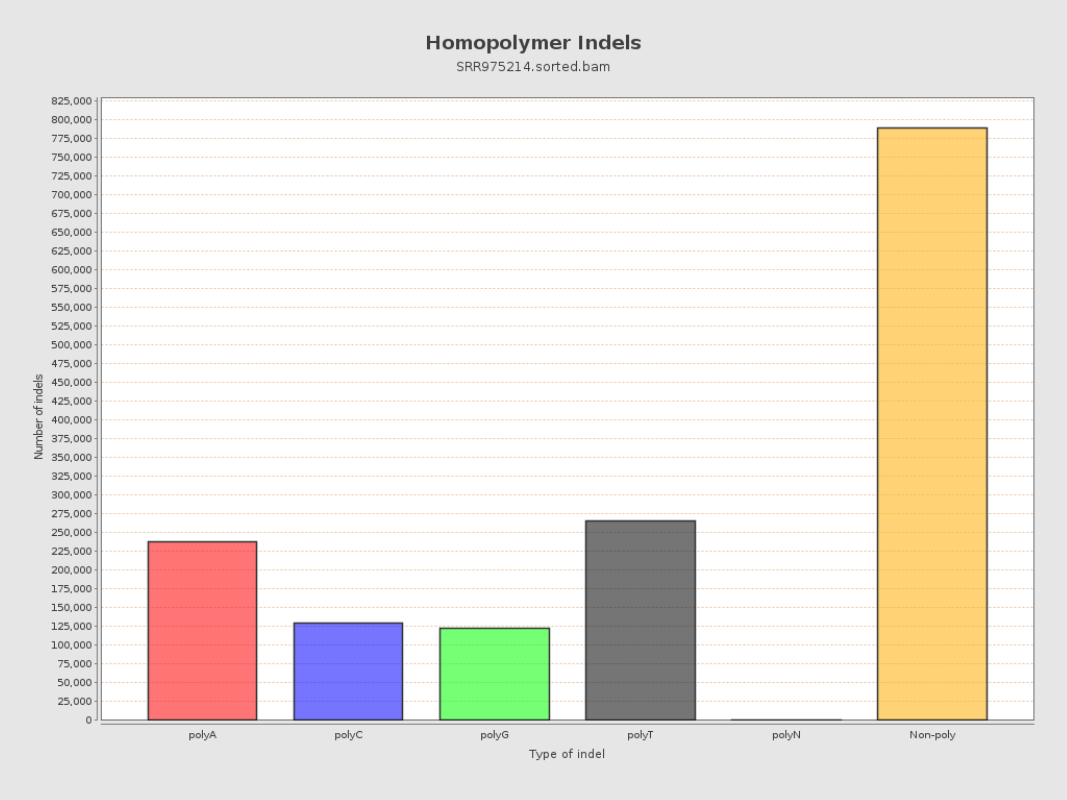
9. Results : Mapped Reads GC-content Distribution



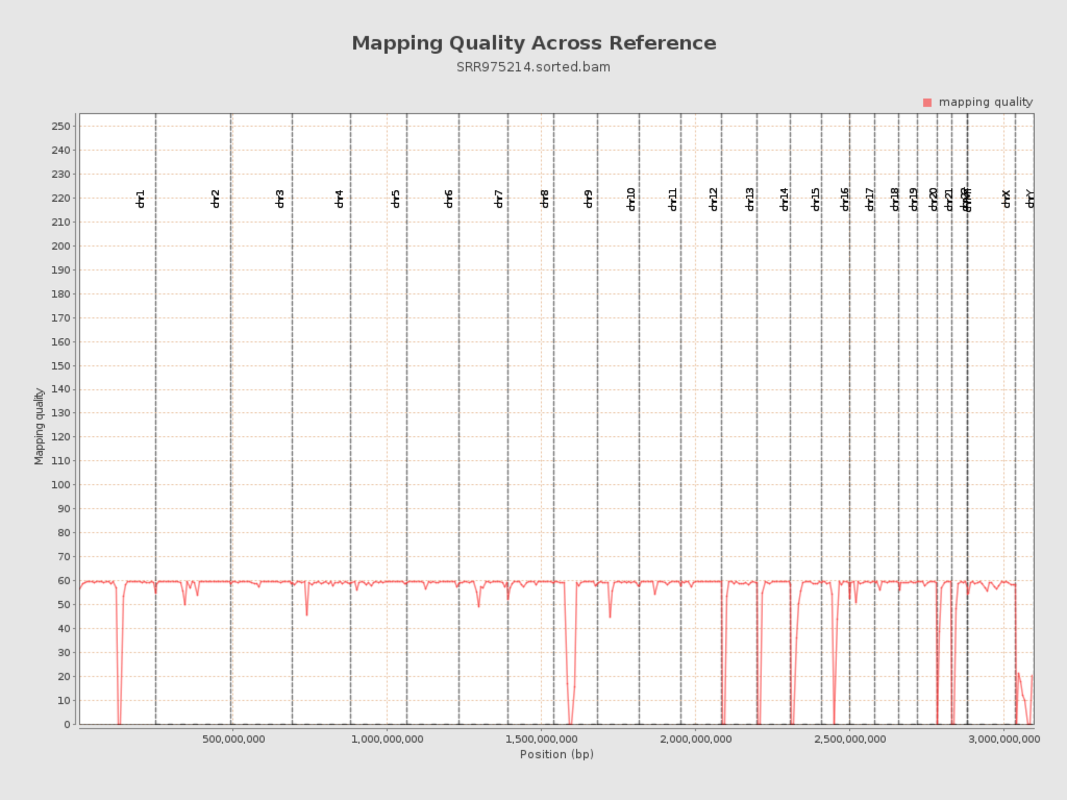
10. Results : Mapped Reads Clipping Profile



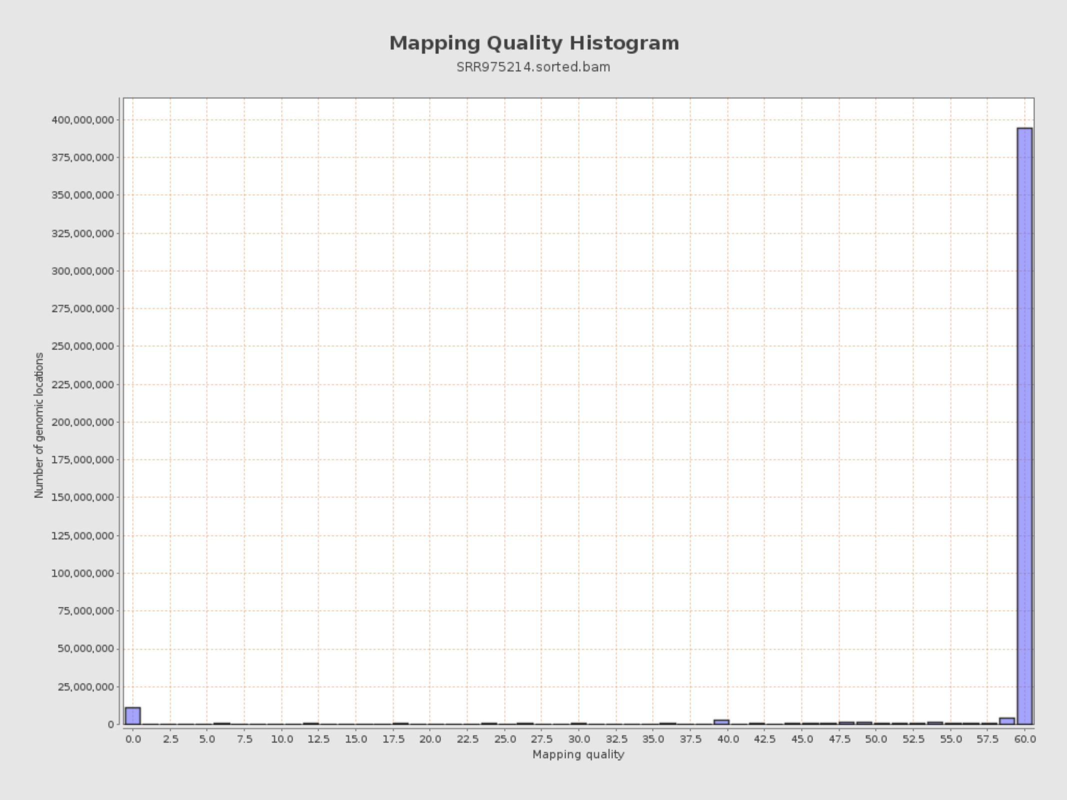
11. Results : Homopolymer Indels



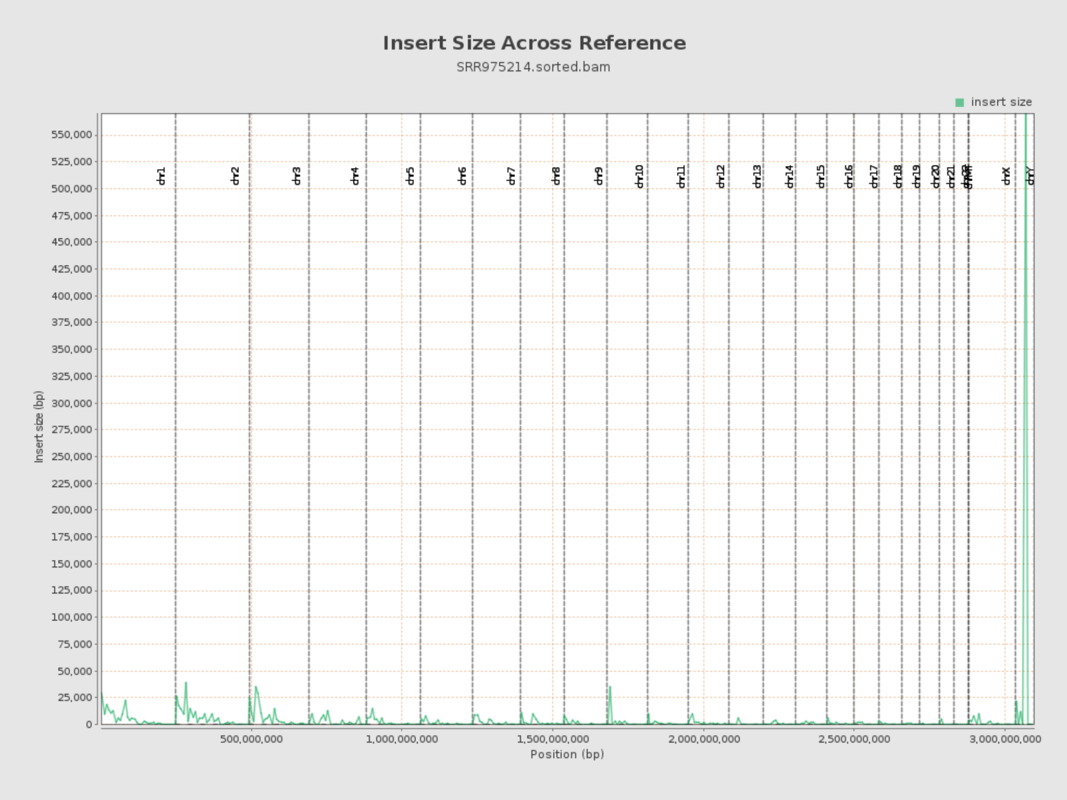
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram