Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:22:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975197.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_SRR975197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975197_1.fastq.gz SRR975197_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:22:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,774
Mapped reads	2,202,912 / 98.88%
Unmapped reads	24,862 / 1.12%
Mapped paired reads	2,202,912 / 98.88%
Mapped reads, first in pair	1,102,842 / 49.5%
Mapped reads, second in pair	1,100,070 / 49.38%
Mapped reads, both in pair	2,195,440 / 98.55%
Mapped reads, singletons	7,472 / 0.34%
Secondary alignments	0
Supplementary alignments	29,152 / 1.31%
Read min/max/mean length	30 / 151 / 151.64
Duplicated reads (estimated)	379,120 / 17.02%
Duplication rate	15.96%
Clipped reads	1,593,145 / 71.51%

2.2. ACGT Content

Number/percentage of A's	89,690,805 / 29.72%
Number/percentage of C's	60,314,513 / 19.99%
Number/percentage of T's	89,151,354 / 29.54%
Number/percentage of G's	62,583,298 / 20.74%
Number/percentage of N's	16,202 / 0.01%

GC Percentage	40.73%

2.3. Coverage

Mean	0.0976
Standard Deviation	1.5503

2.4. Mapping Quality

Mean Mapping Quality	53.48

2.5. Insert size

Mean	95,332.51
Standard Deviation	2,974,425.5
P25/Median/P75	140 / 173 / 220

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	3,736,645
Insertions	67,176
Mapped reads with at least one insertion	2.89%
Deletions	127,097
Mapped reads with at least one deletion	5.54%
Homopolymer indels	46.76%

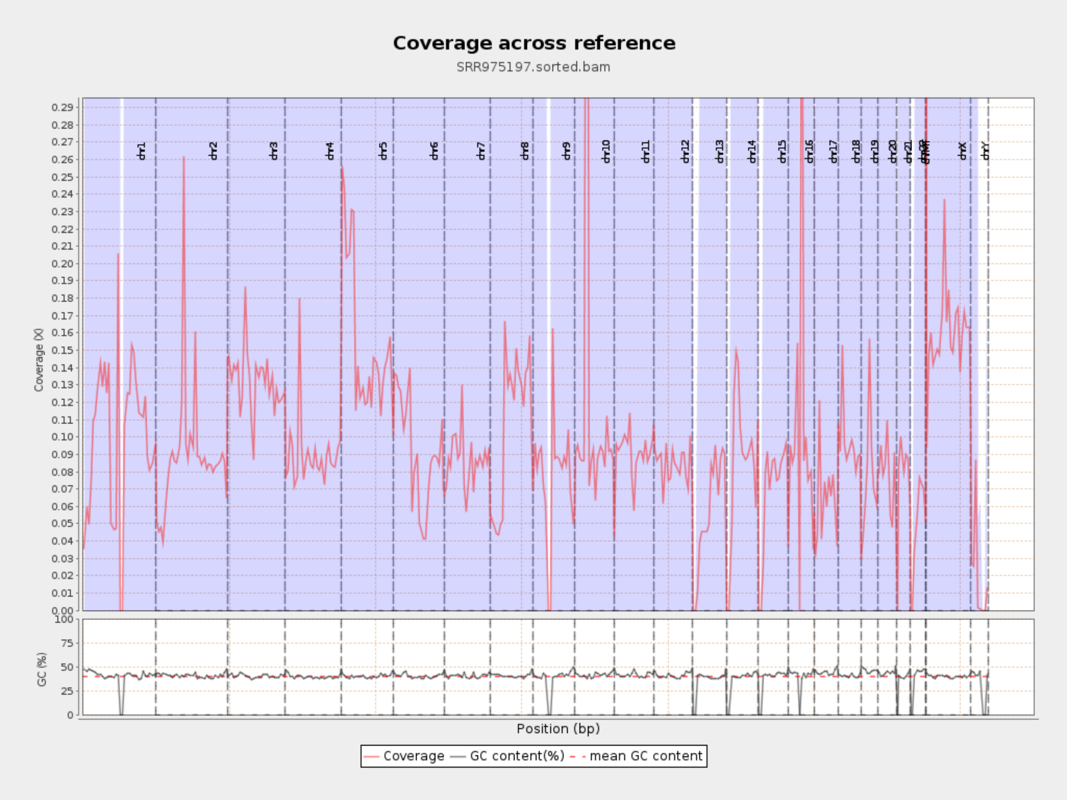
2.7. Chromosome stats

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

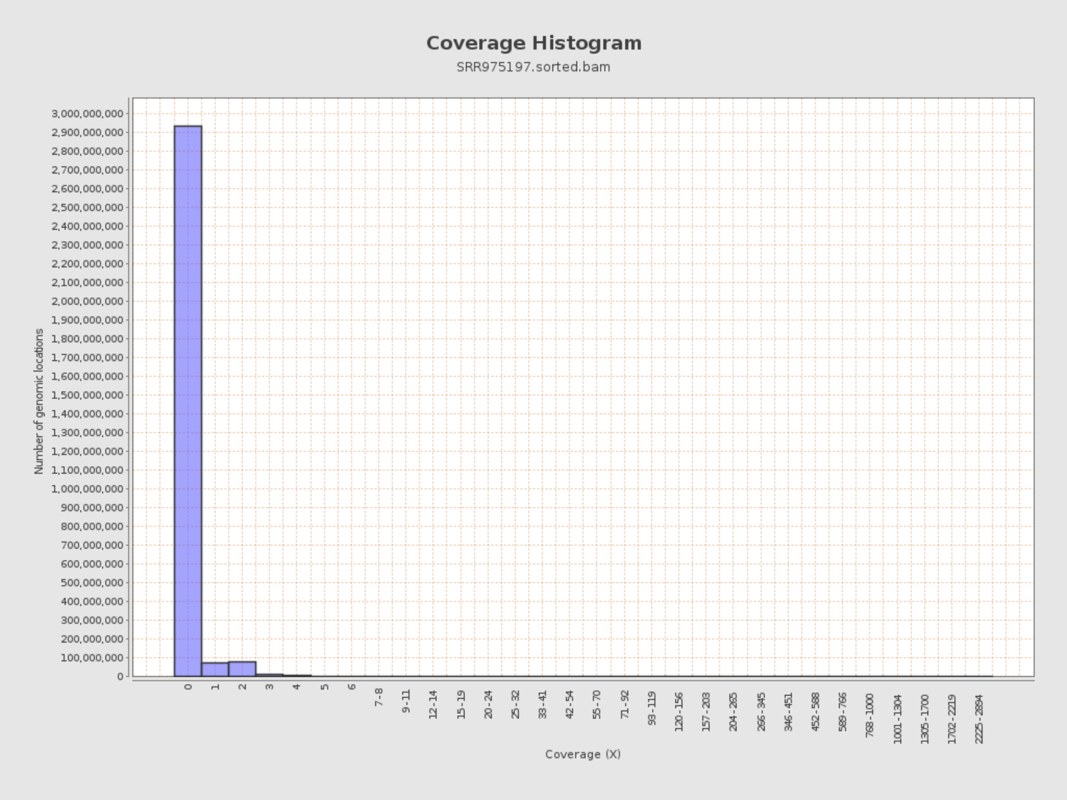
		bases	coverage	deviation
chr1	249250621	24944857	0.1001	1.7556
chr2	243199373	21921765	0.0901	1.2384
chr3	198022430	26151042	0.1321	0.5875
chr4	191154276	17208280	0.09	0.7654
chr5	180915260	28194565	0.1558	0.5877
chr6	171115067	15662534	0.0915	0.6726
chr7	159138663	13769846	0.0865	0.8332
chr8	146364022	15725452	0.1074	0.5947
chr9	141213431	10988329	0.0778	1.6927
chr10	135534747	16403063	0.121	5.4584
chr11	135006516	12215333	0.0905	0.775
chr12	133851895	11255544	0.0841	0.4165
chr13	115169878	6531356	0.0567	0.3382
chr14	107349540	9217090	0.0859	0.4356
chr15	102531392	6938950	0.0677	0.372
chr16	90354753	10132265	0.1121	2.5701
chr17	81195210	5201934	0.0641	1.1901
chr18	78077248	7620927	0.0976	1.7124
chr19	59128983	4681754	0.0792	1.0083
chr20	63025520	4991696	0.0792	0.4685
chr21	48129895	3710511	0.0771	0.5591
chr22	51304566	2510680	0.0489	0.3265
chrMT	16571	51296	3.0955	2.653
chrX	155270560	24827426	0.1599	0.7374

chrY	59373566	1134951	0.0191	1.2896

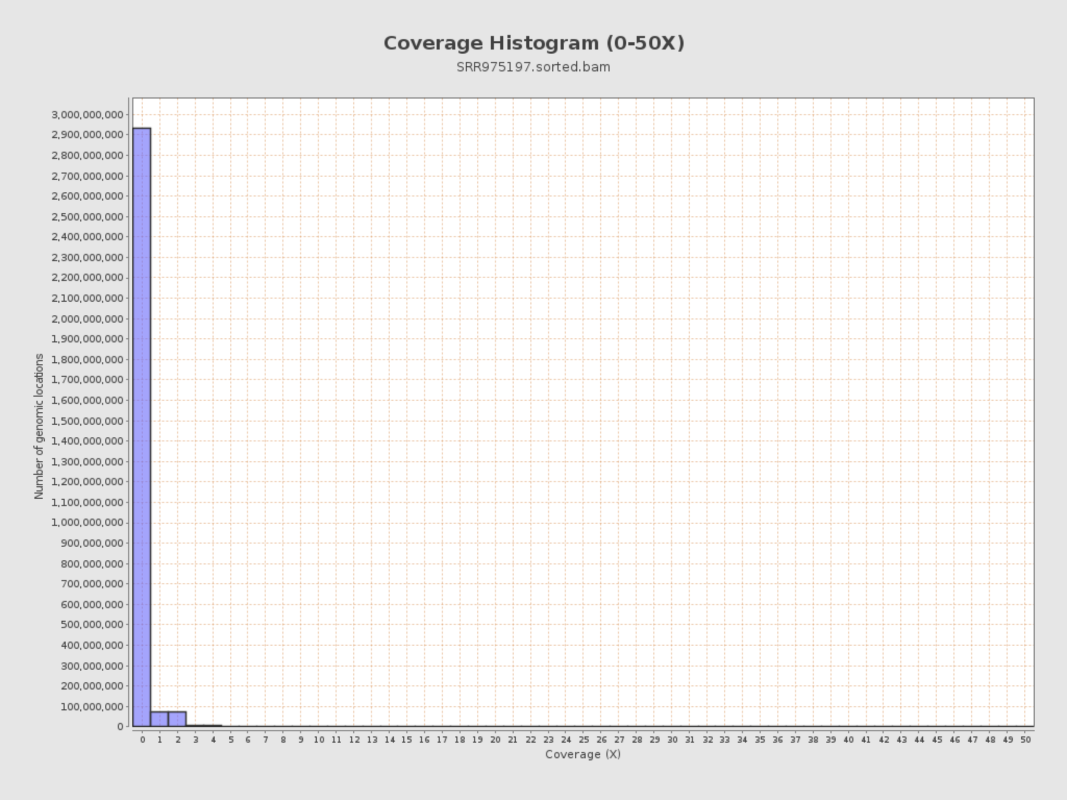
3. Results : Coverage across reference



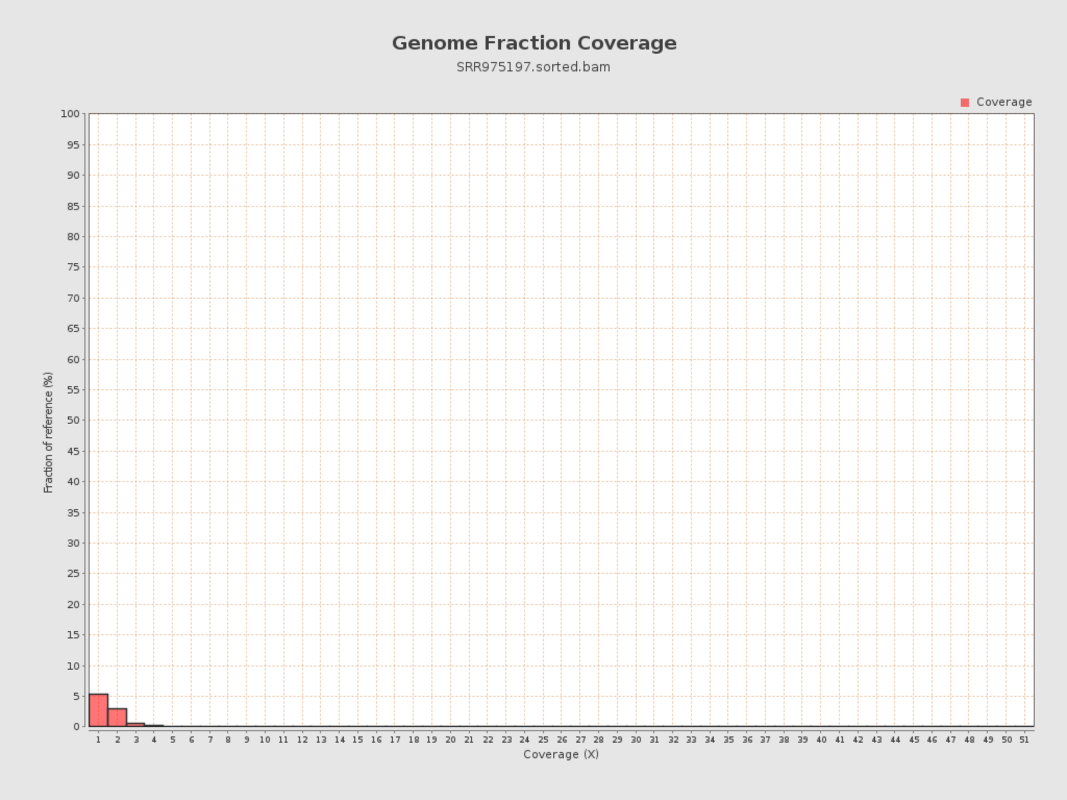
4. Results : Coverage Histogram



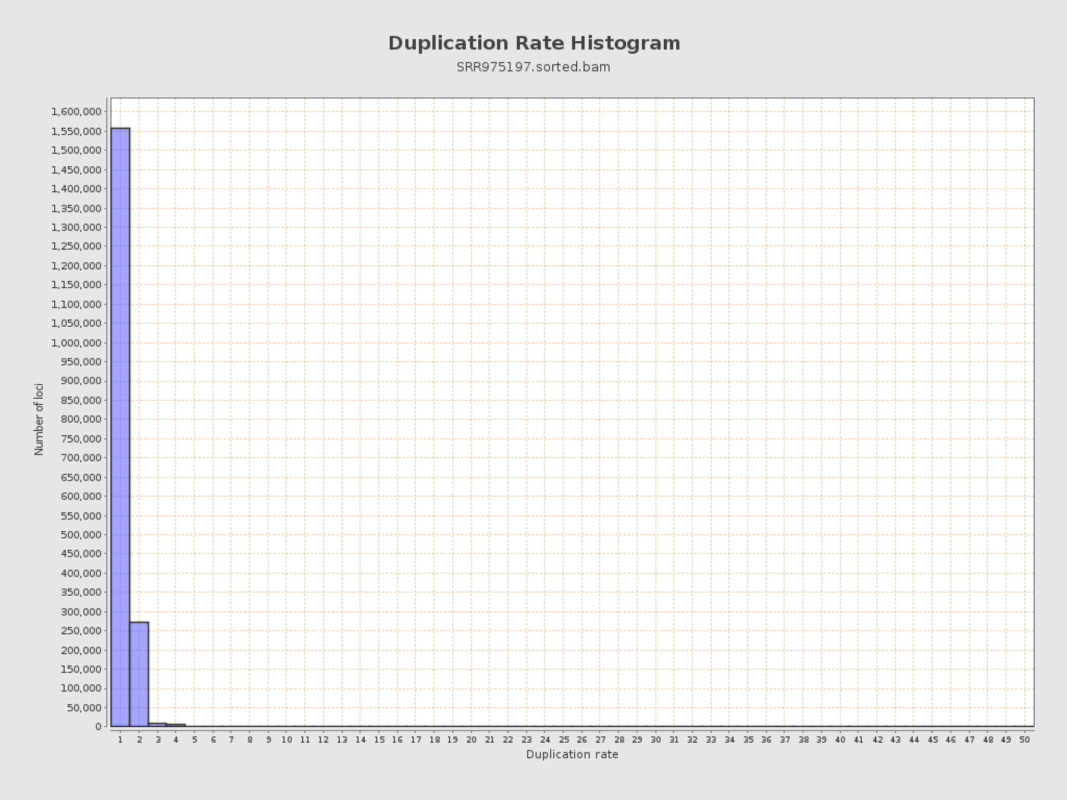
5. Results : Coverage Histogram (0-50X)



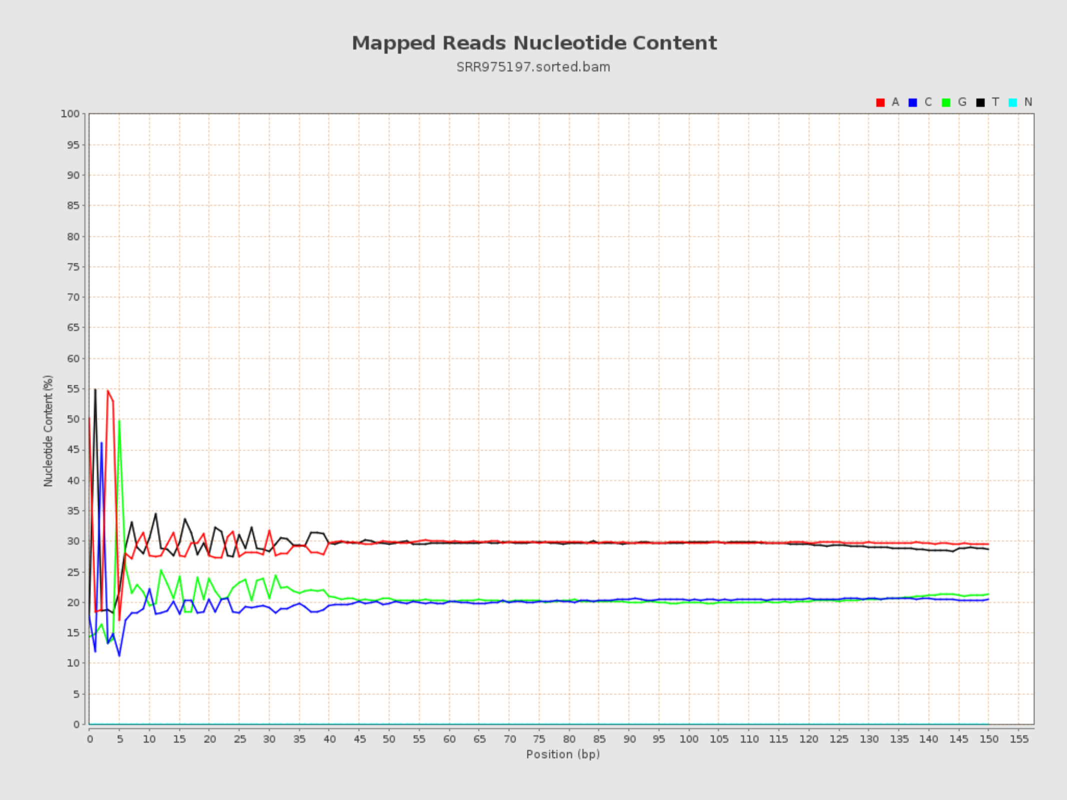
6. Results : Genome Fraction Coverage



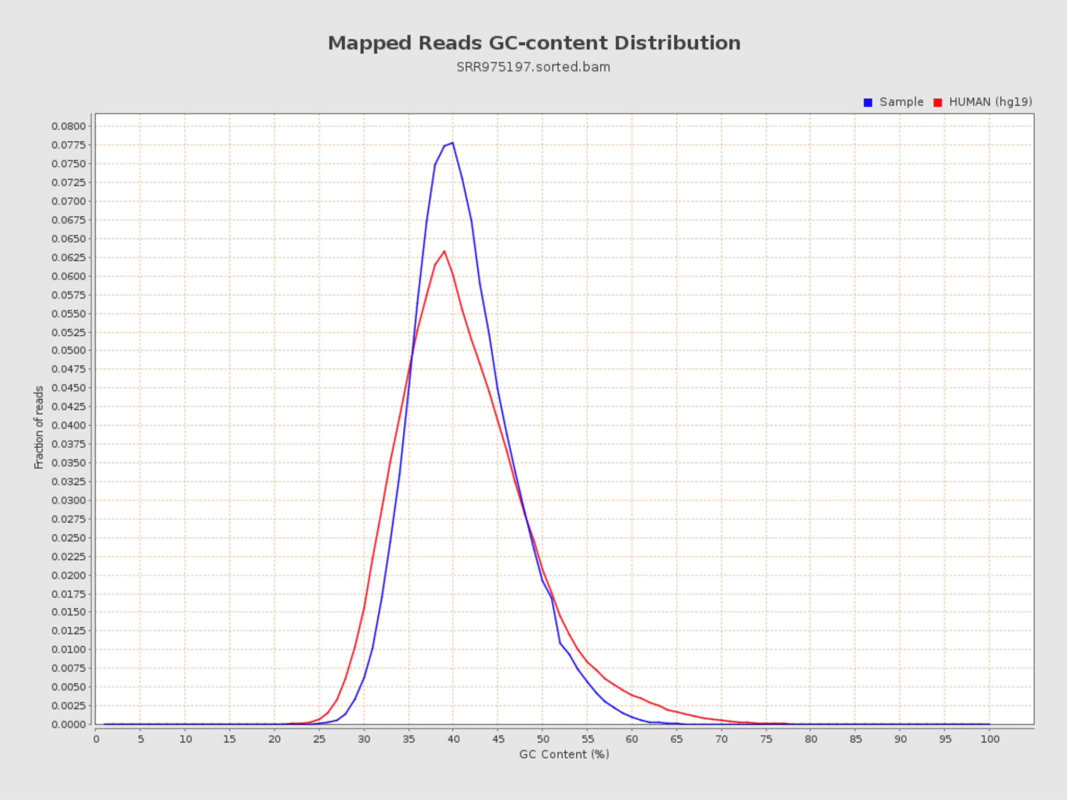
7. Results : Duplication Rate Histogram



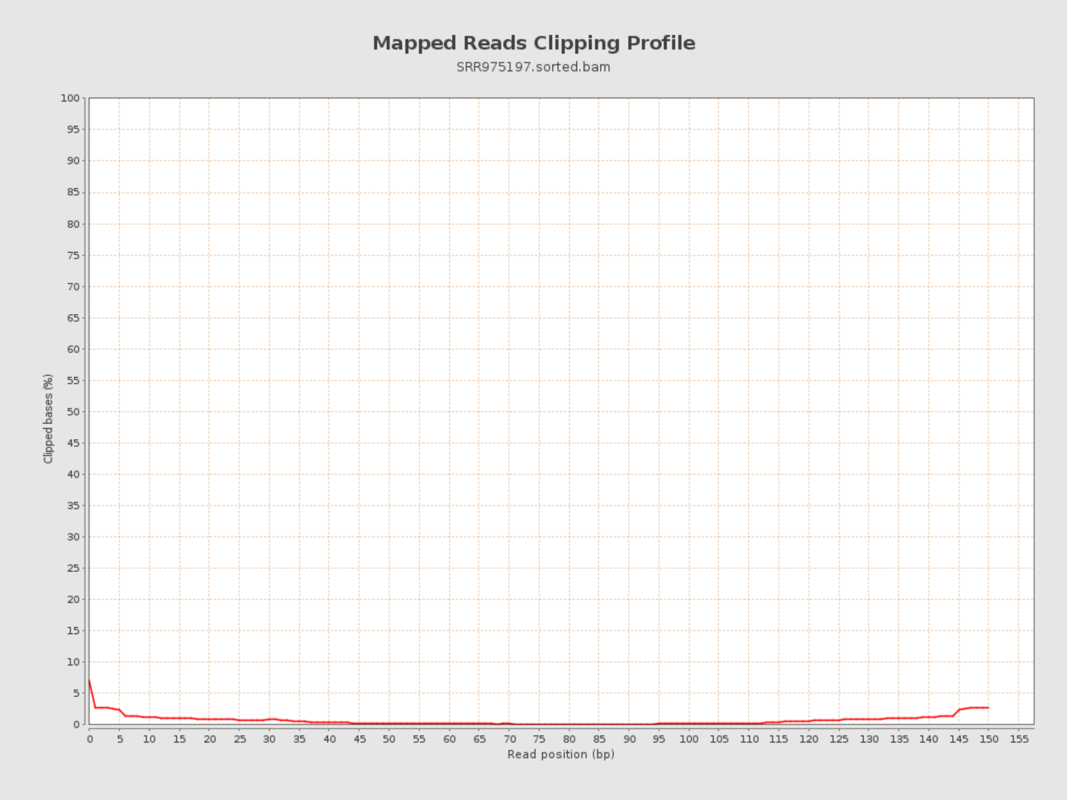
8. Results : Mapped Reads Nucleotide Content



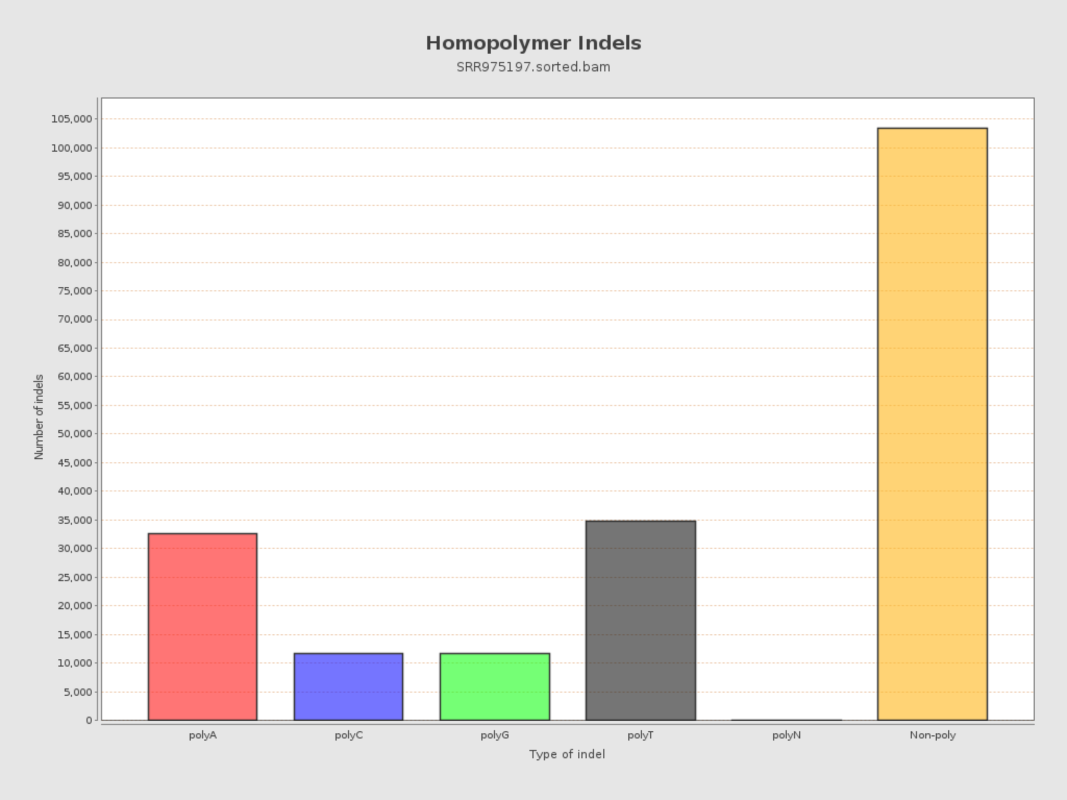
9. Results : Mapped Reads GC-content Distribution



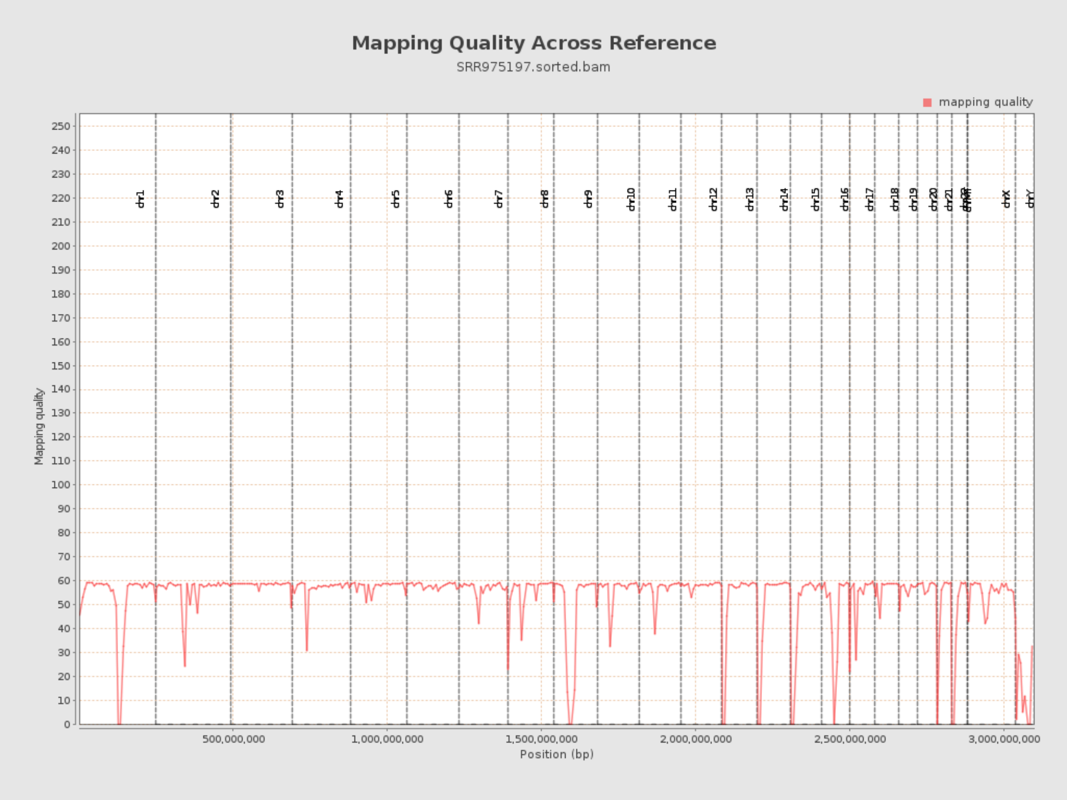
10. Results : Mapped Reads Clipping Profile



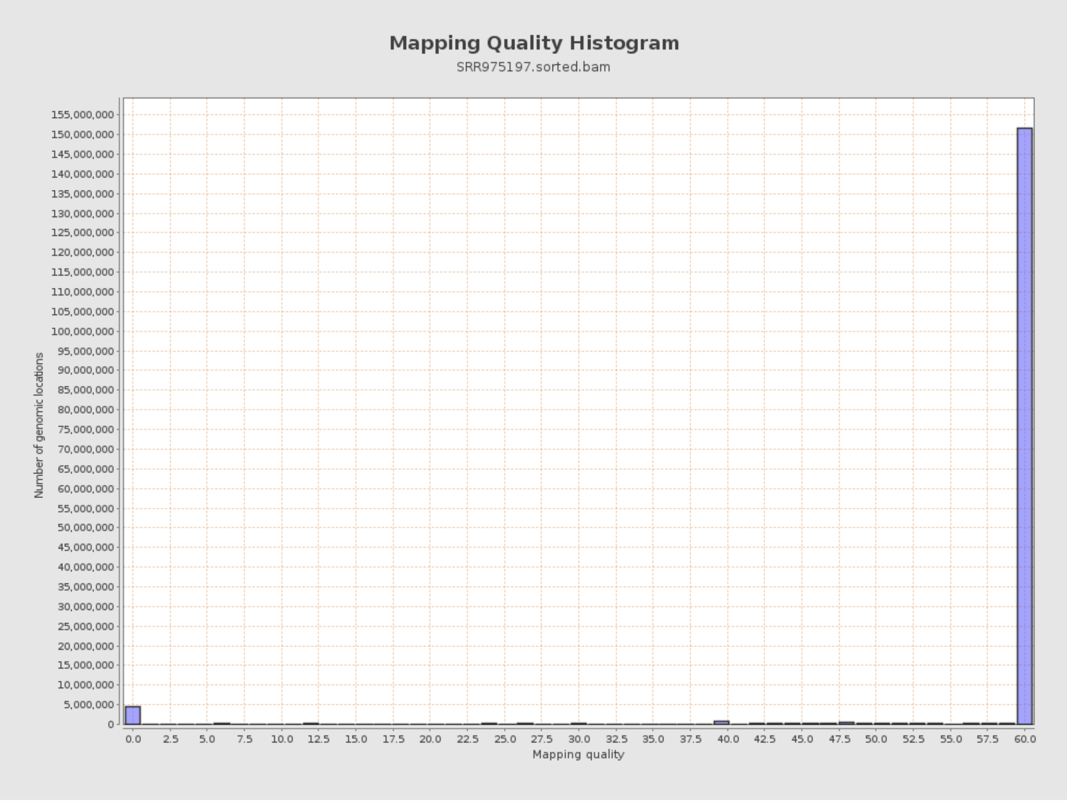
11. Results : Homopolymer Indels



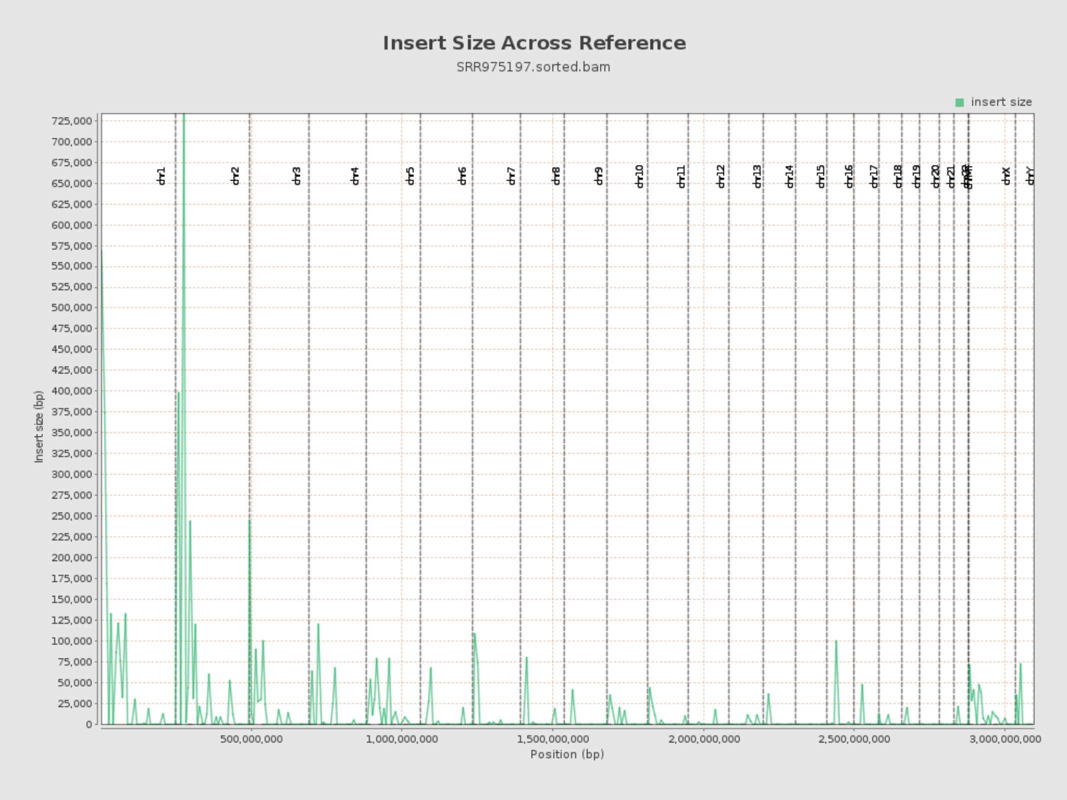
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram