Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:32:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975232.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_SRR975232 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975232_1.fastq.gz SRR975232_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:32:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975232.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,231,910
Mapped reads	44,144,718 / 99.8%
Unmapped reads	87,192 / 0.2%
Mapped paired reads	44,144,718 / 99.8%
Mapped reads, first in pair	22,074,318 / 49.91%
Mapped reads, second in pair	22,070,400 / 49.9%
Mapped reads, both in pair	44,082,476 / 99.66%
Mapped reads, singletons	62,242 / 0.14%
Secondary alignments	0
Supplementary alignments	169,683 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	26,068,512 / 58.94%
Duplication rate	42.28%
Clipped reads	25,399,369 / 57.42%

2.2. ACGT Content

Number/percentage of A's	1,087,177,811 / 26.06%
Number/percentage of C's	975,474,881 / 23.39%
Number/percentage of T's	1,098,323,298 / 26.33%
Number/percentage of G's	1,010,140,563 / 24.22%
Number/percentage of N's	116,840 / 0%

GC Percentage	47.6%

2.3. Coverage

Mean	1.3479
Standard Deviation	18.8692

2.4. Mapping Quality

Mean Mapping Quality	56.01

2.5. Insert size

Mean	218,100.26
Standard Deviation	4,643,580.79
P25/Median/P75	190 / 233 / 282

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	28,217,416
Insertions	394,595
Mapped reads with at least one insertion	0.88%
Deletions	995,654
Mapped reads with at least one deletion	2.22%
Homopolymer indels	46.58%

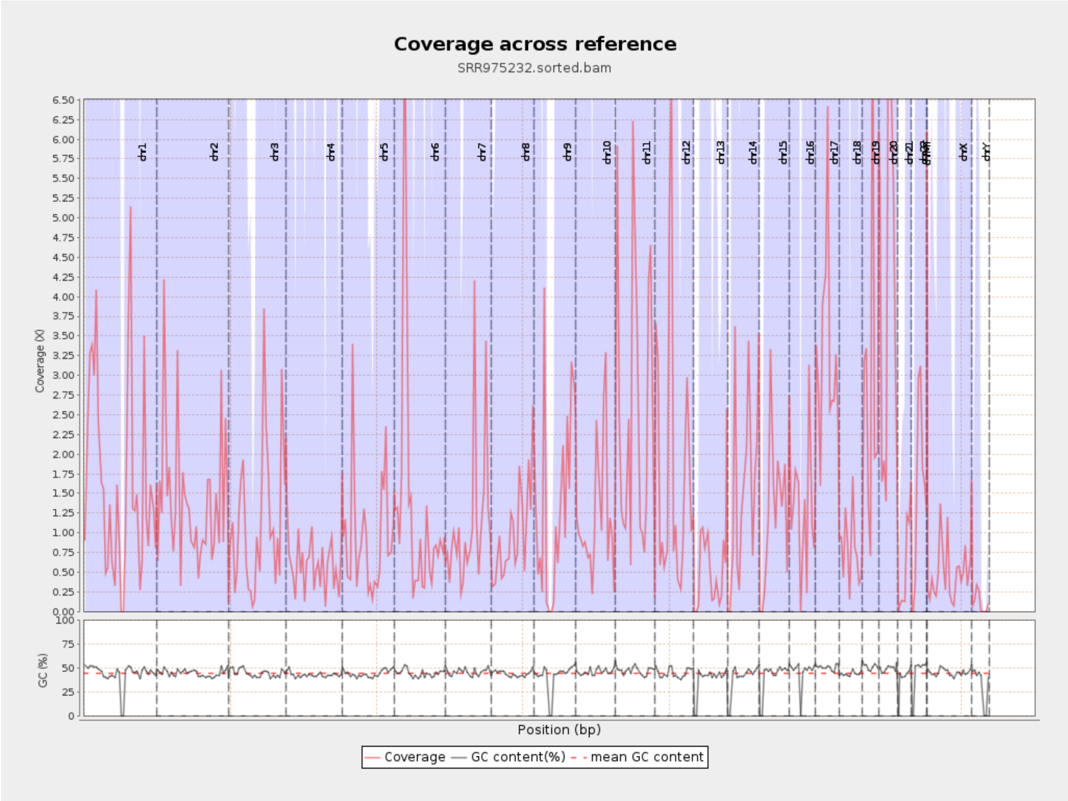
2.7. Chromosome stats

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

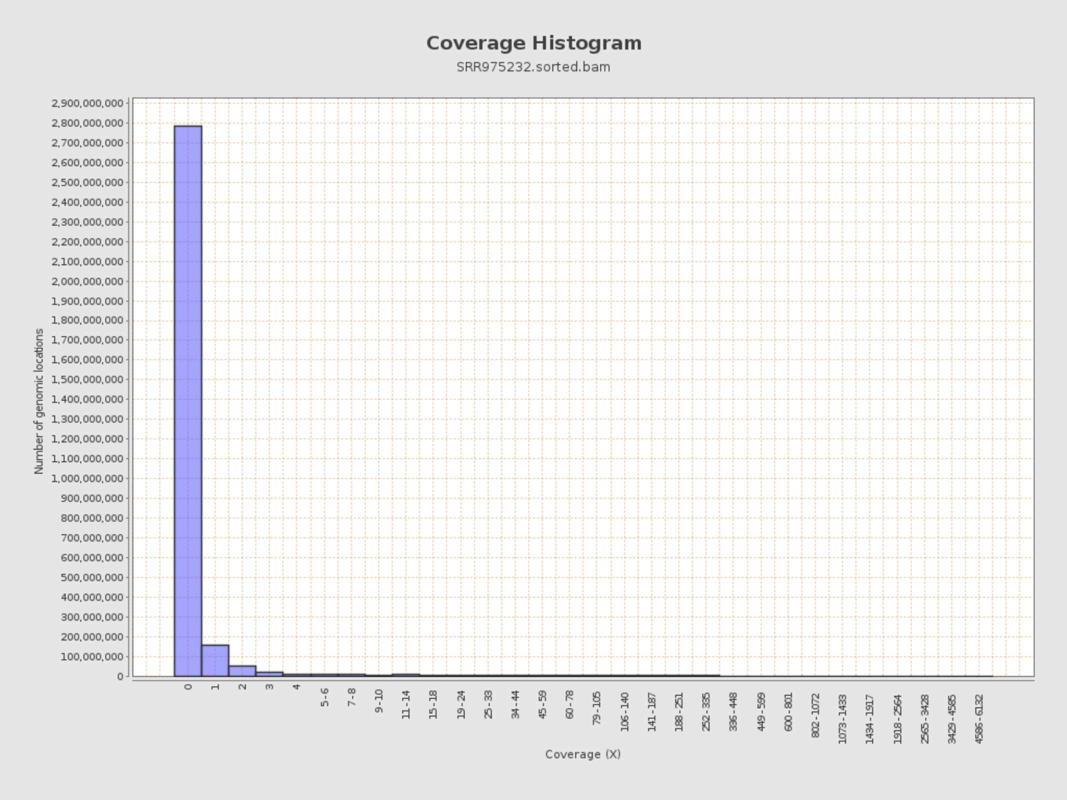
		bases	coverage	deviation
chr1	249250621	411352313	1.6504	20.0133
chr2	243199373	340598822	1.4005	17.7415
chr3	198022430	225054758	1.1365	15.6458
chr4	191154276	112969884	0.591	9.3162
chr5	180915260	175356706	0.9693	14.6089
chr6	171115067	222946423	1.3029	18.3621
chr7	159138663	178509578	1.1217	16.8533
chr8	146364022	144567266	0.9877	14.8808
chr9	141213431	182569312	1.2929	17.5574
chr10	135534747	166144876	1.2258	17.0202
chr11	135006516	346442166	2.5661	28.5513
chr12	133851895	257363937	1.9228	24.5217
chr13	115169878	59531025	0.5169	9.4245
chr14	107349540	159964648	1.4901	19.4344
chr15	102531392	122085448	1.1907	14.7516
chr16	90354753	116578318	1.2902	15.9279
chr17	81195210	268605598	3.3081	33.3779
chr18	78077248	61839459	0.792	13.3585
chr19	59128983	176876559	2.9914	31.9023
chr20	63025520	250253648	3.9707	42.6896
chr21	48129895	29160466	0.6059	9.9178
chr22	51304566	79319534	1.5461	19.9865
chrMT	16571	101251	6.1101	9.2667
chrX	155270560	77535891	0.4994	8.2065

chrY	59373566	6957349	0.1172	3.4379

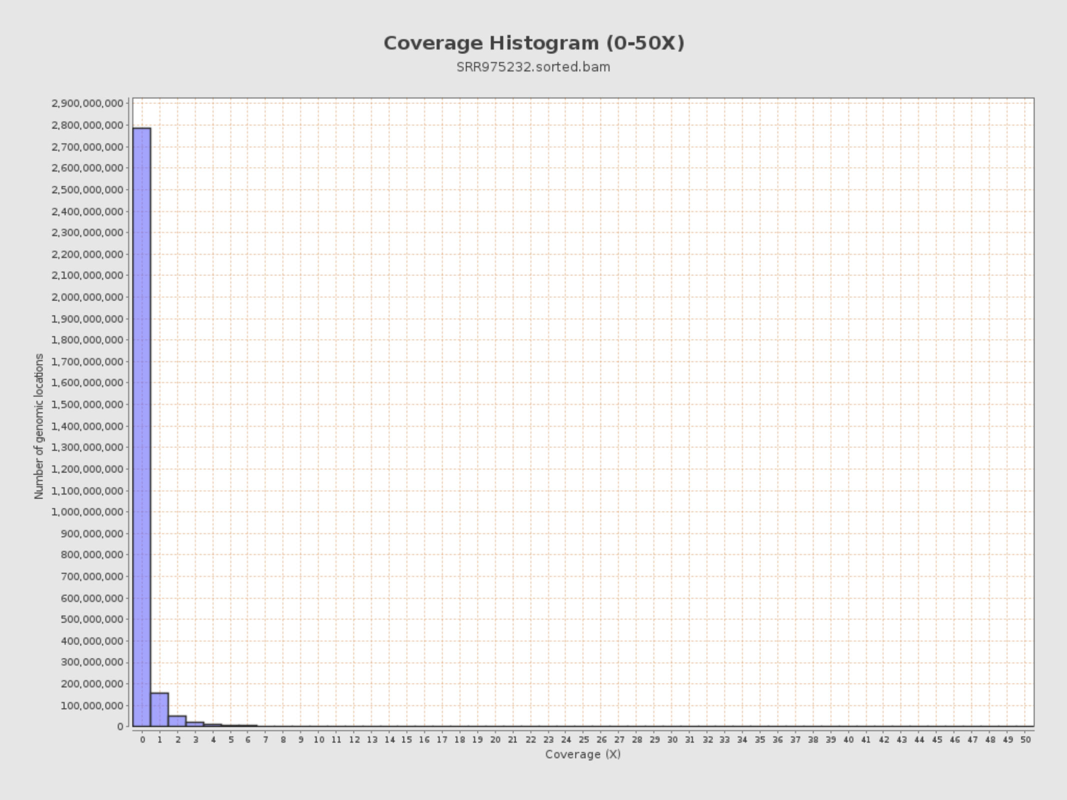
3. Results : Coverage across reference



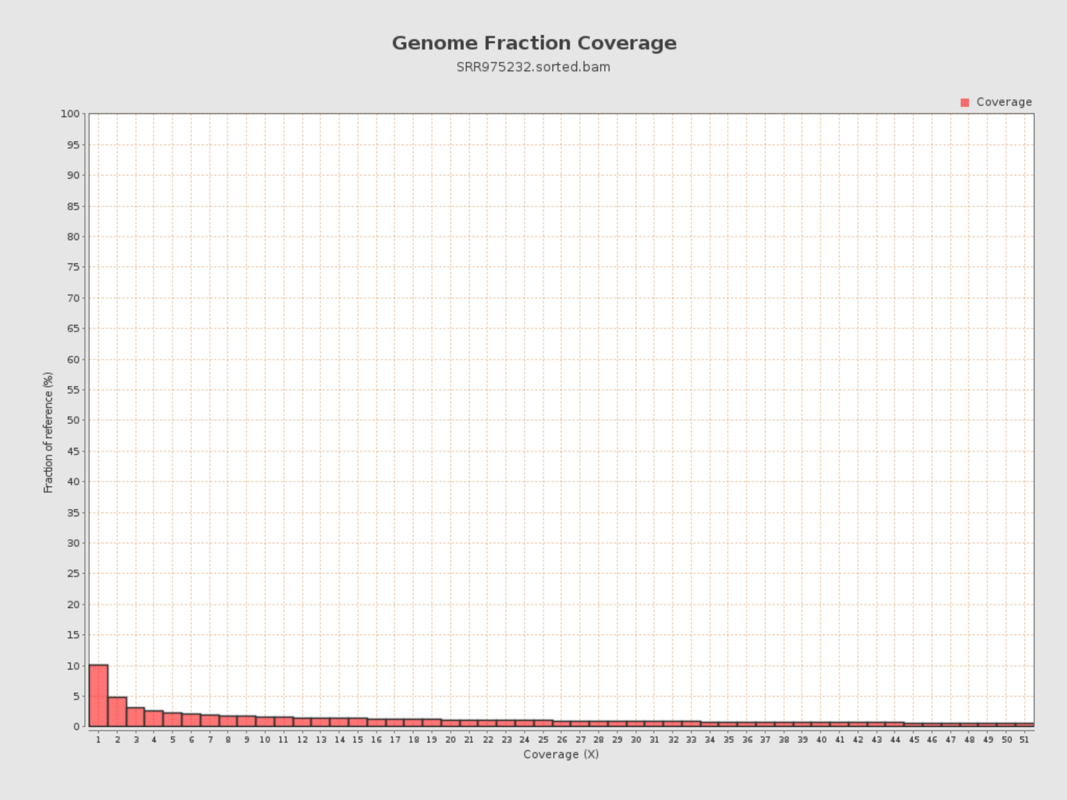
4. Results : Coverage Histogram



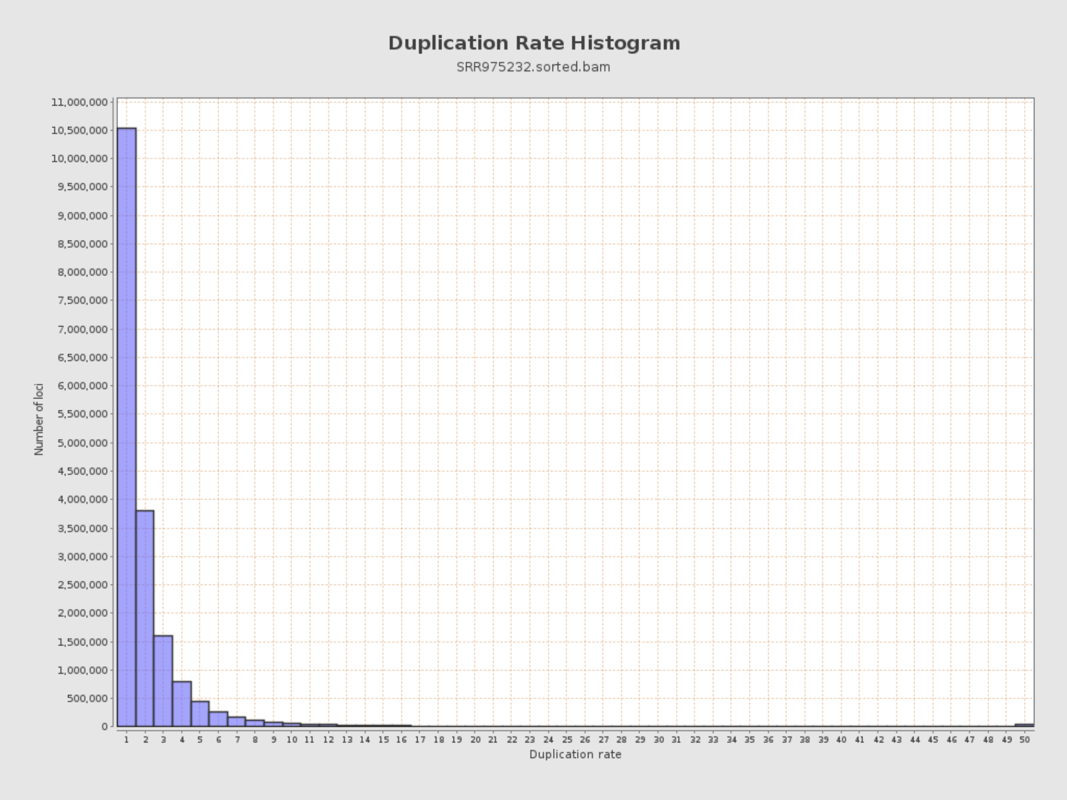
5. Results : Coverage Histogram (0-50X)



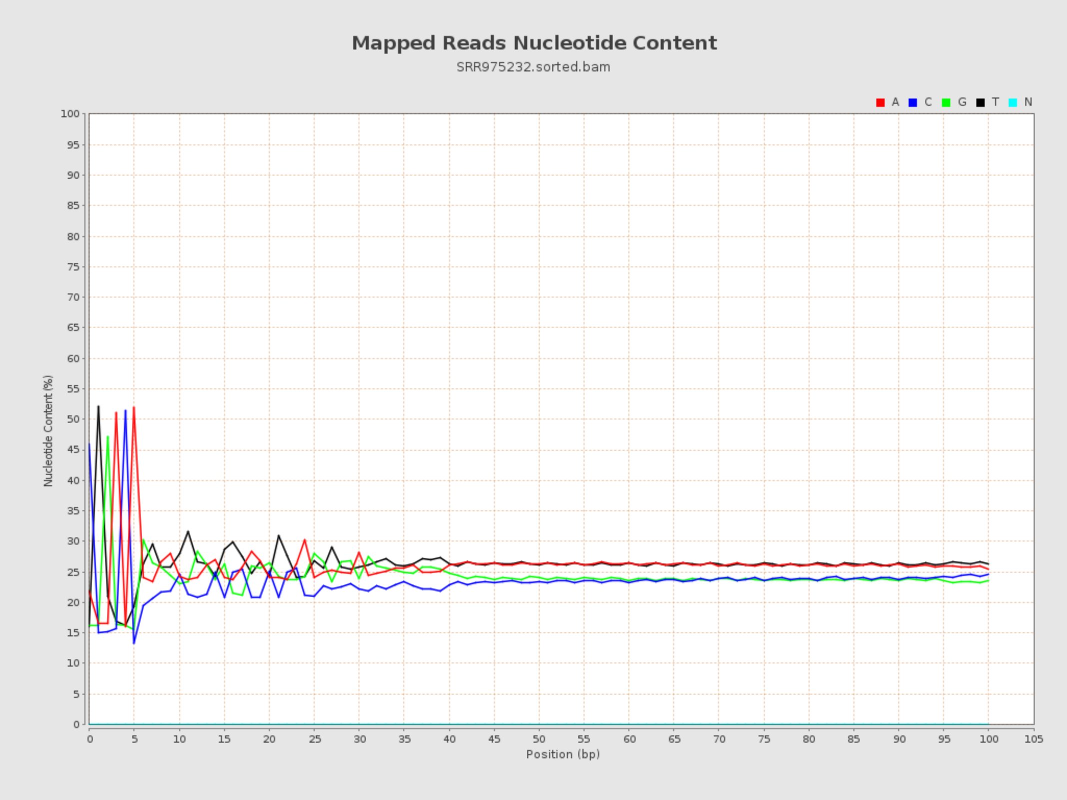
6. Results : Genome Fraction Coverage



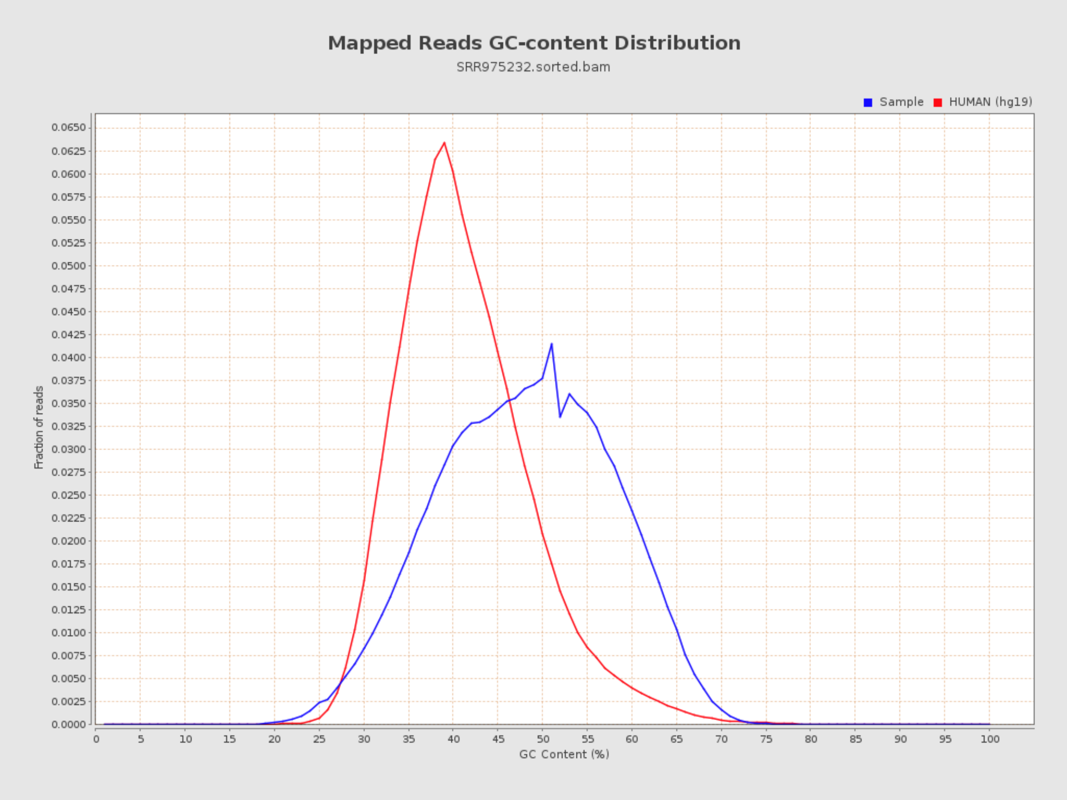
7. Results : Duplication Rate Histogram



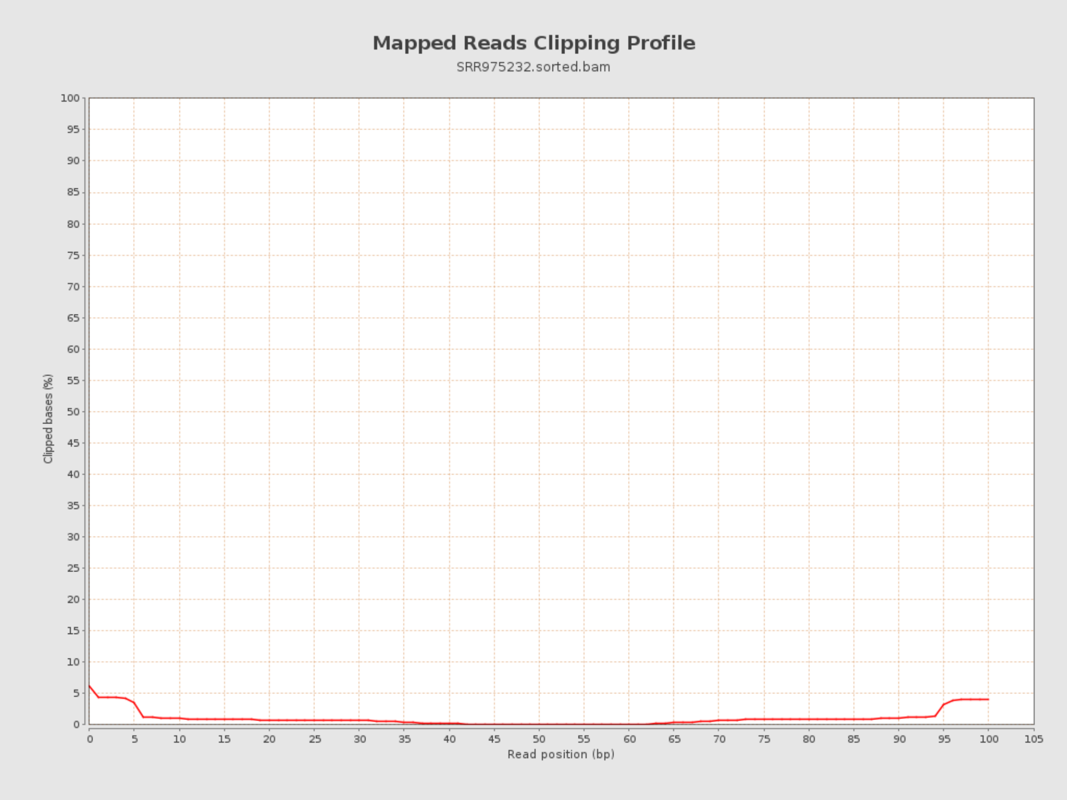
8. Results : Mapped Reads Nucleotide Content



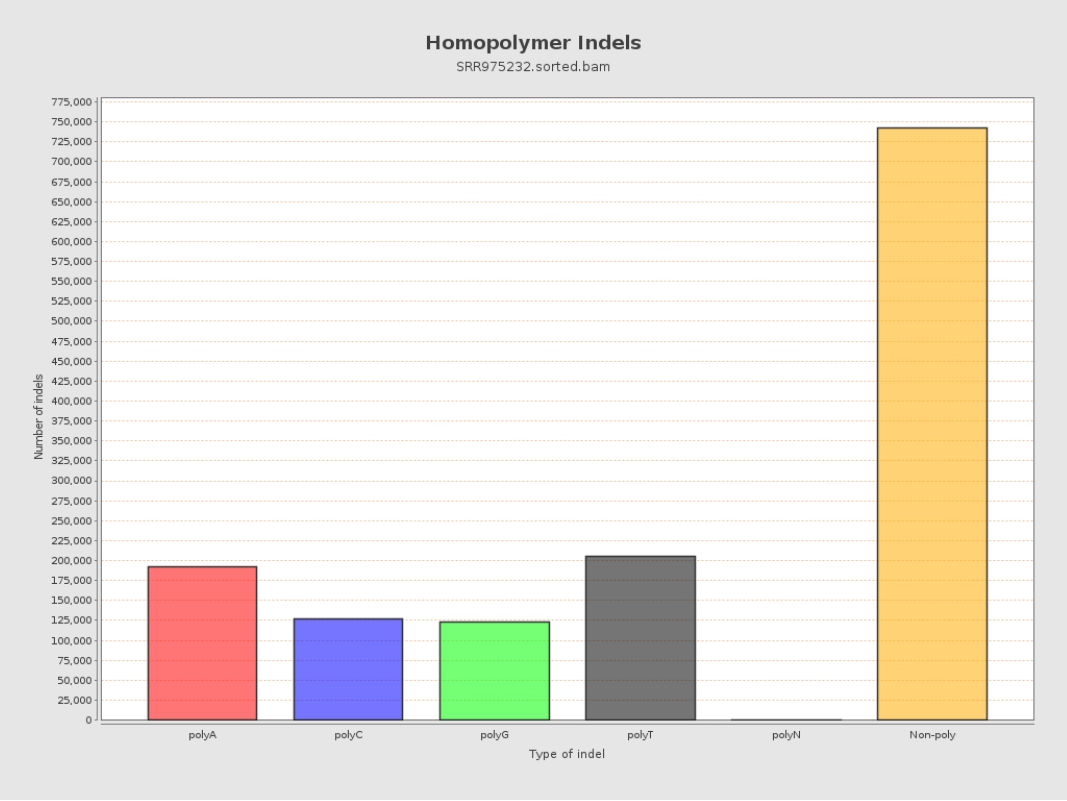
9. Results : Mapped Reads GC-content Distribution



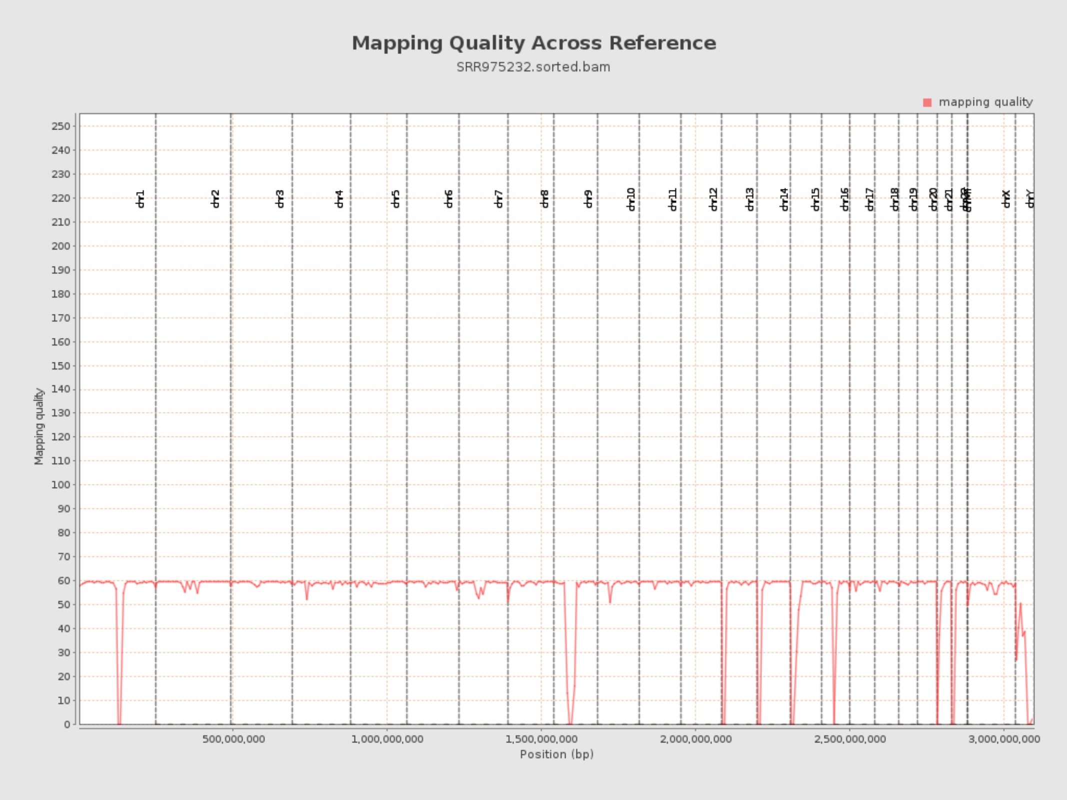
10. Results : Mapped Reads Clipping Profile



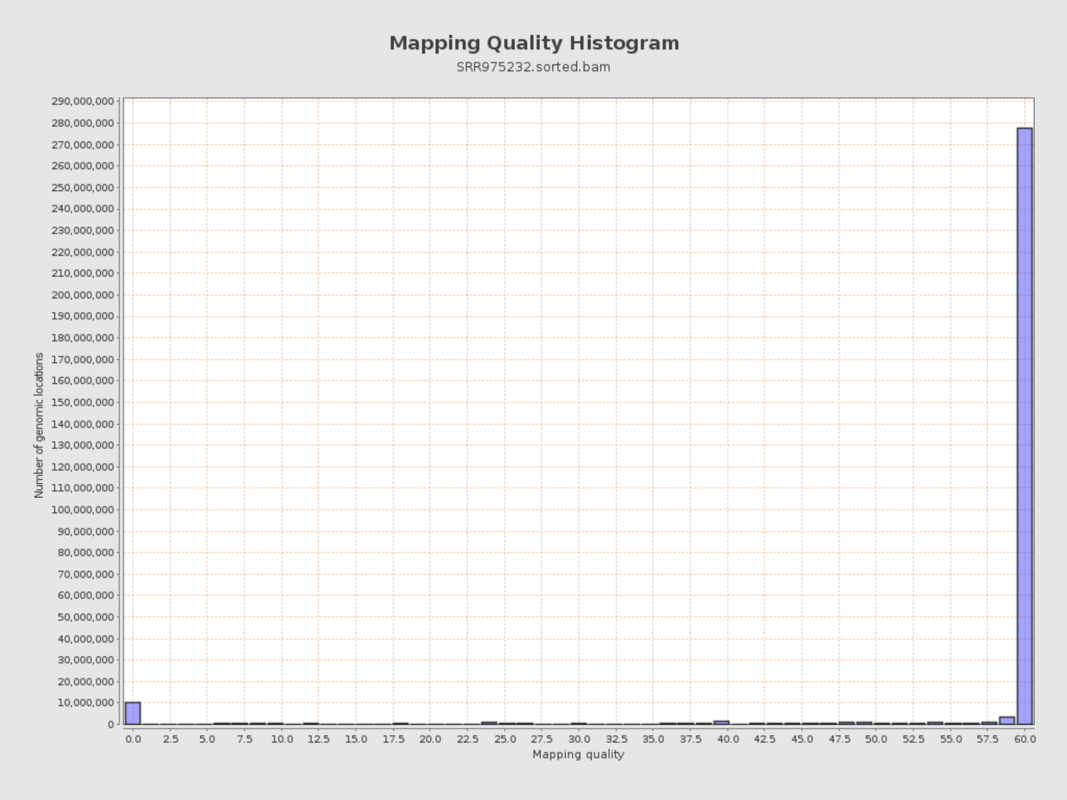
11. Results : Homopolymer Indels



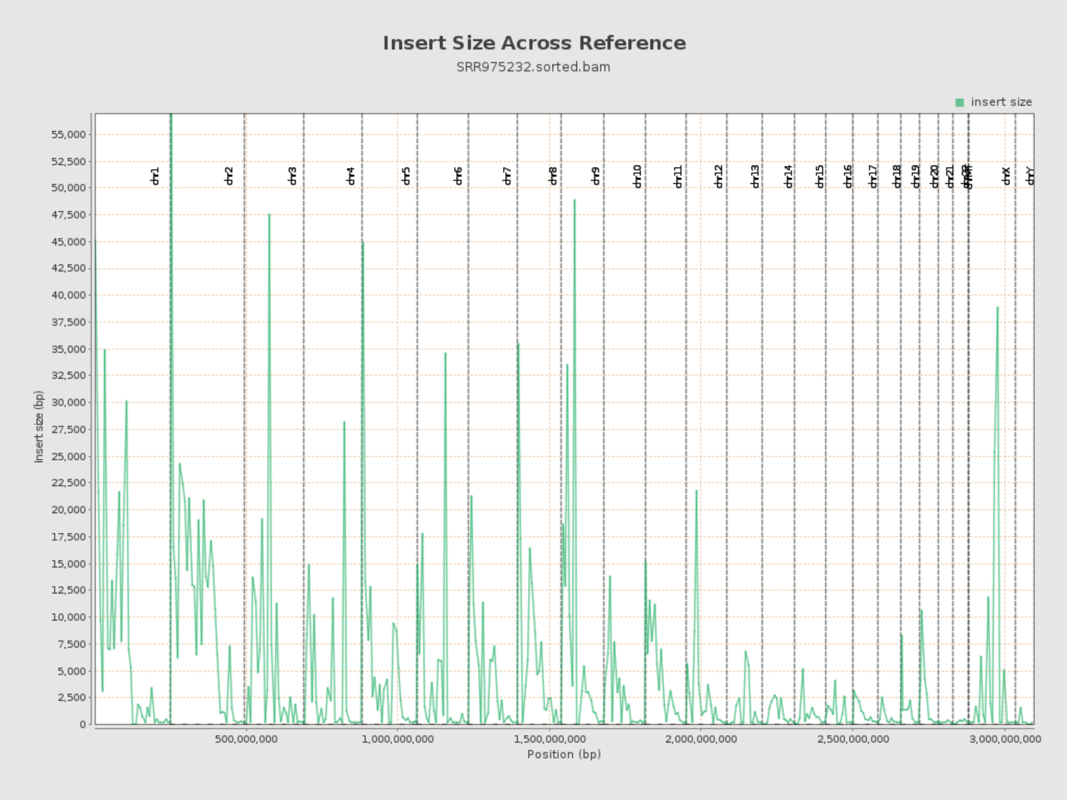
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram