Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:02:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975230.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_SRR975230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975230_1.fastq.gz SRR975230_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:02:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	108,769,624
Mapped reads	108,568,566 / 99.82%
Unmapped reads	201,058 / 0.18%
Mapped paired reads	108,568,566 / 99.82%
Mapped reads, first in pair	54,290,998 / 49.91%
Mapped reads, second in pair	54,277,568 / 49.9%
Mapped reads, both in pair	108,517,714 / 99.77%
Mapped reads, singletons	50,852 / 0.05%
Secondary alignments	0
Supplementary alignments	1,539,095 / 1.42%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	72,010,793 / 66.2%
Duplication rate	54.91%
Clipped reads	59,870,030 / 55.04%

2.2. ACGT Content

Number/percentage of A's	2,354,051,671 / 22.27%
Number/percentage of C's	2,922,888,381 / 27.65%
Number/percentage of T's	2,419,581,884 / 22.89%
Number/percentage of G's	2,875,022,998 / 27.19%
Number/percentage of N's	406,863 / 0%

GC Percentage	54.84%

2.3. Coverage

Mean	3.4155
Standard Deviation	39.4131

2.4. Mapping Quality

Mean Mapping Quality	56.03

2.5. Insert size

Mean	87,633.23
Standard Deviation	2,981,911.74
P25/Median/P75	122 / 142 / 167

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	29,930,983
Insertions	615,136
Mapped reads with at least one insertion	0.56%
Deletions	566,847
Mapped reads with at least one deletion	0.51%
Homopolymer indels	34.49%

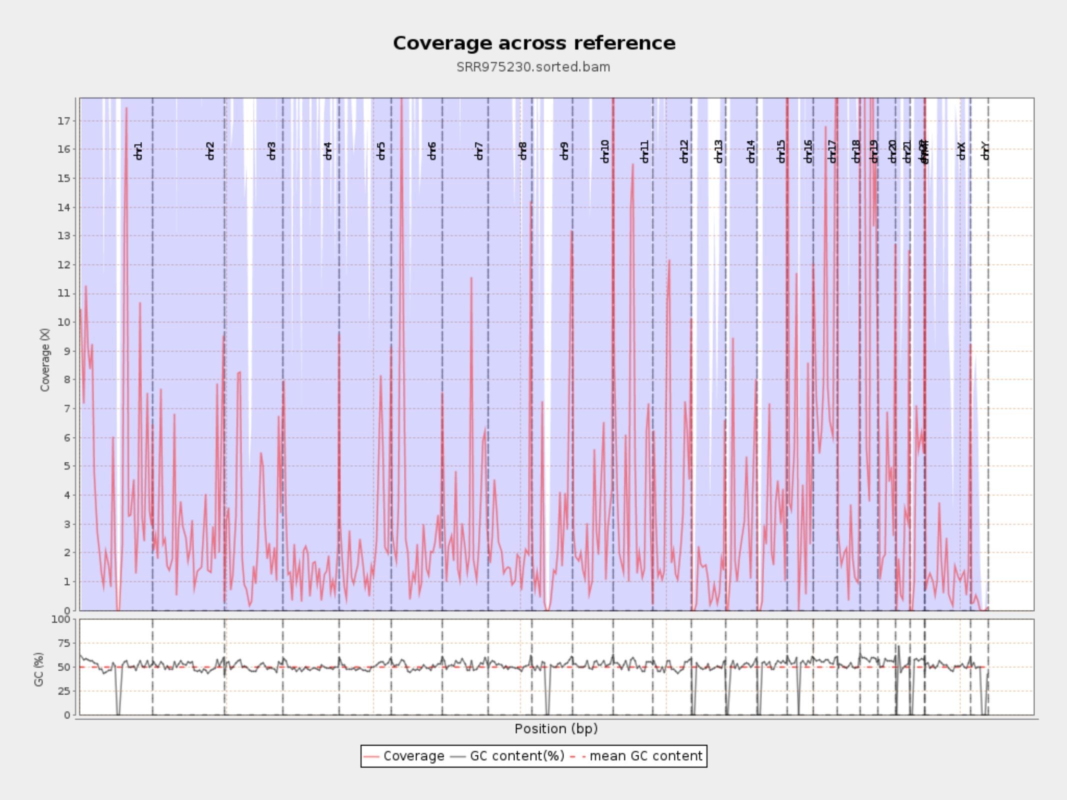
2.7. Chromosome stats

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

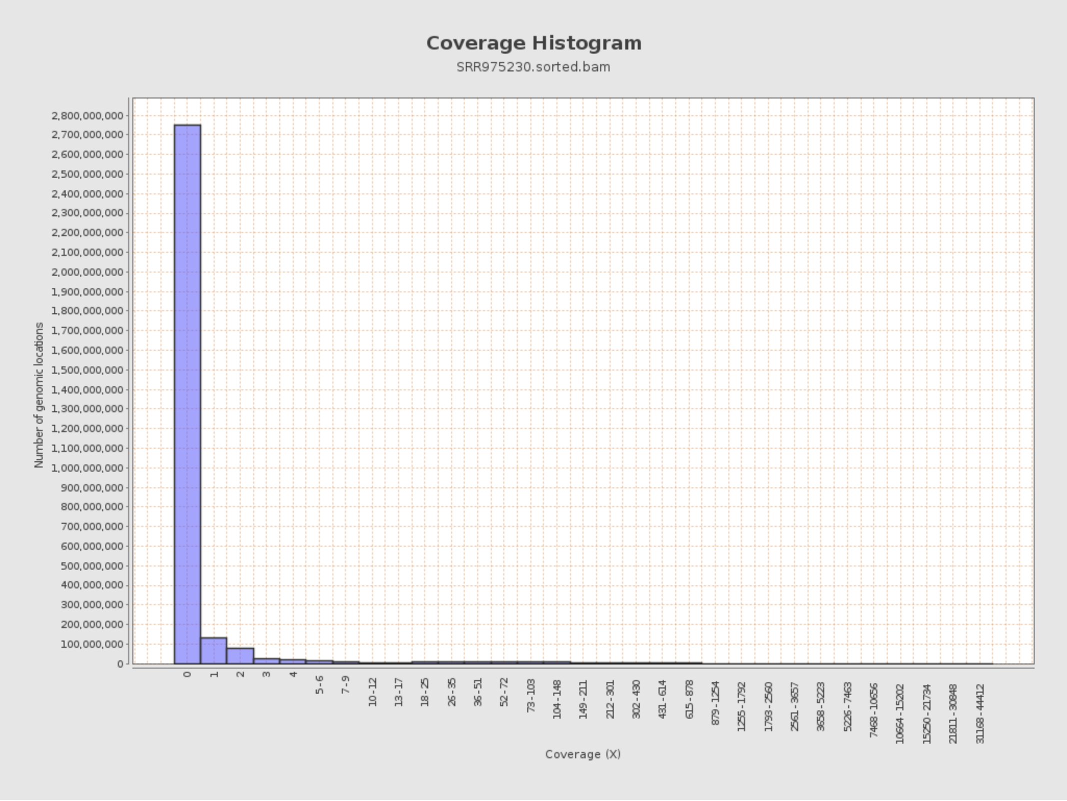
		bases	coverage	deviation
chr1	249250621	1237847395	4.9663	49.637
chr2	243199373	703686457	2.8935	33.1487
chr3	198022430	545390481	2.7542	30.424
chr4	191154276	305998302	1.6008	22.0486
chr5	180915260	455693867	2.5188	31.0395
chr6	171115067	516226093	3.0168	34.8338
chr7	159138663	512561984	3.2209	35.73
chr8	146364022	363790062	2.4855	31.7555
chr9	141213431	407290248	2.8842	32.3527
chr10	135534747	358329851	2.6438	30.6754
chr11	135006516	700799116	5.1909	48.0811
chr12	133851895	544498523	4.0679	40.9748
chr13	115169878	119684207	1.0392	15.8152
chr14	107349540	334128991	3.1125	35.1325
chr15	102531392	264616058	2.5808	26.7026
chr16	90354753	501235902	5.5474	50.1052
chr17	81195210	789730451	9.7263	70.5562
chr18	78077248	147133093	1.8845	26.8934
chr19	59128983	933193904	15.7823	104.9757
chr20	63025520	259771318	4.1217	39.7942
chr21	48129895	133459266	2.7729	78.5682
chr22	51304566	221582944	4.319	37.4375
chrMT	16571	701376	42.3255	52.6306
chrX	155270560	204638166	1.3179	17.0871

chrY	59373566	11262984	0.1897	4.8092

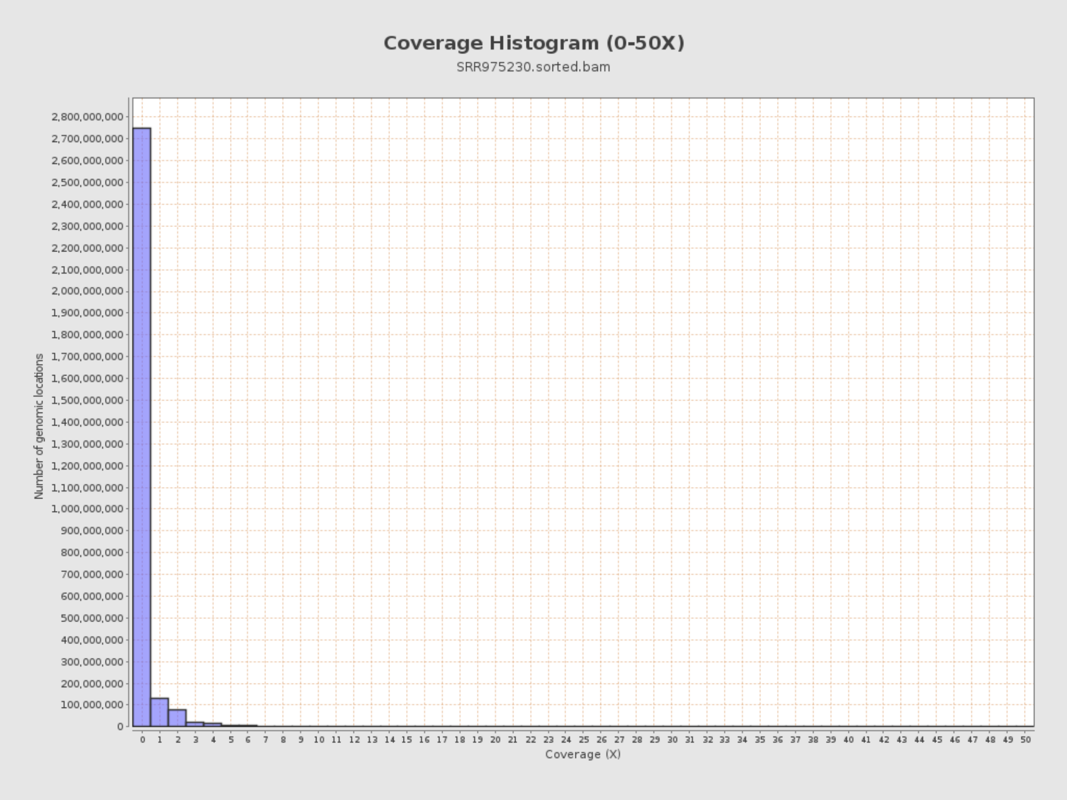
3. Results : Coverage across reference



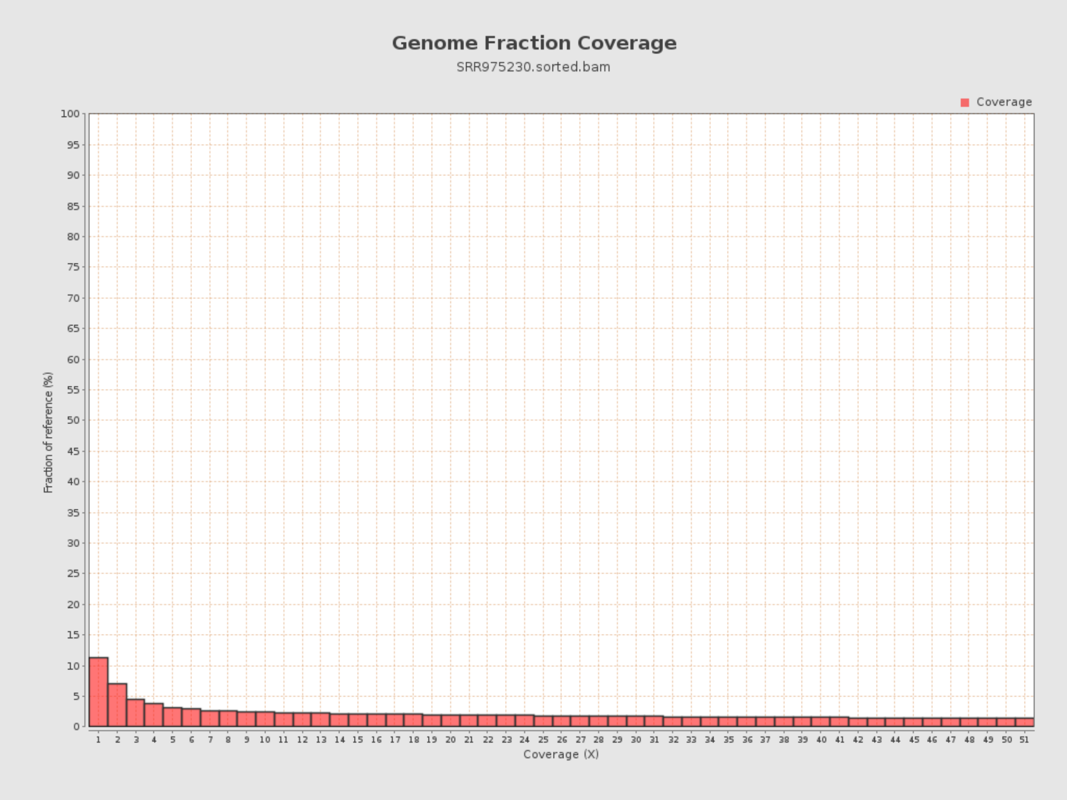
4. Results : Coverage Histogram



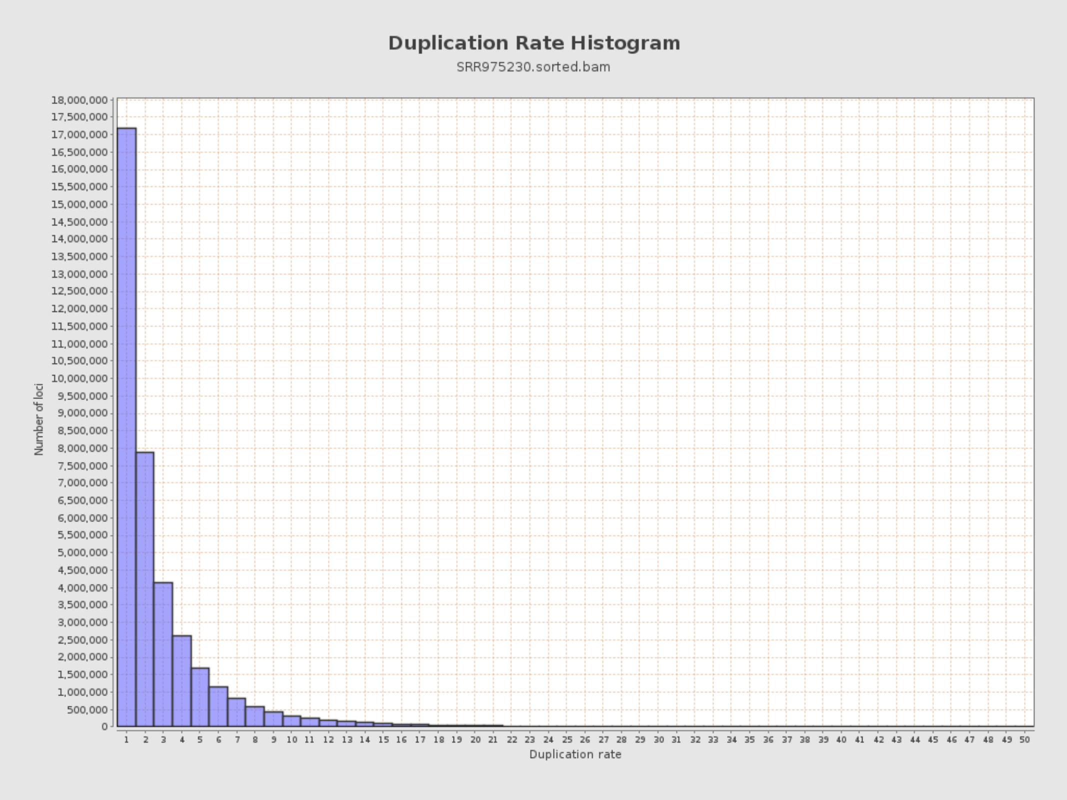
5. Results : Coverage Histogram (0-50X)



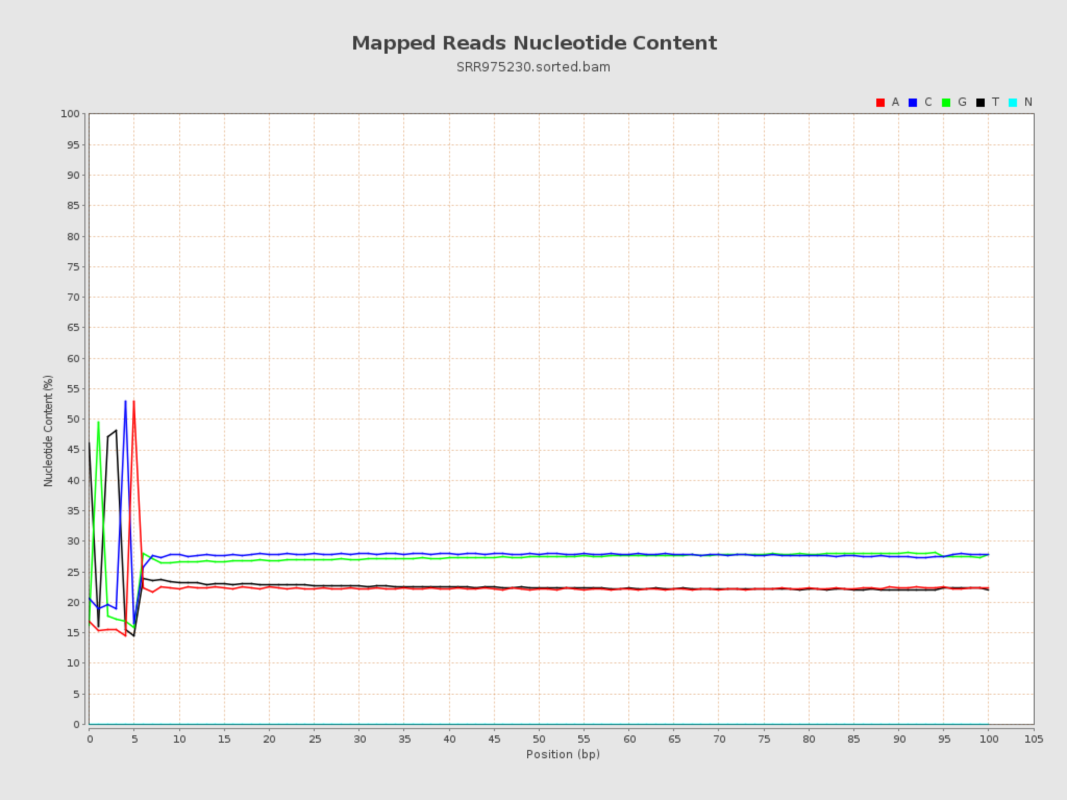
6. Results : Genome Fraction Coverage



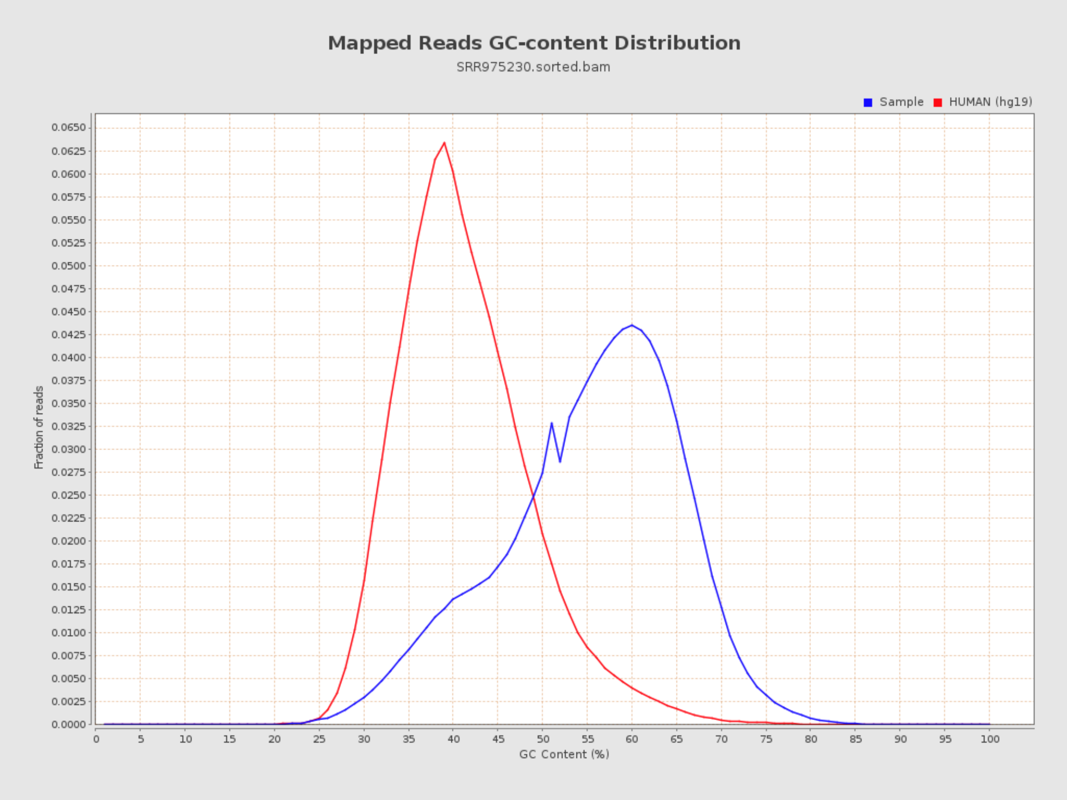
7. Results : Duplication Rate Histogram



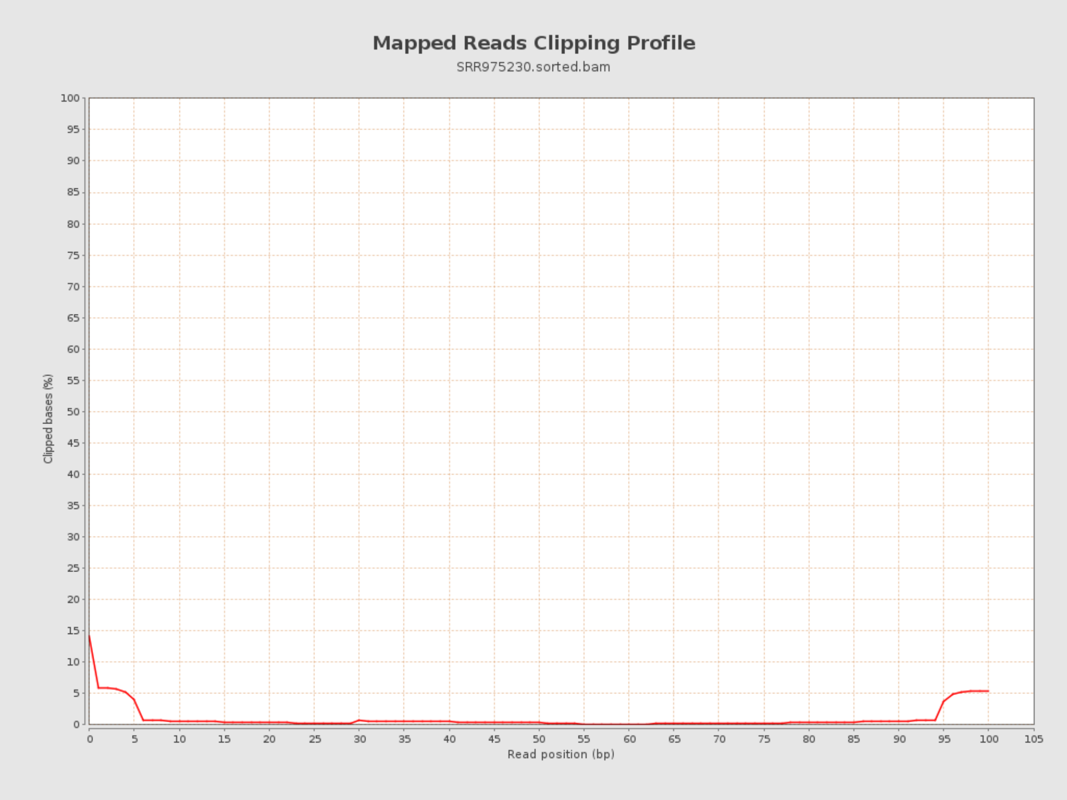
8. Results : Mapped Reads Nucleotide Content



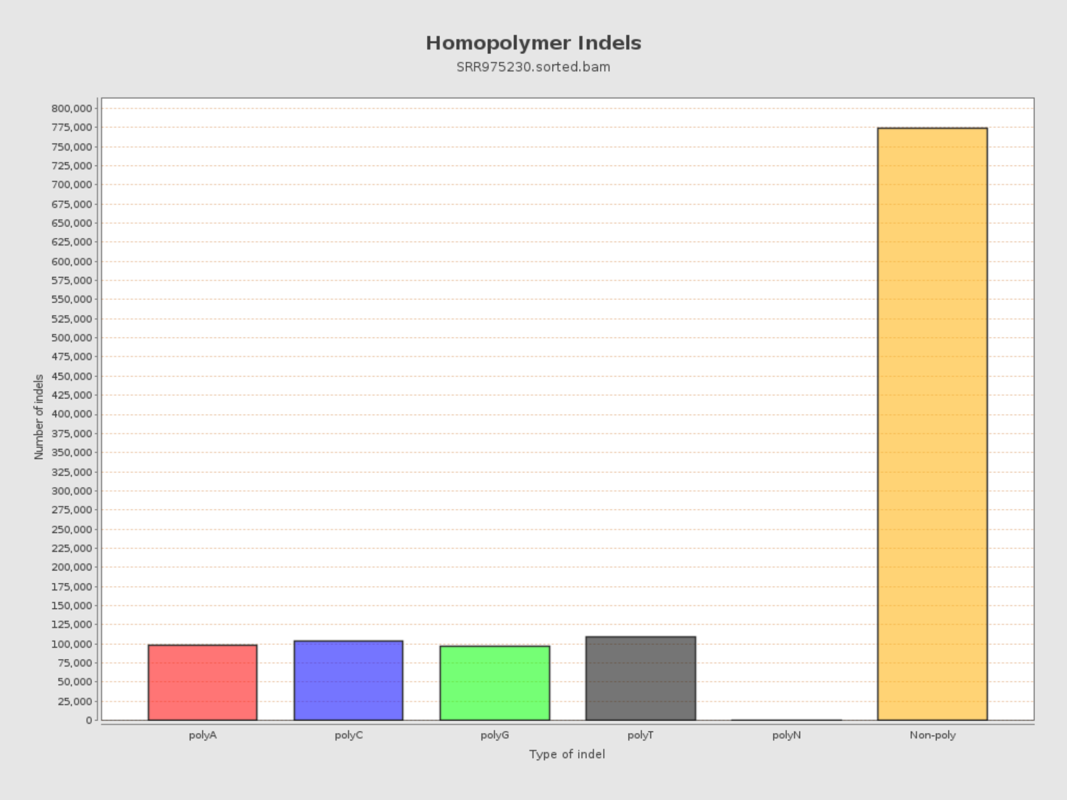
9. Results : Mapped Reads GC-content Distribution



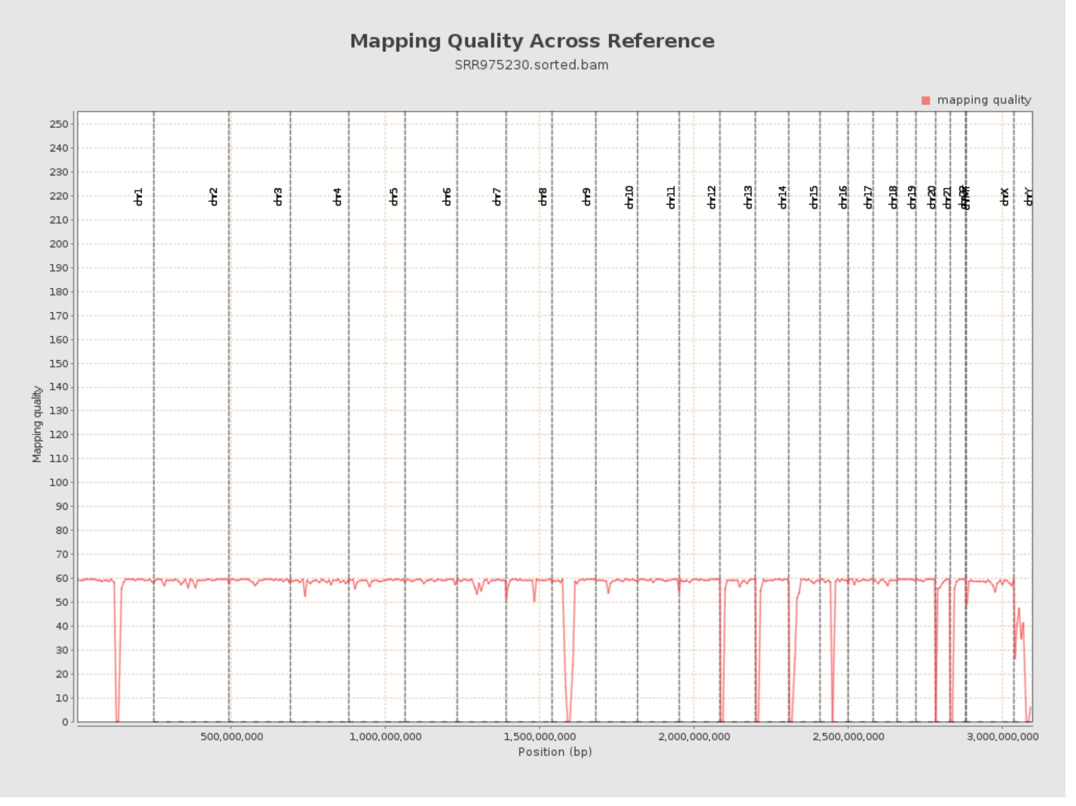
10. Results : Mapped Reads Clipping Profile



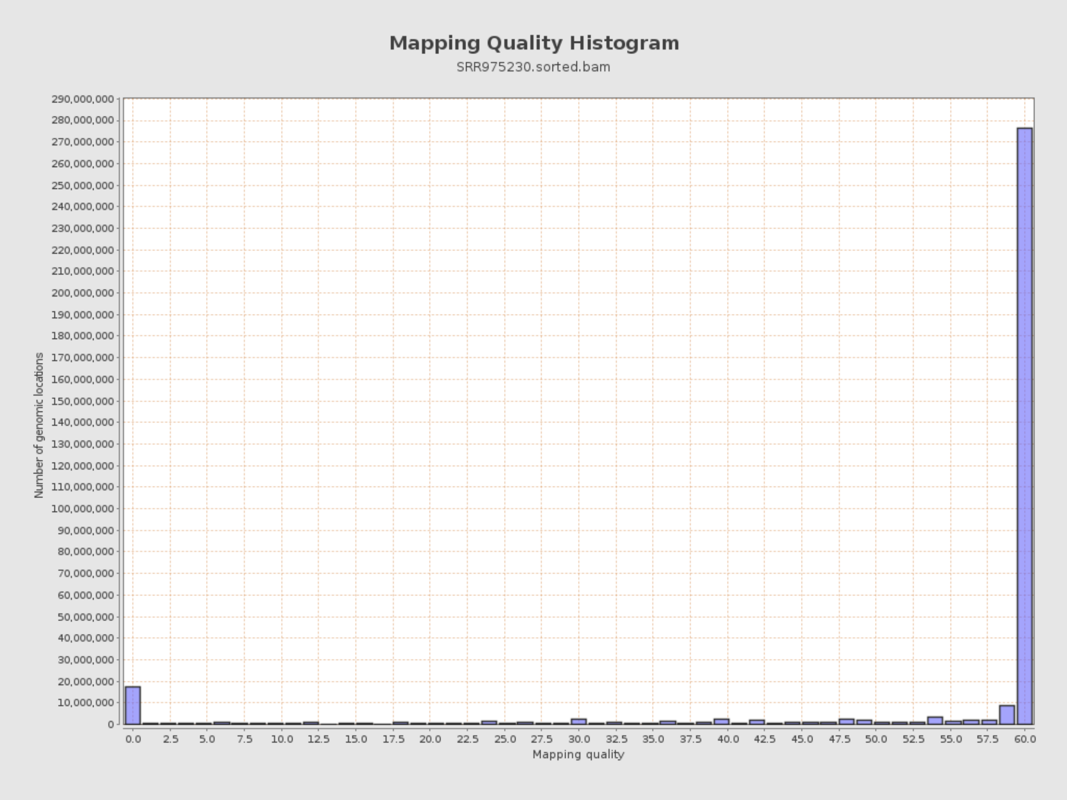
11. Results : Homopolymer Indels



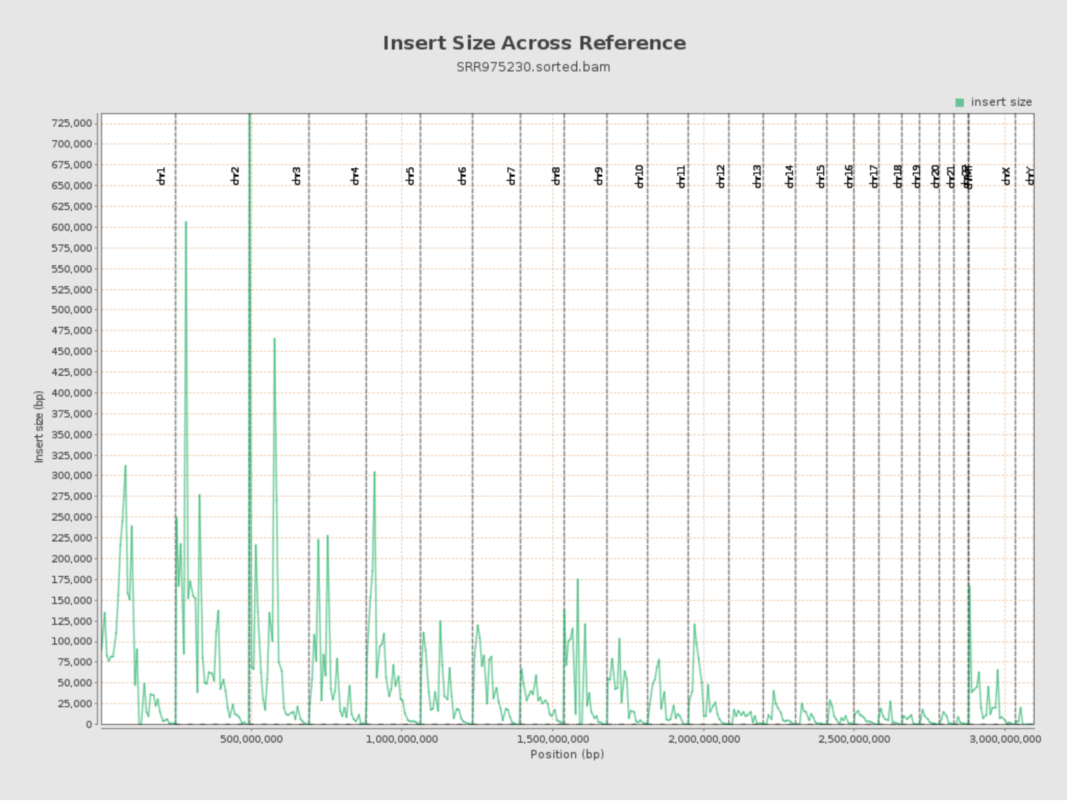
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram