Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 05:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975200.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_SRR975200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975200_1.fastq.gz SRR975200_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 05:47:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,817,004
Mapped reads	36,746,682 / 99.81%
Unmapped reads	70,322 / 0.19%
Mapped paired reads	36,746,682 / 99.81%
Mapped reads, first in pair	18,373,703 / 49.91%
Mapped reads, second in pair	18,372,979 / 49.9%
Mapped reads, both in pair	36,701,120 / 99.69%
Mapped reads, singletons	45,562 / 0.12%
Secondary alignments	0
Supplementary alignments	95,599 / 0.26%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	20,758,839 / 56.38%
Duplication rate	42.27%
Clipped reads	21,646,767 / 58.8%

2.2. ACGT Content

Number/percentage of A's	934,286,838 / 27.27%
Number/percentage of C's	729,261,076 / 21.28%
Number/percentage of T's	974,476,654 / 28.44%
Number/percentage of G's	787,994,988 / 23%
Number/percentage of N's	237,050 / 0.01%

GC Percentage	44.28%

2.3. Coverage

Mean	1.1072
Standard Deviation	17.5958

2.4. Mapping Quality

Mean Mapping Quality	55.8

2.5. Insert size

Mean	105,355.83
Standard Deviation	3,125,891.56
P25/Median/P75	188 / 232 / 282

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	17,819,604
Insertions	374,389
Mapped reads with at least one insertion	1%
Deletions	764,002
Mapped reads with at least one deletion	2.04%
Homopolymer indels	46.11%

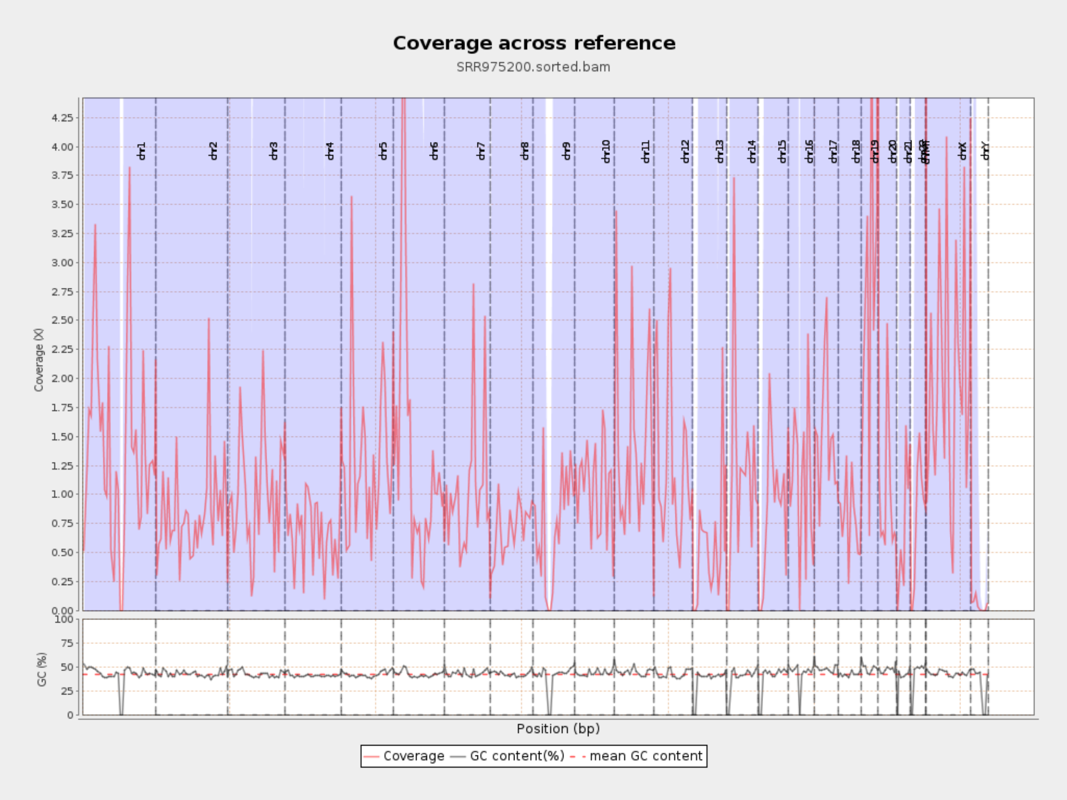
2.7. Chromosome stats

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

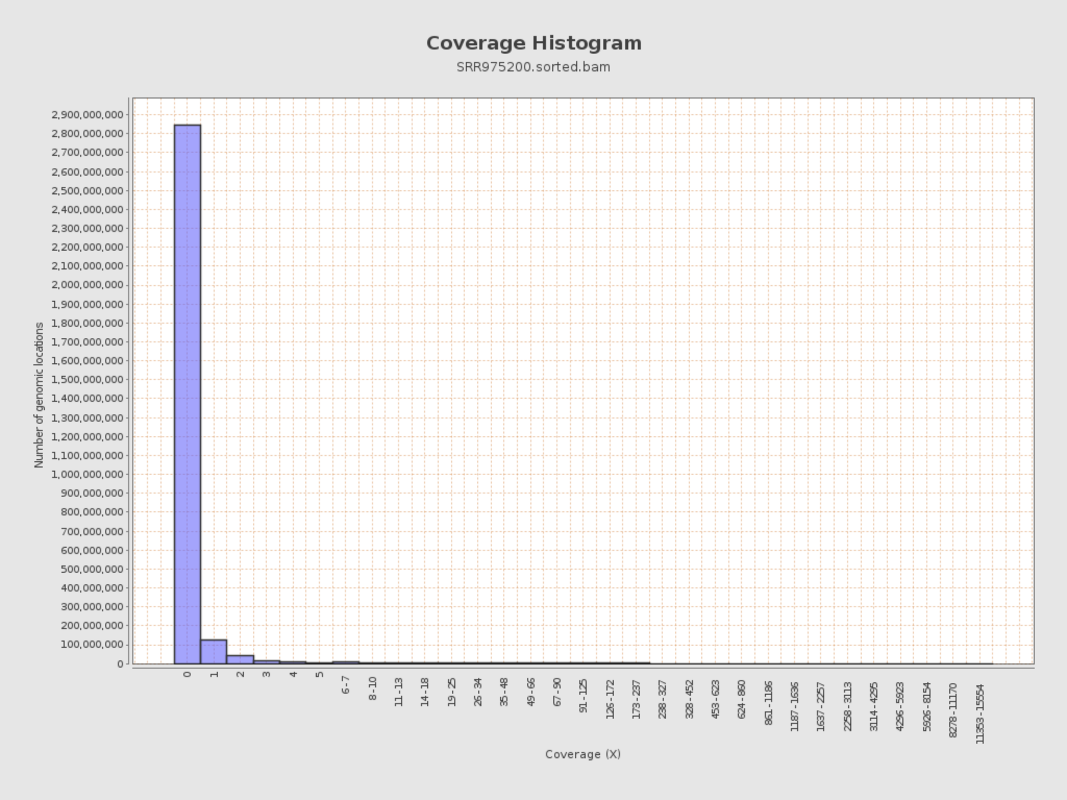
		bases	coverage	deviation
chr1	249250621	353353279	1.4177	19.1712
chr2	243199373	205692195	0.8458	12.6497
chr3	198022430	198710690	1.0035	14.9567
chr4	191154276	127762040	0.6684	12.0575
chr5	180915260	238694365	1.3194	18.5624
chr6	171115067	228916193	1.3378	19.1565
chr7	159138663	165803694	1.0419	16.5683
chr8	146364022	103631263	0.708	10.7912
chr9	141213431	100841071	0.7141	11.3335
chr10	135534747	145824156	1.0759	15.9233
chr11	135006516	195415967	1.4475	18.5283
chr12	133851895	177090632	1.323	16.8829
chr13	115169878	63651414	0.5527	13.349
chr14	107349540	127895907	1.1914	18.7537
chr15	102531392	84236749	0.8216	11.3046
chr16	90354753	97967770	1.0843	14.0937
chr17	81195210	123958696	1.5267	19.6681
chr18	78077248	62954309	0.8063	13.6926
chr19	59128983	173599942	2.936	46.941
chr20	63025520	60583136	0.9612	15.6015
chr21	48129895	34429904	0.7154	11.7678
chr22	51304566	40933524	0.7979	11.512
chrMT	16571	112869	6.8112	14.5305
chrX	155270560	312514324	2.0127	29.762

chrY	59373566	2868879	0.0483	2.4171

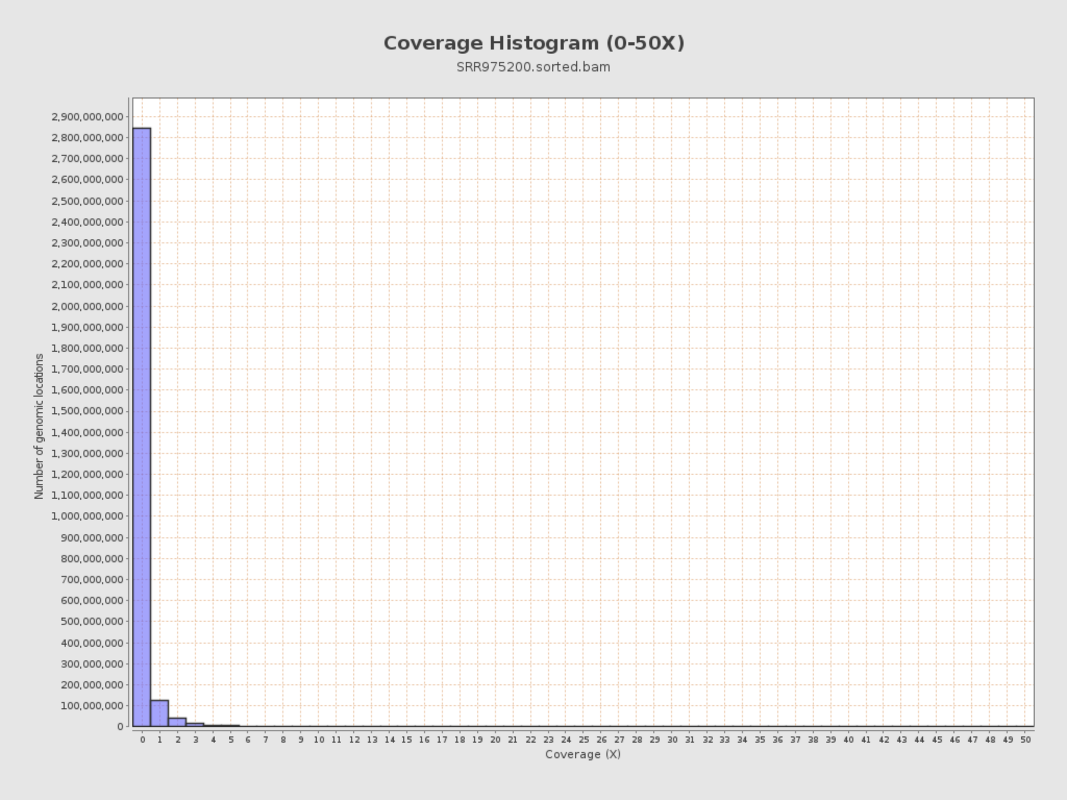
3. Results : Coverage across reference



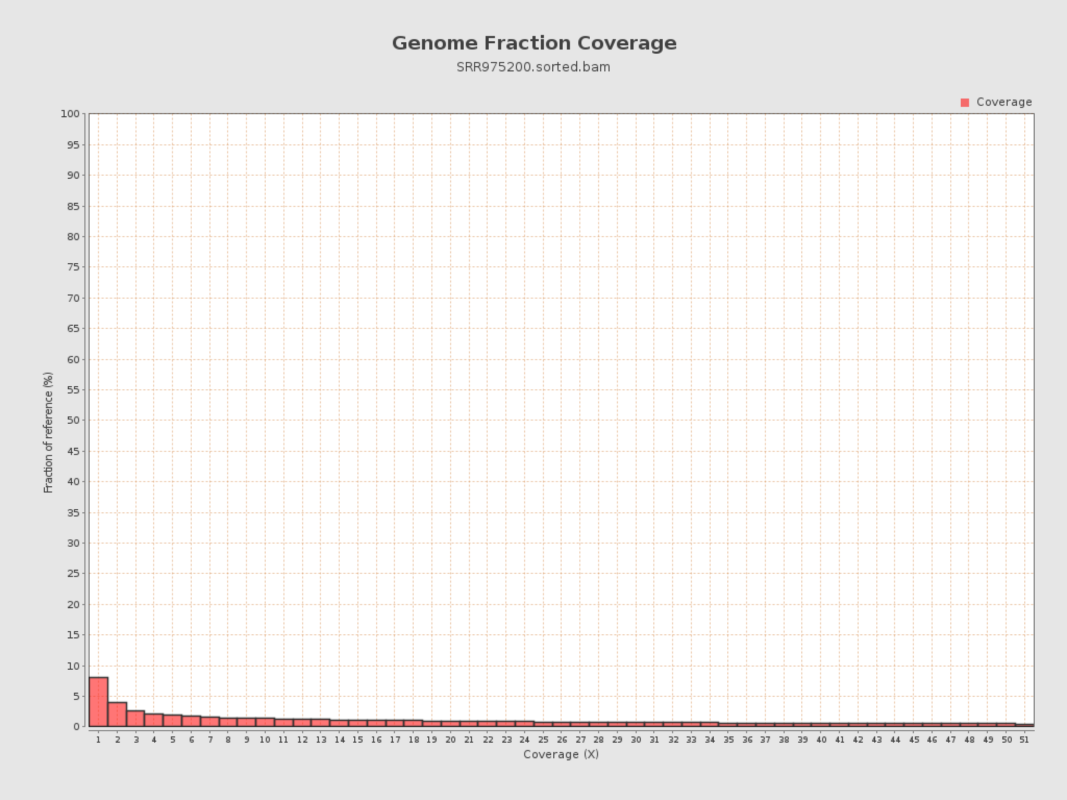
4. Results : Coverage Histogram



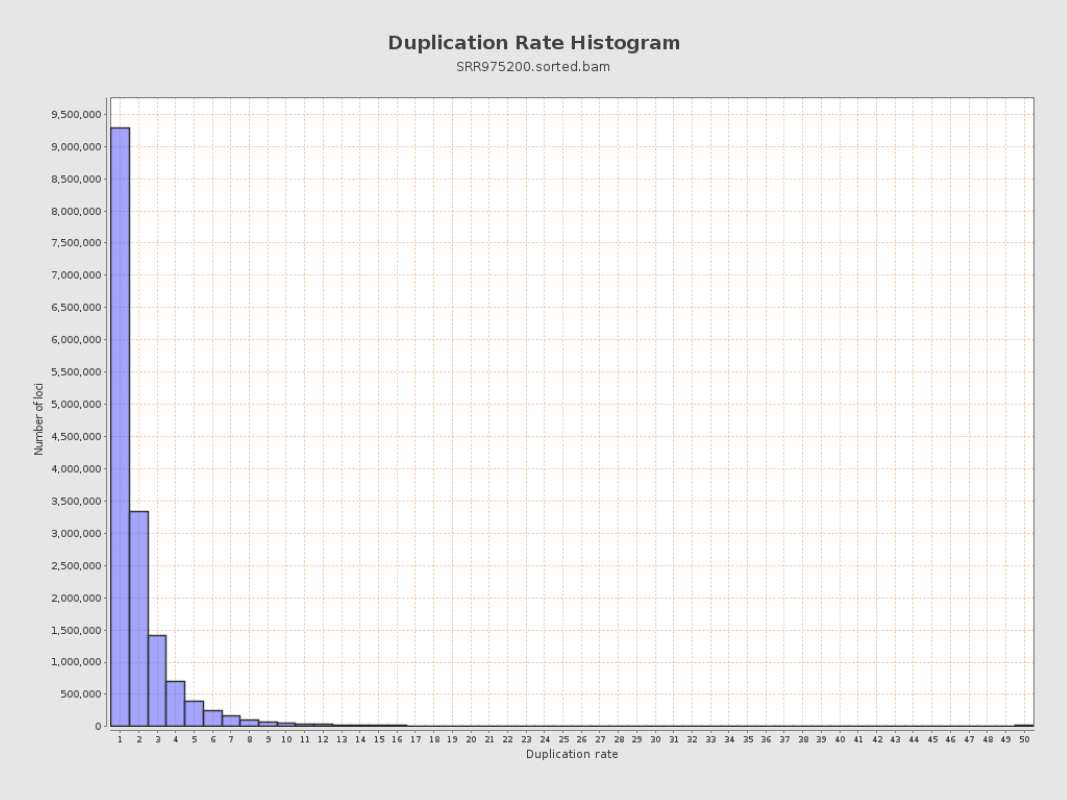
5. Results : Coverage Histogram (0-50X)



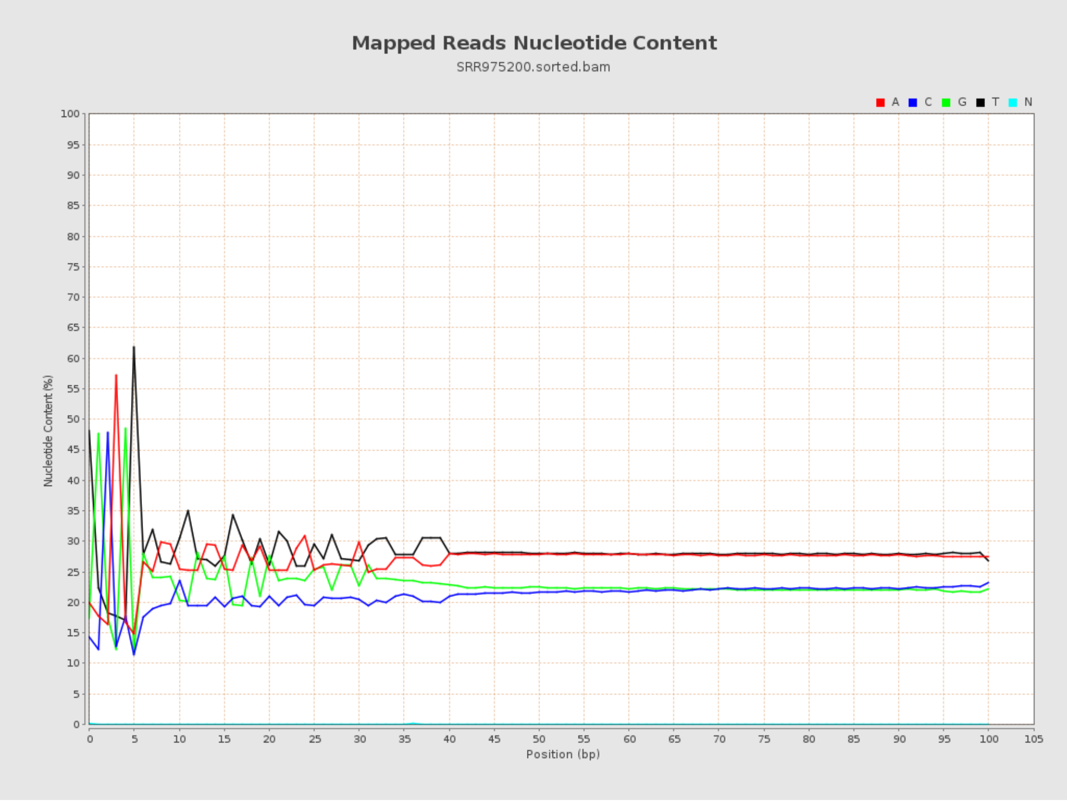
6. Results : Genome Fraction Coverage



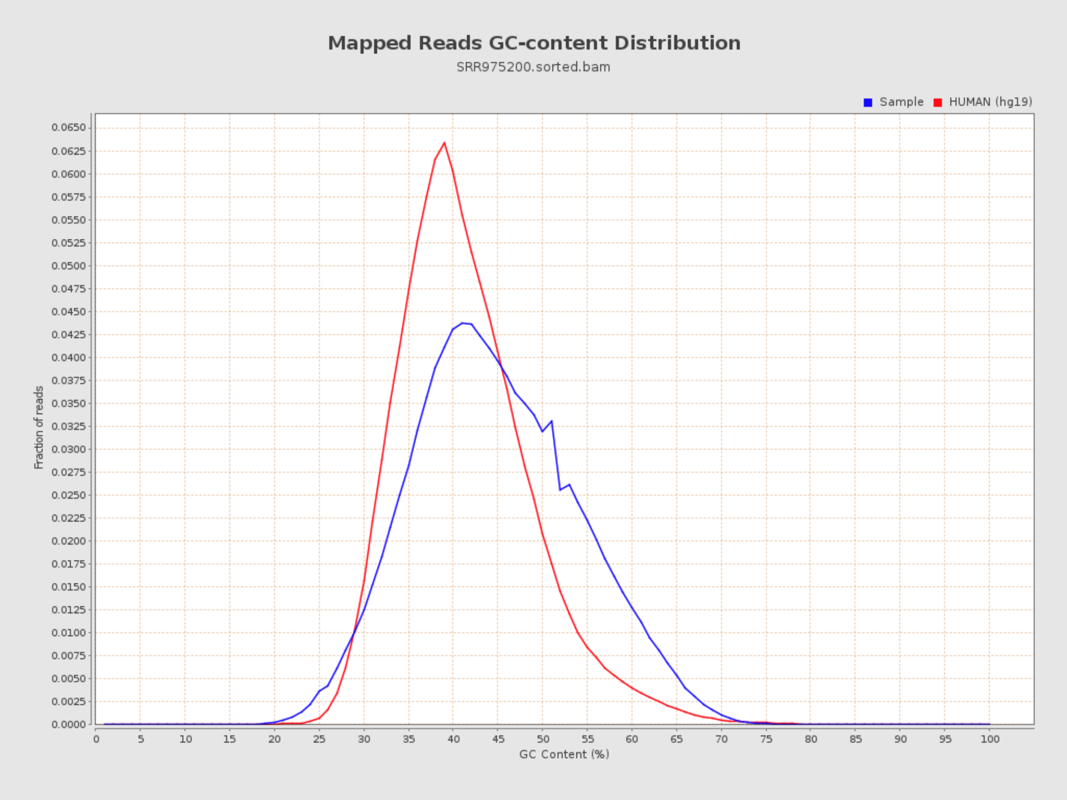
7. Results : Duplication Rate Histogram



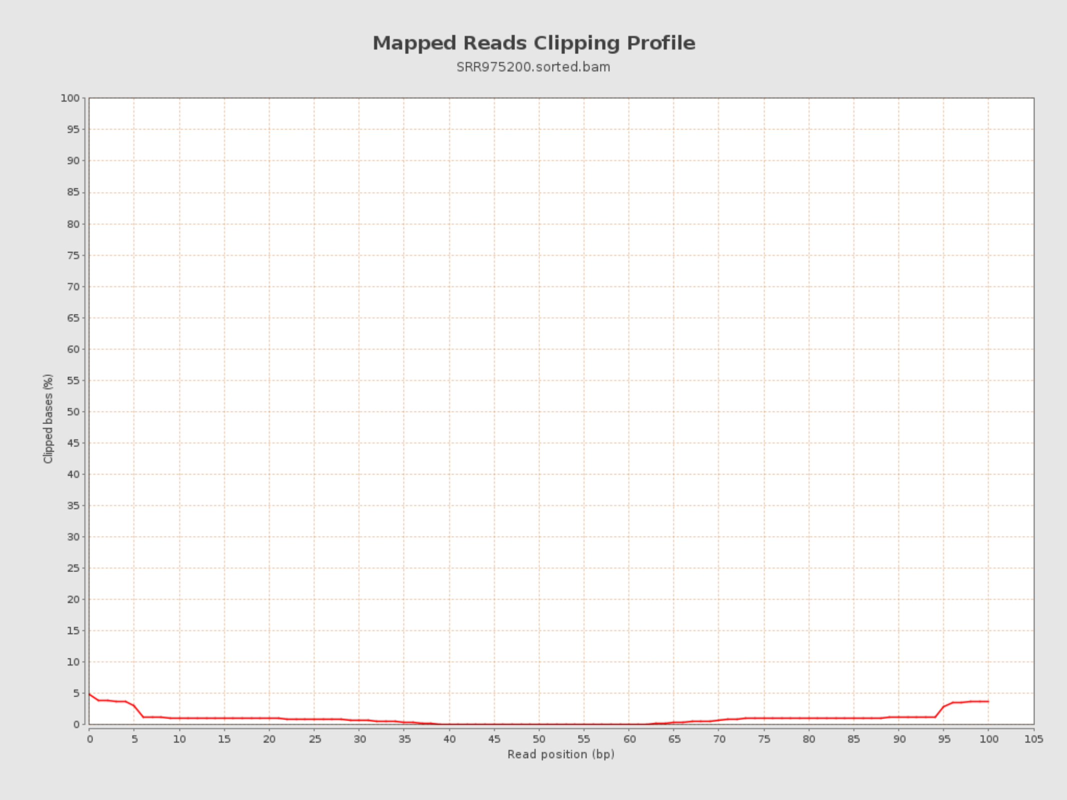
8. Results : Mapped Reads Nucleotide Content



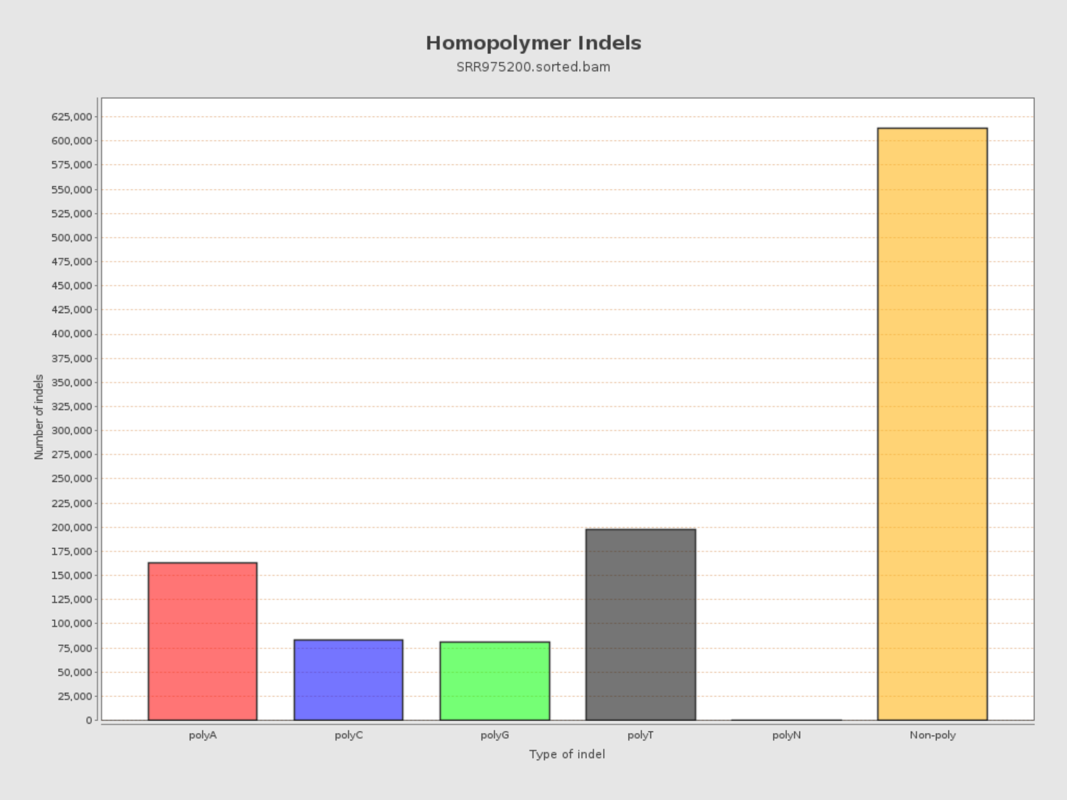
9. Results : Mapped Reads GC-content Distribution



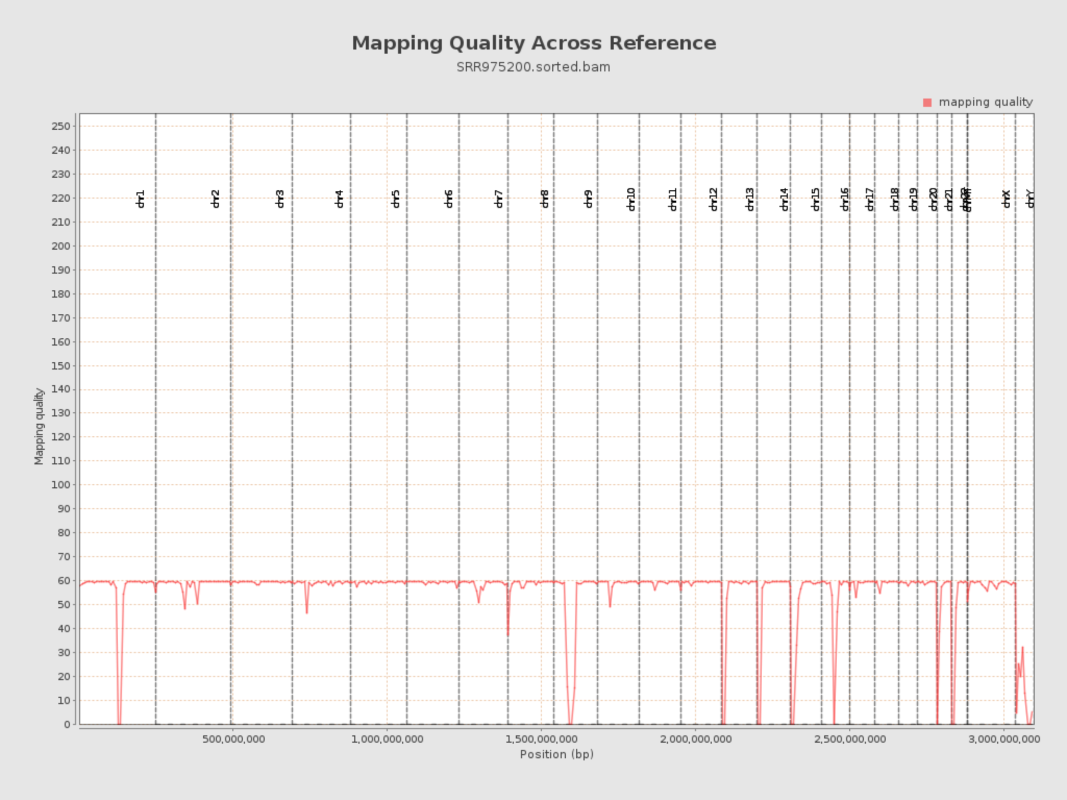
10. Results : Mapped Reads Clipping Profile



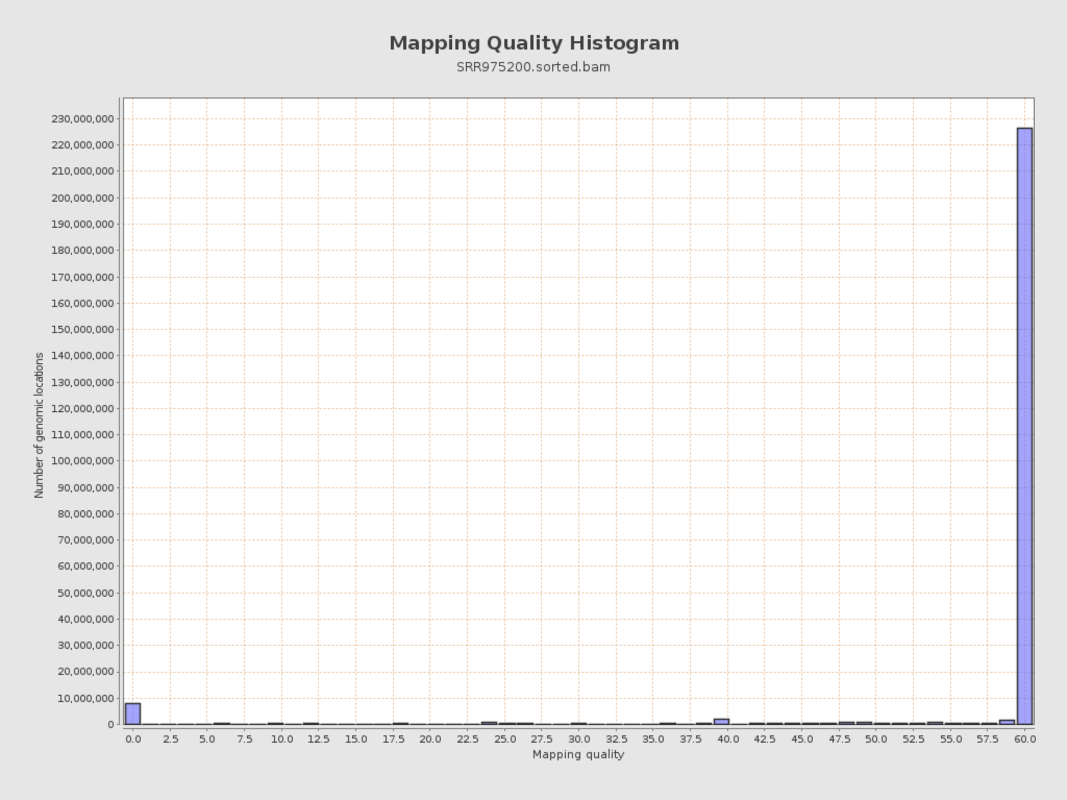
11. Results : Homopolymer Indels



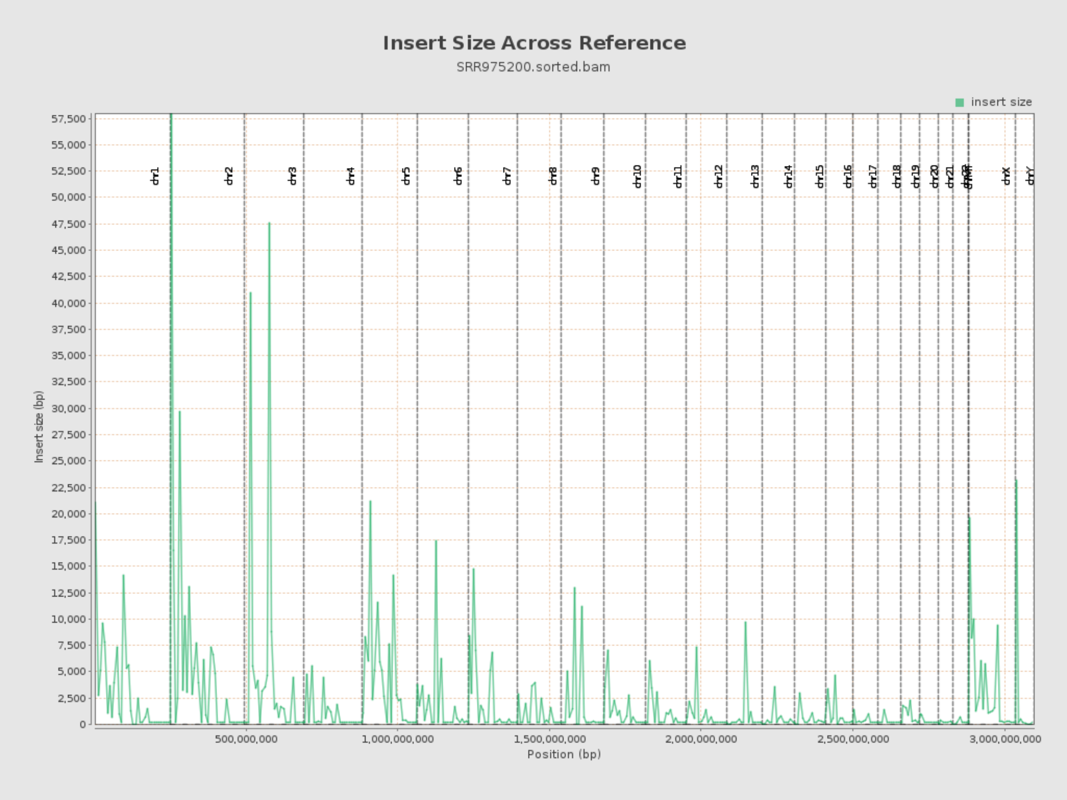
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram