Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:55:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975333.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_SRR975333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975333_1.fastq.gz SRR975333_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:55:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,576,714
Mapped reads	3,513,725 / 98.24%
Unmapped reads	62,989 / 1.76%
Mapped paired reads	3,513,725 / 98.24%
Mapped reads, first in pair	1,755,458 / 49.08%
Mapped reads, second in pair	1,758,267 / 49.16%
Mapped reads, both in pair	3,495,864 / 97.74%
Mapped reads, singletons	17,861 / 0.5%
Secondary alignments	0
Supplementary alignments	18,729 / 0.52%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	240,998 / 6.74%
Duplication rate	3.52%
Clipped reads	2,161,102 / 60.42%

2.2. ACGT Content

Number/percentage of A's	93,929,393 / 29.49%
Number/percentage of C's	60,017,230 / 18.84%
Number/percentage of T's	96,135,283 / 30.18%
Number/percentage of G's	68,400,731 / 21.48%
Number/percentage of N's	6,898 / 0%

GC Percentage	40.32%

2.3. Coverage

Mean	0.1029
Standard Deviation	1.3864

2.4. Mapping Quality

Mean Mapping Quality	52.65

2.5. Insert size

Mean	73,255.25
Standard Deviation	2,507,144.73
P25/Median/P75	133 / 164 / 207

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	2,502,497
Insertions	52,182
Mapped reads with at least one insertion	1.44%
Deletions	104,454
Mapped reads with at least one deletion	2.91%
Homopolymer indels	46.07%

2.7. Chromosome stats

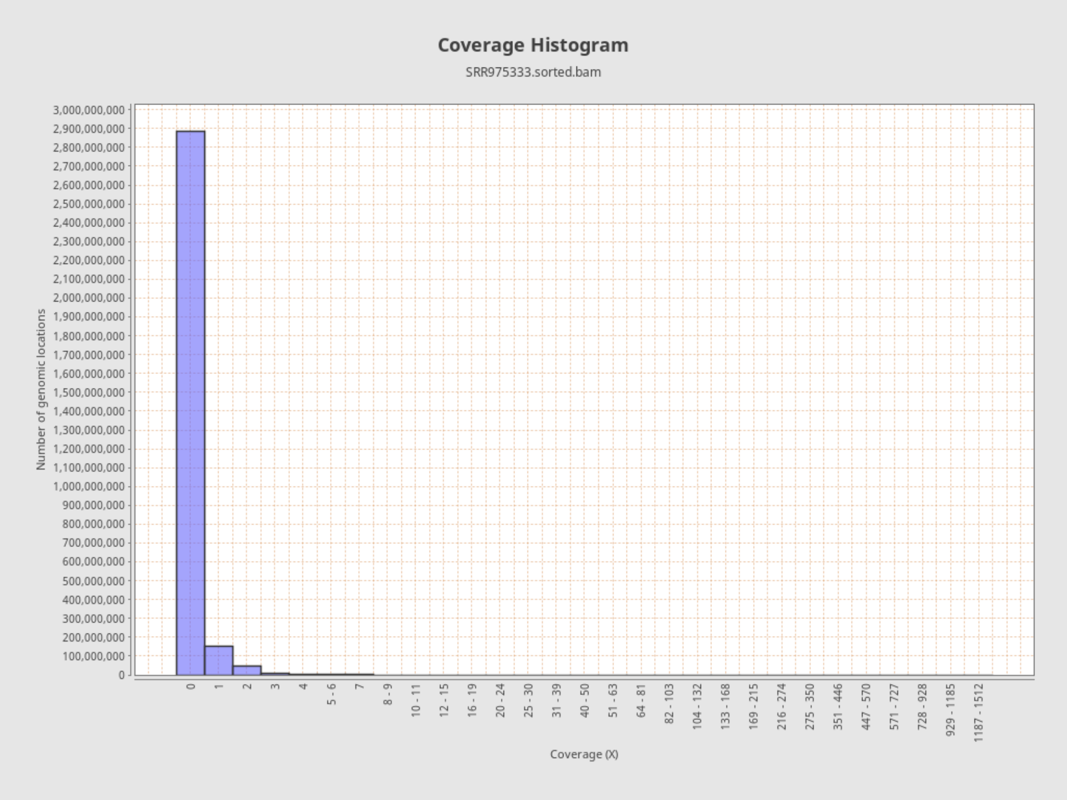
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	23073751	0.0926	1.1376
chr2	243199373	29567477	0.1216	1.6626
chr3	198022430	21796051	0.1101	0.4622
chr4	191154276	20603972	0.1078	1.0834
chr5	180915260	19648139	0.1086	0.4405
chr6	171115067	18380823	0.1074	1.1529
chr7	159138663	18119673	0.1139	1.8068
chr8	146364022	17241807	0.1178	0.6844
chr9	141213431	13962420	0.0989	1.7205
chr10	135534747	17093472	0.1261	3.4445
chr11	135006516	14880105	0.1102	0.8829
chr12	133851895	14168585	0.1059	0.4284
chr13	115169878	9849558	0.0855	0.377
chr14	107349540	9873471	0.092	0.4441
chr15	102531392	8925223	0.087	0.3885
chr16	90354753	11679719	0.1293	2.9098
chr17	81195210	7260895	0.0894	1.3513
chr18	78077248	9756515	0.125	1.9857
chr19	59128983	3958714	0.067	0.7092
chr20	63025520	6337597	0.1006	0.4925
chr21	48129895	4238052	0.0881	0.5644
chr22	51304566	2832841	0.0552	0.341
chrMT	16571	74302	4.4839	3.8864
chrX	155270560	10138214	0.0653	0.5007

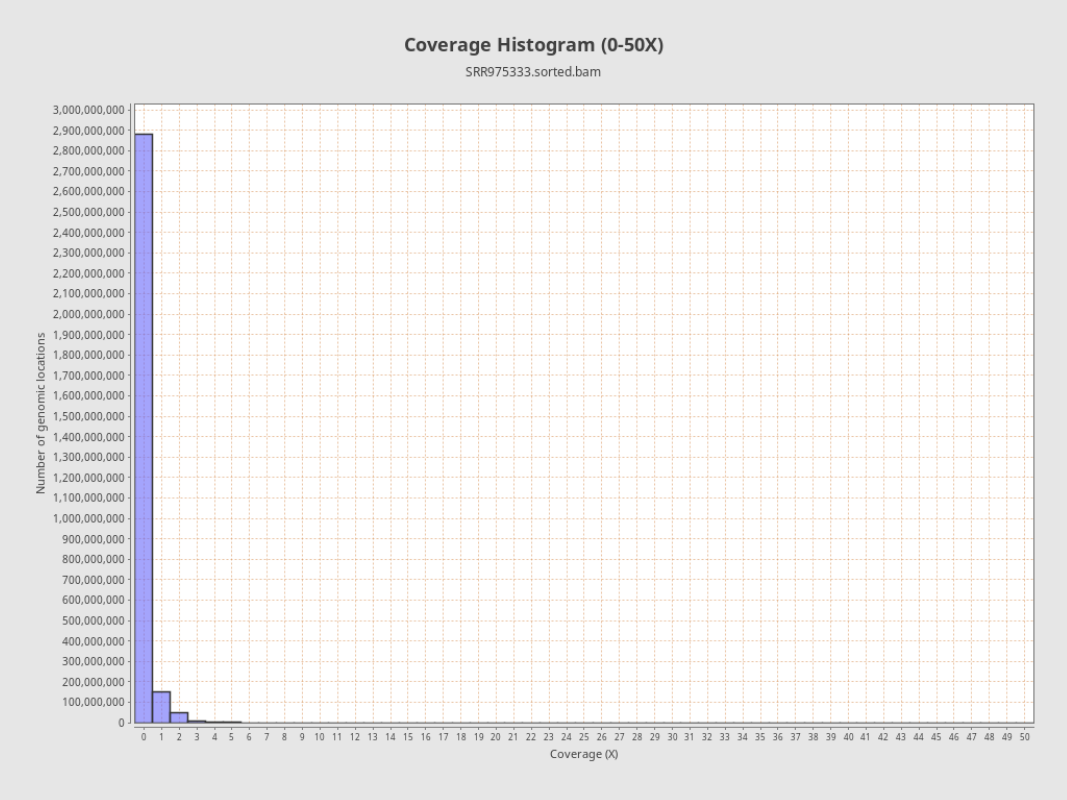
chrY	59373566	5220356	0.0879	2.2536

3. Results : Coverage across reference

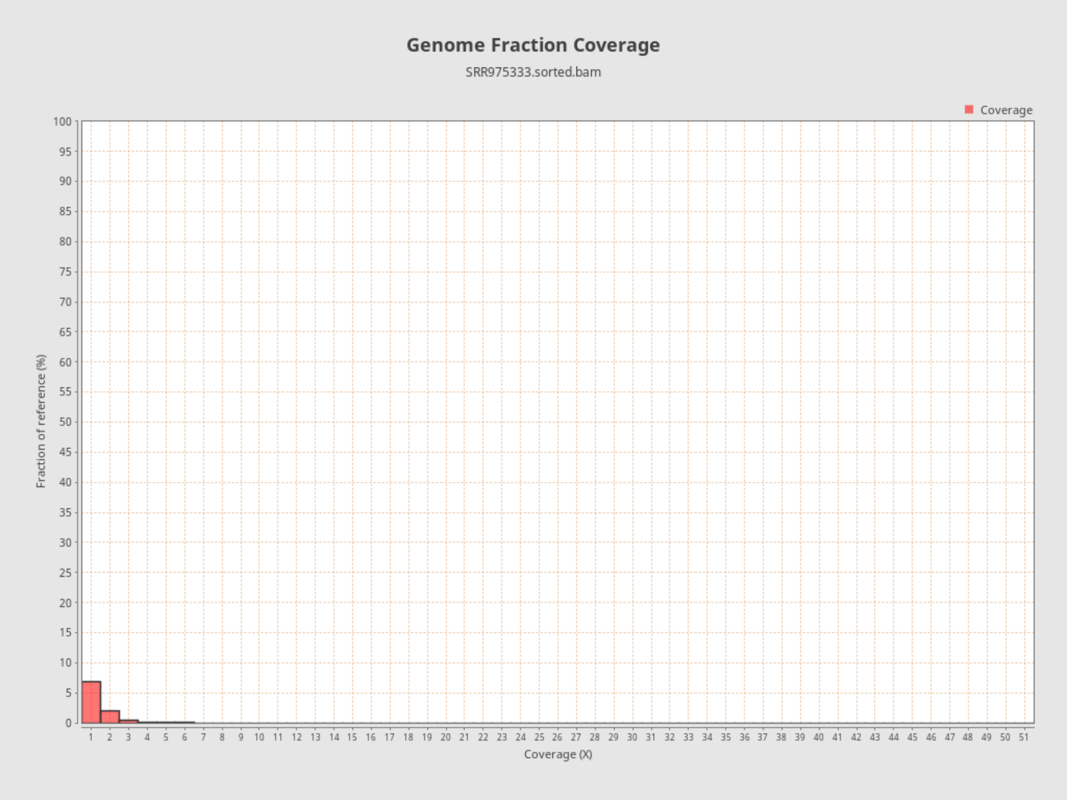
4. Results : Coverage Histogram



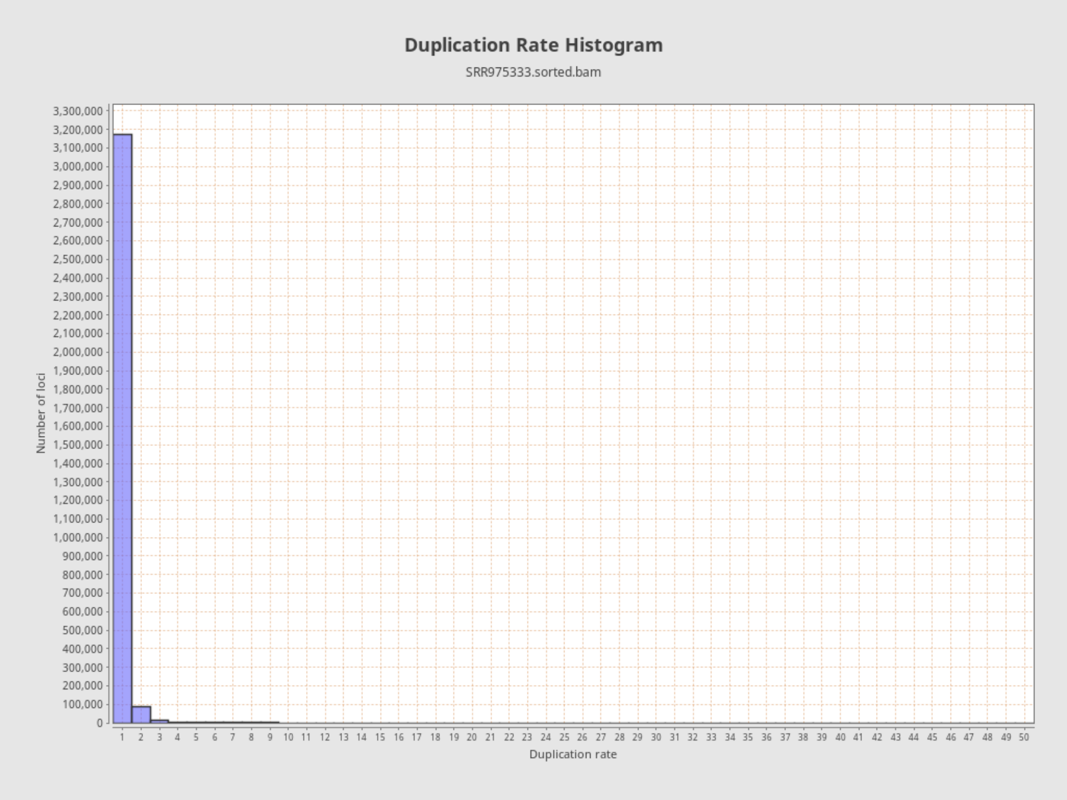
5. Results : Coverage Histogram (0-50X)



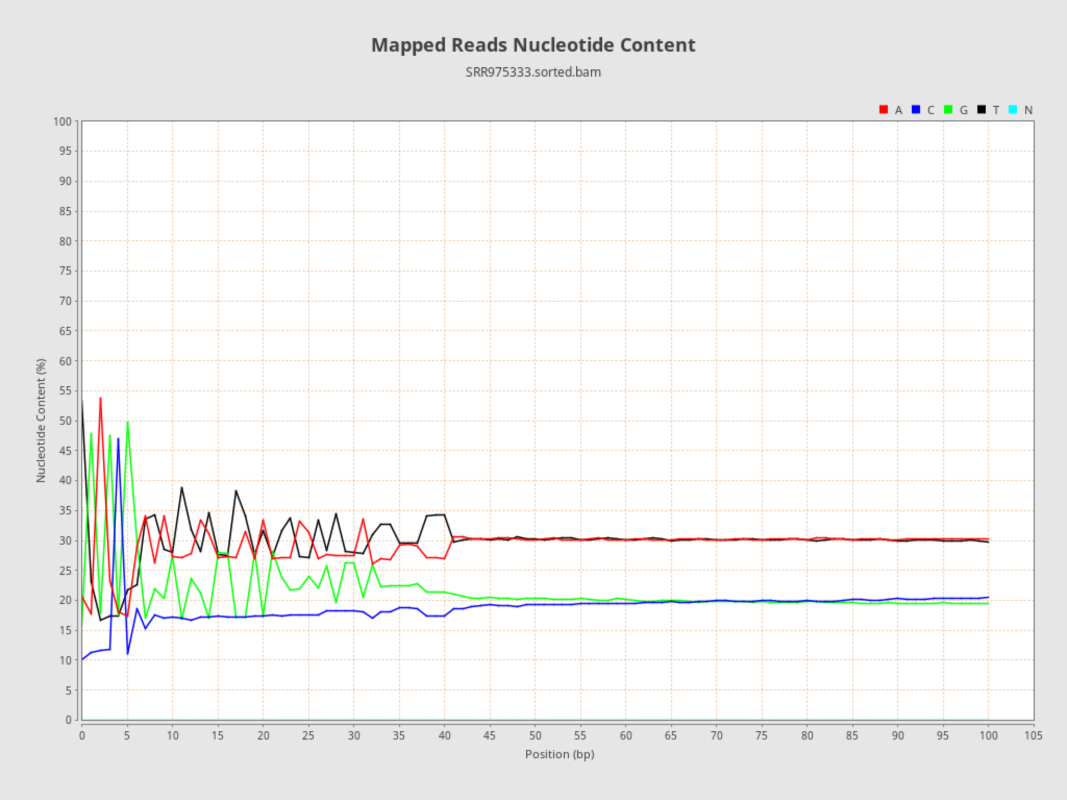
6. Results : Genome Fraction Coverage



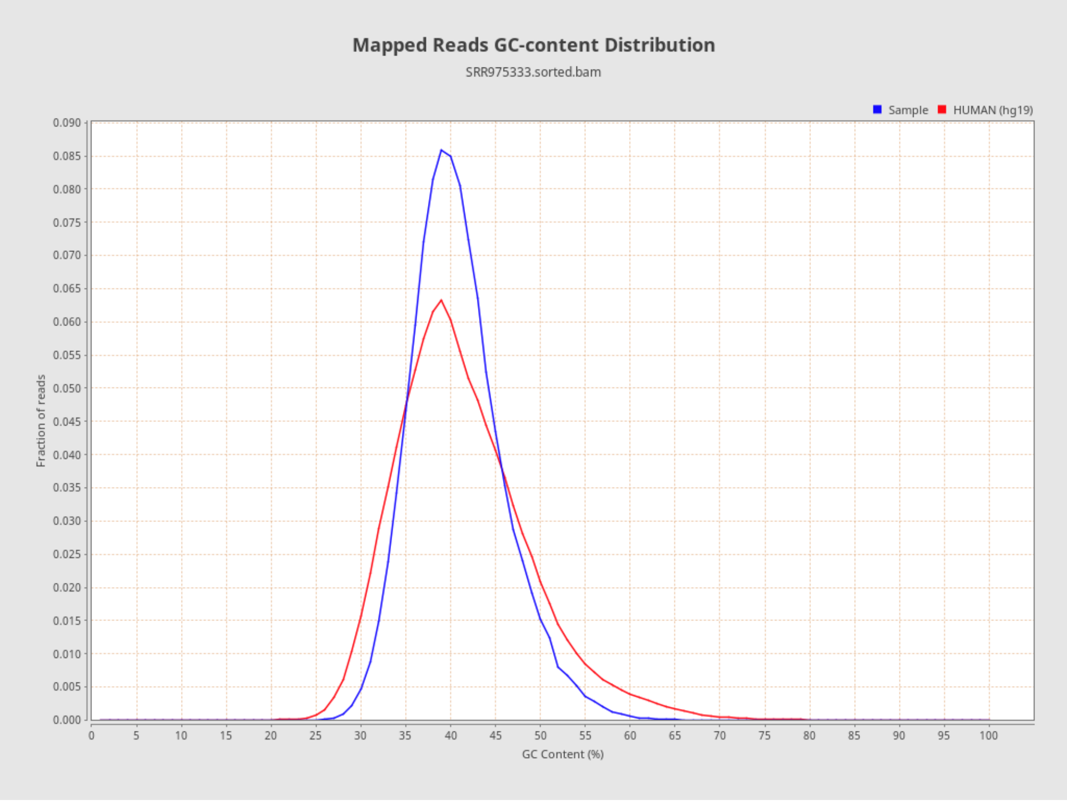
7. Results : Duplication Rate Histogram



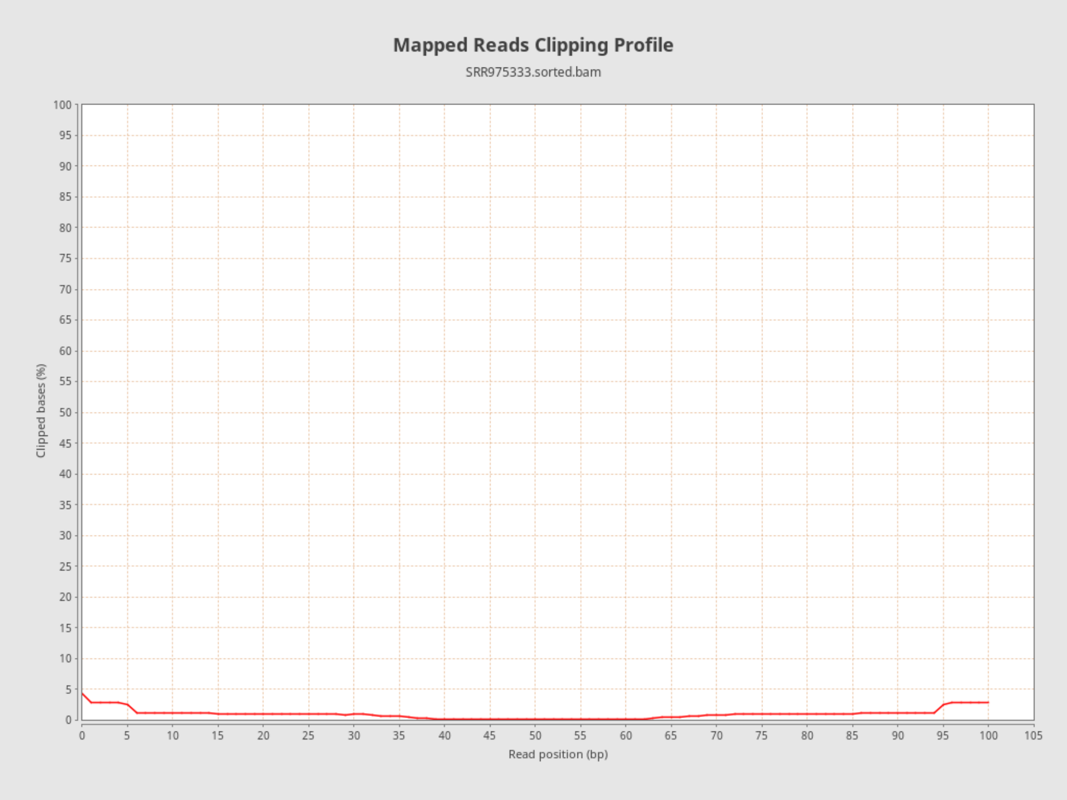
8. Results : Mapped Reads Nucleotide Content



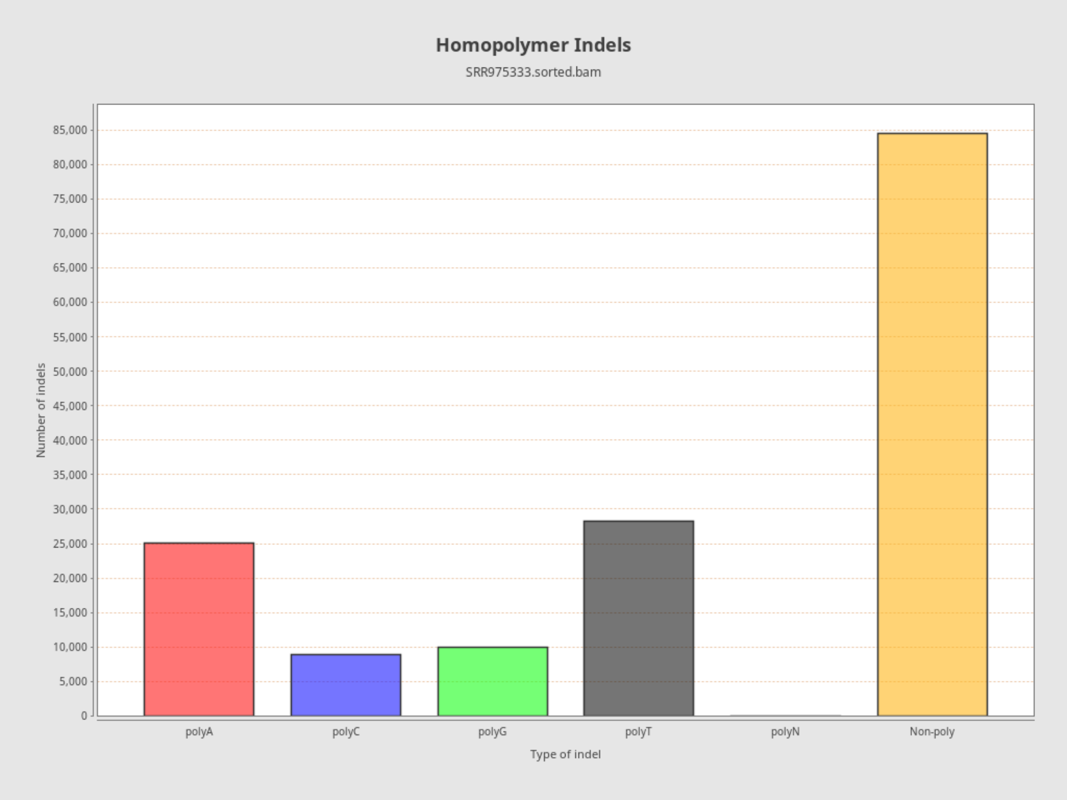
9. Results : Mapped Reads GC-content Distribution



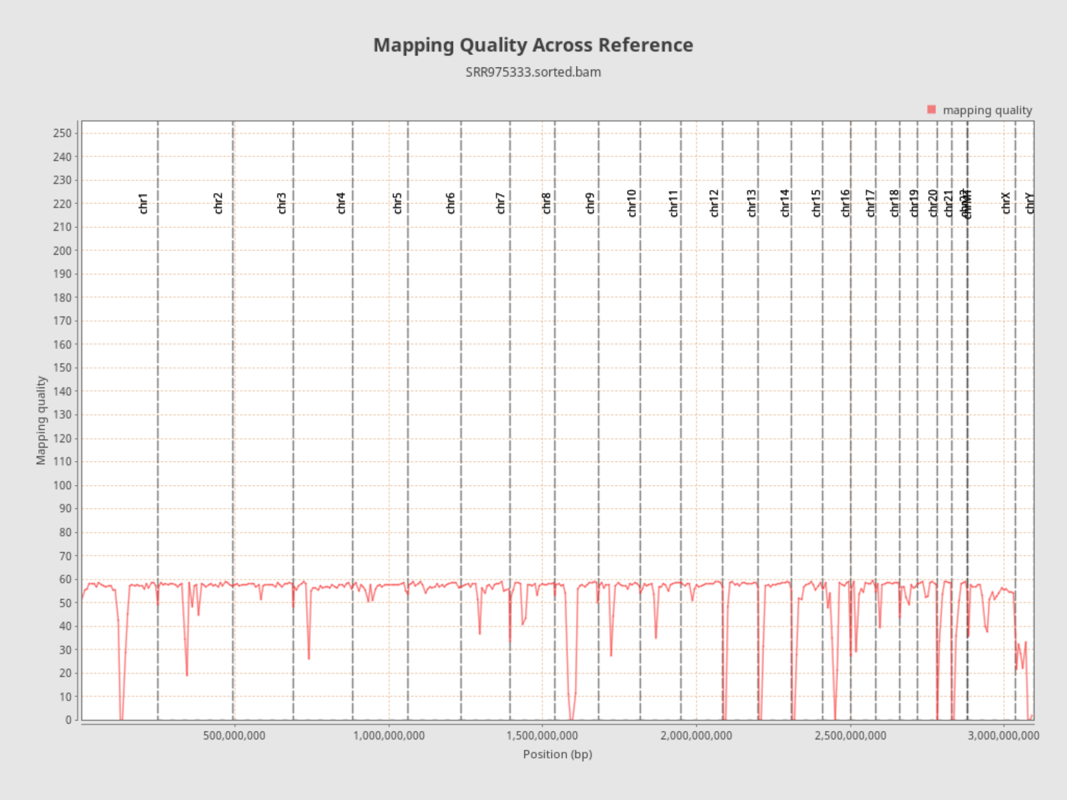
10. Results : Mapped Reads Clipping Profile



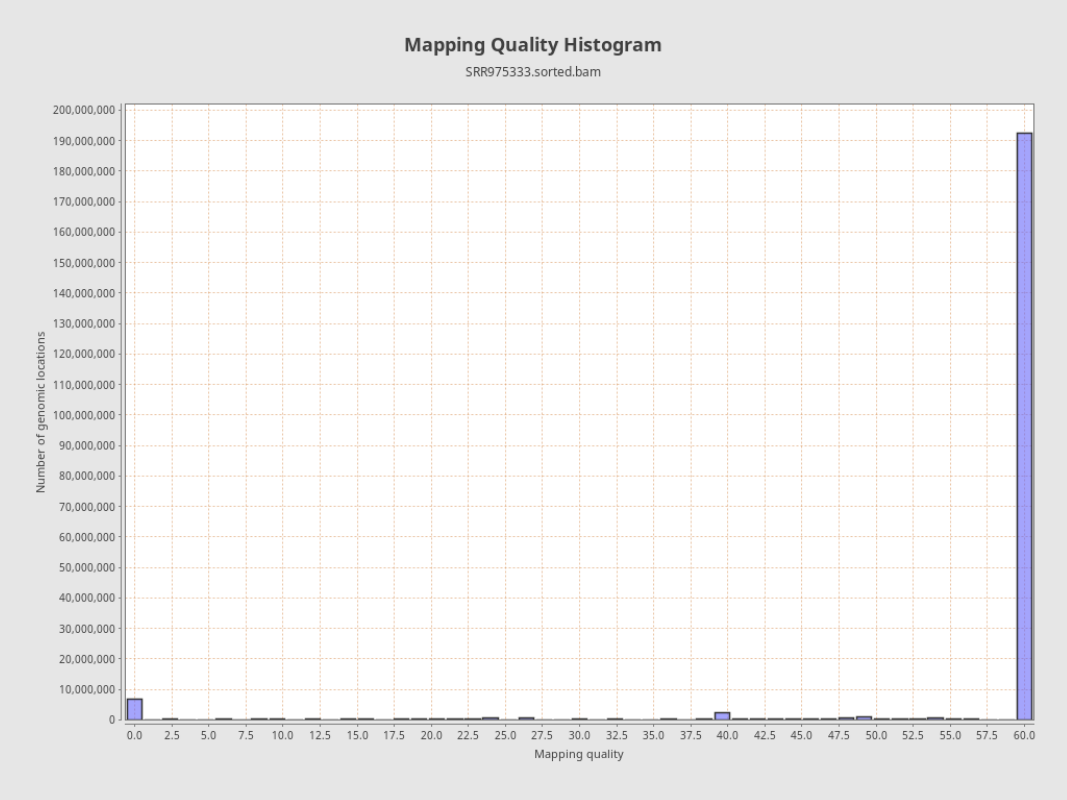
11. Results : Homopolymer Indels



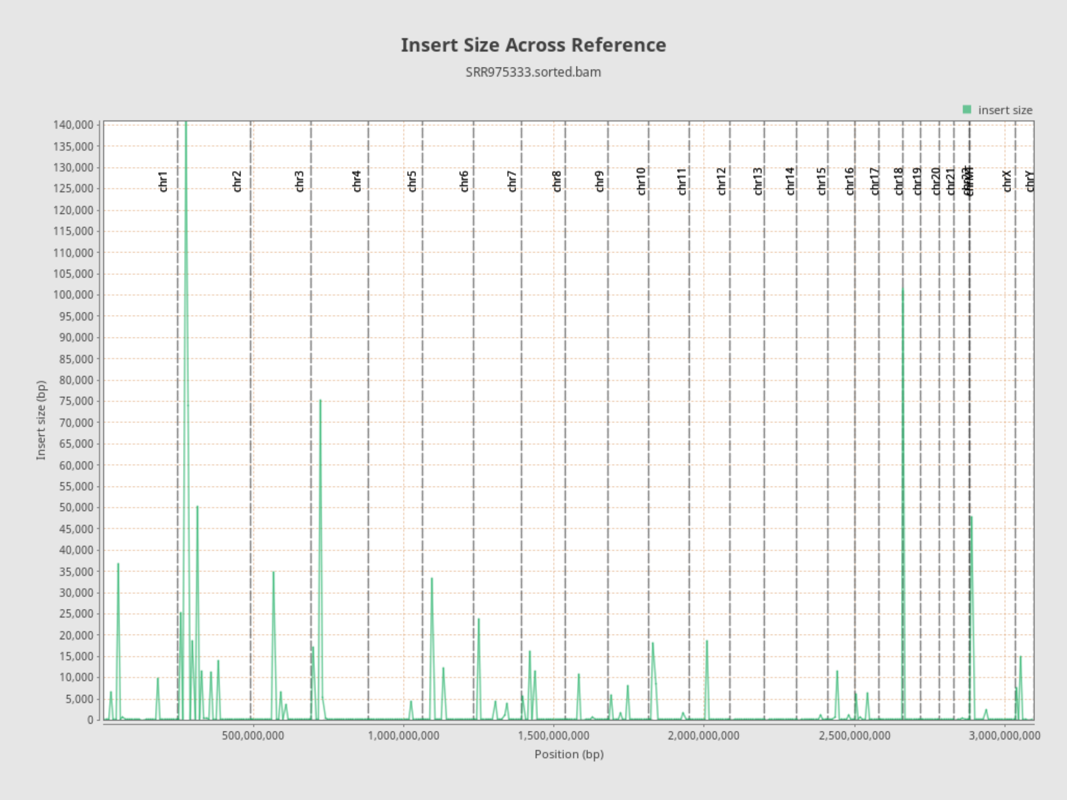
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram