Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 07:12:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975267.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_SRR975267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975267_1.fastq.gz SRR975267_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 07:12:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,895,866
Mapped reads	77,748,178 / 99.81%
Unmapped reads	147,688 / 0.19%
Mapped paired reads	77,748,178 / 99.81%
Mapped reads, first in pair	38,887,570 / 49.92%
Mapped reads, second in pair	38,860,608 / 49.89%
Mapped reads, both in pair	77,685,212 / 99.73%
Mapped reads, singletons	62,966 / 0.08%
Secondary alignments	0
Supplementary alignments	144,884 / 0.19%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	50,671,096 / 65.05%
Duplication rate	50.09%
Clipped reads	42,806,846 / 54.95%

2.2. ACGT Content

Number/percentage of A's	1,903,003,651 / 26.21%
Number/percentage of C's	1,668,986,702 / 22.99%
Number/percentage of T's	1,912,062,037 / 26.34%
Number/percentage of G's	1,775,011,652 / 24.45%
Number/percentage of N's	315,236 / 0%

GC Percentage	47.44%

2.3. Coverage

Mean	2.3458
Standard Deviation	32.1831

2.4. Mapping Quality

Mean Mapping Quality	56.31

2.5. Insert size

Mean	62,106.05
Standard Deviation	2,457,504.17
P25/Median/P75	151 / 187 / 235

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	45,156,391
Insertions	670,894
Mapped reads with at least one insertion	0.85%
Deletions	1,676,298
Mapped reads with at least one deletion	2.12%
Homopolymer indels	47.97%

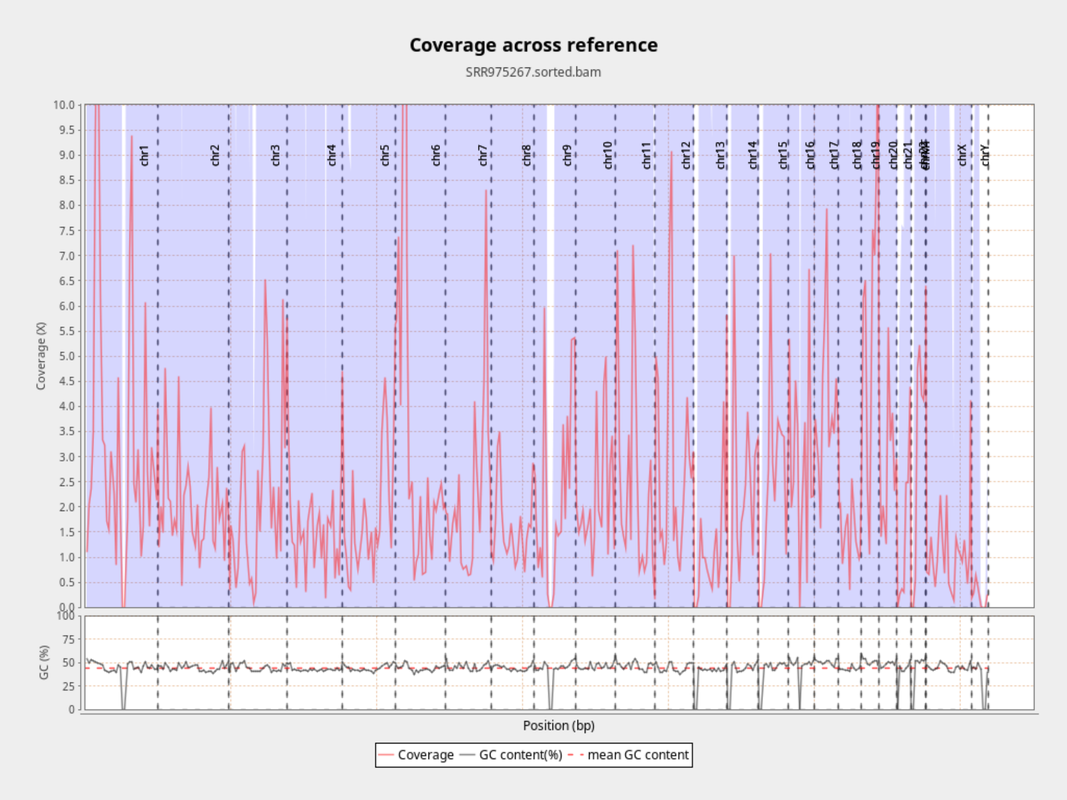
2.7. Chromosome stats

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

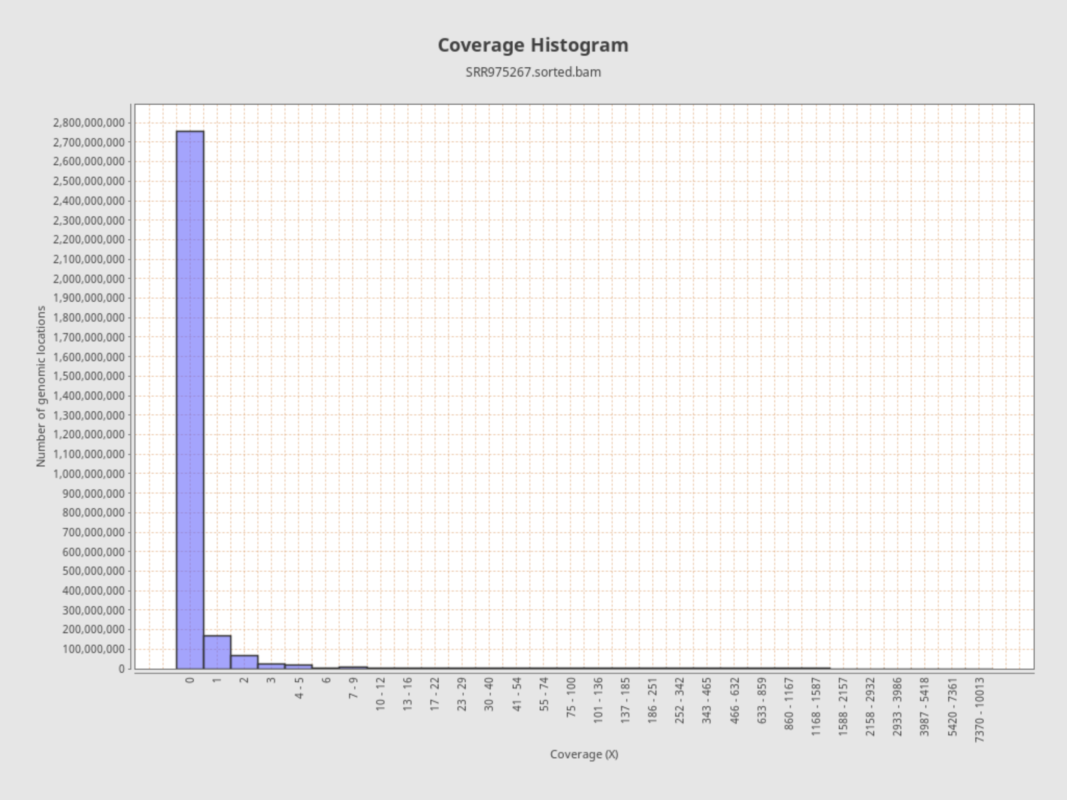
		bases	coverage	deviation
chr1	249250621	835373886	3.3515	40.2339
chr2	243199373	491213204	2.0198	26.8749
chr3	198022430	439159901	2.2177	31.308
chr4	191154276	285576520	1.494	22.8473
chr5	180915260	325982925	1.8019	27.1853
chr6	171115067	679951232	3.9736	53.8961
chr7	159138663	360190868	2.2634	32.4564
chr8	146364022	236155641	1.6135	23.9362
chr9	141213431	296912828	2.1026	29.4096
chr10	135534747	301944445	2.2278	29.3133
chr11	135006516	349250235	2.5869	31.4709
chr12	133851895	396185159	2.9599	34.8164
chr13	115169878	130368507	1.132	21.0871
chr14	107349540	232751483	2.1682	28.4969
chr15	102531392	258905670	2.5251	31.4571
chr16	90354753	257312658	2.8478	34.0955
chr17	81195210	334293798	4.1172	42.1211
chr18	78077248	116535827	1.4926	24.5716
chr19	59128983	346317754	5.857	50.4164
chr20	63025520	188015541	2.9832	37.2782
chr21	48129895	67329698	1.3989	22.7357
chr22	51304566	156330007	3.0471	35.2997
chrMT	16571	106003	6.3969	15.5373
chrX	155270560	162242143	1.0449	17.4338

chrY	59373566	13359731	0.225	7.8246

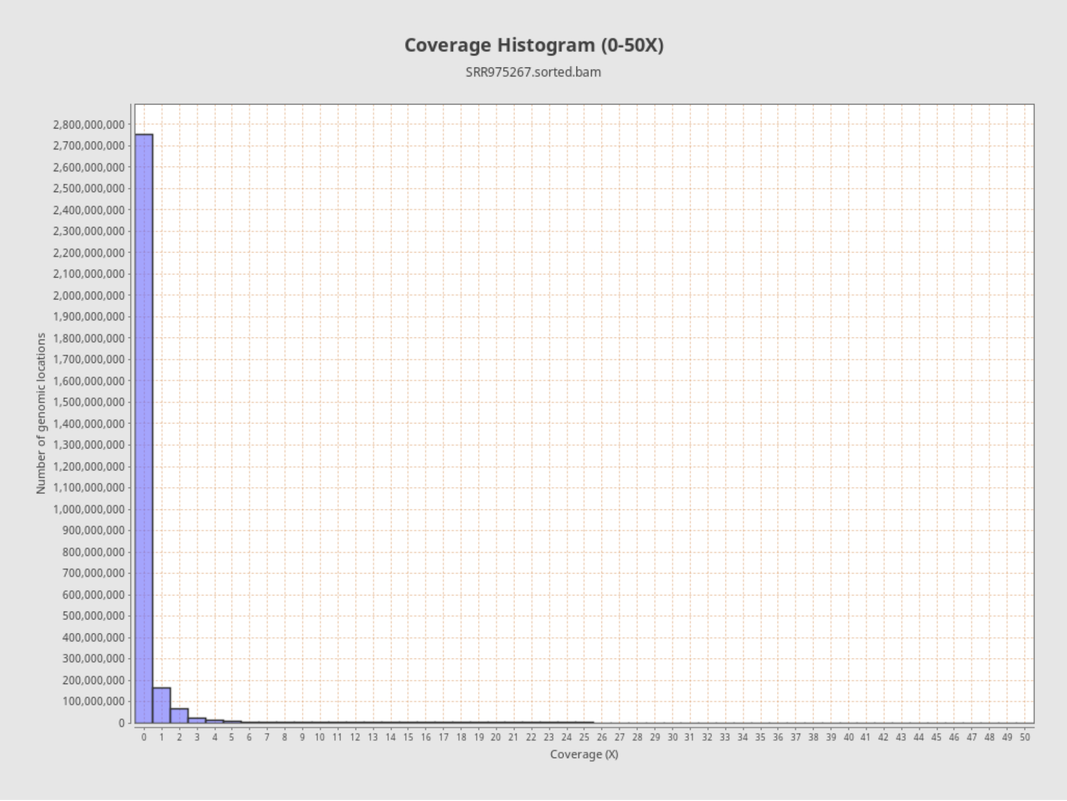
3. Results : Coverage across reference



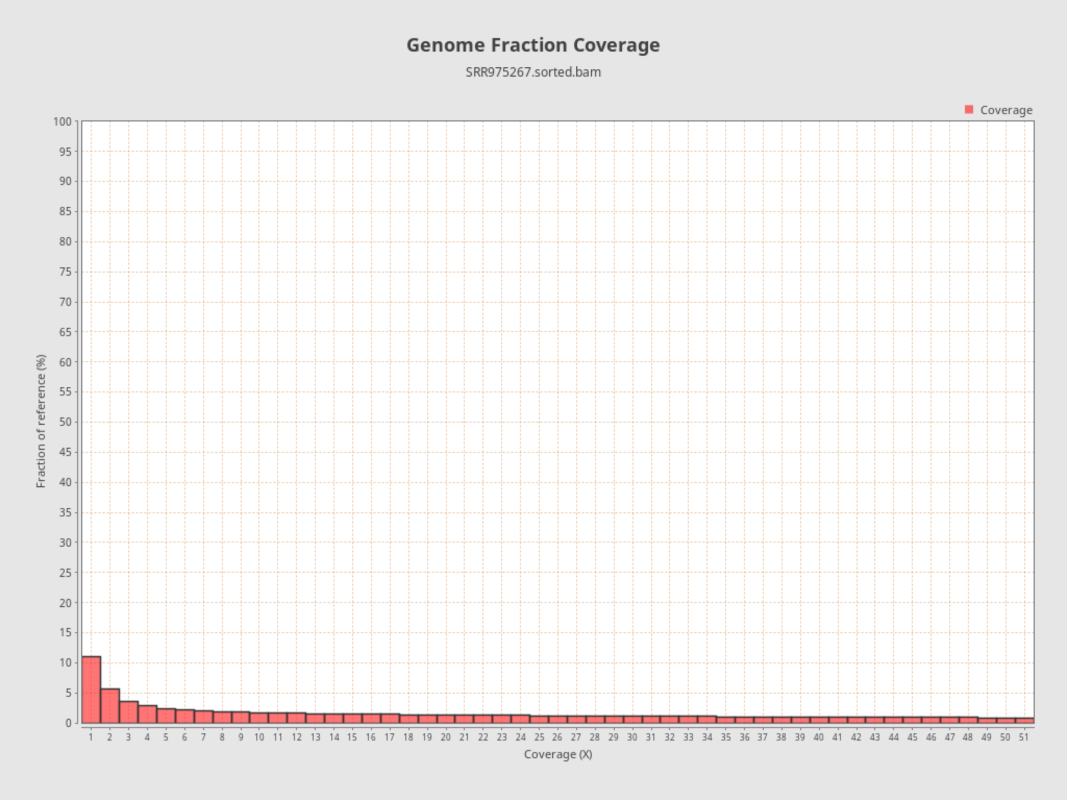
4. Results : Coverage Histogram



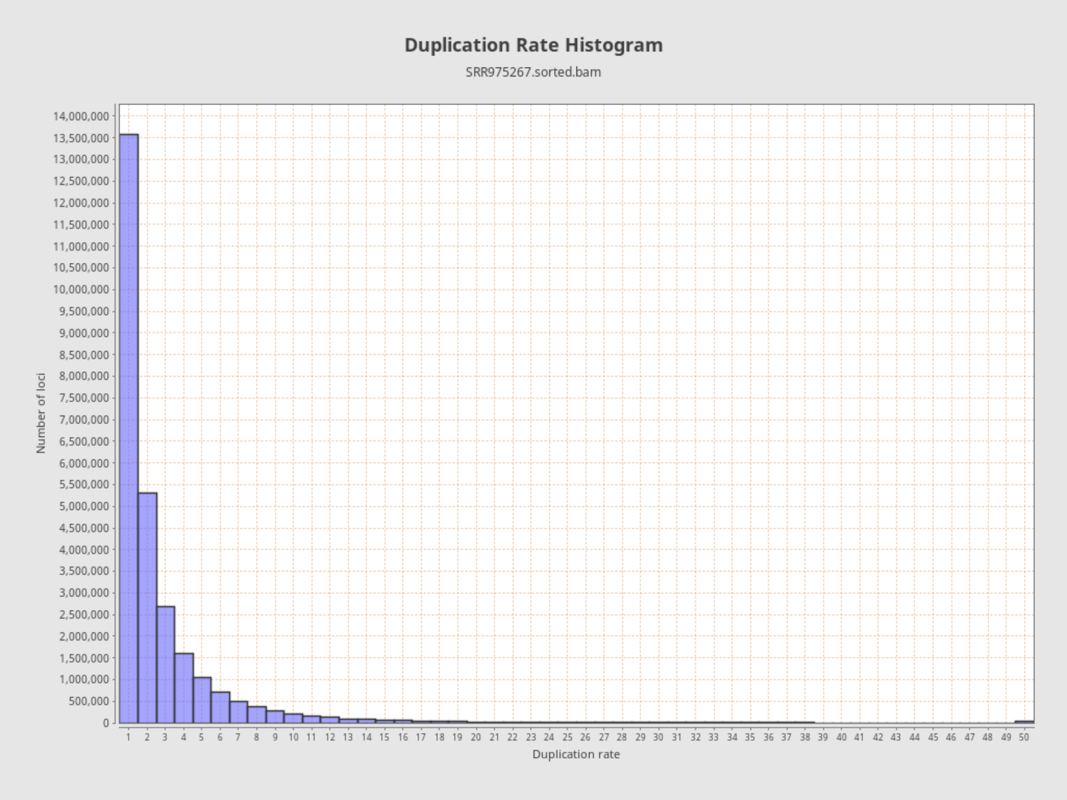
5. Results : Coverage Histogram (0-50X)



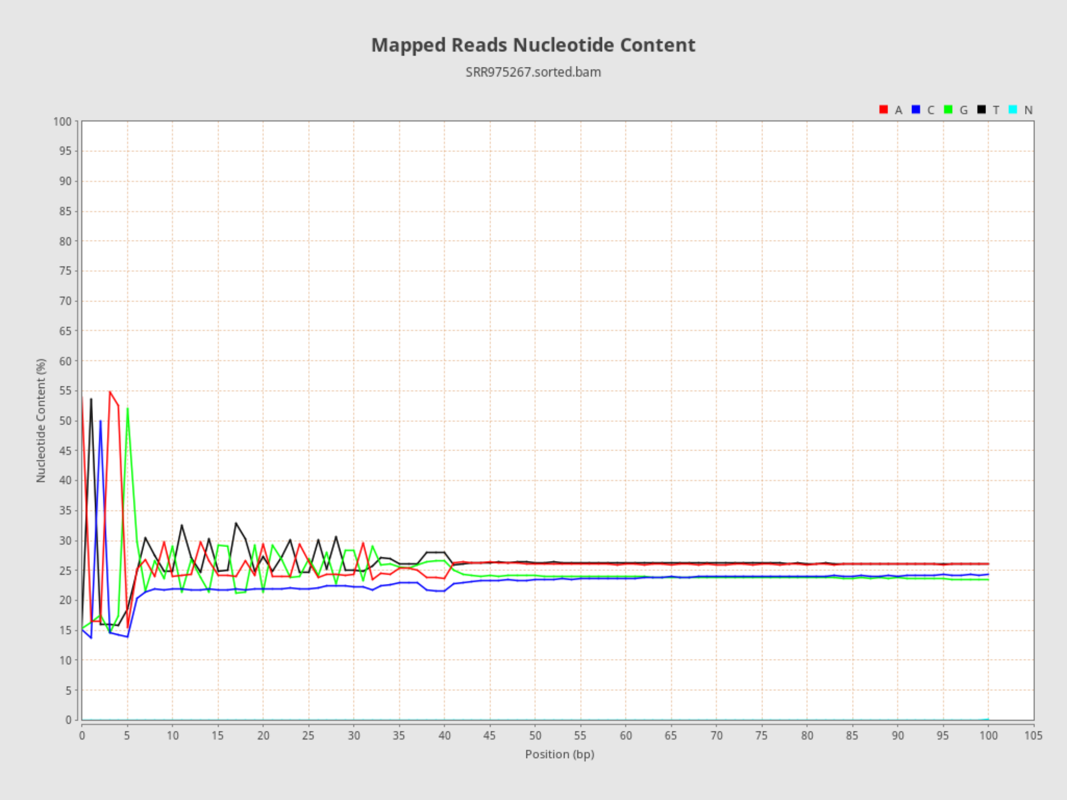
6. Results : Genome Fraction Coverage



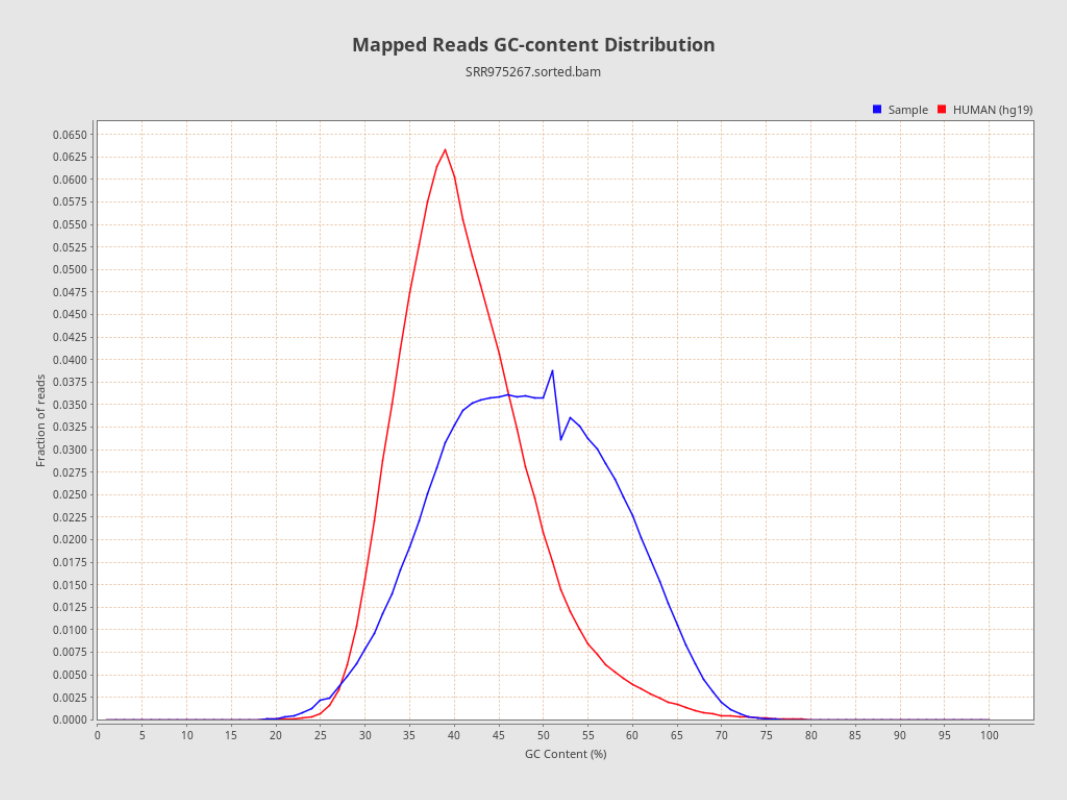
7. Results : Duplication Rate Histogram



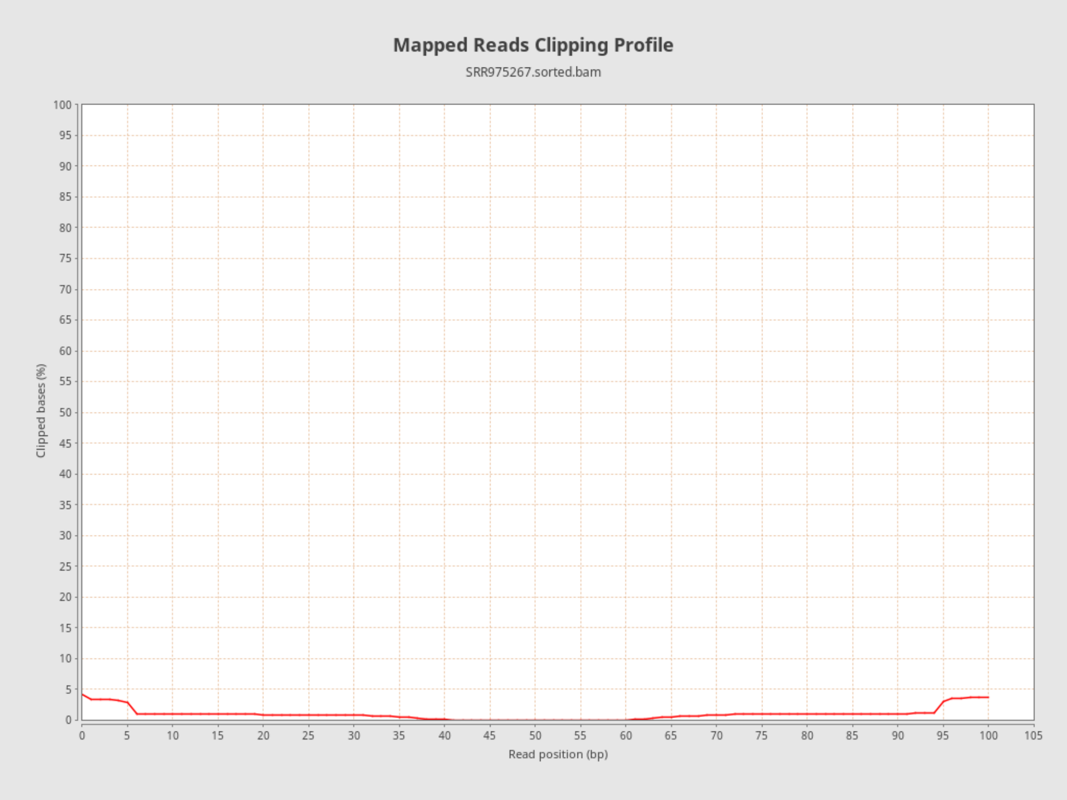
8. Results : Mapped Reads Nucleotide Content



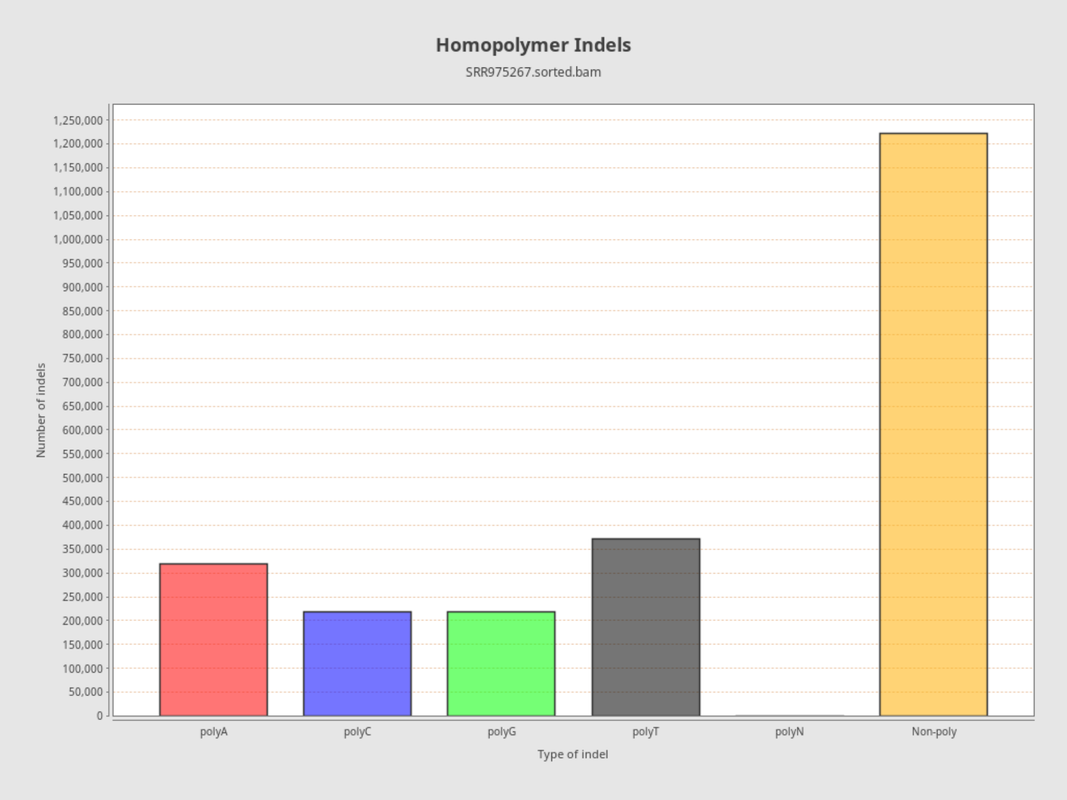
9. Results : Mapped Reads GC-content Distribution



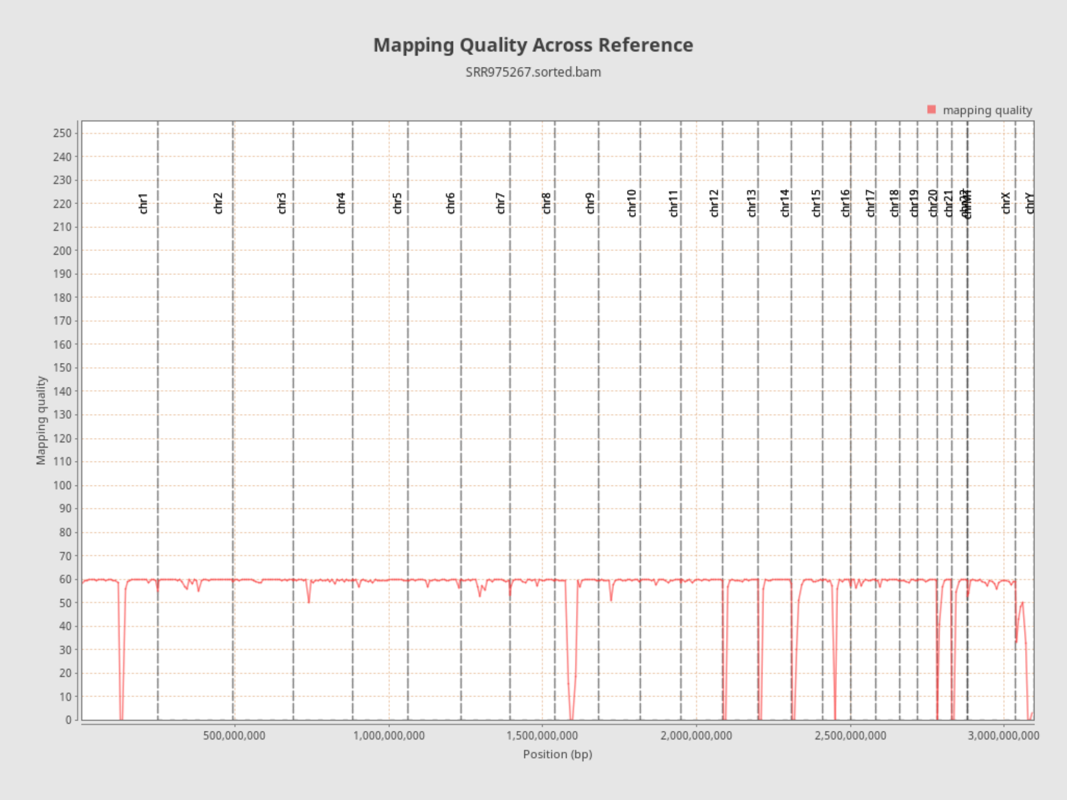
10. Results : Mapped Reads Clipping Profile



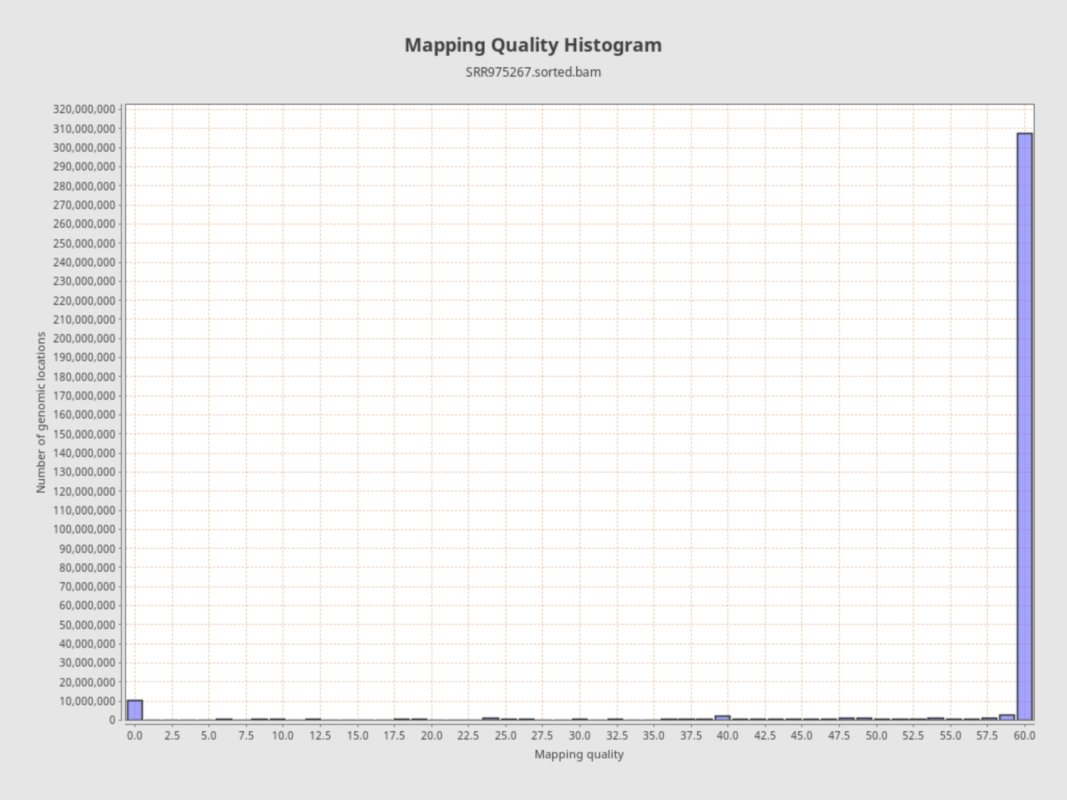
11. Results : Homopolymer Indels



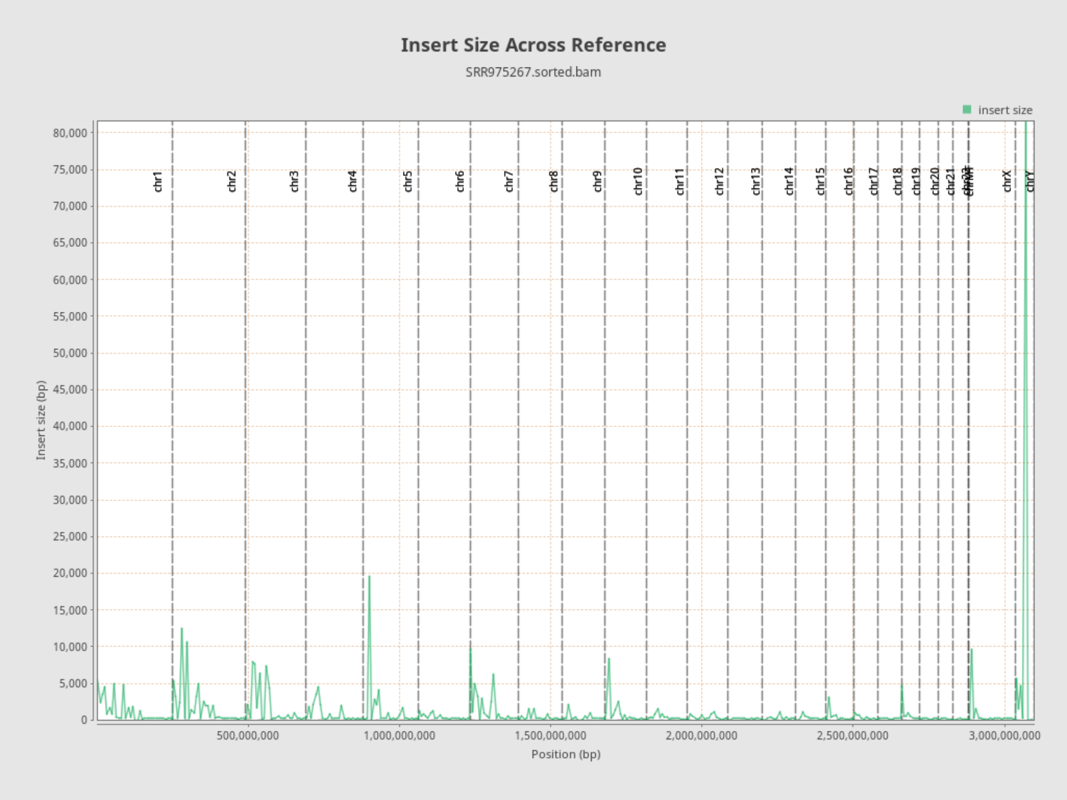
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram