Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/26 11:47:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976567.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_SRR2976567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976567_1.fastq.gz SRR2976567_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 26 11:47:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,505,194,148
Mapped reads	1,482,610,631 / 98.5%
Unmapped reads	22,583,517 / 1.5%
Mapped paired reads	1,482,610,631 / 98.5%
Mapped reads, first in pair	744,298,048 / 49.45%
Mapped reads, second in pair	738,312,583 / 49.05%
Mapped reads, both in pair	1,468,159,300 / 97.54%
Mapped reads, singletons	14,451,331 / 0.96%
Secondary alignments	0
Supplementary alignments	1,783,297 / 0.12%
Read min/max/mean length	20 / 101 / 97.3
Duplicated reads (estimated)	444,621,459 / 29.54%
Duplication rate	26.98%
Clipped reads	45,294,454 / 3.01%

2.2. ACGT Content

Number/percentage of A's	43,159,319,215 / 29.94%
Number/percentage of C's	28,810,377,350 / 19.98%
Number/percentage of T's	43,440,547,671 / 30.13%
Number/percentage of G's	28,693,310,463 / 19.9%
Number/percentage of N's	57,583,690 / 0.04%

GC Percentage	39.89%

2.3. Coverage

Mean	46.58
Standard Deviation	496.1623

2.4. Mapping Quality

Mean Mapping Quality	53.86

2.5. Insert size

Mean	17,169.98
Standard Deviation	1,222,503.66
P25/Median/P75	161 / 215 / 290

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	764,978,368
Insertions	12,380,530
Mapped reads with at least one insertion	0.81%
Deletions	14,703,293
Mapped reads with at least one deletion	0.96%
Homopolymer indels	41.13%

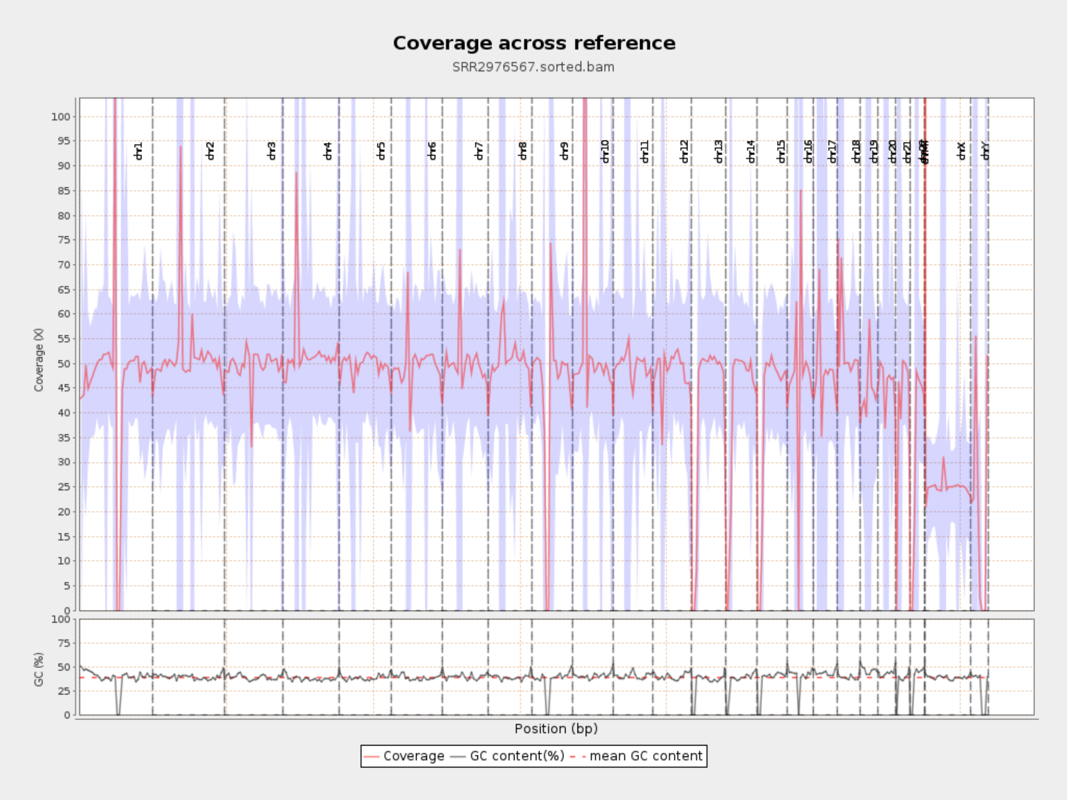
2.7. Chromosome stats

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

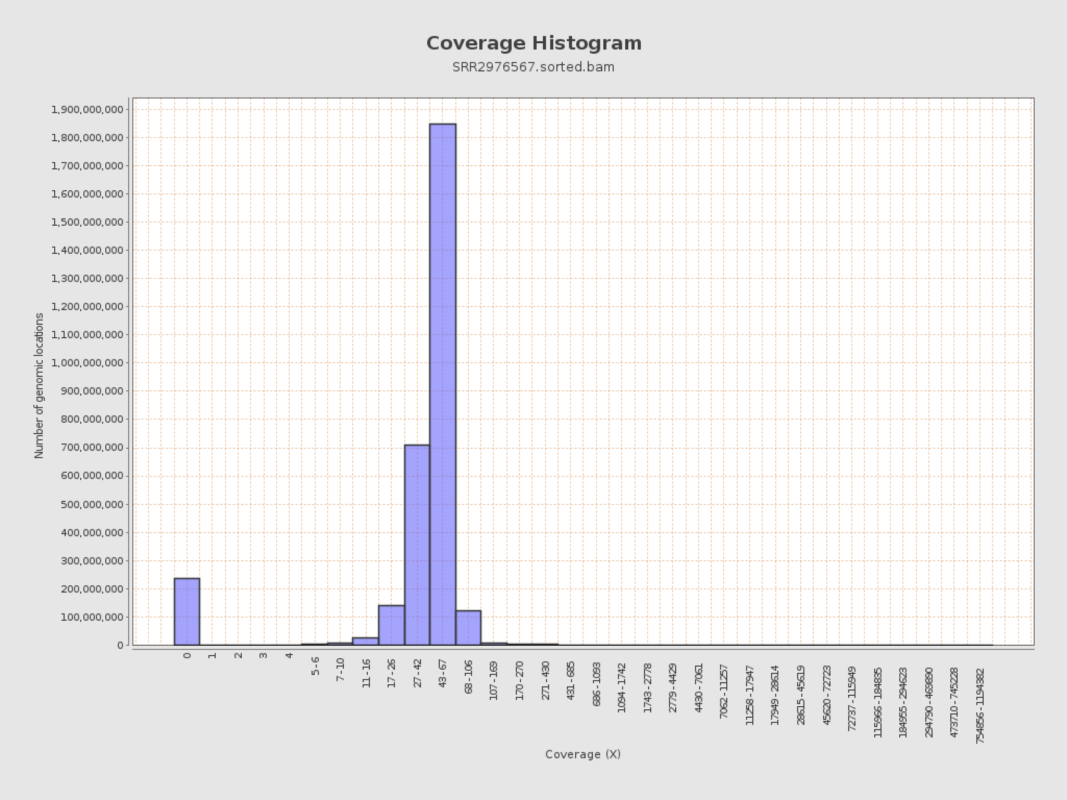
		bases	coverage	deviation
chr1	249250621	11882470442	47.6728	1,226.7824
chr2	243199373	12561003908	51.649	299.5728
chr3	198022430	9805763819	49.5185	44.2022
chr4	191154276	9996032535	52.293	321.7452
chr5	180915260	8973127136	49.5985	43.146
chr6	171115067	8550276096	49.968	205.8654
chr7	159138663	7977295055	50.128	490.2562
chr8	146364022	7456184765	50.9427	578.8279
chr9	141213431	6222794011	44.0666	590.8613
chr10	135534747	7463893127	55.07	876.4037
chr11	135006516	6671862058	49.4188	295.3799
chr12	133851895	6485070877	48.4496	33.0102
chr13	115169878	4801989808	41.6948	24.592
chr14	107349540	4383974740	40.8383	44.8181
chr15	102531392	4044586708	39.4473	24.318
chr16	90354753	4291882283	47.5003	307.9399
chr17	81195210	3869468859	47.6564	302.9968
chr18	78077248	4124331401	52.8237	701.6222
chr19	59128983	2632349312	44.5188	510.4789
chr20	63025520	2902441606	46.0518	72.5601
chr21	48129895	2023178977	42.0358	138.3341
chr22	51304566	1629175084	31.755	123.29
chrMT	16571	234482679	14,150.1828	1,909.944
chrX	155270560	3884760282	25.0193	117.9819

chrY	59373566	1329117986	22.3857	339.2274

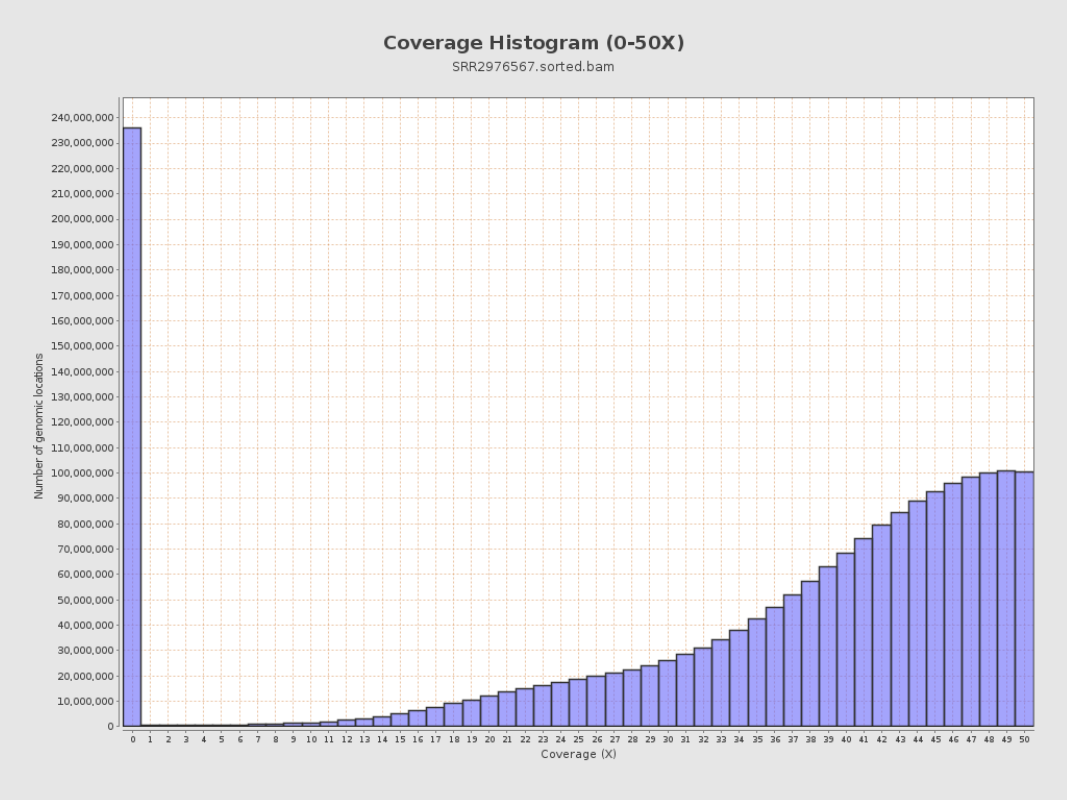
3. Results : Coverage across reference



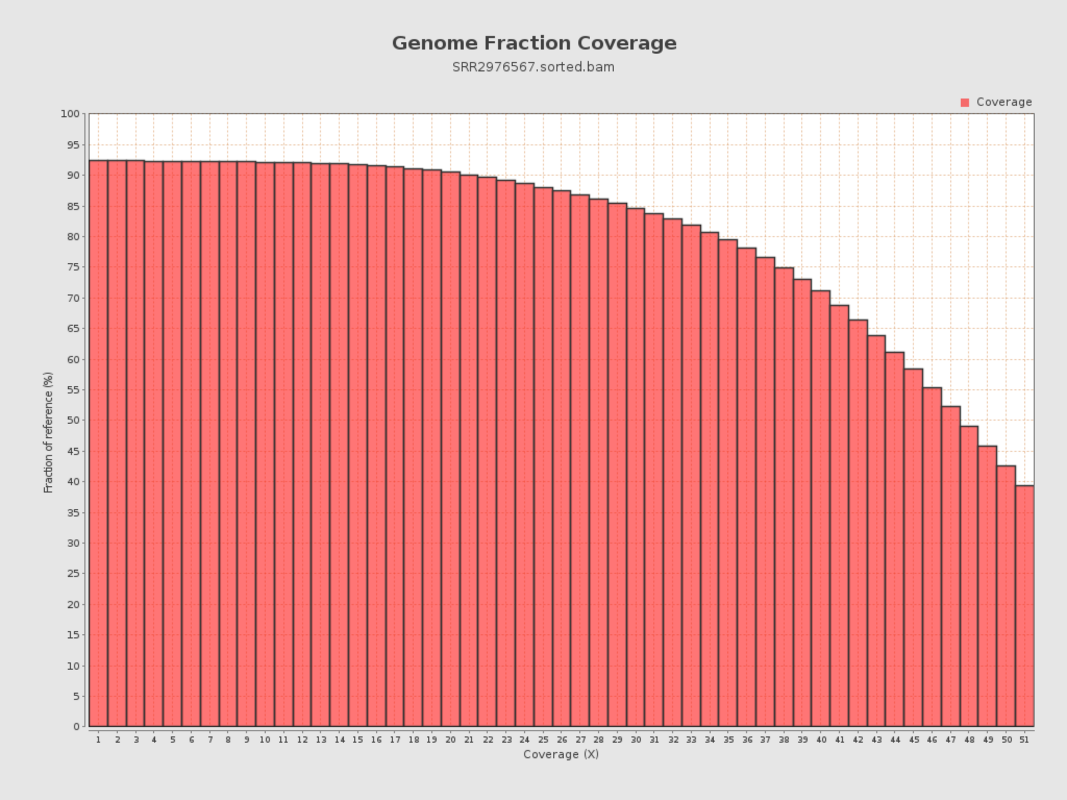
4. Results : Coverage Histogram



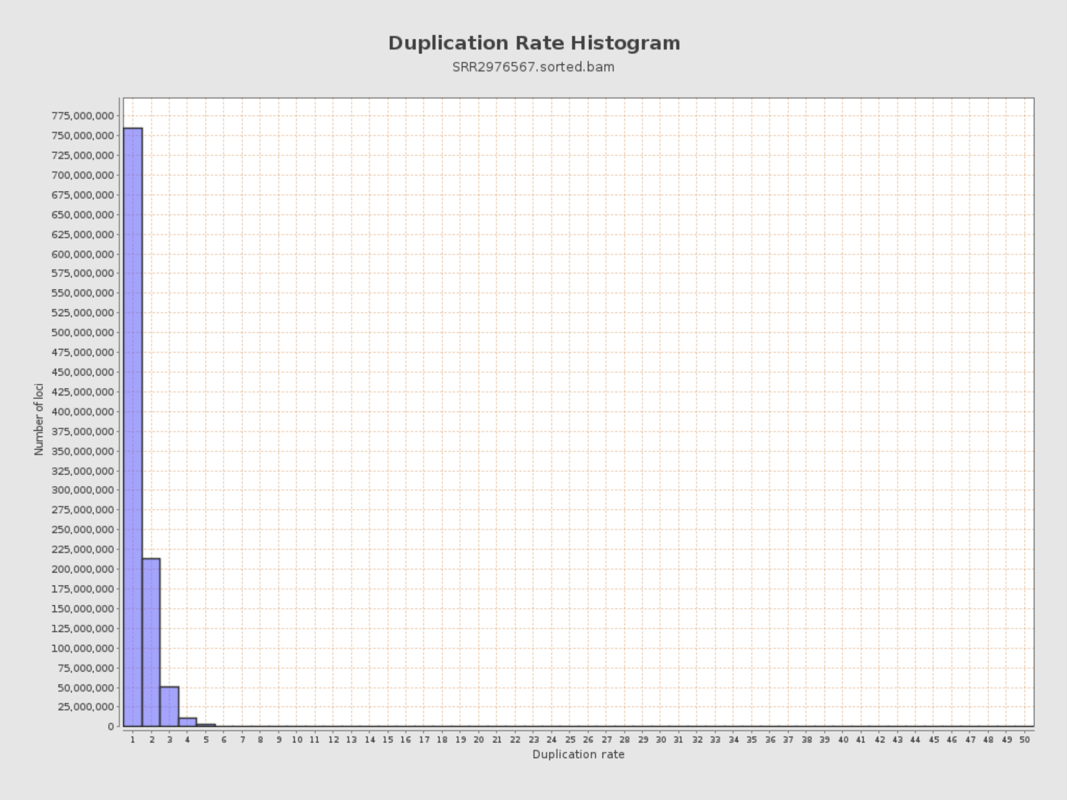
5. Results : Coverage Histogram (0-50X)



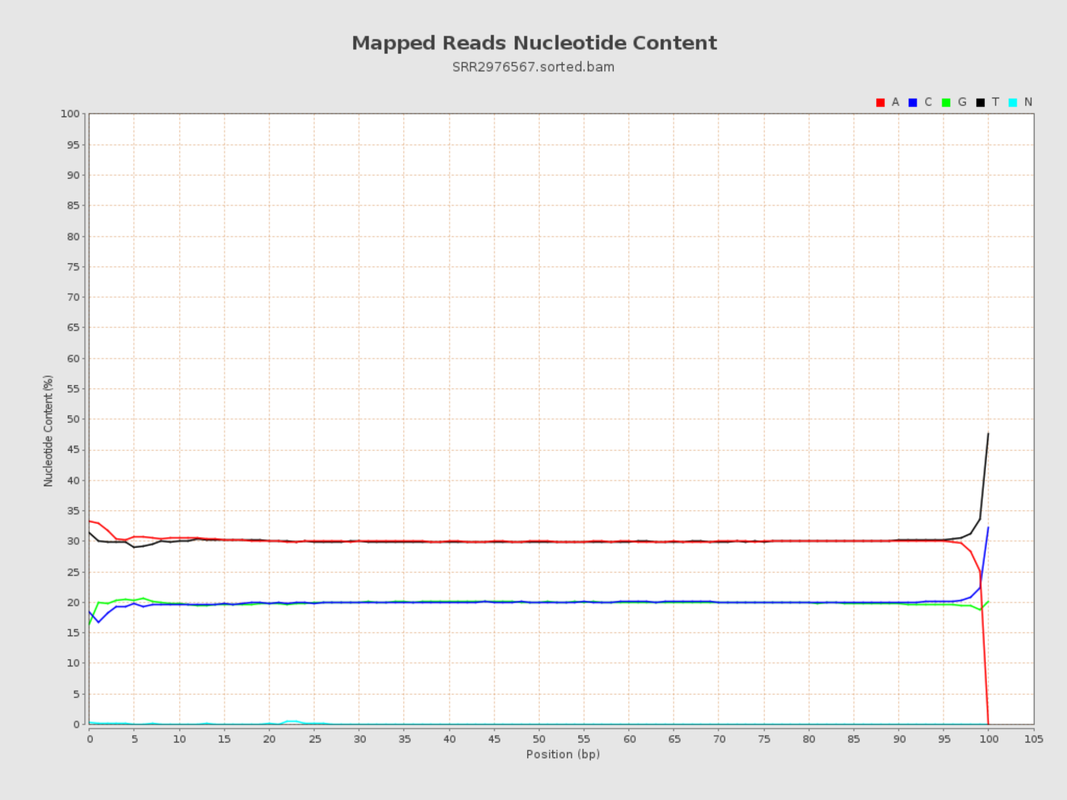
6. Results : Genome Fraction Coverage



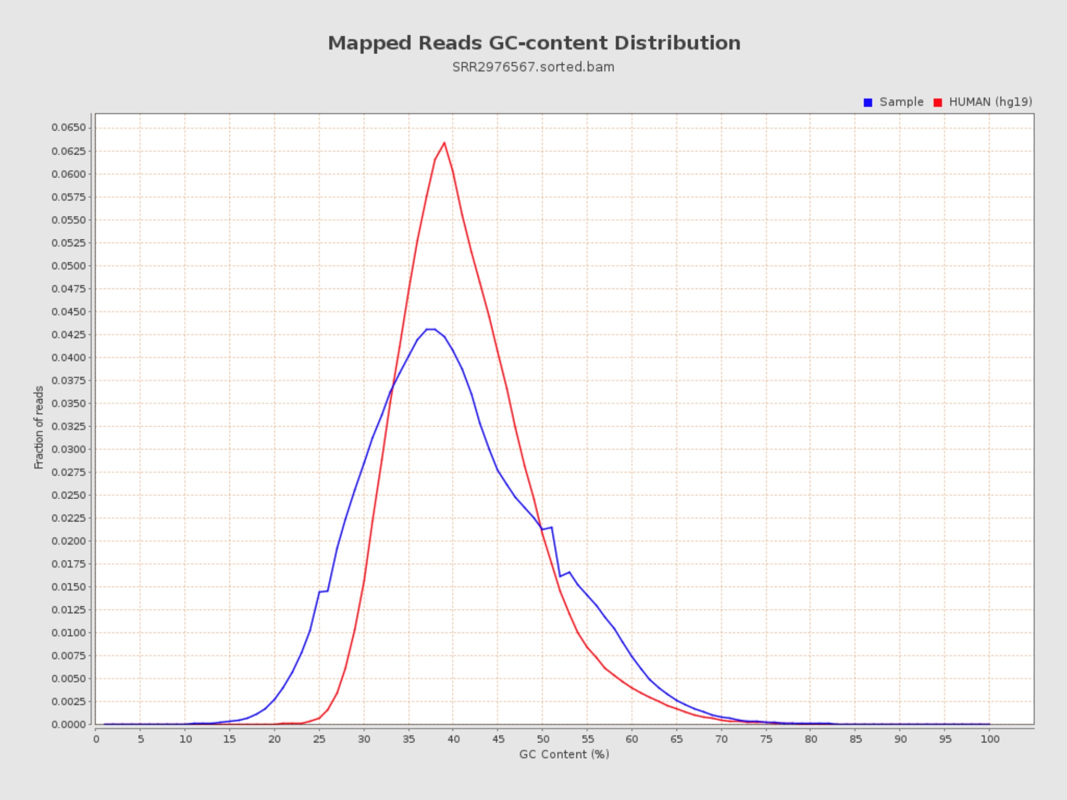
7. Results : Duplication Rate Histogram



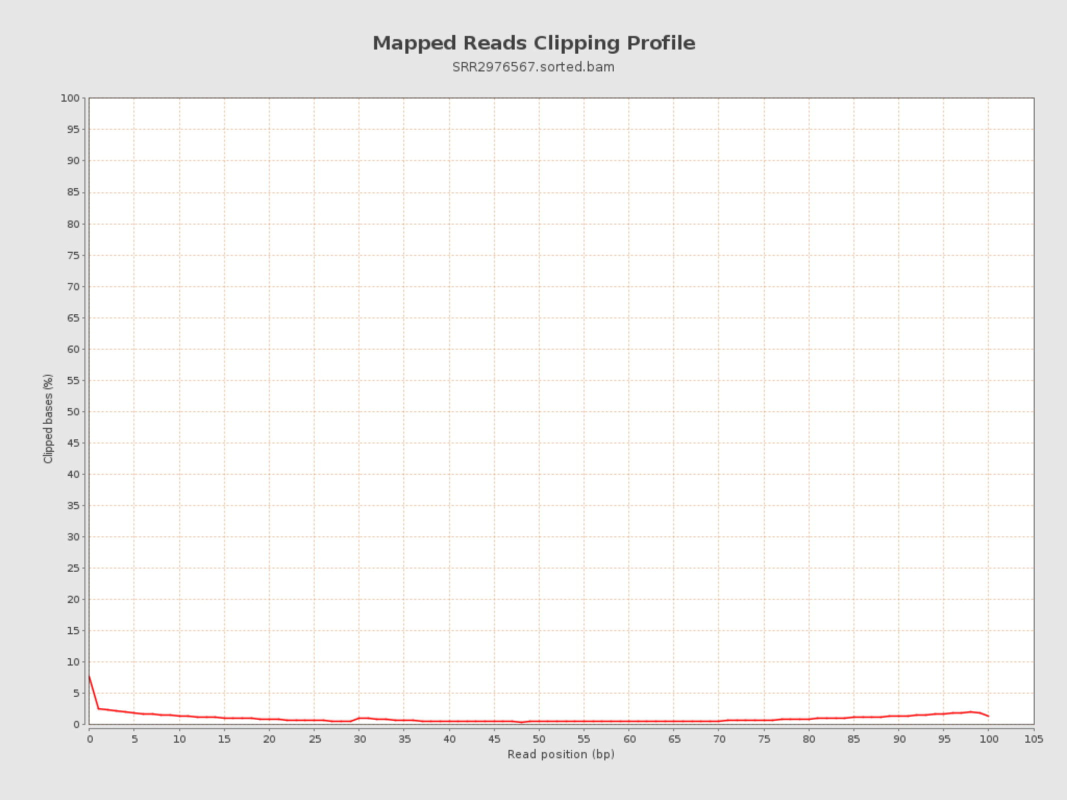
8. Results : Mapped Reads Nucleotide Content



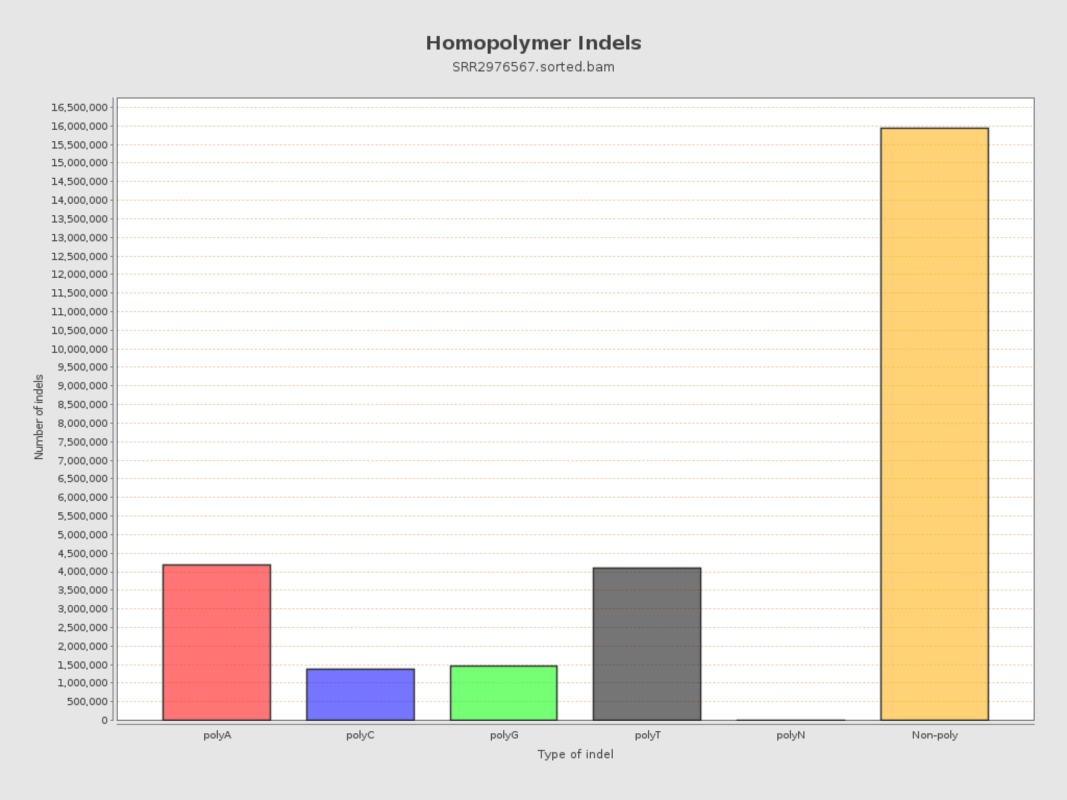
9. Results : Mapped Reads GC-content Distribution



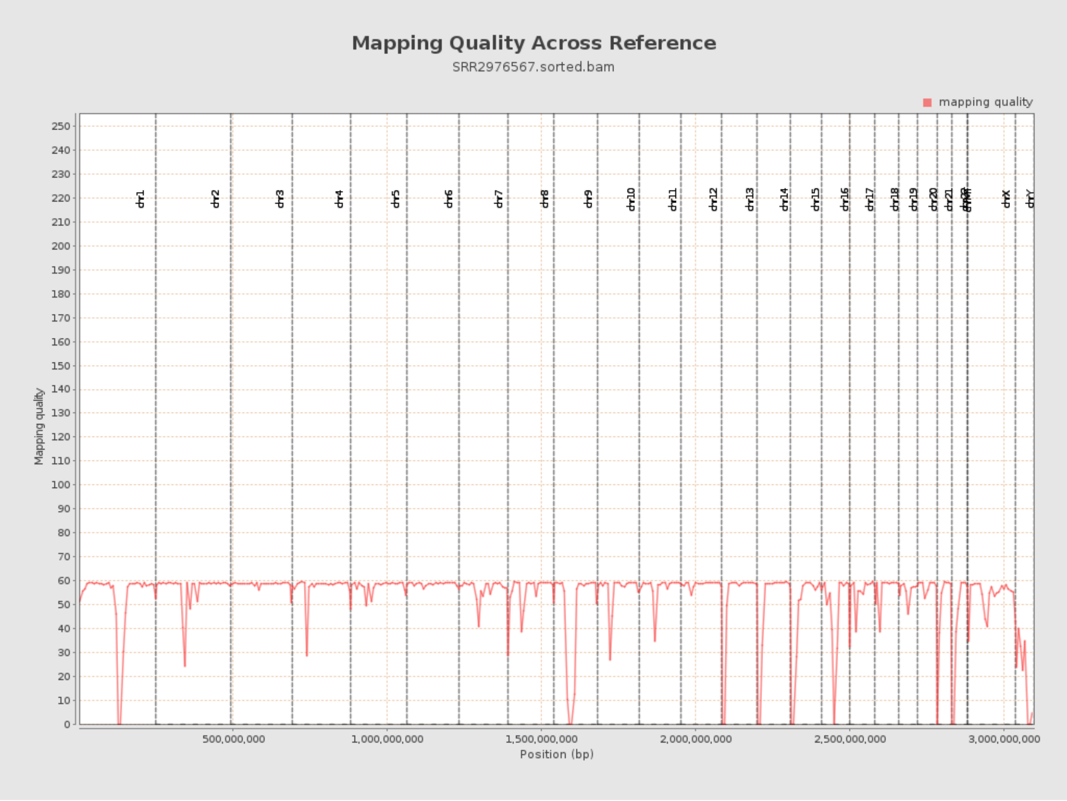
10. Results : Mapped Reads Clipping Profile



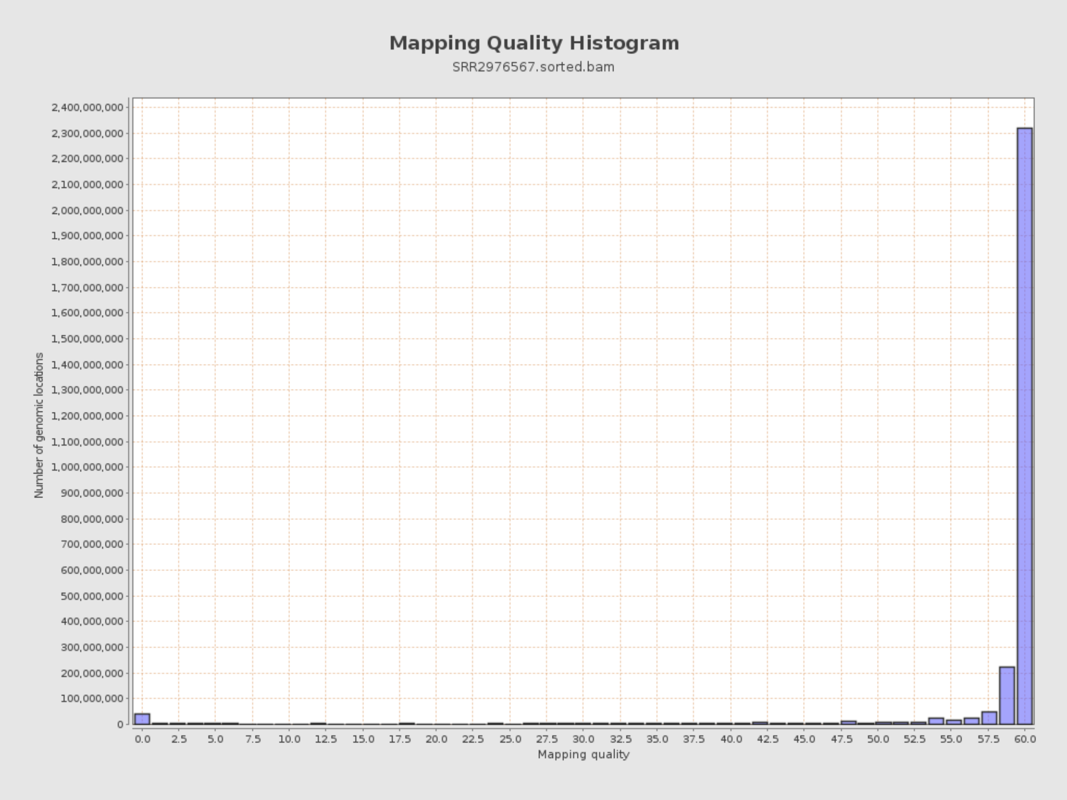
11. Results : Homopolymer Indels



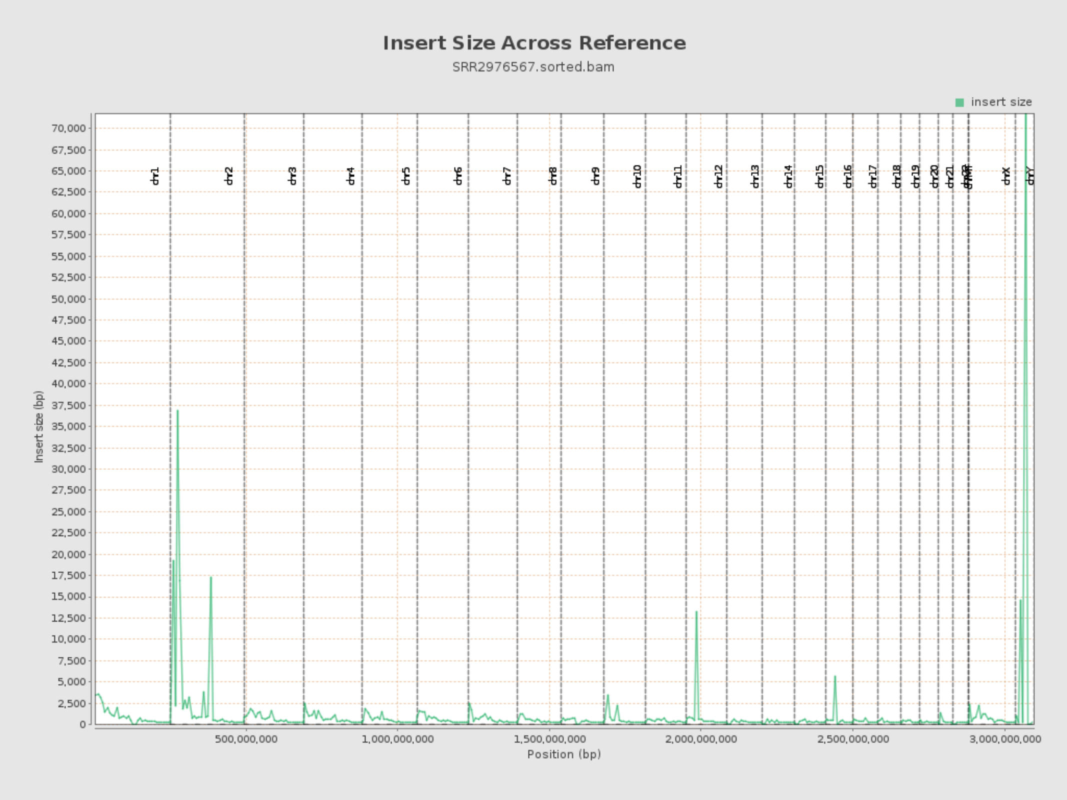
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram