Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/29 07:59:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976571.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_SRR2976571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976571_1.fastq.gz SRR2976571_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 29 07:59:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,400,564,016
Mapped reads	1,379,368,729 / 98.49%
Unmapped reads	21,195,287 / 1.51%
Mapped paired reads	1,379,368,729 / 98.49%
Mapped reads, first in pair	694,985,772 / 49.62%
Mapped reads, second in pair	684,382,957 / 48.86%
Mapped reads, both in pair	1,362,152,434 / 97.26%
Mapped reads, singletons	17,216,295 / 1.23%
Secondary alignments	0
Supplementary alignments	10,645,454 / 0.76%
Read min/max/mean length	20 / 100 / 96.1
Duplicated reads (estimated)	491,321,098 / 35.08%
Duplication rate	32.92%
Clipped reads	101,575,520 / 7.25%

2.2. ACGT Content

Number/percentage of A's	39,626,489,610 / 30.04%
Number/percentage of C's	26,241,010,997 / 19.89%
Number/percentage of T's	39,699,264,544 / 30.09%
Number/percentage of G's	26,214,788,866 / 19.87%
Number/percentage of N's	135,816,238 / 0.1%

GC Percentage	39.76%

2.3. Coverage

Mean	42.6216
Standard Deviation	56.7925

2.4. Mapping Quality

Mean Mapping Quality	54.26

2.5. Insert size

Mean	32,246.59
Standard Deviation	1,701,420.56
P25/Median/P75	181 / 231 / 303

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	1,283,244,741
Insertions	14,584,493
Mapped reads with at least one insertion	1.04%
Deletions	10,960,240
Mapped reads with at least one deletion	0.78%
Homopolymer indels	45.32%

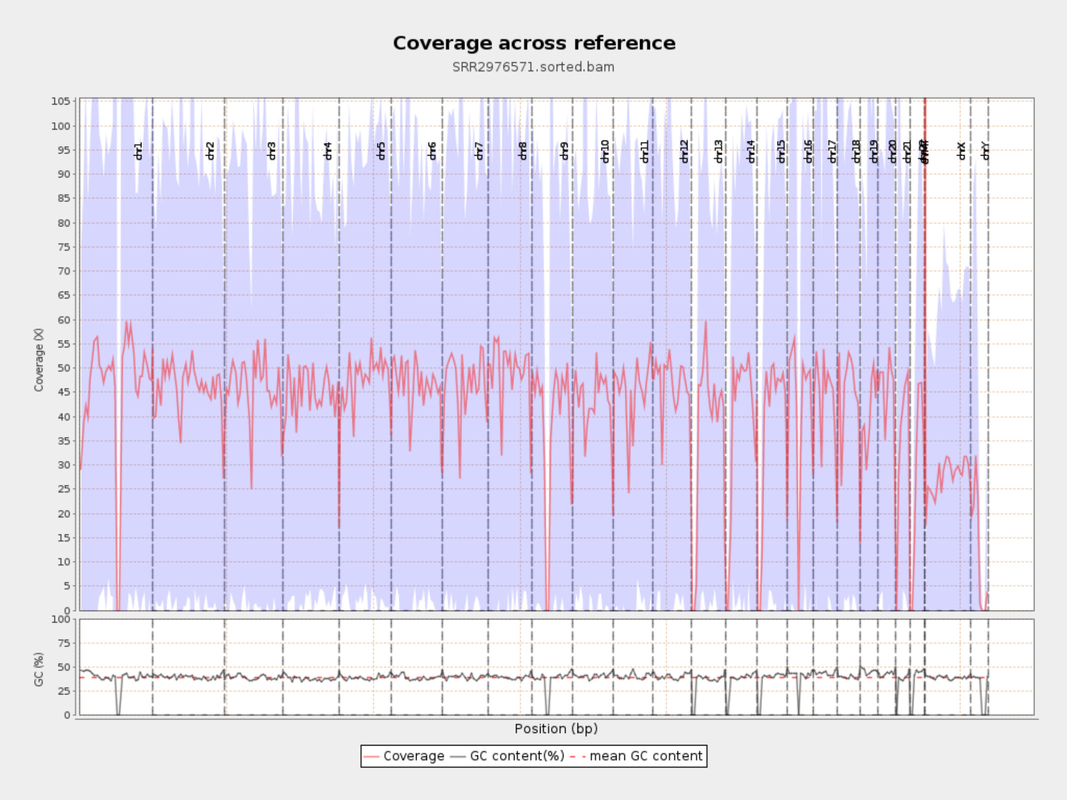
2.7. Chromosome stats

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

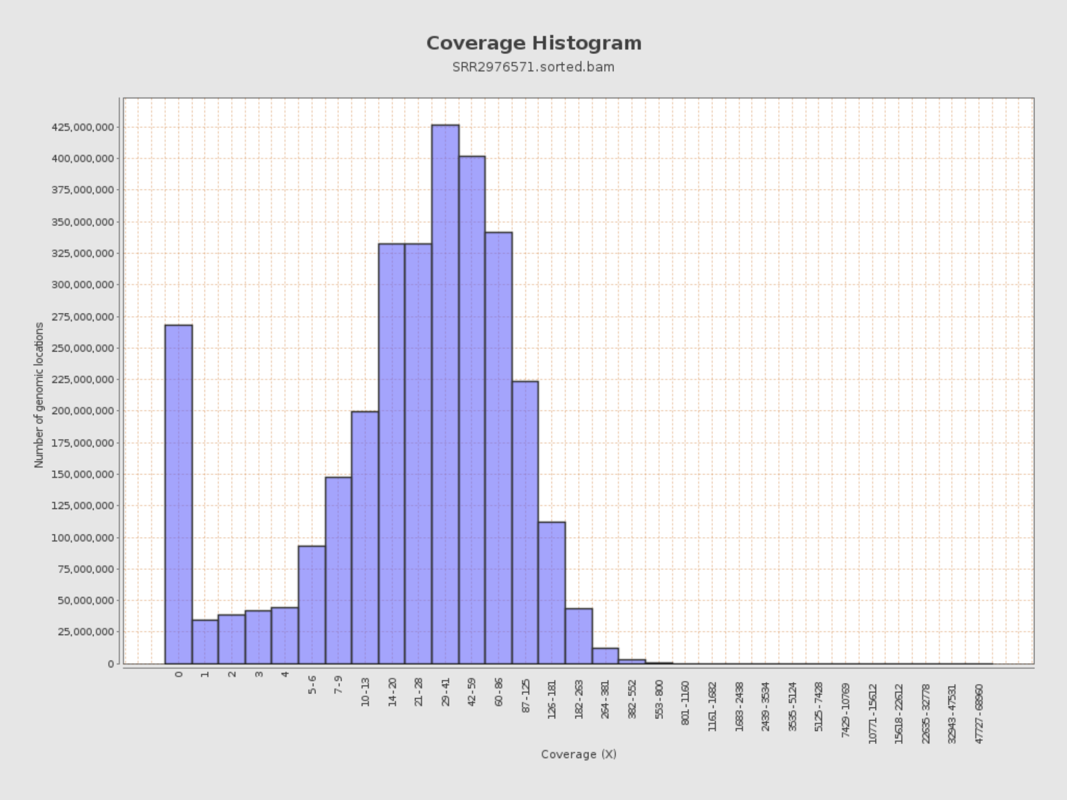
		bases	coverage	deviation
chr1	249250621	11500829290	46.1416	89.7831
chr2	243199373	11235890512	46.2003	51.3712
chr3	198022430	9161599357	46.2655	46.5126
chr4	191154276	8664173641	45.3256	49.3416
chr5	180915260	8588933060	47.4749	46.6893
chr6	171115067	8032622632	46.9428	56.3687
chr7	159138663	7377410975	46.3584	51.329
chr8	146364022	7230682548	49.402	51.5482
chr9	141213431	5388810351	38.1607	57.5704
chr10	135534747	5908877926	43.5968	68.3711
chr11	135006516	6076617566	45.0098	49.9393
chr12	133851895	6208347510	46.3822	49.3434
chr13	115169878	4300819555	37.3433	44.3843
chr14	107349540	4173159449	38.8745	46.928
chr15	102531392	3840338486	37.4552	46.5079
chr16	90354753	3718437915	41.1538	51.3314
chr17	81195210	3542161710	43.6253	76.272
chr18	78077248	3607755753	46.2075	67.8646
chr19	59128983	2344945365	39.6581	65.0107
chr20	63025520	2864928087	45.4566	52.2723
chr21	48129895	1727970503	35.9022	64.5179
chr22	51304566	1393582509	27.1629	41.4793
chrMT	16571	19170642	1,156.879	321.0842
chrX	155270560	4296531162	27.6713	36.2475

chrY	59373566	738726882	12.442	39.4236

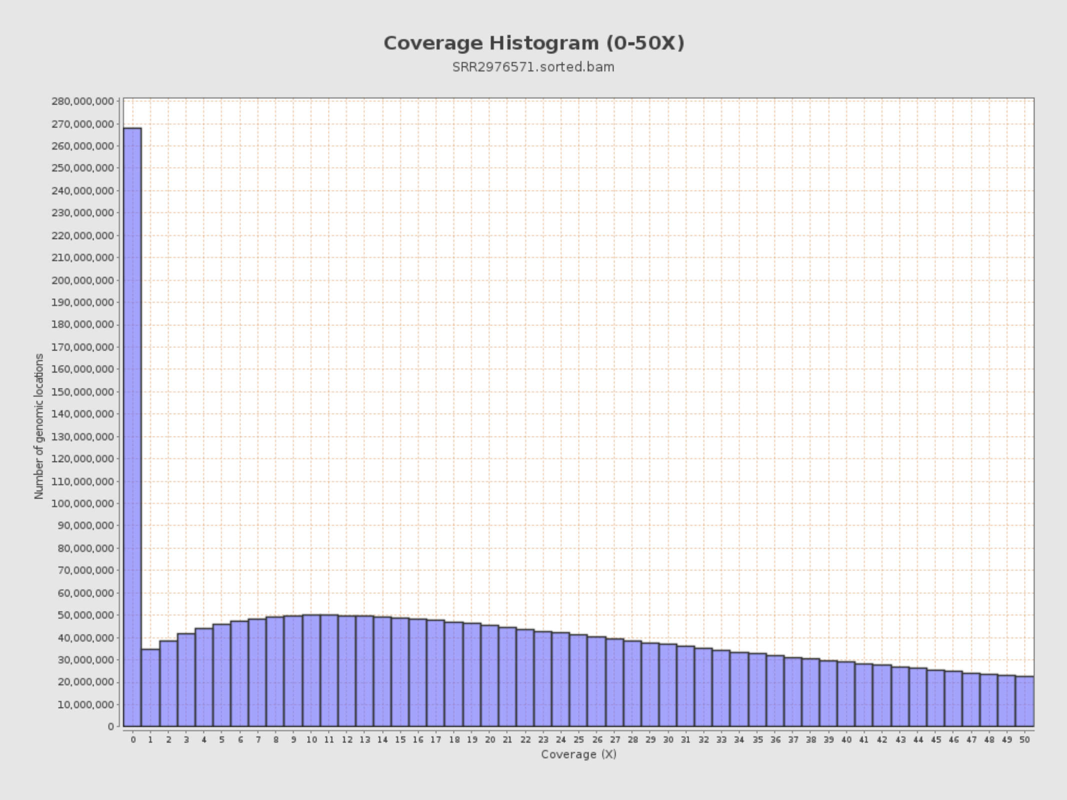
3. Results : Coverage across reference



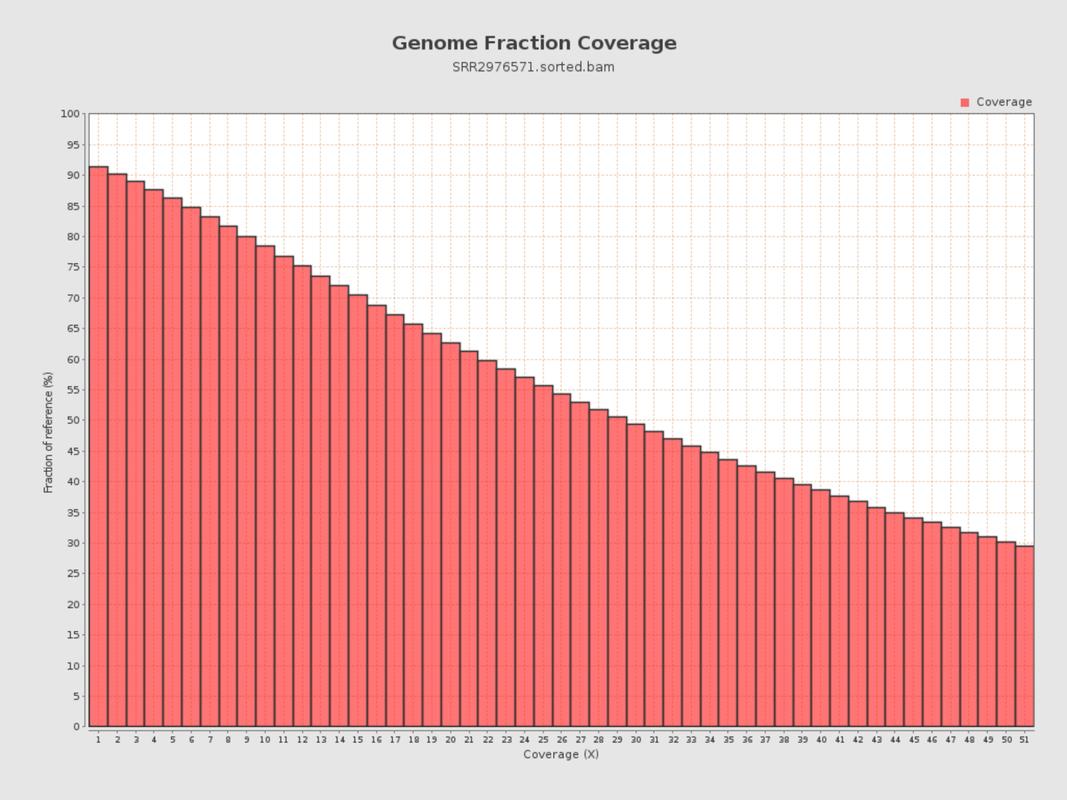
4. Results : Coverage Histogram



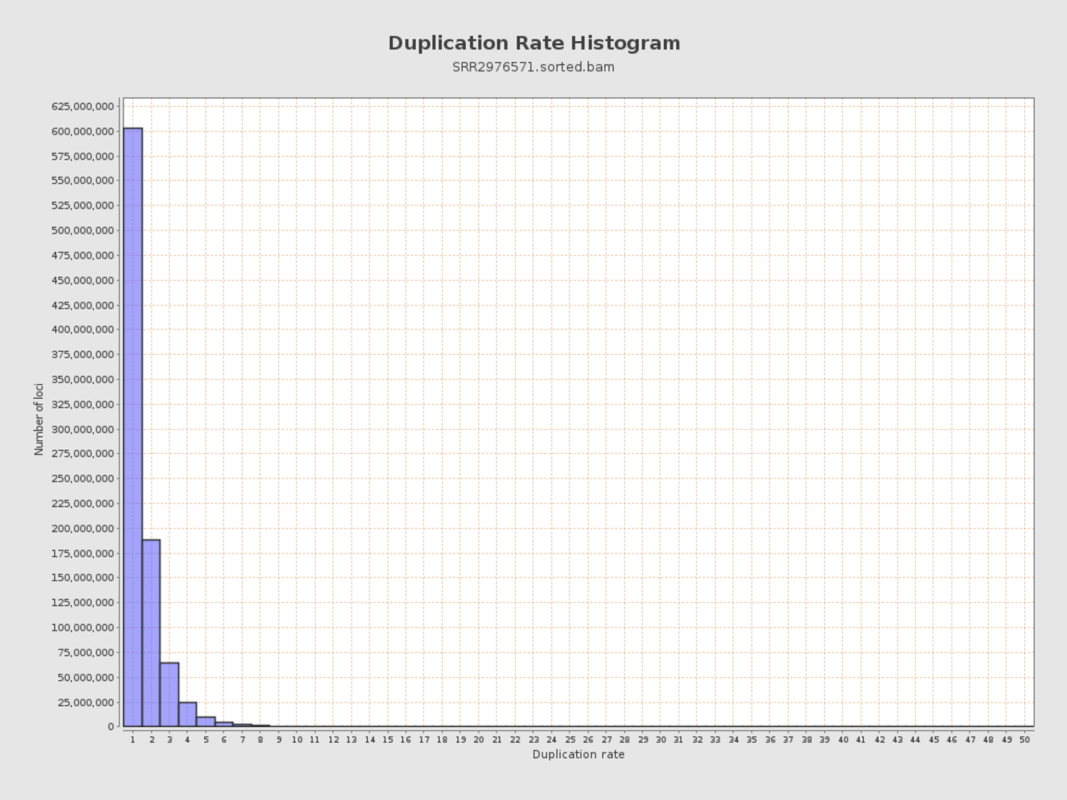
5. Results : Coverage Histogram (0-50X)



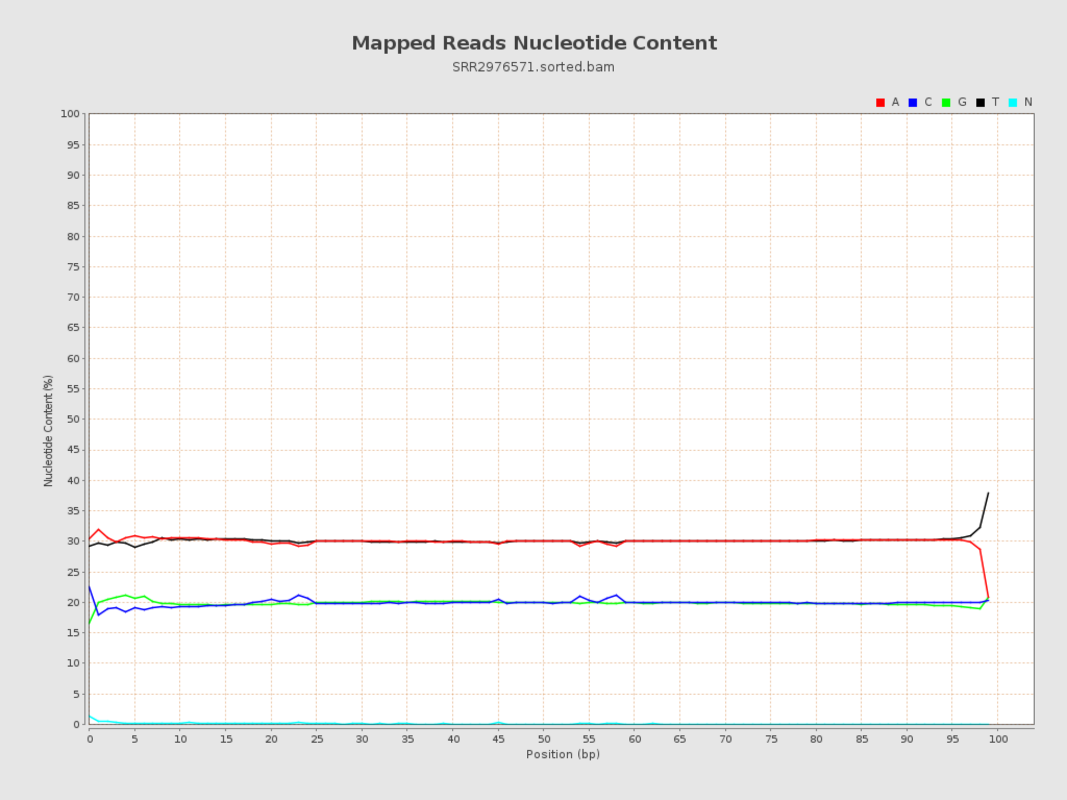
6. Results : Genome Fraction Coverage



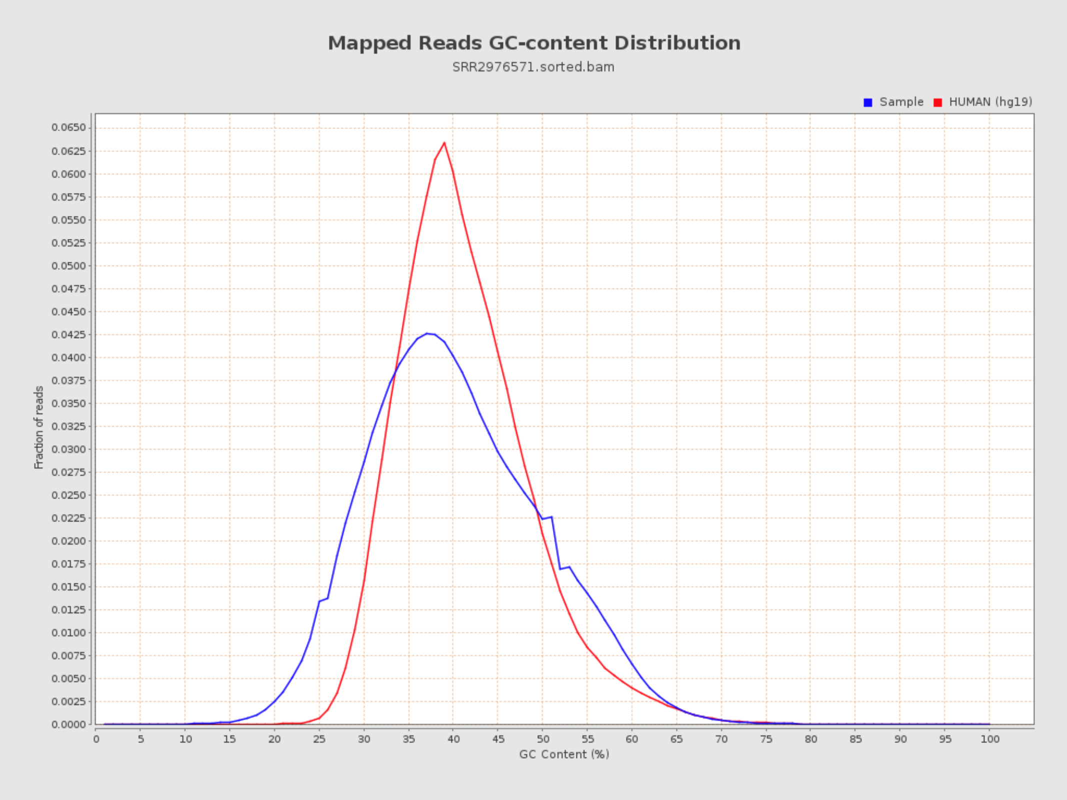
7. Results : Duplication Rate Histogram



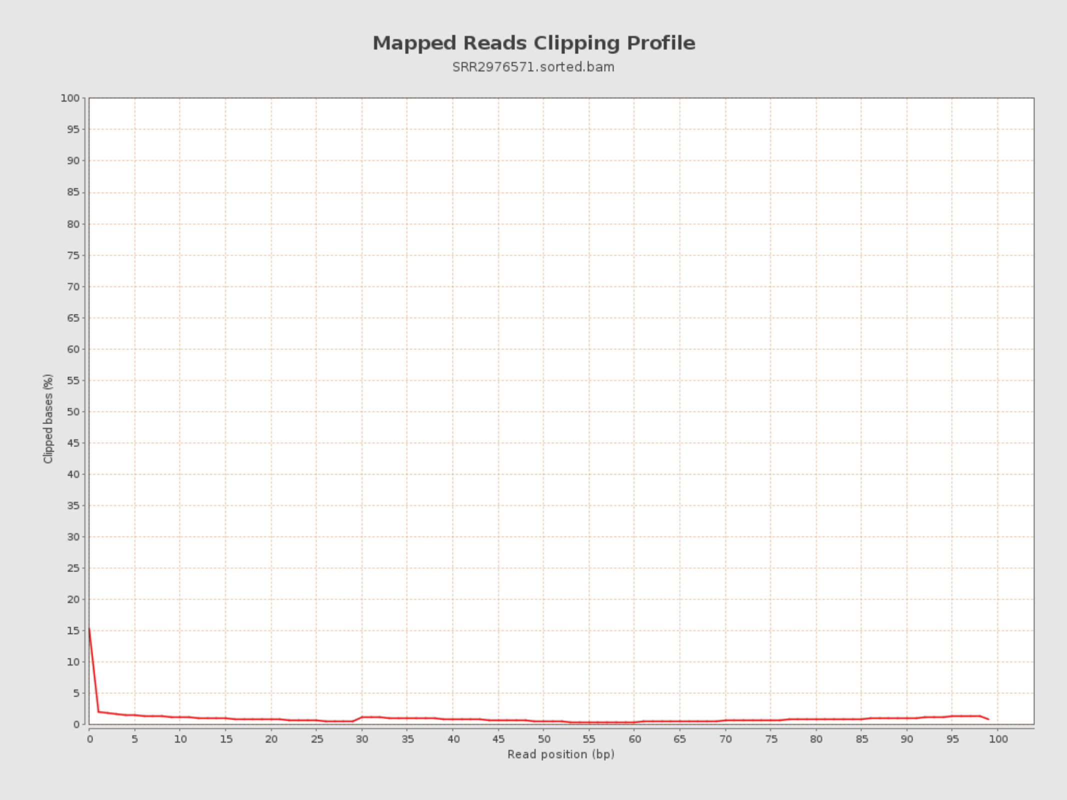
8. Results : Mapped Reads Nucleotide Content



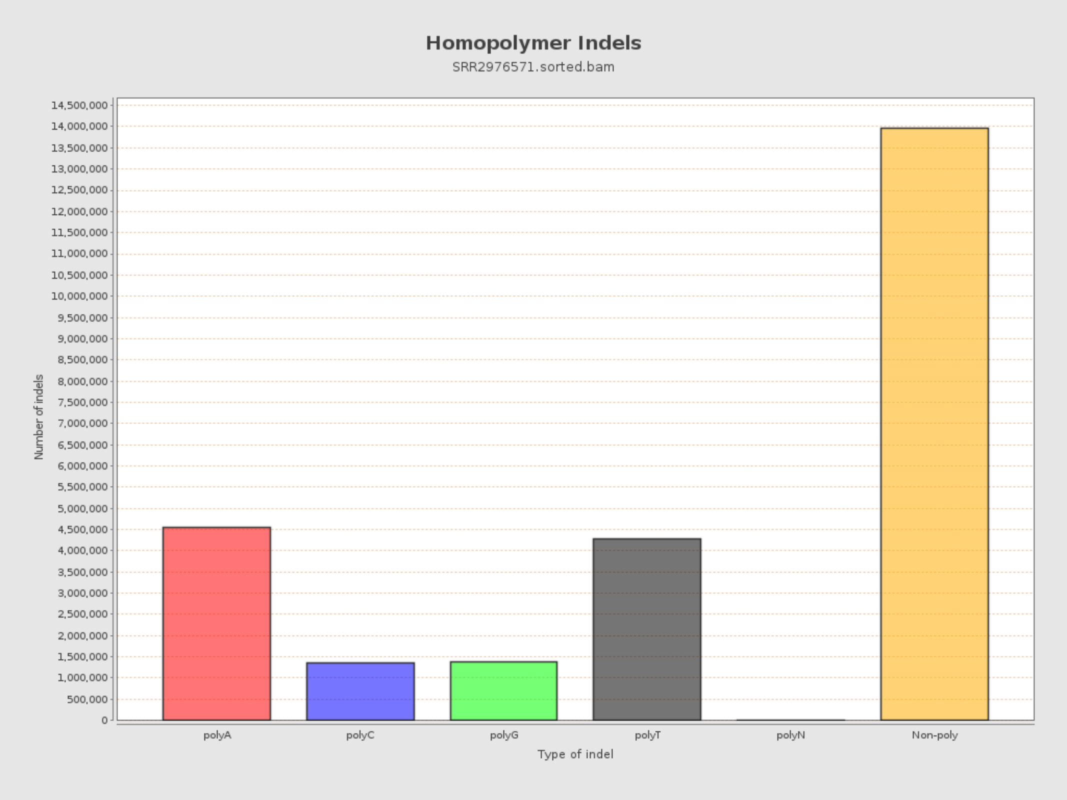
9. Results : Mapped Reads GC-content Distribution



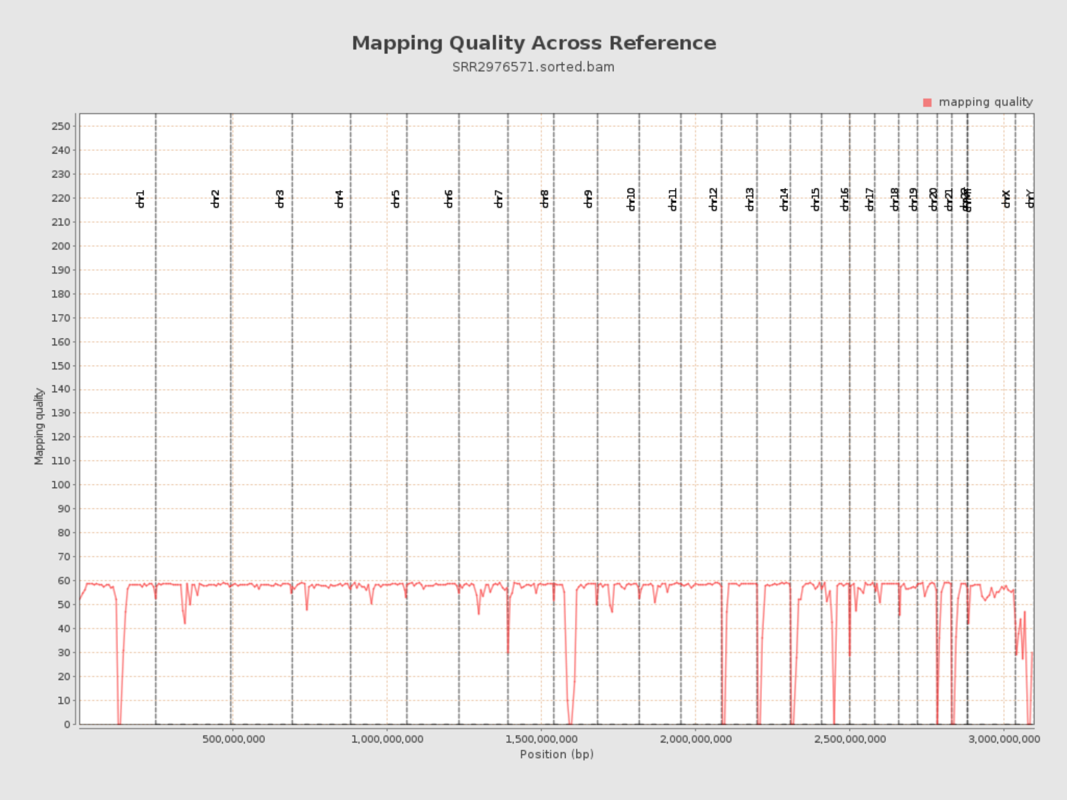
10. Results : Mapped Reads Clipping Profile



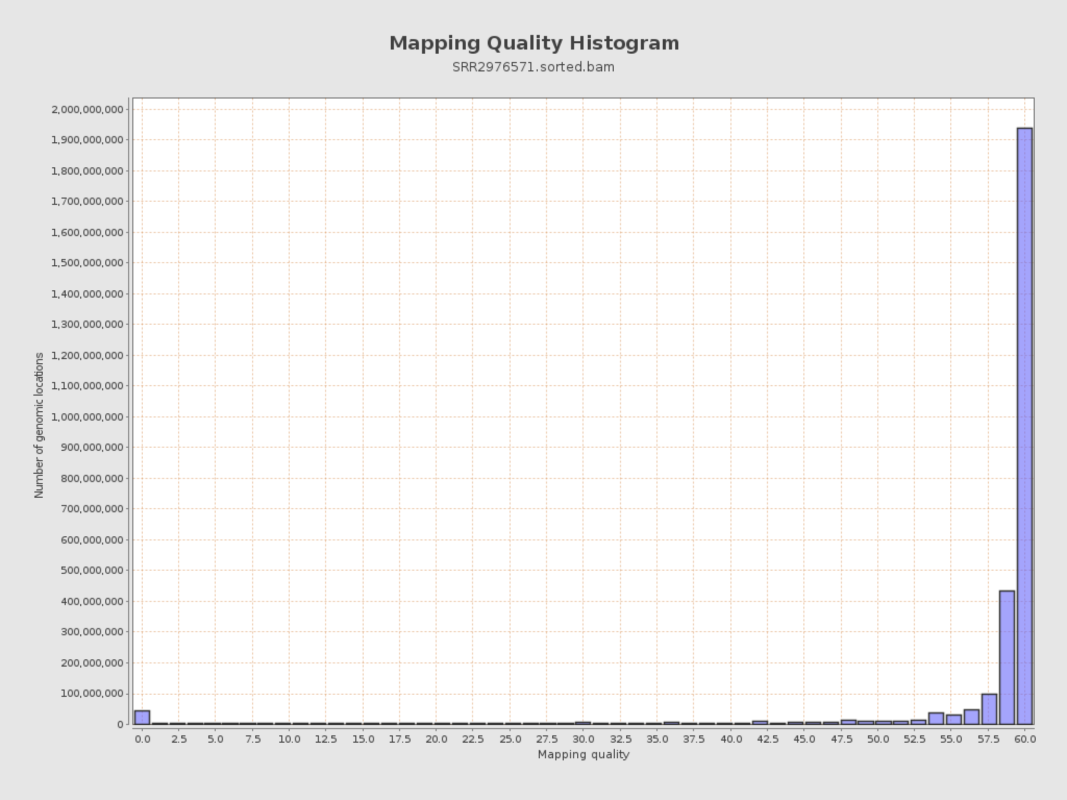
11. Results : Homopolymer Indels



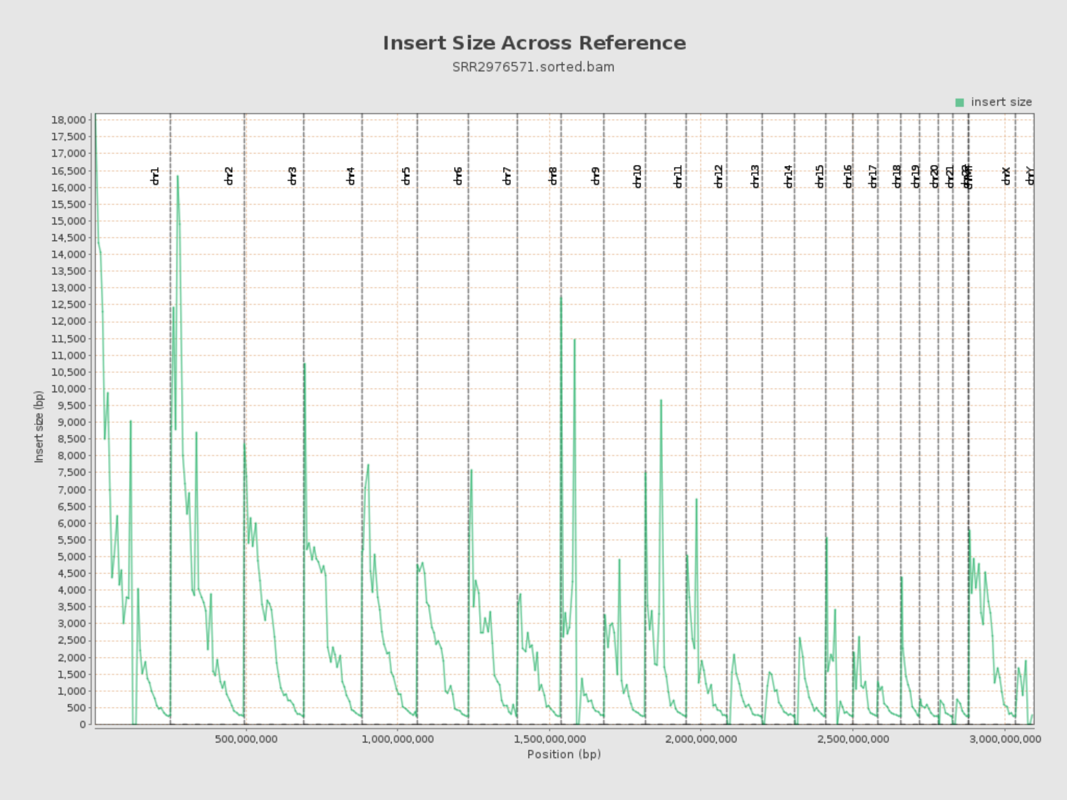
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram