Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/28 08:32:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976570.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_SRR2976570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976570_1.fastq.gz SRR2976570_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 28 08:32:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,450,059,946
Mapped reads	1,431,436,063 / 98.72%
Unmapped reads	18,623,883 / 1.28%
Mapped paired reads	1,431,436,063 / 98.72%
Mapped reads, first in pair	719,913,603 / 49.65%
Mapped reads, second in pair	711,522,460 / 49.07%
Mapped reads, both in pair	1,416,204,746 / 97.67%
Mapped reads, singletons	15,231,317 / 1.05%
Secondary alignments	0
Supplementary alignments	10,579,937 / 0.73%
Read min/max/mean length	20 / 100 / 96.33
Duplicated reads (estimated)	497,956,342 / 34.34%
Duplication rate	32.73%
Clipped reads	78,350,498 / 5.4%

2.2. ACGT Content

Number/percentage of A's	41,292,383,849 / 30.03%
Number/percentage of C's	27,301,187,453 / 19.85%
Number/percentage of T's	41,283,356,785 / 30.02%
Number/percentage of G's	27,525,513,213 / 20.02%
Number/percentage of N's	121,014,240 / 0.09%

GC Percentage	39.87%

2.3. Coverage

Mean	44.4323
Standard Deviation	50.7458

2.4. Mapping Quality

Mean Mapping Quality	54.32

2.5. Insert size

Mean	32,030.28
Standard Deviation	1,707,835.78
P25/Median/P75	184 / 237 / 312

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	869,902,933
Insertions	14,545,526
Mapped reads with at least one insertion	1%
Deletions	10,616,294
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.48%

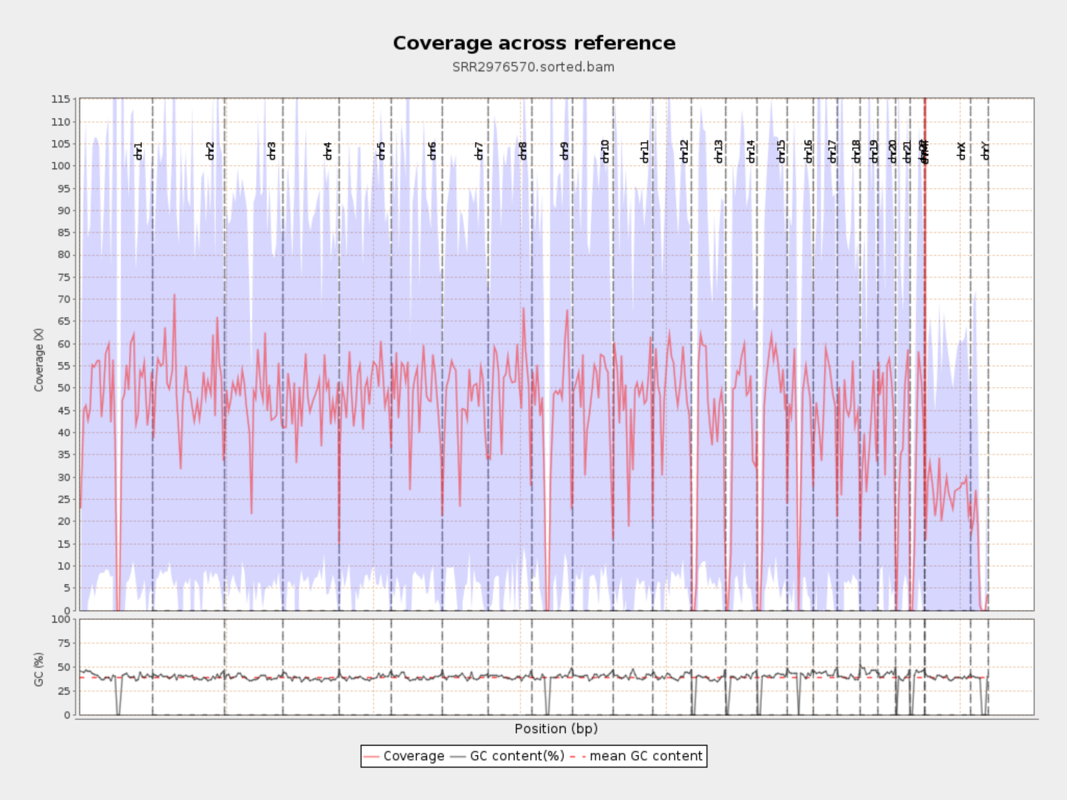
2.7. Chromosome stats

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

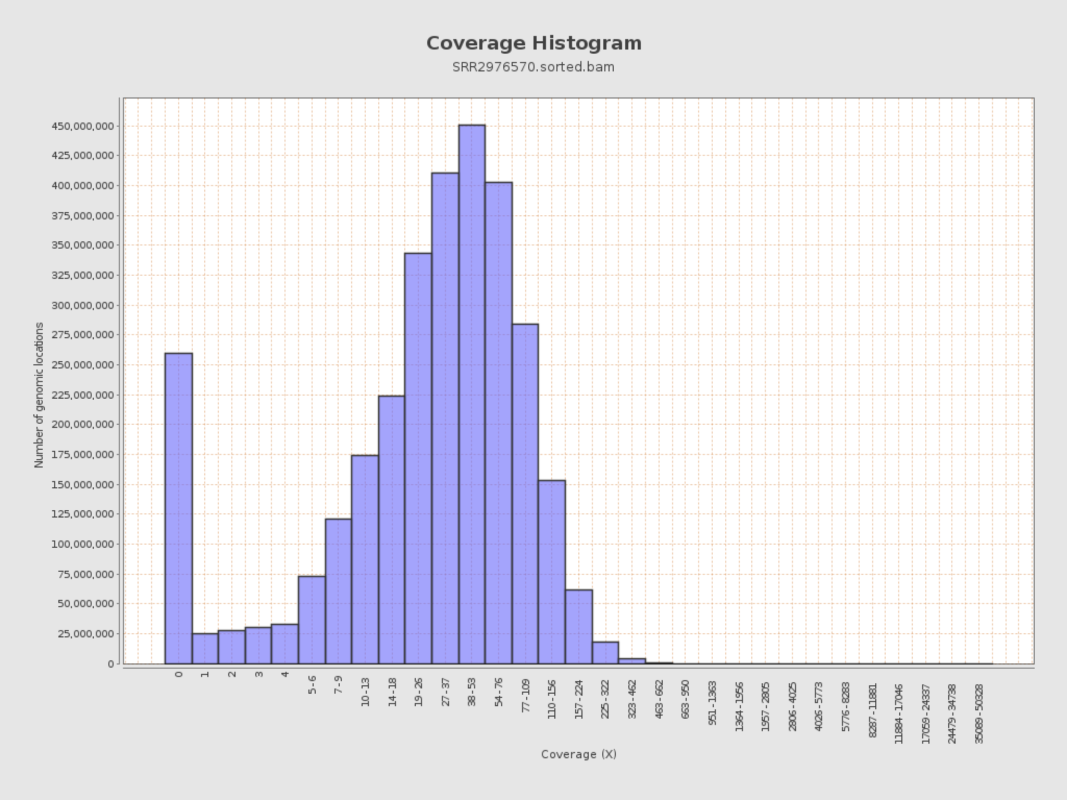
		bases	coverage	deviation
chr1	249250621	11572713616	46.43	72.1775
chr2	243199373	12296465462	50.5613	47.8587
chr3	198022430	9437524690	47.6589	43.0898
chr4	191154276	9043548224	47.3102	45.7216
chr5	180915260	8885337159	49.1133	44.0375
chr6	171115067	8458765309	49.4332	51.6128
chr7	159138663	7306060039	45.91	44.4368
chr8	146364022	7481793574	51.1177	47.8649
chr9	141213431	5908875020	41.8436	53.3723
chr10	135534747	6565441418	48.441	58.6918
chr11	135006516	6362563679	47.1278	48.015
chr12	133851895	6761774322	50.5168	46.4444
chr13	115169878	4635273219	40.2473	42.8599
chr14	107349540	4319468852	40.2374	45.3601
chr15	102531392	4423029582	43.1383	47.5257
chr16	90354753	3610730563	39.9617	45.1106
chr17	81195210	3700867779	45.5799	60.9907
chr18	78077248	3472681378	44.4775	54.3532
chr19	59128983	2212783610	37.423	54.3549
chr20	63025520	2997869559	47.566	48.1868
chr21	48129895	1740386842	36.1602	57.7746
chr22	51304566	1590055493	30.9925	42.8475
chrMT	16571	37117359	2,239.8986	533.9572
chrX	155270560	4086163669	26.3164	31.1983

chrY	59373566	641537904	10.8051	29.9893

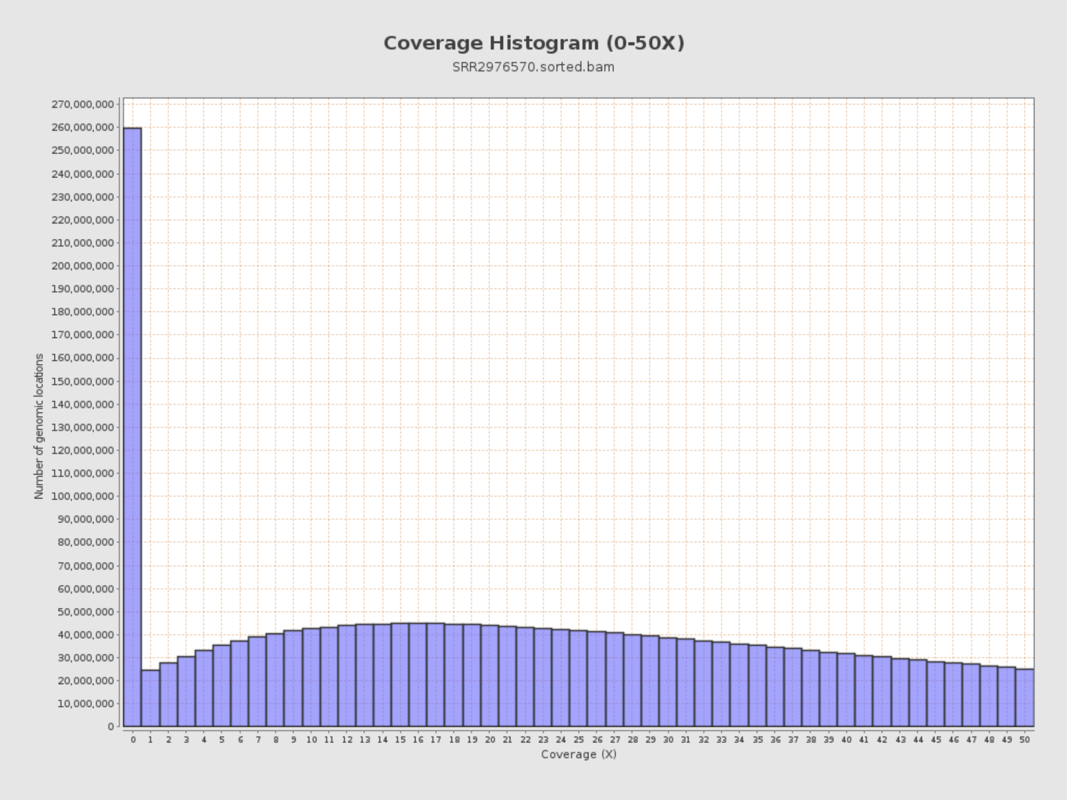
3. Results : Coverage across reference



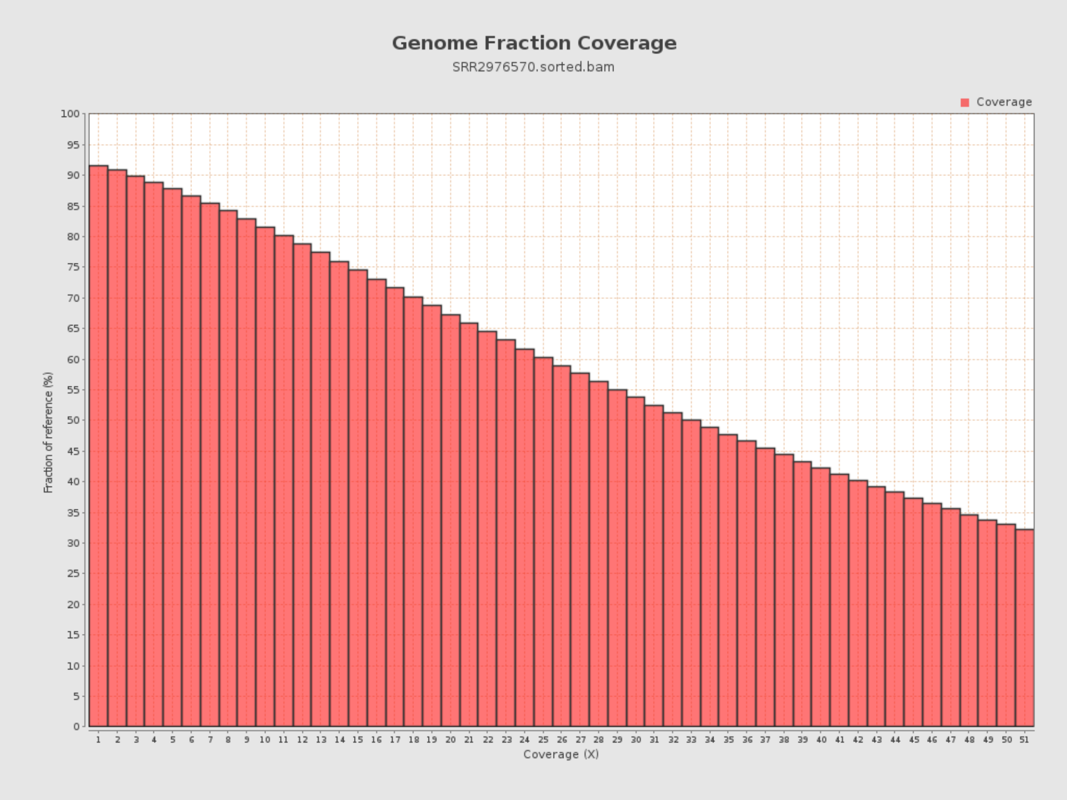
4. Results : Coverage Histogram



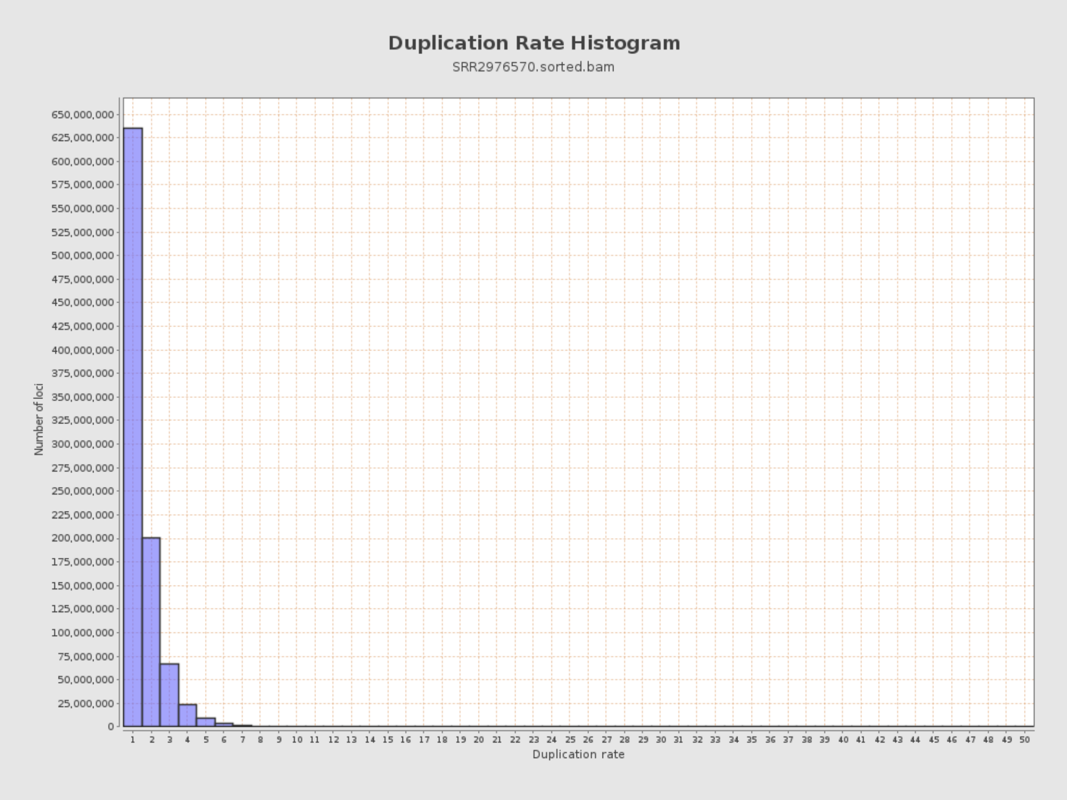
5. Results : Coverage Histogram (0-50X)



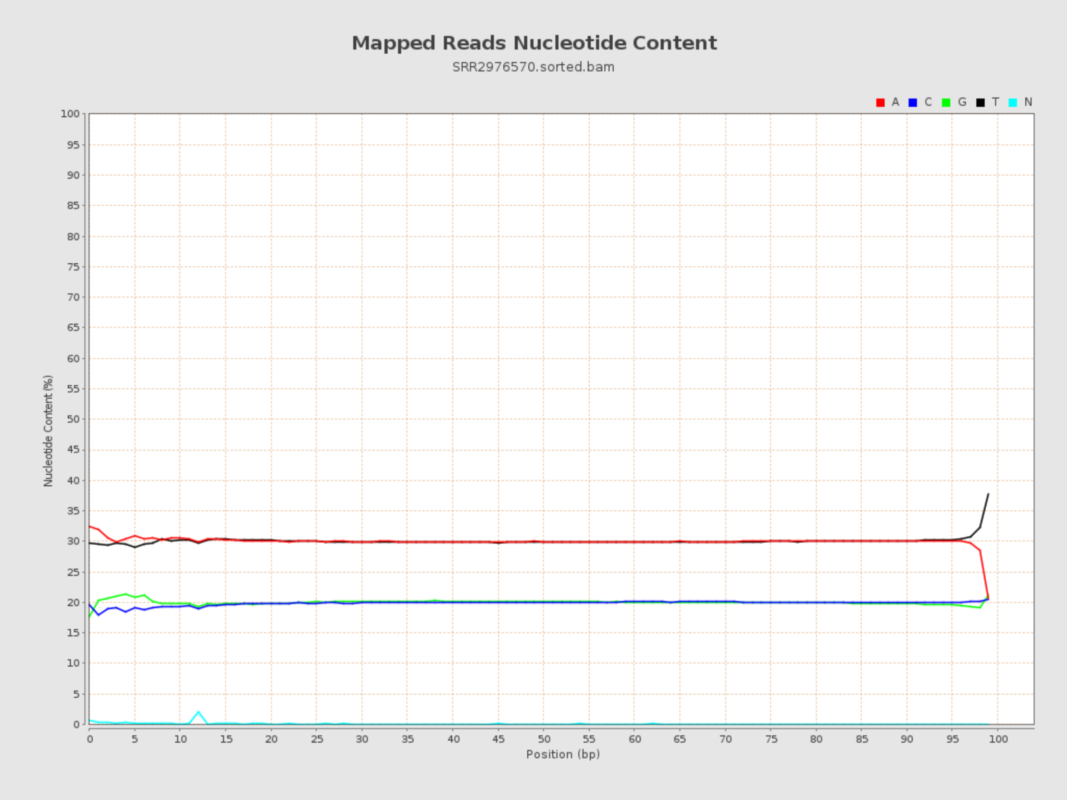
6. Results : Genome Fraction Coverage



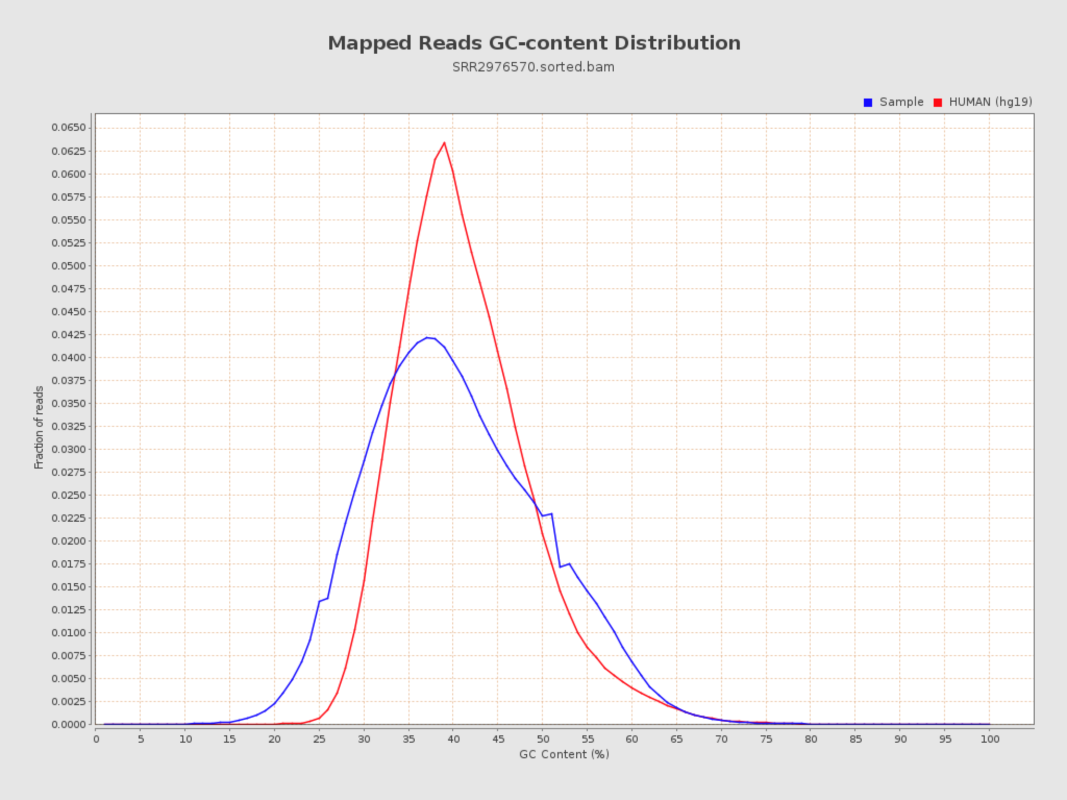
7. Results : Duplication Rate Histogram



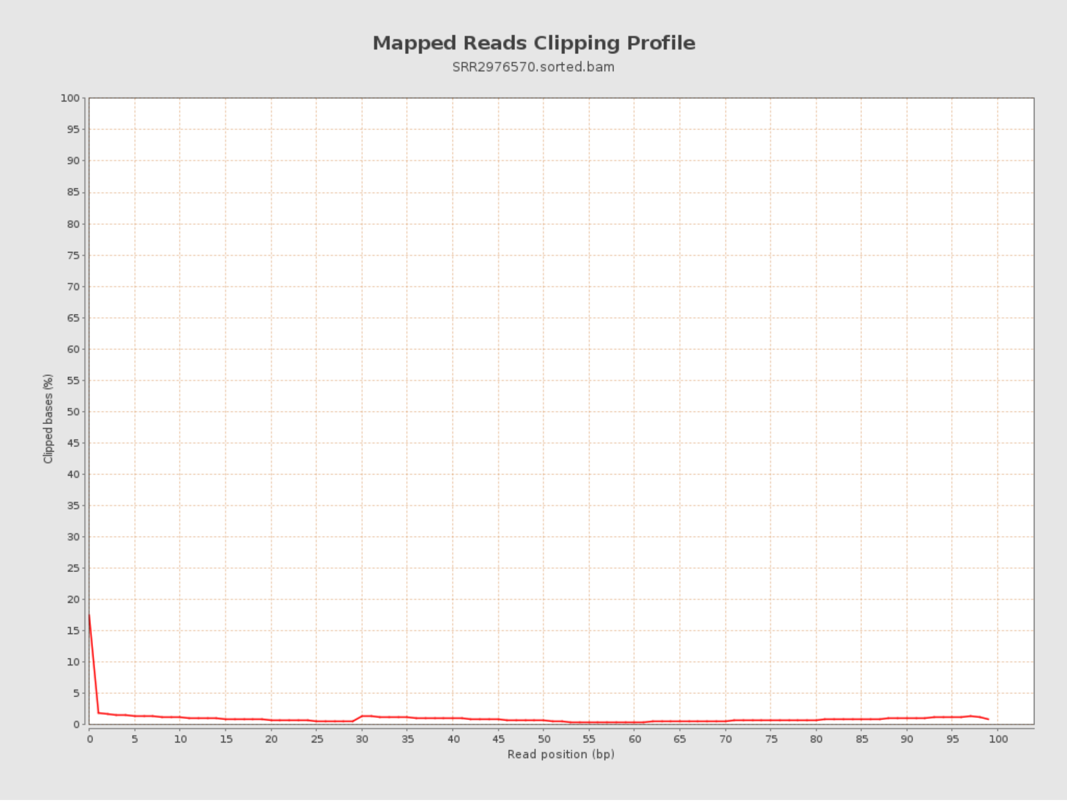
8. Results : Mapped Reads Nucleotide Content



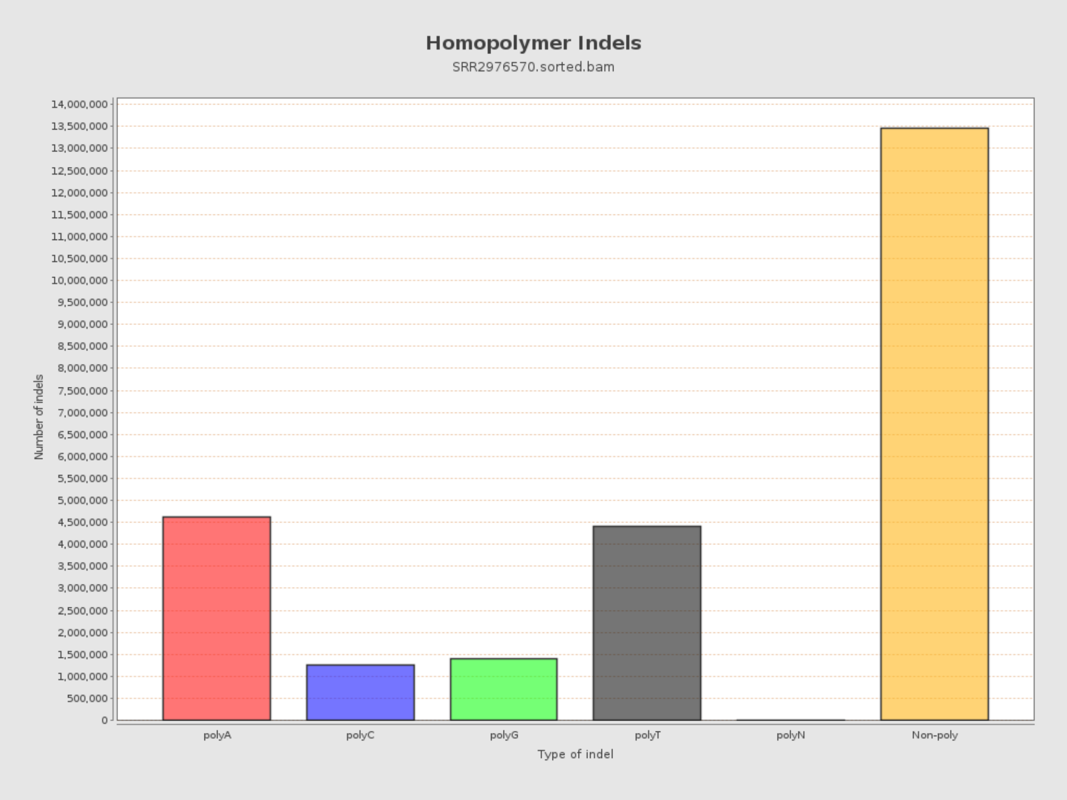
9. Results : Mapped Reads GC-content Distribution



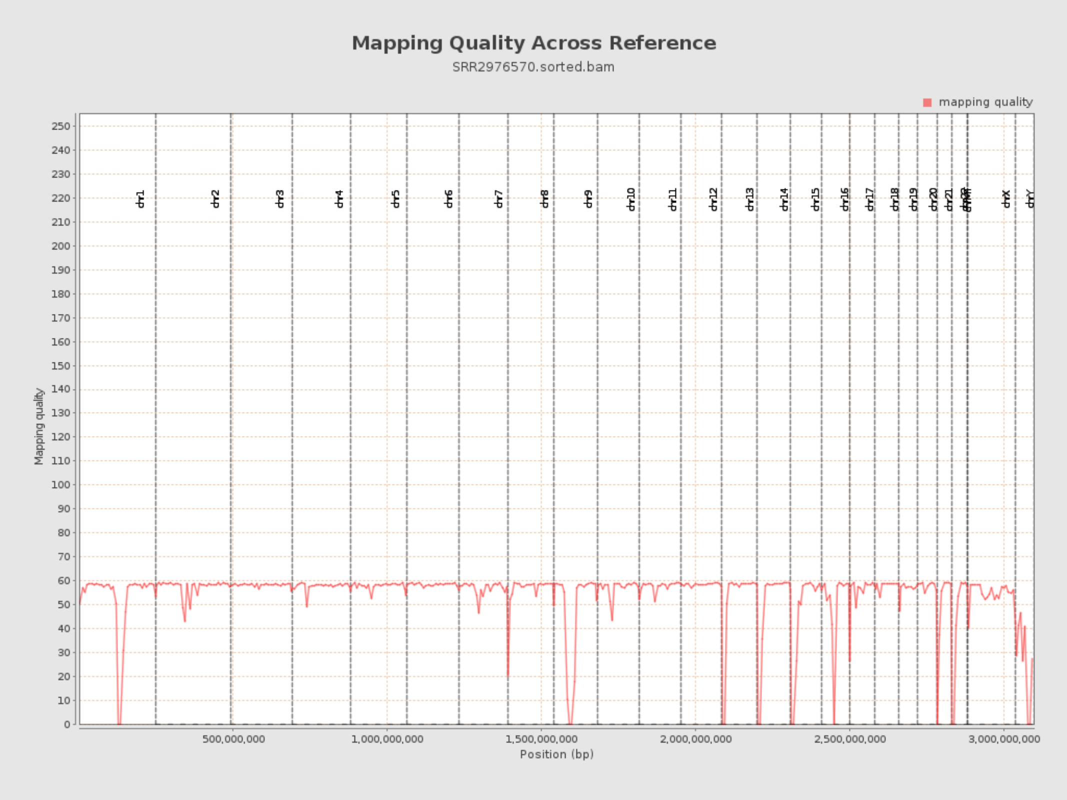
10. Results : Mapped Reads Clipping Profile



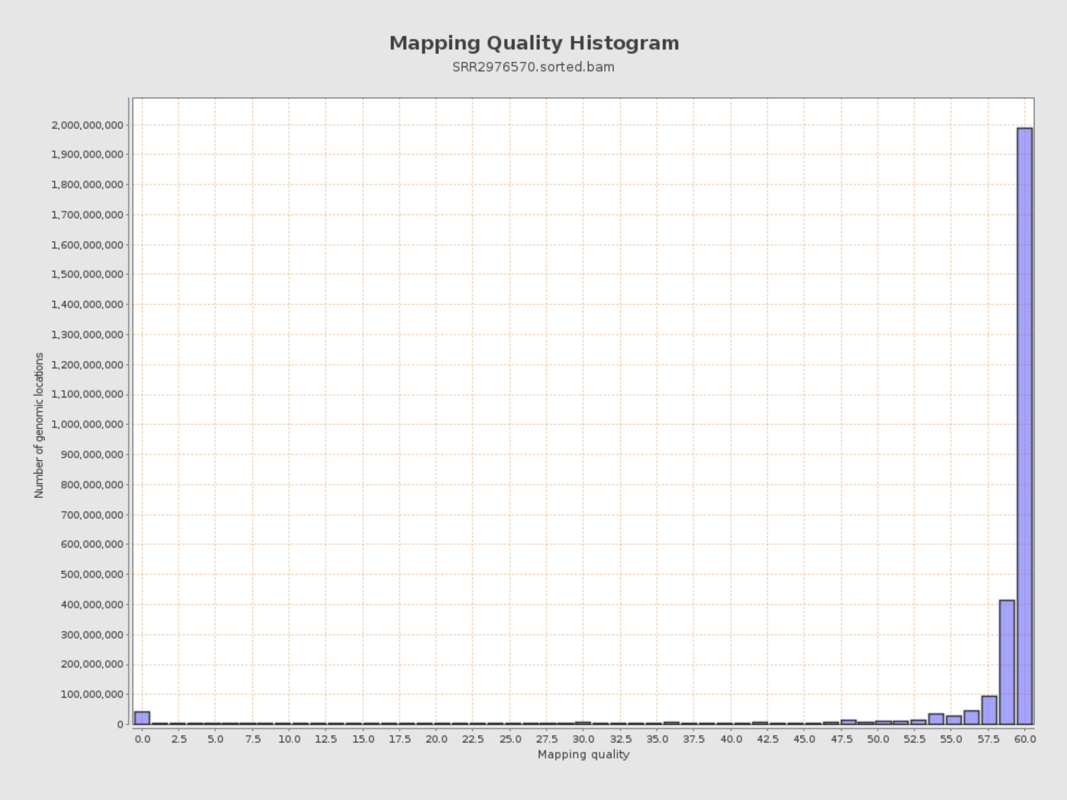
11. Results : Homopolymer Indels



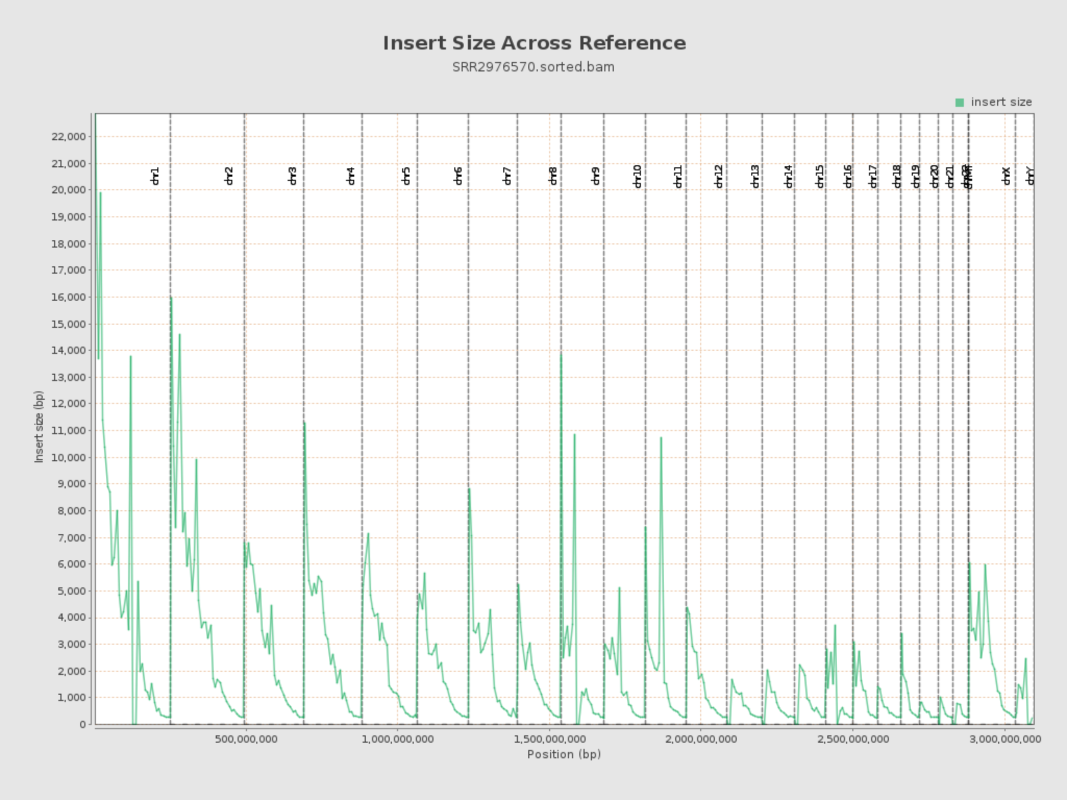
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram