Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/22 22:31:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976562.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_SRR2976562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976562_1.fastq.gz SRR2976562_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 22 22:31:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	366,809,340
Mapped reads	364,368,464 / 99.33%
Unmapped reads	2,440,876 / 0.67%
Mapped paired reads	364,368,464 / 99.33%
Mapped reads, first in pair	182,989,933 / 49.89%
Mapped reads, second in pair	181,378,531 / 49.45%
Mapped reads, both in pair	362,401,446 / 98.8%
Mapped reads, singletons	1,967,018 / 0.54%
Secondary alignments	0
Supplementary alignments	11,877,237 / 3.24%
Read min/max/mean length	20 / 249 / 234.07
Duplicated reads (estimated)	50,082,421 / 13.65%
Duplication rate	12.13%
Clipped reads	38,939,982 / 10.62%

2.2. ACGT Content

Number/percentage of A's	24,428,400,488 / 28.95%
Number/percentage of C's	17,729,760,602 / 21.01%
Number/percentage of T's	24,261,536,176 / 28.75%
Number/percentage of G's	17,960,420,184 / 21.28%
Number/percentage of N's	1,503,134 / 0%

GC Percentage	42.3%

2.3. Coverage

Mean	27.2671
Standard Deviation	41.8476

2.4. Mapping Quality

Mean Mapping Quality	55.53

2.5. Insert size

Mean	77,911.83
Standard Deviation	2,714,739.63
P25/Median/P75	487 / 541 / 622

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	572,250,701
Insertions	8,127,606
Mapped reads with at least one insertion	2.12%
Deletions	10,546,029
Mapped reads with at least one deletion	2.76%
Homopolymer indels	46.98%

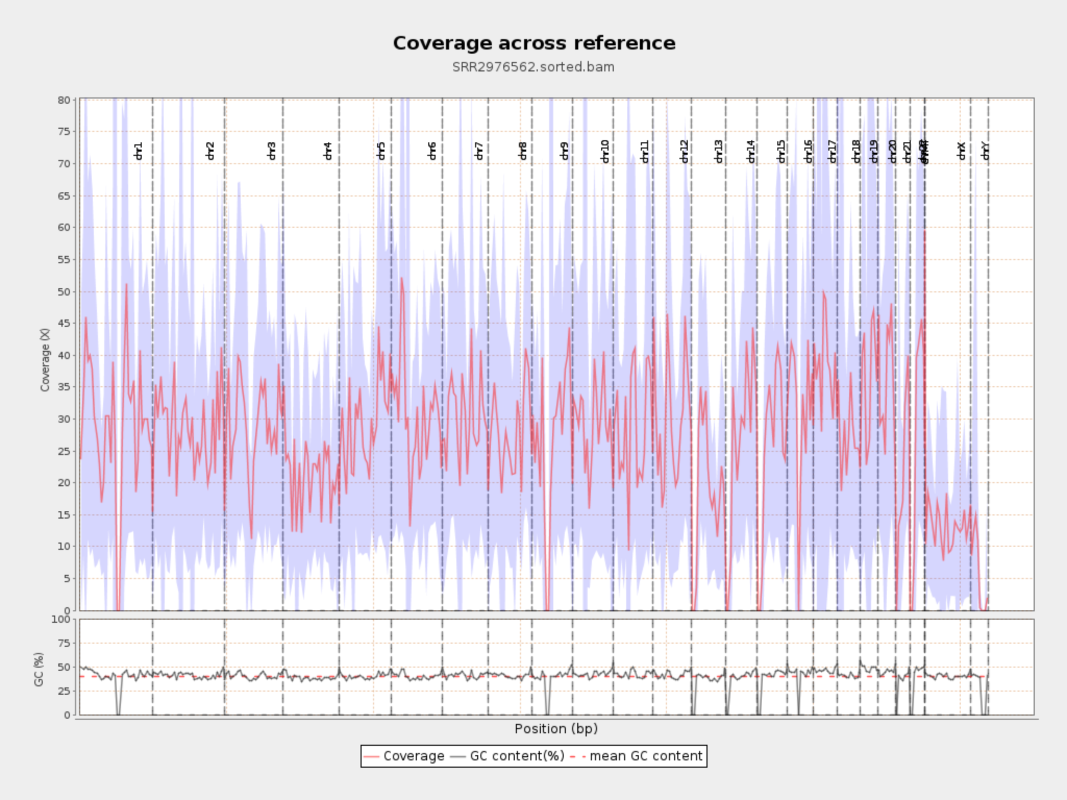
2.7. Chromosome stats

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

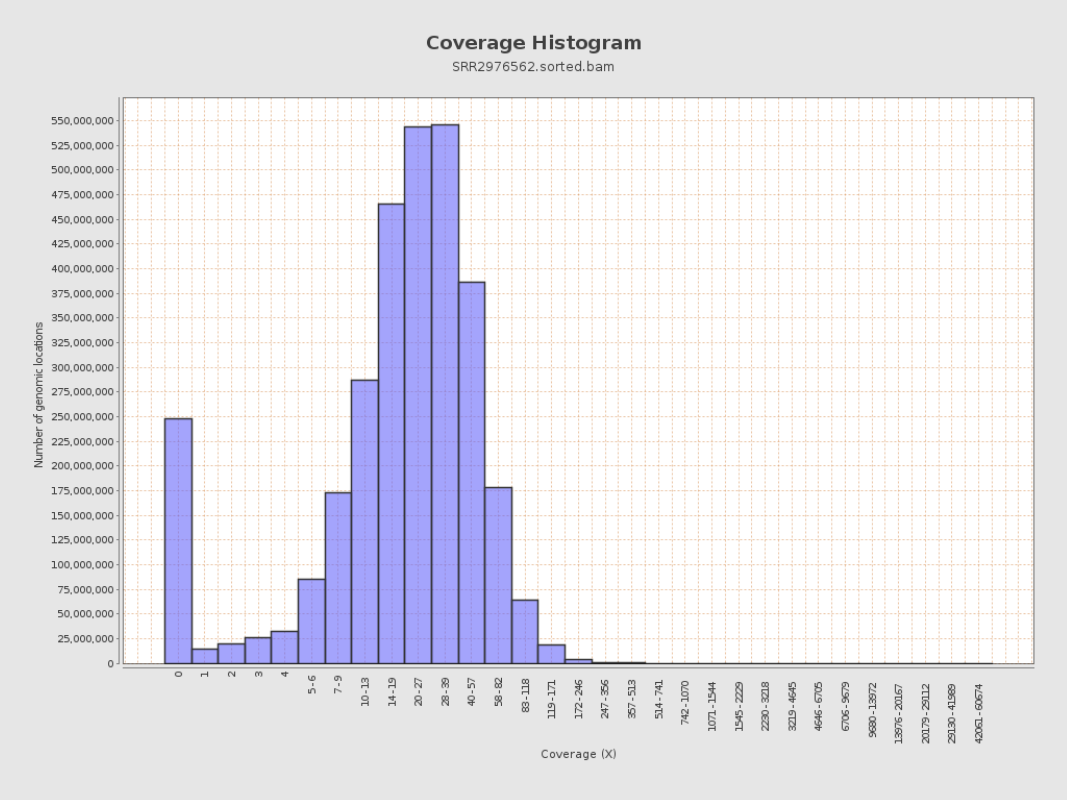
		bases	coverage	deviation
chr1	249250621	7262396556	29.1369	67.2782
chr2	243199373	7001819580	28.7905	31.757
chr3	198022430	5788309094	29.2306	21.6051
chr4	191154276	4084877148	21.3695	18.2089
chr5	180915260	5339825418	29.5156	22.8245
chr6	171115067	5247989373	30.6694	35.7784
chr7	159138663	4807514383	30.2096	27.0811
chr8	146364022	4143567007	28.31	23.6106
chr9	141213431	3785208621	26.8049	85.9498
chr10	135534747	4013880696	29.6151	62.0607
chr11	135006516	3891896876	28.8275	31.6889
chr12	133851895	4052169636	30.2735	25.4669
chr13	115169878	2167081642	18.8164	18.069
chr14	107349540	2835142414	26.4104	24.9227
chr15	102531392	2546366004	24.835	24.0378
chr16	90354753	2811910267	31.1208	28.9355
chr17	81195210	3146004563	38.7462	70.843
chr18	78077248	2138165929	27.3853	77.0464
chr19	59128983	2196478631	37.1472	51.3337
chr20	63025520	2289745942	36.3305	30.2438
chr21	48129895	1061835381	22.0619	28.5421
chr22	51304566	1413169503	27.5447	30.9648
chrMT	16571	990037	59.7452	21.468
chrX	155270560	2024842462	13.0407	14.7015

chrY	59373566	359302622	6.0516	26.0536

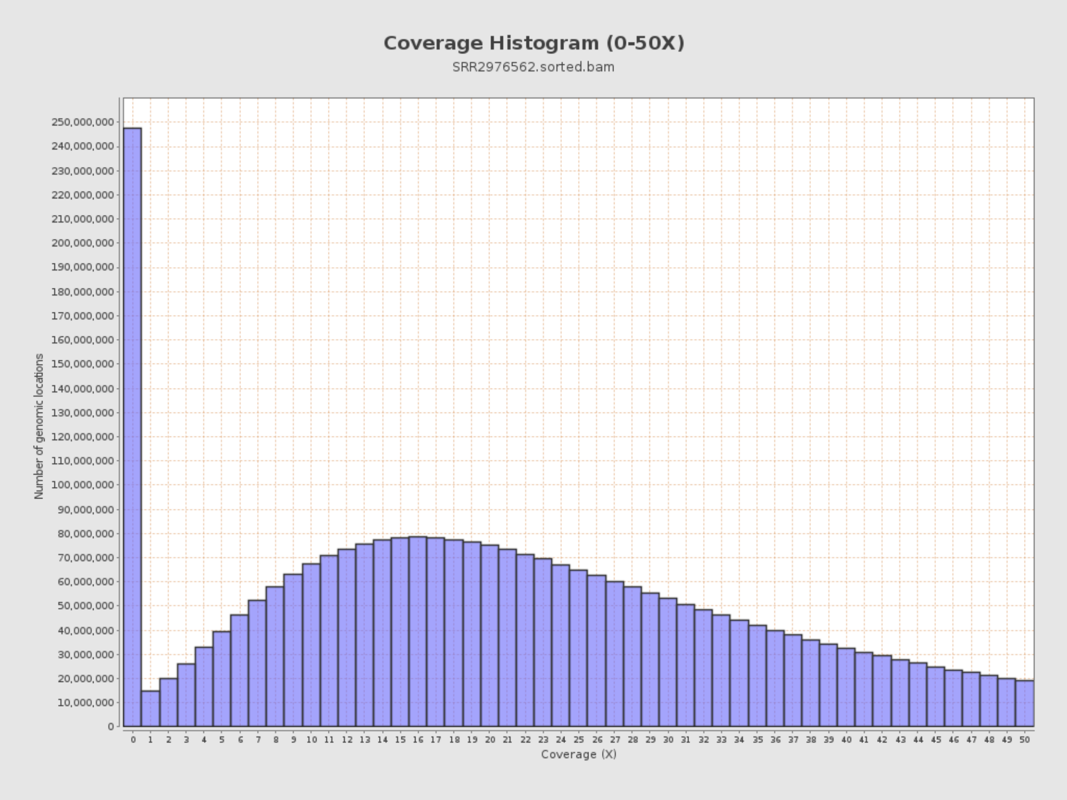
3. Results : Coverage across reference



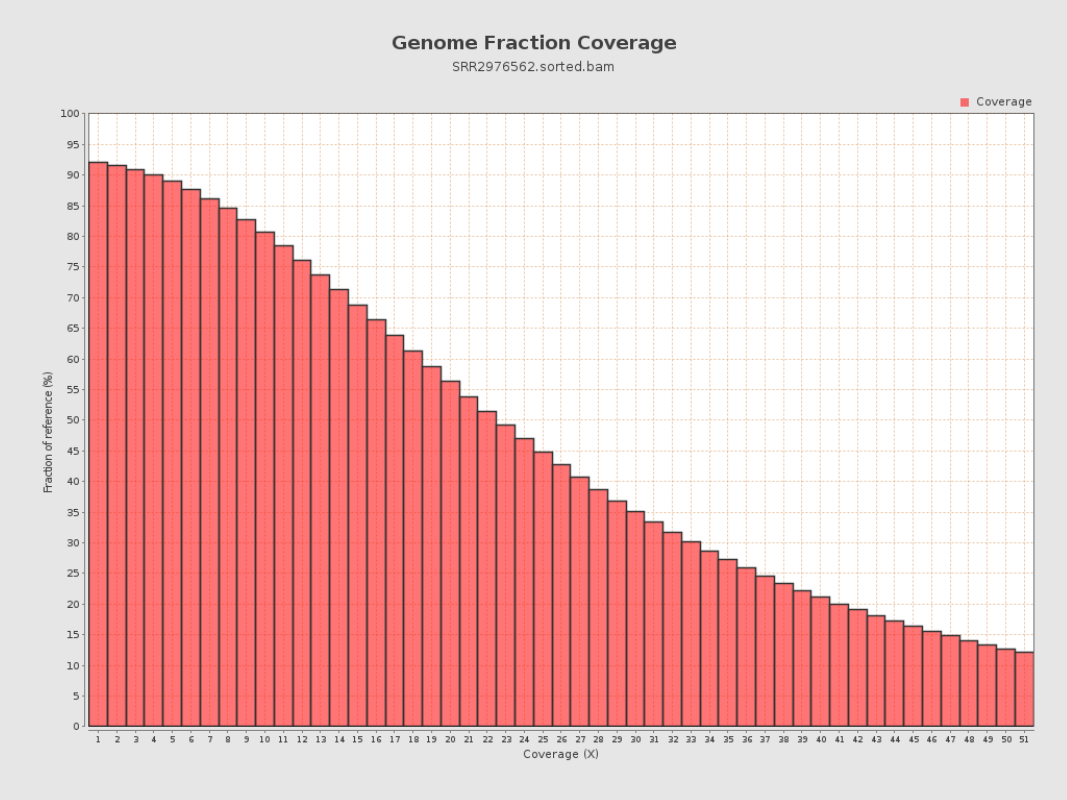
4. Results : Coverage Histogram



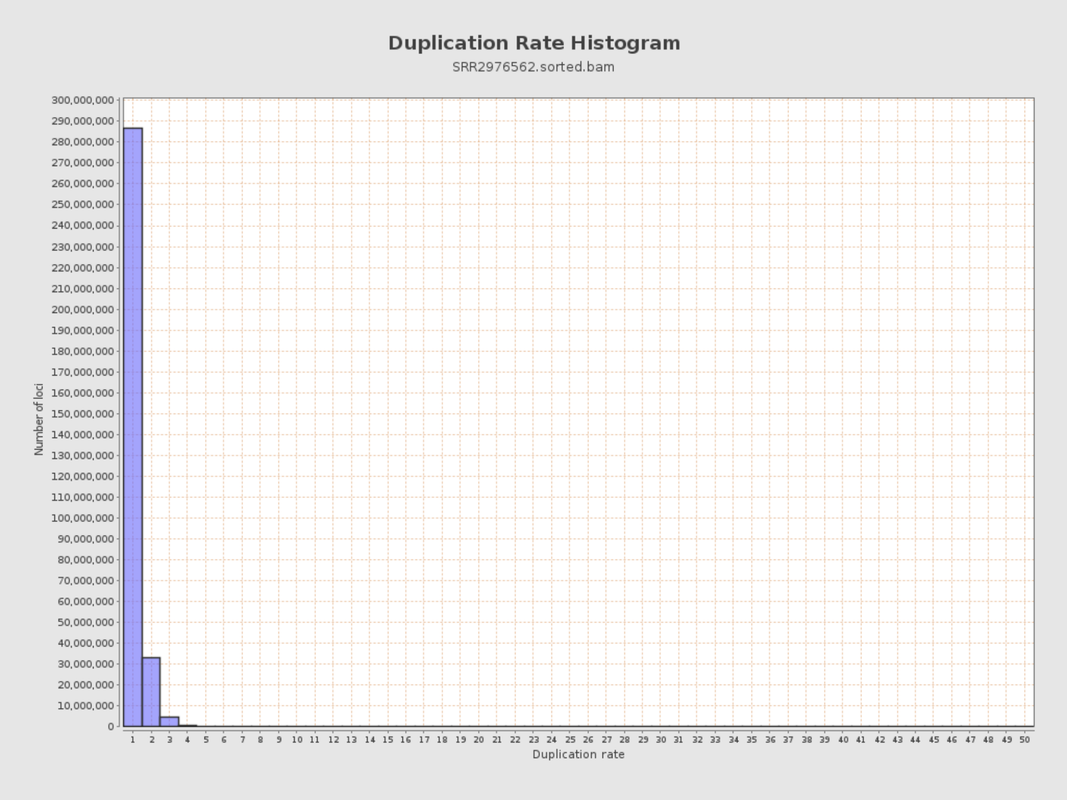
5. Results : Coverage Histogram (0-50X)



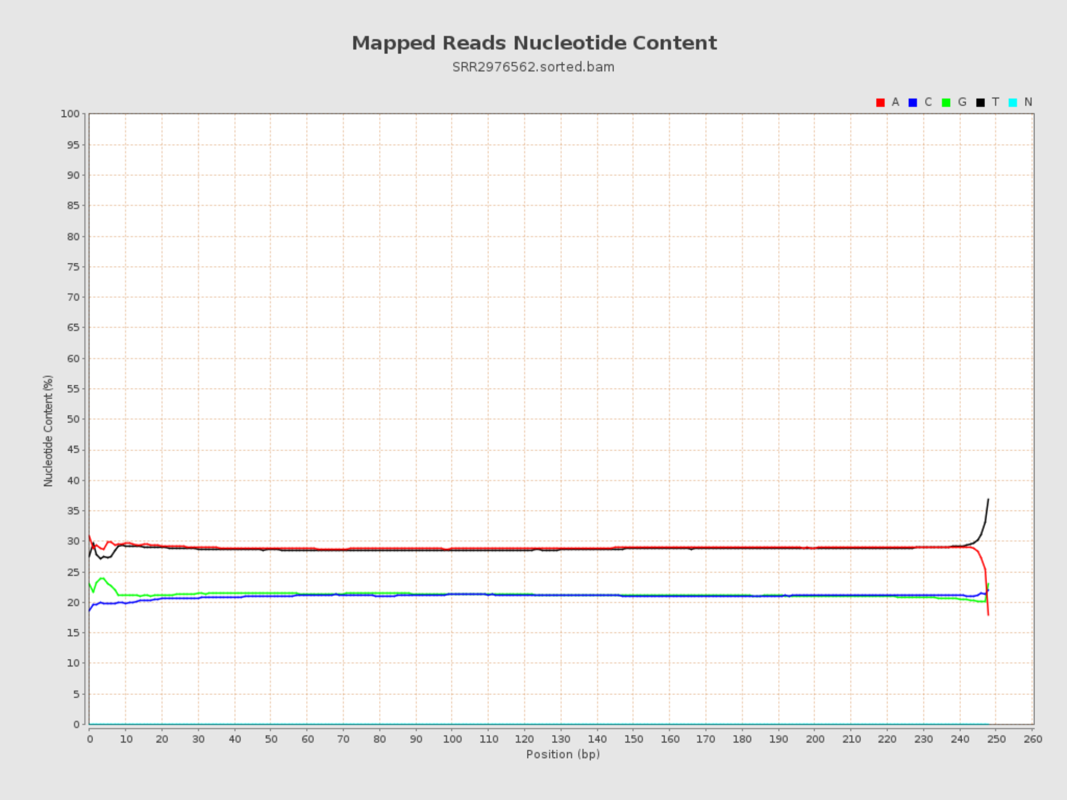
6. Results : Genome Fraction Coverage



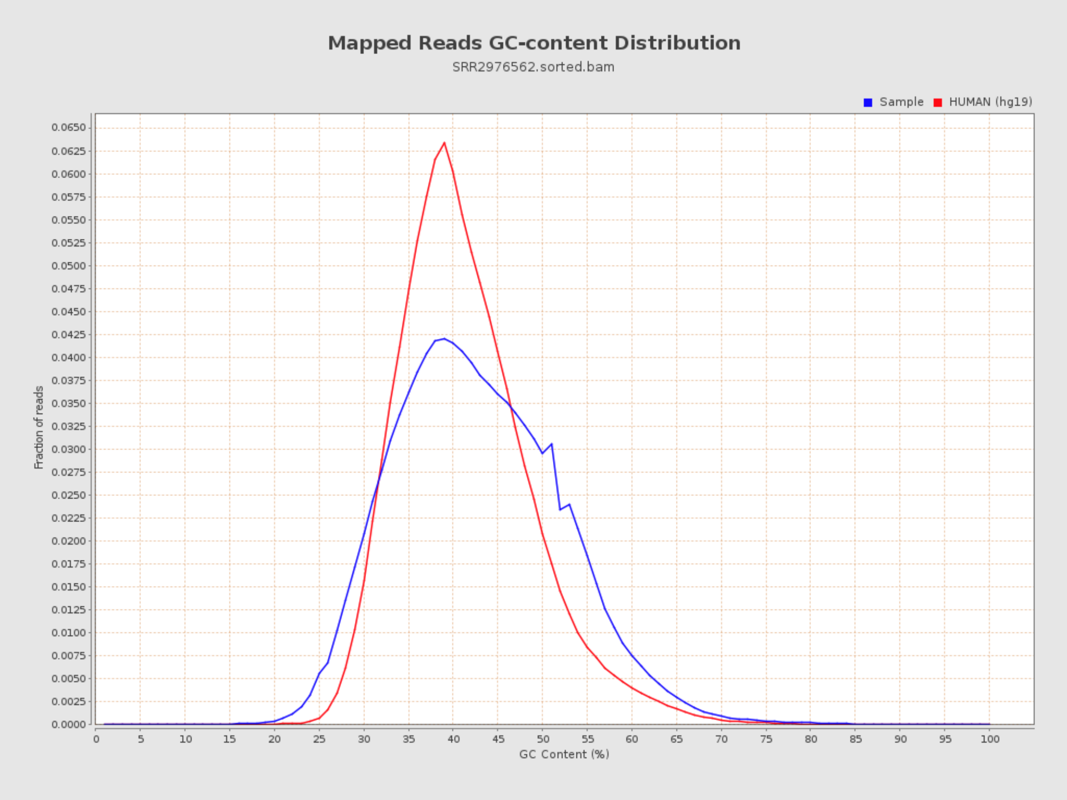
7. Results : Duplication Rate Histogram



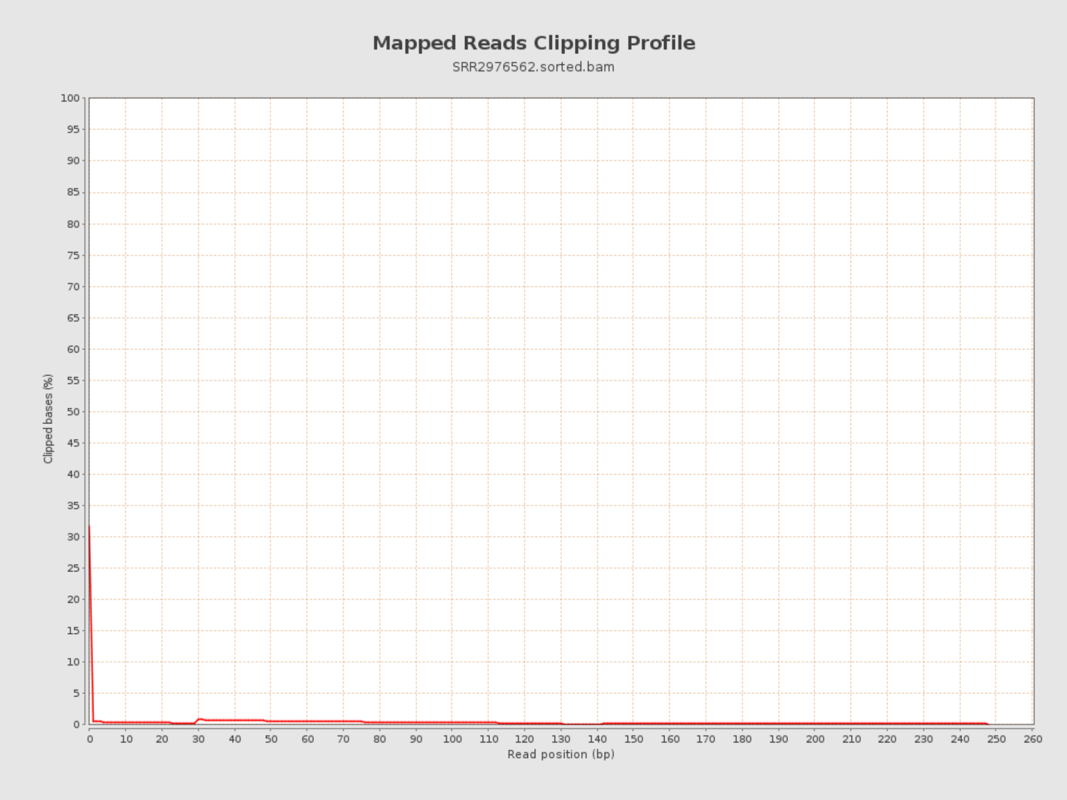
8. Results : Mapped Reads Nucleotide Content



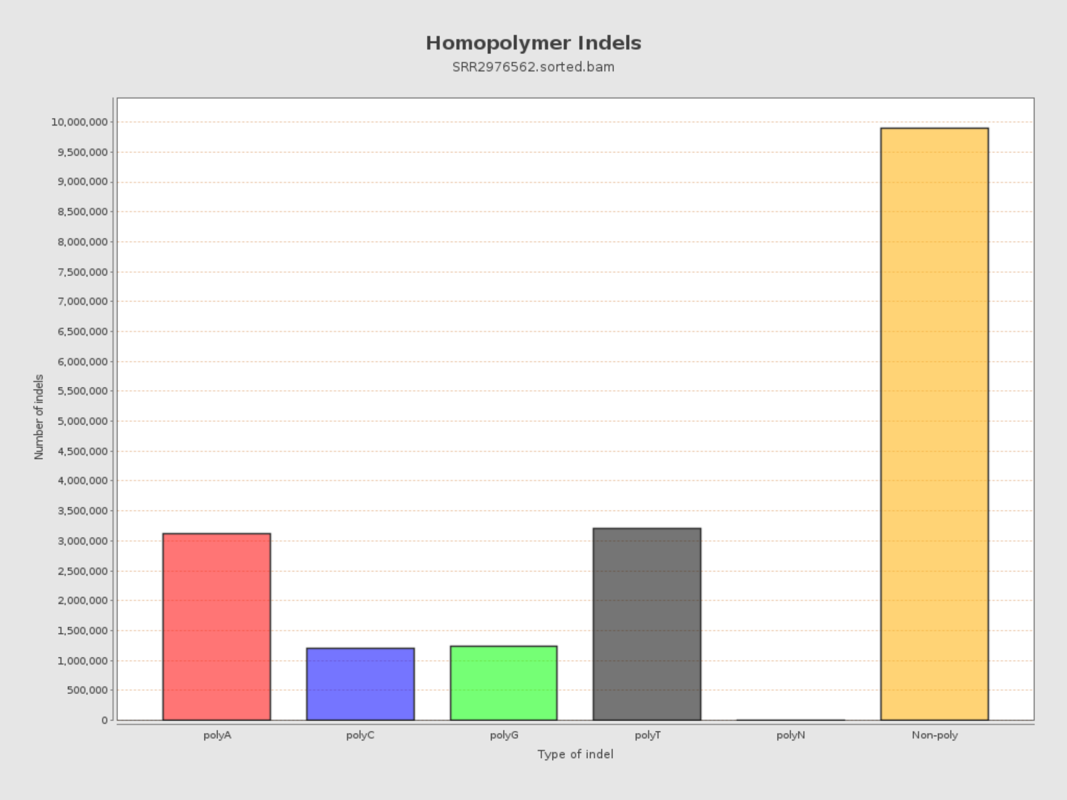
9. Results : Mapped Reads GC-content Distribution



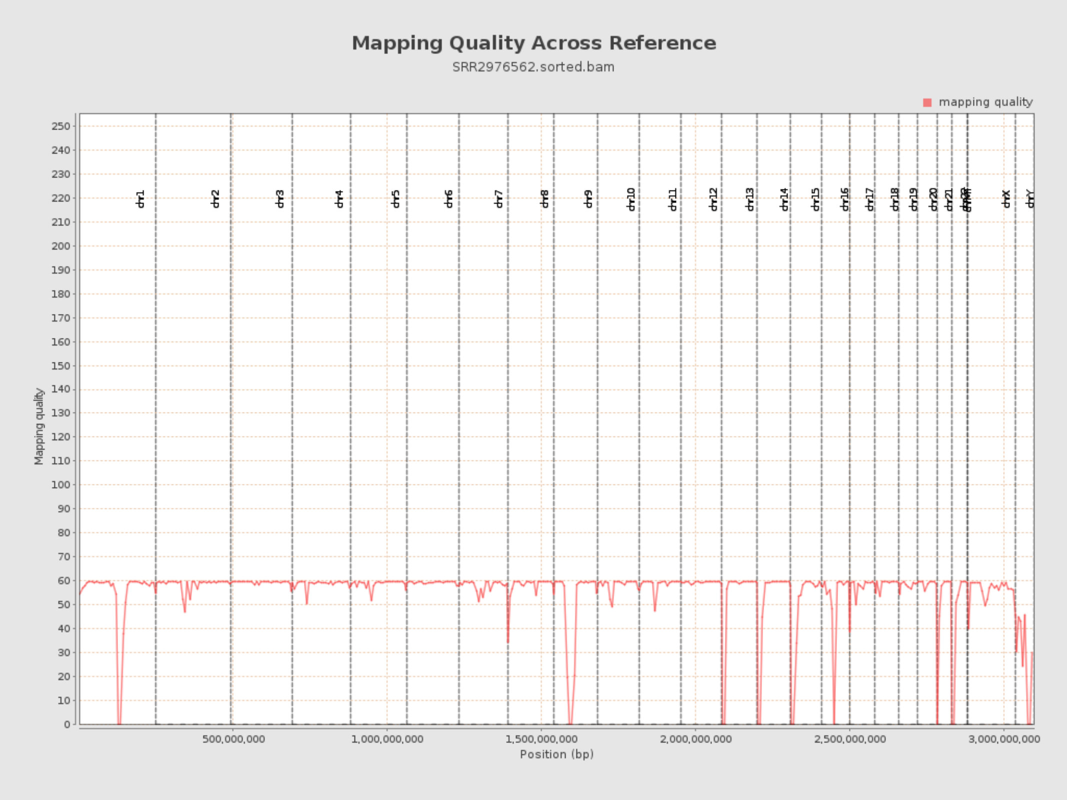
10. Results : Mapped Reads Clipping Profile



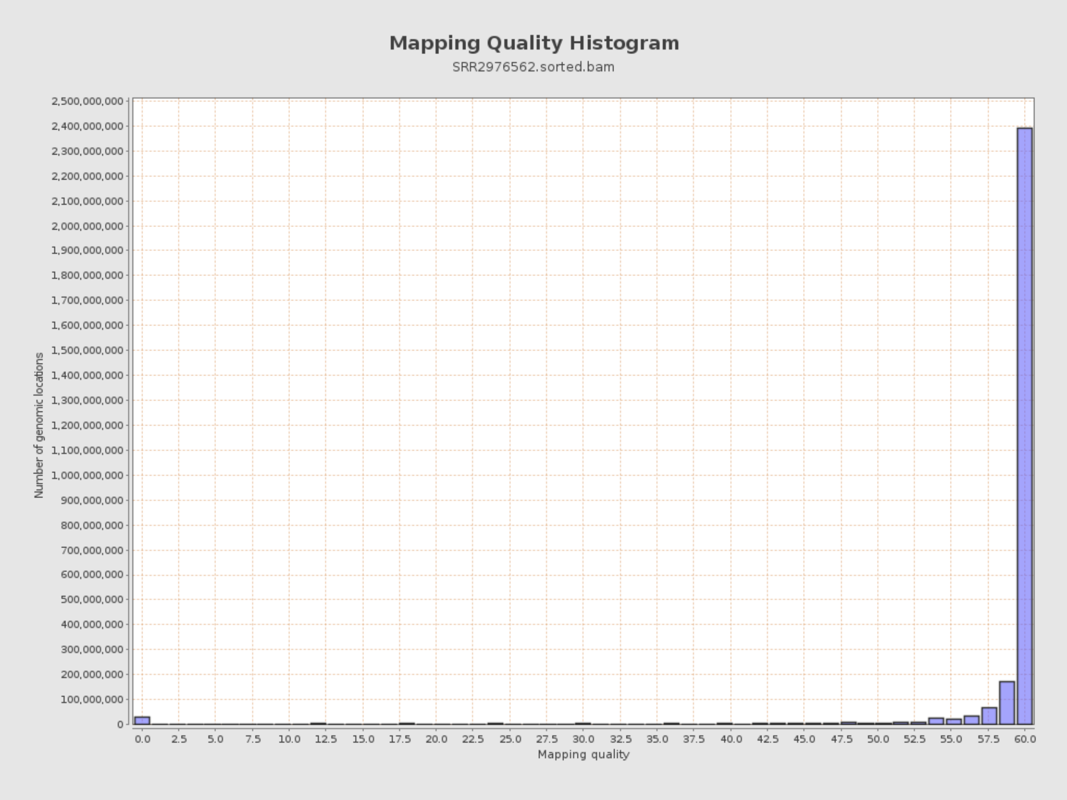
11. Results : Homopolymer Indels



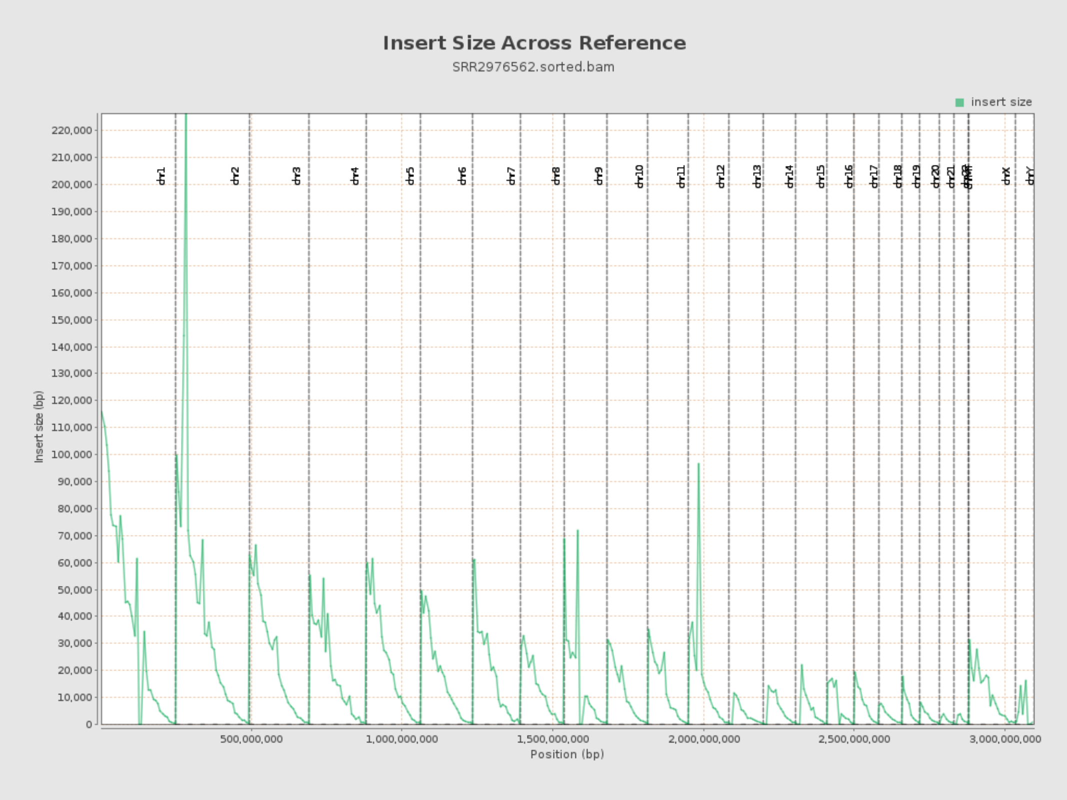
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram