Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/23 20:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976564.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_SRR2976564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976564_1.fastq.gz SRR2976564_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 23 20:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976564.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	686,734,540
Mapped reads	676,744,656 / 98.55%
Unmapped reads	9,989,884 / 1.45%
Mapped paired reads	676,744,656 / 98.55%
Mapped reads, first in pair	340,063,764 / 49.52%
Mapped reads, second in pair	336,680,892 / 49.03%
Mapped reads, both in pair	671,449,108 / 97.77%
Mapped reads, singletons	5,295,548 / 0.77%
Secondary alignments	0
Supplementary alignments	2,102,703 / 0.31%
Read min/max/mean length	20 / 150 / 142.97
Duplicated reads (estimated)	122,214,909 / 17.8%
Duplication rate	13.57%
Clipped reads	33,017,269 / 4.81%

2.2. ACGT Content

Number/percentage of A's	28,342,543,005 / 29.39%
Number/percentage of C's	19,794,080,951 / 20.52%
Number/percentage of T's	28,510,431,299 / 29.56%
Number/percentage of G's	19,791,270,795 / 20.52%
Number/percentage of N's	2,168,358 / 0%

GC Percentage	41.05%

2.3. Coverage

Mean	31.1637
Standard Deviation	323.248

2.4. Mapping Quality

Mean Mapping Quality	54.43

2.5. Insert size

Mean	23,125.31
Standard Deviation	1,435,959.51
P25/Median/P75	359 / 408 / 464

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	813,880,555
Insertions	10,366,590
Mapped reads with at least one insertion	1.44%
Deletions	11,836,874
Mapped reads with at least one deletion	1.67%
Homopolymer indels	42.24%

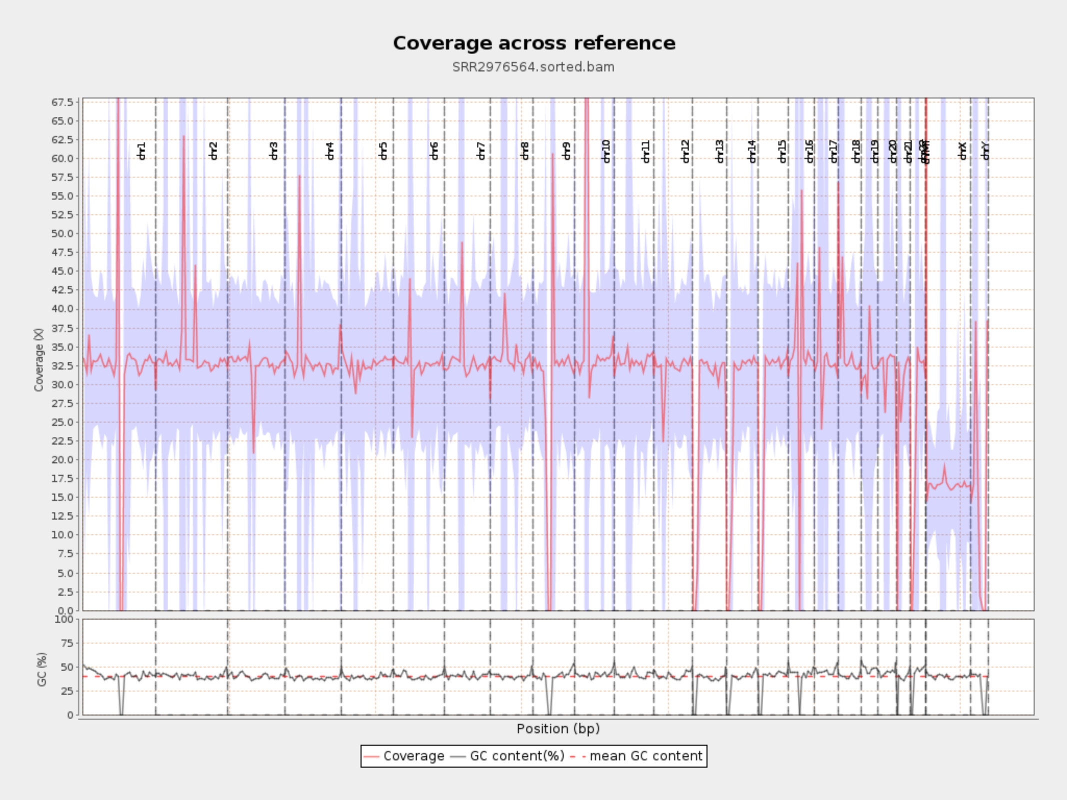
2.7. Chromosome stats

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

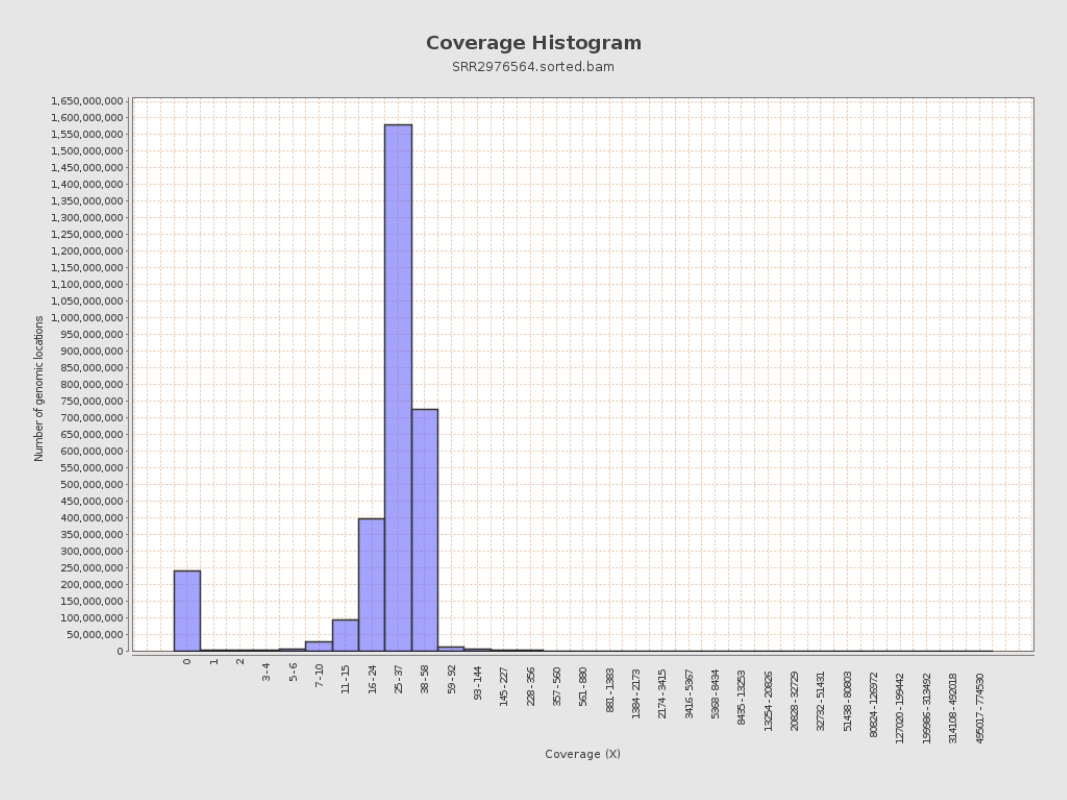
		bases	coverage	deviation
chr1	249250621	7974258714	31.9929	769.0888
chr2	243199373	8361015709	34.3793	192.4738
chr3	198022430	6440441150	32.5238	16.1139
chr4	191154276	6454289498	33.7648	222.6571
chr5	180915260	5897715641	32.5993	28.9265
chr6	171115067	5619313093	32.8394	134.9052
chr7	159138663	5322025524	33.4427	330.0293
chr8	146364022	4923788803	33.6407	228.9916
chr9	141213431	4272663763	30.2568	595.2598
chr10	135534747	5014324640	36.9966	564.0979
chr11	135006516	4464223395	33.0667	132.6213
chr12	133851895	4303726682	32.1529	18.0873
chr13	115169878	3099634636	26.9136	16.0715
chr14	107349540	2927019895	27.2663	22.2543
chr15	102531392	2750966294	26.8305	17.2268
chr16	90354753	3029639662	33.5305	189.1667
chr17	81195210	2712686101	33.4094	187.2894
chr18	78077248	2755687564	35.2944	450.1722
chr19	59128983	1912248831	32.3403	323.8796
chr20	63025520	2048813005	32.5077	53.163
chr21	48129895	1364183570	28.3438	90.1783
chr22	51304566	1186328107	23.1232	64.6372
chrMT	16571	106658821	6,436.4746	771.7684
chrX	155270560	2579780988	16.6147	37.3794

chrY	59373566	951973490	16.0336	248.2852

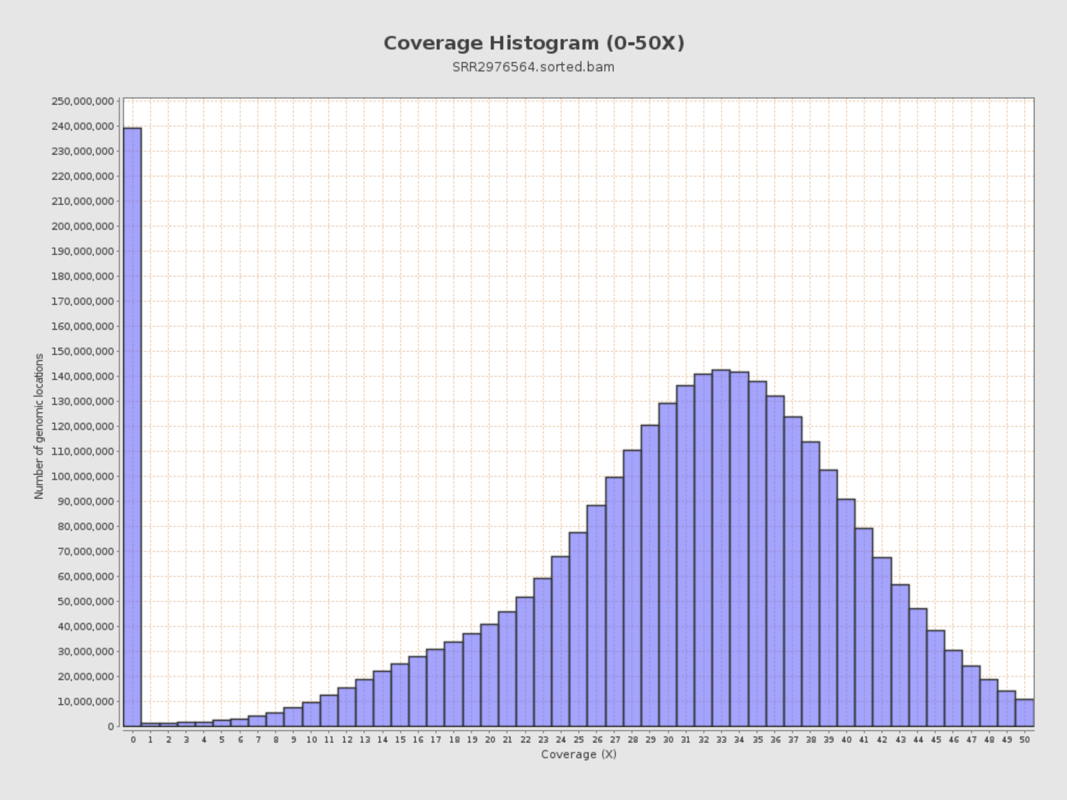
3. Results : Coverage across reference



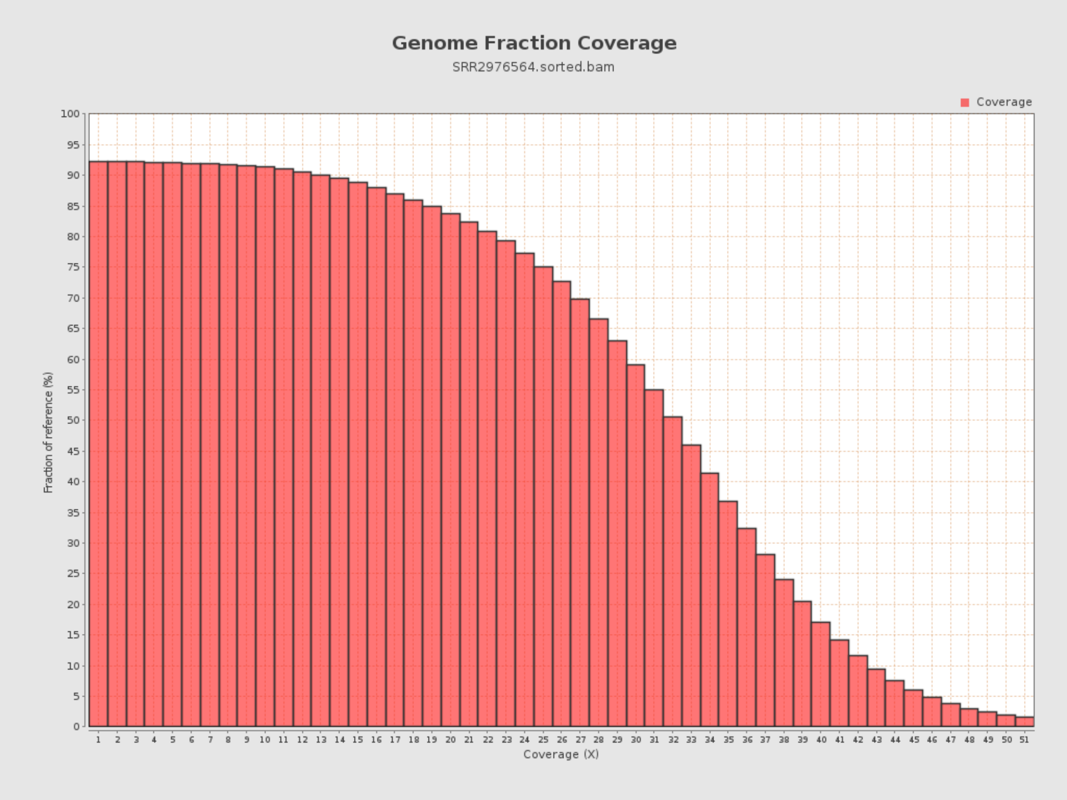
4. Results : Coverage Histogram



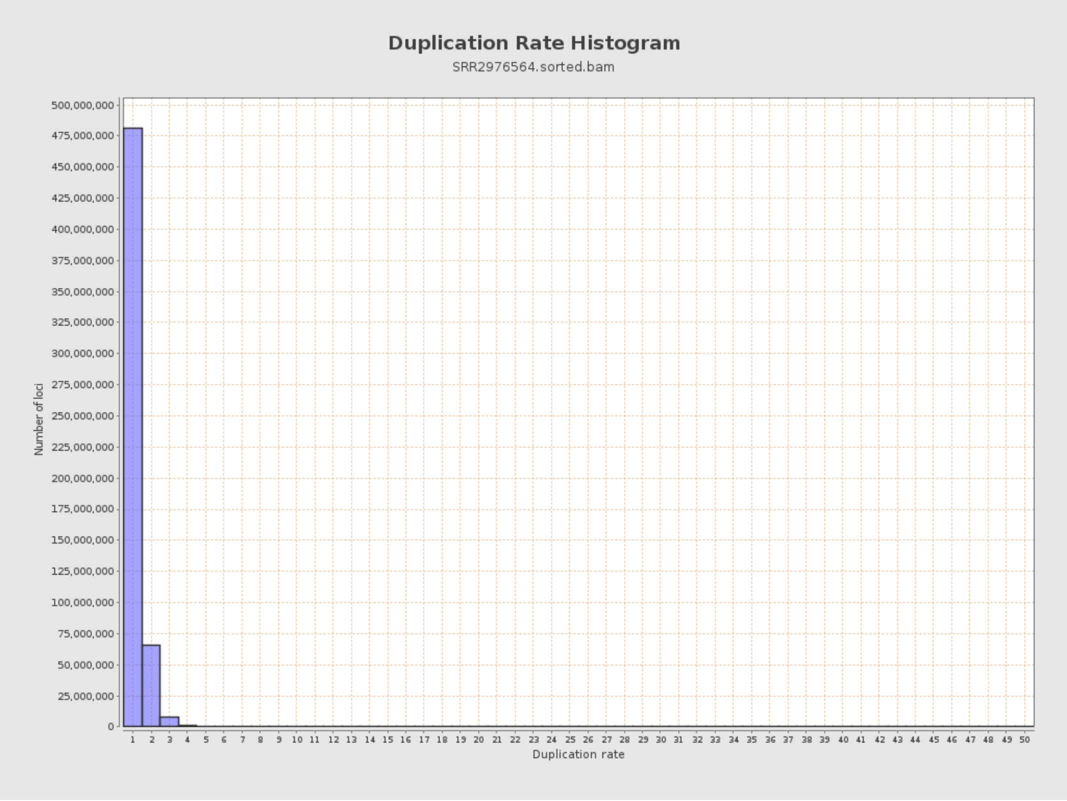
5. Results : Coverage Histogram (0-50X)



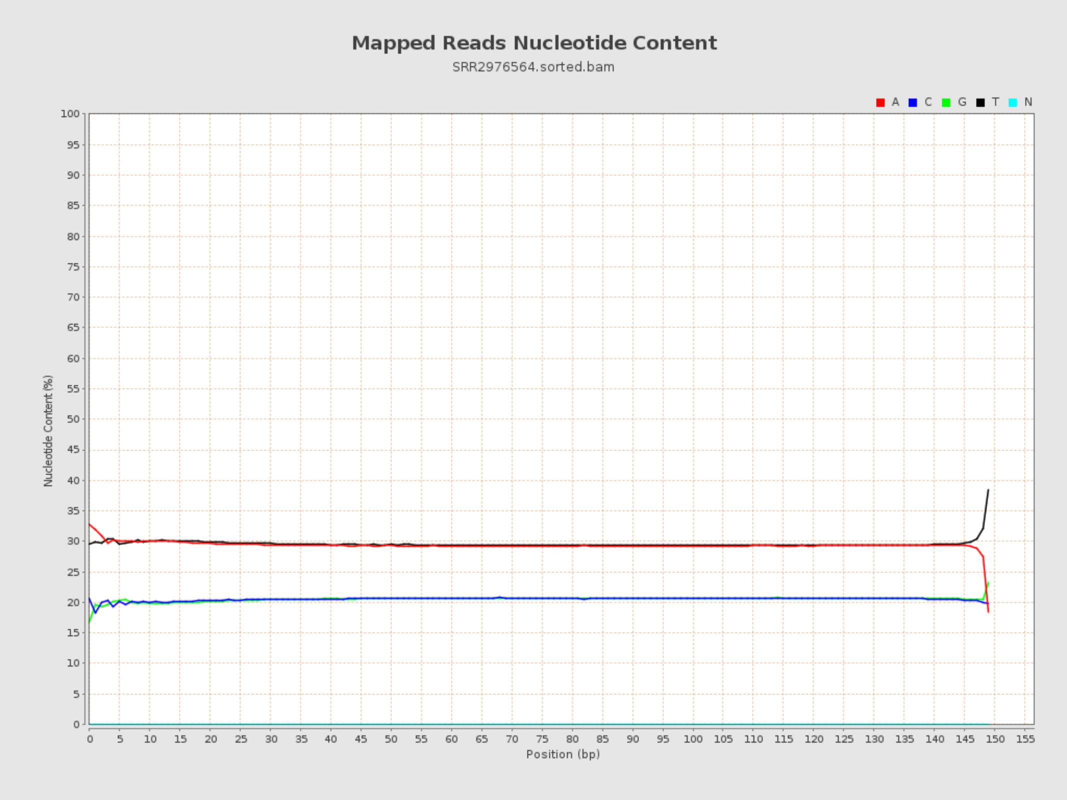
6. Results : Genome Fraction Coverage



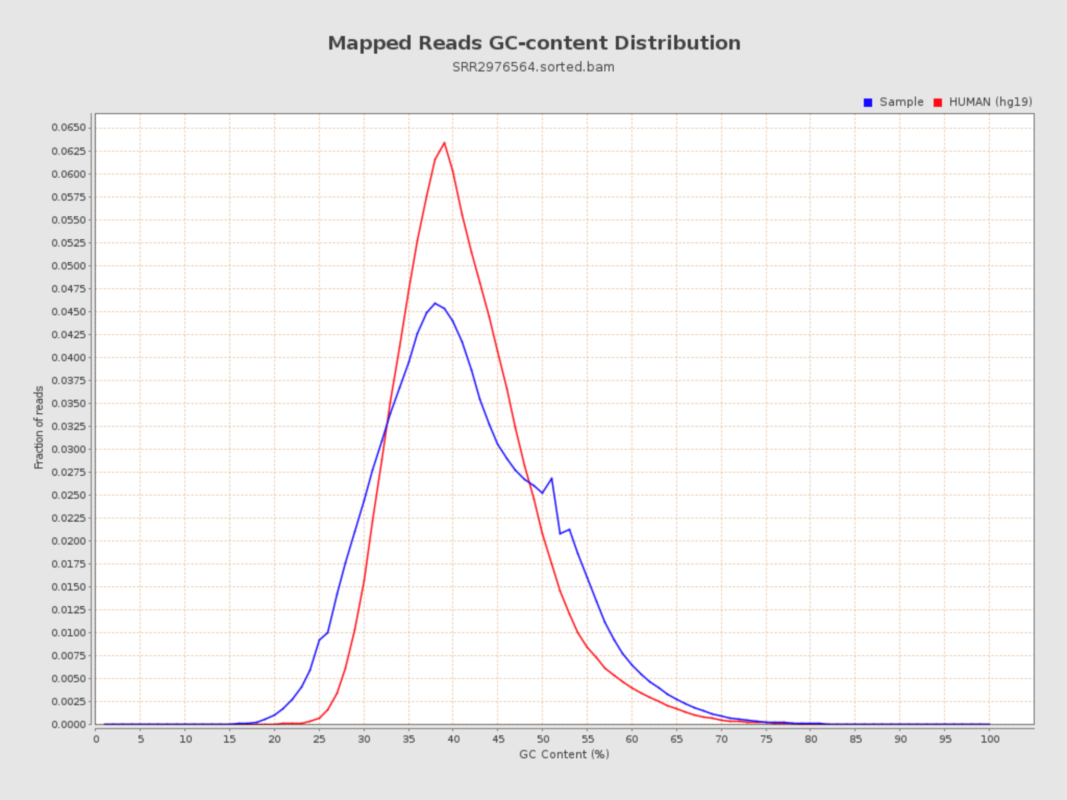
7. Results : Duplication Rate Histogram



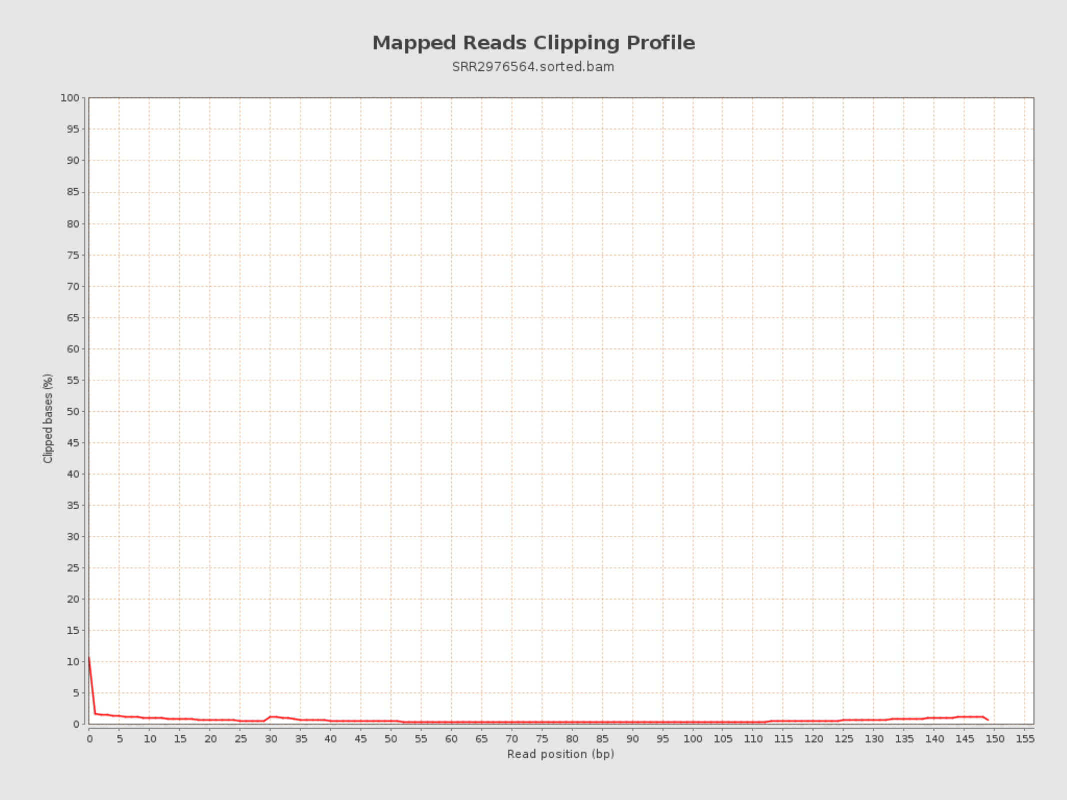
8. Results : Mapped Reads Nucleotide Content



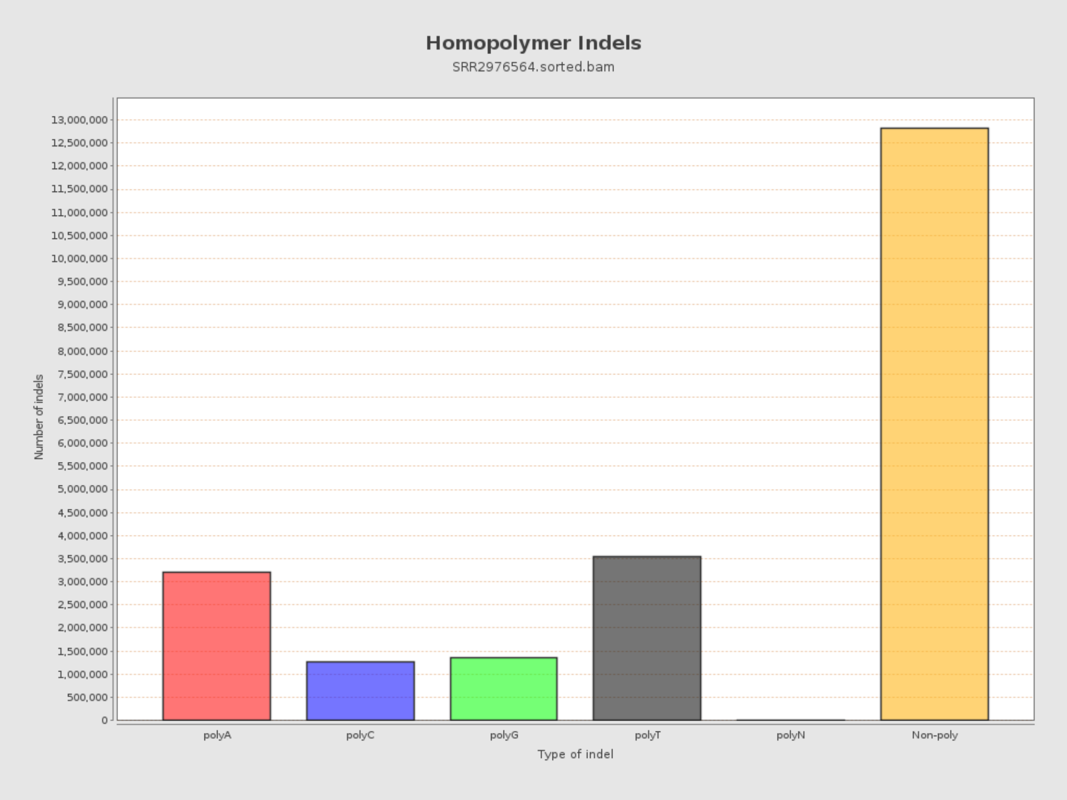
9. Results : Mapped Reads GC-content Distribution



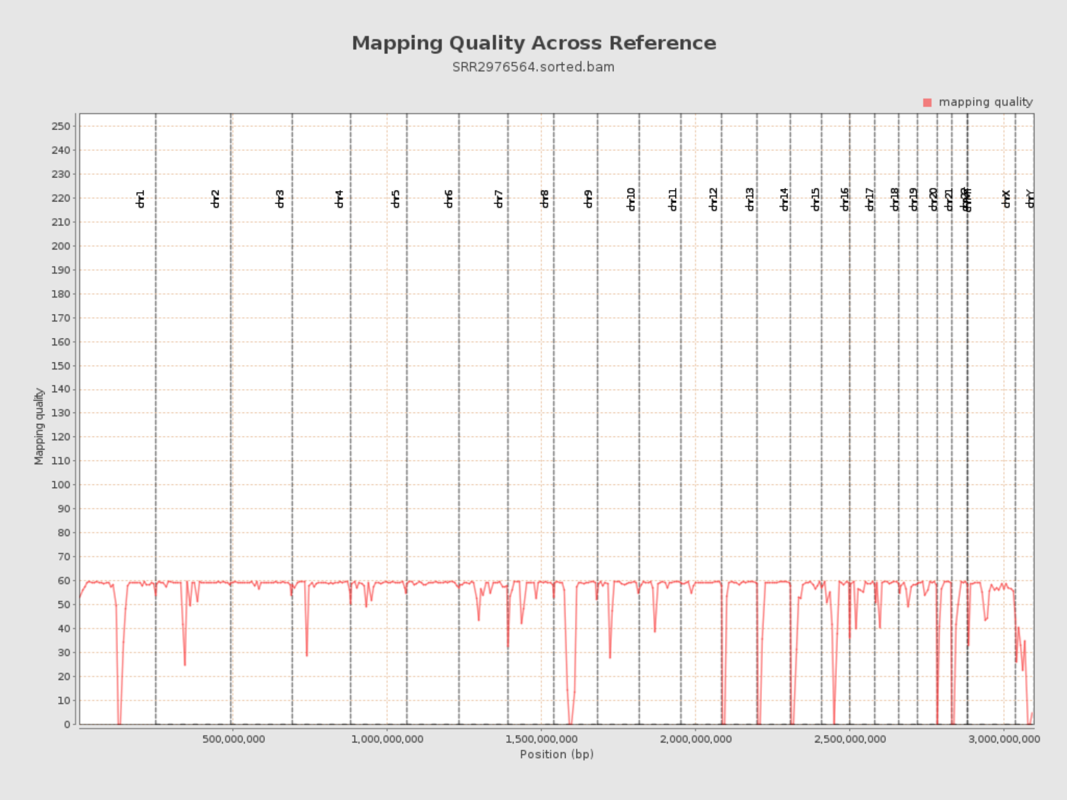
10. Results : Mapped Reads Clipping Profile



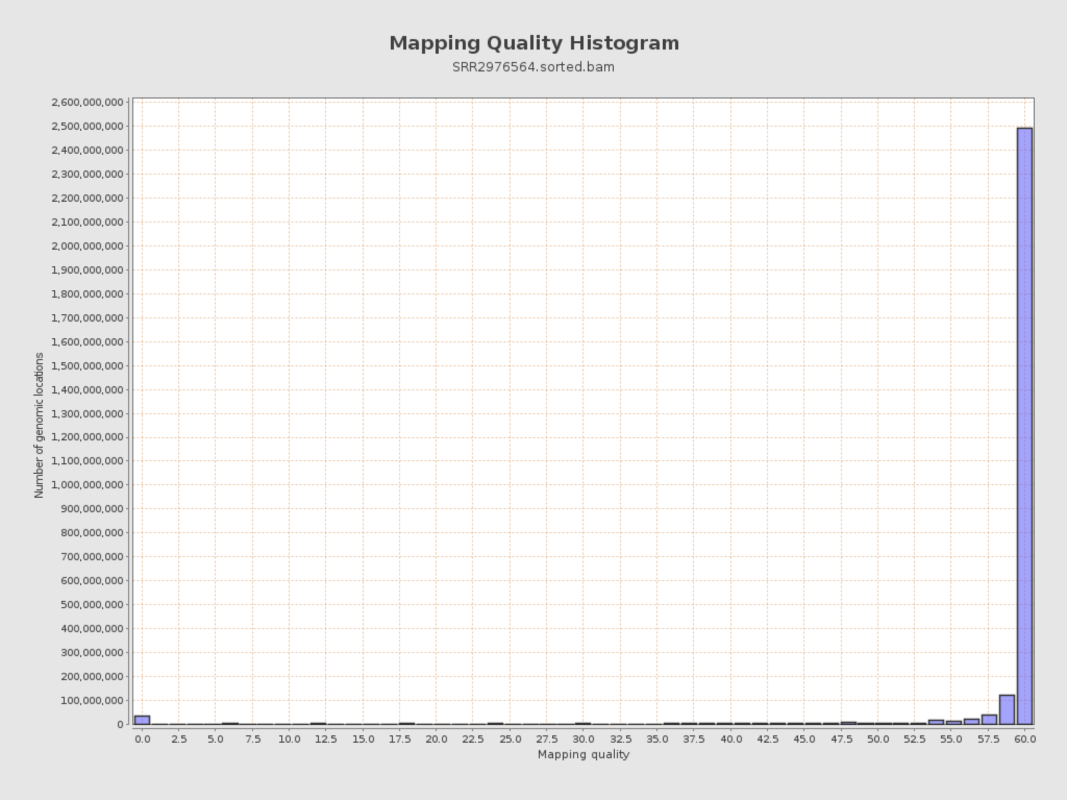
11. Results : Homopolymer Indels



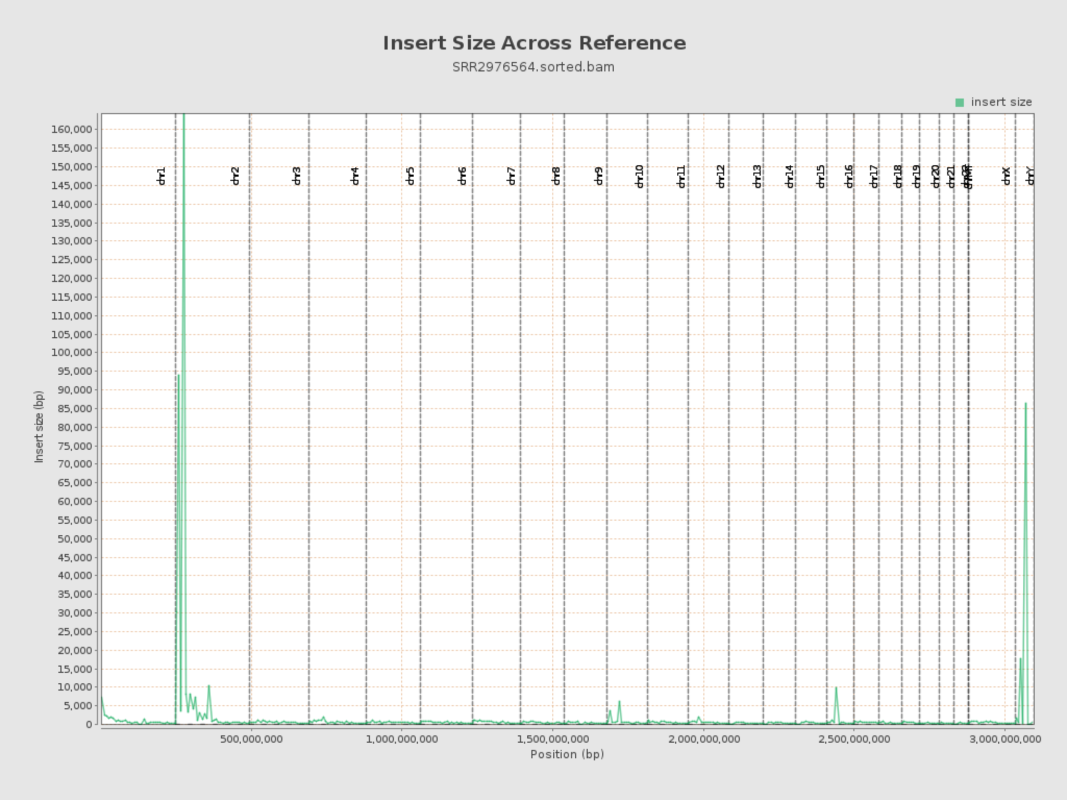
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram