Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/24 22:40:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976565.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_SRR2976565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976565_1.fastq.gz SRR2976565_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 24 22:40:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	779,966,256
Mapped reads	767,380,905 / 98.39%
Unmapped reads	12,585,351 / 1.61%
Mapped paired reads	767,380,905 / 98.39%
Mapped reads, first in pair	385,289,964 / 49.4%
Mapped reads, second in pair	382,090,941 / 48.99%
Mapped reads, both in pair	762,010,106 / 97.7%
Mapped reads, singletons	5,370,799 / 0.69%
Secondary alignments	0
Supplementary alignments	2,361,952 / 0.3%
Read min/max/mean length	20 / 150 / 143.33
Duplicated reads (estimated)	148,781,791 / 19.08%
Duplication rate	15.07%
Clipped reads	36,338,991 / 4.66%

2.2. ACGT Content

Number/percentage of A's	32,198,518,958 / 29.34%
Number/percentage of C's	22,566,679,125 / 20.56%
Number/percentage of T's	32,367,247,009 / 29.49%
Number/percentage of G's	22,603,747,645 / 20.6%
Number/percentage of N's	2,508,555 / 0%

GC Percentage	41.16%

2.3. Coverage

Mean	35.4609
Standard Deviation	355.4756

2.4. Mapping Quality

Mean Mapping Quality	54.44

2.5. Insert size

Mean	23,087.14
Standard Deviation	1,437,641.83
P25/Median/P75	346 / 394 / 451

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	879,005,084
Insertions	11,711,065
Mapped reads with at least one insertion	1.43%
Deletions	13,378,507
Mapped reads with at least one deletion	1.66%
Homopolymer indels	42.27%

2.7. Chromosome stats

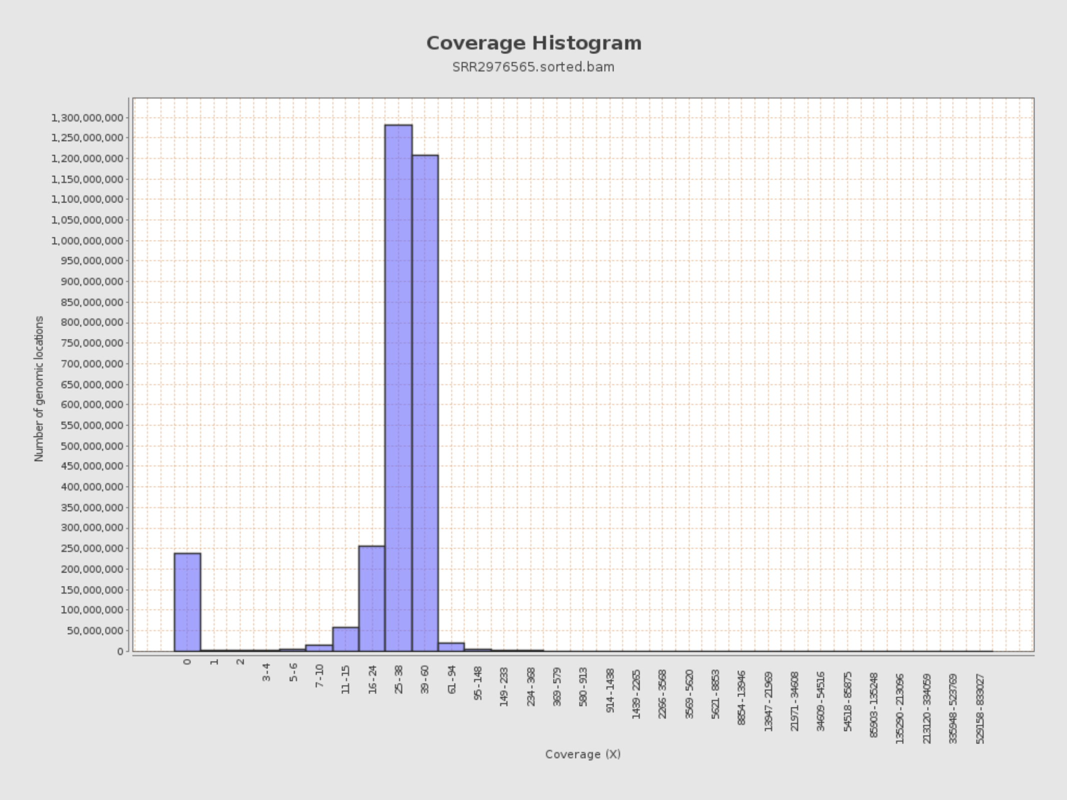
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	**coverage**	**deviation**
chr1	249250621	9085140218	36.4498	832.467
chr2	243199373	9507661118	39.0941	211.8845
chr3	198022430	7324820576	36.9899	18.4757
chr4	191154276	7303162963	38.2056	248.6707
chr5	180915260	6690821859	36.9832	32.7877
chr6	171115067	6382047723	37.2968	148.8603
chr7	159138663	6038592111	37.9455	364.2651
chr8	146364022	5595645324	38.231	267.8628
chr9	141213431	4857593125	34.3989	662.9001
chr10	135534747	5688667966	41.972	624.8409
chr11	135006516	5083069100	37.6505	144.2842
chr12	133851895	4901902651	36.6218	21.1535
chr13	115169878	3516105739	30.5297	18.1282
chr14	107349540	3336462152	31.0804	25.1702
chr15	102531392	3139495587	30.6198	19.5129
chr16	90354753	3456610238	38.256	208.3732
chr17	81195210	3109770798	38.2999	202.5969
chr18	78077248	3139354738	40.2083	506.0217
chr19	59128983	2201184866	37.2268	356.7685
chr20	63025520	2346800409	37.2357	60.4515
chr21	48129895	1550941492	32.2241	101.0761
chr22	51304566	1365747587	26.6204	66.6296
chrMT	16571	156788597	9,461.6256	1,077.7211
chrX	155270560	2929517238	18.8672	41.2824

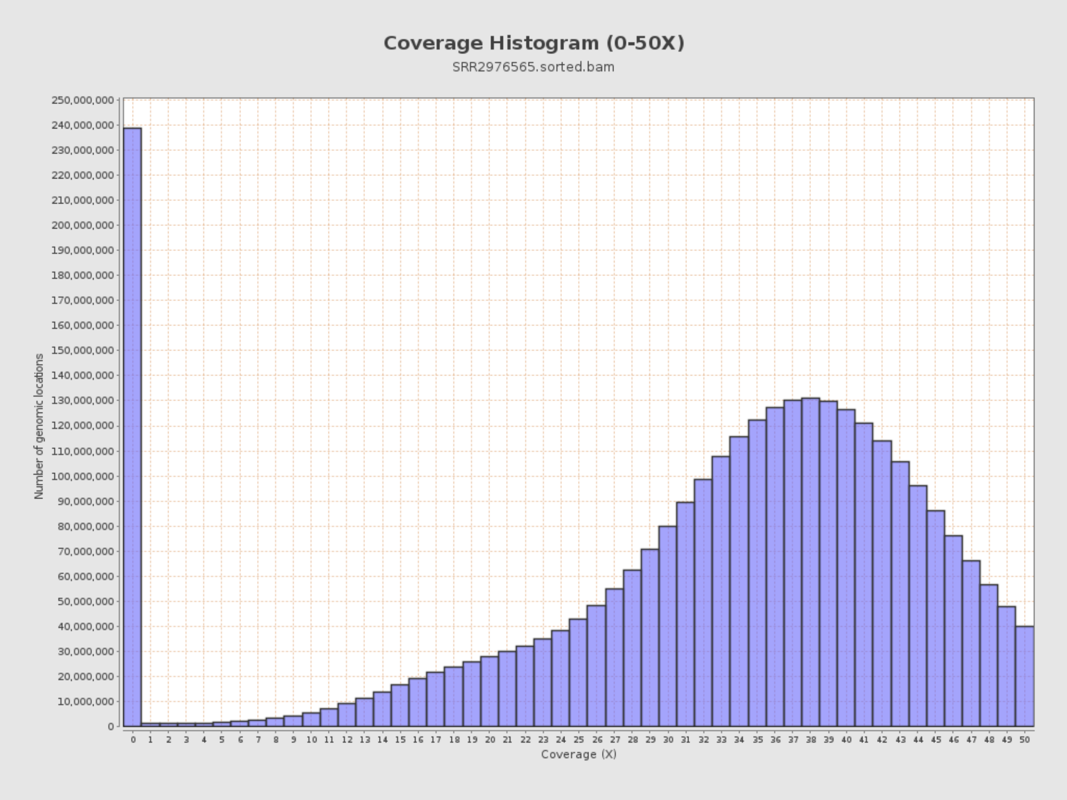
chrY	59373566	1068172888	17.9907	274.7486

3. Results : Coverage across reference

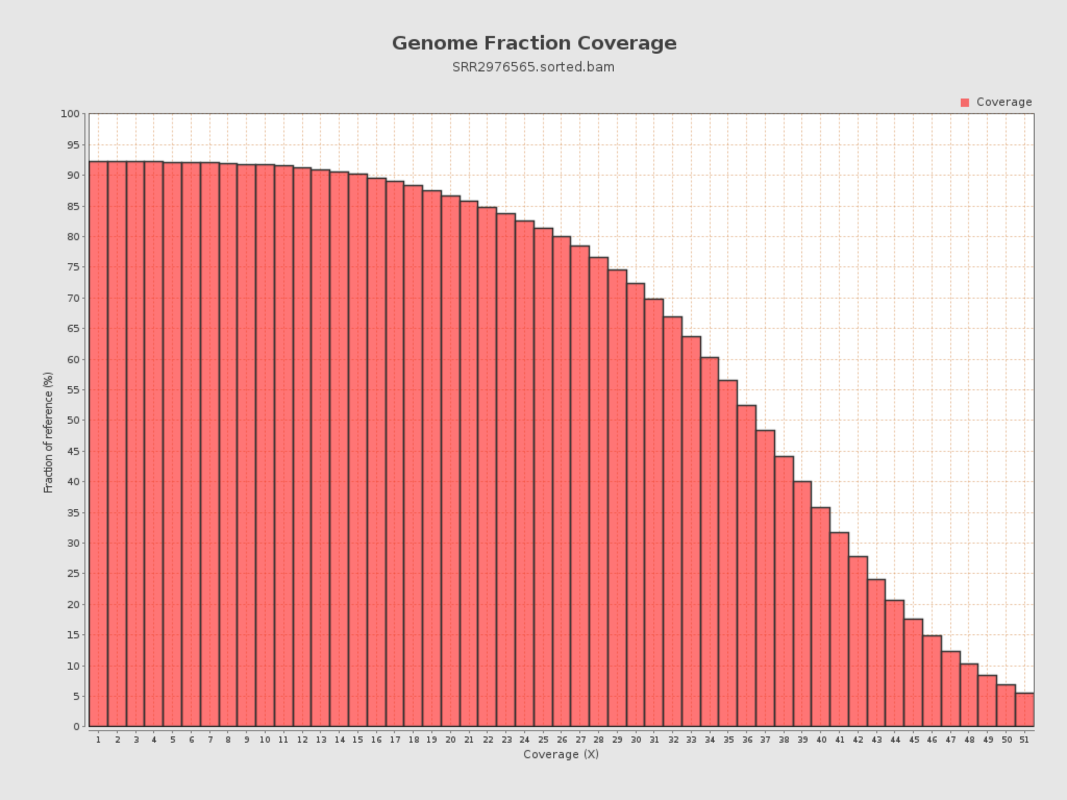
4. Results : Coverage Histogram



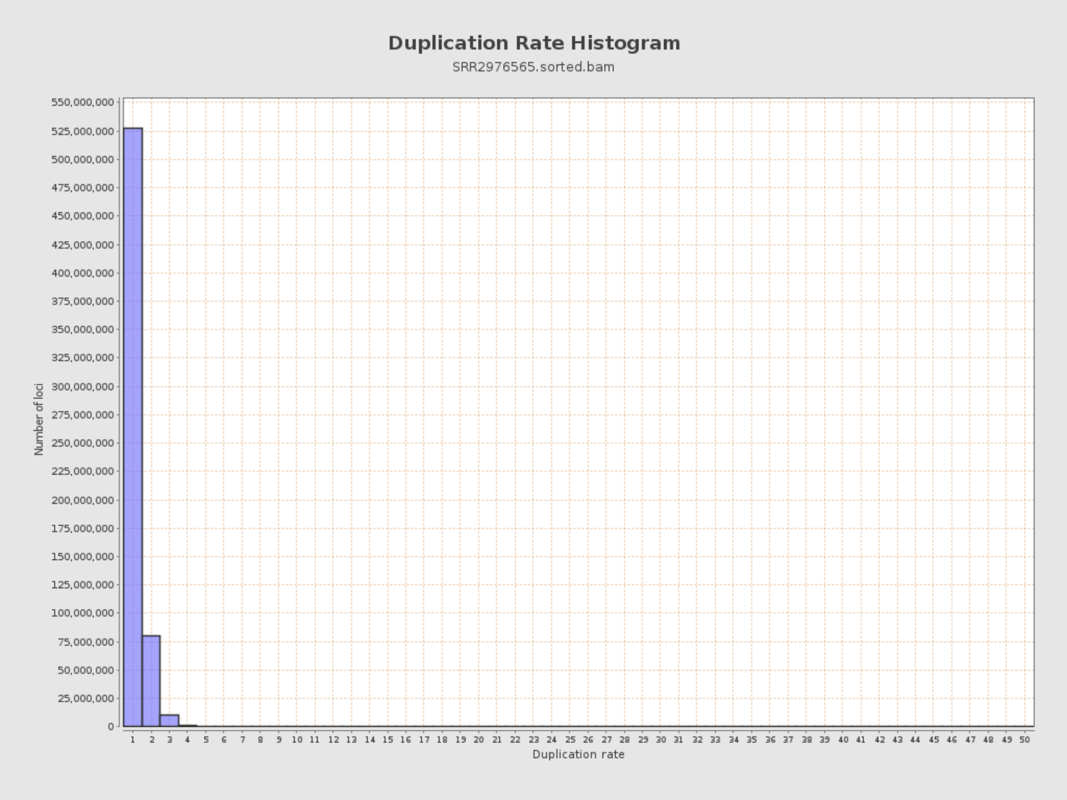
5. Results : Coverage Histogram (0-50X)



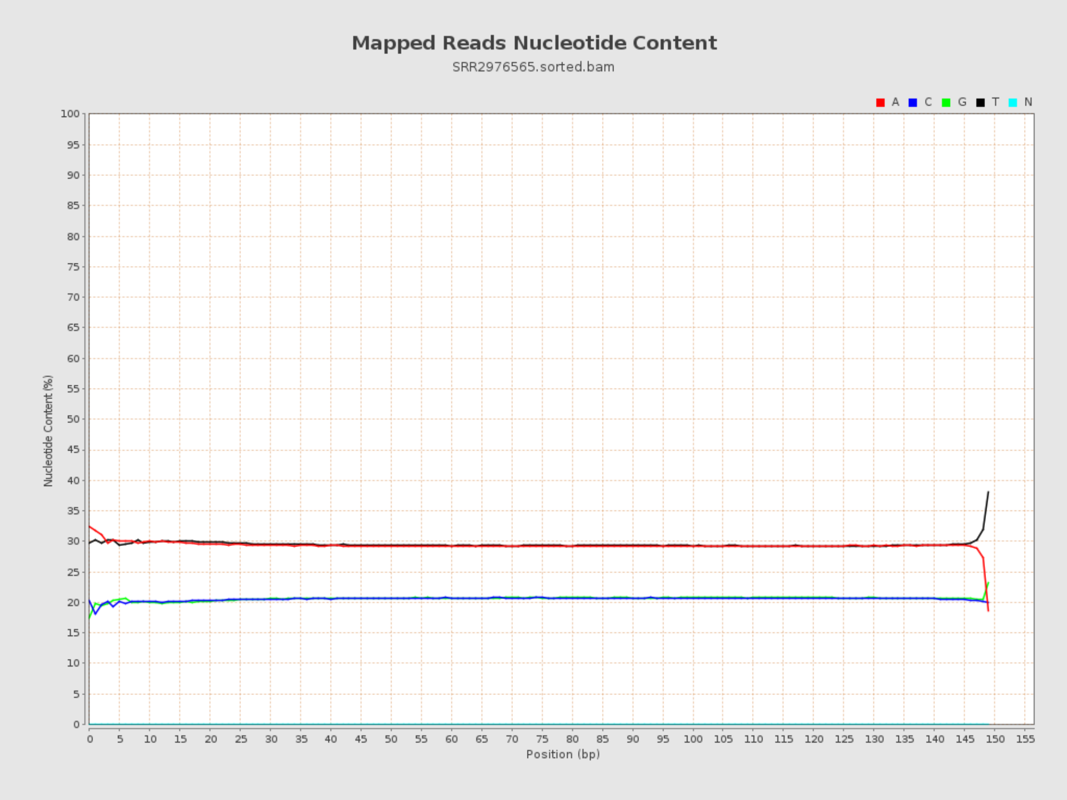
6. Results : Genome Fraction Coverage



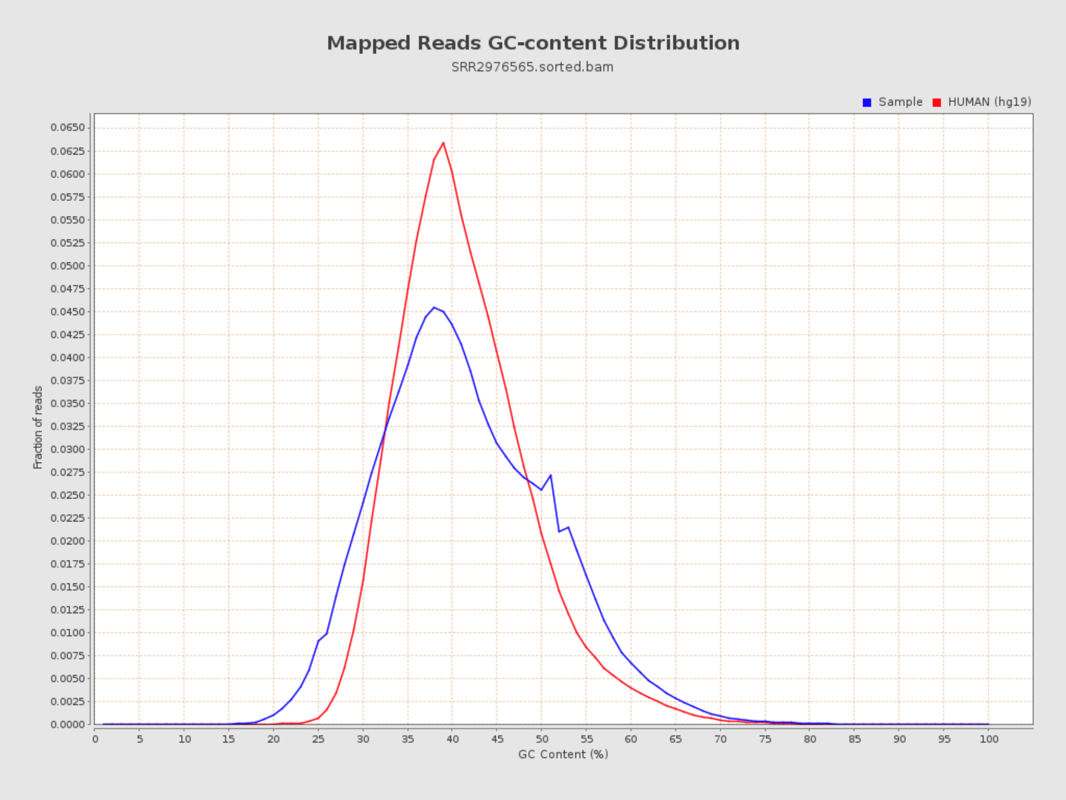
7. Results : Duplication Rate Histogram



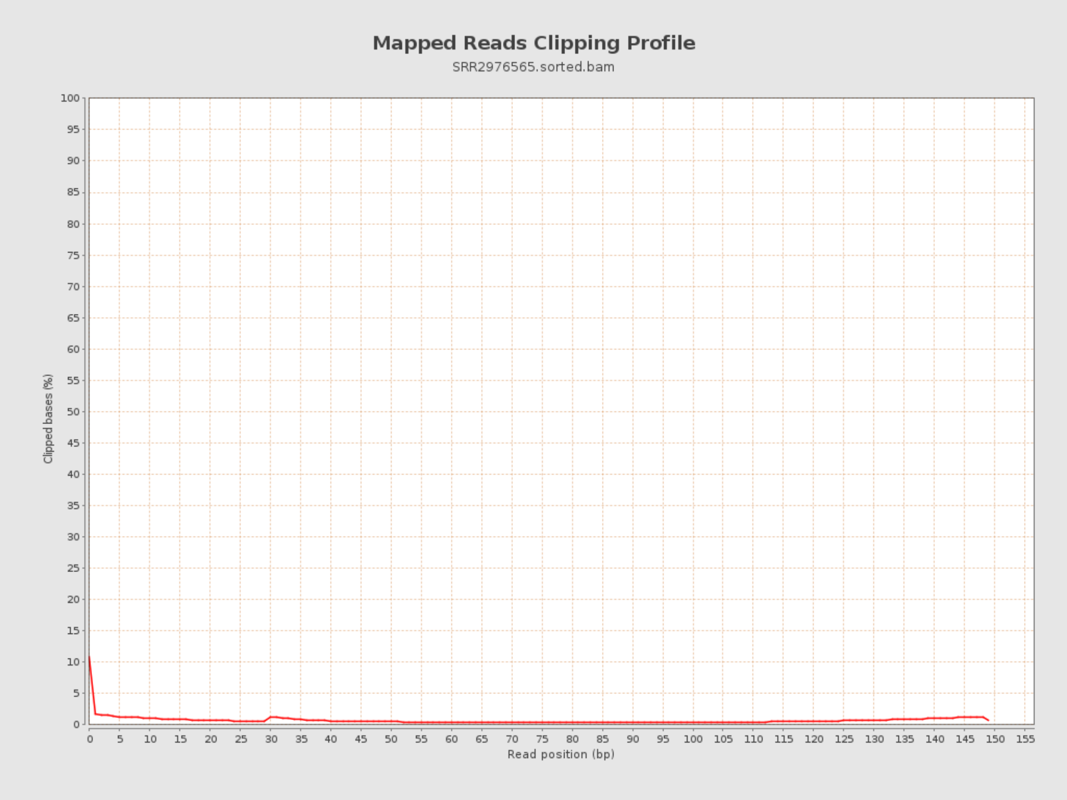
8. Results : Mapped Reads Nucleotide Content



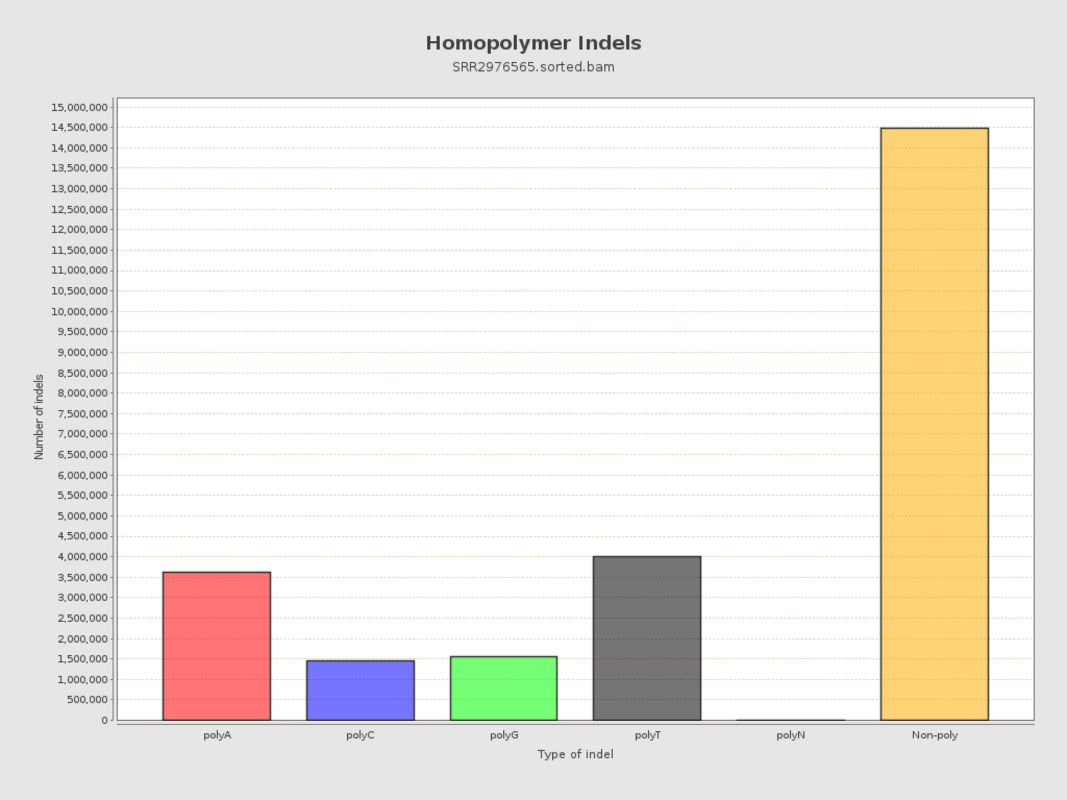
9. Results : Mapped Reads GC-content Distribution



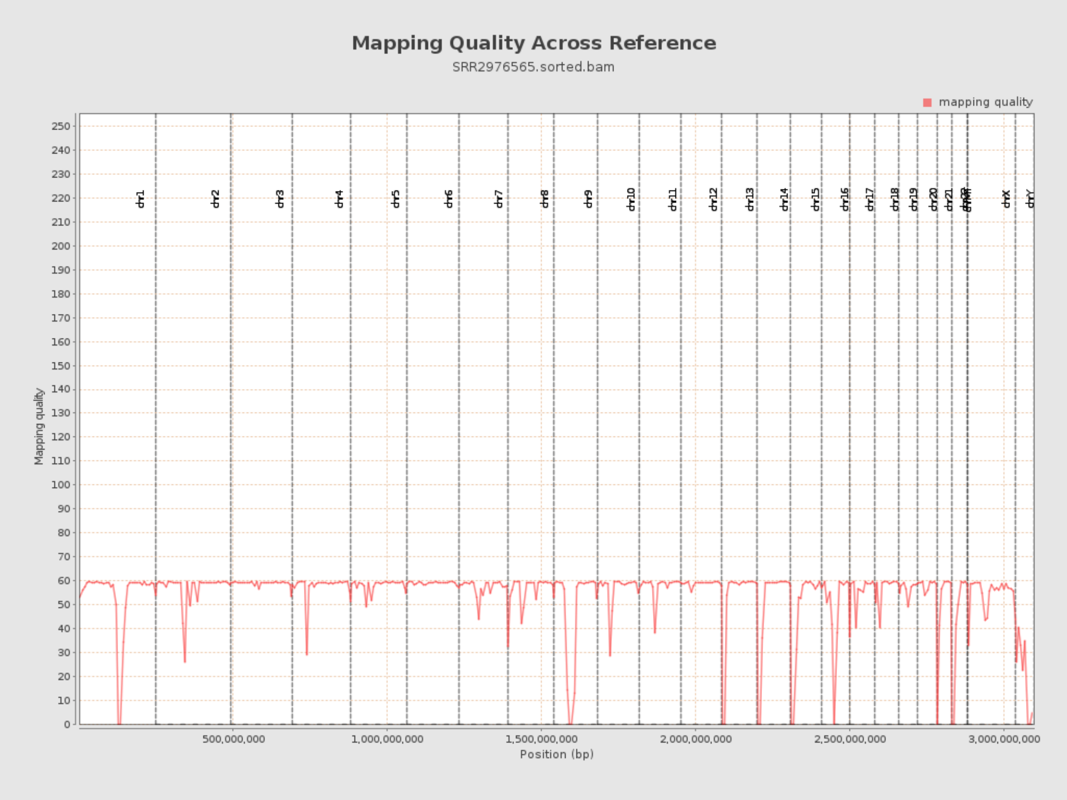
10. Results : Mapped Reads Clipping Profile



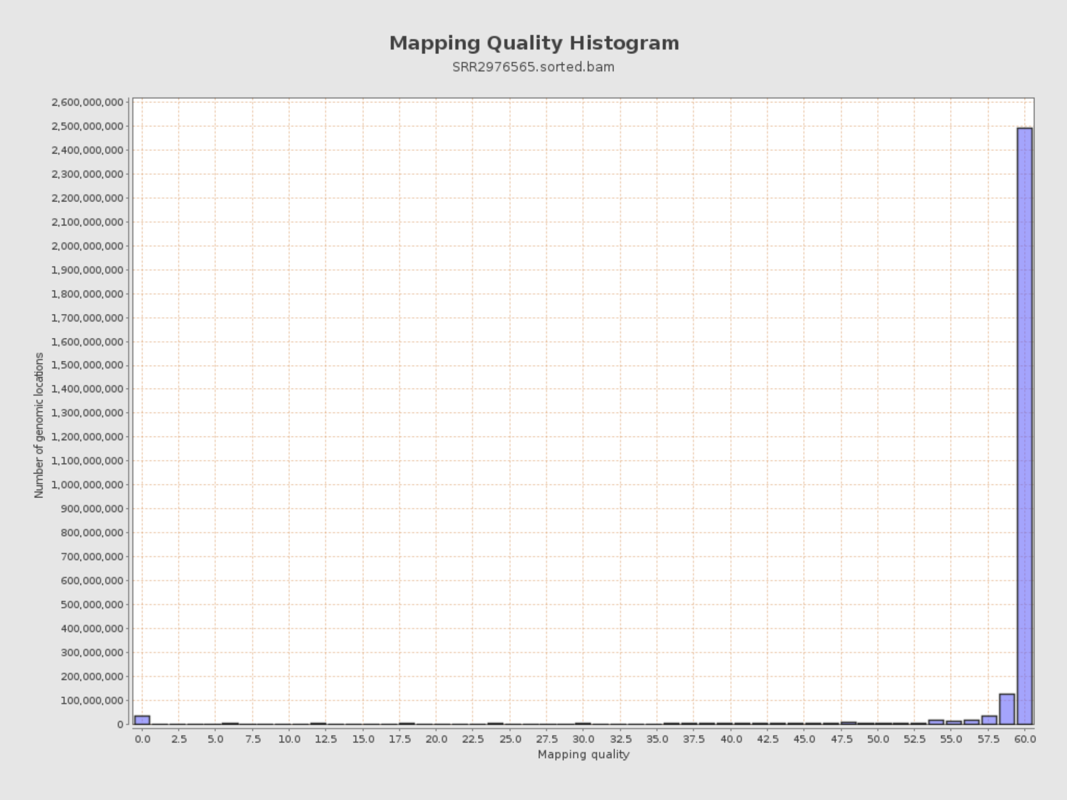
11. Results : Homopolymer Indels



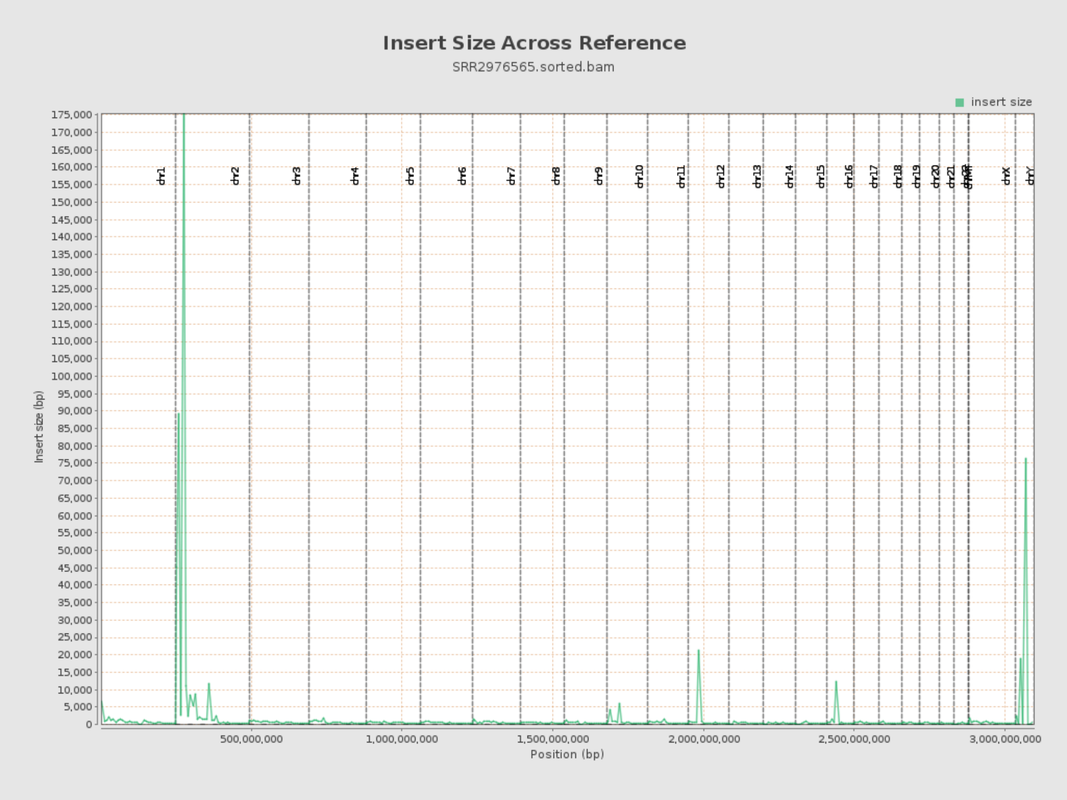
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram