Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:41:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714169.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_ERR9714169 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:41:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	887,840
Mapped reads	764,490 / 86.11%
Unmapped reads	123,350 / 13.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,344 / 4.54%
Read min/max/mean length	30 / 151 / 138.66
Duplicated reads (estimated)	753,517 / 84.87%
Duplication rate	39.31%
Clipped reads	721,252 / 81.24%

2.2. ACGT Content

Number/percentage of A's	30,229,053 / 30.82%
Number/percentage of C's	18,744,001 / 19.11%
Number/percentage of T's	27,603,249 / 28.14%
Number/percentage of G's	21,509,262 / 21.93%
Number/percentage of N's	712 / 0%
GC Percentage	41.04%

2.3. Coverage

Mean	0.0322

Standard Deviation	20.0175

2.4. Mapping Quality

Mean Mapping Quality	40.86

2.5. Mismatches and indels

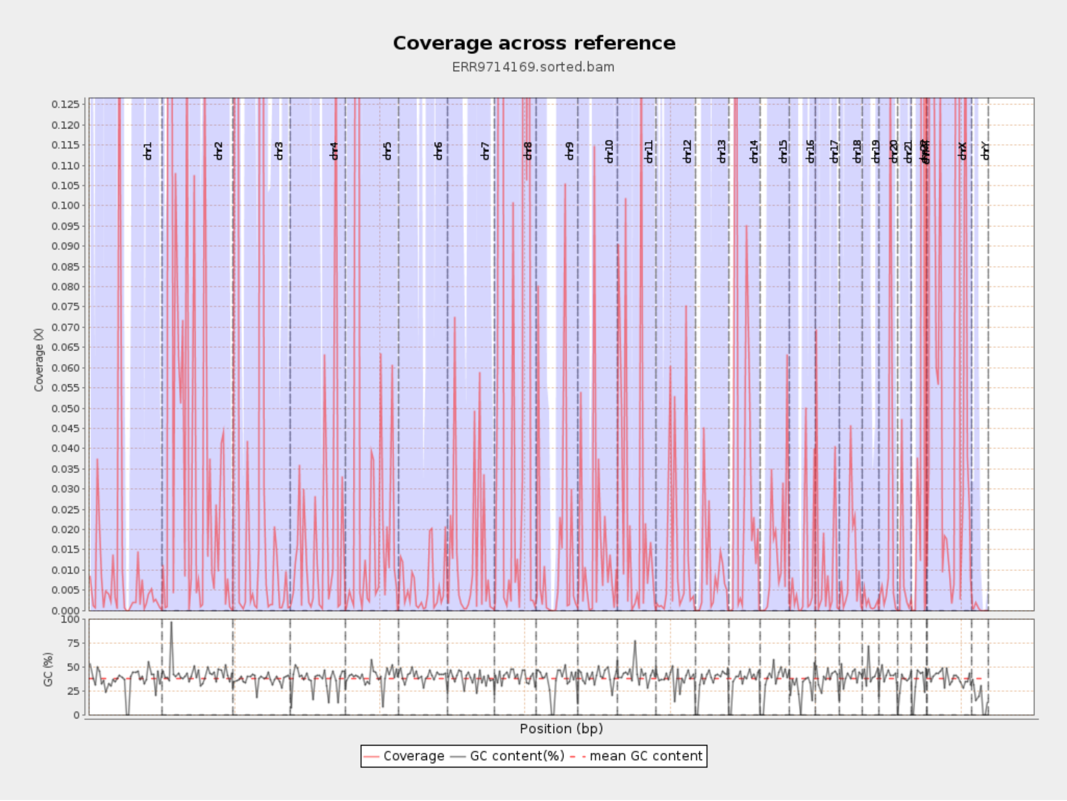
General error rate	3.71%
Mismatches	3,451,727
Insertions	83,452
Mapped reads with at least one insertion	10%
Deletions	299,816
Mapped reads with at least one deletion	37.79%
Homopolymer indels	26.37%

2.6. Chromosome stats

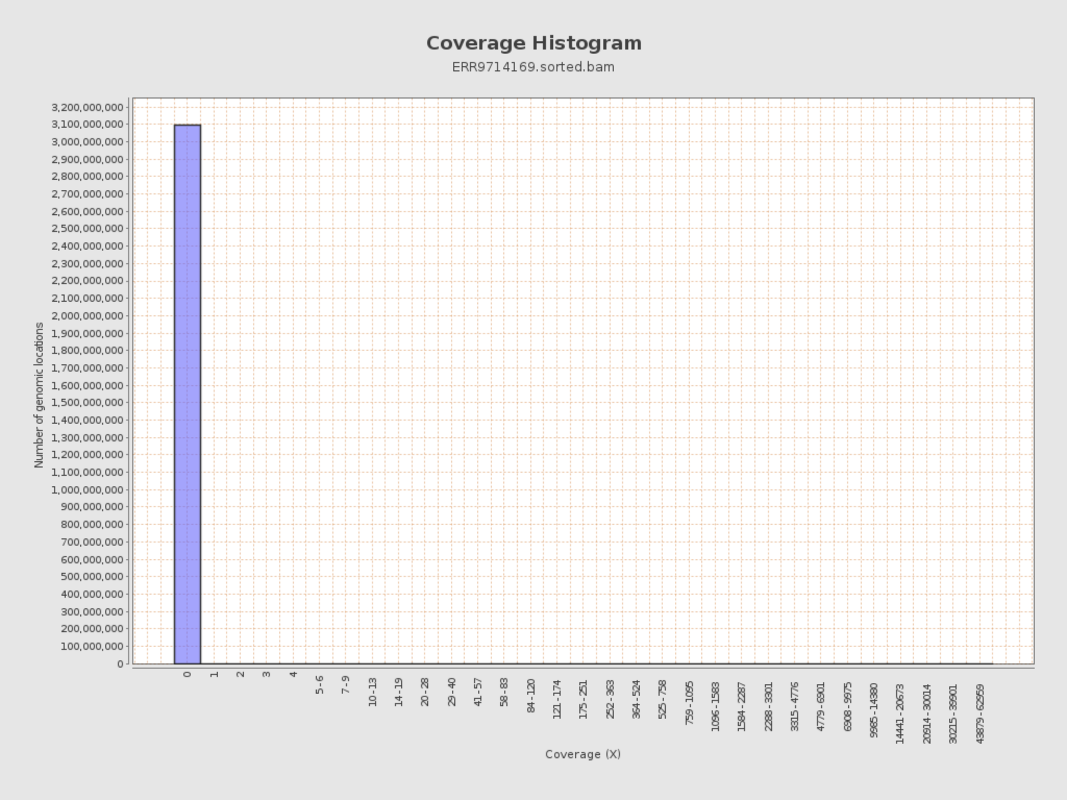
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2502161	0.01	6.0916
chr2	243199373	13809900	0.0568	26.1982
chr3	198022430	8474177	0.0428	25.8609
chr4	191154276	3594781	0.0188	7.1899
chr5	180915260	6712876	0.0371	17.8562
chr6	171115067	1068111	0.0062	1.4626
chr7	159138663	2321504	0.0146	3.6023

chr8	146364022	22303763	0.1524	69.0753
chr9	141213431	2213030	0.0157	7.0227
chr10	135534747	2431829	0.0179	4.6495
chr11	135006516	3746607	0.0278	8.8627
chr12	133851895	2063943	0.0154	5.1123
chr13	115169878	1048960	0.0091	2.4101
chr14	107349540	3620940	0.0337	12.2198
chr15	102531392	1523999	0.0149	3.2572
chr16	90354753	861730	0.0095	3.576
chr17	81195210	1100071	0.0135	3.8831
chr18	78077248	914165	0.0117	2.1396
chr19	59128983	109626	0.0019	0.3723
chr20	63025520	1232417	0.0196	10.375
chr21	48129895	446757	0.0093	2.659
chr22	51304566	3663375	0.0714	23.6124
chrMT	16571	32363	1.953	13.933
chrX	155270560	13926150	0.0897	23.1509
chrY	59373566	24121	0.0004	0.1487

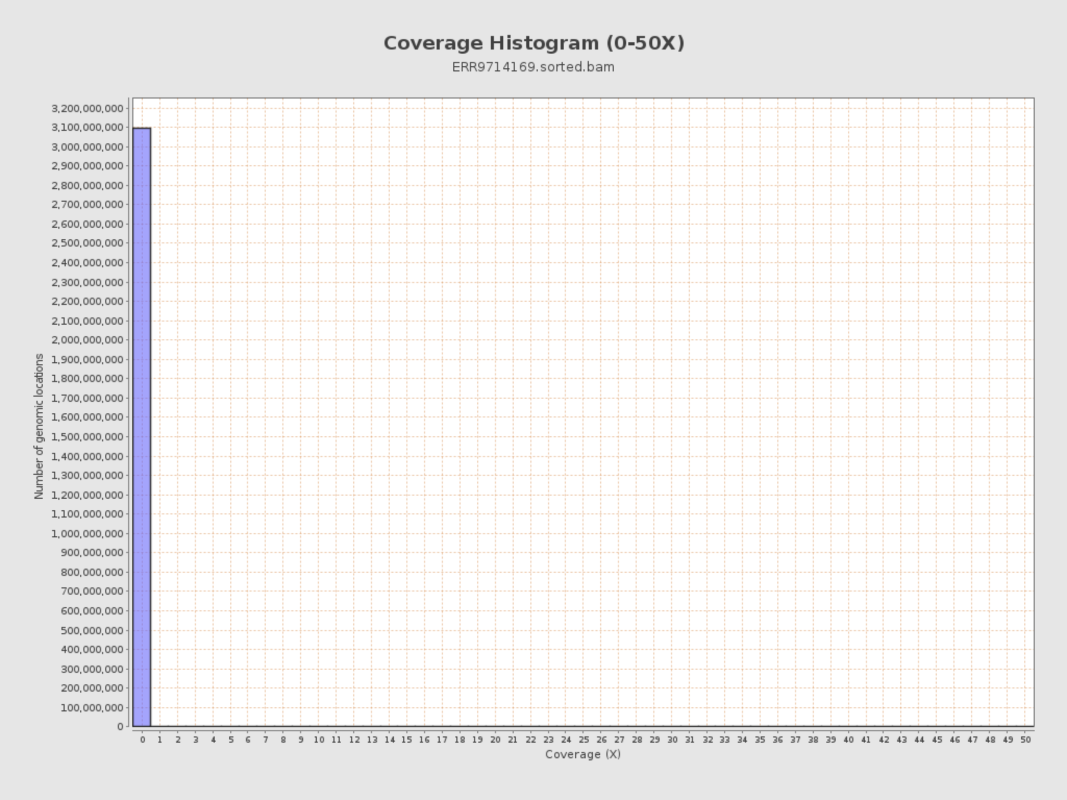
3. Results : Coverage across reference



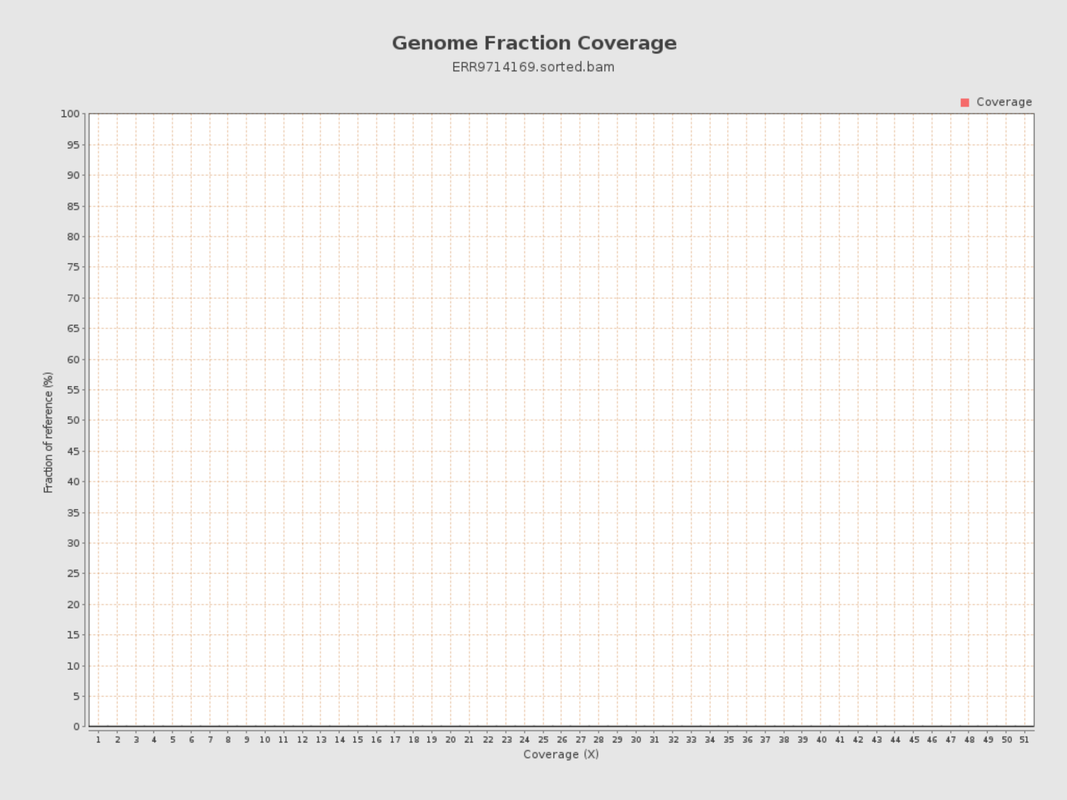
4. Results : Coverage Histogram



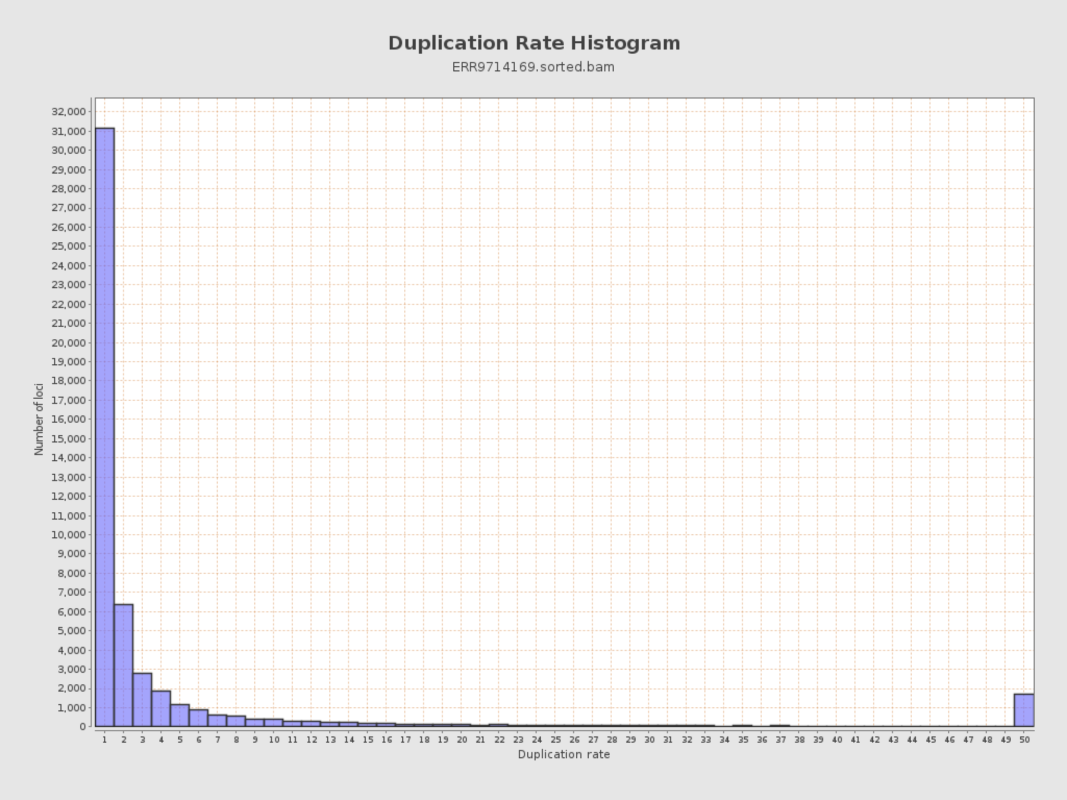
5. Results : Coverage Histogram (0-50X)



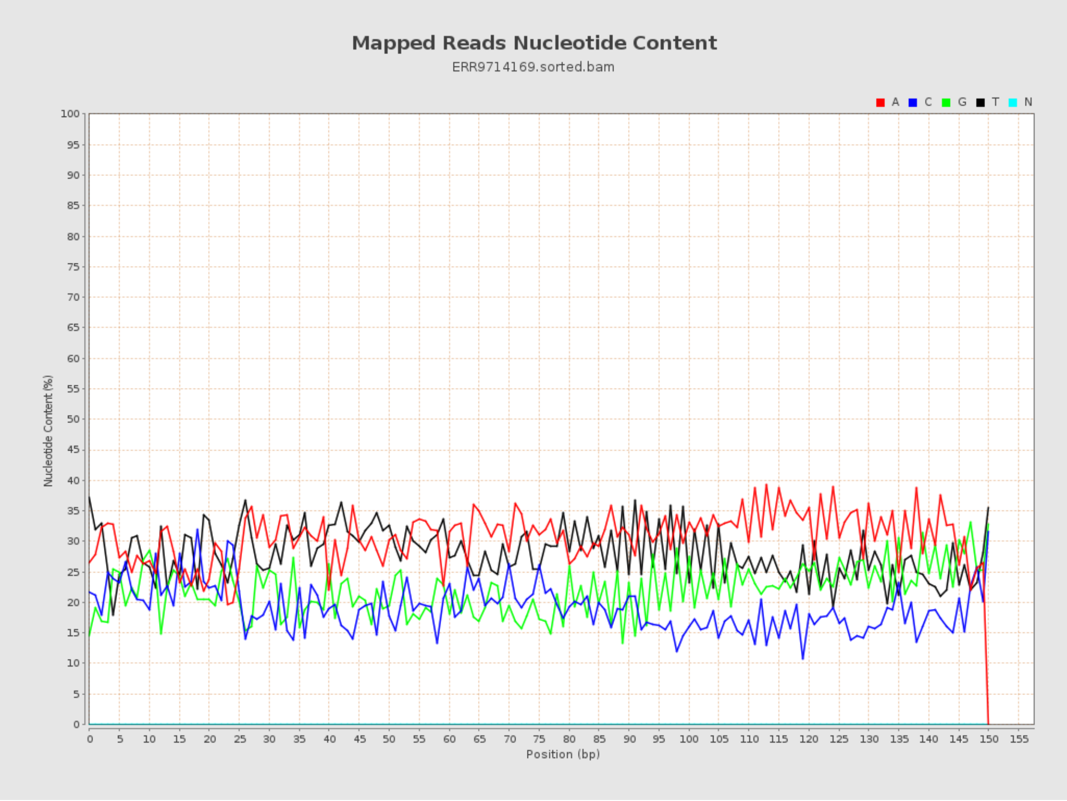
6. Results : Genome Fraction Coverage



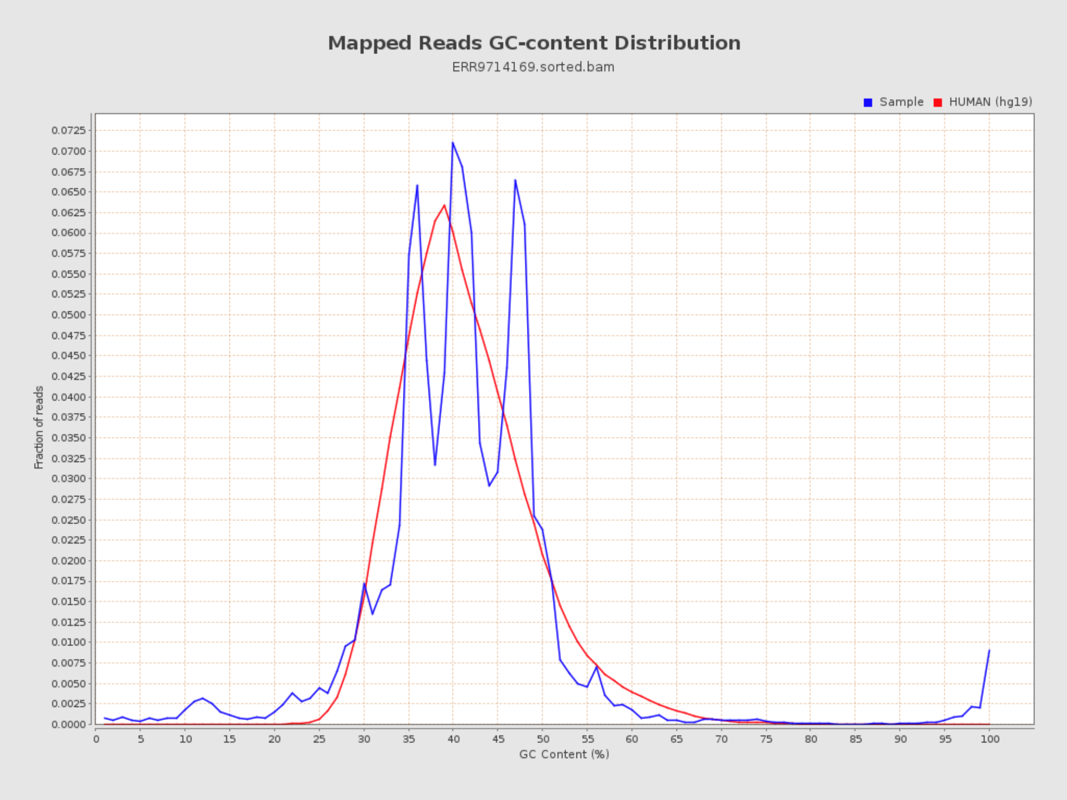
7. Results : Duplication Rate Histogram



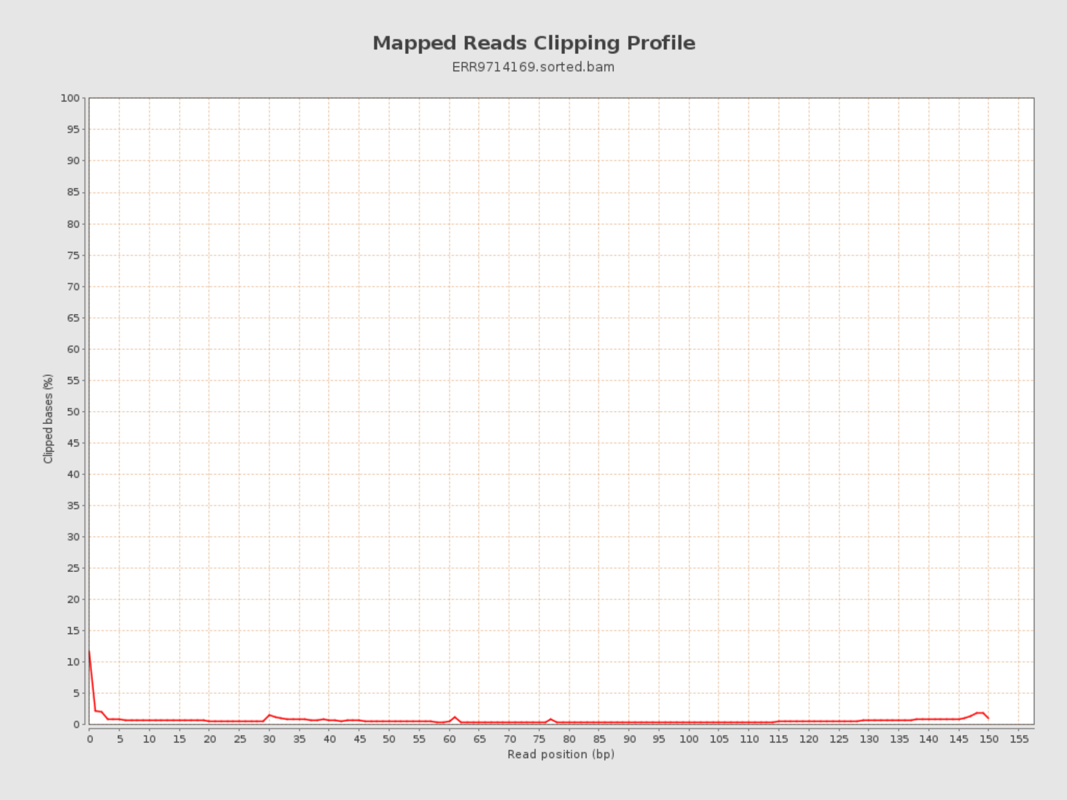
8. Results : Mapped Reads Nucleotide Content



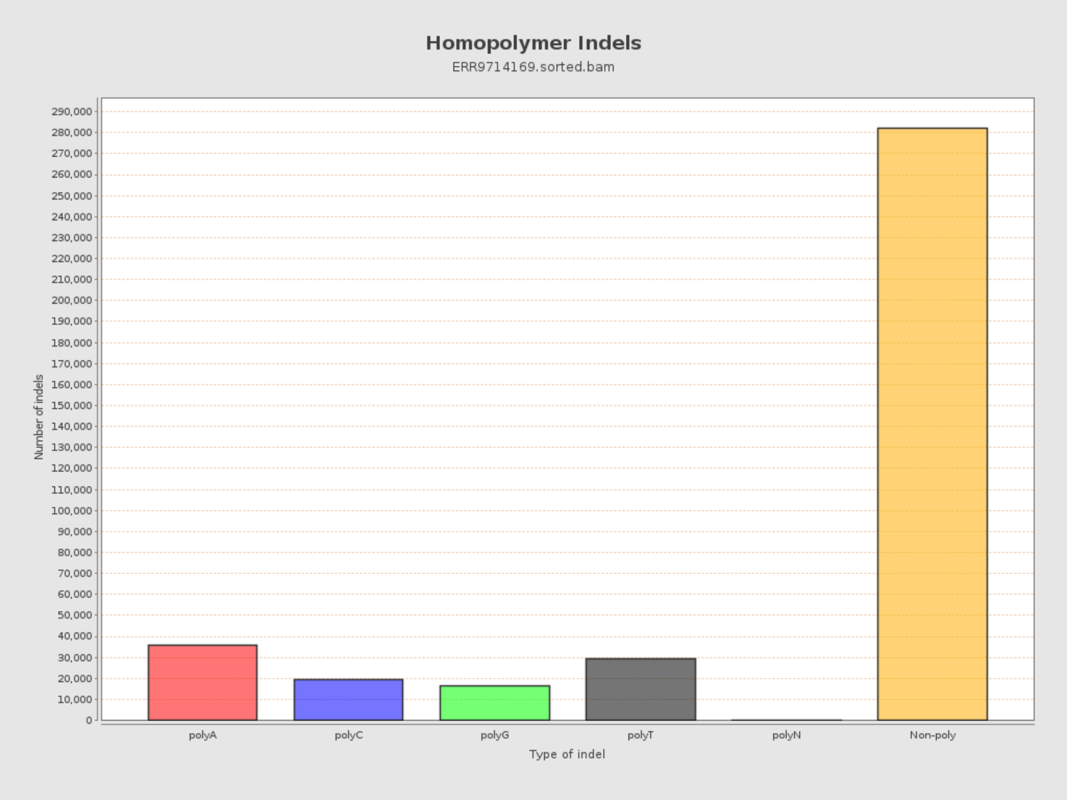
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



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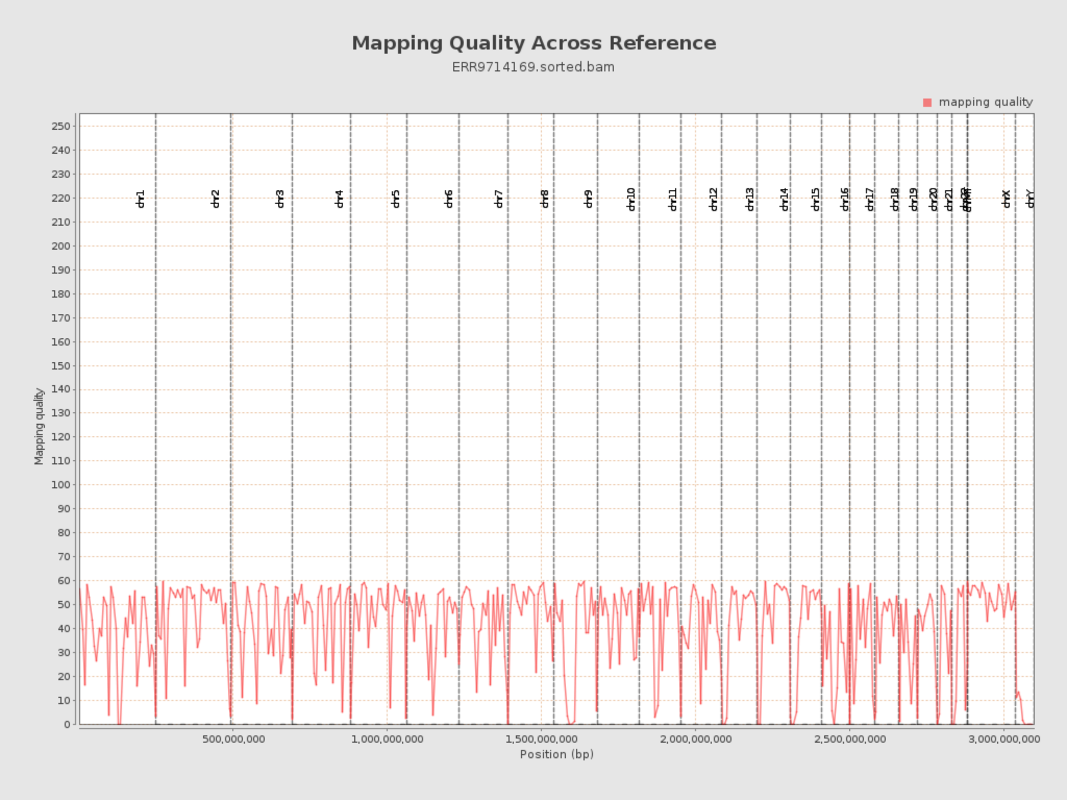
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram