Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:03:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714155.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_ERR9714155 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714155.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:03:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714155.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,119,608
Mapped reads	379,859 / 33.93%
Unmapped reads	739,749 / 66.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,548 / 2.64%
Read min/max/mean length	30 / 151 / 84.6
Duplicated reads (estimated)	336,591 / 30.06%
Duplication rate	41.58%
Clipped reads	346,486 / 30.95%

2.2. ACGT Content

Number/percentage of A's	11,262,035 / 25%
Number/percentage of C's	7,414,050 / 16.46%
Number/percentage of T's	10,255,493 / 22.77%
Number/percentage of G's	16,109,001 / 35.77%
Number/percentage of N's	496 / 0%
GC Percentage	52.23%

2.3. Coverage

Mean	0.0148

Standard Deviation	11.16

2.4. Mapping Quality

Mean Mapping Quality	49.61

2.5. Mismatches and indels

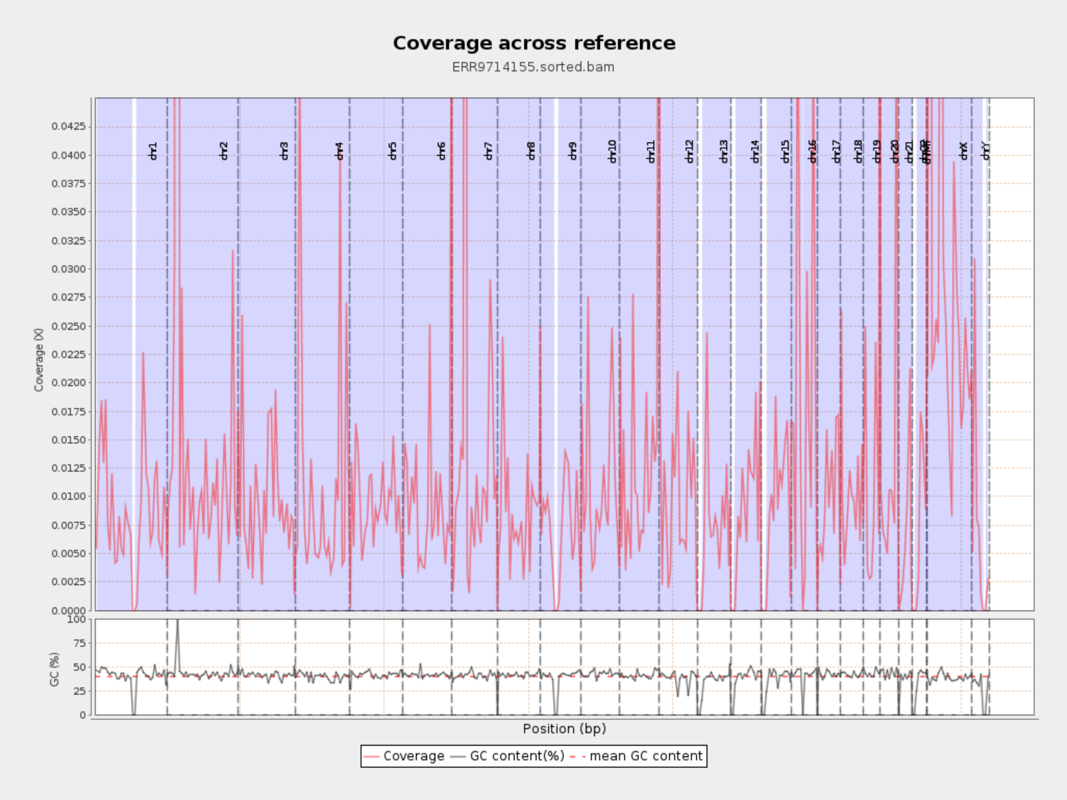
General error rate	3.78%
Mismatches	1,473,347
Insertions	54,735
Mapped reads with at least one insertion	12.82%
Deletions	112,860
Mapped reads with at least one deletion	28.31%
Homopolymer indels	31.12%

2.6. Chromosome stats

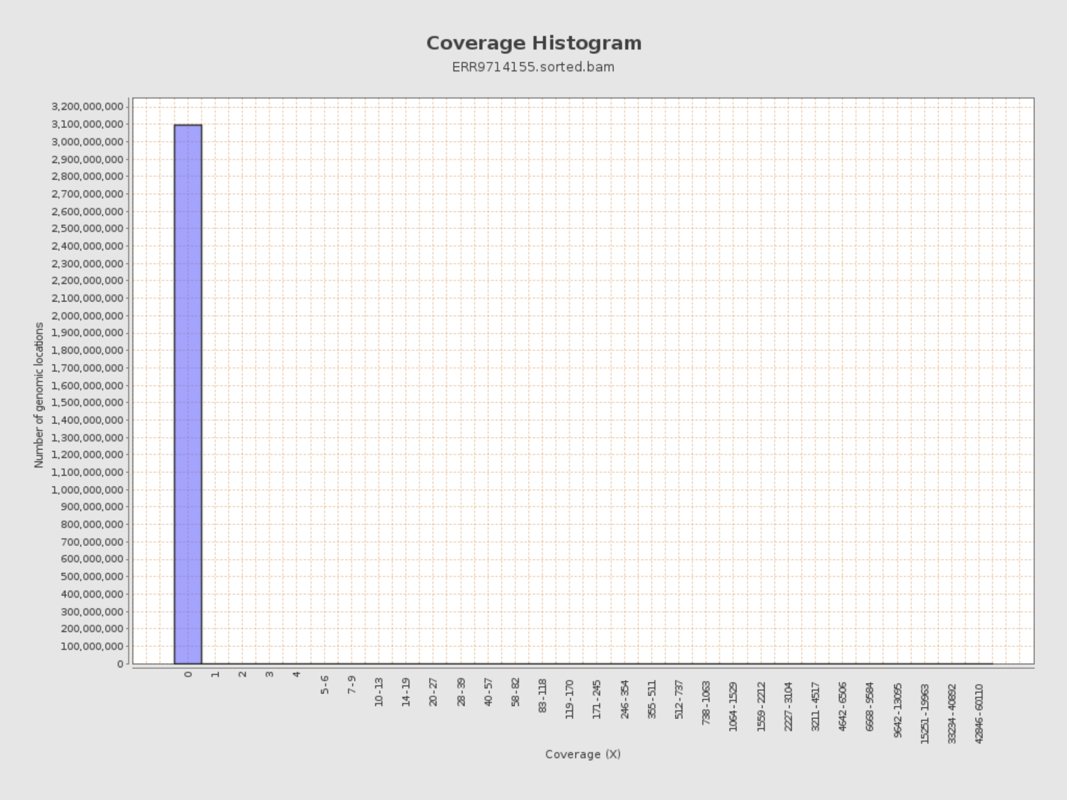
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2136245	0.0086	0.8451
chr2	243199373	11315983	0.0465	37.5255
chr3	198022430	1922064	0.0097	1.0026
chr4	191154276	2096190	0.011	2.475
chr5	180915260	1733742	0.0096	0.8533
chr6	171115067	1684470	0.0098	1.344
chr7	159138663	2734631	0.0172	7.6086

chr8	146364022	1247994	0.0085	0.7926
chr9	141213431	1016841	0.0072	0.6592
chr10	135534747	1498860	0.0111	1.4484
chr11	135006516	1593791	0.0118	1.4724
chr12	133851895	1332727	0.01	1.622
chr13	115169878	821717	0.0071	0.8521
chr14	107349540	977048	0.0091	1.05
chr15	102531392	917946	0.009	1.0911
chr16	90354753	1684797	0.0186	4.3983
chr17	81195210	809652	0.01	1.1365
chr18	78077248	794443	0.0102	0.9527
chr19	59128983	942466	0.0159	3.9237
chr20	63025520	954099	0.0151	2.6309
chr21	48129895	316497	0.0066	1.4606
chr22	51304566	393479	0.0077	0.8716
chrMT	16571	526918	31.7976	257.5017
chrX	155270560	5802683	0.0374	12.8954
chrY	59373566	417236	0.007	1.5168

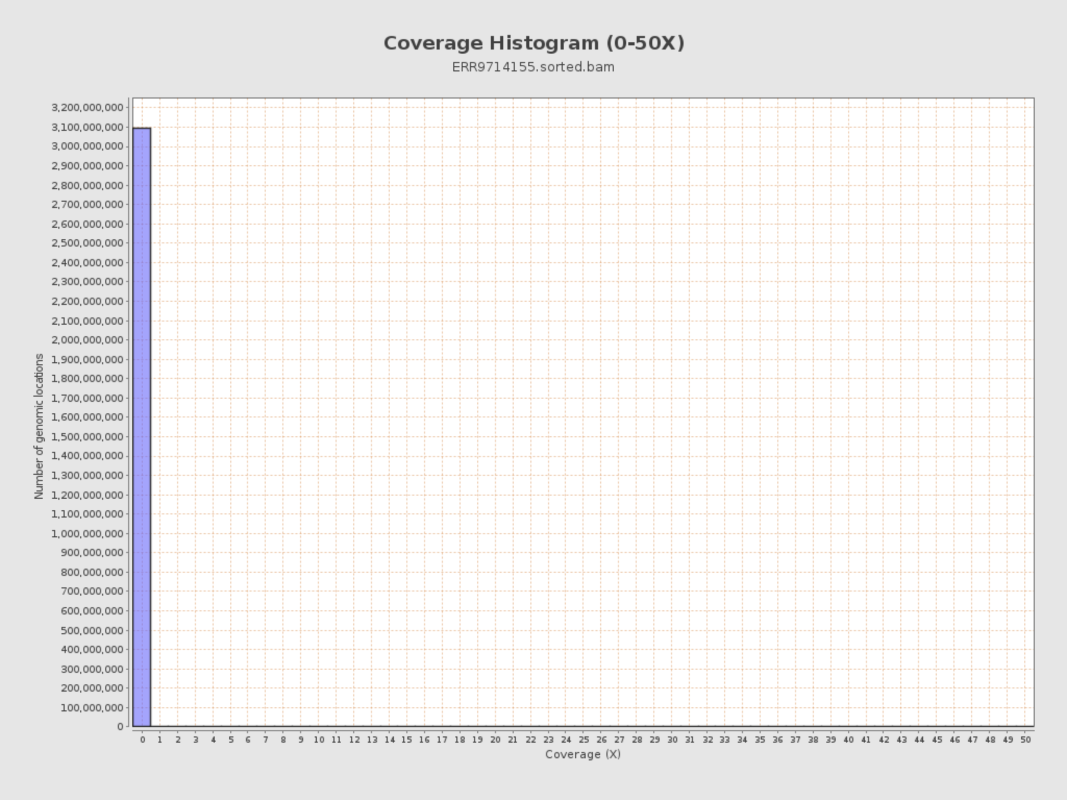
3. Results : Coverage across reference



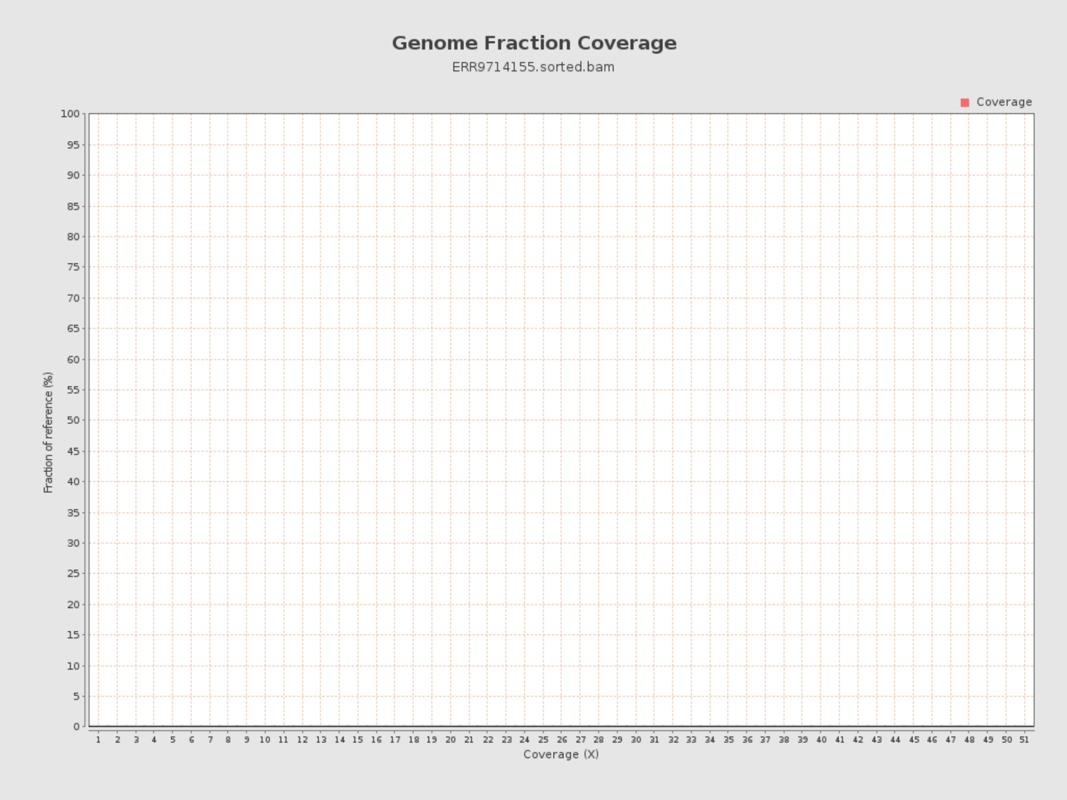
4. Results : Coverage Histogram



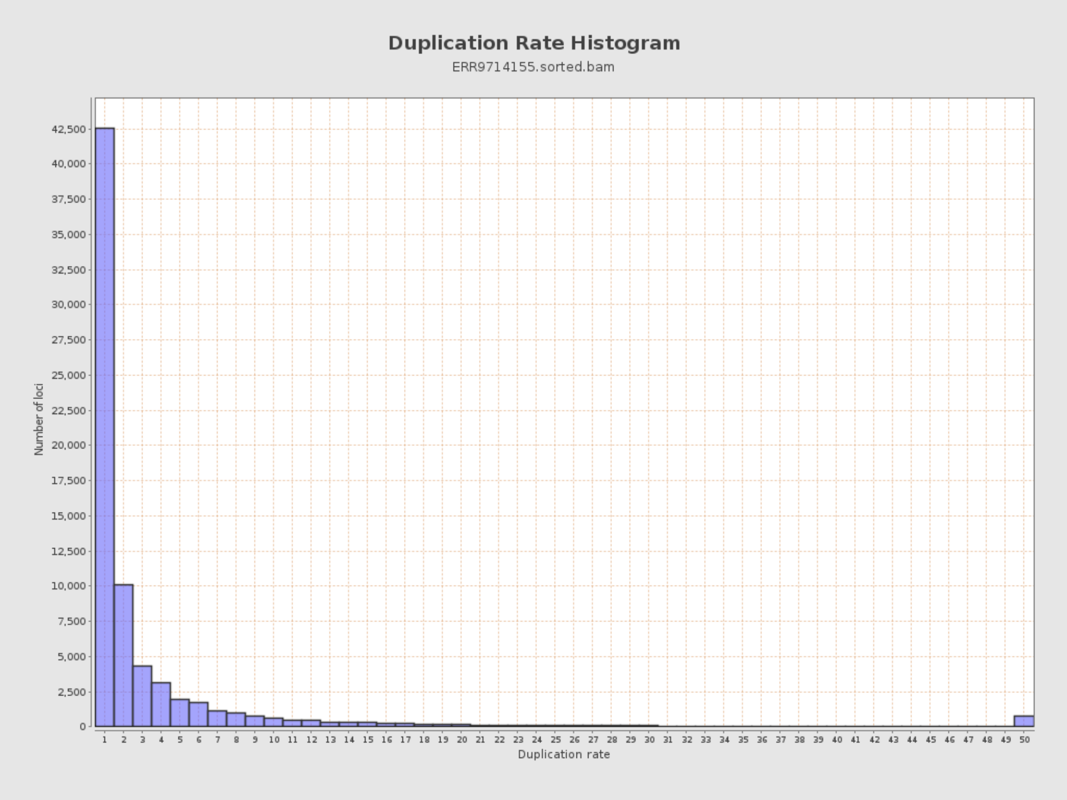
5. Results : Coverage Histogram (0-50X)



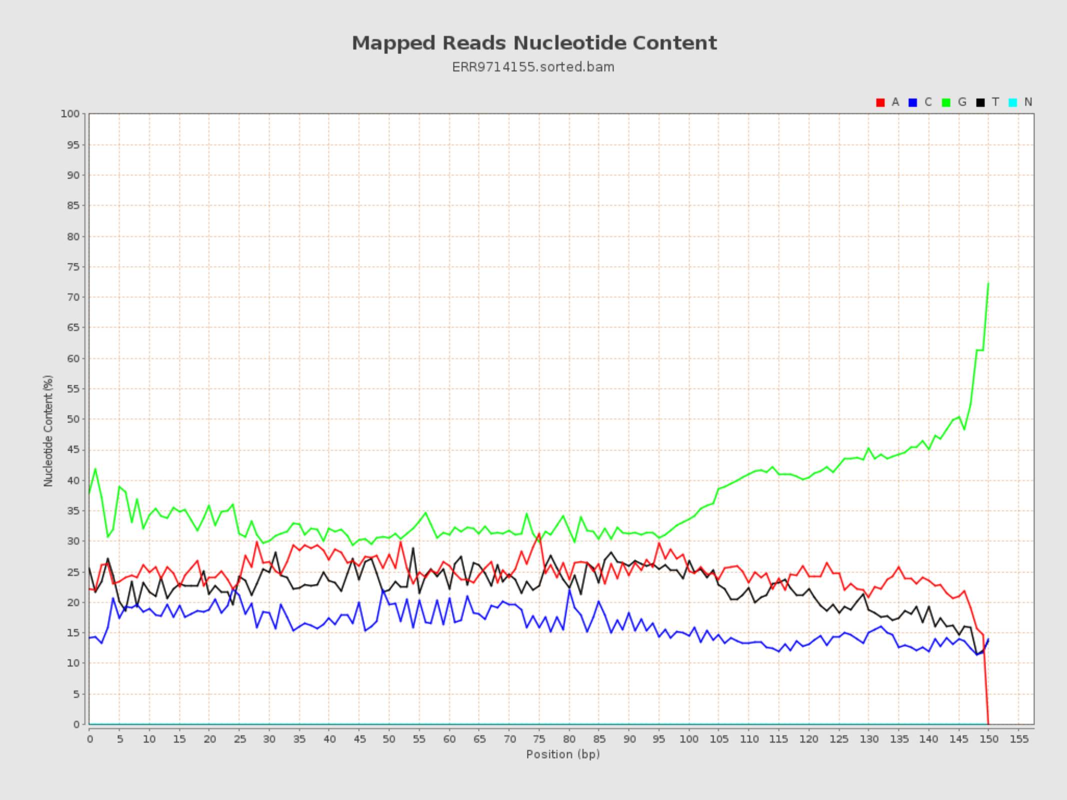
6. Results : Genome Fraction Coverage



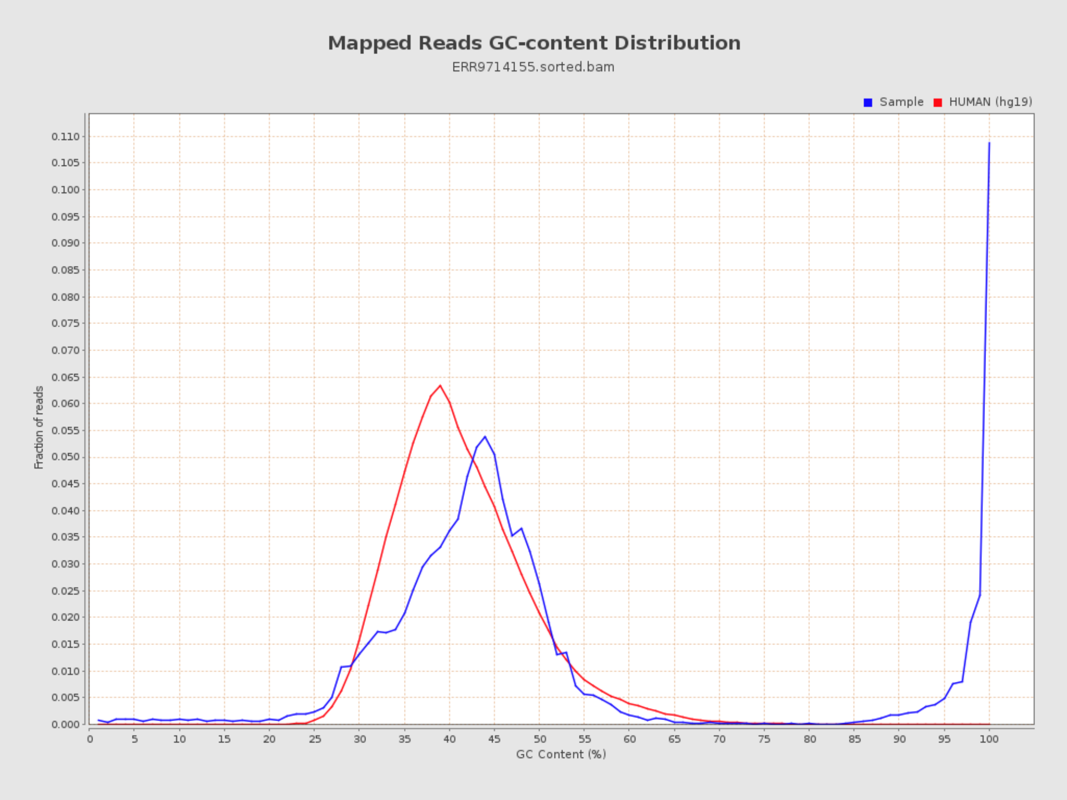
7. Results : Duplication Rate Histogram



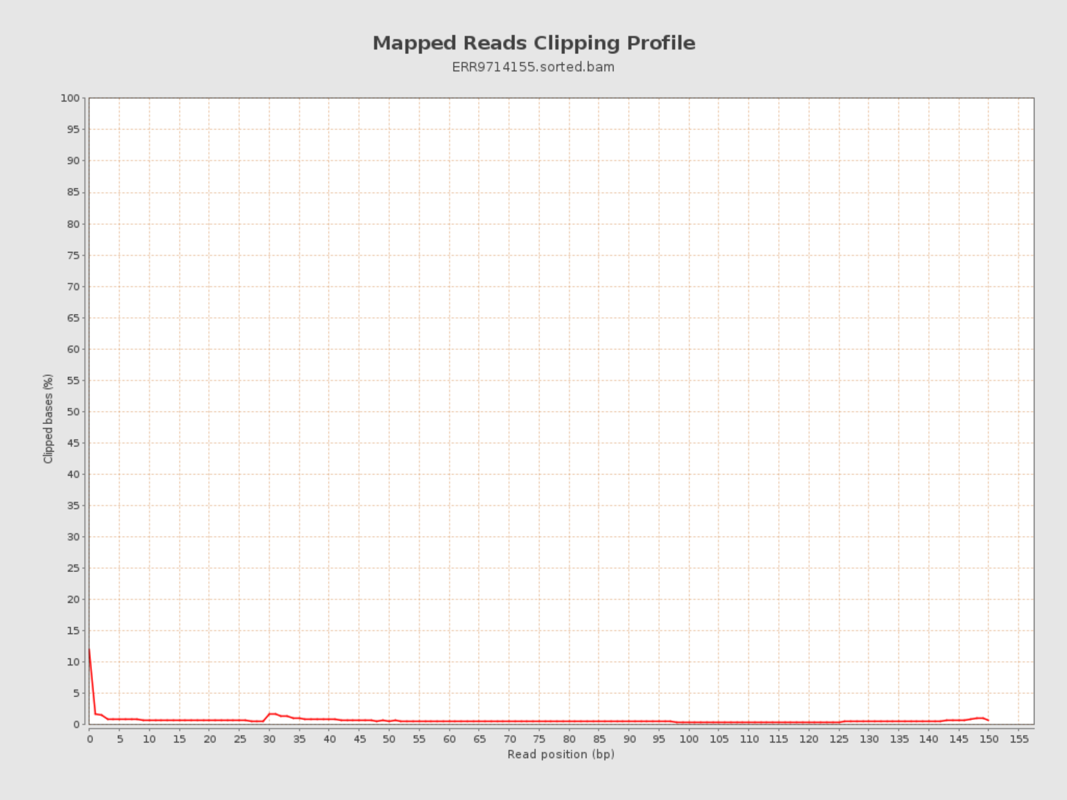
8. Results : Mapped Reads Nucleotide Content



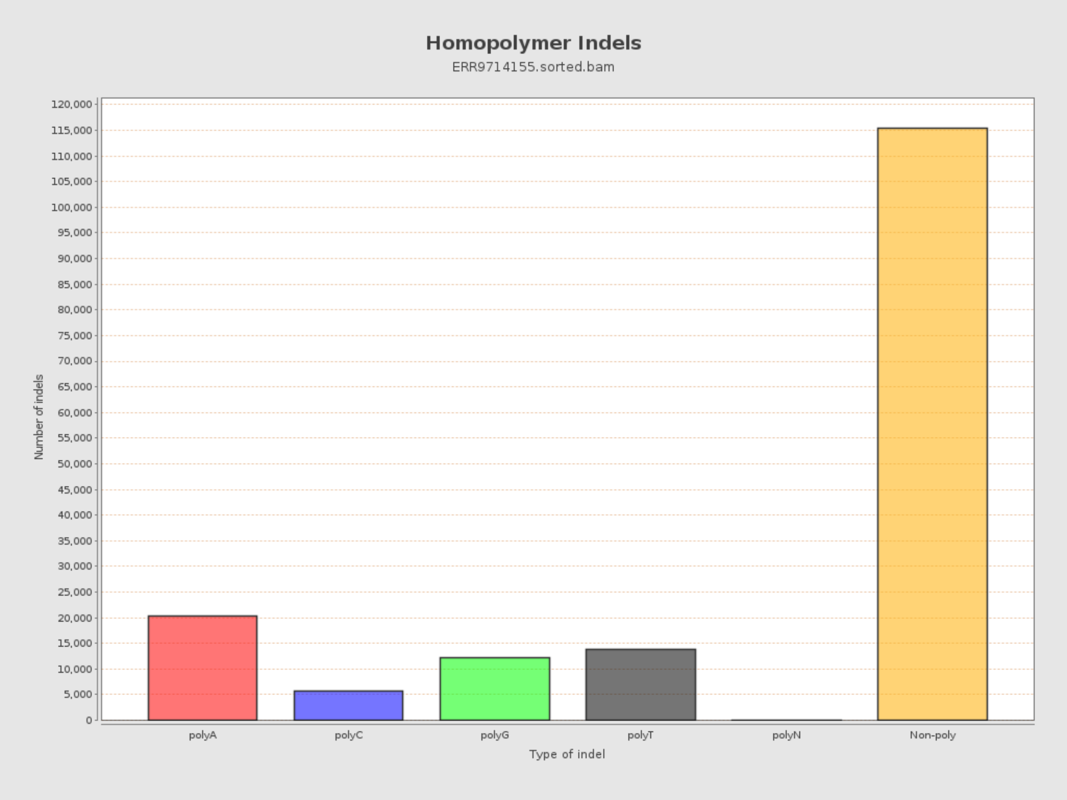
9. Results : Mapped Reads GC-content Distribution



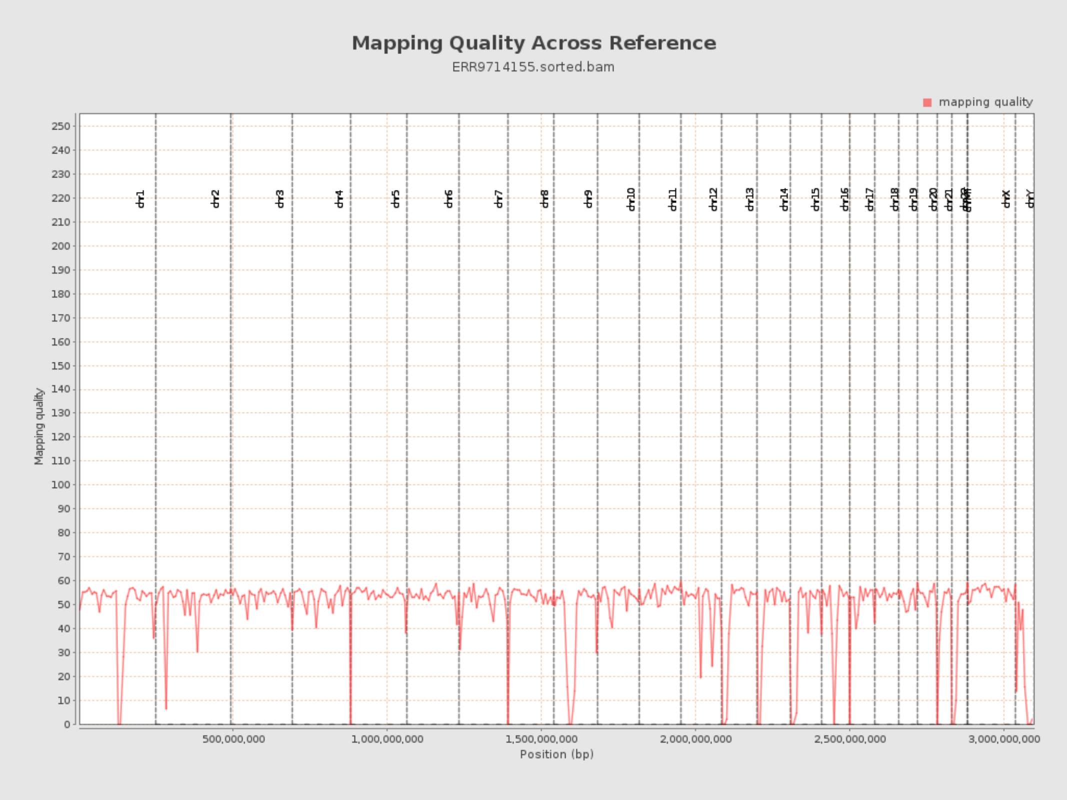
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram