Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:32:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714053.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_ERR9714053 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:32:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	487,384
Mapped reads	79,678 / 16.35%
Unmapped reads	407,706 / 83.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,719 / 0.56%
Read min/max/mean length	30 / 151 / 62.61
Duplicated reads (estimated)	77,988 / 16%
Duplication rate	24.86%
Clipped reads	45,097 / 9.25%

2.2. ACGT Content

Number/percentage of A's	282,592 / 3.46%
Number/percentage of C's	110,281 / 1.35%
Number/percentage of T's	143,572 / 1.76%
Number/percentage of G's	7,641,033 / 93.44%
Number/percentage of N's	191 / 0%
GC Percentage	94.79%

2.3. Coverage

Mean	0.0026

Standard Deviation	9.781

2.4. Mapping Quality

Mean Mapping Quality	17.3

2.5. Mismatches and indels

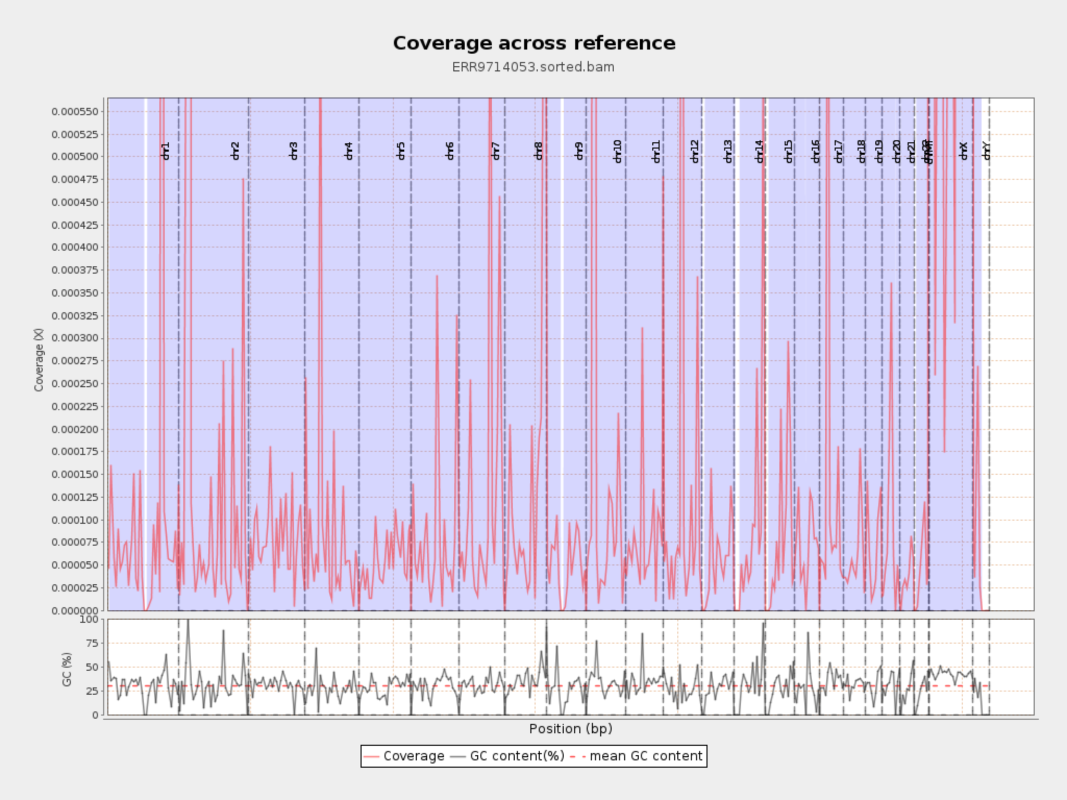
General error rate	3.26%
Mismatches	199,910
Insertions	9,359
Mapped reads with at least one insertion	7.55%
Deletions	4,462
Mapped reads with at least one deletion	5.31%
Homopolymer indels	65.25%

2.6. Chromosome stats

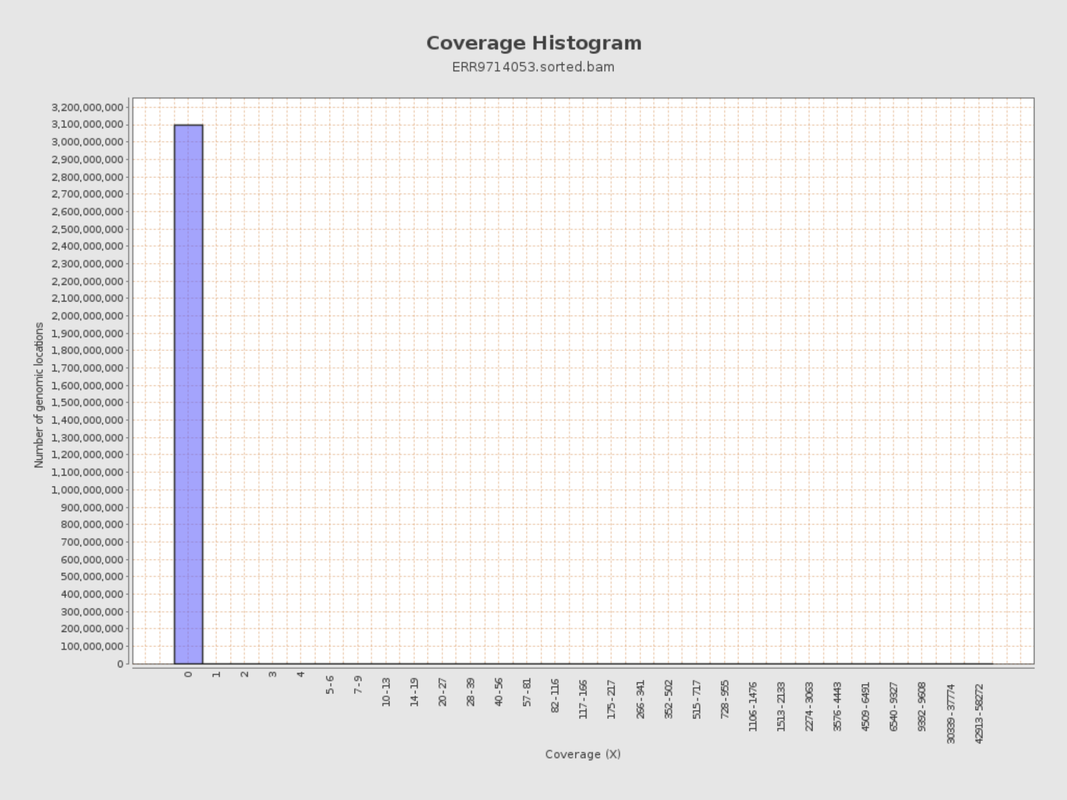
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37385	0.0001	0.2567
chr2	243199373	7629073	0.0314	34.8934
chr3	198022430	15724	0.0001	0.015
chr4	191154276	17969	0.0001	0.039
chr5	180915260	10079	0.0001	0.0105
chr6	171115067	13709	0.0001	0.0282
chr7	159138663	22040	0.0001	0.0859

chr8	146364022	23276	0.0002	0.0487
chr9	141213431	7439	0.0001	0.0129
chr10	135534747	32094	0.0002	0.3466
chr11	135006516	10932	0.0001	0.0304
chr12	133851895	24511	0.0002	0.1362
chr13	115169878	6541	0.0001	0.0105
chr14	107349540	11057	0.0001	0.083
chr15	102531392	8431	0.0001	0.0307
chr16	90354753	6633	0.0001	0.0143
chr17	81195210	13351	0.0002	0.1418
chr18	78077248	4549	0.0001	0.0126
chr19	59128983	4057	0.0001	0.0216
chr20	63025520	6039	0.0001	0.0357
chr21	48129895	1897	0	0.0082
chr22	51304566	2350	0	0.0087
chrMT	16571	5824	0.3515	2.1346
chrX	155270560	280121	0.0018	0.2608
chrY	59373566	2899	0	0.0187

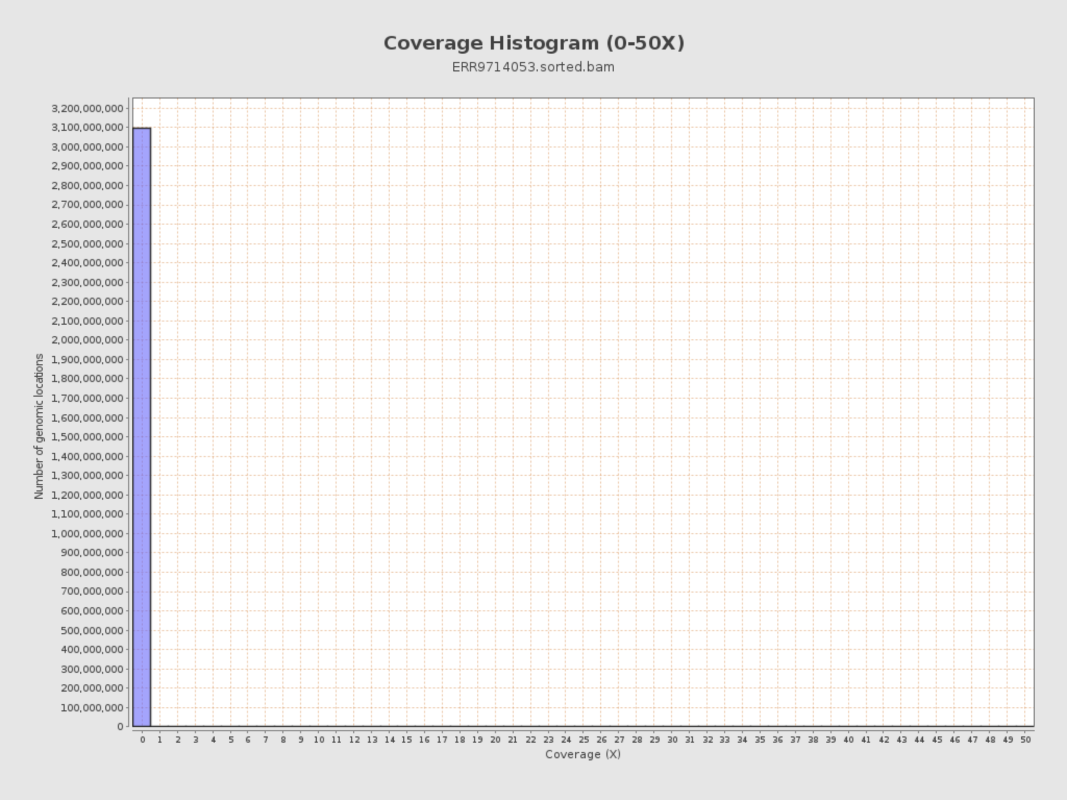
3. Results : Coverage across reference



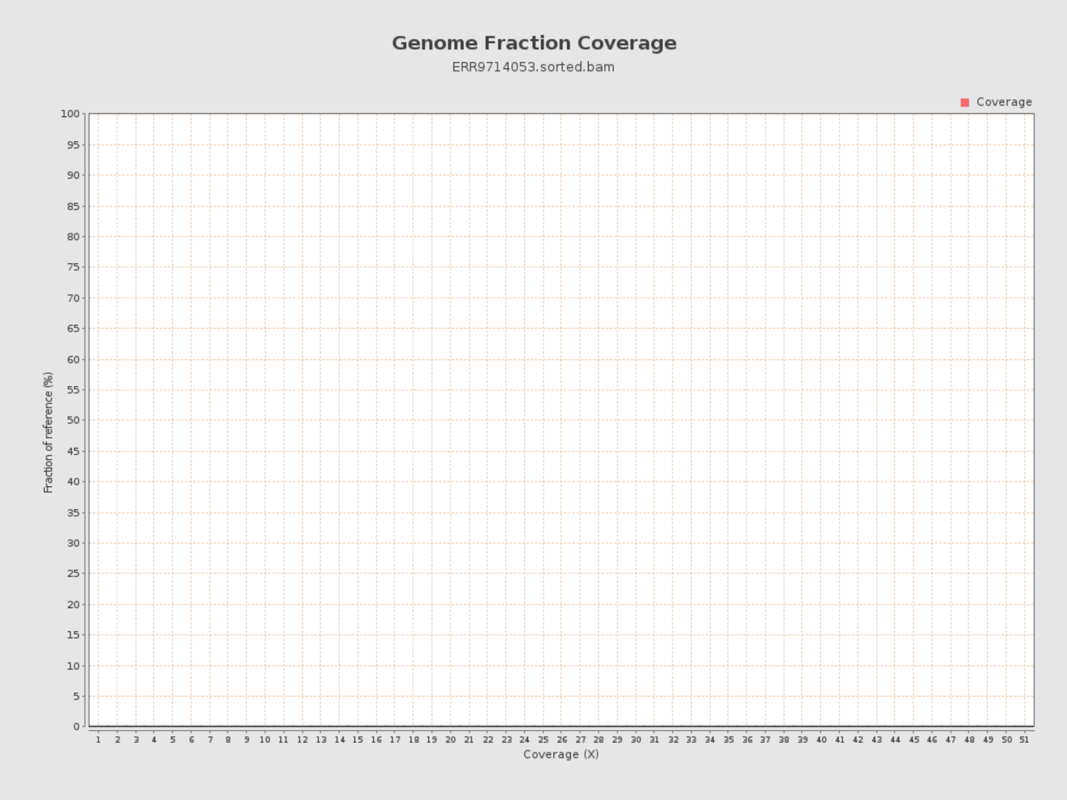
4. Results : Coverage Histogram



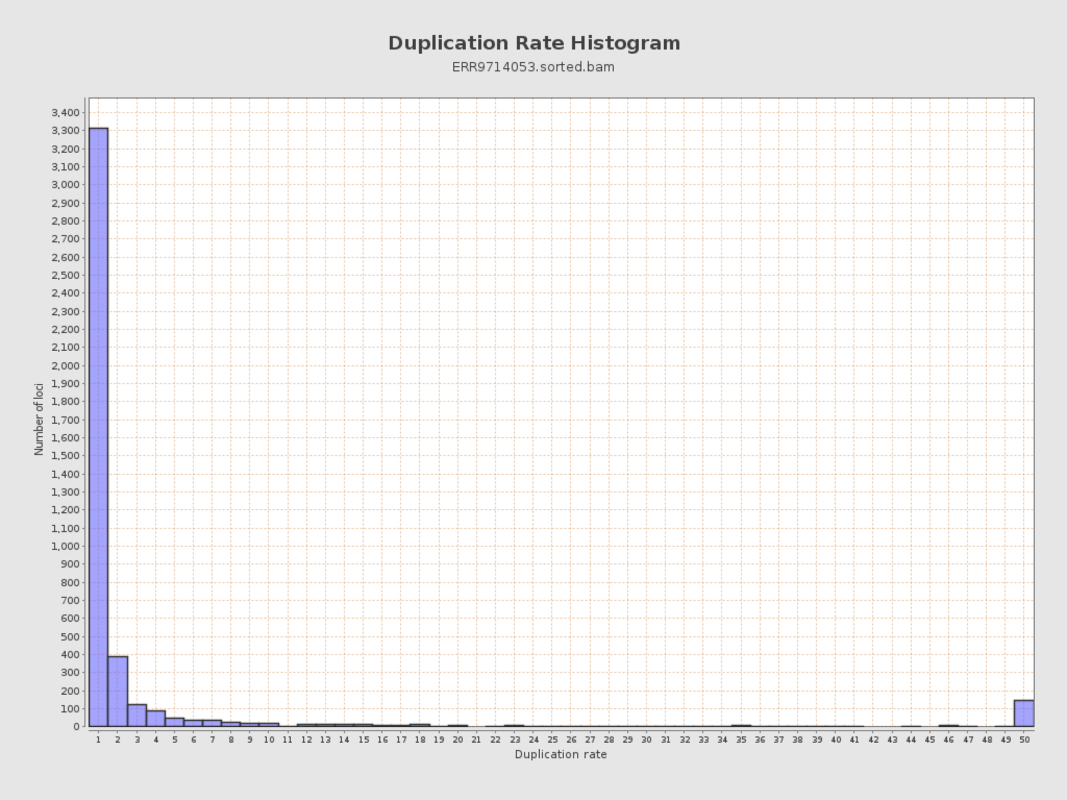
5. Results : Coverage Histogram (0-50X)



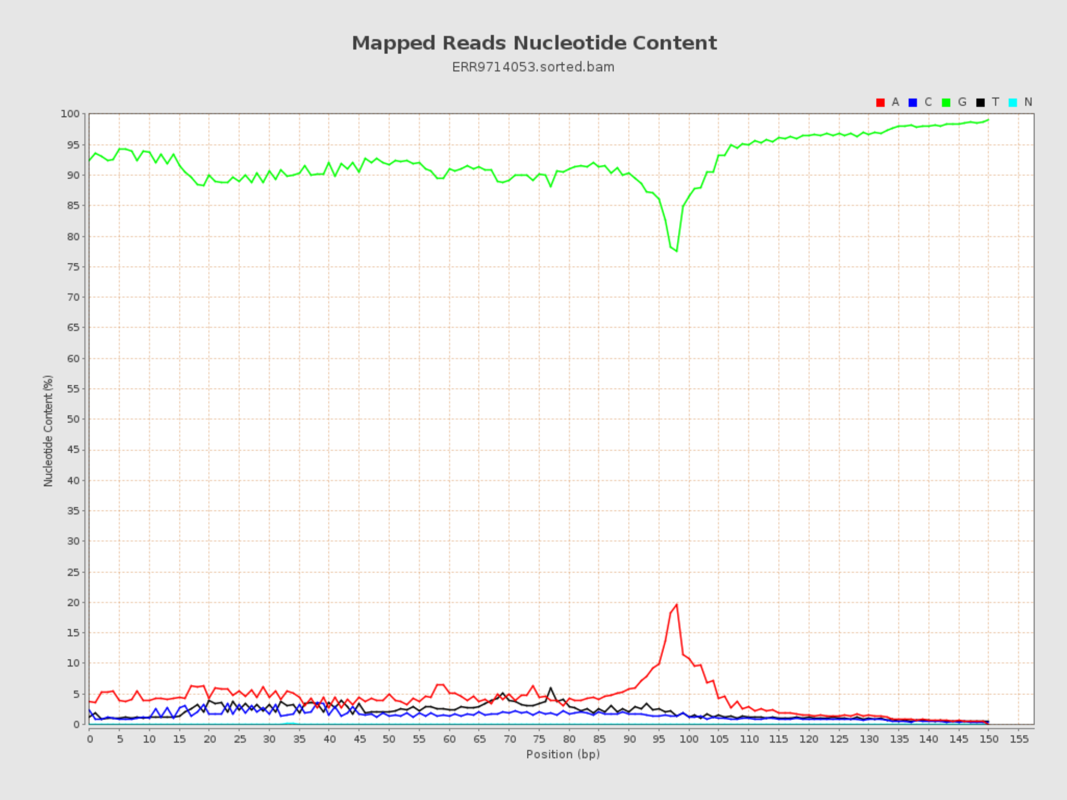
6. Results : Genome Fraction Coverage



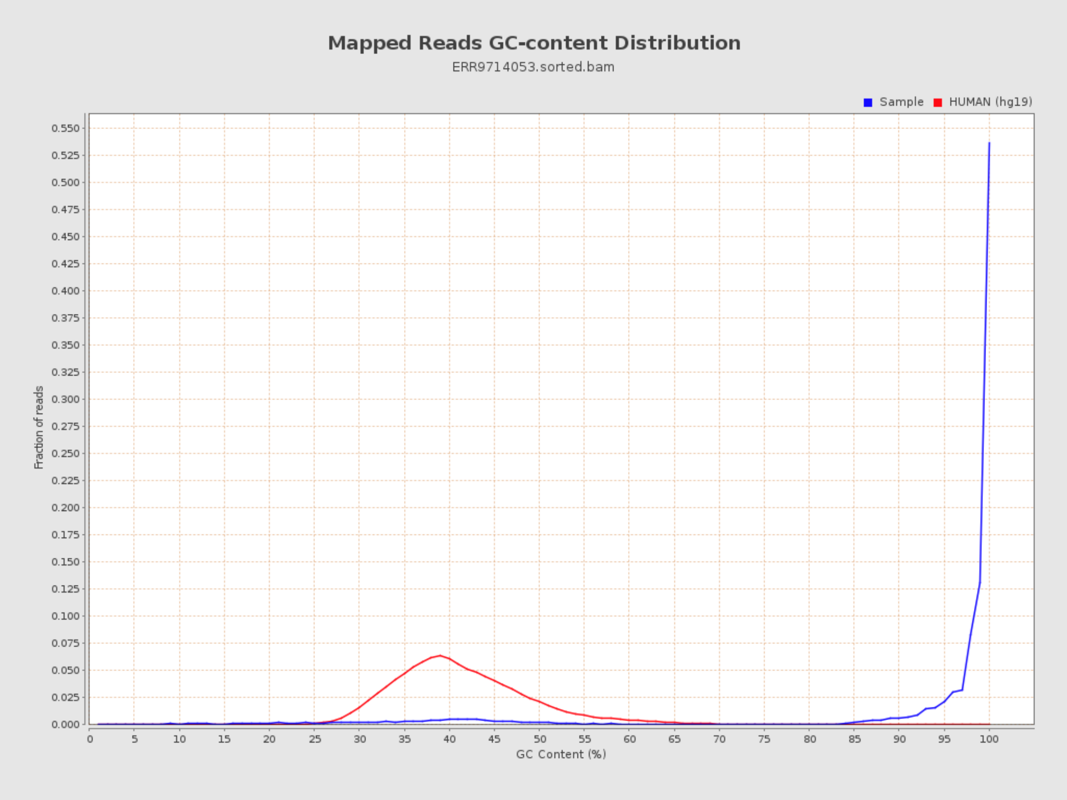
7. Results : Duplication Rate Histogram



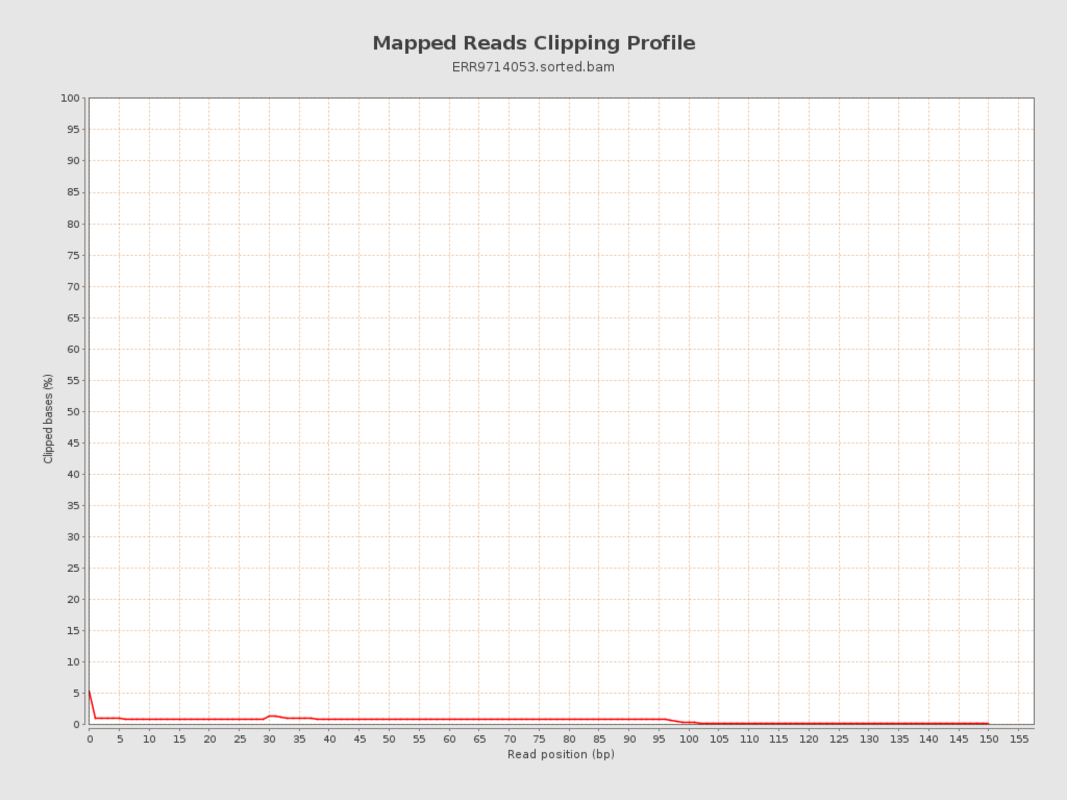
8. Results : Mapped Reads Nucleotide Content



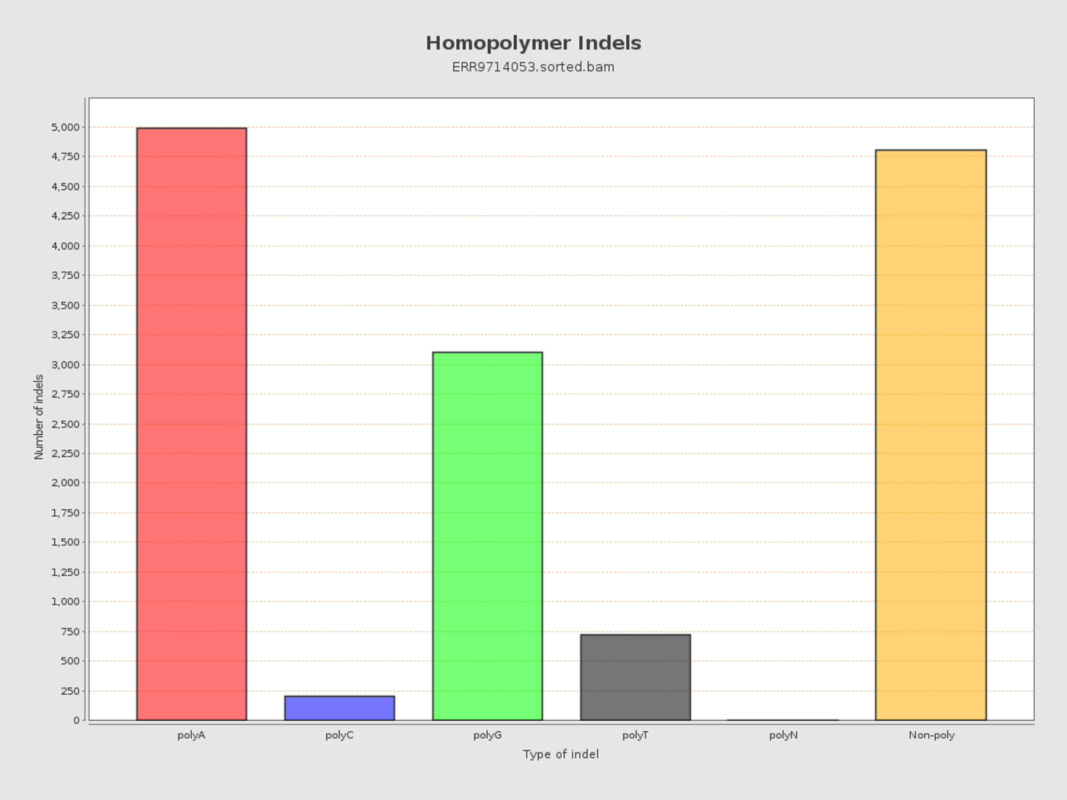
9. Results : Mapped Reads GC-content Distribution



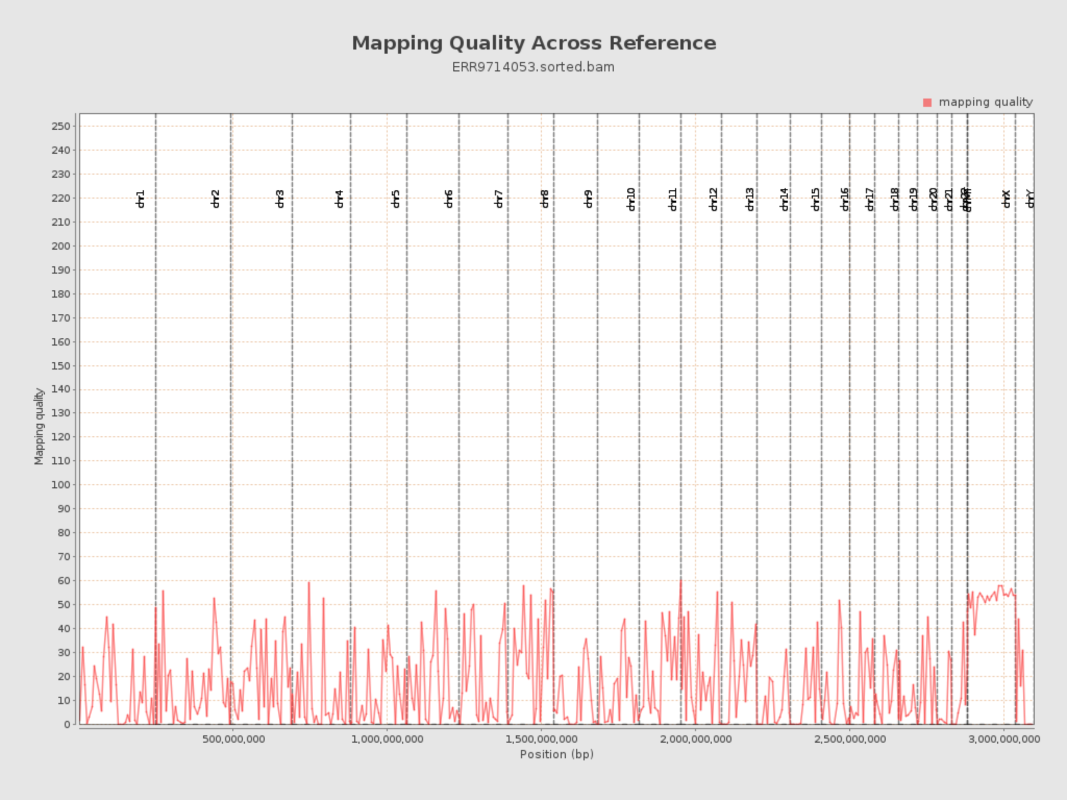
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram