Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:29:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714052.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_ERR9714052 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:29:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	478,152
Mapped reads	73,861 / 15.45%
Unmapped reads	404,291 / 84.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,329 / 0.28%
Read min/max/mean length	30 / 151 / 61.75
Duplicated reads (estimated)	72,020 / 15.06%
Duplication rate	35.27%
Clipped reads	41,183 / 8.61%

2.2. ACGT Content

Number/percentage of A's	264,713 / 3.51%
Number/percentage of C's	142,436 / 1.89%
Number/percentage of T's	171,395 / 2.27%
Number/percentage of G's	6,955,403 / 92.32%
Number/percentage of N's	161 / 0%
GC Percentage	94.21%

2.3. Coverage

Mean	0.0024

Standard Deviation	8.8266

2.4. Mapping Quality

Mean Mapping Quality	10.87

2.5. Mismatches and indels

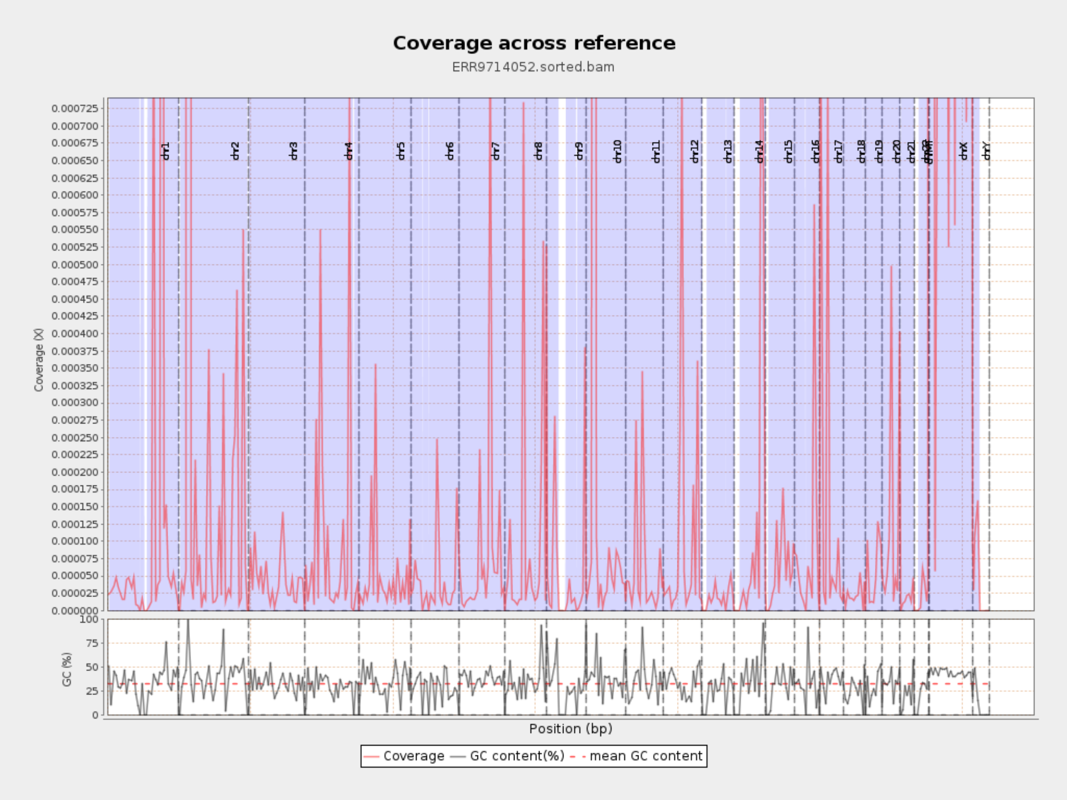
General error rate	3.3%
Mismatches	194,884
Insertions	7,925
Mapped reads with at least one insertion	7.69%
Deletions	4,810
Mapped reads with at least one deletion	6.32%
Homopolymer indels	57.64%

2.6. Chromosome stats

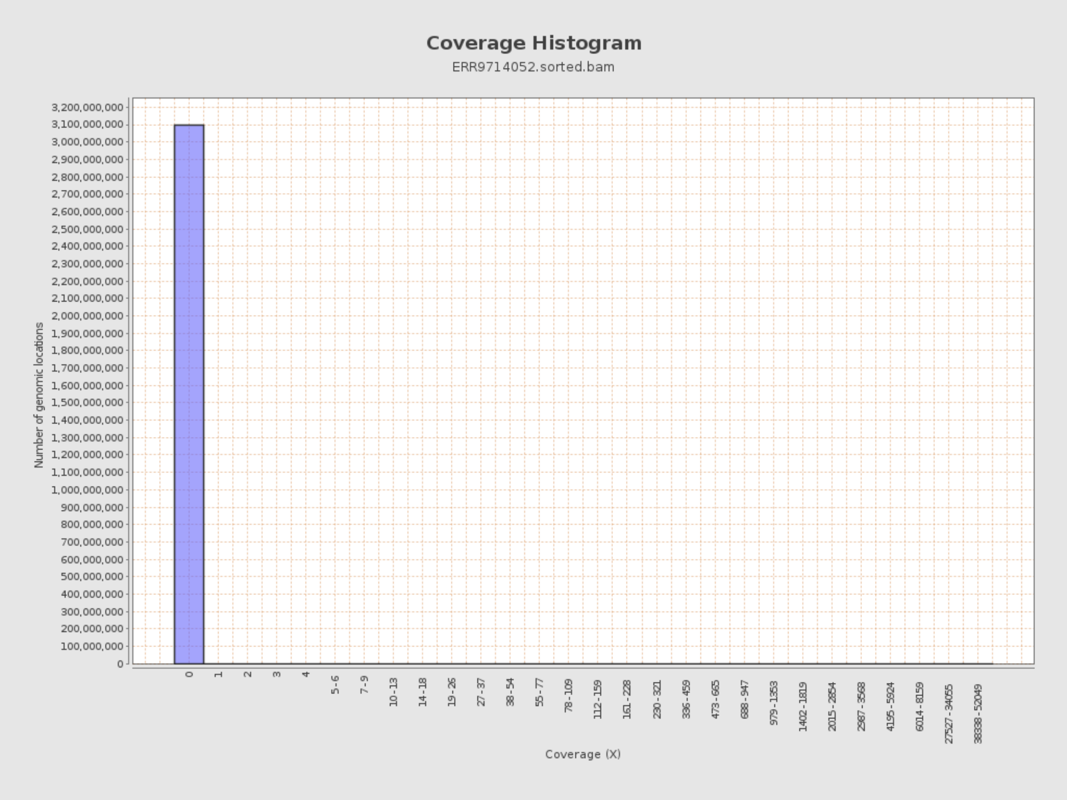
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	50418	0.0002	0.4143
chr2	243199373	6907939	0.0284	31.4838
chr3	198022430	8806	0	0.0149
chr4	191154276	19527	0.0001	0.048
chr5	180915260	9237	0.0001	0.0195
chr6	171115067	7102	0	0.0165
chr7	159138663	14383	0.0001	0.0889

chr8	146364022	15423	0.0001	0.0418
chr9	141213431	7839	0.0001	0.0233
chr10	135534747	41545	0.0003	0.5506
chr11	135006516	8832	0.0001	0.0369
chr12	133851895	14612	0.0001	0.0594
chr13	115169878	2094	0	0.0052
chr14	107349540	15888	0.0001	0.096
chr15	102531392	5924	0.0001	0.0201
chr16	90354753	8621	0.0001	0.0376
chr17	81195210	15059	0.0002	0.1201
chr18	78077248	1692	0	0.0068
chr19	59128983	3279	0.0001	0.0161
chr20	63025520	7479	0.0001	0.0371
chr21	48129895	868	0	0.0061
chr22	51304566	995	0	0.006
chrMT	16571	2133	0.1287	1.5595
chrX	155270560	388335	0.0025	0.4033
chrY	59373566	2208	0	0.0151

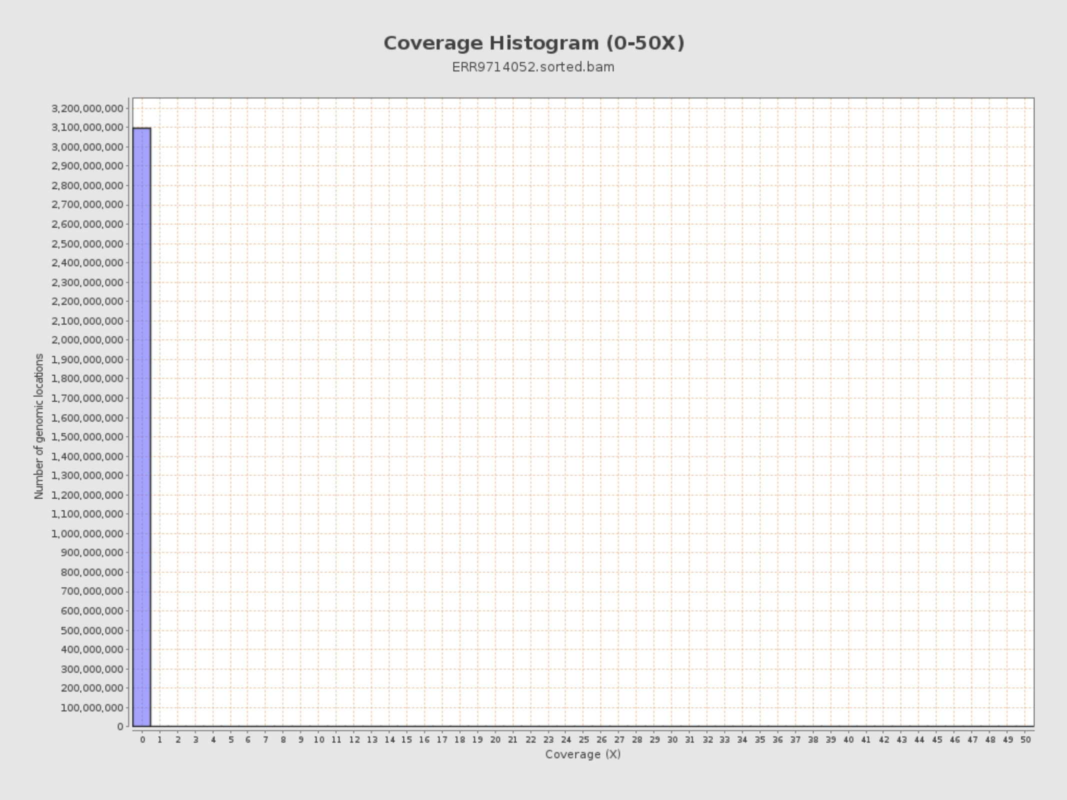
3. Results : Coverage across reference



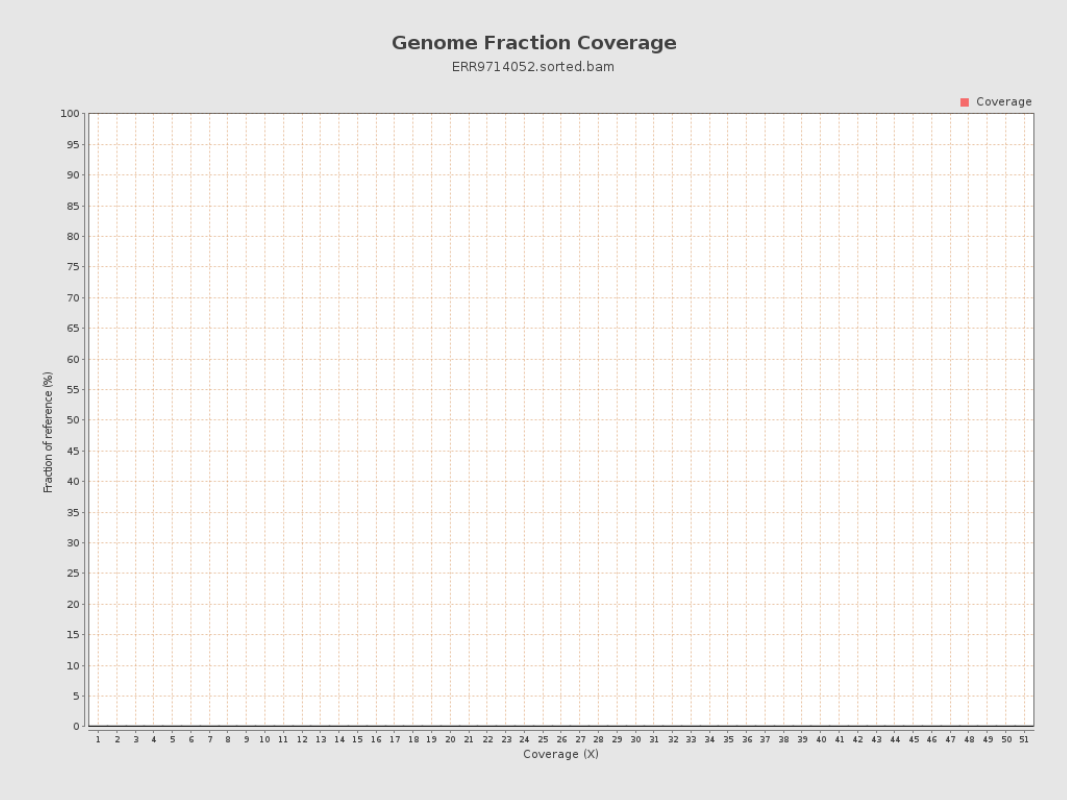
4. Results : Coverage Histogram



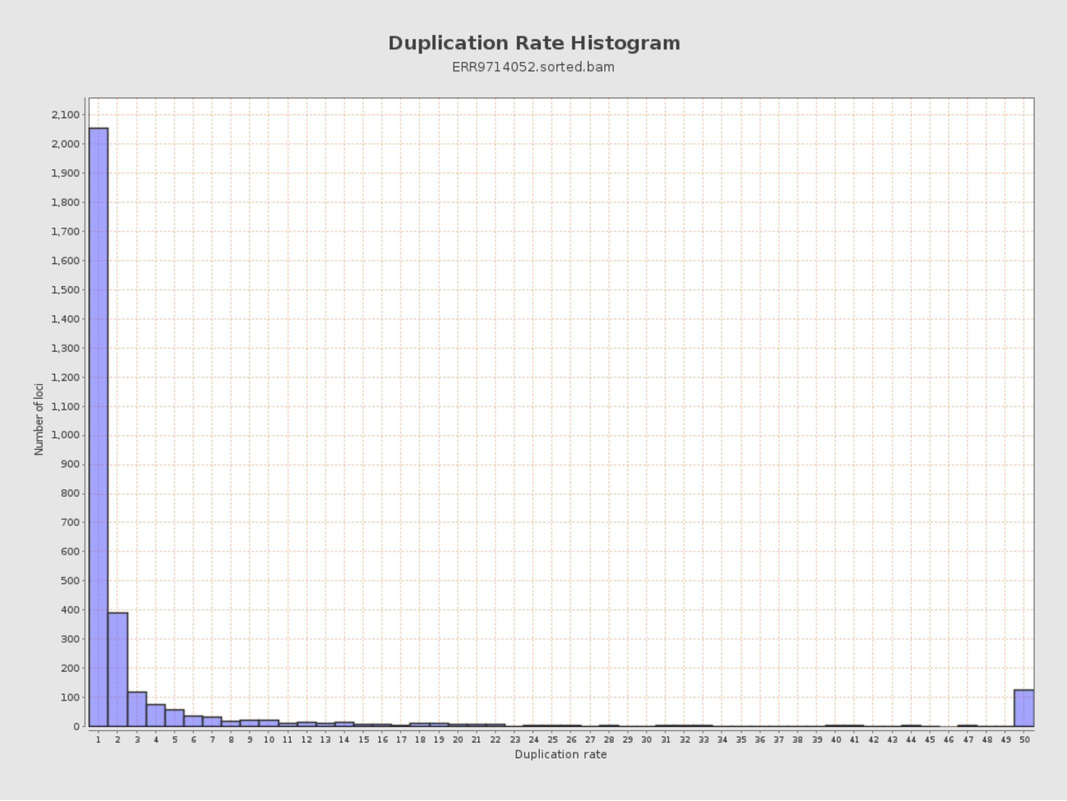
5. Results : Coverage Histogram (0-50X)



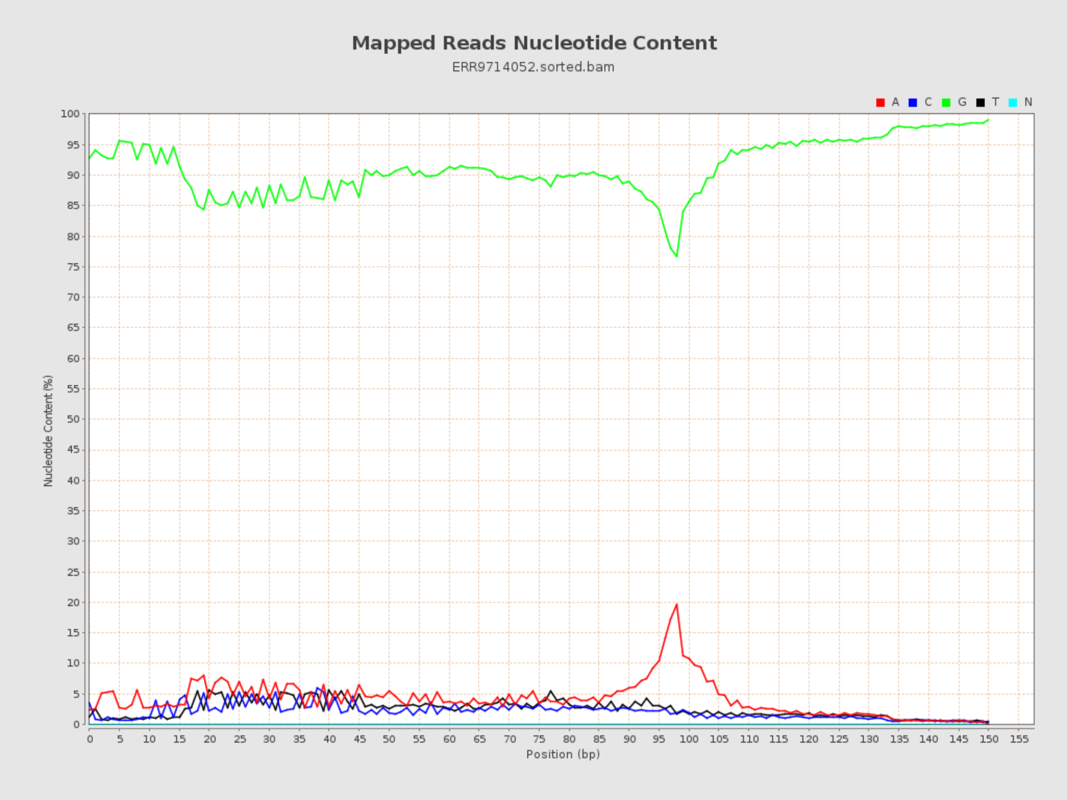
6. Results : Genome Fraction Coverage



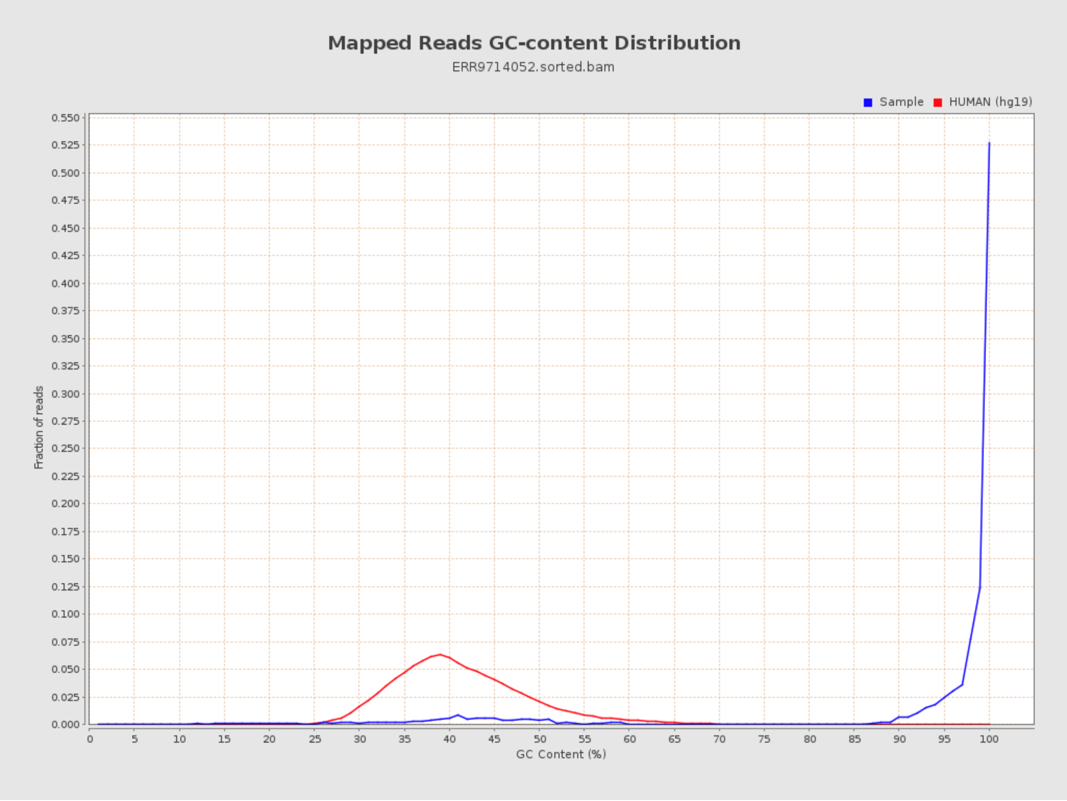
7. Results : Duplication Rate Histogram



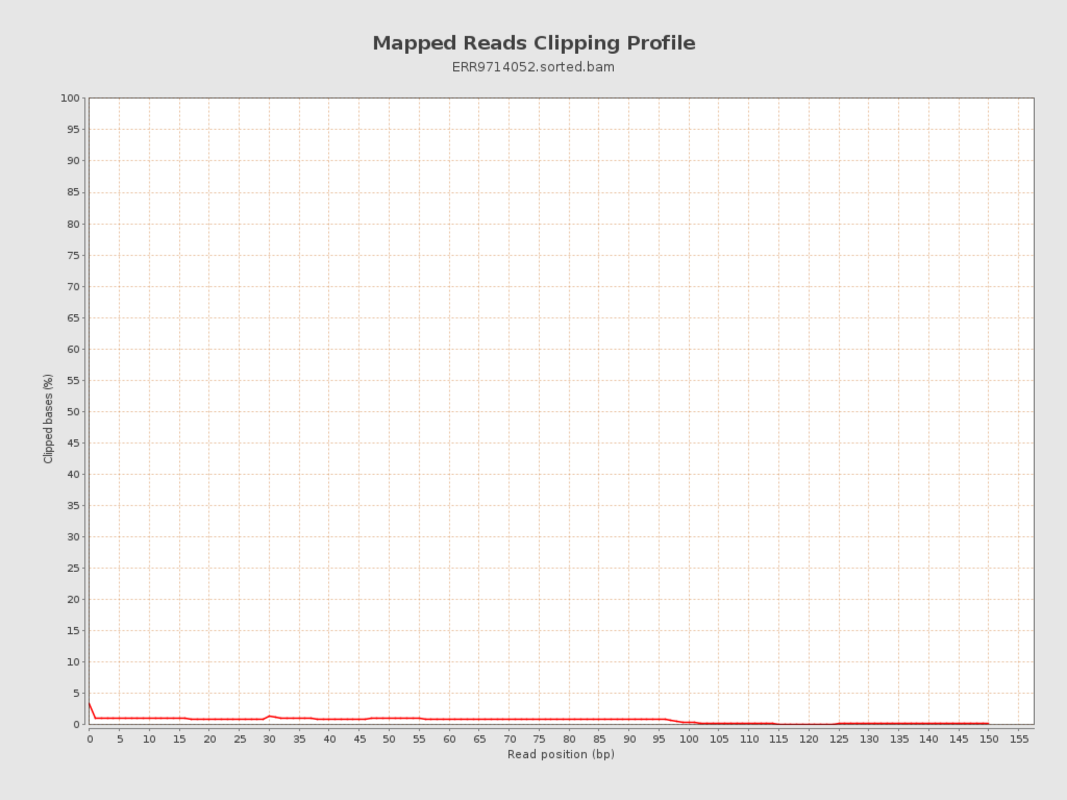
8. Results : Mapped Reads Nucleotide Content



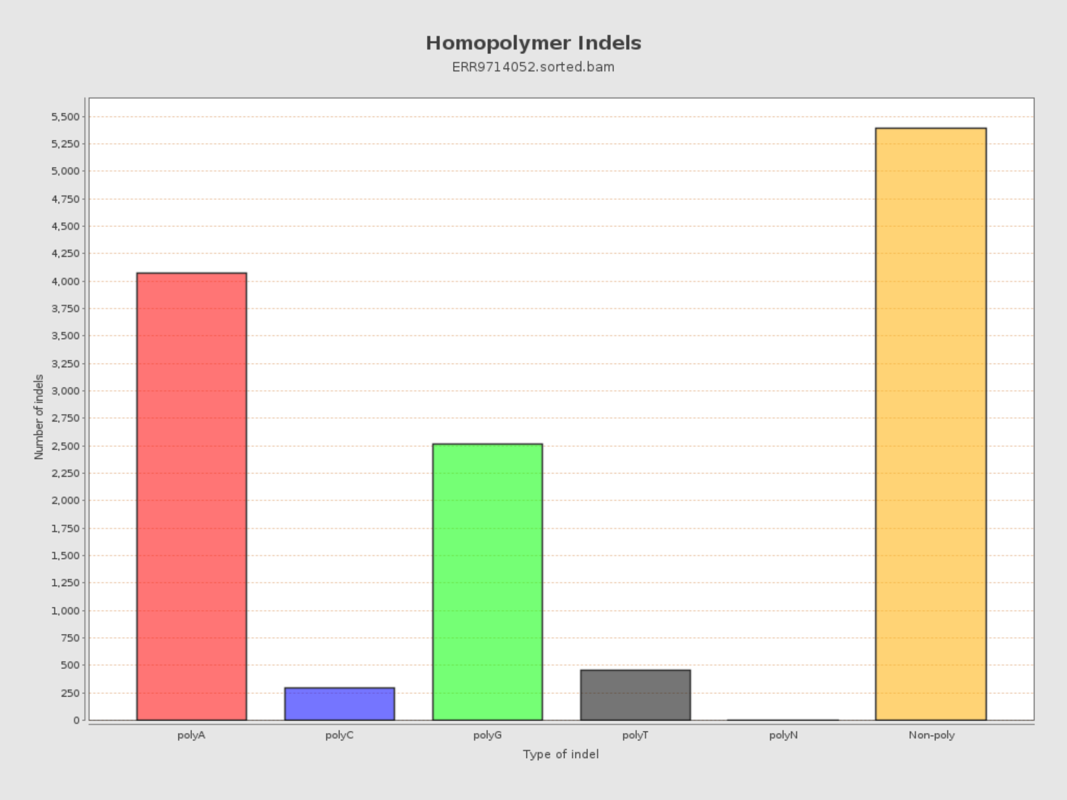
9. Results : Mapped Reads GC-content Distribution



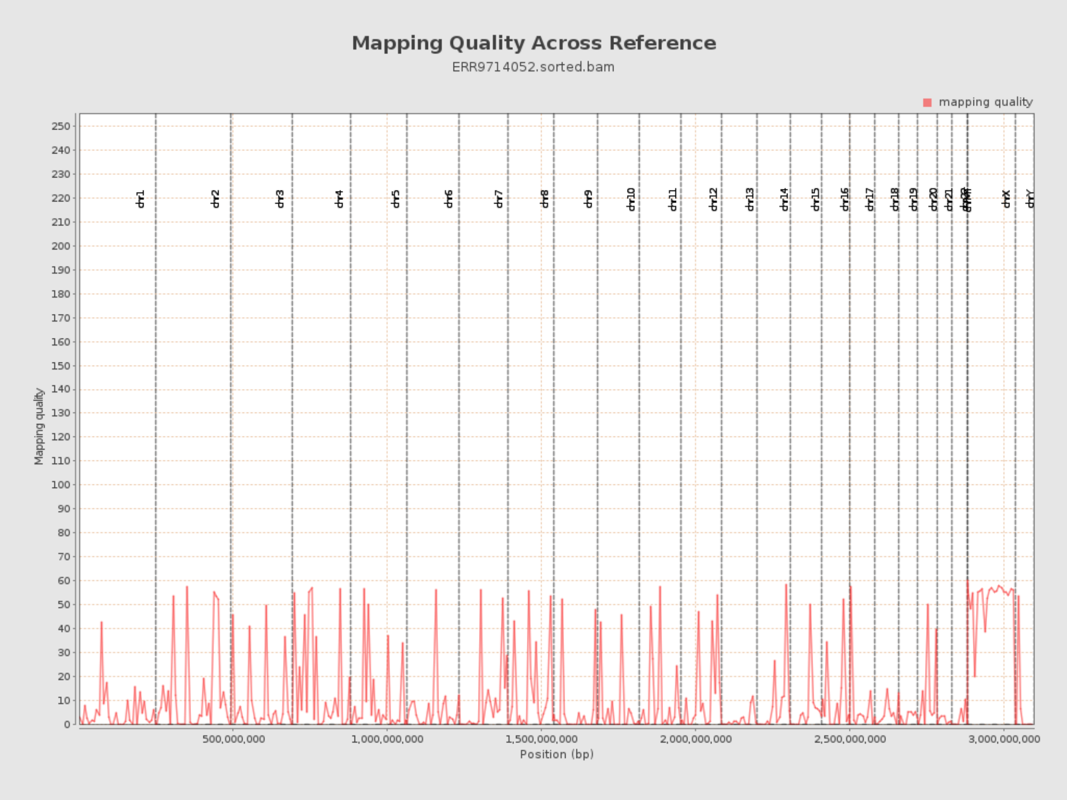
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram