Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:22:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714049.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_ERR9714049 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:22:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	462,682
Mapped reads	73,776 / 15.95%
Unmapped reads	388,906 / 84.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,389 / 0.3%
Read min/max/mean length	30 / 151 / 60.64
Duplicated reads (estimated)	72,645 / 15.7%
Duplication rate	36.9%
Clipped reads	39,257 / 8.48%

2.2. ACGT Content

Number/percentage of A's	153,004 / 2.02%
Number/percentage of C's	64,444 / 0.85%
Number/percentage of T's	81,369 / 1.07%
Number/percentage of G's	7,270,904 / 96.05%
Number/percentage of N's	145 / 0%
GC Percentage	96.9%

2.3. Coverage

Mean	0.0025

Standard Deviation	9.323

2.4. Mapping Quality

Mean Mapping Quality	12.88

2.5. Mismatches and indels

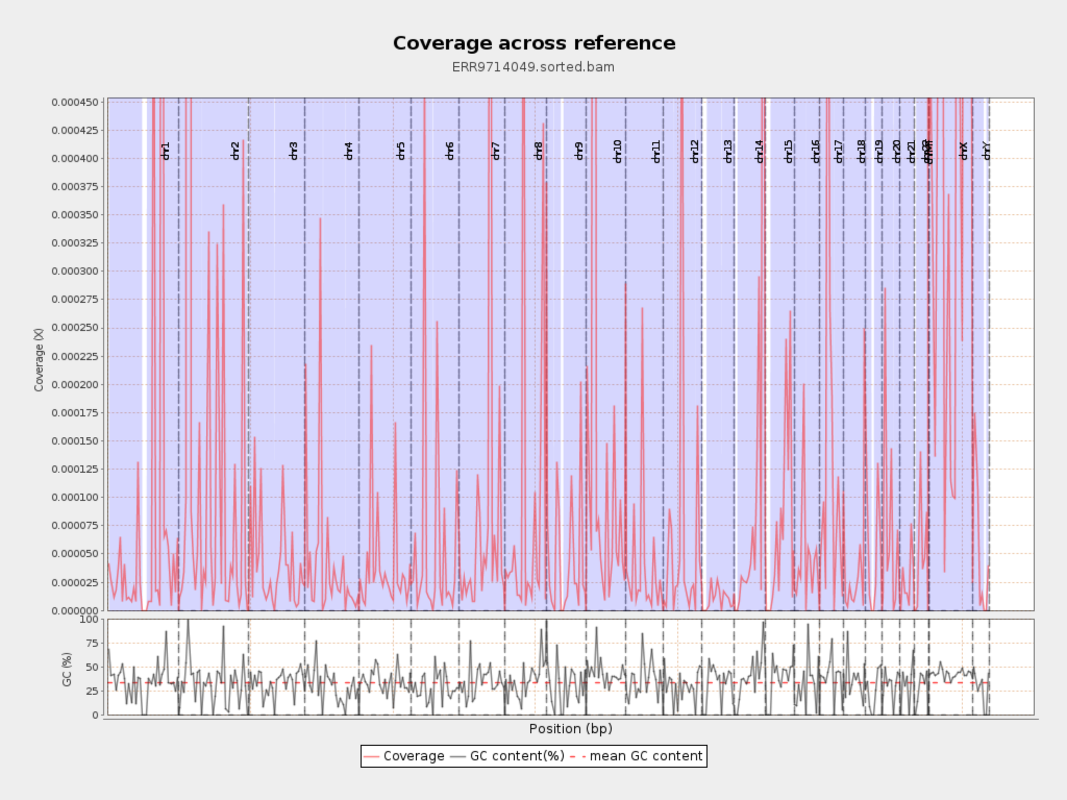
General error rate	3.26%
Mismatches	187,261
Insertions	8,652
Mapped reads with at least one insertion	8.11%
Deletions	3,540
Mapped reads with at least one deletion	4.62%
Homopolymer indels	63.05%

2.6. Chromosome stats

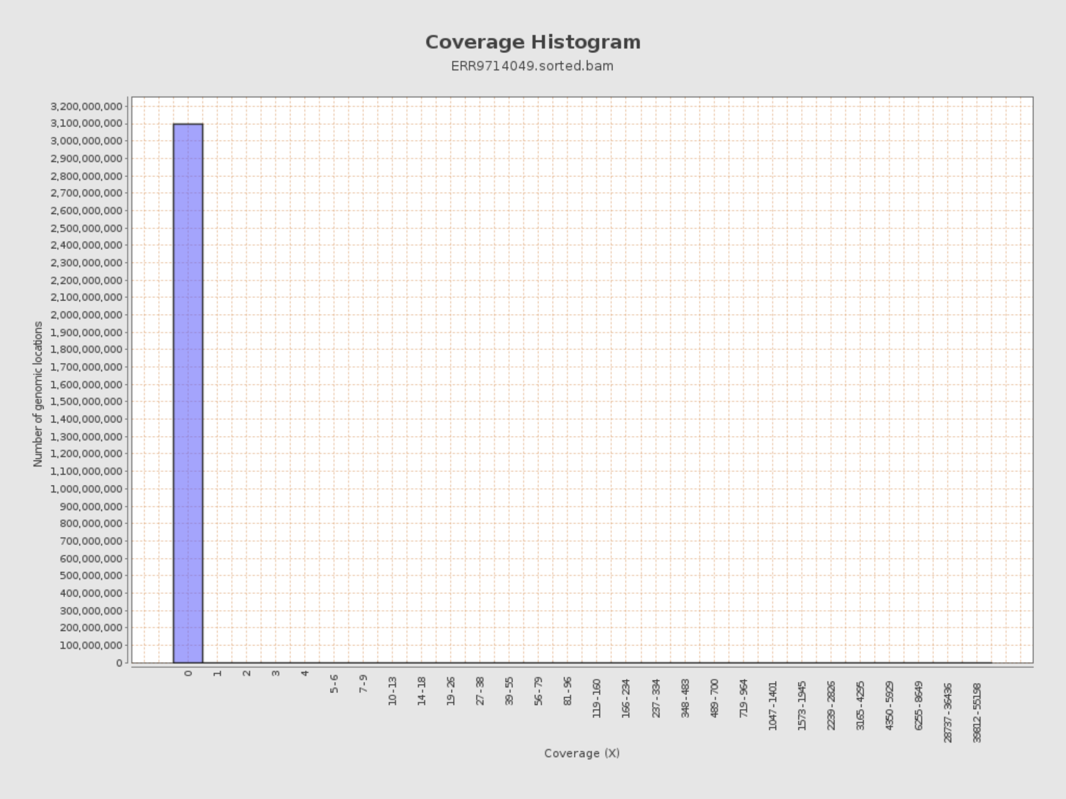
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25456	0.0001	0.165
chr2	243199373	7298282	0.03	33.2611
chr3	198022430	8150	0	0.0152
chr4	191154276	8232	0	0.0183
chr5	180915260	7605	0	0.0128
chr6	171115067	10035	0.0001	0.0218
chr7	159138663	15198	0.0001	0.1101

chr8	146364022	14057	0.0001	0.0411
chr9	141213431	6627	0	0.0151
chr10	135534747	23559	0.0002	0.2113
chr11	135006516	6039	0	0.0265
chr12	133851895	9844	0.0001	0.0493
chr13	115169878	1219	0	0.0036
chr14	107349540	13544	0.0001	0.1317
chr15	102531392	7376	0.0001	0.0212
chr16	90354753	4131	0	0.0125
chr17	81195210	13181	0.0002	0.1166
chr18	78077248	2841	0	0.0252
chr19	59128983	2945	0	0.0158
chr20	63025520	4711	0.0001	0.0252
chr21	48129895	1353	0	0.0096
chr22	51304566	2437	0	0.0144
chrMT	16571	1636	0.0987	0.5698
chrX	155270560	93843	0.0006	0.0897
chrY	59373566	3319	0.0001	0.0124

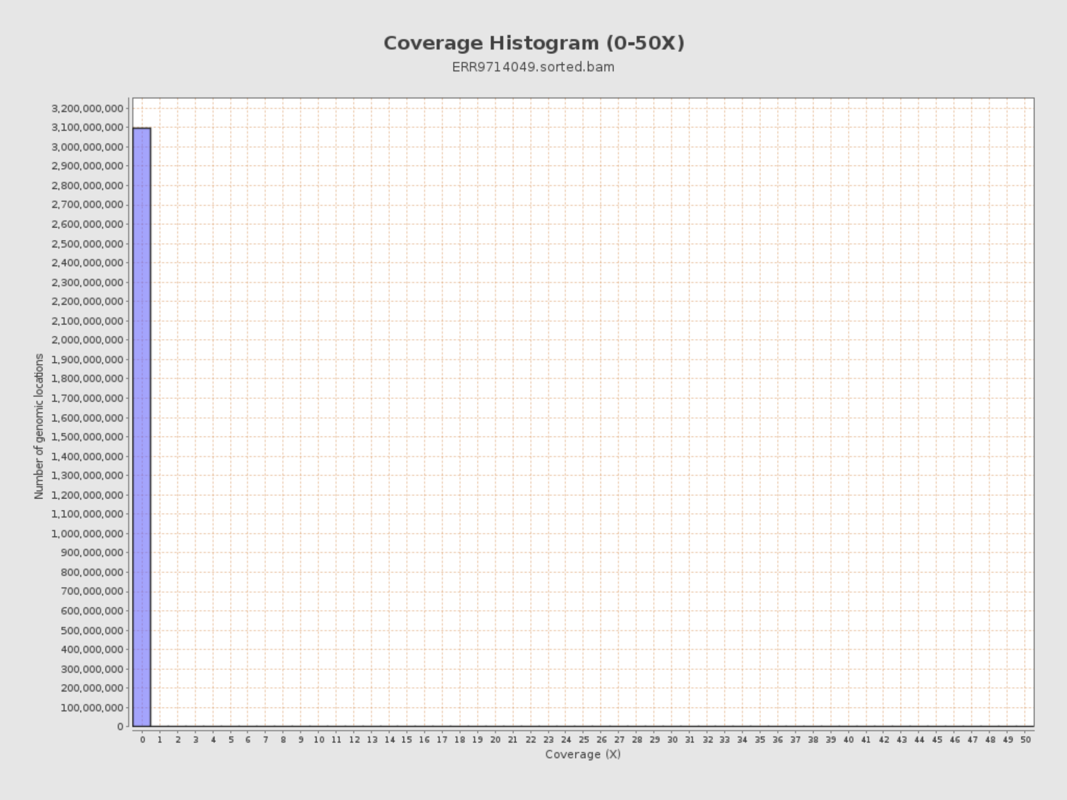
3. Results : Coverage across reference



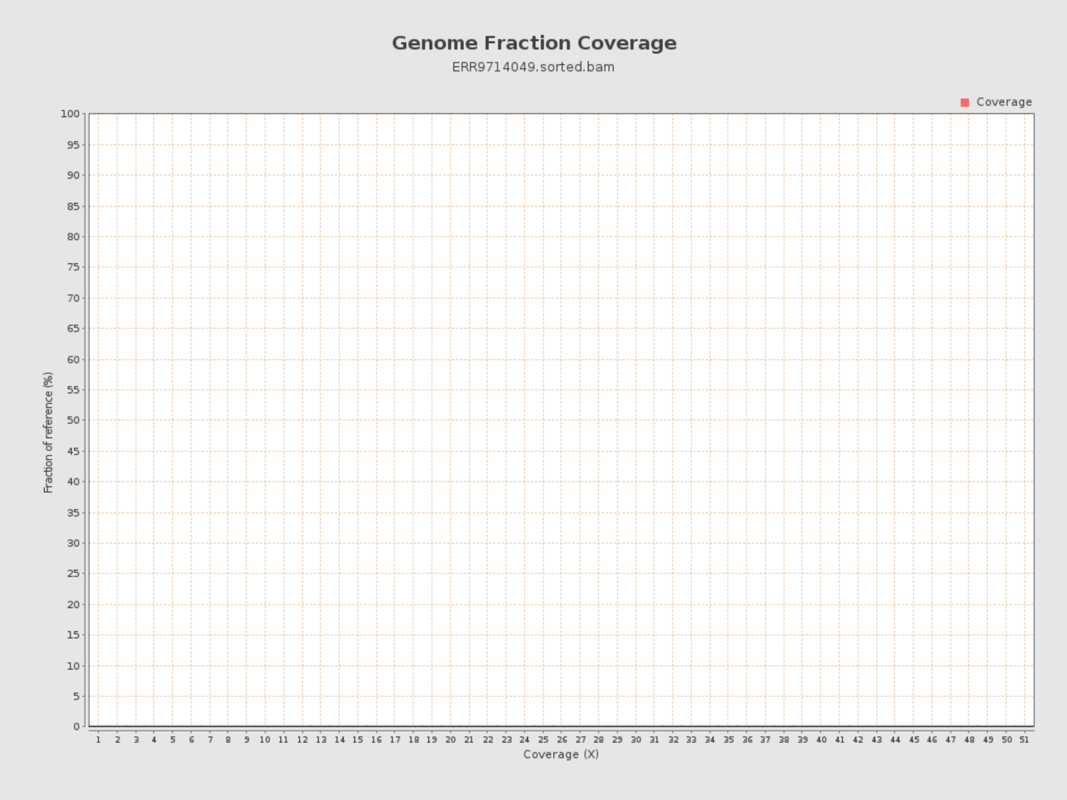
4. Results : Coverage Histogram



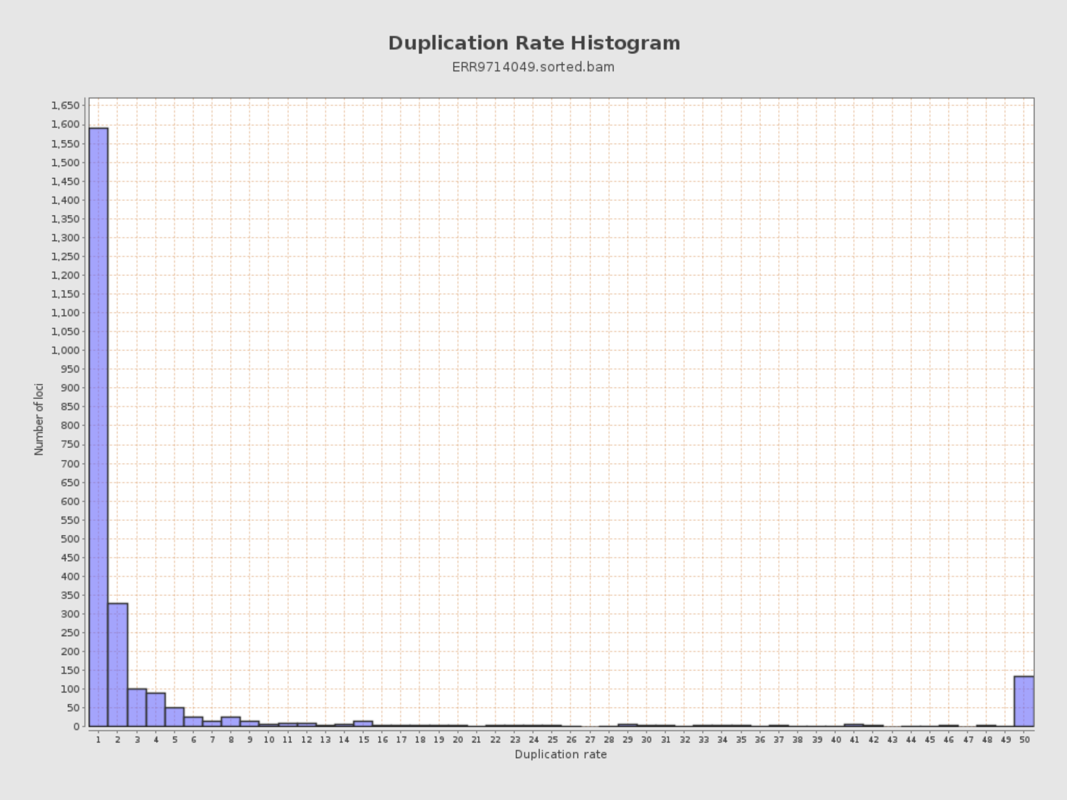
5. Results : Coverage Histogram (0-50X)



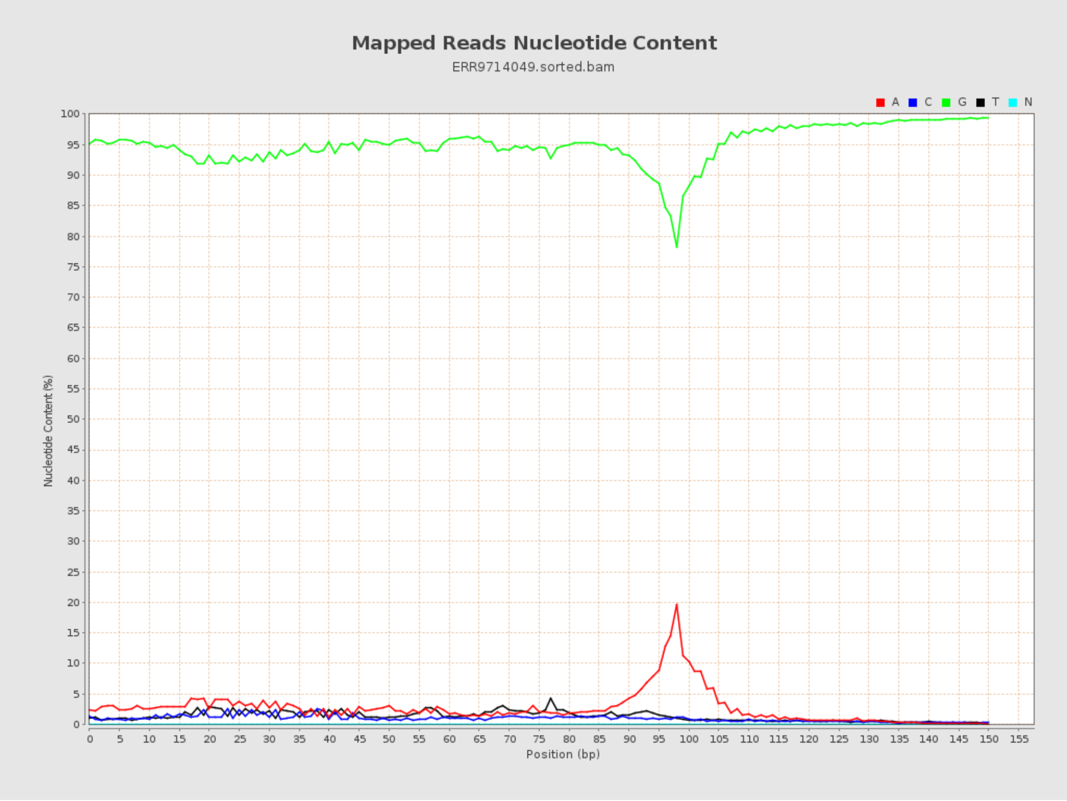
6. Results : Genome Fraction Coverage



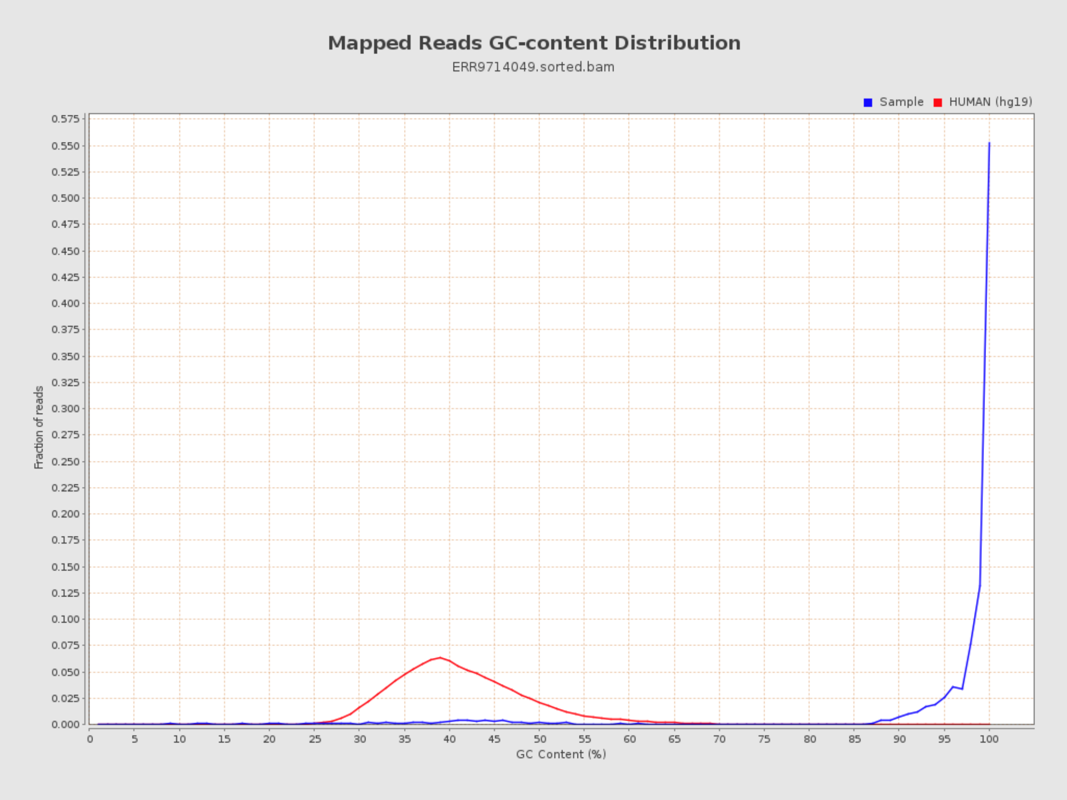
7. Results : Duplication Rate Histogram



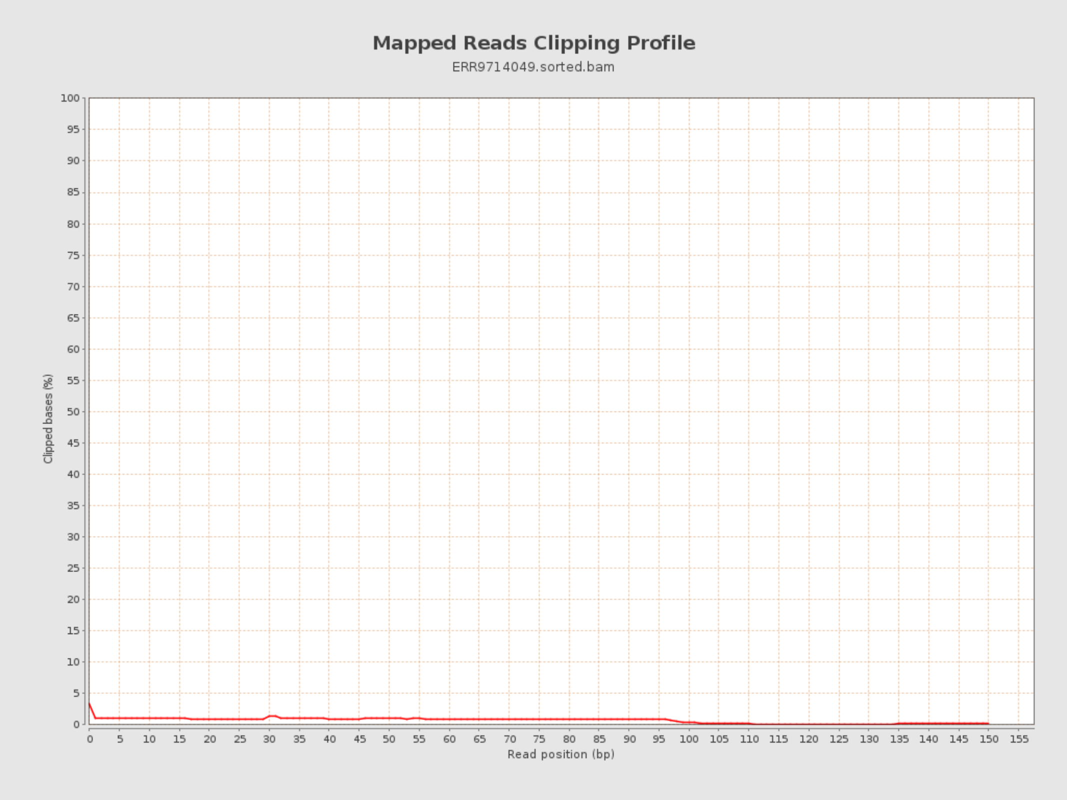
8. Results : Mapped Reads Nucleotide Content



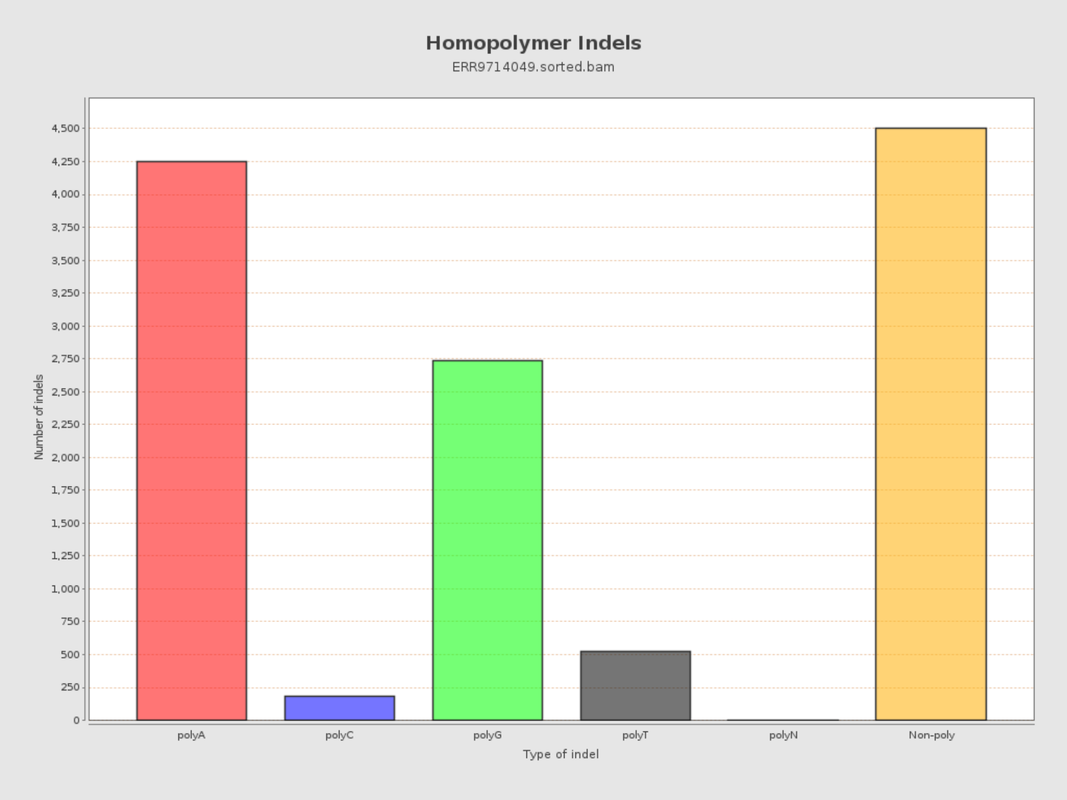
9. Results : Mapped Reads GC-content Distribution



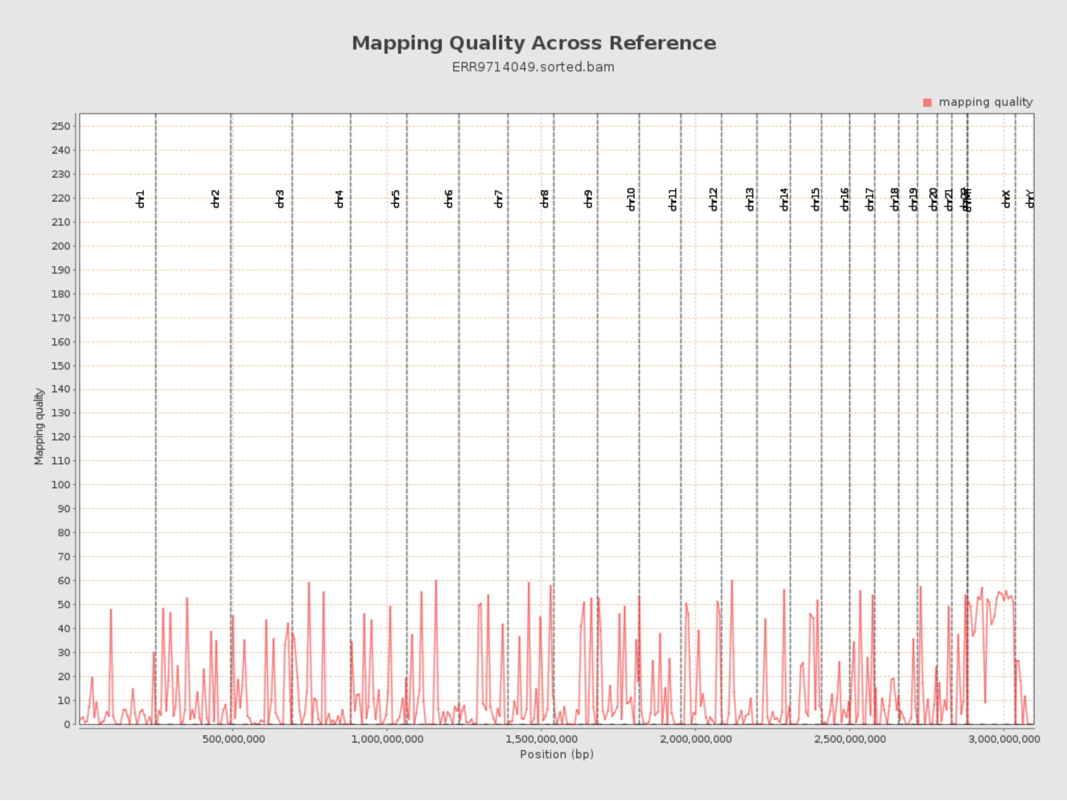
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram