Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:43:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714186.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_ERR9714186 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714186.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:43:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	58,818
Mapped reads	8,272 / 14.06%
Unmapped reads	50,546 / 85.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	205 / 0.35%
Read min/max/mean length	30 / 151 / 66.06
Duplicated reads (estimated)	7,607 / 12.93%
Duplication rate	37.59%
Clipped reads	4,941 / 8.4%

2.2. ACGT Content

Number/percentage of A's	45,530 / 5.31%
Number/percentage of C's	27,161 / 3.17%
Number/percentage of T's	32,687 / 3.82%
Number/percentage of G's	751,338 / 87.7%
Number/percentage of N's	24 / 0%
GC Percentage	90.87%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.9364

2.4. Mapping Quality

Mean Mapping Quality	9.43

2.5. Mismatches and indels

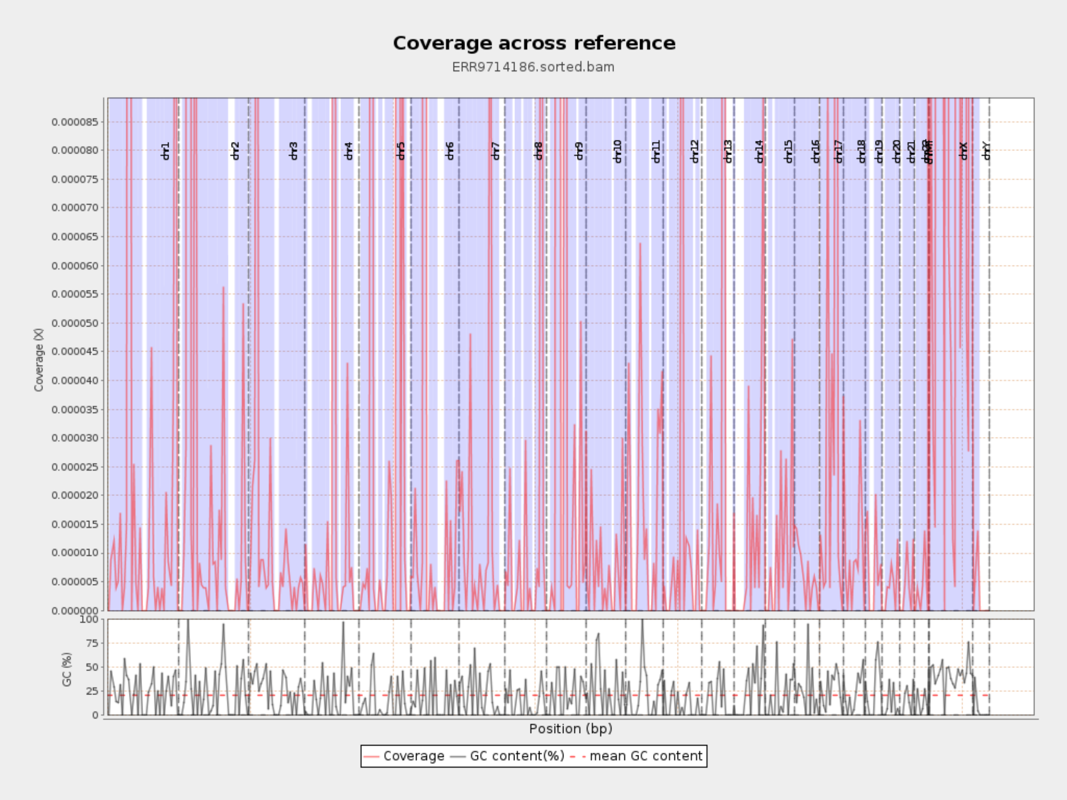
General error rate	3.11%
Mismatches	21,814
Insertions	777
Mapped reads with at least one insertion	6.53%
Deletions	629
Mapped reads with at least one deletion	7.34%
Homopolymer indels	51.92%

2.6. Chromosome stats

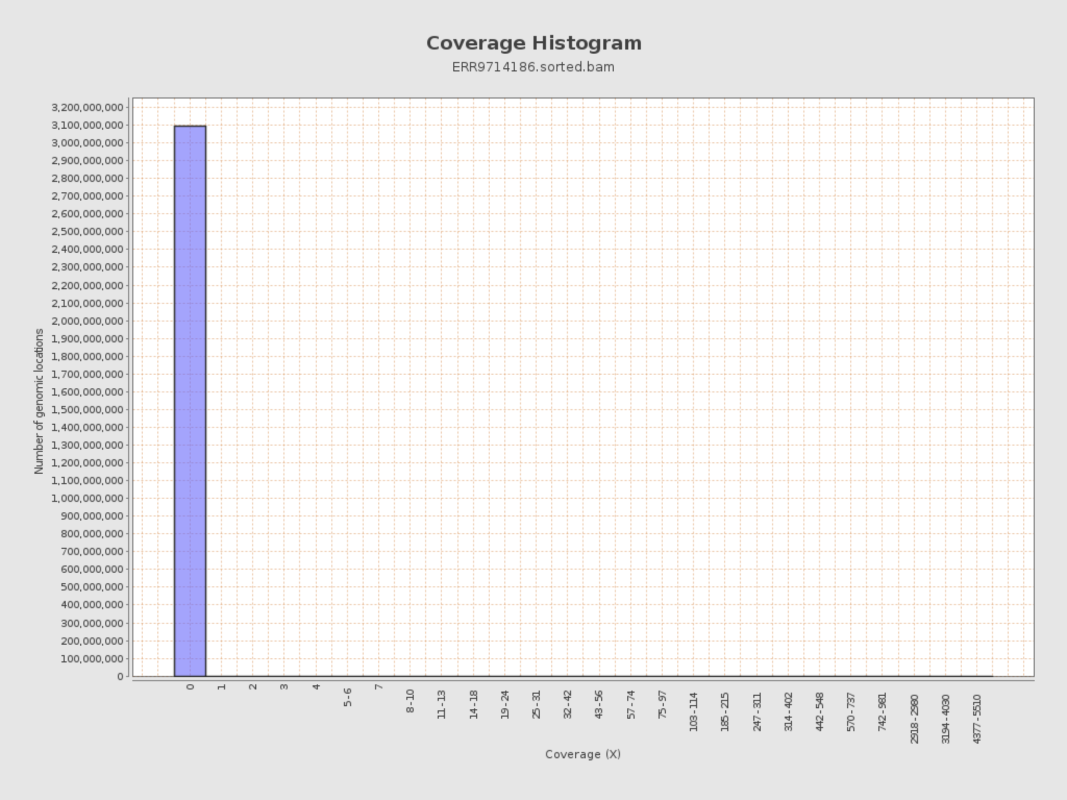
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7253	0	0.0227
chr2	243199373	735694	0.003	3.3386
chr3	198022430	2996	0	0.0099
chr4	191154276	3486	0	0.0156
chr5	180915260	10891	0.0001	0.0425
chr6	171115067	19653	0.0001	0.0829
chr7	159138663	2335	0	0.0172

chr8	146364022	2408	0	0.011
chr9	141213431	11116	0.0001	0.0437
chr10	135534747	970	0	0.0039
chr11	135006516	2314	0	0.0059
chr12	133851895	2215	0	0.0148
chr13	115169878	3831	0	0.0231
chr14	107349540	1649	0	0.0121
chr15	102531392	1097	0	0.0044
chr16	90354753	561	0	0.0026
chr17	81195210	3592	0	0.0242
chr18	78077248	746	0	0.0034
chr19	59128983	425	0	0.0029
chr20	63025520	263	0	0.002
chr21	48129895	221	0	0.0021
chr22	51304566	201	0	0.002
chrMT	16571	297	0.0179	0.1327
chrX	155270560	45741	0.0003	0.0942
chrY	59373566	139	0	0.0015

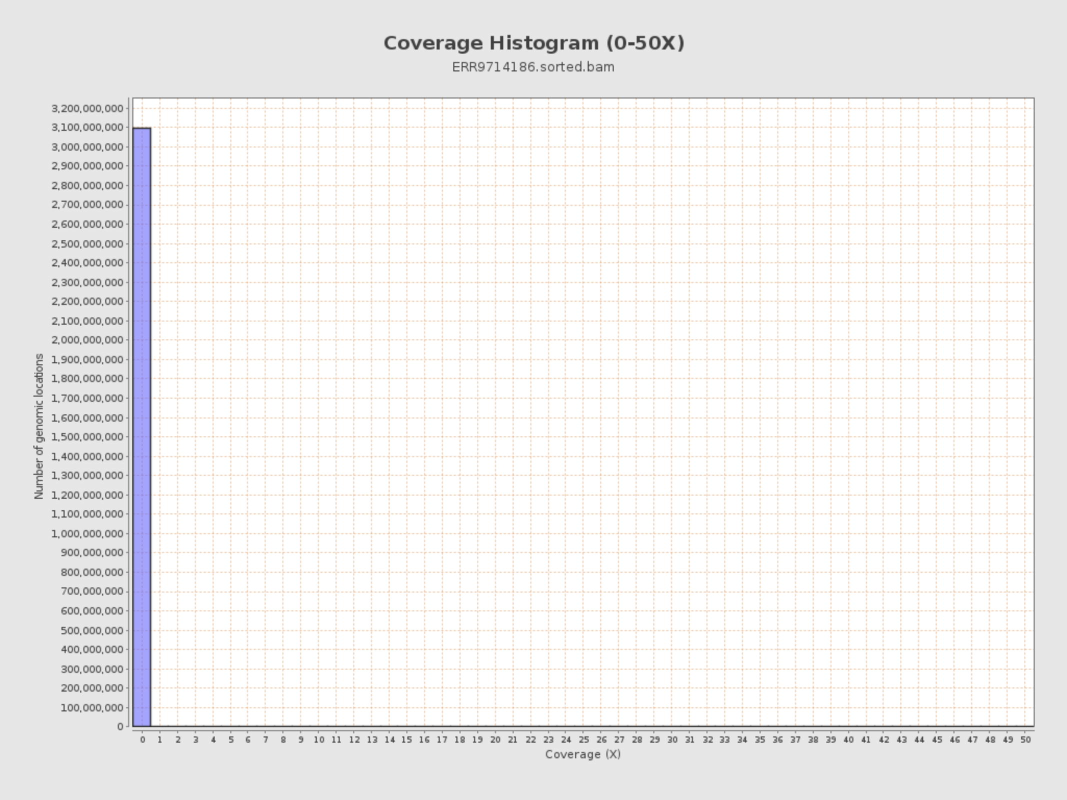
3. Results : Coverage across reference



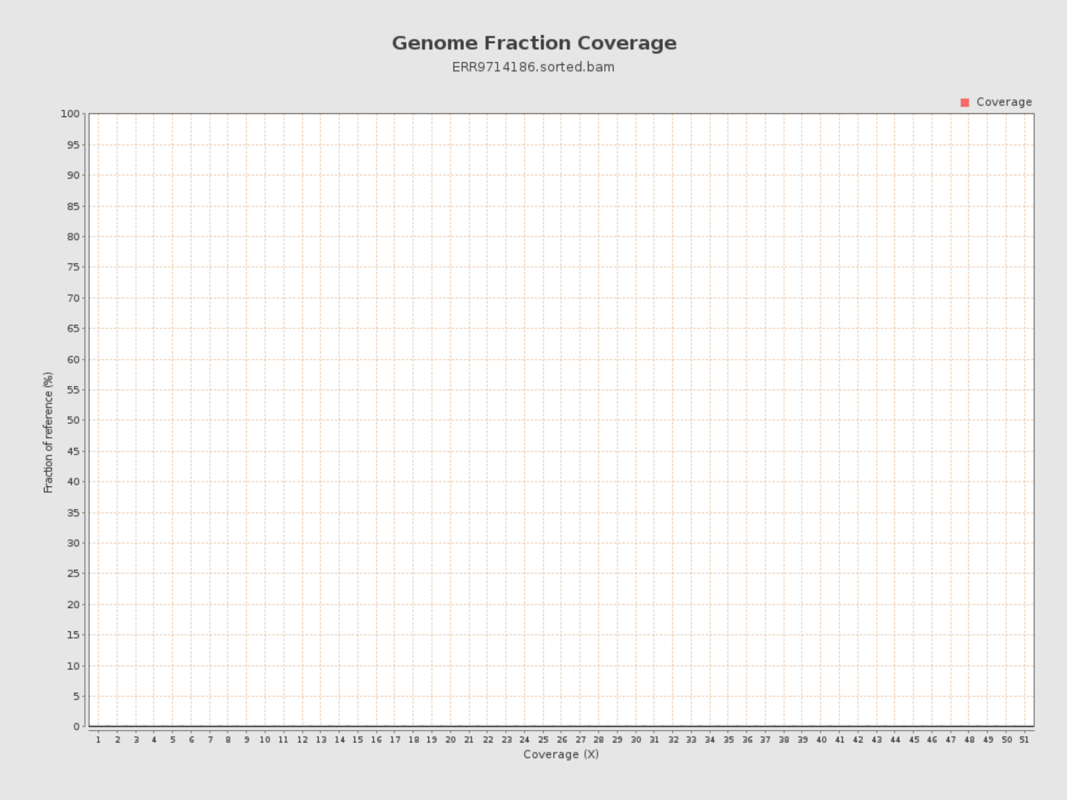
4. Results : Coverage Histogram



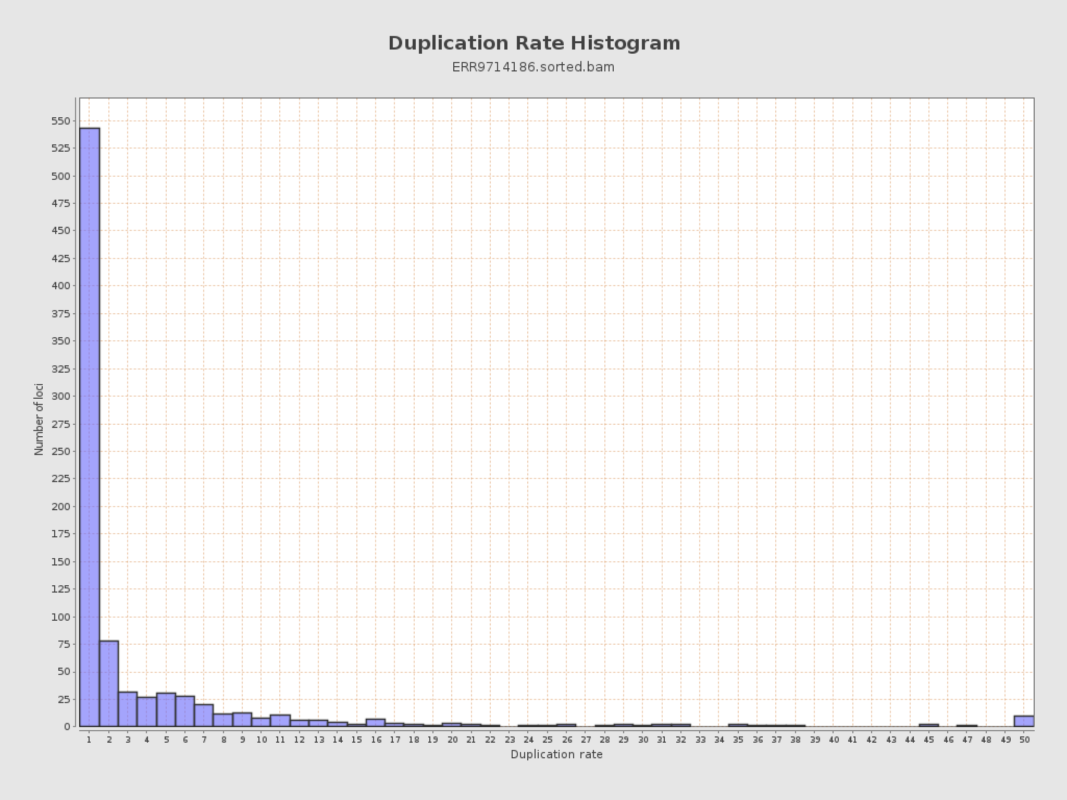
5. Results : Coverage Histogram (0-50X)



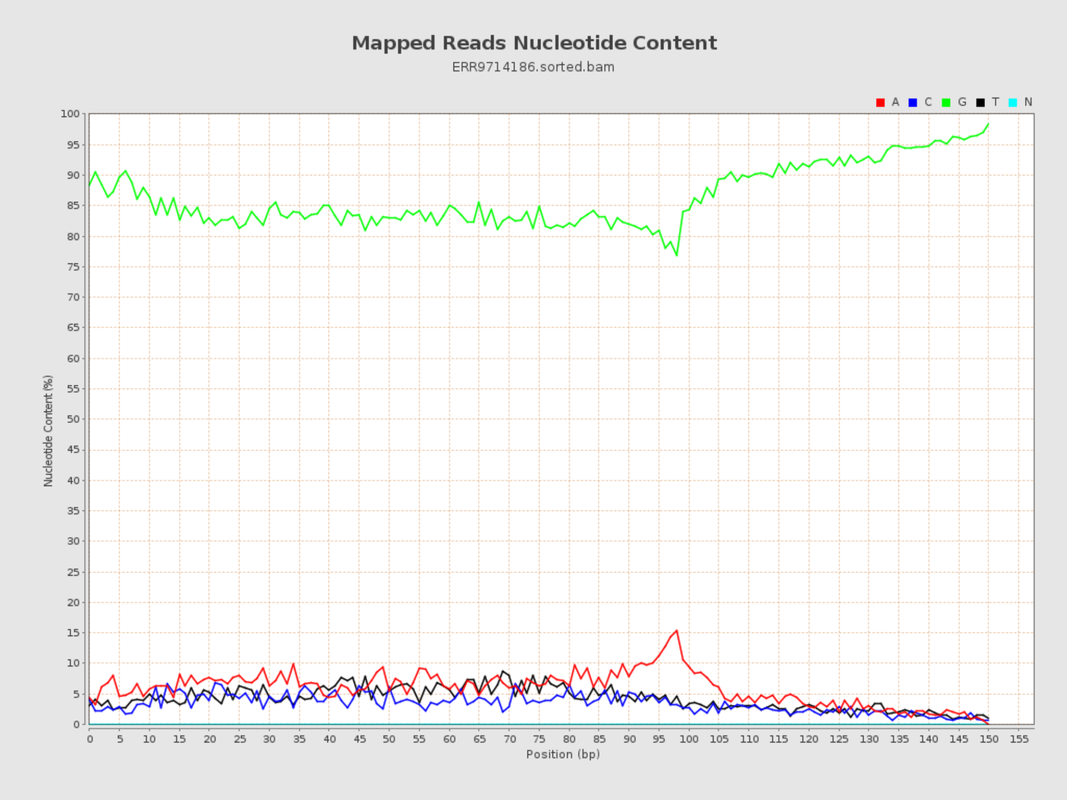
6. Results : Genome Fraction Coverage



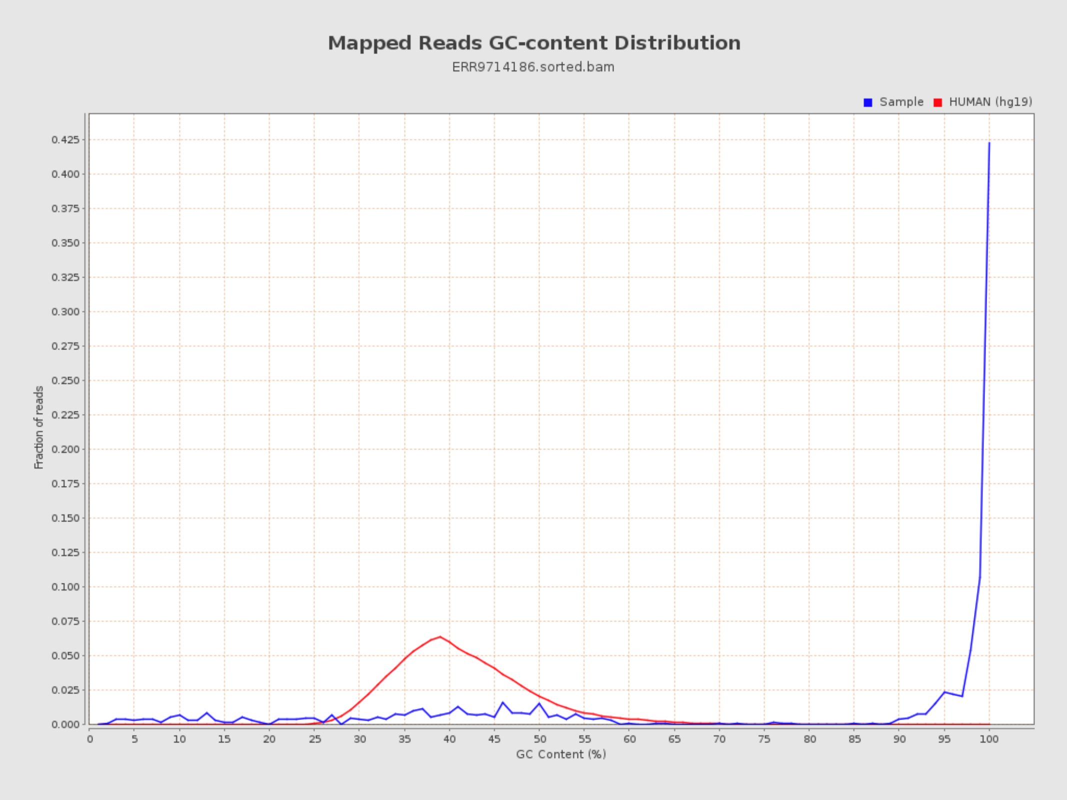
7. Results : Duplication Rate Histogram



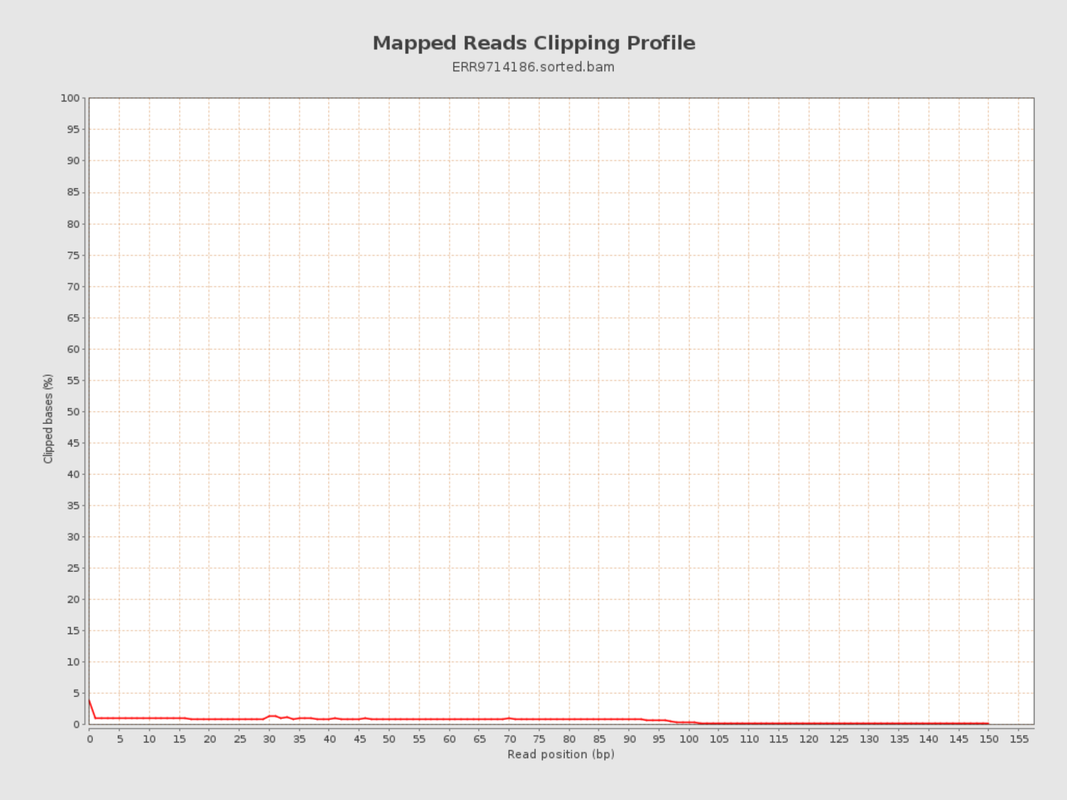
8. Results : Mapped Reads Nucleotide Content



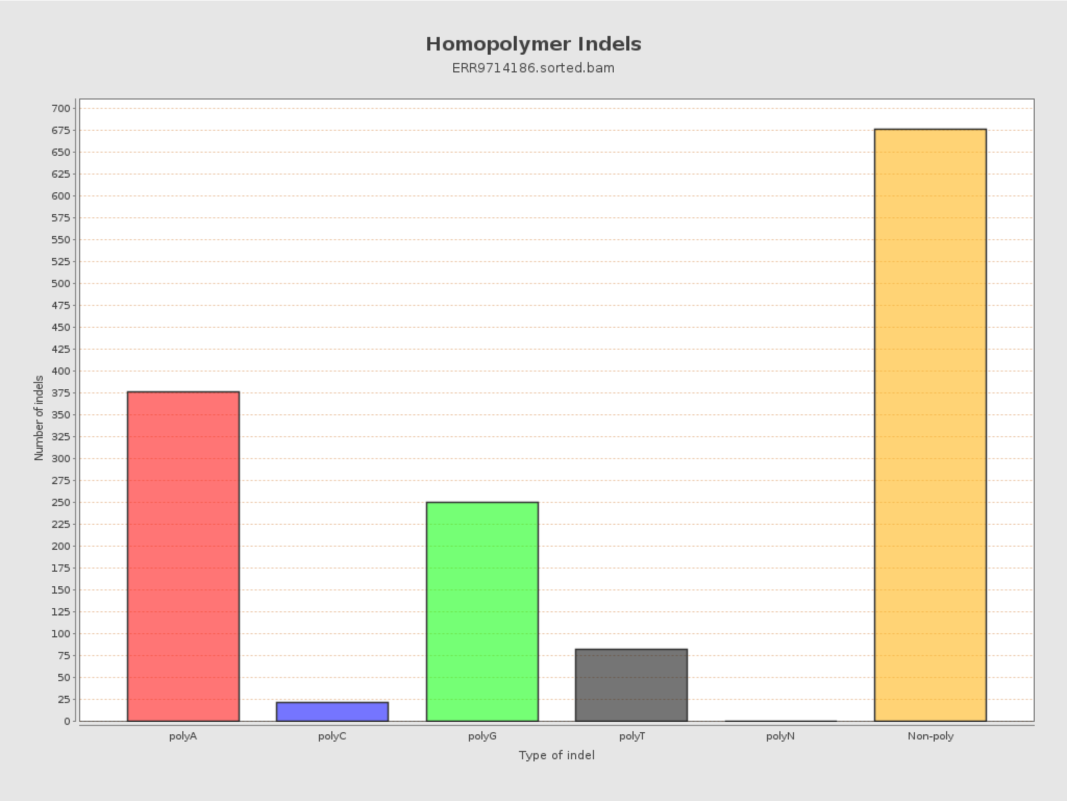
9. Results : Mapped Reads GC-content Distribution



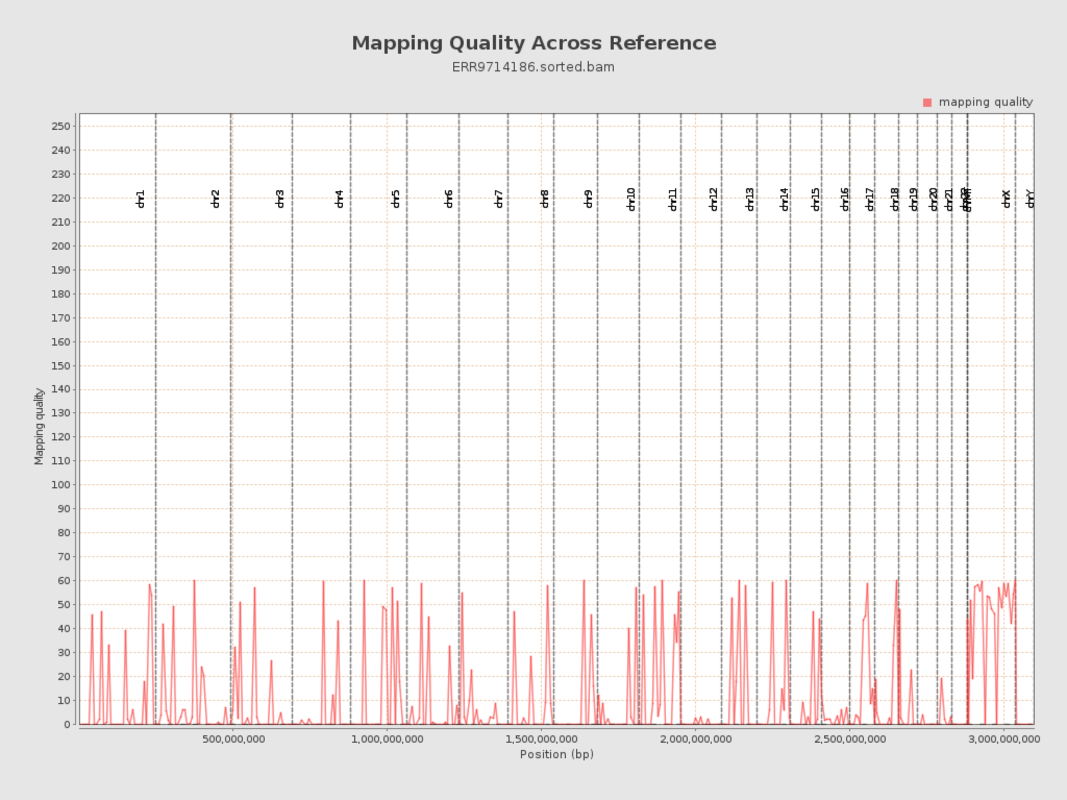
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram