Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:46:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714171.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_ERR9714171 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714171.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:46:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714171.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,729,792
Mapped reads	115,333 / 6.67%
Unmapped reads	1,614,459 / 93.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,398 / 0.14%
Read min/max/mean length	30 / 151 / 53.16
Duplicated reads (estimated)	110,832 / 6.41%
Duplication rate	28.64%
Clipped reads	80,373 / 4.65%

2.2. ACGT Content

Number/percentage of A's	496,628 / 4.95%
Number/percentage of C's	259,518 / 2.58%
Number/percentage of T's	337,280 / 3.36%
Number/percentage of G's	8,944,655 / 89.09%
Number/percentage of N's	1,636 / 0.02%
GC Percentage	91.68%

2.3. Coverage

Mean	0.0033

Standard Deviation	10.6441

2.4. Mapping Quality

Mean Mapping Quality	19.66

2.5. Mismatches and indels

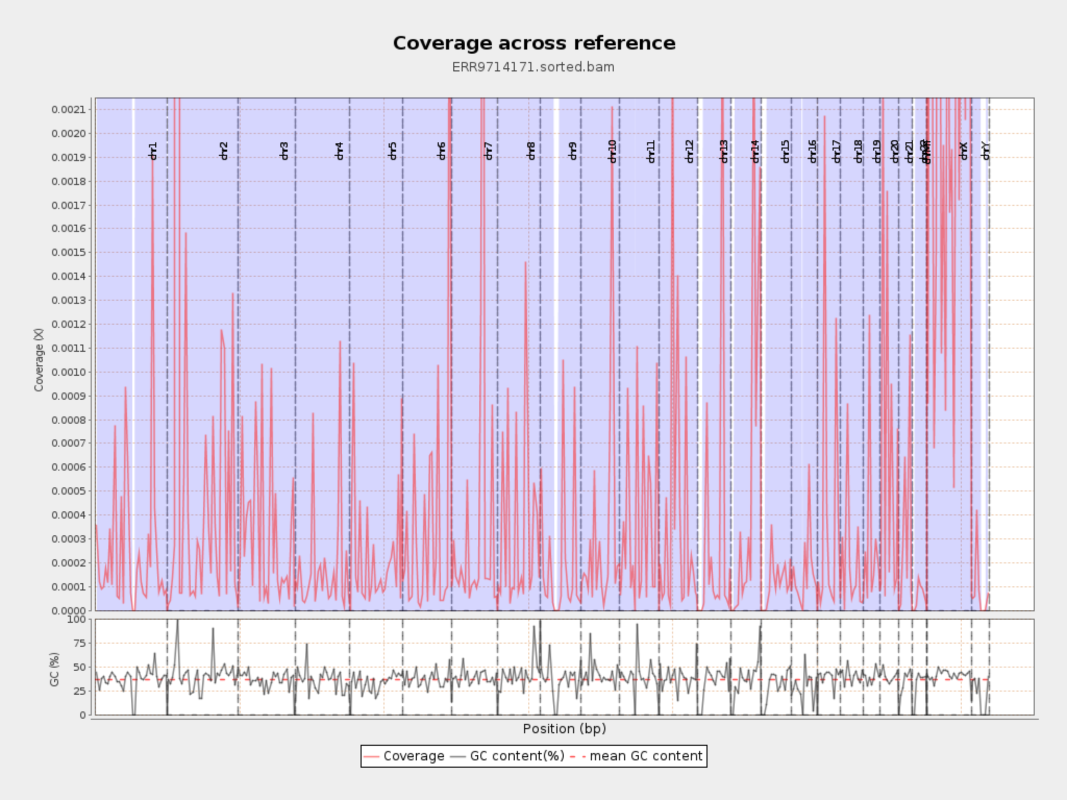
General error rate	3.05%
Mismatches	237,842
Insertions	10,661
Mapped reads with at least one insertion	6.51%
Deletions	6,848
Mapped reads with at least one deletion	5.73%
Homopolymer indels	55.74%

2.6. Chromosome stats

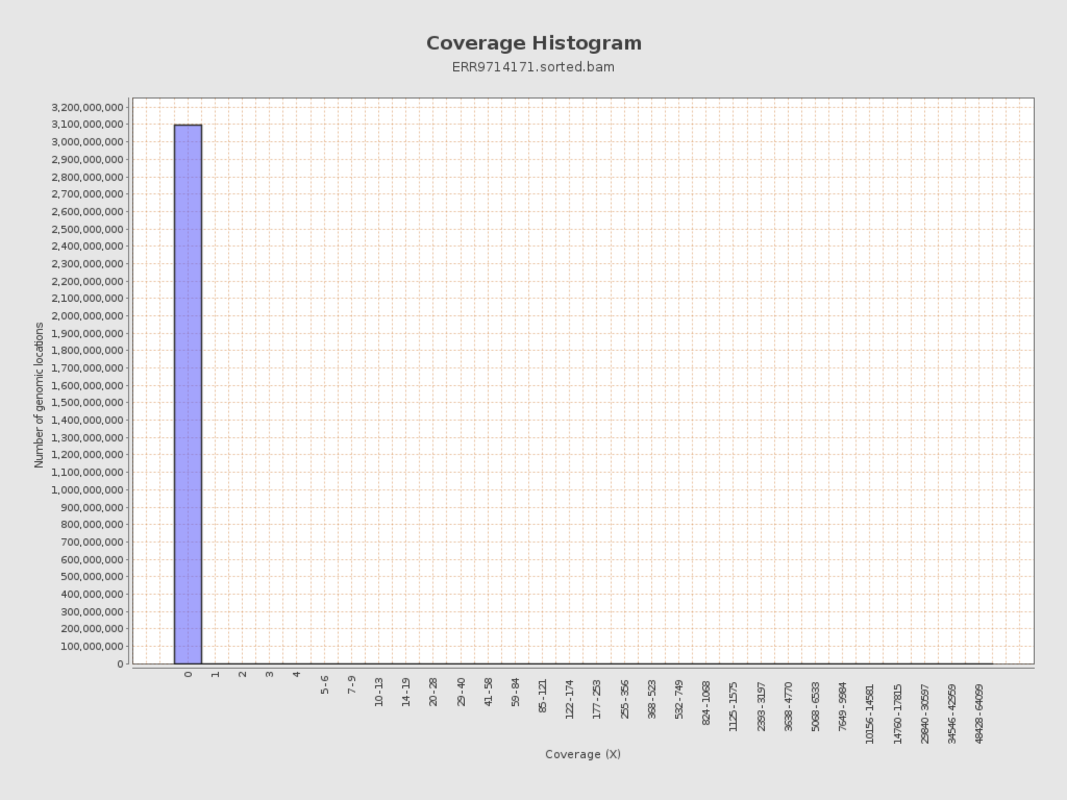
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	66452	0.0003	0.083
chr2	243199373	8853812	0.0364	37.9705
chr3	198022430	66176	0.0003	0.1053
chr4	191154276	36074	0.0002	0.065
chr5	180915260	42028	0.0002	0.0684
chr6	171115067	67557	0.0004	0.1621
chr7	159138663	69109	0.0004	0.4439

chr8	146364022	53200	0.0004	0.1187
chr9	141213431	29687	0.0002	0.0762
chr10	135534747	42846	0.0003	0.0901
chr11	135006516	50566	0.0004	0.1435
chr12	133851895	56229	0.0004	0.1659
chr13	115169878	33776	0.0003	0.165
chr14	107349540	59339	0.0006	0.3335
chr15	102531392	12413	0.0001	0.0294
chr16	90354753	14775	0.0002	0.0465
chr17	81195210	35541	0.0004	0.188
chr18	78077248	16234	0.0002	0.0641
chr19	59128983	17560	0.0003	0.1
chr20	63025520	45114	0.0007	0.3467
chr21	48129895	17607	0.0004	0.1052
chr22	51304566	3009	0.0001	0.012
chrMT	16571	12117	0.7312	6.4292
chrX	155270560	370186	0.0024	0.331
chrY	59373566	5220	0.0001	0.0296

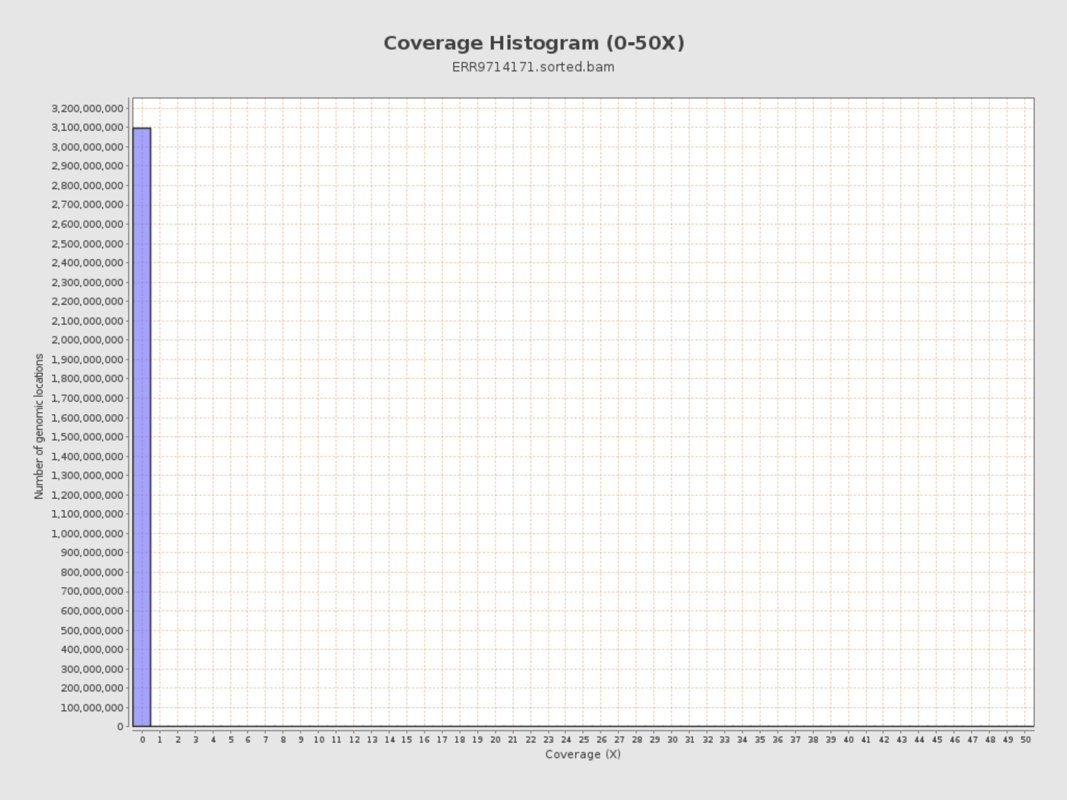
3. Results : Coverage across reference



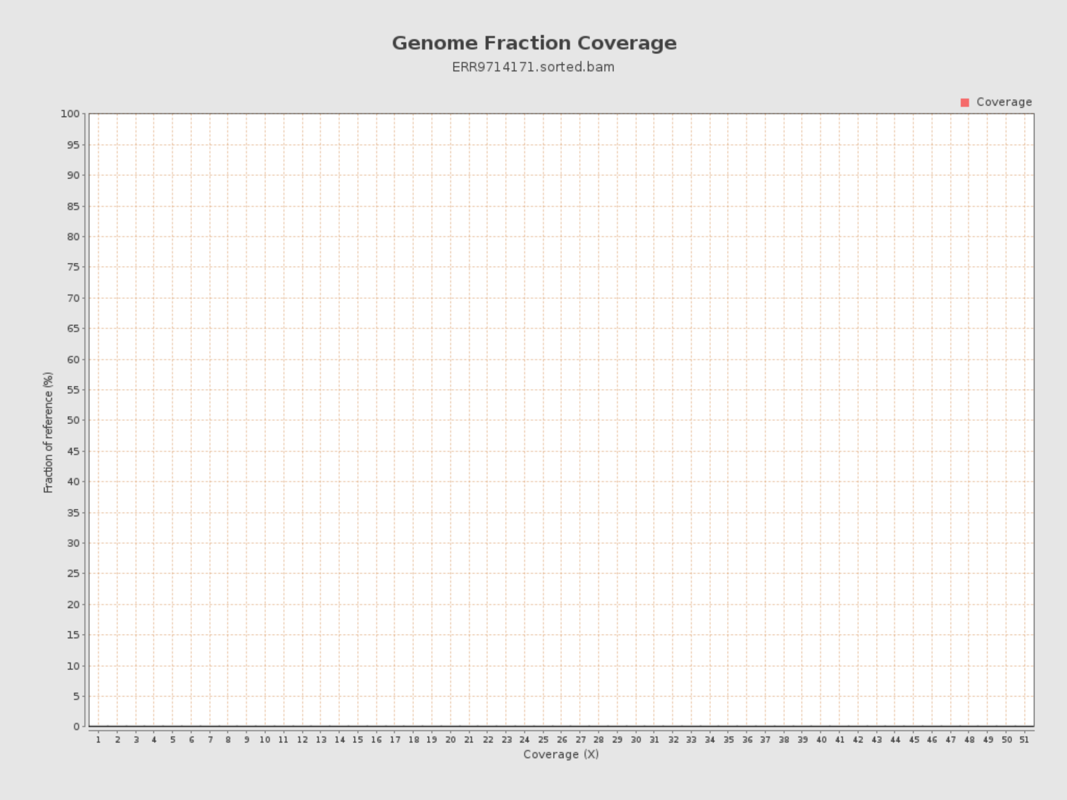
4. Results : Coverage Histogram



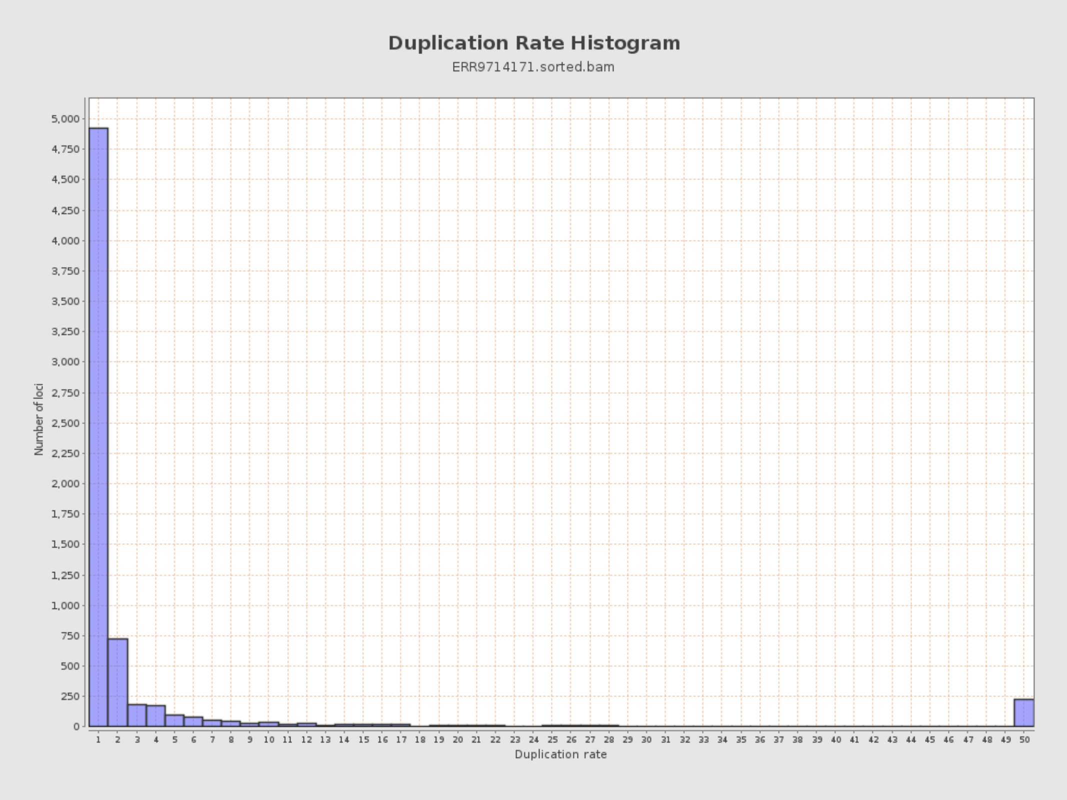
5. Results : Coverage Histogram (0-50X)



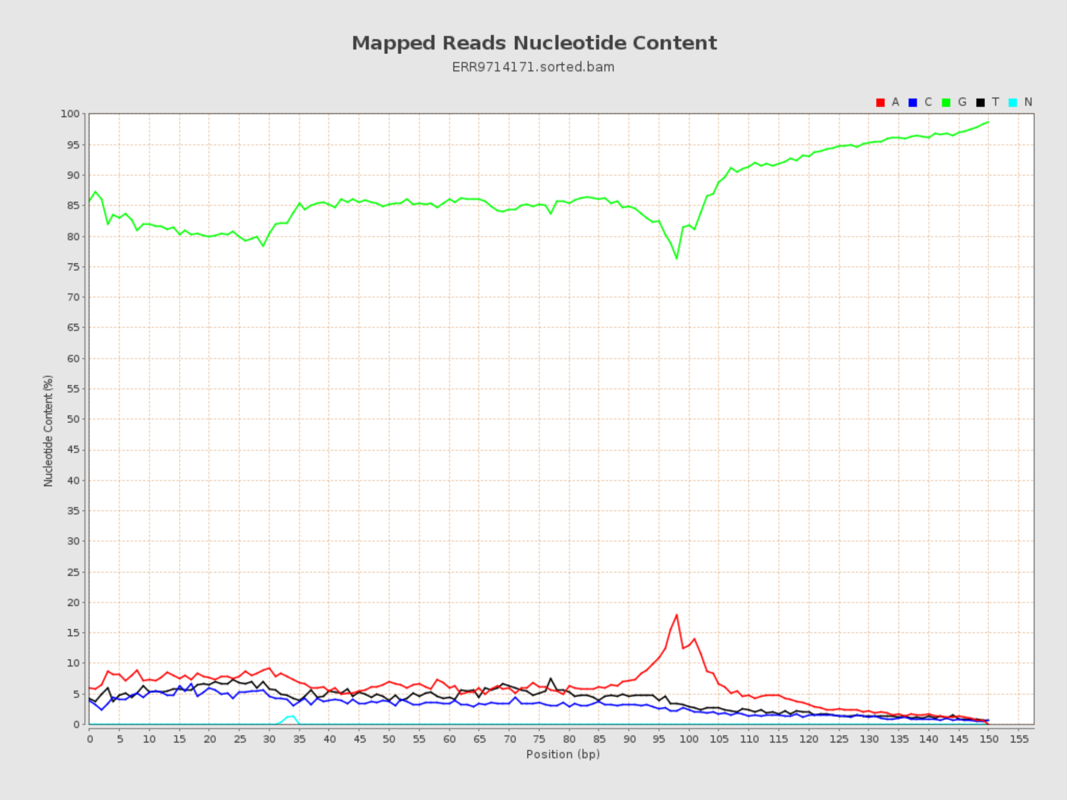
6. Results : Genome Fraction Coverage



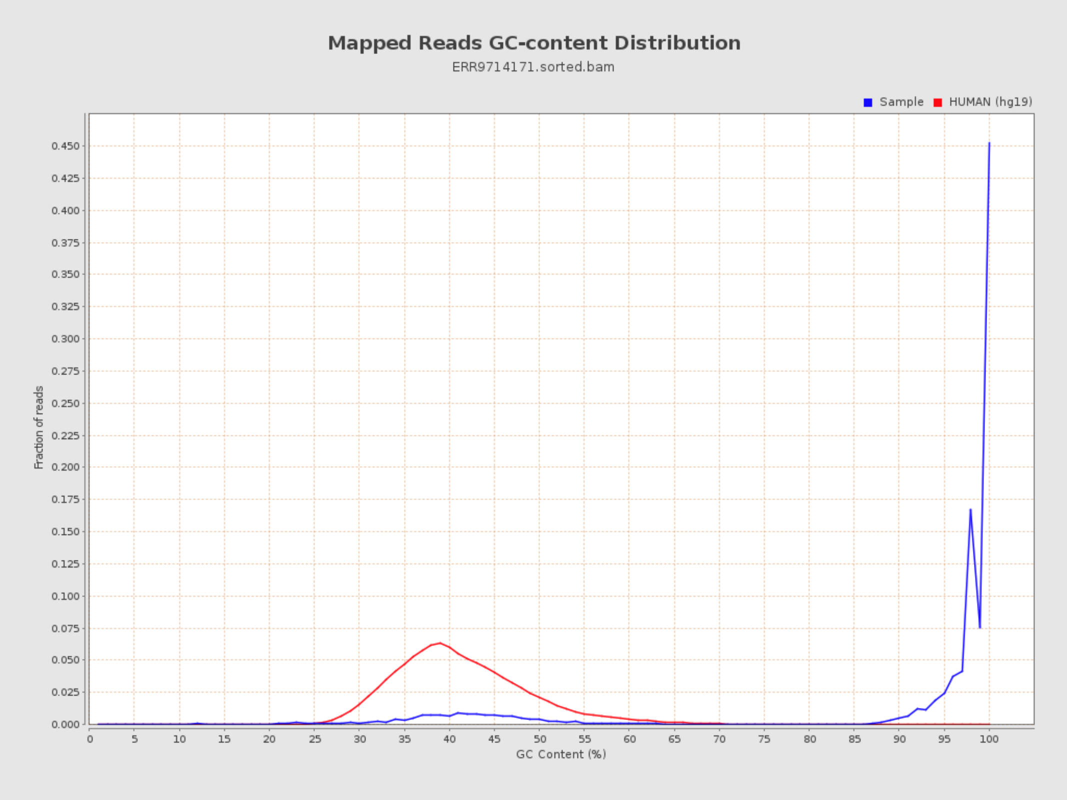
7. Results : Duplication Rate Histogram



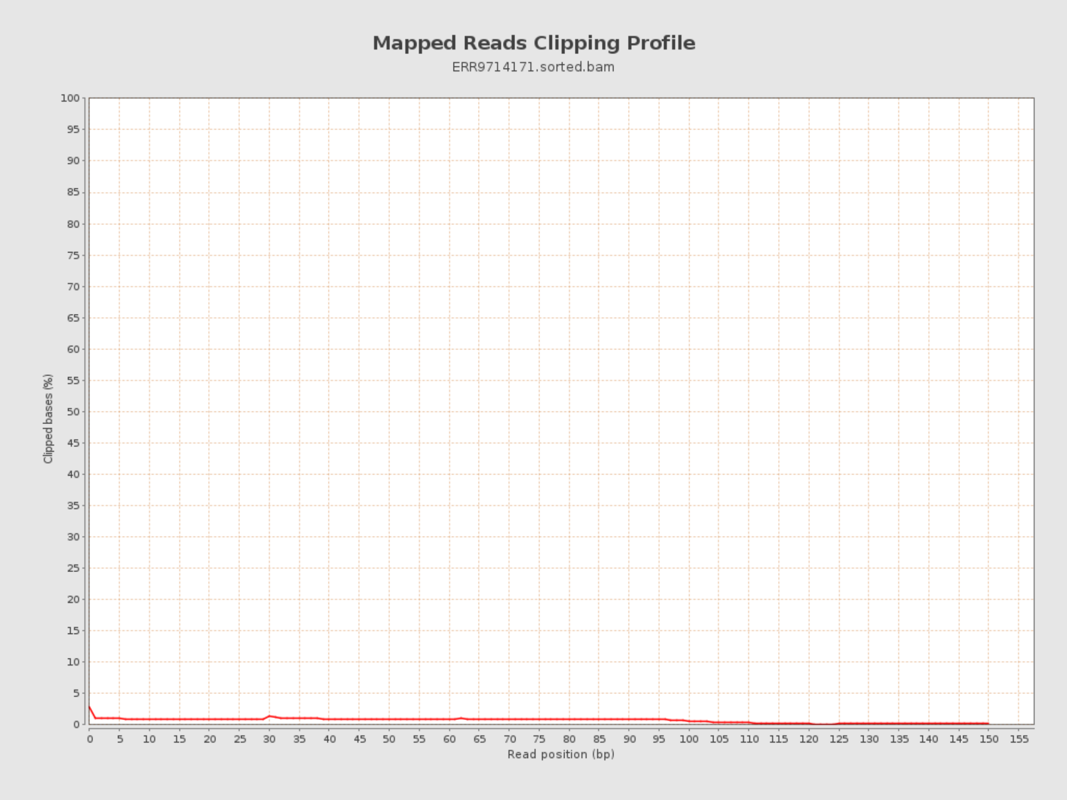
8. Results : Mapped Reads Nucleotide Content



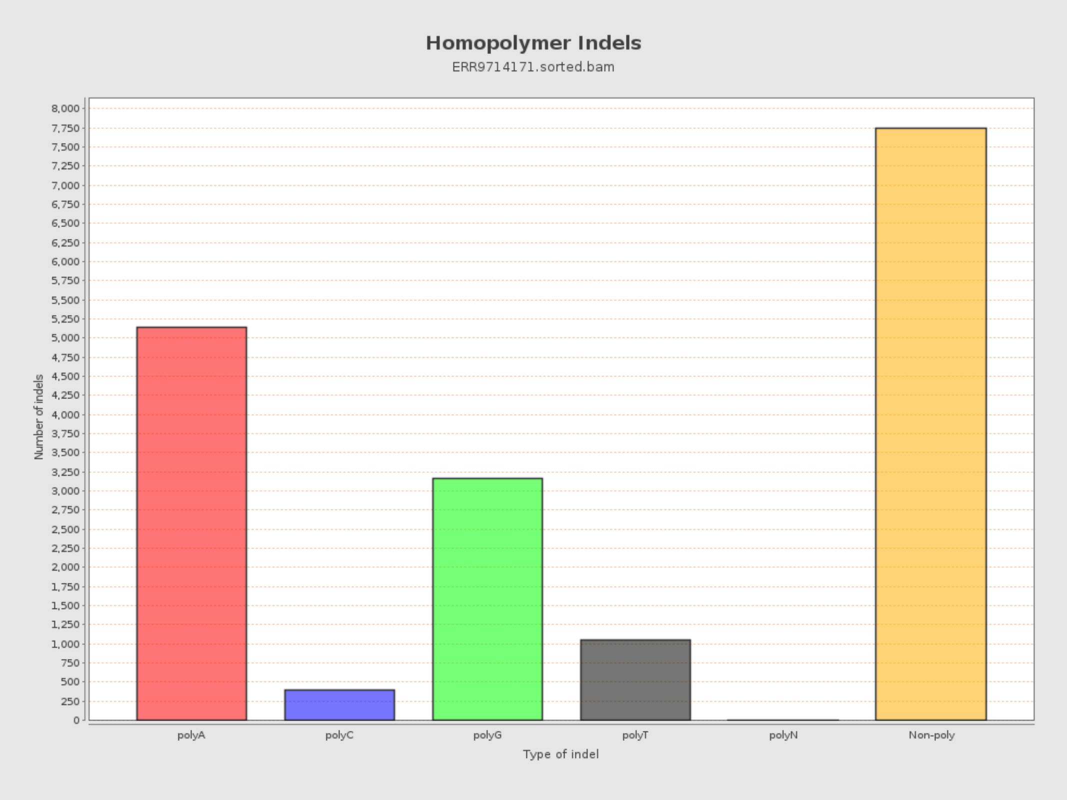
9. Results : Mapped Reads GC-content Distribution



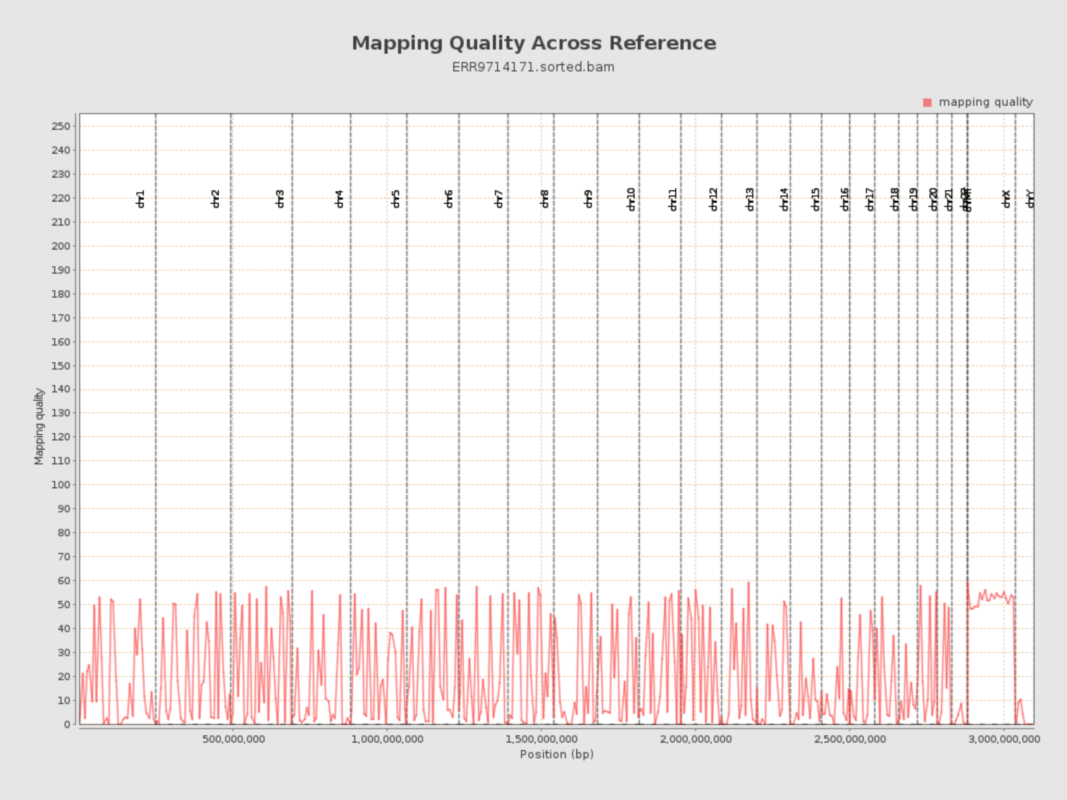
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram