Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:42:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714185.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_ERR9714185 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:41:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,904
Mapped reads	9,866 / 17.34%
Unmapped reads	47,038 / 82.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	166 / 0.29%
Read min/max/mean length	30 / 151 / 63.58
Duplicated reads (estimated)	8,988 / 15.8%
Duplication rate	40.13%
Clipped reads	6,261 / 11%

2.2. ACGT Content

Number/percentage of A's	52,576 / 5.95%
Number/percentage of C's	30,430 / 3.45%
Number/percentage of T's	39,872 / 4.51%
Number/percentage of G's	760,223 / 86.08%
Number/percentage of N's	15 / 0%
GC Percentage	89.53%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.9502

2.4. Mapping Quality

Mean Mapping Quality	12.31

2.5. Mismatches and indels

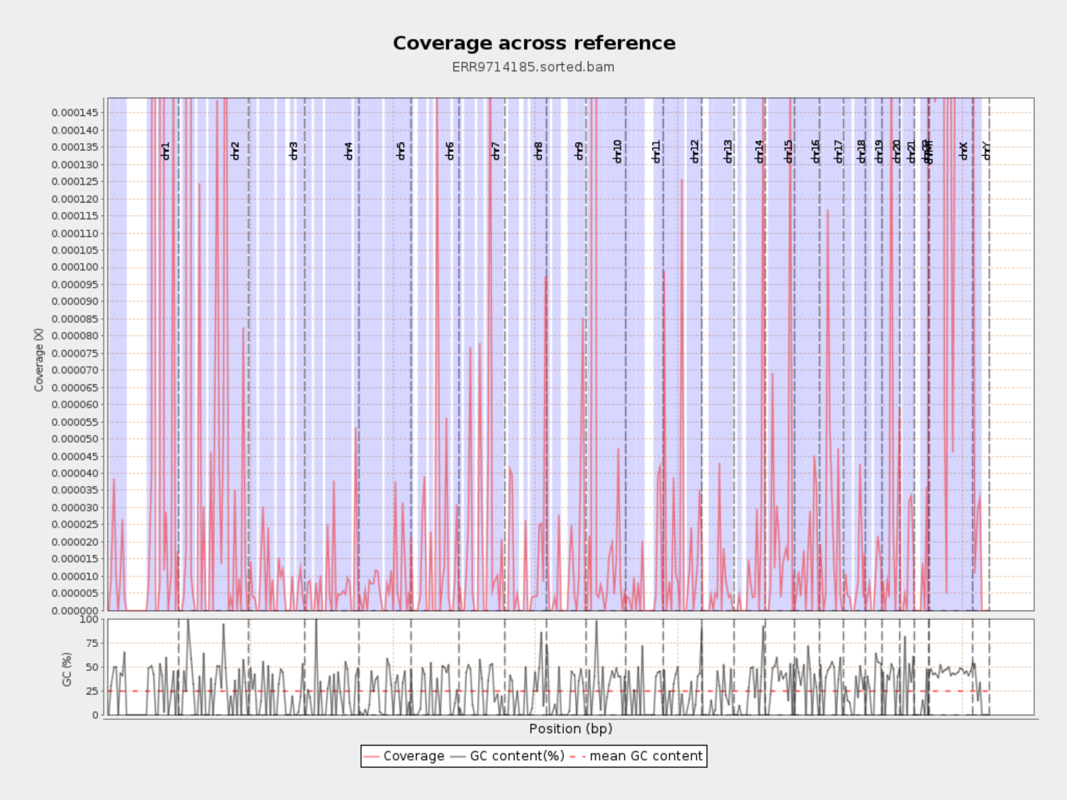
General error rate	3.03%
Mismatches	21,440
Insertions	848
Mapped reads with at least one insertion	6.13%
Deletions	522
Mapped reads with at least one deletion	5.05%
Homopolymer indels	55.55%

2.6. Chromosome stats

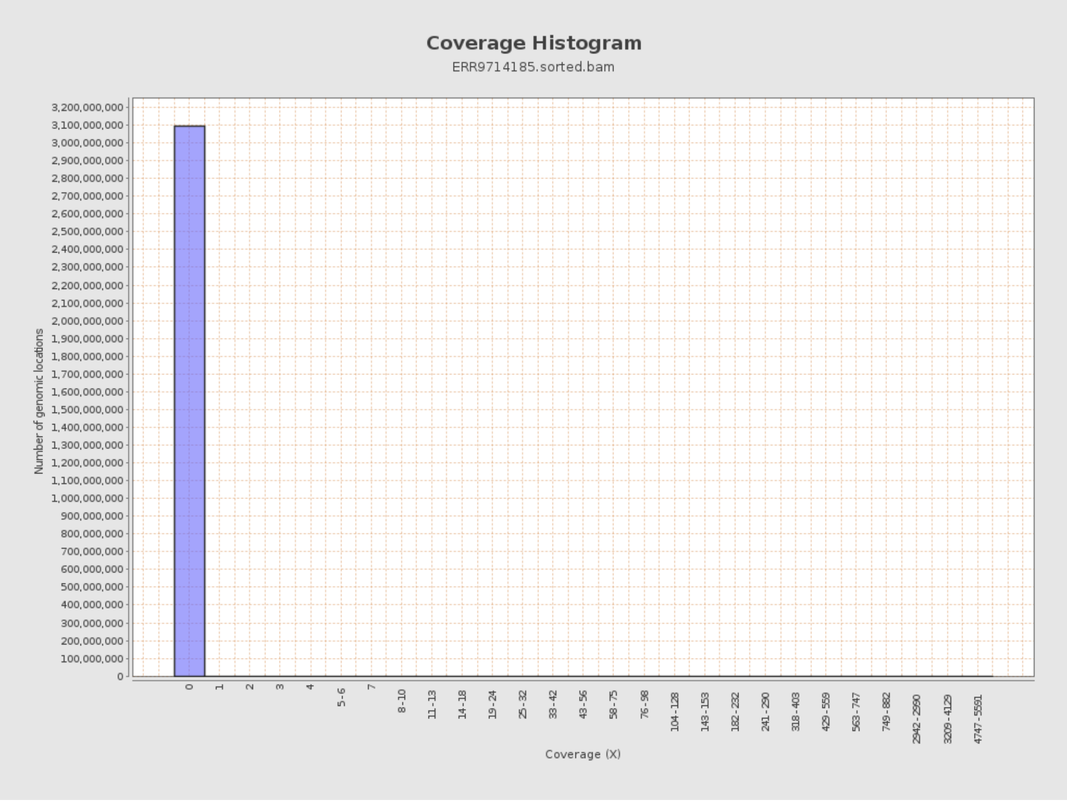
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33356	0.0001	0.2791
chr2	243199373	741033	0.003	3.3674
chr3	198022430	1339	0	0.0032
chr4	191154276	1555	0	0.0036
chr5	180915260	1413	0	0.0034
chr6	171115067	2966	0	0.0073
chr7	159138663	3802	0	0.0187

chr8	146364022	2076	0	0.0061
chr9	141213431	1886	0	0.0049
chr10	135534747	24427	0.0002	0.3613
chr11	135006516	1048	0	0.0043
chr12	133851895	2950	0	0.0106
chr13	115169878	710	0	0.0031
chr14	107349540	1897	0	0.0179
chr15	102531392	2743	0	0.0171
chr16	90354753	1286	0	0.0048
chr17	81195210	2236	0	0.0115
chr18	78077248	682	0	0.0036
chr19	59128983	454	0	0.0032
chr20	63025520	2035	0	0.0103
chr21	48129895	636	0	0.0049
chr22	51304566	387	0	0.0041
chrMT	16571	4455	0.2688	1.1911
chrX	155270560	49316	0.0003	0.0402
chrY	59373566	1210	0	0.0071

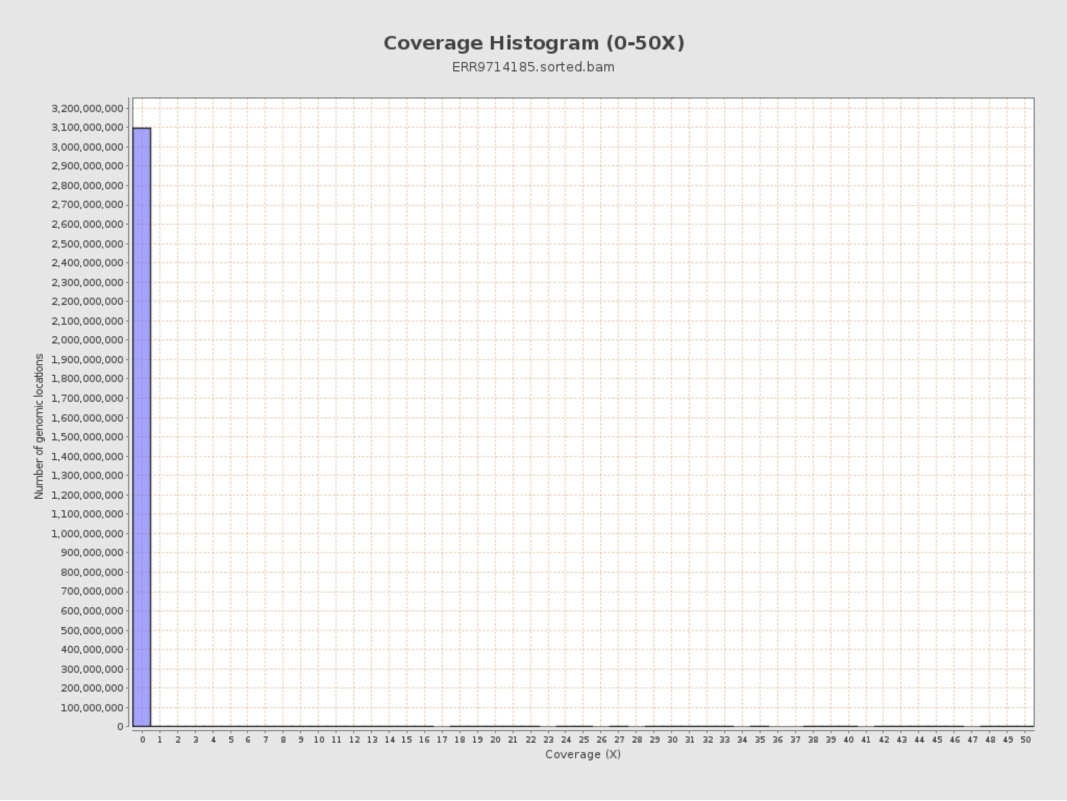
3. Results : Coverage across reference



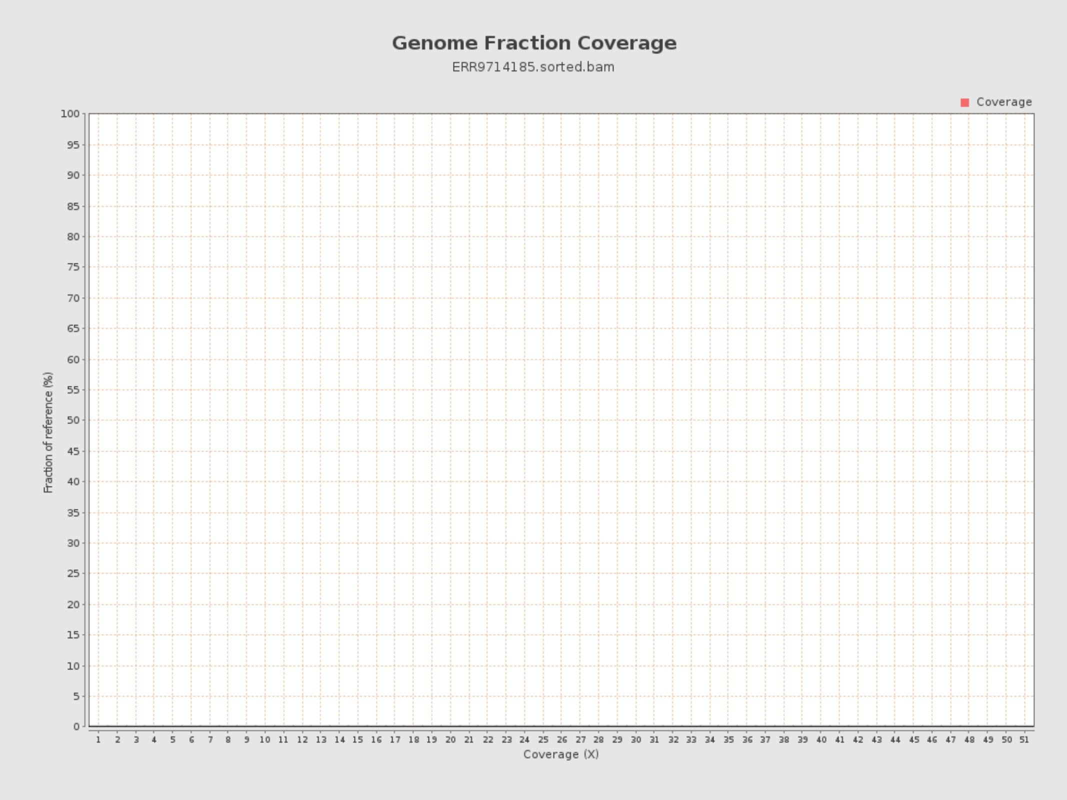
4. Results : Coverage Histogram



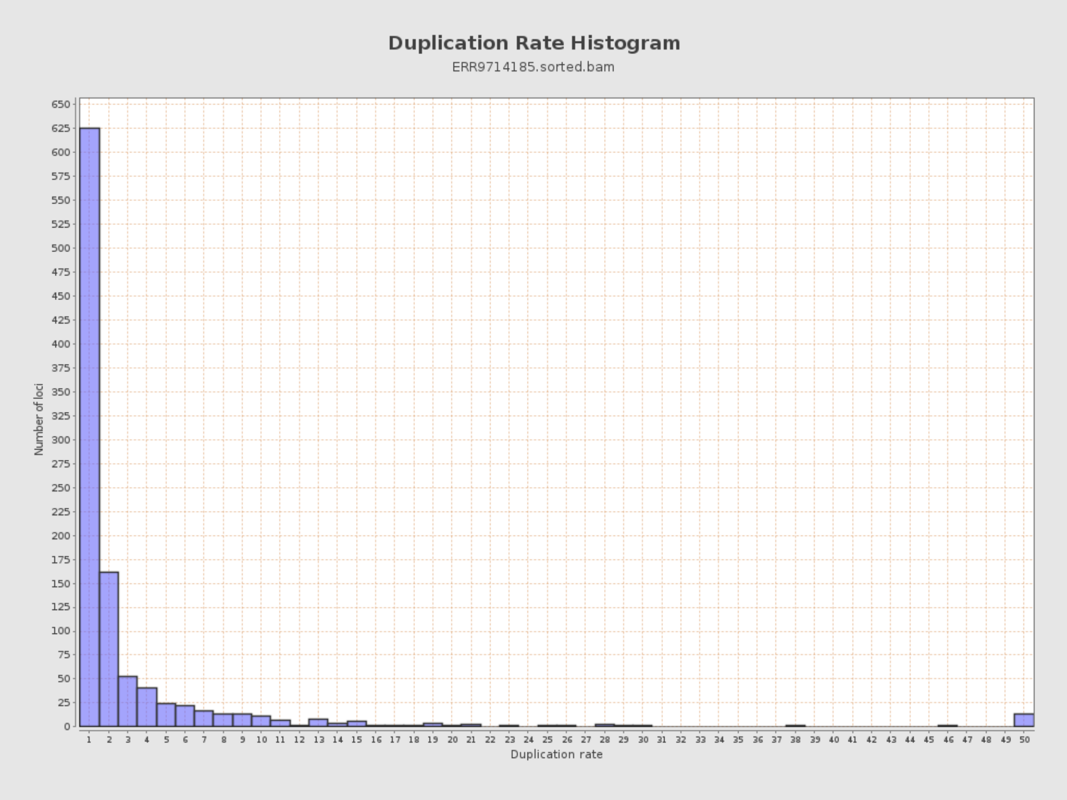
5. Results : Coverage Histogram (0-50X)



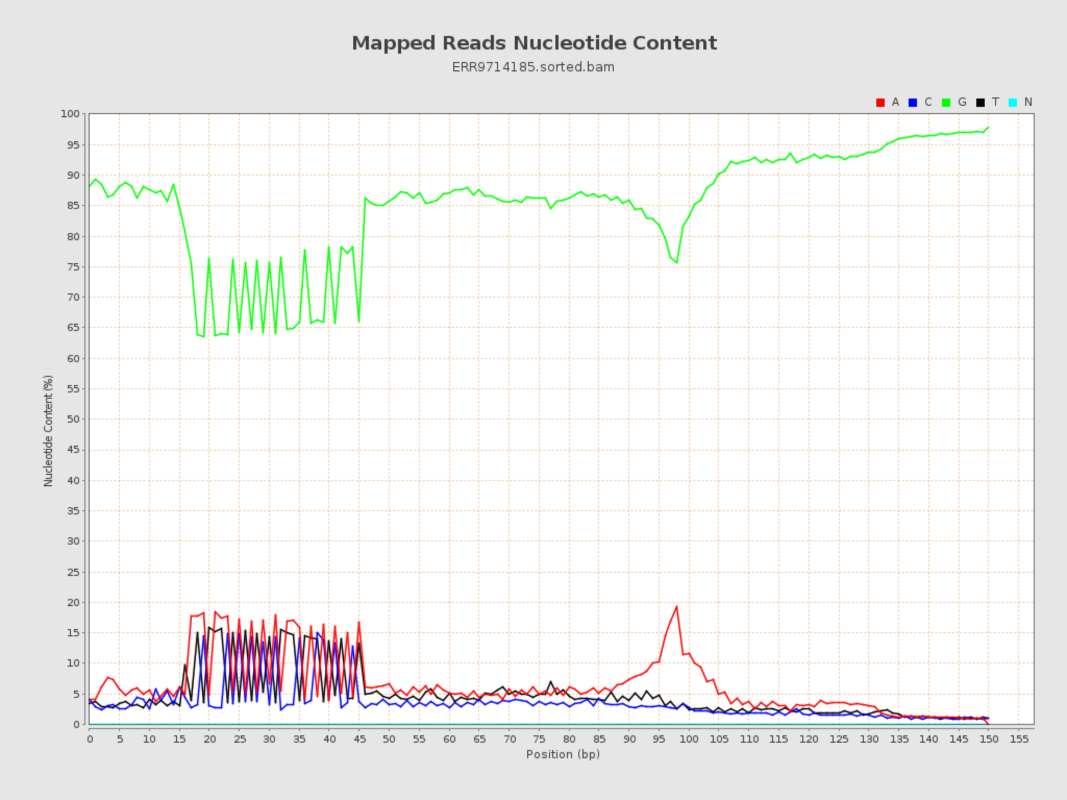
6. Results : Genome Fraction Coverage



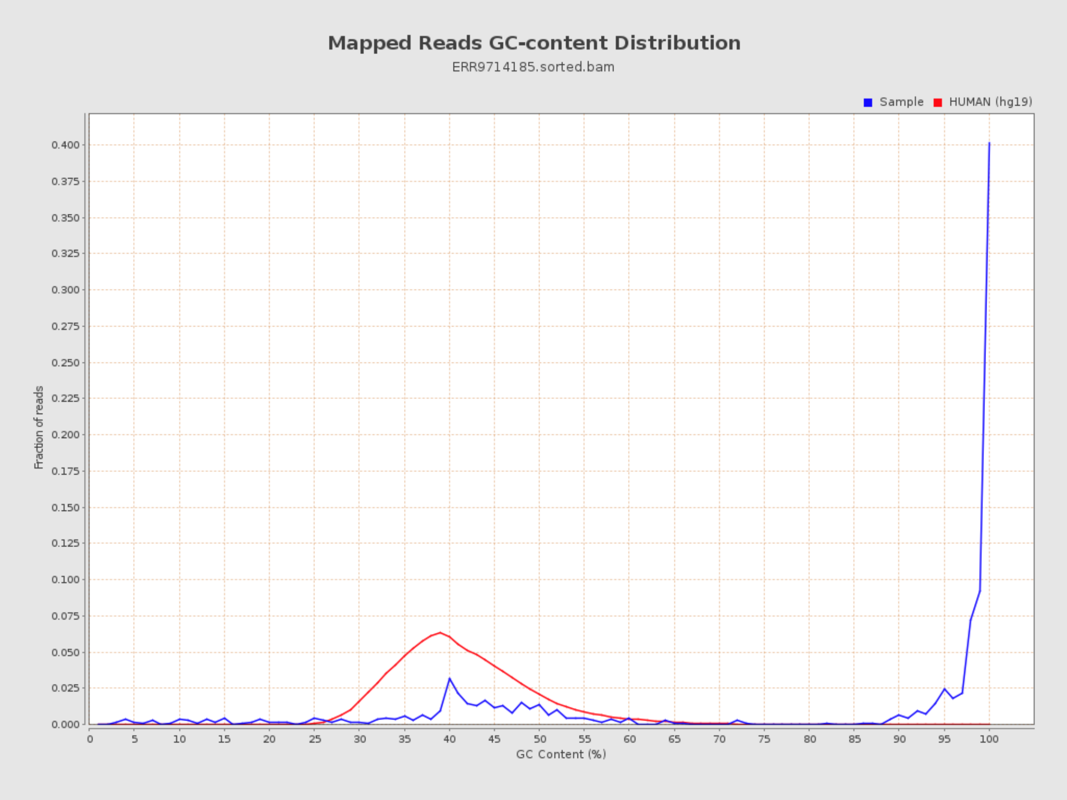
7. Results : Duplication Rate Histogram



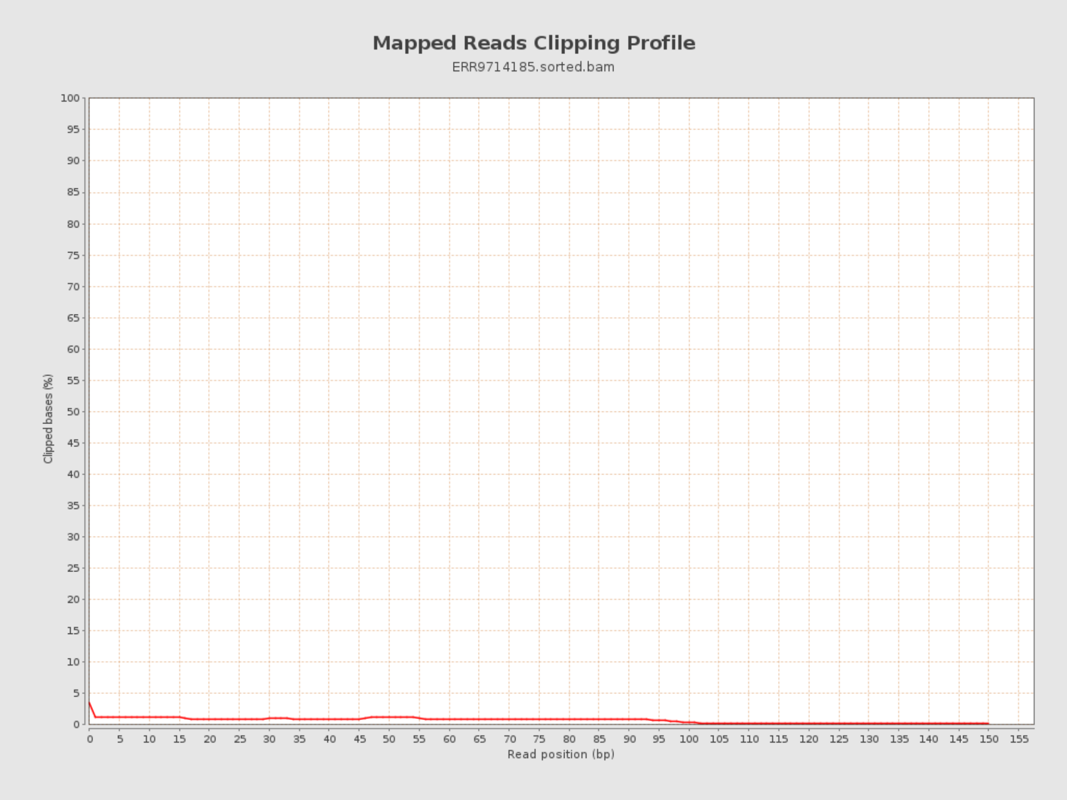
8. Results : Mapped Reads Nucleotide Content



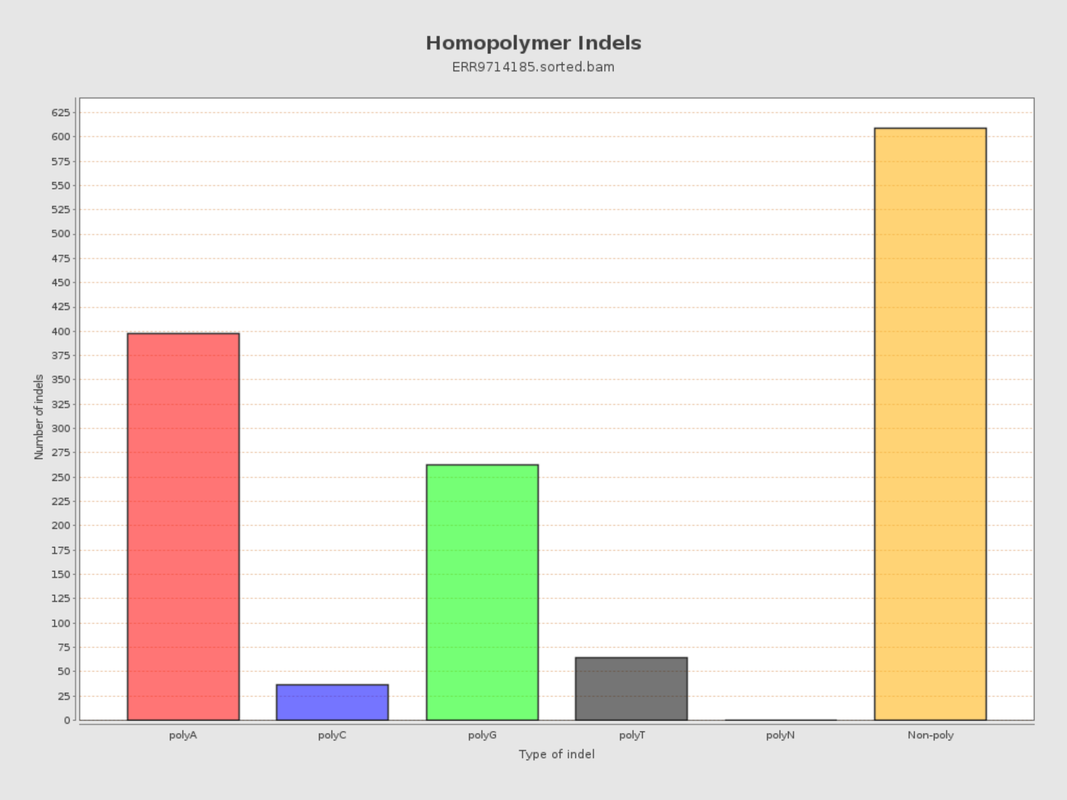
9. Results : Mapped Reads GC-content Distribution



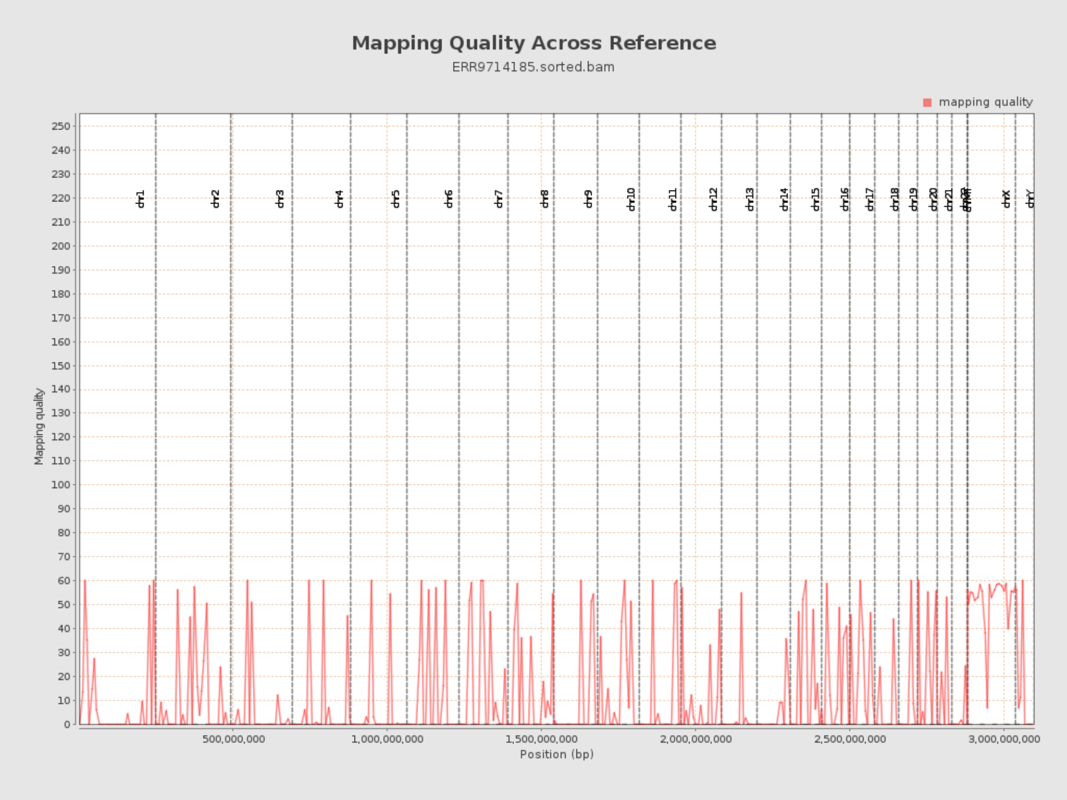
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram