Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:34:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714166.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_ERR9714166 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714166.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:34:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714166.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	816,878
Mapped reads	753,222 / 92.21%
Unmapped reads	63,656 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,325 / 3.83%
Read min/max/mean length	30 / 151 / 142.87
Duplicated reads (estimated)	728,021 / 89.12%
Duplication rate	39.41%
Clipped reads	723,877 / 88.62%

2.2. ACGT Content

Number/percentage of A's	25,463,857 / 26.96%
Number/percentage of C's	20,525,114 / 21.73%
Number/percentage of T's	24,251,877 / 25.68%
Number/percentage of G's	24,203,339 / 25.63%
Number/percentage of N's	627 / 0%
GC Percentage	47.36%

2.3. Coverage

Mean	0.0311

Standard Deviation	14.6176

2.4. Mapping Quality

Mean Mapping Quality	46.79

2.5. Mismatches and indels

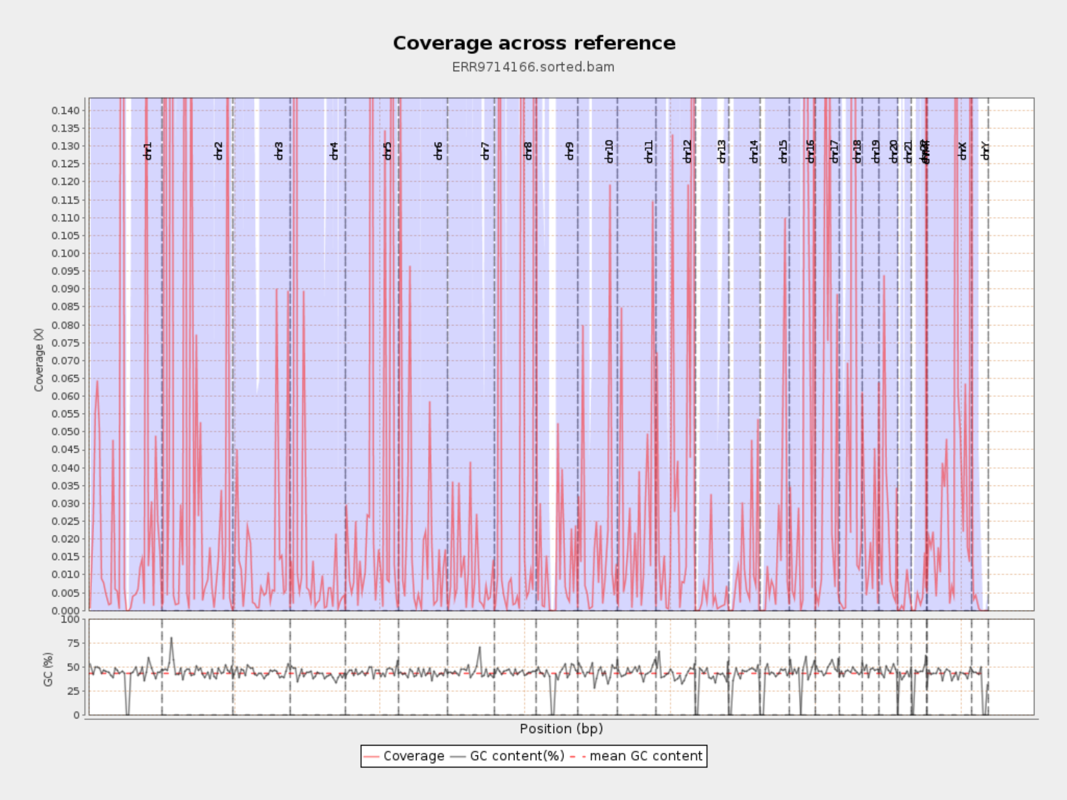
General error rate	4.25%
Mismatches	3,639,932
Insertions	143,943
Mapped reads with at least one insertion	18.68%
Deletions	304,937
Mapped reads with at least one deletion	38.63%
Homopolymer indels	28.18%

2.6. Chromosome stats

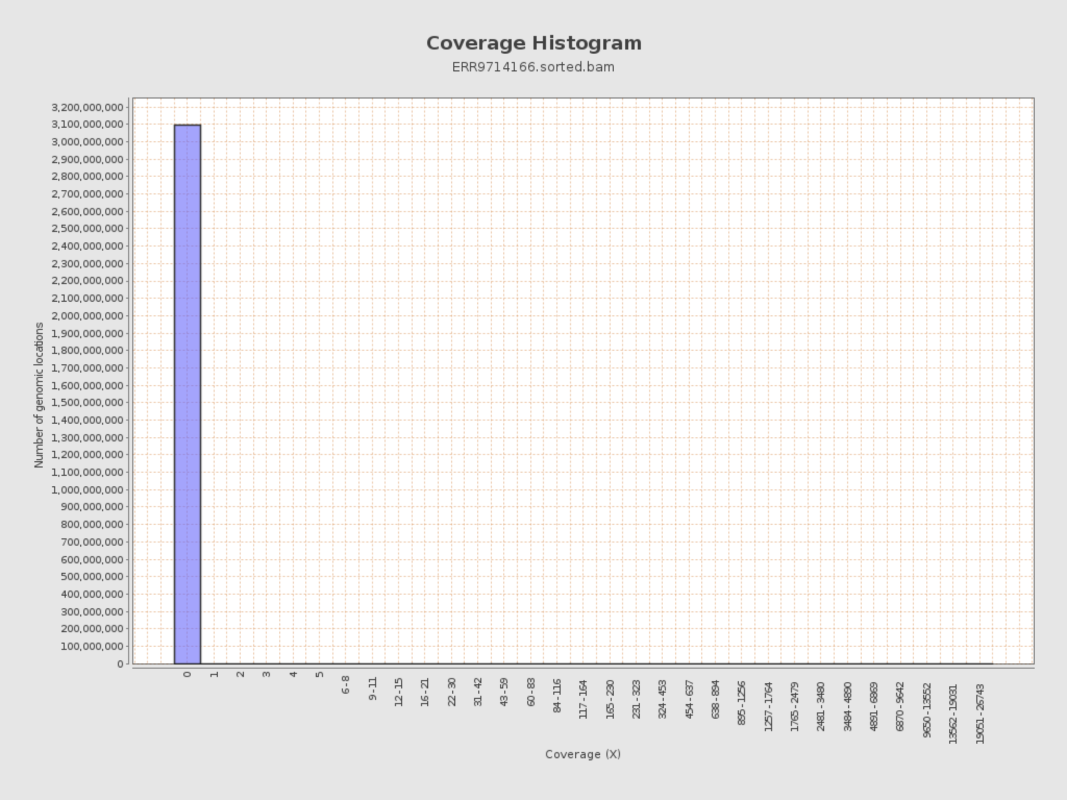
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8304995	0.0333	17.3981
chr2	243199373	13093774	0.0538	20.6684
chr3	198022430	3023768	0.0153	5.3736
chr4	191154276	5294339	0.0277	18.8073
chr5	180915260	7734680	0.0428	17.577
chr6	171115067	3814657	0.0223	7.6857
chr7	159138663	1819365	0.0114	2.7581

chr8	146364022	7851452	0.0536	25.6996
chr9	141213431	1693800	0.012	2.9148
chr10	135534747	2970656	0.0219	6.9989
chr11	135006516	3703109	0.0274	6.6447
chr12	133851895	6351466	0.0475	18.8845
chr13	115169878	569811	0.0049	1.8081
chr14	107349540	1484513	0.0138	3.4143
chr15	102531392	1979186	0.0193	6.7234
chr16	90354753	6111008	0.0676	22.0852
chr17	81195210	4638523	0.0571	15.4096
chr18	78077248	6260198	0.0802	34.8426
chr19	59128983	1214661	0.0205	4.0474
chr20	63025520	1621720	0.0257	7.2579
chr21	48129895	153493	0.0032	0.9008
chr22	51304566	219155	0.0043	1.0276
chrMT	16571	23859	1.4398	11.1972
chrX	155270560	6250318	0.0403	9.6843
chrY	59373566	133788	0.0023	0.8051

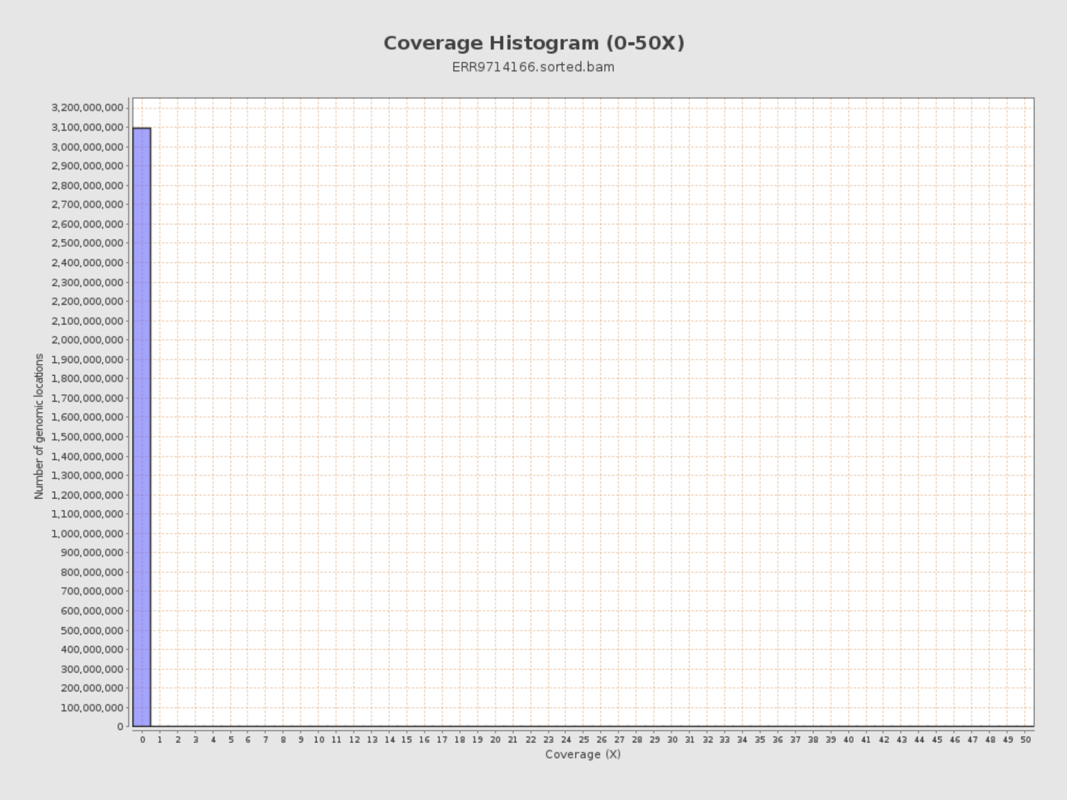
3. Results : Coverage across reference



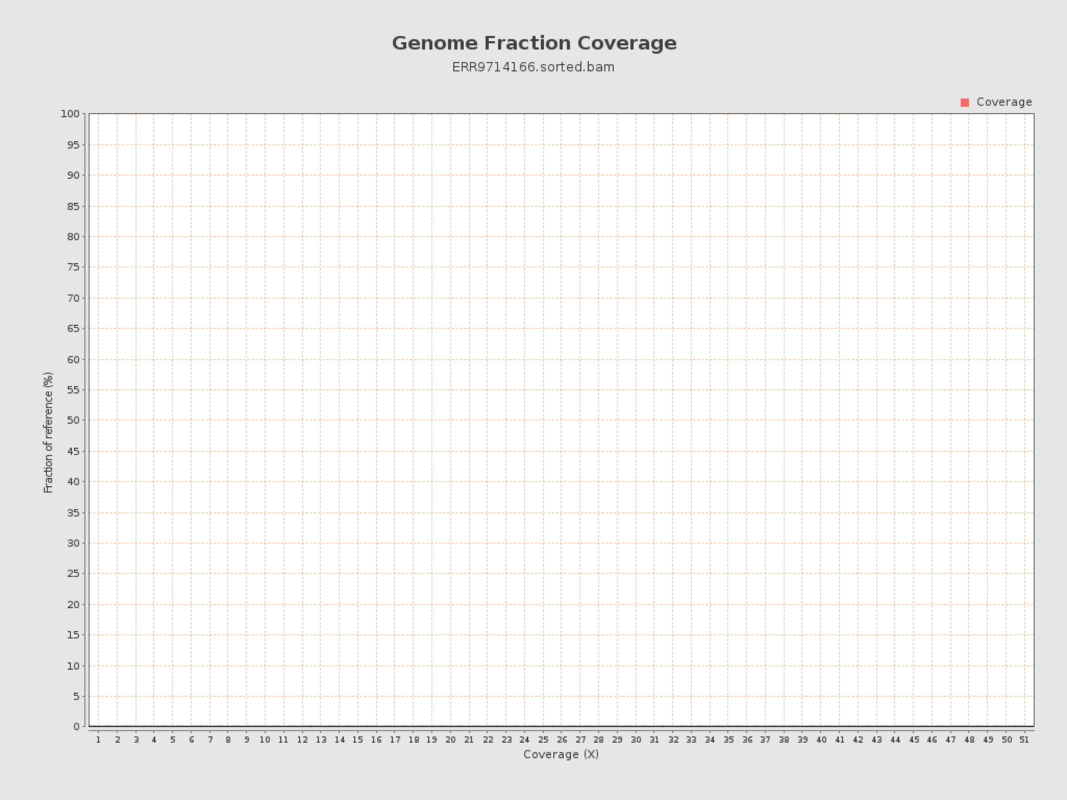
4. Results : Coverage Histogram



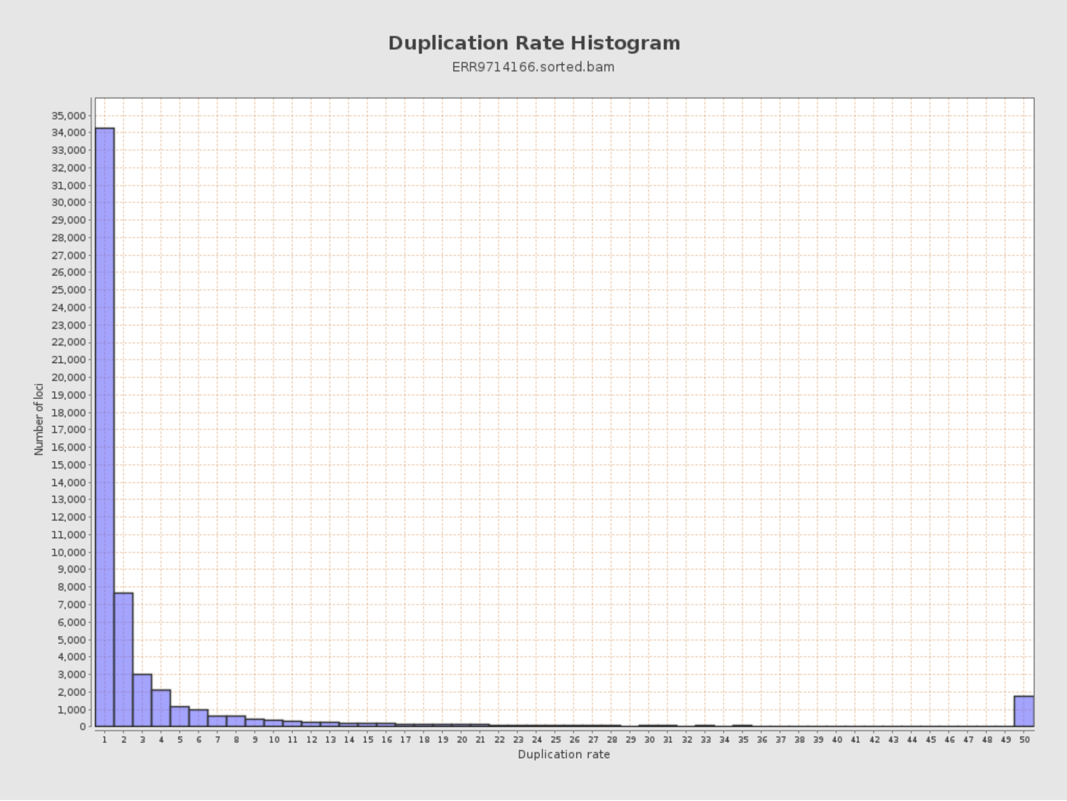
5. Results : Coverage Histogram (0-50X)



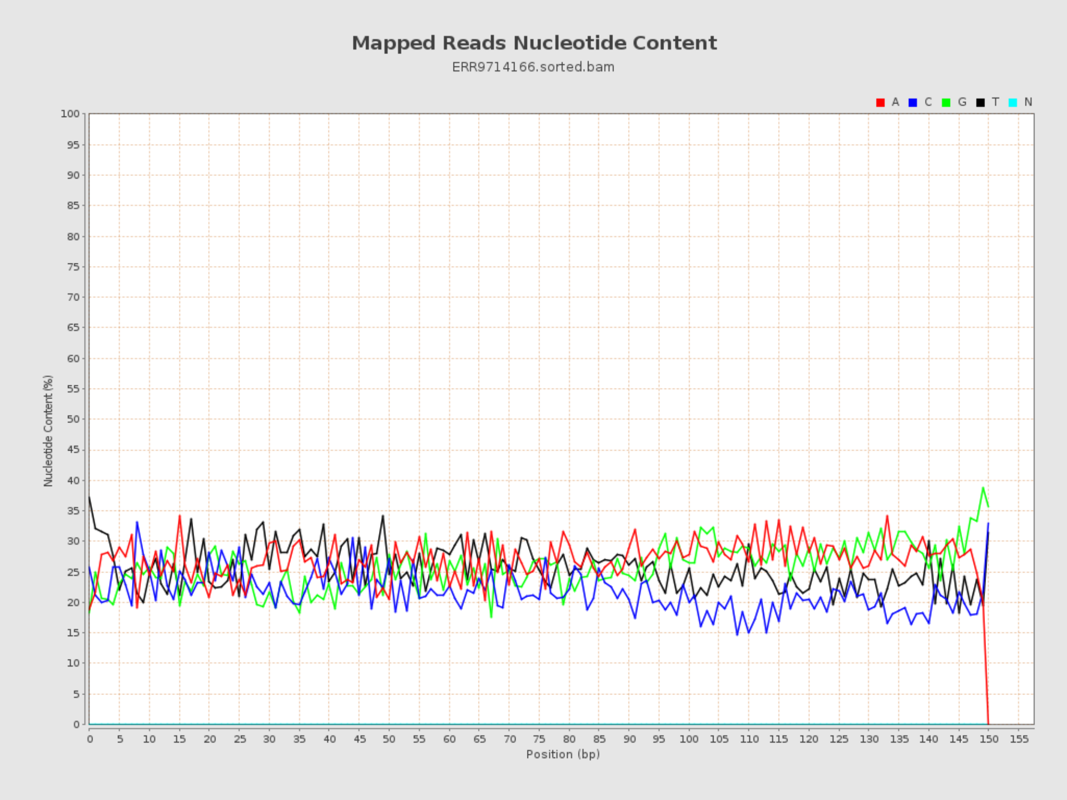
6. Results : Genome Fraction Coverage



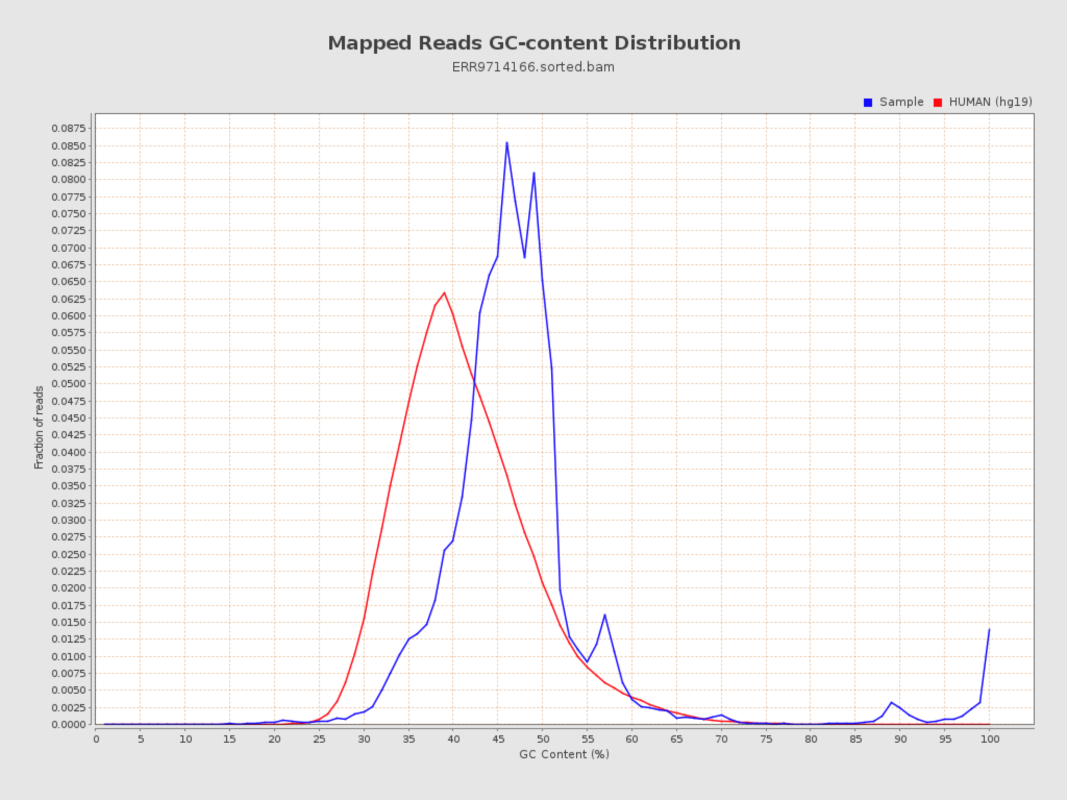
7. Results : Duplication Rate Histogram



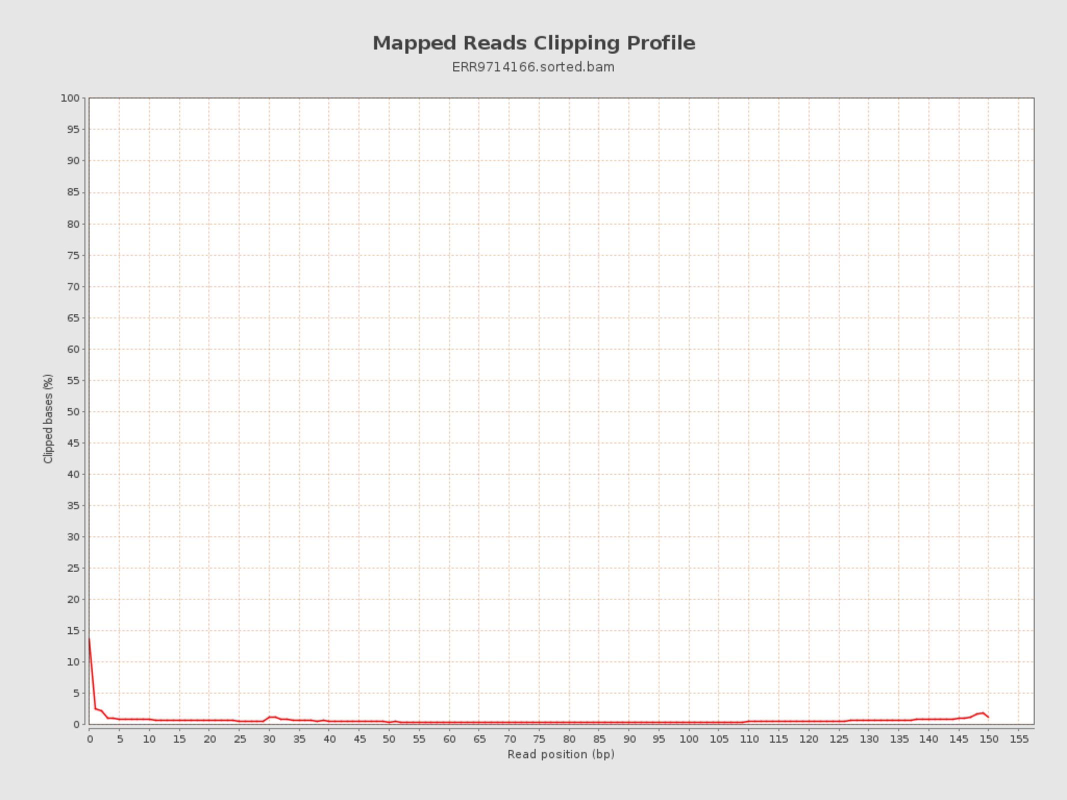
8. Results : Mapped Reads Nucleotide Content



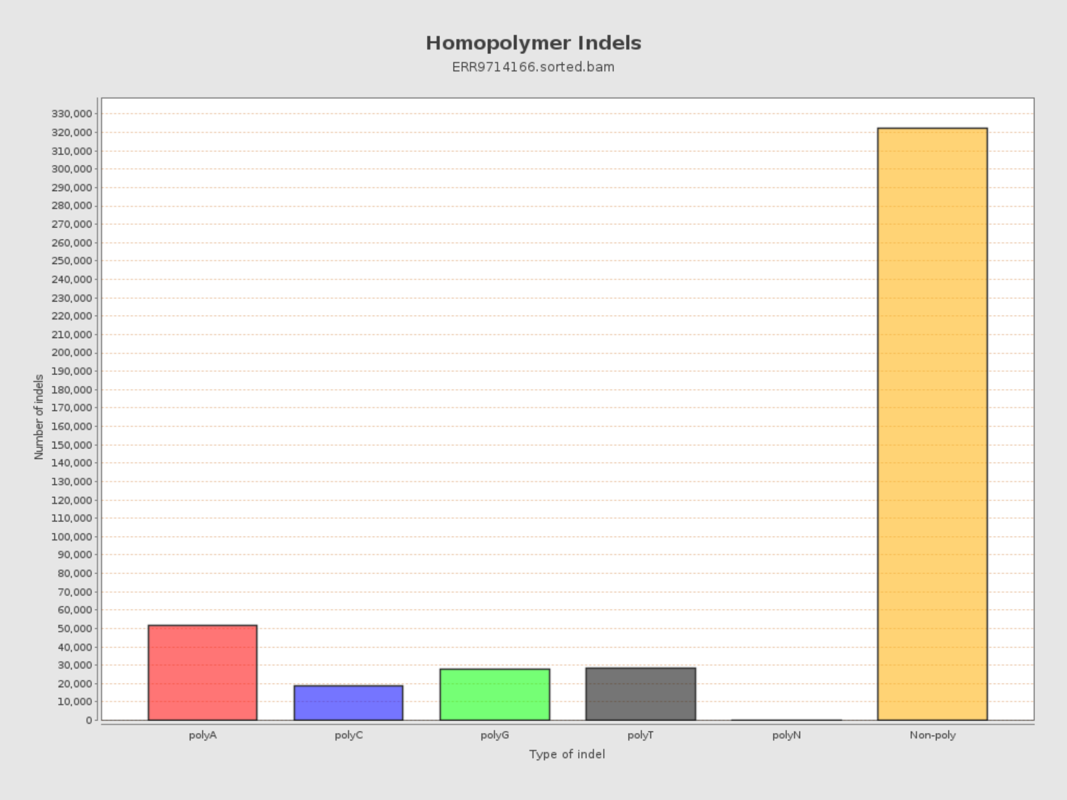
9. Results : Mapped Reads GC-content Distribution



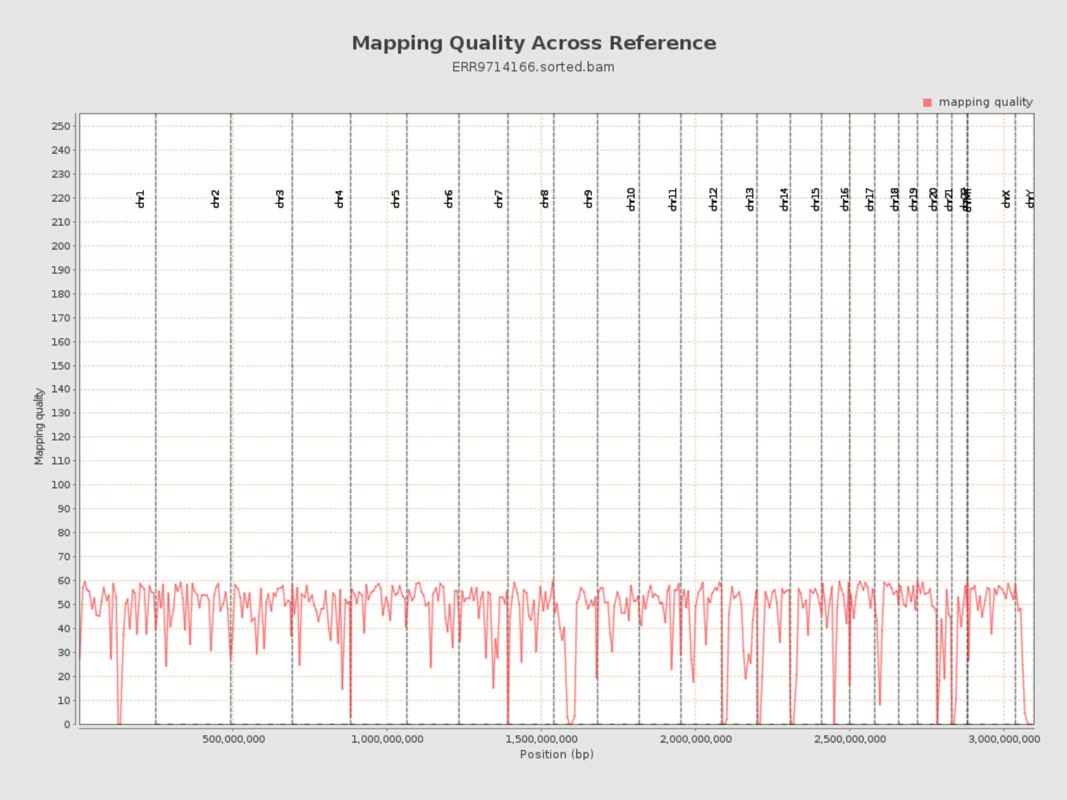
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram