

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:40:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714258.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_ERR9714258 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:40:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,310
Mapped reads	2,617 / 21.26%
Unmapped reads	9,693 / 78.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	186 / 1.51%
Read min/max/mean length	30 / 151 / 74.69
Duplicated reads (estimated)	1,660 / 13.48%
Duplication rate	44.09%
Clipped reads	2,160 / 17.55%

2.2. ACGT Content

Number/percentage of A's	56,080 / 20.35%
Number/percentage of C's	45,030 / 16.34%
Number/percentage of T's	52,472 / 19.04%
Number/percentage of G's	122,048 / 44.28%
Number/percentage of N's	1 / 0%
GC Percentage	60.62%

2.3. Coverage

Mean	0.0001

Standard Deviation	0.095
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2.4. Mapping Quality

Mean Mapping Quality	19.07
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2.5. Mismatches and indels

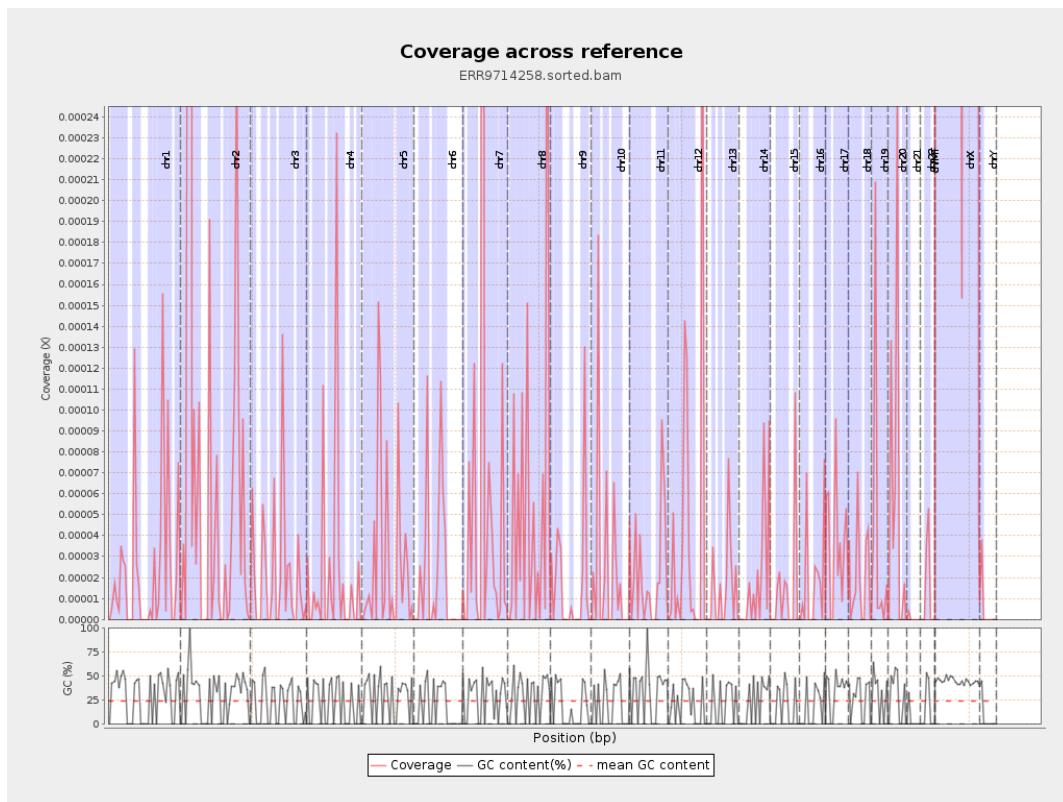
General error rate	3.67%
Mismatches	9,015
Insertions	187
Mapped reads with at least one insertion	5.24%
Deletions	597
Mapped reads with at least one deletion	22.01%
Homopolymer indels	35.84%

2.6. Chromosome stats

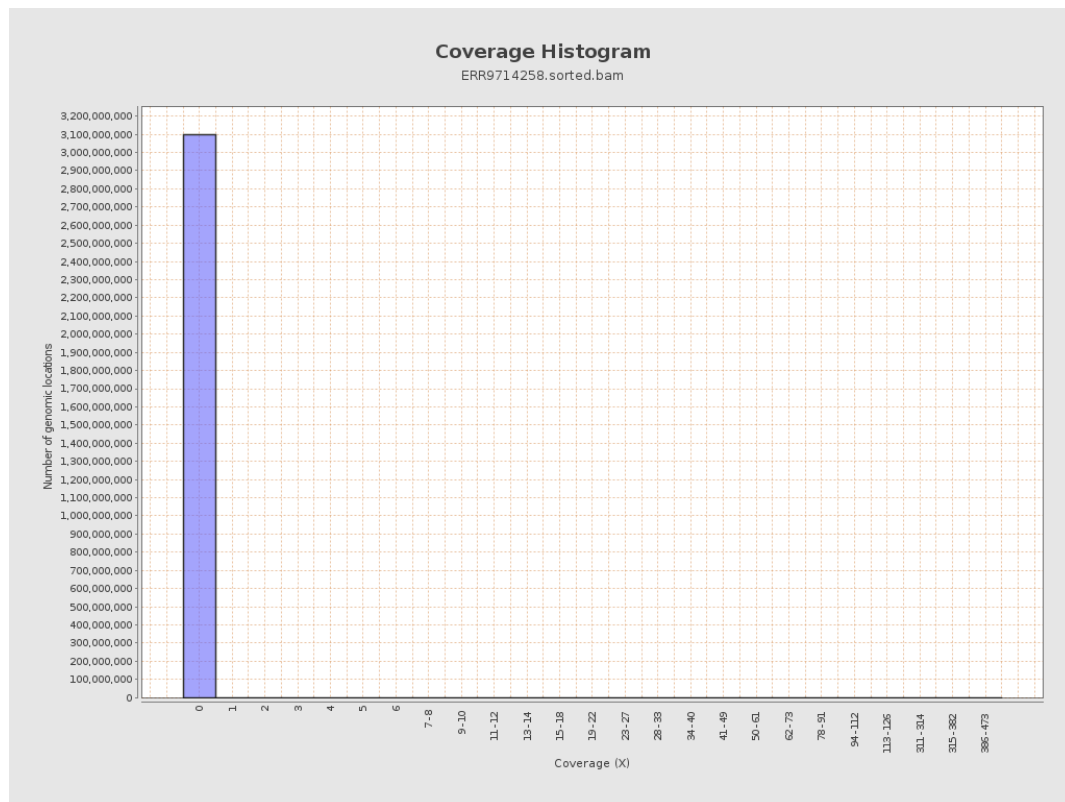
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5966	0	0.0164
chr2	243199373	90633	0.0004	0.3275
chr3	198022430	4123	0	0.007
chr4	191154276	4033	0	0.0085
chr5	180915260	5089	0	0.012
chr6	171115067	3337	0	0.009
chr7	159138663	10178	0.0001	0.0394

chr8	146364022	8229	0.0001	0.0216
chr9	141213431	2290	0	0.0085
chr10	135534747	3185	0	0.0209
chr11	135006516	2774	0	0.0073
chr12	133851895	5785	0	0.0168
chr13	115169878	1612	0	0.006
chr14	107349540	2153	0	0.0083
chr15	102531392	1409	0	0.0054
chr16	90354753	1696	0	0.0068
chr17	81195210	2897	0	0.0089
chr18	78077248	1606	0	0.0075
chr19	59128983	2185	0	0.0121
chr20	63025520	3877	0.0001	0.0206
chr21	48129895	31	0	0.0008
chr22	51304566	693	0	0.0051
chrMT	16571	754	0.0455	0.3124
chrX	155270560	115362	0.0007	0.0887
chrY	59373566	333	0	0.0044

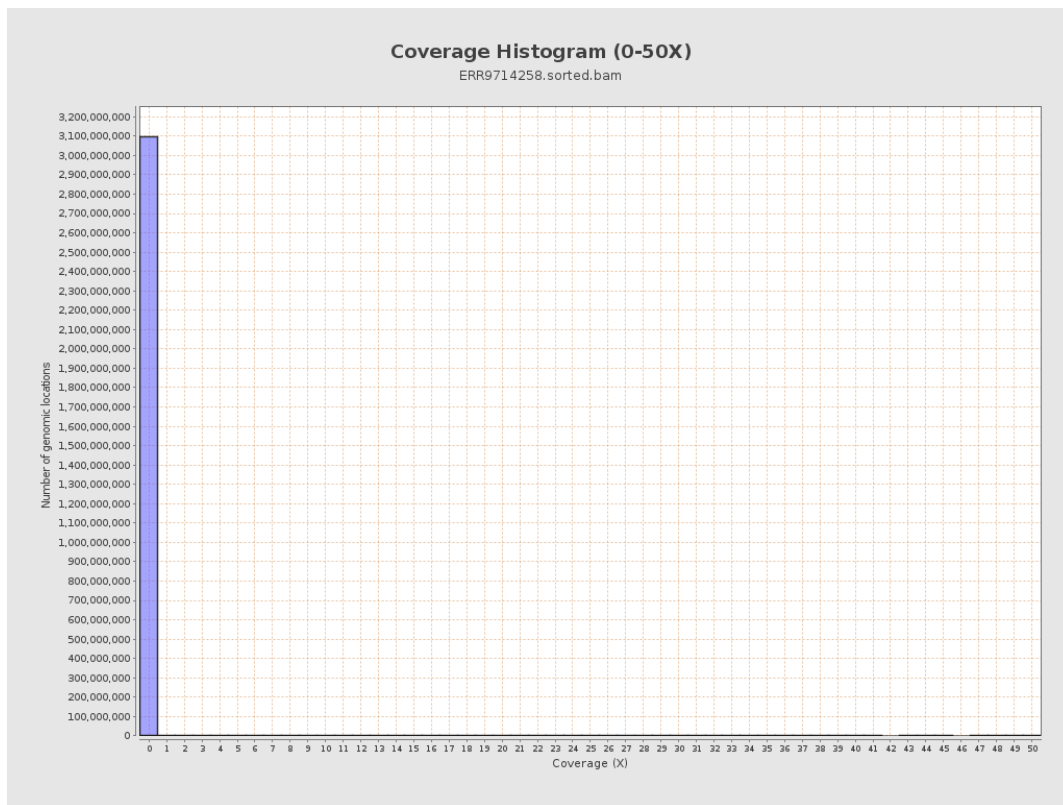
3. Results : Coverage across reference



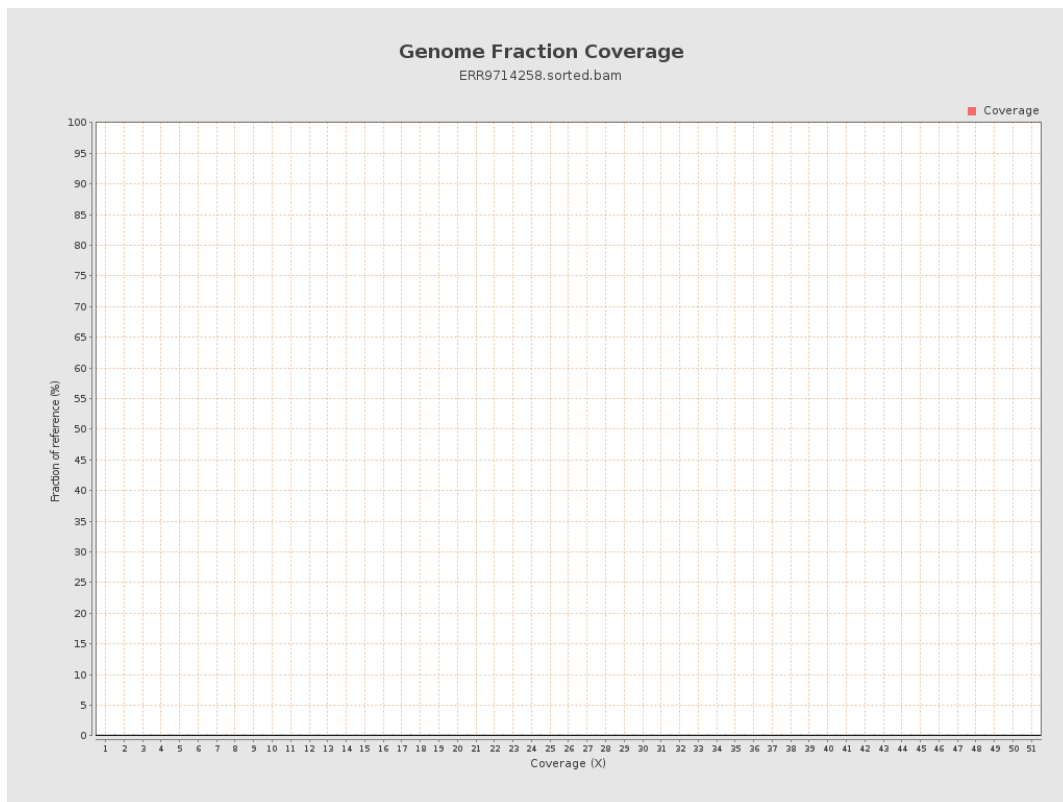
4. Results : Coverage Histogram



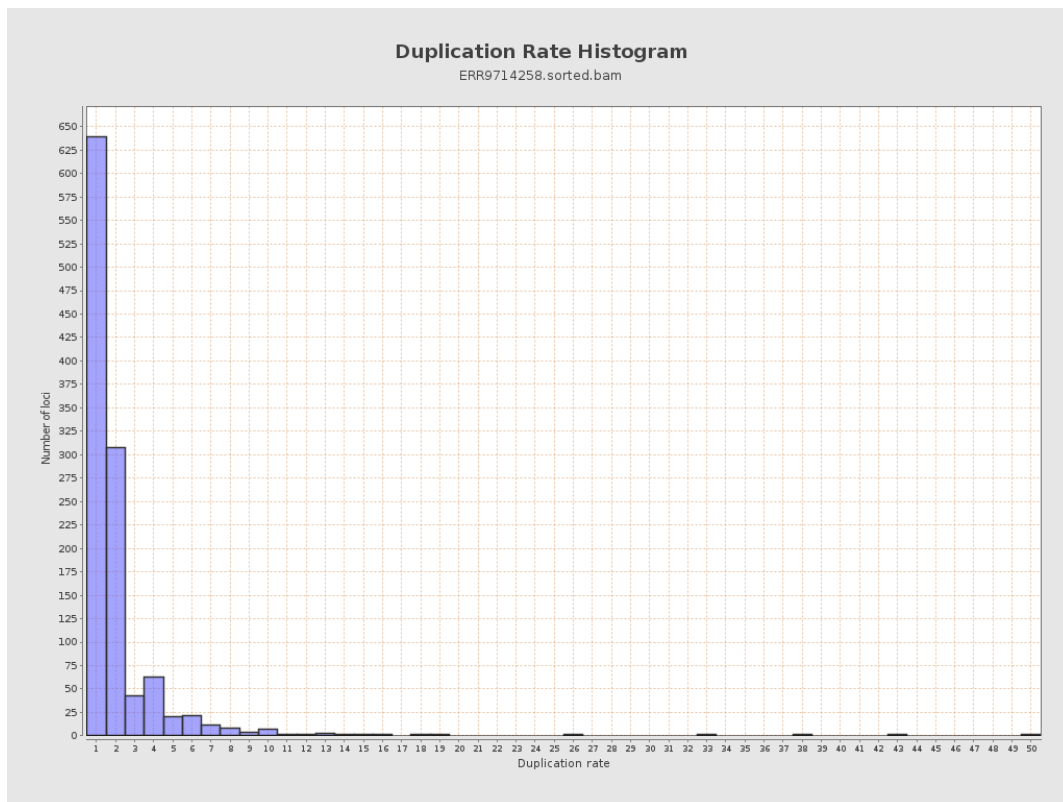
5. Results : Coverage Histogram (0-50X)



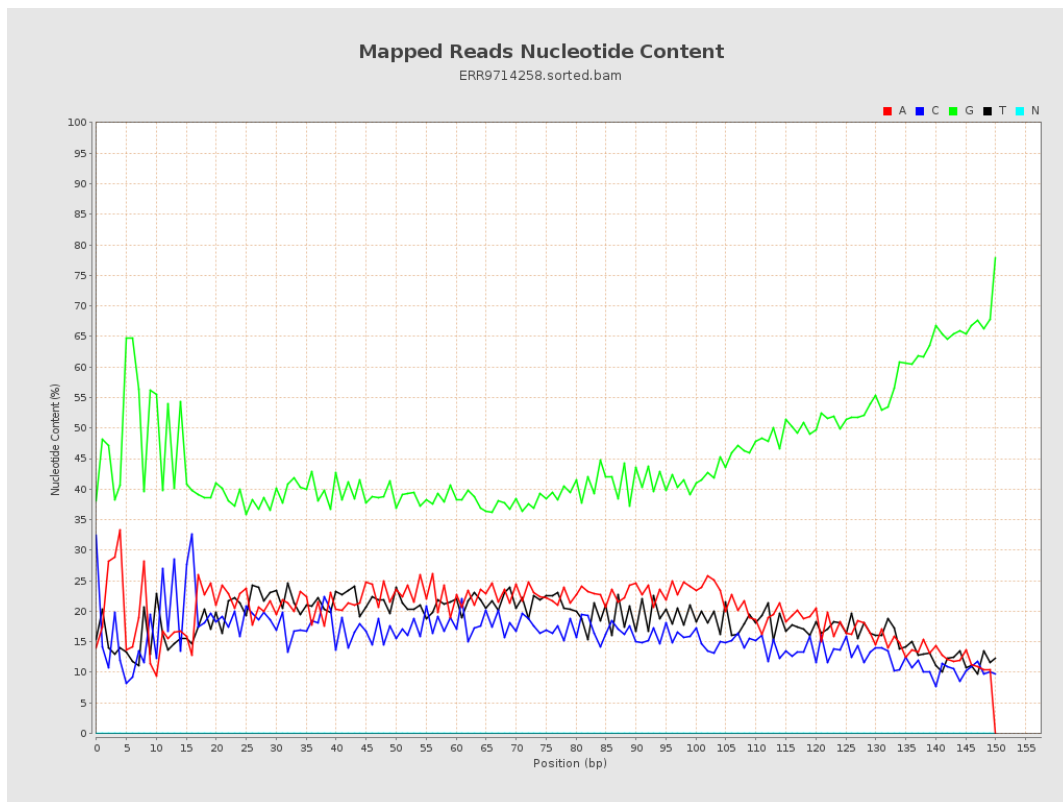
6. Results : Genome Fraction Coverage



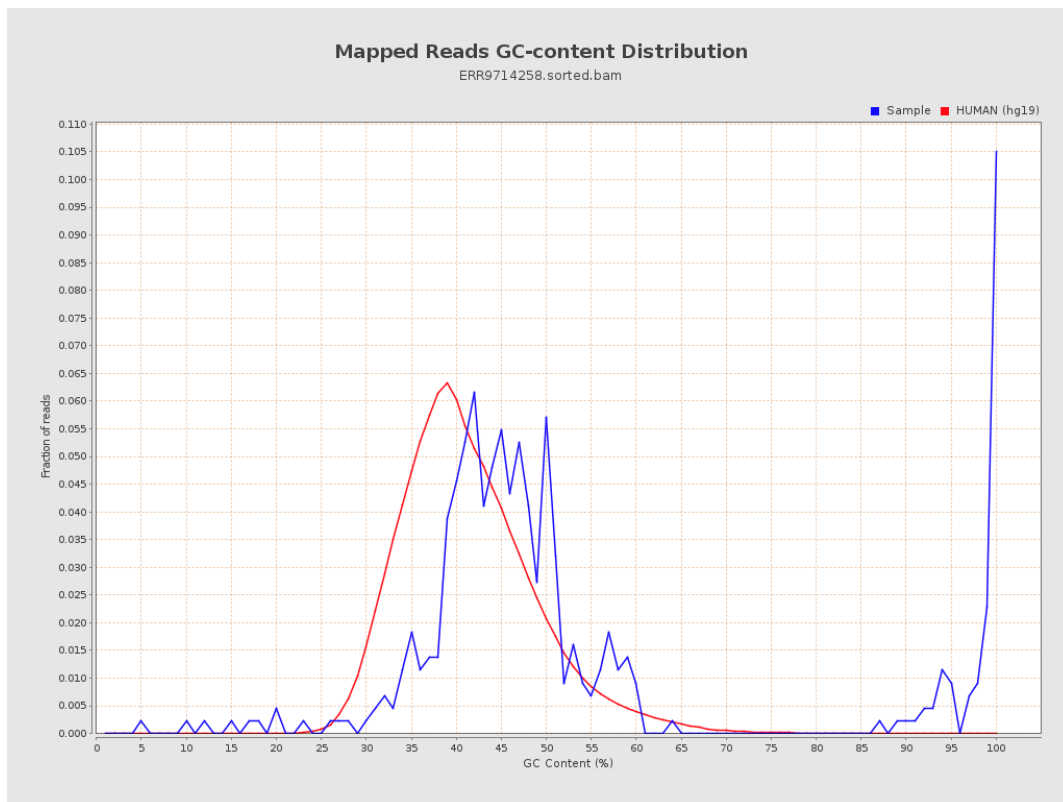
7. Results : Duplication Rate Histogram



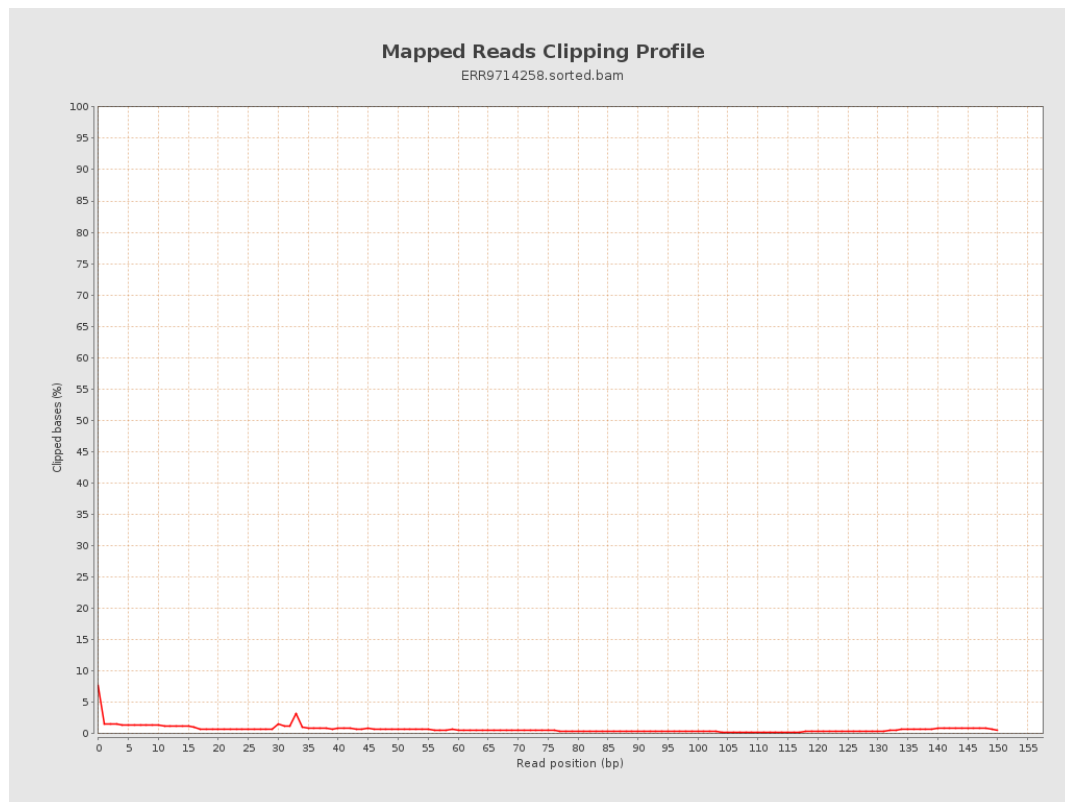
8. Results : Mapped Reads Nucleotide Content



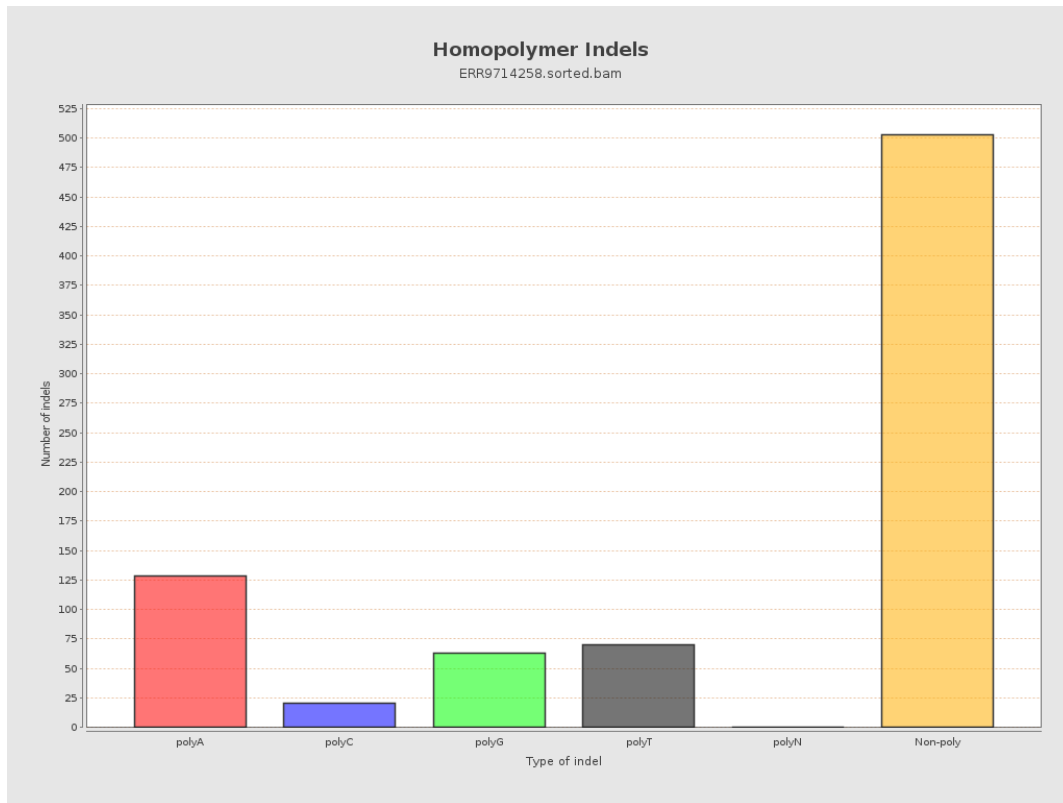
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

