

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:06:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714241.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_ERR9714241 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714241.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:06:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714241.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	249,342
Mapped reads	69,042 / 27.69%
Unmapped reads	180,300 / 72.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,809 / 1.13%
Read min/max/mean length	30 / 151 / 82.61
Duplicated reads (estimated)	57,615 / 23.11%
Duplication rate	41.88%
Clipped reads	61,167 / 24.53%

2.2. ACGT Content

Number/percentage of A's	1,847,242 / 22.98%
Number/percentage of C's	1,418,808 / 17.65%
Number/percentage of T's	1,731,915 / 21.54%
Number/percentage of G's	3,040,644 / 37.82%
Number/percentage of N's	204 / 0%
GC Percentage	55.47%

2.3. Coverage

Mean	0.0026

Standard Deviation	2.0224
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2.4. Mapping Quality

Mean Mapping Quality	46.73
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2.5. Mismatches and indels

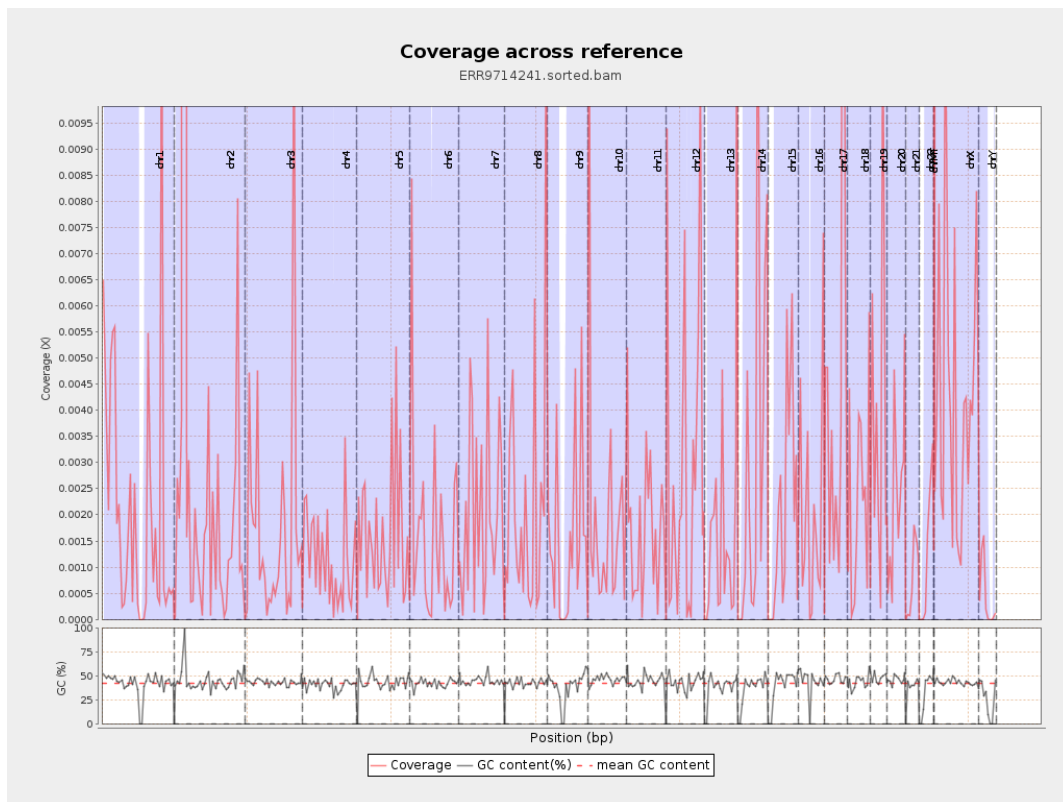
General error rate	4.13%
Mismatches	295,870
Insertions	8,595
Mapped reads with at least one insertion	11.51%
Deletions	23,857
Mapped reads with at least one deletion	32.35%
Homopolymer indels	32.11%

2.6. Chromosome stats

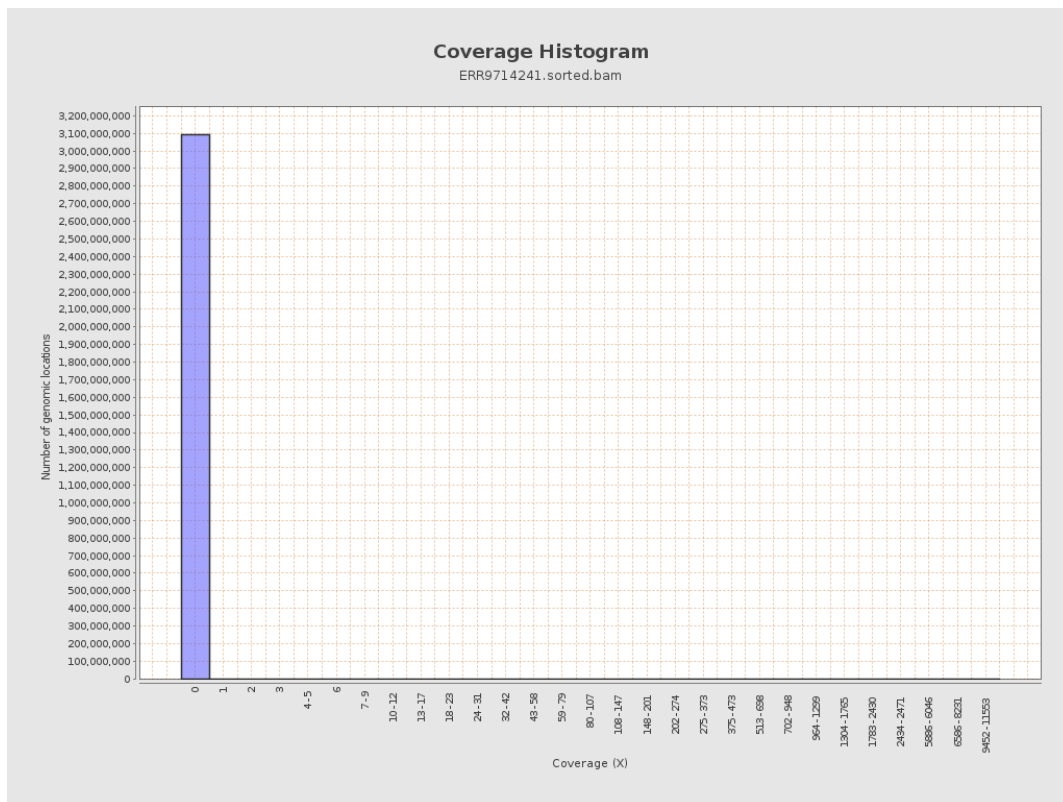
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	531375	0.0021	0.439
chr2	243199373	1979821	0.0081	6.9661
chr3	198022430	345207	0.0017	0.5859
chr4	191154276	217698	0.0011	0.2195
chr5	180915260	294601	0.0016	0.3241
chr6	171115067	268095	0.0016	0.424
chr7	159138663	328746	0.0021	0.4565

chr8	146364022	324240	0.0022	0.4873
chr9	141213431	214879	0.0015	0.3262
chr10	135534747	286100	0.0021	0.705
chr11	135006516	220385	0.0016	0.2969
chr12	133851895	382617	0.0029	0.6301
chr13	115169878	175147	0.0015	0.3706
chr14	107349540	327345	0.003	0.9238
chr15	102531392	215874	0.0021	0.3977
chr16	90354753	185101	0.002	0.3902
chr17	81195210	430557	0.0053	1.5948
chr18	78077248	182558	0.0023	0.5087
chr19	59128983	223069	0.0038	0.5428
chr20	63025520	149156	0.0024	0.4322
chr21	48129895	36339	0.0008	0.1101
chr22	51304566	61151	0.0012	0.1959
chrMT	16571	105847	6.3875	51.6349
chrX	155270560	662496	0.0043	0.4307
chrY	59373566	27161	0.0005	0.1141

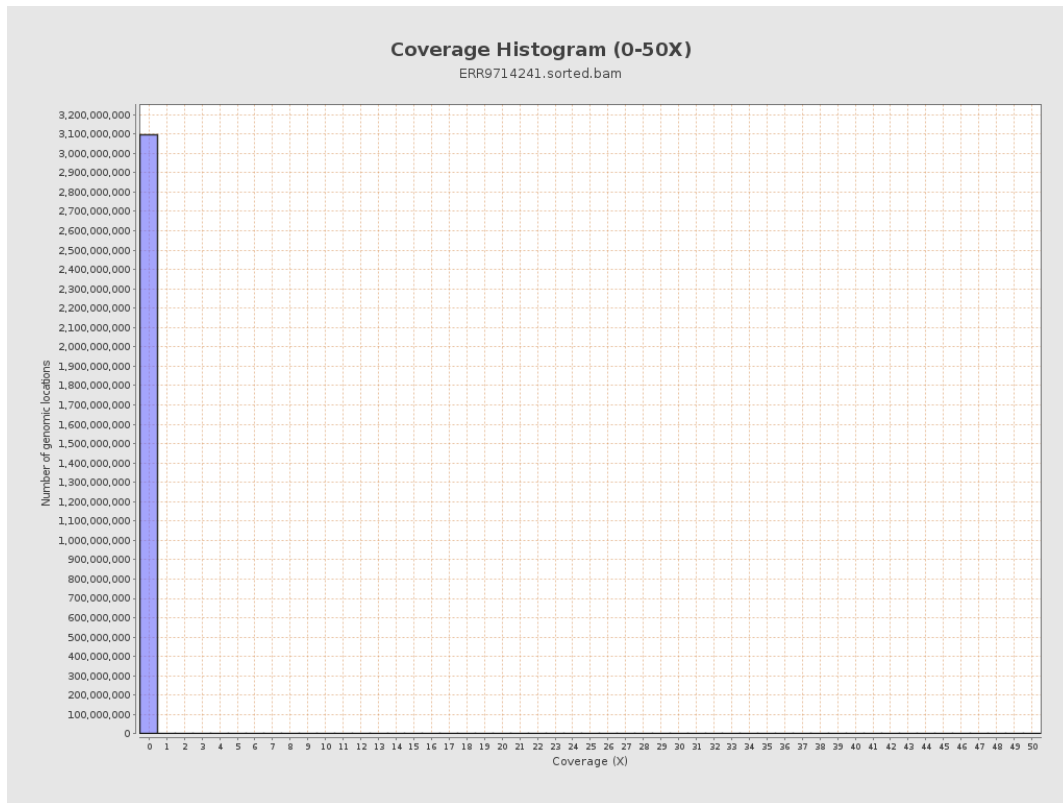
3. Results : Coverage across reference



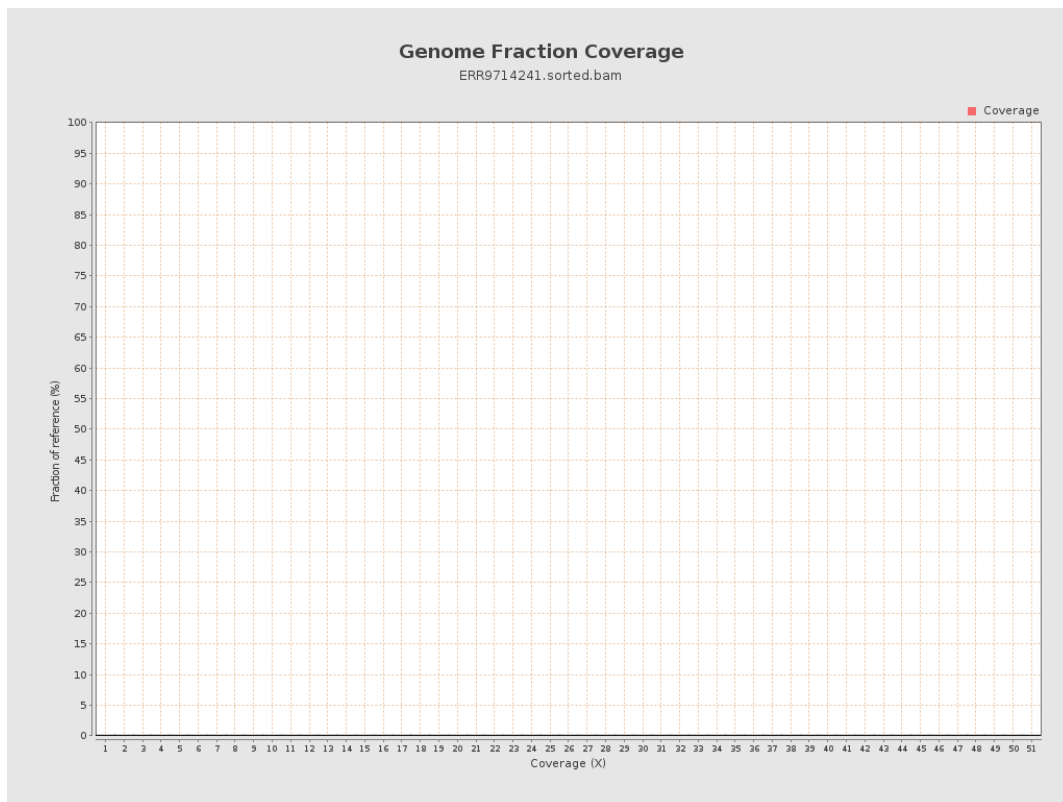
4. Results : Coverage Histogram



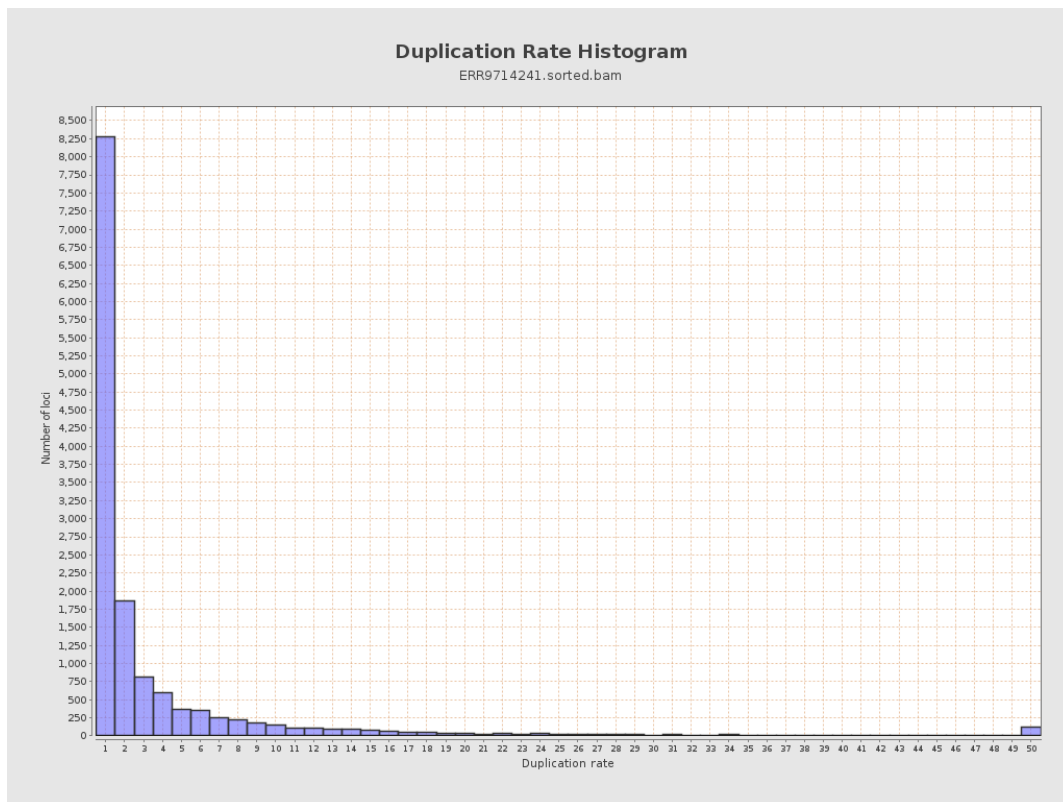
5. Results : Coverage Histogram (0-50X)



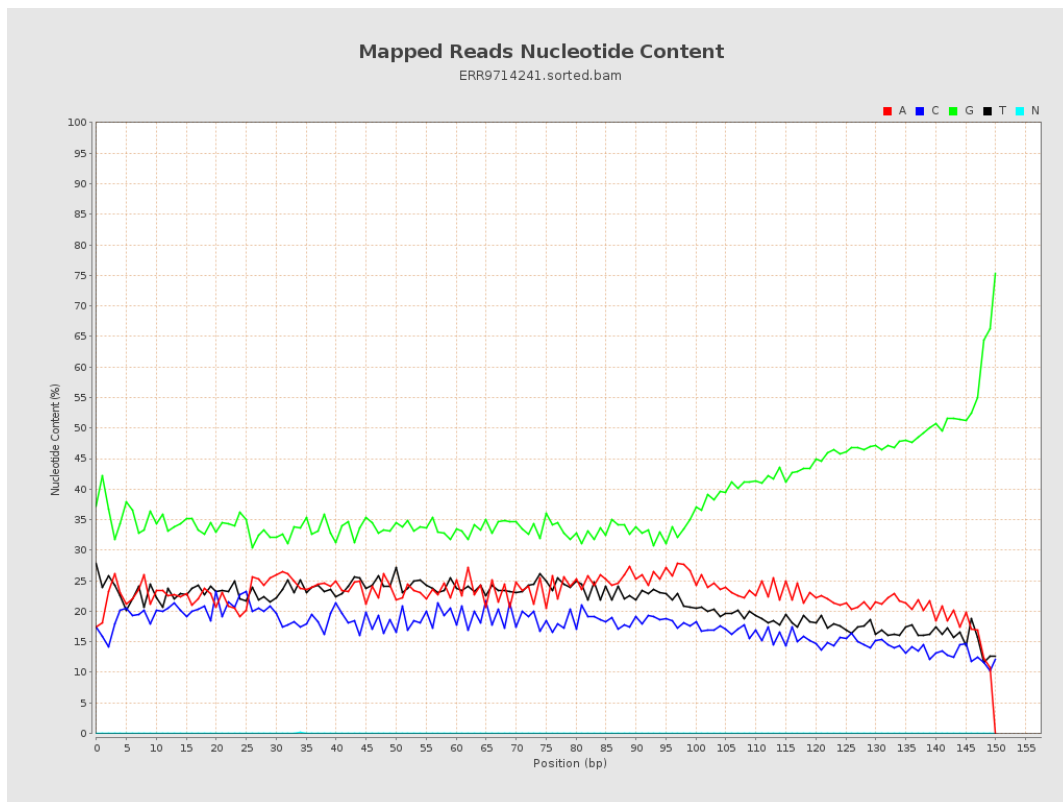
6. Results : Genome Fraction Coverage



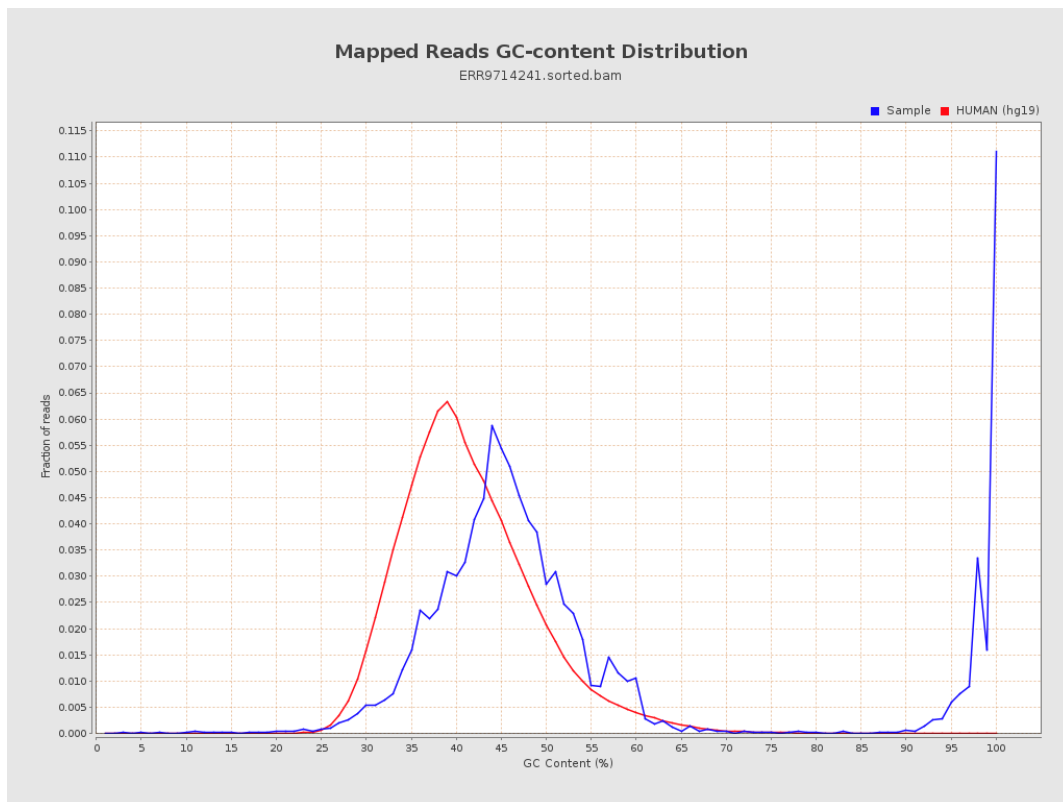
7. Results : Duplication Rate Histogram



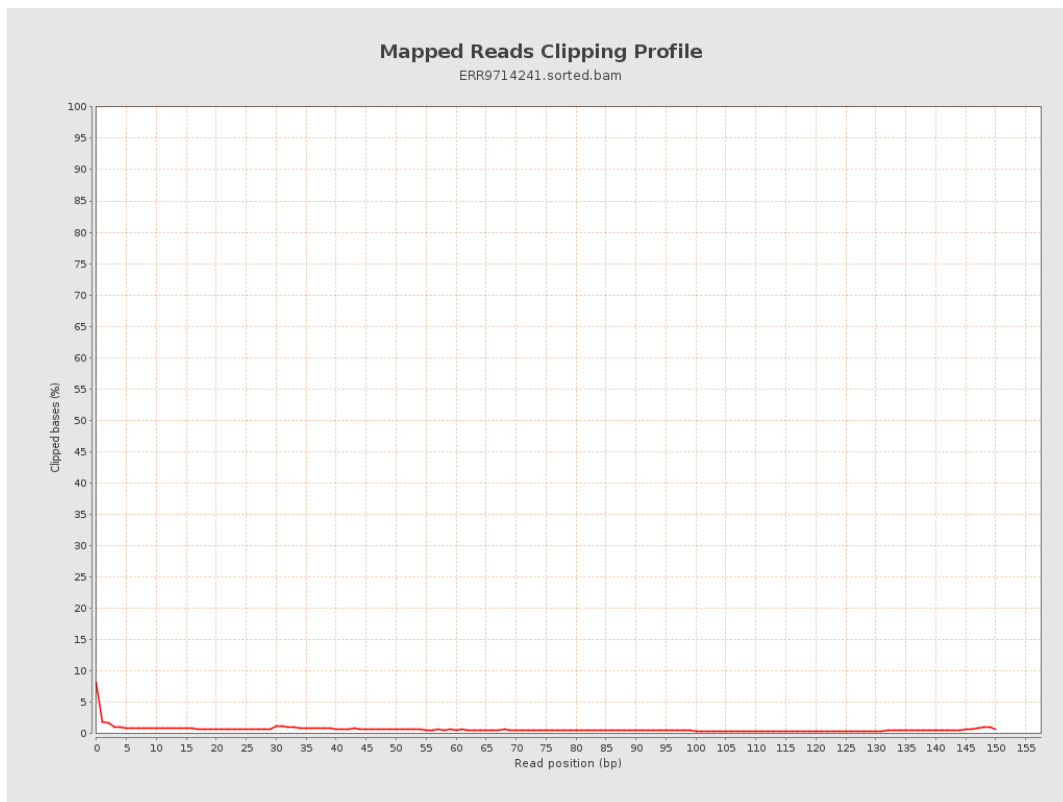
8. Results : Mapped Reads Nucleotide Content



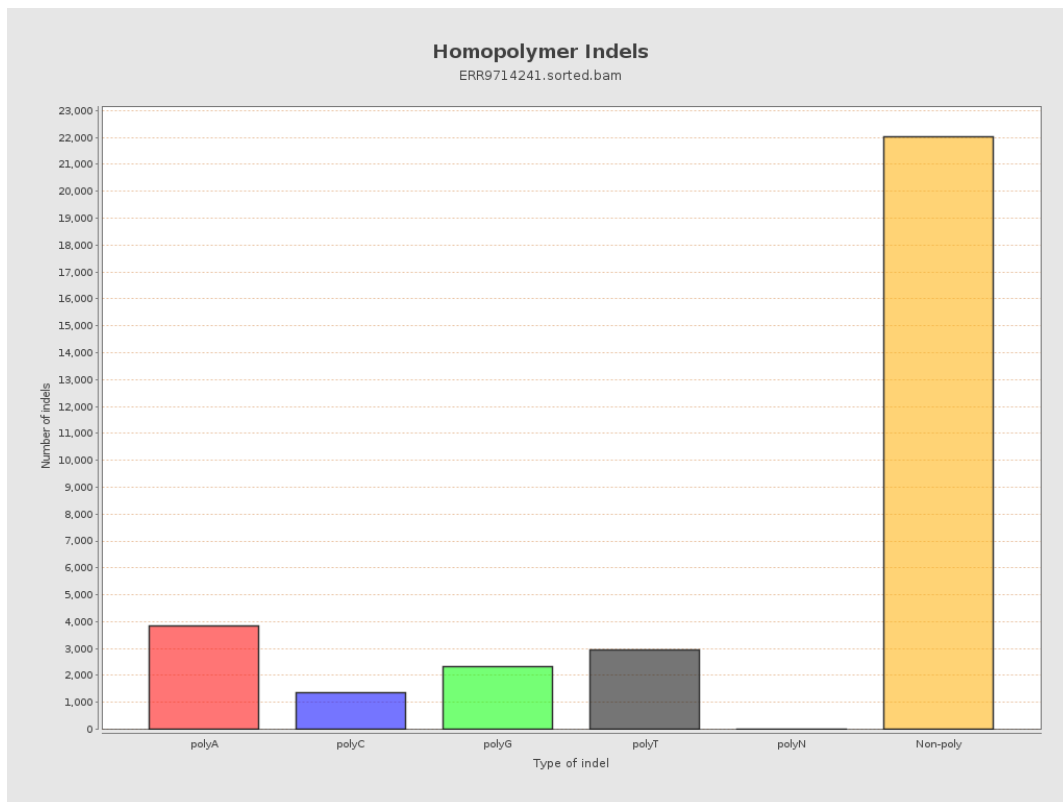
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

