

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714260.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_ERR9714260 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	246,400
Mapped reads	199,126 / 80.81%
Unmapped reads	47,274 / 19.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,991 / 2.43%
Read min/max/mean length	30 / 151 / 131.07
Duplicated reads (estimated)	163,124 / 66.2%
Duplication rate	42.39%
Clipped reads	186,863 / 75.84%

2.2. ACGT Content

Number/percentage of A's	6,716,440 / 26.65%
Number/percentage of C's	5,512,382 / 21.87%
Number/percentage of T's	6,357,334 / 25.23%
Number/percentage of G's	6,615,127 / 26.25%
Number/percentage of N's	141 / 0%
GC Percentage	48.12%

2.3. Coverage

Mean	0.0083

Standard Deviation	2.1993
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2.4. Mapping Quality

Mean Mapping Quality	52.14
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2.5. Mismatches and indels

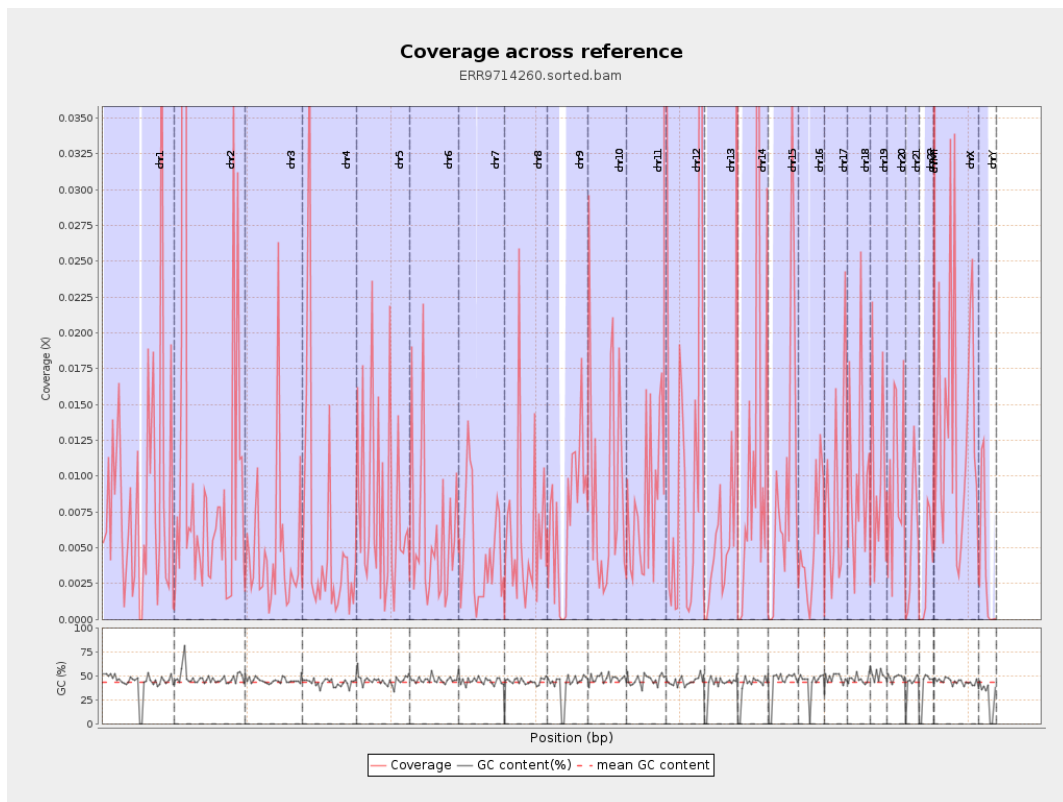
General error rate	4.37%
Mismatches	1,019,621
Insertions	27,026
Mapped reads with at least one insertion	13.05%
Deletions	88,795
Mapped reads with at least one deletion	42.39%
Homopolymer indels	29.19%

2.6. Chromosome stats

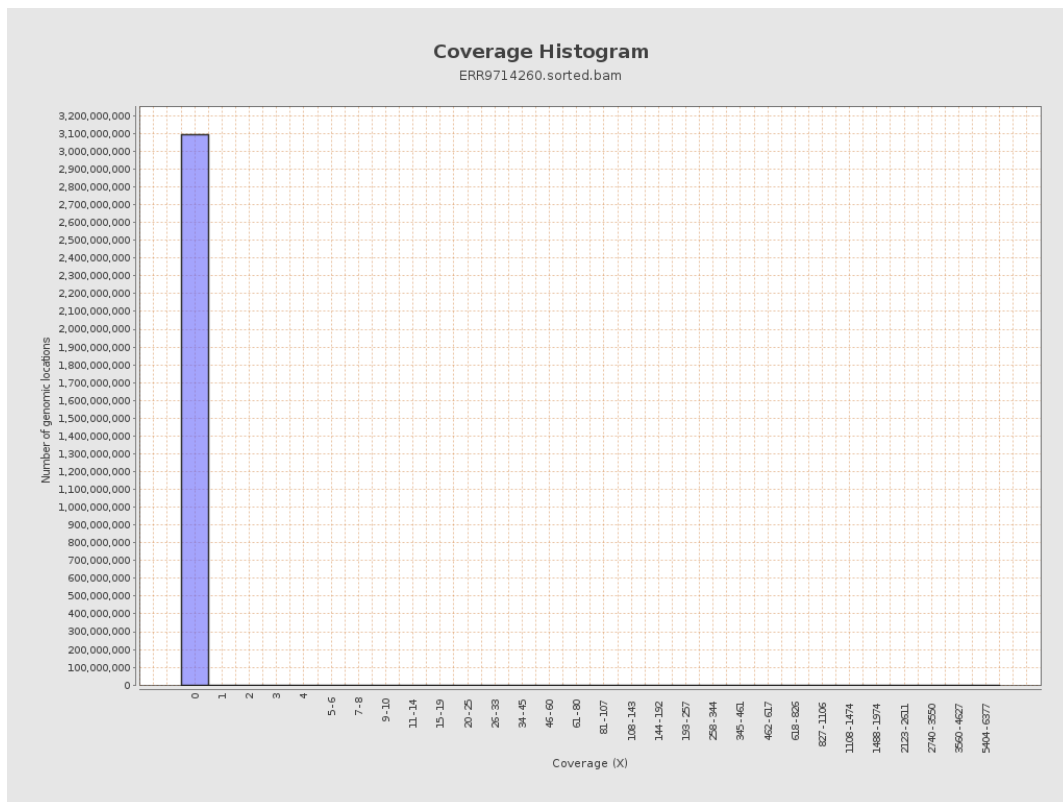
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2101686	0.0084	1.7282
chr2	243199373	3255422	0.0134	4.8166
chr3	198022430	940098	0.0047	0.9216
chr4	191154276	1010269	0.0053	1.3262
chr5	180915260	1377469	0.0076	1.5886
chr6	171115067	1022230	0.006	1.0755
chr7	159138663	766319	0.0048	0.7795

chr8	146364022	874482	0.006	1.3859
chr9	141213431	990766	0.007	1.1002
chr10	135534747	1250186	0.0092	1.6269
chr11	135006516	1253479	0.0093	1.6079
chr12	133851895	1844334	0.0138	4.6226
chr13	115169878	722307	0.0063	1.4926
chr14	107349540	1286362	0.012	3.7221
chr15	102531392	954006	0.0093	1.7338
chr16	90354753	475700	0.0053	0.7016
chr17	81195210	750100	0.0092	1.6492
chr18	78077248	826520	0.0106	2.0867
chr19	59128983	574460	0.0097	1.1197
chr20	63025520	630574	0.01	1.3341
chr21	48129895	265757	0.0055	1.1769
chr22	51304566	187497	0.0037	0.5942
chrMT	16571	30382	1.8334	14.7143
chrX	155270560	2140552	0.0138	1.5061
chrY	59373566	226722	0.0038	0.6711

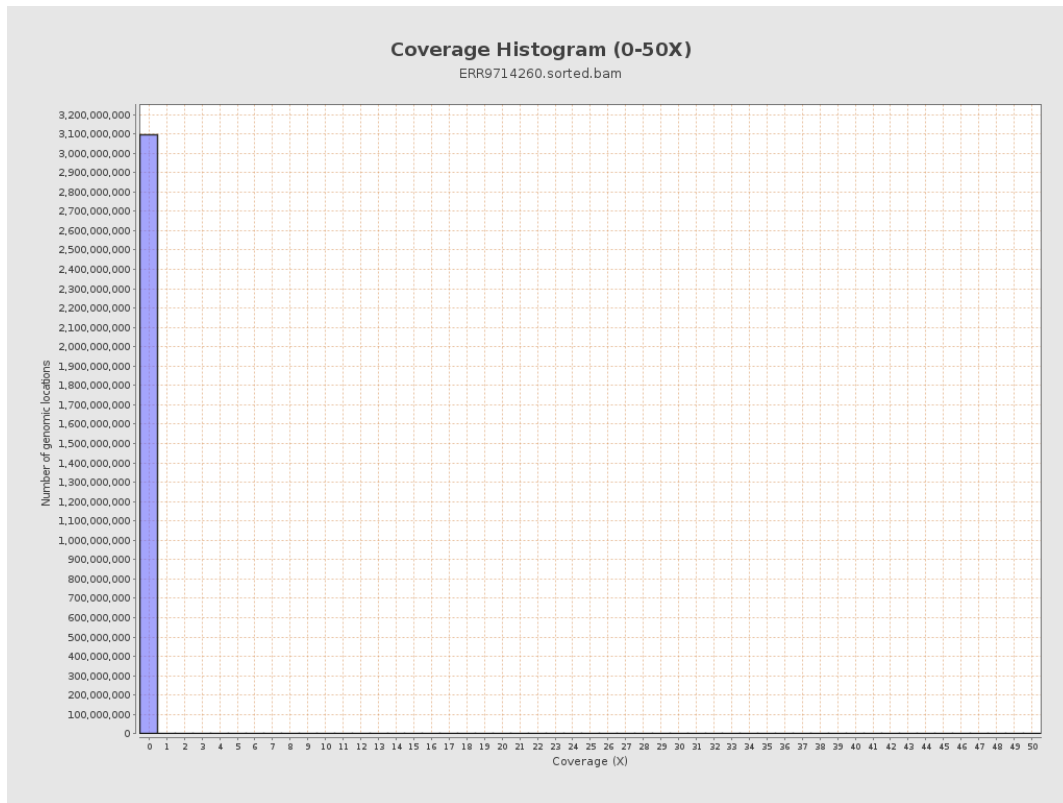
3. Results : Coverage across reference



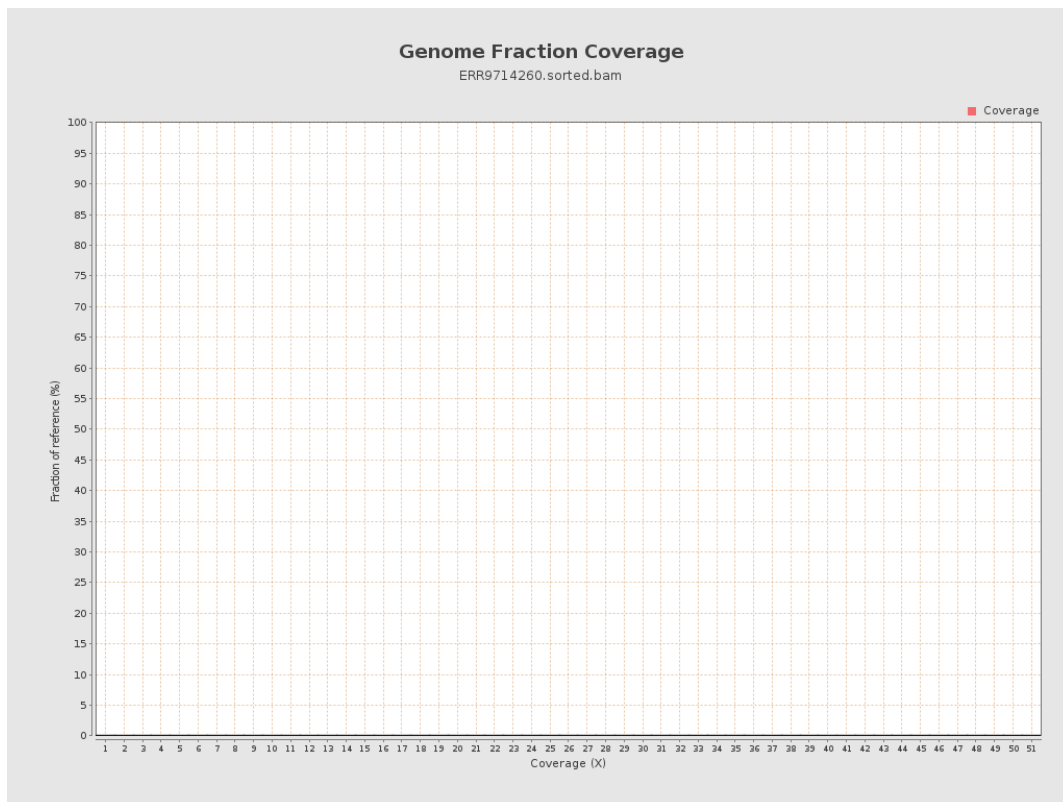
4. Results : Coverage Histogram



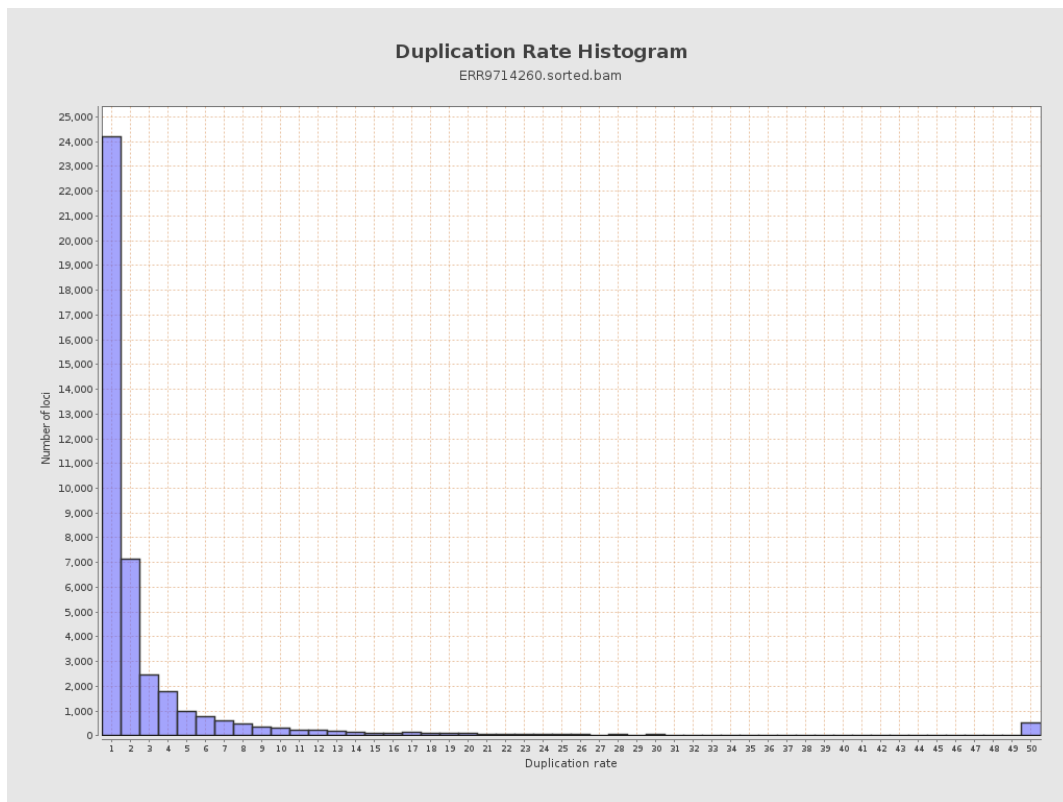
5. Results : Coverage Histogram (0-50X)



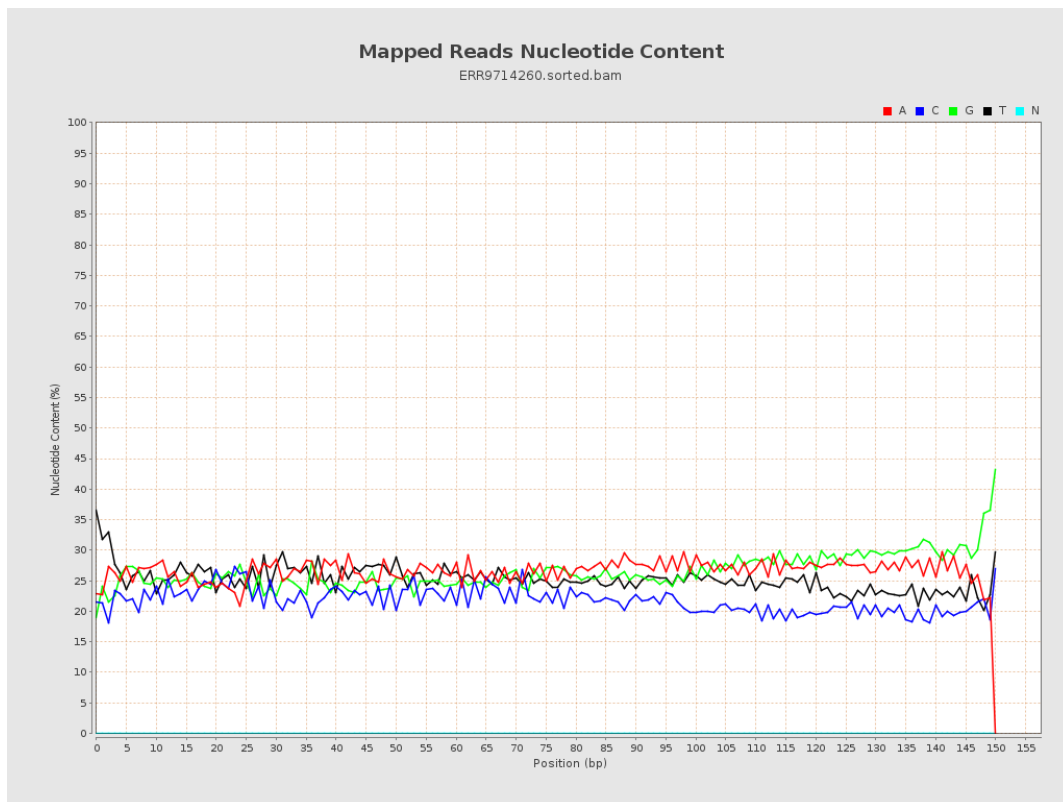
6. Results : Genome Fraction Coverage



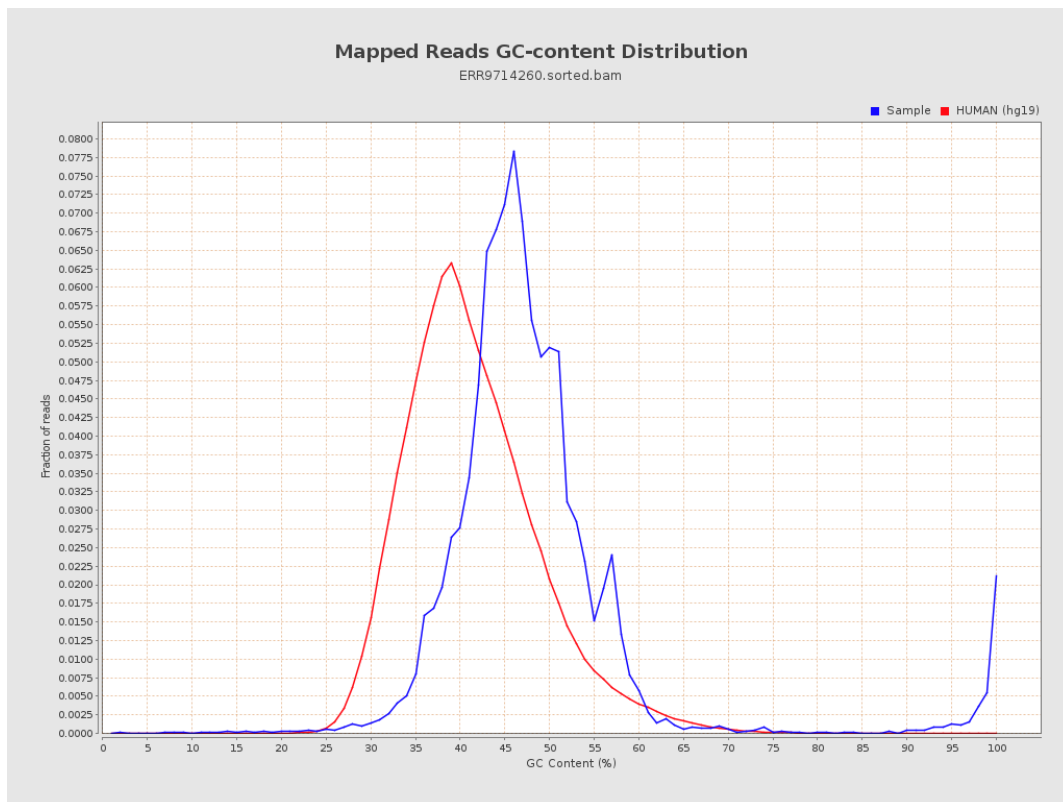
7. Results : Duplication Rate Histogram



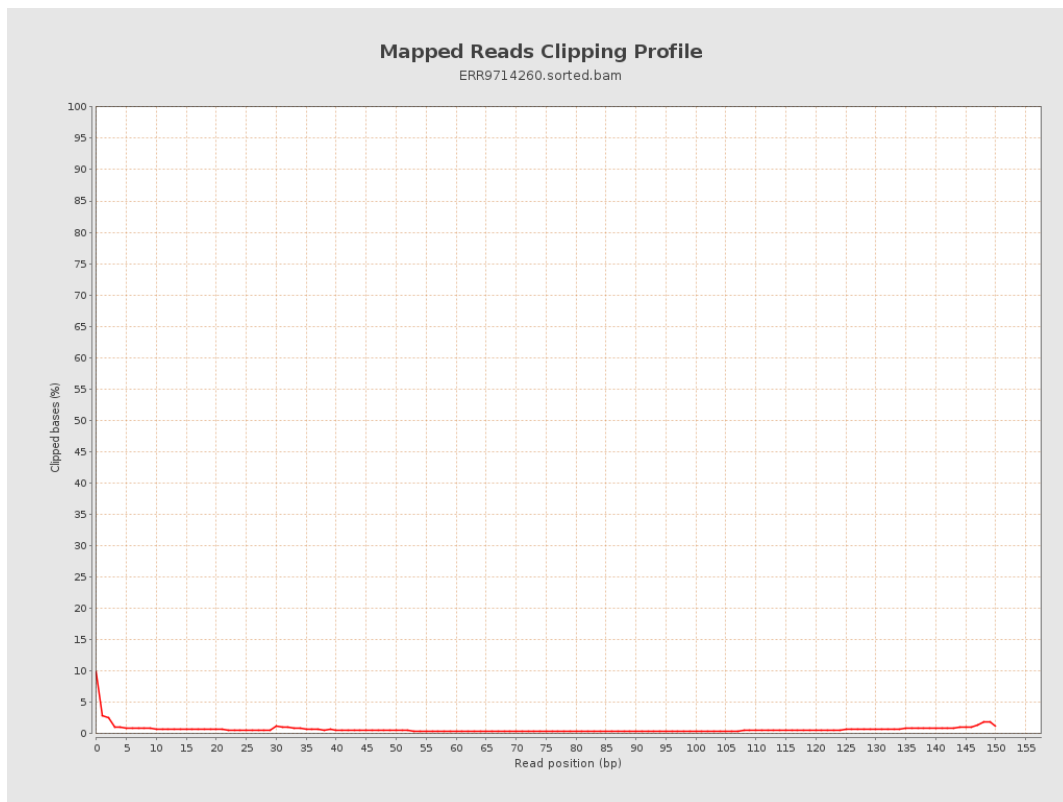
8. Results : Mapped Reads Nucleotide Content



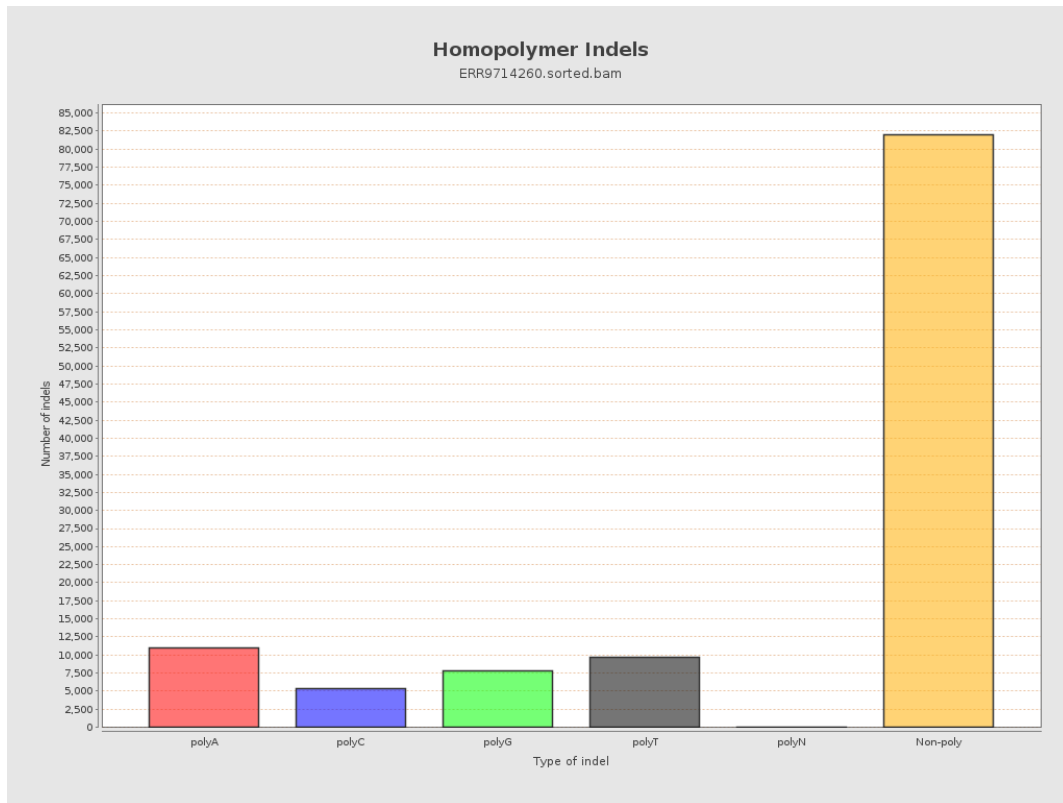
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

