

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:59:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714135.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_ERR9714135 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:59:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	705,416
Mapped reads	514,623 / 72.95%
Unmapped reads	190,793 / 27.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,291 / 2.45%
Read min/max/mean length	30 / 151 / 124.09
Duplicated reads (estimated)	430,771 / 61.07%
Duplication rate	43.39%
Clipped reads	485,360 / 68.8%

2.2. ACGT Content

Number/percentage of A's	18,161,396 / 28%
Number/percentage of C's	13,634,026 / 21.02%
Number/percentage of T's	17,239,425 / 26.58%
Number/percentage of G's	15,823,178 / 24.4%
Number/percentage of N's	371 / 0%
GC Percentage	45.42%

2.3. Coverage

Mean	0.0214

Standard Deviation	2.9522
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2.4. Mapping Quality

Mean Mapping Quality	52.39
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2.5. Mismatches and indels

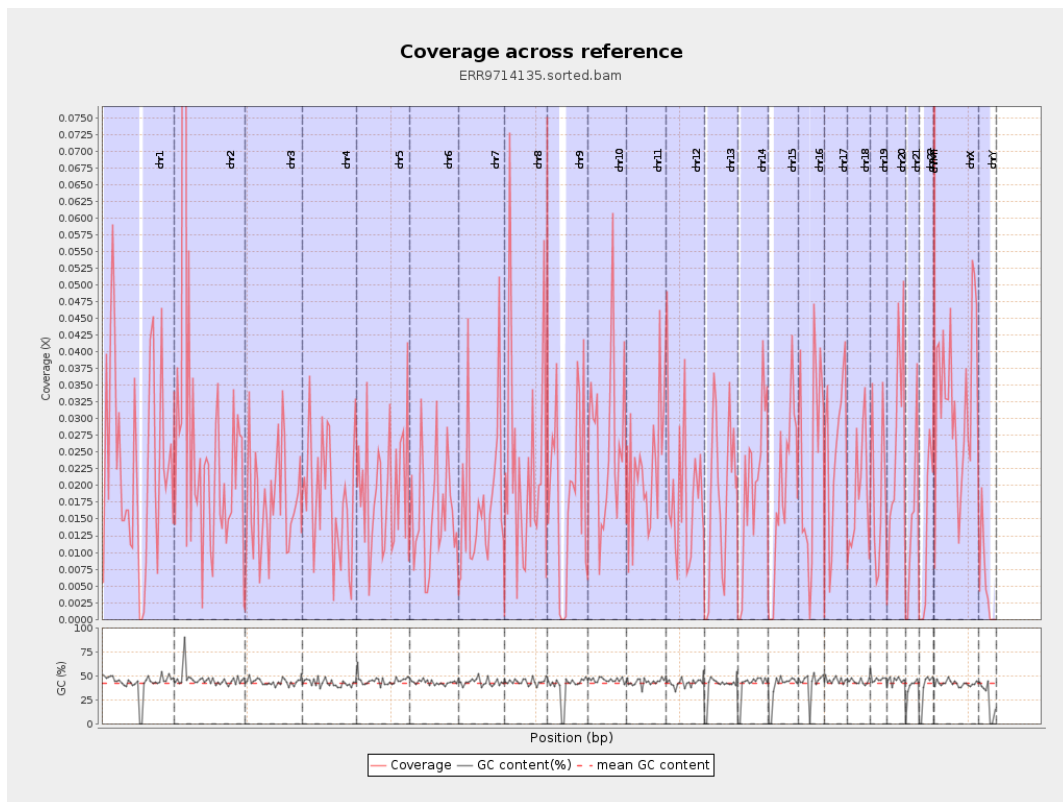
General error rate	4.29%
Mismatches	2,540,185
Insertions	72,764
Mapped reads with at least one insertion	13.62%
Deletions	217,040
Mapped reads with at least one deletion	40.14%
Homopolymer indels	29.1%

2.6. Chromosome stats

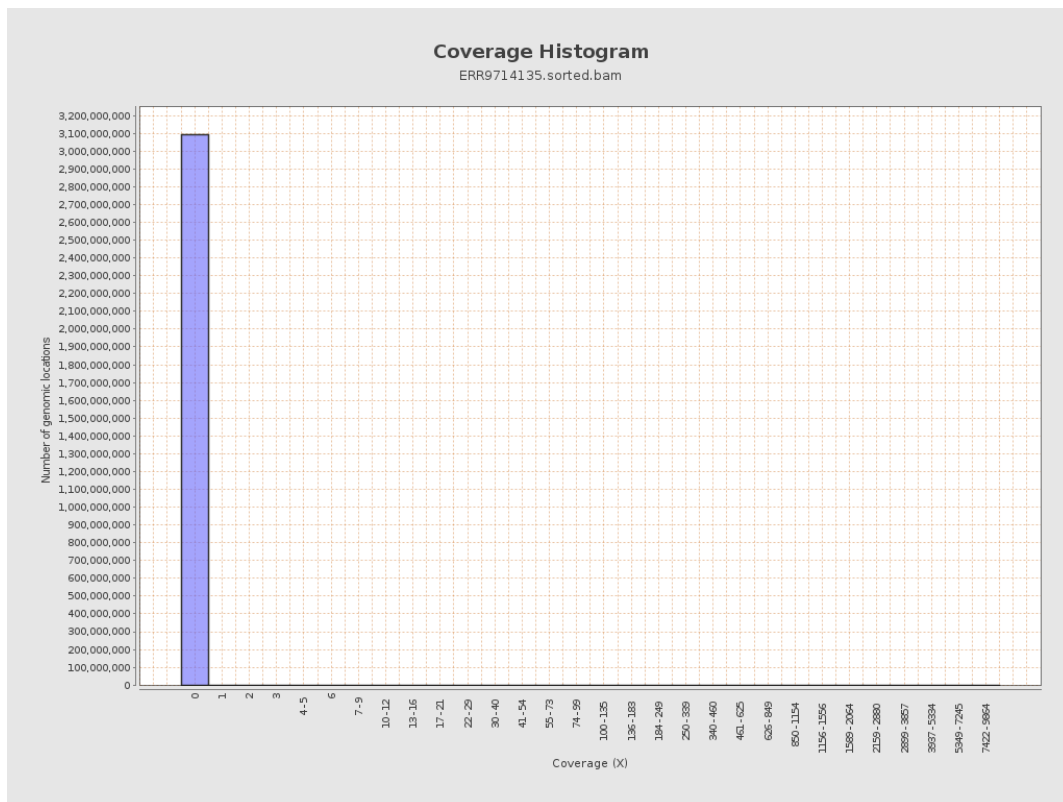
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5660434	0.0227	2.3831
chr2	243199373	7210931	0.0297	7.0143
chr3	198022430	3539859	0.0179	1.6801
chr4	191154276	3494014	0.0183	2.0586
chr5	180915260	3557334	0.0197	1.8976
chr6	171115067	2651637	0.0155	1.4329
chr7	159138663	2791229	0.0175	1.9042

chr8	146364022	3248130	0.0222	2.5934
chr9	141213431	2706313	0.0192	2.2914
chr10	135534747	3622554	0.0267	2.5221
chr11	135006516	2980824	0.0221	2.113
chr12	133851895	2521277	0.0188	1.9338
chr13	115169878	2044827	0.0178	2.0598
chr14	107349540	2142617	0.02	1.8667
chr15	102531392	1934427	0.0189	1.809
chr16	90354753	2207638	0.0244	2.6426
chr17	81195210	2066148	0.0254	2.5604
chr18	78077248	1522224	0.0195	1.7742
chr19	59128983	1026802	0.0174	1.615
chr20	63025520	1699027	0.027	2.3374
chr21	48129895	676926	0.0141	1.9896
chr22	51304566	665886	0.013	1.4276
chrMT	16571	737218	44.4884	406.2745
chrX	155270560	5096474	0.0328	2.1856
chrY	59373566	316347	0.0053	0.8982

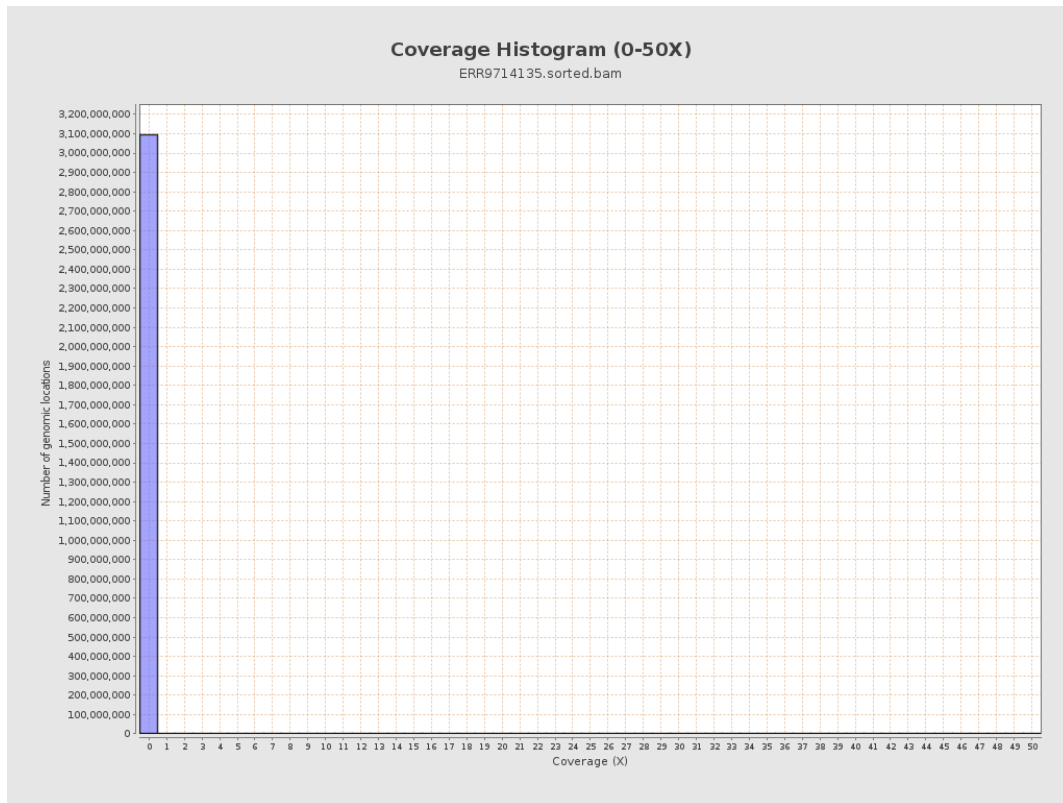
3. Results : Coverage across reference



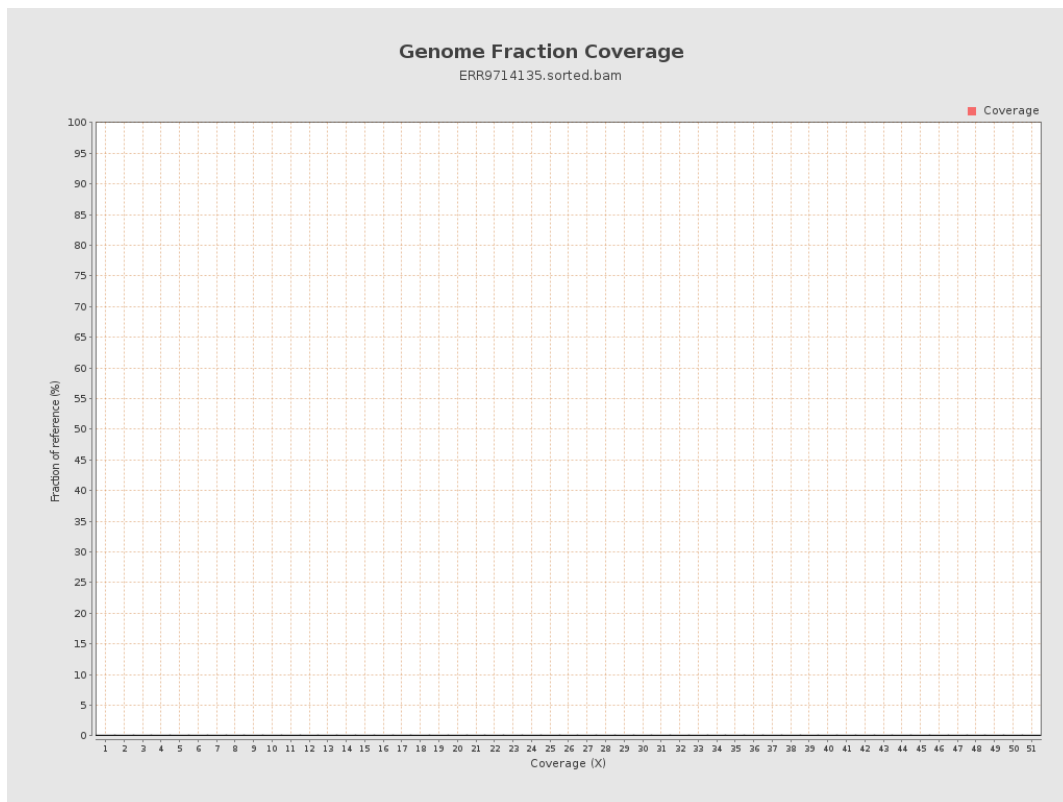
4. Results : Coverage Histogram



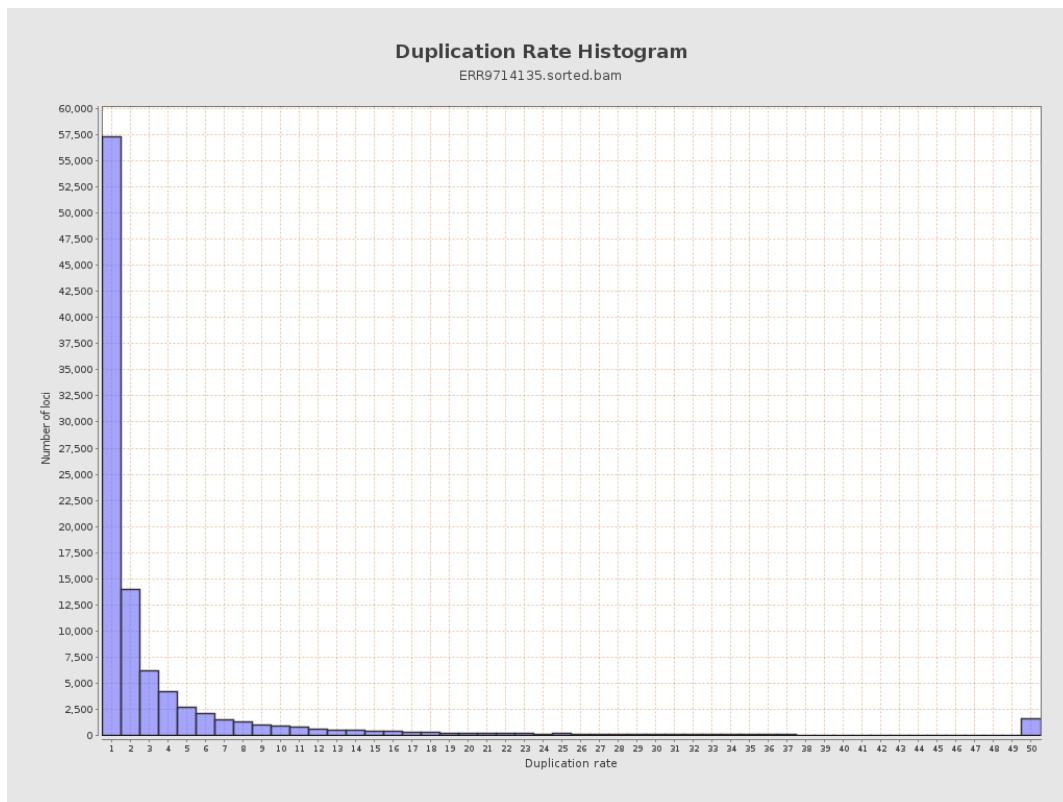
5. Results : Coverage Histogram (0-50X)



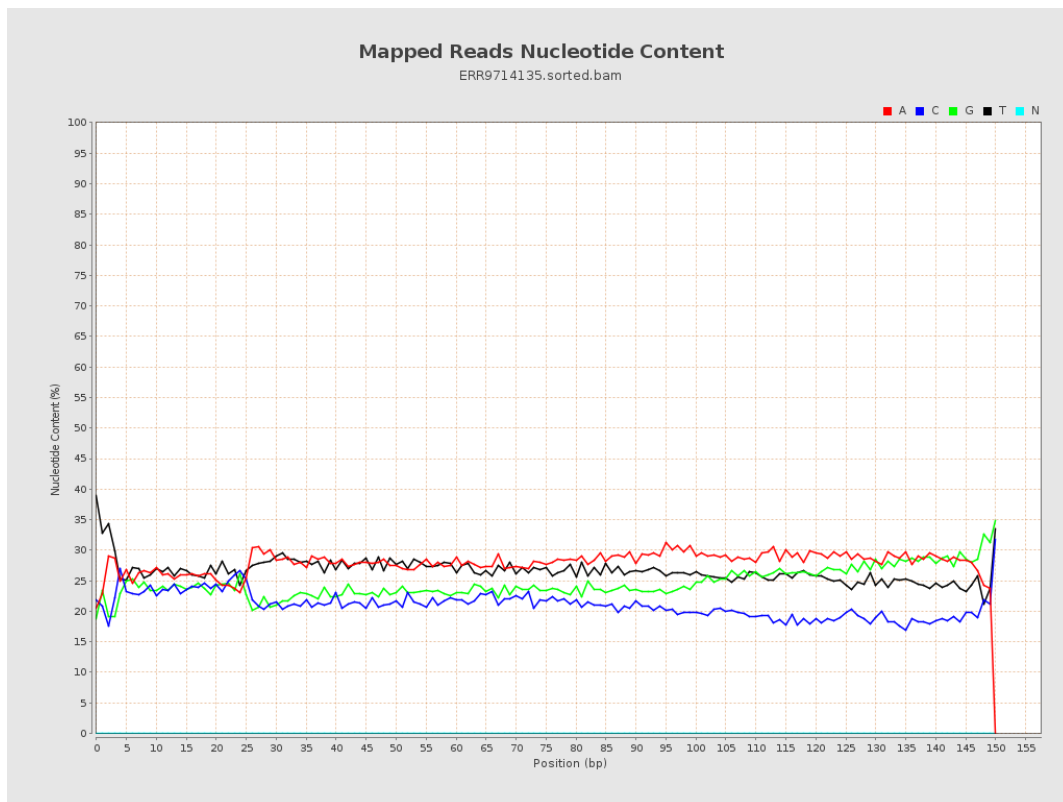
6. Results : Genome Fraction Coverage



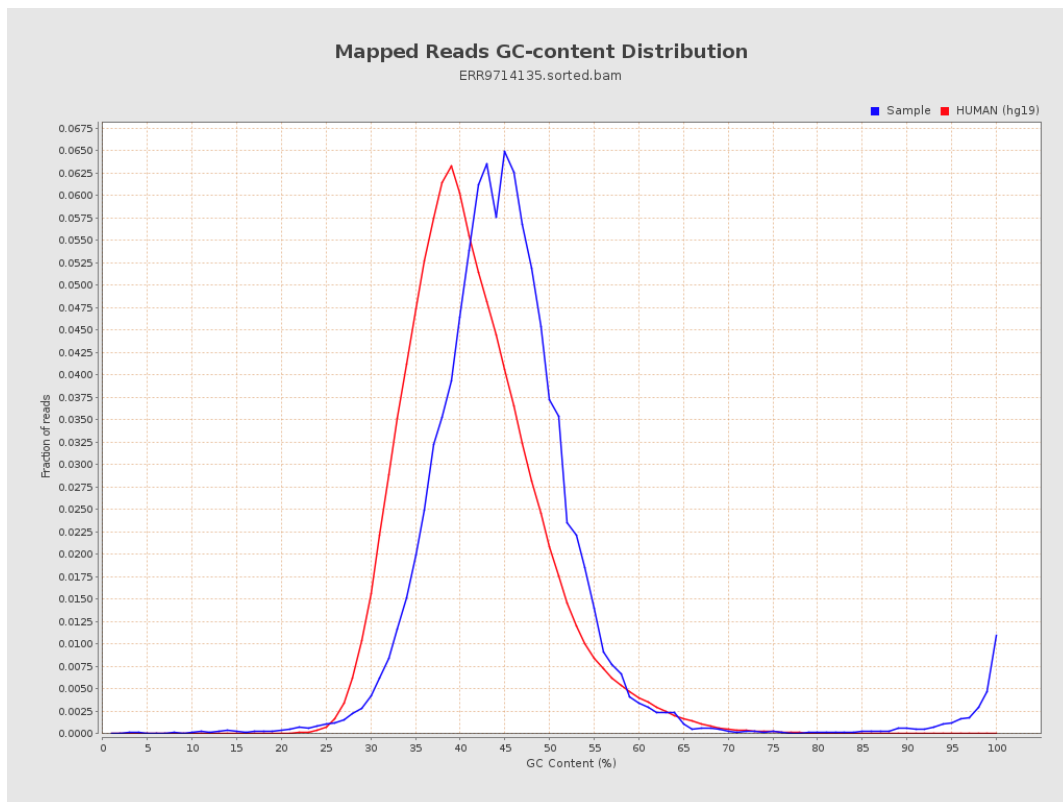
7. Results : Duplication Rate Histogram



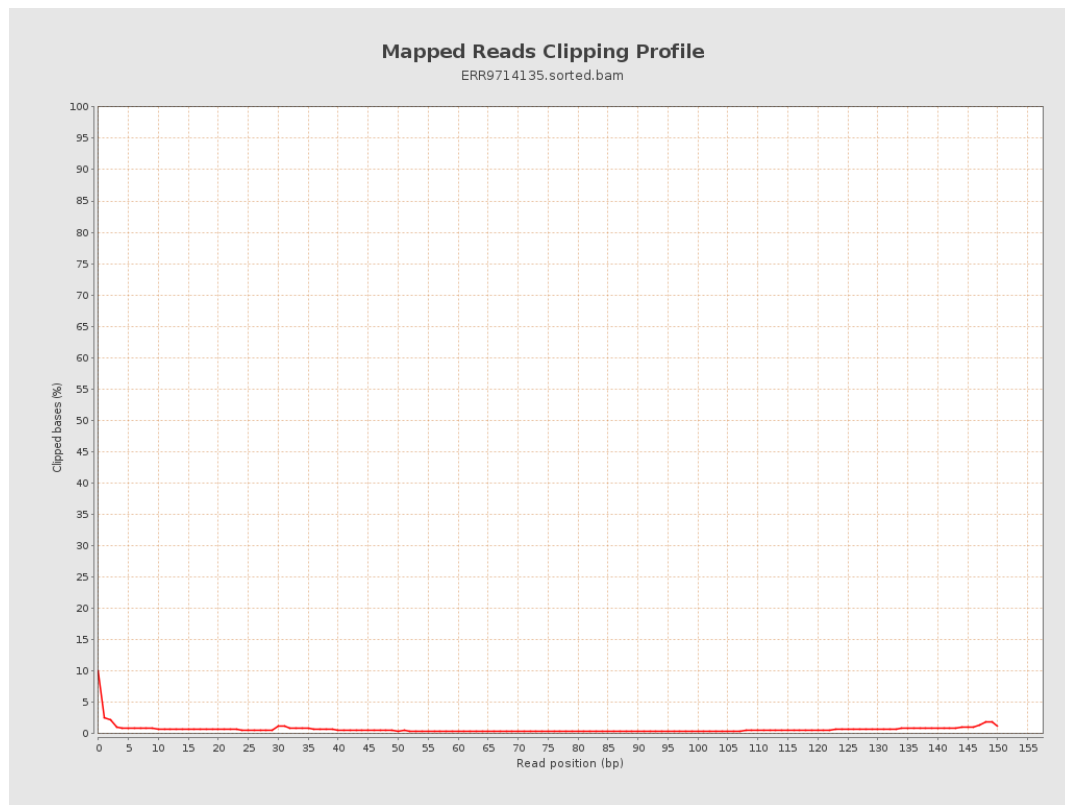
8. Results : Mapped Reads Nucleotide Content



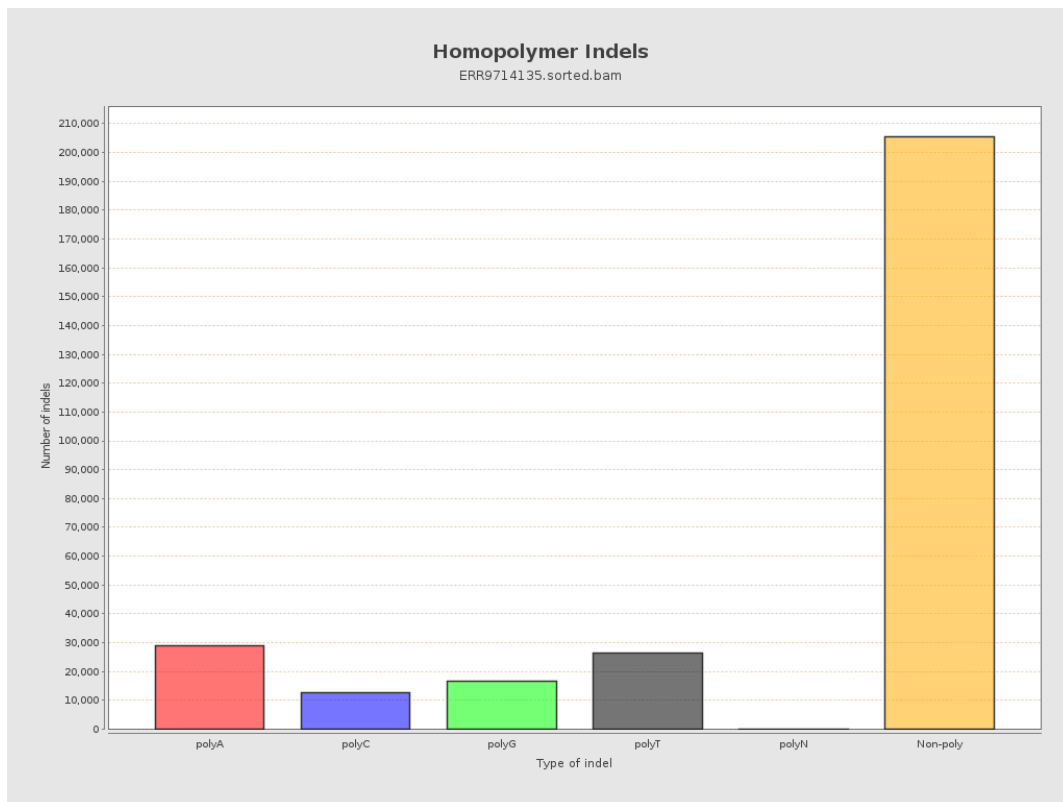
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

