

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:20:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714121.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_ERR9714121 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:20:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	654,230
Mapped reads	481,397 / 73.58%
Unmapped reads	172,833 / 26.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,118 / 2.01%
Read min/max/mean length	30 / 151 / 125.44
Duplicated reads (estimated)	421,205 / 64.38%
Duplication rate	43.95%
Clipped reads	442,383 / 67.62%

2.2. ACGT Content

Number/percentage of A's	16,750,184 / 27.35%
Number/percentage of C's	12,474,604 / 20.37%
Number/percentage of T's	15,942,097 / 26.03%
Number/percentage of G's	16,075,787 / 26.25%
Number/percentage of N's	508 / 0%
GC Percentage	46.62%

2.3. Coverage

Mean	0.0203

Standard Deviation	5.381
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2.4. Mapping Quality

Mean Mapping Quality	51.66
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2.5. Mismatches and indels

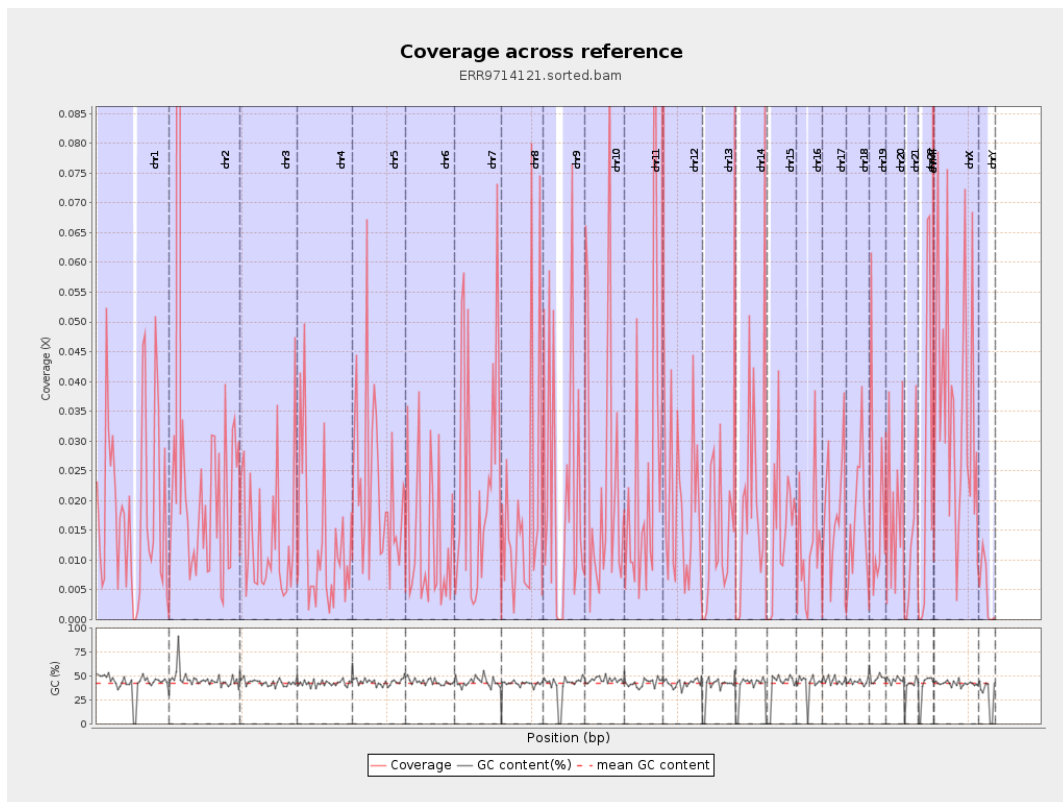
General error rate	4.66%
Mismatches	2,655,609
Insertions	74,928
Mapped reads with at least one insertion	14.83%
Deletions	233,396
Mapped reads with at least one deletion	45.04%
Homopolymer indels	29.63%

2.6. Chromosome stats

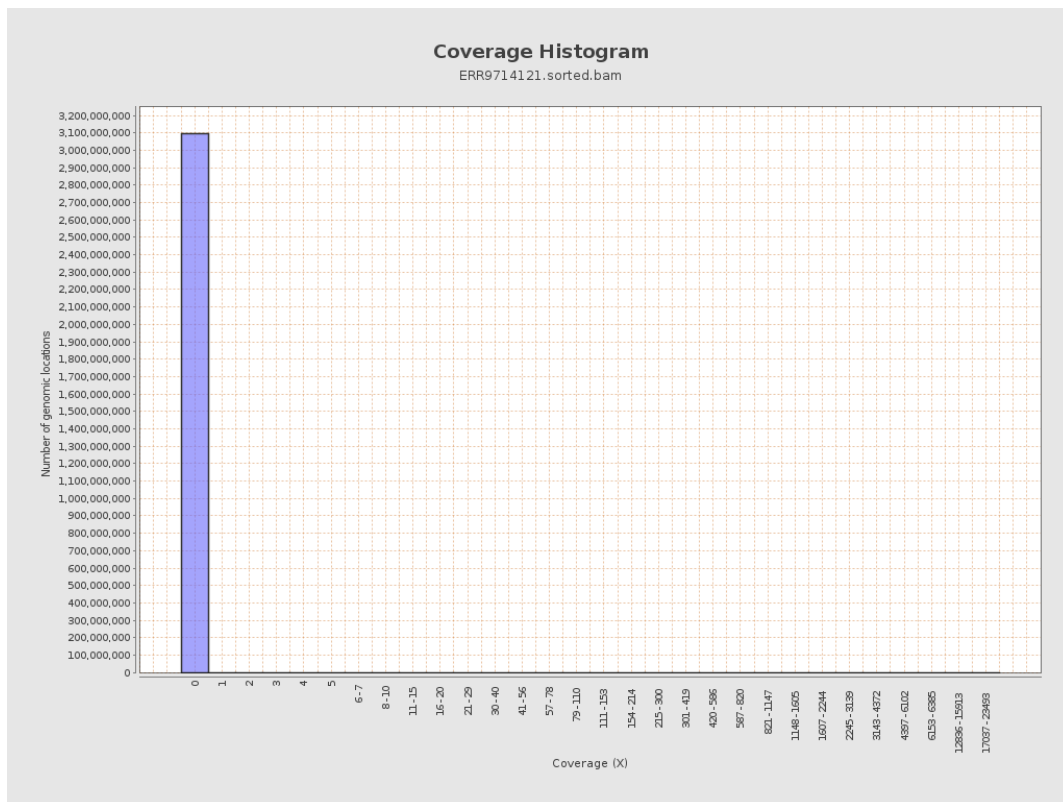
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4505514	0.0181	2.9792
chr2	243199373	8187365	0.0337	14.767
chr3	198022430	2702972	0.0136	2.5128
chr4	191154276	2505507	0.0131	2.0299
chr5	180915260	4000399	0.0221	3.948
chr6	171115067	2226715	0.013	2.2698
chr7	159138663	3689353	0.0232	4.6612

chr8	146364022	2713307	0.0185	3.8053
chr9	141213431	2777449	0.0197	3.6015
chr10	135534747	3349327	0.0247	5.0372
chr11	135006516	3455382	0.0256	7.0547
chr12	133851895	2607279	0.0195	2.6894
chr13	115169878	1672200	0.0145	2.2654
chr14	107349540	2393059	0.0223	4.2554
chr15	102531392	1598115	0.0156	1.9884
chr16	90354753	1091671	0.0121	1.49
chr17	81195210	1488547	0.0183	2.635
chr18	78077248	1322097	0.0169	1.9407
chr19	59128983	1107247	0.0187	2.5292
chr20	63025520	1172040	0.0186	2.8954
chr21	48129895	578306	0.012	2.3635
chr22	51304566	1273719	0.0248	6.3827
chrMT	16571	375133	22.6379	180.8308
chrX	155270560	5648153	0.0364	3.8057
chrY	59373566	266405	0.0045	0.9313

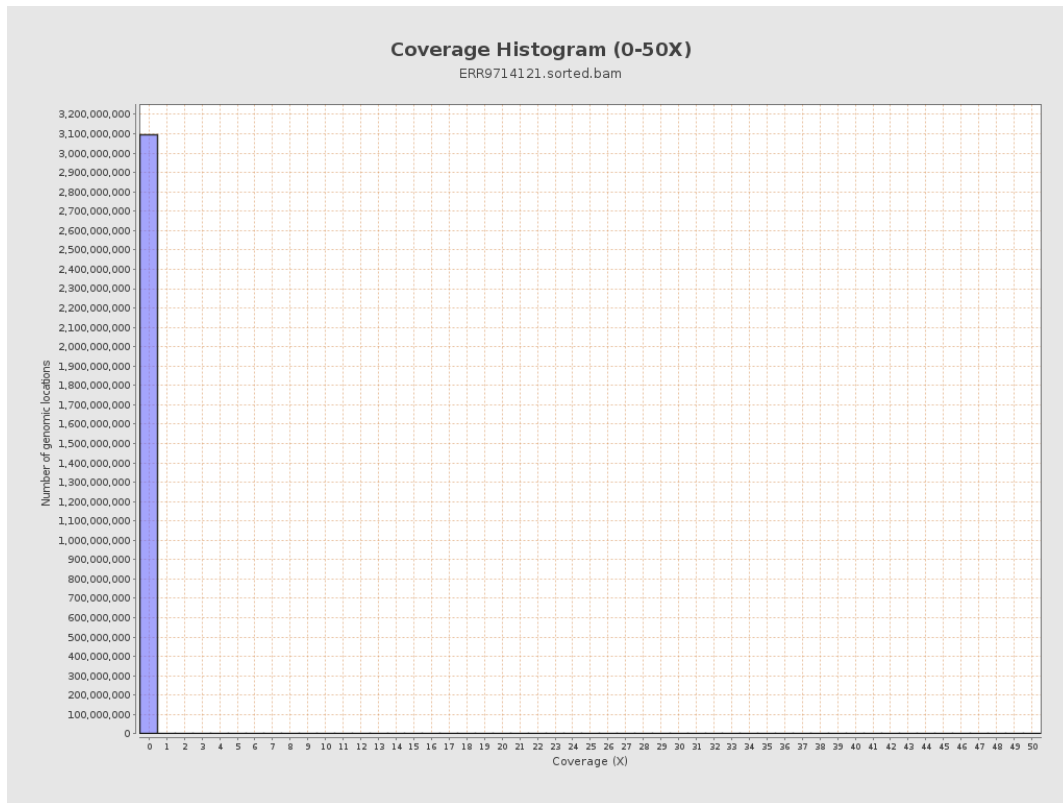
3. Results : Coverage across reference



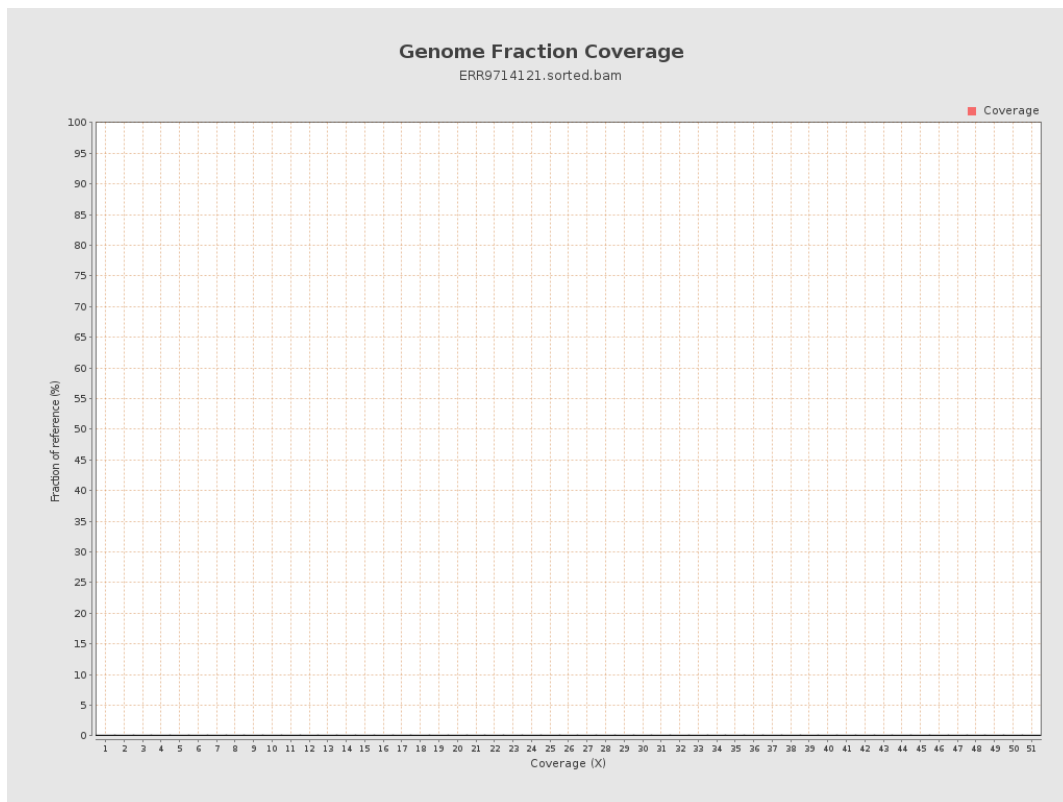
4. Results : Coverage Histogram



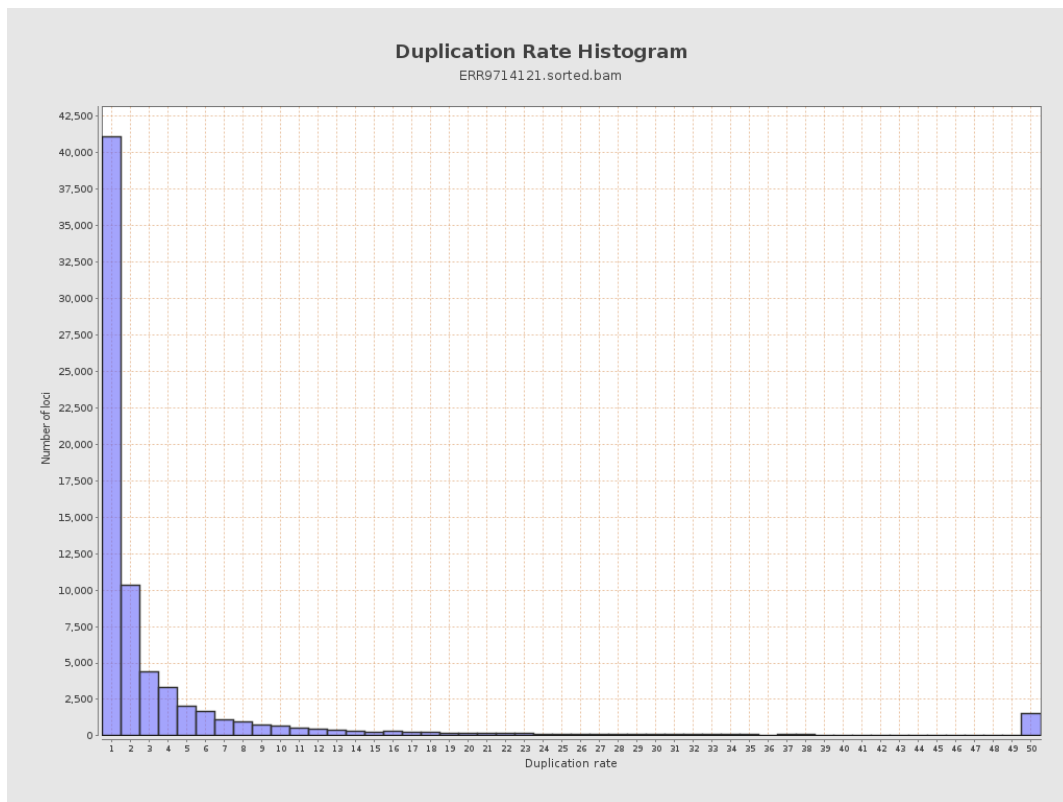
5. Results : Coverage Histogram (0-50X)



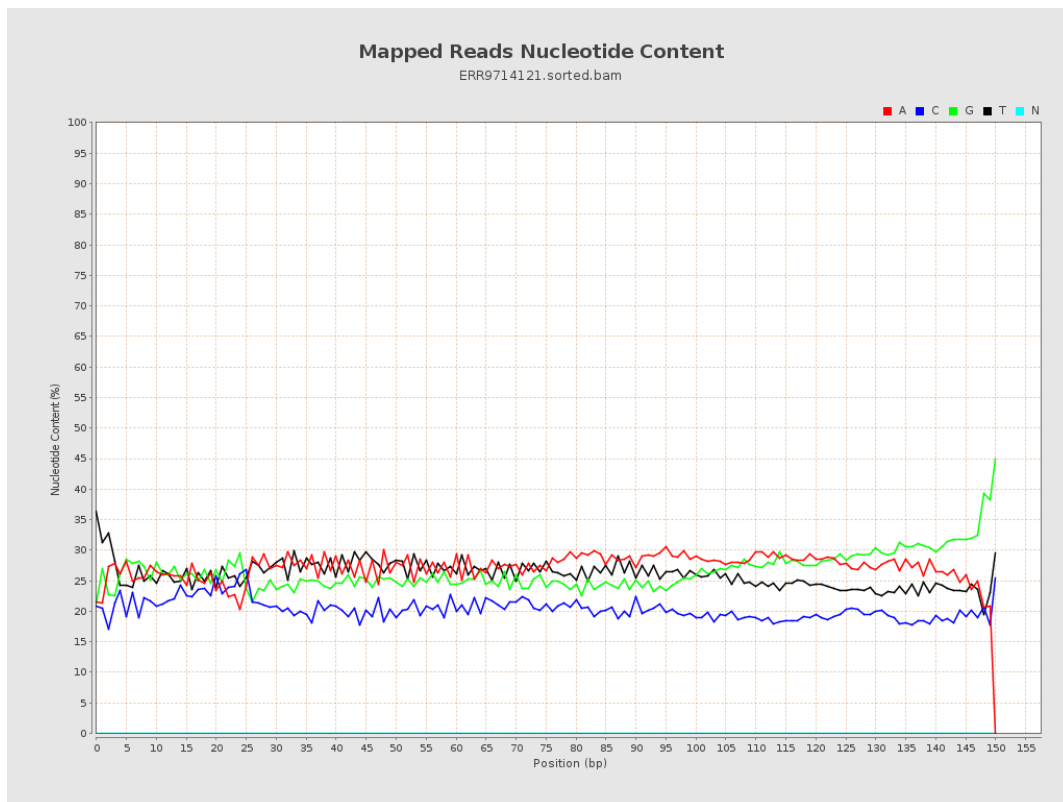
6. Results : Genome Fraction Coverage



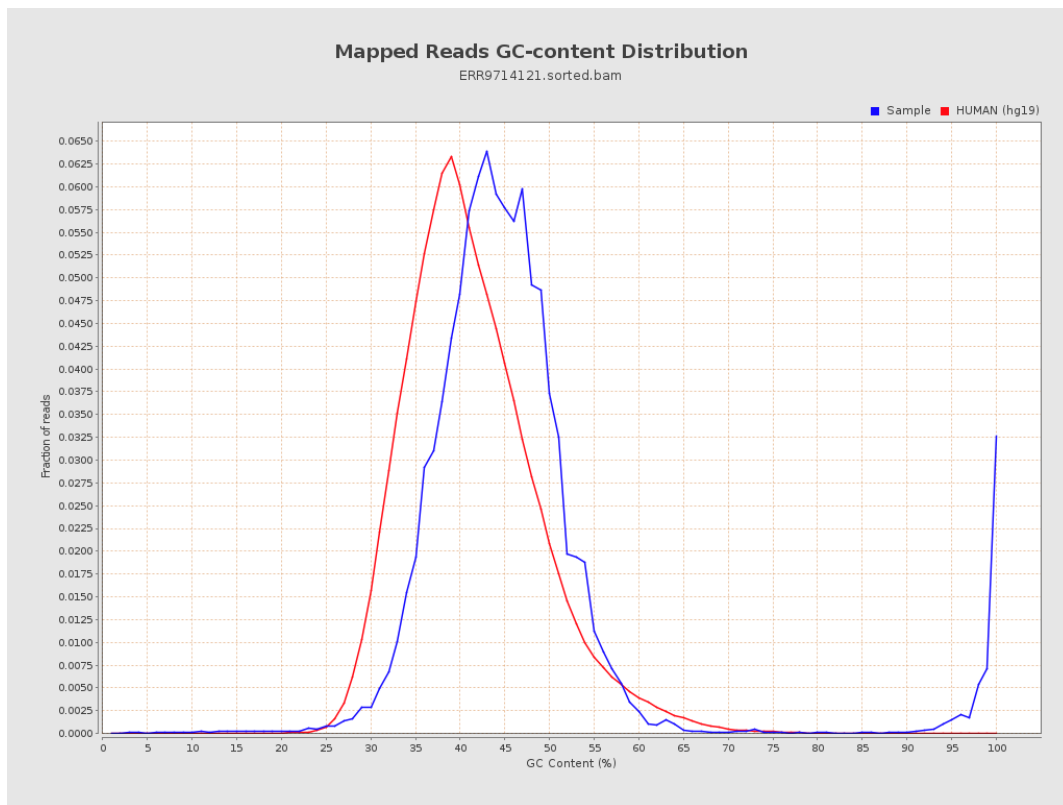
7. Results : Duplication Rate Histogram



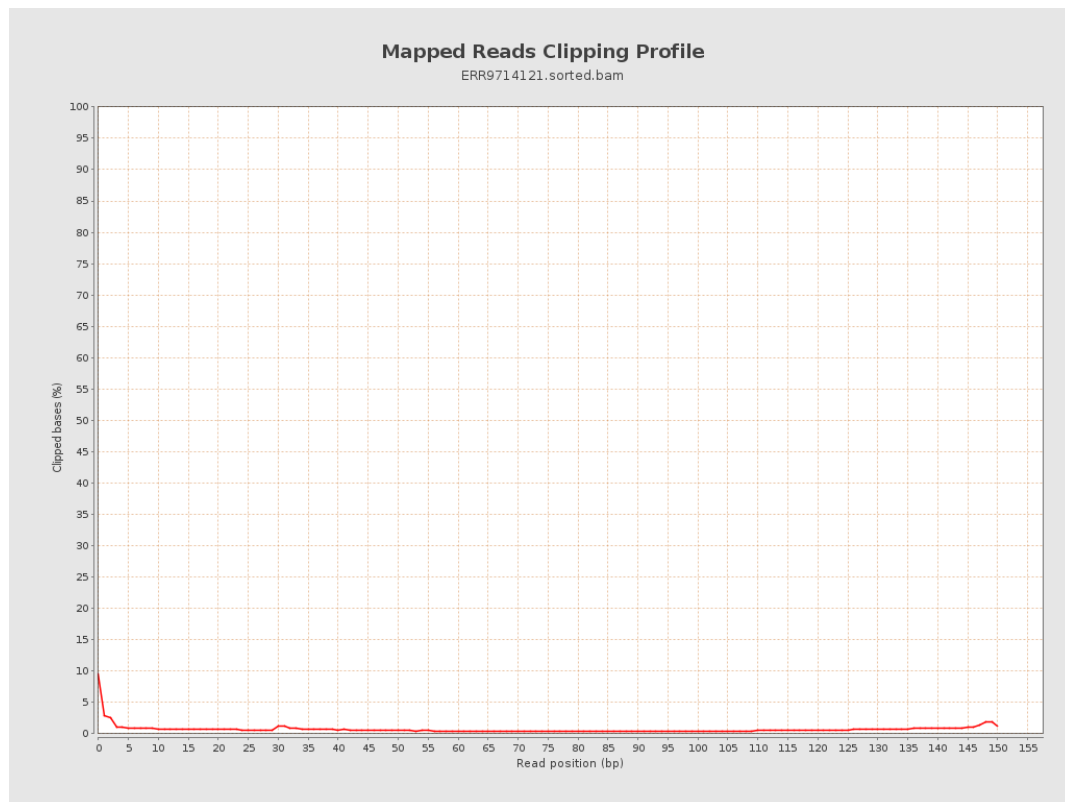
8. Results : Mapped Reads Nucleotide Content



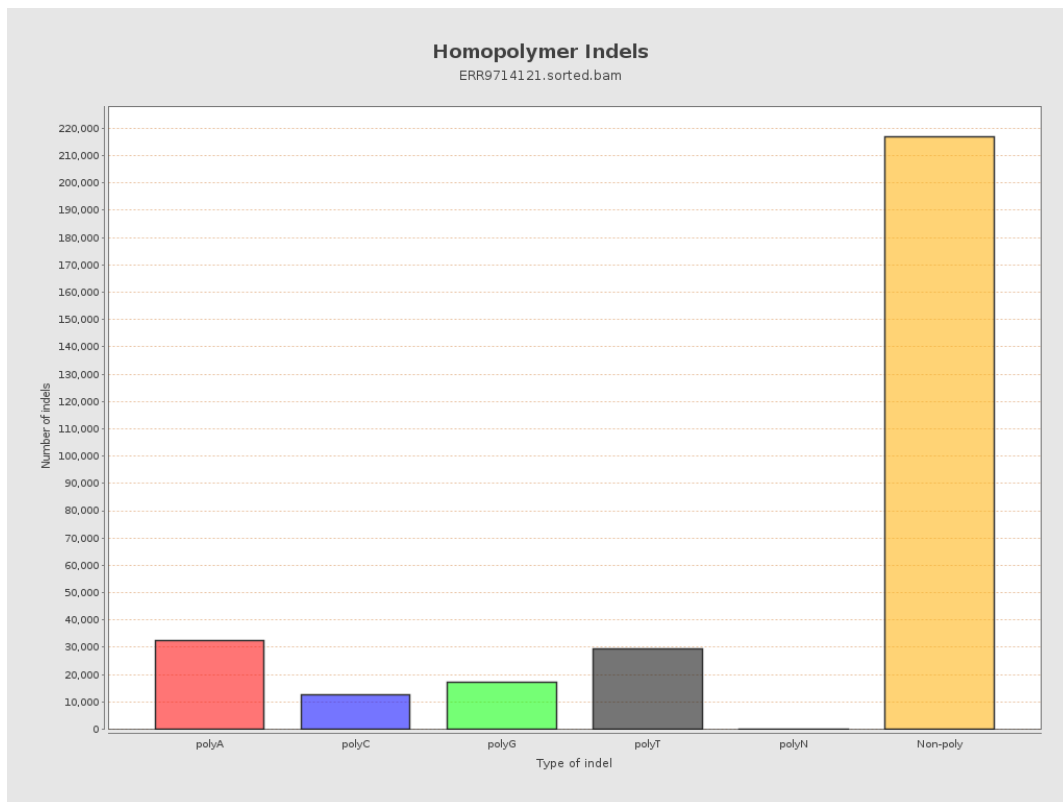
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

