

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:27:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714217.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_ERR9714217 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:27:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	169,812
Mapped reads	37,101 / 21.85%
Unmapped reads	132,711 / 78.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,292 / 0.76%
Read min/max/mean length	30 / 151 / 71.36
Duplicated reads (estimated)	33,031 / 19.45%
Duplication rate	46.57%
Clipped reads	26,659 / 15.7%

2.2. ACGT Content

Number/percentage of A's	606,032 / 15.18%
Number/percentage of C's	492,600 / 12.34%
Number/percentage of T's	551,118 / 13.8%
Number/percentage of G's	2,342,845 / 58.68%
Number/percentage of N's	54 / 0%
GC Percentage	71.02%

2.3. Coverage

Mean	0.0013

Standard Deviation	2.3354
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2.4. Mapping Quality

Mean Mapping Quality	35.72
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2.5. Mismatches and indels

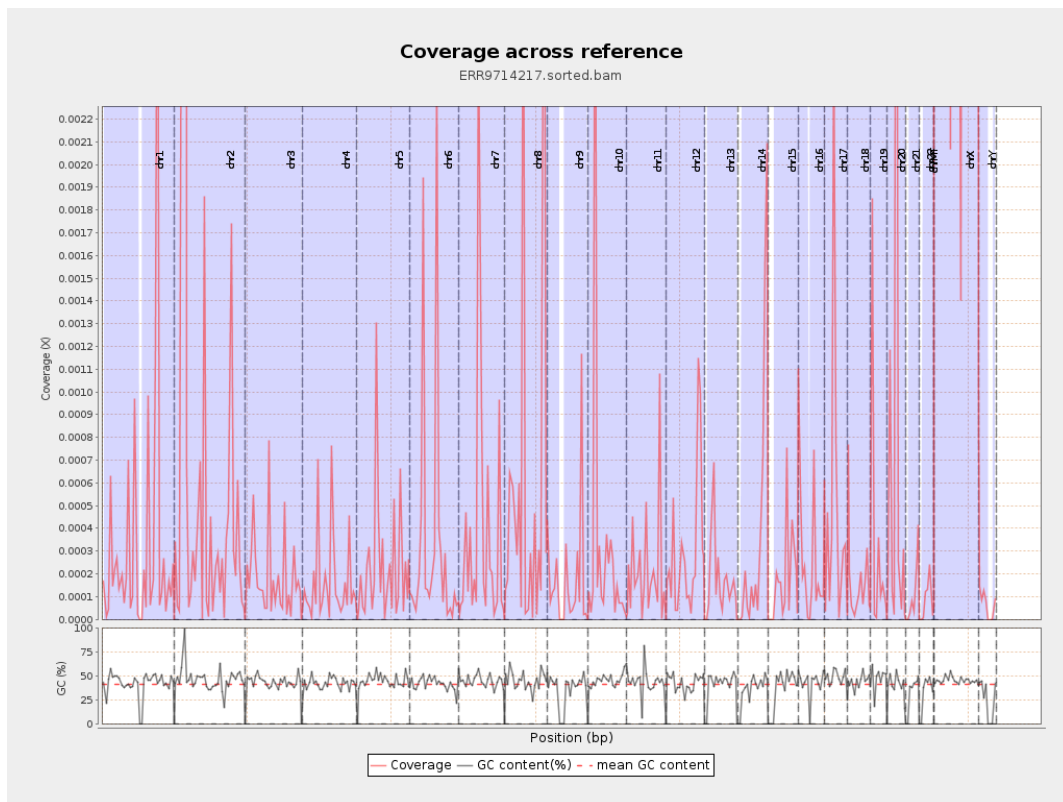
General error rate	3.56%
Mismatches	124,404
Insertions	3,032
Mapped reads with at least one insertion	5.91%
Deletions	6,881
Mapped reads with at least one deletion	18%
Homopolymer indels	38.9%

2.6. Chromosome stats

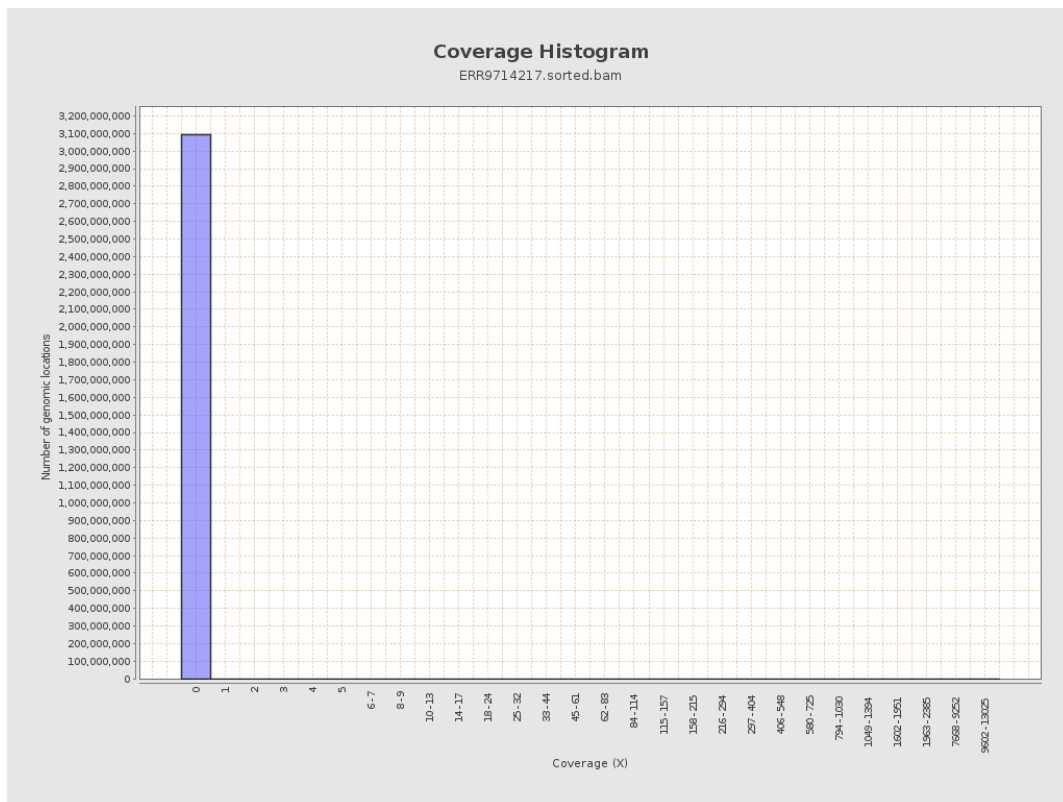
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	86688	0.0003	0.325
chr2	243199373	1965761	0.0081	8.2728
chr3	198022430	37005	0.0002	0.0413
chr4	191154276	31805	0.0002	0.0439
chr5	180915260	43110	0.0002	0.0743
chr6	171115067	57902	0.0003	0.1141
chr7	159138663	58364	0.0004	0.1389

chr8	146364022	90785	0.0006	0.2479
chr9	141213431	24597	0.0002	0.0623
chr10	135534747	46679	0.0003	0.4151
chr11	135006516	30202	0.0002	0.0525
chr12	133851895	38736	0.0003	0.0701
chr13	115169878	19370	0.0002	0.0454
chr14	107349540	42321	0.0004	0.1375
chr15	102531392	18701	0.0002	0.0485
chr16	90354753	23690	0.0003	0.0594
chr17	81195210	39714	0.0005	0.135
chr18	78077248	12371	0.0002	0.0311
chr19	59128983	20002	0.0003	0.1471
chr20	63025520	53755	0.0009	0.3137
chr21	48129895	5343	0.0001	0.0242
chr22	51304566	4177	0.0001	0.0179
chrMT	16571	1644	0.0992	0.4947
chrX	155270560	1289482	0.0083	1.0176
chrY	59373566	3770	0.0001	0.0135

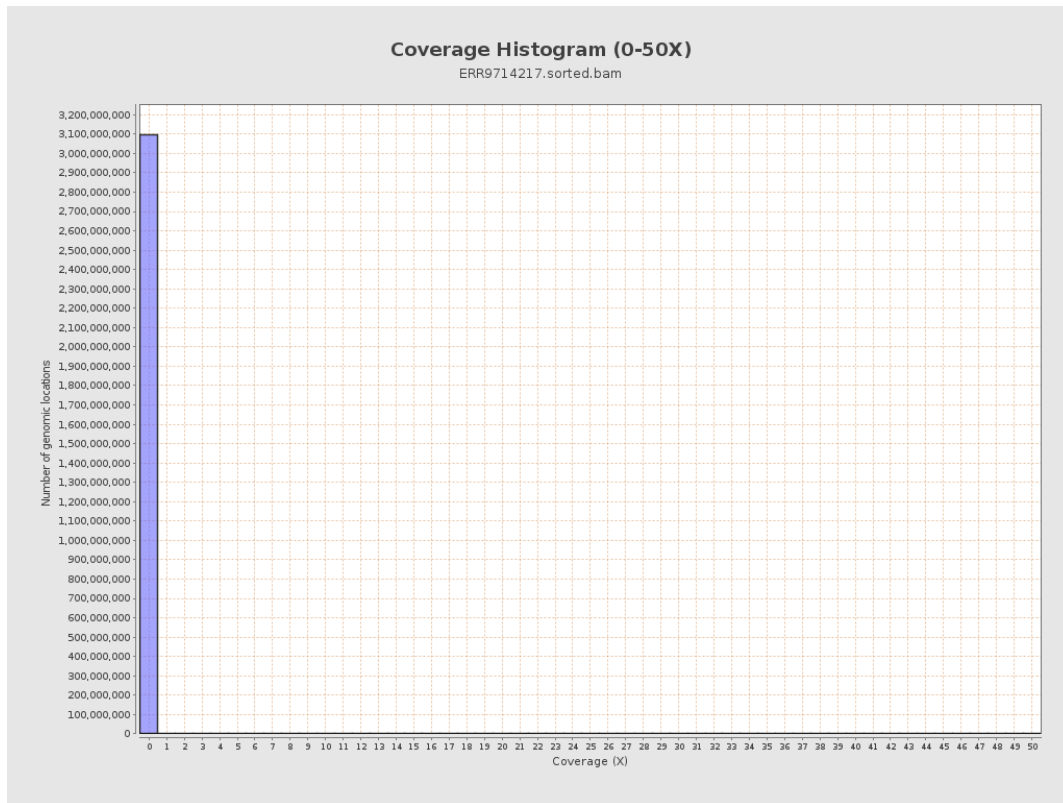
3. Results : Coverage across reference



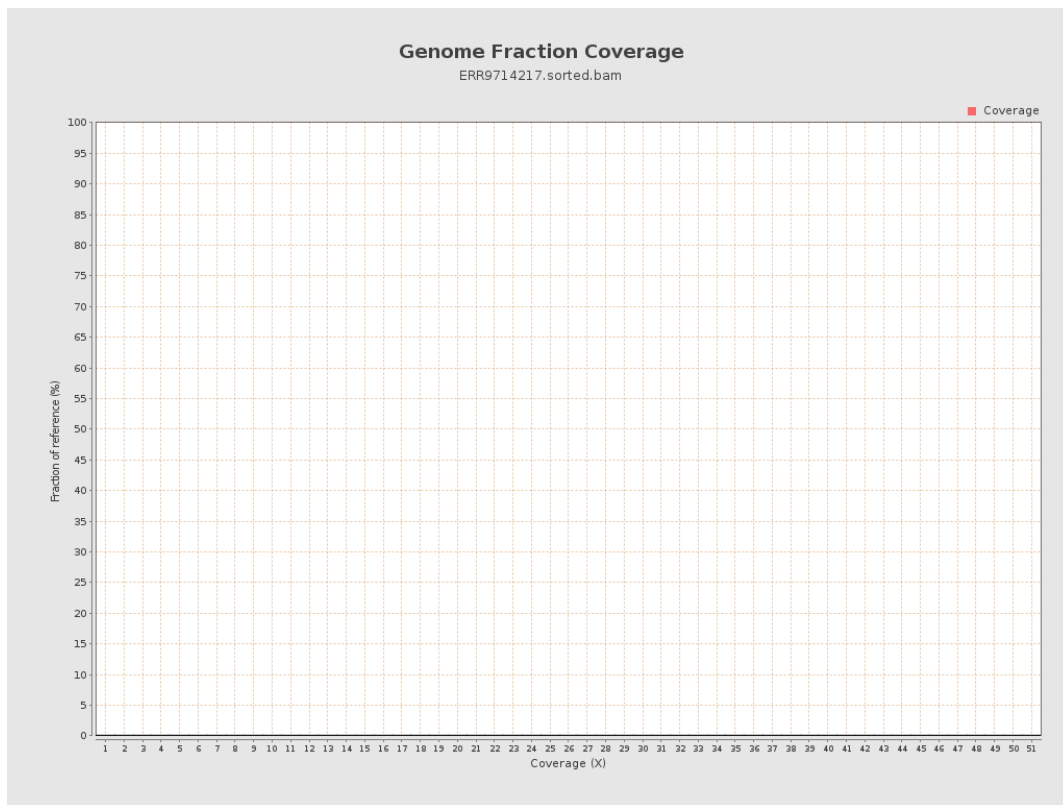
4. Results : Coverage Histogram



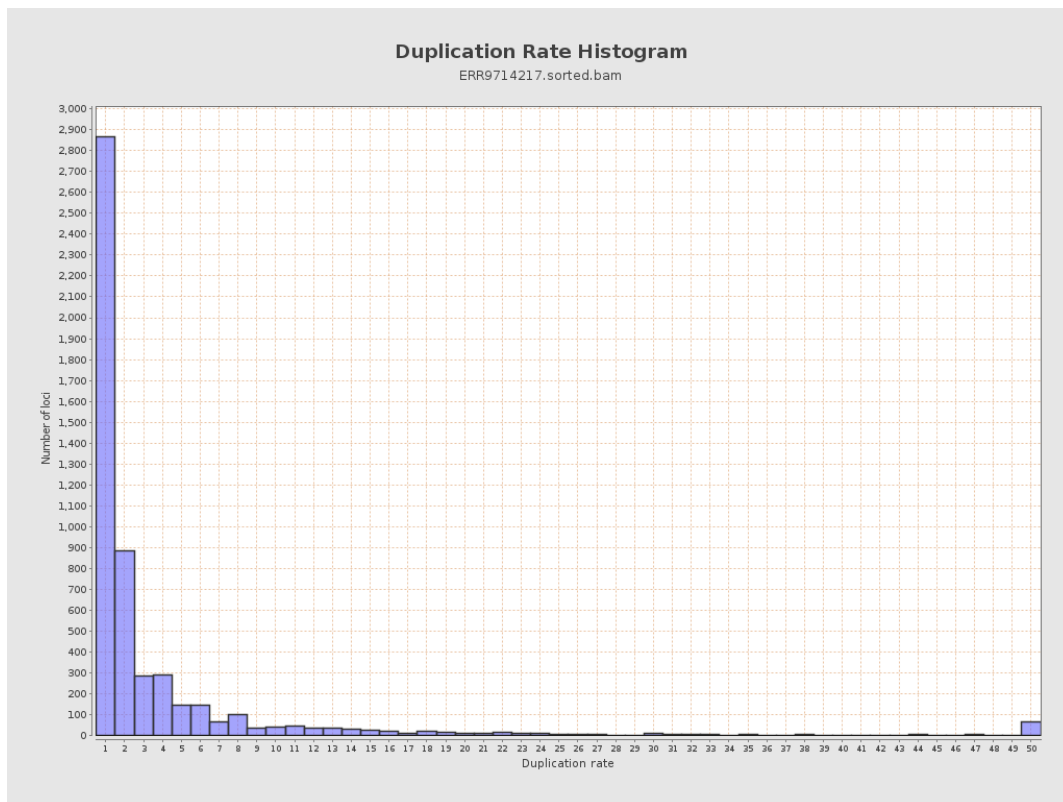
5. Results : Coverage Histogram (0-50X)



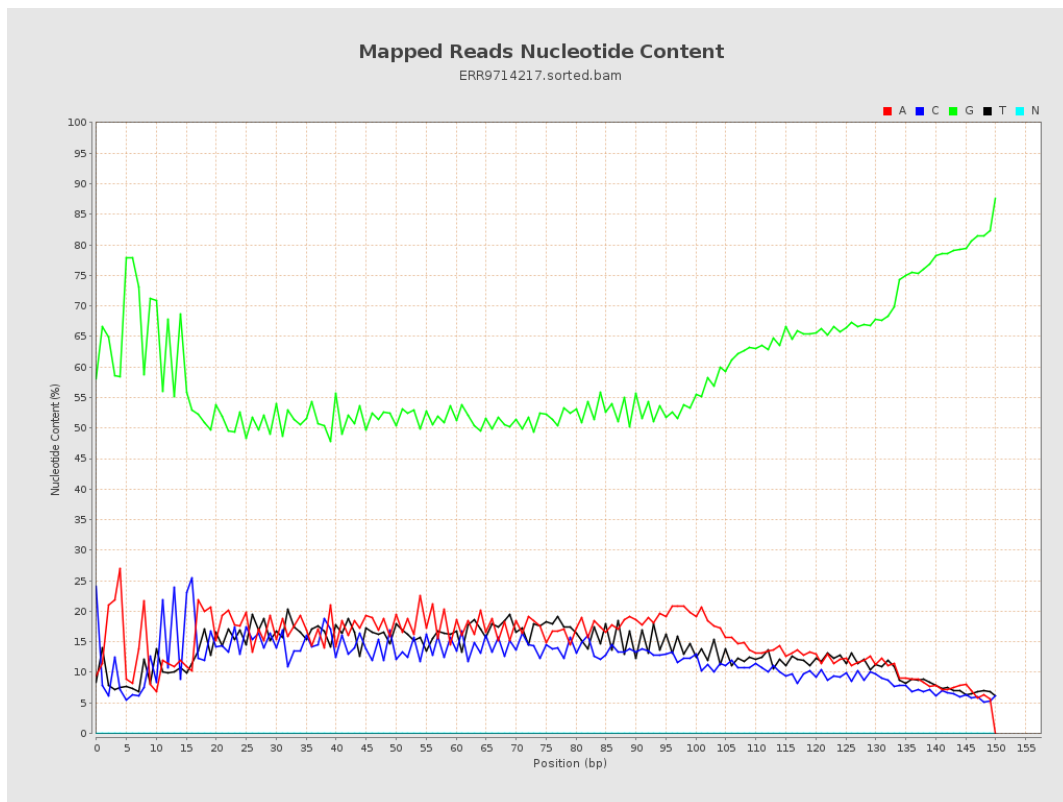
6. Results : Genome Fraction Coverage



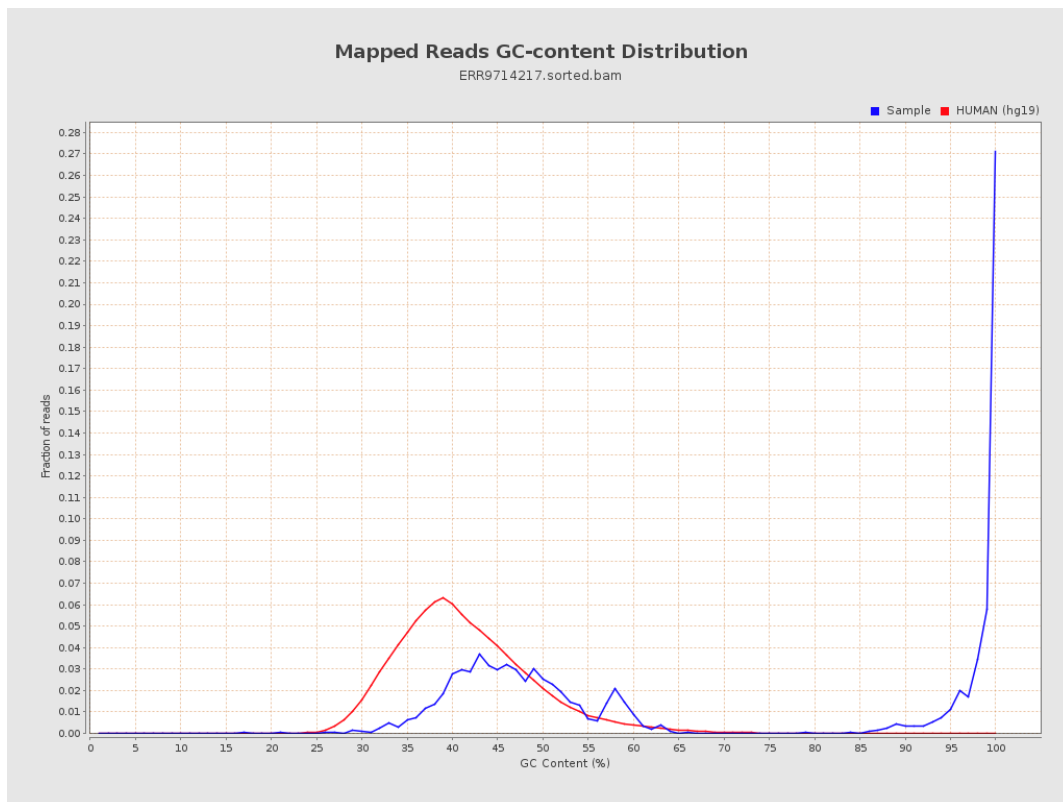
7. Results : Duplication Rate Histogram



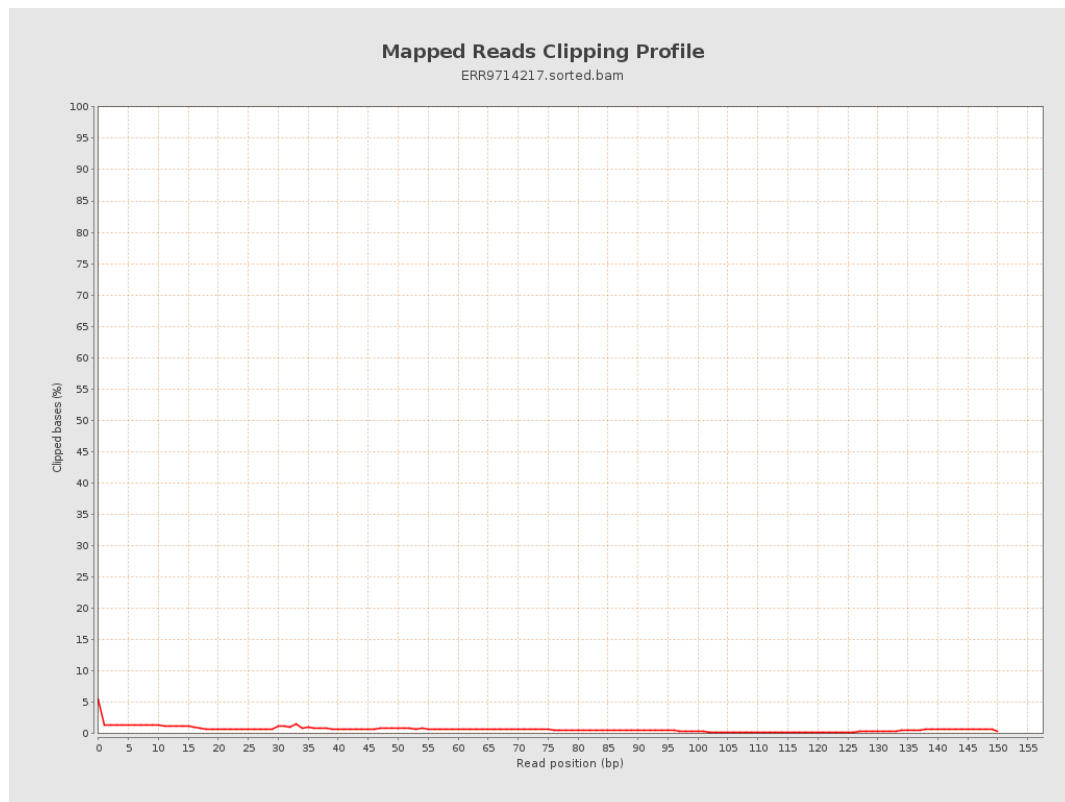
8. Results : Mapped Reads Nucleotide Content



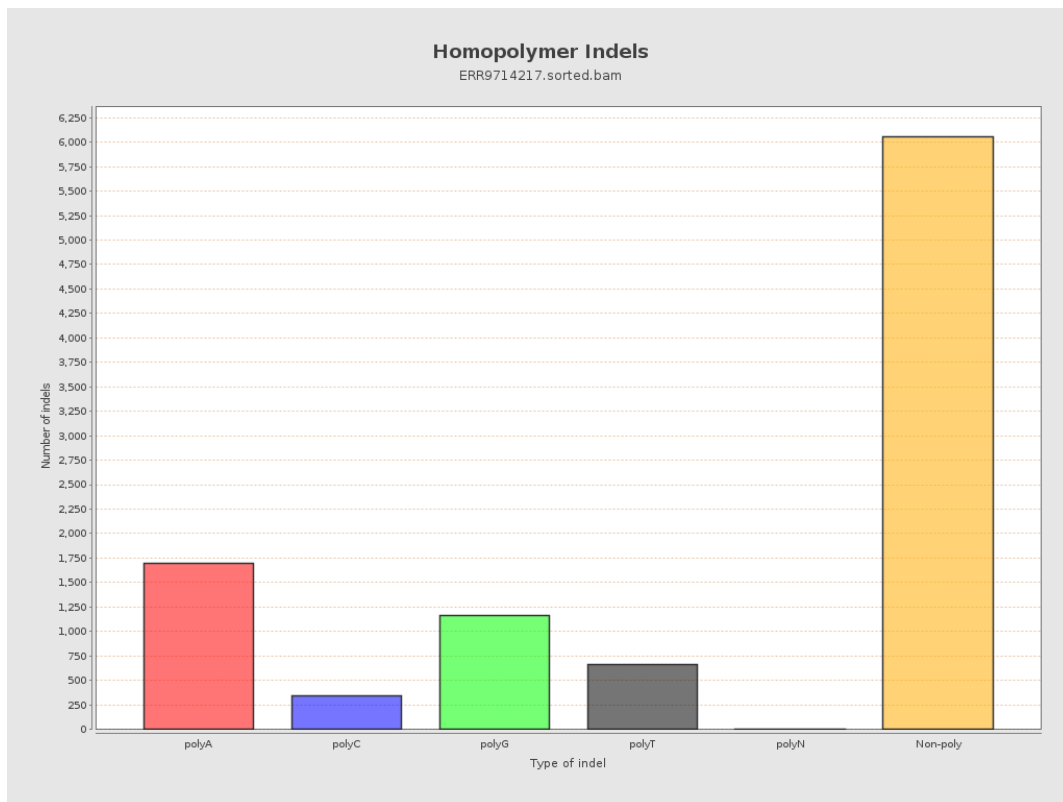
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

