

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:21:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714142.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_ERR9714142 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:21:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	896,214
Mapped reads	433,493 / 48.37%
Unmapped reads	462,721 / 51.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,443 / 3.29%
Read min/max/mean length	30 / 151 / 98.12
Duplicated reads (estimated)	375,799 / 41.93%
Duplication rate	43.6%
Clipped reads	407,209 / 45.44%

2.2. ACGT Content

Number/percentage of A's	13,820,645 / 26.68%
Number/percentage of C's	9,354,758 / 18.06%
Number/percentage of T's	12,909,678 / 24.92%
Number/percentage of G's	15,720,614 / 30.34%
Number/percentage of N's	602 / 0%
GC Percentage	48.4%

2.3. Coverage

Mean	0.017

Standard Deviation	7.8874
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2.4. Mapping Quality

Mean Mapping Quality	50.53
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2.5. Mismatches and indels

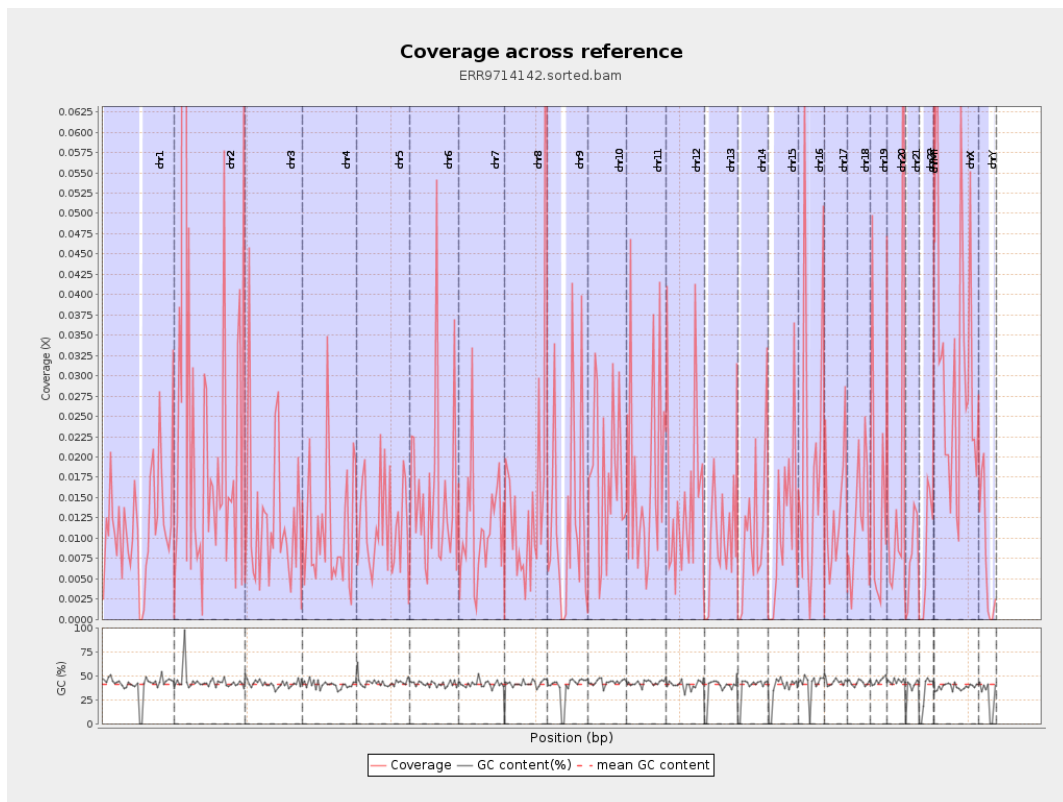
General error rate	3.97%
Mismatches	1,839,013
Insertions	61,615
Mapped reads with at least one insertion	13.02%
Deletions	144,877
Mapped reads with at least one deletion	31.9%
Homopolymer indels	30.93%

2.6. Chromosome stats

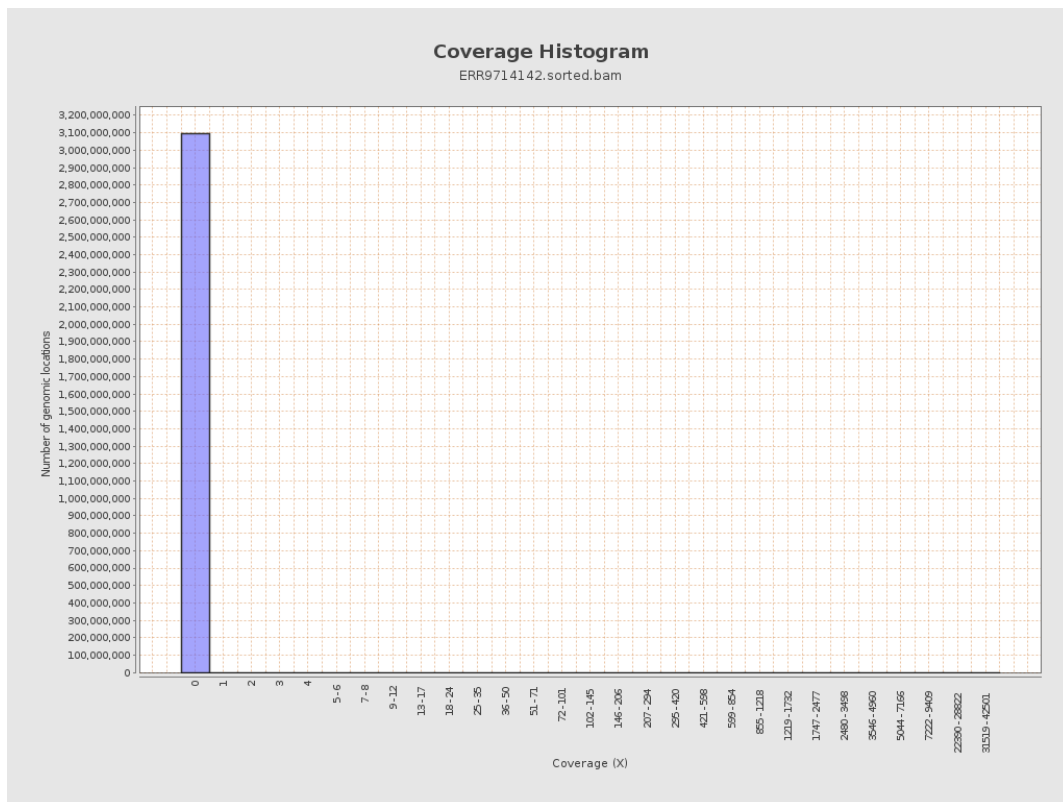
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2878614	0.0115	1.5353
chr2	243199373	10764926	0.0443	26.3399
chr3	198022430	2449850	0.0124	1.6764
chr4	191154276	2126871	0.0111	1.6187
chr5	180915260	2163431	0.012	1.3026
chr6	171115067	2615471	0.0153	2.1501
chr7	159138663	1809767	0.0114	1.6691

chr8	146364022	2516540	0.0172	5.4289
chr9	141213431	1760938	0.0125	1.8382
chr10	135534747	2426734	0.0179	1.9854
chr11	135006516	2333054	0.0173	2.2701
chr12	133851895	1940572	0.0145	2.0565
chr13	115169878	1094596	0.0095	1.1807
chr14	107349540	1194651	0.0111	1.274
chr15	102531392	1142924	0.0111	1.5136
chr16	90354753	1808139	0.02	4.6025
chr17	81195210	1095524	0.0135	1.7141
chr18	78077248	998960	0.0128	1.314
chr19	59128983	856664	0.0145	2.6141
chr20	63025520	1329983	0.0211	5.8199
chr21	48129895	369129	0.0077	0.7729
chr22	51304566	465837	0.0091	0.922
chrMT	16571	1227626	74.0828	592.3591
chrX	155270560	4871049	0.0314	4.1108
chrY	59373566	450162	0.0076	1.2192

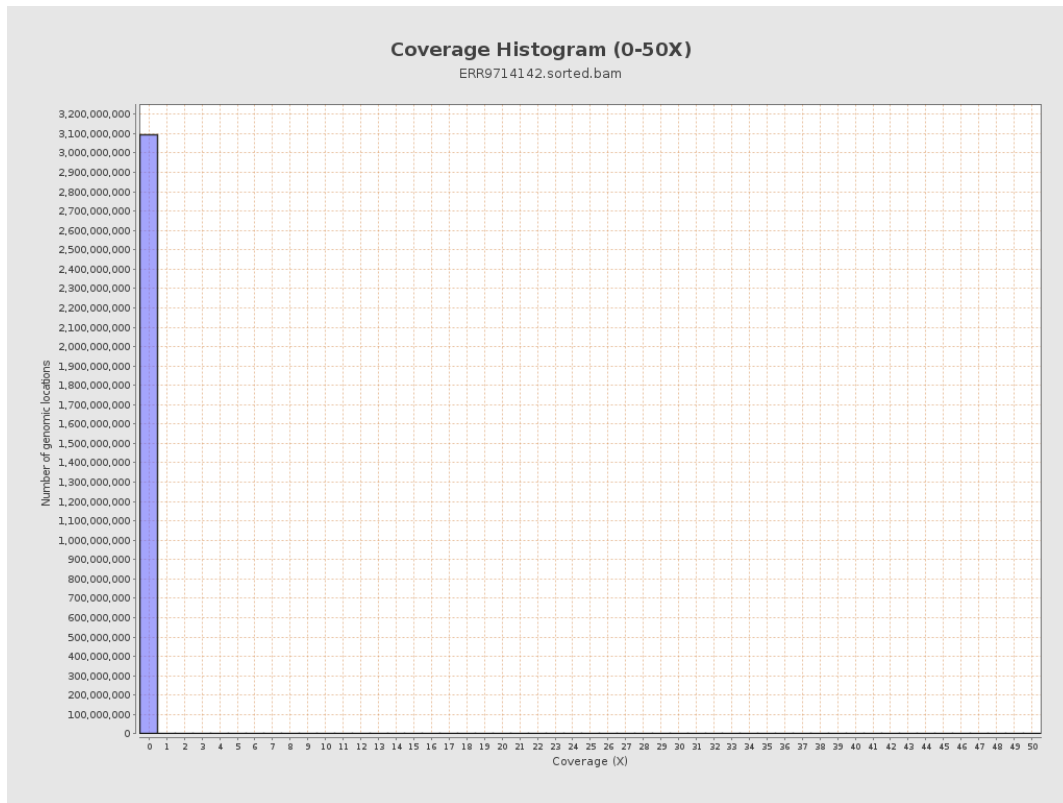
3. Results : Coverage across reference



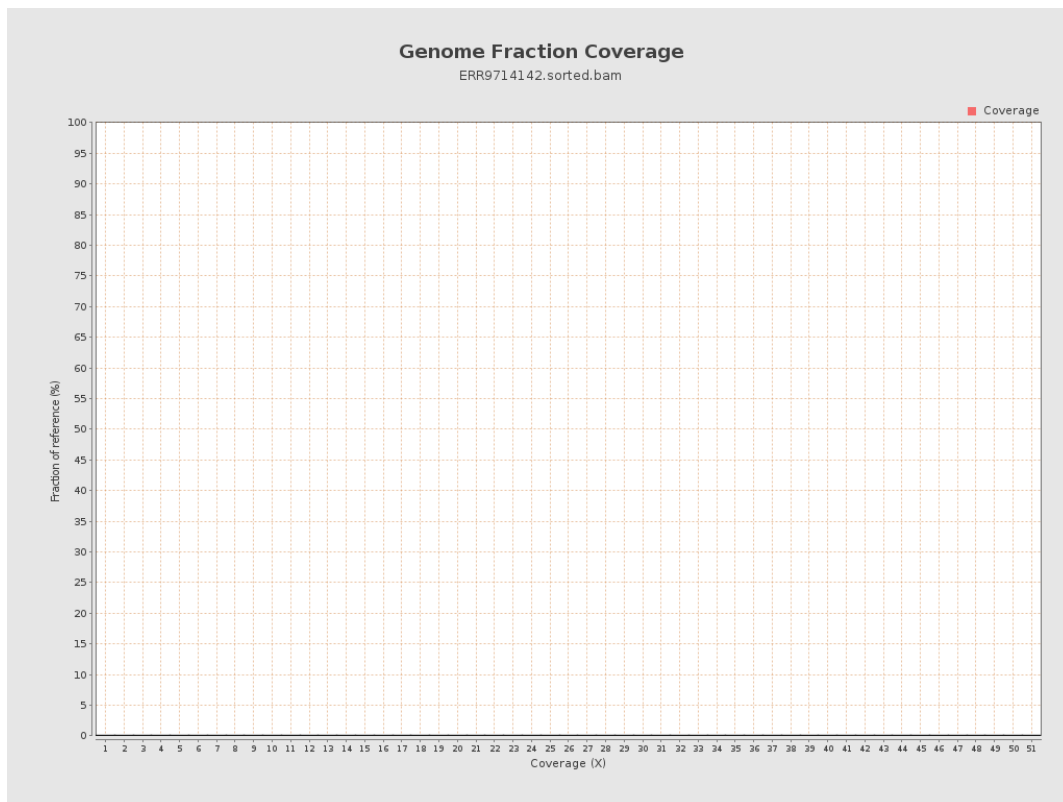
4. Results : Coverage Histogram



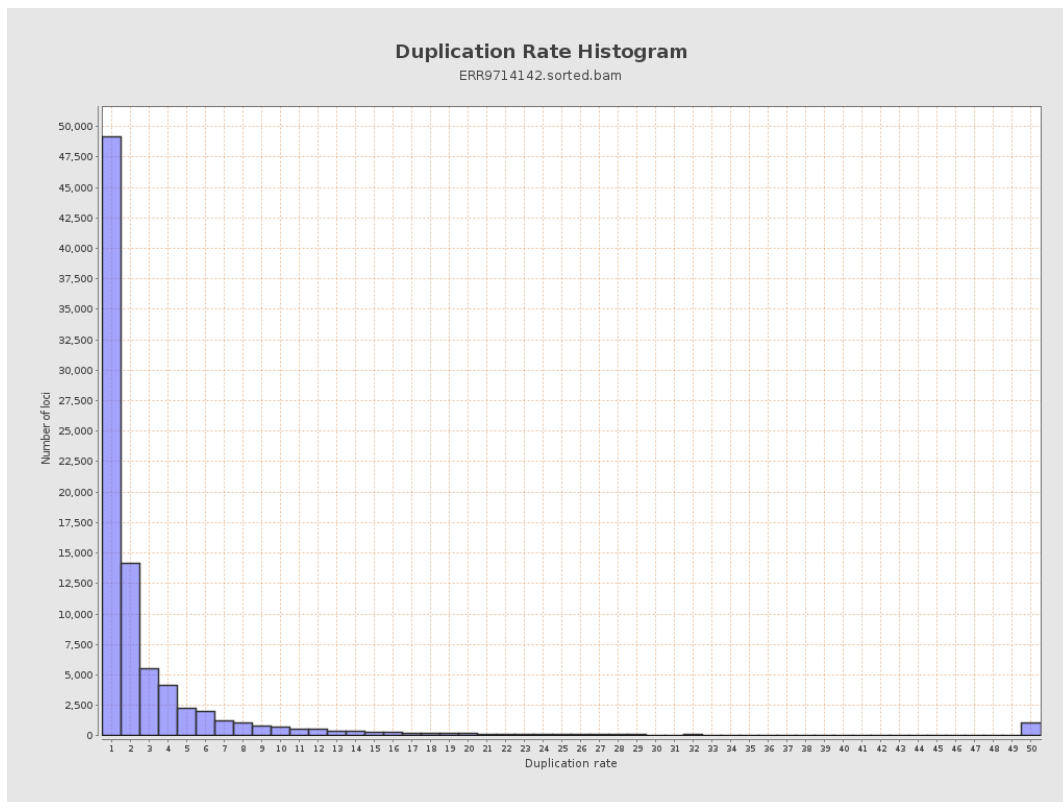
5. Results : Coverage Histogram (0-50X)



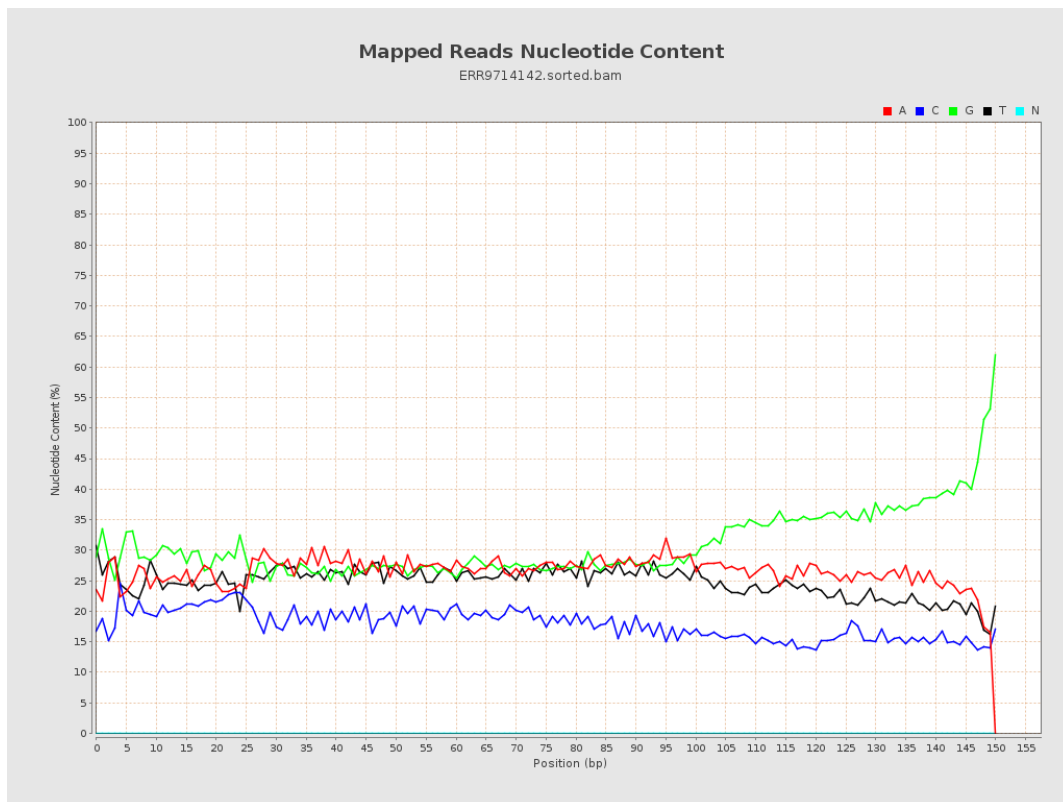
6. Results : Genome Fraction Coverage



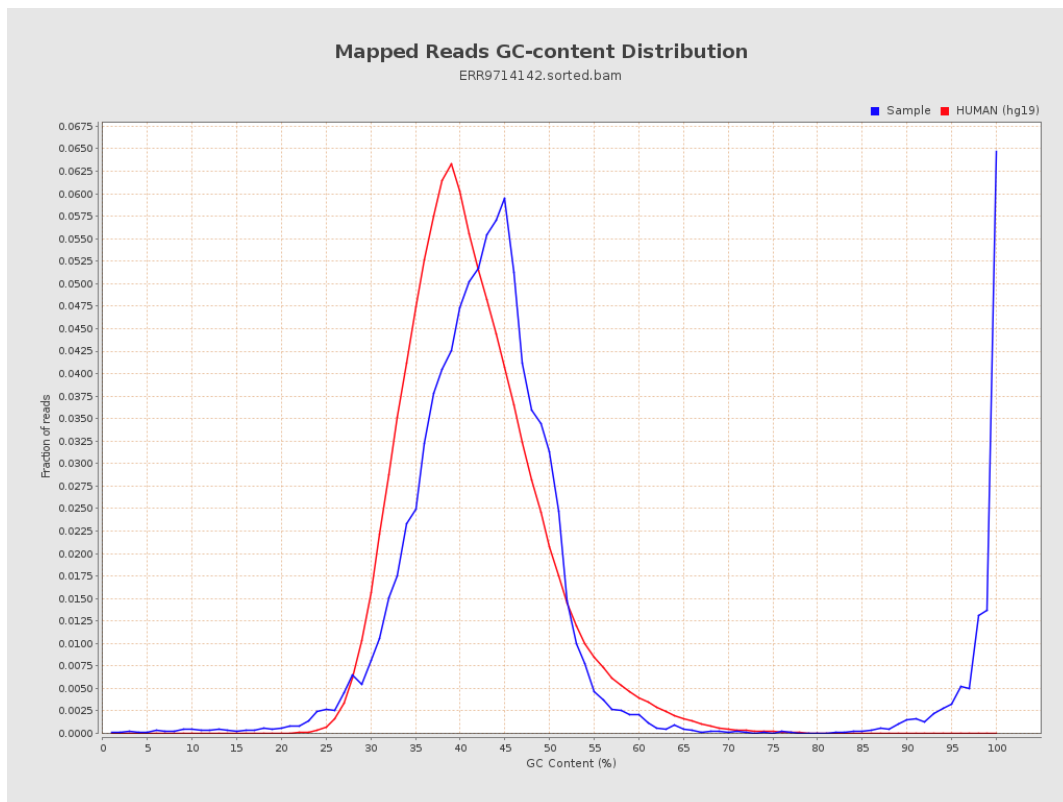
7. Results : Duplication Rate Histogram



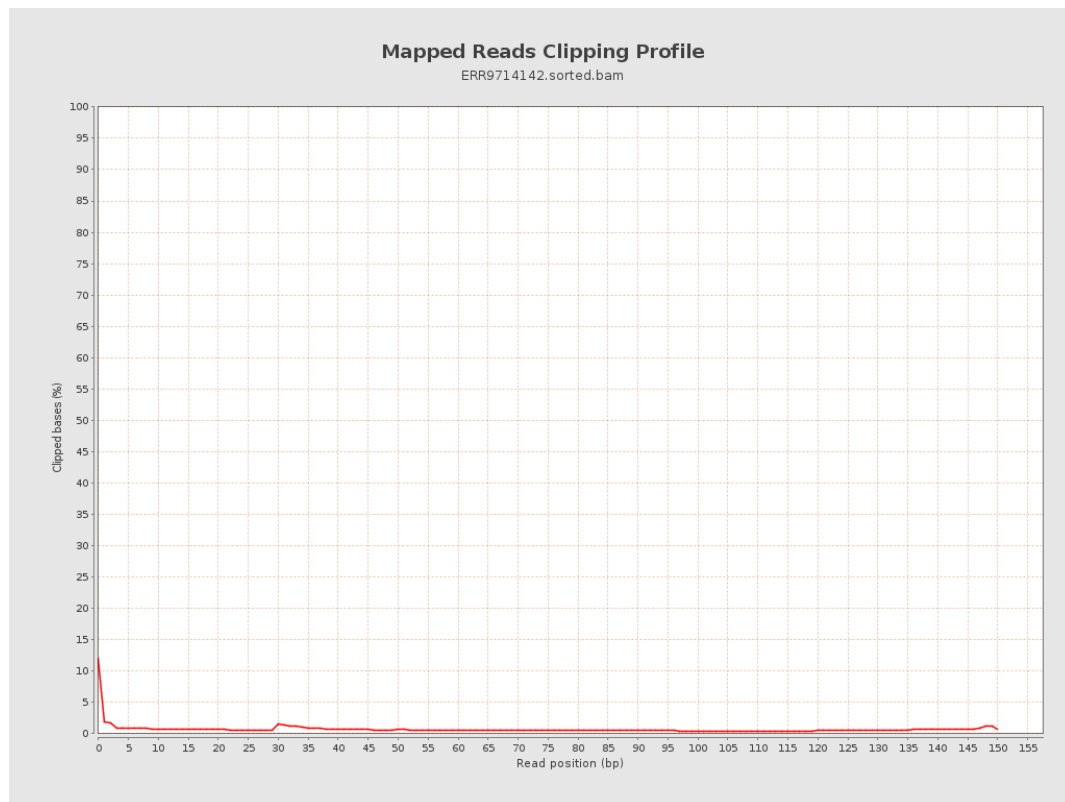
8. Results : Mapped Reads Nucleotide Content



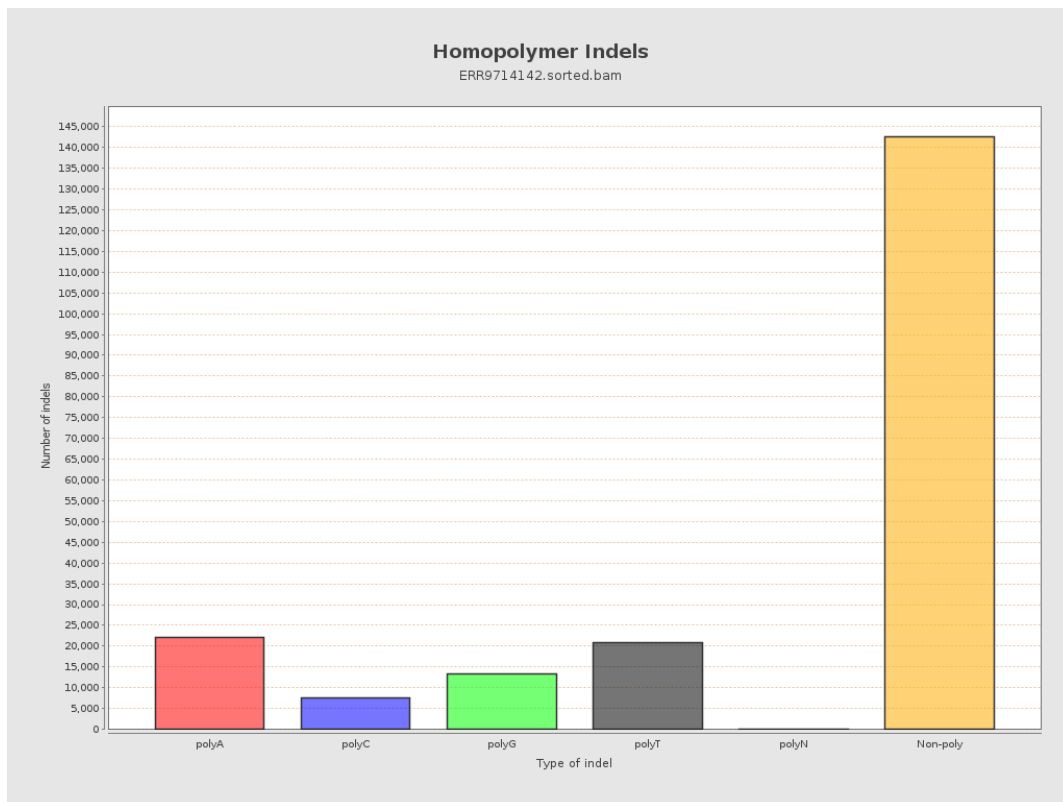
9. Results : Mapped Reads GC-content Distribution



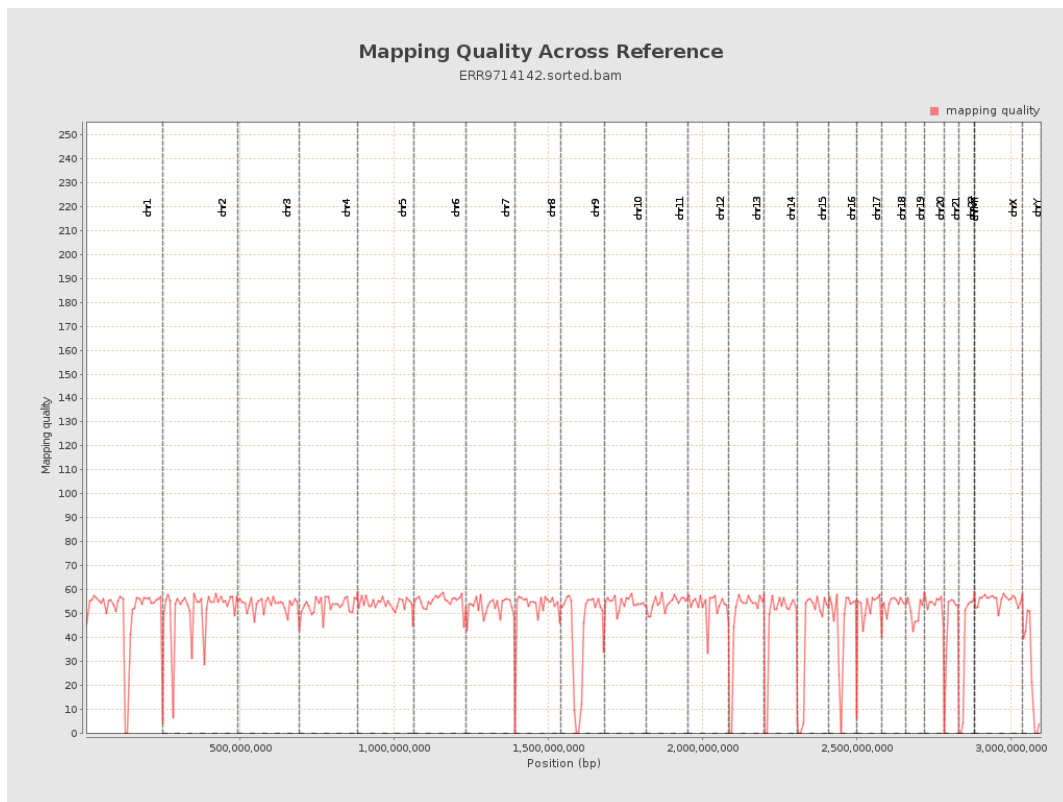
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

