

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:38:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714056.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_ERR9714056 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:38:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	303,018
Mapped reads	231,230 / 76.31%
Unmapped reads	71,788 / 23.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,671 / 2.2%
Read min/max/mean length	30 / 151 / 128.15
Duplicated reads (estimated)	191,581 / 63.22%
Duplication rate	43.4%
Clipped reads	212,278 / 70.05%

2.2. ACGT Content

Number/percentage of A's	8,094,940 / 27.44%
Number/percentage of C's	5,986,148 / 20.29%
Number/percentage of T's	7,733,578 / 26.22%
Number/percentage of G's	7,681,923 / 26.04%
Number/percentage of N's	220 / 0%
GC Percentage	46.34%

2.3. Coverage

Mean	0.0098

Standard Deviation	2.5161
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2.4. Mapping Quality

Mean Mapping Quality	50.51
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2.5. Mismatches and indels

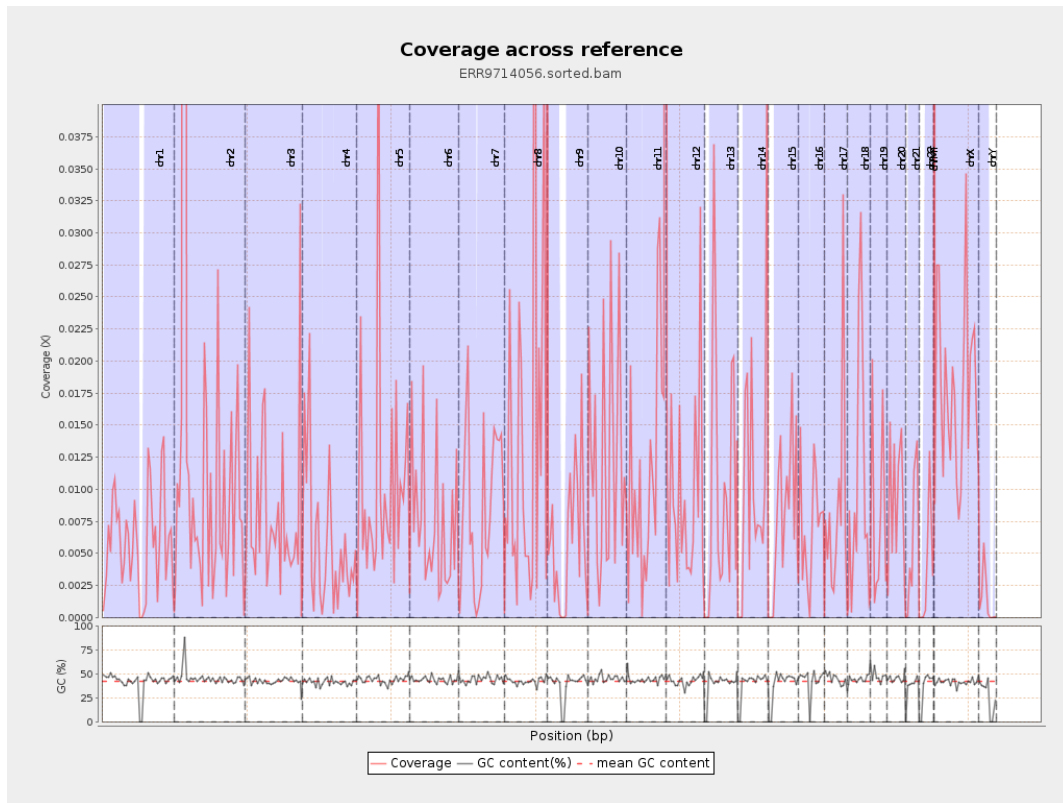
General error rate	4.83%
Mismatches	1,322,496
Insertions	35,501
Mapped reads with at least one insertion	14.75%
Deletions	115,685
Mapped reads with at least one deletion	46.34%
Homopolymer indels	29.54%

2.6. Chromosome stats

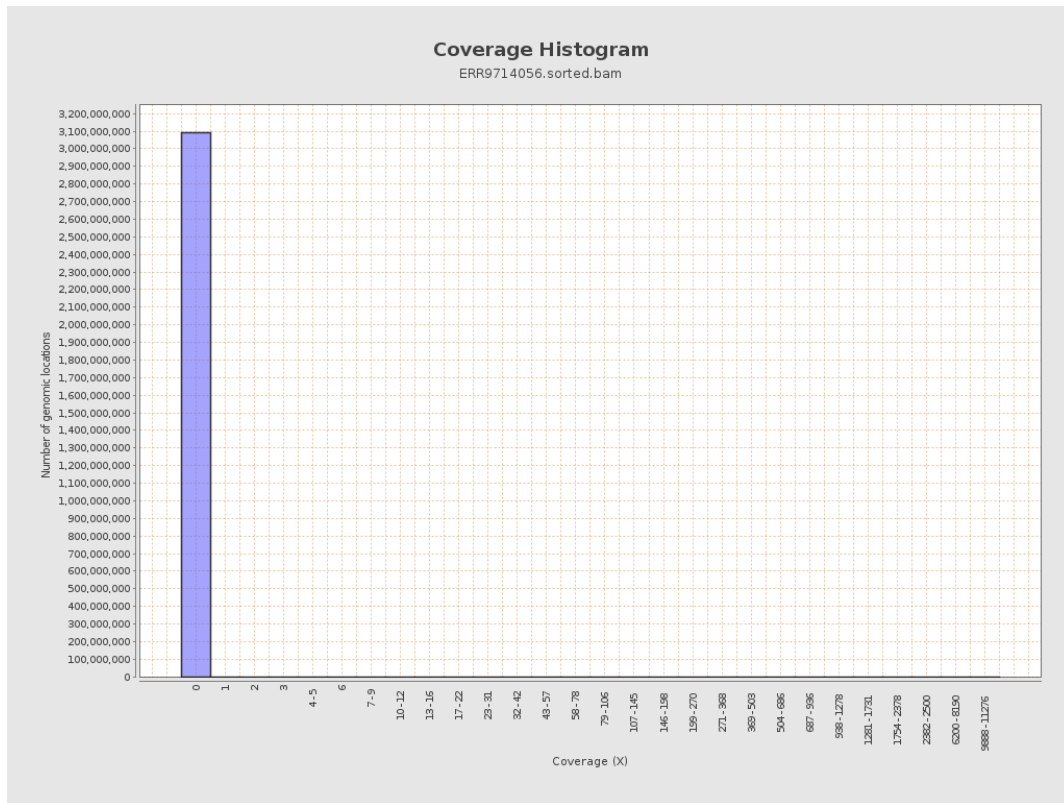
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1444640	0.0058	0.8891
chr2	243199373	4076900	0.0168	7.1678
chr3	198022430	1693039	0.0085	1.377
chr4	191154276	1076500	0.0056	0.9882
chr5	180915260	1983305	0.011	2.0533
chr6	171115067	1238719	0.0072	1.0646
chr7	159138663	1356490	0.0085	1.1649

chr8	146364022	2149108	0.0147	3.2024
chr9	141213431	904337	0.0064	1.0235
chr10	135534747	1692979	0.0125	1.7011
chr11	135006516	1632253	0.0121	2.0567
chr12	133851895	1241111	0.0093	1.561
chr13	115169878	1114661	0.0097	1.5882
chr14	107349540	1186308	0.0111	2.3077
chr15	102531392	825298	0.008	1.1124
chr16	90354753	639441	0.0071	0.8988
chr17	81195210	672978	0.0083	2.0001
chr18	78077248	866152	0.0111	1.5261
chr19	59128983	443460	0.0075	1.1008
chr20	63025520	575279	0.0091	1.2659
chr21	48129895	285213	0.0059	1.0374
chr22	51304566	185991	0.0036	0.6047
chrMT	16571	109871	6.6303	51.4393
chrX	155270560	2759659	0.0178	1.5467
chrY	59373566	88611	0.0015	0.2935

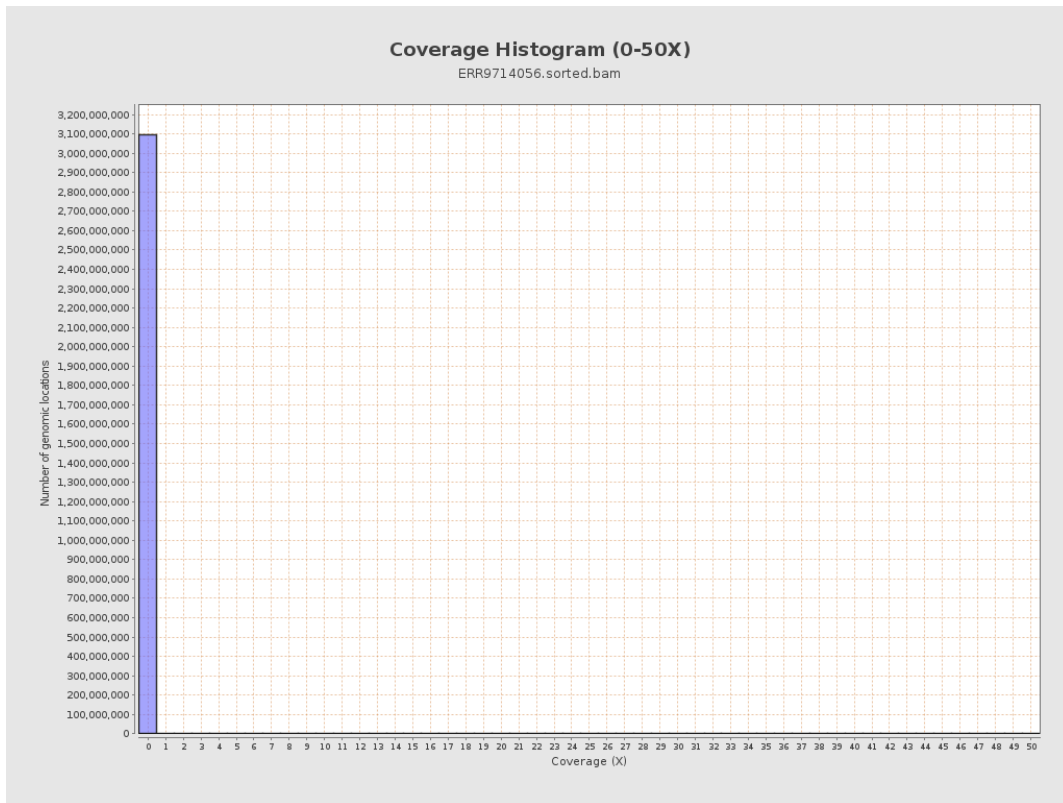
3. Results : Coverage across reference



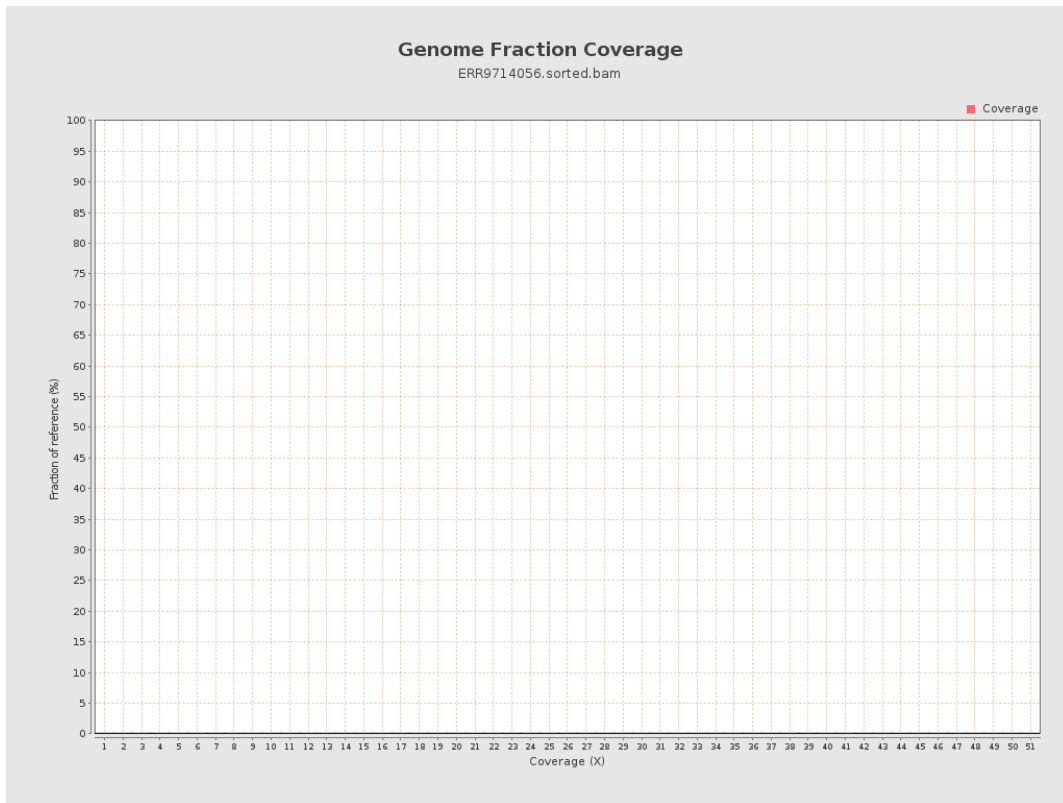
4. Results : Coverage Histogram



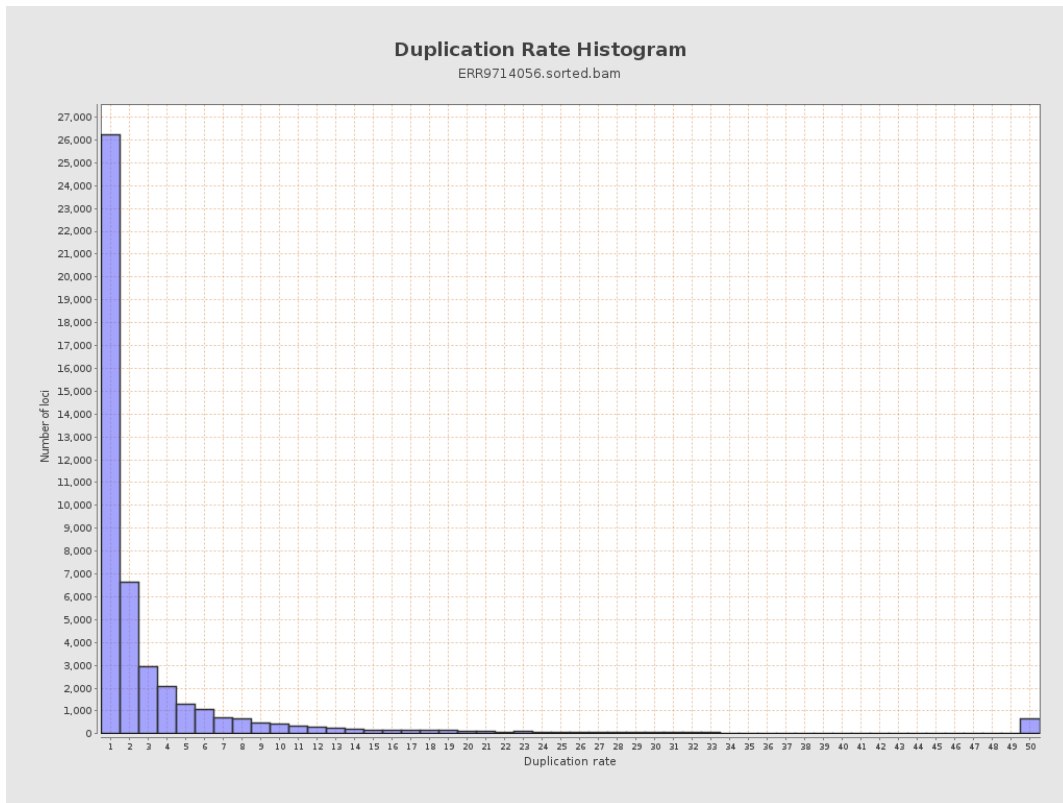
5. Results : Coverage Histogram (0-50X)



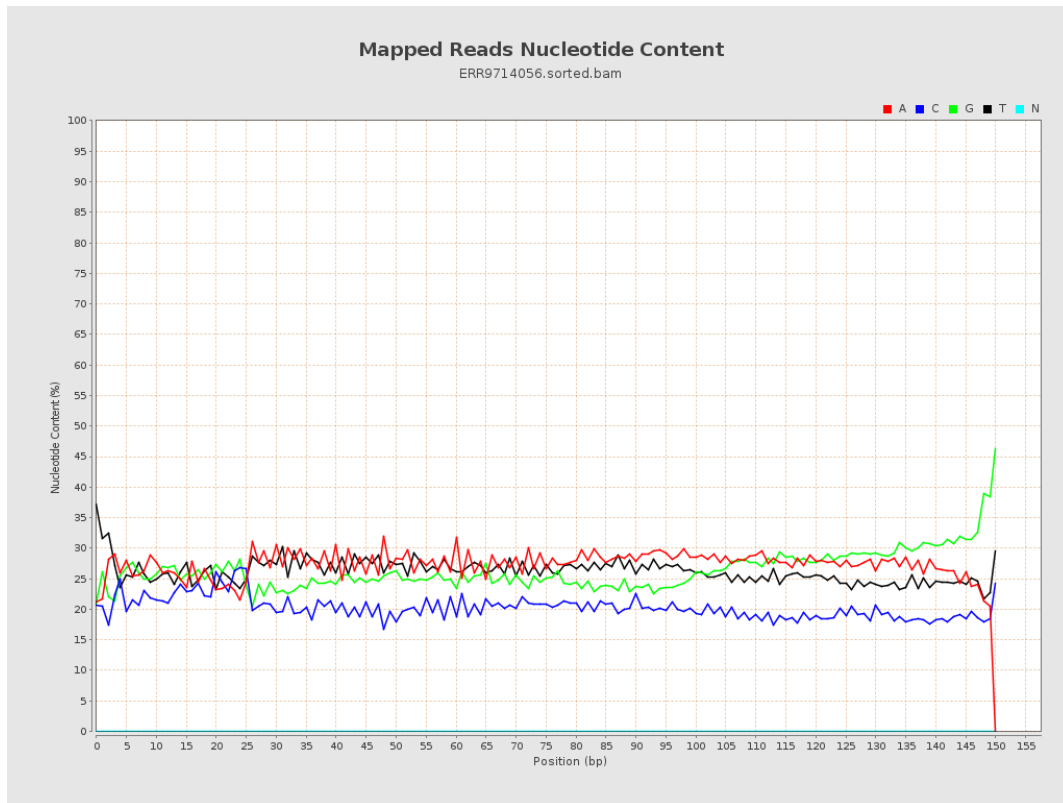
6. Results : Genome Fraction Coverage



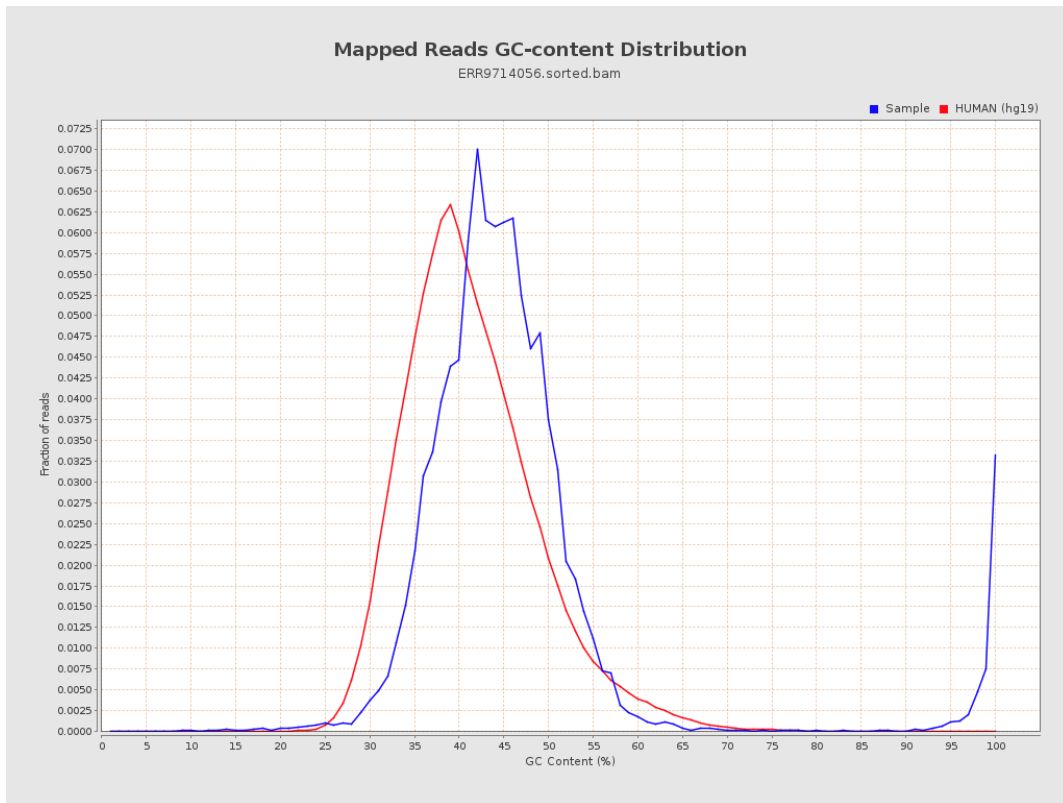
7. Results : Duplication Rate Histogram



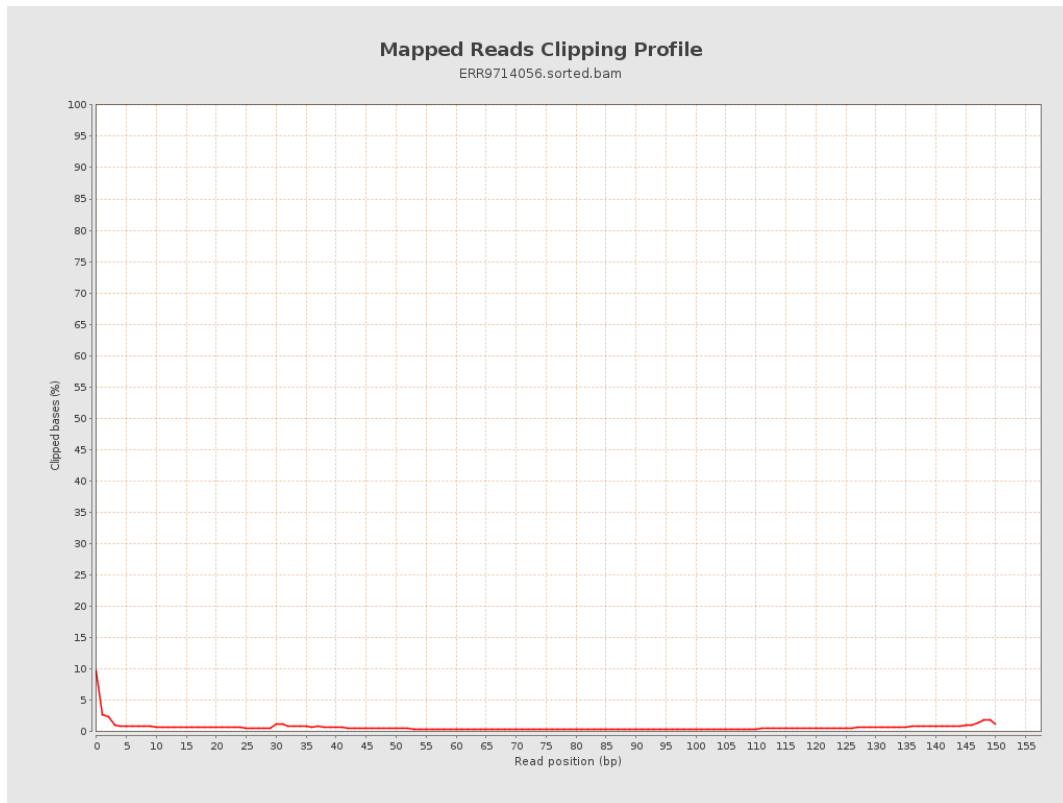
8. Results : Mapped Reads Nucleotide Content



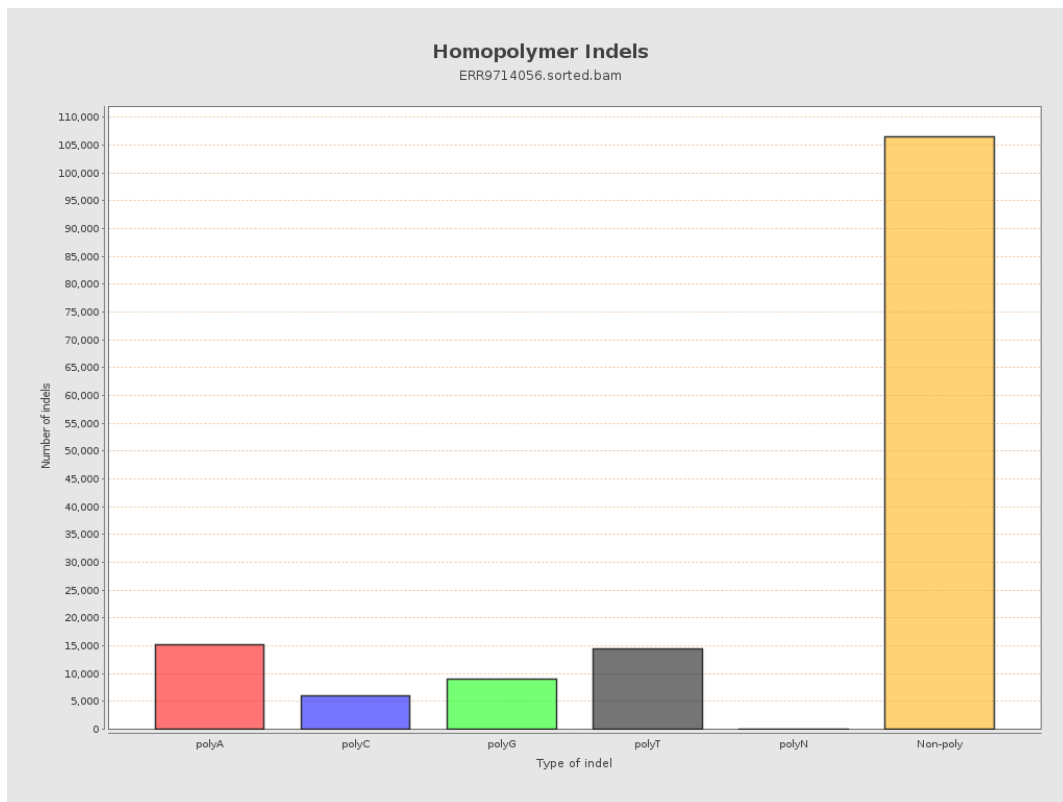
9. Results : Mapped Reads GC-content Distribution



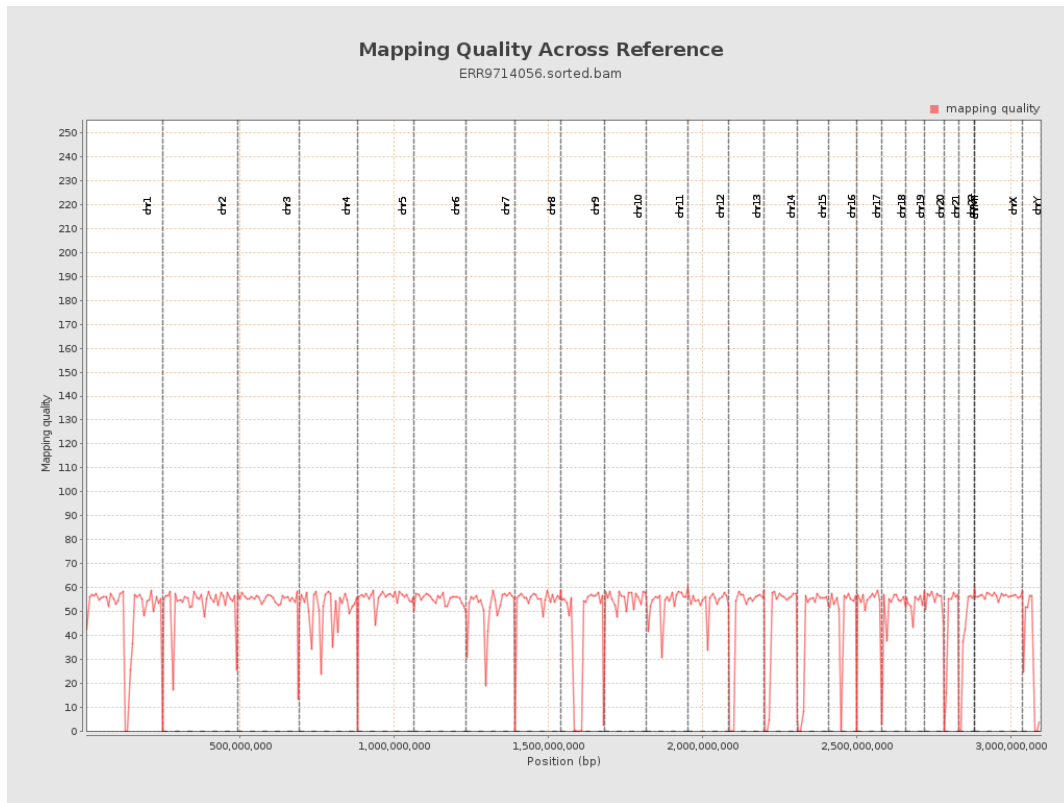
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

