

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:05:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714094.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_ERR9714094 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:05:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	721,888
Mapped reads	213,713 / 29.6%
Unmapped reads	508,175 / 70.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,525 / 1.46%
Read min/max/mean length	30 / 151 / 84.43
Duplicated reads (estimated)	178,796 / 24.77%
Duplication rate	42.45%
Clipped reads	184,298 / 25.53%

2.2. ACGT Content

Number/percentage of A's	5,860,696 / 23.1%
Number/percentage of C's	4,177,965 / 16.47%
Number/percentage of T's	5,505,937 / 21.7%
Number/percentage of G's	9,822,275 / 38.72%
Number/percentage of N's	325 / 0%
GC Percentage	55.19%

2.3. Coverage

Mean	0.0083

Standard Deviation	6.9182
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2.4. Mapping Quality

Mean Mapping Quality	50.2
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2.5. Mismatches and indels

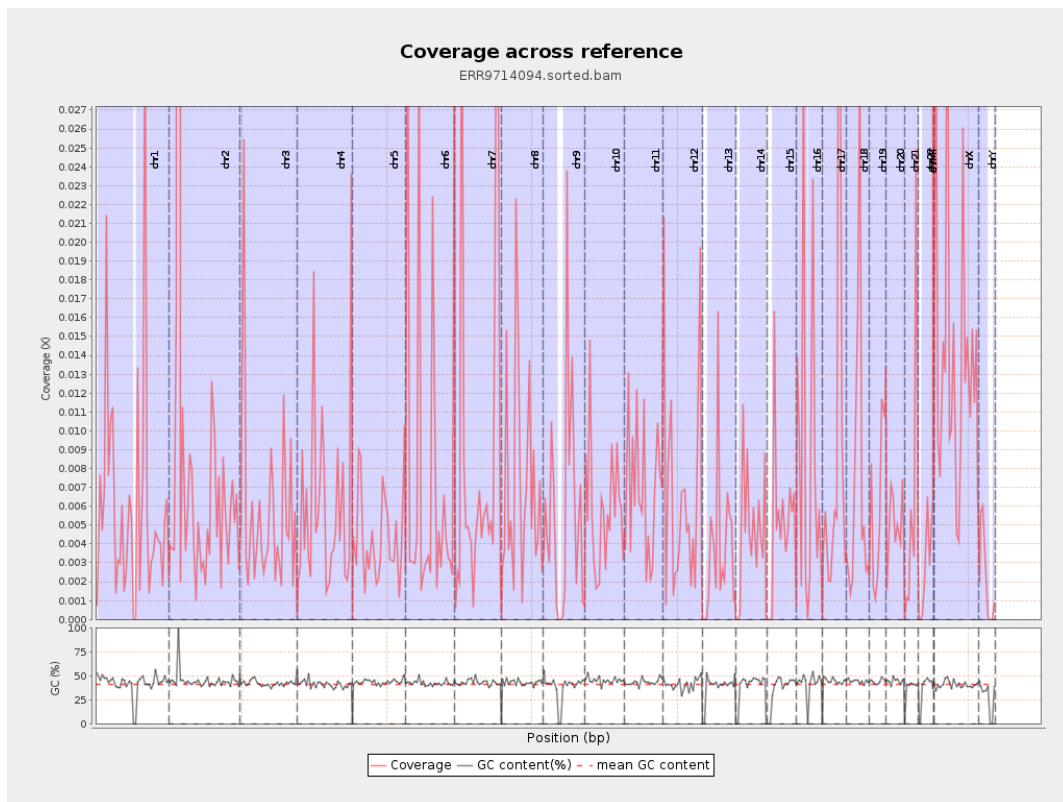
General error rate	3.84%
Mismatches	862,835
Insertions	27,964
Mapped reads with at least one insertion	11.59%
Deletions	66,298
Mapped reads with at least one deletion	29.79%
Homopolymer indels	33.26%

2.6. Chromosome stats

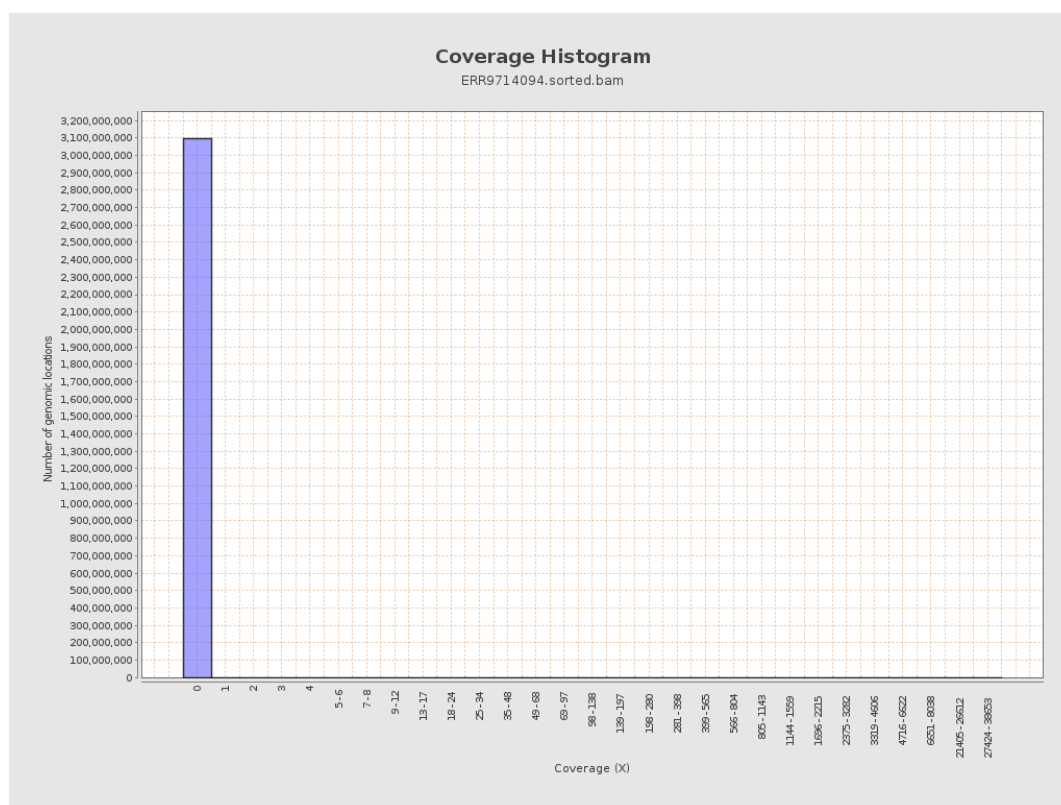
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1520130	0.0061	1.2143
chr2	243199373	6925131	0.0285	24.2784
chr3	198022430	1069820	0.0054	1.0948
chr4	191154276	1164718	0.0061	0.9166
chr5	180915260	780587	0.0043	0.4543
chr6	171115067	1326840	0.0078	1.8732
chr7	159138663	1383862	0.0087	2.3234

chr8	146364022	1053038	0.0072	1.0494
chr9	141213431	796719	0.0056	1.0298
chr10	135534747	800094	0.0059	0.74
chr11	135006516	913602	0.0068	0.7305
chr12	133851895	861334	0.0064	0.9692
chr13	115169878	416181	0.0036	0.6479
chr14	107349540	500223	0.0047	0.5776
chr15	102531392	506988	0.0049	0.8701
chr16	90354753	758859	0.0084	1.9686
chr17	81195210	697135	0.0086	1.6295
chr18	78077248	579939	0.0074	1.4126
chr19	59128983	348691	0.0059	0.785
chr20	63025520	324053	0.0051	0.5883
chr21	48129895	296362	0.0062	1.834
chr22	51304566	141919	0.0028	0.3309
chrMT	16571	253075	15.2722	127.3772
chrX	155270560	2208859	0.0142	1.9313
chrY	59373566	126474	0.0021	0.2975

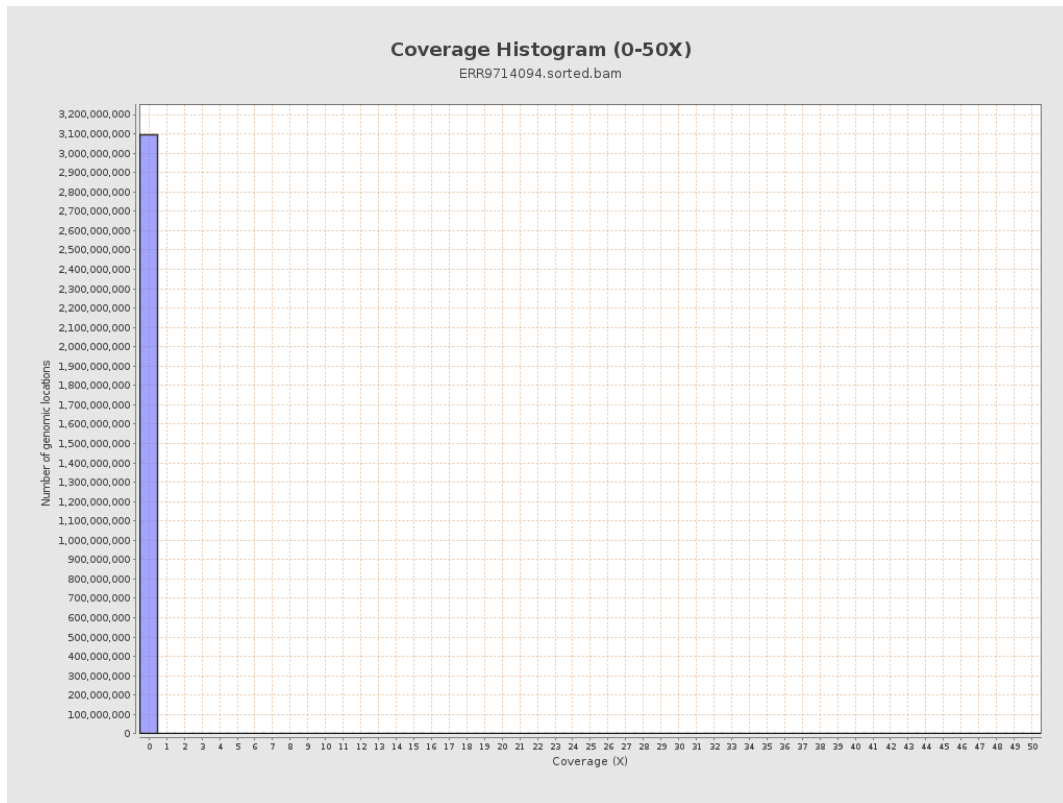
3. Results : Coverage across reference



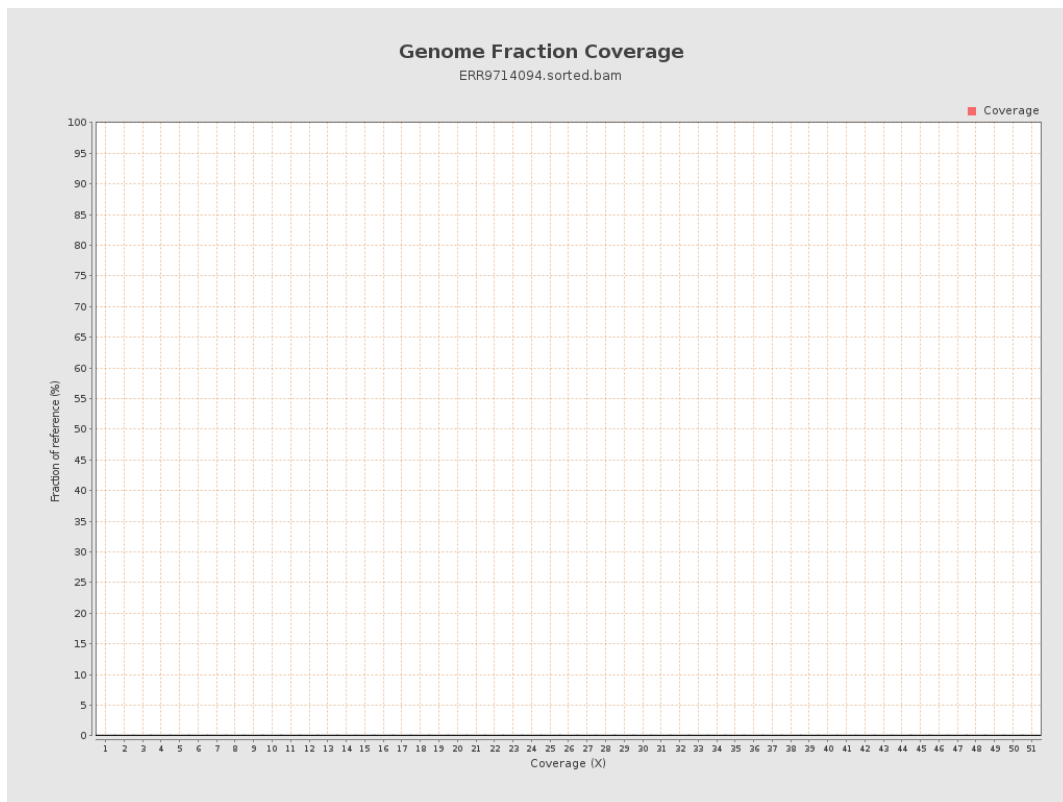
4. Results : Coverage Histogram



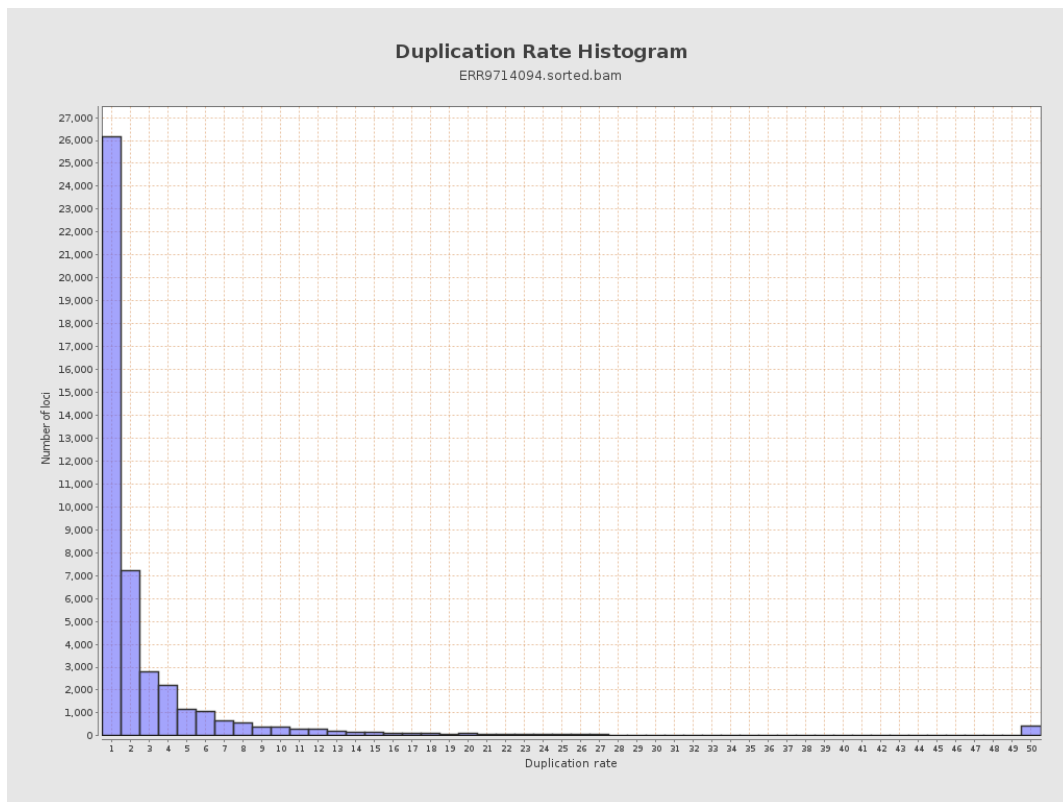
5. Results : Coverage Histogram (0-50X)



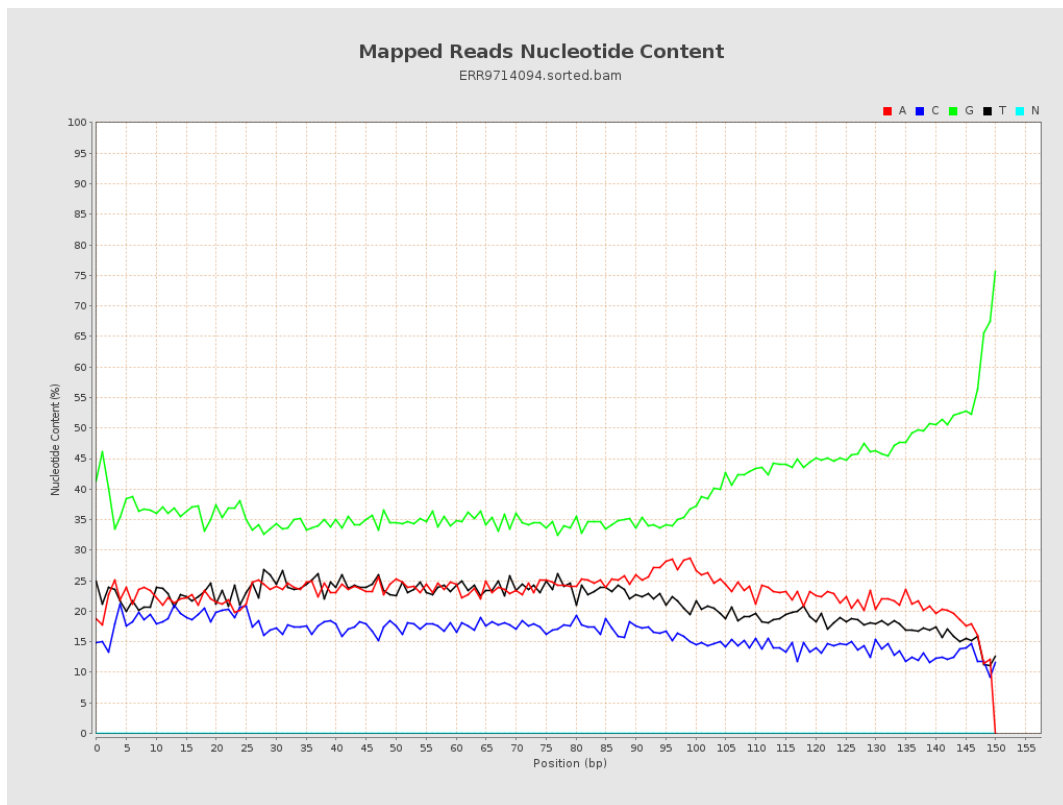
6. Results : Genome Fraction Coverage



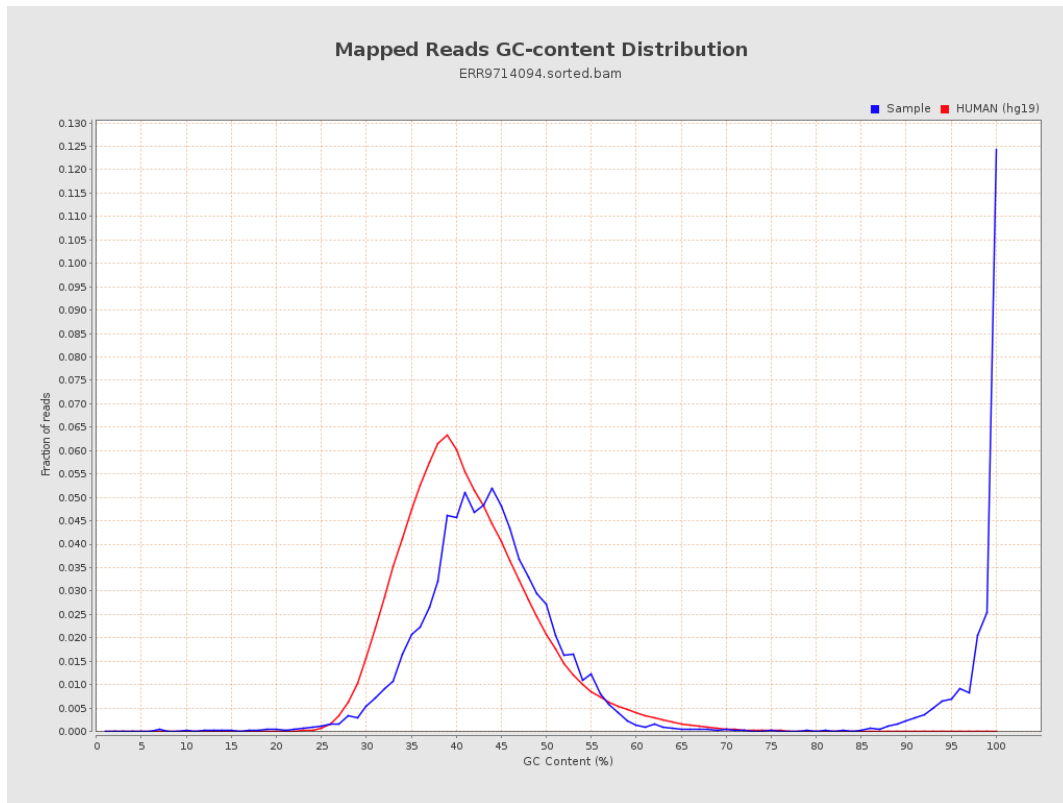
7. Results : Duplication Rate Histogram



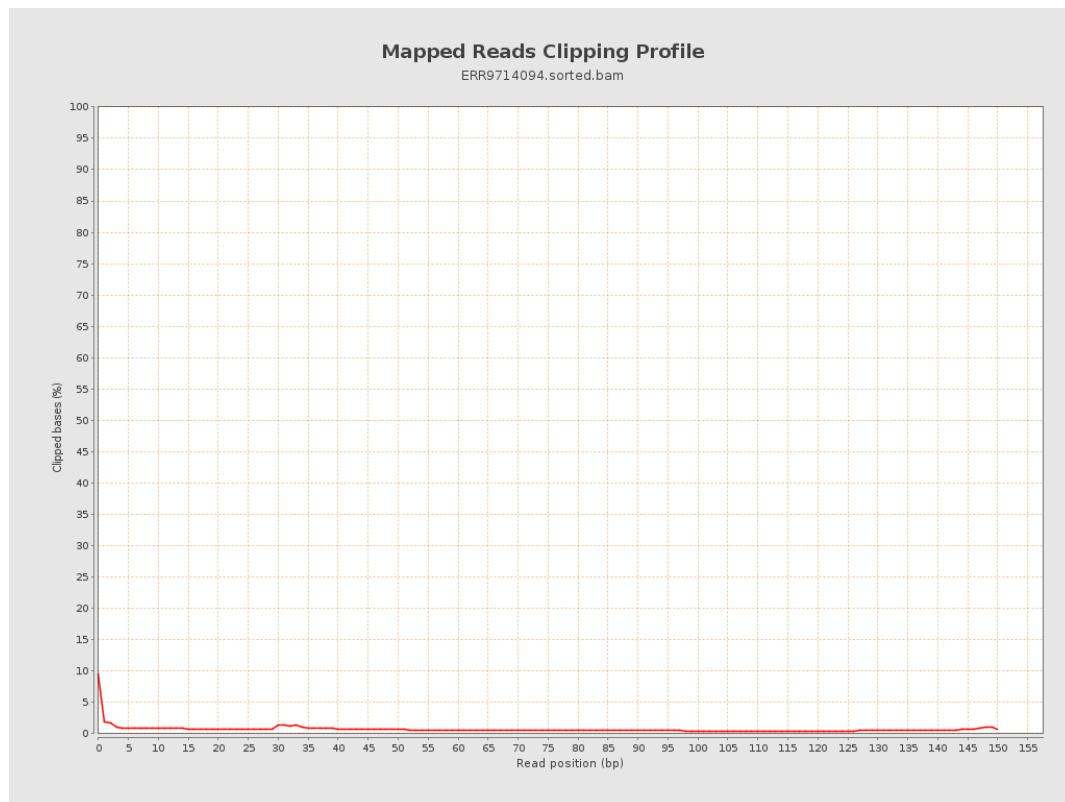
8. Results : Mapped Reads Nucleotide Content



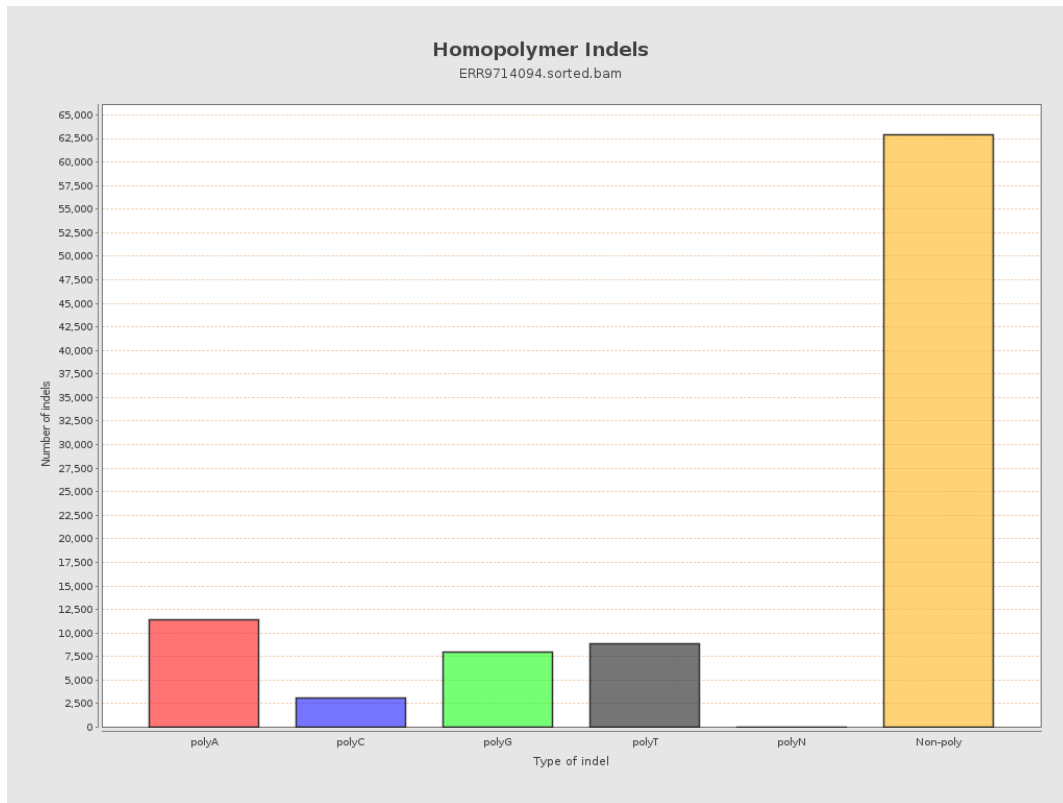
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

