

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:58:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714065.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_ERR9714065 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:58:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	409,716
Mapped reads	174,190 / 42.51%
Unmapped reads	235,526 / 57.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,715 / 1.39%
Read min/max/mean length	30 / 151 / 97.82
Duplicated reads (estimated)	149,641 / 36.52%
Duplication rate	41.84%
Clipped reads	156,843 / 38.28%

2.2. ACGT Content

Number/percentage of A's	5,553,917 / 25.73%
Number/percentage of C's	4,235,521 / 19.63%
Number/percentage of T's	5,286,553 / 24.5%
Number/percentage of G's	6,505,164 / 30.14%
Number/percentage of N's	291 / 0%
GC Percentage	49.77%

2.3. Coverage

Mean	0.0071

Standard Deviation	3.1076
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2.4. Mapping Quality

Mean Mapping Quality	48.93
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2.5. Mismatches and indels

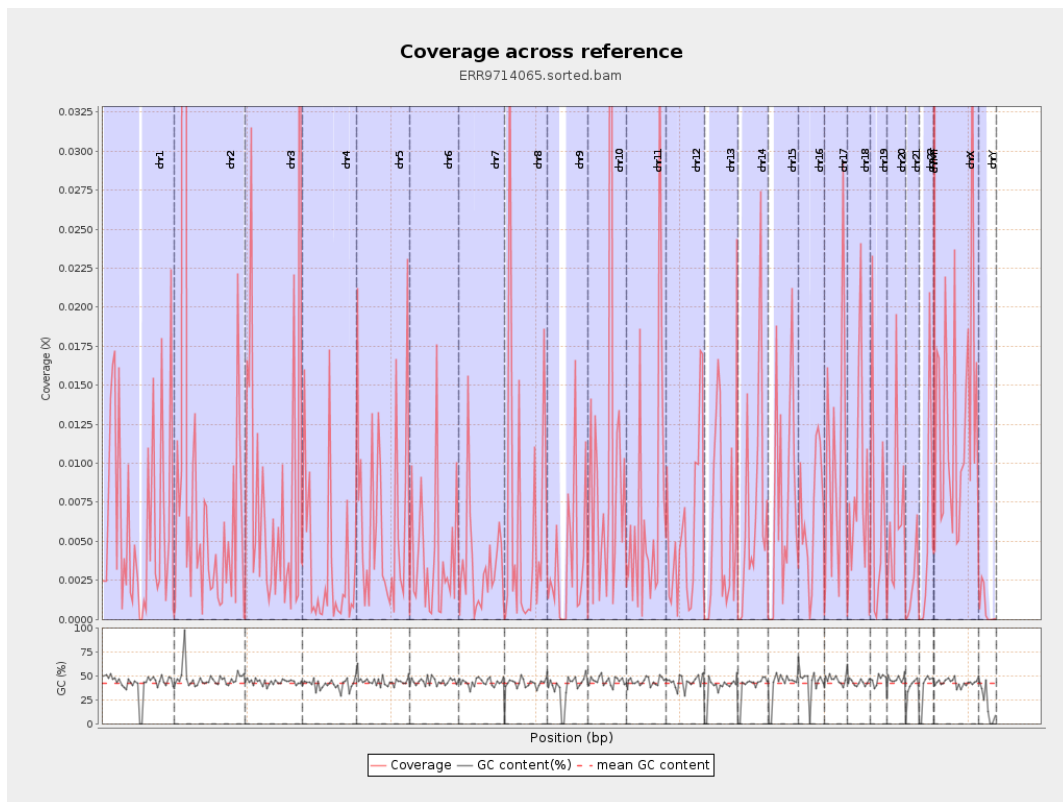
General error rate	4.44%
Mismatches	879,916
Insertions	25,352
Mapped reads with at least one insertion	13.77%
Deletions	76,592
Mapped reads with at least one deletion	41.07%
Homopolymer indels	32.37%

2.6. Chromosome stats

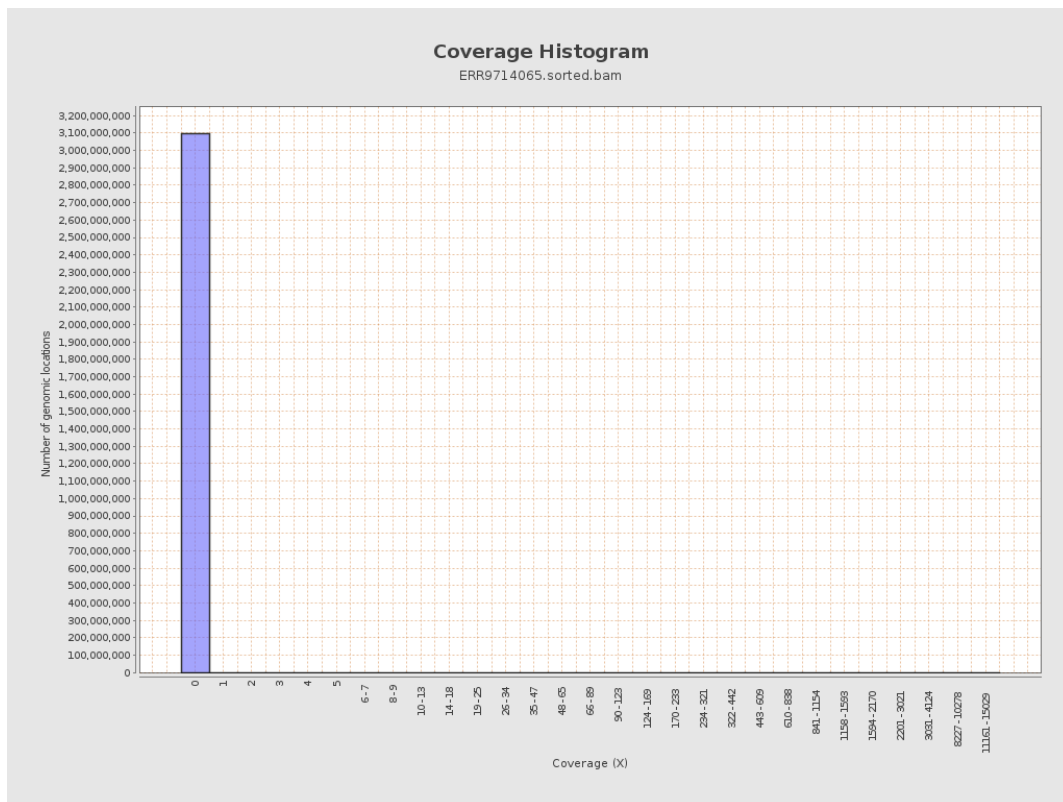
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1559195	0.0063	1.1275
chr2	243199373	3491792	0.0144	9.3956
chr3	198022430	1893405	0.0096	3.8044
chr4	191154276	617032	0.0032	0.8493
chr5	180915260	1121158	0.0062	1.1237
chr6	171115067	697865	0.0041	0.829
chr7	159138663	551401	0.0035	0.6173

chr8	146364022	867796	0.0059	1.7008
chr9	141213431	507052	0.0036	0.6564
chr10	135534747	1437483	0.0106	3.6348
chr11	135006516	964972	0.0071	1.3369
chr12	133851895	753808	0.0056	1.0654
chr13	115169878	671228	0.0058	1.3021
chr14	107349540	717103	0.0067	1.728
chr15	102531392	739748	0.0072	1.3687
chr16	90354753	609990	0.0068	0.9424
chr17	81195210	848107	0.0104	2.1545
chr18	78077248	681071	0.0087	1.3737
chr19	59128983	351282	0.0059	1.0392
chr20	63025520	433088	0.0069	1.2895
chr21	48129895	101136	0.0021	0.3065
chr22	51304566	253037	0.0049	1.1331
chrMT	16571	116559	7.0339	58.2849
chrX	155270560	2010637	0.0129	1.6463
chrY	59373566	45720	0.0008	0.194

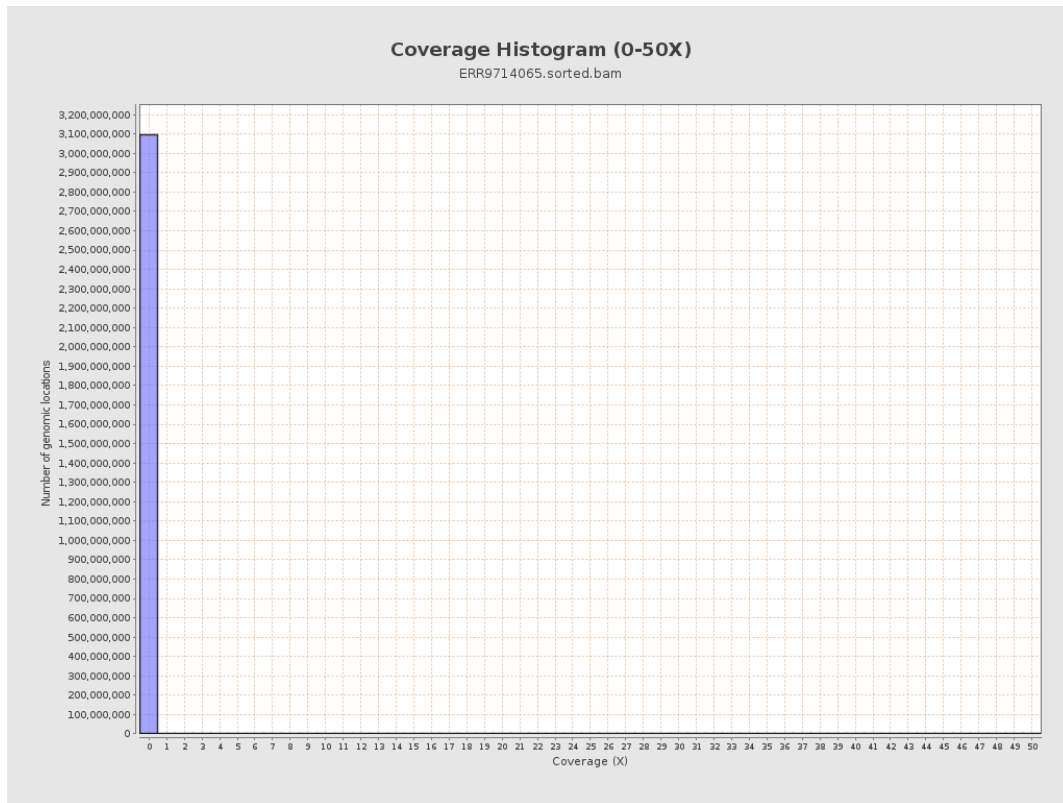
3. Results : Coverage across reference



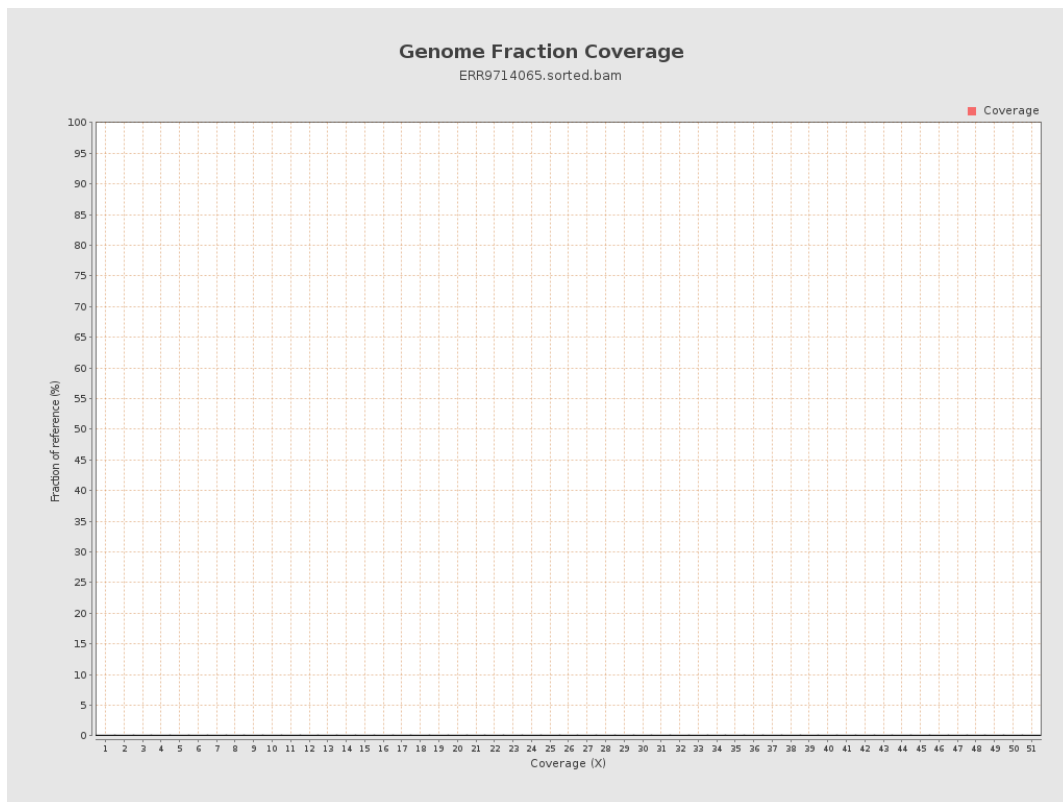
4. Results : Coverage Histogram



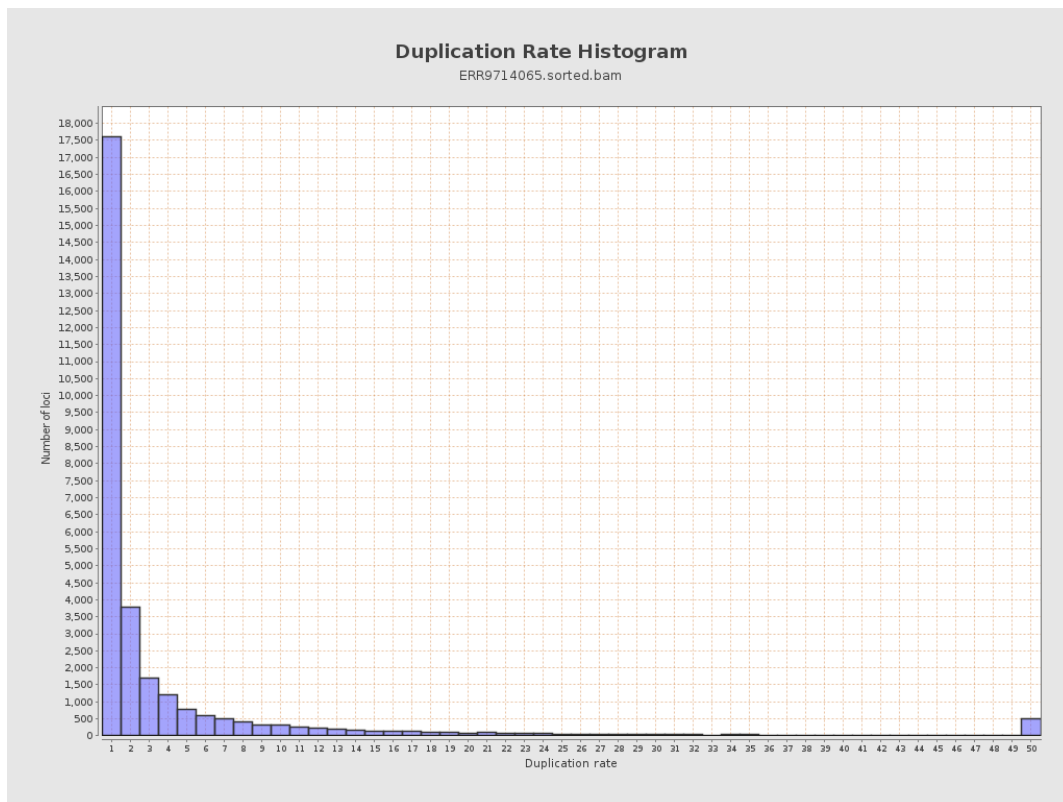
5. Results : Coverage Histogram (0-50X)



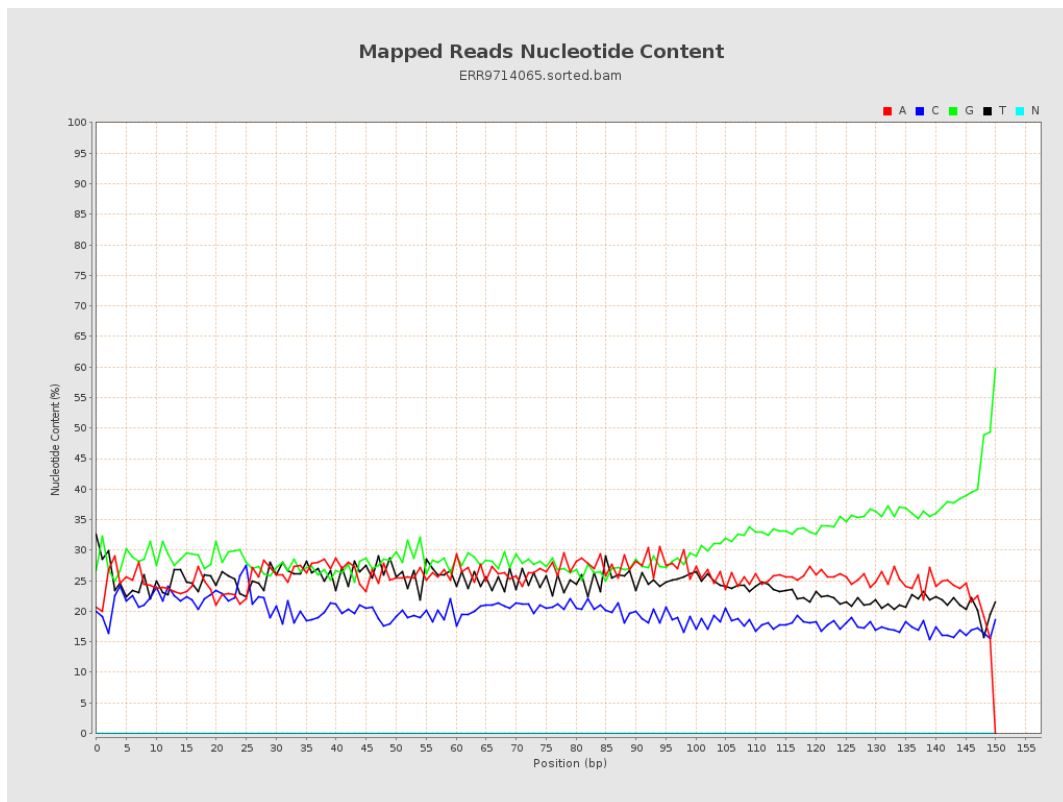
6. Results : Genome Fraction Coverage



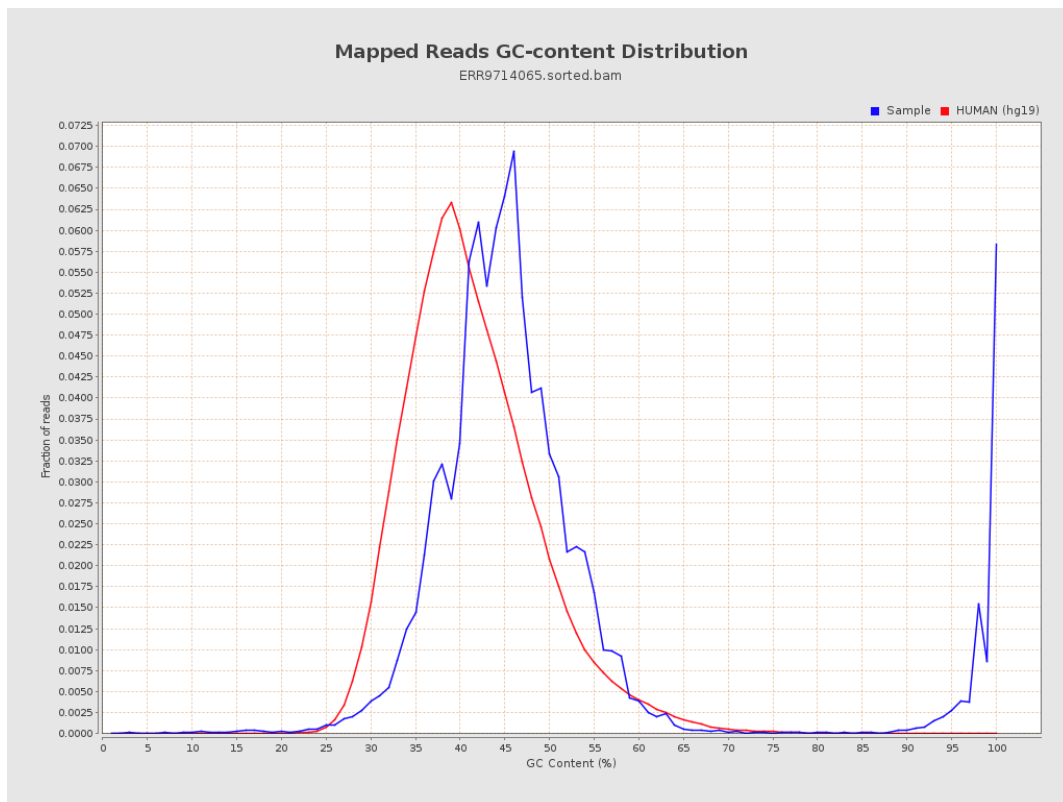
7. Results : Duplication Rate Histogram



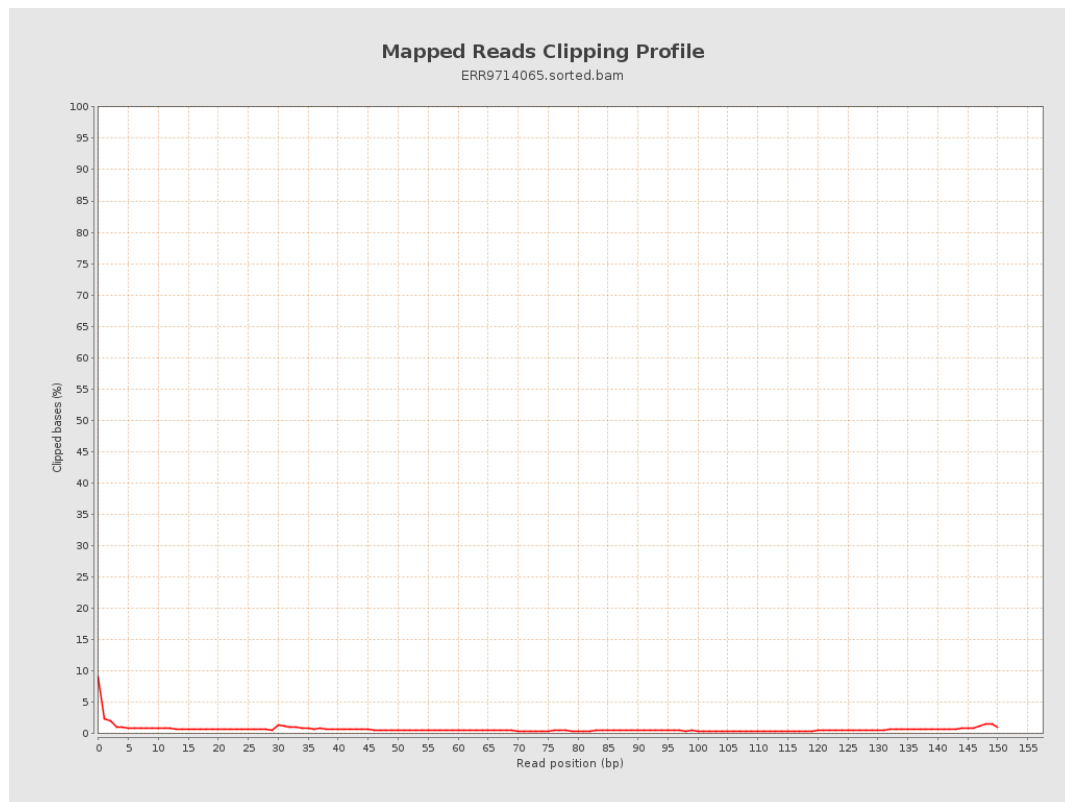
8. Results : Mapped Reads Nucleotide Content



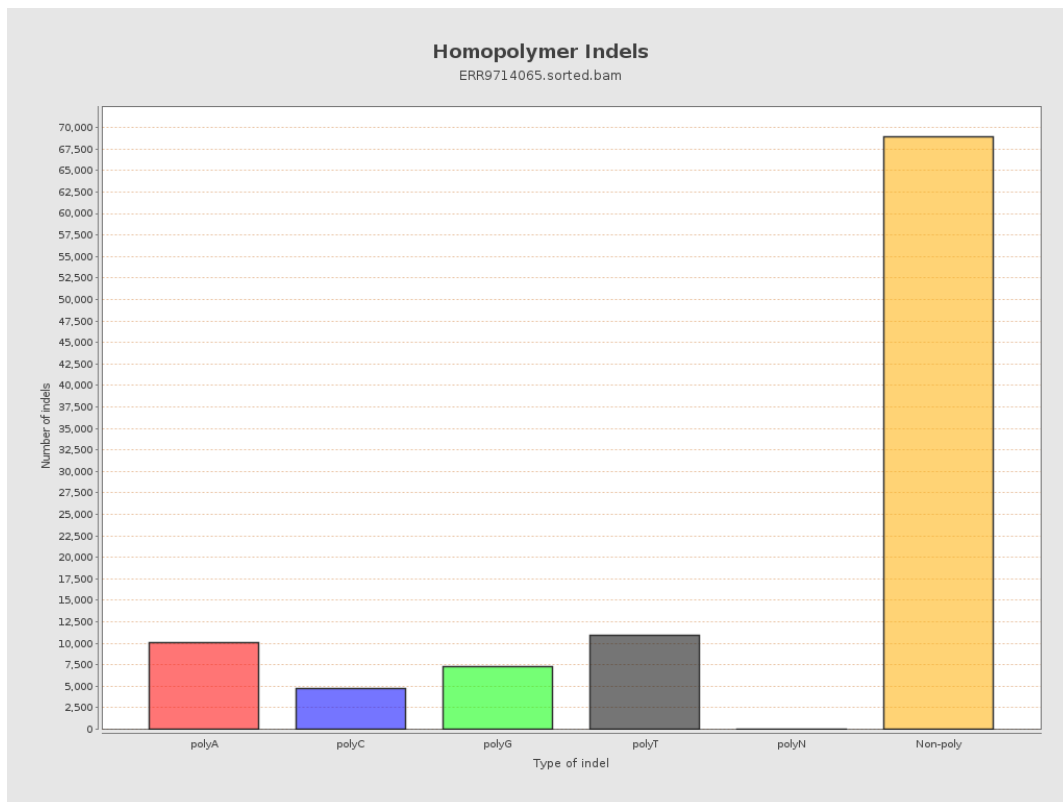
9. Results : Mapped Reads GC-content Distribution



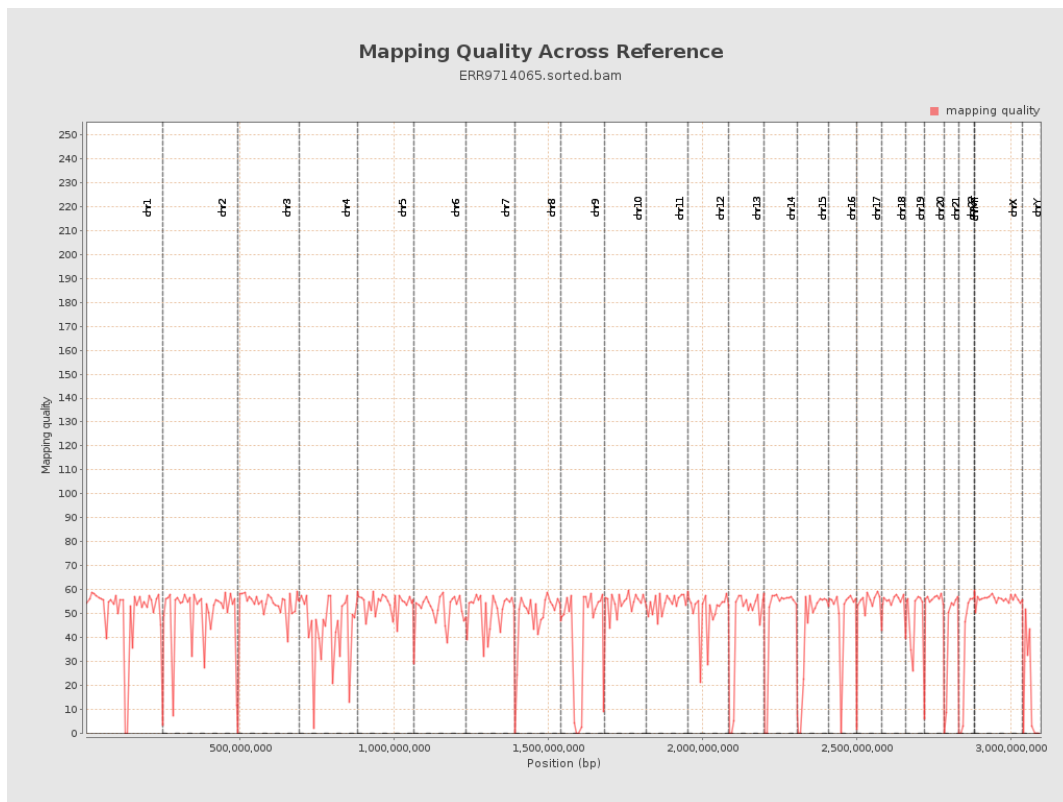
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

