

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:42:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714085.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_ERR9714085 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:42:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	619,972
Mapped reads	197,449 / 31.85%
Unmapped reads	422,523 / 68.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,835 / 0.62%
Read min/max/mean length	30 / 151 / 80.18
Duplicated reads (estimated)	191,014 / 30.81%
Duplication rate	35.24%
Clipped reads	165,914 / 26.76%

2.2. ACGT Content

Number/percentage of A's	5,798,761 / 23.36%
Number/percentage of C's	4,526,512 / 18.23%
Number/percentage of T's	6,082,629 / 24.5%
Number/percentage of G's	8,418,356 / 33.91%
Number/percentage of N's	360 / 0%
GC Percentage	52.14%

2.3. Coverage

Mean	0.0081

Standard Deviation	16.2892
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2.4. Mapping Quality

Mean Mapping Quality	30.39
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2.5. Mismatches and indels

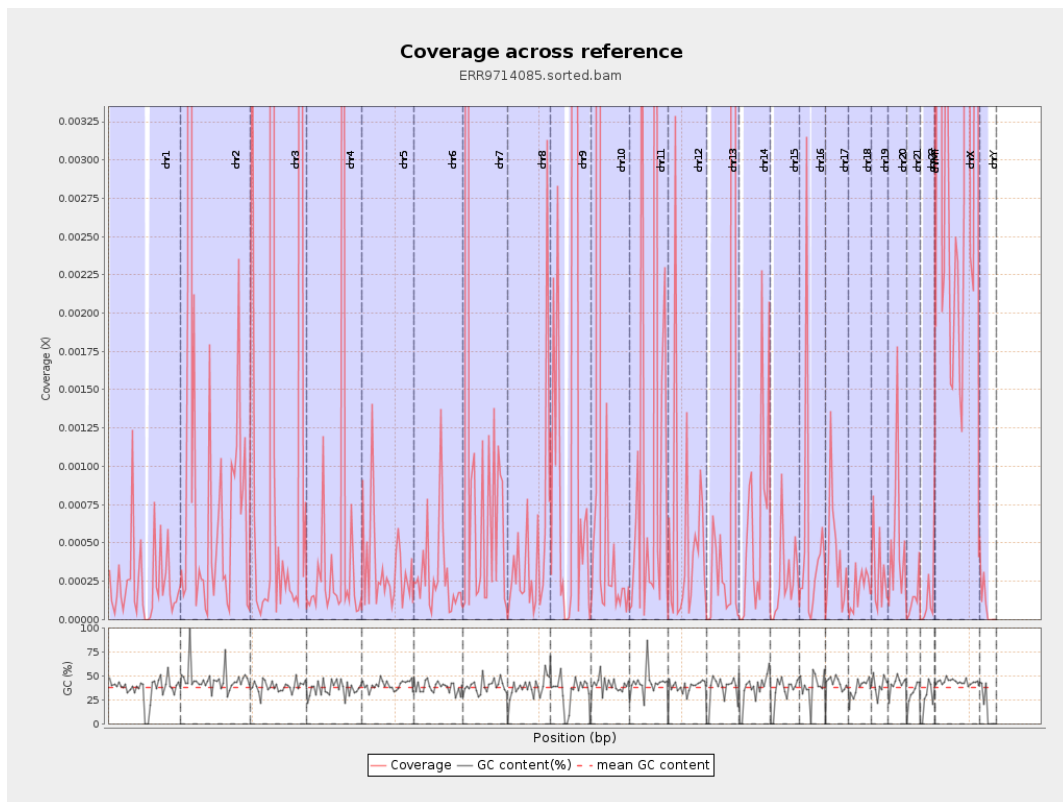
General error rate	2.84%
Mismatches	662,029
Insertions	11,416
Mapped reads with at least one insertion	5.09%
Deletions	59,427
Mapped reads with at least one deletion	29.05%
Homopolymer indels	48.51%

2.6. Chromosome stats

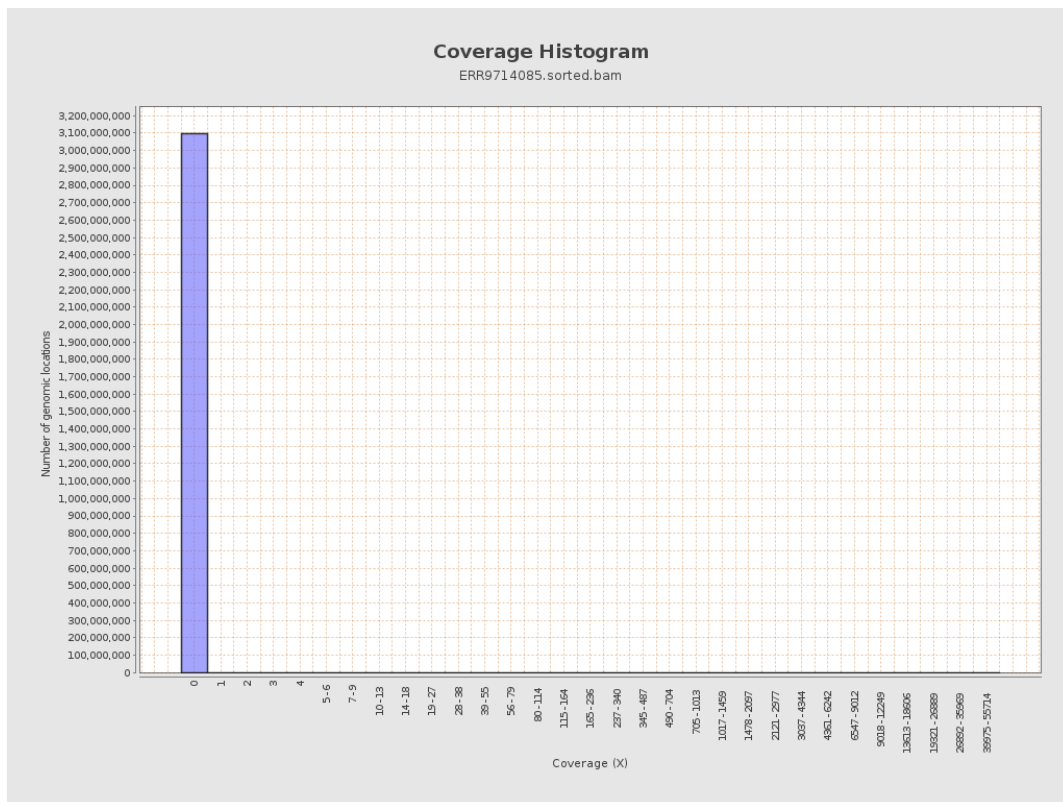
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	59656	0.0002	0.0432
chr2	243199373	3919545	0.0161	16.3715
chr3	198022430	8296024	0.0419	45.8218
chr4	191154276	116535	0.0006	0.454
chr5	180915260	62966	0.0003	0.0623
chr6	171115067	49218	0.0003	0.0637
chr7	159138663	209550	0.0013	0.7547

chr8	146364022	68199	0.0005	0.1585
chr9	141213431	257176	0.0018	0.92
chr10	135534747	874965	0.0065	5.371
chr11	135006516	196026	0.0015	0.6991
chr12	133851895	74233	0.0006	0.1657
chr13	115169878	269149	0.0023	2.2553
chr14	107349540	69207	0.0006	0.1629
chr15	102531392	25801	0.0003	0.0401
chr16	90354753	47627	0.0005	0.1794
chr17	81195210	33132	0.0004	0.1118
chr18	78077248	16123	0.0002	0.0335
chr19	59128983	17586	0.0003	0.0734
chr20	63025520	34877	0.0006	0.0959
chr21	48129895	6089	0.0001	0.0191
chr22	51304566	6171	0.0001	0.024
chrMT	16571	8940756	539.5423	4,422.2313
chrX	155270560	1344359	0.0087	6.598
chrY	59373566	6913	0.0001	0.0297

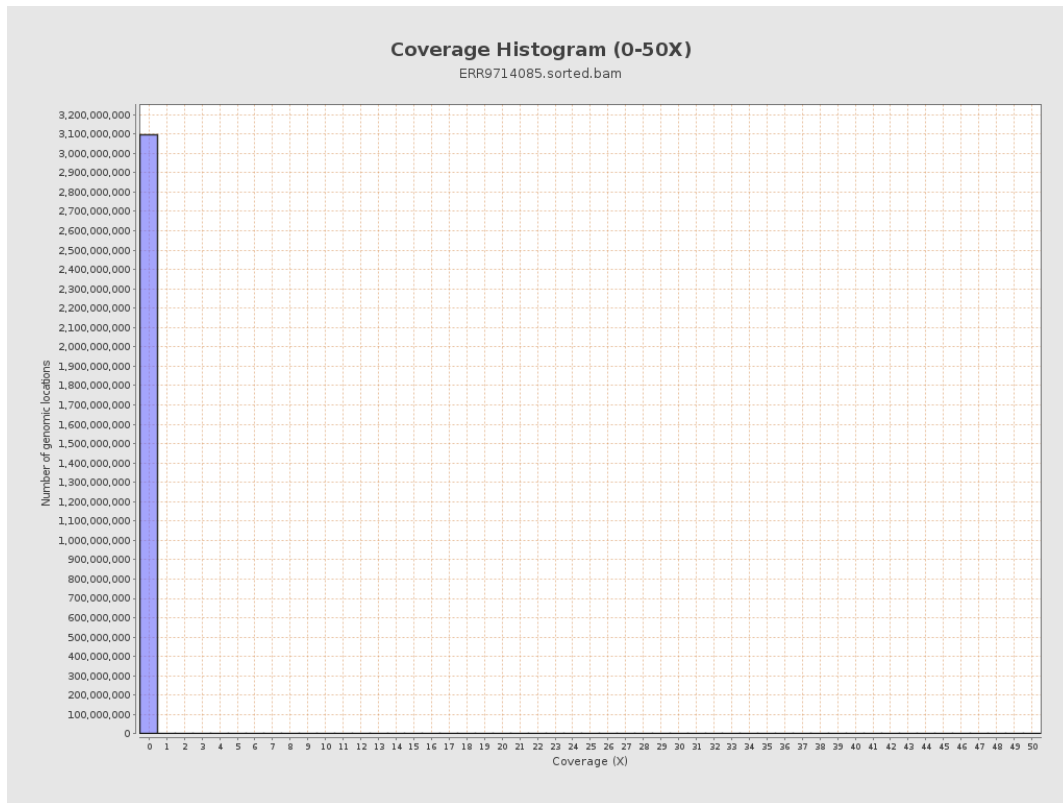
3. Results : Coverage across reference



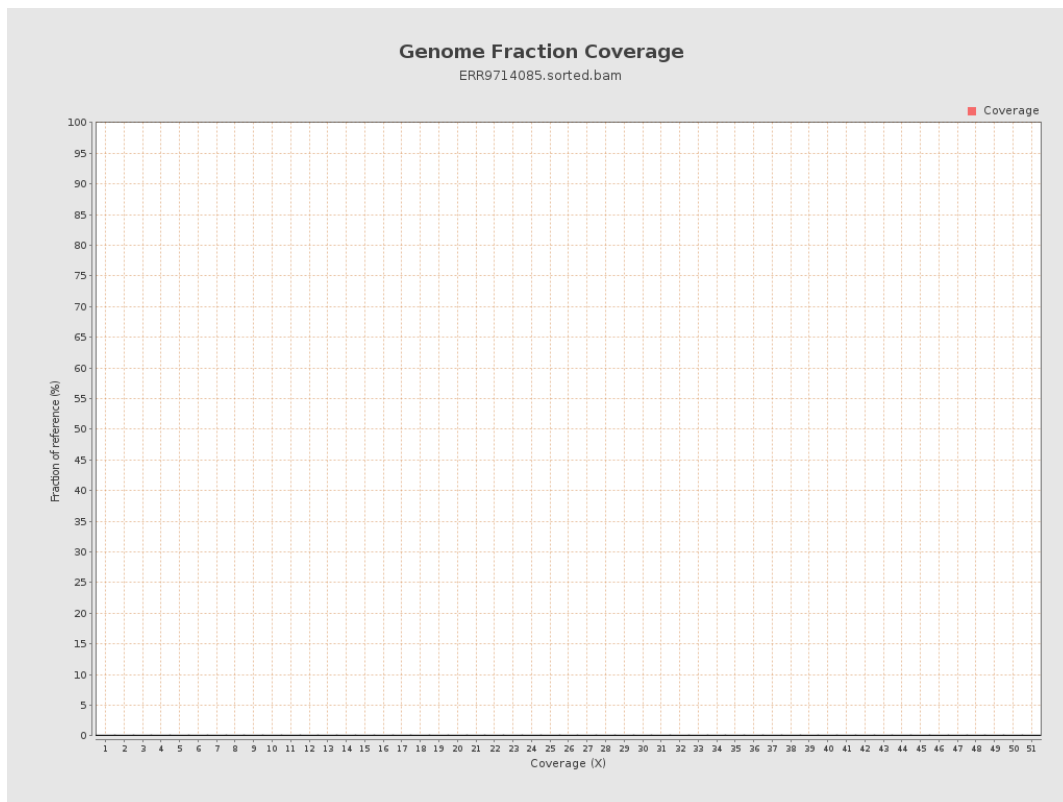
4. Results : Coverage Histogram



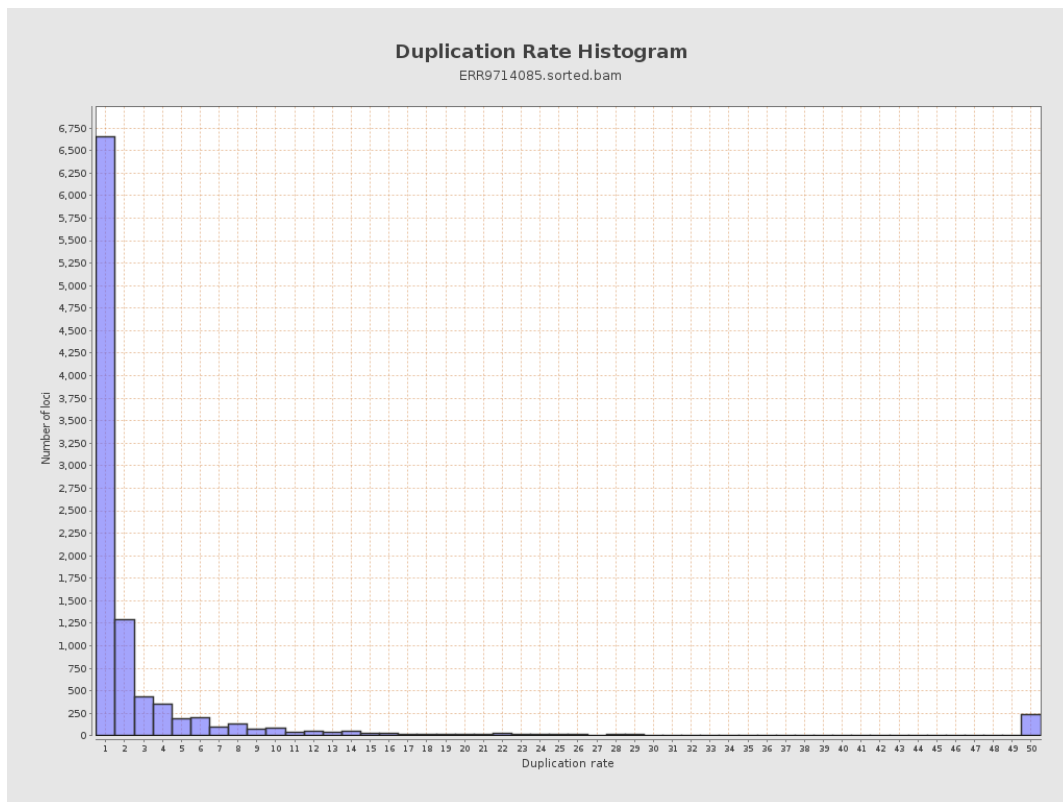
5. Results : Coverage Histogram (0-50X)



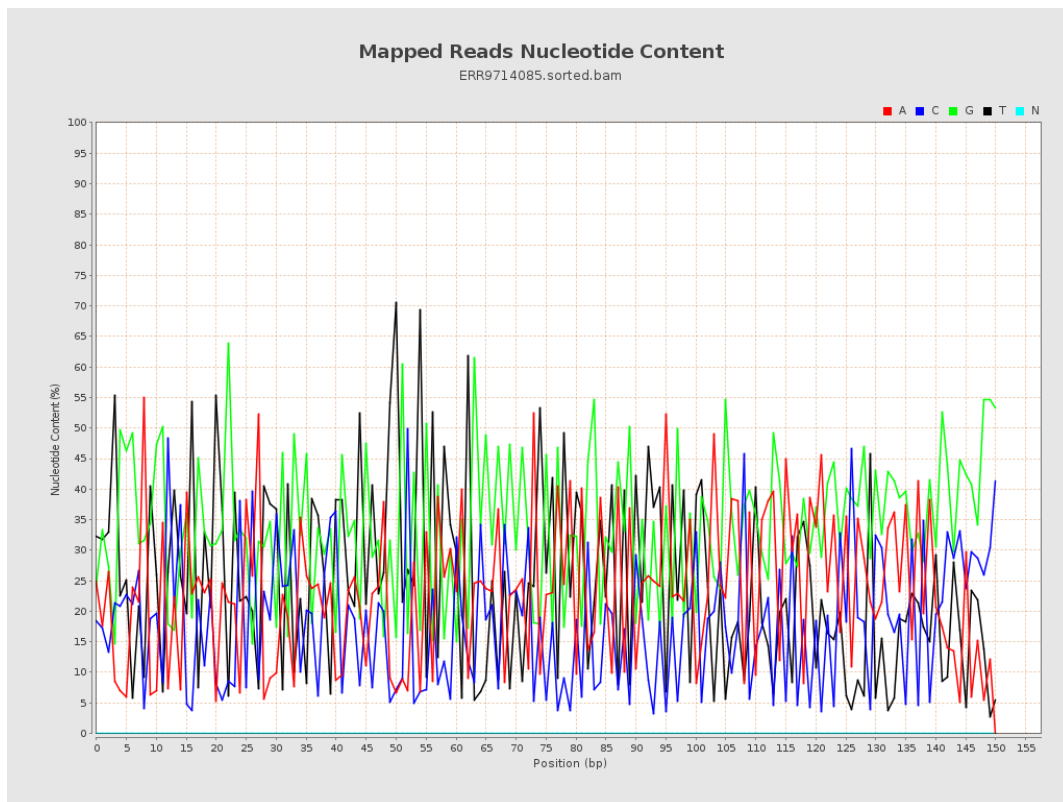
6. Results : Genome Fraction Coverage



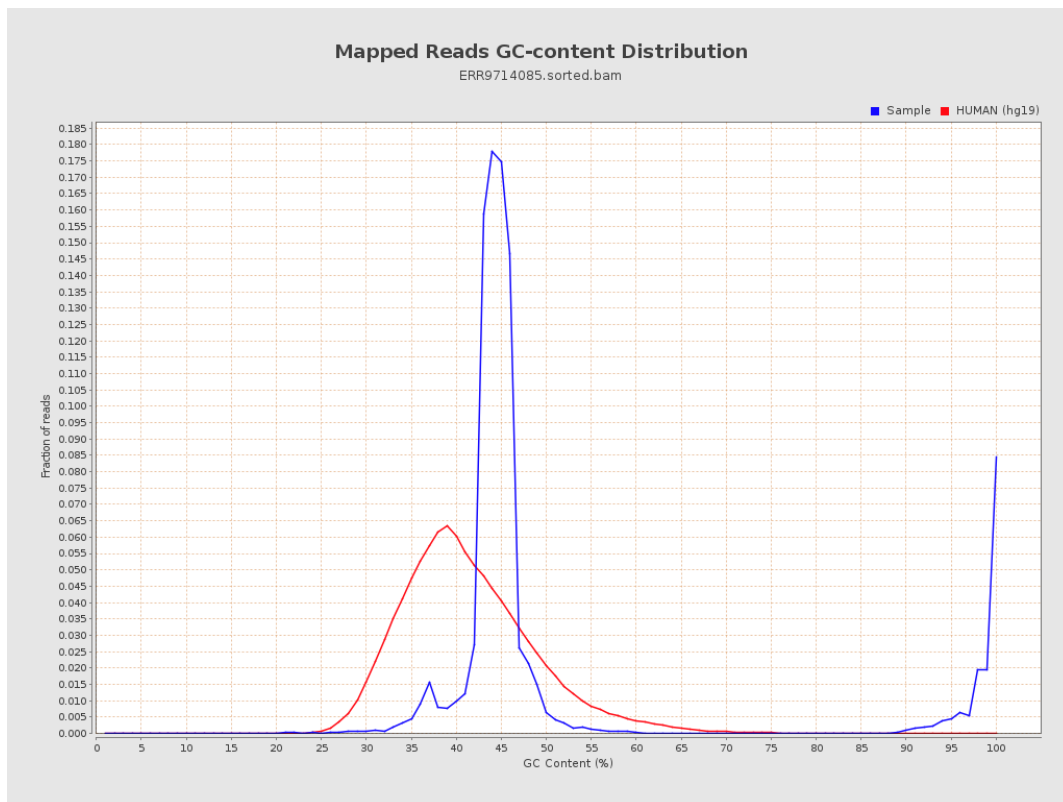
7. Results : Duplication Rate Histogram



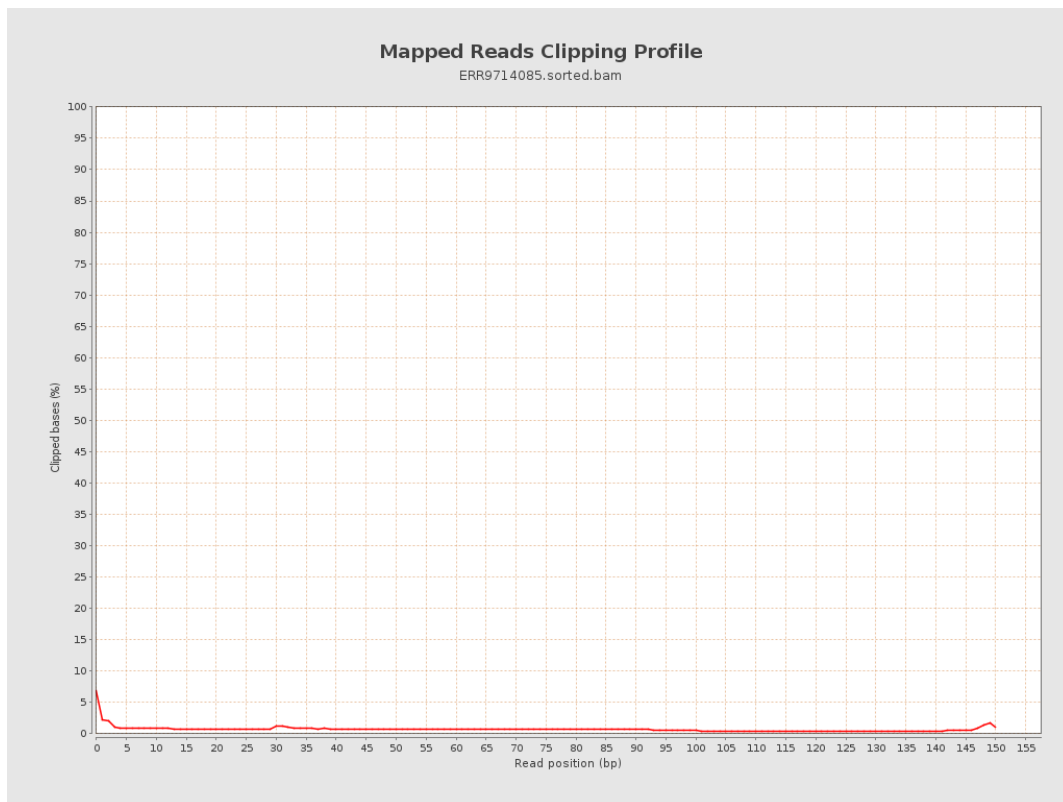
8. Results : Mapped Reads Nucleotide Content



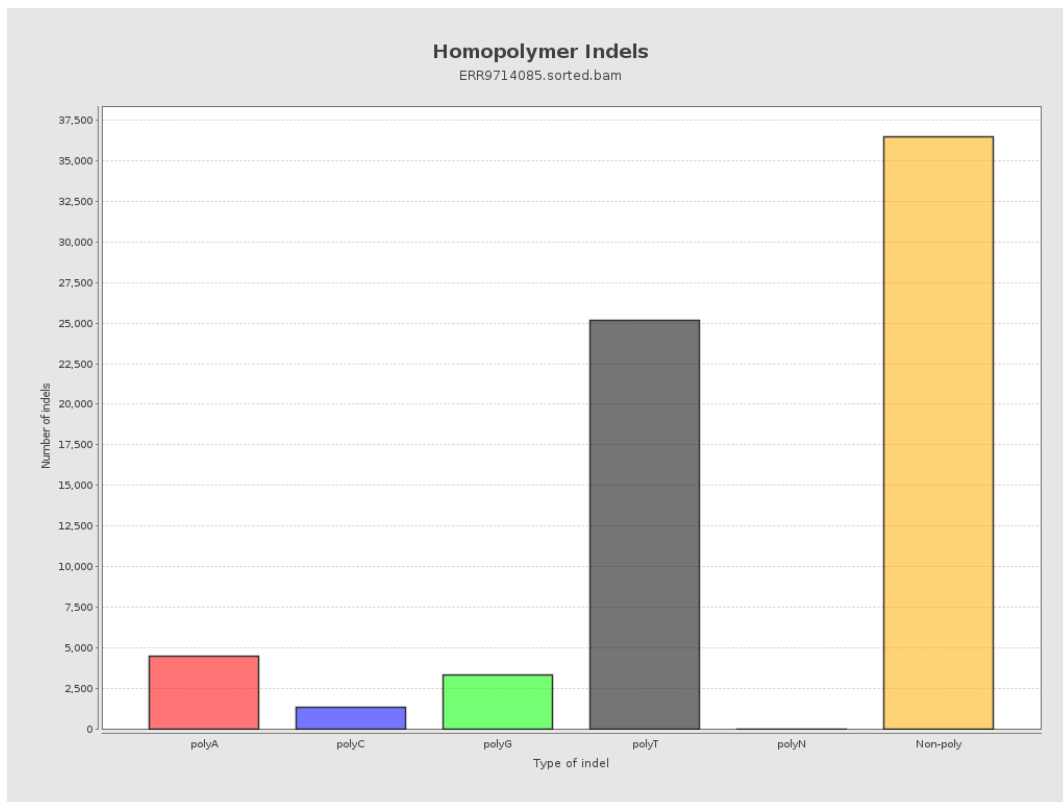
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

