

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714228.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_ERR9714228 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:43:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	175,170
Mapped reads	75,846 / 43.3%
Unmapped reads	99,324 / 56.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,892 / 1.65%
Read min/max/mean length	30 / 151 / 99.66
Duplicated reads (estimated)	61,566 / 35.15%
Duplication rate	42.08%
Clipped reads	69,312 / 39.57%

2.2. ACGT Content

Number/percentage of A's	2,360,014 / 25.35%
Number/percentage of C's	1,846,759 / 19.83%
Number/percentage of T's	2,247,318 / 24.14%
Number/percentage of G's	2,857,071 / 30.68%
Number/percentage of N's	112 / 0%
GC Percentage	50.52%

2.3. Coverage

Mean	0.0031

Standard Deviation	1.309
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2.4. Mapping Quality

Mean Mapping Quality	49.29
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2.5. Mismatches and indels

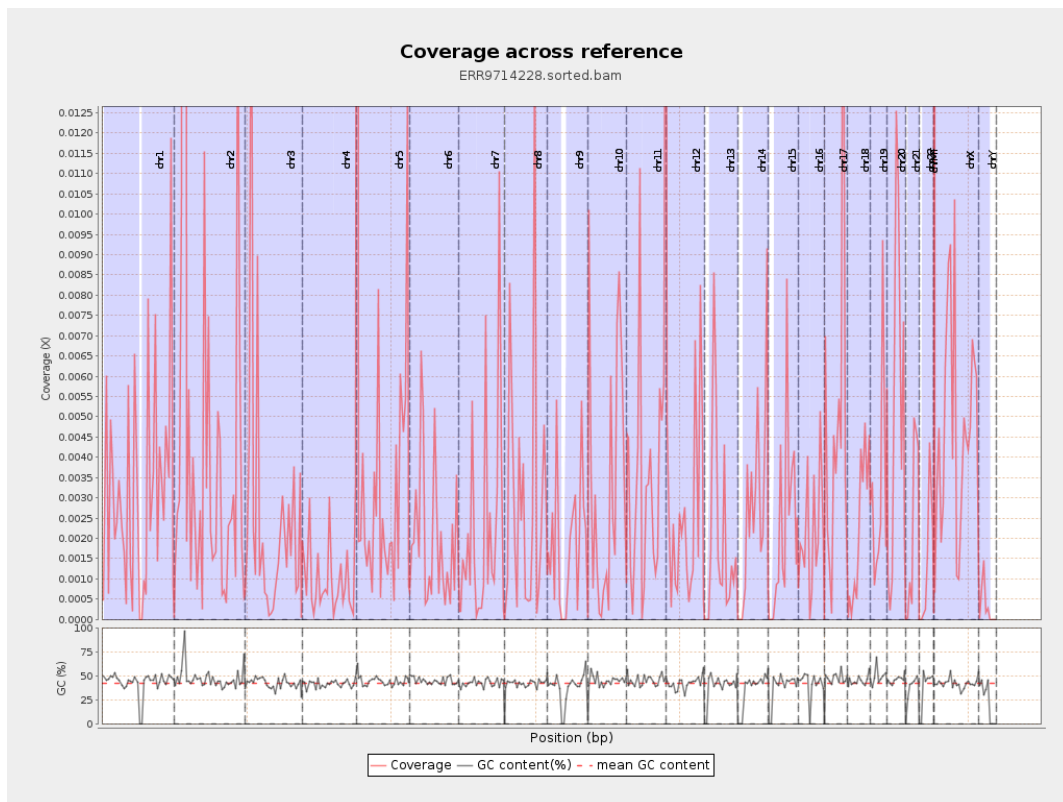
General error rate	4.27%
Mismatches	369,853
Insertions	9,423
Mapped reads with at least one insertion	11.76%
Deletions	32,938
Mapped reads with at least one deletion	40.53%
Homopolymer indels	29.34%

2.6. Chromosome stats

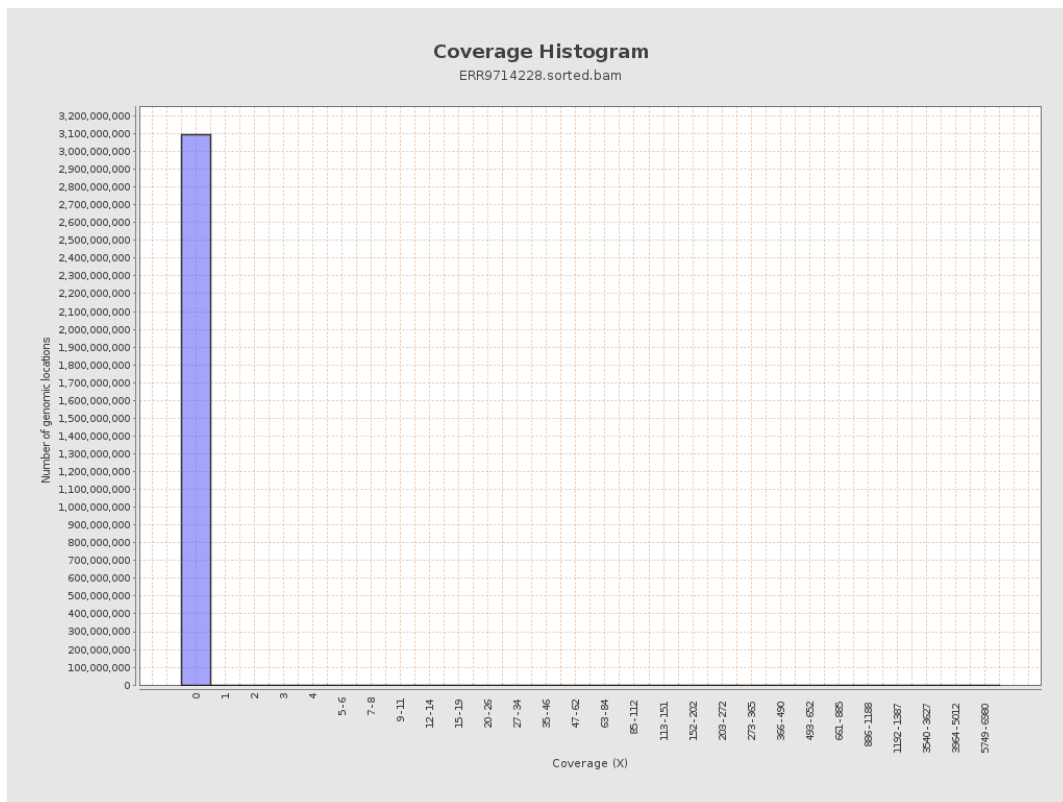
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	773780	0.0031	0.5284
chr2	243199373	1829068	0.0075	4.2571
chr3	198022430	511954	0.0026	0.7456
chr4	191154276	193132	0.001	0.1633
chr5	180915260	595675	0.0033	0.6267
chr6	171115067	340543	0.002	0.3809
chr7	159138663	354771	0.0022	0.5632

chr8	146364022	425931	0.0029	0.7906
chr9	141213431	256439	0.0018	0.3909
chr10	135534747	431916	0.0032	0.5216
chr11	135006516	456613	0.0034	0.5915
chr12	133851895	340952	0.0025	0.4387
chr13	115169878	221126	0.0019	0.4
chr14	107349540	301706	0.0028	0.5489
chr15	102531392	227120	0.0022	0.4396
chr16	90354753	184276	0.002	0.3444
chr17	81195210	401818	0.0049	1.3009
chr18	78077248	174816	0.0022	0.3501
chr19	59128983	180698	0.0031	0.4426
chr20	63025520	333947	0.0053	0.8952
chr21	48129895	104670	0.0022	0.4451
chr22	51304566	66744	0.0013	0.2469
chrMT	16571	45699	2.7578	15.5826
chrX	155270560	731298	0.0047	0.4792
chrY	59373566	21117	0.0004	0.0921

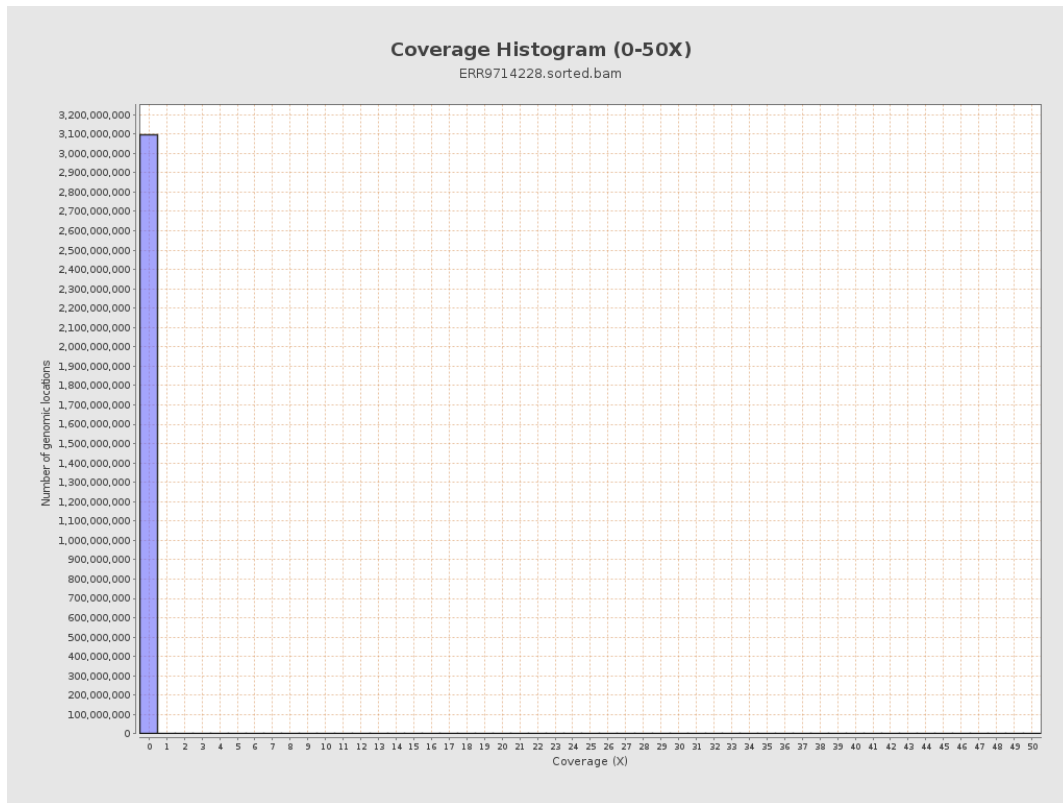
3. Results : Coverage across reference



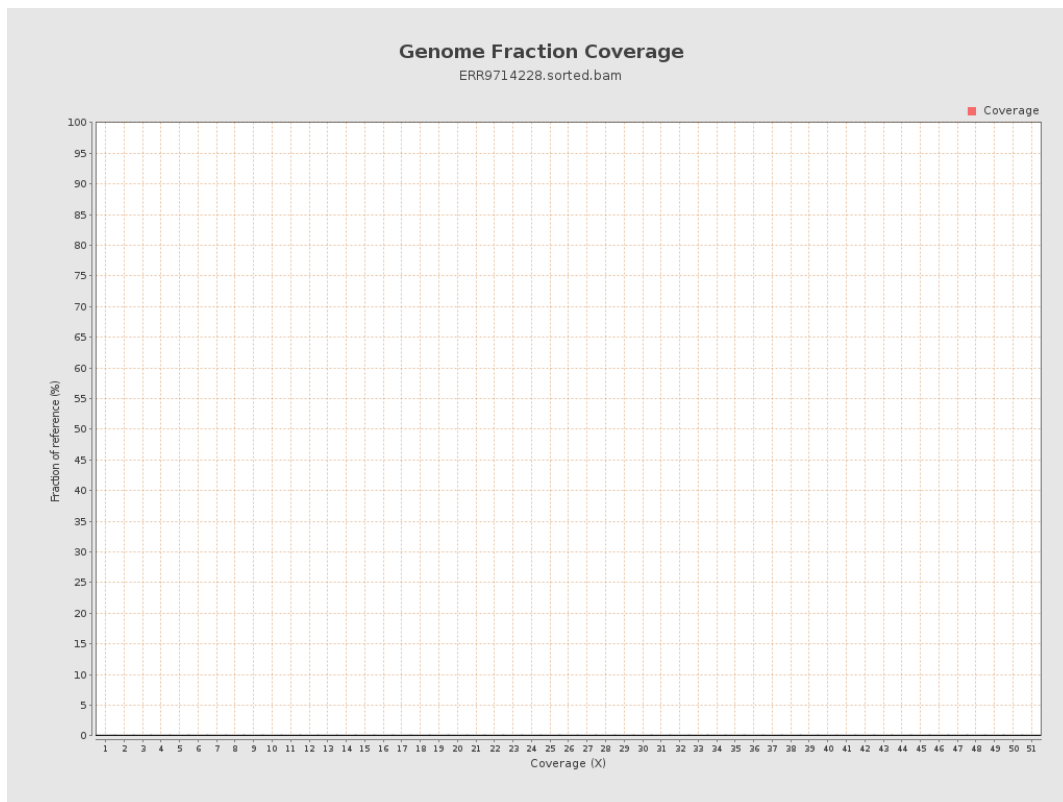
4. Results : Coverage Histogram



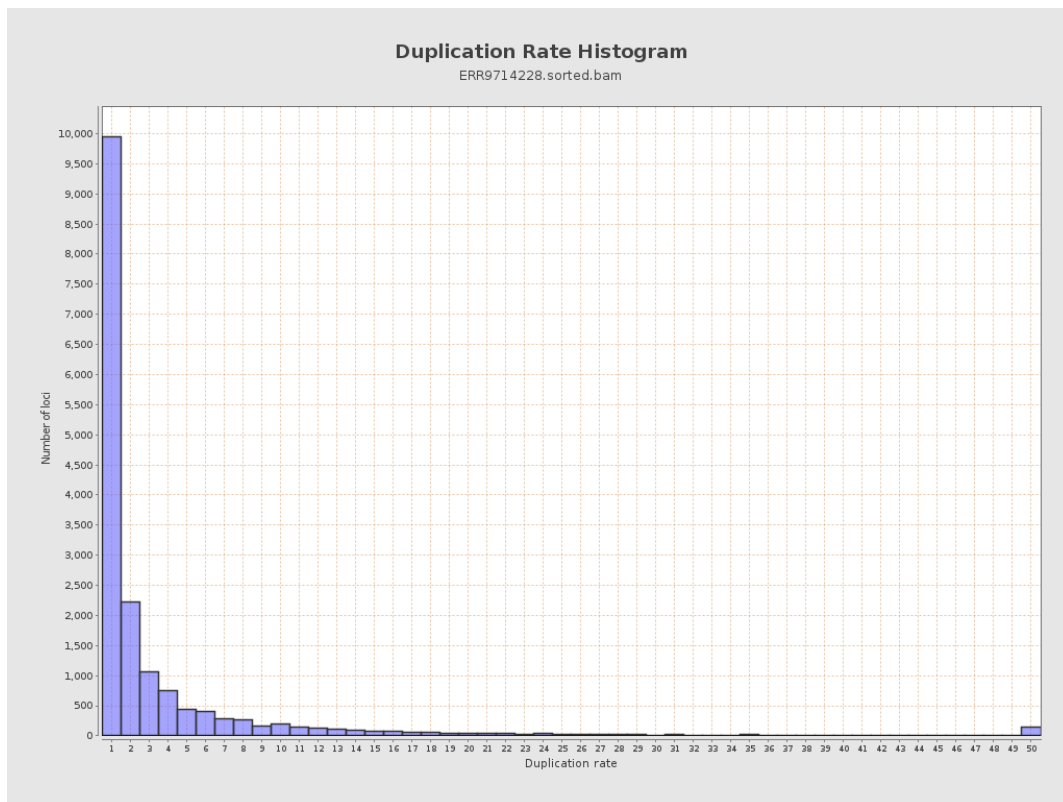
5. Results : Coverage Histogram (0-50X)



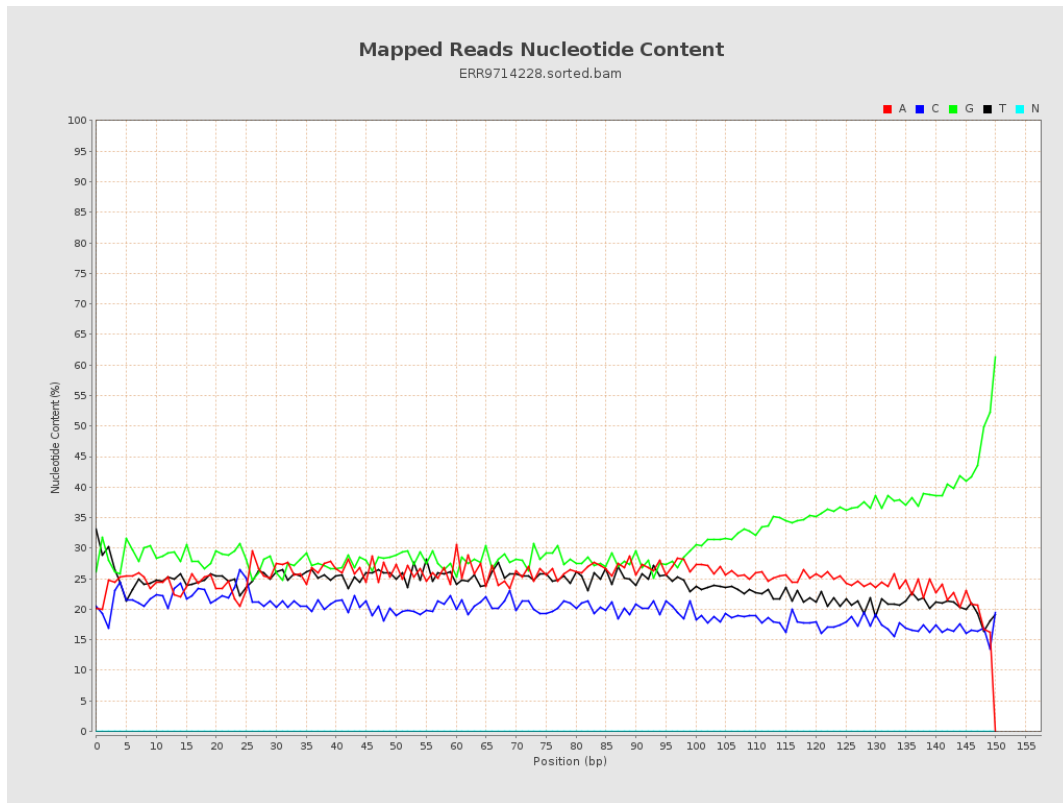
6. Results : Genome Fraction Coverage



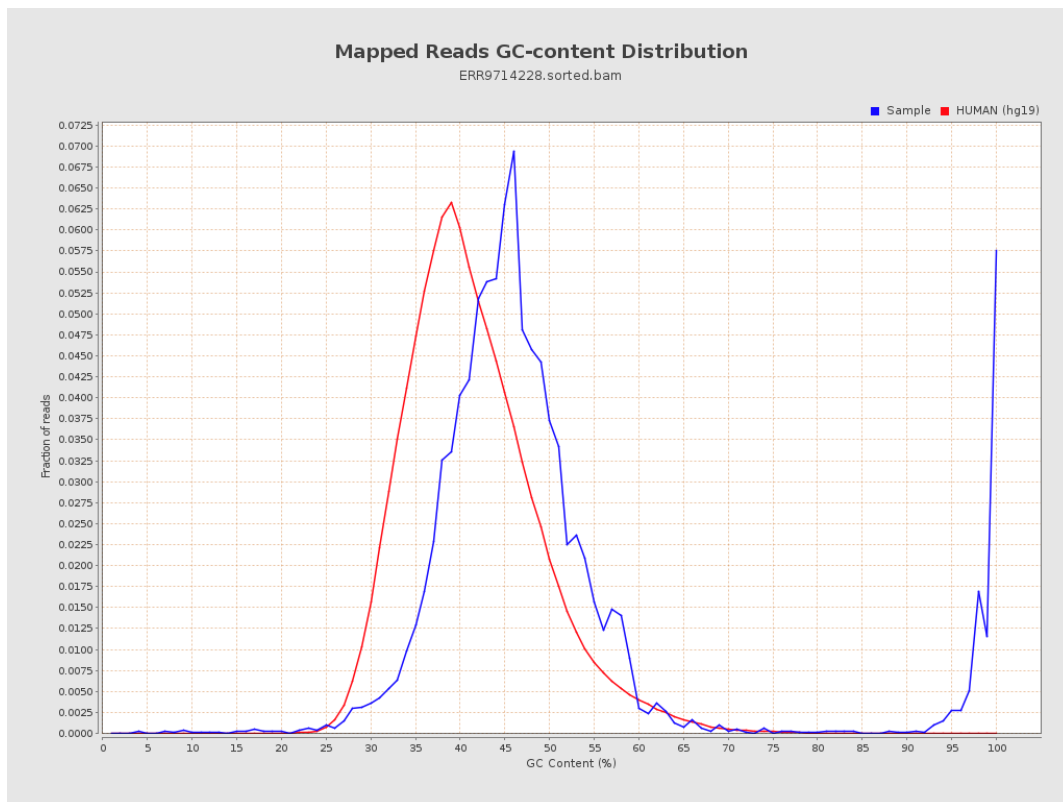
7. Results : Duplication Rate Histogram



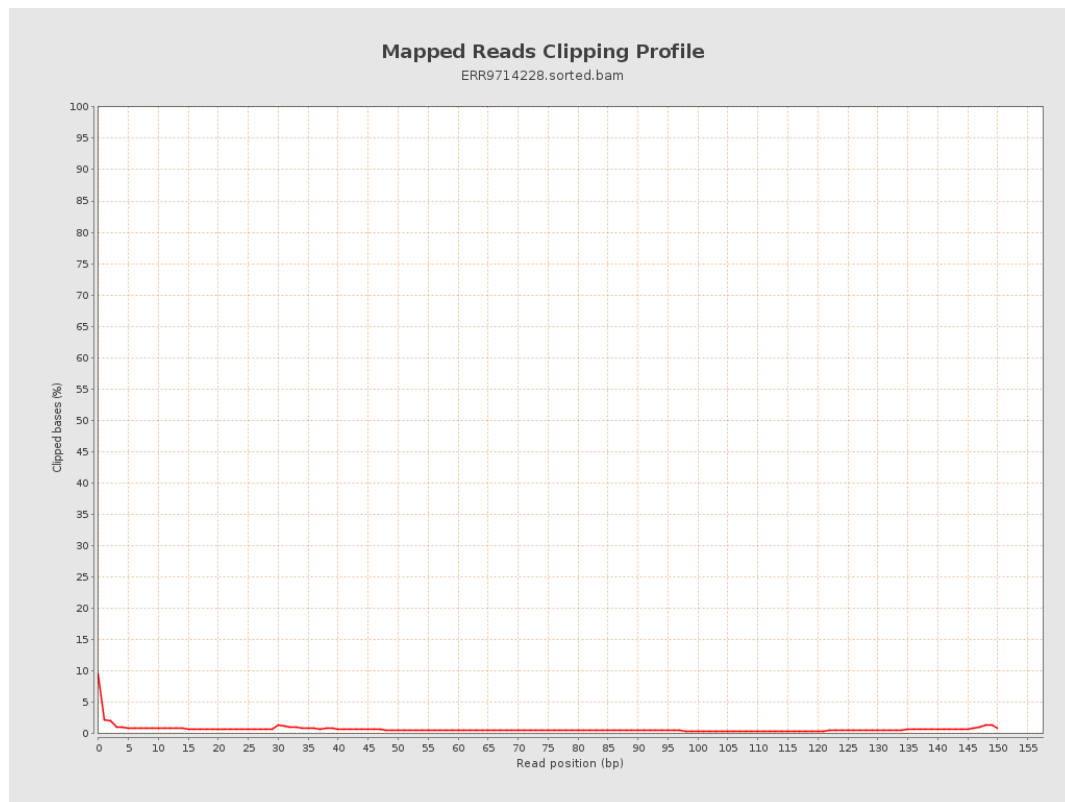
8. Results : Mapped Reads Nucleotide Content



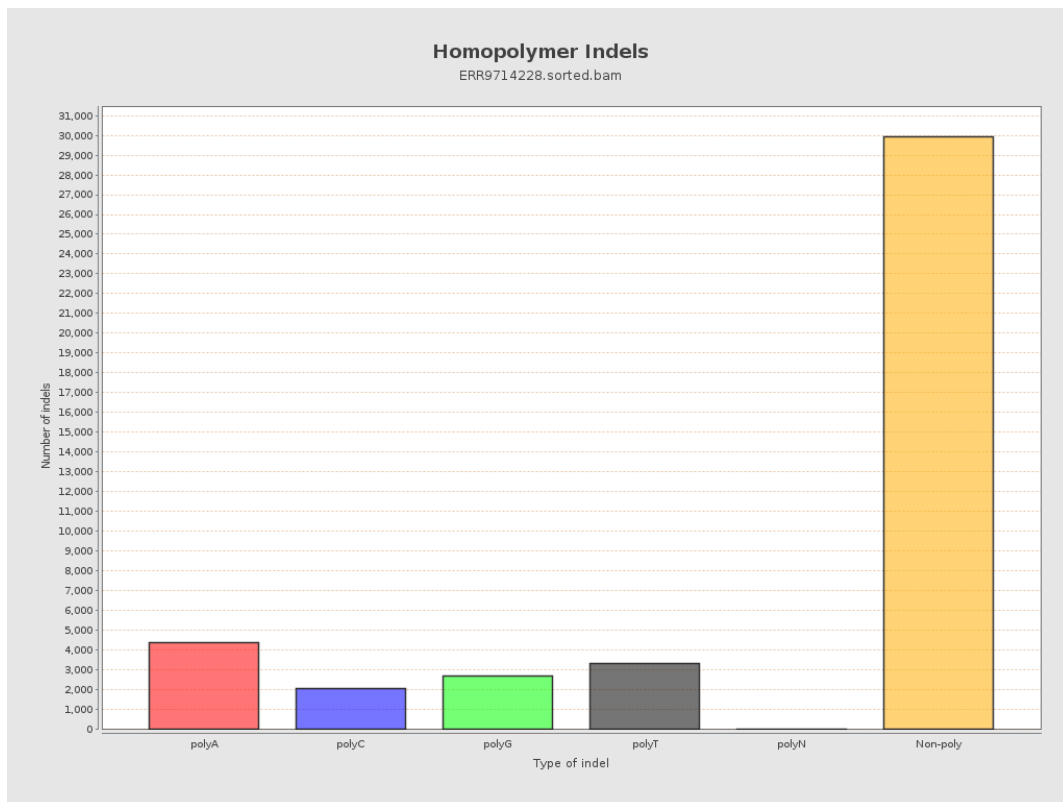
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

