

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714246.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_ERR9714246 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:16:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	348,510
Mapped reads	52,313 / 15.01%
Unmapped reads	296,197 / 84.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,231 / 0.35%
Read min/max/mean length	30 / 151 / 60.76
Duplicated reads (estimated)	50,013 / 14.35%
Duplication rate	26.62%
Clipped reads	30,656 / 8.8%

2.2. ACGT Content

Number/percentage of A's	226,743 / 4.44%
Number/percentage of C's	111,031 / 2.17%
Number/percentage of T's	146,461 / 2.87%
Number/percentage of G's	4,621,597 / 90.51%
Number/percentage of N's	176 / 0%
GC Percentage	92.69%

2.3. Coverage

Mean	0.0017

Standard Deviation	5.7905
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2.4. Mapping Quality

Mean Mapping Quality	18.9
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2.5. Mismatches and indels

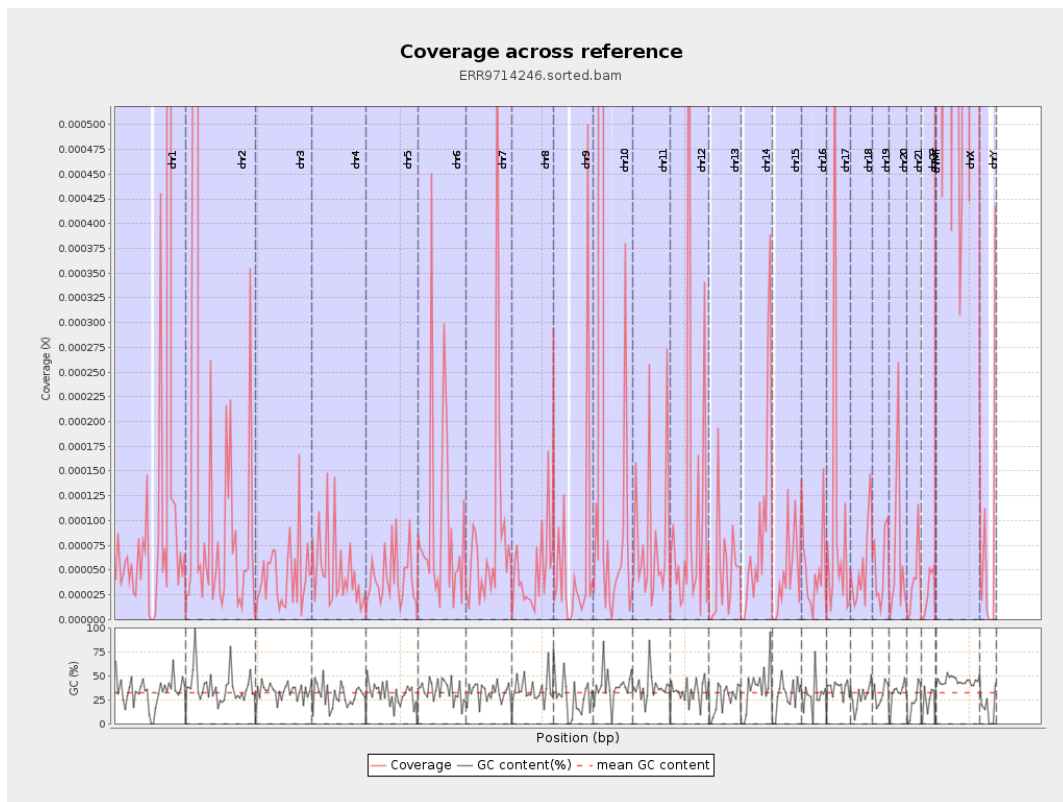
General error rate	3.35%
Mismatches	129,089
Insertions	5,935
Mapped reads with at least one insertion	7.57%
Deletions	3,123
Mapped reads with at least one deletion	5.76%
Homopolymer indels	61.35%

2.6. Chromosome stats

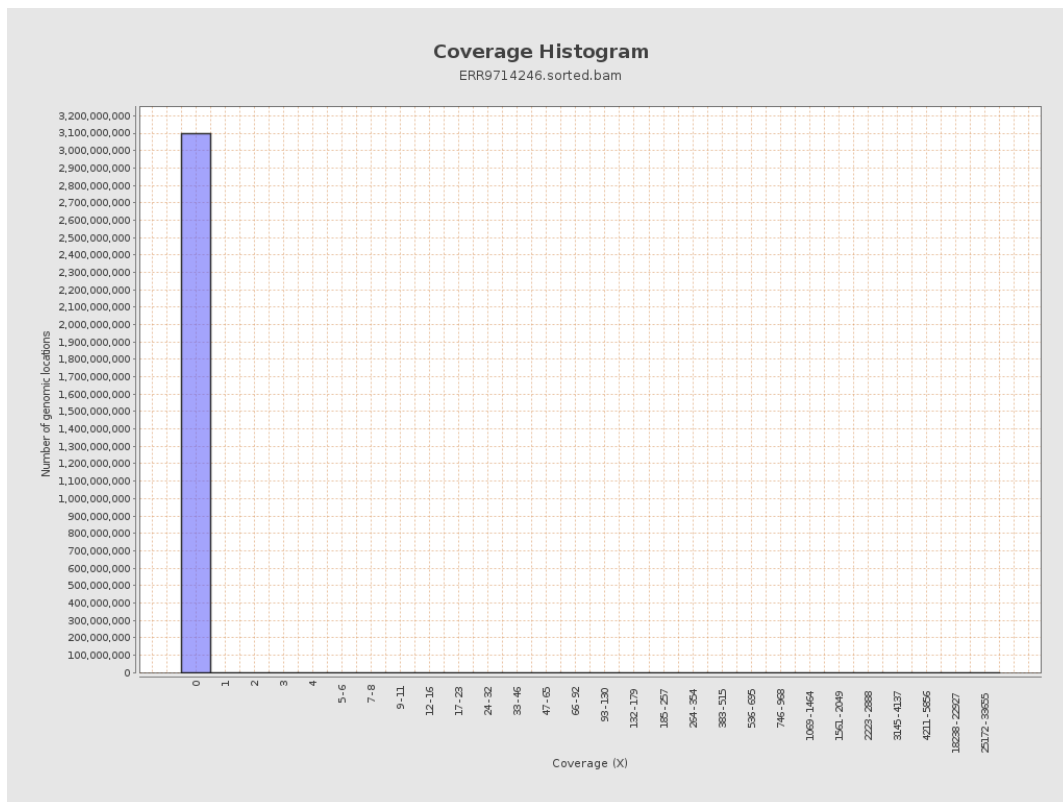
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	85554	0.0003	0.7966
chr2	243199373	4573897	0.0188	20.6277
chr3	198022430	8640	0	0.0104
chr4	191154276	9234	0	0.0098
chr5	180915260	7701	0	0.0095
chr6	171115067	15750	0.0001	0.0281
chr7	159138663	14329	0.0001	0.065

chr8	146364022	6897	0	0.0127
chr9	141213431	8261	0.0001	0.0273
chr10	135534747	76236	0.0006	1.0465
chr11	135006516	10583	0.0001	0.0291
chr12	133851895	15815	0.0001	0.0632
chr13	115169878	5482	0	0.0098
chr14	107349540	10079	0.0001	0.0528
chr15	102531392	4718	0	0.0136
chr16	90354753	4589	0.0001	0.0101
chr17	81195210	8731	0.0001	0.0897
chr18	78077248	4244	0.0001	0.0161
chr19	59128983	3088	0.0001	0.0122
chr20	63025520	4348	0.0001	0.0239
chr21	48129895	2008	0	0.0081
chr22	51304566	1379	0	0.0054
chrMT	16571	13099	0.7905	5.5731
chrX	155270560	222809	0.0014	0.2269
chrY	59373566	4493	0.0001	0.0126

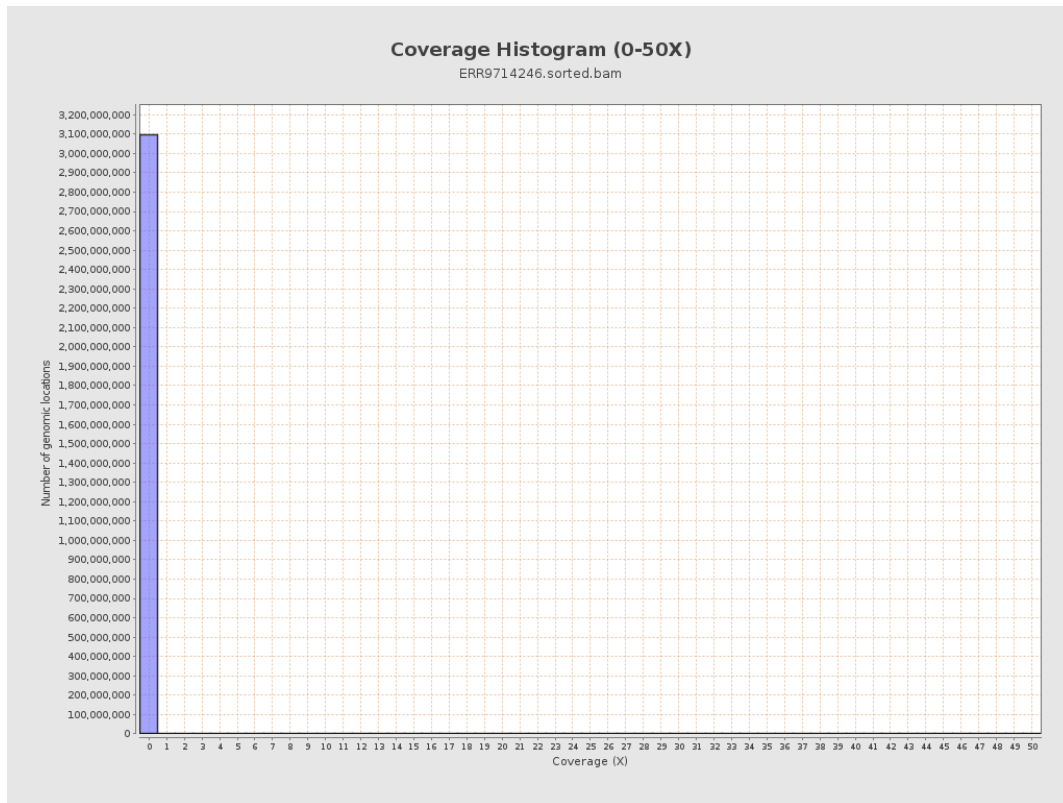
3. Results : Coverage across reference



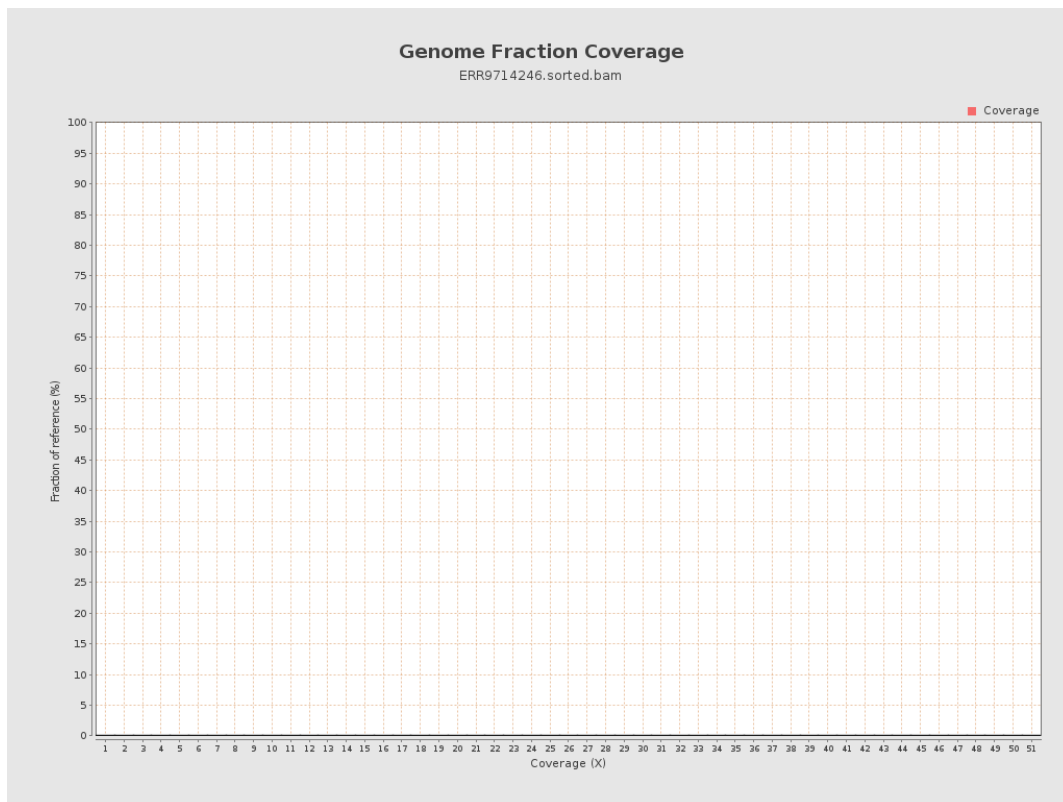
4. Results : Coverage Histogram



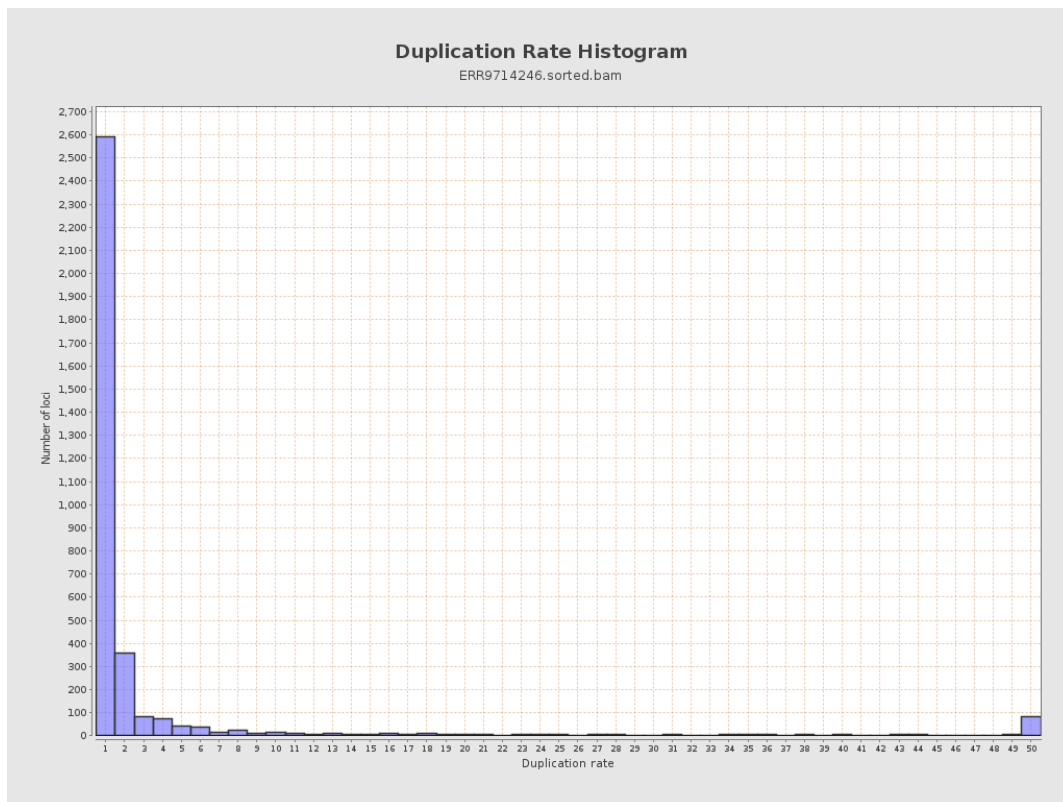
5. Results : Coverage Histogram (0-50X)



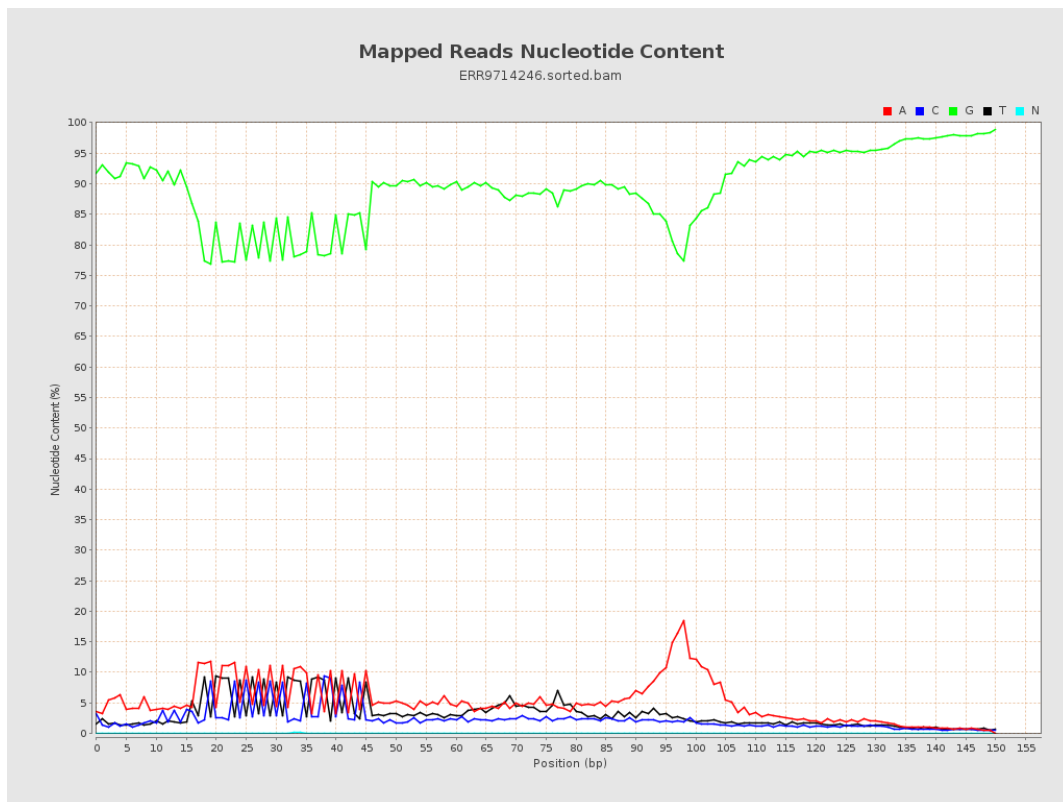
6. Results : Genome Fraction Coverage



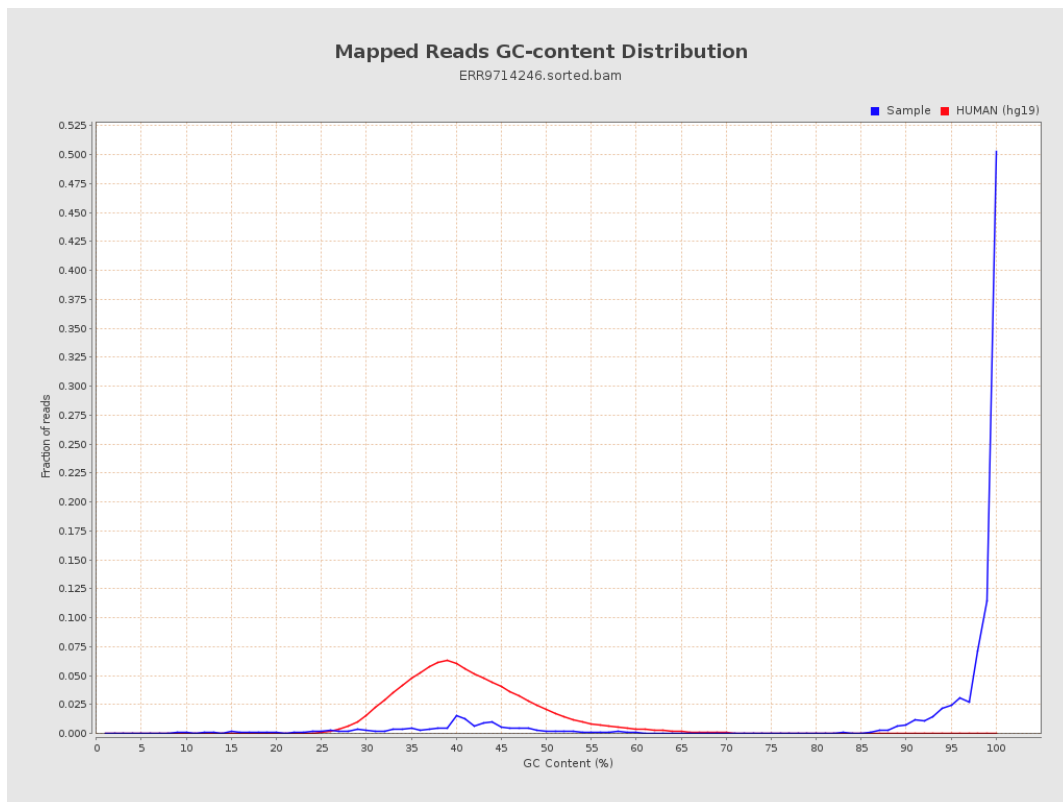
7. Results : Duplication Rate Histogram



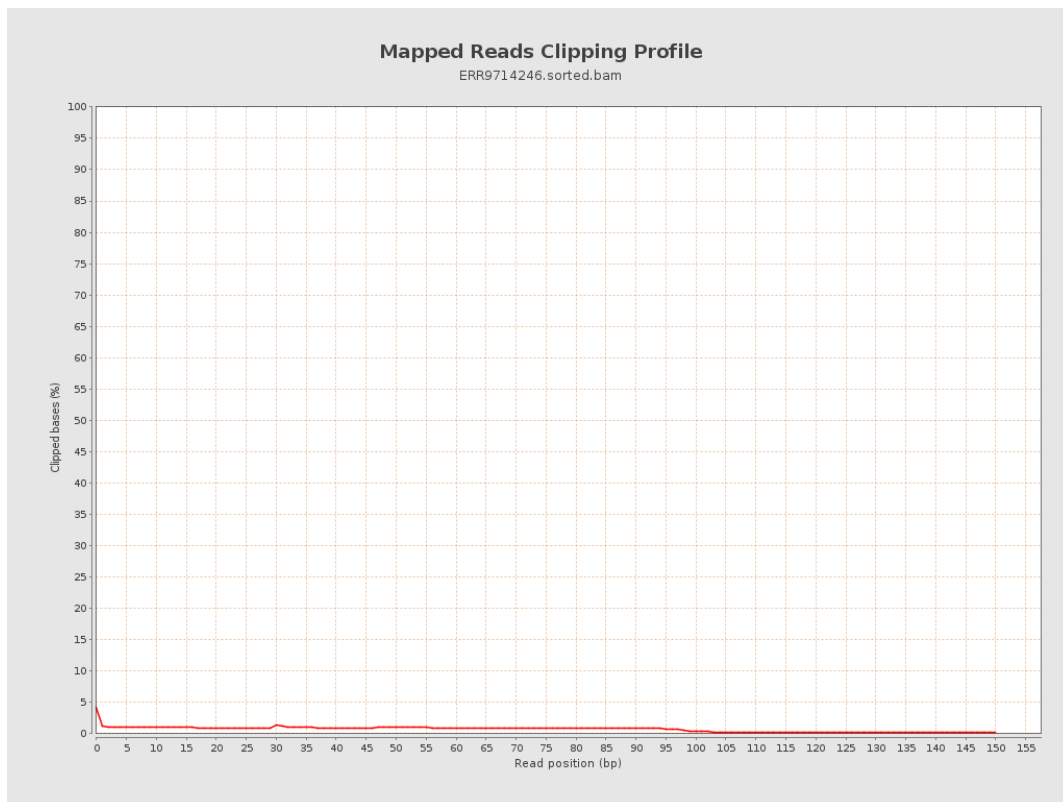
8. Results : Mapped Reads Nucleotide Content



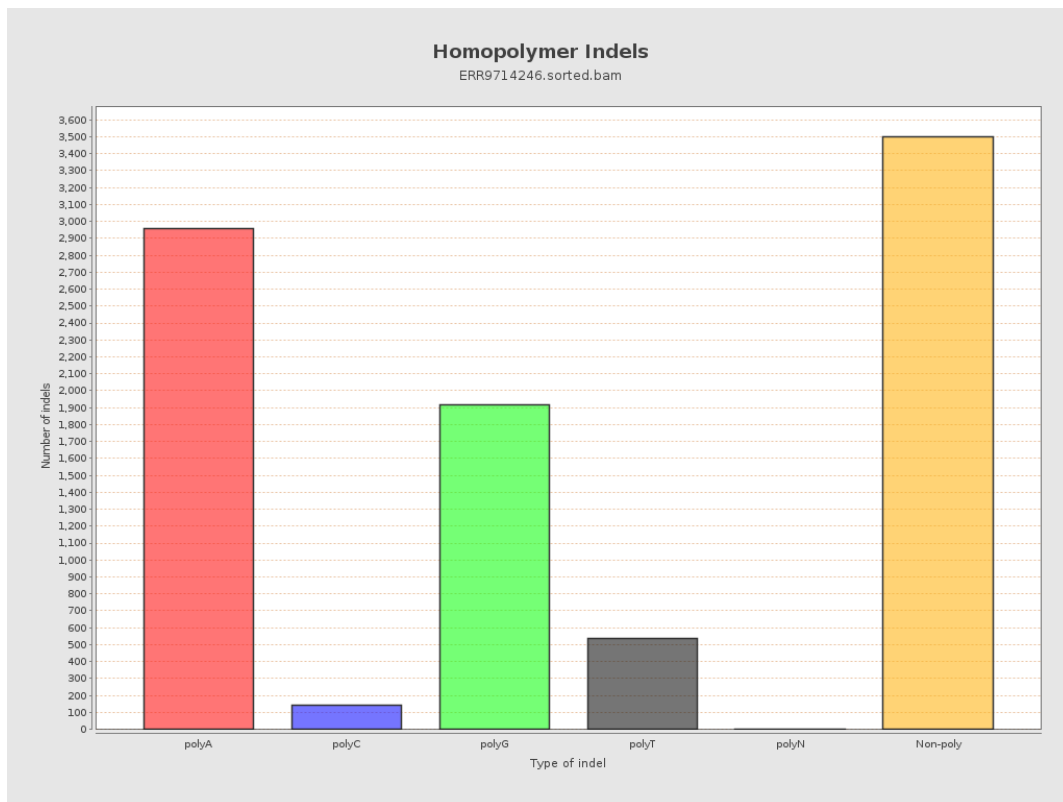
9. Results : Mapped Reads GC-content Distribution



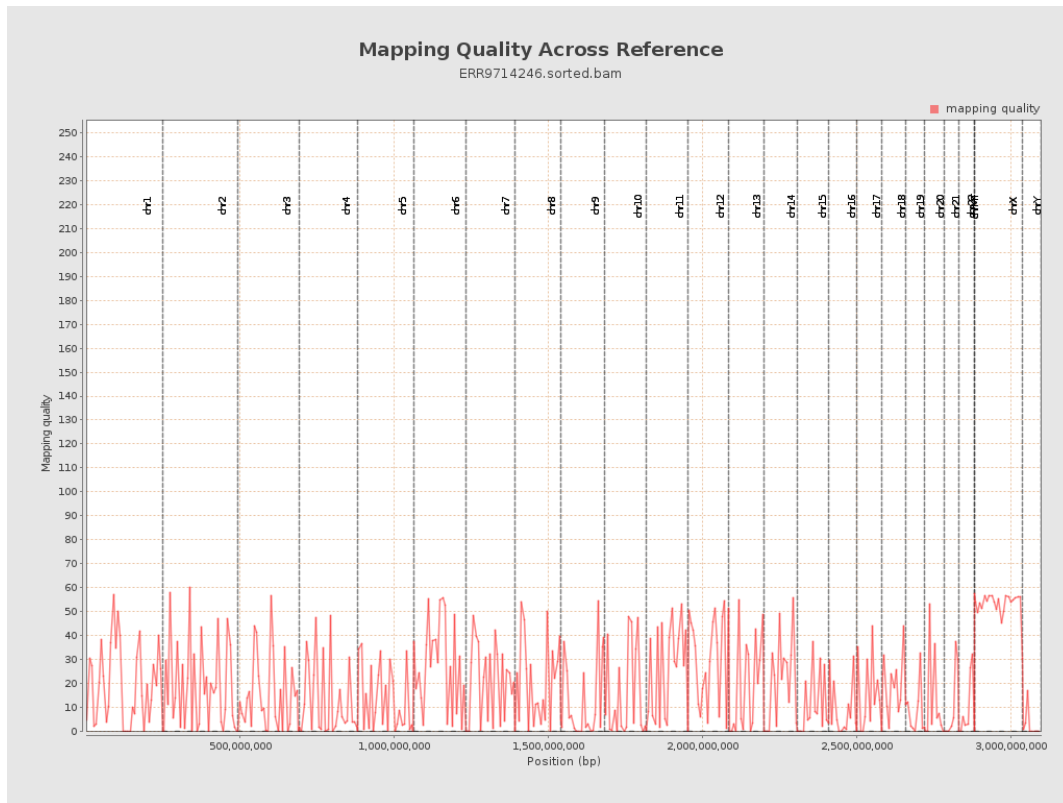
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

