

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:45:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714229.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_ERR9714229 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:45:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	257,194
Mapped reads	36,756 / 14.29%
Unmapped reads	220,438 / 85.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	912 / 0.35%
Read min/max/mean length	30 / 151 / 60.93
Duplicated reads (estimated)	35,673 / 13.87%
Duplication rate	30.73%
Clipped reads	20,094 / 7.81%

2.2. ACGT Content

Number/percentage of A's	119,854 / 3.18%
Number/percentage of C's	50,942 / 1.35%
Number/percentage of T's	65,788 / 1.75%
Number/percentage of G's	3,530,566 / 93.72%
Number/percentage of N's	69 / 0%
GC Percentage	95.07%

2.3. Coverage

Mean	0.0012

Standard Deviation	4.4959
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2.4. Mapping Quality

Mean Mapping Quality	12.43
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2.5. Mismatches and indels

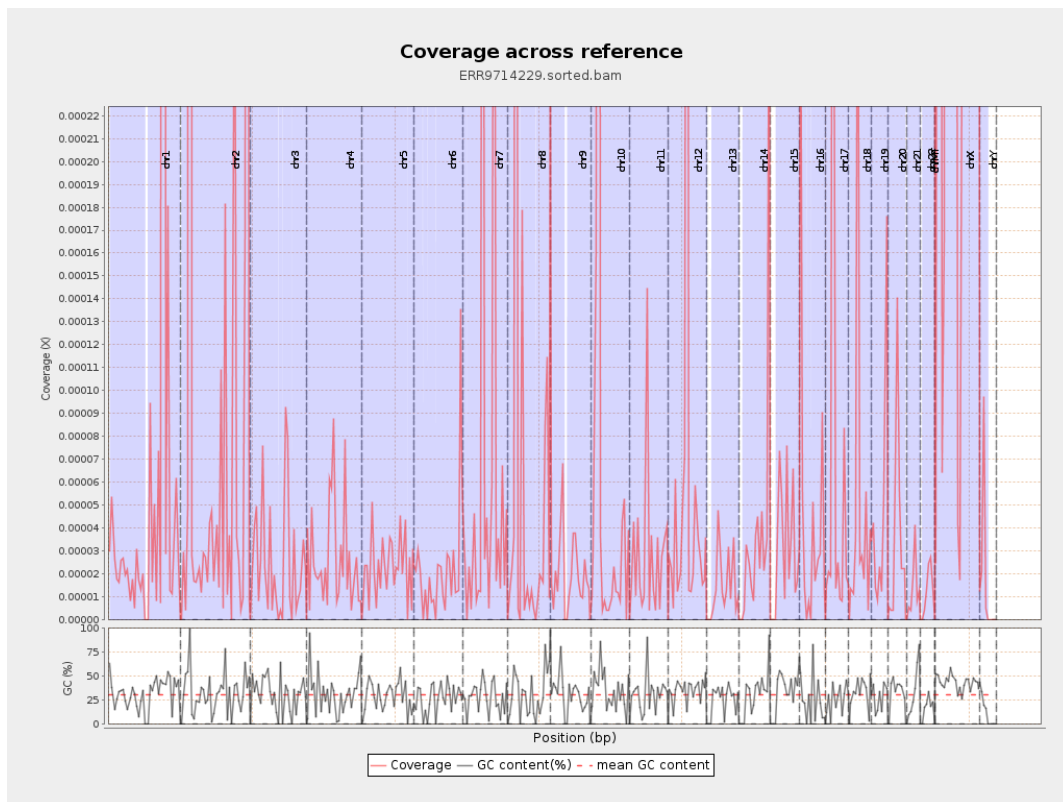
General error rate	3.33%
Mismatches	95,055
Insertions	4,293
Mapped reads with at least one insertion	7.6%
Deletions	1,991
Mapped reads with at least one deletion	5.15%
Homopolymer indels	63.62%

2.6. Chromosome stats

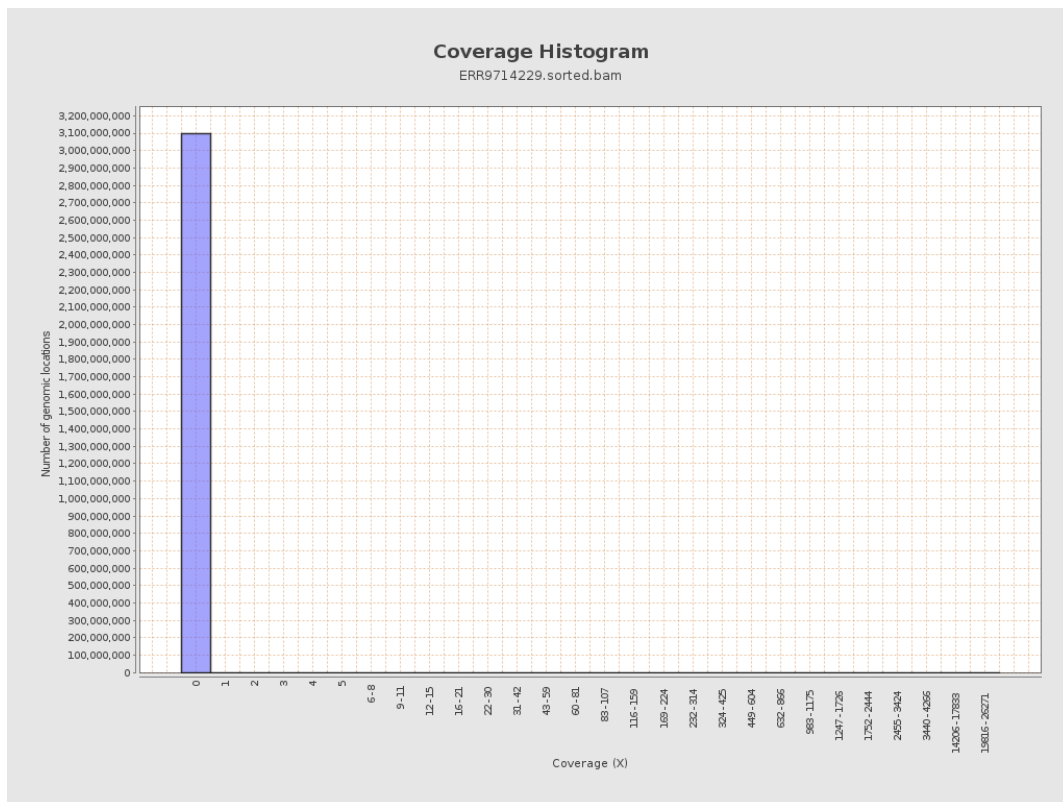
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28770	0.0001	0.2465
chr2	243199373	3531605	0.0145	16.0356
chr3	198022430	4929	0	0.0081
chr4	191154276	5163	0	0.0077
chr5	180915260	4058	0	0.0057
chr6	171115067	3730	0	0.0082
chr7	159138663	12435	0.0001	0.0557

chr8	146364022	10273	0.0001	0.0459
chr9	141213431	3067	0	0.007
chr10	135534747	26265	0.0002	0.3549
chr11	135006516	3797	0	0.0152
chr12	133851895	9808	0.0001	0.0545
chr13	115169878	1675	0	0.0047
chr14	107349540	4733	0	0.039
chr15	102531392	3173	0	0.0103
chr16	90354753	3896	0	0.0203
chr17	81195210	5267	0.0001	0.0625
chr18	78077248	4373	0.0001	0.0278
chr19	59128983	2654	0	0.0157
chr20	63025520	2437	0	0.0131
chr21	48129895	659	0	0.0044
chr22	51304566	641	0	0.0039
chrMT	16571	3483	0.2102	1.6618
chrX	155270560	99473	0.0006	0.1274
chrY	59373566	1015	0	0.0077

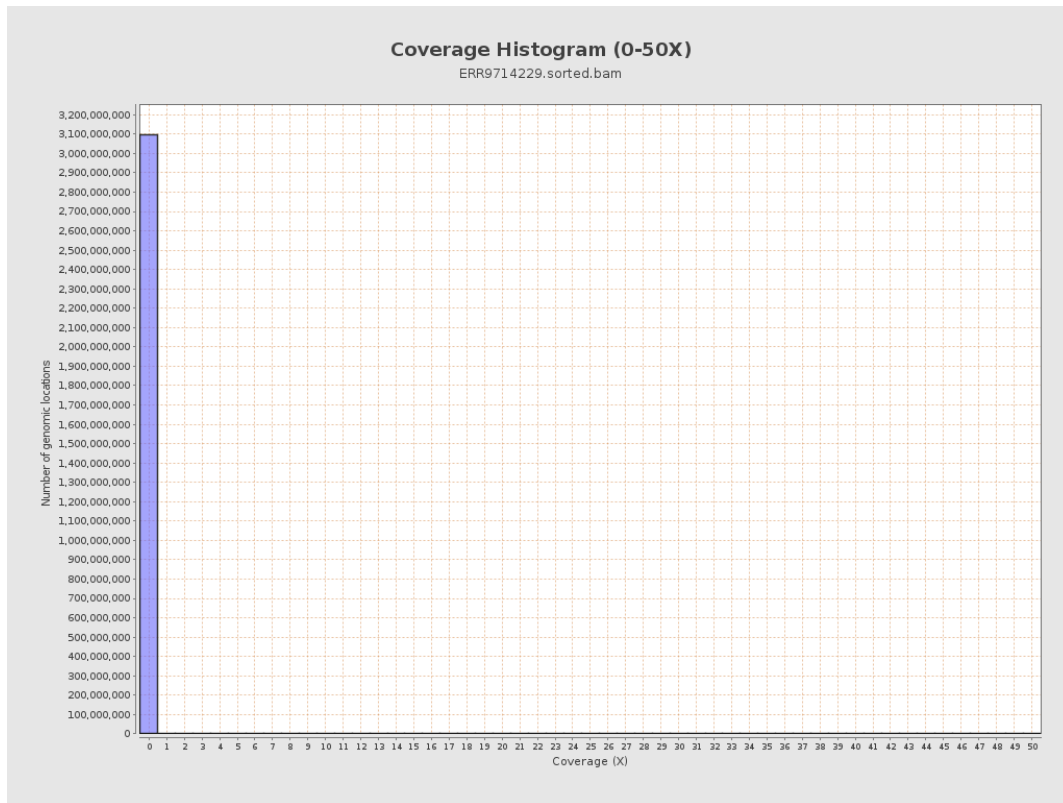
3. Results : Coverage across reference



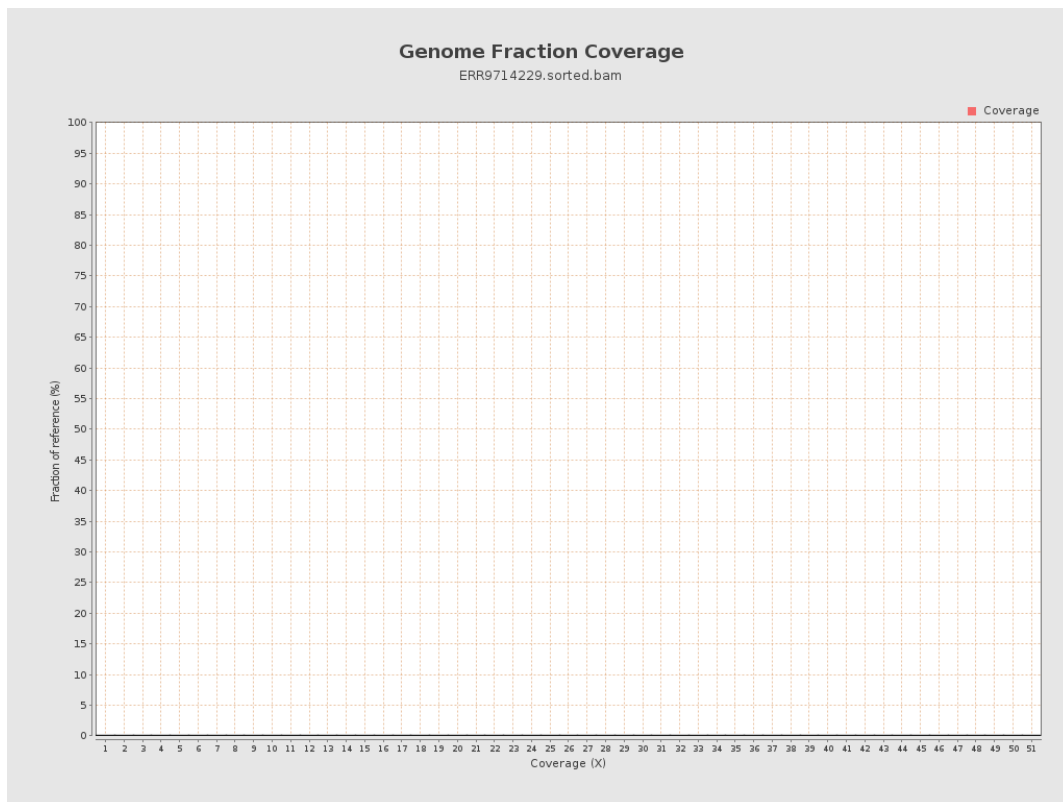
4. Results : Coverage Histogram



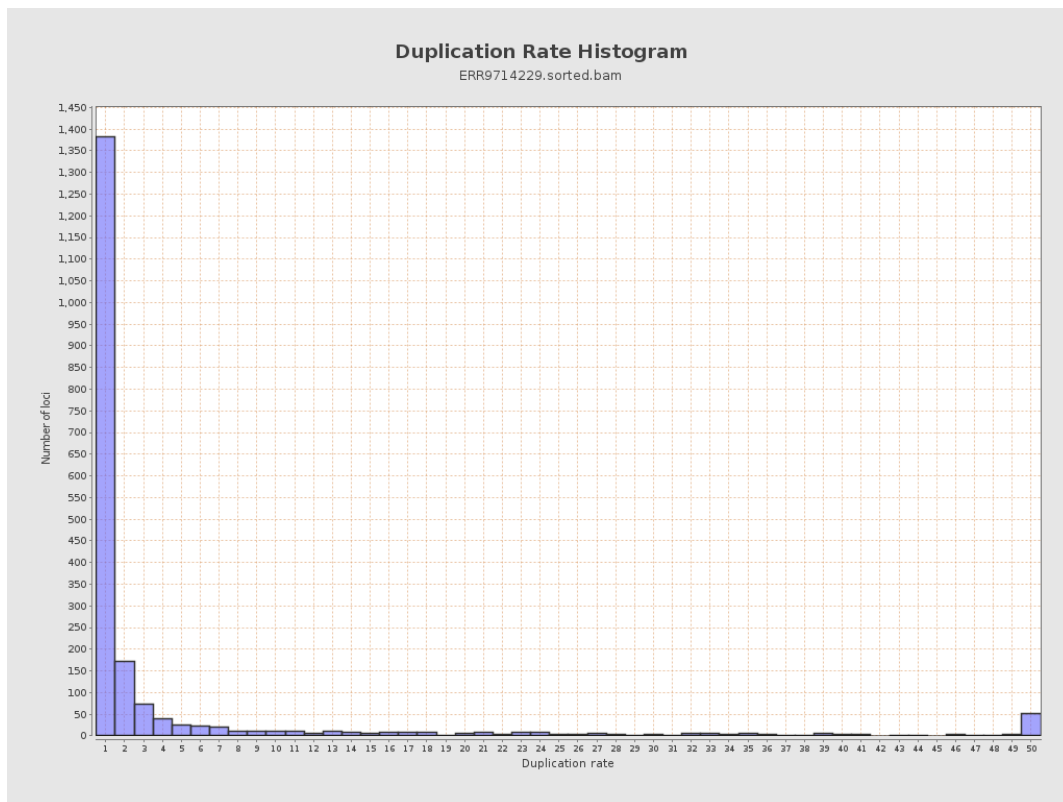
5. Results : Coverage Histogram (0-50X)



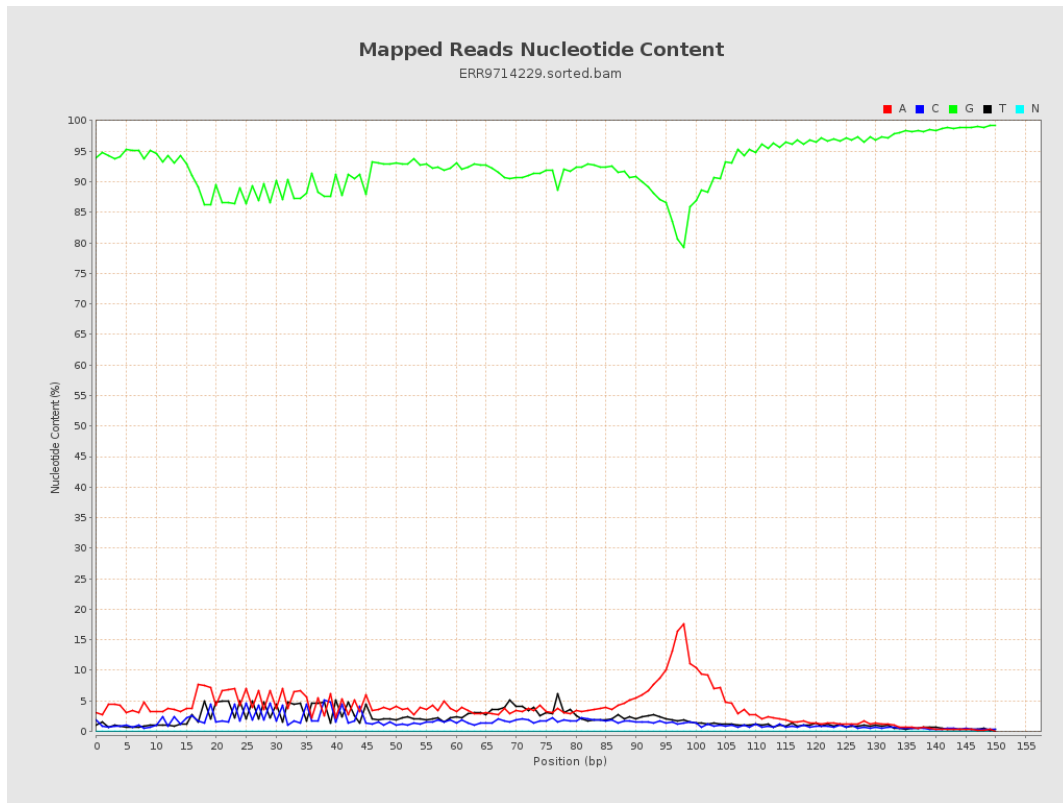
6. Results : Genome Fraction Coverage



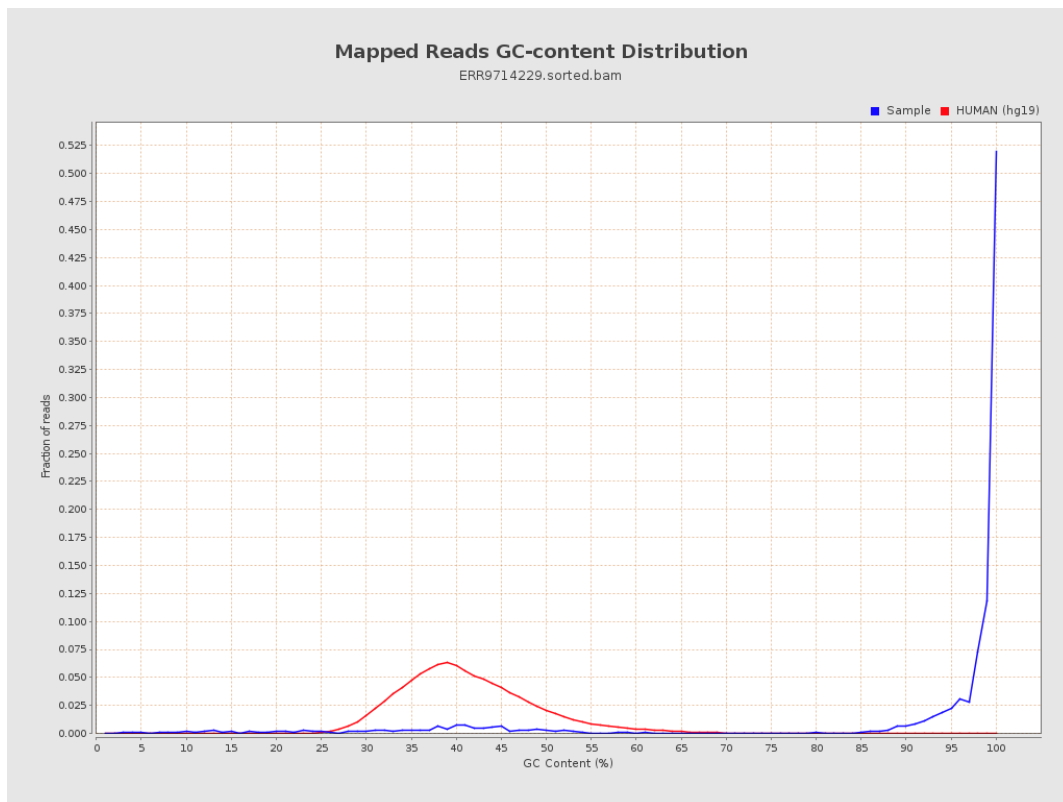
7. Results : Duplication Rate Histogram



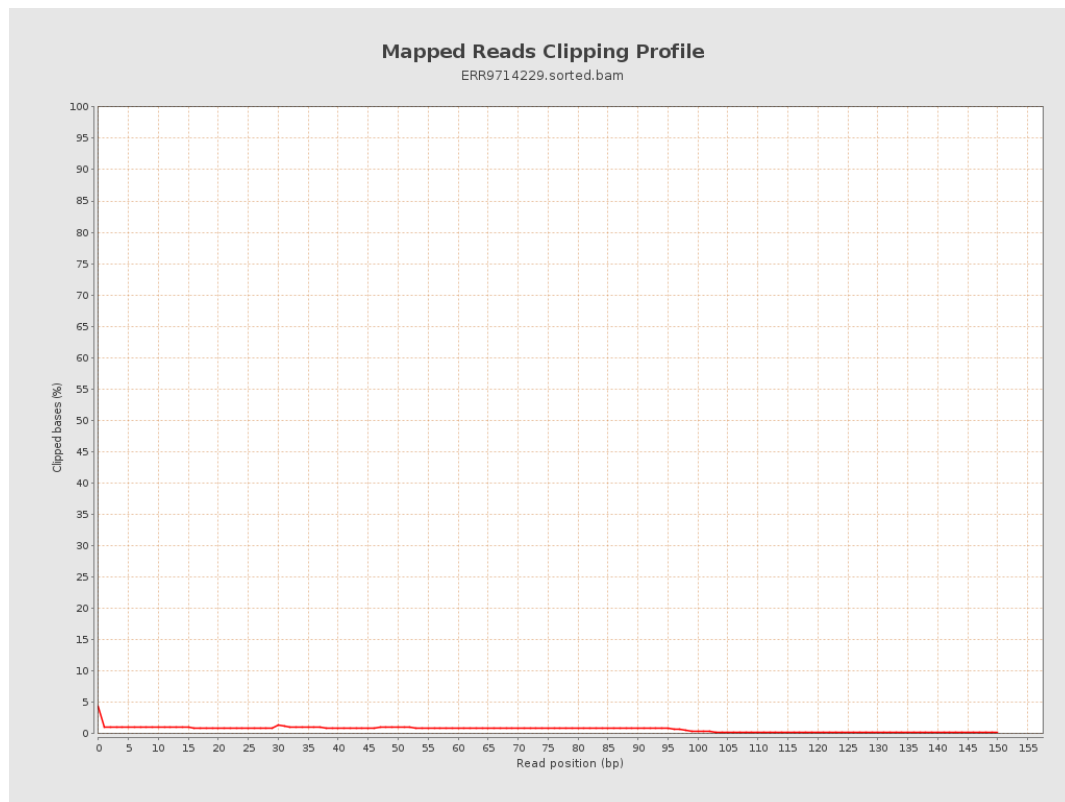
8. Results : Mapped Reads Nucleotide Content



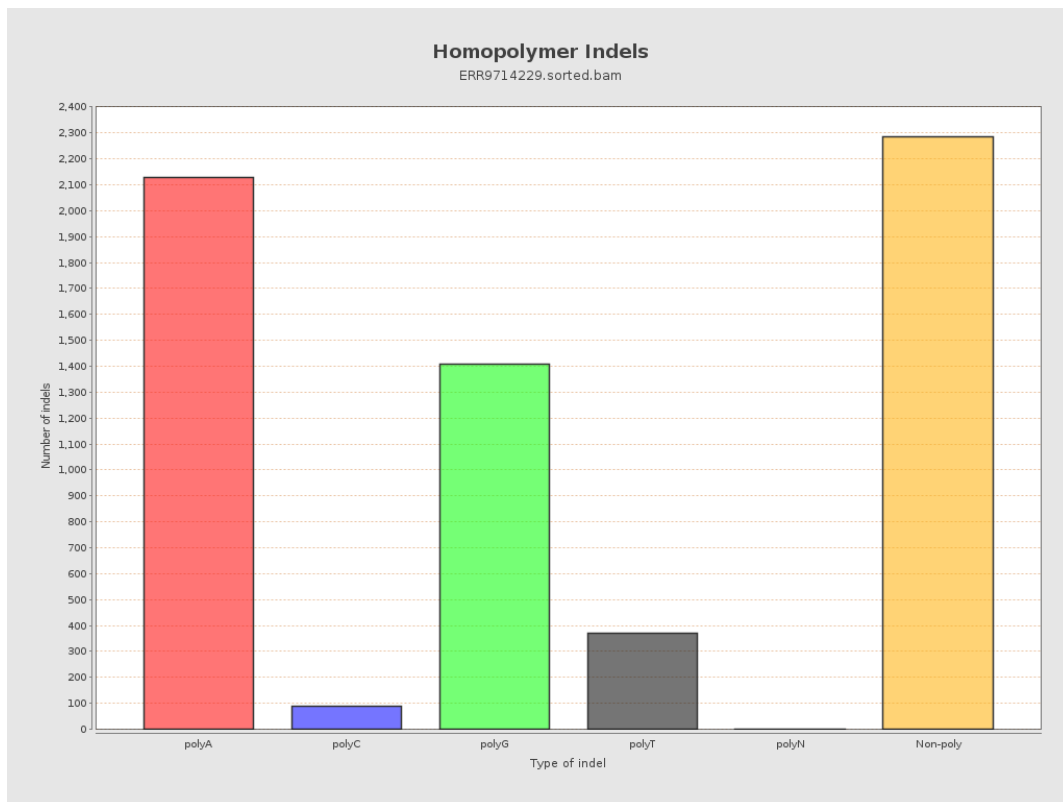
9. Results : Mapped Reads GC-content Distribution



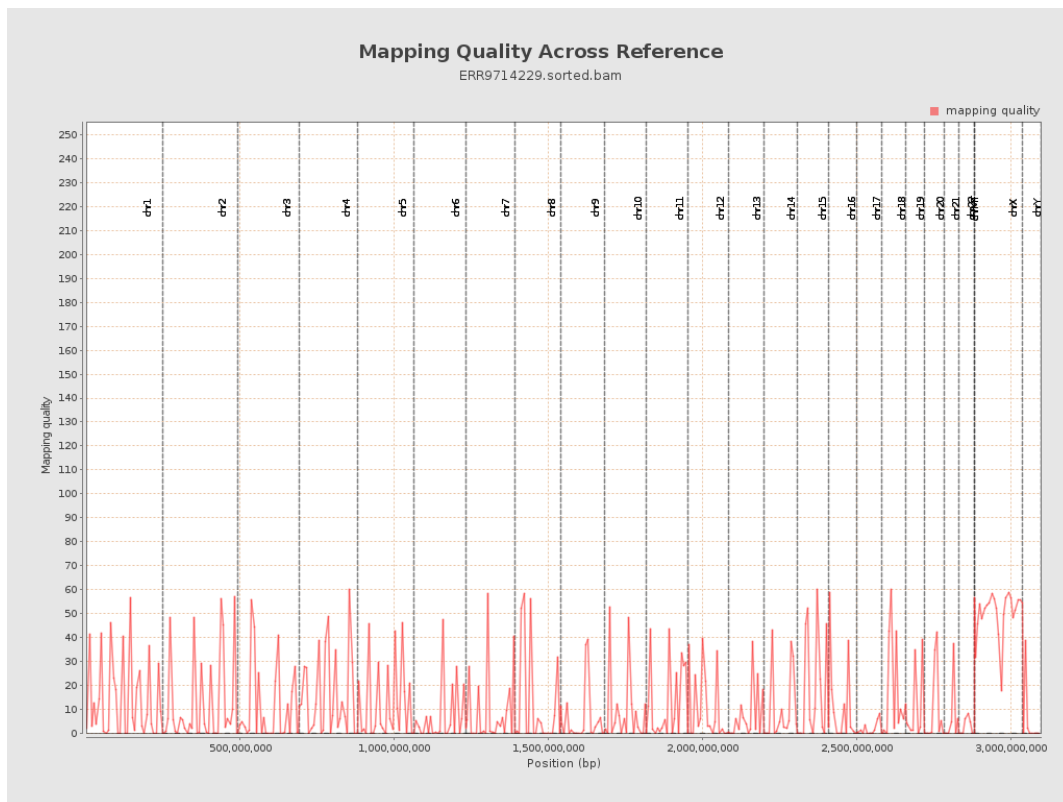
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

