Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:21:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714213.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_ERR9714213 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:21:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	156,724
Mapped reads	25,985 / 16.58%
Unmapped reads	130,739 / 83.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	400 / 0.26%
Read min/max/mean length	30 / 151 / 61.9
Duplicated reads (estimated)	25,276 / 16.13%
Duplication rate	40.13%
Clipped reads	13,858 / 8.84%

2.2. ACGT Content

Number/percentage of A's	65,333 / 2.47%
Number/percentage of C's	29,797 / 1.13%
Number/percentage of T's	39,416 / 1.49%
Number/percentage of G's	2,511,510 / 94.91%
Number/percentage of N's	53 / 0%
GC Percentage	96.04%

2.3. Coverage

Mean	0.0009

Standard Deviation	3.2438

2.4. Mapping Quality

Mean Mapping Quality	6.85

2.5. Mismatches and indels

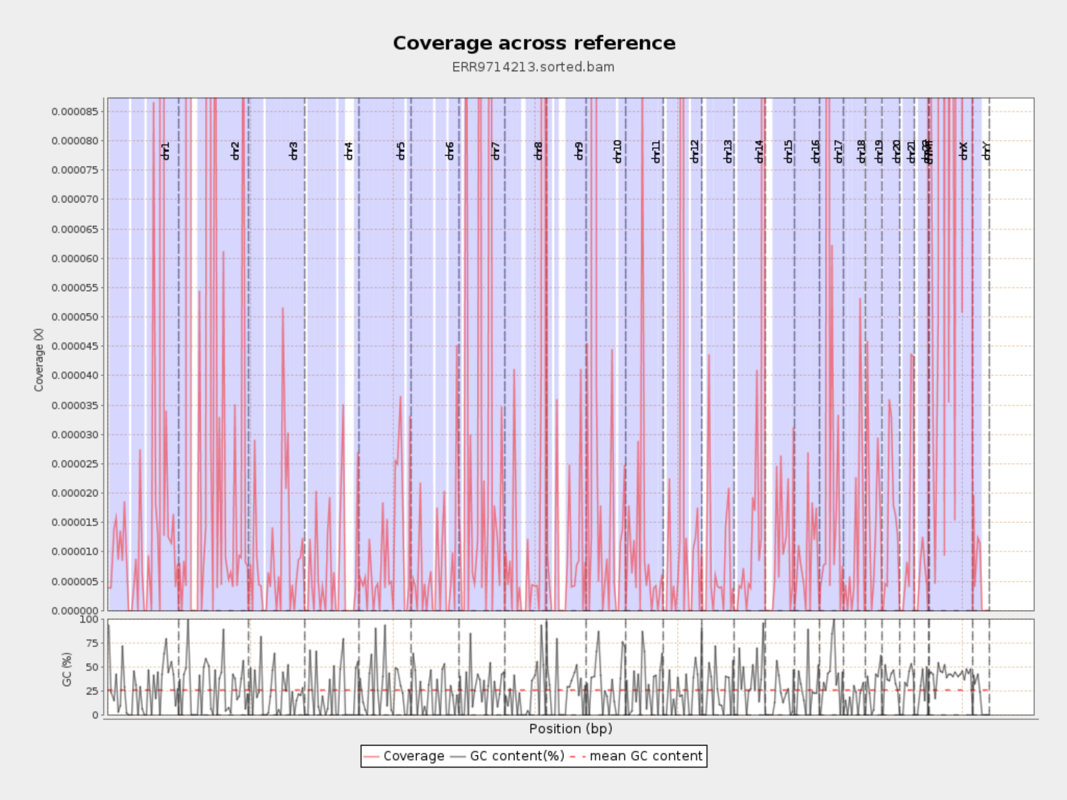
General error rate	3.15%
Mismatches	64,997
Insertions	2,745
Mapped reads with at least one insertion	7.27%
Deletions	1,229
Mapped reads with at least one deletion	4.56%
Homopolymer indels	61.1%

2.6. Chromosome stats

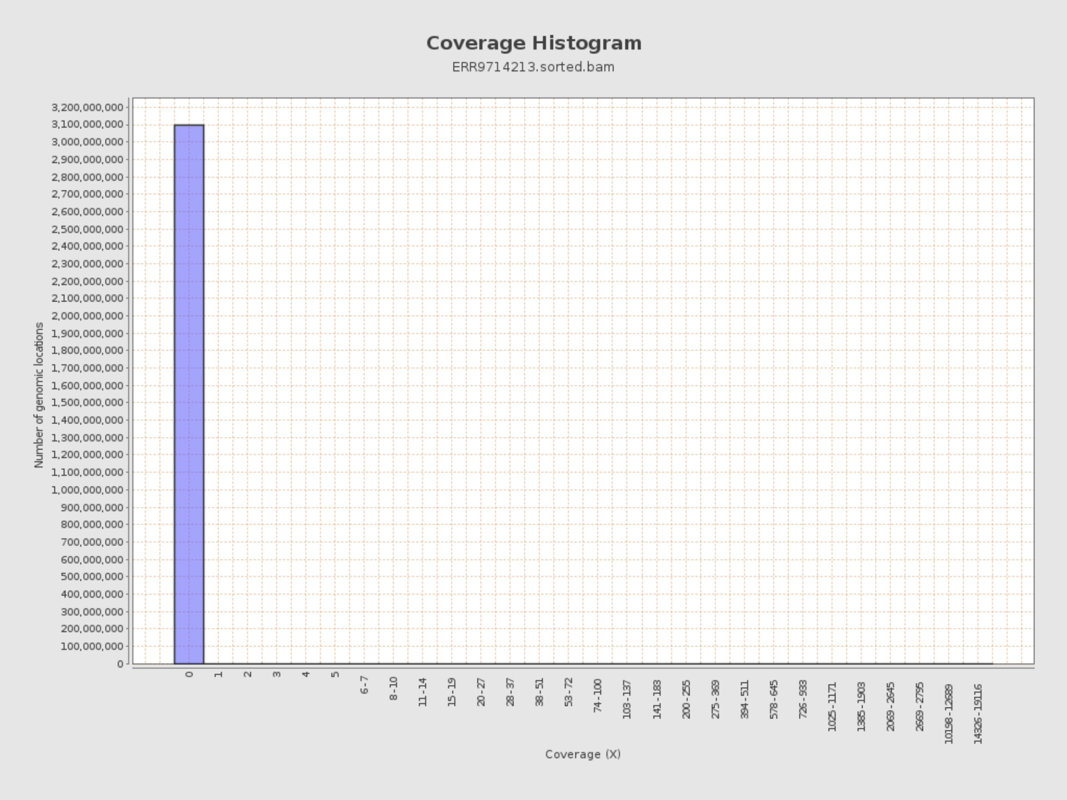
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21165	0.0001	0.2114
chr2	243199373	2514961	0.0103	11.5691
chr3	198022430	1801	0	0.004
chr4	191154276	1272	0	0.0042
chr5	180915260	1617	0	0.0034
chr6	171115067	1253	0	0.0038
chr7	159138663	5688	0	0.0294

chr8	146364022	10738	0.0001	0.0656
chr9	141213431	1297	0	0.0046
chr10	135534747	19524	0.0001	0.2743
chr11	135006516	1585	0	0.0092
chr12	133851895	3289	0	0.0228
chr13	115169878	812	0	0.0042
chr14	107349540	3349	0	0.039
chr15	102531392	946	0	0.0048
chr16	90354753	830	0	0.0042
chr17	81195210	3370	0	0.0378
chr18	78077248	815	0	0.005
chr19	59128983	955	0	0.0074
chr20	63025520	965	0	0.0072
chr21	48129895	674	0	0.0051
chr22	51304566	260	0	0.0025
chrMT	16571	294	0.0177	0.132
chrX	155270560	53874	0.0003	0.0745
chrY	59373566	318	0	0.0028

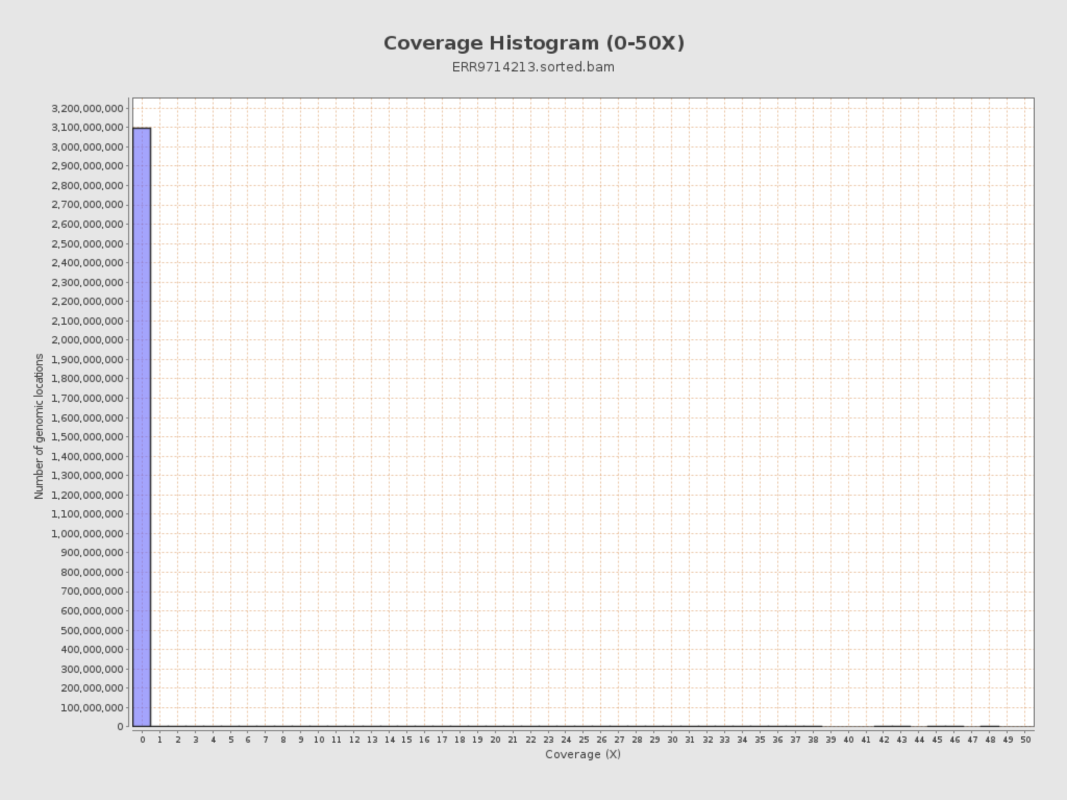
3. Results : Coverage across reference



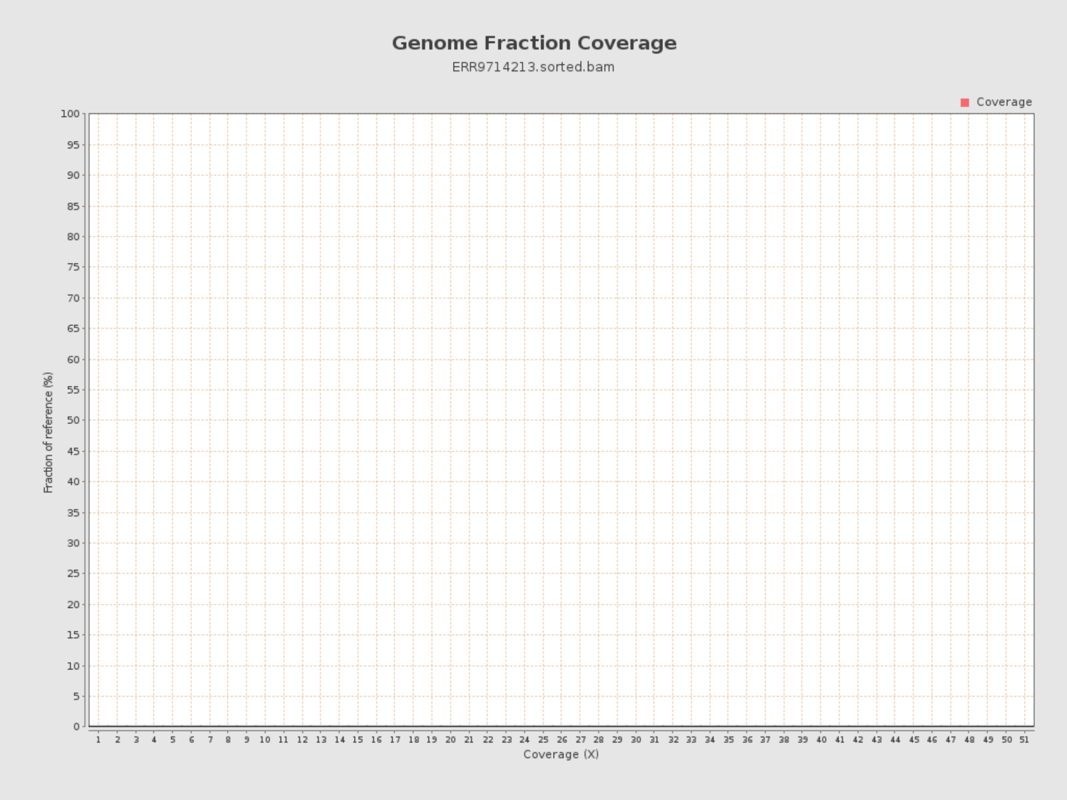
4. Results : Coverage Histogram



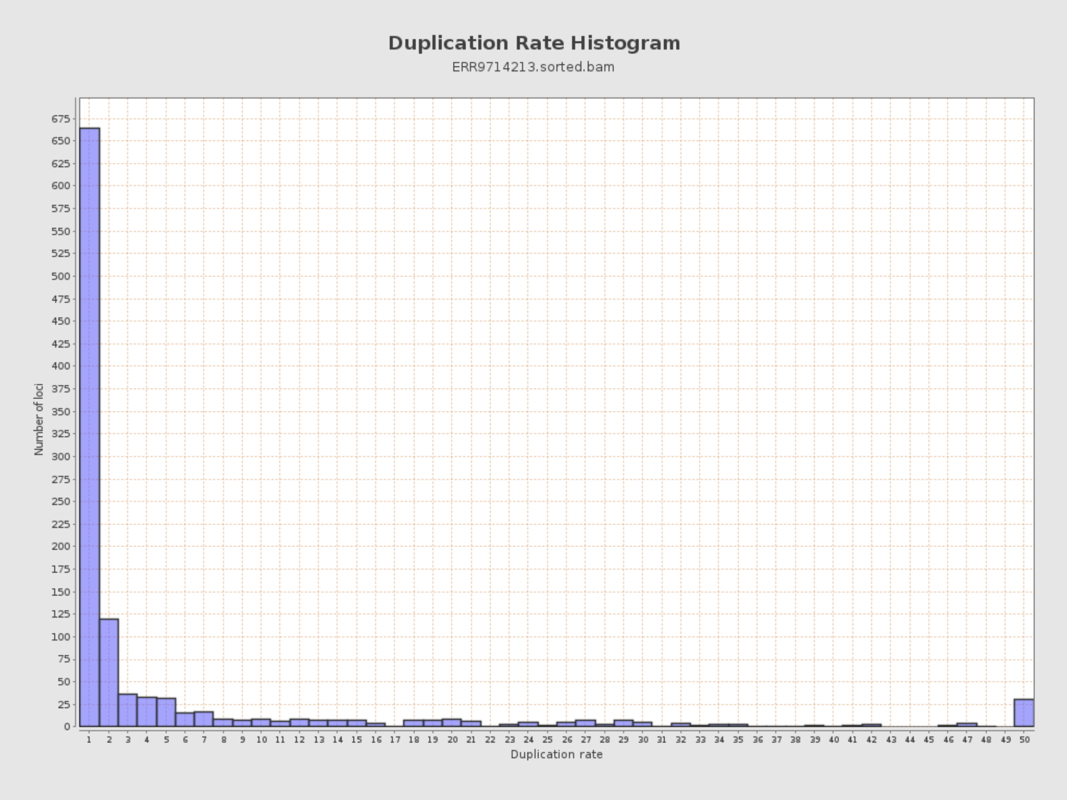
5. Results : Coverage Histogram (0-50X)



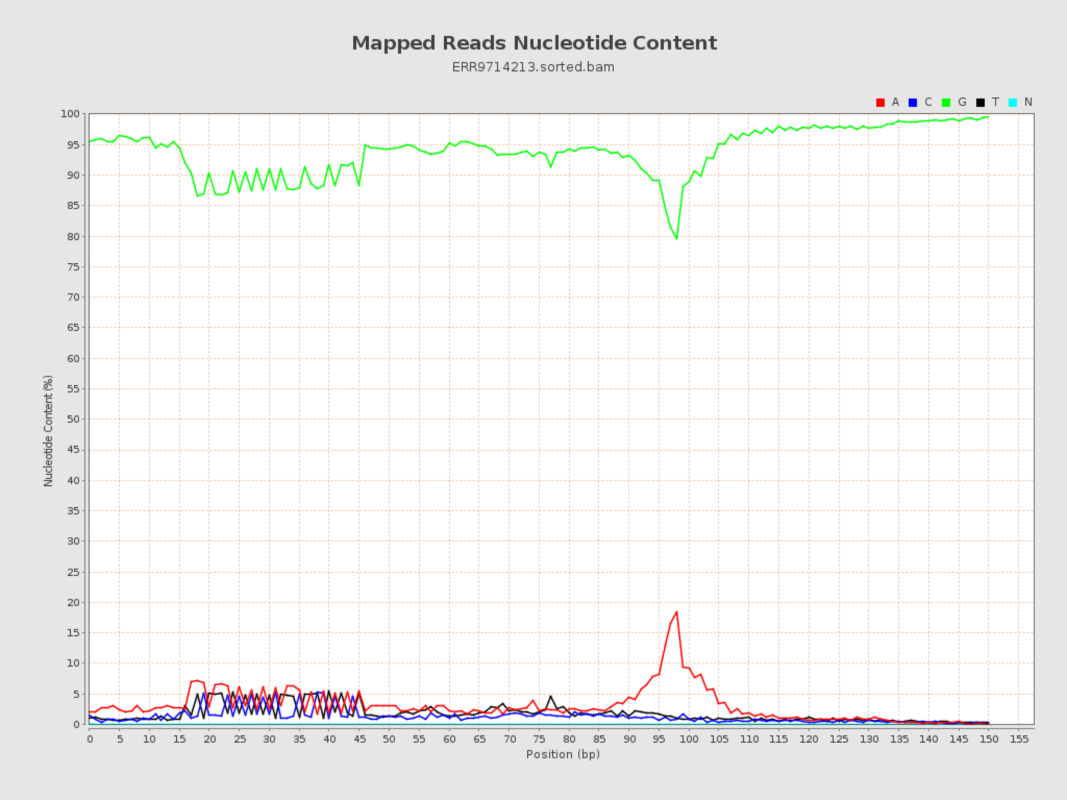
6. Results : Genome Fraction Coverage



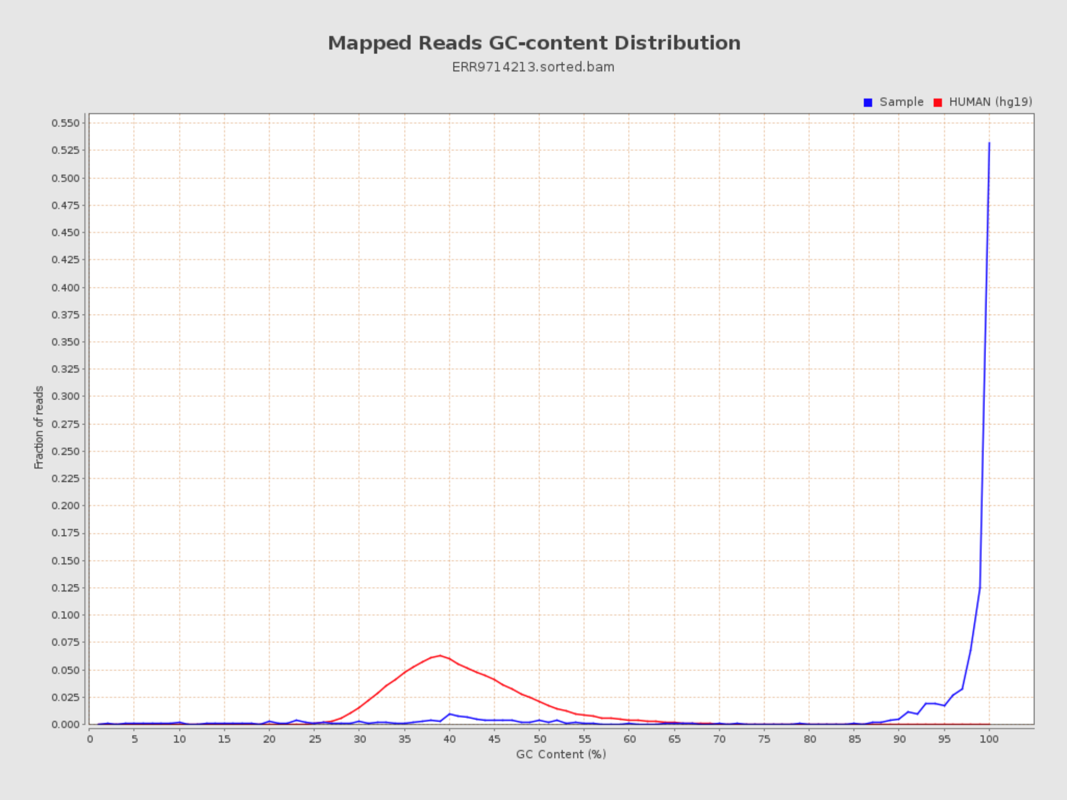
7. Results : Duplication Rate Histogram



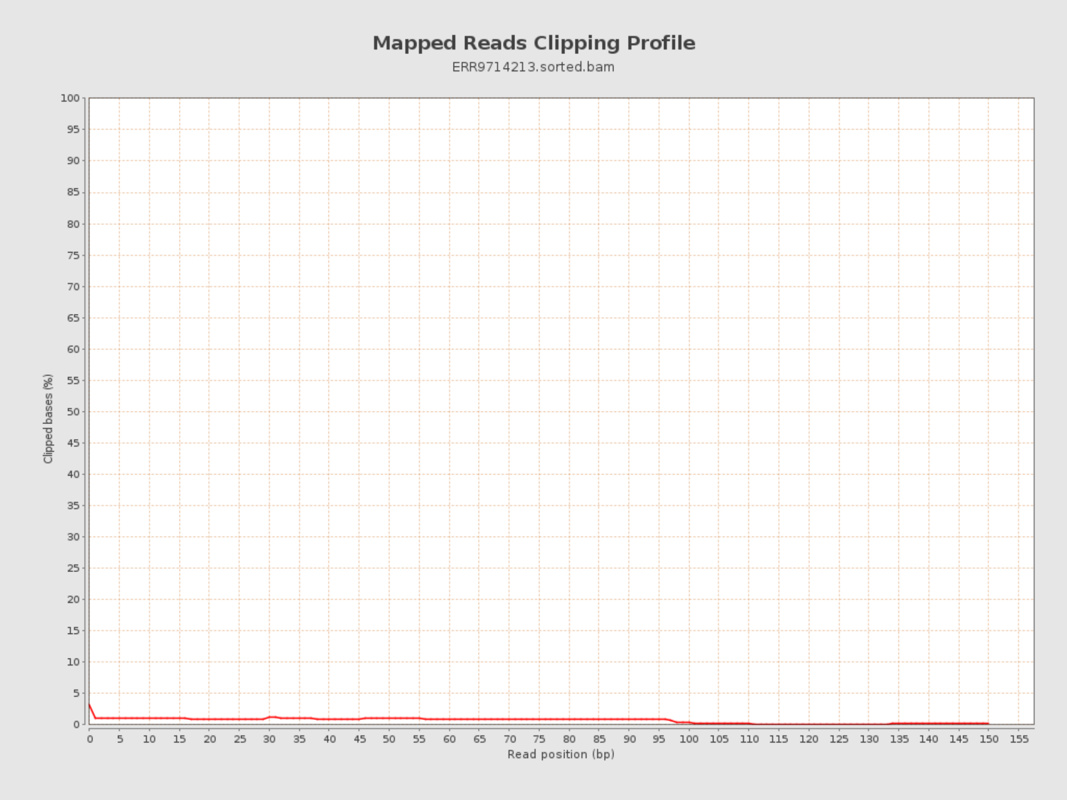
8. Results : Mapped Reads Nucleotide Content



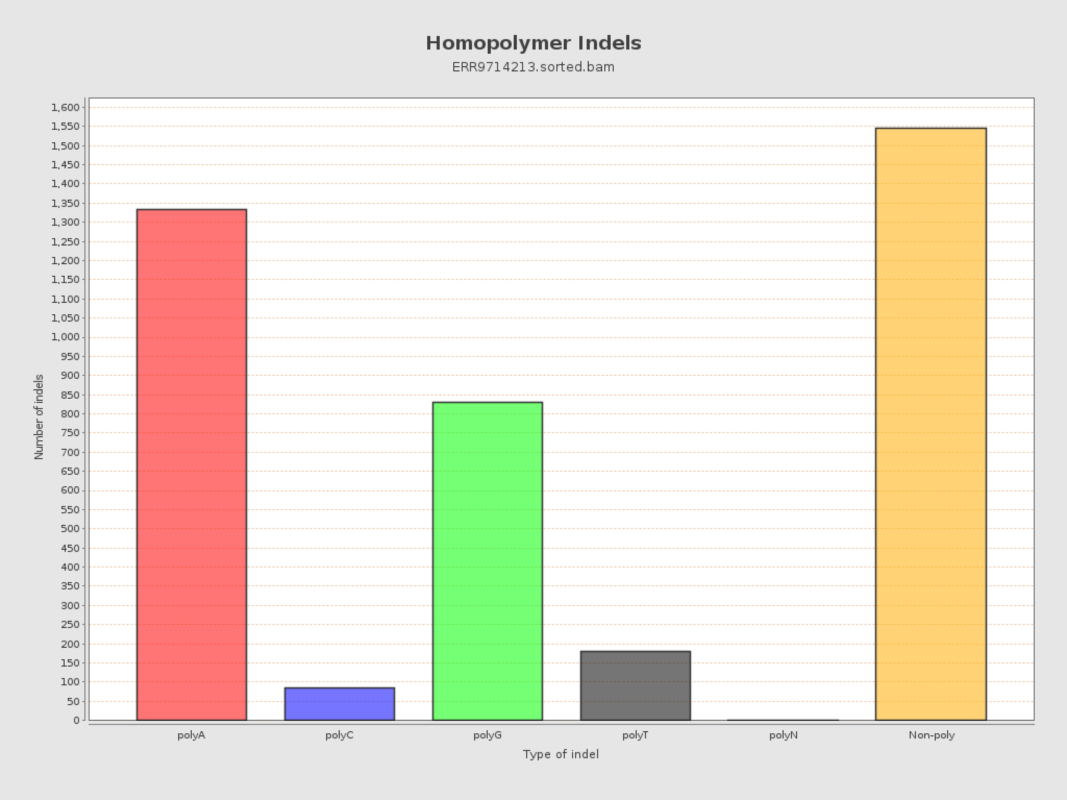
9. Results : Mapped Reads GC-content Distribution



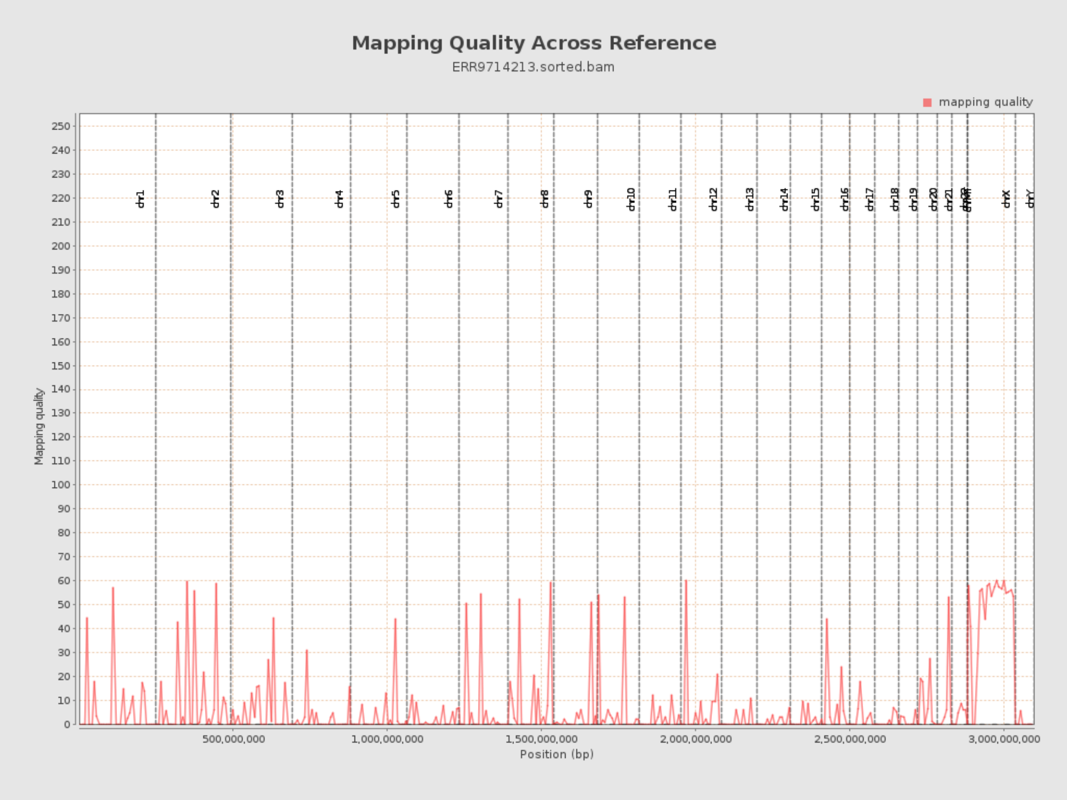
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram