Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:17:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714211.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_ERR9714211 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:17:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	124,278
Mapped reads	17,248 / 13.88%
Unmapped reads	107,030 / 86.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	443 / 0.36%
Read min/max/mean length	30 / 151 / 66.57
Duplicated reads (estimated)	15,834 / 12.74%
Duplication rate	37.05%
Clipped reads	10,797 / 8.69%

2.2. ACGT Content

Number/percentage of A's	146,281 / 8.1%
Number/percentage of C's	94,646 / 5.24%
Number/percentage of T's	114,655 / 6.35%
Number/percentage of G's	1,450,136 / 80.3%
Number/percentage of N's	76 / 0%
GC Percentage	85.55%

2.3. Coverage

Mean	0.0006

Standard Deviation	1.752

2.4. Mapping Quality

Mean Mapping Quality	13.37

2.5. Mismatches and indels

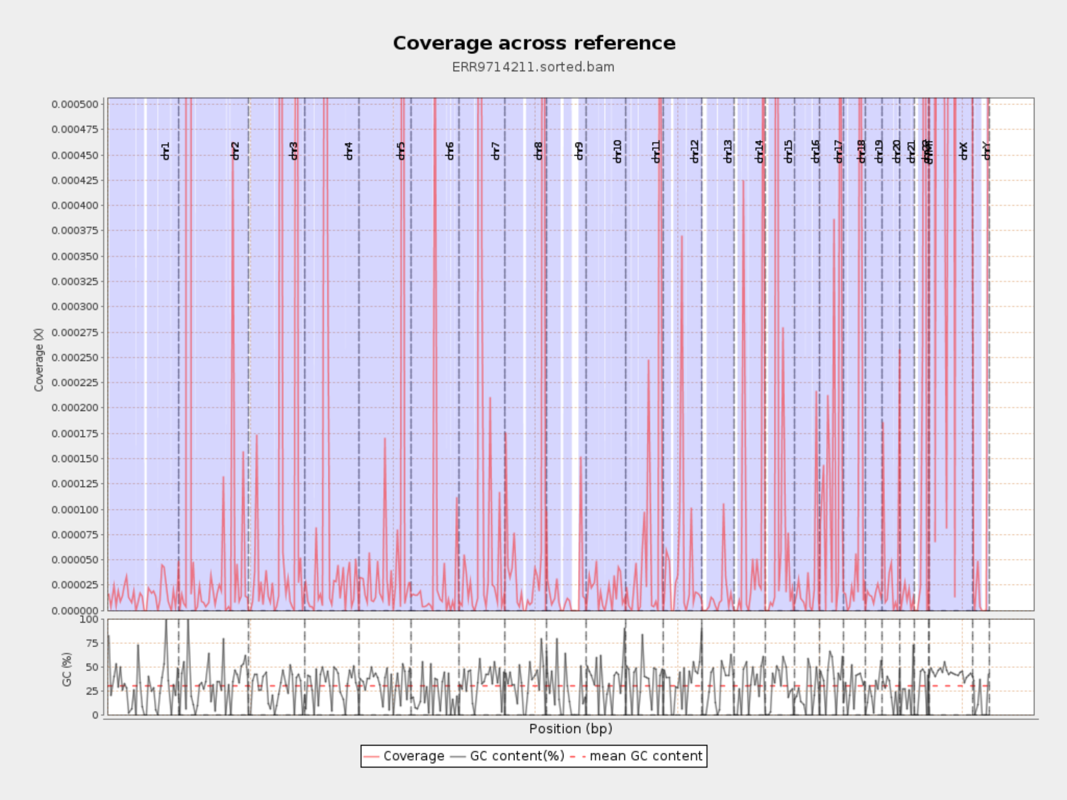
General error rate	3.29%
Mismatches	49,729
Insertions	1,638
Mapped reads with at least one insertion	6.48%
Deletions	1,780
Mapped reads with at least one deletion	9.97%
Homopolymer indels	48.89%

2.6. Chromosome stats

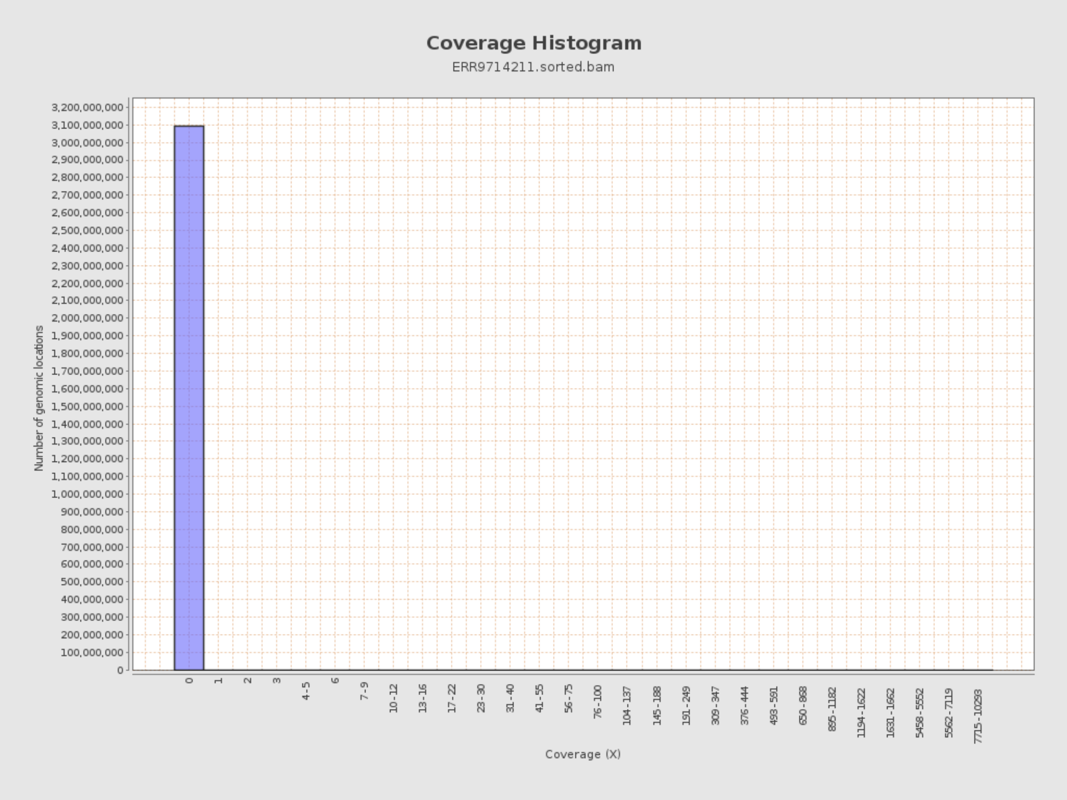
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3817	0	0.0053
chr2	243199373	1375808	0.0057	6.2445
chr3	198022430	24857	0.0001	0.0819
chr4	191154276	15341	0.0001	0.0484
chr5	180915260	14592	0.0001	0.0491
chr6	171115067	7431	0	0.0372
chr7	159138663	27323	0.0002	0.1305

chr8	146364022	15709	0.0001	0.0778
chr9	141213431	2516	0	0.0151
chr10	135534747	2659	0	0.0056
chr11	135006516	11839	0.0001	0.0511
chr12	133851895	6475	0	0.0267
chr13	115169878	1667	0	0.007
chr14	107349540	10209	0.0001	0.0422
chr15	102531392	13835	0.0001	0.0835
chr16	90354753	2798	0	0.0131
chr17	81195210	14272	0.0002	0.0586
chr18	78077248	7545	0.0001	0.055
chr19	59128983	924	0	0.0041
chr20	63025520	2747	0	0.0188
chr21	48129895	635	0	0.0049
chr22	51304566	10636	0.0002	0.1015
chrMT	16571	0	0	0
chrX	155270560	239305	0.0015	0.2617
chrY	59373566	5171	0.0001	0.0158

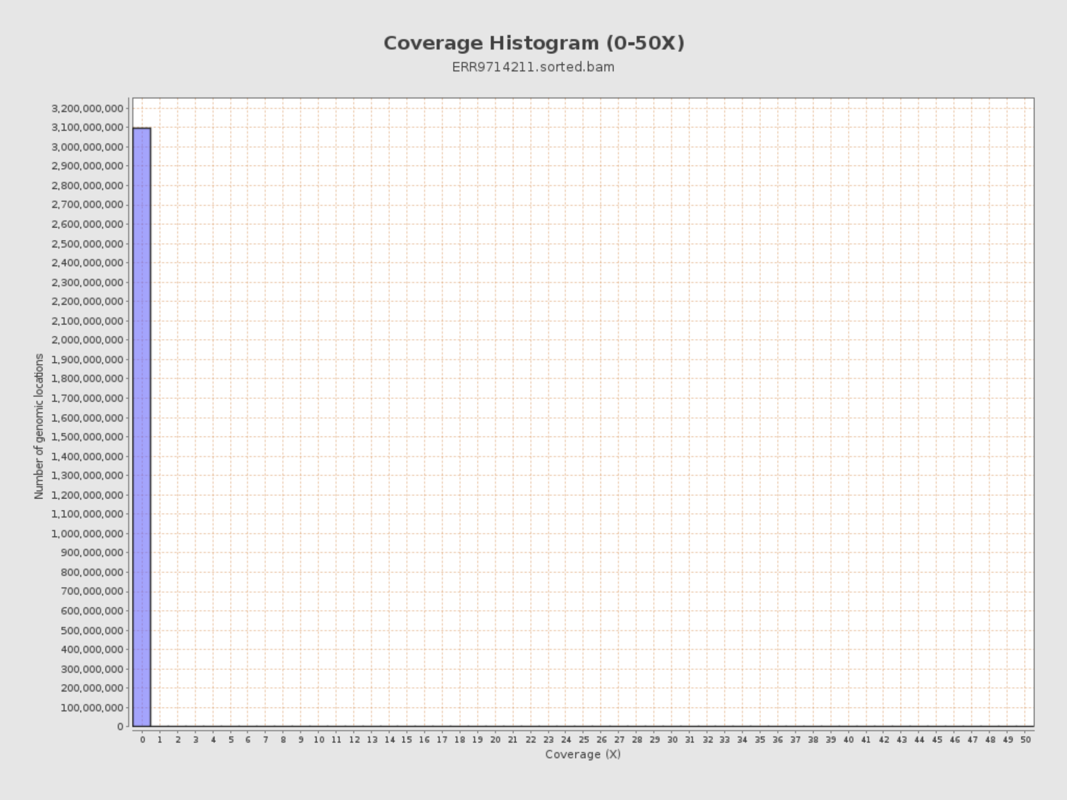
3. Results : Coverage across reference



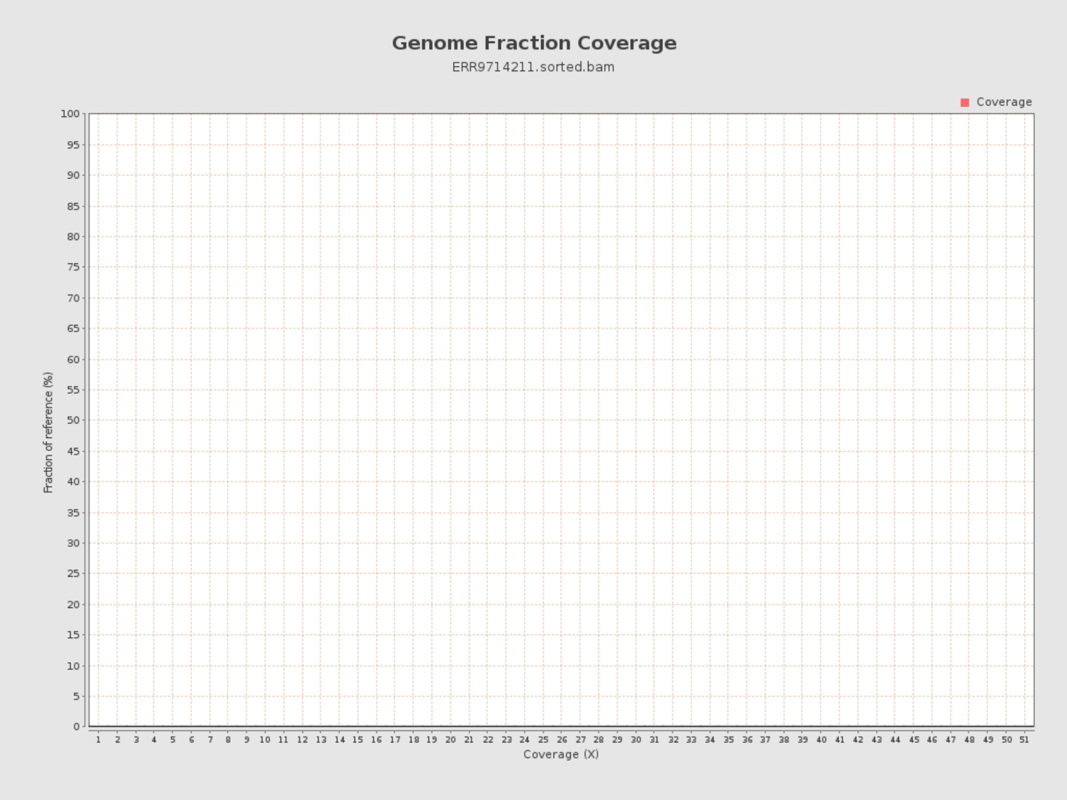
4. Results : Coverage Histogram



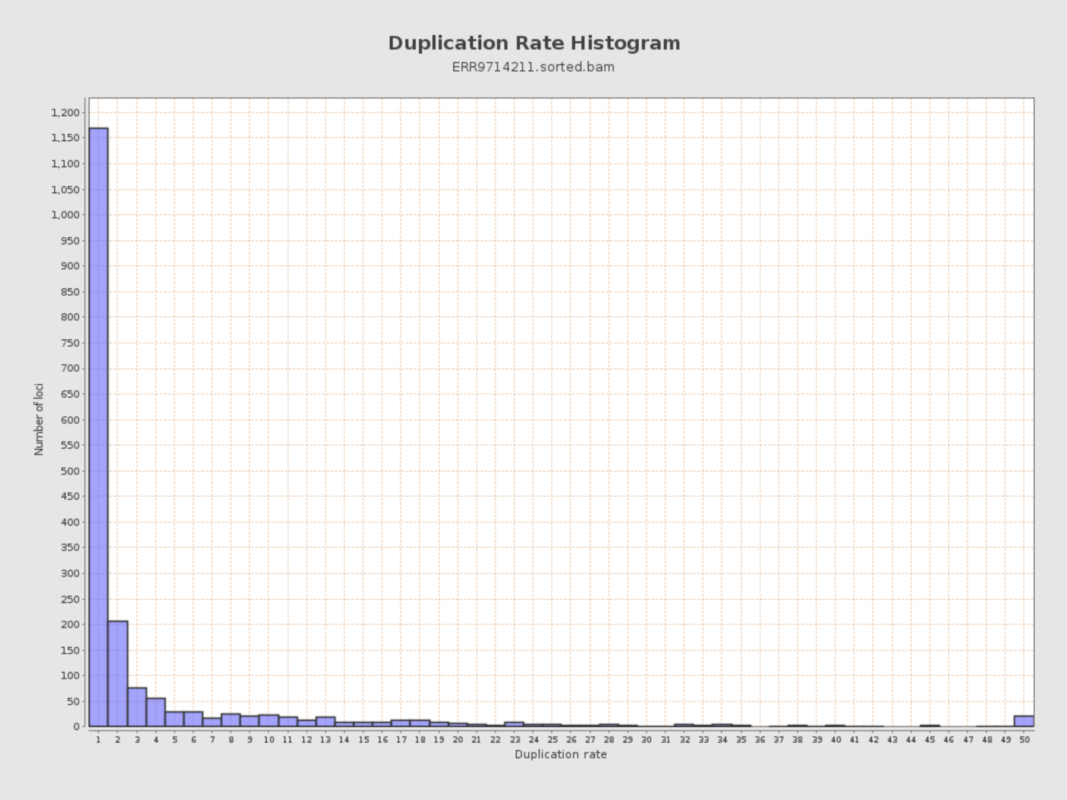
5. Results : Coverage Histogram (0-50X)



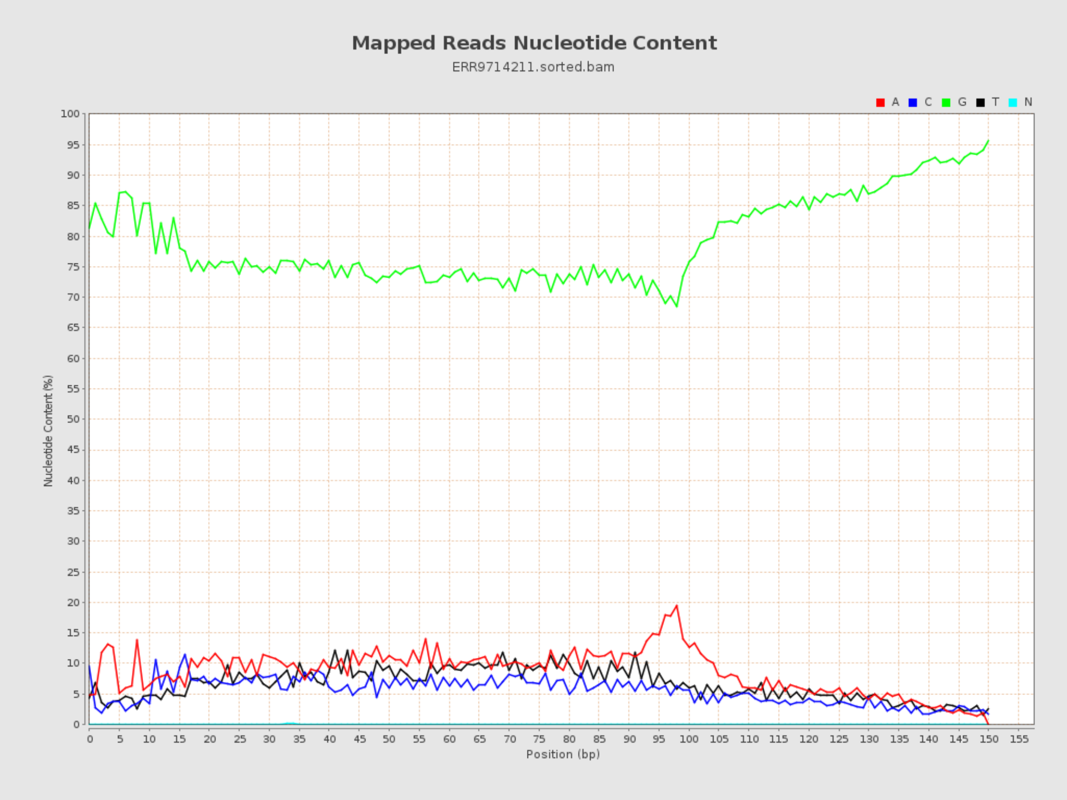
6. Results : Genome Fraction Coverage



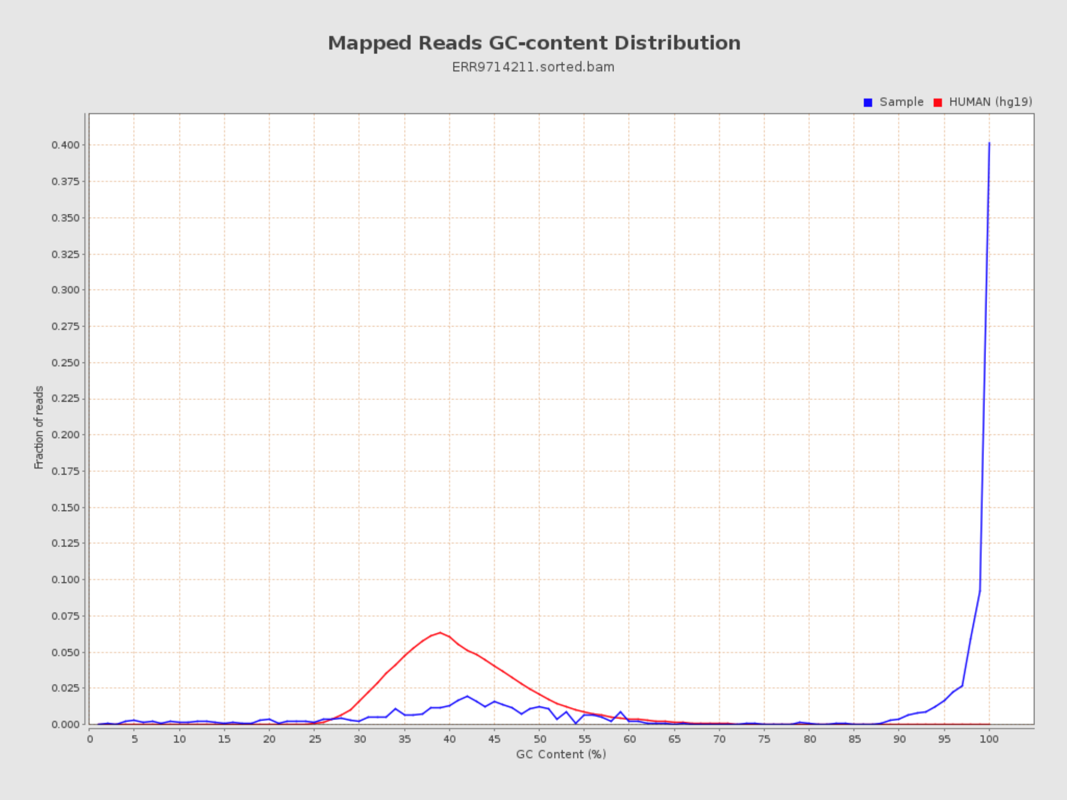
7. Results : Duplication Rate Histogram



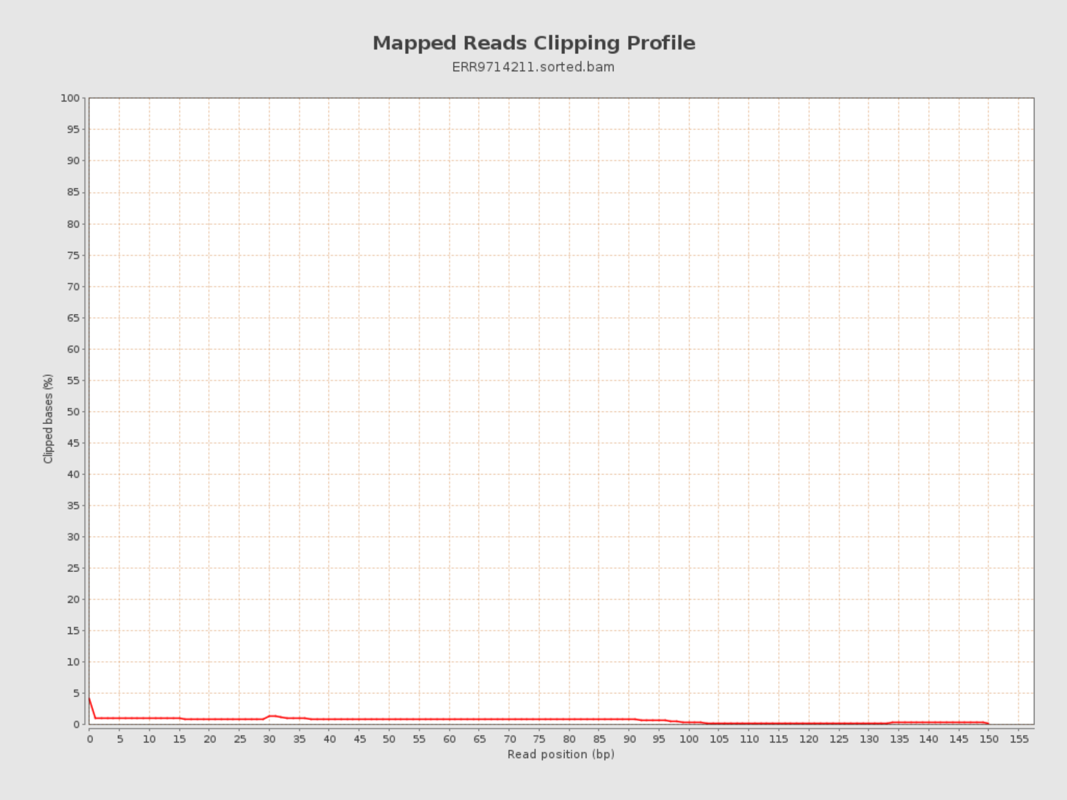
8. Results : Mapped Reads Nucleotide Content



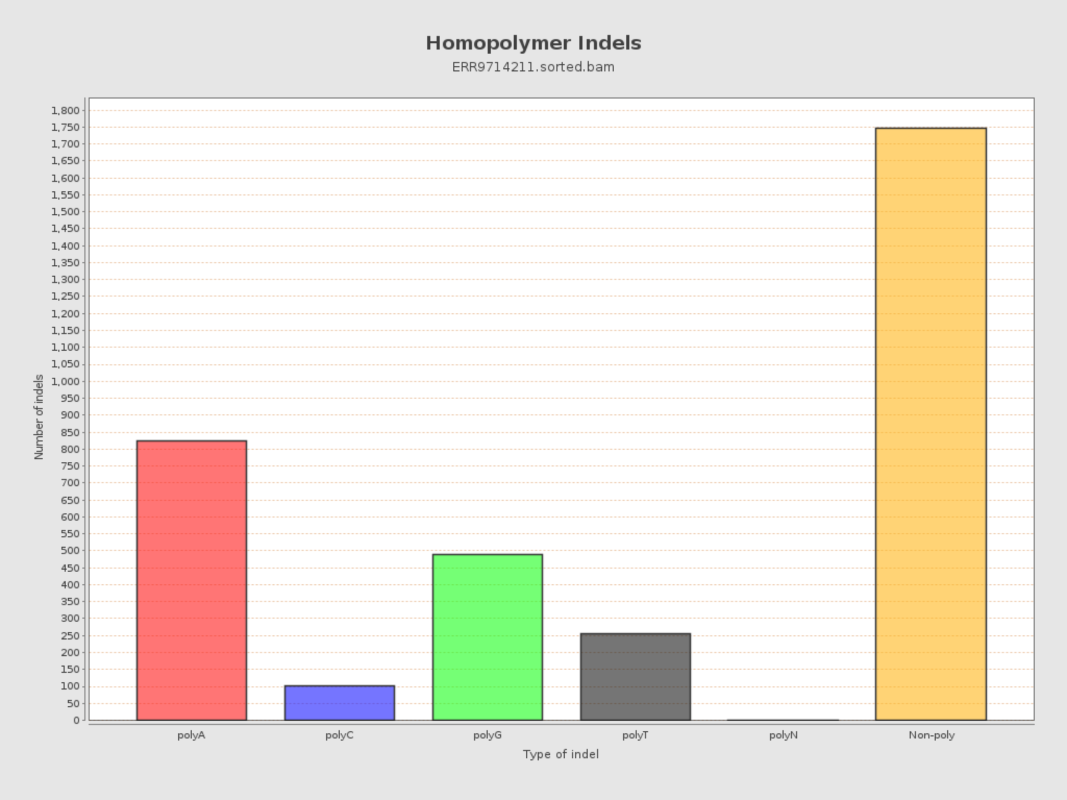
9. Results : Mapped Reads GC-content Distribution



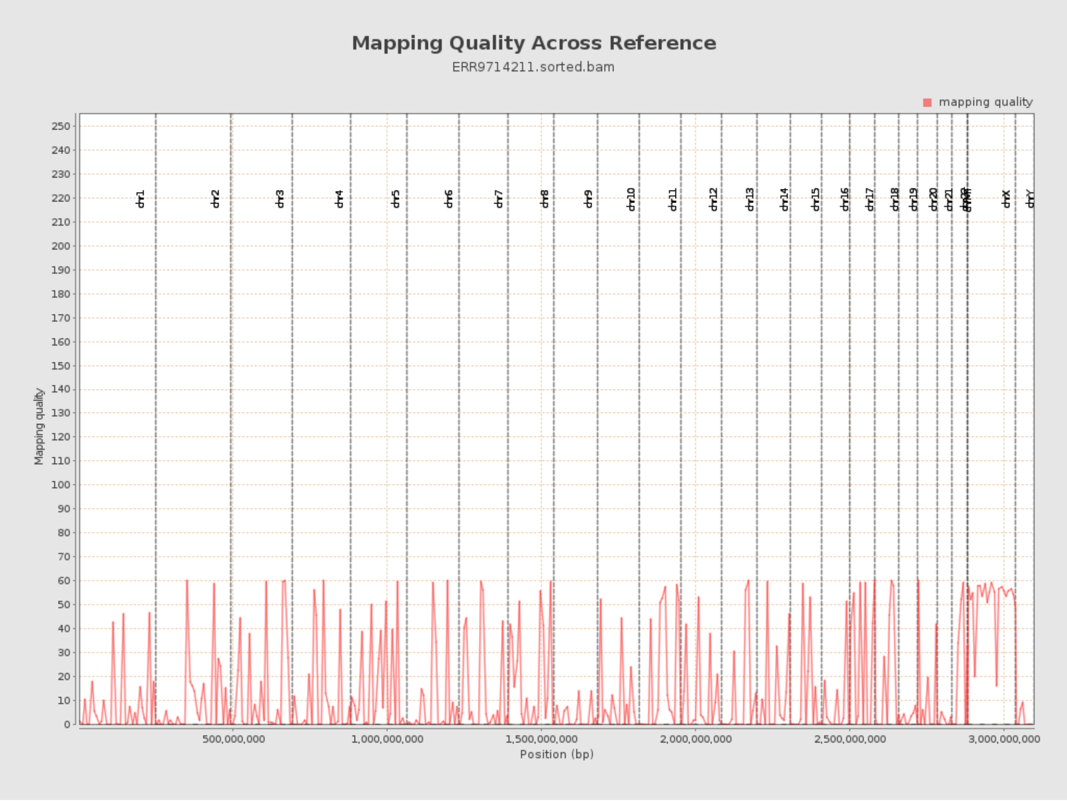
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram