Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:19:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714161.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_ERR9714161 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:19:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	779,886
Mapped reads	682,218 / 87.48%
Unmapped reads	97,668 / 12.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,789 / 0.49%
Read min/max/mean length	30 / 151 / 138.76
Duplicated reads (estimated)	671,387 / 86.09%
Duplication rate	31.85%
Clipped reads	625,550 / 80.21%

2.2. ACGT Content

Number/percentage of A's	25,089,234 / 29.68%
Number/percentage of C's	16,958,866 / 20.06%
Number/percentage of T's	23,181,806 / 27.42%
Number/percentage of G's	19,305,187 / 22.84%
Number/percentage of N's	581 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0274

Standard Deviation	92.3444

2.4. Mapping Quality

Mean Mapping Quality	13.87

2.5. Mismatches and indels

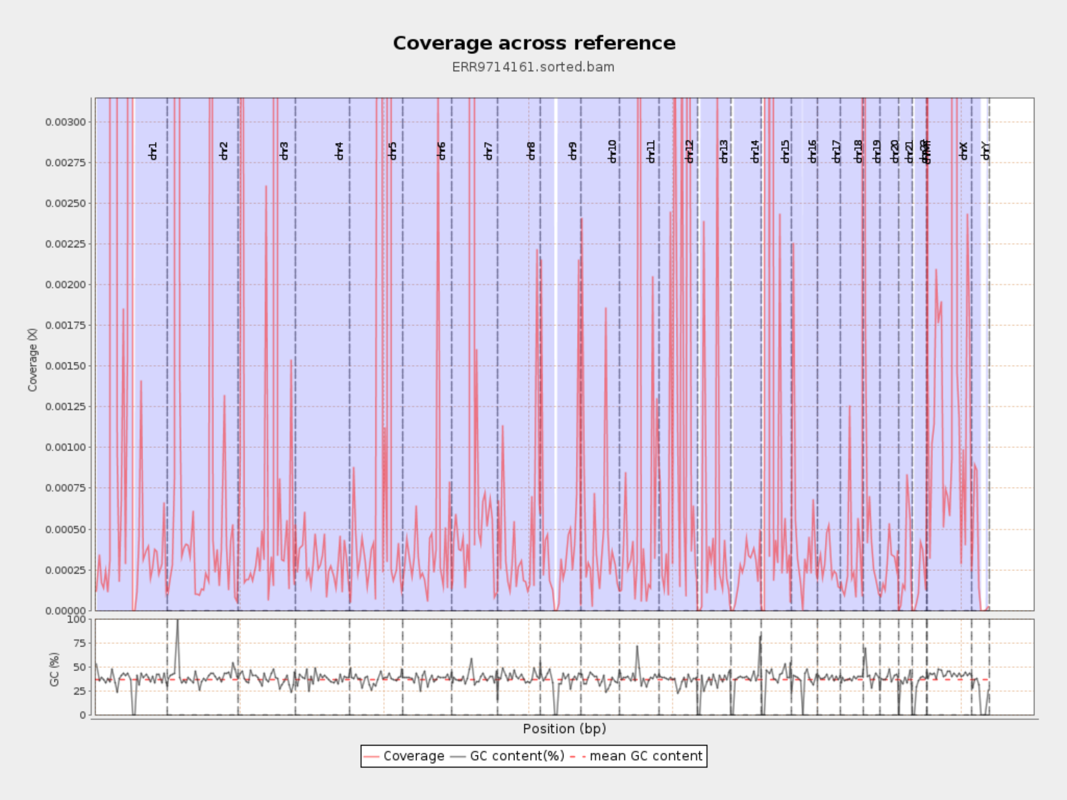
General error rate	3.66%
Mismatches	2,113,491
Insertions	272,003
Mapped reads with at least one insertion	39.17%
Deletions	56,691
Mapped reads with at least one deletion	8.08%
Homopolymer indels	14.18%

2.6. Chromosome stats

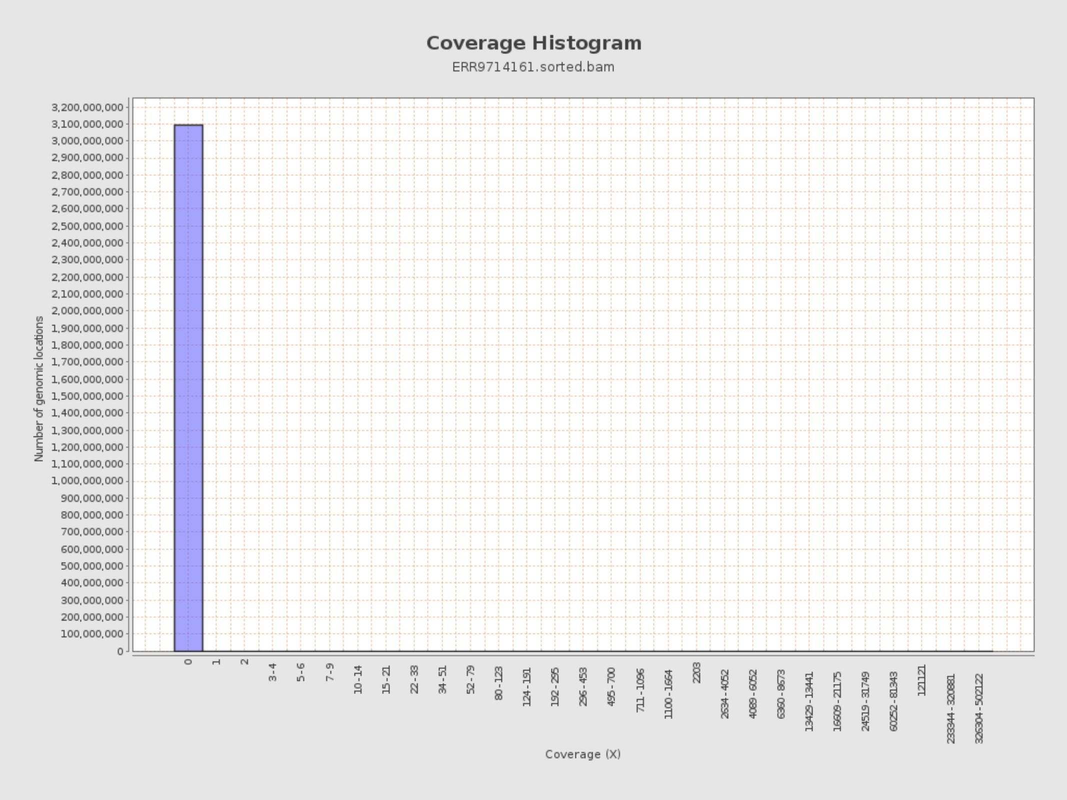
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5276959	0.0212	22.2481
chr2	243199373	1348407	0.0055	5.2801
chr3	198022430	10699156	0.054	62.6192
chr4	191154276	57618	0.0003	0.0526
chr5	180915260	64261852	0.3552	375.3229
chr6	171115067	77672	0.0005	0.2726
chr7	159138663	971497	0.0061	5.7176

chr8	146364022	65620	0.0004	0.1838
chr9	141213431	69184	0.0005	0.283
chr10	135534747	71710	0.0005	0.2576
chr11	135006516	118403	0.0009	0.212
chr12	133851895	174758	0.0013	0.8102
chr13	115169878	63351	0.0006	0.3593
chr14	107349540	26779	0.0002	0.0581
chr15	102531392	427945	0.0042	0.7701
chr16	90354753	43983	0.0005	0.2493
chr17	81195210	23110	0.0003	0.0483
chr18	78077248	25384	0.0003	0.0927
chr19	59128983	141044	0.0024	0.5248
chr20	63025520	17483	0.0003	0.0446
chr21	48129895	13953	0.0003	0.0777
chr22	51304566	10128	0.0002	0.0421
chrMT	16571	8401	0.507	3.8253
chrX	155270560	724463	0.0047	2.9343
chrY	59373566	16784	0.0003	0.125

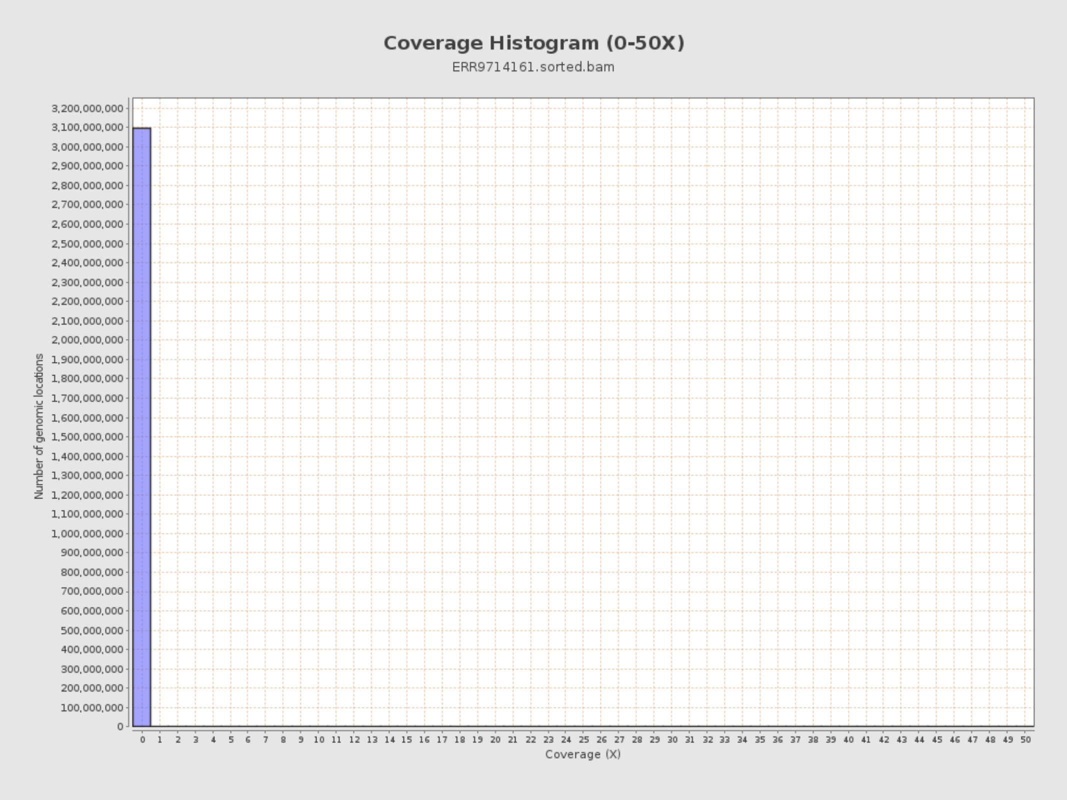
3. Results : Coverage across reference



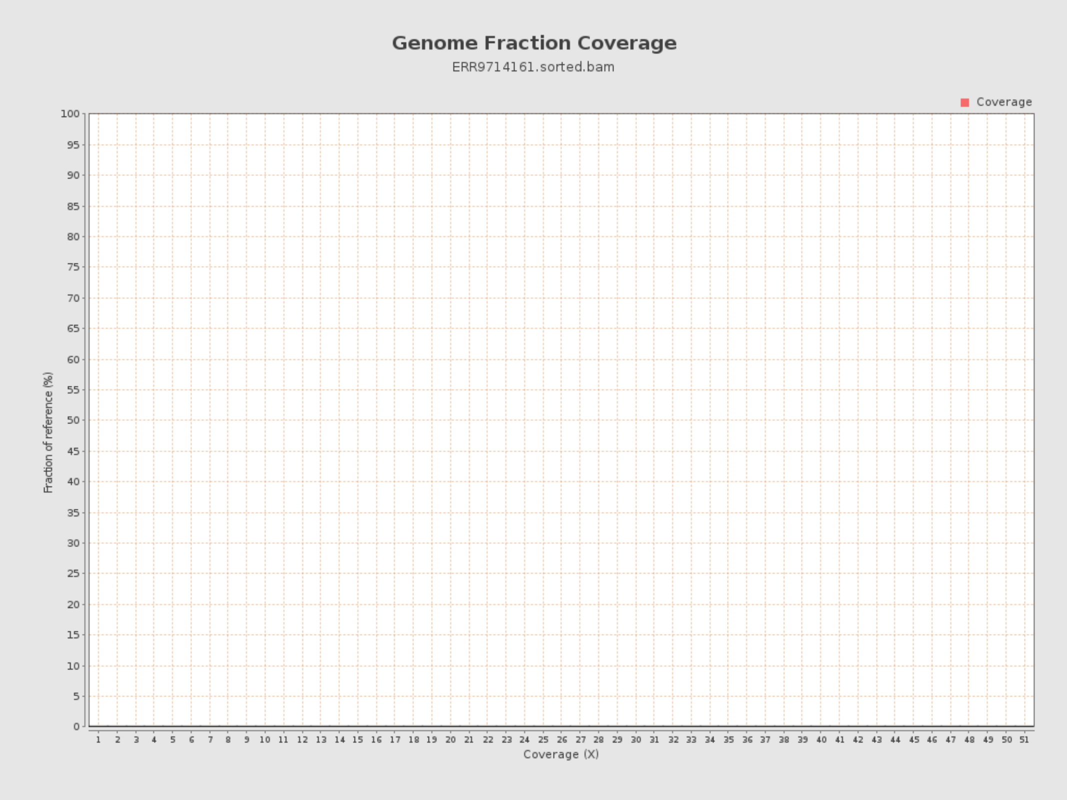
4. Results : Coverage Histogram



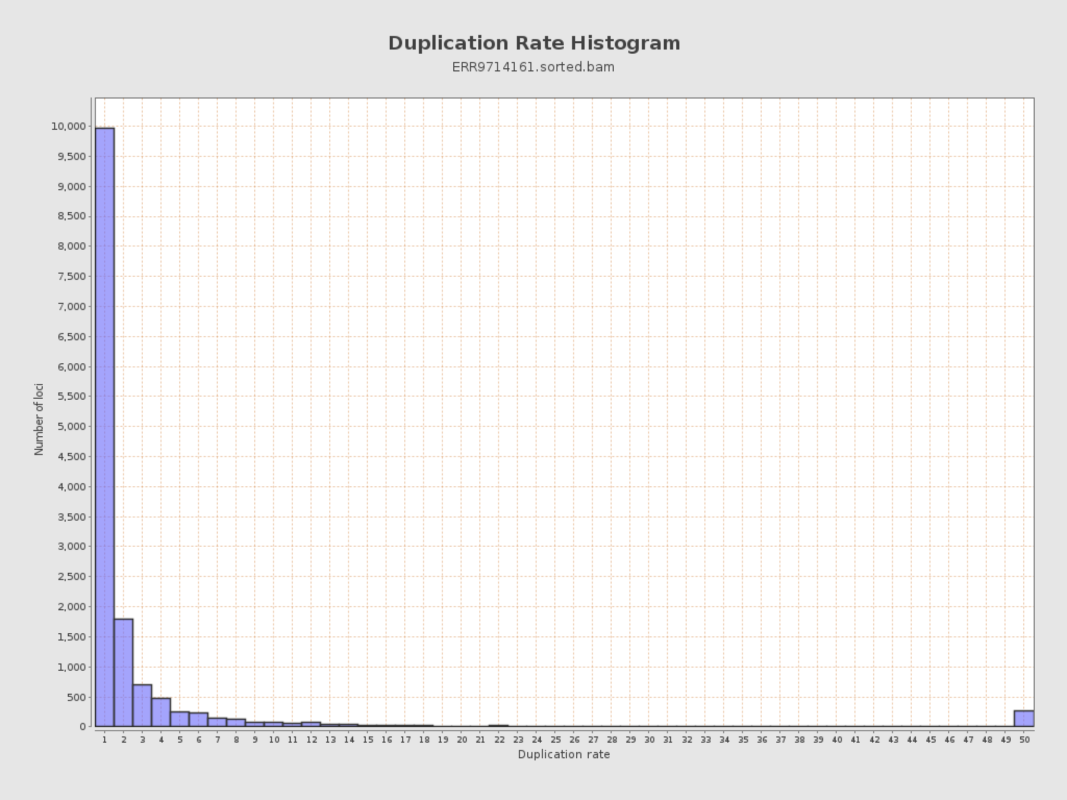
5. Results : Coverage Histogram (0-50X)



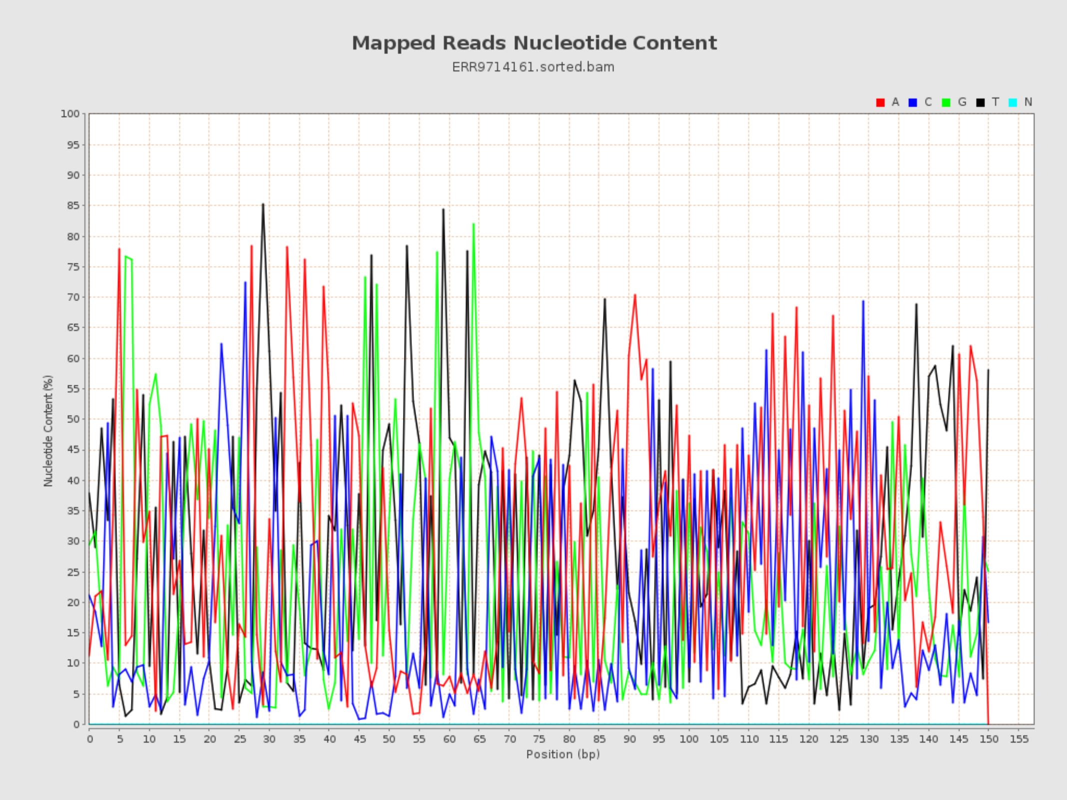
6. Results : Genome Fraction Coverage



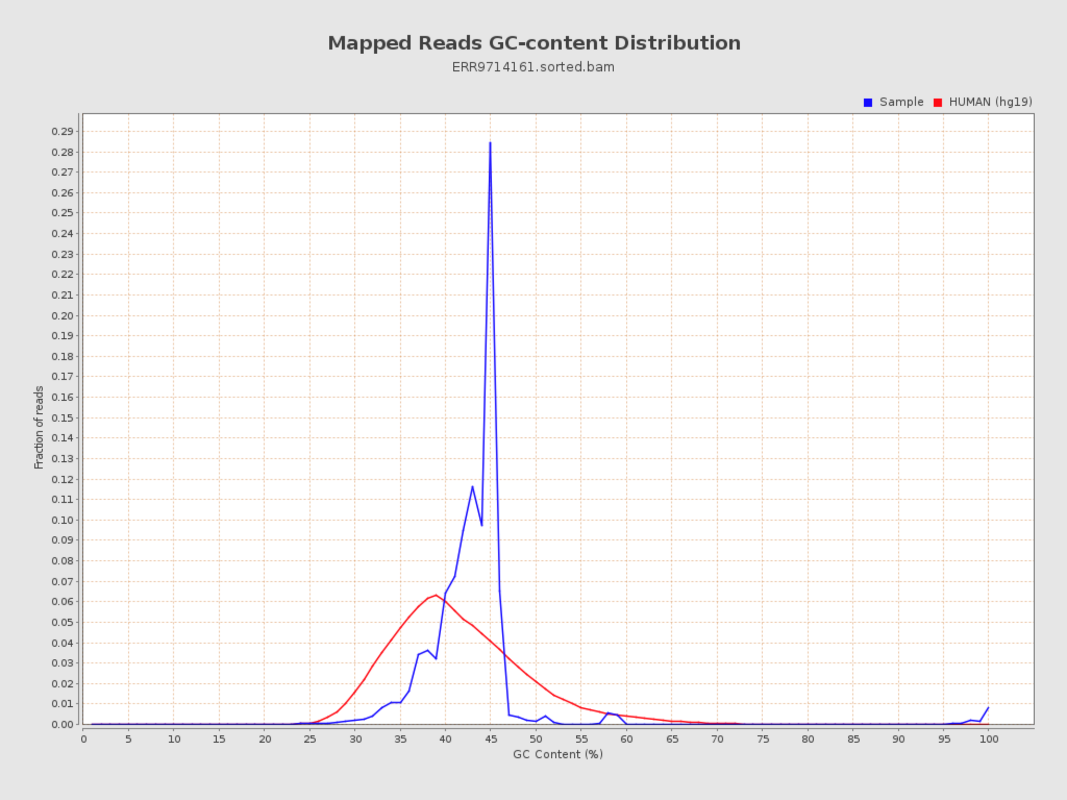
7. Results : Duplication Rate Histogram



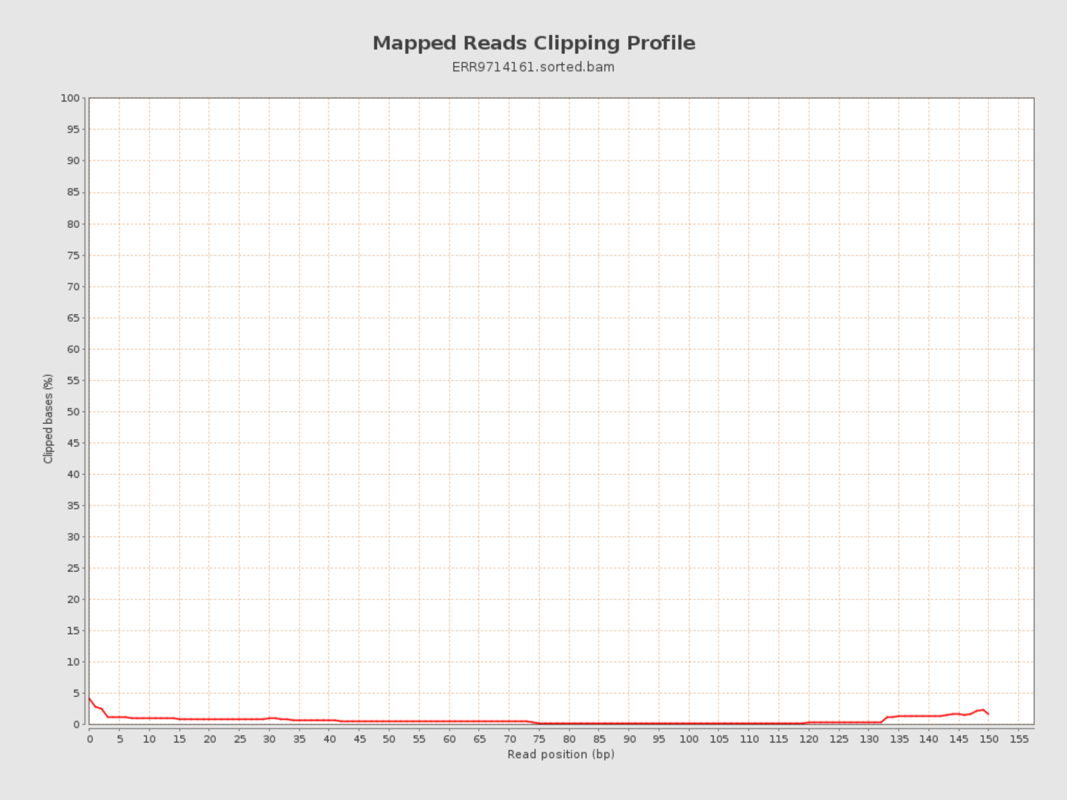
8. Results : Mapped Reads Nucleotide Content



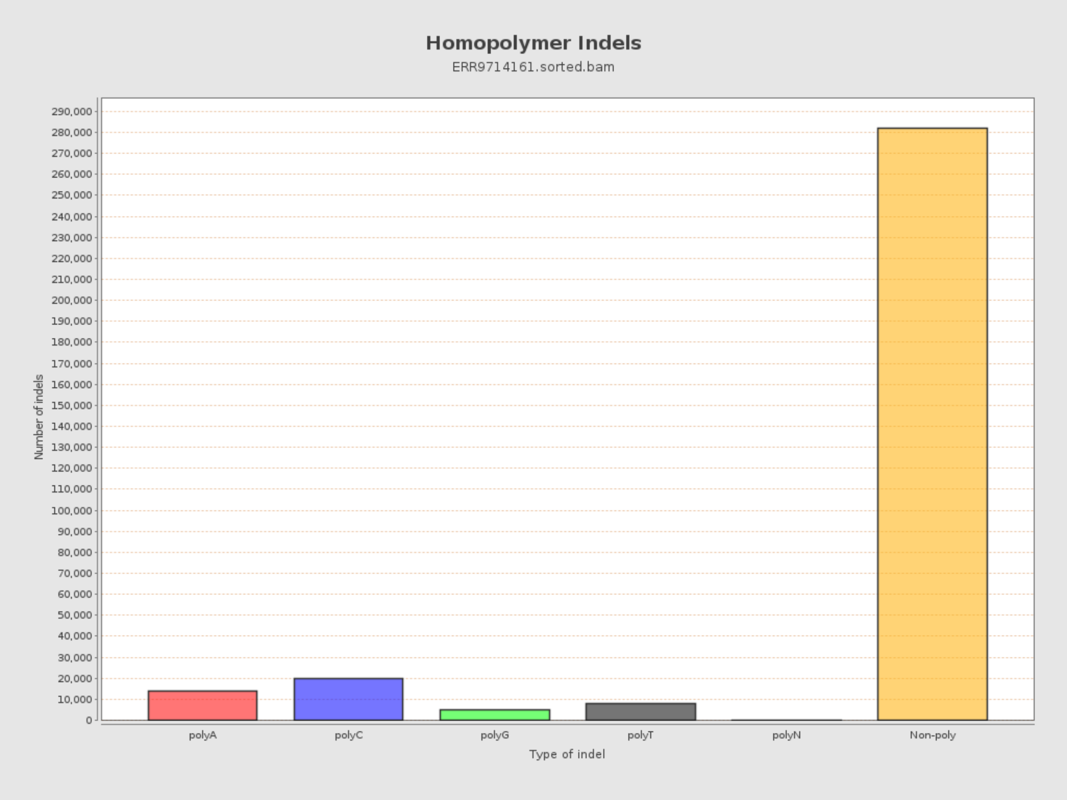
9. Results : Mapped Reads GC-content Distribution



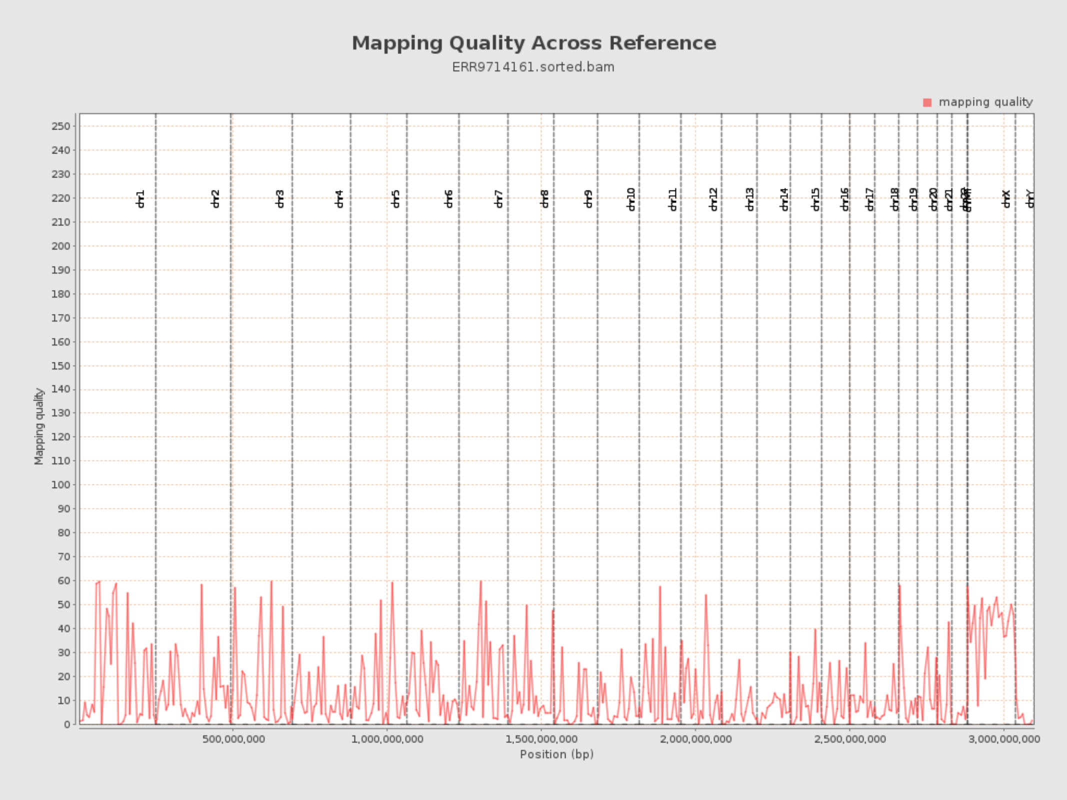
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram