Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:35:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714255.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_ERR9714255 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714255.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:35:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714255.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	420,460
Mapped reads	60,540 / 14.4%
Unmapped reads	359,920 / 85.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,943 / 0.46%
Read min/max/mean length	30 / 151 / 60.55
Duplicated reads (estimated)	59,402 / 14.13%
Duplication rate	24.47%
Clipped reads	33,214 / 7.9%

2.2. ACGT Content

Number/percentage of A's	172,540 / 2.75%
Number/percentage of C's	61,070 / 0.97%
Number/percentage of T's	79,658 / 1.27%
Number/percentage of G's	5,970,259 / 95.01%
Number/percentage of N's	154 / 0%
GC Percentage	95.98%

2.3. Coverage

Mean	0.002

Standard Deviation	7.6114

2.4. Mapping Quality

Mean Mapping Quality	17.06

2.5. Mismatches and indels

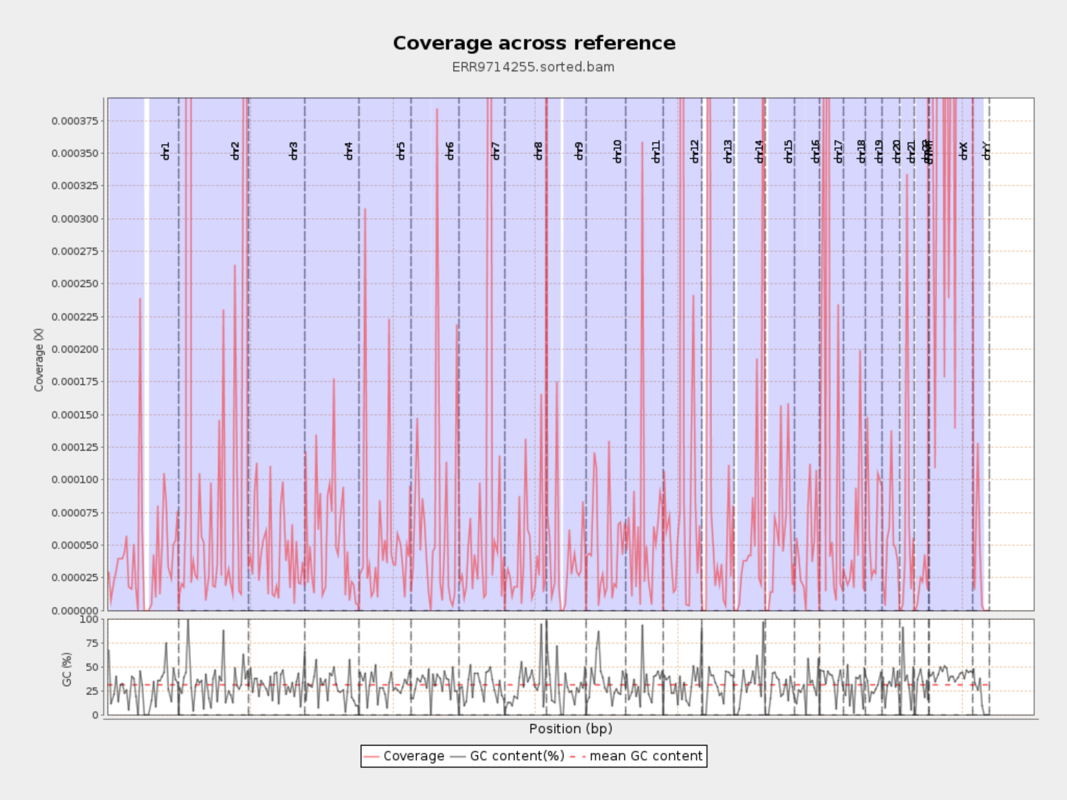
General error rate	3.3%
Mismatches	153,664
Insertions	7,398
Mapped reads with at least one insertion	7.81%
Deletions	3,017
Mapped reads with at least one deletion	4.78%
Homopolymer indels	66.47%

2.6. Chromosome stats

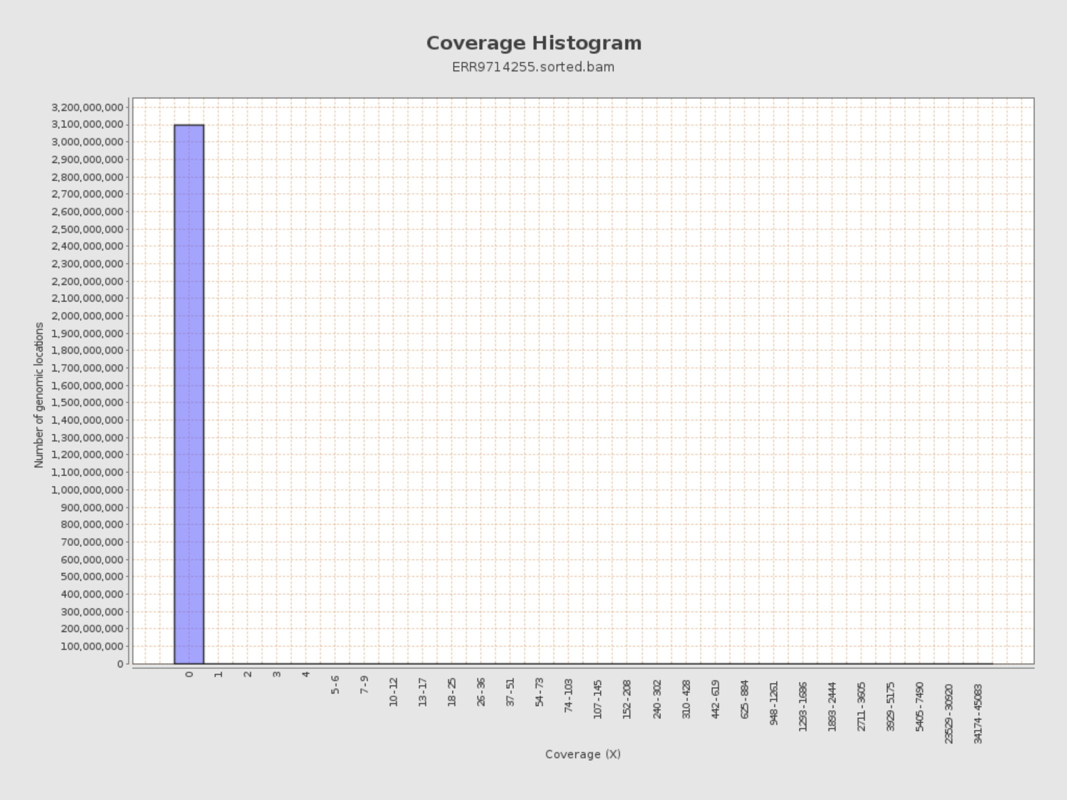
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10369	0	0.0124
chr2	243199373	5995586	0.0247	27.1553
chr3	198022430	8815	0	0.0117
chr4	191154276	10295	0.0001	0.0141
chr5	180915260	10210	0.0001	0.0155
chr6	171115067	11560	0.0001	0.0195
chr7	159138663	15419	0.0001	0.0798

chr8	146364022	6205	0	0.0182
chr9	141213431	6296	0	0.0165
chr10	135534747	6432	0	0.0128
chr11	135006516	8842	0.0001	0.0378
chr12	133851895	19535	0.0001	0.1009
chr13	115169878	9517	0.0001	0.0466
chr14	107349540	8642	0.0001	0.0719
chr15	102531392	5813	0.0001	0.0191
chr16	90354753	4307	0	0.01
chr17	81195210	14525	0.0002	0.1222
chr18	78077248	3894	0	0.0117
chr19	59128983	4147	0.0001	0.0148
chr20	63025520	3196	0.0001	0.0126
chr21	48129895	3800	0.0001	0.0317
chr22	51304566	935	0	0.0044
chrMT	16571	13117	0.7916	3.2957
chrX	155270560	114229	0.0007	0.1106
chrY	59373566	1610	0	0.0083

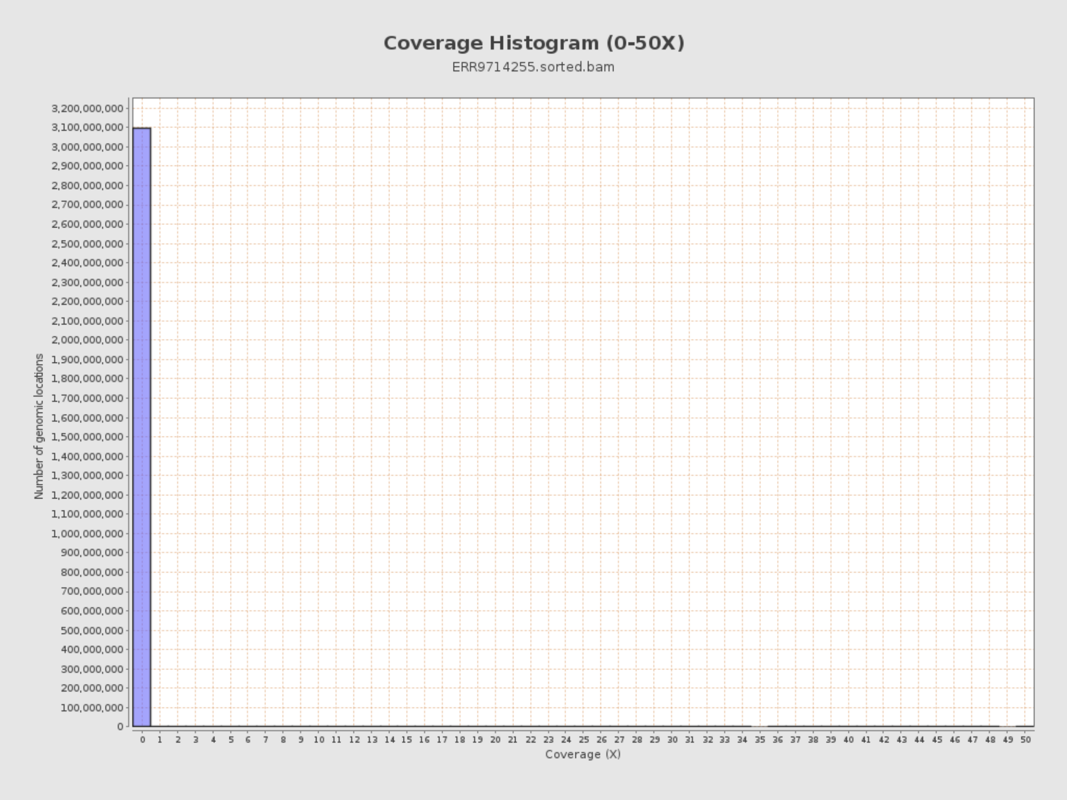
3. Results : Coverage across reference



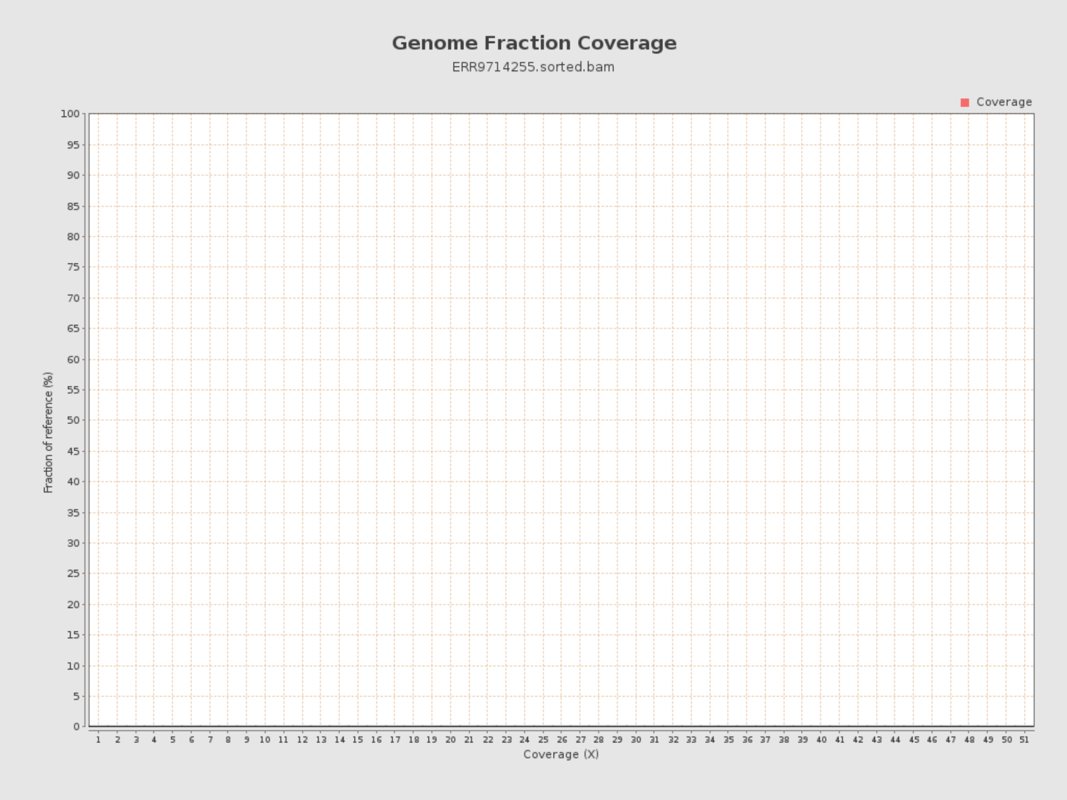
4. Results : Coverage Histogram



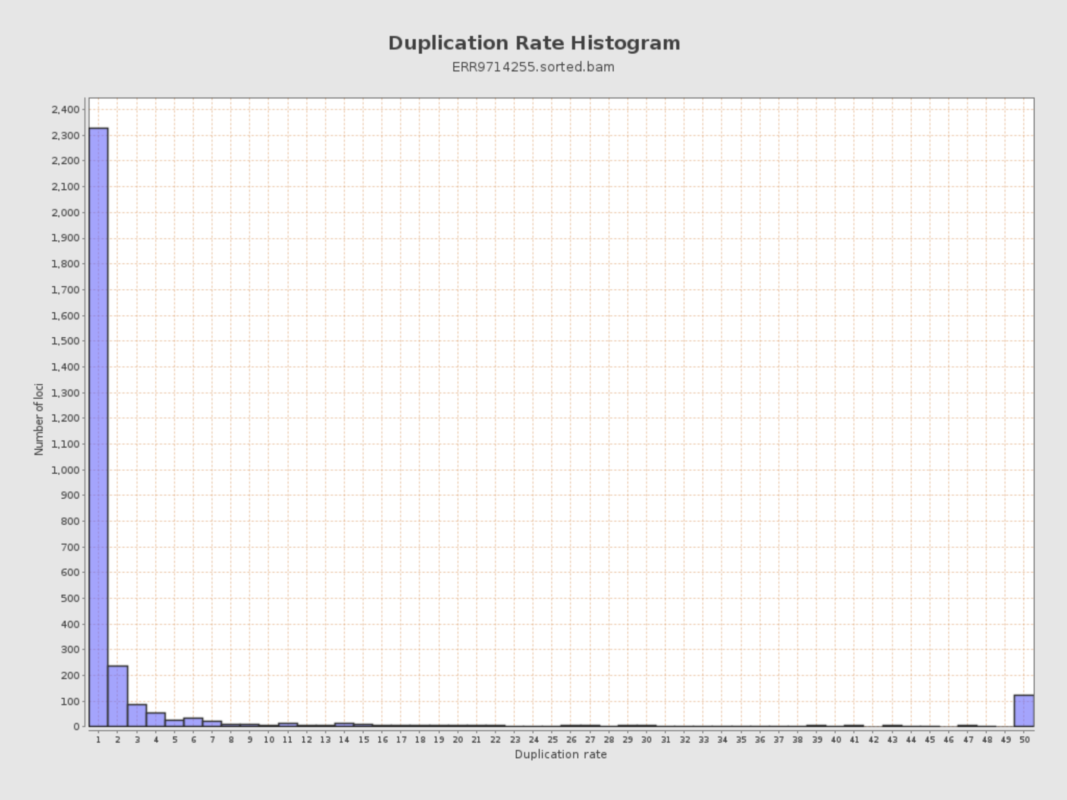
5. Results : Coverage Histogram (0-50X)



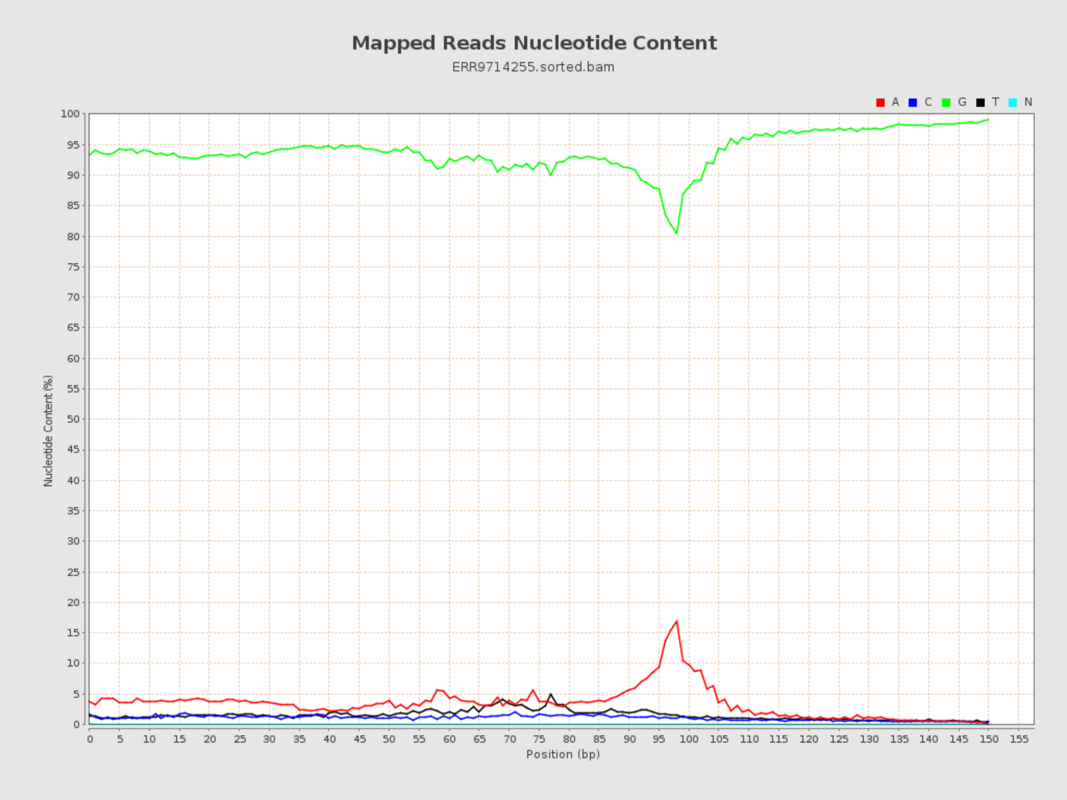
6. Results : Genome Fraction Coverage



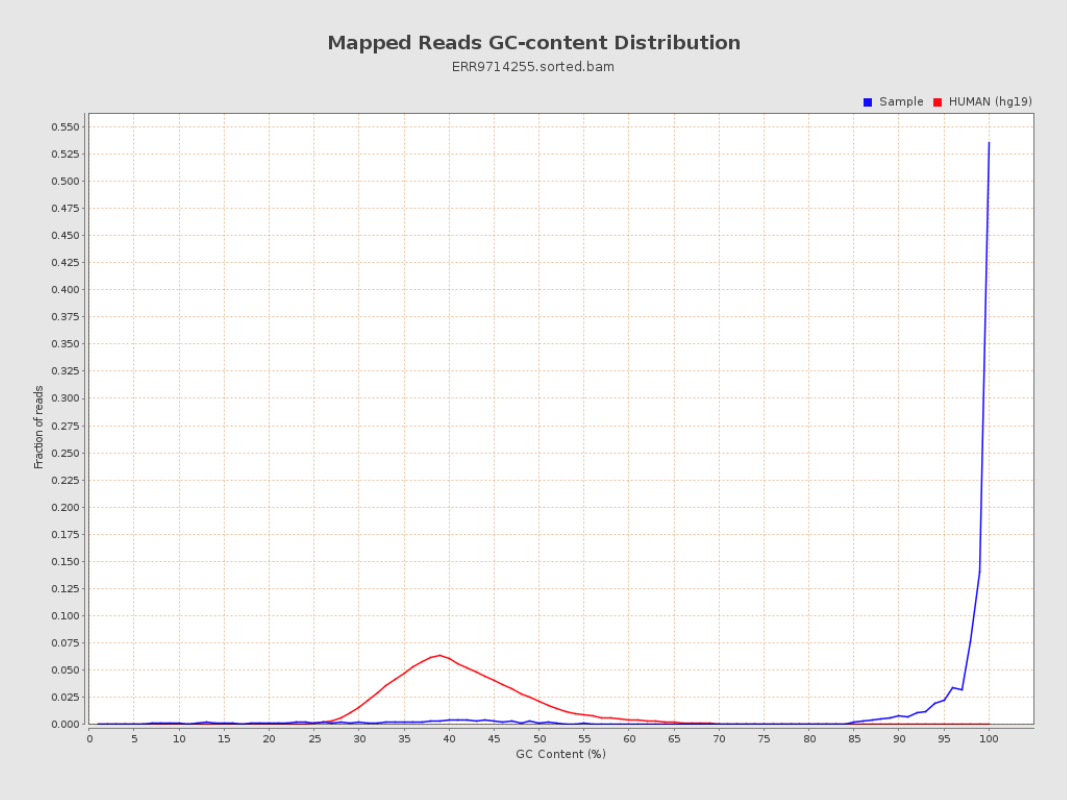
7. Results : Duplication Rate Histogram



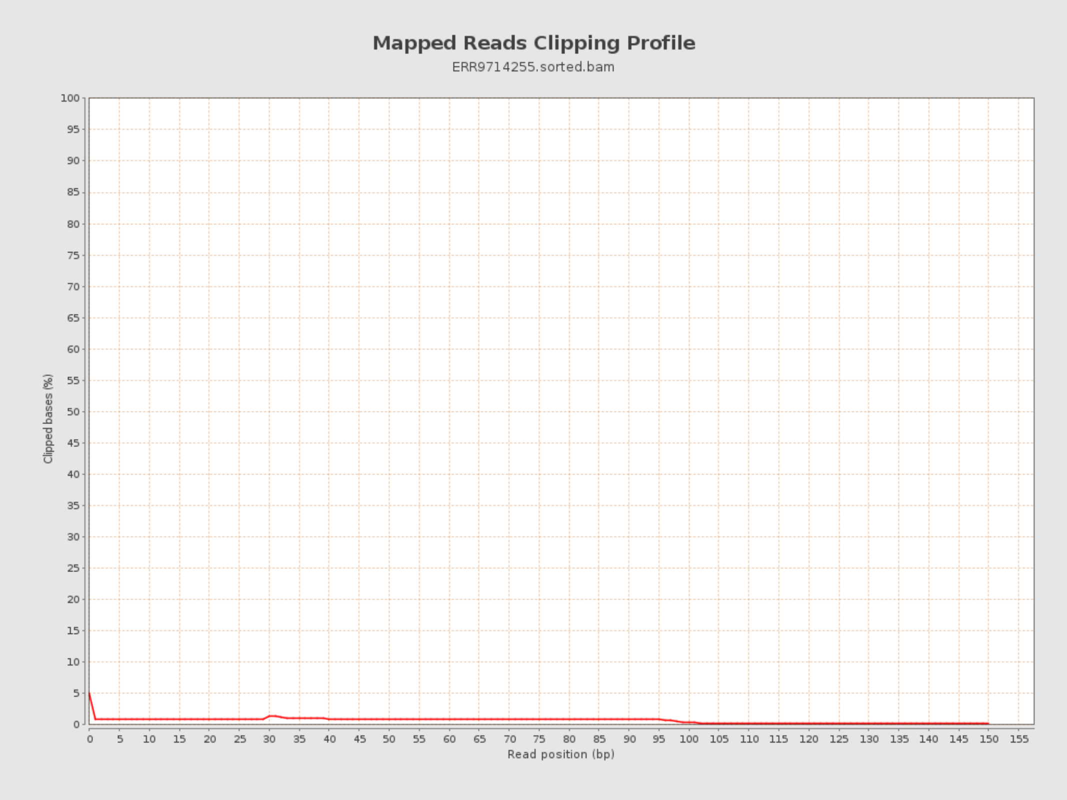
8. Results : Mapped Reads Nucleotide Content



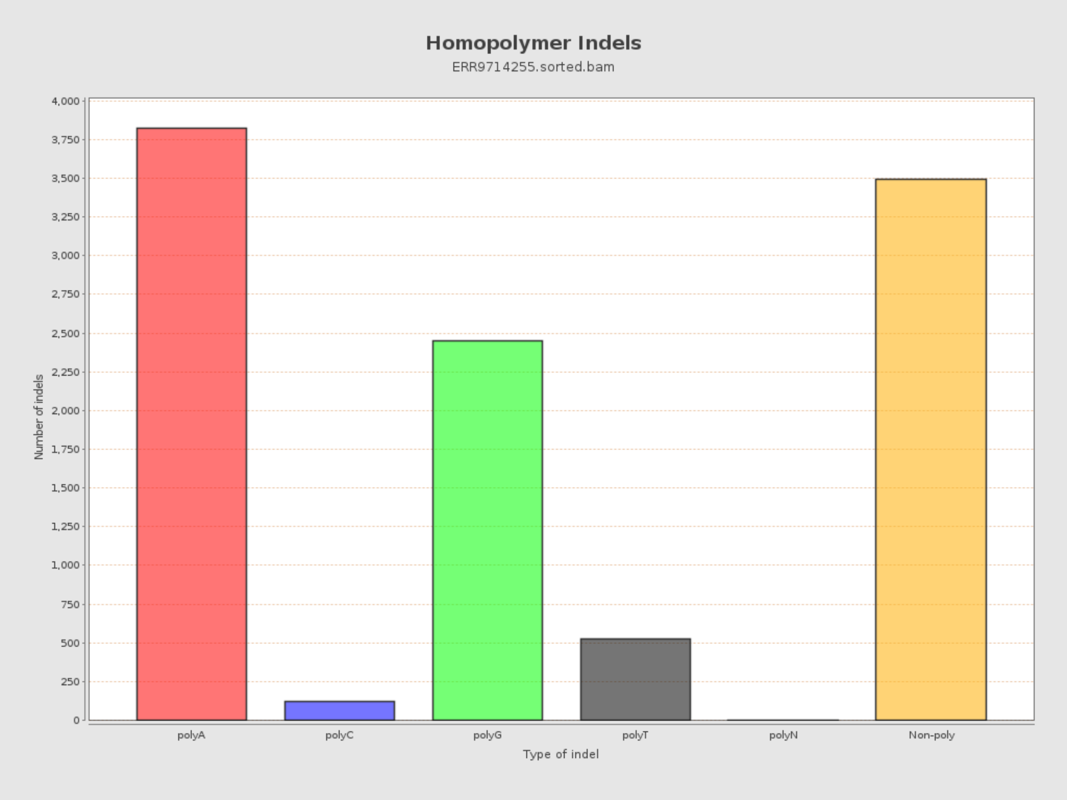
9. Results : Mapped Reads GC-content Distribution



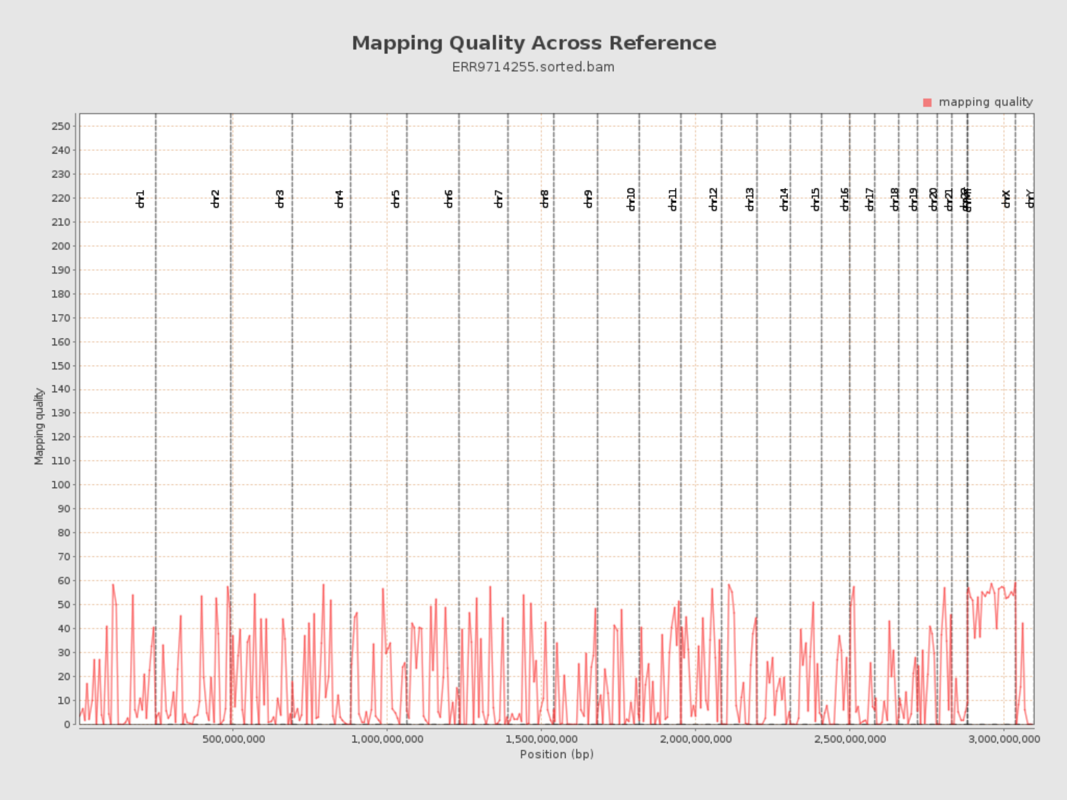
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram