Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:15:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714073.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_ERR9714073 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	455,242
Mapped reads	223,783 / 49.16%
Unmapped reads	231,459 / 50.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,766 / 0.61%
Read min/max/mean length	30 / 151 / 100.24
Duplicated reads (estimated)	213,891 / 46.98%
Duplication rate	32.88%
Clipped reads	211,252 / 46.4%

2.2. ACGT Content

Number/percentage of A's	8,085,402 / 32.07%
Number/percentage of C's	4,393,184 / 17.43%
Number/percentage of T's	6,595,043 / 26.16%
Number/percentage of G's	6,134,054 / 24.33%
Number/percentage of N's	201 / 0%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0083

Standard Deviation	27.1484

2.4. Mapping Quality

Mean Mapping Quality	36.02

2.5. Mismatches and indels

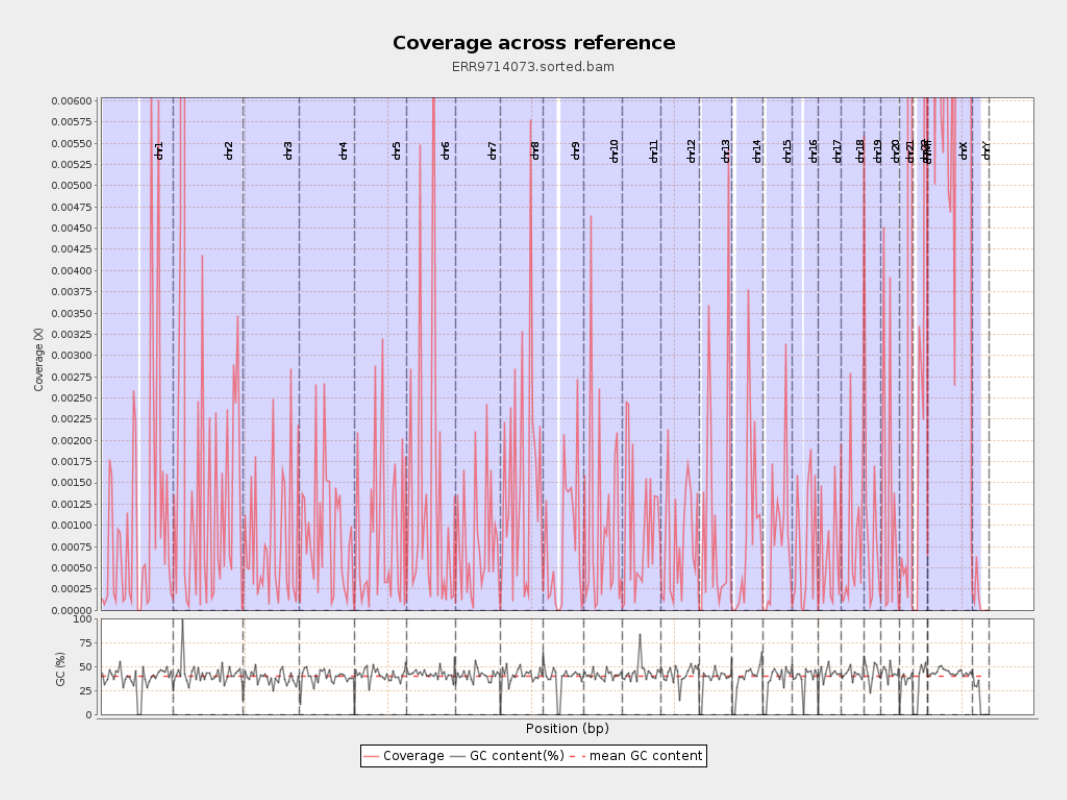
General error rate	4.09%
Mismatches	1,024,276
Insertions	8,488
Mapped reads with at least one insertion	3.52%
Deletions	58,602
Mapped reads with at least one deletion	25.13%
Homopolymer indels	16.49%

2.6. Chromosome stats

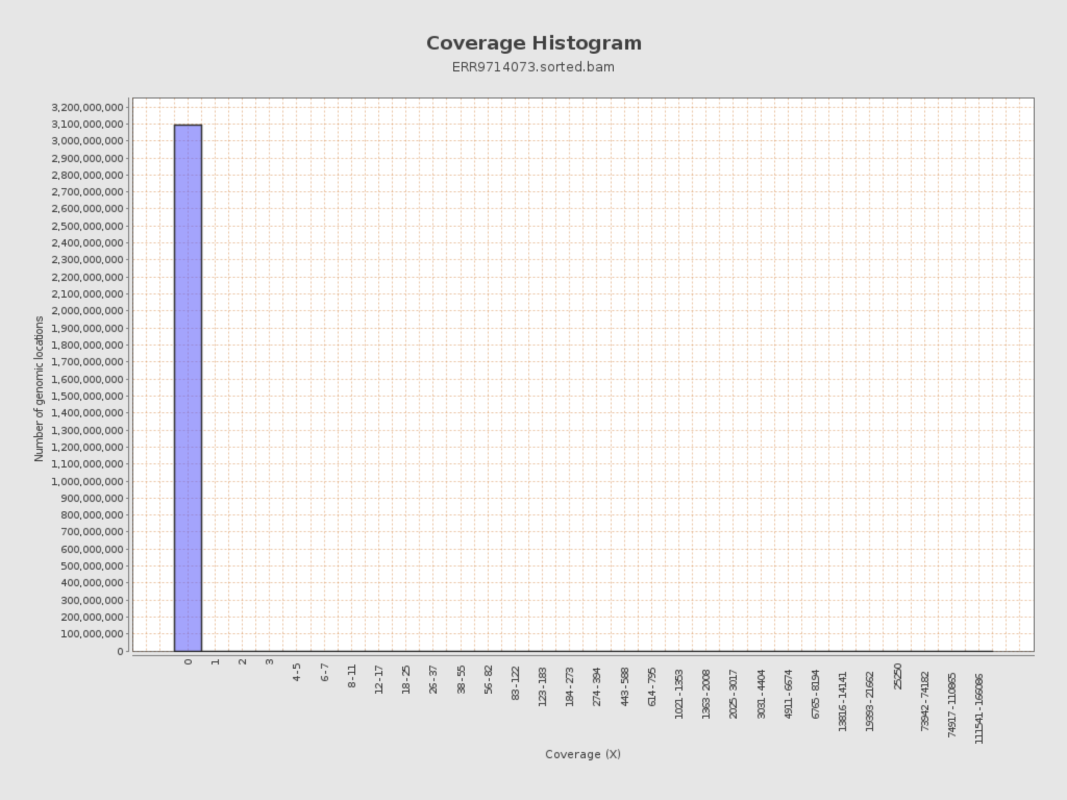
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	269449	0.0011	0.3066
chr2	243199373	1535615	0.0063	5.1269
chr3	198022430	170735	0.0009	0.21
chr4	191154276	176834	0.0009	0.2254
chr5	180915260	159211	0.0009	0.2249
chr6	171115067	223917	0.0013	0.3474
chr7	159138663	126519	0.0008	0.2155

chr8	146364022	228225	0.0016	0.3599
chr9	141213431	110505	0.0008	0.1652
chr10	135534747	140445	0.001	0.242
chr11	135006516	133449	0.001	0.2059
chr12	133851895	111930	0.0008	0.1848
chr13	115169878	122456	0.0011	0.3454
chr14	107349540	103588	0.001	0.2203
chr15	102531392	88903	0.0009	0.1874
chr16	90354753	66856	0.0007	0.141
chr17	81195210	54488	0.0007	0.1579
chr18	78077248	61416	0.0008	0.1815
chr19	59128983	55006	0.0009	0.1755
chr20	63025520	84605	0.0013	0.3647
chr21	48129895	20116870	0.418	217.4086
chr22	51304566	160922	0.0031	0.474
chrMT	16571	41362	2.496	16.5956
chrX	155270560	1415328	0.0091	0.9335
chrY	59373566	8011	0.0001	0.036

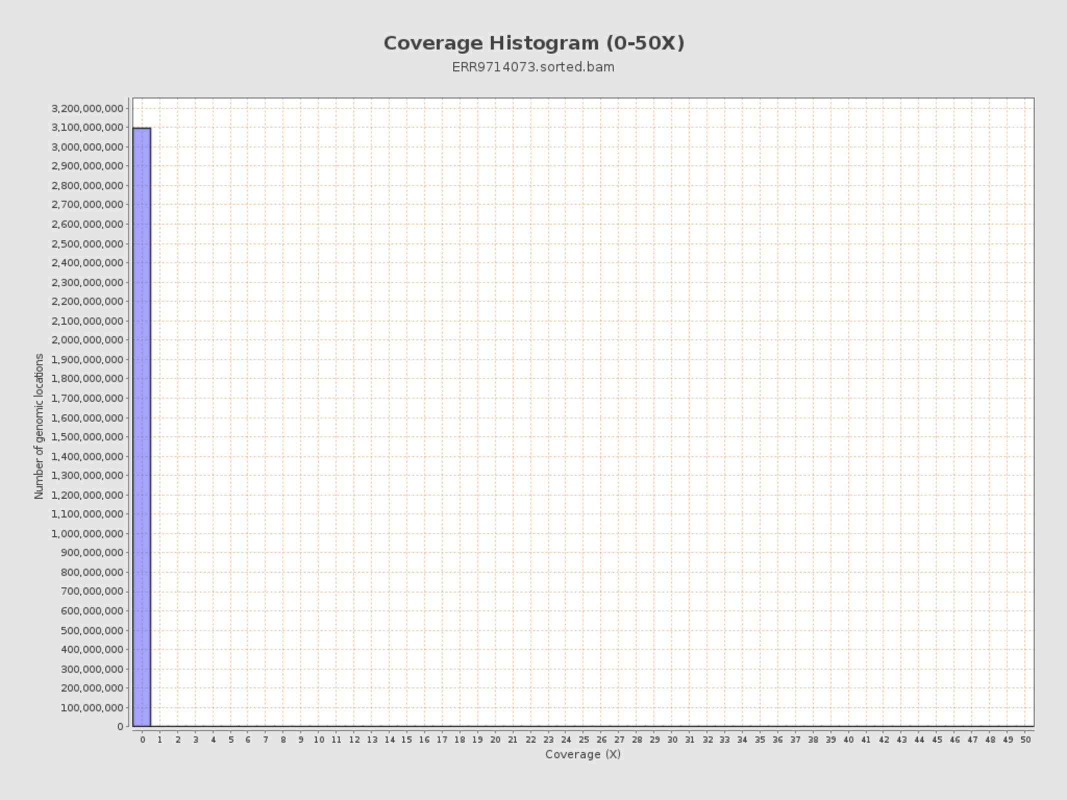
3. Results : Coverage across reference



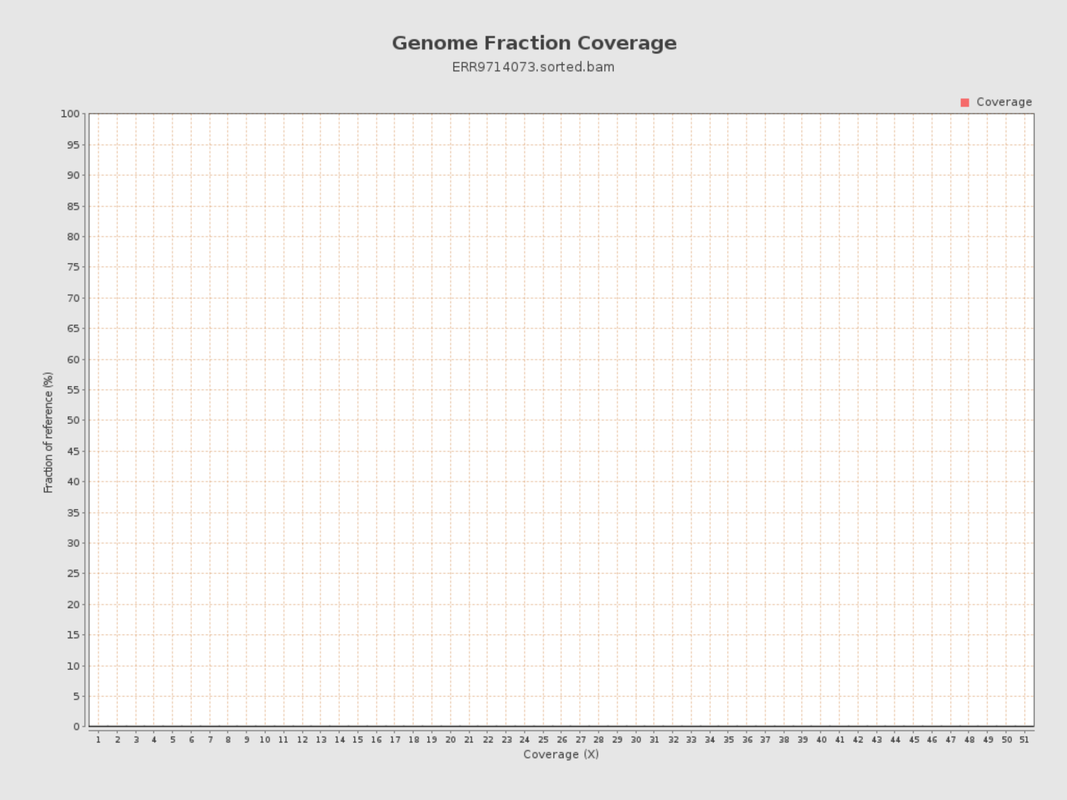
4. Results : Coverage Histogram



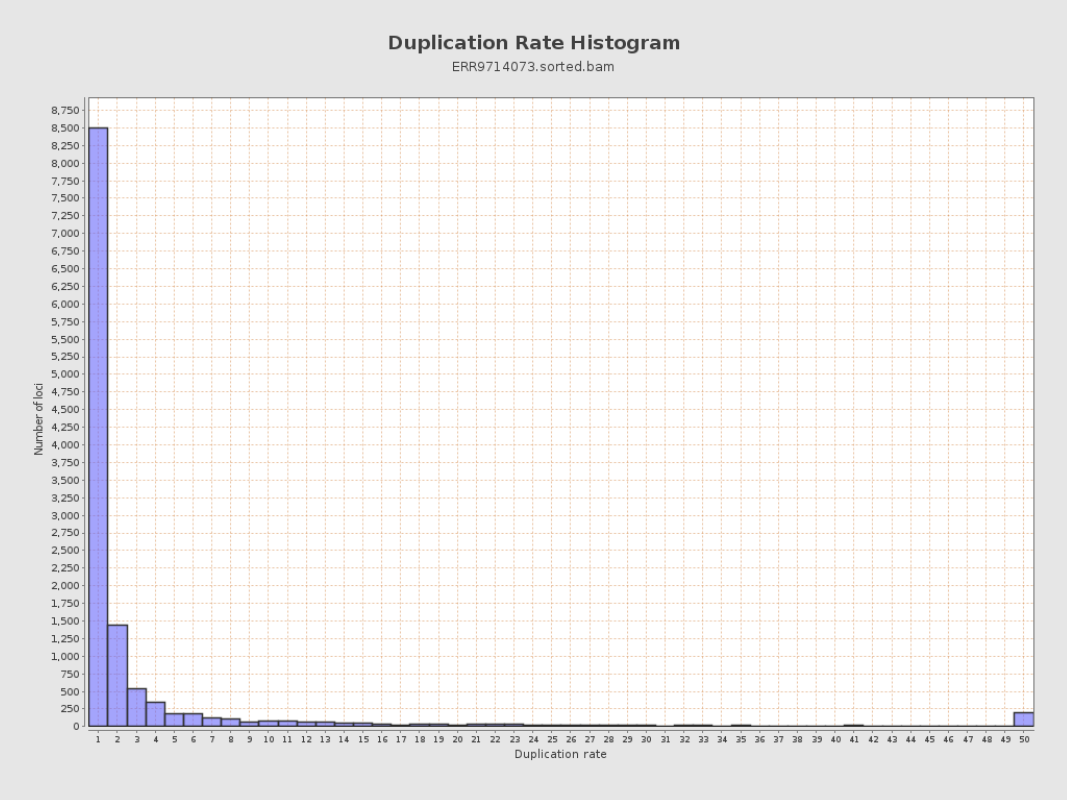
5. Results : Coverage Histogram (0-50X)



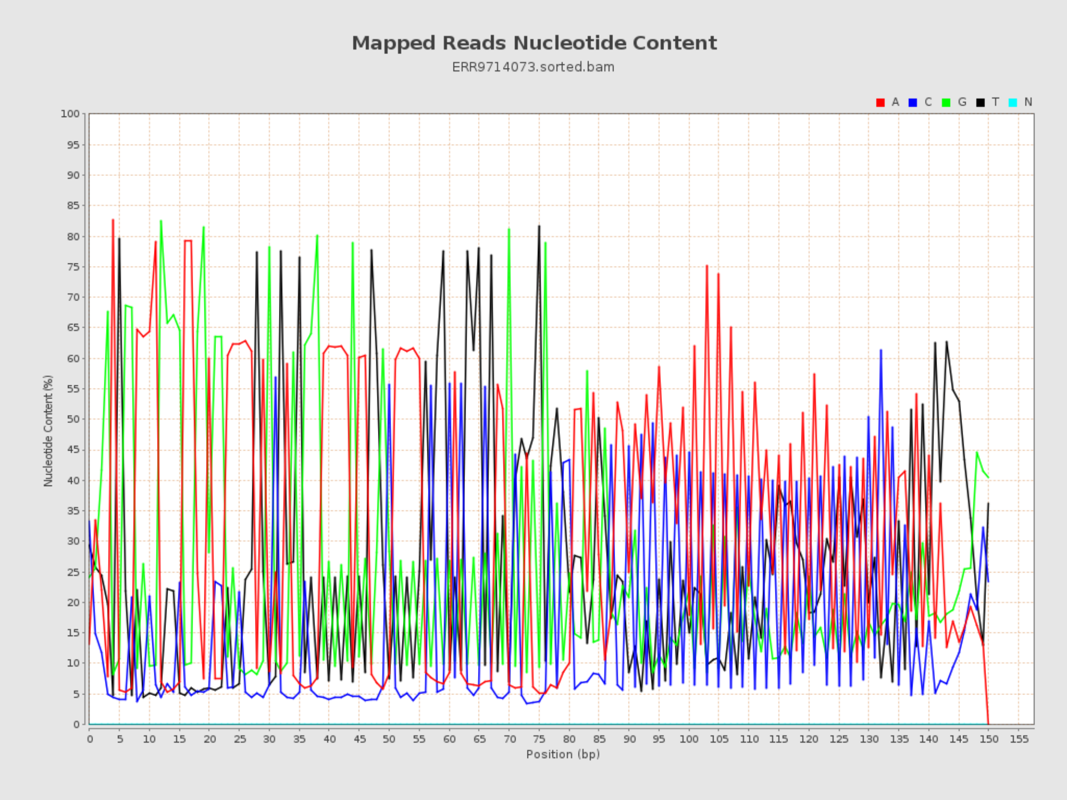
6. Results : Genome Fraction Coverage



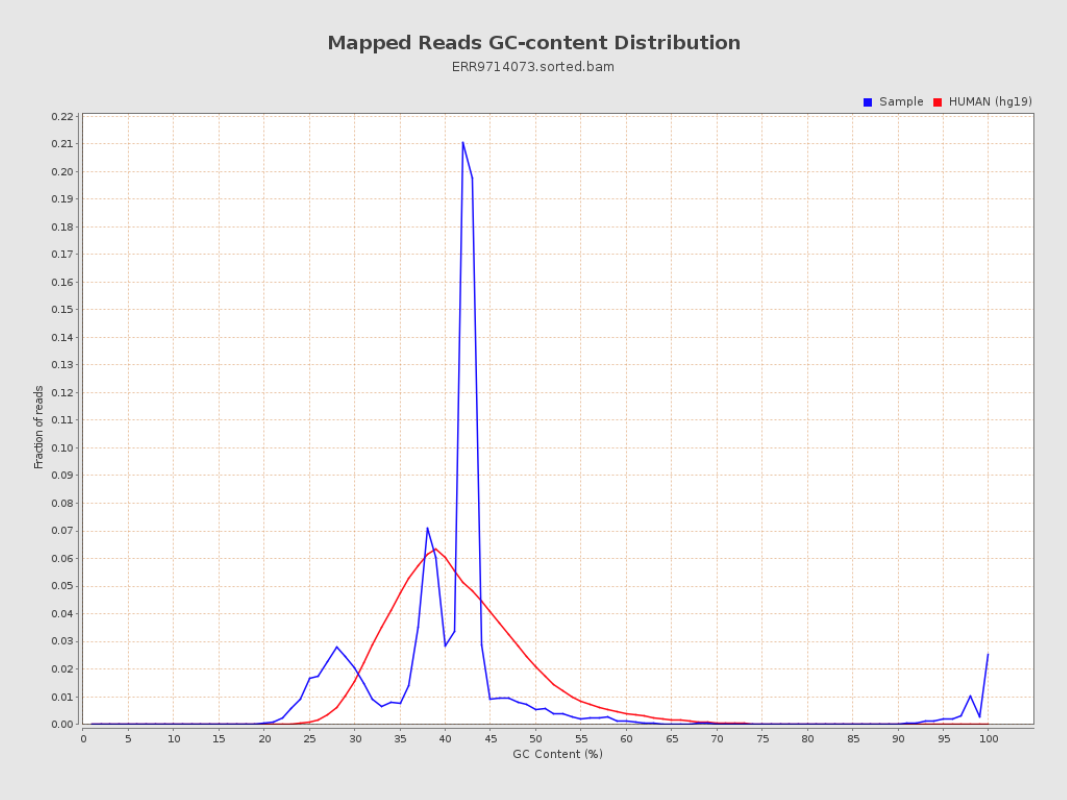
7. Results : Duplication Rate Histogram



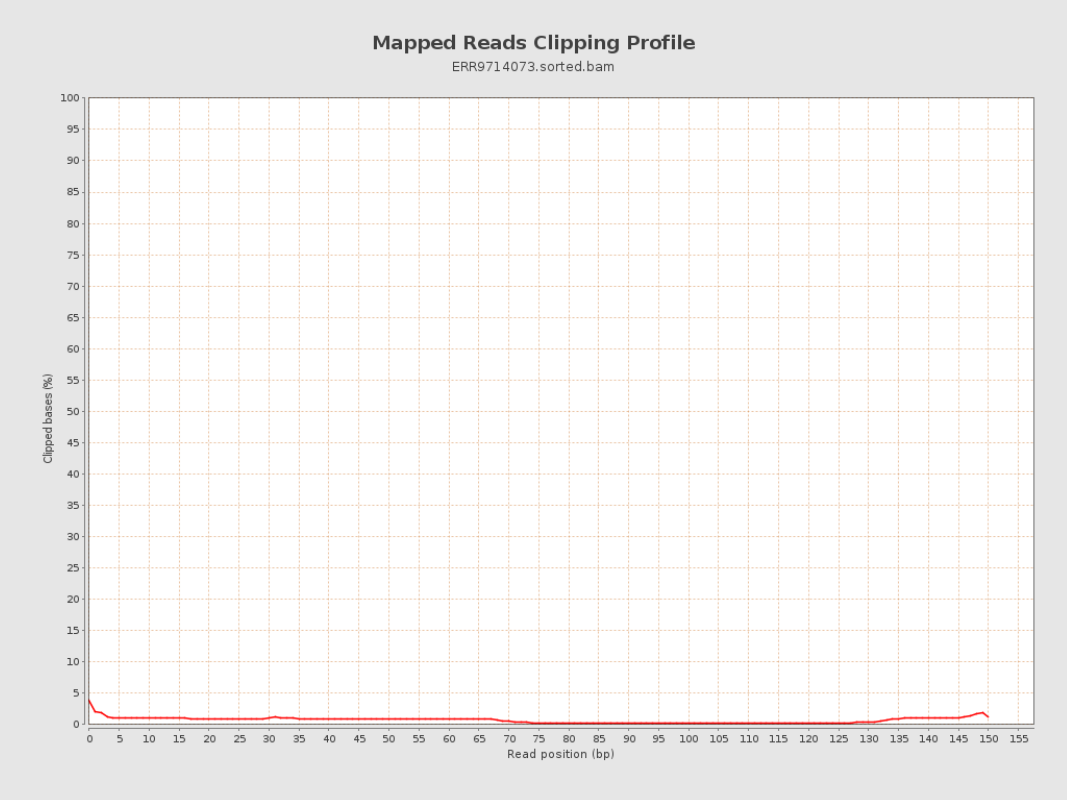
8. Results : Mapped Reads Nucleotide Content



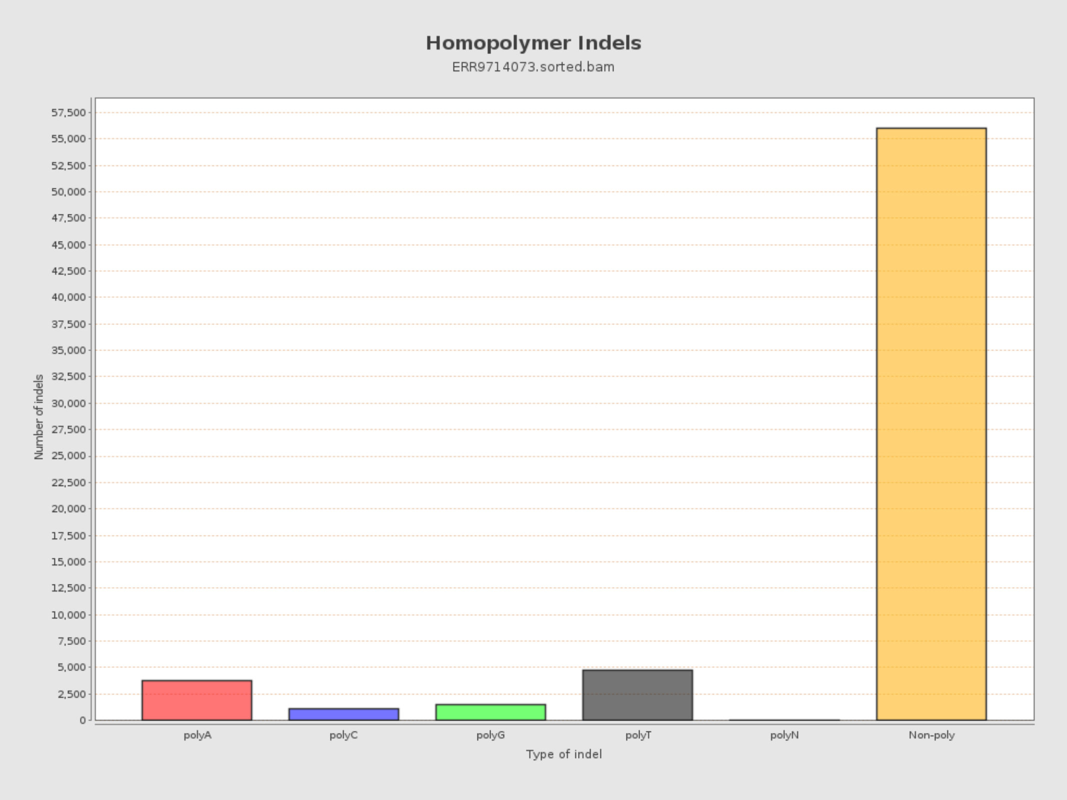
9. Results : Mapped Reads GC-content Distribution



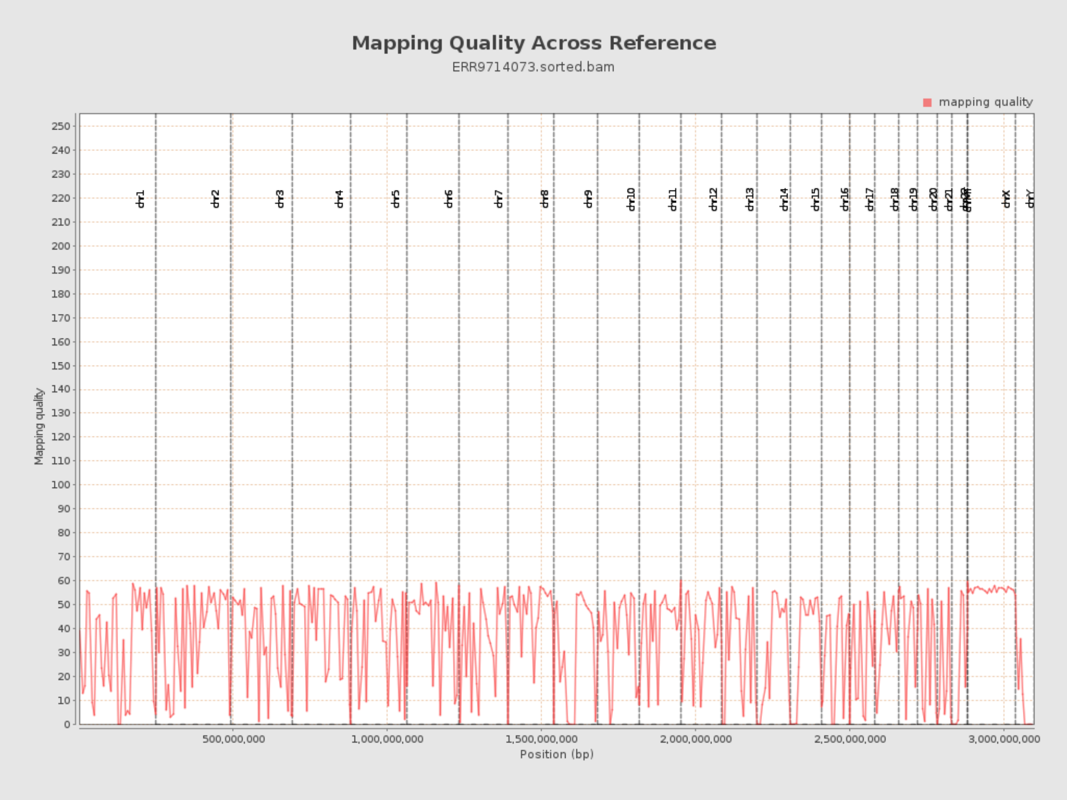
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram