Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:54:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714133.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_ERR9714133 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:54:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	662,688
Mapped reads	549,257 / 82.88%
Unmapped reads	113,431 / 17.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,243 / 2.45%
Read min/max/mean length	30 / 151 / 133.97
Duplicated reads (estimated)	488,386 / 73.7%
Duplication rate	44.38%
Clipped reads	518,270 / 78.21%

2.2. ACGT Content

Number/percentage of A's	18,583,624 / 26.74%
Number/percentage of C's	15,363,659 / 22.11%
Number/percentage of T's	17,574,753 / 25.29%
Number/percentage of G's	17,978,695 / 25.87%
Number/percentage of N's	618 / 0%
GC Percentage	47.97%

2.3. Coverage

Mean	0.023

Standard Deviation	6.706

2.4. Mapping Quality

Mean Mapping Quality	51.61

2.5. Mismatches and indels

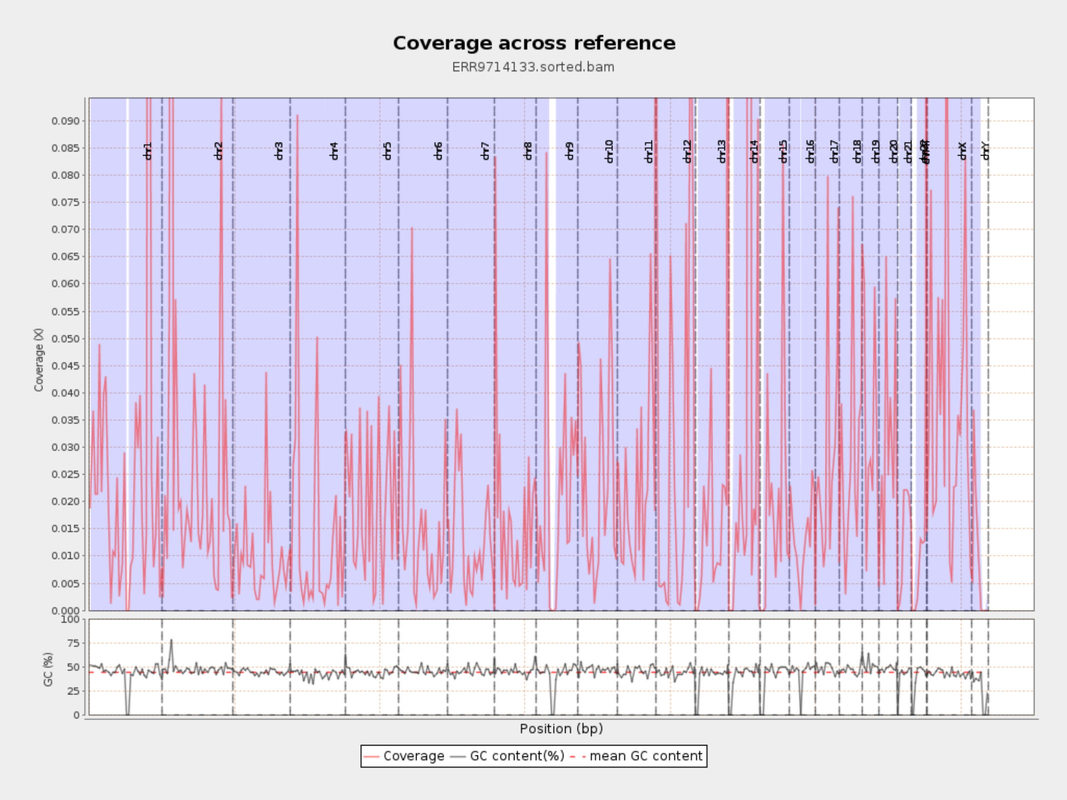
General error rate	4.44%
Mismatches	2,869,394
Insertions	76,716
Mapped reads with at least one insertion	13.41%
Deletions	249,257
Mapped reads with at least one deletion	43.15%
Homopolymer indels	29.81%

2.6. Chromosome stats

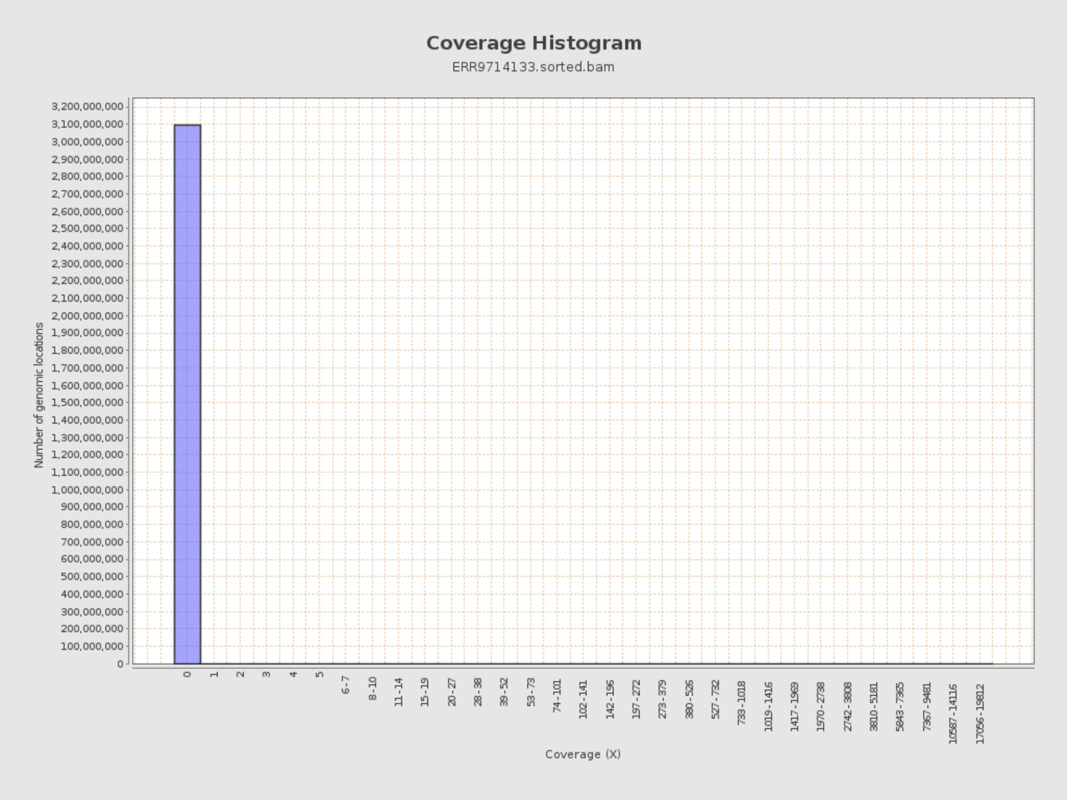
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6434979	0.0258	7.0515
chr2	243199373	8505808	0.035	11.1854
chr3	198022430	1976280	0.01	1.4037
chr4	191154276	2712239	0.0142	3.2215
chr5	180915260	3566443	0.0197	3.5113
chr6	171115067	2793860	0.0163	3.1449
chr7	159138663	2069931	0.013	2.2209

chr8	146364022	2554482	0.0175	3.9906
chr9	141213431	2775835	0.0197	4.5592
chr10	135534747	3305362	0.0244	3.7296
chr11	135006516	3339266	0.0247	4.1554
chr12	133851895	4142935	0.031	6.8052
chr13	115169878	2590431	0.0225	8.1678
chr14	107349540	4846755	0.0451	22.6048
chr15	102531392	2104406	0.0205	3.3388
chr16	90354753	1219991	0.0135	1.6778
chr17	81195210	2432031	0.03	4.7821
chr18	78077248	2130842	0.0273	5.4821
chr19	59128983	1918257	0.0324	3.6027
chr20	63025520	1999447	0.0317	4.2161
chr21	48129895	632211	0.0131	1.9211
chr22	51304566	409920	0.008	1.0686
chrMT	16571	135372	8.1692	68.89
chrX	155270560	5945123	0.0383	4.4746
chrY	59373566	546919	0.0092	1.7495

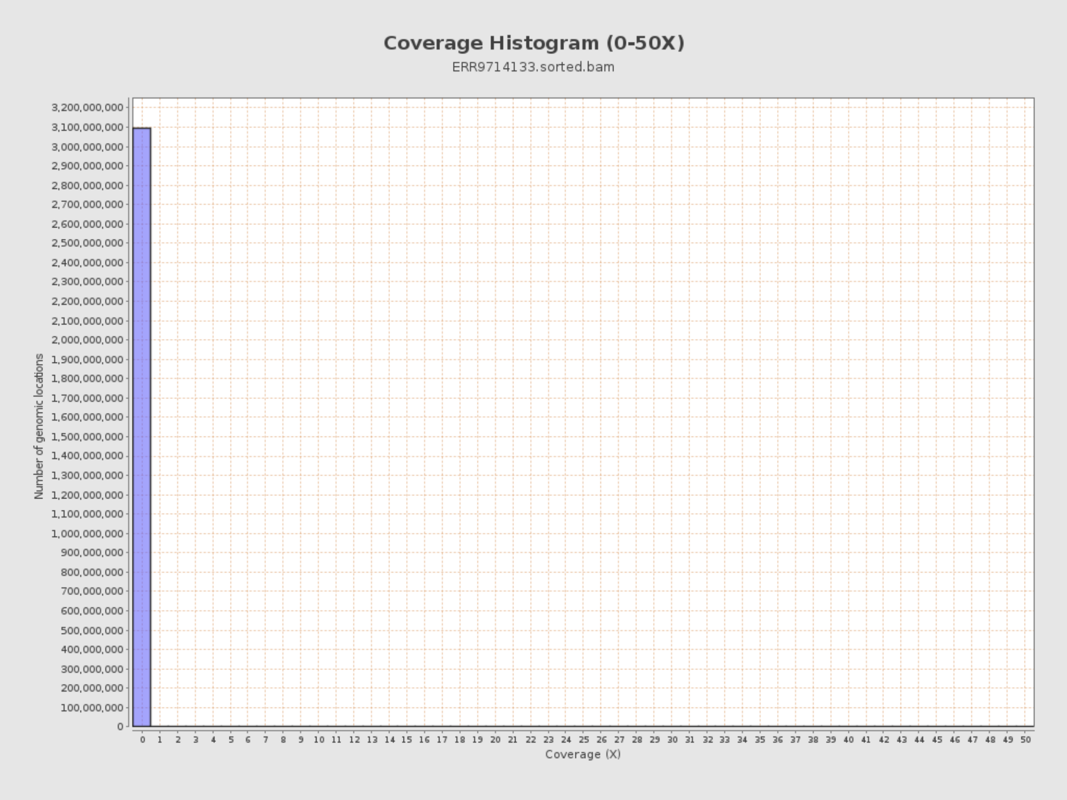
3. Results : Coverage across reference



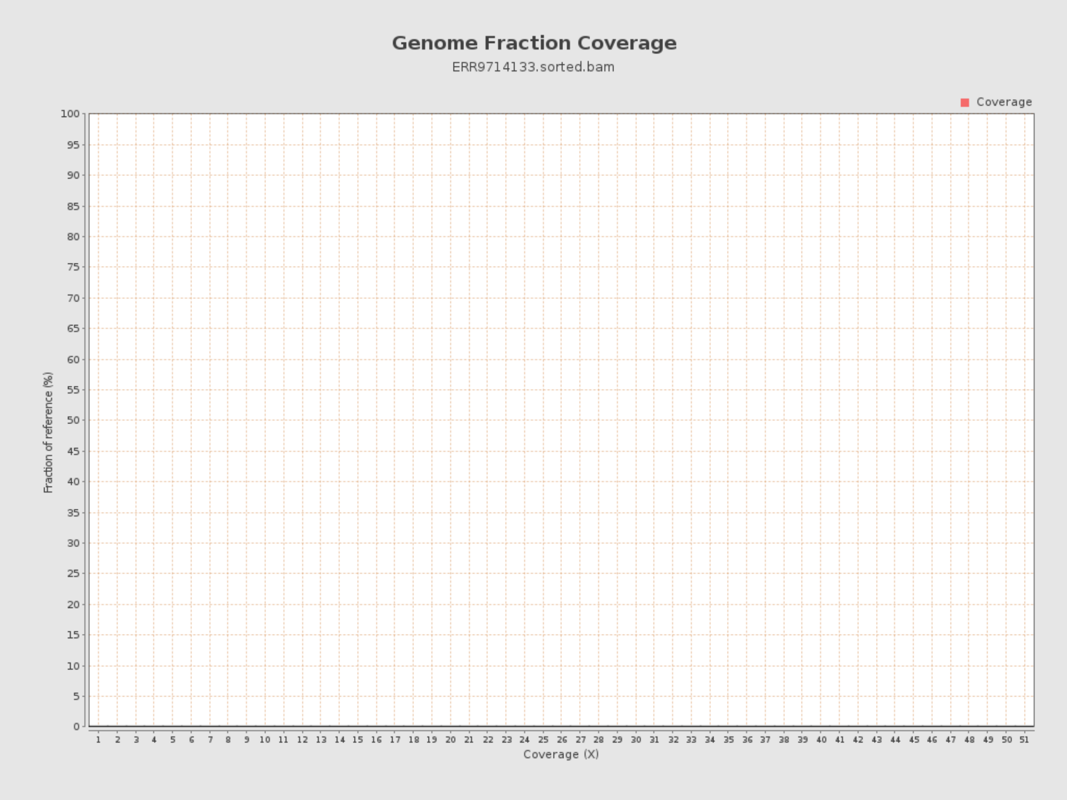
4. Results : Coverage Histogram



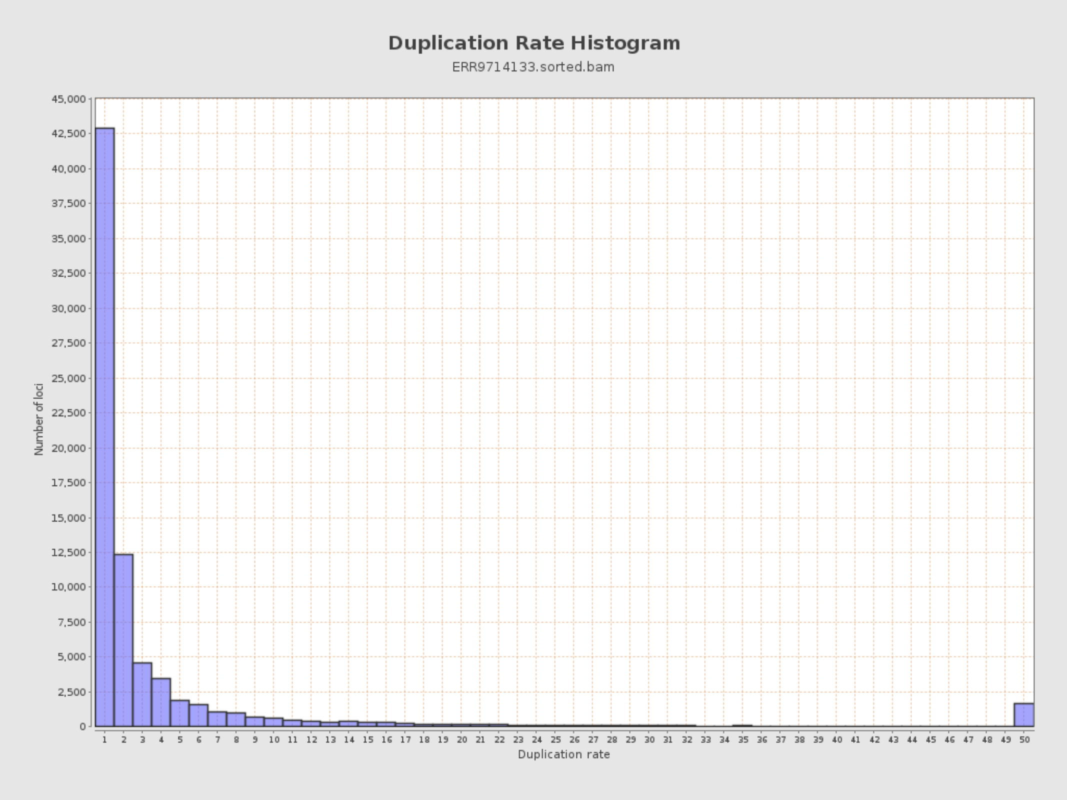
5. Results : Coverage Histogram (0-50X)



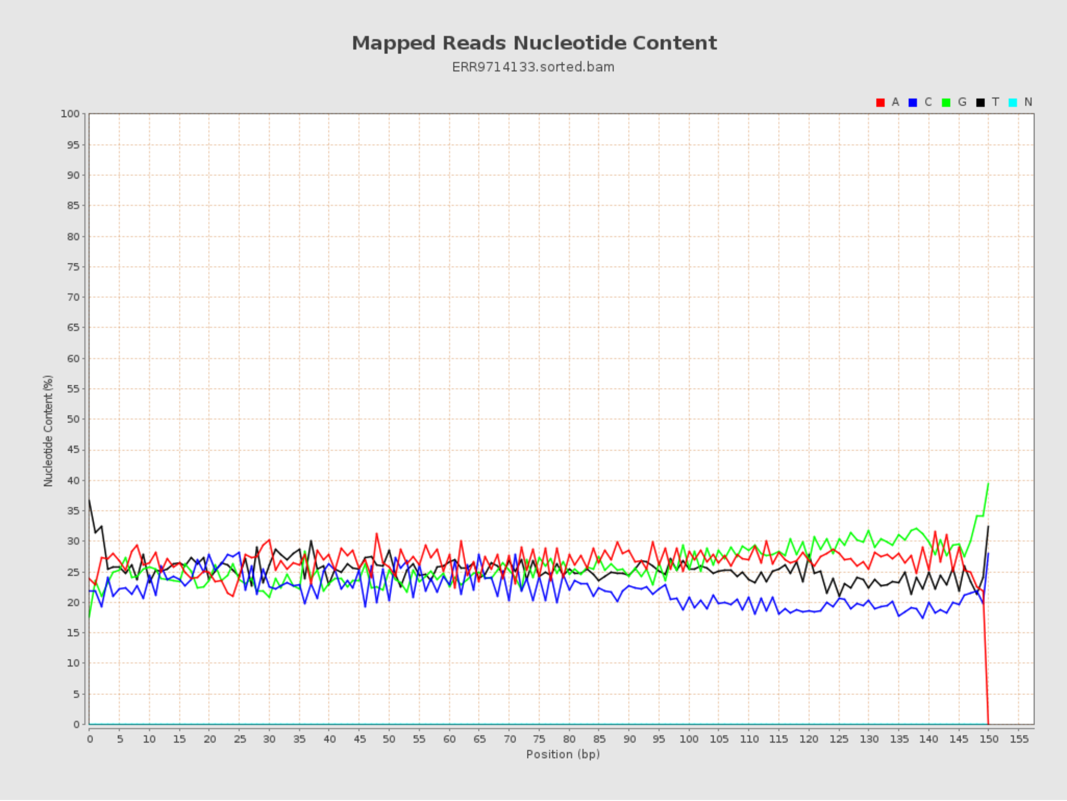
6. Results : Genome Fraction Coverage



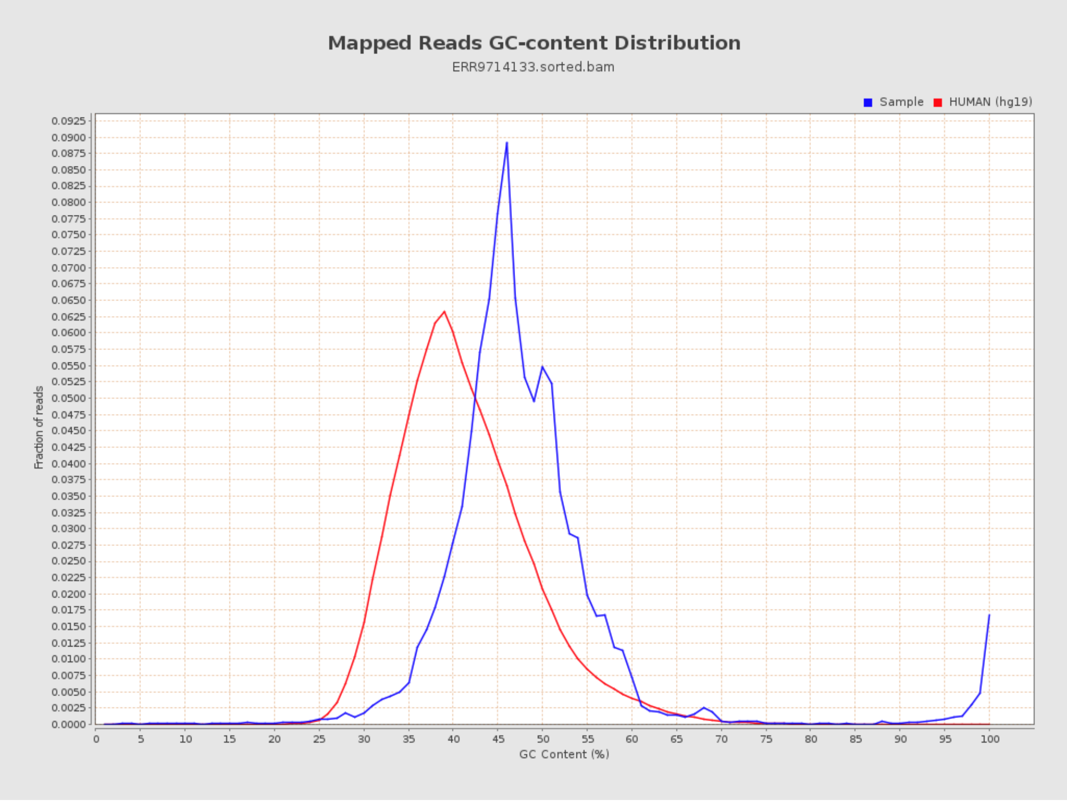
7. Results : Duplication Rate Histogram



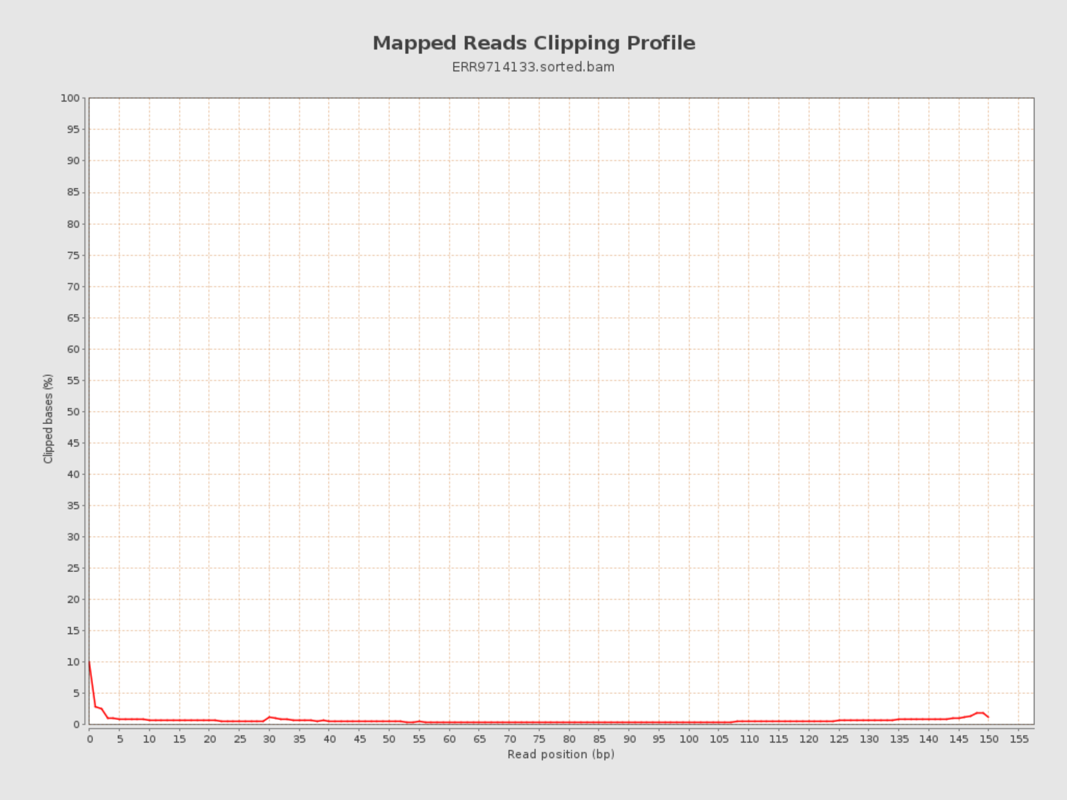
8. Results : Mapped Reads Nucleotide Content



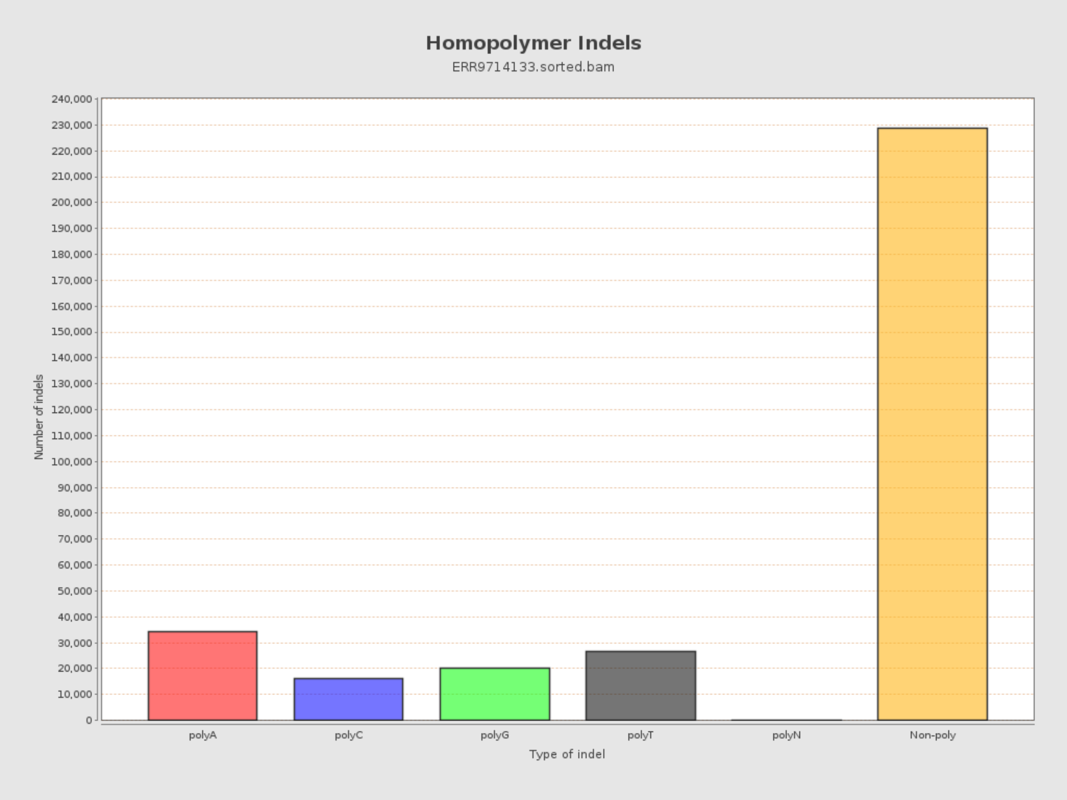
9. Results : Mapped Reads GC-content Distribution



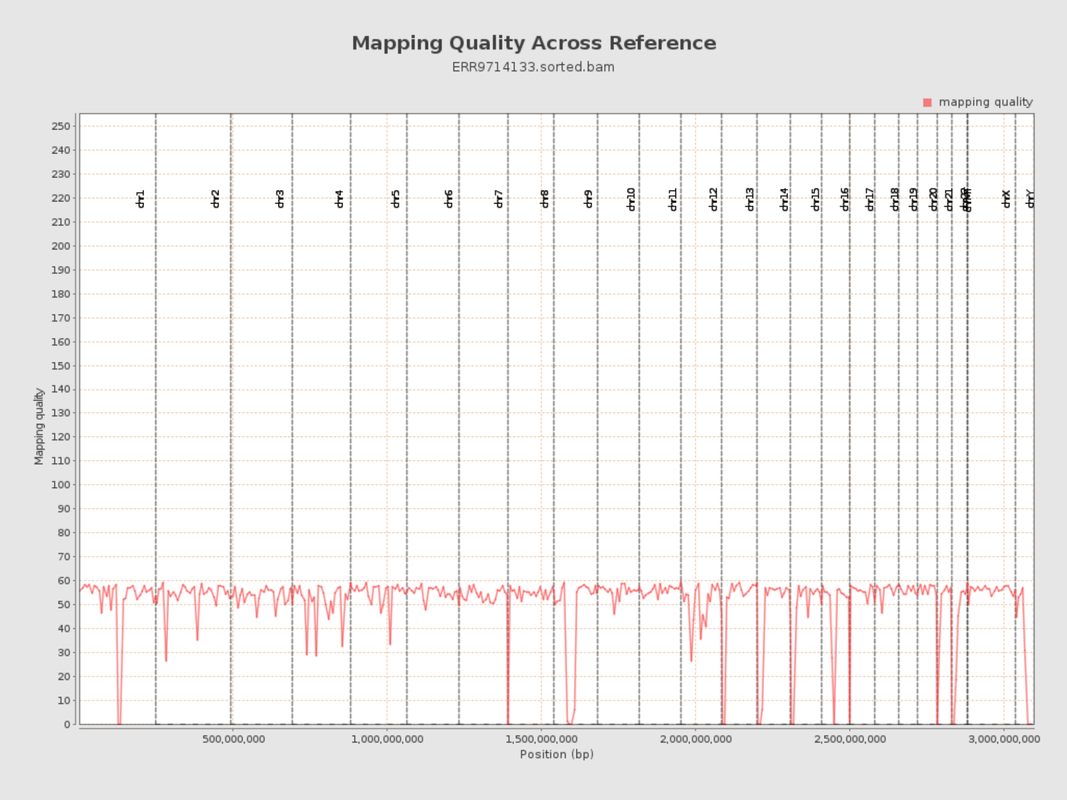
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram