Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:41:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714149.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_ERR9714149 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714149.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:41:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714149.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	727,482
Mapped reads	590,243 / 81.14%
Unmapped reads	137,239 / 18.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,320 / 2.79%
Read min/max/mean length	30 / 151 / 132.53
Duplicated reads (estimated)	521,580 / 71.7%
Duplication rate	43.13%
Clipped reads	552,734 / 75.98%

2.2. ACGT Content

Number/percentage of A's	21,008,444 / 28.02%
Number/percentage of C's	15,347,586 / 20.47%
Number/percentage of T's	19,867,428 / 26.5%
Number/percentage of G's	18,749,286 / 25.01%
Number/percentage of N's	659 / 0%
GC Percentage	45.48%

2.3. Coverage

Mean	0.0248

Standard Deviation	4.995

2.4. Mapping Quality

Mean Mapping Quality	51.24

2.5. Mismatches and indels

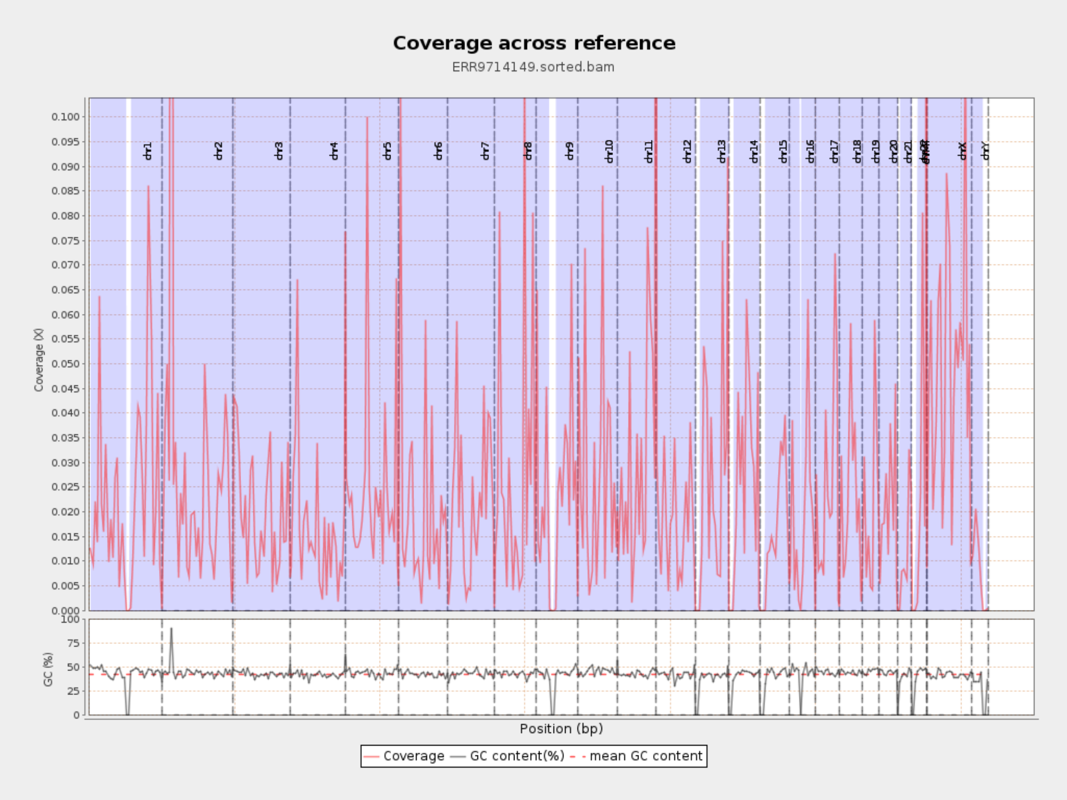
General error rate	4.81%
Mismatches	3,390,523
Insertions	84,677
Mapped reads with at least one insertion	13.79%
Deletions	302,272
Mapped reads with at least one deletion	47.21%
Homopolymer indels	29.83%

2.6. Chromosome stats

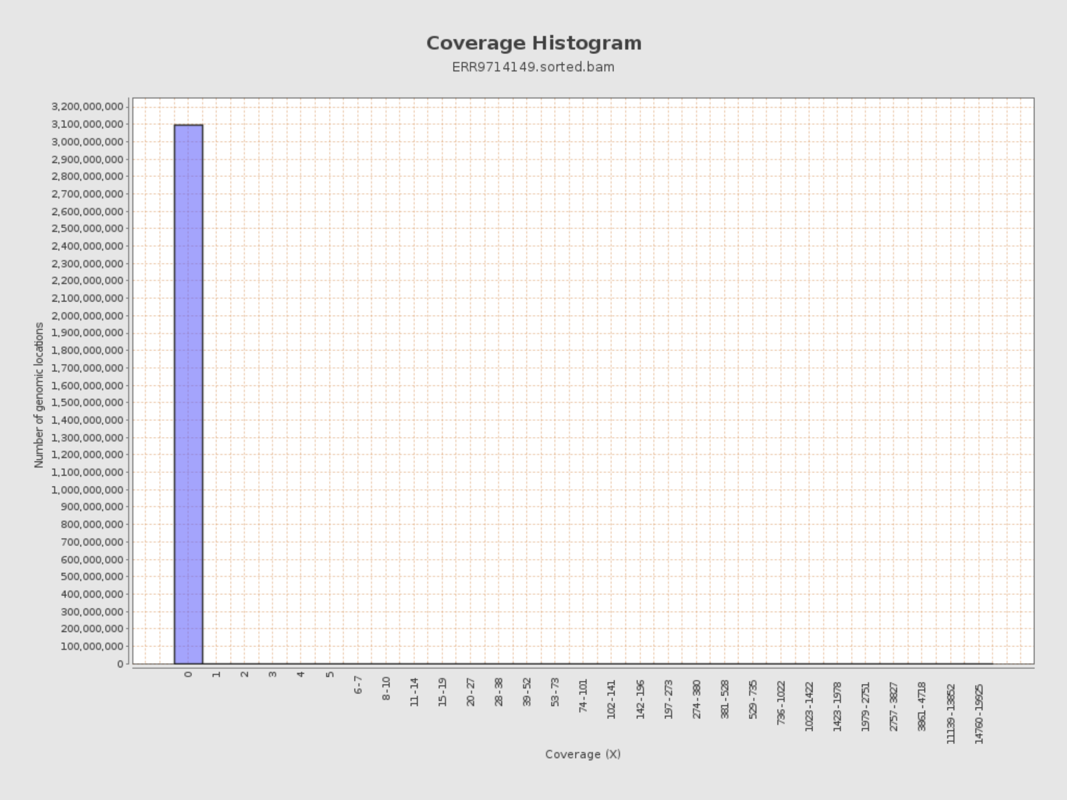
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5726289	0.023	3.6679
chr2	243199373	8562659	0.0352	12.6501
chr3	198022430	3983622	0.0201	2.7562
chr4	191154276	3147383	0.0165	2.4489
chr5	180915260	4611970	0.0255	4.207
chr6	171115067	3625329	0.0212	3.3365
chr7	159138663	3512959	0.0221	2.9274

chr8	146364022	4153266	0.0284	4.698
chr9	141213431	3092240	0.0219	3.2265
chr10	135534747	3844736	0.0284	5.0106
chr11	135006516	4069536	0.0301	4.9611
chr12	133851895	2393423	0.0179	2.6777
chr13	115169878	2879970	0.025	3.8601
chr14	107349540	2862764	0.0267	3.7291
chr15	102531392	1681339	0.0164	1.9062
chr16	90354753	1729133	0.0191	2.5827
chr17	81195210	2141760	0.0264	3.9791
chr18	78077248	1801696	0.0231	2.7241
chr19	59128983	1199417	0.0203	2.5011
chr20	63025520	1399412	0.0222	2.8338
chr21	48129895	550076	0.0114	1.6605
chr22	51304566	1053650	0.0205	3.7656
chrMT	16571	653728	39.4501	311.4979
chrX	155270560	7735035	0.0498	5.0361
chrY	59373566	461714	0.0078	1.3049

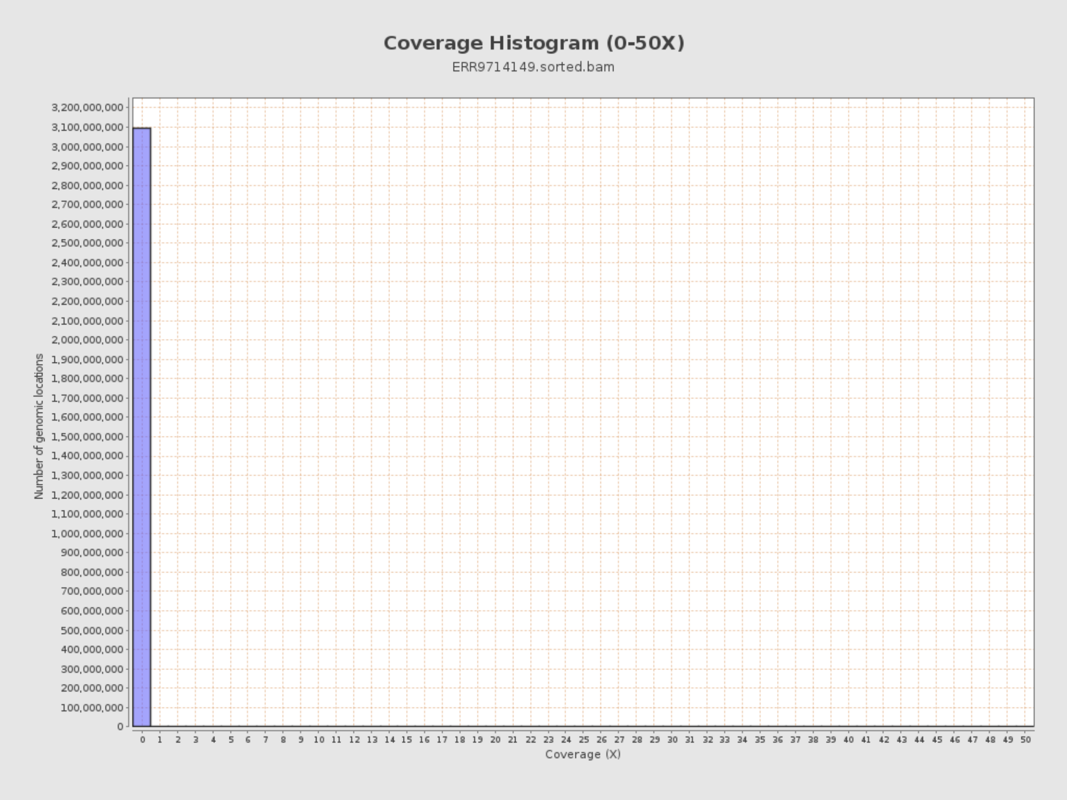
3. Results : Coverage across reference



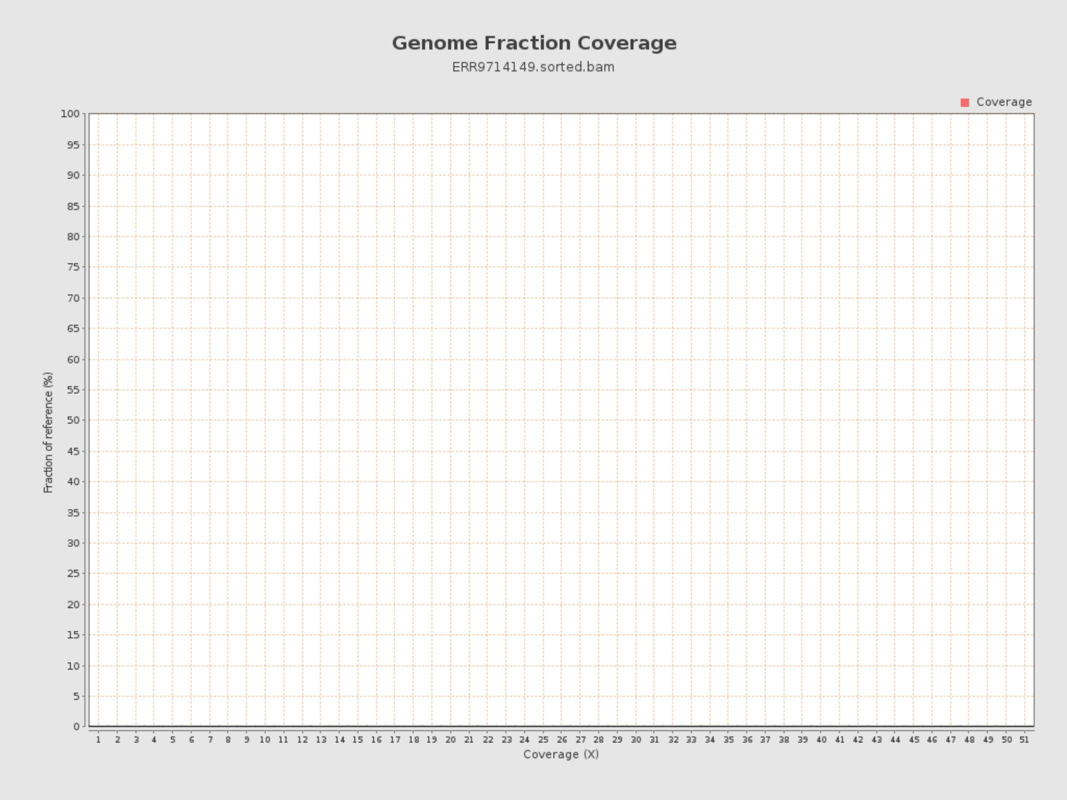
4. Results : Coverage Histogram



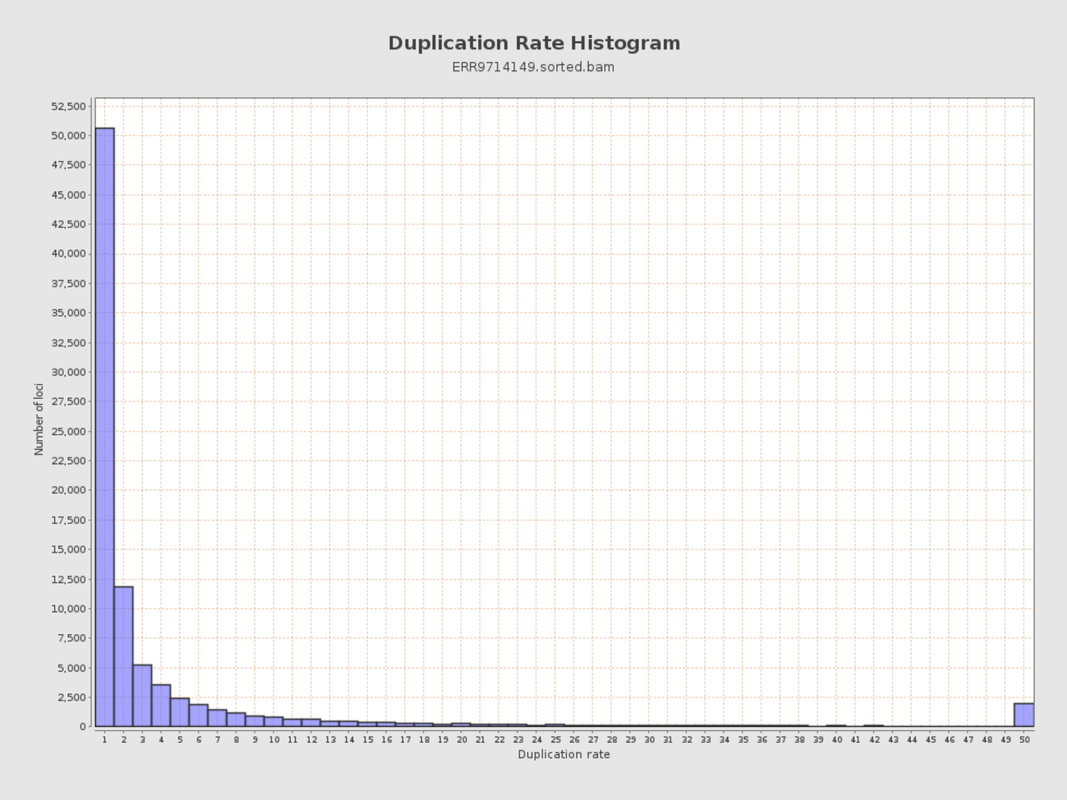
5. Results : Coverage Histogram (0-50X)



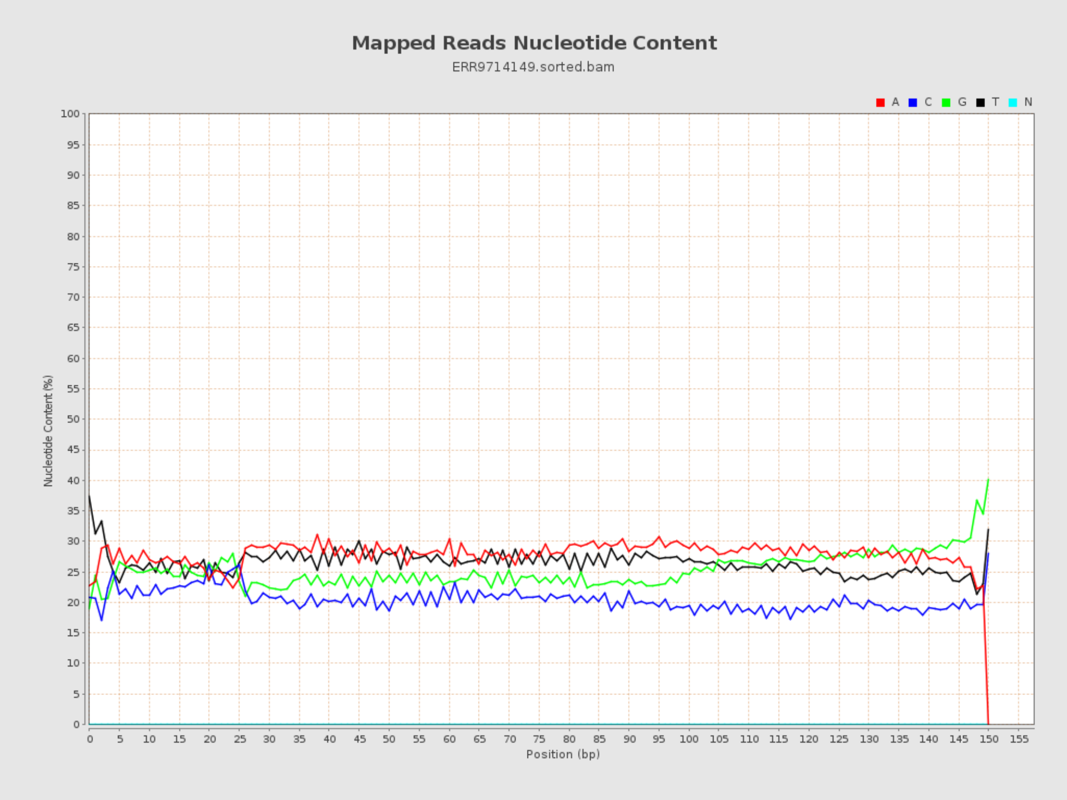
6. Results : Genome Fraction Coverage



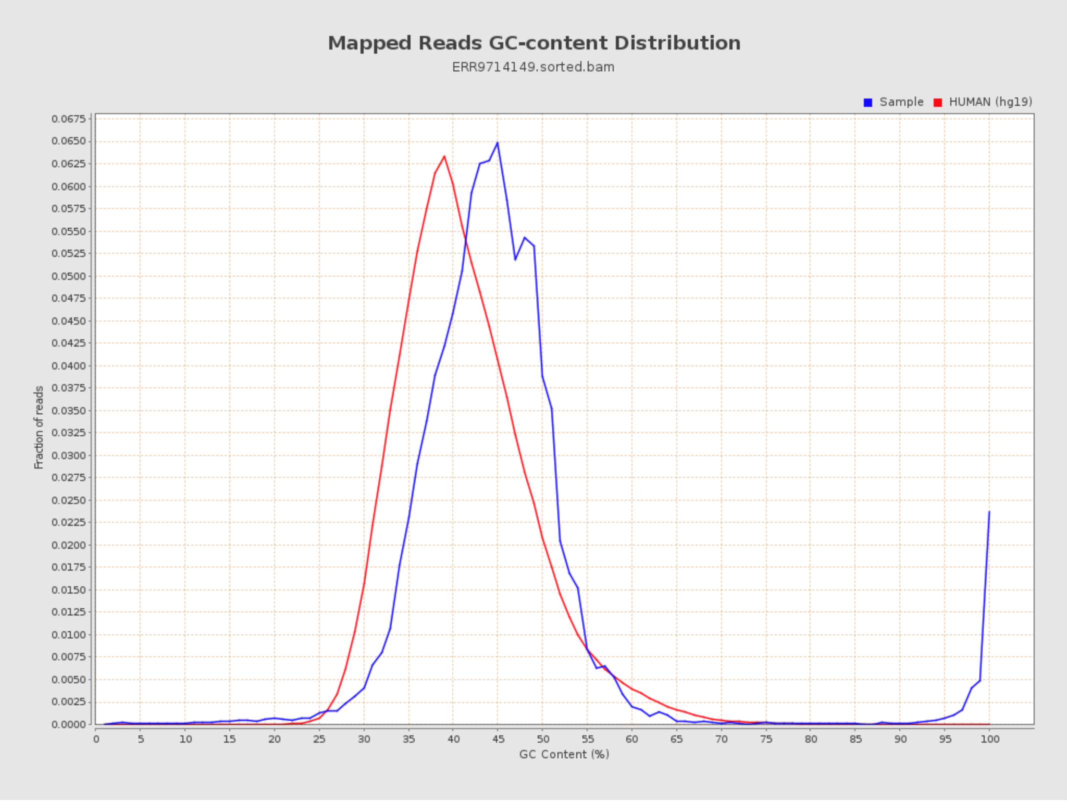
7. Results : Duplication Rate Histogram



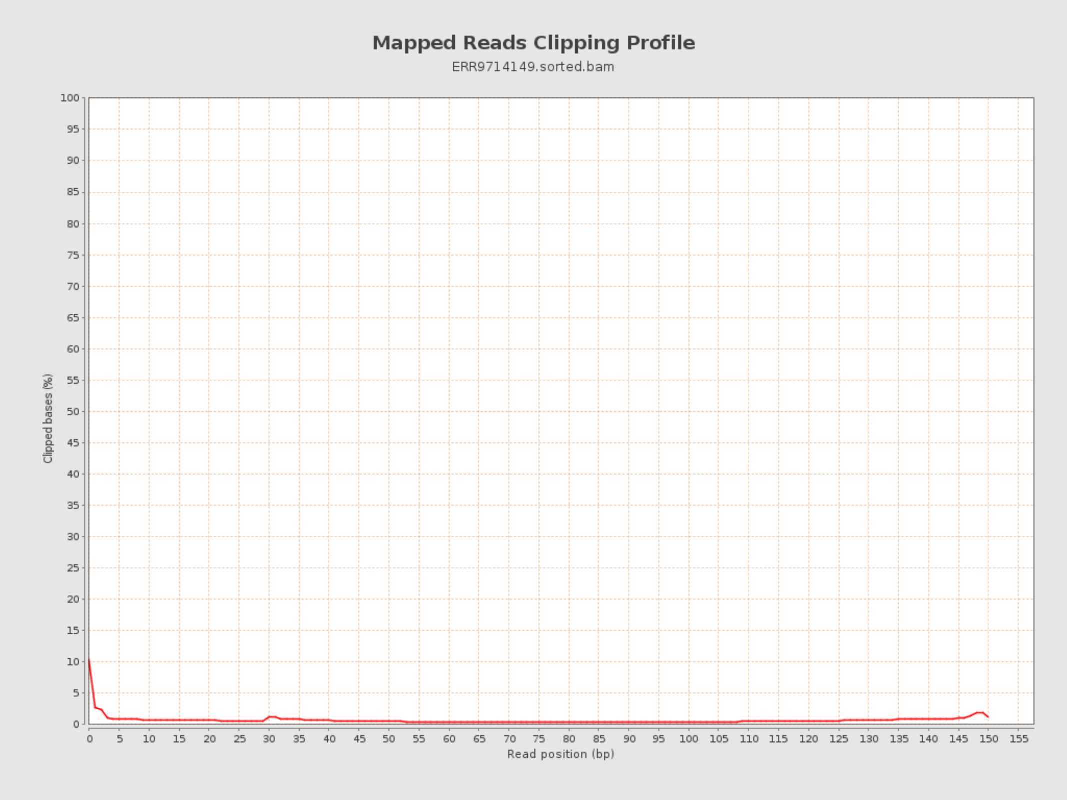
8. Results : Mapped Reads Nucleotide Content



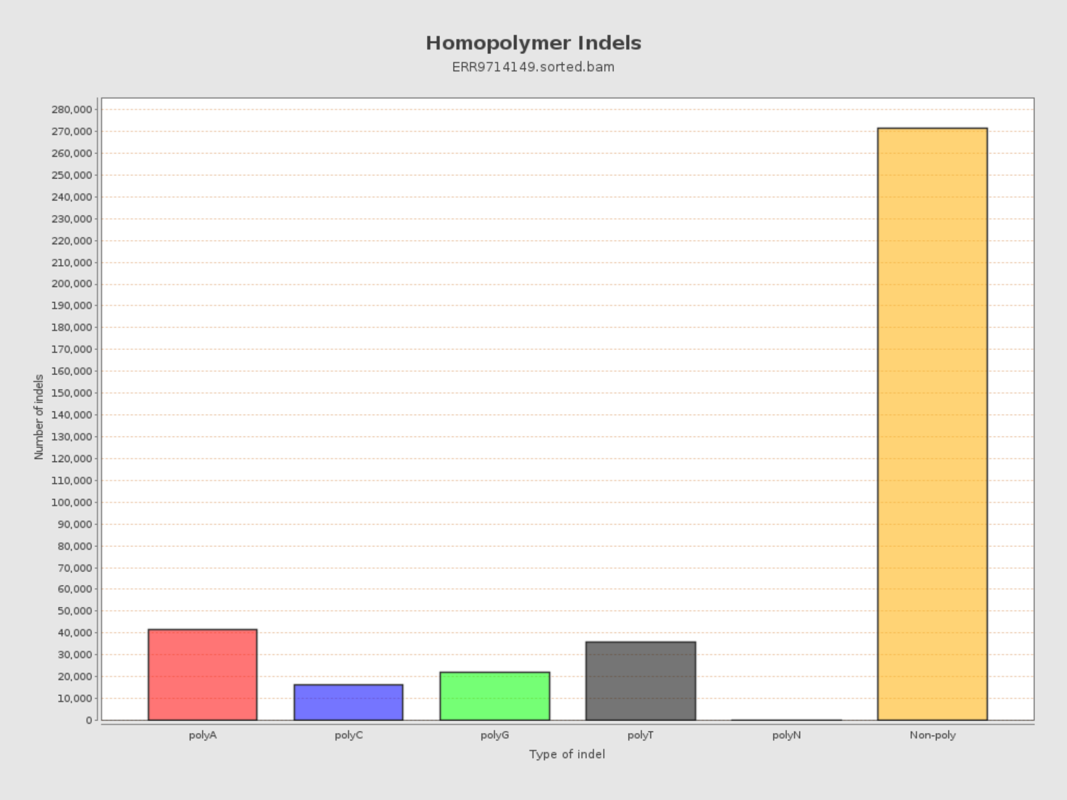
9. Results : Mapped Reads GC-content Distribution



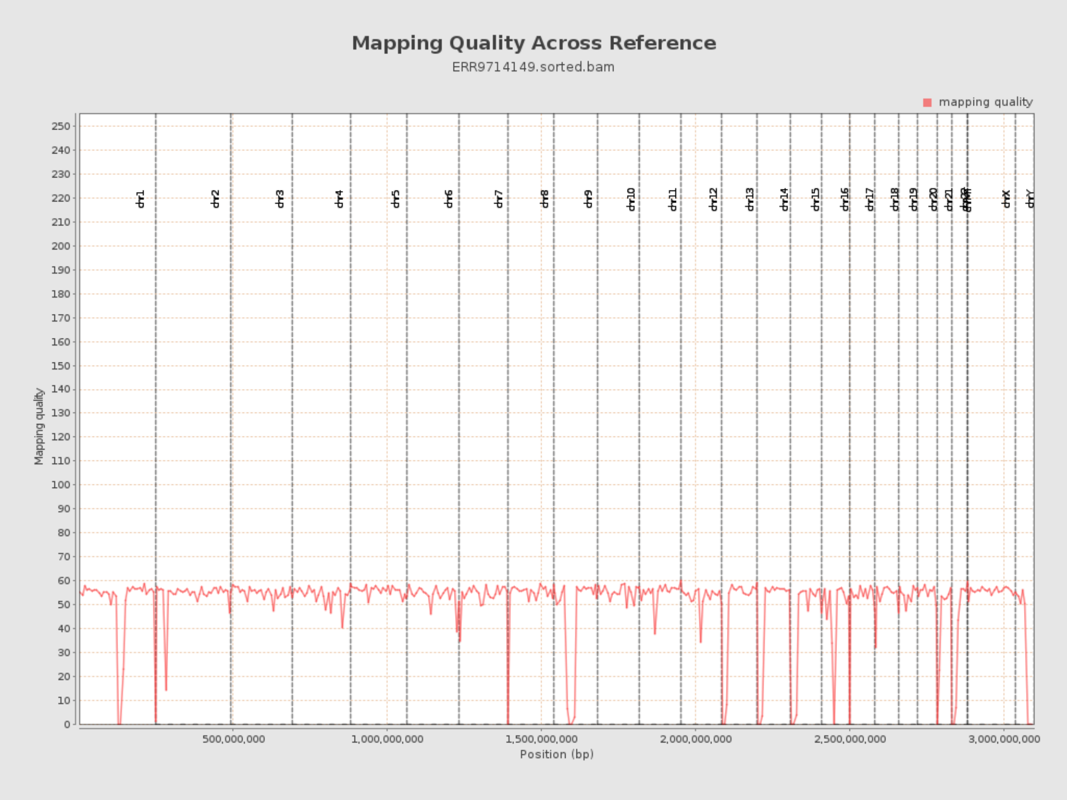
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram