Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 18:11:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714071.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_ERR9714071 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 18:11:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	513,218
Mapped reads	126,060 / 24.56%
Unmapped reads	387,158 / 75.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,095 / 0.99%
Read min/max/mean length	30 / 151 / 79.34
Duplicated reads (estimated)	113,907 / 22.19%
Duplication rate	38.96%
Clipped reads	111,151 / 21.66%

2.2. ACGT Content

Number/percentage of A's	3,321,876 / 22.67%
Number/percentage of C's	2,653,567 / 18.11%
Number/percentage of T's	3,113,205 / 21.24%
Number/percentage of G's	5,566,985 / 37.98%
Number/percentage of N's	354 / 0%
GC Percentage	56.09%

2.3. Coverage

Mean	0.0048

Standard Deviation	3.7258

2.4. Mapping Quality

Mean Mapping Quality	44.2

2.5. Mismatches and indels

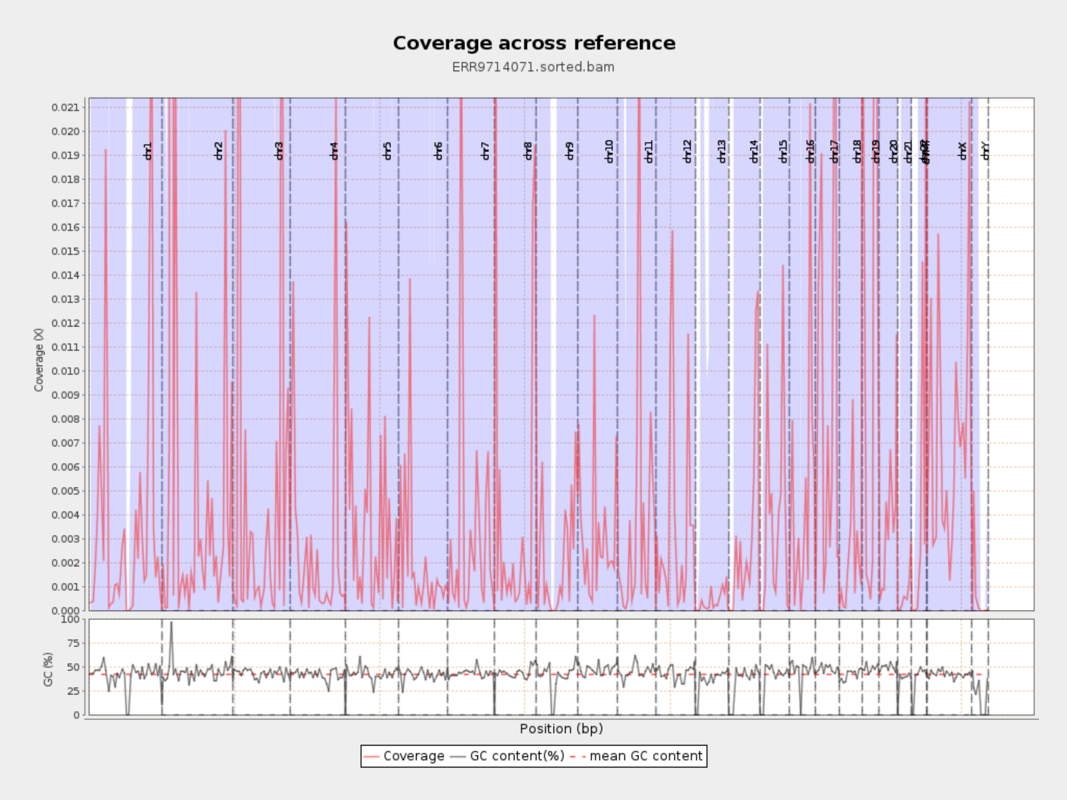
General error rate	4.13%
Mismatches	555,384
Insertions	16,047
Mapped reads with at least one insertion	11.81%
Deletions	45,657
Mapped reads with at least one deletion	33.72%
Homopolymer indels	29.81%

2.6. Chromosome stats

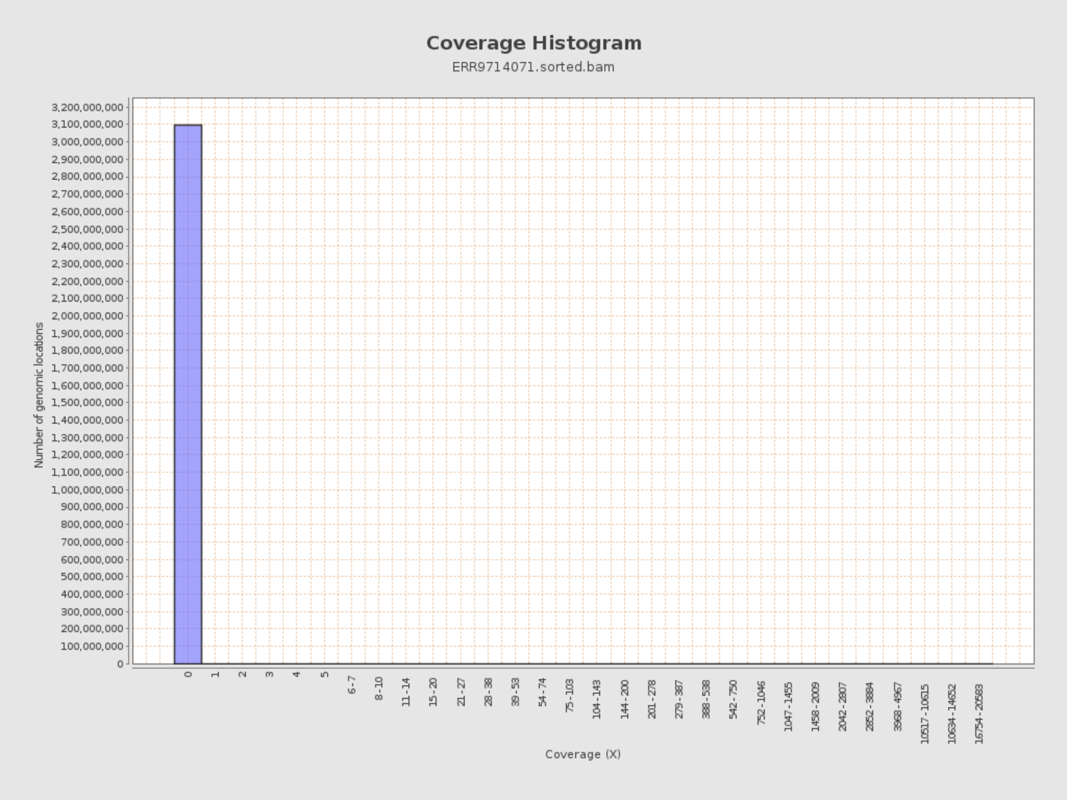
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	876260	0.0035	1.1967
chr2	243199373	3856921	0.0159	12.4973
chr3	198022430	1077529	0.0054	2.6421
chr4	191154276	524904	0.0027	1.1841
chr5	180915260	687413	0.0038	0.8292
chr6	171115067	339036	0.002	0.4977
chr7	159138663	521053	0.0033	1.3824

chr8	146364022	668523	0.0046	1.6773
chr9	141213431	287661	0.002	0.4719
chr10	135534747	432777	0.0032	0.7443
chr11	135006516	545114	0.004	1.4244
chr12	133851895	495985	0.0037	1.0081
chr13	115169878	48555	0.0004	0.0934
chr14	107349540	355412	0.0033	0.9106
chr15	102531392	400347	0.0039	1.0464
chr16	90354753	446110	0.0049	1.407
chr17	81195210	692473	0.0085	2.5928
chr18	78077248	169629	0.0022	0.4737
chr19	59128983	709621	0.012	2.4577
chr20	63025520	221564	0.0035	0.6116
chr21	48129895	33332	0.0007	0.1417
chr22	51304566	196963	0.0038	1.2576
chrMT	16571	144291	8.7074	58.4158
chrX	155270560	1147154	0.0074	0.8365
chrY	59373566	43908	0.0007	0.3826

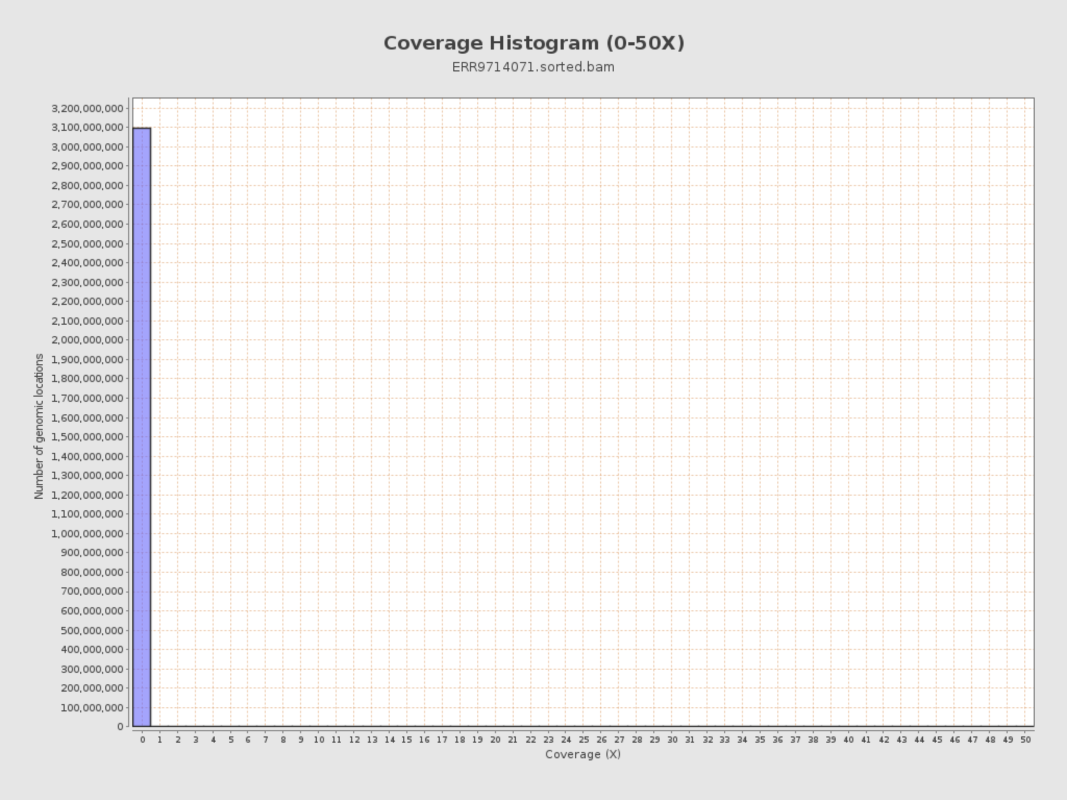
3. Results : Coverage across reference



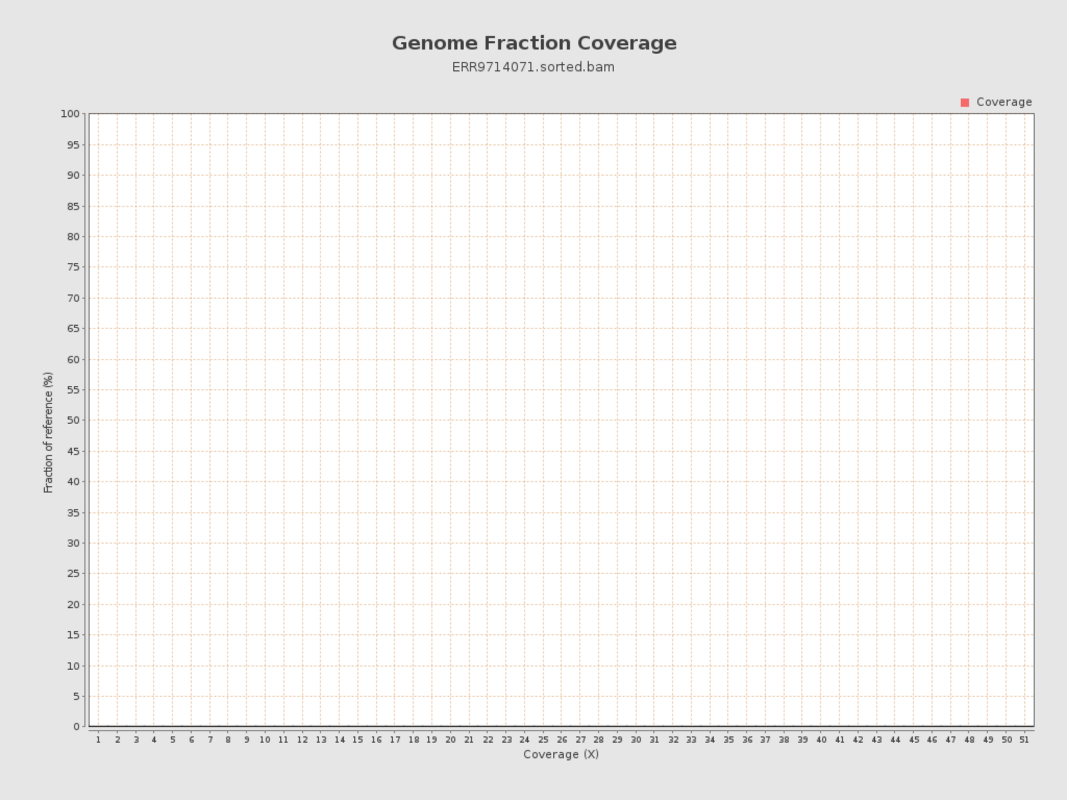
4. Results : Coverage Histogram



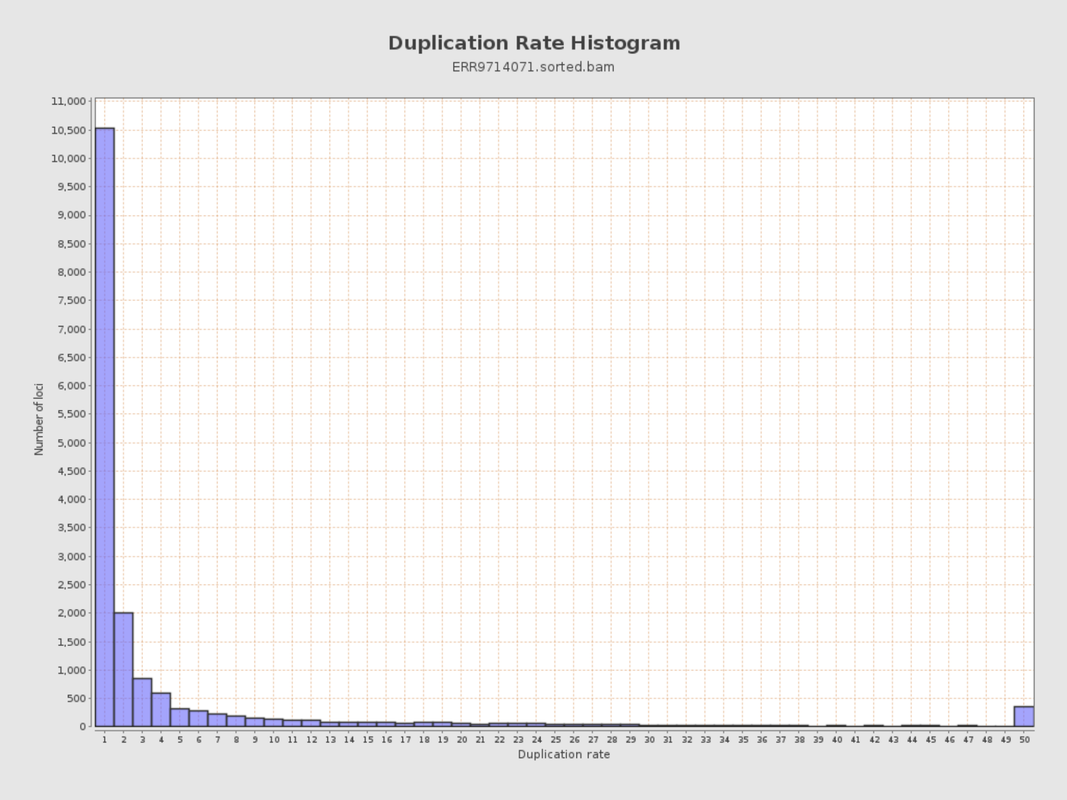
5. Results : Coverage Histogram (0-50X)



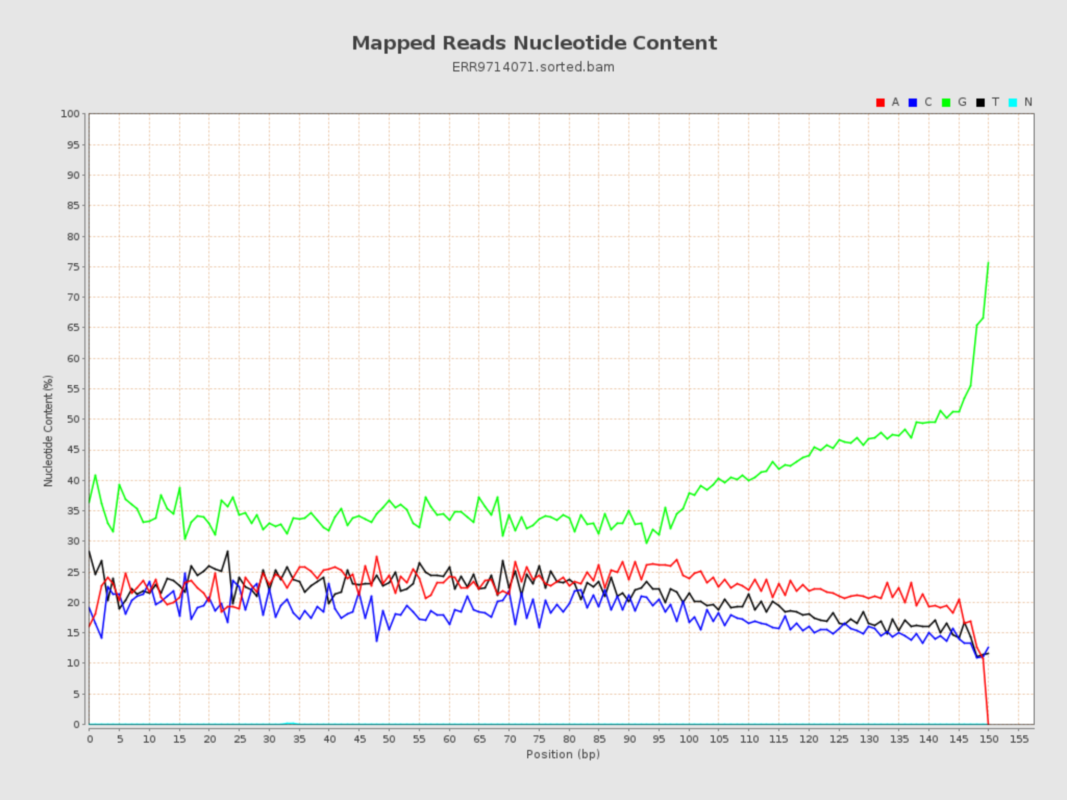
6. Results : Genome Fraction Coverage



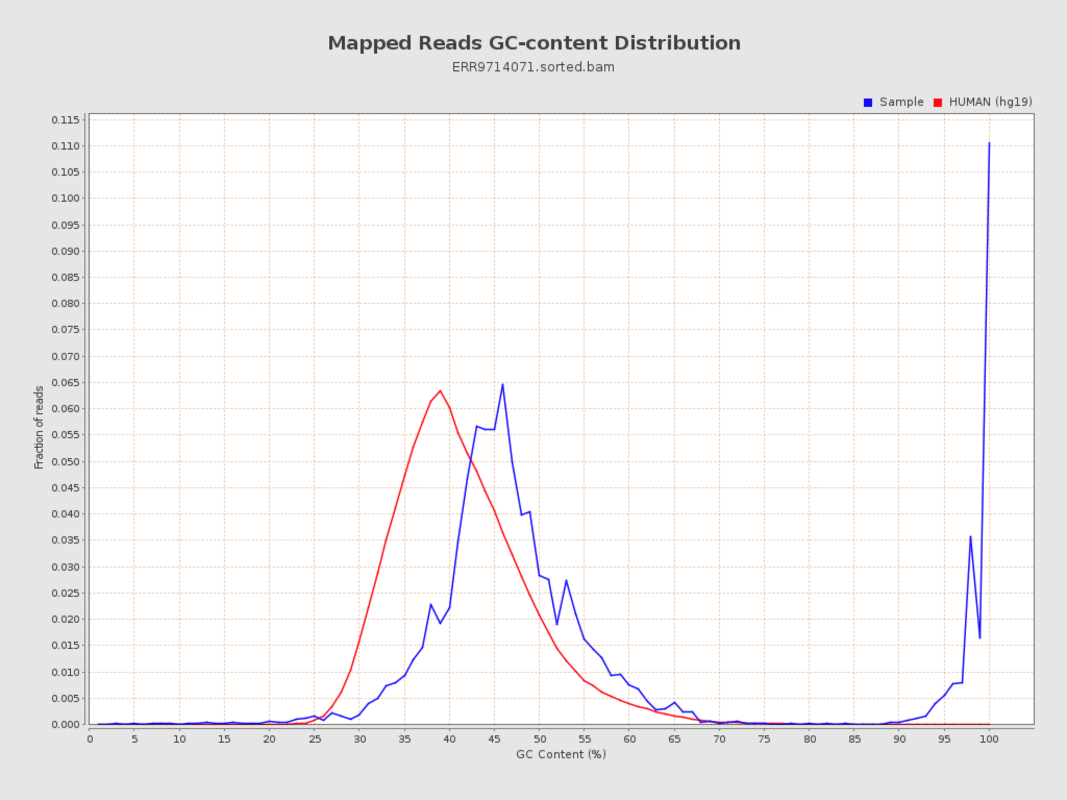
7. Results : Duplication Rate Histogram



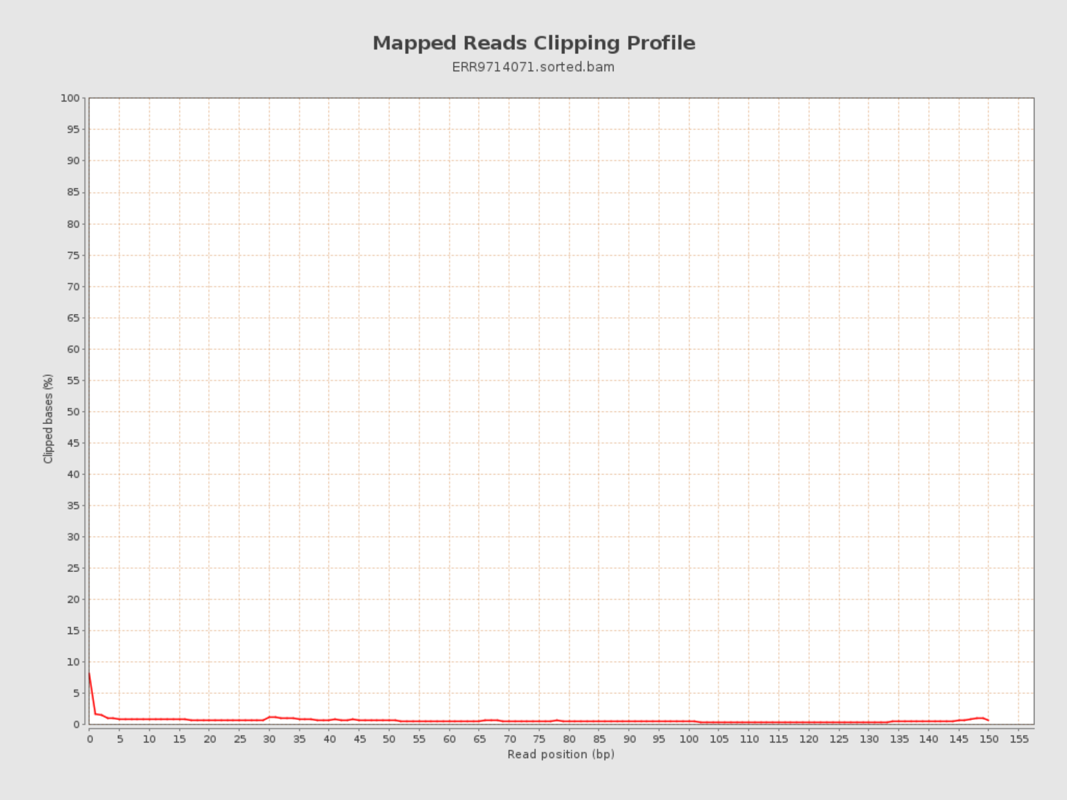
8. Results : Mapped Reads Nucleotide Content



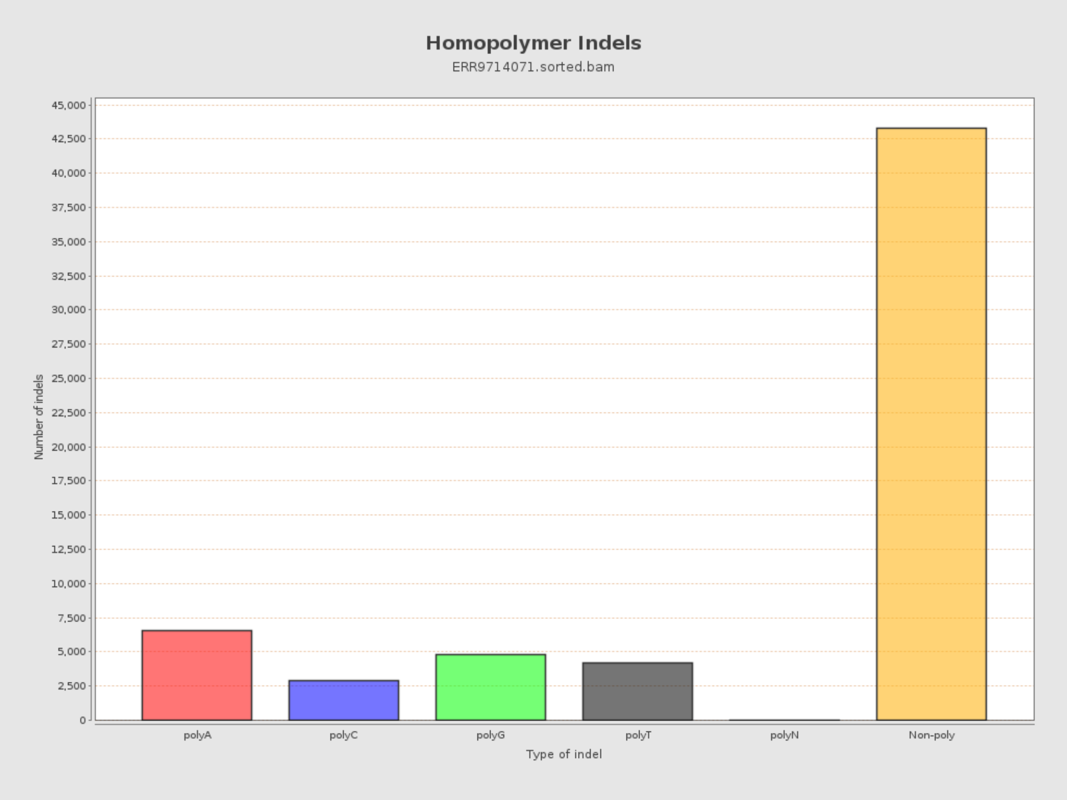
9. Results : Mapped Reads GC-content Distribution



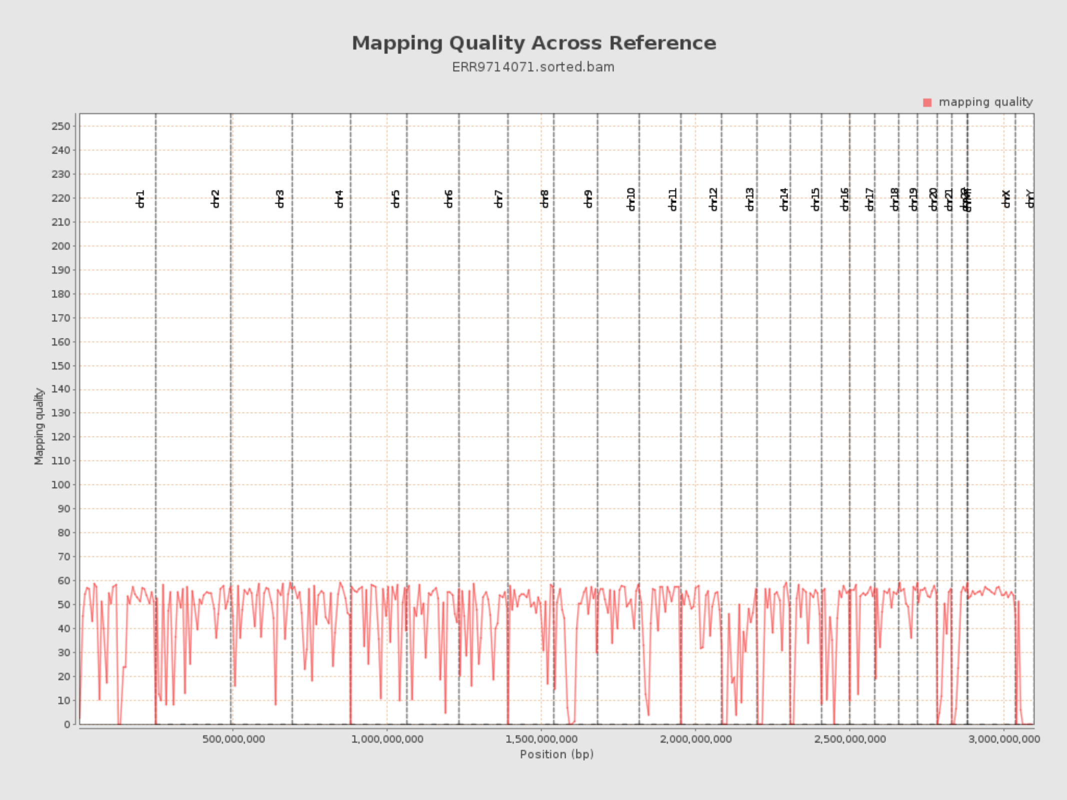
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram