Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:57:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714113.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_ERR9714113 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:57:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	634,126
Mapped reads	453,510 / 71.52%
Unmapped reads	180,616 / 28.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,749 / 2.48%
Read min/max/mean length	30 / 151 / 123.11
Duplicated reads (estimated)	397,955 / 62.76%
Duplication rate	43.75%
Clipped reads	422,376 / 66.61%

2.2. ACGT Content

Number/percentage of A's	15,704,752 / 27.5%
Number/percentage of C's	11,534,098 / 20.2%
Number/percentage of T's	14,838,489 / 25.98%
Number/percentage of G's	15,029,878 / 26.32%
Number/percentage of N's	562 / 0%
GC Percentage	46.52%

2.3. Coverage

Mean	0.0189

Standard Deviation	4.9786

2.4. Mapping Quality

Mean Mapping Quality	50.95

2.5. Mismatches and indels

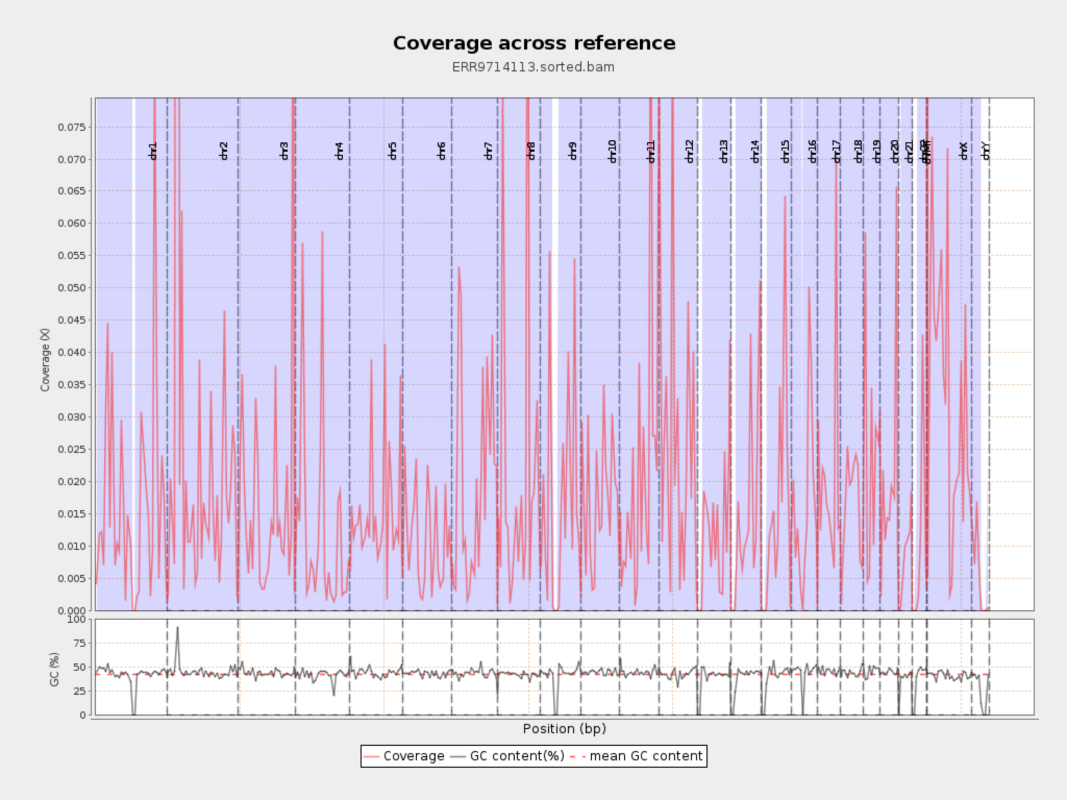
General error rate	4.7%
Mismatches	2,508,038
Insertions	62,671
Mapped reads with at least one insertion	13.17%
Deletions	222,374
Mapped reads with at least one deletion	45.38%
Homopolymer indels	31.36%

2.6. Chromosome stats

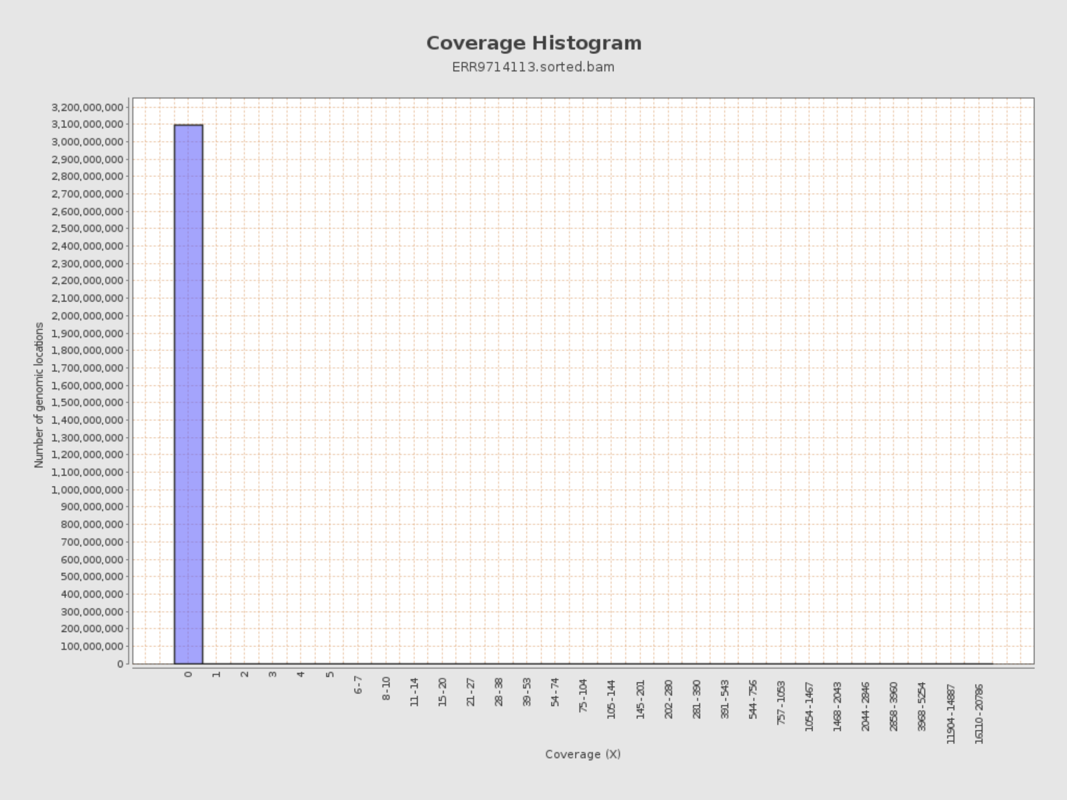
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4239829	0.017	3.5486
chr2	243199373	7675118	0.0316	13.4513
chr3	198022430	3595903	0.0182	4.2261
chr4	191154276	2361708	0.0124	2.633
chr5	180915260	2901677	0.016	2.2137
chr6	171115067	1882971	0.011	1.4007
chr7	159138663	3088649	0.0194	3.1965

chr8	146364022	3202355	0.0219	5.2364
chr9	141213431	2328719	0.0165	3.4639
chr10	135534747	2342103	0.0173	2.252
chr11	135006516	2852559	0.0211	5.6905
chr12	133851895	3560377	0.0266	4.3649
chr13	115169878	1310999	0.0114	1.8531
chr14	107349540	1637371	0.0153	3.3587
chr15	102531392	1620339	0.0158	2.5099
chr16	90354753	1523806	0.0169	2.602
chr17	81195210	1715810	0.0211	3.8043
chr18	78077248	1289460	0.0165	2.1783
chr19	59128983	1404590	0.0238	3.7233
chr20	63025520	1309536	0.0208	3.6613
chr21	48129895	392068	0.0081	0.9362
chr22	51304566	501884	0.0098	1.922
chrMT	16571	340563	20.5517	163.048
chrX	155270560	5115759	0.0329	3.3447
chrY	59373566	311954	0.0053	1.0908

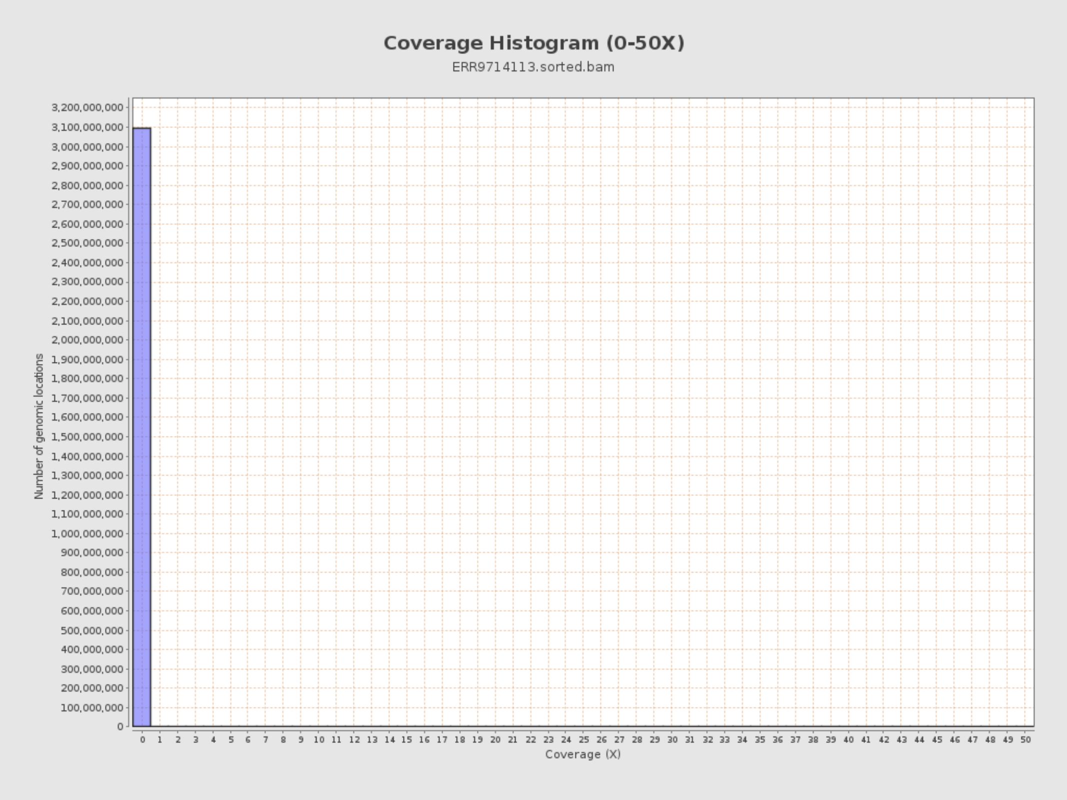
3. Results : Coverage across reference



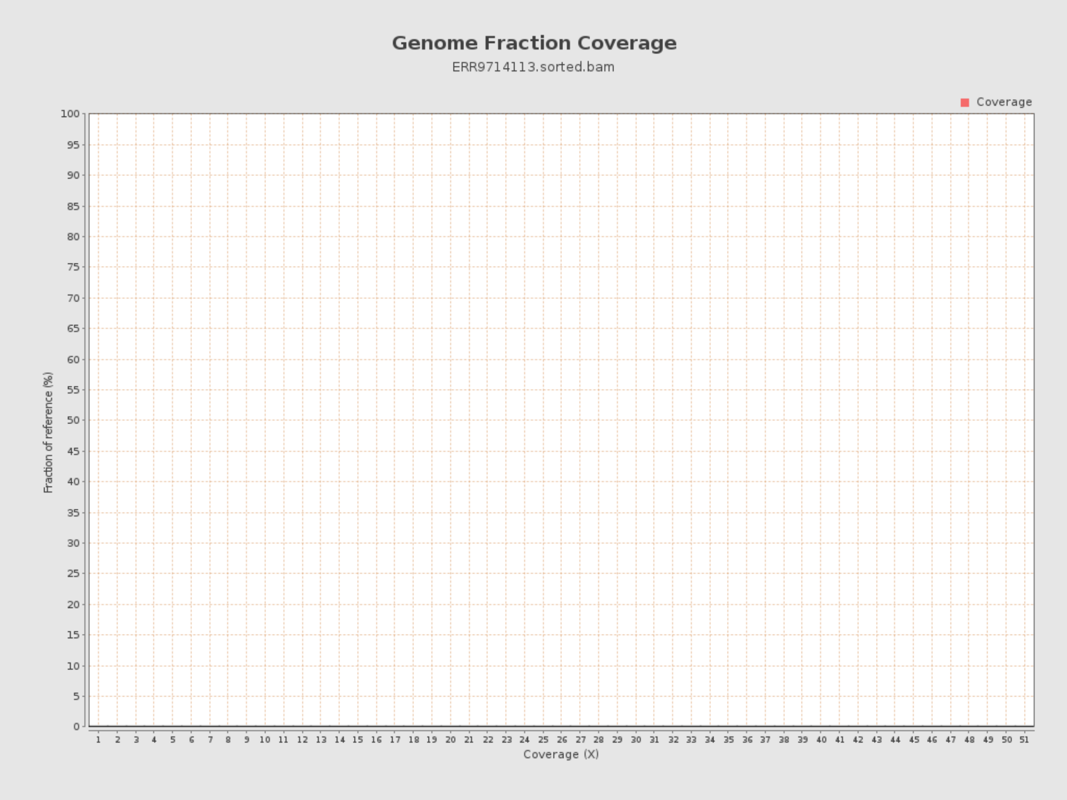
4. Results : Coverage Histogram



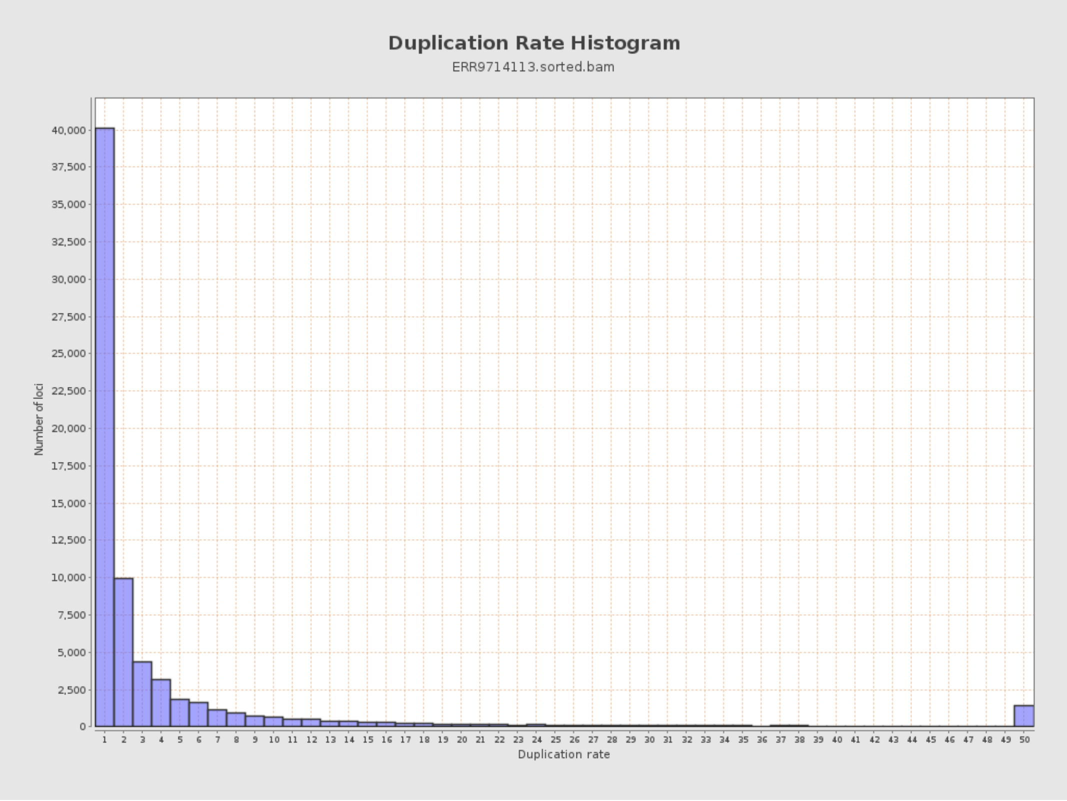
5. Results : Coverage Histogram (0-50X)



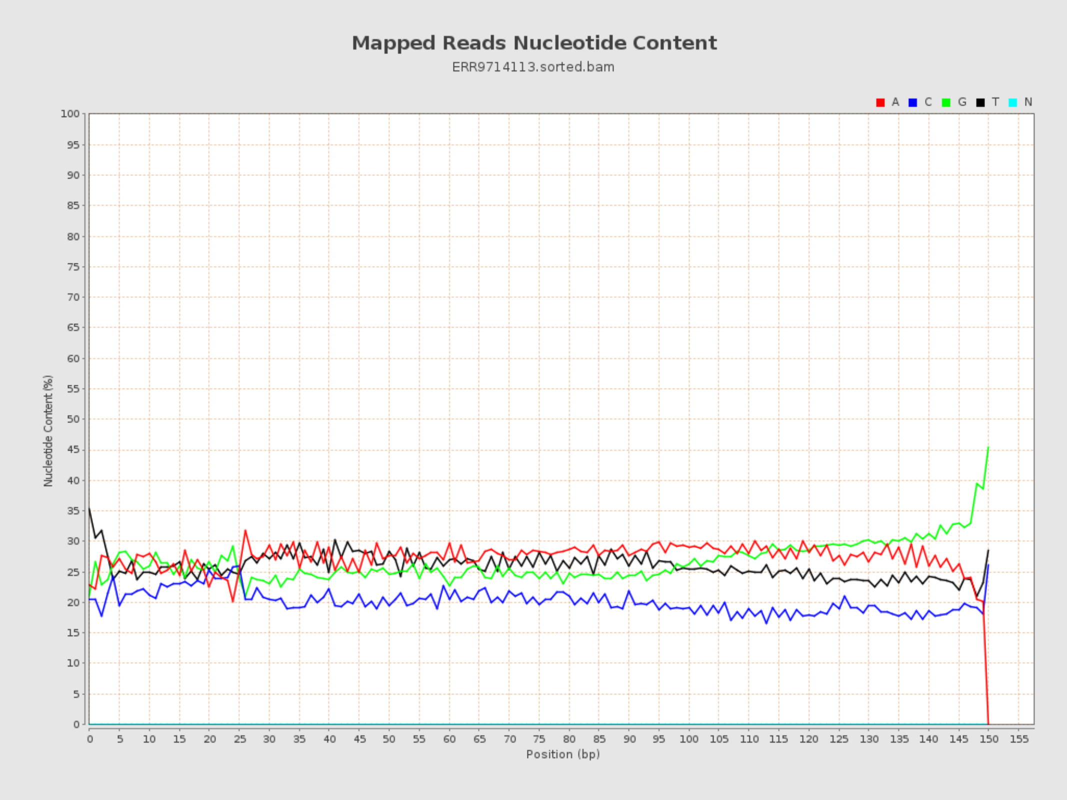
6. Results : Genome Fraction Coverage



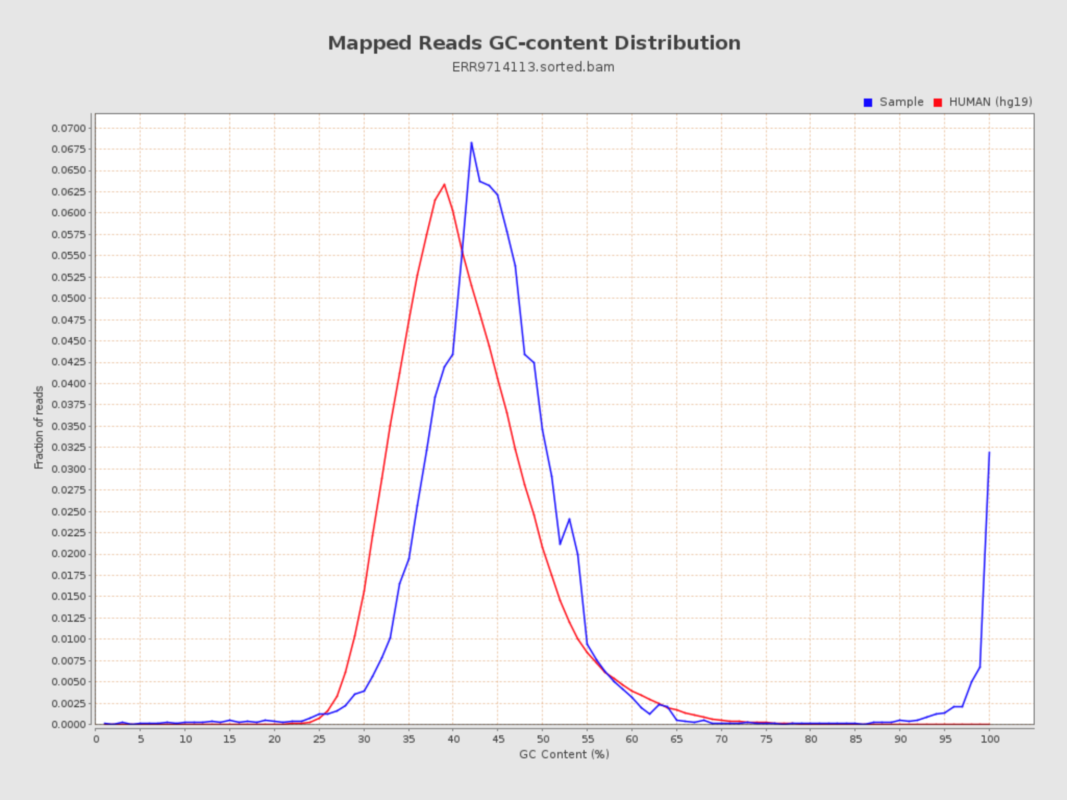
7. Results : Duplication Rate Histogram



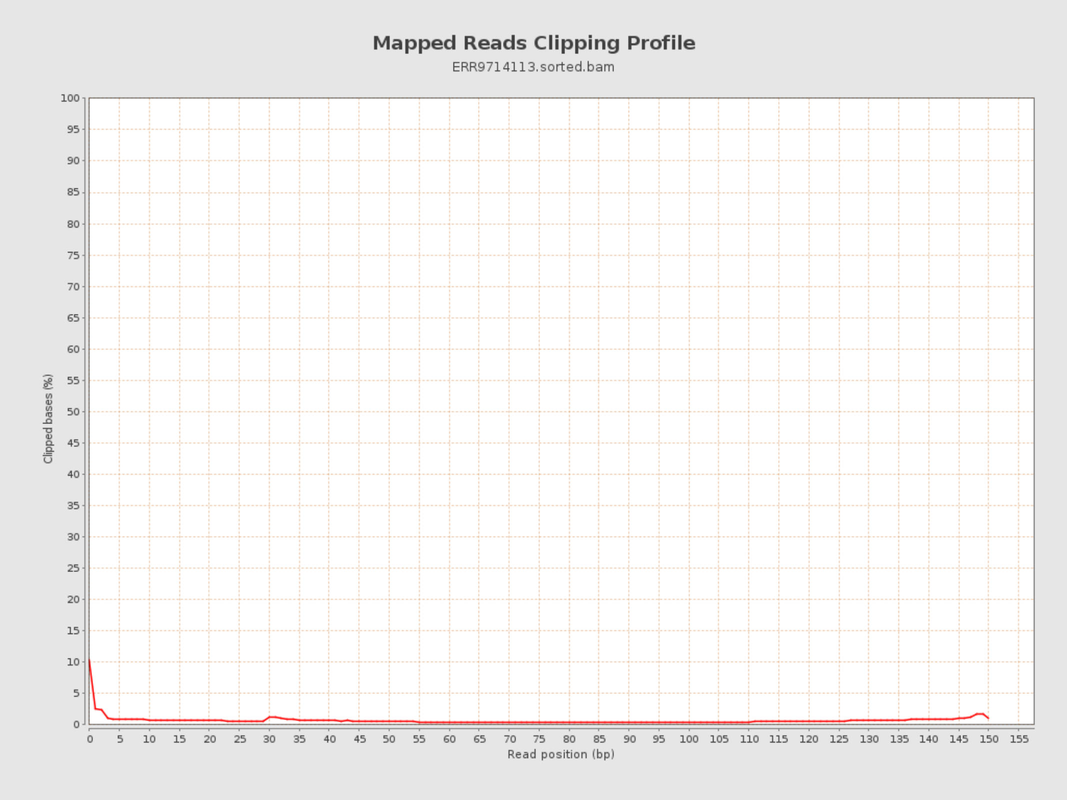
8. Results : Mapped Reads Nucleotide Content



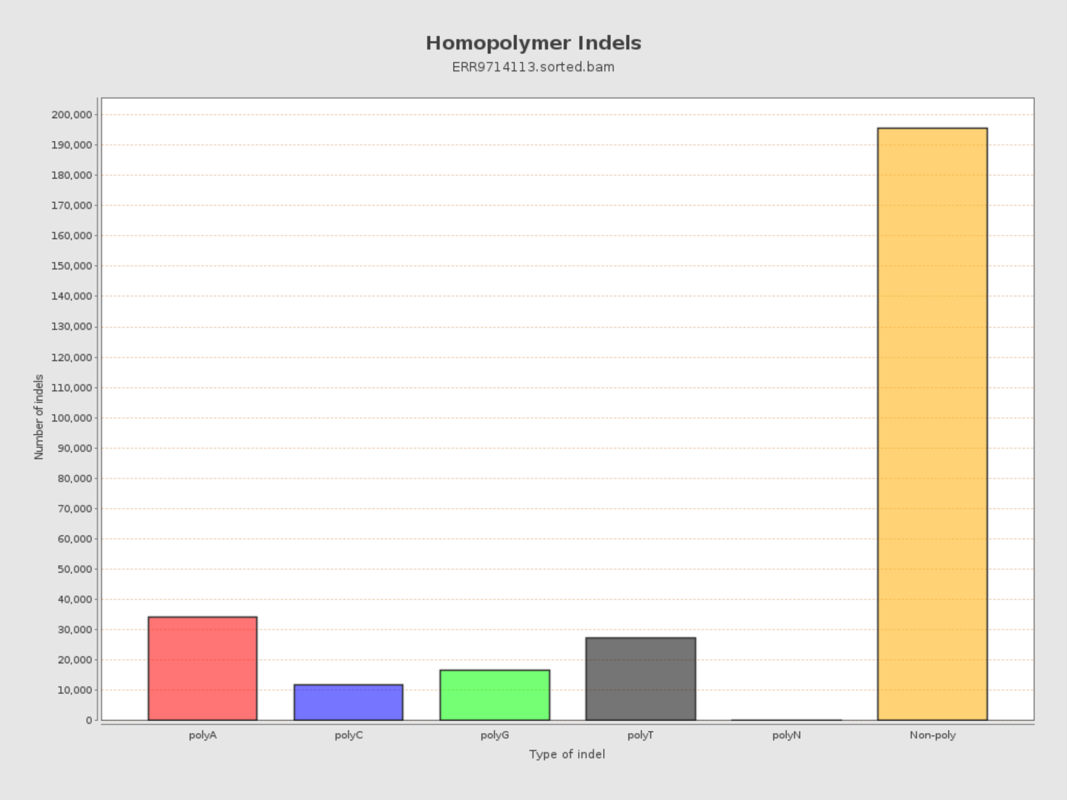
9. Results : Mapped Reads GC-content Distribution



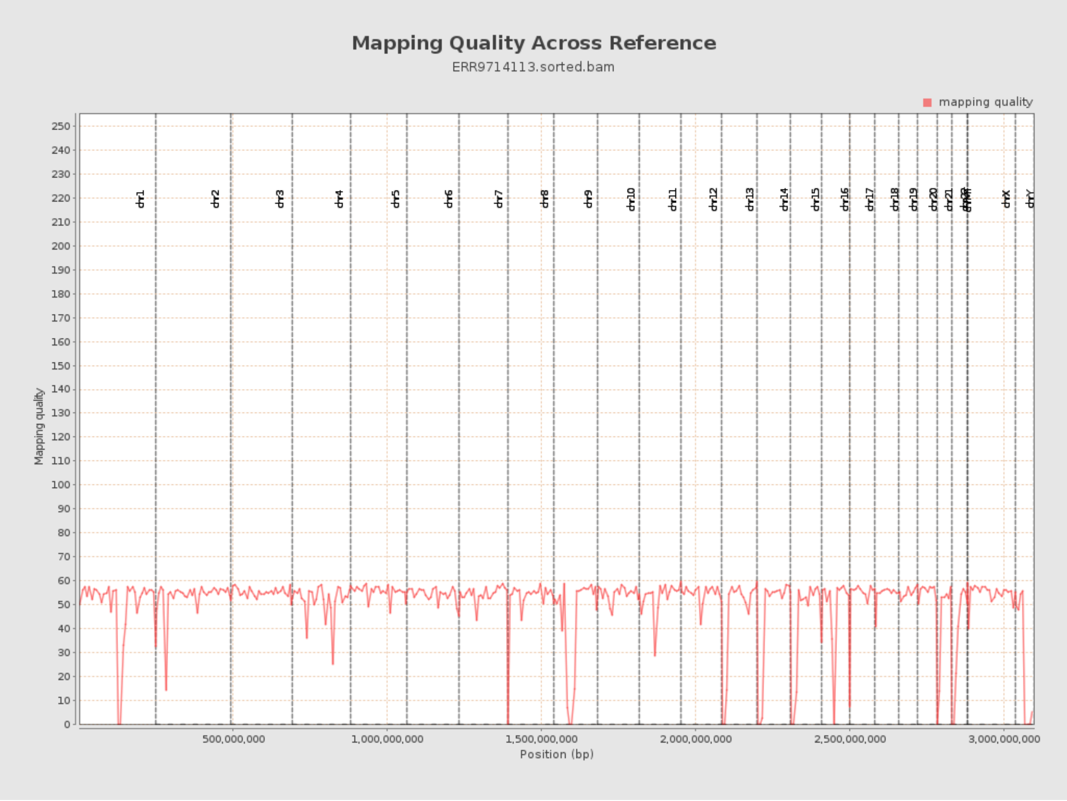
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram