Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:44:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714108.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_ERR9714108 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714108.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:44:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714108.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	849,174
Mapped reads	213,899 / 25.19%
Unmapped reads	635,275 / 74.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,602 / 0.54%
Read min/max/mean length	30 / 151 / 73.99
Duplicated reads (estimated)	204,964 / 24.14%
Duplication rate	38.61%
Clipped reads	179,992 / 21.2%

2.2. ACGT Content

Number/percentage of A's	5,772,350 / 22.21%
Number/percentage of C's	4,620,159 / 17.78%
Number/percentage of T's	5,750,270 / 22.12%
Number/percentage of G's	9,846,926 / 37.89%
Number/percentage of N's	683 / 0%
GC Percentage	55.66%

2.3. Coverage

Mean	0.0084

Standard Deviation	15.2941

2.4. Mapping Quality

Mean Mapping Quality	31.62

2.5. Mismatches and indels

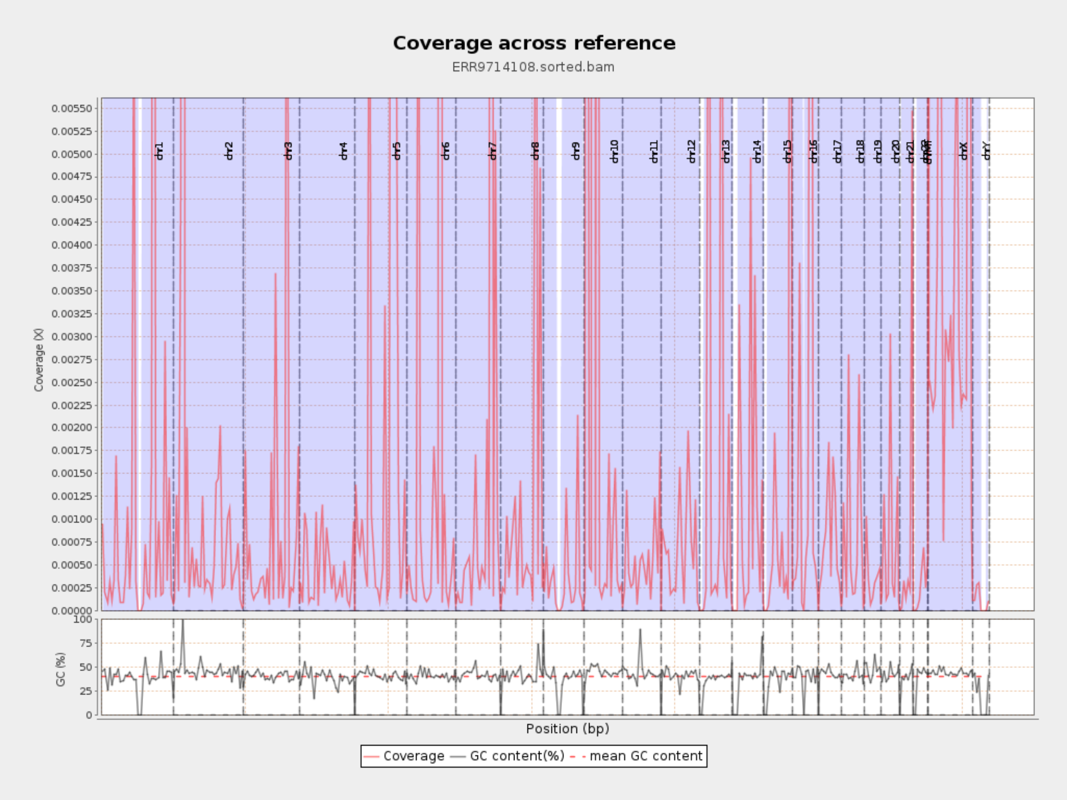
General error rate	3.54%
Mismatches	659,485
Insertions	52,443
Mapped reads with at least one insertion	23.1%
Deletions	40,950
Mapped reads with at least one deletion	18.5%
Homopolymer indels	41.47%

2.6. Chromosome stats

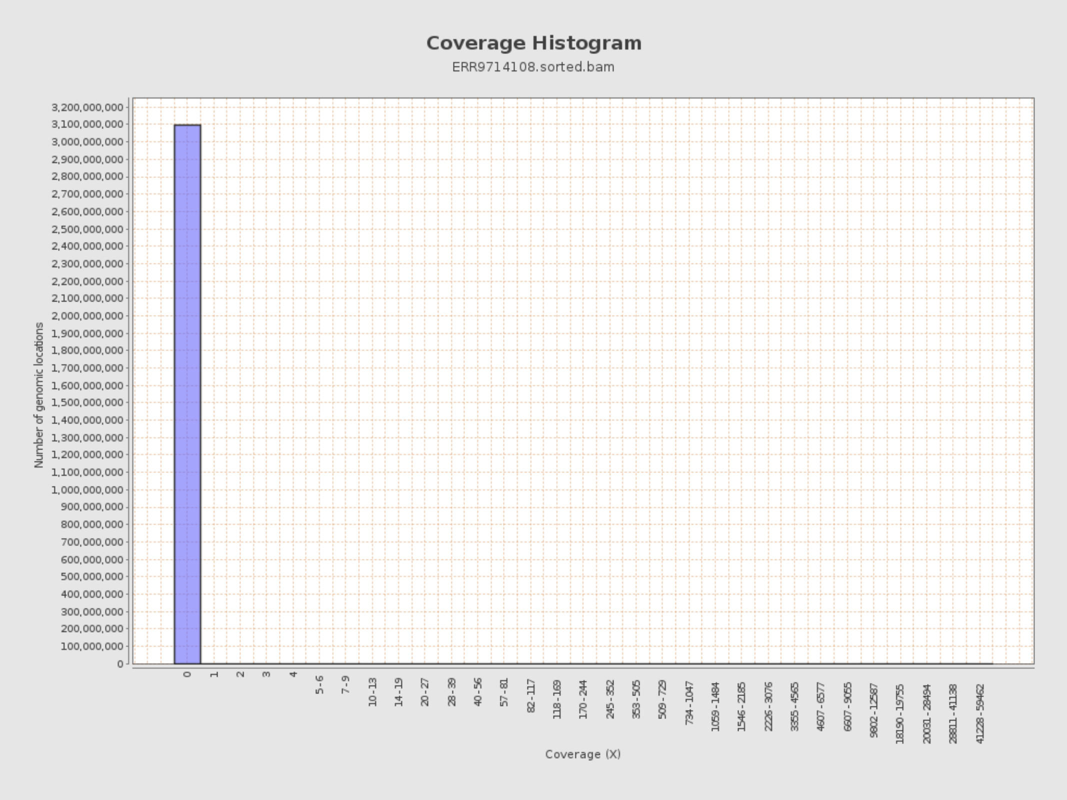
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	362909	0.0015	0.9648
chr2	243199373	5242974	0.0216	21.996
chr3	198022430	200172	0.001	0.3443
chr4	191154276	83902	0.0004	0.0815
chr5	180915260	424776	0.0023	0.952
chr6	171115067	1994121	0.0117	11.2535
chr7	159138663	500197	0.0031	2.4483

chr8	146364022	177745	0.0012	0.4744
chr9	141213431	52536	0.0004	0.0765
chr10	135534747	8073661	0.0596	52.4839
chr11	135006516	76015	0.0006	0.0994
chr12	133851895	93854	0.0007	0.1366
chr13	115169878	206743	0.0018	0.7896
chr14	107349540	125408	0.0012	0.3624
chr15	102531392	136714	0.0013	0.7266
chr16	90354753	181807	0.002	1.0507
chr17	81195210	63290	0.0008	0.1508
chr18	78077248	71486	0.0009	0.2612
chr19	59128983	21322	0.0004	0.0742
chr20	63025520	51797	0.0008	0.2221
chr21	48129895	34864	0.0007	0.2007
chr22	51304566	13004	0.0003	0.0565
chrMT	16571	7288568	439.8388	3,530.5449
chrX	155270560	620962	0.004	0.4843
chrY	59373566	6877	0.0001	0.0216

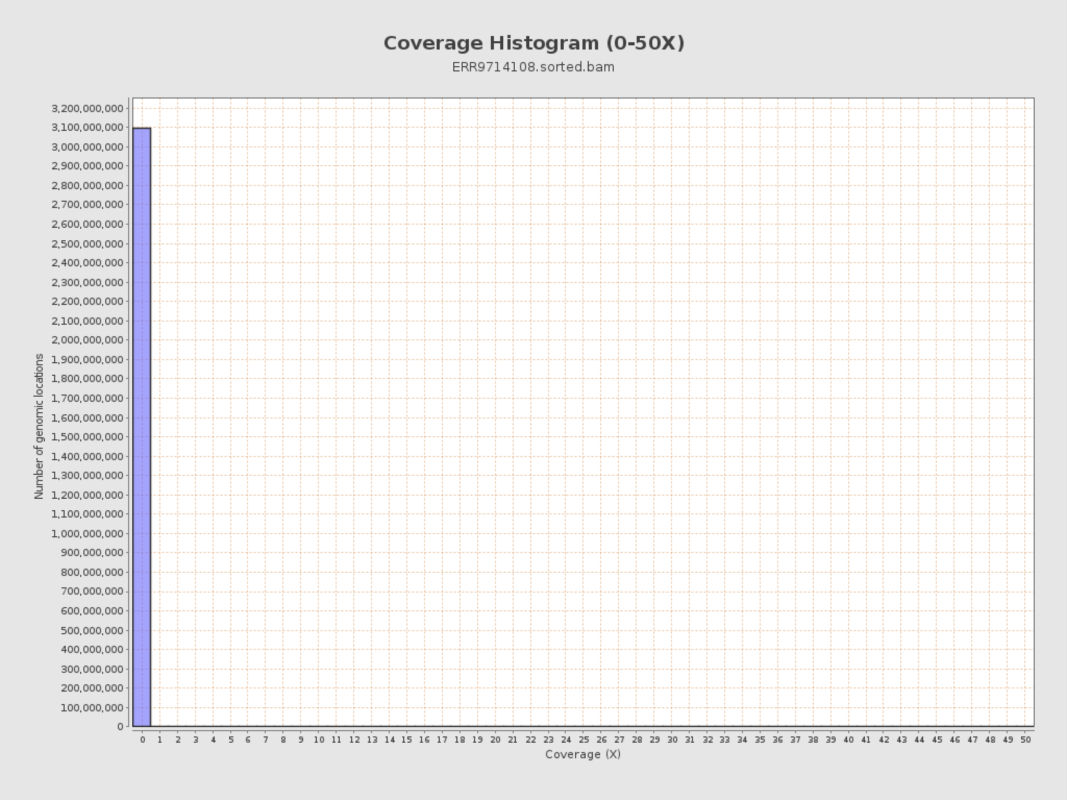
3. Results : Coverage across reference



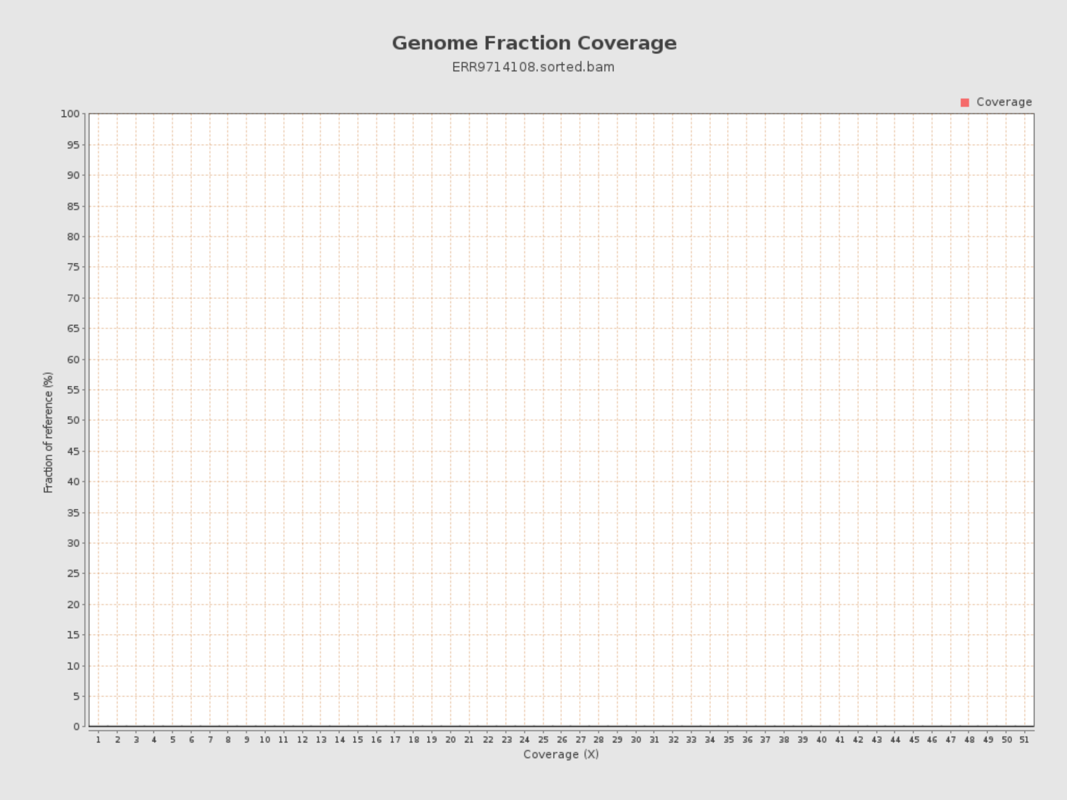
4. Results : Coverage Histogram



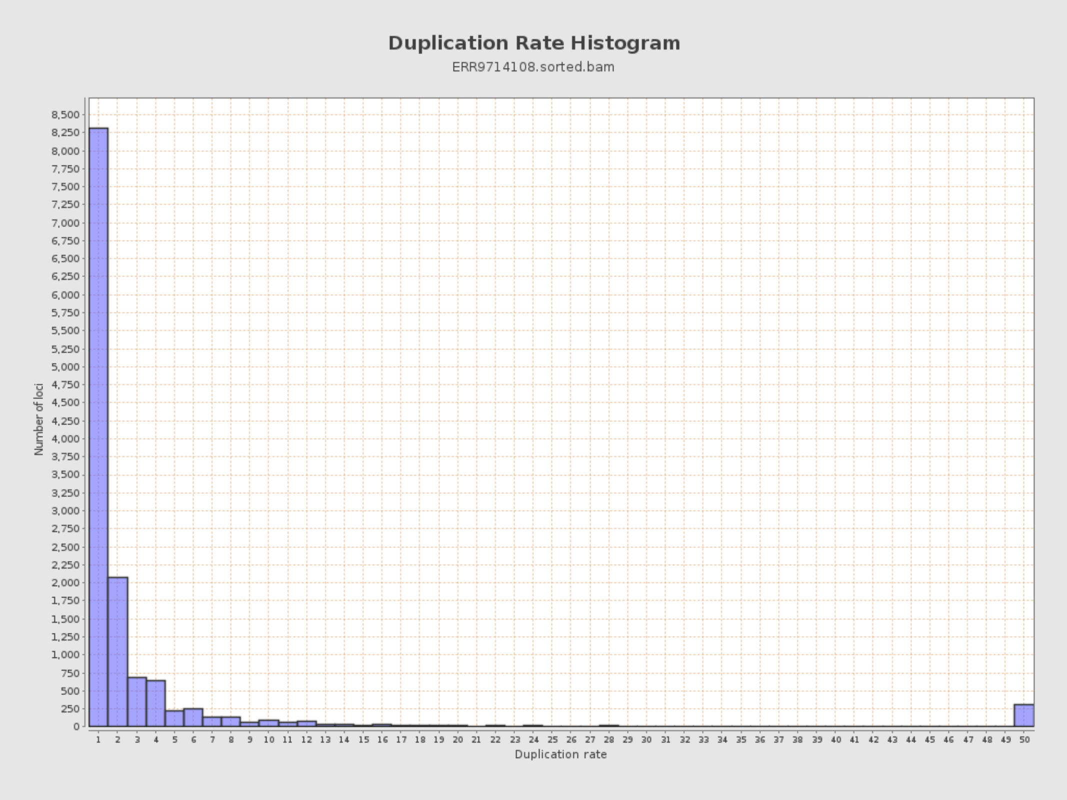
5. Results : Coverage Histogram (0-50X)



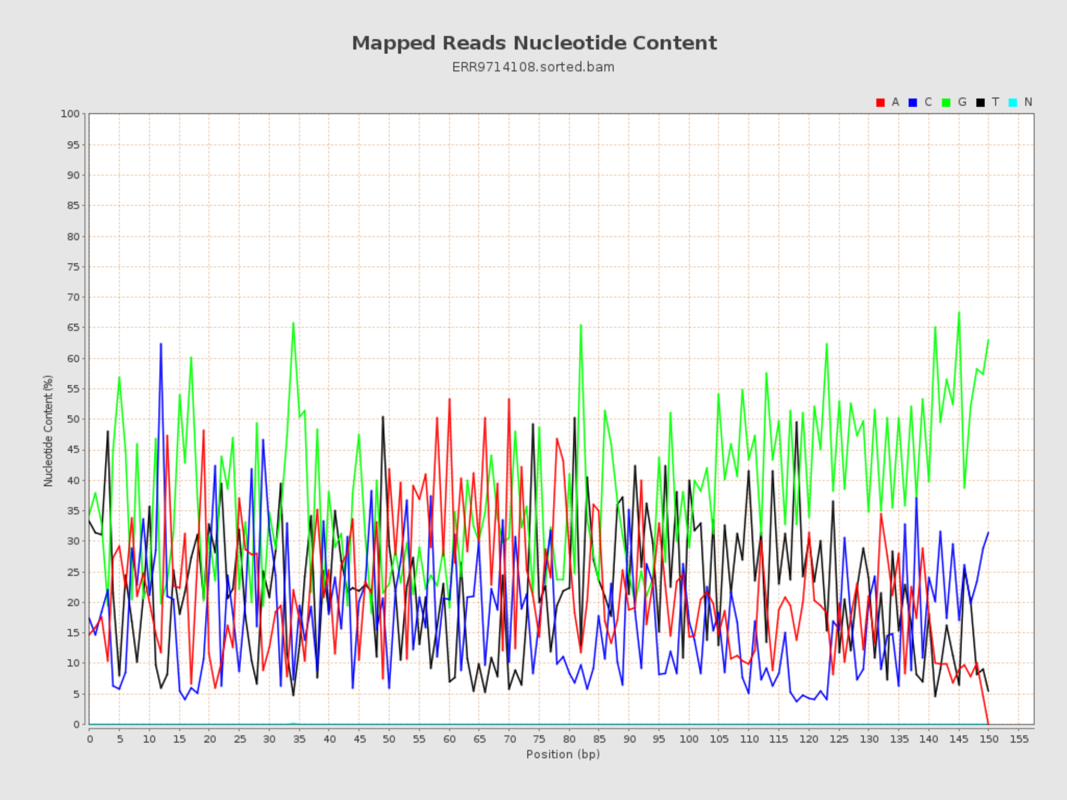
6. Results : Genome Fraction Coverage



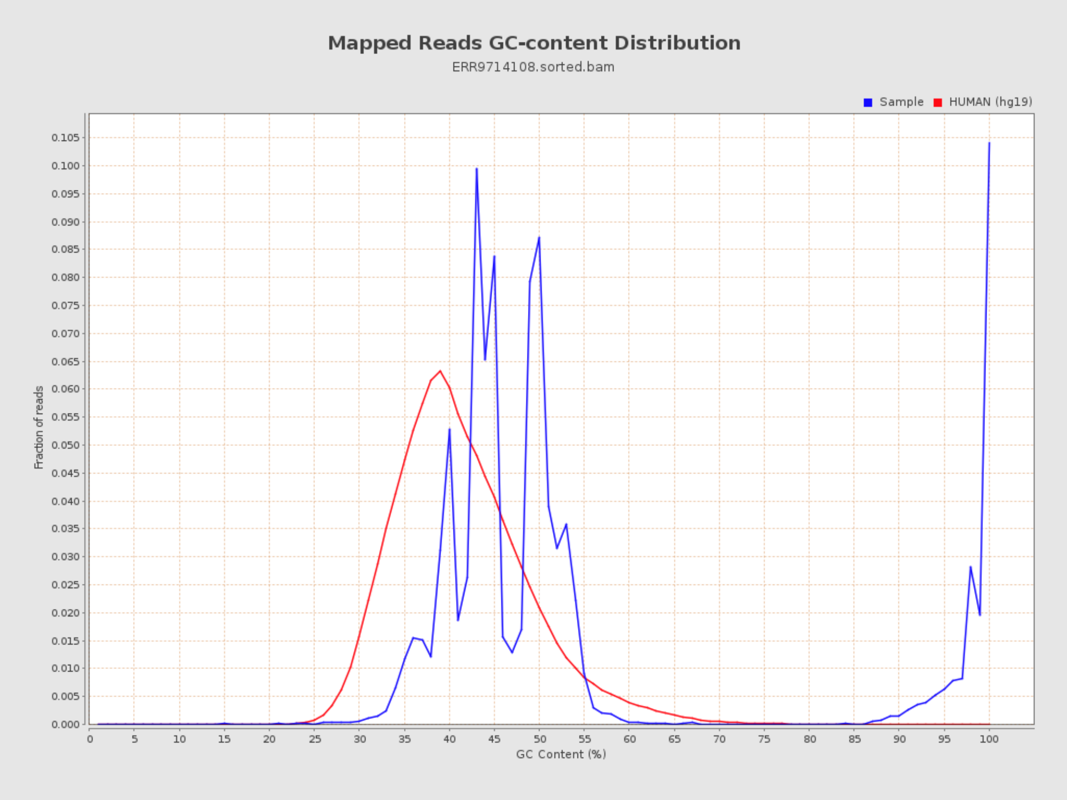
7. Results : Duplication Rate Histogram



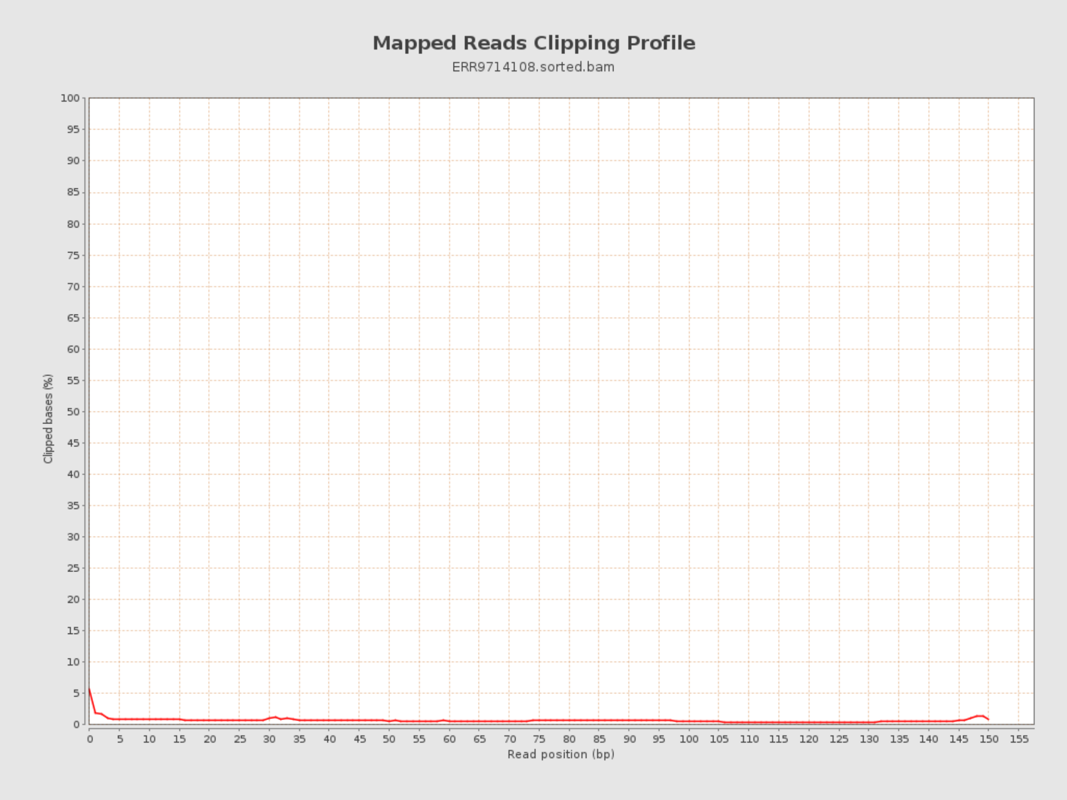
8. Results : Mapped Reads Nucleotide Content



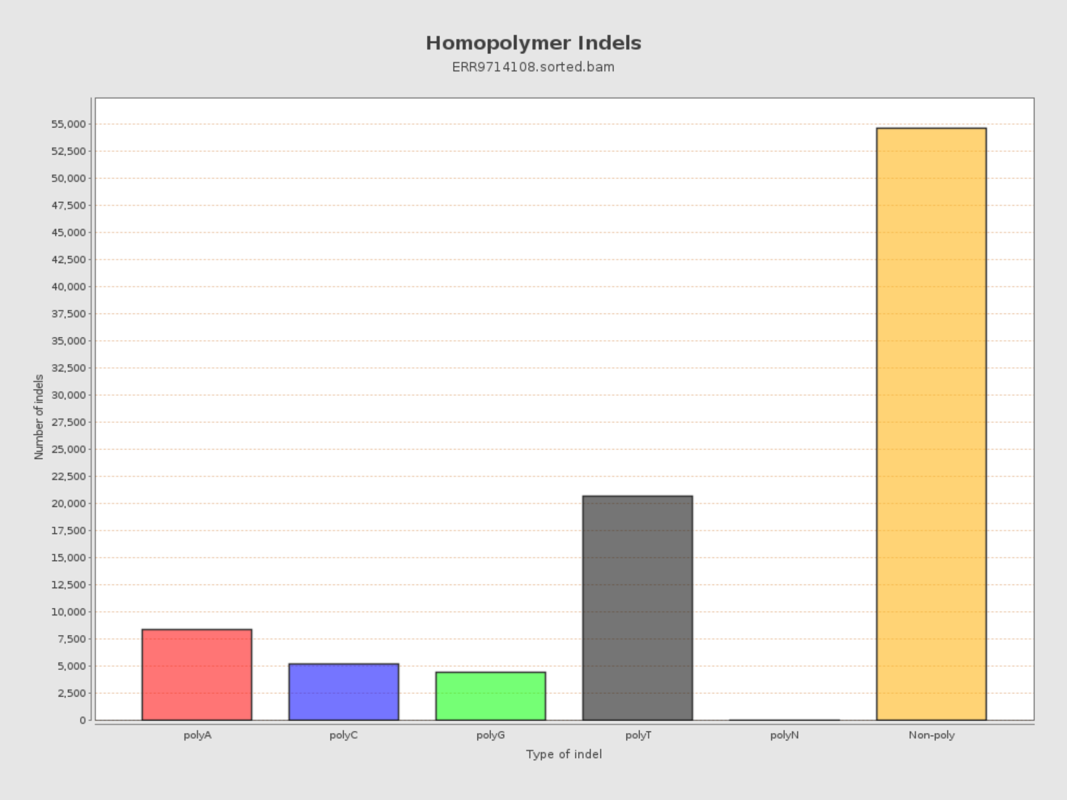
9. Results : Mapped Reads GC-content Distribution



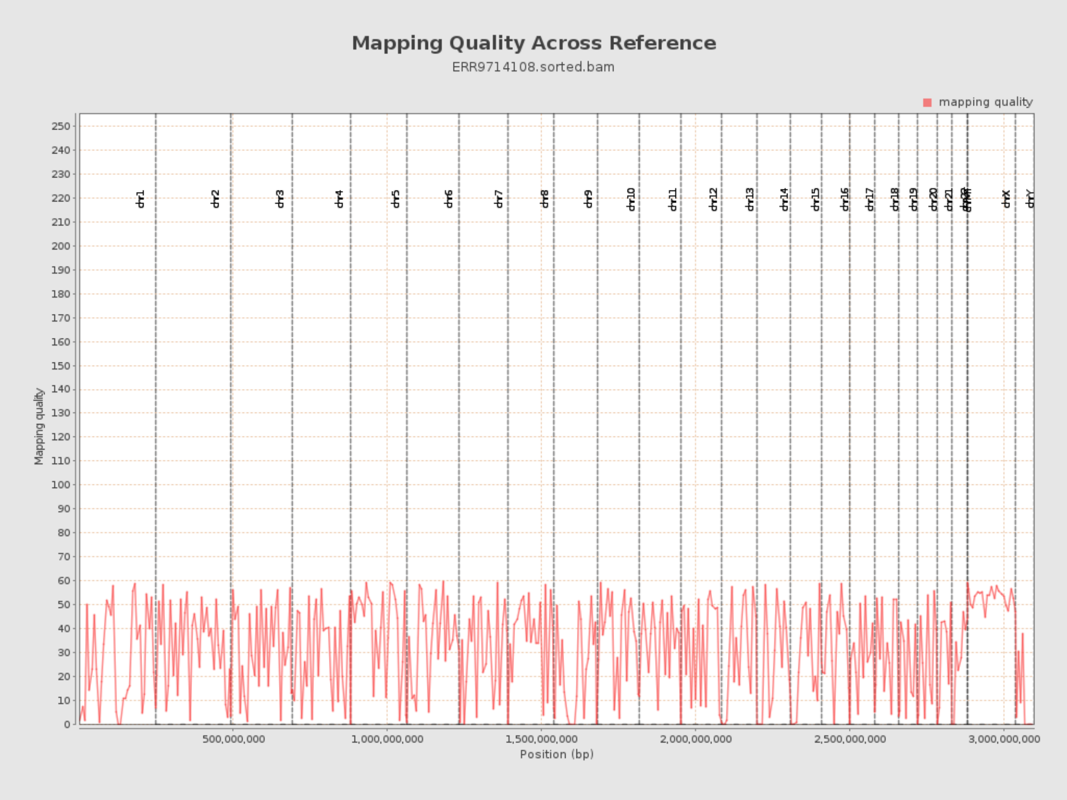
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram