Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 19:54:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714112.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_ERR9714112 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 19:54:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,324
Mapped reads	5,905 / 26.45%
Unmapped reads	16,419 / 73.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	260 / 1.16%
Read min/max/mean length	30 / 151 / 82.68
Duplicated reads (estimated)	4,256 / 19.06%
Duplication rate	47.15%
Clipped reads	4,860 / 21.77%

2.2. ACGT Content

Number/percentage of A's	140,282 / 21.3%
Number/percentage of C's	123,625 / 18.77%
Number/percentage of T's	129,574 / 19.67%
Number/percentage of G's	265,239 / 40.27%
Number/percentage of N's	2 / 0%
GC Percentage	59.03%

2.3. Coverage

Mean	0.0002

Standard Deviation	0.1888

2.4. Mapping Quality

Mean Mapping Quality	25.78

2.5. Mismatches and indels

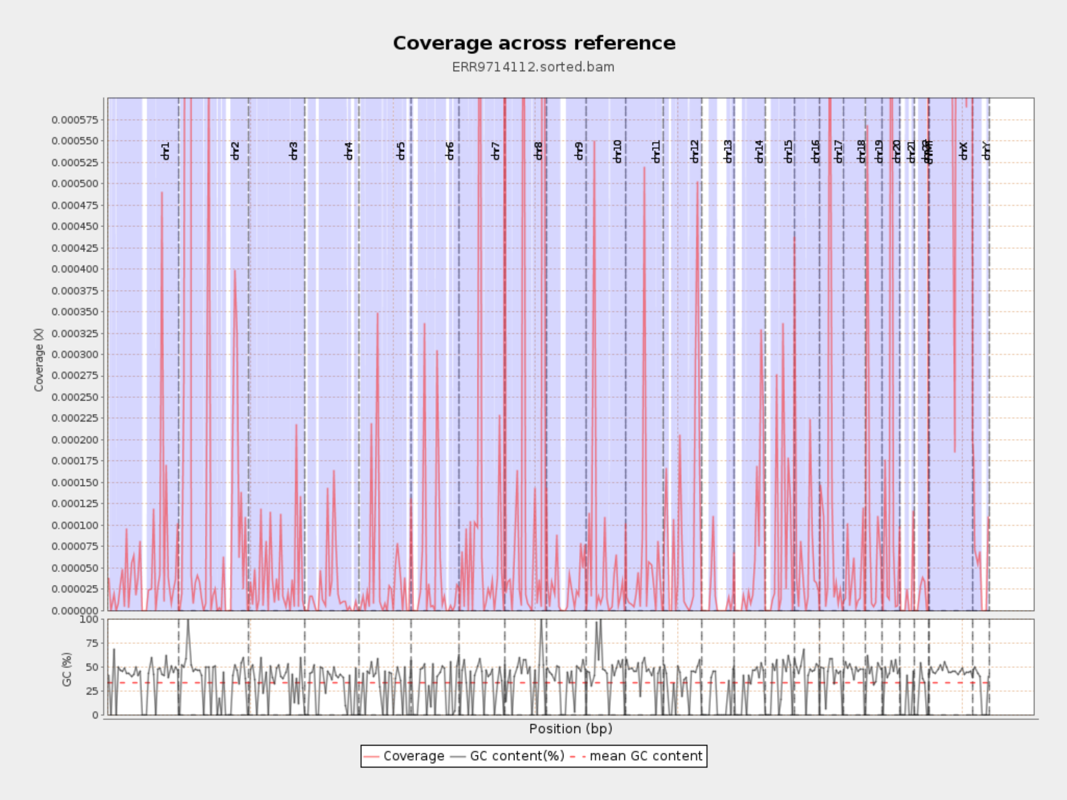
General error rate	3.81%
Mismatches	23,067
Insertions	385
Mapped reads with at least one insertion	5.06%
Deletions	1,570
Mapped reads with at least one deletion	25.76%
Homopolymer indels	34.27%

2.6. Chromosome stats

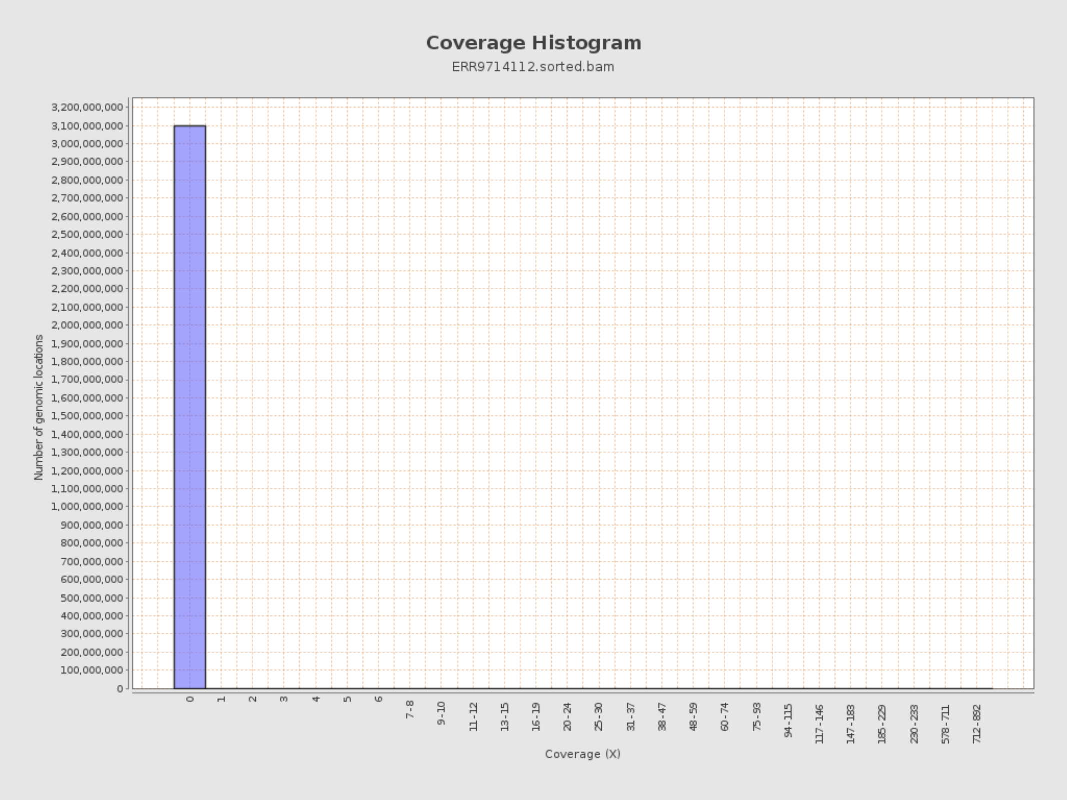
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12591	0.0001	0.0448
chr2	243199373	171438	0.0007	0.6132
chr3	198022430	8373	0	0.0142
chr4	191154276	4677	0	0.0091
chr5	180915260	8191	0	0.0191
chr6	171115067	7817	0	0.0179
chr7	159138663	15262	0.0001	0.0526

chr8	146364022	30070	0.0002	0.1251
chr9	141213431	4089	0	0.0091
chr10	135534747	7975	0.0001	0.0636
chr11	135006516	7799	0.0001	0.0205
chr12	133851895	12974	0.0001	0.034
chr13	115169878	1714	0	0.0063
chr14	107349540	7219	0.0001	0.024
chr15	102531392	7764	0.0001	0.0222
chr16	90354753	6523	0.0001	0.0187
chr17	81195210	10646	0.0001	0.0393
chr18	78077248	2877	0	0.0117
chr19	59128983	6729	0.0001	0.0447
chr20	63025520	10925	0.0002	0.0683
chr21	48129895	768	0	0.0055
chr22	51304566	790	0	0.0056
chrMT	16571	539	0.0325	0.2128
chrX	155270560	319806	0.0021	0.3002
chrY	59373566	3292	0.0001	0.0127

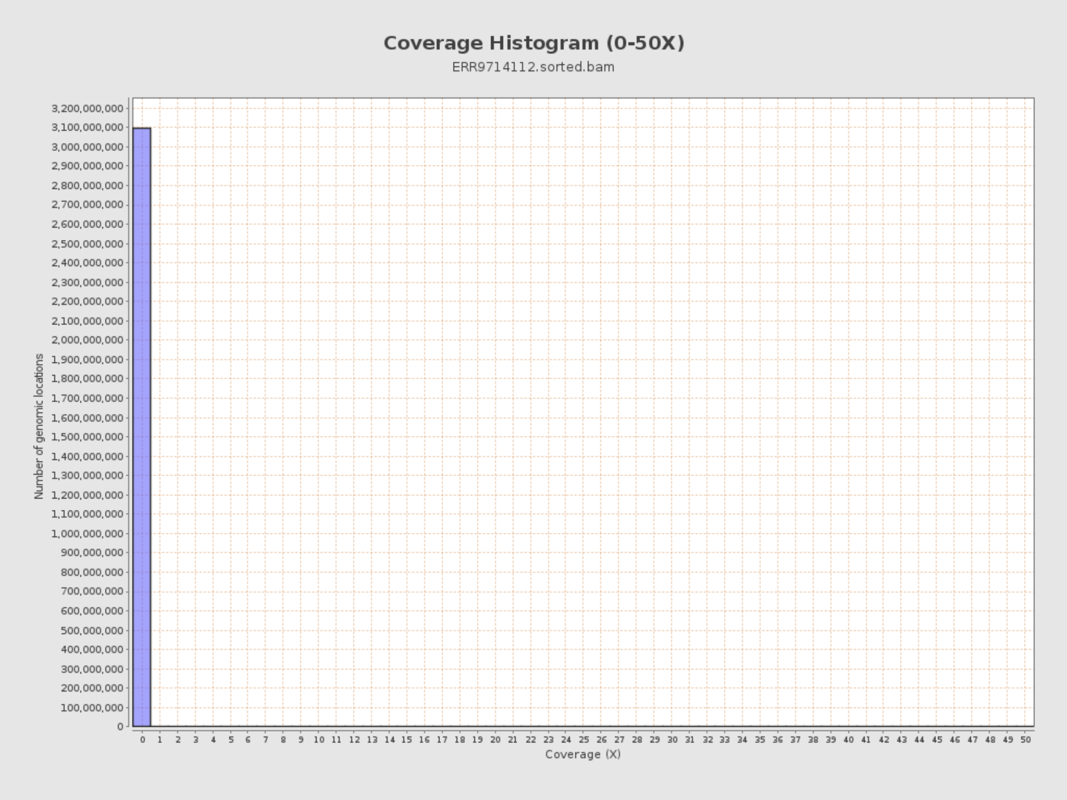
3. Results : Coverage across reference



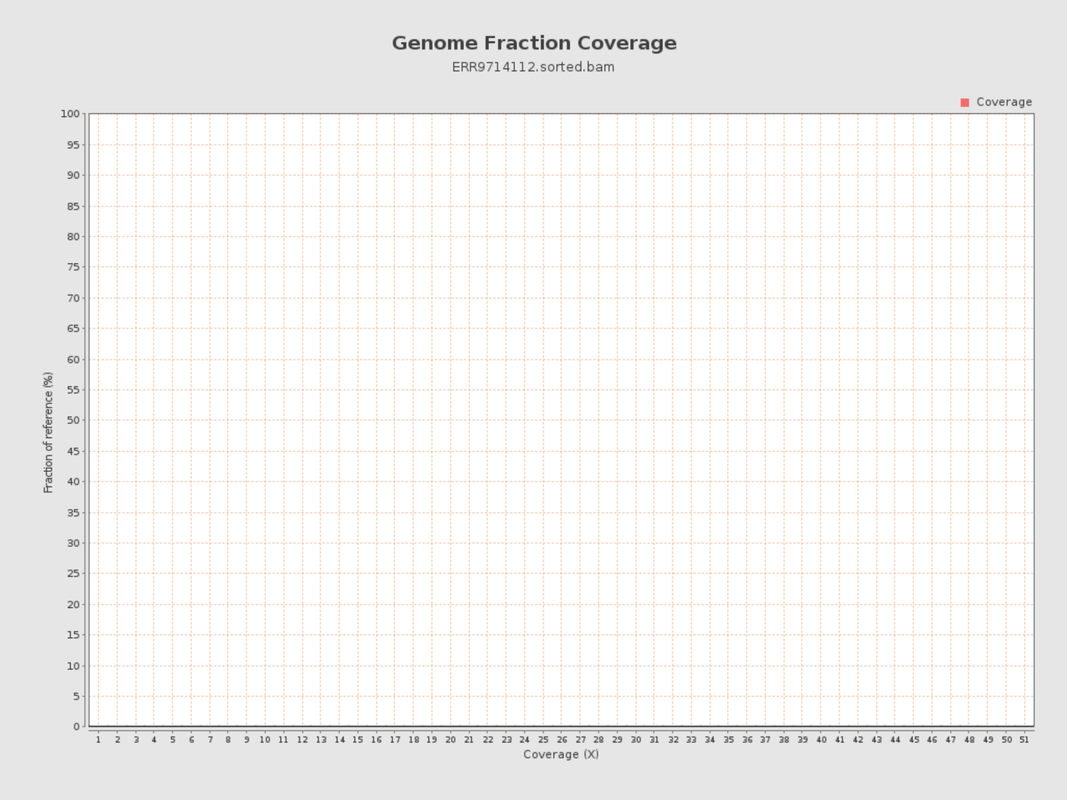
4. Results : Coverage Histogram



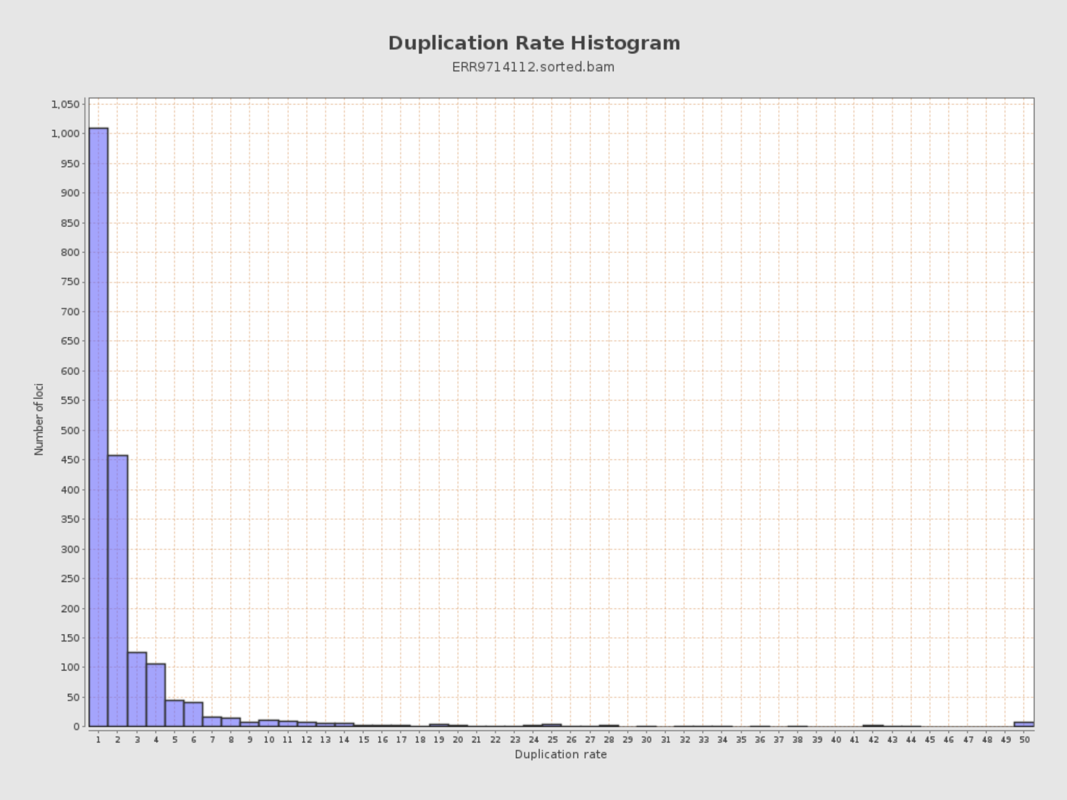
5. Results : Coverage Histogram (0-50X)



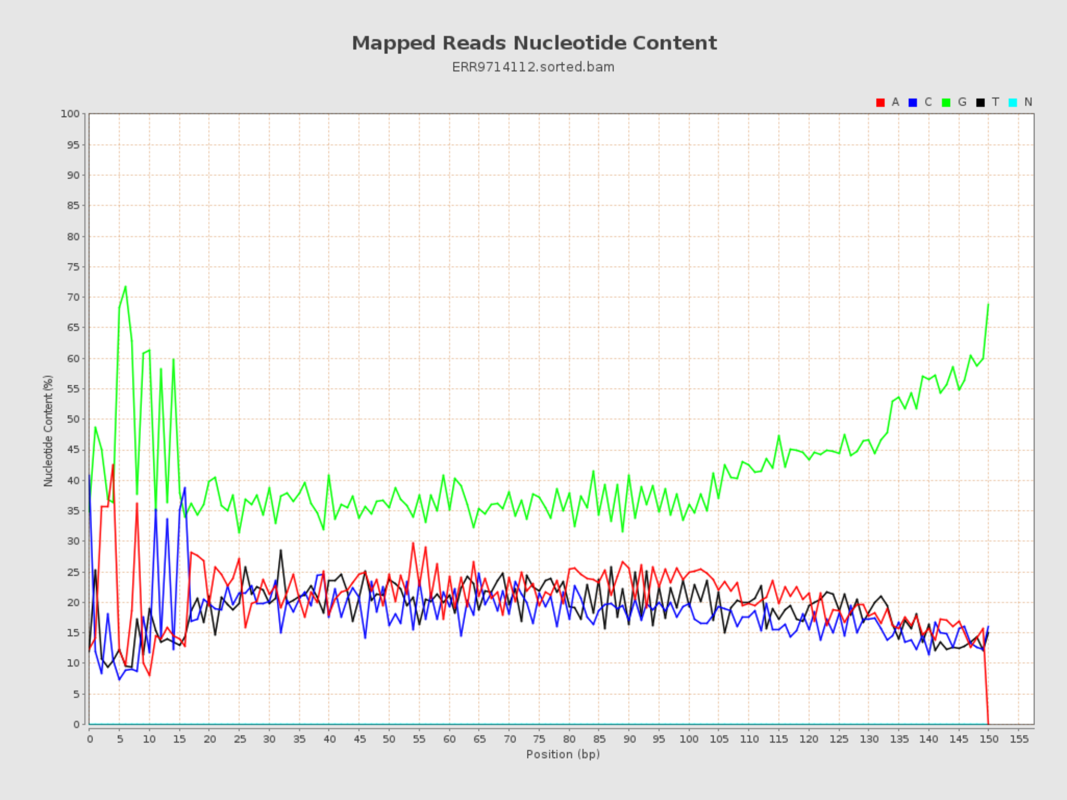
6. Results : Genome Fraction Coverage



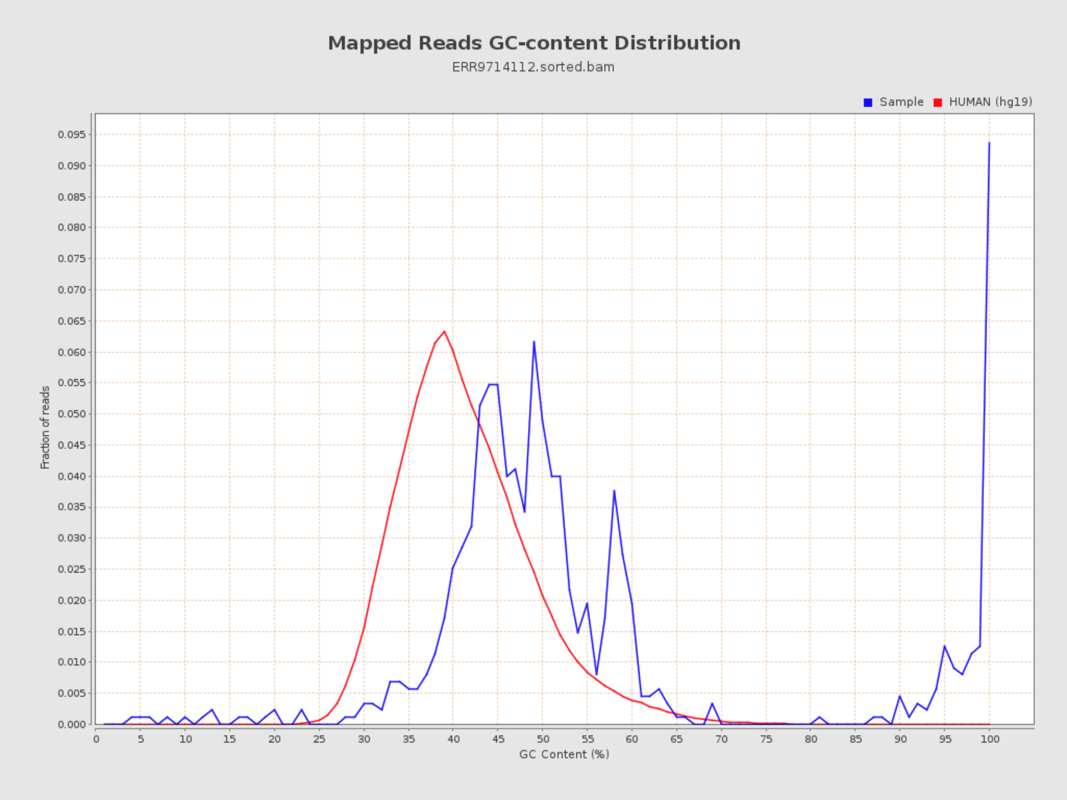
7. Results : Duplication Rate Histogram



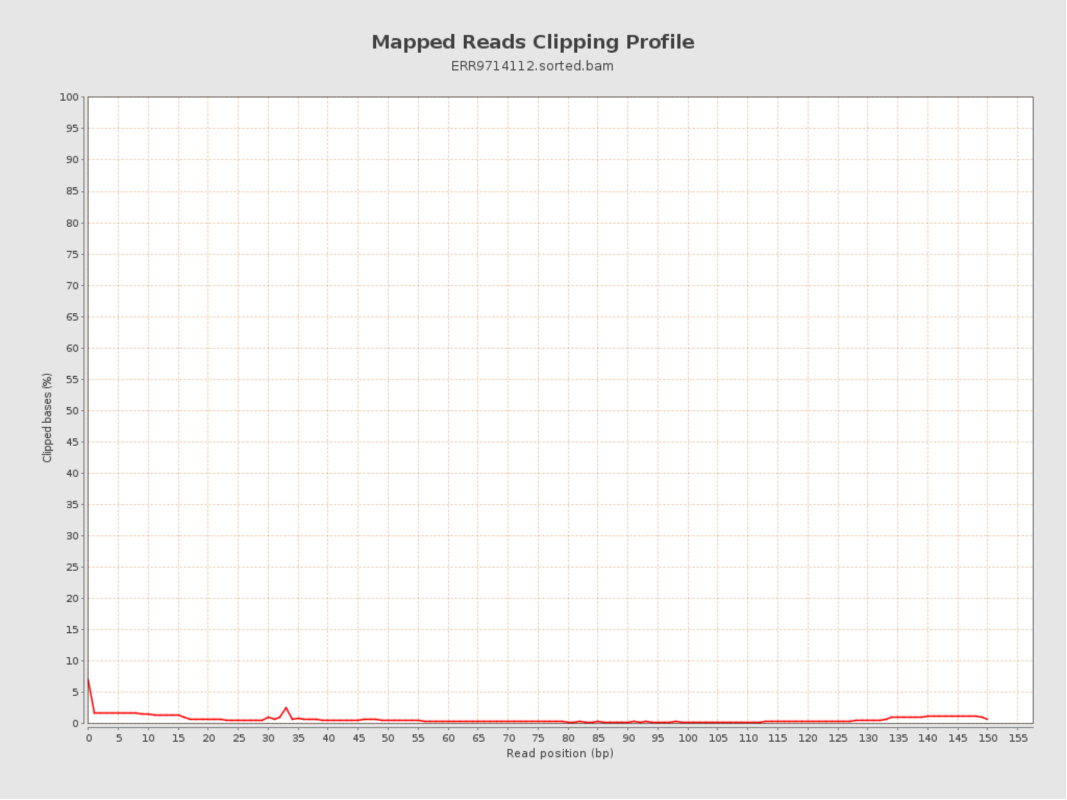
8. Results : Mapped Reads Nucleotide Content



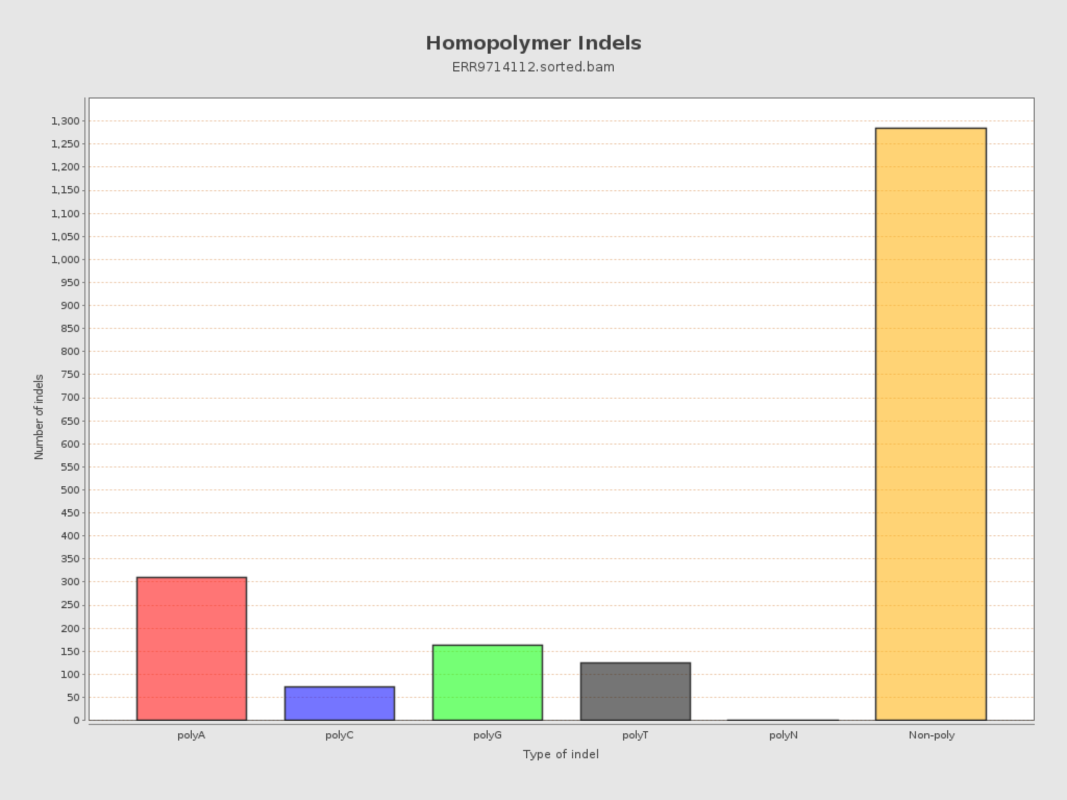
9. Results : Mapped Reads GC-content Distribution



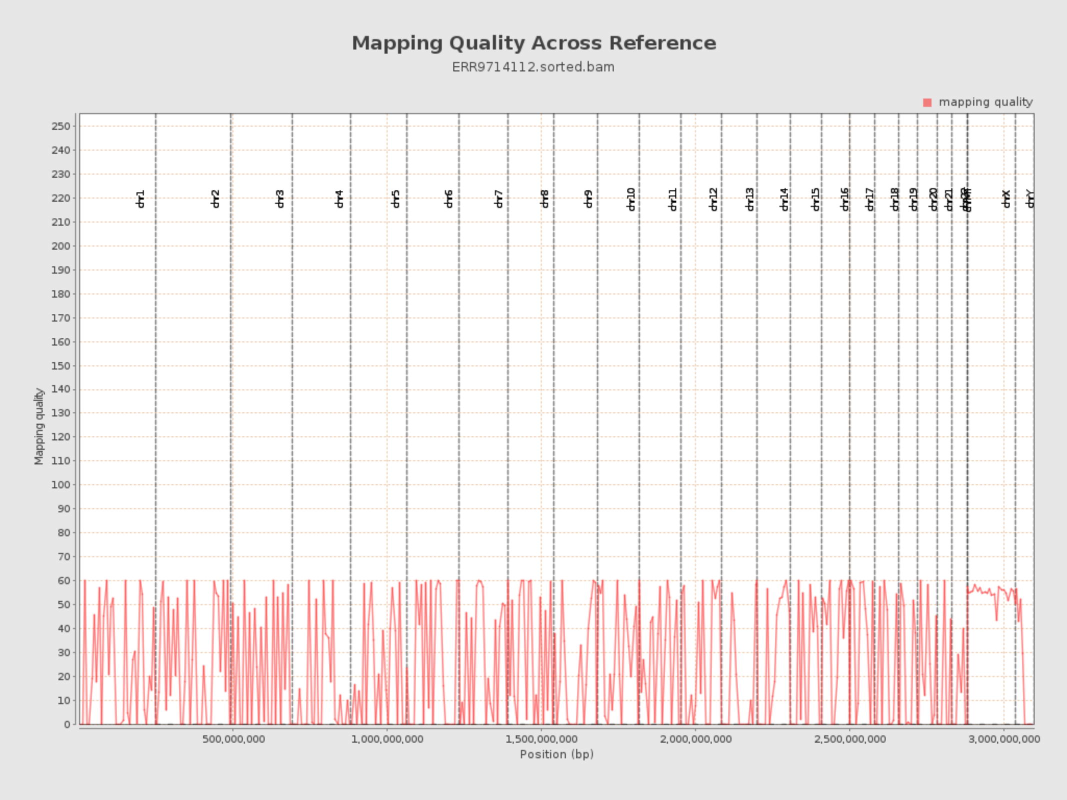
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram