Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:04:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714201.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_ERR9714201 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:04:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	107,214
Mapped reads	25,253 / 23.55%
Unmapped reads	81,961 / 76.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	835 / 0.78%
Read min/max/mean length	30 / 151 / 74.6
Duplicated reads (estimated)	21,832 / 20.36%
Duplication rate	49.62%
Clipped reads	18,615 / 17.36%

2.2. ACGT Content

Number/percentage of A's	469,906 / 16.68%
Number/percentage of C's	393,780 / 13.97%
Number/percentage of T's	431,417 / 15.31%
Number/percentage of G's	1,522,860 / 54.04%
Number/percentage of N's	36 / 0%
GC Percentage	68.01%

2.3. Coverage

Mean	0.0009

Standard Deviation	1.4337

2.4. Mapping Quality

Mean Mapping Quality	32.15

2.5. Mismatches and indels

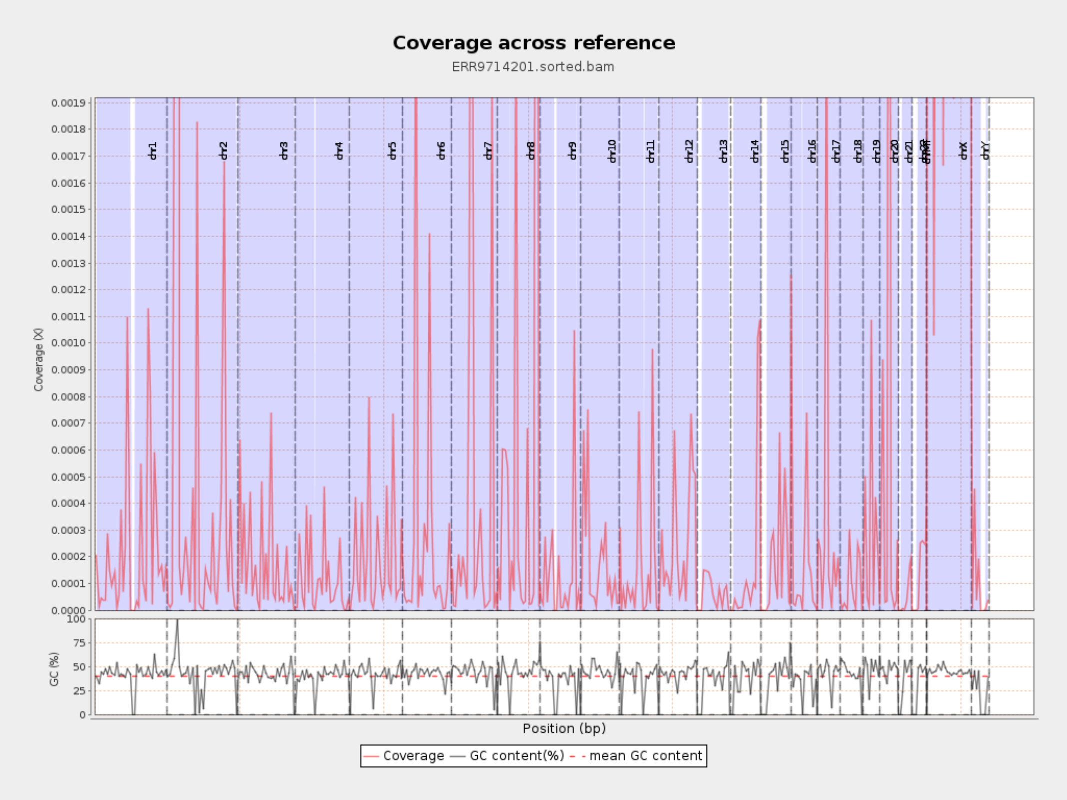
General error rate	3.61%
Mismatches	91,636
Insertions	1,990
Mapped reads with at least one insertion	5.88%
Deletions	5,513
Mapped reads with at least one deletion	21.26%
Homopolymer indels	36.79%

2.6. Chromosome stats

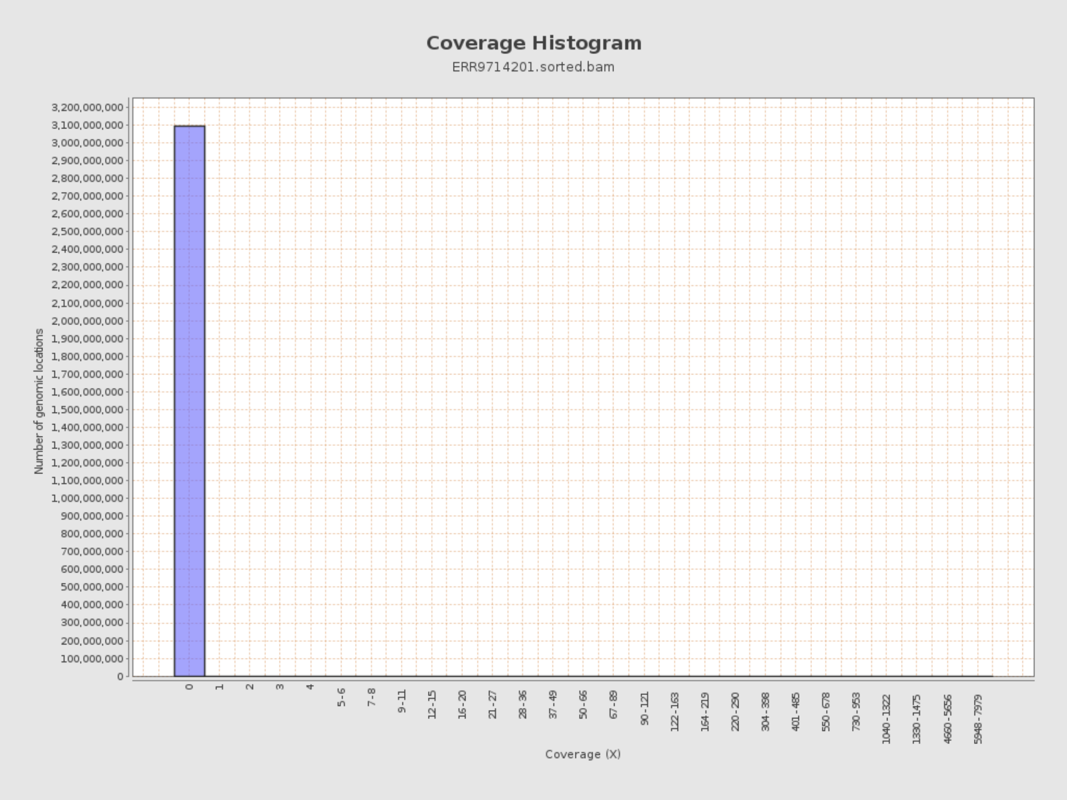
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55167	0.0002	0.0913
chr2	243199373	1210206	0.005	5.0587
chr3	198022430	34986	0.0002	0.0465
chr4	191154276	21781	0.0001	0.0322
chr5	180915260	35443	0.0002	0.0574
chr6	171115067	50540	0.0003	0.1179
chr7	159138663	69626	0.0004	0.2126

chr8	146364022	85301	0.0006	0.2995
chr9	141213431	18947	0.0001	0.0551
chr10	135534747	24853	0.0002	0.0978
chr11	135006516	22520	0.0002	0.0467
chr12	133851895	32615	0.0002	0.0557
chr13	115169878	7146	0.0001	0.0162
chr14	107349540	20445	0.0002	0.0774
chr15	102531392	17988	0.0002	0.0424
chr16	90354753	18010	0.0002	0.0662
chr17	81195210	29854	0.0004	0.0741
chr18	78077248	7453	0.0001	0.0222
chr19	59128983	17552	0.0003	0.0824
chr20	63025520	48151	0.0008	0.2853
chr21	48129895	2680	0.0001	0.0208
chr22	51304566	6763	0.0001	0.0266
chrMT	16571	0	0	0
chrX	155270560	1015752	0.0065	0.8171
chrY	59373566	5671	0.0001	0.0287

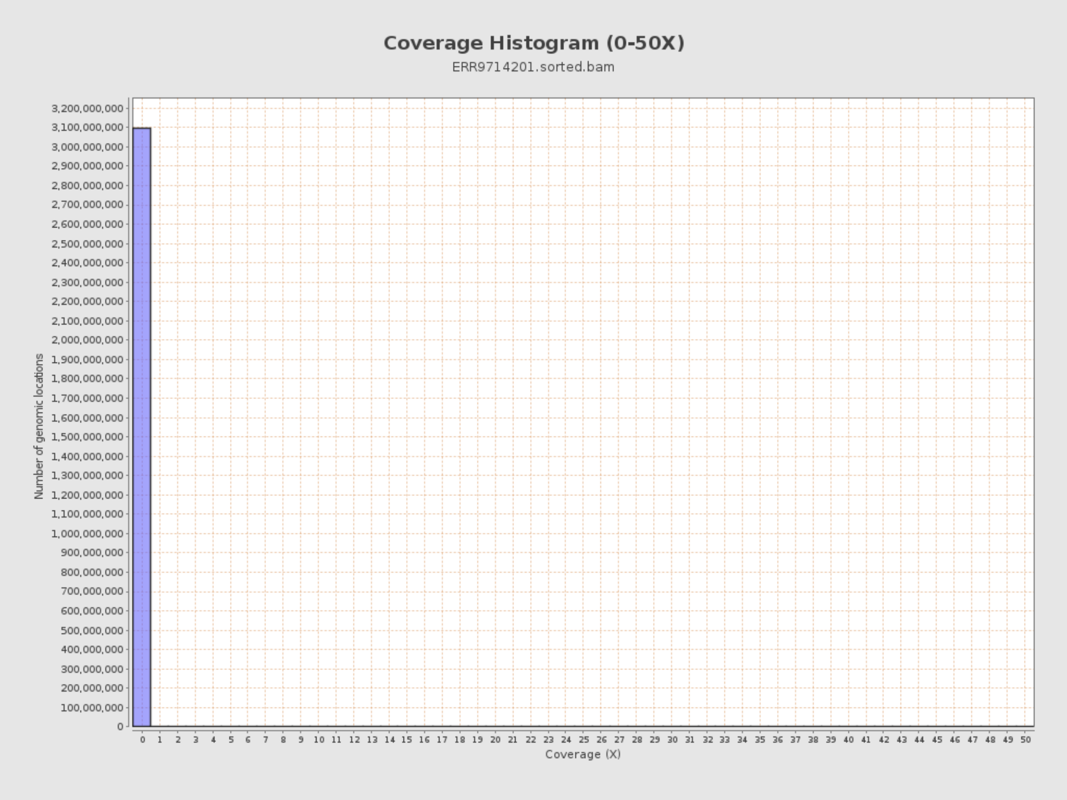
3. Results : Coverage across reference



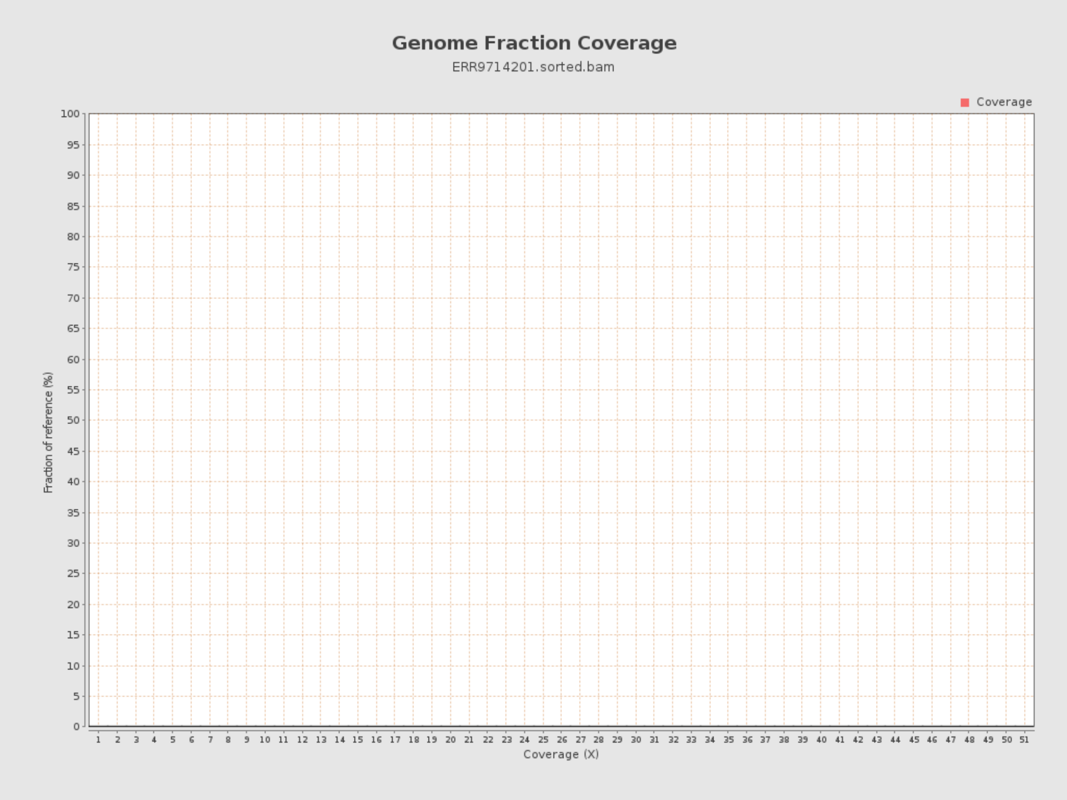
4. Results : Coverage Histogram



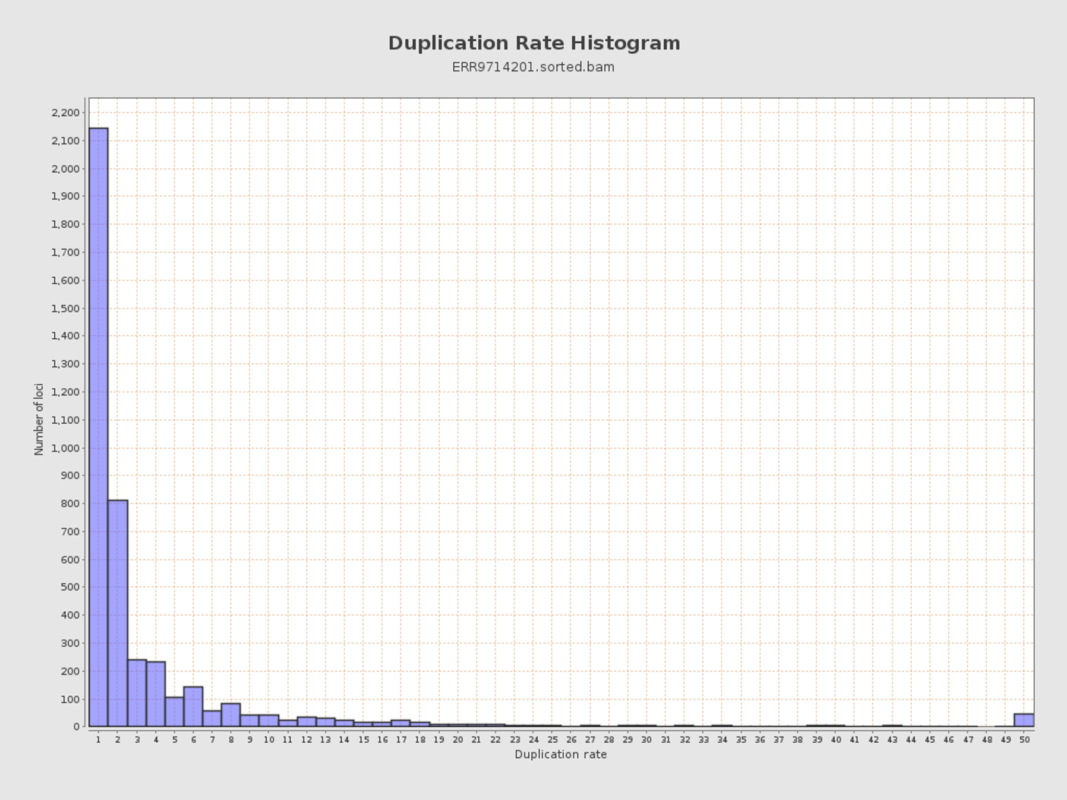
5. Results : Coverage Histogram (0-50X)



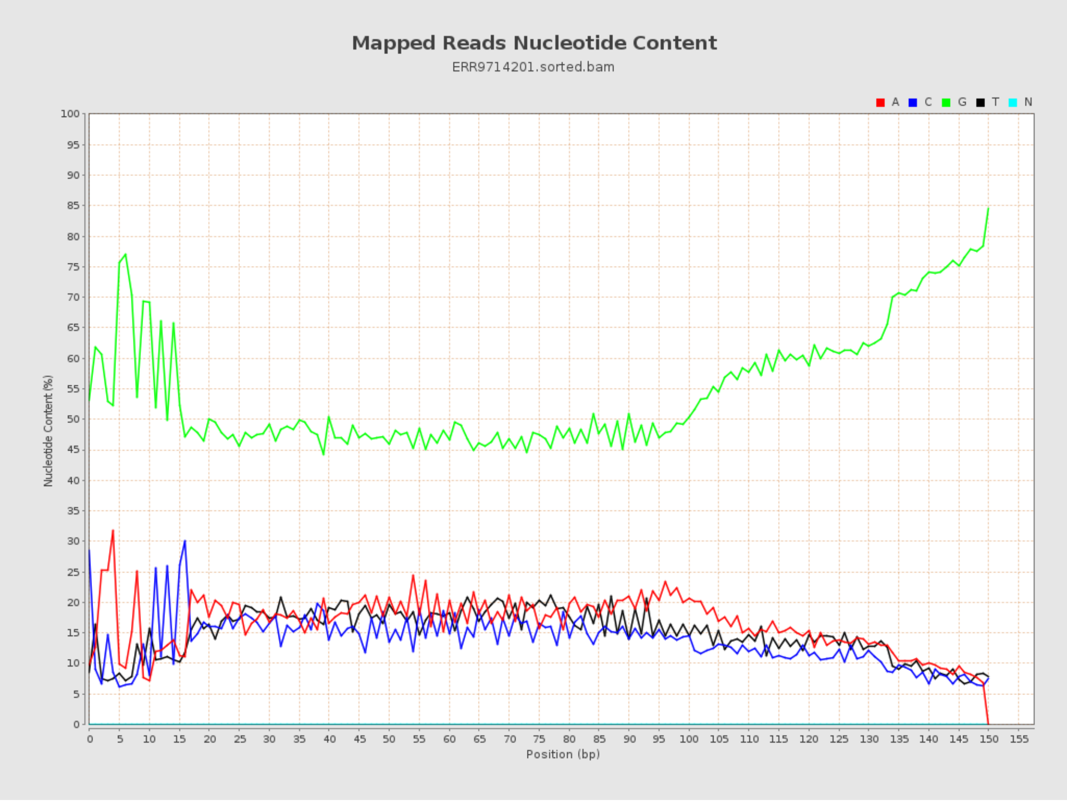
6. Results : Genome Fraction Coverage



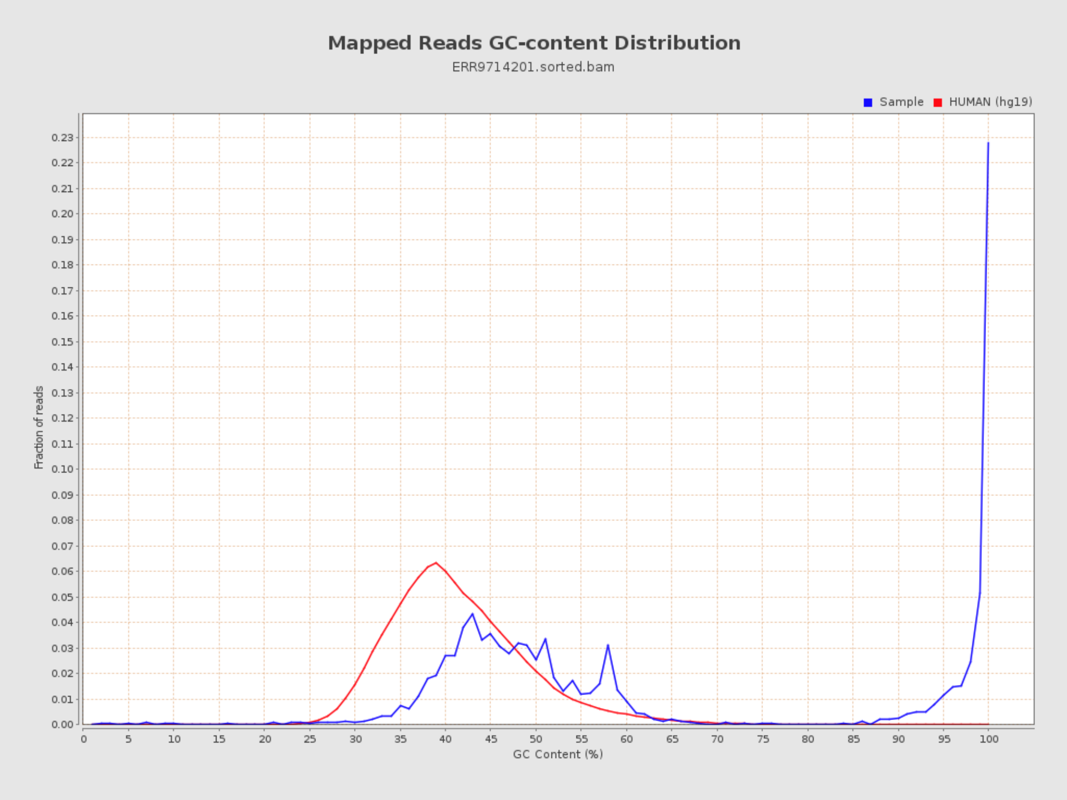
7. Results : Duplication Rate Histogram



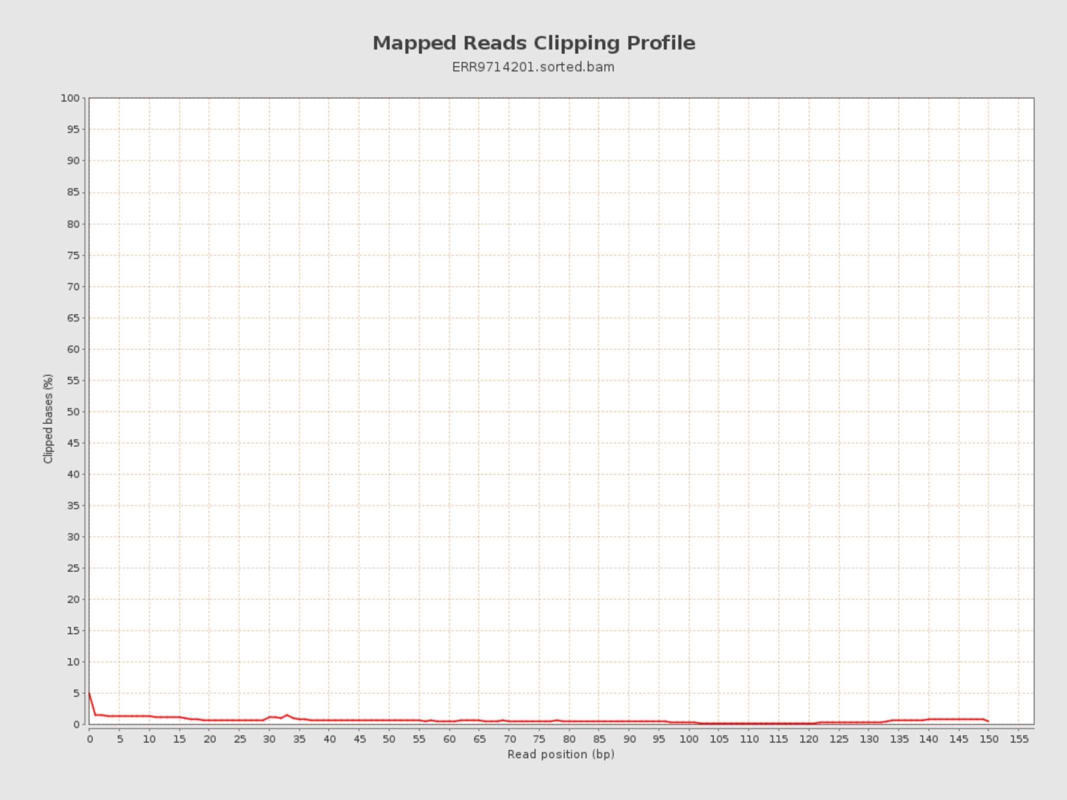
8. Results : Mapped Reads Nucleotide Content



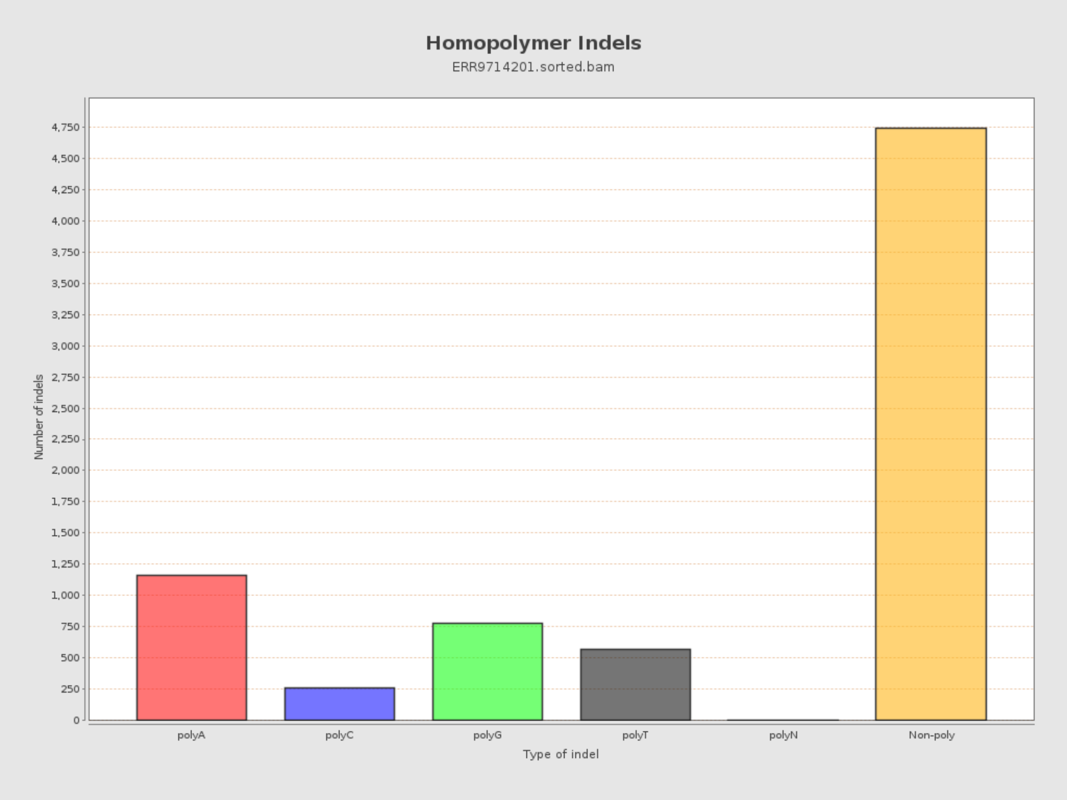
9. Results : Mapped Reads GC-content Distribution



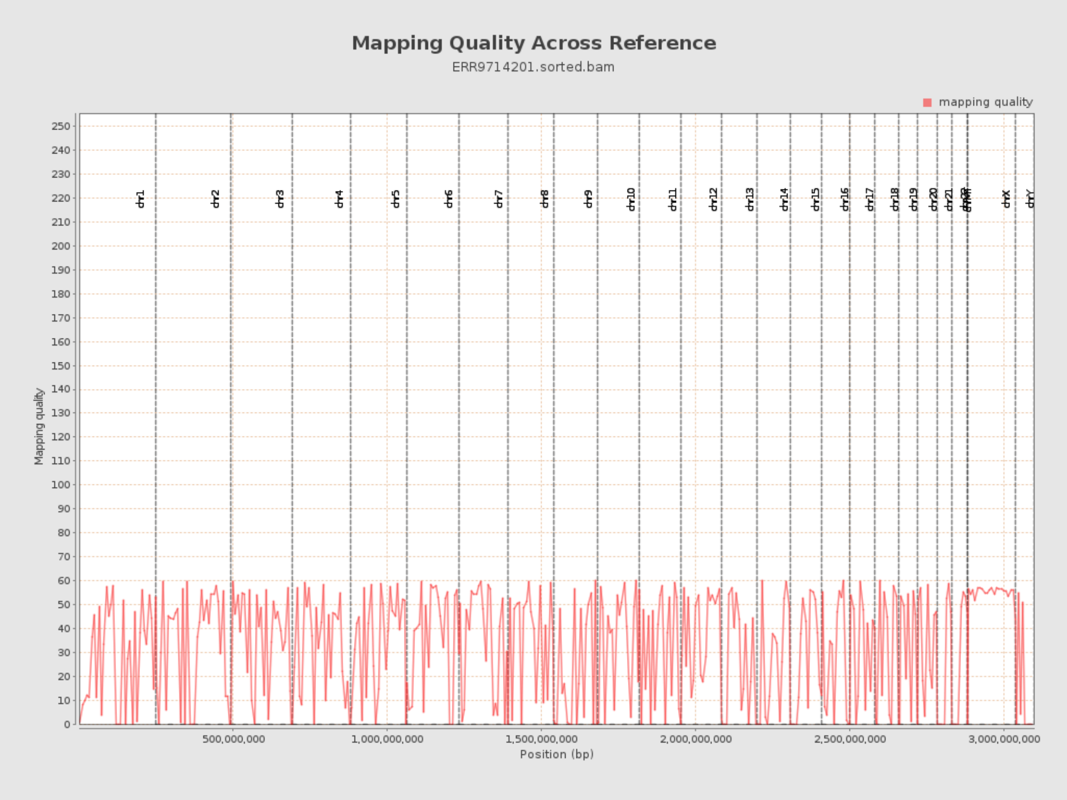
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram