Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:29:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714164.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_ERR9714164 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:29:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	922,480
Mapped reads	268,850 / 29.14%
Unmapped reads	653,630 / 70.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,069 / 0.87%
Read min/max/mean length	30 / 151 / 116.26
Duplicated reads (estimated)	213,933 / 23.19%
Duplication rate	42.24%
Clipped reads	249,700 / 27.07%

2.2. ACGT Content

Number/percentage of A's	9,406,092 / 27.47%
Number/percentage of C's	7,183,218 / 20.98%
Number/percentage of T's	8,977,578 / 26.22%
Number/percentage of G's	8,673,494 / 25.33%
Number/percentage of N's	224 / 0%
GC Percentage	46.31%

2.3. Coverage

Mean	0.0114

Standard Deviation	2.1843

2.4. Mapping Quality

Mean Mapping Quality	52.28

2.5. Mismatches and indels

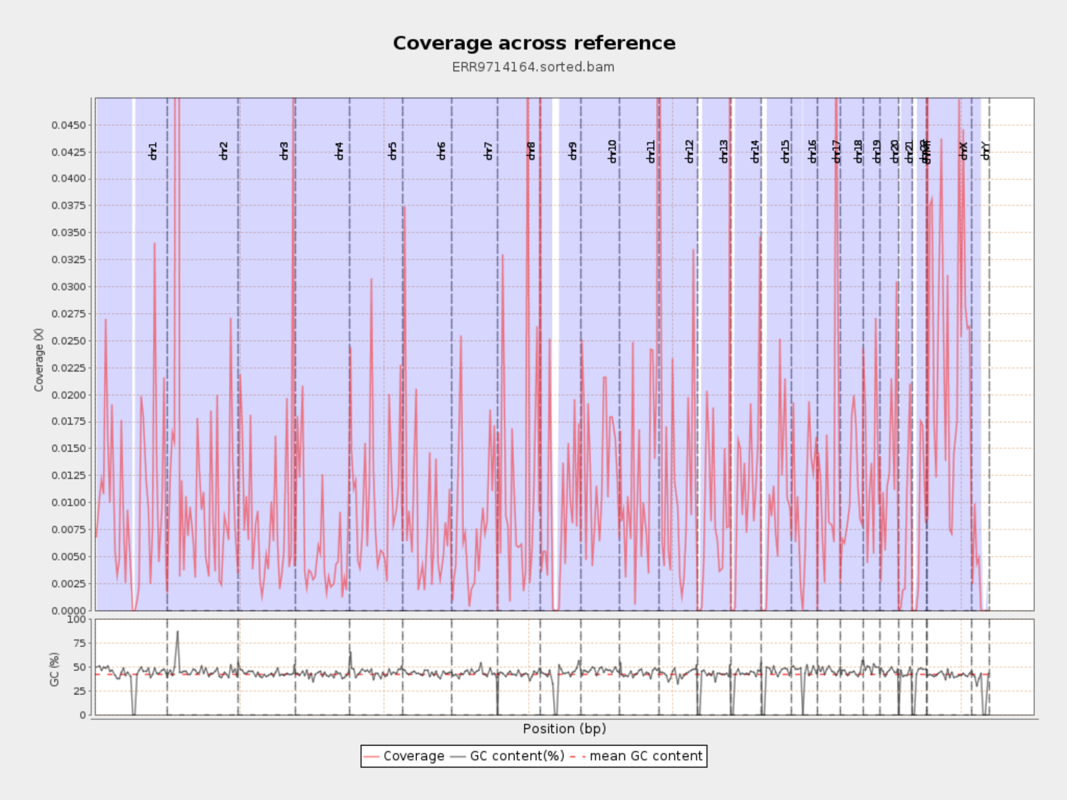
General error rate	4.89%
Mismatches	1,572,510
Insertions	38,457
Mapped reads with at least one insertion	13.71%
Deletions	144,991
Mapped reads with at least one deletion	49.76%
Homopolymer indels	30.39%

2.6. Chromosome stats

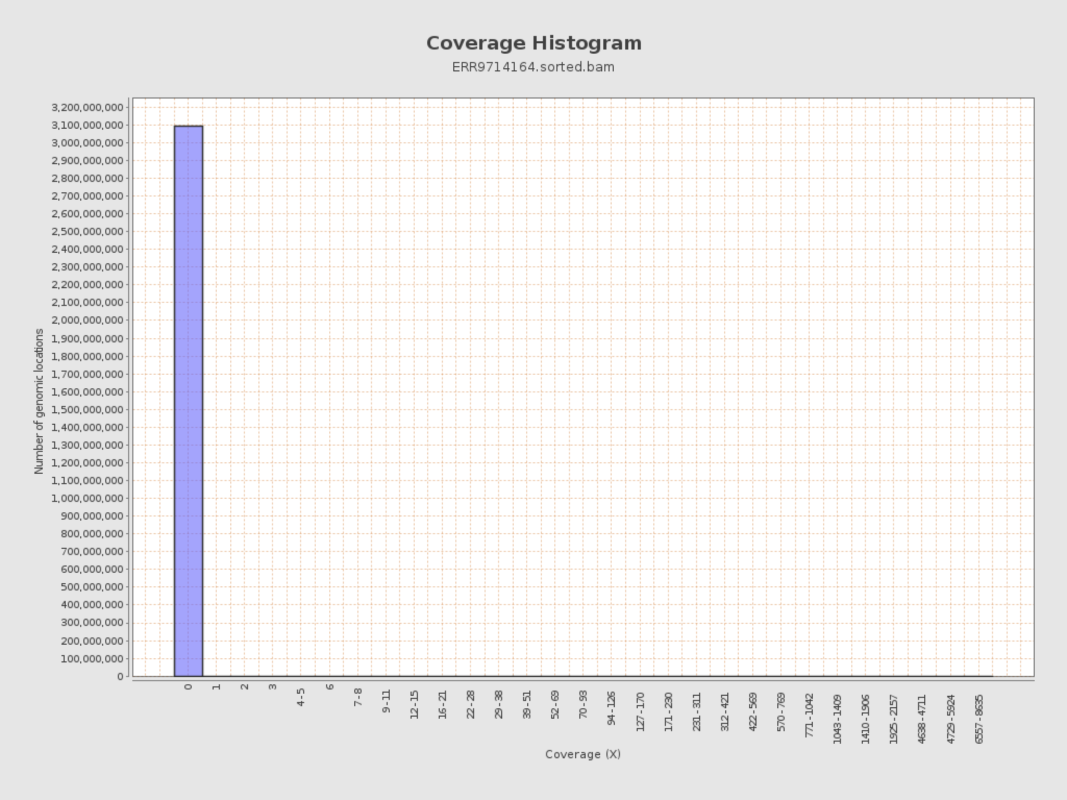
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2528714	0.0101	1.2905
chr2	243199373	3909397	0.0161	5.6772
chr3	198022430	1918880	0.0097	1.7984
chr4	191154276	1114883	0.0058	0.7542
chr5	180915260	1932372	0.0107	1.6498
chr6	171115067	1490908	0.0087	1.238
chr7	159138663	1298248	0.0082	1.0101

chr8	146364022	1798836	0.0123	2.3175
chr9	141213431	1186799	0.0084	1.1593
chr10	135534747	1859526	0.0137	1.6166
chr11	135006516	1702388	0.0126	1.8421
chr12	133851895	1697549	0.0127	2.0779
chr13	115169878	1034552	0.009	1.3846
chr14	107349540	1248611	0.0116	1.5299
chr15	102531392	976404	0.0095	0.9286
chr16	90354753	948474	0.0105	1.1456
chr17	81195210	1204816	0.0148	2.5946
chr18	78077248	875392	0.0112	1.3557
chr19	59128983	797431	0.0135	1.4393
chr20	63025520	854889	0.0136	1.6871
chr21	48129895	335255	0.007	1.3059
chr22	51304566	379792	0.0074	0.8377
chrMT	16571	36626	2.2102	13.5985
chrX	155270560	3871115	0.0249	2.0897
chrY	59373566	161457	0.0027	0.4767

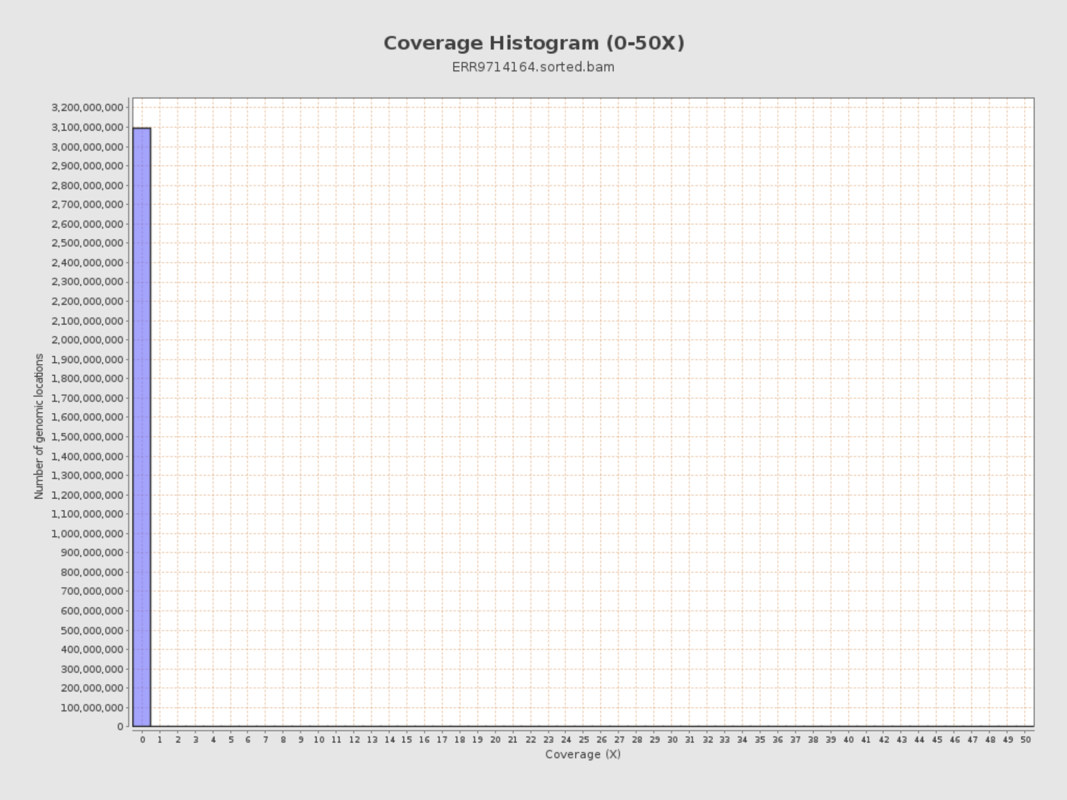
3. Results : Coverage across reference



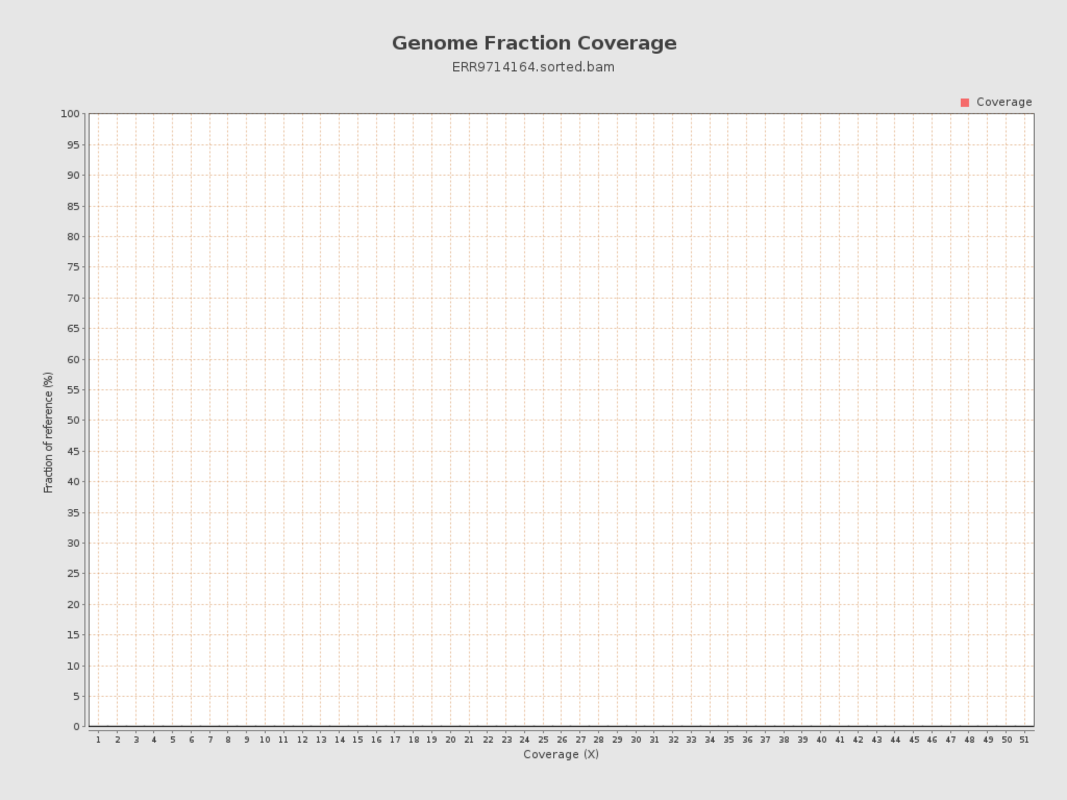
4. Results : Coverage Histogram



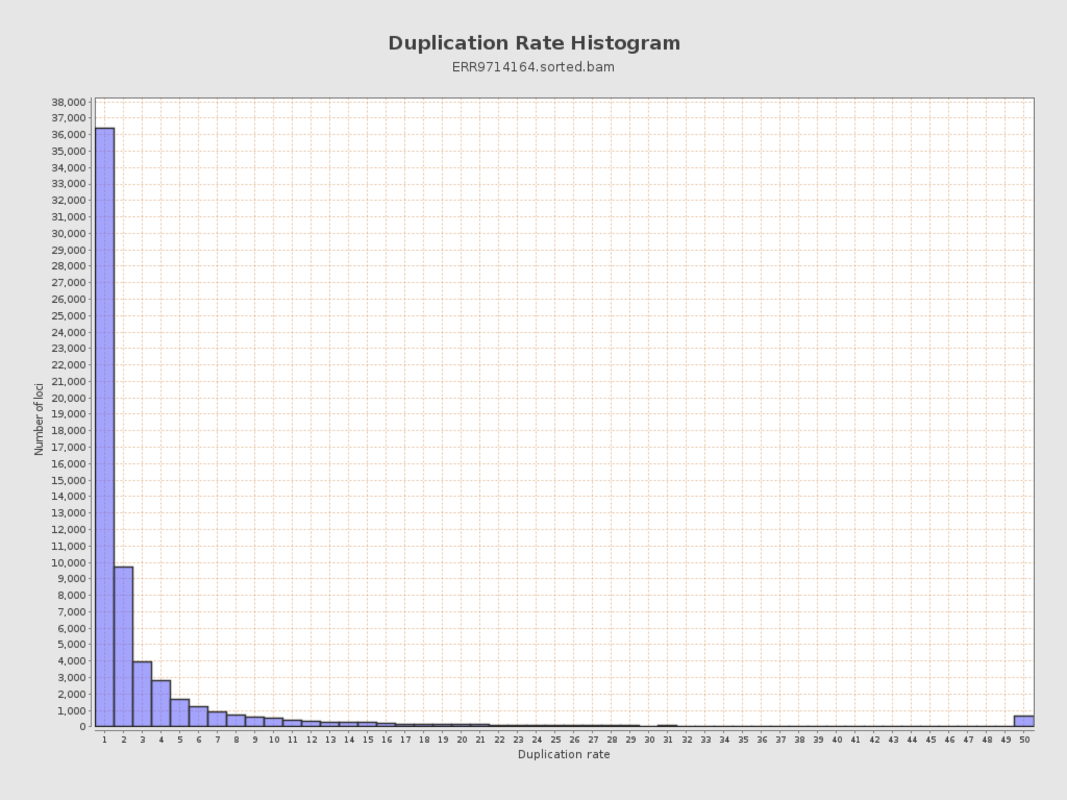
5. Results : Coverage Histogram (0-50X)



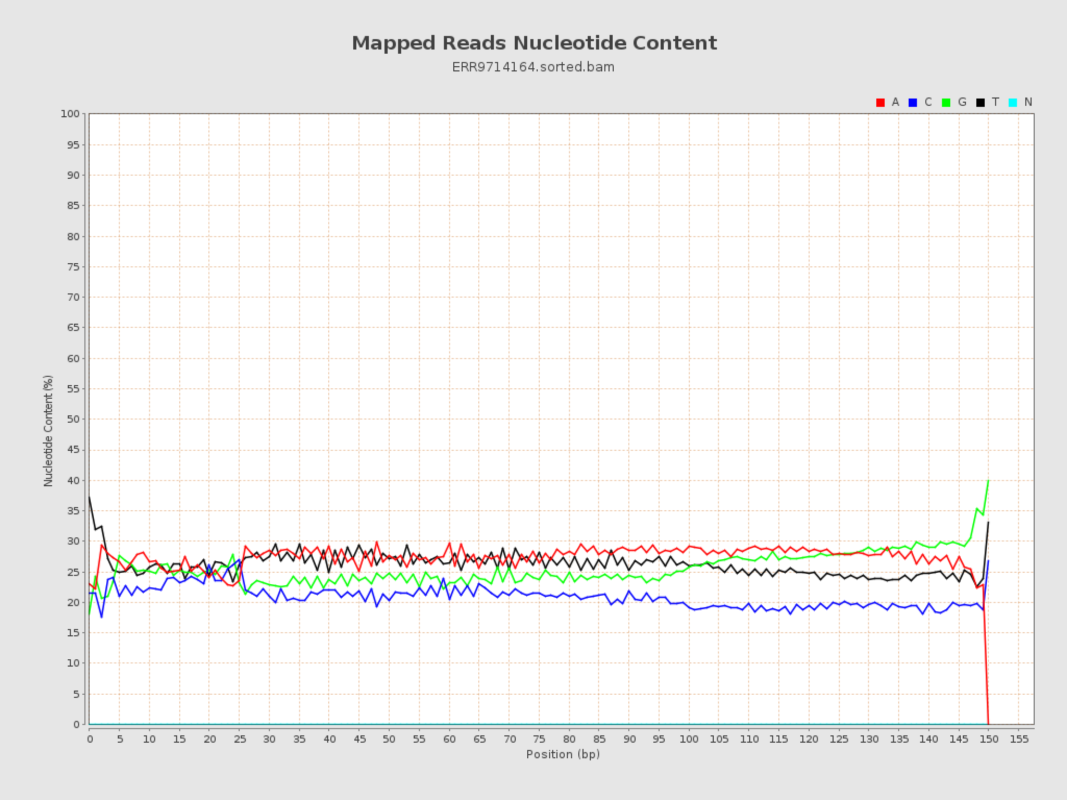
6. Results : Genome Fraction Coverage



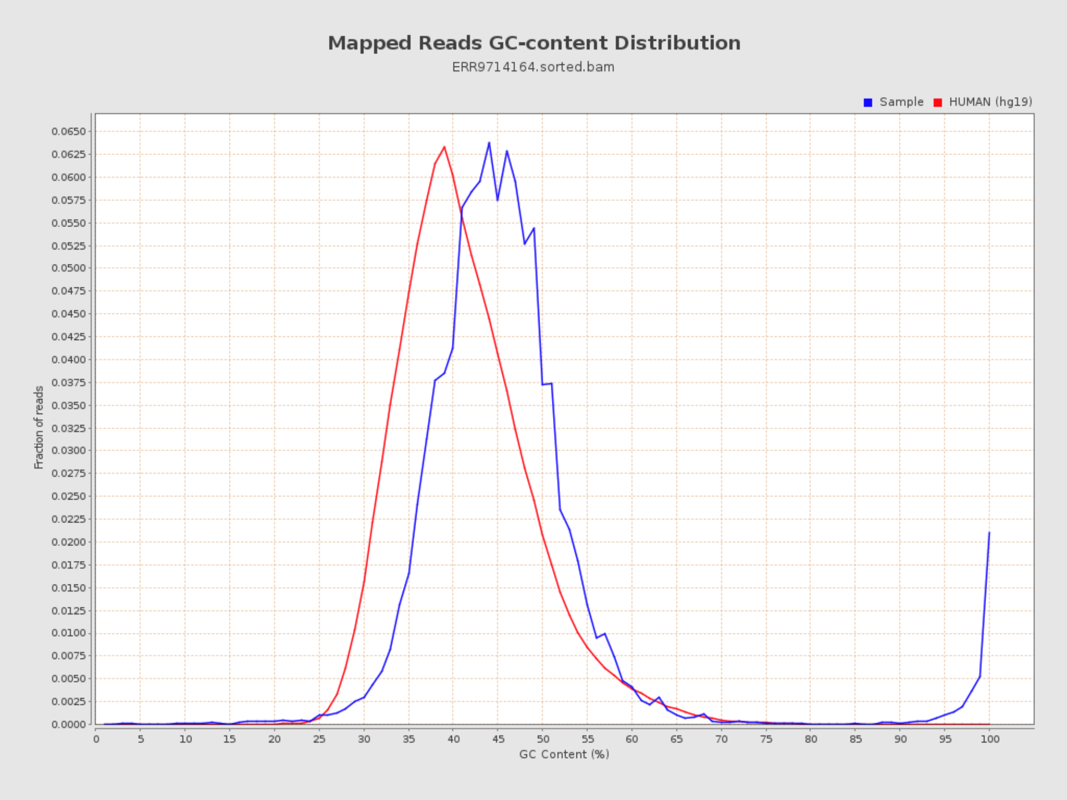
7. Results : Duplication Rate Histogram



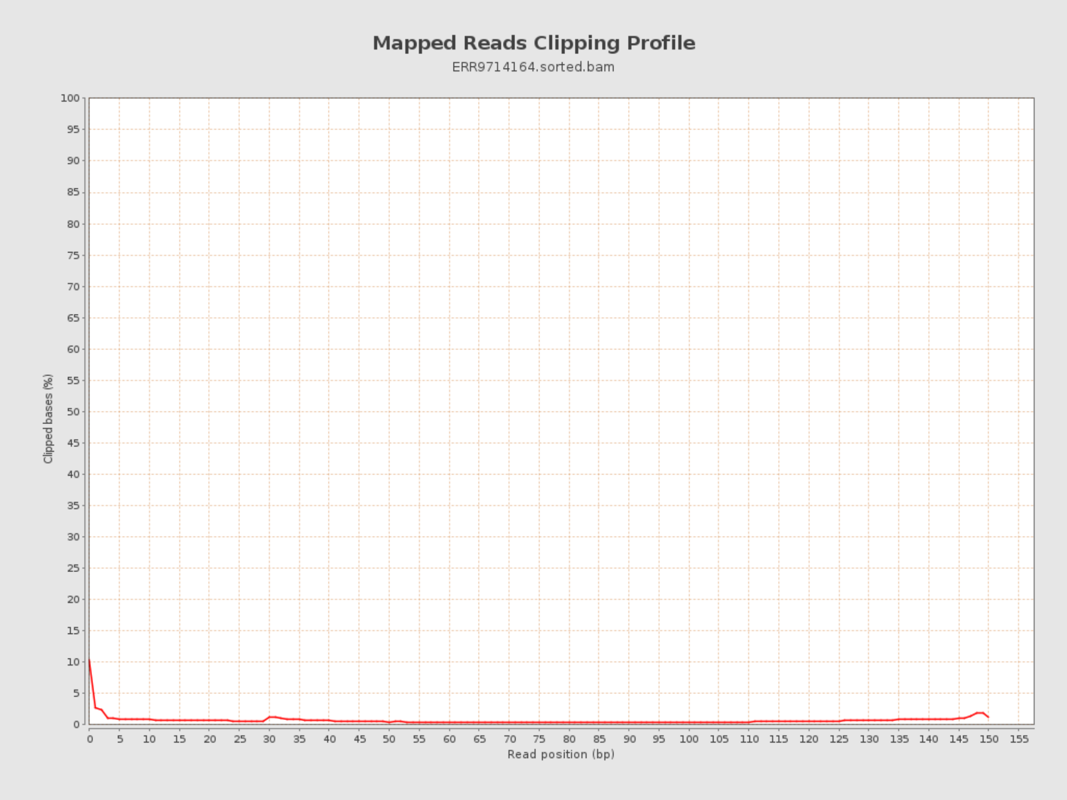
8. Results : Mapped Reads Nucleotide Content



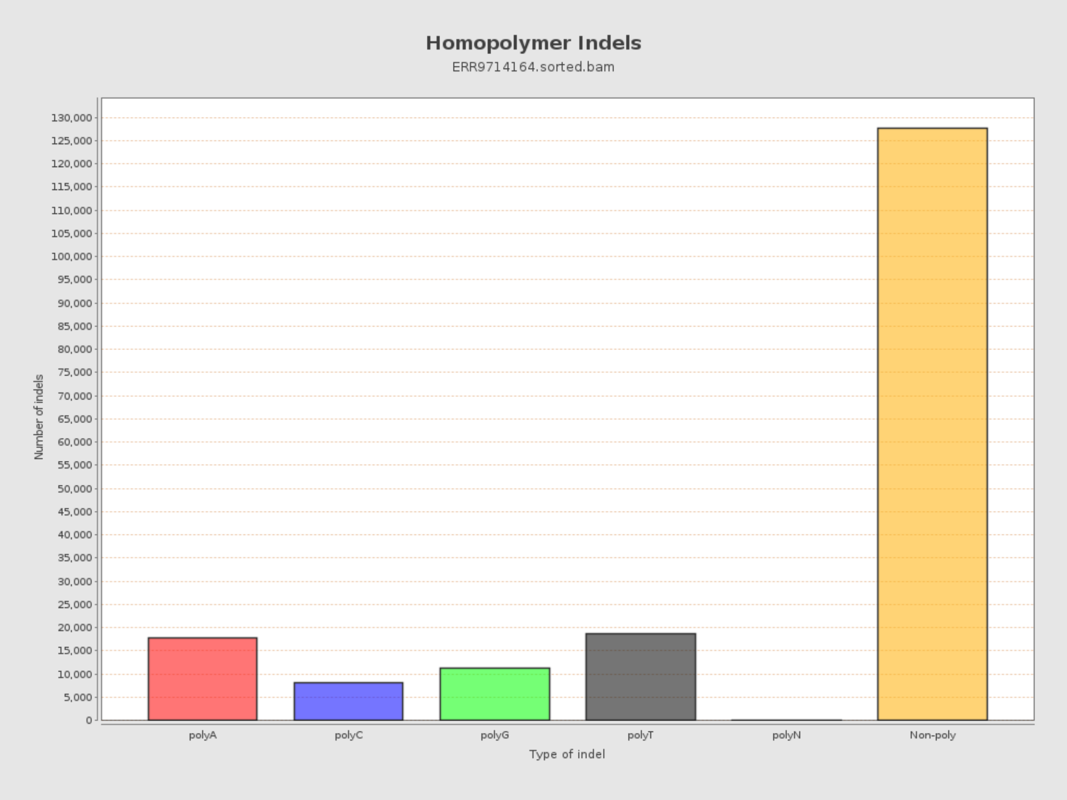
9. Results : Mapped Reads GC-content Distribution



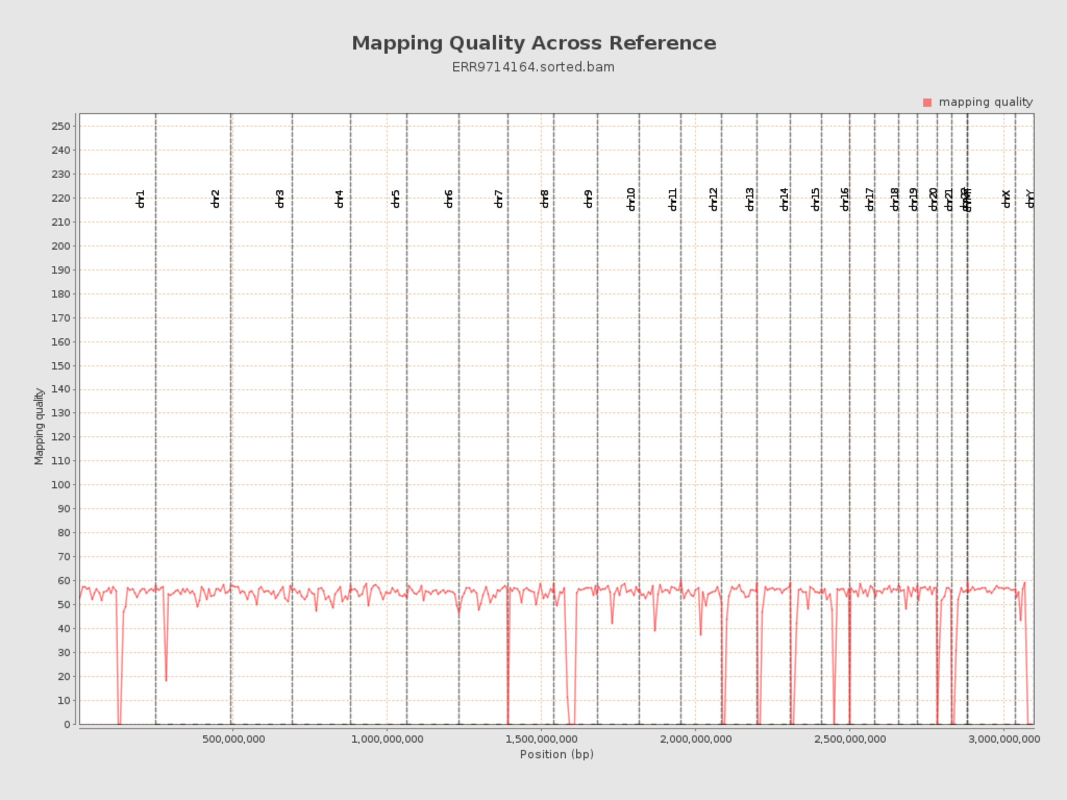
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram