Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:50:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714061.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_ERR9714061 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:49:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	308,500
Mapped reads	255,899 / 82.95%
Unmapped reads	52,601 / 17.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,178 / 2.98%
Read min/max/mean length	30 / 151 / 134.55
Duplicated reads (estimated)	195,432 / 63.35%
Duplication rate	41.85%
Clipped reads	243,696 / 78.99%

2.2. ACGT Content

Number/percentage of A's	8,907,615 / 27.57%
Number/percentage of C's	7,036,150 / 21.78%
Number/percentage of T's	8,462,659 / 26.2%
Number/percentage of G's	7,899,581 / 24.45%
Number/percentage of N's	239 / 0%
GC Percentage	46.23%

2.3. Coverage

Mean	0.0106

Standard Deviation	1.2217

2.4. Mapping Quality

Mean Mapping Quality	52.53

2.5. Mismatches and indels

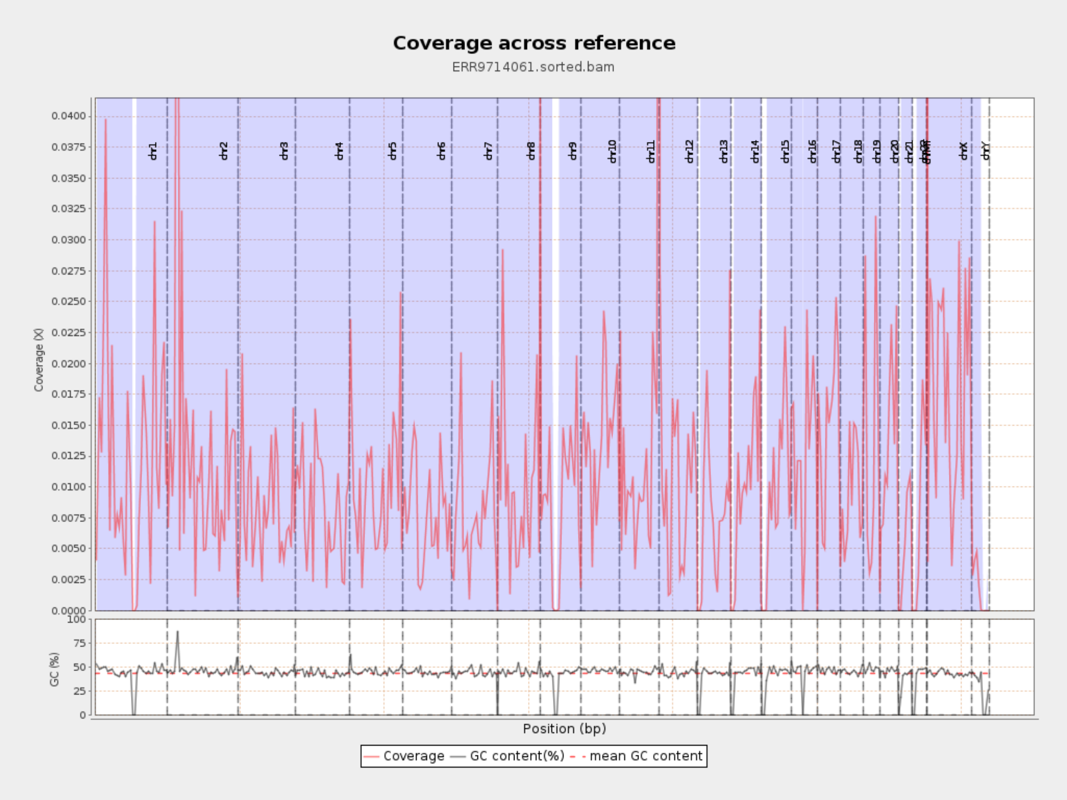
General error rate	4.2%
Mismatches	1,242,856
Insertions	36,366
Mapped reads with at least one insertion	13.78%
Deletions	108,470
Mapped reads with at least one deletion	40.52%
Homopolymer indels	28.51%

2.6. Chromosome stats

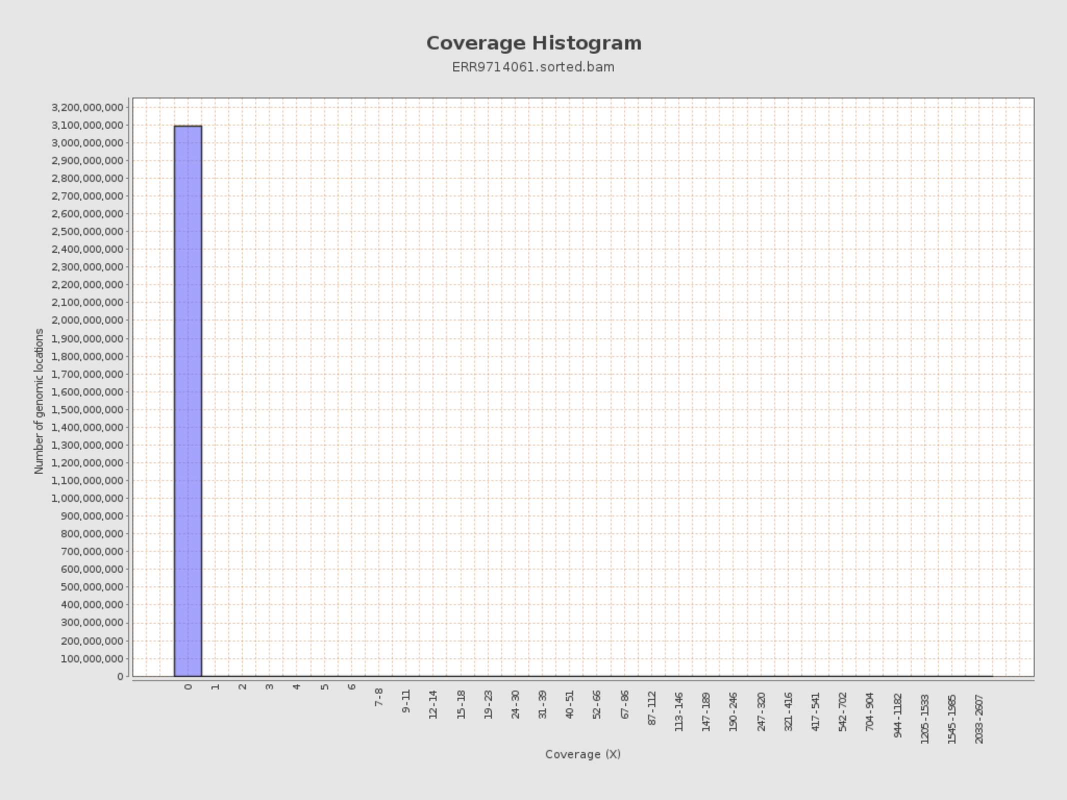
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3060074	0.0123	1.3072
chr2	243199373	3209953	0.0132	2.3085
chr3	198022430	1667542	0.0084	0.7764
chr4	191154276	1584766	0.0083	0.9433
chr5	180915260	1811227	0.01	0.9363
chr6	171115067	1326292	0.0078	0.7495
chr7	159138663	1254234	0.0079	0.7875

chr8	146364022	1449482	0.0099	1.1093
chr9	141213431	1276709	0.009	0.9214
chr10	135534747	1906005	0.0141	1.3017
chr11	135006516	1503934	0.0111	1.0955
chr12	133851895	1374429	0.0103	0.9922
chr13	115169878	874466	0.0076	0.9738
chr14	107349540	1118336	0.0104	1.1243
chr15	102531392	955792	0.0093	0.856
chr16	90354753	1167970	0.0129	1.3349
chr17	81195210	1221344	0.015	1.5519
chr18	78077248	760345	0.0097	0.8776
chr19	59128983	769818	0.013	1.4175
chr20	63025520	893222	0.0142	1.181
chr21	48129895	265313	0.0055	0.5279
chr22	51304566	421505	0.0082	0.8919
chrMT	16571	200152	12.0785	110.0523
chrX	155270560	2760804	0.0178	1.2099
chrY	59373566	99859	0.0017	0.2696

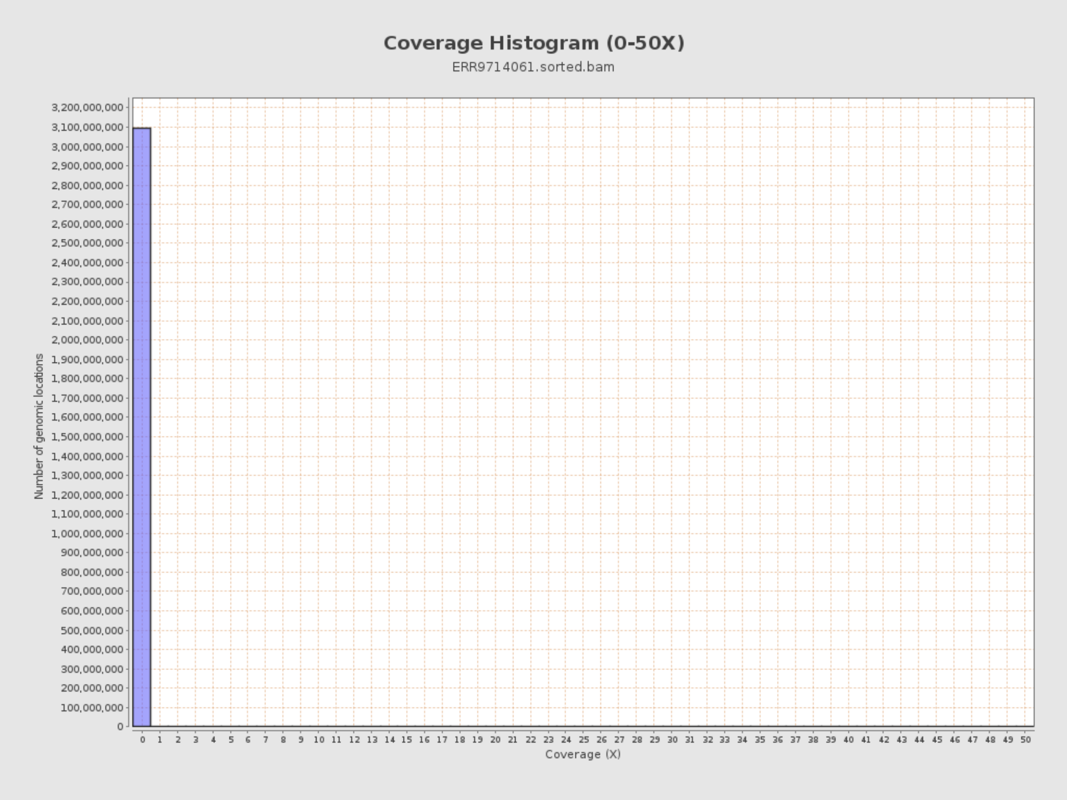
3. Results : Coverage across reference



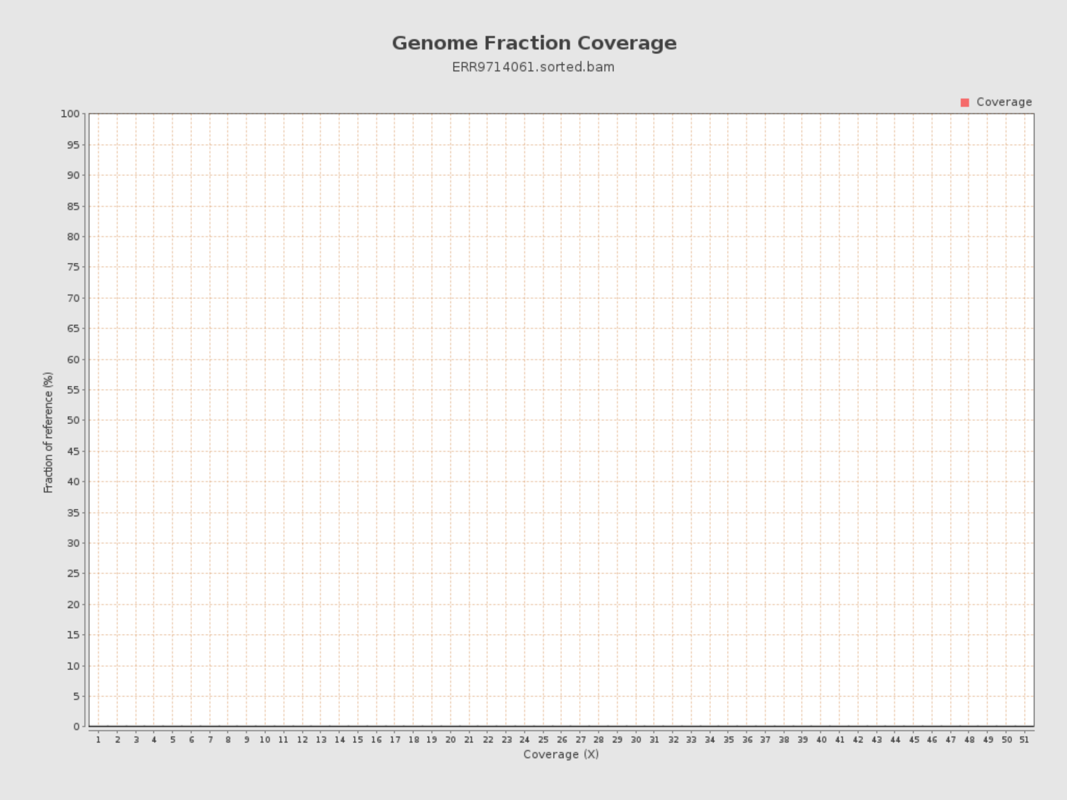
4. Results : Coverage Histogram



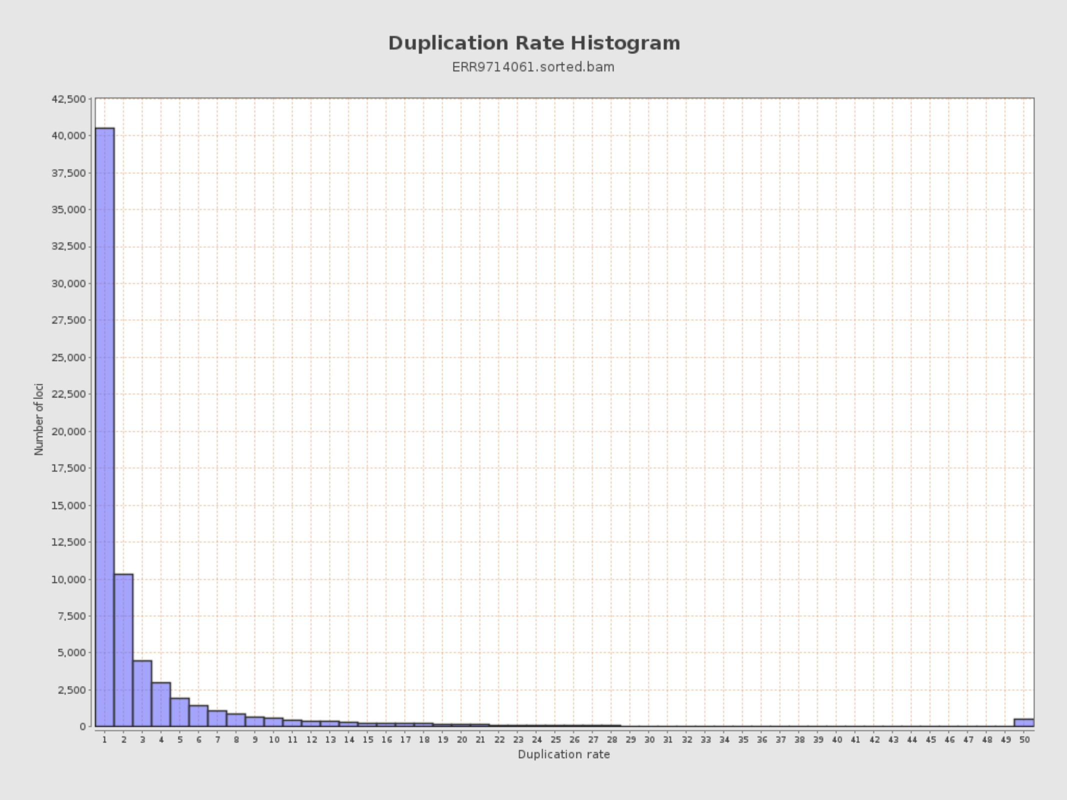
5. Results : Coverage Histogram (0-50X)



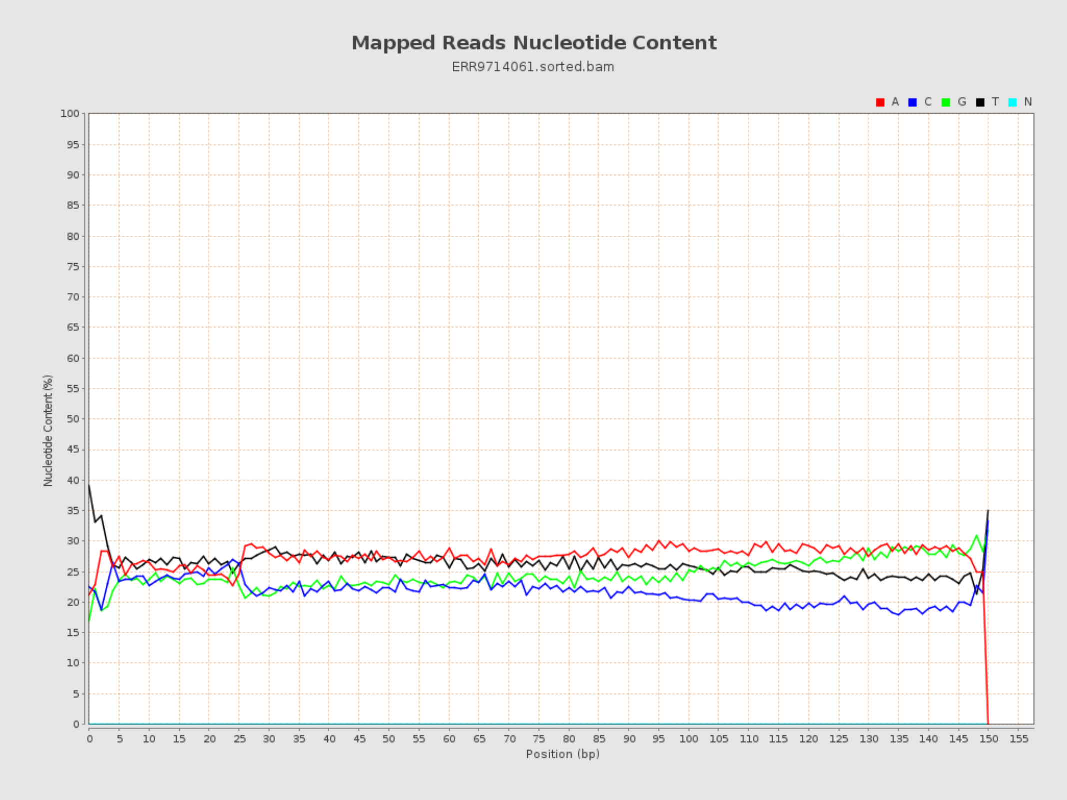
6. Results : Genome Fraction Coverage



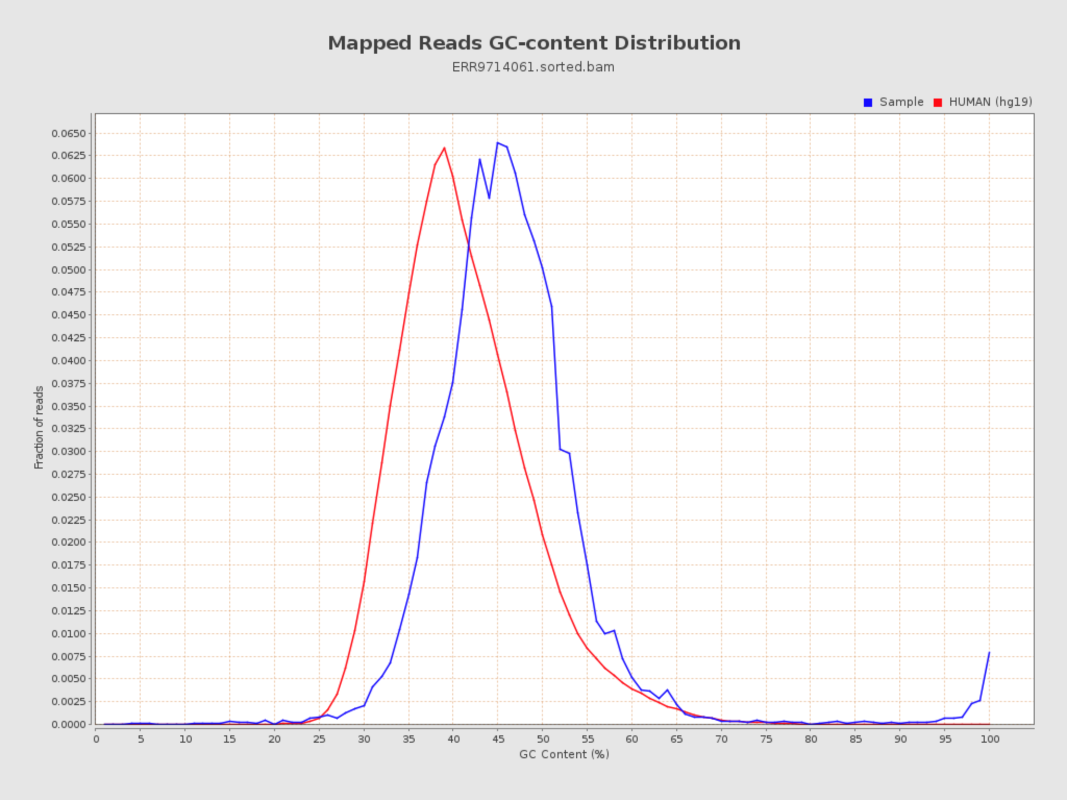
7. Results : Duplication Rate Histogram



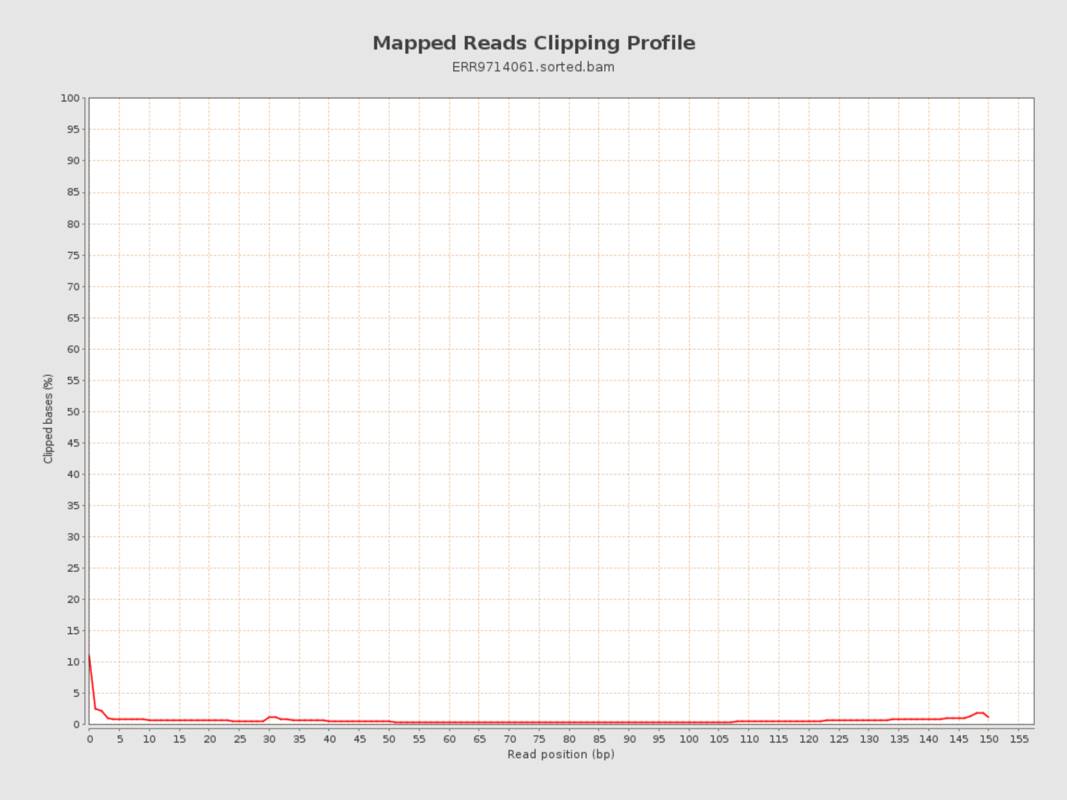
8. Results : Mapped Reads Nucleotide Content



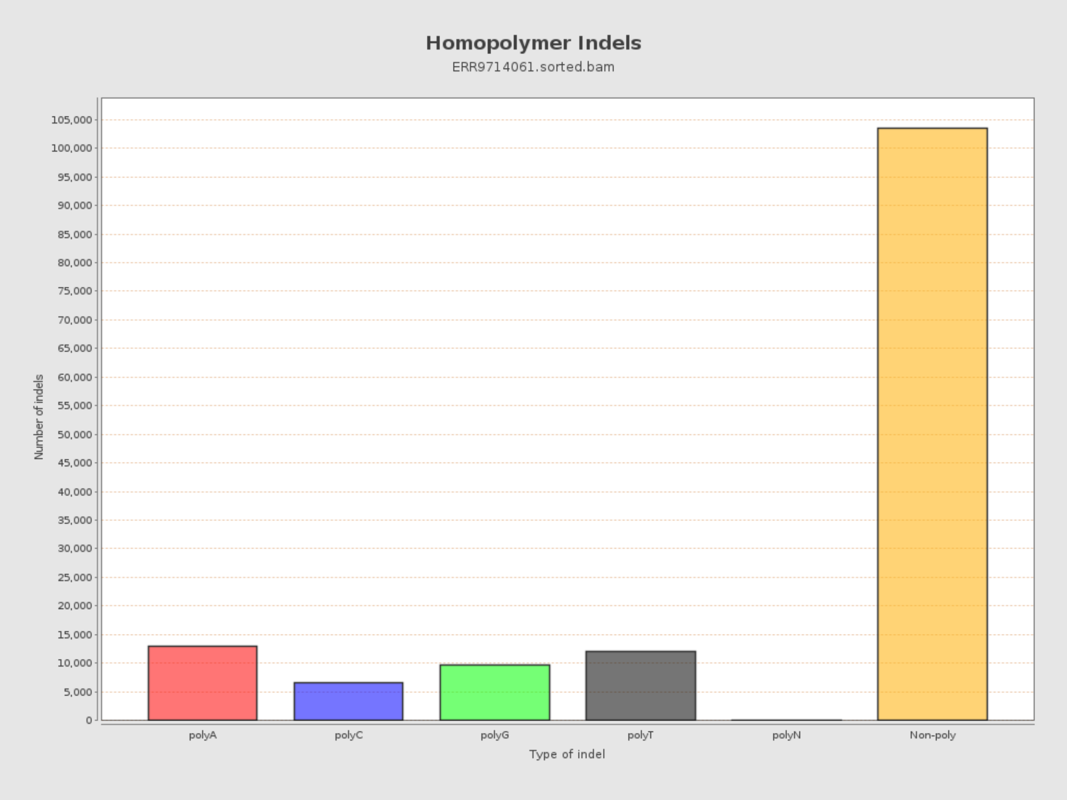
9. Results : Mapped Reads GC-content Distribution



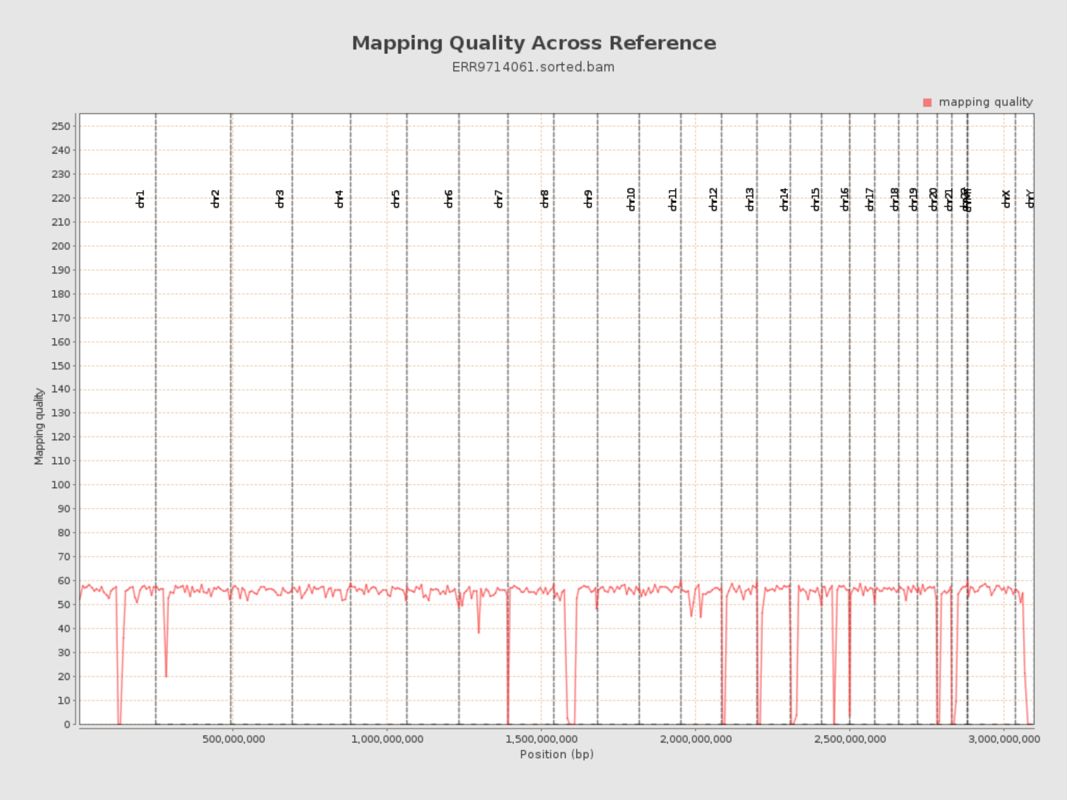
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram