Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:06:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714116.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_ERR9714116 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:06:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	814,086
Mapped reads	331,344 / 40.7%
Unmapped reads	482,742 / 59.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,317 / 0.78%
Read min/max/mean length	30 / 151 / 89.31
Duplicated reads (estimated)	313,487 / 38.51%
Duplication rate	33.81%
Clipped reads	288,549 / 35.44%

2.2. ACGT Content

Number/percentage of A's	9,707,950 / 24.42%
Number/percentage of C's	7,175,748 / 18.05%
Number/percentage of T's	9,231,855 / 23.22%
Number/percentage of G's	13,644,691 / 34.32%
Number/percentage of N's	690 / 0%
GC Percentage	52.36%

2.3. Coverage

Mean	0.013

Standard Deviation	13.5044

2.4. Mapping Quality

Mean Mapping Quality	31.21

2.5. Mismatches and indels

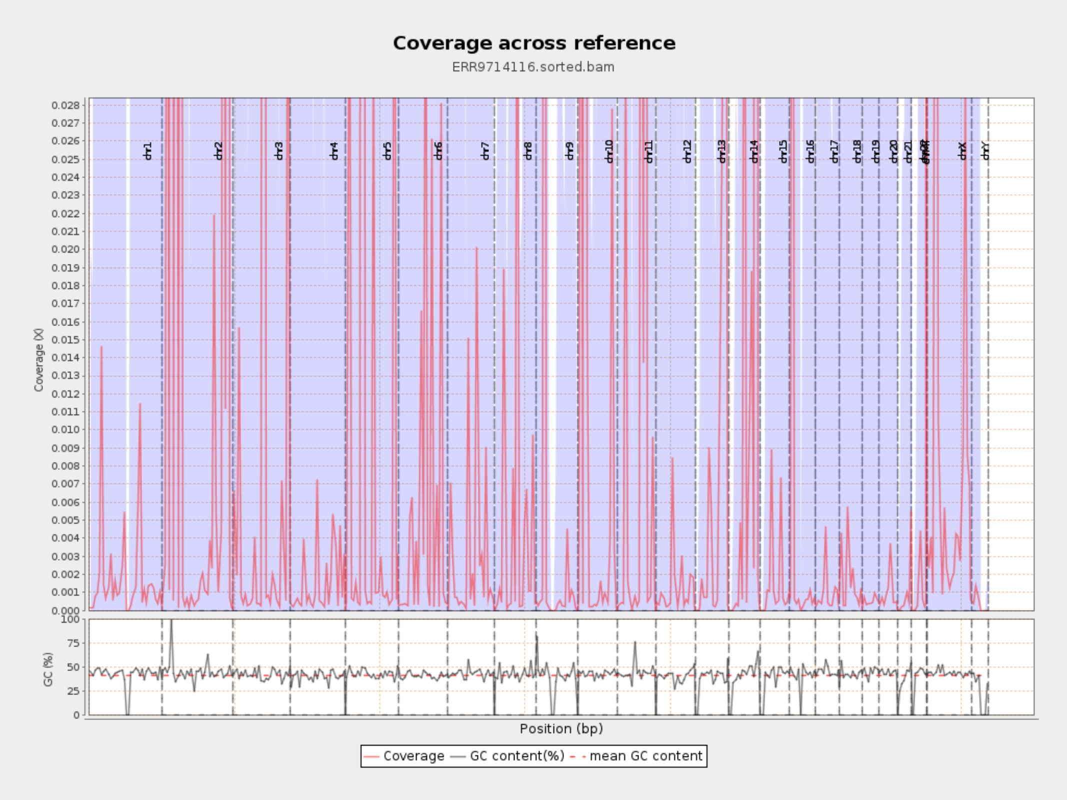
General error rate	3.19%
Mismatches	1,108,336
Insertions	38,919
Mapped reads with at least one insertion	10.93%
Deletions	95,038
Mapped reads with at least one deletion	27.61%
Homopolymer indels	30.27%

2.6. Chromosome stats

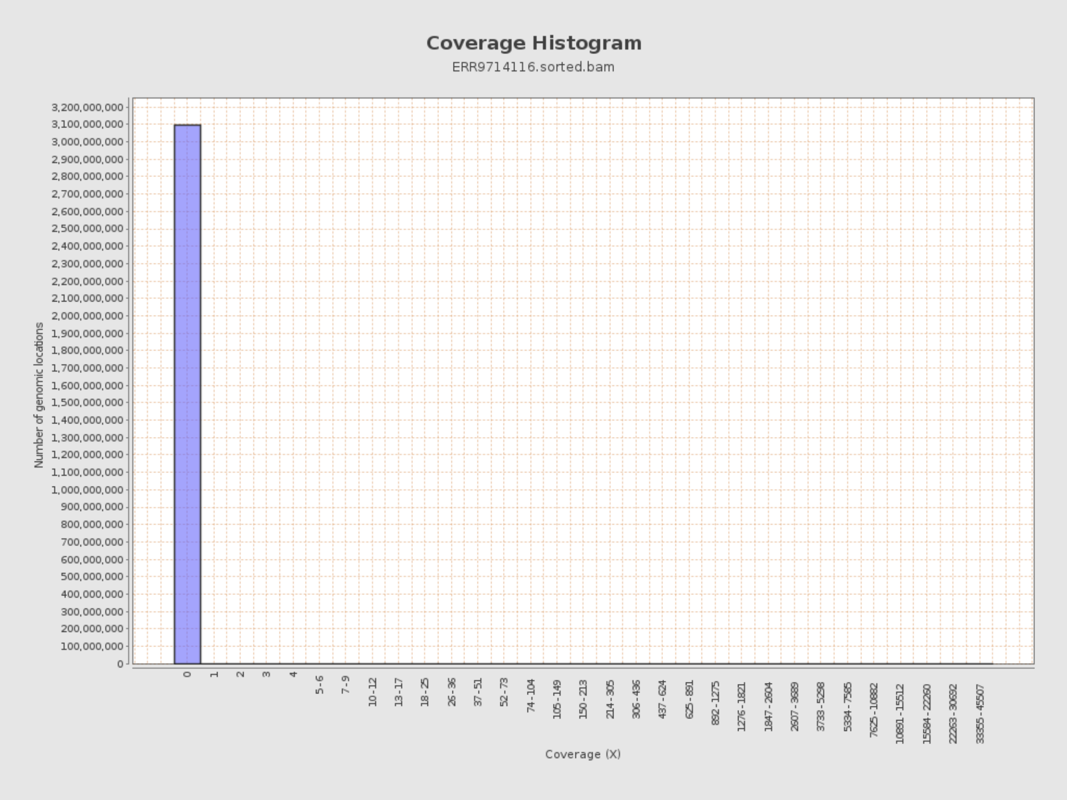
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	504115	0.002	0.5877
chr2	243199373	13731892	0.0565	32.2051
chr3	198022430	2276450	0.0115	8.8047
chr4	191154276	305796	0.0016	0.4174
chr5	180915260	4461030	0.0247	23.3757
chr6	171115067	1118795	0.0065	2.3563
chr7	159138663	534496	0.0034	1.3383

chr8	146364022	771911	0.0053	2.4364
chr9	141213431	824251	0.0058	2.5957
chr10	135534747	4569124	0.0337	22.8131
chr11	135006516	1950055	0.0144	6.5432
chr12	133851895	181833	0.0014	0.4605
chr13	115169878	1282940	0.0111	4.6368
chr14	107349540	4721181	0.044	32.3664
chr15	102531392	173817	0.0017	0.5862
chr16	90354753	590517	0.0065	4.4931
chr17	81195210	84008	0.001	0.2594
chr18	78077248	134771	0.0017	0.4105
chr19	59128983	31028	0.0005	0.0708
chr20	63025520	63649	0.001	0.2918
chr21	48129895	42452	0.0009	0.3091
chr22	51304566	44224	0.0009	0.2699
chrMT	16571	347937	20.9967	169.315
chrX	155270560	1415840	0.0091	2.8761
chrY	59373566	20727	0.0003	0.1032

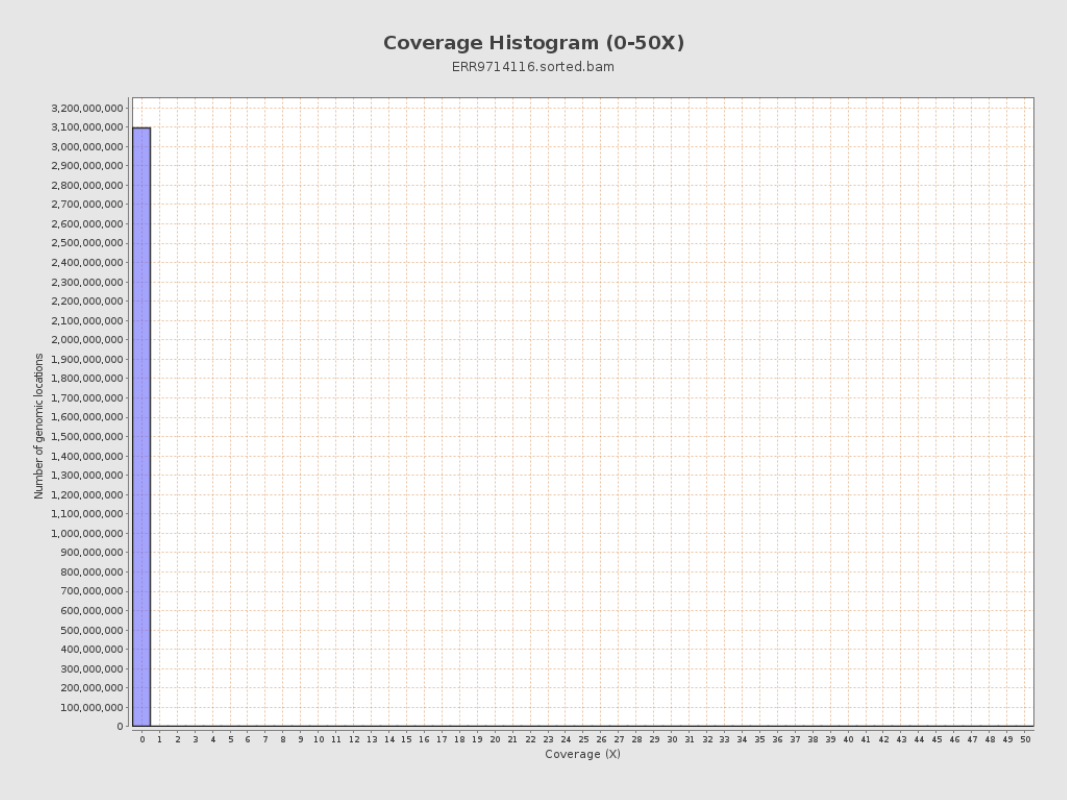
3. Results : Coverage across reference



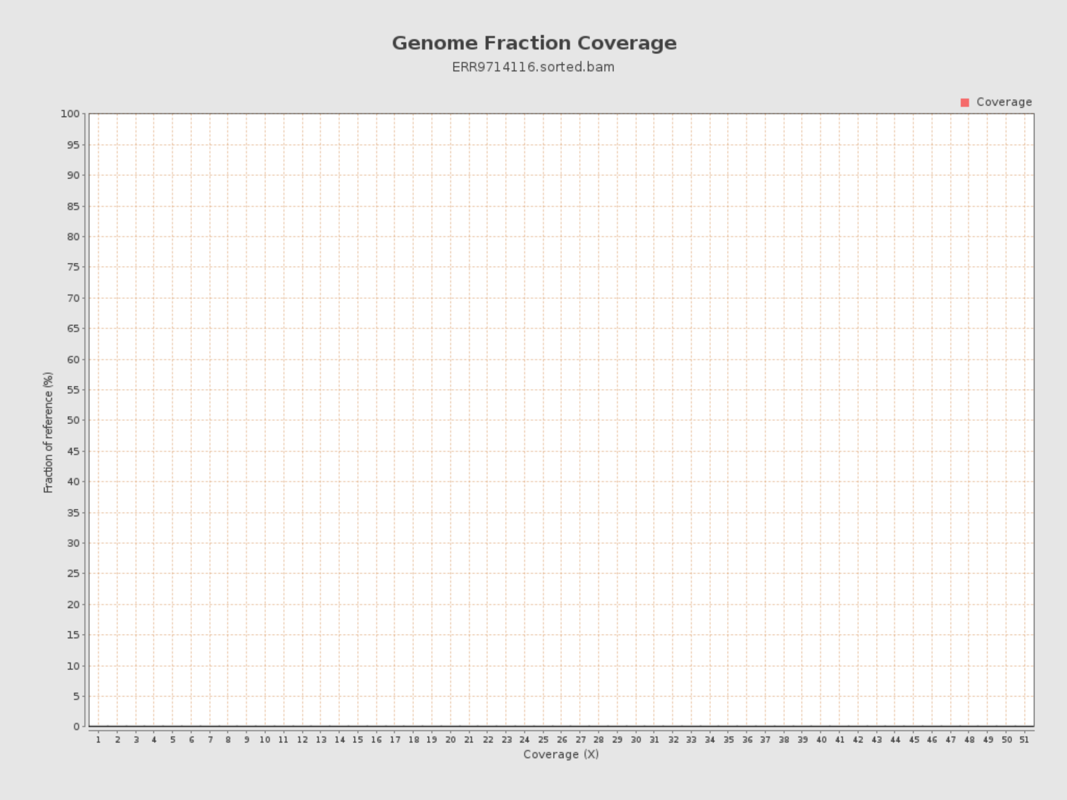
4. Results : Coverage Histogram



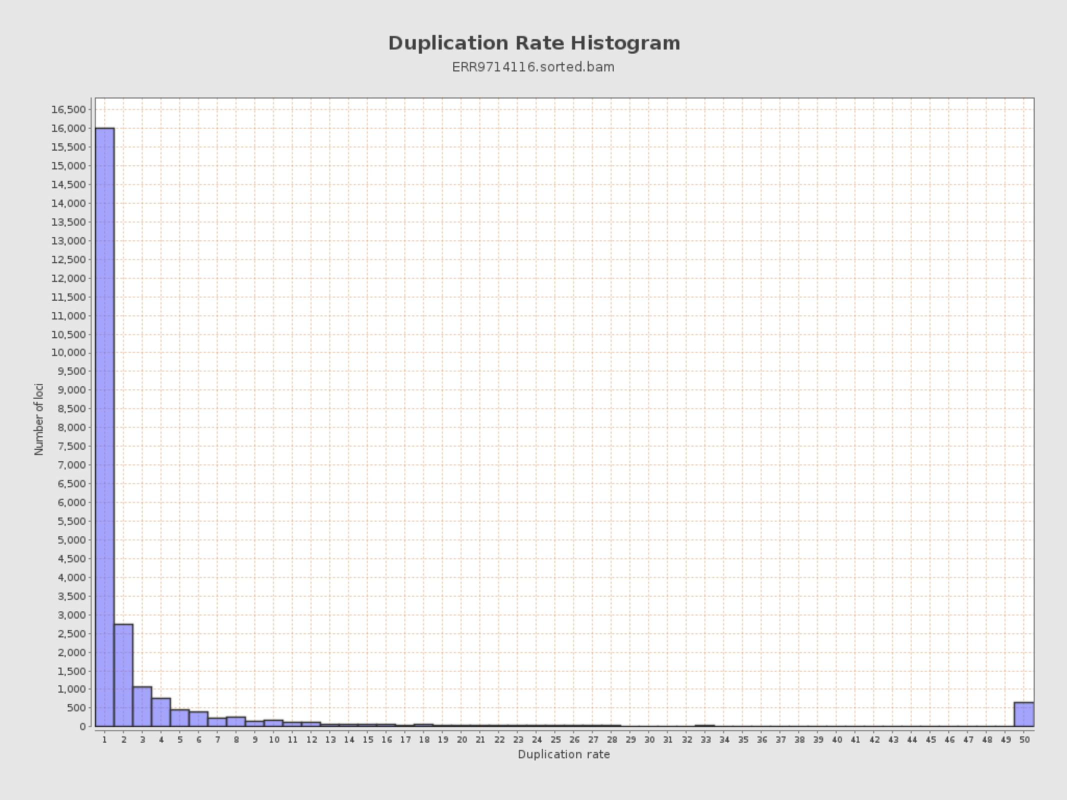
5. Results : Coverage Histogram (0-50X)



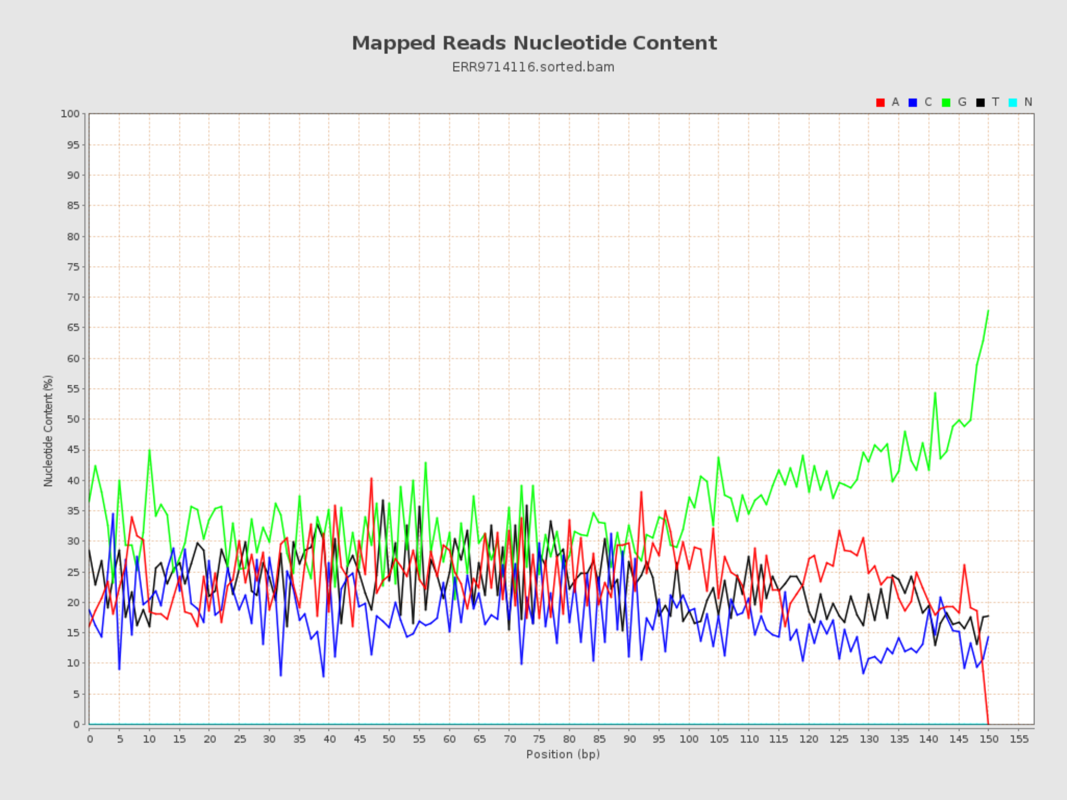
6. Results : Genome Fraction Coverage



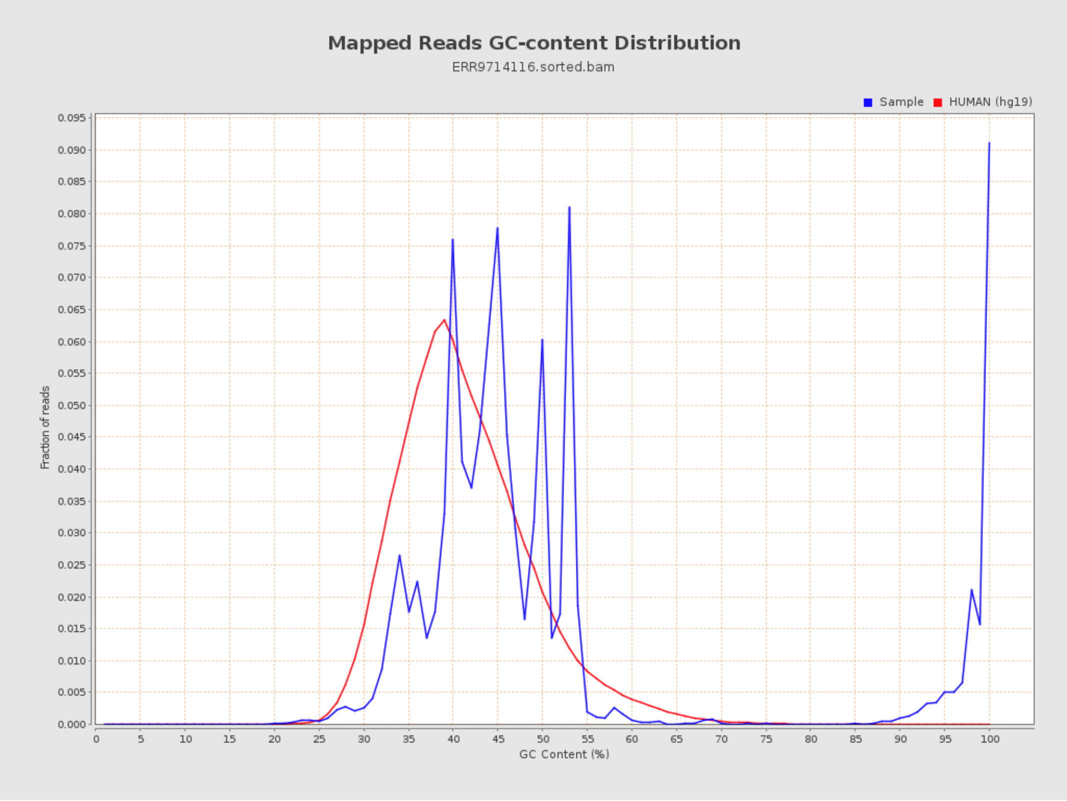
7. Results : Duplication Rate Histogram



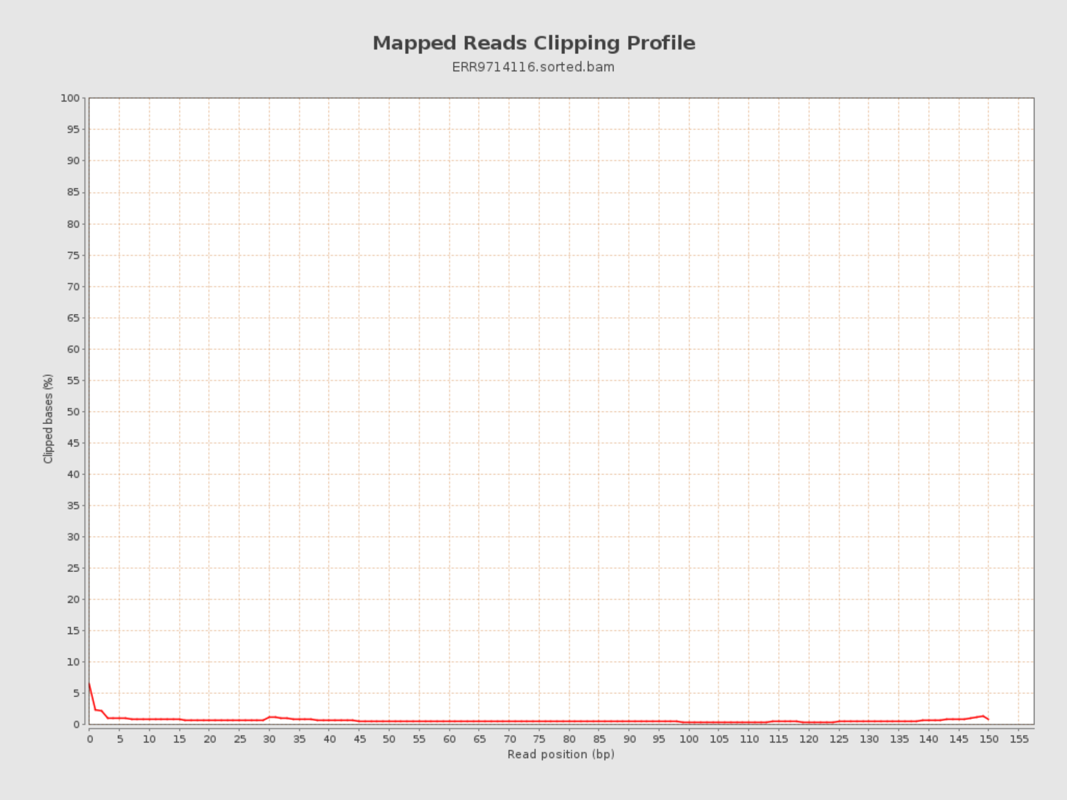
8. Results : Mapped Reads Nucleotide Content



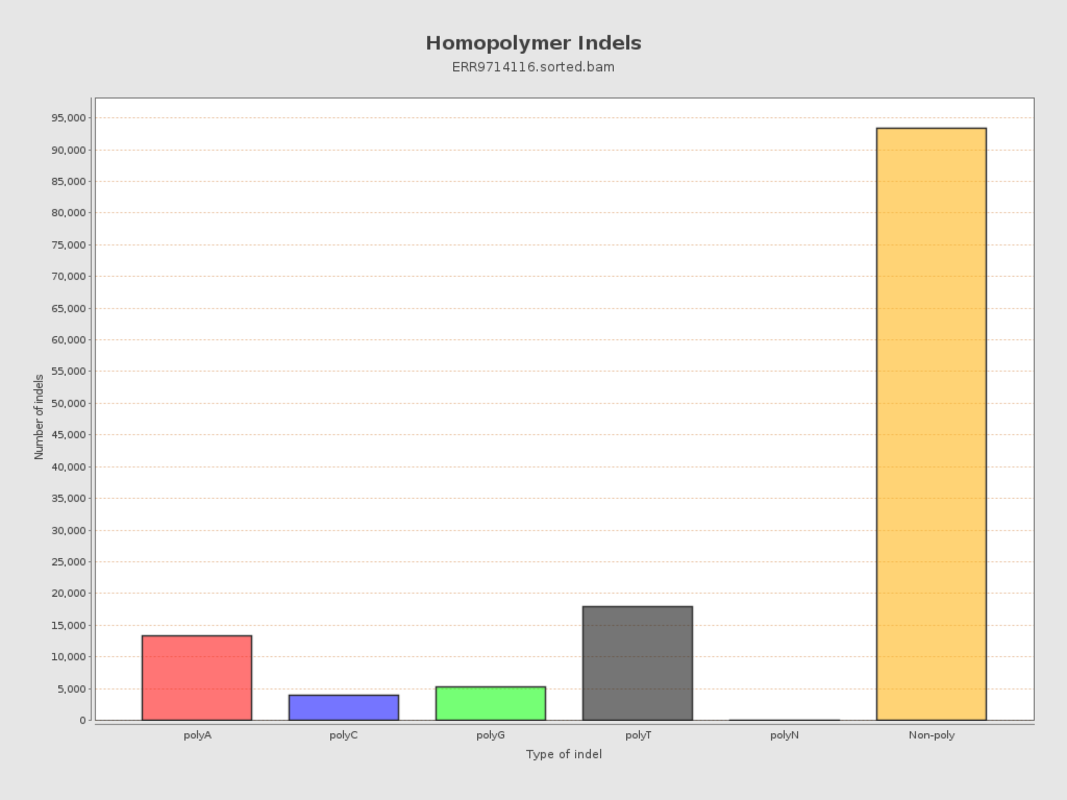
9. Results : Mapped Reads GC-content Distribution



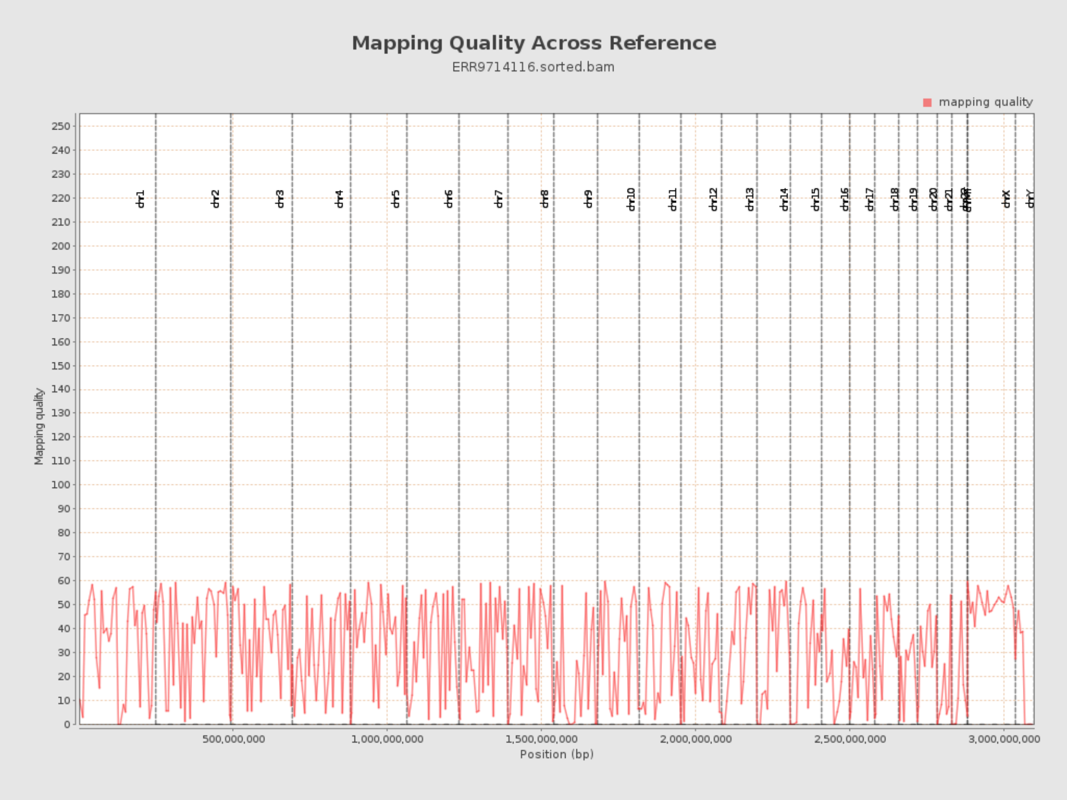
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram