Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 17:36:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714055.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_ERR9714055 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 17:36:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	272,526
Mapped reads	256,618 / 94.16%
Unmapped reads	15,908 / 5.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,208 / 2.64%
Read min/max/mean length	30 / 151 / 144.98
Duplicated reads (estimated)	246,221 / 90.35%
Duplication rate	32.92%
Clipped reads	241,807 / 88.73%

2.2. ACGT Content

Number/percentage of A's	9,101,832 / 28.46%
Number/percentage of C's	6,781,306 / 21.2%
Number/percentage of T's	8,490,275 / 26.55%
Number/percentage of G's	7,606,454 / 23.79%
Number/percentage of N's	178 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.0106

Standard Deviation	15.4731

2.4. Mapping Quality

Mean Mapping Quality	27.03

2.5. Mismatches and indels

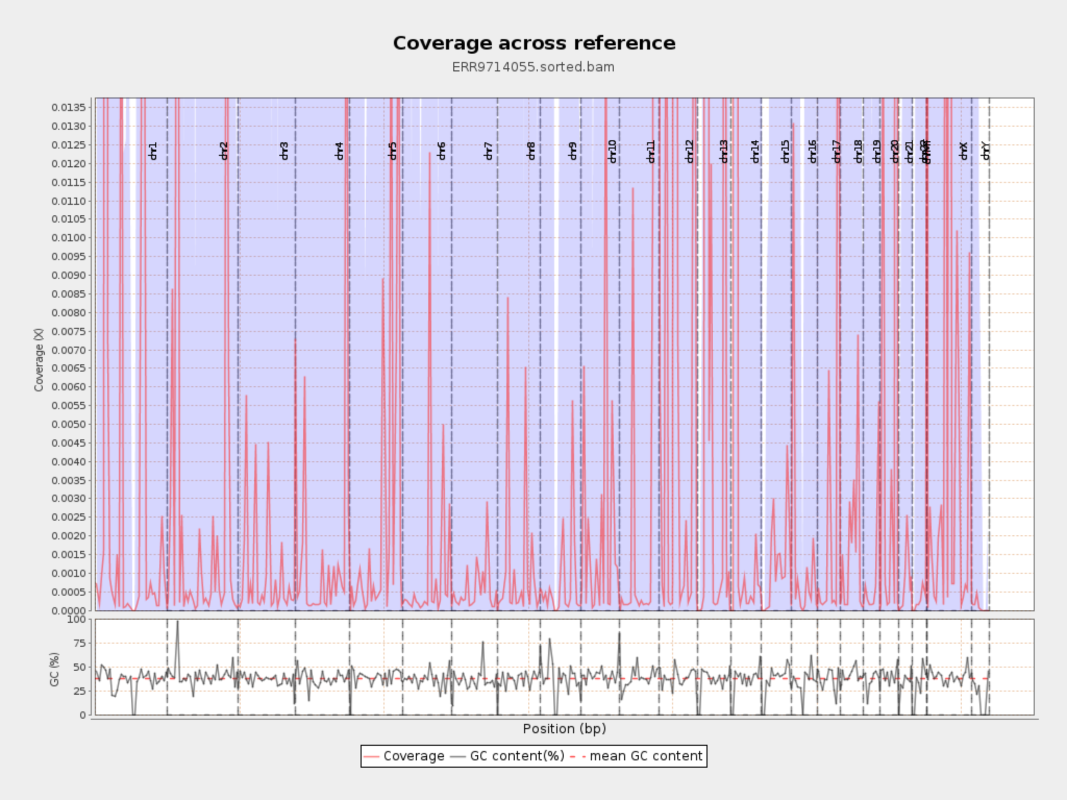
General error rate	4.59%
Mismatches	1,383,429
Insertions	32,255
Mapped reads with at least one insertion	12.28%
Deletions	135,243
Mapped reads with at least one deletion	49.56%
Homopolymer indels	29.38%

2.6. Chromosome stats

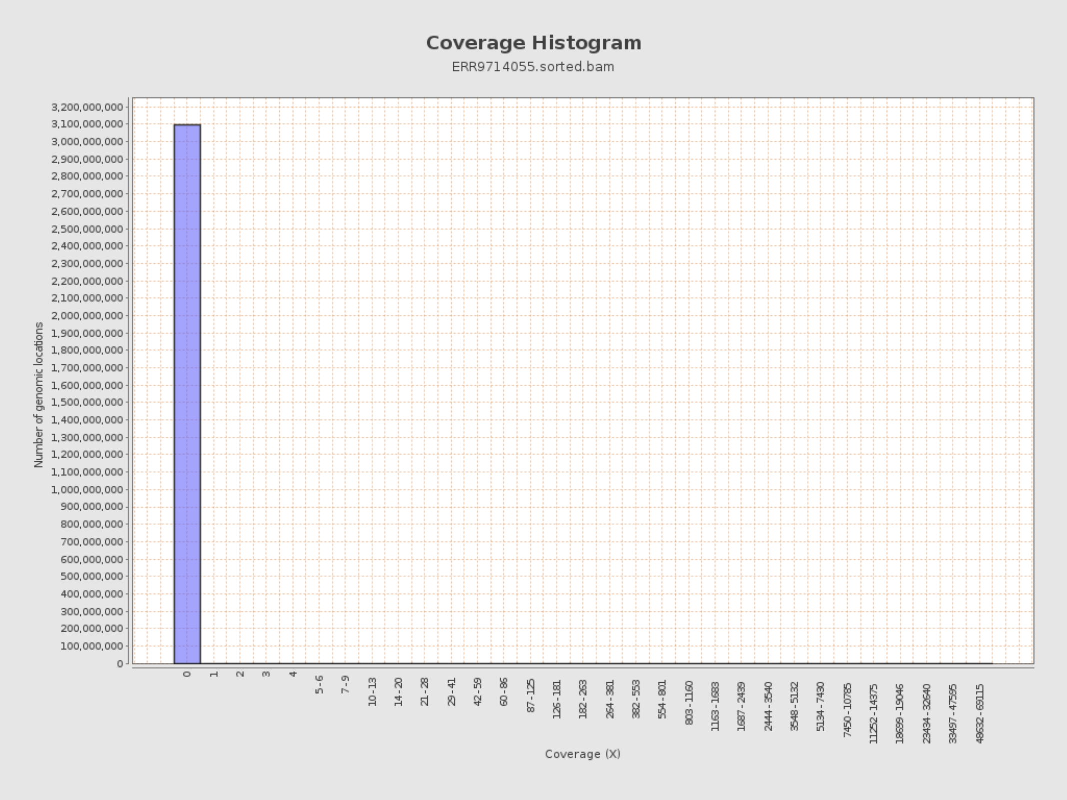
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1568388	0.0063	3.722
chr2	243199373	725277	0.003	1.3797
chr3	198022430	196474	0.001	0.2764
chr4	191154276	382328	0.002	1.0385
chr5	180915260	545385	0.003	1.0056
chr6	171115067	194749	0.0011	0.5976
chr7	159138663	94329	0.0006	0.1831

chr8	146364022	180354	0.0012	0.3785
chr9	141213431	114664	0.0008	0.2166
chr10	135534747	325396	0.0024	0.8561
chr11	135006516	19384096	0.1436	71.8061
chr12	133851895	1499838	0.0112	5.5638
chr13	115169878	1788515	0.0155	10.0515
chr14	107349540	1930771	0.018	11.8528
chr15	102531392	141453	0.0014	0.4695
chr16	90354753	144024	0.0016	0.8451
chr17	81195210	274466	0.0034	1.1954
chr18	78077248	150450	0.0019	0.5516
chr19	59128983	60533	0.001	0.3145
chr20	63025520	1781367	0.0283	11.7646
chr21	48129895	36974	0.0008	0.1893
chr22	51304566	56099	0.0011	0.3334
chrMT	16571	12916	0.7794	5.5353
chrX	155270560	1096210	0.0071	2.1377
chrY	59373566	6405	0.0001	0.0252

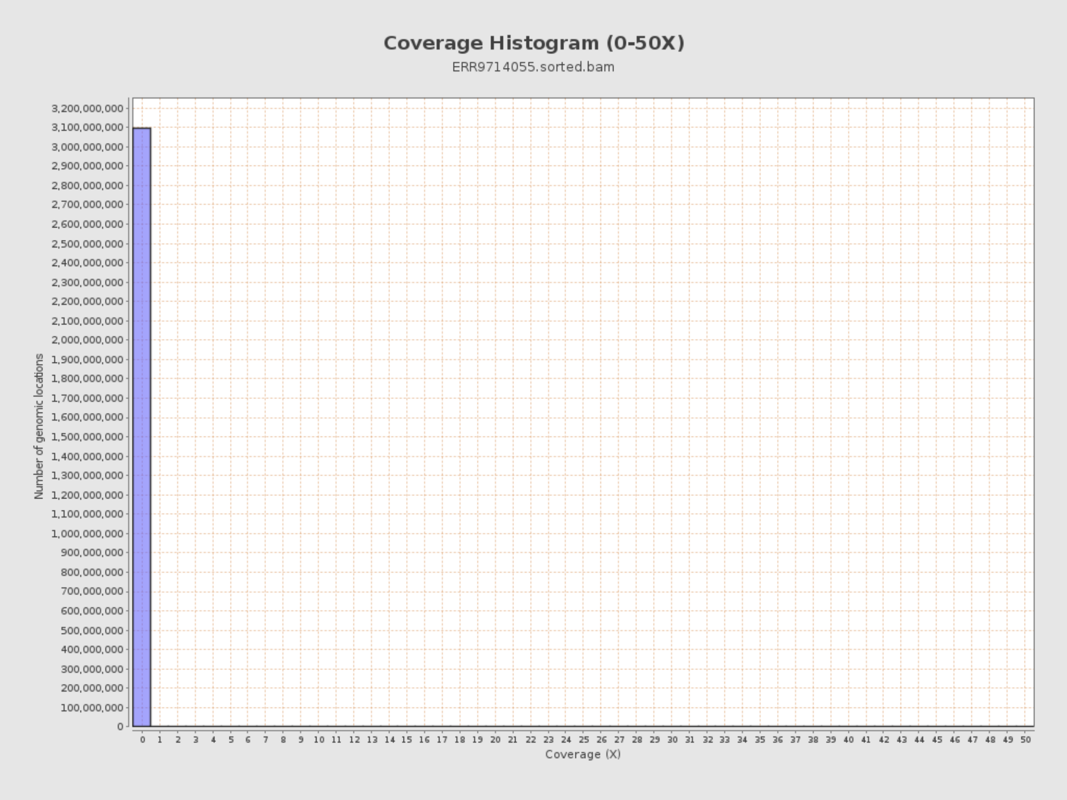
3. Results : Coverage across reference



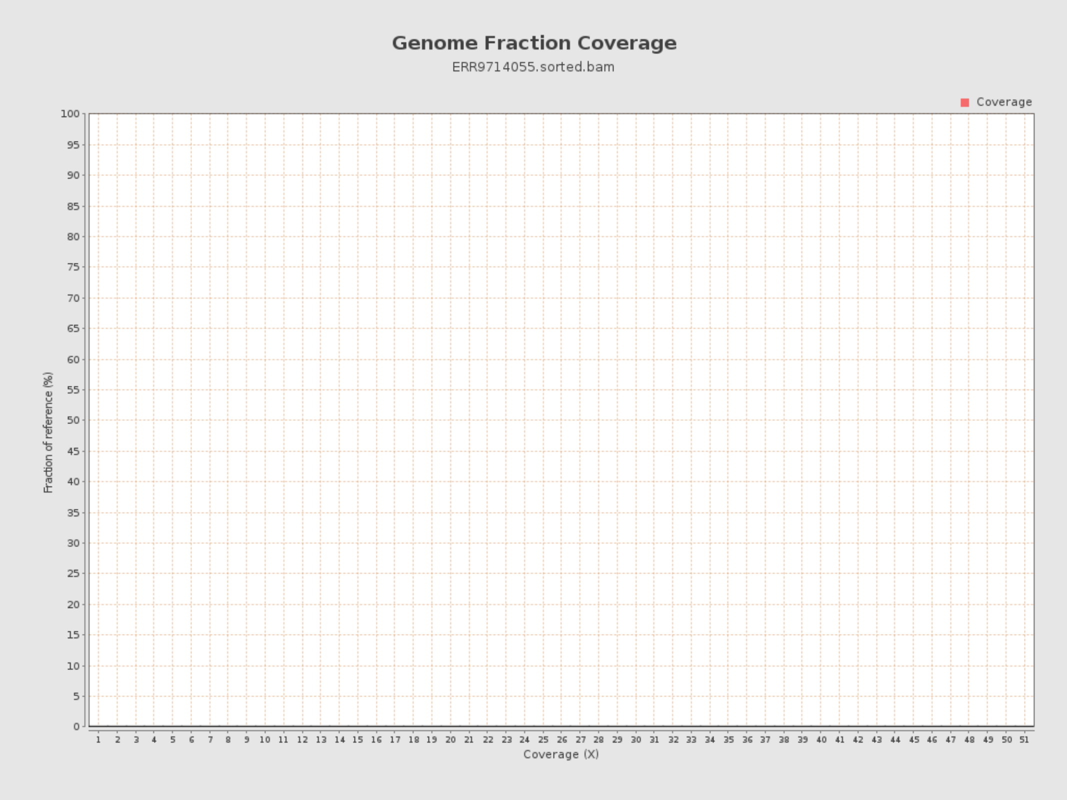
4. Results : Coverage Histogram



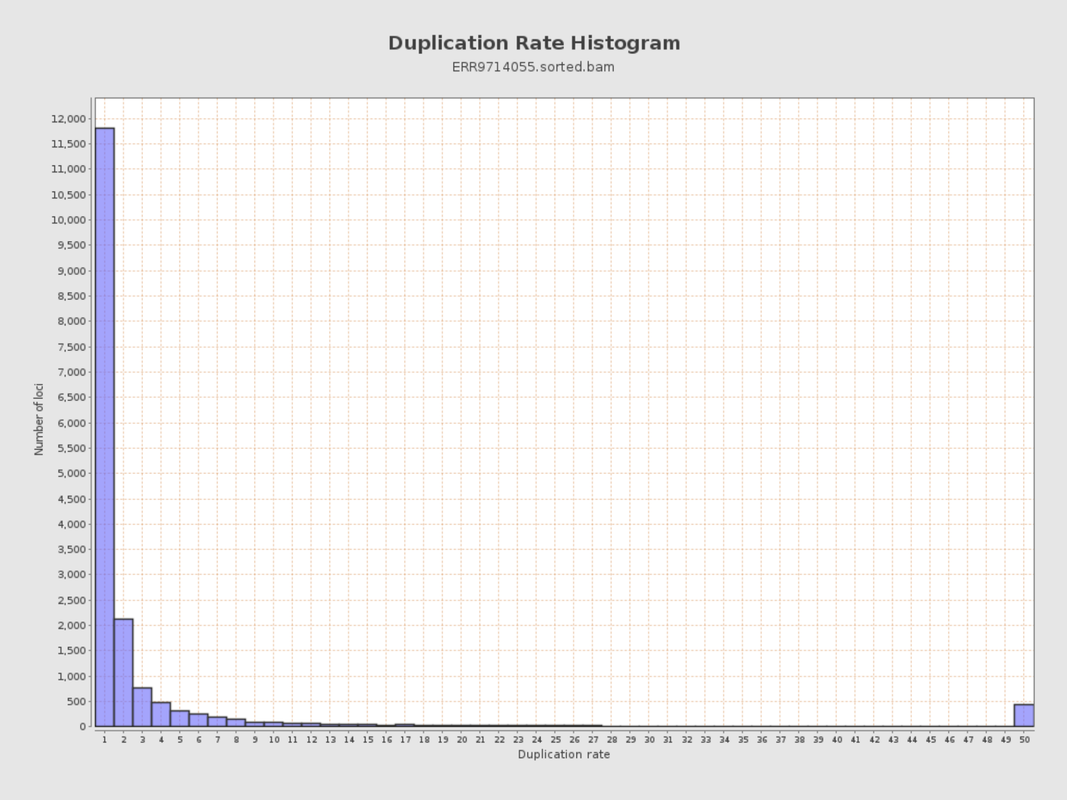
5. Results : Coverage Histogram (0-50X)



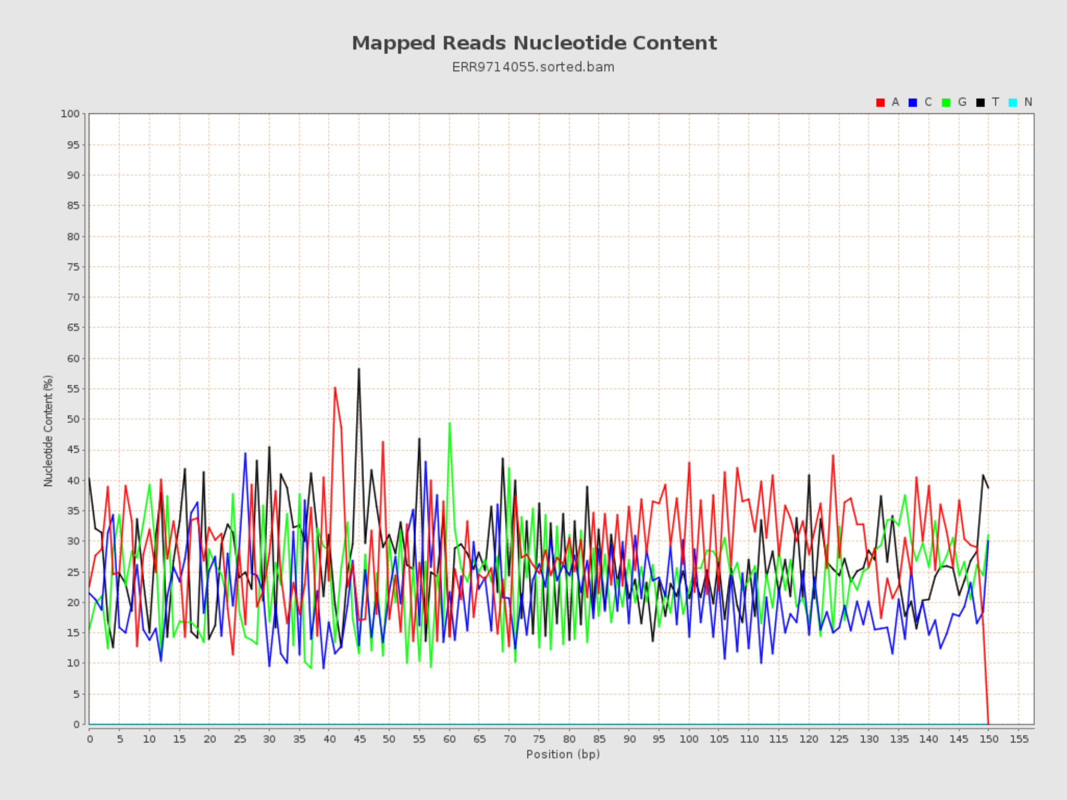
6. Results : Genome Fraction Coverage



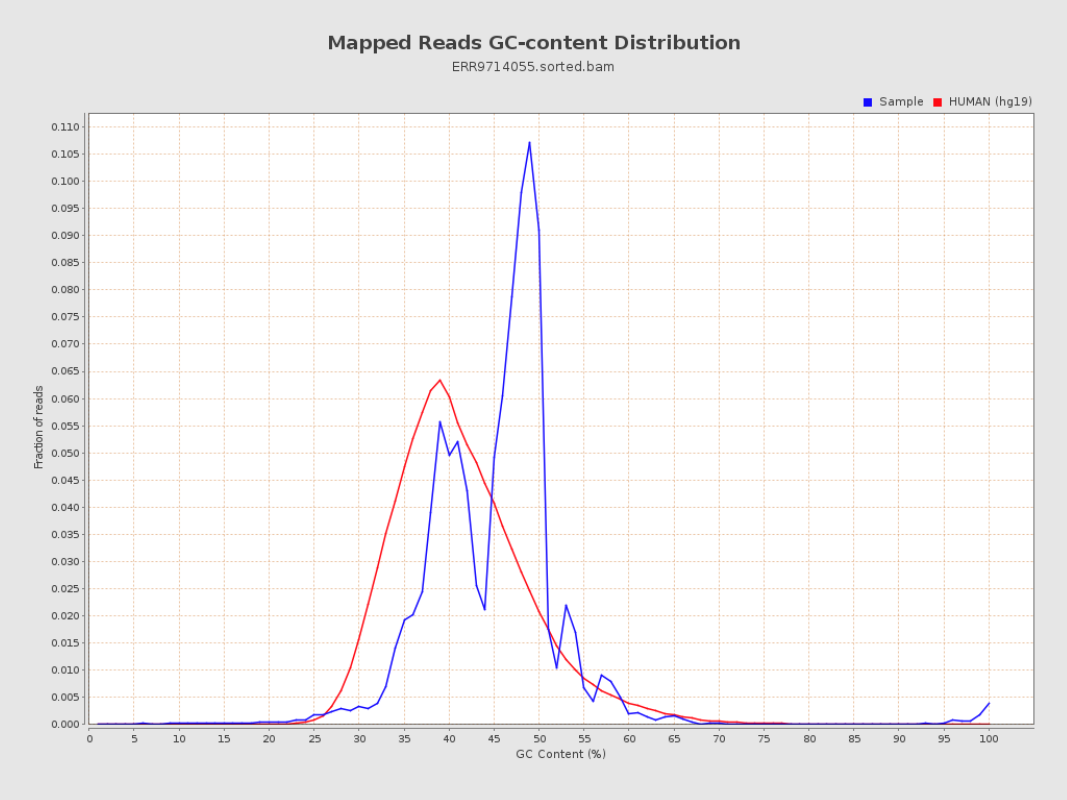
7. Results : Duplication Rate Histogram



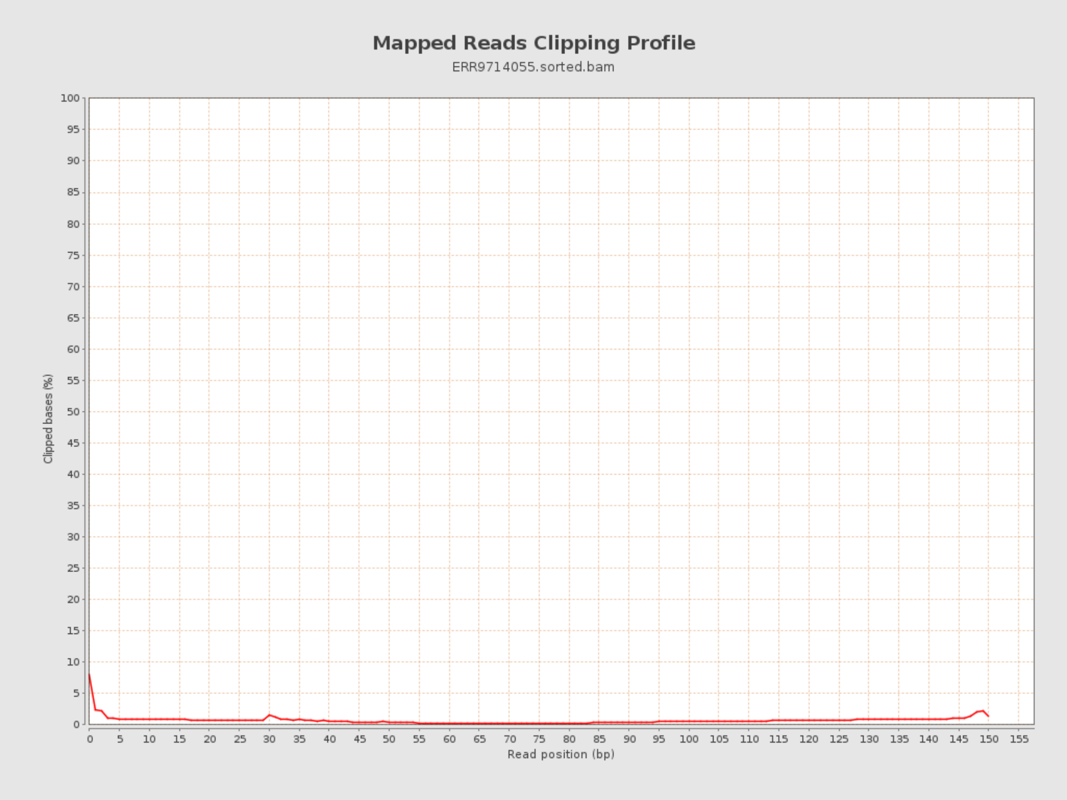
8. Results : Mapped Reads Nucleotide Content



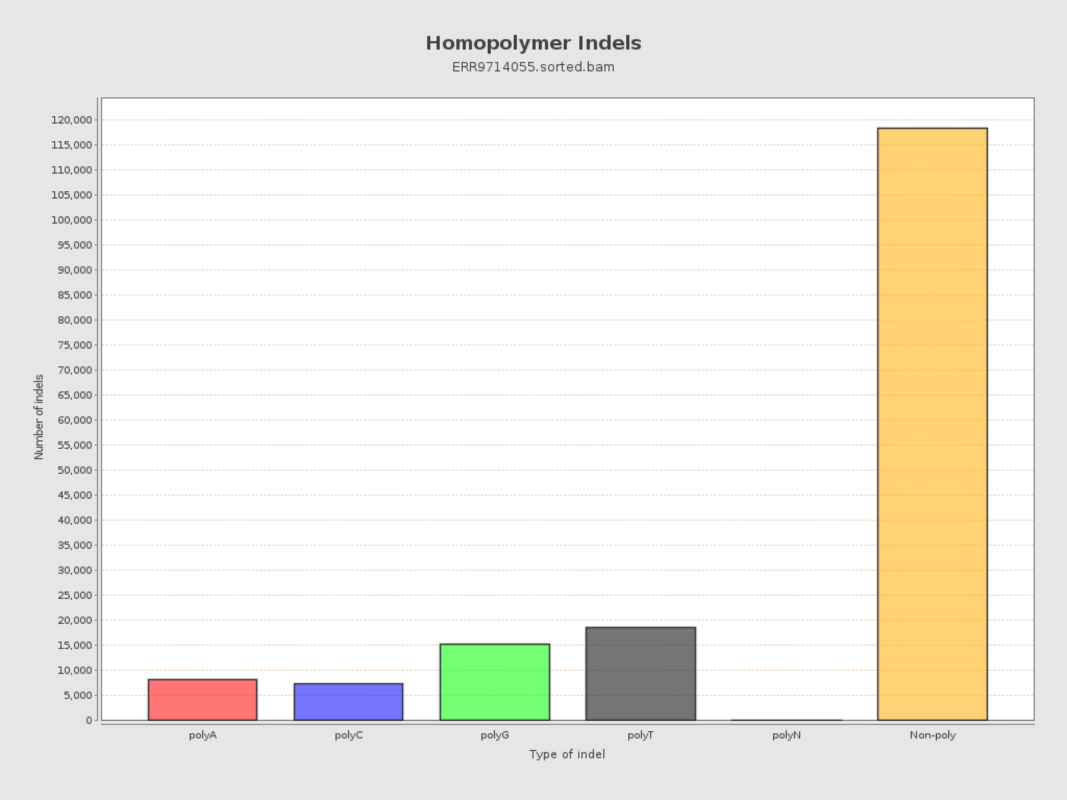
9. Results : Mapped Reads GC-content Distribution



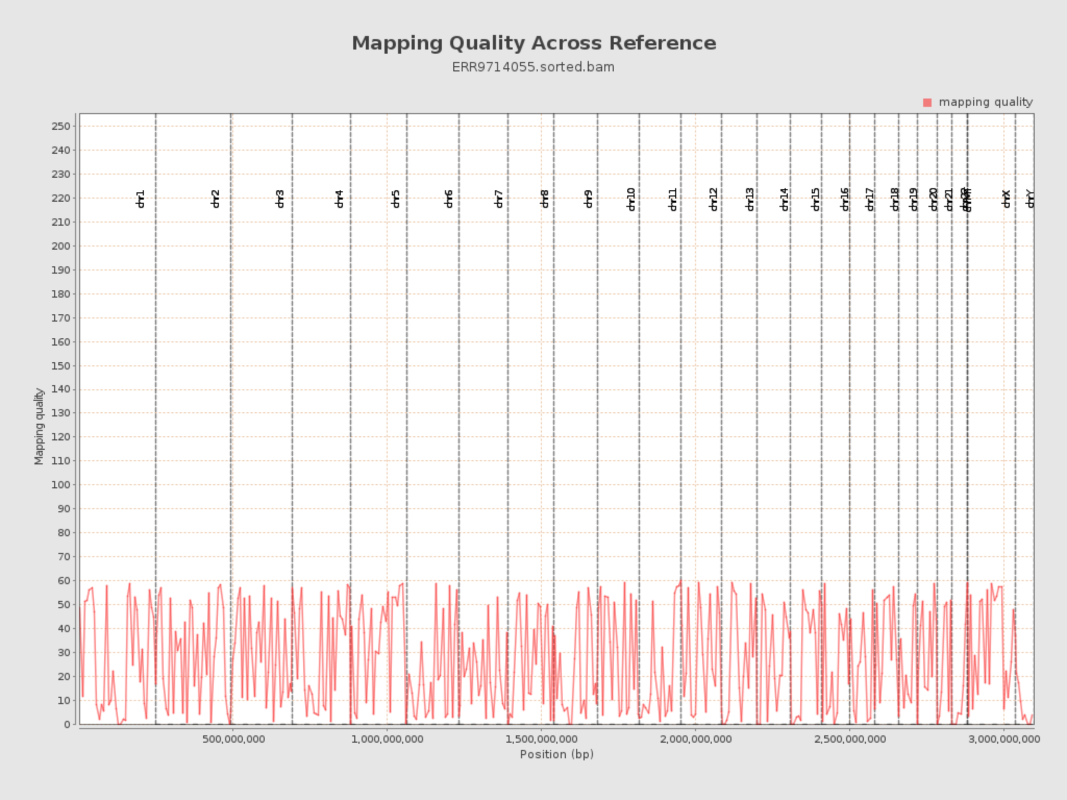
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram