Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:11:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714139.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_ERR9714139 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:11:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	659,508
Mapped reads	591,361 / 89.67%
Unmapped reads	68,147 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,328 / 2.93%
Read min/max/mean length	30 / 151 / 140.51
Duplicated reads (estimated)	509,633 / 77.27%
Duplication rate	43.08%
Clipped reads	560,410 / 84.97%

2.2. ACGT Content

Number/percentage of A's	21,256,658 / 28.39%
Number/percentage of C's	15,949,547 / 21.3%
Number/percentage of T's	20,115,618 / 26.87%
Number/percentage of G's	17,542,055 / 23.43%
Number/percentage of N's	517 / 0%
GC Percentage	44.74%

2.3. Coverage

Mean	0.0247

Standard Deviation	2.7482

2.4. Mapping Quality

Mean Mapping Quality	52.54

2.5. Mismatches and indels

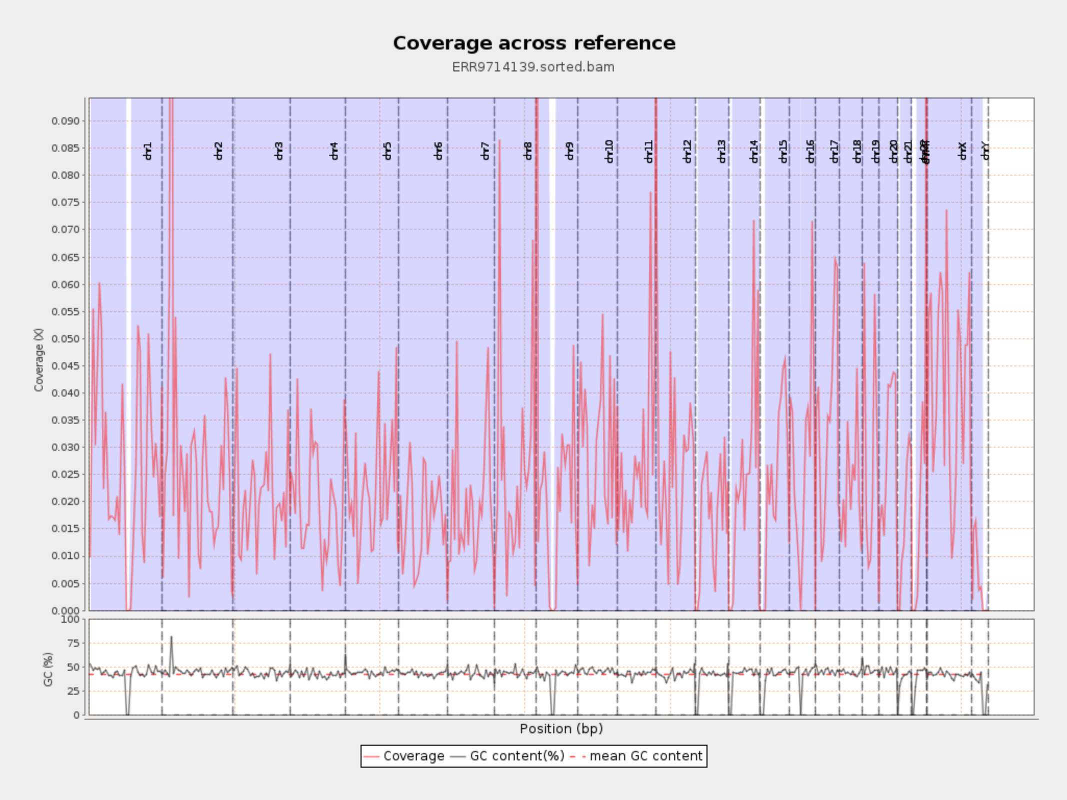
General error rate	4.35%
Mismatches	2,964,262
Insertions	88,562
Mapped reads with at least one insertion	14.57%
Deletions	255,497
Mapped reads with at least one deletion	41.04%
Homopolymer indels	27.92%

2.6. Chromosome stats

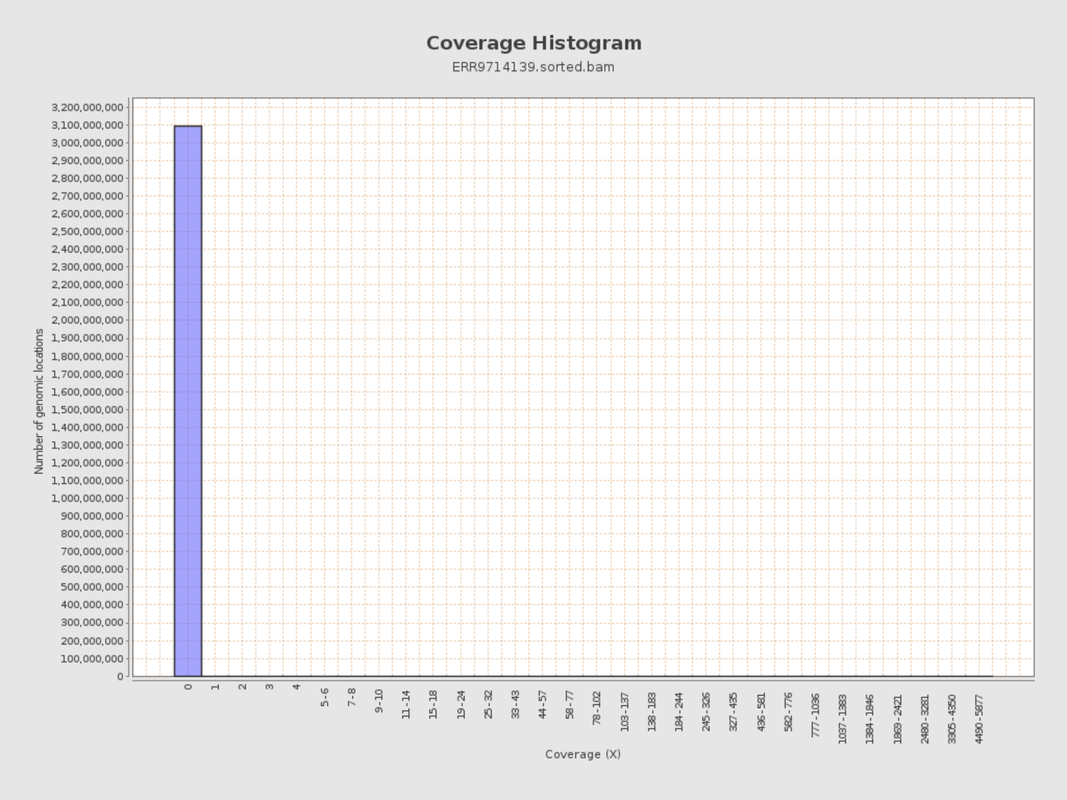
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6640724	0.0266	2.8005
chr2	243199373	7263636	0.0299	4.8191
chr3	198022430	4179212	0.0211	2.044
chr4	191154276	3811709	0.0199	2.2425
chr5	180915260	4093757	0.0226	2.1904
chr6	171115067	2859830	0.0167	1.5759
chr7	159138663	3222274	0.0202	2.1659

chr8	146364022	3750960	0.0256	2.6764
chr9	141213431	2937590	0.0208	2.4271
chr10	135534747	4118740	0.0304	2.7794
chr11	135006516	3656444	0.0271	2.6762
chr12	133851895	3515162	0.0263	2.7848
chr13	115169878	1911041	0.0166	1.6794
chr14	107349540	2737718	0.0255	2.8171
chr15	102531392	2401583	0.0234	2.2761
chr16	90354753	2513203	0.0278	3.1146
chr17	81195210	2870481	0.0354	3.6654
chr18	78077248	1774272	0.0227	2.267
chr19	59128983	1592536	0.0269	3.0531
chr20	63025520	1904191	0.0302	2.5781
chr21	48129895	771574	0.016	1.7189
chr22	51304566	843647	0.0164	1.7716
chrMT	16571	227946	13.7557	124.8901
chrX	155270560	6449208	0.0415	2.9573
chrY	59373566	317344	0.0053	0.8996

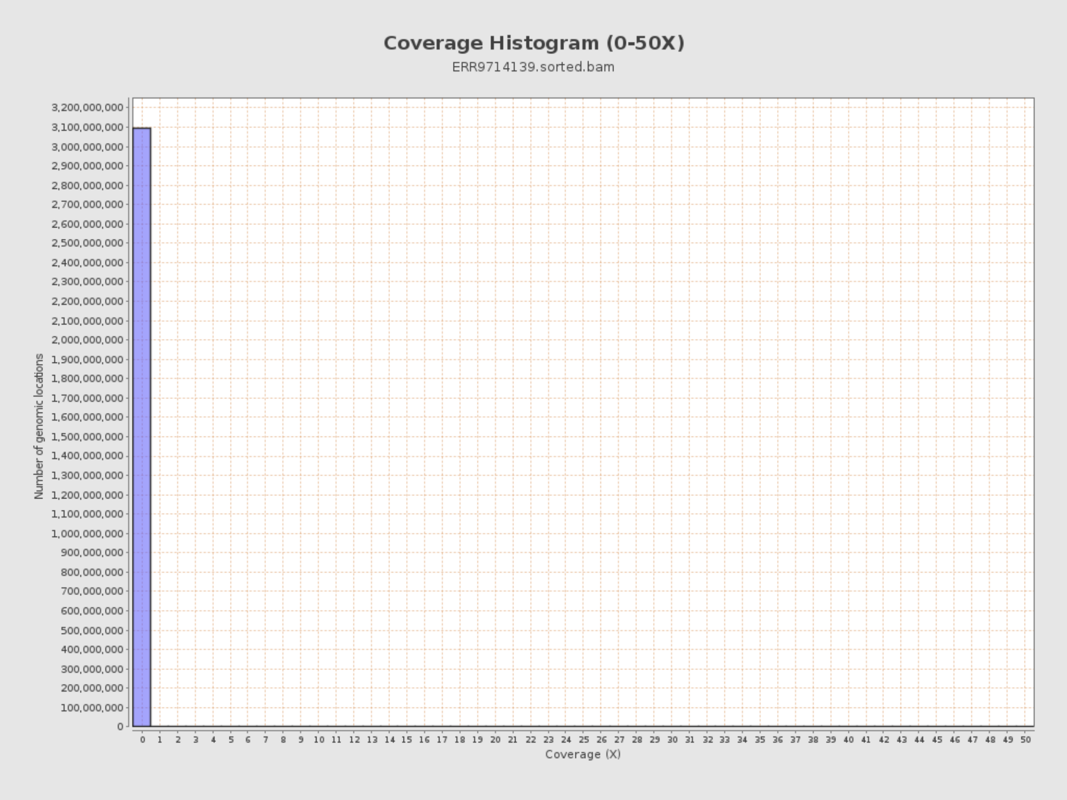
3. Results : Coverage across reference



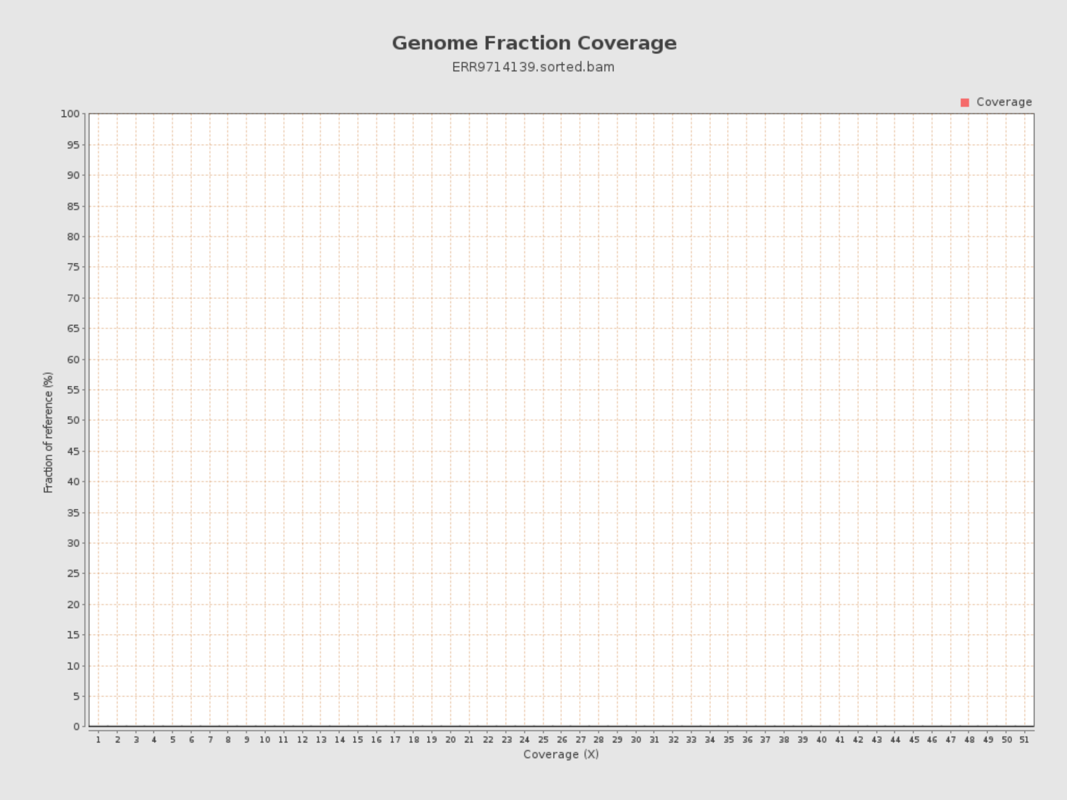
4. Results : Coverage Histogram



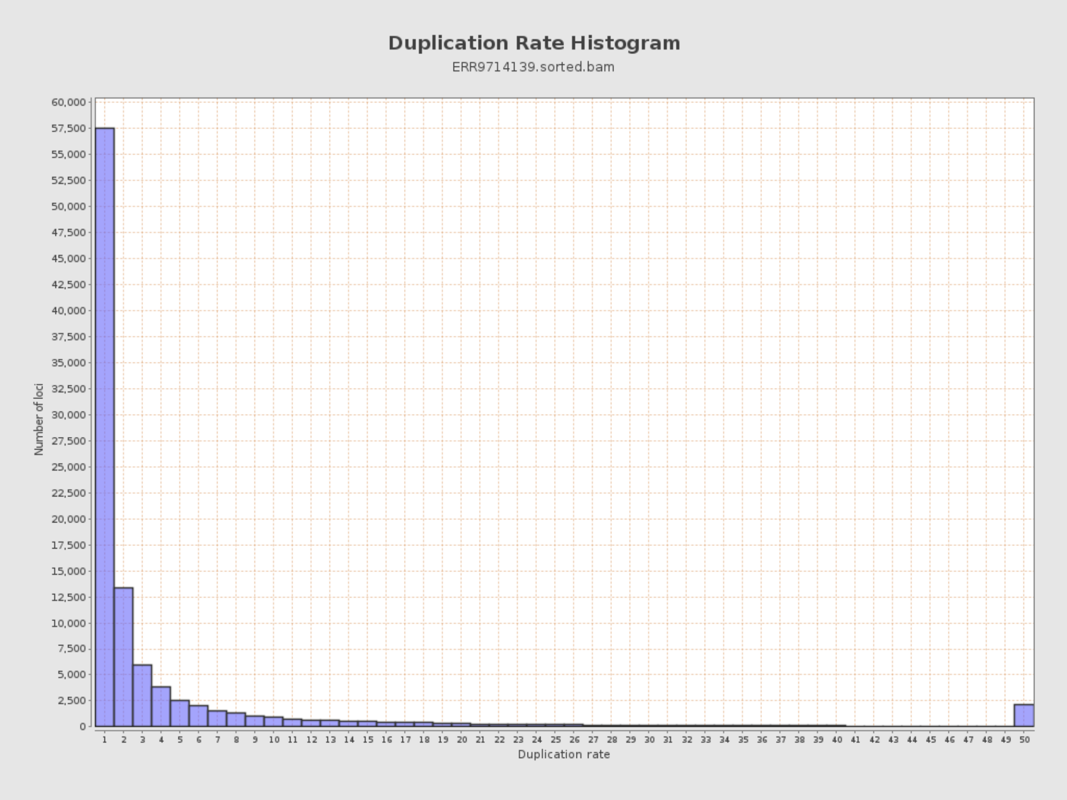
5. Results : Coverage Histogram (0-50X)



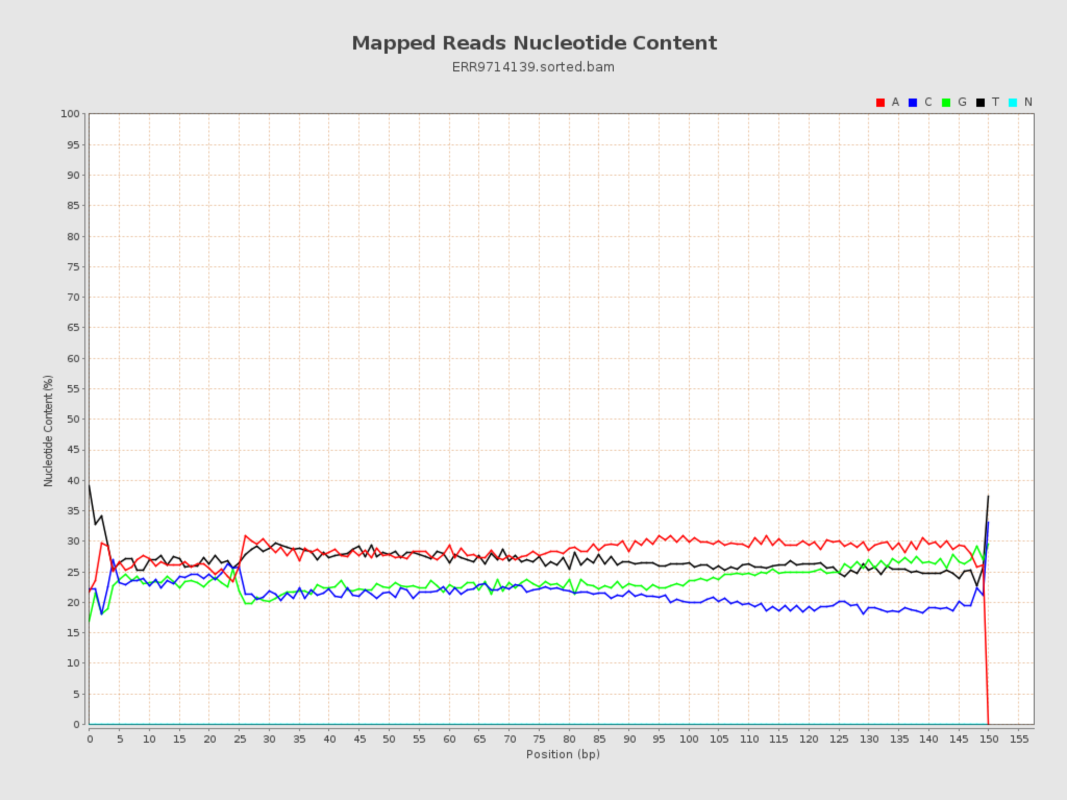
6. Results : Genome Fraction Coverage



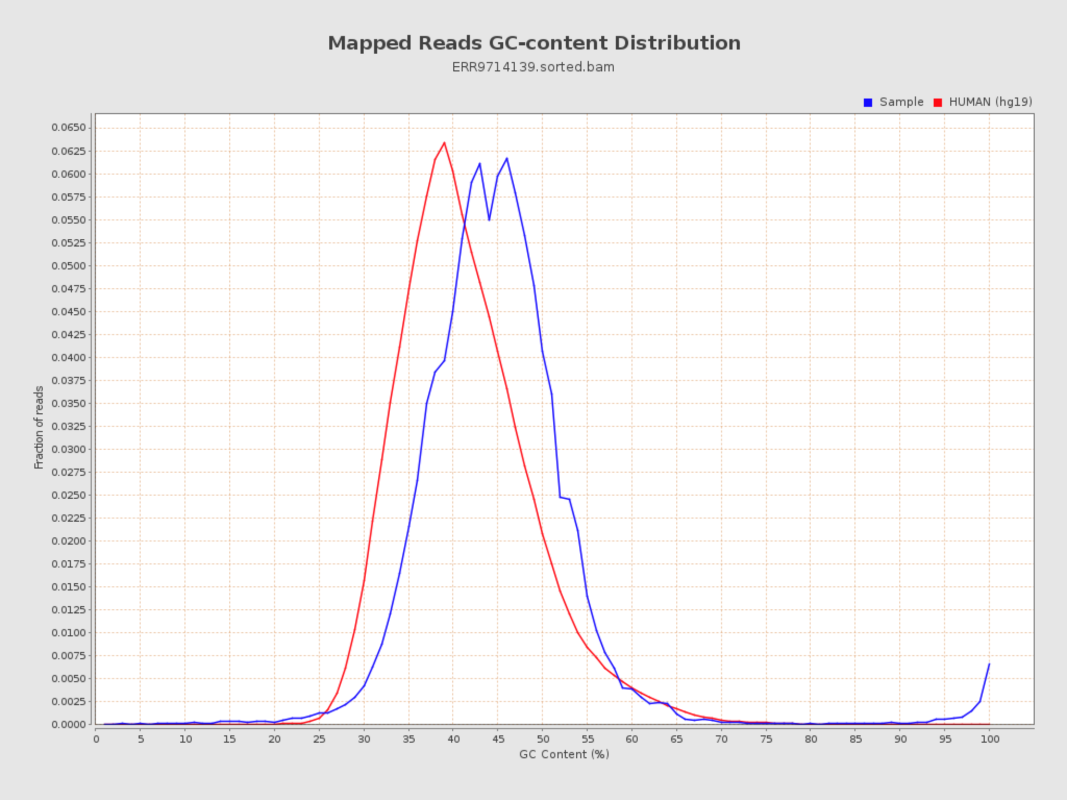
7. Results : Duplication Rate Histogram



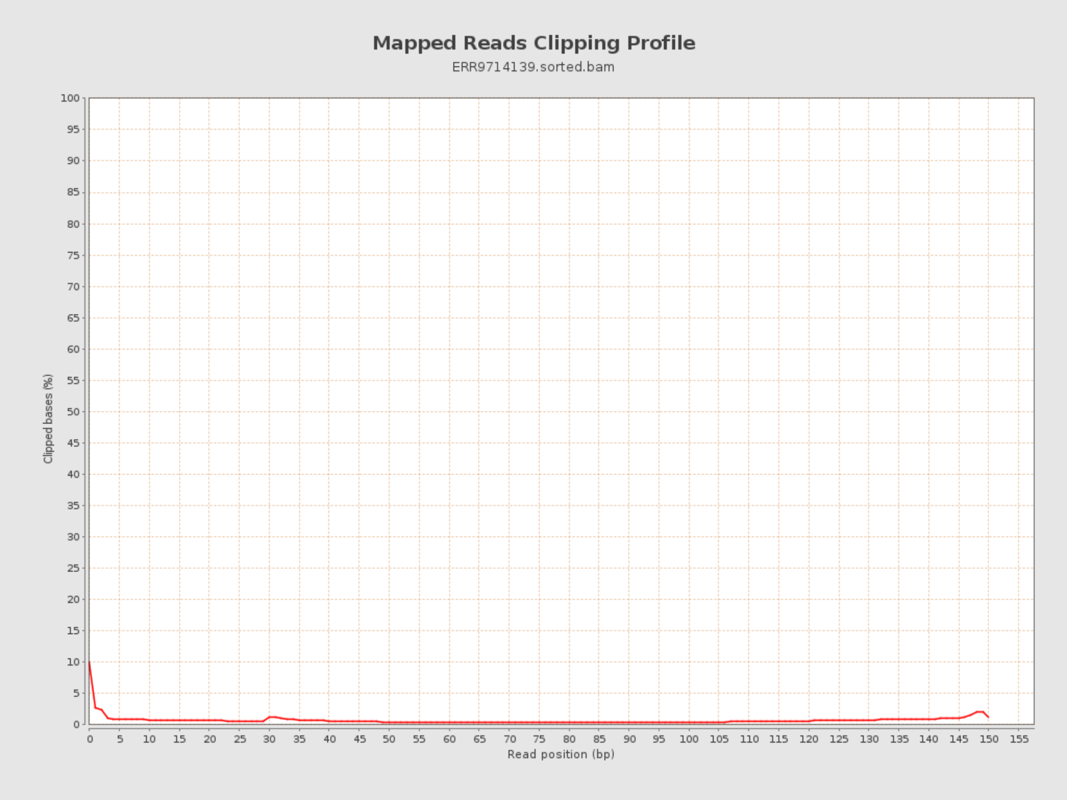
8. Results : Mapped Reads Nucleotide Content



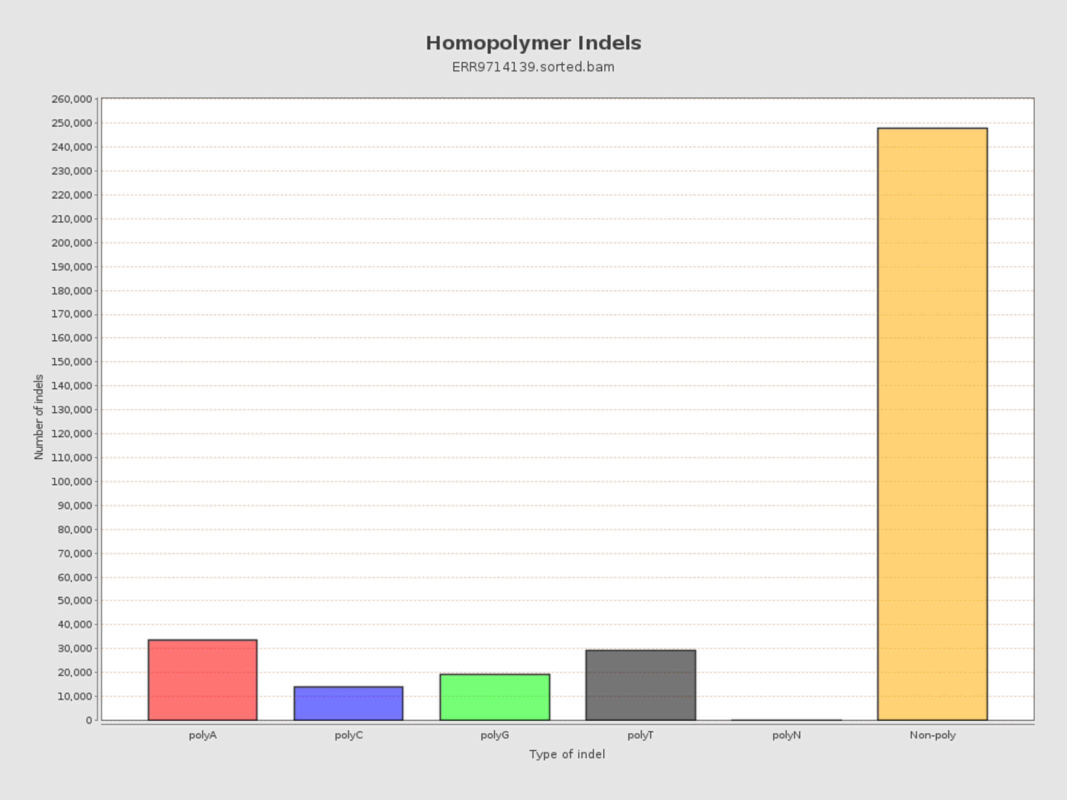
9. Results : Mapped Reads GC-content Distribution



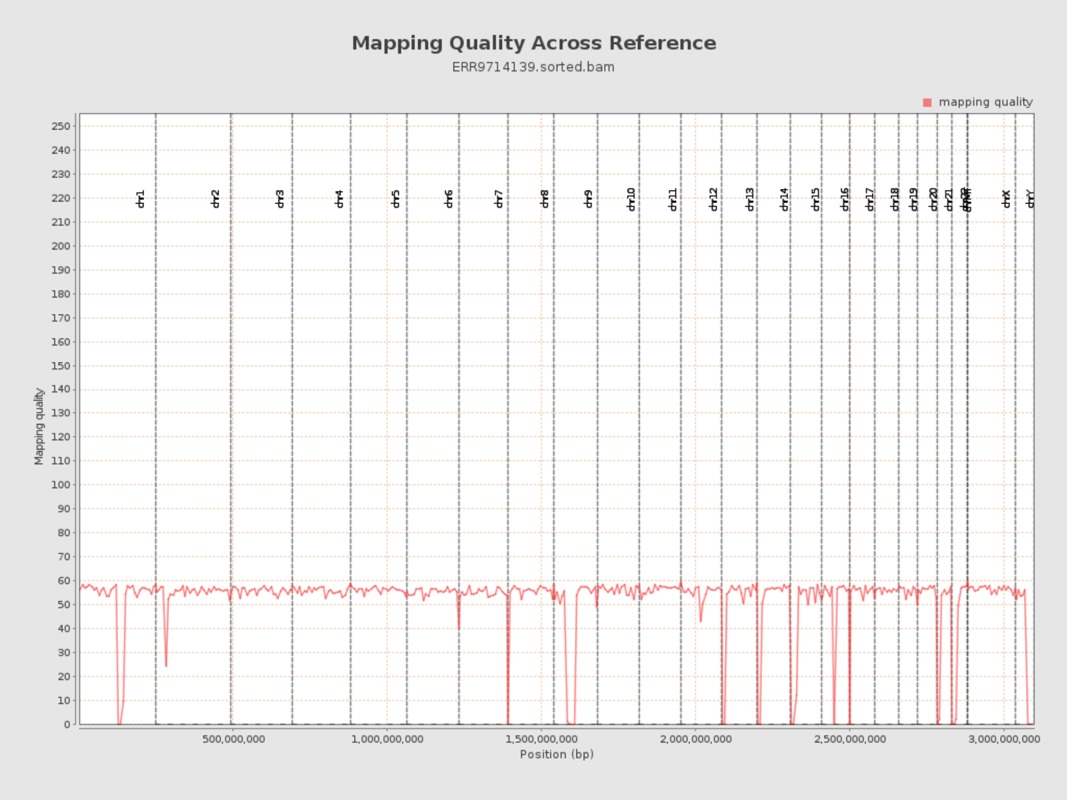
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram