Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:29:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714145.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_ERR9714145 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:29:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	38,806
Mapped reads	7,453 / 19.21%
Unmapped reads	31,353 / 80.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	220 / 0.57%
Read min/max/mean length	30 / 151 / 71.4
Duplicated reads (estimated)	4,802 / 12.37%
Duplication rate	37.37%
Clipped reads	6,476 / 16.69%

2.2. ACGT Content

Number/percentage of A's	189,711 / 23.03%
Number/percentage of C's	137,215 / 16.66%
Number/percentage of T's	179,817 / 21.83%
Number/percentage of G's	316,911 / 38.48%
Number/percentage of N's	20 / 0%
GC Percentage	55.13%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.2305

2.4. Mapping Quality

Mean Mapping Quality	37.35

2.5. Mismatches and indels

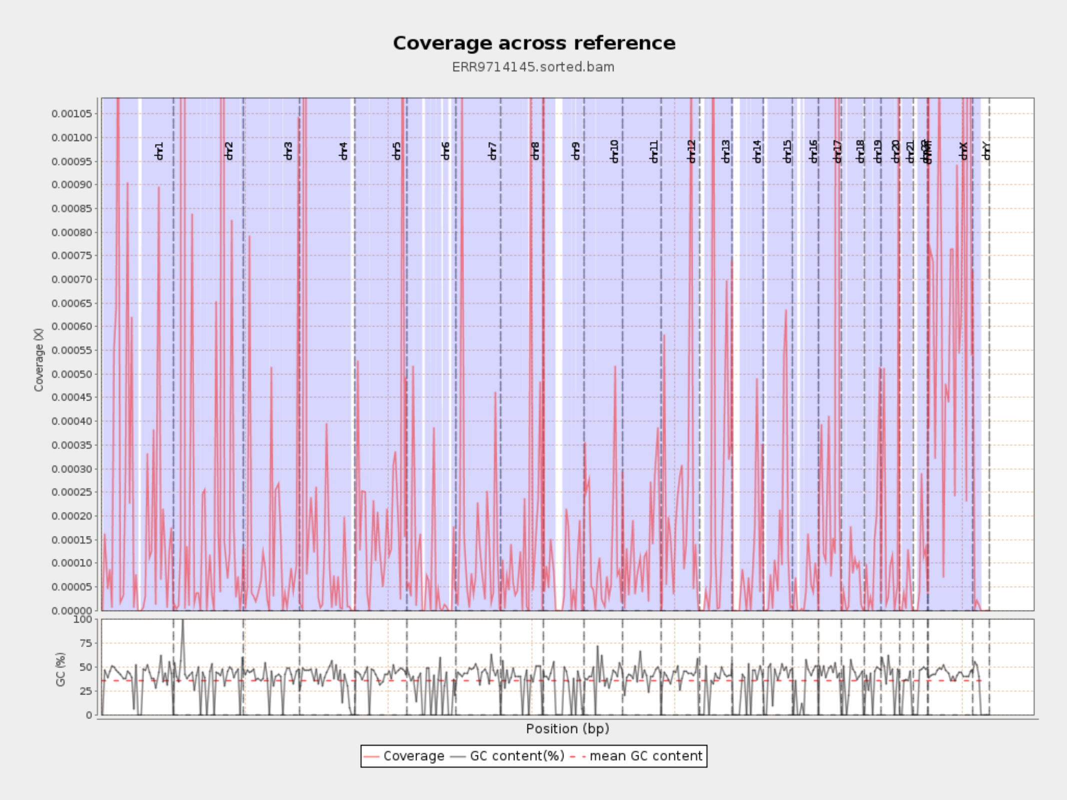
General error rate	4.17%
Mismatches	29,061
Insertions	1,157
Mapped reads with at least one insertion	14.21%
Deletions	2,252
Mapped reads with at least one deletion	28.07%
Homopolymer indels	37.61%

2.6. Chromosome stats

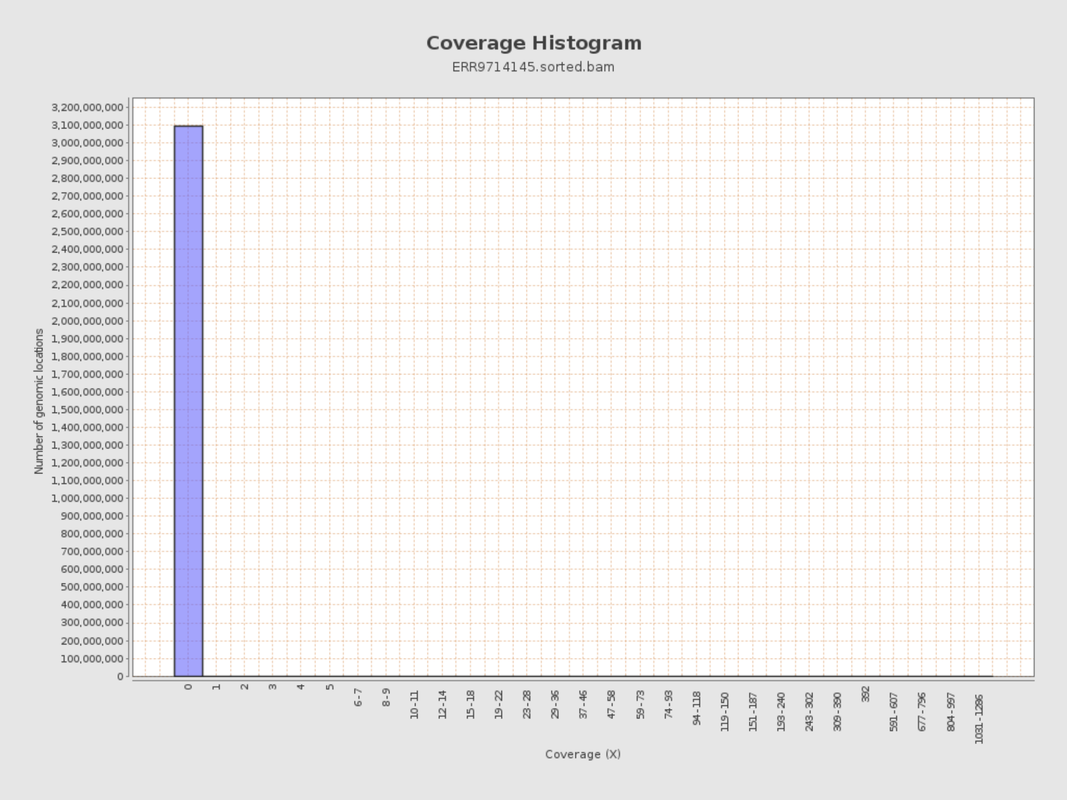
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	59079	0.0002	0.06
chr2	243199373	237895	0.001	0.7674
chr3	198022430	30234	0.0002	0.0552
chr4	191154276	34305	0.0002	0.1057
chr5	180915260	40457	0.0002	0.0569
chr6	171115067	13352	0.0001	0.0286
chr7	159138663	25064	0.0002	0.0528

chr8	146364022	22385	0.0002	0.0493
chr9	141213431	10647	0.0001	0.0202
chr10	135534747	17322	0.0001	0.0304
chr11	135006516	18013	0.0001	0.0267
chr12	133851895	30551	0.0002	0.0582
chr13	115169878	28454	0.0002	0.0849
chr14	107349540	10483	0.0001	0.0306
chr15	102531392	14264	0.0001	0.0324
chr16	90354753	4046	0	0.0108
chr17	81195210	59924	0.0007	0.34
chr18	78077248	4781	0.0001	0.0139
chr19	59128983	7821	0.0001	0.0381
chr20	63025520	11915	0.0002	0.0604
chr21	48129895	1814	0	0.0086
chr22	51304566	4519	0.0001	0.0213
chrMT	16571	32230	1.945	13.9886
chrX	155270560	113801	0.0007	0.0866
chrY	59373566	4029	0.0001	0.0237

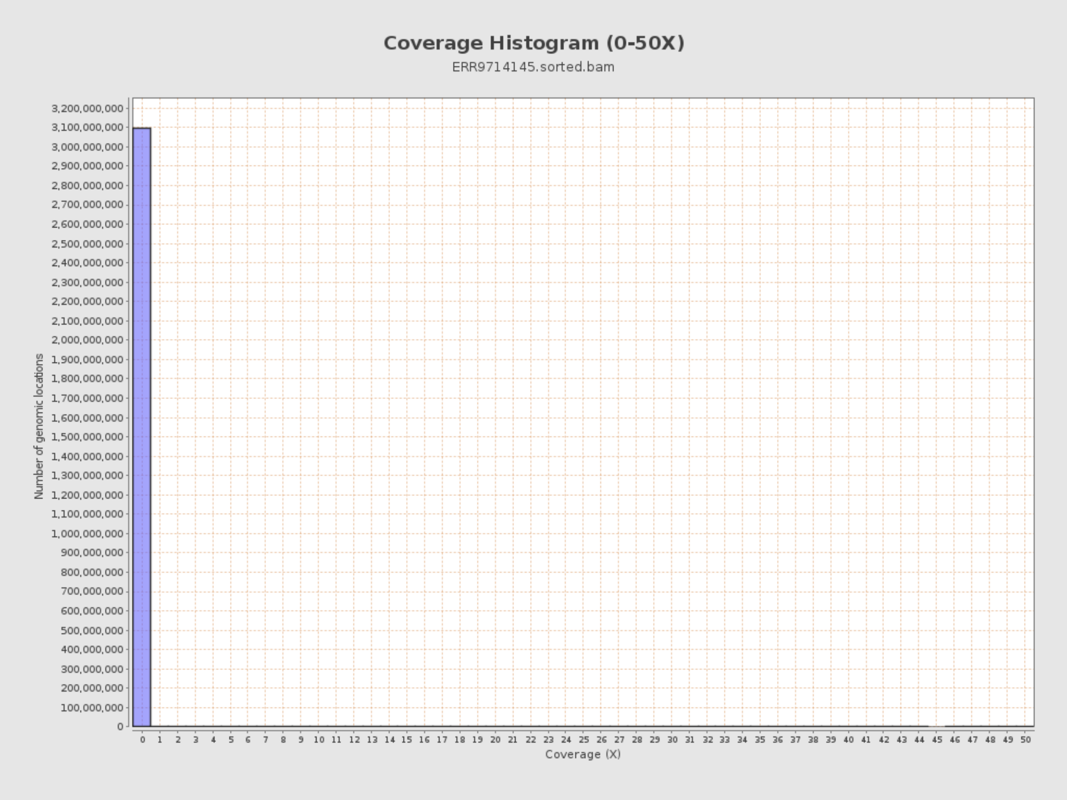
3. Results : Coverage across reference



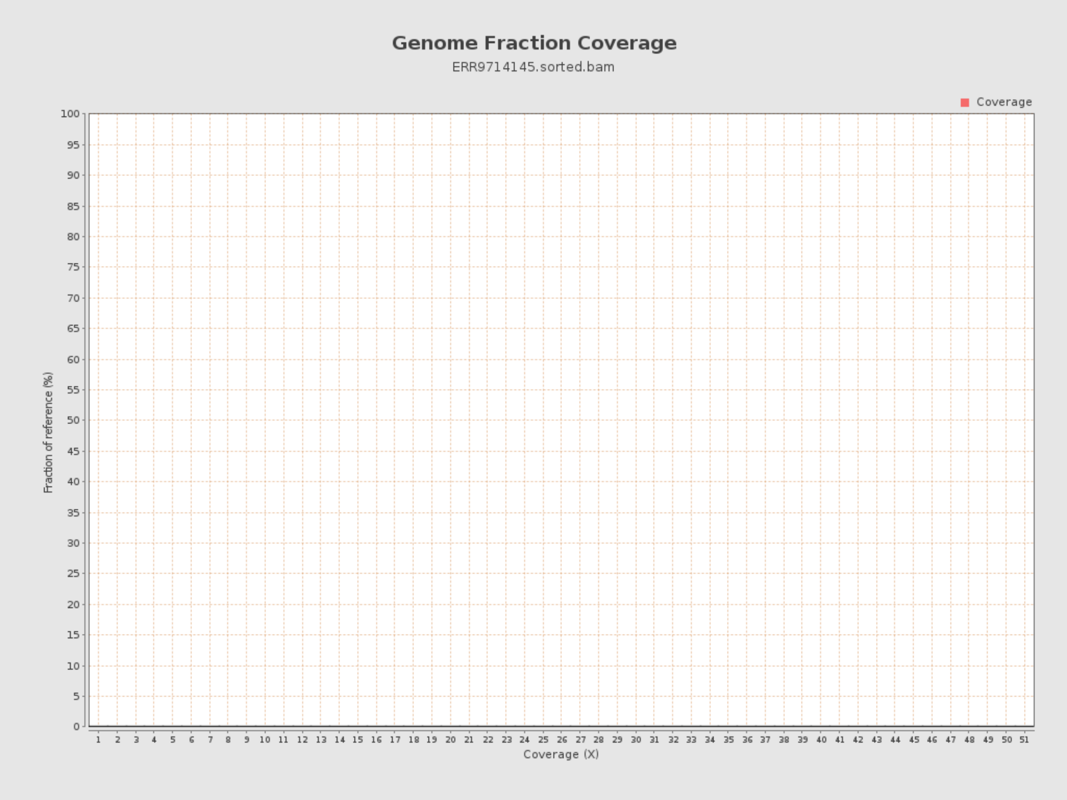
4. Results : Coverage Histogram



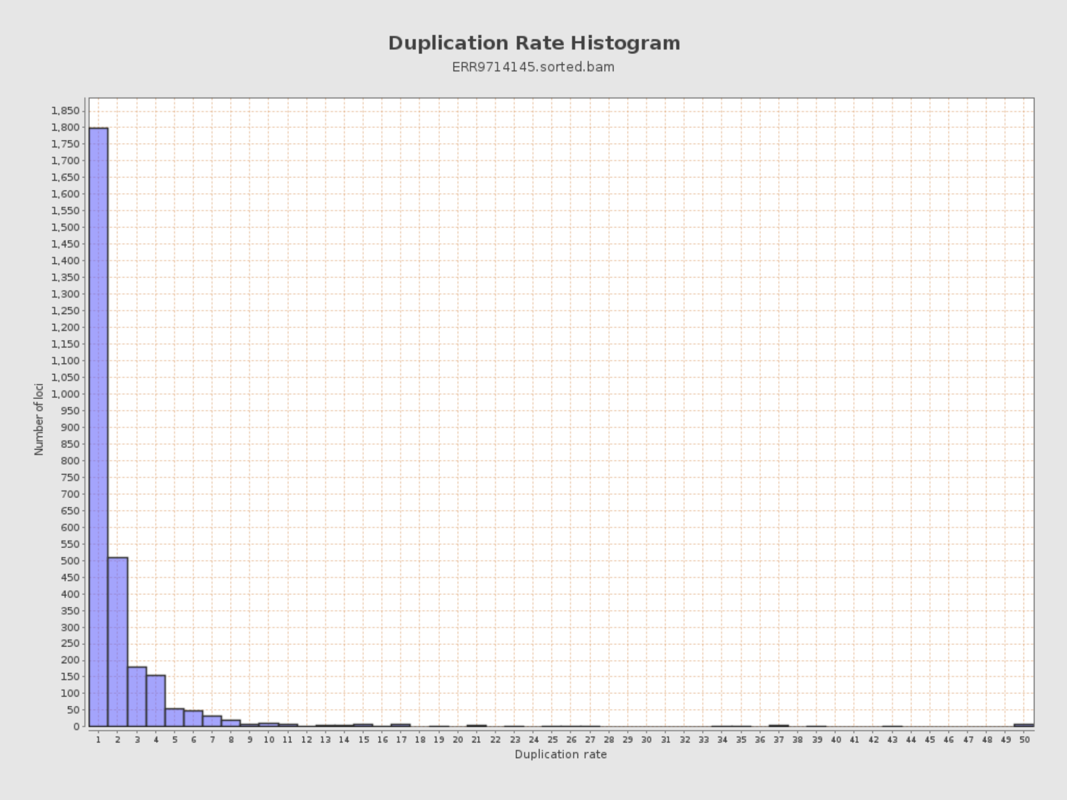
5. Results : Coverage Histogram (0-50X)



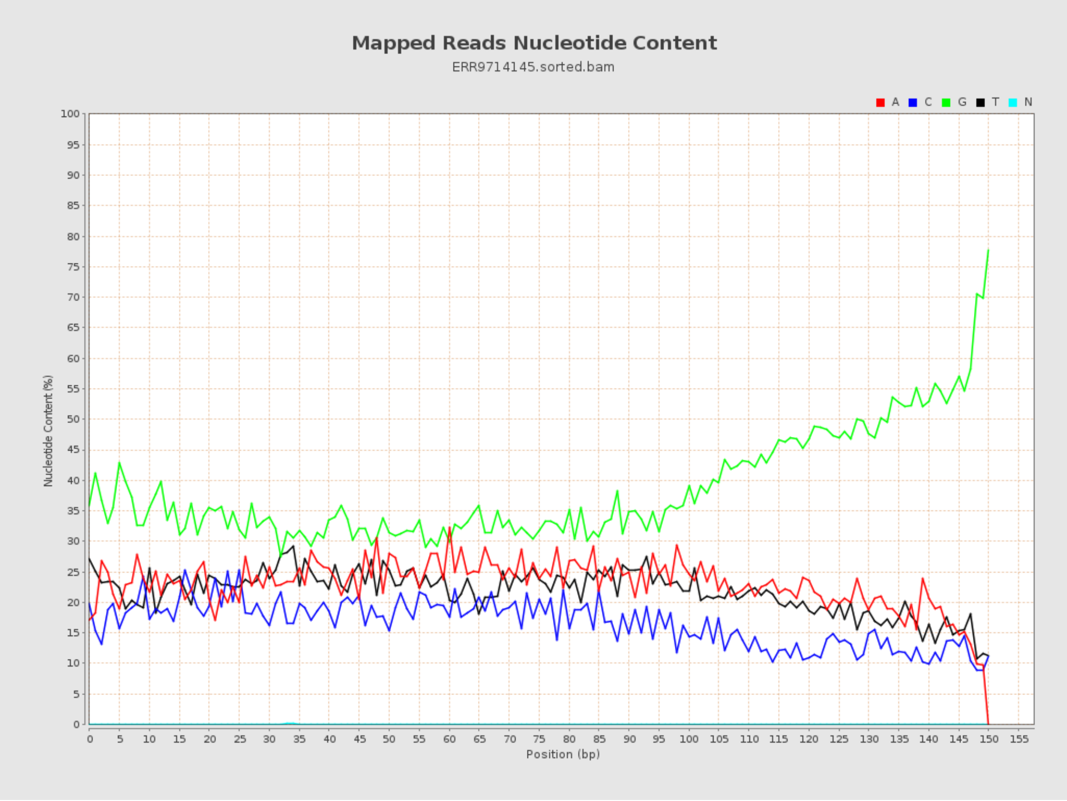
6. Results : Genome Fraction Coverage



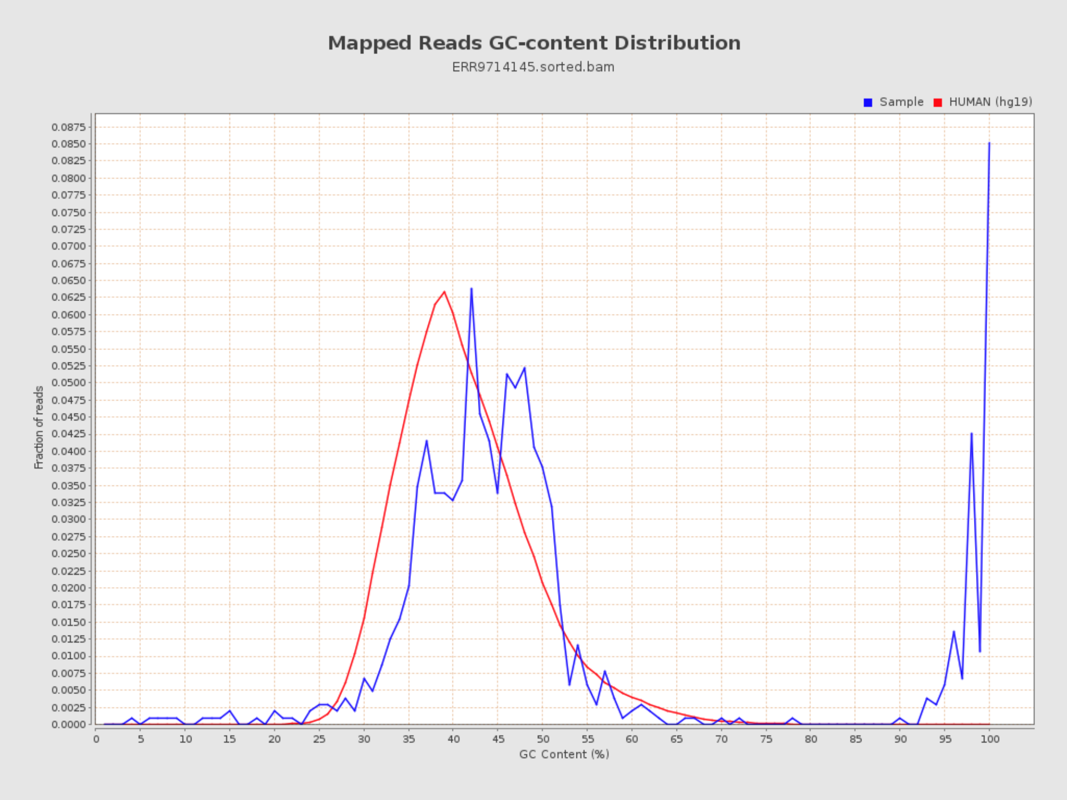
7. Results : Duplication Rate Histogram



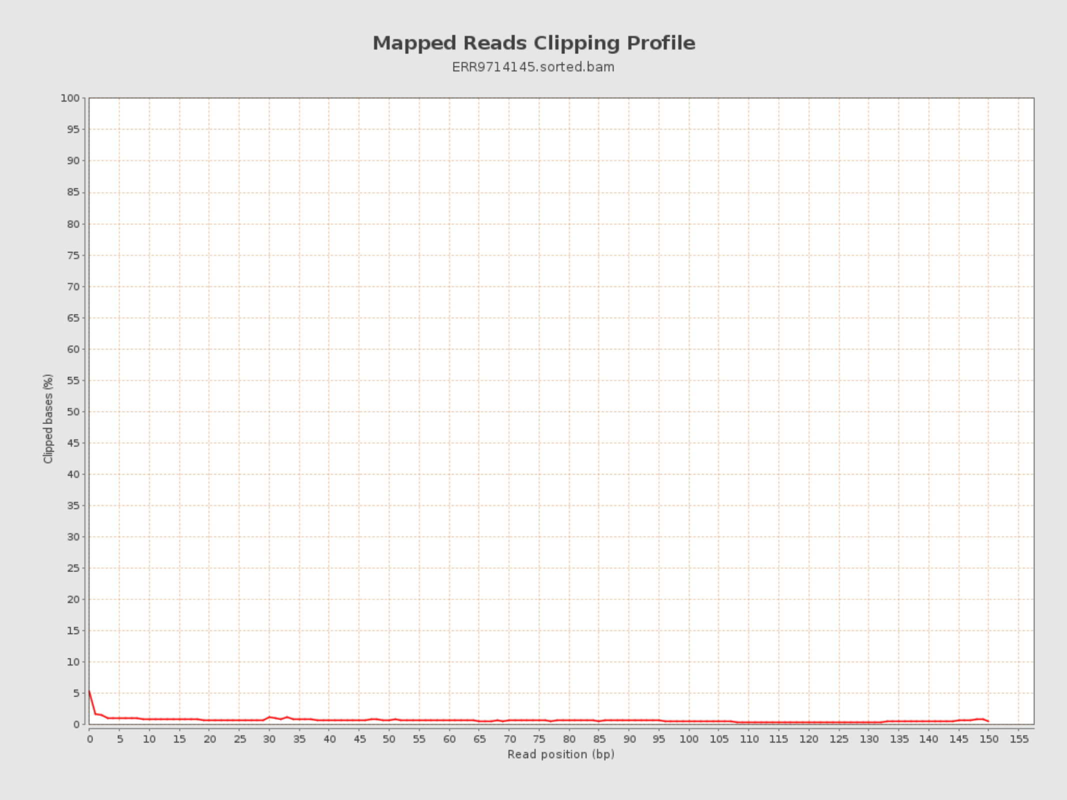
8. Results : Mapped Reads Nucleotide Content



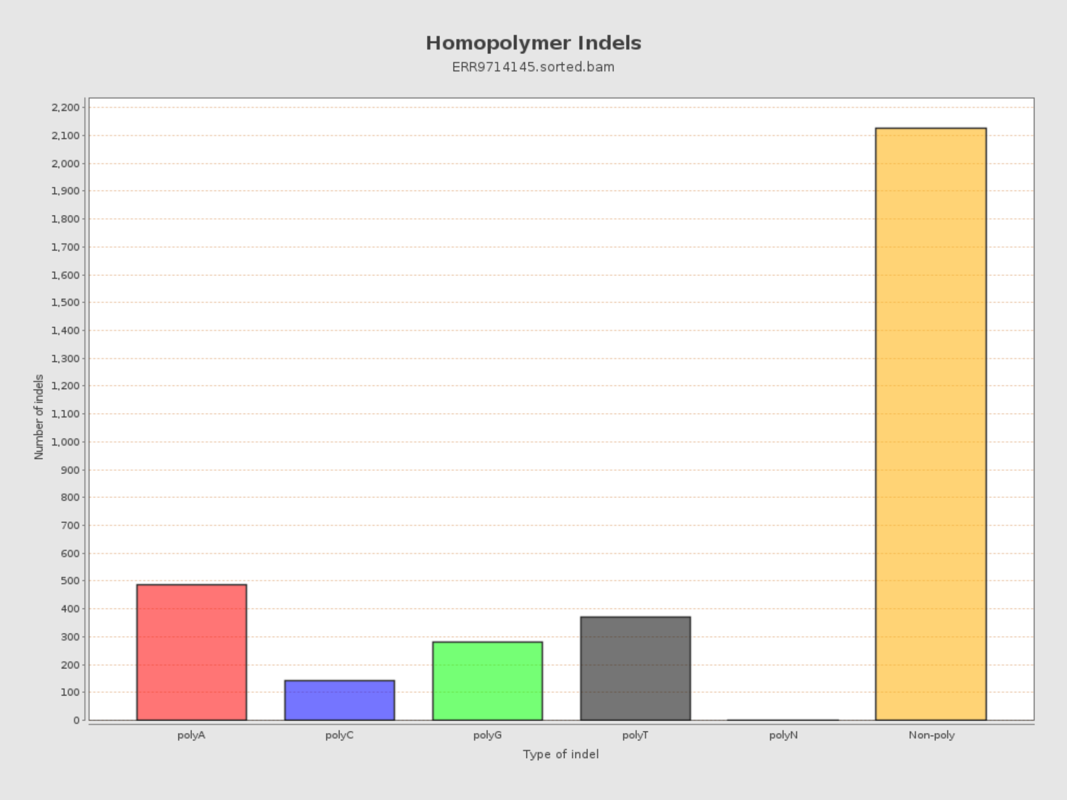
9. Results : Mapped Reads GC-content Distribution



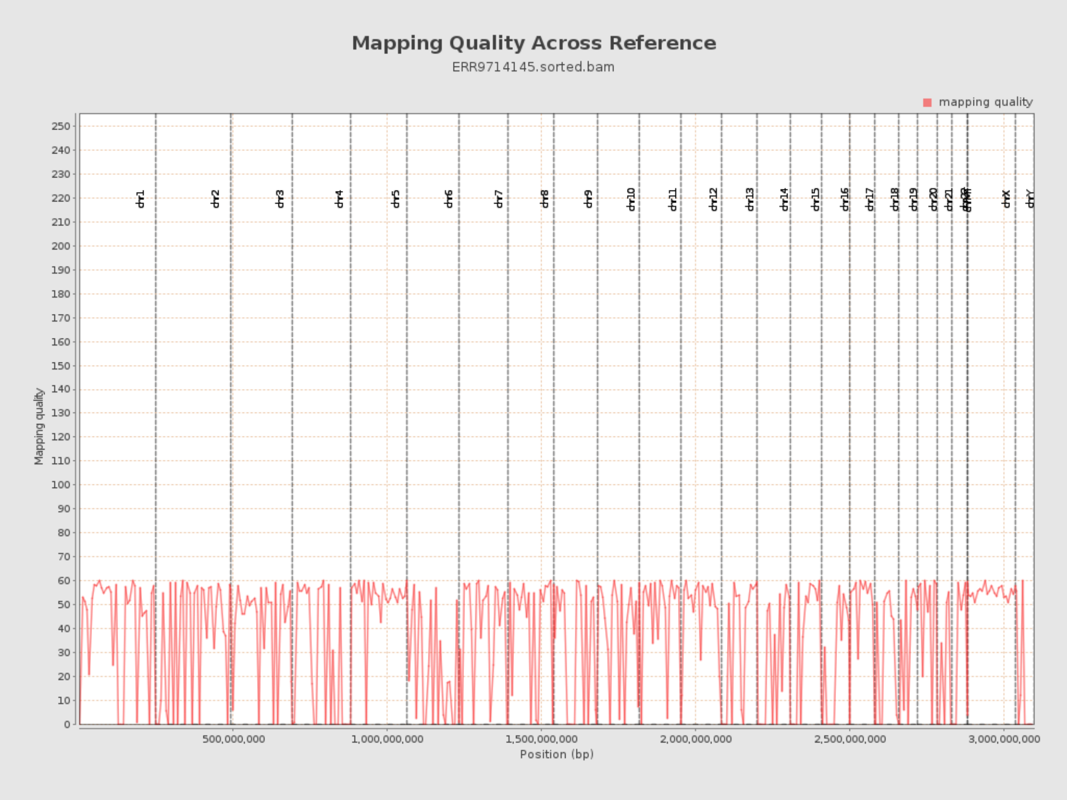
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram