Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:58:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714197.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_ERR9714197 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714197.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:58:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	93,824
Mapped reads	23,827 / 25.4%
Unmapped reads	69,997 / 74.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	953 / 1.02%
Read min/max/mean length	30 / 151 / 80.88
Duplicated reads (estimated)	20,290 / 21.63%
Duplication rate	50%
Clipped reads	19,289 / 20.56%

2.2. ACGT Content

Number/percentage of A's	559,473 / 21.19%
Number/percentage of C's	482,269 / 18.27%
Number/percentage of T's	524,493 / 19.87%
Number/percentage of G's	1,073,781 / 40.67%
Number/percentage of N's	36 / 0%
GC Percentage	58.94%

2.3. Coverage

Mean	0.0009

Standard Deviation	0.7665

2.4. Mapping Quality

Mean Mapping Quality	34.01

2.5. Mismatches and indels

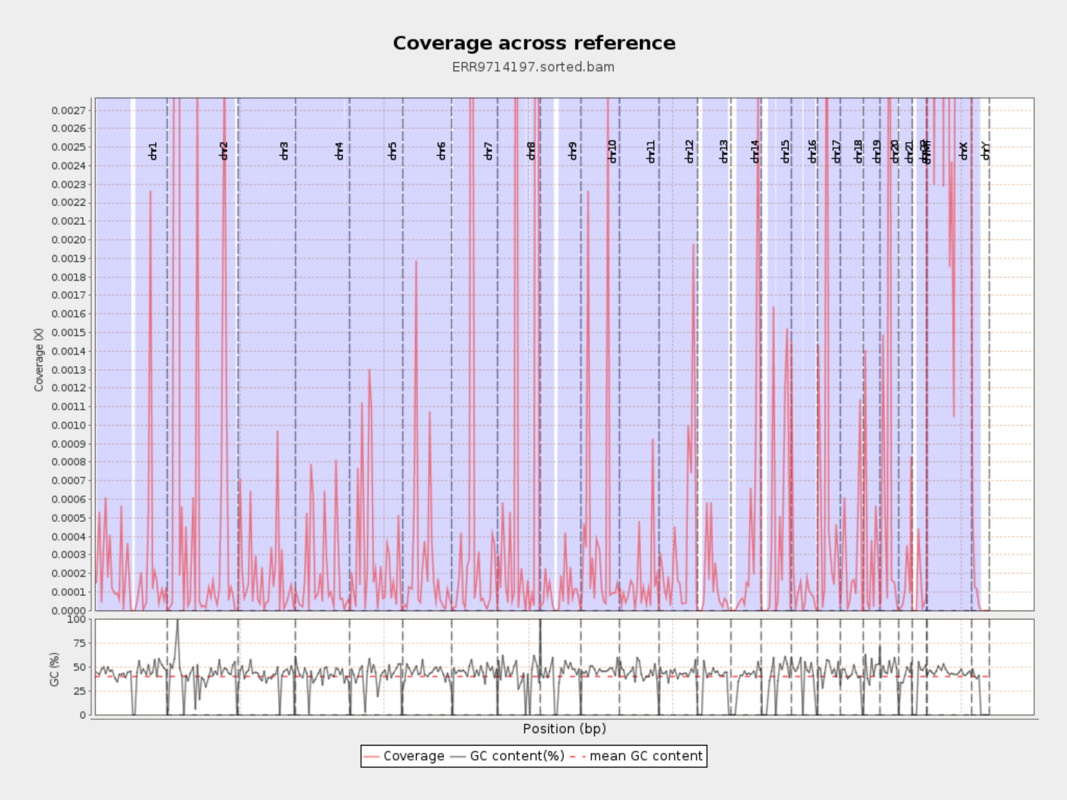
General error rate	3.59%
Mismatches	87,786
Insertions	1,493
Mapped reads with at least one insertion	5.02%
Deletions	5,731
Mapped reads with at least one deletion	23.01%
Homopolymer indels	32.81%

2.6. Chromosome stats

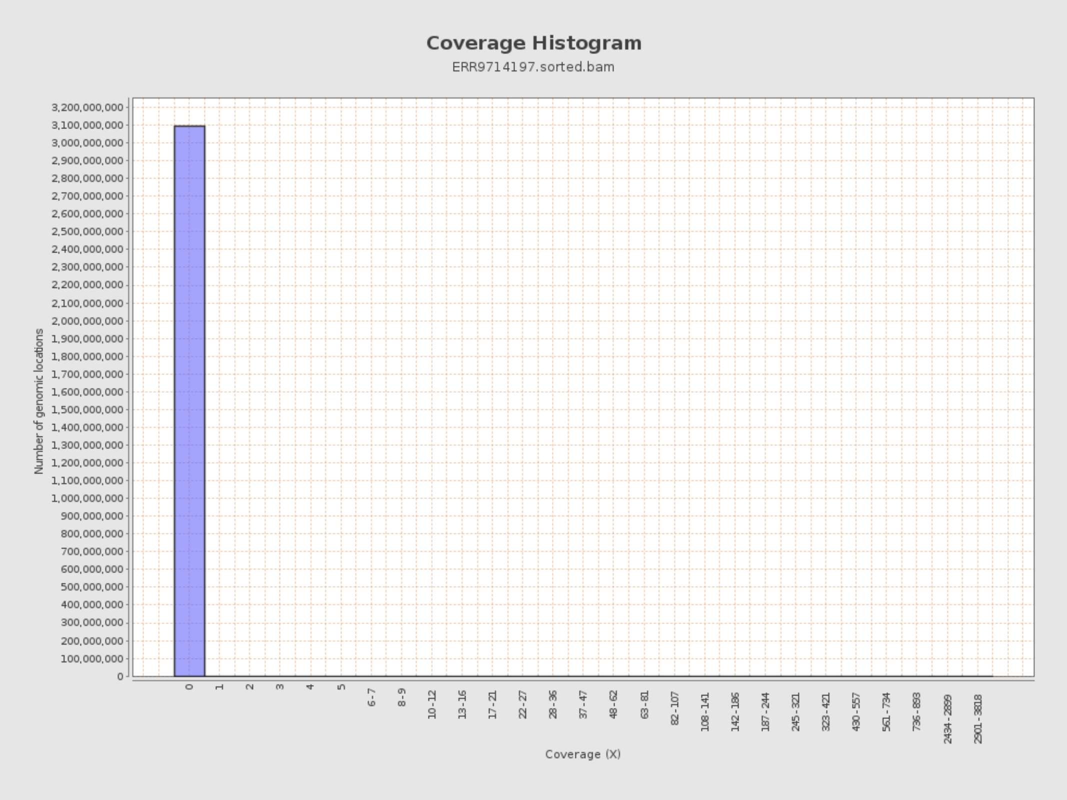
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60478	0.0002	0.2079
chr2	243199373	705556	0.0029	2.5694
chr3	198022430	38789	0.0002	0.0552
chr4	191154276	40879	0.0002	0.0638
chr5	180915260	56436	0.0003	0.0953
chr6	171115067	44242	0.0003	0.0757
chr7	159138663	70137	0.0004	0.3083

chr8	146364022	130274	0.0009	0.5159
chr9	141213431	14447	0.0001	0.028
chr10	135534747	60397	0.0004	0.3069
chr11	135006516	21479	0.0002	0.041
chr12	133851895	50237	0.0004	0.1021
chr13	115169878	15879	0.0001	0.0472
chr14	107349540	49799	0.0005	0.1635
chr15	102531392	46859	0.0005	0.1269
chr16	90354753	14342	0.0002	0.0578
chr17	81195210	60939	0.0008	0.1677
chr18	78077248	23758	0.0003	0.0681
chr19	59128983	20280	0.0003	0.1172
chr20	63025520	60089	0.001	0.3644
chr21	48129895	8723	0.0002	0.0431
chr22	51304566	5899	0.0001	0.0429
chrMT	16571	1555	0.0938	0.472
chrX	155270560	1081020	0.007	0.8522
chrY	59373566	4820	0.0001	0.0282

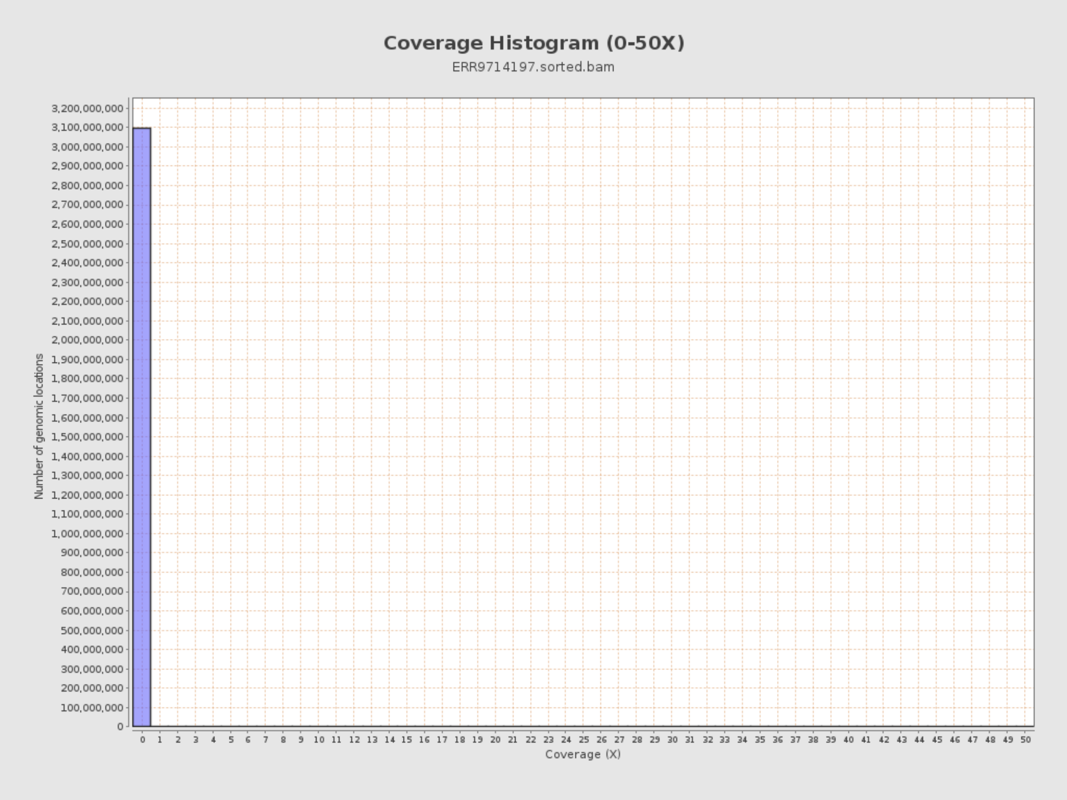
3. Results : Coverage across reference



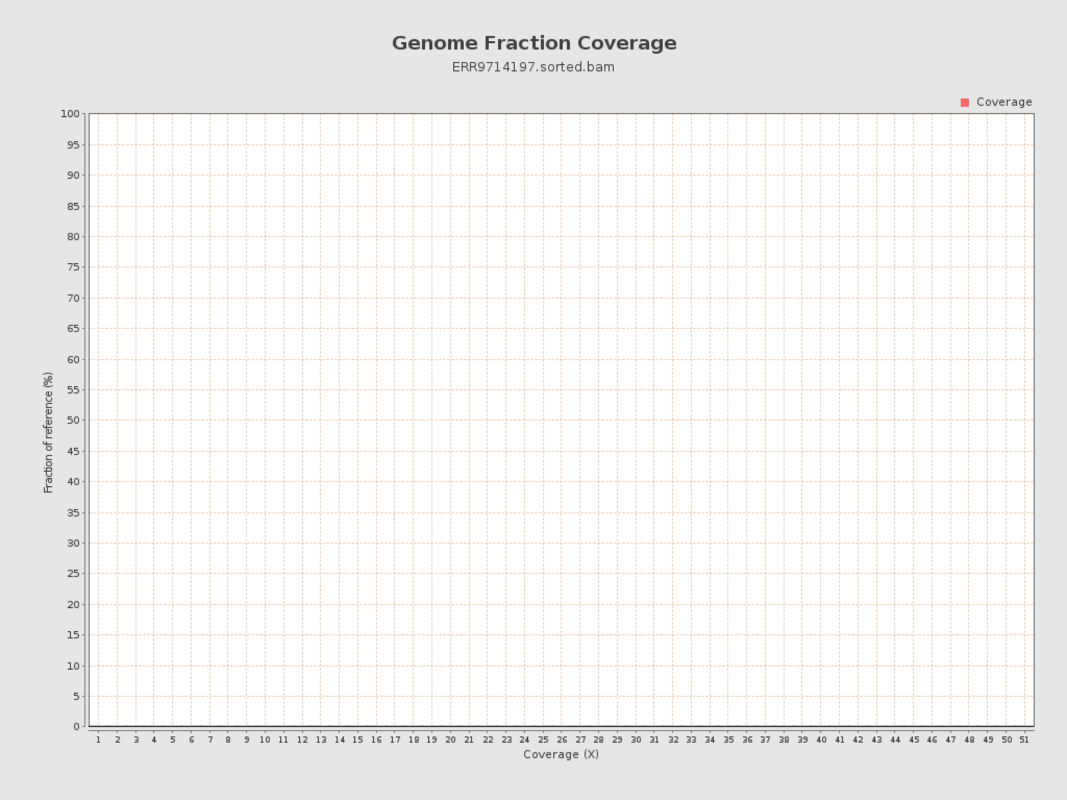
4. Results : Coverage Histogram



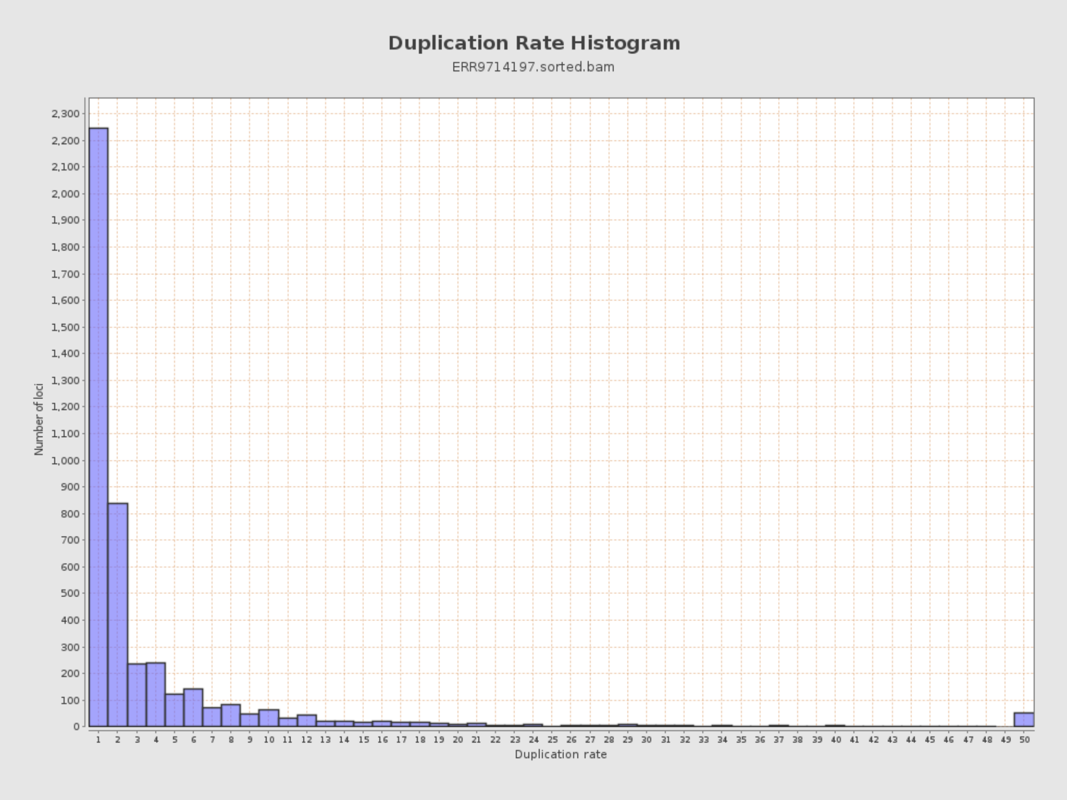
5. Results : Coverage Histogram (0-50X)



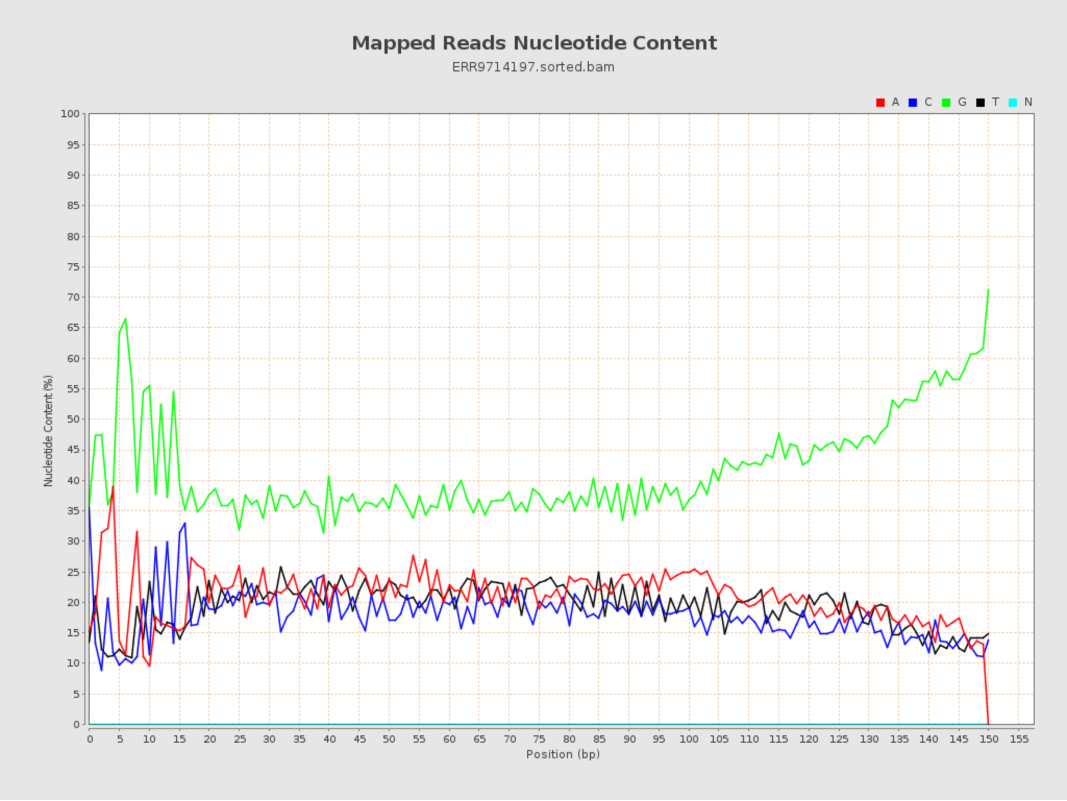
6. Results : Genome Fraction Coverage



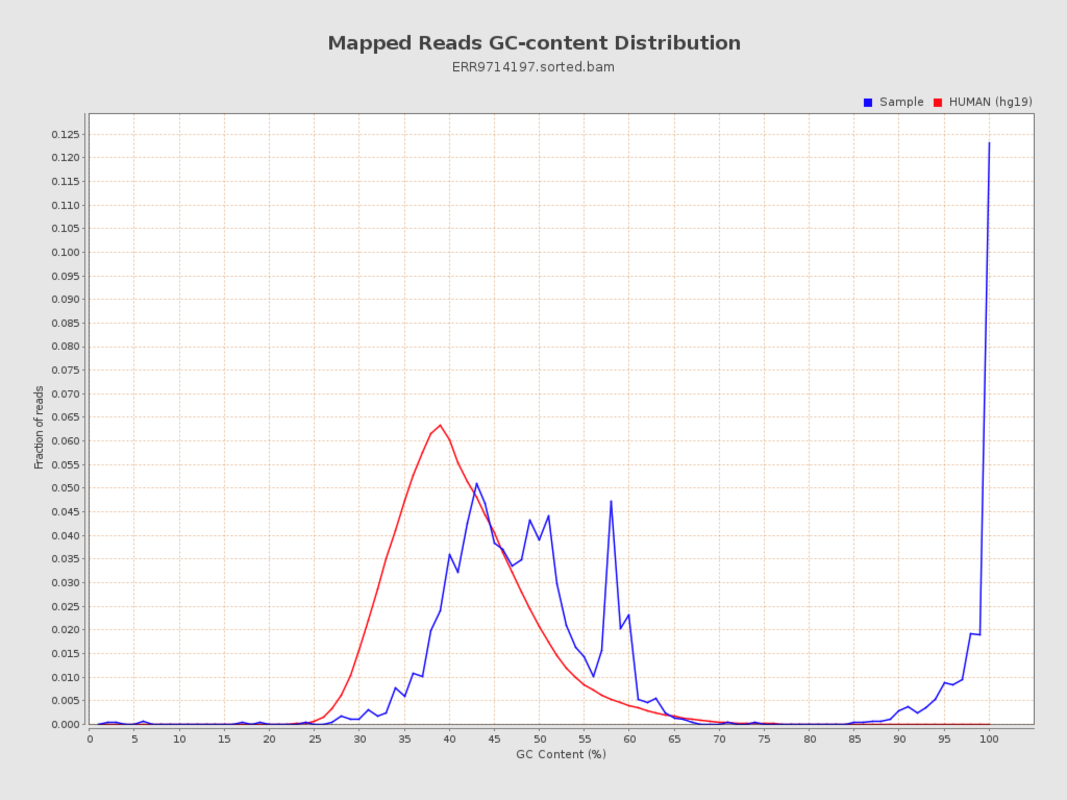
7. Results : Duplication Rate Histogram



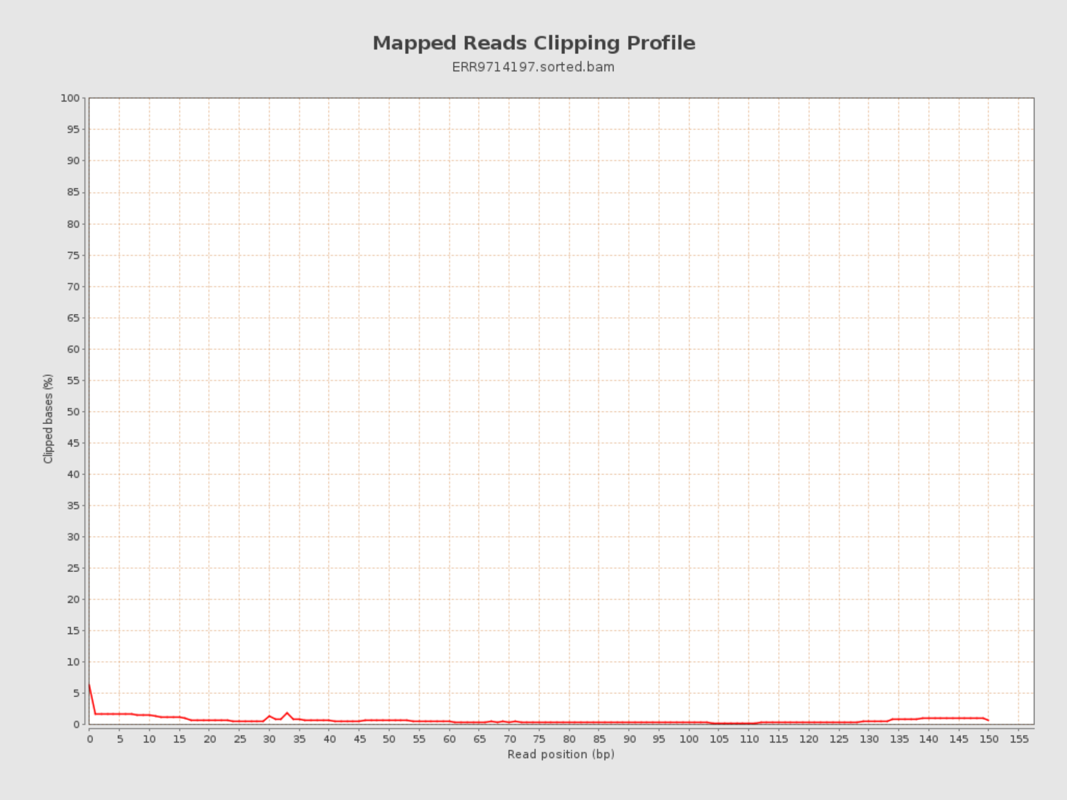
8. Results : Mapped Reads Nucleotide Content



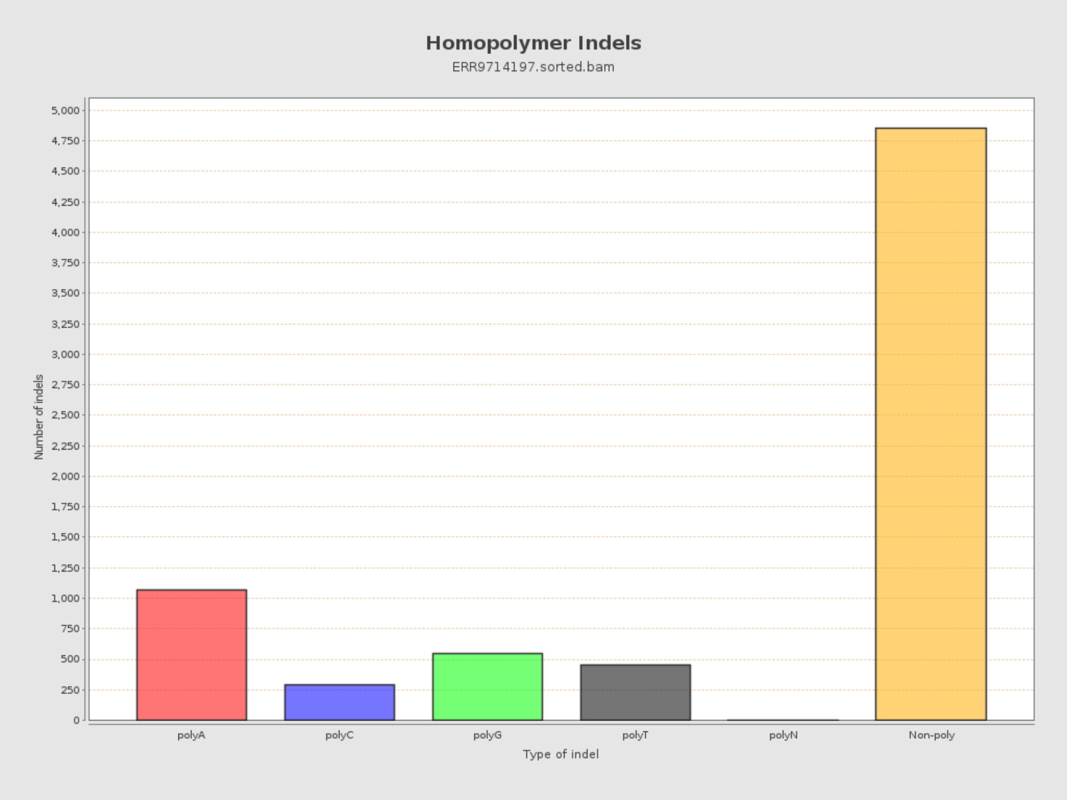
9. Results : Mapped Reads GC-content Distribution



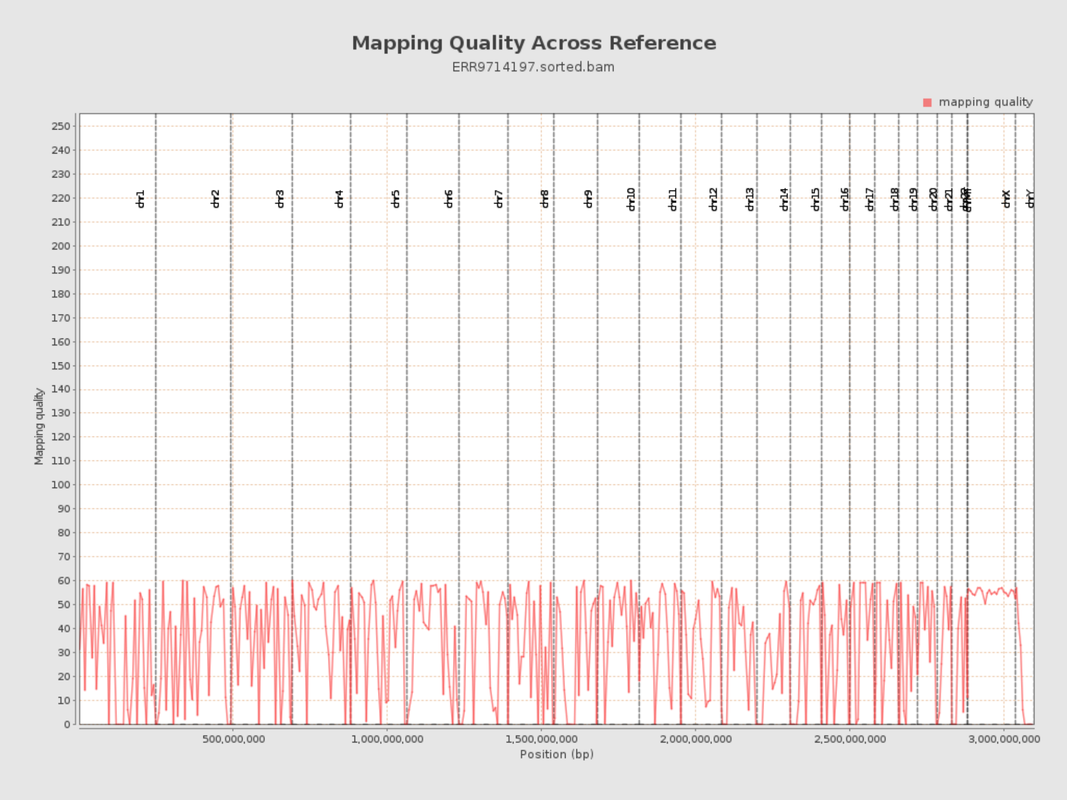
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram