Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:35:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714127.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_ERR9714127 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714127.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:35:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714127.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	651,458
Mapped reads	514,159 / 78.92%
Unmapped reads	137,299 / 21.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,897 / 2.29%
Read min/max/mean length	30 / 151 / 131.98
Duplicated reads (estimated)	449,067 / 68.93%
Duplication rate	44.59%
Clipped reads	473,459 / 72.68%

2.2. ACGT Content

Number/percentage of A's	18,285,677 / 27.69%
Number/percentage of C's	13,640,200 / 20.66%
Number/percentage of T's	17,419,771 / 26.38%
Number/percentage of G's	16,687,459 / 25.27%
Number/percentage of N's	548 / 0%
GC Percentage	45.93%

2.3. Coverage

Mean	0.0218

Standard Deviation	4.7331

2.4. Mapping Quality

Mean Mapping Quality	51.9

2.5. Mismatches and indels

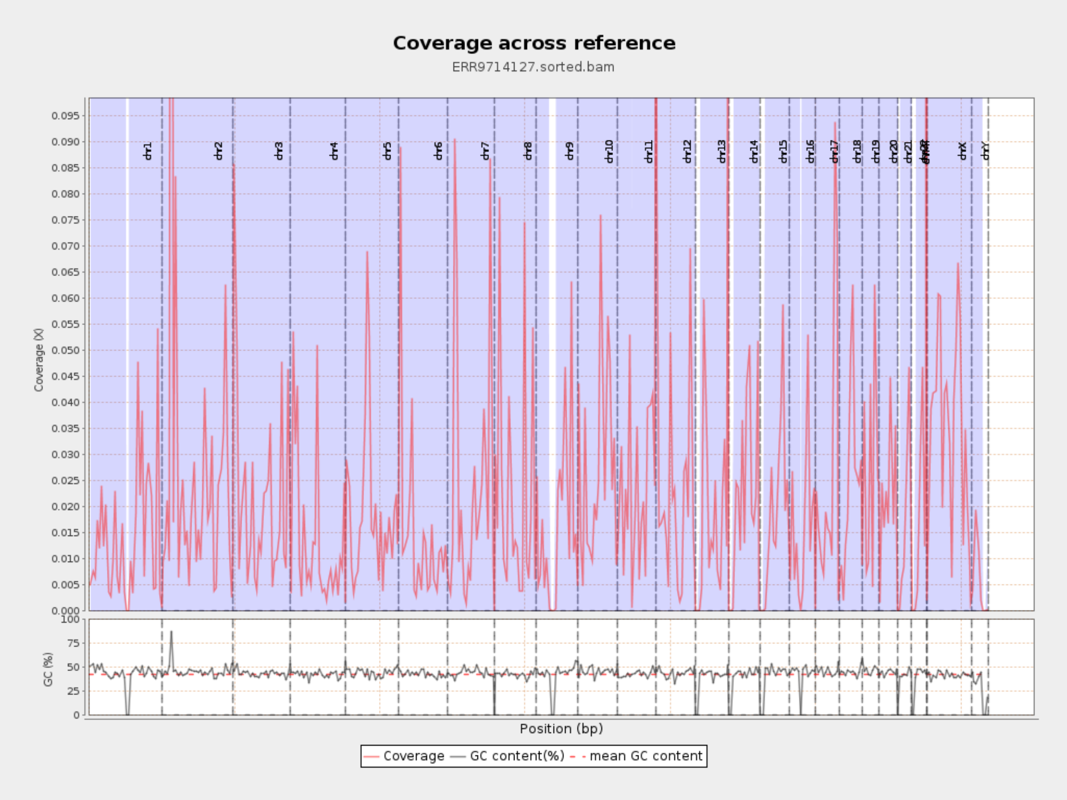
General error rate	4.61%
Mismatches	2,814,707
Insertions	79,504
Mapped reads with at least one insertion	14.85%
Deletions	251,712
Mapped reads with at least one deletion	45.3%
Homopolymer indels	29.81%

2.6. Chromosome stats

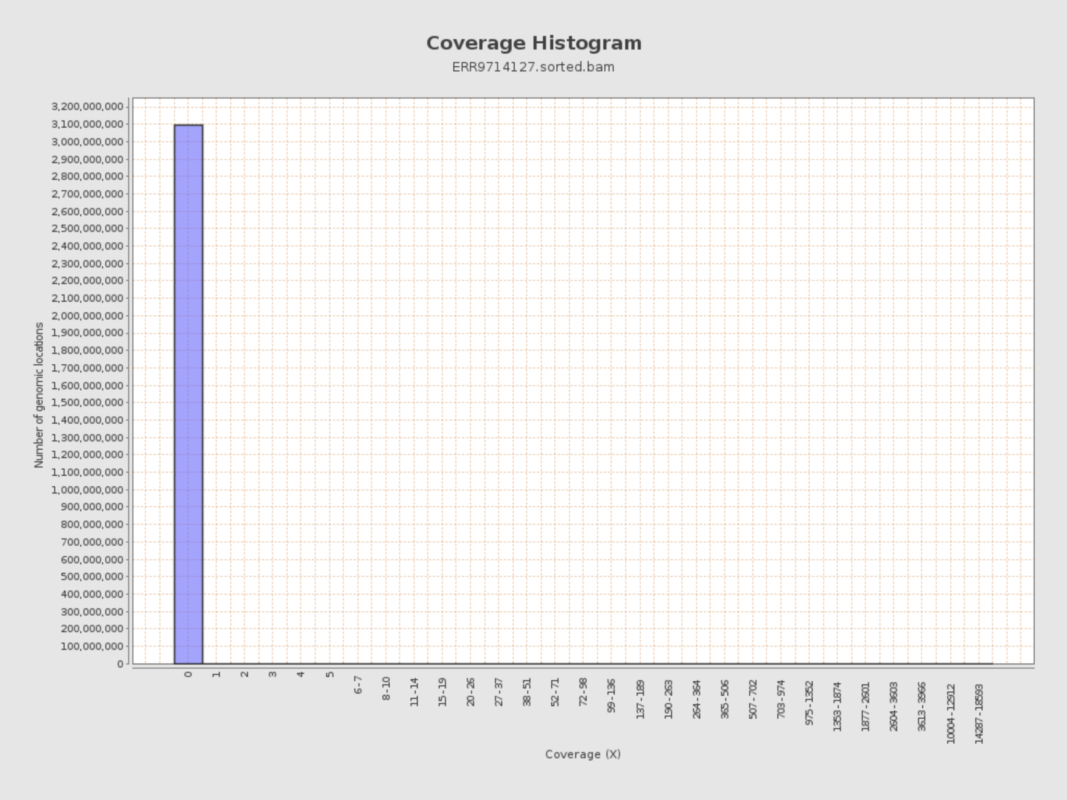
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3565994	0.0143	2.5745
chr2	243199373	8303879	0.0341	11.8935
chr3	198022430	4348585	0.022	3.7306
chr4	191154276	2655608	0.0139	2.6668
chr5	180915260	3468490	0.0192	3.9453
chr6	171115067	2557911	0.0149	2.6532
chr7	159138663	3897451	0.0245	5.3068

chr8	146364022	3449179	0.0236	3.7435
chr9	141213431	2241957	0.0159	2.5626
chr10	135534747	3885848	0.0287	4.5067
chr11	135006516	3190321	0.0236	3.3456
chr12	133851895	3180962	0.0238	3.7396
chr13	115169878	2056793	0.0179	2.7464
chr14	107349540	2416348	0.0225	3.5657
chr15	102531392	1935795	0.0189	2.2612
chr16	90354753	1488079	0.0165	2.027
chr17	81195210	2166605	0.0267	5.2755
chr18	78077248	1948679	0.025	3.7813
chr19	59128983	1567245	0.0265	4.2952
chr20	63025520	1430431	0.0227	3.1201
chr21	48129895	792166	0.0165	3.0944
chr22	51304566	799896	0.0156	2.6057
chrMT	16571	452727	27.3204	206.5757
chrX	155270560	5421431	0.0349	3.3537
chrY	59373566	342844	0.0058	1.1582

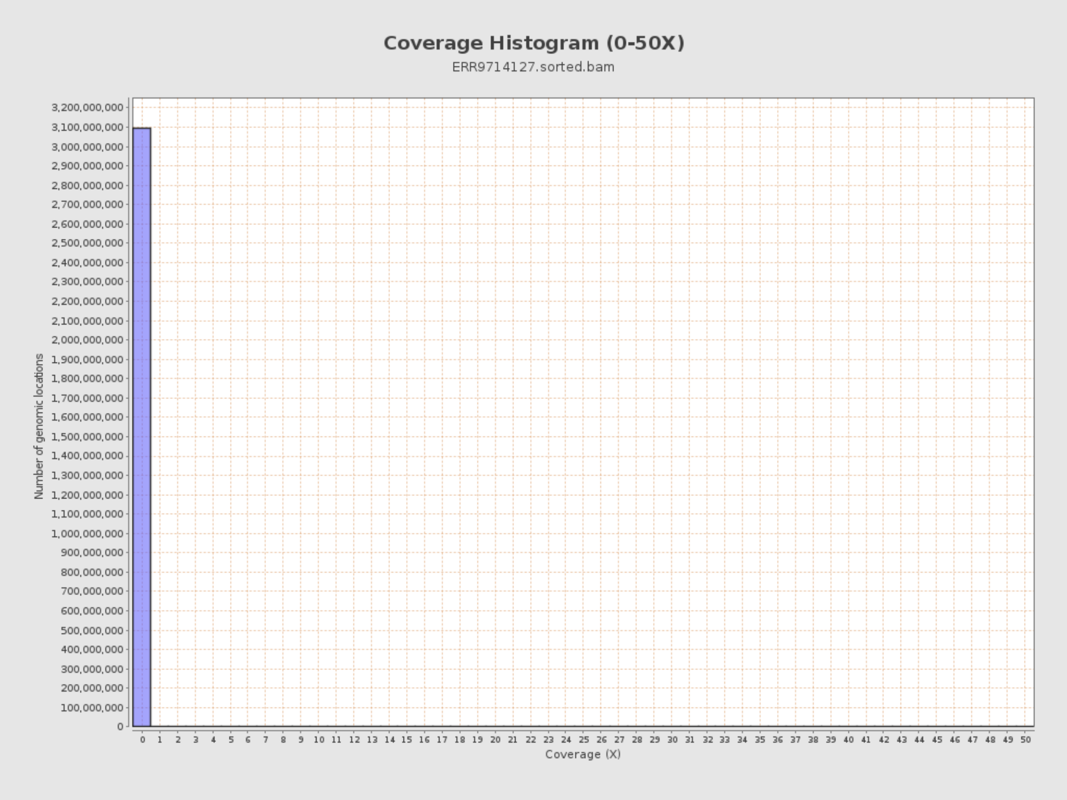
3. Results : Coverage across reference



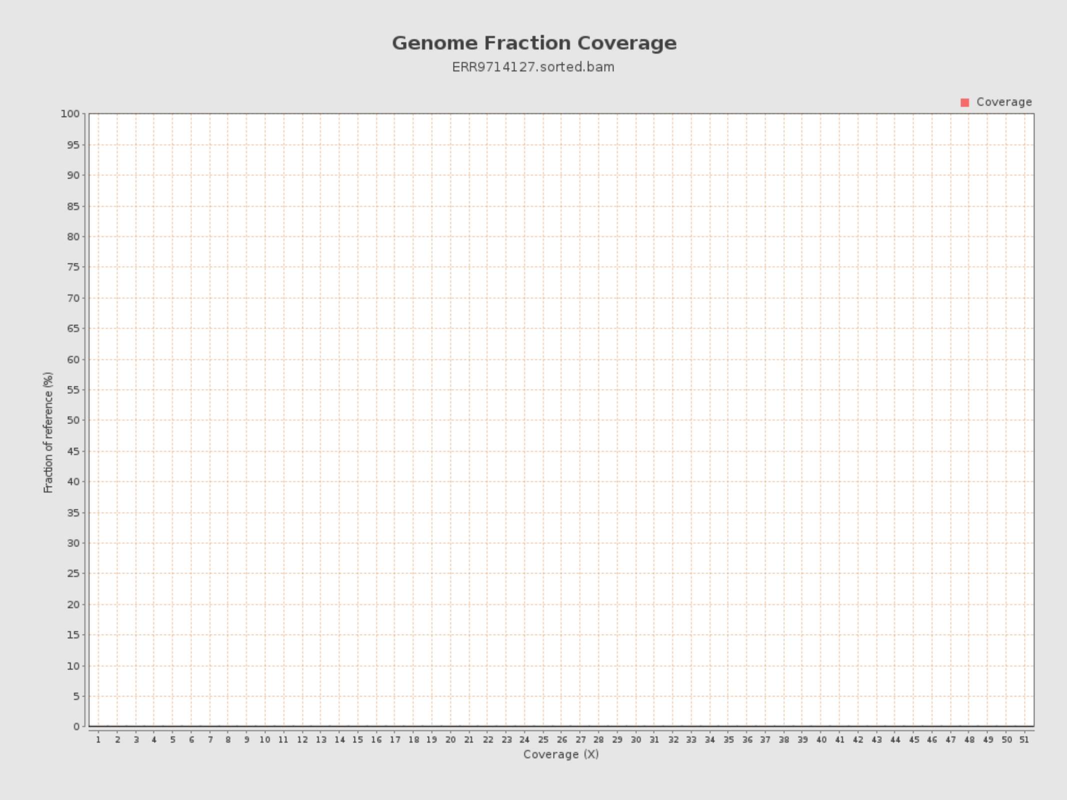
4. Results : Coverage Histogram



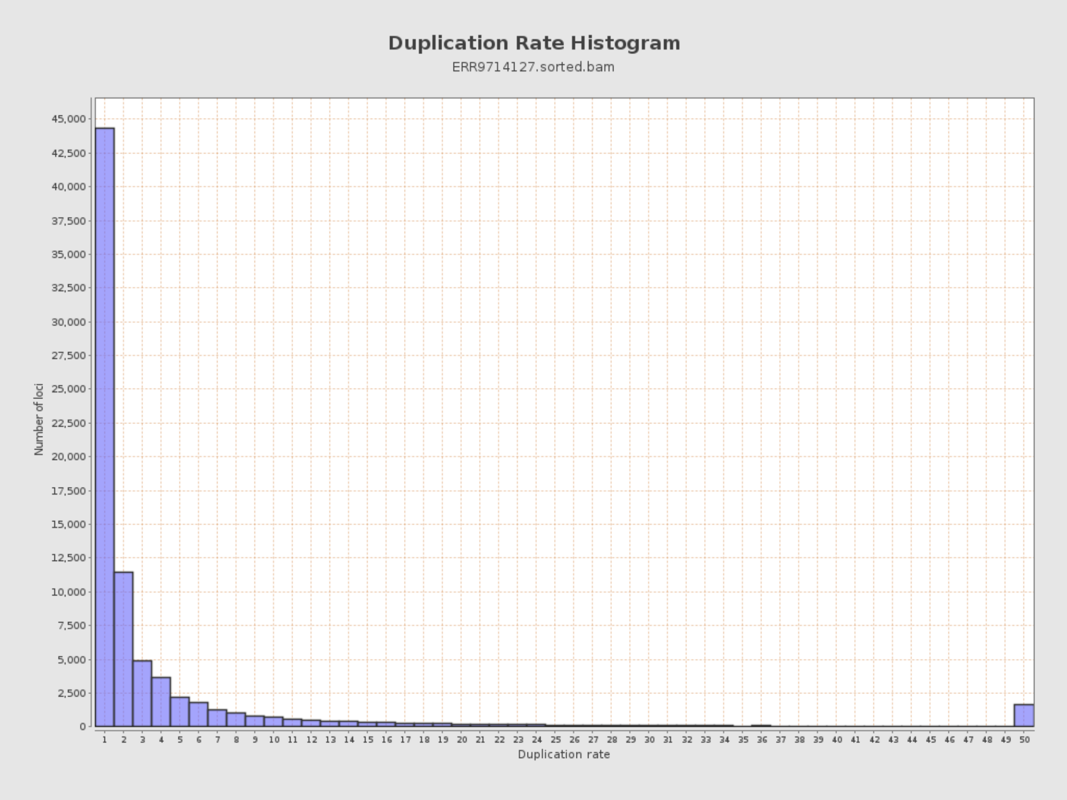
5. Results : Coverage Histogram (0-50X)



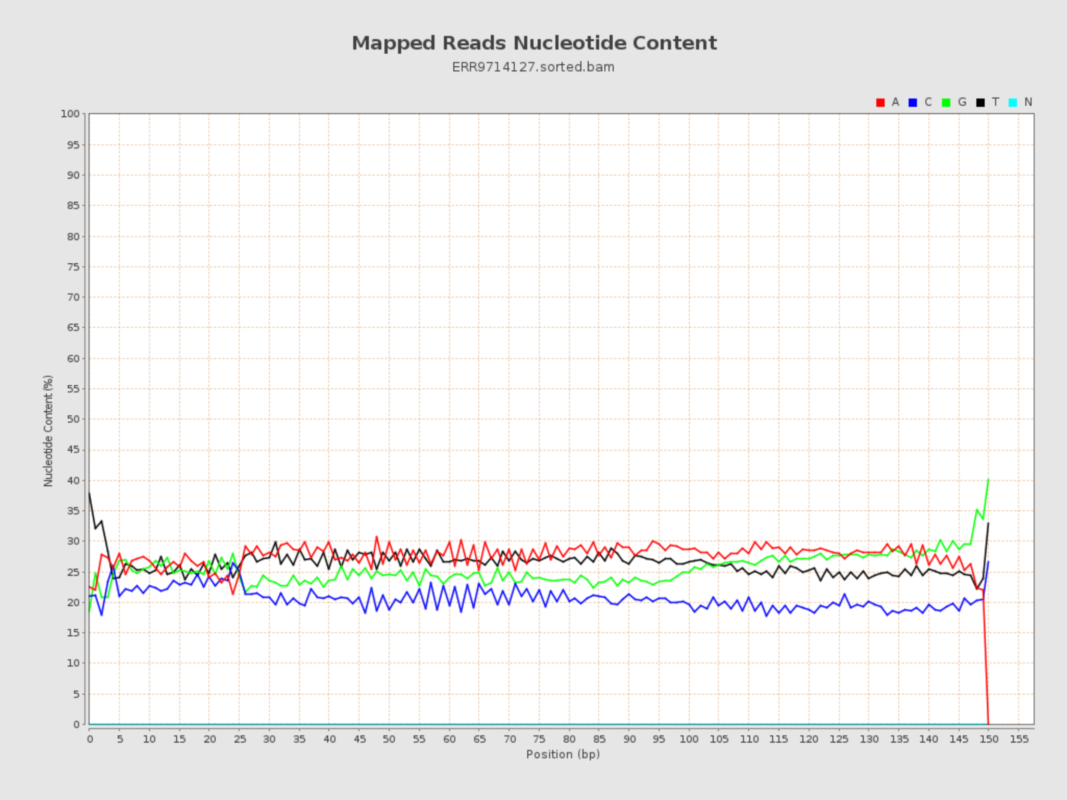
6. Results : Genome Fraction Coverage



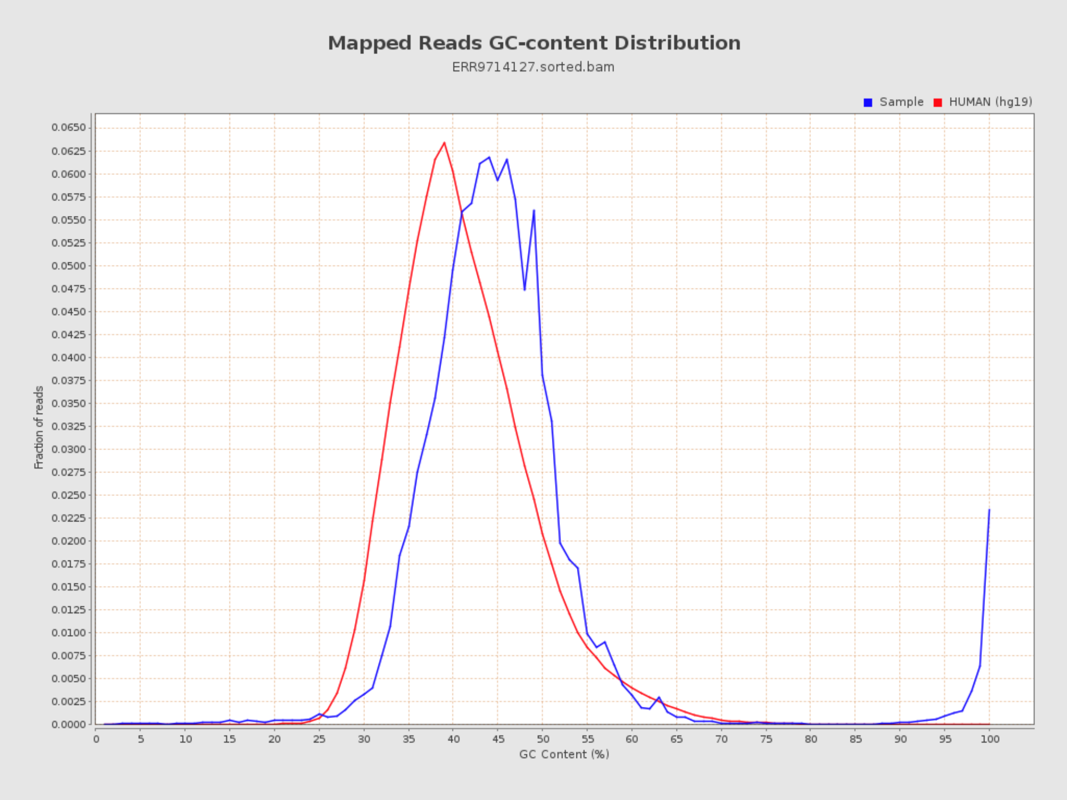
7. Results : Duplication Rate Histogram



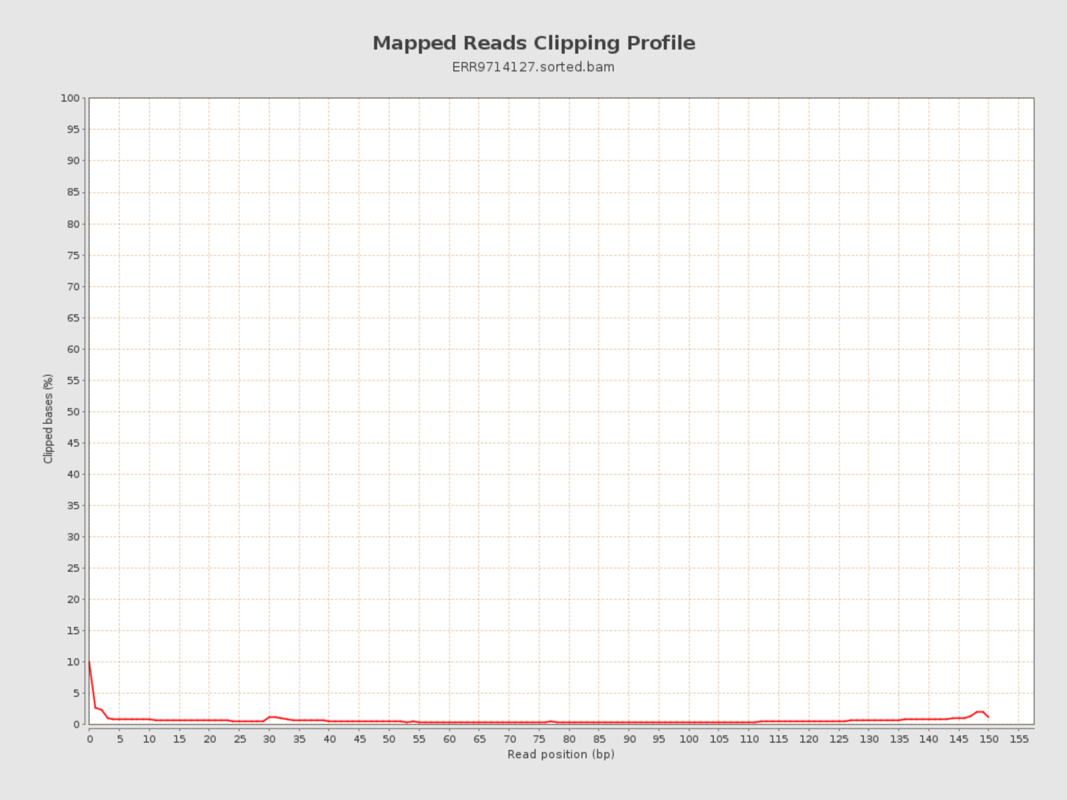
8. Results : Mapped Reads Nucleotide Content



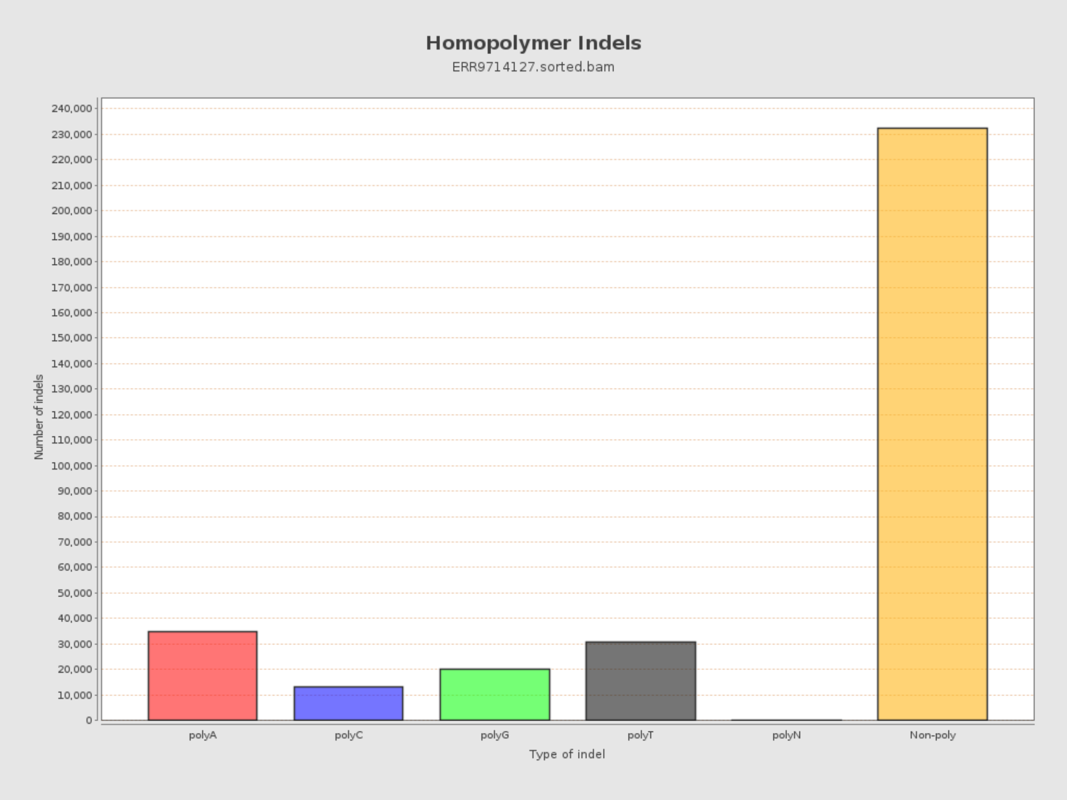
9. Results : Mapped Reads GC-content Distribution



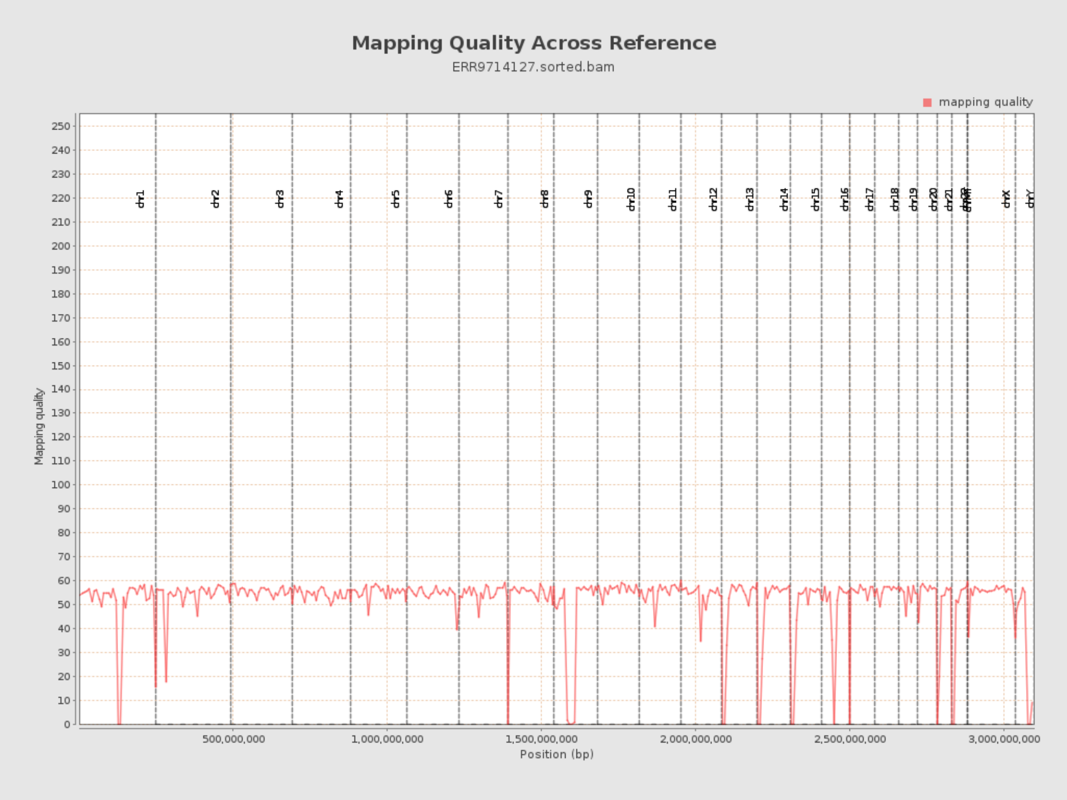
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram