Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:56:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714134.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_ERR9714134 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:56:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,470
Mapped reads	7,635 / 22.81%
Unmapped reads	25,835 / 77.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	273 / 0.82%
Read min/max/mean length	30 / 151 / 71.97
Duplicated reads (estimated)	5,811 / 17.36%
Duplication rate	46.11%
Clipped reads	5,935 / 17.73%

2.2. ACGT Content

Number/percentage of A's	147,043 / 18.13%
Number/percentage of C's	122,870 / 15.15%
Number/percentage of T's	134,038 / 16.53%
Number/percentage of G's	406,967 / 50.19%
Number/percentage of N's	7 / 0%
GC Percentage	65.34%

2.3. Coverage

Mean	0.0003

Standard Deviation	0.3587

2.4. Mapping Quality

Mean Mapping Quality	27.92

2.5. Mismatches and indels

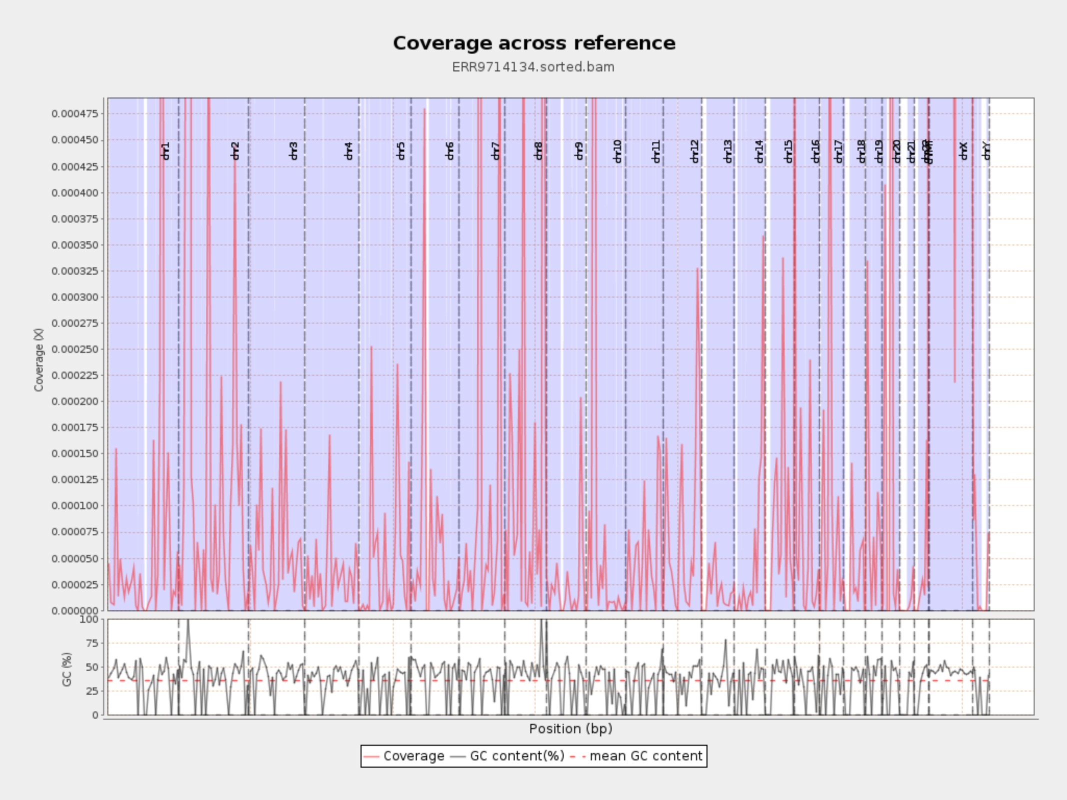
General error rate	3.66%
Mismatches	26,675
Insertions	578
Mapped reads with at least one insertion	5.46%
Deletions	1,652
Mapped reads with at least one deletion	21.1%
Homopolymer indels	36.59%

2.6. Chromosome stats

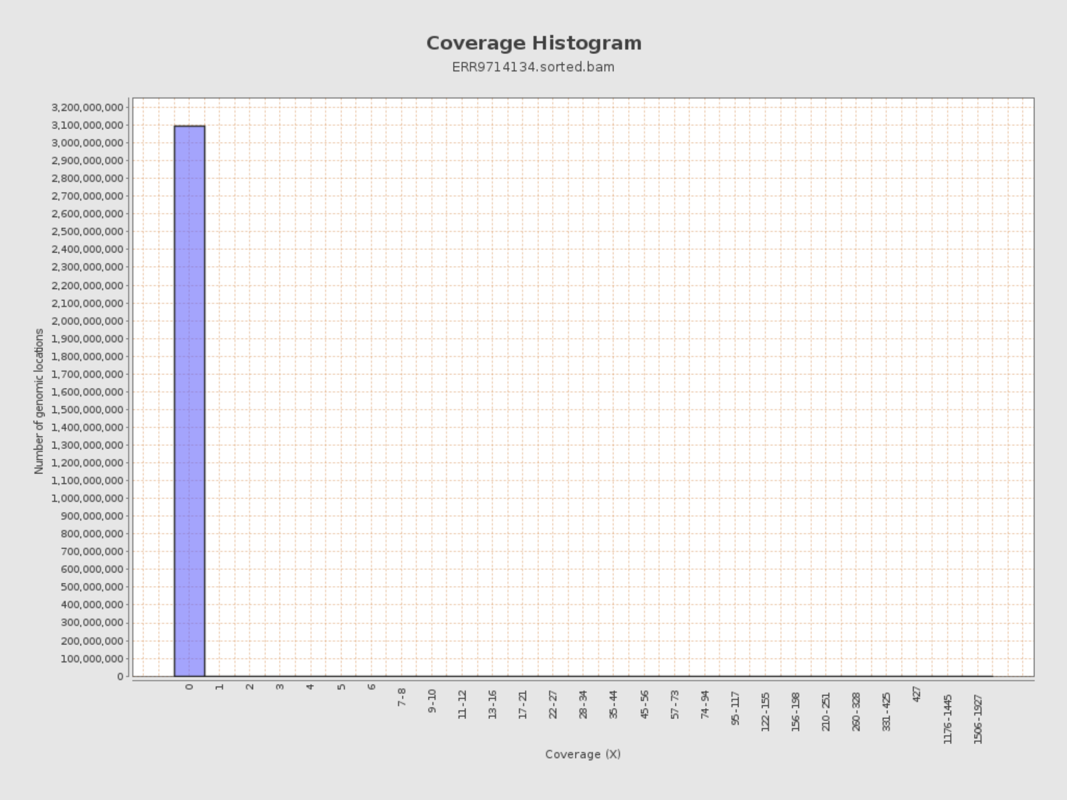
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19196	0.0001	0.1086
chr2	243199373	312986	0.0013	1.2489
chr3	198022430	11153	0.0001	0.0138
chr4	191154276	6588	0	0.0093
chr5	180915260	8882	0	0.0165
chr6	171115067	10220	0.0001	0.0201
chr7	159138663	20736	0.0001	0.0701

chr8	146364022	26265	0.0002	0.0714
chr9	141213431	3765	0	0.0119
chr10	135534747	11850	0.0001	0.1386
chr11	135006516	6762	0.0001	0.0115
chr12	133851895	10674	0.0001	0.0236
chr13	115169878	2145	0	0.0065
chr14	107349540	6167	0.0001	0.0197
chr15	102531392	7692	0.0001	0.0191
chr16	90354753	7778	0.0001	0.0284
chr17	81195210	9473	0.0001	0.0323
chr18	78077248	2526	0	0.0122
chr19	59128983	4991	0.0001	0.0274
chr20	63025520	12433	0.0002	0.077
chr21	48129895	344	0	0.0027
chr22	51304566	1797	0	0.0113
chrMT	16571	834	0.0503	0.3063
chrX	155270560	316328	0.002	0.2647
chrY	59373566	2060	0	0.0094

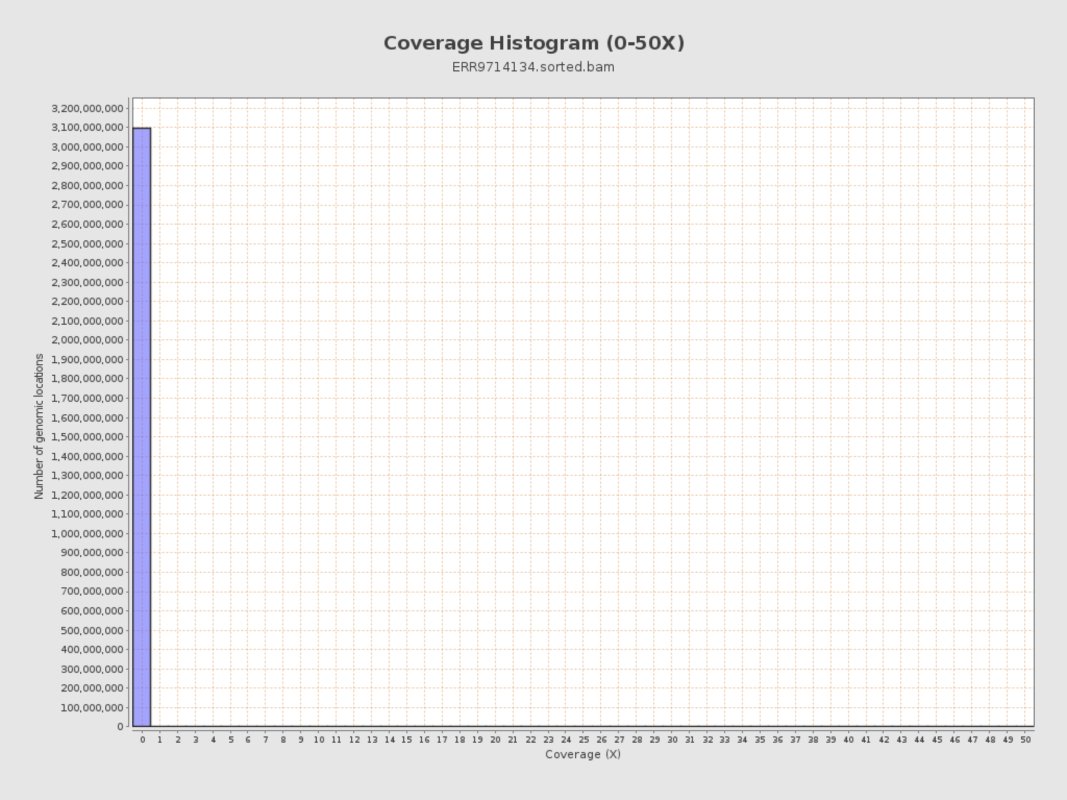
3. Results : Coverage across reference



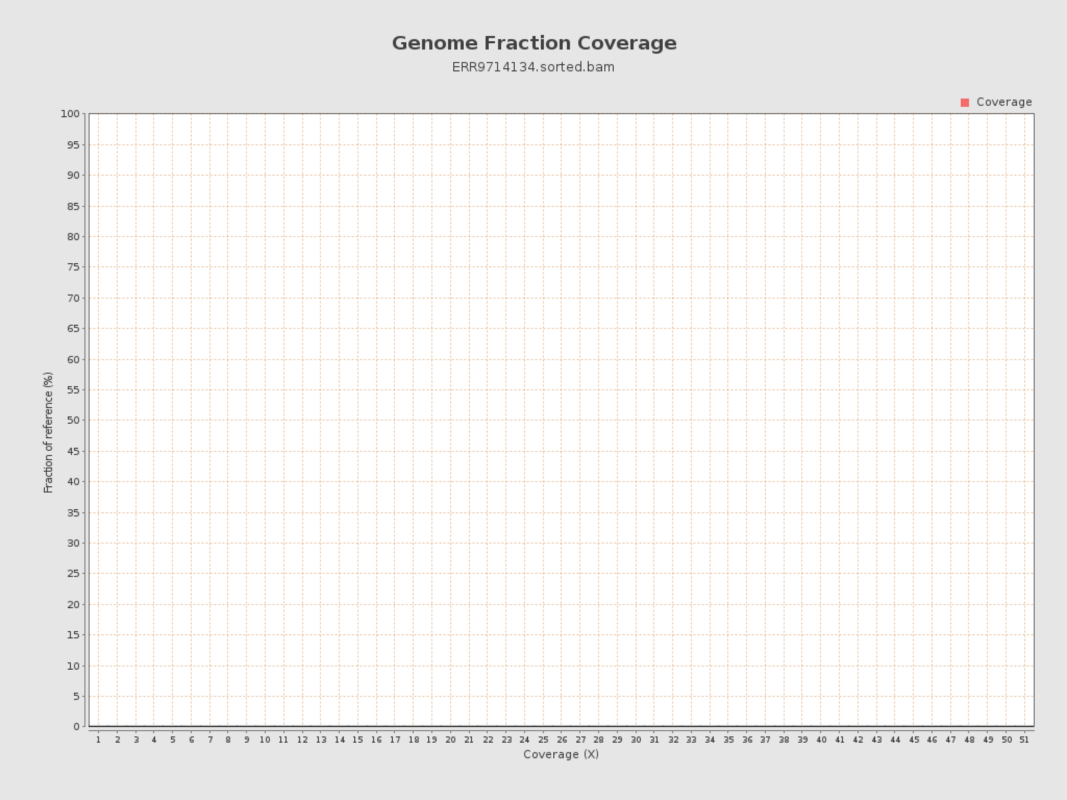
4. Results : Coverage Histogram



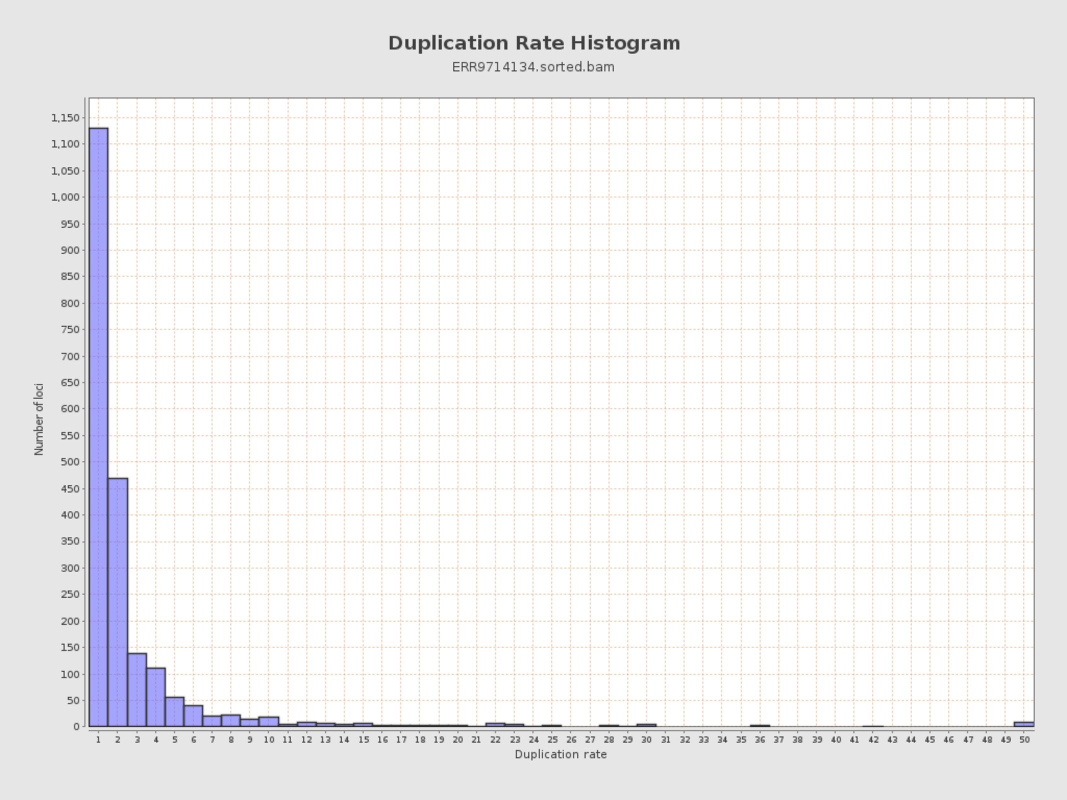
5. Results : Coverage Histogram (0-50X)



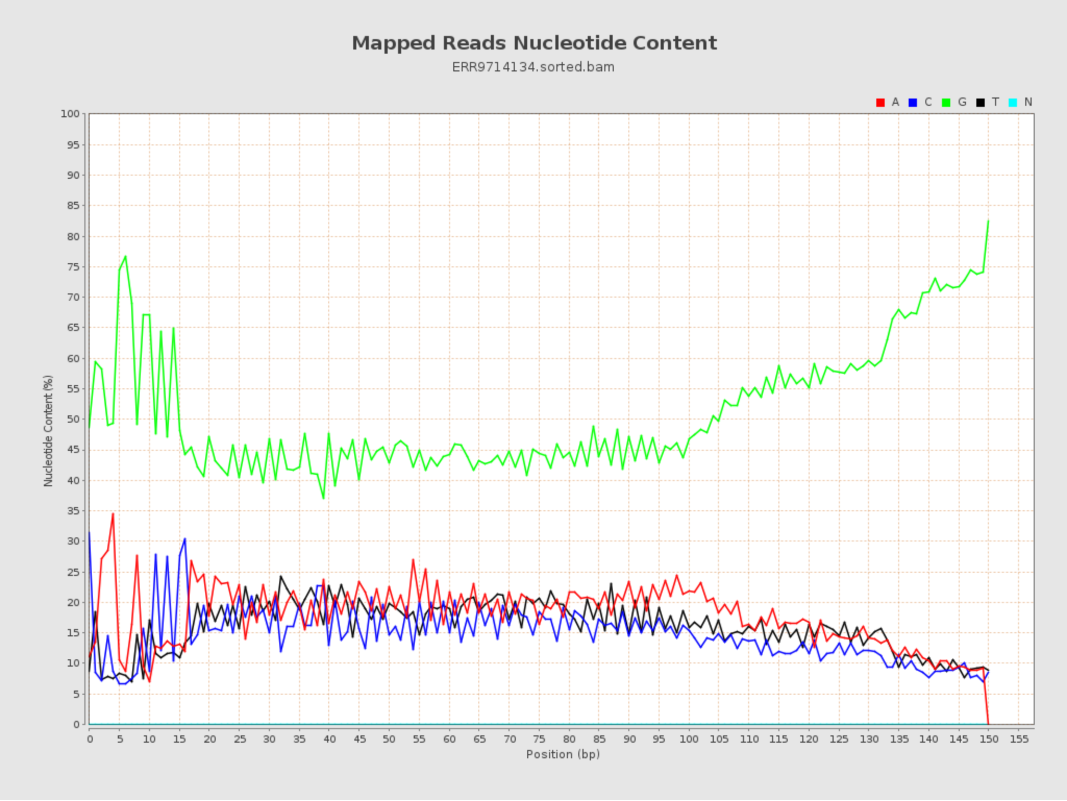
6. Results : Genome Fraction Coverage



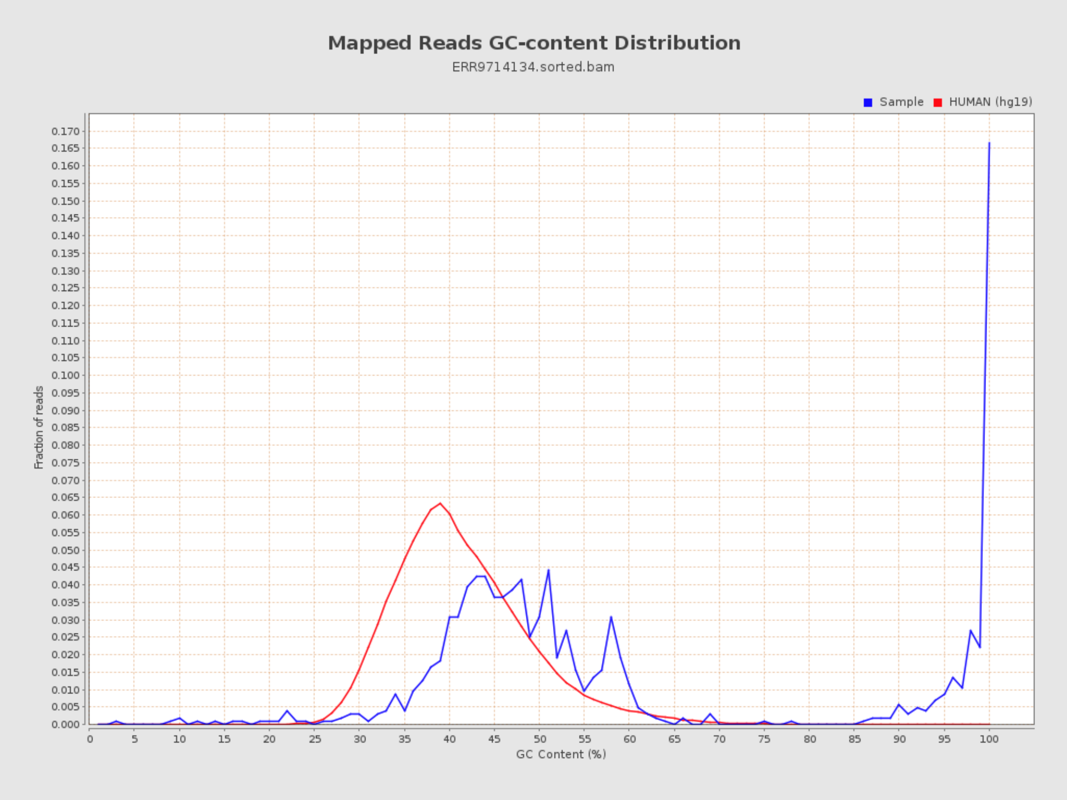
7. Results : Duplication Rate Histogram



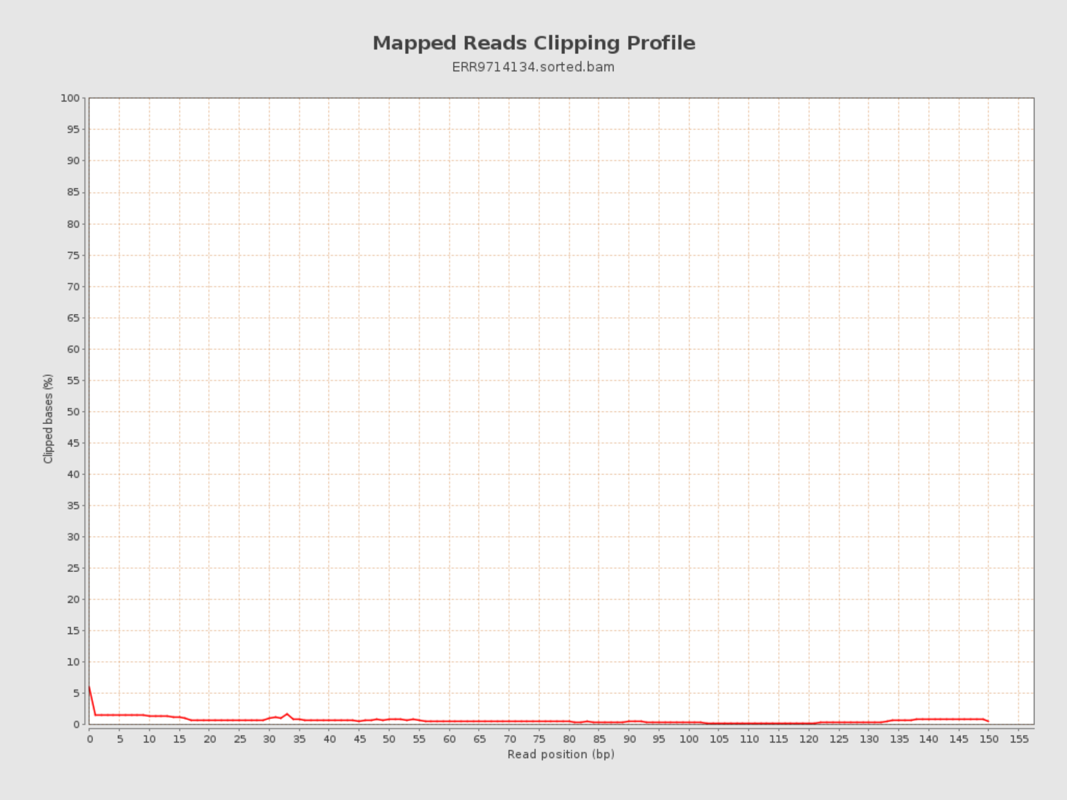
8. Results : Mapped Reads Nucleotide Content



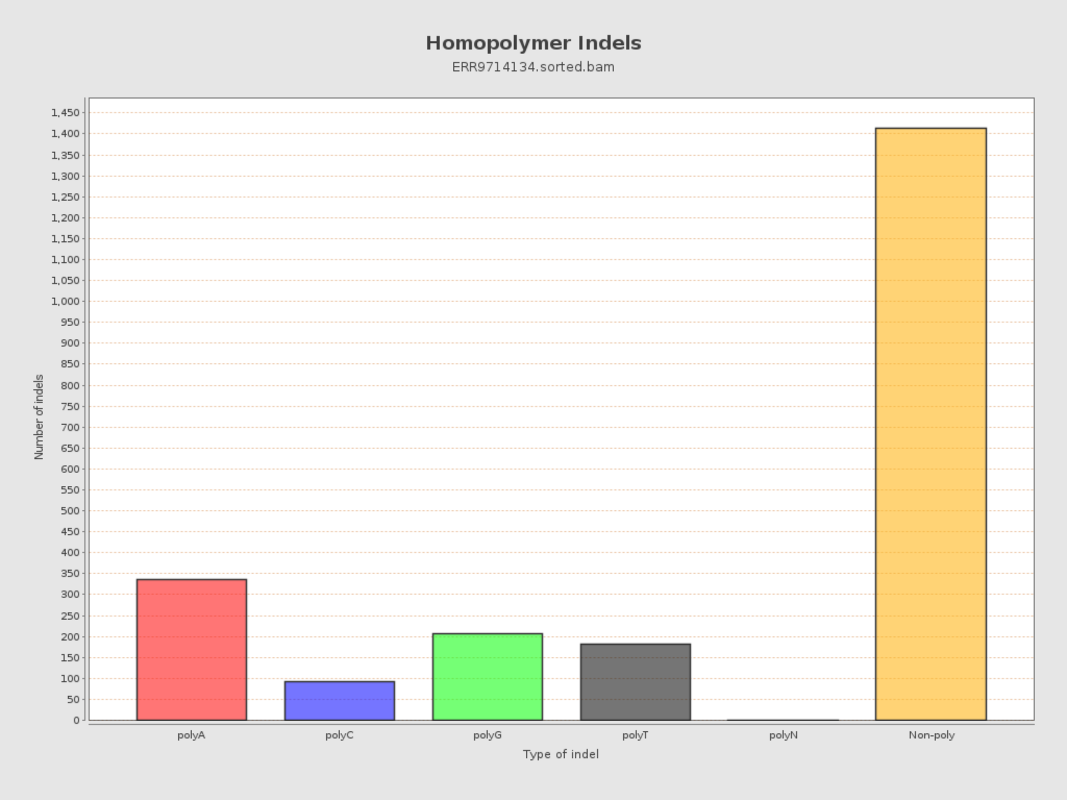
9. Results : Mapped Reads GC-content Distribution



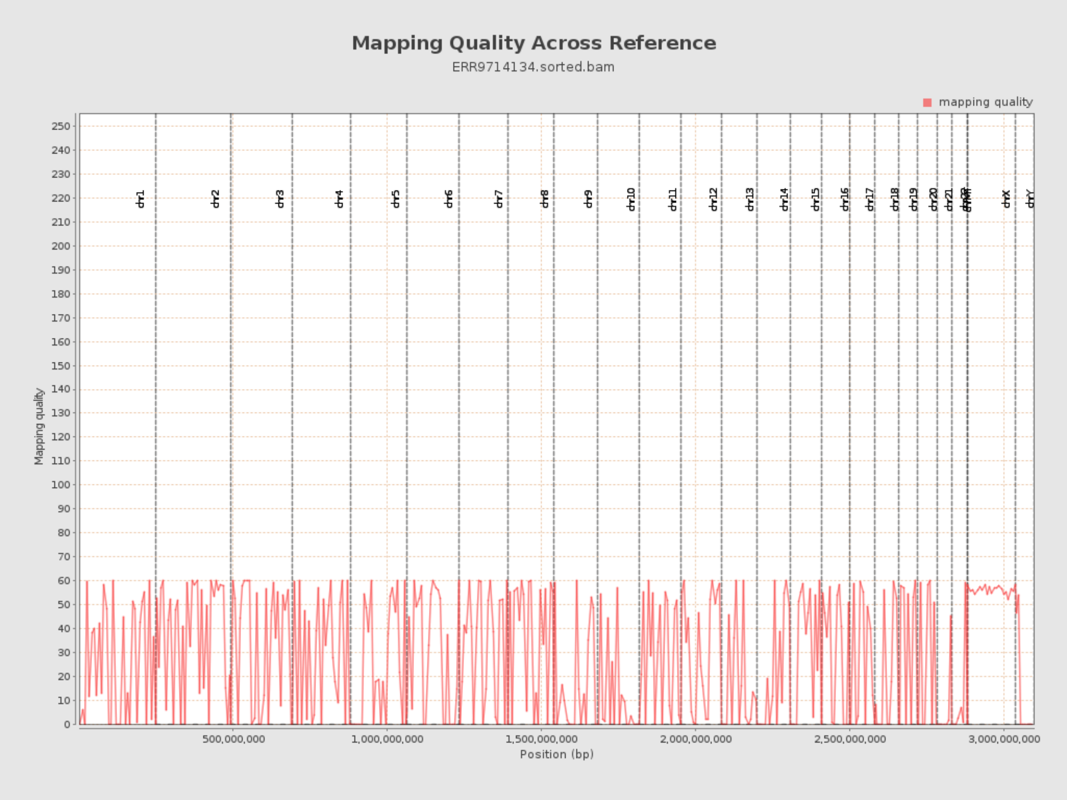
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram