Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:38:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714148.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_ERR9714148 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:38:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	659,640
Mapped reads	633,866 / 96.09%
Unmapped reads	25,774 / 3.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,240 / 2.77%
Read min/max/mean length	30 / 151 / 148.16
Duplicated reads (estimated)	637,251 / 96.61%
Duplication rate	23.99%
Clipped reads	612,497 / 92.85%

2.2. ACGT Content

Number/percentage of A's	24,042,138 / 29.52%
Number/percentage of C's	17,920,482 / 22%
Number/percentage of T's	22,512,294 / 27.64%
Number/percentage of G's	16,976,157 / 20.84%
Number/percentage of N's	567 / 0%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0267

Standard Deviation	77.4934

2.4. Mapping Quality

Mean Mapping Quality	18.08

2.5. Mismatches and indels

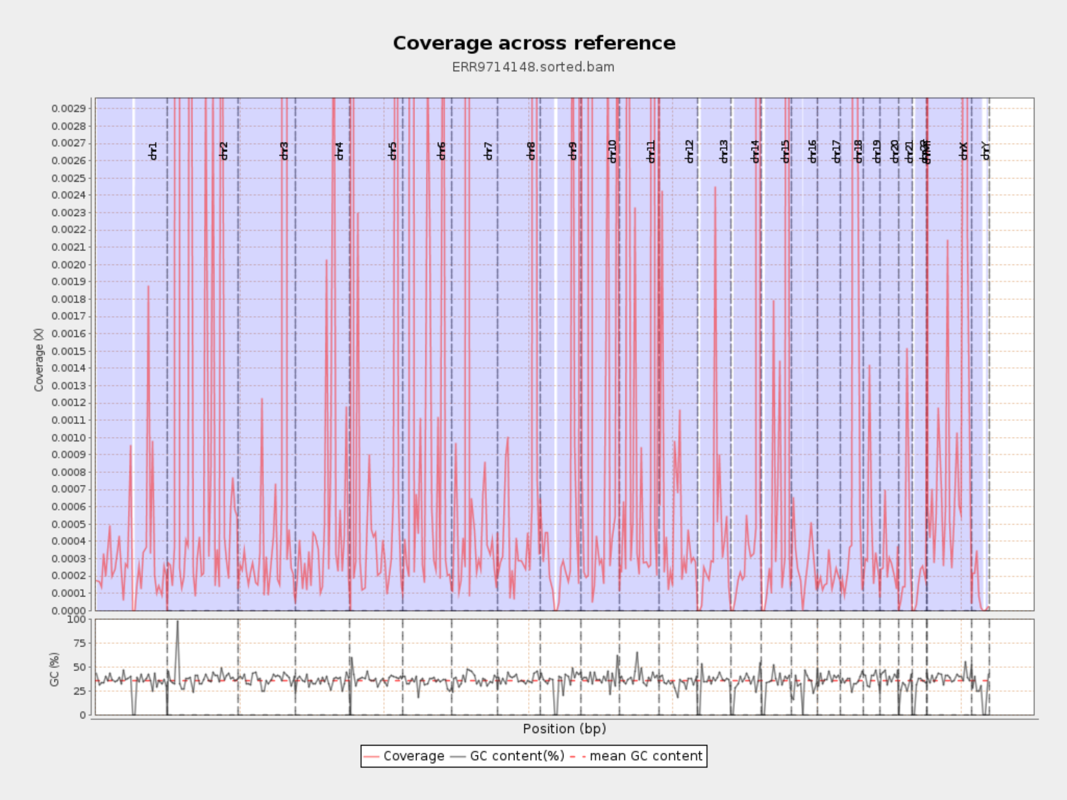
General error rate	4.48%
Mismatches	2,773,973
Insertions	254,600
Mapped reads with at least one insertion	39.58%
Deletions	169,424
Mapped reads with at least one deletion	25.89%
Homopolymer indels	48.95%

2.6. Chromosome stats

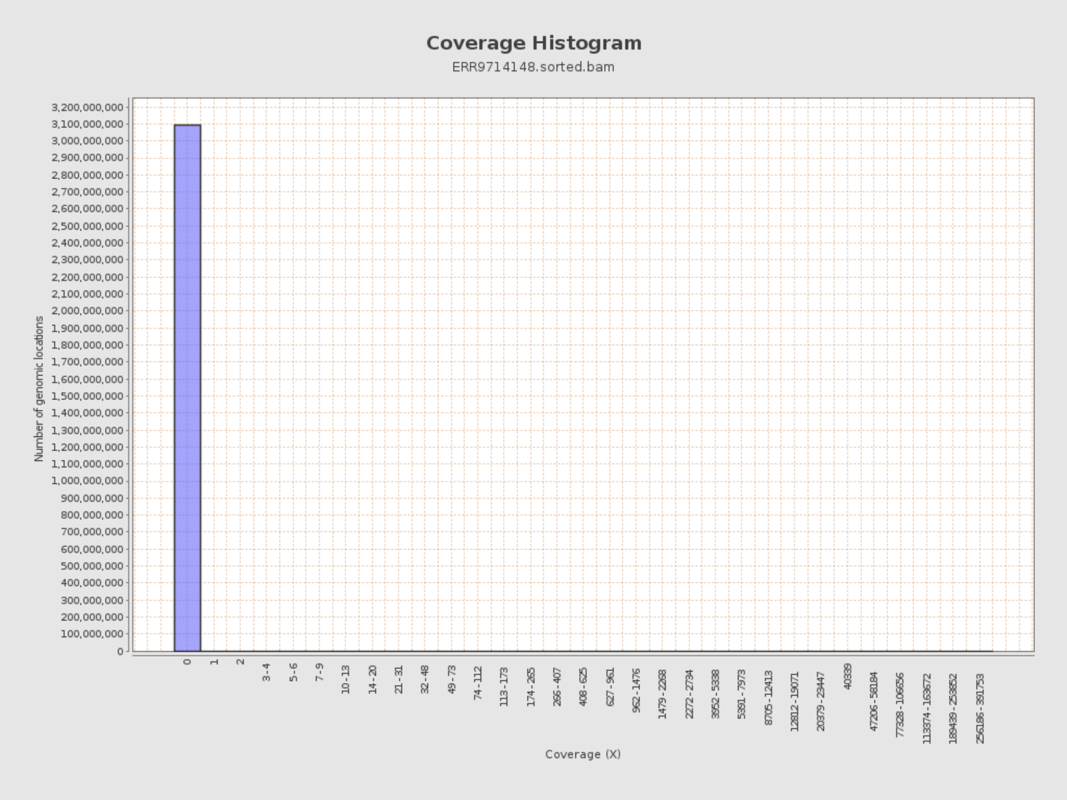
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	79198	0.0003	0.138
chr2	243199373	568962	0.0023	1.5396
chr3	198022430	3236689	0.0163	18.5327
chr4	191154276	106190	0.0006	0.1946
chr5	180915260	23683632	0.1309	130.5482
chr6	171115067	369512	0.0022	1.5687
chr7	159138663	813982	0.0051	5.3194

chr8	146364022	211389	0.0014	0.8852
chr9	141213431	85817	0.0006	0.2302
chr10	135534747	1645296	0.0121	11.4662
chr11	135006516	332016	0.0025	1.7139
chr12	133851895	69884	0.0005	0.1584
chr13	115169878	50323	0.0004	0.2047
chr14	107349540	50511655	0.4705	378.938
chr15	102531392	161567	0.0016	0.9203
chr16	90354753	25227	0.0003	0.0612
chr17	81195210	15036	0.0002	0.021
chr18	78077248	127697	0.0016	1.2274
chr19	59128983	25676	0.0004	0.2452
chr20	63025520	18294	0.0003	0.0374
chr21	48129895	17280	0.0004	0.273
chr22	51304566	10217	0.0002	0.0729
chrMT	16571	65933	3.9788	33.5638
chrX	155270560	304527	0.002	0.9878
chrY	59373566	6462	0.0001	0.021

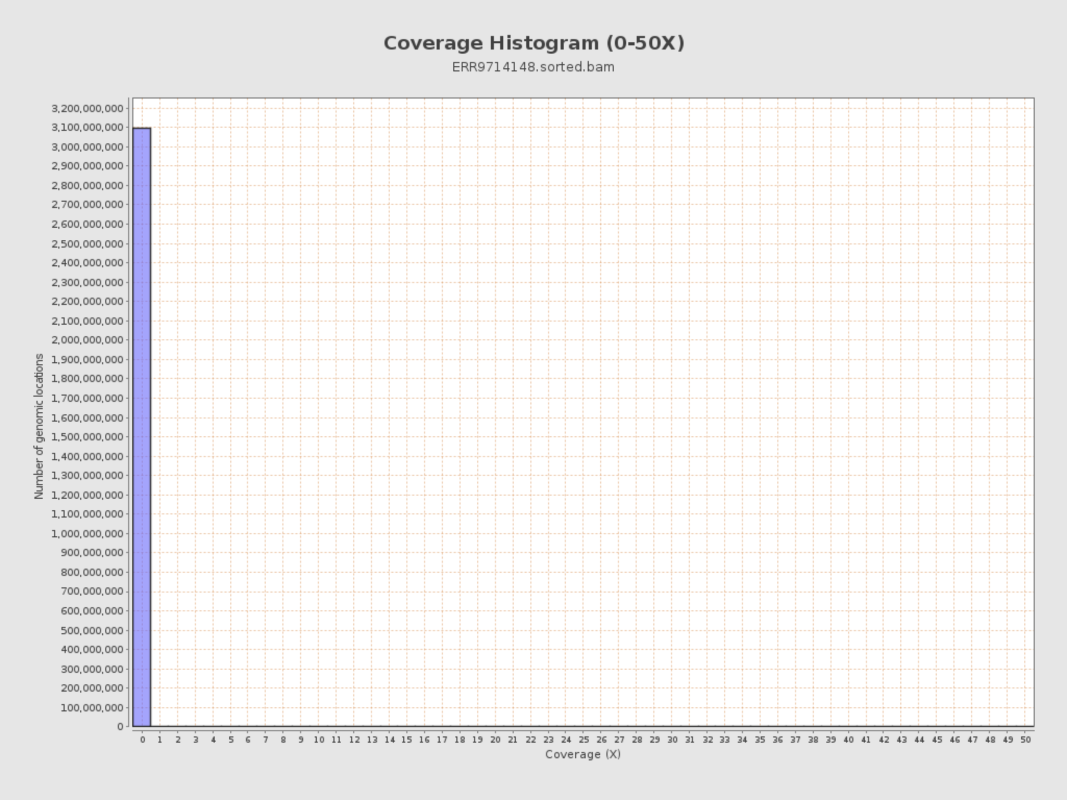
3. Results : Coverage across reference



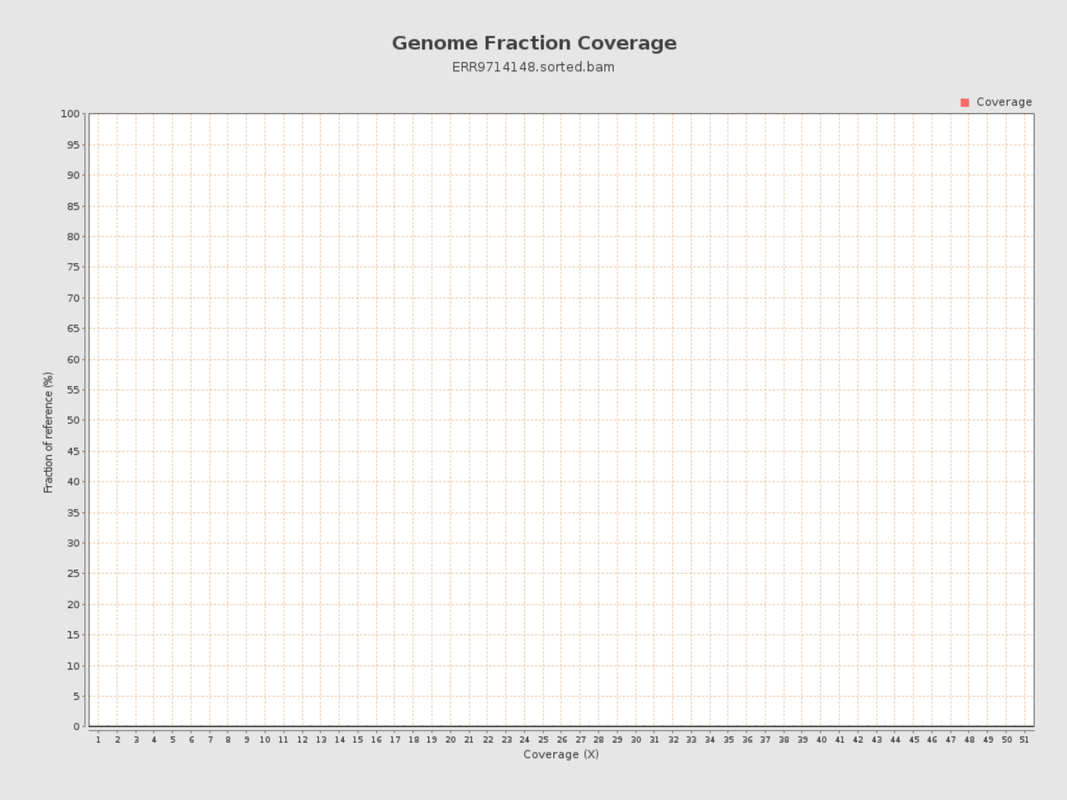
4. Results : Coverage Histogram



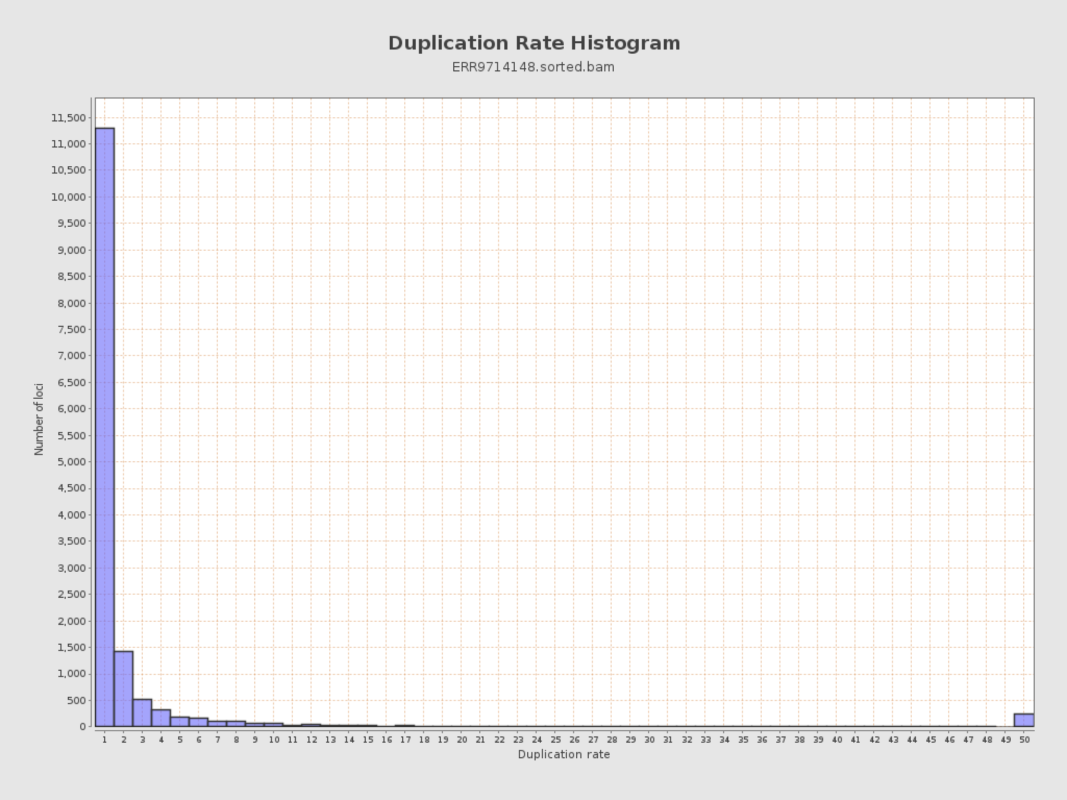
5. Results : Coverage Histogram (0-50X)



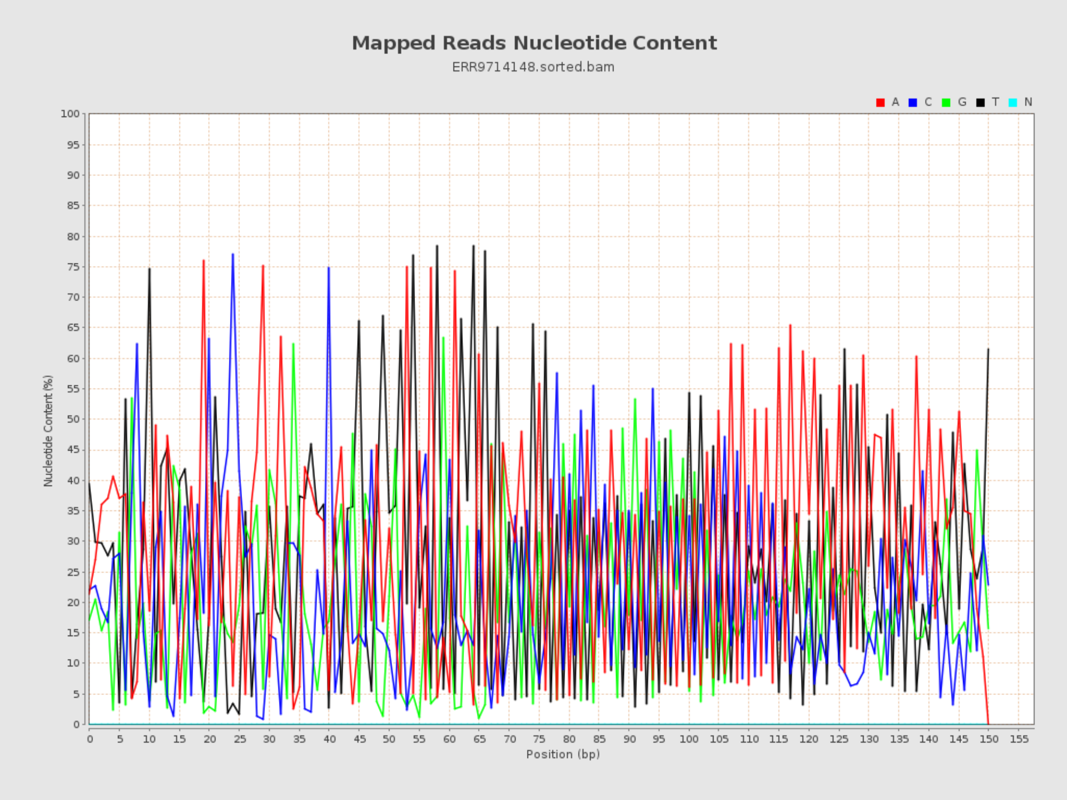
6. Results : Genome Fraction Coverage



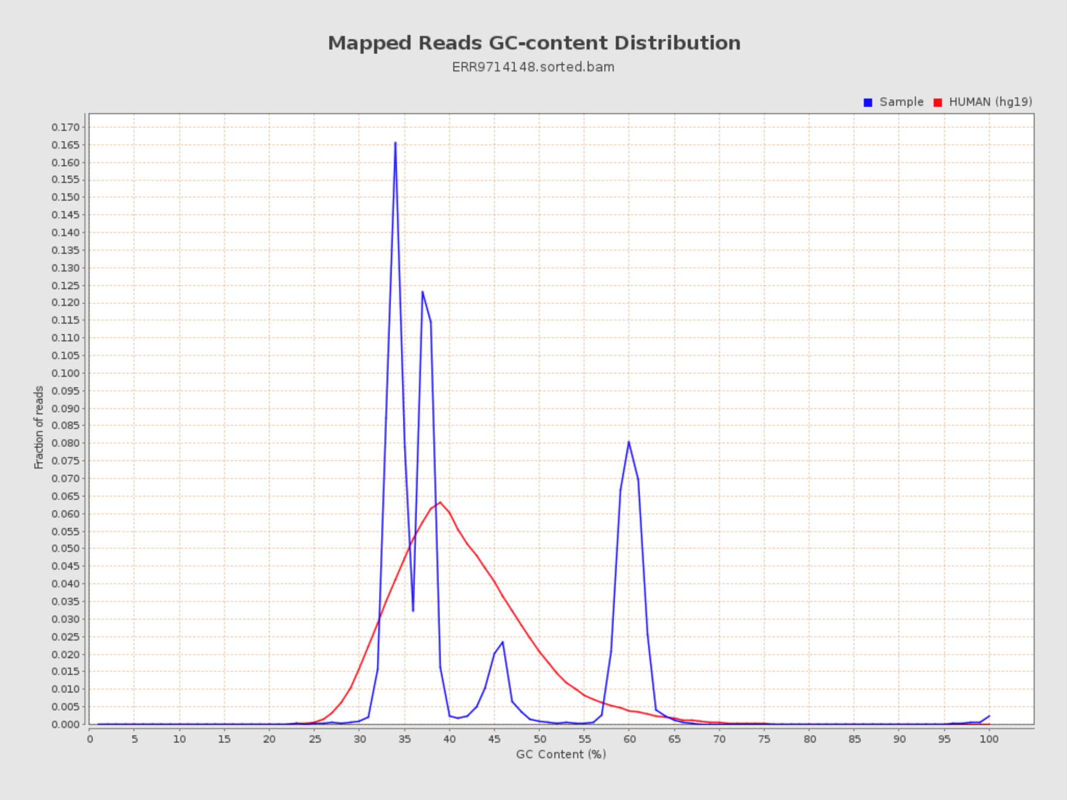
7. Results : Duplication Rate Histogram



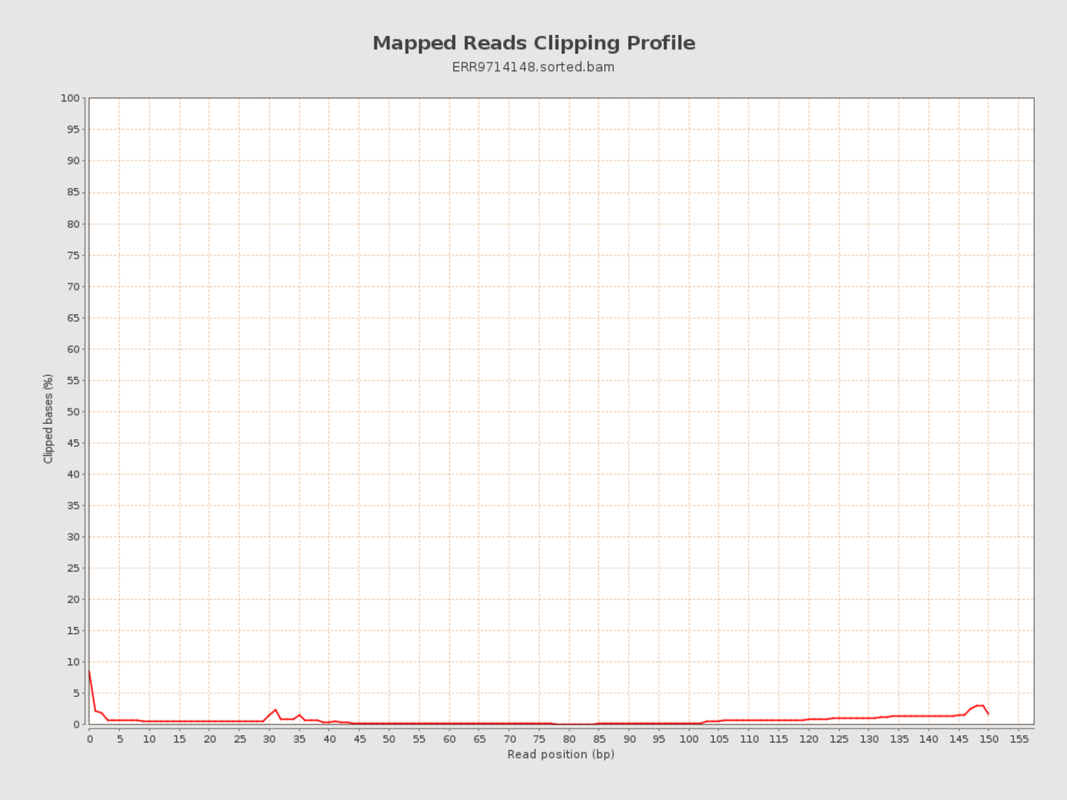
8. Results : Mapped Reads Nucleotide Content



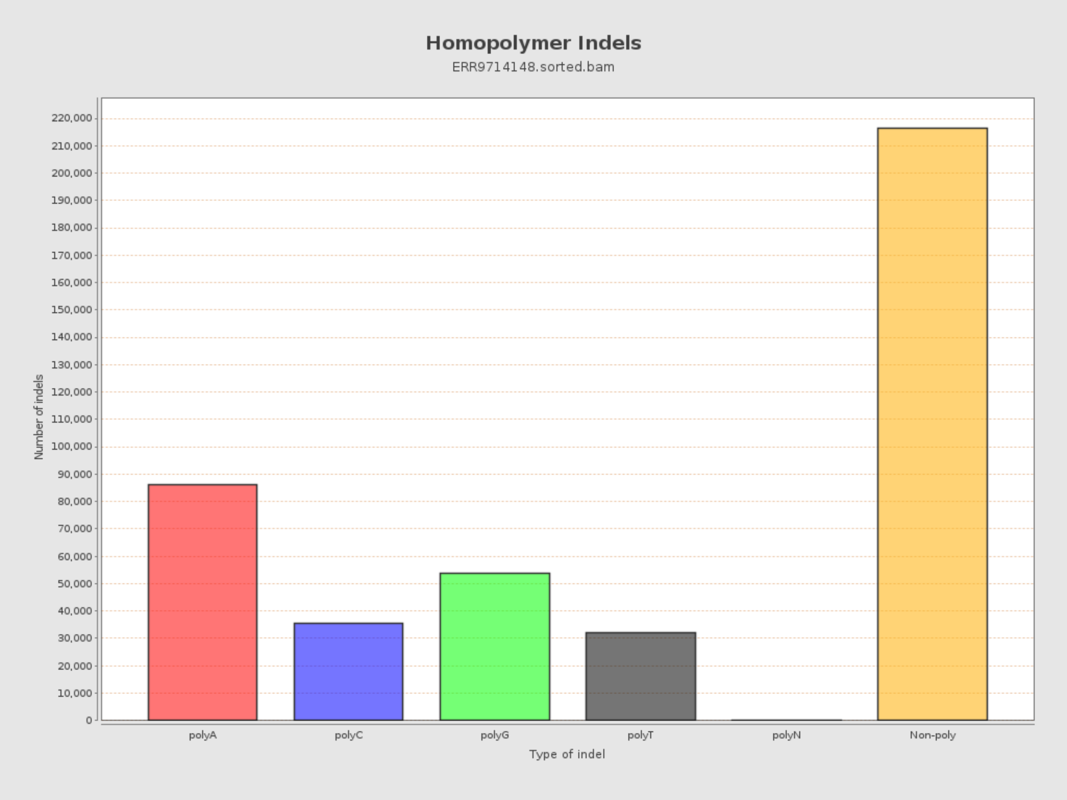
9. Results : Mapped Reads GC-content Distribution



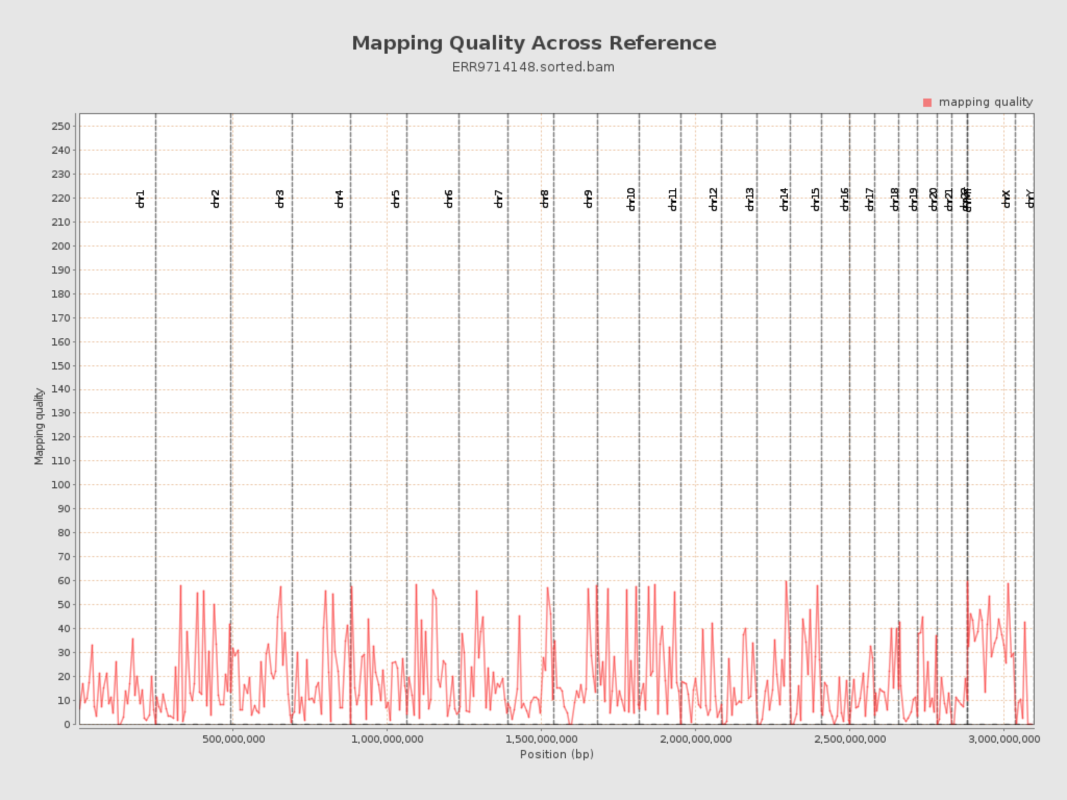
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram