Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 22:09:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714158.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_ERR9714158 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 22:09:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	809,978
Mapped reads	543,765 / 67.13%
Unmapped reads	266,213 / 32.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,181 / 2%
Read min/max/mean length	30 / 151 / 131.12
Duplicated reads (estimated)	484,297 / 59.79%
Duplication rate	44%
Clipped reads	514,045 / 63.46%

2.2. ACGT Content

Number/percentage of A's	18,540,607 / 26.77%
Number/percentage of C's	15,503,391 / 22.39%
Number/percentage of T's	17,565,530 / 25.37%
Number/percentage of G's	17,639,045 / 25.47%
Number/percentage of N's	570 / 0%
GC Percentage	47.86%

2.3. Coverage

Mean	0.0229

Standard Deviation	5.9658

2.4. Mapping Quality

Mean Mapping Quality	51.87

2.5. Mismatches and indels

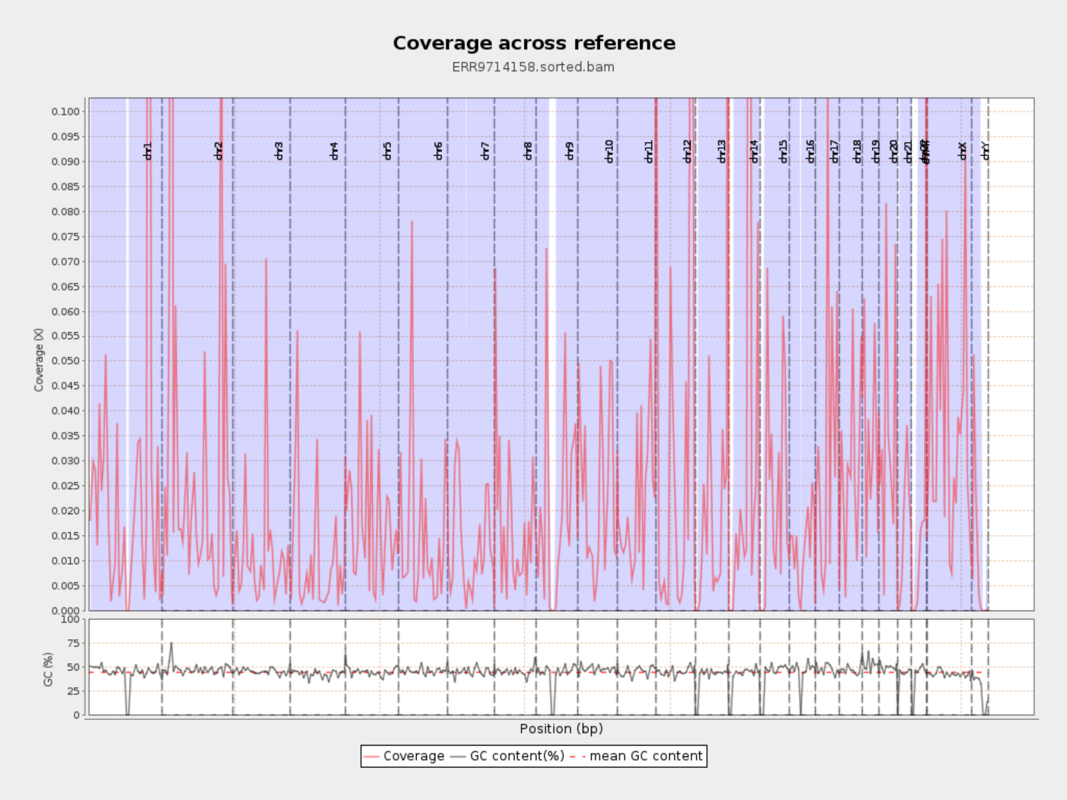
General error rate	4.44%
Mismatches	2,874,111
Insertions	73,601
Mapped reads with at least one insertion	13.04%
Deletions	256,181
Mapped reads with at least one deletion	44.71%
Homopolymer indels	30.44%

2.6. Chromosome stats

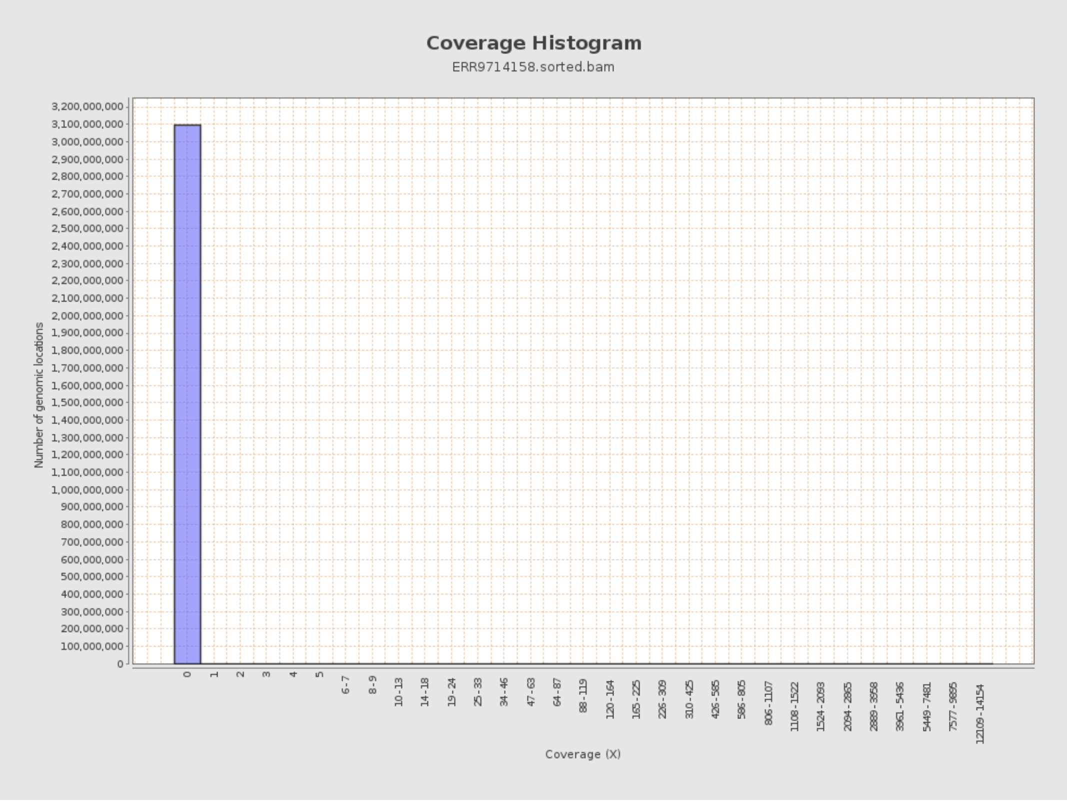
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6391830	0.0256	7.4105
chr2	243199373	8624295	0.0355	10.2361
chr3	198022430	2305906	0.0116	2.3935
chr4	191154276	2023063	0.0106	2.1644
chr5	180915260	3274949	0.0181	3.3523
chr6	171115067	2707358	0.0158	3.3219
chr7	159138663	2080484	0.0131	2.124

chr8	146364022	2600942	0.0178	3.7004
chr9	141213431	2722170	0.0193	4.1041
chr10	135534747	3285052	0.0242	3.664
chr11	135006516	2990378	0.0221	3.2065
chr12	133851895	4365922	0.0326	7.694
chr13	115169878	2828507	0.0246	8.2009
chr14	107349540	3871106	0.0361	16.2448
chr15	102531392	2444214	0.0238	3.9207
chr16	90354753	1184805	0.0131	1.7297
chr17	81195210	2824121	0.0348	6.1826
chr18	78077248	2160317	0.0277	5.3073
chr19	59128983	2039199	0.0345	3.7859
chr20	63025520	2301700	0.0365	5.3499
chr21	48129895	761207	0.0158	2.875
chr22	51304566	541385	0.0106	1.2904
chrMT	16571	92393	5.5756	44.5429
chrX	155270560	5794566	0.0373	3.6619
chrY	59373566	646912	0.0109	2.4314

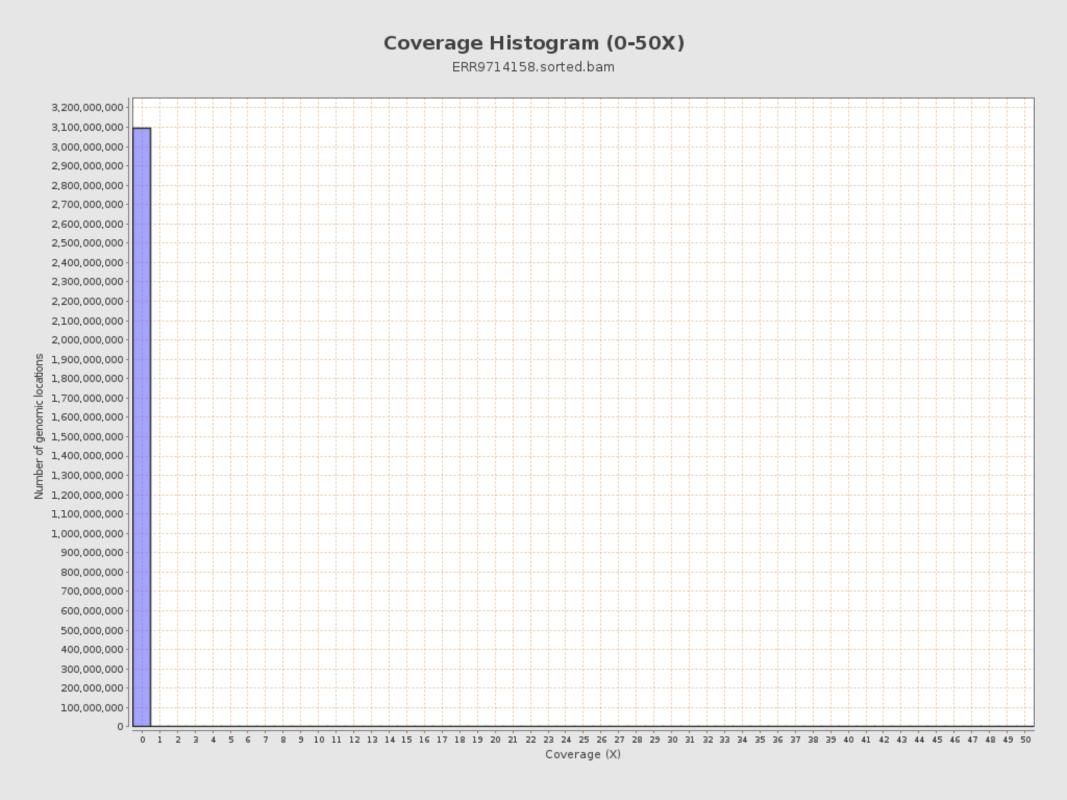
3. Results : Coverage across reference



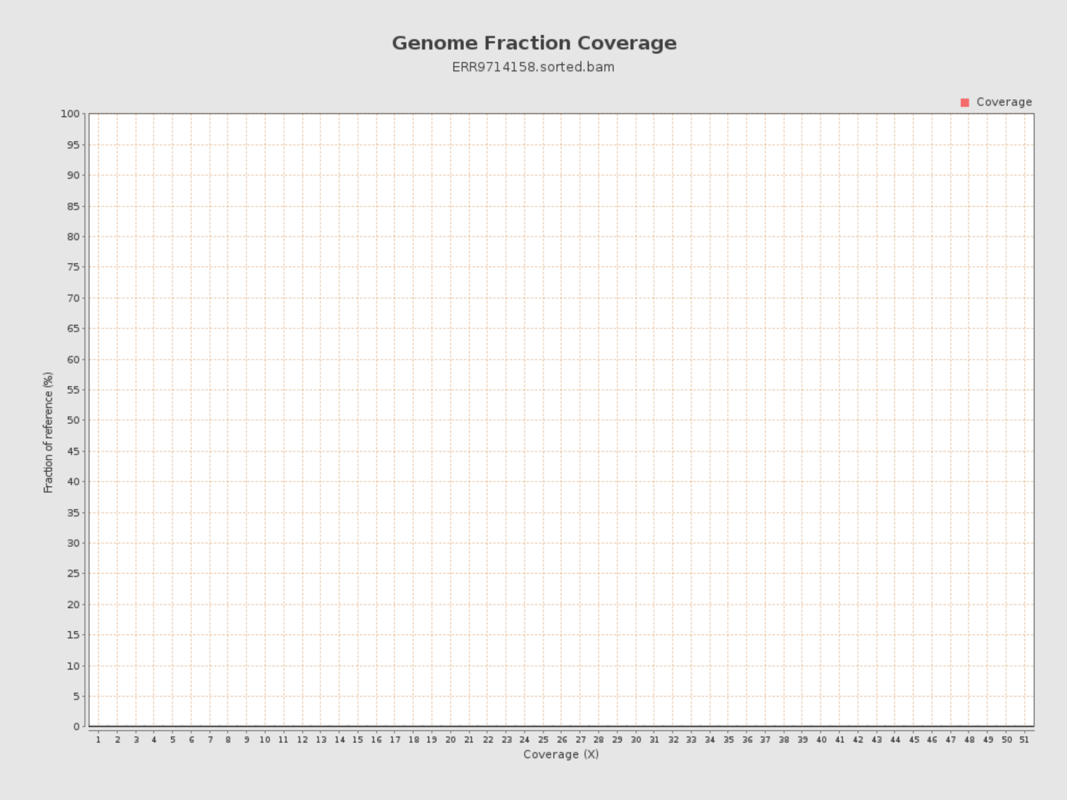
4. Results : Coverage Histogram



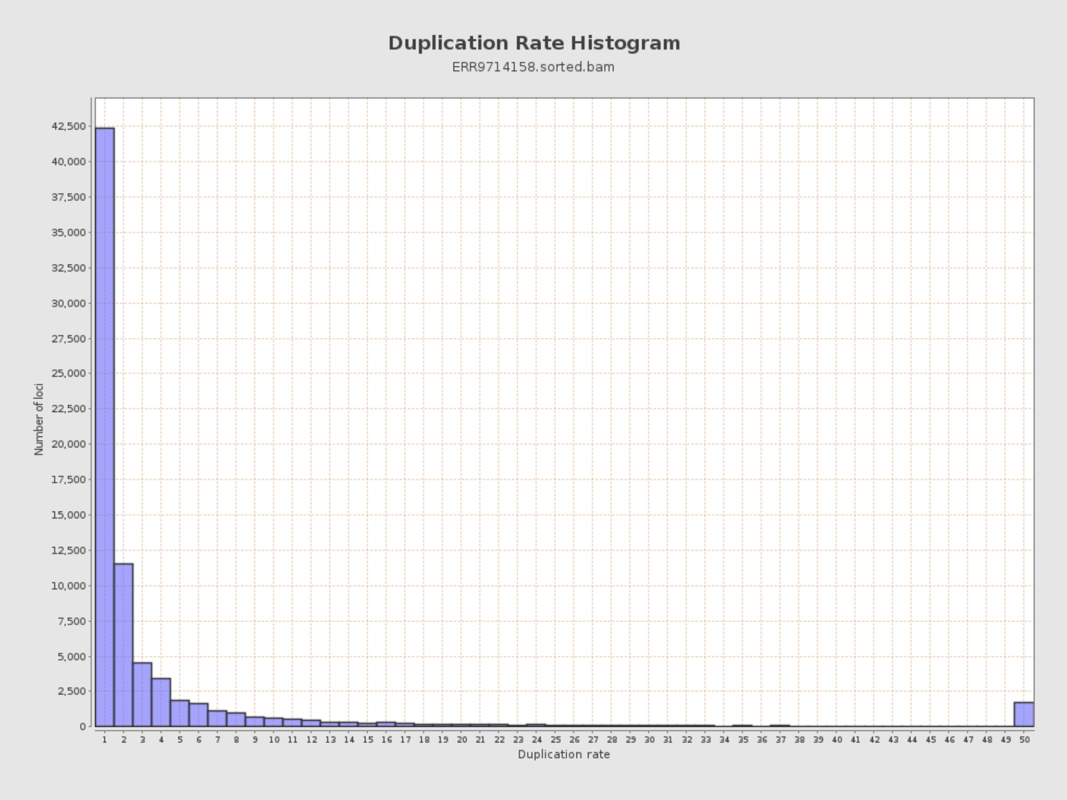
5. Results : Coverage Histogram (0-50X)



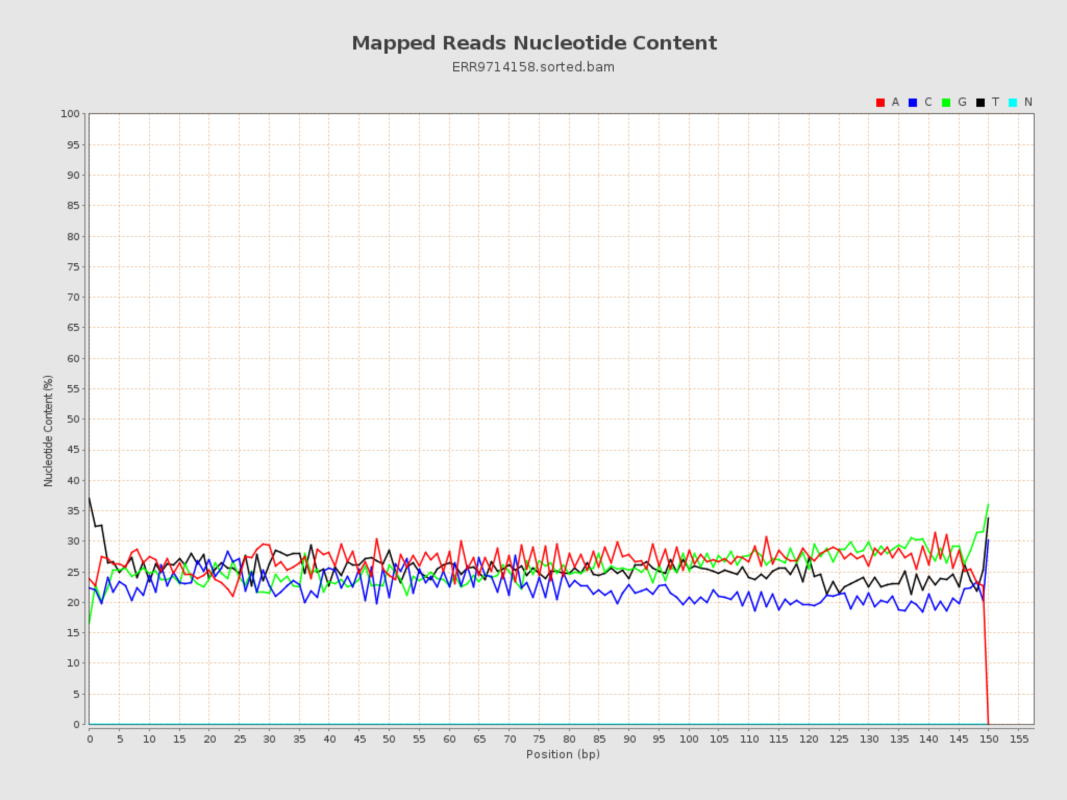
6. Results : Genome Fraction Coverage



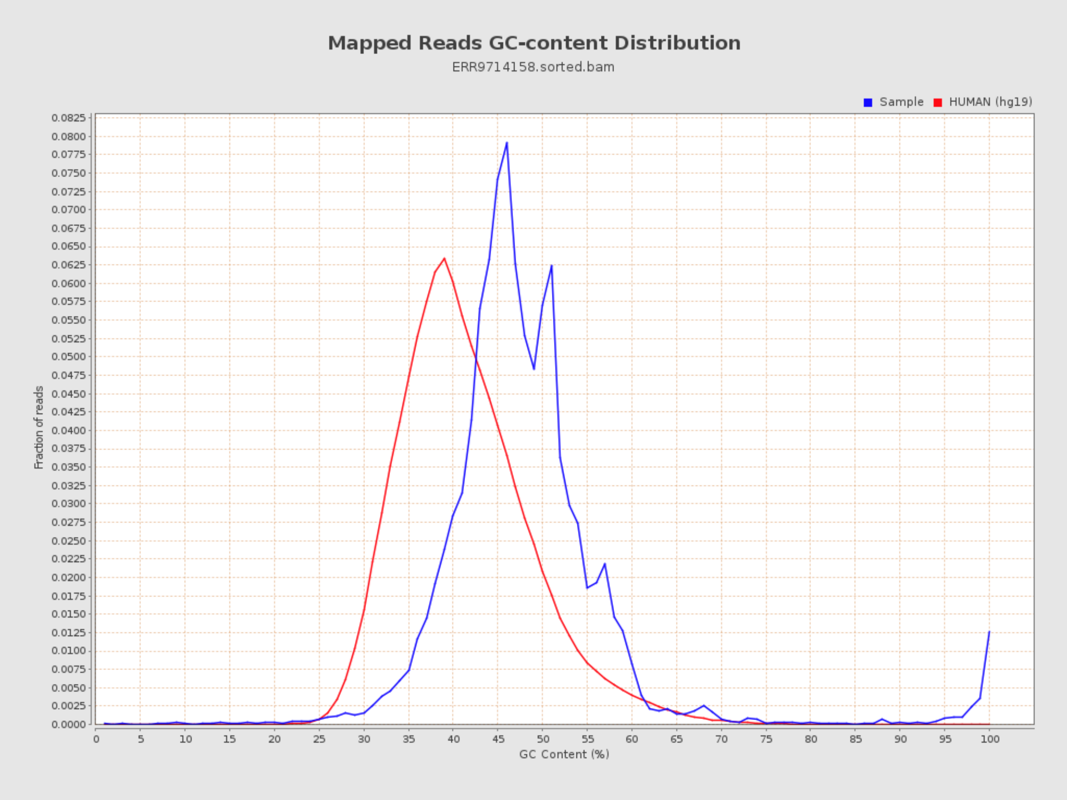
7. Results : Duplication Rate Histogram



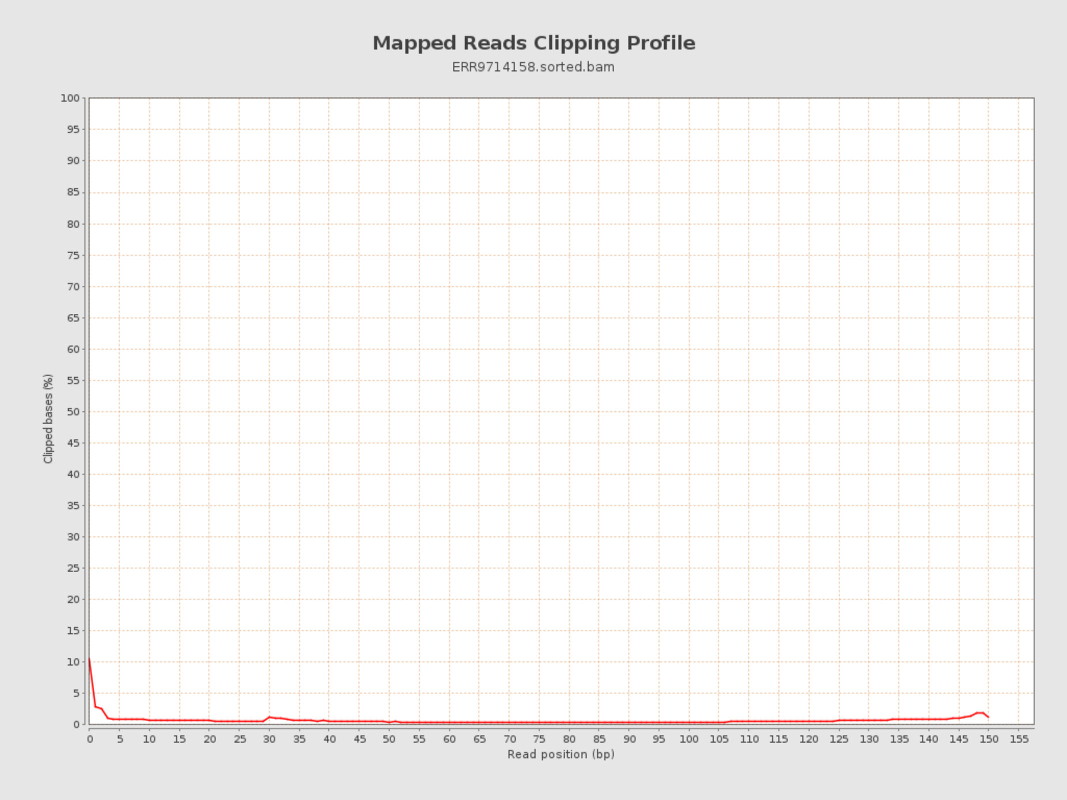
8. Results : Mapped Reads Nucleotide Content



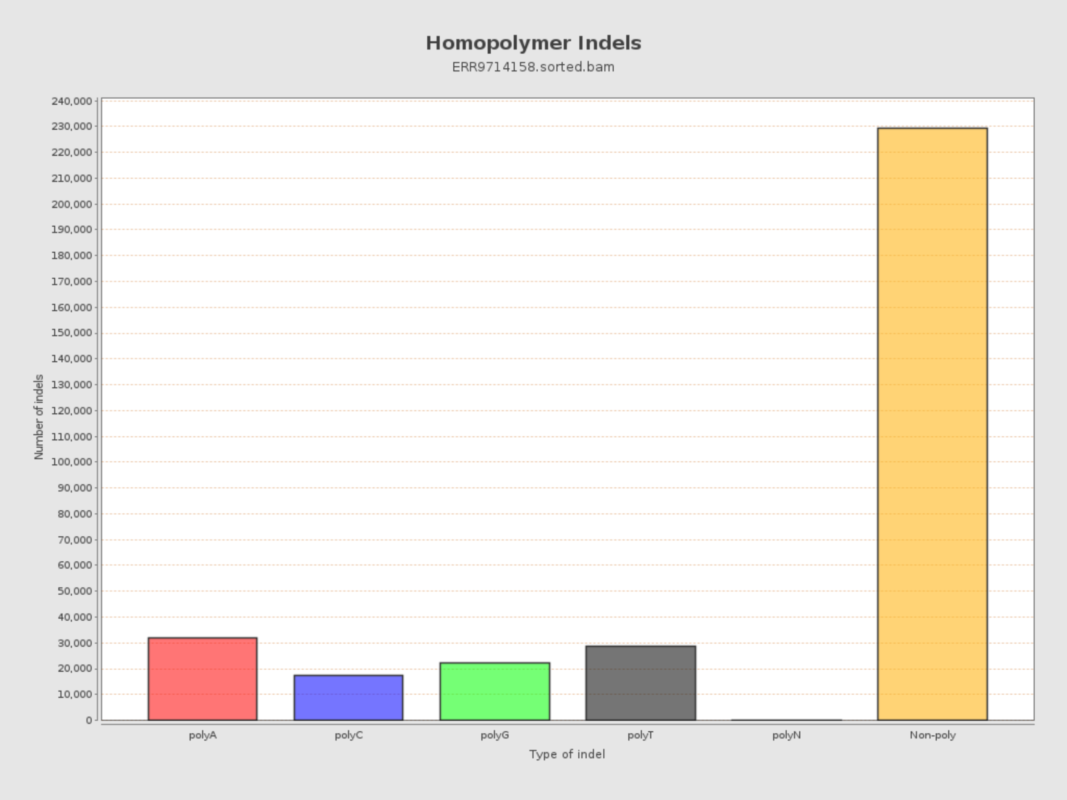
9. Results : Mapped Reads GC-content Distribution



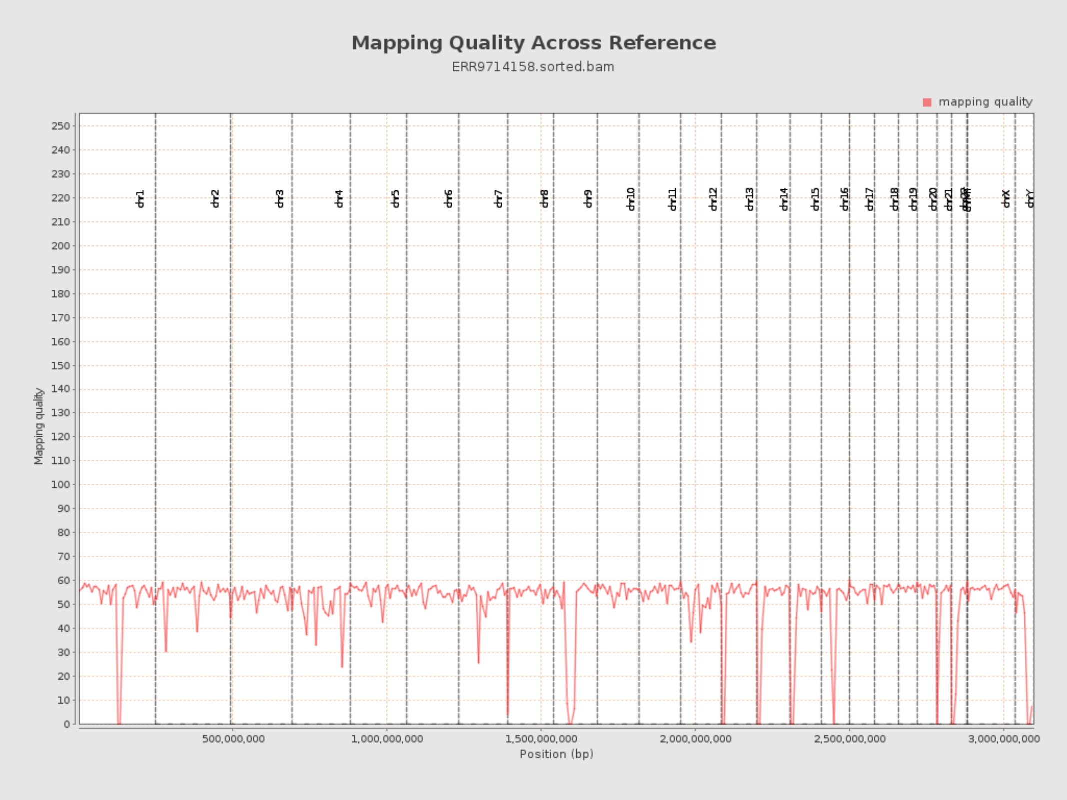
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram