Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:05:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714137.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_ERR9714137 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714137.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:05:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	669,532
Mapped reads	550,746 / 82.26%
Unmapped reads	118,786 / 17.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,350 / 2.89%
Read min/max/mean length	30 / 151 / 134.21
Duplicated reads (estimated)	463,118 / 69.17%
Duplication rate	44.38%
Clipped reads	520,379 / 77.72%

2.2. ACGT Content

Number/percentage of A's	19,509,305 / 28%
Number/percentage of C's	14,784,523 / 21.22%
Number/percentage of T's	18,547,604 / 26.62%
Number/percentage of G's	16,823,031 / 24.15%
Number/percentage of N's	558 / 0%
GC Percentage	45.37%

2.3. Coverage

Mean	0.0229

Standard Deviation	2.9057

2.4. Mapping Quality

Mean Mapping Quality	52.77

2.5. Mismatches and indels

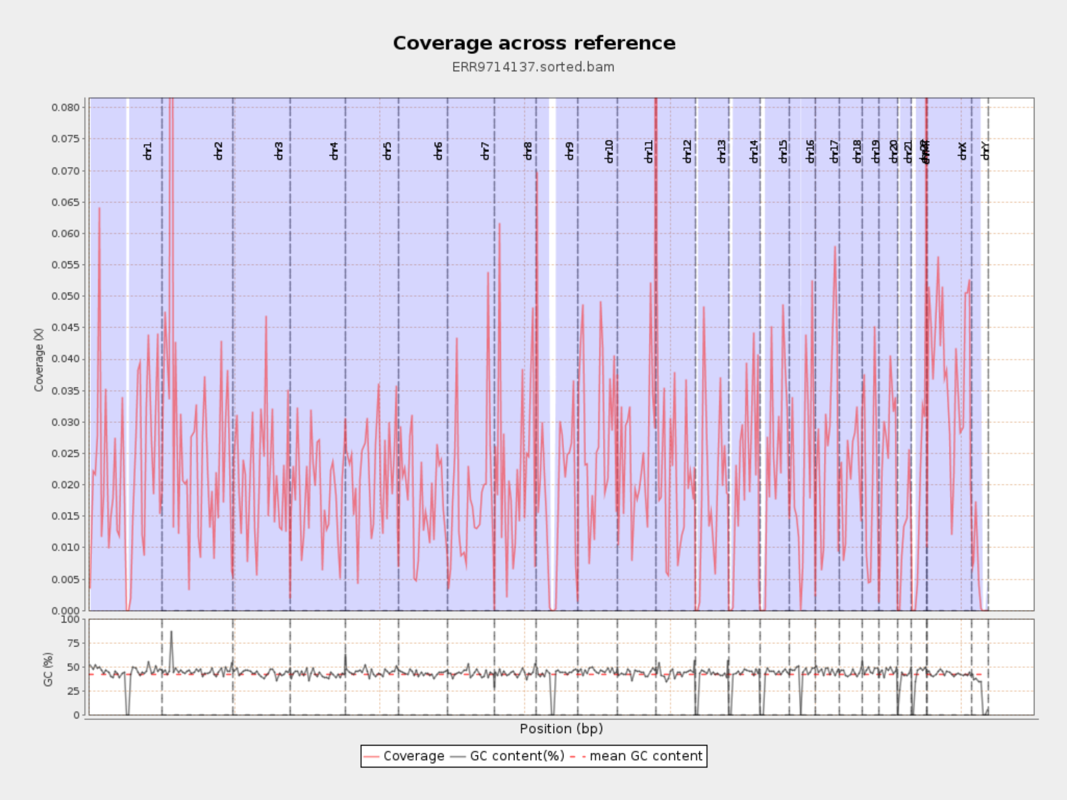
General error rate	4.18%
Mismatches	2,670,507
Insertions	78,094
Mapped reads with at least one insertion	13.81%
Deletions	232,875
Mapped reads with at least one deletion	40.46%
Homopolymer indels	28.75%

2.6. Chromosome stats

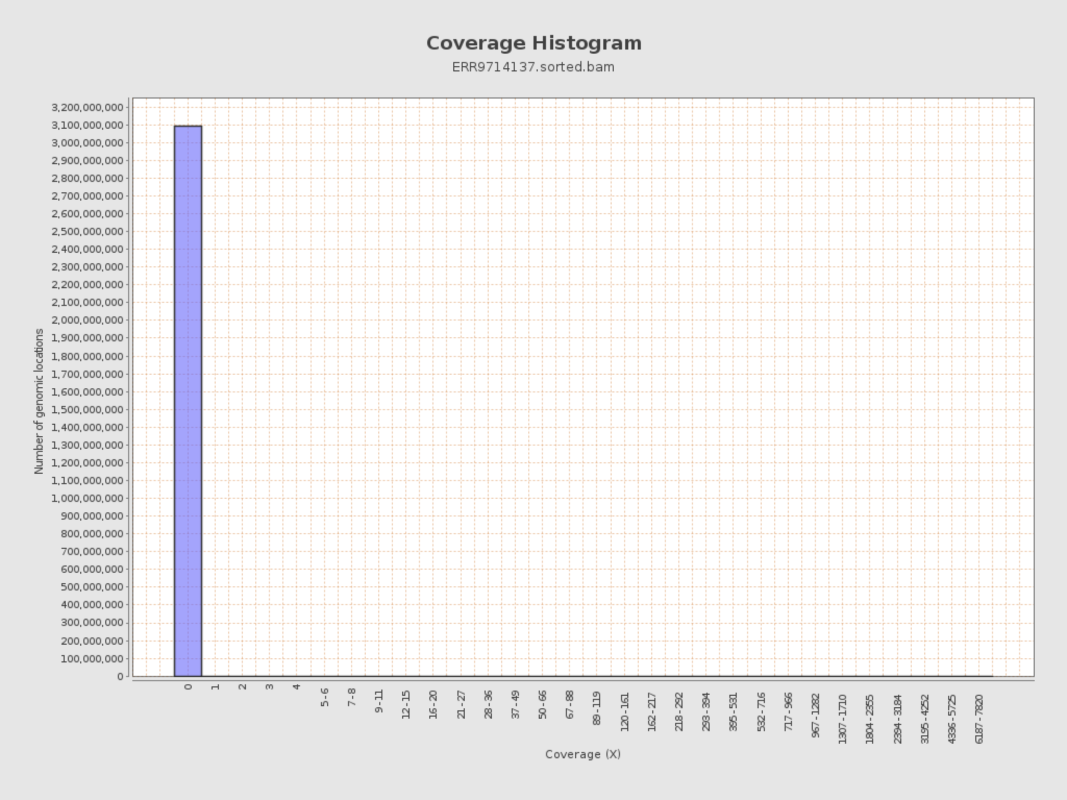
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5498838	0.0221	2.2341
chr2	243199373	7448738	0.0306	5.8758
chr3	198022430	4179323	0.0211	1.9083
chr4	191154276	3605626	0.0189	1.9708
chr5	180915260	3965983	0.0219	2.0028
chr6	171115067	2982527	0.0174	1.5527
chr7	159138663	2917416	0.0183	1.7669

chr8	146364022	3364798	0.023	2.4814
chr9	141213431	2530087	0.0179	1.761
chr10	135534747	3908364	0.0288	2.7603
chr11	135006516	3420524	0.0253	2.3901
chr12	133851895	2864263	0.0214	1.9142
chr13	115169878	2051236	0.0178	2.0545
chr14	107349540	2381332	0.0222	2.3582
chr15	102531392	2410208	0.0235	2.2956
chr16	90354753	2043624	0.0226	2.3229
chr17	81195210	2312239	0.0285	3.0055
chr18	78077248	1693095	0.0217	1.885
chr19	59128983	1137874	0.0192	2.0912
chr20	63025520	1706331	0.0271	2.2418
chr21	48129895	548986	0.0114	1.0034
chr22	51304566	811925	0.0158	1.7289
chrMT	16571	997938	60.222	546.6439
chrX	155270560	5966804	0.0384	2.3117
chrY	59373566	264343	0.0045	0.6414

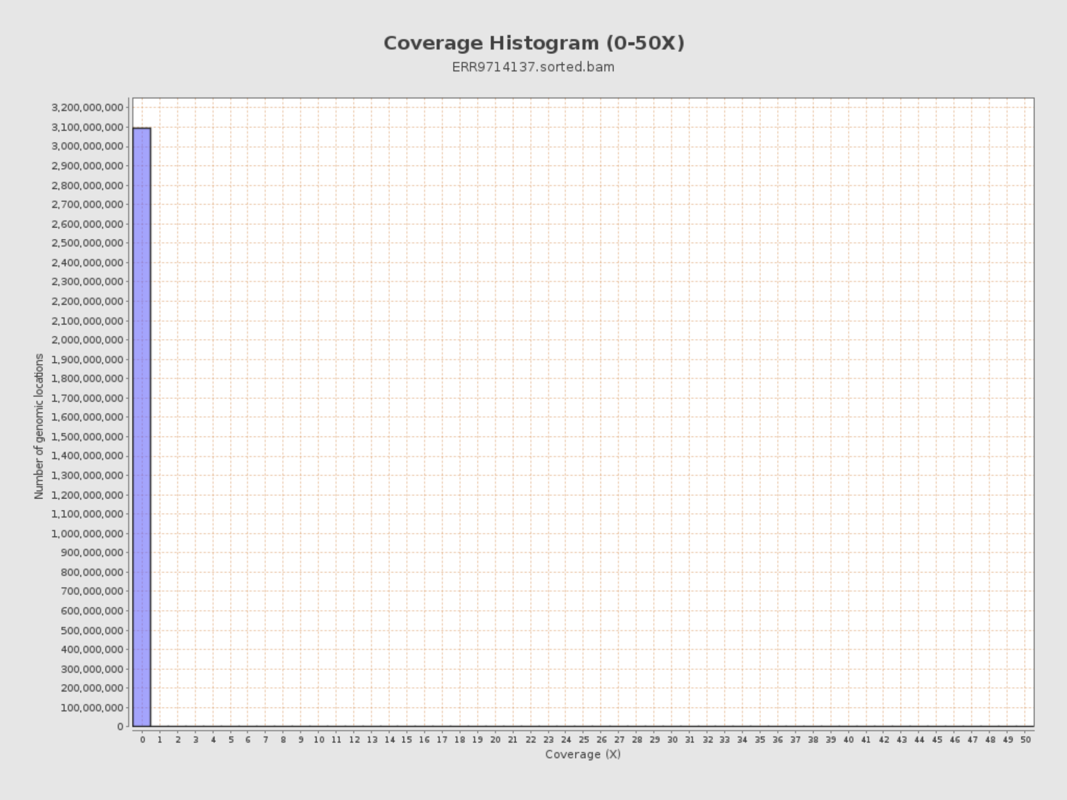
3. Results : Coverage across reference



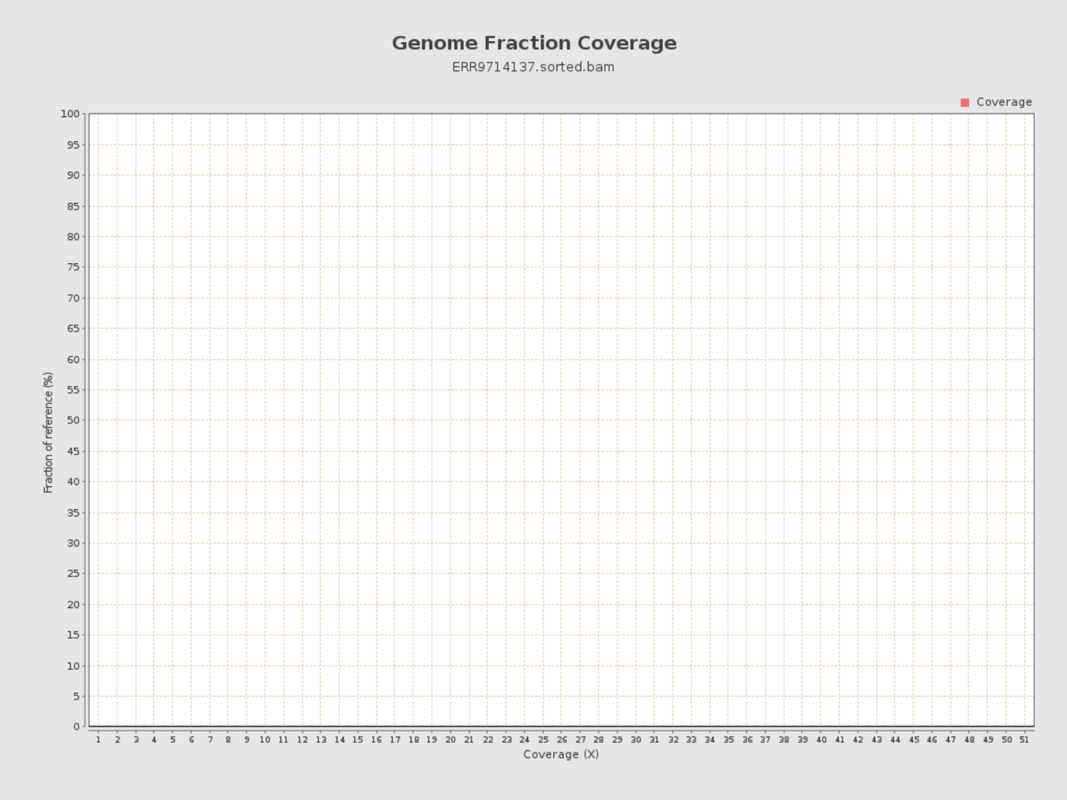
4. Results : Coverage Histogram



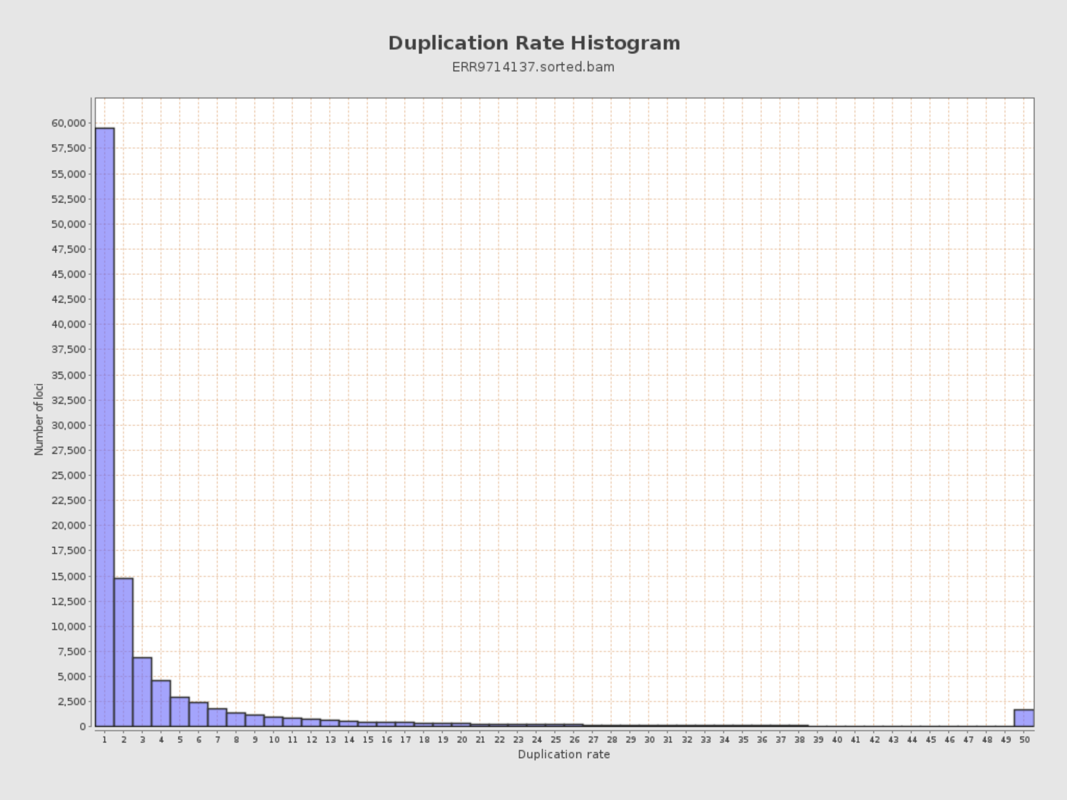
5. Results : Coverage Histogram (0-50X)



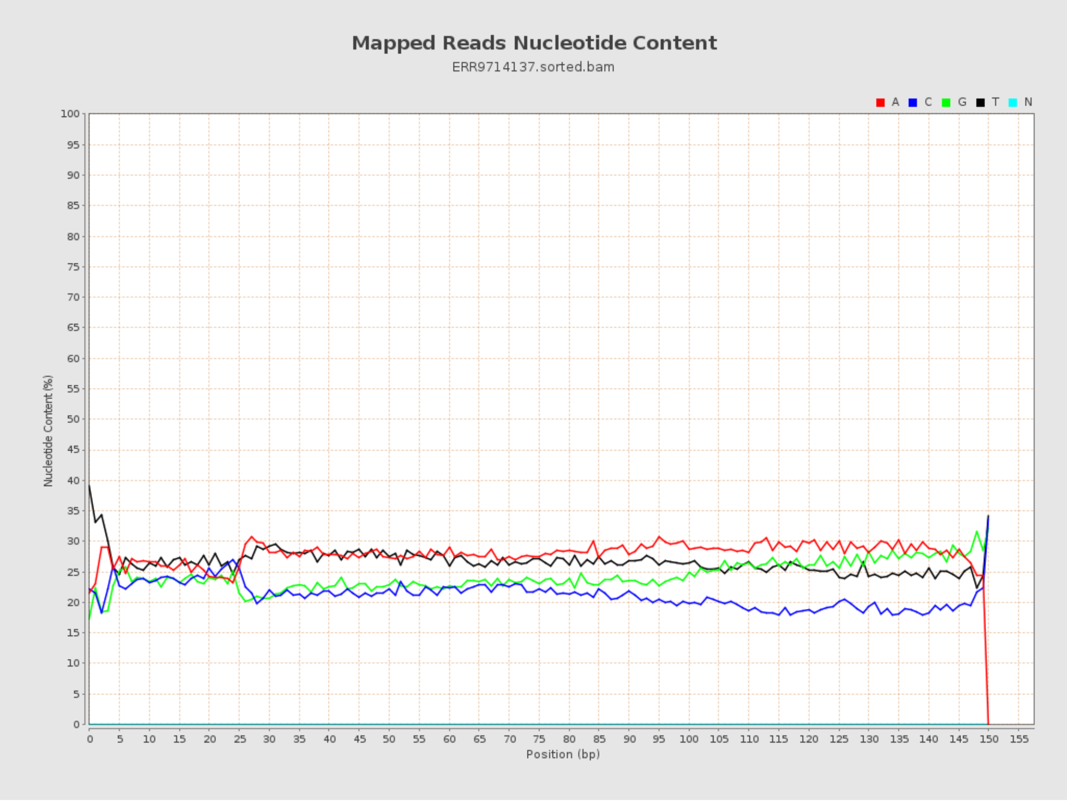
6. Results : Genome Fraction Coverage



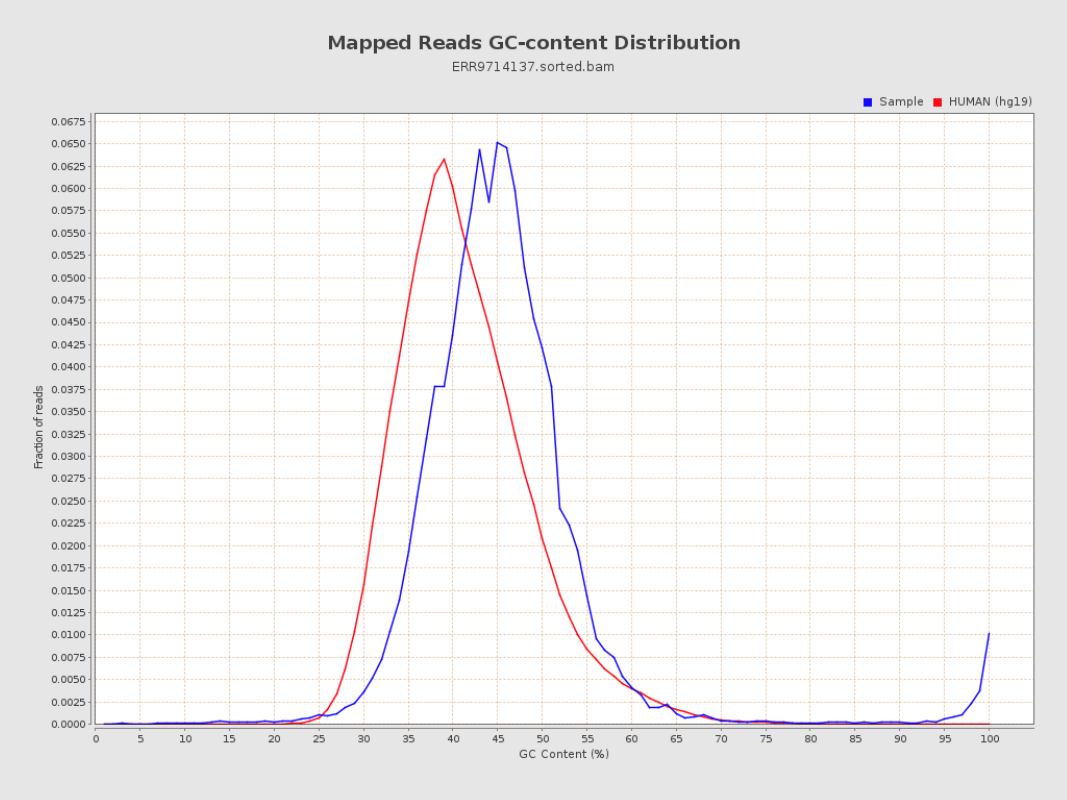
7. Results : Duplication Rate Histogram



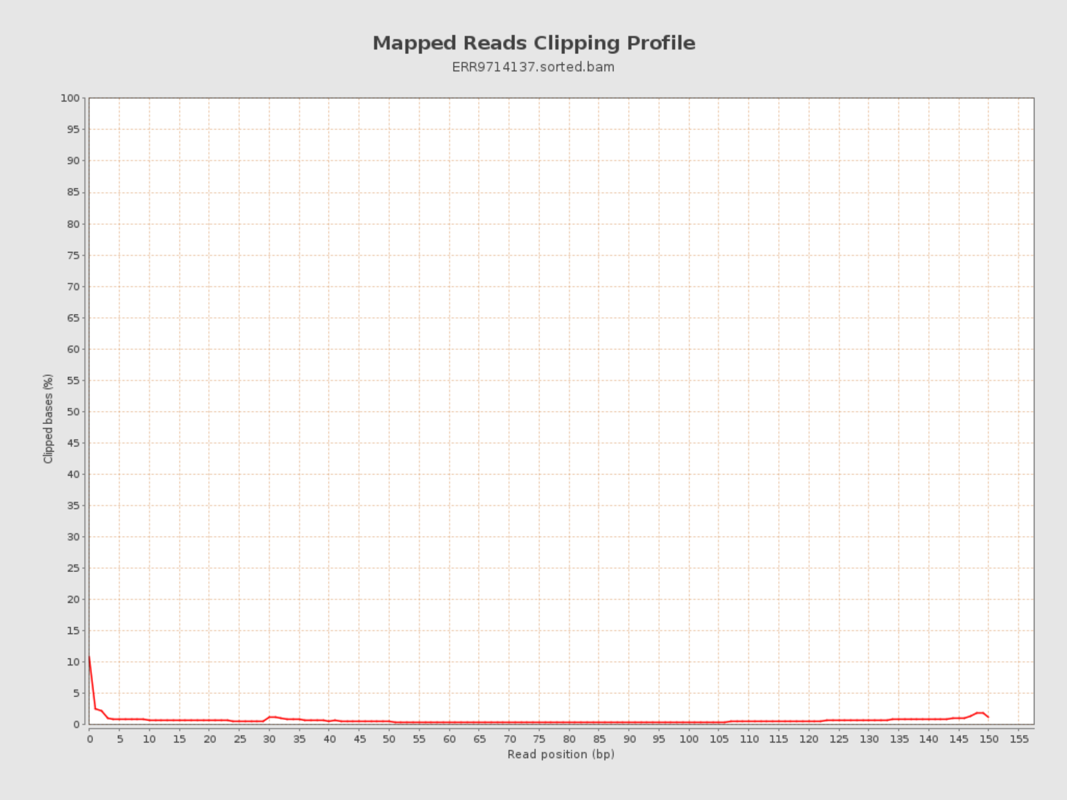
8. Results : Mapped Reads Nucleotide Content



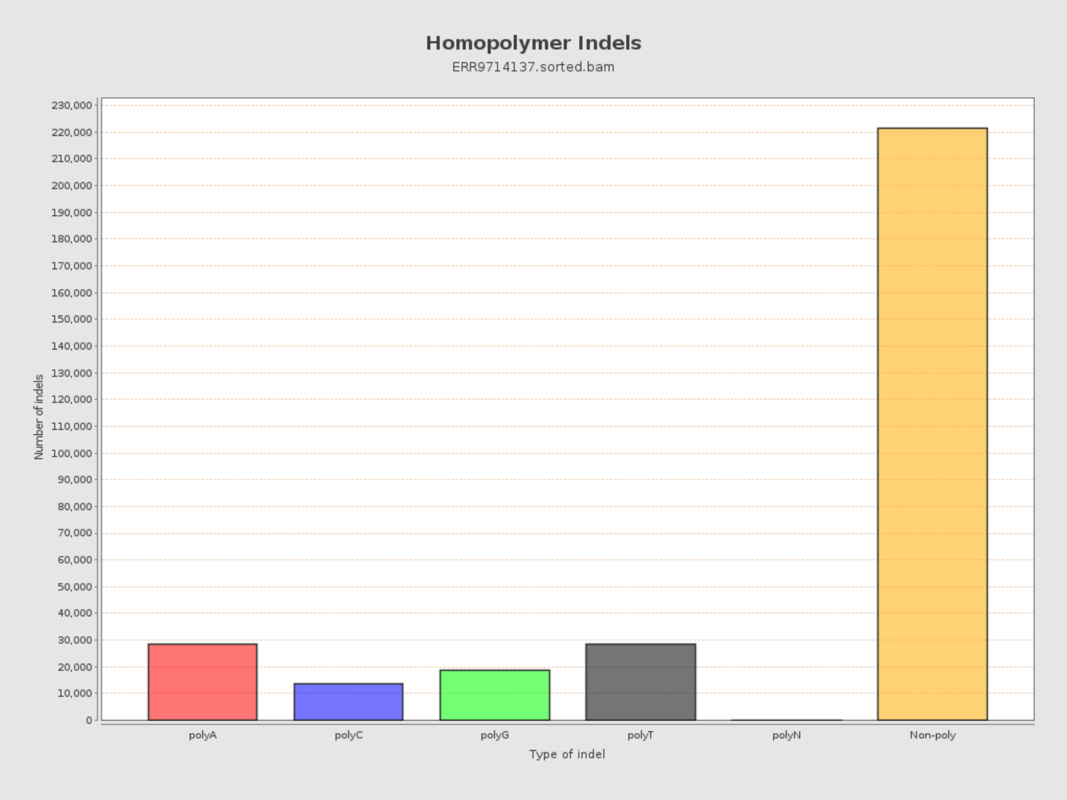
9. Results : Mapped Reads GC-content Distribution



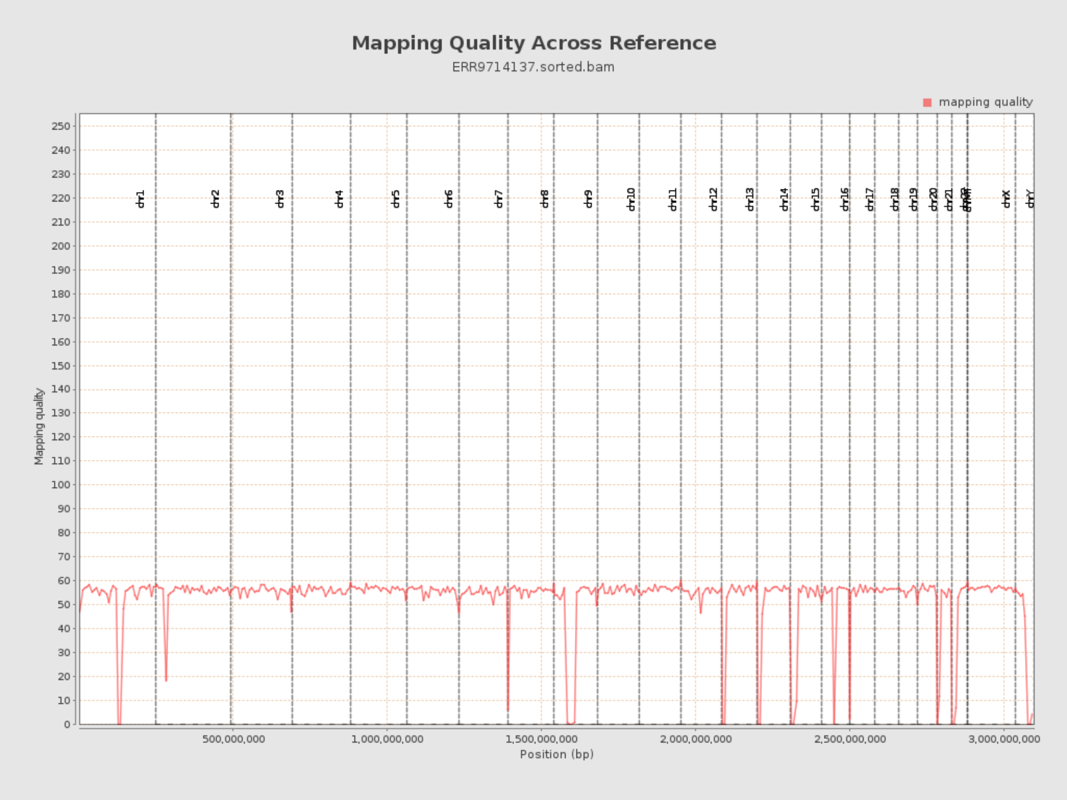
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram