Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 21:55:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714153.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_ERR9714153 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 21:55:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	756,664
Mapped reads	654,326 / 86.48%
Unmapped reads	102,338 / 13.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,935 / 2.63%
Read min/max/mean length	30 / 151 / 138.06
Duplicated reads (estimated)	591,464 / 78.17%
Duplication rate	43.78%
Clipped reads	620,840 / 82.05%

2.2. ACGT Content

Number/percentage of A's	22,410,372 / 26.87%
Number/percentage of C's	18,835,948 / 22.58%
Number/percentage of T's	21,217,080 / 25.44%
Number/percentage of G's	20,950,671 / 25.12%
Number/percentage of N's	587 / 0%
GC Percentage	47.7%

2.3. Coverage

Mean	0.0276

Standard Deviation	7.3543

2.4. Mapping Quality

Mean Mapping Quality	51.47

2.5. Mismatches and indels

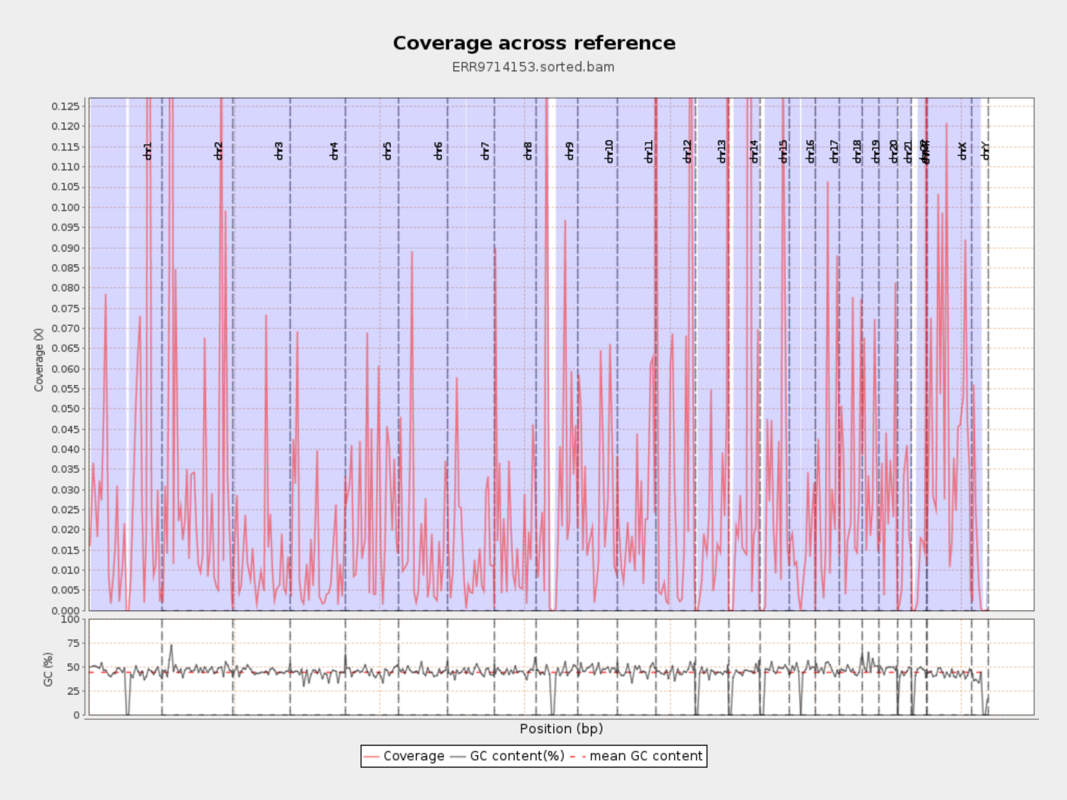
General error rate	4.41%
Mismatches	3,451,391
Insertions	88,000
Mapped reads with at least one insertion	13%
Deletions	304,359
Mapped reads with at least one deletion	44.15%
Homopolymer indels	29.91%

2.6. Chromosome stats

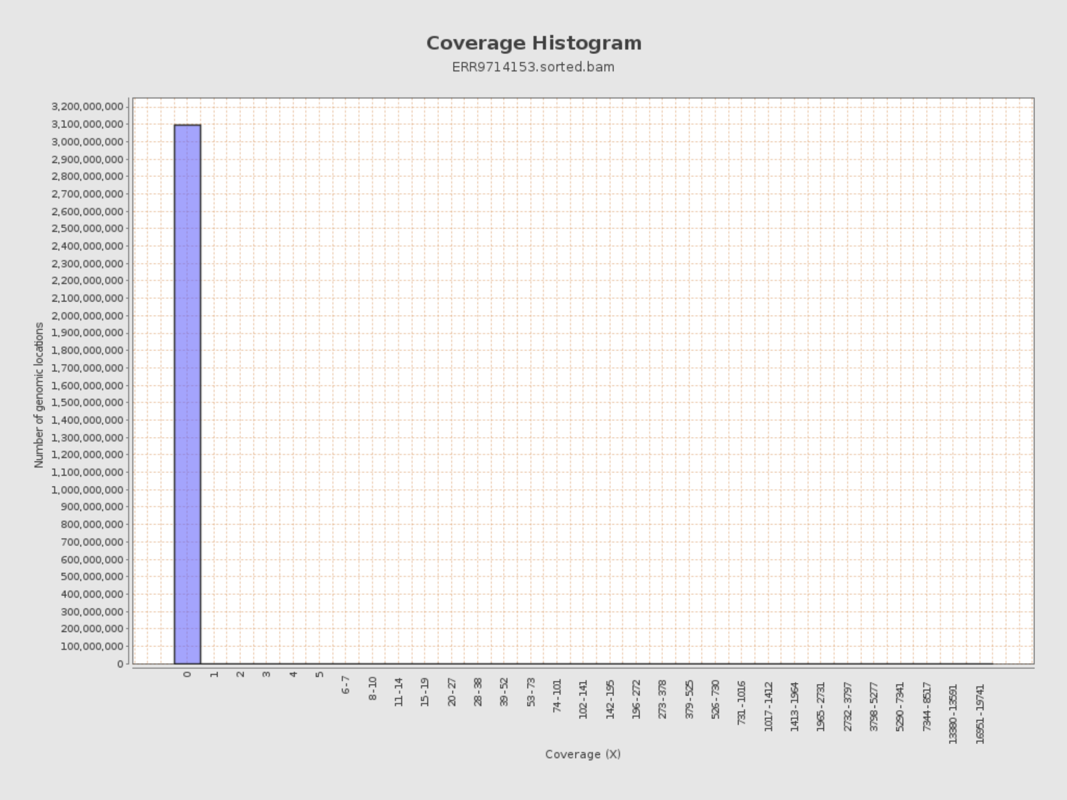
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7775143	0.0312	8.2292
chr2	243199373	10123044	0.0416	11.3445
chr3	198022430	2603703	0.0131	2.3664
chr4	191154276	2728885	0.0143	2.956
chr5	180915260	4589445	0.0254	4.5136
chr6	171115067	3152392	0.0184	3.4478
chr7	159138663	2390202	0.015	2.4297

chr8	146364022	3196530	0.0218	4.7123
chr9	141213431	4312191	0.0305	8.099
chr10	135534747	3890052	0.0287	4.4664
chr11	135006516	3730887	0.0276	4.7262
chr12	133851895	4766460	0.0356	9.3962
chr13	115169878	3036838	0.0264	8.0621
chr14	107349540	4838987	0.0451	22.3811
chr15	102531392	3363406	0.0328	6.1528
chr16	90354753	1390968	0.0154	2.0746
chr17	81195210	2968100	0.0366	6.3619
chr18	78077248	2506088	0.0321	6.9599
chr19	59128983	2065773	0.0349	3.703
chr20	63025520	2064145	0.0328	4.1224
chr21	48129895	848499	0.0176	3.4702
chr22	51304566	517049	0.0101	1.1411
chrMT	16571	152981	9.2319	77.3804
chrX	155270560	7645268	0.0492	5.1256
chrY	59373566	687345	0.0116	2.7909

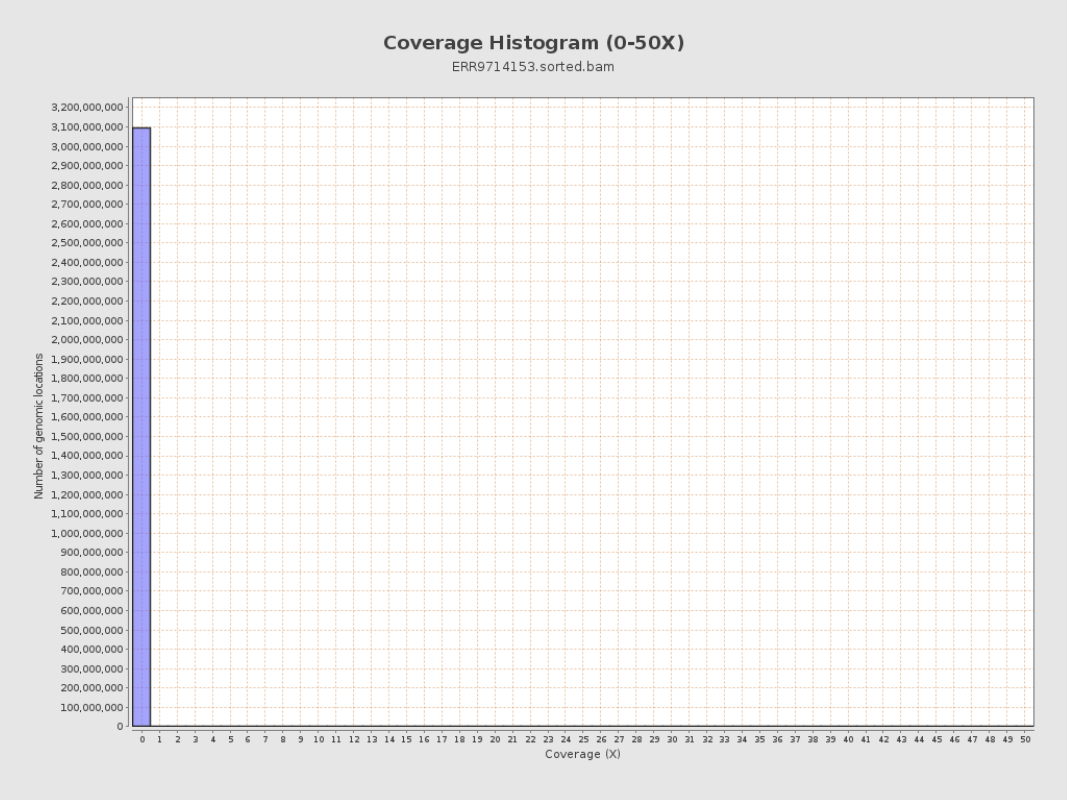
3. Results : Coverage across reference



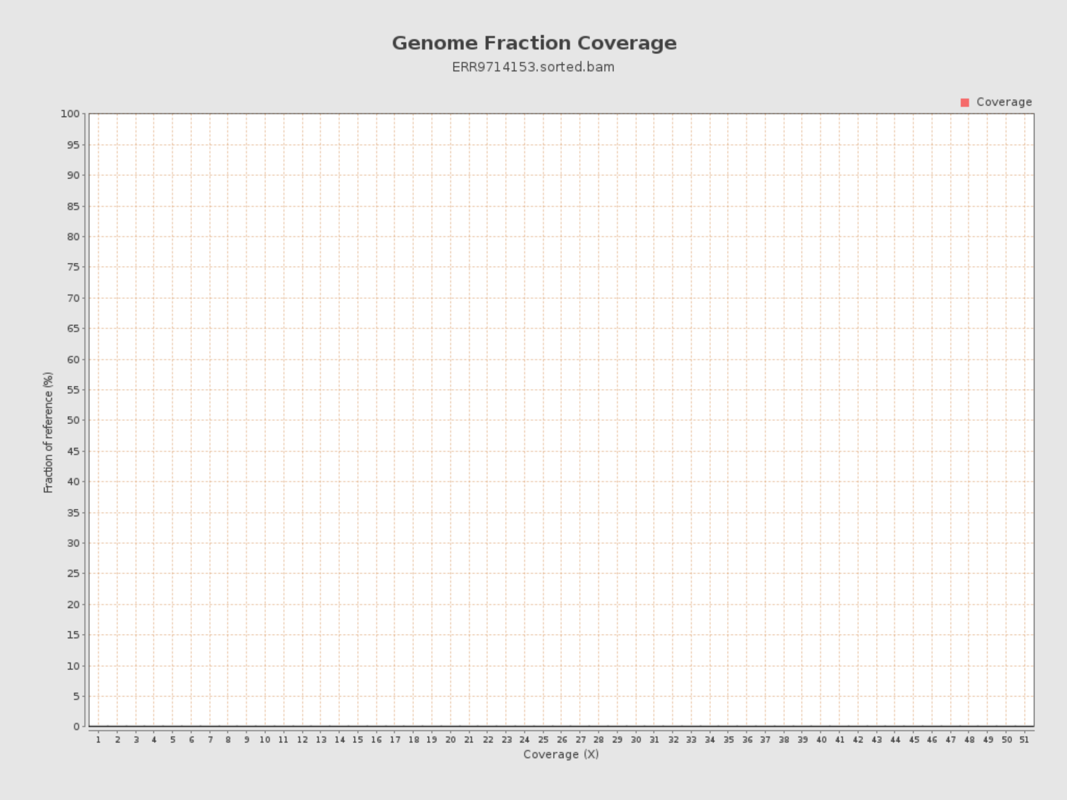
4. Results : Coverage Histogram



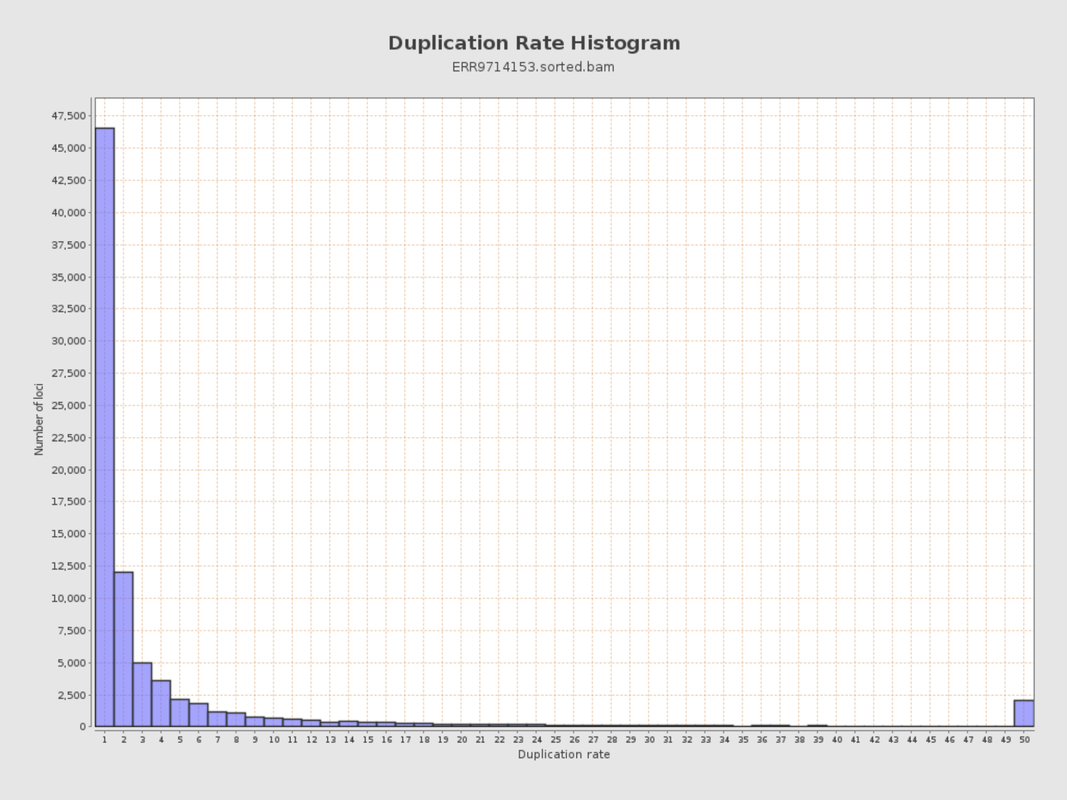
5. Results : Coverage Histogram (0-50X)



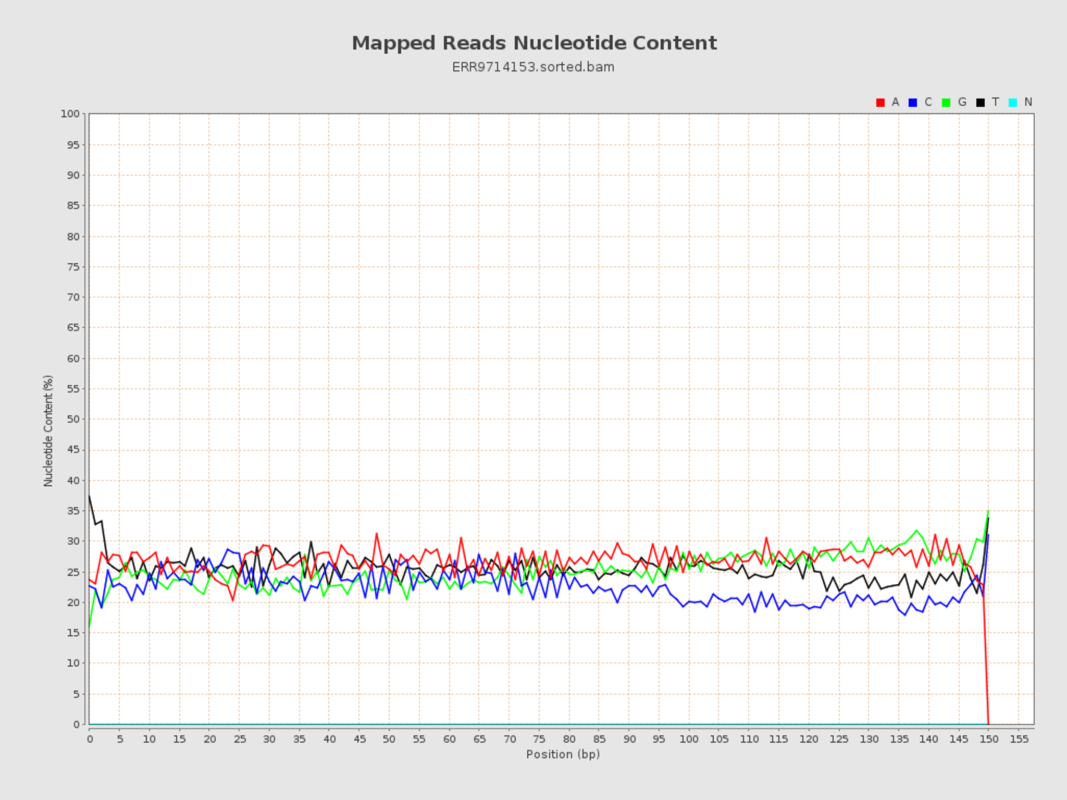
6. Results : Genome Fraction Coverage



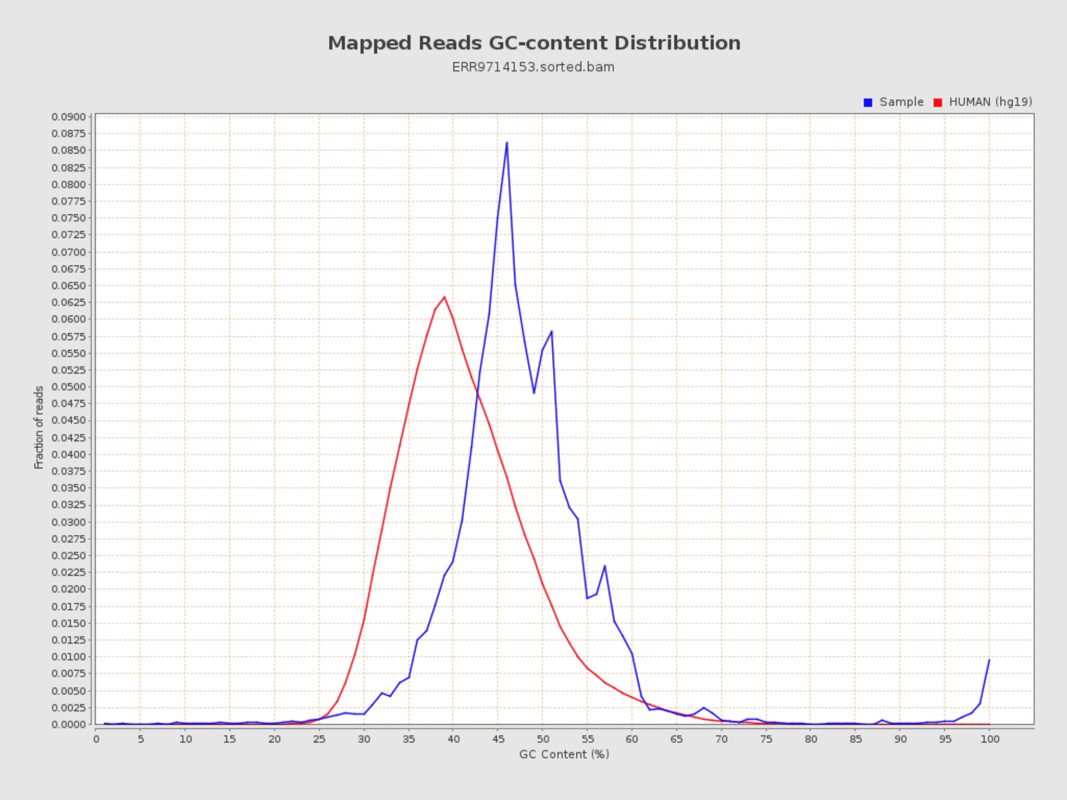
7. Results : Duplication Rate Histogram



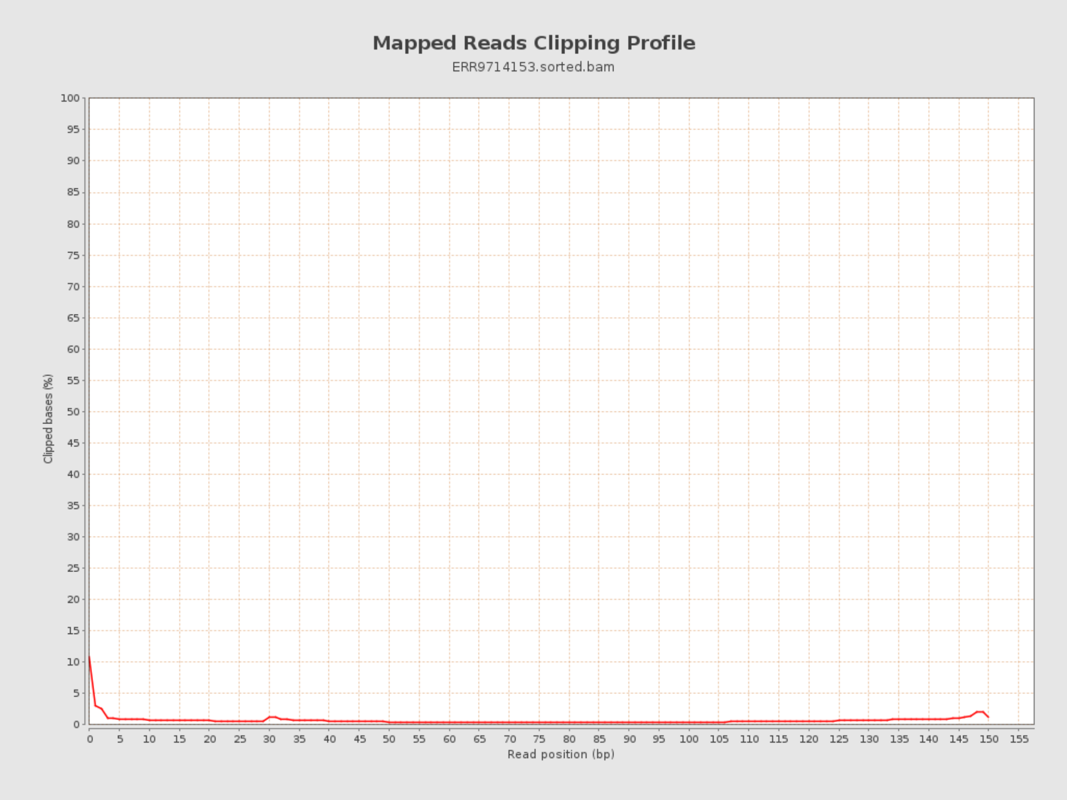
8. Results : Mapped Reads Nucleotide Content



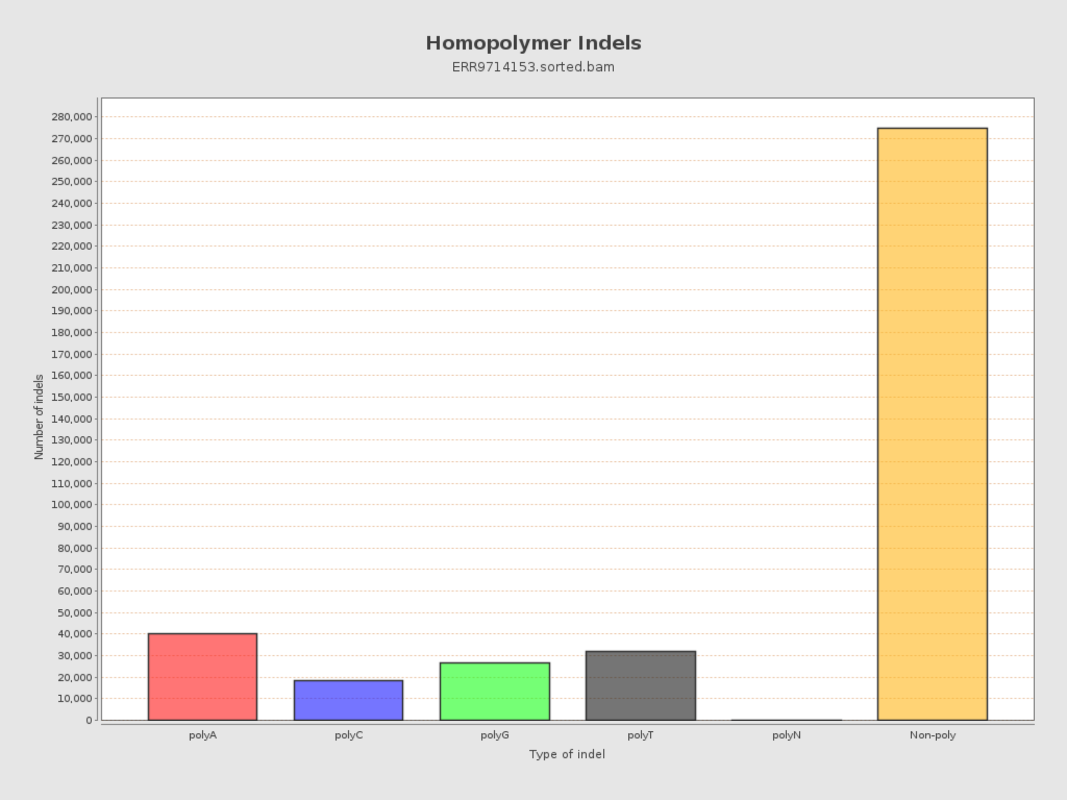
9. Results : Mapped Reads GC-content Distribution



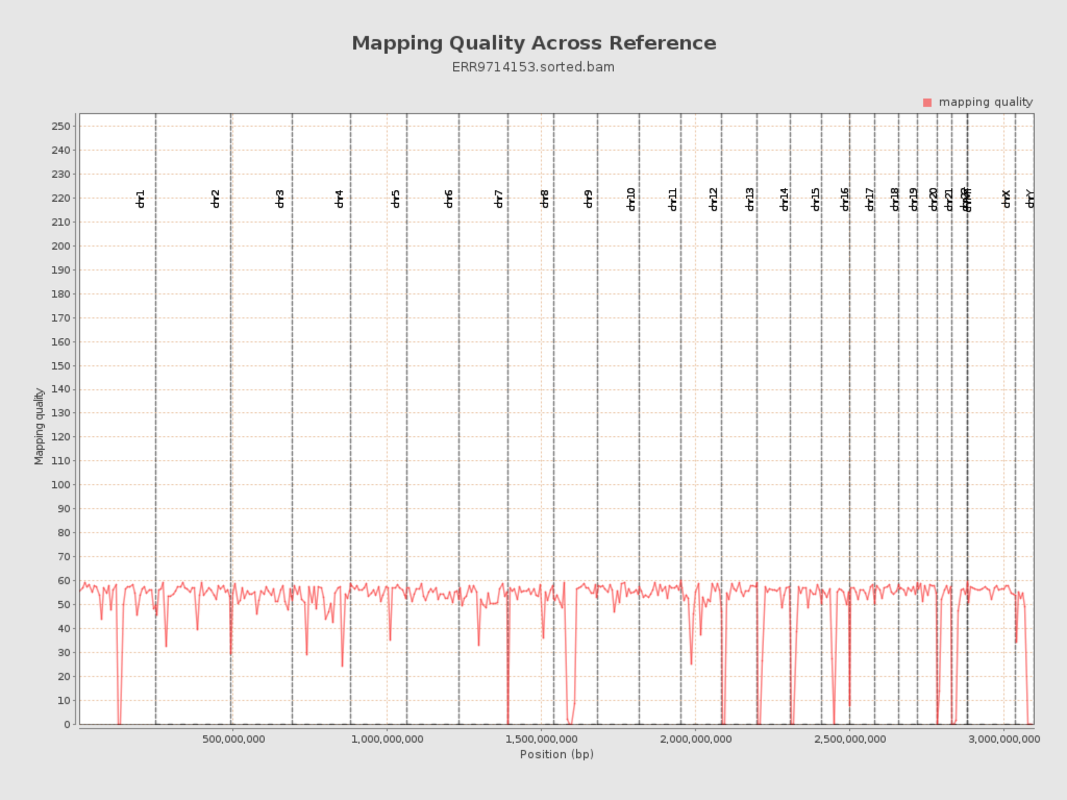
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram