Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:30:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714253.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_ERR9714253 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:30:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	260,022
Mapped reads	93,903 / 36.11%
Unmapped reads	166,119 / 63.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,700 / 1.04%
Read min/max/mean length	30 / 151 / 114.88
Duplicated reads (estimated)	67,518 / 25.97%
Duplication rate	39.9%
Clipped reads	86,584 / 33.3%

2.2. ACGT Content

Number/percentage of A's	3,264,820 / 27.63%
Number/percentage of C's	2,385,006 / 20.19%
Number/percentage of T's	3,098,005 / 26.22%
Number/percentage of G's	3,066,476 / 25.96%
Number/percentage of N's	103 / 0%
GC Percentage	46.14%

2.3. Coverage

Mean	0.0039

Standard Deviation	0.9972

2.4. Mapping Quality

Mean Mapping Quality	51.38

2.5. Mismatches and indels

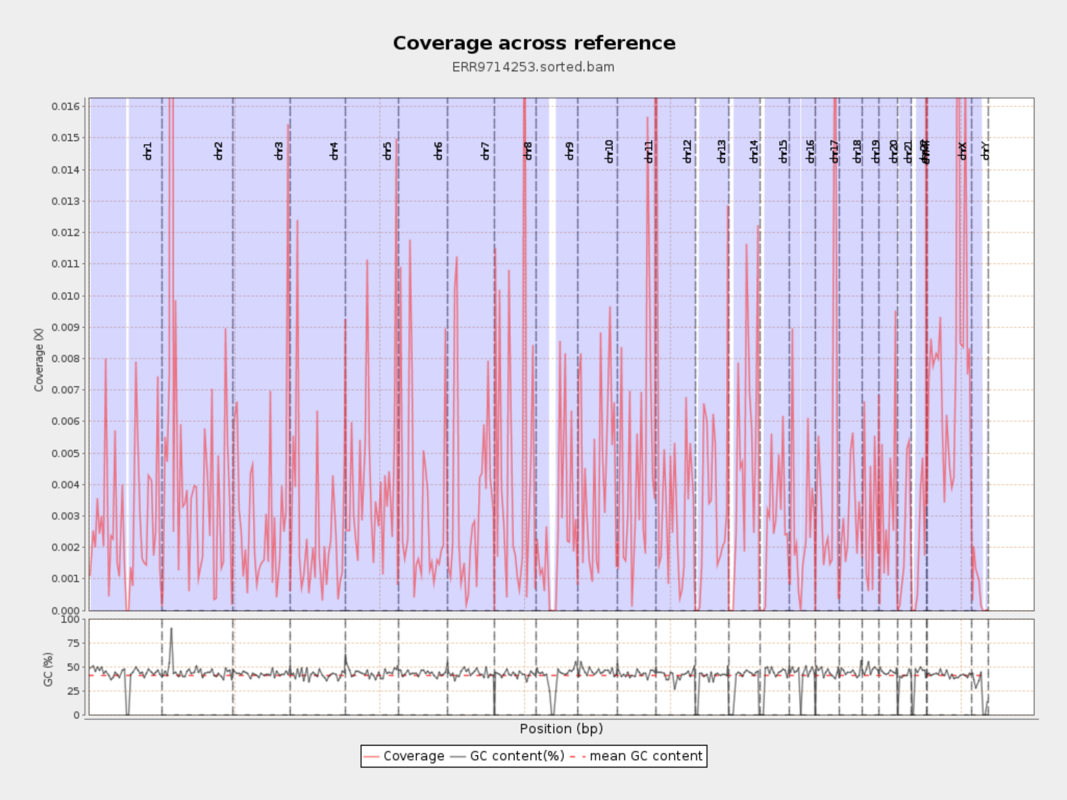
General error rate	4.9%
Mismatches	541,502
Insertions	13,424
Mapped reads with at least one insertion	13.57%
Deletions	47,558
Mapped reads with at least one deletion	46.79%
Homopolymer indels	30.76%

2.6. Chromosome stats

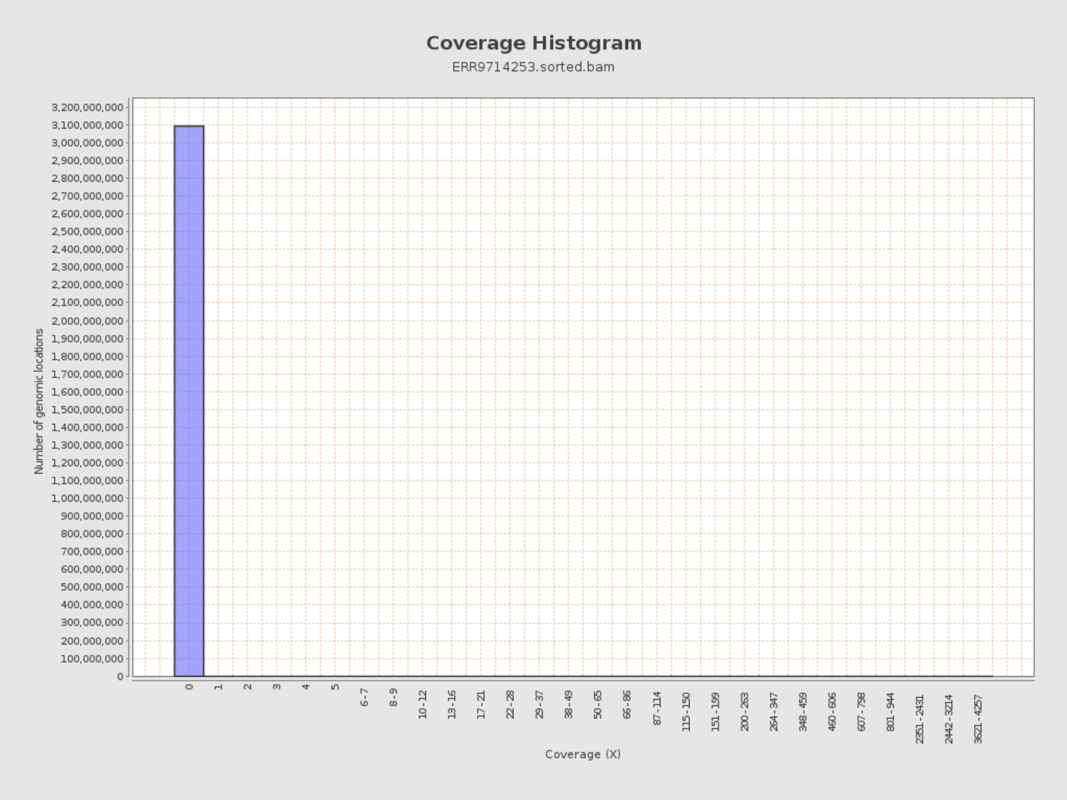
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	679505	0.0027	0.4063
chr2	243199373	1591139	0.0065	2.7114
chr3	198022430	626990	0.0032	0.6403
chr4	191154276	485696	0.0025	0.4184
chr5	180915260	768941	0.0043	0.7389
chr6	171115067	588862	0.0034	0.67
chr7	159138663	561618	0.0035	0.563

chr8	146364022	744079	0.0051	1.2054
chr9	141213431	351247	0.0025	0.4569
chr10	135534747	621027	0.0046	0.6189
chr11	135006516	653255	0.0048	0.9752
chr12	133851895	485276	0.0036	0.6224
chr13	115169878	359026	0.0031	0.4868
chr14	107349540	511776	0.0048	0.7602
chr15	102531392	283867	0.0028	0.2949
chr16	90354753	254741	0.0028	0.4537
chr17	81195210	373626	0.0046	1.259
chr18	78077248	233797	0.003	0.3817
chr19	59128983	181781	0.0031	0.4466
chr20	63025520	213970	0.0034	0.5135
chr21	48129895	107187	0.0022	0.3523
chr22	51304566	93899	0.0018	0.2287
chrMT	16571	32318	1.9503	13.7992
chrX	155270560	1281814	0.0083	0.9368
chrY	59373566	36505	0.0006	0.0998

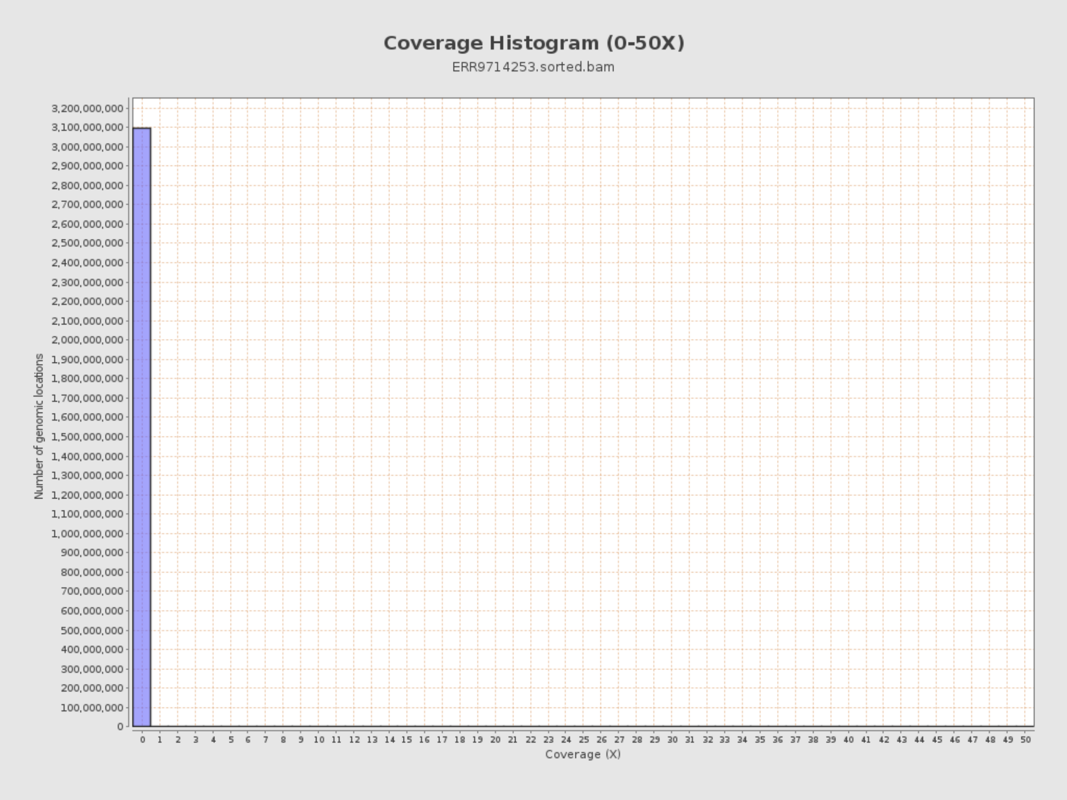
3. Results : Coverage across reference



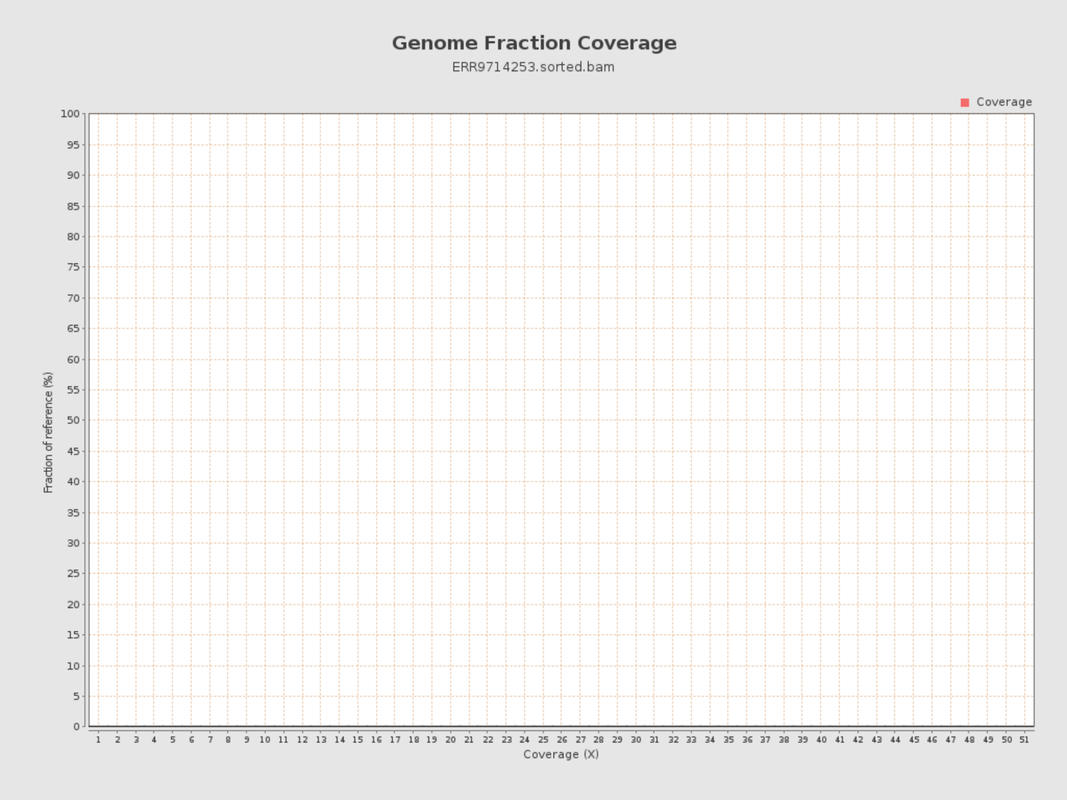
4. Results : Coverage Histogram



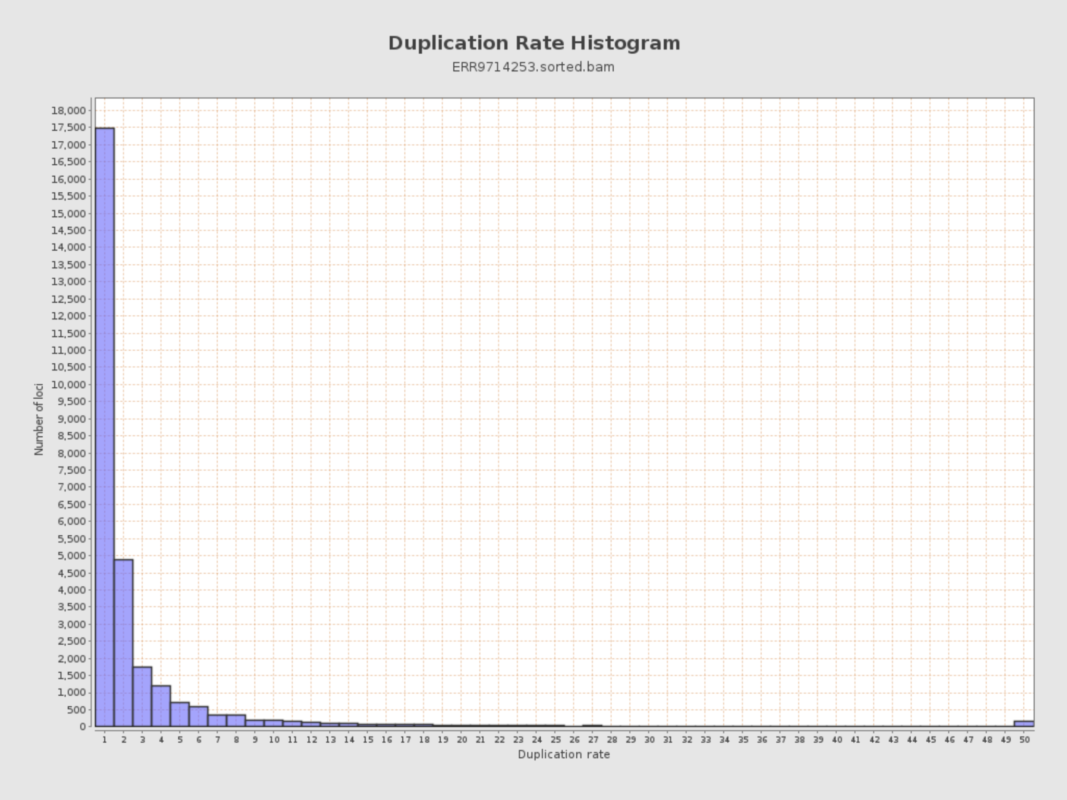
5. Results : Coverage Histogram (0-50X)



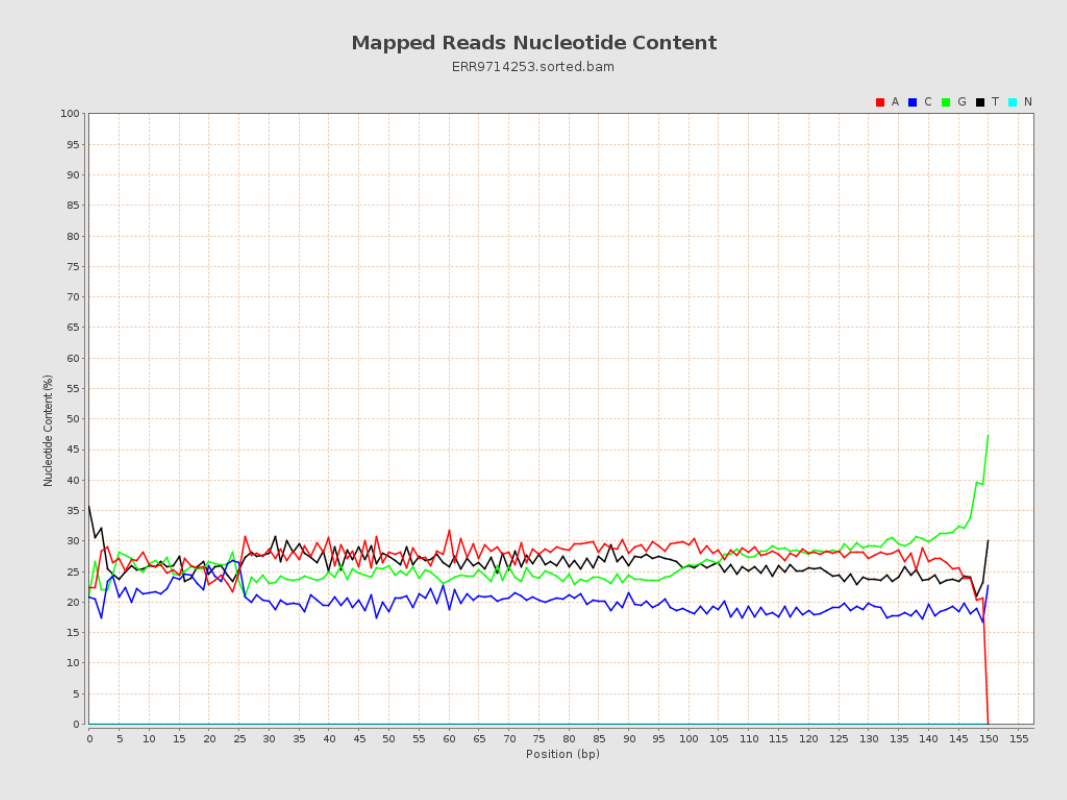
6. Results : Genome Fraction Coverage



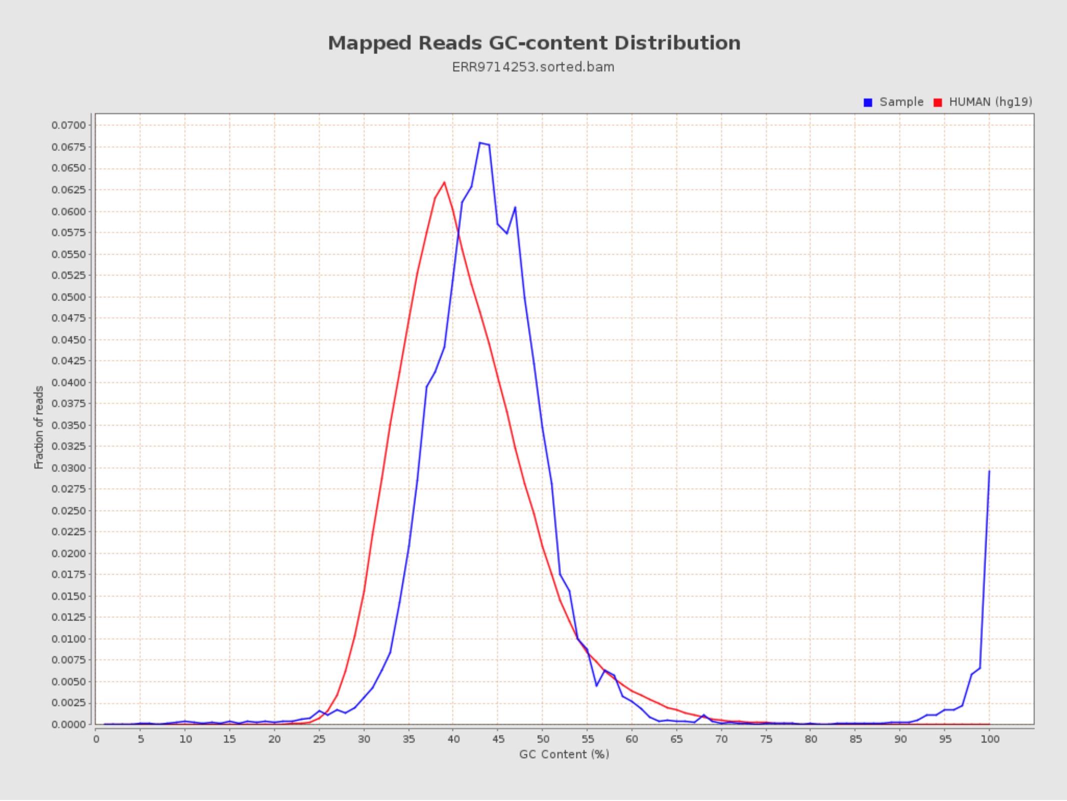
7. Results : Duplication Rate Histogram



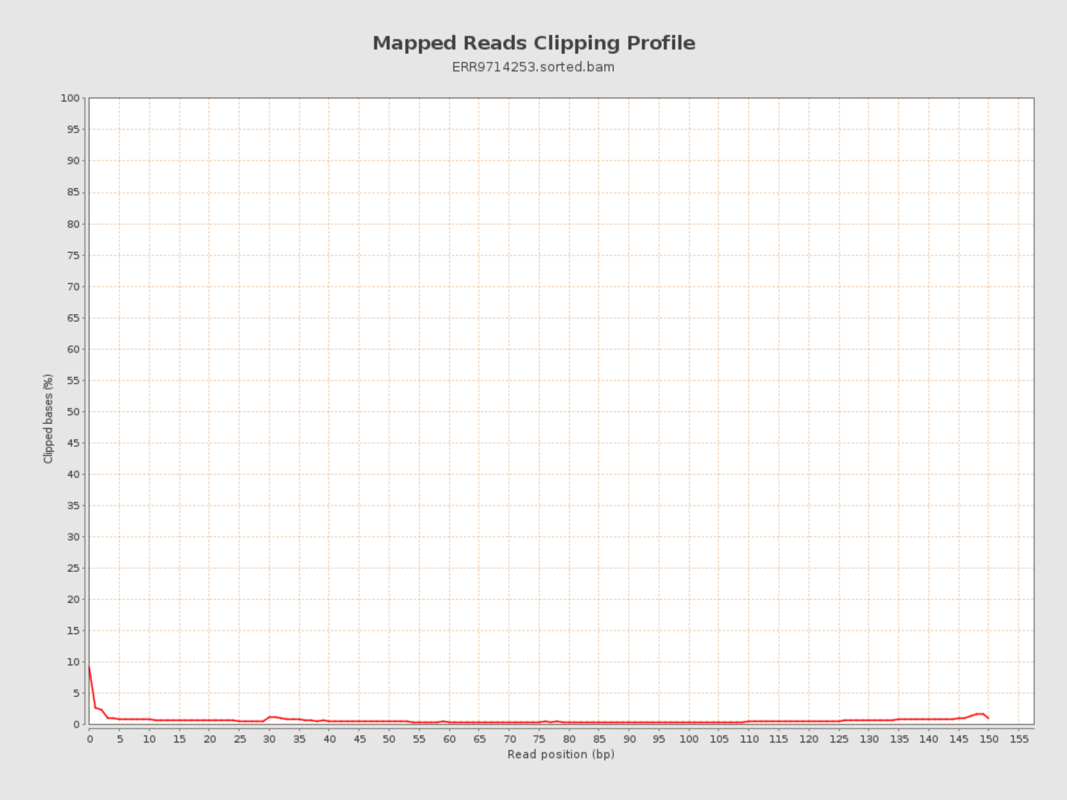
8. Results : Mapped Reads Nucleotide Content



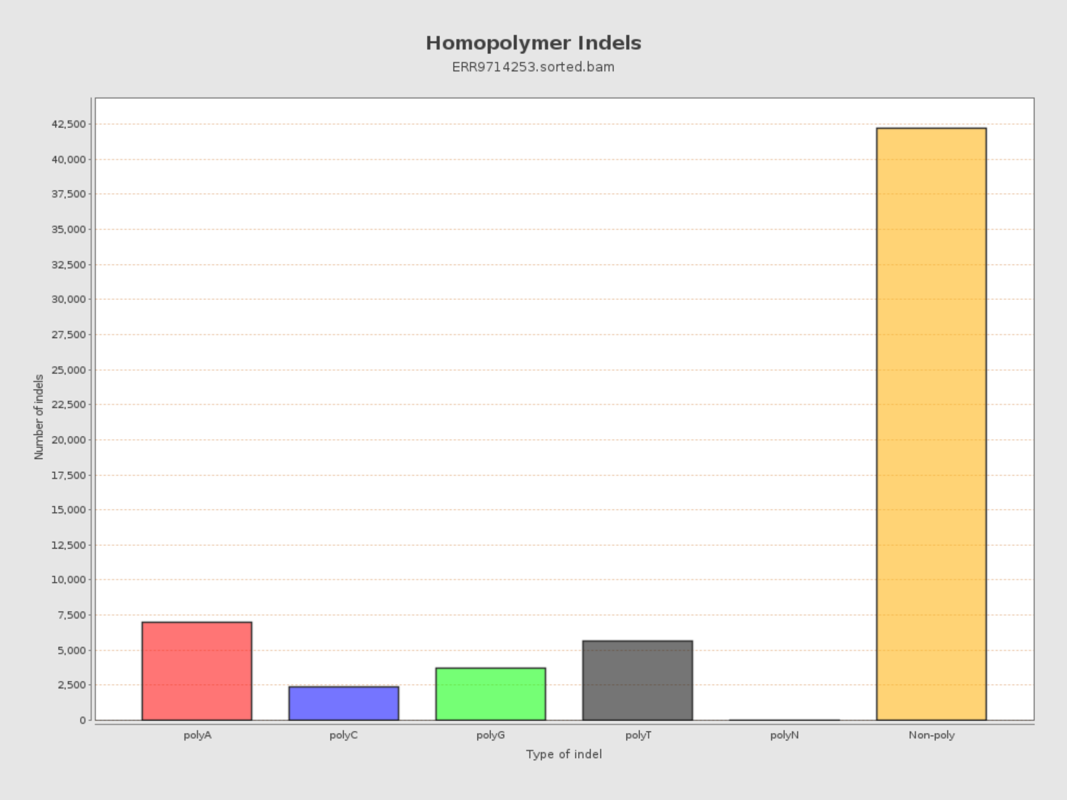
9. Results : Mapped Reads GC-content Distribution



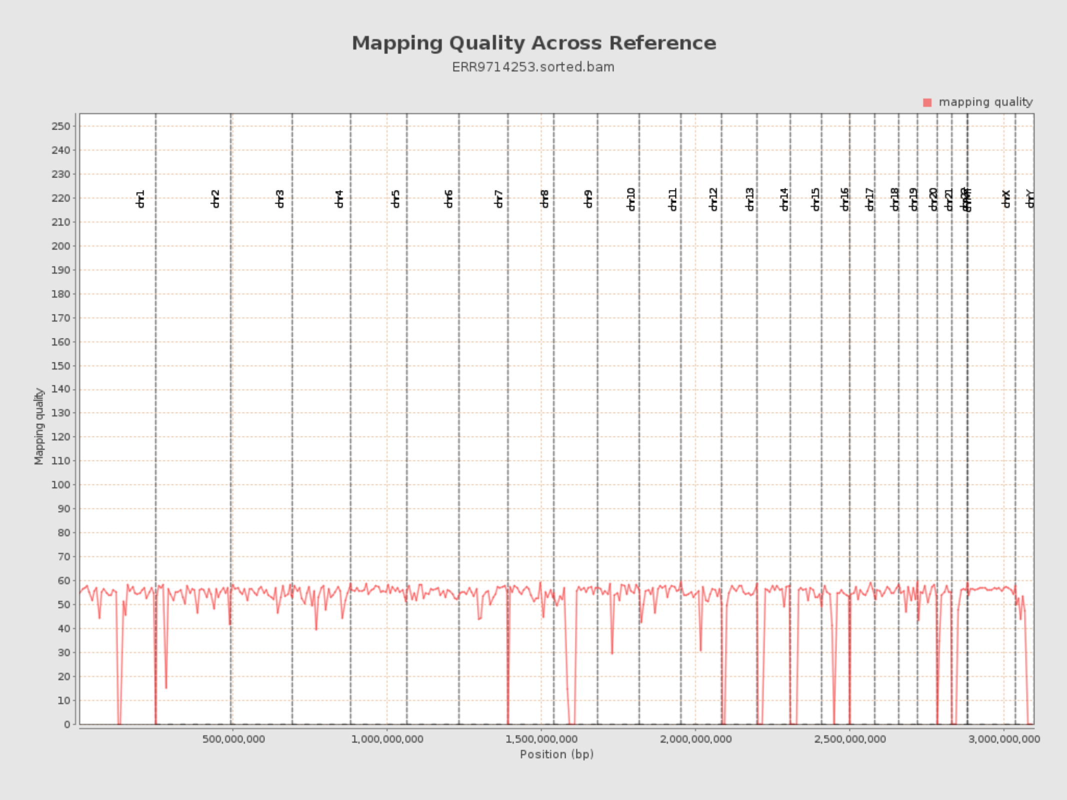
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram