Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:00:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714175.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_ERR9714175 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:00:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,163,788
Mapped reads	906,810 / 77.92%
Unmapped reads	256,978 / 22.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,812 / 2.73%
Read min/max/mean length	30 / 151 / 128.5
Duplicated reads (estimated)	792,453 / 68.09%
Duplication rate	44.08%
Clipped reads	849,529 / 73%

2.2. ACGT Content

Number/percentage of A's	33,653,610 / 28.99%
Number/percentage of C's	23,437,872 / 20.19%
Number/percentage of T's	32,067,328 / 27.63%
Number/percentage of G's	26,913,066 / 23.19%
Number/percentage of N's	981 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0382

Standard Deviation	5.7403

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Mismatches and indels

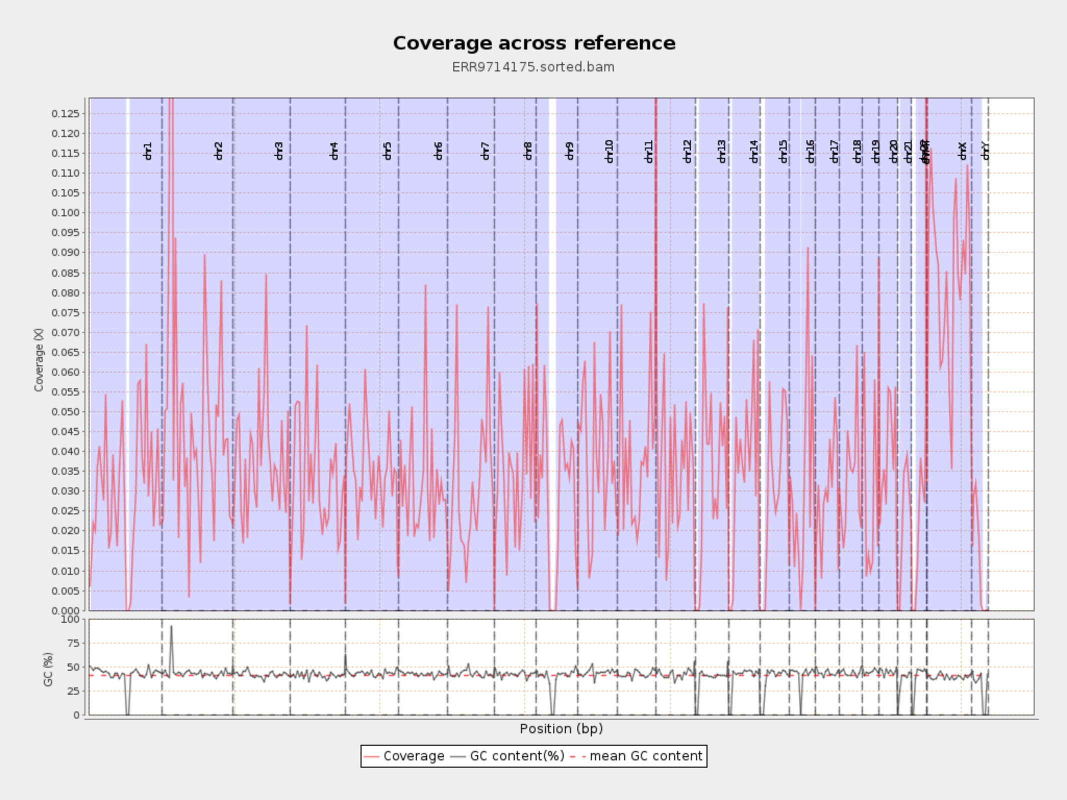
General error rate	3.98%
Mismatches	4,234,965
Insertions	123,189
Mapped reads with at least one insertion	13.19%
Deletions	353,664
Mapped reads with at least one deletion	37.3%
Homopolymer indels	29.75%

2.6. Chromosome stats

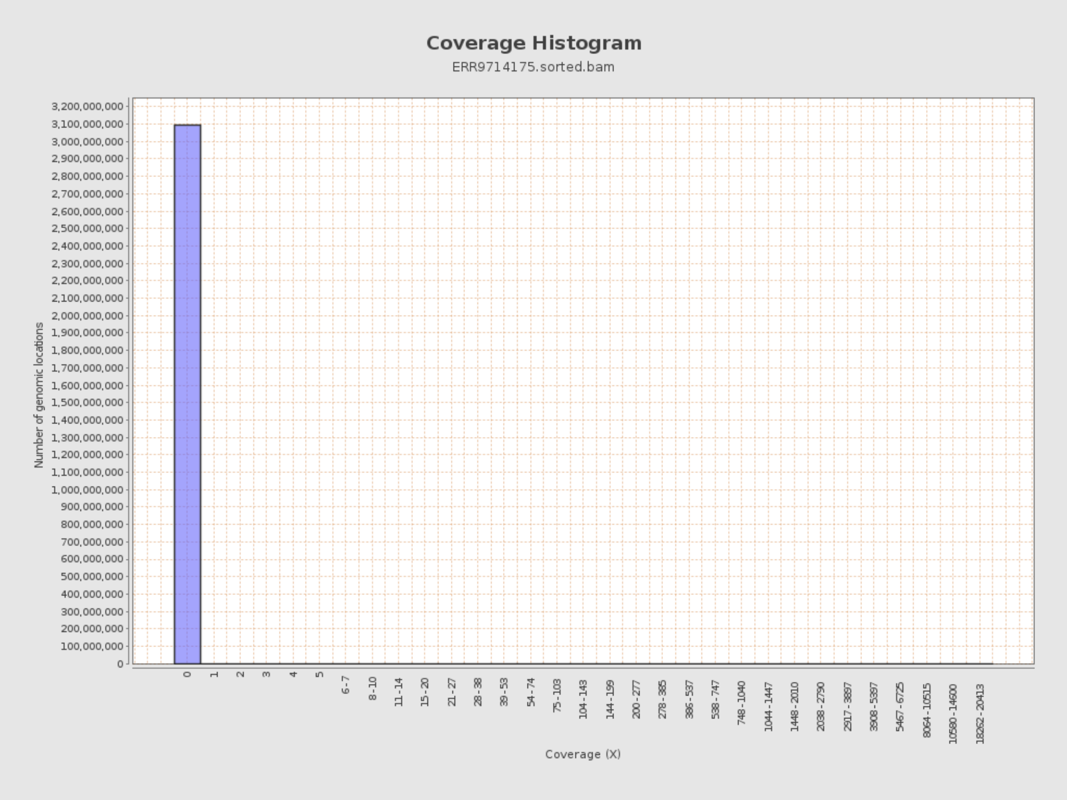
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7518157	0.0302	2.6614
chr2	243199373	13304928	0.0547	10.5397
chr3	198022430	7488096	0.0378	3.2546
chr4	191154276	6366414	0.0333	3.3334
chr5	180915260	6408450	0.0354	3.0217
chr6	171115067	5403601	0.0316	2.4802
chr7	159138663	5073802	0.0319	2.7181

chr8	146364022	5246262	0.0358	3.193
chr9	141213431	4097426	0.029	2.7465
chr10	135534747	5529234	0.0408	3.8123
chr11	135006516	5075484	0.0376	3.0869
chr12	133851895	4643509	0.0347	3.2459
chr13	115169878	3833063	0.0333	3.2492
chr14	107349540	3890617	0.0362	3.5576
chr15	102531392	3133148	0.0306	2.6571
chr16	90354753	2821308	0.0312	2.7132
chr17	81195210	2448762	0.0302	2.779
chr18	78077248	2573276	0.033	2.5345
chr19	59128983	1736209	0.0294	3.6681
chr20	63025520	2459039	0.039	3.3241
chr21	48129895	1041890	0.0216	1.983
chr22	51304566	944609	0.0184	1.7541
chrMT	16571	3555766	214.5776	1,697.7179
chrX	155270560	12865801	0.0829	3.8649
chrY	59373566	708732	0.0119	1.4791

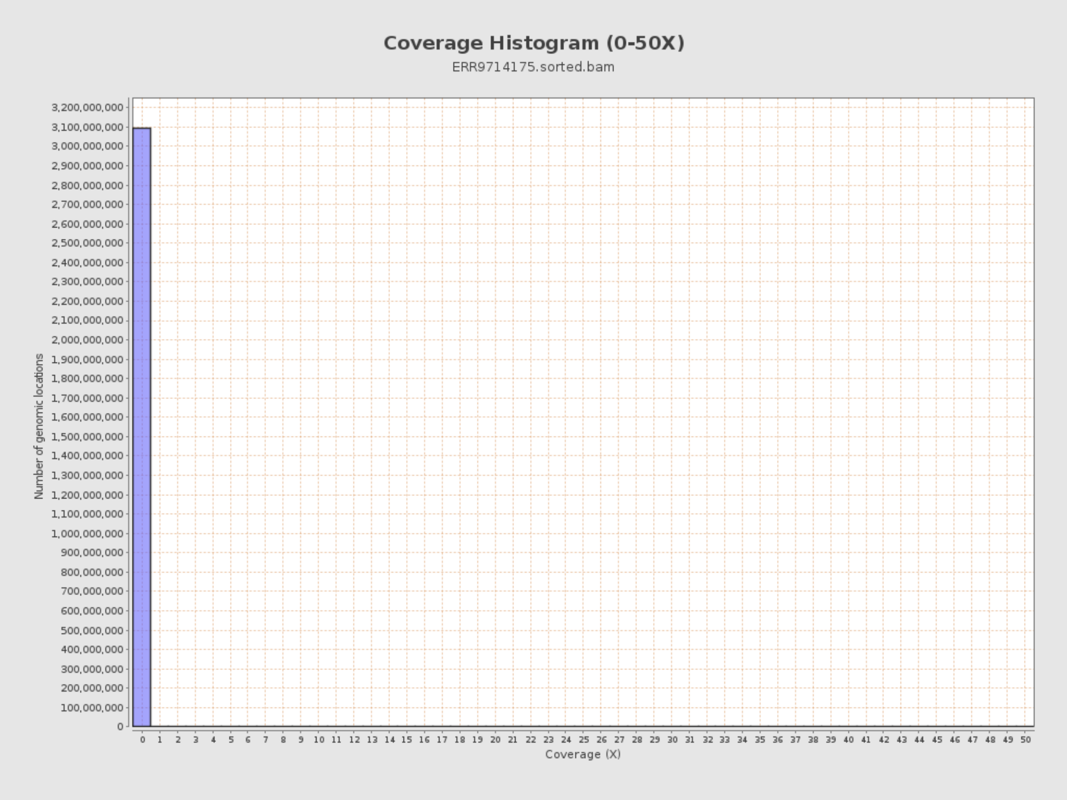
3. Results : Coverage across reference



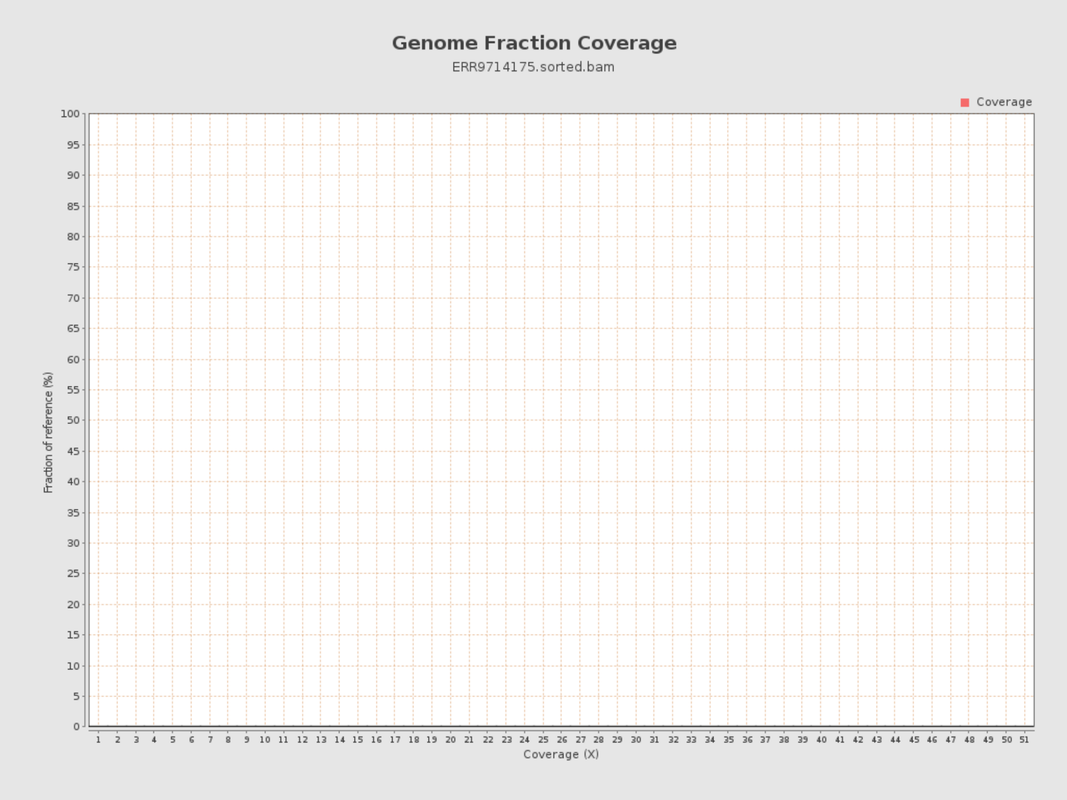
4. Results : Coverage Histogram



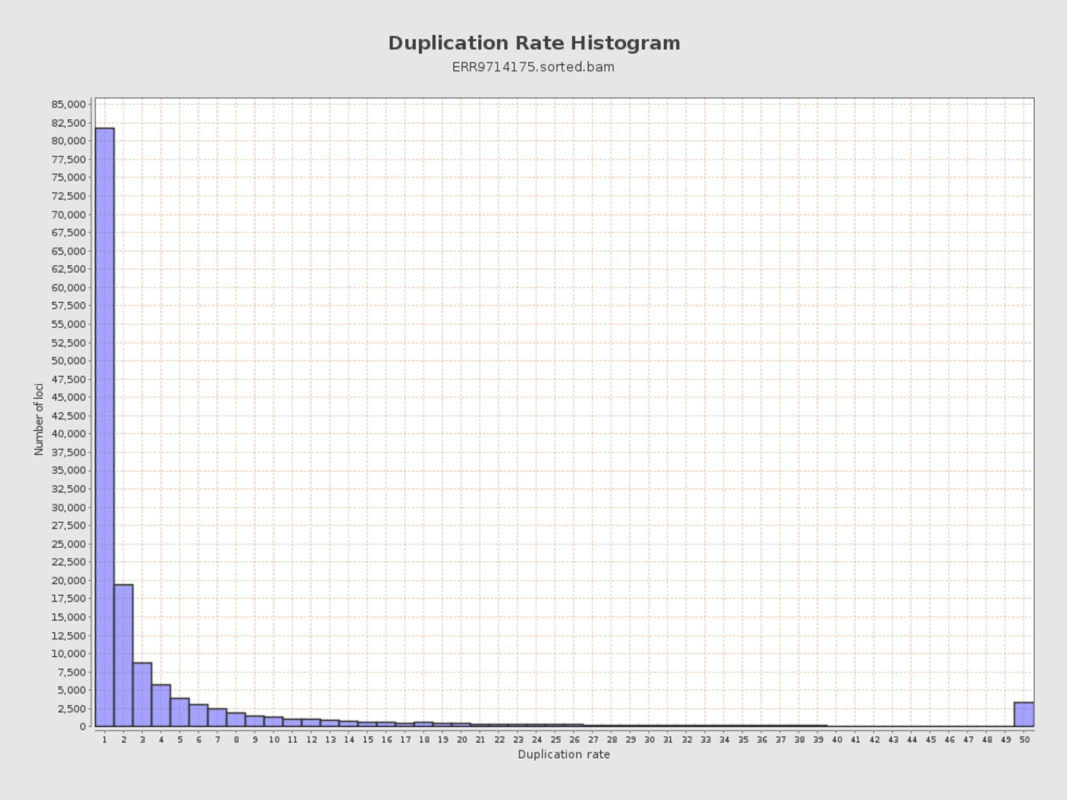
5. Results : Coverage Histogram (0-50X)



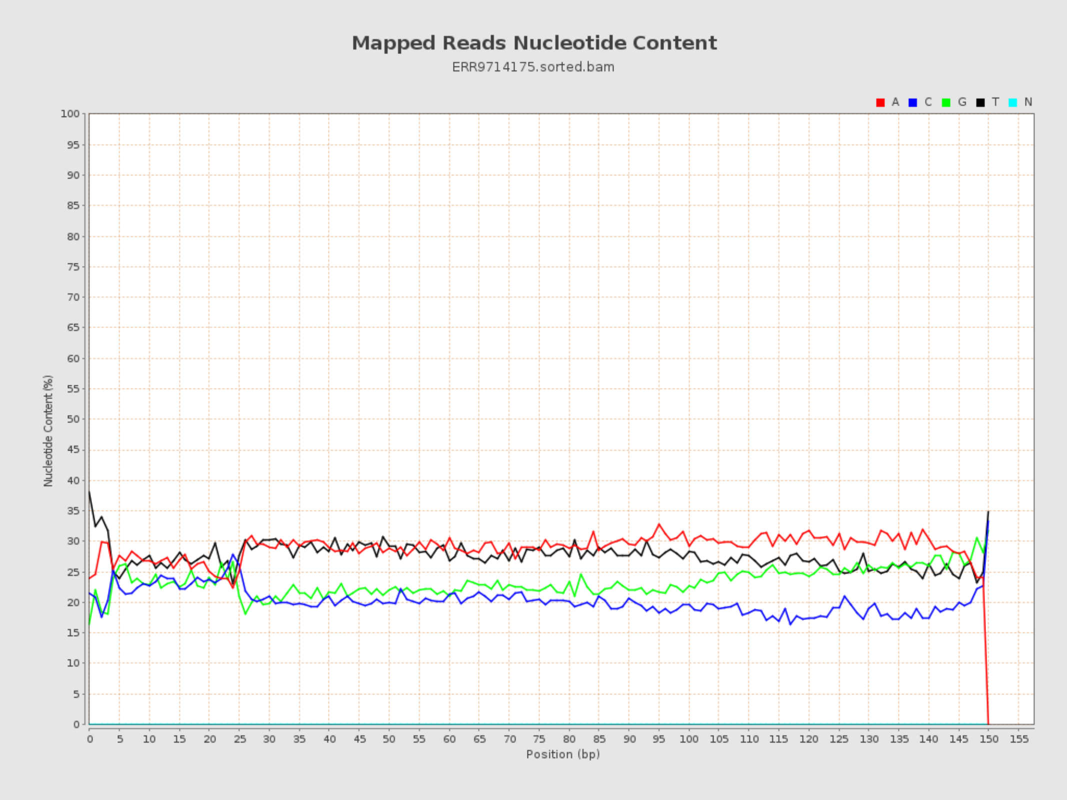
6. Results : Genome Fraction Coverage



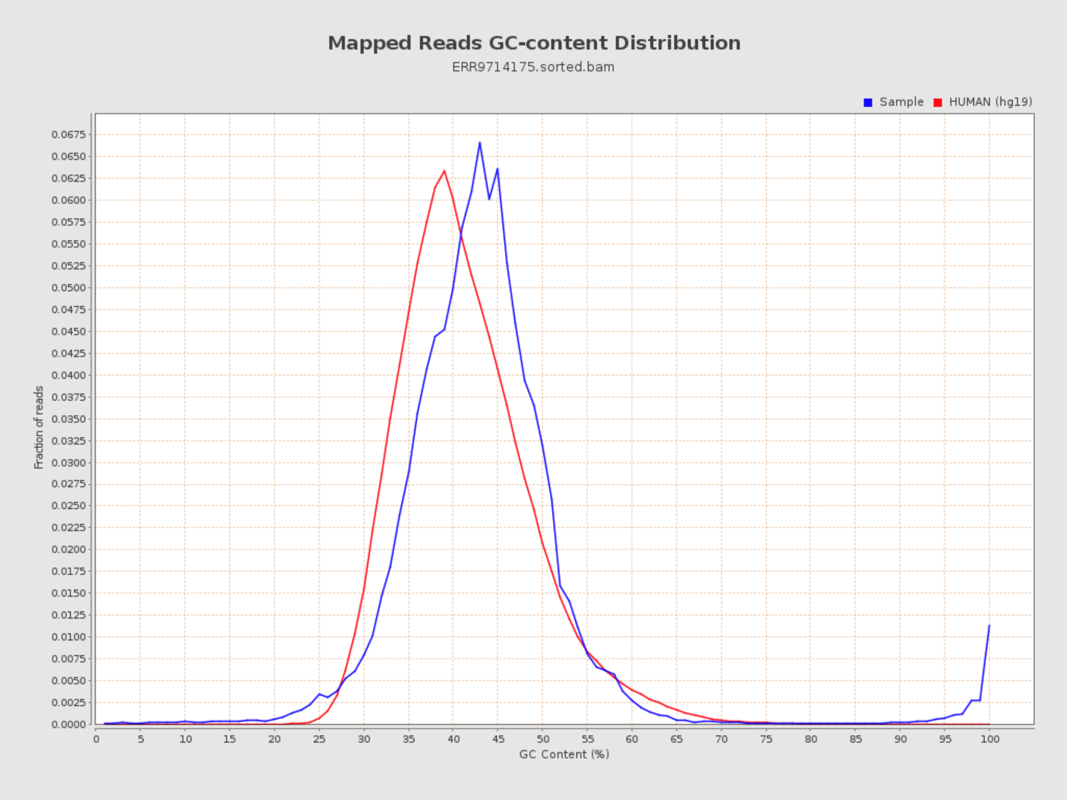
7. Results : Duplication Rate Histogram



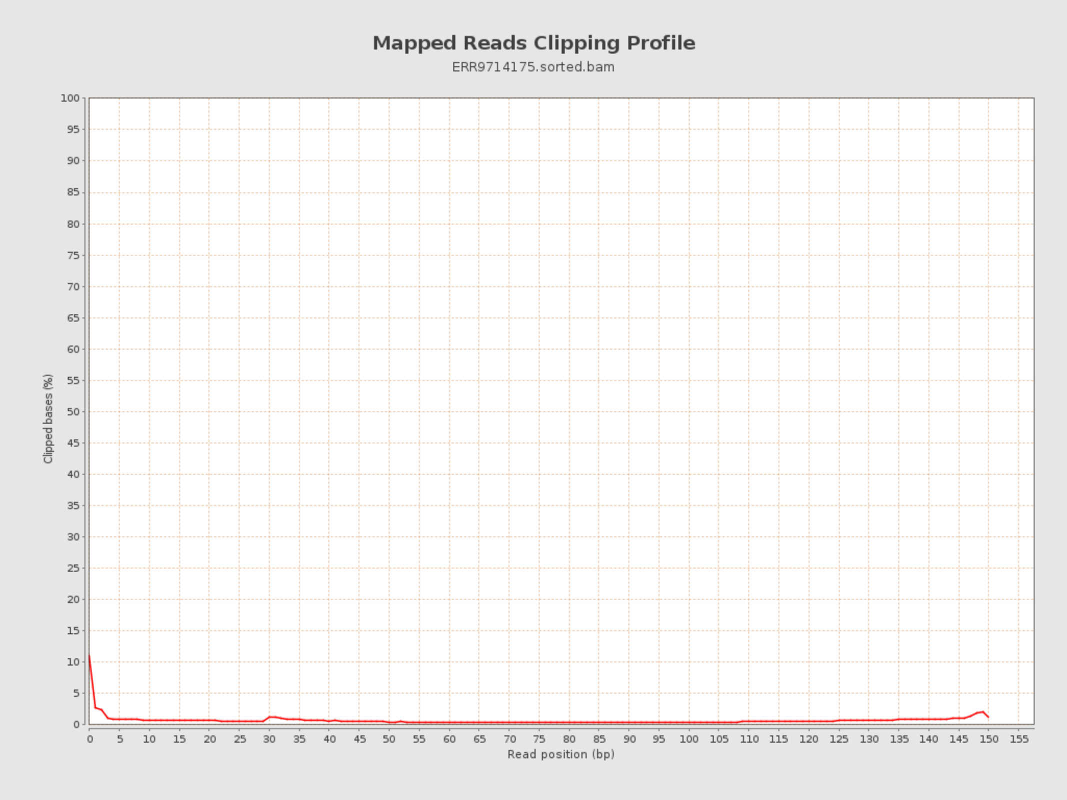
8. Results : Mapped Reads Nucleotide Content



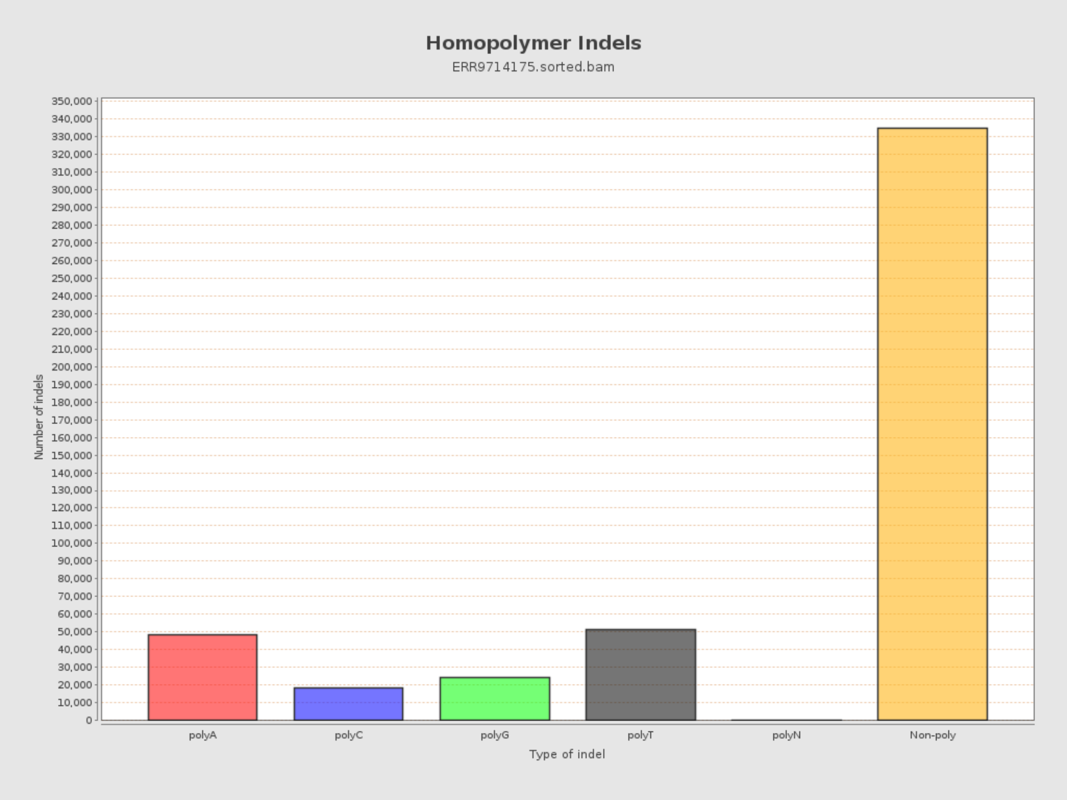
9. Results : Mapped Reads GC-content Distribution



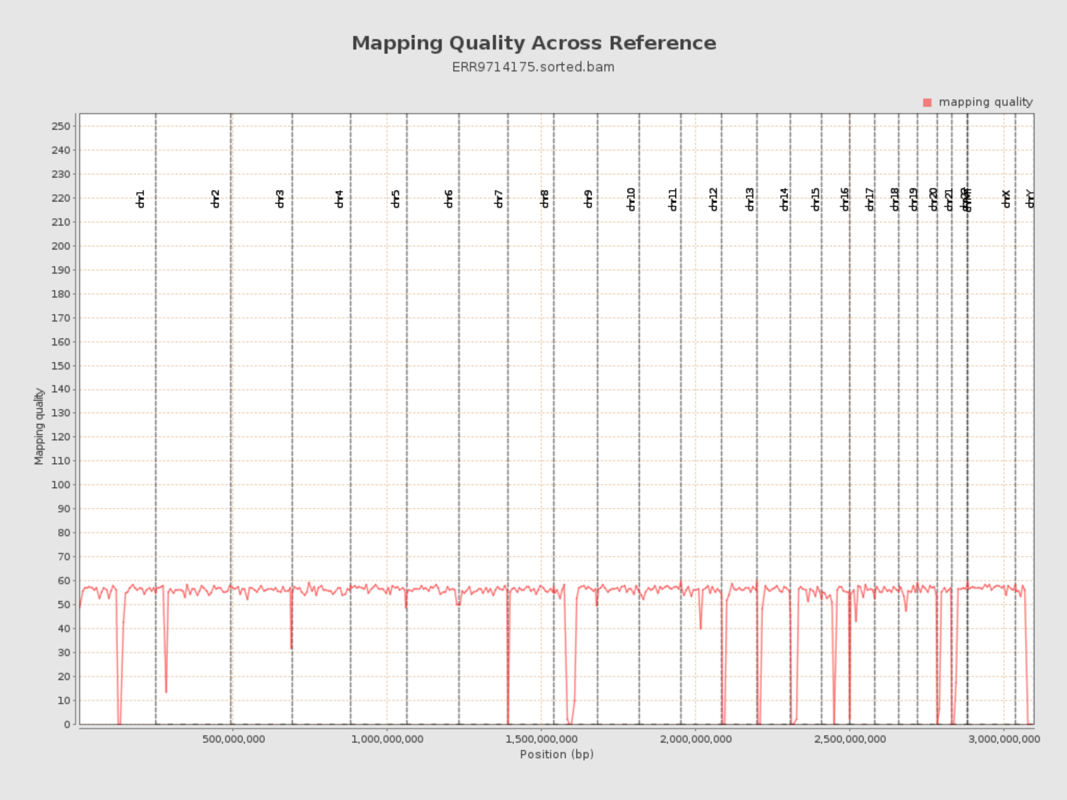
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram