Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 23:39:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714184.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_ERR9714184 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 23:39:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,125,676
Mapped reads	2,013,237 / 94.71%
Unmapped reads	112,439 / 5.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	134,388 / 6.32%
Read min/max/mean length	30 / 151 / 146.8
Duplicated reads (estimated)	2,071,264 / 97.44%
Duplication rate	32.34%
Clipped reads	2,017,362 / 94.9%

2.2. ACGT Content

Number/percentage of A's	73,367,941 / 29.14%
Number/percentage of C's	51,279,182 / 20.37%
Number/percentage of T's	72,658,733 / 28.86%
Number/percentage of G's	54,454,127 / 21.63%
Number/percentage of N's	1,755 / 0%
GC Percentage	42%

2.3. Coverage

Mean	0.0824

Standard Deviation	85.3181

2.4. Mapping Quality

Mean Mapping Quality	24.89

2.5. Mismatches and indels

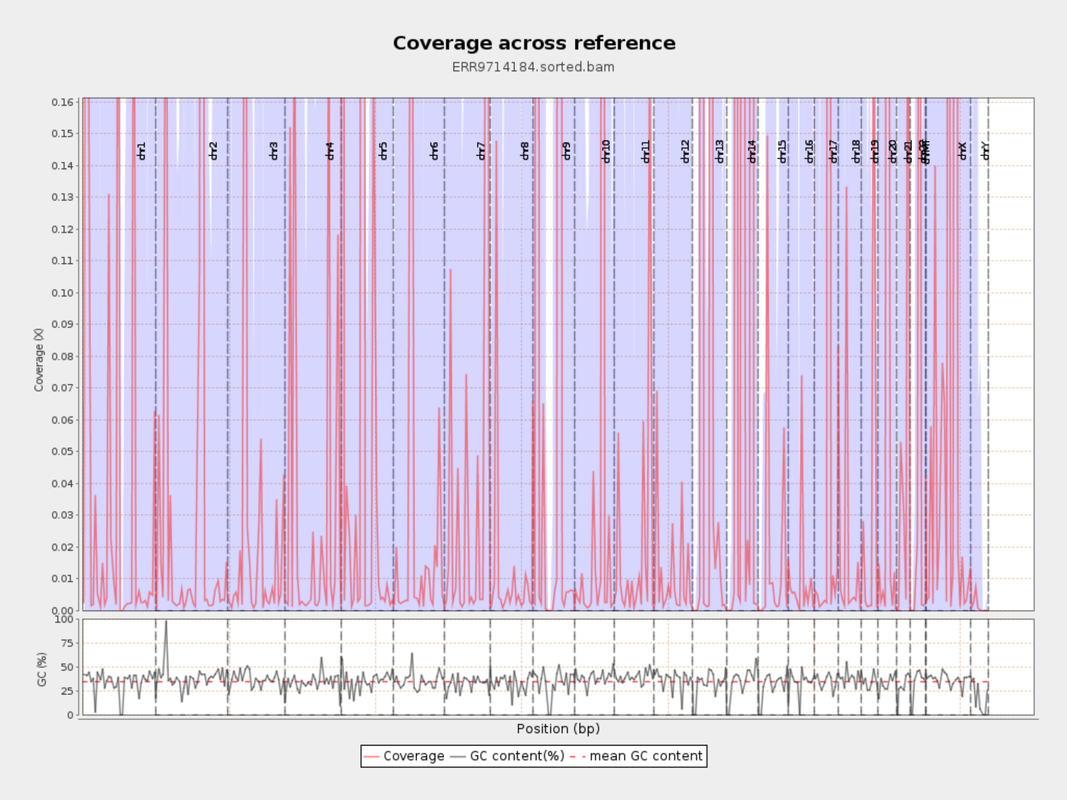
General error rate	3.95%
Mismatches	8,054,371
Insertions	366,235
Mapped reads with at least one insertion	17.6%
Deletions	547,419
Mapped reads with at least one deletion	25.61%
Homopolymer indels	23.77%

2.6. Chromosome stats

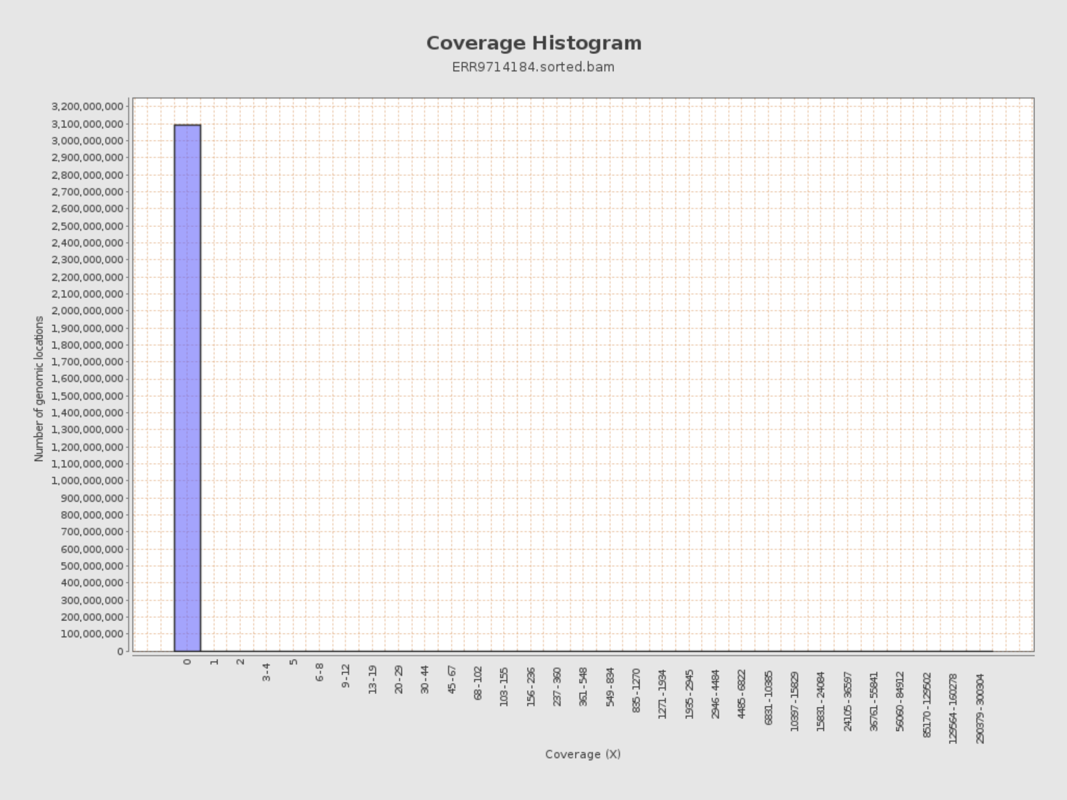
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11956148	0.048	26.3999
chr2	243199373	9896952	0.0407	25.7951
chr3	198022430	4776914	0.0241	13.0675
chr4	191154276	6274561	0.0328	15.1274
chr5	180915260	25362552	0.1402	99.8159
chr6	171115067	4958775	0.029	15.383
chr7	159138663	7986136	0.0502	26.7646

chr8	146364022	1805378	0.0123	6.4202
chr9	141213431	35834148	0.2538	158.5315
chr10	135534747	10345641	0.0763	65.062
chr11	135006516	2893375	0.0214	11.059
chr12	133851895	1642242	0.0123	4.4706
chr13	115169878	53315260	0.4629	330.6531
chr14	107349540	34491291	0.3213	137.4316
chr15	102531392	1889849	0.0184	9.6755
chr16	90354753	983121	0.0109	5.4556
chr17	81195210	15702301	0.1934	115.2793
chr18	78077248	1641848	0.021	9.2821
chr19	59128983	1846565	0.0312	16.9728
chr20	63025520	4713657	0.0748	42.6177
chr21	48129895	2625149	0.0545	23.7653
chr22	51304566	3036064	0.0592	24.6157
chrMT	16571	698	0.0421	0.3436
chrX	155270560	11049234	0.0712	26.489
chrY	59373566	92684	0.0016	0.52

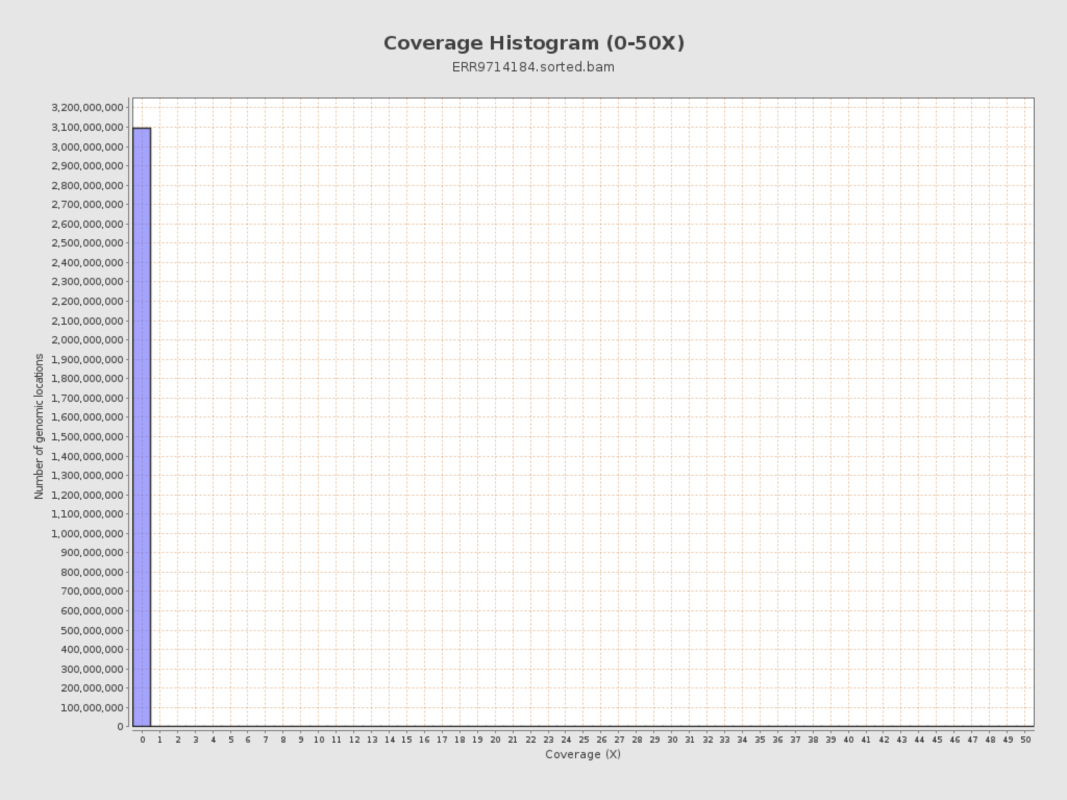
3. Results : Coverage across reference



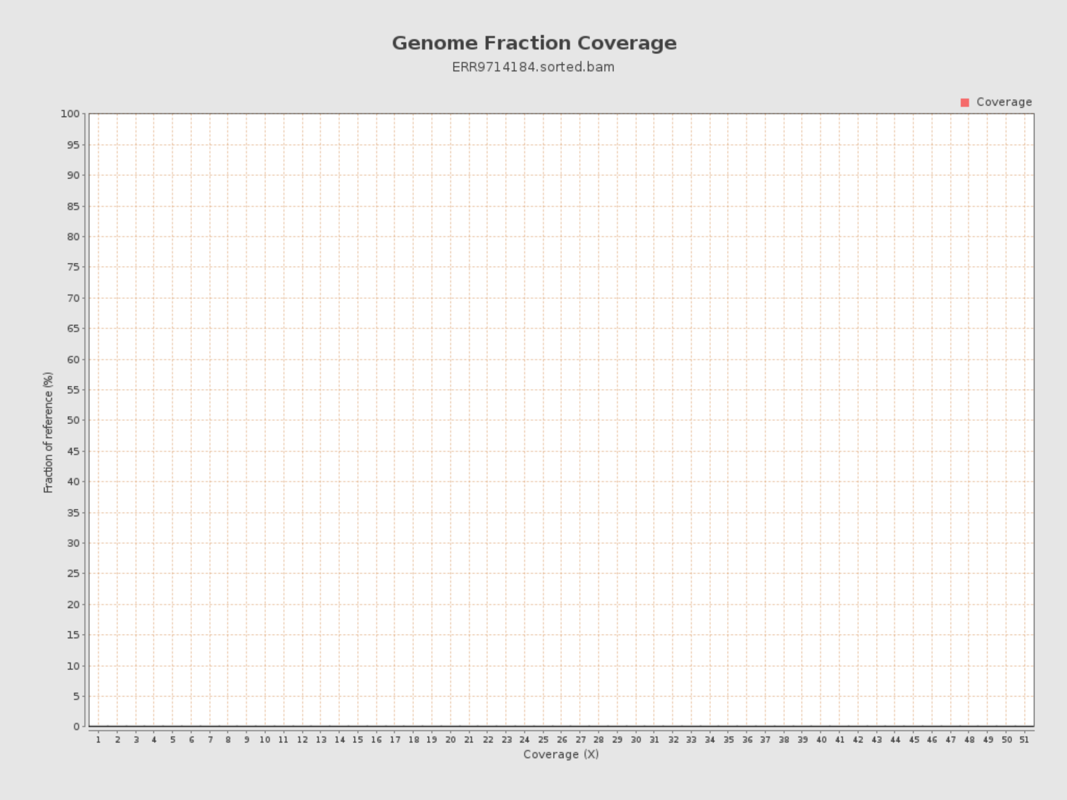
4. Results : Coverage Histogram



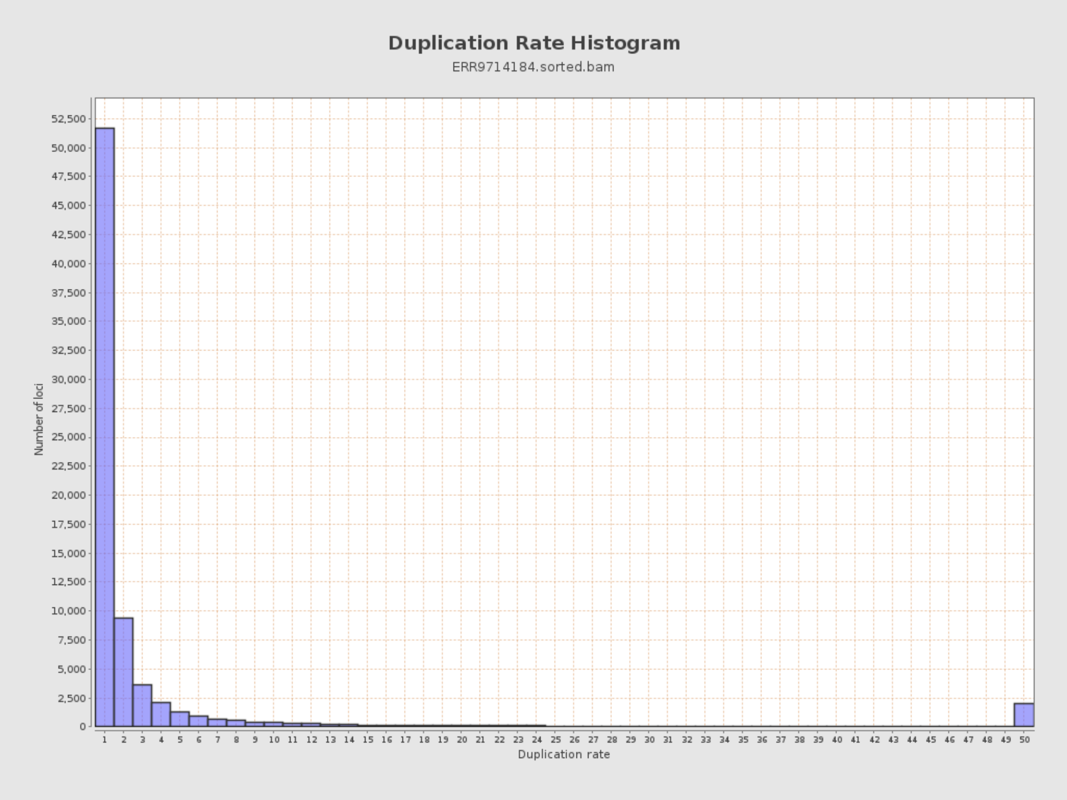
5. Results : Coverage Histogram (0-50X)



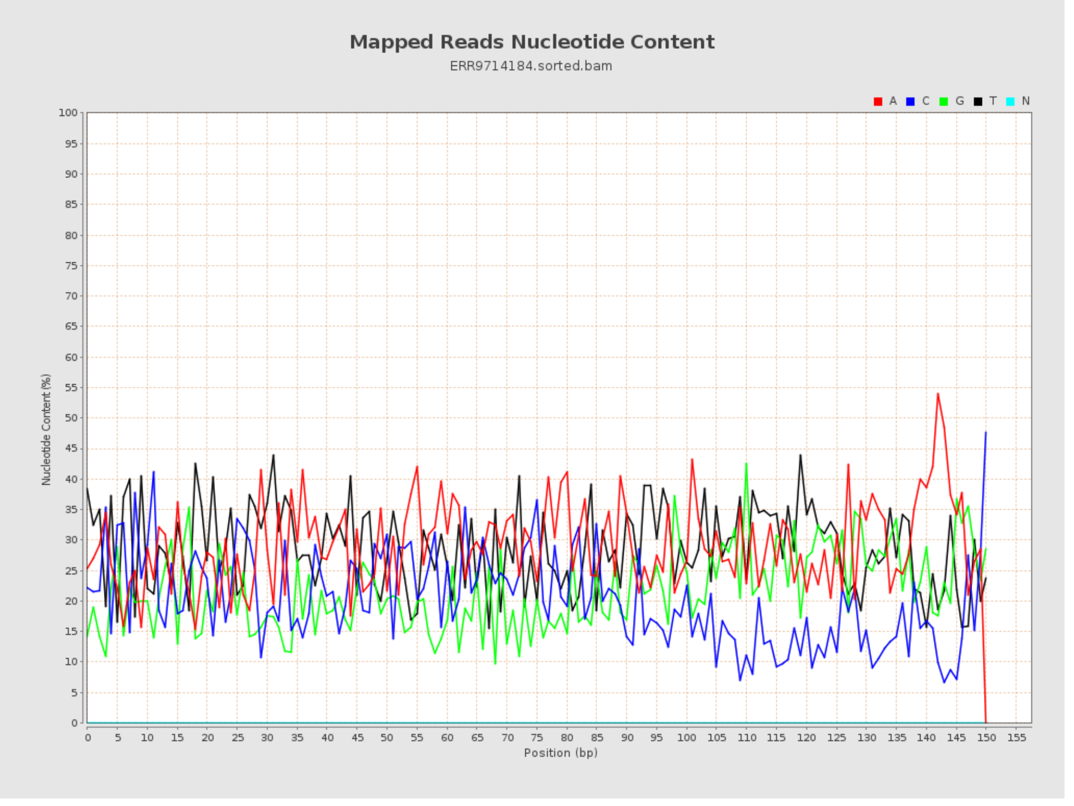
6. Results : Genome Fraction Coverage



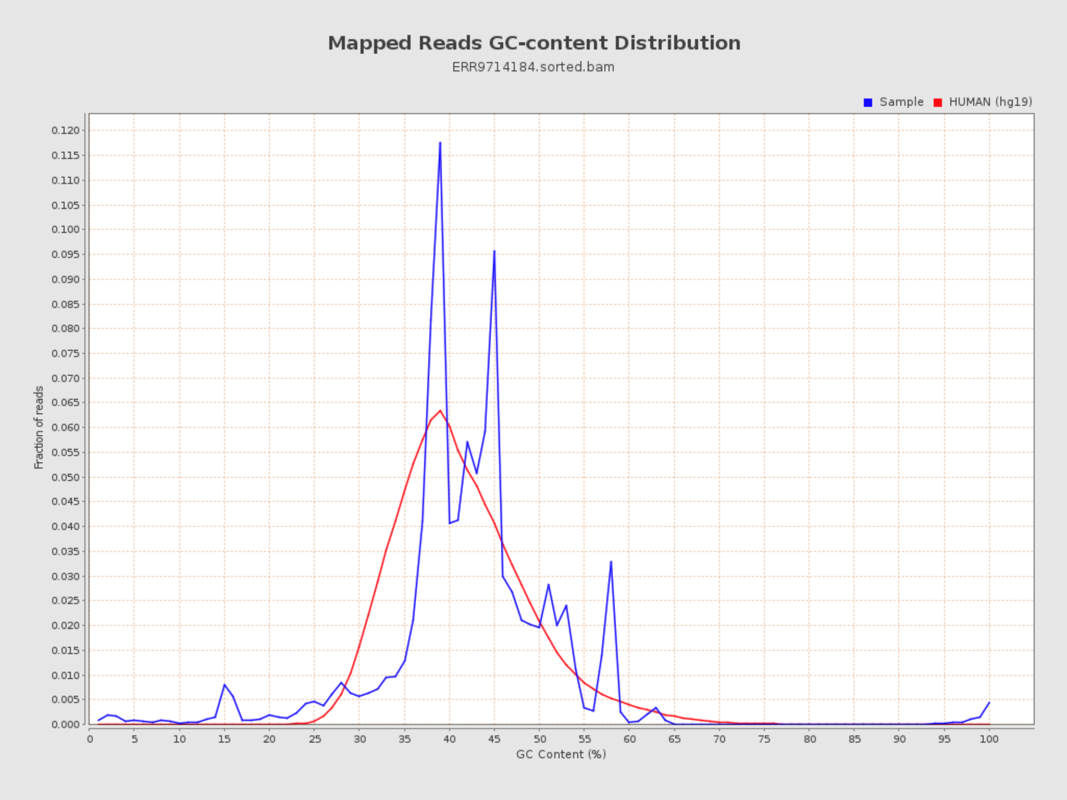
7. Results : Duplication Rate Histogram



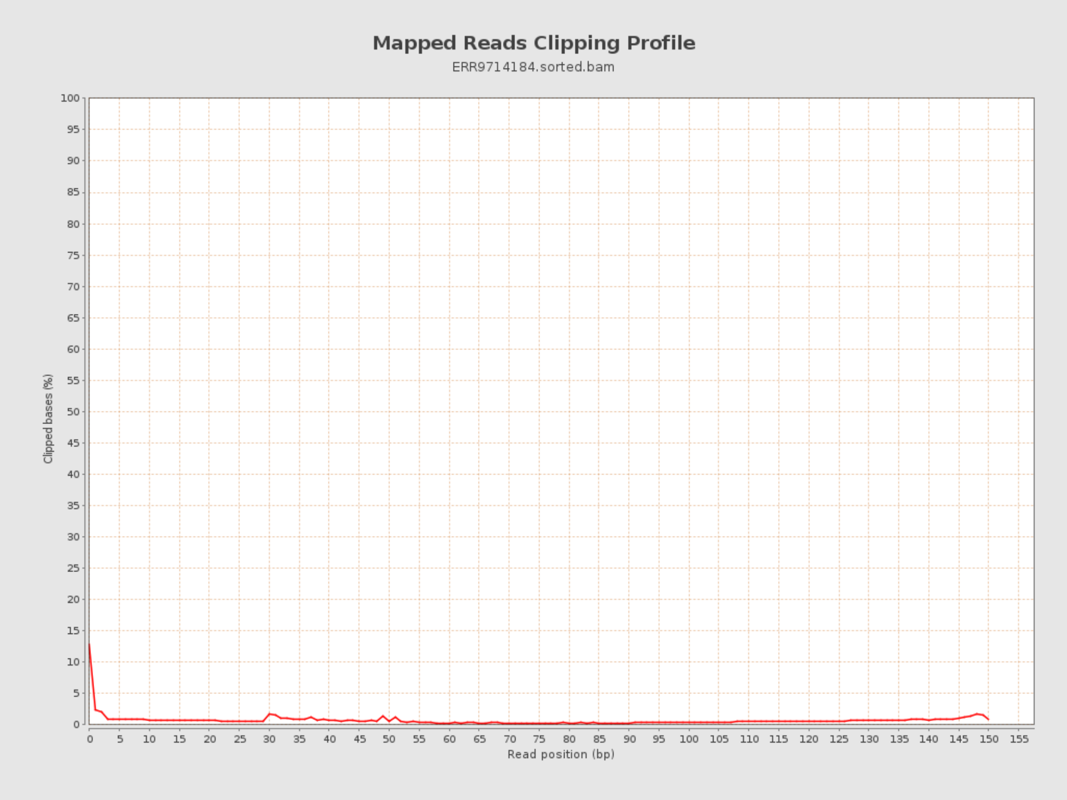
8. Results : Mapped Reads Nucleotide Content



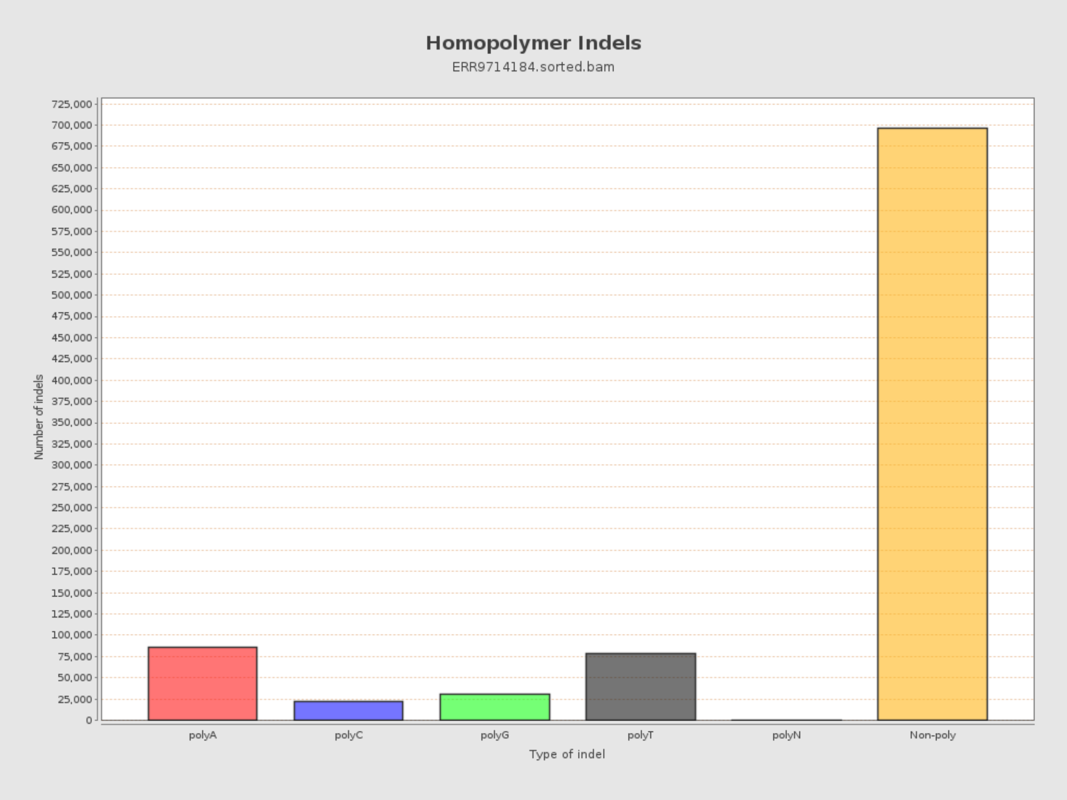
9. Results : Mapped Reads GC-content Distribution



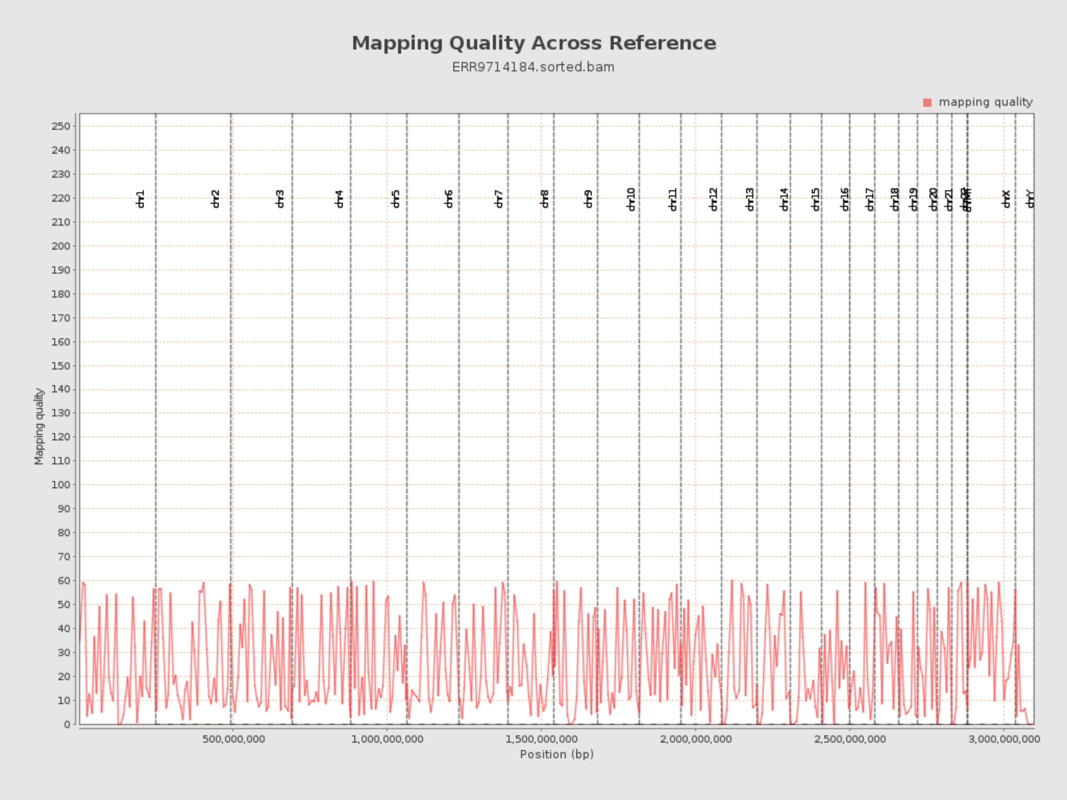
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram