Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 01:49:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714263.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_ERR9714263 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 01:49:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	392,918
Mapped reads	90,051 / 22.92%
Unmapped reads	302,867 / 77.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,123 / 0.79%
Read min/max/mean length	30 / 151 / 71.31
Duplicated reads (estimated)	63,667 / 16.2%
Duplication rate	36.96%
Clipped reads	82,219 / 20.93%

2.2. ACGT Content

Number/percentage of A's	2,713,431 / 25.99%
Number/percentage of C's	1,842,281 / 17.64%
Number/percentage of T's	2,526,396 / 24.2%
Number/percentage of G's	3,359,017 / 32.17%
Number/percentage of N's	162 / 0%
GC Percentage	49.81%

2.3. Coverage

Mean	0.0034

Standard Deviation	1.7727

2.4. Mapping Quality

Mean Mapping Quality	51

2.5. Mismatches and indels

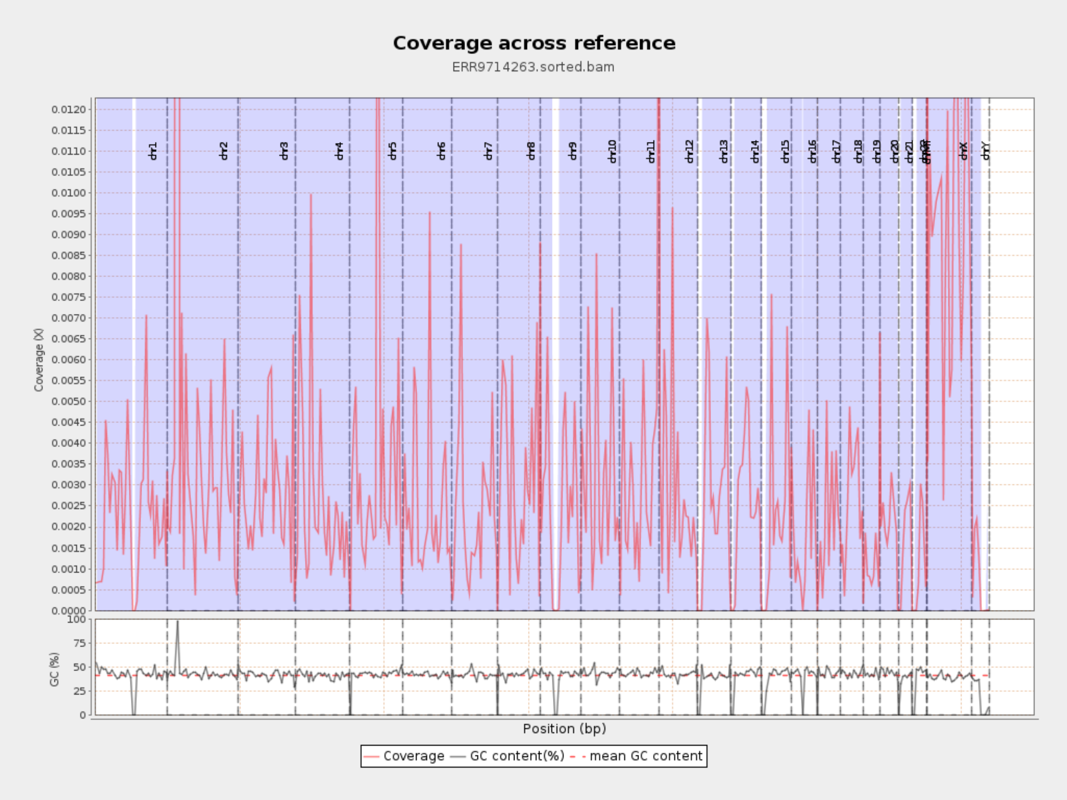
General error rate	3.75%
Mismatches	356,256
Insertions	10,596
Mapped reads with at least one insertion	10.98%
Deletions	28,841
Mapped reads with at least one deletion	30.54%
Homopolymer indels	28.7%

2.6. Chromosome stats

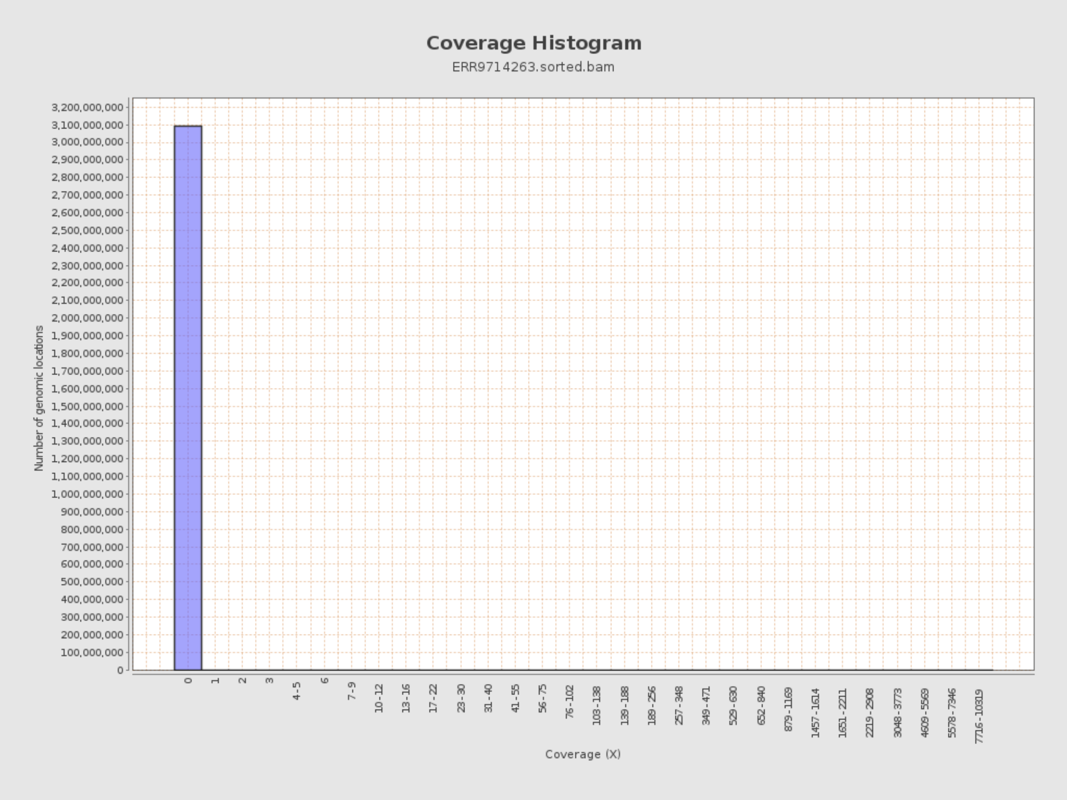
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	575262	0.0023	0.2865
chr2	243199373	2217791	0.0091	6.1519
chr3	198022430	587207	0.003	0.3291
chr4	191154276	496720	0.0026	0.4827
chr5	180915260	661740	0.0037	1.0231
chr6	171115067	438142	0.0026	0.3247
chr7	159138663	386720	0.0024	0.3409

chr8	146364022	447209	0.0031	0.3783
chr9	141213431	354965	0.0025	0.2879
chr10	135534747	442250	0.0033	0.3456
chr11	135006516	402505	0.003	0.3053
chr12	133851895	383128	0.0029	0.4425
chr13	115169878	323417	0.0028	0.3245
chr14	107349540	285061	0.0027	0.3385
chr15	102531392	243995	0.0024	0.3352
chr16	90354753	169245	0.0019	0.2354
chr17	81195210	173715	0.0021	0.2843
chr18	78077248	217797	0.0028	0.2923
chr19	59128983	71756	0.0012	0.1894
chr20	63025520	133124	0.0021	0.1919
chr21	48129895	81824	0.0017	0.1902
chr22	51304566	55000	0.0011	0.1553
chrMT	16571	1828	0.1103	0.8739
chrX	155270560	1416858	0.0091	0.6319
chrY	59373566	44228	0.0007	0.1126

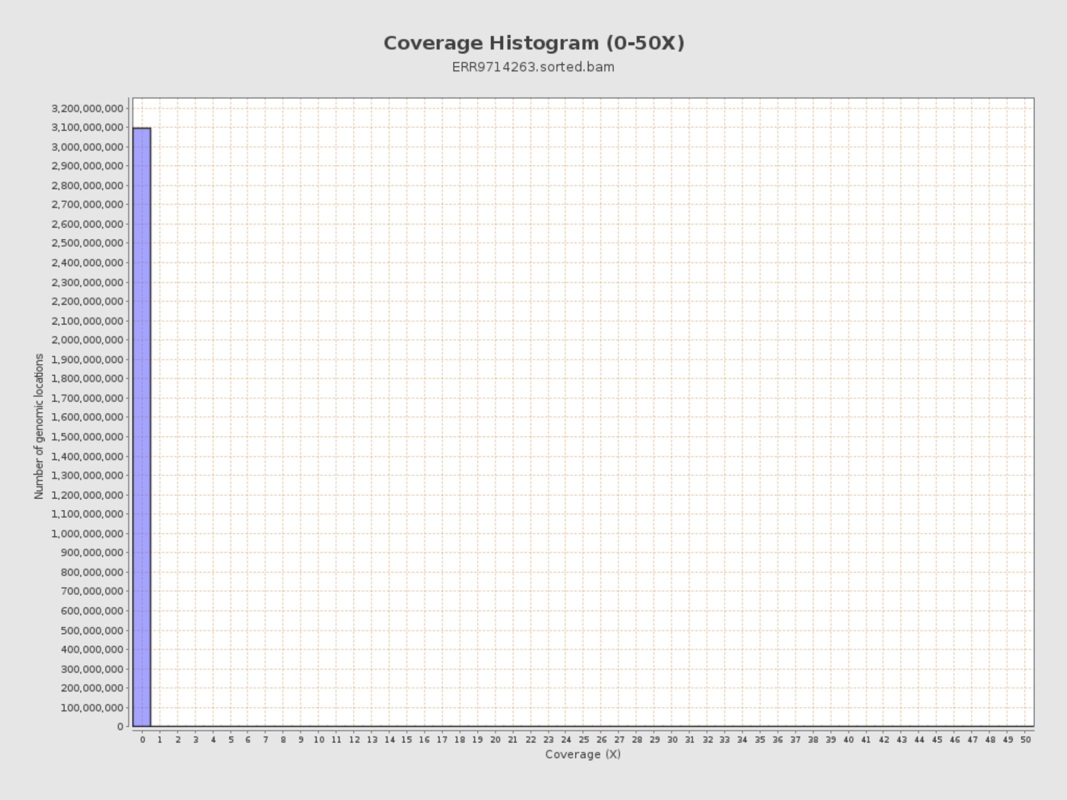
3. Results : Coverage across reference



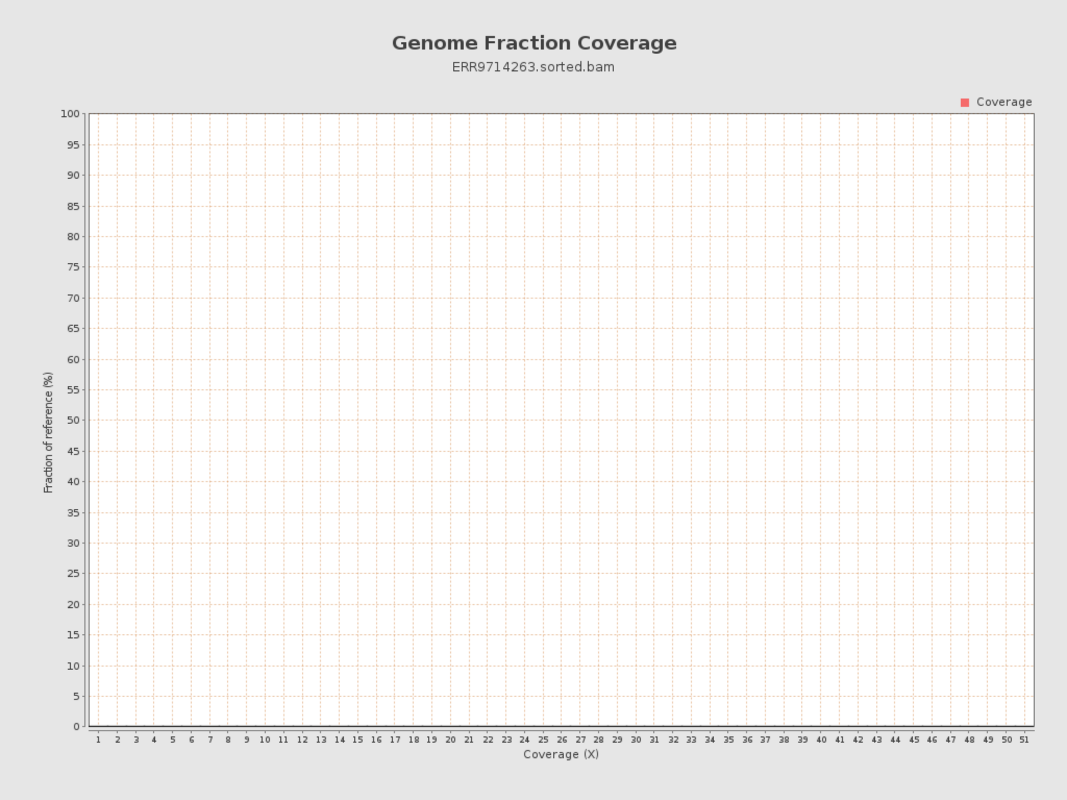
4. Results : Coverage Histogram



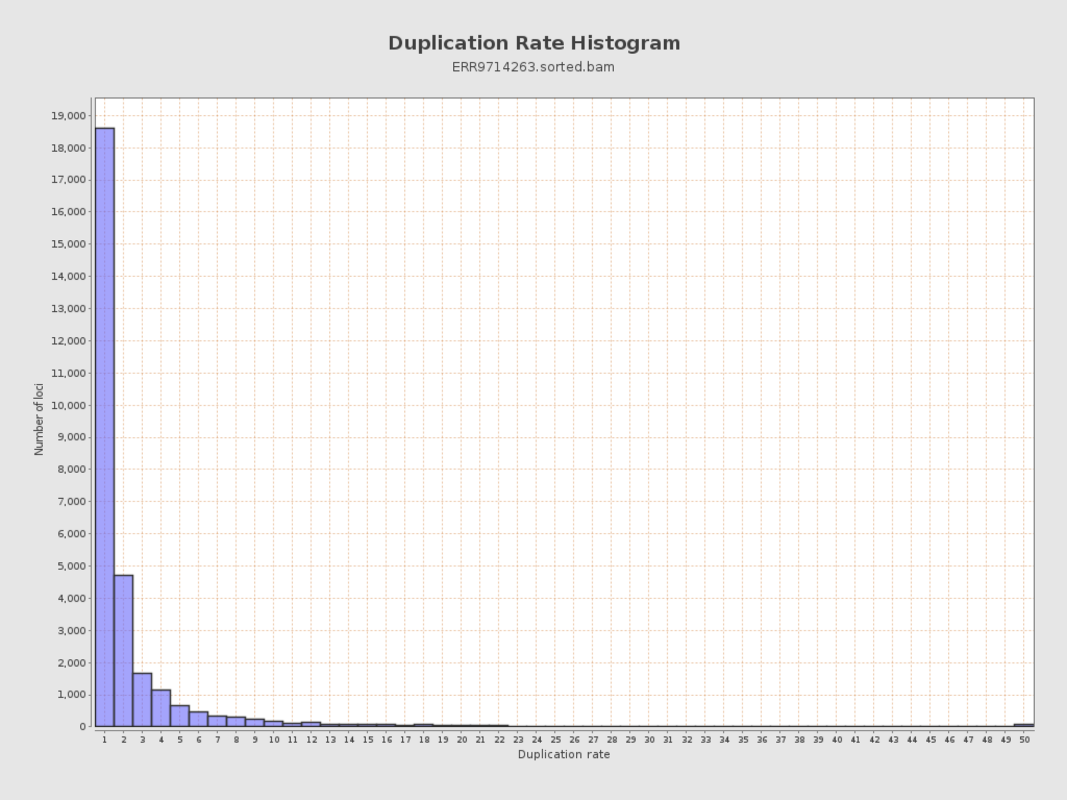
5. Results : Coverage Histogram (0-50X)



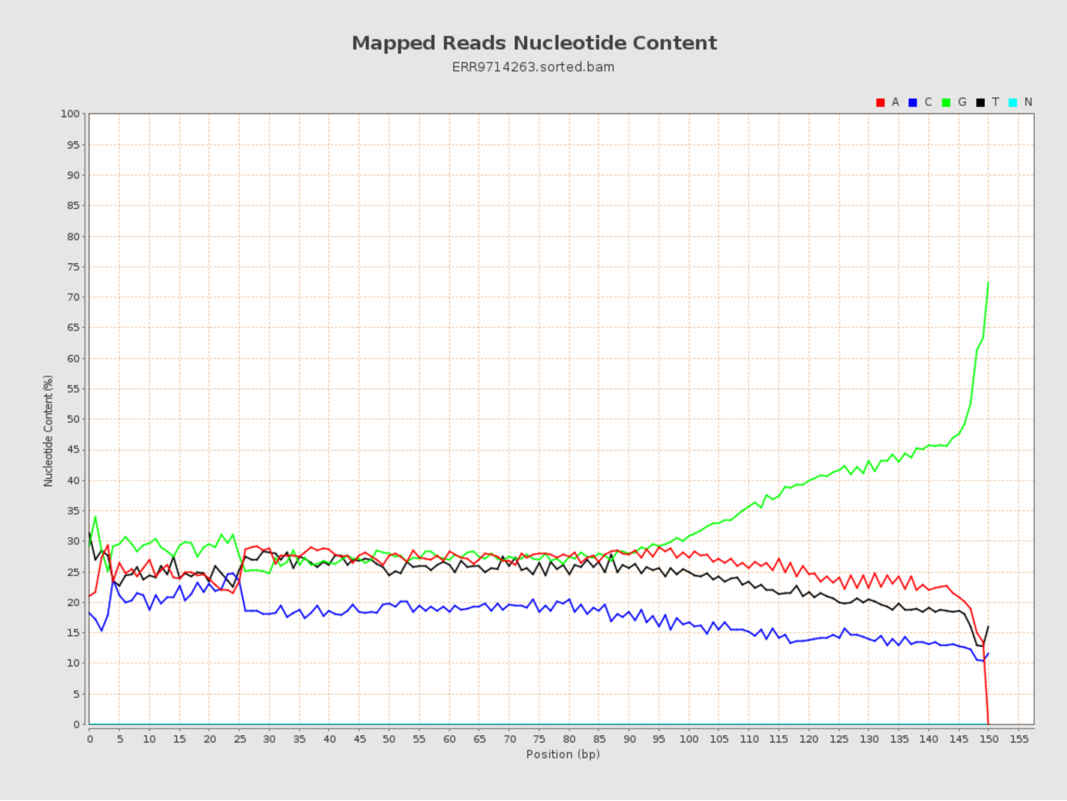
6. Results : Genome Fraction Coverage



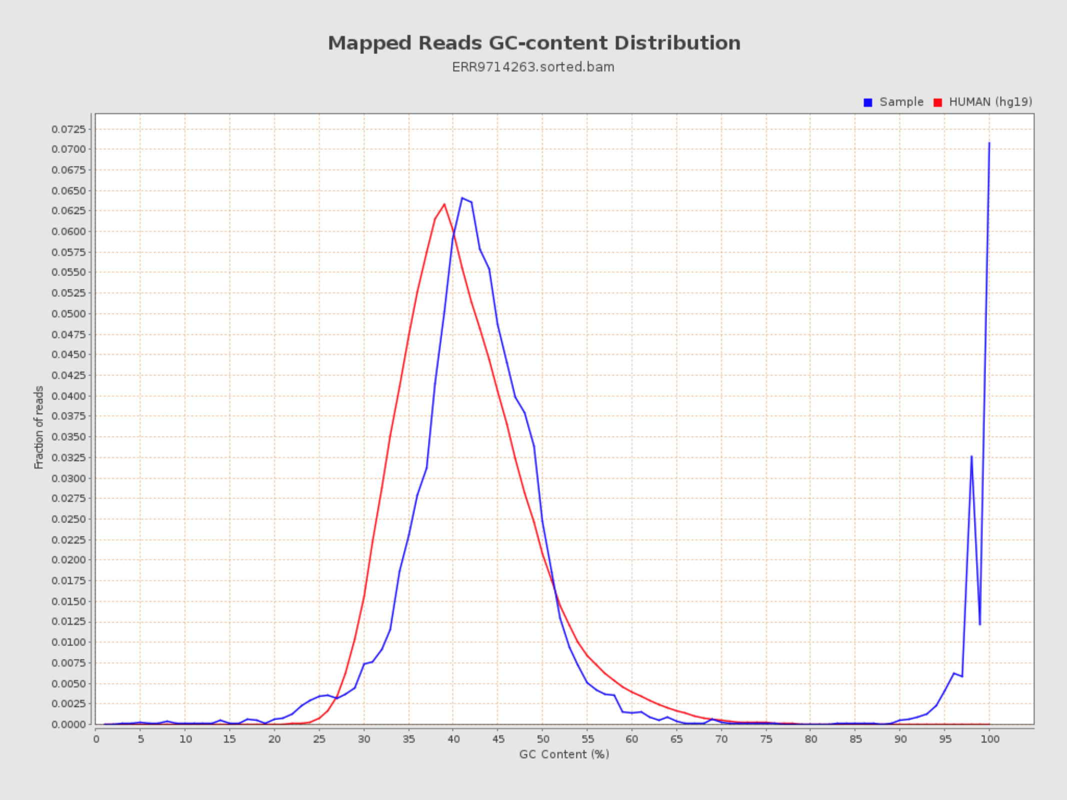
7. Results : Duplication Rate Histogram



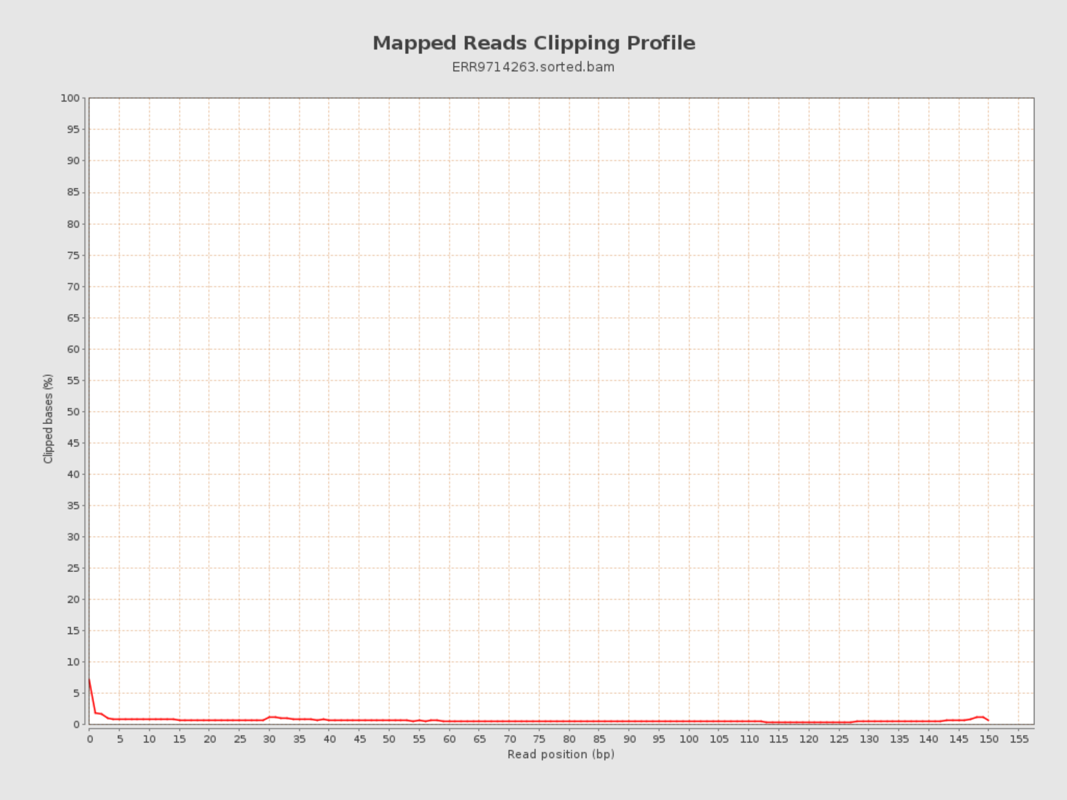
8. Results : Mapped Reads Nucleotide Content



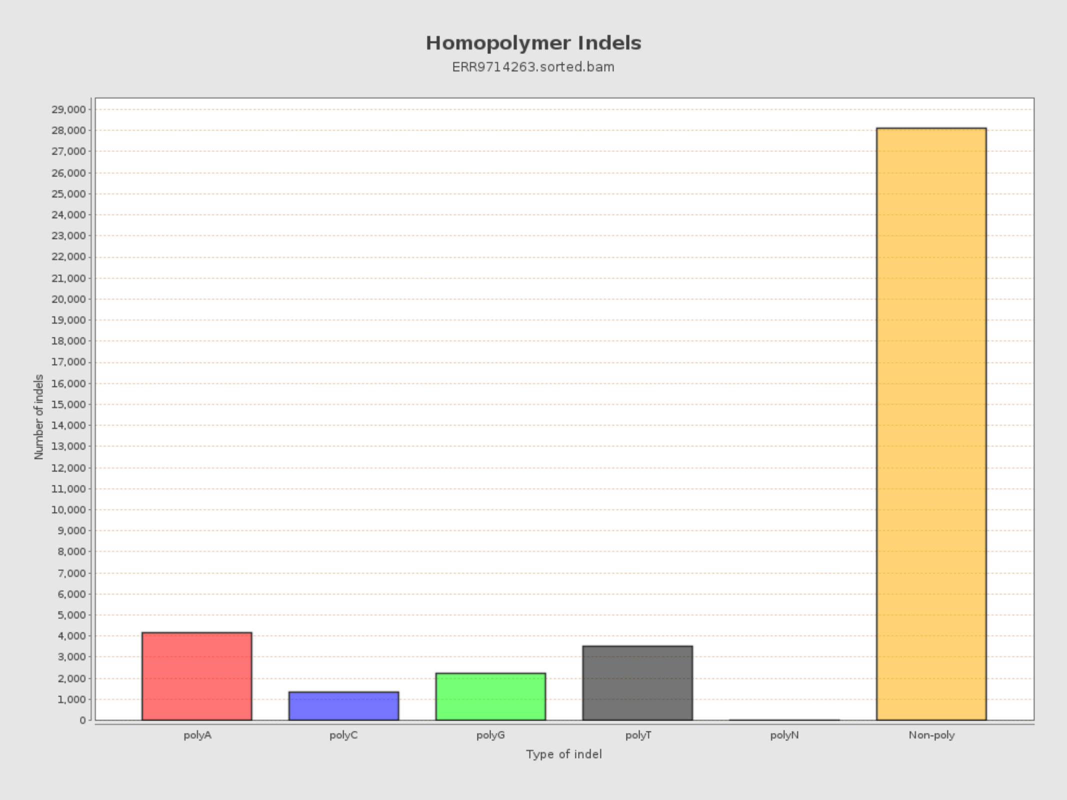
9. Results : Mapped Reads GC-content Distribution



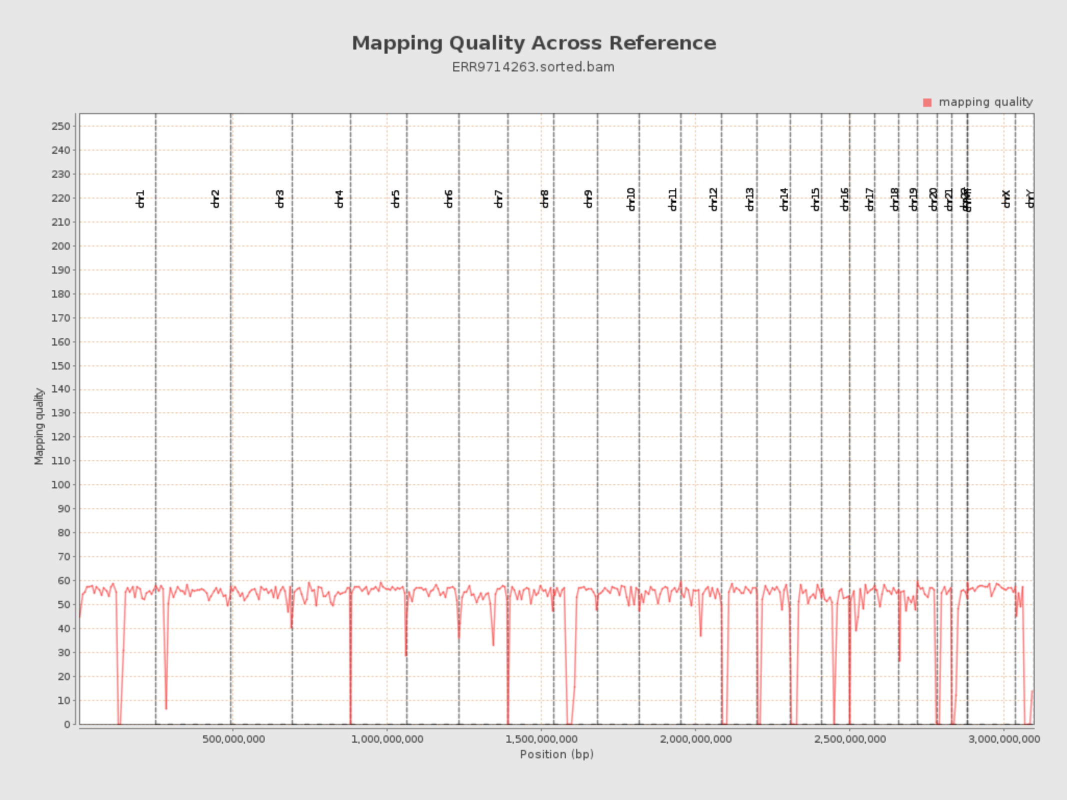
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram