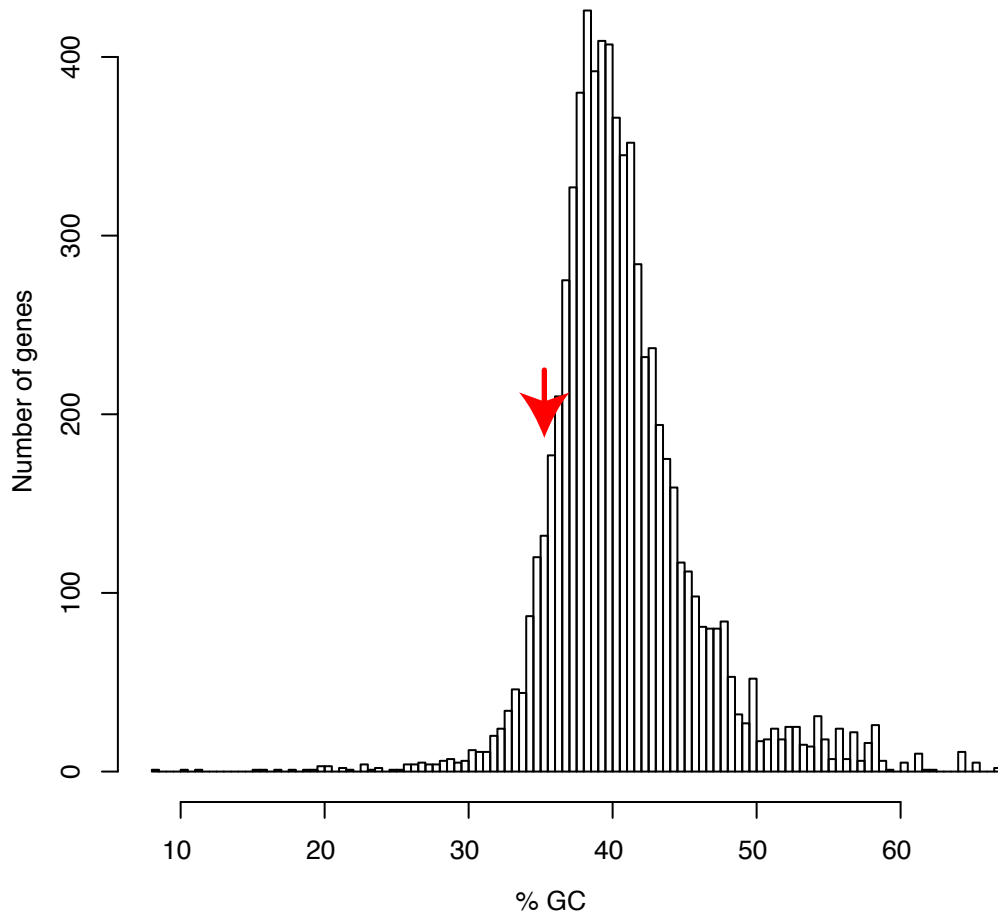


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Figure S2



The GC content of YFP is similar to that of native *S. cerevisiae* genes. Because EMS preferentially causes mutations at G-C base pairs, we compared the percentage of nucleotides that are either guanine or cytosine (%GC) in the YFP coding sequence to the %GC in coding sequences of genes endogenous to the *S. cerevisiae* genome (median %GC = 39.95%) is shown with the %GC of YFP (35.56%) indicated with a red arrow. Sequences for *S. cerevisiae* genes are from the Saccharomyces Genome Database EF3 assembly (Ensembl, Release 64).