The ability to modulate gene expression is an important genetic tool in systems biology and biotechnology. Here, we demonstrate that a previously published easy and fast PCR-based method for modulating gene expression in lactic acid bacteria is also applicable to Corynebacterium glutamicum. We constructed constitutive promoter libraries based on various combinations of a previously reported C. glutamicum -10 consensus sequence (ggnTAv/c/t)aaTgg) and the Escherichia coli -35 consensus, either with or without an AT-rich region upstream. A promoter library based on consensus sequences frequently found in low-GC Gram-positive microorganisms was also included. The strongest promoters were found in the library with a -35 region and a C. glutamicum -10 consensus, and this library also represents the largest activity span. Using the alternative -10 consensus TATAAT, which can be found in many other prokaryotes, resulted in a weaker but still useful promoter library. The upstream AT-rich region did not appear to affect promoter strength in C. glutamicum. In addition to the constitutive promoters, a synthetic inducible promoter library, based on the E. coli lac-promoter, was constructed by randomizing the 17-bp spacer between -35 and -10 consensus sequences and the sequences surrounding these. The inducible promoter library was shown to result in β-galactosidase activities ranging from 284 to 1,665 Miller units when induced by IPTG, and the induction fold ranged from 7–59. We find that the synthetic promoter library (SPL) technology is convenient for modulating gene expression in C. glutamicum and should have many future applications, within basic research as well as for optimizing industrial production organisms.