

**P003** Transcriptome analysis leading to the identification of novel promoters for high level expression in *S.cerevisiae*  
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We describe the identification and application of novel high expression promoters from *S.cerevisiae*.

We used Affymetrix Genechips to measure transcript levels for ~6000 *S. cerevisiae* genes during exponential (glucose) and stationary (ethanol) growth phases. We identified and cloned the promoters of eleven genes that showed either (i) the highest constitutive transcription over both glucose and ethanol growth phase; (ii) the greatest induced transcription on entry into stationary phase. Luciferase reporter constructs were generated for each promoter and luciferase levels expressed by each promoter construct were measured and compared with expression from a previously reported strong heterologous promoter (*PRB1*). Further studies were performed to examine the effects of media (rich vs minimal) and scale (10ml shake flask, 500 ml shake flask, 5L fermenter) on luciferase expression. This work identified (amongst others) the *ZEO1* (YOL109W) and *HOR7* (YMR251W-A) as promoters that direct transcription at a level several fold higher than previously reported strong promoters, in both rich and minimal media and over a range of culture scales.

These promoters have since been integrated into our expression systems, and used to successfully express a wide variety of heterologous proteins.