**The expression of NOX from synthetic promoters reveals an important role of the redox status in regulating secondary metabolism of *Saccharopolyspora erythraea***

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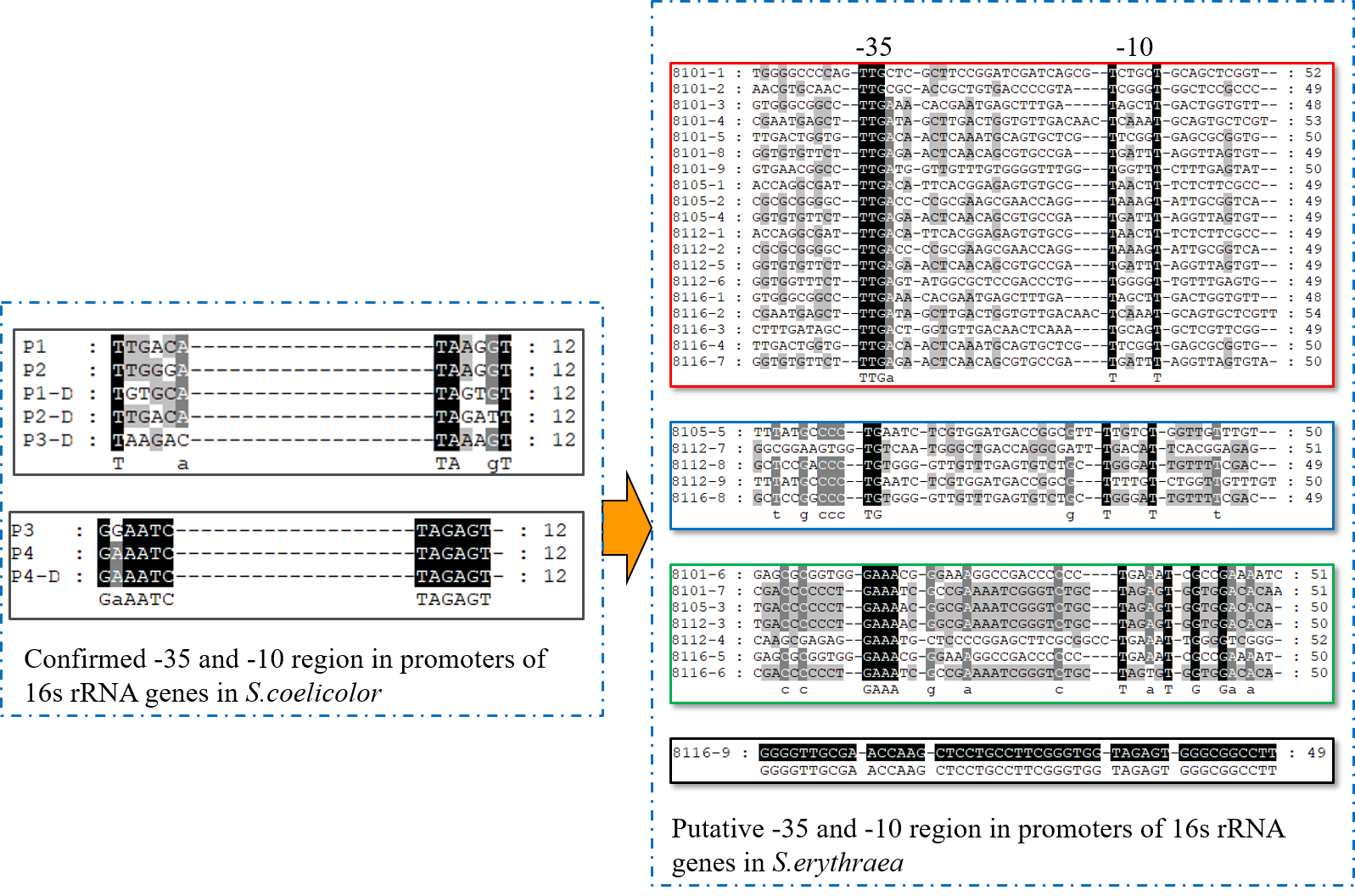
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# Figure S1. Search for putative 16s rRNA promoters in *S. erythraea*. In the left panel -35 and -10 regions of 16s rRNA genes in *S. coelicolor* were listed and summarized with black and grey background. P1/P2/P3/P4 are the promoter names in *S .coelicolor*. The consensus sequences were employed to identify the putative -35 and -10 regions in *S. erythraea* by searching for similar sequences upstream of the coding sequences of 16s rRNA genes in *S. erythraea* in the right panel. 8101/8105/8112/8116 are locus tags of 16s rRNA genes in *S. erythraea*. Numbers at the end of sequences indicate their length. The upstream, -35 region, spacer, -10 region and the downstream were separated from each other by “-” gaps.

5’-ATGTCCAAGATCGTCGTCGTCGGCGCCAACCACGCCGGCACCGCCTGCATCAACACCATGCTGGACAACTTCGGCAACGAGAACGAGATCGTCGTCTTCGACCAGAACTCCAACATCTCCTTCCTGGGCTGCGGCATGGCCCTGTGGATCGGCGAGCAGATCGACGGCGCCGAGGGCCTGTTCTACTCCGACAAGGAGAAGCTGGAGGCCAAGGGCGCCAAGGTCTACATGAACTCCCCGGTCCTGTCCATCGACTACGACAACAAGGTCGTCACCGCCGAGGTCGAGGGCAAGGAGCACAAGGAGTCCTACGAGAAGCTGATCTTCGCCACCGGCTCCACCCCGATCCTGCCGCCGATCGAGGGCGTCGAGATCGTCAAGGGCAACCGCGAGTTCAAGGCCACCCTGGAGAACGTCCAGTTCGTCAAGCTGTACCAGAACGCCGAGGAGGTCATCAACAAGCTGTCCGACAAGTCCCAGCACCTGGACCGCATCGCCGTCGTCGGCGGCGGCTACATCGGCGTCGAGCTGGCCGAGGCCTTCGAGCGCCTGGGCAAGGAGGTCGTCCTGGTCGACATCGTCGACACCGTCCTGAACGGCTACTACGACAAGGACTTCACCCAGATGATGGCCAAGAACCTGGAGGACCACAACATCCGCCTGGCCCTGGGCCAGACCGTCAAGGCCATCGAGGGCGACGGCAAGGTCGAGCGCCTGATCACCGACAAGGAGTCCTTCGACGTCGACATGGTCATCCTGGCCGTCGGCTTCCGCCCGAACACCGCCCTGGCCGACGGCAAGATCGAGCTGTTCCGCAACGGCGCCTTCCTGGTCGACAAGAAGCAGGAGACCTCCATCCCGGGCGTCTACGCCGTCGGCGACTGCGCCACCGTCTACGACAACGCCCGCAAGGACACCTCCTACATCGCCCTGGCCTCCAACGCCGTCCGCACCGGCATCGTCGGCGCCTACAACGCCTGCGGCCACGAGCTGGAGGGCATCGGCGTCCAGGGCTCCAACGGCATCTCCATCTACGGCCTGCACATGGTCTCCACCGGCCTGACCCTGGAGAAGGCCAAGGCCGCCGGCTACAACGCCACCGAGACCGGCTTCAACGACCTGCAGAAGCCGGAGTTCATGAAGCACGACAACCACGAGGTCGCCATCAAGATCGTCTTCGACAAGGACTCCCGCGAGATCCTGGGCGCCCAGATGGTCTCCCACGACATCGCCATCTCCATGGGCATCCACATGTTCTCCCTGGCCATCCAGGAGCACGTCACCATCGACAAGCTGGCCCTGACCGACCTGTTCTTCCTGCCGCACTTCAACAAGCCGTACAACTACATCACCATGGCCGCCCTGACCGCCGAGAAGTGA -3’

# Figure S2. Coding sequence of NADH oxidase after codon optimization.



# Figure S3. Concentration of residual glucose for E3 and E3::F1F0ATPase (E3H) in 1 L fermenters with 600 mL minimal liquid medium.