Table A1 The oligonucleotides used in this work

Name	Sequence
Oligo 1	5′TGTGGATACCGGC3′
Oligo 2	5′AAGGTTATTATTA3′
FP Stab	5′GGCCTTCCTGTAGCCAGCTTTCATCAAC3′
RP Stab	5'ACGCGTCGACCGATCCGGACAACCGATGAAAG3′
RP1-8311	5′GGCTGTGGGAGTTTCTGAATTG3′
RP2-10412	5′TGGTCATTCCGTTGGTCGTA3′
FP1-92512	5′CACAGATACGTACAGAAAGACATTCAGG3′
FP2-10412	5′GCGGAACACTGGCAAATCATG3′
FP2-42213	5′CTCATGAGACAATAACCCTGATAAATG3′
RP2-42213	5′TAAGGGCGACACGGAAATG′3′

Figure A1

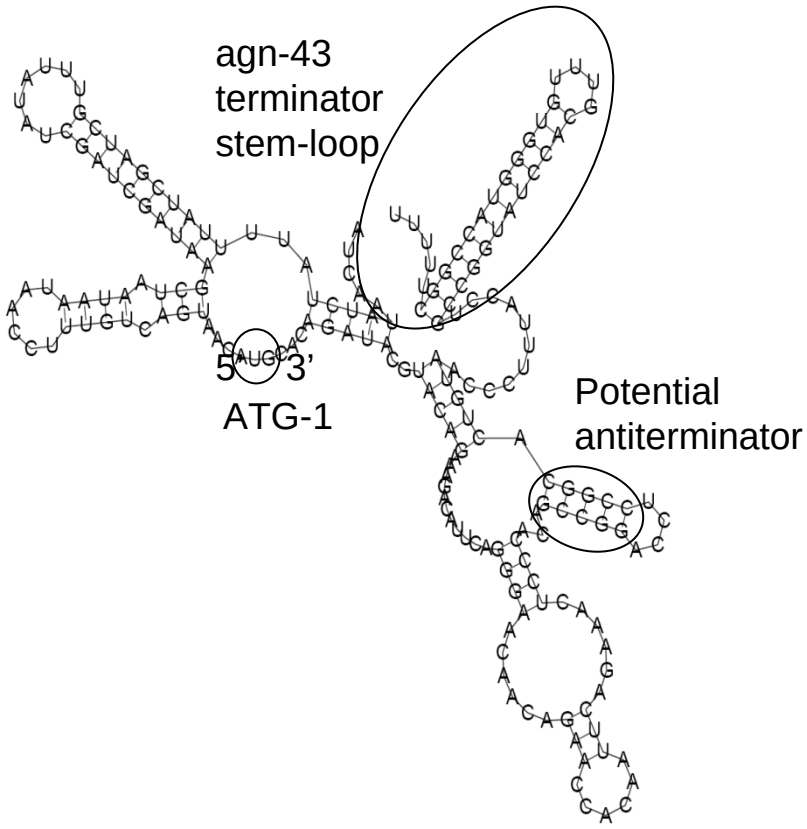

Figure A1: Secondary structure prediction for the fully folded *agn*^{K12} leader RNA, modeled by the RNAfold WebServer. Regions corresponding to ATG-1 (as it has been called in the body of the manuscript), the agn-43 terminator stem/loop and a potential antiterminator sequence are identified.

Figure A2

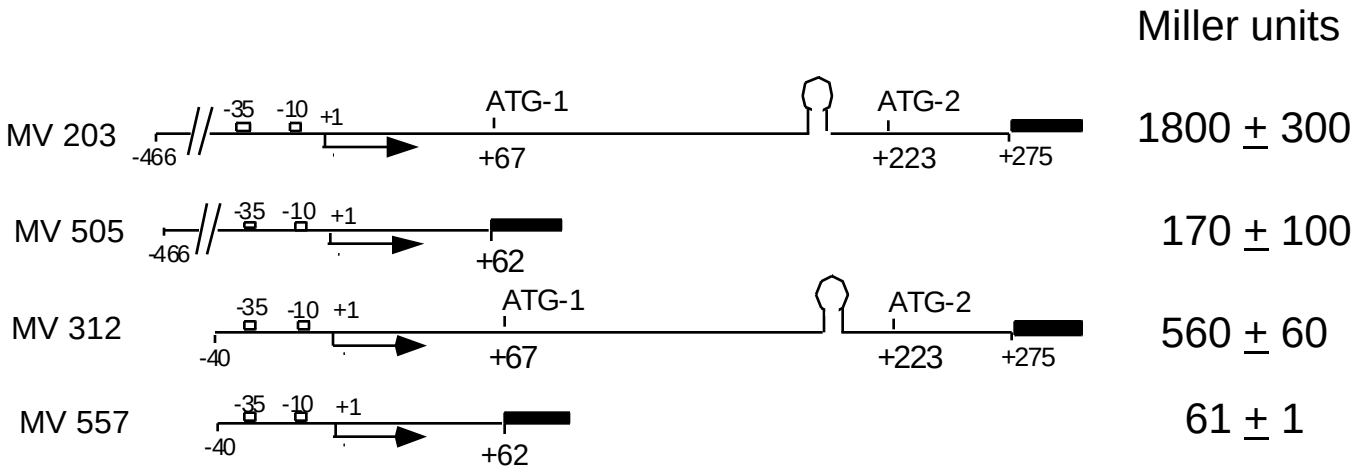

Figure A2: The leader region downstream of the promoter is important for *agn*^{K12} regulation: effect of a large deletion. The various cartoons represent the constructs that were tested. The black rectangles represent the *lacZ* reporter gene, containing its own SD and ATG start site. The promoter +1 transcription start site (arrow) as well as the two *agn*^{K12} translational start sites, ATG-1 and ATG-2 are indicated. The approximate position of the stem-loop in the leader region is also shown. The top two construct have *agn*^{K12} sequence up to -466, the bottom two up to -40. On the right the measured expression levels for each construct are shown in Miller Units. For the upstream-truncated constructs (compare MV203 with MV312, and MV505 with MV557) the expression of the reporter gene is lower by about 3 fold. On the other hand the effect of a downstream truncation is about ten-fold (Compare MV203 with MV505, and MV312 with MV557).

Figure A3

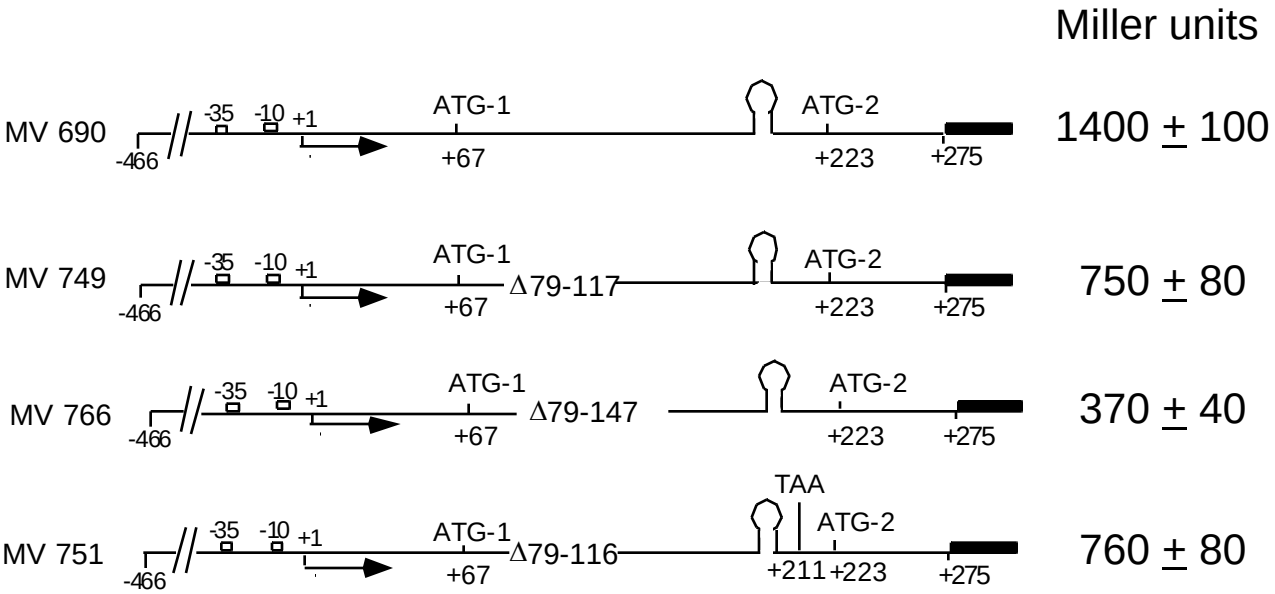

Figure A3: The leader region downstream of the promoter is important for *agn*^{K12} regulation: effects of two in-frame (MV749 and MV766) and one out of frame deletion (MV 751) in the *agn*^{K12} leader region on LacZ expression levels in *agn*^{K12}*'-lacZ* translational fusions. The deletions in MV749 and MV751 are very similar in size, and they reduce LacZ expression by similar extents even though the out of frame deletion of MV751 introduced a stop codon TAA at +211 (upstream of ATG-2), as indicated. The deletion of MV766 is greater by about 30 bp, and it result in an additional decrease in lacZ expression. For additional information see the legend of figure A2.