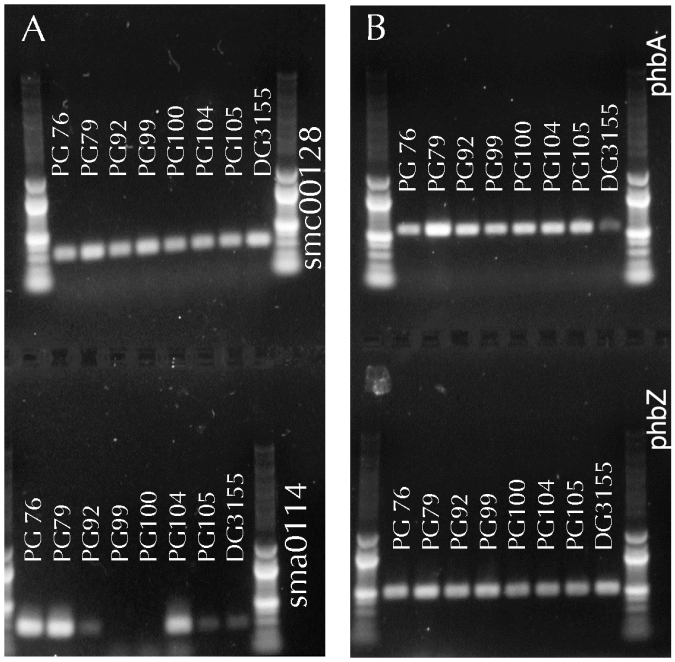
Supplementary Table 1. Primers used for RT PCR experiments

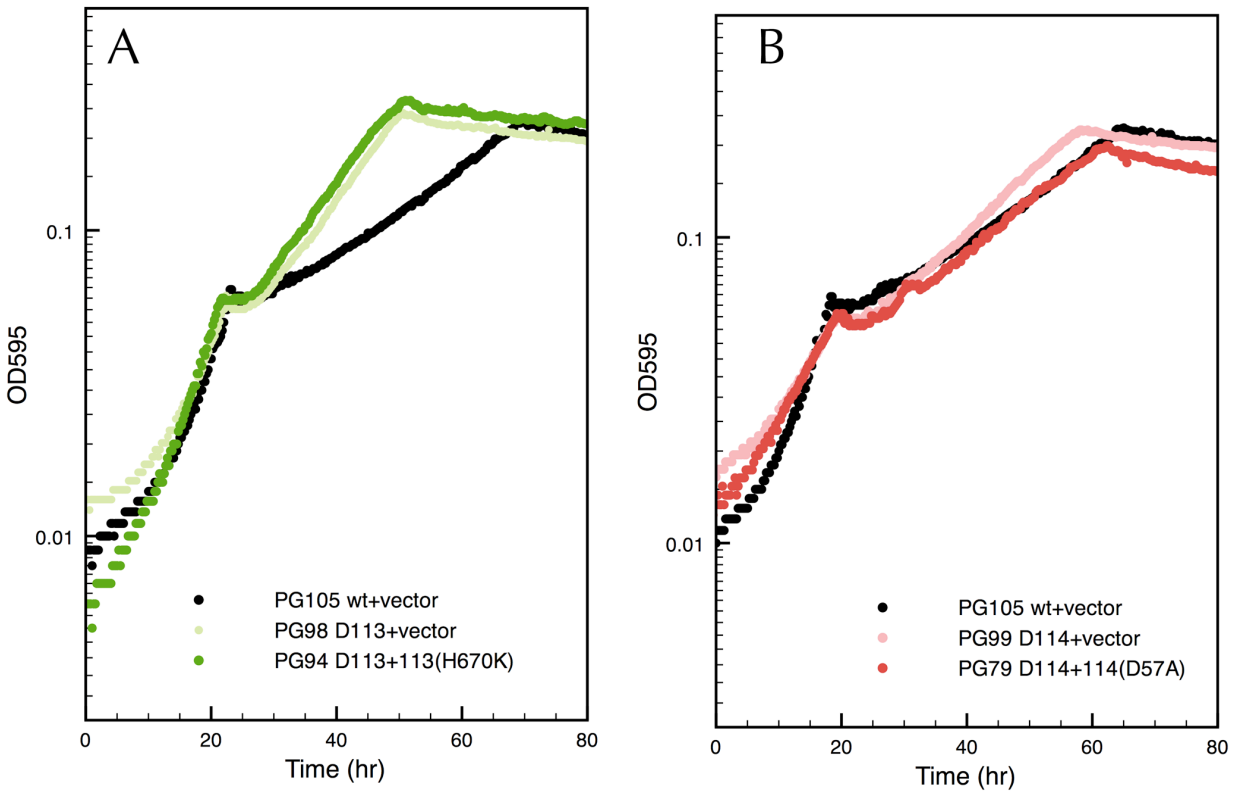
Primer Sequence	**Primer Name**[a]
TTACAGGCGTTCCACGCACAT	*phbA* RT-Rev
ACGGCTACCACATGGGCATCA	*phbA* Fwd
ATCGCTCCGCCATTGACGTT	*phbA* Rev
GGCAGCGCATGTTGCATGAA	*phaZ* RT-Rev
GAGCCGTTCTGCAACCTCATACAT	*phaZ* Fwd
TGAAGCCGGAAAGCTGGAGAAAG	*phaZ* Rev
GCGTAACCTTCCTGGTCCTTCA	*smc00128* RT-rev
AGTTCGACGAGCTGGATCGGT	*smc00128* Rev
ATATCGTGATCATACTCGCCCTGC	*smc00128* Fwd
GTTCTCGTGGTCGAAGACGAAT	*sma0114* Fwd
TCCTTTGAGATCTGCACGAGTACG	*sma0114* RT-Rev
GGCTTCCAGTTCGCTGTCCAAA	*sma0014* Rev

[a] Target gene name is first, followed by RT-Rev if the primer was used as the primer for reverse transcription, or Fwd/Rev if it was used for the subsequent PCR reactions

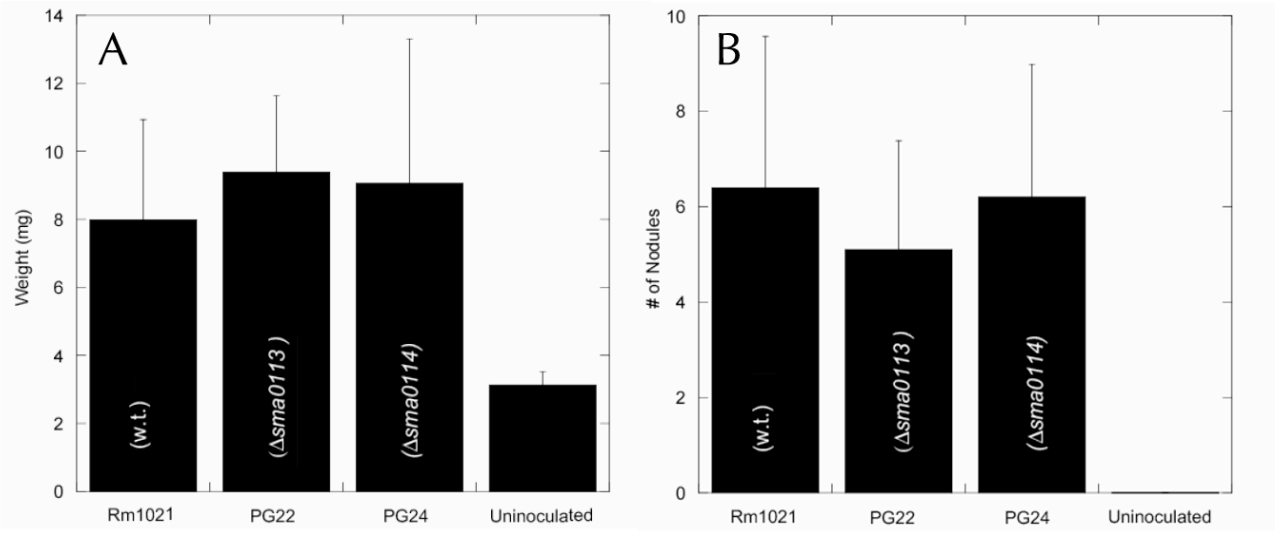


Strain	Relevant genotype
PG76	Δ*sma0114* with overexpressed *sma0114*
PG79	Δ*sma0114* with overexpressed *sma0114*-D57A
PG92	Δ*sma0113* with overexpressed *sma0113*
PG99	Δ*sma0114* with overexpression vector only
PG100	Δ*sma0113*Δ*sma0114*
PG104	Δ*sma0113*Δ*sma0114* with overexpressed *sma0113* and *sma0114*
PG105	Rm1021(w.t.) with overexpression vector only
DG3155	Rm1021 *phbA*::Tn5-233

Supplemental Fig 1. Typical RT-PCR results. A) Shows the RT PCR products from the control gene *smc00128* (top) and from *sma0114* (bottom). B) Shows the RT PCR products from *phbA* (top) and from *phaZ* (bottom). The Tn5-233 insertion into *phbA* in strain DG3155 is upstream of the binding sites for the *phbA* RT-PCR primers. The faint band in the lane with DG3155 RT-PCR product is likely due to transcription of phbA arising from transcription within Tn5-233. In strain DG3155 the *phbA* gene is interrupted at the 86th codon. RT-PCR experiments were done as described in Materials and Methods. The table denotes the relevant genotypes of the strains used in the experiments shown in panels A and B.



Supplemental Figure 2. Effects of mutations which render Sma0113 nonphosphorylatable (strain PG94 *sma0113*-H670K, panel A) and Sma0114 nonphosphorylatable (strain PG79 *sma0114*-D57A, panel B). Cultures were grown in M9 minimal medium with 0.05% succinate plus 0.1% lactose. The curves were time-shifted to align them at point of succinate exhaustion, in order to more readily compare the length of the diauxic lag.



Supplementary Figure 3. Effect of *sma0113* and *sma0114* deletions on nodulation of alfalfa. Alfalfa seedlings grown on BNM were inoculated as described in Materials and Methods. Panel A shows the shoot dry weight 30 days after inoculation. Panel B shows the number of nodules per plant 30 days after inoculation. 10 plants were inoculated with each, strain and the error bars represent standard deviations. There was no statistical difference between wild-type and the *sma0113* and *sma0114* mutants in shoot weight or nodule number at $P<0.05$. All strains were significantly different from the uninoculated control at a $P<0.05$.