TABLE S2. Primers used in this study.

Primer	Sequence* (5'—3')	Restriction enzyme† and use
P1	GTTGCCGTCCCTGGTATGG	PCR *ntrC* from the *A. vinelandii* genome
P2	GTGGACACGGCATAGATTTC	PCR *ntrC* from the *A. vinelandii* genome
P3	AGAGCTCAGCCATGCCCAGGAG	*Sac*I; *ntrC* deletion mutation construction
P4	AGAGCTCGGCTTGGGCAGGTATTC	*Sac*I; *ntrC* deletion mutation construction
P5	AAATCTAGAAGCAGCGCTTCGAAAC	*Xba*I; PCR *nasAB* promoter region from the *A. vinelandii* genome
P6	TGGATCCATGCCGGCCAGCACCGGAGAG	*Bam*HI; PCR *nasAB* promoter region from the *A.*

		vinelandii genome
P8	AGCTGGGGCCGCAATTC	PCR tandem *rrnB1* from pPROBE-NT
P9	ATTCAGCTTCCGATC	PCR tandem *rrnB1* from pPROBE-NT
P10	CCGACAGAACGGGATAGGACAAAGGCGTC	*nasAB* leader small ORF mutation
P11	CCTATCCCGTTCTGTCAAAGGCGTC	*nasAB* leader small ORF mutation
P12	GCAGTGTTTCCCGACAGGAATGGACAAAGGCGTC	*nasAB* leader hairpin II deletion mutation
P13	CTGTCGGGAAACACTGC	*nasAB* leader hairpin II deletion mutation
P14	GGGGATCGGAAGCTGAATG	Confirmation of tested sequence in pVnflacZ(a/b)
P15	GTCTCATGAGCGGATAC	Confirmation of *vnf* in pWhite
P16	AGTCGACAAGCTTCCTCGCTCACTGACTC	*Sal*I, *Hind*III; PCR *bla* and pM1 of pBbluscript II KS

		(+)
P17	AGAGCTCAGGTGGCACTTTTCG	PCR *bla* and pM1 of pBbluscript II KS (+)
P18	GTATTACCGCCTTTGAGTG	Confirmation of *vnf* in pWhite
P19	GTGATCTGTCGGTTTTC	*nasAB* leader hairpin I deletion mutation
P20	AAACCGACAGATCACATAAACGTGGAGGGCAGTG	*nasAB* leader hairpin I deletion mutation
P21	AAATCTAGAACCAAGACAGTGCAAG	*Xba*I; *nasAB* promoter deletion construction
P22	AAATCTAGAAACCCCATAAGAGG	*Xba*I; *nasAB* promoter deletion construction
P23	AAATCTAGAGCTCTGCTCGCCCTGTTG	*Xba*I; *nasAB* promoter deletion construction
P24	AAATCTAGAGTCATCCGTGAAAC	*Xba*I; *nasAB* promoter deletion

		construction
P25	CAAGGCGATTAAGTTGGGTAAC	Confirmation of tested sequence in pVnflacZ(a/b)
P26	GTAAAACGACGGCCAGTG	pBluescript II KS(+) sequencing
P27	CAGGAAACAGCTATGAC	pBluescript II KS(+) sequencing
P28	TAACACAGCCCCTATATCGAGAAAACCGAC	σ^{54} binding site mutation
P29	TATAGGGGCTGTGTTAGTTTCACGGATGACTG	σ^{54} binding site mutation
P30	CAGAACGGGAATGGACAATTTTTGTTTTCCGCTTTC	Terminator hairpin deletion mutation
P31	AATTGTCCATTCCCGTTCTG	Terminator hairpin deletion mutation
P32	AAGGATCCGCTTATGTGATCTGTCG	*Bam*HI; Transcriptional fusion construction
P33	AAAGAGCTCATCATCTCGCCCAGTTC	*Sac*I; PCR *vnf* sequence
P34	AAACGCCTCGAGAAGAGCATG	*Xho*I; PCR *vnf* sequence

P35	CGCCTGGCTCGACGAATG	*nasA* promoter region cloning confirmation
P36	GTCCATTCCCGTTCTGTC	*nasA* promoter region cloning confirmation
P37	TCGAATTCCATGCTGCGCATCCTCCTG	*EcoR*I; Clone *nasT* into pDK6
P38	ATAGATCTCAGCTTCCCAGCATGTCGTGCATG	*Bgl*II; Clone *nasT* into pDK6
P39	ATAGAATTCCATGACAGACCACCACGCA ACTTC	*EcoR*I; Clone *nasS* into pDK6
P40	ATAAGATCTTTAGGAGGATGCGCAG	*Bgl*II; Clone *nasS* into pDK6
P41	TCCGTTGTGGGGAAAGTTATC	Construct pBTW
P42	AGCGGCCGCTCACAATTCCACAC	Construct pBTW
P43	AGAGCGGCCGCCGACAGATCACATAAG	*Not*I; PCR *nasA´-´lacZ* fragment

* The underlined sequences are the restriction sites.

† Restriction enzymes that can digest the underlined sequences.