```
Reciever domain (REC)
                                                                          phosphorylation
Gsul_GnfM    MLLNRILVADDEESMRWVLSKALRKKGFTVDLARDGEEALRLIQSNEYDLAILDIKMPGF   60
Kpne_NtrC    MQRGIAWIVDDDSSIRWVLERALTGAGLSCTTFESGNEVLDALTTKTPDVLLSDIRMPGM   60
Ecol_NtrC    MQRGIVWVVDDDSSIRWVLERALAGAGLTCTTFENGAEVLEALASKTPDVLLSDIRMPGM   60

Gsul_GnfM    TGLELLDKVRELKHDLLMVIMTAEASMKNAVEAMKRGAYDYITKPFDLDVIDAIIE   116
Kpne_NtrC    DGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVD   116
Ecol_NtrC    DGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVE   116

Gsul_GnfM    KVHKAREITSQMTILREELKERYHLEK   143
Kpne_NtrC    -----RAISHYQEQQQPRNAPISSPTA   138
Ecol_NtrC    -----RAISHYQEQQQPRNVQLNGPTT   138

AAA/Sigma54_activation domain
                                               Walker A
Gsul_GnfM    NIIGNSPAMREVYKTIGKVAPSDVTVLVQGESGTGKELIARAIHFNSKRIGKPFIALNCA   203
Kpne_NtrC    DIIGEAPAMQDVFRIIGRLSRSSISVLINGESGTGKELVAHALHRHSPRSKAPFIALNMA   198
Ecol_NtrC    DIIGEAPAMQDVFRIIGRLSRSSISVLINGESGTGKELVAHALHRHSPRAKAPFIALNMA   198

                     sigma54 binding            Walker B
Gsul_GnfM    AIPKDLLESELFGFEKGAFTGAVERKLGKFEQANGGTIFLDEIGDMPLDLQAKILRVLQE   263
Kpne_NtrC    AIPKDLIESELFGHEKGAFTGANTVRQGRFEQADGGTLFLDEIGDMPLDVQTRLLRVLAD   258
Ecol_NtrC    AIPKDLIESELFGHEKGAFTGANTIRQGRFEQADGGTLFLDEIGDMPLDVQTRLLRVLAD   258

                                 AAA minimum consensus
Gsul_GnfM    KEVTRTGGSQNIAVDVRIVAATNQNLEELVRKKQFREDLFYRLNVVPIQLVPLRERKEDV   323
Kpne_NtrC    GQFYRVGGYAPVKVDVRIIAATHQNLEQRVQEGKFREDLFHRLNVIRVHLPPLRERREDI   318
Ecol_NtrC    GQFYRVGGYAPVKVDVRIIAATHQNLEQRVQEGKFREDLFHRLNVIRVHLPPLRERREDI   318

Gsul_GnfM    PLLVDYFLQNACAELEVSPKKCSPEAMALLTTHSWPGNVRELENTIKRAVILSSDPLLTP   383
Kpne_NtrC    PRLARHFLQIAARELGVEAKQLHPETETALTRLAWPGNVRQLENTCRWLTVMAAGQEVLT   378
Ecol_NtrC    PRLARHFLQVAARELGVEAKLLHPETEAALTRLAWPGNVRQLENTCRWLTVMAAGQEVLI   378

Gsul_GnfM    SDFPGLRARQTGSE   397
Kpne_NtrC    QDLPSELFETTVPD   392
Ecol_NtrC    QDLPGELFESTVAE   392

Gsul_GnfM    ATAADDLS-----LEALVDMKLRASLTNLDKMESGDI   429
Kpne_NtrC    SPTQMQPDSWATLLGQWADRALRSGHQNL--------   421
Ecol_NtrC    STSQMQPDSWATLLAQWADRALRSGHQNL--------   421

DNA-binding domain (HTH)
                           Helix-Turn-Helix
Gsul_GnfM    YNLVLKQIERPLIRFVLEKTRGNQVKGAEILGINRNTLRKKIQELGIELRKD   481
Kpne_NtrC    LSEAQPEMERTLLTTALRHTQGHKQEAARLLGWGRNTLTRKLKELGME----   469
Ecol_NtrC    LSEAQPELERTLLTTALRHTQGHKQEAARLLGWGRNTLTRKLKELGME----   469
```

Figure S1. GnfM. (A) Domain organization of GnfM. (B) Comparison of *G. sulfurreducens* GnfM with NtrC. *G. sulfurreducens* GnfM (Gsul, GenBank accession number, AAR34331) and NtrC homologues from *Escherichia coli* (Ecol, AAC76866) and *Klebsiella pneumoniae* (Kpne, CAA26923) are aligned. The boxes contain the conserved regions found in the EBP family containing the receiver domain, including the phosphorylation site, the Walker A and B motifs, the GAFTGA sigma54 binding motif, the AAA minimum consensus, and the helix-turn-helix motif (1).

```
Gsul    M----------TTEEKKEEFLATVIDSVGDGVIVIDLDGRIALMNPAAEEISGISRRQAV
Gmet    M----------SPESPNEAFLATIIDSVGDGVIVIDLGGRITLMNPAAEEIIAISRRQAM
Gura    V-----------TTEHLQEYYANIIDSVGDGVIVLDIQGVITLLNPAAEEIAGISRRQAK
Rcap    M---NLPPP------------GIIWNSLPLPALMLDVNDRVIEINPAAELFLNLSARALK
Kpne    MATGTLPDA------------GQILNSLINSILLVDDDLAVHYANPAAQQLLAQSSRKLF
Ecol    MATGTQPDA------------GQILNSLINSILLIDDNLAIHYANPAAQQLLAQSSRKLF

Gsul    GHRFALVFHREAVLREMVGKTATSGMTISDHE-NIVIRKLKQL-TPVSATTFPLMLPHGE
Gmet    GHPFAALLGSQEILVDMVAKTAATGMTISDNE-NIVIRKAKQL-TPVAVTTFPLLRQDGE
Gura    GAHFSALFKGEDILLEMVNKTAATGMTISDHE-NIVLKMTGRL-IPISATTSPLLMANGE
Rcap    GQALGERLAISAPLEEIFARVRKNRSALFVNDVDLTTGERAPVQCNLQAAPIA---DDPE
Kpne    GTPLPELLSYFSLNIGLMQESLAAGQGFTDNEVTLVIDGRSHI-LSLTAQRLP-------
Ecol    GTPLPELLSYFSLNIELMQESLEAGQGFTDNEVTLVIDGRSHI-LSVTAQRMP-------
                                              *
Gsul    TTGTILVLRDITSIRELEDAVRNADRLSTLGTLAAGLAHEIKNPLGGIKGAAQLLELELP
Gmet    PIGTILMLRDLTNIRELEDAVRHADRLSTLGTLAAGLAHEIKNPLGGIKGAAQLLEMELP
Gura    RIGTILILRDLTNIRELEEAVRQADRLSTLGALAAGLAHEIKNPLGGIKGAAQLLEMELP
Rcap    TVLLLISPREIADRLGRASMVKSAARSAGIG-MAEMLAHEIKNPLAGIAGAAQLLSMGLS
Kpne    EGYILLEMAPMDNQRRLSQEQLQHAQQIAARDLVRGLAHEIKNPLGGLRGAAQLLSKALP
Ecol    DGMILLEMAPMDNQRRLSQEQLQHAQQVAARDLVRGLAHEIKNPLGGLRGAAQLLSKALP

Gsul    TESELRDNVRIMLKEVERVNRIVEELLALASPRGLQLSKVNLHKVIGDILTLQKRSTEGK
Gmet    PESELRDNVRVVVREVDRVNRIVEELLALSSPRKLQLTKVNLHKILGDIVTLRKRATEGK
Gura    DNAELRDCTRVMLKEVQRVNRIVEELLELASPRKLDLTKVNLHKILGDIILLQKRTVDDR
Rcap    GED--LELTDLIVDETRRIVKLLEQVEQFGNVRPPEMKPVNIHDVLDRARKSAGVGFGA-
Kpne    DPA-LMEYTKVIIEQADRLRNLVDRLLGPQHP-GMHVTE-SIHKVAERVVKLVSMELPD-
Ecol    DPS-LLEYTKVIIEQADRLRNLVDRLLGPQLP-GTRVTE-SIHKVAERVVTLVSMELPD-

Gsul    NVAFQQQFDPSIPPILADEGLLTQLFLNLVKNAMEAVDDG-GCIRVASRVISDYSMTQK-
Gmet    SVTFQQQFDPSIPPILADEGLLTQLFLNLIKNAVEAVDER-GTIRVASRVLSDYSMTPK-
Gura    RVTFQQHFDPSIPPILADEALLTQLFLNLIKNAVEAVGAV-GLIKVSSRVLADYSMTQK-
Rcap    HMLIVEDYDPSVPPTLGDADQLTQVFLNLLKNASEAAKGQ-GTIRL--RTFYDYALRLRR
Kpne    NVKLVRDYDPSLPELPHDPDQIEQVLLNIVRNALQALGPEGGEITL--RTRTAFQLTLH-
Ecol    NVRLIRDYDPSLPELAHDPDQIEQVLLNIVRNALQALGPEGGEIIL--RTRTAFQLTLH-

Gsul    --GERRSRMVAIDVADDGPGIPPERLEQLFTPFFTTKTKGTGLGLAICQKIVTEHRGMIK
Gmet    --GERRSRMVAVDVRDDGPGIPREQLEQLFTPFFTTKAKGTGLGLAICQKIVTEHRGMLK
Gura    --GEGRSRMVAIEVSDDGPGILKEQLEHLFTPFYTTKAKGTGLGLAICHKIVAEHRGMIR
Rcap    PDGGGSAVPLQVEVIDDGPGIPADIASSIFEPFVSGRENGTGLGLALVSKIISEHNGWIS
Kpne    --GVRYRLAARIDVEDNGPGIPSHLQDTLFYPMVSGREGGTGLGLSIARSLIDQHSGKIE
Ecol    --GERYRLAARIDVEDNGPGIPPHLQDTLFYPMVSGREGGTGLGLSIARNLIDQHSGKIE

Gsul    VESYPGKGTTFTVMLPLIQ---
Gmet    VESDPGTGTTFTVMLPLIQ---
Gura    VDSEPTKGTTFTVMLPLIQ---
Rcap    VESAPGR-TLFRISLPVAPKEL
Kpne    FTSWPGH-TEFSVYLPIRK---
Ecol    FTSWPGH-TEFSVYLPIRK---
```

Figure S2. Comparison of GnfL homologues with NtrB. GnfL homologues from *G. sulfurreducens* (Gsul, GenBank accession number, AAR34331), *G. metallireducens* (Gmet, ABB32781), and *G. uraniireducens* (Gura, ABQ25121), and NtrB homologues from *Escherichia coli* (Ecol, AAC76866), *Klebsiella pneumoniae* (Kpne, CAA26923) and *Rhodobacter capsulatus* (Rcap, CAA51074) are aligned. NtrB homologues have a PAS domain at the N-terminus. A putative autophosphorylation site is indicated by an asterisk.

Gsul	**E**VEL**LKE**QV**EDLKE**TL**E**S**RK**IV**EKAKG**I**LM**QN**QGL**T**E**P**EA**F**R**KM**QK**L**AMDKRK**SM**RQIA**E**AIL**LT**E**A
Gmet	**E**VET**LKE**EV**EDLKE**IL**E**S**RK**V**IEKAKG**V**LM**RN**QGLSE**P**EA**F**R**RM**QK**L**AMDKRK**SM**RQIA**E**AIL**LT**E**
Gura	**E**IDE**LKE**QV**EDLKE**T**IE**S**RK**V**IEKAKG**V**LM**RT**QGLSE**P**EA**F**R**KM**QK**L**AMDKRK**SL**RQIA**D**AIL**LT**E**S
Ppro	**E**VDG**LKE**KID**DL**R**E**V**IE**N**RK**I**IE**R**AKG**M**LM**ETER**LSE**AD**A**Y**R**TL**QK**M**AMDKRK**TL**RQ**VADS**IL**KSAK
Paer	**E**MAK**LK**QKT**E**Q**L**QDR**I**AGQAR**I**NQ**AK**VL**LM**QRH**G**WD**E**R**EA**HQHLSRE**AM**KR**R**EPILK**IA**QEL**L**GN**E**PSA
Kpne	**E**LQQ**L**SGQLAS**LK**DAL**E**E**RK**L**IEKAK**SV**LM**TY**QG**MQ**E**EQ**A**WQALR**K**M**AMDK**NQRMVE**IA**R**A**L**L**TVKALWRVTPK

Figure S3. GnfR. The C-terminal ANTAR domains of GnfR homologues are compared with those of known antiterminators. GnfR homologues from *G. sulfurreducens* (Gsul, GenBank accession number, AAR36216), *G. metallireducens* (Gmet, ABB30902), *G. uraniireducens* (Gura, ABQ25350), and *P. propionicus* (Ppro, ABL01052), and AmiR from *P. aeruginosa* (Paer, CAA32023) and NasR from *K. pneumoniae* (Kpne, AAA25101) are aligned.

```
                                                     -24         -12
Gsul_nifH  TTGCTTGCCTGTAAAGCTTAGTTAATTCAGTGTGTTGCTGGTTGGCATGGACGGTGCTAT
Gmet_nifH  GGGGGAAGGAGCAAAGTCAAGTAATTACAATGGGTTGATTTTTGGCACGGTCAGTGCTTT
Gura_nifH  TCTGTGGAAATAAAAAGTCCGTCATTTCAGCTTGTTAGCAGTTGGCATGGTCAATGCTAA
                       ***     ** * * **    ***     ****** ** *  ****

                   +1
Gsul_nifH  ACCACTATCAAACATACAGACGA------GAATACGCCGGAGTATTCG----CTGCTGAA
Gmet_nifH  ATCTGTTTCAAAT-CAATAACGA------GAATACGCCGGAGTATTCG----CTGCTGAA
Gura_nifH  AGTAAAGCCATACATCATAGCGATGATCTGAATACGCTGCGGTATTCGACTATTATATGT
           *       ** *        ***      ******** *  *******     *

Gsul_nifH  CGCAGGCAAGGGCGCCACCATTAAACGGAAATGGGGCGCCTTTTTTGTTGCCCCGAACAT
Gmet_nifH  CGCAGGCAAGGGCGCCACCAATAT-CACCATTGGGGCGCCTTTTTTGTTGCCCCGCAAAC
Gura_nifH  CACAGGCAAAGGCGCCACCATAAT---TCAATGGGGCGCCTTTTTTGTTGCCCCGAAAAT
           * ******* **********  *      * ************************ * *

Gsul_nifH  TCCCAGGCAGTCCACGGATTGGTGGACGAAAGGAGACAGGACATG
Gmet_nifH  CATTAGAGGCTC----AGACCCAGGGCGAAAGGAGAAACATCATG
Gura_nifH  TCACTTGCGGTCCACAGATTAGTGGACGAAAGGAG-CAGAACATG
                     **           ** *********  *   ****
```

Figure S4. Alignment of the 5’ untranslated regions of *nifH*. The putative transcription termination signals are highlighted in grey. Highly conserved dinucleotides GG and GC in RpoN-dependent –24/-12 promoter elements are indicated by bold letters. The transcription initiation site for Gsul_*nifH* is indicated in bold by +1. Translation initiation codon, ATG, is underlined with bold letters. Gsul; *G. sulfurreducens*, Gmet; *G. metallireducens*, Gura; *G. uraniireducens*.

(A)

RpoD; CTAGATTC**TTGACA**TAAAAGTGGTATTAAAG**TACTTA**TTTACTCAAAG
TAAGAACTGTATTTTCACCATAATTTCATGAATAAATGAGTTTCCTAG

RpoD-TTS(WT); CTAGATTC**TTGACA**TAAAAGTGGTATTAAAG**TACTTA**TTTACTCAAAGAAGGGCGCCACCATTAAACGGAAATGGGGCGCCTTTTTTGTTG
TAAGAACTGTATTTTCACCATAATTTCATGAATAAATGAGTTTCTTCCCGCGGTGGTAATTTGCCTTTACCCCGCGGAAAAAACAACCTAG

RpoD-TTS(-up); CTAGATTC**TTGACA**TAAAAGTGGTATTAAAG**TACTTA**TTTACTCAAAGAAACGGAAATGGGGCGCCTTTTTTGTTG
TAAGAACTGTATTTTCACCATAATTTCATGAATAAATGAGTTTCTTTGCCTTTACCCCGCGGAAAAAACAACCTAG

RpoD-TTS(-down);CTAGATTC**TTGACA**TAAAAGTGGTATTAAAG**TACTTA**TTTACTCAAAGAAGGGCGCCACCATTAAACGGATTTTGTTG
TAAGAACTGTATTTTCACCATAATTTCATGAATAAATGAGTTTCTTCCCGCGGTGGTAATTTGCCTAAAACAACCTAG

RpoD-TTS(mut); CTAGATTC**TTGACA**TAAAAGTGGTATTAAAG**TACTTA**TTTACTCAAAGAAGGGCGCCACCATTAAACGGAAAT**ACATACAACA**TTTTGTTG
TAAGAACTGTATTTTCACCATAATTTCATGAATAAATGAGTTTCTTCCCGCGGTGGTAATTTGCCTTTATGTATGTTGTAAAACAACCTAG

(B)

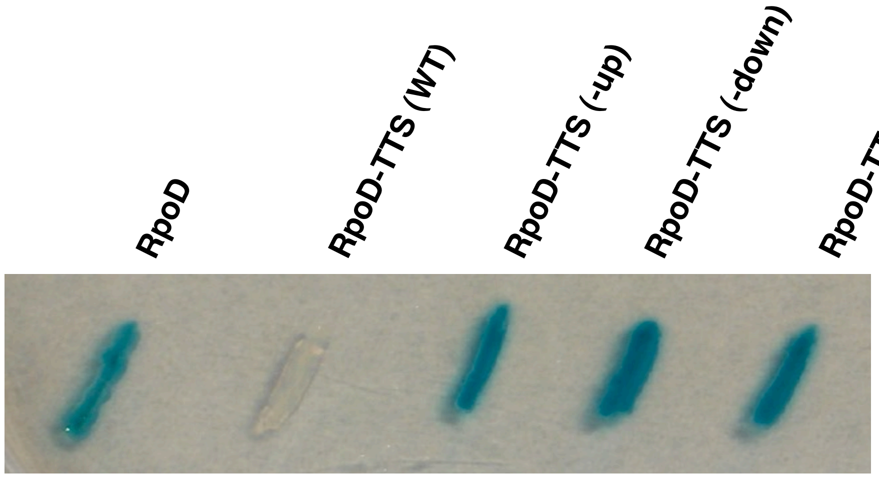

Figure S5. *lacZ* fusion assays for transcription termination signals. (A) Sequences of promoters used for *lacZ* fusion assays (Figure 10D). RpoD-dependent -35/-10 promoter elements are underlined with bold letters. The regions predicted to form the stem structure are underlined. Mutated nucleotides from the wild-type sequence are indicated in bold. (B) A picture of the strains grown on an X-gal plate (Figure 10D).

Table S1. Primers used in this study. Recognition sequences for restriction enzymes are underlined.

Name	Sequence	Enzyme
Primer extension assays		
NifH-PE	CCGTAGATCGCTACCTGTCTC	
GlnB-PE	ATCCAGCTTGAACGGTTTGATAATC	
GnfK-PE	TCCTTTTCTGCTATGTACTTC	
GnfR-PE	TCGTCGCATATAAGGACACTTC	
GdhA-PE	TGATAGATGCCCTGAAGTTTC	
Construction of EBP expression vectors		
0300-Fwd	TCTCATATGGGACAGCAGTGGGTCAAC	NdeI
0300-Rev	TCTCTCGAGTGCAAGAGACGTGGAAATTAC	XhoI
0372-Fwd	TCTCATATGCCCGCAACCATACTGATC	NdeI
0372-Rev	TCTCTCGAGCGGCCCCTGGTCCCGGGTTATGCCGAA	XhoI
0598-Fwd	TCTCATATGGAAAACATTGATGTACTTGTA	NdeI
0598-Rev	TCAAGCTTGTTCGTCATCTGGTTACGTAC	HindIII
0776-Fwd	TCTCATATGCTCAAGGCGAAAATACTCA	NdeI
0776-Rev	TCTCTCGAGTTCGTCGTCGGCCGGGACGCCTC	XhoI
0811-Fwd	TCTCATATGAACGAAACGATACTCGTCGTGGAC	NdeI
0811-Rev	TCTCTCGAGTTTTTTAGCGTCGATCCCGTAAC	XhoI
0963-Fwd	TCTCATATGCCGATCGTGTCAGATAAAAAGCGCA	NdeI
0963-Rev	TCTCTCGAGGGCGTAGTCTTCGCGGCGGATA	XhoI
1003-Fwd	TCTCATATGTTACTGAACCGCATATTGGT	NdeI
1003-Rev	TCTCTCGAGGTCTTTTCTCAGTTCGATGCCCA	XhoI
1129-Fwd	TCTCATATGAAAGAGCGGACCAAAATCC	NdeI
1129-Rev	TCAAGCTTGAGCGGCATGCCGAGCCGCCGCATC	HindIII
1320-Fwd	TCTCATATGGCTGAAGAGCGGCAACCT	NdeI
1320-Rev	TCTCTCGAGTTTTTTTCTCTCCGGTGCAGTGATC	XhoI
1495-Fwd	TCTCATATGGAAATTCATGTTCTCGTA	NdeI
1495-Rev	TCTCTCGAGCTCCTCATCCATGCCAAATTTTGCCA	XhoI
1940-Fwd	TCTCATATGGAAAAACTGCTGATCGTC	NdeI
1940-Rev	TCTCTCGAGCCCACTTATCCCGTGTTTTTCATCA	XhoI
2041-Fwd	TCTCATATGAAAAAGCGGATACTGGTC	NdeI
2041-Rev	TCTCTCGAGATCGATGCCGAATTCCTTGAGCTTGTA	XhoI
2915-Fwd	TCTCATATGAGAAAGACAAAGATACTGGT	NdeI
2915-Rev	TCAAGCTTTTTAAGGAAGCCGAACTTCTTCA	HindIII
3363-Fwd	TCTCATATGGAGCCGATAATTACCGAC	NdeI
3363-Rev	TCAAGCTTTTGTCTGTCCCCCTGCGGCATATC	HindIII
Promoter for DNA-binding assays		
GnfK-Pro1	CGAGATCATGGGCCTCGAC	
GnfK-Pro2	AGAACGAAGATGTTATATA	
NifH-Pro1	TTGCCGAGGCGATTCTGCTGAC	
NifH-Pro2	AGCAACACACTGAATTAAC	
GlnB-Pro1	AAGCGTGATGCAGAACTGTC	
GlnB-Pro2	TAAACAGAGAGAAAAATCCAAC	
GdhA-Pro1	ATCCTCCCATCATCGTGGTC	
GdhA-Pro2	TGATAGATGCCCTGAAGTTTC	
3409-Pro1	TGTATGTAATTTAAATGCA	
3409-Pro2	GTGCCACAGTGGAAAAC	
Probe for footprint assays		
GnfK-F1	TCTCTAGACGAGATCATGGGCCTCGAC	

GnfK-F2	TCGGATCCGTTAGGCACGAGGCA
GdhA-F1	TCTCTAGACAACAACCGGTCCGTCCA
GdhA-F2	TCGGATCCCCTGATTAAAATGTAGACA

lacZ fusion assays

gnfK

-243T	TCTCTAGACGAGATCATGGGCCTCGAC
-111T	TCGAATTCGACTGGTGATTGAAAAAGC
-88T	TCGAATTCTTAATCGAGGTGACGGCCGGTC
-129B	TCGAATTCACAAAAAGAAAAGCCGCC
-106B	TCGAATTCTGCCCAATATTTCAGCA
+32B	AGCGCATTTGCCATGGGTCAC

gdhA

WT12T	CTAGAAAATTTGCCGATAAATCAGGCAATTGCCCACCTCAACA
WT12B	CGTGATGTTGAGGTGGGCAATTGCCTGATTTATCGGCAAATTTT
WT34T	TCACGCCATGCACAGTTTT**GG**TGCAGTACGT**GC**ATAAAATGCAGGCAATCG
WT34B	GATCCGATTGCCTGCATTTTATGCACGTACTGCACCAAAACTGTGCATGG
Mut34T	TCACGCCAATGTACGTTTT**GG**TGCAGTACGT**GC**ATAAAATTACTTATATCG
Mut34B	GATCCGATATAAGTAATTTTATGCACGTACTGCACCAAAACGTACATTGG

Construction of pCDNdeII

NdeI-Fwd	AATTGACTGACTGAGAAGGAGATATACATATGCCCTCGAGTCTAGAG
NdeI-Rev	AATTCTCTAGACTCGAGGGCATATGTATATCTCCTTCTCAGTCAGTC

Construction of overexpression vectors for GnfL-K and GnfM in *Geobacter*

GnfLK-Fwd	CTCAGATCTGAATTCCATGCTTCCTCACGGCGAAAC	BglII, EcoRI
GnfLK-Rev	TCTCTAGACTACTGAATCAGGGGGAGCATC	XbaI
GnfM-Fwd	TCTCATATGTTACTGAACCGCATATTGGT	NdeI
GnfM-Rev	TCTCTCGAGAAGCTTCAGTCTTTTCTCAGTTCGA	XhoI, HindIII

Construction of overexpression vectors for GnfL-K and GnfM in *E. coli*

GnfLK-Fwd	TCTCATATGCTTCCTCACGGCGAAAC	NdeI
GnfLK-Rev	TCAAGCTTCTGAATCAGGGGGAGCATCAC	HindIII
GnfM-Fwd	TCTCATATGTTACTGAACCGCATATTGGT	NdeI
GnfM-Rev	TCTCTCGAGGTCTTTTCTCAGTTCGATGCCCA	XhoI

Construction of mutants

GnfK-D1	TCTCTAGATGATCGCCGAATGGATCCAC	XbaI
GnfK-D2	TCGAATTCCTTTTCTGCTATGTACTTC	EcoRI
GnfK-D3	TCTAAGCTTCATTCGCACCAGCCAGAAC	HindIII
GnfK-D4	TCGGATCCATAACCGGTTGGTAGACC	BamHI
GnfR-D1	TCGGATCCTCGCGCCTGAAGAGCGCCTC	BamHI
GnfR-D2	ACGTCGGGAAGCTTGGCAAAC	HindIII
GnfR-D3	TCGAATTCACGGAGCCCGAAGCGTTCCGCA	EcoRI
GnfR-D4	TCTCTAGAAGCCGACCTTGAGCACGTCC	XbaI
Km-Fwd	GCATGAGAATTCCTGACGGAACAGCGGGAAGTCCAGC	EcoRI
Km-Rev	GCTATGAAGCTTTCATAGAAGGCGGCGGTGGAATCGAA	HindIII

Primer extension assays

NifH-R1	CCTGCGTTCAGCAGCGAATAC
NifH-R2	CCGTAGATCGCTACCTGTCTC

GlnB-PE	ATCCAGCTTGAACGGTTTGATAATC	
Overexpression of GnfK and GnfR		
GnfK-Fwd	TCTCATATGGCAAATGCGCTTGCGAAGTA	NdeI
GnfK-Rev	TCTCTCGAGCTCGGCTGCGACAAAGGTGAGCGTA	XhoI
GnfR-Fwd	TCTCATATGATTTTAGTGCGAAGTGTCCTTA	NdeI
GnfR-Rev	TCTCTCGAGCGCTTCGGTCAGCAGAATCGCCTC	XhoI

Table S2. Alignment of the RpoN-dependent –24/-12 promoter elements of the nitrogen-fixation genes. The –24/-12 promoter elements for *nifH*, *glnB*, *gnfK*, *gnfR*, and *gdhA* of *G. sulfurreducens* were assigned from the transcription initiation sites determined by the primer extension assays (Figure 1A). Other –24/-12 promoter elements were identified by comparing the promoter regions of the nitrogen-fixation genes. It is likely that the *glnB* operon contains *glnA*, the *nifEN* operon contains *nifEN* and *nifX* in this order, the Gsul_0938 homologue operon contains a gene encoding a hypothetical protein, *glnK* and *amtB* in this order, and the Gsul_2799 homologue operon contains genes encoding a putative radical SAM domain protein and a putative acetyltransferase. Highly conserved dinucleotides GG and GC in RpoN-dependent –24/-12 promoter elements are indicated by bold letters. Gsul; *G. sulfurreducens*, Gmet; *G. metallireducens*, Gura; *G. uraniireducens*.

Gene	**-24** **-12**
Gsul_nifH	GGTT**GG**CATGGACGGT**GC**TATA
Gmet_nifH	TTTT**GG**CACGGTCAGT**GC**TTTA
Gura_nifH	AGTT**GG**CATGGTCAAT**GC**TAAA
Gsul_nifEN	GATT**GG**CACGTGGGGT**GC**AAAG
Gmet_nifEN	CCTT**GG**CACGTCACCT**GC**TAAC
Gura_nifEN	GATT**GG**CACGGCAAAT**GC**TCAA
Gsul_nifV	GCCT**GG**CACGGCTCGT**GC**TAAT
Gmet_nifV	GCGT**GG**CACGCCTTGT**GC**TTTA
Gura_nifV	TACT**GG**CATGCCTATT**GC**TTGA
Gsul_glnB	TTTA**GG**CAGACTATTT**GC**TTTT
Gmet_glnB	TTTG**GG**CAAAGTATTT**GC**TTTG
Gura_glnB	TCTT**GG**CAGATAATTT**GC**TATA
Gsul_0938	GAGT**GG**CACGGCCTAT**GC**TAAA
Gmet_0693	TGAT**GG**CATGCCTTAT**GC**TAAT
Gura_3367	ATGT**GG**CACGGCTTGT**GC**TTTT
Gsul_gnfK	TTCT**GG**CATGCCTCGT**GC**CTAA
Gmet_gnfK	TTCT**GG**CACGCCTCGT**GC**CTAC
Gura_gnfK	TGTT**GG**CATGACTTAT**GC**CTTT
Gsul_gnfR	GATT**GG**AACACTTTAT**GC**TGAA
Gmet_gnfR	CCTT**GG**AACGGTTTAT**GC**TGAA
Gura_gnfR	GATT**GG**AATGGTTCGT**GC**TTTT
Gsul_2799	TTGT**GG**CACGCTTAGT**G**TTAAG
Gmet_0681	TTCT**GG**CACGCTTAAT**GC**CATA
Gura_1209	ATCT**GG**CACGCTTCAT**G**TTAAT
Gsul_gdhA	TTTT**GG**TGCAGTACGT**GC**ATAA
Gmet_gdhA	TTTT**GG**TGCACCCTCT**GC**ATAT
Gura_gdhA	TTAT**GG**TGCACTATGT**GC**ATAT

Table S3. Conservation of EBPs in *Geobacter* species. Presence and absence of homologues of *G. sulfurreducens* EBPs are indicated by + and -, respectively.

sulfurreducens	*metallireducens*	*uraniireducens*
GSU0280 (EBP1)	-	-
GSU0300 (EBP2)	+	+
GSU0359 (EBP3)	+	-
GSU0372 (EBP4)	+	+
GSU0470 (EBP5)	-	+
GSU0598 (EBP6)	+	+
GSU0776 (EBP7)	+	+
GSU0811 (EBP8)	+	+
GSU0841 (EBP9)	-	+
GSU0963 (EBP10)	+	+
GSU1003 (EBP11)	+	+
GSU1039 (EBP12)	-	-
GSU1129 (EBP13)	+	+
GSU1250 (EBP14)	-	+
GSU1320 (EBP15)	+	+
GSU1495 (EBP16)	+	+
GSU1653 (EBP17)	-	+
GSU1940 (EBP18)	+	+
GSU1989 (EBP19)	+	-
GSU2041 (EBP20)	+	+
GSU2506 (EBP21)	-	-
GSU2524 (EBP22)	-	+
GSU2581 (EBP23)	-	-
GSU2753 (EBP24)	-	+
GSU2915 (EBP25)	+	+
GSU3217 (EBP26)	-	+
GSU3363 (EBP27)	+	+
GSU3418 (EBP28)	-	+

Table S4. Predicted GnfM-binding sites. The sequences were identifed by comparing the promoter regions of the nitrogen-fixation genes. It is likely that the *glnB* operon contains *glnA*, the *nifEN* operon contains *nifEN* and *nifX* in this order, the Gsul_0938 homologue operon contains a gene encoding a hypothetical protein, *glnK* and *amtB* in this order, and the Gsul_2799 homologue operon contains genes encoding a putative radical SAM domain protein and a putative acetyltransferase. Highly conserved dinucleotides GG and GC in RpoN-dependent –24/-12 promoter elements are indicated by bold letters. Gsul; *G. sulfurreducens*, Gmet; *G. metallireducens*, Gura; *G. uraniireducens*.

Gene/operon	sequence
Gsul_nifH	TGATTAATTGTTGTGCA
Gsul_nifH	TGCATGGGAAAGAGGCG
Gmet_nifH	TGGCTATTCCTTGAGCA
Gmet_nifH	TGAACAGGAAAGAGGCG
Gura_nifH	TGATTAAATATTGTGCA
Gura_nifH	TGCTGACCGATAAAGCG
Gsul_nifEN	TGAGCAAATCCATCCCG
Gmet_nifEN	TGCATAAAATGTGTGCA
Gura_nifEN	TGCCCAATAATTGGGCA
Gsul_nifV	TGCCCGATATTTGGGCA
Gmet_nifV	TGTTTATAAAACAGTCA
Gura_nifV	TGTGTAAAAAAGAGGCA
Gsul_glnB	TGCTCATTTGGTATGCA
Gsul_glnB	TGCCTTTATTTTGTGCT
Gmet_glnB	TGCTTCTGATTTGTGCA
Gmet_glnB	TGCCTTATTTTTGAGCT
Gura_glnB	TGCCCATCCATTGGGCA
Gura_glnB	TGCTCAATTTATAAGCT
Gsul_0938	TGATGCGCTGATGTTCA
Gsul_0938	TGCATAAATAATGGGCA
Gmet_0693	TGCTTATATAATGTGCA
Gmet_0693	TGGAGGTGGCGTAAGCG
Gura_3367	TGCCTGGAAATGAAACG
Gura_3367	TGCATAAAAAATAATCA
Gsul_gnfK	TGCTGAAATATTGGGCA
Gsul_gnfK	TGATTGAAAAAGCGGCA
Gmet_gnfK	TGCCTCAATTGTGGGCG
Gmet_gnfK	TGCCTAAATGGTGTGCA
Gura_gnfK	TGCGCTATTTGTGGGCA
Gura_gnfK	TGCATGCTTTTTCAGCA
Gsul_gnfR	TGAAGCCCAGTTCCACA
Gsul_gnfR	TGCCCGAAACCCTGACA
Gmet_gnfR	TGAAGCTCACCTCCACC
Gmet_gnfR	TGGTTCCTGAAACGGCA
Gura_gnfR	TGAAGCTCGCCTCCACG
Gura_gnfR	TGCCCGAAACATGAACG
Gsul_2799	TGCCCCAGCGATCCTCA
Gsul_2799	TGCCCAACAATTAGTCA

Gmet_0681	TGGTGGAAGGTGCTGCA
Gmet_0681	TGCCTGTTTTTTAATCC
Gura_1209	TGCCGGTAAGGGATGCA
Gura_1209	TGCCTAAATATTAATCA
Gsul_gdhA	TGCCGATAAATCAGGCA
Gsul_gdhA	TGCCCACCTCAACATCA
Gsul_gdhA	TGCACAGTTTTGGTGCA
Gsul_gdhA	TGCATAAAATGCAGGCA
Gmet_gdhA	TGCCGCAAATTCGGGCA
Gmet_gdhA	TGCCTCTTTATGCATCG
Gmet_gdhA	GCGCATTTTTTGGTGCA
Gmet_gdhA	TGCATATATAAGTGGCG
Gura_gdhA	TGACTAAATAATACGCA
Gura_gdhA	TGTGCACGTTAAGTGCT
Gura_gdhA	TGCCTATTTATGGTGCA
Gura_gdhA	TGCATATTATTTAATCG

Reference

1. Schumacher,J., Joly,N., Rappas,M., Zhang,X. and Buck,M. (2006) Structures and organisation of AAA+ enhancer binding proteins in transcriptional activation. *J. Struct. Biol.,* **156,** 190-199.