Table 1. Putative attenuation regulation in bacteria.

The notes. Taxa and genes with regulation are shown; empty cells mean no regulation. LEU- and LEU1-elements are located upstream *leuA*; other regulations are various cases of attenuation.

Phylum and class	Genes						
α-proteobacteria	*ilvB, I*	*trpE*	*hisS*	*pheST*	*thrA*	*leuA*	*leuA*
β-proteobacteria	*ilvB*	*trpE*		*pheA*	*thrS*	*leuA*	*leuA, ilvB*
γ-proteobacteria	*ilvB, G*	*trpE*	*hisG*	*pheA, S*	*thrA*	*leuA*	
δ-proteobacteria	*ilvB*	*trpS*			*thrA, S*	*leuA*	
Actinobacteria	*ilvB, I, D*	*trpE, S, BE, BA*					*leuA*
Bacteroides/Chlorobi	*ilvD*	*trpE*	*hisG*				
Firmicutes	*ilvD, lysQ*	*trpB*	*hisZ*				
Thermotogae		*trpE*	*hisS*				
Chloroflexi	*ilvD*						

Table 2. Bacteria with predicted attenuation regulation.

The notes. The acronyms are given for bacterial species names, strains or close species.

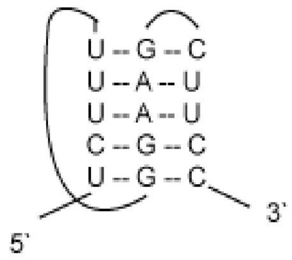
Phylum/class	Order	Species	Reduced species manes
Actinobacteria	Actinomycetales	*Corynebacterium diphtheriae*	DIP
		Corynebacterium efficiens	CE
		Corynebacterium glutamicum	cg, cgR
		Corynebacterium jeikeium	jk
		Streptomyces avermitilis	SAV
		Streptomyces coelicolor	SCO
		Streptomyces venezuelae	SVE
		Streptomyces scabies	SCA
		Thermobifida fusca	Tfu
		Thermomonospora fusca	RTFU
		Nocardia farcinica	nfa
		Saccharopolyspora erythraea	SACE
		Kineococcus radiotolerans	Krad
		Mycobacterium avium	MAV
		Mycobacterium bovis	BCG
		Mycobacterium leprae	ML
		Mycobacterium tuberculosis	MtubH
		Mycobacterium sp. KMS	Mkms
		Mycobacterium marinum	Mma
		Mycobacterium smegmatilis	MSMEG
		Mycobacterium vanbaalenii	Mvan
		Mycobacterium ulcerans	MUL
		Mycobacterium gilvum	Mgil
		Mycobacterium flavescens	Mflv
		Mycobacterium microti	Micro
		Tropheryma whipplei	TW
		Frankia alni	FRAAL
		Frankia sp.	Francci3, Franeanl
		Nocardioides sp.	Noca
		Clavibacter michiganensis	CLAV
		Salinispora arenicola	Sare
		Salinispora tropica	Strop
		Arthrobacter aurescens	Aaur
		Arthrobacter sp.	Arth
		Leifsonia xyli	Lxx
		Brevibacterium linens	Blin
		Rhodococcus jostii	RHA1
		Rhodococcus equi	Req
		Actinomyces naeslundii	Anae
		Janibacter sp.	JNB
		Acidothermus cellulolyticus	Acel
		Atopobium minutum	Amin
	Bifidobacteriales	*Bifidobacterium longum*	BLO
		Bifidobacterium adolescentis	BAD
	unclassified Actinobacteria	*marine actinobacterium*	MAR
Alpha-proteobacteria	Rhodobacterales	*Roseobacter denitrificans*	RD1
		Roseobacter sp.	RSK20926
		Roseovarius sp.	RTM1035
		Roseovarius nubinhibens	ISM
		Sulfitobacter sp.	NAS141
		Silicibacter sp.	TM1040
		Oceanicola granulosus	OG2516
		Oceanicola batsensis	OB2597
		Oceanicaulis alexandrii	OA2633
		Loktanella vestfoldens	SKA53
		Sagittula stellata	SSE37
		Dinoroseobacter shibae	Dshi
		Jannaschia sp.	Jann
		Rhodobacter sphaeroides	Rsph17025
		Rhodobacterales bacterium	RB2654, RB2150, OM2255
		Stappia aggregata	SIAM614
		Hyphomonas neptunium	HNE

		Maricaulis maris	Mmar
	Rhizobiales	*Fulvimarina pelagi*	FP2506
		Brucella melitensis	BAB1, BME
		Brucella ovis	BOV
		Brucella suis	BR
		Brucella abortus	BruAb1
		Aurantimonas sp.	SI859A1
		Rhodopseudomonas palustris	RPE, RPC
		Agrobacterium tumefaciens	Atu
		Ochrobactrum anthropi	Oant
		Sinorhizobium meliloti	SMc
		Sinorhizobium medicae	Smed
		Rhizobium etli	RHE
		Rhizobium leguminosarum	RL
		Mesorhizobium loti	ml
		Mesorhizobium sp.	Meso
		Bradyrhizobium sp.	BRAD, BRADO
		Bradyrhizobium japonicum	blr
		Xanthobacter autotrophicus	Xaut
		Methylobacterium extorquens	Mext
		Methylobacterium sp.	M446
		Azorhizobium caulinodans	AZC
		Nitrobacter sp.	NB311A
		Nitrobacter winogradskyi	Nwi
		Nitrobacter hamburgensis	Nham
		Candidatus Pelagibacter	SAR11
		Bartonella quintana	BQ
	Caulobacterales	*Caulobacter crescentus*	CC
		Caulobacter sp.	Caul
	Rhodospirillales	*Magnetospirillum magnetotactic*	Magn
		Magnetospirillum magneticum	amb
		Granulibacter bethesdensis	GbCGDNIH1
		Rhodospirillum rubrum	Rru
	Sphingomonadales	*Zymomonas mobilis*	ZMO
		Sphingomonas wittichii	Swit
	unclassif. Proteobacteria	*Magnetococcus* sp. Mc-1	Mmc1
	unclassif. Proteobacteria	*Mariprofundus ferrooxydans*	SPV1
	unclassif. Alphaproteobacteria	*alpha proteobacterium*	OM2255
Beta-proteobacteria	Burkholderiales	*Bordetella pertussis*	BP
		Bordetella bronchiseptica	BB
		Bordetella parapertussis	BPP
		Bordetella avium	Bavium, Bav
		Ralstonia eutropha	H16, Reut
		Ralstonia metallidurans	Rmet
		Ralstonia solanacearum	RSc
		Ralstonia pickettii	Rpic
		Delftia acidovorans	Daci
		Polaromonas sp.	Bpro
		Burkholderia thailandensis	BTH
		Burkholderia pseudomallei	Bpse110, BURPS
		Burkholderia mallei	BmalP
		Burkholderia vietnamiensis	Bcep1808
		Burkholderia ambifaria	BamMC406
		Burkholderia cepacia	Bamb
		Burkholderia cenocepacia	Bcen2424
		Burkholderia sp.	Bcep18194
		Burkholderia fungorum	Bcep
		Burkholderia dolosa	BdolA
		Burkholderia multivorans	Bmul
		Burkholderia xenovorans	Bxe
		Burkholderia phytofirmans	Bphyt
		Herminiimonas arsenicoxydans	HEAR
		Janthinobacterium sp.	mma
		Polynucleobacter sp.	Pnuc
		Acidovorax sp.	Ajs
		Methylibium petroleiphilum	Mpe
		Comamonas testosteroni	Ctes
	Rhodocyclales	*Azoarcus* sp.	azo
		Dechloromonas aromatica	Daro
	Neisseriales	*Chromobacterium violaceum*	CV

	Methylophilales	*Methylobacillus flagellatus*	Mfla
	Nitrosomonadales	*Nitrosospira multiformis*	Nmul
Delta-proteobacteria	Desulfobacterales	*Desulfotalea psychrophila*	DP
		Desulfovibrio desulfuricans	Dde
		Desulfococcus oleovorans	Dole
		Lawsonia intracellularis	LI
	Desulfuromonadales	*Geobacter sulfurreducens*	GSU
		Geobacter bemidjiensis	Gbem
		Geobacter uraniumreducens	Gura
		Geobacter sp.	Geob, GeobDRAFT
		Desulfuromonas acetoxidans	Dace
		Pelobacter propionicus	Ppro
		Pelobacter carbinolicus	Pcar
	Syntrophobacterales	*Syntrophus aciditrophicus*	SYN
		Syntrophobacter fumaroxidans	Sfum
	Myxococcales	*Stigmatella aurantiaca*	STIAU
		Myxococcus xanthus	MXAN
		Plesiocystis pacifica	PPSIR1
	Bdellovibrionales	*Bdellovibrio bacteriovorus*	Bd
	unclassif. Deltaproteobacteria	*delta proteobacterium*	MldD
Gamma-proteobacteria	Enterobacteriales	*Escherichia coli*	EcE, EcE24377A
		Salmonella typhi	t, t1219
		Salmonella enterica	STY, Sententer
		Salmonella typhimurium	STM
		Klebsiella pneumoniae	KPN
		Yersinia pestis	YPN, YpAngola, YPIP275
		Yersinia mollaretii	YmolA
		Yersinia bercovieri	YberA
		Yersinia pseudotuberculosis	Yps, YpsIP31758, YpsIP
		Yersinia frederiksenii	YfreA
		Yersinia enterocolitica	YE
		Yersinia intermedia	YintA
		Citrobacter koseri	CKO
		Shigella dysenteriae	SDY
		Shigella flexneri	S, SFV
		Shigella boydii	SbBS, SbBs512, SboyB
		Shigella sonnei	SSON
		Enterobacter sp. 638	Ent, Ent638
		Enterobacter sakazakii	ESA
		Erwinia carotovora	ECA
		Serratia proteamaculans	Spro
		Photorhabdus luminescens	plu
		Sodalis glossinidius	SG
	Pasteurellales	*Pasteurella multocida*	PMO, PM
		Haemophilus influenzae	HI, NTHI
		Haemophilus somnus	HSM
		Mannheimia haemolytica	Mannh
	Vibrionales	*Vibrionales bacterium*	VSWAT, VSWAT3
		Photobacterium profundum	P3TCK, PBPRA, PBPR
		Photobacterium sp. SKA34	SKA, SKA34
		Vibrio fischeri	VF
		Vibrio cholerae	VC, VCO395, A5A
		Vibrio parahaemolyticus	VP, A79
		Vibrio vulnificus	VV, VV1
		Vibrio angustum	VAS14
		Vibrio shilonii	VSAK1
		Vibrio harveyi	VIBHAR, A1Q
		Vibrio sp. MED222, Ex25	MED222, Vex2w
		Vibrio alginolyticus	V12G01
		Vibrio splendidus	V12B01
	Alteromonadales	*Moritella* sp. PE36	PE36
		Shewanella oneidensis	SO
		Shewanella sp. MR-4, W3181	Shewmr, Sputw3181, Sputw
		Shewanella baltica	Sbal, Sbal195, Sbal223
		Shewanella putrefaciens	Sput, Sputcn32, Sput200
		Shewanella sediminis	Ssed
		Shewanella frigidimarina	Sfri
		Shewanella denitrificans	Sden
		Shewanella loihica	Shew

		Shewanella pealeana	Spea
		Shewanella woodyi	Swoo, SwooD
		Shewanella amazonensis	Sama
		Colwellia psychrerythraea	CPS
		Alteromonadales bacterium	ATW7
		Pseudoalteromonas haloplanktis	PSHA, PSHAa
		Pseudoalteromonas tunicata	PTD2
		Pseudoalteromonas atlantica	Patl
		Alteromonas macleodii	MADE
		Psychromonas ingrahamii	Ping
		Psychromonas sp. CNPT3	PCNPT3
		Idiomarina loihiensis	IL
		Idiomarina baltica	OS
	Aeromonadales	*Aeromonas salmonicida*	ASA
		Aeromonas hydrophila	AHA
	Xanthomonadales	*Xanthomonas campestris*	XC
		Xanthomonas oryzae	XOO
		Xylella fastidioza	Xfaso
	Pseudomonadales	*Pseudomonas putida*	Pput
		Pseudomonas syringae	PSPTO
		Pseudomonas fluorescens	PFL
Firmicutes	Bacillales	*Bacillus halodurans*	BH
		Bacillus cereus	Bcer
		Bacillus thuringiensis	BT9727; BALH
		Bacillus anthracis	BATI
		Bacillus weihenstephanensis	BcerKBAB4
		Listeria welshimeri	lwe
		Listeria monocytogenes	lmo
		Listeria innocua	lin
		Staphylococcus aureus	SA
		Staphylococcus epidermidis	SERP
		Staphylococcus haemolyticus	SH
		Staphylococcus saprophyticus	SSP
		Geobacillus thermodenitrificans	GTNG
	Clostridiales	*Clostridium difficile*	CD
	Lactobacillales	*Lactococcus lactis*	LACR
Bacteroidetes/ Chlorobi	Chlorobiales	*Chlorobium tepidum*	CT
	Bacteroidales	*Bacteroides fragilis*	BF
		Bacteroides vulgatus	BVU
		Bacteroides thetaiotaomicron	BT
		Bacteroides uniformis	BACUNI
		Bacteroides ovatus	BACOVA
		Bacteroides caccae	BACCAC
		Parabacteroides distasonis	BDI
		Parabacteroides merdae	PARMER
		Porphyromonas gingivalis	PGN
	Flavobacteriales	*Flavobacterium psychrophilum*	FP
		Flavobacterium johnsoniae	Fjoh
		Flavobacteria bacterium	FBBAL38
		Flavobacteriales bacterium	FB2170
		Croceibacter atlanticus	CA2559
		Gramella forsetii	GFO
		Robiginitalea biformata	RB2501
		Dokdonia donghaensis	MED134
		Leeuwenhoekiella blandensis	MED217
		Psychroflexus torquis	P700755
		Polaribacter irgensii	PI23P
		Polaribacter dokdonensis	MED152
	Sphingobacteriales	*Cytophaga hutchinsonii*	CHU
		Microscilla marina	M23134
		Algoriphagus sp. PR1	ALPR1
	environmental samples	*unidentified eubacterium*	SCB49
Thermotogae	Thermotogales	*Thermotoga maritima*	TM
		Thermotoga petrophila	Tpet
Cloroflexi	Herpetosiphonales	*Herpetosiphon aurantiacus*	Haur

Fig. 1. RNA triplex upstream gene *hisG* in *E. coli*. The “third shoulder” of the triplex: UCUUU; the shoulders of the helix: GGAAG and CUUCC.



`5` CCUGACUAG`**`UCUUU`**`CAGGCGAUGUGUGCU`**`GGAAG`**`ACAUUCAGAU`**`CUUCC`**`AGUG 3``

Fig. 2. LEU1-pseudoknot upstream gene *leuA* in *D. shibae.* Under regulation is the leader peptide gene with leucine codons. The left shoulder of the helix adjoins the codons. The stem is absent.

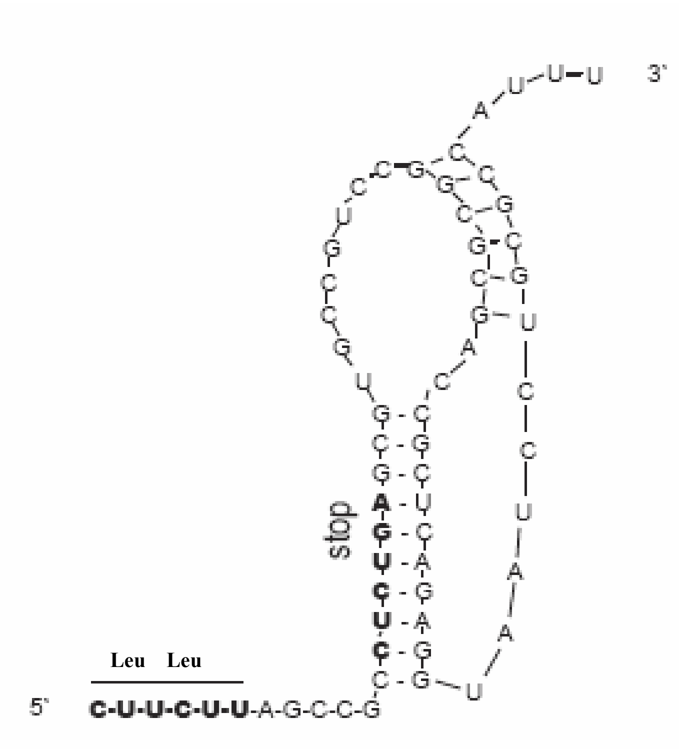


Fig. 3. LEU-regulation of gene *leuA* in *M. bovis*. Under regulation is the leader peptide gene with leucine codons. The stem is a helix. Its left shoulder has sequence UGCUCC and adjoins the leucine codons; the right shoulder adjoins the ribosome binding site.

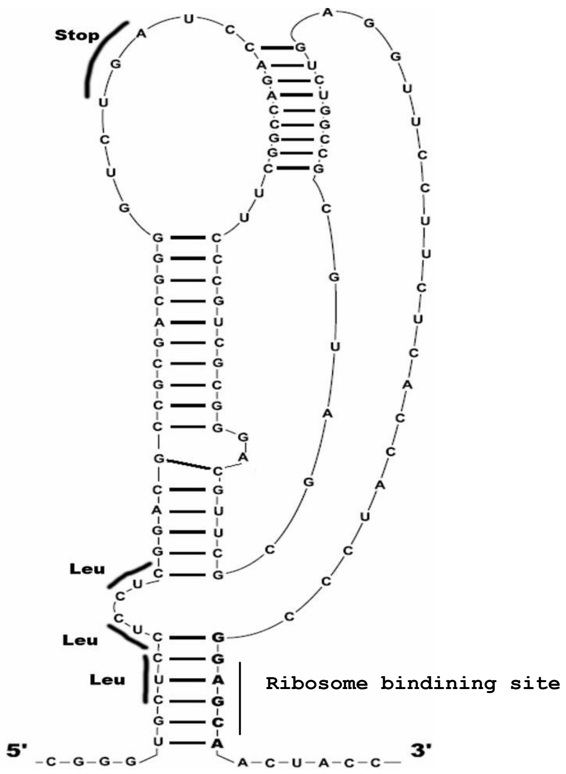


Fig. 4. Classic attenuation regulation: a) *pheST* operon in α-proteobacteria, b) *pheA* gene in β-proteobacteria**.** Species acronyms are given in Table 2. The start and regulatory codons of the leader peptide gene are in bold; the alternative start codon is in green; stop codon - in bold italic; terminator – in yellow; antiterminator – underlined. Here, unlike in other Figures, the alignment is not given.

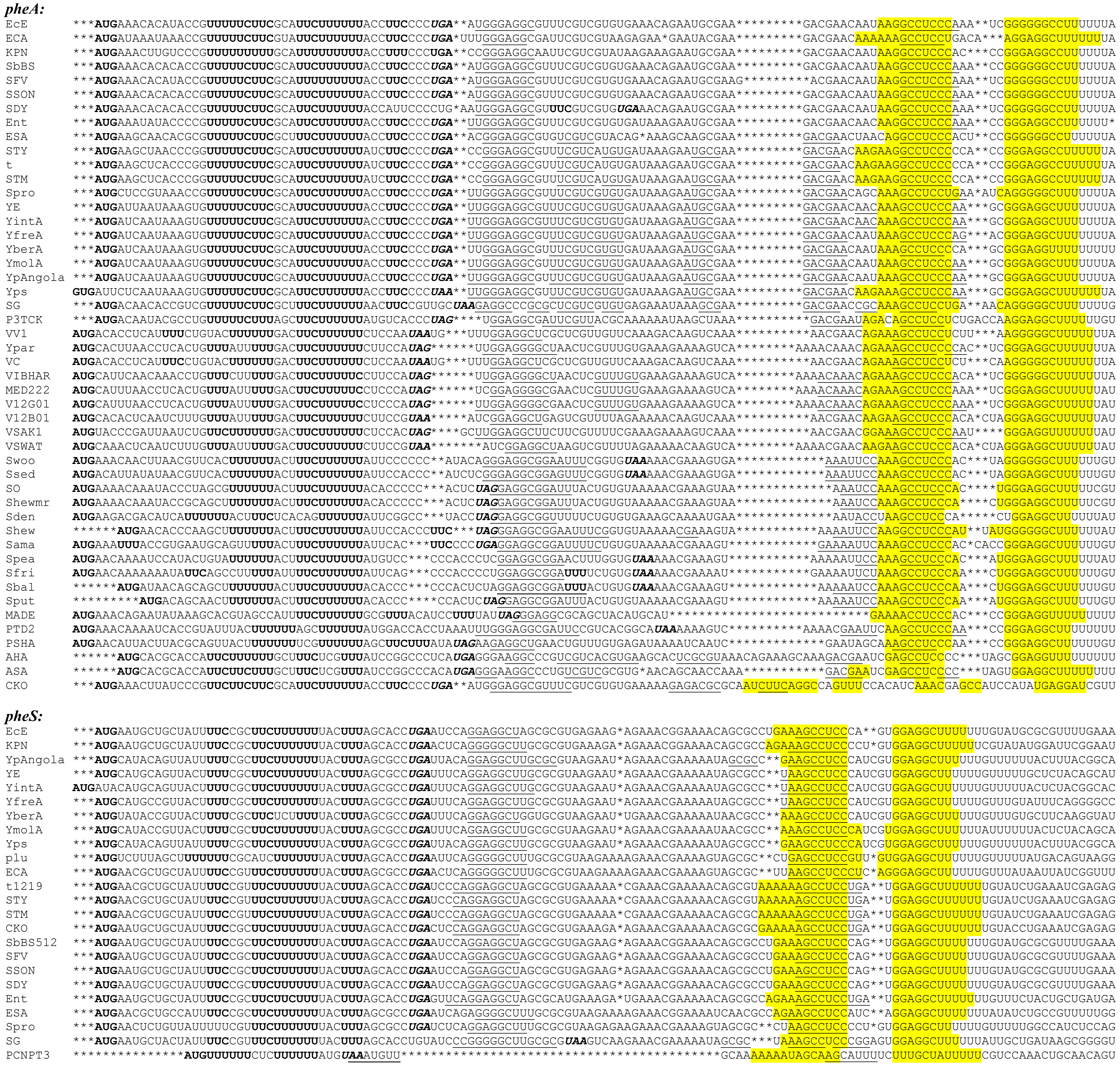
a) *pheST:*

Mmar
AUGAGCAAUGCGACGUAC**UUUUUU**GCGGCCUAU**UUU**GACAACGCAACCCGGGUGGGGGCGGUGGCCGGC***UAG***AUUGUGCGACAGCGCAACGAAACCAGGGCCUCCCCCACGGGGAGGCCCUUUUCUUUUGUCUGAAGGGAUUACACAC
OA2633
AUGACAGCAAACCUC**UUUUUCUUC**GGCGGCUAU**UUC**UAUCGUCCCCAUGGGGCCGGU***UGA***CGCUGCUUGCUUGCAAGAAAAAGUCACCAGCCCCGCCCGAUGGCGGGGUUUUUUAUUGGAGAAACGGCA
ml
AUGGGGAACCCGCGCUGGCACGGCUGGCGCGGG**UUCUUU**UGUCUC***UGA***UGUCUGAACUUUCAACUUAAAAGUGACUUCCACUUUAAAGUCGACUUCCAACGUAGCGAGUUUGACCC
RB2150
AUGGGUCGG**UUU**ACAAUCAAAUUAUCUUUAAAUAACCUCCAAAGUGGAGGU**UUUUUU**AUG**UUU*UAG***GAAACCGCGUUAAUGGUUUGGUCCUCGGCACUAUCGCCCAUGGUAUCGGUACAGCCAAAGCGGUACAGCUAAGCGAACAAGCUGGCGCUUUUGCUU
Mmc1
AUGUACUGUUCUACAAUUUUGACUAUUUUCUGAGCCAUCCCACCGCCA**UUUUUC**AUA**UUU**GGGAAGGGGGGAUGUCCU**UUC**ACGGUGGUU***UGA***UUGGAGGCGUGGUGGCUUGCCUGCUCUACGCUCGCAAAAGCCAGAUUCCGUGUUUAAUGUUGGCGGAUUUGGUCUU

b) *pheA:*

BP, BB
GUGGCC**UUCUUC**AAGGUGCUGGGUUCGUAUCCGGCGCAA***UAG***GGCCACGGCGUGGUUGACGCACACCAGGCGGCCGCCGUGACGGAGCGUGUGUCCGUCCGGCGCUGCCAUAUUGUUUUUCUGCAGGU
BPP
GUGGCC**UUCUUC**AAGGUGCUGGGUUCGUAUCCGGCGCAA***UAG***GGCCACGGCGUGGUUGACGCACACCAGGCGGCCGGCGUGACGGAGCGUGUGUCCGUCCGGCGCUGCCAUAUUGUUUUUCUGCAGGU

Fig. 5. Classic attenuation regulation of genes *pheA* and *pheS* in γ-proteobacteria. Designations as in Figure 4.



pheA:

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EcE      ***AUGAAACACAUACCGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**AUGGGAGGCGUUUCGUCGUGUGAAACAGAAUGCGAA*********GACGAACAAUAAGGCCUCCCAAA**UCGGGGGGCCUUUUUUA
ECA      ***AUGAUAAAUAAACCGUUUUUCUUCGUAUUCUUUUUUUACCUUCCCCUGA*UUUGGGAGGCGAUUCGUCGUAAGAGAA*GAAUACGAA*********GACGAACAAAAAAGCCUCCUGACA***AGGAGGCUUUUUUUA
KPN      ***AUGAAACUUGUCCCGUUUUUUUUUGCAUUUUUUUUUACCUUUCCCUGA**CCGGGAGGCAAUUCGUCGUAUAAGAAAGAAUGCGAA*********GACGAACAAUAAGGCCUCCCAC***CCGGGAGGCCUUUUUUA
SbBS     ***AUGAAACACACACCGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**AUGGGAGGCGUUUCGUCGUGUGAAACAGAAUGCGAA*********GACGAACAAUAAGGCCUCCCAAA**CCGGGGGGCCUUUUUUA
SFV      ***AUGAAACACAUACCGUUUUUCUUCGCAUUUUUUUUUACCUUCCCCUGA**AUGGGAGGCGUUUCGUCGUGUGAAACAGAAUGCGAAG*********ACGAACAAUAAGGCCUCCCAAA**UCGGGGGGCCUUUUUUA
SSON     ***AUGAAACACACACCGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**AUGGGAGGCGUUUCGUCGUGUGAAACAGAAUGCGAA*********GACGAACAAUAAGGCCUCCCAAA**CCGGGGGGCCUUUUUUA
SDY      ***AUGAAACACACACCGUUUUUCUUCGCAUUCUUUUUUUACCAUUCCCCUG*AAUGGGAGGCGUUUCGUCGUGUGAAACAGAAUGCGAA*********GACGAACAAUAAGGCCUCCCAAA**UCGGGGGGCCUUUUUUA
Ent      ***AUGAAAUAUACCCCGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAACAAGGCCUCCCAAA**CCGGGAGGCCUUUUUU*
ESA      ***AUGAAGCAACACGCGUUUUUCUUCGCUUUCUUUUUUUACCUUCCCCUGA**ACGGGAGGCGUGUCGUCGUACAG*AAAGCAAGCGAA*********GACGAACUAACAGGCCUCCCACU**CCGGGGGGCCUUUUUUA
STY      ***AUGAAGCUAACCCGGUUUUUCUUCGCAUUCUUUUUUUAUCUUCCCCUGA**CCGGGAGGCGUUUCGUCAUGUGAUAAAGAAUGCGAA*********GACGAACAAGAAGGCCUCCCCCA**CCGGGAGGCCUUUUUUA
t        ***AUGAAGCUCACCCGGUUUUUCUUCGCAUUCUUUUUUUAUCUUCCCCUGA**CCGGGAGGCGUUUCGUCAUGUGAUAAAGAAUGCGAA*********GACGAACAAGAAGGCCUCCCCCA**CCGGGAGGCCUUUUUUA
STM      ***AUGAAGCUCACCCGGUUUUUCUUCGCAUUCUUUUUUUAUCUUCCCCUGA**CCGGGAGGCGUUUCGUCAUGUGAUAAAGAAUGCGAA*********GACGAACAAGAAGGCCUCCCCCA**CCGGGAGGCCUUUUUUA
Spro     ***AUGCUCCGUAAACCGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAGCAAAGCCUCCUGAA*AUCAGGGGGCUUUUUUA
YE       ***AUGAUUAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAACAAAGCCUCCCAA***GCGGGAGGCUUUUUUUA
YintA    ***AUGAUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAACAAAGCCUCCCAA***GCGGGAGGCUUUUUUUA
YfreA    ***AUGAUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAAUAAAGCCUCCCAG***ACGGGAGGCUUUUUUUA
YberA    ***AUGAUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAAUAAAGCCUCCCCA***GCGGGAGGUUUUUUUUU
YmolA    ***AUGAUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAAUAAAGCCUCCCAA***GCGGGAGGCUUUUUUUA
YpAngola ***AUGAUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAAUAAAGCCUCCCAA***GCGGGAGGCUUUUUUUA
Yps      GUGAUUCUCAAUAAAGUGUUUUUCUUCGCAUUCUUUUUUUACCUUCCCCUAA**UUGGGAGGCGUUUCGUCGUGUGAUAAAGAAUGCGAA*********GACGAACAAGAAAGCCUCCCAA***GCGGGAGGCUUUUUUUA
SG       ***AUGACAACACCGUCGUUUUUCUUCGCUUUCUUUUUUUAACUUCCGUUGCUAAGAGGCCCGCGCUCGUCGUGUGAGAAAUAAAGCGAA*********GACGAACCGCAAAGCCUCCUGA**AACAGGGGGCUUUUUUUG
P3TCK    ***AUGACAAUACGCCUGUUUUUCUUUAGCUUCUUUUUUUAUGUCACCCUAG****UGGAGGCGAUUCGUUACGCAAAAAAUAAGCUAAA**********GACGAAUAGACAGCCUCCUCUGACCAAGGAGGCUUUUUUGU
VV1      AUGACACCUCAUUUUCUGUACUUUUUUGACUUCUUUUUUUCUCCAAUAAUG***UUUGGAGGCUCGCUCGUUGUUCAAAGACAAGUCAAA*********AACGAACAGAAAGCCUCCUCUU***AAGGGGGCUUUUUUUA
Ypar     AUGCACUUAACCUCACUGUUUAUUUUUGACUUCUUUUUUUCUUCCAUAG*****UUGGAGGGGCUAACUCGUUUGUGAAAGAAAAGUCA*******AAAACAAACAGAAAGCCUCCCCAC**UCGGGAGGCUUUUUUUA
VC       AUGACACCUCAUUUCCUGUACUUUUUUGACUUCUUUUUUUCUCCAAUAAUG***UUUGGAGGCUCGCUCGUUGUUCAAAGACAAGUCAAA*********AACGAACAGAAAGCCUCCUCU***CAAGGGGGCUUUUUUUA
VIBHAR   AUGCAUUCAACAAACCUGUUUCUUUUUGACUUCUUUUUCCUUCCAUAG*****UUGGAGGGGCUAACUCGUUUGUGAAAGAAAAGUCA*******AAAACAAACAGAAAGCCUCCCACA**UCGGGGGGCUUUUUUUA
MED222   AUGCAUUUAACCUCACUGUUUAUUUUUGACUUCUUUUUCCUCCCAUAG*****UCGGAGGGGCGAACUCGUUUGUGAAAGAAAAGUCA*******AAAACAAACAGAAAGCCUCCCAAA**UCGGGAGGCUUUUUUUAU
V12G01   AUGCAUUUAACCUCACUGUUUAUUUUUGACUUCUUUUUCCUCCCAUAG*****UUGGAGGGGCGAACUCGUUUGUGAAAGAAAAGUCA*******AAAACAAACAGAAAGCCUCCCAAA**UCGGGAGGCUUUUUUUAU
V12B01   AUGCACACUCAAUCUUUGUUUAUUUUUGACUUCUUUUUUUCUUCCGUAA*****AUCGGAGGCUGAGUCGUUUUAGAAAAACAAGUCAAA*********AACGAACAAGAAGCCUCCCACA*CUAGGGAGGCUUUUUUAU
VSAK1    AUGUACCCGAUUAAUCUGUUCUUUUUUGACUUCUUUUUUUCUCCACUAG****GCUUGGAGGCUUCUUCGUUUUCGAAAGAAAAGUCAAA*********AACGAACGGAAAGCCUCCCAAU****GGGAGGUUUUUUUAU
VSWAT    AUGCAAACUCAAUCUUUGUUUAUUUUUGACUUCUUUUUUUCUUCCGUAA******AUCGGAGGCUAAGUCGUUUUAGAAAAACAAGUCA*******AAAACGAACAAGAAGCCUCCCACA*CUAGGGAGGCUUUUUUAU
Swoo     AUGAAACAACUUAACGUUCACUUUUUUACUUUCUUUUUUUAUUCCCCCC**AUACAGGGAGGCGGAAUUUCGGUGUAAAAACGAAAGUGA***********AAAUUCCAAAGCCUCCCAC***UAGGGGGGCUUUUUUGU
Ssed     AUGACAUUAUAUAACGUUCACUUUUUUACUUUCUUUUUUUAUUCCACCC**AUCUCGGGAGGCGGAGUUUCGGUGUAAAAACGAAAGUGA***********AAAUUCCAAAGCCUCCCAC***UAGGGAGGCUUUUUUGU
SO       AUGAAAACAAAUACCCUAGCGUUUUUUACUUUCUUUUUUUACACCCCC***ACUCUAGGAGGCGGAUUUACUGUGUAAAAACGAAAGUAA************AAAUCCAAAGCCUCCCAC****UGGGAGGCUUUUUUCGU
Shewmr   AUGAAAACAAAUACCGCAGCUUUUUUUACUUUCUUUUUUUACACCCCC***ACUCUAGGAGGCGGAUUUACUGUGUAAAAACGAAAGUAA************AAAUCCAAAGCCUCCCA****CUGGGAGGCUUUUUUCGU
Sden     AUGAAGACGACAUCAUUUUUUACUUUCUCACAGUUUUUUAUUCGGCC***UACCUAGGAGGCGGUUUUUCUGUGUGAAAGCAAAAUGAA************AAUACCUAAGCCUCCCA*****CUGGAGGCUUUUUUAU
Shew     ******AUGAACACCCAAGCUUUUUUUACUUUCUUUUUUUAUUCCACCCUUC***UAGGGAGGCGGAAUUUCGGUGUAAAAACGAAAGUA**********AAAAUUCCAAGGCCUCCCAU**UAUGGGGGGCUUUUUUAU
Sama     AUGAAAUUUACCGUGAAUGCAGUUUUUACUUUCUUUUUUUAUUCAC***UUCCCCUGAGGAGGCGGAUUUUCUGUGUAAAAACGAAAGU**********GAAAAUUCAAAGCCUCCCAC*CACCGGGAGGCUUUUUUGU
Spea     AUGAACAAAAUCCAUACUGUAUUUUUUACUUUCUUUUUUUAUGUCC***CCCACCCUCGGAGGCGGAACUUUGGUGUAAAAACGAAAGU**********AAAAAUUCCAAAGCCUCCCAC***AUGGGAGGCUUUUUUAU
Sfri     AUGAACAAAAAAAAUAUUCAGCCUUUUUAUUUUCUUUUUUUAUUCAG***CCCACCCCUGGAGGCGGAUUUUCUGUGUAAAAACGAAAAU**********GAAAAUUCUAAAGCCUCCCAA***CUGGGAGGCUUUUUUGU
Sbal     ******AUGAUAACAGCAGCUUUUUUUACUUUCUUUUUUUACACCC***CCCACUCUAGGAGGCGGAUUUACUGUGUAAAAACGAAAGU***********AAAAAUCCAAAGCCUCCCAA***CUGGGAGGCUUUUUUGU
Sput     *********AUGACAGCAACUUUUUUUACUUUCUUUUUUUACACCC****CCACUCUAGGAGGCGGAUUUACUGUGUAAAAACGAAAGU***********AAAAAUCCAAAGCCUCCCAA***AUGGGAGGCUUUUUUGU
MADE     AUGAAACAGAAUAUAAAGCACGUAGCCAUUUUCUUUUUUUGCGUUUACAUCCUUUUAUUAGGGAGGCGCAGCUACAUGCAU*************************GAAAACCUCCCAC***CCGGGAGGUUUUUUUUU
PTD2     AUGAAACAAAAUCACCGUAUUUACUUUUUUAGCUUUUUUUAUGGACCACCUAAAUUUGGGAGGCGAUUCCGUCACGGCAUAAAAAAGUC**********AAAACGAAUUCAAGCCUCCCAA***CCGGGAGGCUUUUUUUU
PSHA     AUGAACAUUACUUACGCAGUUACUUUUUUUCGUUUUUUAGCUUCUUUAUAUAGAAGAGGCUGAACUGUUUGUGAGAUAAAAUCAAUC************GAAUAGCAAAGCCUCCCAA***CCGGGAGGCUUUUUUGU
AHA      ******AUGCACGCACCAUUCUUUUUUGCUUUCUCGUUUAUCCGGCCCUCAUGAGGGAAGGCCCGUCGUCACGUGAAGCACUCGCGUAAACAGAAAGCAAAGACGAAUCGAGCCUCCCC***UAGCGGAGGUUUUUUUUU
ASA      ******AUGCACGCACCAUUCUUCUUUGCUUUCUCGUUUAUCCGGCCCACAUGAGGGAAGGCCCUGUCGUCGCGUG*AACAGCAACCAAA**********GACGAAUCGAGCCUCCCC***UAGUGGAGGCUUUUUUUU
CKO      ***AUGAAACUUAUCCCGUUCUUCUUCGCAUUCUUUUUUUACCUUCCCCUGA**AUGGGAGGCGUUUCGUCGUGUGAAAAAGAGACGCGCAAUCUUCAGGCCAGUUUCCACAUCAAACGAGCCAUCCAUAUGAGGAUCGUU
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pheS:

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EcE      ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAAUCCAGGAGGCUAGCGCGUGAGAAG*AGAAACGGAAAACAGCGCCUGAAAGCCUCCCA**GUGGAGGCUUUUUUUGUAUGCGCGUUUUGAAA
KPN      ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAACUCAGGGGGCUUGCGCGUGAAAGA*AGAAACGGAAAACAGCGCCAGAAAGCCUCCCCU*GUGGAGGCUUUUUUCGUAUAUGGAUUCGGAAU
YpAngola ***AUGCAUACAGUUAUUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUACAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAGCGCC**GAAGCCUCCCAUCGUGGAGGCUUUUUGUUUUUUACUUUACGGCA
YE       ***AUGCAUGCAGUUACUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUUCAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAGCGCC**UAAGCCUCCCAUCGUGGAGGCUUUUUUGUUUUUGCUCUACAGCAU
YintA    AUGAUACAUGCAGUUACUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUUCAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAGCGCC**UAAGCCUCCCAUCGUGGAGGCUUUUUUGUUUUUACUCUACGGCAC
YfreA    ***AUGCAUGCCGUUACUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUUCAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAGCGCC**UAAGCCUCCCAUCGUGGAGGCUUUUUUGUUUGUAUUUCAGGGGCC
YberA    ***AUGUAUACCGUUACUUUUCGCUUCUCUUUUUACUUUAGCGCCUGAUUUCAGGAGGCUGGUGCGUAAGAAU*UGAAACGAAAAAUAACGCC**AAAGCCUCCCAUCGUGGAGGCUUUUUUGUUUGUGCUUCAAGGUAU
YmolA    ***AUGCAUACCGUUACUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUUCAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAACGCC**AAAGCCUCCCAUCGUGGAGGCUUUUUUAUUUUUUACUCUACAGCA
Yps      ***AUGCAUACAGUUAUUUUUCGCUUCUUUUUUUACUUUAGCGCCUGAUUACAGGAGGCUUGCGCGUAAGAAU*AGAAACGAAAAAUAGCGCC**GAAGCCUCCCAUCGUGGAGGCUUUUUUGUUUUUUACUUUACGGCA
plu      ***AUGUCUUUAGCUUUUUUUCGCAUCUUUUUUUACUUUAGCACCUGAAUUCAGGGGGCUUUGCGCGUAAGAAAAGAAACGAAAAGUAGCGC**CUGAGCCUCCGUU*GUGGAGGCUUUUUUGUUUUUAUGACAGUAAGG
ECA      ***AUGAACGCUGCUAUUUUCCGUUUCUUUUUUUACUUUAGCGCCUGAACUCAGGGGGCUUUGCGCGUAAGAAAAGAAACGAAAAGUAGCGC**UUAAGCCUCCCUC*AGGGAGGCUUUUUUGUUUAUAAUUAUCGGUUU
t1219    ***AUGAACGCUGCUAUUUUCCGUUUCUUUUUUUACUUUAGCACCUGAUCCCAGGAGGCUAGCGCGUGAAAAA*CGAAACGAAAAACAGCGUAAAAAAGCCUCCUGA**UGGAGGCUUUUUUUGUAUCUGAAAUCGAGAG
STY      ***AUGAACGCUGCUAUUUUCCGUUUCUUUUUUUACUUUAGCACCUGAUCCCAGGAGGCUAGCGCGUGAAAAA*CGAAACGAAAAACAGCGUAAAAAAGCCUCCUGA**UGGAGGCUUUUUUUGUAUCUGAAAUCGAGAG
STM      ***AUGAACGCUGCUAUUUUCCGUUUCUUUUUUUACUUUAGCACCUGAUCCCAGGAGGCUAGCGCGUGAAAAA*CGAAACGAAAAACAGCGCAAAAAAGCCUCCUGA**UGGAGGCUUUUUUUGUAUCUGAAAUCGAGAG
CKO      ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGACUCCAGGAGGCUAGCGCGUGAAAGA*AGAAACGAAAAACAGCGCGAAAAAGCCUCCUGA**UGGAGGCUUUUUUUGUACCUGAAAUCGAGAG
SbBS512  ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAAUCCAGGAGGCUAGCGCGUGAGAAG*AGAAACGGAAAACAGCGCCUGAAAGCCUCCCAG**UGGAGGCUUUUUUUGUAUGCGCGUUUUGAAA
SFV      ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAAUCCAGGAGGCUAGCGCGUGAGAAG*AGAAACGGAAAACAGCGCCUGAAAGCCUCCCAG**UGGAGGCUUUUUUUGUAUGCGCGUUUUGAAA
SSON     ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAAUCCAGGAGGCUAGCGCGUGAGAAG*AGAAACGGAAAACAGCGCCUGAAAGCCUCCCAG**UGGAGGCUUUUUUUGUAUGCGCGUUUUGAAA
SDY      ***AUGAAUGCUGCUAUUUUCCGCUUCUUUUUUUACUUUAGCACCUGAAUCCAGGAGGCUAGCGCGUGAGAAG*AGAAACGGAAAACAGCGCCUGAAAGCCUCCCAG**UGGAGGCUUUUUUUGUAUGCGCGUUUUGAAA
Ent      ***AUGAAUGCUGCUAUUUUCCGCUUCUUCUUUUACUUUAGCACCUGAGUUCAGGAGGCUAGCGCAUGAAAGA*UGAAACGAAAAACAGCGCCAGAAAGCCUCCUGA**UGGAGGCUUUUUUUGUUUCUACUGCUGAUGA
ESA      ***AUGAACGCUGCCAUUUUCCGCUUCUUUUUUUACUUUAGCGCCUGAAUCAGAGGGGCUUUGCGCGUAAGAAAAGAAACGGAAAAUCAACGCCAGAAGCCUCCCAUC**AGGAGGCUUUUUUUAUAUCUGCCGUUUUUGG
Spro     ***AUGAACUCUGUUAUUUUUCGUUUCUUUUUUUACUUUAGCGCCUGAUCUCAGGAGGCUUUGCGCGUAAGAGAAGAAACGAAAAGUAGCGC**CUAAGCCUCCCCU*GUGGAGGCUUUUUUGUUUUUGGCCAUCUCCAG
SG       ***AUGAAUGCUACUAUUUUCCGUUUCUUUUUUUACUUUAGCACCUGUAUCCCGGGGGCUUGCGCGUAAGUCAAGAAACGAAAAAUAGCGC***UAAAGCCUCCCGGAGUGGAGGCUUUUUUAUUGCUGAUAAGCGGGGU
PCNPT3   **************AUGUUUUUUCUCUUUUUUAUGUAAAUGUU*****************************************GCAAAAAAAUAGCAAGCAUUUUCUUUGCUAUUUUUCGUCCAAACUGCAACAGU
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Fig. 6. Phylogenetic tree of the regulatory regions of genes *pheA* and *pheS* in γ- proteobacteria. Species names and their acronyms are given in Table 2.

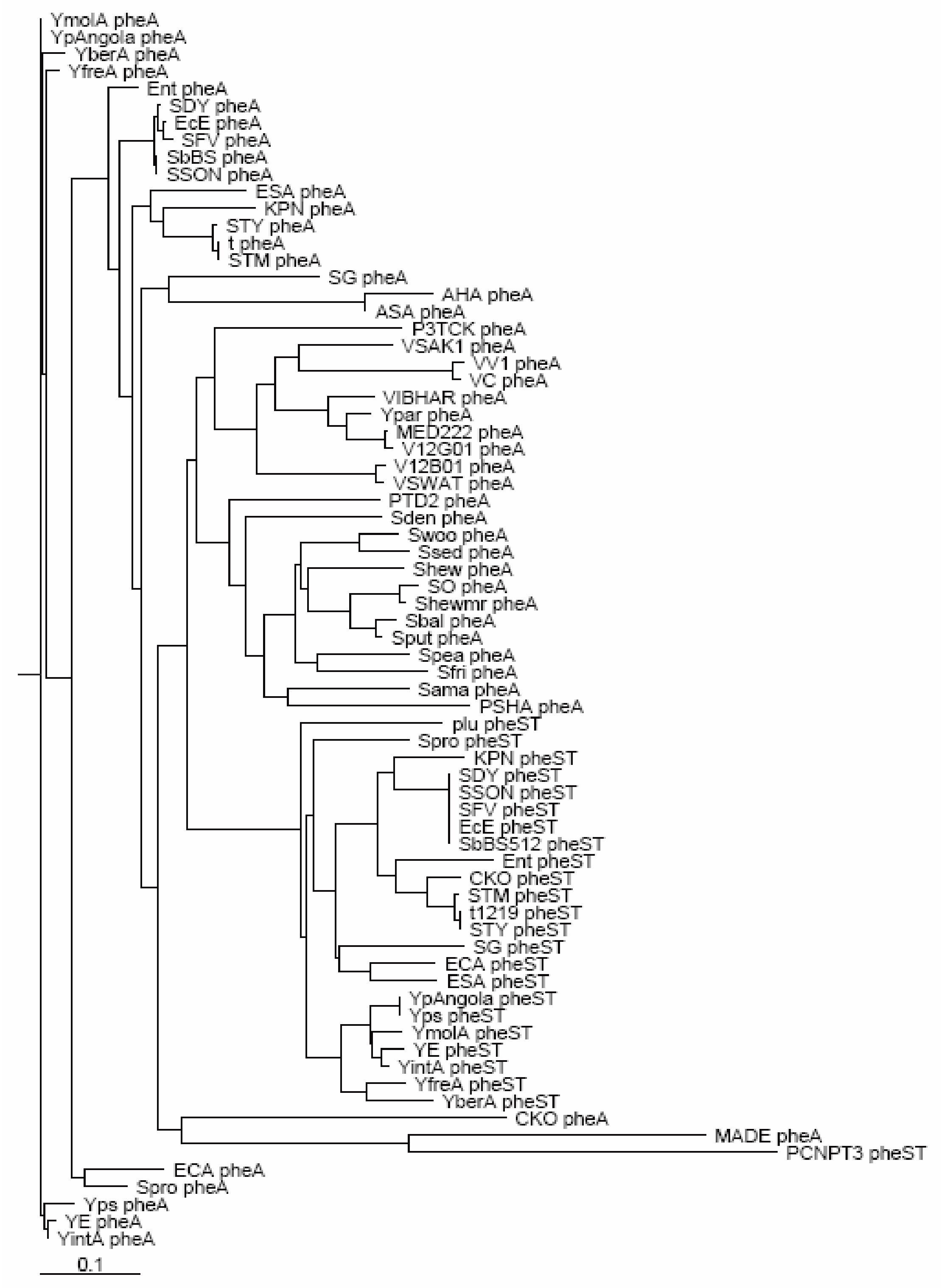


Fig. 7. Classic attenuation regulation: a) *thrA* gene in α-proteobacteria, b) *thrA* and *thrS* genes in δ-proteobacteria. Designations as in Figure 4, alignment is absent. Paralogs of *thrS* designated as numbers. In *Bdellovibrio bacteriovorus* (Bb thrS1) the antiterminator (double underlined) does not fully overlap with the terminator and requires a co-antiterminator (single underlined). Antiterminator and co-terminator (in blue) do not coexist.

a) *thrA:*

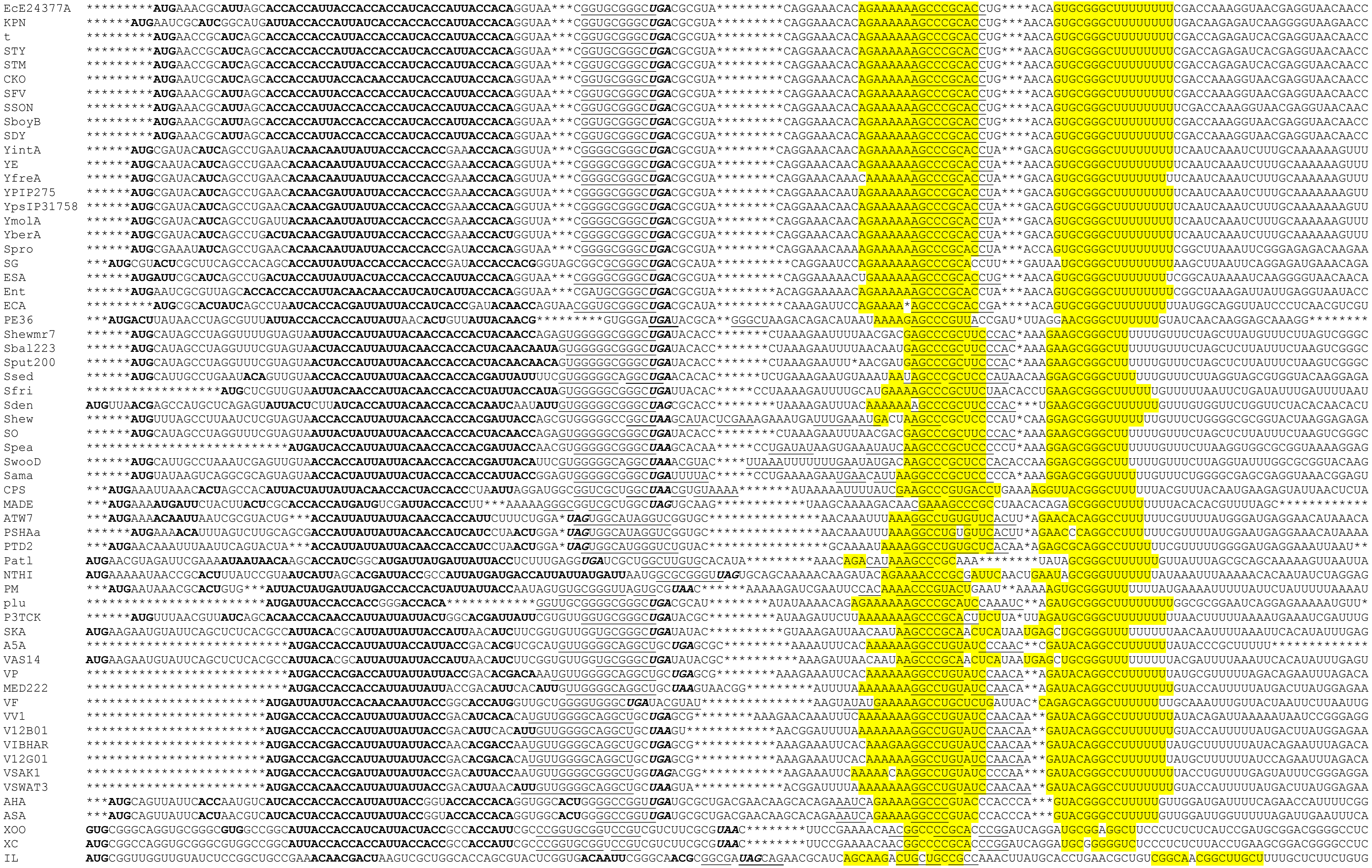
OM2255
AUGAUUAUUAUUACCACCCUUGUCAGGGCGGACGUUGGU***UAG***UGCAUGUUCACAAAUCAUCUGAAGCCCGCUAAAGUAGCGGGCUUUUUUGUUUUACCAGUAUCAAUUUUUCGAACUAGGAGUUCAC

b) *thrA, thrS:*

MXAN_thrA
GUGCUG**ACCACCACCACCACGACCACGACGACU**CCCCGCCGGGCGCGGUGGUC***UAG***CGACGGAACCACCUUGGUUUCCAGCUCGGCCCCGCGCUCUCCGGCGCGGGGCUUUUUUGUUUUCACAUGCCGCAGGAGCCCCGACAUGCAGCCCUCCUCGCAGUCG

Bd_thrS1
AUGAAUUUG**AUUACGACA**GAU**AUU**AAA**ACA**AGAAGUUUGCAGAGCUCUCUUGCGAAGUCUGCA**ACGACA**AAC***UAG***ACGGCGCACUUAAGCGACGCUAGAAUUUAACUUAAAUUACUCCGGCGAAGCCGGAGUGUAAGCCAGUGGAGGUUUACCAUUAGCAAGUUUGAA
MXAN_thrS1
GUGAGCUUCGUC**AUCACCACCACGACCACC**GGC**ACCACGACU**CGCUUCGGCGGGCGUGGA**ACC**GUGCGCGUC**ACG**UGG***UGA***GCUGACGAACGCACGGUUCCCUGCCCCGCCUUCUCCGGCCGGGGCAACCGUGCGCUCGCUCAGCGCUCCGACCGGAUGGCGUUUCAC
STIAU_thrS1
ACCAGC**AUG**AAGUUCAGCCAGCUC**ACGACU**CGC**ACGACCACU**CCCCGC**ACC**GGCGGGCGAGCGGCUGUGCGC**ACG*UAA***GCUGAGCGCGCGGACACCGCAGCCCCGCCGGGACAUCCGGACUGGGGCGCACCGCGCGAAUCGCUUCACCCCCGCUCCGGAC
Bd_thrS2
AUGAGCUUUGACCUGUCUUUCAGCCUC**AUU**CUUGUUUUCGCC**ACC**CCGGCG**ACCACC**CCG***UAG***GGGUCUAUAAUCUAUUGGCCGCCCAACUGGCGGCCCCGACGCAUUUUUCCAUAUUUUUAUAAAAUUUUAAGAUCCGCUGAAGCGGAGAGAGAUUUAUU

Fig. 8. Classic attenuation regulation of gene *thrA* in γ-proteobacteria. Designations as in Figure 4.



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EcE24377A  *********AUGAAACGCAUUAGCACCACCAUUACCACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG****ACAGUGCGGGCUUUUUUUUCGACCAAAGGUAACGAGGUAACAACC
KPN        ******AUGAAUCGCAUCGGCAUGAUUACCACCAUUAUCACCACCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUUGACAAGAGAUCAAGGGGUAAGAACC
t          *********AUGAACCGCAUCAGCACCACCACCAUUACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUCGACCAGAGAUCACGAGGUAACAACC
STY        *********AUGAACCGCAUCAGCACCACCACCAUUACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUCGACCAGAGAUCACGAGGUAACAACC
STM        *********AUGAACCGCAUCAGCACCACCACCAUUACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUCGACCAGAGAUCACGAGGUAACAACC
CKO        *********AUGAAUCGCAUCAGCACCACCAUUACCACAACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUCGACCAAAGGUAACGAGGUAACAACC
SFV        *********AUGAAACGCAUUAGCACCACCAUUACCACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG****ACAGUGCGGGCUUUUUUUUCGACCAAAGGUAACGAGGUAACAACC
SSON       *********AUGAAACGCAUUAGCACCACCAUUACCACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG****ACAGUGCGGGCUUUUUUUUUCGACCAAAGGUAACGAGGUAACAAC
SboyB      *********AUGAAACGCAUUAGCACCACCAUUACCACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG****ACAGUGCGGGCUUUUUUUUCGACCAAAGGUAACGAGGUAACAACC
SDY        *********AUGAAACGCAUUAGCACCACCAUUACCACCACCAUCACCAUUACCACAGGUAA***CGGUGCGGGCUGACGCGUA*********CAGGAAACACAGAAAAAAGCCCGCACCUG****ACAGUGCGGGCUUUUUUUUCGACCAAAGGUAACGAGGUAACAACC
YintA      ******AUGCGAUACAUCAGCCUGAAUACAACAAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAACAGAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAGUUU
YE         ******AUGCAAUACAUCAGCCUGAACACAACAAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAACAGAAAAAAGCCCGCACCUA***AACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAGUUU
YfreA      ******AUGCGAUACAUCAGCCUGAACACAACAAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAAACAAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAGUUU
YPIP275    ******AUGCGAUACAUCAGCCUGAACACAACGAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAAUAGAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAAGUU
YpsIP31758 ******AUGCGAUACAUCAGCCUGAACACAACGAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAACAGAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAAGUU
YmolA      ******AUGCGAUACAUCAGCCUGAUUACAACAAUUAUUACCACCACCGAAACCACAGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAACAGAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAGUUU
YberA      ******AUGCGAUACAUCAGCCUGACUACAACGAUUAUUACCACCACCGAAACCACUGGUUA***CGGGGCGGGCUGACGCGUA********CAGGAAACAACAGAAAAAAGCCCGCACCUA***GACAGUGCGGGCUUUUUUUUUCAAUCAAAUCUUUGCAAAAAAGUUU
Spro       ******AUGCGAAAUAUCAGCCUGAACACAACAAUUAUUACCACCACCGAUACCACAGGUAA***CGGGGCGGGCUGACGCGUA********CAGGAAACAAAAGAAAAAAGCCCGCACCUA***ACCAGUGCGGGCUUUUUUUUCGGCUUAAAUUCGGGAGAGACAAGAA
SG         ***AUGCGUACUCGCUUCAGCCACAGCACCAUUAUUACCACCACCACCGAUACCACCACGGGUAGCGGCGCGGGCUGACGCAUA**********CAGGAAUCCAGAAAAAAGCCCGCACCUU***GAUAAUGCGGGCUUUUUUUUAAGCUUAAUUCAGGAGAUGAAACAGA
ESA        ******AUGAUUCGCAUCAGCCUGACUACCAUUAUUACUACCACCACCAUUACCACAGGUAA***CGGGGCGGGCUGACGCGUA*********CAGGAAAAACUGAAAAAAGCCCGCACCUG***AACAGUGCGGGCUUUUUUUUCGGCAUAAAAUCAAGGGGUAACAACA
Ent        ******AUGAAUCGCGUUAGCACCACCACCAUUACAACAACCAUCAUCAUUACCACAGGUAA***CGAUGCGGGCUGACGCGUA********ACAGGAAAAACAGAAAAAAGCCCGCACCUA***AACAGUGCGGGCUUUUUUUUCGGCUAAAGAUUAUUGAGGUAAUACC
ECA        *********AUGCGCACUAUCAGCCUAAUCACCACGAUUAUUACCAUCACCGAUACAACCAGUAACGGUGCGGGCUGACGCAUA*********CAAAGAUUCCAGAAAA*AGCCCGCACCGA****ACAGUGCGGGCUUUUUUUUUAUGGCAGGUUAUCCCUCAACGUCGU
PE36       ***AUGACUUAUAACCUAGCGUUUAUUACCACCACCAUUAUUAACACUGUUAUUACAACG*********GUGGGAUGAUACGCA**GGGCUAAGACAGACAUAAUAAAAGAGCCCGUUACCGAU*UUAGGAACGGGCUUUUUUGUAUCAACAAGGAGCAAAGG********
Shewmr7    ******AUGCAUAGCCUAGGUUUUGUAGUAAUUACCAUUAUUACAACCACCACUACAACCAGAGUGGGGGCGGGCUGAUACACC*******CUAAAGAAUUUUAACGACGAGCCCGCUUCCCAC*AAAGAAGCGGGCUUUUUUGUUUCUAGCUUAUGUUUCUUAGUCGGGC
Sbal223    ******AUGCAUAGCCUAGGUUUCGUAGUAACUACCAUUAUUACAACCACCACUACAACAAUAGUGGGGGCGGGCUGAUACACC*******CUAAAGAAUUUUAACAAUGAGCCCGCUUCCCAC*AAAGAAGCGGGCUUUUUUGUUUCUAGCUCUUAUUUCUAAGUCGGGC
Sput200    ******AUGCAUAGCCUAGGUUUCGUAGUAACUACCAUUAUUACAACCACCACUACAACAACAGUGGGGGCGGGCUGAUACACC*******CUAAAGAAUUU*AACGAUGAGCCCGCUUCCCAC*AAAGAAGCGGGCUUUUUUGUUUCUAGCUCUUAUUUCUAAGUCGGGC
Ssed       ******AUGCAUUGCCUGAAUACAGUUGUAACCACCAUUAUUACAACCACCACGAUUAUUUUCGUGGGGGCAGGCUGAACACAC******UCUGAAAGAAUGUAAAUAAUAGCCCGCUCCCAUAACAAGGAGCGGGCUUUUUUGUUUCUUAGGUAGCGUGGUACAAGGAGA
Sfri       ******************AUGCUCGUUGUAAUUACAACCAUUACAACCACCACUAUUACCAUAGUGGGGGCGGGCUGAUUACAC*****CCUAAAAGAUUUUGCAUGAAAAGCCCGCUUCUAACACCUGAAGCGGGCUUUUUUGUUUUUAAUUCUGAUAUUUGAUUUUAAU
Sden       AUGUUAACGAGCCAUGCUCAGAGUAUUACUCUUAUCACCAUUACAACCACCACAAUCAAUAUUGUGGGGGCGGGCUAGCGCACC********UAAAAGAUUUACAAAAAAAGCCCGCUUCCCAC***UGAAGCGGGCUUUUUUGUUUGUGGUUCUGGUUCUACACAACACU
Shew       ******AUGUUUAGCCUUAAUCUCGUAGUAACCACCAUUAUUACAACCACCACGAUUACCAGCGUGGGGGCCGGCUAAGCAUACUCGAAAGAAAUGAUUUGAAAUGACUAAGCCCGCUCCCCAU*CAAGGAGCGGGUUUUUUUGUUUCUGGGGCGCGGUACUAAGGAGAGA
SO         ******AUGCAUAGCCUAGGUUUCGUAGUAAUUACUAUUAUUACAACCACCACUACAACCAGAGUGGGGGCGGGCUGAUACACC********CUAAAGAAUUUAACGACGAGCCCGCUUCCCAC*AAAGAAGCGGGCUUUUUUGUUUCUAGCUCUUAUUUCUAAGUCGGGC
Spea       ***************************AUGAUCACCAUUAUUACAACCACCACGAUUACCAACGUGGGGGCGGGCUAAGCACAA*****CCUGAUAUAAGUGAAAUAUCAAGCCCGCUCCCCCU*AAAGGAGCGGGCUUUUUUGUUUCUUAAGGUGGCGCGGUAAAAGGAG
SwooD      ******AUGCAUUGCCUAAAUCGAGUUGUAACCACCAUUAUUACAACCACCACGAUUACAUUCGUGGGGGCAGGCUAAACGUAC****UUAAAUUUUUUUGAAUAUGACAAGCCCGCUCCCACACCAAGGAGCGGGCUUUUUUGUUUCUUAGGUAUUUGGCGCGGUACAAG
Sama       ******AUGUAUAAGUCAGGCGCAGUAGUAACCACUAUUAUUACUACCACCACCAUUACCGGAGUGGGGGCGGGCUGAUUUUAC*****CCUGAAAAGAAUGAACAUUAAGGCCCGCUCCCCCA*AAAGGAGCGGGUUUUUUGUUUCUGGGGCGAGCGAGGUAAACGGAGU
CPS        ***AUGAAAUUAAACACUAGCCACAUUACUAUUAUUACAACCACUACCACCCUAAUUAGGAUGGCGGUCGCUGGCUAACGUGUAAAA*******AUAAAAAUUUUAUCGAAGCCCGUGACCUGAAAAGGUUACGGGCUUUUUUACGUUUACAAUGAAGAGUAUUAACUCUA
MADE       ***AUGAAAAUGAUUCUACUUACUCGCACCACCAUGAUGUCGAUUACCACCUU***AAAAAGGGCGGUCGCUGGCUAGUGCAAG************UAAGCAAAAGACAACGAAAGCCCGCCUAACACAGAGCGGGCUUUUUUUUACACACGUUUUAGC************
ATW7       ***AUGAAAACAAUUAAUCGCGUACUG***ACCAUUAUUAUUACAACCACCAUUCUUUCUGGA*UAGUGGCAUAGGUCGGUGC***************AACAAAUUUAAAGGCCUGUGUUCACUU*AGAACACAGGCCUUUUUUCGUUUUAUGGGAUGAGGAACAUAAACA
PSHAa      ******AUGAAAACAUUUAGUCUUGCAGCGACCAUUAUUAUUACAACCAUCAUCCUAACUGGA*UAGUGGCAUAGGUCGGUGC***************AACAAAUUUAAAGGCCUGUGUUCACUU*AGAACCAGGCCUUUUUUCGUUUUAUGGAAUGAGGAAACAUAAAA
PTD2       ***AUGAACAAAUUUAAUUCAGUACUA***ACCAUUAUUAUUACAACCACCAUCCUAACUGGA*UAGUGGCAUGGGUCUGUAC****************GCAAAAUAAAAGGCCUGUGCUCACAA*AGAGCGCAGGCCUUUUUUCGUUUUUGGGGAUGAGGAAAUUAAU**
Patl       AUGAACGUAGAUUCGAAAAUAAUAACAAGCACCAUCGGCAUGAUUAUGAUUAUUACCUCUUUGAGGUGAUCGCUGGCUUGUGCACAUA*********AAACAGACAUAAAGCCCGCAAA********UAUAGCGGGCUUUUUUGUUAUUUAGCGCAGCAAAAAGUUAAUUA
NTHI       AUGAAAAAUAACCGCACUUUAUCCGUAAUCAUUAGCACGAUUACCGCCAUUAUGAUGACCAUUAUUAUGAUUAAUGGCGCGGGUUAGUGCAGCAAAAACAAGAUACAGAAAACCCGCGAUUCAACUGAAUAGCGGGUUUUUUUUAUAAAUUUAAAAACACAAUAUCUAGGAG
PM         ***AUGAAUAAACGCACUGUG***AUUACUAUGAUUAUGACCACCACUAUUAUUACCAAUAGUGUGCGGGUUAGUGCGUAAC******AAAAAGAUCGAAUUCCACAAAACCCGUACUGAAU**AAAAAGUGCGGGUUUUUUUAUGAAAAUUUUUAUUCUAUUUUUAAAAU
plu        ************************AUGAUUACCACCACCGGGACCACA************GGUUGCGGGGCGGGCUGACGCAU********AUAUAAAACAGAGAAAAAAGCCCGCAUCCAAAUC**AGAUGCGGGCUUUUUUUUGGCGCGGAAUCAGGAGAAAAAUGUU*
P3TCK      ******AUGUUUAACGUUAUCAGCACAACCACAACCAUUAUUAUUACUGGCACGAUUAUUCGUGUUGGUGCGGGCUGAUACGC*********AUAAGAUUCUUAAAAAAAGCCCGCACUUCUUA*UUAGAUGCGGGCUUUUUUUUUAACUUUUUAAAAUGAAAUCGAUUUG
SKA        AUGAAGAAUGUAUUCAGCUCUCACGCCAUUACACGCAUUAUUAUUACCAUUAACAUCUUCGGUGUUGGUGCGGGCUGAUAUAC**********GUAAAGAUUAACAAUAAGCCCGCAACUCAUAAUGAGCUGCGGGUUUUUUUUUAACAAUUUUAAAUUCACAUAUUUGAG
A5A        ***************************AUGACCACCAUUAUUACCAUUACCGACACGUCGCAUGUUGGGGCAGGCUGCUGAGCGC*********AAAAUUUCACAAAAAAGGCCUGUAUCCCAAC**CGAUACAGGCCUUUUUUUAUACCCGCUUUUUU************
VAS14      AUGAAGAAUGUAUUCAGCUCUCACGCCAUUACACGCAUUAUUAUUACCAUUAACAUCUUCGGUGUUGGUGCGGGCUGAUAUACGC**********AAAGAUUAACAAUAAGCCCGCAACUCAUAAUGAGCUGCGGGUUUUUUUUUACGAUUUUAAAUUCACAUAUUUGAGU
VP         ***************************AUGACCACGACCAUUAUUAUUACCGACACGACAAAUGUUGGGGCAGGCUGCUGAGCG********AAAGAAAUUCACAAAAAAGGCCUGUAUCCAACA**AGAUACAGGCCUUUUUUUAUGCGUUUUUAGACAGAAUUUAGACA
MED222     ***************************AUGACCACCACCAUUAUUAUUACCGACAUUCACAUUGUUGGGGCAGGCUGCUAAGUAACGG*********AUUUUAAAAAAAAGGCCUGUAUCCAACA**AGAUACAGGCCUUUUUUUGUACCAUUUUUAUGACUUAUGGAGAA
VF         ************************AUGAUUAUUACCACAACAAUUACCGGCACCAUGGUUGCUGGGGUGGGCUGAUACGUAU***************AAGUAUAUGAAAAAGCCUGCUCUGAUUAC*CAGAGCAGGCUUUUUUUUGCAAAUUUGUUACUAAUUCUUAAUUG
VV1        ************************AUGACCACCACCAUUAUUAUUACCGACAUCACACAUGUUGGGGCAGGCUGCUGAGCG********AAAGAACAAAUUUCAAAAAAAAGGCCUGUAUCCAACAA**GAUACAGGCCUUUUUUUAUACAGAUUAAAAAUAAUCCGGGAGG
V12B01     ************************AUGACCACCACCAUUAUUAUUACCGACAUUCACAUUGUUGGGGCAGGCUGCUAAGU************AACGGAUUUUAAAAAAAAGGCCUGUAUCCAACAA**GAUACAGGCCUUUUUUUGUACCAUUUUUAUGACUUAUGGAGAA
VIBHAR     ************************AUGACCACGACCAUUAUUAUUACCAACACGACCAAUGUUGGGGCAGGCUGCUGAGCG***********AAAGAAAUUCACAAAGAAGGCCUGUAUCCAACAA**GAUACAGGCCUUUUUUUAUGCUUUUUUAUACAGAAUUUAGACA
V12G01     ************************AUGACCACGACCAUUAUUAUUACCGACACGACACAUGUUGGGGCAGGCUGCUGAGCG***********AAAGAAAUUCACAAAAAAGGCCUGUAUCCAACAA**GAUACAGGCCUUUUUUUAUGCUUUUUUAUCCAGAAUUUAGACA
VSAK1      ************************AUGACCACCACGAUUAUUAUUACCGACAUUACCAAUGUUGGGGCGGGCUGGUAGACGG***********AAGAAAUUCAAAAACAAGGCCUGUAUCCCCAA***GAUACGGGCCUUUUUUUUACCUGUUUUGAGUAUUUCGGGAGGA
VSWAT3     ************************AUGACCACAACCAUUAUUAUUACCGACAUUAACAUUGUUGGGGCAGGCUGCUAAGUA************ACGGAUUUUAAAAAAAAGGCCUGUAUCCAACAA**GAUACAGGCCUUUUUUUGUACCAUUUUUAUGACUUAUGGAGAA
AHA        ***AUGCAGUUAUUCACCAAUGUCAUCACCACCACCAUUAUUACCGGUACCACCACAGGUGGCACUGGGGCCGGUUGAUGCGCUGACGAACAAGCACAGAAAUCAGAAAAGGCCCGUACCCACCCA***GUACGGGCCUUUUUGUUGGAUGAUUUUCAGAACCAUUUUCGG
ASA        ***AUGCAGUUAUUCACUAACGUCAUCACUACCACCAUUAUUACCGGUACCACCACAGGUGGCACUGGGGCCGGUUGAUGCGCUGACGAACAAGCACAGAAAUCAGAAAAGGCCCGUACCCACCCA***GUACGGGCCUUUUUGUUGGAUUGGUUUUUAGAUUGAAUUUCA
XOO        GUGCGGGCAGGUGCGGGCGUGGCCGGCAUUACCACCAUCAUUACUACCGCCACCAUUCGCCCGGUGCGGUCCGUCGUCUUCGCGUAAC********UUCCGAAAACAACGGCCCCGCACCCGGAUCAGGAUGCGGAGGCUUCCCUCUCUCAUCCGAUGCGGACGGGGCCUC
XC         AUGCGGCCAGGUGCGGGCGUGGCCGGCAUUACCACCACCAUUACCACCGCCACCAUUCGCCCGGUGCGGUCCGUCGUCUUCGCGUAAC********UUCCGAAAACAACGGCCCCGCACCCGGAUCAGGAUGCGGGGGUCUCCCUCUCUUACCUGAAGCGGACGGGGCCUC
IL         AUGCGGUUGGUUGUAUCUCCGGCUGCCGAAACAACGACUAAGUCGCUGGCACCAGCGUACUCGGUGACAAUUCGGGCAACGCGGCGAUAGCAGAACGCAUCAGCAAGACUGCUGCCGCCAAACUUAUGCACCUGAACGCUGUCGGCAACGGCUUGCUUUUGCUCUUCUGUG
```

Fig. 9. Classic attenuation regulation of gene *thrS* in β-proteobacteria. Designations as in Figure 4.

Bcep	**AUGACA**CCGCGA**ACG**UUG**ACC**GAA**ACCACU**UCGGAGCGACGC***UAG***UCGAGGACCACUUUCGCCAAUGUAGUUUGCAGGAAAUGU*GAA*UGCGGCCCCUCGAAAGCGGGGCCGCAUUUUUUUUAGCUUGUUUGAUGG****
Bcen2424	**AUGACA**CCGCGA**ACG**UUG**ACC**GAA**ACCACU**UCGGAGCGACGC***UAG***UCGAGGAACGUUUUCGCCCUUUCAGUCUGAGUGAAGUAUCGAA*UGCGGCCCCUCGAAAGCGGGGCCGCAUUUUUUUUGUCGCGAAUUUUUUU****
BURPS	**AUGACA**CCGCGA**ACG**UUG**ACC**GAA**ACC**CAUUCGGAGCGACGC***UAG***UCGAGGAACGUUUUCGCCUUGUG*GUUUUGA***AGUAUCGGA*UGCGGCCCCUCGAAAGCGGGGCCGCAUUUUUUUUGUUGCGCGUUUCAUUGUU
Bcep1808	**AUGACA**CCGCGA**ACG**UUG**ACC**GAA**ACC**UUUUCGGAGCGACGC***UAG***UCGAGGAACGUUUUCGCCCUUUCAGUCUGAGUGAAGUAUCGAA*UGCGGCCCCUCGAAAGCGGGGCCGCAUUUUUUUUGUCGCGAAAUUCCGCGCG
CV	**GUG**AAAUCCUUGCGA**ACUACCACAACC**CGACAU**ACU**CACGAAAGC***UGA***GCCUUGCGGUUGG**********ACCAUGCGAAAAAGAAGUGCGGCUCAG**********GCCGCACUUUUUUUUUACCCUUUUGCUUU***
Mfla	**ACCACA**AAAGAAAGCAAA**ACC**UUGAUGCCUGAGUGCGGCAAGGUUUGUGAG***UAG*****************UAAGUAGUAAGGAAGUGGCGACGCGGC*****CAAAGGCAUGCCCGAUCGCUCUUUUUUCAAUAUCCCUUUUA

Fig. 10. Phylogenetic tree of the gene *thrS* paralogs in δ-proteobacteria. Species names and their acronyms are given in Table 2.

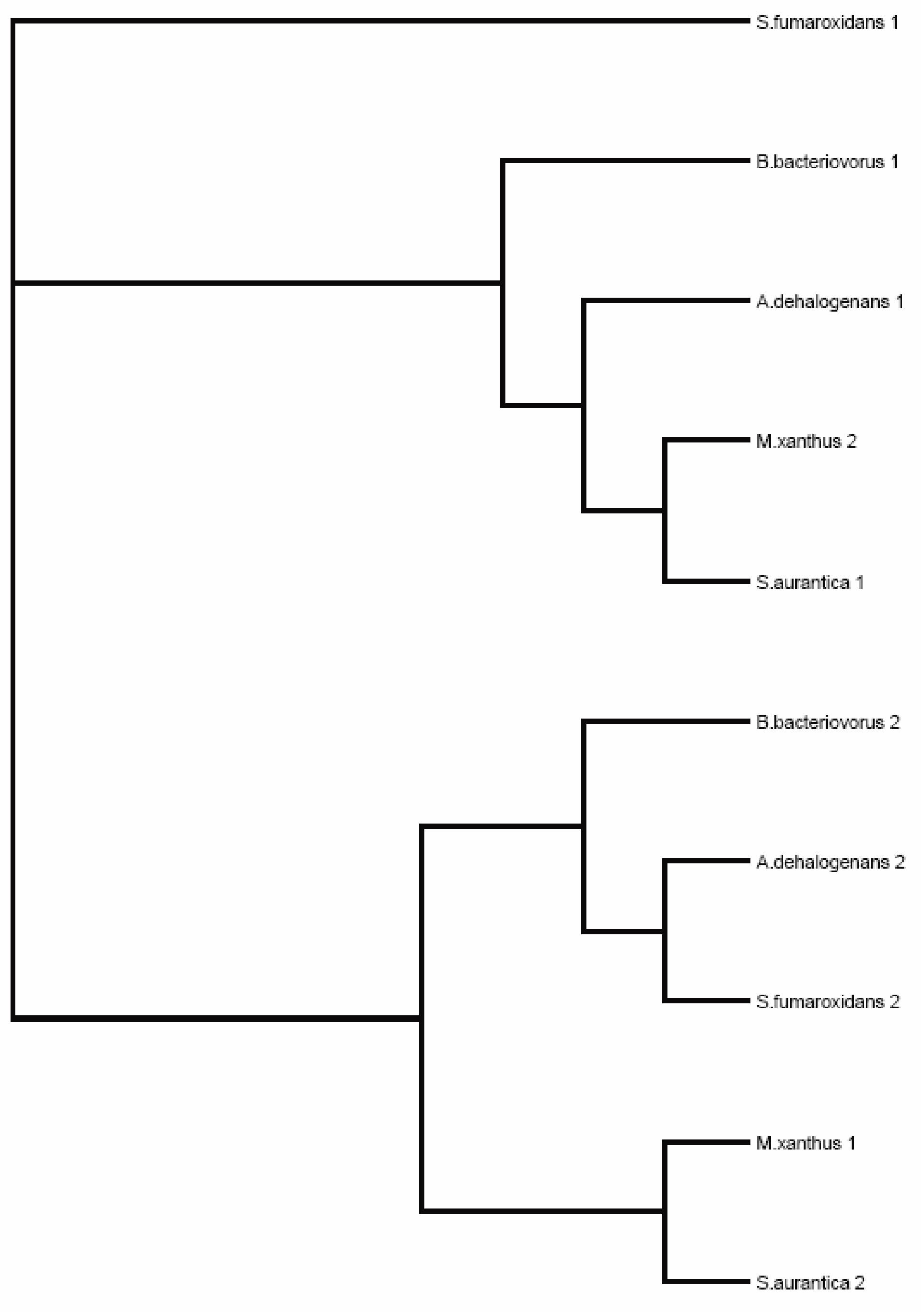

Fig. 11. Phylogenetic tree of the regulatory regions of gene *thrS* paralogs in δ-proteobacteria. Species names and their acronyms are given in Table 2.

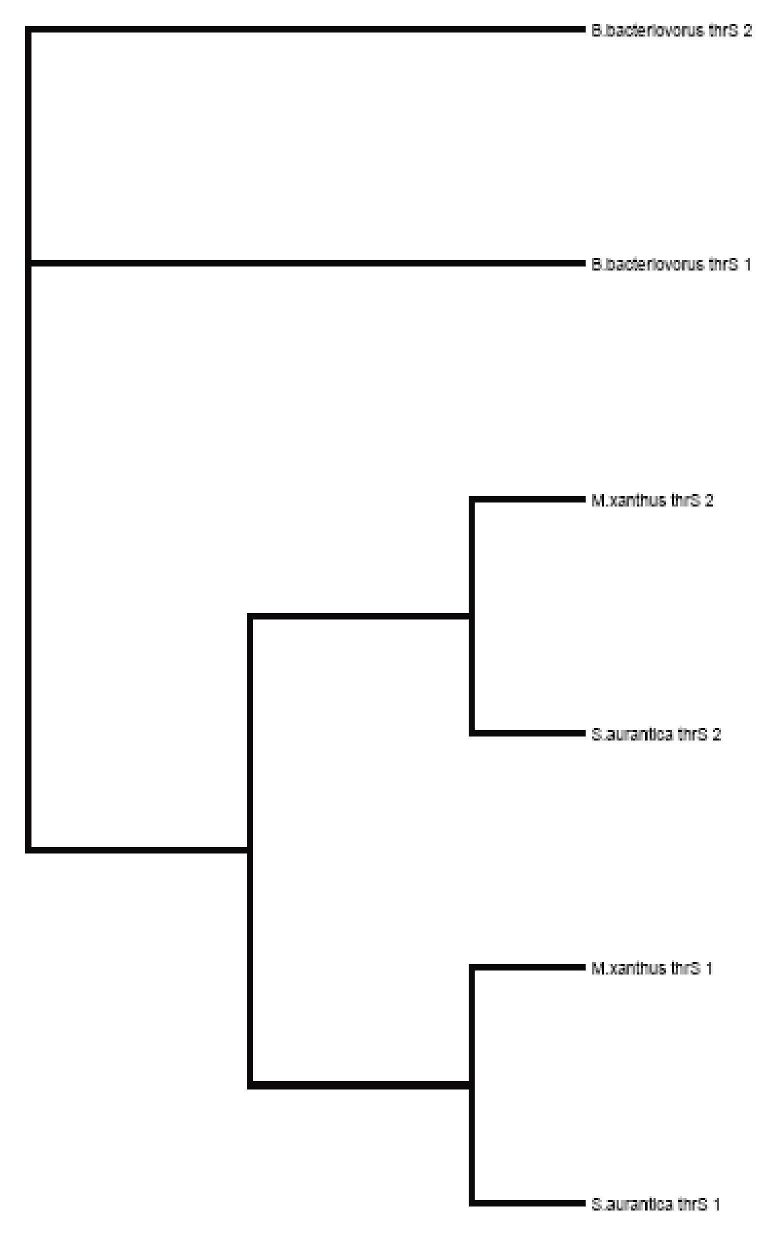

Fig. 12. Classic attenuation regulation: a) *trpE, trpS, trpBE, trpBA* operons in actinobacteria; b) *trpB* gene in Bacillales (Firmicutes). Designations as in Figure 4.

a)

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DIP_trpBE   ************************AUGAAUGCACAUAACUGGUGGUGGCGCGCUUAACC*GCGGGCC*GUUUU***CACGCAUUCAUUUC************AAC**AGGCUCGCCUUGUCCA*****ACAAGCAGCGGGCCUUUUUGUUAGC*
DIP_trpBA   ***************AUGAUGAAUGCAGCUUUCAAGUUCUUCUGGUGGCGCGCCUAGCAGGCGGGCCCCUUUUGUGUGAGCAUUCACCACACAACUUUUGGAAACACAAGCCCGCGUAU***************CGCGGGCUUUUUCGUAUAU*
CE_trpE     ******GUGAACAACUUCUGUCAAUCCCAGGGCACCCAGUGGUGGUGGCGCGCUAGAUAAGCGGGCCCACGGAUCACCAAGUUGUUUUCACACUGAAGAUUU***CAAGGCUCGUGUACUUCGUUCGACGAAGCAGCGGGCCUUUU*GUGGUU*
cg_trpE     ******GUGAAUAACUCUUGUCUCAGUCAAAGCACCCAGUGGUGGUGGCGCGCUAACUAAGCGAGCCUGACACCUCAAGUUGUUUUCACUU**UGAUGAAUUUUUUAAGGCUCGU**ACUUCGUUCGACGAAGAAGCGGGCCUUUU*GUGGUU*
SAV_trpS    ***************AUGACUACGCGUACGUGUACCCAGCAGUGGUGGGCCGCCUGA*CGGCG*GCCGUACACACGUAUGUACUC*********************AACGGCCGCCGCCU*************CGGCGGCCGUUCUCGUUUCU*
SAV_trpE    ***************AUGUUCGCGCACUCGAUCCAGAACUGGUGGUGGACCGCUCAUCCGGCG*GCCCACUGACUGCGCGU***********ACGCAAGACUUCGCGAAGGCCGCCC**************GAGGGGCGGCCUUUCGUGUUUCC
SCO_trpE    ***************AUGUUCGCGCACUCGACCCGGAACUGGUGGUGGACCGCUCACCCGGCG*GCCCACUGACUGCGCGCG***********ACUCAAGACUCGCGAAGGCCGCCC**************GAGGGGCGGCCUUCGGUGUUUUC
SVE_trpE    ***************AUGUUCGCGCACUCGACCCGGAACUGGUGGUGGACCGCUCACCCGGCG*GCCCACUGAUCGCGCGU**********ACACGGAUCACACGCACAGGCCGCCC**************GAGGGGCGGCCUUUCUCG*****
Tfu_trpE    ************AUGCGACCGGCACUGACUUUCCAGCAGUGGUGGCGCCGCUGGUAGGCGGCGCUUCUGGUUCGCAU******************UCCUGAGACCUGGCGACCGCCC************GGACCGGCGGUCGUUUCUGUUGUC*
nfa_trpS    UGGCCUCGAACCAGCCGCAUCUCACGCCGGAGGCGCGGAUGGUGGGCUCGUACCUGAUGGGGCAACGGGUGCCCUACCCG*********************CUGCCGGUGCCCGCCCAGCAGGU*****CACCGGCGGGUACUACCUGCUCGU*
SACE_trpS   ***************************************AUGUGGUGGGCCGCCCAC*GGGCG*GCCCGGACGCUUCGCGCACUGACCAACGCGAACCGGUCGCCAUCAGGCGGCCGACGCGAAUCGCGGUCAUCCUGGUGGCGGCAAGGACC*
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b) *trpB:*

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BH   AUGUGUUGGUGGUGGCAGUAAUGCGAUAGGAACGUUUUACCCAUUUUUAGAGGAUGACGUGAAGCUUAUCGGCGUGGAAGCGGCGGGCAAAGGAGUCGAGACUUCUCAACAUGCGGCGACGAUU***ACGAAAGGACGAGUAGGUGUCAUUCACGGAUCGAUGACCUACUUGCUUCAG
BALH UUGUAUUGGUGGUGGGAGUAACGCAAUGGGAAUGUUUUAUCCGUUCGUACACGAUGAAGAAGUUGCUCUUUACGGCGUAGAAGCAGCUGGAAAAGGUGUUCAUACAGAAAAGCAUGCAGCAACUUUAACGAAAGGAAGCGUCGGUGUUUUACACGGAU***CAAUGAUGUAUCUUCUA
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Fig. 13. Phylogenetic tree of the regulatory regions of genes *trpE* and *trpS* in actinobacteria. Species names and their acronyms are given in Table 2.

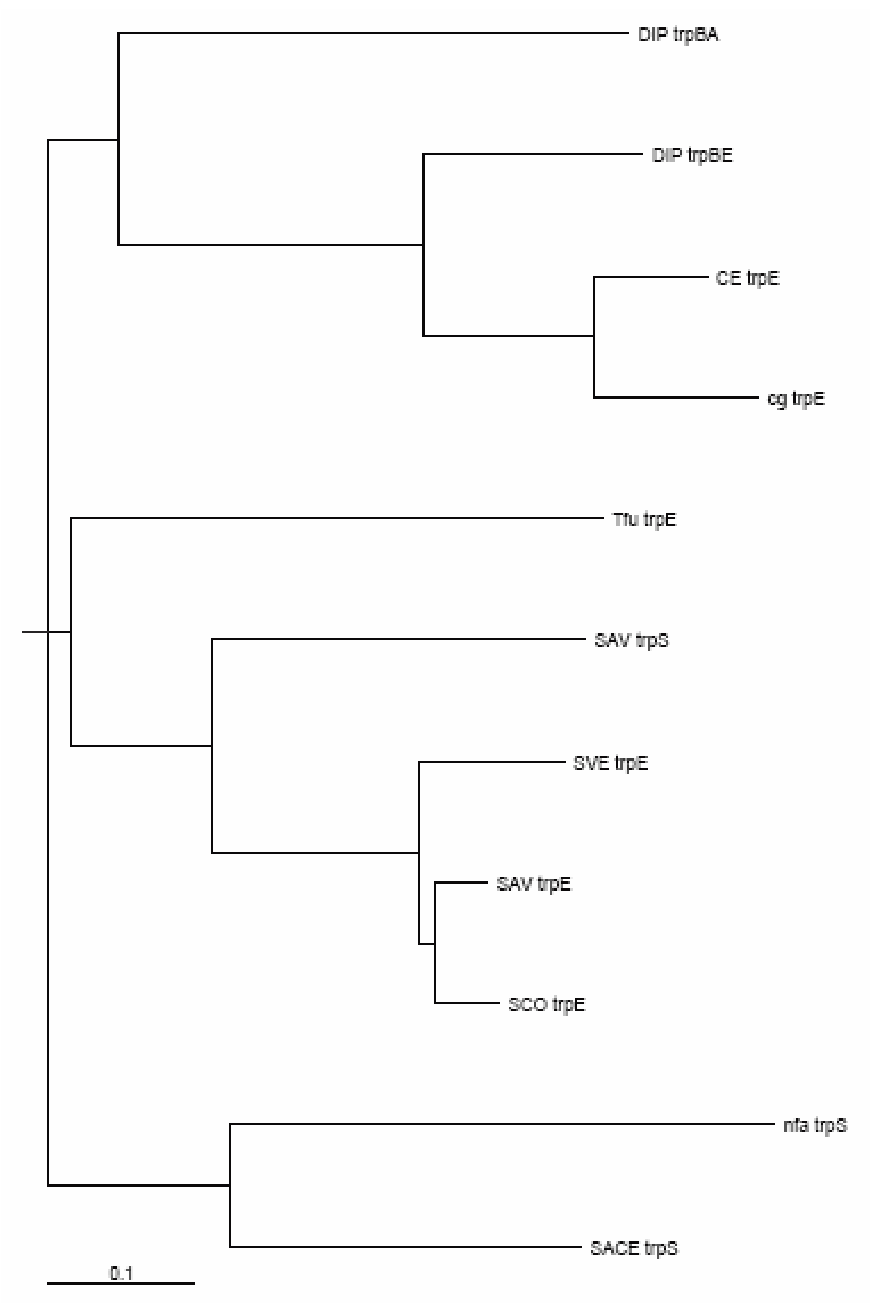

Fig. 14. Classic attenuation regulation of gene *trpE* in α-proteobacteria. Designations as in Figure 4.

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blr      ***AUGAGCACCGCCGUCCGCCCAGCCCGUCUUUGGUGGCGCACCUCCUAAGA***GGUGGCCGGUGCGAUUUCUU***********UUCCCAAAAUCGUCGAAGGUCGCCCACGCA**********GUGCGGCGGCCUGAUCGUUUGUCCUGUGUG
BRADO    ***AUGAGCACUGUCGUCCGCCCAGCCCGUCUCUGGUGGCGCACCUUUUAAAA***GGUGGCCGGUGCGAUUCAUU*********UGACAUUCGAUCGCAGAGGGGCCGCCACGCAG*************CGGCGGCUUCCGGUUGGUCCUGUGUGG
Nham     ***AUGAACACCGUCGCCCGCCUGACCCGUCUCUGGUGGCCCACCUUCUGAA****GGUGGCCGGUGCGAUUUUGU*********UUCAGUUUUGAUCGUCAAAGGCCGUCAUGCAGA***********ACGACGGCCUUUUUUCGUUUGUCCUGUG
NB311A   ***AUGAAUCCUGCCGCUCGCCCGUUCCGUUUCUGGUGGCCCGCUUUCUGAA****GCUGGCCGGCGCGAUUUUGC**********UCAAUUCUAAUCGUCGAAAGCCGUCAUGCAGA***********GCGACGGCCUUUU*UUGUUUGUCCUGUG
RPC      ***AUGCGCACGGCAGCCCGCCUUUCCCGUCUCUGGUGGCCCACCUUCUGAA****GGUGGCCGGUGCGAUUUCCA************UUUUUCCAAUCGUCAAGGCCGUCAACGCAG**********UGCGACGGCCUUUUGUUUGUUUGCCCUGC
Oant     AUGAACAUUUCGCGCAAUAUCGUCAUCAACGGUUGGUGGUGGGCCCGCUAAA****AGCGGCCACGCAGGCGUUUG*******UGCAUUUGCGUUUAGAAAACAGGCCGCUGGGAUUA*********UCCGGCGGCCUUUUUGUUUGGCUGUUUGA
Meso     ************AUGGUUCUAAACGCAAAGCUUUGGUGGUGGGCCCGCUAACG***AGCGGCCGGCGCUAGCAUG*********AGCGUUUGAACUUCGACGAUGGCCGCAGGUGAAA*********ACCGGGCGGCCAUUUUAGUUUGGGGCUUCC
ml       ************AUGCGUUCGACCAAGACCAUUUGGUGGUGGGCCUGCUGACA****GCGGCCUGUUCGAACGCGC*********GUGCGUGAAAAGAGAGGGUGGCCGCAACGGAAA********GUCCGGGCGGCCAUUUGUUUUUUAAAAACCA
BOV      AUGAACAUUUCGCGCAUUAUCGUCAUCAACGGUUGGUGGUGGGCUCGCUAAA****AGCGGCCACGCAGGCGUUCG*******UGCAUAUGCGUUCAGAAGACAGGCCGCUGGGAUUA*********UCUGGCGGCCUUUUUGUUUGGCUGUUGGA
BR       AUGAACAUUUCGCGCAUUAUCGUCAUCAACGGUUGGUGGUGGGCUCGCUAAA****AGCGGCCACGCAGGCGUUCG*******UGCAUAUGCGUUCAGAAGACAGGCCGCUGGGAUUA*********UCCGGCGGCCUUUUUGUUUGGCUGUUGGA
BruAb1   AUGAACAUUUCGCGCAUUAUCGUCAUCAACGGUUGGUGGUGGGCUCGCUAAA****AGCGGCCACGCAGGCGUUCG*******UGCAUAUGCGUUCAGAAGACAGGCCGCUGGGAUUA*********UCCGGCGGCCUUUUUGUUUGGCUGUUGGA
BME      AUGAACAUUUCGCGCAUUAUCGUCAUCAACGGUUGGUGGUGGGCUCGCUAAA****AGCGGCCACGCAGGCGUUCG*******UGCAUAUGCGUUCAGAAGACAGGCCGCUGGGAUUA*********UCCGGCGGCCUUUUUGUUUGGCUGUUGGA
SMc      ******AUGGCAAACACGCAGAACAUUUCGAUCUGGUGGUGGGCUCGCUGAG*****GCGGCCUUGACCAGUCAUG************CGUGAUUGAGAGAUGGAGCCGCCCGGAGAU********UUCGAGGCGGCUUUUUUCGUAUUCGGGCCGC
Smed     ******AUGACAAACACGCAGAACAUUUCGAUCUGGUGGUGGGCUCGCUGA*****GGCGGCCUUGACCAGUCAUG************CGUGAUUGAGAGUUGGAGCCGCCCGGAGAU********UUCGAGGCGGCUUUUUCGUAUUCUGGCCGCG
RHE      ******AUGAUCAAGUCCUUGAACAUCGCUGUUUGGUGGUGGGCUCGCUGA*****GGCGGCCUCGACCAAUCGUGUC********CAAAGACGACGACGAGUGAGCCGCCCGAAA*********CUUCGAGGCGGCUUUUUUGUUUUAUCGCCGCC
RL       ******AUGAUCAAGUCAUUGAACAUUGCUGUUUGGUGGUGGGUUCGCUAA*****GGCGGCCUCGACCAAUCGUGUC***********CAAAGACGACGAGUGAGCCGCCCGAAA*********CUUCGAGGCGGCUUUUUUUGUUUAUGGCCGCC
FP2506   ******AUGACAAACACGCAGAACAUUUCGAUCUGGUGGUGGGCUCGCUGA*****GGCGGCCUUGACCAGUCAUGC************GUGAUUGAGAGUUGGAGCCGCCCGGAGA********UUUCGAGGCGGCUUUUUCGUAUUCUGGCCGCG
Atu      ***AUGAAUAUCGUGUCUAAGAACAUUGCUAACUGGUGGUGGAGCAGCUUUUUG****CGGCCUUGACCAGUCAUGUC***********UUCAGACAAAGUCCAAGCCGCCCGAA**********UUUUCAGGCGGCUUUUUUGUUAUUAUGCCGCC
SIAM614  ***************AUGAACCUGAAAGCAGCUUGGUGGUGGCGCGGCGCGAUAUAGGCGGCCAGCGAUCAGUCAUGCUCUGAAGGGAUCGAGUAUCCAACCAAGGCCGCCGCGGGA*******CACCGCUGGCGGCCUUGGUUCUU**********
OM2255   ***************************AUGAAUUGGUGGUGGCAGUCCCUCUAGGGCUGUUUGUGCGCGUCUAUGUGU*****************CAUAAAAAAAGCCCGAGAU****************UUCGGGCUUUUUUUAUGCUUAUUUUUU
```

Fig. 15. Classic attenuation regulation of gene *trpE* in β-proteobacteria. Designations as in Figure 4.

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BP         ************************AUGCGCAACGCCUCGUGGCGUUGGUGGCGUUUGUCUUCCGGGUGGCGAUGAUUCCCUUCCCGGCCCUGGACGUAUCUGUCGCCUAGAGCCGGAGCUGUGAAGUGCAGCGCCAAGCCCGGAACCCGUAACUGGACCGGGCUUUUUGCUG
BB         ************************AUGCGCAACGCCUCGUGGCGUUGGUGGCGUUUGUCUUCCGGGUGGCGAUGAUUCCCUUCCCGGCCCUGGACGUAUCUGUCGCCUAGAGCCGAAGCUGUGAAGUGCAGCGCCAAGCCCGGAACCCGUAACUGGACCGGGCUUUUUGCUG
BPP        ************************AUGCGCAACGCCUCGUGGCGUUGGUGGCGUUUGUCUUCCGGGUGGCGAUGAUUCCCUUCCCGGCCCUGGACGUAUCUGUCGCCUAGAGCCGAAGCUGUGAAGUGCAGCGCCAAGCCCGGAACCCGUAACUGGACCGGGCUUU******
Bav        ************************AUGCGCAACGCCUCAUGGCGUUGGUGGCGUUUGUCUUCCGGGUGGCGAUAAUCU*CUUCCCGGCCCUAAGCGCGCGUCGCGA*UAGUGCC**************CAAAGCCAAGCCCGGAACCAC*AACAGGACCGGGCUUUUUUGUU
BTH        AUGUUUCUGAACAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCCAACCUCGAUGA**************************************************GGUACGCUGAAGCUC*GUCUUCAGCCCCGUUUUUUGUU
Bpse110    AUGUUUCUGAACAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCCAACCUCGAUGA**************************************************GGUACGCUGAAGCUC*GUCUUCAGCCCCGUUUUUUGUU
BmalP      AUGUUUCUGAACAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCCAACCUCGAUGA**************************************************GGUACGCUGAAGCUC*GUCUUCAGCCCCGUUUUUUGUU
Bcep1808   AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUGACCUCUUCGA***********************************************UGAGGUACGCUGAAGCCC*GUCUUCAGCGCCGUUUUUUAUC
BamMC406   AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCACUAACCUCUUCGA***********************************************UGAGGUACGCUGAGGCAC*GUCUUCAGCGCCGUUUUUUAUC
Bamb       AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCUUCGA***********************************************UGAGGUACGCUGAGGCAC*GUCUUCAGCGCCGUUUUUUAUC
Bcen2424   AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCUUCGA***********************************************UGAGGUACGCUGAAGCAC*GUCUUCAGCGCCGUUUUUUAUC
Bcep18194  AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCUUCGA***********************************************UGAGGUACGCUGAAGCAC*GUCUUCAGCGCCGUUUUUUAUC
BdolA      AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUGACCUCUUCGA***********************************************UGAGGUACGCUGAAGCCC*GUCUUCAGCGCCGUUUUUUAUC
Bmul       AUGUUUCUGAAUAAAAAACGGAGUCUGAGCAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCUUCGA***********************************************UGAGGUACGCUGAAGCAC*GUCUUCAGCGCCGUUUUUUAUC
Bxe        AUGUUUCUGAAUAAAAAACGGAGUCUGAUUAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCGCUU*************************************************GAGGUACGCUGAAGCUCGUCUUCGGCAACCGUUUUUUACU
Bphyt      AUGUUUCUGAAUAAAAAACGGAGUCUGAUUAGCAUCGACCGGGGAGCCUGGCCCUGGCGUCGCUGGUCGCGCUAACCUCGCCU*************************************************GAGGUACGCUGAAGCUCGUCUUCGGCAACCGUUUUUUACU
HEAR       AUGUCUCUCGACAAAAAACGACUCACAACACCAGGCGCUCAUGAGGCCUGGCUAUGGCGAGGCUGGCAAAACUGGUGCUGAA****************CACCAUUUGCCGCUGAUCACCUGCGCGUUUUUUAUCUGCGCAUCUGCUACCCGAUCAGCAACGUUUUUUGAAC
mma        AUGUUUCUCAACAAAAAACGACUCGCAUCACCAGGCGCCCAUGAGGCCUGGCUAUGGCGACGCUGGCAAAUCUGGUCUUAAA**********************************CACCAAUUGCCGCUGAUCGCCUGCGCCCAUUGCGCGAUCAGCAACGUUUUUUGAAC
Reut       AUGUUCUUCAACCGCAAACGCAUCUCUUCUGGCAGUGAUCGGCAGGCUUGGCCCUGGCGUCGCUGGCGCGCCUCCCAACAGGCGUAA*********************AGUGCGUUCGCGAGUCCGCUGAGCGGCCUUCGUACCGAAGGCUCGCCAGCACCGGCCAGGGUGC
Rmet       AUGUUCCUCAACCGCAAACGCAACUUUCUUGGCAGUGAUCGGCAGGCUUGGCCCUGGCGUCGCUGGCGCGCCUCUGAACAGGCGUAAAGUGCGUUCGCGAGUUUCCUGACGGGCUUGCGGGGAUACAUCGGGACUUAUUAAGUCCGCCGCAGUCACCCCCCAAGCUCCG***
RSc        AUGUUCCUGAACCGCAAACGCAUCUUCGCUGGUAGUGACCGGGGGGCCUGGCCCUGGCGACGCUGGCAUGCCCUCGCCCGGGCGUAAGCGUUUGCACGGCUGCUGAUCGUUCCAUUCCGGUUUCCGGCAUCCGGCGCACCCUCGGUGCGCCAGCCUGAGCCGCCUUCGU***
Rpic       AUGUUCCUGAAUCGCAAACGCGUCGACGCUGGUGGUGACCGGGGGGCCUGGCCCUGGCGGCCCUGGCACGCCCUCGUCCGGGCGUAAGCGUUUGCACGGCUGCUGAUCGUUCUUCCUCGGUUUCGGCAUUCCGGCGCGUCACGAGCGCGCCGCCCAAACCACCCCCCGC***
```

Fig. 16. Classic attenuation regulation of gene *trpE* in γ-proteobacteria. Designations as in Figure 4. Duplications of the gene’s regulatory region are marked with “#”.

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SKA_trpE      AUGUUACAGCAAAUUCAAAAUCAACAAUGCGUUUUCUUCAAUAAUUGGUGGUGGCACUCCUACUUACGGGCAGUGUGAAUAGCUGUAAUUCAG*****************************CAAAAUAACAACGAGCCCGCCAUCAA******UGCGGGCUUUUUUA
PBPR_trpE     AUGUUACAGCAAAUUAACCGACAGCUUCGCGCUUUCUUCAUCUCAUGGUGGUGGCACUUCUCUAUACGGUUGUGUGAUUUGCUGUUCCUAAC****************************GGACAGAAUAGACAUAAGCCCGCCAGA*******UGCGGGCUUUUUCA
SO_trpE       ************AUGACUCAGAUUAACGCUUCUUUCAACAUCAUUUGGUGGUGGCACUUCCCAACUUAGCGGGUAGUGUGAAGCUCUGUGCUCA***************UUUGAAAGUAACAGAAUCAACAGAAAAGCCCGCAGAAA*******UGCGGGCUUUUUUG
Sbal_trpE     ************AUGACACACAUUAACGCUUCAUUAAACAUCAUUUGGUGGUGGCACUUCCCAACUUAGCGGGUGGUGUGAAGCUCUGUGCUCA***************UUUGAAAGUGACCAGAAUCAACAAGAAGCCCGCAGAAA*******UGCGGGCUUUUUUG
Sput_trpE     ************AUGACCCACAUUAACGCUUCAUUAAACAUCAUUUGGUGGUGGCACUUCCCAACGUAGCGGGUGGUGUGAAGCUCUGUGCUCA***************UUUGAAAGUGACCAGAAUCAACAAGAAGCCCGCAGAAA*******UGCGGGCUUUUUUG
Sputw_trpE    ************AUGACCCACAUUAACGCUUCAUUAAACAUCAUUUGGUGGUGGCACUUCCCAACGUAGCGGGUGGUGUGAAGCUCUGUGCUCA***************UUUGAAAGUGACCAGAAUCAACAAGAAGCCCGCAGAAA*******UGCGGGCUUUUUUG
Spea_trpE     ************AUGACACAGUUAACAACUUUCCAAAACAUUAAUUGGUGGUGGCACUUCCCAAAUUAGCGGGUGGUGUGGAACUGUGUGCUCA**************GAAAACUGAGACAAGAUUCAACAAGAAAGCCCGCAUACA******CUGCGGGCUUUCUUG
Shew_trpE     ***************AUGACGACGCAGCUAUUCAACAACAUCAACUGGUGGUGGCACUUCCCAACAUAGCGGGUGGUGUGAAUUUCUGUGCUCA**************UGUAAAAGAGACAAGAUUUAAACAAAAAGCCCGCACUCG******AUGCGGGCUUUUUGC
Ssed_trpE     ************AUGAACACAUUUUCACAAGCACAAAACAUUAAUUGGUGGUGGCACUUCCCAACUUAGCGGGUGGUGUGAAACUCUGUGCUCA***************UGUAAAAGAGACAAGAUUCAACAAGAAGCCCGCAUAGA******AUGCGGGCUUUUUUG
Swoo_trpE     ************AUGAACAUUUUUUCUCAAGCACAAAACAUCAAUUGGUGGUGGCACUUCCCUAACUAGCGGGUGGUGUGAAACUCUGUGCUCA***************UGUAAAAGAGACAAGAUUCAACAAUAAGCCCGCAUAGA******UUGCGGGCUUUUUUG
Sfri_trpE     ************AUGACACACUCUUUAGCUUCAUUACACAUUACAUGGUGGUGGCACUUCCCAAAUUAACGGGUGGUGUGAAGCGUUGUGCUCA**************UUUUUAAGAGACAAGAUUUUACCAAAAAGCCCGCAGAGA*******UGUGGGCUUUCUUG
Sden_trpE     ************AUGACACACUCAAACGCAUUUCAACACAUUUCUUGGUGGUGGCACUUCCCAACUUAACGGGCGGUGUGAUGCGUUGUGCUUA******************AUUGACACAAGAAUUAUCCAAAAAGCCCGCACCU********UGCGGGCUUUUUUG
Sama_trpE     ***************AUGAACCCAAUCAUUGCUUCUUUCAUCAACUGGUGGUGGCACUUCCCGAAUACGCGGGUGGUGUGAAGCUUGGUGUGCG**************UUUAACAGACACAAGAUUCAUCGAAAAGGCCCGCACUA********CGCGGCCUUUUUUG
ASA_trpE      ******************AUGCAAACGACUUCCAUCCUGACCAUCUGGUGGUGGCACACUCCCUGACAUGCGGGCGUGUGGUCGUUGCUGUAUC******UGUAAUCUGACAGCAAAUUAAGAACCCAAAGAAAAAGCCCGCUGACCC*****CAGCGGGCUUUUUUA
AHA_trpE      ******************AUGCAAACGACUUCCAUCCUGACCAUCUGGUGGUGGCACACUCCCUGACAUGCGGGCGUGUGGUCGUUGCUGUACC*****UGUAAAUCUGACAGCAAAUAAAGAACCCAAAGAAAAAGCCCGCUGACCC*****CAGCGGGCUUUUUUA
CPS_trpE      ************AUGAACACAGCAAAUACAAACAUAACAUUAAUUUGGUGGUGGCAUAACUCGACAUAAUUGGGUUGUGAUAAUUGCGUGUAUC*************UUAAAAAAGAUGAAUCGAAUUUCAAAAAAACCCGCUCCUGU*****UAGCGGGUUUUUCUC
SFV_trpE      *********************AUGAAAGCAAUUUUCGUACUGAAAGGUUGGUGGC*GCACUUCC**UGAAACGGGCAGUGUAUUCACCAUGCGUAAA************************GCAAUCAGAUACCCAGCCCGCCUAAU******GAGCGGGCUUUUUUU
SbBS512_trpE  *********************AUGAAAGCAAUUUUCGUACUGAAAGCUUGGUGGC*GCACUUCC**UGAAACGGGCAGUGUAUUCACCAUGCGUAAA************************GCAAUCAGAUACCCAGCCCGCCUAAU******GAGCGGGCUUUUUUU
SSON_trpE     *********************AUGAAAGCAAUUUUCGUACUGAAAGCUUGGUGGC*GCACUUCC**UGAAACGGGCAGUGUAUUCACCAUGCGUAAA************************GCAAUCAGAUACCCAGCCCGCCUAAU******GAGCGGGCUUUUUUU
SDY_trpE      *********************AUGAAAGCAAUUUUCGUACUGAAAGGUUGGUGGC*GCACUUCC**UGAAACGGGCAGUGUAUUCACCAUGCGUAAA************************GCAAUCAGAUACCCAGCCCGCCUAAU******GAGCGGGCUUUUUUU
CKO_trpE      *********************AUGAAAGCAACAUUCGUACUGCACGGUUGGUGGC*GCACUUCC**UGAUUUCGGGCAGUGUAUGACGUCUGCAAUA***********************AGCAACCAGAUACCCGGCCCGCCAGAU******GAGCGGGCUUUUUUU
Ent_trpE      *********************AUGAAAGCACAUUUCUCCCAGCACGGUUGGUGGC*GCACUUCC**UGAAUAUCGGGCAGUGUCAUUCGUGUGCGUU**********************ACGAAAACAGAUACCUGGCCCGCGACUA*******UGCGGGCUUUUUUA
ESA_trpE      *********************AUGACUCACAUUUUUUCUCUGCAUGGCUGGUGGC*GUACCUCC**UGAUCCCGGGCGGUGUCUUCACGU*********************************GAGGCAUCGCGCAAGGCGCUGGAUG*****AACUGGGCGUUUGCU
PE36_trpE     ******************AUGCAAAAUAUUACAAACCAAACAAUCAGUUGGUGGUGGCACAUCCCUCUCUAAACGGGCAUGUGAUUUUGUGAUAUCUGCAGUAAAUGUAAAUCUACAAAAAAUAAUAAACAUUAAAGCCCGUUUCAUU****GAAACGGGCUUUUUUA
IL_trpE       *********************AUGUUUUUACGCACAACAACACAACAUUGGUGGUGGCACUUCCCAAACGAGCGGGUGGUGUAGUUGUGCGUGUAACGU*****************AAAUAGCUUCACUUUGAGAAACCCGCUCCUUU*****GAGCGGGUUUUUUAU
OS_trpE       ******************AUGCAACUCGCACAAUUUUCACUACAAGCUUGGUGGUGGCACUUCCCGAAUUAGCGGGUGGUGGUUCUGUGCGCAUACG*******************UAAAUAAGUACAGUUUCGAAAACCGCUCAAC******GAGCGGGUUUUUUUA
Patl_trpE     ************AUGAAUACAGUAUUACGCGUUUCAACUAACUUAAUUUGGUGGUGGCACAUCCCUAACUAGCGGGCUGUGAGCGUAUGUAUUUGUG***********************CGAUUGAACAAGAAAAGCCCGUAUAA********UACGGGCUUUUUUU
PSHAa_trpE    *********************AUGAACAAUUCUACUUUAAACACUAUUUGGUGGUGGCACUCGUAAUUUC**CGGGUGAUGAAUUGUCGUGUCUAAC****************************AAAUAUUCAAAACCCGCAACU*******GUGCGGGUUUUUUUA
PTD2_trpE#1   ***************AUGAAUACUUCAGUUCAAACACUAACAGUAAUUUGGUGGUGGCACUCGUAAAACGCGGGGGGAACUGUCAUGUCU**********************************AACAGUUUUUAAACCCGCCUUG********UGCGGGUUUUUUUA
PTD2_trpE#2   ******************AUGAAUAACUUAGUUAACAAACACAGCUCUUGGUGGUGGCGCCUGAUUUAACGGGACGGAAUACUUGUAACUA**********************************UAGUUUUUCAAGCCCGCACUUUUU***ACUGCGGGCUUUUUU*
MADE_trpE     ******AUGCAUCCUUACAACAUCUCAAAAGUAUUAACAGUUGCAGCUUGGUGGUGGCACUCCCUAACUUAACGGGCGGUGUGCACUGUAGUGCGUG**********************AAUGAAAACACAUAAAGGCCCGUUUA*********UACGGCCUUUUUUU
ATW7_trpE#1   *********************AUGAACAAUUCAAACCUAAACACAAUUUGGUGGUGGCACUCGUAAUUAUCGGGUGAUGAAUUGUCGUGUCUGACAA******************************AAUUUCAAAACCCGCAAAUA*******UGCGGGUUUUUUUA
ATW7_trpE#2   ******************AUGAAUAACGGUAUUACUCUUACACAUCAUUGGUGGUGGCGCCUGGUAUAGCGGGACGGUAAUGAUCUGUUUGUAAUUU**********************AGAUAUCGUUAUUCAAACCCCGCACUGCACAGCAUUGCGGGGUUUU***
EcE_trpE      ************************AUGAAAGCAAUUUUCGUACUGAAAGGUUGGUGGCGCACUUCCUGAAA*CGGGCAGUGUAUUCACCAUGCGUAA***********************AGCAAUCAGAUACCCAGCCCGCCUAAUG******AGCGGGCUUUUUU*
t_trpE        ************************AUGGCAGCGACAUUUGCAUUACACGGUUGGUGGCGCACUUCCUGAUAGCGGGCGGUGUAUGAACAGCUGUAAU**********************CAGCCAAACGAUACCCGGCCCGCCUGUUA******AGCGGGCUUUUUU*
STY_trpE      ************************AUGGCAGCGACAUUUGCAUUACACGGUUGGUGGCGCACUUCCUGAUAGCGGGCGGUGUAUGAACAGCUGUAAU**********************CAGCCAAACGAUACCCGGCCCGCCUGUUA******AGCGGGCUUUUUU*
STM_trpE      ************************AUGGCAGCGACAUUUGCAUUACACGGUUGGUGGCGCACUUCCUGAUAGCGGGCGGUGUAUGAACAGCUGUAAU**********************CAGCCAAACGAUACCCGGCCCGCCUGUUA******AGCGGGCUUUUUU*
KPN_trpE      ***************************AUGCACUUUAUCACUCUGCACAGCUGGUGGCGCACCUCCUGACGACGGGCGGCGUGAUCGCGUUUUGCA*********************UUCAGCAUACAGAUACCCGGCCCGCCAAU*******GAGCGGGCUUUUUA*
Ping_trpE     ******************AUGAUUUUAACAACAAUUUCUCUUAAUGAUUAUUGGUGGCACUCAUUCUCCUAAGCGAGCAAUGAGGUUUUUUUAUAUUCGU**********AUAUUUUCCAAAAAACUAAAUUUUAAGCUCGCAAUA********UGCGGGCUUUUUU*
PCNPT3_trpE   ******************AUGAUUUUUAAUACAAUUACUCUUACUCUUUAUUGGUGGCACUUAUUCUCCCUUCGCGAGCAAUGAGGUUUUUGUGUAU*************AAAAUUUUCCAAAACCAAAUUUAAAAGCUCGCAAAU********UGCGGGCUUUUUU*
Spro_trpE     ************************AUGAAUAAGCAAACUUCUCUUCUUCGUUGGUGGCGUCACUCCCUUUUUCGGGCGGAGUAAUCACGCAUACCUGUCAUCU**************GACACUGCAGAUUCCCUAAGCCCGCUGGU******AACGCGGGCUUUUUU*
ECA_trpE      ***************************************AUGAAGCAUGGUUGGUGGCGCUCUUCCCUCUCGCGGGUGGACUAAUCACGCAUCGCUGUUAUCA**************CACAUGCAGAUAUUCCCAGGCCCGCUUAAC*****UAAGCGGGCUUUUUA*
YPN_trpE      *********************AUGAAGACUUCCCUGAUUUCCUUACUGCGUUGGUGGCAUAUCUCCCUCUCUCGGGCGAUGUAAUCACGCAUAUCCGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGUUUUUUU*
YberA_trpE    *********************AUGAAAACCACUCUGAUCUCCCUACUGCGUUGGUGGCACAUCUCCCUCUCUCGGGCGGUGUAAUCGCGCAUACCAGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGUUUUUUU*
YE_trpE       *********************AUGAAAACUUCCCUAAUUUCCUUACUGCGUUGGUGGCACAUCUCCCUCUUCCGGGCGGUGUAAUCGCGCAUAUCAGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGUUUUUUU*
YintA_trpE    *********************AUGAAAACUUCCCUGAUUUCCUUACUGCGUUGGUGGCACAUCUCCCUCUCUCGGGCGGUGUAAUCACGCAUAUCAGUCACCA**************GACAAUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGCUUUUUU*
YfreA_trpE    *********************AUGAAAACUUCCCUGAUUUCCUUACUGCGUUGGUGGCACAUCUCCCUCACUCGGGCGAUGUAAUCACGCAUAUCAGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGUUUUUUU*
Ymol_trpE     *********************AUGAACACGAUUCUGAUCUCUCUACUGCGUUGGUGGCACAUCUCCCUCACUCGGGCGGUGUAAUCGCGCAUUCCAGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCGAA********UAGCGGGUUUUUUU*
YpsIP_trpE    *********************AUGAAAACUUCCCUGAUUUCCUUACUGCGUUGGUGGCAUAUCUCCCUCUCUCGGGCGAUGUAAUCACGCAUAUCCGUCAUCA**************GACAGUGCAGAUUGCUUCAGCCCGCUAA********UAGCGGGUUUUUUU*
plu_trpE      ************************************AUGACGUCUAUCCGUUGGUGGCAUAACUUCCAGUAAGGGCGGUAUGGUCACGCACAUAAAUCAACA******************GUGCCAAAUUACCAAAACCCGCCUAAU******CAGCGGGUUUUUUU*
SG_trpE       ******************************************AUGCUUCGCUGGUGGCGCCCCCCUU**UAGCGGGUGGUGAAAUCAUGCGUCGCUGUCAUCA************GACAGAGCACGAUCCCAAAUAGCCCGCUGCGU******UAGCGGGUUUUUUA*
VAS14_trpE    ***AUGUUACAGCAAAUUCAAAAUCAACAAUGCGUUUUCUUCAAUAAUUGGUGGUGGCACUCCUACUUACGGGCGGUGUGAAUAGCUGUAACUCAGCAA**************************AAUUGCAACGAGCCCGCCAUCA******AUGCGGGCUUUUUU*
VIBHAR_trpE   ******************************AUGAAUUCUGCAGAUCUUGCUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCAAACGUGUACUUCUAGUUU**************AGAGAAUUAAAUGUCACAAAGCCCGCUACCU******CAGCGGGCUUUUUG*
VSAK1_trpE    ******************************AUGGUUAAUUCUCUACAAGGUUGGUGGCGCACUUGGACACAAUCCGAGUGGGCUUUUUUGCGUGCAUAAUCAA****************AACCUAAUUUGAUUAAAGCCCACUCAAA*****CGAGUGGGCUUUUUU*
VF_trpE2      ******************AUGUCACAGCUUAACAGACAACAAGCAAUCUUAAAAACAUCAGUGGUAAGCUCACGAUGGUGGCACUACUUUGGGUAGUGUUUUG****UGCUAAUUUAUUUUUGACAUAAAUCCACUACCCGCAACUA*******AGCGGGUUUUUUU*
VC_trpE       AAAGCGAAACUUGCUCUGCAUAAUUUCAGUCCAGCGGAUGCUGAACUGGCUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCUCACGUGUAUUUCUAAGUUU****************AGAUACUCACACACCUAGCCCGCCAACU*****UGAGCGGGCUUUUUA*
VV_trpE       AAAGCGAAACUUGCUCUGCAUAACGAGAAUGUCAAUGCAGCAGAGCUCGCUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCUAACGUGUACUUUUAAUAA***************AGAAAAUGAAUCACACAAAGCCCGCUAACC******AUGCGGGCUUUUUA*
VP_trpE       AAAGCGAAAGUUGCUGUUUGCCUUAAUAAGACAAACUCAACAGAUCUUGCUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCUAACGUGUACUUCUAGUUU**************AGAAAAACAAACGUCAUAAAGCCCGCUACUC******AAGCGGGCUUUUUA*
VEx2w_trpE    AAAGCGAAAGUUGCGGUUUGUCUUAAUAAGGCAAACUCAUCAGAUCUUGCUUGGUGGCGCACUUGGACUAGUUCUUGGUGGGCGAACGUAUACUUCUAGUUU**************AUAGAACCAAACGUUGUAAAGCCCGCUACUU******AAGCGGGCUUUUUU*
V12G01_trpE   AAAGCGAAAGUUGCGGUUUGUCUUAAUAAGGCAAACUCAUCAGAUCUUGCUUGGUGGCGCACUUGGACUAGUUCUUGGUGGGCAAACGUAUACUUCUAGUUU**************AUAGAACCAAACGUUGUAAAGCCCGCUACUU******AAGCGGGCUUUUUU*
V12B01_trpE   AAAGAUAAAGUUUUAGAACUUUCUUCAAUAGAAGCAAGUUCAGAGCUUAAUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCUAACGUGUACUUCUAGUUA***AACAGUUUGUUUAUAAAAAAGUUAUCACUAAGCCCGCUUUAA******UAGCGGGCUUUUUA*
VSWAT3_trpE   AAAGAUAAAGUUUUAGAACUUUCUUCAGUAGAAGCAAGUUCAGAGCUUAAUUGGUGGCGCACUUGGACAAGUUCUUGGUGGGCUAACGUAUACUUCUAAUUA***AACAGUUUGUUUAUAAAAAAGUUAUCACUAAGCCCGCUUCCA******UAGCGGGCUUUUUA*
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Fig. 17. Classic attenuation regulation: a) gene *trpE* in Bacteroidetes; b) gene *trpE* in Thermotogae. Designations as in Figure 4. Alignment not shown.

a) *trpE:*

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BF        AUGCAAGUAAAUACAUAUUGGUGGUGGCGCCCGUUACAACUCCGACAGUCGUAAGGGAGCAGCGCUCGUAUGUAUAUACCUCAUUAAAGAUAUAACAGAA**********UUUAGAAAGAGCCCUGUCGCAA*CCUGCGACGGGGCUCUUUUUUUUAA
BVU    ******AUGGUAAAUACAUAUUGGUGGCGUUUCUUACAACUAAACAAGUCGUAAGGGAACCAGACCAUGUAUAUAUACCUGACAUUCUAAAAGGAUAUUC************AAACUGAAGGCCUGUCGUA**CUUACGACAGGCCUUUUUUCGUUAG
FP      *********AUGAACACAUUUUUAAACAAUACUUGGUGGUGGAAUAAUUUACGUCAAACGUCGUGAACUAAUCCUCUAUAUUGUAUUUUUAAAACU**********CAAAAUAUAAAAAAGGCUUGUCAAUCA***CGACAAGCCUUUUUUUUGUGCA
Fjoh    *********************AUGAACAAUACUUGGUGGUGGAACAAUUUACGUCAAACGUCGUGAACGAAGCUUCCUAUGGUAUUUU*************CAAAACUAUAAAUAUAAAAGGCUUGUCA*UCA***CGACAAGCCUUUUUUU******
FB2170  *********AUGAAAAACAGAACAAAUAAUACAUGGUGGUGGAGUAACUUACGAAAAACGUCGUGAGCAAAGCAUCAUUGUAGUAAA**********************ACUAUAUAAAAGGCUUGUCUAUCA***CGACAAGCCUUUUUUAAUUAUA
FBBAL38 *********AUGAUUUCAAUUUUAAACAAUACUUGGUGGUGGUCUAACUUACGUCGAACUUCGUGAGCGAAUCCUGCUAUAGUAUCA**********UUUAAAACCAAAUACAUAGAAAAGGCUUGUCAAUCA***CGACAAGCCUUUUUUUAUUGCC
GFO     ******************AUGAAAAAAAAAUAACUGGUGGUGGAAUAACUUACGUCAAACUUCGUGAGCUAAACUGCUAUUUUCAAUAUAGAA********************AUUAAAAAGGCUUGUUUCA*****CGACAAGCCUUUUUUUAUUGCA
RB2501  *********AUGAAAACAUUGAUUACAACAAACUGGUGGUGGGUAUCUGAUCGCGGAACGUCGUGACCUGAGCCCCCCUGUGUUUGUCCACCAUA********************CCUAAGGCUUGUCUGUCA***CGACAGGCCUUUUUUAAUUUUU
MED134  *********AUGAAAAACAAUACAGUACAUACUUGGUGGUGGAUUACACAACAAUCGUUGUCGUAAGCACGCACCUAUGUACCAUUCAUAUA*************************CAGCCUGUCUUUA*****CGACAGGCUUUUUUUUGUUCU
MED217  *********AUGAAAAACAAAACAGUAAAUACUUGGUGGUGGAUCUCGCAACAGUAAUGUCGUGAAACAACCUUGUAUUUAAAAUUUAAAUAAC*********************UGAAAGGCCUGUCUCA*****CGACAGGCCUUUUUUGUUUCGC
P700755 *********AUGCUUAAAACAAAUAACAAAUCUUGGUGGUGGUCUUUAUUACGUCAAACGUCGUGACUUAGAUCCUGCUAUGUAAAUAUAUCA***********************UAAAGGCUUGUCUAUCA***CGACAAGCCUUUUUUCAUUUAU
MED152  *********AUGAAAAACAGUAUAAACAUAUCUUGGUGGUGGAACUCUCUUAACUAAUAAGUGAGUUUAUACCUGUAUGUAAAAAUAUAU************************UAAAAAGGCUUAUCUCA*****CGAUAAGCCUUUUUCAAUUCAA
PI23P   *********AUGAAAAAUAAUACAAACAAAACUUGGUGGUGGAACUCUCUUAAUUCAUAAGUGAGAUGAAUCCUAUAUGUUUAUAA*********************CAUAAUAAAAAAAGGCUUAUCUCA*****CGAUAAGCCUUUUUUUUAUUAUU
CHU     ***AUGAAAACAAUUACAGGAACUAAACAAUUGUGGUGGUGCGUGAACUAAUCAGUUCGUGAACAUGCUGCUGUGUCCUGUUUGA******************AAAUAUAUCAAAAAAGAGGCUUGCUGU***UCACGGCAAGCCUCUUUUAUUUUAU
M23134  AUGAAUGAAAAAAGUUUACAUAUUACAAGAUGUUGGUGGUGGCACAAAAGAGAACUCUCUUCUGUGAAUAGCCCCGUUGUAUACGUGUAAAACUUUAUUACAUAAAGAUAUAAGCAAAAAGGCUUCCUGU***UCACAGGAAGCCUUUUUGCGUUUUG
ALPR1   *********AUGAAAACAUUCGCAAACAAAUAUUGGUGGUGGCAUUCUUAUUCUUUCCAAAAGGAAGUUUAGAAAGCCCCUGCAAUAAAAUUUGCG******UUACGAUAUAGUAUAAAAGGCUUACUGGAU*UUCCGGUAAGCCUUUUUUAUUGAAA
SCB49   *********AUGCAAACAACAAACAAUCUUACUUGGUGGUGGAAUAACUCUCGACAAAAAUCGUGAGCUAAGCACUAUUUGGUAUAUAUCAUA**********************CAAAAGGCUUGUCAUU***CACGACAAGCCUUUUUUUUUAUU*
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b) *trpE:*

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TM, Tpet
GUGGAGAGGAGUUCAUGGUGGUAUUUGAAACAGGUGAGCGAGACGCGGUGGUAAAAACGAUGGACAACAUUAUGGAGAACAUCAGAAACUUCGACUGGCAGAAGAUAUUCGGAAGUGAAAAGAAAGUAACUUUGAGUGGAGGGGUUGCGUUUUCAAAG
```

Fig. 18. Classic attenuation regulation of gene *trpS* in δ-proteobacteria. Designations as in Figure 4. Conserved antiterminator is lacking and functionally replaced by a set of hairpins (not shown). Alignment not shown.

Dace
AUGACAUUACAGCGA**UGGUGGUGG**CGCUCAGCCUUUAUGGAC***UGA***UCGCGUGCCUUUCGCUUUUUUGACAUCACAGACUGCGCCGGGCACGGCGCGGCAACAAUGAAAUCACACAAGCCGCGAUGAUCGUAUCGCGGCUUGUUUUGUUUUUGGACCUUUU
Dole
GUGCCCGGGCCUGGGCCACGGCCGGCUCCCCGGCCGCCA**UGGUGG**CCUCGCAACUCCUGCUGCUGCUCUGGUUUUCCGUGC***UGA***UCAACGCGGUGCUGGCCGUGUUCAACAUGAUUCCCCUUCCACCCCUGGACGGCAGCCG
Gura
*** **AUG**GUGGAUGGUGGA**UGGUGG**AUGGUGGAUGGUGGAUGG***UAG***UGACGUACCCUGCUUUGGACAACUACUGAAAAGGAGUCUCUAUUAA
Sfum
GUCGCAGGGACA**UGG**CGC**UGGUGG**CCGCCUCCGGACCGA***UGA***CGAAUCUGGUCCUGGCCGGCGCGAGUGCCGUUGUCUAUCGUCUUAUUGUCCUCGGGCU

Fig. 19. Classic attenuation regulation of gene *hisS* in: a) α-proteobacteria, b) Thermotogae. Designations as in Figure 4.

a) *hisS:*

CC *****AUG**ACCCGCACGCCG**CACCAUCAC**GGC**CACCACCACCAU**CCGACCUCGCCUCGCGGGAUCGGCCGGGUCCGCGCGCUC***UAA***AGCCGAGCGUACCCAGCCAGAGCCCCGCCUAGCGGAUGGGGCUUAAGUGCAAGCGCCAUCCGUCGAAGCCUAGAAGCCUU

Caul *****AUG**ACCCGCACGCCG**CACCAUCAC**GGC**CACCACCACCAU**CCGACCUCGCCUCGCGGGAUCGGCCGGGUCCGCGCGCUC***UAA***AGCCGAGCGUACCCAGCCAGAGCCCCGCCUAGCGGAUGGGGCUUAAGUGCAAGCGCCAUCCGUCGAAGCCUAGAAGCCUU

HNE ***********AUG**AACACCGCGCUG**CAU**CUC**CACCACCAUCAC**GCA***UGA***CGCGCCGAAGAGGCGCGAACCGGUCCGGCUGCGCCCUCUGACAAGUGUUCCUUC****************

b) *hisS:*

TM

*****************AUG**UUUUUCGGUGAA**CACCACCAUCAU**UGCUACGGCCCGGCGGUUUCUCCACCGGGUGUG***UGA***UGGUGGGAGAUCGC*********ACGGGCCACGUCGAGAAGACGUGGCCUUUUUGUUUAUCGAAUAAAACCGCAAAGAAGACACCAUUUU

Fig. 20. Classic attenuation regulation of gene *hisG* in γ-proteobacteria. The start and regulatory codons of the leader peptide gene are in bold, the stop codon is in bold italic, the alternative start codon – in green. The antiterminator (helix 1) does not fully overlap with the terminator (helix 4) and requires a co-antiterminator (helix 2). When the antiterminator cannot form at certain ribosome position on RNA strand, the co-terminator is formed (helix 3 cannot coexist with helix 2 but allows the formation of helix 4). The triplex is shown in pink. In *Alteromonadales bacterium* (ATW7) and *Pseudoalteromonas haloplanktis* (PSHA) the triplex is less stable and shown in red italic.

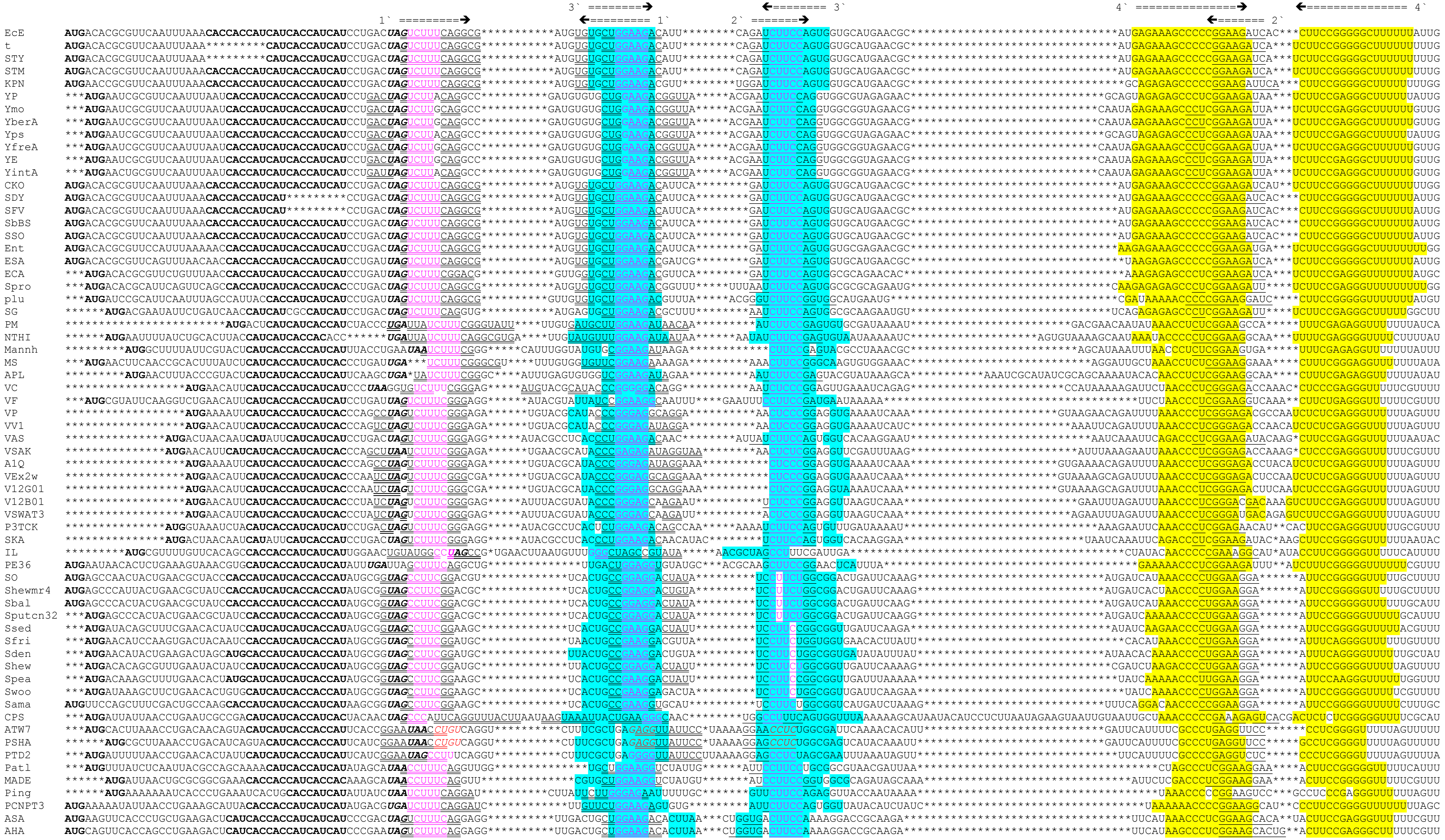

Fig. 21. Classic attenuation regulation of gene *hisZ* in Firmicutes. Designations as in Figure 20. *Listeria welshimeri* and *Listeria monocytogenes* (lwe, lmo) possess classic attenuation. Bacillales possess a weak Py-Pu-Py triplex. In *Clostridium difficile* (CD) from Clostridiales a weak Pu-Pu-Py triplex is shown in red italic.

```
                                                                3`================>                <================= 3`              4`=================>     <================= 4`
                                       1`================>        <================== 1`            2` ==============>                       <============= 2`
Bcer      AUGCUUACACAACUACAUCAUCAUACGUAAAGCCCUUGAACCUAACGUGAAA***ACGUGUAGGUGCAAGGGUUA************UUCCCGUUGUACCUACACGCUA*****************CGAAAGAGCCUUGUAGGUAUAUUUUAUCUACAAGGCUCUUUUUA
BT9727    AUGCUUACACAACUACAUCAUCAUACGUAAAGCCCUUGAACCUAGCGUGAAA***ACGUGUAGGUGCAAGGGUUA************UUCCCGUUGUACCUACACGCUA*****************CGAAAGAGCCUUGUAGGUAUAUUUUAUCUACAAGGCUCUUUUUA
BATI      AUGCUUACACAACUACAUCAUCAUACGUAAAGCCCUUGAACCUAACGUGAAA***ACGUGUAGGUGCAAGGGUUA************UUCCCGUUGUACCUACACGCUA*****************CGAAAGAGCCUUGUAGGUAUAUUUUAUCUACAAGGCUCUUUUUA
BcerKBAB4 AUGCUUACAAAACUACAUCAUCAUACAUGAAACCCUUGAACCUAACGUGAAA***ACGUGUAGGGACAAGGGUUA************UUCCCGUUGUACCUACACUCUA*****************CUAAAGAGCCUUGUAGGUAU**UUUGUCUACAAGGCUCUUUUUA
lwe       AAAAAUGUAAGGACAACACGCCAUCAUCAGUUUGUGGUCCAUACUCAUUUAAAAAAUCUCGCGUAAAAUCCUCAUAACCAAUCAAA*******************************UAAUCUACUUCCAAUCCAAUAUGUAUGAAUAAAUCGCUCGCAUAUUUUUUCUUU
lmo       AAAAAUGCAGCGACAACACACCAUCAUCCGUUUGUGGUCCAUACUCAUUCAAAAAAUCCCGCGUAAAAUCCUCAUAACCAAUCAAA*******************************UAAUCCACUUCAAACCCGAUAUGUAUUAAUAAAUCGCUCGCAUAUUUUUUCUUU
CD        ACAAAAUUAAAUCAUCACCAUCAUCAUAGAUUAAAGGGAUUGUAAUAUGAAAUUAAUUCAUAGACACAAGCCCUGUUUUUAGUGUAAUUGGUCUUGUAUCUAUGAUGGGAAGUAAUUUUAAGAGAAAAUUAUAGCCAUAUAGGUAUAAA**GCCUAUGUGGCUUUUUU**
```

Fig. 22. Classic attenuation regulation of gene *hisG* in Bacteroidetes. Designations as in Figure 4.

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PGN      ******AUGACU****18************CAUCAUCAUUUUUAUAAUUGCAAUCAGGCGAUUUAAAAAUGUAUUGAAUAAAAGCAAAAUA***UUUAUAAACCCGUUUGAGCAAA*UCAAACGGGUUUUUUCAAUUUUA
BF       ******AUGAACAUUACUAUUACACAUCGUCAUCAUCAUUACUCAAUCGAAUAACUCGGUGGCAAGAUGGUAUUGUGUAUAUAUAUGAUAGAA****UACGAGGCUUACCGAUA**AGGUGAGCCUUUUUUAUUUUCUA
BACCAC   ******AUGAAAUAUACAGCUACACAUCAUCAUCAUCAUUUUCCUAACGAAUAACUCGGUGGCAUAGAUGAUAUUGUGUAUACUCUAUAUAACGAUAACAAAGGCUUGCCGAAU*ACGGUAAGCCUUUUUUUUAUUCCC
BT       ******AUGAAAUAUACAGUUGCACAUCAUCAUCAUCAUUUUCCUAACGAAUAACUCGGUGGCGUGAUUGAUAGUGUGUAUAACUCUAUAAAGAU*AACGAAGGCUUACCGAAU*ACGGUAAGCCUUUUUUUAUUUCUG
BACOVA   ******AUGAAAUAUACAGCUACACAUCAUCAUCAUCAUUUUCCUAACGAAUAAUCGGUGGCGUGGAUGAUAUUGUGUAUAACUAUAUAAACGAUA*ACGAAGGCUUACCGAAU*GCGGUAAGCCUUUUUUGUUUUUCA
BACUNI   ******AUGAAGAAUAUCGUUGCACAUCAUCACCAUCAUCAUCCUAACGAAUAACUCGGUGGCGUAUGAGUGUAUAUGUACAACAGAUGACAUAACAGACGAGGCUUGCCGAAUAUUGGUAAGCCUCGUUUUGUUUUCU
BVU      *********AUGGUUAGAACUGCUACACAUCAUCAUCAUUUUCCUAACGAAUAAUUCGGUGGCUAAGGUGAUAUUGUAG**********UAUAAUGAUAUAGGGCUUGCCGAAA*ACGGUAAGCCCUUUUUAUUGCCGG
BDI      ***AUGAAAAUAACGACUACAUUAUAUCACCAUCAUCAUUACAGCGGGCAAUAGUUCGGUGGCUGAAUGGUAUGUAUGUACUC***AUGAUAAAAAGAUAAAGGCUUGCCGUUUUGCGGUAAGCCUUUUUUUGUUGAUA
PARMER   AUGAAAAGUACGGUUCUGCAUCUCCACCAUCAUCAUCAUUACAACGGGCAAUAGUUCGGUGGCUGUGUGGUAUGUAGGAACAUAUGAUAUA**AAUGAAUAAGGCUUGCCGUUU*ACGGUGGGCCUUAUUUUGUUUUUG
FBBAL38  ***AUGAAAGCACAAAACGUACAUCAUCAUCAUUUUUUCACUUACCGUCAGGCGAGCUAAAAAUGUAUUGAUG*****UAACUCAAACAUAUUUUAAAAACCGUCUGUU********UCAGGCGGUUUUUUUGUUUUAAA
FB2170   ******AUGAGAAACCAAAAUACACAUCAUCAUUUUUAUACUUGCUCUCAAGCGAGGUAGAAAUGUAUUGUAGU******AUUUACAACAUAUAGCUAACCCGUUUGAGAA*****AUCAAACGGGUUUUUUGAUUAAUA
FP       ***AUGUCUCUAAAUCAAUUACAUCAUCAUCAUUUUCAUAUUUGCUCUCAGGCGAAGUGUUAAUGGUAUGCGUG*****UAAAUCACAAUAUUCUAAAACCCGUUUGAGUA****CAUCAAACGGGUUUUUUAUUUUCUC
Fjoh     ***AUGAUUUCAAAUCAAUUACAUCAUCAUCAUUUACAUUAUUGCUCUCAAGCGAUGUGUUAAUGGUAUGUGUG*****UAAAUCAUCAUAUUUUAAAACCCGUUUGAGUA****CAUCAAACGGGUUUUUUUAUACCAA
P700755  ***AUGAAAAAUUACAACCUACAUCAUUAUUUAUCUAAUACGCUCAACGCGGUUGGAAUGUAAUAUGUAGAUAG*********UUAAUCAUAUACAAAACCCGUUUGAGCACUAUGCUCUAACGGGUUUUUUAAUUUAAA
GFO      ***AUGAGAAAAUAUACUGUACAUCAUCAUCAUUUUUCUAUCCACGCUCAGGCGAGGUGAAUAUGAUAUGUUGU***AACAUUAACUAAAAUAUCAUAACCCGUUUGAGCA*****AUCAAACGGGUUUUUUUAUUUCUA
MED217   ***AUGAGAAGAACAGUAUUACAUCAUCAUCAUUUUUAUUCACGCACUCAAGCGAGGUAAAGAUGUUGUAUAUGUAAUUUAUAUAUAAAAUAACAAUAACCCGUUUGAGCC****GUUCAAACGGGUUUUCUGUUUAGAA
MED134   ***AUGAAAUUGAACAAAACACAUCAUCACCAUACUACAUUAUUCGCUCAAGCGAGGUAGUUUGGUAUGUAAAU***********AAUUCAUAUAUAAACCCGUUUGAGAU****ACUCAAACGGGUUUUUUCUUUUUUG
RB2501   ******AUGAAGAAGAACACCACACAUCAUCAUAUCGGCUCCUGCGCUCAGGCGAGGUAGCGGUAUAUGUUGUGUUG*****CAGACCACAUAAUCGGACCCGUUUGAGCA*****AUCAAGCGGGUUUUUUUAUUUACA
CA2559   ******AUGAGAAACACACAUACACAUCACCAUUUUUCUAGCAACGCUCAAGCGAUGUAGAUUUGGUAUGUGAAAAA********CUAUAAAUCUAAAACCCGUUUGAGAC****AUUCAAACGGGUUUUUUGAUUUUAU
PI23P    AUGACUUUUAUUCAAGCACAUCAUCAUCAUCAUUUUUACAAUUGCAUUCAAGCGAUUUAAAAAUGUAUUGAAUAAAA******UCAACAUAUUUAUAAACCCGUUUGAGCAA****AUCAAACGGGUUUUUUUAAUUUUA
M23134   UUAGCCACCGCUAACAUCCAUCACCACCCCCAUCAUUUGGCGCAUCAUCAUUGCCAUUAAUUC-70np-UUCAUACAGUUUAGAAUAGAGUCAGGCGCUUUGUACUGCUUCGUAUGCUAAACACACGCCUAUUUUUUGAU
SCB49    AUGAAUACACAAAUACAUCAUCAUCGCUUUAACUCUGGACUACAGUCGAGCAAGAAGUGAUAUGUGUAU***********AAAACAAUAUAUUAUGAAACCCGUCUGAGUAA*****UUAGACGGGUUUUCUGUUUUUAA
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Рис. 23. Classic attenuation regulation of gene *lysQ* in Firmicutes. Designations as in Figure 20. It is a permease-coding gene. In *Lactococcus lactis*, unlike in other firmicutes, it has histidine-dependent regulation, which suggests a change in the enzyme specificity. A weak Pu-Pu-Py triplex is shown in red italic.

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                                                      3` =============→          ←=============== 3`    4` =============→     ←============ 4`
LACR                                1` ============→      ←============== 1`               2` =====→            ←===== 2`
AUGAAUUGCUCAUUGCGCCAUCAUCAUUUGCAUAGAUAAGAGUUGUGUCAUACAGUAGGUAUAGAUACAGCUUUAGAGUACGCUCAAGUAUCUAUGCCGGUGAUUCUCAAGAGACCGGUUGUAAAGACAACUGGUCUUUUUAUUUGUUCGUGCUC
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Fig. 24. Classic attenuation regulation of genes *ilvB* and *ilvI* in actinobacteria. Designations as in Figure 4. The gene is annotated as *ilvI* in *Frankia alni* (FRAAL). In *Rhodococcus jostii* (RHA1) only two (*ilvB4* и *ilvB5*) out of six paralogs have the shown regulations.

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DIP       ************AUGAACAUUAUUCGA***CUUGUAGUGAUUACCACUCGGCGCUUGCCGUAGCGGCUACAAGUCGUUUCCGA*******************************AAAGCGCCCUCGACAGCA****CCACACAUGCUGAGCGGGGGCUUUCCUUAU
CE        ************AUGACCUCAAUUCGACCUGUAGUAAUCGUAGCUGCGCGGCGUUUGCCGUAACGGUUUUCUACAAGUCGUCUCGU****************************CAAGCGCCCUCGACAGUACCCACCACAGUGCUGUUUCGAGGGCUUUGUUGUU
cgR       ************AUGACCAUUAUUCGA***CUUGUAGUAGUAACCGCGCGGCGCCUGCCGUAACGGCCUUCCAAGUCGUCUCGUC******************************AAGCGCCCUCGACAACACUCACCACAGUGUUGGAACGAGGGCUUUCUUGUU
jk        *********AUGGAAUUUACGCAACUAGUACGAGUACUCAUUAUCGAGGGGCGCCACUAGCUACCUCGUUGAGCUCGACACG**********************************GCGCCCCCAGCAACCGACGCAACAGCGUCGGUAAGUUGGGGGCUUUUGUUG
SAV       ********************AUGCGCACCCGAAUUCUCGUACUUGGAAAGCGCGUCGGCUGAGCUGGUGAAGUACCGGACGACCCGGAACACCCAGCGACCGCAC***CCGGCGCGCUCCCCUCGCUUGCC**********UCACGGCACGAGGGGUUUUUUGUU
SCO       ********************AUGCGCACCCGAAUUCUCGUACUUGGAAAGCGCGUCGGCUGAAGCUGGUGACGUCCGGACCGACCCGGACUCCCCGCGACCCACA***CCGACGCGCUCCCCUCGCUUGCC**********UUACGGCACGAGGGGUUUUUUGUU
SCA       ********************AUGCGCACCCGAAUCCUCGUACUUGGAAAGCGCGUCGGCUGAAGCUGGGACCCACCGGACGACGAUCCGGAAUCCCCGGCGACCGUACCCGACGCGCUCCCCUCGCUUGCCC*********UGUGGCAAGGAGGGGUUUUUUGUU
Mma       ******AUGGAUACCGCCGGAACCCCCGGAAAGCUUGUAGUACUUGGUCGGCGCGUUGUUGCCUGACUAGGUCAAUCGA***************************GCACCAACGCGCAACCCUCGUGCAGCAGC*******UGAGCUGACG*GGGGUUUUUUGUU
micro     *****************************AUGCUCGUAGUAAUUGGUCGGCGCGUUGGUGCCUGACUAGCCCAAGCGA*****************************GCACCAACGCGACCCUCGUGCAGCAGC*******UGAGCUGGCGA*GGGUUUUUUCUU
Mflv      ********************AUGCAGACCCUGCUCGUAGUAAUUGGCUCGCGCGUUGAUGCCGCGCUGGCCCUGAUUCGGGCAUAGCA*************CAACCGCAUCAACGCGCACCCUCGUACAGCCGC*******CGGGCUGACG*GGGGUUUUUUGUU
MAV       ******AUGGAUACCGCCGGAAAGCCCGGGAUGCUCGUAGUAAUU***AGGCGCGUUGGUGCCUGAGUUGCCCGUCAGCA*************UGUGAAGCAAUCCAGCACAACGCGCAACCCUCGUGCAGCACA*********AGCUGUCG*GGGGUUUUUUGUU
BCG       ******AUGGACAAGGCCGGAAAGCCCGGGAUGCUCGUAGUAAUUGGUCGGCGCGUUGGUGCCUGACUAGCCCAAGCGA*****************************GCACCAACGCGACCCUCGUGCAGCAGC*******UGAGCUGGCGA*GGGUUUUUUCUU
ML        ******AUGGAUAACGCCGGCCAGCCCGGAAUGUUGGUAGUAAUUUGUCAGCGCGUUGGUGGUUGAGUAGCACUUCAGUA************UUUGAAGCGAUCCAAAGCCAACGCGCAACCCUCGUGCAGCUAG*******UCAGCUGUCGA*GGGUUUUUUGUU
MtubH     ******AUGGACAAGGCCGGAAAGCCCGGGAUGCUCGUAGUAAUUGGUCGGCGCGUUGGUGCCUGACUAGCCCAAGCGA*****************************GCACCAACGCGACCCUCGUGCAGCAGC*******UGAGCUGGCGA*GGGUUUUUUCUU
MUL       ******AUGGAUACCGCCAGAACCCCCGGAAAGCUUGUAGUACUUGGUCGGCGCGUUGUUGCCUGACUAGGUCAAUCGA***************************GCACCAACGCGCAACCCUCGUGCAGCAGC*******UGAGCUGACG*GGGGUUUUUUGUU
Mvan      ********************AUGCAGACCUUGCUCGUAGUAAUUGGGUUGCGCGUUGAUGCCGCGCUAGCCCUGGUUCGGGCAUAGCAAAA************CCGCAUCGACGCGCAACCCUCGUACAGCCGC*******CGGGCUGACG*GGGGUUUUUUGUU
Mgil      ********************AUGCAGACCCUGCUCGUAGUAAUUGGCUCGCGCGUUGAUGCCGCGCUGGCCCUGAUUCGGGCAUAGCACAA*************CCGCAUCAACGCGCACCCUCGUACAGCCGC*******CGGGCUGACG*GGGGUUUUUUGUU
MSMEG     ***************AUGCAGACCCCGGGAGUGCUCGUAGUAAUUGGUUGGCGCGUUGAUGCCGCGCUGGCCCUCUGCCGGGCAUAGCAAAC************CAGCAUCGACGCGCCACCCUCGUACAGCAGC*********CUGCUGACG*GGGGUUUUUUGUU
Mkms      AUGCUCGACGGAGGCGCUUCGGCGCCGACAUCGCUCGUAGUAAUUGGUUGGCGCGUAGAUGCCGCGCUGGCCCUCUGCCGGUGCCGGGCAUAG*******CCACCAGCAUCGACGCGCCACCCUCGAACAGCGGC*********CCGCUGUCGGGGGUUUUUUCUU
Noca      ********************AUGCGCAACGGCAUUCUUGUACGCACGCGACGUGUGAGCUGAGUCGACACGACCGCAGCG****************************CACACGUCACCCCUCGCCGCCCACC**********CGGGCCGAGGGGUUUUUUGUU
nfa       ******************GUGAAUCGAAACGAGUUGCUCGUAAUCGGCCGGCGCGUCCAGCGUUGAGCCUGACUGCCUAGG******UCGAAUACGUCAGCUCGCGUUUGCGACGCGCCACCCUCGAACAGCCAC********GCGCUGUCGAGGGCUUUUUUGUU
Req       ******************GUGAAGCAGAAUGAGUUGCUCGUAAUCGGCCGGCGCGUCGUCGCCUGAGCCGGUUGUUGCAACU******************CGCCAGAUAACGACGCGCCACCCUCGUACAGCU*********GAUGCUGACGA*GGGUUUUUUGUU
Strop     ******************AUGCUUGUCGCCAUGUCGUCGUACCGGUCGCUGCGAGUACUUACCUGAGCGCACUCUCCCACU*************************GAGAGUGCGCUGGCCCCGUGCA**************UCCCGCACGCGGGCUUUUUUGUU
FRAAL     ***************AUGUCUGUGCACAGUCAGAUUCUCGUACGUUCAGAGCGCGCGUAGUCGACGAUC**************************************UCGACCCCGUGCGCCGCCCCUCAGUGCC************CUAGGCACGAGGGGCUUUUUCGU
Franean1  ******AUGCUGCUCGGCAUUCUCGUACGUACGAUUCUCGUAGGCUCGGAGCGCGUGUAGUCGGACCAG**************************AUCGGUCUCCGACCACCCGCGCCGCCCCUCAGUGCC************CAUGGCACGAGGGGUUUUUUCGU
Francci3  ********************GUGCAUCUCGGGAUUCUCGUACGCUCAGAGCGUGCAUAGUCGACGACG**********************************UCGACCUGUGCGCCGCCCCUCAGUGCC*************UCGGCACGAGGGGCUUUUUCGU
Acel      ************GUGCGUUUUAUCGCGCUCGUACUCCGUGGGCGCGCUGGCUGACCGACGGUCAC*********************************************CUGGCGCGCAACCCCUCCGUGCUGC*************GGCACGAGGGGUUUUUUGUU
Krad      ***************AUGCGGUUCCUCGUAGCCAUCGGACAGCGCGCCGGCUGACCAGUUCGGCCG*********************************************AGCGCGCGACCCCUCACACGCCAUC*********CCUGGCUGAGGGGUCUUUUUGC
Aaur      ******AUGAUCACAUUCGUUACCGUCGGCGUCGUCGUCCUUACCAAGCGCGUGGCUUAGCCC*****************************GACUGGUAACGAACCGUCACGCGCAAACCCCUCGAAGAGCCGG**********AAGGCUGAGGGGUUUUUUUAU
Arth      AUGAUCGCAUUCGUUACCAACUGCGCCGCUGCAGAUGCAGUCGUCGUCCUUACCAAGCGCGUGGCUCAAUAGCC*****************CGACUGGUAACGAACCGUCAUGCGCAACCCCUCGAAGAGCCGC**********CAGGCUGAGGGGUUUUUCUAU
Tfu       ***************GUGCAGAGCAACUUUCUGAUUCUCGUACUUGGUCAGCGCGCAGCCCGCUGACCGAGUCGAC***********************************GCUGCGCGCUCCCCUCAACCGCUAC*************GCGGUGGGGGUUUUUUUGU
RTFU      ***************GUGCAGAGCAACUUUCUGAUUCUCGUACUUGGUCAGCGCGCAGCCCGCUGACCGAGUCGAC***********************************GCUGCGCGCUCCCCUCAACCGCUAC*************GCGGUGGGGGUUUUUUUGU
TW        ***************************GUGGCAGGGAUUGUUUUAUAACAAACGCUAUUCUCA*GACCGACCUGAAUA*********************CCGGUGAUGCGUAUAUACCUGAUUUUUGUAAACUUGCCGAAUCGUAUUCAUGCGCAAGUUGCAGGGU
JNB       ******************GUGACCCGCUUCCUCGUACUUCUCUCGGCGCCCGGCCCCUCCUGACAGGUCC**************************************GGCCAGGCGCCUCCCUCCAUCGUCCCC**CAGUACGUGGGACGGAGGGUUUUUUUGU
SACE      ************AUGCAGCGACUGAUCGACCUUCUCGUAAUUUCCUGGCGCGUCGACGCCUAGGAAGUUCGUA******************************CCGUCGACGCGCCAACCCUCGUAAGACCA*****GCGUCUGGUCUGCGGGGUUUUUUCGU
Blin      ***************AUGACUCACCUUCUUGUCGUCGUUAUUACCCAGCGCGCGGAUCUUCCGUAGCCUGUCAACACGACA****************************UGUUCCGCGCGCCCCUACCGA******************AACCGGAGGGGCUUUUUUCA
BAD       ******AUGCCCGAGCUGCGGUUCCUUCCGCGGCCGCGUGUACCGCGAGGCUGUCCGCUCCAUCCACACCAAGUGAGUGGUUGCCGGAUAACGGUAUAA**********AGCAUCGAAACCCUGCCAUCGACG*************GGUGGCAGGGUUUCUUUUA
RHA1_5    ******************GUGAAACAGAAUGAGUUGCUCGUAAUCGGCCGGCGCGUCGUCGCCUGAGUCGAUUCCUUCAACU******************CGCCAGAUAACGACGCGCCACCCUCGUACAGCA*********UCAGCUGACG*GGGGUUUUUUGUU
RHA1_4    ******************************AUGAAGCUCGUCAUUUCCCGGAACCUGGACUGAUC*****************CCCGCGGGUGCGGGGCGGAGAGACGCCUUCGCCCCGCACCCGUCCGGGUACCCGCGCACCAUCCGCACACGAACACGCACAGCC
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Fig. 25. Classic attenuation regulation of genes *ilvB* and *ilvI* in α-proteobacteria. Designations as in Figure 4.

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RD1_ilvB        ***************************AUGACCGAACUAGUCGUCAUUGUGAGAAACACGCGCAUGGGCCGGUAACGGUAGACCAUAGUCUG**ACCCAUGCGCCCCCGCC********AAGACCGGGGGCUUUUUUGUGCGCAAAAGAUAACGGGC
RSK20926_ilvB   ***************************AUGAAAGCCCUAGUCGUAAUCGUAGGAACCAAGCGCAUGGGCCGGUAACGGUAGACCACAAUCGA**ACCCAUGCGCCUCCCCUG******ACAAAGCGGAGGCUUUUUUUAUGCGUAACAGACGAUGUC
RTM1035_ilvB    ***************************AUGGACACACUCGUAUUCAUCGUAGGUAAGUGGCGCAUGGGCCGGUAACGGACACCCUUCGGGUC**CCCCAUGCGCCCCCGG*********AAAACCGGGGGCUUUUUUAUGCGACUUGAAUUGACGUC
NAS141_ilvB     ************AUGACAGAUCUAGCUUUGACAGAUAUCGUCGUCAUUCUAAGACACACGCGCAUGGGCCGGUAACGGCAGACCAUAAUAGU**CACCAUGCGCCCCCGUC*******AAAAUCGGGGGCUUUUUUUGCGCAACGUAUUUUUUGAU
TM1040_ilvB     ***************************AUGGCUCGGCUAGUCGUAAUUGUAGGACACACGCGCAUGGGCCGGUAACGGUAGACCAUAAUCGA**ACCCAUGCGCCUCCGAUCC****UCAAAAUCGGGGGCUUUUUUAUGCGAUACACACUGACGUU
OG2516_ilvB     ***************************AUGGCCGACGUACUCGUACUUAUCAGGGAUUGGCGCAUGGGCCGGUAACGGUUGACCAUAUCUGGUACCCCAUGCGCCUCCGAG*******AAAGUUCGGGGGCUUUUUUGUGCGUGAAACGACGGACGU
OB2597_ilvB     ***************************AUGACCUCGCUAGUGAUCGUAGUAGGAGCUUGGCGCAUGGGCCGGUAACACCGGAACCCCAAGAGGACCCCAUGCGCCCCCGG******AAAACUCCCGGGGGCUUUUUUGUUGGUACGGUACGGCGAUU
SKA53_ilvB      ***************************AUGAUUGUCGUCGUACUAAUCGUGGAUCACAUGCGCAUGGGCCGGUAACGGAUUUUCCAUAAUGA**CCCCAUGCGCCCCCGAC********AAAAUCGGGGGUUUUUUUAUGCCGGAUGCAACGAAACG
SSE37_ilvB      ***************************AUGAUCACUCUAGUAGUCAUCGUAGGAGAAAGGCGCAUGGGCCGCUAACGCGGACACCCUACCAGGUCCCCAUGCGCCCCCGUC******AGCCGAACGGGGGCUUUUUUUUGCCCGCUGCCCACGUGGC
Dshi_ilvB       ***************************AUGCCCCGUAUUGUCGUACUCGUAGAAAACAGGCGCAUGGGCCGGUAACGGACACCCUUCCGAU**CCCCCGUGCGCCCCCG*******AAAACGACCGGGGGUUUUUUUAUGCCCAACCGCAACGACCC
Jann_ilvB       ***************************AUGUCCGACAUUCUCGUACUUGUAGGACAAAGGCGCAUGGGUCGGUAACGGCAUCCAUAAUUGGA***ACCAUGCGCCCCCGGA******UAACCUCCGGGGGCUUUUUUUUGCAUUAUAUAUUCGCACA
Rsph17025_ilvB  ***************************AUGCCUGGUGUCGUACUUCUUGUAGGAAAGCUGCGCAUGGGCCGGUGACGGUUGACCAUAAUCGG*UUCCCAUGCGCCCCCG*******AGUGAAACCGGGGGCUUUUUGUUGCGCGGAUCGCGCGGCCC
RB2654_ilvB1    ***************************GUGGAAAGCCUUGUAGUCAUCGUAGGAUAUAGGCGCAUGGGACGGUAACGGACCCCUGAA***GGUUCCCAUGCGCCCCCGAC******AGAAAAUCGGGGGCUUUUUUAUGACCGGAGAUACGGGCGC
RB2654_ilvB2    ***************************AUGAACGACAUCCUCGUCCUAGUCAGAACCAAGCGCAUGGUCCGGUAACGGAAAUCCAUAA**UGGAAACCAUGCGCCCCCGAC**********AAUCGGGGGUUUUUUUAUGUUUAAAGACGUCAAGUG

FP2506_ilvB     *********************AUGACGAACACGACCAUUCUCGUAAUCGUACGAAGGCGCACACGACCGGCAGCGUAGCUGCCAGGCGAAUGCCACGUGUGCGC*GAAGACAGGGGCCCUCCAGAGGCCCUUUUUUUAUGCUUGCACUUGGUCGGAA
BAB1_ilvB       ************************AUGAACACGAUCAUUAUUCUUGUAGUACGGGCGCGCAUGGGCAGGGUGGUGUAACCACCCGGCGAAAGCU*CCCAUGCGCGAAAGACAGGCUCCCUC***GGGGGCCUUUUUUAUUAUCCAAAUCAGAAAUGA
Oant_ilvB       ************************AUGAACACGAUUAUUAUUCUUGUGGUACGGGCGCGCAUGGGCAGGAUGGUGUAACCAUCCGGCGAAAG*CUCCCAUGCGCGAAAGACAGGCUCCC***UCGGGGGCCUUUUUUAUUAUCCAAAUCAGAAAUGA
SI859A1_ilvB    ************************AUGACAAAGAUCAACAUUCUCGUAGUAGGACGGCGCACACGCGAGGCGGUCUAGGGACCGCCCGGCGAGA*GCCACGUGUGCGCAACUCAAAGGGCCCCAGCGGCCCUUUUUUAUUGCGCCGAGUUCCGACAC
SIAM614_ilvB    ***************************AUGUCGCUCAUUCUAGUAGUAGUAGGAAAGCGCGCCUCCGCGGCGGGAUGAACCCCGUACGGA****CAGGAUGGCGCGCGACCAAGGCUCCC**AAAGGGGCCUUUUUUUGUACCCGCCUCCUGACUUC
Atu_ilvI        *********************AUGAAAAAUCUUAACGUACUUAUCGUGGUGGGACGGCGCAUGGGCAGGAUGGUAUAACCAUCCGGCGAAAG*CACCCAUGCGCUGAAC**GAGGCUCCUC**UAGGGGCCUUUUUUUAUGUCUUCAAACAGGCCCU
SMc_ilvI        *********************AUGAAAAAUUUCGCGGUUAUUCUUGUGGUGGGACGGCGCAUGGGCAGGGUGGUGUAACCAUCCGGCGGUAGCCACCCAUGCGCUGAAC**GAGGCUCCUG**ACGGGGCCUUUUUUUAUGCCUUCAAACACGUUAU
RHE_ilvI        *********************AUGAAAAUCGCAACGGCUCUUAUCGUGGUGGGAAAGCGCAUGGGCAGGAUGGUGUAACCAUCCGGCGACAGCCACCCAUGCGCUAGAUGACAGGCUCCU***CCGGGGCCUUUUUUUGUGCCCGAAUUUCGGGCUU
ml_ilvI         ***************************AUGAAAAAGGCACUUAUCCUGGUGGGAAGGCGCGUGGGCAAGGCGGUGUAACCGCCGGGCGAAAACCUCCCAUGCGCAACACAU*AGGCUCCC**UCGGGGGCCUUUUUUAUU*****************
BRAD_ilvI       ************AUGCGCAAUUUUAUUGCCAUUCUCCUUAUCGUAGUCGUACCCAGGCGCAUCGCCGGGGAUGGCUAGCGGCCAUCCAAAAU***CCGAGCGGUGCGC**AGGGCCUUCC****AGGGCCCUUUUUUAUUGCCCGAACCGACCCCGA
blr_ilvI        ************AUGCGUAACAUUAUUACCAAACUCCUUAUCGCCGUCGUACCCAGGCACACCGCCGGGGAUGGCUAGCUGCCAUCCACAUG***ACAGGCGGUGUGCAUGGGCCCUCUU****CGGGGCCUUUUUUAUUUCCCGAACCCGACACGA
Xaut_ilvB       ************************AUGCGCAAGAUCGUUAUUCUUCUCGUAGGGUGGCGCGCCACUUUUUGUCCAGCCUGAGGGCUGCGGCAG**ACGAGGUGGCGCGUGACGAGGGGCC*UUCGGGCCCCUUCGUCGUUUCUGAAGGGCCUCGGCC
Mext_ilvB       ***************************AUGCGCACGGUUCUUAUCGUAGUGGAAGCGCCACAGACGGGGCGGGCUUGAUCUCAAGCCUGACAGGCCCGGUCGGUGGCGCAUGCAGGGUCCCUC*GGGGCCCUUUUUUAUUGCGCGAAAUCCAGCGGG
M446_ilvB       ***************************AUGCGCGCGGGUCUUAUUGUAGGGUGGGCGCCACGGACGGGGCGGGCUUGAGAGACAGCCCGUGAGCCCGCCGGUGGCGCAUG*CAGGGUCCUUC**GGGGCCCUUUUUUAUUGCCCGAACCGGCCGCUG
AZC_ilvB        ************************AUGCGCAACUUCAUUAUCCUUCUUGUACGUGAGCGCGCCAUCGUCGCGGCGGCCUGACGGGCCGUCCGGG*GACAGGUGGCGCGCGAUCAGGGGCC*UUCGGGCCCCUUCGUUGUUUCUGGAGCUCGGCUCCG
CC_ilvI         ***************************************AUGAUCGUACUUAUGGAGCGGCCGUUCGCGGGGUGACCUCGAAGUCACG**UCGUAGCUCGGUCGCGCGCGCAAAGGUCCU***UCGGGACCUUUUUUCUUUUCCAGCCCCCUCUUCC
Magn_ilvB       ************************AUGCGCACGGUUCUUAUCGUAGUGGAAGCGCCACGGACGGGGCGGGCUUGAGGACAAGCCCGGCA*GGCCCGGUCGGUGGCGCAU*GCAGGGUCCC**UCGGGGCCCUUUUUUAUUGCGCAAAAUCCAACGGG
RPE_ilvB        ************AUGCGCAAUUUUGUUACCCAACUGCUUAUCAUCGUACCCAGGCGCACCGCCUUGGGUGGCUGACGCCAUCCAUGA**********CAGGCGGUGUGACGGGGCCUG*****ACCGGCCCUUUUUUAUUGCCCGAACGACAUACGC
NB311A_ilvB     ******AUGCGCAAUUUUGUUAUCAAGAACCUUGUUCUGAUCCUCGUAACUCGGAACACCGCCCAGGAUGGCUAAGCCGUCCGAAGGGA********AAGGCGGUGUGCCGGGGCCC*****UUCAGGCCCUUUUUUAUUGUUUGCGACGCUGGCGG
Nwi_ilvB        ***AUGCGUAAUUUUGUUACCAGAGAUCUUGUUCCGGUGGUCGUCGUUUCCGGGAGUGCUGUCUGGCGCGGUUGAGCUGUCCCAAU********CAAGGGGCGGUGCGCCGGGCCCU*****CCAAGGGCCUUUUUUCUUAUCCGUGACGGUGGCAA
Nham_ilvB       ******AUGAGCAACUUUGUUACCAAGAUCGUCCUUGUUAUCGUCGUACCCCGGAGCACCGCCCGGGGCGGCUGAGGCCGUCCCAAU********CCAAGGCGGUGUGCCGGGGCCC***UUCAGAGGCCCUUUUUUAUUUCUGCGAUGCAGCGAUC
SAR11_ilvB      ************AUGGAUGUGUUGGUAUUAGAGCAAAAGAUCCAAGUGAAUUGGAUGAAAAAAUUGAAGAAAUGAUUAACACAGAUAGACCUGUUAUUUUUGACUGUCUUGUAGAUCAAGGAGAGAAUUGUUUUCCAAUGAUCCCAUCUGGAAAACC
HNE_ilvB        AUGCCUGAACUCCCAAGAUUGAGGAAACGCCAAGUGCGCGCAUAUAAAGUAGUAAUUCUUAAGUGCCCGUAGCUGCCCUUCGACCA*GGCAGUUGCGGGUGCGCGCACAAAAGGGCUUCCUCCGGGAGCCCUUUUUUCUUGGUCCCUUUGCUCUUUU
```

Fig. 26. Classic attenuation regulation of gene *ilvB* in*:* a-b) β-proteobacteria, c) δ-proteobacteria. Designations in b) and c) as in Figure 4. In yellow is the sequester, in green – the predicted *ilvB* initiation codon. For δ-proteobacteria alignment is not shown.

a)

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BP    GUGCUCAAGGCCGCCAUCGAGUACGGCGGCCCGGCGCUGGUCGACAUCAUCGUCCAGCCGCUGCAGGAAGCGGCGGCCCCGGUCAGCCAGUGGAUGGGCUGAGGCCCGCUUCCUCGAACACGACACGGGCGGGCACAUGACCAGAACAGAACCGGACCAACCGAUGGGCGCGGCUCCGG
BB    GUGCUCAAGGCCGCCAUCGAGUACGGCGGCCCGGCGCUGGUCGACAUCAUCGUCCAGCCGCUGCAGGAAGCGGCGGCCCCGGUCAGCCAGUGGAUGGGCUGAGGCCCGCUUCCUCGAACACGACACGGGCGGGCACAUGACCAGAACAGAACCGGACCAACCGAUGGGCGCGGCUCCGG
BPP   GUGCUCAAGGCCGCCAUCGAGUACGGCGGCCCGGCGCUGGUCGACAUCAUCGUCCAGCCGCUGCAGGAAGCGGCGGCCCCGGUCAGCCAGUGGAUGGGCUGAGGCCCGCUUCCUCGAACACGACACGGGCGGGCACAUGACCAGAACAGAACCGGACCAACCGAUGGGCGCGGCUCCGG
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b)

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Bpro ***************************AUGUUCGAAAACAGUGCGUUUCGAGUCUUGCGACGGCGAAACCAGUCCAGGGUGGUGUUGGACAAGAUGCGCUGAAACAGCAUGGGGAGUUCGGCGGCAGGCUUGUCGCCAUAGUGCUGCGCCAGCUUCAUCAUGCUGUCCUGAACAAUAUC
azo  ************************AUGUUCCGUUCCGCUUCCCUUCCUGUCGUAGCCCUGUCCGUACGCGUAGUAGUAGGCGUAGGCGGUCGCGCGUCGUAGCGGAUAAGGGCACAGGCAAACCACAGCAUUCCCCAACCCCCGCCGGCGCGAAAUGCCGGCGGGGGUUUUUGUUUUUC
Daro AUGAACGCUCCCCGUACCGCCCACCGCUCCAACACUGCCCGCGCAGUGCUGCCGGUCGUCGUACGUGUAGUCGUCGUAAGCGUCGUUACGGACACGCCGUCGCGGAUCGGGUAAGCAGAAGCAGCACAGAACCCC*AACCCCCGCCGGCGC*AAACCGGCGGGGGUUUUGUUUUGGC**
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c)

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STIAU GUGCAGGCCCUCGUCCUCGUAGUAGGCGGAGAGCUCCUUCUUGCGCGCCUUCUUGCGCAUGGGGGCGGCCGCCGUUCUGAGUCGGGAGAAAUCCUCCCCAGGCCGGAACGAAUCAGCCCCGCCCCCGGAAACGGUGGCGGGGUUUUCGUUUUUCGGCUCCCAAAAACCCGUGAUUCG
DP    AUGGCUUAUACUUCUGUAAUUGUAUACUUUUCAUGCUUUCUCCUUUUGGCAAUCCCGUAACAAAAAAAAAGGCCCCGGUUUUUCAACCGCGGCCUUUAGAUCAACUUAUAUAGUAGACAAACAAAACUAAUAAAUUUCUCUCCAGACCGCGCAAGGGCGGAGCAAUAAUAGGCAUGCU
Gura  ************AUGGUCCCUGCCGGGGCAUCGCUGACCGAGAUGGUGCUCGCAUCCUGAGGUAAUGUUCGUAGAGGCGAUCCUCGUGAUCGCCCGAUUGCUGGGCGAGUACAAGAUUCGUCCCUACAGCGAUUUCGGAGGAUUUUC
Ppro  ******************************CUGGUGAUUUUGUCAUUUCCUGAUCCCUGAAAUGAUGUUGCUCUGGUGUCAGACACGUUUUUCCCAGAGAACUCUGUGCCCUCUGUGGCUAUGUACAUUUUCCCGGUUCAUGUUUGCGGAUGGAGUGAUGGU
Sfum  AUGCGUCGCCGCCCGAGAUGGAGCGGGGCAGUCGAUCAGCUCUUGAUUUUCGGAGUCAAUCCAUCAUUAUAAGGACCUUUAAUCUGGGAGCUCACCGGCGGCGAUGCCAUCAUCACGACGGAAGUGGGCCAGCACCAGAUGUGGACCGCCCAGUUCUUCGAAU
```

Fig. 27. Classic attenuation regulation of genes *ilvA*, *ilvB, ilvC, ilvG* in γ-proteobacteria. Designations as in Figure 4.

ilvB:

```
EcE        ************AUGUUCAACGCAAAACUACUACCAACUGCGCUAUCCGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGGAA**CAACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
KPN        AUGAACGCAACCCUGAUCGCUUCGACCCUACUAAAAACCGCGCC***AGCCGCGGUGGUCGUCGUGUCU*********GUGGUGGUCGUCGUCGGCAAUGCGCCGUAGGGUCCGGAA****CAACACGAAUUCCAAACCCCGCCGGCGCAAACCGAGCGGGGUUUUUUGUUGGC
ECA        ACGCACUACUCUUCUUCCACUUCAGCACUACUAAACACCGCGCAUAUUGACGCGGUCGUCGUCGUGCUCGUGGCAGUCGUCGUGGUCGUCGUCGGCAGCGCGCCGUAACGGGUUCCG***AAUCGAAGAUUCUCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUGUUUCU
t          ************AUGCUGAACGCGACCCUACUAACAACUGCGCCAUCUCGCGCAGUGGUCGUCGUGCGU*********GUGGUGGUCGUCGUCGGCAAUGCGCCGUAGGGUCCGGAA***CACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUUGUUUAA
STM, STY   ************AUGCUGAACGCGACCCUACUAACAACUGCGCCAUCUCGCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGUCCGGAA***CACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUUGUUUAA
CKO        ************AUGCUGACUGCGACCCUACUAAAAACUGCGCAACCUGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGGAA**CAACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
YPN        GUGAACUAUUCCACUGCCAAUUUCGCCCUACUAAACACCGCGCAUGUUGCCGCGGUCGUCGUCGUGCGC************GUGGUGGUAGUCGGCAGCGCGCCGUAACGGGUACCGAAUCCAGAAAGAUUCCCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUUUUAUC
Yps        GUGAACUAUUCCACUGCCAAUUUCGCCCUACUAAACACCGCGCAUGUUGCCGCGGUCGUCGUCGUGCGC************GUGGUGGUAGUCGGCAGCGCGCCGUAACGGGUACCGAAUCCAGAAAGAUUCCCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUUUUAUC
YE         AACUAUUCCACUGCUGCUCAUUUCGCUCUACUAAACGCCGCGCAUGUUGACGCGGUAGUUGUCGUGCGC******GUGGUGGUGGUAGUGGUCGGCAGCGCGCCGUAACGGGUACCGAAUCUAGAAAGAUUCCCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUUUUAGC
YfreA      GUGAACUAUUCCACUGCCAAUUUCGCCCUACUAAACACCGCGCAUGUUGACGCGGUAGUCGUCGUGCGC******GUGGUGGUGGUGGUGGUCGGCAGCGCGCCGUAACGGGUACCGAAUCCAGAAAGAUUCCCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUUUUAGC
YintA      GUGAACUAUUCCACUGCCACUUUCAGUCUACAAAAUACUGCGUAUGUUAACGCAGUCGUAGUCGUUCGC***GUGCUAGUGGUGGUGGUGGUCGGCAGCGCGCCGUAACGGGUACCGAAUCCAAAAAGAUUCCCAAACCCCGCCGGCGCCAGCCGAGCGGGGUUUCUUUUUUGC
Ent638     **************AUGACGUCGACCCUACUAAAAACUGCGCUACCAGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGGAU**CAACACACGAAUCCAAAACCCCGCCGGCGCAAACCGGCGGGGUUUUUAGUUUUAA
Spro       GUGAUCGCAUCCUCGCUGACUUCGACCCUACUAGUUACCGCGCUACCAGCCGCGGUGAUGGUCGUCGUG******CGUGUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGUCCGAA*UCAACGCAUCGAUUCCCAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUAGUUUCA
S          ************AUGUUCAACGCAAAACUACUACCAACUGCGCCAUCCGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGG**AACAACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
SSON       ************AUGUUCAACGCAAAACUACUACCAACUGCGCCAUCCGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGG**AACAACACACGAUUCCAAAACCCCGUCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
SbBS512    ************AUGUUCAACGCAAAACUACUACCAACUGCGCUAUCCGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUGGUCGUCGGCAAUGCGCCGUAGGGACUGG**AACAACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
SDY        ************AUGUUCAACGCAAAACUACUACCAACUGCGCCAUCCGCCGCAGUGGUCGUCGUGCGU*********GUGGUGGUCGUCGUCGGCAAUGCGCCGUAGGGACUGG**AACAACACACGAUUCCAAAACCCCGCCGGCGCAAACCGGGCGGGGUUUUUCGUUUAA
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ilvG:

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EcE        *********AUGACAGCCCUUCUACGAGUGAUUAGCUUGGUCGUGAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAGGAAAGGCUUAGAGAUC*********AAGCCUUAACGAACUAAGACCCCGCACCGAAAGGUCCGGGGGUUUUUUUUGACC
t          *********AUGACAGCCCUUCUACGAGUGAUUAGCCUGGUCGUGAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAGGAAAGGCUUAGAAAUC*********AAGCCUUAACGAACUAAGACCCCGCACCGAAAGGUCCGGGGGUUUUUUUUUGGCC
KPN        *********AUGACAGCCCUUCUACGAGUGAUUAGCCUGGUCGUGAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAGGAAAGGCUUAGAAAUC*********AAGCCUUAACGAACUAAGACCCCGCACCGAAAGGUCCGGGGGUUUUUUUUUAUAAC
YP         *********AUGAAAGCAAUUCUCCAAGUGAUUAACCUAGUCCUAAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAAGAAAGGCAUAAAAAUC********AAGCCUUAAUCUCAAGAGAACCCCCGCACCGAAAGGUCCGGGGGUUUUUUUAUUGGC
ECA        *********AUGAAAGCAAUUCUCCAAGUGAUUAACCUAGUCCUAAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAAGAAAGGCAUAAAAAUC********AAGCCUUAAUCUCAAGAGAACCCCCGCACCGAAAGGUCCGGGGGUUUUUUUAUUGGC
YmolA      *********AUGAAAGCGAUUGUCCAAGUGAUUAACCUAGUCCUAAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAAGAAAGGCAUAAAAAUC********AAGCCUUAAUCUCAAGAGAACCCCCGCACCGAAAGGUCCGGGGGUUUUUUUAUUGG
YberA      *********AUGAAAGCGAUUGUCCAAGUGAUUAACCUAGUCCUAAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAAGAAAGGCAUAAAAAUC********AAGCCUUAAUCUCAAGAGAACCCCCGCACCGAAAGGUCCGGGGGUUUUUUUAUUGG
SG         *********AUGAAAGCUGUUGUUCAAGUGAUUAGCCUAGUCGUGAUUAGCGUGGUGGUGAUUAUUAUCCCACCGUGCGGGGCUGCACUUGGACGAAGAAAAGCUUACUAAAC********AAGCUUAAAUCUCAAGAAAACCCCGUACCAAC*UGGUCGGGGGUUUUUUUUGGGG
plu        *********AUGAACACAUUUGUCCUAGUGAUUAGCCUAAUUAUUGUCAGCGUGGUGGUGAUUAUUAUCCCACCGAGCGGGGCUGCACUUGGACGAAGAAAGGCUUAGAAGAA*********CAGCCAAAUCUCUCGAAGACCCCCGCACCGAAAGGCGCGGGGGUUUUUUUUCGAC
ESA        *********AUGACAACCCUUCUACUAGUGAUUAGCCUGGUCGUGAUUAGCGUGGUGGUGAUUAUUAACCCACCGUGCGGGGCUGCACUCGGAAGAAGAAAGGCUUAGAAAUC*********AAGCCUGAAUCAUCGAAAACCCCGCACCGAAAGGUCCGGGGGUUUUUUUAUGAC
AHA        *****************AUGGCCUCCCGUUUCGUCAGCAUUAUUGUGGUCCUAGUGGUGAUUAUUAUCUCACCGCUCGGGGCUCGUUUAGCUGCACGGAACAAGGGAUAGACCCACCACCGGACAGAACGAAACAAGCGACCCCCGAGCCUCACAGCUCGGGGGUUUUUUUUCGAC
ASA        *****************AUGGCCUCCCGUUUCGUCAGCAUUAUUGUGGUCCUAGUGGUGAUUAUUAUCUCACCGCUCGGGGCUCGUUUAGCUGCACGGAACAAGGGAUAGACCCACCACCGGACAGAACGAAACAAGCGACCCCCGAGCCUCACAGCUCGGGGGUUUUUUUUCGAC
VSWAT3     *********AUGAACUUCAACGCUCGCAUUUACGCACUGAUUAACCUGAUUAUCGUAGUCAUUAUUGAGACUGCGCGGGGCGAGUGGGAAAAAAGUAACCACGAAUUA************************GAAAAAACCCCGCACUGACAAGUCCGGGGGUUUUUUCUAAUU
VC0395     *********AUGAACUUGAACGCUCGCAUCAACGCUCUAAUUAACCUAAUUAUCGUGGUCAUUCUAGUGACGACGCGGGGGCGAGUGGGCGAAAAAUAAGUAACCAAAUCC**********************AAAAAACCCCGCACUGAAAAGUCCGGGGGUUUUUUACAAC
A79        *********AUGAACCUAUUCGCUCACAUCAACAACACUGCUAGCCCUGAUUAUCGUGGUCAUUAUUGGCACCGCGCGGGGGCUUGUGGGCGAAAGGUAACCACAAAUU************************ACAAAAAACCCCGCGCUGAAAAGUCCGGGGGUUUUUUACAAC
VV         *********AUGAACUUUGCCGCUCAAAUUAACUCUCUGAUUAACCUGAUUAUCGUGGUCCUCAUUAGCACCGCGCGGGGGAGAGUGGGCGCAAAAUAACCACUAGAUU************************UACAAACCCCGCACUGAAAAGUUCGGGGGUUUUUUUUCAGC
VF         *********AUGACCUUUUUUGCUCAACUGAAUAUUCUGAUUAUUAACAUUCUAGUGGUGAUUCUGGUCACCGCUCGGGGAUGUGUGAGCAAAAAGUAGAGUUACAAGCAC*********************ACUAAAAACCCCAAGCCAACAAGCAAGGGGGUUUUUUAUAAG
A1Q        *********AUGAACUUAUUCGCUCACAUCAACUCACUGCUAGCCCUGAUUAUCGUGGUCAUUAUUGGCACCGCGCGGGGGAUUGUGGGCGAAAGAUAACCACAAAUUA************************CAAAAAACCCCGCACUGAGAAGUCCGGGGGUUUUUUACAAC
VSAK1      *********AUGACUUUUAACGCUCACUCUCGCACUCUGAUUAGCCUGAUUAUUGUGGUCCUGAUUGGUACCGCACGGGGGCAUGUGGGCGGAAAAUAACCACGAGAUU************************CAAAAAACCCCGCACUGAAAAGUCCGGGGGUUUUUUACAAA
V12G01     *********AUGAACCUUUUCGCUCAUAUCAACGCACUGCUAGCCCUGAUUAUCGUGGUCAUUAUUGGCACCGCGCGGGGUAUUGUGGGCGAAAGGUAACCACAAAUUA************************CAAAAAACCCCGCACUGAAAAGUCCGGGGGUUUUUUACAAC
VEx2w      *********AUGAACCUUUUCGCUCAUAUCAACGCACUGCUAGCCCUGAUUAUCGUGGUCAUUAUUGGCACCGCGCGGGGUAUUGUGGGCGAAAGGUAACCACAAAUUA************************CAAAAAACCCCGCACUGAAAAGUCCGGGGGUUUUUUACAAC
V12B01     *********AUGAUUUUUAACGCUCGCAUUUACGCACUGAUUAACCUGAUUAUCGUAGUCAUUAUUAAGACUGCGCGGGGGCGAGUGGGAAGAAAGUAACCACGAAUUA************************GAAAAAACCCCGCACUGAAAAGUCCGGGGGUUUUUUCUAAUU
VAS14      ************AUGCGCUUAACAACAUCUCUCGUACUCAUUAUUAAUGUCAUUGUGGUGAUUAUGUCACCGCAGCGGGGAUUUGCUGGCGCAAAGUAGCGCAAAAGAC********************GCAAACAAAAGCCCCGCACUGAGAAGUUCGGGGGCUUUUUUCAACA
SKA34      ************AUGCGCUUAACAACAUCUCUCGUACUCAUUAUUAAUGUCAUUGUGGUGAUUAUGUCACCGCAGCGGGGAUUUGCUGGCGCAAAGUAGCGCAAGAGAC********************GCAAAUAAAAGCCCCGCACUGAGAAGUUCGGGGGCUUUUUUCAACA
P3TCK      *********AUGCCAUUUAACGCUAAAGCCCUACAACUCAUUAUUAUCGUCAUCGUGGUGAUUAUGUCACCACGAGGGGAGUGCUAGGCGUUAGGUAGCAAGAAACAUA********************ACAAACGCAUAAGCCCCCGCACUGAAAGGUUCGGGGGCUUUUUUAAAUA
PE36       ************AUGUUUGGGUUUACUUCGCGUCUUAUUAUUGUGGUCAGCAUUCUGGUGGUAAUUAUUAAAUUACCAAGCCGGGGACUUACUGCUAAGCGAAAAUAAGCUU************AAUCCAGCAAUAAGAAAACCCCGGUUGA***UAACCGGGGUUUUUUUUGUUU
SO         ************AUGUUUAACCAAGCUGCCAAGCUCAUUCUCGUGAUUAUUACCGUCGUGAUUAUUAAAUCACAGCGGGGGCGGCGCAUGGCAAACUGGUAGACCUAAAAGG*********UUAAAAGUUUCGAAAGAACCCCCCGCUCCGAAAGGACCGGGGGGUUCUUCGUUUU
Sputw3181  ************AUGUUUAACCAAGCUGCCAAGCUCAUUCUCGUGAUUAUUACCGUAGUGAUUAUUAAAUCACAGCGGGGGCGGCGCAUGGCAAACUGGUAGACCUAAAAGG*********UUAAAAGUUUCGAAAGAACCCCCCGCUCCGAAAGGACCGGGGGGUUCUUCGUUUU
Sbal195    ************AUGUUUAACCAAGCUGCCAAGCUCAUUCUCGUGAUUAUUACCGUCGUGAUUAUUAAAUCACAGCGGGGGCGGCGCAUGGCGAACUGAUAGACCUAAAAGG*********UUAAAAGUUUCGAAAGAACCCCCCGCUCCGAAAGGACCGGGGGGUUCUUCGUUUC
Sputcn32   ************AUGUUUAACCAAGCUGCCAAGCUCAUUCUCGUGAUUAUUACCGUCGUGAUUAUUAAAUCACAGCGGGGGCGGCGCAUGGCGAACUGAUAGACCUAAAAGG*********UUAAAAGUUUCGAAAGAACCCCCCGCUCCGAAAGGAUCGGGGGGUUCUUCGUUUC
Ssed       ************AUGUUUAACCAAGUCGCCCUGCUCAUUAUUGAGAUUAUUACCGUCGUGAUUAUUAGAUCACAGCGGGGGCUACGCACGGCGCAUCGACAAACCUAAUUAG*********GUAAAAGAUUGCAACUAACCCCCCGCUCCGAAAGGACCGGGGGGUUUUCGUUUA
Sfri       ************AUGUUAAACCACACAGCCAUUCUCAUUCUCGAAAUUAUUACCGUAGUGAUUAUUAAGUCACAGCGGGGGUGGCGUUUUGGCAACUAGACUGACCUAAGAG**********UCACACAGAUUGCAAAAACCCCCGCUCCGAAAGGACCGGGGGUUUUUUAGUUUU
Sden       ************AUGUUGAACCAAGUCAGCGCCAUUAUCCUCGUGAUUAUUACCGUAGUGAUUAUUAAGUCACAGCGGGGGUGGCGUUUGGCAAUAAAAAUGAUCUAAAAAA************UCAAACAUUGCAAAAACCCCCGCUCCGAAAGGACCGGGGGUUUUUUCGUUUU
Shew       ************AUGUUUAACCAAGCUGCCCUCCUCAUUAUUGAGAUUAUUACCGUAGUGAUUAUUAAAUCACAGCGGGGGCAUCGCAUGGCGCGUCGACACACCUAAUCAG*********GUCAAGAUUGCAACAAGAACCCCCGCUCCGAAAGGACCGGGGGUUUUUUGUUUUU
Spea       ************AUGUUUAACCAAGCUGCCCAGCUCAUUAUUGUGAUUAUUACCGUCGUGAUUAUUAAAUCACAGCGGGGGCUGCGCAUAUUGAAUCGACACACCUAAUCUA**********GGUUUAAGAUUGCAAAAACCCCCGCUCCGAAAGGAACGGGGGUUUUUUCGUAUA
Swoo       ************AUGUUUAACCAAGCCGCCCUACUCAUUAUUGAGAUUAUUACCGUCGUGAUUAUUAAAUCACAGCGGGGGCAAGGCAUGGCAUAUCGACAAACCUAAUUUA*********GGAAAAGAUUGCAACCAACCCCCCGCUCCGAAAGGACCGGGGGUUUUCGUUUU
Sama       ************GUGUUUAACCAGGCUGCCAAGCUCAUUCUCGUGAUUAUUACCGUAGUGAUUAUUAAAUCACAGCGGGGACGGCGCAUGGCAAACUGACAGACCUAAUCCA********GGAAAGAAGUUGCAGAAAGCCCCCCGCUCCGACAGGACCGGGGGGUUUCUCGUUUC
CPS        **************AUGCACAUAUUUAACUCAAUUAUUAUAAACCUUCUCGUCGUGGUGAUUCUUAAAUCAUCUCGAGGGUUUUGUUGAGCUAAAAAAAAGCAUUCAAUC********************AAAUAACAAACCCUCGCUUCGCAAGAACCGAGGGUUUUCUUUUUAG
PSHAa      **************AUGCUUGCAAAUGCACUAAACCUAGUCCUGAUUAUUAUCGUGGUGAUUAUUCCC***GCGAGGGCUUCGUAGUGCUUUAAAAAACUUAAGC************************AUUUAAAAGCCCUCCGCACUUAACCGUUCGGGGGCUUUUUGGUUU
PTD2       ************AUGCUGACAAACACACUUUCUCUAGUCCUAAUUAUUAUCAACGUGGUGAUUAUUAUCACCGCGGGGGCGAGCUAGUGUCUAAGUAAAAUUGCU************************UAAUCACGAACCCCCCGAACUGAAAAGUCCGGGGGUUUUUUGUUUC
Patl       **********************************AUGAUUAACCUUAUUUUAGUUGUAAAUUCGUAAUAUCAUCCUAUUAACGUGGUUGUAAUCUUAUGAAUC****************************GAAAGAUAUAUCCUAAUAUAUUGCUAUAUUGGGAUAUAUAUCUCA
ATW7       **************AUGCUUACAACUGCACUUAAACUAGUCCUGAUUAUUAUCGUGGUGAUUAUUCCCGCGAGGGCUUUGUAGUGCUAUAAACUUGAGCA****************************UUAAAAGCCCUCCGCACUUAACAGUUCGGAGGGCUUUUUAGUUU
Ping       ***AUGCAAGUGAAAUUGUUGAAGUUGUCCGCUCAGGCGUCUGUGGUAUUGCGCGUGGUGAAAAAGCAUUACGCGGUUAAUUUCUGACUAAAUGACCAGAUG****************************ACCAUCAAUGCAAAGUUCAGGAA*****UCUGGCUUUGCAUUUUUUC
PCNPT3     **************AUGUUACAUUUUGUCCUCCUCCUCAUAAUAAUUAUUAGCGUGGUGAUCAUUGGAUCACAGCGGGGGGACGCACGCAUCGAGAAGACAAAAUAAGGUCU***********UCUAAGAUAAAAAAAACCCCCGCUCCGCAAGGAACGGGGGUUUUUUUUUGUUU
PM         ************AUGGCAUUACGCCCUGUACUUAGCAUUAUUAUUAACCUCGUGGUGAUUAUUAUCA*CUGCGGGGCGAGCGCGUUAAUGUUUGACUGUCAAUAAAUAA***************AAAAGAUCAAAUUUAACCCUCGUCUGAUAGCAGAUGAGGGUUUUUUUUACUU
HI         *********AUGCGCGACGACCAGAAAAAGUCUCACGCUUUUGUGCUUUUGGAGCUGAGUGCACCAUAAAUUAUCCUAUGUAAAAAAAUGAAAAGAGUUUCAAUAUAAUGAAAUCUAACAAUCAGUCAAUAAGCAAGCUUAAAGAGCGGUAAAAAUUCACUAAAUUUUUUAGGGGA*
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ilvC:

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XC         ACCUUGAACGCUUCACUGCCCGCGCCCAUCGGCGUGCCGGCGUCGCUUCUCGUGCUCGUACUUAUUACCUCGCCAACCGGUGCGGGACGCGGCUUCGUGUAGGCAACAGACAC***********ACAAGGCUUCGAUCAGACCCCGCACCGGCAACGGCGCGGGGUUUCGCGUUUC
XOO        ************AUGUCCACGCCCUCUGGCGCGUUGGUUGUGUCGCUUCUCGUGCUCGUACUUAUUACCUCGCCAAUCGGUGCGGGACGAGACUUCGUGUAGGCAACAGAC*************ACAAGGCUUCGAUCAGACCCCGCACCGGCAACGGCGCGGGGUUUCGCGUUUC
Xfaso      GCUUCUUCCAACUGUCUUCCCAAUUCUGCUAUUACGGUAGCCUUUCUUCUUAUACUCGUGCUUAUUGCCUGCCCAAACAGUGGGGGACAGGCCAGCGUGUAAACAACAUACAC************UCAGGCUUUGAUCAAACCCCGCAUUGGCAACCUUGCGGGGUUUUGUUUUUU
```

ilvA:

```
Pput       ******************************AUGAAUACAUUCCCGCACGUGAACGCCAUUAUUAUUACCGCCAUUAUCAGCUUGGCGGGCUAGCGCGUACGUGC********************************ACCGAACCCGCCCUGG******AGGCGGGUUUUUUCUCUC
PSPTO      ***************************AUGAACCUCAUCAAGCAAAACCUCGGCCAGAUUAUUAUUACCGUCAUUCCAGUCAUGGCGGGUUAGCCGACGUUUGC*********************************AAAAAACCCGCCCUGG******AGGCGGGUUUUUUCUGUC
PFL        ***************************AUGACUUUCCCUGCAUAUCGUUUCCAGCCAAGCAUUAUUACCGCCAUUCCUUAUUGGCGGGCUUGCUGACGACUGCA**********************************CCCAACCCGCCCUGG******AGGCGGGUUUUUUCUCUC
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Fig. 28. Phylogenetic tree of the regulatory regions of genes *ilvA*, *ilvB, ilvC, ilvG* in γ-proteobacteria. Species names and acronyms are given in Table 2.

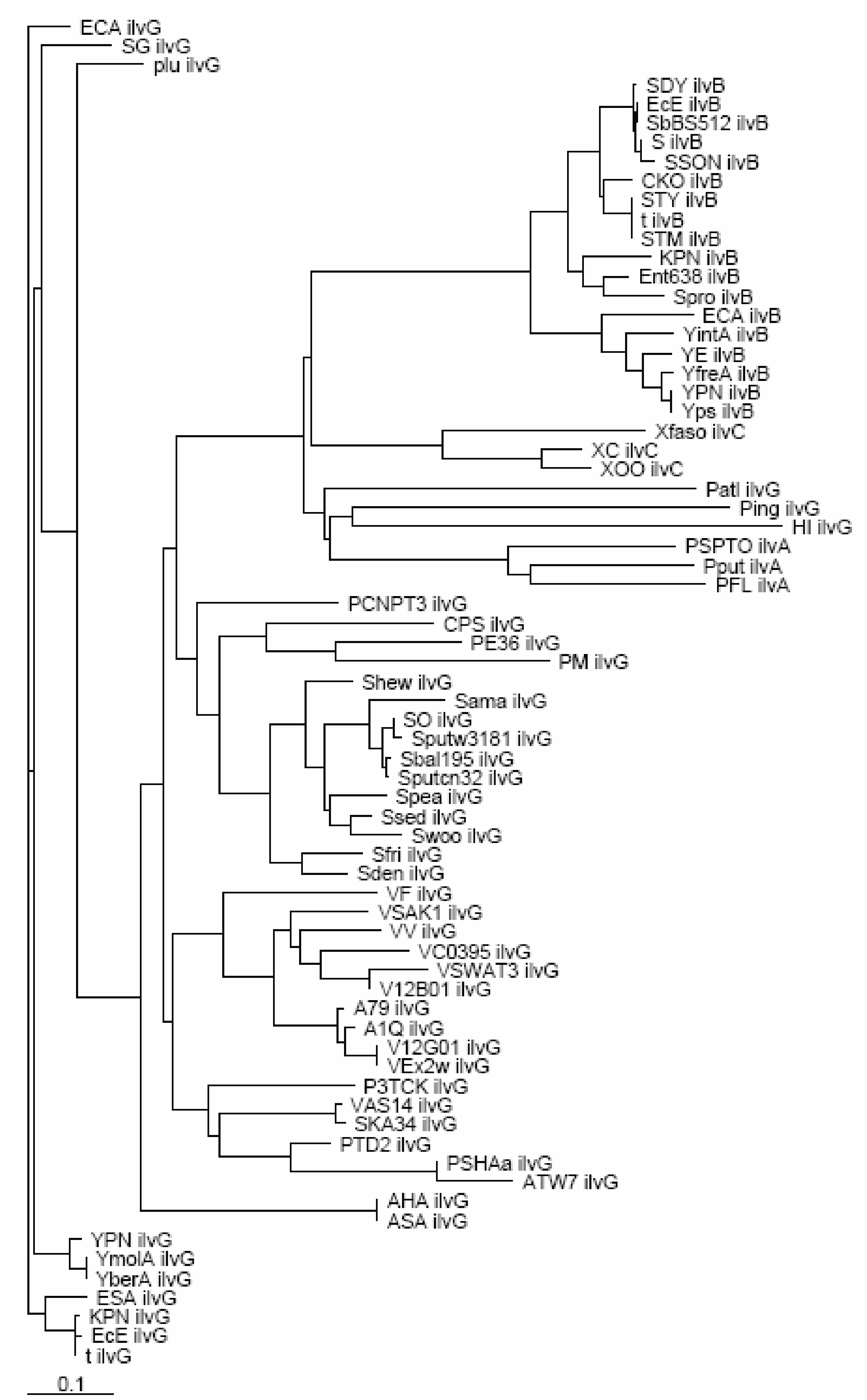

Fig. 29. Probability of the *ilvB* gene termination in δ-proteobacteria. Species names and acronyms are given in Table 2.

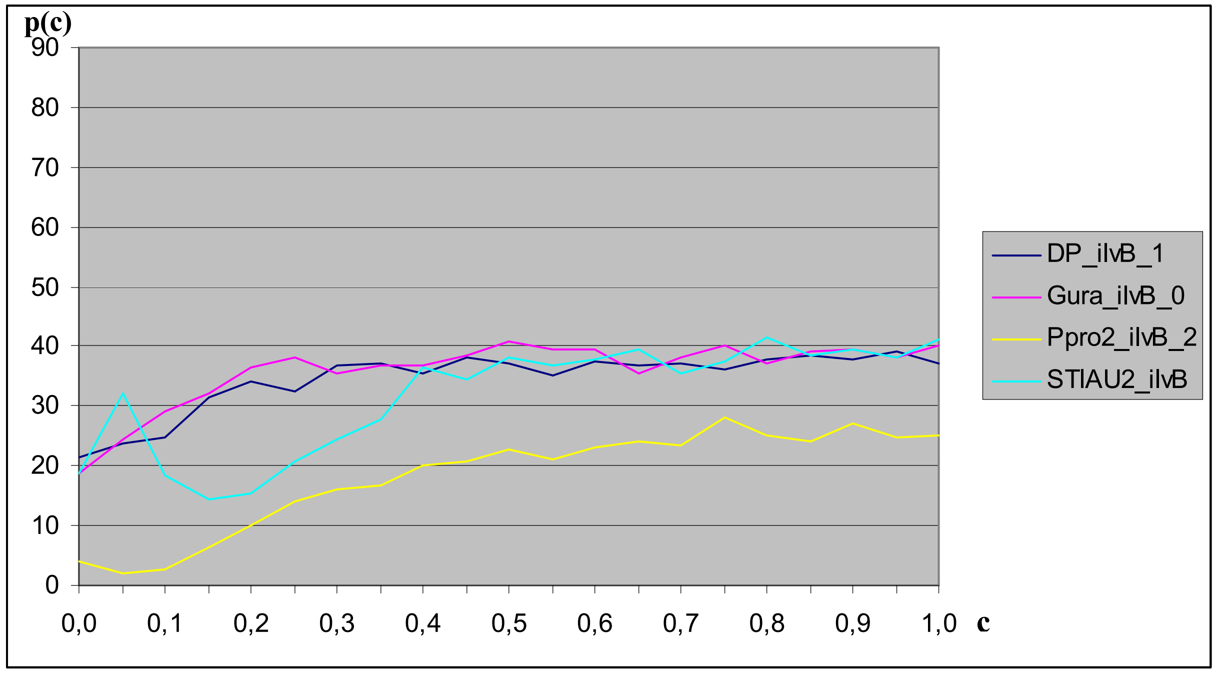

Fig. 30. Classic attenuation regulation of gene *ilvD* in: a) actinobacteria, b) Chloroflexi, c) Bacteroidetes/Chlorobi. Designations as in Figure 4.

a)

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CE     GUGCCACCAUCCAGUGUGACGGUGUGAUUCGAACCAGAGAACCGAUCGCCGUCGGACAUCCUAUUCUGCUUUGGAUUCCGCCGCUCCCAGCCCACCUCACCCGGUCCGGGCAUGGUGAGGCGGCAUCCGAGAUUUUUCCCCUUU
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b)

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Haur   AUGAAUAAUCGUCCCGCGUUUAUUAUUAUUAGCAACCUCCUUAGCCUCGUAAUCGUCGUCAUUACGCGGUCACUUUUGUGUGGGAGGGGCUAACAAGCCUCGCGGGUAGUUCAAAAGAACUCAAGCCCCUCCCAAUCGGGAGGGGCUUUUGAUUUGUGAUUAAGUUA
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c)

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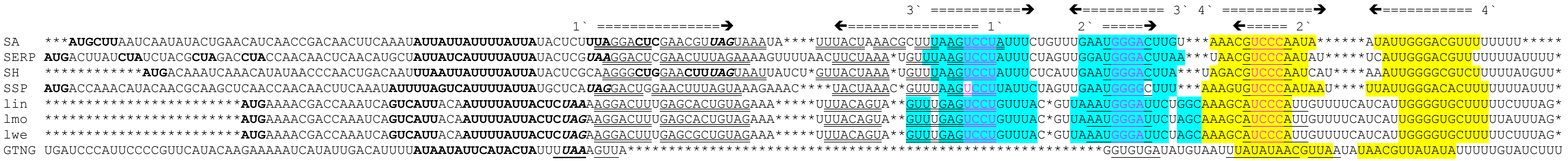
BDI    *********************AUGAACAACGUAUUGCAUAUUAUUCUCGUGGUGGUCCUUCUAGUCAUUAGUAGGUAAGGAGAAAGGUGUGUAAGAAGUUGUGAAGUCGUA******GAGAUAUUUCUUAAGCCUUUCUCCA**UAUAGGGAAAGGCUUUUUUUAUU
PARMER ******************AUGAUGAACAAUGUAUUGCAUAUUAUUCUCGUGGUGGUCCUUCUAGUCAUUAGCAGGUAAGGAGAAAGGUGUGCAAGAAAUUGUGAAGUCGUA****UAAAGAUAUUUCUUAAGCCUUUCUCCA**UACAGAGAAGGCUUUUUUAAUA
BACOVA ***AUGUUACAUACAUCUAUUAACCUAGCAGUCCUGCAUAUUAUUCGCGUCGUGGUGGUCCCAUCAAG******AGCGUGAGAAAGGUUUUUGUGUUGUAUGUGUUCGUACCAUAAAAGAUAGAAUUUAGAGCCUUUCUCACUUGUGUGAGGAAGGCUCUUUAAUUA
BACCAC ***AUGUUACAUACAUCUAUUAACCUAGCAGUUUUGCAUAUUAUUCGCGUCGUGGUGGUCCCAUCAAG******AGCGUGAGAAAGGUUUUGUGUUGUAUGU*GUUCGUACCAUAAAAGAUAGAAUUUAGAGCCUUUCUCACUGAUGUGAGAGAGGCUCUUUAAUUA
BF     AUGAAUAAUCAUACAUCAAUUAACCUGGCAGUCCUGCAUAUUAUUCGCGUCGUGGUGAUUCCAUCAAG******AGCGUGAGAAAGGUUAUGUAUGUAUUCG*****UACAGAUAGAAGAUAUGAUUUAGAGCCUUUCUCACUACAGUGGGGAAGGCUCUUUACUUA
BVU    AUGAAUAUUACUACUCUAAAUAACCUGGCAGUCCUGCAUAUUAUUCGCGUCGUGGUGGUCACACUGGG******AGCGUGAGAAAGGUUGUGUAUGUGUAGU****UGUACAUAUAAAGAAAUAAUUGAAAGCCUUUCUCACA*UGGUGAGGAAGGCUUUUUCAAUA
MED217 ******AUGAAAACAGCAAUUCGUGUAC******GUUCUAUUAUUGUCAUUAACGGUAGUUGAU******************************************GCGGAACGUCAUAUUUAAAUAAUAGACCUUCCGUUAA****ACUGGAAGGUUUUUUUUUGA
SCB49  ************************************************GUGGUCAUUAUACCAAUUCUAUAUUAGCCACUA*********************************CAGAAGCCAAACAAAAAGGAUUUGA***********CGAAGCUCUUUUACUAG
CT    CCCCUCCUCUCCGGUAUUACCCUUACCGUAUCGGUACCGCUUGUACACGUACGAAUUAUCGUAGCCUGACCCGCCGUCAGCCCGUUUCCAGGUCCAUCGUAUUUUC***CGCGACAAUACAUCAGACUUCAAGGCUUCGGGACAGGCAGGCCCGGACUUUUGUUUUUC
```

Fig. 31. Classic attenuation regulation of gene *ilvD* in Firmicutes. Designations as in Figure 20. In *Geobacillus thermodenitrificans* (GTNG) regulation is predicted by Yanovsky.



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                                                                                                                  3` ===========→     ←========== 3` 4` ===========→      ←=========== 4`
                                                                     1` ===============→             ←================ 1`          2` =====→          ←===== 2`
SA   ***AUGCUUAAUCAAUAUACUGAACAUCAACCGACAACUUCAAAUAUUAUUAUUUUAUUAUACUCUUUAGGACUCGAACGUUAGUAAAUA****UUUACUAAACGCUUUAAGUCCUAUUUCUGUUUGAAUGGGACUUGU***AAACGUCCCAAUA******AUAUUGGGACGUUUUUUUU*****
SERP AUGACUUAUCUAUCUACGCUAGACCUACCAACAACUCAACAUGCUAUUAUCAUUUUAUUAUACUCGUAAGGACUCGAACUUUAGAAAAGUUUUAACUUCUAAA*UGUUUAAGUCCUAUUUCUAGUUGGAUGGGACUUAA***UAACGUCCCAAUAU*****UCAUUGGGACGUUUUUUUAUUUU*
SH   ************AUGACAAAUCAAACAUAUAACCCAACUGACAAUUUAAUUAUUUUAUUAUACUCGCAAGGGCUGGAACUUUAGUAAUUAUCU*GUUACUAAA*UGUUUAAGUCCUAUUUCUCAUUGAAUGGGACUUA***UAGACGUCCCAAUCAU****AAAUUGGGGCGUCUUUUUAUGUU*
SSP  AUGACCAAACAUACAACGCAAGCUCAACCAACAACUUCAAAUAUUUUAGUCAUUUUAUUAUGCUCAUAGGACUGGAACUUUAGUAAAGAAAC****UACUAAAC*GUUUAAGUCCUUAUUCUAGUUGAAUGGGGCUUU***AAAGUGUCCCAAUAAU****UUAUUGGGACACUUUUUUUAUUU*
lin  ************************AUGAAAACGACCAAAUCAGUCAUUACAAUUUUAUUACUCUAAAAGGACUUUGAGCACUGUAGAAA*****UUUACAGUA**GUUUGAGUCCUGUUUAC*GUUAAAUGGGAUUCUGGCAAAGCAUCCCAUUGUUUUCAUCAUUGGGGUGCUUUUUCUUUAG*
lmo  ************************AUGAAAACGACCAAAUCAGUCAUUACAAUUUUAUUACUCUAGAAGGACUUUGAGCACUGUAGAAA*****UUUACAGUA**GUUUGAGUCCUGUUUAC*GUUAAAUGGGAUUCUAGCAAAGCAUCCCAUUGUUUUCAUCAUUGGGGUGCUUUUUAUUUAG*
lwe  ************************AUGAAAACGACCAAAUCAGUCAUUACAAUUUUAUUACUCUAGAAGGACUUUGAGCGCUGUAGAAA*****UUUACAGUA**GUUUGAGUCCUGUUUAC*GUUAAAUGGGAUUCUAGCAAAGCAUCCCAUUGUUUUCAUCAUUGGGGUGCUUUUUCUUUAG*
GTNG UGAUCCCAUUCCCCGUUCAUACAAGAAAAAUCAUAUUGACAUUUUAUAAUAUUCAUACUAUUUUAAAGUUA**********************************************************GGUGUGAUAUGUAAUUUAUAUAACGUUAAUAUAACGUUAUAUAUUUUUGUAUCUUU
```

Fig. 32. Probability of the *ilvD* operon termination in *Staphylococcus* and *Listeria*. a) *Staphylococcus*, b) *Listeria,* helix energies are calculated without accounting for RNA triplexes, c) *Listeria,* helix energies are calculated accounting for RNA triplexes. Species names and acronyms are given in Table 2.

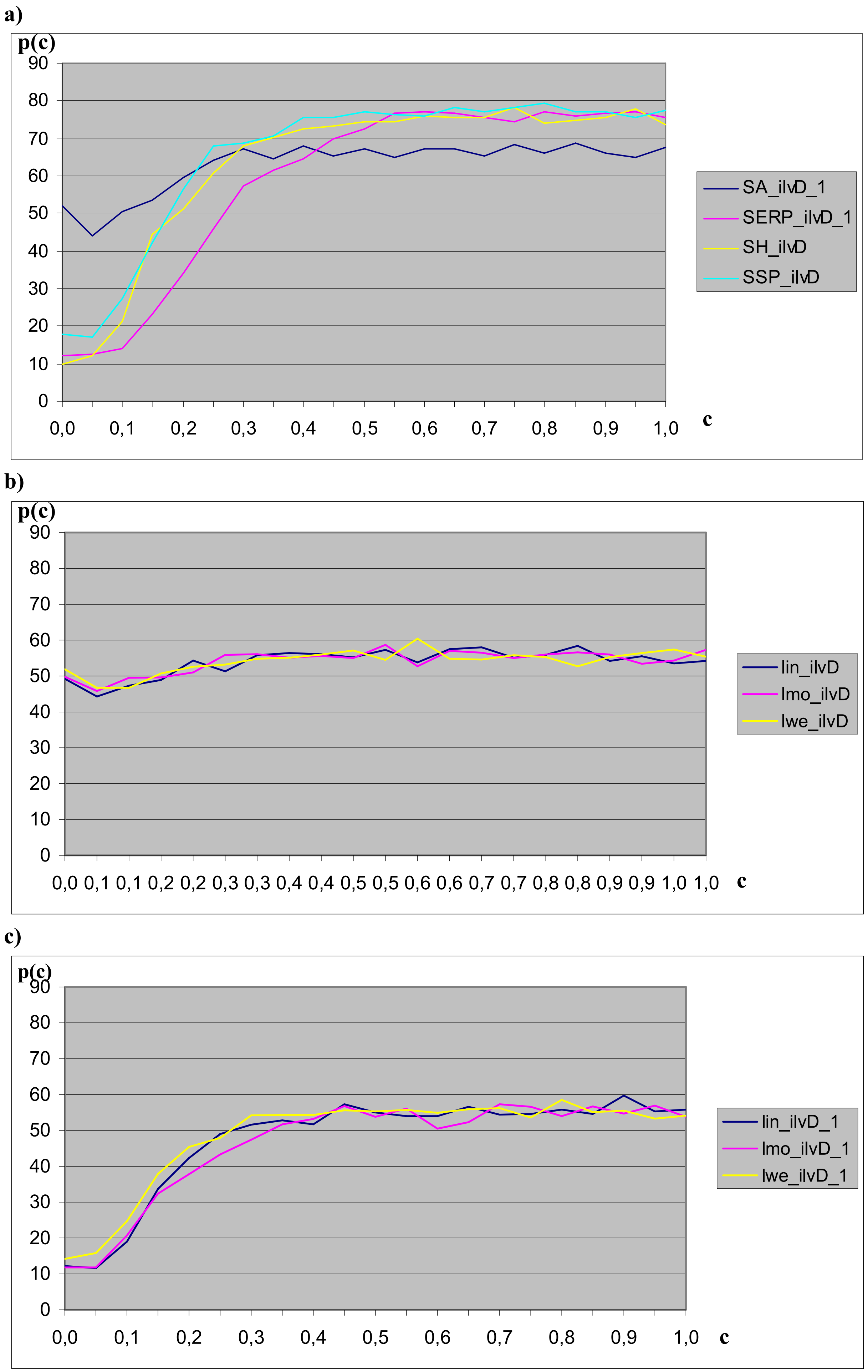

Fig. 33. Classic attenuation regulation of gene *leuA* in: a) α-proteobacteria, b) β-proteobacteria, c) δ-proteobacteria. Designations as in Figure 4.

a)

```
Caul  ************************AUGAACGUCGCGCGCCAACUGCUUUCGCUUCGGCUUACCAACCCCUGGGCGCUCUAGGGGCACGC*UUCGUCGUGGCCGGGCGCGCAGGGGAUGACUGAUCCAUCGCCGCCCCGCACGCAGACACCUUCCGACGAGUAGCUCC*
CC    ************************AUGACUGUCACGCGCGACCUGCUUUCGCUUCGGCUUAUCAGCCCCUGGGCGCUCUAGGGCCGCGCAUCGUCGUGGCCGGGCGCACAGGGGAUGAUUGAACCCGCAGCCCGCACGCAGACACACCCCUUUCGACGAGUACUUUC
blr   GUGGCUCUGGCCGCCGCCACGAUCCCGGCCGCGCUGCUGCCCACCCUCCUUCUUGGCGGCCUUCUUCUUACUUGCCCCUGAGGGCCGGCUGGGCGCCACGCGCCUGGGCGCUCAGGGGUUGGUCGAGAUCACCGGACACCUCAAGCGCCCAGCACUGAACGGCGCAAA
SPV1  ******AUGAACUUUUAUACGCACACAUCCGUUUUUACGCGUCAGUACCUGCUACUGCGACUACGGCUGUGUGUCUGCUGAACGCGUUUCAGUAACAGAUAUACAGGCCGCGCUUACCCCGCGGCCUUUUUUUAUGCCCUGUUUGAGUUGCUAAUCUGAGG*******
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b)

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Bxe   ACCCUAUCGCUACUACUAGCCCGCUCCACCGGGCUAGGUCUGCUGCUGCGCGCUUCCGUCUGAAACACCCGAAGCACCGCUCAAUUCCCCAGUAACUGACCCAGCCCCGGUUUCCGACCGGCGGCCCAGUUAUGUCUUUUCG**************************
Bphyt ***CUAUCGCUACUACUAGCCCCCUCUACCGGGCUAGGUCUGCUGCUGCGCGCUUCCAUCUGAUACACCCGAAGCACCGCAAAAUUCCCCAGUAACUGACCCAGCCCCGGUUUUCGACCGGCGCCUCGUCAUGUCUUUUCGUCGUCCG********************
Bpro  ******************AUGAAACAAAUUUCGCUUGCACUAUUGCUAUCUGCCAACGGGCGGAGACGGUAGCGCGCACG*******CGUACACCCAAUUCAACGGCCCGUUUGC**AACAGCAACGGGCCGUUUUUCUUUGGGUUGCUGGUUUUUGAAAUCUUCAAA
Daci  ******************AUGCAAUACCUGUCGCUAGCUCUACUACUGAUGUCCAACGGGCAGAGACAGUAGCGCGCGCG*******UACAUACCUACUUUCACGGCCCGUUUGC**ACCAGCGACGGGCCGUUUUGCAUUUGUGGGGUCGC****************
Ajs   ******************AUGCAUUUCCUGUCGCUAGCACUACUACUGAACUUGUCCCUCGGGCAGGCAUAGUAGCGCGC***GCGUACACACCUACUUCCCACGGCCCGUGAGC**ACCAGCGACGGGCCGUUUUUGUUUUUCCGGGGUCGCUGGAGCACAGGUCAG
Mpe   *********AUGACGUUUCGCGCCCGCUUUUCGCUGCUGCUACUGCUAGGAGUGCCCUGCGCGCGCUGAUUGCACACGUC*****CCGUCGUUUCUGCAUCCACGGCCCGCGCGCUUCCUGCUCGCGGGCCGUUUUGUUUAGUCCUCGACCUUCGUAUCUUCGCUGGA
Ctes  ******************AUGCAAAACCUGUCGCUAGCUCUACUACUAAUGUCCAACGGGCAGAGAAAGUAGCGCGCGCG***UACAAACACACCCUACUUGGCGGCCCGUAGCA***UCAGCGACGGGCCGUUUUUGCUUUUGGGCGUCGCUGGAGCUGGGUUCAAU
BURPS AUGACCGCAUUUUCCCGCCCCUUCCUUCUUCUAGCCGGUGCGCCGCUACGCGCGCUAGCGCUAGCGCGCCUGCCGCGCUGACCGUUUUCGCCCUCCGUCGAGCUUCGUCUGUUGUCUAGCGUCGCCUGCGGUGGCGCGAGCUUCAUCACGUGUGUUUCCCCAUUCGAC
```

c)

```
DP     ***************************AUGAACUUUAUCUCUCUCCUCCUACUAGCAUGCCUAUUAUUGCUCCGCCCUUGCGCGGUCUGGAGAGAAAUUUAUUAGUUUUGUUUGUCUACUAUAUAAGUUGAUCUAAAGGCCGCGGUU***GAAAAACCGGGGCCUUUUUUUUUGUU
SYN    ***GUGGCAAAUAGAGAAAGGGCCGAUAUCCUGUUAGACAGCCUGUUGCUUCUGGGCCUCGCCCUUCUGUGCCUUGCUUUCCAUCGCCCGGUCUUUUCAGGUCAACCGUAAACGAAGAAAAAAAAGAAAAACUGAAAGGCCAUGGGC**GGAAAGCUCAUGGCCUUUUU*******
Sfum   ******************AUGAUCCAGGCUCUCGUCCUAUCCCUACUUCUUCUCGACCUGAAUGGUCGGACGCGGAGACCUCGUGCCUUUCUCUUGCCCGCGCUCUGAAGCGCGCUGCAUACCGUCCAAACC**UAAGGCCAUGGGG***GAAACUCCAUGGCCUUUUUGUUUU**
STIAU  ******************GUGUCCGUCGUUGCUCGGGUGGCCGGCCUCCUUCUUGGCGCGCUUCUUCUUCUUCUUGCGCACGGGGCCGGGCCACCGUUCUGAGACUGGAUGAACC*****CCAGGCUGGAACGAAAAGCCCCGCCCCCGGAAACGGAGGCGGGGUUUUCGUUUUUC
PPSIR1 AUGACCCGGUGCAUCCCCACGACUGCUGCCCUCCUCGGAGCGCGCGACCUACUCGUCCUCGACGGUGGGCUGCUCCUCCUCGUGGAGGUCUGCGUGGUGUGAACUAGGUCCUACGGCACCU******UCCACGCAGACCCACCCGCCA***UUUUGGCCGGUGGUUUUUUUGCGU*
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Fig. 34. Classic attenuation regulation of gene *leuA* in γ-proteobacteria. Designations as in Figure 4.

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KPN            ******AUGAUUCGCACCGCUCGUAUCACCAGCCUACUACUACUAAACGCAUGCCAUUUGCGCGGUAGGCUGUUGGGCGACGUUCAGCGUUAAGUCAUCUUCCAGCAAGACUAU**************AAAACCCGCGCCUUG****GCGCGGGUUUUUUUAU**********
ECA            *********AUGUUCAAGUUUACUGUCCUACUAAGCCUACUACUAAACGCAUCCUUCUUGCGCGGUAGGUUUGUGGGCAGACUUCAGAACUAAGUUUCUCGCCACACGAUAC***************AAAAACCCGCGCUGAU****GCGCGGGUUUUUUUUU**********
EcE24377A      ******AUGACUCACAUCGUUCGCUUUAUCGGUCUACUACUACUAAACGCAUCUUCUUUGCGCGGUAGACGAGUGAGCGGCAGCCAGCAUUAAGCCAGCACGCAGUCAAAC**************AAAAAACCCGCGCCAUU****GCGCGGGUUUUUUUAU*********
SbBS512,S,SSON ******AUGACUCACAUCGUUCGCUUUAUCGGUCUACUACUACUAAACGCAUCUUCUUUGCGCGGUAGACGAGUGAGCGGCAUCCAGCAUUAAGCCAGCACGCAGUCAAAC**************AAAAAACCCGCGCCAUU****GCGCGGGUUUUUUUAUGCCCGAAGCG
SDY            ******AUGACUCACAUCGUUCGCUUUAUCGGUCUACUACUA***AACGCAUCUUCUUUGCGCGGUAGACGAGUGAGCGGCAUCCAGCAUUAAGCCAGCACGCAGUCAAAC**************AAAAAACCCGCGCCAUU****GCGCGGGUUUUUUUAUGCCCGAAGCG
Spro           ******AUGAACUCUACUUUCCGUCUACUAGGCCUACUACUU***AACGCAUCUUGUUUGCGCGGUAUGCCGGUGGACGCAGUUCAGAGCUGAUUCAGCCCACCUCAUAAC*****************AAACCCGCGCUACU****GCGCGGGUUUUUUUUUACCCGCUUAG
YPIP275        ******AUGUUCUACUCAACCCGUCUACUAAGCCUACUACUU***AACGCAUCUCUCUUGCGCGGUAUGUUGGUGGACGGAAAUCA****UGAUUCAGCCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUGU*********
YpsIP31758     ******AUGUUCUACUCAACCCGUCUACUAAGCCUACUACUU***AACGCAUCUCUCUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGCCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUAUCCGCUGAG
YE             ******AUGUUCUACUCAACCCGUCUACUAGGCCUACUACUU***AACGCAUCUCUCUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGUCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUACCCGCUAAG
YberA          ******AUGUUCUACUCAACCCGCCUACUAAGCCUACUACUA***AACGCAUCUCACUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGUCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUACCCGCAAAG
YfreA          ******AUGUUCUACUCAACCCGUCUACUAGGCCUACUACUU***AACGCAUCUCUCUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGUCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUACCCGCAAAG
YmolA          ******AUGUUCUACUCAACCCGCCUACUCAGCCUACUACUA***AACGCAUCUCACUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGUCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUACCCGCUAAG
YintA          ******AUGUUCUACUCAACCCGUCUACUAAGCCUACUACUU***AACGCAUCUCACUUGCGCGGUAUGUUGGUGGACGGAAAUCAGAACUGAUUCAGUCAUCAAGAUUAAC*****************AAGCCCGCGCAAAU****GCGCGGGUUUUUUUUUACCCGCUAAG
SG             ******AUGUUCAAGUCUAUCCGUCUACUAAGCCUACUACUA***CACGUAGAAUUGAUGCGCGGCAGGCUGGUGCACGGUAUUCAGAACUGAAUUCGGGCCACUCCAGAUU***************AAAACCCGCGCACUACU**GCGCGGGUUUUUUUAUGCCUGGCGUG
Plu            ******AUGAUUCACUCAAUUUGUCUACUAAACCUACUACUC***AUCGUAUCUGAUAUGCGCGGUAUGCUGGUGGACAGAAAACAGAGUUGAUUCAAAACAGAGUUGGUCCAAACCAGACAUUAACAAGAACCCGCGCCAA*****GCGCGGGUUUUUUUUACCUGCUGGGC
Ent638         ******AUGAUUCGUACCGUUCGUUCUCUCAGCCUACUACUACUAAACGCAUCUCUUUUGCGCGGUAGGCUGGCGAACGAAAUUCAACGUUGAAUCGUCUCCAGUAAA****************CAAGAAACCCGCGCCAUU****GCGCGGGUUUUUUUAUGCU*******
ESA            ******AUGAUUCGCAUCGUUCGUUUCGCUGGUCUACUACUACUAAACGCAUCCUCAGUGCGCGGUAGACUGGUGCGCGACGUUCAGCGGUAACGCUUGAGUCAGGUCAUCAGAAAU********AAAAAACCCGCGCCGCU****GCGCGGGUUUUUUUAUGCUCACGCAA
t              ******AUGUCAUAUAUCGUUCGUUUCACUGGGCUACUACUACUCAACGCAUUUAUUGUGCGCGGUAGACCGGUGGGCGGCAUUCAACAUUAAGUCAGCUCGAAGUCAAAC****************AAAACCCGCGCCGUU****GUGCGGGUUUUUUUAU*********
Sententer      ******AUGUCACAUAUCGUUCGUUUCACUGGGCUACUACUACUCAACGCAUUUAUUGUGCGCGGUAGACCGGUGGGCGGCAUUCAACAUUAAGUCAGCUCGAAGUCAAAC****************AAAACCCGCGCCGUU****GCGCGGGUUUUUUUAUGCCUGACGCA
STM            ******AUGUCACAUAUCGUUCGUUUCACUGGGCUACUACUACUCAACGCAUUUAUUGUGCGCGGUAGACCGGUGGGCGGCAUUCAACAUUAAGUCAGCUCGAAGUCAAAC****************AAAACCCGCGCCGUU****GCGCGGGUUUUUUUAUGCCUGACGCA
CKO            ******AUGAUUCGUAUCGCUCGCUUUAACGGUCUACUACUACUAAACGCAUCUUCGUUGCGCGGUAGACUGGUGAGCGACAUUCAGCAUUAAGUCAGCAUCAGUAAGAUU***************AAAAACCCGCGCCGUU****GCGCGGGUUUUUUUAUGCUCGAAGCA
HSM            ******AUGUUUGACAUUCUUUCUCUGUUACUCAAUUUACGACUAUCACAUUUCUUGUGCGGAUAAAUUGUGGAACAAAGAAAUAUAGUUAAACAUGUCAGUU***************************GACCCGCACAAGUAAAAUGCGGGUUUUUUUGUAUCUAAAAUC
NTHI           ******AUGUUUCGUAUUGUUUCUUUAUCUCUCAACCUGCUGCUCUCACAUUUUGCGUGCGGCUAAGUUGUGGAUAAAAAACAGUCAGAUGUAAAUACCCAAUUUU************************AAACCCGCACUUUAUAAGUCGCGGGUUUUUUGUCUAAAAAAUAC
PM             **************AUGUGUUCUUUAUCUCUCAACCUUCUGCUCACACAGUCAUUGUGCGGCUAGGUUGUGGAUAAAAAACAGUAAAAUAUC*************************CCACAAAUUAGACCCGCACAUGU****AAGCGGGUCUUUUUUAUGAAAACGA
Sfri           ******AUGAACACACAAUCAGUUUUACUCGGACUCCUUCUCCUCUCA**CGCAUAUCCUGCGCGGAGUCCUUUGUGUUACAUGCAAAA*UAAUUCAUUAAGCAUACAC******************AAACCCCGCGCUAAU**AGUCGCGGGGUUUUUUUUAGCCCUUUUG
Sden           ******AUGAAACACACUUACUUGCAACUCGGACUCCUUCUCCUCUCU***GACAUUUUUGUGCGGAGUGUGUGGUGUUGCAAGUAAAACAGCAAAAUUAACACU**********************AAACCCGCGCUAAUC***GUCGCGGGUUUUUUGUUUUUAGGCCCA
SO             ******AUGAAUAGAAUUAGCAGCAAACUCGACCUCCUCCUUCUCUCUCUCGCGCCAAAAACGCGGAGGUCUUAGUGUUGCUCGCUCGAUAGAUAGGCAAAACACUCAU******************AAACCCCGCACUAAU***GUUGCGGGGUUUUUUGUAUCU******
Spea           ******AUGAAAUAUACCGAUGCACUACUAGGACUCCUUAUUCUCAUUCUCGCAGAACCUGCGCGGAGGACUUAGUGCUAUACGCUUUAAAAUGAGCCUGCAUUAAU*******************AAACCCCGCAAAUA*****GAGCGGGGUUUUUUGUAUUUUAAUCG
Sama           ******AUGAAUAGAAUUGUUUCACUAAUCAACCUCCUUCUCCUUACUCUCGCAAUCCCUGCGCGGAGGAAUUAGUGUCGCACGCUCGCUAGCCAAGCAAAGCCUUC*****************ACAAAACCCCGCGCCAACC***ACGCGGGGUUUUUUGUUUUCAAACAC
Swoo           ******AUGAAUAUUAGCCGUGCAUUACUCAACCUCCUCAUUCUCAUUCUCGCAGUUUCUGCGCGGAGGAUGUAGUGUUGCACGCUUGAUUAGAGUCACCAACAUUC********************AAAACCCCGCGCUACGAA**UCGCGGGGUUUUUUGUUUUUGUACCC
Shewmr4        ******AUGAAUAGAAUUAGCAGCAAACUCGACCUCCUCCUUCUCUCUCUCGCGCCACAAACGCGGAGGUCUUAGUGUUGCUCGCUCGAUAGAUAGGCAAAGCAUU******************CACAAACCCCGCACCAAUG***UUGCGGGGUUUUUUGUAUCUGAAUAC
Sbal195        ******AUGAAUAGAAUUAGCAGCAAACUCGACCUCCUCCUCUCUCUCCUCGCGGUUUAUACGCGGAGGUCUUAGUGUUGCACGCUCGAUAAAUAGGCAAAGCAUU******************CACAAACCCCGCACCAAUG***UUGCGGGGUUUUUUGUAUCUGAAUAC
Sput           ******AUGAAUAUUAUUAGCCGCAAACUCGACCUCCUCCUCUCUCUCCUUGCGGUUUAUACGCGGAGGUCUUAGUGUUGCACGCUCGAUAAAGAGGCAAAGCAUU******************CACAAACCCCGCACAAAUG***UUGCGGGGUUUUUUGUAUCUGAAUAC
Shew           ***AUGACGACUAUUAACCGUGCACUCCUCAGCCUCCUUAUUCUCAUUCUCGCAGGUCCUGCGCGGAGAAUGUAGUGUUGCACGCUUAAUAACACACCCAUCAUU*******************CAUAAACCCCGCGCCCAAC**AACGCGGGGUUUUUUUGUUUAUGGAUU
Ssed           ******AUGAAAAUUAAAAGUGCAUUACUCAACCUCCUCAUUCUCAUUCUCGCAGAUUCUGCGCGGAGGAUGUAGUGUUGCACGCUCGAUAGAAGUACCAGCAUU*******************CACAAACCCCGCGCUAAC**AACCGCGGGGUUUUUUGUUUUAUAUCCC
Ping           *********AUGAAAUUGUUCUGCCCUAUCCUGCUAUCCUUACUCCUGAUGCAAAAUGCGUACGGGUGAUCGGUGGCUGAAUAAAAUCAGUUAAAUUUCC*************************AAAAACCCGUGCCCU*****GCGCGGGUUUUUUUAUAUCCAUAAUA
CPS            ***AUGACCAAAUUGAUUAAGCACAUUAAAAACAACCUCCUCCUCGCACUCAUCGU***GCGCGGCUAGGUUUUGUUGCUUCUUCAAAAGUUUAAAUAUUGAGAACUAAGUA******GAAAUAAAAUAAAACCCGCGCUAAC**AAUCGCGGGUUUUUUUAUGUCCGCAGUU
MADE           *********AUGCGUAUUCGUUUUCUUCUUCUAUCUCUACUCCUUAUGGCAGCCAGACUGCACGGGUAGAUUGCGACCAGCGAUUCAAAUUCAC*****************************AAAAACCCGUGCCAA*****GCACGGGUUUUUUUUUAACUAUUUAA
ATW7           AUGCAAAAUAUUCGUUUAAUUACACUAAAAACUUAACCUCUUACUGCUAUGGCAAGUAA*GCGGGGAUUAGUGUGUUUGCAUUGAGUUGAACAUU*******************************AAAAACCCCGCAAUU*******GCGGGGUUUUUUUUAUCUCGCGGC
PSHAa          AUGCAUAUUAUUCGUUUAAUUACACUAAAACUGAACCUCUUACUGCUAUGGCAAGUGA*GCGGGGAUUAGUGUGUUUGCAUUGAGCUAAACAU********************************AAAAAAACCCCGCACUU*******GCGGGGUUUUUUUUAUCUCGCGGU
PTD2           AUGCAAAUAACAUCAUUAUUAACACUGAAUAUUAAACUCUCUCUCUUACUUAAGAGCGAUGGGGUUUAGUGUAUUUGCAUUAAGAGAUACGUUAC******************************AAAAACCCCGCUUUA******GUCGGGGUUUUUUUAUGUCUAUAAA
Pat1           ************AUGACAUCAUUACUACUAUCAACUCUACUUCUGCUGGCAGCAAGACUGCACGGGUAGGUUGUAAGCGAAACGCAAACAAUAACU*****************************AAAAACCCGUGCUUAGC**AGCACGGGUUUUUUCGUUUAAGUGCCU
VC0395         ************AUGCGUUUUUCUCUCCUGCUAGGCCUACUACUGAUCGUGGAACCAUCACGCGGGUAGGCUGUGGACGAAAAACACCACACAAGAU*****************************AAAAAACCCGCAGCUGA*****UGCGGGUUUUUUUAUAGCCGAUUUU
VV1            ******AUGACAGCACAUUUUUCUUUCCUACUGAACCUCCUCCUCAUCGUGACAAGAUCGCGCGGGUAGGCUGUGGAAGAAAAAUAAACCACACAGAAUAACAACU**************************AGCCCGCACAUCG****AUGCGGGCUUUUUAUAUCCAAACAC
VAS14          ******AUGAAAAAACGUUUCUCUUUACUCCUUAGCCUCCUCCUUAUCGUGACUUAAAUCGCGCGGUUGCUUUUGAGUGGGAAACGCCACUAAAGAUUUU**************************AAAACCCGCGCAACU***UGCGCGGGUUUUUUCAUAUAUCGACUA
VSAK1          ******GUGUCAUUACGUUUUUCUCUACUCCUGAACCUCCUCCUUAUCGUGAAAACAUCGCGCGGGUAGGUUGUGGACGAAAAACACCACUAAGAAUUCU**************************AAAAAAACCCGCUUAGAC****AAGCGGGUUUUUUUAUAUCGAUUGAA
VEx2w          ******AUGUCAGCUCAUUUUUCUAUUCUGCUUAGCCUCCUCCUGAUCGUGACCAGUUCGCGCGGGUAGGCUGUGGAAGAAAAAUAACCACACCAAUUUCU**************************AAGAACCCGCAUGAGA****AUGCGGGUUUUUUUAUAUCUAAAUAC
V12G01         ******AUGUCAGCUCAUUUUUCUAUCCUGCUUAGCCUCCUCCUGAUCGUGACCAGUUCGCGCGGGUAGGCUGUGGAAGAAAAAUAACCACACCAAUUUCU**************************AAGAACCCGCAUGAGA****AUGCGGGUUUUUUUAUAUCUAAAUAC
A1Q            ******AUGUCAGCACGCUUUUCUAUCCUGCUUAGCCUCCUCCUUAUCGUGACCAAUUCGCGCGGGUAGGCUGUGGAAGAAAAAUAACCACACCAAUUUCU*************************AAGAAACCCGCAUGCAA****AUGCGGGUUUUUUUAUAUCUAAAUAC
VP             ******AUGUCAGCUCAUUUUUCUAUCCUGCUUAGCCUCCUCCUUAUCGUGACCAGUUCGCGCGGGUAGGCUGUGGAAGAAAAAUAACCACACCAAUUUCU**************************UAGAAACCCGCAUGAAA****AUGCGGGUUUUUUUAUAUCUAAAUAC
VF             ******AUGAAAACAGUAUCUUCUUUUGCUCUAAACCUCCUCCUGAUCGUGAACAUCUCACGCGGGUAGGUUAUGGACCAAAAGAAACCAUAAACCAAAUUUU************************AAAACCCGCUAACCA****UGGCGGGUUUUUUUAUGGAUAUCCGU
V12B01         ******AUGAUUUUUUCUUCUUCUCUACUGCUGAAACUUCUCCUUAUCGUGAACCAAUCGCGCGGGUAAGUUGUGGGUCAAGAACUACACAAAUAUU*****************************AAAACCCGCACUGA******GCGGGUUUUUUUGUAACUGGCACU
VSWAT3         ******AUGAUUUUUUCUUCUUCUCGACUGCUGAAACUUCUCCUUAUCGUGAACCAAUCGCGCGGGUAAGUUGUGGGUCAAGAACUACACAAAUAUU*****************************AAAACCCGCGCUGA******GCGGGUUUUUUUGUAACUGGCACU
SKA34          **************************GUGGUGGCACUCCUACUUACGGGCAGUGUGAAUAGCUGUAAUUCAGCAAAAUAACAA******************************************CGAGCCCGCCAUC*****AAUGCGGGCUUUUUUAUAACGGCGAAU
PBPRA          ******AUGAAAAAUCGUUUCUCUUUACUCUUAAGCCUCCUCCUUAUCGUGAAUAAUUCGCGCGGGUAGCUUAUAGGUGAGAAACACCACAUAAGAAUCU***************************AAAAACCCGCGCAGUC***UGCGCGGGUUUUUGCAUAUUACAGAGC
ASA            ******AUGCAUAUUGCCGCUCCGCUACUACUACUCUCCCUA***AUCGCGACCAGUC*GCGCGGGAUCCUUGUAGCCGGGCUCAGGCAUAGCCGGAAUUUAC*************************AAAAACCCGUGCACCCU***GCACGGGUUUUUUUAUGCCGCCGCAG
AHA            ******AUGCGUAUUGCCGCUCCGCUACUACUAAUCUCCCUA***AUCGCGACCAGUC*GCGCGGGAUCCUUGUAGCCGGGCUCAGGCAUAGCCGGAAUUUAC*************************AAAAACCCGUGCACCCU***GCACGGGUUUUUUUAUGCCAACGCAG
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Fig. 35. LEU-regulation of gene *leuA* in actinobacteria. Helix shoulders forming the pseudoknot are in yellow and underlined. The stem of LEU-element is in upper case, the putative Shine-Dalgarno sequence – in italic.

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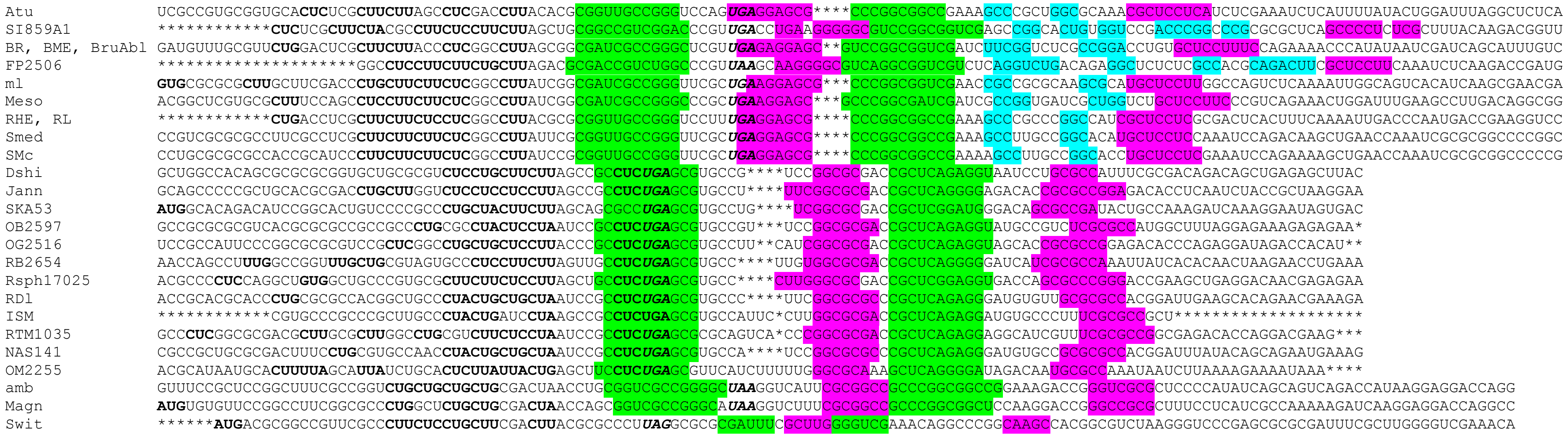
DIP      cuucUCCUUCuu******cgccgcggcgggucacaggcuuaacgucccuuaca****************cacagccggcuc***cccgucgcgga**guucu**********aguguagccggcug************************************************caacaagaacccacguGAAGGAaacua*****
CE       GCUCuUCUUcuu******cgccgcggcgggucccagaggucauaa*************************gcgaccggcac***cccgucgcgga**guuu************guguugccggucgugaacccg*******caacagcgcuagaguuugauuccagaaacaagcgcacacuccacgaAAGAuGAGCa********
cgR      cuacuUCUUCUU******cgccgcggcgggucccagaggucuuaa************************cacgaccggcau***cccgucgcgga**guuu***********gguguugccggucgug*****************************************gacccacccaaaacuuuuuAAGAAGGuugaa******
Jk       cuGCUUCUgcga*********cgcggcggggcucaaagguucuaagagauuuggguuuacagcccaacgaccgaccggca***ccccgucgcgga**cuuu***********ggcguugccggucgggaaaaca***********************************accaagaacaaacaauucuucucAGGAGCcc******
Krad     gagaacCUCCUCCUUC***gucgccgcggcggggccag*******************************cuaggccggucu**ccccgucgcgggaccucgucgu********gcg*cgccggcc**************************************gccgcaccagccgcugaagaccgcGAACGAGGAGaacgaa***
MAV      cgggUGCUCCuccucggacgccgcgacggggucugauu*******************************ccagaccggcuu***cccgucgcgggu*guucgc*********gaug*cgccggucug**********************************************agguuccuucugauauccccGGAGCAaucacc*
BCG      cgggUGCUCCuccucggacgccgcgacggggucugau********************************ccagaccggcuu***cccgucgcgggacguucgc*********gaug*cgccggucug**********************************************agguuccuucucaccaucccGGAGCAacuacc*
Aaur     augcuUCUUcuu***agcugccgcggcgaggccugaaagcuauc************************ugaagcugggccau*ccucgccgcgga**guucc**********guuguguccggcuaagcuuuca*****************************************cuuaguucuuagagaaAAGGccacacguc**
Arth     gaacugCUUcuucuuagcugccgcggcgaggccucagacgcgaucuagcgc***********************aaggccaauccucgucgcgga**guugu**********guug**cccggccaccuuucac******************************************ccaggaaccacagaaaAGGccccgauagua
ML       cagguaCUCCuccucgaacgccgcgacggggucugau*******************************cccagaccggcug***cccguuguggaa*guucacu*********aug*cgccggucug**********************************************agguuccuucucacauc*ccGGAGcaauuauu*
MtubH    cgggugCUCCuccucggacgccgcgacggggucugau********************************ccagaccggcuu***cccgucgcgggacguucgc*********gaug*cgccggucug**********************************************agguuccuucucaccaucccGGAGcaacuacc*
SAV      gcacuccucCUCCuuggucgccgcgacgaggccuga***********************************cggccggcac***cucgucgcggg**gucgaa**********ccg*cgccgcccacagcacgcuccgaccg*****accuucggcgccucgccgaccucgacugcugacgucgcaugaccacGGAGgcacuccgc
Strop    gcguugcuuCUCCuuggucgccgcggcggggccuga***********************************cggccggcac***cucgucgcggg**gucgaa**********ccg*cgccgcccgcuccg***********acccguucuucggcgccucgccgaccucgacugcugacgucacaugaccacGGAGgcacuccgc
Mkms     cgggcgCUCCuucucggccgccgcggcggggucuga*********************************ccagaccggcuu***cccgucgcgggu*guucgc*********gaug*cgccggucga************************************************gucccucgucaaacucccGGAGcaaucgauc
Mma      cgggUGCUCCuccucggacgccgcgacggggccugau********************************ccagaccggcuu***cccgucgcggg*uguucg*********cgaug*cgccggucugaa*********************************************guuccuucucgccacccccGGAGCAacuacc*
Blin     agguugcUCCUCcuuccuugccgcgacgaguccugau**********************************cggacagcaca**cucgucgcgga**guuuuu*********caua*ugcugauuuag***********************************************cacacgaugaaugauuGAGGAacc*******
RHA1     gcacucCUCCuu***gguugccgcgacggggucugau********************************ccagacuggcuu***cccgucgcggg**guuu*********cucgug*cgccggucgacac******************************agccguuggacucagaaaguccacaucgaaucuGGAGaucaauccc
MAR      cugcucCUCCuu***agcugccgcgacgaguccuaau************************************ccaggccc**acucgucgcgga**guuuguc**********auuggcugaccagauccguaacga****************************guggcccacaaggcuuugagaacagcaGGAGcacaga***
MSMEG    cggguGCUCCuucucggacgccgcggcggggucuga*********************************ucagaccggcuu***cccgucgcggg*uguuu********cgcgaug*cgccggucga**************************************************gucccguccaacucccGGAGCcaagaacu
Mvan     cggguGCUCCuucucggacgccgcgacggggucuga*********************************ccagaccggccu***cccgucgcggg*uguuu********cgcgaug*cgccggucugaaguccc**********************************************cuagaccuuuuccGGAGCaccgaa**
MUL      cggguGCUCCuccucggacgccgcgacggggccugau********************************ccagaccggcuu***cccgucgcggg*uguucgc*********gaug*cgccggucugaag*********************************************uuccuucucgccacccccGGAGCaacuacc*
Franean1 gcgcugCUUCuucuuaggugccgcggcggggccugauccgauccgga********************gagauggcuggcuu**ccccgccgcgga**guucuc**********gug*cgucagcgcuggguccc***************************gcucggcgggggauaaccgccggcucuuccgagGAAGcaggagca
FRAAL    cugcuccuccuu***agccgccgcggcggggccugau*********************************ccagcuggcuu**ccccgucgcgg**uguucuc**********gug*cgccagcguc*******gggauccucgcggucaugguggcccggcggucacgcccagcccgggcggccgcccguccggcgc********
Francci3 cugcuuCUCCUu***agccgccgcggcggggccugau******************************accugagcuggcuu**ccccgucgcgg**uguuuuc**********gug*ugucagcgucgggauccucgccauccggcgguccagcguccaggugcgaccugacgcuccucugcuggaggaagcAGGAGca*******
Noca     cucgcguucuccucgcggcuucgccgcgggagaucggcuga****************************gacguucgagcguucauugccgaugaccggcaaagggucagcccgca*agcaggauga***cgugaccgcaacucggccccugcgguggucugagccggagguucugucccugcgacgcgaccugga**********
Mgil     cguguGCUCCuucucggacgccgcgacggggucugau********************************ccagaccggcuu***cccgucgcggg*uguucgc**********gaugcgccggucug***********************************************acuuccccaagaccuuuccGGAGCacccc***
CLAV     ggccgcCUCCUCcuuagucgccgcggcgaggccugau*************************************ccggcccu*ccucgucgcgga**guccc**************gucacggcugac****************************************************ccgauaccgacGAGGAGacgacc***
Sare     gggcuGCUCCUCcuuagcugccgcggcgagggccuguaag****************************cagaggccgaccc**cccuccccgcgg**agucuggc******guugcgccgucggccg*************************************************uccuuccggacaccacGAGGAGCccacgcau
SCO      GGGCUgCUUCuccuuagcugccgcggcgagggccuguag********************************aggccgacu**cccuccccgcgg**agcuuggu********ggugccgucggccguccuuccg*************gacacgcggacgacgcggacaccgccgagauccgcggacaucacGAGGAGCCCacgcca
Tfu      gagcuGCUCCUGcuuagcggccgcggcgggggccgauaa********************************gggccggcu**cccucgccgcgga*gguucgacc*****ugucugcugucggccg******************************************cacgaccgcaagaaaaagucucaCGGGAGCguauucac
Lxx      ggcCUGAUUCUCcuuagcugccgcgacgaauccuaag***********************************uuccgggccuccuucgucgcgg**aguuc**************gucguuggcucuccc*****************************************gaccagaccgcgaaGAGAuAUCGGacc********
Nfa      cgggcucUUCUUCucggccgccgcgacggggucugau*********************************cggaccggc****ucccgucgcgg**gguu***********aagccgugccggucgaccc****************************************auuacuggauuccaccaacccuGGAGAAuugc***
Anae     gugagcCUCCUGcuuagucgccgcggcggggccuga**********************************caggccggca**ccccgaccgcggc*ugacuc**********guccugcucggccacguucgcg**********************************************gccgcguuccuCAGGAGucag*****
Amin     GCAAGAcUucuucuauggacagauuaguaguaucuauaa********************uuaucgcaucucgcgccgguuu*******uaguggagcuauugaa****************cgguuuga****************************************************AUCaUUGUaaucccuacuuuuuauuu
JNB      cgucuccUUCUUcucu***gccgcggcgaggccugaa*********************************ucggcccu*****ccucgucgcggag**uucgcu*********gugcccauggcugagcacacg*******************************************acgagcagugaguaGAGGcgagaa*****
SACE     acgCGGGGcGAGCuuacucgccgcggcaggggcuga**********************************cgggccggcg***accugcugcggggaggucgc**********gca*cgccgguccacc*********************************************guccgguGUUCUCCCGaaaggucaccc*****
Acel     uaccuucugcUGCuCGG*cg*cguugcgggcccuga***************************cgagcaacggcacgau*********gcccggcu*gauauu******cgaugcauuugugcugcgggc***************************************gcucgcgacguccgguuaucaaCCGGCGcuggaugac
Micro    cgGGUGCUccuccucggacgccgcgacggggucugauc********************************cagaccggcuu***cccgucgcgggacguucgcg***********acacuaggaagc****************************agcacuaaugauuuucuuaucuucuccgcAGCAUCgacggcgccagccgac
Mflv     cguGUGCUCCuucucggacgccgcgacggggucugauc********************************cagaccggcuu***cccgucgcggguguucgcgaug***********cgccggucug***********************************************acuuccccaagaccuuuccGGAGCACccc***
Req      cgcgcgCUCCuucuuggguggccgcggcggggucugauc********************************cagacuggcc***acccgucgcggguccucuccgug***********cgccggucgccu*****************************cagcugucgggcucucuacaguccacaaccaaccuGGAGaucgauucc
SCA      GGGCUgCUUCuccuuagcugccgcggcgagggccuguagucg*****************************aggccgaccc**cccuccccgcggugcuuuggcguugcg*******ucgucggccg*************************************************uccuuuccggaccaucGAGGAGCCCacgcau
RTFU     GAGCUgcuccugcuuagcggccgcggcgggggccgauaa********************************gggccggcu**cccucgccgcggagguucgaccugucugc******ugucggccgc******************************************acgaccgcaagaaaaAGuCUCACGggagcguauucac
BLO      ggcguggaUCUGGagggcggccgcgacgug**cugggc*****************************aucugggcgucg*****cccgccgcggagggcgcacgcu*****auuggcugucggugcucac************************************************cgagcugaagaaCCGGGgc*********
```

Fig. 36. LEU-regulation of gene *leuA* in α-proteobacteria. The start and regulatory codons of the leader peptide are in bold, the stop codon is in bold italic, the left shoulder – in green, the right shoulder – in violet.



```
Atu              UCGCCGUGCGGUGCACUCUCGCUUCUUAGCCUCGACCUUACACGCGGUUGCCGGGUCCAGUGAGGAGCG****CCCGGCGGCCGAAAGCCCGCUGGCGCAAACGCUCCUCAUCUCGAAAUCUCAUUUUAUACUGGAUUUAGGCUCUCA
SI859A1          ************CUCUCGCUUCUACGCCUUCUCCUUCUUAGCUGCGGCCGUCGGACCCGUUGACCUGAAGGGGGCGUCCGGCGGUCGAGCCGGCACUGUGGUCCGACCCGGCCCGCGCGCUCAGCCCCUCUCGCUUUACAAGACGGUU
BR, BME, BruAbl  GAUGUUUGCGUUCUGGACUCGCUUCUUACCCUCGGCCUUAGCGGCGAUCGCCGGGCUCGUUGAGAGGAGC**GUCCGGCGGUCGAUCUUCGGUCUCGCCGGACCUGUGCUCCUUUCCAGAAAACCCAUAUAAUCGAUCAGCAUUUGUC
FP2506           *********************GGCCUCCUUCUUCUGCUUAGACGCGACCGUCUGGCCCGUUAAGCAAGGGGCGUCAGGCGGUCGUCUCAGGUCUGACAGAGGCUCUCUCGCCACGCAGACUUCGCUCCUUCAAAUCUCAAGACCGAUG
ml               GUGCGCGCGCUUGCUUCGACCCUGCUUCUUCUCGGCCUUAUCGGCGAUCGCCGGGUUCGCUGAAGGAGCG***CCCGGCGGUCGAACCGCCGCGCAAGCGCAUGCUCCUUGGCCAGUCUCAAAAUUGGCAGUCACAUCAAGCGAACGA
Meso             ACGGCUCGUGCGCUUUCCAGCCUCCUUCUUCUCGGCCUUAUCGGCGAUCGCCGGGCCCGCUGAAGGAGC***GCCCGGCGAUCGAUCGCCGGUGAUCGCUGGUCUGCUCCUUCCCGUCAGAAACUGGAUUUGAAGCCUUGACAGGCGG
RHE, RL          ************CUGACCUCGCUUCUUCUCCUCGGCCUUACGCGCGGUUGCCGGGUCCUUUGAGGAGCG****CCCGGCGGCCGAAAGCCCGCCCGGCCAUCGCUCCUCGCGACUCACUUUCAAAAUUGACCCAAUGACCGAAGGUCC
Smed             CCGUCGCGCGCCUUCGCCUCGCUUCUUCUUCUCGGCCUUAUUCGCGGUUGCCGGGUUCGCUGAGGAGCG****CCCGGCGGCCGAAAGCCUUGCCGGCACAUGCUCCUCCAAAUCCAGACAAGCUGAACCAAAUCGCGCGGCCCCGGC
SMc              CCUGCGCGCGCCACCGCAUCCCUUCUUCUUCUCGGCCUUAUCCGCGGUUGCCGGGUUCGCUGAGGAGCG****CCCGGCGGCCGAAAAGCCUUGCCGGCACCUGCUCCUCGAAAUCCAGAAAAGCUGAACCAAAUCGCGCGGCCCCCG
Dshi             GCUGGCCACAGCGCGCGCGGUGCUGCGCGUCUCCUGCUUCUUAGCCGCCUCUGAGCGUGCCG****UCCGGCGCGACCGCUCAGAGGUAAUCCUGCGCCAUUUCGCGACAGACAGCUGAGAGCUUAC
Jann             GCAGCCCCCGCUGCACGCGACCUGCUUGGUCUCCUCCUCCUUAGCCGCCUCUGAGCGUGCCU****UUCGGCGCGACCGCUCAGGGGAGACACCGCGCCGGAGACACCUCAAUCUACCGCUAAGGAA
SKA53            AUGGCACAGACAUCCGGCACUGUCCCCGCCCUGCUACUUCUUAGCAGCGCCUGAGCGUGCCUG****UCGGCGCGACCGCUCGGAUGGGACAGCGCCGAUACUGCCAAAGAUCAAAGGAAUAGUGAC
OB2597           GCCGCGCGCGUCACGCGCGCCGCCGCCCUGCGCCUACUCCUAAUCCGCCUCUGAGCGUGCCGU***UCCGGCGCGACCGCUCAGAGGUAUGCCGUCUCGCGCCAUGGCUUUAGGAGAAAGAGAGAA*
OG2516           UCCGCCAUUCCCGGCGCGCGUCCGCUCGGCCUGCUGCUCCUUACCCGCCUCUGAGCGUGCCUU**CAUCGGCGCGACCGCUCAGAGGUAGCACCGCGCCGGAGACACCCAGAGGAUAGACCACAU**
RB2654           AACCAGCCUUUGGCCGGUUUGCUGCGUAGUGCCCUCCUUCUUAGUUGCCUCUGAGCGUGCC****UUGUGGCGCGACCGCUCAGGGGGAUCAUCGCGCCAAAUUAUCACACAACUAAGAACCUGAAA
Rsph17025        ACGCCCCUCCAGGCUGUGGCUGCCCGUGCGCUUCUUCUCCUUAGCUGCCUCUGAGCGUGCC****CUUGGGCGCGACCGCUCGGAGGUGACCAGCGCCCGGGACCGAAGCUGAGGACAACGAGAGAA
RDl              ACCGCACGCACCCUGCGCGCCACGGCUGCCCUACUGCUGCUAAUCCGCCUCUGAGCGUGCCC****UUCGGCGCGCCCGCUCAGAGGGAUGUGUUGCGCGCCACGGAUUGAAGCACAGAACGAAAGA
ISM              ************CGUGCCCGCCCGCUUGCCCUACUGAUCCUAAGCCGCCUCUGAGCGUGCCAUUC*CUUGGCGCGACCGCUCAGAGGAUGUGCCCUUUCGCGCCGCU********************
RTM1035          GCCCUCGGCGCGACGCUUGCGCUUGGCCUGCGUCUUCUCCUAAUCCGCCUCUGAGCGCGCAGUCA*CCCGGCGCGACCGCUCAGAGGAGGCAUCGUUUCGCGCCGGCGAGACACCAGGACGAAG***
NAS141           CGCCGCUGCGCGACUUUCCUGCGUGCCAACCUACUGCUGCUAAUCCGCCUCUGAGCGUGCCA****UCCGGCGCGCCCGCUCAGAGGGAUGUGCCGCGCGCCACGGAUUUAUACAGCAGAAUGAAAG
OM2255           ACGCAUAAUGCACUUUUAGCAUUAUCUGCACUCUUAUUACUGAGCUUCCUCUGAGCGUUCAUCUUUUUGGGCGCAAAGCUCAGGGGAUAGACAAUGCGCCAAAUAAUCUUAAAAGAAAAUAAA****
amb              GUUUCCGCUCCGGCUUUCGCCGGUCUGCUGCUGCUGCGACUAACCUGCGGUCGCCGGGGCUAAGGUCAUUCGCGGCCGCCCGGCGGCCGGAAAGACCGGGUCGCGCUCCCCAUAUCAGCAGUCAGACCAUAAGGAGGACCAGG
Magn             AUGUGUGUUCCGGCCUUCGGCGCCCUGGCUCUGCUGCGACUAACCAGCGGUCGCCGGGCAUAAGGUCUUUCGCGGCCGCCCGGCGGCUCCAAGGACCGGGCCGCGCUUUCCUCAUCGCCAAAAAGAUCAAGGAGGACCAGGCC
Swit             ******AUGACGCGGCCGUUCGCCCUUCUCCUGCUUCGACUUACGCGCCCUUAGGCGCGCGAUUUCGCUUGGGGUCGAAACAGGCCCGGCAAGCCACGGCGUCUAAGGGUCCCGAGCGCGCGAUUUCGCUUGGGGUCGAAACA
```

Fig. 37. LEU-regulation of gene *leuA* in β-proteobacteria. Designations as in Figure 36.

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BP,BB,BPP ***************GUGUCCCCCACCGCCCUAUCGCUACUACGCCUACCGAUCGGUUGCCGGGCCUAGUGCCCCGUGGUA*GCUCGGCAGCCGUACGCUCGCCACACGCGUUUUCCCCCGUUUUAUUAAACUGAAUCCGGCCGAUUUACGG
H16       CUGGCAUCGGGCCGCGCCCUGCGCGCUUCCUCGCUACUGCUAAGCCUAUCGACCGGUUGCCGGGCCUAGUGCCCCGUGGCA*GUUCGGCAGCCUUUC****GCCACCGUUUCUUCCGUUUUUCCUUUACUUCCCUUAG*************
Rmet      CUGCUGUCGUGCCGCGCCCUGGGCGCUUCCUCGCUACUGCUAAGCCUACCGAUCGGUUGCCGGGCCUAGAGCCCUGUGGCA*GUUCGGCAGCCUUUC****GCCACCGUUUUUCCGUCCGUUUUCCGUUUUUGACGCAUUCGUCGCAUCUUC
mma       ************AUGAGCUUCGCUCGUUCAUUGGCUUUGCUAUUGCUACCGAUCGGUUACCUGACCUAGCGCAC*GUGGCA*GUCAGGUAGCCCAAU***CGCCACCCCUGACGCUUUCCCCGAUUGAACCGAAUUUAAGGAUUUAUC****
HEAR      GCAACAUUGUCCGCCGCGAUCGCCCAUGCUCGCGCUCUGCUACUGCUACCGAUCGGUUAUCUGGCCUAGCGUUGCGUGGCAAGUCAGGUAGCCUUCC****GCCACACCGAAUCUCCCCUAUUCAGCAAGCAAGGAAAAACCAUCAUGAUGU
Bavium    AUCUCCCUCCUGGGCACUUUCGCUGCCCUAGCGCUACCGCUACGCCUACCGAUCGGUUGCCGGGCCUAGUGCCCCGUGGUA*GCUCGGCAGCCGUUCGCUCGCCACACGUCUUUCCCCUGUUUUAAACCCUGAAUUCGCCUGCGCCG*****
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