

	σ factor: name [known/deduced consensus if available]
	known promoters (when no consensus can be clearly deduced)
	SIGffRid output motifs

^{m4} links SIGffRid motifs to known promoter(s) it overlap

Table 1: SIGffRid results compared with known SFBSs motif

Motifs are presented as follow: DNA_motif (R ratio, LRT likelyhood ratio test).
(for *S. coelicolor*: $R \geq 0.48$, $LRT \geq 3.84$; for *S. avermitilis*: $R \geq 0.44$, $LRT \geq 3.84$)

σ factor: HrdB	
known HrdB-dependent promoters overlapped by SIGffRid output motifs	
?n ₇ taggct (SCO0598 ^{m4} , sigBp2) [1]	
ttgaccn ₁₈ tacggg (SCO1429 ^{m3} , chiD) [2, 3]	
ttgacan ₁₈ cacctt (SCO5003 ^{m1m2} , chiA) [3]	
ttgaccn ₁₇ tattct (SCO5376 ^{m3} , chiC) [2, 3]	
ttgacan ₁₇ caaatt (SCO5673 ^{m1} , chiB) [3]	
ttgacan ₁₇ tagatt (SCOr09 ^{m1} , rrnDp2) [4, 5]	
other HrdB promoters strongly similar to SIGffRid motifs	
tgggcan ₁₈ taggat (SCO2026, gltBp1) [6]	
ttgagcn ₁₈ taggtt (SCO0561, furA) [7]	
ttgtcan ₁₈ tagcat (SCO3471) [8]	
ttgactggn ₁₄ ttgagt (SCO7263, chiF) [3]	
ttgaacn ₁₈ tagtgt (SCO2082, ftsZ2p) [9]	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
tgacan _{17,20} an ₃ t (0.50, 116.11) ^{m1}	
ttgacn _{19,20} ancnt (0.61, 65.76) ^{m2}	ttgacn _{18,19} tac (0.47, 28.69)
ttgan _{18,19} cta (0.60, 62.49) ^{m3}	ttgan _{18,19} cta (0.49, 43.35)
	ttgn _{18,20} ccta (0.47, 67.51)
	ttgn _{17,19} cata (0.47, 45.32)
cngn _{18,21} taggct (0.67, 100.33) ^{m4}	cngn _{18,22} taggct (0.62, 101.89)
σ factor: SigR ggaatn₁₈ggt [10]	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
ggaatn _{16,19} ggt (0.49, 54.69)	ggaatn _{17,19} ggtg (0.51, 30.98)
gggaan _{18,20} cggt (0.48, 42.97)	
	ggaatn _{17,18} ggtg (0.44, 25.36)
σ factor: BldN cgtaacn₁₆cggtga (SCO4768) [11]	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
cgtaan _{18,19} ggt (0.57, 20.04)	gtaacn _{17,18} ggt (0.52, 17.81)

σ factor: ? , motif similar <i>Bacillus subtilis</i> SigE binding site [12] <i>catattn</i> ₁₄ <i>cataca</i>	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>catan</i> _{15,17} <i>tac</i> (0.54, 35.40)	
σ factor (?) involved in sporulation regulation	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>cngn</i> _{14,16} <i>agtaa</i> (0.49, 67.26)	
<i>agtaan</i> _{13,15} <i>cng</i> (0.48, 58.48)	
DNA-damage inducible promoters motif <i>ttgtcagtggn</i>₆<i>taggg</i> [13]	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>tgtcagtn</i> _{14,15} <i>tng</i> (0.59, 37.76)	<i>tgtcagtn</i> _{14,15} <i>tng</i> (0.49, 36.73)
<i>tgtcagtn</i> ₁₄ <i>tng</i> (0.63, 36.63)	
SIGffRid output motifs (spacer range: 8 to 14)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>tgtcagtn</i> _{9,12} <i>ang</i> (0.85, 62.24)	
<i>tgtcagtn</i> _{12,14} <i>tng</i> (0.64, 43.08)	<i>tgtcagtn</i> _{12,14} <i>tng</i> (0.48, 36.05)
TFBS consensus for: BldD <i>agtgan</i>_m<i>tcacc</i> (SCO) [14]	
SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>[ta]gtgan</i> _{18,20} <i>tn</i> ₂ <i>c</i> (0.57, 269.95)	<i>[ta]gtgan</i> _{18,20} <i>tn</i> ₂ <i>c</i> (0.48, 242.80)
<i>[ta]gtgan</i> _{16,18} <i>cnt</i> (0.55, 290.18)	<i>[ta]gtgan</i> _{15,19} <i>gn</i> ₂ <i>t</i> (0.47, 400.42)
<i>tgtn</i> _{18,20} <i>tna</i> (0.50, 69.54)	<i>tgtn</i> _{18,20} <i>tna</i> (0.49, 99.17)
<i>tnan</i> _{16,18} <i>tgtga</i> (0.57, 101.85)	<i>tnan</i> _{16,18} <i>tgtga</i> (0.46, 100.52)
<i>tgtn</i> _{17,18} <i>tnt</i> (0.55, 76.95)	
<i>tntn</i> _{16,19} <i>ctgtga</i> (0.48, 35.58)	
Other interesting SIGffRid output motifs (spacer range: 14 to 20)	
<i>S. coelicolor</i>	<i>S. avermitilis</i>
<i>taan</i> _{17,21} <i>gtta</i> (0.73, 27.68)	<i>taan</i> _{17,21} <i>gtta</i> (0.48, 18.33)
<i>cgggn</i> _{13,15} <i>tta</i> (0.48, 80.37)	
<i>cccg</i> _{14,15} <i>gtaa</i> (0.52, 45.87)	

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