

Table 1. Putative attenuation regulation in bacteria. 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						
$\alpha$ -proteobacteria	<i>ilvB, I</i>	<i>trpE</i>	<i>hisS</i>	<i>pheST</i>	<i>thrA</i>	<i>leuA</i>	<i>leuA</i>
$\beta$ -proteobacteria	<i>ilvB</i>	<i>trpE</i>		<i>pheA</i>	<i>thrS</i>	<i>leuA</i>	<i>leuA, ilvB</i>
$\gamma$ -proteobacteria	<i>ilvB, G</i>	<i>trpE</i>	<i>hisG</i>	<i>pheA, S</i>	<i>thrA</i>	<i>leuA</i>	
$\delta$ -proteobacteria	<i>ilvB</i>	<i>trpS</i>			<i>thrA, S</i>	<i>leuA</i>	
Actinobacteria	<i>ilvB, I, D</i>	<i>trpE, S, BE, BA</i>					<i>leuA</i>
Bacteroides/Chlorobi	<i>ilvD</i>	<i>trpE</i>	<i>hisG</i>				
Firmicutes	<i>ilvD, lysQ</i>	<i>trpB</i>	<i>hisZ</i>				
Thermotogae		<i>trpE</i>	<i>hisS</i>				
Chloroflexi	<i>ilvD</i>						