

**Table S1:** Strains and plasmids used in this study.

<b>Strains</b>		
<i>B. cenocepacia</i> J2315	Wild type (Wt), ET-12 lineage, CF isolate, LMG 16656	Lab collection
$\Delta brrF$	J2315 <i>brrF</i> deletion mutant	This study
Wt-VC	J2315 + pSCrhaM2	[8]
Wt-pBrrF-d1	J2315 + pM2- <i>brrF</i> -d1	This study
Wt-pBrrF-d2	J2315 + pM2- <i>brrF</i> -d2	This study
Wt-pBrrF-d3	J2315 + pM2- <i>brrF</i> -d3	This study
$\Delta brrF$ -VC	$\Delta brrF$ + pSCrhaM2	This study
$\Delta brrF$ -pBrrF-d1	$\Delta brrF$ + pBrrF-d1	This study
$\Delta brrF$ -pBrrF-d2	$\Delta brrF$ + pBrrF-d2	This study
$\Delta brrF$ -pBrrF-d3	$\Delta brrF$ + pBrrF-d3	This study
<b>Plasmids</b>		
pSCrhaM2	Derivative of pSCrhaB2, RBS and start codons removed, <i>ori<sub>pBBR1</sub></i> , <i>rhaR</i> and <i>RhaS-P<sub>rhaB</sub></i> , T <sub>p</sub> <sup>r</sup>	[8]
pBrrF-d1	pSCrhaM2 overexpressing sRNA BrrF from 80 nt upstream of the putative processing site to 49 nt downstream of the computationally predicted terminator	This study
pBrrF-d2	Derivative of pBrrF-d1, overexpressing BrrF from the putative processing site to 49 nt downstream of the computationally predicted terminator	This study
pBrrF-d3	Derivative of pBrrF-d1, with point mutations at position 8 and 9, replacing guanosine residues with cytosine residues	This study