

In silico Work Preformed

Stage 1 - Shuttle Vector Design

Shuttle vectors with based on the pMTL8000 modular vector series were designed to quickly test which ketone production operon (KPO) would be most suitable before stable integration into the *C. sporogenes* genome.

Shuttle Vectors designed for KPO DBHB_A

The following plasmid vectors variants in table 1 below have been designed for testing of the DBHB_A operon.

Table 1 - List of pMTL8000 modular shuttle vectors designed to test KPO DBHB_A.

Vector	Description	Vector Map	Primer table (Primers to amplify fragments with overhangs suitable for HiFi assembly)	Gel of expected fragments needed to assemble vector (run on a 1% agarose gel)
pMTL82151-Px-DBHB _A	No promoter as a negative control - no expression of KPO genes.	Figure 1-A.	Table 2	Figure 1-B.
pMTL82151-Pntnh-DBHB _A	Expression of KPO genes dependent upon sigma factor <i>botR</i> expression.	Figure 2-A.	Table 3	Figure 2-B.
pMTL82151-Plac-DBHB _A	Expression of KPO genes dependent on presence of lactose (inducible system)	Figure 3-A.	Table 4	Figure 3-B.
pMTL82151-Pfdx-DBHB _A	Constitutive expression of KPO genes using the native <i>fdx</i> promoter as a positive control.	Figure 4-A.	Table 5	Figure 4-B.

DBHB_A KPO vector maps, primer tables and agarose gel simulations

pMTL82151-Px-DBHB_A

Table 2 - Primer table to amplify fragments needed to assemble pMTL82151-pX-DBHB_A by HiFi assembly

Gene Name/ Fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Thiolase (<i>thl</i>)	thl_pMTL_Px_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	ctgtatccatatgaaagaag ttttaatagcttag	1199
	thl_pMTL_(A)_R		ccttttaaatctgacttttc tagcaatattg	
Acetoacetate CoA- transferase subunit A/B (<i>ctfA</i> / <i>B</i> & <i>ctfB</i>)	ctfA/B_pMTL_(A)_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtgttagatttaaagg agggattaaaatgaac	1363
	ctfA/B_pMTL_(A)_R		tcgtctttctcaaacagcca tgggtctaag	
3-hydroxybutanoate dehydrogenase (<i>bdhA</i>)	bdhA_pMTL_(A)_F	<i>Streptococcus</i> <i>dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttagagaaagacg aggatagtatc	509
	bdhA_pMTL_(A)_R		ttattttatgctacaataa gctgatccc	
Vector Backbone	Vec_pMTL_(A)_F	pMT82151	ttatttgtagcataaaaata agaagctgcatt	5010
	Vec_pMTL_Px_R		cttcattcatatggatacagc ggccgcg	

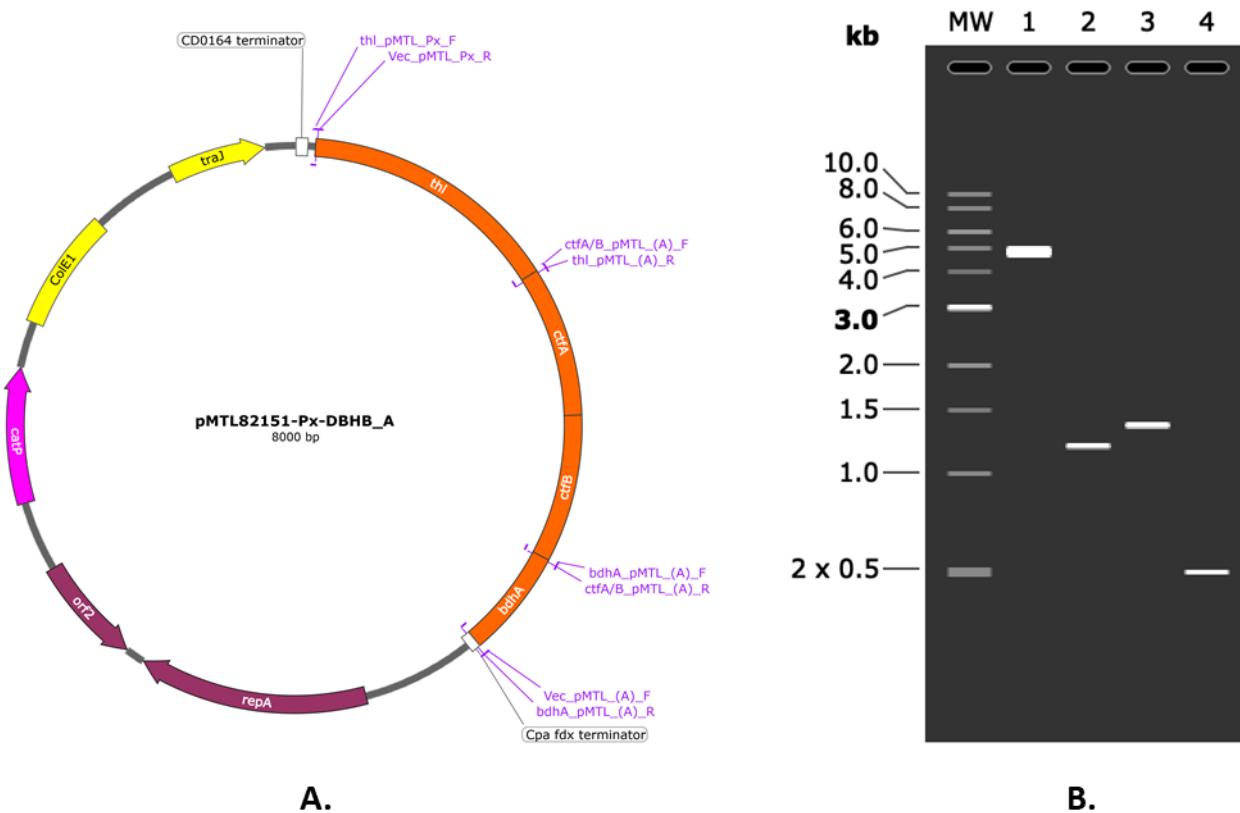
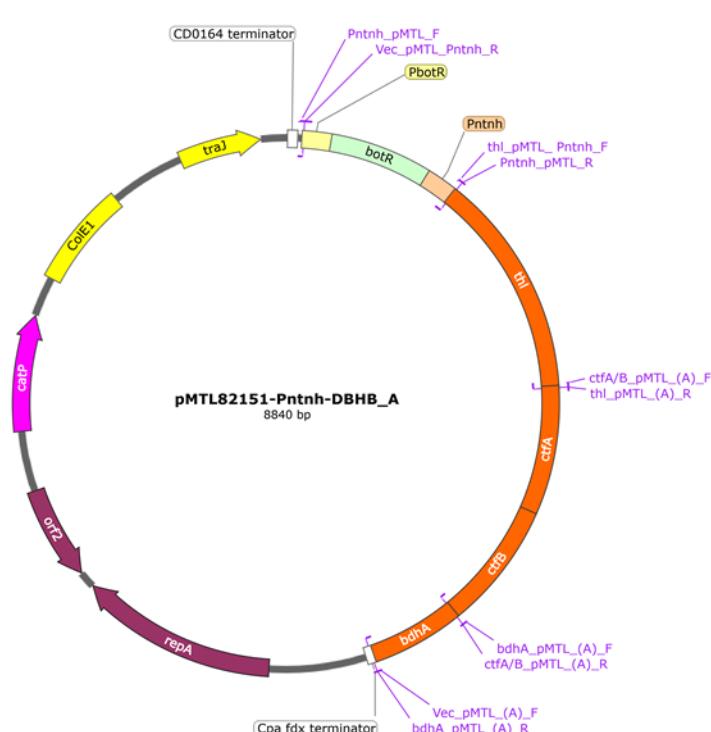


Figure 1 - pMTL82151-Px-DBHB_A Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-thl; 3-ctfA/B; 4- bdhA.

pMTL82151-Pntnh-DBHB_A

Table 3 – Primer table to amplify fragments needed to assemble pMTL82151-pntnh-DBHB_A by HiFi assembly.

Gene Name/ Fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Pntnh promoter	Pntnh_pMTL_F	<i>C. botulinum</i> ATCC 3502 gDNA	atgagtcgaccctaaaatttaaatatcaaattttttatgtttac	873
	Pntnh_pMTL_R		cttcttcataatctaaccaccctctaaatttttcc	
Thiolase (<i>thl</i>)	thl_pMTL_Pntnh_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	gtggtagatgaaagaaggtagttatagcttag	1199
	thl_pMTL(A)_R		cctttaaatctagactttctagcaatattg	
Acetoacetate CoA- transferase subunit A/B (<i>ctfA</i> / <i>B</i>)	ctfA/B_pMTL(A)_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtctagattaaaaggaggataaaatgaa	1363
	ctfA/B_pMTL(A)_R		tgcgtttctctaaacagccatgggtctaag	
3-hydroxybutanoate dehydrogenase (<i>bdhA</i>)	bdhA_pMTL(A)_F	<i>Streptococcus</i> <i>dysgalactiae</i> <i>subsp. equisimilis</i> AC2713 gDNA	ggctgttagagaaaagacgaggatgtatc	509
	bdhA_pMTL(A)_R		ttattttatgtacaaaataagctgattttcc	
Vector Backbone	Vec_pMTL(A)_F	pMTL82151	ttattttagcataaaaataagaaggctgcatt	4997
	Vec_pMTL_Pntnh_R		aaattttagggtcgactcatagctgtttc	



A.

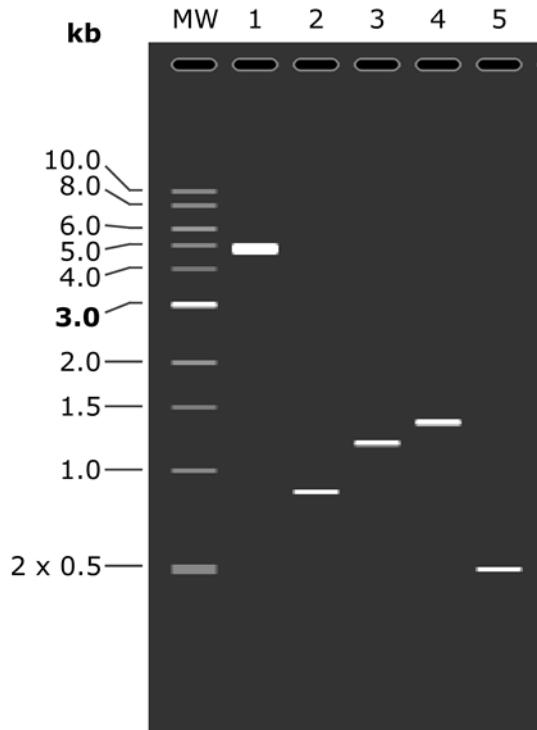
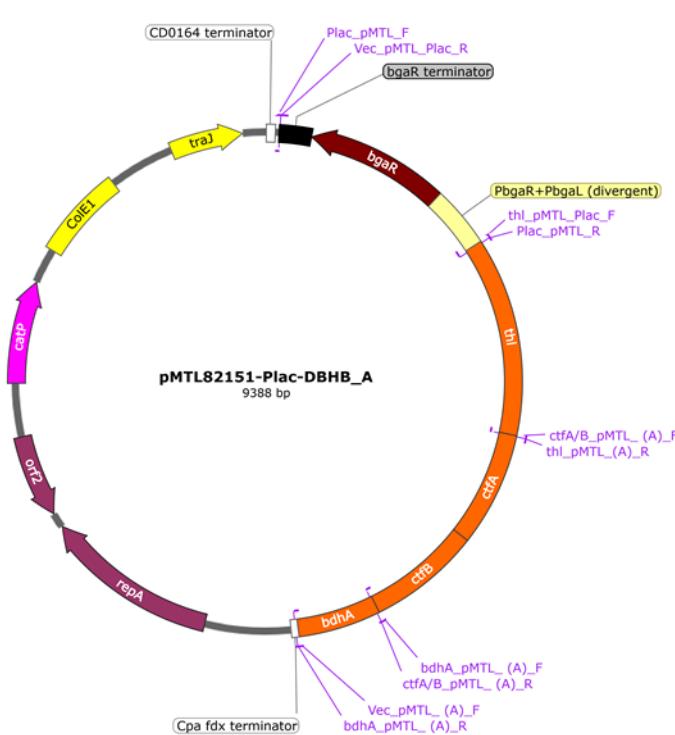


Figure 2 - pMTL82151-Pntnh-DBHB_A Vector plasmid annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Pntnh; 3-thl; 4-ctfA/B; 5-bdhA.

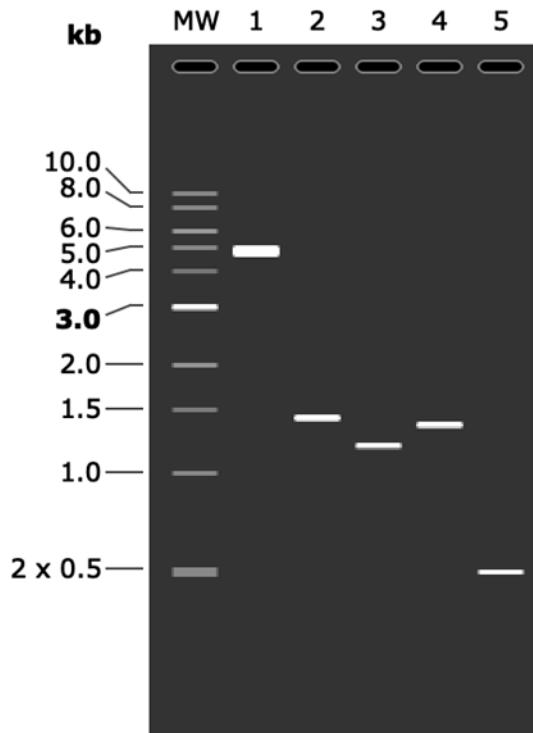
pMTL82151-Plac-DBHB_A

Table 4 - Primer table to amplify fragments needed to assemble pMTL82151-plac-DBHB_A by HiFi assembly.

Gene Name/ Fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Plac promoter	Plac_pMTL_F	<i>C. perfringens</i> gDNA	atgaggctgactaatttagat attaattctaaattaatgtcaa ataaatatag	1421
	Plac_pMTL_R		cttcttcatatccatccc atacatataaaataattatg	
Thiolase (<i>thl</i>)	thl_pMTL_Plac_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	ggagggtaaaatgaaagaa gtttaatagctag	1199
	thl_pMTL_(A)_R		ccttttaatcttagacttttc tagcaatattg	
Acetoacetate CoA- transferase subunit A/B (<i>ctfA</i> / <i>B</i> & <i>ctfB</i>)	ctfA/B_pMTL_(A)_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtcttagatttaaagg agggattaaaatgaac	1363
	ctfA/B_pMTL_(A)_R		tcgtcttctctaaacagcca tgggtctaag	
3-hydroxybutanoate dehydrogenase (<i>bdhA</i>)	bdhA_pMTL_(A)_F	<i>Streptococcus</i> <i>dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttttagagaaagacga ggatagtatc	509
	bdhA_pMTL_(A)_R		ttattttatgtctacaataaa gctgatttcc	
Vector Backbone	Vec_pMTL_(A)_F	pMTL82151	ttattttagcataaaaataaa gaaggcctgcatt	4997
	Vec_pMTL_Plac_R		atctaaatttagtcgactcata gctgttcc	



A.



B.

Figure 3 - pMTL82151-Plac-DBHBA Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Plac; 3--thl; 4-ctfA/B; 5-bdhA.

pMTL82151-Pfdx-DBHBA

Table 5 - Primer table to amplify fragments needed to assemble pMTL82151-pfdx-DBHBA by HiFi assembly.

Gene Name/fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Pfdx promoter	Pfdx_pMTL_F	<i>C. sporogenes</i> 10696 gDNA	atgagtcgacgttagtagc ctgcgaaataag	223
	Pfdx_pMTL_R		cttttccatatgtaacacac ctccttaaaaattac	
Thiolase (<i>thl</i>)	thl_pMTL_Pfdx_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	tgtgttacatatgaaagaag ttgttaatagctag	1199
	thl_pMTL_(A)_R		ccttttaaatcttagactttc tagcaatattg	
Acetoacetate CoA-transferase subunit A/B (<i>ctfA</i> / <i>B</i> & <i>ctfB</i>)	ctfA/B_pMTL_(A)_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtgcgtatggaaaagg agggattaaaatgaac	1363
	ctfA/B_pMTL_(A)_R		tcgtttttctcaaacagcca tgggtctaag	
3-hydroxybutanoate dehydrogenase (<i>bdhA</i>)	bdhA_pMTL_(A)_F	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttagagaaaagacga ggatagttatc	509
	bdhA_pMTL_(A)_R		ttattttatgtctacaataa gctgattttc	
Vector Backbone	Vec_pMTL_(A)_F	pMTL82151	ttatttgttagcataaaaataa gaaggctgcatt	4997
	Vec_pMTL_Pfdx_R		gctactacacgtcgactcat agctgtttc	

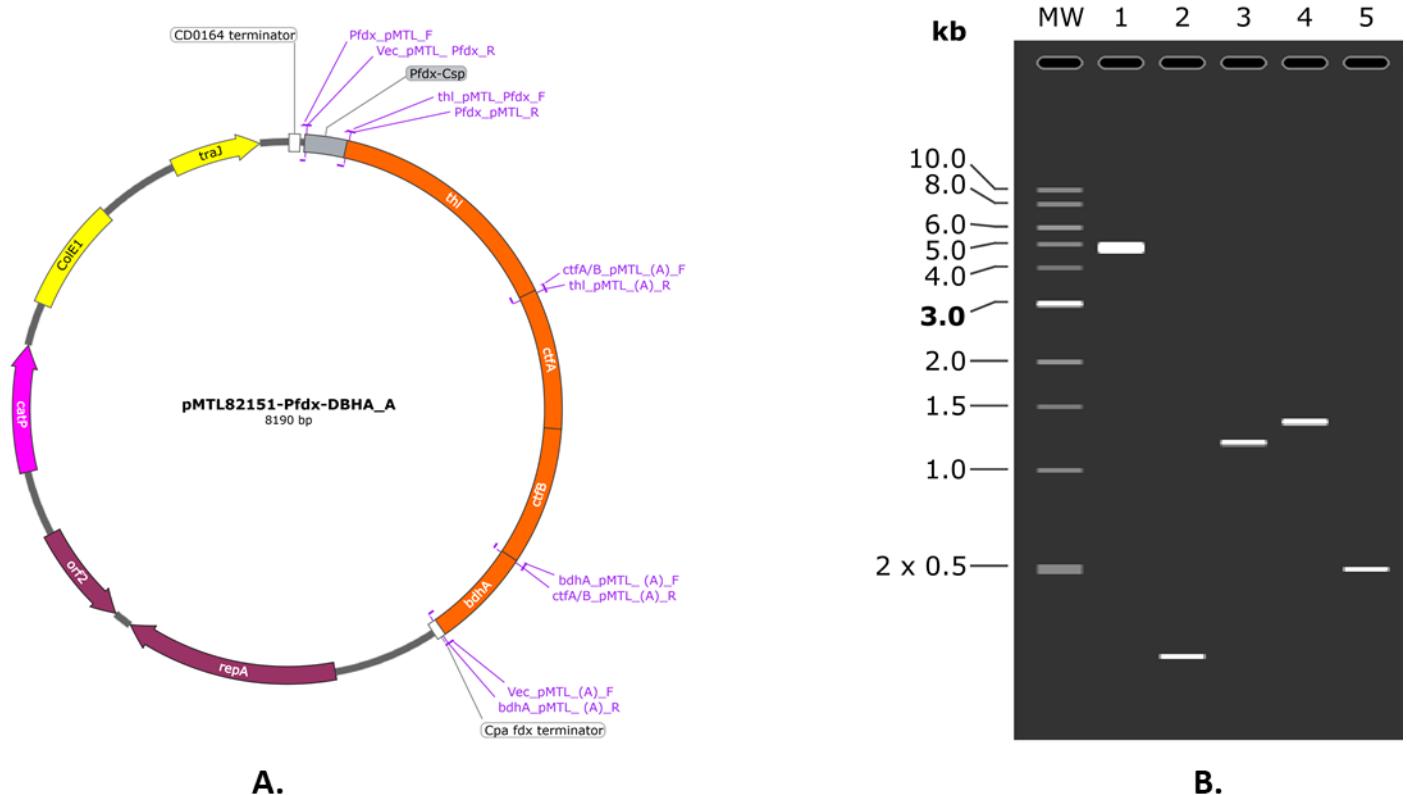


Figure 4 - pMTL82151-pfdx-DBHBA Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Pfdx; 3--thl; 4- ctfA/B; 5-bdhA.

Shuttle Vectors designed for KPO DBHB_B

The following plasmid vectors variants in table 6 below have been designed for testing of the DBHB_B operon.

Table 6 - List of pMTL8000 modular shuttle vectors designed to test KPO DBHB_B.

Vector	Description	Vector Map	Primer table (Primers to amplify fragments with overhangs suitable for HiFi assembly)	Gel of expected fragments needed to assemble vector (run on a 1% agarose gel)
pMTL82151-Px-DBHB _B	No promoter as a negative control - no expression of KPO genes.	Figure 5-A.	Table 7	Figure 5-B.
pMTL82151-Pntnh-DBHB _B	Expression of KPO genes dependent upon sigma factor <i>botR</i> expression.	Figure 6-A.	Table 8	Figure 6-B.
pMTL82151-Plac-DBHB _B	Expression of KPO genes dependent on presence of lactose (inducible system)	Figure 7-A.	Table 9	Figure 7-B.
pMTL82151-Pfdx-DBHB _B	Constitutive expression of KPO genes using the native <i>fdx</i> promoter as a positive control.	Figure 8-A.	Table 10	Figure 8-B.

DBHB_B KPO vector maps, primer tables and agarose gel simulations

pMTL82151-Px-DBHB_B

Table 7 - Primer table to amplify fragments needed to assemble pMTL82151-pX-DBHB_B by HiFi assembly.

Gene Name/fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Thiolase (<i>thl</i>)	<i>thl_pMTL_Px_F</i>	<i>C. acetobutylicum</i> ATCC 824 gDNA	ctgtatccatatgaaagaagttgttaatagcttag	1199
	<i>thl_pMTL_(B)_R</i>		tctcacaaaggctgactttcttagcaatattg	
Acetoacetyl-CoA reductase (<i>phbB</i>)	<i>phbB_pMTL_(B)_F</i>	<i>Cupriavidus necator</i> gDNA	aaagtgcgtactttgtgagagacaaggcag	784
	<i>phbB_pMTL_(B)_R</i>		agtaacaaaggatttgcattgtgctgcc	
Thioesterase II (<i>tesB</i>)	<i>tesB_pMTL_(B)_F</i>	<i>Escherichia coli</i> gDNA	catgcaataactttgtactggagagttatag	901
	<i>tesB_pMTL_(B)_R</i>		ttatttttatattaattgtgattacgcacac	
Vector Backbone	<i>Vec_pMTL_(B)_F</i>	pMTL82151	aatcacaattaaataaaaataagaaggctgcattt	5010
	<i>Vec_pMTL_Px_R</i>		cttcattcatatggatacagcggccgcg	

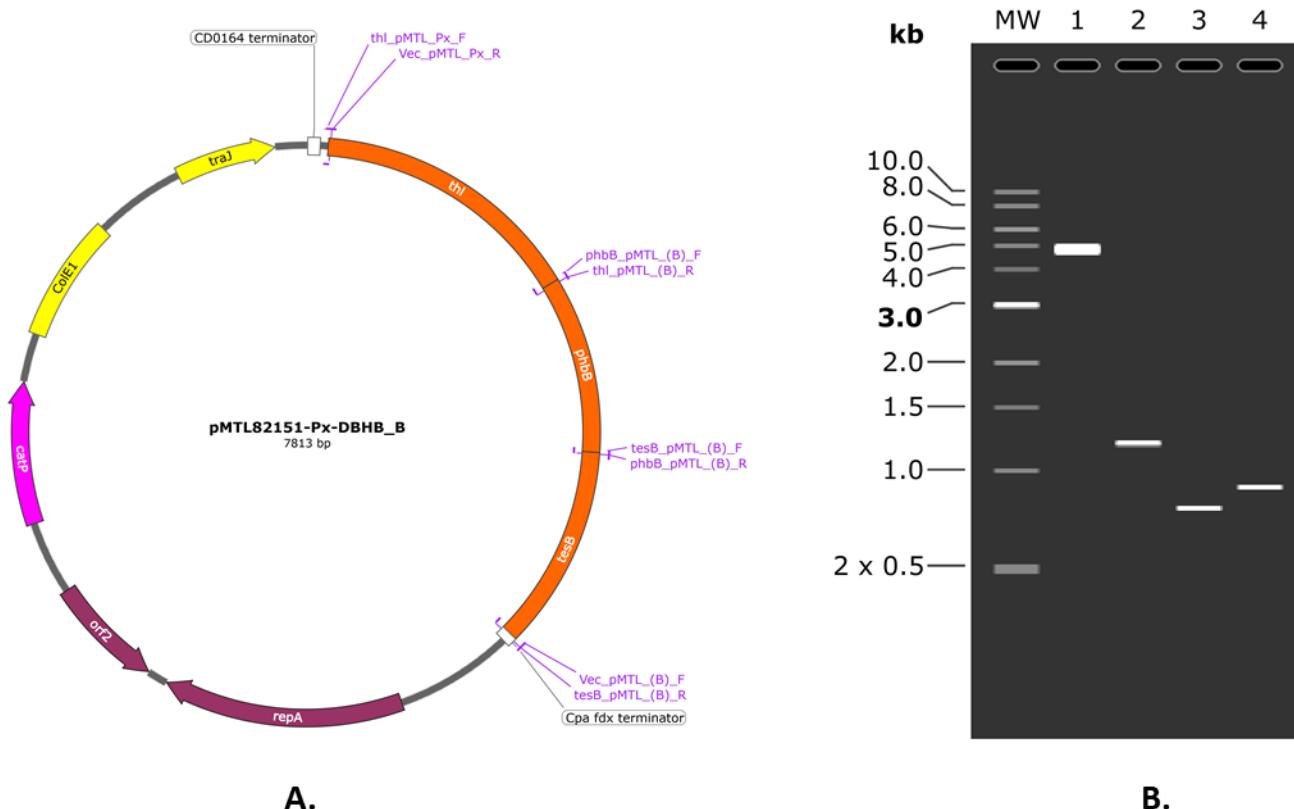
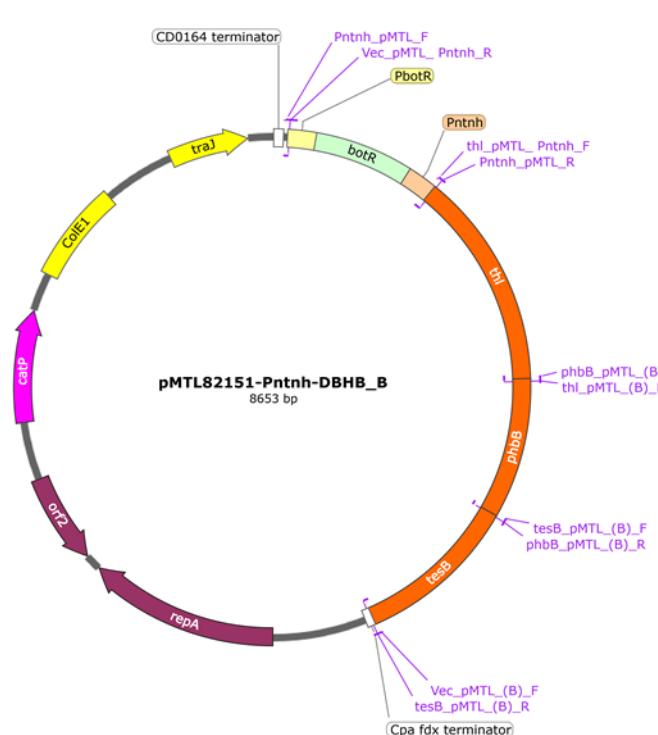


Figure 5 - pMTL82151-Px-DBHB_B Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-thl; 3-phbB; 4-tesB.

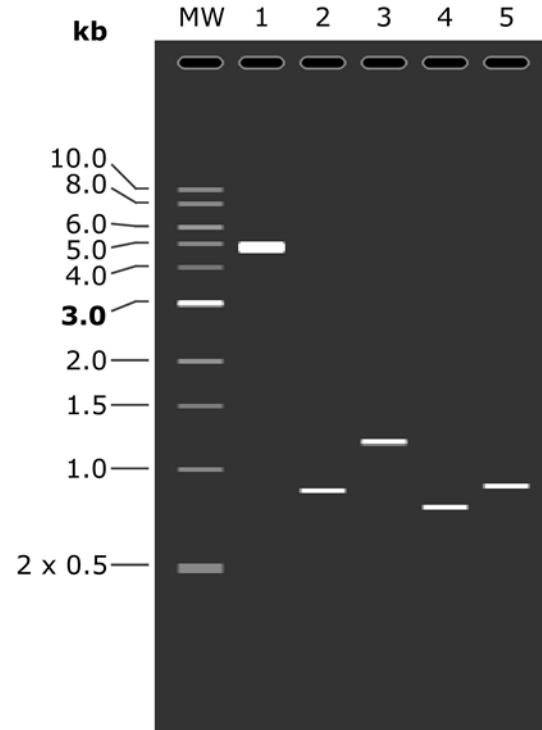
pMTL82151-Pntnh-DBHB_B

Table 8- Primer table to amplify fragments needed to assemble pMTL82151-pntnh-DBHB_B by HiFi assembly.

Gene Name/ Fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Pntnh promoter	Pntnh_pMTL_F	<i>C. botulinum</i> ATCC 3502 gDNA	atgagtcgaccctaaaattaaatatcaaattttattgtatgttac	873
	Pntnh_pMTL_R		cttctttcatatctaaccaccctctaaattttatcc	
Thiolase (thl)	thl_pMTL_ Pntnh_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	gtggtagatgatgaaagaaggtaatagctag	1199
	thl_pMTL_(B)_R		tctcacaaagctagcactttcttagcaatattg	
Acetoacetyl- CoA reductase (phbB)	phbB_pMTL_(B)_F	<i>Cupriavidus necator</i> gDNA	aaagtgcgtactttgtgagagacaaggcag	784
	phbB_pMTL_(B)_R		agtaacaaagttattgcattgtgcgtcccc	
Thioesterase II (tesB)	tesB_pMTL_(B)_F	<i>Escherichia coli</i> gDNA	catgcaataacttttactggagagttatgtat	901
	tesB_pMTL_(B)_R		ttatTTTATTAAATTGTTGATTACGATCAC	
Vector Backbone	Vec_pMTL_(B)_F	pMTL82151	aatcacaattaaataaaaataagaaggcgcatttg	4997
	Vec_pMTL_ Pntnh_R		aaatttttagggtcgactcatagctgtttc	



A.



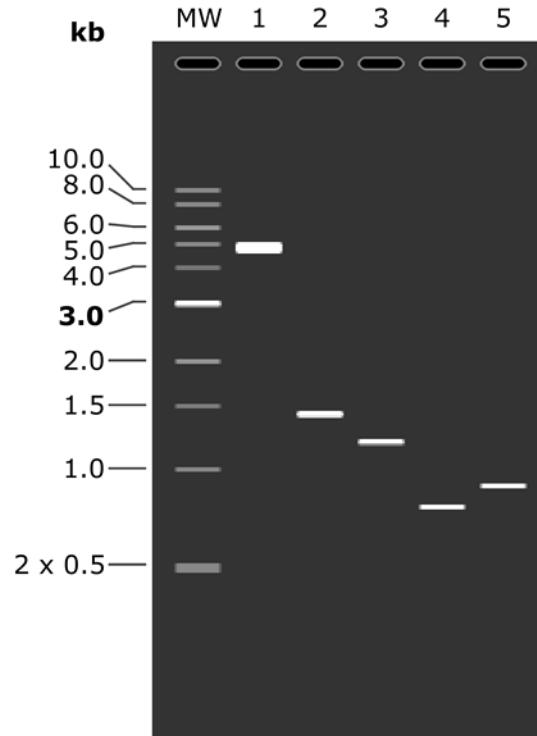
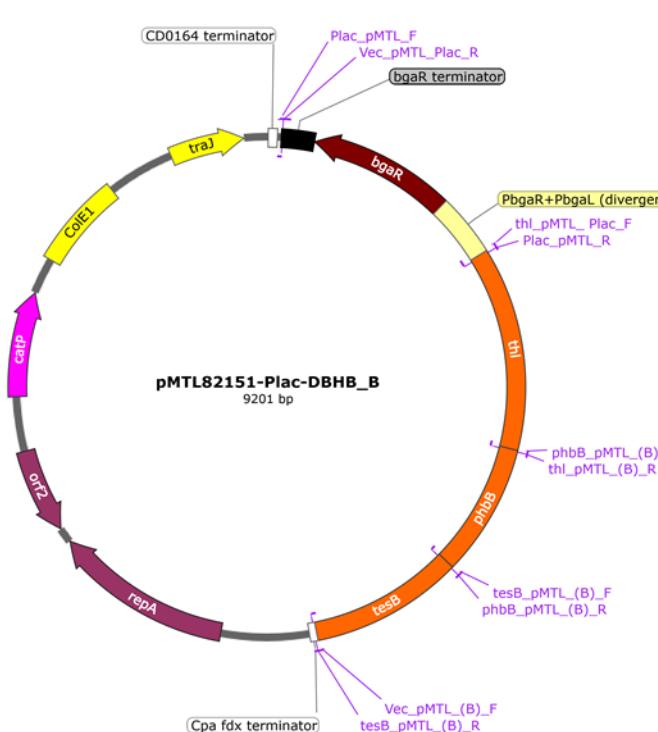
B.

Figure 6 - pMTL82151-Pntnh-DBHB_B Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Pntnh; 3-thl; 4-phbB; 5-tesB.

pMTL82151-Plac-DBHB_B

Table 9 - Primer table to amplify fragments needed to assemble pMTL82151-plac-DBHB_B by HiFi assembly.

Gene Name/ Fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Plac promoter	Plac_pMTL_F	<i>C. perfringens</i> gDNA	atgagtcgactaatttagatattaattctaaattaagtgaaattaatata	1421
	Plac_pMTL_R		tttctttcattttaccctcccaatacattaaaaataattatg	
Thiolase (<i>thl</i>)	thl_pMTL_Plac_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	ggagggtaaaatgaaagaagttgaatagctag	1199
	thl_pMTL_(B)_R		tctcacaaagctagcactttctgcataatattg	
Acetoacetyl- CoA reductase (<i>phbB</i>)	phbB_pMTL_(B)_F	<i>Cupriavidus</i> <i>necator</i> gDNA	aaagtgcgtactttgtgagagacaaggcag	784
	phbB_pMTL_(B)_R		agtaacaagttattgcattgtgcgtgc	
Thioesterase II (<i>tesB</i>)	tesB_pMTL_(B)_F	<i>Escherichia coli</i> gDNA	catgcaataactttgtactggagagttat	901
	tesB_pMTL_(B)_R		ttatttttatttaatttgtgattacgcac	
Vector Backbone	Vec_pMTL_(B)_F	pMTL82151	aatcacaattaaataaaaaataagaaggcctgcattt	4997
	Vec_pMTL_		atctaaatttagtcactcatagctgtttc	



A.

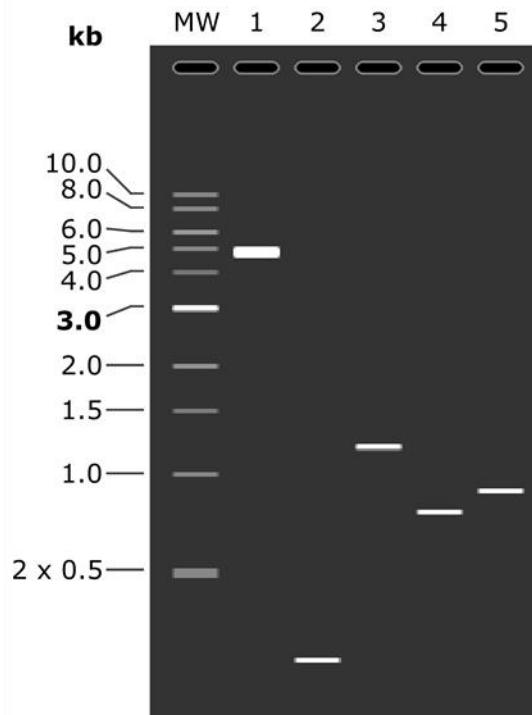
B.

Figure 7 - pMTL82151-Plac-DBHB_B Vector plasmid annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Plac; 3-thl; 4-phbB; 5-tesB.

pMTL82151-Pfdx-DBHB_B

Table 10 - Primer table to amplify fragments needed to assemble pMTL82151-pfdx-DBHB_B by HiFi assembly.

Gene Name/fragment	Primer name	Template	Primer 5' to 3'	Amplicon size (bp)
Pfdx promoter	Pfdx_pMTL_F	<i>C. sporogenes</i> 10696 gDNA	atgagtcgacgtgttagtagccgcggaaataag	223
	Pfdx_pMTL_R		cttcttcatatgtAACACACCTCCTAAATTAC	
Thiolase (<i>thl</i>)	thl_pMTL_Pfdx_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	tgtgttacatatgtAAAGAGTTGAATAGCTAG	1199
	thl_pMTL_Pfdx(B)_R		ttcacaaaggctgactttcttagcaatattg	
Acetoacetyl-CoA reductase (<i>phbB</i>)	phbB_pMTL_(B)_F	<i>Cupriavidus necator</i> gDNA	aaagtgcgtactttgtggagagacaaggcag	784
	phbB_pMTL_(B)_R		agtaacaaggatttgcattgtgcgtcccc	
Thioesterase II (<i>tesB</i>)	tesB_pMTL_(B)_F	<i>Escherichia coli</i> gDNA	catcaataactttgtactggagagttatgt	901
	tesB_pMTL_(B)_R		ttatTTTATTAAATTGATTGATTACGCATCAC	
Vector Backbone	Vec_pMTL_(B)_F	pMTL82151	aatcacaattaaaaataagaaggctgcatttg	4997
	Vec_pMTL_Pfdx_R		gctactacacgtcgactcatagctgtttc	



A.

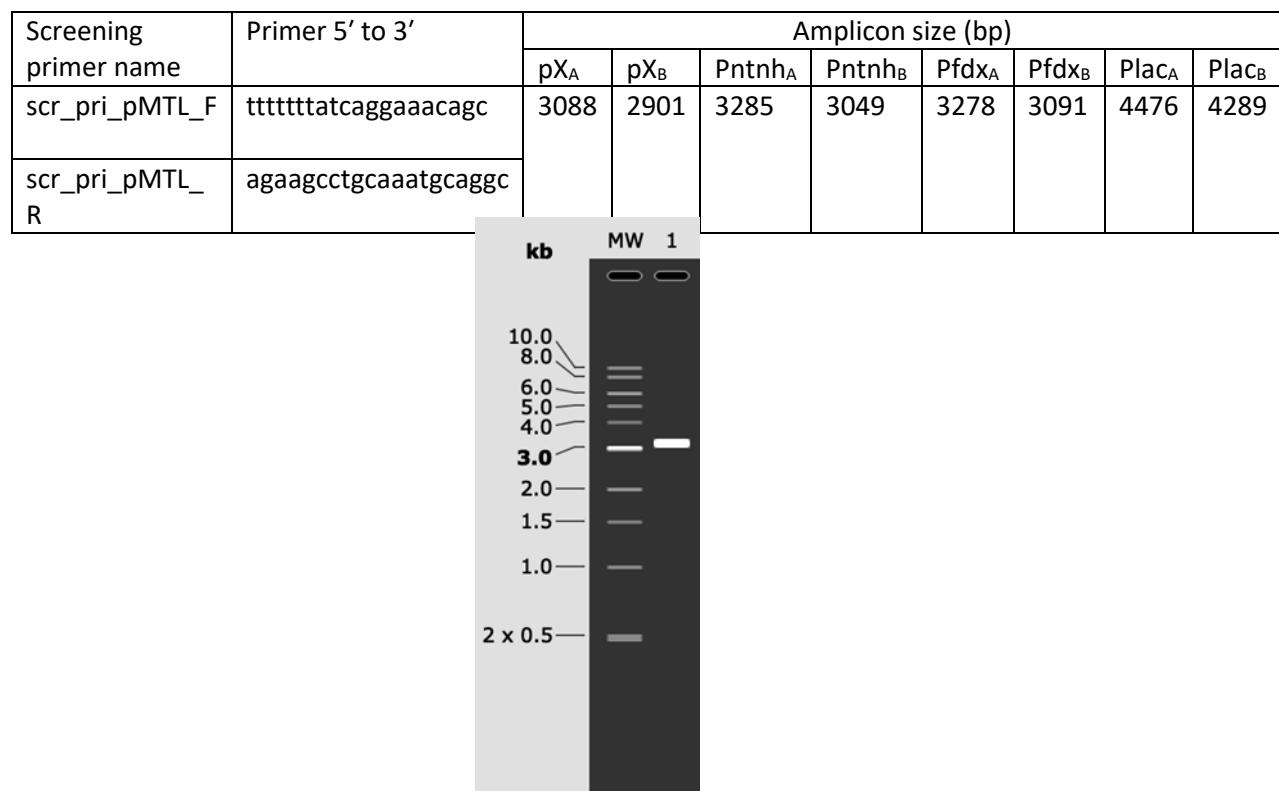
B.

Figure 8 - pMTL82151-Pfdx-DBHB_B Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Pfdx; 3-thl; 4-phbB; 5-tesB.

Shuttle vector screening primers

To confirm the successful construction of the shuttle vectors by HiFi assembly in E.coli, primers needed to be designed that bind in the vector backbone to allow amplification across the entire inserted KPO operons. The screening primer sequences and expected band sizes are found in table 11 below. These primers can also be used to confirm the presence of the shuttle vectors in *C. sporogenes* after conjugation. Figure 9 demonstrates what this would look like when run on an agarose gel by electrophoresis.

*Table 11 - Screening primers sequences and band sizes for shuttle vectors to confirm assembly and/or presence in *C. sporogenes**



*Figure 9 - A 1% agarose gel stimulation demonstrating the band size expected if the pMTL82151-Pfdx-DBHBA is correctly assembled vector (or present in *C. sporogenes* genome) – MW- Ladder; 1- pMTL82151-Pfdx-DBHBA*

Stage 2 – Genomic Integration Vector Design

Once tested using shuttle vectors the most suitable pathway (DBHBA in our ‘dry lab’ project) would be integrated into the *C. sporogenes* genome to allow stable expression of the KPO without the need to maintain the plasmid vector by antibiotic selection. To integrate the DBHBA KPO with the three promotor variants for alternative expression profiles we would use the RiboCas system. Below in table 12 outlines the three vectors that would be created.

Table 12 - List of RiboCas vectors designed to integrate the DBHBA KPO into the *C. sporogenes* genome

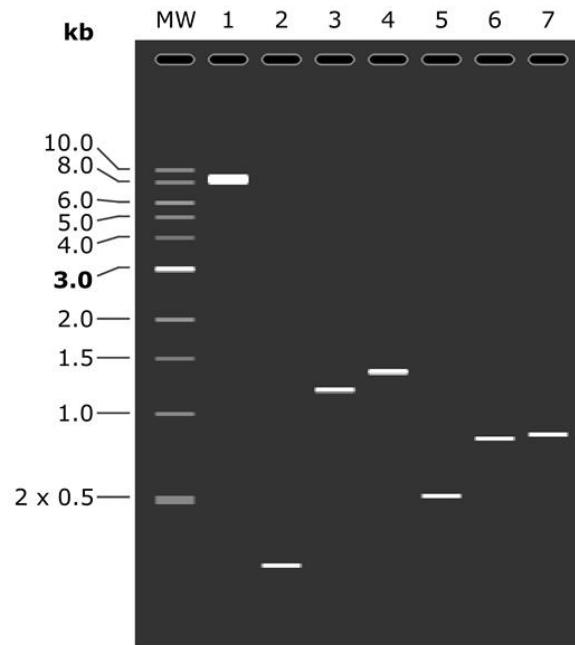
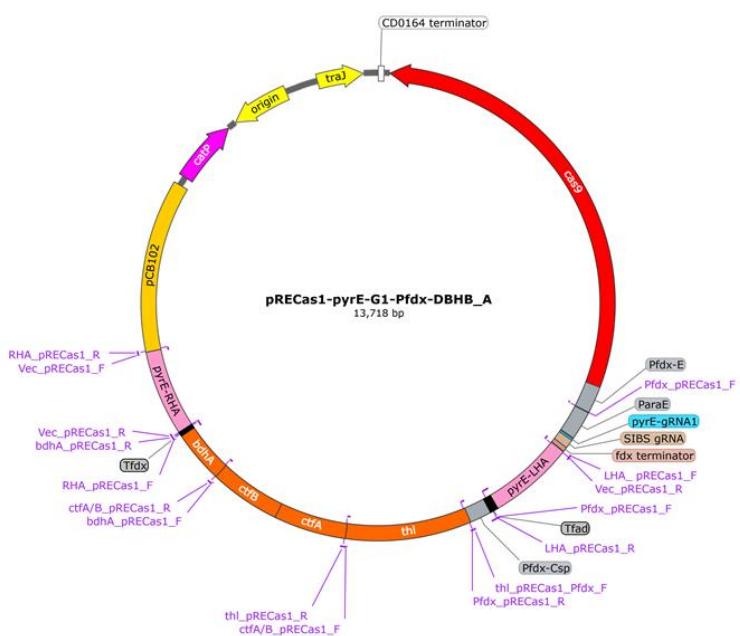
Vector	Vector Map	Primer table (Primers to amplify fragments with overhangs suitable for HiFi assembly)	Gel of expected fragments needed to assemble vector (run on a 1% agarose gel)
pRECas1-Pfdx-DBHB _A	Figure 10-A.	Table 13	Figure 10-B.
pRECas1-Pntnh-DBHB _A	Figure 11-A.	Table 14	Figure 11-B.
pRECas1-Plac-DBHB _A	Figure 12-A.	Table 15	Figure 12-B.

RiboCas DBHB_A KPO vector maps, primer tables and agarose gel simulations

pRECas1-Pfdx-DBHB_A

Table 13 - Primer table to amplify fragments needed to assemble pRECas1-Pfdx-DBHB_A by HiFi assembly.

Gene Name/ Fragment	Primer Name	Template	Primer 5' to 3'	Amplicon size (bp)
Pfdx promotor	Pfdx_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	attgtggcagactttatttatcttattgattttcattttaat gtgttagtagctgcgaaat	260
	Pfdx_pRECas1_R		cttccttcatatgtAACACACCTCCTAAATTAC	
Thiolase (<i>thl</i>)	thl_pRECas1_Pfdx_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	tgtgttacatatgtAAAGAAGTTGTAATAGCTG	1199
	thl_pRECas1_R		ccttttaaatcttagcactttctagcaatattg	
Acetoacetate CoA-transferase subunit A/B (<i>ctfA</i> / <i>& ctfB</i>)	ctfA/B_pRECas1_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtgcataattaaaaggaggattaaatgaac	1363
	ctfA/B_pRECas1_R		tgcgtttctctaaacagccatgggtctaag	
3-hydroxybutanoate dehydrogenase (<i>bhdA</i>)	bhdA_pRECas1_F	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttttagaaaaAGACGAGGATAGTATC	529
	bhdA_pRECas1_R		aaggcctgcaaattgcaggctttatTTTatctacaataagct gattttcc	
Right Homology Arm (RHA)	RHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	agcctgcattgcaggctttatTTTatTTTaaaATAAGG AGTGTC	840
	RHA_pRECas1_R		gcggcgcgcactcccataaataatcttg	
Vector Backbone	Vec_pRECas1_F	pRECas1-ΔpyrE::PbotR-botR (from Nottingham IGEM 2019 project)	atggggagttggcgccgcattttt	8806
	Vec_pRECas1_R		aaggtaatcgacgtcataaaaataagaaggcctgcaaatg	
Left Homology Amr (LHA)	LHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	ttatgacgtcgattgaccttaatcctaaagaag	856
	LHA_pRECas1_R		taaagtctgccacaattggcagactttatTTtatTTGC agttatatatTTCTCTTataact	



A.

B.

Figure 10 -*pRECcas1-Pfdx-DBHB_A* Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-*Pfdx*; 3-*thl*; 4-*ctfA/B*; 5-*bhdA*; 6-*RHA*; 7-*LHA*.

pRECas1-Pntnh-DBHB_A

Table 14 - Primer table to amplify fragments needed to assemble pRECas1-Pntnh-DBHB_A by HiFi assembly.

Gene Name/ Fragment	Primer Name	Template	Primer 5' to 3'	Amplicon size (bp)
Pntnh promotor	Pntnh_pRECas1_F	<i>C. botulinum</i> ATCC 3502 gDNA	attgtggcagacttattttatctattgattttcatttta	910
	Pntnh_pRECas1_R		atcctaaaattttaaatatatc cttccttcataatctaaccaccctccaaatttatttc	
Thiolase (<i>thl</i>)	<u>thl_pRECas1_Pntnh_F</u>	<i>C. acetobutylicum</i> ATCC 824 gDNA	gtggtagatataaaaaaaaggagttgttaatgcgtat	1199
	<u>thl_pRECas1_R</u>		ccttttaatctacgtactttctacgtcaatattg	
Acetoacetate CoA- transferase subunit A/B (<i>ctfA</i> / & <i>ctfB</i>)	ctfA/B_pRECas1_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtgcataattaaaaggagggattaaaatgaac	1363
	ctfA/B_pRECas1_R		tgcgtttctctaaacagccatgggtctaag	
3- hydroxybutan oate dehydrogenas e (<i>bdhA</i>)	<u>bdhA_pRECas1_F</u>	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttttagagaaagacgaggatagtatc	529
	<u>bdhA_pRECas1_R</u>		aaggcgtcaatgcaggcttttatctacaataag ctgttttcc	
Right Homology Arm (RHA)	RHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	agcctgcattgcaggcttttatattttaaaataag gaggttc	840
	RHA_pRECas1_R		gcggcgcccaactccccataataatcttg	
Vector Backbone	Vec_pRECas1_F	pRECas1- ApvrE::PbotR-botR (from Nottingham IGEM 2019 project)	atggggagttggcgccgcgcattttt	8806
	Vec_pRECas1_R		aaggtaatcgacgtcataaaaataagaagcctgcaaatg	
Left Homology Amr (LHA)	LHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	ttatgacgtcattgacctaattctaaagaag	856
	LHA_pRECas1_R		taaagtctgccacaatttggcagactttatctattgg cagttatcttcccttatact	

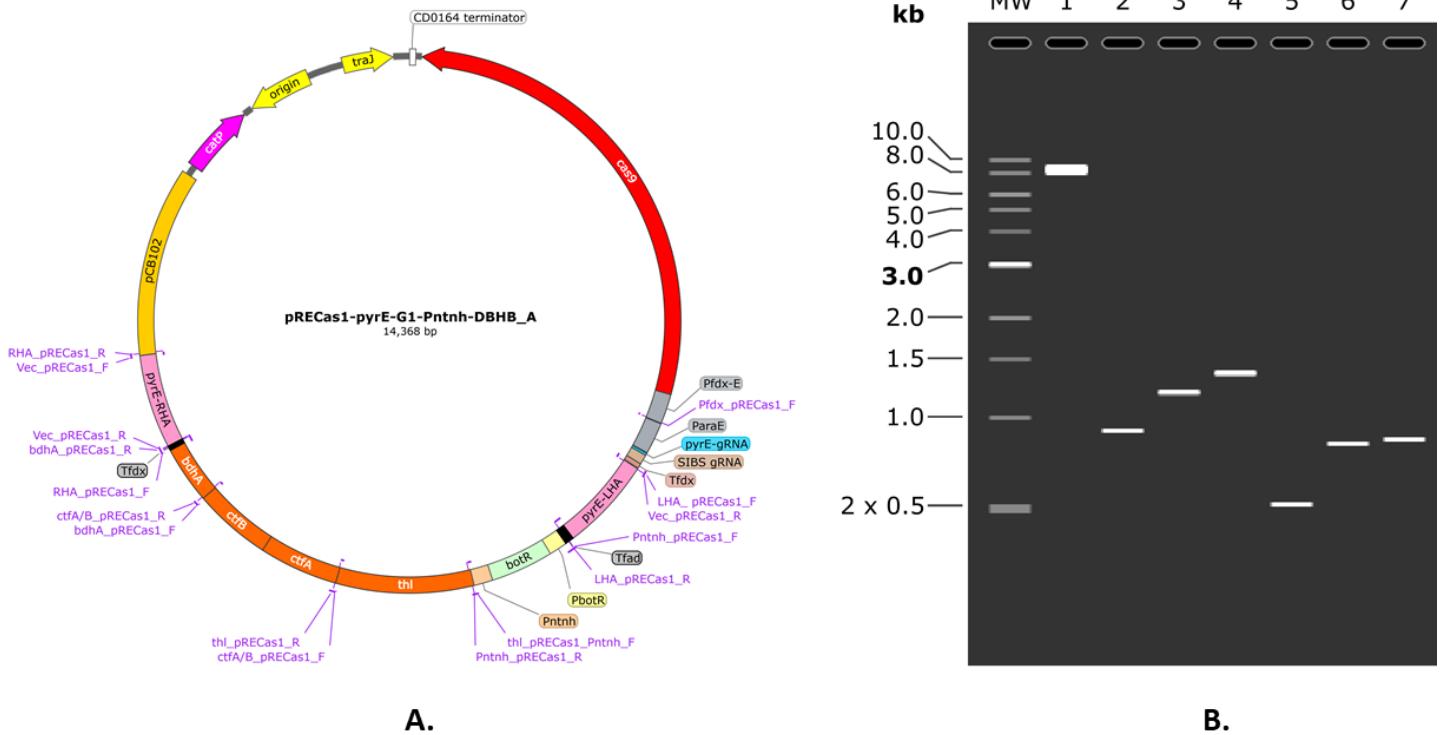


Figure 11 - pRECas1-Pntnh-DBHB_A Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1- Vector Backbone; 2-Pntnh; 3-thl; 4-ctfA/B; 5-bdhA; 6-RHA; 7-LHA.

pRECas1-Plac-DBHB_A

Table 15 - Primer table to amplify fragments needed to assemble pRECas1-Plac-DBHB_A by HiFi assembly.

Gene Name/ Fragment	Primer Name	Template	Primer 5' to 3'	Amplicon size (bp)
Plac promotor	Plac_pRECas1_F	<i>C. perfringens</i> gDNA	attgtggcagactttatTTtatctattgatttatttcattttta attatTTtagatTTaaattct	1458
	Plac_pRECas1_R		cTCTTTCatTTTaccCcccaatTTaaaataattatg	
Thiolase (thl)	thl_pRECas1_Plac_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	ggagggtaaaatgaaagaaggTTgtaatAGCTG	1199
	thl_pRECas1_R		cCTTTaaatCTGactTTCTGcaatTTG	
Acetoacetate CoA- transferase subunit A/B (ctfA/ & ctfB)	ctfA/B_pRECas1_F	<i>C. acetobutylicum</i> ATCC 824 gDNA	aaagtgcTAGATTAAAGGGGATTAAGAAC	1363
	ctfA/B_pRECas1_R		TcgTCTTCTCAAACAGCCATGGGTCAAG	
3- hydroxybutano ate dehydrogenas e (bdhA)	bdhA_pRECas1_F	<i>Streptococcus</i> <i>dysgalactiae</i> subsp. <i>equisimilis</i> AC2713 gDNA	ggctgttagAGAAAGACGAGGATAGTAC	529
	bdhA_pRECas1_R		aaggcTGCaaATGcaggCTTATTTatcAAAG CTGATTTC	
Right Homology Arm (RHA)	RHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	agccTgcATTGcaggCTTATTTatTTAAAG GAGTGTC	840
	RHA_pRECas1_R		gcggcgcGCCAACTCCCCATAAATAATCTG	
Vector Backbone	Vec_pRECas1_F	pRECas1- ΔpyRE::PbotR-botR (from Nottingham IGEM 2019 project)	atggggagTTGGCGCCGCCATTATT	8806
	Vec_pRECas1_R		aaggTcaATGcACGTcATAAAATAAGAAGCCTGCAAATG	
Left Homology Arm (LHA)	LHA_pRECas1_F	<i>C. sporogenes</i> 10696 gDNA	ttatGacGTCATTGACCTAAATCCTAAAGAAG	856
	LHA_pRECas1_R		tAAAGTCTGCCAAATTGTCAGACTTTATCTATTGG CAGTTATCTCTCCCTTACT	

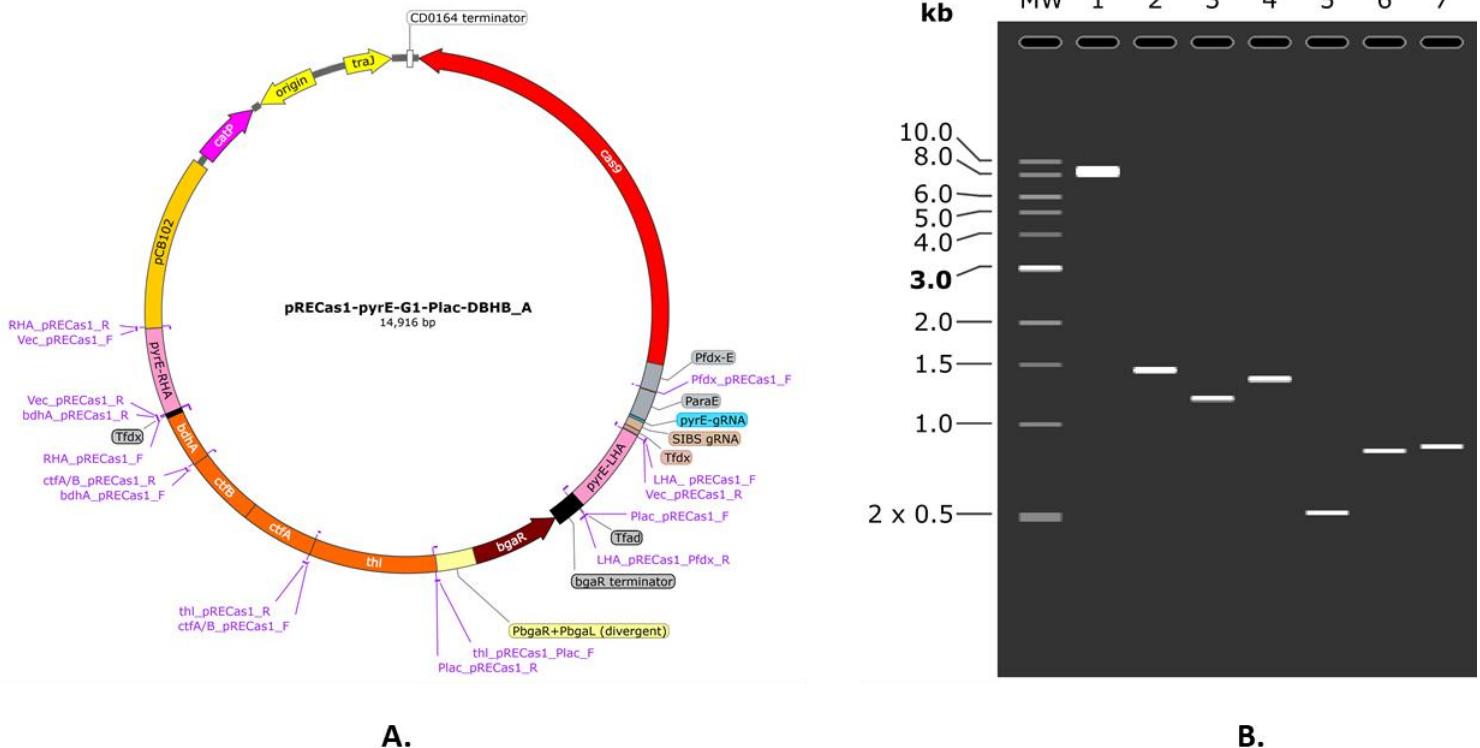


Figure 12- pRECas1-Plac-DBHBA Vector plasmid map annotated with primer binding sites (A.) and 1% agarose gel stimulation (B.) of expected fragment sizes needed to create vector – MW- Ladder; 1-Vector backbone2-Plac; 3-thl; 4-ctfA/B; 5-bdhA; 6-RHA; 7-LHA.

Genomic integration screening primers

To confirm the successful construction of the integration vectors by HiFi assembly in *E.coli*, primers needed to be designed that bind in the vector backbone to allow amplification across the region of the vector including the DBHBA operon, homology arms and sgRNA region. These primers and the expected band sizes for the three vectors are shown in table 16 below.

Table 16 - Screening primers to confirm successful assembly of the RiboCas integration vectors in *E.coli*.

Vector screening primer name	Primer 5' to 3'	Amplicon size (bp)		
		Pntnh _A	Pfdx _A	Plac _A
sgRNA-F	cctttcatttacaattcatacg	5277	5319	6517
pCB102-R	ctgttatgcctttgactatc			

A second set of screening primers needed to be designed to allow screening of *C. sporogenes* colonies following conjugation with the RiboCas integration vectors. These primers bind in the *C. sporogenes* genome either side of the *pyrE* locus in which the DBHBA KPO is to be integrated into. The primer sequences can be found in table 17 below and the binding locations of these primers is demonstrated in figure 13.

Table 17 - Screening primers to confirm successful integration of the DBHBA variants into the *C. sporogenes* genome.

Genomic screening primer name	Primer 5' to 3'	Amplicon size (bp)		
		Pntnh _A	Pfdx _A	Plac _A
scr_pri_pRECas1_F	actgcagttacaataggAACAGC	3623	3741	4639
scr_pri_pRECas1_R	tctttgtctaaaaatacttggtttgc			

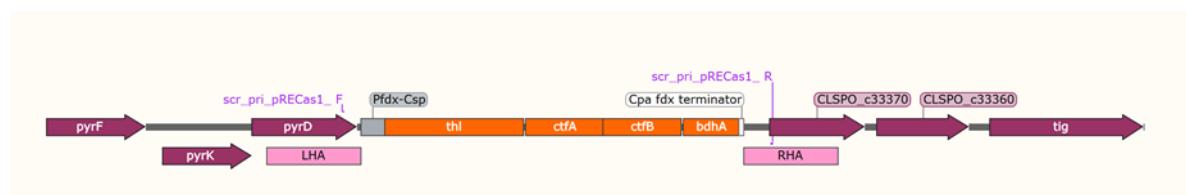


Figure 13- *C. sporogenes* pyrE locus with DBHBA KPO driven by the native fdx promoter replacing the pyrE gene with the genomic screening primers binding sites shown.

How this would be implemented in the wet lab

If the wet lab was available to use these are the steps we would have followed to create the vectors we have designed, which we have outlined above. The process of making both the shuttle and genomic integration vectors is the same. The difference in the process comes when conjugating into *C. sporogenes* – which is described below.

Step 1

Extraction of gDNA (from organisms stated in primers tables) using genomic DNA extraction kit (See Protocol 1 in Experiments Page).

Step 2

Amplification of DNA fragments needed to construct vectors using KOD Hot Start Master Mix and primers from table(s) 2-5, 7-10 for shuttle vectors and tables 13-15 for integration vectors. See protocol 2 for example reaction setup and thermocycler conditions.

Step 3

Load PCR reactions on 1% agarose gel and separate by electrophoresis (Protocol 3).

Step 4

Extract bands (expected as shown in figures 1-B. to 8-B. and 10-B. to 12-B.) using a DNA gel extraction kit (as outlined in protocol 4) and quantify DNA concentrations obtained using Thermo Scientific Nanodrop (see protocol 5).

Step 5

Setup the NEBuilder HiFi DNA assembly reaction with the amplified fragments to be assembled following the ratios suggested in manufacturer's protocol (protocol 6).

Step 6

After HiFi incubation transform reaction mixture into the NEB 5-alpha competent 2 “cloning” *E. coli* cells provided in the HiFi cloning kit following the manufactures transformation protocol (protocol 7) and plating onto Luria-Bertani (LB) agar supplemented with chloramphenicol (at 25 µg/mL) – to select for successful transformants (plates made following protocol 8).

Step 7

Screen any colonies that appear on the transformation plates by colony PCR using primers in table 11 for shuttle vectors and table 16 for RiboCas integration vectors - following protocol 9.

Analyse PCR products by gel electrophoresis (protocol 3) looking for band sizes outlined in table 11 and 16 for the respective vectors.

Step 8

Inoculate 5 mL of LB broth containing chloramphenicol (at a final concentration of 12.5 µg/mL) with a colony identified from the gel as being correctly assembled (with the expected band size). From this liquid culture extract the plasmid from the bacteria suing a miniprep kit- following protocol 10. The plasmid DNA can then be sent to be sanger sequenced, preparing the samples as per the sequencing company’s requirements (using the same primers used in the colony PCR), to ensure the correct sequence is has been assembled.

Step 9

The extracted plasmid is then transformation into a conjugation donor *E.coli* strain CA434 by electroporation following protocol 11 and again plate on LB+ Chloramphenicol (25 µg/mL) selection plates.

Step 10

Once the plasmid vectors (both the shuttle and genomic integration vectors) have been assembled and transformed into the conjugation donor *E.coli* strain as outlined above they can be conjugated into *C. sporogenes* 10696. The steps carried out will differ depending on if conjugating the preliminary shuttle vector or the vectors for genomic integration of the KPO operon.

For the shuttle vectors

Follow the conjugation protocol outlined in protocol 12. Once trans-conjugants appear on the selection plates pick single colonies and screen by colony PCR and gel electrophoresis (as in protocol 9 and 3 respectively) using primers in table 16 for presence of the shuttle vector plasmid. Restreak confirmed trans-conjugant colonies onto TYG selective plates with thiampenicol (15µg/mL) to ensure the shuttle plasmid is maintained.

For the genomic integration vectors

Follow the conjugation protocol outlined in protocol 12. Once trans-conjugants appear on the selection plates pick single colonies and restreak onto reduced TYG plates supplemented with Thiamphenicol , D-Cycloserine and Theophylline (final concentrations of 15µg/mL, 250µg/mL and 15µg/mL respectively). After incubation in the anaerobic cabinet overnight any colonies that appear to the theophylline plates should be successful mutants. Screen these colonies to grow by colony PCR and gel electrophoresis (as in protocol 9 and 3 respectively) using primers in table 17 for successful integration of the KPO operon in the

C. sporogenes genome. Choose a mutant colony confirmed by the colony PCR lose the plasmid as described in protocol 13.

The mutant with the plasmid lost can then be stored at -80°C in a TGY-glycerol (10% v/v) stock. The genomic DNA can be extracted as in protocol 1 and sent externally for sanger sequencing to confirm the operon has been correctly inserted with no errors.

Further steps

Growth and spore assays to characterise the DBHB_A KPO integrated strains and gas chromatography analysis of strain supernatants to determine whether our *C. sporogenes* strains produce the desired concentrations of DBHB and which promotor variant may be most suitable.