

Figure S1 Sequence of the pYOGM081 plasmid containing the iGM gene insertion module. In a version of the plasmid not containing the HA-tag (pTJH001), nucleotides 4,954–5,101 are removed and replaced with a stop codon (TAA) and a *Hin*dIII site (Materials and Methods). In plasmids containing the *ADH1* (pTJH002), *TEF* (pTJH003), and *CUP1* (pTJH004) promoters for driving the expression of a gene introduced between the Gateway cloning sites, nucleotides 2,755–3,232 are replaced with the respective sequences shown below (Materials and Methods).

Figure S1 (continued).

	TATA region of CYC1				
		1,620 	1,640 	1,660 	1,680 I
pYOGM081 map	TGTGCTCTGTATGTATAT	TAAAACTCTTGTTTTCTT	CTTTTCTCTAAATATTCTTT	CCTTATACATTAGGTC	CTTTGTAGC
	TATA region of CYC1	1700	1 720	1,740 GFP co	ding sequence
pYOGM081 map	ATAAATTACTATACTTC	1,700 I FATAGACACGCAAACACA	1,720 I A A A T A C A C A C T A A A T T A C C	GGATCAATTCGGGGGA1	J 1
	GFP coding sequence				
		1,780 	1,800 	1,820 	1,840 I
pYOGM081 map	AAAGGAGAAGAACTTTT	CACTGGAGTGGTCCCAGT	TCTTGTTGAATTAGATGGCG	ATGTTAATGGGC AAAAA	ATTCTCTGT
	GFP coding sequence	4.000	4.000	4 000	4.000
pYOGM081 map	C AGTGGAGAGGGTGAAG	1,860 	1,880 A A C T T A C C C T T A A T T T T A T T	1,900 I TGCACTACTGGGAAGCT	1,920 A C C T G T T C
prodividor map	GFP coding sequence	JIGAIGEAACAIACGGAA	AACTTACCCTTAATTTATT	T de Re l'Ac l'add A Ade l	TACCIOTIC
	or r soung soquenes	1,940 	1,960 I	1,980 	2,000
pYOGM081 map	CATGGCCAACACTTGTC	ACTACTTTCTCTTATGGT		CCCAGATCATATGAAAG	CAGCATGAC
	GFP coding sequence				
		2,020	2,040	2,060	2,080
pYOGM081 map		GCCCGAAGGTTATGTACA	.GGAAAGAACTATATTTACA	AAGATGACGGGAACTAG	LAAGACACG
	GFP coding sequence	2,100 I	2,120	2,140 	2,160
pYOGM081 map	TGCTGAAGTCAAGTTTG/		I ATAGAATCGAGTTAAAAGGT		ATGGAAACA
	GFP coding sequence				
		2,180 	2,200 	2,220 	2,240
pYOGM081 map		GAATACAACTATAACTCA	CATAATGTATACATCATGGG	AGACAAACCAAAGAATO	GGCATCAAA
	GFP coding sequence	2,260	2,280	2,300	2,320
pYOGM081 map	GTTAACTTCAAAATTAG/	T ACACAACATTAAAGATGG	I A A G C G T T C A A T T A G C A G A C C	ATTATCAACAAAATAC1	TCCAATTGG
,	GFP coding sequence				
		2,340	2,360 I	2,380	2,400
pYOGM081 map	CGATGGCCCTGTCCTTT	TACCAGACAACCATTACC	TGTCCACACAATCTGCCCTT	TCCAAAGATCCCAACGA	AAAGAGAG
	GFP coding sequence	0.400		0.400	0.400
pYOGM081 map	ATCACATGATCCTTCTTC	2,420 I G A G T T T G T A A C A G C T G C T	2,440 I AGGATTACACATGGCATGGA	2,460 I T G A A C T A T A C A A A t a a C	2,480
ртобиют пар	CYC1 terminator	3AGTTTGTAACAGCTGCT	Addrineheniddeniddn	IGAACTATACAAA	344666146
	OTOT terminator	2,500 	2,520 	2,540 	2,560
pYOGM081 map	AGGAGGGCCGCATCATG	TAATTAGTTATGTCACGC	TTACATTCACGCCCTCCCCC	CACATCCGCTCTAACCC	GAAAAGGAA
	CYC1 terminator				
		2,580 	2,600	2,620	2,640
pYOGM081 map		AGTCTAGGTCCCTATTTA	ATTITITATAGTTATGTTAG	TATTAAGAACGTTATTI	TATATTTCA
	CYC1 terminator	2,660	2,680	2,700	2,720
pYOGM081 map	AATTTTCTTTTTTCT	TGTACAGACGCGTGTACG	I ICATGTAACATTATACTGAAA	ACCTTGCTTGAGAAGG1	TTTTGGGAC
		HindIII/Stul cloning j			
	CYC1 terminator	2,740	GAL1-10 promoter 2,760	2,780	2,800
pYOGM081 map	 GCTCGAAGGCTTTAATT	·	I CGGATTAGAAGCCGCCGAGC	l	<u> </u>
	GAL1-10 promoter				
		2,820 	2,840 	2,860 I	2,880
pYOGM081 map	TCTCCTCCGTGCGTCCTC	CGTCTTCACCGGTCGCGT	TCCTGAAACGCAGATGTGCC	TCGCGCCGCACTGCTCC	CGAACAATA
	GAL1-10 promoter	2,900	2,920	2,940	2,960
pYOGM081 map	AAGATTCTACAATACTAG	I	AGGAAAATTGGCAGTAACC	I	1
,	GAL1-10 promoter				
		2,980 	3,000 I	3,020 	3,040 I
pYOGM081 map	GAATCAAATTAACAACCA	ATAGGATGATAATGCGAT	TAGTTTTTTAGCCTTATTTC	TGGGGTAATTAATCAG	GAAGCGAT
	GAL1-10 promoter	3,060	3,080	3,100	0.400
pYOGM081 map	GATTITIGATCTATTAAC	I	3,080 I AGCTGCATAACCACTTTAAC	l	3,120 T.C.A.G.T.T.G
p. oomoo, map	GAL1-10 promoter	THE POWER STANK			
		3,140 	3,160	3,180	3,200
pYOGM081 map	TATTACTTCTTATTCAA		CAAAAATTGTTAATATACC		AAGGAGAAA

Figure S1 (continued).

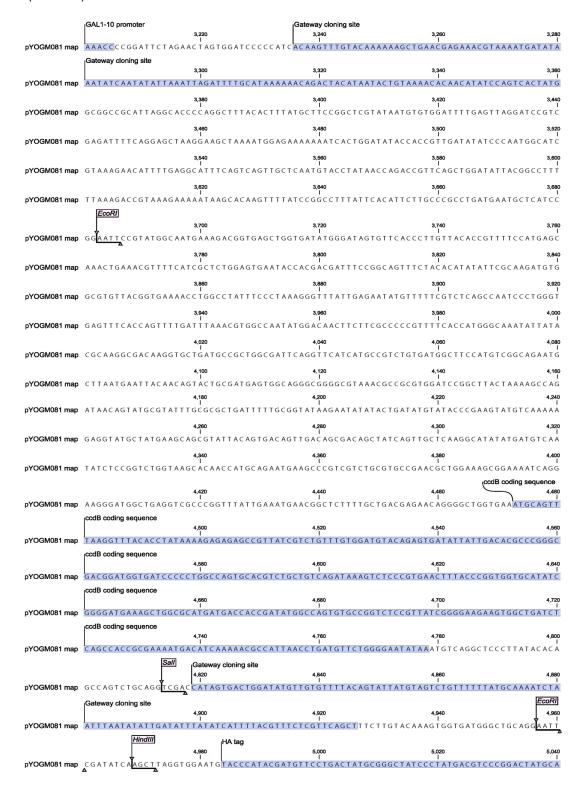


Figure S1 (continued).

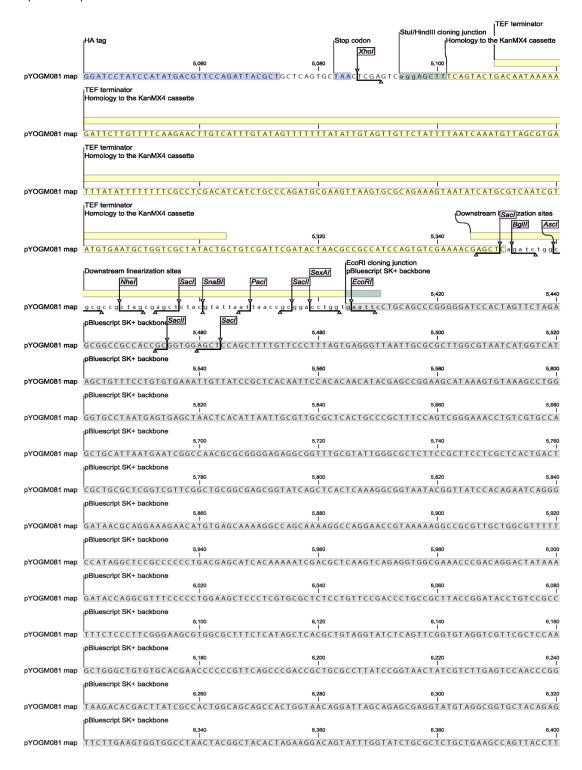


Figure S1 (continued).

	pBluescript SK+ backbone						
		6,420 	6,440 	6,460	6,480 		
pYOGM081 map	CGGAAAAAGAGTTGGTAC	GCTCTTGATCCGGCAAACAA	ACCACCGCTGGTAGCGGTGG	TTTTTTGTTTGCAAGCAGC	AGA		
	pBluescript SK+ backbone	0.500	0.500	0.540	0.500		
pYOGM081 map	TTACGCGCAGAAAAAAA	6,500 	6,520 I GATCTTTTCTACGGGGTCTG	6,540 I ACGCTCAGTGGAACGAAAACT	6,560 I		
prodividorniap							
	pBluescript SK+ backbone	6,580	6,600	6,620	6,640		
pYOGM081 map	L CGTTAAGGGATTTTGGTC	T TATGAGATTATCAAAAAGGA	TCTTCACCTAGATCCTTTTA.	AATTAAAAATGAAGTTTTAA	ATC		
	pBluescript SK+ backbone						
		6,660 I	6,680 I	6,700 I	6,720 I		
pYOGM081 map		AGTAAACTTGGTCTGACAGT	TACCAATGCTTAATCAGTGA	GGCACCTATCTCAGCGATCTC	STC		
	pBluescript SK+ backbone	6,740	6,760	6,780	6,800		
pYOGM081 map	TATTTCGTTCATCCATAC	l		AGGGCTTACCATCTGGCCCC			
p	pBluescript SK+ backbone						
		6,820	6,840	6,860	6,880		
pYOGM081 map	GCTGCAATGATACCGCG <i>A</i>	NGACCCACGCTCACCGGCTC	CAGATTTATCAGCAATAAAC	CAGCCAGCCGGAAGGGCCGAG	GCG		
	pBluescript SK+ backbone						
		6,900 	6,920 	6,940	6,960 		
pYOGM081 map		TTTATCCGCCTCCATCCAG	TCTATTAATTGTTGCCGGGA	AGCTAGAGTAAGTAGTTCGC	CAG		
	pBluescript SK+ backbone	6,980	7,000	7,020	7,040		
pYOGM081 map	TTAATAGTTTGCGCAACO	l		T CGTTTGGTATGGCTTCATTC			
	pBluescript SK+ backbone						
		7,060	7,080 I	7,100	7,120 I		
pYOGM081 map	TCCGGTTCCCAACGATCA	AAGGCGAGTTACATGATCCC	CCATGTTGTGCAAAAAGCG	GTTAGCTCCTTCGGTCCTCC	GAT		
	pBluescript SK+ backbone						
		7,140 	7,160 	7,180 	7,200 		
pYOGM081 map		GGCCGCAGTGTTATCACTC	ATGGTTATGGC AGC ACTGC A	TAATTCTCTTACTGTCATGC	LAI		
	pBluescript SK+ backbone	7,220	7,240 	7,260	7,280		
pYOGM081 map	CCGTAAGATGCTTTTCTG	I STGACTGGTGAGTACTCAAC		I GTATGCGGCGACCGAGTTGC1	TCT		
	pBluescript SK+ backbone						
		7,300 	7,320 	7,340 	7,360 		
pYOGM081 map	TGCCCGGCGTCAATACGG	G A T A A T A C C G C G C C A C A T A	GCAGAACTTTAAAAGTGCTC	ATCATTGGAAAACGTTCTTCC	3GG		
	pBluescript SK+ backbone	7,380	7.400	7,420	7,440		
pYOGM081 map	GCGAAAACTCTCAAGGAT	I	7,400 I AGTTCGATGTAACCCACTCG [*]	TGCACCCAACTGATCTTCAG			
procinos map	pBluescript SK+ backbone						
	policion profes de desigono	7,460	7,480	7,500	7,520		
pYOGM081 map	CTTTTACTTTCACCAGCG	GTTTCTGGGTGAGCAAAAAC	AGG A AGG C A A A A T G C C G C A A	A A A A G G G A A T A A G G G C G A C A C	CGG		
	pBluescript SK+ backbone						
		7,540 	7,560 	7,580	7,600 I		
pYOGM081 map	AAATGTTGAATACTCATA	CTCTTCCTTTTTCAATATT	ATTGAAGCATTTATCAGGGT:	TATTGTCTCATGAGCGGATAG	Z A T		
	pBluescript SK+ backbone	7,620	7,640	7,660	7,680		
pYOGM081 map	ATTTGAATGTATTTAGAA	l	l	T AGTGCCACCTAAATTGTAAG(- 1		
,	pBluescript SK+ backbone						
		7,700 I	7,720 I	7,740	7,760 I		
pYOGM081 map	TAATATTTTGTTAAAATT	CGCGTTAAATTTTTGTTAA	ATCAGCTCATTTTTTAACCA	AT AGGCCGAAATCGGCAAAA1	TCC		
	pBluescript SK+ backbone						
=VOCM004		7,780	7,800 	7,820 	7,840 		
pYOGM081 map	CTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTG						
	pBluescript SK+ backbone	7,860	7,880	7,900	7,920		
pYOGM081 map	L GACTCCAACGTCAAAGGG	I GCGAAAAACCGTCTATCAGG	I GCGATGGCCCACTACGTGAAG	I CCATCACCCTAATCAAGTTTT	TTT		
	pBluescript SK+ backbone						
		7,940 	7,960 	7,980 	8,000 I		
pYOGM081 map	GGGGTCGAGGTGCCGTAA	AGCACTAAATCGGAACCCT	A A A G G G A G C C C C G A T T T A G	AGCTTGACGGGGAAAGCCGG	C G A		

Figure S1 (continued).

	pBluescript SK+ backbone							
		8,020 I	8,040 I	8,060 I	8,080 I			
pYOGM081 map	ACGTGGCGAGAAAGGAAGGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTA							
	pBluescript SK+ backbone							
		8,100	8,120	8,140	8,160 I			
pYOGM081 map	ACCACCACACCCGCCGC	GCTTAATGCGCCGCTACAGG	GCGCGTCCCATTCGCCATTC	AGGCTGCGCAACTGTTGGGA	AGG			
	_I pBluescript SK+ backbone							
		8,180	8,200	8,220	8,240			
pYOGM081 map	GCGATCGGTGCGGGCCT	CTTCGCTATTACGCCAGCTG	GCGAAAGGGGGATGTGCTGC	AAGGCGATTAAGTTGGGTAA	CGC			
	ipBluescript SK+ backbone							
		8,260	8,280	8,300	8,320			
pYOGM081 map	CAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAGCGCGCGTAATACGACTCACTATAGGGCGAATTGGGT							
	script SK+ backbone							
	1							
pYOGM081 map	ACCGGGCCCCCC							

ADH1 promoter

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Figure S1 (continued).

CUP1 promoter

