

Supplementary Data

Gene	Organism		
	<i>Ensifer</i> sp. FP291	<i>Ensifer</i> sp. HP113	<i>Ensifer</i> sp. HP127
16S rDNA	MH173836	MH173834	MH170308.2
recA	MK246816	MK246817	MK246818
sinI	MH234519	MH234520	MH234518
sinR	MH238425	MH238426	MH238427
traI	MH238428	MH238429	MH238430
traR	MH238431	MH238432	MH238433
expR	MN433628	MN433629	MH238434

Table S1: GenBank Nucleotide Accession numbers of the submitted sequences

Isolate	Closest match	Query cover	E value	Identity
FP 163	<i>Providencia vermicola</i> strain PCX7 16S ribosomal RNA gene	99%	0.0	96%
FP 292	<i>Providencia vermicola</i> strain UN26 16S ribosomal RNA gene	98%	0.0	96%
HP 114	<i>Brevundimonas diminuta</i> partial 16S rRNA gene, strain 1309-W2	100%	0.0	100%
HP 118	<i>Rhizobium rosettiformans</i> strain W3 16S ribosomal RNA gene	99%	0.0	100%
HP 120	<i>Klebsiella pneumoniae</i> strain VRBG-52 16S ribosomal RNA gene	100%	0.0	100%
HP 123	<i>Rhizobium pusense</i> strain S19 16S ribosomal RNA gene	99%	0.0	100%
HP 125	<i>Arthrobacter globiformis</i> strain B-4S-7 16S ribosomal RNA gene	84%	7e-89	97%
HP 126	<i>Klebsiella pneumoniae</i> strain VRBG-52 16S ribosomal RNA gene	100%	0.0	100%
Sa 111	<i>Ochrobactrum pseudogrignonense</i> strain RD_MATFB_05 16S rRNA gene	99%	0.0	94%
Sa 112	<i>Ochrobactrum pseudogrignonense</i> strain YH5-3 16S ribosomal RNA gene	99%	0.0	95%
Su 141	<i>Ochrobactrum pseudogrignonense</i> strain PS17 16S ribosomal RNA gene	99%	0.0	98%

Table S2 16S sequence BLAST analysis of isolates not selected for detailed study

16S Sequences of the isolates not used for detailed study

>16S_HP114

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CCGGCTAACTTCGTGCCAGCAGCCGCGGTAATACGAAGGGGGCTAGCGTTGCTCGGAATTACTGGGCGTAAA
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>16S_HP118

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GATGTTGGTATC

>16S_HP120

AGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGTGAGTAATGTCTGGGAACTGCCTG
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GGGCCTCATGCCATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGA
TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAAGTCTGAGACACGGTCCAGACTCCTACGGGAGGCAG
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AGCACCGGCTAACTCCGTGCCAGCAGCCGCGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGCG
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>16S_HP123

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TAACGCATTAACATTCCGCCTGGGGAGTACGGTCGCAAGATTAAACTCAAAGGAATTGACGGGGGGCCCGC
ACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGCAGAACCCTTACCAGCTCTTGACATTCGGGGTAT
GGGCATTGGAGACGATGTCTTCAGTTAGGCTGGCCCCAGAACAGGTGCTGCATGGCTGTGTCGACGCTCGTG
TCGTGAGATGTTGGT

 >16S_HP126 TCGAGCGGTAGCACAGAGAGCTTGCTCTCGGGTGACGAGCGGCGGACGGGTGAGTAATGTCTGGGAAACTGC CTGATGGAGGGGGATAAATACTACTGGAAACGGTAGCTAATAACGCATAAACGTCGCAAGACCAAAGTGGGGGACC TTCGGGCCCTCATGCCATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGA CGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAAGTGAAGACACGGTCCAGACTCCTACGGGAGG CAGCAGTGGGGAAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCCGGTGTATGAAGAAGGCCCTTCG GGTTGTAAGAGTACTTTACAGCGGGGAGGAAGGCGATAAGGTTAATAACCTTGTTCGATTGACGTTACCCGCAGA AGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAAACGGAGGGTGCAAGCGTTAATCGGAATTACTGG GCGTAAAGCGCACGACGAGGCGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGAACGTCATTG AACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATCGGTAGAGATCTGG AGGAATACCGGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCAAA AGGATTAGATACCTTGGTAGTCCACGCCGTAAACGATGTTCGATTGGAGGTTGTGCCCTTGAGGCGTGGCTT CCGGAGCTAACCGTTAAATCGACCGCTTGGGGAGTAGCGGCCGAAGGTTAAAACTCAAATGAATTGACGGG GGCCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCC ACAGAACTTGCCAGAGATGGCTTGGTGCCCTTCGGGAACGTGTGAGACAGGTGCTGCATGGCTGTCTGTAGCTC CTGTTGTGAAATGTTGGGTATC
 >16S_SA111 GGAGCGGCAGACGGGTGAGTAACGCGTGGAATCTACCTTTTGCTACGGAATAACTCAGGGAAACTTGTGCT AATACCGTATGTGCCCTTTTGGGGAAAGATTTATCGGCAAAAGGATGAGCCCGCGTTGGATTAGCTAGTTGGT GGGGTAAAGGGCCACCAAGGCGACGATCCATAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGAC ACGGCCACACTCCTACGGGAGGCAGCAGTGGGGAAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATGC CGCGTAGTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCCCGGTGAAGATAATGACGGTCAACCGGAGAAGA AGCCCCGGCTAACTTCATGCCAGCGGCCGCGGTAATACAAAAGGGGCTAGCGTTGTTCCGATTACTGGGCG TAAAGCGCACGTAGGCGGACTTTTAAAGTCAAGGGTGAAATCCAGAGCTCAACTCTGGAAGTGCCTTTGATA CTGGAAGTCTTGAGTATGGTAGAGGTGAGTGGAATTCGAGGTGTAGAGGTGAAATTCATAGATATCGGAGGA ACACCGTGGCGAAGGCGCTACTGGGCATTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCATGAGGAT TAGATACCTTGGTAGTCCACGCCGTGACGATGAAGTTACCGTCCGGGTGTTACTCTTCGGTGGCGCAGCTAAC GCATTAACATTCCGCCTGGGAGTACGGTCGCAAATTAAACTCTAAGGATTGACGGGGCACGCACAGCGTGGA GCAGTGGTTAATTCGAGCACGCGCACAACTTACCGCCTTGACATACGGTCGCGAACAGAGATGTGTCTTCAG TCGGCTGGACCGATACGGTGCTGCATGGTGTCTGCTCACTCGGT
 >16S_SA112 GGGAGCGGCAGACGGGTGAGTAACGCGTGGAATCTACCTTTTGCTACGGAATAACTCAGGGAAACTTGTGC TAATACCGTATGTGCCCTTTTGGGGAAAGATTTATCGGCAAAAGGATGAGCCCGCGTTGGATTAGCTAGTTGG TGGGGTAAAGGCCACCAAGGCGACTATCCATAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGACA CAGGCGCCACACTCCTACGGGAGGCAGCAGTGGGGAAATATTGGACAATGGGCGCAAGCCTGATCCAGCCATG CCGCGTAGTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCCCGGTGAAGATAATGACGGTAACCGGAGAA AAAGCCCCGGCTAACTTCATGCCAGCGGCCGCGGTAATACAAAAGGGGCTAGCGTTGTTCCGATTACTGGG CGTAAAGCGCACGTAGGCGGACTTTTAAAGTCAAGGGTGAAATCCCAGAGCTCAACTCTGGAAGTGCCTTTGA TACTGGAAGTCTTGAGTATGGTAGAGGTGAGTGGAAATCCGAGTGATAGAGGTGAAATTCATAGATATTCTGA GGAACCCAGTGGCGAAGGCGGCTACTGGACCATTACTGACGCTGAGGTGCGAAAGCGTGGGGAGCATGAGGAT GATTAATACCCGGTAGTCCACGCCGTAAACGATGATGTTAACCGTCGGGTGTTACACTTCGGTGGCGCAGCTAA ACGCATTAAACATTCCGCCTGGGGATTACGGTCGCAAATTAAACTCTAAGGATTGACGGGGGCACGCACAACC GTGAACATGTGGTTTATTCAAGCACGCGCACAACTTACGGCCTTGACATACAGTTCGCGAACAGAGAGTGTCT TCATTCTGTGGACGGATACGGTGCTCATGGTGTCTCACTCGGTCTGAGAGTTGGTATC
 >16S_SU141 GCAAGTCGAGCGCCCCGAGGGGAGCGGCAGACGGGTGAGTAACGCGTGGAATCTACCTTTTGCTACGGAA TAACTCAGGGAAACTTGTGCTAATACCGTATGTGCCCTTTTGGGGAAAGATTTATCGGCAAAAGGATGAGCCC CGTTTGAGATTAGCTAATTGGTGGGTAAAGGCCACCAAGGCGACGATCCATAGCTGGTCTGAGAGGATGAT CAGCCACACTGGGACTGAGACACGGCCCCACACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGC GCAAGCCTGATCCAGCCATGCCGCGTGAGTGATGAAGGCCCTAGGGTTGTAAAGCTCTTTCACCGGTGAAGA TAATGACGGTACCGGAGAAAAAGCCCCGGCTAACTTCATGCCAGCGGCCGCGGTAATACAAAAGGGGCTAG CGTTGTTCCGATTACTGGGCGTAAAGCGCAGTAGGGCGGACTTTTAAAGTCAAGGGTGAAATCCCAGAGCTC AACTCTGGAAGTCCCTTTGATACCTGGAAGTCTTGAGTATGGTAGAGGTGAGTGAATTCGAGTGTAGAGGT GAAATTCGTAGATATTCTGAGGAACACCAGTGGCGAAGGCGGCTCACTGGACCATT
 >16S_FP163 TGTAGAGGTTAAGTCCCGCAACGAGCAAAAGTATTGTGTCTGGGACTGCCCTTGGTGGGGGGGGATATACAGT GAAAGGGGTAGATTATCCACATCGGGTCCCGACCAAAAAGAGGGAGATTTTGGGGCCTCGCCCTCTCATAT GTGCCGATAGGGGAATCTCTTGTGGGGGGGGTAGGCGCTCCTAGGGGACAACCTCCATCTCGGCTGAGAGAA GGACACGCCCACTGGGGAAAGTGAAACGGGCTCCACACCCACGCGGGGGGCGGTGGGGGAAATTTTTCAC TGGGGCCCCGCTGAGACACCCCTTTCCCGCGT

>16S_FP292 TTGCTTCCCGCTGACGAGCGGCGGACGGGTGAGTAATGTATGGGGATCTGCCCGATAGAGGGGGATAACCAC TGGAAACGGTGGCTAATACCGCATAATCTCTTAGGAGCAAAGCAGGGGAACCTCGGTCTTGCGCTATCGGA TGAACCCATATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGA GGATGATCAGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCAC AATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCCTAGGGTTGTAAAGTACTTTCAGTC GGGAGGAAGGCGTTGATGCTAATATCATCAACGATTGACGTTACCGACGGAAGAAGCACCGGCTAACTCCGT GCCAGCAGCCGCGTAATACGGAGGGTGCAAGCGTTAATCGGAATT
>16S_HP125 TGGCGAACAGATGAGTAACACGTGAGTAACCTGCCCTTGACTCTGGGATAAGCCTGGGAACTGGGTCTAAT ACCGGATATGACCTTCCATCGCATGGTGGTTGGTGAAAGCTTTTGTGGTTTTGGATGGACTCGTGGCCTAT CTCTTGTTGGT
>16S_HP128 CGCAAAAAAATAGAGGGAGATTTTGGGCCCTCGCCCTATCAGATGTGCCCATATGATAATCGCGAGTGGGGG GGGTAAGCGCTCATAGGCGACAATATCCAAATCGGCTCAGAGAAGGACACCCCCACTGGGGAACCTGAAACC GGTTCACACCCACGCGGGGGGCGTGGGGGGAAATTTTGCACTGGGGGCCCGCCCCATACACCCCTTCCC GCGTGTAAAAAAGCGTTTGGGGTT

Table S3: 16S Sequences of the isolates not used for detailed study

		10 ⁶ cfu/g of soil				10 ⁶ cfu/g of soil			
		<i>Ensifer</i> sp. HP127				<i>Ensifer</i> sp. HP113			
		Wk1	wk2	Wk3	Wk5	Wk1	wk2	Wk3	Wk5
Primary	Proximal	4.36 (0.10)a	6.42 (0.10)b	6.23 (0.07)c	6.56 (0.07)d	4.80 (0.13)a	5.58 (0.27)B	6.48 (0.58)c	6.31 (0.08)d
	Subprox.	4.59 (0.11)a	4.98 (0.03)b	4.26 (0.48)c	5.73 (0.04)d	4.63 (0.13)a	5.42 (0.22)b	5.20 (1.09)C	5.10 (0.13)d
	Central	4.42 (0.10)a	4.77 (0.07)b	3.52 (0.10)c	5.21 (0.15)d	4.20 (0.17)a	4.31 (0.20)b	4.98 (0.14)C	5.18 (0.22)d
	Subdistal	4.46 (0.15)a	4.52 (0.07)b	2.87 (0.10)c	5.20 (0.17)d	4.36 (0.10)a	2.85 (0.14)B	4.40 (0.21)C	4.75 (0.38)d
	Distal	3.46 (0.15)a	3.80 (0.04)b	2.67 (0.17)c	3.42 (0.10)d	3.10 (0.17)a	3.00 (0.11)B	3.19 (0.16)c	3.38 (0.21)d
Secondary	Prox. Prox.	4.36 (0.10)	3.42 (0.10)	4.36 (0.17)	6.36 (0.10)	3.36 (0.10)	4.45 (0.23)	5.55 (0.27)	5.98 (0.09)
	Prox. Cent.	3.30 (0.00)	3.36 (0.10)	4.46 (0.17)	4.36 (0.10)	4.30 (0.00)	3.89 (0.08)	4.16 (0.09)	5.08 (0.19)
	Prox., Dist.	2.63 (0.06)	2.77 (0.07)	4.09 (0.10)	2.20 (0.17)	3.42 (0.10)	3.30 (0.11)	3.81 (0.07)	3.79 (0.01)
	Cent. Prox.	5.95 (0.05)	4.67 (0.06)	4.03 (0.10)	5.52 (0.07)	3.97 (0.06)	4.15 (0.18)	4.89 (0.18)	5.67 (0.20)
	Cent., Cent	3.92 (0.08)	3.67 (0.19)	2.87 (0.17)	4.42 (0.10)	2.92 (0.08)	2.20 (0.10)	3.55 (0.17)	4.01 (0.08)
	Cent., Dist.	3.52 (0.07)	2.75 (0.05)	3.81 (0.10)	4.36 (0.10)	3.42 (0.10)	1.05 (0.09)	2.41 (0.06)	3.01 (0.08)
	Dist., Prox.			2.49 (0.24)	4.36 (0.10)		1.32 (0.07)	2.73 (0.06)	3.88 (0.06)
	Dist., Cent.			4.36 (0.17)	3.36 (0.10)	1.03 (0.09)		2.44 (0.09)	3.98 (0.05)
Thin new roots from:	Dist., Dist			3.69 (0.30)	3.42 (0.10)				2.69 (0.07)
	1° Prox.		4.66 (0.10)	4.19 (0.03)		1.05 (0.19)	3.44 (0.07)	3.97 (0.24)	5.18 (0.19)
	1° Subprox.		3.56 (0.07)	3.69 (0.35)	4.42 (0.10)		4.05 (0.09)	4.63 (0.18)	3.49 (0.13)
	1° Central		3.42 (0.10)	2.83 (0.17)	3.42 (0.10)			2.00 (0.09)	2.77 (0.08)
	1° Subdist.		2.20 (0.17)	4.10 (0.17)	4.36 (0.10)				4.41 (0.09)
	1° Distal			3.20 (0.24)	3.20 (0.17)			2.14 (0.15)	1.25 (0.08)
	2° PP				4.20 (0.17)		2.08 (0.04)		4.05 (0.16)
	2° PC				3.10 (0.17)				2.84 (0.09)
	2° PD				2.11 (0.16)				
	2° CP				3.36 (0.10)				3.10 (0.10)
	2° CC				4.20 (0.17)				3.69 (0.17)
	2° CD				3.42 (0.10)				

Table S4: Spatiotemporal distribution pattern of *Ensifer* sp. HP127 and *Ensifer* sp. HP113 when inoculated in soil at 10⁶ cfu/g of soil. The labels follow the same notation style as mentioned in Figure 4.1. The values refer to mean log₁₀ (cfu/cm of root) of respective strains from different regions of the roots at week 1, 2, 3 and 5 (Wk1-5) (n=3). Values in parenthesis indicate SD. Only the values in **boldface** are shown for statistical significance comparison. Values with same alphabet across the row are compared with each other. Values with same case across the row are statistically non-significant whereas values with different case (lower and upper) across the row are statistically significant. (**p ≤ 0.01; *p≤0.05; n=3). Cells highlighted in grey indicate the roots hadn't emerged, whereas cells highlighted in blue denote that no bacteria were recovered.

		Week1		Week2		Week3		Week5	
		Control	Test	Control	Test	Control	Test	Control	Test
Primary	P	5.56 (0.07)	3.98 (0.12)***	5.81 (0.12)	3.76 (0.21)***	6.42 (0.10)	4.59 (0.23)***	6.68 (0.15)	4.73 (0.09)***
	SP	3.36 (0.10)	3.05 (0.05) ^{ns}	4.42 (0.10)	2.95 (0.06)**	5.36 (0.10)	4.42 (0.14)*	5.35 (0.37)	4.56 (0.14)*
	C	1.42 (0.10)	1.42 (0.12) ^{ns}	3.95 (0.05)	3.95 (0.16) ^{ns}	4.89 (0.11)	4.63 (0.11) ^{ns}	4.13 (0.24)	4.82 (0.12) ^{ns}
	SD	1.10 (0.17)	2.36 (0.13)**	1.10 (0.17)	1.20 (0.09) ^{ns}	1.87 (0.11)	3.30 (0.09)***	1.81 (0.18)	3.36 (0.21)***
	D	1.00 (0.00)	1.87 (0.11)*	1.00 (0.00)	2.84 (0.12)**	1.10 (0.17)	3.10 (0.23)***		3.36 (0.07)
Secondary	PP	4.36 (0.10)	3.46 (0.04)*	4.93 (0.08)	3.46 (0.13)*	5.00 (0.68)	5.11 (0.21) ^{ns}	4.82 (0.11)	4.10 (0.20) ^{ns}
	PC	3.52 (0.07)	1.52 (0.05)***	3.36 (0.10)	1.10 (0.05)***	4.36 (0.10)	4.20 (0.16) ^{ns}	3.36 (0.10)	4.20 (0.27)***
	PD	3.36 (0.10)		1.10 (0.17)	1.10 (0.09) ^{ns}	1.83 (0.16)	2.10 (0.08)*	1.20 (0.17)	2.20 (0.13)***
	CP	1.20 (0.17)	3.13 (0.21)**	2.20 (0.17)	2.52 (0.12) ^{ns}	2.52 (0.46)	4.20 (0.16)***	2.23 (0.40)	4.52 (0.05)***
	CC	1.10 (0.17)		1.36 (0.01)	2.36 (0.05)*	2.36 (0.10)	3.20 (0.14)**	2.36 (0.36)	3.20 (0.16)*
	CD			1.10 (0.18)	2.20 (0.13)*	1.65 (0.50)	2.16 (0.19)**		2.01 (0.06)
	DP					1.20 (0.17)		1.98 (0.32)	1.84 (0.12) ^{ns}
	DC					1.36 (0.10)			
	DD								
Thin roots from:	1° P				2.95 (0.13)	1.77 (0.50)	3.46 (0.17)***		4.56 (0.20)
	1° sp				2.20 (0.06)		2.53 (0.14)	1.44 (0.39)	4.36 (0.24)***
	1° C				1.10 (0.08)		2.26 (0.07)		3.20 (0.09)
	1° Sd				1.00 (0.10)	1.48 (0.30)	3.30 (0.13)***	1.52 (0.47)	2.03 (0.13)**
	1° D								1.52 (0.06)
	2° PP								4.36 (0.27)
	2° PC								3.26 (0.13)
	2° PD								1.46 (0.03)
	2° CP								2.10 (0.14)
	2° CC								1.56 (0.06)
	2° CD								

Table S5: Colonization dynamics of *Ensifer* sp. HP113 on the root when coated on root and the soil is inoculated with *Ensifer* HP127 at 10⁶ cfu/g of soil (test), or if the soil is sterile (control). The labels follow the same notation style as mentioned in Figure 4.1. The values refer to avg. log₁₀ (cfu/ml) of respective strain in respective areas of the roots at week 1, 2, 3 and 5 (Wk1-5) calculated from three independent observations, each with technical repeats. Values in parenthesis indicates SD. Values of control are compared with that of the test for statistical significance. * denotes p≤0.05, ** denotes p≤0.01 and *** denotes p≤0.001 calculated from individual unpaired t-tests. ns stands for non-significant.

		Week1		Week2		Week3		Week5	
		Control	Test	Control	Test	Control	Test	Control	Test
Primary	P	4.36 (0.34)	3.93 (0.20)*	6.42 (0.26)	3.98 (0.19)**	6.23 (0.30)	4.56 (0.21)*	5.56 (0.29)	5.56 (0.13) ^{ns}
	SP	4.59 (0.14)	2.67 (0.16)**	4.98 (0.21)	3.52 (0.14)*	4.26 (0.19)	4.03 (0.33) ^{ns}	5.73 (0.07)	5.42 (0.47) ^{ns}
	C	4.42 (0.19)	3.92 (0.27)*	4.77 (0.13)	4.20 (0.14) ^{ns}	3.52 (0.22)	4.36 (0.14)*	5.21 (0.30)	5.36 (0.15) ^{ns}
	SD	4.46 (0.21)	4.95 (0.31) ^{ns}	4.52 (0.17)	4.52 (0.16) ^{ns}	2.87 (0.13)	3.42 (0.15)*	5.20 (0.16)	4.36 (0.08)*
	D	3.36 (0.16)	3.52 (0.11) ^{ns}	3.80 (0.22)	4.42 (0.25)*	2.67 (0.12)	3.10 (0.21)**	3.42 (0.04)	3.00 (0.13) ^{ns}
Secondary	PP	4.36 (0.11)	3.63 (0.13)*	3.42 (0.09)	2.70 (0.10)**	4.36 (0.19)	2.10 (0.13)**	6.36 (0.28)	4.69 (0.09)*
	PC	3.30 (0.06)	3.67 (0.17) ^{ns}	3.36 (0.11)	2.52 (0.13)*	4.46 (0.28)	3.10 (0.18)*	4.36 (0.13)	4.36 (0.21) ^{ns}
	PD	2.63 (0.31)		2.77 (0.16)	2.73 (0.21) ^{ns}	4.09 (0.31)	4.36 (0.29) ^{ns}	2.20 (0.07)	2.98 (0.19) ^{ns}
	CP	5.95 (0.34)	4.52 (0.26)**	4.67 (0.14)	4.20 (0.16) ^{ns}	4.03 (0.26)	3.42 (0.21)*	5.52 (0.14)	5.42 (0.23) ^{ns}
	CC	3.92 (0.04)		3.67 (0.13)	3.80 (0.09) ^{ns}	2.87 (0.05)	4.10 (0.27)**	4.42 (0.12)	3.20 (0.07)*
	CD	3.52 (0.11)		2.75 (0.14)	2.69 (0.12) ^{ns}	3.81 (0.21)	3.42 (0.23) ^{ns}	4.36 (0.17)	3.55 (0.06)*
	DP					2.49 (0.13)	3.26 (0.31)*	4.36 (0.26)	2.93 (0.04)**
	DC					4.36 (0.23)	2.10 (0.11)**	3.36 (0.14)	3.36 (0.15) ^{ns}
	DD					3.69 (0.14)	1.83 (0.09)***	3.42 (0.23)	3.26 (0.25) ^{ns}
Thin roots from:	1° P			4.66 (0.13)	3.10 (0.16)*	4.19 (0.31)	2.98 (0.13)**		
	1° sp			3.56 (0.19)	2.52 (0.11)**	3.69 (0.47)	1.20 (0.15)***	4.42 (0.21)	3.52 (0.20)*
	1° C			3.42 (0.20)	4.46 (0.21)**	2.83 (0.16)	3.20 (0.23)*	3.42 (0.19)	3.77 (0.16) ^{ns}
	1° Sd			2.20 (0.05)	2.36 (0.22) ^{ns}	4.10 (0.33)	2.10 (0.17)**	4.36 (0.21)	3.36 (0.06)*
	1° D					3.20 (0.17)		3.20 (0.19)	3.10 (0.07) ^{ns}
	2° PP							4.20 (0.25)	3.36 (0.23)*
	2° PC							3.10 (0.16)	2.26 (0.12)**
	2° PD							2.11 (0.08)	2.10 (0.04) ^{ns}
	2° CP							3.36 (0.14)	3.63 (0.34) ^{ns}
	2° CC							4.20 (0.26)	2.59 (0.06)*
	2° CD							3.42 (0.18)	2.50 (0.02)**

Table S6: Colonization dynamics of *Ensifer* sp. HP127 on the root when inoculated in soil at 10⁶ cfu/g of soil in the presence (test) or absence (control) of *Ensifer* sp. HP113 as the root-coated strain. The labels follow the same notation style as mentioned in Figure 4.1. The values refer to avg. log₁₀ (cfu/ml) of respective strain in respective areas of the roots at week 1, 2, 3 and 5 (Wk1-5) calculated from three independent observations, each with technical repeats. Values in parenthesis indicates SD. Values of control are compared with that of the test for statistical significance. * denotes p≤0.05, ** denotes p≤0.01 and *** denotes p≤0.001 calculated from individual unpaired t-tests. ns stands for non-significant.

		Week1		Week2		Week3		Week5	
		Control	Test	Control	Test	Control	Test	Control	Test
Primary	P	5.06 (0.10)	4.80 (0.21) ^{ns}	6.06 (0.10)	5.60 (0.14) [*]	7.39 (0.09)	5.81 (0.09) [*]	7.47 (0.07)	5.76 (0.13) ^{**}
	SP	5.16 (0.27)	5.06 (0.34) ^{ns}	6.00 (0.00)	4.40 (0.06) ^{**}	5.87 (0.09)	4.00 (0.07) [*]	5.10 (0.17)	5.46 (0.06) ^{ns}
	C	4.92 (0.03)	4.20 (0.05) ^{ns}	4.74 (0.29)	4.16 (0.19) ^{ns}	4.72 (0.06)	3.08 (0.11) [*]	4.34 (0.18)	4.22 (0.02) ^{ns}
	SD	4.88 (0.06)	3.08 (0.12) [*]	2.47 (0.07)	1.55 (0.07) [*]	3.00 (0.18)	2.22 (0.20) [*]	2.32 (0.15)	2.55 (0.14) ^{ns}
	D	4.76 (0.15)	2.00 (0.05) ^{**}	2.32 (0.15)		2.02 (0.14)	1.88 (0.09) ^{ns}	2.10 (0.17)	1.56 (0.07) [*]
Secondary	PP	4.47 (0.07)	2.44 (0.06) ^{**}	4.29 (0.11)	3.25 (0.21) [*]	5.26 (0.07)	4.87 (0.21) [*]	4.54 (0.06)	4.21 (0.23) ^{ns}
	PC	3.99 (0.04)	2.14 (0.14) ^{ns}	4.30 (0.00)	2.87 (0.13) ^{**}	4.20 (0.17)	4.01 (0.06) ^{ns}	3.55 (0.15)	3.01 (0.19) ^{ns}
	PD	3.00 (0.00)		2.60 (0.21)		2.10 (0.17)	1.11 (0.09) [*]		
	CP	2.19 (0.19)	2.04 (0.11) ^{ns}	2.09 (0.18)	2.17 (0.06) ^{ns}	2.80 (0.13)	1.54 (0.11) [*]	3.16 (0.10)	3.29 (0.13) ^{ns}
	CC	1.60 (0.17)	1.04 (0.05) ^{ns}	1.63 (0.10)	1.34 (0.09) ^{ns}	2.02 (0.14)		2.65 (0.05)	2.11 (0.04) ^{ns}
	CD	1.43 (0.23)	1.00 (0.06) ^{ns}	1.20 (0.17)		1.19 (0.19)		1.36 (0.10)	
	DP							2.26 (0.07)	
	DC							1.42 (0.10)	
	DD								
Thin roots from:	1° P								1.14 (0.01)
	1° sp							2.36 (0.10)	
	1° C					2.54 (0.49)		2.26 (0.24)	
	1° SD					1.56 (0.50)			
	1° D					1.88 (0.13)		2.10 (0.17)	0.51 (0.08) ^{**}
	2° PP								
	2° PC								
	2° PD								
	2° CP							0.67 (0.58)	
	2° CC								
	2° CD							0.83 (0.76)	

Table S7: Colonization dynamics of *Ensifer* sp. HP127 on the root when coated on root and the soil is inoculated with *Ensifer* HP113 at 10⁶ cfu/g of soil (test), or if the soil is sterile (control). The labels follow the same notation style as mentioned in Figure 4.1. The values refer to avg. log₁₀ (cfu/ml) of respective strain in respective areas of the roots at week 1, 2, 3 and 5 (Wk1-5) calculated from three independent observations, each with technical repeats. Values in parenthesis indicates SD. Values of control are compared with that of the test for statistical significance. * denotes p≤0.05, ** denotes p≤0.01 and *** denotes p≤0.001 calculated from individual unpaired t-tests. ns stands for non-significant.

		Week1		Week2		Week3		Week5	
		Control	Test	Control	Test	Control	Test	Control	Test
Primary	P	4.80 (0.07)	3.71 (0.11) *	5.58 (0.26)	4.26 (0.13) *	6.48 (0.27)	4.84 (0.07) **	6.31 (0.20)	5.12 (0.17) *
	SP	4.63 (0.16)	3.55 (0.13) *	5.42 (0.07)	4.44 (0.17) *	5.20 (0.31)	3.84 (0.19) **	5.10 (0.16)	4.51 (0.08) *
	C	4.20 (0.23)	4.11 (0.14) ^{ns}	4.31 (0.16)	4.42 (0.26) ^{ns}	4.98 (0.35)	4.22 (0.27) ^{ns}	5.18 (0.19)	5.49 (0.06) ^{ns}
	SD	4.36 (0.14)	4.61 (0.08) ^{ns}	2.85 (0.14)	3.41 (0.14) *	4.40 (0.14)	4.91 (0.06) ^{ns}	4.75 (0.14)	5.24 (0.24) *
	D	3.10 (0.09)	3.44 (0.18) ^{ns}	3.00 (0.19)	3.74 (0.07) ^{ns}	3.19 (0.07)	4.60 (0.16) **	3.38 (0.28)	5.10 (0.34) **
Secondary	PP	3.36 (0.05)	2.02 (0.15) *	4.45 (0.11)	1.57 (0.07) **	5.55 (0.21)	2.01 (0.14) ***	5.98 (0.26)	2.57 (0.08) ***
	PC	4.30 (0.24)	3.44 (0.05) *	3.89 (0.06)	3.08 (0.16) ^{ns}	4.16 (0.12)	2.81 (0.17) ***	5.08 (0.07)	3.30 (0.16) **
	PD	3.42 (0.09)	3.51 (0.09) ^{ns}	3.30 (0.17)	2.41 (0.14)	3.81 (0.11)	2.44 (0.16) **	3.79 (0.16)	4.92 (0.18) *
	CP	3.97 (0.15)	3.81 (0.17) ^{ns}	4.15 (0.16)	4.43 (0.09) ^{ns}	4.89 (0.08)	4.19 (0.13) ^{ns}	5.67 (0.19)	5.43 (0.11) ^{ns}
	CC	2.92 (0.05)	3.55 (0.20) *	2.20 (0.14)	1.36 (0.04) *	3.55 (0.21)	3.02 (0.11) ^{ns}	4.01 (0.17)	4.81 (0.23) ^{ns}
	CD	3.42 (0.04)	3.37 (0.21) ^{ns}	1.05 (0.05)	2.07 (0.05) *	2.41 (0.16)	2.81 (0.17) ^{ns}	3.01 (0.23)	2.84 (0.07) *
	DP		2.12 (0.04)	1.32 (0.09)		2.73 (0.05)	2.88 (0.07) ^{ns}	3.88 (0.05)	4.76 (0.16) *
	DC	1.03 (0.04)				2.44 (0.07)	2.02 (0.21) ^{ns}	3.98 (0.14)	4.22 (0.14) *
	DD		1.00 (0.04)				1.13 (0.20)	2.69 (0.10)	
Thin roots from:	1° P	1.05 (0.06)	1.00 (0.08) ^{ns}	3.44 (0.01)	2.19 (0.19) *	3.97 (0.09)	3.22 (0.17) ^{ns}	5.18 (0.16)	4.30 (0.17) ^{ns}
	1° SP			4.05 (0.14)	2.55 (0.11) **	4.63 (0.21)	3.83 (0.10) **	3.49 (0.17)	2.33 (0.16) *
	1° C		0.88 (0.09)		3.10 (0.07)	2.00 (0.14)		2.77 (0.20)	1.94 (0.11) *
	1° SD		1.22 (0.10)				3.44 (0.11)	4.41 (0.29)	3.04 (0.16) **
	1° D					2.14 (0.04)	1.10 (0.16) *	1.25 (0.11)	
	2° PP			2.08 (0.06)	1.40 (0.14) **			4.05 (0.21)	1.80 (0.34) ***
	2° PC				1.11 (0.17)			2.84 (0.08)	
	2° PD								
	2° CP						1.04 (0.04)	3.10 (0.13)	
	2° CC							3.69 (0.06)	
	2° CD								

Table S8: Colonization dynamics of *Ensifer sp.* HP113 on the root when inoculated in soil at 10⁶ cfu/g of soil in the presence (test) or absence (control) of *Ensifer sp.* HP127 as the root-coated strain. The labels follow the same notation style as mentioned in Figure 4.1. The values refer to avg. log₁₀ (cfu/ml) of respective strain in respective areas of the roots at week 1, 2, 3 and 5 (Wk1-5) calculated from three independent observations, each with technical repeats. Values in parenthesis indicates SD. Values of control are compared with that of the test for statistical significance. * denotes p≤0.05, ** denotes p≤0.01 and *** denotes p≤0.001 calculated from individual unpaired t tests. ns stands for

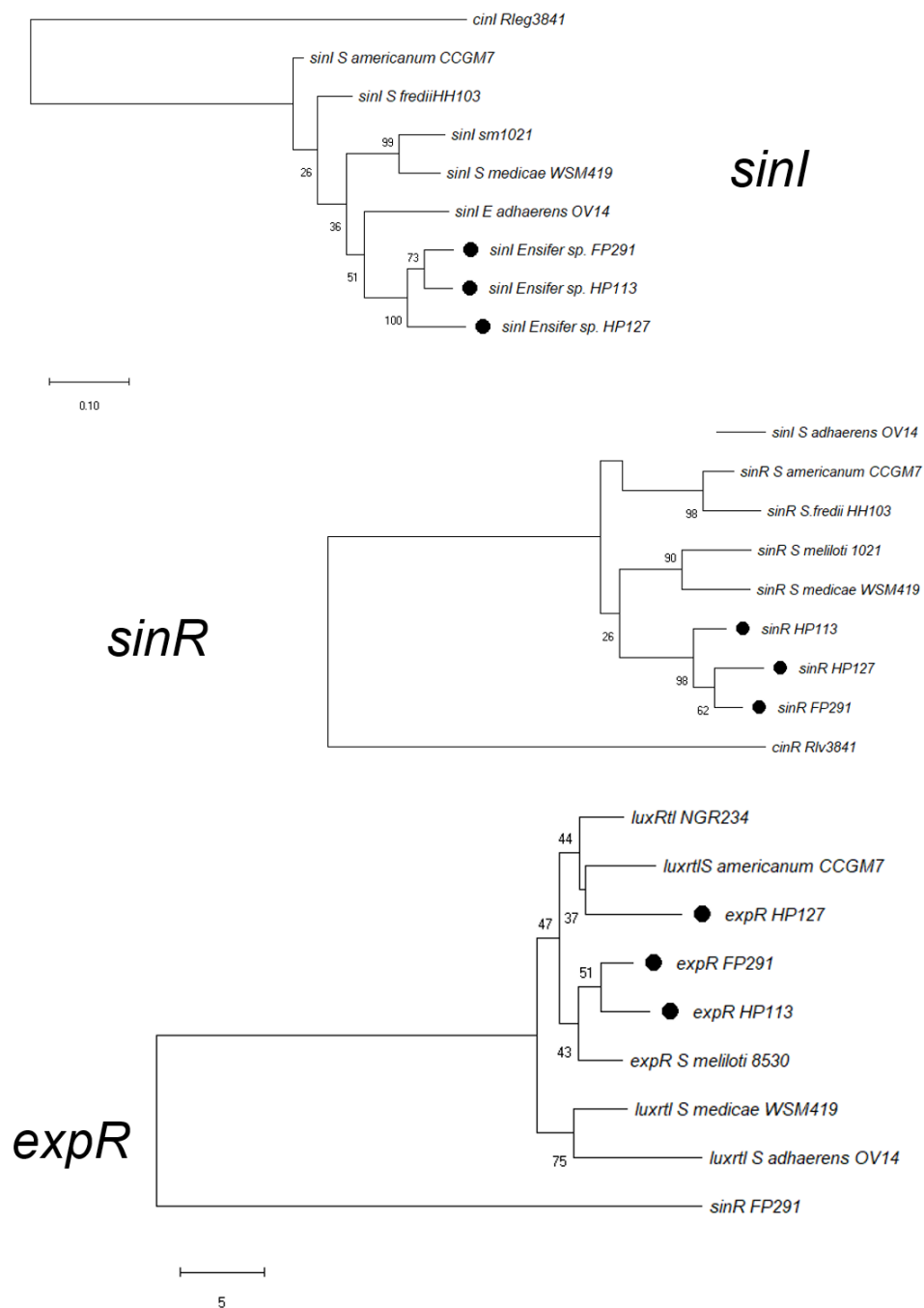


Figure S1A Neighbour joining trees of sinI, traI and expR. Sequences of this study are indicated with a bold sphere.

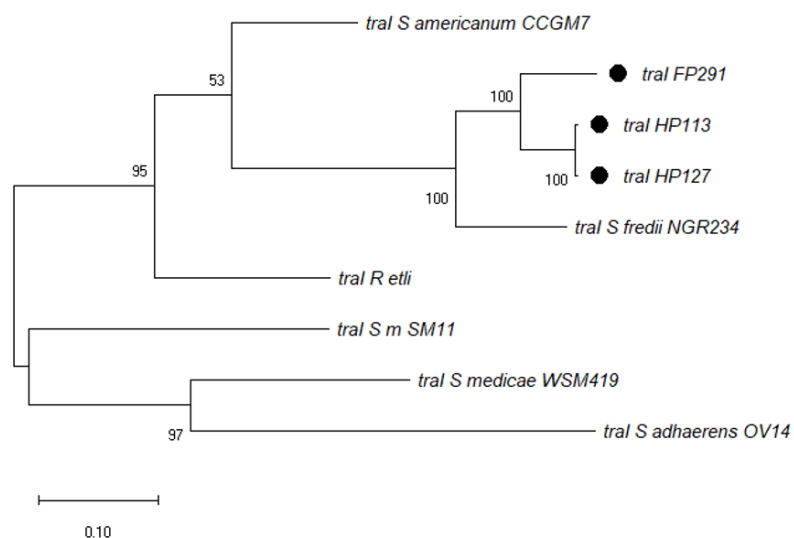
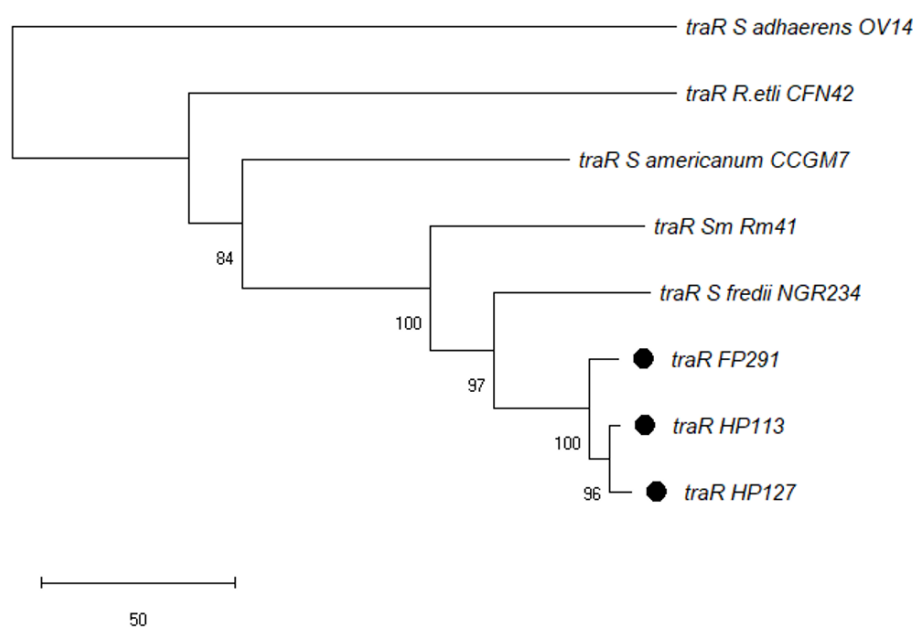
traI*traR*

Figure S1B Neighbour joining trees of *traI* and *traR*. Sequences of this study are indicated with a bold sphere.



Figure S2A Detection of conserved domains in sinI, traI, sinR and traR from the homologues detected in Ensifer nodulating pigeon pea

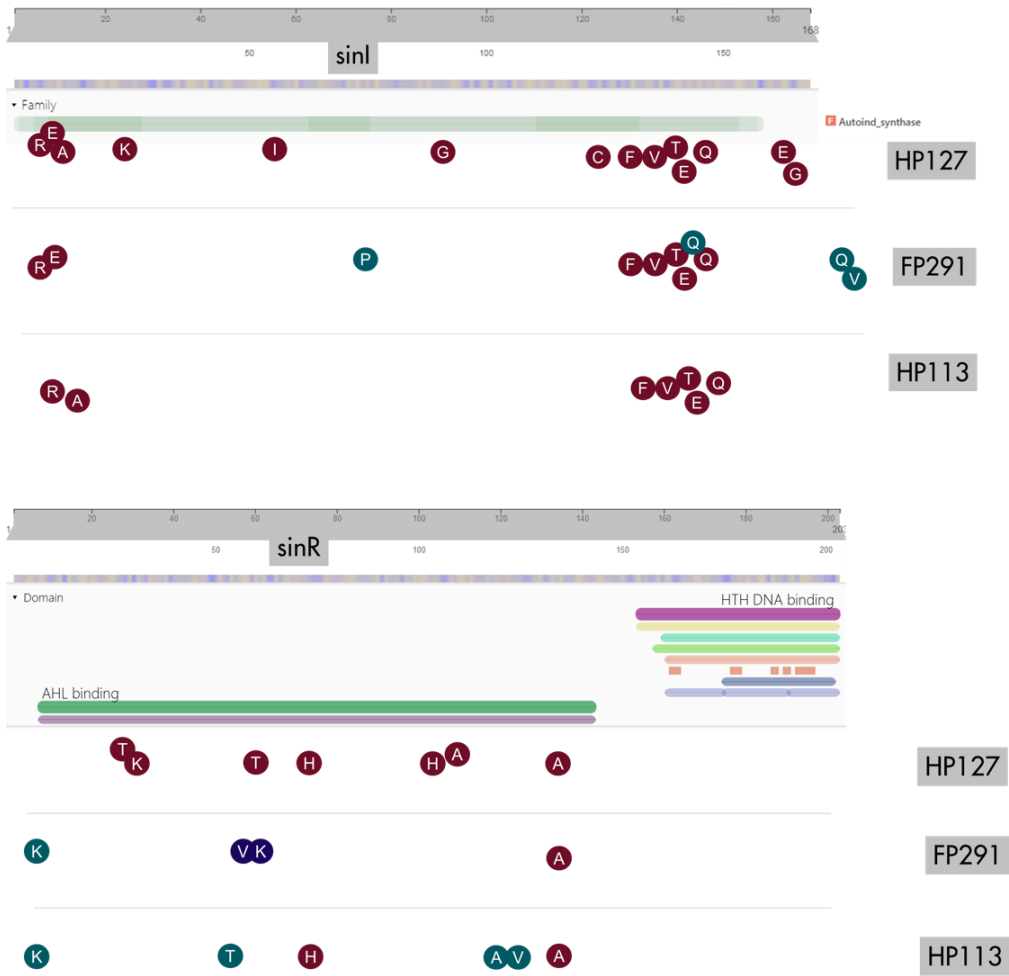


Figure S2B Mapping of amino acid differences in the sinI and sinR homologues across detected domains. Amino acids are shown as single letter code in sphere at length in the sequence corresponding to their location. Blue and Green spheres indicate the amino acids varying across the three isolates as well.

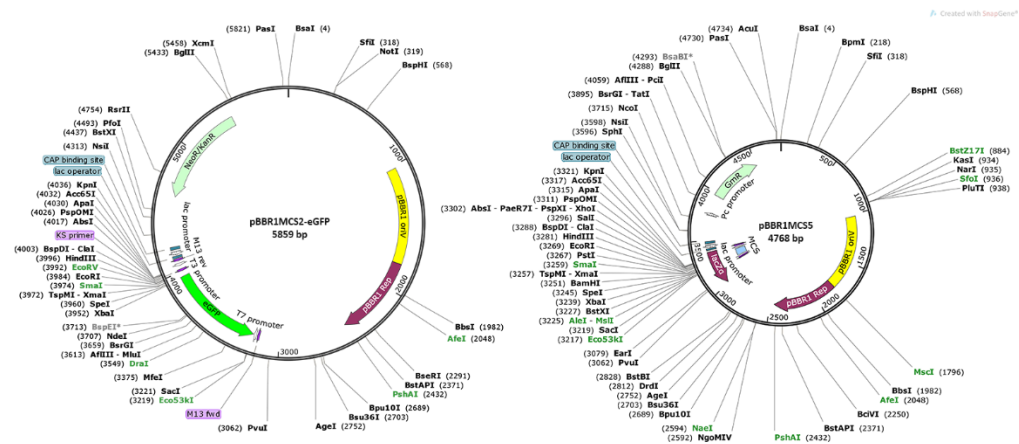


Figure S3B Plasmid maps of pBBR1MCS2-eGFP and pBBR1MCS5 (used in chapter 3)