

Supplemental file one containing the following information:

- 1) Seven DNA sequences of *pltR* gene of strain Pf-5, LK298, LK361, LK362, LK363, LK364 and LK365.
- 2) Alignment of the seven *pltR* DNA sequences
- 3) Alignment of the seven PltR protein sequences
- 4) Two DNA sequences of *gfp* in the transcriptional fusion of *prnA::gfp(AGA)* and *prnA::gfp(CGC)* (Figure 5A).
- 5) Alignment of the two *gfp* DNA sequences
- 6) Alignment of the two GFP protein sequences

1-1) *pltR*-Pf-5 (PFL_2785)

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1 ATGAAGGCGC TAGGCGTTGT CAATGACATA GACCTTTATA TATCCGTAAC TAAAACGGGT
61 AGTTTCTCCG AAACAGGAAG ACTACTTGGC ATCCCACCTT CTTCGGTGAT GCGCAGAATC
121 AATAGCCTCG AAAAAGAAGT TGAAACCTGT CTATTCAATC GATCGACAAA ATGCTTGATA
181 CTTACCGAAA CAGGCCTGCT CTTTCTCGAA CATGCAAAGA ACATCTCGAG ATGCATTGGG
241 CATGCTAGAT CAGAAGTAAA AGAACACACT GCATCGACCC TTGGCGTTCT CAAGGTTTCA
301 GCACCCGTGG CCTTTGGACG GCGCCATGTA GCGCCTTTAT TGAGCAGAAT ACTGAACCAT
361 CATCCCGGTT TGAATATTGA ATTCTCGCTT AACGACAAAG CTCTCGACCC CAGCATCGAT
421 AACGTCGATA TCTGTATCAA GCTGGGCATA TTGCCGGACA GTAATCTGAT TCCAACGAAA
481 CTTGCGGATA TGCGGCGCGT GCTCTGCGCA AGCCCGGAAT ACATCCGGCA ACACGGCTGT
541 CCGCAAACCT TTGAAGACCT GTACCAACAT GCCTGCCTGA TCCACAGCAC CTGCAGCAAC
601 TTCTCACTGA CTTGGCAATT CAAGGTCGAT GGCCTGCTCA AGAAGCTCAT GCCCAGCAGC
661 CGGCTATCGG TCAACAGTTC CGAGTTGCTG GTGGACGGCG CCCTTCAGGG CATAGGAATC
721 ATCCACGCGC CCACCTGGCT GGTGCATGAA CAGATCGCCA GCGGCCAACT GGTGTGCTG
781 CTCGACGAAT ATTGCGAGGC CGATCCGCAA CAGGGAGCGA TCTACGCACT GAGGGCACGC
841 AGCAGCGTTG TCCCGGCCAA GACCCGCCTG TTCATCAATG AGTTGAAACG CTCGATCGGC
901 AGCACGCCTT ACTGGGACTT GCCGTTTGAA AAGGAAATAC CGCAGACCCT GGCCACCCTG
961 CATTTCGATA CCGCAATGCA TTCAGCGCTT TCCAGAGCGA CCACCTTGCA AGACAAGAGC
1021 CAGACATCAT GA
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1-2) *pltR*-LK298

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1 ATGAAGGCGC TGGGCGTGGT GAACGACATC GACCTGTACA TCAGCGTGAC CAAGACGGGC
61 AGCTTCAGCG AGACCGGCCG GCTCCTGGGC ATCCCGCCCA GCAGCGTCAT GCGCCGCATC
121 AACTCGCTCG AAAAGGAGCT CGAGACCTGC CTGTTCAACC GCTCCACCAA GTGCCTGATC
181 CTGACCGAGA CGGGCCTGCT GTTCCTGGAA CACGCCAAGA ACATCAGCCG CTGCATCGGC
241 CACGCCCCGA GCGAAGTCAA GGAACATACC GCGAGCACCC TCGGCGTCCT GAAGGTGTCTG
301 GCGCCGGTCC CGTTCGGCCG TCGCCATGTC GCCCGCTCC TGAGCCGCAT CCTGAACCAC
361 CACCCGGGGC TGAAGATCGA ATTCTCGCTG AACGATAAGG CCCTGGACCC GTCGATCGAC
421 AATGTGCGAC TCTGCATCAA GCTCGGCATC CTGCCGGATT CCAACCTCAT CCCGACCAAA
481 CTGGCCGATA TGCGCCGCGT GCTGTGCGCG TCGCCGGAGT ACATCCGCCA GCATGGCTGC
541 CCGCAGACCC TCGAGGACCT GTACCAGCAC GCCTGCCTGA TCCACTCGAC CTGCAGCAAC
601 TTCAGCCTCA CCTGGCAGTT CAAGGTCGAC GGCCTCCTGA AGAAACTGAT GCCGTCCAGC
661 CGCCTCTCCG TCAACTCCTC CGAACTGCTG GTCGACGGCG CGCTCCAGGG CATCGGCATC
721 ATCCACGCCC CGACCTGGCT CGTGCATGAG CAGATCGCCA GCGGCCAGCT GGTGAGCCTC
781 CTCGACGAGT ACTGCGAGGC GGACCCGCAG CAAGGCGCCA TCTACGCCCT CCGCGCGCGT
841 TCGTCCGTGG TCCCGGCCAA GACCCGGCTC TTCATCAACG AGCTGAAGCG CAGCATCGGC
901 AGCACCCCCT ACTGGGACCT CCCGTTTGAA AAAGAAATCC CGCAGACCCT GGCCACCCTG
961 CACTTCGACA CCGCCATGCA CTCCGCCCTG AGCCGCGCCA CCACCTGCA GGACAAGAGC
1021 CAGACATCAT GA
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1-3) *pltR*-LK361

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1 ATGAAGGCGC TGGGCGTGGT CAATGACATC GACCTGTACA TCTCCGTGAC TAAAACGGGT
61 AGTTTCTCCG AAACAGGAAG ACTCCTGGGC ATCCCACCTT CTTCGGTGAT GCGCAGAATC
121 AATAGCCTCG AAAAAAGAACT CGAAACCTGT CTGTTCAATC GATCGACAAA ATGCTTGATC
181 CTGACCGAAA CAGGCCTGCT CTTTCTCGAA CATGCAAAGA ACATCTCGAG ATGCATTGGG
241 CATGCTAGAT CAGAAGTCAA AGAACACACT GCATCGACCC TCGGCGTCCT CAAGGTGTCA
301 GCACCCGTGG CCTTTGGACG GCGCCATGTC GCGCCTTTAT TGAGCAGAAT CCTGAACCAT
361 CATCCCGGTT TGAAAATTGA ATTCTCGCTG AACGACAAAG CTCTCGACCC CAGCATCGAT
421 AACGTCGATA TCTGTATCAA GCTGGGCATC TTGCCGGACA GTAATCTGAT TCCACGAAA
481 CTGGCGGATA TGCGGCGCGT GCTCTGCGCA AGCCCGGAAT ACATCCGGCA ACACGGCTGT
541 CCGCAAACTC TCGAAGACCT GTACCAACAT GCCTGCCTGA TCCACAGCAC CTGCAGCAAC
601 TTCTCACTGA CCTGGCAATT CAAGGTCGAT GGCCTGCTCA AGAAGCTCAT GCCCAGCAGC
661 CGGCTCTCGG TCAACAGTTC CGAGTTGCTG GTGGACGGCG CCCTCCAGGG CATCGGAATC
721 ATCCACGCGC CCACCTGGCT GGTGCATGAA CAGATCGCCA GCGGCCAACT GGTGTCGCTG
781 CTCGACGAAT ACTGCGAGGC CGATCCGCAA CAGGGAGCGA TCTACGCACT GAGGGCACGC
841 AGCAGCGTGG TCCCGGCCAA GACCCGCCCTG TTCATCAATG AGTTGAAACG CTCGATCGGC
901 AGCAGCGCCTT ACTGGGACTT GCCGTTTGAA AAGGAAATCC CGCAGACCCT GGCACCCCTG
961 CATTTCGATA CCGCAATGCA TTCAGCGCTG TCCAGAGCGA CCACCTTGCA AGACAAGAGC
1021 CAGACATCAT GA

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1-4) *pltR*-LK362

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1 ATGAAGGCGC TAGGCGTTGT CAATGACATA GACCTTTATA TATCCGTAAC CAAAACGGGC
61 AGTTTCTCCG AAACAGGCAG ACTACTTGGC ATCCCGCCCT CTTCGGTGAT GCGCAGAATC
121 AATAGCCTCG AAAAAAGAACT TGAAACCTGT CTATTCAATC GATCGACAAA ATGCTTGATA
181 CTTACCGAAA CAGGCCTGCT CTTTCTCGAA CATGCAAAGA ACATCTCGAG ATGCATTGGG
241 CATGCCAGAT CAGAAGTAAA AGAACACACC GCATCGACCC TTGGCGTTCT CAAGGTTTCA
301 GCACCCGTGG CCTTTGGCCG GCGCCATGTA GCGCCGTTAT TGAGCAGAAT ACTGAACCAT
361 CATCCCGGGT TGAAAATTGA ATTCTCGCTT AACGACAAAG CCCTCGACCC CAGCATCGAT
421 AACGTCGATA TCTGTATCAA GCTGGGCATA TTGCCGGACA GTAATCTGAT TCCGACGAAA
481 CTTGCGGATA TGCGGCGCGT GCTCTGCGCA AGCCCGGAAT ACATCCGGCA ACACGGCTGT
541 CCGCAAAACC TTGAAGACCT GTACCAACAT GCCTGCCTGA TCCACAGCAC CTGCAGCAAC
601 TTCTCACTGA CCTGGCAATT CAAGGTCGAT GGCCTGCTCA AGAAGCTCAT GCCCAGCAGC
661 CGGCTATCGG TCAACAGTTC CGAGTTGCTG GTGGACGGCG CCCTTCAGGG CATAGGCATC
721 ATCCACGCGC CCACCTGGCT GGTGCATGAA CAGATCGCCA GCGGCCAACT GGTGTCGCTG
781 CTCGACGAAT ATTGCGAGGC CGATCCGCAA CAGGGCGCGA TCTACGCACT GAGGGCACGC
841 AGCAGCGTTG TCCCGGCCAA GACCCGCCCTG TTCATCAATG AGTTGAAACG CTCGATCGGC
901 AGCAGGCCCT ACTGGGACTT GCCGTTTGAA AAGGAAATAC CGCAGACCCT GGCACCCCTG
961 CATTTCGATA CCGCAATGCA TTCAGCGCTT TCCAGAGCGA CCACCTTGCA AGACAAGAGC
1021 CAGACATCAT GA

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1-5) *pltR*-LK363

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1 ATGAAGGCGC TAGGCGTTGT CAATGACATA GACCTTTATA TATCCGTAAC TAAAACGGGT
61 AGTTTCTCCG AAACAGGAAG ACTACTTGGC ATCCCACCTA GCTCGGTGAT GCGCAGAATC
121 AATAGCCTCG AAAAAAGAACT TGAAACCTGC CTATTCAATC GCTCGACAAA ATGCCTGATA
181 CTTACCGAAA CAGGCCTGCT CTTCTCGAA CATGCCAAGA ACATCTCGAG ATGCATTGGG
241 CATGCTAGAT CAGAAGTAAA AGAACACACT GCGTCGACCC TTGGCGTTCT CAAGGTTTCA
301 GCGCCCGTGG CCTTCGACG GCGCCATGTA GCGCCTTTAC TGAGCAGAAT ACTGAACCAT
361 CATCCCGGTC TGAAAATTGA ATTCTCGCTT AACGACAAAG CTCTCGACCC CAGCATCGAT

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421	AACGTCGATA	TCTGCATCAA	GCTGGGCATA	CTGCCGGACA	GTAATCTGAT	TCCAACGAAA
481	CTTGCGGATA	TGCGGCGCGT	GCTCTGCGCG	AGCCCCGGAAT	ACATCCGGCA	ACACGGCTGC
541	CCGCAAACTC	TTGAAGACCT	GTACCAACAT	GCCTGCCTGA	TCCACAGCAC	CTGCAGCAAC
601	TTCTCACTGA	CCTGGCAATT	CAAGGTCGAT	GGCCTGCTCA	AGAAAGTCAT	GCCCAGCAGC
661	CGGCTATCGG	TCAACAGTTC	CGAGTGCTG	GTGGACGGCG	CCCTTCAGGG	CATAGGAATC
721	ATCCACGCGC	CCACCTGGCT	GGTGATGAA	CAGATCGCCA	GCGGCCAACT	GGTGTGCTG
781	CTCGACGAAT	ATTGCGAGGC	CGATCCGCAA	CAGGGAGCGA	TCTACGCCCT	GAGGGCGCGC
841	AGCAGCGTTG	TCCCGGCCAA	GACCCGCCCTG	TTCATCAATG	AGCTGAAACG	CTCGATCGGC
901	AGCACGCCTT	ACTGGGACCT	CCCGTTGCAA	AAGGAAATAC	CGCAGACCCT	GGCCACCCTG
961	CATTTCGATA	CCGCCATGCA	TTCAGCGCTT	TCCAGAGCGA	CCACCCTGCA	AGACAAGAGC
1021	CAGACATCAT	GA				

1-6) *pltR*-LK364

1	ATGAAGGCGC	TAGGCGTTGT	CAATGACATA	GACCTTTATA	TATCCGTAAC	TAAAACGGGT
61	AGCTTCTCCG	AAACAGGACG	GCTACTTGGC	ATCCCACCTT	CTTCGGTGAT	GCGCCGCATC
121	AATAGCCTCG	AAAAAGAACT	TGAAACCTGT	CTATTCAATC	GATCGACAAA	ATGCTTGATA
181	CTTACCGAAA	CAGGCCTGCT	CTTTCTCGAA	CATGCAAAGA	ACATCTCGCG	CTGCATCGGG
241	CATGCTCGGT	CAGAAGTAAA	AGAACACACT	GCATCGACCC	TTGGCGTTCT	CAAGGTTTCA
301	GCACCCGTGG	CCTTTGGACG	GCGCCATGTA	GCGCCTCTCT	TGAGCCGCAT	ACTGAACCAT
361	CATCCCGGTT	TGAAAATCGA	ATTCTCGCTT	AACGACAAAG	CTCTCGACCC	CAGCATCGAT
421	AACGTCGATA	TCTGTATCAA	GCTGGGCATA	TTGCCGGACT	CCAATCTGAT	CCCAACGAAA
481	CTTGCGGATA	TGCGGCGCGT	GCTCTGCGCA	AGCCCCGGAAT	ACATCCGGCA	ACACGGCTGT
541	CCGCAAACTC	TTGAAGACCT	GTACCAACAT	GCCTGCCTGA	TCCACAGCAC	CTGCAGCAAC
601	TTCTCACTGA	CCTGGCAATT	CAAGGTCGAT	GGCCTGCTCA	AGAAAGTCAT	GCCCAGCAGC
661	CGGCTATCGG	TCAACTCCTC	CGAGTTGCTG	GTGGACGGCG	CCCTTCAGGG	CATAGGAATC
721	ATCCACGCGC	CCACCTGGCT	GGTGATGAA	CAGATCGCCA	GCGGCCAACT	GGTGTGCTG
781	CTCGACGAAT	ATTGCGAGGC	CGATCCGCAA	CAGGGAGCGA	TCTACGCACT	GCGCGCACGC
841	AGCAGCGTTG	TCCCGGCCAA	GACCCGCCCTG	TTCATCAATG	AGTTGAAACG	CTCGATCGGC
901	AGCACGCCTT	ACTGGGACTT	GCCGTTTGAA	AAGGAAATAC	CGCAGACCCT	GGCCACCCTG
961	CATTTCGATA	CCGCAATGCA	TTCAGCGCTT	TCCCGCGCGA	CCACCTTGCA	AGACAAGAGC
1021	CAGACATCAT	GA				

1-7) *pltR*-LK365

1	ATGAAGGCGC	TAGGCGTTGT	CAATGACATA	GACCTTTATA	TATCCGTAAC	TAAAACGGGT
61	AGTTTCTCCG	AAACAGGACG	GCTACTTGGC	ATCCCACCTT	CTTCGGTGAT	GCGCCGCATC
121	AATAGCCTCG	AAAAAGAACT	TGAAACCTGT	CTATTCAATC	GATCGACAAA	ATGCTTGATA
181	CTTACCGAAA	CAGGCCTGCT	CTTTCTCGAA	CATGCAAAGA	ACATCTCGCG	CTGCATTGGG
241	CATGCTCGGT	CAGAAGTAAA	AGAACACACT	GCATCGACCC	TTGGCGTTCT	CAAGGTTTCA
301	GCACCCGTGG	CCTTTGGACG	GCGCCATGTA	GCGCCTTTAT	TGAGCCGCAT	ACTGAACCAT
361	CATCCCGGTT	TGAAAATTGA	ATTCTCGCTT	AACGACAAAG	CTCTCGACCC	CAGCATCGAT
421	AACGTCGATA	TCTGTATCAA	GCTGGGCATA	TTGCCGGACA	GTAATCTGAT	TCCAACGAAA
481	CTTGCGGATA	TGCGGCGCGT	GCTCTGCGCA	AGCCCCGGAAT	ACATCCGGCA	ACACGGCTGT
541	CCGCAAACTC	TTGAAGACCT	GTACCAACAT	GCCTGCCTGA	TCCACAGCAC	CTGCAGCAAC
601	TTCTCACTGA	CCTGGCAATT	CAAGGTCGAT	GGCCTGCTCA	AGAAAGTCAT	GCCCAGCAGC
661	CGGCTATCGG	TCAACAGTTC	CGAGTTGCTG	GTGGACGGCG	CCCTTCAGGG	CATAGGAATC
721	ATCCACGCGC	CCACCTGGCT	GGTGATGAA	CAGATCGCCA	GCGGCCAACT	GGTGTGCTG
781	CTCGACGAAT	ATTGCGAGGC	CGATCCGCAA	CAGGGAGCGA	TCTACGCACT	GAGGGCACGC
841	AGCAGCGTTG	TCCCGGCCAA	GACCCGCCCTG	TTCATCAATG	AGTTGAAACG	CTCGATCGGC
901	AGCACGCCTT	ACTGGGACTT	GCCGTTTGAA	AAGGAAATAC	CGCAGACCCT	GGCCACCCTG
961	CATTTCGATA	CCGCAATGCA	TTCAGCGCTT	TCCCGCGCGA	CCACCTTGCA	AGACAAGAGC
1021	CAGACATCAT	GA				

2) Alignment of the seven *pltR* DNA sequences

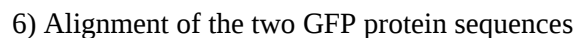
Consensus	1	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150
Identity	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
1. <i>pltR</i> Pf-5	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
2. <i>pltR</i> LK298	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
3. <i>pltR</i> LK361	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
4. <i>pltR</i> LK362	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
5. <i>pltR</i> LK363	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
6. <i>pltR</i> LK364	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
7. <i>pltR</i> LK365	ATG	AAG	GCG	CTA	GCG	GTT	GTC	AAT	GAC	CTT	TAT	ATA	GTC	CTA	ATG	ATG
Consensus	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	
Identity	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
1. <i>pltR</i> Pf-5	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
2. <i>pltR</i> LK298	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
3. <i>pltR</i> LK361	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
4. <i>pltR</i> LK362	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
5. <i>pltR</i> LK363	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
6. <i>pltR</i> LK364	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
7. <i>pltR</i> LK365	CTA	TTT	AAT	GAA	TGC	AAA	TGC	TTC	ATA	CTT	ACC	GAA	ACA	GCG	CTG	
Consensus	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	
Identity	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
1. <i>pltR</i> Pf-5	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
2. <i>pltR</i> LK298	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
3. <i>pltR</i> LK361	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
4. <i>pltR</i> LK362	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
5. <i>pltR</i> LK363	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
6. <i>pltR</i> LK364	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
7. <i>pltR</i> LK365	GCA	CCG	GTC	GCT	TTC	GGA	GCG	CAT	GTA	GCG	CCT	TTA	TTC	AGA	AGA	
Consensus	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	
Identity	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
1. <i>pltR</i> Pf-5	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
2. <i>pltR</i> LK298	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
3. <i>pltR</i> LK361	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
4. <i>pltR</i> LK362	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
5. <i>pltR</i> LK363	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
6. <i>pltR</i> LK364	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
7. <i>pltR</i> LK365	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
Consensus	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	
Identity	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
1. <i>pltR</i> Pf-5	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
2. <i>pltR</i> LK298	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
3. <i>pltR</i> LK361	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
4. <i>pltR</i> LK362	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
5. <i>pltR</i> LK363	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
6. <i>pltR</i> LK364	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
7. <i>pltR</i> LK365	TTC	GCG	GAC	AGT	AAT	CTG	ATT	CCA	ACG	AAA	CTT	GCG	GAT	ATG	GCG	
Consensus	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	
Identity	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
1. <i>pltR</i> Pf-5	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
2. <i>pltR</i> LK298	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
3. <i>pltR</i> LK361	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
4. <i>pltR</i> LK362	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
5. <i>pltR</i> LK363	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
6. <i>pltR</i> LK364	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
7. <i>pltR</i> LK365	CAG	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
Consensus	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	
Identity	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
1. <i>pltR</i> Pf-5	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
2. <i>pltR</i> LK298	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
3. <i>pltR</i> LK361	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
4. <i>pltR</i> LK362	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
5. <i>pltR</i> LK363	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
6. <i>pltR</i> LK364	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
7. <i>pltR</i> LK365	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
Consensus	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	
Identity	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
1. <i>pltR</i> Pf-5	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
2. <i>pltR</i> LK298	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
3. <i>pltR</i> LK361	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
4. <i>pltR</i> LK362	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
5. <i>pltR</i> LK363	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
6. <i>pltR</i> LK364	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	
7. <i>pltR</i> LK365	AGC	ATC	GCG	AGC	GAA	CTG	GTC	GCG	CTC	GTC	GTC	GTC	GTC	GTC	GTC	

3) Alignment of the seven *PltR* protein sequences

Consensus	1	20	30	40	50	60	70	80	90	100
Identity	M	K	A	L	G	V	N	D	I	D
1. <i>PltR</i> Pf-5	M	K	A	L	G	V	N	D	I	D
2. <i>PltR</i> LK298	M	K	A	L	G	V	N	D	I	D
3. <i>PltR</i> LK361	M	K	A	L	G	V	N	D	I	D
4. <i>PltR</i> LK362	M	K	A	L	G	V	N	D	I	D
5. <i>PltR</i> LK363	M	K	A	L	G	V	N	D	I	D
6. <i>PltR</i> LK364	M	K	A	L	G	V	N	D	I	D
7. <i>PltR</i> LK365	M	K	A	L	G	V	N	D	I	D
Consensus	110	120	130	140	150	160	170	180	190	200
Identity	R	R	H	V	A	P	L	L	S	R
1. <i>PltR</i> Pf-5	R	R	H	V	A	P	L	L	S	R
2. <i>PltR</i> LK298	R	R	H	V	A	P	L	L	S	R
3. <i>PltR</i> LK361	R	R	H	V	A	P	L	L	S	R
4. <i>PltR</i> LK362	R	R	H	V	A	P	L	L	S	R
5. <i>PltR</i> LK363	R	R	H	V	A	P	L	L	S	R
6. <i>PltR</i> LK364	R	R	H	V	A	P	L	L	S	R

4-2) *gfp-prnA::gfp*(CGC)

5) Alignment of the two *gfp* DNA sequences



	1	10	20	30	40	50	60	70	80	90	100	
Consensus	MSKGEELFTGVVPEILVELDGDVNGHKFSVSSEGEEDATYGLTLKFICTTGKLPVWPPTLVTTLTYGVCESRYPDHMKRHDFFKSAMPFEGYVQERTIFFKDD											
Identity												
1. gfp-prmA::gfp(AGA)	MSKGEELFTGVVPEILVELDGDVNGHKFSVSSEGEEDATYGLTLKFICTTGKLPVWPPTLVTTLTYGVCESRYPDHMKRHDFFKSAMPFEGYVQERTIFFKDD											
2. gfp-prmA::gfp(CGC)	MSKGEELFTGVVPEILVELDGDVNGHKFSVSSEGEEDATYGLTLKFICTTGKLPVWPPTLVTTLTYGVCESRYPDHMKRHDFFKSAMPFEGYVQERTIFFKDD											
Consensus	110	120	130	140	150	160	170	180	190	200		
Identity	GNYKTRAEVKEEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSQLADHYQONTPIGDGPEVLLPDNHYLSTQSA											
1. gfp-prmA::gfp(AGA)	GNYKTRAEVKEEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSQLADHYQONTPIGDGPEVLLPDNHYLSTQSA											
2. gfp-prmA::gfp(CGC)	GNYKTRAEVKEEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSQLADHYQONTPIGDGPEVLLPDNHYLSTQSA											
Consensus	210	220	230	239								
Identity	LSKDDNEKRDHNVLLFVTAAGITHGMDLYK											
1. gfp-prmA::gfp(AGA)	LSKDDNEKRDHNVLLFVTAAGITHGMDLYK											
2. gfp-prmA::gfp(CGC)	LSKDDNEKRDHNVLLFVTAAGITHGMDLYK											