

Supplementary Figure 1. The phenotype comparison of the engineered heterologous expression strains. (A) Front side of agar plate with strain *S. albus* 9B10; (B) Back side of agar plate with strain *S. albus* 9B10; (C) Front side of agar plate with strain *S. albus* pJTU2554; (D) Back side of agar plate with strain *S. albus* pJTU2554.



Supplementary Figure 2. HPLC profiles of the fermentation extracts of engineered heterologous expression strains. I: *S. albus* 9B10-1; II: *S. albus* 9B10-2; III: *S. albus* 9B10- Δ *E7*; IV: *S. albus* 9B10- Δ *A*; V: *S. albus* 9B10- Δ *S3*; VII: *S. albus* 9B10- Δ *S7*; VIII: *S. albus* 9B10 with reduced nitrogen source (removing the ammonium acetate and decreasing the yeast extract to 1g/L in the fermentation medium).



Supplementary Figure 3. Selected COSY and HMBC correlations for compounds 4, 6-8, and 10-11.



Supplementary Figure 4. Maps of the *rub* and *R1128* biosynthetic gene cluster.



Supplementary Figure 5. MS and NMR data (measured in DMSO-*d*₆) of **1** and **2** with or without ¹⁵N-labeled anthranilic acid feeding. (A) ¹⁵N NMR spectrum of **1** obtained after feeding with ¹⁵N-labeled anthranilic acid; (B) HRESIMS analysis of **1** obtained after feeding with ¹⁵N-labeled anthranilic acid; (C) ¹⁵N NMR spectrum of **2** obtained after feeding with ¹⁵N-labeled anthranilic acid; (D) HRESIMS analysis of **2** obtained after feeding with ¹⁵N-labeled anthranilic acid; (E) ¹⁵N NMR spectrum of **2** obtained after feeding with ¹⁵N-labeled anthranilic acid; (E) ¹⁵N-labeled anthranilic acid.



Supplementary Figure 6. HRESIMS analysis of compound 10.



Supplementary Figure 7. HRESIMS analysis of compound 11.



Supplementary Figure 8. HRESIMS analysis of compound 12.





Supplementary Figure 9. HRESIMS analysis of compound 13.





Supplementary Figure 10. HRESIMS analysis of compound 14.



Supplementary Figure 11. HRESIMS analysis of compound 15.





Supplementary Figure 12. HRESIMS analysis of compound 16.









Supplementary Figure 14. HRESIMS analysis of compound 18.

User Spectra



Supplementary Figure 15. HRESIMS analysis of compound 19.



Supplementary Figure 16. (A) Proposed mechanism for the pyridyl moiety formation from intermediate **4**; (B) the enlarged ¹H NMR spectra of **4** in D₂O after 5 minutes (spectra I and IV, left), 2 hours (spectra II and V, middle) and 4 hours (spectra III and VI, right) incubation.



Supplementary Figure 17. The proposed central role of the reactive 1,5-dione moiety (blue) in accessing a diverse pyridine chemical universe including (A) rubolones and (B) selected natural alkaloids for which are potentially involved in the non-enzymatical pyridine formation using the intermediacy of the 1,5-dione moiety.



Supplementary Figure 18. Gene replacement of *orf1-7* using the PCR-targeting method. (A) Scheme for the construction of *orf1-7* replacement mutant. (B) Confirmation of plasmid p9B10-1 by restriction endonuclease BamHI. Lane M: DNA molecular ladder. Lane 9B10-1: Restriction fragments from the p9B10-1 (11259 bp, 9647 bp, 6601 bp, 4209 bp, 4123 bp, 3299 bp, 2376 bp, 858 bp, 20 bp).



Supplementary Figure 19. Gene replacement of *orf30-37* using the PCR-targeting method. (A) Scheme for the construction of *orf30-37* replacement mutant. (B) Confirmation of plasmid p9B10-2 by restriction endonuclease BamHI. Lane M: DNA molecular ladder. Lane 9B10-2: Restriction fragments from the p9B10-2 (11259 bp, 10062 bp, 6601 bp, 4123 bp, 3299 bp, 2376 bp, 1473 bp, 858 bp, 844 bp, 37 bp).



Supplementary Figure 20. Gene replacement of *rubS1* using the PCR-targeting method. (A) Scheme for the construction of *rubS1* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubS1$, PCR product from *S. albus* 9B10- $\Delta S1$ mutant.



Supplementary Figure 21. Gene replacement of *rubS2* using the PCR-targeting method. (A) Scheme for the construction of *rubS2* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubS2$, PCR product from *S. albus* 9B10- $\Delta S2$ mutant.



Supplementary Figure 22. Gene replacement of *rubS3* using the PCR-targeting method. (A) Scheme for the construction of *rubS3* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubS3$, PCR product from *S. albus* 9B10- $\Delta S3$ mutant.



Supplementary Figure 23. Gene replacement of *rubS7* using the PCR-targeting method. (A) Scheme for the construction of *rubS7* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubS7$, PCR product from *S. albus* 9B10- $\Delta S7$ mutant.



Supplementary Figure 24. Gene replacement of *rubA* using the PCR-targeting method. (A) Scheme for the construction of *rubA* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubA$, PCR product from *S. albus* 9B10- ΔA mutant.



Supplementary Figure 25. Gene replacement of *rubB* using the PCR-targeting method. (A) Scheme for the construction of *rubB* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubB$, PCR product from *S. albus* 9B10- ΔB mutant.



Supplementary Figure 26. Gene replacement of *rubC* using the PCR-targeting method. (A) Scheme for the construction of *rubC* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubC$, PCR product from *S. albus* 9B10- ΔC mutant.



Supplementary Figure 27. Gene replacement of *rubE7* using the PCR-targeting method. (A) Scheme for the construction of *rubE7* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubE7$, PCR product from *S. albus* 9B10- $\Delta E7$ mutant.



Supplementary Figure 28. Gene replacement of *rubE9* using the PCR-targeting method. (A) Scheme for the construction of *rubE9* replacement mutant. (B) Confirmation of mutant by PCR using the primers listed in supplementary Table 6. Lane M: DNA molecular ladder. Lane WT, PCR product from the *S. albus* 9B10. Lane $\Delta rubE9$, PCR product from *S. albus* 9B10- $\Delta E9$ mutant.



Supplementary Figure 29. ¹H NMR spectrum of compound 3 in DMSO-*d*₆.



Supplementary Figure 30. HRESIMS analysis of compound 3.



Supplementary Figure 31. ¹H NMR spectrum of compound 4 in DMSO-*d*₆.



Supplementary Figure 32. ¹³C NMR spectrum of compound 4 in DMSO-d₆.



Supplementary Figure 33. ¹H-¹H COSY NMR spectrum of compound 4 in DMSO-*d*₆.



Supplementary Figure 34. HSQC NMR spectrum of compound **4** in DMSO-*d*₆.



Supplementary Figure 35. HMBC NMR spectrum of compound 4 in DMSO-d₆.



Supplementary Figure 36. HRESIMS analysis of compound 4.



Supplementary Figure 37. ¹H NMR spectrum of compound 5 in CD₃OD.



Supplementary Figure 38. ¹³C NMR spectrum of compound **5** in CD₃OD.



Supplementary Figure 39. HRESIMS analysis of compound 5.



Supplementary Figure 40. ¹H NMR spectrum of compound 6 in CD₃OD.



Supplementary Figure 41. ¹³C NMR spectrum of compound 6 in CD₃OD.



Supplementary Figure 42. ¹H-¹H COSY NMR spectrum of compound 6 in CD₃OD.





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User Spectra



Supplementary Figure 45. HRESIMS analysis of compound 6.



Supplementary Figure 46. ¹H NMR spectrum of compound 7 in DMSO-*d*₆.



Supplementary Figure 47. ¹³C NMR spectrum of compound 7 in DMSO-d₆.



Supplementary Figure 48. ¹H-¹H COSY NMR spectrum of compound 7 in DMSO-*d*₆.



Supplementary Figure 49. HSQC NMR spectrum of compound 7 in DMSO-d₆.



Supplementary Figure 50. HMBC NMR spectrum of compound 7 in DMSO-d₆.



Supplementary Figure 51. HRESIMS analysis of compound 7.



Supplementary Figure 52. ¹H NMR spectrum of compound 8 in DMSO-*d*₆.



Supplementary Figure 53. ¹³C NMR spectrum of compound 8 in DMSO-d₆.



Supplementary Figure 54. ¹H-¹H COSY NMR spectrum of compound 8 in DMSO-*d*₆.



Supplementary Figure 55. HSQC NMR spectrum of compound 8 in DMSO-d₆.



Supplementary Figure 56. HMBC NMR spectrum of compound 8 in DMSO-d₆.



Supplementary Figure 57. HRESIMS analysis of compound 8.



Supplementary Figure 58. ¹H NMR spectrum of compound 10 in DMSO-*d*₆.





Supplementary Figure 59. ¹⁹F NMR spectrum of compound 10 in DMSO-*d*₆.



Supplementary Figure 60. ¹³C NMR spectrum of compound 10 in DMSO-*d*₆.



Supplementary Figure 61. HSQC NMR spectrum of compound 10 in DMSO-d₆.



Supplementary Figure 62. HMBC NMR spectrum of compound 10 in DMSO-d₆.



Supplementary Figure 63. ¹H-¹H COSY NMR spectrum of compound **10** in DMSO-*d*₆.



Supplementary Figure 64. ¹H NMR spectrum of compound 11 in DMSO-*d*₆.



Supplementary Figure 65. ¹³C NMR spectrum of compound 11 in DMSO-d₆.



Supplementary Figure 66. HSQC NMR spectrum of compound 11 in DMSO-d₆.



Supplementary Figure 67. HMBC NMR spectrum of compound 11 in DMSO-d₆.



Supplementary Figure 68. ¹H-¹H COSY NMR spectrum of compound 11 in DMSO-*d*₆.







Supplementary Figure 70. ¹H NMR spectrum of compound 4 in D₂O after 5 minutes incubation.



Supplementary Figure 71. ¹H NMR spectrum of compound **4** in D₂O after 2 hours incubation.



Supplementary Figure 72. ¹H NMR spectrum of compound **4** in D₂O after 4 hours incubation.

				Closest sequence similarity				
Protein	Size	Category	Function	Protein, Origin	Positives/	Accession No.		
	<u>(a</u> a)				Identities			
RubS1	492	sugar	FAD-linked oxidoreductase	AknOx, Streptomyces	65/52	Q0PCD7		
		U U		galilaeus				
RubN1	135	hypothetical	Unknown	Sgcj, Streptomyces	56/43	40VM		
		protein		carzinostaticus				
RubS2	204	sugar	dTDP-4-keto-6-deoxy-D-glucose	StrM, Streptomyces	63/46	P29783		
		-	3,5-epimerase	griseus				
RubS3	310	sugar	dTDP-glucose-4-ketoreductase	NovS, Streptomyces	56/44	Q9L9E9		
_				niveus				
RubS4	343	sugar	dTDP-glucose 4,6 dehydratase	NovT, Streptomyces	75/63	Q9L9E8		
D 1 05	000			niveus	75/50	D07770		
RubS5	289	sugar	Giucose-1-phosphate	RIDA, Snigella flexneri	15/58	P3///9		
Dut 00	070		tnymidylyltransterase	Azop Vonerhilus	45/00			
RubS6	278	sugar	NAD dependent	AZOB, Xenophilus	45/29	USKUU/		
Dub07	204	sugar	epimerase/denydratase	azovoraris ElmGT Streptomuces	18/36	005250		
RUDOI	304	sugar	Giycosyllansielase	olivaceus	40/30	U 3L7L3		
RuhR	345	regulation	SARP family transcriptional	Dnrl Streptomyces	54/39	P25047		
	0-0	regulation	regulator	peucetius	0 1/00	. 200 11		
RubN2	115	hypothetical	Unknown	AcrR. Sciscionella	69/51	WP 02050192		
	110	protein	Charlown	marina	50/01	0		
RubA	311	oxvdenase	F420-dependent oxidoreductase	SsuD. Amvcolatopsis	79/68	AIJ25240		
	.	5.7, 9011000		methanolica 239				
RubB	518	oxygenase	Oxygenase	ZhuM, Streptomyces	67/55	AAG30200.1		
	-	,,	20	sp. R1128	-			
RubC	389	oxygenase	naphthocyclinone hydroxylase	ActVA 5, Streptomyces	59/45	CAA41641		
			. , , , ,	coelicolor A3(2)				
RubE1	319	PKS	β-ketoacylsynthase III (KSIII)	ZhuH, Streptomyces	78/61	AAG30194.1		
			,	sp. R1128				
RubE2	91	PKS	Acyl carrier protein (ACP)	ZhuG, Streptomyces	73/53	AAG30194.1		
				sp. R1128				
RubE3	306	PKS	Acyl transferase (AT)	ZhuC, Streptomyces	67/56	AAG30190.1		
				sp. R1128				
RubE4	84	PKS	Acyl carrier protein (ACP)	ZhuN, Streptomyces	82/68	AAG30201.1		
				sp. R1128				
RubE5	164	PKS	Bifunctional	ZhuJ, Streptomyces	76/69	AAG30197.1		
			cyclase/dehydratase	sp. R1128				
RubE6	251	PKS	Cyclase	Zhul, Streptomyces	88/79	AAG30196.1		
				sp. R1128				
RubE7	206	PKS	NADH dehydrogenase	McyH1, Streptomyces	80/69	AFG19428		
				flaveolus				
RubE8	409	PKS	β-ketoacylsynthase II (KSα)	ZhuB, Streptomyces	88/79	AAG30189.1		
				sp. R1128				
RubE9	400	PKS	Chain length factor (CLF/KSβ)	ZhuA, Streptomyces	81/71	AAG30188.1		
				sp. R1128				

Supplementary Table 1. Deduced roles of genes in *rub* gene cluster based on sequence homology.

NI-	3	4		5			
NO.	δΗ	δc	$\delta_{ m H}$	COSY	HMBC	δ	$\delta_{ m H}$
2	2.55 (s)	20.82	2.46 (s)		4, 3	125.42	6.89 (s)
3		169.33				163.49	
4	8.12 (s)	106.34	7.61 (s)		6, 3, 2	113.71	7.42 (s)
5		161.41				139.00	
6		122.14				184.54	
7		133.84				136.11	
8		150.12				108.40	7.03 (s)
9		nd				165.73	
10	6.50 (s)	119.54	6.48 (brs)	12	12, 8	109.53	6.48 (s)
11		nd				166.55	
12	6.69 (s)	126.62	7.07 (brs)	10	13, 10, 7, 6	111.94	
13		186.39				189.72	
14		115.07				124.01	
15		195.96				151.51	
16	3.03 (t, 7.1)	43.20	2.81 (t, 7.2)	17	18, 17, 15	39.36	3.09 (t, 7.6)
17	1.65 (m)	16.96	1.53 (m)	18, 16	18, 16, 15	25.42	1.60 (m)
18	0.93 (t, 7.3)	13.80	0.89 (t, 7.4)	17	17, 16	14.86	0.99 (t, 7.3)

Supplementary Table 2. NMR data of **3** and **4** in DMSO- d_6 , and **5** in CD₃OD (δ in ppm, J in Hz).

^and means not detected in the NMR spectra.

No	6					7				8			
NO.	δ _C	δ _Η	COSY	HMBC	δ _C	δ _Η	COSY	HMBC	δ _C	δ _Η	COSY	HMBC	
1	171.86												
2	132.77				51.91	2.12 (dd,13.6, 1.7), 2.80 (overlapped)	4	16, 15, 14, 4, 3	22.77	2.17 (s)			
3	159.72				207.86	2.00 (0001100000)			157.73				
4	113.41	7.50 (s)		14,13, 6, 5, 3, 2, 1	55.29	2.36 (dd,13.0, 1.6), 2 79 (overlapped)	2	14, 6, 5, 3, 2	116.31	8.51 (s)			
5	138.25				74.25	2.10 (0001100000)			161.61				
6	183.76				40.04	2.52 (overlapped) 3.30 (d. 16.5)		14, 12, 8, 7, 5, 4	107.54				
7 8 9	135.60 108.22 166.36	6.98 (d, 1.9)	10	13, 12, 10, 7, 6	146.23 107.98 164.59	6.08 (brs)	10	12, 10, 6	137.69 170.87 161.22				
10 11	109.49 165.42	6.45 (d, 1.9)	8	12, 9, 8	99.91 164.60	6.02 (d, 1.9)	8	9, 8	114.45 185.74	6.36 (s)		12, 11, 9, 8	
12 13 14 15	111.97 189.33 123.85 147.15				111.35 203.21 59.65 75.95				118.51 192.57 121.32 154.82	6.46 (s)		13, 10, 6	
16	35.86	3.18 (t, 7.6)	17	18, 17, 15, 14, 2	43.97	1.40 (td, 3.7, 13.0), 1.63 (td, 4.3, 13.0)	17	18, 17, 15, 14, 2,	30.57	2.82 (m), 2.49 (m)	17	18, 17, 15, 14	
17	25.32	1.63 (m)	18, 16	18, 16, 15	17.40	1.26 (m), 1.52 (m)	18, 16	18, 16	21.66	1.32 (m)	18, 16	18, 16, 15	
18 1'	15.13	1.07 (t, 7.3)	17	17, 16	14.60	0.86 (t, 7.2)	17	17, 16	13.99	0.71 (t, 6.9)	17	17, 16	
1 2'									129.02				
_ 3'									129.03	7.77	4'		
4'									133.80	7.91	3'		
5' 6'									131.53	7.82	6' 5'	1' 2' 7'	
ю 7'									132.30	8.21	5	2,7	
OH-5						5.29 (brs)		14, 6, 5					
OH-11						12.89 (s)		13, 12, 11, 10					
OH-15						4.81 (s)		15, 14, 2					

Supplementary Table 3. NMR data of **6** in CD₃OD and **7-8** in DMSO- d_6 (δ in ppm, J in Hz).

	10				11				
No.	δc	δΗ	δF	HMBC	COSY	δc	δн	HMBC	COSY
2	22.75	2.17 (s)		4, 3		22.87	2.17 (s)	4, 3	
3	158.46					158.57			
4	115.90	8.50 (s)		14, 3, 2		115.90	8.47 (s)	14, 3, 2	
5	161.53					161.53			
6	111.41					111.45			
7	137.69					137.69			
8	170.02					169.83			
9	165.39					165.53			
10	130.07					130.08			
11	183.56					183.49			
12	117.27	6.47 (s)		13, 11, 10, 7, 6		117.00	6.46 (s)	13, 11, 10, 7, 6	
13	192.79					192.98			
14	120.88					120.82			
15	154.70					154.83			
16	30.38	2.48 (m)		18, 17, 14	H-17	30.51	2.48 (m)		H-17
		2.84 (m)					2.89 (m)		
17	21.67	1.30 (m)		18, 16	H-18, H-16	21.59	1.33 (m)		H-18, H-16
18	13.88	0.73 (t. 7.1)		17, 16	H-17	13.97	0.72 (t. 6.1)	17.16	H-17
19	104.55	5.14 (s)		20, 10, 9		104.55	5.13 (s)	20, 10, 9	
20	83.11	- (-)		-, -, -		83.09	(-)	-, -, -	
21	74.07	3.82 (brs)		20. 10	H-22, OH-21	74.10	3.82 (brs)	20.10	H-22, OH-21
22	70.31	3.49 (brs)		24, 21, 20	H-23, OH-22, H-21	70.35	3.48 (brs)	,	OH-22, H-21
23	70.26	3.78 (m)		24, 22, 21, 19	H-24, H-22	70.23	3.78 (m)		H-24, H-22
24	16.69	1.07 (d. 6.2)		23, 22	H-23	16.69	1.07 (d. 5.9)	23. 22	H-23
1'	129.79					128.31		,	
2'	132.45					134.44			
3'	131.58	7.91 (m)		5'. 1'	H-4'	129.97	7.71 (m)	5'	H-4'
4'	120.44	7.77 (m)		6'. 2'	H-3'	131.23	8.01 (m)	2'	H-3'
5'	162.39	()	-108.22	- ,	-	135.19	()		-
6'	118.82	7.94 (m)		4'. 2'		130.75	7.75 (m)	4'. 2'	
7'	164.06	,		.,_		165.43		.,_	
OH-20		5.77 (s)					5.78 (s)	19	
OH-21		7.66 (brs)			H-21		7.68 (brs)	21.20	H-21
OH-22		4.69 (s)			H-22		4.67 (s)	23	H-22

Supplementary Table 4. NMR data of compounds **10** and **11** in DMSO- d_6 (δ in ppm, J in Hz).

Supplementary Table 5. Strains and plasmids used and generated in this study.

Strains/Plasmid	Purpose	Sources
Strains		
E. coli		
DH10B	Host strain for cloning	Invitrogen
BW25113/pIJ790	Host strain for PCR targeting	Ref. 10
ET12567/pUZ8002	Donor strain for conjugation	Ref. 11
XL1-blue MR	Host strain for genomic library	Agilent Technologies
DH5a/BT340	Host strain for in-frame deletion	Ref. 12
Streptomyces		
Streptomyces sp. KIB-H033	Rubrolones wild type producing strain	This study
Streptomyces albus J1074	Host strain for heterologous expression	Ref. 13
S. albus 9B10	Streptomyces albus J1074 integrated with plasmid 9B10 which contains <i>rub</i> biosynthetic gene cluster	This study
S. albus 9B10-1	orf1-orf7 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-2	orf30-orf37 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆S1	rubS1 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆S2	rubS2 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆S3	rubS3 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆S7	rubS7 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆A	rubA inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆B	rubB inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆C	rubC inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆E7	rubE7 inactivation mutant of S. albus 9B10	This study
S. albus 9B10-∆E9	rubE9 inactivation mutant of S. albus 9B10	This study
Plasmids		
pJTU2554	Apr ^r , Cosmid vector for genomic library construction	Ref. 10
pJTU6722	Ery ^r , Vector for PCR targeting	Constructed by Prof. Meifeng Tao
p9B10	Apr ^r , Cosmid which contains <i>rub</i> biosynthetic gene cluster	This study
p9B10-1	Apr ^r , gene inactivation clone used for orf1-orf7 mutant	This study
p9B10-2	Apr ^r , gene inactivation clone used for orf30-orf37 mutant	This study
p9B10-∆S <i>1</i>	Apr ^r , gene inactivation clone used for <i>rubS1</i> mutant	This study
p9B10-∆S2	Apr ^r , gene inactivation clone used for <i>rubS2</i> mutant	This study
p9B10-∆S3	Apr ^r , gene inactivation clone used for <i>rubS3</i> mutant	This study
p9B10-∆S7	Apr ^r , gene inactivation clone used for <i>rubS7</i> mutant	This study
p9B10-ΔA	Apr ^r , gene inactivation clone used for <i>rubA</i> mutant	This study
p9B10-Δ <i>B</i>	Apr ^r , gene inactivation clone used for <i>rubB</i> mutant	This study
p9B10-ΔC	Apr ^r , gene inactivation clone used for <i>rubC</i> mutant	This study
p9B10-Δ <i>E7</i>	Apr ^r , gene inactivation clone used for <i>rubE7</i> mutant	This study
p9B10-Δ <i>E9</i>	Apr ^r , gene inactivation clone used for <i>rubE9</i> mutant	This study

Supplementary Table 6. Primers used for constructing and confirming the mutants.

Primers	Targeted	Sequences
	genes	
For PCR		
targeting		
Tar-H2517-F	orf1-orf7	5'-CTCCGACGCCGTCGGTGAAATCTTTTCAGGAGGAAGTCCattccggggatccgtcgacc-3'
Tar-H2511-R		5'-GTGCACCCGCAACAGCGAGTACTGGATCCTGCGCACCGGtgtaggctggagctgcttc-3'
Tar-H2518-F	rubS1	5'-ACCGTCCGGCCCGGCGACCCGCGCTACGACGACCTGGCGattccggggatccgtcgacc-3'
Tar-H2518-R		5'-CCGCGCTCTCGATCTCCGTGCGGGCGGCATCGGTGCTCGtgtaggctggagctgcttc-3'
Tar-H2549-F-	orf30-orf37	5'-CCGGCACCCTCGCGGCGGGCATCTTCGCGGTCGGCACCCattccggggatccgtcgacc-3'
Tar-H2542-R		5'-TTCGGGTTCCGACCGAGGCAGGACAGCGGGCCGGTCCGCtgtaggctggagctgcttc-3'
Tar-H2541-F	rubE9	5'-CCGATGAGGCCGCCCGCAGTCGTCACCGGGATCGGGGTGattccggggatccgtcgacc-3'
Tar-H2541-R		5'-GGGTCCCGCTTCGGGTTCCGACCGAGGGCGGCGGGGGTCAtgtaggctggagctgcttc-3'
Tar-H2539-F	rubE7	5'-GCAACGACGGCGCGCACGGCTCCTGGCGCTGGACGCGGCGattccggggatccgtcgacc-3'
Tar-H2539-R		5'-AGCGCAAACCCGTGCACGAGGTCGCCCAGGCGGAGGTCAtgtaggctggagctgcttc-3'
Tar-H2528-F	rubA	5'-CTGCGCAAACCGATCTCTGAAATGGGGTGCTGGGCAATGattccggggatccgtcgacc-3'
Tar-H2528-R		5'-GCCCGGGCCGCCGGGTCCGGGCACCGGGCCCGGCGGTCAtgtaggctggagctgcttc-3'
Tar-H2530-F	rubB	5'-ACCCGCGTCGGCTGCCGTCGCCGATGGGAGTGGGAGATGattccggggatccgtcgacc-3'
Tar-H2530-R		5'-GGTCACCACGTCGACGCGTCCGGCCCAGCCGGCGGCCGTtgtaggctggagctgcttc-3'
Tar-H2531-F	rubC	5'-CCGAAGGAGACTGATGTGACGCACCCAGTAGCCGCCGGGattccggggatccgtcgacc-3'
Tar-H2531-R		5'-TGCCGGGGACGGCAGGGCGGCGGCCGGGTGCACGGGTCAtgtaggctggagctgcttc-3'
Tar-H2520-F	rubS2	5'-ACAACGTGCGGCCGCGCCTCGCCCCCGGAGCCGAAGACCattccggggatccgtcgacc-3'
Tar-H2520-R		5'-GCGGCCGGCACGGCGGGGGGCGCGGGGGGGGGGGGGGG
Tar-H2521-F	rubS3	5'-GCCACAGGGCGAGGTCCGCGTCGGAGGGGCCGCTGTCGGattccggggatccgtcgacc-3'
Tar-H2521-R		5'-GGCAGTCGGCGGTGCGGTCACCGCCCGGCCCGGGGGGGCtgtaggctggagctgcttc-3'
Tar-H2525-F	rubS7	5'-ATTGCCGACTCCTCGACAAAGGGCGTATGCGCAGCCATGattccggggatccgtcgacc-3'
Tar-H2525-R		5'-CTCCGCGGTCAGTTGTGTCCTGTCGGCGGCGACACCCAGtgtaggctggagctgcttc-3'
For gene		
validation		
H2518-check-F	rubS1	5'-GTGAGTGTTCCTTGAGCAA-3'
H2518-check-R		5'-GAACTTGCGGATGTCCTC-3'
H2541-check-F	rubE9	5'-CAACCTGCACGAACCGGATC-3'
H2541-check-R		5'-AGCACATGACGAAGGGCCTG-3'
H2539-check-F	rubE7	5'-TGCGCGAGATGGTCGAGGAGTA-3'
H2539-check-R		5'-CGGAAGTCAGCAGGTCCACGAAT-3'
H2528-check-F	rubA	5'-CATGGTCGCATTCTGTCCTCTCAT-3'
H2528-check-R		5'-GCGTTCATCGAGCACTGGAAGT-3'
H2530-check-F	rubB	5'-CTGCCTCAGCCATTGCTCAAGA-3'
H2530-check-R		5'-GGTGCGTCACATCAGTCTCCTTC-3'
H2531-check-F	rubC	5'-AGCGTGACCGAAGCGATGCA-3'
H2531-check-R		5'-AACACCTCAGCGGCGTCGAT-3'
H2520-check-F	rubS2	5'-GGACATCCGCAAGTTCAT-3'
H2520-check-R		5'-CTGCACTACGTCAACACT-3'
H2521-check-F	rubS3	5'-GCCTGAAGCTGATCCTGT-3'
H2521-check-R		5'-GATCGACGACGAGGAT-3'
H2525-check-F	rubS7	5'-GCGGCTACTTGACGATGTCCTC-3'
H2525-check-R		5'-GCTACCACGAGTACCTGATGTTCT-3'

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