

SUPPLEMENTARY INFORMATION

SUPPLEMENTARY TABLES AND FIGURES

TABLE S1. The amino acid sequence identity of protein used in the phylogenetic tree.

	CebE_griseus	CebE_reticuli	SCO2795	SCO7555	SCAB_2421	SCAB_15521	SCAB_57751	SCAB_77271	GEO1108	GEO5601	GEO7671
CebE_griseus	100	47.99	46.28	49.4	47.79	34.55	47.09	39.76	34.47	48,05	39.76
CebE_reticuli		1000	51.38	45.61	45.75	32.51	46.83	36.02	32.05	79.05	36.56
SCO2795			100	47.95	47.21	29.41	71.39	33.48	29.19	51.58	34.8
SCO7555				100	90.59	33.1	47.46	36.22	33.1	45.25	35.95
SCAB_2421					100	32.33	46.19	35.14	32.08	46.06	35.41
SCAB_15521						100	30.47	29.92	96.48	34.1	29.66
SCAB_57751							100	35.14	29.17	46.93	34.64
SCAB_77271								100	30.31	36.05	98.8
GEO1108									100	33.9	30.18
GEO5601										100	36.79
GEO7671											100

TABLE S2. Summary of sequencing and assembly results for the RNA samples.

Sample	Clean Reads	Q30 (%)	Mapping Ratio
36h-1	6313294	96.17%	95.46%
36h-2	6842781	96.13%	97.94%
36h-3	5436705	96.26%	97.72%
72h-1	4276641	96.21%	96.72%
72h-2	6796329	96.38%	94.90%
72h-3	4974938	96.19%	96.43%
120h-1	6549152	96.05%	93.73%
120h-2	6307468	96.10%	94.60%
120h-3	8986765	96.39%	98.00%

TABLE S3. Primers used in this study. The restriction sites are underlined.

Primers	Sequence (5'→3')	Description
1108F (<i>Nde</i> I)	CCCATATGGTGGGCTCGGATTCC	Gene Cloning
1108R (<i>Xho</i> I)	CCCTCGAGTCAGTTCACCCCCT	
5601F (<i>Nde</i> I)	CCCATATGATGGACGGCGGCTC	
5601R (<i>Bam</i> HI)	CGGGATCCTCACTGGCCGAGCACGT	
7671F (<i>Nde</i> I)	CCCATATGATGGAGGGCGATGC	
7671R (<i>Xho</i> I)	CCCTCGAGTCACTTCAGCGAGTCCA	Gene Knockout
5601①F	CGGGATCCTCGGCTCCGGCGCCCGCTGC	
5601①R	GGAGGACGCACCAGCTCCAAAGAGGCACTC	
5601②F	TTGGAGCTGGTGCCTCCTGATGCCC	
5601②R	CCAAGCTTCAGATCCGGGAGCGGGTCGT	
7671①F	CGGGATCCCTGCGCGACCTCTGCCGACGT	
7671①R	ACTGGGACCTCATCGGTGGACAGGGCGAATT	
7671②F	TCCACCGATGAGGTCCCAGTCGTGCAGC	
7671②R	CCAAGCTTATGGCCTCGACGACATC	
5601①VF	ACAGCAGCACGAACACCAGC	Knockout Verification
5601①VR	CAGCCCGATAACCGAAGACA	
7671①VF	CGAGGATGAAGGTGAAGTTGTC	
7671①VR	TCTGGGCTGCCTGGTAGTGC	
5601F	CCTTCGGAGTCTTCGGCTA	qRT-PCR
5601R	AGTAGACCGAGGTCTTGG	
7671F	GACCAGTACGAGGTGCTCTG	
7671R	TCGTAGATGTTCCGGAGGTC	

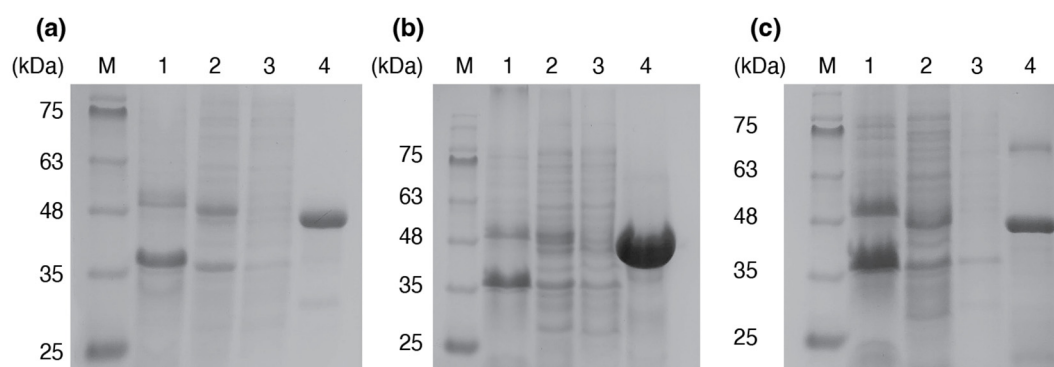


FIGURE S1 SDS-PAGE spectrums of the purification process of three putative CebE protein of CebE¹¹⁰⁸ **(a)**, CebE⁵⁶⁰¹ **(b)**, and CebE⁷⁶⁷¹ **(c)**. Lane M, marker; Lane 1, crude enzyme extract; Lane 2, inclusion body; Lane 3, effluent from the washing process; Lane 4, elution by 500 mM imidazole.

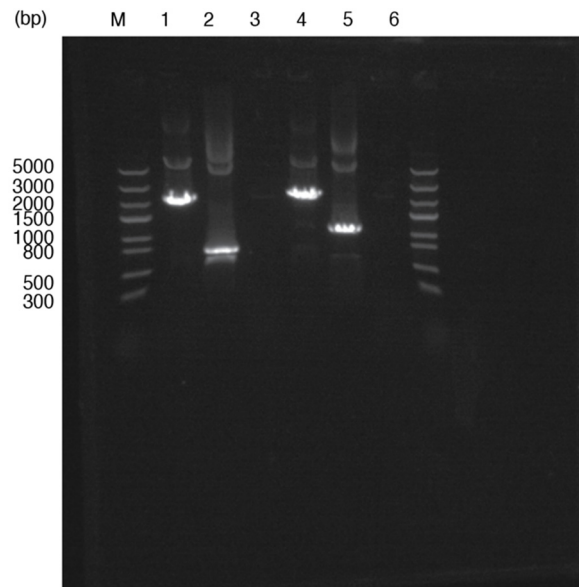


FIGURE S2 PCR verification of the in-frame deletion *Streptomyces* mutants Δ *GEO5601* and Δ *GEO7671*. Lane M, marker; Lane 1, positive control of *GEO5601* (2046 bp); Lane 2, mutant that only carrying the deleted *GEO5601* fragment (688 bp); Lane 3, negative control with no template supplementation; Lane 4, positive control of *GEO7671* (2272 bp); Lane 5, mutant that only carrying the deleted *GEO7671* fragment (1063 bp); Lane 6, negative control with no template supplementation.

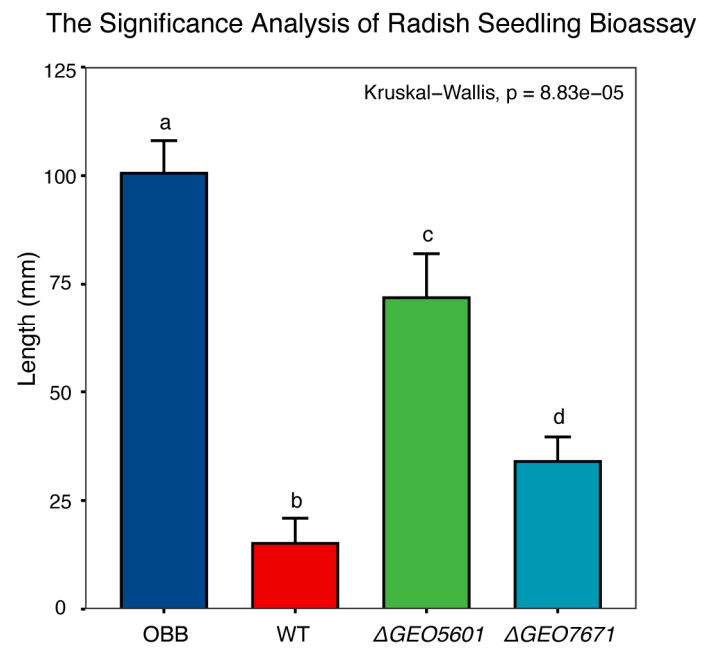


FIGURE S3 The significance analysis of radish seedling bioassay.