

1 **Supplementary Information**

2 **Characterization and functional evidence for Orf2 of**
3 ***Streptomyces* sp. 139 as a novel dipeptidase E.**

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Table S1 Expression levels of significantly upregulated peptidase coding genes
(log2FoldChange $\geq$ 2)

Gene_id	log2FoldChange	p-Value	Pfam	Gene_description
F3L20_RS27855	3.68577	6.53E-05	PF05547	M6 family peptidase
F3L20_RS27130	3.65849	1.00E-04	PF05576	S37 family peptidase
F3L20_RS04500	3.55891	1.46E-03	PF00082	S8 family peptidase
F3L20_RS24255	3.16802	2.47E-04	PF00877	C40 family peptidase
F3L20_RS00325	3.02962	7.40E-04	PF00768	S11 family peptidase
F3L20_RS24445	2.88784	2.37E-03	PF00883	M17 family peptidase
F3L20_RS26635	2.84759	1.98E-03	PF11838	M1 family peptidase
F3L20_RS08700	2.32071	1.12E-03	PF00082	S8 family peptidase
F3L20_RS22500	2.20113	3.58E-03	PF01546	M20 family peptidase

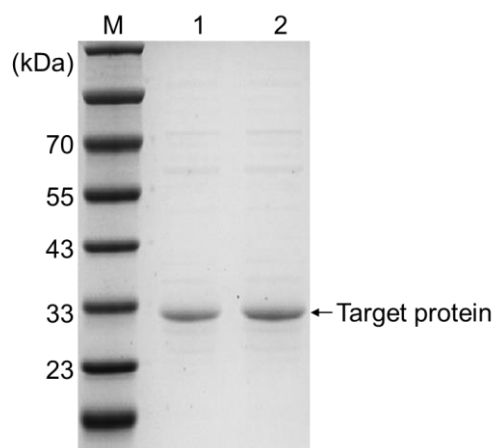
Table S2 The expression of oligopeptides, dipeptides and amino acid transferases coding genes

Gene_id	log2FoldChange	p-Value	Pfam	Gene_description
F3L20_RS05800	3.64513	3.10E-06	PF00528	amino acid ABC transporter permease
F3L20_RS07915	3.24702	5.23E-04	PF00528	amino acid ABC transporter permease
F3L20_RS07920	2.88639	2.11E-03	PF00528	amino acid ABC transporter permease
F3L20_RS32195	-1.35932	2.52E-02	PF00528	amino acid ABC transporter permease
F3L20_RS05800	3.64513	3.10E-06	PF00528	amino acid ABC transporter permease
F3L20_RS06610	2.69791	8.56E-03	PF12911	oligopeptide transport permease
F3L20_RS05045	2.22275	9.33E-03	PF12911	oligopeptide transport permease
F3L20_RS06630	3.81674	6.62E-05	PF08352	oligopeptide/dipeptide transporter
F3L20_RS05065	3.49627	1.44E-05	PF08352	oligopeptide/dipeptide transporter
F3L20_RS06625	3.47494	3.74E-04	PF08352	oligopeptide/dipeptide transporter
F3L20_RS05060	2.80960	2.20E-04	PF08352	oligopeptide/dipeptide transporter

Table S3 The expression of ATP synthase coding genes

Gene_id	log2FoldChange	p-Value	Pfam	Gene_description
F3L20_RS06140	3.03740	1.08E-02	PF00430	F0F1 ATP synthase subunit B
F3L20_RS06155	2.99991	8.84E-03	PF00231	F0F1 ATP synthase subunit gamma
F3L20_RS06160	2.78124	2.12E-02	PF00306	F0F1 ATP synthase subunit beta
F3L20_RS06150	2.76311	1.93E-02	PF02874	F0F1 ATP synthase subunit alpha
F3L20_RS06145	2.44886	2.65E-02	PF00213	F0F1 ATP synthase subunit delta
F3L20_RS06130	2.32692	2.30E-02	PF00119	F0F1 ATP synthase subunit A
F3L20_RS06165	2.07781	2.98E-02	PF02823	F0F1 ATP synthase subunit epsilon

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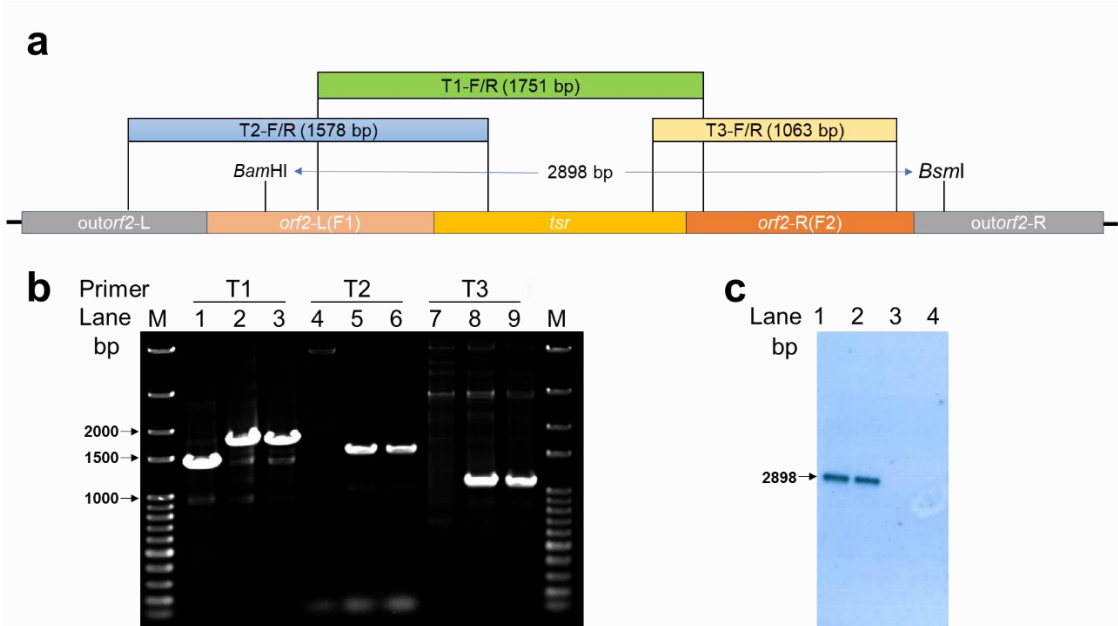


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34 Fig.S1 SDS-PAGE analysis of the Orf2. M, Blue Plus[®] V Protein Marker. Lanes 1-2,

35 Orf2.

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40 Fig. S2 *orf2* mutant strain construction and validation

41 Fig. S2 a: The primers and restriction enzyme cleavage sites used for verification on

42 the mutant strain genome. b: Lane 1, 2 and 3 were used T1-(F/R) primers for PCR

43 validation of WT, mutant 1 and mutant 2, respectively; Lane 4, 5 and 6 were used T2-

44 (F/R) primers for PCR validation of WT, mutant 1 and mutant 2, respectively; Lane 7,

45 8 and 9 were used T3-(F/R) primers for PCR validation of WT, mutant 1 and mutant 2,

46 respectively. c: Southern blot autoradiograph of *orf2* mutants and WT with *tsr* as a probe.

47 Lane 1 and 2 were chromosome DNA of *orf2* mutants digested with *Bam*HI and *Bsm*I;

48 Lane 3 and 4 were chromosome DNA of WT digested with *Bam*HI and *Bsm*I.

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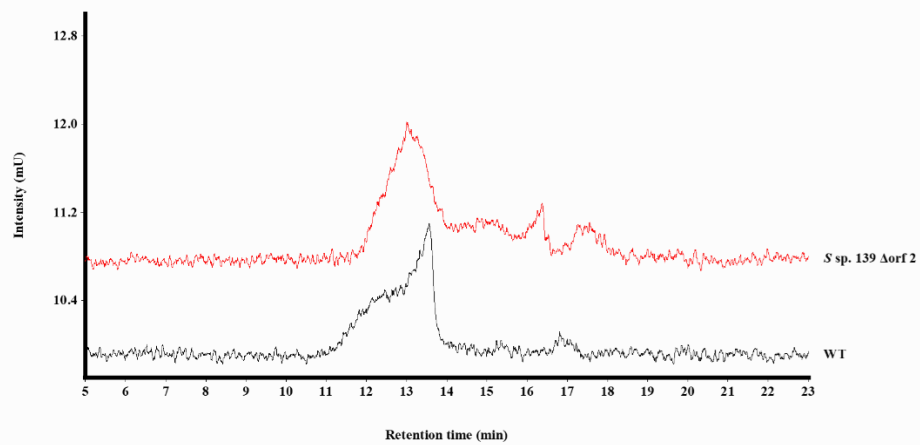
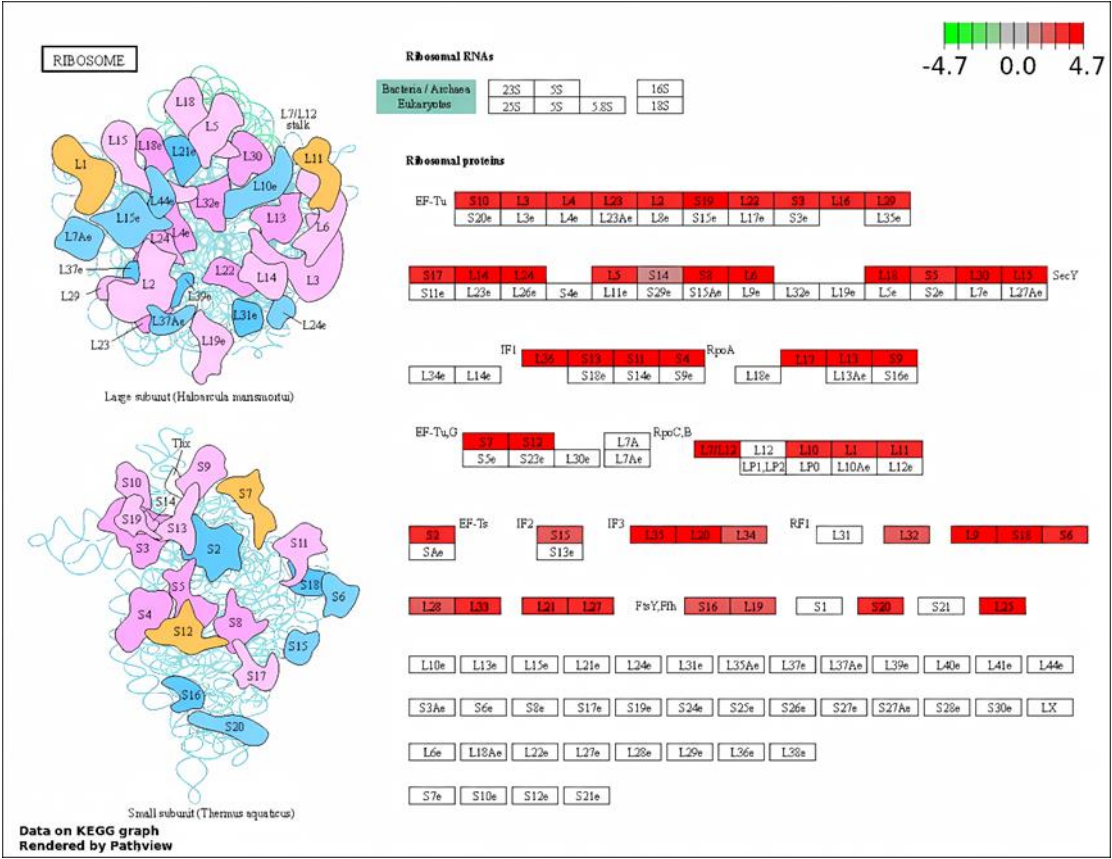


Fig. S3 Molecular distribution of crude polysaccharide from *Streptomyces* sp. 139 Δ
 $orf2$ and WT strain via GPC analysis

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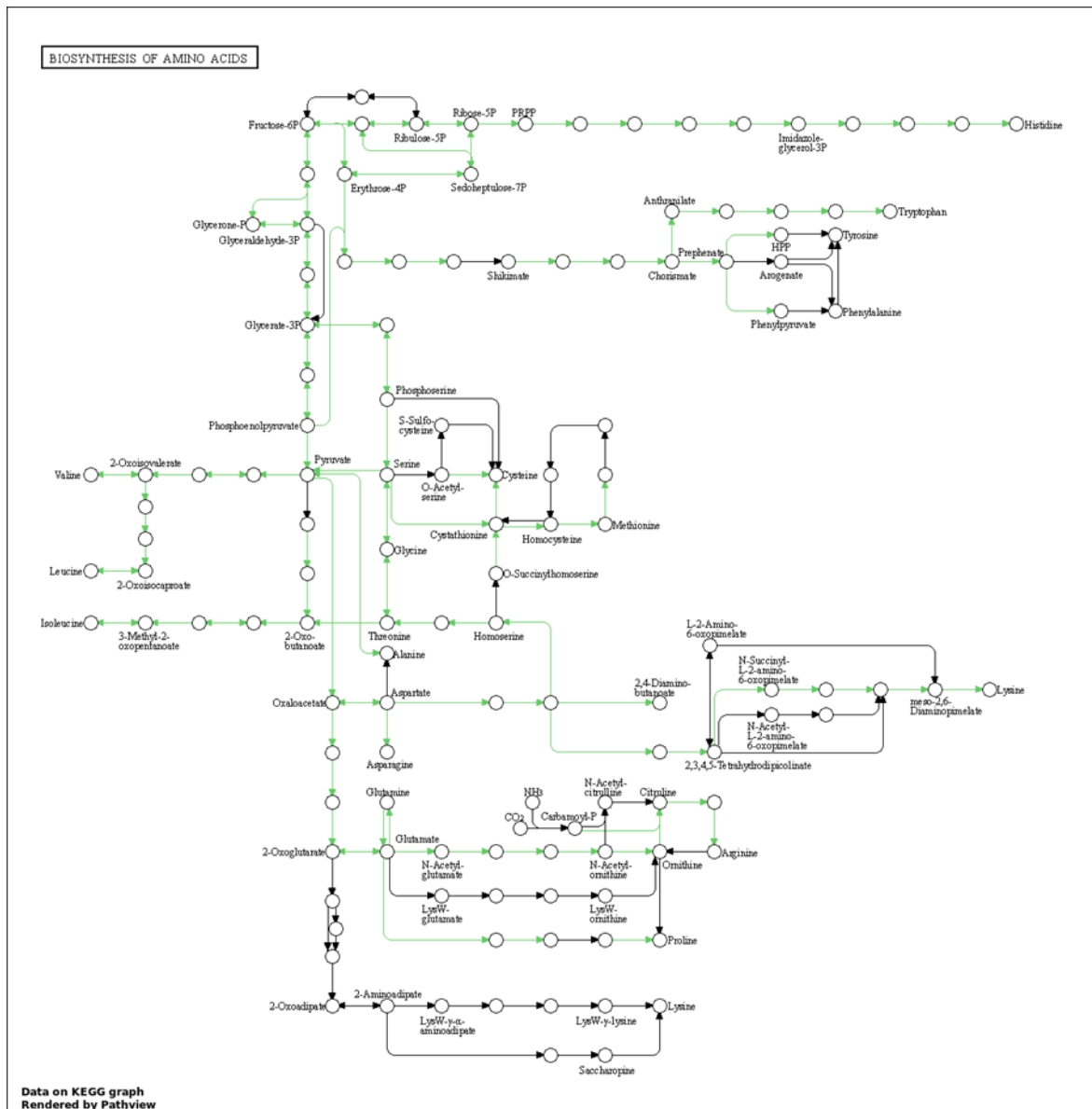


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56 Fig. S4 Expression of key genes of ribosome pathway

57 The color of the square to which the gene belongs represents its expression level, which

58 increases sequentially from green (log2foldchange=-4.7) to red (log2foldchange=4.7).



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60 Fig. S5 Amino acid biosynthetic pathway

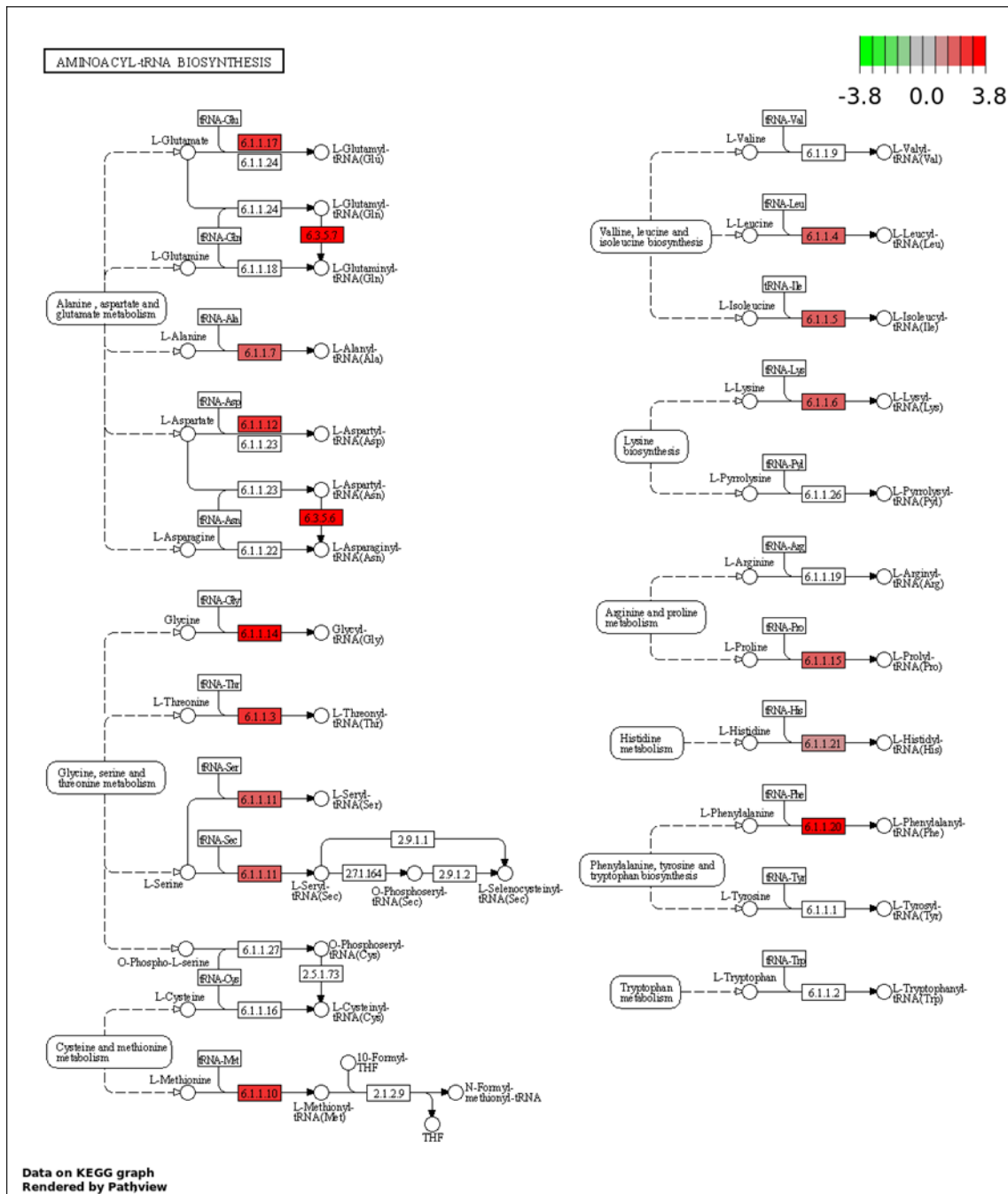


Fig. S6 Aminoacyl tRNA synthesis pathway