

Bioinformatic Analysis of Secondary Metabolite Biosynthetic Potential in Pathogenic *Fusarium*

Chao Lin ¹, Xi-long Feng ¹, Yu Liu ¹, Zhao-chen Li ¹, Xiu-Zhang Li ² and Jianzhao Qi ^{1,*}

¹ Shaanxi Key Laboratory of Natural Products & Chemical Biology, College of Chemistry & Pharmacy, North-west A&F University, Yangling, Xianyang 712100, China

² State Key Laboratory of Plateau Ecology and Agriculture, Qinghai Academy of Animal and Veterinary Sciences, Qinghai University, Xining 810016, China

* Correspondence: qjz@nwafu.edu.cn

Supplementary Table.	3
Table S1: The 35 pathogenic <i>Fusarium</i> species used in this study.	3
Table S2: BGC statistics based on antiSMASH predictions.	4
Table S3: The 16 identified BGCs for GCF network establishment.	5
Table S4: Sequence identities (%) of Ffsc4 and its homologues.	6
Table S5: Sequence identities (%) of Ffsc6 and its homologues.	7
Table S6: Sequence identities (%) of STC5 and homologues.	8
Table S7: Sequence identities (%) of STC3 and homologues.	9
Table S8: Sequence identities (%) of CLM1 and homologues.	10
Table S9: Sequence identities (%) of TRI5 and homologues.	11
Table S10: Sequence identities (%) of FlvE and homologues.	12
Table S11: Sequence identities (%) of DpfgD and homologues.	13
Table S12: Sequence identities (%) of GGS and homologues.	14
Table S13: Sequence identities (%) of CPS/KS and homologues.	16
Table S14: Sequence identities (%) of DpfgB and homologues.	17
Table S15: Sequence identities (%) of FgMS, FoFs and homologues.	18
Table S16: Sequence identities (%) of ERG7 and homologues.	19
Table S17: Sequence identities (%) of CarRA and homologues.	20
Table S18: Sequence identities (%) of DMATS1 and homologues.	21
Table S19: Sequence identities (%) of BEA1 and homologues.	22
Supplementary Figures.	23
Figure S1: GCF network of 1733 predicted biosynthetic gene cluster (BGC) from 35 pathogenic <i>Fusarium</i> species caculated by BiG-SCAPE pipeline and visualised with Cytoscape.	23
Figure S2: Cluster analysis of terpenoid synthase and their homologues based on phylogenetic tree.	24
Figure S3: Comparison of <i>Flv</i> BGCs from different species.	25
Figure S4: Phylogenetic tree-based cluster analysis of GGPP-related enzymes.	26
Figure S5: Comparison of <i>dpfg</i> BGCs from different pathogenic <i>Fusarium</i> species.	27
Figure S6: The predicted three-dimensional structure of protein of FgMS (A), FGSG_01738 (B), FGRMN_7913 (C), FPCIR_12113 (D), FPANT_13888 (E) and FoFs(F) predicted by Alphafold.	28
Figure S7: Phylogenetic tree-based cluster analysis of CarRA and its homologues.	29
Figure S8: Domain comparison of NPS1 and its homologues(A), comparison of the BGCs containing <i>nps1</i> from different species(B).	30
Figure S9: Domain comparison of NPS2 and its homologues.	31
Figure S10: Domain comparison of NPS6 and its homologues.	32
Figure S11: Domain comparison of SidE and its homologues.	33
Figure S12: Domain comparison of SidC and its homologues.	34
Figure S13: Domain comparison of ESYN1 and its homologues.	35
Figure S14: Domain comparison of PesF and its homologues.	36
Figure S15: Domain comparison of HTS1 and its homologues.	37
Figure S16: Comparison of <i>Bea</i> BGCs from different pathogenic fungi.	38
Figure S17: Comparative analysis of AclP and its homologues. Comparison of the amino acid sequence identity of AclP and its homologues(A), comparison of the structural domains of AclP and its homologues(B), structure of cyclo-(L-Phe-L-Phe)(C).	39
Figure S18: Comparison of <i>Acl</i> BGCs from different species.	40
Figure S19: Comparison of the BGCs containing <i>nrps4</i> from different <i>Fusarium</i> species.	41
Figure S20: Comparison of the BGCs containing <i>nrps5</i> from different <i>Fusarium</i> species.	42
Figure S21: Comparison of the BGCs containing <i>nrps7</i> and PKS6 from different <i>Fusarium</i> species.	43
Figure S22: Structures of sansalvamide (A), comparison of the amino acid sequence identity of NRPS30 and its homologues (B), domain comparison of NRPS30 and its homologues (C), comparison of the BGC for aurofusarin and its similar BGCs (D).	44

Figure S23: Comparison of the amino acid sequence identity of Chry1 and its homologues (A), domain comparison of Chry1 and its homologues (B), comparison of <i>chry</i> BGCs from different <i>Fusarium</i> species.	45
Figure S24: Comparison of the amino acid sequence identity of GRA1 and its homologues (A), domain comparison of GRA1 and its homologues (B), comparison of the BGC for Gramillin A, Gramillin B and its similar BGCs (C), structure of Gramillin A and Gramillin B (D).	46
Figure S25: Domain comparison of <i>apf1</i> and its homologues (A), comparison of <i>apf</i> BGCs from different <i>Fusarium</i> species (B).	47
Figure S26: Domain comparison of <i>FrbI</i> and its homologues (A), domain comparison of PKS-NRPS1 and its homologues (B), domain comparison of <i>FUS1</i> and its homologues (C).	48
Figure S27: Phylogenetic tree-based cluster analysis of PKS-related enzymes.	49
Figure S28: Comparison of <i>gpy</i> BGCs from different <i>Fusarium</i> species.	50
Figure S29: Comparison of <i>fsr</i> BGCs from different <i>Fusarium</i> species.	51
Figure S30: Comparison of <i>FUBB</i> GCGs from different <i>Fusarium</i> species.	52
Figure S31: Comparison of <i>bik</i> BGCs from different <i>Fusarium</i> species.	53
Figure S32: Comparison of <i>FPY</i> BGCs from different <i>Fusarium</i> species.	54
Figure S33: Comparison of <i>fog</i> BGCs from different <i>Fusarium</i> species.	55
Figure S34: Comparison of the amino acid sequence identity of <i>SdnO</i> and its homologues (A), domain comparison of <i>SdnO</i> and its homologues (B).	56
Figure S35: Comparison of <i>DEPB</i> GCGs from different <i>Fusarium</i> species.	57
Figure S37: Domain comparison of <i>PKS40</i> and its homologues.	59
Figure S39: Comparison of the amino acid sequence identity of <i>Alt5</i> and its homologues (A), domain comparison of <i>Alt5</i> and its homologues (B).	61
Figure S40: Domain comparison of <i>DpfgA</i> and its homologues.	62
Figure S41: Domain comparison of <i>FSL1</i> and its homologues (A), comparison of <i>FSLB</i> GCGs from different <i>Fusarium</i> species (B).	63
Figure S42: Domain comparison of <i>Bet1</i> and its homologues (A), comparison of <i>bet</i> BGCs from different species (B).	64
Figure S43: Domain comparison of <i>G433</i> and its homologues (A), comparison of the BGC for <i>G433</i> and its similar BGCs (B).	65
Figure S44: Comparison of the amino acid sequence identity of <i>Alt5</i> and its homologues (A), domain comparison of <i>FUM1</i> and its homologues (B), comparison of <i>FUMB</i> GCGs from different <i>Fusarium</i> species (C).	66
Figure S45: Domain comparison of <i>ZEA1</i> and its homologues (A), domain comparison of <i>ZEA2</i> and its homologues (B).	67
Figure S46: Domain comparison of <i>PkhA</i> and its homologues (A), domain comparison of <i>PkhB</i> and its homologues (B).	68
Figure S47: Comparison of <i>luc</i> BGCs from different <i>Fusarium</i> species.	69
Figure S48: Amino acid sequence identity comparison (A) and domain comparison (B) of newly discovered PKS-NRPSs in 35 pathogenic <i>Fusarium</i> species.	70
Figure S49: Comparison of <i>smB</i> BGCs from different <i>Fusarium</i> species.	71
Figure S50: Comparison of <i>fsa</i> BGCs and <i>PKS-NRPSB</i> GCGs from different <i>Fusarium</i> species.	72
Figure S51: Comparison of <i>icc</i> BGCs from different <i>Fusarium</i> species.	73
Figure S52: Comparison of the amino acid sequence identity of <i>FsdS</i> and its homologues (A), domain comparison of <i>FsdS</i> and its homologues (B), comparison of <i>fsdB</i> GCGs from different <i>Fusarium</i> species (C).	74
Figure S53: Domain comparison of <i>ACE1</i> and its homologues (A), comparison of <i>ACEB</i> GCGs from different species (B).	75
Figure S54: Domain comparison of <i>ThnA</i> and its homologues (A), comparison of <i>thn</i> BGCs from different species (B).	76
Figure S55: Domain comparison of <i>CghG</i> and its homologues.	77
Figure S56: Domain comparison of <i>LCI18_013989</i> and <i>jgi.p_Fustri_620762</i> .	78
Figure S57: Cluster analysis of NRPS-like sequences based on phylogenetic tree.	79
References.	80

Supplementary Table.

Table S1: The 35 pathogenic *Fusarium* species used in this study.

Species	Pathogenicity	Accession No.	Reference
<i>Fusarium oxysporum</i>	Wilt diseases	GCF_000271745.1	[1]
<i>Fusarium fujikuroi</i>	Bakanae disease	GCF_900079805.1	[2]
<i>Fusarium solani-melongenae</i>	<i>Fusarium</i> Root and Stem Rot in <i>Sweet potatoes</i>	GCA_023101225.1	[3]
<i>Fusarium vanettenii</i>	rot disease	GCF_000151355.1	[4]
<i>Fusarium odoratissimum</i>	<i>Fusarium</i> wilt of banana	GCF_000260195.1	[5]
<i>Fusarium proliferatum</i>	Vascular Wilt on Cowpea (<i>Vigna unguiculata</i>) in Brazil	GCF_900067095.1	[6]
<i>Fusarium graminearum</i>	<i>Fusarium</i> head blight in small-grain cereals	GCF_000240135.3	[7]
<i>Fusarium pseudograminearum</i>	wheat crown rot disease	GCF_000303195.2	[8]
<i>Fusarium mangiferae</i>	mango malformation disease (MMD)	GCF_900044065.1	[9]
<i>Fusarium culmorum</i>	root rot and head blight in wheat.	GCA_016952355.1	[10]
<i>Fusarium solani</i>	Root Rot and Stem Canker on Storage Roots of Sweet Potato	GCF_020744495.1	[11]
<i>Fusarium redolens</i>	American Ginseng Root Rot	GCF_020744475.1	[12]
<i>Fusarium flagelliforme</i>	Maize Leaf Blight	GCF_020744385.1	[13]
<i>Fusarium musae</i>	post-harvest disease in bananas and systemic and superficial infection in humans.	GCF_019915245.1	[14]
<i>Fusarium falciforme</i>	Leaf Blight in <i>Acacia mangium</i>	GCF_026873545.1	[15]
<i>Fusarium venenatum</i>	foot and root rot of wheat (<i>Triticum aestivum</i>)	GCF_900007375.1	[16]
<i>Fusarium tricinctum</i>	<i>Fusarium</i> head blight (FHB) and root rot	GCA_020744515.1	[17]
<i>Fusarium poae</i>	<i>Fusarium</i> Head Blight of Wheat	GCF_019609905.1	[18]
<i>Fusarium keratoplasticum</i>	associated with human infection	GCF_025433545.1	[19]
<i>Fusarium graminum</i>	<i>Fusarium</i> head blight (FHB) of small grain cereals	GCA_013266165.1	[20]
<i>Fusarium napiforme</i>	disseminated fusariosis	GCA_013396005.1	[21]
<i>Fusarium mexicanum</i>	agent of mango and big-leaf mahogany malformation in Mexico	GCA_013396015.1	[22]
<i>Fusarium decemcellulare</i>	Inflorescence Wilt and Vascular and Flower Necrosis of Rambutan (<i>Nephelium lappaceum</i>), Longan (<i>Dimocarpus longan</i>), and Mango (<i>Mangifera indica</i>)	GCA_013266205.1	[23]
<i>Fusarium acutatum</i>	permanent wilting of chickpea cuttings and killed cells	GCA_012932015.1	[24]
<i>Fusarium subglutinans</i>	Maize pathogen	GCF_013396075.1	[25]
<i>Fusarium verticillioides</i>	kernel and ear rot of maize	GCF_000149555.1	[26]
<i>Fusarium avenaceum</i>	Wheat pathogen		[27]
<i>Fusarium globosum</i>	Chlorosis and necrosis of wheat leaves and maize stems	GCA_013396165.1	[28]
<i>Fusarium mundagurra</i>	producer of fumonisins	GCA_013396205.1	[29]
<i>Fusarium pseudocircinatum</i>	Mango Malformation Disease	GCA_013396035.1	[30]
<i>Fusarium denticulatum</i>	chlorotic leaf distortion with deformation of young leaves and stunted vines.	GCA_013396175.1	[31]
<i>Fusarium pseudoanthophilum</i>	were capable of infecting vegetables such as tomatoes, bell and cayenne peppers,	GCA_013395995.1	[32]
<i>Fusarium anthophilum</i>	produced at least one of the analyzed mycotoxins	GCA_013364935.1	[33]
<i>Fusarium sarcochroum</i>	dry root rot, crown, trunk or twig canker or twig dieback of citrus trees	GCA_013266185.1	[34]
<i>Fusarium moniliforme</i>	ear rot and stalk rot of corn and infection of corn kernels		[35]

Table S2: BGC statistics based on antiSMASH predictions.

Species	BGC Type							Total
	NRPS	PKS	RiPP	Terpene	Hybird	Indole	Other	
<i>Fusarium oxysporum</i>	19	8	2	9	6	2	1	47
<i>Fusarium fujikuroi</i>	16	8	4	12	9	1	2	52
<i>Fusarium solani-melonigenae</i>	15	11	1	6	4	1	1	39
<i>Fusarium vanettenii</i>	14	12	1	6	3	1	1	38
<i>Fusarium odoratissimum</i>	15	8	2	11	6	2	1	45
<i>Fusarium proliferatum</i>	22	11	4	13	8	2	1	61
<i>Fusarium graminearum</i>	15	7	4	11	10	0	1	48
<i>Fusarium pseudograminearum</i>	14	5	2	10	9	0	0	40
<i>Fusarium mangiferae</i>	17	7	3	13	9	3	1	53
<i>Fusarium culmorum</i>	14	7	2	12	5	0	1	41
<i>Fusarium solani</i>	14	11	1	5	7	1	1	40
<i>Fusarium redolens</i>	18	9	4	11	7	2	0	51
<i>Fusarium flagelliforme</i>	18	7	2	9	6	1	1	44
<i>Fusarium musae</i>	18	7	2	11	5	2	1	46
<i>Fusarium falciforme</i>	13	13	1	5	5	1	1	39
<i>Fusarium venenatum</i>	14	5	5	12	8	0	0	44
<i>Fusarium tricinctum</i>	20	9	6	11	10	3	1	60
<i>Fusarium poae</i>	15	9	4	14	5	0	1	48
<i>Fusarium keratoplasticum</i>	11	11	1	6	7	1	1	38
<i>Fusarium graminum</i>	16	12	6	9	5	2	1	51
<i>Fusarium napiforme</i>	17	13	4	10	7	3	1	55
<i>Fusarium mexicanum</i>	18	14	2	11	11	3	1	60
<i>Fusarium decemcellulare</i>	22	17	3	12	6	3	1	64
<i>Fusarium acutatum</i>	18	11	3	11	8	2	1	54
<i>Fusarium subglutinans</i>	19	13	3	11	6	3	1	56
<i>Fusarium verticillioides</i>	17	12	1	6	7	2	1	46
<i>Fusarium avenaceum</i>	19	12	5	12	9	2	2	61
<i>Fusarium globosum</i>	22	14	3	13	7	2	1	62
<i>Fusarium mundagurra</i>	21	15	3	10	5	2	1	57
<i>Fusarium pseudocircinatum</i>	16	14	5	11	8	1	1	56
<i>Fusarium denticulatum</i>	15	15	2	13	11	1	1	58
<i>Fusarium pseudoanthophilum</i>	19	13	5	12	6	2	1	58
<i>Fusarium anthophilum</i>	23	15	5	13	7	1	1	65
<i>Fusarium sarcochroum</i>	16	11	10	9	7	2	0	55
<i>Fusarium moniliforme</i>	17	12	1	6	7	2	1	46

Table S3: The 16 identified BGCs for GCF network establishment.

Type	GCF	Identified BGC	Representative Compound	Reference
PKS I	<i>fsr</i> _GCF	<i>fsr</i> BGC	oxyjavanicin	[36]
	<i>BIK</i> _GCF	<i>BIK</i> BGC	bikaverin	[37]
	<i>ACTT</i> /PKS19_GCF	<i>ACTT</i> /PKS19BGC	fujikurin A-D ACT-Toxin II	[38, 39]
	<i>DEP</i> _GCF	<i>DEP</i> BGC	depudecin	[40]
	<i>alt</i> _GCF	<i>alt</i> BGC	alternapyrone alternapyrone B-F	[41, 42]
Terpene	<i>SQS1</i> _GCF	<i>SQS1</i> BGC	squalestatin S1	[43]
	<i>Ffsc</i> _GCF	<i>Ffsc</i> BGC	koraiol	[44]
	<i>GA</i> _GCF	<i>GA</i> _BGC	gibberellin	[45]
	<i>Tri</i> _GCF	<i>tri</i> BGC	deoxynivalenol nivalenol trichodiene-11-one	[46-48]
NRPS	<i>chry</i> _GCF	<i>chry</i> BGC	chrysogine	[49]
	<i>san</i> _GCF	<i>san</i> BGC	sansaivamide	[50]
	<i>aba</i> _GCF	<i>aba</i> BGC	AbT1 KK-1	[51, 52]
	<i>APS</i> _GCF	<i>APS</i> BGC	apicidin	[53]
PKS- NRPS- Hybrid	<i>FSL</i> _GCF	<i>FSL</i> BGC	fusarielin H	[54]
	<i>ZEA</i> _GCF	<i>ZEABGC</i>	zearalenone	[55]
Other	<i>has</i> _GCF	<i>has</i> BGC	hexadehydroastechrome	[56]
	<i>fsd</i> _GCF	<i>fsd</i> BGC	fusaridione A	[57]

Table S4: Sequence identities (%) of Ffsc4 and its homologues.

FNAPI_ 12378	FPANT_ _5545	J7337_0 10974	FDENT_ _14120	FPCR_ 8416	FMEXI_ _13175	FSUBG_ _8956	FANTH_ _11676	FACUT_ _6830	FMUN_ D_8404	FGLOB_ 1_10057	Ffsc4(F FUJ_12 585)	FPRO_ 12247	FMAN_ 11750	BKA55 DRAFT _562495	BKA59 DRAFT _435158	jgi-p_F ustri1_1 03320	FGRM N_1905	FGSG_ 11327	HYE67_ 005221	FPSE_0 5683	FPOAC 1_00750 2	FVRRE S_10751	FPOAC 1_01296 7	FPOAC 1_01381 3	FPOAC 1_00389 4	B016D RAFT _345894	BKA59 DRAFT _497532	FSARC _7662	FDECE _5463
100	99.18	99.4	98.08	98.9	97.53	98.08	97.53	97.81	97.53	96.44	96.71	96.99	97.26	95.89	88.49	87.12	86.07	81.94	81.64	82.47	81.1	81.94	77.47	77.2	83.33	85.36	77.57	83.79	75.35
99.18	100	99.4	97.81	98.63	97.26	97.81	97.26	97.53	97.26	96.16	96.44	96.71	96.99	95.62	88.22	87.4	85.79	82.22	81.92	82.74	81.37	82.22	77.75	77.47	83.33	85.08	77.26	83.79	74.79
99.4	99.4	100	98.51	99.4	97.91	98.51	97.91	98.51	98.21	97.01	97.31	97.31	97.61	96.12	88.06	87.16	85.71	82.73	82.69	83.28	82.09	82.73	78.74	78.44	85.05	85.84	78.23	83.83	79.88
98.08	97.81	98.51	100	98.63	97.26	97.81	97.26	97.53	97.26	96.16	96.44	96.71	96.99	96.16	87.95	86.85	85.52	81.94	81.64	82.47	81.1	81.94	77.47	77.2	82.54	85.36	77.88	83.79	74.79
98.9	98.63	99.4	98.63	100	98.08	98.63	98.08	98.36	98.08	96.99	97.26	97.53	97.81	96.44	88.77	87.4	86.35	82.5	82.19	83.01	81.64	82.5	78.02	77.75	84.13	85.91	78.5	84.34	75.35
97.53	97.26	97.91	97.26	98.08	100	99.18	98.08	96.99	96.71	96.71	96.44	97.26	97.53	95.62	87.67	86.3	85.24	82.5	82.19	82.74	81.64	82.5	78.02	77.75	83.33	85.64	78.82	84.62	75.62
98.08	97.81	98.51	97.81	98.63	99.18	100	98.9	97.53	97.26	97.26	96.99	97.81	98.08	96.16	88.22	86.85	85.79	82.78	82.47	83.29	81.92	82.78	78.3	78.02	84.13	86.19	78.82	84.34	75.62
97.53	97.26	97.91	97.26	98.08	98.08	98.9	100	96.99	96.71	96.99	96.71	97.53	97.81	96.16	87.67	86.3	85.24	82.78	82.47	83.29	81.92	82.78	78.3	78.02	84.13	86.19	78.82	84.34	75.62
97.81	97.53	98.51	97.53	98.36	96.99	97.53	96.99	100	98.08	96.99	96.99	97.53	97.81	96.16	88.22	86.85	85.79	82.78	82.47	83.29	82.19	82.22	77.75	77.47	82.54	85.64	77.57	84.07	75.07
97.53	97.26	98.21	97.26	98.08	96.71	97.26	96.71	98.08	100	96.99	96.99	97.53	97.81	95.89	88.49	86.85	86.07	82.5	82.47	83.01	81.92	82.5	78.57	78.3	84.13	85.91	77.88	84.34	75.62
96.44	96.16	97.01	96.16	96.99	96.71	97.26	96.99	96.99	96.99	100	98.08	99.45	99.18	95.89	87.95	86.58	85.79	82.22	81.92	82.74	81.64	82.22	78.3	78.3	84.13	85.64	77.88	84.07	75.07
96.71	96.44	97.31	96.44	97.26	96.44	96.99	96.71	96.99	96.99	98.08	100	98.63	98.36	96.16	87.95	86.58	86.35	82.5	82.19	83.01	81.92	82.5	78.3	78.3	83.33	85.91	78.5	84.34	75.62
96.99	96.71	97.31	96.71	97.53	97.26	97.81	97.53	97.53	97.53	99.45	98.63	100	99.73	96.44	88.22	87.12	86.35	82.78	82.47	83.29	82.19	82.78	78.3	78.3	83.33	86.19	78.19	84.34	75.35
97.26	96.99	97.61	96.99	97.81	97.53	98.08	97.81	97.81	97.81	99.18	98.36	99.73	100	96.71	88.49	87.4	86.63	83.06	82.74	83.56	82.47	83.06	78.57	78.3	84.13	86.46	78.5	84.62	75.62
95.89	95.62	96.12	96.16	96.44	95.62	96.16	96.16	96.16	95.89	95.89	96.16	96.44	96.71	100	87.12	85.75	84.68	82.78	82.47	83.29	81.92	82.78	78.02	77.75	84.13	86.19	79.13	85.16	75.62
88.49	88.22	88.06	87.95	88.77	87.67	88.22	87.67	88.22	88.49	87.95	87.95	88.22	88.49	87.12	100	96.02	90.03	81.44	81.15	81.97	81.15	81.72	76.5	76.23	83.33	84.89	77.02	83.38	73.2
87.12	87.4	87.16	86.85	87.4	86.3	86.85	86.3	86.85	86.85	86.58	86.58	87.12	87.4	85.75	96.02	100	88.41	81.16	80.87	81.69	81.15	81.44	76.23	75.96	81.75	84.07	76.4	82.56	72.65
86.07	85.79	85.71	85.52	86.35	85.24	85.79	85.24	85.79	86.07	85.79	86.35	86.35	86.63	84.68	90.03	88.41	100	80.83	80.28	81.11	80	81.11	76.67	76.39	83.47	83.57	76.9	80.61	71.91
81.94	82.22	82.73	81.94	82.5	82.5	82.78	82.78	82.78	82.5	82.22	82.5	82.78	83.06	82.78	81.44	81.16	80.83	100	99.45	99.72	97.51	98.34	85.83	85.56	84.3	93.85	78.48	80.83	70.87
81.64	81.92	82.69	81.64	82.19	82.19	82.47	82.47	82.47	82.47	81.92	82.19	82.47	82.74	82.47	81.15	80.87	80.28	99.45	100	99.18	96.99	97.78	85.48	85.21	84.13	93.39	78.19	80.55	70.72
82.47	82.74	83.28	82.47	83.01	82.74	83.29	83.29	83.29	83.01	82.74	83.01	83.29	83.56	83.29	81.97	81.69	81.11	99.72	99.18	100	97.27	98.34	85.75	85.48	84.13	94.21	78.5	81.1	71.55
81.1	81.37	82.09	81.1	81.64	81.64	81.92	81.92	82.19	81.92	81.64	81.92	82.19	82.47	81.92	81.15	81.15	80	97.51	96.99	97.27	100	97.51	84.11	83.84	83.33	93.11	77.88	80.6	70.8
81.94	82.22	82.73	81.94	82.5	82.5	82.78	82.78	82.22	82.5	82.22	82.5	82.78	83.06	82.78	81.72	81.44	81.11	98.34	97.78	98.34	97.51	100	85.83	85.56	85.12	93.85	78.48	81.11	71.15
77.47	77.75	78.74	77.47	78.02	78.02	78.3	78.3	77.75	78.57	78.3	78.3	78.3	78.57	78.02	76.5	76.23	76.67	85.83	85.48	85.75	84.11	85.83	100	99.73	100	85.67	76.64	77.26	69.34
77.2	77.47	78.44	77.2	77.75	77.75	78.02	78.02	77.47	78.3	78.3	78.3	78.3	78.3	77.75	76.23	75.96	76.39	85.56	85.21	85.48	83.84	85.56	99.73	100	99.21	85.4	76.32	76.99	69.06
83.33	83.33	85.05	82.54	84.13	83.33	84.13	84.13	82.54	84.13	84.13	83.33	83.33	84.13	84.13	83.33	81.75	83.47	84.3	84.13	84.13	83.33	85.12	100	99.21	100	86.51	78.79	80.95	67.2
85.36	85.08	85.84	85.36	85.91	85.64	86.19	86.19	85.64	85.91	85.64	85.91	86.19	86.46	86.19	84.89	84.07	83.57	93.85	93.39	94.21	93.11	93.85	85.67	85.4	86.51	100	79	83.43	74.37
77.57	77.26	78.23	77.88	78.5	78.82	78.82	78.82	77.57	77.88	77.88	78.5	78.19	78.5	79.13	77.02	76.4	76.9	78.48	78.19	78.5	77.88	78.48	76.64	76.32	78.79	79	100	80.86	70.72
83.79	83.79	83.83	83.79	84.34	84.62	84.34	84.34	84.07	84.34	84.07	84.34	84.34	84.62	85.16	83.38	82.56	80.61	80.83	80.55	81.1	80.6	81.11	77.26	76.99	80.95	83.43	80.86	100	76.57
75.35	74.79	79.88	74.79	75.35	75.62	75.62	75.62	75.07	75.62	75.07	75.62	75.35	75.62	75.62	73.2	72.65	71.91	70.87	70.72	71.55	70.8	71.15	69.34	69.06	67.2	74.37	70.72	76.57	100

Table S5: Sequence identities (%) of Ffsc6 and its homologues.

BKA5 5DRA FT_67 8444	FOIG _1479 6	FOY G_139 12	FMA N_132 18	Ffsc6(FFUJ_ 10353)	FGLO B1_91 81	FPRO _1386 1	FDEN T_419 3	FPCI R_133 13	FMEX I_210 9	FSUB G_793 5	FACU T_671 0	FMU ND_9 317	FNAP I_668 0	FPAN T_656 8	FVEG _1370 7	J7337 _0122 60	FSAR C_823 0	jgi_p_ Fustri 1_457 669	BKA5 9DRA FT_48 8114	FPOA C1_00 5877	FVRR ES_06 486	HYE6 7_001 787	FGSG _0349 4
100	95.15	94.61	88.68	88.41	85.35	88.95	86.46	85.68	85.48	79.51	84.37	87.4	83.56	84.11	84.66	84.66	67.31	74.29	75.34	70.64	71.23	68.22	67.67
95.15	100	98.38	92.45	92.18	87.61	92.18	89.23	88.65	87.67	81.13	86.25	89.59	86.58	86.85	87.4	87.67	65.66	74.58	74.79	70.64	71.23	68.22	67.67
94.61	98.38	100	92.99	92.72	88.17	92.45	89.5	88.38	87.4	80.86	86.52	89.32	86.3	86.58	87.12	87.4	65.66	74.29	74.52	70.36	70.96	67.95	67.67
88.68	92.45	92.99	100	98.38	92.96	97.3	89.5	88.65	87.67	81.4	84.64	89.32	86.58	87.95	87.95	88.49	64.84	71.75	71.51	68.98	68.49	65.75	65.21
88.41	92.18	92.72	98.38	100	94.37	98.92	89.78	88.92	87.95	81.67	85.18	89.59	86.85	88.22	88.22	88.77	64.56	72.32	72.05	69.25	69.04	66.3	65.75
85.35	87.61	88.17	92.96	94.37	100	94.37	85.31	85.88	84.18	84.7	90.16	85.88	83.33	84.75	83.9	84.46	64.76	70.2	71.35	68.19	68.48	65.62	65.04
88.95	92.18	92.45	97.3	98.92	94.37	100	89.78	88.92	87.95	81.67	85.18	89.59	86.85	88.22	87.67	88.22	65.38	72.32	72.6	69.81	69.59	66.85	66.3
86.46	89.23	89.5	89.5	89.78	85.31	89.78	100	97.53	92.86	87.64	85.16	94.51	92.58	92.31	92.31	92.86	63.79	69.86	70.11	67.69	68.72	66.2	65.36
85.68	88.65	88.38	88.65	88.92	85.88	88.92	97.53	100	92.18	81.59	78.61	93.26	92.57	91.91	91.91	92.45	63.39	70.42	69.4	67.49	67.49	64.21	63.39
85.48	87.67	87.4	87.67	87.95	84.18	87.95	92.86	92.18	100	88.14	82.21	95.15	91.64	92.72	92.99	93.53	62.88	70.99	71.19	66.76	67.04	64.54	65.1
79.51	81.13	80.86	81.4	81.67	84.7	81.67	87.64	81.59	88.14	100	84.73	87.33	81.77	85.44	85.44	85.98	60.92	66.67	66.04	63.04	63.61	60.38	59.84
84.37	86.25	86.52	84.64	85.18	90.16	85.18	85.16	78.61	82.21	84.73	100	84.37	77.47	81.67	81.13	81.67	61.14	69.75	69.29	63.84	64.67	61.96	61.14
87.4	89.59	89.32	89.32	89.59	85.88	89.59	94.51	93.26	95.15	87.33	84.37	100	94.88	96.23	95.69	96.23	63.43	70.99	71.19	67.87	68.42	65.65	64.82
83.56	86.58	86.3	86.58	86.85	83.33	86.85	92.58	92.57	91.64	81.77	77.47	94.88	100	95.42	93.8	94.34	62.6	68.45	68.7	66.2	66.76	64.54	63.16
84.11	86.85	86.58	87.95	88.22	84.75	88.22	92.31	91.91	92.72	85.44	81.67	96.23	95.42	100	96.23	96.77	61.5	69.3	69.53	66.76	67.31	64.54	63.99
84.66	87.4	87.12	87.95	88.22	83.9	87.67	92.31	91.91	92.99	85.44	81.13	95.69	93.8	96.23	100	99.19	62.05	68.45	68.7	65.93	66.48	63.71	63.16
84.66	87.67	87.4	88.49	88.77	84.46	88.22	92.86	92.45	93.53	85.98	81.67	96.23	94.34	96.77	99.19	100	62.05	68.73	68.98	65.93	66.48	63.71	63.16
67.31	65.66	65.66	64.84	64.56	64.76	65.38	63.79	63.39	62.88	60.92	61.14	63.43	62.6	61.5	62.05	62.05	100	70	70.27	68.94	70	68.11	67.57
74.29	74.58	74.29	71.75	72.32	70.2	72.32	69.86	70.42	70.99	66.67	69.75	70.99	68.45	69.3	68.45	68.73	70	100	93.89	80.56	80.28	79.72	79.72
75.34	74.79	74.52	71.51	72.05	71.35	72.6	70.11	69.4	71.19	66.04	69.29	71.19	68.7	69.53	68.7	68.98	70.27	93.89	100	80.11	80.86	80.32	80.32
70.64	70.64	70.36	68.98	69.25	68.19	69.81	67.69	67.49	66.76	63.04	63.84	67.87	66.2	66.76	65.93	65.93	68.94	80.56	80.11	100	94.55	91.83	91.28
71.23	71.23	70.96	68.49	69.04	68.48	69.59	68.72	67.49	67.04	63.61	64.67	68.42	66.76	67.31	66.48	66.48	70	80.28	80.86	94.55	100	92.45	91.91
68.22	68.22	67.95	65.75	66.3	65.62	66.85	66.2	64.21	64.54	60.38	61.96	65.65	64.54	64.54	63.71	63.71	68.11	79.72	80.32	91.83	92.45	100	98.65
67.67	67.67	67.67	65.21	65.75	65.04	66.3	65.36	63.39	65.1	59.84	61.14	64.82	63.16	63.99	63.16	63.16	67.57	79.72	80.32	91.28	91.91	98.65	100

Table S6: Sequence identities (%) of STC5 and homologues.

FPC IR_3 536	FPA NT_ 9745	FDE NT_ 6295	FAC UT_ 9293	FSU BG_ 1573	FAN TH_ 5434	FME XL_4 348	FPR O_1 5464	STC 5(FF UJ_1 1739)	FGL OB1 _235 9	FM AN_ 1488 7	FOY G_1 5697	FOI G_1 0183	FGS G_0 8181	HYE 67_0 0026 0	FPS E_10 885	FVR RES _046 82	FPO AC1 _004 210	FSA RC_ 5213
100	97. 76	96. 76	97. 51	96. 51	96. 51	95. 76	96. 51	95. 26	96. 01	97. 26	94. 51	94. 76	88. 53	89. 53	88. 78	86. 28	87. 03	80. 1
97. 76	100	96. 76	98. 25	97. 51	97. 51	96. 76	97. 26	96. 01	97. 01	97. 51	94. 76	95. 26	88. 53	89. 53	89. 28	86. 53	87. 53	80. 37
96. 76	96. 76	100	97. 26	96. 26	96. 26	95. 76	96. 51	95. 26	96. 01	97. 01	95. 01	95. 51	88	89. 03	88. 28	85. 79	86. 78	79. 58
97. 51	98. 25	97. 26	100	97. 76	97. 76	97. 26	98	96. 76	97. 51	98. 75	95. 76	95. 76	89. 6	90. 52	89. 53	87. 03	88. 03	80. 1
96. 51	97. 51	96. 26	97. 76	100	100	98	97. 26	96. 01	97. 26	97. 51	94. 76	95. 01	88. 53	89. 53	89. 03	86. 78	87. 78	80. 89
96. 51	97. 51	96. 26	97. 76	100	100	98	97. 26	96. 01	97. 26	97. 51	94. 76	95. 01	88. 53	89. 53	89. 03	86. 78	87. 78	80. 89
95. 76	96. 76	95. 76	97. 26	98	98	100	96. 76	96. 01	96. 76	97. 51	94. 26	94. 51	87. 2	88. 28	87. 78	85. 29	86. 78	79. 58
96. 51	97. 26	96. 51	98	97. 26	97. 26	96. 76	100	98. 25	99	98. 75	95. 76	96. 51	88. 27	89. 03	88. 78	87. 78	88. 28	80. 89
95. 26	96. 01	95. 26	96. 76	96. 01	96. 01	96. 01	98. 25	100	97. 76	97. 51	94. 51	95. 26	87. 2	88. 28	87. 78	86. 53	87. 03	79. 84
96. 01	97. 01	96. 01	97. 51	97. 26	97. 26	96. 76	99	97. 76	100	98. 25	95. 26	96. 51	88	88. 53	88. 03	86. 78	87. 28	80. 63
97. 26	97. 51	97. 01	98. 75	97. 51	97. 51	97. 51	98. 75	97. 51	98. 25	100	95. 76	96. 01	89. 07	89. 78	88. 78	86. 78	87. 78	80. 37
94. 51	94. 76	95. 01	95. 76	94. 76	94. 76	94. 26	95. 76	94. 51	95. 26	95. 76	100	98. 25	87. 47	87. 53	87. 03	85. 54	85. 79	80. 89
94. 76	95. 26	95. 51	95. 76	95. 01	95. 01	94. 51	96. 51	95. 26	96. 51	96. 01	98. 25	100	86. 67	87. 53	87. 03	86. 28	86. 53	81. 68
88. 53	88. 53	88	89. 6	88. 53	88. 53	87. 2	88. 27	87. 2	88	89. 07	87. 47	86. 67	100	98. 94	96. 54	90. 67	91. 2	78. 37
89. 53	89. 53	89. 03	90. 52	89. 53	89. 53	88. 28	89. 03	88. 28	88. 53	89. 78	87. 53	87. 53	98. 94	100	96. 77	91. 52	92. 02	79. 32
88. 78	89. 28	88. 28	89. 53	89. 03	89. 03	87. 78	88. 78	87. 78	88. 03	88. 78	87. 03	87. 03	96. 54	96. 77	100	92. 02	92. 52	79. 58
86. 28	86. 53	85. 79	87. 03	86. 78	86. 78	85. 29	87. 78	86. 53	86. 78	86. 78	85. 54	86. 28	90. 67	91. 52	92. 02	100	98. 25	78. 53
87. 03	87. 53	86. 78	88. 03	87. 78	87. 78	86. 78	88. 28	87. 03	87. 28	87. 78	85. 79	86. 53	91. 2	92. 02	92. 52	98. 25	100	78. 8
80. 1	80. 37	79. 58	80. 1	80. 89	80. 89	79. 58	80. 89	79. 84	80. 63	80. 37	80. 89	81. 68	78. 37	79. 32	79. 58	78. 53	78. 8	100

Table S7: Sequence identities (%) of STC3 and homologues.

FVRRES_13838	FGLOB1_629	STC3(FFUJ_04067)	FPRO_03449
100	82.38	81.9	81.43
82.38	100	99.16	98.88
81.9	99.16	100	98.6
81.43	98.88	98.6	100

Table S8: Sequence identities (%) of CLM1 and homologues.

FPSE_07410	HYE67_0111 82	CLM1(FGSG _10397)	FVRRES_137 51	FDECE_1558 3	jgi.p_Fustri1 _646467	BKA59DRAF T_555427
100	99.12	98.23	76.7	71.04	71.6	71.98
99.12	100	99.12	76.7	71.04	71.89	72.27
98.23	99.12	100	76.7	71.34	71.6	71.98
76.7	76.7	76.7	100	72.97	75.51	76.45
71.04	71.04	71.34	72.97	100	78.57	79.53
71.6	71.89	71.6	75.51	78.57	100	95.39
71.98	72.27	71.98	76.45	79.53	95.39	100

Table S9: Sequence identities (%) of TRI5 and homologues.

FPSE_12160	HYE67_0018 32	FGSG_03537	FPOAC1_005 923	FVRRES_065 32	TRI5(TOX5)	B0J16DRAF T_404726
100	97.07	98.13	91.73	92.27	92	85.52
97.07	100	97.6	90.4	90.93	90.4	84.99
98.13	97.6	100	91.47	92	91.47	86.33
91.73	90.4	91.47	100	97.88	96.82	88.24
92.27	90.93	92	97.88	100	98.68	87.97
92	90.4	91.47	96.82	98.68	100	87.17
85.52	84.99	86.33	88.24	87.97	87.17	100

Table S10: Sequence identities (%) of FlvE and homologues.

LCI18_010754	LCI18_011228	NECHADRAFT_97884	NCS54_01458300	NCS57_01441900	flvE
100.00	100.00	95.15	91.67	96.52	50.90
100.00	100.00	95.15	91.67	96.52	50.90
95.15	95.15	100.00	90.29	95.66	52.25
91.67	91.67	90.29	100.00	93.06	47.70
96.52	96.52	95.66	93.06	100.00	50.65
50.90	50.90	52.25	47.70	50.65	100.00

Table S11: Sequence identities (%) of DpfgD and homologues.

FPSE_10841	dpfgD(FGSG_04591)	jgi.p_Fustri1_542810	BKA55DRAFT_506145
100	93.23	87.38	89.73
93.23	100	86.24	87.92
87.38	86.24	100	93.88
89.73	87.92	93.88	100

Table S12: Sequence identities (%) of GGS and homologues.

FDE CE_ 1297 3	NCS 57_0 0750 400	NCS 54_0 0710 300	LCH 8_01 1732	BOJ1 5DR AFT _391 762	NEC HA DR AFT _695 30	FSA RC_ 1442 4	FGR MN _446 2	jgl-p _Fus tri1_ 1332 2	BKA 59D RAF T_46 2499	BOJ1 6DR AFT _677 42	FVR RES _035 20	FPO AC1 _003 180	HYE 67_0 1087 9	FPS E_00 459	FGS G_1 0097	BKA 55D RAF T_50 8582	FOI G_0 7211	FOY G_0 8127	FAC UT_ 3379	FME XL1 0918	FAN TH_ 4007	FSU BG_ 9424	FPC IR_9 600	FGL OB1 _119 67	FPR O_0 7922	FFU J_07 352	GG S	FM AN_ 0752 8	FDE NT_ 1333 8	FM UN D_9 065	J733 7_00 5732	FVE G_0 2819	FPA NT_ 8144	FNA PL1 3184
100	88.7	88.7	88.46	88.46	87.98	86.47	83.09	83.33	83.57	82.61	82.61	82.61	81.64	81.4	82.13	84.62	84.13	84.13	83.41	83.41	85.28	83.41	83.17	83.41	83.41	82.93	83.17	83.41	83.41	83.17	83.41	83.65	82.93	
88.7	100	99.52	99.04	98.81	98.33	90.1	86.71	87.2	87.68	85.51	86.47	86.23	85.27	85.02	85.75	87.26	87.5	87.5	86.54	86.78	87.82	86.78	86.54	87.02	87.02	86.54	87.02	86.78	86.78	86.3	86.78	87.02	86.3	
88.7	99.52	100	99.04	99.29	98.33	89.86	86.47	86.96	87.44	85.27	86.47	86.23	85.51	85.27	85.99	87.26	87.5	87.5	86.54	86.78	87.82	86.78	86.54	87.02	87.02	86.54	87.02	86.78	86.78	86.3	86.78	87.02	86.3	
88.46	99.04	99.04	100	98.8	98.33	90.1	86.23	86.71	87.2	85.02	86.47	86.23	85.51	85.27	85.99	87.02	87.26	87.26	86.3	86.54	87.56	86.54	86.3	86.78	86.78	86.3	86.78	86.54	86.54	86.06	86.54	86.78	86.06	
88.46	98.81	99.29	98.8	100	98.57	89.61	85.75	86.23	86.71	84.54	85.75	85.51	84.78	84.54	85.27	86.54	86.78	86.82	85.06	86.31	86.06	85.82	86.3	86.78	86.3	85.82	86.3	86.06	86.06	85.58	86.06	86.3	85.58	
87.98	98.33	98.33	98.33	98.57	100	88.89	85.02	85.51	85.99	84.3	85.02	84.78	84.06	83.82	84.54	86.3	86.54	86.58	85.82	86.8	85.82	85.82	86.06	86.06	86.06	85.58	86.06	85.82	85.82	85.34	86.82	86.06	85.34	
86.47	90.86	89.1	90.61	89.88	100	89.89	89.9	89.9	90.38	89.18	88.7	88.94	88.22	87.98	88.22	91.11	91.59	91.59	91.11	90.87	91.62	91.11	90.87	91.11	91.11	91.62	87	91.11	91.11	91.87	91.11	91.11	90.62	
83.09	86.71	86.47	86.23	85.75	85.02	89.9	100	97.12	97.6	89.66	90.38	90.62	89.42	89.42	89.18	91.59	91.07	92.07	91.59	91.83	92.39	91.59	90.35	90.87	90.87	90.38	90.62	91.35	91.11	91.11	91.35	91.59	91.87	
83.33	87.2	86.96	86.71	86.23	85.51	89.9	97.12	100	99.52	89.9	90.62	90.87	89.66	89.66	89.42	92.07	92.07	92.07	91.59	92.07	92.39	91.35	91.35	91.35	91.35	90.87	91.11	91.35	91.11	91.35	91.11	91.35	91.59	91.87
83.57	87.68	87.44	87.2	86.71	85.99	90.38	97.6	99.52	100	90.14	90.87	91.11	89.9	89.9	89.66	92.07	92.55	92.55	92.07	92.55	92.89	91.31	91.83	91.83	91.83	91.35	91.59	91.83	91.59	91.83	91.59	91.83	92.07	91.35
82.61	85.51	85.27	85.02	84.54	84.3	89.18	89.66	89.9	90.14	100	94.23	93.75	93.27	93.03	93.03	92.07	92.07	92.07	90.87	91.11	91.37	91.35	90.87	90.87	90.87	90.38	90.62	90.87	90.62	90.38	90.87	90.87	90.38	
82.61	86.47	86.47	86.47	85.75	85.02	88.7	90.38	90.62	90.87	94.23	100	98.32	97.12	96.88	96.88	92.79	93.03	93.03	91.59	92.07	92.13	92.07	91.59	92.31	92.07	92.07	91.59	91.83	91.59	91.35	91.59	91.35	91.59	91.59
82.61	86.23	86.23	86.23	85.51	84.78	88.94	90.62	90.87	91.11	93.75	98.32	100	97.6	97.36	97.36	93.03	93.27	93.27	91.83	92.31	92.39	92.31	91.83	92.07	91.83	91.83	91.35	91.59	91.83	91.59	91.83	91.83	91.83	91.83
81.64	85.27	85.51	85.51	84.78	84.06	88.22	89.42	89.66	89.9	93.27	97.12	97.6	100	99.28	99.28	92.07	92.07	92.07	90.87	91.35	91.37	91.35	90.87	90.87	90.87	90.38	90.62	87.62	90.38	90.62	90.87	90.87	90.38	
81.4	85.02	85.27	85.27	84.54	83.82	87.98	89.42	89.66	89.9	93.03	96.88	97.36	99.28	100	99.04	91.83	91.83	91.83	90.62	91.11	91.12	91.11	90.62	90.62	90.62	90.14	90.38	90.62	90.38	90.14	90.62	90.62	90.14	
82.13	85.75	85.99	85.99	85.27	84.54	88.22	89.18	89.42	89.66	93.03	96.88	97.36	99.28	99.04	100	91.83	91.83	91.83	90.62	91.11	91.62	91.11	90.62	90.62	90.62	90.14	90.38	90.62	90.62	90.38	90.62	84.09	90.38	
84.62	87.26	87.26	87.02	86.54	86.3	91.11	91.59	92.07	92.07	92.07	92.79	93.03	92.07	91.83	91.83	100	98.8	98.8	97.61	97.37	97.73	97.61	97.13	97.13	97.13	96.65	96.89	97.61	97.37	97.13	97.61	97.13	97.13	
84.13	87.5	87.5	87.26	86.78	86.54	91.59	92.07	92.07	92.55	92.07	93.27	93.27	92.07	91.83	91.83	98.8	100	100	98.56	98.33	98.74	98.56	98.33	98.09	98.09	97.61	97.85	98.56	98.33	98.33	98.56	98.09	98.09	
84.13	87.5	87.5	87.26	86.78	86.54	91.59	92.07	92.07	92.55	92.07	93.27	93.27	92.07	91.83	91.83	98.8	100	100	98.56	98.33	98.74	98.56	98.33	98.09	98.09	97.61	97.85	98.56	98.33	98.33	98.56	98.09	98.09	

83. 41	86. 54	86. 54	86. 3	85. 82	85. 58	91. 11	91. 59	91. 59	92. 07	90. 87	91. 59	91. 83	90. 87	90. 62	90. 62	97. 61	98. 56	98. 56	10 0	99. 28	99. 75	99. 52	99. 52	98. 8	99. 04	99. 04	98. 56	98. 8	99. 52	99. 28	99. 04	99. 52	99. 04	99. 04
83. 41	86. 78	86. 78	86. 54	86. 06	85. 82	90. 87	91. 83	92. 07	92. 55	91. 11	92. 07	92. 31	91. 35	91. 11	91. 11	97. 37	98. 33	98. 33	99. 28	10 0	99. 75	99. 76	99. 28	98. 56	98. 8	98. 8	98. 33	98. 56	99. 28	99. 04	98. 56	99. 28	98. 8	98. 8
85. 28	87. 82	87. 82	87. 56	87. 31	86. 8	91. 62	92. 39	92. 39	92. 89	91. 37	92. 13	92. 39	91. 37	91. 12	91. 62	97. 73	98. 74	98. 74	99. 75	99. 75	10 0	10 0	99. 49	98. 74	98. 99	98. 99	98. 48	98. 74	99. 49	99. 49	99. 24	99. 75	99. 24	99. 24
83. 41	86. 78	86. 78	86. 54	86. 06	85. 82	91. 11	91. 59	91. 83	92. 31	91. 35	92. 07	92. 31	91. 35	91. 11	91. 11	97. 61	98. 56	98. 56	99. 52	99. 76	10 0	10 0	99. 52	98. 8	99. 04	99. 04	98. 56	98. 8	99. 52	99. 28	98. 8	99. 52	99. 04	99. 04
83. 17	86. 54	86. 54	86. 3	85. 82	85. 58	90. 87	91. 35	91. 35	91. 83	90. 87	91. 59	91. 83	90. 87	90. 62	90. 62	97. 61	98. 56	98. 56	99. 52	99. 28	99. 49	99. 52	10 0	98. 8	99. 04	99. 04	98. 56	98. 8	99. 52	99. 28	98. 8	99. 52	99. 04	99. 04
83. 41	87. 02	87. 02	86. 78	86. 3	86. 06	91. 11	90. 87	91. 35	91. 83	90. 87	92. 31	92. 07	90. 87	90. 62	90. 62	97. 13	98. 33	98. 33	98. 8	98. 56	98. 74	98. 8	98. 8	10 0	99. 76	99. 76	99. 28	99. 52	98. 8	98. 56	98. 56	98. 8	98. 33	98. 33
83. 41	87. 02	87. 02	86. 78	86. 3	86. 06	91. 11	90. 87	91. 35	91. 83	90. 87	92. 07	91. 83	90. 87	90. 62	90. 62	97. 13	98. 09	98. 09	99. 04	98. 8	98. 99	99. 04	99. 04	99. 76	10 0	10 0	99. 52	99. 76	99. 04	98. 8	98. 33	99. 04	98. 56	98. 56
83. 41	87. 02	87. 02	86. 78	86. 3	86. 06	91. 11	90. 87	91. 35	91. 83	90. 87	92. 07	91. 83	90. 87	90. 62	90. 62	97. 13	98. 09	98. 09	99. 04	98. 8	98. 99	99. 04	99. 04	99. 76	10 0	10 0	99. 52	99. 76	99. 04	98. 8	98. 33	99. 04	98. 56	98. 56
82. 93	86. 54	86. 54	86. 3	85. 82	85. 58	90. 62	90. 38	90. 87	91. 35	90. 38	91. 59	91. 35	90. 38	90. 14	90. 14	96. 65	97. 61	97. 61	98. 56	98. 33	98. 48	98. 56	98. 56	99. 28	99. 52	99. 52	10 0	99. 28	98. 56	98. 33	97. 85	98. 56	98. 09	98. 09
83. 17	87. 02	87. 02	86. 78	86. 3	86. 06	90. 87	90. 62	91. 11	91. 59	90. 62	91. 83	91. 59	90. 62	90. 38	90. 38	96. 89	97. 85	97. 85	98. 8	98. 56	98. 74	98. 8	98. 8	99. 52	99. 76	99. 76	99. 28	10 0	98. 8	98. 56	98. 09	98. 8	98. 33	98. 33
83. 41	86. 78	86. 78	86. 54	86. 06	85. 82	91. 11	91. 35	91. 35	91. 83	90. 87	91. 59	91. 83	90. 87	90. 62	90. 62	97. 61	98. 56	98. 56	99. 52	99. 28	99. 49	99. 52	99. 52	98. 8	99. 04	99. 04	98. 56	98. 8	10 0	99. 76	98. 8	99. 52	99. 04	99. 04
83. 41	86. 78	86. 78	86. 54	86. 06	85. 82	91. 11	91. 11	91. 11	91. 59	90. 62	91. 35	91. 59	90. 62	90. 38	90. 62	97. 37	98. 33	98. 33	99. 28	99. 04	99. 49	99. 28	99. 28	98. 56	98. 8	98. 8	98. 33	98. 56	99. 76	10 0	99. 04	99. 76	99. 28	99. 28
83. 17	86. 3	86. 3	86. 06	85. 58	85. 34	90. 87	91. 11	91. 11	91. 59	90. 38	91. 35	91. 59	90. 38	90. 14	90. 38	97. 13	98. 33	98. 33	99. 04	98. 56	99. 24	98. 8	98. 8	98. 56	98. 33	98. 33	97. 85	98. 09	98. 8	99. 04	10 0	99. 28	98. 8	99. 04
83. 41	86. 78	86. 78	86. 54	86. 06	85. 82	91. 11	91. 35	91. 35	91. 83	90. 87	91. 59	91. 83	90. 87	90. 62	90. 87	97. 61	98. 56	98. 56	99. 52	99. 28	99. 75	99. 52	99. 52	98. 8	99. 04	99. 04	98. 56	98. 8	99. 52	99. 76	99. 28	10 0	99. 52	99. 52
83. 65	87. 02	87. 02	86. 78	86. 3	86. 06	91. 11	91. 59	91. 59	92. 07	90. 87	91. 59	91. 83	90. 87	90. 62	84. 09	97. 13	98. 09	98. 09	99. 04	98. 8	99. 24	99. 04	99. 04	98. 33	98. 56	98. 56	98. 09	98. 33	99. 04	99. 28	98. 8	99. 52	10 0	99. 04
82. 93	86. 3	86. 3	86. 06	85. 58	85. 34	90. 62	90. 87	90. 87	91. 35	90. 38	91. 11	91. 35	90. 38	90. 14	90. 38	97. 13	98. 09	98. 09	99. 04	98. 8	99. 24	99. 04	99. 04	98. 33	98. 56	98. 56	98. 09	98. 33	99. 04	99. 28	99. 04	99. 52	99. 04	10 0

Table S13: Sequence identities (%) of CPS/KS and homologues.

FSARC _13126	jgi.p_F ustri1_ 538881	FDECE _7075	LCI18_ 013895	FNAPI _4141	FOIG_ 09083	FGLO B1_618 6	FPRO_ 08705	CPS/K S(FFUJ _14336)	FMAN _08250	FOYG_ 08942	FACUT _8682	FPRO_ 16062	FANT H_6278	FSUBG _10000	FMEXI _710	FDEN T_1408 6	FMUN D_1569 7	J7337_0 05030	FPANT _11050
100	54.24	57.43	49.33	41.67	43.54	53.77	53.7	52.91	52.28	52.7	52.54	52.54	54.07	53.62	53.33	52.28	52.7	52.12	53.02
54.24	100	70.04	65.15	51.98	55.8	64.76	65.01	65.78	65.89	65.89	65.64	66.17	66.63	65.31	64.83	65.36	66.31	65.85	65.15
57.43	70.04	100	77.15	54.56	59.08	66.38	66.6	66.74	66.53	66.53	66.6	65.33	66.63	65.22	65.26	65.58	66.63	66.63	66.53
49.33	65.15	77.15	100	64.4	57.62	60.6	61.97	61.63	61.43	63.57	62.14	61.75	63.18	60.85	61.05	61.43	62.21	59.88	60.85
41.67	51.98	54.56	64.4	100	75.72	62.55	63.29	62.9	63.1	63.29	65.28	64.09	62.9	60.97	61.51	66.27	65.87	67.66	68.25
43.54	55.8	59.08	57.62	75.72	100	76.19	77.34	79.08	78.43	80.83	78.38	78	78.43	75.82	76.91	78.87	79.74	77.56	78.65
53.77	64.76	66.38	60.6	62.55	76.19	100	96.9	85.55	85.01	85.12	84.57	83.71	84.26	82.85	83.94	83.4	85.97	83.3	84.15
53.7	65.01	66.6	61.97	63.29	77.34	96.9	100	85.61	84.87	84.98	84.54	83.49	84.14	82.54	83.61	83.19	85.92	82.85	83.93
52.91	65.78	66.74	61.63	62.9	79.08	85.55	85.61	100	89.08	86.13	85.91	85.28	84.66	83.07	84.14	84.35	86.97	83.74	85.08
52.28	65.89	66.53	61.43	63.1	78.43	85.01	84.87	89.08	100	85.71	86.44	86.12	85.92	84.44	85.61	84.77	86.34	83.52	85.5
52.7	65.89	66.53	63.57	63.29	80.83	85.12	84.98	86.13	85.71	100	85.17	85.28	85.4	83.81	84.45	83.82	86.24	82.63	84.24
52.54	65.64	66.6	62.14	65.28	78.38	84.57	84.54	85.91	86.44	85.17	100	85.47	85.49	84.22	84.75	85.28	87.07	86.62	86.86
52.54	66.17	65.33	61.75	64.09	78	83.71	83.49	85.28	86.12	85.28	85.47	100	89.38	89.19	89.48	88.01	86.65	84.06	84.23
54.07	66.63	66.63	63.18	62.9	78.43	84.26	84.14	84.66	85.92	85.4	85.49	89.38	100	91.96	91.7	87.39	86.45	83.96	84.45
53.62	65.31	65.22	60.85	60.97	75.82	82.85	82.54	83.07	84.44	83.81	84.22	89.19	91.96	100	92.17	86.46	84.76	81.93	83.07
53.33	64.83	65.26	61.05	61.51	76.91	83.94	83.61	84.14	85.61	84.45	84.75	89.48	91.7	92.17	100	87.18	85.71	83.52	84.35
52.28	65.36	65.58	61.43	66.27	78.87	83.4	83.19	84.35	84.77	83.82	85.28	88.01	87.39	86.46	87.18	100	88.55	84.97	86.03
52.7	66.31	66.63	62.21	65.87	79.74	85.97	85.92	86.97	86.34	86.24	87.07	86.65	86.45	84.76	85.71	88.55	100	86.97	89.39
52.12	65.85	66.63	59.88	67.66	77.56	83.3	82.85	83.74	83.52	82.63	86.62	84.06	83.96	81.93	83.52	84.97	86.97	100	90.98
53.02	65.15	66.53	60.85	68.25	78.65	84.15	83.93	85.08	85.5	84.24	86.86	84.23	84.45	83.07	84.35	86.03	89.39	90.98	100

Table S14: Sequence identities (%) of DpfgB and homologues.

DER45 DRAF T_6180 20	KAF25 _00342 3	HG530 _01394 2	FAVG 1_1269 8	H9Q72 _00356 7	H9Q73 _00381 7	H9Q70 _01408 9	TPAR_ 03748	XA68_ 13016	FNYG _13150	F53441 _8896	FOMA 001_g1 8868	LZL87 _01391 6	DER46 DRAF T_6903 67	Forpe1 208_v0 11544	FCUL G_000 07167	FPSE5 266_10 837	MDCF G8_L OCUS 587785	FPSE_ 10837	MDCF G202_ LOCU S51873 6	FAUS T_1142 1	MDCF U1_LO CUS56 7934	dpfgB _FGS G_122 22_ 17.1	FGRA MCM L3066_ 01t157 17.1	MDCF G5_L OCUS 178956	FGRA MPH1 _01T15 659	NXS19 _00800 5
100	98.34	98.76	98.35	91.32	91.86	90.78	80.58	76.57	90.4	87.19	93.14	90.99	92.61	93.04	91.21	91.63	91.21	88.78	91.21	91.21	91.21	92.35	90.79	90.38	91.56	65.35
98.34	100	99.17	98.76	92.12	93.02	91.71	81.74	76.99	90.96	88.38	94.29	92.24	93.48	93.91	90.04	90.46	90.46	87.98	90.46	90.46	90.46	91.33	90.04	89.63	90.79	64.22
98.76	99.17	100	99.59	92.15	93.02	91.75	80.99	76.57	90.96	88.02	94.29	91.85	93.48	93.91	91.21	91.63	91.21	88.78	91.21	91.21	91.21	92.35	90.79	90.38	91.56	65.35
98.35	98.76	99.59	100	92.15	93.02	91.75	80.99	76.57	90.96	88.02	93.71	91.42	93.04	93.48	91.21	91.63	91.21	88.78	91.21	91.21	91.21	92.35	90.79	90.38	91.56	65.35
91.32	92.12	92.15	92.15	100	99.42	99.51	80.58	75.73	89.27	84.3	91.43	88.41	90	89.57	89.54	89.96	89.96	86.83	89.96	89.96	89.96	91.18	89.54	89.12	89.33	63.6
91.86	93.02	93.02	93.02	99.42	100	100	81.4	78.49	90.7	90.7	91.86	91.86	91.86	91.86	90	90.59	90.59	89.12	90.59	90.59	90.59	90.59	90.59	90	90.59	80.81
90.78	91.71	91.75	91.75	99.51	100	100	79.61	72.41	86.52	81.55	90.65	87.31	89.18	88.66	87.86	88.35	88.35	84.3	88.35	88.35	88.35	89.05	87.86	87.38	87.5	65.62
80.58	81.74	80.99	80.99	80.58	81.4	79.61	100	77.82	77.97	77.37	80.57	78.63	80.43	80.43	82.01	82.43	82.85	80.98	82.85	82.85	82.85	81.76	82.43	82.43	82.67	58.77
76.57	76.99	76.57	76.57	75.73	78.49	72.41	77.82	100	75.71	74.48	76.57	75.22	75.65	76.09	77.54	77.54	77.54	76.59	77.54	77.54	77.54	78.82	77.54	77.12	78.22	57.02
90.4	90.96	90.96	90.96	89.27	90.7	86.52	77.97	75.71	100	92.09	93.71	91.53	91.53	91.53	88.51	90.23	90.23	88.08	90.23	90.23	90.23	92.35	90.23	90.23	90.23	81.36
87.19	88.38	88.02	88.02	84.3	90.7	81.55	77.37	74.48	92.09	100	93.71	91.14	88.02	88.43	85.77	87.03	87.03	89.76	87.03	87.03	87.03	92.94	86.61	86.19	92.44	66.23
93.14	94.29	94.29	93.71	91.43	91.86	90.65	80.57	76.57	93.71	93.71	100	98.86	98.86	98.86	93.02	94.77	94.77	93.29	94.77	94.77	94.77	95.88	94.77	94.19	94.77	85.14
90.99	92.24	91.85	91.42	88.41	91.86	87.31	78.63	75.22	91.53	91.14	98.86	100	93.39	92.98	90	91.3	91.3	93.97	91.3	91.3	91.3	95.88	90.87	90.43	94.14	69.82
92.61	93.48	93.48	93.04	90	91.86	89.18	80.43	75.65	91.53	88.02	98.86	93.39	100	99.17	92.07	93.39	93.39	93.47	93.39	93.39	93.39	95.88	92.95	92.51	94.59	69.82
93.04	93.91	93.91	93.48	89.57	91.86	88.66	80.43	76.09	91.53	88.43	98.86	92.98	99.17	100	92.51	93.83	93.83	93.97	93.83	93.83	93.83	95.88	93.39	92.95	95.05	69.82
91.21	90.04	91.21	91.21	89.54	90	87.86	82.01	77.54	88.51	85.77	93.02	90	92.07	92.51	100	98.76	98.35	94.71	98.35	98.35	98.35	98.27	97.93	97.52	96.93	70.18
91.63	90.46	91.63	91.63	89.96	90.59	88.35	82.43	77.54	90.23	87.03	94.77	91.3	93.39	93.83	98.76	100	99.59	96.15	99.59	99.59	99.59	100	99.17	98.76	98.25	71.49
91.21	90.46	91.21	91.21	89.96	90.59	88.35	82.85	77.54	90.23	87.03	94.77	91.3	93.39	93.83	98.35	99.59	100	96.15	99.81	100	99.63	100	99.44	99.26	98.86	71.49
88.78	87.98	88.78	88.78	86.83	89.12	84.3	80.98	76.59	88.08	89.76	93.29	93.97	93.47	93.97	94.71	96.15	96.15	100	96.15	96.15	96.15	99.33	95.67	95.19	97.07	68.29
91.21	90.46	91.21	91.21	89.96	90.59	88.35	82.85	77.54	90.23	87.03	94.77	91.3	93.39	93.83	98.35	99.59	99.81	96.15	100	100	99.9	100	99.63	97.86	99.05	71.49
91.21	90.46	91.21	91.21	89.96	90.59	88.35	82.85	77.54	90.23	87.03	94.77	91.3	93.39	93.83	98.35	99.59	100	96.15	100	100	100	100	99.59	99.17	98.25	71.49
91.21	90.46	91.21	91.21	89.96	90.59	88.35	82.85	77.54	90.23	87.03	94.77	91.3	93.39	93.83	98.35	99.59	99.63	96.15	99.9	100	100	100	99.81	97.97	99.24	71.49
92.35	91.33	92.35	92.35	91.18	90.59	89.05	81.76	78.82	92.35	92.94	95.88	95.88	95.88	95.88	98.27	100	100	99.33	100	100	100	100	100	99.42	100	90.75
90.79	90.04	90.79	90.79	89.54	90.59	87.86	82.43	77.54	90.23	86.61	94.77	90.87	92.95	93.39	97.93	99.17	99.44	95.67	99.63	99.59	99.81	100	100	99.44	99.05	71.49
90.38	89.63	90.38	90.38	89.12	90	87.38	82.43	77.12	90.23	86.19	94.19	90.43	92.51	92.95	97.52	98.76	99.26	95.19	97.86	99.17	97.97	99.42	99.44	100	99.24	71.05
91.56	90.79	91.56	91.56	89.33	90.59	87.5	82.67	78.22	90.23	92.44	94.77	94.14	94.59	95.05	96.93	98.25	98.86	97.07	99.05	98.25	99.24	100	99.05	99.24	100	72.44
65.35	64.22	65.35	65.35	63.6	80.81	65.62	58.77	57.02	81.36	66.23	85.14	69.82	69.82	69.82	70.18	71.49	71.49	68.29	71.49	71.49	71.49	90.75	71.49	71.05	72.44	100

Table S15: Sequence identities (%) of FgMS, FoFs and homologues.

FgMS	FGSG_01738	FoFs	FGRMN_7913	FPCIR_12113	FPANT_13888
100	98.65	32.23	29.12	29.35	29.59
98.65	100	31.25	27.39	27.87	28.25
32.23	31.25	100	28.78	28.8	29.67
29.12	27.39	28.78	100	79.33	80.05
29.35	27.87	28.8	79.33	100	96.94
29.59	28.25	29.67	80.05	96.94	100

Table S16: Sequence identities (%) of ERG7 and homologues.

ERG7(A0A0E0 SP71)	LCI18_ 004508	NECH ADRAF T_72055	B0J15D RAFT_ 490730	NCS57_ 0116210 0	B0J15D RAFT_ 467131	NCS54_ 0141840 0	NCS57_ 0140030 0	FDECE _3328	BKA59 DRAFT _535453	FSARC _2617
100	80.45	80.1	80.45	80.08	56.64	56.58	56.72	58.39	49.68	58.59
80.45	100	98.04	98.82	97.91	58.13	58.89	59.02	60.85	52.44	59.95
80.1	98.04	100	98.3	97.65	57.72	58.48	58.62	60.44	51.94	59.81
80.45	98.82	98.3	100	98.43	57.86	58.62	58.75	60.85	52.6	60.22
80.08	97.91	97.65	98.43	100	57.99	58.75	58.89	60.71	52.44	60.08
56.64	58.13	57.72	57.86	57.99	100	96.34	96.75	74.52	59.15	71.45
56.58	58.89	58.48	58.62	58.75	96.34	100	98.37	75.72	59.08	71.27
56.72	59.02	58.62	58.75	58.89	96.75	98.37	100	75.85	59.57	71.68
58.39	60.85	60.44	60.85	60.71	74.52	75.72	75.85	100	63.59	77.66
49.68	52.44	51.94	52.6	52.44	59.15	59.08	59.57	63.59	100	68.35
58.59	59.95	59.81	60.22	60.08	71.45	71.27	71.68	77.66	68.35	100

Table S17: Sequence identities (%) of CarRA and homologues.

BAKA5 5DRA FT_65 2263	FOYG _15802	FOIG _10085	FNAP I_9157	J7337_ 013307	FVEG _10718	FMU ND_1 581	FPAN T_457 7	FPCIR _12421	FDEN T_702 0	FACU T_109 5	FPRO _15512	FGLO B1_67 42	carRA (FFUJ _11802)	FMA N_149 45	FMEX I_3381	FSUB G_785 0	FANT H_697 1
100	96.72	97.59	95.69	95.69	95.69	94.66	96.38	96.03	93.45	95.69	95.17	94.48	95.52	94.83	95.17	95.17	94.07
96.72	100	98.79	96.38	96.03	96.03	95.34	96.72	96.03	93.79	96.72	96.55	95.86	96.9	96.21	96.55	96.21	95.56
97.59	98.79	100	97.24	96.9	96.9	95.86	97.59	96.9	94.83	97.24	97.07	96.38	97.41	96.72	97.07	96.72	95.74
95.69	96.38	97.24	100	97.93	97.93	97.24	98.62	97.93	95.69	97.93	97.41	97.07	98.1	97.76	98.45	97.76	97.04
95.69	96.03	96.9	97.93	100	99.14	97.24	98.62	97.93	95.17	98.1	97.07	96.72	97.76	97.07	97.41	97.41	96.48
95.69	96.03	96.9	97.93	99.14	100	96.72	98.45	97.76	95	97.93	96.9	96.55	97.59	97.07	97.41	97.24	96.48
94.66	95.34	95.86	97.24	97.24	96.72	100	98.28	97.24	94.83	97.41	96.38	96.38	97.07	96.72	97.07	97.41	96.48
96.38	96.72	97.59	98.62	98.62	98.45	98.28	100	98.97	96.21	98.79	97.76	97.41	98.45	97.76	98.1	98.45	97.59
96.03	96.03	96.9	97.93	97.93	97.76	97.24	98.97	100	96.03	98.28	97.59	97.24	98.28	97.59	97.93	98.28	97.41
93.45	93.79	94.83	95.69	95.17	95	94.83	96.21	96.03	100	95.52	95.17	94.48	95.52	95.17	95.52	95.69	94.63
95.69	96.72	97.24	97.93	98.1	97.93	97.41	98.79	98.28	95.52	100	98.1	97.76	98.79	98.1	98.45	98.45	97.59
95.17	96.55	97.07	97.41	97.07	96.9	96.38	97.76	97.59	95.17	98.1	100	98.79	98.45	97.76	98.1	97.76	96.85
94.48	95.86	96.38	97.07	96.72	96.55	96.38	97.41	97.24	94.48	97.76	98.79	100	98.1	97.41	98.1	97.76	96.85
95.52	96.9	97.41	98.1	97.76	97.59	97.07	98.45	98.28	95.52	98.79	98.45	98.1	100	98.45	98.79	98.45	97.59
94.83	96.21	96.72	97.76	97.07	97.07	96.72	97.76	97.59	95.17	98.1	97.76	97.41	98.45	100	98.97	98.62	97.59
95.17	96.55	97.07	98.45	97.41	97.41	97.07	98.1	97.93	95.52	98.45	98.1	98.1	98.79	98.97	100	99.31	98.15
95.17	96.21	96.72	97.76	97.41	97.24	97.41	98.45	98.28	95.69	98.45	97.76	97.76	98.45	98.62	99.31	100	98.7
94.07	95.56	95.74	97.04	96.48	96.48	96.48	97.59	97.41	94.63	97.59	96.85	96.85	97.59	97.59	98.15	98.7	100

Table S18: Sequence identities (%) of DMATS1 and homologues.

FDECE _2611	BKA55 DRAFT _596100	FOIG_1 5822	FOYG_ 12928	FGLOB 1_12591	DMAT S1(FFU J_09179)	FACUT _4333	FMEXI _13958	FSUBG _13334	FANTH _2382	FMUN D_7075	FNAPI _658	FPANT _11676	FDENT _259	J7337_0 11243	FVEG_ 09966
100	65.66	67.93	67.7	64.45	66.67	64.85	65.64	65.88	65.94	65.88	65.17	65.88	65.64	65	65.94
65.66	100	78.61	77.11	73.32	74.31	73.07	72.07	73.07	74.06	75.12	74.13	72.89	73.88	79.39	74.38
67.93	78.61	100	92.74	86.38	86.36	84.94	83.33	84.04	84.93	88.29	84.07	82.9	85.95	86.67	85.2
67.7	77.11	92.74	100	83.8	87.08	85.88	83.8	84.27	85.17	88.06	84.78	84.07	86.18	84.93	85.68
64.45	73.32	86.38	83.8	100	91.17	82.39	80.33	81.5	82.34	84.31	81.03	80.56	81.97	85.22	83.53
66.67	74.31	86.36	87.08	91.17	100	86.87	83.05	83.53	84.25	87.59	84.96	84.25	85.44	86.09	86.16
64.85	73.07	84.94	85.88	82.39	86.87	100	84.04	84.74	85.68	87.79	86.15	84.51	86.62	84.64	86.16
65.64	72.07	83.33	83.8	80.33	83.05	84.04	100	94.38	95.7	86.18	82.44	82.2	83.61	82.32	83.29
65.88	73.07	84.04	84.27	81.5	83.53	84.74	94.38	100	96.42	86.89	83.37	82.67	83.84	84.06	83.77
65.94	74.06	84.93	85.17	82.34	84.25	85.68	95.7	96.42	100	86.87	83.77	83.77	84.25	84.06	84.01
65.88	75.12	88.29	88.06	84.31	87.59	87.79	86.18	86.89	86.87	100	89.98	89.04	91.38	91.07	90.97
65.17	74.13	84.07	84.78	81.03	84.96	86.15	82.44	83.37	83.77	89.98	100	93.71	91.61	89.63	90.5
65.88	72.89	82.9	84.07	80.56	84.25	84.51	82.2	82.67	83.77	89.04	93.71	100	89.98	88.18	89.31
65.64	73.88	85.95	86.18	81.97	85.44	86.62	83.61	83.84	84.25	91.38	91.61	89.98	100	92.22	93.59
65	79.39	86.67	84.93	85.22	86.09	84.64	82.32	84.06	84.06	91.07	89.63	88.18	92.22	100	98.56
65.94	74.38	85.2	85.68	83.53	86.16	86.16	83.29	83.77	84.01	90.97	90.5	89.31	93.59	98.56	100

Table S19: Sequence identities (%) of BEA1 and homologues.

FVR RES_ 12556	FPO AC1_ 01150 0	BKA 55DR AFT_ 67790 2	FOY G_12 900	FOIG _1579 3	FMA N_12 971	FGL OB1_ 2217	BEA1 (FFUJ _0929 6)	FPR O_13 541	FAC UT_8 369	J7337 _0112 63	FVE G_16 703	FPCI R_12 112	FDE NT_2 45	FMU ND_ 5269	FAN TH_2 399	FME XI_40 09	FSUB G_13 646
100	89.93	66.16	66.00	66.04	65.60	65.6	65.22	65.41	65.49	56.19	67	65.36	65.21	65.44	65.41	65.4	65.65
89.93	100	66.45	66.55	66.4	66.09	66.18	65.84	65.79	66.01	56.28	67.77	66.01	65.82	66.05	65.76	65.91	65.88
66.16	66.45	100	91.07	91.39	88.55	88.68	89.05	88.39	90.01	70.79	89.19	89.26	89.84	90.08	89.3	89.09	88.82
66.00	66.55	91.07	100	97.55	90.18	90.49	90.62	90.33	91.80	72.70	90.45	90.53	91.15	91.61	90.55	90.87	90.15
66.04	66.40	91.39	97.55	100	90.47	90.66	90.78	90.59	92.38	73.14	90.95	90.79	91.35	92	90.87	90.88	90.45
65.60	66.09	88.55	90.18	90.47	100	95.09	94.83	94.64	90.52	70.9	90.05	89.45	89.64	90.11	89.05	88.96	88.27
65.60	66.18	88.68	90.49	90.66	95.09	100	95.09	95.76	90.42	70.07	89.95	89.13	89.48	89.85	89.12	89.06	88.6
65.22	65.84	89.05	90.62	90.78	94.83	95.09	100	95.76	90.9	70.94	90.22	89.25	89.86	90.23	89.3	89.47	88.78
65.41	65.79	88.39	90.33	90.59	94.64	95.76	95.76	100	90.33	70.07	90.09	88.9	89.26	89.79	88.99	88.8	88.34
65.49	66.01	90.01	91.80	92.38	90.52	90.42	90.9	90.33	100	72.03	91.35	91.13	91.73	91.99	90.8	90.52	90.12
56.19	56.28	70.79	72.70	73.14	70.9	70.07	70.94	70.07	72.03	100	97.68	73.72	74.06	71.88	69.88	71.36	70.69
67.00	67.77	89.19	90.45	90.95	90.05	89.95	90.22	90.09	91.35	97.68	100	92.07	92.56	90.9	89.5	89.73	89.46
65.36	66.01	89.26	90.53	90.79	89.45	89.13	89.25	88.9	91.13	73.72	92.07	100	95.19	90.94	90.01	89.89	89.67
65.21	65.82	89.84	91.15	91.35	89.64	89.48	89.86	89.26	91.73	74.06	92.56	95.19	100	91.54	90.53	90.19	89.94
65.44	66.05	90.08	91.61	92.00	90.11	89.85	90.23	89.79	91.99	71.88	90.9	90.94	91.54	100	90.87	90.78	90.55
65.41	65.76	89.30	90.55	90.87	89.05	89.12	89.3	88.99	90.8	69.88	89.5	90.01	90.53	90.87	100	93.9	93.47
65.40	65.91	89.09	90.87	90.88	88.96	89.06	89.47	88.8	90.52	71.36	89.73	89.89	90.19	90.78	93.9	100	93.73
65.65	65.88	88.82	90.15	90.45	88.27	88.6	88.78	88.34	90.12	70.69	89.46	89.67	89.94	90.55	93.47	93.73	100

Supplementary Figures.

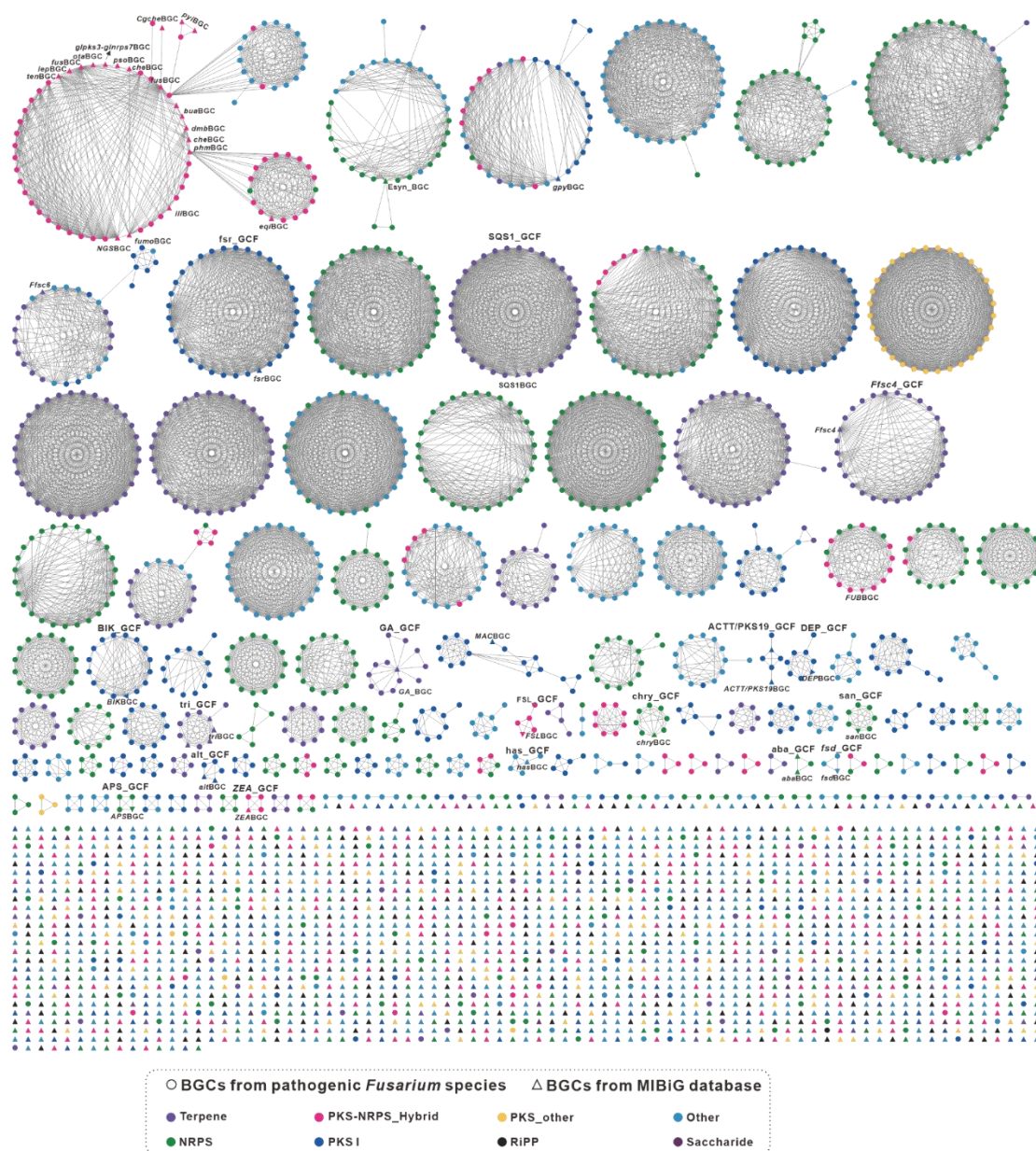


Figure S1: GCF network of 1733 predicted biosynthetic gene cluster (BGC) from 35 pathogenic *Fusarium* species caculated by BiG-SCAPE pipeline and visualised with Cytoscape.

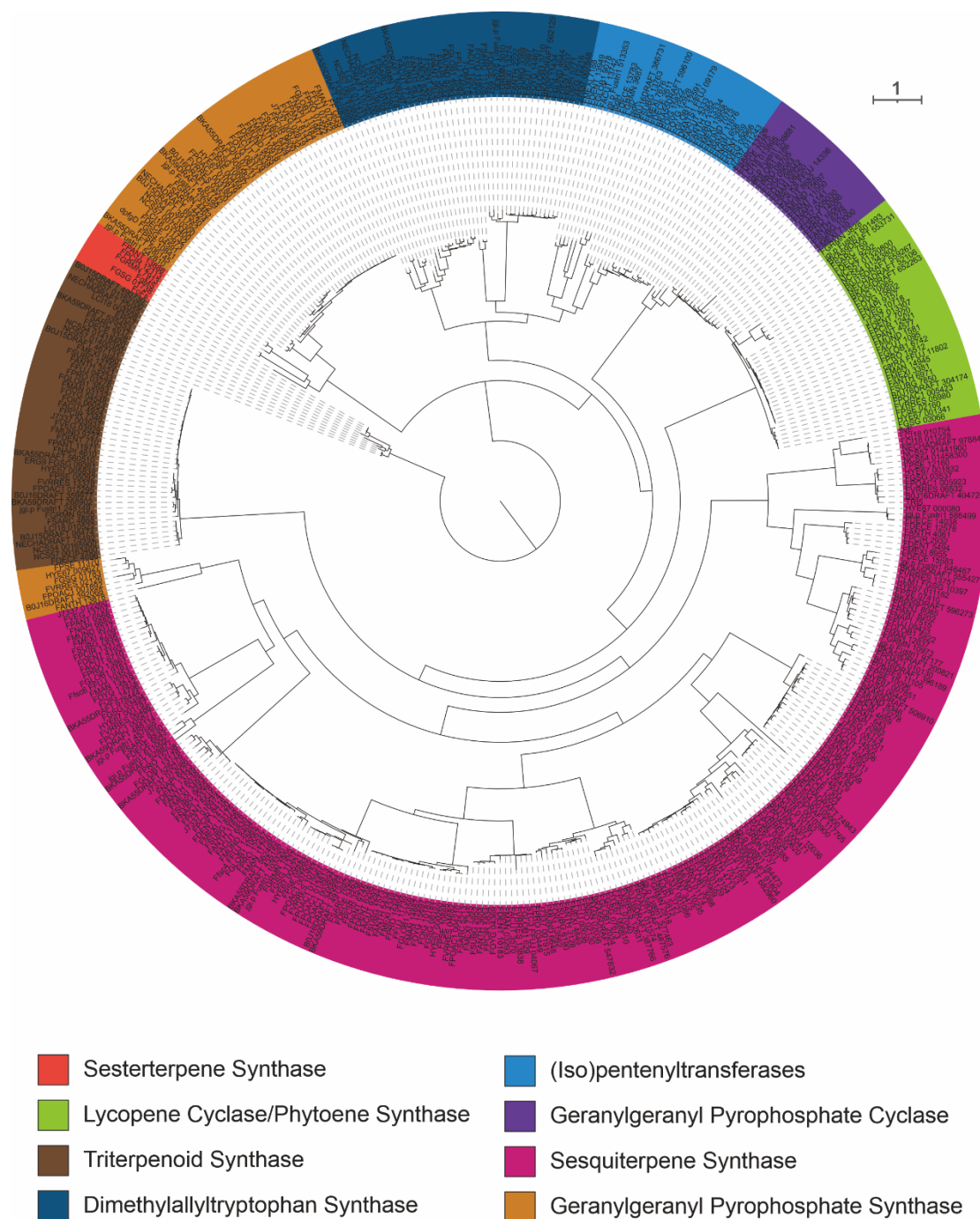


Figure S2: Cluster analysis of terpenoid synthase and their homologues based on phylogenetic tree.

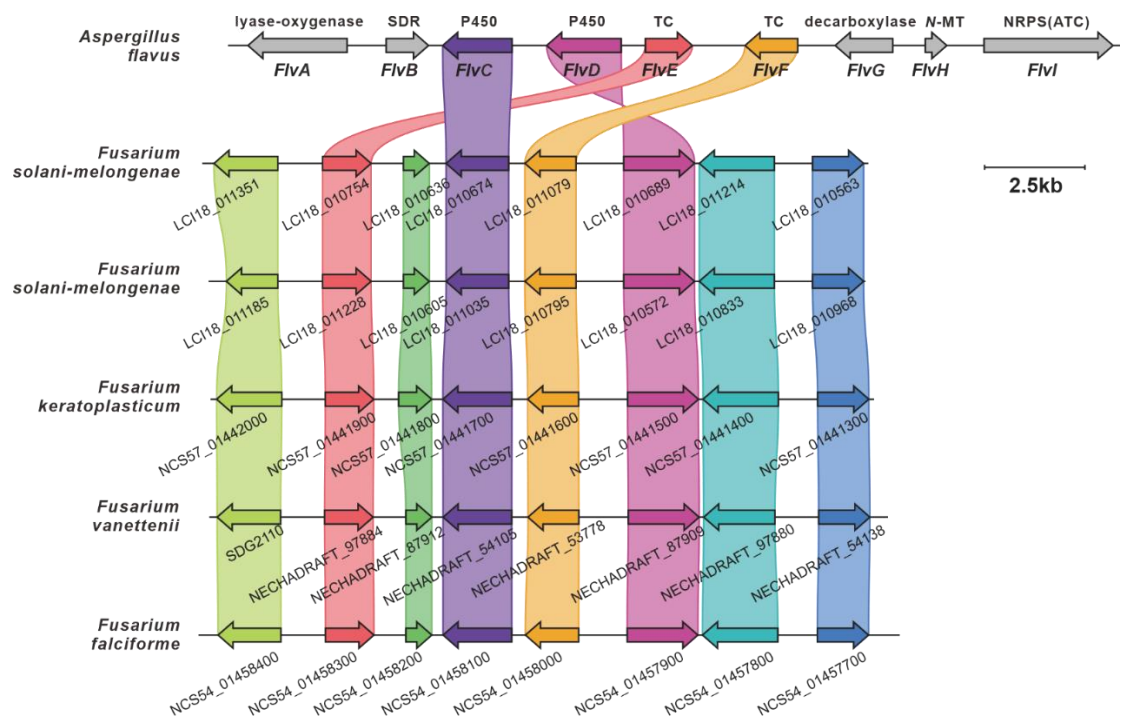


Figure S3: Comparison of *FlvBGCs* from different species.

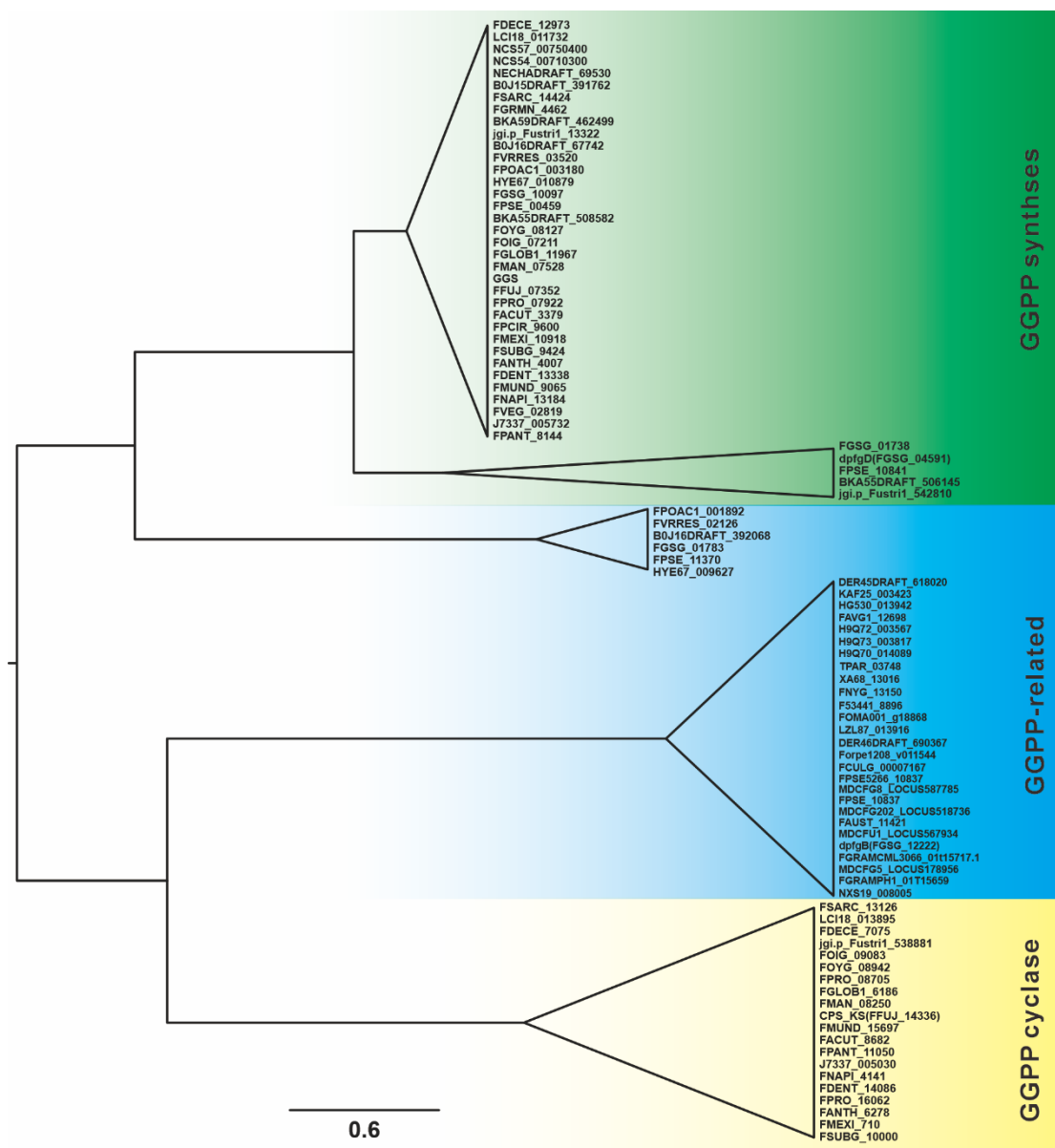


Figure S4: Phylogenetic tree-based cluster analysis of GGPP-related enzymes.

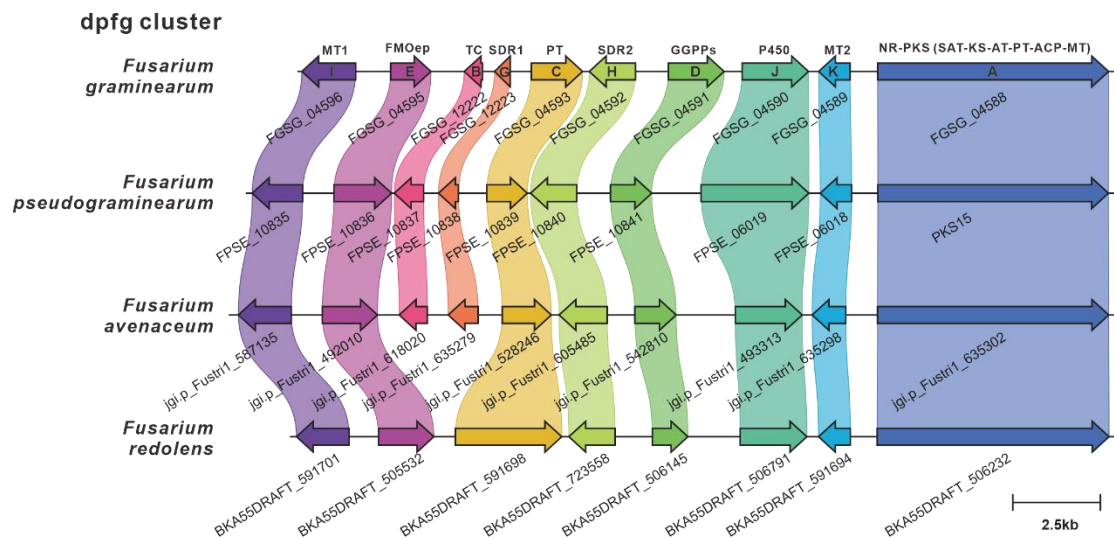


Figure S5: Comparison of *dpfg*BGCs from different pathogenic *Fusarium* species.

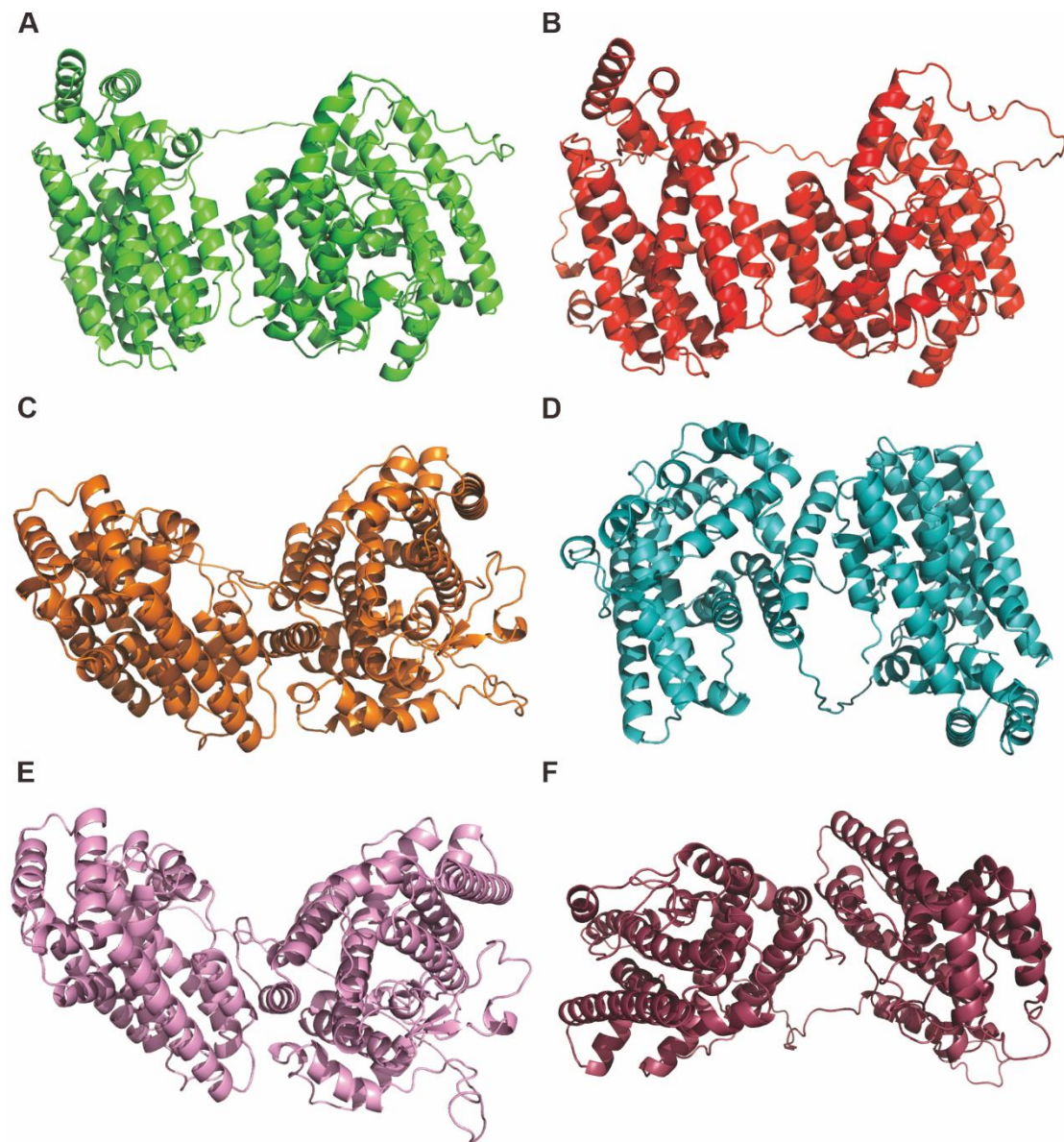


Figure S6: The predicted three-dimensional structure of protein of FgMS (A), FGSG_01738 (B), FGRMN_7913 (C), FPCIR_12113 (D), FPANT_13888 (E) and FoFs(F) **predicted by AlphaFold**.

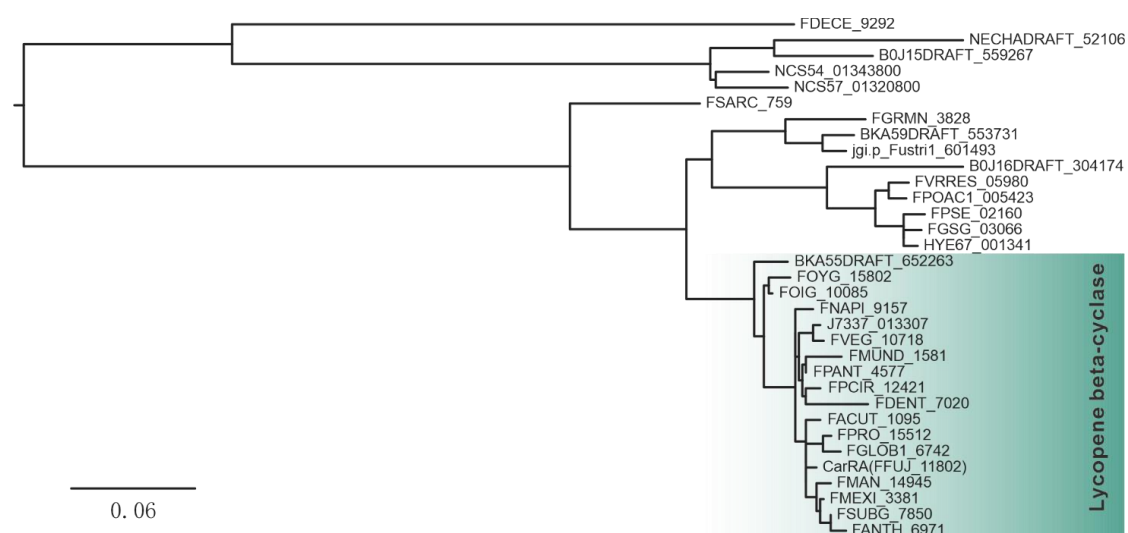


Figure S7: Phylogenetic tree-based cluster analysis of CarRA and its homologues.

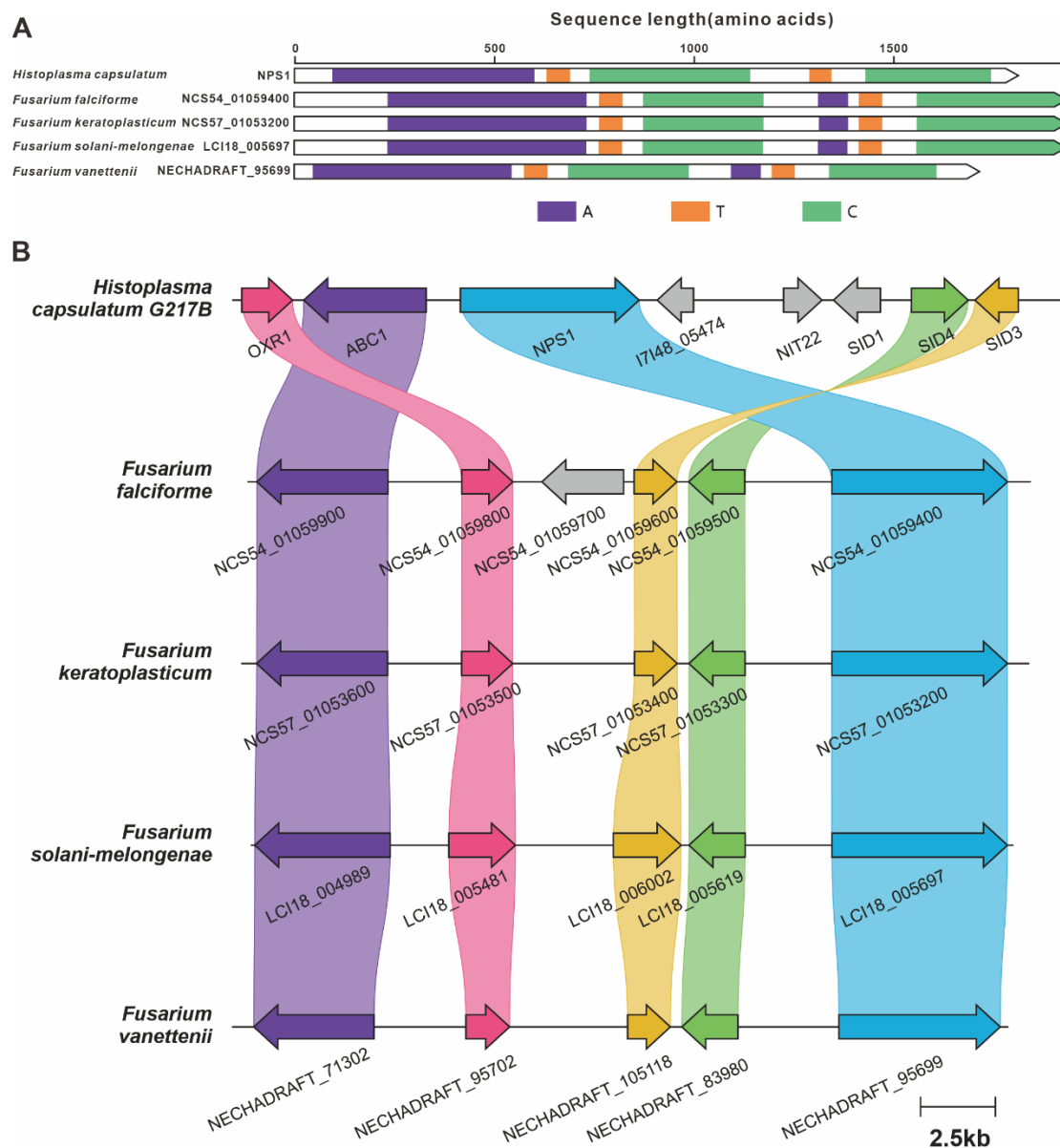


Figure S8: Domain comparison of NPS1 and its homologues(A), comparison of the BGCs containing *nps1* from different species(B).

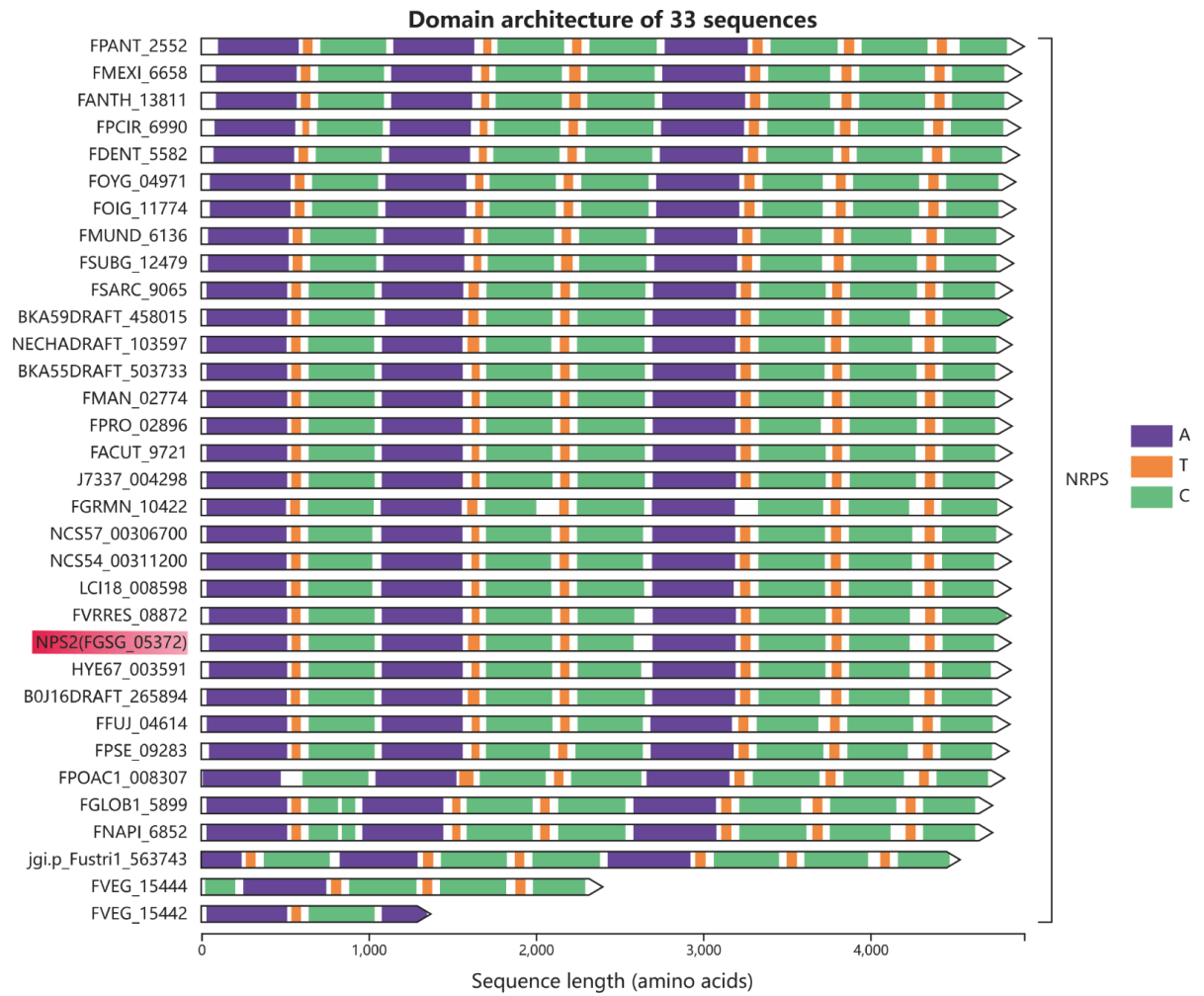


Figure S9: Domain comparison of NPS2 and its homologues.

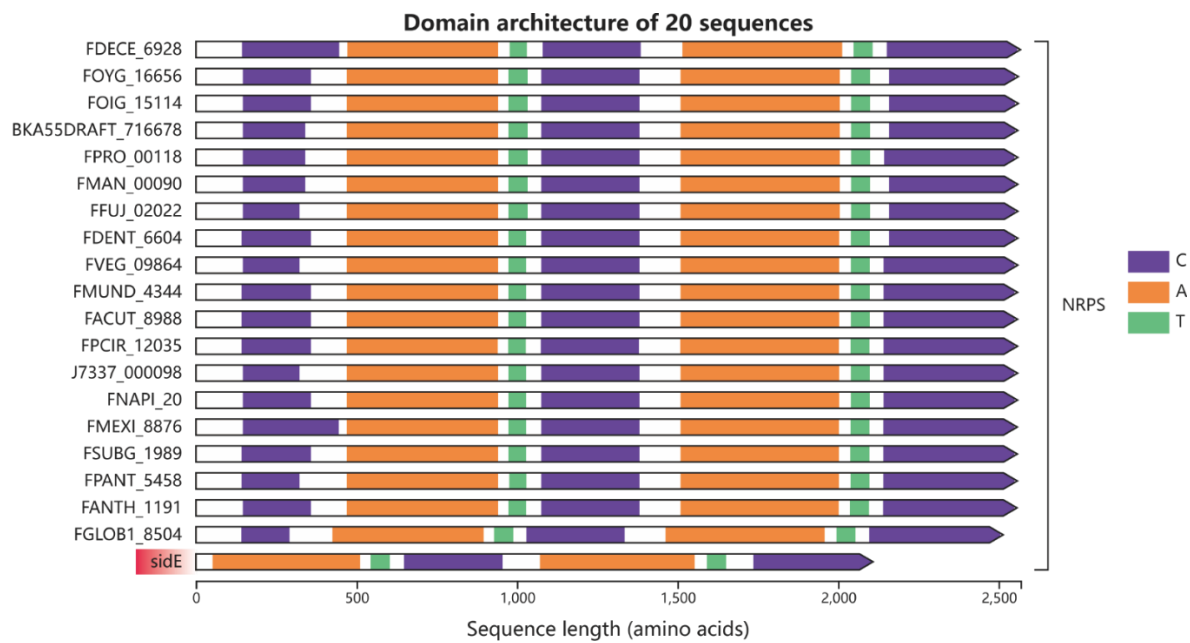


Figure S11: Domain comparison of SidE and its homologues.

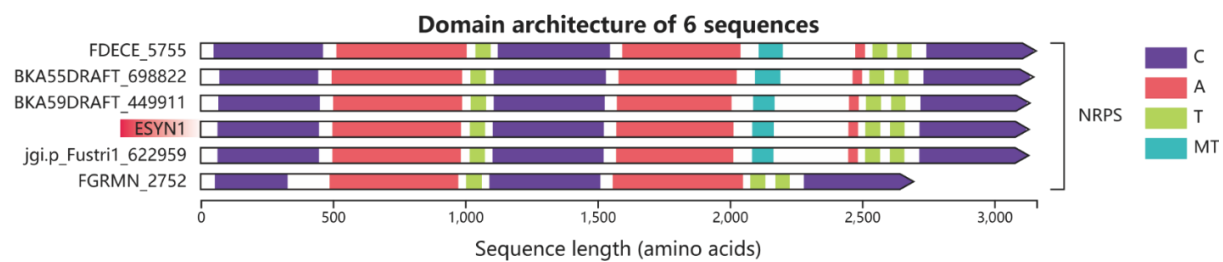


Figure S13: Domain comparison of ESYN1 and its homologues.

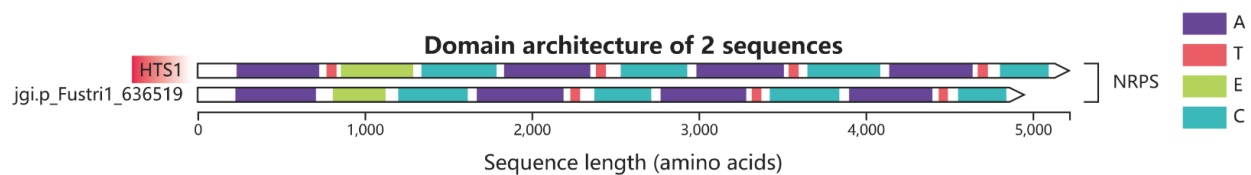


Figure S15: Domain comparison of HTS1 and its homologues.

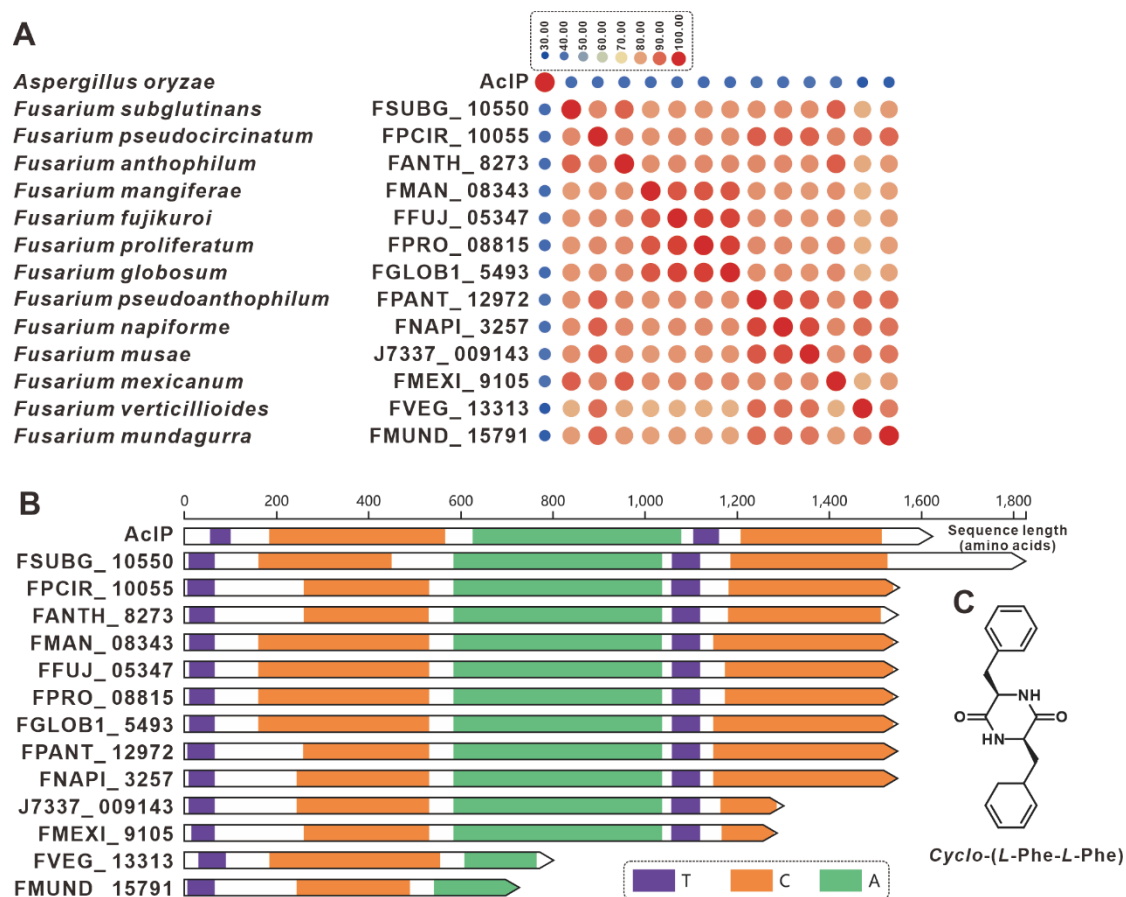


Figure S17: Comparative analysis of AclP and its homologues. Comparison of the amino acid sequence identity of AclP and its homologues(A), comparison of the structural domains of AclP and its homologues(B), structure of cyclo-(L-Phe-L-Phe)(C).

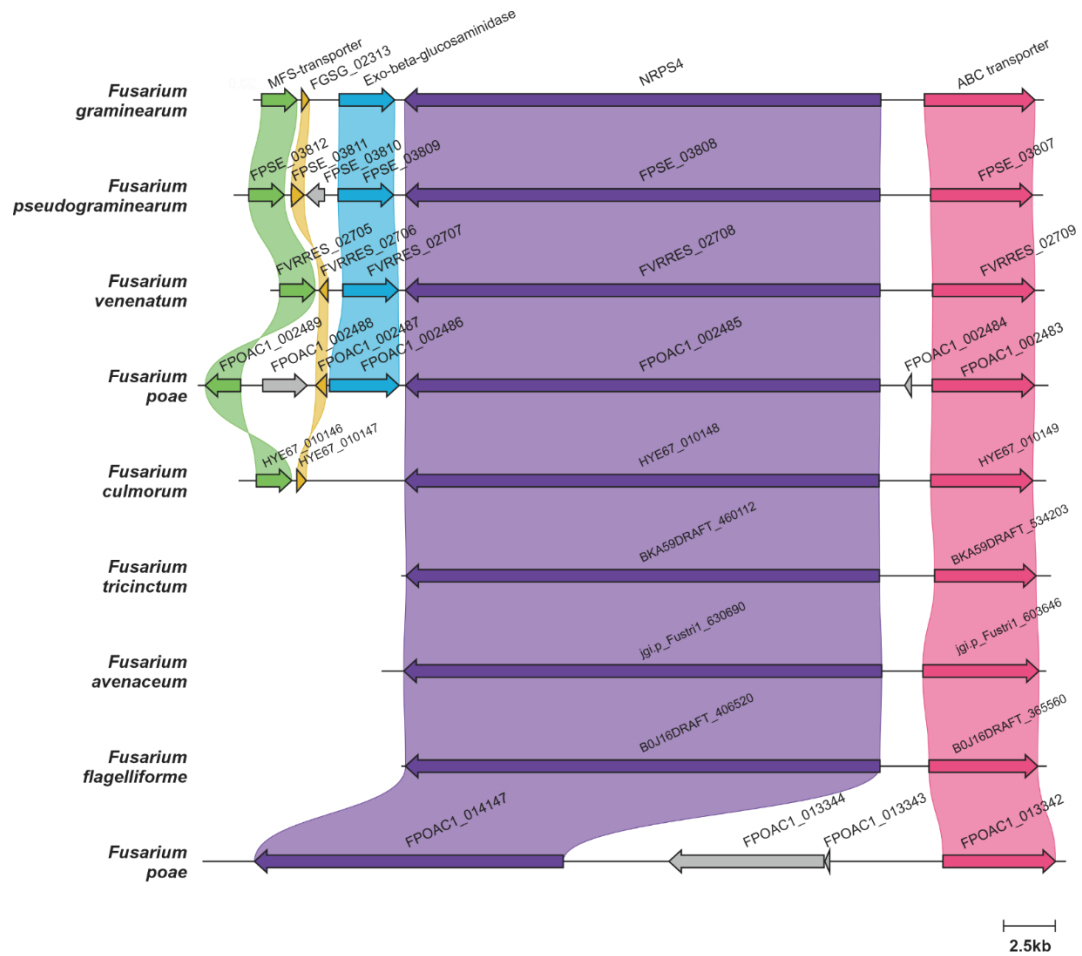


Figure S19: Comparison of the BGCs containing *nrps4* from different *Fusarium* species.

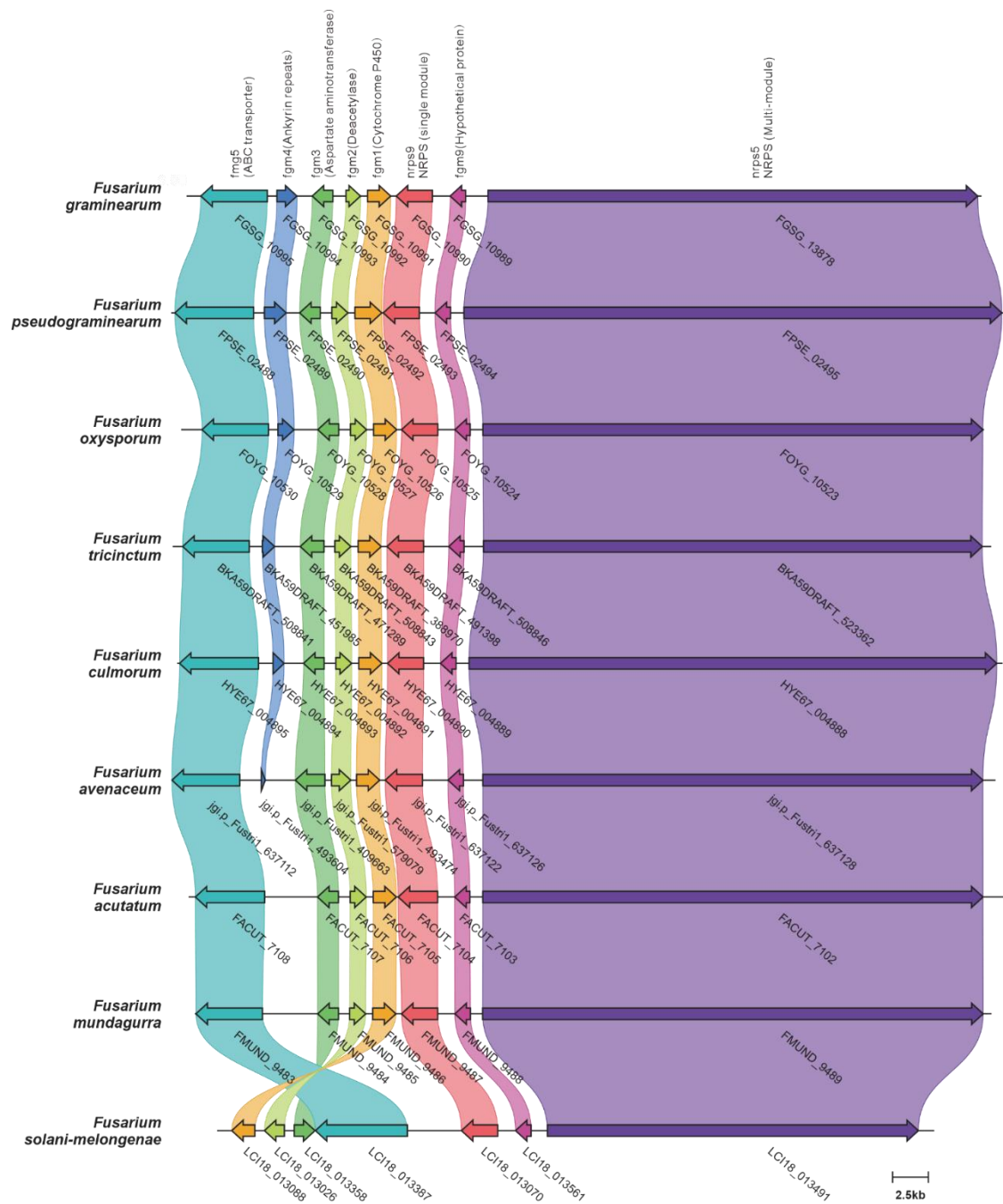


Figure S20: Comparison of the BGCs containing *nrps5* from different *Fusarium* species.

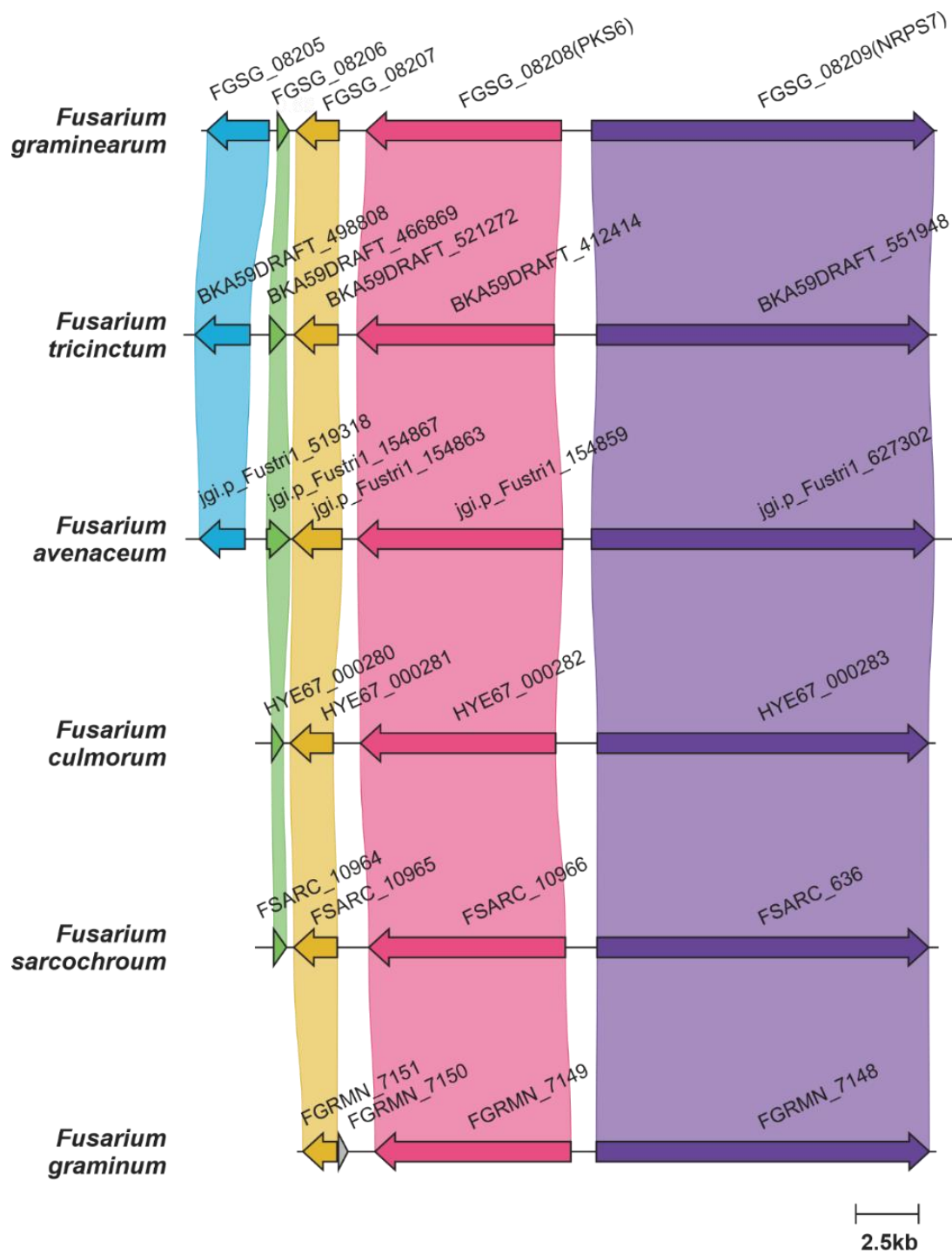


Figure S21: Comparison of the BGCs containing *nrps7* and PKS6 from different *Fusarium* species.

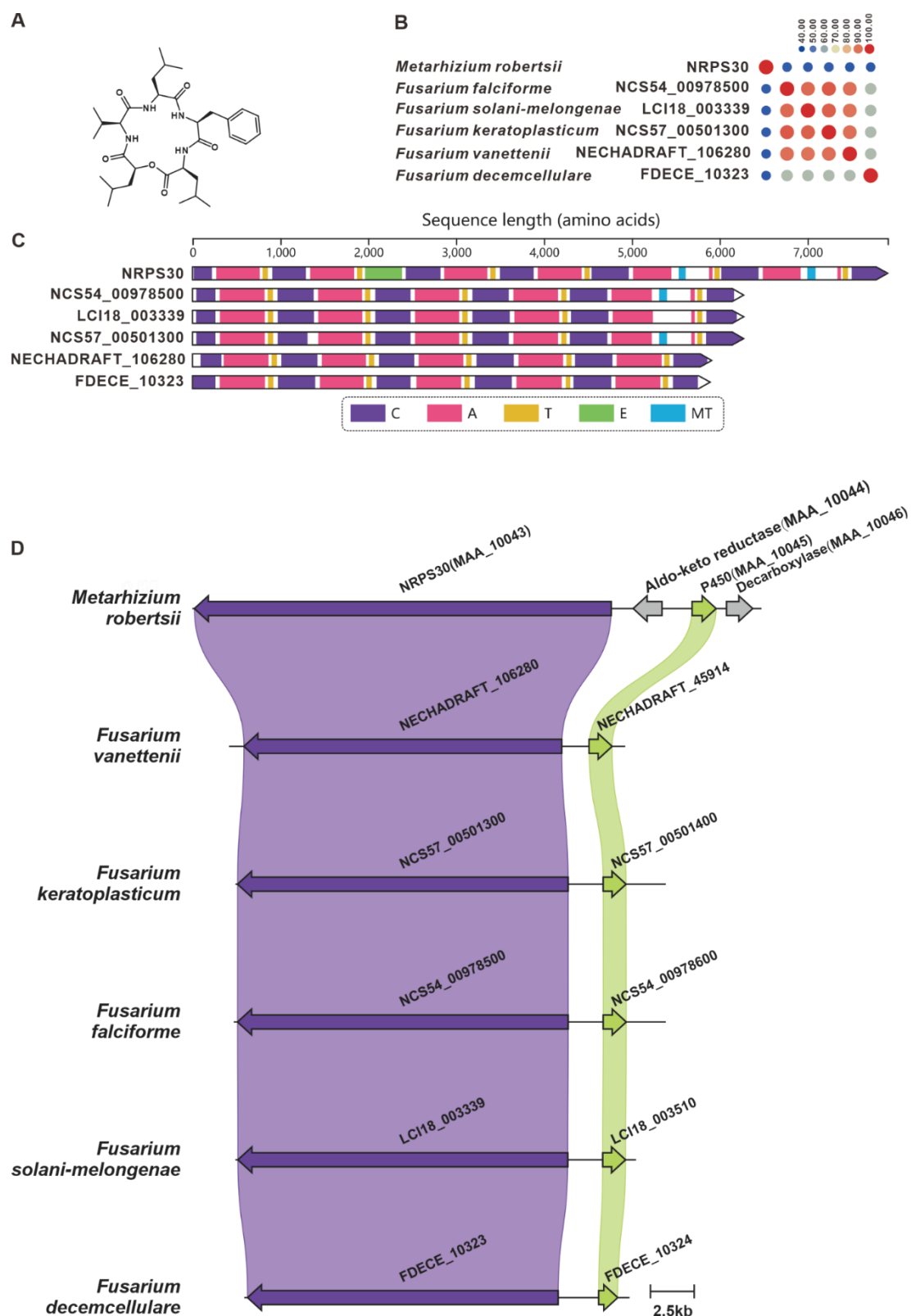
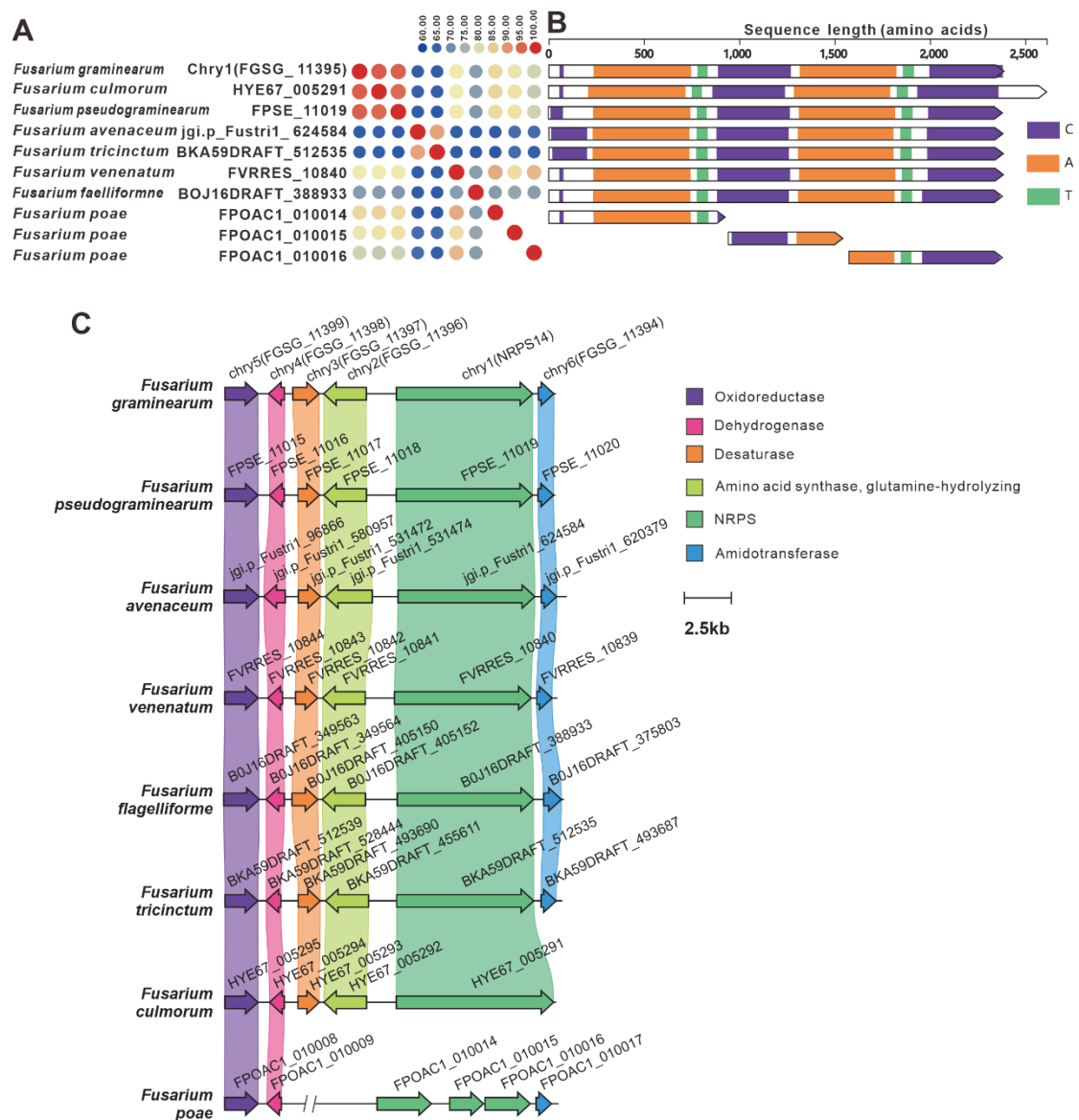


Figure S22: Structures of sansalvamide (A), comparison of the amino acid sequence identity of NRPS30 and its homologues (B), domain comparison of NRPS30 and its homologues (C), comparison of the BGC for aurofusarin and its similar BGCs (D).



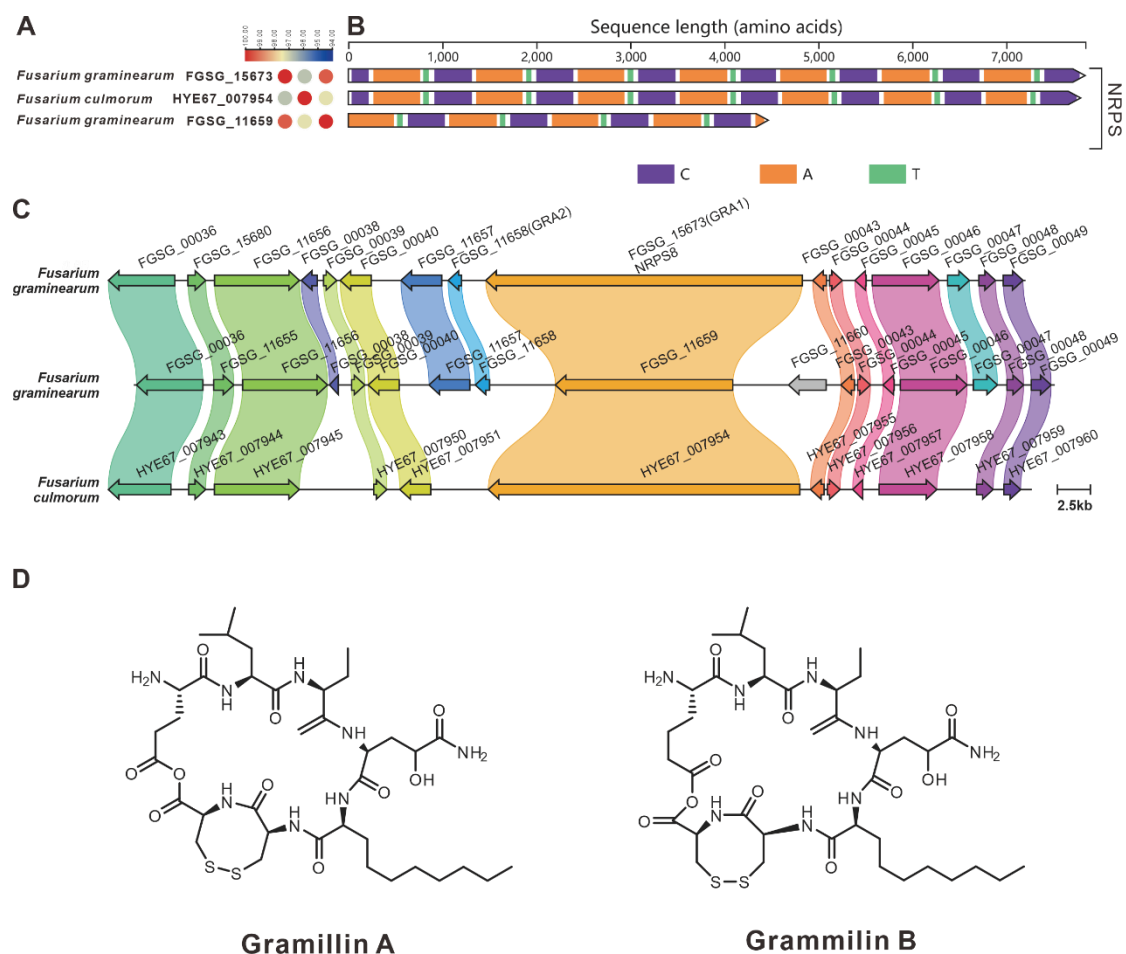


Figure S24: Comparison of the amino acid sequence identity of GRA1 and its homologues (A), domain comparison of GRA1 and its homologues (B), comparison of the BGC for Gramillin A, Gramillin B and its similar BGCs (C), structure of Gramillin A and Gramillin B (D).

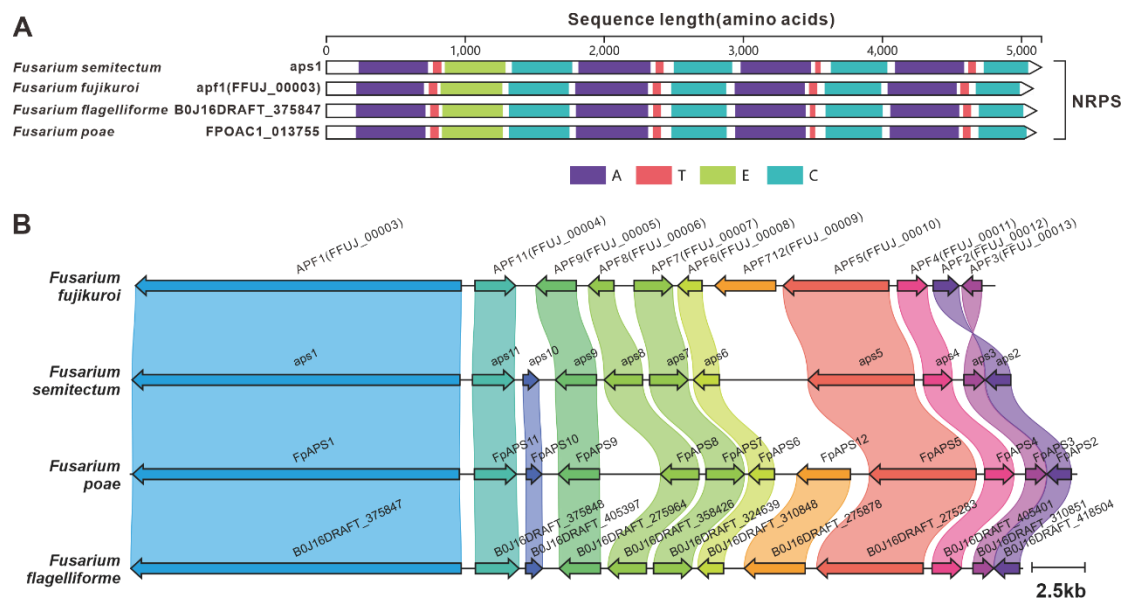


Figure S25: Domain comparison of apf1 and its homologues (A), comparison of apfBGCs from different *Fusarium* species (B).

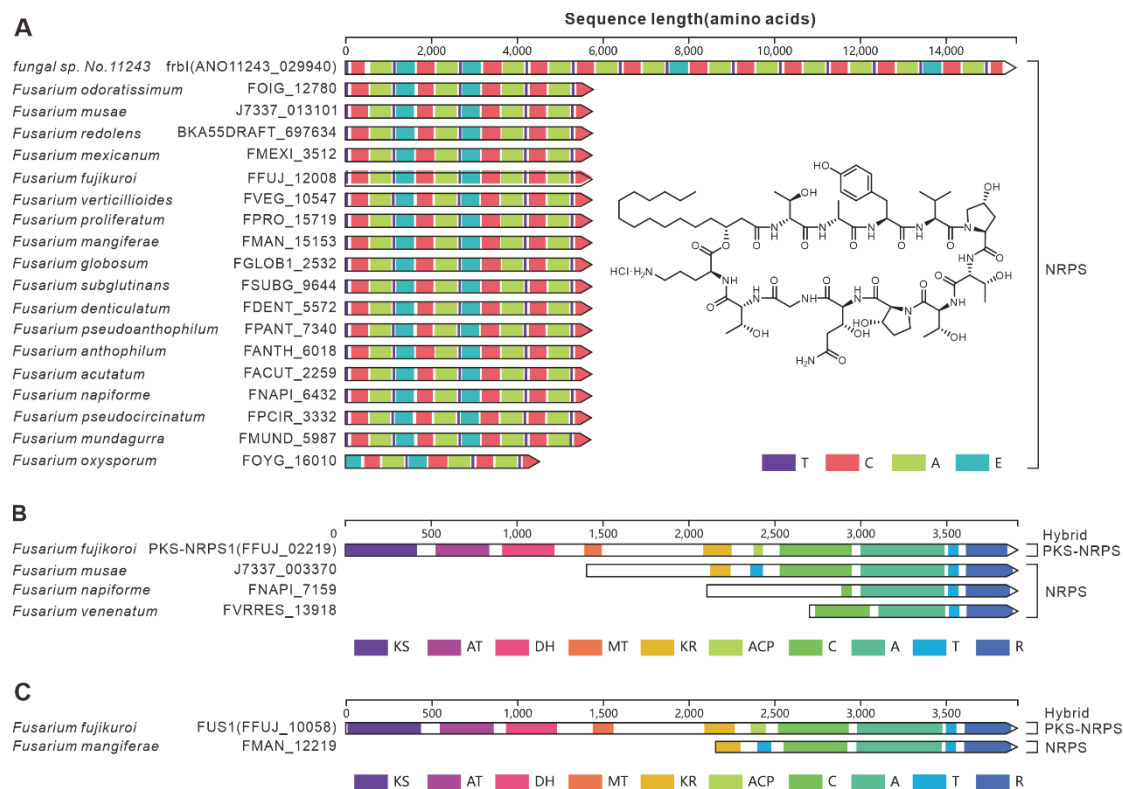


Figure S26: Domain comparison of FrbI and its homologues (A), domain comparison of PKS-NRPS1 and its homologues (B), domain comparison of FUS1 and its homologues (C).

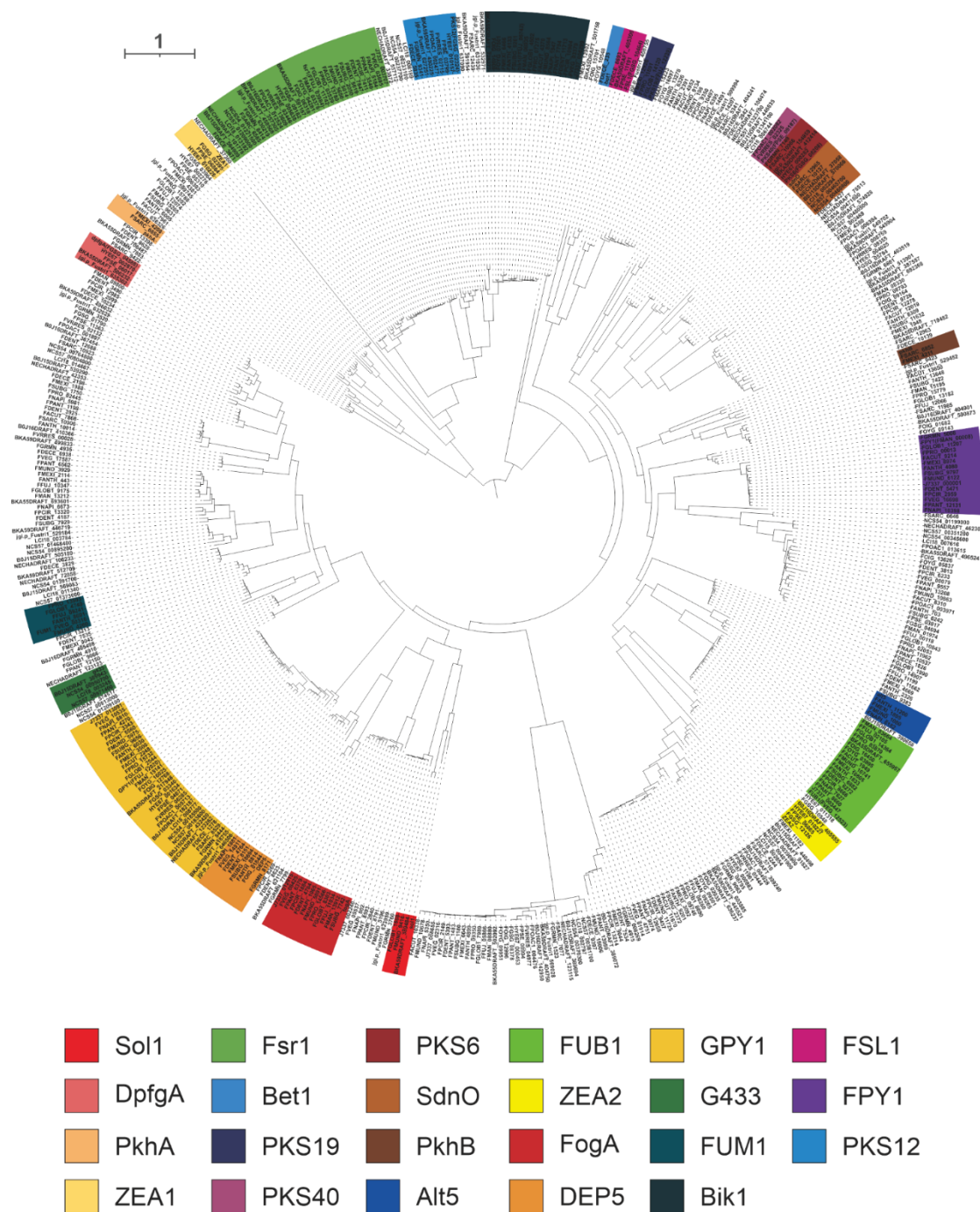


Figure S27: Phylogenetic tree-based cluster analysis of PKS-related enzymes.

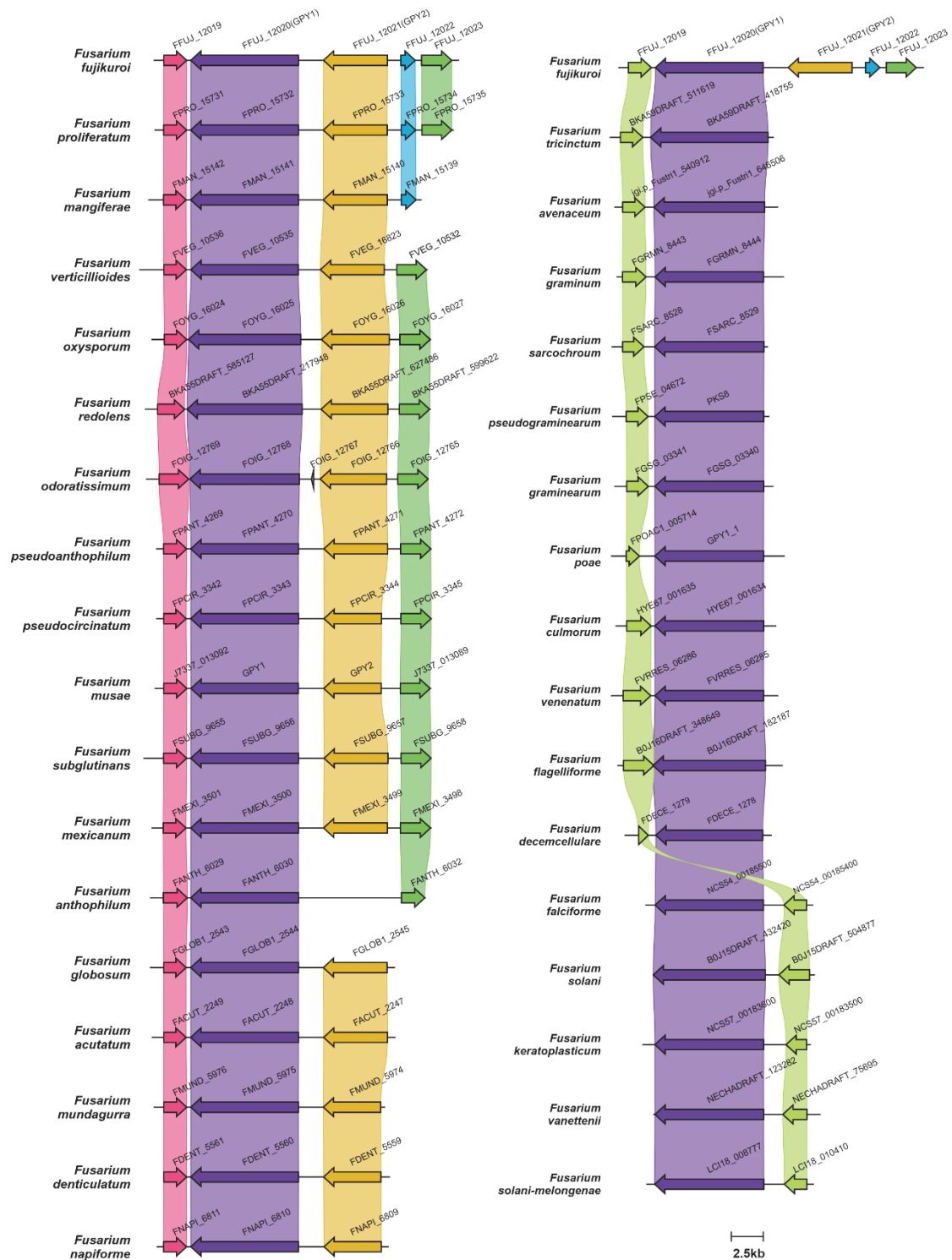


Figure S28: Comparison of *gpy*BGCs from different *Fusarium* species.

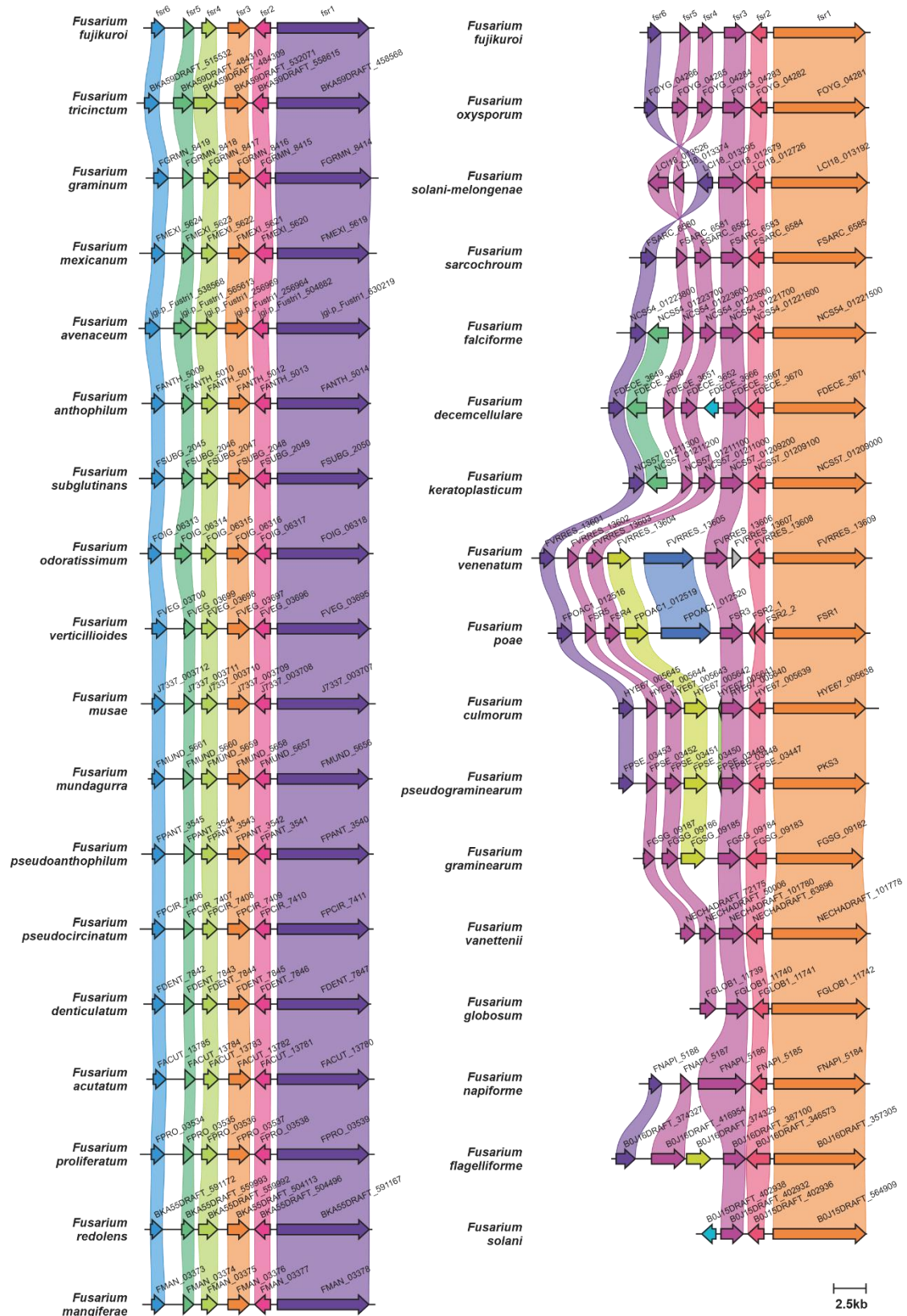


Figure S29: Comparison of *fsrBGCs* from different *Fusarium* species.

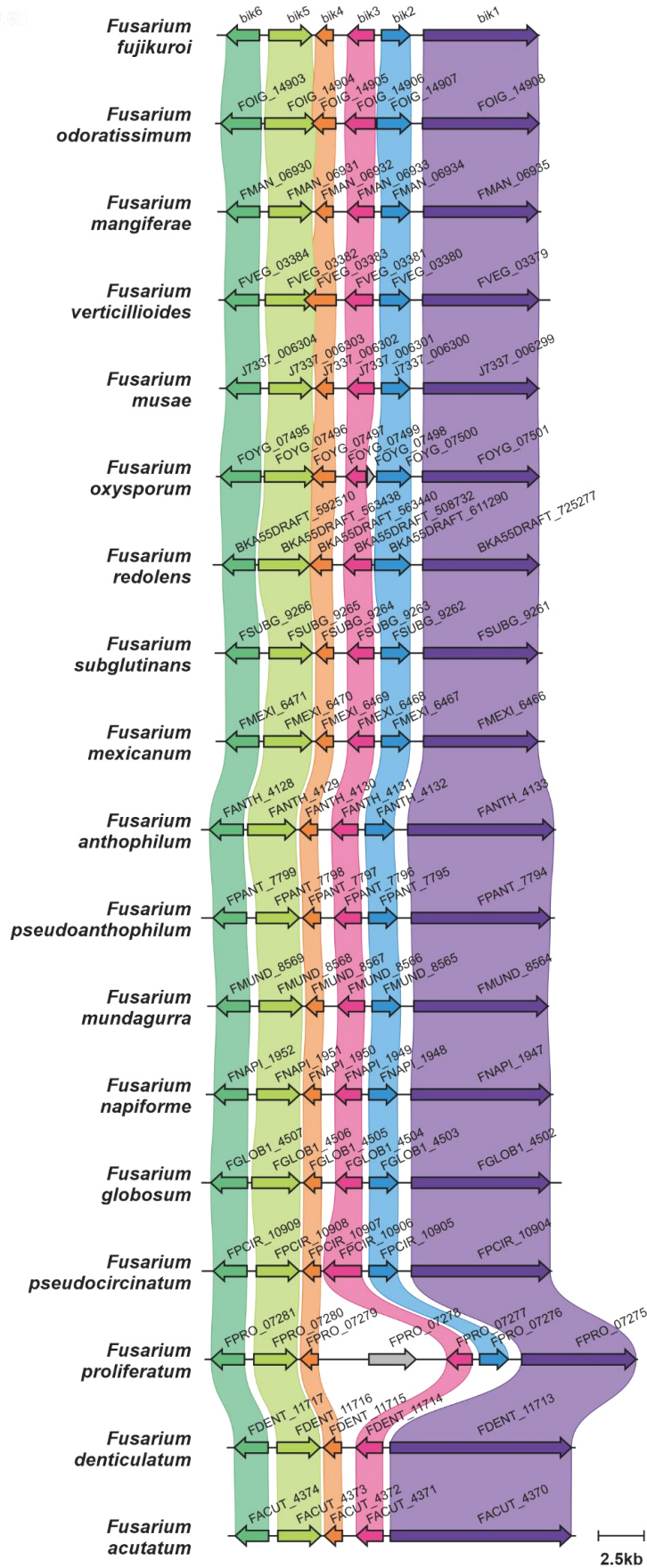


Figure S31: Comparison of *bik*BGCs from different *Fusarium* species.

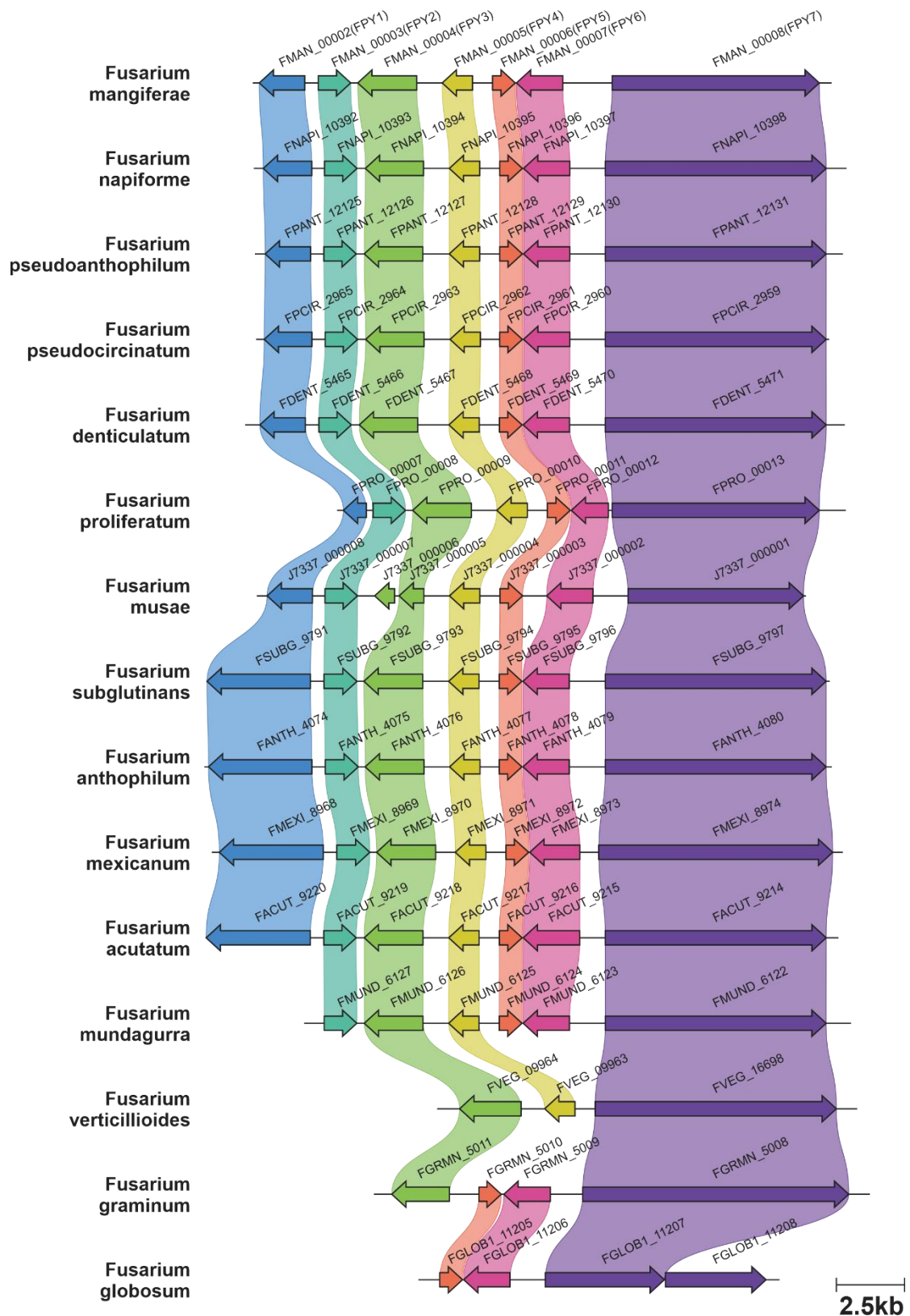


Figure S32: Comparison of FPYBGCs from different *Fusarium* species.

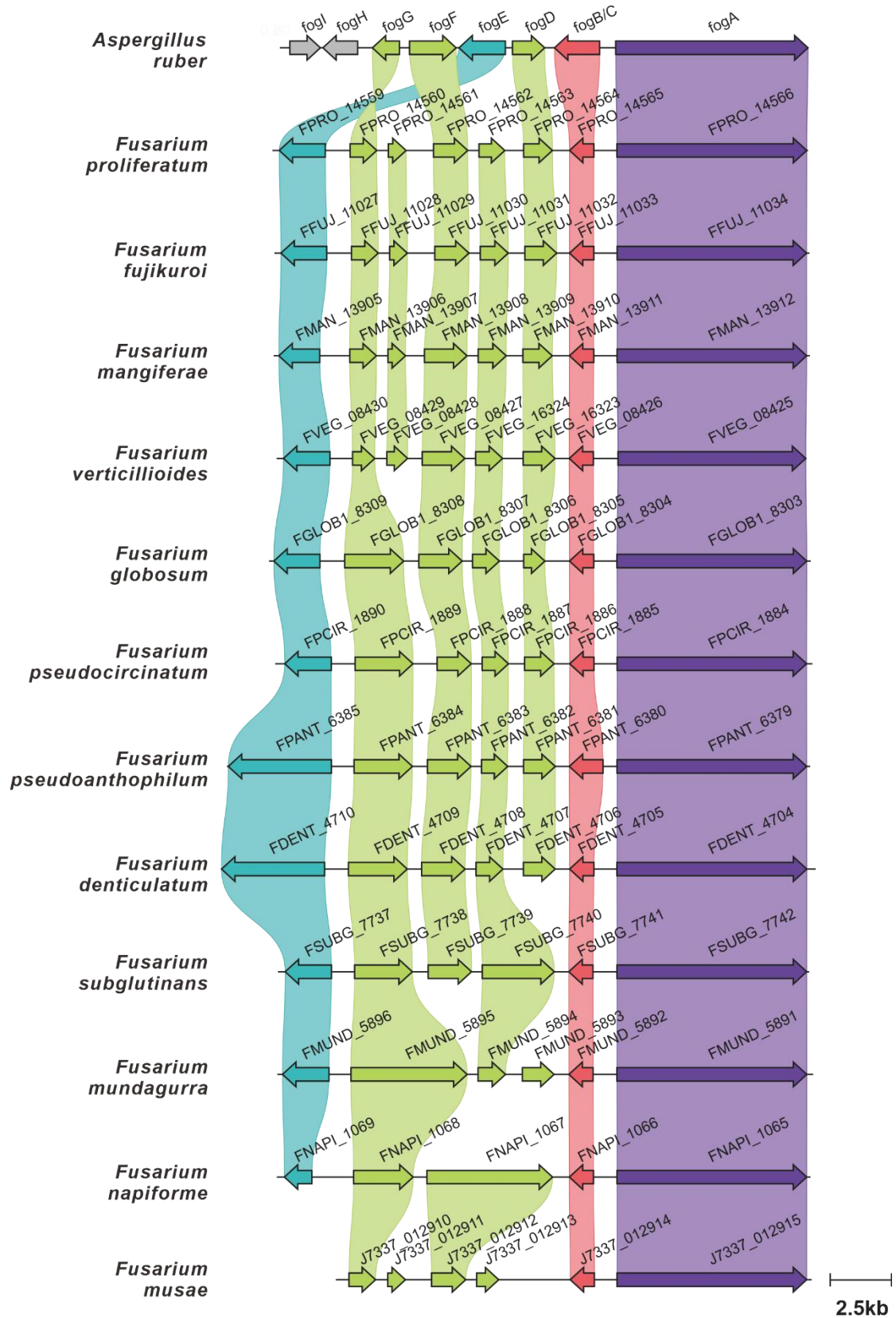


Figure S33: Comparison of *fog*BGCs from different *Fusarium* species.

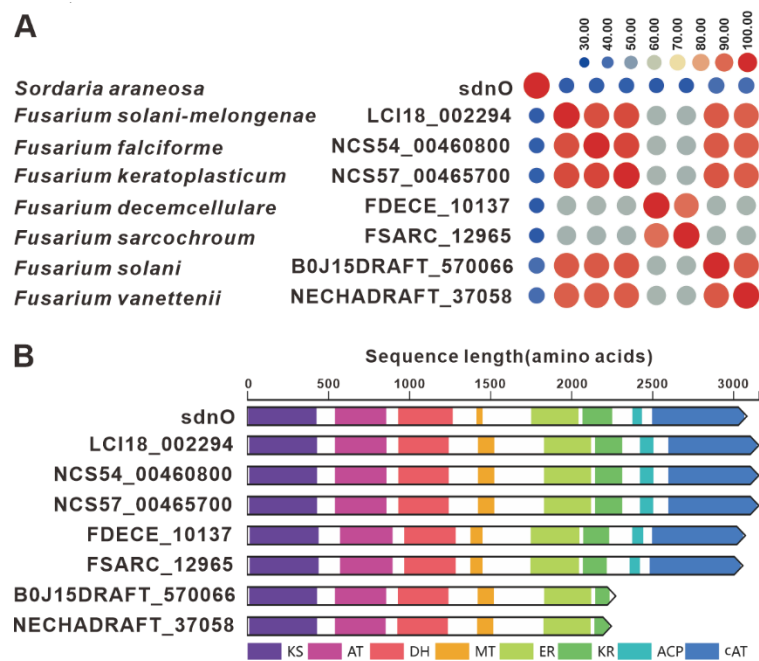


Figure S34: Comparison of the amino acid sequence identity of SdnO and its homologues (A), domain comparison of SdnO and its homologues (B).

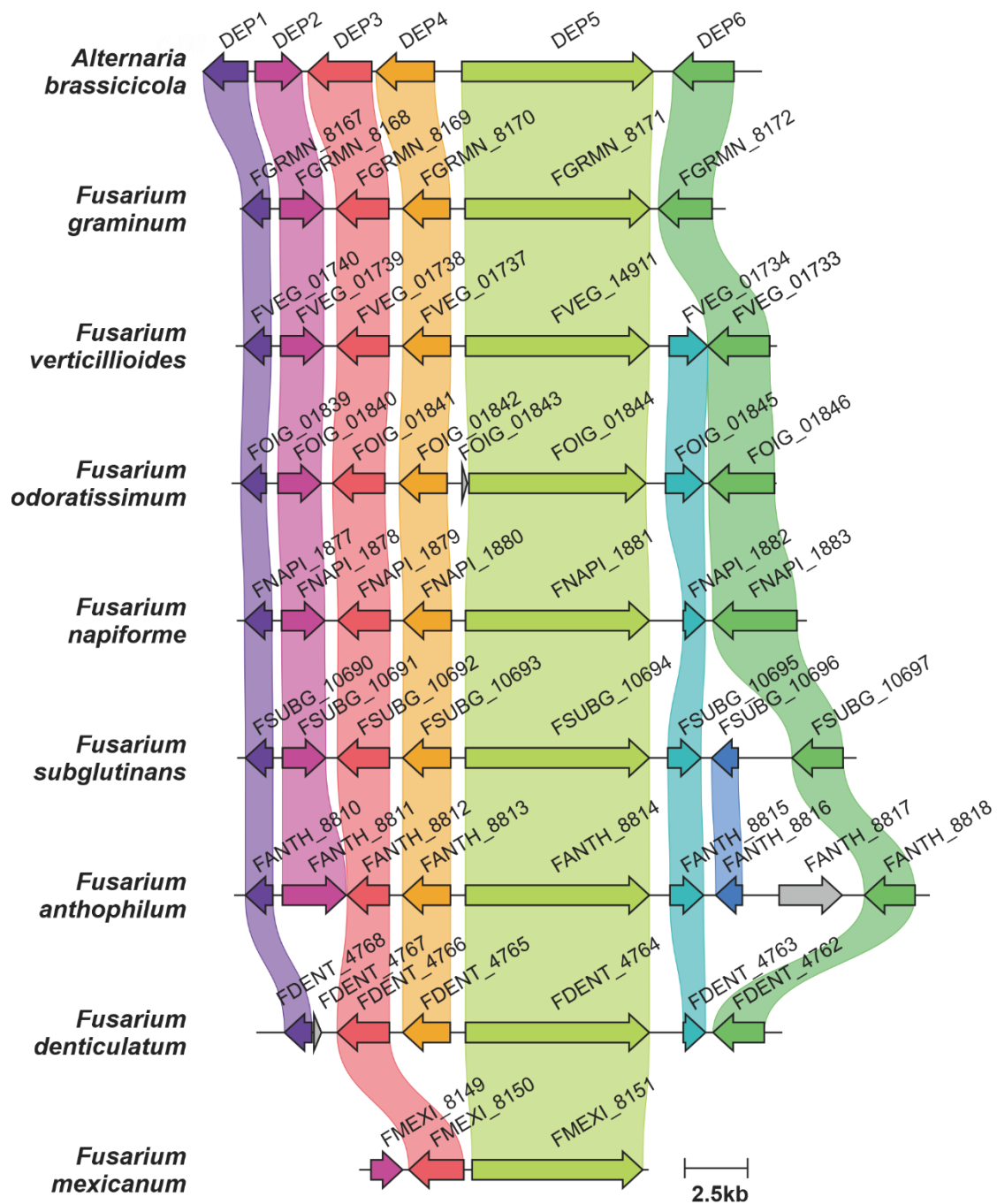


Figure S35: Comparison of *DEPBGCs* from different *Fusarium* species.

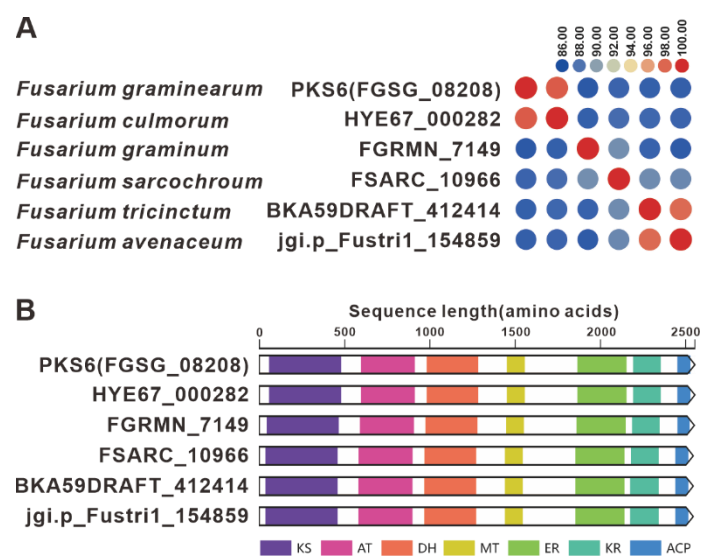


Figure S36: Comparison of the amino acid sequence identity of PKS6 and its homologues (A), domain comparison of PKS6 and its homologues (B).

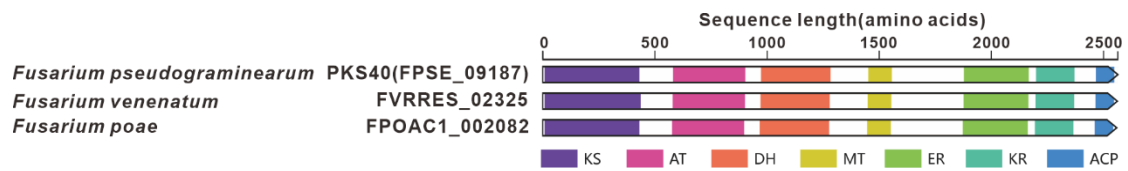


Figure S37: Domain comparison of PKS40 and its homologues.

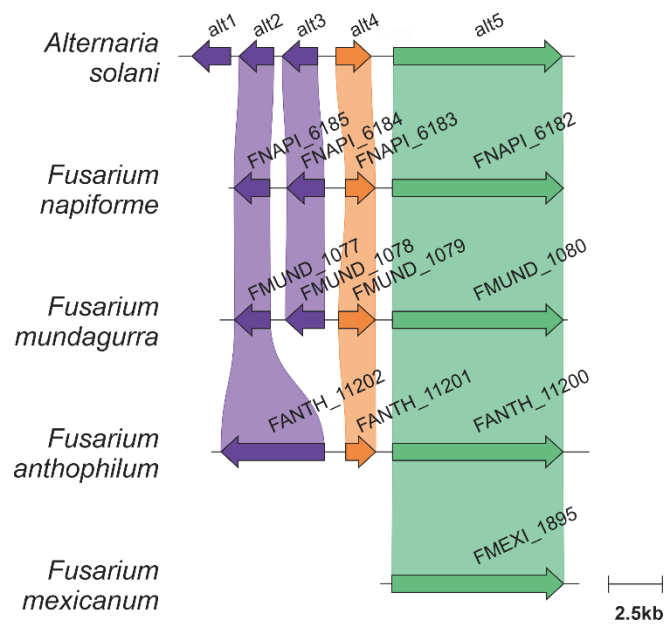


Figure S38: Comparison of *altBGCs* from different *Fusarium* species.

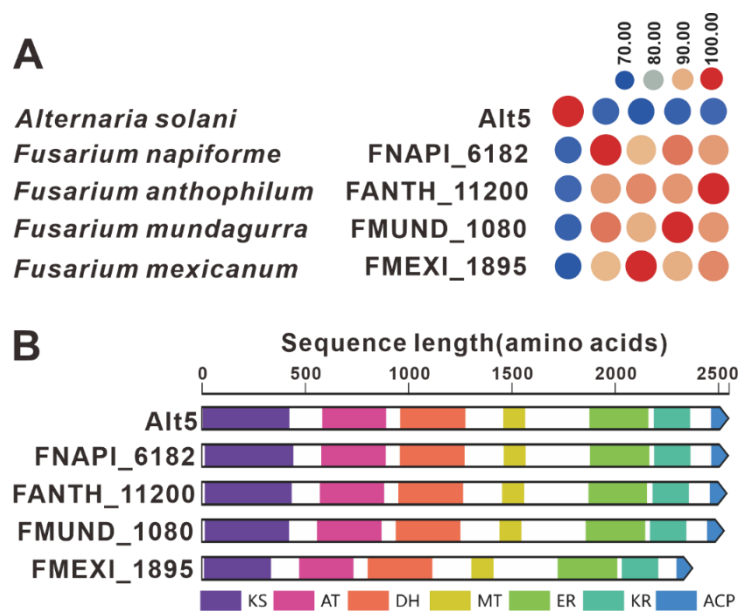


Figure S39: Comparison of the amino acid sequence identity of Alt5 and its homologues (A), domain comparison of Alt5 and its homologues (B).

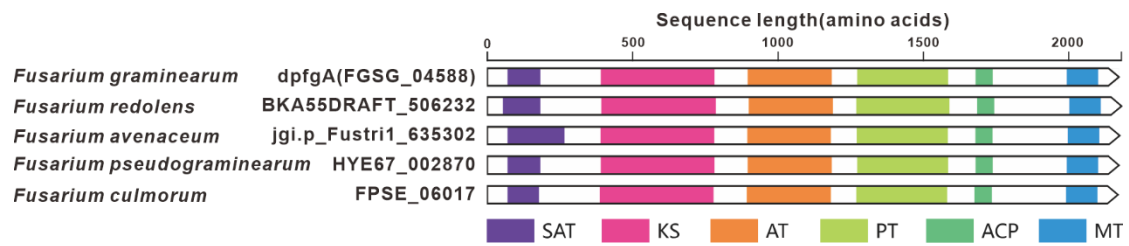


Figure S40: Domain comparison of DpfgA and its homologues.

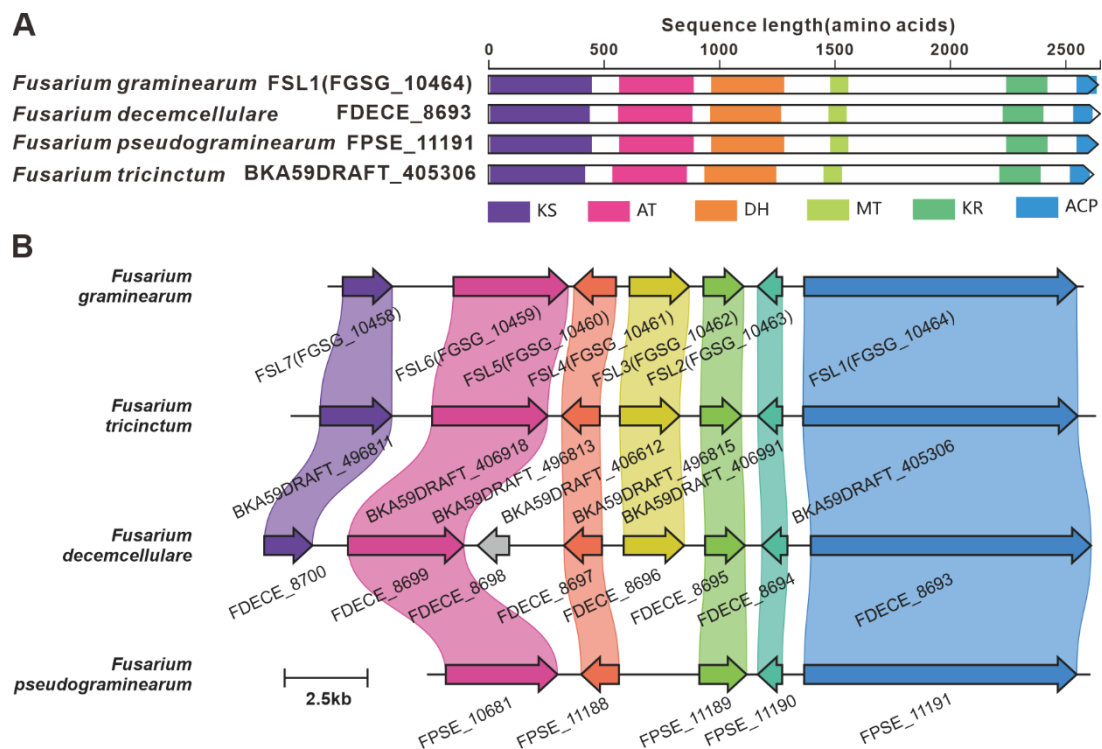


Figure S41: Domain comparison of FSL1 and its homologues (A), comparison of FSLBGCs from different *Fusarium* species (B).

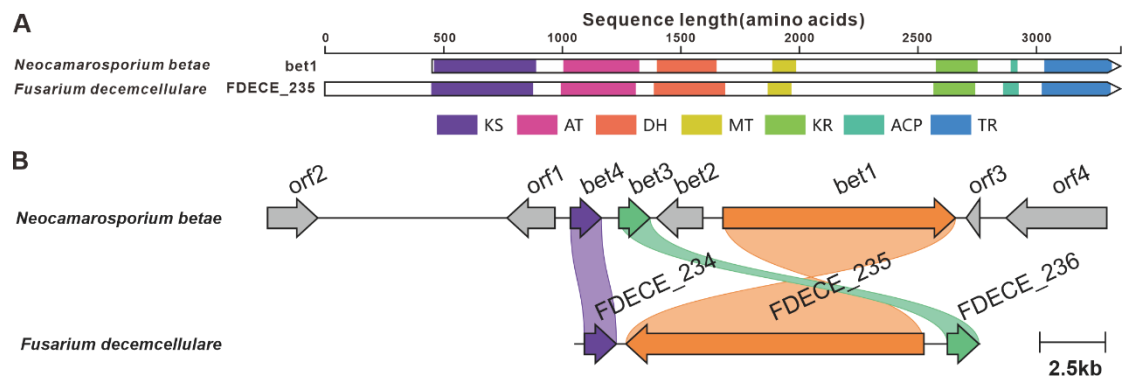


Figure S42: Domain comparison of Bet1 and its homologues (A), comparison of *bet*BGCs from different species (B).

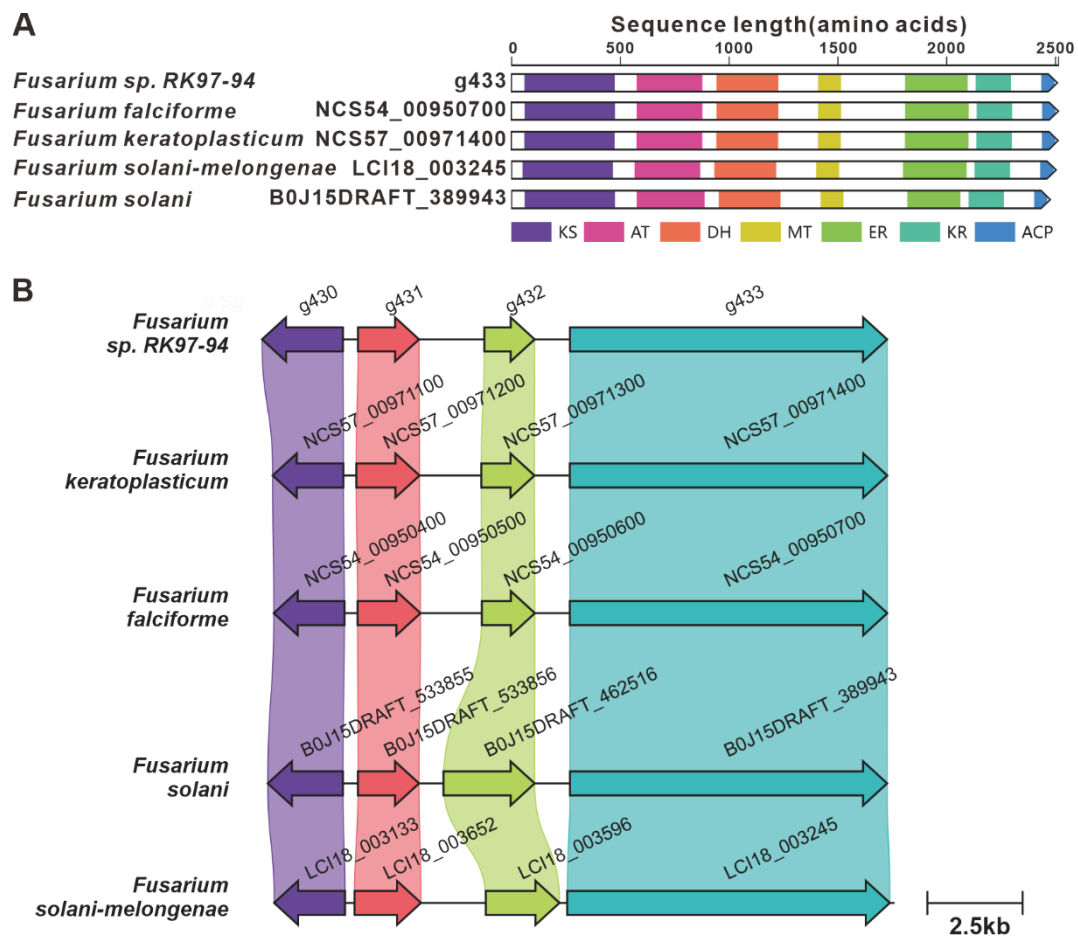


Figure S43: Domain comparison of G433 and its homologues (A), comparison of the BGC for G433 and its similar BGCs (B).

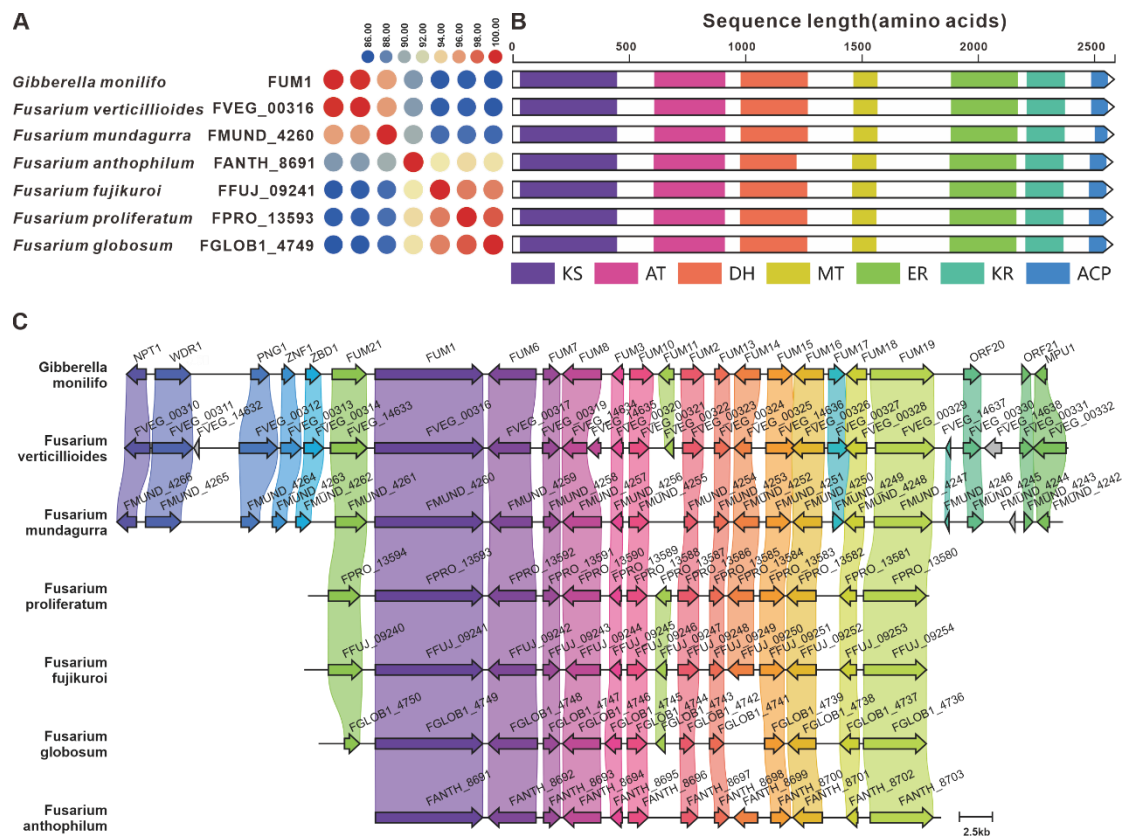


Figure S44: Comparison of the amino acid sequence identity of Alt5 and its homologues (A), domain comparison of FUM1 and its homologues (B), comparison of *FUMBGCs* from different *Fusarium* species (C).

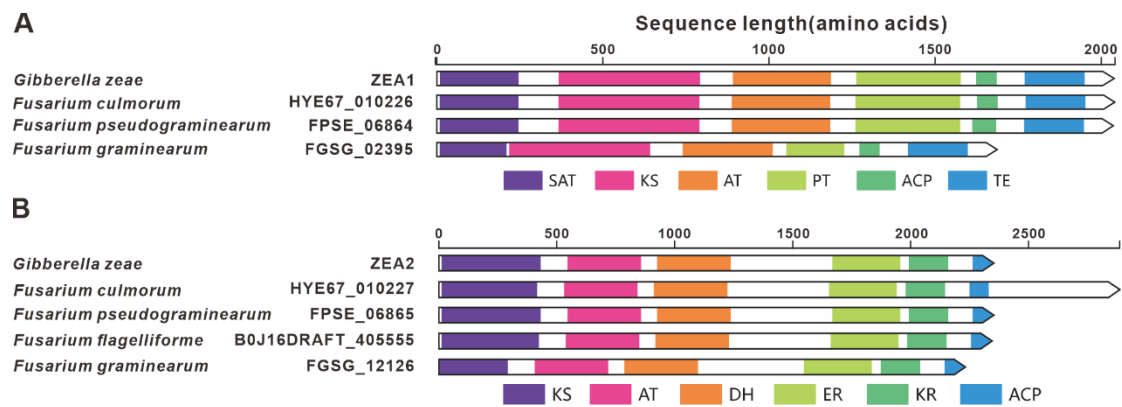


Figure S45: Domain comparison of ZEA1 and its homologues (A), domain comparison of ZEA2 and its homologues (B).

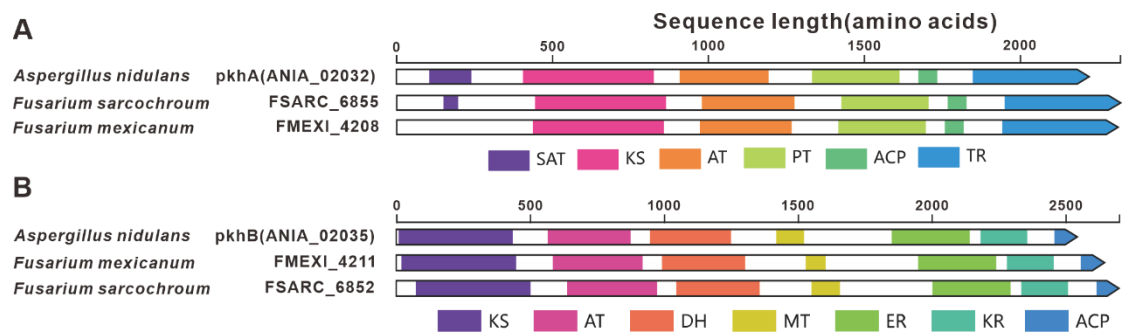


Figure S46: Domain comparison of PkhA and its homologues (A), domain comparison of PkhB and its homologues (B).

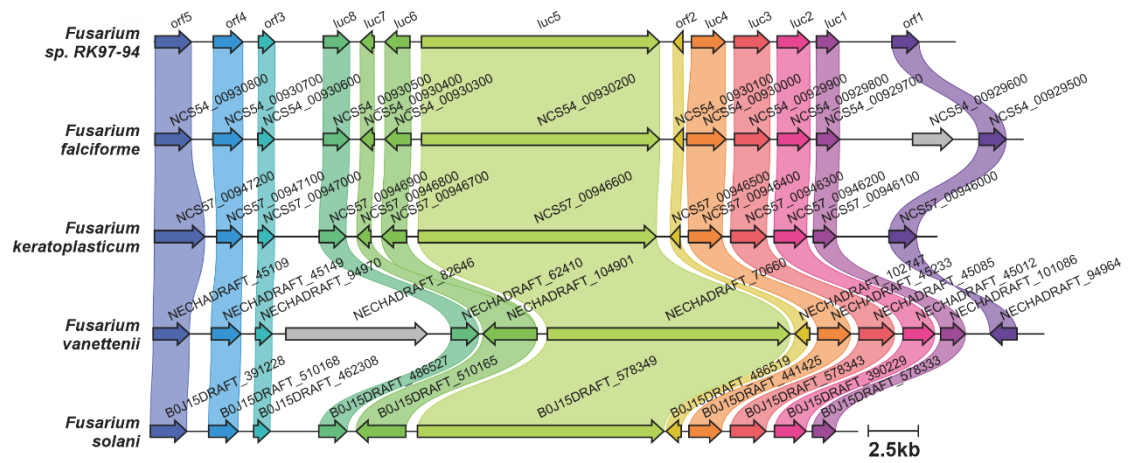


Figure S47: Comparison of *luc*BGCs from different *Fusarium* species.

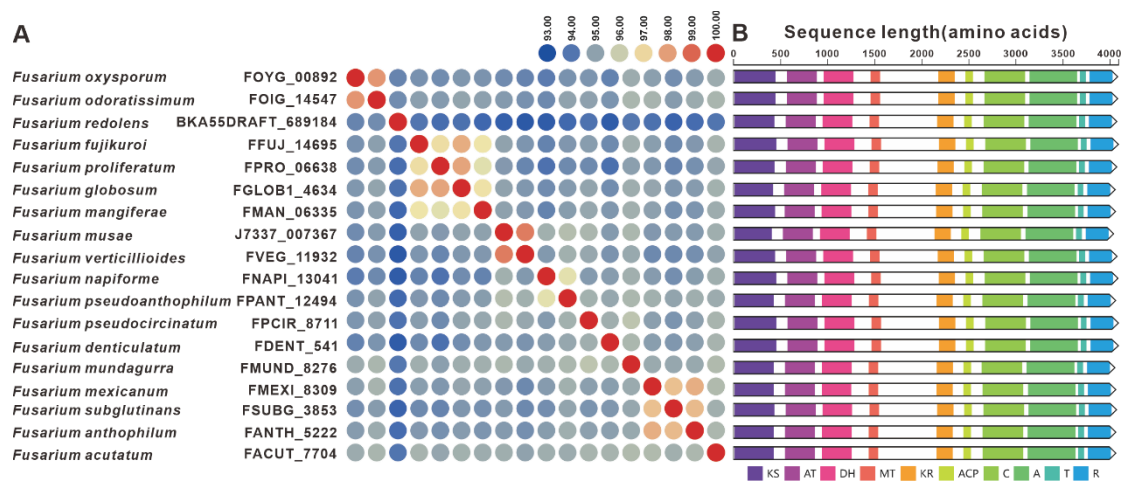


Figure S48: Amino acid **sequence** identity comparison (A) and domain comparison (B) of newly discovered PKS-NRPSs in 35 pathogenic *Fusarium* species.

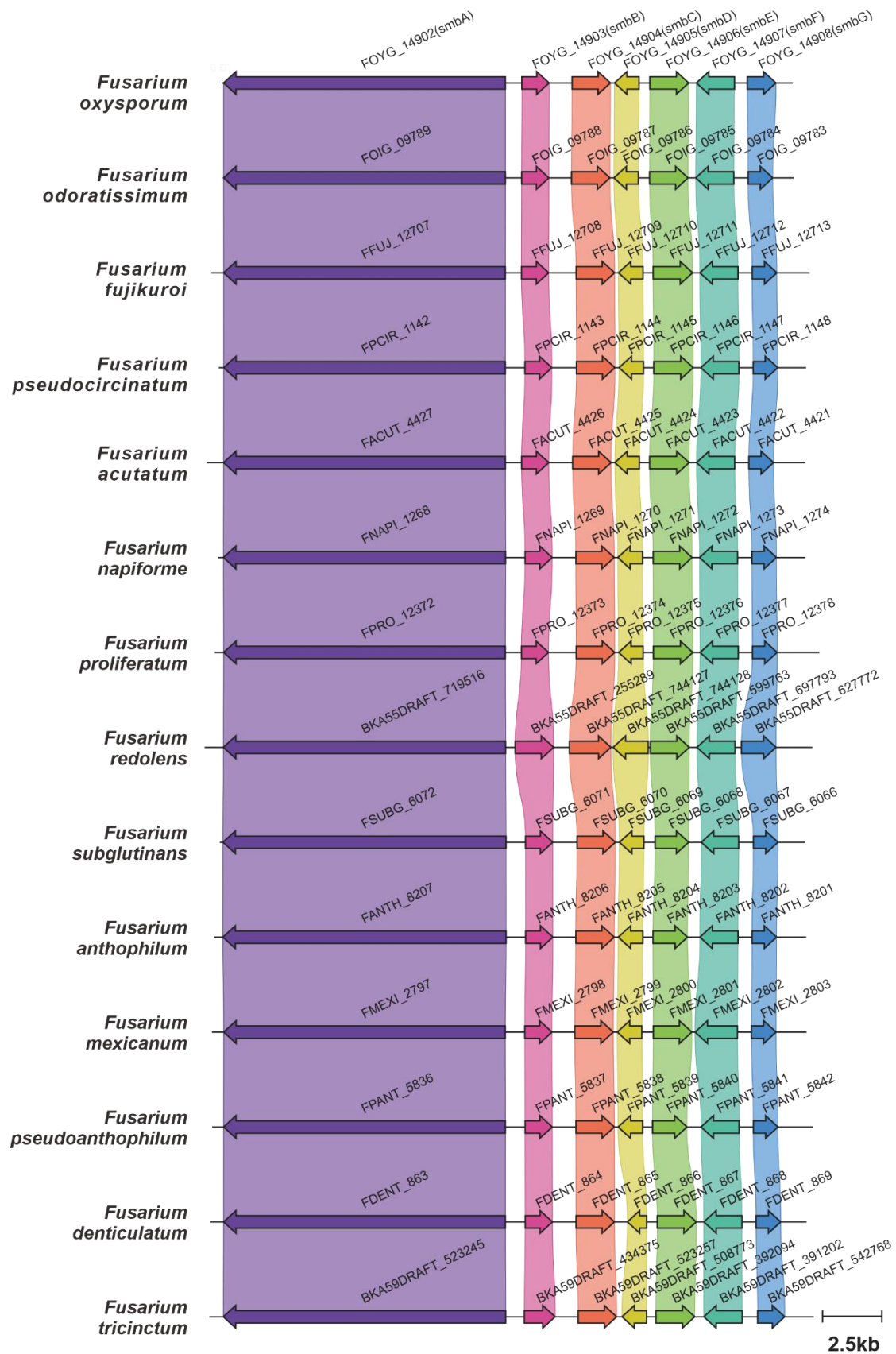


Figure S49: Comparison of *smb*BGCs from different *Fusarium* species.

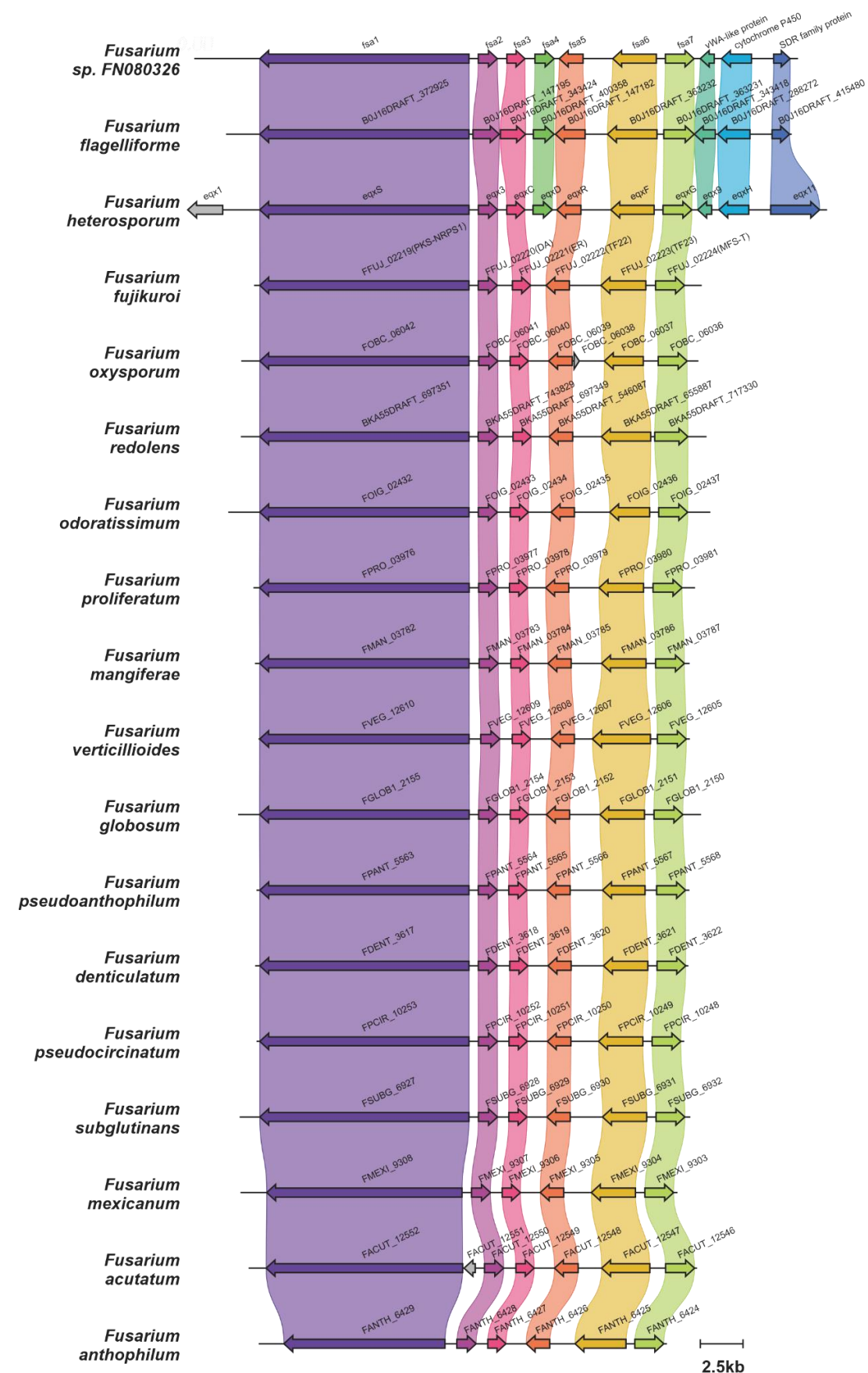


Figure S50: Comparison of *fsa*BGCs and *PKS-NRPS*BGCs from different *Fusarium* species.

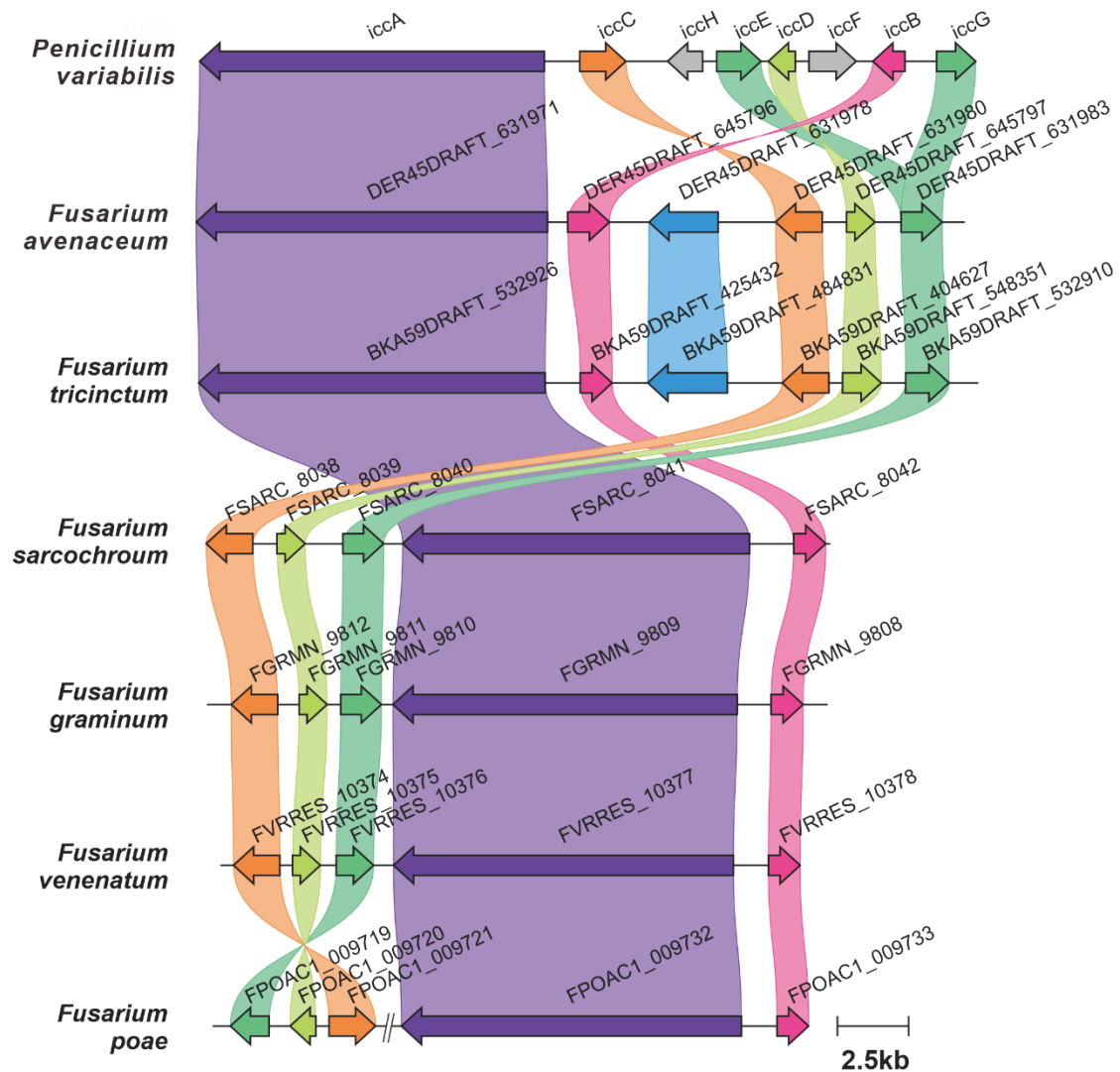


Figure S51: Comparison of *icc*BGCs from different *Fusarium* species.

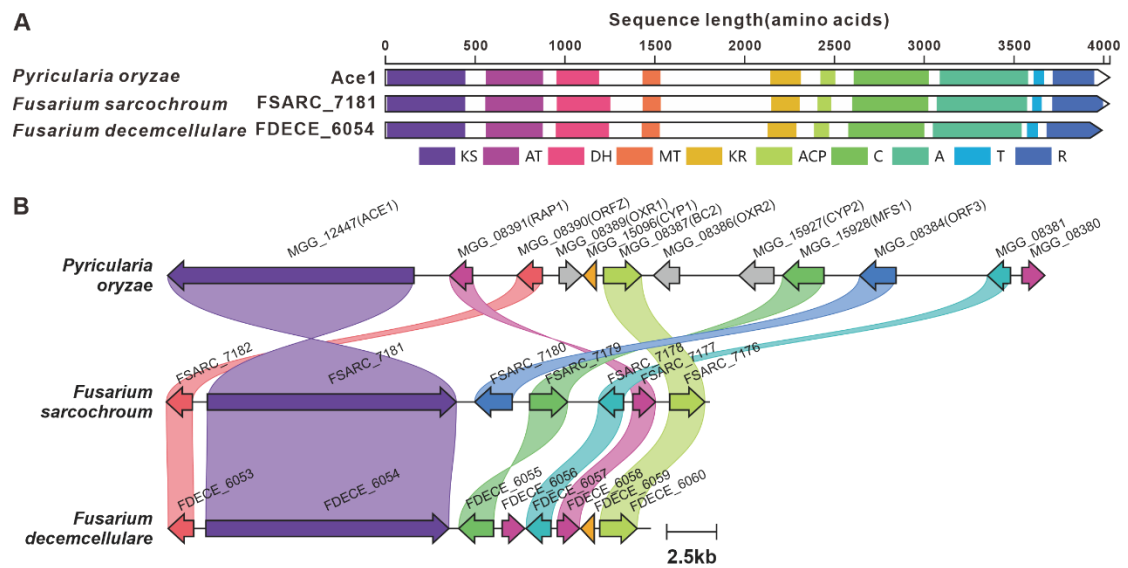


Figure S53: Domain comparison of ACE1 and its homologues (A), comparison of ACEBGCs from different species (B).

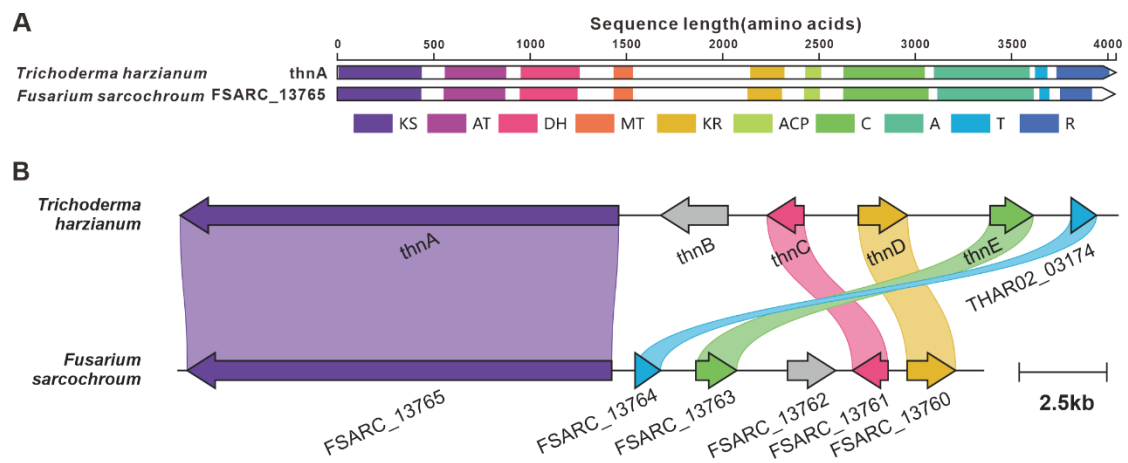


Figure S54: Domain comparison of ThnA and its homologues (A), comparison of *thn*BGCs from different species (B).

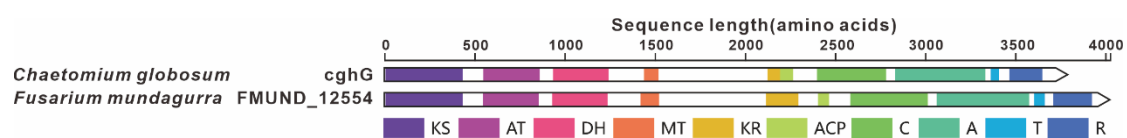


Figure S55: Domain comparison of CghG and its homologues.

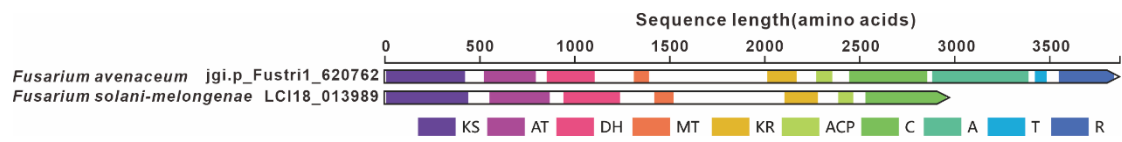


Figure S56: Domain comparison of LCI18_013989 and jgi.p_Fustri_620762.

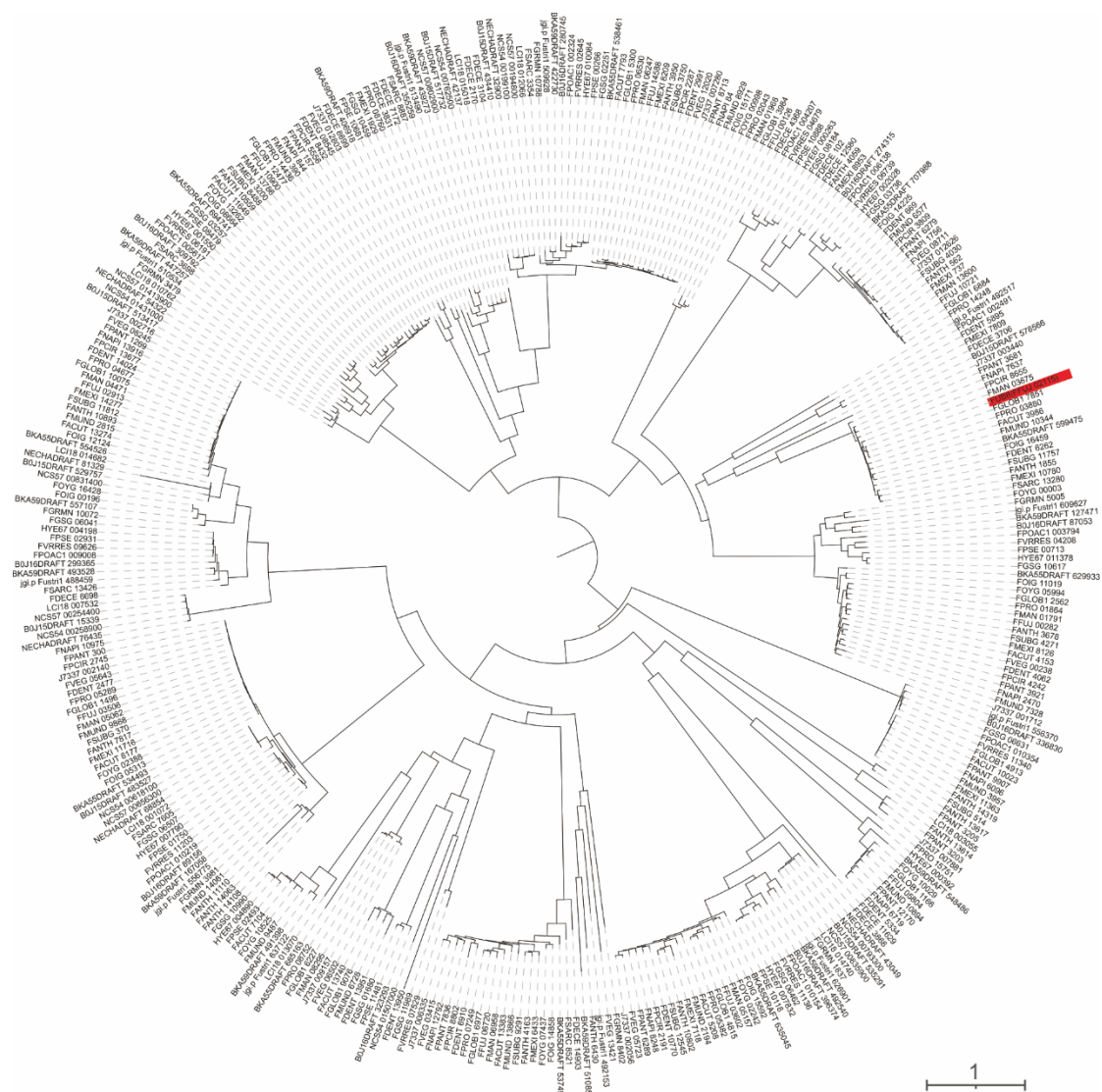


Figure S57: Cluster analysis of NRPS-like sequences based on phylogenetic tree. Sequence with a red background indicate that the sequence has been characterised.

References.

1. Michielse, C.B. and M. Rep, *Pathogen profile update: Fusarium oxysporum*. MOL PLANT PATHOL, 2009. **10**(3): p. 311-324.
2. Matic, S., M.L. Gullino, and D. Spadaro, *The puzzle of bakanae disease through interactions between Fusarium fujikuroi and rice*. FRONT BIOSCI, 2017. **9**(2): p. 333-344.
3. Xie, S.Y., et al., *Whole-Genome Sequencing and Comparative Genome Analysis of Fusarium solani-melongenae Causing Fusarium Root and Stem Rot in Sweetpotatoes*. MICROBIOL SPECTR, 2022. **10**(4): p. e00683-22.
4. Debbarma, R., et al., *First report of root rot disease on Solanum lycopersicum L. caused by Fusarium vanettenii in India*. J PHYTOPATHOL, 2021. **169**(11-12): p. 752-756.
5. van Westerhoven, A.C., et al., *Dissemination of Fusarium wilt of banana in Mozambique caused by Fusarium odoratissimum Tropical Race 4*. PLANT DIS, 2023. **107**(ja): p. 628-632.
6. Farias, O.R., et al., *Occurrence of Fusarium proliferatum Causing Vascular Wilt on Cowpea (Vigna unguiculata) in Brazil*. PLANT DIS, 2022. **106**: p. 1992.
7. Drakopoulos, D., et al., *Control of Fusarium graminearum in Wheat With Mustard-Based Botanicals: From in vitro to in planta*. FRONT MICROBIOL, 2020. **11**: p. 1595.
8. Xie, Y., et al., *A Megabirnavirus Alleviates the Pathogenicity of Fusarium pseudograminearum to Wheat*. PHYTOPATHOLOGY, 2022. **112**(5): p. 1175-1184.
9. Atanasoff-Kardjalieff, A.K., et al., *Biosynthesis of Fusapyrone Depends on the H3K9 Methyltransferase, FmKmt1, in Fusarium mangiferae*. FRONT FUNGAL BIOL, 2021. **2**.
10. Scherm, B., et al., *Fusarium culmorum: causal agent of foot and root rot and head blight on wheat*. MOL PLANT PATHOL, 2013. **14**(4): p. 323-341.
11. Wang, R.-Y., et al., *First Report of Fusarium solani Causing Fusarium Root Rot and Stem Canker on Storage Roots of Sweet Potato in China*. PLANT DIS, 2014. **98**(1): p. 160-160.
12. Fan, S., et al., *American Ginseng Root Rot Caused by Fusarium redolens in China*. PLANT DIS, 2021. **105**: p. 2734.
13. Xu, X., et al., *Fusarium Species Associated with Maize Leaf Blight in Heilongjiang Province, China*. J FUNGI, 2022. **8**(11): p. 1170.
14. Degradi, L., et al., *Exploring Mitogenomes Diversity of Fusarium musae from Banana Fruits and Human Patients*. MICROORGANISMS, 2022. **10**(6): p. 1115.
15. Wang, C.G., et al., *First Report of Fusarium falciforme Causing Leaf Blight in Acacia mangium in China*. PLANT DIS, 2022. **0**(0): p. PDIS-07-22-1583-PDN.
16. Rigorth, K.S., M.R. Finckh, and A. Šišić, *First Report of Fusarium venenatum Causing Foot and Root Rot of Wheat (Triticum aestivum) in Germany*. PLANT DIS, 2021. **105**(6): p. 1855.
17. Wang, Y., R. Wang, and Y. Sha, *Distribution, pathogenicity and disease control of Fusarium tricinctum*. FRONT MICROBIOL, 2022. **13**: p. 939927.
18. Ghimire, B., et al., *First Report of Fusarium poae Causing Fusarium Head Blight of Wheat in Georgia, U.S.A*. PLANT DIS, 2021. **105**(2): p. 491-491.
19. Chiewchanvit, S., et al., *Melanization of Fusarium keratoplasticum (F. solani Species Complex) During Disseminated Fusariosis in a Patient with Acute Leukemia*. MYCOPATHOLOGIA, 2017. **182**(9-10): p. 879-885.
20. Chen, Y., H.C. Kistler, and Z. Ma, *Fusarium graminearum Trichothecene Mycotoxins: Biosynthesis, Regulation, and Management*. ANNU REV PHYTOPATHOL, 2019. **57**: p. 15-39.
21. de Souza, M., et al., *Fusarium napiforme systemic infection: case report with molecular characterization and antifungal susceptibility tests*. SPRINGERPLUS, 2014. **3**: p. 492.
22. Santillán-Mendoza, R., et al., *Genetic diversity of Fusarium mexicanum, causal agent of mango and big-leaf mahogany malformation in Mexico*. MOL BIOL REP, 2019. **46**(4): p. 3887-3897.
23. Serrato-Díaz, L.M., et al., *First Report of Fusarium decemcellulare Causing Inflorescence Wilt*

- and Vascular and Flower Necrosis of Rambutan (*Nephelium lappaceum*), Longan (*Dimocarpus longan*), and Mango (*Mangifera indica*). PLANT DIS, 2015. **99**(8): p. 1187.
24. Gopalakrishnan, S., et al., Chickpea wilt: identification and toxicity of 8-O-methyl-fusarubin from *Fusarium acutatum*. PHYTOCHEMISTRY, 2005. **66**(13): p. 1536-1539.
 25. Ferrigo, D., et al., Influence of H₂O₂-Induced Oxidative Stress on In Vitro Growth and Moniliformin and Fumonisin Accumulation by *Fusarium proliferatum* and *Fusarium subglutinans*. TOXINS, 2021. **13**(9): p. 653.
 26. Blacutt, A.A., et al., *Fusarium verticillioides*: Advancements in Understanding the Toxicity, Virulence, and Niche Adaptations of a Model Mycotoxigenic Pathogen of Maize. PHYTOPATHOLOGY, 2018. **108**(3): p. 312-326.
 27. Mesny, F., et al., Genetic determinants of endophytism in the Arabidopsis root mycobiome. NAT COMMUN, 2021. **12**(1): p. 7227.
 28. Gagkaeva, T.Y., O.P. Gavrilova, and A.S. Orina, First Report of *Fusarium globosum* Associated with Barley Grain in the Southwestern Part of Siberia. PLANT DIS, 2019. **103**(3): p. 588-588.
 29. Ono, L.T., et al., Fungal communities in Brazilian cassava tubers and food products. INT J FOOD MICROBIOL, 2023. **384**: p. 109909.
 30. Freeman, S., et al., First Report of Mango Malformation Disease Caused by *Fusarium pseudocircinatum* in Mexico. PLANT DIS, 2014. **98**(11): p. 1583.
 31. González, M.S., et al., First Report of *Fusarium denticulatum* from Sweet Potato in Venezuela. PLANT DIS, 2003. **87**(2): p. 202.
 32. Amobonye, A., et al., Characterisation, pathogenicity and hydrolytic enzyme profiling of selected *Fusarium* species and their inhibition by novel coumarins. ARCH MICROBIOL, 2021. **203**(6): p. 3495-3508.
 33. Nicolli, C.P., et al., *Fusarium fujikuroi* species complex in Brazilian rice: Unveiling increased phylogenetic diversity and toxigenic potential. INT J FOOD MICROBIOL, 2020. **330**: p. 108667.
 34. Sandoval-Denis, M., et al., Symptomatic Citrus trees reveal a new pathogenic lineage in *Fusarium* and two new *Neocosmospora* species. PERSOONIA, 2018. **40**: p. 1-25.
 35. Nelson, P.E., Taxonomy and biology of *Fusarium moniliforme*. MYCOPATHOLOGIA, 1992. **117**(1-2): p. 29-36.
 36. Studt, L., et al., Biosynthesis of fusarubins accounts for pigmentation of *Fusarium fujikuroi* perithecia. APPL ENVIRON MICROBIOL, 2012. **78**(12): p. 4468-4480.
 37. Son, S.W., et al., Bikaverin and fusaric acid from *Fusarium oxysporum* show antioomycete activity against *Phytophthora infestans*. J Appl Microbiol, 2008. **104**(3): p. 692-698.
 38. von Barga, K.W., et al., Isolation and Structure Elucidation of Fujikurins A-D: Products of the PKS19 Gene Cluster in *Fusarium fujikuroi*. J NAT PROD, 2015. **78**(8): p. 1809-1815.
 39. Miyamoto, Y., et al., ACTTS3 Encoding a Polyketide Synthase Is Essential for the Biosynthesis of ACT-Toxin and Pathogenicity in the Tangerine Pathotype of *Alternaria alternata*. MOL PLANT MICROBE IN, 2010. **23**(4): p. 406-414.
 40. Wight, W.D., et al., Biosynthesis and Role in Virulence of the Histone Deacetylase Inhibitor Depudecin from *Alternaria brassicicola*. Molecular Plant-Microbe Interactions®, 2009. **22**(10): p. 1258-1267.
 41. Li, H., et al., Chemical Ecogenomics-Guided Discovery of Phytotoxic alpha-Pyrone from the Fungal Wheat Pathogen *Parastagonospora nodorum*. ORG LETT, 2018. **20**(19): p. 6148-6152.
 42. Fujii, I., et al., An iterative type I polyketide synthase PKSN catalyzes synthesis of the decaketide alternapyrone with regio-specific octa-methylation. CHEM BIOL, 2005. **12**(12): p. 1301-1309.
 43. Bonsch, B., et al., Identification of genes encoding squalenstatin S1 biosynthesis and in vitro production of new squalenstatin analogues. CHEM COMMUN, 2016. **52**(41): p. 6777-6780.
 44. Brock, N.L., et al., Genetic dissection of sesquiterpene biosynthesis by *Fusarium fujikuroi*.

- CHEMBIOCHEM, 2013. **14**(3): p. 311-315.
45. Hwang, I.S. and I.P. Ahn, *Multi-Homologous Recombination-Based Gene Manipulation in the Rice Pathogen Fusarium fujikuroi*. Plant Pathol J, 2016. **32**(3): p. 173-181.
 46. Kimura, M., et al., *The trichothecene biosynthesis gene cluster of Fusarium graminearum F15 contains a limited number of essential pathway genes and expressed non-essential genes*. FEBS LETT, 2003. **539**(1-3): p. 105-110.
 47. Lee, T., et al., *Tri13 and Tri7 determine deoxynivalenol- and nivalenol-producing chemotypes of Gibberella zeae*. APPL ENVIRON MICROBIOL, 2002. **68**(5): p. 2148-2154.
 48. Tokai, T., et al., *Screening of putative oxygenase genes in the Fusarium graminearum genome sequence database for their role in trichothecene biosynthesis*. FEMS Microbiol Lett, 2005. **251**(2): p. 193-201.
 49. Wollenberg, R.D., et al., *Chrysogine Biosynthesis Is Mediated by a Two-Module Nonribosomal Peptide Synthetase*. J NAT PROD, 2017. **80**(7): p. 2131-2135.
 50. Romans-Fuertes, P., et al., *Identification of the non-ribosomal peptide synthetase responsible for biosynthesis of the potential anti-cancer drug sansalvamide in Fusarium solani*. CURR GENET, 2016. **62**(4): p. 799-807.
 51. Slightom, J.L., et al., *Cloning and molecular characterization of the gene encoding the Aureobasidin A biosynthesis complex in Aureobasidium pullulans BP-1938*. GENE, 2009. **431**(1-2): p. 67-79.
 52. Yoshimi, A., et al., *Heterologous Production of a Novel Cyclic Peptide Compound, KK-1, in Aspergillus oryzae*. Front Microbiol, 2018. **9**: p. 690.
 53. Jin, J.M., et al., *Functional characterization and manipulation of the apicidin biosynthetic pathway in Fusarium semitectum*. MOL MICROBIOL, 2010. **76**(2): p. 456-466.
 54. Droce, A., et al., *Functional Analysis of the Fusarielin Biosynthetic Gene Cluster*. MOLECULES, 2016. **21**(12): p. 1701.
 55. Kim, Y.T., et al., *Two different polyketide synthase genes are required for synthesis of zearalenone in Gibberella zeae*. MOL MICROBIOL, 2005. **58**(4): p. 1102-1113.
 56. Yin, W.B., et al., *A nonribosomal peptide synthetase-derived iron(III) complex from the pathogenic fungus Aspergillus fumigatus*. J Am Chem Soc, 2013. **135**(6): p. 2064-2067.
 57. Kakule, T.B., et al., *Two related pyrrolidinedione synthetase loci in Fusarium heterosporum ATCC 74349 produce divergent metabolites*. ACS Chem Biol, 2013. **8**(7): p. 1549-1557.