**Figure S1.** Phylogenetic relationship of paralogs with regards to the respective hostrange-associated gene. FCIR = *Fusarium circinatum*; FFRAC = *Fusarium fracticaudum*; FPIN = *Fusarium pininemorale*; FSUB = *Fusarium subglutinans*.

0GI664981 hypothetical protein CEK27 010469 Eusarium fuikuroi	
XAE5651472 1 hypothetical protein E25203 4124 Eucarium on NPBL 25303	
<sup>1</sup> Ki 00/1722 1 Uppharacterized protein 1 2000 12552 Eugerium fuikurei	
Colog2414 humathatical anatain OCKOE 040470 Europium fuillunai	
<sup>al</sup> QGI83741.1 hypothetical protein CEK25 010470 Fusarium fujikurol	
SCV36416.1 uncharacterized protein FFB14 06087 Fusarium fujikuroi	
KLP07619.1 Uncharacterized protein Y057 10642 Fusarium fujikuroi	
SCN67810.1 uncharacterized protein FFB20 02786 Fusarium fujikuroi	
XP 023432735.1 uncharacterized protein FFUJ 06645 Fusarium fujikuroi IMI 58289	
RKL45032.1 hypothetical protein BFJ72 g3682 Fusarium proliferatum	
🗤 🕅 KAG4284514.1 hypothetical protein FPRO06 08893 Fusarium proliferatum	
KAG4266723.1 hypothetical protein FPRO04 13195 Fusarium proliferatum	
KAF4332319.1 hypothetical protein FBEOM 13883 Fusarium beomiforme	
EXL60708.1 hypothetical protein FOCG 00001 Fusarium oxysporum f. sp. radicis-lycopersici 26381	
🔐 🖁 🤻 KK65457.1 hypothetical protein BFJ69 g16270 Fusarium oxysporum	
<sup>La</sup> KAF5650722.1 hypothetical protein F52700 264 Fusarium sp. NRRL 52700	
TXP 046093088.1 uncharacterized protein BGZ61DRAFT 488089 Ilyonectria robusta	
៉ៅ 🔓 KAF5251455.1 hypothetical protein FOXYS1 14775 Fusarium oxysporum	
گری P 003040533.1 uncharacterized protein NECHADRAFT 102246 Fusarium vanettenii 77-13-4	
۰۱ CAH0037048.1 unnamed protein product Clonostachys rhizophaga	
Γ <sup>L1</sup> KAF5011794.1 hypothetical protein FDECE 2084 Fusarium decemcellulare	
RGP71800.1 hypothetical protein FSPOR 3166 Fusarium sporotrichioides	
KAH7201206.1 hypothetical protein DER44DRAFT 869666 Fusarium oxysporum	
KAH7214239.1 hypothetical protein BKA60DRAFT 85524 Fusarium oxysporum	
RKL03503.1 hypothetical protein BFJ71 g4045 Fusarium oxysporum	
EWZ95925.1 hypothetical protein FOWG 03442 Fusarium oxysporum f. sp. lycopersici MN25	
EXL55613.1 hypothetical protein FOCG 06178 Fusarium oxysporum f. sp. radicis-lycopersici 26381	
EWZ36079.1 hypothetical protein FOZG 11847 Fusarium oxysporum Fo47	
<sup>a</sup> XP 018250082.1 hypothetical protein FOXG 11720 Fusarium oxysporum f. sp. lycopersici 4287	
<sup>a</sup> RYC83508.1 hypothetical protein BEJ63 vAg13627 Fusarium oxysporum f. sp. parcissi	
KAH7473780.1 hypothetical protein FOMA001 g11966 Fusarium gyvsporum f. sp. matthiolae	
<sup>60</sup> r KAH7009575.1 hypothetical protein EDB80DRAFT 775984 llyopectria destructans	
XP 003000736.1 conserved hypothetical protein Verticillium alfalfae VaMs.102	
<sup>61</sup> KAH7381031.1 hypothetical protein BKA64DRAFT 764882 Leotiomycetes sp. MPI-SDFR-AT-0126	
<sup>10</sup> XP 046050612.1 uncharacterized protein BKA55DRAFT 510361 Fusarium redolens	
<sup>65</sup> L X CONCERNMENT AND A CONCERNMENT OF CONCERNMENT. OF CONCERNMENT OF CONCERNMENT OF CONCERNMENT OF CONCERNMENT OF CONCERNMENT OF CONCERNMENT OF CONCERNENT OF CONCERNENT OF CONCERNMENT OF CONCERNATINA OF CONCERNME	
XP 0012127831 predicted protein Aspergillus terreus NIH2624	
$\frac{1}{100}$ KEX52045.1 hypothetical protein GO26.0030190 Talaromyces marneffei PM1	
<sup>01</sup> <sup>00</sup> KAE5658804.1 hypothetical protein ECIPC 12732 Eusarium circinatum	
CIP 10 gene 25.58	
KAE5570120.1 hypothetical protein EPCIP 11270 Eusarium pseudooircinatum	
<sup>60</sup> KAE7525556 1 hypothetical protein C7054 d5204 Neopertaletionsis clavisnora	
KAF7555566.1 hypothetical protein G7054 g5204 Neopestalotiopsis clavispora	
<sup>10</sup> <sup>13</sup> VD 00722626261 humathatical protein E6E 14 007300 Neopestalotiopsis sp. 37M	
<sup>02</sup> DOESC 400.4 kurseth stigel anstein OEDEC 00.401 Ourseus sub-s	
$1^{1}$	
<sup>10</sup> KAB8349827.1 hypothetical protein FH972 023840 Carpinus rangiana	
KXH26978.1 hypothetical protein CNYM01 14149 Collectotrichum hymphaeae SA-01	
KAG/038026.1 ester cyclase Colletotrichum scovillei	
XP 035336908.1 uncharacterized protein HER10 EVM0001562 Colletotrichum scovillei	
PVH98527.1 hypothetical protein DM02DRAFT 673320 Periconia macrospinosa	
KAF4304208.1 hypothetical protein GTA08 BOTSD008526 Botryosphaeria dothidea	
KIM93405.1 hypothetical protein OIDMADRAFT 46214 Oidiodendron maius Zn	
KAF5019518.1 hypothetical protein F66182 8460 Fusarium sp. NRRL 66182	

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The evolutionary history of FCIR 10 gene 25.58 and its paralog FCIR 10 gene 25.59 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.

QKD60524.1 hypothetical protein FOBC 14701 Fusarium oxysporum Fo47 ËWZ32632.1 hypothetical protein FOZG 14175 Fusarium oxysporum Fo47 RKK11837.1 hypothetical protein BFJ65 g13713 Fusarium oxysporum f. sp. cepae RYC92606.1 hypothetical protein BFJ63 vAg4665 Fusarium oxysporum f. sp. narcissi EXL45534.1 hypothetical protein FOCG 12911 Fusarium oxysporum f. sp. radicis-lycopersici 26381 PCD26826.1 hypothetical protein AU210 013248 Fusarium oxysporum f. sp. radicis-cucumerinum RKK96705.1 hypothetical protein BFJ71 g7659 Fusarium oxysporum KAH7469539.1 hypothetical protein FOMA001 g14256 Fusarium oxysporum f. sp. matthiolae %P 018247343.1 hypothetical protein FOXG 20180 Fusarium oxysporum f. sp. lycopersici 4287 <sup>1</sup> XP 031032436.1 uncharacterized protein FOYG 13326 Fusarium oxysporum NRRL 32931 EMT71408.1 Putative transcriptional regulatory protein C3C7.04 Fusarium odoratissimum XP 031061798.1 uncharacterized protein FOIG 08727 Fusarium odoratissimum NRRL 54006 RKK88301.1 hypothetical protein BFJ69 g157 Fusarium oxysporum SCO90821.1 uncharacterized protein FRV6 14949 Fusarium oxysporum EXM19604.1 hypothetical protein FOTG 12456 Fusarium oxysporum f. sp. vasinfectum 25433 EXA35913.1 hypothetical protein FOVG 13030 Fusarium oxysporum f. sp. pisi HDV247 EXK83213.1 hypothetical protein FOQG 12565 Fusarium oxysporum f. sp. raphani 54005 EXL77406.1 hypothetical protein FOPG 08173 Fusarium oxysporum f. sp. conglutinans race 2 54008 KAG7003897.1 putative transcriptional regulatory protein Fusarium oxysporum f. sp. conglutinans 0.1 KAG7003898.1 putative transcriptional regulatory protein Fusarium oxysporum f. sp. conglutinans KAH7154038.1 fungal-specific transcription factor domain-containing protein Fusarium sp. MPI-SDFR-AT-0072 0.0 KAG7405371.1 putative transcriptional regulatory protein Fusarium oxysporum f. sp. rapae KAF4968676.1 hypothetical protein FSARC 3962 Fusarium sarcochroum <sup>••</sup>FFRAC 10 gene 17.128 <sup>2</sup>XP 041683625.1 uncharacterized protein FMAN 13738 Fusarium mangiferae <sup>•••</sup> KAF5558712.1 transcriptional regulatory Fusarium phyllophilum - KAF5551680.1 c6 zinc finger domain-containing protein Fusarium mexicanum xP 036536024.1 transcriptional regulatory Fusarium subglutinans الم 🖁 FFRAC 10 gene 17.127

— KAF4454431.1 putative transcriptional regulatory protein C3C7.04 Fusarium austroafricanum

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The evolutionary history of FFRAC 10 gene 17.127 and its paralog FFRAC 10 gene 17.128 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.

QGI66498.1 hypothetical protein CEK27 010469 Fusarium fujikuroi	
KAF5651472.1 hypothetical protein F25303 4124 Fusarium sp. NRRL 25303	
KLO94733.1 Uncharacterized protein LW93 13552 Fusarium fujikuroi	
QGI83741.1 hypothetical protein CEK25 010470 Fusarium fujikuroi	
SCV36416.1 uncharacterized protein FFB14 06087 Fusarium fujikuroi	
KLP07619.1 Uncharacterized protein Y057 10642 Fusarium fujikuroi	
SCN67810.1 uncharacterized protein FFB20 02786 Fusarium fujikuroi	
XP 023432735.1 uncharacterized protein FFUJ 06645 Fusarium fujikuroi IMI 58289	
🔐 🗍 RKL45032.1 hypothetical protein BFJ72 g3682 Fusarium proliferatum	
KAG4284514.1 hypothetical protein FPRO06 08893 Fusarium proliferatum	
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KAF4332319.1 hypothetical protein FBEOM 13883 Fusarium beomiforme	
EXL60708.1 hypothetical protein FOCG 00001 Fusarium oxysporum f. sp. radicis-lycopersici 26381	
KKK65457.1 hypothetical protein BFJ69 g16270 Fusarium oxysporum	
مدا 🖉 KAF5650722.1 hypothetical protein F52700 264 Fusarium sp. NRRL 52700	
La FFRAC 6 gene 42.88	
مدا الآلي XP 003040533.1 uncharacterized protein NECHADRAFT 102246 Fusarium vanettenii 77-13-4	
MKAF5251455.1 hypothetical protein FOXYS1 14775 Fusarium oxysporum	
CAG9945759.1 unnamed protein product Clonostachys rosea f. rosea IK726	
CAH0037048.1 unnamed protein product Clonostachys rhizophaga	
KAF5011794.1 hypothetical protein FDECE 2084 Fusarium decemcellulare	
GP71800.1 hypothetical protein FSPOR 3166 Fusarium sporotrichioides	
L <sup></sup> KAH7201206.1 hypothetical protein DER44DRAFT 869666 Fusarium oxysporum	
KAH7214239.1 hypothetical protein BKA60DRAFT 85524 Fusarium oxysporum	
EWZ36079.1 hypothetical protein FOZG 11847 Fusarium oxysporum Fo47	
Line EXL55613.1 hypothetical protein FOCG 06178 Fusarium oxysporum f. sp. radicis-lycopersici 26381	
EWZ95925.1 hypothetical protein FOWG 03442 Fusarium oxysporum f. sp. lycopersici MN25	
KAH/4/3/80.1 hypothetical protein FOMA001 g11966 Fusarium oxysporum f. sp. matthiolae	
<sup>4</sup> PV02250082.1 hypothetical protein FOXG 11/20 Fusarium oxysporum f. sp. lycopersici 4287	
RYC83508.1 hypothetical protein BFJ63 vAg13627 Fusarium oxysporum f. sp. narcissi	
<sup>10</sup> KAU3200575 4 hum athenia la protein BFJ/1 g4045 Fusarium oxysporum	
<sup>0.1</sup> 0 <sup>2</sup> VR 000007004 concerned humoth sticel anstein Visitial and Visitial And	
<sup>02</sup> KAUZ202000736.1 conserved hypothetical protein Verticilium alrainae Vams.102	
<sup>60</sup> VD 046050610.1 up obstactorized protein BKA64DRAF1 764882 Leotiomycetes sp. MPI-SDFR-A1-0126	
<sup>0.5</sup> [] XP 046050612.1 uncharacterized protein BKA55DRAF1 510361 Fusarium redolens	
<sup>62</sup> KAE4204208 1 hypothetical protein CTA08 BOTSD008526 Botsycophastic dethidee	
AF4304208. I hypothetical protein GTA08 BOTSD008526 Botryosphaena dotnidea	
PVH98527.1 hypothetical protein DM02DRAF1 675320 Periconia macrospinosa	
<sup>67</sup> KEX52045.1 by notherical protein CO26.0020190. Talaramyose manaffei DM1	
KAC7525586 1 hypothetical protein G2050 Alegoestalotionsis clavispora	
<sup>40</sup> KAE30023471 hypothetical protein E8E14 007300 Neopestalotionsis sp. 37M	
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$^{02}$ $^{01}$ KAB83498271 by pothetical protein EH972 023840 Carpinus fanciana	
$1^{1}$ POE564891 hypothetical protein CEP56 33461 Quercus suber	
<sup>6</sup> KXH26978.1 hypothetical protein CNYM01 14149 Colletotrichum nymphaeae SA-01	
KAG7038026.1 ester cyclase Colletotrichum scovillei	
<sup>33</sup> XP 035336908.1 uncharacterized protein HER10 EVM0001562 Colletotrichum scovillei	
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The evolutionary history of FFRAC\_10\_gene\_24.123 and its paralog FFRAC\_6\_gene\_42.88 was inferred by using the Maximum Likelihood method and JTT matrix-based model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.

<sup>®</sup>XP 031885015.1 uncharacterized protein CGMCC3 g8468 Colletotrichum fructicola KAF4915754.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum fructicola <sup>°°</sup>KAF4806151.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum siamense KAF4853354.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum siamense XP 036496744.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum siamense KAH9238749.1 hypothetical protein K456DRAFT 48947 Colletotrichum gloeosporioides 23 KAF4866399.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum siamense KAF4927814.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum viniferum <sup>%</sup>XP 037180051.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum aenigma KAF4838607.1 Anhydro-N-acetylmuramic acid kinase Colletotrichum tropicale KAH0432359.1 hypothetical protein CcaCcLH18 06439 Colletotrichum camelliae EQB54052.1 hypothetical protein CGLO 06162 Colletotrichum gloeosporioides Cg-14 XP 045259484.1 Transaldolase Colletotrichum gloeosporioides ÅAF0320780.1 transaldolase Colletotrichum asianum XP 038742152.1 uncharacterized protein CkaCkLH20 09870 Colletotrichum karsti OAA63383.1 Anhydro-N-acetylmuramic acid kinase Sporothrix insectorum RCEF 264 XP 007911936.1 putative anhydro-n-acetylmuramic acid kinase protein Phaeoacremonium minimum UCRPA7 r KAH7139854.1 anhydro-N-acetylmuramic acid kinase partial Dactylonectria estremocensis KAH7129230.1 anhvdro-N-acetylmuramic acid kinase Dactylonectria macrodidyma KAF7550950.1 hypothetical protein G7Z17 g5369 Cylindrodendrum hubeiense KAH7007337.1 anhydro-N-acetylmuramic acid kinase llyonectria destructans <sup>b</sup>XP 046097701.1 anhydro-N-acetylmuramic acid kinase llyonectria robusta KAH6974191.1 anhydro-N-acetylmuramic acid kinase Ilyonectria sp. MPI-CAGE-AT-0026 KFA50069.1 hypothetical protein S40293 08607 Stachybotrys chartarum IBT 40293 KEY64558.1 hypothetical protein S7711 03624 Stachybotrys chartarum IBT 7711 KAH8897610.1 anhydro-N-acetylmuramic acid kinase Thozetella sp. PMI 491 VUC37874.1 unnamed protein product Clonostachys rosea CAH0044290.1 unnamed protein product Clonostachys solani CAG9983471.1 unnamed protein product Clonostachys byssicola CAG9946511.1 unnamed protein product Clonostachys rosea f. rosea IK726 CAH0014875.1 unnamed protein product Clonostachys rhizophaga <sup>1</sup>°CAH0056914.1 unnamed protein product Clonostachys solani PKS06042.1 hypothetical protein jhhlp 007876 Lomentospora prolificans PWI65654.1 hypothetical protein PCL 06859 Purpureocillium lilacinum XP 018176045.1 transaldolase Purpureocillium lilacinum KAF5529811.1 transaldolase Fusarium mexicanum KAF5675701.1 transaldolase Fusarium circinatum FPIN 12 gene 2.24 FPIN 12 gene 2.12 <sup>3</sup> XP 016213002.1 hypothetical protein PV09 05775 Verruconis gallopava 0.5 - XP 040779106.1 uncharacterized protein M406DRAFT 70239 Cryphonectria parasitica EP155 KAH8758749.1 anhydro-N-acetylmuramic acid kinase Hyaloscypha sp. PMI 1271 ÅAH8748353.1 anhydro-N-acetylmuramic acid kinase Hyaloscypha finlandica XP 024728320.1 anhydro-N-acetylmuramic acid kinase Hyaloscypha bicolor E <sup>®</sup>PMD33884.1 anhydro-N-acetylmuramic acid kinase Hyaloscypha variabilis F XP 013318671.1 hypothetical protein PV05 02637 Exophiala xenobiotica <sup>11</sup> XP 013268416.1 hypothetical protein Z518 09005 Rhinocladiella mackenziei CBS 650.93 XP 008725873.1 hypothetical protein G647 03305 Cladophialophora carrionii CBS 160.54 ÖCT49387.1 Anhydro-N-acetylmuramic acid kinase Cladophialophora carrionii KIW64920.1 hypothetical protein PV04 07222 Phialophora americana XP 007741568.1 anhydro-N-acetylmuramic acid kinase Cladophialophora psammophila CBS 110553 XP 016618981.1 hypothetical protein Z519 07296 Cladophialophora bantiana CBS 173.52 XP 016627192.1 hypothetical protein Z520 11126 Fonsecaea multimorphosa CBS 102226 XP 018697313.1 hypothetical protein AYL99 03173 Fonsecaea erecta XP 016242955.1 hypothetical protein PV07 11005 Cladophialophora immunda OQU94048.1 hypothetical protein CLAIMM 00467 Cladophialophora immunda XP 022500457.1 hypothetical protein AYO20 05295 Fonsecaea nubica XP 022510144.1 hypothetical protein AYO21 07652 Fonsecaea monophora XP 013281216.1 hypothetical protein Z517 09854 Fonsecaea pedrosoi CBS 271.37 XP 016246407.1 hypothetical protein PV07 09305 Cladophialophora immunda - TKA29430.1 hypothetical protein B0A50 03442 Salinomyces thailandica KAF7167777.1 hypothetical protein CNMCM6106 003220 Aspergillus hiratsukae <sup>2</sup>XP 040698708.1 uncharacterized protein ASPSYDRAFT 92939 Aspergillus sydowii CBS 593.65 OJJ65798.1 hypothetical protein ASPBRDRAFT 35651 Aspergillus brasiliensis CBS 101740 XP 041549370.1 uncharacterized protein APUU 10004A Aspergillus puulaauensis XP 040732550.1 uncharacterized protein BHQ10 004046 Talaromyces amestolkiae <sup>1</sup>XP 035340352.1 uncharacterized protein TRUGW13939 01257 Talaromyces rugulosus - KAE8152338.1 Anhydro-N-acetylmuramic acid kinase Aspergillus avenaceus xP 013322967.1 hypothetical protein T310 10051 Rasamsonia emersonii CBS 393.64 🗠 XP 040668230.1 uncharacterized protein ASPVEDRAFT 83965 Aspergillus versicolor CBS 583.65 KIV80998.1 hypothetical protein PV11 08452 Exophiala sideris ີ່ GFZ48433.1 hypothetical protein JCM24511 06181 Saitozyma sp. JCM 24511 RSH91604.1 hypothetical protein EHS25 008973 Saitozyma podzolica KAI1123679.1 anhydro-N-acetylmuramic acid kinase Nemania abortiva KAI0096453.1 anhydro-N-acetylmuramic acid kinase Nemania sp. FL0031 KAI0868258.1 anhydro-N-acetylmuramic acid kinase Hypoxylon argillaceum KAI1150283.1 anhydro-N-acetylmuramic acid kinase Nemania diffusa RWA14205.1 hypothetical protein EKO27 g896 Xylaria grammica KAI0416674.1 anhydro-N-acetylmuramic acid kinase Xylaria grammica GDZ33912.1 anhydro-N-acetylmuramic acid kinase Bifidobacteriaceae bacterium MCC02031 WP 003838372.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium dentium WP 196329681.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium dentium WP 137652915.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium moukalabense WP 033501798.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium catenulatum WP 172144273.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium sp. DSM 109963 WP 214304355.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium miconisargentati WP 033517701.1 anhydro-N-acetylmuramic acid kinase Bifidobacterium scardovii RQP12227.1 anhydro-N-acetylmuramic acid kinase Microbacteriaceae bacterium MBV9921319.1 anhydro-N-acetylmuramic acid kinase Pseudonocardia sp. WP 101579331.1 anhydro-N-acetylmuramic acid kinase Bacillus canaveralius WP 125929096.1 anhydro-N-acetylmuramic acid kinase Bacillus canaveralius WP 188498745.1 anhydro-N-acetylmuramic acid kinase Pullulanibacillus pueri WP 144274066 1 anhydro-N-acetylmuramic acid kinase Raoultella planticola WP 181591817.1 anhydro-N-acetylmuramic acid kinase Klebsiella pneumoniae PLN19352.1 anhydro-N-acetylmuramic acid kinase Klebsiella pneumoniae MBV9290708.1 anhydro-N-acetylmuramic acid kinase Hyphomicrobiales bacterium MBV8970116.1 anhydro-N-acetylmuramic acid kinase Verrucomicrobia bacterium <sup>43</sup> WP 080863943.1 MULTISPECIES: anhydro-N-acetylmuramic acid kinase Agrobacterium tumefaciens complex WP 227319878.1 anhydro-N-acetylmuramic acid kinase Acidisoma silvae الله 227319878:1 annyaru-אראבינין אווא אווא 27319878:1 annyaru-אראבינין אווא 227319878:1 annyaru-אראבינין אווא אין WP 159014438:1 annydro-N-acetylmuramic acid kinase Acidisoma sp. S159

The evolutionary history of FPIN\_12\_gene\_2.12 and its paralog FPIN\_12\_gene\_2.24 was inferred by using the Maximum Likelihood method and the Le Gascuel model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.





The evolutionary history of FSUB 25 gene 2.21 and its paralog FSUB 37 gene 0.24 was inferred by using the Maximum Likelihood method and the Le Gascuel model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site (next to the branches). Evolutionary analyses were conducted in MEGA11.