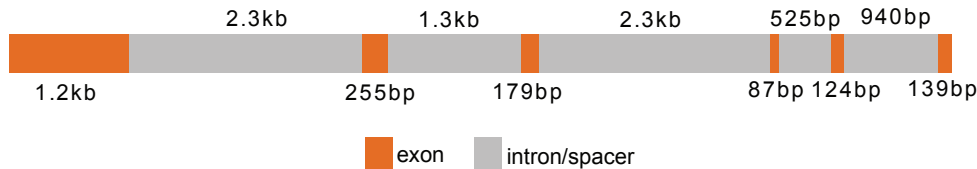


A

(1)

<i>B. tabaci</i> MEAM1 ArgG	MSGDQIKKIVLAYSGGLDTSSIIIPWLKENYNCEVVAFAVDIGQDRADLDGVEKKALQSGASECHVVDLREEIRDVYPTLQTGALYEETYLIGTSMARP	100
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	MS----KRVILAYSGGEEKSVIANWLQCNRYGEIITFTADLGQFKKIELAYKKAKVLGKIKMYIEDLKESFVTKMICHFRFRANTIIECGKKIGASIVRE	96
<i>B. tabaci</i> Asia II 3 ArgG	MSGDKIKKIVLAYSGGLDTSSIIIPWLKENYNCEVVAFAVDIGOERADLDG-----	50
<i>B. tabaci</i> MEAM1 ArgG	ITAKAQVELALRLGADAVAHGATGKGNDUVRFEFTAFATAPOLKVVAPWREWDLRSKEALLNYLKERNIH-TTATLEKI-TSRDENAWHISTEGGELEDF	198
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	LIILRLIEIAKLNKTTNISYGTIKKSKDLIRLLDSTYSINFIKIIAPWRDLNFISONKERTVFKKKFSNEFVQKHISCVNNDFLIHFSKCCCLDNT	196
<i>B. tabaci</i> Asia II 3 ArgG	-----LALRLGADAVAHGATGKGNDUVRFEFTAFATAPOLKVVAPWREWDLRSKEALLNYLKERNIH-TTATLEKI-TSRDENAWHISTEGGELEDF	140
<i>B. tabaci</i> MEAM1 ArgG	ANAPNKAANVWTVDPDAPDKPETVTIAIEKGRIVGVNGEKLTFYGLLEKLNALGAKHGVRIDIVENRIIVIKSRGCYETPGGTLMMTALRALEQLVLL	298
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	WNEAKKRCCLNSNFFKNTPDKFTYDITDFKQGNPTSINSEVLKSHEIMIKLNNLGSKHGIGRVNKRYYGSG-----LKA	271
<i>B. tabaci</i> Asia II 3 ArgG	ANAPNKAANVWTVDPDAPDKPETVTIAIEKGRIVGVNGEKLSEFACLEKLNALGAKHGVRIDIVENRI-----LVLD	214
<i>B. tabaci</i> MEAM1 ArgG	RDCYKWKQQLGHEMAVYVVDGKWFAPLTKSILAAAFSLAEVVDGEVVLQLYKGRATAIKKTSFKSLYSEEFATFGGEDEVYDHSAGGPIR--LFSLSARI	396
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	RCCY---ENPGVTILHAHRAIESFTLDHEILQIKD-----ILMPLIA-----ENVYTVNLWTKIKMLKALIDTSQKYVNGIVIRIKLYKGV/VLI	353
<i>B. tabaci</i> Asia II 3 ArgG	RDCYKWRQOLGHEMAVYVVDGKWFAPLTKSILAAAFSLAGGGGGEVVLQLYKGSATAIKKTSFKSLYSEEFATFGGEDEVYDHSAGGPIR--LFSLSARI	312
<i>B. tabaci</i> MEAM1 ArgG	RAIRDOKKILMRGRRQSSSRRLDATIRAPWMCELHTEKLKASWFLFPVTEACCAARRASPVLTGNSGGYNTKPKQISNSVFENLHSFFSFRKKIVLSFPQ	496
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	IGTKSDQ-----	360
<i>B. tabaci</i> Asia II 3 ArgG	RAIRDOKK-----	320
<i>B. tabaci</i> MEAM1 ArgG	MNARKEAIFITAPGCNYSMSMDVRVAYRKIEGALTFLARDGMRMLRCALGLAVITLDSFSCSTENSLRCNVIRSFMGKPCETVVKNRLLRSSLRTPCLLI	596
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	-----	360
<i>B. tabaci</i> Asia II 3 ArgG	-----	320
<i>B. tabaci</i> MEAM1 ArgG	LSHSFKWQIDRYIAKYATRLILRVWNPTVEVLCTKGSTRGSLERSPNLDSKPNENIFHARGKKCQNHCF	664
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs ArgG	-----	360
<i>B. tabaci</i> Asia II 3 ArgG	-----	320

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B

(1)

<i>B. tabaci</i> MEAM1 ArgH	-----MHRFQMALWGSRFTEAADQRFKLFNLSLRFDYRLAEQDIIGSIAWSMALVTWNILTSOEQKELESALNTLLAEVNSHFEQIPQSD	85
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	-----MKNFKKFWIGRKKSTCKLVNFTASINFDYRLVYHDKVSIHAKMLEIVGLLTLLKESQLIINGKKNIEKDINNEKTINWFTK	83
<i>P. venusta</i> ASL-1	MSDTIEINKTVELNKSATDKTKLWNCQCEQDISFEFLQFNCSITEDEILYADDIEGSIHVTLMLSECQIIEQRRERQIVETLGNIKDDIEKGKVEL	99
<i>P. venusta</i> ASL-2	-----MHSCGDLVKEEKKTIIINTLNETEGDINDNKIELKTE	37
<i>B. tabaci</i> MEAM1 ArgH	AEDIHSWVESRLIEVVALGKKLHTGRSRNDQVITEPGVNVVSYGKETFFMIVNPMMLSCQVATDKLWCKAQVNDLLIATRGDQALITTTEATQDILMPG	185
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	LEDVHMNIENANLIKKIGNIGKKLHTGRSRNDQTS-----TDIIRLVLEKIDKTKLTKTKRSLNLNLAISESDTIMPG	156
<i>P. venusta</i> ASL-1	LEDIHMNIEAELINRIGDIGRKLHTGRSRNDQVI-----TDLRLIFTRKNIKIILELVSTISRLTQLADQYAHVMPG	172
<i>P. venusta</i> ASL-2	LEDIHMNIESELIKRIGDIGRKLHTGRSRNDQIV-----TDLRLYTRKHIDIIEILLLTMHMLDHSKHKHTIMPG	110
<i>B. tabaci</i> MEAM1 ArgH	YTHLQRAQVFSFAHWCLAYVEMLARDETNRDITLKRLDMSPLGCGALAGTAYPIDNEQLAAWLGASATRNSLDTSVDRDYLILILSNAATGMVHLSRFA	285
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	FTHLQIAQPIITFGHHILAWHEMISRDRHERILECRKRINTPLGSAALAGTTPINRNIIKDLLGFDHITENSLDAVSDRDRDAIEFTSVSSILLMHLRMC	256
<i>P. venusta</i> ASL-1	FTHFQFAQPIISVGHYLLAYACMEKRDVERFLECRKRVNPNPLGSAALAGTTHPINHLLTQLLHFDQPSSENSLDAISDRDIEFISDCSQTIMHLSRIS	272
<i>P. venusta</i> ASL-2	FTHFQTAQPIISVGHYLLAYASMEKRDNRHLECRKRVTNPNPLGSAALAGTTHPINRYLTSKLLDFTDKPSNSLDSISDRDFVIEFISDCQTIMHLSRIS	210
<i>B. tabaci</i> MEAM1 ArgH	EDLIFFNTGEASFVELSDKVTSGSSIMPQKKNPDALELIRGKCGRVQCAITGMLTTLKALPLAYNKNQEDKEGLFDADVTLGCLQMAALVLDGIRVKK	385
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	EELIFWTSPLPDDFIELPDCCTGSSIMPQKKNPDIPELIRGKTGRIYGNLNLIVLMKSQPLAYNKNQEDKEPLFDTEFVINDNFINTIKFLKINP	356
<i>P. venusta</i> ASL-1	EEFIIFMNPQDFVALPDSLLTGSSIMPQKKNPDMLELIRGKSGRIYGNLNLITIMKSQPLAYNKDFQCKQPLFDSIKTITMTLTADEILNNVQFN	372
<i>P. venusta</i> ASL-2	EEFIIFMNPQDFVELTLESEFTLGSSIMPQKKNPVLELIRGKTGRIYANLINILTTMKCOTLAYNKDLOEDKIPLFDTVDNIMCLVAFGKLEKSIFNE	310
<i>B. tabaci</i> MEAM1 ArgH	PRCRHAEQSTANSTELADYLVAKGLPFREAHHLVGRVVEAQAQCVPLAAMSLQELKKESDVVEEDVYPVLELQSCLEKNCAGKGVAAHQAVALAEAK	485
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	KKMYLSALCNYSTATDFADYLVVRGVPFERDAHSIVGKVYVYGGITNQKNENEIYIEKLEEFSSNKIDEELEVLITLGESINTRNHIGGTAENOVRSALRAK	456
<i>P. venusta</i> ASL-1	TKX-----	375
<i>P. venusta</i> ASL-2	KQMYETAKGFISTDLADYLVKGLPFRTSHEIVGSIKKVCNEKHRTSPLSETELEKTHSYKDDIIDIDICENSRYKNHIGGTSPEQWKISVONFR	410
<i>B. tabaci</i> MEAM1 ArgH	ERIILKSEP-----	493
<i>Ca. Portiera aleyrodidarum</i> TV ArgH	KIKKILLG-----	464
<i>P. venusta</i> ASL-1	-----	375
<i>P. venusta</i> ASL-2	FVILKIKTNKLEPKFSY	426

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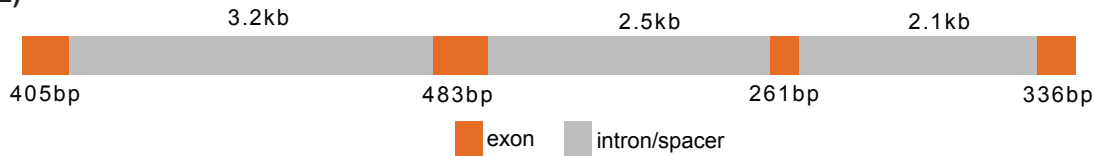


Fig. S2

C

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<i>B. tabaci</i> MEAM1 DapF	MAENAHQIRGRKLQIRIQRPKKHKMHNVRRSKFYHHTDRRKTAMMIGISIGSLTTYIGMAVGFVKSLAVDENHRPKSHS	100
<i>Ca. Portiera aleyrodidarum</i> TV DapF	-----MIIDFIN	7
<i>Ca. Hamiltonella defensa</i> DapF	-----MCSLGNDFVIIDAVT	15
<i>Planococcus citri</i> DapF	-----MLEKIDEVKMHGLGNDFVIIVKSEN	24
<b>DAP epimerase</b>		
<i>B. tabaci</i> MEAM1 DapF	QNVSF--ADQIRRLADRLHGVGFDQLLVVERSPEDVDVDFHYRIFNVDSSEVAQCGNGARCFARFVQLQHLRKRDLHVSTASG-RRMVLSTTPDDQVRV	197
<i>Ca. Portiera aleyrodidarum</i> TV DapF	QYFLIN--KTIHKYLSNRNLGVGFDQLLLVEIHNNHHFDFYRIFNANGSEVENCGNGARCLAKFLFDKRLTNKTIHIVETYGGHILLYININNNNLISV	105
<i>Ca. Hamiltonella defensa</i> DapF	QNVHLR--SEFICRLANRHTGIGFDQLLLLEFPNSPELDFHYRIFNADGSEVFCGNGARCLGRFVHLKGLTNKKNIQVSTKT--VKMQIHIEEKNQICV	111
<i>Planococcus citri</i> DapF	LLSSORNKOVAMEISNRRTGIGCDQFVWYEKIRTSYYNMT--LYNIDGSFVKICGNAARCLAKLISDETGEKEFTIKSTIKDLKCRINEHTVTVMGKV	122
<i>B. tabaci</i> MEAM1 DapF	NMGEPVLEERLIPFRTPPTNKTTETLYHMD----NVTFGCVSLGNPHCVVQVQSVKTAQVDTLGAMLETHERFPERTNVGFMVEVDPGHIHLRVFERGVG-E	292
<i>Ca. Portiera aleyrodidarum</i> TV DapF	NFGKP-LIKGFKIKTPISQ---FKLID-----LF-IVSIGNPHAVLIIVSNINTIPINILGNFIENNLFIETKINVGFMQIISPSLIKLRVFERGVGGE	194
<i>Ca. Hamiltonella defensa</i> DapF	NMGEPDFFPKTIPFRSKTIK--KIYELDVAEQKLLCGIVSMGNPHCIHQVEKLDSDQIKLIGPLLGCPSFPPEGTNVGFMQIIDRKHIHLRVYERAG-E	208
<i>Planococcus citri</i> DapF	SFOEP-WMPSMEKIRSVTEP--FAEDLS-----NLIDVDVANPHLVIFGIFTESNKL-LVGKKLONLEYELGVDNVSEVTIKD-NKIHVFIWFERGAG-P	210
<b>DAP epimerase</b>		
<i>B. tabaci</i> MEAM1 DapF	TRACGSNACAAVCGVROGALA--SPVRVDLPGGTLRVTWAG-LGQPVYLTGPAVHVYDGFIDLGNK-	356
<i>Ca. Portiera aleyrodidarum</i> TV DapF	TMACGTGACAAVSFGIKLGYLNRNKSIVKILPGGNLKINNLGGLYNSLYMSGYVKKVEDGSIEVFN--	260
<i>Ca. Hamiltonella defensa</i> DapF	TQACGSGACAAVSIGVQDILLD--EKVHVEQKGGNLDICIKG-TGHCLYMTGPADHVYDGVIHMSFKP	273
<i>Planococcus citri</i> DapF	TLACGSAACASFASSLKFGVLE--SPSEVIFTLGNISMSEON---GDLLMTGETTFVAEGKYYHYF--	271

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D

<i>B. tabaci</i> LysA	-----MAGIVPLSNHFTYRNNELYCEDIPVANLAEKYGTPLYVYSQAAILKQLOALQFAFSELK-P-LVCYSVKANSNLSILRLLAEHSGGF	85
<i>Ca. Portiera aleyrodidarum</i> TV LysA	-----MTFQFYRG-ILFIENISCLKIAKKFGTPCYVYSKKEIHKYFNYYKYQLSLNHENICAYALKANSNIAILNLSQLGSGF	79
<i>Ca. Hamiltonella defensa</i> LysA-1	MKSELFSPNVQVFQPQRLTPLLNDIEIRA-FIYTTPEKLTAYVKKYGSPLHLIWPENLQNLTALRTALQKLH-RHLIFYAVKVKKSQALLESAAKSGIGA	98
<i>Ca. Hamiltonella defensa</i> LysA-2	-----MREQNVKV	8
<i>B. tabaci</i> Asia II 3 LysA	-----MAGIVPPWNHFTYRNNELYCEDIPVANLAEKYGTPLYVYSQAAILKQLOALQFAFSELK-P-LVCYSVKANSNLSILRLLAEHSGGF	85
<i>B. tabaci</i> LysA	DVVS GGELKRV S----VAGGQARQTVFAGVGKTDDEIAAGLTAGVLMFNVESEELDAIVRVAQSKRIQAPVALRINPDVDPKTHRYISTGHKESKFGMD	181
<i>Ca. Portiera aleyrodidarum</i> TV LysA	DI V SIGELEKVL----IAGGDPKKIVYSGVAKKKQEIKRALKVGIKCFNVEFQEMDRINEIARLKNKANISIRINENVDAKTHPYISTGLKSNKFGIS	175
<i>Ca. Hamiltonella defensa</i> LysA-1	DVSSLYEMRAAR----KSGIPYSKICASGPSKTSIFLTDLITHDAC-ISIDSTEEFEI KALVAH--IQPAHRVRVLLRYRESFLPISRFGMKSKDLALC	191
<i>Ca. Hamiltonella defensa</i> LysA-2	DAVSLGEIERALKANFIPGESSDIIFTADLLDKMTLKKVIQLNIP-VNAGSIDMLEIQIGQAVSG---HPVWIRINPGFGHGHKKNTIGGENSKHGI-	102
<i>B. tabaci</i> Asia II 3 LysA	DVVS GGELKRV S----VAGGQARQTVFAGVGKTDDEIAAGLTAGVLMFNVESEELDAIVRVAQSKRIQAPVALRINPDVDPKTHRYISTGHKESKFGMD	181
<i>B. tabaci</i> LysA	IQRSLLAEKFKGSES-IKMIGIHMHIGSQITTTTAYSSAAAKSVDIITRLREMCHPTDFWNMGGGFGISYDGKTSPTS---ISEFA---AAVVPSTRK--	272
<i>Ca. Portiera aleyrodidarum</i> TV LysA	IDKA-EEAYFYANSLTNIKVIGIDFHIGSQILNLNLFLEALDNIILLIKKLYKKIKILNILDIGGGLGVNYK-KINFYKFLIKKYF---TTL CERILANI	270
<i>Ca. Hamiltonella defensa</i> LysA-1	LDKL--ASLKKQ----CHFLGFHFL-SGY-CKTRIEAIRELHPMITRAHSLGIKAQLMNIGGGLPVQYVDQHKYQTY-LKEHSPADYDHQKPPLSFY	281
<i>Ca. Hamiltonella defensa</i> LysA-2	WHEDLPKALEKIAQYQ-LKLIGFHMHIGSGV-NYQHLKKVCDAIVEQVIKLNQD---ISAISAGGGLSVPYKKGEKEVD--IEHYYNLWHRARKKISKHF	195
<i>B. tabaci</i> Asia II 3 LysA	IQRSLLAEKFKGSES-IKMIGIHMHIGSQITTTTAYSSAAAKSVDIITRLREMCHPTDFWNMGGGFGISYDGKTSPTS---ISEFA---AAVVPSTRK--	272
<i>B. tabaci</i> LysA	-TGCRIVMEP--GRVIVGNAGILISRVIYTKVSGEKRFLIQDAAMNDLIRPSLYESFHGIWPKVP-AGFPSPPDDETSR-INGTKLCDVVGPFVCSGD	367
<i>Ca. Portiera aleyrodidarum</i> TV LysA	-HNIEIILEP--GRSILANTGVLLTSVEIIKKTKIKNEAIVDAGMNDIFIRPAFYNAWHNIEV-----LINKVK-YYKKLFYDIVGPICESD	354
<i>Ca. Hamiltonella defensa</i> LysA-1	PYEGELNGAQWLSRLLLSHYKADFSLADYLNQKLTALALEPGRSIVDQCAITVR-VTRVKLLRRDRWVIFVEGSSSACETWFSSEF--LVDPIILAEQ	378
<i>Ca. Hamiltonella defensa</i> LysA-2	GHPVNIETEP--GRFLVAESGVLIQIRAIKNMGSQHYIIVDAGFNDLMRPAMYGSYHRISLL-----PADGRVSKK-HIKTV--VAGPICESGD	282
<i>B. tabaci</i> Asia II 3 LysA	-TGCRIVMEP--GRVIVGNAGILISRVIYTKVSGEKRFLIQDAAMNDLIRPSLYESFHGIWPKVP-AGFPSPPDDETSR-INGTKLCDVVGPFVCSGD	361
<i>B. tabaci</i> LysA	FLAQD-----RAIPPLNRGELIAIFSAGAYGMT-MASNYNSRPRPAELLVNGSGVVVARR-RETDDLIAEELNPLS	437
<i>Ca. Portiera aleyrodidarum</i> TV LysA	FLGKK-----RYINKLSQNDLIVHSVGAYGFV-MSSNYNTRKRPSELLVDKNQFLIRE-SDSLKSLCKNEYVNLF	424
<i>Ca. Hamiltonella defensa</i> LysA-1	KGPHRTCLSCQAFIAGHSCLDEDIISHRFIHPMLPQAGDFLVYSNTAGYQMDLLENRFHRHPIPHISLFDKQCA---	454
<i>Ca. Hamiltonella defensa</i> LysA-2	VFTQNQNACLETVYPPAFVDDYIFHNTGAYGAS-MSSNYNSRPLIPEVLLKNGEVQLIRR-RQTIEELISLEIF---	356
<i>B. tabaci</i> Asia II 3 LysA	-----	361

Fig. S2

E

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<i>B. tabaci</i> MEAM1 CM	-----MDCACASWIRNNVKVNIVIFEEVENRDLILNQKELST	37
<i>B. tabaci</i> Asia II 3 CM	-----	1
<i>Ca. Hamiltonella defensa</i> CM	-----	1
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs CM	MNKKFKPYIKYIGNIDYOILKLISHRAKLVSQIOLADDKONCSYNNGHEDRYFYSIKTSNKGPLSNKVLISKIFKSIVSACLKEKKKSQVAYLGPEGTFTO	100
<i>B. tabaci</i> MEAM1 CM	NSTWHKTGAKMGFIESALMVMVSLCLFV-----DVHPKSVAVCHPQTAEVCHPQTAEANAD---ASTGAMIILSLATTLNDRMEYMKIVAGDK	123
<i>B. tabaci</i> Asia II 3 CM	-----MGFIESALMAMA-SLCLFV-----DVHKSVA-----VCHPQTAEVCHPOT---AD---TC-G-----RFD-----GN-	50
<i>Ca. Hamiltonella defensa</i> CM	-----MSLIGINEIELLINQRFY-----YMEDIA-----AYKAEK-CLAIEDL---EQ---EK-----RIL-----RN-	46
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs CM	QAVLKVFCKSTKSTIPVKDVERTTENKIMNYGVVPVENSTEGIVNNTFDSFISSNLKIGGEIILSIHHHLLIDKONINKNIDKIYSHOOSFSOCRDLWLKNN	200
<i>B. tabaci</i> MEAM1 CM	YKKGKPVEDLPREKVMNSAVANASAEGLDPSNVRFPIQAQMDVAKDIQRTY--IAGWQVRPE-KWEPRALEEVR-EFTSADDAK-----ILRLSRQQL	213
<i>B. tabaci</i> Asia II 3 CM	YD--HPVPG--RD-----AEQS-DGVHERRGAG--QAQMDVAKDIQRTY--IAGWQAR--EVGA-EGSRGGQGAADDAK-----ILRLSRQQL	121
<i>Ca. Hamiltonella defensa</i> CM	-----AMLL-----AEQK--GITPNSIGSFSSALIHAAKLIQCRY--QSDWQKKSITKHPQNLQAMRYKLLQLNDSL-----IERVYQALI	119
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs CM	VPNAKKIAVASNAHASNLTOYKKNS-AAAGDLAASY-YSLLKLAKNTEDRINNYTRFLILSDKDVAFTGYDKTY-LMAYINNOIGSFYLLIEPFVRYNI	297
<i>B. tabaci</i> MEAM1 CM	ELGGFCEAYRAQ---IYRSLTAPHITDAHRKLLVD-TLFCVTLKQ-----	254
<i>B. tabaci</i> Asia II 3 CM	TLGGFCEAYRAQ---IYRSLTAPYITDEHRKLLVD-TLFCVKLKQ-----	162
<i>Ca. Hamiltonella defensa</i> CM	AGQKEKTTSGS---MIKMIHHPQLSETHKRKIIVT-ALQATHLIQ-----	160
<i>Ca. Portiera aleyrodidarum</i> BT-B-HRs CM	NILRLTTRPAPENKGVWNYIFLEUKGHRKSKLVEKTLLEETYRGAEKILGSFPEOLTTRI	359

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F

<i>B. tabaci</i> MEAM1 BioA	MNLAER--DRKI LWHPFTQERTAPFIPIAVKRAEGPTITLVDDRAYLDDLSSWWVNLHGHAHEKTAGATYEQSRLEHVIIFAGFTHEPAVTLCEKLRALLP	98
<i>Cardinium endosymbiont</i> cBtQ1 BioA	MPLKER--DCKV LWHPFTQAKTAEPLIAIKRGYGSYLYDTDDKPYLDLISSWWVNLHGHAHEGIAKAIYAQSLTLEHVIIFAGFTHEPAVQLCEKLOPLLP	98
<i>Ca. Hamiltonella defensa</i> BioA	MNKDDLDFDRHF IWHPHYTRMIDPLPCYPVKSAAQGVELILTDGRRLIDGMSSWWAAIHGYNCRELNQALHQQIEKMSHVMFGGITHSPAIDLCRQLIALTP	100
<i>Planococcus citri</i> BioA	MSILEK--DRSI IWHPFETOEKTAAPPILITKGKDSYLYDDKNNKYLDLVSSWWVNIHGHANDETSNATYNOCRKLEHVIIFAGFTHEPAVTLCDLSLTSLLP	98
<i>B. tabaci</i> MEAM1 BioA	QKLSKFFFSNDNGSTAVEVALKMSYQYWWNKDERDKTVFLSFEQAYHGDTFGAMSVG-VTSGFHDPTSRLLFFSVLTIPFFETWI--GDDQVERK-EIHALQ	194
<i>Cardinium endosymbiont</i> cBtQ1 BioA	G-FSKFFFSNDNGSTAVEVALKMAQQYWHNQGVKRTIFLSFDGGYHGDTFGAMSIG-VKSGFHTLFSDLFFSVLTIPFPATWD--GDEATQNK-EAYALE	193
<i>Ca. Hamiltonella defensa</i> BioA	DPLDCVELADSGSVSVEVALKMALQYWHAKG-ERRSKILSFRQGYHGDTFGALSVCDPENSMQALYQGYVAKNLFAPAPPAYQFSEYFFDAPWNNEEIQ	199
<i>Planococcus citri</i> BioA	SPLRKFFFSNDNGSTAVEVAMKMSYQWKNQO-YHKPLEVAEDGGYHGDTWGVMSVS-VKSGFHDAFEKVVEPVLYAPFPDTWL--EDDKVDEK-EANSII	193
<i>B. tabaci</i> MEAM1 BioA	ILERHLQADAHKIAALILEPLVQGASGMRMCRPEFVSRAVNLAHQYGILIIIFDEIMTGFGRTGSYFALEQVNFVPDFICVSKGLTGGFLPLAITATTDRI	294
<i>Cardinium endosymbiont</i> cBtQ1 BioA	VLASHLSTSCDAIVLVLEPLIQGANGMOMCRPAFVEQVHVLVRNYGILVIFDEVMTGFGRTGTIFYCFEQINIIIPDFICLAKGLTGGFLPLALTVTTEKV	293
<i>Ca. Hamiltonella defensa</i> BioA	AFSQIIEETNNTDIAAVILEPIVQAGGGMRIYHPAFLREVSALCERHQILLIADIEIATGFGRTGRLFACNYAAIAPDILCLGKALTGGYITLSATLCTREV	299
<i>Planococcus citri</i> BioA	VLROHLETNRNINSAIVLEPLVOGASGMRMCRASEIDKVTTLVREFDILVIFDEVMTGFGRTGTIFYFALDOTNAVPDFICLSKGIITGGFLPLSLTVTTOKI	293
<i>B. tabaci</i> MEAM1 BioA	YDAFLSEHNTKAFAGHGSYNTANPLGCAAGIASIELELTQPDIMAKLNRHILTHKKKELEKLSVAFTDIHRIKRVGTGTIAAFDI-PYAQL--LKPFLFKGLLL	391
<i>Cardinium endosymbiont</i> cBtQ1 BioA	YKVEWDDALNKSFAHGHGSYNTANPLGCAAAIASLDLLMEESTMQSIQAIHDAHTKAIVNLPVK----HR-RVTGTIAAFDL-ENPQT--FKRKCLEQGLLI	385
<i>Ca. Hamiltonella defensa</i> BioA	ANAISKKGAG-CFMHGPTFMANPLACAVANANLAILARHEWQPVKAIENQLWAEISPLSAI-----RASRYFGCTGVRRDRGD--RNEKSSRCGLIT	389
<i>Planococcus citri</i> BioA	YDSFLINDNEDKAFAGHGSYTGNEPVTCAAASVAFKILTDLKTKNNIASINTIHRNRINELKKNCKNVOHARITGTIAAFDVKENVOVKFKKEKCFEDGILI	393
<i>B. tabaci</i> MEAM1 BioA	RPLGNTITFLPPYCTSDLELEGAYKTVAETLRKSVGDNFGQGVN	434
<i>Cardinium endosymbiont</i> cBtQ1 BioA	RPLGNNAVYLLPPYSTTVSELEKAYEKTNNIIKII-----	419
<i>Ca. Hamiltonella defensa</i> BioA	T-----	390
<i>Planococcus citri</i> BioA	RPINRSVYVILPPYCTADEINVAVDVETIKCTNEE-----	427

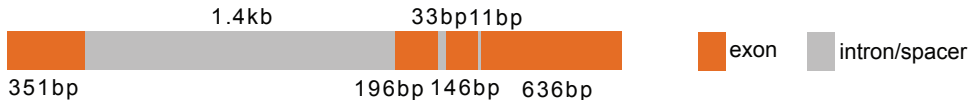
Fig. S2

G

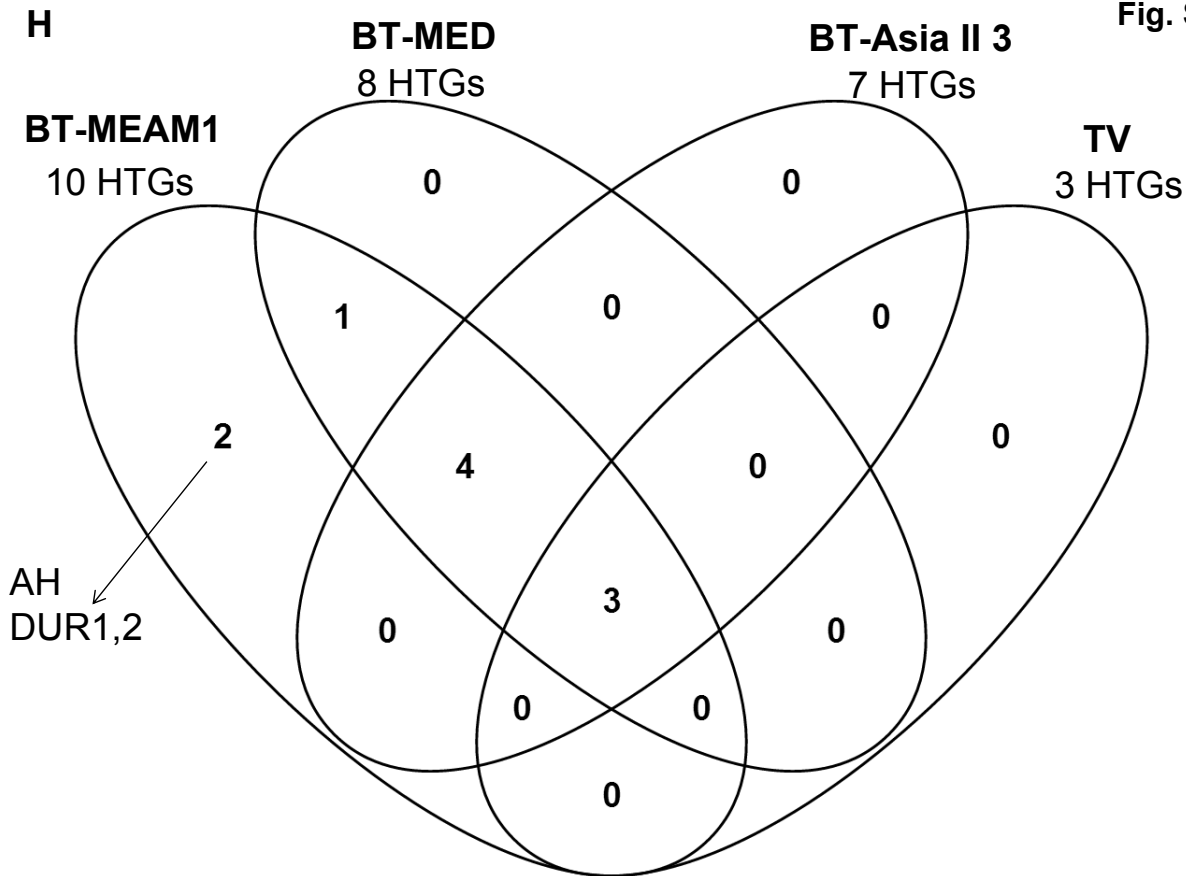
(1)

<i>B. tabaci</i> MEAM1 BioB	MALR--WSLEEA LRVFKLPADLMYQAQSTHRANFNPNEQISTLLSIKTGACPENCSCYCPQSAYYKTEIKKEPLMDLAEVVAAAKAAKEGGSTRFCMGA	98
<i>Ca. Hamiltonella defensa</i> BioB	MPKQVTWTLQKQDAFFEQELLELLFTAQOIHRQHFDPQVQISTLLSIKTGACPENCCKYCPQSARMRTGLKSEKLMOVEQVLASARQAKAAGATRFMGA	100
<i>Planococcus citri</i> BioB	MSGK--WSVVQASKIFNLISLPFLFYKAQTVHRENFDAETIQISTLLSIKTGKCPENCSCYCPQSIHHKTNIKSEPLMDISKVIEAAKAAKANGSTRFCMGA	98
<i>B. tabaci</i> Asia II 3 BioB	MALR--WSLEEA LRVFKLPADLMYQAQSTHRANFNPNEQISTLLSIKTGACPENCSCYCPQSAYYKTEIKKEPLMDLAEVVAAAKAAKEGGSTRFCMGA	98
<i>B. tabaci</i> MEAM1 BioB	AWRGPTDRNLPLVCDMVKEVKKLGLGETCVTLGLLKDRHAVQLKEAGLDFYNHNIDTSPEYYKKIISTRTFEDRIRTLHVNRNAGIKVCCGGILGMGENTE	198
<i>Ca. Hamiltonella defensa</i> BioB	AWKNPHTRDMBYLEQMVKGVKAMGMETCMVLTGLTLDKTDADRLANAGLDYYNHNIDTSPEFYSSVITTRTYQERLDTLDEVROAGIKVCSGGIIGMGESPK	200
<i>Planococcus citri</i> BioB	AWRGPTSKTLPQVCEMVKEVKKLGMETCVTLGLLKEEHAVALKDAGLDYYNHNIDTSPEYYEKIITTRTFENRIQTLHVNRNADIKVCCGGILGMGETTE	198
<i>B. tabaci</i> Asia II 3 BioB	AWRGPTDRNLPLVCDMVKEVKKLGLGETCVTLGLLKDRHAVQLKEAGLDFYNHNIDTSPEYYKKIISTRTFEDRIRTLHVNRNAGIKVCCGGILGMGENTE	198
<i>B. tabaci</i> MEAM1 BioB	DRIKMLLVLANLEPPESVPINOLIPIPGTPLADADPVEGTDVFRTIALTRVMMPKAYIRLSAGRENMSEEMQTLCLAGVNSIFYGEKLLTAKNFQPSK	298
<i>Ca. Hamiltonella defensa</i> BioB	DRAGLLVQLANLSPPPESIPINMLVKVKGTFFEHKEDLDVDFIRTIIVARIIMPEASYVRLSAGREKNEQTQALCFMAGANSIFYGSKLLTTSNPSEDK	300
<i>Planococcus citri</i> BioB	DRIKMLLVLANLETPESVPINOLMKIPGTPLEDDVDIDPTEFVRTIGVARVMMPKSYIRLSAGRENMSEELQALCFMAGVNSIFYGEKLLTAKNFQPSK	298
<i>B. tabaci</i> Asia II 3 BioB	DRIKMLL-----GTDFVRTIALTRVMMPKAYIRLSAGRENMSEEMQTLCLAGVNSIFYGEKLLTAKNFQPSK	266
<i>B. tabaci</i> MEAM1 BioB	DDQLLSKLGF-----KMEIDETPASSQCKEAAIG-----	328
<i>Ca. Hamiltonella defensa</i> BioB	DVQLFRQLGLNPQWTQVKTAPPEKIFVNLSENSSLFAQNQVEVEQKDEASSFFYNAAI	358
<i>Planococcus citri</i> BioB	DDILLDKLGY-----KASL-----ASA-----	316
<i>B. tabaci</i> Asia II 3 BioB	DDRLLSKLGF-----KMEIDETPANSQCKEAAIG-----	296

(2)



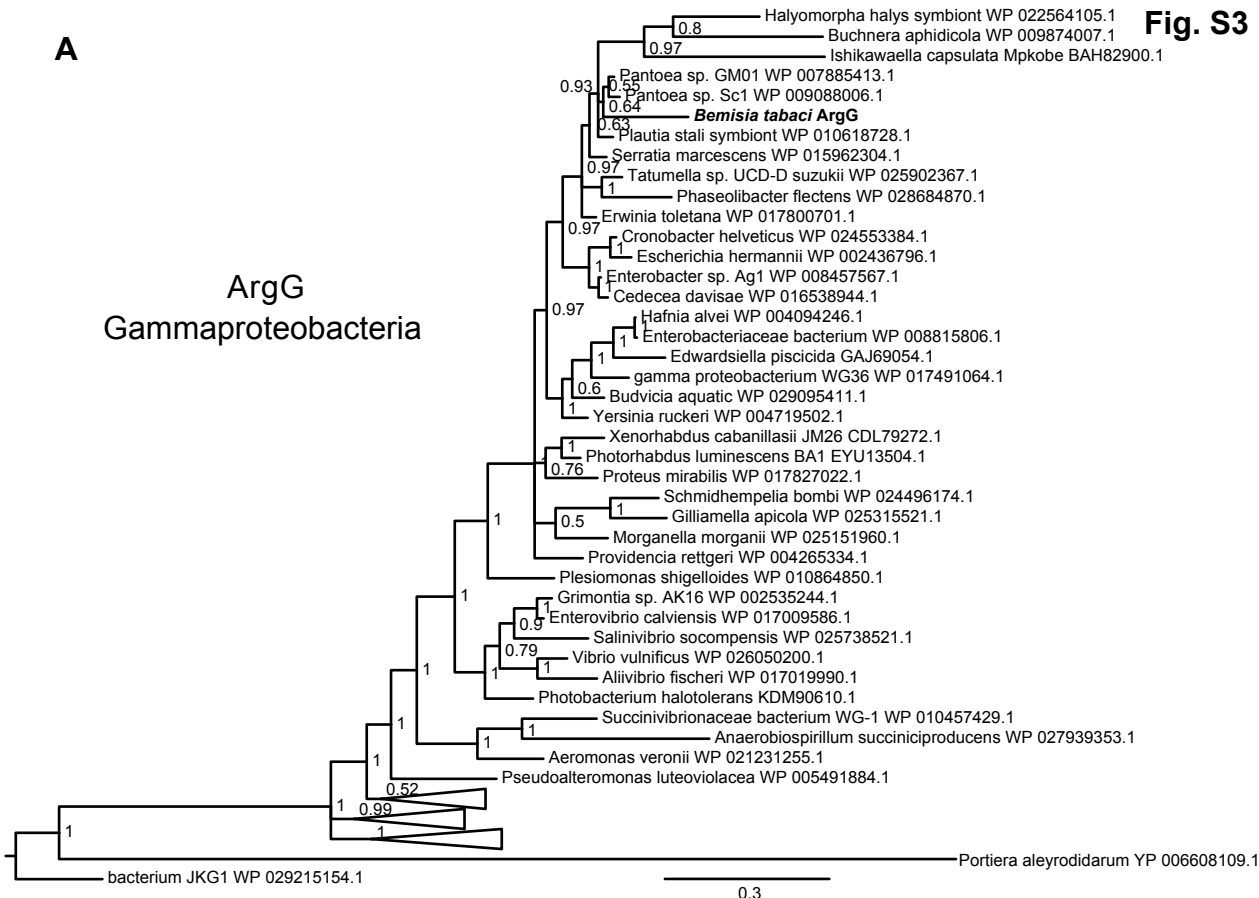
**Fig. S2**





**A****Fig. S3**

# ArgG Gammaproteobacteria

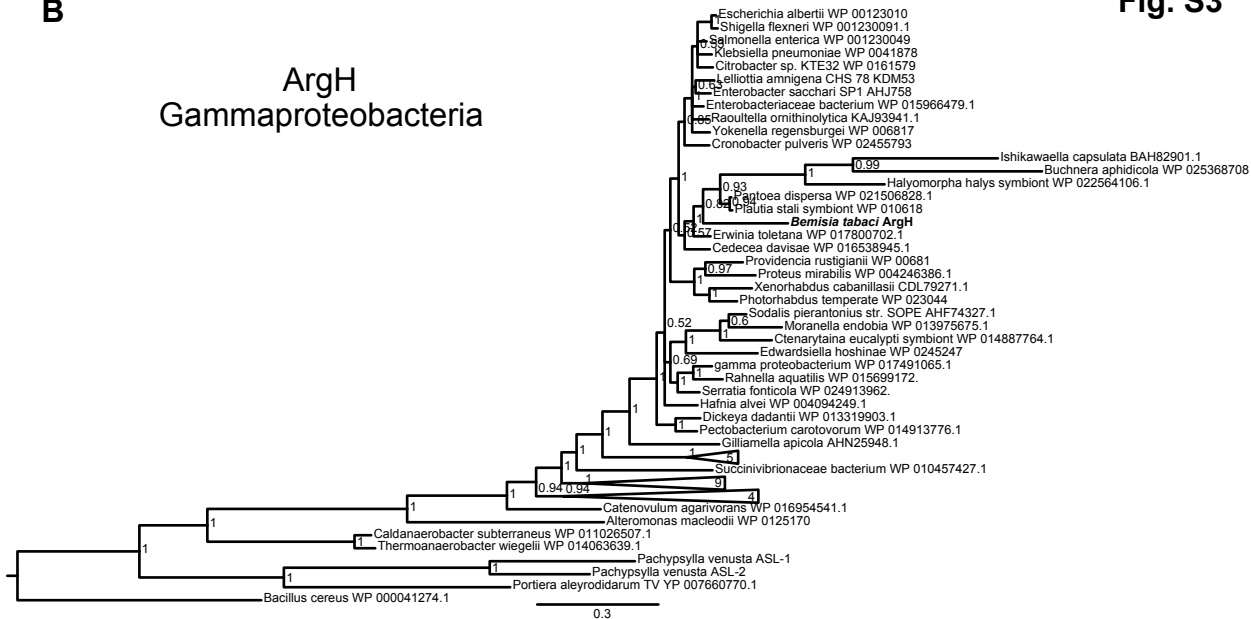


0.3

B

Fig. S3

# ArgH Gammaproteobacteria



C

Fig. S3

DapB  
Alphaproteobacteria

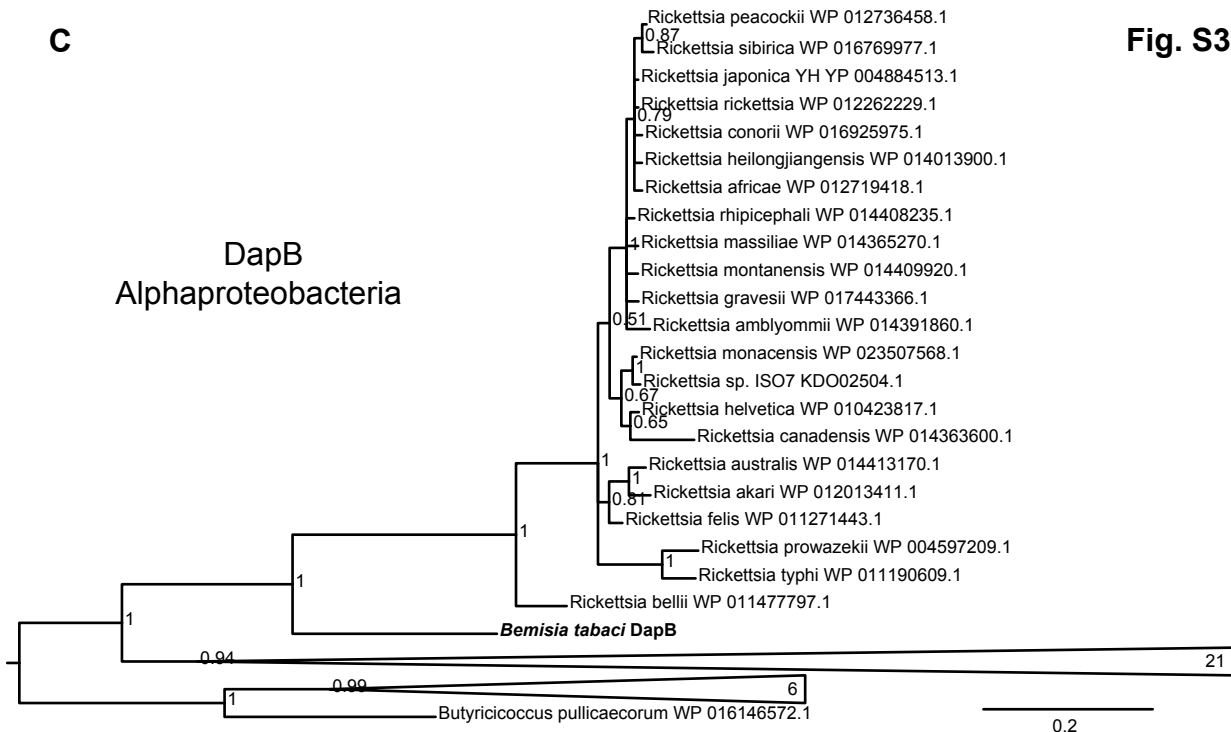
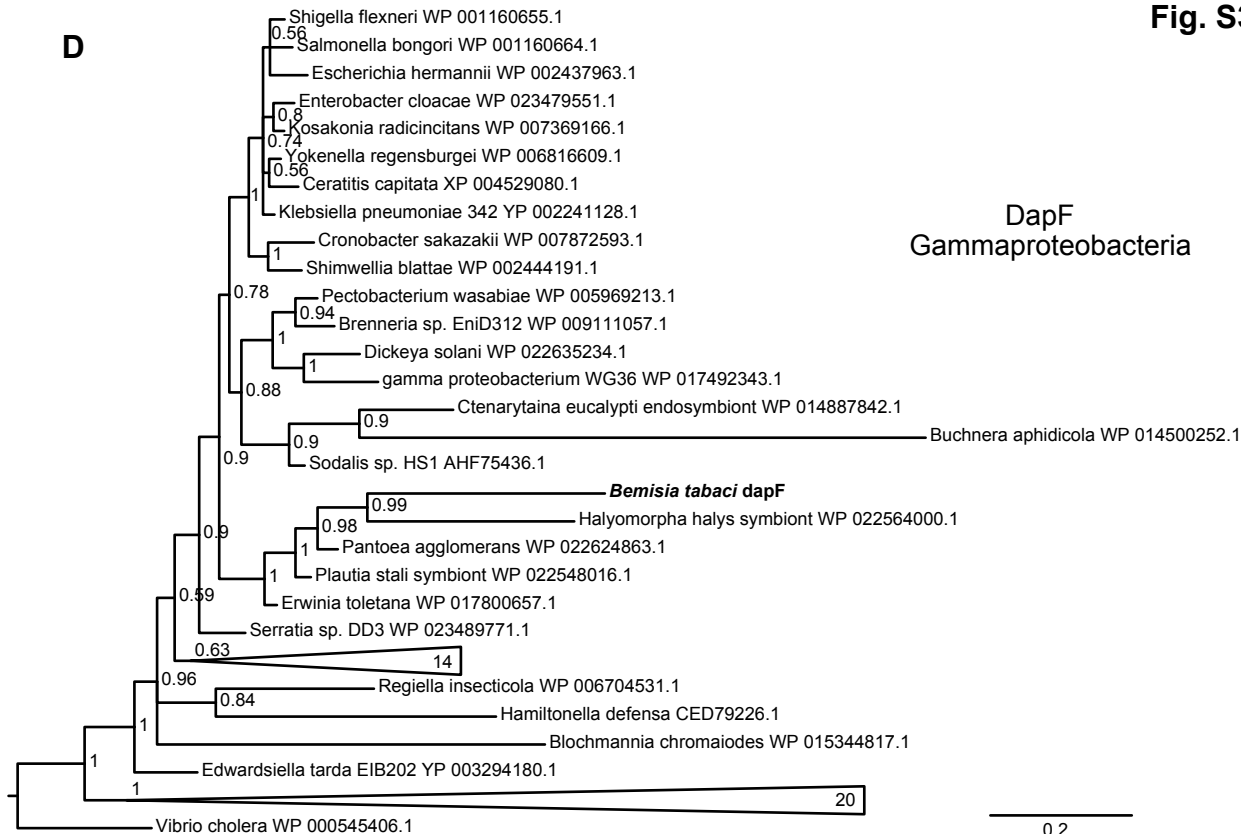


Fig. S3

D



0.2

E

# LysA Planctomycetes

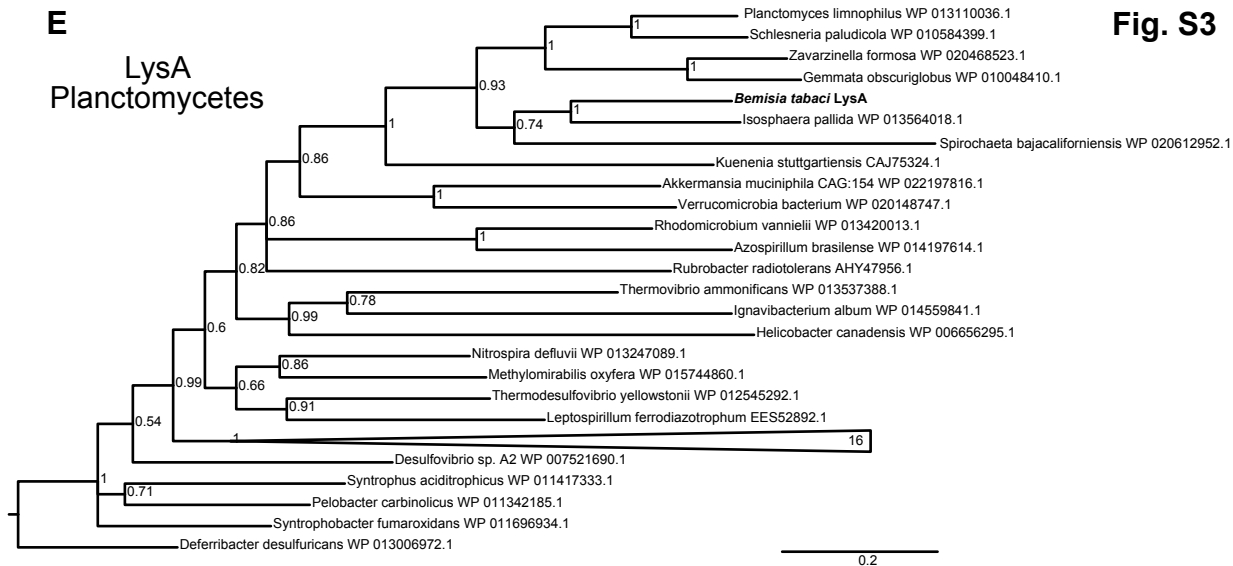


Fig. S3

Fig. S3

F

CM  
Gammaproteobacteria

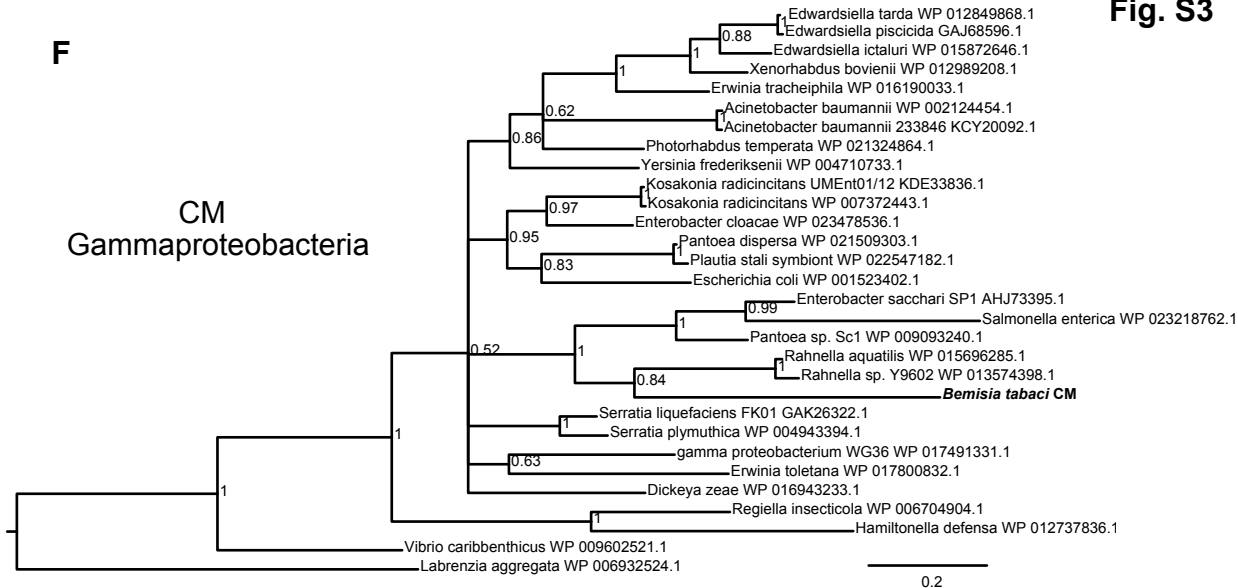
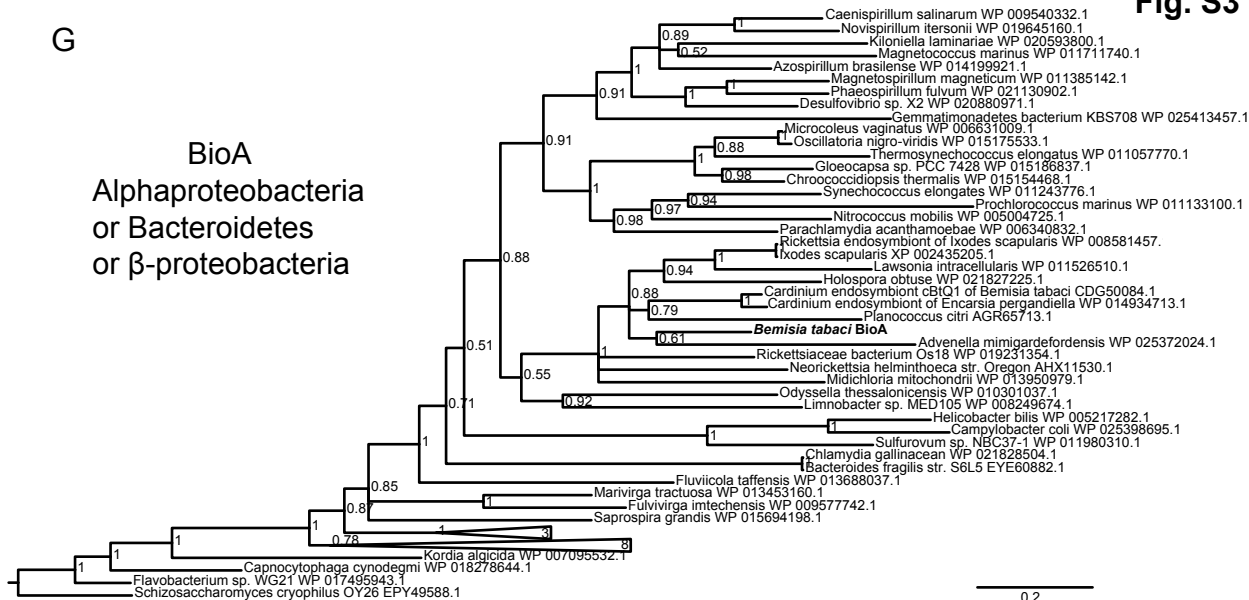


Fig. S3

G

BioA

Alphaproteobacteria  
or Bacteroidetes  
or  $\beta$ -proteobacteria



0.2

Fig. S3

H

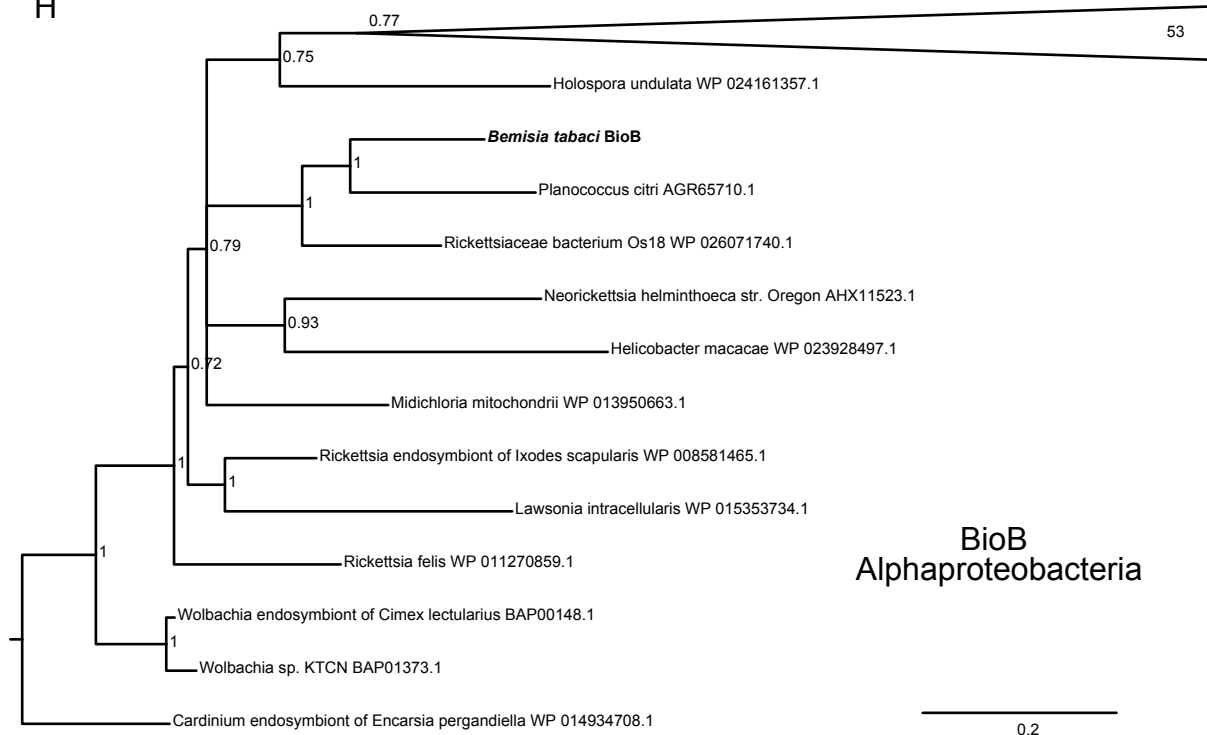
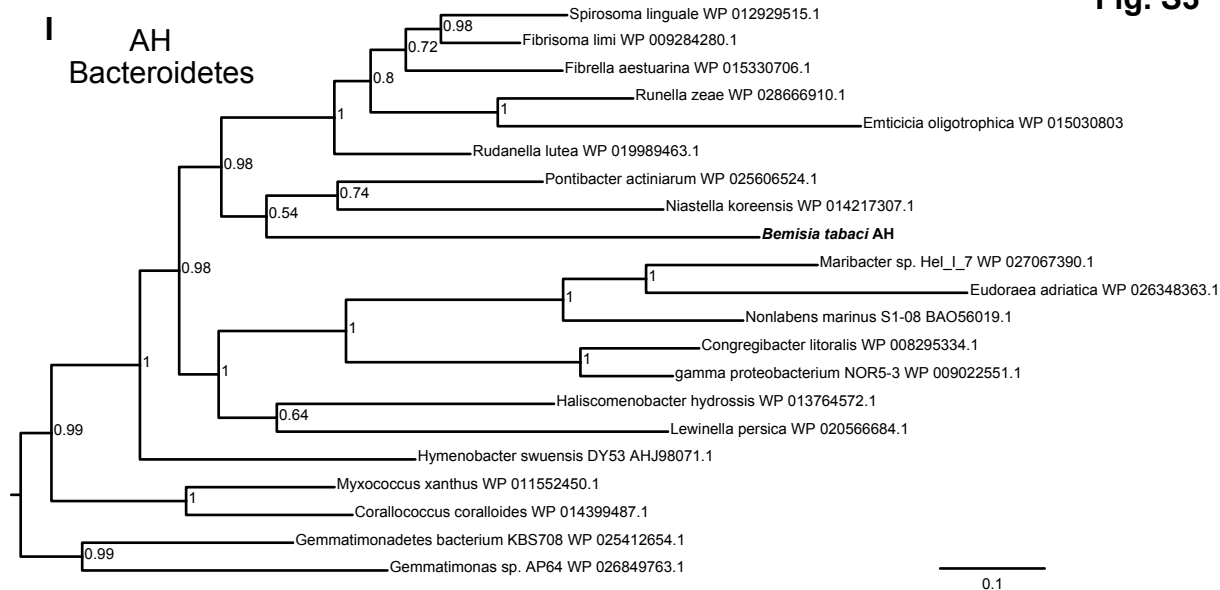




Fig. S3



J

Fig. S3

DUR1,2  
Gammaproteobacteria

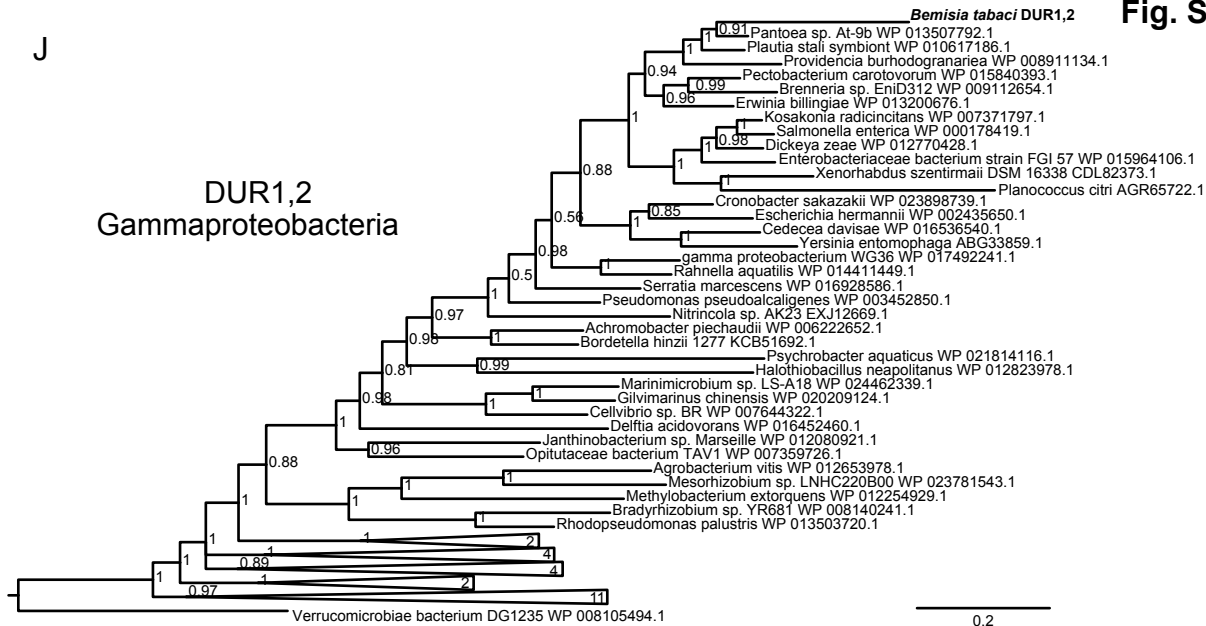
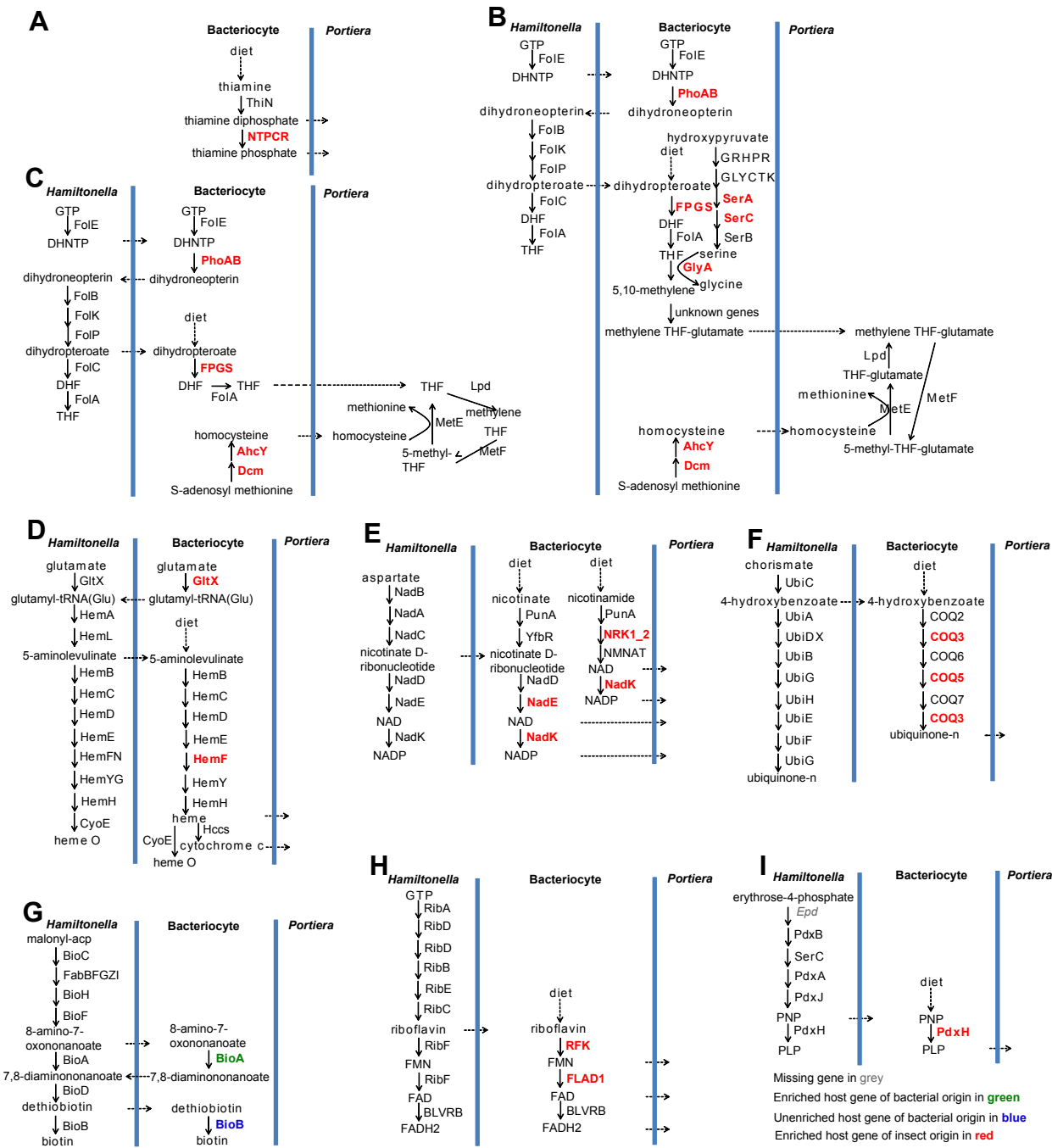
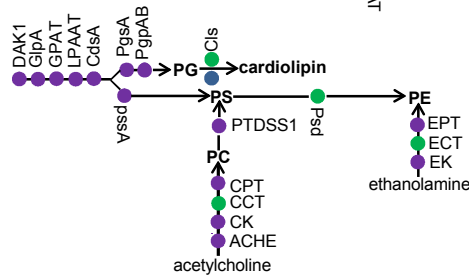
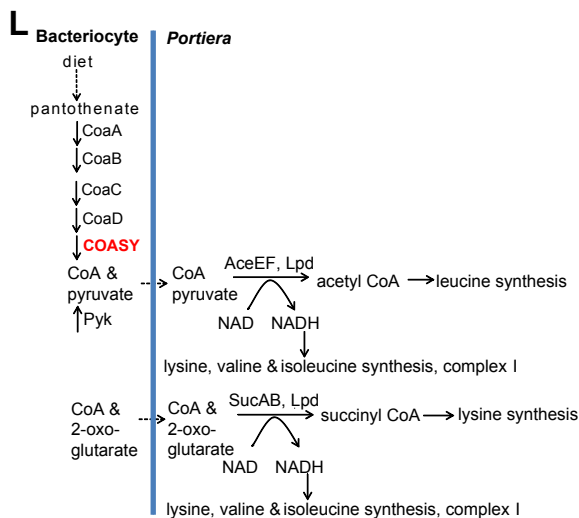
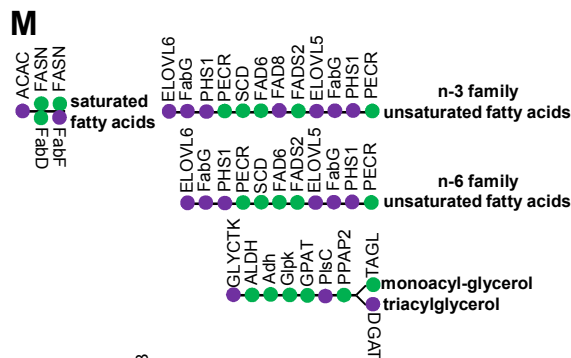
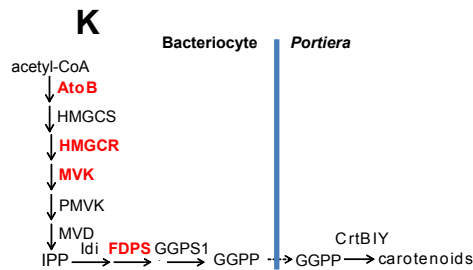
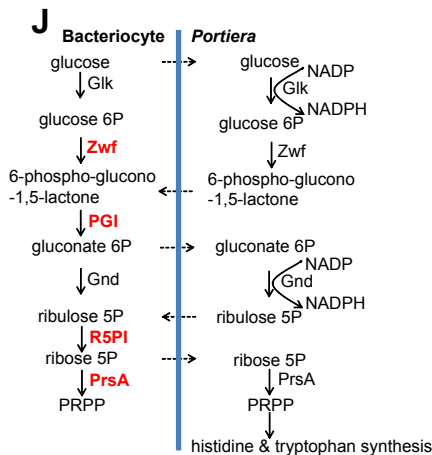


Fig. S4



**Fig. S4**



Portiera

Unenriched host gene of insect origin

Enriched host gene of insect origin in **red** or **green**