

List of supplementary tables and figures.

Table S1 – Strains sequenced and assembly information (n=72)

Table S2 – Genetic clusters obtained using BAPS

Table S3 – Genes commonly found to be under positive selection in the three subspecies (n=14)

Table S4 - Recombining genes in *X. fastidiosa* subsp. *pauca* strains 9a5c and U24D (Citrus)

Table S5 – Recombination genes for *X. fastidiosa* 32 (Coffee)

Table S6 - Genes found to be under selection in each subspecies

Table S7 – Recombining genes for each *X. fastidiosa* subspecies

Table S8 – Genes found in the accessory genome of each subspecies

Figure S1 - Phylogeny of *X. fastidiosa* strains (n=72) and pan-genome visualization

Figure S2 - Detection of temporal signal in the dataset

Figure S3 - Rate comparison amongst subspecies. The boxplot (A) was constructed by merging the rate of evolution of each branch (internal and external) of the *X. fastidiosa* subsp. *fastidiosa*, *pauca* and *multiplex* clades together (obtained through rate-dating) as illustrated by the colored frames (B)

Figure S4 - Comparison between clonalFrameML and FastGEAR. (A) ClonalFrameML output, (B) FastGEAR output, (C) comparison between the genes found to be recombining between the two algorithms that were mapped to the *X. fastidiosa* reference genome

Table S1 – Strains sequenced and assembly information (n=72). Strain names in parentheses represent synonyms.

Name	N50	L50	Total length	Country	Host	Subspecies	Isolation date	Accession
CO33	176,135	6	2,681,926	Italy	<i>Coffea arabica</i>	?	2015	SAMN04100274
MUL0034	2,642,186	1	2,666,577	USA	<i>Morus alba</i>	<i>morus</i>	2003	SAMN03081485
Mul-MD	134,146	6	2,520,555	USA	<i>Morus alba</i>	<i>morus</i>	2011	SAMN02630185
Ann-1	44,355	22	2,729,755	USA	<i>Nerium oleander</i>	<i>sandyi</i>		SAMN03081476
Xf_ATCC_35879	500,648	2	2,522,328	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	1987	SAMN02997312
DSM10026	89,916	11	2,431,652	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	1987	SAMN05660380
EB92-1	44,355	22	2,729,755	USA	<i>Sambucus</i> sp.	<i>fastidiosa</i>	1992	SAMN02471770
SLO	97,628	8	2,450,910	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	1994	SAMN09941414
STL	99,345	8	2,424,461	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	1998	SAMN09941416
Temecula1	2,519,802	1	2,521,148	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	1998	SAMN02603844
Baja	97,614	9	2,466,363	Mexico	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2001	SAMN09941403
M23	2,535,690	1	2,535,690	USA	<i>Prunus dulcis</i>	<i>fastidiosa</i>	2003	SAMN02598408
Stag's Leap	559,515	2	2,510,798	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2005	SAMN04485942
GB514	2,491,203	1	2,517,383	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2006	SAMN02603754
CFBP8073	67,596	13	2,582,150	Mexico	<i>Coffea canephora</i>	<i>fastidiosa</i>	2012	SAMN04075659
Napa1	89,536	9	2,458,708	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2015	SAMN09941406
RACD01AG	97,645	8	2,512,383	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941411
RACD01AH	99,072	8	2,452,920	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941412
RACD01AE	99,072	9	2,467,249	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941409
RACD01AI	97,646	8	2,470,105	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941413
RACD01AF	102,728	8	2,469,725	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941410
RACD01AC	99,072	9	2,463,313	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941408
CV23	97,316	9	2,448,559	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2012	SAMN09941404
maple5	97,637	9	2,450,181	USA	<i>Acer</i> sp.	<i>fastidiosa</i>	2001	SAMN09941405

Xf43	408,369	3	2,555,687	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2011	SAMN09941432
Xf44	554,557	3	2550801	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>		SAMN09941433
Xf50 (WM1-1)	165,74	6	2,492,684	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2009	SAMN09941434
Xf51 (CCPM1)	90,053	9	2,462,048	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>	2010	SAMN09941435
Xf99	539,544	2	2,572,129	USA	<i>Vitis vinifera</i>	<i>fastidiosa</i>		SAMN09941436
Xf ATCC 35871	106,692	7	2,416,255	USA	<i>Prunus domestica</i>	<i>multiplex</i>	1983	SAMN02441559
Xf40 (ATCC_700964)	1,902,928	1	2,439,135	USA	<i>Vitis vinifera</i>	<i>multiplex</i>	1997	SAMN09941430
Sy-VA	119,241	7	2,475,880	USA	<i>Platanus occidentalis</i>	<i>multiplex</i>	2002	SAMN02709772
M12	2,475,130	1	2,475,130	USA	<i>Prunus dulcis</i>	<i>multiplex</i>	2003	SAMN02598402
Griffin-1	74,017	12	2,387,314	USA	<i>Quercus rubra</i>	<i>multiplex</i>	2006	SAMN02472062
Xf10	239,591	4	2,658,817	USA	<i>Olea europea</i>	<i>multiplex</i>	2011	SAMN09941418
Xf11	262,018	4	2,665,076	USA	<i>Olea europea</i>	<i>multiplex</i>	2011	SAMN09941419
CFBP8416	113,891	6	2,466,748	France	<i>Polygala myrtifolia</i>	<i>multiplex</i>	2015	SAMN04546448
CFBP8417	118,419	8	2,504,981	France	<i>Spartium junceum</i>	<i>multiplex</i>	2015	SAMN04546482
CFBP8418	96,035	9	2,513,969	France	<i>Spartium junceum</i>	<i>multiplex</i>	2015	SAMN04546487
polygala	90937	9	2,645,094	USA	<i>Polygala myrtifolia</i>	<i>multiplex</i>	2016	SAMN09941407
Dixon	201,792	4	2,622,328	USA	<i>Prunus dulcis</i>	<i>multiplex</i>	2002	SAMN02441075
Xf20 (BH-Elm)	235,14	4	2507844	USA	<i>Ulmus</i> sp.	<i>multiplex</i>	2010	SAMN09941420
Xf21 (RBCF119)	210,272	5	2617044	USA	<i>Carya illinoensis</i>	<i>multiplex</i>	2012	SAMN09941421
Xf22 (AlmaEM3)	95,305	9	2472098	USA	<i>Vaccinium</i> sp.	<i>multiplex</i>	2011	PUIY00000000
Xf23 (BBI-64)	197,029	4	2,516,923	USA	<i>Vaccinium</i> sp.	<i>multiplex</i>	2009	PUJA00000000
Xf24 (BB08-1)	509,227	3	2,533,721	USA	<i>Vaccinium</i> sp.	<i>multiplex</i>	2008	PUIZ00000000
Xf25 (L95-1)	100,59	7	2,702,760	USA	<i>Lupinus</i> sp.	<i>multiplex</i>	1995	SAMN09941425
Xf26	113,305	7	2,833,668	USA	<i>Ambrosia</i> sp.	<i>multiplex</i>		SAMN09941426
Xf27	139,761	6	2,571,357	USA	<i>Iva annua</i>	<i>multiplex</i>		SAMN09941427
Xf28	93,473	9	2,603,215	USA	<i>Helianthus</i> sp.	<i>multiplex</i>		SAMN09941428
Xf29	284,274	4	2,823,167	USA	<i>Platanus</i> sp.	<i>multiplex</i>		SAMN09941429
Xf41	284,274	4	2,823,167	USA	<i>Prunus domestica</i>	<i>multiplex</i>		SAMN09941430

CFBP8072	87,332	11	2,496,662	Ecuador	<i>Coffea arabica</i>	<i>pauca</i>	2012	SAMN04075656
9a5c	2,679,306	1	2,731,750	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1992	SAMN02603773
11399	183,019	6	2,736,060	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1996	SAMN02786837
J1a12	2,519,802	1	2,867,237	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1998	SAMN03166204
6c	264,629	19	2,603,975	Brazil	<i>Coffea arabica</i>	<i>pauca</i>	1999	SAMN02471371
CVC0251	135,651	7	2,740,246	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1999	SAMN03862120
CVC0256	116,891	7	2,702,144	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1999	SAMN03862121
U24D	2,681,334	1	2,681,334	Brazil	<i>Citrus sinensis</i>	<i>pauca</i>	1998	SAMN03154423
32	104,769	9	2,607,546	Brazil	<i>Coffea arabica</i>	<i>pauca</i>	2002	SAMN02471372
COF0324	100,091	9	2,772,556	Brazil	<i>Coffea sp.</i>	<i>pauca</i>	2006	SAMN03862122
Pr8x	2,666,242	1	2,666,242	Brazil	<i>Prunus domestica</i>	<i>pauca</i>	2008	SAMN03166213
COF0407	56,951	15	2,538,474	Costa Rica	<i>Coffea sp.</i>	<i>pauca</i>	2009	SAMN03862125
OLS0478	246,999	4	2,555,411	Costa Rica	<i>Nerium oleander</i>	<i>pauca</i>	2011	SAMN03862124
De_donno	2,508,465	1	2,508,465	Italy	<i>Olea europaea</i>	<i>pauca</i>	2014	SAMN06765826
CoDiRO	375,307	3	2,542,932	Italy	<i>Olea europaea</i>	<i>pauca</i>	2014	SAMN03247589
OLS0479	68,456	11	2,539,963	Costa Rica	<i>Nerium oleander</i>	<i>pauca</i>	2015	SAMN03862123
509	135,076	6	2,524,895	Italy	<i>Olea europaea</i>	<i>pauca</i>	2016	SAMN09941401
sq	169,317	5	2,526,020	Italy	<i>Olea europaea</i>	<i>pauca</i>	2016	SAMN09941415
w2	2,508,465	1	2,508,465	Italy	<i>Olea europaea</i>	<i>pauca</i>	2016	SAMN09941417
1129	168,009	6	2,621,148	Italy	<i>Olea europaea</i>	<i>pauca</i>	2016	SAMN09941402

Table S2 – Strain genetic assignments to various clusters obtained using BAPS.

BAPS	No Recombination		With Recombination		Subspecies
	Lineage	Cluster	Lineage	Cluster	
Ann-1	1	1	3	1	<i>Xf. sandyi</i>
CO33	1	1	3	1	
Mul-MD	1	1	3	1	<i>Xf. morus</i>
MUL0034	1	1	3	1	<i>Xf. morus</i>
32	2	2	1	2	<i>Xf. pauca</i>
509	2	2	1	3	<i>Xf. pauca</i>
1129	2	2	1	3	<i>Xf. pauca</i>
11399	2	2	1	2	<i>Xf. pauca</i>
6c	2	2	1	2	<i>Xf. pauca</i>
9a5c	2	2	1	2	<i>Xf. pauca</i>
CFBP8072	2	2	1	3	<i>Xf. pauca</i>
CoDiRO	2	2	1	3	<i>Xf. pauca</i>
COF0324	2	2	1	2	<i>Xf. pauca</i>
COF0407	2	2	1	3	<i>Xf. pauca</i>
CVC0251	2	2	1	2	<i>Xf. pauca</i>
CVC0256	2	2	1	2	<i>Xf. pauca</i>
De donno	2	2	1	3	<i>Xf. pauca</i>
J1a12	2	2	1	2	<i>Xf. pauca</i>
OLS0478	2	2	1	3	<i>Xf. pauca</i>
OLS0479	2	2	1	3	<i>Xf. pauca</i>
Pr8x	2	2	1	2	<i>Xf. pauca</i>
sq	2	2	1	3	<i>Xf. pauca</i>
U24D	2	2	1	2	<i>Xf. pauca</i>
w2	2	2	1	3	<i>Xf. pauca</i>
CFBP8416	3	3	2	4	<i>Xf. multiplex</i>
CFBP8417	3	3	2	4	<i>Xf. multiplex</i>
CFBP8418	3	3	2	4	<i>Xf. multiplex</i>
Dixon	3	3	2	4	<i>Xf. multiplex</i>
Griffin1	3	3	2	4	<i>Xf. multiplex</i>
M12	3	3	2	4	<i>Xf. multiplex</i>
polygala	3	3	2	4	<i>Xf. multiplex</i>
Sy-VA	3	3	2	4	<i>Xf. multiplex</i>
Xf ATCC 35871	3	3	2	4	<i>Xf. multiplex</i>
Xf10	3	3	2	4	<i>Xf. multiplex</i>
Xf11	3	3	2	4	<i>Xf. multiplex</i>
Xf20	3	3	2	4	<i>Xf. multiplex</i>
Xf21	3	3	2	4	<i>Xf. multiplex</i>
Xf22	3	3	2	4	<i>Xf. multiplex</i>
Xf23	3	3	2	4	<i>Xf. multiplex</i>
Xf24	3	3	2	4	<i>Xf. multiplex</i>
Xf25	3	3	2	4	<i>Xf. multiplex</i>
Xf26	3	3	2	4	<i>Xf. multiplex</i>
Xf27	3	3	2	4	<i>Xf. multiplex</i>
Xf28	3	3	2	4	<i>Xf. multiplex</i>
Xf29	3	3	2	4	<i>Xf. multiplex</i>
Xf40	3	3	2	4	<i>Xf. multiplex</i>

Xf41	3	3	2	4	<i>Xf. multiplex</i>
Baja	4	4	3	5	<i>Xf. fastidiosa</i>
CFBP8073	4	4	3	5	<i>Xf. fastidiosa</i>
CV23	4	4	3	5	<i>Xf. fastidiosa</i>
DSM10026	4	4	3	5	<i>Xf. fastidiosa</i>
EB92_1	4	4	3	5	<i>Xf. fastidiosa</i>
GB514	4	4	3	5	<i>Xf. fastidiosa</i>
M23	4	4	3	5	<i>Xf. fastidiosa</i>
maple5	4	4	3	5	<i>Xf. fastidiosa</i>
Napa1	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AC	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AE	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AF	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AG	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AH	4	4	3	5	<i>Xf. fastidiosa</i>
RACD01AI	4	4	3	5	<i>Xf. fastidiosa</i>
SLO	4	4	3	5	<i>Xf. fastidiosa</i>
Stag's_Leap	4	4	3	5	<i>Xf. fastidiosa</i>
STL	4	4	3	5	<i>Xf. fastidiosa</i>
Temecula1	4	4	3	5	<i>Xf. fastidiosa</i>
Xf ATCC 35879	4	4	3	5	<i>Xf. fastidiosa</i>
Xf43	4	4	3	5	<i>Xf. fastidiosa</i>
Xf44	4	4	3	5	<i>Xf. fastidiosa</i>
Xf50	4	4	3	5	<i>Xf. fastidiosa</i>
Xf51	4	4	3	5	<i>Xf. fastidiosa</i>
Xf99	4	4	3	5	<i>Xf. fastidiosa</i>

Table S3 – Genes commonly found to be under positive selection in the three subspecies, namely *fastidiosa*, *multiplex* and *pauca* (n=14).

Gene Name	Description	Length	GO IDs
<i>pilY1_2</i>	pilus tip-associated	1219	F:GO:0046872; C:GO:0009289
PD_1130	hypothetical protein	69	
PD_1506	hemolysin-type calcium binding	1562	F:GO:0005509; C:GO:0016021; C:GO:0005576; P:GO:0009405
<i>frpC</i>	peptidase M23	999	F:GO:0005509
PD_1721	DUF1566 domain-containing	156	
PD_1731	hypothetical protein	79	
PD_1671	GGDEF domain-containing response regulator	566	P:GO:0000160; C:GO:0005622
PD_1100	addiction module antitoxin	93	
PD_1128	DUF1566 domain-containing	154	
PD_1187	DUF3277 domain-containing	145	
PD_1593	hypothetical protein	142	C:GO:0016021
PD_1285	filamentous hemagglutinin N-terminal domain-containing	3698	
PD_1249	hemagglutinin	91	
<i>pspA_3</i>	filamentous hemagglutinin N-terminal domain-containing	3377	

Table S4 - Recombining genes in subsp. *pauca* strains 9a5c and U24D (Citrus)

SeqName	Cluster of origin	Description	Length	GO IDs
XF_0260	1	phosphomannomutase	34473	F:GO:0000287; P:GO:0005975; F:GO:0016868
XF_1844	1	ammonia channel	41013	F:GO:0008519; P:GO:0072488; C:GO:0016021
XF_1087	1	cardiolipin synthase	163683	F:GO:0003824
XF_1479	1	oligopeptidase B	221074	P:GO:0006508; F:GO:0004252; F:GO:0004177; F:GO:0070008
dnaE	1	DNA polymerase III subunit alpha	251908	F:GO:0003677; F:GO:0008408; P:GO:0090305; F:GO:0003887; C:GO:0005737; P:GO:0006260; P:GO:0071897
XF_2551	1	peptidase	268870	P:GO:0006508; C:GO:0016021; F:GO:0008236
XF_2708	1	cellulase	288633	P:GO:0005975; F:GO:0004553
XF_2544	1	type IV-A pilus assembly ATPase	301513	F:GO:0005524; P:GO:0009297; P:GO:0015031; F:GO:0008565
XF_0287	1	long-chain fatty acid-- ligase	327270	F:GO:0003824; P:GO:0008152
ffh	1		333580	
glnS	1	glutamine--tRNA ligase	404597	F:GO:0005524; C:GO:0005737; F:GO:0004819; P:GO:0006424; P:GO:0006425
XF_0029	1	type IV pilus modification	429829	C:GO:0016021
XF_0588	1	DUF2066 domain-containing	438469	
XF_2118	1	hypothetical protein	458781	
XF_1957	1	energy transducer	459791	C:GO:0016021; P:GO:0006810
XF_1486	1	DUF2252 domain-containing	476003	
XF_2208	1	amino acid permease	563583	C:GO:0016021; F:GO:0015171; P:GO:0003333
XF_2366	1	polysaccharide biosynthesis	650043	C:GO:0016021
XF_2367	1	undecaprenyl-phosphate glucose phosphotransferase	744154	C:GO:0016021
hisA	1	1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase	766813	C:GO:0005737; F:GO:0003949; P:GO:0000105
hisD	1	histidinol dehydrogenase	769571	F:GO:0008270; F:GO:0051287; P:GO:0055114; P:GO:0000105; F:GO:0004399
hisI	1	bifunctional phosphoribosyl-AMP cyclohydrolase phosphoribosyl-ATP diphosphatase	772371	F:GO:0005524; F:GO:0004636; F:GO:0004635; C:GO:0005737; P:GO:0000105
XF_2739	1	DEAD DEAH box helicase	793965	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; P:GO:0009307
XF_0167	1	membrane	902389	C:GO:0016021
mfd	1	transcription-repair coupling factor	916676	F:GO:0005524; C:GO:0005737; P:GO:0000716; P:GO:0006355; F:GO:0004386; F:GO:0003684
msbA	1	lipid A export permease ATP-binding	953525	F:GO:0005524; P:GO:0006869; F:GO:0034040; P:GO:0055085; C:GO:0043190
XF_1258	1	mechanosensitive ion channel family	955188	P:GO:0055085; C:GO:0016021
mutL	1	DNA mismatch repair	975291	F:GO:0005524; P:GO:0006298; F:GO:0030983
nuoH	1	NADH:ubiquinone oxidoreductase subunit H	1012313	F:GO:0048038; C:GO:0016021; P:GO:0055114; C:GO:0005886; F:GO:0016655
XF_2433	1	multidrug MFS transporter	1070583	C:GO:0016021
XF_0256	1	glucose-1-phosphate thymidyltransferase	1205905	F:GO:0008879; F:GO:0046872; P:GO:0045226
XF_0407	1	oxidoreductase	1226108	F:GO:0003723; C:GO:0005737; F:GO:0008168; P:GO:0006364; P:GO:0032259
rlmL	1	23S rRNA methyltransferase	1229480	F:GO:0003723; C:GO:0005737; F:GO:0070043; F:GO:0052915; P:GO:0070476
XF_1330	1	hybrid sensor histidine kinase response regulator	1248155	F:GO:0000155; P:GO:0000160; P:GO:0023014; C:GO:0005622
XF_2165	1	RNA-binding transcriptional accessory	1281627	F:GO:0003676; P:GO:0006139
XF_2452	1	rifampin ADP-ribosyl transferase	1312740	P:GO:0051301; C:GO:0005737; F:GO:0016740; P:GO:0051304
XF_1073	1	succinate dehydrogenase iron-sulfur subunit	1316757	F:GO:0008177; F:GO:0046872; F:GO:0009055; F:GO:0051538; P:GO:0006099; F:GO:0051539; F:GO:0051537
XF_2225	1	aspartate kinase	1394223	F:GO:0050661; F:GO:0004072; P:GO:0009067; P:GO:0055114; P:GO:0016310; F:GO:0016597; F:GO:0004412
trpE	1	anthranilate synthase component I	1421536	P:GO:0000162; F:GO:0004049
XF_1517	1	type II secretion system	1483924	F:GO:0005524; F:GO:0008565; P:GO:0015628; C:GO:0015627
XF_2442	1	agmatine deiminase	25367	F:GO:0004668; P:GO:0009446

glk	1	glucokinase	387987	F:GO:0005524; P:GO:0051156; C:GO:0005737; P:GO:0006096; F:GO:0004340
XF_2023	1	DUF2461 domain-containing	459791	
XF_0296	1	restriction endonuclease subunit S	693353	F:GO:0003677; P:GO:0006304
XF_2733	1	DUF3375 domain-containing	717217	
hflX	1	GTPase	766813	F:GO:0000287; F:GO:0005525; C:GO:0005737; F:GO:0003924
XF_2721	1	DEAD DEAH box helicase	785718	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0004519; F:GO:0004386; P:GO:0006304
XF_2369	1	polysaccharide biosynthesis	1145697	C:GO:0016021; P:GO:0009103
purH	1	phosphoribosylaminoimidazolecarboxamide formyltransferase	1157259	F:GO:0003937; P:GO:0006189; F:GO:0004643
XF_1213	1	GTP-binding	1440506	F:GO:0005525; F:GO:0003746; F:GO:0003924; P:GO:0006414
XF_1516	1	membrane	1455153	P:GO:0009405; C:GO:0019867
XF_2133	1	ABC transporter ATP-binding	1523607	F:GO:0016887; F:GO:0005524
	1	agmatine deiminase	25367	F:GO:0004668; P:GO:0009446
	1	asparagine synthase B	70777	P:GO:0006529; F:GO:0004066
	1	cytochrome o ubiquinol oxidase subunit I	195650	F:GO:0004129; F:GO:0005506; C:GO:0016021; P:GO:1902600; F:GO:0016682; P:GO:0009060; C:GO:0070469; F:GO:0020037
	1	glucokinase	388214	F:GO:0005524; P:GO:0051156; C:GO:0005737; P:GO:0006096; F:GO:0004340
	1	restriction endonuclease subunit S	693353	F:GO:0003677; P:GO:0006304
	1	DUF3375 domain-containing	718266	
	1	DEAD DEAH box helicase	785698	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0004519; F:GO:0004386; P:GO:0006304
	1	DEAD DEAH box helicase	790529	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; F:GO:0004386; P:GO:0009307
	1	DEAD DEAH box helicase	792410	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; P:GO:0009307
	1	NAD-dependent DNA ligase	848126	P:GO:0006281; F:GO:0003911; F:GO:0046872; P:GO:0006260; P:GO:0006266
	1	site-specific DNA-methyltransferase	885582	F:GO:0003677; F:GO:0008170; P:GO:0006306
	1	phosphoenolpyruvate synthase	1119400	F:GO:0005524; P:GO:0006094; F:GO:0046872; P:GO:0016310; P:GO:0006090; F:GO:0008986
	1	polysaccharide biosynthesis	1145697	C:GO:0016021; P:GO:0009103
	1	phosphoribosylaminoimidazolecarboxamide formyltransferase	1157259	F:GO:0003937; P:GO:0006189; F:GO:0004643
	1	cell surface	1306513	P:GO:0009405; C:GO:0019867
	1	GTP-binding	1438913	F:GO:0005525; F:GO:0003746; F:GO:0003924; P:GO:0006414
	1	ABC transporter ATP-binding	1523607	F:GO:0016887; F:GO:0005524
	1	DNA ligase (NAD(+))	848199	P:GO:0006281; F:GO:0003911; F:GO:0046872; P:GO:0006260; P:GO:0006266
XF_1078	3	DNA internalization-related competence Rec2	174148	C:GO:0016021; P:GO:0030420
dapE	3	succinyl-diaminopimelate desuccinylase	217602	F:GO:0008270; P:GO:0009089; P:GO:0006508; F:GO:0009014; F:GO:0008237; F:GO:0050897; P:GO:0019877
fmt	3	methionyl-tRNA formyltransferase	344824	F:GO:0004479; P:GO:0071951; P:GO:0006413
XF_2441	3	hypothetical protein	693704	
XF_1648	3	phage recombination Bet	734356	F:GO:0003677; P:GO:0006259
gyrA	3	DNA gyrase subunit A	747936	F:GO:0003677; F:GO:0005524; C:GO:0005737; P:GO:0006261; C:GO:0005694; F:GO:0003918; P:GO:0006265
XF_2725	3	DEAD DEAH box helicase	791366	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; F:GO:0004386; P:GO:0009307
XF_0910	3	ubiquinol cytochrome C oxidoreductase	1061796	F:GO:0009055; C:GO:0016021; F:GO:0020037
XF_0033	3	pilus assembly	1088543	C:GO:0016021; F:GO:0008565; P:GO:0015628; C:GO:0015627
recG	3	ATP-dependent DNA helicase	1191182	F:GO:0003676; F:GO:0005524; P:GO:0006281; P:GO:0032508; P:GO:0006310; F:GO:0004003
XF_2438	3	30S ribosomal S1	1278699	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412
XF_2022	3	exodeoxyribonuclease I	1309426	F:GO:0003676; P:GO:0006281; P:GO:0090305; F:GO:0008852
XF_1610	3	carbohydrate kinase	1313819	P:GO:0016310; F:GO:0016773; F:GO:0016301
XF_1072	3	fumarate reductase	1315936	F:GO:0008177; F:GO:0050660; P:GO:0006099; P:GO:0022900; C:GO:0005886
XF_0050	3		1467051	
sucC	3	succinate-- ligase subunit beta	1358581	F:GO:0000287; F:GO:0005524; F:GO:0016746; F:GO:0030145; P:GO:0006099; F:GO:0004775
gmd	3	GDP-mannose 4,6-dehydratase	418322	F:GO:0070401; P:GO:0019673; F:GO:0008446
XF_1521	3	general secretion pathway	470944	C:GO:0016021
ligA	3	NAD-dependent DNA ligase	848396	P:GO:0006281; F:GO:0003911; F:GO:0046872; P:GO:0006260; P:GO:0006266
XF_2539	3	fimbrial	1088217	C:GO:0016021; P:GO:0007155; C:GO:0009289

	3	agmatine deiminase	25679	F:GO:0004668; P:GO:0009446
	3	oligopeptidase B	220718	P:GO:0006508; F:GO:0004252; F:GO:0070008
	3	GDP-mannose 4,6-dehydratase	418440	F:GO:0070401; P:GO:0019673; F:GO:0008446
	3	---NA---	428403	
	3	general secretion pathway	470944	C:GO:0016021
	3	histidinol dehydrogenase	768871	F:GO:0008270; F:GO:0051287; P:GO:0055114; P:GO:0000105; F:GO:0004399
	3	restriction endonuclease subunit R	784846	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0004519; P:GO:0006304
	3	DEAD DEAH box helicase	789302	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; F:GO:0004386; P:GO:0009307
	3	NAD-dependent DNA ligase	848396	P:GO:0006281; F:GO:0003911; F:GO:0046872; P:GO:0006260; P:GO:0006266
	3	fimbrial	1087816	C:GO:0016021; P:GO:0007155; C:GO:0009289
	3	glycerol-3-phosphate 1-O-acyltransferase	1102993	P:GO:0016024; F:GO:0004366; C:GO:0005886
	3	ATP-dependent DNA helicase	1190491	
	3	cell surface	1301098	P:GO:0009405; C:GO:0019867
XF_0151	4	phosphomannomutase	33385	P:GO:0005975; F:GO:0016868; C:GO:0016021
XF_0118	4	asparagine synthase B	71806	P:GO:0006529; F:GO:0004066
XF_1496	4	#NOM?	124806	C:GO:0009279; F:GO:0004872; P:GO:0006810
ccmC	4	heme ABC transporter permease	139911	F:GO:0015232; C:GO:0016021; P:GO:0017004; F:GO:0020037; P:GO:0015886
cysH	4	phosphoadenosine phosphosulfate reductase	198937	P:GO:0070814; C:GO:0005737; F:GO:0004604; P:GO:0019379
cysI	4	assimilatory sulfite reductase (NADPH) hemo subunit	200866	F:GO:0050661; P:GO:0070814; F:GO:0046872; P:GO:0019344; P:GO:0055114; F:GO:0051539; F:GO:0004783; P:GO:0000103; C:GO:0009337; F:GO:0020037
XF_2260	4		266052	
groL	4	molecular chaperone	426197	F:GO:0005524; C:GO:0005737; F:GO:0051082; P:GO:0042026
XF_1650	4	hypothetical protein	725194	
hisC	4	histidinol-phosphate aminotransferase	768390	F:GO:0030170; F:GO:0080130; P:GO:0000105; F:GO:0004400
hisG	4	ATP phosphoribosyltransferase	771833	F:GO:0000287; F:GO:0005524; C:GO:0005737; F:GO:0003879; P:GO:0000105
XF_2728	4	type I restriction-modification system subunit M	784559	F:GO:0003677; P:GO:0090305; F:GO:0008170; F:GO:0004519; P:GO:0009307; P:GO:0032775; F:GO:0009007
XF_1968	4	site-specific DNA-methyltransferase	886367	F:GO:0003677; F:GO:0008170; P:GO:0032775; F:GO:0009007
mrda	4	penicillin-binding 2	950603	C:GO:0016021; F:GO:0008658
mtnB	4	methylthioribulose-1-phosphate dehydratase	961431	F:GO:0046570; F:GO:0008270; C:GO:0005737; P:GO:0019284; P:GO:0019509
XF_0311	4	NADH dehydrogenase	1001342	F:GO:0009055; C:GO:0016020; F:GO:0030151; F:GO:0008137; F:GO:0051539; P:GO:0042773
nuoD	4	NADH dehydrogenase	1011674	F:GO:0050136; F:GO:0048038; F:GO:0051287; P:GO:0055114; P:GO:0006810; C:GO:0005886
XF_0316	4	NADH-quinone oxidoreductase subunit L	1014898	C:GO:0016021; F:GO:0008137; P:GO:0042773
pfp	4	6-phosphofructokinase	1063304	F:GO:0047334; C:GO:0005737; F:GO:0046872; P:GO:0006002; P:GO:0061615; P:GO:0046835; F:GO:0003872
XF_1259	4	phosphoenolpyruvate synthase	1121223	F:GO:0005524; P:GO:0006094; F:GO:0046872; P:GO:0016310; P:GO:0006090; F:GO:0008986
purM	4	phosphoribosylaminoimidazole synthetase	1159212	F:GO:0005524; C:GO:0005737; P:GO:0006189; F:GO:0004641
queA	4	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1169740	P:GO:0008616; C:GO:0005737; F:GO:0016740; F:GO:0016853
XF_0255	4	dTDP-glucose 4,6-dehydratase	1206624	F:GO:0008460; P:GO:0009225
rlmJ	4	23S rRNA (adenine(2030)-N(6))-methyltransferase	1227052	F:GO:0003723; P:GO:0070475; F:GO:0036307
secA	4	pre translocase subunit	1321733	F:GO:0005524; P:GO:0006605; C:GO:0005737; F:GO:0046872; P:GO:0065002; P:GO:0017038; F:GO:0005886
XF_1363	4	lytic murein transglycosylase	1328443	C:GO:0042597; F:GO:0004553
smc	4	chromosome segregation SMC	1334450	F:GO:0003677; F:GO:0005524; P:GO:0007062; C:GO:0005737; P:GO:0006260; P:GO:0030261; C:GO:0005694
XF_0243	4	acriflavin resistance	1367089	C:GO:0016021; P:GO:0006810; F:GO:0005215
XF_2223	4	threonine synthase	1395955	F:GO:0030170; P:GO:0006520
XF_0082	4	pilus assembly	1495276	P:GO:0061077; C:GO:0030288; P:GO:0071555; P:GO:0043711
XF_1252	4	alpha-2-macroglobulin family	1514280	F:GO:0004866; P:GO:0010951
XF_1611	4	N-acylglucosamine 2-epimerase	1526987	F:GO:0003824
XF_1465	4	N-acetylglucosamine-6-phosphate	24768	P:GO:0005975; P:GO:0006044; F:GO:0008448

		deacetylase		
XF_1029	4	glutaryl-7-ACA acylase	171905	P:GO:0006508; F:GO:0008239
XF_1389	4	cytochrome o ubiquinol oxidase subunit I	193607	F:GO:0004129; F:GO:0005506; C:GO:0016021; P:GO:1902600; F:GO:0016682; P:GO:0009060; C:GO:0070469; F:GO:0020037
XF_0081	4	fimbrial biogenesis outer membrane usher	338050	C:GO:0016021; C:GO:0009279; P:GO:0006810; F:GO:0005215
XF_2747	4	HrgA protein	503809	
XF_0775	4	acyltransferase	545838	F:GO:0016746; C:GO:0016021
XF_2742	4	DNA methyltransferase	662667	F:GO:0003677; F:GO:0008170; P:GO:0006306
XF_0614	4	AE003907_2hypothetical protein XF_0614	720303	C:GO:0016021
hslU	4	ATP-dependent protease	798735	F:GO:0016887; F:GO:0005524; C:GO:0009376; F:GO:0070011; P:GO:0006508; P:GO:0043335
plsB	4	glycerol-3-phosphate 1-O-acyltransferase	1104496	P:GO:0016024; F:GO:0004366; C:GO:0005886
XF_1068	4	aminomethyl transferase	1517837	F:GO:0008168; P:GO:0032259
XF_1529	4	cell surface	1302200	P:GO:0009405; C:GO:0019867
	4	glutaryl-7-ACA acylase	171905	P:GO:0006508; F:GO:0008239
	4	cytochrome o ubiquinol oxidase subunit I	193607	F:GO:0004129; F:GO:0005506; C:GO:0016021; P:GO:1902600; F:GO:0016682; P:GO:0009060; C:GO:0070469; F:GO:0020037
	4	Oligopeptidase B	220526	P:GO:0006508; F:GO:0004252; F:GO:0070008
	4	fimbrial biogenesis outer membrane usher	338348	C:GO:0016021; C:GO:0009279; P:GO:0006810; F:GO:0005215
	4	DUF2461 domain-containing	459407	
	4	HrgA protein	505063	
	4	acyltransferase	546207	F:GO:0016746; C:GO:0016021
	4	DNA methyltransferase	662646	F:GO:0003677; F:GO:0008170; P:GO:0006306
	4	hypothetical protein	693537	
	4	AE003907_2hypothetical protein XF_0614	720303	C:GO:0016021
	4	phage recombination Bet	734190	F:GO:0003677; P:GO:0006259
	4	Type I restriction-modification M subunit	782524	F:GO:0003677; F:GO:0008170; P:GO:0006306
	4	type I restriction endonuclease subunit R	789751	F:GO:0003677; F:GO:0005524; P:GO:0009305; F:GO:0009035; F:GO:0004386; P:GO:0009307
	4	DEAD DEAH box helicase	793357	F:GO:0003677; F:GO:0005524; P:GO:0009305; F:GO:0009035; F:GO:0004386; P:GO:0009307
	4	ATP-dependent protease	798772	F:GO:0016887; F:GO:0005524; C:GO:0009376; F:GO:0070011; P:GO:0006508; P:GO:0043335
	4	large conductance mechanosensitive channel	955001	F:GO:0005216; P:GO:0034220; C:GO:0016021; C:GO:0005886
	4	glycerol-3-phosphate 1-O-acyltransferase	1102300	P:GO:0016024; F:GO:0004366; C:GO:0005886
	4	glycerol-3-phosphate 1-O-acyltransferase	1104409	P:GO:0016024; F:GO:0004366; C:GO:0005886
	4	carbohydrate kinase	1313188	P:GO:0016310; F:GO:0016773; F:GO:0016301
	4	aminomethyl transferase	1518553	F:GO:0008168; P:GO:0032259

Table S5 – Recombination genes for *X. fastidiosa* 32 (Coffee).

SeqName	Cluster of origin	Description	Length	GO IDs
XF_0260	1	phosphomannomutase	2504	F:GO:0000287; P:GO:0005975; F:GO:0016868
XF_1455	1	hybrid sensor histidine kinase response regulator	2982	F:GO:0000155; P:GO:0000160; P:GO:0023014; C:GO:0005622
XF_1087	1	cardiolipin synthase	4320	F:GO:0003824
XF_1389	1	cytochrome o ubiquinol oxidase subunit I	2042	F:GO:0004129; F:GO:0005506; C:GO:0016021; P:GO:1902600; F:GO:0016682; P:GO:0009060; C:GO:0070469; F:GO:0020037
XF_1479	1	oligopeptidase B	355	P:GO:0006508; F:GO:0004252; F:GO:0004177; F:GO:0070008
metX	1	homoserine O-acetyltransferase	750	F:GO:0004414; P:GO:0009086; C:GO:0005737
XF_0620	1	cytochrome c biogenesis	725	C:GO:0005623; C:GO:0016021; P:GO:0045454
XF_2708	1	cellulase	639	P:GO:0005975; F:GO:0004553
XF_2544	1	type IV-A pilus assembly ATPase	4268	F:GO:0005524; P:GO:0009297; P:GO:0015031; F:GO:0008565
XF_0671	1	3-ketoacyl-ACP reductase	605	F:GO:0004316; F:GO:0051287; P:GO:0055114; P:GO:0006633
glk	1	glucokinase	2265	F:GO:0005524; P:GO:0051156; C:GO:0005737; P:GO:0006096; F:GO:0004340
XF_1464	1	iron dicitrate transport regulator	1463	P:GO:0005975; F:GO:0008483; F:GO:0030246
XF_2266	1	glycerol-3-phosphate dehydrogenase	6157	P:GO:0006072; C:GO:0009331; F:GO:0052591; P:GO:0055114
gmk	1	guanylate kinase	447	F:GO:0005524; P:GO:0005737; P:GO:0046710; P:GO:0046037; F:GO:0004385; P:GO:0016310
XF_0029	1	type IV pilus modification	679	C:GO:0016021
XF_0588	1	DUF2066 domain-containing	1077	
XF_2448	1	ABC transporter substrate-binding	1578	
XF_2445	1	coagulation factor 5 8 type domain-containing	1868	F:GO:0003824
XF_2118	1	hypothetical protein XFUD_09200	288	
XF_1838	1	nucleoside-diphosphate sugar epimerase	1483	
XF_1458	1	class I SAM-dependent methyltransferase	2784	
XF_2750	1	hypothetical protein	1205	
XF_1508	1	DUF1631 domain-containing	1826	
XF_2444	1	family	298	C:GO:0016021
XF_2366	1	polysaccharide biosynthesis	648	C:GO:0016021
XF_2733	1	DUF3375 domain-containing	178	
XF_2367	1	undecaprenyl-phosphate glucose phosphotransferase	3065	C:GO:0016021
XF_2721	1	DEAD DEAH box helicase	677	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0004519; F:GO:0004386; P:GO:0006304
XF_2739	1	DEAD DEAH box helicase	1226	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; F:GO:0004386; P:GO:0009307
kup	1	potassium transporter Kup	7136	F:GO:0015079; P:GO:0071805; C:GO:0016021; C:GO:0005886
XF_1419	1	---NA---	113	
XF_0259	1	mannose-1-phosphate guanyltransferase	1530	P:GO:0000271; F:GO:0004475; F:GO:0016853
mdh	1	malate dehydrogenase	1416	P:GO:0005975; F:GO:0030060; P:GO:0006108; P:GO:0006099
XF_2385	1	acriflavine resistance B	5163	C:GO:0016021; P:GO:0006810; F:GO:0005215
msbA	1	lipid A export permease ATP-binding	2610	F:GO:0005524; P:GO:0006869; F:GO:0034040; P:GO:0055085; C:GO:0043190
XF_0401	1	response regulator receiver	2934	P:GO:0000160; C:GO:0005622
nuoC	1	NADH dehydrogenase	572	F:GO:0048038; F:GO:0008137; P:GO:0055114; P:GO:0006810; C:GO:0005886
nuoD	1	NADH dehydrogenase	2598	F:GO:0050136; F:GO:0048038; F:GO:0051287; P:GO:0055114; P:GO:0006810; C:GO:0005886
XF_2009	1	Xaa-Pro aminopeptidase	3036	P:GO:0006508; F:GO:0004177; F:GO:0030145
XF_2433	1	multidrug MFS transporter	2241	C:GO:0016021
XF_1259	1		709	
XF_1402	1	phosphoenolpyruvate-- phosphotransferase	3224	C:GO:0005737; F:GO:0046872; P:GO:0009401; P:GO:0016310; F:GO:0008965; F:GO:0016301
XF_1553	1	adenylosuccinate lyase	552	F:GO:0004018; P:GO:0044208; P:GO:0006189; F:GO:0070626
purH	1	phosphoribosylaminoimidazolecarboxamide formyltransferase	6147	F:GO:0003937; P:GO:0006189; F:GO:0004643
recB	1	exodeoxyribonuclease V subunit beta	1443	F:GO:0000287; F:GO:0003677; F:GO:0005524; P:GO:0090305; P:GO:0032508; P:GO:0000724; F:GO:0004003; F:GO:0008854
rlmL	1		4291	
XF_2165	1	RNA-binding transcriptional accessory	3612	F:GO:0003676; P:GO:0006139

XF_1200	1	pseudouridine synthase	1142	P:GO:0001522; F:GO:0003723; F:GO:0009982
XF_2452	1	rifampin ADP-ribosyl transferase	2439	P:GO:0051301; C:GO:0005737; F:GO:0016740; P:GO:0051304
XF_1073	1	succinate dehydrogenase iron-sulfur subunit	820	F:GO:0008177; F:GO:0046872; F:GO:0009055; F:GO:0051538; P:GO:0006099; F:GO:0051539; F:GO:0051537
smc	1	chromosome segregation SMC	2721	F:GO:0003677; F:GO:0005524; P:GO:0007062; C:GO:0005737; P:GO:0006260; P:GO:0030261; C:GO:0005694
XF_1295	1	SMR domain	318	F:GO:0046872; P:GO:0019430; P:GO:0055114; F:GO:0004784
XF_2225	1	aspartate kinase	2205	F:GO:0050661; F:GO:0004072; P:GO:0009067; P:GO:0055114; P:GO:0016310; F:GO:0016597; F:GO:0004412
XF_1213	1	GTP-binding	4285	F:GO:0005525; F:GO:0003746; F:GO:0003924; P:GO:0006414
uppP	1	UDP pyrophosphate phosphatase	1330	P:GO:0008360; P:GO:0009252; C:GO:0016021; P:GO:0046677; F:GO:0050380; P:GO:0016310; P:GO:0071555; P:GO:0016311; F:GO:0016301; C:GO:0005886
XF_1527	1	type II secretion system	2368	F:GO:0008565; P:GO:0015628; C:GO:0009279; C:GO:0015627
XF_1329	1	polyisoprenoid-binding	1239	
XF_2203	1	elongation factor P	324	F:GO:0003746; C:GO:0005737; P:GO:0006414
Unkown	1	agmatine deiminase	776	F:GO:0004668; P:GO:0009446
Unkown	1	helicase SNF2	813	F:GO:0003677; F:GO:0005524; F:GO:0016787
Unkown	1	phage recombination Bet	196	F:GO:0003677; P:GO:0006259
Unkown	1	mannosyltransferase	3787	F:GO:0016757
XF_2442	3	agmatine deiminase	240	
argD	3	acetylornithine aminotransferase	2278	F:GO:0030170; P:GO:0006526; C:GO:0005737; F:GO:0003992
XF_1078	3	transporter	3133	C:GO:0016021; P:GO:0030420
XF_2241	3	peptidase S1	933	P:GO:0006508; F:GO:0004252
XF_1428	3	glutamate--cysteine ligase	1542	P:GO:0006750; F:GO:0004357
glnS	3	glutamine--tRNA ligase	388	F:GO:0005524; C:GO:0005737; F:GO:0004819; P:GO:0006424; P:GO:0006425
gmd	3	GDP-mannose 4,6-dehydratase	969	F:GO:0070401; P:GO:0019673; F:GO:0008446
XF_0598	3	PKHD-type hydroxylase	1785	F:GO:0031418; F:GO:0005506; F:GO:0016706; P:GO:0055114
XF_1837	3	DUF2145 domain-containing	334	
XF_2679	3	acid virulence B	365	
XF_0820	3	peptidase M20	688	
XF_0596	3	DUF2271 domain-containing	347	
XF_1966	3	helicase SNF2	386	F:GO:0003677; F:GO:0005524; F:GO:0004386
gyrB	3	DNA gyrase subunit B	1887	F:GO:0000287; F:GO:0003677; F:GO:0005524; C:GO:0005737; P:GO:0006261; C:GO:0005694; F:GO:0003918; P:GO:0006265
hisC	3	histidinol-phosphate aminotransferase	601	F:GO:0030170; F:GO:0080130; P:GO:0000105; F:GO:0004400
lepA	3	elongation factor 4	1126	F:GO:0005525; P:GO:0045727; F:GO:0003746; F:GO:0003924; F:GO:0043022; P:GO:0006414; C:GO:0005886
XF_0887	3	mannosyltransferase	1028	F:GO:0016757
XF_2235	3	penicillin-binding 1C	1198	P:GO:0009252; F:GO:0008658; F:GO:0008955
pcm	3	-L-isoaspartate O-methyltransferase	774	P:GO:0030091; C:GO:0005737; F:GO:0004719; P:GO:0006479
XF_2539	3	fimbrial	1005	C:GO:0016021; P:GO:0007155; C:GO:0009289
queC	3	7-cyano-7-deazaguanine synthase	868	F:GO:0005524; F:GO:0008270; P:GO:0008616; F:GO:0016879
XF_2438	3	30S ribosomal S1	1416	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412
XF_2022	3	exodeoxyribonuclease I	517	F:GO:0003676; P:GO:0006281; P:GO:0090305; F:GO:0008852
XF_1610	3	carbohydrate kinase	630	P:GO:0016310; F:GO:0016773; F:GO:0016301
XF_1072	3	fumarate reductase	1652	F:GO:0008177; F:GO:0050660; P:GO:0006099; P:GO:0022900; C:GO:0005886
XF_2206	3	3-phosphoglycerate dehydrogenase	1676	F:GO:0051287; F:GO:0004617; P:GO:0006564; P:GO:0055114; F:GO:0016597
Unkown	3	oligopeptidase B	191	P:GO:0006508; F:GO:0004252; F:GO:0070008
Unkown	3	coagulation factor 5 8 type domain-containing	1387	F:GO:0003824
Unkown	3	ion transporter	459	F:GO:0005249; P:GO:0071805; C:GO:0008076
Unkown	3	electron transfer flavo -ubiquinone oxidoreductase	393	F:GO:0004174; P:GO:0055114; F:GO:0051536
Unkown	3	L-ascorbate oxidase	1589	F:GO:0005507; F:GO:0016491; P:GO:0055114
Unkown	3	dTDP-4-dehydrorhamnose reductase	193	P:GO:0055114; F:GO:0008831
Unkown	3	hybrid sensor histidine kinase response regulator	1080	
Unkown	3	carbohydrate kinase	96	P:GO:0016310; F:GO:0016773; F:GO:0016301
Unkown	3	DNA helicase II	612	F:GO:0003677; F:GO:0005524; C:GO:0005737; F:GO:0004003; P:GO:0006268
XF_0151	4	phosphomannomutase	1220	P:GO:0005975; F:GO:0016868; C:GO:0016021
ccmC	4	heme ABC transporter permease	1524	F:GO:0015232; C:GO:0016021; P:GO:0017004; F:GO:0020037; P:GO:0015886

XF_0132	4	copper oxidase	1539	F:GO:0005507; F:GO:0016491; P:GO:0055114; C:GO:0042597
cysNC	4	adenylyltransferase	1173	F:GO:0005525; F:GO:0005524; P:GO:0070814; F:GO:0003924; F:GO:0004020; F:GO:0004781; P:GO:0016310; P:GO:0000103
dapD	4	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	1150	C:GO:0005737; P:GO:0009089; F:GO:0008666; P:GO:0019877
XF_1062	4	phosphogluconate dehydratase	2292	P:GO:0009255; F:GO:0004456
XF_0993	4	multidrug transporter	3082	C:GO:0016021
XF_2474	4	EF-P beta-lysylation	1310	F:GO:0003824; F:GO:0046872; F:GO:0051539
XF_2134	4	ligand-gated channel	1271	C:GO:0009279; F:GO:0004872; P:GO:0006810
XF_2550	4	family hemolysin secretion activation	1678	P:GO:0015031
fumC	4	class II fumarate hydratase	2294	P:GO:0006099; F:GO:0004333; P:GO:0006106; C:GO:0045239
glmS	4	glucosamine--fructose-6-phosphate aminotransferase	2847	P:GO:0005975; C:GO:0005737; F:GO:0004360; P:GO:0006541; P:GO:1901137; F:GO:0030246
XF_0268	4	MFS transporter	1138	C:GO:0016021; P:GO:0008643; F:GO:0005215
XF_2023	4	DUF2461 domain-containing	734	
XF_1434	4	peptidase	370	
XF_1299	4	DNA methylase	467	P:GO:0006281; F:GO:0016491; F:GO:0008168; P:GO:0055114; P:GO:0032259
XF_2549	4	#NOM?	876	C:GO:0009279; F:GO:0004872; P:GO:0006810
XF_2208	4	amino acid permease	1985	C:GO:0016021; F:GO:0015171; P:GO:0003333
XF_2261	4	oligopeptide OPT family	4689	P:GO:0055085; C:GO:0016021
XF_2742	4	DNA methyltransferase	734	F:GO:0003677; F:GO:0008170; P:GO:0006306
XF_0439	4	beta-glucosidase	1074	P:GO:0005975; F:GO:0004553
XF_0296	4	restriction endonuclease subunit S	2293	F:GO:0003677; P:GO:0090305; F:GO:0004519; P:GO:0006304
XF_1918	4	hypothetical protein B398_05435	1650	
XF_1298	4	electron transfer flavo -ubiquinone oxidoreductase	1364	F:GO:0016491; P:GO:0055114; F:GO:0051536
XF_1648	4	phage recombination Bet	322	F:GO:0003677; P:GO:0006259
XF_1507	4	family oxidoreductase	815	P:GO:0006779; C:GO:0005737; F:GO:0004109; P:GO:0055114; F:GO:0051536
hisA	4	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	1356	C:GO:0005737; F:GO:0003949; P:GO:0000105
XF_2728	4	type I restriction-modification system subunit M	2244	F:GO:0003677; P:GO:0090305; F:GO:0008170; F:GO:0004519; P:GO:0009307; P:GO:0032775; F:GO:0009007
XF_2725	4	DEAD DEAH box helicase	4030	F:GO:0003677; F:GO:0005524; P:GO:0090305; F:GO:0009035; F:GO:0004386; P:GO:0009307
map	4	type I methionyl aminopeptidase	1174	P:GO:0070084; F:GO:0046872; P:GO:0006508; F:GO:0070006
XF_1968	4	site-specific DNA-methyltransferase	282	F:GO:0003677; F:GO:0008170; P:GO:0032775; F:GO:0009007
opgD	4	glucan biosynthesis D	2383	P:GO:0009250; F:GO:0003824; C:GO:0042597; F:GO:0030246
mfd	4	transcription-repair coupling factor	3466	F:GO:0005524; C:GO:0005737; P:GO:0000716; P:GO:0006355; F:GO:0004386; F:GO:0003684
XF_1302	4	ABC transporter ATP-binding	3816	F:GO:0016887; F:GO:0005524
mtnC	4	haloacid dehalogenase	666	F:GO:0000287; P:GO:0043716; F:GO:0043715; P:GO:0019284; P:GO:0019509; P:GO:0016311; F:GO:0043874
murC	4	UDP-N-acetylmuramate--alanine ligase	2115	P:GO:0008360; P:GO:0051301; F:GO:0005524; C:GO:0005737; P:GO:0009252; F:GO:0008763; P:GO:0071555; P:GO:0007049
murF	4	UDP-N-acetylmuramoylalanyl-D-glutamyl-6-diaminopimelate--D-alanyl-D-alanine ligase	3413	P:GO:0008360; P:GO:0051301; F:GO:0005524; C:GO:0005737; P:GO:0009252; P:GO:0071555; F:GO:0047480; P:GO:0007049
pepA	4	leucyl aminopeptidase	2768	C:GO:0005737; P:GO:0006508; F:GO:0008235; F:GO:0004177; F:GO:0030145
XF_2677	4	L-ascorbate oxidase	989	F:GO:0005507; F:GO:0016491; P:GO:0055114
purM	4	phosphoribosylaminoimidazole synthetase	1952	F:GO:0005524; C:GO:0005737; P:GO:0006189; F:GO:0004641
recC	4	exodeoxyribonuclease V subunit gamma	3271	F:GO:0003677; F:GO:0005524; P:GO:0090305; P:GO:0032508; P:GO:0000724; F:GO:0004003; C:GO:0009338; F:GO:0008854
rep	4	ATP-dependent DNA helicase Rep	1571	F:GO:0005524; F:GO:0008408; P:GO:0090305; F:GO:0004003; P:GO:0006268; F:GO:0003697
XF_0257	4	dTDP-4-dehydrorhamnose 3,5-epimerase	126	F:GO:0008830
XF_0258	4	dTDP-4-dehydrorhamnose reductase	503	P:GO:0055114; F:GO:0008831
XF_2730	4	threonine transporter	966	C:GO:0016021; P:GO:0006865; C:GO:0005886
XF_1552	4	transcriptional regulator	1531	
XF_1330	4	hybrid sensor histidine kinase response regulator	1535	F:GO:0000155; P:GO:0000160; P:GO:0023014; C:GO:0005622
XF_0547	4	type electron transport complex subunit B	522	F:GO:0046872; F:GO:0009055; C:GO:0016020; P:GO:0055114; F:GO:0051539; F:GO:0051537
secA	4	pre translocase subunit	3586	F:GO:0005524; P:GO:0006605; C:GO:0005737; F:GO:0046872; P:GO:0005002; P:GO:0017038; C:GO:0005886

smpB	4	#NOM?	1309	F:GO:0003723; C:GO:0005737; P:GO:0070929
XF_0352	4	(p)ppGpp synthetase	7332	P:GO:0015969; F:GO:0016597; F:GO:0016787
XF_2223	4	threonine synthase	1285	F:GO:0030170; P:GO:0006520
XF_0050	4	DNA helicase II	467	F:GO:0003677; F:GO:0005524; C:GO:0005737; F:GO:0004003; P:GO:0006268
valS	4	valyl-tRNA synthetase	849	F:GO:0004832; F:GO:0005524; P:GO:0006438; C:GO:0005737; P:GO:0006450; F:GO:0002161
XF_1637	4	glycosyl transferase	647	C:GO:0016021; F:GO:0016740
XF_0845	4	glycoside hydrolase family 3	1488	P:GO:0005975; F:GO:0004553
XF_1252	4	alpha-2-macroglobulin family	3380	F:GO:0004866; P:GO:0010951
XF_1068	4	glycine cleavage T	515	F:GO:0016740
XF_2133	4	ABC transporter ATP-binding	4335	F:GO:0016887; F:GO:0005524
Unkown	4	cytochrome o ubiquinol oxidase subunit I	1045	F:GO:0004129; F:GO:0005506; C:GO:0016021; P:GO:1902600; F:GO:0016682; P:GO:0009060; C:GO:0070469; F:GO:0020037
Unkown	4	Oligopeptidase B	2702	P:GO:0006508; F:GO:0004252; F:GO:0070008
Unkown	4	acid virulence B	380	
Unkown	4	DUF3375 domain-containing	193	
Unkown	4	helicase SNF2	555	F:GO:0003677; F:GO:0005524; F:GO:0016787
Unkown	4	DNA gyrase subunit B	1830	F:GO:0000287; F:GO:0003677; F:GO:0005524; C:GO:0005737; P:GO:0006261; C:GO:0005694; F:GO:0003918; P:GO:0006265
Unkown	4	---NA---	57	
Unkown	4	phosphoenolpyruvate synthase	2571	F:GO:0005524; P:GO:0006094; F:GO:0046872; P:GO:0016310; P:GO:0006090; F:GO:0008986
Unkown	4	exodeoxyribonuclease V subunit beta	2606	F:GO:0000287; F:GO:0003677; F:GO:0005524; P:GO:0090305; P:GO:0032508; P:GO:0000724; F:GO:0004003; F:GO:0008854
Unkown	4	chromosome segregation SMC	1528	F:GO:0003677; F:GO:0005524; P:GO:0007062; C:GO:0005737; P:GO:0006260; P:GO:0030261; C:GO:0005694
Unkown	4	type II secretion system	2995	P:GO:0051301; F:GO:0003677; C:GO:0005737; P:GO:0015074; F:GO:0008565; P:GO:0007059; P:GO:0015628; C:GO:0009279; C:GO:0015627; F:GO:0009037; P:GO:0007049; P:GO:0006313

Table S6 – Gene found to be under selection in each subspecies

Subspecies	SeqName	Description	GO Names
all	pilY1_2	pilus tip-associated	F:metal ion binding; C:pilus
all	PD_1130	hypothetical protein	
all	PD_1506	hemolysin-type calcium binding	F:calcium ion binding; C:integral component of membrane; C:extracellular region; P:pathogenesis
all	frpC	peptidase M23	F:calcium ion binding
all	PD_1721	DUF1566 domain-containing	
all	PD_1731	hypothetical protein	
all	PD_1671	GGDEF domain-containing response regulator	P:phosphorelay signal transduction system; C:intracellular
all	PD_1100	addiction module antitoxin	
all	PD_1128	DUF1566 domain-containing	
all	PD_1187	DUF3277 domain-containing	
all	PD_1593	hypothetical protein	C:integral component of membrane
all	PD_1285	filamentous hemagglutinin N-terminal domain-containing	
all	PD_1249	hemagglutinin	
all	pspA_3	filamentous hemagglutinin N-terminal domain-containing	
Xff	napA	nitric oxide dioxygenase	F:oxygen binding; F:FAD binding; F:metal ion binding; P:oxygen transport; P:response to nitrosative stress; P:oxidation-reduction process; F:oxygen transporter activity; P:response to toxic substance; F:nitric oxide dioxygenase activity; F:heme binding
Xff	aroQ	3-dehydroquinate dehydratase	P:aromatic amino acid family biosynthetic process; F:3-dehydroquinate dehydratase activity; P:chorismate biosynthetic process
Xff	fabZ	3-hydroxyacyl-ACP dehydratase	F:3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity; C:cytoplasm; P:lipid A biosynthetic process; P:fatty acid biosynthetic process
Xff	lexA	transcriptional repressor	F:DNA binding; P:DNA repair; P:negative regulation of transcription, DNA-templated; P:transcription, DNA-templated; P:DNA replication; P:proteolysis; F:serine-type endopeptidase activity; P:SOS response
Xff	mntP	MNTP_XYLFT ame: Full= manganese efflux pump	P:manganese ion transmembrane transport; C:integral component of membrane; F:manganese ion transmembrane transporter activity; C:plasma membrane
Xff	pilY1_3	1 homolog	F:metal ion binding; C:pilus
Xff	rpoZ	DNA-directed RNA polymerase subunit omega	F:DNA binding; F:DNA-directed 5'-3' RNA polymerase activity; P:transcription, DNA-templated
Xff	pheS	phenylalanyl-tRNA synthetase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; F:phenylalanine-tRNA ligase activity; P:phenylalanyl-tRNA aminoacylation; F:tRNA binding
Xff	gltX	glutamate--tRNA ligase	F:ATP binding; C:cytoplasm; F:glutamate-tRNA ligase activity; F:tRNA binding; P:glutamyl-tRNA aminoacylation

Xff	tilS	tRNA(Ile)-lysine synthetase	F:ATP binding; F:ligase activity, forming carbon-nitrogen bonds; C:cytoplasm; P:tRNA modification
Xff	PD_0970	hypothetical protein	
Xff	PD_1419	RTX toxin Ca ²⁺ -binding	
Xff	PD_0874	GNAT family N-acetyltransferase	F:N-acetyltransferase activity
Xff	PD_2080	DUF4194 domain-containing	
Xff	dpoL	DNA polymerase	F:DNA binding; F:DNA-directed DNA polymerase activity; P:DNA replication; P:DNA biosynthetic process
Xff	PD_0373	hypothetical protein	
Xff	PD_1138	DUF4224 domain-containing	
Xff	priA	primosomal N	F:DNA binding; F:ATP binding; F:zinc ion binding; F:ATP-dependent DNA helicase activity; P:DNA unwinding involved in DNA replication; C:primosome complex; P:DNA replication, synthesis of RNA primer
Xff	PD_0014	hypothetical protein	C:integral component of membrane
Xff	PD_0933	Zonular occludens toxin	C:integral component of membrane
Xff	bcp	thiol peroxidase	F:peroxidase activity; P:cellular oxidant detoxification; P:oxidation-reduction process
Xff	pilB	type IV-A pilus assembly ATPase	F:ATP binding; P:pilus assembly; P:protein transport; F:protein transporter activity
Xff	PD_0389	XRE family transcriptional regulator	F:sequence-specific DNA binding
Xff	mrkD	fimbrial adhesin precursor	P:cell adhesion; C:pilus
Xff	PD_0126	conserved hypothetical protein	
Xff	phaF	poly(hydroxyalcanoate) granule associated	
Xff	PD_0127	DUF2326 domain-containing	
Xff	grxC	glutaredoxin	C:cell; F:protein disulfide oxidoreductase activity; F:electron carrier activity; P:cell redox homeostasis; P:oxidation-reduction process
Xff	PD_0511	hypothetical protein	C:integral component of membrane
Xff	PD_0573	polyisoprenoid-binding	
Xff	PD_2050	response regulator receiver	P:phosphorelay signal transduction system; P:phosphorylation; F:kinase activity; C:intracellular
Xff	mreC	rod shape-determining	P:regulation of cell shape
Xff	PD_0968	XRE family transcriptional regulator	F:sequence-specific DNA binding
Xff	folC	bifunctional tetrahydrofolate synthase dihydrofolate synthase	F:tetrahydrofolylpolyglutamate synthase activity; F:ATP binding; P:tetrahydrofolylpolyglutamate biosynthetic process
Xff	fabG	3-ketoacyl-ACP reductase	F:3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity; F:NAD binding; P:oxidation-reduction process; P:fatty acid biosynthetic process
Xff	rimI	ribosomal- -alanine acetyltransferase	P:N-terminal protein amino acid acetylation; F:N-acetyltransferase activity

Xff	frpC_1	Haemolysin-type calcium binding domain	F:calcium ion binding; C:extracellular region; P:pathogenesis
Xff	PD_0729	Taurine catabolism dioxygenase family	F:oxidoreductase activity; P:oxidation-reduction process
Xff	PD_1149	transcriptional regulator	
Xff	PD_0835	helicase SNF2	F:DNA binding; F:ATP binding; F:helicase activity
Xff	PD_1031	hypothetical protein	C:integral component of membrane
Xff	PD_1472	conserved hypothetical protein	
Xff	PD_1459	hypothetical protein	
Xff	PD_1926	fimbrial	C:integral component of membrane; P:cell adhesion; C:pilus
Xff	pspB	autotransporter domain-containing	P:proteolysis; F:serine-type endopeptidase activity
Xff	PD_1424	hypothetical protein	
Xff	PD_2020	TPR repeat-containing	
Xff	ushA	5'-nucleotidase	F:nucleotide binding; F:magnesium ion binding; C:cytoplasm; F:5'-nucleotidase activity; P:dephosphorylation; P:nucleotide metabolic process
Xff	PD_1010	hypothetical protein PD_1010	
Xff	eda	2-dehydro-3-deoxyphosphogluconate aldolase	P:metabolic process; F:2-dehydro-3-deoxy-phosphogluconate aldolase activity; F:4-hydroxy-2-oxoglutarate aldolase activity
Xff	PD_0971	DUF3277 domain-containing	
Xff	PD_1974	conserved hypothetical protein	C:integral component of membrane
Xff	rne	ribonuclease E	F:magnesium ion binding; P:RNA phosphodiester bond hydrolysis, endonucleolytic; F:zinc ion binding; F:RNA binding; C:cytoplasm; P:tRNA processing; F:ribonuclease E activity; P:rRNA processing; P:mRNA catabolic process; C:cytoplasmic side of plasma membrane; F:endoribonuclease activity
Xff	ampE	membrane	C:integral component of membrane
Xff	PD_0969	phage-related protein	C:integral component of membrane
Xff	PD_1069	uroporphyrin-III C-methyltransferase	C:integral component of membrane; F:methyltransferase activity; P:methylation
Xff	PD_0616	hypothetical protein	
Xff	yjcE	Na ⁺ H ⁺ antiporter	F:solute:proton antiporter activity; C:integral component of membrane; P:hydrogen ion transmembrane transport
Xff	algU	DNA-directed DNA polymerase	F:DNA binding; F:DNA-directed DNA polymerase activity; P:DNA replication; P:DNA biosynthetic process
Xff	hemY	porphyrin biosynthesis	C:integral component of membrane; P:heme metabolic process
Xff	PD_0956	peptidase	
Xff	PD_1844	hypothetical protein	
Xff	PD_0039	conserved hypothetical protein	C:integral component of membrane
Xff	gpo	glutathione peroxidase	P:response to oxidative stress; F:glutathione peroxidase activity; P:cellular oxidant detoxification; P:oxidation-reduction process

Xff	PD_0605	cytochrome C oxidase	
Xff	PD_0962	hypothetical protein	
Xff	tnp	IS1327 transposase	F:nucleic acid binding; P:DNA integration
Xff	PD_1415	RTX toxin Ca2+-binding	
Xff	ftsY	signal recognition particle-docking	F:GTP binding; P:cell division; P:SRP-dependent cotranslational protein targeting to membrane; C:cytoplasm; F:GTPase activity; C:intrinsic component of plasma membrane
Xff	PD_0772	DUF4065 domain-containing	
Xff	PD_0299	RTX toxin Ca2+-binding	
Xff	PD_0301	RTX toxin Ca2+-binding	
Xff	PD_0842	conserved hypothetical protein	C:integral component of membrane
Xff	rsuA	pseudouridine synthase	P:pseudouridine synthesis; F:RNA binding; F:pseudouridine synthase activity
Xff	PD_0578	hypothetical protein PD_0578	
Xff	PD_1282	hypothetical protein	C:integral component of membrane
Xff	dpoL_3	truncated phage-related DNA polymerase	
Xfm	hemC	prophobilinogen deaminase	P:peptidyl-pyrromethane cofactor linkage; F:hydroxymethylbilane synthase activity; P:protoporphyrinogen IX biosynthetic process
Xfm	hisH	imidazole glycerol phosphate synthase subunit	C:cytoplasm; P:glutamine metabolic process; F:imidazoleglycerol-phosphate synthase activity; P:histidine biosynthetic process
Xfm	prs	ribose-phosphate pyrophosphokinase	F:magnesium ion binding; F:ATP binding; P:ribonucleoside monophosphate biosynthetic process; C:cytoplasm; P:nucleotide biosynthetic process; F:ribose phosphate diphosphokinase activity; P:phosphorylation; F:kinase activity; P:5-phosphoribose 1-diphosphate biosynthetic process
Xfm	lola	outer membrane lipo carrier	F:lipoprotein transporter activity; C:periplasmic space; P:lipoprotein transport
Xfm	msbA	lipid A export permease ATP-binding	F:ATP binding; P:lipid transport; F:lipid-transporting ATPase activity; P:transmembrane transport; C:ATP-binding cassette (ABC) transporter complex
Xfm	rimK	ribosomal S6 modification	F:magnesium ion binding; F:ATP binding; P:cellular protein modification process; F:acid-amino acid ligase activity; F:manganese ion binding; P:translation
Xfm	rlmN	23S rRNA (adenine(2503)-C(2))-methyltransferase	F:rRNA (adenine-C2-)-methyltransferase activity; C:cytoplasm; F:metal ion binding; P:rRNA base methylation; F:tRNA (adenine-C2-)-methyltransferase activity; F:4 iron, 4 sulfur cluster binding; F:tRNA binding; F:rRNA binding; P:tRNA methylation
Xfm	ileS	isoleucine--tRNA ligase	P:isoleucyl-tRNA aminoacylation; F:ATP binding; F:zinc ion binding; F:isoleucine-tRNA ligase activity; C:cytoplasm; P:regulation of translational fidelity; F:aminoacyl-tRNA editing activity
Xfm	xerC	tyrosine recombinase	P:cell division; F:DNA binding; C:cytoplasm; P:DNA integration; P:chromosome segregation; F:tyrosine-based site-specific recombinase activity; P:cell cycle; P:transposition, DNA-mediated
Xfm	PD_1186	hypothetical protein	
Xfm	PD_0518	alpha-2-macroglobulin family	F:endopeptidase inhibitor activity; P:negative regulation of endopeptidase activity

Xfm	hsf	cell surface	P:pathogenesis; C:outer membrane
Xfm	PD_1971	M48 family peptidase	F:zinc ion binding; C:membrane; P:proteolysis; P:chaperone-mediated protein folding; C:periplasmic space; F:metalloendopeptidase activity
Xfm	trxB	thioredoxin reductase	C:cytoplasm; P:removal of superoxide radicals; F:thioredoxin-disulfide reductase activity; P:oxidation-reduction process
Xfm	lysC	bifunctional aspartate kinase homoserine dehydrogenase I	F:NADP binding; F:aspartate kinase activity; P:aspartate family amino acid biosynthetic process; P:oxidation-reduction process; P:phosphorylation; F:amino acid binding; F:homoserine dehydrogenase activity
Xfm	PD_1352	hypothetical protein	C:integral component of membrane
Xfm	argE	acetylornithine deacetylase	P:metabolic process; F:acetylornithine deacetylase activity
Xfm	estA	autotransporter domain-containing esterase	F:carboxylic ester hydrolase activity
Xfm	PD_1470	segregation and condensation B	P:cell division; C:cytoplasm; P:chromosome separation
Xfm	PD_1669	conserved hypothetical protein	C:integral component of membrane
Xfm	PD_1009	hypothetical protein	
Xfm	nohA	Phage DNA packaging Nu1	
Xfm	gyrB	DNA gyrase subunit B	F:magnesium ion binding; F:DNA binding; F:ATP binding; C:cytoplasm; P:DNA-dependent DNA replication; C:chromosome; F:DNA topoisomerase type II (ATP-hydrolyzing) activity; P:DNA topological change
Xfm	PD_0994	hypothetical protein	C:integral component of membrane
Xfm	parC	DNA topoisomerase IV subunit A	F:DNA binding; F:ATP binding; P:chromosome segregation; C:chromosome; F:DNA topoisomerase type II (ATP-hydrolyzing) activity; P:DNA topological change; C:extrinsic component of plasma membrane
Xfm	mucD	family serine endoprotease	F:2-alkenal reductase [NAD(P)] activity; P:proteolysis; F:serine-type endopeptidase activity; P:oxidation-reduction process
Xfm	PD_1703	lipase	P:lipid catabolic process; F:triglyceride lipase activity
Xfm	gluP	glucose galactose MFS transporter	C:Gram-negative-bacterium-type cell wall; C:integral component of membrane; F:galactose transmembrane transporter activity; P:galactose transport; F:glucose transmembrane transporter activity; P:glucose transmembrane transport
Xfm	PD_0538	hypothetical protein	
Xfm	traC	DNA primase	
Xfm	pilA	prepilin-type cleavage methylation domain-containing	C:integral component of membrane; P:cell adhesion; C:pilus
Xfm	tolA	cell envelope integrity	C:integral component of membrane; P:transport; F:transporter activity
Xfm	PD_2045	DUF3106 domain-containing	
Xfm	PD_1158	conserved hypothetical protein	
Xfm	PD_1431	hypothetical protein PD_1431	
Xfm	PD_2068	Uncharacterized conserved	

Xfm	recD	exodeoxyribonuclease V subunit alpha	F:DNA binding; F:ATP binding; P:nucleic acid phosphodiester bond hydrolysis; P:DNA duplex unwinding; P:double-strand break repair via homologous recombination; F:ATP-dependent DNA helicase activity; C:exodeoxyribonuclease V complex; F:exodeoxyribonuclease V activity
Xfm	PD_1347	DUF1376 domain-containing	
Xfm	PD_1511	hypothetical protein	C:integral component of membrane
Xfm	tldD	metalloprotease	P:proteolysis; F:metallopeptidase activity
Xfm	PD_1003	hypothetical protein	
Xfm	dnaJ_1	cytochrome c biogenesis	F:unfolded protein binding; P:protein folding
Xfm	PD_1112	conserved hypothetical protein	C:integral component of membrane
Xfp	bamD	outer membrane assembly factor	P:Gram-negative-bacterium-type cell outer membrane assembly; C:cell outer membrane; P:protein insertion into membrane
Xfp	dapF	diaminopimelate epimerase	F:diaminopimelate epimerase activity; C:cytoplasm; P:lysine biosynthetic process via diaminopimelate
Xfp	PD_1253	elongation factor P	F:translation elongation factor activity; C:cytoplasm; P:translational elongation
Xfp	tsf	elongation factor Ts	F:translation elongation factor activity; C:cytoplasm; P:translational elongation
Xfp	fabA	3-hydroxydecanoyl-ACP dehydratase	F:3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity; C:cytoplasm; F:3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase activity; F:trans-2-decenoyl-acyl-carrier-protein isomerase activity; P:fatty acid biosynthetic process
Xfp	foIE	GTP cyclohydrolase I	F:GTP binding; F:zinc ion binding; C:cytoplasm; F:GTP cyclohydrolase I activity; P:7,8-dihydroneopterin 3'-triphosphate biosynthetic process; P:tetrahydrofolate biosynthetic process; P:one-carbon metabolic process
Xfp	hmp	nitric oxide dioxygenase	F:oxygen binding; F:FAD binding; F:metal ion binding; P:oxygen transport; P:response to nitrosative stress; P:oxidation-reduction process; F:oxygen transporter activity; P:response to toxic substance; F:nitric oxide dioxygenase activity; F:heme binding
Xfp	lifO	lipase chaperone	P:lipid catabolic process; C:integral component of membrane; F:unfolded protein binding; P:protein folding; C:plasma membrane
Xfp	minE	cell division topological specificity factor	P:cell division; P:regulation of barrier septum assembly; P:cell cycle
Xfp	nadA	quinolinate synthetase	P:quinolinate biosynthetic process; C:cytoplasm; F:metal ion binding; P:NAD biosynthetic process; F:4 iron, 4 sulfur cluster binding; F:quinolinate synthetase A activity; F:transferase activity, transferring alkyl or aryl (other than methyl) groups
Xfp	nadE	NAD synthetase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:NAD+ synthase (glutamine-hydrolyzing) activity; F:ATP binding; P:NAD biosynthetic process
Xfp	mutL	DNA mismatch repair	F:ATP binding; P:mismatch repair; F:mismatched DNA binding
Xfp	pncB	nicotinate phosphoribosyltransferase	F:nicotinate-nucleotide diphosphorylase (carboxylating) activity; F:nicotinate phosphoribosyltransferase activity; P:NAD biosynthetic process; P:nicotinate nucleotide biosynthetic process; F:ligase activity
Xfp	pgk	phosphoglycerate kinase	F:ATP binding; C:cytoplasm; F:phosphoglycerate kinase activity; P:glycolytic process
Xfp	pilY1_1	fimbrial assembly	C:type IV pilus; F:metal ion binding; P:type IV pilus-dependent motility

Xfp	prmC	-(glutamine-N5) release factor-specific	F:nucleic acid binding; F:protein-glutamine N-methyltransferase activity; P:peptidyl-glutamine methylation
Xfp	psd	phosphatidylserine decarboxylase	P:phosphatidylethanolamine biosynthetic process; F:phosphatidylserine decarboxylase activity; C:plasma membrane
Xfp	pyrF	orotidine 5 -phosphate decarboxylase	P:'de novo' pyrimidine nucleobase biosynthetic process; F:orotidine-5'-phosphate decarboxylase activity; P:'de novo' UMP biosynthetic process
Xfp	rimP	ribosome maturation factor	C:cytoplasm; P:ribosomal small subunit biogenesis
Xfp	rplM	50S ribosomal L13	F:structural constituent of ribosome; C:ribosome; P:translation
Xfp	rpsQ	30S ribosomal S17	F:structural constituent of ribosome; C:ribosome; F:rRNA binding; P:translation
Xfp	rsmG	16S rRNA methyltransferase	C:cytoplasm; F:rRNA (guanine-N7-)-methyltransferase activity; P:rRNA (guanine-N7)-methylation
Xfp	slyX	SLYX_XYLFT ame: Full= homolog	
Xfp	proS	proline--tRNA ligase	F:ATP binding; C:cytoplasm; P:regulation of translational fidelity; F:proline-tRNA ligase activity; F:aminoacyl-tRNA editing activity; P:prolyl-tRNA aminoacylation
Xfp	PD_1275	Holliday junction resolvase	F:nucleic acid binding; P:nucleic acid phosphodiester bond hydrolysis; C:cytoplasm; F:nuclease activity; P:rRNA 5'-end processing
Xfp	PD_0964	hypothetical protein	
Xfp	PD_0965	hypothetical protein	
Xfp	lpdA	dihydrolipoamide dehydrogenase	C:cell; F:flavin adenine dinucleotide binding; P:cell redox homeostasis; P:oxidation-reduction process; F:dihydrolipoyl dehydrogenase activity
Xfp	PD_1014	phage-type endonuclease	F:DNA binding; P:nucleic acid phosphodiester bond hydrolysis; F:nuclease activity
Xfp	PD_1954	family transporter	C:integral component of membrane
Xfp	PD_1790	hypothetical protein	
Xfp	clp	transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated; C:intracellular
Xfp	PD_2046	hypothetical protein	C:integral component of membrane
Xfp	PD_1317	MBL fold metallo-hydrolase	F:hydrolase activity
Xfp	PD_1414	conserved hypothetical protein	C:integral component of membrane
Xfp	PD_0866	integral membrane	C:integral component of membrane
Xfp	PD_0978	DUF2184 domain-containing	
Xfp	pspA	hemagglutinin-like secreted	
Xfp	PD_0123	hypothetical protein	
Xfp	tctE	sensor histidine kinase	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfp	PD_0780	hypothetical protein	
Xfp	PD_2091	hypothetical protein	
Xfp	PD_1416	hypothetical protein	C:integral component of membrane

Xfp	PD_0512	bacteriophage terminase large (ATPase) subunit and inactivated derivatives	
Xfp	PD_1720	hypothetical protein	
Xfp	PD_1330	hypothetical protein	
Xfp	PD_1332	glyoxalase	F:dioxygenase activity; F:lyase activity; P:oxidation-reduction process
Xfp	PD_0806	DUF1631 domain-containing	
Xfp	mutT_1	NUDIX hydrolase	F:hydrolase activity
Xfp	gumJ	lipopolysaccharide biosynthesis	C:integral component of membrane
Xfp	PD_1211	lipase	P:lipid catabolic process; F:triglyceride lipase activity
Xfp	slpD	peptidase S33	P:proteolysis; C:integral component of membrane; F:peptidase activity
Xfp	PD_1907	hypothetical protein	
Xfp	PD_0103	membrane	C:integral component of membrane
Xfp	ctp	peptidase S41	P:proteolysis; F:serine-type peptidase activity
Xfp	PD_1509	hypothetical protein	C:integral component of membrane
Xfp	PD_1173	tail	
Xfp	PD_1122	hypothetical protein	
Xfp	algC	phosphomannomutase phosphoglucomutase	P:carbohydrate metabolic process; F:intramolecular transferase activity, phosphotransferases; C:integral component of membrane
Xfp	PD_1002	Prophage antirepressor	
Xfp	PD_2025	N-acetylmuramoyl-L-alanine amidase	P:peptidoglycan catabolic process; F:N-acetylmuramoyl-L-alanine amidase activity
Xfp	sspA	stringent starvation A	F:transferase activity
Xfp	thiD	phosphomethylpyrimidine kinase	F:ATP binding; F:phosphomethylpyrimidine kinase activity; P:phosphorylation; P:thiamine biosynthetic process
Xfp	PD_0312	outer membrane	
Xfp	PD_1405	conserved hypothetical protein	
Xfp	PD_0997	---NA---	
Xfp	PD_0076	glycosyl transferase	F:transferase activity
Xfp	PD_1717	DUF86 domain-containing	
Xfp	PD_1508	hypothetical protein	
Xfp	phoA	alkaline phosphatase	P:dephosphorylation; F:alkaline phosphatase activity
Xfp	tonB_3	energy transducer	C:integral component of membrane; P:transport
Xfp	lysC_1	diaminopimelate decarboxylase	F:diaminopimelate decarboxylase activity; F:aspartate kinase activity; P:lysine biosynthetic process via diaminopimelate; P:phosphorylation; F:amino acid binding
Xfp	PD_0858	DUF4440 domain-containing	F:calmodulin binding; F:calmodulin-dependent protein kinase activity; P:protein phosphorylation
Xfp	PD_0834	hypothetical protein	
Xfp	trx	Thioredoxin domain-containing	C:cell; F:protein disulfide oxidoreductase activity; P:glycerol ether metabolic process; P:cell redox homeostasis; P:oxidation-

reduction process			
Xfp	PD_0147	hypothetical protein	C:integral component of membrane
Xfp	apbE	FAD: FMN transferase	F:metal ion binding; P:protein flavinylation; F:transferase activity; C:plasma membrane
Xfp	PD_0564	conserved hypothetical protein	
Xfp	PD_1127	hypothetical protein	
Xfp	PD_0775	hypothetical protein	C:integral component of membrane
Xfp	PD_0160	---NA---	
Xfp	PD_1421	RTX toxin Ca ²⁺ -binding	
Xfp	korB	transcriptional repressor	F:DNA binding
Xfp	moeB_1	molybdopterin-synthase adenylyltransferase	F:small protein activating enzyme activity
Xfp	PD_0789	recombinase family	F:DNA binding; F:recombinase activity; C:integral component of membrane; P:DNA recombination
Xfp	PD_1843	conserved hypothetical protein	
Xfp	PD_1770	transferase hexapeptide (six repeat-containing)	
Xfp	PD_1978	hypothetical protein	C:integral component of membrane
Xfp	PD_0585	hypothetical protein	C:integral component of membrane
Xfp	PD_0008	TPR repeat-containing	

Table S7 – Recombining genes for each *Xylella* subspecies

Genetic Cluster	Gene	Description	GO Names
Xff	cls	cardiolipin synthase	F:cardiolipin synthase activity; C:integral component of membrane; C:plasma membrane; P:cardiolipin biosynthetic process
Xff	PD_0125	peptidase C1	F:nucleotide binding; P:proteolysis; F:cysteine-type peptidase activity
Xff	pyrE	orotate phosphoribosyltransferase	F:magnesium ion binding; P:'de novo' UMP biosynthetic process; F:orotate phosphoribosyltransferase activity
Xff	SLO_37511_37909_2	cardiolipin synthase	F:cardiolipin synthase activity; C:integral component of membrane; C:plasma membrane; P:cardiolipin biosynthetic process
Xff	SLO_134200_134390_2	peptidase C1	F:nucleotide binding; P:proteolysis; F:cysteine-type peptidase activity
Xff	enpP	alkaline phosphatase family	P:nucleic acid phosphodiester bond hydrolysis; F:phosphodiesterase I activity

Xff	SLO_359977_360255_2	orotate phosphoribosyltransferase	F:magnesium ion binding; P:'de novo' UMP biosynthetic process; F:orotate phosphoribosyltransferase activity
Xff	carA	carbamoyl phosphate synthase small subunit	F:ATP binding; P:'de novo' pyrimidine nucleobase biosynthetic process; P:arginine biosynthetic process; P:glutamine metabolic process; F:carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity; P:'de novo' UMP biosynthetic process
Xff	PD_0008	TPR domain component of system	
Xff	slpD	peptidase S33	P:proteolysis; C:integral component of membrane; F:peptidase activity
Xff	copB	copper resistance B	P:cellular copper ion homeostasis; F:copper ion binding; C:cell outer membrane
Xff	Xylella_fastidiosa_Strain_CFBP8073_48377_48503_4	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xff	Xylella_fastidiosa_Strain_CFBP8073_48968_49160_4	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xff	cyoB	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xff	folB	dihydroneopterin aldolase	F:dihydroneopterin aldolase activity; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process
Xff	Xylella_fastidiosa_Strain_CFBP8073_113629_113727_4	glucokinase	F:ATP binding; P:glucose 6-phosphate metabolic process; P:glycolytic process; F:glucokinase activity
Xff	Xylella_fastidiosa_Strain_CFBP8073_113728_113900_2	glucokinase	F:ATP binding; P:glucose 6-phosphate metabolic process; P:glycolytic process; F:glucokinase activity
Xff	PD_0680	glucokinase	F:ATP binding; P:glucose 6-phosphate metabolic process; P:glycolytic process; F:glucokinase activity
Xff	PD_0386	phosphoglycerate mutase	
Xff	Xylella_fastidiosa_Strain_CFBP8073_133967_134099_2	peptidase C1	F:nucleotide binding; P:proteolysis; F:cysteine-type peptidase activity

Xff	Xylella_fastidiosa_Strain_CFBP8073_134100_134601_4	peptidase C1	P:proteolysis; F:cysteine-type peptidase activity
Xff	Xylella_fastidiosa_Strain_CFBP8073_150262_150300_4	---NA---	
Xff	PD_0679	antibiotic resistance	C:integral component of membrane
Xff	PD_1080	family pyridoxal phosphate-dependent enzyme	
Xff	PD_1741	hypothetical protein	
Xff	Xylella_fastidiosa_Strain_CFBP8073_216414_216456_4	---NA---	
Xff	hemL	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1-semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process
Xff	Xylella_fastidiosa_Strain_CFBP8073_279571_279646_1	organic solvent ABC transporter	
Xff	ttg2D	organic solvent ABC transporter	
Xff	PD_2039	multicopper oxidase family	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xff	pstA	phosphate ABC transporter permease	C:integral component of plasma membrane; F:inorganic phosphate transmembrane transporter activity; P:phosphate ion transmembrane transport
Xff	Xylella_fastidiosa_Strain_CFBP8073_368386_368486_4	---NA---	
Xff	recJ	ssDNA-specific exonuclease	F:nucleic acid binding; F:5'-3' exonuclease activity; P:DNA repair; P:nucleic acid phosphodiester bond hydrolysis; P:DNA recombination
Xff	rnt	ribonuclease T	F:magnesium ion binding; F:nucleic acid binding; P:RNA phosphodiester bond hydrolysis, exonucleolytic; P:tRNA processing; F:exoribonuclease activity, producing 5'-phosphomonoesters
Xff	rsgA	ribosome small subunit-dependent GTPase A	F:GTP binding; F:metal ion binding; F:GTPase activity
Xff	Xylella_fastidiosa_Strain_CFBP8073_437264_437887_4	Fe-S cluster assembly	
Xff	PD_0286	Fe-S cluster assembly	
Xff	thiD	phosphomethylpyrimidine kinase	F:ATP binding; F:phosphomethylpyrimidine kinase activity; P:phosphorylation; P:thiamine biosynthetic process

Xff	thrB	homoserine kinase	F:homoserine kinase activity; F:ATP binding; C:cytoplasm; P:threonine biosynthetic process; P:phosphorylation
Xff	PD_1899	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1	F:ATP binding; P:tRNA threonylcarbamoyladenine modification
Xff	PD_0061	pilus assembly	P:chaperone-mediated protein folding; C:outer membrane-bounded periplasmic space; P:cell wall organization; P:pilus organization
Xff	PD_1162	N-acylglucosamine 2-epimerase	F:catalytic activity
Xff	atpF	ATP synthase subunit B	C:proton-transporting ATP synthase complex, coupling factor F(o); C:integral component of membrane; C:plasma membrane; F:proton-transporting ATP synthase activity, rotational mechanism; P:plasma membrane ATP synthesis coupled proton transport
Xff	atpH	ATP synthase FOF1 subunit delta	C:proton-transporting ATP synthase complex, catalytic core F(1); C:plasma membrane; F:proton-transporting ATP synthase activity, rotational mechanism; P:plasma membrane ATP synthesis coupled proton transport
Xff	dapB	dihydrodipicolinate reductase	F:NADP binding; F:oxidoreductase activity, acting on CH or CH2 groups, NAD or NADP as acceptor; C:cytoplasm; F:NAD binding; P:lysine biosynthetic process via diaminopimelate; F:4-hydroxy-tetrahydrodipicolinate reductase; P:oxidation-reduction process; P:diaminopimelate biosynthetic process
Xff	PD_0274	16S rRNA (guanine(966)-N(2))-methyltransferase	F:nucleic acid binding; P:rRNA methylation; F:16S rRNA (guanine(966)-N(2))-methyltransferase activity
Xff	X_fastidiosa_M23_133800_134390_2	peptidase C1	F:nucleotide binding; P:proteolysis; F:cysteine-type peptidase activity
Xff	PD_0121	hypothetical protein	C:integral component of membrane
Xff	X_fastidiosa_M23_359977_360593_2	orotate phosphoribosyltransferase	F:magnesium ion binding; P:'de novo' UMP biosynthetic process; F:orotate phosphoribosyltransferase activity
Xff	PD_1845	fructose-bisphosphate aldolase	P:glycolytic process; F:fructose-bisphosphate aldolase activity
Xff	orn	oligoribonuclease	F:nucleic acid binding; P:RNA phosphodiester bond hydrolysis, exonucleolytic; C:cytoplasm; F:exoribonuclease activity, producing 5'-phosphomonoesters
Xff	attO	family transcriptional regulator	F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated; F:sequence-specific DNA binding
Xff	rmd	GDP-mannose 4,6	

dehydratase			
Xff	xf44_494065_494099_4	---NA---	
Xff	engB	GTP-binding	F:magnesium ion binding; F:GTP binding; P:cell division; F:GTPase activity; P:cell cycle
Xff	htpG	molecular chaperone	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress
Xff	xf51_39573_39861_4	---NA---	
Xff	xf51_66226_66261_4	---NA---	
Xff	ttcA	tRNA 2-thiocytidine(32) synthetase	F:ATP binding; C:cytoplasm; P:tRNA processing
Xff	fabD	malonyl -acyl carrier transacylase	F:[acyl-carrier-protein] S-malonyltransferase activity; P:metabolic process
Xff	nuoI	NADH-quinone oxidoreductase subunit	
Xff	Xylella_fastidiosa_EB92_1_344171_344895_4	phosphate ABC transporter permease	C:integral component of plasma membrane; F:inorganic phosphate transmembrane transporter activity; P:phosphate ion transmembrane transport
Xff	Xylella_fastidiosa_EB92_1_449978_450635_4	Homoserine kinase	F:homoserine kinase activity; F:ATP binding; C:cytoplasm; P:threonine biosynthetic process; P:phosphorylation
Xf morus	nagA	N-acetylglucosamine-6-phosphate deacetylase	P:carbohydrate metabolic process; P:N-acetylglucosamine metabolic process; F:N-acetylglucosamine-6-phosphate deacetylase activity
Xf morus	ygjT	Integral membrane	C:integral component of membrane
Xf morus	yadF	carbonate dehydratase	F:ATP binding; F:zinc ion binding; P:'de novo' pyrimidine nucleobase biosynthetic process; P:arginine biosynthetic process; P:glutamine metabolic process; F:carbonate dehydratase activity; F:carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity; P:'de novo' UMP biosynthetic process; P:carbon utilization
Xf morus	X_fastidiosa_MUL0034_41646_41697_2	---NA---	
Xf morus	dapF	diaminopimelate epimerase	F:diaminopimelate epimerase activity; C:cytoplasm; P:lysine biosynthetic process via diaminopimelate
Xf morus	X_fastidiosa_MUL0034_59749_60016_2	RNA polymerase-binding	F:zinc ion binding
Xf morus	engB	GTP-binding	F:magnesium ion binding; F:GTP binding; P:cell division; F:GTPase activity; P:cell cycle
Xf morus	PD_1491	lysine 2,3-aminomutase	F:catalytic activity; F:metal ion binding; F:4 iron, 4 sulfur cluster binding

Xf morus	folD	methenyltetrahydrofolate cyclohydrolase	P:methionine biosynthetic process; P:purine nucleotide biosynthetic process; P:folic acid-containing compound biosynthetic process; P:tetrahydrofolate interconversion; P:oxidation-reduction process; P:histidine biosynthetic process; F:methenyltetrahydrofolate cyclohydrolase activity; F:methylenetetrahydrofolate dehydrogenase (NADP+) activity
Xf morus	folP	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xf morus	ftsY	signal recognition particle-docking	F:GTP binding; P:cell division; P:SRP-dependent cotranslational protein targeting to membrane; C:cytoplasm; F:GTPase activity; C:intrinsic component of plasma membrane
Xf morus	gluP_1	MFS transporter	C:Gram-negative-bacterium-type cell wall; C:integral component of membrane; F:fucose transmembrane transporter activity; F:galactose transmembrane transporter activity; P:galactose transport; F:glucose transmembrane transporter activity; P:fucose transport; P:glucose transmembrane transport
Xf morus	glmS_1	iron dicitrate transport regulator	P:carbohydrate metabolic process; F:glutamine-fructose-6-phosphate transaminase (isomerizing) activity; F:carbohydrate binding
Xf morus	X_fastidiosa_MUL0034_129525_131614_2	general secretion pathway	C:integral component of membrane; P:protein secretion; C:plasma membrane
Xf morus	yxaH	DUF418 domain-containing	C:integral component of membrane
Xf morus	pilV	---NA---	
Xf morus	PD_1461	acyltransferase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:transferase activity, transferring acyl groups; P:nitrogen compound metabolic process
Xf morus	PD_2086	hypothetical protein	
Xf morus	PD_2038	DUF2272 domain-containing	
Xf morus	X_fastidiosa_MUL0034_176738_177123_2	haloacid dehalogenase	C:integral component of membrane
Xf morus	PD_0816	CDP-glycerol glycerophosphotransferase	F:CDP-glycerol glycerophosphotransferase activity; C:membrane
Xf morus	PD_0570	polyketide cyclase	C:integral component of membrane
Xf morus	PD_0409	hypothetical protein	
Xf morus	PD_1992	YdiU family protein	
Xf morus	PD_0090	right-handed parallel beta-helix repeat-containing	

Xf morus	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	C:cytoplasm; F:1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity; P:histidine biosynthetic process
Xf morus	lexA	family transcriptional regulator	F:DNA binding; P:DNA repair; P:negative regulation of transcription, DNA-templated; P:transcription, DNA-templated; P:DNA replication; P:proteolysis; F:serine-type endopeptidase activity; P:SOS response
Xf morus	lpxD	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	P:lipid A biosynthetic process; F:N-acyltransferase activity
Xf morus	lpxH	UDP-2,3-diacylglycosamine hydrolase	C:cytoplasm; F:pyrophosphatase activity; P:lipid A biosynthetic process
Xf morus	lysC_1	diaminopimelate decarboxylase	F:diaminopimelate decarboxylase activity; F:aspartate kinase activity; P:lysine biosynthetic process via diaminopimelate; P:phosphorylation; F:amino acid binding
Xf morus	X_fastidiosa_MUL0034_270705_272304_2	efflux RND transporter periplasmic adaptor subunit	P:transmembrane transport; C:membrane
Xf morus	mgo	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xf morus	mtnC	2,3-diketo-5-methylthio-1-phosphopentane phosphatase	F:magnesium ion binding; F:2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase activity; F:2,3-diketo-5-methylthiopentenyl-1-phosphate enolase activity; P:L-methionine salvage from S-adenosylmethionine; P:L-methionine salvage from methylthioadenosine; P:dephosphorylation; F:acireductone synthase activity
Xf morus	mutY	A G-specific adenine glycosylase	F:DNA binding; P:base-excision repair; F:DNA N-glycosylase activity; F:4 iron, 4 sulfur cluster binding
Xf morus	nrdB	ribonucleotide-diphosphate reductase subunit beta	F:ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor; F:metal ion binding; P:DNA replication; P:deoxyribonucleoside diphosphate metabolic process; P:oxidation-reduction process
Xf morus	nuoD	NADH dehydrogenase	F:NADH dehydrogenase (quinone) activity; F:quinone binding; F:NAD binding; P:oxidation-reduction process; P:transport; C:plasma membrane
Xf morus	oxyR	transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated

Xf morus	panC	pantoate--beta-alanine ligase	P:pantothenate biosynthetic process; F:ATP binding; C:cytoplasm; F:pantoate-beta-alanine ligase activity
Xf morus	PD_2039	multicopper oxidase family	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf morus	PD_0279	diguanylate cyclase	C:integral component of membrane
Xf morus	recJ	single-stranded-DNA-specific exonuclease	F:nucleic acid binding; F:5'-3' exonuclease activity; P:DNA repair; P:nucleic acid phosphodiester bond hydrolysis; P:DNA recombination
Xf morus	X_fastidiosa_MUL0034_370517_372826_2	ATP-dependent DNA helicase	F:nucleic acid binding; F:ATP binding; P:DNA repair; F:ATP-dependent 3'-5' DNA helicase activity; P:DNA replication; P:DNA duplex unwinding; P:DNA recombination; P:SOS response; C:intracellular
Xf morus	rfbA	glucose-1-phosphate thymidyltransferase	F:glucose-1-phosphate thymidyltransferase activity; F:metal ion binding; P:extracellular polysaccharide biosynthetic process
Xf morus	ribA_1	3,4-dihydroxy-2-butanone-4-phosphate synthase	F:metal ion binding; P:riboflavin biosynthetic process; F:3,4-dihydroxy-2-butanone-4-phosphate synthase activity
Xf morus	PD_1665	oxidoreductase	F:RNA binding; C:cytoplasm; F:methyltransferase activity; P:rRNA processing; P:methylation
Xf morus	X_fastidiosa_MUL0034_391974_392129_2	50S ribosomal L21	F:structural constituent of ribosome; C:ribosome; F:rRNA binding; P:translation
Xf morus	rsgA	ribosome small subunit-dependent GTPase A	F:GTP binding; F:metal ion binding; F:GTPase activity
Xf morus	secG	pre translocase subunit	P:protein transmembrane transport; F:P-P-bond-hydrolysis-driven protein transmembrane transporter activity; C:integral component of membrane; P:protein secretion
Xf morus	PD_0707	family transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated
Xf morus	PD_1216	phosphatase	F:protein serine/threonine phosphatase activity; P:protein dephosphorylation
Xf morus	PD_0286	Fe-S cluster assembly	
Xf morus	PD_0507	surface antigen (D15):Surface antigen variable number	C:integral component of membrane; C:cell outer membrane
Xf morus	trpD_1	anthranilate synthase component II	P:glutamine metabolic process; F:transferase activity; F:anthranilate synthase activity
Xf morus	PD_0748	tRNA threonylcarbamoyladenosine biosynthesis	P:proteolysis; P:tRNA threonylcarbamoyladenosine modification; F:peptidase activity
Xf morus	ttcA	tRNA 2-thiocytidine(32) synthetase	F:ATP binding; C:cytoplasm; P:tRNA processing
Xf morus	X_fastidiosa_MUL0034_	polyisoprenoid-binding	

	485992_487159_2		
Xf morus	X_fastidiosa_MUL0034_488835_489334_2	D-hexose-6-phosphate mutarotase	P:carbohydrate metabolic process; F:carbohydrate binding; F:isomerase activity
Xf morus	zipA	cell division	P:FtsZ-dependent cytokinesis; C:integral component of plasma membrane; C:cell division site
Xf morus	PD_0682	family transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated
Xf morus	dapE	succinyl-diaminopimelate desuccinylase	F:zinc ion binding; P:lysine biosynthetic process via diaminopimelate; P:proteolysis; F:succinyl-diaminopimelate desuccinylase activity; F:metallopeptidase activity; F:cobalt ion binding; P:diaminopimelate biosynthetic process
Xf morus	X_fastidiosa_MUL0034_80566_81085_4	colicin transporter	P:protein transport; C:integral component of membrane; F:protein transporter activity
Xf morus	X_fastidiosa_MUL0034_92486_92936_4	dihydroneopterin aldolase	F:dihydroneopterin aldolase activity; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process
Xf morus	PD_1080	family pyridoxal phosphate enzyme	
Xf morus	X_fastidiosa_MUL0034_176582_176737_4	---NA---	
Xf morus	PD_1577	ligand-binding SH3	
Xf morus	X_fastidiosa_MUL0034_229871_230080_4	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1-semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process
Xf morus	holC	---NA---	
Xf morus	PD_1517	P60 family	F:hydrolase activity
Xf morus	mutS	DNA mismatch repair	F:ATP binding; P:mismatch repair; F:mismatched DNA binding; F:damaged DNA binding
Xf morus	nuoE	NADH dehydrogenase	F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduction process; F:2 iron, 2 sulfur cluster binding
Xf morus	kdtA	3-deoxy-D-manno-octulosonic acid transferase	C:integral component of membrane; F:transferase activity
Xf morus	PD_1170	ABC transporter ATP-binding	F:ATPase activity; F:ATP binding
Xf morus	copB	copper resistance B	
Xf morus	pefK	general secretion pathway	C:integral component of membrane; P:protein secretion
Xf morus	PD_0174	haloacid dehalogenase	C:integral component of membrane
Xf morus	mtrC	efflux RND transporter periplasmic adaptor subunit	P:transmembrane transport; C:membrane

Xf morus	recQ	ATP-dependent DNA helicase	F:nucleic acid binding; F:ATP binding; P:DNA repair; F:ATP-dependent 3'-5' DNA helicase activity; P:DNA replication; P:DNA duplex unwinding; P:DNA recombination; P:SOS response; C:intracellular
Xf morus	rplU	50S ribosomal L21	F:structural constituent of ribosome; C:ribosome; F:rRNA binding; P:translation
Xf morus	PD_0573	polyisoprenoid-binding	
Xf morus	PD_1306	D-hexose-6-phosphate mutarotase	P:carbohydrate metabolic process; F:carbohydrate binding; F:isomerase activity
Xf morus	tolQ	colicin transporter	P:protein transport; C:integral component of membrane; F:protein transporter activity
Xf morus	folB	dihydroneopterin aldolase	F:dihydroneopterin aldolase activity; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process
Xf morus	Xylella_fastidiosa_Mul-MD_133454_133568_4	---NA---	
Xf morus	hemL	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1-semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process
Xf morus	Xylella_fastidiosa_Mul-MD_419721_419758_4	---NA---	
Xf sandyi	mrp	sodium:proton antiporter	F:ATPase activity; F:ATP binding; F:metal ion binding; F:iron-sulfur cluster binding
Xf sandyi	Xylella_fastidiosa_strain_CO33_41646_41721_1	copper resistance	P:cellular copper ion homeostasis; F:copper ion binding; C:cell outer membrane
Xf sandyi	dapE	succinyl-diaminopimelate desuccinylase	F:zinc ion binding; P:lysine biosynthetic process via diaminopimelate; P:proteolysis; F:succinyl-diaminopimelate desuccinylase activity; F:metallopeptidase activity; F:cobalt ion binding; P:diaminopimelate biosynthetic process
Xf sandyi	Xylella_fastidiosa_strain_CO33_59749_60056_1	molecular chaperone	F:zinc ion binding
Xf sandyi	PD_1491	EF-P beta-lysylation	F:catalytic activity; F:metal ion binding; F:4 iron, 4 sulfur cluster binding
Xf sandyi	Xylella_fastidiosa_strain_CO33_113629_114216_1	glucokinase	F:ATP binding; P:glucose 6-phosphate metabolic process; P:glycolytic process; F:glucokinase activity
Xf sandyi	PD_0056	hypothetical protein AOT81_05400	
Xf sandyi	PD_0679	antibiotic resistance	C:integral component of membrane
Xf sandyi	PD_1053	DUF58 domain-containing	C:integral component of membrane
Xf sandyi	PD_1056	histidine triad nucleotide-binding	F:catalytic activity
Xf sandyi	Xylella_fastidiosa_strain_CO33_230081_230202_1	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1-semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process

Xf sandyi	kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	P:keto-3-deoxy-D-manno-octulosonic acid biosynthetic process; C:cytoplasm; F:3-deoxy-8-phosphooctulonate synthase activity
Xf sandyi	ppiD	peptidylprolyl isomerase	F:peptidyl-prolyl cis-trans isomerase activity; C:membrane; C:integral component of membrane; P:protein peptidyl-prolyl isomerization; F:isomerase activity
Xf sandyi	rnaSA3	ribonuclease	P:RNA phosphodiester bond hydrolysis, endonucleolytic; F:RNA binding; F:endoribonuclease activity
Xf sandyi	PD_1754	peptidoglycan editing factor	
Xf sandyi	nagA	N-acetylglucosamine-6-phosphate deacetylase	P:carbohydrate metabolic process; P:N-acetylglucosamine metabolic process; F:N-acetylglucosamine-6-phosphate deacetylase activity
Xf sandyi	slpD	peptidase S33	P:proteolysis; F:peptidase activity
Xf sandyi	Xylella_fastidiosa_strain_CO33_55197_55452_2	succinyl-diaminopimelate desuccinylase	F:zinc ion binding; P:lysine biosynthetic process via diaminopimelate; P:proteolysis; F:succinyl-diaminopimelate desuccinylase activity; F:metallopeptidase activity; F:cobalt ion binding; P:diaminopimelate biosynthetic process
Xf sandyi	rpfF	enoyl- hydratase	P:metabolic process; F:isomerase activity
Xf sandyi	folB	dihydroneopterin aldolase	F:dihydroneopterin aldolase activity; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process
Xf sandyi	acvB_1	virulence	
Xf sandyi	pilV	type IV pilus modification	C:membrane; C:integral component of membrane
Xf sandyi	Xylella_fastidiosa_strain_CO33_149862_149900_2	---NA---	
Xf sandyi	Xylella_fastidiosa_strain_CO33_163324_163486_2	family pyridoxal phosphate enzyme	
Xf sandyi	traB	conjugal transfer	C:integral component of membrane
Xf sandyi	PD_0021	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xf sandyi	hup	DNA-binding	F:DNA binding; P:chromosome condensation
Xf sandyi	mtnD	acireductone dioxygenase	F:iron ion binding; P:L-methionine salvage from S-adenosylmethionine; P:L-methionine salvage from methylthioadenosine; F:acireductone dioxygenase [iron(II)-requiring] activity; F:nickel cation binding; F:acireductone dioxygenase (Ni2+-requiring) activity; P:oxidation-reduction process
Xf sandyi	rsgA	RSGA_XYLF2 ame: Full=Small ribosomal subunit biogenesis GTPase	F:GTP binding; F:metal ion binding; F:GTPase activity
Xf sandyi	ttcA	tRNA 2-thiocytidine(32)	F:ATP binding; C:cytoplasm; P:tRNA

		synthetase	processing
Xf sandyi	adhP	hydroxyacid dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf sandyi	apaH	bis(5'-nucleosyl)-tetraphosphatase	F:bis(5'-nucleosyl)-tetraphosphatase (symmetrical) activity
Xf sandyi	copB	copper resistance	P:cellular copper ion homeostasis; F:copper ion binding; C:cell outer membrane
Xf sandyi	PD_0852	colicin V synthesis	C:integral component of membrane; P:toxin biosynthetic process
Xf sandyi	folA	dihydrofolate reductase	F:NADP binding; P:nucleotide biosynthetic process; P:oxidation-reduction process; P:phosphorylation; P:tetrahydrofolate biosynthetic process; F:dihydrofolate reductase activity; P:glycine biosynthetic process; F:kinase activity; P:one-carbon metabolic process
Xf sandyi	dnaK	molecular chaperone	F:ATP binding; F:unfolded protein binding; P:protein folding
Xf sandyi	dps	DNA starvation stationary phase protection	F:oxidoreductase activity, oxidizing metal ions; P:cellular iron ion homeostasis; C:cell; F:DNA binding; F:ferric iron binding; P:oxidation-reduction process; P:response to stress
Xf sandyi	gshI	glutamate--cysteine ligase	P:glutathione biosynthetic process; F:glutamate-cysteine ligase activity
Xf sandyi	Xylella_fastidiosa_strain_CO33_87605_87635_4	---NA---	
Xf sandyi	folP	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xf sandyi	PD_0680	glucokinase	F:ATP binding; P:glucose 6-phosphate metabolic process; P:glycolytic process; F:glucokinase activity
Xf sandyi	PD_0850	chemotaxis	P:chemotaxis; P:signal transduction; F:signal transducer activity
Xf sandyi	Xylella_fastidiosa_strain_CO33_129355_129573_4	---NA---	
Xf sandyi	PD_0125	peptidase C1	P:proteolysis; F:cysteine-type peptidase activity
Xf sandyi	PD_0503	hypothetical protein	
Xf sandyi	PD_0806	DUF1631 domain-containing	
Xf sandyi	PD_1172	hypothetical protein	
Xf sandyi	PD_1219	hypothetical protein	
Xf sandyi	PD_1080	family pyridoxal phosphate-dependent enzyme	
Xf sandyi	PD_1073	SPOR domain-containing	F:peptidoglycan binding
Xf sandyi	PD_0570	polyketide cyclase	C:integral component of membrane
Xf sandyi	PD_0075	zinc CHCC-type	

Xf sandyi	PD_0146	membrane	P:cellular amino acid metabolic process; C:outer membrane
Xf sandyi	xrvA	histone-like nucleoid- structuring	F:DNA binding; P:regulation of transcription, DNA-templated; C:intracellular
Xf sandyi	hemB	delta-aminolevulinic acid dehydratase	F:porphobilinogen synthase activity; F:metal ion binding; P:tetrapyrrole biosynthetic process
Xf sandyi	hemL	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1- semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process
Xf sandyi	hflX	GTPase	F:magnesium ion binding; F:GTP binding; C:cytoplasm; F:GTPase activity
Xf sandyi	yrbE	ABC transporter permease	P:transport; C:ATP-binding cassette (ABC) transporter complex
Xf sandyi	mutS	DNA mismatch repair	F:ATP binding; P:mismatch repair; F:mismatched DNA binding; F:damaged DNA binding
Xf sandyi	panC	pantoate--beta-alanine ligase	P:pantothenate biosynthetic process; F:ATP binding; C:cytoplasm; F:pantoate-beta- alanine ligase activity
Xf sandyi	pcm_1	-L-isoaspartate O- methyltransferase	F:protein-L-isoaspartate (D-aspartate) O- methyltransferase activity; P:protein methylation
Xf sandyi	PD_2039	L-ascorbate oxidase	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf sandyi	prmB	ribosomal L3 N(5)- glutamine methyltransferase	F:nucleic acid binding; F:protein-glutamine N- methyltransferase activity; P:peptidyl- glutamine methylation; C:ribosome; P:DNA methylation on adenine; F:site-specific DNA- methyltransferase (adenine-specific) activity
Xf sandyi	pstA	phosphate ABC transporter permease	C:integral component of plasma membrane; F:inorganic phosphate transmembrane transporter activity; P:phosphate ion transmembrane transport
Xf sandyi	rhlB	ATP-dependent RNA helicase	F:ATP binding; F:RNA binding; C:cytoplasm; F:ATP-dependent RNA helicase activity; P:RNA catabolic process
Xf sandyi	PD_1665	oxidoreductase	F:RNA binding; C:cytoplasm; F:methyltransferase activity; P:rRNA processing; P:methylation
Xf sandyi	PD_0761	transcriptional regulator	
Xf sandyi	serS	seryl-tRNA synthetase	P:selenocysteinyl-tRNA(Sec) biosynthetic process; F:ATP binding; C:cytoplasm; P:selenocysteine biosynthetic process; F:serine-tRNA ligase activity; P:seryl-tRNA aminoacylation
Xf sandyi	slt	---NA---	
Xf sandyi	PD_0286	Fe-S cluster assembly	
Xf sandyi	thrB	Homoserine kinase	F:homoserine kinase activity; F:ATP binding; C:cytoplasm; P:threonine biosynthetic process; P:phosphorylation

Xf sandyi	PD_0748	tRNA threonylcarbamoyladenosi ne biosynthesis	P:proteolysis; P:tRNA threonylcarbamoyladenosine modification; F:peptidase activity
Xf sandyi	PD_0485	ABC transporter ATP- binding	F:ATPase activity; F:ATP binding
Xf sandyi	bamB	outer membrane assembly factor	P:Gram-negative-bacterium-type cell outer membrane assembly; C:membrane; C:cell outer membrane; P:protein insertion into membrane
Xf sandyi	X_fastidiosa_sandyi_An n-1_151395_151881_1	antibiotic resistance	C:integral component of membrane
Xf sandyi	PD_1854	---NA---	
Xf sandyi	rfbA	glucose-1-phosphate thymidyltransferase	F:glucose-1-phosphate thymidyltransferase activity; F:metal ion binding; P:extracellular polysaccharide biosynthetic process
Xf sandyi	X_fastidiosa_sandyi_An n-1_425065_425457_1	lytic murein transglycosylase	C:periplasmic space; F:hydrolase activity, hydrolyzing O-glycosyl compounds
Xf sandyi	X_fastidiosa_sandyi_An n-1_494182_494432_1	hydrolase	P:metabolic process; F:hydrolase activity
Xf sandyi	PD_2050	response regulator receiver	
Xf sandyi	yadF	carbonate dehydratase	F:zinc ion binding; F:carbonate dehydratase activity; P:carbon utilization
Xf sandyi	X_fastidiosa_sandyi_An n-1_55130_55797_2	succinyl-diaminopimelate desuccinylase	F:zinc ion binding; P:lysine biosynthetic process via diaminopimelate; P:proteolysis; F:succinyl-diaminopimelate desuccinylase activity; F:metallopeptidase activity; F:cobalt ion binding; P:diaminopimelate biosynthetic process
Xf sandyi	engB	GTP-binding HSR1-related	F:magnesium ion binding; F:GTP binding; P:cell division; F:GTPase activity; P:cell cycle
Xf sandyi	tolR_1	biopolymer transporter	P:protein transport; C:integral component of membrane; C:plasma membrane; F:transporter activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_87806_87922_2	regulator of pathogenicity	P:metabolic process; F:isomerase activity
Xf sandyi	glmS_1	iron dicitrate transport regulator	P:carbohydrate metabolic process; F:transaminase activity; F:carbohydrate binding
Xf sandyi	X_fastidiosa_sandyi_An n-1_146290_146478_2	type IV pilus modification	C:integral component of membrane
Xf sandyi	X_fastidiosa_sandyi_An n-1_146553_146800_2	hypothetical protein D934_01230	
Xf sandyi	X_fastidiosa_sandyi_An n-1_163178_163260_2	family pyridoxal phosphate enzyme	
Xf sandyi	X_fastidiosa_sandyi_An n-1_190024_190284_2	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xf sandyi	PD_0409	AE003947_7hypothetical protein XF_1117	
Xf sandyi	X_fastidiosa_sandyi_An n-1_241360_241864_2	DNA-binding	F:DNA binding; P:chromosome condensation

Xf sandyi	miaA	tRNA dimethylallyltransferase	F:ATP binding; P:tRNA processing; F:tRNA dimethylallyltransferase activity
Xf sandyi	mltB	lytic murein transglycosylase B	
Xf sandyi	X_fastidiosa_sandyi_An n-1_296032_296572_2	acireductone dioxygenase	F:iron ion binding; P:L-methionine salvage from S-adenosylmethionine; P:L-methionine salvage from methylthioadenosine; F:acireductone dioxygenase [iron(II)-requiring] activity; F:nickel cation binding; F:acireductone dioxygenase (Ni2+-requiring) activity; P:oxidation-reduction process
Xf sandyi	nrdB	ribonucleotide-diphosphate reductase subunit beta	F:ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor; F:metal ion binding; P:DNA replication; P:deoxyribonucleoside diphosphate metabolic process; P:oxidation-reduction process
Xf sandyi	PD_1170	multidrug ABC transporter ATP-binding	F:ATPase activity; F:ATP binding
Xf sandyi	PD_1631	quinone oxidoreductase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf sandyi	X_fastidiosa_sandyi_An n-1_3109_3599_4	hydroxyacid dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf sandyi	ahcY	S-adenosyl-L-homocysteine hydrolase	C:cytoplasm; F:adenosylhomocysteinase activity; P:one-carbon metabolic process
Xf sandyi	bioB	biotin synthase	F:iron ion binding; F:biotin synthase activity; F:4 iron, 4 sulfur cluster binding; P:biotin biosynthetic process; F:2 iron, 2 sulfur cluster binding
Xf sandyi	X_fastidiosa_sandyi_An n-1_27742_28179_4	alpha beta hydrolase	P:proteolysis; F:peptidase activity
Xf sandyi	cmk	cytidylate kinase	F:cytidylate kinase activity; F:ATP binding; P:nucleotide phosphorylation; C:cytoplasm; P:pyrimidine nucleotide metabolic process
Xf sandyi	X_fastidiosa_sandyi_An n-1_41523_41816_4	copper resistance	P:cellular copper ion homeostasis; F:copper ion binding; C:cell outer membrane
Xf sandyi	X_fastidiosa_sandyi_An n-1_48033_48238_4	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xf sandyi	cyoB	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xf sandyi	exoA	DNA-(apurinic or apyrimidinic site) lyase	P:DNA repair; P:nucleic acid phosphodiester bond hydrolysis; F:DNA-(apurinic or apyrimidinic site) lyase activity;

			F:exodeoxyribonuclease III activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_87625_87805_4	regulator of pathogenicity	F:catalytic activity; P:metabolic process
Xf sandyi	frr	dihydropteroate synthase	P:translational termination; C:cytoplasm; F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_123203_123660_4	chemotaxis	P:chemotaxis; P:signal transduction; F:signal transducer activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_133763_134801_4	peptidase C1	P:proteolysis; F:cysteine-type peptidase activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_146142_146289_4	type IV pilus modification	C:integral component of membrane
Xf sandyi	X_fastidiosa_sandyi_An n-1_149784_150300_4	DUF1631 domain- containing	
Xf sandyi	PD_1035	SCP2 domain-containing	
Xf sandyi	PD_1067	hypothetical protein	
Xf sandyi	X_fastidiosa_sandyi_An n-1_163261_163670_4	family pyridoxal phosphate enzyme	
Xf sandyi	PD_1143	hypothetical protein	F:catalytic activity; P:metabolic process
Xf sandyi	PD_2038	DUF2272 domain- containing	
Xf sandyi	PD_1298	hypothetical protein	C:integral component of membrane
Xf sandyi	PD_0161	membrane	C:integral component of membrane
Xf sandyi	xpsl	general secretion pathway I	C:integral component of membrane
Xf sandyi	PD_1165	nucleo polynucleotide- associated enzyme	C:viral nucleocapsid
Xf sandyi	X_fastidiosa_sandyi_An n-1_216834_217255_4	histone-like nucleoid- structuring	F:DNA binding; P:regulation of transcription, DNA-templated; C:intracellular
Xf sandyi	hemF	coproporphyrinogen oxidase	F:protein homodimerization activity; C:cytoplasm; F:coproporphyrinogen oxidase activity; F:metal ion binding; P:oxidation- reduction process; P:protoporphyrinogen IX biosynthetic process
Xf sandyi	X_fastidiosa_sandyi_An n-1_229871_230080_4	glutamate-1-semialdehyde aminotransferase	F:pyridoxal phosphate binding; C:cytoplasm; F:transaminase activity; F:glutamate-1- semialdehyde 2,1-aminomutase activity; P:protoporphyrinogen IX biosynthetic process
Xf sandyi	hisA	1-(5-phosphoribosyl)-5- [(5-phosphoribosylamino)met hylideneamino] imidazole- 4-carboxamide isomerase	C:cytoplasm; F:1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino]imi dazole-4-carboxamide isomerase activity; P:histidine biosynthetic process
Xf sandyi	holC	DNA polymerase III subunit chi	F:DNA binding; F:DNA-directed DNA polymerase activity; P:DNA replication; P:DNA biosynthetic process
Xf sandyi	PD_0615	luciferase	F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; P:oxidation-reduction

			process
Xf sandyi	PD_1858	membrane	C:integral component of membrane
Xf sandyi	ttg2D	organic solvent ABC transporter	
Xf sandyi	X_fastidiosa_sandyi_An n-1_318469_318624_4	pantoate--beta-alanine ligase	P:pantothenate biosynthetic process; F:ATP binding; C:cytoplasm; F:pantoate-beta-alanine ligase activity
Xf sandyi	X_fastidiosa_sandyi_An n-1_328217_328496_4	multicopper oxidase family	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xf sandyi	X_fastidiosa_sandyi_An n-1_335633_337602_4	peptidylprolyl isomerase	F:peptidyl-prolyl cis-trans isomerase activity; C:integral component of membrane; P:protein peptidyl-prolyl isomerization
Xf sandyi	X_fastidiosa_sandyi_An n-1_343781_344902_4	phosphate ABC transporter permease	C:integral component of plasma membrane; F:inorganic phosphate transmembrane transporter activity; P:phosphate ion transmembrane transport
Xf sandyi	radA	DNA repair	F:ATP binding; P:DNA repair; F:DNA-dependent ATPase activity; F:metal ion binding; F:methyltransferase activity; F:damaged DNA binding; P:methylation
Xf sandyi	rbfA	ribosome-binding factor A	C:cytoplasm; P:rRNA processing
Xf sandyi	recQ	ATP-dependent DNA helicase	F:nucleic acid binding; F:ATP binding; P:DNA repair; F:ATP-dependent 3'-5' DNA helicase activity; P:DNA replication; P:DNA duplex unwinding; P:DNA recombination; P:SOS response; C:intracellular
Xf sandyi	actR	two-component system response regulator	P:phosphorelay signal transduction system; F:sequence-specific DNA binding; C:intracellular
Xf sandyi	X_fastidiosa_sandyi_An n-1_380781_381787_4	oxidoreductase	F:RNA binding; C:cytoplasm; F:methyltransferase activity; P:rRNA processing; P:methylation
Xf sandyi	rnd	ribonuclease D	F:nucleotide binding; F:nucleic acid binding; F:3'-5' exonuclease activity; P:RNA phosphodiester bond hydrolysis, exonucleolytic; P:tRNA processing; F:ribonuclease D activity; C:intracellular
Xf sandyi	rpiA	ribose-5-phosphate isomerase	P:pentose-phosphate shunt, non-oxidative branch; F:ribose-5-phosphate isomerase activity
Xf sandyi	rpoD	RNA polymerase sigma factor	P:transcription initiation from bacterial-type RNA polymerase promoter; F:DNA binding; F:sigma factor activity; F:transcription factor activity, sequence-specific DNA binding; C:cytoplasm; P:regulation of transcription, DNA-templated
Xf sandyi	PD_0707	family transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated

Xf sandyi	speA	arginine decarboxylase	P:arginine catabolic process; F:arginine decarboxylase activity; F:metal ion binding; P:spermidine biosynthetic process
Xf sandyi	PD_1216	serine threonine-phosphatase	F:protein serine/threonine phosphatase activity; P:protein dephosphorylation
Xf sandyi	sucB	dihydrolipoamide succinyltransferase	F:dihydrolipoyllysine-residue succinyltransferase activity; C:oxoglutarate dehydrogenase complex; P:tricarboxylic acid cycle; P:L-lysine catabolic process to acetyl-CoA via saccharopine
Xf sandyi	X_fastidiosa_sandyi_An_n-1_450209_450787_4	Homoserine kinase	F:homoserine kinase activity; F:ATP binding; C:cytoplasm; P:threonine biosynthetic process; P:phosphorylation
Xf sandyi	X_fastidiosa_sandyi_An_n-1_464314_465745_4	tRNA 2-thiocytidine(32) synthetase	F:ATP binding; C:cytoplasm; P:tRNA processing
Xf sandyi	uppS	UDP diphosphate synthase	F:magnesium ion binding; P:regulation of cell shape; P:peptidoglycan biosynthetic process; P:cell wall organization; F:di-trans,poly-cis-decaprenylcistransferase activity
Xf sandyi	xpsD	type II secretion system	F:protein transporter activity; P:protein secretion by the type II secretion system; C:cell outer membrane; C:type II protein secretion system complex
Xf sandyi	PD_1306	D-hexose-6-phosphate mutarotase	P:carbohydrate metabolic process; F:carbohydrate binding; F:isomerase activity
Xf sandyi	PD_0199	transcriptional regulator	
Xfm	polygala_6257_7385_3	adenosylhomocysteinase	C:cytoplasm; F:adenosylhomocysteinase activity; P:one-carbon metabolic process
Xfm	polygala_168272_168541_4	peptidoglycan-binding domain-containing	
Xfm	Xylella_fastidiosa_Strain_CFBP8072_280961_281061_4	ABC transporter permease	
Xfm	Xylella_fastidiosa_Strain_CFBP8416_12688_12936_4	---NA---	
Xfm	Xylella_fastidiosa_Strain_CFBP8416_222654_222791_4	---NA---	
Xfm	Xylella_fastidiosa_Strain_CFBP8416_304967_304995_4	---NA---	
Xfm	Xylella_fastidiosa_Strain_CFBP8416_306538_306609_4	---NA---	
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_2687_3518_3	NAD(P)-dependent alcohol dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process

Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_21339_22250_3	serine threonine kinase	P:Gram-negative-bacterium-type cell outer membrane assembly; C:cell outer membrane; F:protein serine/threonine kinase activity; P:protein phosphorylation; P:protein insertion into membrane
Xfm	bfr	bacterioferritin	P:cellular iron ion homeostasis; C:cell; F:ferric iron binding; P:iron ion transport; P:oxidation- reduction process; F:ferroxidase activity
Xfm	cmk	cytidylate kinase	F:cytidylate kinase activity; F:ATP binding; P:nucleotide phosphorylation; C:cytoplasm; P:pyrimidine nucleotide metabolic process
Xfm	fabB_1	3-oxoacyl-ACP synthase	P:metabolic process; F:transferase activity
Xfm	PD_1615	prepilin-type N-terminal cleavage methylation domain-containing	F:protein transporter activity; P:protein secretion by the type II secretion system; C:type II protein secretion system complex
Xfm	folE	GTP cyclohydrolase	F:GTP binding; F:zinc ion binding; C:cytoplasm; F:GTP cyclohydrolase I activity; P:7,8-dihydroneopterin 3'-triphosphate biosynthetic process; P:tetrahydrofolate biosynthetic process; P:one-carbon metabolic process
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_97413_97788_3	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_128541_129191_3	membrane	C:integral component of membrane
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_153444_155324_3	sulfite exporter family	C:integral component of membrane; C:plasma membrane
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_207484_210415_3	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_234149_234718_3	GTPase	F:magnesium ion binding; F:GTP binding; C:cytoplasm; F:GTPase activity
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_236335_237095_3	DNA polymerase III subunit delta	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	htrB	lipid A biosynthesis lauroyl acyltransferase	C:integral component of plasma membrane; F:lauroyltransferase activity; P:lipopolysaccharide biosynthetic process; P:lipid A biosynthetic process; P:Kdo2-lipid A biosynthetic process
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_274513_275578_3	S-adenosylmethionine synthetase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; P:S-adenosylmethionine biosynthetic process; F:methionine adenosyltransferase activity; P:one-carbon metabolic process
Xfm	Xylella_fastidiosa_strain _sycamore_Sy- VA_277158_277992_3	tRNA dimethylallyltransferase	F:ATP binding; P:tRNA processing; F:tRNA dimethylallyltransferase activity

Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_321405_321916_3	pyridoxine 5 -phosphate synthase	P:pyridoxine biosynthetic process; C:cytoplasm; F:pyridoxine 5'-phosphate synthase activity
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_325638_326560_3	two-component sensor histidine kinase	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_343515_344170_3	phosphatidylserine decarboxylase	P:phosphatidylethanolamine biosynthetic process; F:phosphatidylserine decarboxylase activity; C:plasma membrane
Xfm	rsmH	16S rRNA (cytosine(1402)-N(4))-methyltransferase	C:cytoplasm; P:rRNA base methylation; F:rRNA (cytosine-N4-)-methyltransferase activity
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_423976_425803_3	murein transglycosylase	C:periplasmic space; F:hydrolase activity, hydrolyzing O-glycosyl compounds
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_442547_443935_3	lipopolysaccharide biosynthesis	C:integral component of membrane; F:phospho-N-acetylmuramoyl-pentapeptide-transferase activity
Xfm	Xylella_fastidiosa_strain_sycamore_Sy-VA_478650_480440_3	type II secretion system	F:protein transporter activity; P:protein secretion by the type II secretion system; C:cell outer membrane; C:type II protein secretion system complex
Xfm	X_fastidiosa_M12_2624_91_262573_4	acetyltransferase	
Xfm	PD_1974	DUF4019 domain-containing	
Xfm	xf20_239858_241409_3	molecular chaperone	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress
Xfm	ispB	octaprenyl-diphosphate synthase	F:heptaprenyl diphosphate synthase activity; P:isoprenoid biosynthetic process
Xfm	yggB	mechanosensitive ion channel	P:transmembrane transport; C:integral component of membrane
Xfm	PD_0274	16S rRNA (guanine(966)-N(2))-methyltransferase	F:nucleic acid binding; P:rRNA methylation; F:16S rRNA (guanine(966)-N(2))-methyltransferase activity
Xfm	uppS	UDP diphosphate synthase	F:magnesium ion binding; P:regulation of cell shape; P:peptidoglycan biosynthetic process; P:cell wall organization; F:di-trans,poly-cis-decaprenylcistransferase activity
Xfm	PD_1754	peptidoglycan editing factor	
Xfm	xf21_21339_22276_3	serine threonine kinase	P:Gram-negative-bacterium-type cell outer membrane assembly; C:cell outer membrane; F:protein serine/threonine kinase activity; P:protein phosphorylation; P:protein insertion into membrane
Xfm	xf21_128541_129524_3	membrane	C:integral component of membrane
Xfm	xf21_173456_173506_1	---NA---	
Xfm	xf21_277137_277801_3	tRNA	F:ATP binding; P:tRNA processing; F:tRNA

		dimethylallyltransferase	dimethylallyltransferase activity
Xfm	pdxJ	pyridoxine 5 -phosphate synthase	P:pyridoxine biosynthetic process; C:cytoplasm; F:pyridoxine 5'-phosphate synthase activity
Xfm	PD_2039	multicopper oxidase family	F:copper ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xfm	xf21_343560_344170_3	phosphatidylserine decarboxylase	P:phosphatidylethanolamine biosynthetic process; F:phosphatidylserine decarboxylase activity; C:plasma membrane
Xfm	apaH	bis(5 -nucleosyl)-tetrphosphatase	F:bis(5'-nucleosyl)-tetrphosphatase (symmetrical) activity
Xfm	bamB	serine threonine kinase	P:Gram-negative-bacterium-type cell outer membrane assembly; C:cell outer membrane; F:protein serine/threonine kinase activity; P:protein phosphorylation; P:protein insertion into membrane
Xfm	xf22_30718_31483_3	family DNA-binding transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated; F:alanine racemase activity
Xfm	xf22_46803_51004_3	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	dapA	dihydrodipicolinate synthase	C:cytoplasm; P:lysine biosynthetic process via diaminopimelate; F:4-hydroxy-tetrahydrodipicolinate synthase; P:diaminopimelate biosynthetic process
Xfm	exbB	biopolymer transporter	P:protein transport; C:integral component of membrane; F:protein transporter activity
Xfm	exbD1	biopolymer transporter	P:protein transport; C:integral component of membrane; C:plasma membrane; F:transporter activity
Xfm	xf22_85790_86761_3	3-oxoacyl-ACP synthase	F:3-oxoacyl-[acyl-carrier-protein] synthase activity; P:fatty acid biosynthetic process
Xfm	xf22_96541_97788_3	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xfm	xf22_138693_139081_3	hypothetical protein	C:integral component of membrane
Xfm	xf22_145037_145435_3	hypothetical protein	
Xfm	xf22_148224_150348_3	DUF1631 domain-containing	
Xfm	xf22_154281_155324_3	sulfite exporter family	C:integral component of membrane; C:plasma membrane
Xfm	PD_0225	serine threonine kinase	F:protein serine/threonine kinase activity; P:protein phosphorylation
Xfm	xf22_159470_159575_3	SCP2 domain-containing	

Xfm	xf22_159799_160015_3	SCP2 domain-containing	
Xfm	PD_1764	peptidoglycan-binding domain-containing	
Xfm	xf22_178522_180430_3	family	C:integral component of membrane
Xfm	xf22_197535_197963_3	SET domain-containing - lysine N-methyltransferase	
Xfm	xf22_201118_201740_3	DUF3011 domain-containing	
Xfm	PD_1577	ligand-binding SH3	
Xfm	PD_0333	rhomboid family intramembrane serine protease	P:proteolysis; C:integral component of membrane; F:serine-type endopeptidase activity
Xfm	xf22_235589_237095_3	ATP phosphoribosyltransferase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; F:ATP phosphoribosyltransferase activity; P:histidine biosynthetic process
Xfm	xf22_242975_246402_3	dihydroxy-acid dehydratase	P:isoleucine biosynthetic process; F:dihydroxy-acid dehydratase activity; F:metal ion binding; P:valine biosynthetic process; F:4 iron, 4 sulfur cluster binding
Xfm	xf22_256989_257330_3	Lipoate- ligase B	F:octanoyltransferase activity; C:cytoplasm; F:lipoyl(octanoyl) transferase activity; P:cellular protein modification process; F:ligase activity; P:lipoate biosynthetic process
Xfm	lolD	ABC transporter ATP-binding	F:ATPase activity; F:lipoprotein transporter activity; F:ATP binding; C:ATP-binding cassette (ABC) transporter complex; P:lipoprotein transport
Xfm	xf22_274513_275864_3	S-adenosylmethionine synthetase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; P:S-adenosylmethionine biosynthetic process; F:methionine adenosyltransferase activity; P:one-carbon metabolic process
Xfm	xf22_276946_277801_3	tRNA dimethylallyltransferase	F:ATP binding; P:tRNA processing; F:tRNA dimethylallyltransferase activity
Xfm	xf22_286220_287675_3	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xfm	xf22_292519_292788_3	N-ethylammelane chlorohydrolase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
Xfm	nuoE	NADH dehydrogenase	F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduction process; F:2 iron, 2 sulfur cluster binding
Xfm	xf22_325600_326560_3	two-component sensor histidine kinase	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfm	pilU	twitching motility	F:ATP binding; P:transport

Xfm	psd	phosphatidylserine decarboxylase	P:phosphatidylethanolamine biosynthetic process; F:phosphatidylserine decarboxylase activity; C:plasma membrane
Xfm	xf22_359948_360533_3	orotate phosphoribosyltransferase	F:magnesium ion binding; P:'de novo' UMP biosynthetic process; F:orotate phosphoribosyltransferase activity
Xfm	xf22_362988_364815_3	DNA repair	F:ATP binding; P:DNA repair; F:DNA-dependent ATPase activity; F:metal ion binding; F:methyltransferase activity; F:damaged DNA binding; P:methylation
Xfm	rfbA	glucose-1-phosphate thymidyltransferase	F:glucose-1-phosphate thymidyltransferase activity; F:metal ion binding; P:extracellular polysaccharide biosynthetic process
Xfm	xf22_375586_375897_3	dolichol-phosphate mannosyltransferase	F:transferase activity, transferring glycosyl groups
Xfm	rpml	50S ribosomal L35	F:structural constituent of ribosome; C:ribosome; P:translation
Xfm	xf22_438302_438842_3	cysteine desulfurase	
Xfm	xf22_443564_443881_3	class I SAM-dependent methyltransferase	F:methyltransferase activity; P:methylation
Xfm	tatC	pre translocase subunit	C:integral component of plasma membrane; C:TAT protein transport complex; F:protein transmembrane transporter activity; P:protein transport by the Tat complex
Xfm	yueF	AI-2E family transporter	C:integral component of membrane
Xfm	xf22_470091_471207_3	2-octaprenyl-6-methoxyphenyl hydroxylase	F:FAD binding; F:2-octaprenyl-6-methoxyphenol hydroxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen; P:oxidation-reduction process; P:ubiquinone biosynthetic process
Xfm	xf23_46803_51142_3	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	dacC	D-alanyl-D-alanine carboxypeptidase	F:serine-type D-Ala-D-Ala carboxypeptidase activity; P:proteolysis
Xfm	xf23_96257_97788_3	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xfm	xf23_112000_112637_3	gamma-glutamyltransferase	P:glutathione metabolic process; F:gamma-glutamyltransferase activity
Xfm	xf23_133157_133453_3	hypothetical protein P910_001404	
Xfm	PD_0503	hypothetical protein	
Xfm	xf23_178427_180430_3	family	C:integral component of membrane

Xfm	PD_1706	reactive intermediate imine deaminase	
Xfm	PD_0695	SET domain-containing - lysine N-methyltransferase	
Xfm	xf23_236099_237095_3	DNA polymerase III subunit delta	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	xf23_239117_240399_3	molecular chaperone	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress
Xfm	lipB	Lipoate- ligase B	F:octanoyltransferase activity; C:cytoplasm; F:lipoyl(octanoyl) transferase activity; P:cellular protein modification process; F:ligase activity; P:lipoate biosynthetic process
Xfm	metK	S-adenosylmethionine synthetase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; P:S-adenosylmethionine biosynthetic process; F:methionine adenosyltransferase activity; P:one-carbon metabolic process
Xfm	xf23_286220_288102_3	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xfm	xf23_325692_326560_3	two-component sensor	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfm	ruvA	ATP-dependent DNA helicase	F:DNA binding; F:ATP binding; P:DNA repair; P:DNA duplex unwinding; P:DNA recombination; C:Holliday junction helicase complex; F:four-way junction helicase activity; P:SOS response
Xfm	parA_1	Cobyrinic acid ac-diamide synthase	
Xfm	csd	cysteine desulfurase	F:cysteine desulfurase activity; F:pyridoxal phosphate binding; P:cysteine metabolic process
Xfm	xf23_469316_472372_3	2-octaprenyl-6-methoxyphenyl hydroxylase	F:FAD binding; F:2-octaprenyl-6-methoxyphenol hydroxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen; P:oxidation-reduction process; P:ubiquinone biosynthetic process
Xfm	xf24_10403_10515_3	---NA---	
Xfm	xf24_23952_25533_3	tetratricopeptide repeat	
Xfm	xf24_30585_31483_3	family DNA-binding transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation

			of transcription, DNA-templated; F:alanine racemase activity
Xfm	xf24_47126_50413_3	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	xf24_83298_84054_3	malonyl -ACP transacylase	F:[acyl-carrier-protein] S-malonyltransferase activity; P:metabolic process
Xfm	xf24_85790_86997_3	3-oxoacyl-ACP synthase	F:3-oxoacyl-[acyl-carrier-protein] synthase activity; P:fatty acid biosynthetic process
Xfm	xf24_112000_112925_3	gamma-glutamyltransferase	P:glutathione metabolic process; F:gamma-glutamyltransferase activity
Xfm	uptE	outer membrane	
Xfm	PD_1894	sulfite exporter family	C:integral component of membrane; C:plasma membrane
Xfm	PD_1035	SCP2 domain-containing	
Xfm	traB	family	C:integral component of membrane
Xfm	PD_1759	iron transporter	F:transition metal ion binding
Xfm	xf24_209475_211496_3	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	hisG	ATP phosphoribosyltransferase	F:magnesium ion binding; F:ATP binding; C:cytoplasm; F:ATP phosphoribosyltransferase activity; P:histidine biosynthetic process
Xfm	xf24_243904_245743_3	dihydroxy-acid dehydratase	P:isoleucine biosynthetic process; F:dihydroxy-acid dehydratase activity; F:metal ion binding; P:valine biosynthetic process; F:4 iron, 4 sulfur cluster binding
Xfm	yecS	ABC transporter permease	C:integral component of membrane; P:transport; C:plasma membrane
Xfm	xf24_286394_287916_3	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xfm	xf24_355327_356119_3	formyltetrahydrofolate deformylase	P:'de novo' IMP biosynthetic process; F:amino acid binding; F:hydroxymethyl-, formyl- and related transferase activity; P:one-carbon metabolic process; F:formyltetrahydrofolate deformylase activity
Xfm	xf24_362988_364725_3	DNA repair	F:ATP binding; P:DNA repair; F:DNA-dependent ATPase activity; F:metal ion binding; F:methyltransferase activity; F:damaged DNA binding; P:methylation
Xfm	sdhA	succinate dehydrogenase flavo subunit	F:succinate dehydrogenase (ubiquinone) activity; F:flavin adenine dinucleotide binding; P:tricarboxylic acid cycle; P:electron transport chain; C:plasma membrane

Xfm	slt	soluble lytic murein transglycosylase precursor	C:periplasmic space; F:hydrolase activity, hydrolyzing O-glycosyl compounds
Xfm	PD_1452	lipopolysaccharide biosynthesis	C:integral component of membrane; F:phospho-N-acetylmuramoyl-pentapeptide-transferase activity
Xfm	xf24_470091_470782_3	2-octaprenyl-6-methoxyphenyl hydroxylase	F:FAD binding; F:2-octaprenyl-6-methoxyphenol hydroxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen; P:oxidation-reduction process; P:ubiquinone biosynthetic process
Xfm	pilV	type IV pilus modification	C:integral component of membrane
Xfm	PD_0021	prepilin-type N-terminal cleavage methylation domain-containing	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	xf25_233636_233826_4	GTPase	F:magnesium ion binding; F:GTP binding; C:cytoplasm; F:GTPase activity
Xfm	nagA	N-acetylglucosamine-6-phosphate deacetylase	P:carbohydrate metabolic process; P:N-acetylglucosamine metabolic process; F:N-acetylglucosamine-6-phosphate deacetylase activity
Xfm	PD_0008	tetratricopeptide repeat	
Xfm	PD_0682	family DNA-binding transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated; F:alanine racemase activity
Xfm	xf26_47126_50700_3	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	xf26_83298_84077_3	malonyl -ACP transacylase	F:[acyl-carrier-protein] S-malonyltransferase activity; P:metabolic process
Xfm	fabH_1	3-oxoacyl-ACP synthase	F:3-oxoacyl-[acyl-carrier-protein] synthase activity; P:fatty acid biosynthetic process
Xfm	xf26_111975_112618_3	gamma-glutamyltransferase	P:glutathione metabolic process; F:gamma-glutamyltransferase activity
Xfm	glmS_1	iron dicitrate transport regulator	P:carbohydrate metabolic process; F:glutamine-fructose-6-phosphate transaminase (isomerizing) activity; F:carbohydrate binding
Xfm	PD_0125	peptidase C1	F:nucleotide binding; P:proteolysis; F:cysteine-type peptidase activity
Xfm	PD_0121	hypothetical protein	C:integral component of membrane
Xfm	PD_1937	DUF3011 domain-containing	

Xfm	xf26_207484_211449_3	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	hflD	high frequency lysogenization	C:cytoplasm; C:plasma membrane
Xfm	xf26_234149_234797_3	GTPase	F:magnesium ion binding; F:GTP binding; C:cytoplasm; F:GTPase activity
Xfm	hisA	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	C:cytoplasm; F:1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity; P:histidine biosynthetic process
Xfm	xf26_236107_237095_3	DNA polymerase III subunit delta	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	xf26_239075_240399_3	molecular chaperone	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress
Xfm	xf26_244296_245743_3	dihydroxy-acid dehydratase	P:isoleucine biosynthetic process; F:dihydroxy-acid dehydratase activity; F:metal ion binding; P:valine biosynthetic process; F:4 iron, 4 sulfur cluster binding
Xfm	PD_1806	methionine ABC transporter substrate-binding	
Xfm	xf26_286220_287916_3	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xfm	PD_1489	N-ethylammelane chlorohydrolase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
Xfm	xf26_293707_293733_3	---NA---	
Xfm	mtnC	acireductone synthase	F:magnesium ion binding; F:2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase activity; F:2,3-diketo-5-methylthiopentenyl-1-phosphate enolase activity; P:L-methionine salvage from S-adenosylmethionine; P:L-methionine salvage from methylthioadenosine; P:dephosphorylation; F:acireductone synthase activity
Xfm	xf26_304806_304966_3	endonuclease V	F:magnesium ion binding; P:DNA repair; P:nucleic acid phosphodiester bond hydrolysis; F:deoxyribonuclease V activity; C:cytoplasm
Xfm	phoQ	two-component sensor histidine kinase	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfm	purU	formyltetrahydrofolate deformylase	P:'de novo' IMP biosynthetic process; F:amino acid binding; F:hydroxymethyl-, formyl- and related transferase activity; P:one-carbon metabolic process; F:formyltetrahydrofolate

			deformylase activity
Xfm	radA	DNA repair	F:ATP binding; P:DNA repair; F:DNA-dependent ATPase activity; F:metal ion binding; F:damaged DNA binding
Xfm	xf26_375642_375897_3	dolichol-phosphate mannosyltransferase	F:transferase activity, transferring glycosyl groups
Xfm	PD_0162	methyltransferase	F:methyltransferase activity; P:methylation
Xfm	xf26_470277_470782_3	2-octaprenyl-6-methoxyphenyl hydroxylase	F:FAD binding; F:2-octaprenyl-6-methoxyphenol hydroxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen; P:oxidation-reduction process; P:ubiquinone biosynthetic process
Xfm	xf28_173455_173506_1	---NA---	
Xfm	PD_1621	membrane	C:integral component of membrane
Xfm	xf29_129553_129573_4	---NA---	
Xfm	hflX	GTPase	F:magnesium ion binding; F:GTP binding; C:cytoplasm; F:GTPase activity
Xfm	xf29_478650_479898_3	type II secretion system	F:protein transporter activity; P:protein secretion by the type II secretion system; C:cell outer membrane; C:type II protein secretion system complex
Xfm	adhP	NAD(P)-dependent alcohol dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xfm	ahcY	S-adenosyl-L-homocysteine hydrolase	C:cytoplasm; F:adenosylhomocysteinase activity; P:one-carbon metabolic process
Xfm	ctpA	peptidase S41	P:proteolysis; F:serine-type peptidase activity
Xfm	cyoB	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	fabD	malonyl -ACP transacylase	F:[acyl-carrier-protein] S-malonyltransferase activity; P:metabolic process
Xfm	folP	dihydropteroate synthase	F:metal ion binding; P:folic acid biosynthetic process; P:tetrahydrofolate biosynthetic process; F:dihydropteroate synthase activity
Xfm	ggt	gamma-glutamyltransferase	P:glutathione metabolic process; F:gamma-glutamyltransferase activity
Xfm	PD_1461	acyltransferase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:transferase activity, transferring acyl groups; P:nitrogen compound metabolic process

Xfm	PD_0806	DUF1631 domain-containing	
Xfm	PD_1613	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	holB	DNA polymerase III subunit delta	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	htpG	molecular chaperone	F:ATP binding; C:cytoplasm; F:unfolded protein binding; P:protein folding; P:response to stress
Xfm	ilvD	dihydroxy-acid dehydratase	P:isoleucine biosynthetic process; F:dihydroxy-acid dehydratase activity; F:metal ion binding; P:valine biosynthetic process; F:4 iron, 4 sulfur cluster binding
Xfm	miaA	tRNA dimethylallyltransferase	F:ATP binding; P:tRNA processing; F:tRNA dimethylallyltransferase activity
Xfm	mgo	malate:quinone oxidoreductase	F:malate dehydrogenase (menaquinone) activity; F:malate dehydrogenase (quinone) activity; C:integral component of membrane; P:tricarboxylic acid cycle
Xfm	nfi	endonuclease V	F:magnesium ion binding; P:DNA repair; P:nucleic acid phosphodiester bond hydrolysis; F:deoxyribonuclease V activity; C:cytoplasm
Xfm	nrdB	ribonucleotide-diphosphate reductase subunit beta	F:ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor; F:metal ion binding; P:DNA replication; P:deoxyribonucleoside diphosphate metabolic process; P:oxidation-reduction process
Xfm	purM	phosphoribosylformylglycinamide cyclo-ligase	F:ATP binding; C:cytoplasm; P:'de novo' IMP biosynthetic process; F:phosphoribosylformylglycinamide cyclo-ligase activity
Xfm	pyrE	orotate phosphoribosyltransferase	F:magnesium ion binding; P:'de novo' UMP biosynthetic process; F:orotate phosphoribosyltransferase activity
Xfm	dpm1	dolichol-phosphate mannosyltransferase	F:transferase activity, transferring glycosyl groups
Xfm	ubiH	2-octaprenyl-6-methoxyphenyl hydroxylase	F:FAD binding; F:2-octaprenyl-6-methoxyphenyl hydroxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen; P:oxidation-reduction process; P:ubiquinone biosynthetic process
Xfm	xpsD	type II secretion system	F:protein transporter activity; P:protein secretion by the type II secretion system; C:cell outer membrane; C:type II protein secretion system complex
Xfm	PD_0199	transcriptional regulator	

Xfm	zipA	cell division	P:FtsZ-dependent cytokinesis; C:integral component of plasma membrane; C:cell division site
Xfm	Xylella_fastidiosa_ATCC_35871_18809_19898_3	outer membrane assembly factor	P:Gram-negative-bacterium-type cell outer membrane assembly; C:integral component of membrane; C:cell outer membrane; P:protein insertion into membrane
Xfm	cdsA	phosphatidate cytidyltransferase	F:phosphatidate cytidyltransferase activity; C:integral component of membrane; P:CDP-diacylglycerol biosynthetic process
Xfm	Xylella_fastidiosa_ATCC_35871_38400_38640_3	cytidylate kinase	F:cytidylate kinase activity; F:ATP binding; P:nucleotide phosphorylation; C:cytoplasm; P:pyrimidine nucleotide metabolic process
Xfm	Xylella_fastidiosa_ATCC_35871_44340_45368_3	peptidase S41	P:proteolysis; F:serine-type peptidase activity
Xfm	Xylella_fastidiosa_ATCC_35871_47340_50490_3	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfm	dxr	1-deoxy-D-xylulose 5-phosphate reductoisomerase	F:1-deoxy-D-xylulose-5-phosphate reductoisomerase activity; F:metal ion binding; F:NADPH binding; P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; P:oxidation-reduction process; P:terpenoid biosynthetic process; F:isomerase activity
Xfm	Xylella_fastidiosa_ATCC_35871_83298_84045_3	malonyl -ACP transacylase	F:[acyl-carrier-protein] S-malonyltransferase activity; P:metabolic process
Xfm	Xylella_fastidiosa_ATCC_35871_86214_86855_3	3-oxoacyl-ACP synthase	F:3-oxoacyl-[acyl-carrier-protein] synthase activity; P:fatty acid biosynthetic process
Xfm	Xylella_fastidiosa_ATCC_35871_90789_91309_3	pre-pilin like leader sequence	F:protein transporter activity; P:protein secretion by the type II secretion system; C:type II protein secretion system complex
Xfm	gcvR	Glycine cleavage system regulatory	P:regulation of transcription, DNA-templated
Xfm	alkB	alkylated DNA repair	P:DNA repair; F:oxidoreductase activity; C:integral component of membrane; F:methyltransferase activity; P:oxidation-reduction process; P:methylation
Xfm	Xylella_fastidiosa_ATCC_35871_148224_14894_0_3	Nitrilase cyanide hydratase and apolipo N-acyltransferase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; F:transferase activity, transferring acyl groups; P:nitrogen compound metabolic process
Xfm	Xylella_fastidiosa_ATCC_35871_197535_19800	SET domain-containing -lysine N-methyltransferase	

7_3

Xfm	Xylella_fastidiosa_ATCC_35871_208902_21041_5_3	pilus assembly	C:integral component of membrane; P:type IV pilus biogenesis
Xfm	Xylella_fastidiosa_ATCC_35871_236496_23709_5_3	DNA polymerase III subunit delta	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	lexA	transcriptional repressor	F:DNA binding; P:DNA repair; P:negative regulation of transcription, DNA-templated; P:transcription, DNA-templated; P:DNA replication; P:proteolysis; F:serine-type endopeptidase activity; P:SOS response
Xfm	lpxA	acyl-[acyl-carrier-]--UDP-N-acetylglucosamine O-acyltransferase	C:cytoplasm; F:acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity; P:lipid A biosynthetic process
Xfm	PD_1422	UDP-3-O-[3-hydroxymyristoyl]glucosamine N-acyltransferase	F:transferase activity, transferring acyl groups
Xfm	htrB_1	lipid A biosynthesis lauroyl acyltransferase	F:transferase activity, transferring acyl groups; C:integral component of membrane
Xfm	Xylella_fastidiosa_ATCC_35871_290873_29142_2_3	mechanosensitive ion channel	P:transmembrane transport; C:integral component of membrane
Xfm	ptsA	phosphoenolpyruvate--phosphotransferase	C:cytoplasm; F:metal ion binding; P:phosphoenolpyruvate-dependent sugar phosphotransferase system; P:phosphorylation; F:phosphoenolpyruvate-protein phosphotransferase activity; F:kinase activity
Xfm	Xylella_fastidiosa_ATCC_35871_362988_36467_2_3	DNA repair	F:ATP binding; P:DNA repair; F:DNA-dependent ATPase activity; F:metal ion binding; F:damaged DNA binding
Xfm	PD_0327	RIP metalloprotease	F:metal ion binding; P:proteolysis; C:integral component of membrane; F:metalloendopeptidase activity; C:plasma membrane
Xfm	Xylella_fastidiosa_ATCC_35871_410731_41122_8_3	16S rRNA (guanine(966)-N(2))-methyltransferase	F:nucleic acid binding; P:rRNA methylation; F:16S rRNA (guanine(966)-N(2))-methyltransferase activity
Xfm	rmd	GDP-6-deoxy-D-lyxo-4-hexulose reductase	
Xfm	Xylella_fastidiosa_ATCC_35871_473452_47408_4_3	UDP diphosphate synthase	F:magnesium ion binding; P:regulation of cell shape; P:peptidoglycan biosynthetic process; P:cell wall organization; F:di-trans,poly-cis-decaprenylcistransferase activity
Xfm	Xylella_fastidiosa_ATCC_35871_489610_49018_7_3	peptidoglycan editing factor	

Xfm	dmt	dolichol-phosphate mannosyltransferase	F:transferase activity, transferring glycosyl groups; C:integral component of membrane
Xfp1	cyoA	ubiquinol oxidase subunit II	F:cytochrome o ubiquinol oxidase activity; F:cytochrome-c oxidase activity; F:copper ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; P:electron transport chain; C:plasma membrane; C:respiratory chain
Xfp1	Italy_1129_47263_4768 1_3	ubiquinol oxidase subunit II	F:cytochrome o ubiquinol oxidase activity; F:cytochrome-c oxidase activity; F:copper ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; P:electron transport chain; C:plasma membrane; C:respiratory chain
Xfp1	cyoB	cytochrome o ubiquinol oxidase subunit I	F:cytochrome-c oxidase activity; F:iron ion binding; C:integral component of membrane; P:hydrogen ion transmembrane transport; F:oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor; P:aerobic respiration; C:respiratory chain; F:heme binding
Xfp1	ilvD	dihydroxy-acid dehydratase	P:isoleucine biosynthetic process; F:dihydroxy-acid dehydratase activity; F:metal ion binding; P:valine biosynthetic process; F:4 iron, 4 sulfur cluster binding
Xfp1	dmt	dolichol-phosphate mannosyltransferase	F:transferase activity, transferring glycosyl groups; C:integral component of membrane
Xfp2	mltB	murein transglycosylase	
Xfp2	carA	carbamoyl-phosphate synthase small subunit	F:ATP binding; P:'de novo' pyrimidine nucleobase biosynthetic process; P:arginine biosynthetic process; P:glutamine metabolic process; F:carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity; P:'de novo' UMP biosynthetic process
Xfp2	X_fastidiosa_9a5c_1061 47_106520_2	MFS transporter	C:Gram-negative-bacterium-type cell wall; C:integral component of membrane; F:fucose transmembrane transporter activity; F:galactose transmembrane transporter activity; P:galactose transport; F:glucose transmembrane transporter activity; P:fucose transport; P:glucose transmembrane transport
Xfp2	nuoE	NADH dehydrogenase	F:oxidoreductase activity; F:metal ion binding; P:oxidation-reduction process; F:2 iron, 2 sulfur cluster binding
Xfp2	purM	phosphoribosylaminoimid azole synthetase	F:ATP binding; C:cytoplasm; P:'de novo' IMP biosynthetic process; F:phosphoribosylformylglycinamide cyclo- ligase activity

Xfp2	X_fastidiosa_9a5c_1065 21_106810_3	L-fucose:H ⁺ symporter permease	C:Gram-negative-bacterium-type cell wall; C:integral component of membrane; F:fucose transmembrane transporter activity; F:galactose transmembrane transporter activity; P:galactose transport; F:glucose transmembrane transporter activity; P:fucose transport; P:glucose transmembrane transport
Xfp2	yggB	mechanosensitive ion channel family	P:transmembrane transport; C:integral component of membrane
Xfp2	purN	phosphoribosylglycinamid e formyltransferase	F:phosphoribosylglycinamide formyltransferase activity; P:'de novo' IMP biosynthetic process
Xfp2	ykgJ	ferredoxin	
Xfp2	X_fastidiosa_9a5c_2945 07_295155_4	methylthioribulose-1- phosphate dehydratase	F:methylthioribulose 1-phosphate dehydratase activity; F:zinc ion binding; C:cytoplasm; P:L-methionine salvage from S- adenosylmethionine; P:L-methionine salvage from methylthioadenosine
Xfp2	queA	---NA---	
Xfp2	X_fastidiosa_9a5c_4220 73_422373_4	pre translocase subunit	P:protein transmembrane transport; F:P-P- bond-hydrolysis-driven protein transmembrane transporter activity; C:integral component of membrane; P:protein secretion
Xfp2	PD_0061	pilus assembly	P:chaperone-mediated protein folding; C:outer membrane-bounded periplasmic space; P:cell wall organization; P:pilus organization
Xfp2	PD_0575	polyisoprenoid-binding protein	
Xfp2	gumC	polysaccharide biosynthesis	C:integral component of membrane; P:lipopolysaccharide biosynthetic process
Xfp2	X_fastidiosa_J1a12_346 799_347066_3	polysaccharide biosynthesis	C:integral component of membrane; P:lipopolysaccharide biosynthetic process
Xfp2	cmk	cytidylate kinase	F:cytidylate kinase activity; F:ATP binding; P:nucleotide phosphorylation; C:cytoplasm; P:pyrimidine nucleotide metabolic process
Xfp2	X_fastidiosa_J1a12_283 206_283722_4	murein transglycosylase	
Xfp2	gluP_1	MFS transporter	C:Gram-negative-bacterium-type cell wall; C:integral component of membrane; F:fucose transmembrane transporter activity; F:galactose transmembrane transporter activity; P:galactose transport; F:glucose transmembrane transporter activity; P:fucose transport; P:glucose transmembrane transport
Xfp2	X_fastidiosa_Pr8x_2621 15_262573_2	acetyltransferase	F:transferase activity
Xfp2	PD_1028	polyisoprenoid-binding	

Xfp2	holC	DNA polymerase III subunit chi	F:DNA binding; F:DNA-directed DNA polymerase activity; P:DNA replication; P:DNA biosynthetic process
Xfp2	yrbE	ABC transporter permease	
Xfp2	mtnB	methylthioribulose-1-phosphate dehydratase	F:methylthioribulose 1-phosphate dehydratase activity; F:zinc ion binding; C:cytoplasm; P:L-methionine salvage from S-adenosylmethionine; P:L-methionine salvage from methylthioadenosine
Xfp2	secG	pre translocase subunit	P:protein transmembrane transport; F:P-P-bond-hydrolysis-driven protein transmembrane transporter activity; C:integral component of membrane; P:protein secretion
Xfp2	Xylella_fastidiosa_32_2 35053_235093_2	---NA---	
Xfp2	PD_1422	---NA---	
Xfp2	yecS	ABC transporter permease	C:membrane; C:integral component of membrane; P:transport; C:plasma membrane
Xfp2	spsQ	glycosyl transferase	C:integral component of membrane; F:transferase activity
Xfp2	rfbD_1	dTDP-4-dehydrorhamnose 3,5-epimerase	F:dTDP-4-dehydrorhamnose 3,5-epimerase activity; F:transferase activity
Xfp2	PD_0551	ABC transporter	
Xfp2	Xylella_fastidiosa_32_3 74590_374849_4	dTDP-4-dehydrorhamnose 3,5-epimerase	F:dTDP-4-dehydrorhamnose 3,5-epimerase activity
Xfp2	speA	arginine decarboxylase	P:arginine catabolic process; F:arginine decarboxylase activity; F:metal ion binding; P:spermidine biosynthetic process

Table S8 - Gene found in the accessory genome of each subspecies

Subspecies	SeqName	Description	GO Names
Xff	PD_0908	hypothetical protein PD_0908	C:integral component of membrane
Xff	PD_0915	filamentous phage Cf1c related	C:integral component of membrane
Xff	PD_1400	conserved hypothetical protein	C:integral component of membrane
Xff	PD_1416	hypothetical protein	C:integral component of membrane
Xff	PD_0609	pilus assembly	C:integral component of membrane
Xff	PD_0435	hypothetical protein	C:integral component of membrane
Xff	PD_0922	hypothetical protein	C:integral component of membrane
Xff	PD_1780	Phosphate starvation-inducible	F:ATP binding
Xff	PD_0906	Phage related	F:DNA binding
Xff	algU	DNA-directed DNA polymerase	F:DNA binding; F:DNA-directed DNA polymerase activity; P:DNA replication; P:DNA biosynthetic process

Xff	dpnA	DNA methyltransferase	F:DNA binding; F:N-methyltransferase activity; P:DNA methylation
Xff	hsdS	restriction endonuclease subunit S	F:DNA binding; P:DNA modification
Xff	PD_1606	Phage integrase family	F:DNA binding; P:DNA recombination; P:DNA integration
Xff	PD_1802	polysaccharide deacetylase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:carbohydrate metabolic process
Xff	PD_1803	polysaccharide deacetylase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds; P:carbohydrate metabolic process
Xff	dcm	DNA cytosine methyltransferase	F:methyltransferase activity; P:methylation
Xff	rlpA	rare lipo A	F:peptidoglycan binding
Xff	hemF	coproporphyrinogen III oxidase	F:protein homodimerization activity; C:cytoplasm; F:coproporphyrinogen oxidase activity; F:metal ion binding; P:oxidation-reduction process; P:protoporphyrinogen IX biosynthetic process
Xff	higB	XRE family transcriptional regulator	F:sequence-specific DNA binding
Xff	PD_0954	transcriptional regulator	F:sequence-specific DNA binding
Xff	asnB	asparagine synthase B	P:asparagine biosynthetic process; F:asparagine synthase (glutamine-hydrolyzing) activity
Xff	xylA	glycoside hydrolase family 3	P:carbohydrate metabolic process; F:beta-glucosidase activity; F:scopolin beta-glucosidase activity
Xff	xseB	exodeoxyribonuclease VII small subunit	P:DNA catabolic process; P:nucleic acid phosphodiester bond hydrolysis; C:cytoplasm; C:exodeoxyribonuclease VII complex; F:exodeoxyribonuclease VII activity
Xff	ribF	bifunctional riboflavin kinase FMN adenylyltransferase	P:FAD biosynthetic process; F:ATP binding; P:FMN biosynthetic process; P:riboflavin biosynthetic process; F:riboflavin kinase activity; P:phosphorylation; F:FMN adenylyltransferase activity
Xff	nspV	restriction endonuclease	P:nucleic acid phosphodiester bond hydrolysis; F:Type II site-specific deoxyribonuclease activity; P:DNA metabolic process
X f f	PD_0424	dihydroxyacetone kinase	P:phosphorylation; F:kinase activity
Xff	PD_0955	extracellular serine protease	P:proteolysis; F:peptidase activity
Xff	PD_1423	RTX toxin Ca ²⁺ -binding	None
Xff	PD_1240	hemagglutinin	None

Xff	PD_0914	DUF2523 domain-containing	None
Xff	PD_1000	DUF1376 domain-containing	None
Xff	PD_1004	conserved hypothetical protein	None
Xff	PD_1417	RTX toxin Ca ²⁺ -binding	None
Xff	PD_2079	DUF3375 domain-containing	None
Xff	PD_1117	phage antirepressor	None
Xff	PD_1118	hypothetical protein	None
Xff	PD_1418	hypothetical protein	None
Xff	PD_1002	phage antirepressor	None
Xff	PD_0942	hypothetical protein	None
Xff	PD_1424	hypothetical protein	None
Xff	PD_1321	phage-related protein	None
Xff	PD_1239	DUF596 domain-containing	None
Xff	PD_2107	DUF596 domain-containing	None
Xff	PD_1510	hypothetical protein	None
Xff	PD_0069	hypothetical protein, partial	None
Xff	PD_1193	phage-related protein	None
Xff	PD_1328	phage-related protein	None
Xff	PD_1522	hypothetical protein	None
Xff	PD_2092	hypothetical protein	None
Xff	PD_1249	hemagglutinin	None
Xff	PD_1426	hypothetical protein	None
Xff	PD_1346	hypothetical protein	None
Xff	PD_1241	DUF596 domain-containing	None
Xff	PD_0919	hypothetical protein PD_0919	None
Xff	PD_2111	DUF596 domain-containing	None
Xff	PD_0578	hypothetical protein PD_0578	None
Xfm	ddl	D-alanine--D-alanine ligase	F:magnesium ion binding; P:regulation of cell shape; F:ATP binding; F:D-alanine-D-alanine ligase activity; C:cytoplasm; P:peptidoglycan biosynthetic process; F:manganese ion binding; P:cell wall organization
Xfm	PD_1420	hypothetical protein	C:integral component of membrane
Xfm	cvaC	colicin V synthesis	C:integral component of membrane
Xfm	PD_0045	hypothetical protein	C:integral component of membrane
Xfm	PD_1112	conserved hypothetical protein	C:integral component of membrane
Xfm	PD_0310	pathogenicity	C:integral component of membrane
Xfm	lip	triacylglycerol lipase	C:integral component of membrane; F:hydrolase activity

Xfm	hemY	porphyrin biosynthesis	C:integral component of membrane; P:heme metabolic process
Xfm	int_6	3-ketoacyl-ACP reductase	F:3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity; C:cytoplasm; P:poly-hydroxybutyrate biosynthetic process; P:oxidation-reduction process; F:acetoacetyl-CoA reductase activity
Xfm	hsdM_1	SAM-dependent DNA methyltransferase	F:DNA binding; F:N-methyltransferase activity; P:DNA methylation
Xfm	PD_1013	phage recombination Bet	F:DNA binding; P:DNA metabolic process
Xfm	int	integrase family	F:DNA binding; P:DNA recombination; P:DNA integration
Xfm	dpoL_1	phage-related DNA polymerase	F:DNA-directed DNA polymerase activity; P:DNA biosynthetic process
Xfm	pepQ	X-Pro dipeptidase	F:hydrolase activity
Xfm	xanA	phosphomannomutase phosphoglucomutase	F:magnesium ion binding; P:carbohydrate metabolic process; F:phosphomannomutase activity
Xfm	ubiG_1	class I SAM-dependent methyltransferase	F:methyltransferase activity; P:methylation
Xfm	rhIE	RNA helicase	F:nucleic acid binding; F:ATP binding; F:helicase activity
Xfm	ushA	5'-nucleotidase	F:nucleotide binding; F:magnesium ion binding; C:cytoplasm; F:5'-nucleotidase activity; P:dephosphorylation; P:nucleotide metabolic process
Xfm	guaB	IMP dehydrogenase	F:nucleotide binding; F:metal ion binding; F:IMP dehydrogenase activity; P:oxidation-reduction process; P:GMP biosynthetic process
Xfm	PD_0853	SPOR domain-containing	F:peptidoglycan binding; C:integral component of membrane
Xfm	cheA	chemotaxis-related kinase	F:phosphorelay sensor kinase activity; P:chemotaxis; C:cytoplasm; P:phosphorelay signal transduction system; P:signal transduction by protein phosphorylation; P:peptidyl-histidine phosphorylation
Xfm	PD_0348	glycine cleavage T	F:transferase activity
Xfm	htrB_1	lipid A biosynthesis lauroyl acyltransferase	F:transferase activity, transferring acyl groups; C:integral component of membrane
Xfm	fucA1	alpha-L-fucosidase	P:carbohydrate metabolic process; F:alpha-L-fucosidase activity

Xfm	xerC	tyrosine recombinase	P:cell division; F:DNA binding; C:cytoplasm; P:DNA integration; P:chromosome segregation; F:tyrosine-based site-specific recombinase activity; P:cell cycle; P:transposition, DNA-mediated
Xfm	sufD	Fe-S cluster assembly	P:iron-sulfur cluster assembly
Xfm	rpfA	aconitate hydratase	P:metabolic process; F:4 iron, 4 sulfur cluster binding; F:aconitate hydratase activity
Xfm	msrA	peptide-methionine (S)-S-oxide reductase	P:protein repair; P:response to oxidative stress; P:cellular protein modification process; F:peptide-methionine (S)-S-oxide reductase activity; P:oxidation-reduction process
Xfm	glpG	rhomboid family intramembrane serine protease	P:proteolysis; C:integral component of membrane; F:serine-type endopeptidase activity
Xfm	PD_1237	rhomboid family intramembrane serine protease	P:proteolysis; C:integral component of membrane; F:serine-type endopeptidase activity
Xfm	pspB	autotransporter domain-containing	P:proteolysis; F:serine-type endopeptidase activity
Xfm	mrdB	rod shape-determining	P:regulation of cell shape; P:cell division; C:integral component of membrane; P:cell cycle
Xfm	btuE	glutathione peroxidase	P:response to oxidative stress; F:glutathione peroxidase activity; P:cellular oxidant detoxification; P:oxidation-reduction process
Xfm	PD_0730	AEC family transporter	P:transmembrane transport; C:integral component of membrane
Xfm	mexC	efflux RND transporter periplasmic adaptor subunit	P:transmembrane transport; C:plasma membrane
Xfm	fumC	fumarate hydratase	P:tricarboxylic acid cycle; F:fumarate hydratase activity; P:fumarate metabolic process; C:tricarboxylic acid cycle enzyme complex
Xfm	PD_1351	Baseplate J	None
Xfm	PD_1786	hypothetical protein	None
Xfm	PD_1658	sulfate transporter	None
Xfm	PD_1243	DUF596 domain-containing	None
Xfm	PD_2117	DUF596 domain-containing	None
Xfm	PD_1431	hypothetical protein PD_1431	None
Xfm	PD_2068	Uncharacterized conserved	None
Xfm	PD_1592	hypothetical protein	None
Xfm	PD_1726	prophage antirepressor	None
Xfm	PD_1245	DUF596 domain-containing	None
Xfm	PD_2106	hypothetical protein	None

Xfm	PD_1844	hypothetical protein	None
Xfm	PD_1355	hypothetical protein	None
Xfm	PD_0179	DUF885 family	None
Xfp	ispH	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	P:dimethylallyl diphosphate biosynthetic process; F:metal ion binding; P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; F:3 iron, 4 sulfur cluster binding; P:oxidation-reduction process; F:4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity; P:terpenoid biosynthetic process
Xfp	yneN	family disulfide reductase	C:cell; F:antioxidant activity; F:oxidoreductase activity; P:cellular oxidant detoxification; P:cell redox homeostasis; P:oxidation-reduction process
Xfp	pth	peptidyl-tRNA hydrolase	C:cytoplasm; F:aminoacyl-tRNA hydrolase activity; P:translation
Xfp	rimP	ribosome maturation factor	C:cytoplasm; P:ribosomal small subunit biogenesis
Xfp	PD_1066	rhodanese-like domain-containing	C:integral component of membrane
Xfp	PD_0884	DUF2726 domain-containing	C:integral component of membrane
Xfp	PD_0381	DUF1640 domain-containing	C:integral component of membrane
Xfp	PD_0014	hypothetical protein	C:integral component of membrane
Xfp	PD_0109	RDD family	C:integral component of membrane
Xfp	PD_0394	phosphoesterase	C:integral component of membrane
Xfp	PD_0017	hypothetical protein	C:integral component of membrane
Xfp	PD_1718	hypothetical protein	C:integral component of membrane
Xfp	PD_0932	hypothetical protein, partial	C:integral component of membrane
Xfp	PD_1896	DUF1684 domain-containing	C:integral component of membrane
Xfp	PD_1533	hypothetical protein	C:integral component of membrane
Xfp	PD_1354	hypothetical protein XfasM23_1439	C:integral component of membrane
Xfp	PD_0103	membrane	C:integral component of membrane
Xfp	PD_1917	hypothetical protein	C:integral component of membrane
Xfp	PD_1511	hypothetical protein	C:integral component of membrane
Xfp	PD_0808	hypothetical protein	C:integral component of membrane
Xfp	PD_0242	biotin lipoyl-binding	C:integral component of membrane
Xfp	PD_1125	hypothetical protein	C:integral component of membrane
Xfp	pgpB	phosphatase PAP2 family	C:integral component of membrane
Xfp	PD_0585	hypothetical protein	C:integral component of membrane
Xfp	PD_1926	prepilin-type cleavage methylation domain-containing	C:integral component of membrane; P:cell adhesion; C:pilus

Xfp	PD_1684	ribosomal small subunit bTHX	C:ribosome
Xfp	PD_0350	succinate cytochrome b556 subunit	C:succinate dehydrogenase complex; F:electron carrier activity; C:integral component of membrane; P:tricarboxylic acid cycle; F:succinate dehydrogenase activity
Xfp	fabG	3-oxoacyl-ACP reductase	F:3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity; F:NAD binding; P:oxidation-reduction process; P:fatty acid biosynthetic process
Xfp	PD_1305	3-alpha-hydroxysteroid dehydrogenase	F:androsterone dehydrogenase (B-specific) activity; P:oxidation-reduction process
Xfp	mnmA	tRNA 2-thiouridine(34) synthase	F:ATP binding; C:cytoplasm; F:methyltransferase activity; F:sulfurtransferase activity; F:tRNA binding; P:tRNA modification; P:methylation
Xfp	pgk	phosphoglycerate kinase	F:ATP binding; C:cytoplasm; F:phosphoglycerate kinase activity; P:glycolytic process
Xfp	metG	methionyl-tRNA synthetase	F:ATP binding; F:methionine-tRNA ligase activity; C:cytoplasm; F:metal ion binding; P:methionyl-tRNA aminoacylation; F:tRNA binding
Xfp	frpC	peptidase M23	F:calcium ion binding
Xfp	PD_0858	family oxidoreductase	F:calmodulin binding; F:calmodulin-dependent protein kinase activity; P:protein phosphorylation
Xfp	PD_1799	D-alanyl-D-alanine carboxypeptidase family	F:carboxypeptidase activity; P:proteolysis
Xfp	PD_0796	conserved hypothetical protein	F:catalytic activity; F:flavin adenine dinucleotide binding
Xfp	PD_0918	hypothetical protein	F:DNA binding
Xfp	recD	exodeoxyribonuclease V subunit alpha	F:DNA binding; F:ATP binding; P:nucleic acid phosphodiester bond hydrolysis; P:DNA duplex unwinding; P:double-strand break repair via homologous recombination; F:ATP-dependent DNA helicase activity; C:exodeoxyribonuclease V complex; F:exodeoxyribonuclease V activity
Xfp	traE	DNA topoisomerase	F:DNA binding; F:DNA topoisomerase type I activity; P:DNA topological change
Xfp	PD_0789	recombinase family	F:DNA binding; F:recombinase activity; C:integral component of membrane; P:DNA recombination
Xfp	act	family transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated

Xfp	oxyR	Transcriptional regulator	F:DNA binding; F:transcription factor activity, sequence-specific DNA binding; P:transcription, DNA-templated; P:regulation of transcription, DNA-templated
Xfp	cybB	cytochrome B561	F:electron carrier activity; P:respiratory electron transport chain; C:integral component of membrane
Xfp	PD_0482	flavodoxin	F:FMN binding
Xfp	wrbA	flavodoxin family	F:FMN binding; F:oxidoreductase activity; F:electron carrier activity; P:oxidation-reduction process
Xfp	PD_0238	M48 family peptidase	F:hydrolase activity
Xfp	PD_0380	VRR-NUC domain-containing	F:hydrolase activity, acting on ester bonds
Xfp	suhB	inositol monophosphatase	F:inositol monophosphate 1-phosphatase activity; F:metal ion binding; P:phosphatidylinositol phosphorylation; F:inositol monophosphate 3-phosphatase activity; P:inositol phosphate dephosphorylation; F:inositol monophosphate 4-phosphatase activity
Xfp	nfuA	Fe-S biogenesis	F:iron ion binding; P:protein maturation; F:4 iron, 4 sulfur cluster binding; P:iron-sulfur cluster assembly
Xfp	aat	leucyl phenylalanyl-tRNA--transferase	F:leucyltransferase activity; C:cytoplasm; P:protein catabolic process
Xfp	PD_1547	family methyltransferase	F:methyltransferase activity; P:methylation
Xfp	PD_0874	GNAT family N-acetyltransferase	F:N-acetyltransferase activity
Xfp	tnp	IS1327 transposase	F:nucleic acid binding; P:DNA integration
Xfp	ydfG	SDR family NAD(P)-dependent oxidoreductase	F:oxidoreductase activity; P:oxidation-reduction process
Xfp	tctE	sensor histidine kinase	F:phosphorelay sensor kinase activity; F:ATP binding; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfp	rpfC	response regulator	F:phosphorelay sensor kinase activity; P:phosphorelay signal transduction system; C:integral component of membrane; P:signal transduction by protein phosphorylation; C:intracellular
Xfp	PD_0576	hybrid sensor histidine kinase response regulator	F:phosphorelay sensor kinase activity; P:phosphorelay signal transduction system; P:signal transduction by protein phosphorylation; C:intracellular; P:peptidyl-histidine phosphorylation

Xfp	gumB	polysaccharide export	F:polysaccharide transmembrane transporter activity; P:polysaccharide transport; C:membrane
Xfp	PD_1338	phosphotyrosine phosphatase	F:protein tyrosine phosphatase activity; P:peptidyl-tyrosine dephosphorylation
Xfp	aceE	pyruvate dehydrogenase (acetyl-transferring) homodimeric type	F:pyruvate dehydrogenase (acetyl-transferring) activity; P:oxidation-reduction process
Xfp	nuoA	NADH-quinone oxidoreductase subunit A	F:quinone binding; C:integral component of membrane; F:NADH dehydrogenase (ubiquinone) activity; P:oxidation-reduction process; P:transport; C:plasma membrane
Xfp	PD_0072	RNA-binding	F:RNA binding
Xfp	PD_1177	addiction module antitoxin	F:sequence-specific DNA binding
Xfp	PD_0813	XRE family transcriptional regulator	F:sequence-specific DNA binding
Xfp	rpmD	50S ribosomal L30	F:structural constituent of ribosome; C:large ribosomal subunit; P:translation
Xfp	dinJ	XRE family transcriptional regulator	F:toxic substance binding; P:single-species biofilm formation; F:bacterial-type RNA polymerase core promoter proximal region sequence-specific DNA binding
Xfp	PD_1881	phosphotransferase	F:transferase activity
Xfp	gst	glutathione S-transferase	F:transferase activity
Xfp	PD_0791	MBL fold metallo-hydrolase	F:zinc ion binding; F:N-acylphosphatidylethanolamine-specific phospholipase D activity
Xfp	yahK	NAD(P)-dependent alcohol dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xfp	adhP	hydroxyacid dehydrogenase	F:zinc ion binding; F:oxidoreductase activity; P:oxidation-reduction process
Xfp	fcy1	tRNA adenosine(34) deaminase	F:zinc ion binding; F:tRNA-specific adenosine-34 deaminase activity; P:tRNA wobble adenosine to inosine editing
Xfp	egl	cellulase	P:carbohydrate metabolic process; F:cellulase activity
Xfp	PD_1408	autolytic lysozyme	P:carbohydrate metabolic process; P:cell wall macromolecule catabolic process; P:peptidoglycan catabolic process; F:lysozyme activity
Xfp	lptE	Rare lipo B	P:Gram-negative-bacterium-type cell outer membrane assembly; C:cell outer membrane
Xfp	lifO	lipase chaperone	P:lipid catabolic process; C:integral component of membrane; F:unfolded protein binding; P:protein folding; C:plasma membrane

Xfp	pilH	two-component system response regulator	P:phosphorelay signal transduction system; C:intracellular
Xfp	msrB	methionine sulfoxide reductase B	P:protein repair; P:response to oxidative stress; F:zinc ion binding; P:oxidation-reduction process; F:peptide-methionine (R)-S-oxide reductase activity
Xfp	mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	P:regulation of cell shape; C:peptidoglycan-based cell wall; P:peptidoglycan biosynthetic process; C:integral component of membrane; P:cell wall organization; F:transferase activity, transferring pentosyl groups; C:plasma membrane
Xfp	PD_0497	hypothetical protein	None
Xfp	PD_1018	DUF4224 domain-containing	None
Xfp	PD_0528	autotransporter	None
Xfp	PD_2084	DUF769 domain-containing	None
Xfp	PD_1130	hypothetical protein	None
Xfp	PD_0965	hypothetical protein	None
Xfp	PD_1349	hypothetical protein	None
Xfp	PD_0387	polyisoprenoid-binding	None
Xfp	PD_0516	hypothetical protein	None
Xfp	PD_1527	DUF2321 domain-containing	None
Xfp	xpsJ	general secretion pathway J	None
Xfp	PD_2091	hypothetical protein	None
Xfp	PD_2027	hypothetical protein	None
Xfp	PD_0349	DUF1674 domain-containing	None
Xfp	PD_0004	hypothetical protein	None
Xfp	PD_1176	addiction module antitoxin	None
Xfp	PD_1100	addiction module antitoxin	None
Xfp	PD_0364	phage-related protein	None
Xfp	PD_1556	DUF4198 domain-containing	None
Xfp	PD_0678	class I SAM-dependent methyltransferase	None
Xfp	PD_1571	hypothetical protein	None
Xfp	traN	phage head morphogenesis	None
Xfp	PD_1907	hypothetical protein	None
Xfp	PD_0243	hypothetical protein	None
Xfp	PD_1149	transcriptional regulator	None
Xfp	PD_0838	hypothetical protein	None
Xfp	PD_1932	hypothetical protein P910_001865	None
Xfp	PD_1122	hypothetical protein	None

Xfp	PD_0214	hypothetical protein	None
Xfp	PD_2082	conserved hypothetical cytosolic	None
Xfp	PD_2028	conserved hypothetical protein	None
Xfp	PD_0975	hypothetical protein	None
Xfp	PD_1123	conserved hypothetical protein	None
Xfp	PD_1831	conserved hypothetical protein	None
Xfp	PD_0298	hypothetical protein	None
Xfp	PD_1816	hypothetical protein	None
Xfp	PD_0124	DUF3289 family	None
Xfp	PD_1717	DUF86 domain-containing	None
Xfp	PD_0336	hypothetical protein	None
Xfp	PD_2115	DUF596 domain-containing	None
Xfp	PD_0974	hypothetical protein	None
Xfp	PD_0289	hypothetical protein	None
Xfp	PD_1407	hypothetical protein	None
Xfp	PD_1178	hypothetical protein	None
Xfp	PD_0159	DUF2059 domain-containing	None
Xfp	rmd	NAD-dependent epimerase dehydratase family	None
Xfp	PD_1095	hypothetical protein	None
Xfp	PD_0616	hypothetical protein	None
Xfp	tas	aldo keto reductase	None
Xfp	PD_0028	hypothetical protein	None
Xfp	PD_1116	prophage antirepressor	None
Xfp	PD_2031	DUF2290 domain-containing	None
Xfp	PD_1007	mucin-associated surface (MASP)	None
Xfp	PD_0605	cytochrome C oxidase	None
Xfp	PD_0989	family phage regulatory	None
Xfp	PD_1145	hypothetical protein	None
Xfp	parA	chromosome partitioning	None
Xfp	PD_1722	hypothetical protein	None
Xfp	PD_1599	phage-related protein	None
Xfp	PD_0317	hypothetical protein	None

Figure S1 – Phylogeny of *Xylella fastidiosa* strains (n=72) and pan-genome visualization. (A) Number of genes identified using Roary pipeline and shared among the different genomes. (B) Phylogeny and gene content estimated using Roary and visualized in Phalango colored by subspecies; Genetic clusters identified using BAPS approach removing recombining regions (K=4, No recombination) and leaving recombination segments (K=5, Recombination). Recombination analyses were estimated using FastGEAR.

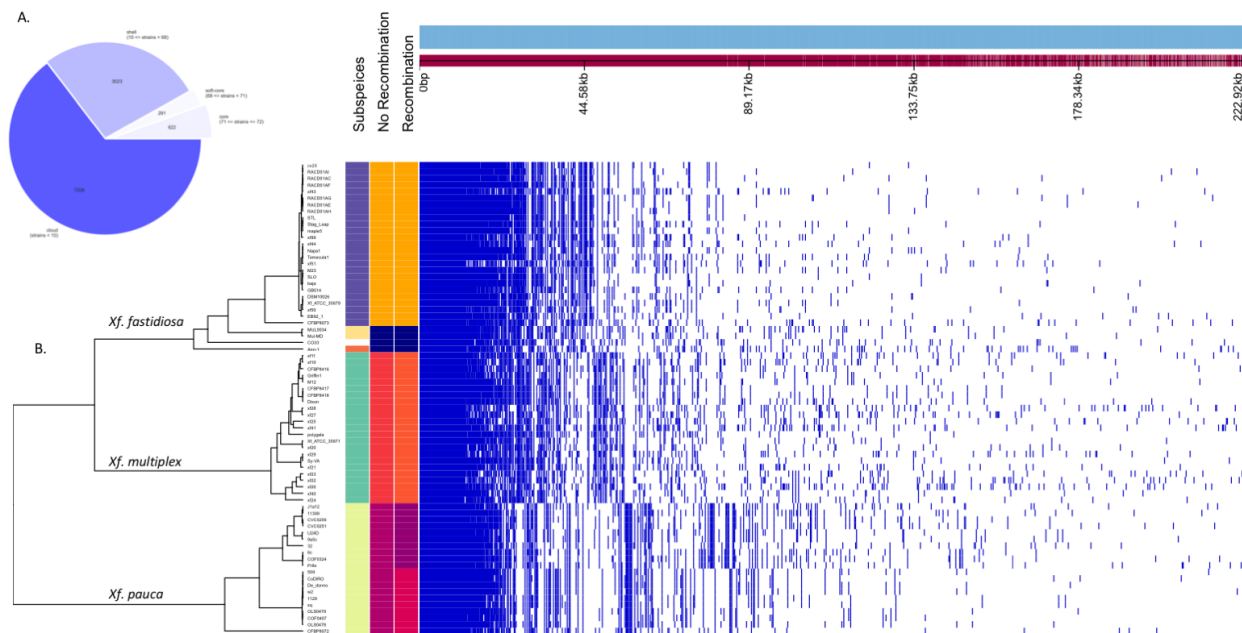


Figure S2: Detection of temporal signal in the dataset.

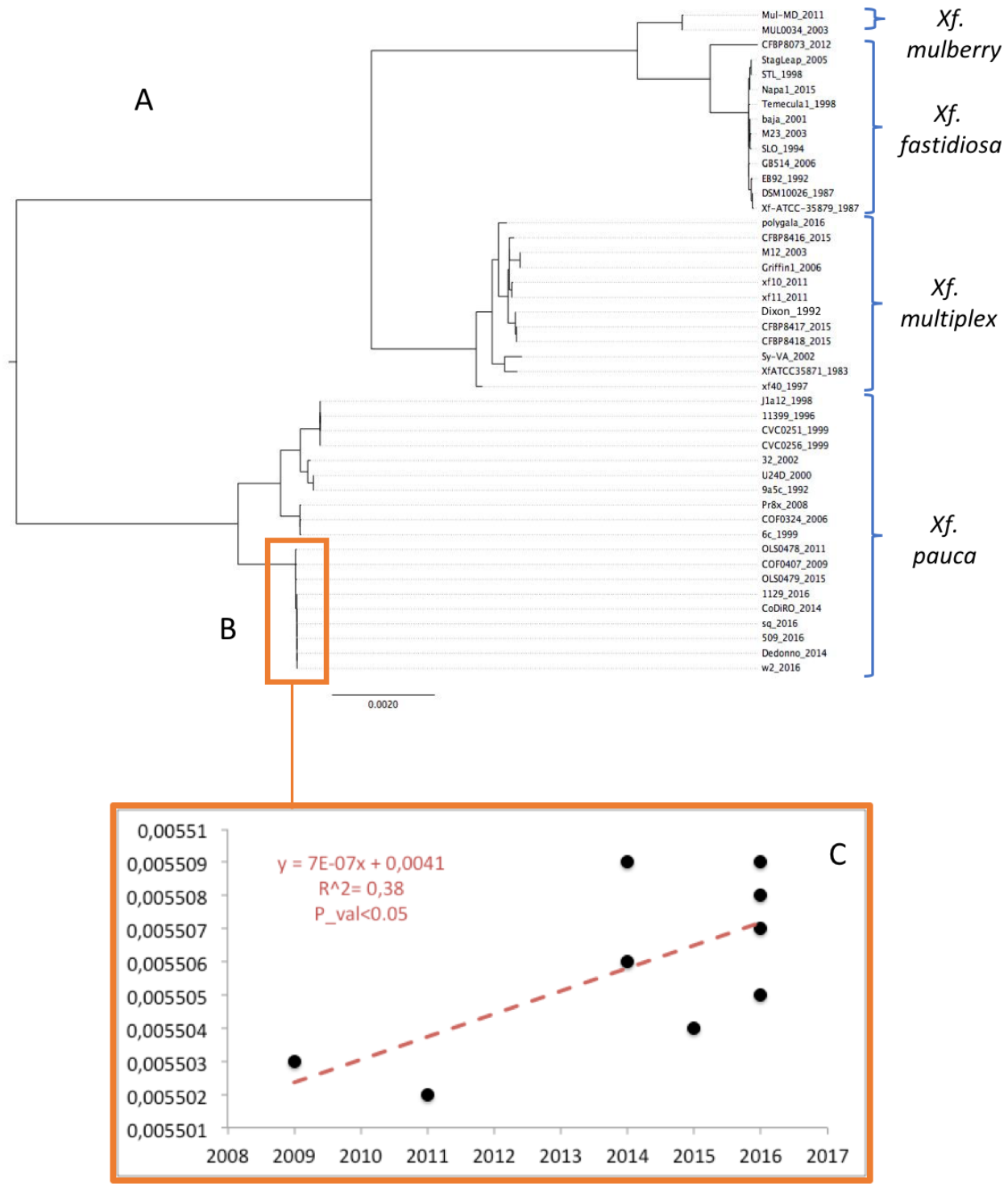


Figure S3: Rate comparison amongst subspecies. The boxplot (A) was constructed by merging the rate of evolution of each branch (internal and external) of the *X. fastidiosa* subsp. *fastidiosa*, *pauca* and *multiplex* clades together (obtained through rate-dating) as illustrated by the colored frames (B).

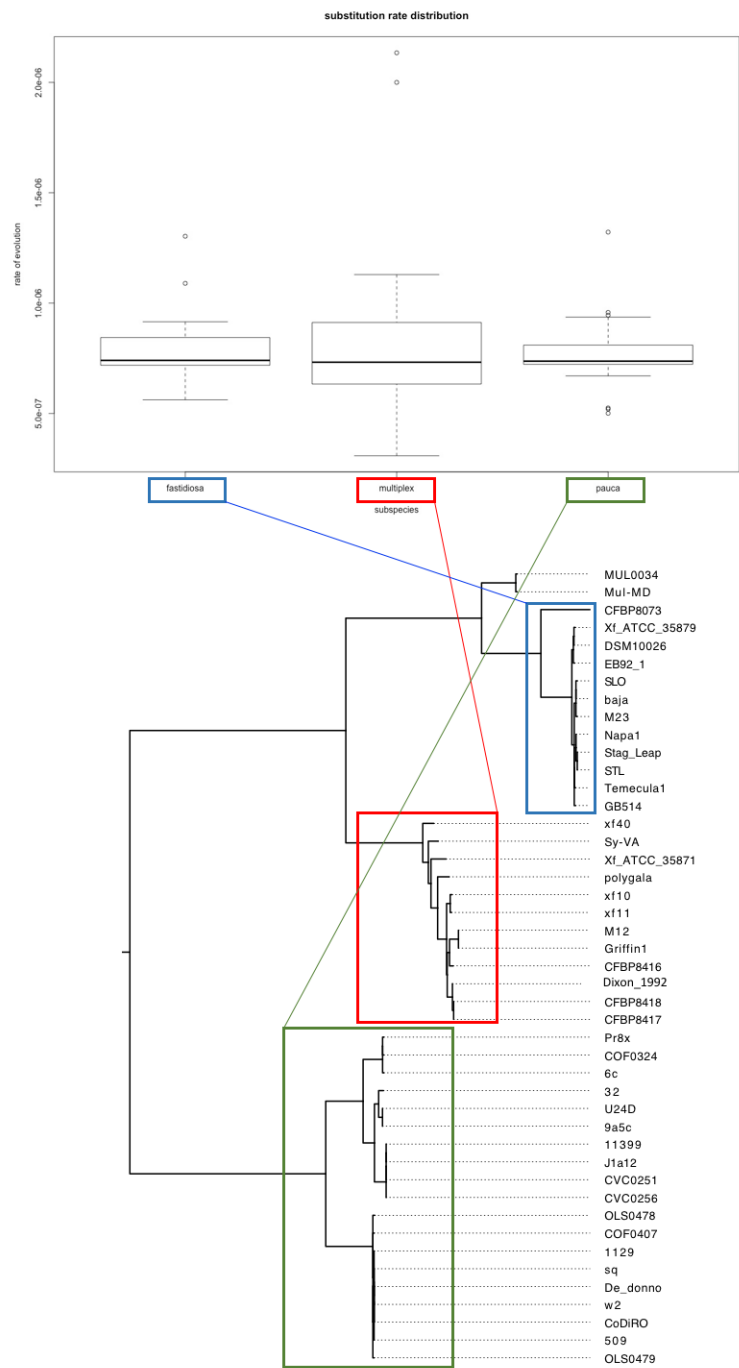


Figure S4 - Comparison between clonalFrameML and FastGEAR. (A) ClonalFrameML output, (B) FastGEAR output, (C) comparison between the genes found to be recombining between the two algorithms which were mapped to the *Xylella fastidiosa* reference genome.

