Supplementary material

Fig. S1. Simplified view of the distance tree of DeltaBLAST results with 5000 *bd* oxidases.

The NJ tree was obtained with all the results of a broad DELTABLAST search using *cydA* of *Bacillus subtilis* (accession: NP_391755) as a query against 5000 species of proteobacteria excluding most δ-proteobacteria and all ε-proteobacteria, as well as Enterobacterales, to reduce sequence redundancy and the complex distribution of δ-proteobacterial oxidases (see Fig. 1 and main text). Major possible instances of Lateral Gene Transfer (LGT) are indicated (see main text).

Fig. S2. Phylogenomic profile of gamma proteobacteria.

The genomes of a selection of taxa representing all the major orders and families of γ-proteobacteria (cf. Rao and Gupta, 2007; Segata et al, 2013), including the taxa shown in Figs. 3-6 of the main article (shown in bold characters), were analysed and presented in a comprehensive phylogenetic tree as described in the Methods (main text).

Table S1. Compilation of the *bd* oxidases most studied in this work.

Fig. S1 - Simplified view of the distance tree (NJ) of DeltaBLAST 5000 of all cytochrome *bd* oxidases.

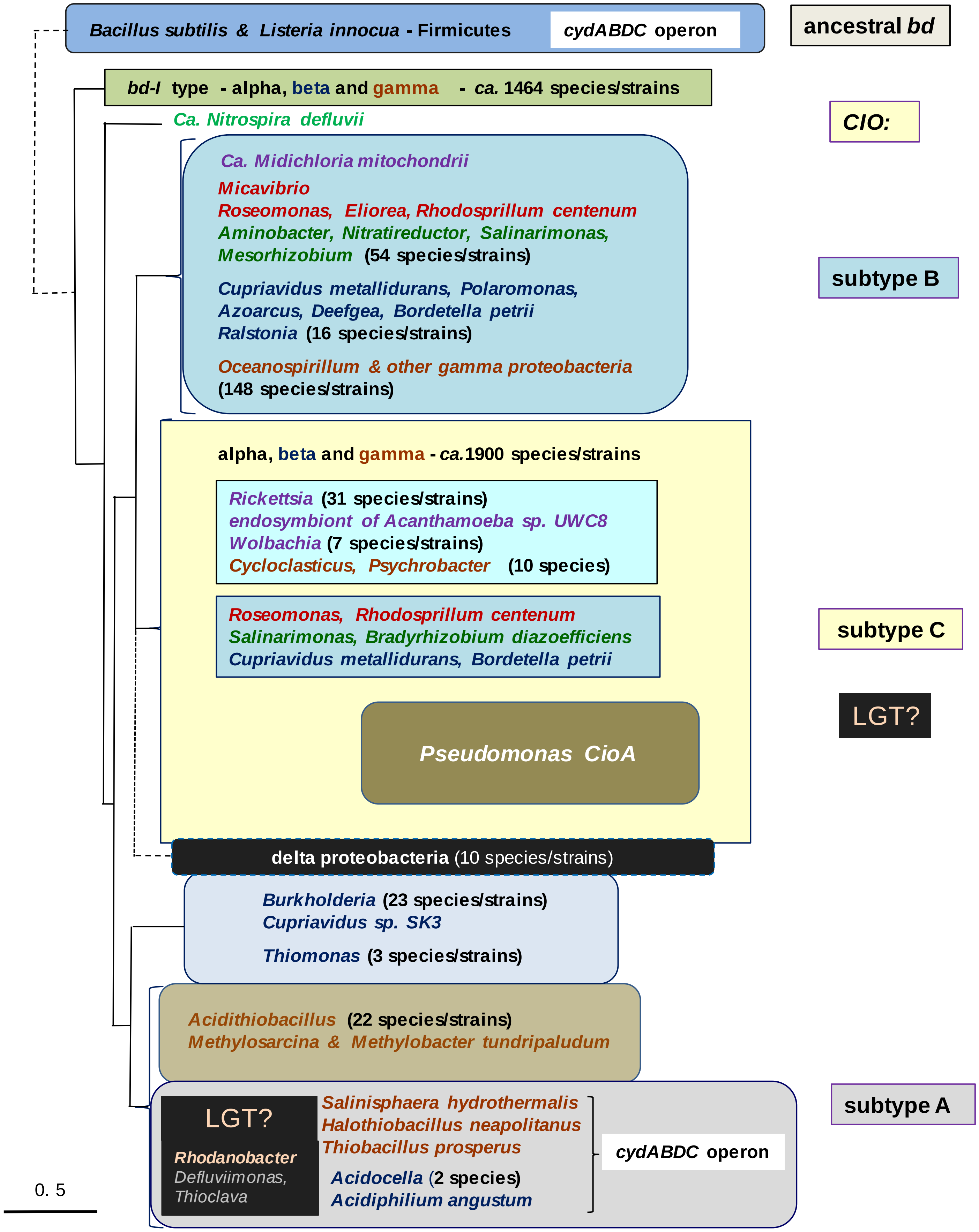

Fig. S1

Figure S2 - Phylogenomics of gamma proteobacteria. In bold are the taxa used in the trees of Figs. 3-6.

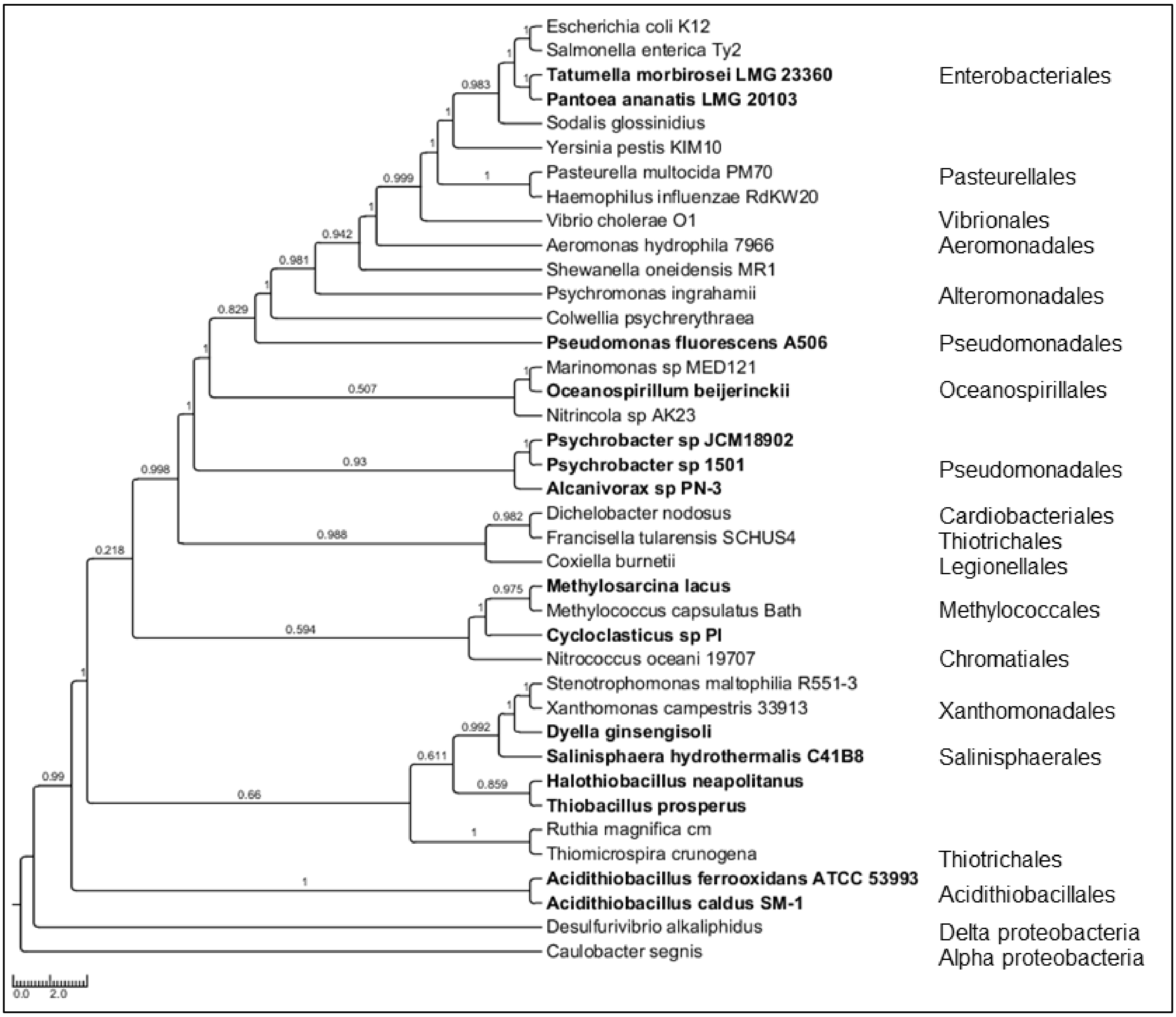

Fig. S2

Table S1. Compilation of the *bd* oxidases most studied in this work.

			cydA (aa)	*cydB* (aa)	
organism	accession	taxonomic group	subunit I	subunit II	classification and notes
		Eubacteria			
Acidocella sp. MX-AZ02	WP_008494833	alpha proteobacteria	**480**	**347**	**CIO subtype A with *cydABDC* cluster**
Acidocella facilis	WP_026438987	alpha proteobacteria	**480**	**347**	**CIO subtype A with *cydABDC* cluster**
Acidiphilium angustum	WP_029312988	alpha proteobacteria	**480**	**348**	**CIO subtype A with *cydABDC* cluster**
Salinisphaera hydrothermalis	KEZ78450	gamma proteobacteria	**478**	**350**	**CIO subtype A with *cydABDC* cluster**
Halothiobacillus neapolitanus	ACX96129	gamma proteobacteria	**483**	**348**	**CIO subtype A with *cydABDC* cluster**
Thiobacillus prosperus	KFZ91409	gamma proteobacteria	**480**	**345**	**CIO subtype A with *cydABDC* cluster**
Tatumella morbirosei	KGD72389	gamma proteobacteria - **enterobacteria**	**481**	**348**	**CIO subtype A,** *cydDC* prepended
Defluviimonas sp. 20V17	KDB01967	alpha proteobacteria	**479**	**348**	CIO subtype A, *cydD* only
Acidithiobacillus caldus	WP_014002943	gamma proteobacteria	**484**	missing	CIO subtype A degenerate
Rhodanobacter sp. 115	EIL96202	gamma proteobacteria	**478**	missing	CIO subtype A degenerate
Methylosarcina lacus	WP_029646396	gamma proteobacteria	**452**	334 in separate cluster	CIO subtype A degenerate
Methylobacter tundripaludum	WP_031436940	gamma proteobacteria	**486**	336 in separate cluster	CIO subtype A degenerate
Acidithiobacillus thiooxidans	WP_024895144	gamma proteobacteria	**482**	**345**	subunit I clustering with subtype A, no *cydDC*
Thiomonas intermedia	Tint_0239, YP_003641981	beta proteobacteria	**494**	**341**	subunit I clustering with subtype A, no *cydDC*
Burkholderia sp. BT03	EUC12370	beta proteobacteria	**463**	**328**	subunit I clustering with subtype A, no *cydDC*
***Ca.* Midichloria mitochondrii**	midi_00095, YP_004679103	alpha proteobacteria	**443**	**316**	CIO subtype B
Rhodospirillum centenum SW	RC1_0287, YP_002296549	alpha proteobacteria	**448**	**335**	CIO subtype B
Micavibrio aeruginosavorus	YP_004864645, MICA_298	alpha proteobacteria	**457**	**335**	CIO subtype B
Mesorhizobium loti	WP_027062122	alpha proteobacteria	**453**	**334**	CIO subtype B
Roseomonas cervicalis ATCC 49957	EFH12552	alpha proteobacteria	**447**	**337**	CIO subtype B
Elioraea tepidiphila	WP_019014234	alpha proteobacteria	**444**	**337**	CIO subtype B
Terasakiella pusilla	WP_028880378	alpha proteobacteria	**449**	**336**	CIO subtype B
Salinarimonas rosea	WP_029030014	alpha proteobacteria	**464**	**340**	CIO subtype B
Oceanospirillum beijerinckii	WP_028301376	gamma proteobacteria	**453**	**332**	CIO subtype B
Teredinibacter turnerae T7901	TERTU_0322, YP_003071988	gamma proteobacteria	**454**	**334**	CIO subtype B
Cupriavidus metallidurans CH34	Rmet_5232 YP_587360	beta proteobacteria	**453**	**345**	CIO subtype B
Polaromonas naphthalenivorans CJ2	Pnap_0495 YP_980736	beta proteobacteria	**470**	**343**	CIO subtype B
beta proteobacterium L13	WP_017509874	beta proteobacteria	**442**	**336**	CIO subtype B
Deefgea rivuli	WP_027467314	beta proteobacteria	**445**	**341**	CIO subtype B
Acetobacter pasteurianus 386B	APA386B_1011	alpha proteobacteria	**477**	**338**	CIO subtype C
Acetobacter pasteurianus IFO 3283-01	APA01_21500	alpha proteobacteria	**477**	**336**	CIO subtype C
Acidiphilium angustum	WP_029312988	alpha proteobacteria	**480**	**348**	CIO subtype C
Acidiphilium cryptum	Acry_2040	alpha proteobacteria	**472**	**341**	CIO subtype C
Acidiphilium multivorum	ACMV_22850	alpha proteobacteria	**472**	**341**	CIO subtype C
Acidomonas methanolica NBRC	GAJ28377	alpha proteobacteria	**477**	**339**	CIO subtype C
Agrobacterium radiobacter K84	Arad_12230	alpha proteobacteria	**475**	**335**	CIO subtype C
alpha bacterium BAL-199	EDP63365	alpha proteobacteria	**473**	**343**	CIO subtype C
Asaia sp. SF2.1	WP_023978129	alpha proteobacteria	**469**	**340**	CIO subtype C
Asticcacaulis benevestitus	WP_018084088	alpha proteobacteria	**471**	**337**	CIO subtype C
Azorhizobium caulinodans ORS 571	AZC_3759	alpha proteobacteria	**478**	**335**	CIO subtype C
Azorhizobium caulinodans ORS 571	AZC_1354	alpha proteobacteria	**470**	**329**	CIO subtype C
Azospirillum lipoferum	AZOLI_p30515	alpha proteobacteria	**465**	**339**	CIO subtype C
Bartonella tamiae	EJF93580	alpha proteobacteria	**468**	**335**	CIO subtype C
Beijerinckia indica	Bind_3288	alpha proteobacteria	**462**	**339**	CIO subtype C
Bradyrhizobium diazefficiens USDA	bll0283 &	alpha proteobacteria	**468**	**328**	CIO subtype C
Bradyrhizobium oligotrophicum S58	S58_06340	alpha proteobacteria	**468**	**336**	CIO subtype C
Bradyrhizobium sp. STM 3843	WP_008973060	alpha proteobacteria	**467**	**343**	CIO subtype C
Bradyrhizobium sp. DFCI-1	WP_021079049	alpha proteobacteria	**468**	**333**	CIO subtype C
Bradyrhizobium sp. Ec3.3	WP_027526639	alpha proteobacteria	**466**	**336**	CIO subtype C
Bradyrhizobium sp. S23321	S23_13360	alpha proteobacteria	**469**	**328**	CIO subtype C
endosymbiont of Acanthamoeba sp.	AIF81514	alpha proteobacteria	**465**	**337**	CIO subtype C
Geminicoccus roseus	WP_027132750	alpha proteobacteria	**479**	**333**	CIO subtype C
Gluconacetobacter or	WP_019086429	alpha proteobacteria	**477**	**339**	CIO subtype C
Gluconacetobacter diazotrophicus PAl 5	Gdia_1472	alpha proteobacteria	**466**	**335**	CIO subtype C
Gluconacetobacter xylinus NBRC 3288	GLX_30020	alpha proteobacteria	**477**	**339**	CIO subtype C
Gluconobacter frateurii	WP_010501967	alpha proteobacteria	**474**	**341**	CIO subtype C
Gluconobacter morbifer	EHH67656	alpha proteobacteria	**476**	**341**	CIO subtype C
Gluconobacter oxydans 621H	GOX0278	alpha proteobacteria	**471**	**341**	CIO subtype C
Gluconobacter oxydans H24	B932_2110	alpha proteobacteria	**474**	**341**	CIO subtype C
Granulibacter bethediensis	GbCGDNIH1_013	alpha proteobacteria	**482**	**342**	CIO subtype C
Hyphomicrobium sp. MC1	HYPMC_4893	alpha proteobacteria	**475**	**337**	CIO subtype C
Inquilinus limosus	WP_026872492	alpha proteobacteria	**465**	**335**	CIO subtype C

Table S1… continued

			cydA (aa)	*cydB* (aa)	
organism	accession	taxonomic group	subunit I	subunit II	classification and notes
		Eubacteria			
Methylobacterium extorquens DSM	EHP90754	alpha proteobacteria	472	335	CIO subtype C
Methylobacterium nodulans	Mnod_3333	alpha proteobacteria	478	335	CIO subtype C
Methylobacterium populi	Mpop_5132	alpha proteobacteria	474	336	CIO subtype C
Methylobacterium radiotolerans	Mrad2831_4861	alpha proteobacteria	470	328	CIO subtype C
Methylobacterium radiotolerans	Mrad2831_4927	alpha proteobacteria	472	335	CIO subtype C
Methylobacterium sp. 4-46	M446_4323	alpha proteobacteria	478	334	CIO subtype C
Methylobacterium sp. 4-46	M446_1250	alpha proteobacteria	482	347	CIO subtype C
Methylobacterium sp. GXF4	EIZ81581	alpha proteobacteria	472	335	CIO subtype C
Methylobacterium extorquens AM1	MexAM1_META1 p4206	alpha proteobacteria	474	336	CIO subtype C
Methylobacterium extorquens AM1	MexAM1_META2 p1123 - plasmid	alpha proteobacteria	472	335	CIO subtype C
Methylobacterium extorquens DM4	METDI4817	alpha proteobacteria	474	336	CIO subtype C
Methylobacterium extorquens PA1	Mext_3834	alpha proteobacteria	474	336	CIO subtype C
Methylocella silvestris BL2	Msil_2188	alpha proteobacteria	472	335	CIO subtype C
Methylocella silvestris BL2	Msil_2644	alpha proteobacteria	474	335	CIO subtype C
Microvirga lotononidis	WP_009493026	alpha proteobacteria	473	335	CIO subtype C
Oligotropha carboxidovorans OM5	OCAR_4639	alpha proteobacteria	468	337	CIO subtype C
Paracoccus denitrificans PD1222	Pden_4010	alpha proteobacteria	467	334	CIO subtype C, also called *qxtAB*
Parvibaculum lavamentivorans DS-1	Plav_0596	alpha proteobacteria	463	336	CIO subtype C
Phaeobacter gallaeciensis DSM 17395	PGA1_c19670	alpha proteobacteria	474	334	CIO subtype C
Pseudovibrio sp. FO-BEG1	PSE_1416	alpha proteobacteria	404	334	CIO subtype C
Rhizobium sp. CF122	EJL50761	alpha proteobacteria	468	331	CIO subtype C
Rhodobacter sphaeroides 2.4.1	RSP_3212	alpha proteobacteria	465	335	CIO subtype C, also called *qxtAB*
Rhodomichrobium vaniellii	Rvan_0181	alpha proteobacteria	464	337	CIO subtype C
Rhodopseudomonas palustris BisA53	RPE_0539	alpha proteobacteria	468	338	CIO subtype C
Rhodopseudomonas palustris BisB5	RPD_4378	alpha proteobacteria	468	334	CIO subtype C
Rhodopseudomonas palustris CA009	RPA4793	alpha proteobacteria	468	336	CIO subtype C
Rhodopseudomonas palustris TIE-1	Rpal_1533	alpha proteobacteria	465	341	CIO subtype C
Rhodospirillum centenum	RC1_0416	alpha proteobacteria	479	339	CIO subtype C
Rickettsia canadensis str. McKiel	A1E_01235	alpha proteobacteria	454	339	CIO subtype C
Rickettsia conorii str. Malish 7	RC0288, NP_359925	alpha proteobacteria	456	339	CIO subtype C
Rickettsia felis URRWXCal2	RF_0333	alpha proteobacteria	456	339	CIO subtype C
Rickettsia massiliae MTU5	RMA_0296, YP_001499104	alpha proteobacteria	430	339	CIO subtype C
Rickettsia parkeri str. Portsmouth	MC1_01625, YP_005392544	alpha proteobacteria	456	339	CIO subtype C
Rickettsia peacockii strain Rustic	RPR_01820	alpha proteobacteria	456	339	CIO subtype C
Rickettsia typhi str. TH1527	RTTH1527_01005	alpha proteobacteria	447	339	CIO subtype C - no COX in genome
Rickettsiaceae bacterium Os18	WP_019231091	alpha proteobacteria	470	339	CIO subtype C
Roseomonas cervicalis ATCC 49957	WP_007003071	alpha proteobacteria	469	354	CIO subtype C
Salinarimonas rosea	WP_029032601	alpha proteobacteria	481	347	CIO subtype C
Sphingobium xenophagum	WP_019054127	alpha proteobacteria	467	332	CIO subtype C
Starkeya novella	Snov_0620	alpha proteobacteria	469	340	CIO subtype C
Starkeya novella	Snov_3535	alpha proteobacteria	474	346	CIO subtype C
Thalassospira profundimaris	EKF07979	alpha proteobacteria	462	332	CIO subtype C
Tistrella mobilis	TMO_b0108	alpha proteobacteria	491	336	CIO subtype C
Wolbachia endosymbiont of Drosophila melanogaster	WD0740	alpha proteobacteria	468	340	CIO subtype C
Wolbachia wRi	YP_002727277	alpha proteobacteria	468	340	CIO subtype C
Zymomonas mobilis subsp. mobilis NCIMB 11163	Za10_1638	alpha proteobacteria	476	340	CIO subtype C
Pseudomonas fluorescens A506	PflA506_4640	gamma proteobacteria	479	335	CIO subtype C, also called *cioAB*
Cycloclasticus sp. P1	YP_006836894, Q91_0351	gamma proteobacteria	470	339	CIO subtype C
Cycloclasticus pugetii	WP_020161758	gamma proteobacteria	470	339	CIO subtype C
Psychrobacter sp. G	PSYCG_08730, YP_008163613	gamma proteobacteria	497	379	CIO subtype C
Psychrobacter sp. JCM 18902	GAF58390	gamma proteobacteria	498	338	CIO subtype C
Psychrobacter sp. 1501(2011)	WP_007395587	gamma proteobacteria	497	338	CIO subtype C
Azotobacter vinelandii DJ	Avin_11050	gamma proteobacteria	476	335	CIO subtype C
Legionella pneumophila subsp. pneumophila	LPO_0235	gamma proteobacteria	456	329	CIO subtype C
Frateuria aurantia DSM 6220	Fraau_2907, YP_005378918	gamma proteobacteria	465	335	CIO subtype C
Salmonella enterica subsp. enterica serovar Thompson str. RM6836	IA1_01940 YP_008612210	gamma proteobacteria - **enterobacteria**	467	336	CIO subtype C
Burkholderia gladioli	WP_013690153	beta proteobacteria	465	336	CIO subtype C
Ralstonia eutropha JMP134	Reut_B4101	beta proteobacteria	483	335	CIO subtype C
Desulfovibrio magneticus RS-1	DMR_06960, YP_002952073	delta proteobacteria	461	338	CIO subtype C
Desulfococcus multivorans	WP_020877073	delta proteobacteria	459	332	CIO subtype C
***Ca.* Nitrospira defluvii**	YP_003798241	Nitrospirales	447	340	**CIO ancestral**

Table S1… continued

			cydA (aa)	*cydB* (aa)	
organism	accession	taxonomic group	subunit I	subunit II	classification and notes
		Eubacteria			
Rhodopseudomonas palustris HaA2	RPB_0929, YP_484550	alpha proteobacteria	**524**	**383**	**_bd_ -I, _cydDC_ appended**
Rhodopseudomonas palustris DX-1	Rpdx1_2434	alpha proteobacteria	**528**	**383**	**_bd_ -I, _cydDC_ appended**
Pleomorphomonas oryzae	WP_026791401	alpha proteobacteria	**527**	**383**	**_bd_ -I, _cydDC_ appended**
Rhodospirillum photometricum	RSPPHO_01249	alpha proteobacteria	**561**	**384**	**_bd_ -I, _cydDC_ appended**
Rhodovulum sp. PH10	WP_008390734	alpha proteobacteria	**531**	**383**	**_bd_ -I, _cydDC_ appended**
Thioclava sp. DT23-4	KEO53817	alpha proteobacteria	**541**	**382**	**_bd_ -I, _cydDC_ appended**
Phaeospirillum molischianum	CCG40832	alpha proteobacteria	**525**	**385**	**_bd_ -I, _cydDC_ appended**
Thioflavicoccus mobilis	Thimo_0355, YP_007242856	gamma proteobacteria	**519**	**377**	**_bd_ -I, _cydDC_ appended**
Dyella ginsengisoli	WP_017460853	gamma proteobacteria	**534**	**377**	**_bd_ -I, _cydDC_ appended**
Frateuria aurantia DSM 6220	Fraau_1563, YP_005377664	gamma proteobacteria	**528**	**378**	**_bd_ -I, _cydDC_ appended**
Pantoea sp. At-9b	Pat9b_04265 YP_004114307	gamma proteobacteria - **enterobacteria**	**480**	**348**	**_bd_ -I, _cydDC_ appended**
Pantoea sp. AS-PWVM4	ERK15167	gamma proteobacteria - **enterobacteria**	**480**	**348**	**_bd_ -I, _cydDC_ appended**
Tatumella morbirosei enterobacteria	KGD72389	gamma proteobacteria - **enterobacteria**	**481**	**348**	**_bd_ -I, _cydDC_ appended**
Kinetoplastibacterium blastocrithidii	BCUE_0079, YP_007449673	beta proteobacteria	**521**	**384**	**_bd_ -I, _cydDC_ appended**
Desulfurivibrio alkaliphilus AHT2	DaAHT2_0790,	delta proteobacteria	**442**	**342**	**_bd_ -I, _cydDC_ appended**
Xanthomonadaceae bacterium 3.5X	KGI78673	gamma proteobacteria	**522**	**377**	**_bd_ -I,** _cydD_ only appended
Coxiella burnetii RSA 493 - cydA2	NP_819973	gamma proteobacteria	**521**	**377**	*subunit I clustering with* ***bd*** **-I**, no *cydDC*
Acidocella sp. MX-AZ02	WP_008494805	alpha proteobacteria	**536**	**379**	**_bd_ -I, _cydDC_ prepended**
Acidiphilium angustum	WP_029312671	alpha proteobacteria	**536**	**379**	**_bd_ -I, _cydDC_ prepended**
Acidiphilium multivorum AIU301	YP_004283908	alpha proteobacteria	**537**	**379**	**_bd_ -I, _cydDC_ prepended**
Acetobacter pasteurianus 386B	APA386B_473	alpha proteobacteria	**537**	**379**	**_bd_ -I, _cydDC_ prepended**
Gluconacetobacter or **Komagataeibacter europaeus**	WP_019092290	alpha proteobacteria	**536**	**379**	**_bd_ -I, _cydDC_ prepended**
Acidomonas methanolica NBRC 104435	GAJ28292	alpha proteobacteria	**535**	**383**	**_bd_ -I, _cydDC_ prepended**
Roseomonas sp. B5	WP_019461856	alpha proteobacteria	**522**	**382**	**_bd_ -I, _cydDC_ prepended**
Rubritepida flocculans	WP_027285067	alpha proteobacteria	**530**	**384**	**_bd_ -I, _cydDC_ prepended**
Tistrella mobilis	TMO_a0189	alpha proteobacteria	**537**	**384**	**_bd_ -I, _cydDC_ prepended**
Rhodospirillum centenum SW	RC1_4036	alpha proteobacteria	**523**	**384**	**_bd_ -I, _cydDC_ prepended**
Oceanibaculum indicum	WP_008945285	alpha proteobacteria	**530**	**384**	**_bd_ -I, _cydDC_ prepended**
Caulobacter sp. K31	Caul_0634	alpha proteobacteria	**526**	**381**	**_bd_ -I, _cydDC_ prepended**
Caulobacter crescentus NA1000	CCNA_00800	alpha proteobacteria	**520**	**383**	**_bd_ -I, _cydDC_ prepended**
Methylobacterium extorquens PA1	Mext_1360	alpha proteobacteria	**529**	**384**	**_bd_ -I, _cydDC_ prepended**
Brucella melitensis biovar Abortus 2308	BAB2_0728	alpha proteobacteria	**504**	**384**	**_bd_ -I, _cydDC_ prepended**
Brucella suis 1330 or melitensis	BMNI_II0476,	alpha proteobacteria	**525**	**384**	**_bd_ -I, _cydDC_ prepended**
Rhizobium etli CIAT 652	RHECIAT_PC0000175	alpha proteobacteria	**526**	**384**	**_bd_ -I, _cydDC_ prepended**
Liberibacter crescens BT-1	B488_01440	alpha proteobacteria	**504**	**366**	**_bd_ -I, _cydDC_ prepended**
Salinisphaera hydrothermalis	KEZ76806	gamma proteobacteria	**526**	**377**	**_bd_ -I, _cydDC_ prepended**
Psychrobacter sp. PRwf-1	PsycPRwf_0327	gamma proteobacteria	**532**	**338**	**_bd_ -I, _cydDC_ prepended**
Variovorax paradoxus B4 - beta	VAPA_1c34620	beta proteobacteria	**537**	**384**	**_bd_ -I, _cydDC_ prepended**
Burkholderia kururiensis	WP_017772623	beta proteobacteria	**529**	**378**	**_bd_ -I, _cydDC_ prepended**
Streptomyces fulvissimus DSM 40593	YP_007932425	**Actinomycetes**	**515**	**333**	subunit I similar to ***bd*** **-I**
Listeria innocua	WP_003772850	**Firmicutes**	**510**	339 in separate cluster	**_bd_ -I degenerate**
Escherichia coli str. K-12 substr. W3110	b0733, NP_415261	gamma proteobacteria - **enterobacteria**	**522**	**379**	**_bd_- I with _cydABX_ , prototypic _bd-I_**
Vibrio cholerae LMA3984-4	VCLMA_B0643 YP_005632513	gamma proteobacteria - **enterobacteria**	**526**	**378**	**_bd_- I with _cydABX_**
Pantoea agglomerans - γ	EZI36193	gamma proteobacteria - **enterobacteria**	**470**	**344**	**_bd_- I with _cydABX_**
Pantoea sp. At-9b - γ	Pat9b_3272 YP_004117124	gamma proteobacteria - **enterobacteria**	**471**	**344**	**_bd_- I with _cydABX_**
Phaeospirillum fulvum	WP_021133524	alpha proteobacteria	**525**	**384**	**_bd_- I with _cydABX_**
Methylocystis sp. SC2	BN69_2246	alpha proteobacteria	**524**	**379**	**_bd_- I with _cydAB_**
Geminicoccus roseus	WP_027133135	alpha proteobacteria	**529**	**379**	**_bd_- I with _cydABX_**
Pleomorphomonas koreensis	WP_026784703	alpha proteobacteria	**525**	**383**	**_bd_- I with _cydABX_**
Inquilinus limosus	WP_026868948	alpha proteobacteria	**525**	**380**	**_bd_- I with _cydABX_**
Novispirillum itersoni	WP_019645898	alpha proteobacteria	**521**	**380**	**_bd_- I with _cydABX_**
Acidithiobac_ferrooxidans	YP_002219519, Lferr_1070	gamma proteobacteria	**544**	**387**	**_bd_- I with _cydABX_**
Acidithiobac_caldus	YP_004749631, Atc_2281	gamma proteobacteria	**546**	**377**	**_bd_- I with _cydABX_**
Thiorhodococcus drewsii	EGV30141	gamma proteobacteria	**534**	**380**	**_bd_- I with _cydABX_**
Methylobacter luteus	WP_027157314	gamma proteobacteria	**521**	**379**	**_bd_- I with _cydABX_**
Methylosarcina fibrata	WP_020563382	gamma proteobacteria	**521**	**379**	**_bd_- I with _cydABX_**
Azotobacter vinelandii DJ	Avin_19890	gamma proteobacteria	**537**	**379**	**_bd_- I with _cydABX_**
Legionella pneumophila 2300/99 Alcoy	lpa_01861	gamma proteobacteria	**510**	**378**	**_bd_- I with _cydAB_**
Methylococcus capsulatus Bath	YP_113575	gamma proteobacteria	**525**	**378**	**_bd_- I with _cydABX_**
Bordetella avium	BAV0991, YP_785514	beta proteobacteria	**525**	**377**	**_bd_- I with _cydABX_**
Thiomonas intermedia (multispecies)	YP_003641759, Tint_0013	beta proteobacteria	**545**	**377**	**_bd_- I with _cydABX_**
Sideroxydans lithotrophicus ES-1	Slit_1151	beta proteobacteria	**521**	**379**	**_bd_- I with _cydABX_**

Table S1… continued – end.

organism	accession	taxonomic group	*cydA* (aa) subunit I	*cydB* (aa) subunit II	classification and notes
		Eubacteria			
Escherichia coli str. K-12 substr. W3110	Y75_p0949	gamma proteobacteria - **enterobacteria**	**514**	**378**	***bd-* I with *appABX*,** also called ***bd-* II**
Methylocystis sp. SC2	BAB2_0728	alpha proteobacteria	**530**	**381**	***bd-* I with *appABX*,** also called ***bd-* II**
Caenispirillum salinarum	WP_009542797	alpha proteobacteria	**532**	**386**	***bd-* I with *appABX***
Defluviimonas sp. 20V17	KDB05436	alpha proteobacteria	**531**	**382**	***bd-* I with *appABX***
***Ca.* Paracaedibacter acanthamoebae**	AIK95954	alpha proteobacteria	**512**	**386**	***bd-* I with *appABX***
Commensalibacter intestini	WP_008854848	alpha proteobacteria	**500**		***bd-* I with *appABX***
Coxiella burnetii RSA 493 - *cydA* 1	CBU_0218, NP_819263	gamma proteobacteria	**516**	**387**	***bd-* I with *appABX***
Francisella philomiragia subsp. philomiragia ATCC 25017	Fphi_0633, YP_001677353	gamma proteobacteria	**584**	**398**	***bd-* I with *appABX***
Dechlorosoma suillum PS	Dsui_1915	beta proteobacteria	**502**	**379**	***bd-* I with *appABX***
Azoarcus sp. BH72 - β	azo1232	beta proteobacteria	**522**	**380**	***bd-* I with *appABX***
Desulfobulbus propionicus DSM 2032	Despr_0567, WP_015723288.	delta proteobacteria	**512**	**383**	***bd-* I with *appABX***
Nitratifractor salsuginis DSM 16511	Nitsa_0601	epsilon proteobacteria	**510**	**376**	***bd-* I with *appABX***
Leptospirillum ferriphilum YSK	AIA30100	Nitrospirales	**534**	**379**	***bd-* I with *appABX***
***Ca.* Odyssella thessalonicensis**	WP_010297580	alpha proteobacteria	**507**	missing	***bd-* I** with *appABX* degenerate
Bacillus subtilis subsp. subtilis str. 168	BSU38760, NP_391755	Firmicutes	**468**	**338**	***cydABDC* operon**, prototypic
Listeria innocua ATCC 33091	EHN60252	Firmicutes	**510**	**340**	***cydABDC* operon**
Bacillus selenitireducens	Bsel_2506	Firmicutes	**459**	**337**	***cydABDC* operon**
Bacillus selenitireducens	Bsel_0543	Firmicutes	**452**	**339**	***cydABDC* operon**
Salsuginibacillus kocurii	WP_018924928	Firmicutes	**447**	**338**	***cydABDC* operon**
Exiguobacterium sp. AT1b	EAT1b_2777	Firmicutes	**462**	**343**	***cydABDC* operon**
Bacillus amyloliquefaciens	BAMF_3713	Firmicutes	**468**	**338**	*cydCD* transporters in a separate cluster
Bacillus subtilis subsp. subtilis str. 168	BSU30710, NP_390949	Firmicutes	**443**	**346**	***ythABC* operon**
Bacillus subtilis subsp. natto BEST195	BSNT_09494, YP_005562287	Firmicutes	**443**	**346**	***ythABC* operon**
Bacillus cellulosilyticus	Bcell_0256	Firmicutes	**451**	**337**	***ythABC* operon**
Bacillus subtilis subsp. subtilis str. RO-NN-1	I33_3129, YP_005558044	Firmicutes	**443**	**346**	***ythABC* operon**
Bacillus amyloliquefaciens subsp. plantarum	BANAU_2983	Firmicutes	**445**	**346**	***ythABC* operon**
Desulfovibrio magneticus RS-1	YP_002954207	delta proteobacteria	**433**	**342**	close to *cydABDC* of Firmicutes
Desulfovibrio sp. X2	EPR44720	delta proteobacteria	**438**	**341**	close to *cydABDC* of Firmicutes
Geobacter daltonii	Geob_0961, YP_002536424	delta proteobacteria	**441**	**340**	close to *cydABDC* of Firmicutes
Myxococcus xanthus DK 1622	MXAN_6913, YP_635027	delta proteobacteria	**445**	**342**	close to *cydABDC* of Firmicutes
		Archaea			
Archaeoglobus sulfaticallidus PM70-1	Asulf_00260, YP_007906286	Euryarchaeota	**506**	**388**	*cydAB* only, no Q loop extension
Methanosarcina barkeri str. Fusaro	Mbar_A0121, YP_303687	Euryarchaeota	**439**	**347**	*cydAB* only
Vulcanisaeta moutnovskia 768-2	VMUT_1510, YP_004245217	Crenarchaeota	**552**	**372**	*cydAB* only, no Q loop extension
Vulcanisaeta distributa DSM 14429	Vdis_1320 , YP_003901757	Crenarchaeota	**469**	**424**	*cydAB* only
Thermoproteus tenax Kra 1	TTX_0142, YP_004891899	Crenarchaeota	**458**	**422**	*cydAB* only
Pyrobaculum neutrophilum V24Sta	Tneu_0322, YP_001793719	Crenarchaeota	**530**	**367**	*cydAB* only, no Q loop extension
***Ca.* Korarchaeum cryptofilum OPF8**	Kcr_1584, YP_001738012	Korarchaeota	**538**	**367**	*cydAB* only, no Q loop extension