Table S1. Putative two-partner secretion systems under the control of LapG orthologs.

Organism	LapD-like	LapG-like	CdrB-like	CdrA-like	Putative Function	C-term. sequence	Length	Class
Pseudomonas aeruginosa **PAO1**	PA1433	PA1434	PA4624	PA4625	cdrA	QGGLGLVSGNYDLAYQGNNLTITKALLNVIADGKTKVYGDADP SLTYQVSGLKNGDSAGSILTGGLNRDAGENVGVYGINQGGLVL TSGNYDLAYQGNDLTITKALLNVFADAKSKQVGTADPALTYQVS GLKNGDSAGQVLAGGLGRVGGEAVGQYDILQGGLALTSGNYQ LNYQGNLLSILPLPVTPGDLGQLAALSDLRELQKGRDPDTPGDA VYRTTTLENPFLENPFLRAYALGMDVSDPNLLPA**TAAG**PAEDAS AKRVGQFTDRPLRAEAESGAG**C**SNQSYLADYWS**C**FNKPLNF	2154	Gamma-proteobacteria
Methylobacterium **sp. 4-46**	none detected	M446_2406 M446_2407 M446_4260	M446_5786	M446_5785	Filamentous haemagglutinin family outer membrane protein	GLVGGEDASVLGGSLTYGGSAQGARNAGSYAITPAGLTSGNYAI TYAPGTLTVTKAPLTVTAGNDAKTYDGRAYSGGNGVSYAGLVG GEDASVLGGSLTYGGSAQGARNAGSYAI**TAAG**LTSGNYGITFVE GILTVAPRPLTVAADAQSRASGQPNPVLTYAVSGLGLVGGDGL AGQLATPATPDSAPGSYPITQGTLAASPDYALTFLNGTLTVTEAV AAAGSAPPVGSPVTASTVTQVLTLNQSLTPYTPPVFQGAGLTSS QGSPLSDPRFDTPVA**C**LSQAA**C**YITPAAPQTGSPSAGR	4855	Alpha-proteobacteria
Burkholderiales bacterium **JOSHI_001**	WP_009550212	BurJ1DRAFT_2236	BurJ1DRAFT_1629	BurJ1DRAFT_1630	Filamentous hemagglutinin family N-terminal domain protein	QITDANALSLGTLSIGALTATSQGDLNLGAGKVAGNLQANSGN GAIGQAGALTVTGTTDLKSGTGAIALSNAGNDLQGVV**TAAG**GP VALATVNKLAVSTVNARGALSLTGASISGVGASTLGVNQFTLTA TGPITLVANTGGIGNVGTEANGLFSNPDILSLNPANSGGMTLTF ANGSIANFAVDSQSQFRTAGIVISTQNEAKKADVWG**C**FGTGI**C** VNLDSTGLFLANAAASATIAAATQEALLRAFGTDNLTAAIQRAFI TKIGVVPPGIDEIEGDLGGAS**C**EPKASGSGIQTAAA**C**NK	4844	Beta-proteobacteria
Rhizobium tropici **CIAT 899**	none detected	RTCIAT899_CH0164 RTCIAT899_CH0941 RTCIAT899_PC05500	RTCIAT899_PC00675	RTCIAT899_PC00680	Filamentous hemagglutinin-like T5SS secreted protein	AITITADTLSKIYGDANPALTYTVGGAGLVNGDTLSGSLSTTAGQ YSNVGSYAITGSFSGSNNYALTYVGGSLSVNQRALTVTADAKSK TYGDANPTLTYAATGLLNGDTLSGSLA**TAAG**QYSDVGAYAITQ GSLANANYAISYMGADLTVNQRAITVAADSLSRRYGLANPALTY TVGGAGLVNRDRLSGGLATSATSLSEPGAYAITQGTLLASANYS MNFVPGALTVEKATNPEPGTQASSVMPSFDASRFAPIRPVSDS TETADGSHDVITDPRFEGTFV**C**LDNGNG**C**VLLPAQATR	3127	Alpha-proteobacteria
Caulobacter **sp. AP07**	none detected	PMI01_01830	PMI01_02255	PMI01_02256	Uncharacterized protein	GVLAATNKTYDGTVAASGSIGLTGLVAGDTVSASGTYAFADKN AGTGKTV**TAAG**VALSGADAGNYTLAPLATTQADILKKGLTGAL AAANKTYDGTTAASGSIGLTGVVAGDTVNASGTYAFADKNAGT GKTVTVSAAALTGLDAANYDLGGVSGGLADILRRQVTVAADSA FKPFGAVDPTLTYRIAVGDLAAGDAFTGGLTRDPGEVPGGYGIT RGTLGLSMNYDLTFTGAVFTIRPFPSSEAGGSMTLKHLVQSPDF TLDWDPEINLTTGGQA**C**PGEG**C**PPQAAMSGSAGGRAVATLR	2071	Alpha-proteobacteria
Nitratireductor pacificus **pht-3B**	none detected	NA2_18545 NA2_18205 NA2_09081	NA2_17801	NA2_17806	Uncharacterized protein	SVNADSKVYDGTTAATGSLGSLSGLIGGDVVGVSGSGSFAFADK NVGTGKTVTVSGLGLTGADAGNYTLAPTATSSADITPATLWVA ANAASMTYGDGVPALGYTYGGLVGGDDASVLTGALASDATSV SNVGSYGITRGSLSAGGNYQIAFTGADVTITRRAVTVRADDLQR AIDEANPDLTYTIISGSLVNGDQPSGGLS**TAAG**VNSPAGGYDID QGSLALSANYDLTYLGGVLTILAEPDVPTPDARPQIHEASPPLPV EADDGTTDT**C**EPVIVRENGPVAVHP**C**NRSYGAWLSAAVE	2053	Alpha-proteobacteria
Sulfuricella denitrificans **skB26**	SCD_n00417	SCD_n00420 SCD_n00418	SCD_n00416	SCD_n00415	Uncharacterized protein	IPLGFSLLFYGTVYTQFWANNNGNISFNGGISSYTPFGPQGAPQ PVISPFFADVDTRNGTSGLMTLRNDIPNQIIVTWDRVGYYSSQA DKLNSFQLVVRGPGYSIPAGEGAIGFFYKTMQWETGGASGGSG GFGGTPAAVGFGDGNANGIVLVGSIENGISGVLNNHHIWFGA NLVPVGEAPVVAATCAQCEVHNALEARRVEPLEPRPTGREPLRI AQDGLVLWATGAGVTVPSFGGIVTANAASAIAAGADPTTLLPA **TAAG**GLGLSAGLDAYSIGGTDY**C**DQVVSGY**C**LPQAGEKAKQ	706	Beta-proteobacteria
Comamonas testosteroni **CNB-1**	WP_034366034.1	CtCNB1_3015	CtCNB1_2446	CtCNB1_2445	Hemolysin	AVDAIHHSVAPGAVQGTQAGPAA**GAAT**ATQTQGQITSNAVA GVAAQESSAQAQASAKVGAAATPESTAADASNARSASSQFNIR TTPPNTRIPGTSLYRQRPEAGALYLVETDPRFTQYKNWLSSDYM LQALQMDPGTVQKRLGDGFYEQQLVQQQIGQLTGRRFLGNYT SNDEQYKDLLQNGATFAQAQGLRPGIELSAAQVAQLTSDIVWL VTKEVTLSDGSRQSVLVPQVYVRVKPRRPGRHRHLAGRLG**C**EP EPFRK**C**RQQRQH**C**GPQHLEHHGREHPESGRPDVWQRRQA**C**S PAGL	2629	Beta-proteobacteria