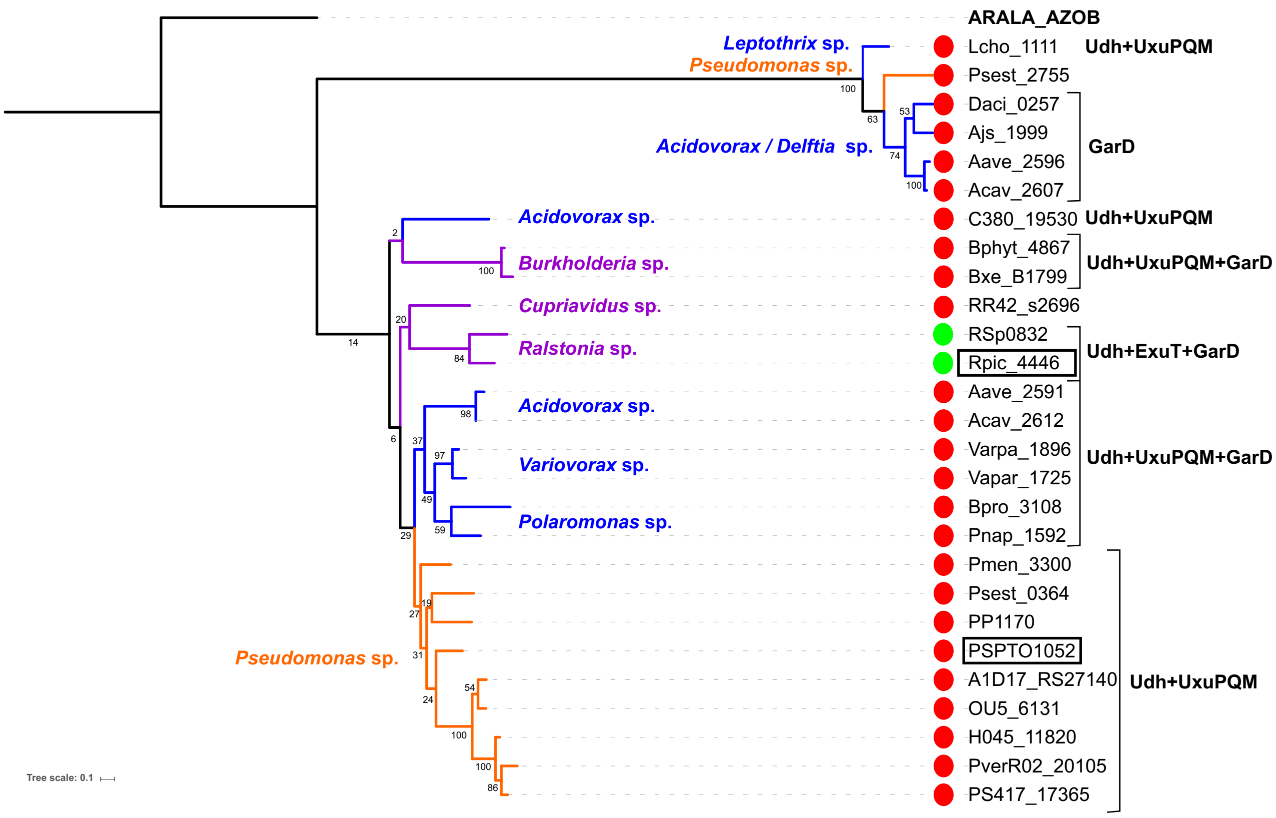
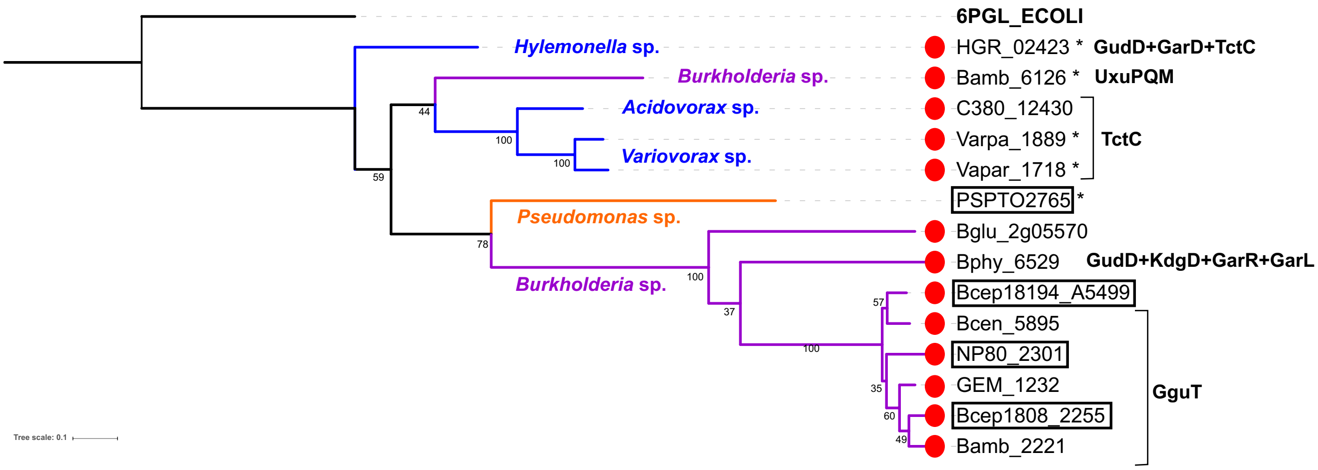
(A) UxuL proteins from the PF08450 family



(B) UxuF proteins from the PF10282 family



<u>Taxonomic groups:</u> **Comamonadaceae**, **Burkholderiaceae**, **Pseudomonadaceae**

FIG S1. Maximum likelihood phylogenetic trees of novel UxuF and UxuL lactonases.

The tree was constructed using the PhyML software; the bootstrap values (100 replicates) are shown for each node.

Representative previously characterized lactonases from both families included as outgroups are in bold:

6-phosphogluconolactonase from *Escherichia coli* (6PGL_ECOLI), L-arabinolactonase from *Azospirillum brasilense* (ARALA_AZOB).

Lactonase genes from the reconstructed GguR and GulR regulons are marked with red ● and green ● circles.

Enzymes biochemically characterized in this work are boxed (▭).

Secreted enzymes as predicted using the SignalP software are marked with asterisk (*).

Genomic clustering of *uxuL* and *uxuF* with other hexuronate utilization genes is shown on the right.

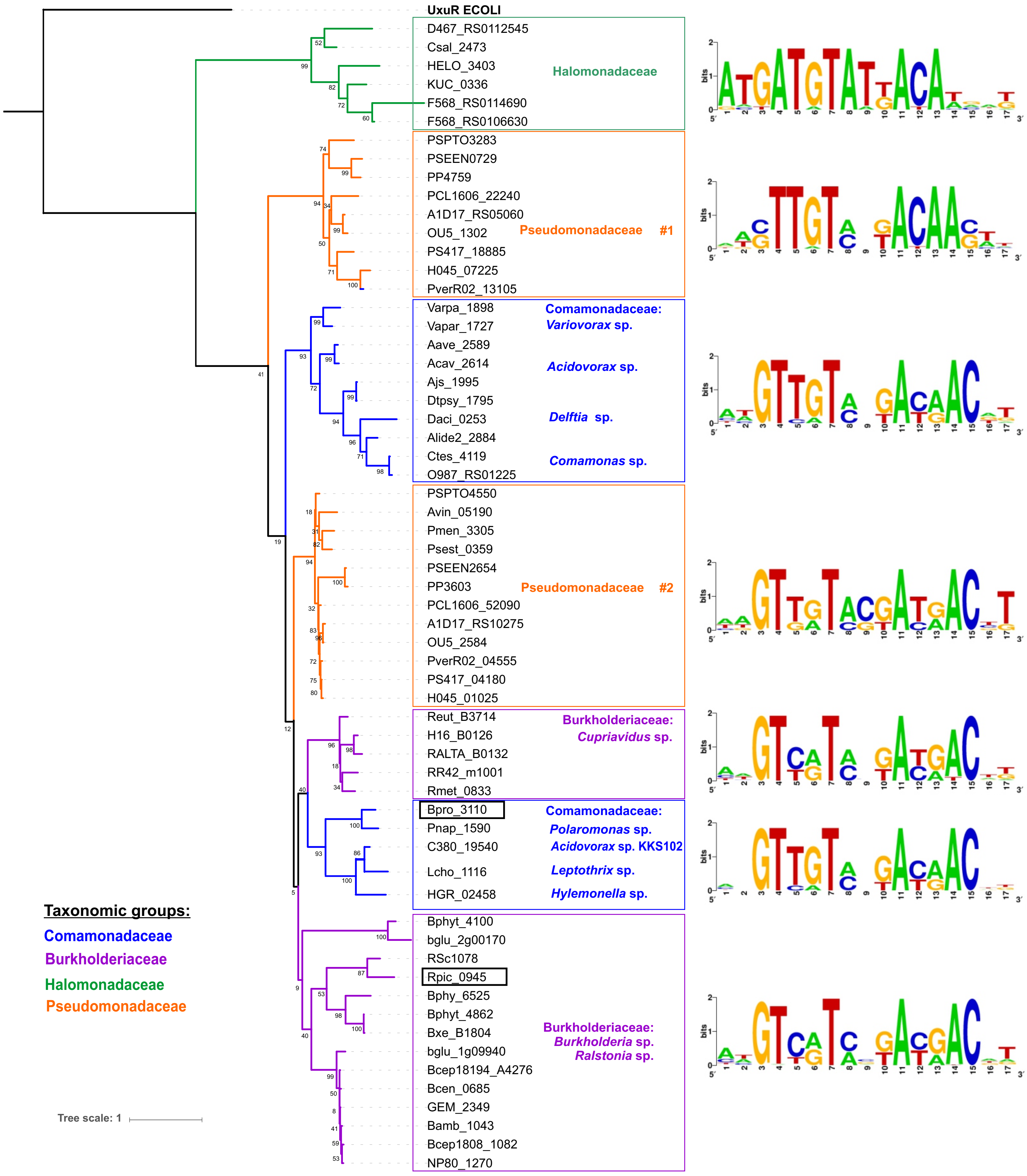


FIG S2. Maximum likelihood phylogenetic tree of the GguR regulators and their DNA motifs.

The tree was constructed using the PhyML software; the bootstrap values (100 replicates) are shown for each node. Regulators characterized in this work are boxed (▭). DNA motifs constructed using the WebLogo tool.

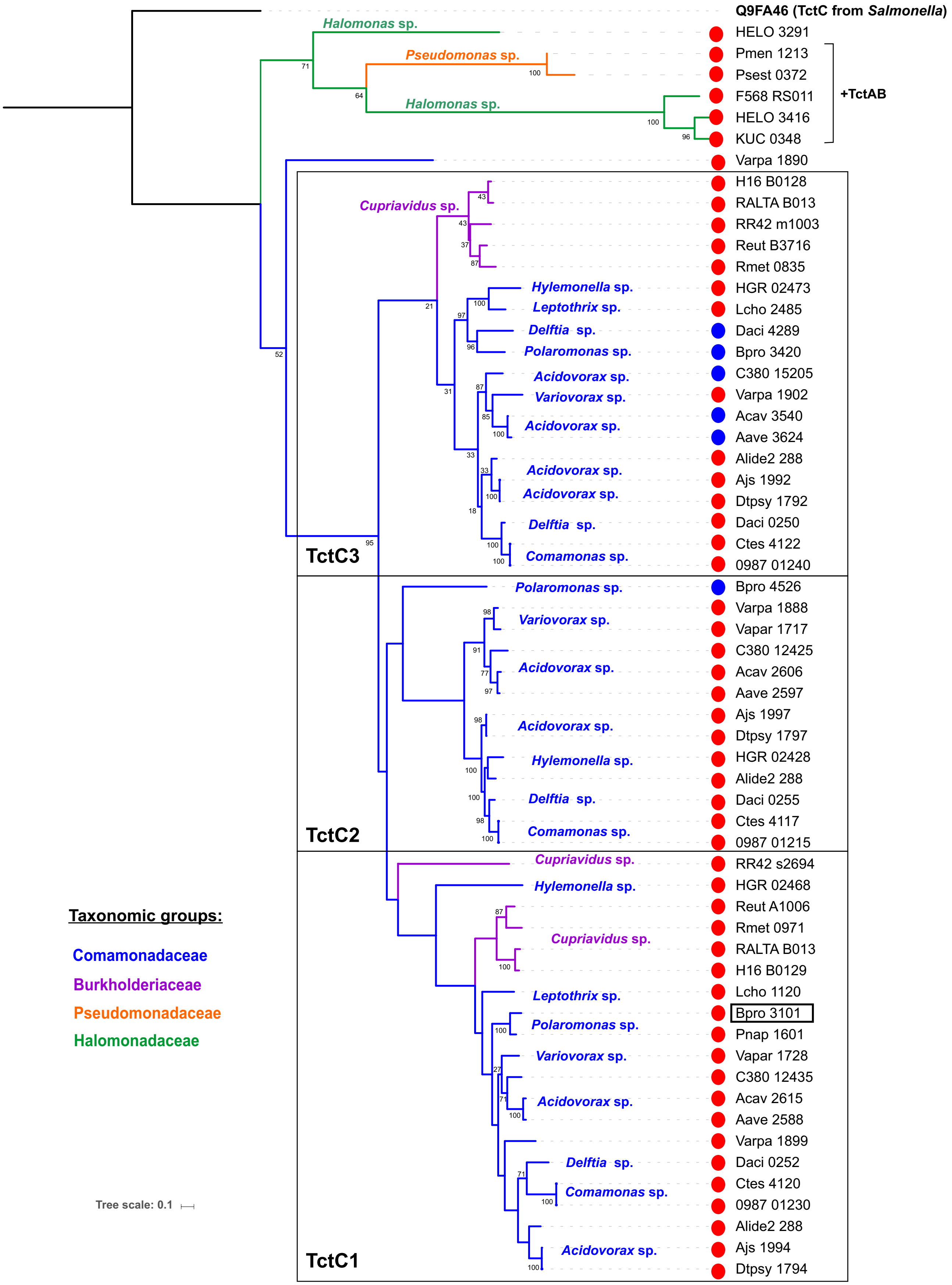


FIG S3. Maximum likelihood phylogenetic tree of novel aldarate transporters TctC.

The tree was constructed using the PhyML software; the bootstrap values (100 replicates) are shown for each node.

Previously characterized TctC protein from *Salmonella* was included as outgroup.

tctC genes from the reconstructed GguR and GudR regulons are marked with red ● and blue ● circles.

Experimentally characterized in this work D-glucarate binding TctC protein is boxed.

Genomic clustering of *tctC* with other aldarate utilization genes is shown on the right.

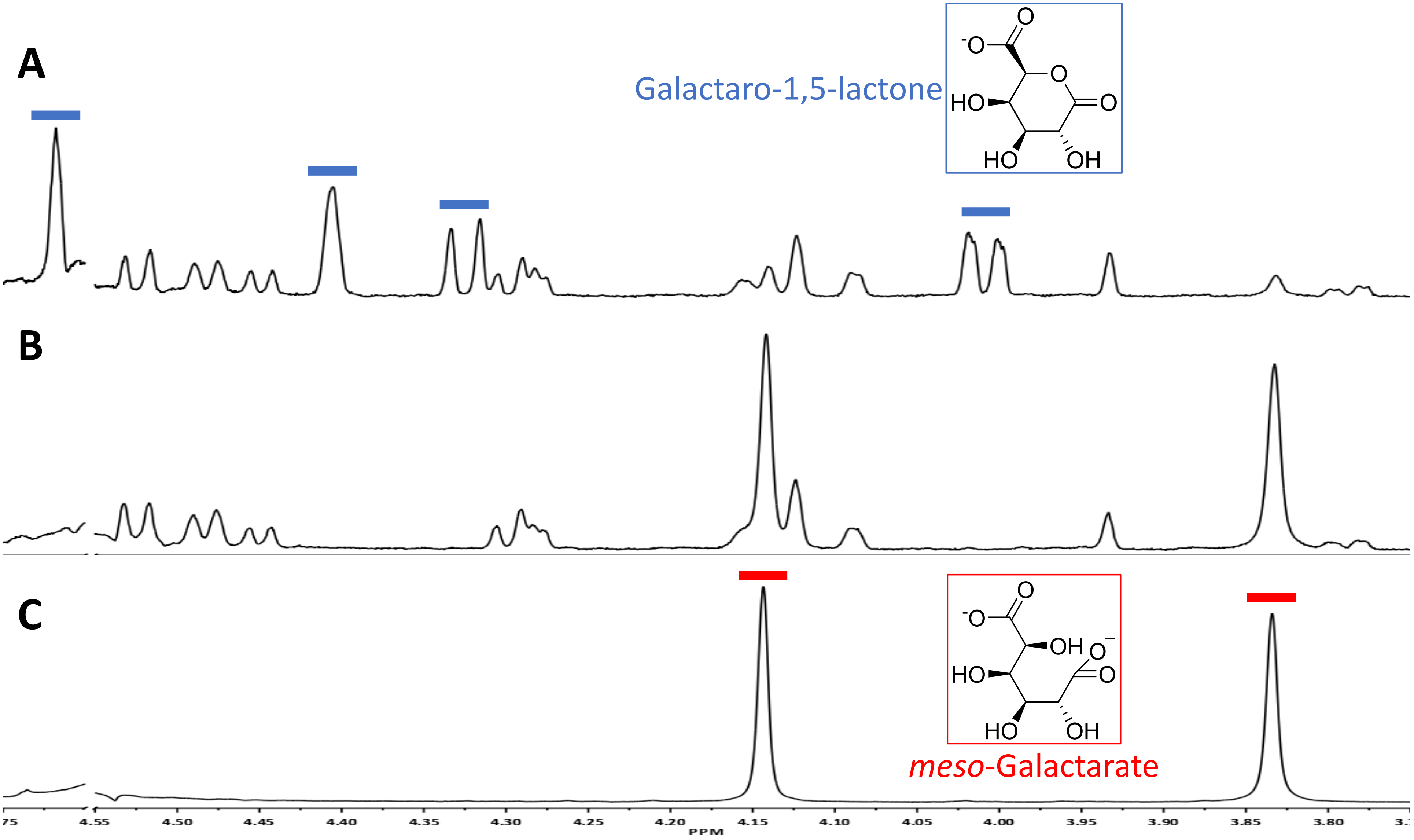


FIG S4 Proton NMR spectra for activity screening of the lactone hydrolase Rpic_4446 from *Ralstonia pickettii*. (A) 1H NMR spectrum of a mixture of galactaro-1,5 & 1,4-lactones. The 1,5-lactone is unstable and converts to the 1,4-lactone spontaneously. (B) Spectrum 2 minutes after the addition of Rpic_4446. The 1,4-lactone peaks remain, while two new peaks emerge. (C) Spectrum of pure *meso*-galactarate. The peaks in (B) match those of *meso*-galactarate, suggesting it to be the product of the lactone hydrolase reaction.

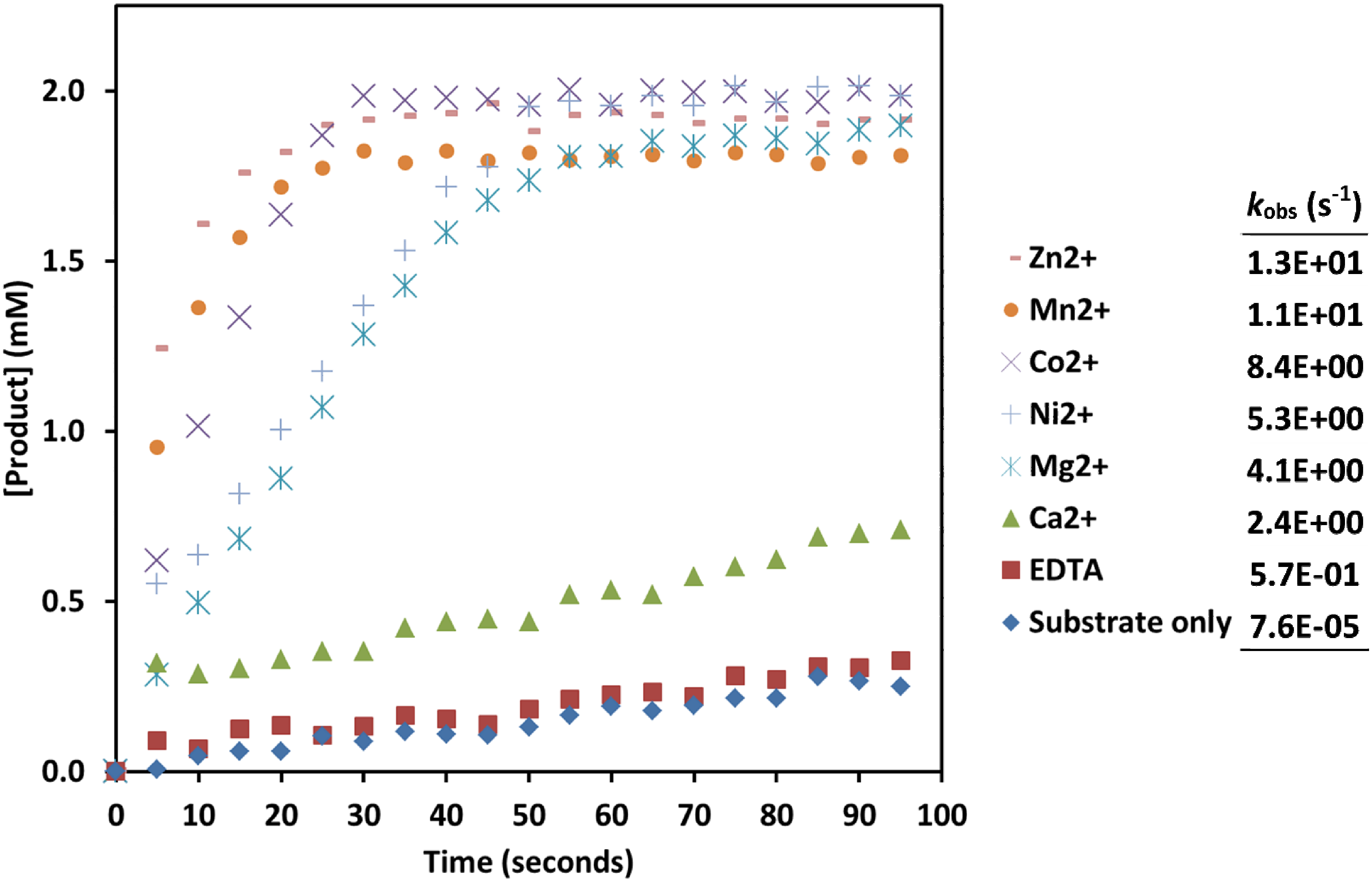


FIG S5 Metal screening of lactone hydrolase from *Ralstonia pickettii* 12J. The reaction was monitored in the presence of Zn^{2+}, Mn^{2+}, Co^{2+}, Ni^{2+}, Mg^{2+}, Ca^{2+}, and EDTA. Blue diamonds represent the progress curve for substrate only. Zn^{2+} is the best activator.

Table S1. Reconstructed catabolic pathways and regulons for hexuronate and aldarate utilization in Proteobacteria.

(A) Distribution of transcriptional regulators, enzymes, and transporters involved in hexuronate/aldarate utilization in the analyzed genomes.

Proteobacterial	Regulators				Upstream enzymes					Downstream enzymes						Transporters					Additional GguR-regulated genes					
Genomes	GguR	GudR	GulR	UdhR	Udh	UxuL	UxuF	Gci	Gli	GarD	GudD	KdgD	KgsD/KgsD2	GarL	GarR	UxuPQM	TctCAB	GarP (GudP)	GguT	ExuT	Pgl	AldE	SerA	Agl	Omp	ExuT-II
Halomonadaceae																										
Halomonas elongata DSM 2581	HELO_3403	-	-	-	HELO_3405	-	-	HELO_340	HELO_340	HELO_3413	HELO_3412	HELO_3417	HELO_3411	-	-	HELO_3410-8	HELO_3414-6, HELO_3291	-	-	-	-	-	-	-	-	-
Halomonas boliviensis LC1	KUC_0336	-	-	-	KUC_0337	-	-	KUC_0339	KUC_0338	KUC_0345	KUC_0344	KUC_0343	KUC_0335	-	-	KUC_0342	KUC_0346-8	-	-	-	-	-	-	-	-	-
Halomonas lutea DSM 23508	F568_RS0106630,F	-	-	-	F568_RS0106625	-	-	F568_RS0	F568_RS01	F568_RS0114680	F568_RS0114685	F568_RS0114660,F	F568_RS0114695	-	-	F568_RS010660	F568_RS0114665-75	-	-	-	-	-	-	-	-	-
Halomonas zhanjiangensis DSM 21076	D467_RS0112545	-	-	-	D467_RS011255	-	-	D467_RS0	D467_RS0	-	-	D467_RS0112665,	D467_RS0112540	-	-	D467_RS011266	-	-	-	-	-	-	-	-	-	-
Chromohalobacter salexigens DSM 3043	Csal_2473	-	-	-	Csal_2474	-	-	Csal_2476	Csal_2475	-	Csal_2481, 86	Csal_2487	Csal_1140	-	-	Csal_2479-77	-	-	-	-	-	-	-	-	-	-
Comamonadaceae																						AldE	SerA			
Acidovorax avenae subsp. citrulli AAC00-1	Aave_2589	Aave_3625	-		Aave_2590	Aave_2591, Aa	-	-	-	Aave_2595	Aave_3623	Aave_2587	Aave_2256	-	-	Aave_2592-4	Aave_3624, Aave_2597, Aave_2588	-	-	-	-	-	Aave_1141	-	-	-
Acidovorax avenae subsp. avenae ATCC 1	Acav_2614	Acav_3542	-		Acav_2613	Acav_2612, Ac	-	-	-	Acav_2608	Acav_3539	Acav_2616	Acav_2884	-	-	Acav_2610-08	Acav_2615, Acav_2606, Acav_3540	-	-	-	-	-	Acav_1151	-	-	-
Acidovorax sp. KKS102	C380_19540	C380_15215	-		C380_19535	C380_19530	C380_12430	-	-	C380-19510	C380_15200	C380_12440, C380	C380_19545	-	-	C380_19525-15	C380_12435, C380_12425, C380_15205	-	-	-	-	C380-19500	C380_12450	-	-	-
Acidovorax sp. JS42	Ajs_1995	-	-		-	Ajs_1999	-	-	-	Ajs_1998	Ajs_1990, Ajs_1996	Ajs_1993	-	-	-	-	Ajs_1997, Ajs_1994, Ajs_1992	-	-	-	-	-	Ajs_1991	-	-	-
Acidovorax ebreus TPSY	Dtpsy_1795	-	-		-	pseudogene	-	-	-	pseudogene	Dtpsy_1790, Dtpsy_	Dtpsy_1793	Dtpsy_1046	-	-	-	Dtpsy_1792, Dtpsy_1794, Dtpsy_1797	-	-	-	-	-	Dtpsy_1791	-	-	-
Alicycliphilus denitrificans BC	Alide2_2884	-	-		-	-	-	-	-	Alide2_2881	Alide2_2889,Alide2_	Alide2_2886	Alide2_2890	-	-	-	Alide2_2887, Alide2_2885,Alide2_2882	-	-	-	-	-	Alide2_2888	-	-	-
Comamonas testosteroni KF-1	Ctes_4119	-	-		-	-	-	-	-	Ctes_4116	Ctes_4124, Ctes_41	Ctes_4121	Ctes_4125	-	-	-	Ctes_4117, Ctes_4120,Ctes_4122	-	-	-	-	-	Ctes_4211	-	-	-
Comamonas testosteroni TK102	0987_RS01225	-	-		-	-	-	-	-	0987_01210	0987_01255,0987_(	0987-01235	0987_01260,0987_2	-	-	-	0987_01215,0987_01230,0987_01240	-	-	-	-	-	0987_01250	-	-	-
Delftia acidovorans SPH-1	Daci_0253	Daci_4288	-		-	Daci_0257	-	-	-	Daci_0256	Daci_0248, Daci_02	Daci_0251	Daci_0247	-	-	-	Daci_4289, Daci_0255, Daci_0252, Daci_0250	-	-	-	-	-	Daci_0249	-	-	-
Hylemonella gracilis ATCC 19624	HGR_02458	-	-		HGR_02453	-	HGR_02423*	-	-	HGR-02418	HGR_02478, HGR_0	HGR-02463	HGR_13374	-	-	HGR_02448-38	HGR_02428, HGR_02468, HGR_02473	-	-	-	-	-	-	-	-	-
Polaromonas sp JS666	Bpro_3110	Bpro_3418, Bpro_45	-		Bpro_3109	Bpro_3108	-	-	-	Bpro_3104	Bpro_3421	Bpro_3419	Bpro_3422	Bpro_3103	Bpro_3102	Bpro_3107-5	Bpro_3101, Bpro_4526, Bpro_3420	-	-	-	-	Bpro_3100	-	-	-	-
Polaromonas naphthalenivorans CJ2	Pnap_1590	Pnap_1131	-		Pnap_1591	Pnap_1592	-	-	-	Pnap_1597	Pnap_1130	Pnap_1596	Pnap_1598	Pnap_1599	Pnap_1600	Pnap_1593-5	Pnap_1601	-	-	-	-	-	-	-	-	-
Variovorax paradoxus EPS	Varpa_1898		-		Varpa_1897	Varpa_1896	Varpa_1889*	-	-	Varpa_1892	Varpa_1903	Varpa_1900	Varpa_1905	-	-	Varpa_1893-5	Varpa_1888,Varpa_1890,Varpa_1899, Varpa_1902	-	-	-	-	-	Varpa_2278	-	-	-
Variovorax paradoxus S110	Vapar_1727	-	-		Vapar_1726	Vapar_1725	Vapar_1718*	-	-	Vapar_1721	Vapar_1731	Vapar_1729	-	-	-	Vapar_1722-4	Vapar_1717, Vapar_1728	-	-	-	-	-	-	-	-	-
Leptothrix cholodnii SP-6	Lcho_1116	-	-		Lcho_1115	Lcho_1111	-	-	-	Lcho_2484	Lcho_1118	Lcho_1117	Lcho_1119	Lcho_1122	Lcho_1123	Lcho_1112-4	Lcho_1120, Lcho_2485	-	-	-	-	-	Lcho_1121	-	-	-
Burkholderiaceae																					Pgl	AldE	SerA	Agl	Omp	
Burkholderia phymatum STM815	Bphy_6525	-	-	Bphy_5674	Bphy_5673	-	Bphy_6529	-	-	Bphy_6382	Bphy_6530	Bphy_6531	Bphy_6526	Bphy_6527	Bphy_6528	-	-	Bphy_6596	-	hy_3128, Bhy_56	-	-	-	-	-	-
Burkholderia phytofirmans PsJN	Bphyt_4862; Bphy	-	-	-	Bphyt_4866	Bphyt_4867	-	-	-	Bphyt_4865	Bphyt_4102	Bphyt_4103; Bphyt	Bphyt_4861	Bphyt_4860	Bphyt_4859	Bphyt_4868-70	-	Bphyt_4863	Bphyt_4101	yt_4857, Bphyt_	Bphyt_4858	-	-	-	Bphyt_4871	-
Burkholderia xenovorans LB400	Bxe_B1804	-	-	-	Bxe_B1800	Bxe_B1799	-	-	-	Bxe_B1801	Bxe_B0539	Bxe_B1802	Bxe_B1805	Bxe_B2034	Bxe_A2462	Bxe_B1798-6	-	Bxe_B1803	-	Bxe_B1806	-	-	-	-	Bxe_B1795	-
Burkholderia ambifaria AMMD	Bamb_1043	-	-	Bamb_5235	Bamb_5236	-	Bamb_2221, Ba	-	-	Bamb_4675	Bamb_1041	Bamb_4676	Bamb_4679	Bamb_3659	Bamb_1817	Bamb_6123-25	-	Bamb_4680	Bamb_2220	b_3566, Bamb_5	Bamb_4904	-	-	Bamb_3565	Bamb_3564	-
Burkholderia lata sp. 383	Bcep18194_A4276	-	-	Bcep18194_B2	Bcep18194_B271	-	Bcep18194_A54	-	-	Bcep18194_B033	Bcep18194_A4275	Bcep18194_B0332	Bcep18194_B0328	ep18194_B17	ep18194_A51	Bcep18194_C74	-	Bcep18194_B0327	ep18194_A54	_B1871, Bcep18	-	-	ep18194_A37	ep18194_B187	ep18194_B187	-
Burkholderia vietnamiensis G4	Bcep1808_1082	-	-	Bcep1808_398	Bcep1808_3989	-	Bcep1808_2255	-	-	Bcep1808_3560	Bcep1808_1081	Bcep1808_3561	Bcep1808_3562	cep1808_480	cep1808_180	Bcep1808_6572-	-	Bcep1808_3563	-	,Bcep1808_3987	Bcep1808_3851	-	-	-	-	-
Burkholderia glumae BGR1	bglu_1g09940,bglu	-	-	-	bglu_1g09950	-	bglu_2g05570	-	-	Bglu_2g03740	Bglu_2g00180	Bglu_2g00190,2g0	Bglu_2g03710	bglu_2g13780	bglu_1g13900	Bglu_2g13770-6	-	Bglu_2g03700	-	Bglu_2g04250	Bglu_2g07210	-	-	Bglu_2g04260	Bglu_2g04270	-
Burkholderia multivorans ATCC BAA-247	NP80_1270	-	-	NP80_3553	NP80_3554	-	NP80_2301	-	-	NP80_5140	NP80_1269	NP80_5141	NP80_5150	NP80_4264	-	NP80_5675-3	-	NP80_5151	NP80_2300	NP80_3552	0_3332,NP80_56	-	NP80_5021	-	NP80_4291	-
Burkholderia cepacia GG4	GEM_2349	-	-	GEM_5231	GEM_5230	-	GEM_1232	-	-	GEM_5883	GEM_2350	GEM_5882	GEM_5879	GEM_4383	-	-	-	GEM_5878	GEM_1233	GEM_5232	-	-	GEM_2880	-	-	-
Burkholderia cenocepacia AU 1054	Bcen_0685	-	-	-	-	-	Bcen_5895	-	-	Bcen_3050	Bcen_0684	Bcen_3049	Bcen_3045	Bcen_4129	Bcen_6199	Bcen_5663-1	-	Bcen_3044	Bcen_5896	Bcen_4207	-	-	Bcen_3830	Bcen_4208	Bcen_4209	-
Cupriavidus eutropha H16	H16_B0126	-	-	-	-	-	-	-	-	H16_B0965	H16_B0127	H16_B0131	H16_B0130	H16_B1180	B0941, H16_A	-	H16_B0128, H16_B0129	-	-	-	-	-	-	-	-	-
Cupriavidus eutropha JMP134	Reut_B3714	-	-	-	-	-	-	-	-	Reut_B3690	Reut_B3715	Reut_B3688	Reut_B3713	Reut_A1499	A1500, Reut_	-	Reut_B3716, Reut_A1006	Reut_B3689	-	-	-	-	-	-	-	-
Cupriavidus metallidurans CH34	Rmet_0833	-	-	-	-	-	-	-	-	Rmet_4734	Rmet_0834	Rmet_4736	Rmet_0832	Rmet_1633	Rmet_1632	-	Rmet_0835, Rmet_0971	Rmet_4735	-	-	-	-	-	-	-	-
Cupriavidus basilensis 4G11	RR42_m1001	-	-	-	RR42_m2279	RR42_s2696	-	-	-	RR42_s1732	RR42_m1002,_m21	RR42_s1730	RR42_m1000	RR42_s1738	s0503, RR42_	-	RR42_m1003,RR42_s2694	RR42_s1731	-	RR42_m2280	-	-	RR42_s2695	-	-	-
Cupriavidus taiwanensis	RALTA_B0132	-	-	-	-	-	-	-	-	RALTA_B0782	RALTA_B0133	RALTA_B0137	RALTA_B0136	RALTA_B1087	B0765, RALTA	-	RALTA_B0134, RALTA_B0135	-	-	-	-	-	-	-	-	-
Ralstonia solanacearum GMI1000	RSc1078	-	RSp0823	-	RSp0831	RSp0832	-	-	-	RSp0830	RSc1079, RSp0829	RSp0826	RSp0827	#NAME?	-	-	-	RSp0828	-	Sc1080, RSp083	-	RSc1083	-	RSc1081	RSc1082	-
Ralstonia pickettii 12J	Rpic_0945	-	Rpic_4453	-	Rpic_4447	Rpic_4446	-	-	-	Rpic_4448	Rpic_0946, Rpic_44	Rpic_4452	Rpic_4451	-	-	-	-	Rpic_4450	-	ic_0947, Rpic_44	-	Rpic_0950	-	Rpic_0948	Rpic_0949	-
Pseudomonadaceae																						AldE				ExuT-II
Pseudomonas mendocina ymp	Pmen_3305	-	-	-	Pmen_3299	Pmen_3300	-	-	-	Pmen_1218	Pmen_1216, Pmen_	Pmen_1215	Pmen_0227	-	-	Pmen_3301-3	Pmen_1211-3	Pmen_1217	-	-	-	Pmen_3306	Pmen_1219	-	-	-
Pseudomonas stutzeri RCH2	Psest_0359	-	-	-	Psest_0365	Psest_0364,Pse	-	-	-	Psest_0377	Psest_0373, Psest_(	Psest_0374	Psest_0375	-	-	Psest_0363-61	Psest_0370-72	-	-	-	-	Psest_0379	Psest_0378	-	-	-
Pseudomonas simiae WCS417	PS417_18885, PS4	-	-	-	PS417_17360	PS417_17365	-	-	-	PS417_04210	PS417_18895	PS417_04195	PS417_04200	-	-	PS417_17370-80	-	PS417_04205	PS417_18890	-	-	PS417_17385	-	-	PS417_17355	PS417_14775
Pseudomonas fluorescens FW300-N1B4	A1D17_RS05060, A	-	-	-	A1D17_RS27145	A1D17_RS2714	-	-	-	A1D17_RS10245	A1D17_RS05070	A1D17_RS10260	A1D17_RS10255	-	-	-	-	A1D17_RS10250	1D17_RS0506	-	-	-	-	-	1D17_RS2715	1D17_RS30165
Pseudomonas entomophila L48	PSEEN2654 , PSEE	-	-	-	-	-	-	-	-	PSEEN2656	PSEEN0731	PSEEN2658	PSEEN2655	-	-	-	-	PSEEN2657	PSEEN0730	-	-	-	-	-	-	-
Pseudomonas putida KT2440	PP3603, PP4759	-	-	-	PP1171	PP1170	-	-	-	PP3601	PP4757	PP3599	PP3602	-	-	PP1169-67	-	PP3600	PP4758	-	-	PP1165	-	-	PP1173	-
Pseudomonas syringae pv. tomato str. DC	PSPTO3283, PSPTC	-	-	-	PSPTO1053	PSPTO1052	PSPTO2765*	-	-	PSPTO4547	PSPTO3285	PSPTO4549	PSPTO3323	-	-	PSPTO1051-49	-	PSPTO4548	PSPTO3284	PSPTO5219	-	PSPTO1047	-	-	PSPTO1054	-
Pseudomonas poae RE_1-1-14	H045_07225, H04	-	-	-	HO45_11815	HO45_11820	-	-	-	H045_01045	H045_07215	H045_01030	H045_01035	-	-	HO45_11825-35	-	H045_01040	H045_07220	-	-	HO45_11840	-	-	H045_11810	H045_09475
Pseudomonas veronii R02	PverR02_13105, P	-	-	-	PverR02_20100	PverR02_2010	-	-	-	PverR02_4590	RverR02_13095	RverR02_04575	RverR02_04580	-	-	PverR02_20110-	-	PverR02_04585	PverR02_1310	-	-	PverR02_2012	-	-	PverR02_2009	PverR02_17090
Pseudomonas chlororaphis PCL1606	PCL1606_22240, P	-	-	-	-	-	-	-	-	PCL1606_52030	PCL1606_22270	PCL1606_52060	PCL1606_52050	-	-	-	-	PCL1606_52040	CL1606_2226	-	-	-	-	-	-	-
Pseudomonas mandelii JR-1	OU5_1302, OU5_2	-	-	-	OU5_6132	OU5_6131	-	-	-	OU5_2576	OU5_1305	OU5_2579	OU5_2578	-	-	OU5_6130-28	-	OU5_2577	OU5_1304	-	-	OU5_6126	-	-	OU5_6133	-
Azotobacter vinelandii AvOP	Avin_05190	-	-	-	-	-	-	-	-	Avin_05250	-	Avin_05220	Avin_05180	-	-	-	-	Avin_05240	-	-	-	-	Avin_05260	-	-	-

Color abbreviations:	Tested in this work: enzymes (UxuL, UxuF), transporters (TctC), and regulators (GguR, GudR)	
genes in GguR regulons	Tested in previous work Udh enzymes	PMID: 25640726
genes in GudR regulons	Tested in previous work KdgD enzymes	PMID: 27855668
genes in GulR regulons	Tested in previous work UxuP transporter	PMID: 25540822
genes in UdhR regulons		
genes in chromosomal loci		
genes in chromosomal loci		
genes in chromosomal loci		
genes in chromosomal loci		

* has Signal peptide (secreted enzyme)

Table S1. Reconstructed catabolic pathways and regulons for hexuronate and aldarate utilization in Proteobacteria.

(B) Reconstructed GguR regulons and predicted GguR-binding sites in the analyzed genomes.

Genome	TF locus tag	Target locus tag	Site position	Site score	Site sequence	Target putative operon
Halomonadaceae						
Chromohalobacter salexigens DSM 3043	Csal_2473	Csal_2479	-339	5.53	ATGATGTATgACAaCAT	uxuPQM-gci-gli-udh--gguR
		Csal_2487	-57	5.51	ATGATGTATgACATgAT	kdgD-gudD-TRAP-gudD
Halomonas elongata DSM 2581	HELO_3403	HELO_3410	-102	5.01	ATGATGTATTAtAagAg	uxuPQM-gci-gli-udh-X-gguR
		HELO_3417	-64	5.54	ATGATGTATTACATgAg	kdgD-tctCAB-garD-gudD-kgsD
		HELO_3291	-207	5.44	ATGATGTATTACATgAa	tctC2
Halomonas boliviensis LC1	KUC_0336	KUC_0343	-76	5.19	ATGATGTATTACATagg	kdgD-uxuPQM-gci-gli-udh-gguR-kgsD
		KUC_0348	-203	5.39	ATGATGTATTACATagT	tctCAB-garD-gudD
		KUC_0336	-124	4.76	AcGATaTAATACAaCcT	gguR
Halomonas lutea DSM 23508	F568_RS0106630, F568_RS0114690	F568_RS0106595	-90	5.21	ATGATGTATgACATaAg	kdgD2-uxuPQM-gci-gli-udh-gguR
		F568_RS0114660	-87	4.81	ATGATGTATgACAcCtT	kdgD1-tctCAB-garD-gudD-gguR2-kgsD
Halomonas zhanjiangensis DSM 21076	D467_RS0112545	D467_RS0112560	-38	5.18	gTGATGTATTACAaCAT	kdgD1-gli-udh-gguR-kgsD
		D467_RS0112665	-85	4.92	ATGATGTATgACAaatT	kdgD2-uxuPQM-gci
		D467_RS0112585	-314	4.39	AatATGTATgACATgtg	porin-kdgM-rhgT- pmeA-pelY
Comamonadaceae						
Acidovorax avenae subsp. citrulli AAC00-1	Aave_2589	Aave_2589	-37	5.22	ATGTTGTCGTACAACGC	gguR
		Aave_2590	-18	5.22	GCGTTGTACGACAACAT	udh-uxuL1-uxuPQM-garD-uxuL2-tctC2
		Aave_2588	-37	4.73	CAGTTGTATGATGACGT	tctC1-kdgD
Acidovorax avenae subsp. avenae ATCC 19860	Acav_2614	Acav_2613	-43	5.22	gcGTTGTaCGACAACAT	udh-uxuL1-uxuPQM-garD-uxuL2-tctC2
		Acav_2614	-39	5.22	ATGTTGTCGtACAACgc	gguR
		Acav_2615	-43	4.87	AaGTTGTatGAtgACgT	tctC-kdgD
Acidovorax sp. KKS102	C380_19540	C380_19535	-68	4.84	tcGTTGTatGACAACtg	udh-uxuL1-uxuPQM-garD-X-aldE
		C380_19540	-71	4.84	caGTTGTCatACAACga	gguR
		C380_19545	-168	5.06	ATGTTGTaCGAtgACAT	kgsD
		C380_12430	-348	4.54	taGTcaTCGtACAACtg	uxuF-tctC2
			-146	4.77	tTGTTGTatGACgACAT	
		C380_12435	-246	4.77	ATGTcGTCatACAACAa	tctC-kdgD-DUF4440-serA
			-44	4.54	caGTTGTaCGAtgACta	
Acidovorax sp. JS42	Ajs_1995	Ajs_1994	-50	5.02	ATGTTGTACGATGACGT	tctC1-kdgD-tctC3-serA-gudD
		Ajs_1995	-38	5.22	ATGTTGTCTGATAACGT	gguR
		Ajs_1996	-75	5.22	ACGTTATCAGACAACAT	gudD2-tctC2-garD-uxuL2
Acidovorax ebreus TPSY	Dtpsy_1795	Dtpsy_1795	-38	5.14	ATGTTGTCttAtAACgT	gguR
		Dtpsy_1796	-78	5.14	AcGTTaTaaGACAACAT	gudD2-tctC2
		Dtpsy_1794	-50	5.02	ATGTTGTaCGAtgACgT	tctC1-kdgD-tctC3-serA-gudD
Alicycliphilus denitrificans BC	Alide2_2884	Alide2_2883	-21	4.73	AaGTcaTCaGACgACAT	gudD2-tctC2-garD
		Alide2_2884	-103	4.73	ATGTcGTCtGAtgACtT	gguR
		Alide2_2885	-80	4.92	ATGTTGTatGAtgACAT	tctC1-kdgD-tctC3-serA-gudD-kgsD
Comamonas testosteroni KF-1 (old)	CtesDRAFT_4119	CtesDRAFT_4118	-79	5.38	caGTTGTaCGACAACAT	gudD2-tctC2-garD
		CtesDRAFT_4119	-81	5.38	ATGTTGTCGtACAACtg	gguR
		CtesDRAFT_4120	-42	4.40	taGTTGTatGAtgACtg	tctC1-kdgD-tctC3-X-serA-gudD-kgsD
Comamonas testosteroni TK102	O987_RS01225	O987_01220	-79	5.38	caGTTGTaCGACAACAT	gudD2-tctC2-garD
		O987_01225	-81	5.38	ATGTTGTCGtACAACtg	gguR
		O987_01230	-42	4.40	taGTTGTatGAtgACtg	tctC1-kdgD-tctC3-tctC4-serA-gudD-kgsD
Delftia acidovorans SPH-1	Daci_0253	Daci_0252	-42	5.23	CAGTTGTACGACAACTG	tctC1-kdgD-tctC3-serA-gudD-kgsD
		Daci_0253	-25	5.48	ACGTTGTCGTACAACTT	gguR
		Daci_0254	-74	5.48	AAGTTGTACGACAACGT	gudD2-tctC2-garD-uxuL2
Hylemonella gracilis ATCC 19624	HGR_02458	HGR_02453	-95	5.02	tTGTTGTaCGACAACtg	udh-uxuPQM-gudD2-tctC3-uxuF-garD
		HGR_02458	-105	5.02	caGTTGTCGtACAACAa	gguR
		HGR_02463	-112	4.91	ATGTTGTaCGAtgACtg	kdgD-tctC1-tctC2-gudD
Polaromonas sp JS666	Bpro_3110	Bpro_3110	-60	4.58	AGGTTGTCTGATGACTG	gguR
		Bpro_3109	-96	4.58	CAGTCATCAGACAACCT	udh-uxuL1-uxuPQM-garD-garL-garR-tctC1-aldE
Polaromonas naphthalenivorans CJ2	Pnap_1590	Pnap_1590	-57	4.68	ACGTTGTCTGATGACTC	gguR
		Pnap_1591	-99	4.68	GAGTCATCAGACAACGT	udh-uxuL1-uxuPQM-kdgD-garD-kgsD-garL-garR-tctC1
Variovorax paradoxus S110	Vapar_1727	Vapar_1726	-39	5.02	taGTTGTaCGACAACAg	udh-uxuL1-uxuPQM-garD-X-tctC3-uxuF-tctC2
		Vapar_1727	-39	5.02	cTGTTGTCGtACAACta	gguR
		Vapar_1728	-44	4.54	taGTTGTaCGAtgACtg	tctC1-kdgD-DUF4440-gudD
Variovorax paradoxus EPS	Varpa_1898	Varpa_1897	-148	5.02	taGTTGTaCGACAACAg	udh-uxuL1-uxuPQM-garD-X-tctC4-uxuF-tctC2

		Varpa_1898	-40	5.02	cTGTTGTCGtACAACta	gguR
		Varpa_1899	-78	4.54	taGTTGTaCGAtgACtg	tctC1-kdgD-DUF4440-tctC3-gudD-X-kgsD
Leptothrix cholodnii SP-6	Lcho_1116	Lcho_2484	-66	5.70	ATGTTGTACGACAACAT	garD
		Lcho_1117	-65	5.10	ATGTTGTACGATGACAT	kdgD-gudD-kgsD-tctC1-serA-garL-garR
		Lcho_1115	-95	5.40	ACGTTGTACGACAACTG	udh-uxuPQM-uxuL2
		Lcho_1116	-73	5.40	CAGTTGTCGTACAACGT	gguR
Burkholderiaceae						
Burkholderia phytofirmans PsJN	Bphyt_4862; Bphyt_4100	Bphyt_4100	-332	4.85	AcGTtGTCtGACGACag	gguR2
			-202	4.06	AgGatGTCCGAtGACaa	
		Bphyt_4101	-238	4.06	ttGTCaTCGGACatCcT	gguT-gudD-kdgD2
			-108	4.85	ctGTCGTCaGACaACgT	
		Bphyt_4856	-103	4.56	AcGTtaTCGtACaACTa	udh2-exuT2
		Bphyt_4860	-191	4.67	AgGTCaTCCtACaACaT	garL-garR
			-79	4.34	AAGaCaTaCGACGACcT	
		Bphyt_4861	-160	4.34	AgGTCGTCGtAtGtCTT	kgsD
			-48	4.67	AtGTtGTaGGAtGACcT	
		Bphyt_4862	-69	4.86	cAGTCGTCaGACGACgg	gguR
		Bphyt_4864	-176	4.89	AcGTCaTCCtACaACaT	kdgD-garP
			-81	4.65	ttGTtGTaCGAtGACgT	
		Bphyt_4865	-160	4.65	AcGTCaTCGtACaACaa	garD-udh-uxuL
			-65	4.89	AtGTtGTaGGAtGACgT	
		Bphyt_4868	-302	4.96	AtGTCGTCGtACaACgT	uxuPQM-omp
Burkholderia phymatum STM815	Bphy_6525	Bphy_6382	-67	4.58	ATGTTGTACGATGACGC	garD
		Bphy_6525	-51	4.51	GCGTTGTCGGACAACGT	gguR
		Bphy_6526	-48	4.31	TTGTTGTACGATGACCG	kgsD
			-171	4.49	ATGTCATAGGATGTCTG	
		Bphy_6527	-77	4.49	CAGACATCCTATGACAT	garL-garR-uxuF-gudD-kdgD
			-200	4.31	CGGTCATCGTACAACAA	
		Bphy_6596	-92	4.75	ATGTCGTCAGACAACCT	garP
			-223	4.86	ACGTCGTCGTACAACTG	
Burkholderia ambifaria AMMD	Bamb_1043	Bamb_1041	-270	5.13	AAGTCATCCGACGACTG	gudD
		Bamb_1043	-107	5.13	CAGTCGTCGGATGACTT	gguR
		Bamb_2220	-86	5.12	ATGTCATACGACGACAT	gguT-uxuF
		Bamb_3566	-106	4.80	CAGTCGTCAGATAACGT	exuT-agl-omp
		Bamb_4675	-48	4.82	ATGTCGTATGATGACTA	garD
			-153	4.65	ATGTCATCGTACAACGA	
		Bamb_4676	-207	4.82	TAGTCATCATACGACAT	kdgD
			-102	4.65	TCGTTGTACGATGACAT	
		Bamb_4679	-239	5.00	AcGTCGTCGtAtGACaT	kgsD
		Bamb_4680	28	5.00	AtGTCaTaCGACGACgT	garP
		Bamb_4904	-73	4.43	ATGTAGTACGACGACGT	pgl
		Bamb_6123	-341	4.59	CAGTCATCCTATGACGA	uxuPQM-uxuF2
Burkholderia vietnamiensis G4	Bcep1808_1082	Bcep1808_1081	-333	5.13	AAGTCATCCGACGACTG	gudD
		Bcep1808_1082	-107	5.13	CAGTCGTCGGATGACTT	gguR
		Bcep1808_2255	-239	5.12	ATGTCATACGACGACAT	uxuF
		Bcep1808_3560	-49	4.82	ATGTCGTATGATGACTA	garD
			-155	4.58	ATGTCATCGTACAACGC	
		Bcep1808_3561	-198	4.82	TAGTCATCATACGACAT	kdgD
			-92	4.58	GCGTTGTACGATGACAT	
		Bcep1808_3562	-241	5.00	ACGTCGTCGTATGACAT	kgsD
		Bcep1808_3563	-26	5.00	ATGTCATACGACGACGT	garP
		Bcep1808_3851	-70	4.51	ATGTGATACGACGACGT	pgl
		Bcep1808_6572	-329	4.78	CAGTCATCGGACAACTA	uxuPQM
Burkholderia glumae BGR1	bglu_1g09940; bglu_2g00170	bglu_1g09940	-99	5.06	CAGTCATCGGATGACTT	gguR-udh
		bglu_2g00170	-276	4.05	AgGaCGTCtGACaACaa	gguR2
			-67	4.03	ggGaCaTCGGAtGACaT	
		bglu_2g00180	-207	4.90	ATGTCATCAGACAACGT	gudD-kdgD
		bglu_2g03700	-69	5.10	AAGTTGTACGACGACAT	garP
		bglu_2g03710	-212	5.10	ATGTCGTCGTACAACTT	kgsD
		bglu_2g03730	-186	4.83	CAGTCATCATACAACAT	kdgD
			-75	5.10	ATGTTGTACGATGACAT	
		bglu_2g03740	-164	5.10	ATGTCATCGTACAACAT	garD
			-53	4.83	ATGTTGTATGATGACTG	
		bglu_2g04250	-90	4.50	AAGTGGTACGATGACTG	exuT-agl-omp
		bglu_2g05570	-114	4.76	AAGTTATATGATGACGT	uxuF
		bglu_2g07210	-77	4.93	ATGTCATCGTATGACGT	pgl
		bglu_2g13770	-497	4.83	CAGTCGTCTTATAACAT	uxuPQM
Burkholderia xenovorans LB400	Bxe_B1804	Bxe_B0539	-106	4.89	CTGTCATCGTACAACAT	gudD
		Bxe_B1798	-322	5.08	ATGTCGTCGTACAACAT	uxuPQM-omp
		Bxe_B1801	-159	4.65	ACGTCATCGTACAACAA	garD-udh-uxuL
			-64	4.89	ATGTTGTAGGATGACGT	
		Bxe_B1802	-83	4.65	TTGTTGTACGATGACGT	kdgD-garP
			-178	4.89	ACGTCATCCTACAACAT	
		Bxe_B1804	-70	4.79	CAGTCATCAGACGACGG	gguR
		Bxe_B1805	-48	4.67	ATGTTGTAGGATGACCT	kgsD

		Bxe_B1807	-103	4.56	AcGTtaTCGtACaACTa	udh2-exuT2
Burkholderia lata sp. 383	Bcep18194_A4276	Bcep18194_A4276	-107	5.13	CAGTCGTCGGATGACTT	gguR
		Bcep18194_A4275	-268	5.13	AAGTCATCCGACGACTG	gudD
		Bcep18194_A5498	-89	5.12	ATGTCATACGACGACAT	gguT-uxuF
		Bcep18194_B0327	-25	4.88	ACGTCATACGACGACGT	garP
		Bcep18194_B0328	-239	4.88	ACGTCGTCGTATGACGT	kgsD
		Bcep18194_B0332	-198	4.82	TAGTCATCATACGACAT	kdgD
			-92	4.65	TCGTTGTACGATGACAT	
		Bcep18194_B0333	-154	4.65	ATGTCATCGTACAACGA	garD
			-48	4.82	ATGTCGTATGATGACTA	
		Bcep18194_B1871	-196	4.92	CAGTCGTCAGATAACAT	exuT-agl-omp
		Bcep18194_C7436	-347	4.71	CAGTCATCCTATGACAA	uxuPQM
Burkholderia multivorans ATCC BAA-247	NP80_1270	NP80_1269	-194	5.06	AAGTCaTCCGAtGACTg	gudD
		NP80_1270	-108	5.06	cAGTCaTCGGAtGACTT	gguR
		NP80_2300	-98	5.12	AtGTCaTaCGACGACaT	gguT-uxuF
		NP80_3332	-77	4.50	AAGTaGTaCGAtGACaT	pgl
		NP80_4291	-272	4.55	AAGgCGTCtGACGACTT	omp
		NP80_5140	-153	4.58	AtGTCaTCGtACaACgc	garD
			-47	4.82	AtGTCGTatGAtGACTa	
		NP80_5141	-199	4.82	tAGTCaTCatACGACaT	kdgD
			-93	4.58	gcGTtGTaCGAtGACaT	
		NP80_5150	-237	4.92	AcGTCGTCatAtGACaT	kgsD
		NP80_5151	-27	4.92	AtGTCaTatGACGACgT	garP
		NP80_5675	-367	4.72	cAGTCaTCCtAtaACgT	uxuPQM
		NP80_5676	-177	4.72	AcGTtaTaGGAtGACTg	pgl*
Burkholderia cepacia GG4	GEM_2349	GEM_1233	-86	5.12	AtGTCaTaCGACGACaT	gguT-uxuF
		GEM_2349	-106	5.13	cAGTCGTCGGAtGACTT	gguR
		GEM_2350	-335	5.13	AAGTCaTCCGACGACTg	gudD
		GEM_5878	30	5.00	AtGTCaTaCGACGACgT	garP
		GEM_5879	-239	5.00	AcGTCGTCGtAtGACaT	kgsD
		GEM_5882	-197	4.82	tAGTCaTCatACGACaT	kdgD
		GEM_5883	-50	4.82	AtGTCGTatGAtGACTa	garD
Burkholderia cenocepacia AU 1054	Bcen_0685	Bcen_0684	-266	5.13	AAGTCaTCCGACGACTg	gudD
		Bcen_0685	-108	5.13	cAGTCGTCGGAtGACTT	gguR
		Bcen_3044	-25	5.00	AtGTCaTaCGACGACgT	garP
		Bcen_3045	-239	5.00	AcGTCGTCGtAtGACaT	kgsD
		Bcen_3049	-197	4.82	tAGTCaTCatACGACaT	kdgD
		Bcen_3050	-49	4.82	GAtTCGTatGAtGACTa	garD
		Bcen_4207	-196	4.92	cAGTCGTCaGAtaACaT	exuT-agl-omp
		Bcen_5663	-336	4.48	cAGTCaTCCtAtaACga	uxuPQM
		Bcen_5896	-89	5.00	AtGTCaTaCGACGACgT	gguT-uxuF
Cupriavidus taiwanensis LMG 19424	RALTA_B0132	RALTA_B0132	-91	4.83	CTGTCATCGTATGACTG	gguR
		RALTA_B0133	-109	4.83	CAGTCATACGATGACAG	gudD-tctC3-tctC1
		RALTA_B0137	-301	4.86	AcGTtGTCaGACaACaT	kdgD-kgsD
			-93	4.78	ttGTCGTaCGAtGACTg	
		RALTA_B0782	-155	4.66	ATGTTGTCGTACAACAC	garD
			-54	4.86	ATGTTGTCAGACAACGT	
Cupriavidus eutropha H16	H16_B0126	H16_B0965	-57	5.00	AAGTTGTCAGACAACGT	garD
			-157	4.60	GTGTTATCGTACAACTA	
		H16_B0131	-94	4.71	TTGTCATACGATGACTG	kdgD-kgsD
			-289	4.85	ACGTTGTCCTACAACAT	
		H16_B0126	-81	4.83	CTGTCATCGTATGACTG	gguR
		H16_B0127	-90	4.83	CAGTCATACGATGACAG	gudD-tctC3-tctC1
Cupriavidus basilensis 4G11	RR42_m1001	RR42_m1000	-148	4.57	AtGTtGTaGGAtGtCTT	kgsD
		RR42_m1001	-81	4.49	cgGTCGTCatAtaACTT	gguR
		RR42_m1002	-35	4.49	AAGTtaTatGACGACcg	gudD-tctC3
		RR42_s1730	-97	4.67	tAGTtGTaCGAtGACgT	kdgD
		RR42_s1731	-107	5.07	AAGTCaTaCGAtGACaT	garP- garD
		RR42_s2695	-75	4.71	tAGTCaTaGGAtGACgT	serA-tctC1
		RR42_s2696	-214	4.71	AcGTCaTCCtAtGACTa	uxuL
Cupriavidus eutropha JMP134	Reut_B3714	Reut_A1006	-45	5.00	ATGTTGTATGACGACTG	tctC1
			-180	5.00	ATGTCATCAGACAACAG	
		Reut_B3688	-317	5.02	AtGTCGTCGtAtGACTg	kdgD
			-101	4.67	tAGTtGTaCGAtGACgT	
		Reut_B3689	-284	4.67	AcGTCaTCGtACaACTa	garP-garD
			-68	5.02	cAGTCaTaCGACGACaT	
		Reut_B3713	-96	4.17	AtGTCaTatGAtGtCcT	kgsD
		Reut_B3714	-80	5.04	CAGTCGTCGTATGACTT	gguR
		Reut_B3715	-87	5.04	AAGTCATACGACGACTG	gudD-tctC3
Cupriavidus metallidurans CH34	Rmet_0833	Rmet_0832	-98	4.53	ATGTCATATGATGTCTT	kgsD
		Rmet_0833	-30	4.68	CGGTCGTCGTATGACTT	gguR
		Rmet_0834	-80	4.68	AAGTCATACGACGACCG	gudD-tctC3

		Rmet_4735	-326	4.45	AAGTCaTCGtACaACca	garP-garD
			-77	5.13	AAGTCGTatGACGACaT	
		Rmet_4736	-359	5.13	AtGTCGTCatACGACTT	kdgD
			-110	4.45	tgGTtGTaCGAtGACTT	
		Rmet_0971	-161	5.13	AAGTCATCCGACGACTG	tctC1
Ralstonia pickettii 12J	Rpic_0945	Rpic_0946	-17	4.67	GTGTTGTACGACGACTG	gudD-exuT-agl-omp-aldE
		Rpic_0945	-85	4.67	CAGTCGTCGTACAACAC	gguR
Ralstonia solanacearum GMI1000	RSc1078	RSc1078	-90	4.98	CAGTCGTCGTACAACAT	gguR
		RSc1079	-26	4.98	ATGTTGTACGACGACTG	gudD-exuT-agl-omp-aldE
Pseudomonadaceae						
Pseudomonas entomophila L48	PSEEN0729, PSEEN2654	PSEEN2654	-63	4.80	ATGTGATCGTACAACTG	gguR2
		PSEEN2658	-71	5.50	ATGTTGTACGATAACTT	kdgD-garP-garD-kgsD
		PSEEN0730	-105	5.30	GTGTTGTCGTACAACTT	gguT-gudD
		PSEEN0729	-201	5.30	AAGTTGTACGACAACAC	gguR1
Pseudomonas mendocina ymp	Pmen_3305	Pmen_1214	-450	4.70	ACGTTATCGTACAACAA	gudD2-tctCBA
			-251	5.10	AGGTCATACGACAACAT	
		Pmen_1215	-275	5.10	ATGTTGTCGTATGACCT	kdgD-gudD-garP-garD-serA
			-76	4.70	TTGTTGTACGATAACGT	
		Pmen_3299	-316	4.80	ACGTTGTCATACAACTT	udh-uxuL-uxuPQM-X
			-60	5.00	AAGTCATACGACAACGT	
		Pmen_3306	-54	4.80	CAGTTGTACGATGACAC	aldE
		Pmen_3305	-63	4.80	GTGTCATCGTACAACTG	gguR
Pseudomonas putida KT2440	PP4759,PP3603	PP1173	-251	4.82	tAGTTGTACGACAACac	omp
		PP1171	-43	5.10	AAGTCATACGACAACCT	udh-uxuL-uxuPQM-X-aldE
		PP3599	-71	5.30	AGGTTGTACGATAACTT	kdgD-garP-garD-kgsD
		PP3603	-47	4.60	ATGTGATCGTACAACCG	gguR2
		PP4758	-79	5.10	ATCTTGTCGTACAACTT	gguT-gudD
		PP4759	-104	5.10	AAGTTGTACGACAAGAT	gguR1
Pseudomonas syringae pv. tomato str. DC3000	PSPTO3283, PSPTO4550	PSPTO4549	-77	5.10	CAGTTGTACGATGACTT	kdgD-garP-garD
		PSPTO3323	-163	5.10	AAGTTGTACGATGACTG	kgsD
		PSPTO1054	-297	4.85	tgGTTGTACGACAACcT	omp
		PSPTO1053	-48	5.10	AAGTCATACGACAACAG	udh-uxuL-uxuPQM-X-aldE
		PSPTO5219	-385	4.20	CAGTCATCGTATAACGA	exuT
			-265	5.60	ATGTTGTACGACAACAT	
		PSPTO3283	-128	3.81	AgcTTGTAaTACAAgTc	gguR1
		PSPTO3284	-358	3.81	gAcTTGTAtTACAAgcT	gguT-gudD
Pseudomonas simiae WCS417	PS417_18885, PS417_04180	PS417_04195	-79	4.78	tAGTTaTACGAtgACgT	kdgD-kgsD2-garP-garD
		PS417_17355	-113	4.86	gAGTcaTCGTAtAACTT	omp
			-55	5.20	AtGTTGTACGACgACgT	
		PS417_17360	-36	4.79	tAGTcaTACGACAACcT	udh-uxuL-uxuPQM-aldE
		PS417_14775	-172	4.62	ttGTcaTCCTACAACTg	exuT-II
			-63	5.01	cAGTTGTACGACgACaT	
		PS417_18885	-99	4.26	tgGTTGTCaTACAAgTT	gguR2
		PS417_18890	-257	4.26	AAcTTGTAtGACAACca	gguT-gudD
Pseudomonas fluorescens FW300-N1B4	A1D17_RS05060, A1D17_RS10275	A1D17_RS27150	-117	5.23	AAGTcaTCGTAtAACTT	omp
			-58	5.20	AtGTTGTACGACgACgT	
		A1D17_RS27145	-59	5.11	AAGTcaTACGACAACcT	udh-uxuL-aldE
		A1D17_RS10260	-80	5.11	AAGTTGTACGAtgACcT	kdgD-kgsD2-garP-garD
		A1D17_RS05065	-283	4.36	AAcTTGTAtGACAACac	gguT-gudD
		A1D17_RS05060	-101	4.36	gtGTTGTCaTACAAgTT	gguR1
		A1D17_RS30165	-322	4.69	cAGTTGTACGACgACag	exuT-II
Pseudomonas stutzeri RCH2	Psest_0359	Psest_0373	-394	5.03	AcGTTaTCGTACAACTa	gudD2-tctCBA
			-179	4.68	tAGTcGTACGACgACcT	
		Psest_0374	-288	4.68	AgGTcGTCGTACgACTa	kdgD-kgsD2-garP-garD-serA-aldE
			-73	5.03	tAGTTGTACGAtAACgT	
		Psest_0359	-64	4.84	tAGTTaTCGTACAACTg	gguR
		Psest_0365	-49	4.52	AtGTcaTAtGACAACag	udh-uxuL-uxuPQM
		Psest_2755	-169	4.84	AtGTcaTAtGACAACaT	uxuL2
Pseudomonas poae RE_1-1-14	H045_07225, H045_01025	H045_01030	-81	4.85	tAGTTGTACGAtgACgT	kdgD-kgsD2-garP-garD
		H045_07220	-210	4.41	AAcTTGTAtGACAACaa	gguT-gudD
		H045_07225	-69	4.41	ttGTTGTCaTACAAgTT	gguR1
		H045_11810	-119	4.91	tAGTcaTCGTAtAACTT	omp
			-61	5.38	AtGTTGTACGACAACgT	
		H045_11815	-39	5.11	AAGTcaTACGACAACcT	udh-uxuL-uxuPQM-aldE
		H045_09475	-170	4.75	ctGTcaTCCTACAACcT	exuT-II
			-61	5.01	cAGTTGTACGACgACaT	

Pseudomonas veronii R02	PverR02_13105, PverR02_04555	PverR02_04575	-81	4.85	tAGTTGTACGAtgACgT	kdgD-kgsD2-garP-garD
		PverR02_13100	-265	4.09	tAcTTGTAtGACAACaa	gguT-gudD
		PverR02_13105	-70	4.09	ttGTTGTCaTACAAgTa	gguR1
		PverR02_20095	-116	4.91	tAGTcaTCGTAtAACTT	omp
			-59	5.20	AtGTTGTACGACgACgT	
		PverR02_20100	-39	4.79	tAGTcaTACGACAACcT	udh-uxuL-uxuPQM-aldE
		PverR02_17090	-171	4.57	gtGTcaTCCTACAACTa	exuT-II
			-61	5.01	cAGTTGTACGACgACaT	
Pseudomonas chlororaphis PCL1606	PCL1606_22240, PCL1606_52090	PCL1606_22240	-96	4.76	cAcTTaTCCGACAACTT	gguR1
		PCL1606_22260	-275	4.76	AAGTTGTCGGAtAAgTg	gguT-gudD
		PCL1606_52060	-78	4.79	tAGTTGTACGAtgACcT	kdgD-kgsD2-garP-garD
		PCL1606_52090	-62	4.36	cgGTgaTCGTACAACTT	gguR2
Pseudomonas mandelii JR-1	OU5_1302, OU5_2584	OU5_1302	-80	4.36	gtGTTGTCaTACAAgTT	gguR1
		OU5_1304	-230	4.36	AAcTTGTAtGACAACac	gguT-gudD
		OU5_2579	-79	5.10	AAGTTGTACGAtgACcT	kdgD-kgsD2-garP-garD
		OU5_6133	-74	5.23	AAGTcaTCGTAtAACTT	omp
			-16	5.20	AtGTTGTACGACgACgT	
		OU5_6132	-46	5.11	AAGTcaTACGACAACcT	udh-uxuL-uxuPQM-X-aldE
Azotobacter vinelandii AvOP	Avin_05190	Avin_05220	-73	5.10	AAGTcaTACGAtAACgT	kdgD-garP-garD-serA
		Avin_05180	-120	4.63	AAGTcaTAtGAtgACaT	gguR
		Avin_05190	-214	4.63	AtGTcaTCaTAtgACTT	kgsD

Binding sites experimentally tested in this work

genes in divergons
genes in divergons

4.10 weak sites

Table S1. Reconstructed catabolic pathways and regulons for hexuronate and aldarate utilization in Proteobacteria.

(C) Reconstructed GudR regulons and predicted GudR-binding sites in the analyzed genomes.

Genome	TF locus tag	Target locus tag	Site position	Site score	Site sequence	Target putative operon
Burkholderiales						
Acidovorax avenae subsp. citrulli AAC00-1						
	Aave_3625	Aave_3625	-110	5.9	GGATGTTAACGTTAACATCC	gudR
		Aave_3624	-40	5.9	GGATGTTAACGTTAACATCC	tctC3-gudD
Acidovorax avenae subsp. avenae ATCC 19860	Acav_3542	Acav_3542	-111	6.12	GAATGTTAaCGtTAACATTC	gudR
		Acav_3540	(-1286)	6.12	GAATGTTAaCGtTAACATTC	tctC3-gudD
Acidovorax sp. KKS102	C380_15215	C380_15215	-130	5.61	tAATGTTAaCGtTAACATca	gudR
		C380_15210	-110	5.61	tgATGTTAaCGtTAACATTa	kdgD-tctC3-gudD
Polaromonas sp. JS666	Bpro_4527, Bpro_3418	Bpro_4527	-24	4.9	GCAAGTTAGCGTTAACATCA	gudR2
		Bpro_4526	-79	5.9	AATTGTTAGCGCTAACATTC	tctC2
		Bpro_3418	-33	5.2	GACTGGTAGCGCTATCGTCG	gudR1
		Bpro_3419	-29	6	AAAAGGTAGCGCTACCATTC	kdgD-tctC3-gudD-kgsD
			-2	5.5	CAATGGTAGCGCTACCTTTA	
Polaromonas naphthalenivorans CJ2	Pnap_1131	Pnap_1130	-93	5.7	AAATGTTACCGATAACATTG	gudD
		Pnap_1131	-67	4.67	tgccGgTAtCGgTAtCATTC	gudR
Delftia acidovorans SPH-1	Daci_4288	Daci_4288	-131	4.95	aAATGaTAtCGtTgtCATTt	gudR
		Daci_4289	-118	4.95	aAATGacAaCGaTAtCATTt	tctC3

Binding sites experimentally tested in this work

(transposase) 4.1 weak sites

genes in divergons

genes in divergons

tandem sites

tandem sites

Table S1. Reconstructed catabolic pathways and regulons for hexuronate and aldarate utilization in Proteobacteria.

(D) Reconstructed GulR regulons and predicted GulR-binding sites in the analyzed genomes.

Genome	TF locus tag	Target locus tag	Site position	Site score	Site sequence	Target putative operon
GulR regulon in Ralstonia spp.						
Ralstonia pickettii 12J	Rpic_4453	Rpic_4452	-339	5.37	TCGATTCAAAAacgGTATgGA	kdgD-kgsD-garP-gudD2-garD-udh-uxuL-exuT2
			-104	5.69	TCaATACAAgTTcTGTATtaA	
		Rpic_4453	-256	5.69	TtaATACAgAAcTTGTATtGA	gulR
			-21	5.37	TCcATACcgtTTTTGAATCGA	
Ralstonia solanacearum GMI1000	RSp0823	RSp0823	92	5.06	TCGATAtAcgTTTTGAATCGA	gulR
		RSp0824	-111	5.06	TCGATTCAAAAcgTaTATCGA	uxuL2
		RSp0826	-109	6.05	TCGATTCAAAAaaTGAATtGA	kdgD-kgsD-garP-gudD2-garD-udh-uxuL-pgl-exuT2

Table S1. Reconstructed catabolic pathways and regulons for hexuronate and aldarate utilization in Proteobacteria.

(D) Reconstructed UdhR regulons and predicted UdhR-binding sites in the analyzed genomes.

Genome	TF locus tag	Target locus tag	Site position	Site score	Site sequence	Target putative operon
UdhR regulon in Burkholderia spp.						
Burkholderia phymatum STM815	Bphy_5674	Bphy_5673	-40	6.5	TcGGAAAACGTTTTCCtA	udh
		Bphy_5674	-107	6.5	TaGGAAAACGTTTTCCgA	udhR
		Bphy_5675	-136	6.5	TaGaAAAACGTTTTCCAA	exuT
Burkholderia ambifaria AMMD	Bamb_5235	Bamb_5235	-156	6.6	TcGGAAAACGTTTTCCAA	udhR
		Bamb_5236	-87	6.6	TTGGAAAACGTTTTCCgA	udh
		Bamb_5234	-145	6.2	TTGaAAAACGTTTTCCAt	exuT
Burkholderia lata sp. 383	Bcep18194_B2717	Bcep18194_B2716	-52	6.6	TTGGAAAACGTTTTCCgA	udh
		Bcep18194_B2717	-158	6.6	TcGGAAAACGTTTTCCAA	udhR
		Bcep18194_B2718	-133	5.8	cTGaAAAACGTTTTCCAg	exuT
Burkholderia multivorans ATCC BAA-247	NP80_3553	NP80_3553	-156	6.33	gcGGAAAACGTTTTCCAA	udhR
		NP80_3554	-61	6.33	TTGGAAAACGTTTTCCgc	udh
		NP80_3552	-130	6.2	TTGaAAAACGTTTTCCAt	exuT
Burkholderia cepacia GG4	GEM_5231	GEM_5230	-64	6.2	TTGGAAAACGTTTTCCgg	udh
		GEM_5231	-47	6.2	ccGGAAAACGTTTTCCAA	udhR
		GEM_5232	-142	6.2	TTGaAAAACGTTTTCCAg	exuT
Burkholderia vietnamiensis G4	Bcep1808_3988	Bcep1808_3988	-156	6.2	ccGGAAAACGTTTTCCAA	udhR
		Bcep1808_3989	-88	6.2	TTGGAAAACGTTTTCCgg	udh
		Bcep1808_3987	-143	6.08	TgGaAAAACGTTTTCCAc	exuT

Table S2. (A) Primers used for cloning of analyzed transcriptional regulators.

Gene locus tag	Uniprot ID	Direction / Restriction site	Gene name	Primer sequence
Rpic_0945	B2U998	forward / NdeI	*gguR*	GAGACCATATGCCCACCGCCAGTTC
		reverse / BamHI		CGTACAACATGGATCCGTATTGGCCGG
Bpro_3110	Q128L8	forward / NdeI	*gguR*	CATTTGCTTGTCAACGGTTTTCATATGACCCTCAGGAAAACC
		reverse / BamHI		GCAACAGAGGTGTCACGGATCCAGTCAGGCCTGGTTC
Bpro_3418	Q127G5	forward / NdeI	*gudR*	CGTCGATAGAATCGGCATATGAACCACGAGGAC
		reverse / BamHI		GTGGTGCGGATCCAAATTGCCGGGTCACTC

(B) Primers used for cloning of analyzed lactonases and TctC transporters.

Gene locus tag	Uniprot ID	Direction / Restriction site	Gene name	Primer sequence
Rpic_4446	B2UIY8	forward /	*uxuL*	TACTTCCAATCCATGGATGGCGTTTGAAATGGTGCTTG
		reverse /		TATCCACCTTTACTGTTATCACTCCCCACTACCTGGCGC
PSPTO_1052	Q888H2	forward /	*uxuL*	TACTTCCAATCCATGGATGCCGAACTGATAGTCGATGC
		reverse /		TATCCACCTTTACTGTTAGCCCTGAAAAACGGGTTCCTC
Bcep1808_2255	A4JG52	forward /	*uxuF*	TACTTCCAATCCATGCCGAACACTGATCGCCTGAC
		reverse /		TATCCACCTTTACTGTTAAATCATCGCGATCCAGTTCGCAC
BMULJ_02167	A9AG49	forward /	*uxuF*	TACTTCCAATCCATGCCGAACACTGACCTTCCGAC
		reverse /		TATCCACCTTTACTGTTAGACGATCGCGATCCAGTTCG
Bcep18194_A5499	Q39EM3	forward /	*uxuF*	TACTTCCAATCCATGCCGAACACTGACCGCCCG
		reverse /		TATCCACCTTTACTGTTAGACGATCGCGACCCAGTTC
PSPTO_2765	Q881W7	forward /	*uxuF*	TACTTCCAATCCATGGTGCAGGCAGCTACCTTCG
		reverse /		TATCCACCTTTACTGTTATTTGTCCGGCTGGCTGAGC
Bpro_3101	Q128M7	forward /	*tctC*	TACTTCCAATCCATGCAAACGCCAAACTGGCCGC
		reverse /		TATCCACCTTTACTGTTACTCCAGCTTGATACCCGCG

(C) Candidate regulator-binding sites tested by DNA-binding assays.

Regulator	Organism[1]	First gene locus tag[2]	Regulated operon	DNA fragments used in EMSA and FPA DNA-binding assays[3]
FPA				
Bpro_3110 (GguR)	POL	Bpro_3109	*udh-uxuL1-uxuPQM-garD-garL-garR-tctC1-aldE*	accccCAGTCATCAGACAACCTccccc
		Bpro_3110 (NC)	-	accccatcataagagtacactcccccc
Rpic_0945 (GguR)	RP	Rpic_0946	*gudD-exuT-agl-omp-aldE*	accccGTGTTGTACGACGACTGccccc
		Rpic_0946 (NC)	-	accccatgttacacgcaccgtaccccc
EMSA				
Rpic_0945 (GguR)	RP	Rpic_0946	*gudD-exuT-agl-omp-aldE*	ggggatagtcgcatccGTGTTGTACGACGACTGatgacatacgtggggg
Bpro_3418 (GudR)	POL	Bpro_3419 (sites 1&2)	*kdgD-tctC4-gudD-kgsD*	ggggttcAAAAGGTAGCGCTACCATTCaaggcttCAATGGTAGCGCTACCTTTAcctggggg

[1] RP, *Ralstonia pickettii* 12J; POL, *Polaromonas* sp. JS666.

[2] NC, a negative control DNA fragments contain srambled sequence of the original target DNA fragment.

[3] Candidate binding sites are capitalized. For each DNA fragment, two complimentary single-stranded oligonucleotides have been synthesized by IDT.
The fragments were 5' labeled by either 6-carboxyfluorescein (for FP) or biotin (for EMSA) as marked by red letters.

(D) Primers used for RT-qPCR in *Ralstonia pickettii* 12J.

Gene locus tag	Gene name	Direction	Primer sequence
(I) GulR regulon			
Rpic_4453	*gulR*	forward	ATTGACGCTGAAGGAGATGGTG
		reverse	CACGGCACGGCAATCAG
Rpic_4452	*kdgD*	forward	GTCTACAACCGCGCCAACC
		reverse	GGCCGCCGACATAGGTAAAG
Rpic_4451	*kgsD*	forward	TCCGCATATTCAGGCAGTGG
		reverse	AGTGCGTCGGGCAACAGG
Rpic_4450	*garP*	forward	TGGCGGTCGTGTGGAGAG
		reverse	GTTTCGGACCCTCAGCCTTG
Rpic_4449	*gudD2*	forward	TTGCCGATTTCAAGCTCAAGG
		reverse	TGAGCGACCATGCACCATTC
Rpic_4448	*garD*	forward	GCCGGTGCTGCGTCTG
		reverse	CTGGCGCTTGTTCAGATGTTC
Rpic_4447	*udh*	forward	GTTCGCCAGCTCGAACCAC
		reverse	GCTGTTCGCCAAACACCTTG
Rpic_4446	*uxuL*	forward	CCGCTCGGCAAGCTGTATC
		reverse	ATGTCGTAATCGAAGGCCCAGAC
Rpic_4445	*exuT2*	forward	TGTGGAGCGTGCTGTGGTTC
		reverse	CGACAGAAAGCGCGGAATG
(II) GguR regulon			
Rpic_0945	*gguR*	forward	GTCGCCATTGAGACGGAGTG
		reverse	GAGGTGGCGCTGTCGTTG
Rpic_0946	*gudD*	forward	CGTGCGCCACGAAGAAG
		reverse	ATCGCCGCTCAGCACAC
Rpic_0947	*exuT2*	forward	TCTACCGTTCGCCGAAAGACC
		reverse	AGCGCAATCGCCCAGAAAC
Rpic_0948	*agl*	forward	GGGCTGCTGATTTGCGATG
		reverse	GCTCTTGACGTTGGCCTTCC
Rpic_0949	*omp*	forward	CCCACGTTTGGCGGTCTC
		reverse	AACGCCTGGTAGTCATAACGCATC
Rpic_0950	*aldE*	forward	AACTCGGCTTGCGCTATGTG
		reverse	TGCGGGCGAAATATGGATG

Table S3. Database identifiers for proteins characterized in this work.

Locus tag	UniProt Accession	Name	Genbank Accession	Current Genbank annotation	Newly proposed annotation
Bcep1808_2255	A4JG52	UxuF	ABO55255	3-carboxymuconate cyclase-like protein	Uronate lactonase, PF10282 family
Bcep18194_A5499	Q39EM3	UxuF	ABB09093	3-carboxymuconate cyclase-like protein	Uronate lactonase, PF10282 family
BMULJ_02167	A9AG49	UxuF	BAG44069	6-phosphogluconolactonase	Uronate lactonase, PF10282 family
Bpro_3101	Q128M7	TctC	ABE45015	Uncharacterized protein UPF0065	Substrate binding protein of aldarate transporter, TTT family
Bpro_3110	Q128L8	GguR	ABE45024	transcriptional regulator, GntR family	Transcriptional regulator for hexuronate/aldarate utilization, GntR family
Bpro_3418	Q127G5	GudR	ABE45327	transcriptional regulator, LacI family	Transcriptional regulator for glucarate utilization, LacI family
PSPTO_1052	Q888H2	UxuL	AAO54583	senescence marker protein-30 family protein	Uronate lactonase, PF08450 family
PSPTO_2765	Q881W7	UxuF	AAO56265	conserved hypothetical protein	Uronate lactonase, PF10282 family
Rpic_0945	B2U998	GguR	ACD26095	GntR domain protein	Transcriptional regulator for hexuronate/aldarate utilization, GntR family
Rpic_4446	B2UIY8	UxuL	ACD29539	SMP-30/Gluconolaconase/LRE domain protein	Uronate lactonase, PF08450 family