

Table S2. Reconstructed lactate utilization regulons and candidate binding sites of lactate regulators

Genome	Regulator ID*	Regulated operon name	First gene ID*	Position [†]	Score [‡]	Site sequence [§]	Upstream gene
LldR (R1) regulon for lactate utilization (GntR family) in γ- and β-proteobacteria				cutoff = 5.1			
<i>Escherichia coli</i> K12	LldR	<i>lldP-lldR-lldD</i>	<i>lldP</i>	-216 -90	6.1 5.93	AATTGGC _c CTACCAATT AATTGGCAGTGCCA _c TT	
<i>Shigella flexneri</i> 2a str. 301	SF3643	<i>lldP-lldR-lldD</i>	<i>SF3642</i>	-189 -63	6.1 5.93	AATTGGC _c CTACCAATT AATTGGCAGTGCCA _c TT	
<i>Salmonella typhimurium</i> LT2	STM3693	<i>lldP-lldR-lldD</i>	<i>STM3692</i>	-218 -92	6.1 5.5	AATTGGC _c CTACCAATT tATTGGCAGgACCA _c TT	
<i>Klebsiella pneumoniae</i> MGH78578	fig 573.2.peg.4021	<i>lldP-lldR-lldD</i>	fig 573.2.peg.4020	-89	6.03	AATTGGC _c GgGCCAATT	
<i>Azotobacter vinelandii</i>	Avin2953	<i>lldP-ldhEFG-dldII</i>	<i>Avin2954</i>	-87	5.95	AATTGGTAtTACCAATT	<i>lldR</i>
<i>Pseudomonas entomophila</i> L48	PSEEN0769	<i>lldP-lldD-dldII</i>	<i>PSEEN0768</i>	-62	5.88	AATTGGTctTACCAATT	
<i>Pseudomonas fluorescens</i> Pf-5	PFL_0818	<i>lldP-ldhEFG-dldII</i>	<i>PFL_0817</i>	-67	5.88	AATTGGTctTACCAATT	<i>lldR</i>
<i>Pseudomonas aeruginosa</i> PAO1	PA4769	<i>lldP-lldD-dldII</i>	<i>PA4770</i>	-127	5.88	AATTGGTctTACCAATT	<i>lldR</i>
<i>Pseudomonas putida</i> KT2440	PP4734	<i>lldP-lldD-dldII</i>	<i>PP4735</i>	-67	5.88	AATTGGTctTACCAATT	<i>lldR</i>
<i>Stenotrophomonas maltophilia</i> K279a	fig 40324.1.peg.3656	<i>lldP-lldR-lldD-dld</i>	fig 40324.1.peg.3655	-176 -79	5.11 5.38	AAaTGGTcGgACCAATa tATTGGTACgACCAATa	
<i>Acinetobacter</i> sp. ADP1	ACIAD0107	<i>lldP-lldR-lldD-dld</i>	<i>ACIAD0106</i>	-199 -94	5.52 5.95	AATTGGTAtgACCAATa AATTGGTAaTACCAATT	
<i>Alkalilimnicola ehrlichei</i> MLHE-1	Mlg_2283	<i>ldhEFG-lldP</i>	<i>Mlg_2282</i>	-88	4.18	AAGtGaTttgACCAATa	<i>lldR</i>
<i>Hahella chejuensis</i> KCTC 2396	HCH_01271	<i>ldhEFG-dldII</i>	<i>HCH_01270</i>	-88	5.95	AATTGGTAtTACCAATT	<i>lldR</i>
<i>Chromohalobacter salexigens</i> DSM 3043	CsaI_0403	<i>lldD-dldII</i>	<i>CsaI_0404</i>	-86	5.59	AATTGGTAaTACCAATa	<i>lldR</i>
		<i>lldP</i>	<i>CsaI_2686</i>	-128	5.59	tATTGGTAtTACCAATT	
<i>Chromobacterium violaceum</i> ATCC 12472	CV3037	<i>ldhEGF-dldII-lldP</i>	<i>CV3030</i>	-29	5.88	AATTGGTctTACCAATT	
		<i>lldR</i>	<i>CV3037</i>	-28	<u>4.05</u>	AtccGGTcagACCAATT	
<i>Neisseria meningitidis</i> MC58	NMB1711	<i>lldP</i>	<i>NMB0543</i>	-109	5.88	AATTGGTctTACCAATT	
		<i>NMB1712</i>	<i>NMB1712</i>	-222 14	4.75 4.78	AATTGGactgACCAATc AATTGGTttgACCAcTa	<i>lldR</i>
<i>Dechloromonas aromatica</i> RCB	Daro_1767	<i>ldhEFG-dldII-lldP</i>	<i>Daro_1766</i>	-46	5.52	tATTGGTctTACCAATT	<i>lldR</i>
<i>Rhodoferrax ferrireducens</i> T118	Rfer_0202	<i>ldhEGF</i>	<i>Rfer_0201</i>	-52	5.59	tATTGGTAtTACCAATT	
		<i>lldR</i>	<i>Rfer_0202</i>	-25	5.88	AATTGGTctTACCAATT	
LldR2 (R2) regulon for lactate utilization (LysR family) in <i>Shewanella</i> spp.				cutoff = 5.2			
<i>Shewanella oneidensis</i> MR-1	SO3460	<i>ldhEFG</i>	<i>SO1520</i>	-122	6.21	TAAATTAGggCTACTTATTTA	
<i>Shewanella putrefaciens</i> CN-32	Sputcn32_2769	<i>ldhEFG</i>	<i>Sputcn32_1270</i>	-124	6.2	TAAATTAGgACTACTTATTTc	
<i>Shewanella putrefaciens</i> W3-18-1	Sputw3181_1243	<i>ldhEFG</i>	<i>Sputw3181_2836</i>	-124	6.2	TAAATTAGgACTACTTATTTc	
<i>Shewanella baltica</i> OS155	Sbal_3151	<i>ldhEFG</i>	<i>Sbal_1352</i>	-122	5.69	TAAATTAGggCTACTTATTTc	
<i>Shewanella</i> sp. MR-4	Shewmr4_1106	<i>ldhEFG</i>	<i>Shewmr4_2736</i>	-92	6.28	TAAATTAGcgCTACTTATTTA	
<i>Shewanella</i> sp. MR-7	Shewmr7_1172	<i>ldhEFG</i>	<i>Shewmr7_2809</i>	-92	6.28	TAAATTAGcgCTACTTATTTA	
<i>Shewanella</i> sp. ANA-3	Shewana3_1106	<i>ldhEFG</i>	<i>Shewana3_2906</i>	-92	6.28	TAAATTAGcgCTACTTATTTA	
<i>Shewanella frigidimarina</i>	Sfri_1855	<i>ldhEFG</i>	<i>Sfri_1852</i>	-134	5.22	TtAATTAGcACTACaTtTTat	<i>lldR2</i>

<i>Shewanella loihica</i> PV-4	Shew_3007	<i>ldhEFG</i>	Shew_3004	-155	6.08	TAAATTAGcACTACTTATTat	<i>lldR2</i>
<i>Shewanella pealeana</i> ANG-SQ1	Spea_1178	<i>ldhEFG</i>	Spea_2996	-169	5.8	TAAATTAGcACTACTTtTTac	
<i>Shewanella sediminis</i> HAW-EB3	Ssed_3921	<i>ldhEFG</i>	Ssed_3924	-148	6.08	TAAATTAGcACTACTTATTat	<i>lldR2</i>

LldR3 (R3) regulon for lactate utilization (GntR family) in Bacillales

cutoff = 5.8

<i>Bacillus subtilis</i>	Yvfl (Bsu3415)	<i>ldhEFG</i>	yvflV	-50	6.42	CAGGTCATCAGATGACCTG	
		<i>lldP</i>	yvflH	-79	5.8	CcaGTCATCAGATGAtCat	<i>lldR3</i>
<i>Bacillus halodurans</i> C-125	BH1835	<i>lldP-ldhEFG-yvfl</i>	BH1831	-55	6.1	tAaGTCATCTGATGACCTa	
<i>Bacillus clausii</i> KSM-K16	ABC0978	<i>lldP-ldhEFG-yvfl</i>	ABC0974	-54	6.28	ataGTCATCTGATGACCat	
<i>Bacillus licheniformis</i> ATCC 14580	BL03455	<i>ldhEFG</i>	BL03456	-45	6.36	CAaGTCATCAGATGACCTG	
		<i>lldP</i>	BL03613	-56	6.04	CAtGTCATCAGATGACtaG	<i>lldR3</i>
<i>Geobacillus kaustophilus</i> HTA426	GK0396	<i>ldhEFG</i>	GK0395	-51	5.87	ataGTCATCAGATGACCcG	
		<i>lldP</i>	GK0398	-94	6.1	CcGGTCATCTGATGACtGg	<i>lldR3</i>
<i>Oceanobacillus iheyensis</i> HTE831	OB0369	<i>lldP-yvfl-ldhEFG</i>	OB0368	-72	6.38	aAGGTCATCAGATGACCTt	
<i>Bacillus cereus</i> ATCC 10987	BCE1415	<i>ldhEFG-yvfl</i>	BCE1416	-60	6.17	ttaGTCATCTGATGACCat	

LldR4 (R4) regulon for lactate utilization (GntR family) in Actinobacteria

cutoff = 5.0

<i>Mycobacterium smegmatis</i> str. MC2 155	MSMEG0586	<i>ldhEFG</i>	MSMEG0584	-62	5.5	cgTGTGGTCTGACCACa	<i>lldR4</i>
				-28	6.3	AgTGTGGTCAGACCACAGT	
<i>Mycobacterium</i> sp. JLS	Mjls_4357	<i>ldhEFG</i>	Mjls_4358	-63	5.92	ggTGTGGTCcGACCACAtT	<i>lldR4</i>
				-39	6.34	ACTGTGGTCAGACCACAGc	
<i>Brevibacterium linens</i> BL2	BlinB01001218	<i>ldhEFG</i>	BlinB01001219	-121	5.5	gtTaaGGTCTGACCACAtT	<i>lldR4</i>
		<i>lldP-lldD</i>	BlinB01001150	-43	5.61	ttaGTTGGTCTGACCACa	
<i>Propionibacterium acnes</i> KPA171202	PPA0165	<i>lldP-ldhEFG</i>	PPA0166	-80	5.36	AtatTGGTCgGACCAaAtc	<i>lldR4</i>
<i>Corynebacterium diphtheriae</i> NCTC 13129	DIP0011	<i>lldP-lldR</i>	DIP0012	-123	5.32	tCTGTGGTCTtACCACtGT	
				-109	5.75	ACTGTGGTCAGACCAactc	
<i>Corynebacterium efficiens</i> YS-314	CE2757	<i>lldP2-lldD</i>	CE2761	-30	5.31	ctTGTGGTCTGACCACAtg	

LldR5 (R5) regulon for lactate utilization (LysR family) in Vibrionales

<i>Vibrio cholerae</i> O1 str. N16961	VCA0982	<i>lldP-lldD-dldII</i>	VCA0983	-130	5.77	TAATGAATTTTCATTA	<i>lldR5</i>
<i>Vibrio parahaemolyticus</i> RIMD 2210633	VPA1497	<i>lldP-lldD</i>	VPA1498	-141	5.03	TAATtAtTTTCATTA	<i>lldR5</i>
<i>Vibrio vulnificus</i> CMCP6	VV20796	<i>lldP-lldD-ldhEFG</i>	VV20797	-191	5.21	gAATGAtTTTCATTA	
	PBPRA1412, PBPRA2361, PBPRA2222	<i>lldP1-ldhGEFG1-dldII</i>	PBPRA1411	-70	4.39	aAAcGAATTTTCaTc	<i>lldR5</i>
<i>Photobacterium profundum</i> SS9		<i>dld</i>	PBPRA2224	-356	5.25	TgATGAATTTTCATgA	<i>lldR5</i>
		<i>lldP3-ldhEFG2-lldR2</i>	PBPRA2357	-459	4.57	acAaGAAATTCATcA	
<i>Aeromonas hydrophila</i> ATCC 7966	AHA_2561	<i>lldP-ldhGEFG-dldII</i>	AHA_2560	-131	4.18	ATTGATcAACTTT	<i>lldR5</i>
				-111	5.49	AATGTTgTTCATT	

*Standard gene or protein identifiers are from GenBank.

† Position relative to the start of translation.

‡ Site search cutoff is given on the top. Site scores below cutoff are underlined.

§ Lowercase letters represent positions that do not conform to the consensus.