Table S1 Differentially expressed genes in *Labrenzia aggregata* wild-type and *rpoN* mutant strains

Gene ID	Description	Fold change(Δ*rpoN* / wild-type)
downregulated		
st40_24680	flagellar assembly protein FlaE	-211.88
st40_25155	flagellar L-ring protein FlgH	-86.75
st40_24685	flagellar hook protein FlgK	-82.78
st40_09705	flagellar hook capping protein	-49.55
st40_24690	flagellar protein	-48.94
st40_25165	flagellar basal body rod protein FlgG	-46.85
st40_22780	MFS transporter permease	-40.39
st40_25160	flagellar basal body P-ring biosynthesis protein FlgA	-34.76
st40_25120	flagellar basal body P-ring biosynthesis protein FlgA	-30.03
st40_09700	hypothetical protein	-28.89
st40_25110	hypothetical protein	-28.13
st40_05350	hypothetical protein	-27.61
st40_25170	flagellar basal body rod protein	-21.73
st40_00765	RNA polymerase sigma54 factor	-13.10
st40_21055	hypothetical protein	-12.07
st40_05345	--	-11.04
st40_10350	hypothetical protein	-10.81
st40_12905	hypothetical protein	-10.66
st40_18290	urea ABC transporter ATP-binding protein	-9.98
st40_18300	acylamide amidohydrolase	-9.62
st40_18285	--	-7.72
st40_18295	urea ABC transporter ATP-binding protein	-7.33
st40_18305	ATPase AAA	-6.52
st40_23540	C4-dicarboxylate ABC transporter	-6.42
st40_18280	ABC transporter permease	-6.40
st40_18275	ABC transporter substrate-binding protein	-6.00
st40_12920	hypothetical protein	-5.70
st40_12915	hypothetical protein	-5.31
st40_21910	MFS transporter	-5.26
st40_12910	hypothetical protein	-5.01
st40_14445	Clp protease ClpP	-4.92
st40_18310	--	-4.58
st40_04815	--	-4.57
st40_18260	hypothetical protein	-4.42
st40_23655	4-hydroxyphenylpyruvate dioxygenase	-4.22

st40_00620	precorrin-4 C11-methyltransferase	-4.12
st40_21915	transcriptional regulator	-4.03
st40_12925	TfuA-like core domain-containing protein	-3.91
st40_26740	acyl-CoA dehydrogenase	-3.82
st40_27660	thiamine pyrophosphate-binding protein	-3.81
st40_18255	allantoin permease	-3.75
st40_15130	hypothetical protein	-3.70
st40_28890	formate dehydrogenase	-3.69
st40_28885	formate dehydrogenase	-3.47
st40_00615	precorrin-3B methylase	-3.44
st40_00590	sirohydrochlorin cobaltochelatase	-3.43
st40_10325	hypothetical protein	-3.37
st40_28895	formate dehydrogenase	-3.36
st40_12110	chemotaxis protein	-3.35
st40_12020	5-oxoprolinase	-3.33
st40_28710	hypothetical protein	-3.29
st40_17865	sugar ABC transporter permease	-3.26
st40_24710	2-keto-gluconate dehydrogenase	-3.23
st40_17870	sugar ABC transporter substrate-binding protein	-3.19
st40_08910	protein hupE	-3.09
st40_00605	precorrin-6Y C5%2C15-methyltransferase	-3.06
st40_10860	molybdenum ABC transporter substrate-binding protein	-3.05
st40_05460	hypothetical protein	-2.96
st40_12930	--	-2.95
st40_00595	precorrin isomerase	-2.82
st40_10370	nitrate reductase	-2.81
st40_04645	nitrous-oxide reductase	-2.78
st40_12045	C4-dicarboxylate ABC transporter permease	-2.73
st40_21625	amino acid dehydrogenase	-2.72
st40_06075	methionine gamma-lyase	-2.71
st40_18820	YHS domain-containing protein	-2.70
st40_06515	hypothetical protein	-2.70
st40_18265	amino acid ABC transporter substrate-binding protein	-2.69
st40_12040	C4-dicarboxylate ABC transporter permease	-2.62
st40_00575	membrane protein	-2.51
st40_23980	hypothetical protein	-2.49
st40_26745	FAD-dependent oxidoreductase	-2.49
st40_07730	2'-5' RNA ligase	-2.46
st40_06065	transketolase	-2.41
st40_10375	nitrate reductase	-2.40
st40_15605	hypothetical protein	-2.38
st40_10365	cytochrome C	-2.37
st40_12605	MFS transporter	-2.36
st40_14980	hypothetical protein	-2.32

st40_12035	C4-dicarboxylate ABC transporter substrate-binding protein	-2.31
st40_16800	indolepyruvate ferredoxin oxidoreductase	-2.30
st40_15600	SulA-family protein	-2.27
st40_24725	ABC transporter substrate-binding protein	-2.25
st40_29480	polyhydroxybutyrate depolymerase	-2.25
st40_23030	peptide ABC transporter substrate-binding protein	-2.19
st40_26045	alanine dehydrogenase	-2.19
st40_23125	hypothetical protein	-2.19
st40_03350	hypothetical protein	-2.17
st40_22980	metallo-beta-lactamase	-2.16
st40_25185	chemotaxis protein	-2.16
st40_18270	hypothetical protein	-2.15
st40_21655	permease	-2.15
st40_21660	C4-dicarboxylate ABC transporter permease	-2.11
st40_24520	peroxidase	-2.11
st40_11160	caspase	-2.10
st40_18230	ABC transporter substrate-binding protein	-2.07
st40_17385	haloacid dehalogenase	-2.06
st40_28630	poly(3-hydroxyalkanoate) synthetase	-2.06
st40_10790	TetR family transcriptional regulator	-2.06
st40_16445	hypothetical protein	-2.05
st40_20295	oxidoreductase	-2.05
st40_17235	photosynthetic protein synthase I	-2.04
st40_03670	hypothetical protein	-2.02
st40_11260	Hcp1 family type VI secretion system effector	-2.01
st40_25810	peroxidase	-2.01
st40_12050	transcriptional regulator	-2.00
upregulated		
st40_05590	imidazolonepropionase	2.00
st40_12250	MFS transporter	2.00
st40_28975	acetyltransferase	2.01
st40_13590	30S ribosomal protein S21	2.01
st40_22390	sugar ABC transporter ATP-binding protein	2.02
st40_14030	XRE family transcriptional regulator	2.03
st40_13925	chromate resistance protein ChrB	2.04
st40_17680	TetR family transcriptional regulator	2.04
st40_27005	signal peptide protein	2.04
st40_02865	Na/Pi cotransporter	2.06
st40_08970	hydrolase	2.07
st40_04380	recombinase RecF	2.09
st40_01240	response regulator receiver protein	2.10
st40_05620	tripartite transporter	2.10
st40_27990	tRNA-Met	2.11

st40_13380	Holliday junction resolvase	2.11
st40_16260	septum formation initiator	2.13
st40_17005	homospermidine synthase	2.14
st40_03025	50S ribosomal protein L33	2.15
st40_00235	septum formation inhibitor Maf	2.20
st40_09710	hypothetical protein	2.22
st40_26070	--	2.24
st40_14240	hypothetical protein	2.26
st40_17335	hypothetical protein	2.34
st40_04585	dihydroxyacetone kinase	2.36
st40_04970	hypothetical protein	2.47
st40_27065	YeeE/YedE	2.54
st40_21265	hypothetical protein	2.57
st40_29650	tRNA-Ile	2.59
st40_00240	translation initiation factor IF-1	2.70
st40_04845	ABC transporter substrate-binding protein	2.70
st40_19230	hypothetical protein	2.71
st40_21350	beta-lactamase TEM	2.73
st40_28775	glycerol-3-phosphate transporter ATP-binding subunit	2.74
st40_16995	GCN5 family acetyltransferase	2.78
st40_22630	conjugal transfer protein TrbE	2.99
st40_29215	glycerol 3-phosphate ABC transporter substrate-binding protein	3.05
st40_14225	Dtr system oriT relaxase	3.07
st40_13685	tRNA-Val	3.08
st40_18355	ATPase	3.08
st40_04535	sugar ABC transporter substrate-binding protein	3.12
st40_00290	tRNA-Thr	3.15
st40_14235	conjugal transfer protein TraB	3.18
st40_19225	phosphoadenosine phosphosulfate reductase	3.30
st40_22645	--	3.32
st40_14205	conjugal transfer protein TraG	3.39
st40_27975	tRNA-Ala	3.40
st40_14215	hypothetical protein	3.46
st40_09150	5'-nucleotidase	3.49
st40_19220	sulfite reductase	3.65
st40_27070	sulfurtransferase	4.13
st40_19910	ABC transporter ATP-binding protein	4.20
st40_19915	DeoR family transcriptional regulator	4.23
st40_19905	ABC transporter substrate-binding protein	4.32
st40_07835	tRNA-Leu	4.56
st40_19210	siroheme synthase	4.86
st40_16955	hypothetical protein	5.15
st40_19215	sulfite reductase	5.27

st40_29510	5-deoxyglucuronate isomerase	9.86
st40_29490	3D-(3%2C5/4)-trihydroxycyclohexane-1%2C2-dione hydrolase	11.47
st40_29505	inosose dehydratase	12.46
st40_29500	3D-(3%2C5/4)-trihydroxycyclohexane-1%2C2-dione hydrolase	13.03
st40_24265	myo-inositol 2-dehydrogenase	18.69
st40_24255	RpiR family transcriptional regulator	20.03
st40_29495	5-dehydro-2-deoxygluconokinase	20.81
st40_24260	inositol 2-dehydrogenase	22.79
st40_24245	ATPase	30.09
st40_24240	ABC transporter ATP-binding protein	47.01
st40_24250	sugar ABC transporter substrate-binding protein	74.44

Table S2 OD_{570} values from the GN2 MicroPlate kit (Biolog) of *L. aggregata* LZB033

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0.058	0.34	0.09	0	0.012	0.218	0.374	0.545	0.414	0.542	0.574
B	0.438	0.528	0.456	0.472	0.282	0.649	0.385	0.146	0.149	0.646	0.562	0.196
C	0.278	0.131	0.161	0.148	0.174	0.491	0.741	0.634	0.191	0.054	0.379	0.546
D	0.171	0.477	0.13	0.176	0.09	0.129	0.565	0.149	0.438	0.54	0.841	0.084
E	0.306	0.502	0.554	0.365	0.194	0.582	0.102	0.457	0.094	0.27	0	0.56
F	0.491	0.136	0.147	0.504	0.087	0.405	0.478	0.11	0.115	0.595	0.135	0.349
G	0.28	0.264	0.298	0.276	0.312	0.371	0.562	0.068	0.085	0.446	0.104	0.141
H	0.266	0.24	0.141	0.134	0.068	0.075	0.108	0.119	0.583	0.119	0.45	0.37

Table S3 OD_{570} values from the GN2 MicroPlate kit (Biolog) of *L. aggregata* Δ*rpoN**

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0.035	0.378	0.109	0	0	0.163	0.184	0.68	0.132	0.634	0.66
B	0.396	0.343	0.217	0.288	0.219	0.481	0.239	0	0.234	0.385	0.351	0.101
C	0.272	0.052	0.156	0.038	0.137	0.33	0.369	0.459	0.178	0	0.208	0.29
D	0.15	0.354	0.058	0.169	0.047	0.178	0.52	0	0.426	0.357	0.557	0.070
E	0.262	0	0.493	0	0.060	0.480	0	0.306	0	0.185	0	0.114
F	0	0.043	0.118	0.359	0	0.218	0.275	0.336	0.136	0.366	0.127	0.362
G	0.235	0.184	0.254	0.231	0.257	0.398	0.439	0	0.158	0.297	0.343	0.180
H	0.446	0.223	0.071	0.145	0.002	0	0.171	0	0.552	0.241	0.319	0.300

*: Values from wells highlighted in green were reductions. While those in red were increases.

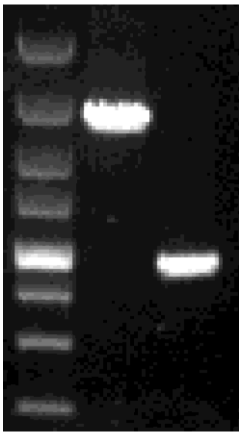

Figure S1 PCR confirmation of the construction of Δ*rpoN*. From left to right: DL5000 DNA marker, wild-type, Δ*rpoN*.

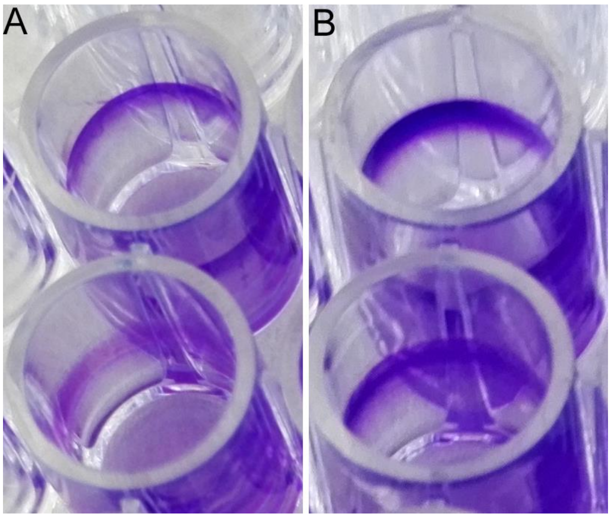

Figure S2 Stain of biofilm formed by *L. aggregata* strains incubated for (A) 24 h and (B) 48 h, upper: LZB033, down: Δ*rpoN*.