

## Supplementary materials

**Table S1.** The major altered metabolic pathways in *S. aureus* ATCC8095 induced by the GMPE.

Metabolic Pathway	Gene ID	Fold Change	Gene Description
Ribosome	EQG65_11565	2.250	30S ribosomal protein S11
	EQG65_11570	2.398	30S ribosomal protein S13
	EQG65_11575	2.448	50S ribosomal protein L36
	EQG65_11595	2.562	50S ribosomal protein L15
	EQG65_11555	2.681	50S ribosomal protein L17
	EQG65_08510	3.008	50S ribosomal protein L27
	EQG65_14300	3.228	50S ribosomal protein L34
	EQG65_11650	3.257	50S ribosomal protein L29
	EQG65_02705	3.380	30S ribosomal protein S7
	EQG65_11600	3.398	50S ribosomal protein L30
	EQG65_11610	3.444	50S ribosomal protein L18
	EQG65_02380	3.473	50S ribosomal protein L25
	EQG65_08040	3.532	50S ribosomal protein L33
	EQG65_02695	3.550	50S ribosomal protein L7-like protein
	EQG65_11625	3.568	Type Z 30S ribosomal protein S14
	EQG65_02700	3.579	30S ribosomal protein S12
	EQG65_11605	3.595	30S ribosomal protein S5
	EQG65_06500	3.686	30S ribosomal protein S15
	EQG65_11630	3.720	50S ribosomal protein L5
	EQG65_11615	3.733	50S ribosomal protein L6
	EQG65_11525	3.784	30S ribosomal protein S9
	EQG65_11635	3.805	50S ribosomal protein L24
	EQG65_11530	3.826	50S ribosomal protein L13
	EQG65_01735	3.843	30S ribosomal protein S18
	EQG65_11640	3.939	50S ribosomal protein L14
	EQG65_11620	4.009	30S ribosomal protein S8
	EQG65_06310	4.044	30S ribosomal protein S16
	EQG65_10975	4.178	Type B 50S ribosomal protein L31
	EQG65_01725	4.205	30S ribosomal protein S6
	EQG65_11655	4.302	50S ribosomal protein L16
	EQG65_11670	4.304	30S ribosomal protein S19
	EQG65_11645	4.347	30S ribosomal protein S17
	EQG65_11665	4.656	50S ribosomal protein L22
	EQG65_11660	4.665	30S ribosomal protein S3
	EQG65_02655	4.767	50S ribosomal protein L11
	EQG65_11680	4.848	50S ribosomal protein L23
	EQG65_11675	4.930	50S ribosomal protein L2
	EQG65_06405	5.149	30S ribosomal protein S2
	EQG65_08520	5.170	50S ribosomal protein L21
	EQG65_08215	5.198	30S ribosomal protein S20
	EQG65_06325	5.206	50S ribosomal protein L19
	EQG65_11690	5.248	50S ribosomal protein L3
	EQG65_11685	5.264	50S ribosomal protein L4
	EQG65_02660	5.414	50S ribosomal protein L1

	EQG65_11695	5.539	30S ribosomal protein S10
	EQG65_02675	6.426	50S ribosomal protein L7/L12
	EQG65_08665	7.772	50S ribosomal protein L35
	EQG65_08890	7.936	30S ribosomal protein S4
	EQG65_02670	7.942	50S ribosomal protein L10
	EQG65_08660	8.055	50S ribosomal protein L20
Purine metabolism	EQG65_13860	0.024	Carbamate kinase
	EQG65_05945	0.059	Carbamate kinase
	EQG65_13755	0.093	Anaerobic ribonucleoside-triphosphate reductase
	EQG65_03735	0.359	Class 1b ribonucleoside-diphosphate reductase subunit $\alpha$
	EQG65_03740	0.472	Class 1b ribonucleoside-diphosphate reductase subunit $\beta$
	EQG65_01860	2.344	IMP dehydrogenase
	EQG65_11585	2.413	Adenylate kinase
	EQG65_11905	2.429	Urease subunit alpha
	EQG65_01865	2.543	Glutamine-hydrolyzing GMP synthase
	EQG65_02425	3.095	Hypoxanthine phosphoribosyltransferase
	EQG65_11895	3.113	Urease subunit gamma
	EQG65_10200	3.237	Adenylosuccinate lyase
	EQG65_08765	3.252	Pyruvate kinase
	EQG65_08460	3.312	Adenine phosphoribosyltransferase
	EQG65_11900	3.957	Urease subunit beta
	EQG65_06890	4.976	GMP reductase
	EQG65_01850	5.085	Xanthine phosphoribosyltransferase
	EQG65_05375	6.772	5-(carboxyamino)imidazole ribonucleotide mutase
	EQG65_05390	7.780	Phosphoribosylformylglycinamide synthase subunit PurS
	EQG65_05380	9.637	5-(carboxyamino)imidazole ribonucleotide synthase
	EQG65_05385	10.026	Phosphoribosylaminoimidazolesuccinocarboxamide synthase
	EQG65_05425	10.852	Phosphoribosylamine--glycine ligase
	EQG65_05400	13.131	Phosphoribosylformylglycinamide synthase subunit PurL
	EQG65_05420	13.262	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
	EQG65_05415	14.297	Phosphoribosylglycinamide formyltransferase
	EQG65_05410	15.616	Phosphoribosylformylglycinamide cyclo-ligase
	EQG65_00095	16.494	Adenylosuccinate synthase
Alanine, aspartate and glutamate metabolism	EQG65_13415	0.070	L-glutamate gamma-semialdehyde dehydrogenase
	EQG65_04810	0.150	NAD-specific glutamate dehydrogenase
	EQG65_11150	0.172	Glutamine--fructose-6-phosphate transaminase (isomerizing)
	EQG65_08830	0.220	Alanine dehydrogenase
	EQG65_07440	0.463	Alanine dehydrogenase
	EQG65_06680	2.208	Type I glutamate--ammonia ligase
	EQG65_02190	5.136	Glutamate synthase subunit $\beta$
	EQG65_02185	5.608	Glutamate synthase large subunit
	EQG65_07660	5.839	Asparaginase
	EQG65_05395	13.761	Phosphoribosylformylglycinamide synthase subunit PurQ
	EQG65_05405	14.775	Amidophosphoribosyltransferase
Pyrimidine metabolism	EQG65_06130	15.489	Carbamoyl-phosphate synthetase large subunit
	EQG65_06125	19.069	Carbamoyl-phosphate synthetase small subunit
	EQG65_01440	0.028	Pseudouridine-5'-phosphate glycosidase

	<i>EQG65_11055</i>	0.137	Pyrimidine-nucleoside phosphorylase
	<i>EQG65_06420</i>	2.255	UMP kinase
	<i>EQG65_07655</i>	2.508	(d)CMP kinase
	<i>EQG65_02760</i>	2.707	Deoxynucleoside kinase
	<i>EQG65_08335</i>	3.362	Uridine kinase
	<i>EQG65_10965</i>	3.370	Thymidine kinase
	<i>EQG65_13595</i>	4.843	Quinone-dependent dihydroorotate dehydrogenase
	<i>EQG65_11010</i>	5.962	CTP synthase
	<i>EQG65_06105</i>	8.209	Bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase PyrR
	<i>EQG65_06140</i>	12.374	Orotate phosphoribosyltransferase
	<i>EQG65_06135</i>	12.955	Orotidine-5'-phosphate decarboxylase
	<i>EQG65_06120</i>	22.780	Dihydroorotase
	<i>EQG65_06115</i>	30.276	Aspartate carbamoyltransferase
Fatty acid biosynthesis	<i>EQG65_00950</i>	0.073	Long-chain fatty acid--CoA ligase
	<i>EQG65_08315</i>	0.457	Acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
	<i>EQG65_07920</i>	2.312	Acetyl-CoA carboxylase biotin carboxyl carrier protein
	<i>EQG65_06270</i>	2.520	3-oxoacyl-[acyl-carrier-protein] reductase
	<i>EQG65_06265</i>	2.705	[acyl-carrier-protein] S-malonyltransferase
	<i>EQG65_07915</i>	2.771	Acetyl-CoA carboxylase biotin carboxylase subunit
	<i>EQG65_06540</i>	2.847	SDR family NAD(P)-dependent oxidoreductase
	<i>EQG65_04940</i>	3.089	Beta-ketoacyl-[acyl-carrier-protein] synthase II
	<i>EQG65_08780</i>	4.037	Acetyl-CoA carboxylase carboxyltransferase subunit beta
	<i>EQG65_08775</i>	4.062	Acetyl-CoA carboxylase carboxyltransferase subunit alpha
	<i>EQG65_04935</i>	5.502	Ketoacyl-ACP synthase III
Protein export	<i>EQG65_13950</i>	0.423	Accessory Sec system translocase SecA2
	<i>EQG65_06305</i>	2.006	Signal recognition particle protein
	<i>EQG65_13970</i>	2.085	Accessory Sec system protein translocase subunit SecY2
	<i>EQG65_01625</i>	2.284	Twin-arginine translocase TatA/TatE family subunit
	<i>EQG65_11590</i>	2.326	Preprotein translocase subunit SecY
	<i>EQG65_01620</i>	2.561	Twin-arginine translocase subunit TatC
	<i>EQG65_10815</i>	2.579	Membrane protein insertase YidC
	<i>EQG65_03855</i>	2.590	Preprotein translocase subunit SecA
	<i>EQG65_04850</i>	3.062	Signal peptidase IB
	<i>EQG65_08470</i>	3.388	Protein translocase subunit SecDF
	<i>EQG65_06095</i>	3.405	Lipoprotein signal peptidase
	<i>EQG65_04845</i>	3.472	Signal peptidase I
Carotenoid biosynthesis	<i>EQG65_13470</i>	0.103	Glycosyl-4%2C4'-diaponeurosporenoate acyltransferase
	<i>EQG65_13465</i>	0.125	Diapolycopene oxygenase
	<i>EQG65_13460</i>	0.212	4%2C4'-diaponeurosporenoate glycosyltransferase
	<i>EQG65_13450</i>	0.232	Dehydrosqualene desaturase
	<i>EQG65_13455</i>	0.312	Dehydrosqualene synthase
Arginine biosynthesis	<i>EQG65_13875</i>	0.014	Arginine deiminase
	<i>EQG65_13870</i>	0.015	Ornithine carbamoyl transferase
	<i>EQG65_05940</i>	0.042	Ornithine carbamoyl transferase
	<i>EQG65_11195</i>	0.094	Arginase
Aminoacyl-tRNA	<i>EQG65_08945</i>	2.034	Tyrosine--tRNA ligase

biosynthesis	<i>EQG65_02465</i>	2.052	Lysine--tRNA ligase
	<i>EQG65_08435</i>	2.232	Aspartate--tRNA ligase
	<i>EQG65_09115</i>	2.439	Leucine--tRNA ligase
	<i>EQG65_06195</i>	2.777	Methionyl-tRNA formyltransferase
	<i>EQG65_08575</i>	2.796	Valine--tRNA ligase
	<i>EQG65_08440</i>	2.823	Histidine--tRNA ligase
	<i>EQG65_08110</i>	2.953	Glycine--tRNA ligase
	<i>EQG65_06445</i>	3.241	Proline--tRNA ligase
	<i>EQG65_05770</i>	3.281	Phenylalanine--tRNA ligase subunit beta
	<i>EQG65_10165</i>	4.021	Asp-tRNA (Asn)/Glu-tRNA (Gln) amidotransferase subunit GatC
	<i>EQG65_05765</i>	4.057	Phenylalanine--tRNA ligase subunit alpha
	<i>EQG65_10155</i>	4.146	Asp-tRNA (Asn)/Glu-tRNA (Gln) amidotransferase subunit GatB
	<i>EQG65_10160</i>	4.280	Asp-tRNA (Asn)/Glu-tRNA (Gln) amidotransferase subunit GatA
	<i>EQG65_06075</i>	4.401	Isoleucine--tRNA ligase
Carbon fixation in photosynthetic organisms	<i>EQG65_08705</i>	0.013	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>EQG65_09275</i>	0.032	Phosphoenolpyruvate carboxykinase (ATP)
	<i>EQG65_13195</i>	0.134	Fructose-1%2C6-bisphosphatase
	<i>EQG65_06920</i>	2.036	Transketolase
	<i>EQG65_03980</i>	3.277	Triose-phosphate isomerase
	<i>EQG65_03975</i>	3.496	Phosphoglycerate kinase
	<i>EQG65_03970</i>	3.781	Type I glyceraldehyde-3-phosphate dehydrogenase
PTS	<i>EQG65_11000</i>	3.929	Fructose-bisphosphate aldolase
	<i>EQG65_01540</i>	0.021	PTS sugar transporter subunit IIA
	<i>EQG65_01530</i>	0.056	PTS ascorbate transporter subunit IIC
	<i>EQG65_01025</i>	0.084	PTS sugar transporter subunit IIA
	<i>EQG65_01535</i>	0.106	PTS sugar transporter subunit IIB
	<i>EQG65_01035</i>	0.143	PTS galactitol transporter subunit IIC
	<i>EQG65_01030</i>	0.195	PTS galactitol transporter subunit IIB
	<i>EQG65_13910</i>	0.430	PTS mannose transporter subunit IIABC
	<i>EQG65_03560</i>	24.254	PTS fructose transporter subunit IIC
	<i>EQG65_03555</i>	28.586	1-phosphofructokinase

**Table S2.** The major altered metabolic pathways in *E. sakazakii* CMCC45401 mediated by the GMPE.

Metabolic Pathway	Gene ID	Fold Change	Gene Description
Tryptophan metabolism	AFK63_10145	2.043	Hydroperoxidase
	AFK63_04175	2.046	Indolepyruvate decarboxylase
	AFK63_02085	3.317	Peroxidase
ABC transporters	AFK63_15425	0.163	Capsule biosynthesis protein
	AFK63_07285	0.204	Nitrate/bicarbonate ABC transporter substrate-binding protein
	AFK63_12140	0.224	Glutamine ABC transporter substrate-binding protein
	AFK63_12150	0.237	Glutamine ABC transporter ATP-binding protein
	AFK63_12145	0.255	Glutamine ABC transporter permease
	AFK63_04315	0.295	Heme ABC transporter permease
	AFK63_04505	0.315	Amino acid ABC transporter permease
	AFK63_12390	0.349	Molybdenum ABC transporter ATP-binding protein
	AFK63_04500	0.360	Amino acid ABC transporter permease
	AFK63_04490	0.381	Histidine ABC transporter substrate-binding protein HisJ
	AFK63_16815	0.400	Amino acid ABC transporter permease
	AFK63_16810	0.408	Amino acid ABC transporter substrate-binding protein
	AFK63_15090	0.415	Thiamine ABC transporter substrate-binding protein
	AFK63_16820	0.433	Amino acid ABC transporter permease
	AFK63_04495	0.435	Histidine ABC transporter substrate-binding protein HisJ
	AFK63_12970	1.779	ABC transporter
	AFK63_19755	1.789	Leucine ABC transporter substrate-binding protein
	AFK63_00740	1.799	Maltose transporter
	AFK63_11885	1.821	Putrescine transporter ATP-binding subunit
	AFK63_01455	1.824	Sugar ABC transporter ATP-binding protein
	AFK63_08460	1.829	Choline ABC transporter permease
	AFK63_18595	1.845	Sugar ABC transporter ATP-binding protein
	AFK63_18600	1.868	Ribose ABC transporter permease
	AFK63_18485	2.015	Phosphate ABC transporter substrate-binding protein
	AFK63_01450	2.177	Sugar ABC transporter substrate-binding protein
	AFK63_12985	2.187	ABC transporter substrate-binding protein
	AFK63_00745	2.458	Sugar ABC transporter substrate-binding protein
	AFK63_19775	2.551	Leucine/isoleucine/valine transporter permease subunit
	AFK63_19780	2.573	Leucine/isoleucine/valine transporter ATP-binding subunit
	AFK63_19785	2.765	Leucine/isoleucine/valine transporter ATP-binding subunit
	AFK63_19770	3.149	Branched-chain amino acid transporter permease subunit LivH
	AFK63_19280	3.162	Xylose transporter
	AFK63_06125	3.497	Sugar ABC transporter substrate-binding protein
	AFK63_00750	3.726	Maltose/maltodextrin transporter ATP-binding protein
	AFK63_06130	3.765	L-arabinose transporter ATP-binding protein
	AFK63_19285	3.994	D-xylose transporter subunit XylF
Fructose and mannose metabolism	AFK63_06860	1.769	PTS mannose transporter subunit IIAB
	AFK63_05265	1.816	Fructose-bisphosphate aldolase
	AFK63_08160	2.291	Mannose-6-phosphate isomerase
	AFK63_05020	2.405	1-phosphofructokinase
	AFK63_19290	4.281	Xylose isomerase
	AFK63_05425	6.011	Phosphomannomutase
	AFK63_05405	8.932	GDP-fucose synthetase

	AFK63_05400	9.129	GDP-mannose 4%2C6-dehydratase
	AFK63_05420	13.341	Mannose-1-phosphate guanyltransferase
Fatty acid degradation	AFK63_06955	1.935	Long-chain fatty acid--CoA ligase
	AFK63_17080	2.113	3-ketoacyl-CoA thiolase
	AFK63_14360	2.388	Acyl-CoA dehydrogenase
	AFK63_17075	2.668	Multifunctional fatty acid oxidation complex subunit alpha
	AFK63_08175	5.512	Alcohol dehydrogenase
Butanoate metabolism	AFK63_08680	0.305	Succinate dehydrogenase
	AFK63_12550	1.959	Succinate dehydrogenase
	AFK63_12555	2.020	Succinate dehydrogenase
	AFK63_08185	2.029	Pyruvate-flavodoxin oxidoreductase
	AFK63_08940	2.209	3-oxoacyl-ACP reductase
	AFK63_07645	3.368	Formate acetyltransferase
Glycosphingolipid biosynthesis	AFK63_17760	2.158	$\alpha$ -galactosidase
	AFK63_12700	2.290	$\beta$ -N-acetylhexosaminidase
Starch and sucrose metabolism	AFK63_06140	1.901	Trehalose phosphatase
	AFK63_19875	1.921	Glycogen branching protein
	AFK63_13750	2.059	Maltodextrin glucosidase
	AFK63_19935	2.077	Maltose phosphorylase
	AFK63_06145	2.258	Trehalose-6-phosphate synthase
	AFK63_08030	2.335	$\beta$ -phosphoglucomutase
	AFK63_01700	2.383	PTS cellobiose transporter subunit IIC
	AFK63_09960	2.699	$\beta$ -D-glucoside glucohydrolase
	AFK63_19260	3.972	$\alpha$ -amylase
	AFK63_01705	4.086	PTS lactose transporter subunit IIB
	AFK63_15600	4.313	PTS cellobiose transporter subunit IIC
	AFK63_02320	7.040	6-phospho-beta-glucosidase
Lysine degradation	AFK63_16040	1.807	Putrescine--2-oxoglutarate aminotransferase
	AFK63_12535	1.900	Dihydrolipoamide succinyltransferase
	AFK63_16660	2.441	Succinate-semialdehyde dehydrogenase
Other glycan degradation	AFK63_14170	2.011	$\beta$ -D-galactosidase
Benzoate degradation	AFK63_08975	2.202	Tautomerase PptA

**Table S3.** Bacterial strains and media used in this study.

Bacterial strain	Culture medium	Source
<i>Aeromonas hydrophila</i>	TSB	LS-SHOU, China
<i>Aeromonas hydrophila</i> ATCC35654	TSB	ATCC, United States
<i>Enterobacter cloacae</i> ATCC13047	TSB	Biobw, China
<i>Enterobacter cloacae</i>	LB	LS-SHOU, China
<i>Enterobacter sakazakii</i> CMCC45401	TSB	Biobw, China
<i>Escherichia coli</i> ATCC8739	TSB	Biobw, China
<i>Escherichia coli</i> K12	TSB	IIM, China
<i>Escherichia coli</i> ATCC25922	LB	ATCC, United States
<i>Listeria monocytogenes</i> ATCC19115	BHI	Biobw, China
<i>Pseudomonas aeruginosa</i> ATCC9027	TSB	Biobw, China
<i>Pseudomonas aeruginosa</i> ATCC27853	TSB	Biobw, China
<i>Salmonella enterica</i> subsp. <i>enterica</i> (ex Kauffmann and Edwards) Le Minor and Popoff serovar Choleraesuis ATCC13312	TSB	ATCC, United States
<i>Salmonella enterica</i> subsp. <i>enterica</i> (ex Kauffmann and Edwards) Le Minor and Popoff serovar Vellore ATCC15611	TSB	ATCC, United States
<i>Salmonella paratyphi</i> -A CMCC50093	TSB	GCCC, China
<i>Shigella dysenteriae</i> CMCC51252	TSB	GCCC, China
<i>Shigella flexneri</i> CMCC51572	TSB	GCCC, China
<i>Shigella flexneri</i> ATCC12022	TSB	ATCC, United States
<i>Shigella flexneri</i> CMCC51574	TSB	GCCC, China
<i>Shigella sonnei</i> ATCC25931	TSB	ATCC, United States
<i>Shigella sonnei</i> CMCC51592	TSB	GCCC, China
<i>Staphylococcus aureus</i> GIM1.160	TSB	GCCC, China
<i>Staphylococcus aureus</i> ATCC25923	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC8095	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC29213	TSB	ATCC, United States
<i>Staphylococcus aureus</i> ATCC6538	TSB	ATCC, United States
<i>Staphylococcus aureus</i> GIM1.441	TSB	LS-SHOU, China
<i>Vibrio alginolyticus</i>	TSB	LS-SHOU, China
<i>Vibrio alginolyticus</i> ATCC17749	TSB	ATCC, United States
<i>Vibrio alginolyticus</i> ATCC33787	TSB	ATCC, United States
<i>Vibrio fluvialis</i> ATCC33809	Marine 2216	ATCC, United States
<i>Vibrio harvey</i> ATCC BAA-1117	Marine 2216	ATCC, United States
<i>Vibrio harveyi</i> ATCC33842	Marine 2216	ATCC, United States
<i>Vibrio metschnikovii</i> ATCC700040	Marine 2216	ATCC, United States
<i>Vibrio mimicus</i> bio-56759	TSB	Biobw, China
<i>Vibrio parahaemolyticus</i> ATCC17802	TSB	ATCC, United States
<i>Vibrio parahaemolyticus</i> B3-13	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B4-10	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B5-29	TSB	LS-SHOU, China
<i>Vibrio parahaemolyticus</i> B9-35	TSB	LS-SHOU, China
<i>Vibrio vulnificus</i> ATCC27562	TSB	Biobw, China
<i>Vibrio vulnificus</i>	TSB	LS-SHOU, China

ATCC: American Type Culture Collection, United States; GCCC, Guangdong Culture Collection Center, Guangzhou, China; IIM, Institute of Industrial Microbiology, Shanghai, China; LS-SHOU, Laboratory stock, Shanghai Ocean University, Shanghai, China.