Supplementary Table 1 Primers and restriction digest sites used in the present study

Targer gene	primer	Restriction digest site
ansB	sense primer:5'-CGAGCTCATGGAGTTTTTCAAAAAGACgg-3' antisense primer: 5'-CCCTCGAGTTAGTACTGATTGAAGA-3'	*Sal*I-*Xho*I
SodB	sense primer:5'-GCCGGATCCATGTCATTCGAATTACCT-3' antisense primer:5'-CGGAAGCTTTTATGCAGCGAGATTTTT-3'	*BamH*I-*Hind*III
hemX	sense primer: 5'-GTA GGATCC ATGACGGAACAAGA-3' antisense primer: 5'-ATT GAATTC TTATTCTCCTTGCGGC-3'	*BamH*I-*EcoR*I
*fdoG**	sense primer: 5'-TA GGATCC ATGCAGGTCAGCAGAAG-3' antisense primer: 5'-AT GAATTC CATCCCCATATTGCCGA-3	*BamH*I-*EcoR*I
*fdnG**	sense primer: 5'-ATA GAATTC ATGGACGTCAGTCGCA-3 antisense primer: 5'-AAC AAGCTT TTACGCCTTCTCGATG-3'	*EcoR*I-*Xho*I
fdnH	sense primer: 5'-TATGAATTC ATGGCTATGGAAACGC-3' antisense primer: 5'-TTGCTCGAG TTACTCATGATGATCCT-3'	*EcoR*I-*Xho*I
*narG**	sense primer: 5'- ACG GGATCC ATGAGTAAATTCCTG-3' antisense primer: 5'-TGCCTCGAG TTTCACATCGTCATAG-3'	*BamH*I-*Xho*I

*: A fragment of these genes was cloned.

Supplementary Table 2 Identification proteins of *E. coil* K-12 membrane fractions by MALDI-TOF MS/MS analysis.

Spot No.	Protein	Gene name	Location [a]	Swissprot No.	Predicted MW	Protein Score	Total Ion Score	Total Ion C. I. %
1	Formate dehydrogenase-O, major subunit	*fdoG*	C	P32176	112,431	593	394	100
2	Respiratory nitrate reductase 1 alpha chain	*narG*	I	P09152	140,401	465	217	100
3	Respiratory nitrate reductase 1 alpha chain	*narG*	I	P09152	140,401	323	124	100
4	Respiratory nitrate reductase 1 alpha chain	*narG*	I	P09152	140,401	279	130	100
5	Outer membrane protein assembly factor yaeT	*yaeT*	O	P0A941	90,497	519	273	100
6	Formate dehydrogenase, nitrate-inducible, major subunit	*fdnG*	P	P24183	112,845	266	149	100
7	Outer membrane protein assembly factor yaeT	*yaeT*	O	P0A941	90,497	124	60	100
8	Formate dehydrogenase-O, major subuni	*fdoG*	C	P32176	112,431	545	364	100
9	Peptidyl-prolyl cis-trans isomerase D	*ppiD*	I	P0ADY1	68,108	249	176	100
10	PTS system mannose-specific EIIAB component	*manX*	C/I	P69798	35,026	543	386	100
11	60 kDa chaperonin - Escherichia coli O6	*groL*	C	P0A6F6	57,293	388	306	100
12	Respiratory nitrate reductase 1 beta chain	*narH*	I	P11349	58,029	389	254	100
13	Fumarate reductase flavoprotein subunit	*frdA*	C	P00363	65,930	487	354	100
14	NADH-quinone oxidoreductase subunit C/D	*nuoC*	I	P33599	68,651	397	278	100
15	Glycerol-3-phosphate acyltransferase	*plsB*	I	P0A7A7	91,324	271	154	100
16	Formate acetyltransferase 1	*pflB*	C	P09373	85,303	441	270	100
17	NADH-quinone oxidoreductase subunit G	*nuoG*	I	P33602	100,236	528	376	100
18	NADH-quinone oxidoreductase subunit G	*nuoG*	I	P33602	100,236	499	327	100

19	Elongation factor G	*fusA*	C	P0A6M9	77,533	499	268	100
20	Anaerobic dimethyl sulfoxide reductase chain A precursor	*dmsA*	I	P18775	903,413	458	318	100
21	30S ribosomal protein S1	*rpsA*	C	P0AG68	61,123	408	304	100
22	Chaperone protein dnaK	*dnaK*	C/I	P0A6Y9	69,073	215	167	100
23	Fumarate reductase flavoprotein subunit	*frdA*	C	P00363	65,930	461	336	100
24	D-lactate dehydrogenase	*dld*	I	P06149	64,572	364	251	100
25	Succinate dehydrogenase flavoprotein subunit	*sdhA*	I	P0AC42	64,381	558	432	100
26	Succinate dehydrogenase flavoprotein subunit	*sdhA*	I	P0AC42	64,381	508	383	100
27	Succinate dehydrogenase flavoprotein subunit	*sdhA*	I	P0AC42	64,381	448	368	100
28	Succinate dehydrogenase flavoprotein subunit	*sdhA*	I	P0AC42	64,381	471	351	100
29	Bifunctional purine biosynthesis protein purH	*purH*	C	Q8FB68	57,257	382	240	100
30	Phosphoenolpyruvate carboxykinase [ATP]	*pckA*	C	Q8FCU4	59,606	460	368	100
31	Anaerobic dimethyl sulfoxide reductase chain A precursor	*dmsA*	I	P18775	90,341	86	52	99.987
32	ATP synthase subunit alpha	*atpA*	I	P0ABB1	55,188	610	462	100
33	ATP synthase subunit beta	*atpD*	I	P0ABB5	50,294	602	410	100
34	Aerobic glycerol-3-phosphate dehydrogenase	*glpD*	C	P13035	56,715	413	257	100
35	Aspartate ammonia-lyase	*aspA*	C	P0AC39	52,323	212	141	100
36	NADH-quinone oxidoreductase subunit F	*nuoF*	P	P31979	49,261	312	197	100
37	Enolase	*eno*	C	P0A6Q0	45,626	380	256	100
38	Elongation factor Tu	*tufA*	C/I	P0A6N2	43,286	489	316	100
39	6-phosphogluconate dehydrogenase	*gnd*	C	P00350	51,449	341	174	100
40	Serine hydroxymethyltransferase	*glyA*	C	P0A826	45,288	436	285	100

41	2,3-bisphosphoglycerate-independent	*gpmI*	C	P37689	56,158	259	153	100
42	Trigger factor	*tig*	C	Q8FKA7	48,221	217	160	100
43	3-oxoacyl-[acyl-carrier-protein] synthase 1	*fabB*	C	P0A953	42,586	73	58	99.998
44	Phosphoglycerate kinase	*pgk*	C	P0A7A0	41,093	491	384	100
45	Hydrogenase-1 large chain	*hyaB*	I	P0ACD8	66,211	69	23	94.62
46	Fructose-bisphosphate aldolase class 2	*fbaA*	U	P0AB71	39,123	260	190	100
47	UDP-glucose 4-epimerase	*galE*	C	P09147	37,242	425	307	100
48	Maltose-binding periplasmic protein precursor	*malE*	P	P0AEX9	43,360	391	261	100
49	Dihydroorotate dehydrogenase	*pyrD*	I	P0A7E1	36,751	580	420	100
50	Maltose-binding periplasmic protein precursor	*malE*	P	P0AEX9	43,360	104	86	100
51	Glyceraldehyde-3-phosphate dehydrogenase A	*gapA*	C	P0A9B3	35,510	470	398	100
52	L-asparaginase 2 precursor	*ansB*	P	P00805	36,828	47	24	
53	D-galactose-binding periplasmic protein precursor	*mglB*	P	P0AEE5	35,690	276	105	100
54	Outer membrane protease ompP precursor-	*ompP*	O	P34210	35,477	425	270	100
55	Signal peptidase I	*lepB*	I	P00803	35,938	206	156	100
56	Lipoprotein yfgL precursor	*yfgL*	O	P77774	41,861	446	328	100
57	L-lactate dehydrogenase [cytochrome]	*lldD*	I	Q8FCB1	42,687	205	84	100
58	L-lactate dehydrogenase [cytochrome]	*lldD*	I	Q8FCB1	42,687	202	101	100
59	Maltose/maltodextrin import ATP-binding protein malK	*malK*	I	P68187	40,965	502	429	100
60	Putative uroporphyrinogen-III C-methyltransferase	*hemX*	I	P09127	42,937	516	345	100
61	D-alanyl-D-alanine carboxypeptidase dacA precursor	*dacA*	I	P0AEB3	44,416	311	160	100

62	Lipoprotein yfgL precurso	*yfgL*	O	P77774	41,861	463	338	100
63	Lipoprotein 34 precursor	*nlpB*	O	P0A903	36,820	371	249	100
64	PTS system mannose-specific EIIAB component	*manX*	C/I	P69798	35,026	480	310	100
65	Mannose permease IID component	*manZ*	I	P69806	31,283	217	170	100
66	UPF0169 lipoprotein yfiO precursor	*yfiO*	O	P0AC0	27,812	424	267	100
67	Small-conductance mechanosensitive channel	*mscS*	I	P0C0S1	30,877	499	391	100
68	Formate dehydrogenase, nitrate-inducible, cytochrome b556(fdn) subunit	*fdnI*	I	P0AEK7	25,351	109	87	100
69	Respiratory nitrate reductase 1 gamma chain	*narI*	I	P11350	25,480	167	145	100
70	Fumarate reductase iron-sulfur subunit	*frdB*	C	P0AC48	27,105	287	220	100
71	Uncharacterized ABC transporter ATP-binding protein yhbG	*yhbG*	I	P0A9V	26,784	283	206	100
72	ATP synthase gamma chain	*atpG*	I	P0ABA7	31,557	486	336	100
73	Protein YdgA precursor	*ydgA*	I	P77804	54,689	112	83	100
74	Succinate dehydrogenase iron-sulfur subunit	*sdhB*	I	P07014	26,752	242	164	100
75	Succinate dehydrogenase iron-sulfur subunit	*sdhB*	I	P07014	26,752	246	180	100
76	Phosphatidylserine decarboxylase proenzyme	*psd*	I	P0A8K2	35,912	89	40	99.892
77	Elongation factor Ts	*tsf*	C	P0A6P2	30,404	343	241	100
78	Tagatose-1,6-bisphosphate aldolase gatY	*gatY*	C	P37192	30,793	152	70	100
79	Cysteine synthase A	*cysK*	C	P0ABK5	34,468	310	237	100
81	Succinate dehydrogenase iron-sulfur subunit	*sdhB*	C	P07014	26,752	331	228	100
82	Superoxide dismutase [Fe]	*sodB*	C/I	P0AGD4	21,253	497	453	100
83	Alkyl hydroperoxide reductase subunit C	*ahpC*	C	P0AE09	20,748	341	271	100

84	NADH-quinone oxidoreductase subunit G	*nuoG*	I	P33602	100,236	501	364	100
85	Uridine phosphorylase	*udp*	C	P12758	27,142	132	70	100
86	NADH-quinone oxidoreductase subunit G	*nuoG*	I	Q8XCX2	100,240	361	260	100
87	Fumarate reductase flavoprotein subunit	*frdA*	C	P00363	65,930	170	129	100
88	Formate dehydrogenase, cytochrome b556(fdo) subunit	*fdoI*	I	P0AEL0	24,606			
89	Formate dehydrogenase, nitrate-inducible, iron-sulfur subunit	*fdnH*	I	P0AAJ3	32,218	59	45	99.949
90	Uncharacterized ABC transporter ATP-binding protein yhbG	*yhbG*	I	P0A9V	26,784	178	87	100
91	Outer membrane protein assembly factor yaeT precursor	*yaeT*	O	P0A941	90,497	311	154	100
93	Pyruvate dehydrogenase E1 component	*aceE*	C	P0AFG8	99,668	115	46	100
94	Outer membrane protein OmpW precursor	*ompW*	O	P0A915	22,928	120	85	100
95	Outer membrane protein Slp	*slp*	O	P37194	20,982	341	271	100
96	Uncharacterized lipoprotein ybjP	*ybjP*	O	P75818	19,009			

[a]: O, outer membrane protein; I, inner membrane protein; C, cytoplasmic protein; P, periplasmic protein; U, unknown.