

Table S1 The eleven single base mutations in the genome of strain 4WGX

Position	Sequence change	Gene	Protein change	Protein function	Ref
199908	C→T	<i>bamA</i>	R661C	outer membrane protein assembly factor BamA	[1]
419625	G→T	<i>brnQ</i>	V271F	branched chain amino acid transporter BrnQ	[2]
547694	A→G	<i>fdrA</i>	E38E	putative oxamate carbamoyltransferase FdrA	[3]
556858	A→T	<i>ybcJ</i>	L36Q	putative RNA-binding protein YbcJ	[4]
624402	C→T	<i>fepB</i>	R99C	ferric enterobactin ABC transporter periplasmic binding protein	[5]
1065700	C→T	<i>agp</i>	R415C	glucose-1-phosphatase	[6]
1093686	T→C	<i>dgcT</i>	V130A	putative diguanylate cyclase DgcT	[7]
1303712	A→G	<i>oppB</i>	S273G	murein tripeptide ABC transporter/oligopeptide ABC transporter inner membrane subunit OppB	[8]
2019202	C→T	<i>fliK</i>	T171I	flagellar hook-length control protein	[9]
2866111	A→G	<i>ygbN</i>		putative transporter YgbN	[10]
2906975	C→G	<i>eno</i>	D450H	enolase	[11]

References

1. Doyle, M.T.; Bernstein, H.D. BamA forms a translocation channel for polypeptide export across the bacterial outer membrane. *Mol. Cell.* **2021**,*81*,2000-2012.
2. Dutta, S.; Corsi, I.D.; Bier, N.; Koehler, T.M. BrnQ-type branched-chain amino acid transporters influence *Bacillus anthracis* growth and virulence. *mBio.* **2022**,*25*, e0364021.
3. Kim, N.Y.; Lee, Y.J.; Park, J.W.; Kim, S.N.; Kim, E.Y.; Kim, Y.; Kim, O.B. An *Escherichia coli* FdrA Variant Derived from Syntrophic Coculture with a Methanogen Increases Succinate Production Due to Changes in Allantoin Degradation. *mSphere.* **2021**,*6*,e0065421.
4. Volpon, L.; Lievre, C.; Osborne, M.J.; Gandhi, S.; Iannuzzi, P.; Larocque, R.; Cygler, M.; Gehring, K.; Ekiel, I. The solution structure of YbcJ from *Escherichia coli* reveals a recently discovered *alphal* motif involved in RNA binding. *J. Bacteriol.*

2003,185,4204-4210.

5. Chu, B.C.; Otten, R.; Krewulak, K.D.; Mulder, F.A.; Vogel, H.J. The solution structure, binding properties, and dynamics of the bacterial siderophore-binding protein FepB. *J. Biol. Chem.* **2014**,289,29219-29234.

6. Lee, D.C.; Cottrill, M.A.; Forsberg, C.W.; Jia, Z. Functional insights revealed by the crystal structures of *Escherichia coli* glucose-1-phosphatase. *J. Biol. Chem.* **2003**,278,31412-31418.

7. Tagliabue, L.; Antoniani, D.; Maciąg, A.; Bocci, P.; Raffaelli, N.; Landini, P. The diguanylate cyclase YddV controls production of the exopolysaccharide poly-N-acetylglucosamine (PNAG) through regulation of the PNAG biosynthetic *pgaABCD* operon. *Microbiology.* **2010**,156,2901-2911.

8. Masulis, I.S.; Sukharycheva, N.A.; Kiselev, S.S.; Andreeva, Z.S.; Ozoline, O.N. Between computational predictions and high-throughput transcriptional profiling: in depth expression analysis of the OppB trans-membrane subunit of *Escherichia coli* OppABCDF oligopeptide transporter. *Res. Microbiol.* **2020**,171,55-63.

9. Minamino, T.; Inoue, Y.; Kinoshita, M.; Namba, K. FliK-Driven Conformational Rearrangements of FlhA and FlhB Are Required for Export Switching of the Flagellar Protein Export Apparatus. *J. Bacteriol.* **2020**,202, e00637-19.

10. Lolkema, J.S. Domain structure and pore loops in the 2-hydroxycarboxylate transporter family. *J. Mol. Microbiol. Biotechnol.* **2006**,11,318-325.

11. Poyner, R.R.; Larsen, T.M.; Wong, S.W.; Reed, G.H. Functional and structural changes due to a serine to alanine mutation in the active-site flap of enolase. *Arch.*

Biochem. Biophys. **2002**,401,155-163.