

Additional file 3. Genomic context and flux-converging pattern analyses for shikimic acid and putrescine production in

Escherichia coli

Reaction	Gene	<i>C₇J_B</i> (Glucose)	Enzyme	Metabolism	EC number	Score					
						>0.95	>0.9	>0.85	>0.8	>0.75	>0.7
Central metabolism											
The detailed information of grouped reactions in central metabolism of <i>E. coli</i> is represented in Supporting Information of Park et al. (2010)[1].											
For shikimic acid production											
DDPA	<i>aroG</i>		3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase	Shikimate biosynthetic pathway	2.5.1.54			<i>tyrA</i>			
DHQS	<i>aroB</i>	<i>C₇J_B</i>	3-dehydroquinate synthase	Shikimate biosynthetic pathway	4.2.3.4	<i>aroK, aroL, aroA, aroE, aroD</i>	<i>aroC, ydiB</i>			<i>kdsA, alaS</i>	<i>ileS, hofQ, pheA, mrcA, pfs, ubiE</i>
DHQD	<i>aroD</i>	<i>C₇J_B</i>	3-dehydroquinate dehydratase	Shikimate biosynthetic pathway	4.2.1.10	<i>ydiB, aroB</i>	<i>aroA, aroE, ydiN, aroK</i>	<i>ydiM</i>		<i>aroC</i>	
SHK3Dr	<i>aroE</i> <i>ydiB</i>	<i>C₇J_B</i>	shikimate dehydrogenase	Shikimate biosynthetic pathway	1.1.1.25	<i>aroB, aroA</i>	<i>aroC, aroD</i>	<i>yrdB, rimN, yrdD</i>		<i>rimL, aroK</i>	<i>smf, smg, aroL</i>

For putrescine production

GLUDy	<i>gdhA</i>	C ₅ J _{CE} / C ₅ J _{DE} / C ₅ J _B	glutamate dehydrogenase	Putrescine biosynthetic pathway	1.4.1.4						
ACGS	<i>argA</i>	C ₇ J _{CE} / C ₇ J _{DE} / C ₇ J _B	N- acetylglutamate synthase	Putrescine biosynthetic pathway	2.3.1.1	<i>argC</i>	<i>argH</i>	<i>argB</i>	<i>argE</i>	<i>topA</i>	
ACGK	<i>argB</i>	C ₇ J _{CE} / C ₇ J _{DE} / C ₇ J _B	acetylglutamate kinase	Putrescine biosynthetic pathway	2.7.2.8	<i>argC</i>	<i>argH, astC, argD</i>	<i>argA</i>	<i>argE, argI</i>	<i>argF, argG</i>	<i>carA</i>
AGPR	<i>argC</i>	C ₇ J _{CE} / C ₇ J _{DE} / C ₇ J _B	N-acetyl-g- glutamyl- phosphate reductase	Putrescine biosynthetic pathway	1.2.1.38	<i>argB, argA</i>	<i>argH, astC, argD</i>			<i>rplM, rpsI, argG, argI, argF, argR</i>	<i>argE, rimK</i>
ACOTA	<i>argD</i>	C ₇ J _{CE} / C ₇ J _{DE} / C ₇ J _B	acetylornithine transaminase	Putrescine biosynthetic pathway	2.6.1.11		<i>argC, argB</i>				
ACODA	<i>argE</i>	C ₇ J _{CE} / C ₇ J _{DE} / C ₇ J _B	acetylornithine deacetylase	Putrescine biosynthetic pathway	3.5.1.16				<i>argB, argC, argA</i>		
ORNDc	<i>speC</i> <i>speF</i>	C ₅ J _{CE} / C ₅ J _{DE} / C ₅ J _B	Ornithine decarboxylase	Putrescine biosynthetic pathway	4.1.1.17				<i>potE</i> <i>potE</i>		

References

1. Park JM, Kim TY, Lee SY: **Prediction of metabolic fluxes by incorporating genomic context and flux-converging pattern analyses.** *Proc Natl Acad Sci U S A* 2010, **107**:14931-14936.