

**S4 Table. Sequence evolution of *evgS* based on dN/dS analysis.**

	All 10 <i>E. coli</i> isolates			Group A			Group B2		
Gene	dN <sup>a</sup>	dS <sup>b</sup>	dN/dS <sup>c</sup>	dN	dS	dN/dS	dN	dS	dN/dS
<i>evgS</i>	0.0116	0.1143	0.1013	0.0016 <sup>d</sup> , 0.0006 <sup>e</sup>	0.0051 <sup>d</sup> , 0.0014 <sup>e</sup>	0.3240 <sup>d</sup> , 0.4409 <sup>e</sup>	0.0009 <sup>f</sup> , 0.0011 <sup>g</sup>	0.0116 <sup>f</sup> , 0.0152 <sup>g</sup>	0.0802 <sup>f</sup> , 0.0744 <sup>g</sup>
<i>evgS</i> (1-537)	0.0136	0.1232	0.1101	0.0027	0.0114	0.2328	0.0006	0.0057	0.1131
<i>evgS</i> (87-234)	0.0146	0.1269	0.1149	0.0059	0.0131	0.4529	0	0	ND <sup>h</sup>
<i>evgA</i>	0	0.0609	0	0	0	ND <sup>h</sup>	0	0.0079	0
<i>yfdE</i>	0.0064	0.0965	0.0658	0	0.0105	0	0.0043	0.0498	0.0856
<i>barA</i>	0.0004	0.0671	0.0056	0	0.0031	0	0.0004	0.0388	0.0097
<i>arcB</i>	0.0008	0.0627	0.0134	0.0004	0	ND <sup>h</sup>	0.0003	0.0139	0.0239

<sup>a</sup>dN – Average number of substitutions per non-synonymous site

<sup>b</sup>dS – Average number of substitutions per synonymous site

<sup>c</sup>dN/dS – Ratio of rates of non-synonymous (dN) and synonymous (dS) substitutions; also known as Ka/Ks

<sup>d,f</sup> values corresponding to the *E. coli* strains included in this study belonging to phylogenetic groups A and group B2, respectively

<sup>e,g</sup> values corresponding to all the *E. coli* strains from phylogenetic groups A and B2, respectively, derived from the MLST-based tree (Lasaro, Liu et al. 2014)

<sup>h</sup>ND – Not determined

Lasaro, M., Z. Liu, et al. (2014). "Escherichia coli isolate for studying colonization of the mouse intestine and its application to two-component signaling knockouts." *J Bacteriol* **196**(9): 1723-1732.