

Table 2 The joint histogram divergence of trinucleotide transition probability matrixes of bacterial genomes

	<i>L. lac_MG</i>	<i>L. lac_SK</i>	<i>L. lac_I1</i>	<i>S. pyo_M1</i>	<i>P. pen_AT</i>	<i>S. aur_US</i>	<i>A. met_QY</i>
<i>L. lac_MG</i>	0						
<i>L. lac_SK</i>	35.674	0					
<i>L. lac_I1</i>	87.366	89.496	0				
<i>S. pyo_M1</i>	1 020.933	1 043.886	1 202.584	0			
<i>P. pen_AT</i>	1 090.625	1 111.164	1 193.150	1 230.305	0		
<i>S. aur_US</i>	1 291.842	1 311.779	1 324.448	1 475.062	1 062.187	0	
<i>A. met_QY</i>	2 305.814	2 344.976	2 570.574	1 586.869	1 916.826	1 768.208	0