Table 1 The Euclidian distance of trinucleotide transition probability matrixes of bacterial genomes

	*L. lac*_MG	*L. lac*_SK	*L. lac*_I1	*S. pyo*_M1	*P. pen*_AT	*S. aur*_US	*A. met*_QY
*L. lac*_MG	0						
*L. lac*_SK	0. 044	0					
*L. lac*_I1	0. 062	0. 073	0				
*S. pyo*_M1	0. 291	0. 295	0. 308	0			
P. pen_AT	0. 321	0. 324	0. 324	0. 305	0		
*S. aur*_US	0. 392	0. 396	0. 390	0. 392	0. 334	0	
*A. met*_QY	0. 382	0. 388	0. 397	0. 320	0. 349	0. 372	0