

Table S1. Average nucleotide identity values between the genome of strain V-78 and closely related type strains inferred by the Protologger using FastANI (v1.2) algorithm (Jain et al. 2018)

Strain code	Type strain	ANI(%)
Strain V-78	<i>Plesiomonas shigelloides</i>	97.1
	<i>Obesumbacterium proteus</i>	78.9
	<i>Serratia ficaria</i>	78.9
	<i>Pectobacterium parmentieri</i>	78.7
	<i>Enterobacter hormaechei</i>	78.7
	<i>Salmonella enterica</i>	78.7
	<i>Cronobacter sakazakii</i>	78.7
	<i>Yersinia entomophaga</i>	78.7
	<i>Yersinia pestis</i>	78.6
	<i>Chania multitudinisentens</i>	78.6
	<i>Sodalis praecaptivus</i>	78.6
	<i>Lonsdalea quercina</i>	78.5
	<i>Serratia quinivorans</i>	78.5
	<i>Enterobacter cloacae</i>	78.5
	<i>Citrobacter amalonaticus</i>	78.4
	<i>Serratia fonticola</i>	78.4
	<i>Serratia proteamaculans</i>	78.2
	<i>Pantoea allii</i>	78.1
	<i>Serratia nematodiphila</i>	78.1
	<i>Klebsiella pneumoniae</i>	78.1
	<i>Hafnia paralvei</i>	77.9
	<i>Citrobacter freundii</i>	77.9
	<i>Rouxiella badensis</i>	77.8
	<i>Citrobacter pasteurii</i>	77.8
	<i>Enterobacter ludwigii</i>	77.8
	<i>Enterobacter soli</i>	77.7
	<i>Serratia marcescens</i>	77.6
	<i>Raoultella planticola</i>	77.6
	<i>Pantoea cypripedii</i>	77.6
	<i>Citrobacter braakii</i>	77.5
	<i>Serratia grimesii</i>	77.5
	<i>Buttiauxella brennerae</i>	77.5
	<i>Buttiauxella noackiae</i>	77.5
	<i>Citrobacter werkmanii</i>	77.5
	<i>Raoultella ornithinolytica</i>	77.5
	<i>Rouxiella chamberiensis</i>	77.5
	<i>Buttiauxella ferragutiae</i>	77.5
	<i>Serratia odorifera</i>	77.5
	<i>Buttiauxella gaviniae</i>	77.4
	<i>Pantoea agglomerans</i>	77.4
	<i>Rouxiella silvae</i>	77.4
	<i>Buttiauxella agrestis</i>	77.3
	<i>Dickeya chrysanthemi</i>	77.3
	<i>Pectobacterium carotovorum</i>	77.3
	<i>Serratia plymuthica</i>	77.2
	<i>Proteus hauseri</i>	76.7