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)

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