

**Table S1.** Genome relatedness among strains Mo2-6<sup>T</sup>, S9, and KG4-3<sup>T</sup> and 50Mo3-2 and their closely related *Staphylococcus* type strains

Taxa: 1, strain Mo2-6<sup>T</sup> (CP150682-3); 2, strain S9 (CP150678-81); 3, strain KG4-3<sup>T</sup> (CP166245-6); 4, strain 50Mo3-2 (CP191146-50); 5, *S. equorum* subsp. *equorum* DSM 20674<sup>T</sup> (CP118982-7); 6, *S. pseudoxylosus* S04009<sup>T</sup> (RCVN000000000); 7, *S. xylosus* NCTC 11043<sup>T</sup> (UHEI000000000)

		dDDH <sup>†</sup> value (%)						
		1	2	3	4	5	6	7
ANI <sup>†</sup> value (%)	1	–	96.3	23.9	24.2	60.1	23.7	23.9
	2	99.6	–	23.9	23.8	59.8	23.7	23.9
	3	80.3	80.2	–	98.9	23.8	59.8	50.5
	4	80.3	80.2	99.9	–	23.8	59.6	50.5
	5	95.0	94.9	80.1	80.0	–	23.7	23.9
	6	80.0	80.0	94.8	94.9	80.0	–	50.6
	7	80.1	80.0	93.1	93.1	80.2	93.2	–

<sup>†</sup>ANI, average nucleotide identity; dDDH, digital DNA–DNA hybridization