Table S1. Statistics for genome assemblies.

Strain*	Read length (# channels)†	# of PE reads‡	# of Contigs§	Size (Mb)¶	N50 (kb)‖	Predicted # CDSs**
S. fredii NGR234*	-	-	-	6.9	-	6322
S. fredii USDA207	32mer (2)	22,136,363	291	6.5	27.8	6995
S. fredii USDA257	32mer (2)	27,603,487	384	7.0	26.7	6723
B. japonicum USDA6	32mer (3)	20,995,355	788	8.7	19.6	7960
B. japonicum USDA110*	-	-	-	9.1	-	8317
B. japonicum USDA122	72mer (0.5)	19,430,723	186	8.9	31	8107
B. japonicum USDA123	32mer (3)	27,393,134	815	9.1	21.6	8361
B. japonicum USDA124	32mer (3)	14,219,973	1285	8.9	19.3	7943