



e-X-tra Fig. S1. Structure analysis of 6,898 SNPs from 16 NGS FOSC from celery with symptoms of Fusarium yellows and 12 reference FOSC from the Broad Institute. All reads were mapped onto the assembled NRRL 34936 (*F. oxysporum* f. sp. *lycopersici* 4287 (Ma et al., 2010). SNPs that could be scored for all isolates were selected and a subset of 6,898 SNPs at a minimum of 5 kb apart were selected and analyzed using *structure* (Falush et al. 2003). FOSC clades are added for reference and mirror the *structure* analysis, except that the 10-gene phylogeny in Fig. 2 has the human pathogenic FOSC NRRL 32931 at the base of clade 3 whereas the isolate in the *structure* analysis here is within FOSC clade 2.