

Table S2. Genome assembly and quality data for the *S. marcescens* strains sequenced in this study.

	Contigs	Avg contig len	Min contig len	Max contig len	Min coverage	Max coverage	Genome size	CDS	% GC	ANI to db11
KZ2	20	240,066	1220	2,786,944	81	3,610	5,035,724	4689	59.8	95.08
KZ11	21	186,739	1221	1,990,358	134	4,000	5,036,791	4691	59.8	95.08
KZ19	24	209,266	1221	842,184	52	1,532	5,226,072	4844	59.5	95.02