



Figure S2. Amplicon sequencing for species identification of the Texas prickly pear isolate.

(A) Ethidium bromide-stained DNA following agarose gel electrophoresis of ladder and PCR products generated using the primer combinations shown at right and, as template, genomic DNA from strain MMY0358. The ladder was GeneRuler DNA Ladder Mix (Thermo Scientific #SM0331). The expected amplicon sizes shown at right reflect *S. cerevisiae* sequence. (B) BLAST alignment results for amplicon #2. Red lines indicate mismatches. (C) BLAST alignment results for amplicon #4. (D) Presumptive sites of primer binding in the reference *S. paradoxus* genome. Bold indicates predicted identity with the template. For *FLO11*, the full amplicon was sequenced and is also shown ("MMY0358 PCR"). The extra three nucleotides 5' of the predicted primer binding site are part of the tandem sequence repeats found in *FLO11* to which the 5'ScereHOfw primer is predicted to anneal. The sequence of one such repeat is shown, and additional copies of this repeat in the sequenced amplicon are shown as arrows in the illustration below. (E) BLAST alignment results for the contig assembled from four *ITS* amplicons (see Materials and Methods).