Supplemental Figure 1. Identification and complementation of the msf1 mutant.

(A) DNA blot analysis. Total DNA from wild type and msf1 was digested with Hind III and BamH I, fractionated by gel electrophoresis, blotted and hybridized with a probe of apHVIII (paromomycin resistance) listed in Suppl. Table 2.
(B) Mapping of the insertion of *apHVIII* in the nuclear genome of *msf1*. Primers used for PCR are indicated and the corresponding PCR products separated by agarose gel electrophoresis are shown. Sequences of the primers are listed in Suppl. Table 2.

(C) Characterization of transformants complementing the *msf1* mutant. Products obtained in the different strains by semi-quantitative RT-PCR are shown. Transcript level of CBLP gene was used as a loading control. Photosynthetic activity was estimated by measuring Φ(II) and is shown on a false color scale. All experiments were repeated more than three times and similar results were obtained.

(D) Immunoblot analysis of the PSI proteins in the indicated strains. Total proteins (20 µg, per lane) were separated by 12% SDS-PAGE followed by immunoblot detection. Similar results were obtained in more than three independent experiments.

(E) Tetrad analysis of a cross between *msf1* and wild type (CC400). Growth patterns of the representative tetrads on TAP (upper) and TAP containing paromomycin (lower) are shown on the left panels. Φ(II) values of the representative tetrads on TAP are shown on the upper-right panel with a false color scale. The lower-right panel shows the PCR analysis of tetrad 1. * unspecific band.