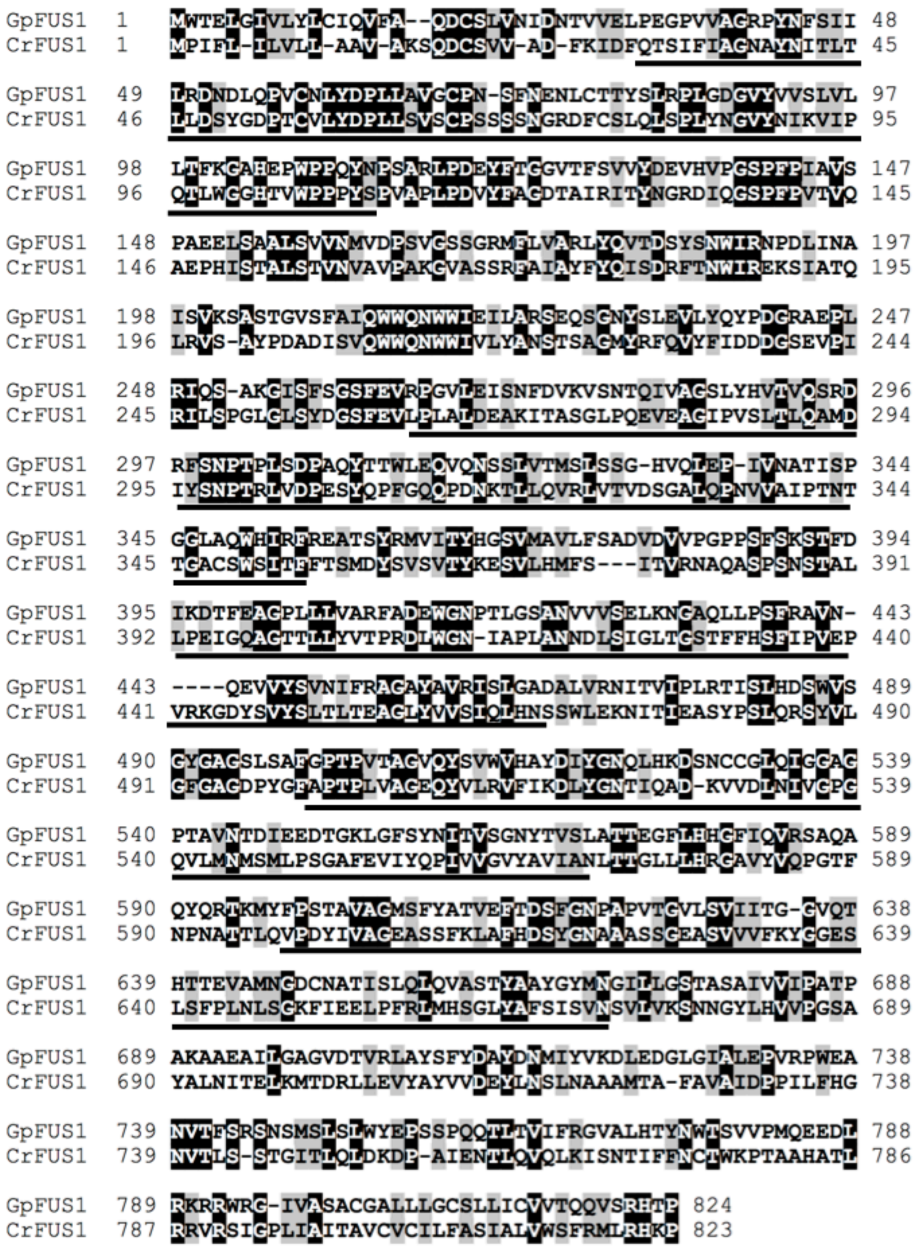

**Figure S6. Alignment of the amino acid sequences of the GpFUS1 and CrFUS1 proteins.** Identical or similar residues have solid or shaded backgrounds, respectively. Underlined residues are aligned in Figure S7. The GC content of *GpFUS1* CDS and introns are mediate (~50%), showing a common feature found in most of the previously identified mating type-specific genes (*CrFUS1*: 47.7%; *CrMID*: 50.5%; *GpMID*: 52.9%; *GpMTD1*: 55.5%).