Supplemental information for *MuTAIL library construction and sequence assembly*

In order to ensure that MuTAIL PCR products were derived exclusively from germinal Mu insertions in three *vp8* mutants (*vp8-umu1*, *vp8-umu2*, and *vp8-umu3*), Mu-inactive *vp8* heterozygous seeds (non-spotted) were selected using the *bz1-mum9* marker for somatic transposition activity. Genomic DNA was prepared from a pool of nine seedlings grown from mixed non-mutant wild type and heterozygous seeds and used for MuTAIL PCR library construction. The library construction and processing and assembly of the sequences were described previously (Settles et al., 2004; McCarty et al, 2005). We obtained single-pass sequence reads from 384 random MuTAIL clones from each of three *vp8* libraries.

In order to identify candidate clones for *vp8* locus, we performed *in silico* subtraction against a large collection MuTAIL sequences derived from UniformMu independent lines (McCarty et al., 2005). The assemblied MuTAIL sequences were further mapped onto maize genomic sequences of Maize Assembled Genomic Island (MAGI, Fu et al, 2005). We reasoned that allelic Mu insertions in the three independent mutants would map to nearby locations in the maize genome. To identify allelic insertions in the dataset we performed a cluster analysis based on BLASTN searches of MAGI using the protocol described in McCarty et al. (2005). As a result of this analysis, we identified MuTAIL sequences from the *vp8-umu1* and *vp8-umu2* libraries that mapped to the same MAGI sequence (MAGI_111554). The MuTAIL sequences that were derived from *vp8* locus of *vp8-umu1* and *vp8-umu2* are available in the GenBank (CC800289 and CC800332 for *vp8-umu1*, CC800544, CC800549, and CC800564 for *vp8-umu2*). Analysis of the MAGI sequence by BLASTX (Altschul et al., 1997) detected proteins that are homologous to glutamate carboxypeptidases from various organisms including homologs of the Arabidopsis ALTERED MERISTEM PROGRAMMING 1 (AMP1) (Helliwell et al., 2001).

In order to confirm presence of Mu insertions in the maize carboxypeptidase gene in the *vp8* mutants, we performed PCR analysis of the three mutant alleles using the gene specific primers and a partially degenerate Mu terminal inverted repeat (TIR) specific primer. By using the gene-specific primers, we confirmed the sites of Mu insertions detected by the MuTAIL PCR products in the *vp8-umu1* and *vp8-umu2* mutants as well as a third Mu insertion in *vp8-umu3* allele using both 5' and 3' gene-specific primers. The PCR-amplified products were sequenced to confirm that they contained *bona fide* Mu flanking sequences matching the MuTAIL products with a 9 bp host duplication (5'TCCGGCTCG3') which is a signature of a Mu insertion.

Fu, Y., Emrich, S.J., Guo, L., Wen, T.J., Ashlock, D.A., Aluru, S., Schnable, P.S. (2005) Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted genes. *Proc. Natl. Acad. Sci. U S A.*, **102**, 12282-12287.