



Supplemental Figure 1. Amino acid sequence alignment of Hsp100/ClpB from *Arabidopsis thaliana* (AtHsp101) (accession no. NP565083), *Thermus thermophilus* ClpB (TtClpB) (accession no. Q9RA63), *Saccharomyces cerevisiae* Hsp104 (ScHsp104) (accession no. NP013074), *Escherichia coli* ClpB (EcClpB) (accession no. NP417083) and ClpA from *E. coli* (accession no. NP415403). Identical residues are highlighted in black and conservative replacements in gray. Secondary structure elements as seen in the *T. thermophilus* ClpB structure appear over the alignment (see Lee et al., 2003). Conserved motifs are indicated below the alignment, as are the positions of the primers used for identification of the tilling mutants. Positions of each of the primary *hot1* mutations are indicated above the alignment in blue, suppressors mutations are in red, and tilling mutations having a wild-type phenotype are indicated in black.