Figure S1

Alignment of CCD1 amino acid sequences. Fourteen CCD1 primary structures deduced from DNA sequences originating from various plant families and including MtCCD1 (bold) are aligned using the program clustal of the HUSAR Genius Sequence Analysis Package and default parameters. Strictly conserved residues are highlighted in white letters on blue background. Residues shaded in red indicate highly conserved amino acids, yellow color marks a lesser degree of conservation. The sequences are displayed in the order of the computed dendrogram. The following sequences were used: CsCCD1, *Crocus sativus* AJ132927; ZmCCD1, *Zea mays* AY773278; AtCCD1, *Arabidopsis thaliana* AJ005813; CmCCD1, *Cucumis melo* DQ269462; RdCCD1, *Rosa damascena* EU327776; MtCCD1, *Medicago truncatula*, FM204879 (this work); PsCCD1, *Pisum sativum* AB080191; PvCCD1, *Phaseolus vulgaris* AY029525; CmCCD1 *Castanea mollisima* EF472600; VvCCD1, *Vitis vinifera*, AY856353; CaCCD1 *Coffea arabica* DQ157170; PhCCD1 *Petunia hybrida* AY576003; SlCCD1A (LeCCD1A) *Solanum lycopersicum* AY576001; SlCCD1B (LeCCD1B) *Solanum lycopersicum* AY576002.