**Additional file 4.** Protein characterisation of the carotenoid cleavage dioxygenases from *A. thaliana* and the *V. vinifera* orthologues present in the grapevine genome

<table>
<thead>
<tr>
<th>CCD</th>
<th>Accession1</th>
<th>Length (aa)</th>
<th>Subcellular localisation2</th>
<th>Transit peptide3</th>
<th>pI4</th>
<th>MW5</th>
<th>Conserved histidines (aa position)6</th>
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</thead>
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<tr>
<td>AtCCD1</td>
<td>At3g63520</td>
<td>538</td>
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<td>H222—H336—H490—H526</td>
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<td>65601.73</td>
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</table>

1 Accession number for the CCD protein sequences in TAIR (At-) (http://www.arabidopsis.org/) and PLAZA version 1 (At- and Vv-)

(http://bioinformatics.psb.ugent.be/plaza_v1/)

2 Softberry Protcomp (http://linux1.softberry.com/berry.phtml) prediction of the subcellular localisation of the predicted CCD protein sequence

3 Length (in amino acids) of predicted transit peptide from Softberry Protcomp prediction

4 Theoretical isoelectric point (pI) of the predicted CCD protein sequence (http://web.expasy.org/compute_pi/)

5 Theoretical molecular weight (MW) of the predicted CCD protein sequence (http://web.expasy.org/compute_pi/)

6 Position of the conserved histidines in the predicted CCD protein sequence (from the multiple protein alignments in Supplementary figure X)