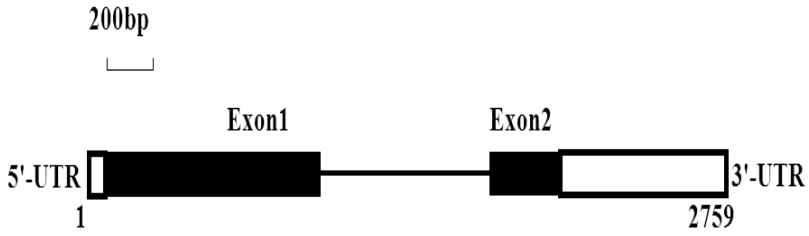
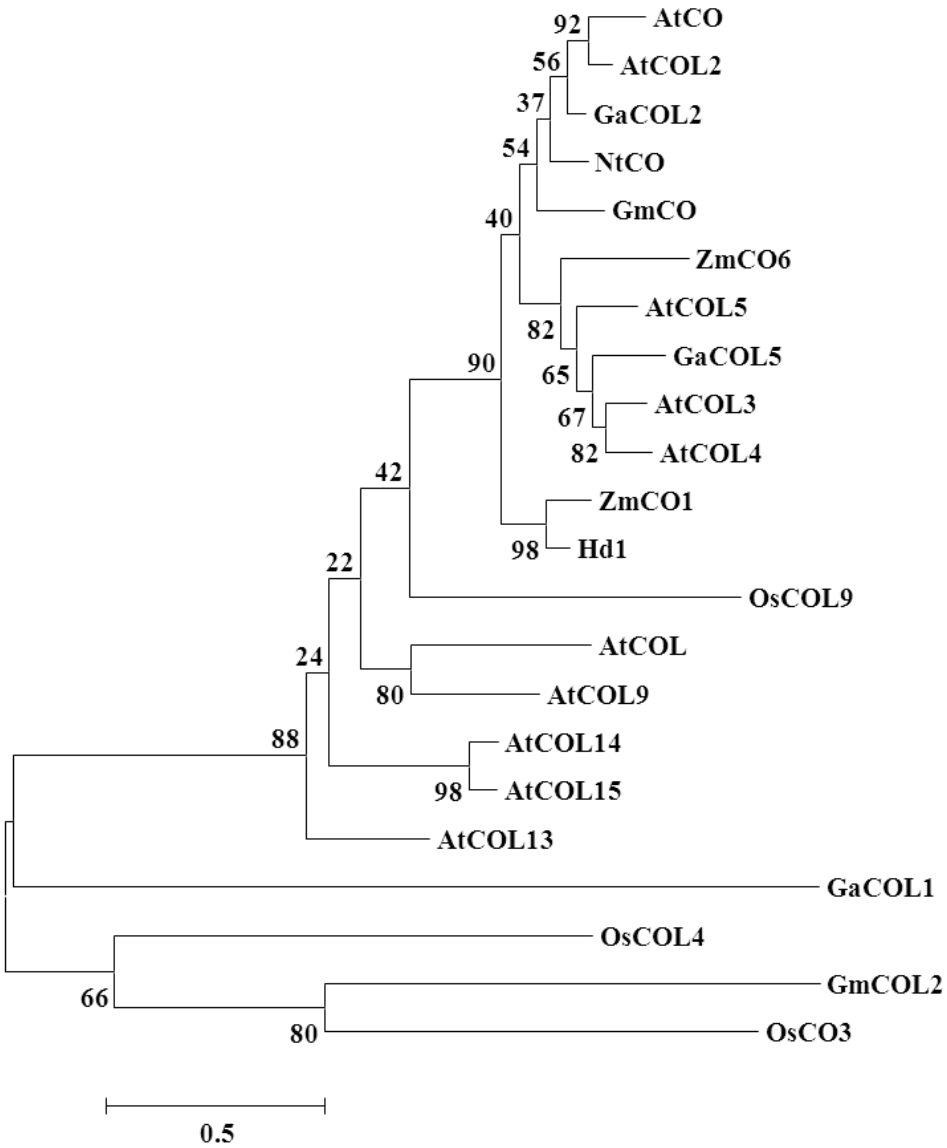
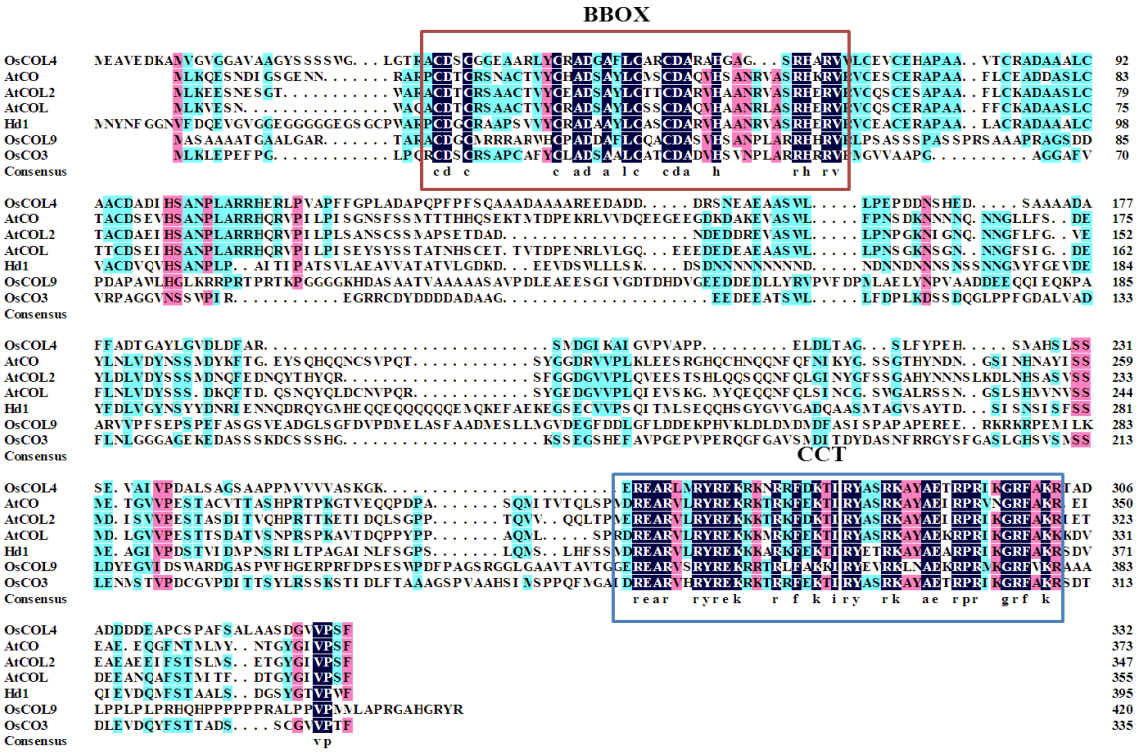
A


200bp
Exon1
Exon2
5'-UTR
3'-UTR
1
2759

B


92
AtCO
56
AtCOL2
37
GaCOL2
54
NtCO
GmCO
40
ZmCO6
AtCOL5
82
GaCOL5
90
65
AtCOL3
67
AtCOL4
82
42
ZmCO1
98
Hd1
22
OsCOL9
AtCOL
24
80
AtCOL9
88
AtCOL14
98
AtCOL15
AtCOL13
GaCOL1
OsCOL4
66
GmCOL2
80
OsCO3
0.5

C



S1 Fig. Exon/intron structure of OsCOL9 and alignment and phylogenetic analysis of OsCOL9 with other COL amino acid sequences. (A) OsCOL9 has two exons (boxes) and one intron (line between the two boxes). Closed boxes indicate coding region, and open boxes show the 5’ and 3’ untranslated regions (UTR). (B) Phylogenetic relationships of OsCOL9 proteins and selected species with the MEGA6 program using the Neighbor-Joining method. The genes and accession numbers were AtCO (CAA64407), AtCOL2 (AAB67880), GaCOL2 (KHG24977), NtCO (AEJ84000), GmCO (ACJ65311), ZmCO6 (NP001148229), AtCOL5 (Q9FHH8), GaCOL5 (KHG29079), AtCOL3 (Q9SK53), AtCOL4 (Q940T9), ZmCO1 (NP001120722), Hd1(AB041837), OsCOL9 (LOC_Os03g50310), AtCOL (CAB78567), AtCOL9 (AEE74583), AtCOL14 (O22800), AtCOL15 (Q9C78E), AtCOL3 (O822256), GaCOL1 (KHG24445), OsCOL4 (AK100097), GmCOL2 (NP001278944), OsCO3 (AB00187). (C) Amino acid sequence alignment of OsCOL9 and other COLs from rice and Arabidopsis. Their gene accession numbers have been showed in (B). The N-terminal conserved domain B-box was highlight marked by red rectangle. The C-terminal CCT domain was highlight marked by blue rectangle.