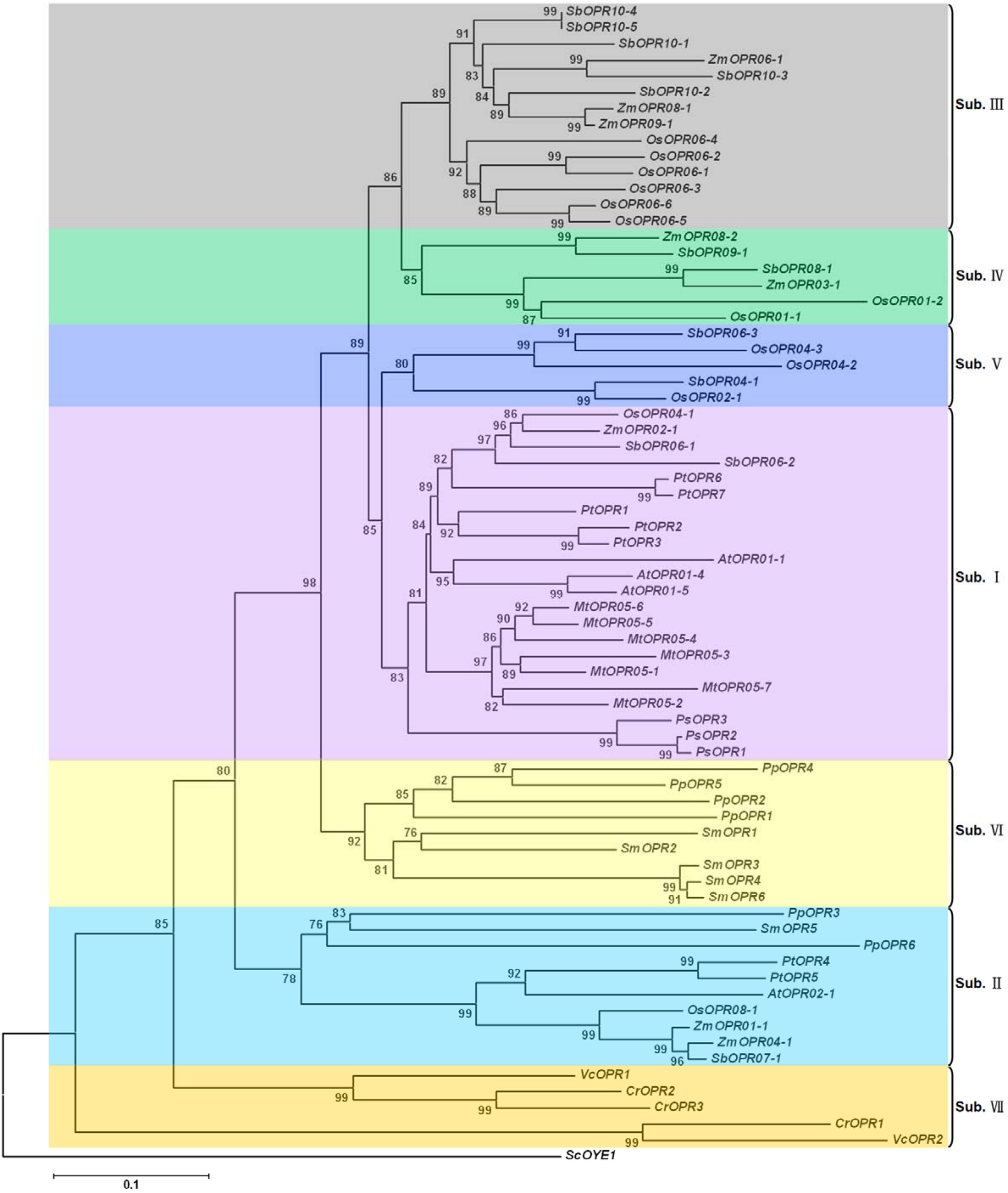
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89
99
ZmOPR09-1
OsOPR06-4
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OsOPR06-2
92
OsOPR06-1
86
OsOPR06-3
88
OsOPR06-6
89
99
OsOPR06-5
Sub. Ⅲ
99
ZmOPR08-2
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SbOPR08-1
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99
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Sub. Ⅳ
91
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89
99
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Sub. Ⅴ
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99
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Sub. Ⅱ
VcOPR1
CrOPR2
99
99
CrOPR3
CrOPR1
99
VcOPR2
Sub. Ⅶ
ScOYE1
0.1

Additional file 5

The rooted maximum-likelihood (ML) phylogenetic tree of OPR genes in 11 representative plants was inferred from the amino acid sequence alignments of the Oxidored_FMN domain (Fig. S1) under the Jones-Taylor-Thornton (JTT) model (Jones et al., 1992), implemented in Phylip v3.68 package (Retief, 2000). The old yellow enzyme 1 (OYE1) of *Saccharomyces cerevisiae* (*ScOYE1*) (Saito et al., 1991) was selected as an out of group marker and its accession number in SWISS-PROT is Q02899. The bootstrap values from 1000 resamplings are given at each node and the branch lengths are drawn to scale. The seven conserved OPR subfamilies are represented as Sub. Ⅰ, Ⅱ, Ⅲ, Ⅳ, Ⅴ, Ⅵ and Ⅶ at the right side of the ML tree.

References

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