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Supporting Information

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Supporting Information

for

Plant Cytochromes CYP74: Biochemical Features, Endocellular Localisation, Activation Mechanism in Plant Defence and Improvements for Industrial Applications

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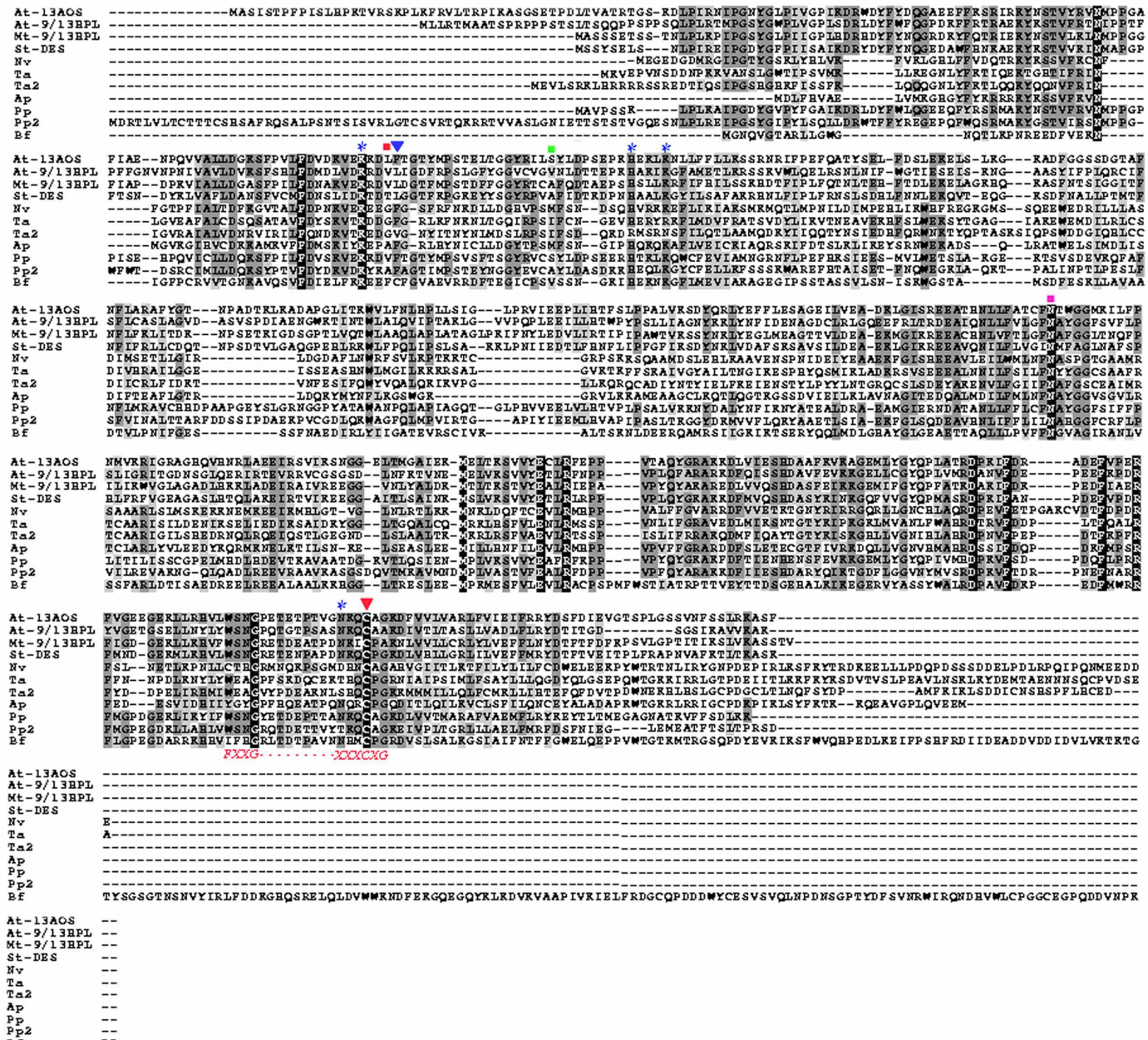
Figure S1. Multiple sequence alignment of plant and animal CYP74 members. Members representative of the four different branches of plant CYP74 enzymes were aligned with *Physcomitrella patens* and animal CYP74 members. Angiosperms: At-9/13 AOS, *Arabidopsis thaliana* AOS, CYP-74A, acc. nr. CAA73184; At-13HPL, *Arabidopsis thaliana* HPL, CYP74B, acc. nr. AAC69871; Mt-9/13 HPL, *Medicago truncatula* HPL, CYP74C, acc. nr. CAC86898; St-DES, *Solanum tubero-sum* DES, CYP74D, acc. nr. CAC28152. Bryophytes: Pp, *Physcomitrella patens*, acc. nrs. CAD 86488, CAD 86489. Cephalochordates: Bf, *Branchiostoma floridae*, acc. nr. ACD88492. Cnidaria: Ap, *Acropora palmata*, acc. nr. B4YFB4; Hm, *Hydra magnipapillata*, acc. nrs: CAP49322, CAP49324; Nv, *Nematostella vectensis*, acc. nr. A7RWD6; Placozoa, Ta, *Trichoplax aderens*, acc. nrs. B3RP47, B3RP49. Residues interacting with haem propionate are indicated by an asterisk.; the highly conserved cysteine is indicated by a triangle; the FxxGx3CxG signature motif with the nine amino acid gap found in CYP74 members is highlighted in yellow. Residues important in determining catalysis and specificity of plant CYP74s are indicated by coloured small squares; these include: N285, F287 and G288 in CYP74C3 (Mt-9/13-HPL) and G324 in At-9/13 AOS. The crucial Phe residue (F137) in At- 9/13 AOS, which, after mutation to a Leu residue, converted the enzyme to an HPL, is also shown by a blue triangle.


At-13AOS
At-9/13HPL
Mt-9/13HPL
St-DES
Nv
Ta
Ta2
Ap
Pp
Pp2
Bf
FXXG- - - - - - - - -XXXCXG