Figure S3. Multiple sequence alignment of HmCYP51, OsCYP51G1, OsCYP51G3, OsCYP74A5, OsCYP74A4 and AtCYP74A1. Assignment of secondary structure elements is based on HmCYP51 and AtCYP74A1 structures. Black frames localize Gotoh’s SRS regions 1-6 identified based on sequence alignment with P450cam, and triangles point to residues constituting the substrate binding site of HmCYP51 (red) and AtCYP74A1 (blue).