Supplementary Information for:

Nuclear receptor phosphorylation in xenobiotic signal transduction

Masahiko Negishi¹, Kaoru Kobayashi², Tsutomu Sakuma³ and Tatsuya Sueyoshi¹

¹Pharmacogenetics section, Reproductive and Developmental Biology Laboratory, National Institute of Environmental Health Sciences, National Institute of Health, Research Triangle Park, North Carolina 27709, USA
²Department of Biopharmaceutics, Meiji Pharmaceutical University, Noshio 2-522-1, Kiyose, Tokyo, 204-8588, Japan
³School of Pharmaceutical Sciences, Ohu University, 31-1 Misumido, Tomita-machi, Koriyama, Fukushima, 963-8611, Japan

All correspondences: Masahiko Negishi at the National Institute of Environmental Health Sciences.

E-mail address, negishi@niehs.nih.gov; Telephone number, 1-984-287-3824
Figure S1: Multiple sequence alignments of two TC-fold zinc fingers in human nuclear receptors.

Within two zinc fingers regions (70 residues in this alignment), only 24 residues are shown, and the others were omitted. Those 24 residues comprise eight cysteine residues functioning as ligands for the zinc atom (#2, 5, 19, 22, 42, 50, 60, 63, highlighted gray), well conserved threonine, serine and tyrosine residues (#10, 14, 18, 29, 38, in blue or red), and 11 residues in which phosphorylation was observed in at least one nuclear receptor. Starting and ending amino acid numbers are indicated for each sequence. Putative secondary structure diagram is depicted above the alignment. Small green letters indicate the residues which are phosphorylated in tissues or cells in vivo, or the residues which were analyzed for the effects of phosphorylation using mutated receptors. Multiple sequence alignment was constructed using Constraint-based Multiple Alignment Tool (COBALT) on NCBI web site. Most phosphorylation sites were collected in PhosphoSitePlus® (139), and some sites were manually determined using literature.