Figure legends

Figure 1. Position of the four *Ciona intestinalis* CYP3-like genes on the genome, as derived from the preliminary assembly of the different scaffold reads to the chromosomes (http://hoya.zool.kyoto-u.ac.jp/chromosomeall.html)

Figure 2. Alignment of *Ciona* CYP3-like genes with human CYP3A4 showing exon-intron boundaries (color coded), substrate recognition sites (underlined), heme binding (blue dotted line) and different helices (red dotted line)

Figure 3. Unrooted phylogenetic tree of clan-3 sequences calculated using Bayesian techniques. Values at branches represent posterior probabilities calculated from 107 generations of Markov Chain Monte Carlo analysis. Four independent replicate analyses provided very similar estimates of posterior probabilities (±0.01). There is strong support (Bayes Factor = 15.6) for the clustering of the *Ciona* genes along with the clam *Mercenaria mercenaria* CYP30 sequence with the CYP3 clade. These phylogenetic results point to a decisive conclusion that the *Ciona* genes are phylogenetically most similar to CYP3 genes

Figure 4. Exon-intron structure of *Ciona* CYP3-like sequences compared to human CYP3A4. The mammalian CYP3As are characterized by a high degree of structural similarity, with well-conserved exon-intron structures. The *Ciona* exon lengths are remarkably similar to those of human CYP3A4. CI19 is a single exon gene that codes for a full-length CYP protein that is 512 amino acids in length. *Ciona* CYPs appear to be more closely related to CYP3s than to other
members of the CYP clan 3 (Supplementary Material Table 3 shows exon information for other Clan-3 CYP genes)