

995 extensions (amino acid residues XX-YY in ZZZ) were removed. The trimmed
996 alignment was used for the generation of an unrooted tree by the neighbor-
997 joining method with 500 bootstrap replicates using MEGA4.1 package (Tamura
998 *et al.*, 2007). The ABC transporters of *D. melanogaster* and *An. gambiae* are
999 indicated with NP and XP prefix accession numbers, respectively. Seven ABC
1000 transporter subfamilies are indicated on the right of tree. Nodes with >50%
1001 bootstrap support were only marked with percentage values.

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1004 **Supplementary Figure 1.** Phylogenetic relationships of three *P. h. humanus*
1005 neuronal component protein families, including (A) voltage-dependent sodium
1006 channel α -subunit (VDSC), (B) sodium channel auxiliary subunit and (C) nicotinic
1007 acetylcholine receptor subunit (nAChR), with respective homologues from *D.*
1008 *melanogaster* (Dm). Deduced amino acid sequences were aligned using
1009 ClustalW (Thompson *et al.*, 1994), and rooted trees were generated from the
1010 alignments by the neighbor-joining method with 500 bootstrap replicates using
1011 MEGA4.1 package (Tamura *et al.*, 2007). The *D. melanogaster* voltage-
1012 dependent calcium channel (Dm VDCC, CG4894-PA), *Homo sapiens* calcium-
1013 activated potassium channel beta 2 subunit (Hs KCNMB2, NP_005828), and *D.*
1014 *melanogaster* *Rdl* GABA receptor subunit (CG10537-PA) were used as
1015 outgroups for the tree generation of VDSC, sodium channel auxiliary subunit, and
1016 nAChR, respectively. Nodes with >50% bootstrap support were only marked with
1017 percentage values.

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1019 **Supplementary Figure 2.** Transcription factor binding motifs observed in
1020 cytochrome P450s of *P. h. humans*. The sequences include 800 base pairs
1021 upstream of all P450 genes' transcription start sites, and 200 base pairs after the
1022 transcription start sites.

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1024 **Supplementary Figure 3.** Transcription factor binding motifs observed in GSTs
1025 of *P. h. humans*. The sequences include 800 base pairs upstream of the genes'
1026 transcription start site, and 200 base pairs after the transcription start site.

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1028 **Supplementary Figure 4.** Transcription factor binding motifs observed in
1029 Esterases of *P. h. humans*. The sequences include 800 base pairs upstream of
1030 the gene's transcription start site, and 200 base pairs after the transcription start
1031 site.