

**Table S6.** Taxa, accession numbers and chromosome location of partial *DIA1R* orthologues.

Species <sup>a</sup>	Protein accession number or identifier	mRNA (or EST) accession number or identifier	Genomic DNA accession number or identifier	Chrom <sup>b</sup>	Intron(s) <sup>c</sup>	Comments
<b>METAZOA</b>						
<b>Chordata</b>						
Vertebrata						
Cephalaspidomorphi						
<i>Petromyzon marinus</i>	-	-	Contig40181	-	Yes	ENSEMBL genomic BLAST
Chondrichthyes						
<i>Leucoraja erinacea</i>	-	EE990465	-	-	-	EST
<i>Squalus acanthias</i>	-	CX663166	-	-	-	EST
Actinopterygii						
<i>Ictalurus punctatus</i>	-	GH685824	-	-	-	EST
Tetrapoda						
Aves						
<i>Taeniopygia guttata</i>	ESTGUP00000006234	ESTGUT00000006296	ESTGUG00000006967	-	Yes	ENSEMBL identifiers First exon appears incorrect on current draft.
Amphibia						
<i>Ambystoma tigrinum</i>	-	CN052543	-	-	-	EST sequence
Mammalia						
<i>Canis familiaris</i>	ENSCAFP000000031380 and ENSCAFP000000021608	ENSRAFT000000036049 and ENSRAFT000000023268	ENSRAFG000000023457 and ENSRAFG000000014656	X	Yes	The first ENSEMBL identifiers match the N-terminal region of <i>DIA1R</i> and the second identifiers match the C-terminal region (both on X chromosome scaffold). Gaps in genomic sequence have led to gene modelling errors.
<i>Cavia porcellus</i>	ENSCPO00000008663	ENSCPOT00000009737	ENSCPOG00000009650	-	Yes	ENSEMBL identifiers
<i>Dasyus novemcinctus</i>	ENSDNOP000000013850	ENSNDNOT000000017850	ENSNDNOG000000017852	-	Yes	ENSEMBL identifiers
<i>Echinops telfairi</i>	ENSETEP000000015464	ENSETET000000019037	ENSETEG000000019037	-	Yes	ENSEMBL identifiers
<i>Erinaceus europaeus</i>	ENSEEUP000000000288	ENSEEUT000000000324	ENSEEUG000000000323	-	Yes	ENSEMBL identifiers
<i>Felis catus</i>	ENSFCAP000000008763	ENSFCAT000000009451	ENSFCAG000000009449	-	Yes	ENSEMBL identifiers
<i>Loxodonta africana</i>	ENSLAFP000000005064	ENSLAFT000000006035	ENSLAFG000000006035	-	Yes	ENSEMBL identifiers
<i>Felis catus</i>	ENSFCAP000000008763	ENSFCAT000000009451	ENSFCAG000000009449	-	Yes	ENSEMBL identifiers
<i>Microcebus murinus</i>	ENSMICP000000013720	ENSMICT000000015048	ENSMICG000000015058	-	Yes	ENSEMBL identifiers

<i>Myotis lucifugus</i>	ENSMLUP0000001597	ENSMLUT0000001744	ENSMLUG0000001741	-	Yes	ENSEMBL identifiers
<i>Ochotona princeps</i>	ENSOPRP00000008092	ENSOPRT00000008840	ENSOPRG00000008844	-	Yes	ENSEMBL identifiers
<i>Oryctolagus cuniculus</i>	ENSOCUP00000012696	ENSOCUT00000014763	ENSOCUG00000014763	-	Yes	ENSEMBL identifiers
<i>Otelemur garnettii</i>	ENSOGAP00000001890	ENSOGAT00000002117	ENSOGAG00000002115	-	Yes	ENSEMBL identifiers
<i>Pan troglodytes</i>	ENSPTRP00000055446	ENSPTRT00000063901	ENSPTRG000000034190	-		ENSEMBL identifiers On the reference database the equivalent sequence is currently annotated as a pseudogene (Accession number XR_020904).
<i>Pongo pygmaeus</i>	ENSPPYP00000022690	ENSPPYT00000023651	ENSPPYG00000029273	X	Yes	ENSEMBL identifiers
<i>Pteropus vampyrus</i>	ENSPVAP00000004149	ENSPVAT00000004383	ENSPVAG00000004383	-	Yes	ENSEMBL identifiers
<i>Rattus norvegicus</i>	XP_576913	XM_576913	NW_048034	X	Yes	A large gap in the current genomic sequence, means the reference database sequence does not correspond to the expected full length protein/mRNA/gene sequence and is incorrect.
<i>Sorex araneus</i>	ENSSARP00000004306	ENSSART00000004738	ENSSARG00000004729	-	Yes	ENSEMBL identifiers
<i>Spermophilus tridecemlineatus</i>	ENSSTOP00000002079	ENSSTOT00000002324	ENSSTOG00000002326	-	Yes	ENSEMBL identifiers Current mRNA is predicted from 8 exons, rather than the expected 5 exons (as for most vertebrate DIA1R sequences). The most likely scenario is that there are several base mis-calls in the genomic sequence, which has led to prediction of 3 incorrect introns, which currently consist of 1, 2, or 2 bp only. This sequence has therefore not been used in our analyses.
<i>Tarsius syrichta</i>	ENSTSY00000012353	ENSTSYT00000013464	ENSTSYG00000013470	-	Yes	ENSEMBL identifiers
<i>Tupaia belangeri</i>	ENSTBEP00000005669	ENSTBET00000006583	ENSTBEG00000006593	-	Yes	ENSEMBL identifiers
<i>Tursiops truncatus</i>	ENSTTRP00000006398	ENSTTRT00000006766	ENSTTRG00000006768	-	Yes	ENSEMBL identifiers

<sup>a</sup>Orthologues are only present in the phylum Metazoa.

<sup>b</sup>Chromosome location, if available.

<sup>c</sup>Intron(s) disrupting coding sequence, if genomic sequence was available.