

Table 1. Mitochondrial COI and cytochrome b genes sequence analyses with regard to 61 cell lines derived from 26 species which cannot be confirmed by mitochondrial PCR analysis,

(1) The results of COI gene sequence analysis.

Species registered by depositors	Name of Cell Line	NCBI ID *	Similarity	A**/B***
Pan troglodytes (Chimpanzee)	HSP-239	Pan troglodytes: KJ192907	98.0%	642 / 655
Pan troglodytes (Chimpanzee)	HSP-250	Pan troglodytes: KJ192907	93.7%	614 / 655
Callithrix jacchus (Common marmoset)	CMES40	Callithrix jacchus: NC_025586	100.0%	658 / 658
Tupaia belangeri (Treeshrew)	T-23	Tupaia belangeri: AJ421453	97.7%	643 / 658
Loxodonta africana (African elephant)	LACF-NaNaI	Loxodonta africana: DQ316069	100.0%	658 / 658
Loxodonta africana (African elephant)	LACF-NaNaII	Loxodonta africana: DQ316069	100.0%	658 / 658
Neovison vison (Mink)	Mv.1.Lu(NBL-7)	Neovison vison: AY377152	99.8%	657 / 658
Neovison vison (Mink)	Mink	Neovison vison: AY377152	99.7%	656 / 658
Neovison vison (Mink)	S+L-Mink	Neovison vison: AY377152	98.9%	648 / 655
Suncus murinus (Asian house shrew)	SEP2	Suncus murinus: KM497424	100.0%	658 / 658
Lagurus lagurus (Steppe Lemming)	LLKF	Lagurus lagurus: KF152989.1	99.1%	639 / 645
Xenopus laevis (African clawed frog)	XTY	Xenopus laevis: NC_001573.1	99.4%	654 / 658
Xenopus laevis (African clawed frog)	XTC-YF	Xenopus laevis: NC_001573.1	99.4%	654 / 658
Xenopus laevis (African clawed frog)	A6	Xenopus laevis: HM102316	100.0%	639 / 639
Xenopus laevis (African clawed frog)	A8	Xenopus laevis: HM102316	100.0%	639 / 639
Cynops pyrrhogaster (Japanese fire belly newt)	CPN4B	Cynops pyrrhogaster: EU880313.1	96.5%	635 / 658
Hynobius tokyoensis (Tokyo salamander)	HTUD1	Hynobius tokyoensis: HM036357	98.8%	650 / 658
Danio rerio (Zebra fish)	BRF41	Danio rerio: NC_002333	100.0%	658 / 658
Oryzias latipes (CAB strain) (Medaka)	OLCAB-e31	Oryzias latipes (Hd-rR) : AB498065	100.0%	658 / 658
Oryzias latipes (CAB strain) (Medaka)	OLCAB-e3	Oryzias latipes (Hd-rR) : AB498065	100.0%	658 / 658
Oryzias latipes (H04C strain) (Medaka)	OLHE-131	Oryzias latipes (Hd-rR) : AB498065	96.7%	637 / 659
Oryzias latipes (HB32 strain) (Medaka)	OLME-104	Oryzias latipes (strain unregistered) : NC_004387	99.5%	655 / 658
Oryzias latipes (Hd-rR strain) (Medaka)	OLHdrR-e3	Oryzias latipes (Hd-rR) : AB498065	100.0%	658 / 658
Oryzias latipes (HNI strain) (Medaka)	OLHNI-2	Oryzias latipes (HNI) : AB498066	100.0%	658 / 658
Oryzias latipes (strain unregistered) (Medaka)	DIT29	Oryzias latipes (Hd-rR) : AB498065	100.0%	658 / 658
Oryzias latipes (strain unregistered) (Medaka)	OLF-136	Oryzias latipes (strain unregistered) : NC_004387	99.4%	654 / 658

Species registered by depositors	Name of Cell Line	NCBI ID *	Similarity	A**/B***
Carassius auratus (Goldfish)	GEM-81	Carassius auratus: KJ874430.1	100.0%	656 / 656
Carassius auratus (Goldfish)	GEM-199	Carassius auratus: KJ874430.1	100.0%	658 / 658
Carassius auratus (Goldfish)	GEM-218	Carassius auratus: KJ874430.1	100.0%	658 / 658
Carassius auratus (Goldfish)	CAEP	Carassius auratus: KJ874430.1	100.0%	658 / 658
Carassius auratus (Goldfish)	CAF	Carassius auratus: KJ874430.1	98.3%	651 / 662
Umbra limi (Mudminnow)	ULF-23	Umbra limi: NC_028282	100.0%	658 / 658
Oreochromis niloticus (Tilapia)	Hepa-T1	Oreochromis niloticus: GU238433.1	79.8%	524 / 657
		Anguilla japonica: AB038556.2	99.8%	657 / 658
Anguilla japonica (Japanese eel)	Hepa-E1	Anguilla japonica: AB038556.2	99.8%	657 / 658
Drosophila melanogaster (Fruit fly)	S2 (Drosophila)	Drosophila melanogaster: U37541	99.8%	657 / 658
Papilio xuthus (Swallowtail butterfly)	NIAS-PX-58	Papilio xuthus: EU105377	100.0%	657 / 657
Papilio xuthus (Swallowtail butterfly)	NIAS-PX-64	Papilio xuthus: EU105377	100.0%	657 / 657
Bombyx mori (Silkworm)	BM-N	Bombyx mori: AB070264	100.0%	658 / 658
Bombyx mori (Silkworm)	BmN4-DR	Bombyx mori: AB070264	98.8%	647 / 655
Bombyx mori (Silkworm)	BmN4-IR	Bombyx mori: AB070264	99.2%	649 / 654
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	SES-MaBr-1	Mamestra brassicae: GQ892864.1	99.8%	656 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	SES-MaBr-3	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	SES-MaBr-4	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	SES-MaBr-5	Mamestra brassicae: GQ892864.1	99.8%	656 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	NIAS-MB-25	Mamestra brassicae: GQ892864.1	99.8%	656 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	NIAS-MB-32	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	NIAS-MaBr-92	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	NIAS-MaBr-93	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	MBHL-2	Mamestra brassicae: GQ892864.1	99.7%	655 / 657
Mamestra brassicae (Cabbage moth, Cabbage armyworm)	MBHL-3	Mamestra brassicae: GQ892864.1	100.0%	657 / 657
Mythimna separata (Oriental armyworm, Northern armyworm)	NIAS-LeSe-11	Mythimna separata: HQ951047	100.0%	658 / 658
Lemyra imparilis (Mulberry tiger moth)	FRI-SpIm-1229	Lemyra imparilis: no registration		
		Mamestra brassicae: GQ892864.1	99.7%	655 / 657
Austrocaligula eucalypti (=Opodiphthera eucalypti) (Emperor gum moth)	Ae	Opodiphthera eucalypti: KF522625.1	99.2%	652 / 657

* NCBI ID following "https://www.ncbi.nlm.nih.gov/nucleotide/" (Data on August 13, 2018)

A** Number of nucleic acid identical to that registered at NCBI

B*** Number of total nucleic acids utilized for the analysis

(2) The results of cytochrome b gene sequence analysis regarding the species which were not confirmed by COI sequence analysis.

Species registered by depositors	Name of Cell Line	NCBI ID *	Similarity	A**/B***
Pelophylax nigromaculatus (Black-spotted pond frog, Dark-spotted frog)	LAH1	Pelophylax nigromaculatus: KT878718.1	74.5%	616 / 827
		Bufo japonicas formosus: AB713498	99.5%	827 / 831
Pelophylax nigromaculatus (Black-spotted pond frog, Dark-spotted frog)	LAH2	Pelophylax nigromaculatus: KT878718.1	90.5%	506 / 559
		Pelophylax porosus brevipodus: AB980777.1	100.0%	559 / 559
Pelophylax porosus brevipodus (Daruma pond frog)	LAH3	Pelophylax porosus brevipodus: AB980777.1	100.0%	559 / 559
Hynobius nebulosus (Clouded salamander)	HNS1A	Hynobius nebulosus: AB266664.1	99.4%	1134 / 1141
Hynobius nebulosus (Clouded salamander)	HNS2	Hynobius nebulosus: AB266664.1	99.2%	1132 / 1141
Hynobius nebulosus (Clouded salamander)	HNS3	Hynobius nebulosus: AB266664.1	97.5%	1112 / 1141
Hynobius nebulosus (Clouded salamander)	HNS4	Hynobius nebulosus: AB266664.1	93.6%	1068 / 1141
Hynobius nebulosus (Clouded salamander)	HNS5	Hynobius nebulosus: AB266664.1	98.9%	1128 / 1141

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