

## SUPPLEMENTARY MATERIAL

### DNA Extraction and PCR amplification methods

Extraction of DNA from all specimens utilised the Qiagen DNeasy Blood and Tissue method on a Qiacube Robot, with final volumes of 200  $\mu$ L. PCR amplification for the mitochondrial cytochrome oxidase subunit I gene (COI) utilised Fish F1 and R1 primers of Ward *et al.* (2005) as shown in Table S-1. The PCR program consisted of the following cycles: 94°C / 3 mins – 1 cycle, 94°C / 20 secs, 60°C / 1 min – 38 cycles, 72°C / 40 secs, 72°C / 5 min – 1 cycle, hold at 10°C. Amplification products were 655 base pairs in size and visualized on a 2% agarose gel. PCR products were cleaned up prior to sequencing using ExoSAP-IT (Affymetrix USB). DNA extractions were done at the Australian Museum (Sydney) and sequencing was conducted at the Australian Genome Research Facility (Sydney)

**Table S1. PCR amplification conditions for COI sequencing of lanternfish and tuna**

PCR product	Stock	<i>per 1 x</i>
MyTaq Red Reagent Buffer (Bioline)	5×	
Fish F1 primer	10 $\mu$ M	
Fish F2 primer	10 $\mu$ M	
MyTaq Red DNA Polymerase (Bioline)	5 Units/ $\mu$ L	
H <sub>2</sub> O		16.3 $\mu$ L
DNA Template		2.5 $\mu$ L
Total		25 $\mu$ L

Ward, R., Zemplak, T., Innes, B., Last, P., and Hebert, P. (2005). DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society B. Biological Sciences* **360**, 1847–1857.  
doi:10.1098/rstb.2005.1716