Table S5. Description of positively selected sites in mitochondrial PCGs.

Species	Gene	Positive Selection Site	Residue Position	Amino Acid		Topological Region
				Foreground Branch	Background Branch	
Allopsontus sp.	*ND2*	2118	181	S	N/S	TMhelix
	ND4	2567	82	E	G/D/S/T/M/L/V/F	inside
	ND5	3266	330	S	S/C/Y/F	inside
		3338	402	G	S	inside
	ND6	3618	122	S	D/N/S/Y/K	outside
	COX2	930	155	S	S/T	outside
	CYTB	1367	106	N	Q/G/E/S/A/D	inside
Allopsontus tibetensis	*ND1*	1884	245	S	G	outside
	ND4	2664	179	N	F/L/W/Q/M/P/G/I	inside
	ND5	3312	376	S	L/S/M/I/V/C	outside
		3434	498	S	S/C/F/G/L/V	inside
Machilontus medogensis	*COX1*	760	484	Y	L/I/T/M/S	inside
	ND2	2161	227	A	N/T/I	inside
	ND5	3430	495	H	S/M/F/H/T/A/W/Y	inside