Table S4. The location of features of ten mitogenomes.

a. *Allopsontus tibetensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	70		
trnQ	L	71	139		
trnM	H	148	220		
ND2	H	221	1252	ATA	TAA
trnW	H	1252	1319		
trnC	L	1319	1385		
trnY	L	1386	1452		
COX1	H	1445	2984	ATT	T
trnL2	H	2985	3049		
COX2	H	3054	3741	ATG	T
trnK	H	3742	3813		
trnD	H	3814	3881		
ATP8	H	3882	4043	ATT	TAA
ATP6	H	4037	4714	ATG	TAA
COX3	H	4714	5499	ATG	TAA
trnG	H	5506	5571		
ND3	H	5569	5925	ATA	TAG
trnA	H	5928	5991		
trnR	H	5999	6063		
trnN	H	6067	6133		
trnS1	H	6134	6200		
trnE	H	6201	6268		
trnF	L	6271	6335		
ND5	L	6338	8068	ATG	TAA
trnH	L	8070	8134		
ND4	L	8136	9485	ATG	TAA
ND4L	L	9479	9778	ATG	TAA
trnT	H	9781	9845		
trnP	L	9846	9910		
ND6	H	9911	10420	ATA	TAA
CYTB	H	10420	11556	ATG	TAA
trnS2	H	11556	11623		
ND1	L	11637	12560	ATA	TAA
trnL1	L	12579	12644		
16S rRNA	L	12645	13945		
trnV	L	13946	14018		
12S rRNA	L	14019	14840		

b. *Allopsontus* sp.

Gene	Strand	From	To	Start	Stop
trnI	H	1	68		
trnQ	L	70	139		
trnM	H	151	217		
ND2	H	221	1252	ATT	TAA
trnW	H	1251	1318		
trnC	L	1318	1385		
trnY	L	1386	1452		
COX1	H	1445	2984	ATT	T
trnL2	H	2985	3049		
COX2	H	3057	3744	ATG	T
trnK	H	3745	3816		
trnD	H	3821	3886		
ATP8	H	3887	4048	ATA	TAA
ATP6	H	4042	4719	ATG	TAA
COX3	H	4719	5504	ATG	TAA
trnG	H	5511	5576		
ND3	H	5577	5930	ATA	TAG
trnA	H	5929	5993		
trnR	H	5997	6061		
trnN	H	6062	6129		
trnS1	H	6130	6196		
trnE	H	6197	6263		
trnF	L	6264	6328		
ND5	L	6334	8073	ATG	TAA
trnH	L	8076	8141		
ND4	L	8145	9500	GTG	TAA
ND4L	L	9494	9793	ATG	TAA
trnT	H	9796	9858		
trnP	L	9859	9923		
ND6	H	9927	10436	ATC	TAA
CYTB	H	10436	11572	ATG	TAA
trnS2	H	11571	11638		
ND1	L	11654	12580	ATA	TAG
trnL1	L	12599	12665		
16S rRNA	L	12666	13980		
trnV	L	13981	14052		
12S rRNA	L	14053	14858		

c. *Pedetontus elegans*

Gene	Strand	From	To	Start	Stop
trnI	H	1	68		
trnQ	L	70	141		
trnM	H	141	210		
ND2	H	211	1248	ATG	TAA
trnW	H	1253	1320		
trnC	L	1320	1389		
trnY	L	1396	1463		
COX1	H	1456	2995	ATT	T
trnL2	H	2996	3060		
COX2	H	3061	3748	ATT	T
trnK	H	3749	3821		
trnD	H	3825	3893		
ATP8	H	3894	4055	ATA	TAA
ATP6	H	4049	4726	ATG	TAA
COX3	H	4726	5508	ATG	TAA
trnG	H	5508	5572		
ND3	H	5573	5926	ATA	TAA
trnA	H	5941	6004		
trnR	H	6007	6072		
trnN	H	6074	6140		
trnS1	H	6141	6210		
trnE	H	6211	6277		
trnF	L	6279	6343		
ND5	L	6343	8081	ATG	TA
trnH	L	8083	8149		
ND4	L	8149	9498	ATG	TAA
ND4L	L	9492	9794	ATG	TAA
trnT	H	9797	9862		
trnP	L	9865	9928		
ND6	H	9935	10447	ATA	TAA
CYTB	H	10451	11587	ATG	TAA
trnS2	H	11586	11653		
ND1	L	11659	12603	ATA	TAA
trnL1	L	12613	12680		
16S rRNA	L	12681	14017		
trnV	L	14018	14091		
12S rRNA	L	14092	14908		

d. *Machilontus medogensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	68		
trnQ	L	69	136		
trnM	H	135	203		
ND2	H	204	1226	ATA	TAG
trnW	H	1236	1307		
trnC	L	1310	1379		
trnY	L	1383	1454		
COX1	H	1489	2988	ATT	TAA
trnL2	H	3002	3068		
COX2	H	3069	3755	ATG	TAA
trnK	H	3760	3831		
trnD	H	3833	3898		
ATP8	H	3899	4060	ATC	TAA
ATP6	H	4057	4731	ATA	TAA
COX3	H	4731	5519	ATG	TAA
trnG	H	5530	5600		
ND3	H	5601	5954	ATT	TAG
trnA	H	5953	6015		
trnR	H	6017	6081		
trnN	H	6090	6157		
trnS1	H	6158	6224		
trnE	H	6226	6292		
trnF	L	6307	6373		
ND5	L	6375	8105	ATC	TAA
trnH	L	8103	8169		
ND4	L	8171	9520	ATG	TAA
ND4L	L	9514	9816	ATG	TAA
trnT	H	9819	9882		
trnP	L	9884	9949		
ND6	H	9951	10475	ATT	TAA
CYTB	H	10475	11611	ATG	TAA
trnS2	H	11616	11683		
ND1	L	11699	12631	ATA	TAA
trnL1	L	12656	12721		
16S rRNA	L	12722	14052		
trnV	L	14053	14125		
12S rRNA	L	14126	14977		

e. *Pedetontus xanthospilus*

Gene	Strand	From	To	Start	Stop
trnI	H	1	69		
trnQ	L	73	146		
trnM	H	146	217		
ND2	H	218	1258	ATG	TAG
trnW	H	1275	1343		
trnC	L	1343	1413		
trnY	L	1414	1485		
COX1	H	1478	3017	ATT	T
trnL2	H	3018	3083		
COX2	H	3089	3776	ATG	T
trnK	H	3777	3848		
trnD	H	3851	3917		
ATP8	H	3918	4079	ATC	TAA
ATP6	H	4073	4750	ATG	TAA
COX3	H	4750	5532	ATG	TAG
trnG	H	5536	5602		
ND3	H	5603	5956	ATA	TAA
trnA	H	5962	6027		
trnR	H	6031	6100		
trnN	H	6103	6166		
trnS1	H	6169	6237		
trnE	H	6245	6310		
trnF	L	6309	6375		
ND5	L	6375	8114	ATG	TAA
trnH	L	8116	8182		
ND4	L	8182	9531	ATG	TAA
ND4L	L	9525	9827	ATG	TAA
trnT	H	9830	9898		
trnP	L	9899	9963		
ND6	H	9964	10488	ATT	TAA
CYTB	H	10492	11628	ATG	TAA
trnS2	H	11627	11693		
ND1	L	11711	12646	ATA	TAA
trnL1	L	12650	12717		
16S rRNA	L	12718	14077		
trnV	L	14078	14150		
12S rRNA	L	14151	15000		

f. *Pedetontus jinxiuensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	69		
trnQ	L	73	146		
trnM	H	147	218		
ND2	H	219	1259	GTG	TAG
trnW	H	1276	1344		
trnC	L	1344	1413		
trnY	L	1414	1481		
COX1	H	1474	3013	ATT	T
trnL2	H	3014	3079		
COX2	H	3086	3773	ATG	T
trnK	H	3774	3845		
trnD	H	3848	3916		
ATP8	H	3917	4078	ATC	TAA
ATP6	H	4072	4749	ATG	TAA
COX3	H	4749	5531	ATG	TAA
trnG	H	5535	5602		
ND3	H	5603	5956	ATA	TAG
trnA	H	5962	6026		
trnR	H	6031	6099		
trnN	H	6101	6167		
trnS1	H	6168	6236		
trnE	H	6244	6309		
trnF	L	6308	6374		
ND5	L	6374	8113	ATG	TAA
trnH	L	8115	8179		
ND4	L	8179	9528	ATG	TAG
ND4L	L	9522	9824	ATG	TAA
trnT	H	9827	9895		
trnP	L	9896	9960		
ND6	H	9964	10485	ATA	TAA
CYTB	H	10489	11625	ATG	TAA
trnS2	H	11624	11690		
ND1	L	11708	12643	ATA	TAA
trnL1	L	12647	12714		
16S rRNA	L	12715	14076		
trnV	L	14077	14149		
12S rRNA	L	14150	15008		

g. *Pedetontus hezhouensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	68		
trnQ	L	73	145		
trnM	H	148	217		
ND2	H	218	1258	GTG	TAG
trnW	H	1272	1339		
trnC	L	1339	1408		
trnY	L	1409	1482		
COX1	H	1475	3014	ATT	T
trnL2	H	3015	3082		
COX2	H	3089	3776	ATG	T
trnK	H	3777	3848		
trnD	H	3852	3919		
ATP8	H	3920	4081	ATT	TAA
ATP6	H	4075	4752	ATG	TAA
COX3	H	4752	5534	ATG	TAA
trnG	H	5541	5607		
ND3	H	5608	5961	ATA	TAA
trnA	H	5966	6031		
trnR	H	6038	6106		
trnN	H	6108	6174		
trnS1	H	6175	6243		
trnE	H	6247	6315		
trnF	L	6318	6386		
ND5	L	6386	8125	ATG	TAA
trnH	L	8127	8191		
ND4	L	8191	9540	ATG	TAA
ND4L	L	9534	9836	ATG	TAA
trnT	H	9839	9906		
trnP	L	9907	9971		
ND6	H	9972	10496	ATC	TAA
CYTB	H	10500	11636	ATG	TAA
trnS2	H	11635	11701		
ND1	L	11721	12650	ATA	TAA
trnL1	L	12660	12727		
16S rRNA	L	12728	14096		
trnV	L	14097	14169		
12S rRNA	L	14170	15035		

h. *Pedetontus nanningensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	69		
trnQ	L	74	148		
trnM	H	150	221		
ND2	H	222	1259	ATG	TAG
trnW	H	1266	1334		
trnC	L	1334	1401		
trnY	L	1402	1474		
COX1	H	1467	3006	ATT	T
trnL2	H	3007	3072		
COX2	H	3078	3765	ATG	T
trnK	H	3766	3837		
trnD	H	3841	3897		
ATP8	H	3911	4072	ATT	TAA
ATP6	H	4066	4743	ATG	TAA
COX3	H	4743	5525	ATG	TAA
trnG	H	5532	5602		
ND3	H	5603	5956	ATA	TAA
trnA	H	5958	6023		
trnR	H	6026	6094		
trnN	H	6096	6161		
trnS1	H	6162	6229		
trnE	H	6236	6304		
trnF	L	6309	6374		
ND5	L	6375	8112	ATG	T
trnH	L	8114	8180		
ND4	L	8180	9529	ATG	TAA
ND4L	L	9523	9825	ATG	TAA
trnT	H	9828	9888		
trnP	L	9897	9968		
ND6	H	9986	10492	ATT	TAA
CYTB	H	10492	11628	ATG	TAA
trnS2	H	11627	11693		
ND1	L	11717	12652	ATG	TAA
trnL1	L	12656	12723		
16S rRNA	L	12724	14102		
trnV	L	14103	14176		
12S rRNA	L	14177	14913		

i. *Pedetontus shenzhenensis*

Gene	Strand	From	To	Start	Stop
trnI	H	1	69		
trnQ	L	74	149		
trnM	H	157	228		
ND2	H	229	1266	ATG	TAA
trnW	H	1273	1343		
trnC	L	1346	1420		
trnY	L	1421	1493		
COX1	H	1486	3025	ATT	T
trnL2	H	3026	3092		
COX2	H	3096	3783	ATG	T
trnK	H	3784	3855		
trnD	H	3859	3926		
ATP8	H	3927	4088	ATT	TAA
ATP6	H	4082	4759	ATG	TAA
COX3	H	4759	5541	ATG	TAA
trnG	H	5546	5613		
ND3	H	5614	5967	ATA	TAA
trnA	H	5968	6035		
trnR	H	6037	6104		
trnN	H	6113	6178		
trnS1	H	6179	6246		
trnE	H	6255	6324		
trnF	L	6325	6391		
ND5	L	6392	8129	ATG	T
trnH	L	8131	8201		
ND4	L	8203	9555	ATG	TAA
ND4L	L	9549	9851	ATG	TAA
trnT	H	9854	9922		
trnP	L	9923	9994		
ND6	H	9995	10519	ATT	TAA
CYTB	H	10524	11660	ATG	TAA
trnS2	H	11659	11726		
ND1	L	11757	12692	ATA	TAG
trnL1	L	12696	12763		
16S rRNA	L	12764	14159		
trnV	L	14160	14232		
12S rRNA	L	14233	15108		

j. *Pedetontus* sp.

Gene	Strand	From	To	Start	Stop
trnI	H	1	70		
trnQ	L	76	151		
trnM	H	158	230		
ND2	H	231	1268	GTG	TAA
trnW	H	1275	1344		
trnC	L	1344	1418		
trnY	L	1419	1493		
COX1	H	1486	3027	ATT	TAA
trnL2	H	3027	3094		
COX2	H	3102	3789	ATG	T
trnK	H	3790	3861		
trnD	H	3867	3931		
ATP8	H	3932	4093	ATT	TAA
ATP6	H	4087	4764	ATG	TAA
COX3	H	4764	5546	ATG	TAA
trnG	H	5551	5619		
ND3	H	5620	5973	ATA	TAA
trnA	H	5979	6046		
trnR	H	6049	6117		
trnN	H	6120	6186		
trnS1	H	6188	6255		
trnE	H	6260	6326		
trnF	L	6325	6391		
ND5	L	6391	8129	ATG	TA
trnH	L	8131	8202		
ND4	L	8202	9551	ATG	TAG
ND4L	L	9545	9847	ATG	TAA
trnT	H	9850	9917		
trnP	L	9918	9984		
ND6	H	9985	10509	ATT	TAA
CYTB	H	10516	11652	ATG	TAA
trnS2	H	11651	11717		
ND1	L	11735	12673	TTG	TAA
trnL1	L	12674	12741		
16S rRNA	L	12742	14124		
trnV	L	14125	14198		
12S rRNA	L	14199	15096		