

DQ087473Microciona	1	PKTLGRITINVIGEPIDERGPIGEEMQAAITHADAPEFVDMNVKQOEILVTGIKVVDLLAPYA
DQ087459Sycon	1	VELTLGRIMNVIGEPIDERGPINAKATAEPTHAEAPEFVDMSEVQOEILETGIVKVVDLLAPYA
DQ087466Leucosolenia	1	PELTLGRIMNVIGEPIDERGPIIDAKASAEPTHAEAPEFVDMSEVQOEILETGIVKVVDLLAPYA
316175_Klon3_Exon	1	-----
DQ087473Microciona	61	KGGKIGLFGGAGVGKTVVIMELINNVAKAHGGCSVFAGVGERTREGNDLYHEMIQGGVTS
DQ087459Sycon	61	KGGKIGLFGGAGVGKTVVIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIVGGVIV
DQ087466Leucosolenia	61	KGGKIGLFGGAGVGKTVVIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIVGGVIV
316175_Klon3_Exon	1	-----REGNDFYHEMITGGVIV
DQ087473Microciona	121	LKDDSSK/VALVYQMNPPGARARVALTGLTVAEYFRDKEGQDVLLFDINIFRFTQAGS
DQ087459Sycon	121	LDKPGSK/VALVYQMNPPGARARVALTGLTVAEYFRDKEGQDVLLFDINIFRFTQAGS
DQ087466Leucosolenia	121	LDKPGSK/VSLVYQMNPPGARARVALTGLTVAEYFRDKEGQDVLLFDINIFRFTQAGS
316175_Klon3_Exon	18	LDKEGSK/VSLVYQMNPPGARAR-----
		*
DQ087473Microciona	180	EVSALLGRIPLLWATSQTLATDMGIMQERITTTQKGSITSVQAVFVPADDLTDPAATTF
DQ087459Sycon	180	EVSALLGRIPSAVGYQPTLATDMGSMQERITTTKEGSITSVQAIYVPADDLTDPAATTF
DQ087466Leucosolenia	180	EVSALLGRIPSAVGYQPTLATDMGSMQERITTP-EGSITSVQAIYVPADDLTDPAATTF
316175_Klon3_Exon		-----
DQ087473Microciona	240	AHLDATTVLSRAISELGIYPAVDPLDSTSRIMDPNIVGAEHYNNVARGVQKILQDYRSLQD
DQ087459Sycon	240	AHLDATTVLSRGI AELGIYPAVDPLDSTSRILDPNIVGQEHYSIARSVQKILQDYKSLQD
DQ087466Leucosolenia	239	AHLDATTVLSRGI AELGIYPAVDPLDSTSRILDPNIVGMEHYTIARSVQKILQDYKSLQD
316175_Klon3_Exon		-----
DQ087473Microciona	300	IIAILGMDELSEEDKLTVAARARKIQRFLSQPFQVAEVFTGKEGKLVLENTISGFQKIIN
DQ087459Sycon	300	IIAILGMDELSEEDKLTVAARARKIQRFLSQPFQVAEVFTGKPGKFFVLEQTIKGFTSILN
DQ087466Leucosolenia	299	IIAILGMDELSEEDKLTVAARARKIQRFLSQPFQVAEVFTGKPGKFFV-----
316175_Klon3_Exon		-----
DQ087473Microciona	360	GELDDIPE
DQ087459Sycon	360	GEHDHIPL
DQ087466Leucosolenia		-----
316175_Klon3_Exon		-----

Additional Figure 1: Amino acid alignment of three sponge ATP Synthetase beta subunit sequences from Genbank (accession numbers DQ087473, DQ087459, DQ087466) and the sequence of *Leucetta chagosensis* (Specimen No. QMG 316175). Location of intron is indicated by a forward slash and * above the site. Black alignment background indicates conserved alignment positions, grey background similar chemical properties, white background variable positions with dissimilar amino acids.

