

Table S1. Mitochondrial Genome Statistics

Species	Mt genome		22 KPC genes		LSUrRNA		SSUrRNA		22 Ymf genes		Control Region	
	Length	A+T	No. of AA	A+T	Length	A+T	Length	A+T	No. of AA	A+T	Length	A+T
<i>T. paravorax</i>	47,369	81.5	6254	79.0	2572	74.2	1568	70.9	6115	84.6	439	89.7
<i>T. malaccensis</i>	47,458	80.1	6315	78.5	2595	72.4	1606	68.9	6187	85.0	491	85.5
<i>T. pigmentosa</i>	47,348	81.5	6294	78.2	2597	74.7	1613	72.3	6065	86.0	556	90.4
<i>T. thermophila</i>	47,577	79.2	6316	75.1	2592	72.2	1606	68.8	6228	84.1	493	84.3
<i>T. pyriformis</i>	47,172	78.7	6487	76.4	2595	73.1	1615	68.7	6305	83.1	437	86.5

Length and A+T content of *Tetrahymena* Mt genomes.

Length is in base pair, and A+T in percentages.