Table S2

**Codon-based test of purifying selection for analysis between *P. caudatum* Hsp70 sequences**

<table>
<thead>
<tr>
<th><em>Paramaecium caudatum</em> PcHsp70</th>
<th>CY1a</th>
<th>CY1b</th>
<th>CY1c</th>
<th>CY2a</th>
<th>CY2b</th>
<th>ER1a</th>
<th>ER1b</th>
<th>ER2a</th>
<th>ER2b</th>
<th>ER2c</th>
<th>MT1a</th>
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</table>

The probability of rejecting the null hypothesis of strict-neutrality \( d_N = d_S \) (above diagonal) in favor of the alternative hypothesis of purifying selection \( d_N < d_S \) (below diagonal) is shown; \( d_S \) and \( d_N \) are the numbers of synonymous and nonsynonymous substitutions per site, respectively. The analyses were conducted using the Nei-Gojobori method and involved 11 nucleotide sequences. All ambiguous positions were removed for each sequence pair with a total of 465 positions in the final dataset. Analyses were conducted in MEGA5.