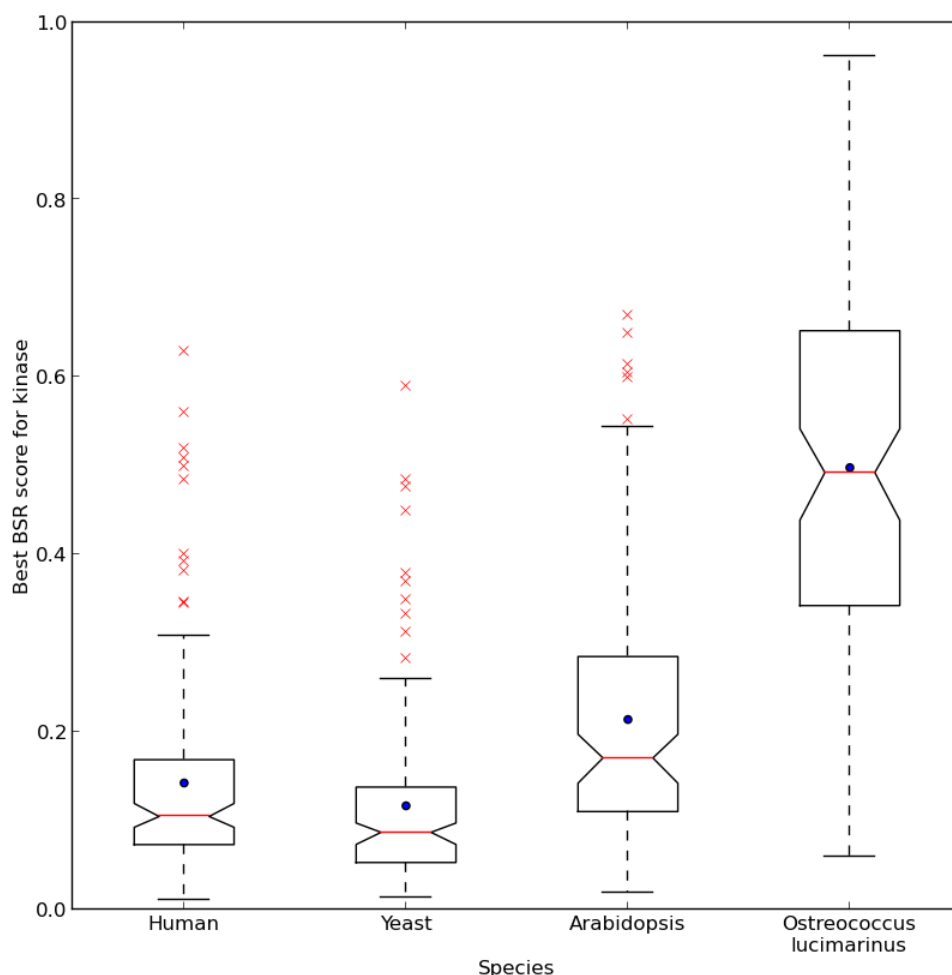


Kinase similarities between *O. tauri* and other model organisms

The following box and whiskers plot shows, for each species, the distributions of the Blast Score Ratio (BSR) similarities of *O. tauri* protein kinases against the best hit in the given species. BSR scores for each *O. tauri* kinase are calculated against the best hit (highest score) found in *H. sapiens*, *S. cerevisiae*, *A. thaliana*, and *O. lucimarinus*. Red crosses show the outliers, whiskers indicate the extremes of the distribution (excluding outliers). Boxes show the upper and lower quartiles, dissected by the red median line. The blue dot indicates the mean. Notches, indicating the 95% confidence interval, were calculated from 100,000 bootstraps. This data shows that *O. tauri* kinases share the largest (median) sequence similarity with *O. lucimarinus*, as expected, followed by *A. thaliana* and then *H. sapiens*. The furthest divergence is to *S. cerevisiae*.



The following table shows the p-values from a two-tailed Mann-Whitney U test comparing for each species the Blast Score Ratio (BSR) similarities of kinases described previously. The comparison is between the vectors of BSR similarities, calculated from *O. tauri* protein kinases to the given species.

Supplemental Information S4

Comparison	P-value
<i>S. cerevisiae</i> - <i>H. sapiens</i>	0.01
<i>A. thaliana</i> - <i>H. sapiens</i>	2.67E-07
<i>A. thaliana</i> - <i>S. cerevisiae</i>	1.24E-12