Supplementary File 1

Analyses of Compact Trichinella Kinomes Reveal a MOS-like Protein Kinase with a Unique N-terminal Domain


*Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Victoria 3010, Australia
†Yourgene Bioscience, Shu-Lin District, New Taipei City 23863, Taiwan
‡Division of Biology, HHMI, California Institute of Technology, Pasadena, California 91125, USA
§Istituto Superiore di Sanità, 00161 Rome, Italy

Figure S1 Trees representing the phylogenetic relationship of eukaryotic protein kinase (ePK) sequences between Trichinella spiralis (T1) and T. pseudospiralis (T4A). Each ePK group is represented by an individual tree (A-I). Nodal support values (Bayesian inference) and sequence identifiers are given at the nodes and tips, respectively

S1 A Protein kinases A, G and C, and other nucleoside-regulated kinases (AGC group)
S1 B Ca²⁺/calmodulin-dependent kinases (CAMK group)
S1 C Casein kinase 1 (CK1 group)
S1 D Cyclin-dependent kinases (CDKs), mitogen-activated protein kinases (MAPKs), glycogen synthase kinases (GSKs) and CDK-like kinases (CMGC group)
S1 E “Other” protein kinases (Other group)
S1 F Receptor guanylate cyclases (RGC group)
S1 G MAPK cascade kinases (STE group)
S1 H Tyrosine kinases (TK group)
S1 I Tyrosine kinase-like kinases (TKL group)
Figure S1 A
AGC group
Figure S1 B
CAMK group
Figure S1 D
CMGC group
Figure S1 E
Other group
Figure S1 F
RGC group
Figure S1 G
STE group
Figure S1 H
TK group
Figure S1 I
TKL group