Chemical proteomic analysis reveals the drugability of the kinome of *Trypanosoma brucei*

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Supporting information

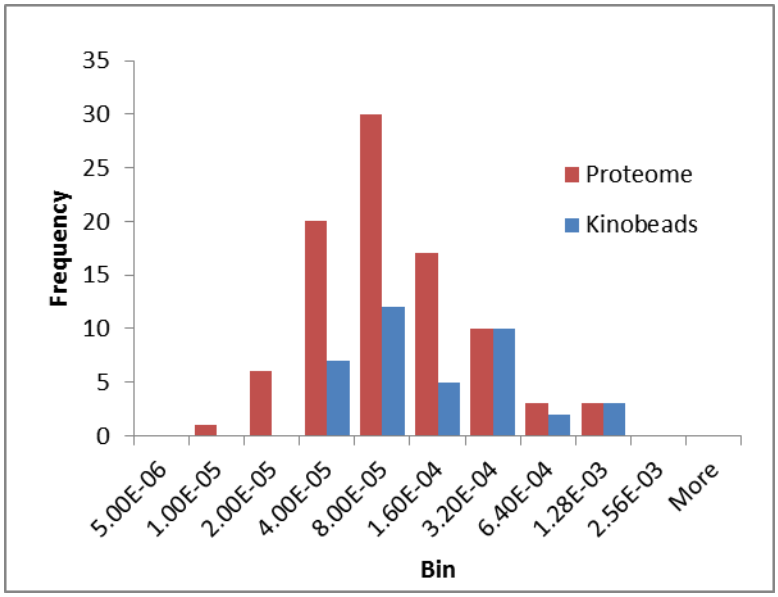

Figure S1. Observation of *T. brucei* protein kinases compared to estimated protein abundance. The protein kinase observed in the *T. brucei* cell lysate or kinobead are binned according to abundance. The abundance of the protein kinases was estimated by spectral counting (Spectrum to Sequence Matches divided by Molecular Weight) using the data contained in Table S3.

Supporting Tables (in a separate .xls file):

Table S1 *Trypanosoma brucei* protein kinase classification

Table S2 Protein profiling data for different kinobeads with *Trypanosoma brucei* cell lysate.

Table S3 Observed proteome of bloodstream form *Trypanosoma brucei*.

Table S4 The expressed kinome of bloodstream form *Trypanosoma brucei*

Table S5 Kinobead profiling of Staurosporine and BMS-387032 against bloodstream form *Trypanosoma brucei* lysates.

Table S6 Kinobead profiling of Trypanosome kinase inhibitors against bloodstream form *Trypanosoma brucei* lysates.

Table S8 Composition of the kinobeads used to profile *Trypanosoma brucei* lysates.