



Figure S3. Score correlations. A subset of the NHLBI profile data set [1] was used to perform this evaluation. For each scoring function, when the best hit per spectrum (analyzed using the analysis program that the scoring function was originally used for) is a true positive, that candidate peptide is scored again using the corresponding scoring function implemented in RAId_aPS. Each true positive best hit thus gives rise to two scores and plotted using the following rule: the first score is used as the ordinate while the second score (from RAId_aPS) is used as the abscissa. Including 500 spectra, panel A is for the RAId score. Panel B is for Hyperscore and contains 495 spectra. The result of K-score is shown in panel C with 310 spectra. Shown with 500 spectra, panel D documents the results for XCorr.

References

1. Alves G, Ogurtsov AY, Wu WW, Wang G, Shen RF, et al. (2007) Calibrating E-values for MS² library search methods. *Biology Direct* 2: 26.