

A high-throughput screening strategy to identify inhibitors of SSB protein-protein interactions in an academic screening facility

Andrew F. Voter, Michael P. Killoran, Gene E. Ananiev, Scott A. Wildman, F. Michael Hoffmann, James L. Keck

Supplemental Material

Corresponding author:

James L. Keck: Department of Biomolecular Chemistry, Room 1135 Biochemistry Building, 420 Henry Mall, University of Wisconsin School of Medicine and Public Health, Madison, WI 53706. Tel: 608-263-1815. Fax: 608-262-5253. Email: jlkeck@wisc.edu

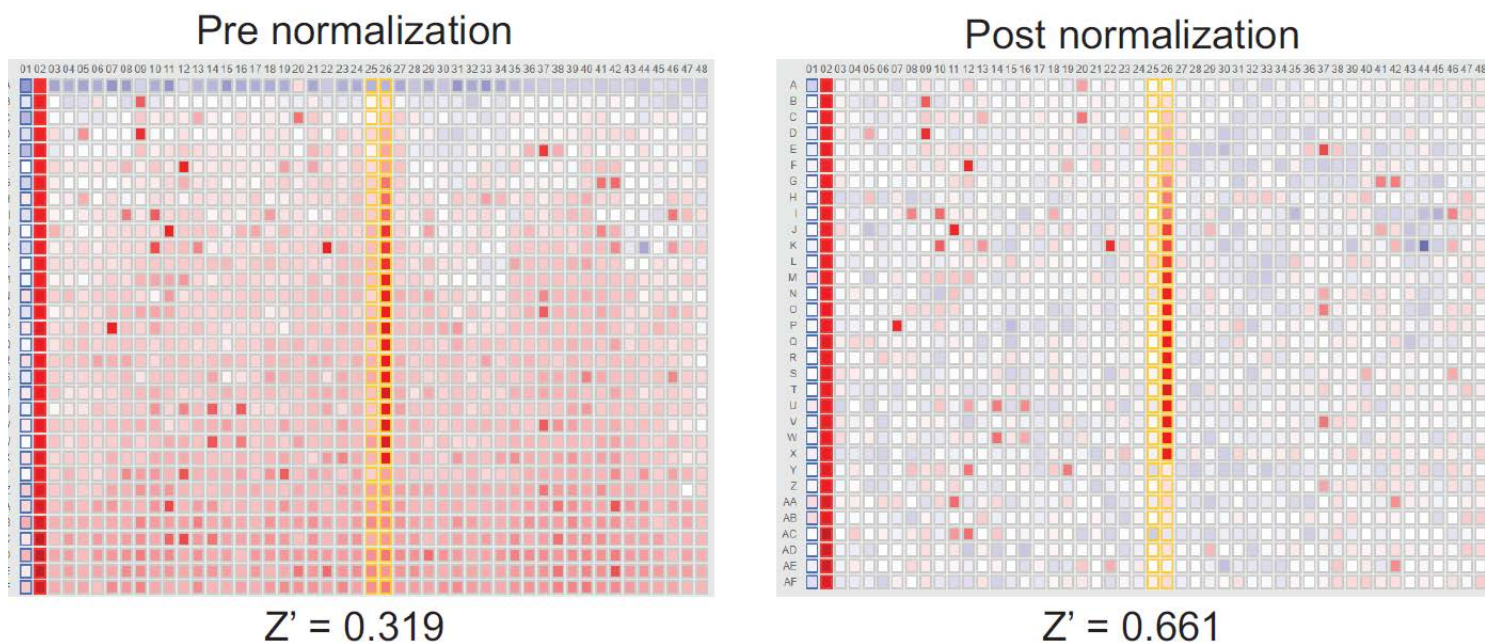


Figure S1. Heat map of a representative 1536-well plate before and after the normalization process. Wells outlined in blue (column 01) and red (column 02) boxes contain negative and positive control peptides respectively, while the wells outlined in yellow contain either DMSO alone (column 25 and bottom of column 26) or a titration of the SSBct positive control peptide (column 26, top). Before normalization (left), a markedly increased signal was noted in the top row of each plate, as well as a vertical signal gradient down the plate. Both problems are resolved after normalization (right) without altering the pattern of hits.

