

Optimizing the detergent concentration conditions for immunoprecipitation (IP) coupled with LC-MS/MS identification of interacting proteins

Li Yang, Haizhen Zhang, James E. Bruce*

Department of Genome Sciences, The University of Washington, Seattle, WA 98195-5065, USA. E-mail: jimbruce@u.washington.edu; Phone: +1-206-543-0220

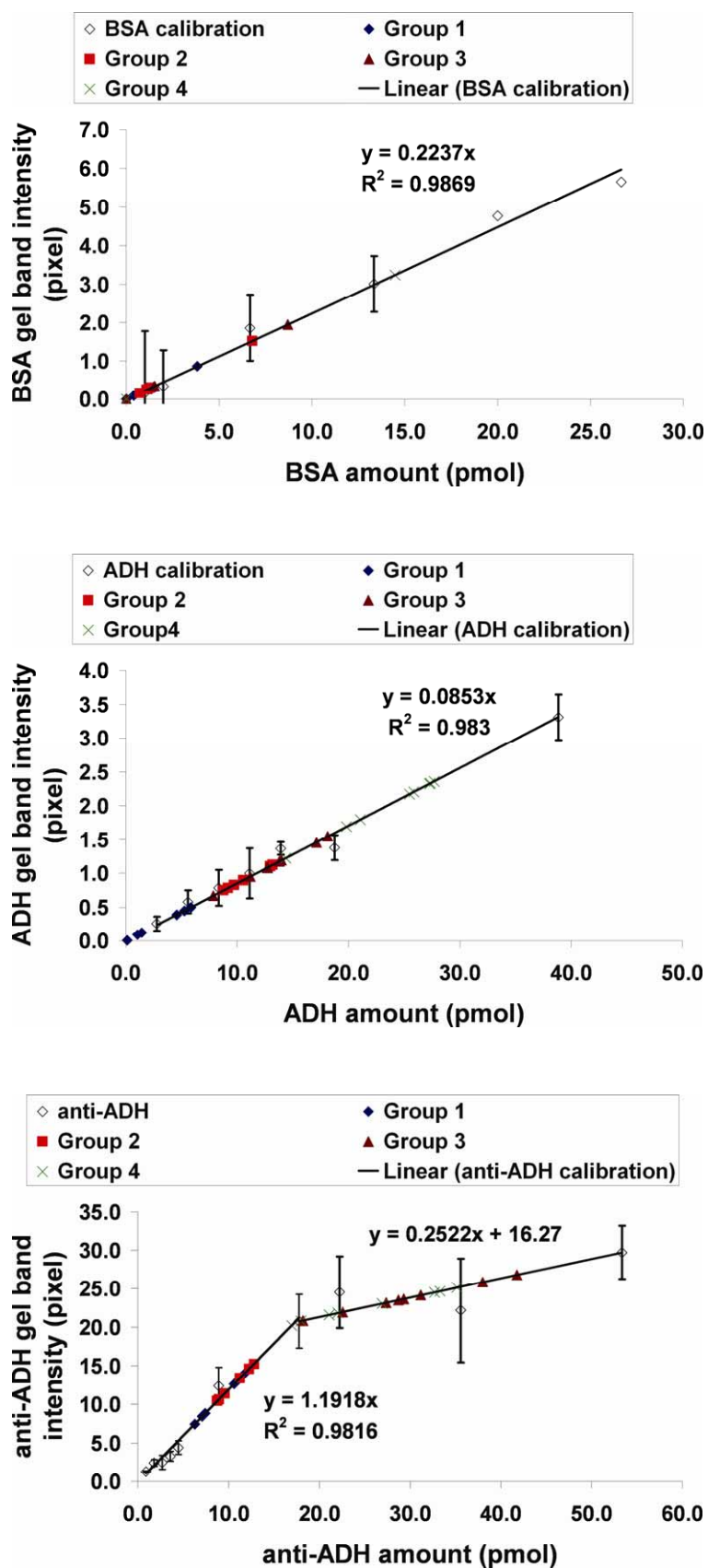


Figure S1. Calibration curves for proteins of ADH system. The data points of all the IP experiments were also marked on the curves: (a) BSA, (b) ADH, (c) anti-ADH.

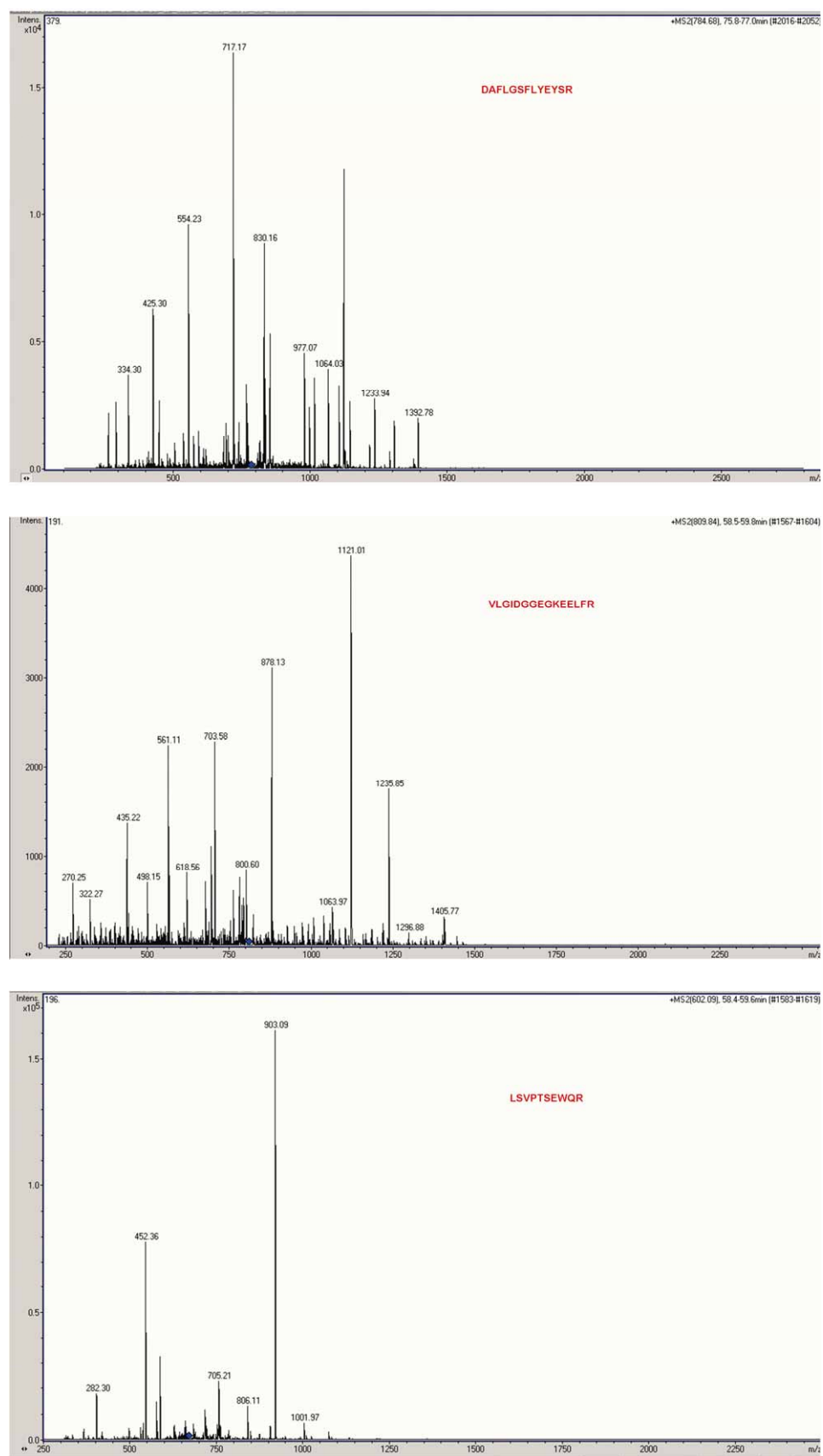


Figure S2. Sample tandem mass spectra. (a) Tandem mass spectrum of BSA peptide. (b) Tandem mass spectrum of ADH peptide. (c) Tandem mass spectrum of anti-ADH peptide.

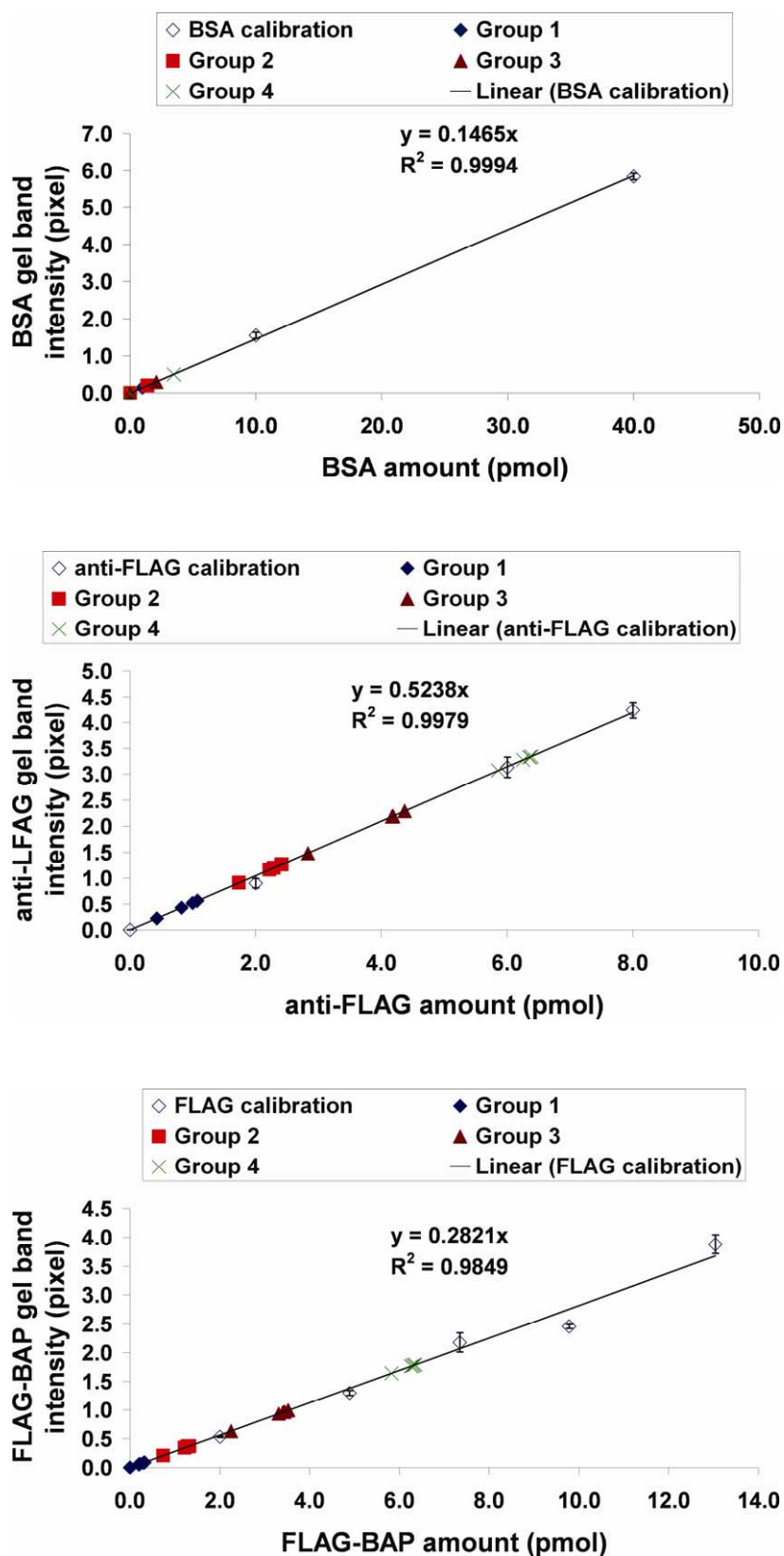


Figure S3. Calibration curves for proteins of FLAG system. The data points of all the IP experiments were also marked on the curves: (a) BSA, (b) FLAG-BAP, (c) anti-FLAG.