## **Description of Additional Supplementary Files**

File Name: Supplementary Data 1

Description: Raw Sanger sequencing trace files for Daedalusexpressed TEAD binding optides. Found in text form in Supplementary Table 4, this data was used to confirm the presence of the properly cloned, sequence-validated TEAD binding optides (TB1G1, TB1G1-L37A, TB1G1-F38A, TB1G2, and TB1G2- W40P) for production as soluble peptides.

File Name: Supplementary Data 2

Description: **TB1G1 SSM sort 2 enrichment values.** Presented here in tabular format is the data found in the heat map in Figure 5b. The values represent the enrichment scores for every possible non-Cys substitution in TB1G1, tested for TEAD binding in SDGF surface display screening (20 nM, monovalent staining). Rows are amino acid substitutions, grouped by chemical category. Columns are the TB1G1 protein sequence, duplicated below the heat map. Enrichment score represents a variant's fold-change in population abundance after two rounds of TEAD sorting versus its input abundance, normalized to TB1G1, and log2-transformed.

File Name: Supplementary Data 3

Description: **High throughput protein content data.** This is the raw and processed high throughput sequencing data used for analysis of surface protein content of the high diversity CDP library, presented in summarized form in Figure 2, Figure 3, and Supplementary Table 3. The Supplementary Methods provide a detailed guide for the generation, processing, and interpretation of this data. The sequences, in the form of DNA or protein for each CDP, were withheld as proprietary information.