Figure S6

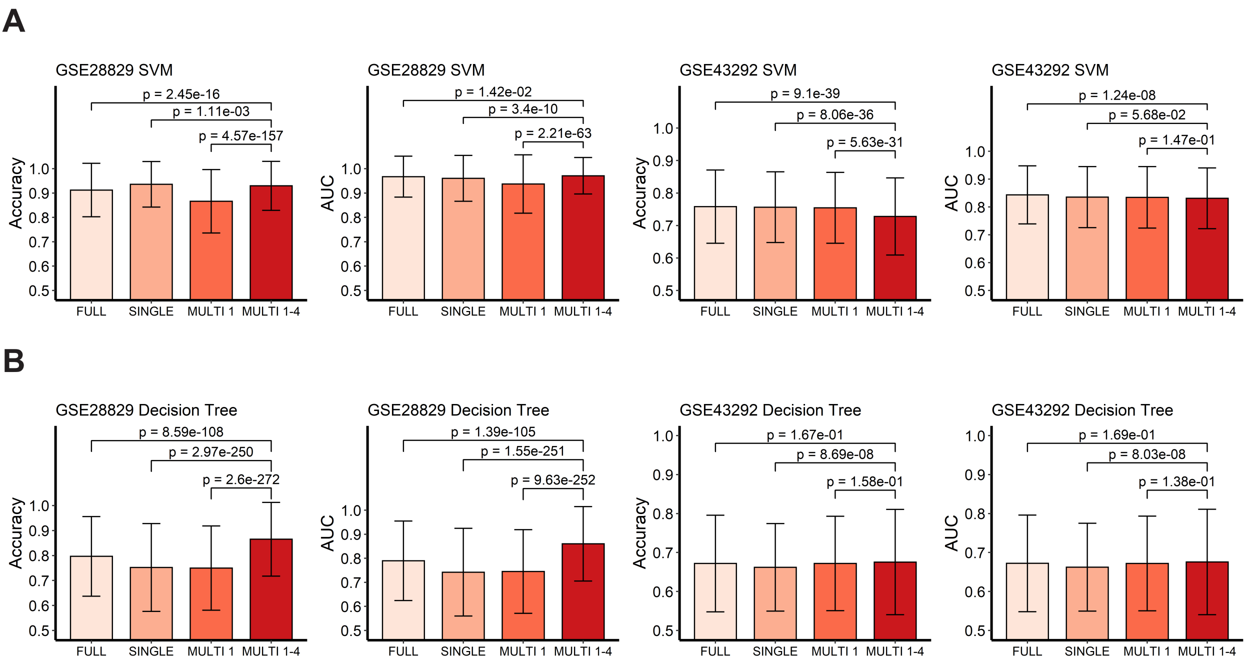

Figure S6 Validation of selected gene sets in independent cohorts

Classification performance based on single-omics (SINGLE), multi-omics component 1 (MULTI 1), and multi-omics component 1-4 (MULTI 1-4) feature subsets as well as the full data (FULL) as a baseline on two independent cohorts GSE28829 and GSE43292. Results were measured by accuracy and AUC using SVM (A) and decision tree (B), respectively, with stratified 5-folds cross-validation and 1,000 random repeats. Results are presented as mean ± SD.