

Figure S8: Pairwise edit distance comparisons between 81 sequence tags designed using barcrawl Frank 2009. We generated these tags using: "barcrawl -l 6 -m 3". Barcrawl uses a hybrid approach to account for substitutions and a single deletion that produces sequence tags approximately equal to a minimum edit distance of two, allowing tags to differentiate samples sufficiently in the presence of insertion, substitution, and deletion errors but not allowing for error correction.

