

Figure S1. Variation in VSIG8 protein level in hair samples from monozygotic twin pairs.

Illustrated are the averages and standard deviations of each twin pair (pooled for the two individuals, each sampled in quadruplicate) for 5 female and 5 male pairs. Spectral counts were not significantly different within twin pairs. The average VSIG8 level from the 5 male pairs was the same as from the highest three female pairs (88 ± 22), but the level in two female pairs was significantly lower (5 ± 4).

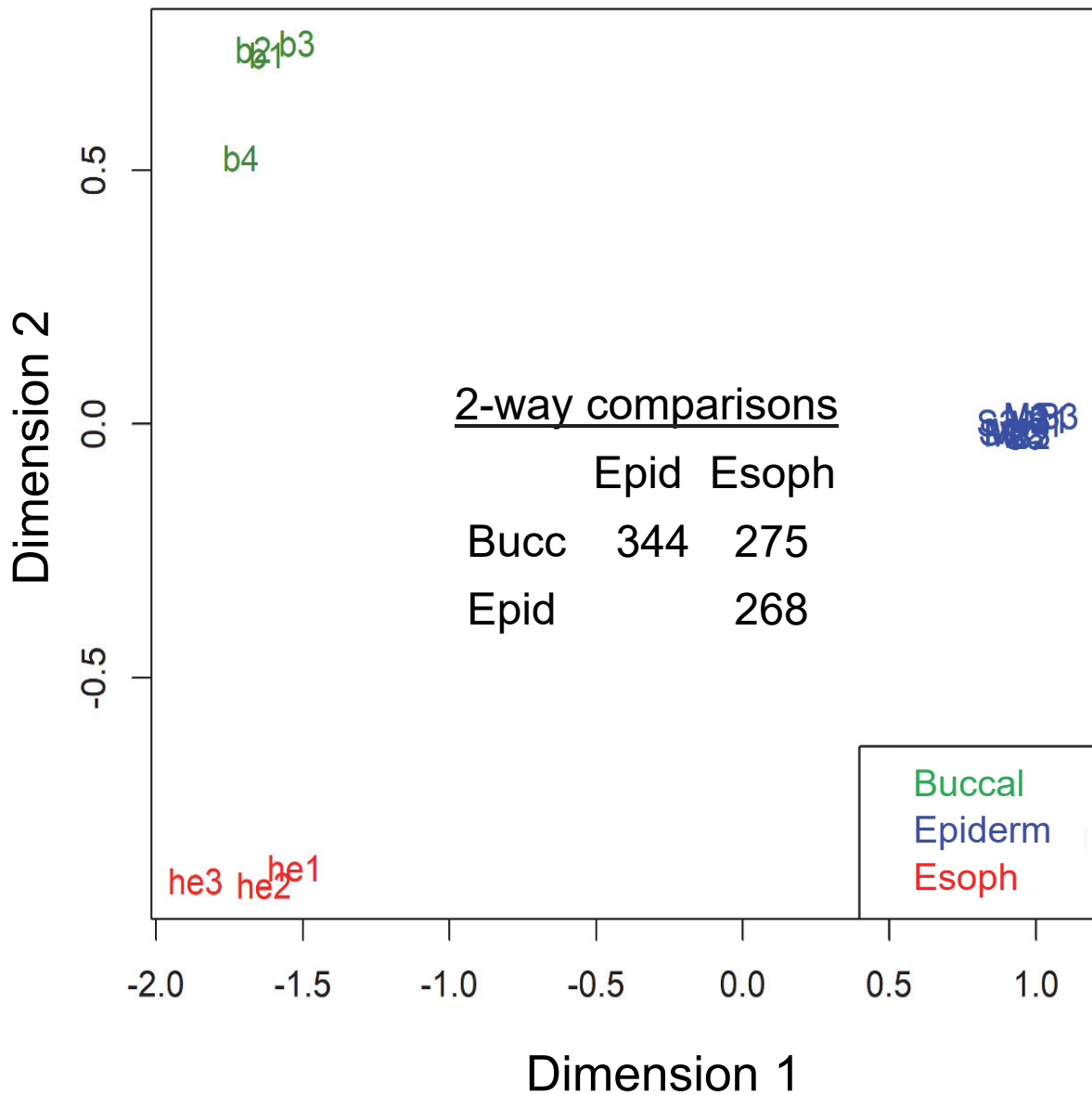


Figure S2. Comparison of buccal, epidermal and esophageal protein profiles. The multidimensional scaling plot of all the samples shows log fold change distances between samples. Prior to analysis, proteins averaging less than 1 weighted spectral count were filtered. Analyses were conducted using the limma-voom Bioconductor pipeline^[58] with limma version 3.32.10, edgeR version 3.18.1, and R version 3.4.4, originally developed for RNA sequencing data. Protein expression was compared between sample types using a one-way ANOVA model in limma, with standard errors of log fold changes adjusted to account for within-subject correlations. Illustrated is a compilation of buccal (4 subjects, b1-b4)), epidermal (4 subjects in triplicate, B1-B3, M1-M3, S1-S3, W1-W3) and esophageal samples (3 subjects, he1-he3).