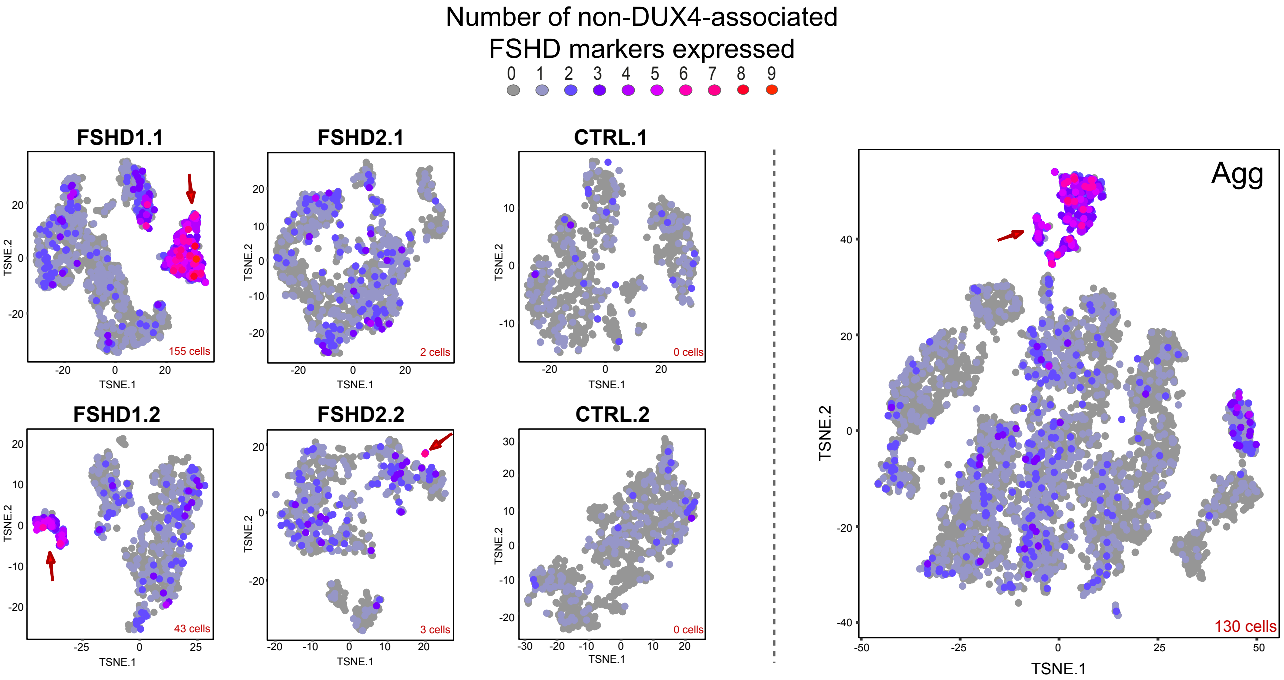

Figure S8. scRNAseq allows for the identification of non-DUX4-associated transcriptional changes in FSHD. t-SNE projections (Cell Ranger) of all samples, colored for the number of non-DUX4-affected FSHD-associated biomarkers being expressed per cell (86 genes previously identified by Yao et al.(4)). The affected population is highlighted with a red arrow.