



Figure 6—figure supplement 1. Microarray transcriptomic data of the NP and AF from four individuals, two of which are young and non-degenerated and the other two aged and degenerated.

(A) boxplots of the normalized data show per-sample distribution of genome-wide expression profiles. (B)–(D) Hierarchical clustering of the 8 microarray samples, based on genome-wide genes (B), matrisome genes (C), or the genes detected by proteomic data only (D). (E)–(H) Scatter plots of probesets between the average expressions of two groups. Red color indicates higher expression in the y-axis samples, and blue indicates higher expression in the x-axis samples. A $\log_2(\text{fold-change})$ of >3 and average expression >10 were used as cutoffs. Multiple instances of a differentially expressed gene are due to multiple probesets design of the array.