

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Differential expression analysis between healthy tissues and NAT in each of the eight tissue types.

File Name: Supplementary Data 2

Description: Genes upregulated/downregulated in comparison of NAT and healthy, and the number of tissue types they were perturbed in.

File Name: Supplementary Data 3

Description: GSEA hallmark gene sets analysis of NAT vs. healthy tissues and NAT vs. tumor.

File Name: Supplementary Data 4

Description: Differential expression analysis between tumors and NAT in each of the eight tissue types.

File Name: Supplementary Data 5

Description: Top 100 upstream regulators of the 18-shared TASA genes as found by Ingenuity Pathway Analysis.

File Name: Supplementary Data 6

Description: Spearman coefficients of the correlations between TASA in the NAT tissue with the expression of genes in the paired tumor samples in each tumor type.

File Name: Supplementary Data 7

Description: Enrichment scores of 30 cell types generated by xCell.