

Supplementary Figure 1. Mean absolute *s* **scores in case study 2.** Results of the multi-omics analysis shown in Figure 3 underwent filtering based on a 5% FDR threshold before calculating the mean absolute *s* values in the six-dimensional analysis (left). Next, the number of gene sets with mean absolute *s* values greater or lower than 0.08 was counted (right) as below this level, mitch precision is lower than expected.