S4 Figure: Samy expression profile under the different conditions studied

The expression level distribution of Samy genes \((n = 102)\) is presented in each condition (described in S2 Fig and S6 Table). A dedicated R package ('mClust') was used to identify the bimodal distributions and classify genes accordingly. In non-inducing conditions (i.e. all conditions except HT, ONA, NAG), a bimodal profile was observed, genes being categorized in the basal (red) or high expression level (green) population. In 'HT', 'ONA' and 'NAG' conditions, the distribution of Samy gene expression was unimodal (population in blue). The data and scripts underlying these panels can be found in S1 Data and S2 Data, respectively.