

Supplementary figure 1: Workflow of the *in-silico* analysis used to identify a new bacterial strain that satisfied the target metabolic profile. Steps in the light blue background resulted in the identification of 77 genomes out of the 6,963 genomes available in the KEGG database with the potential to either degrade prebiotics and enzymes involved in the metabolism of neuroactive compounds (as shown in Figure 1). Steps in the green background led to the identification of 4 *Lactobacillus plantarum* genomes showing the potential to degrade the prebiotics of interest while producing the neuroactive compounds of interest (relevant for Figure 2). This informed the *in-vitro* and *in-vivo* characterization of the new psychobiotic candidate *L. plantarum* APC2688, shown in the step with the orange background (as depicted in Figure 3 and 4).



Supplementary Figure 2: PCA plot of untargeted metabolomics performed on supernatant samples collected at late stationary phase of APC2688 cultures grown in media with different carbon sources. PCA plot constructed using CLR-transformed abundances of every metabolite detected with a confidence on its identity of a level 1 or level 2A (the two highest levels of confidence). Distances between samples were calculated using Euclidian method as suggested for compositional data. Each colour represents a condition as indicated in the legend of the figure.



Supplementary Figure 3: Hatching of the zebrafish eggs and survival of the larvae during the 5 days of exposure to the APC2688 strain supernatant grown on media with different carbon sources. Panel A shows the percentage of zebrafish eggs hatched per day of the experiment. Panel B shows the percentage of surviving fish per day of the experiment. The headers 0.1 and 0.2 correspond to the 0.1% and 0.2% of bacterial supernatant concentration, respectively, administered to the fish water. Colours in the plot represent the different treatment groups as indicated in the legend of the figure.