Legend to Supplemental Fig. S1

Fig. S1. Overall transcription of all *gad* genes in each reference strain in response to acidification in DM at pH 4. Relative normalized (based on the 16S rRNA gene) expression of *gadD1* (□), *gadT1* (Δ), *gadT2* (▲), *gadD2* (■), and *gadD3* (○) in 10403S, LO28 and EGD-e in DM before (0 min) and after (12 and 30 min) acidification in pH 4 achieved with 3 M HCl. Expression of each gene was calculated following Advanced Relative Quantification and normalization based on its relative transcription compared to that of 16S rRNA gene in each strain and time point. To allow comparison of the transcription between different genes in each strain and between strains, all transcription data presented in this figure were expressed as a percentage of the maximal level detected for any gene in any strain. This was *gadD3* of EGD-e after 30 min of acid challenge which showed a relative expression to 16S rRNA of 1.06 10-6 (indicated with dotted lines) and this value was arbitrarily set as 100. The fold change of the expression of each gene in each strain compared to the initial expression at time 0 was calculated and if found above 2.00-fold or below 0.50-fold it is indicated close to each marker. A statistically significant change ($p<0.05$) as estimated by Student's t test is marked by (†). Tukey's multiple comparison test comparison was also carried out between the expression of all genes in each time point and in each strain separately. A result was statistically significant when $p<0.05$ and it is indicated on the graphs by (*). Error bars represent standard deviation.