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## Piezophysiology of genome wide gene expression levels in the yeast *Saccharomyces cerevisiae*

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The legend for figure 4 in the above-mentioned article was inadvertently omitted during file conversion. The legend is as follows:

**Fig. 4.** Functional characterization of induced genes (40MPa) according to the MIPS categories. The genes selected to be induced were grouped according to the functional categories of MIPS using GeneSpring. The percentage was calculated as follows: (number of genes induced by pressure) / (number of genes in the categories) ×100

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