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Author Correction: The MFS efflux pump EmrKY contributes to the survival of *Shigella* within macrophages

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In this Article, Figure 1a is a duplication of Figure 1b. The correct Figure 1 appears below as Figure 1.

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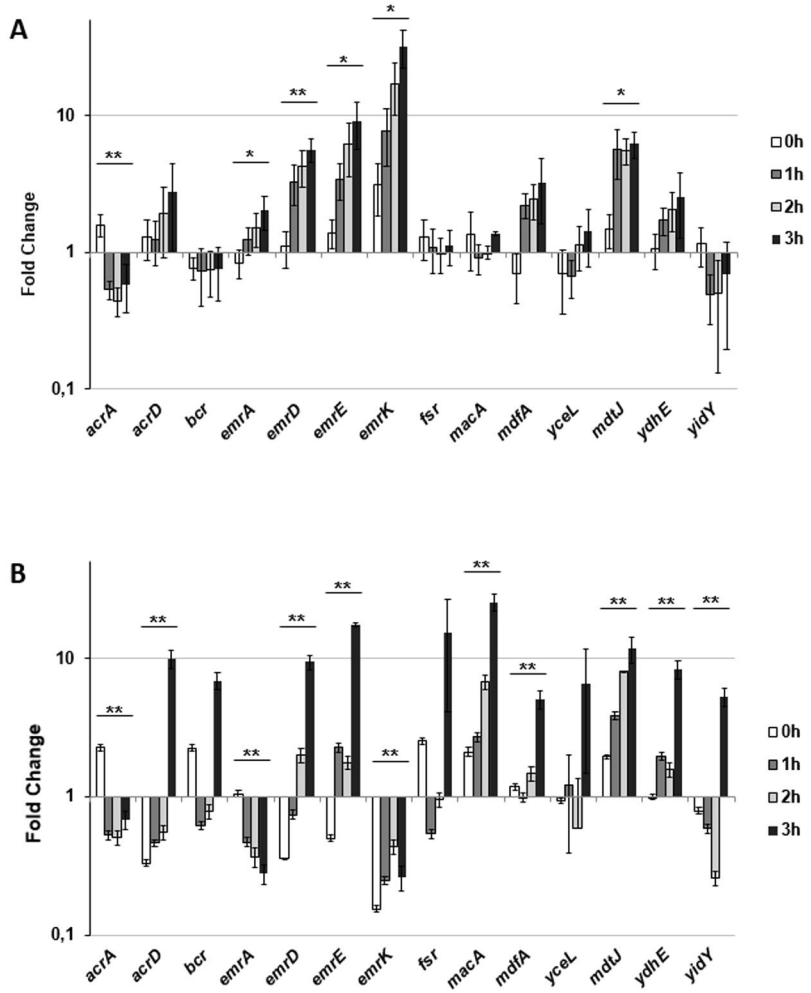

Figure 1. Relative efflux pumps encoding gene transcription during *S. flexneri* infection of (**A**) U937 and (**B**) Caco-2. Quantitative analysis of 14 efflux pump transcripts was performed by means of Q-Real Time PCR assay. Total RNA was extracted from intracellular *S. flexneri* M90T bacteria at various time points p.i., from 0 h (corresponding to bacterial adhesion to the target cells, see MM) up to 3 h. Each infection was repeated three times and at least three wells were run for each sample. The x axis indicates the expression fold-change (RQ value) for each gene on a logarithmic scale. The results are shown relative to the expression of each gene in bacteria grown in RPMI (**A**) or DMEM (**B**) set to 1.00. Statistical significance was determined by a one-tailed ANOVA, and p values are as follows: *$p < 0.05$, **$p < 0.01$. Error bars represent SD.