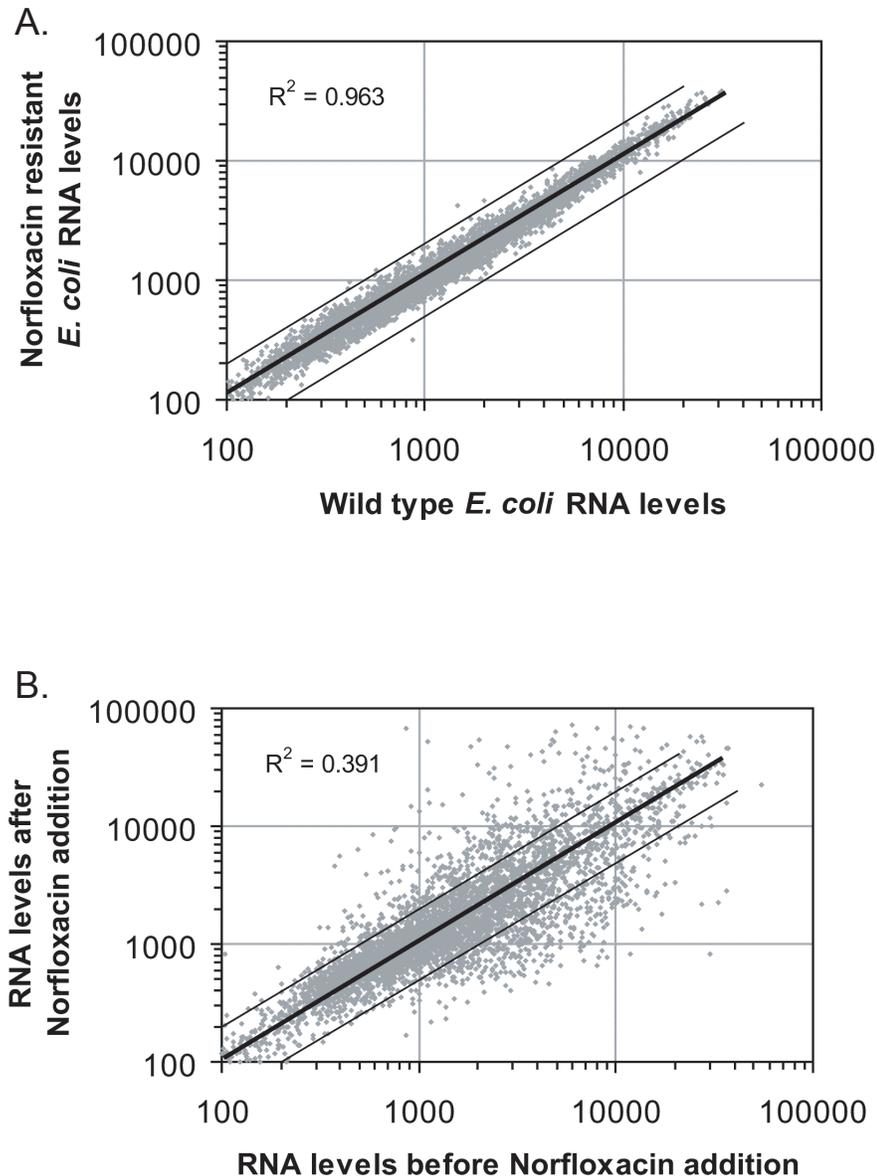


## Additional data file 4

B. Peter et al.



### Additional data file 4. Reproducibility of microarray measurement of RNA levels.

A. Total RNA prepared on separate occasions from a norfloxacin resistant *gyrA<sup>R</sup>parC<sup>R</sup>* strain and the isogenic wild type strain was labeled and applied to the same microarray. RNA from the resistant mutant was reverse transcribed into Cy5-labeled cDNA, and RNA from the wild type was reverse transcribed into Cy3-labeled cDNA. Fluorescence signals for all genes are plotted on a logarithmic scale (base 10), after background subtraction and removal of spots which had an extremely low signal in one or both channels. The thick line represents a linear best-fit line to the data, and hairlines represent twofold changes in either direction. The  $R^2$  value is shown in the upper left. B. A similar quantification of a microarray experiment in which many genes changed their expression level. The wild type strain in A was treated with 15 microg/ml norfloxacin, and RNA from samples taken immediately before and 30min after the treatment was labeled by reverse transcription and applied to a microarray. The microarray data are plotted as in A. Points above the line represent genes that were induced by norfloxacin treatment, and points below the line represent genes that were repressed.