**Statistical analysis**

For testing uniformity of distribution of NTs over cell we assumed the auxiliary hypothesis that poles cover < 50% of cell surface. P-value for this joint hypothesis was computed using quantiles of the Beta distribution. Comparison of cell counts was performed with a binomial generalized linear model using the glm function in R (R Core Team 2019) and - as an additional check – the stan\_glm function from the RStanArm package (Goodrich et al. 2018). Analysis of plasmid transfer and relative expression was performed on the log scale using a linear model with the lm and cor.test functions in R. Where applicable, contrasts and multiple testing corrections were performed with the TukeyHSD function. The difference of spatial distributions of NTs between wild type and Ampicilin-treated bacteria was assessed with Chi-squared test using the chisq.test function in R. Where applicable, we used models with full interactions. Whenever multiple model formulations were considered, we have reported the p-value least favorable to our conclusions. Full code for the statistical analysis can be found in the Supplementary Material.

**References**

R Core Team (2019). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.

Goodrich B, Gabry J, Ali I & Brilleman S. (2018). rstanarm: Bayesian applied regression modeling via Stan. R package version 2.17.4. http://mc-stan.org/