Electronic Supplementary Information

GFP-PspA Expression

GFP-PspA was expressed from the plasmid pEC1 which was constructed by cloning *pspA* into the plasmid pDSW209 with an extended linker sequence, as reported in Engl *et al.* 2009 (1). A culture from a single colony of *MG1655ΔpspA*/pEC1 (1) was grown aerobically overnight at 37 °C in LB medium with ampicillin (100 µg/ml). The next day, 5ml of minimal M63 glucose (0.4%) + ampicillin (100 µg/ml) was inoculated with 100µl of the overnight culture and grown aerobically at 30 °C for 4-6 hours to mid-exponential phase. No inducer was added to the culture as GFP–PspA was produced by leaky expression under the control of a weak P_{trc} promoter, downregulated by the constitutive $LacI_q$ repressor encoded on the plasmid.

Chung-Kennedy Algorithm

The Chung-Kennedy Algorithm (2, 3) is a noise-removal filter that preserves the steps in step-wise signals. A forward and backward window is generated from any given data point to sample the same number of points before and after the point from which the windows are generated. The number of points sampled (i.e. the window size) is variable. The mean and variance of each window is calculated and the output (filtered) value is the one with the smaller variance. This preserves steps as the variance of a window straddling points on both sides of a step-change will be larger than a window with points on only one side. The window size is selected to give the smallest standard deviation between the raw and filtered signals. Only one pass of the filter was applied to the data.

Pairwise Difference Distribution Function

The pairwise difference distribution function (PDDF) (4, 5) for each filtered bleaching trace was calculated as follows. For every data point, its value is subtracted from all data points that follow. For a signal having n data points, the total number of pairwise differences will be equal to $n(n-1)/2$. Subsequently the distribution of these pairwise differences can be calculated using a user-defined number of bins, in this case 2000. The PDDF is then normalised by dividing each bin count with the total number of pairwise differences to give the percentage of the total number of pairwise differences in each bin. The power spectrum of the PDDF was then calculated by fast Fourier transform using the Hanning window.

Four-Parameter Burr Distribution

With the support random variable x ($\gamma \leq x < +\infty$), the probability density function of Burr (4p) distribution is given as (6)

$$f(x) = \frac{\alpha k \left(\frac{x-\gamma}{\beta} \right)^{\alpha-1}}{\beta \left(1 + \left(\frac{x-\gamma}{\beta} \right)^{\alpha} \right)^{k+1}}$$

where k and α are the two shape parameter (k, $\alpha > 0$), β is the scale parameter ($\beta > 0$) and γ is the location parameter. If $\gamma = 0$, it yields the three-parameter Burr distribution. Burr distribution is commonly used to model the household income.

Figure S1

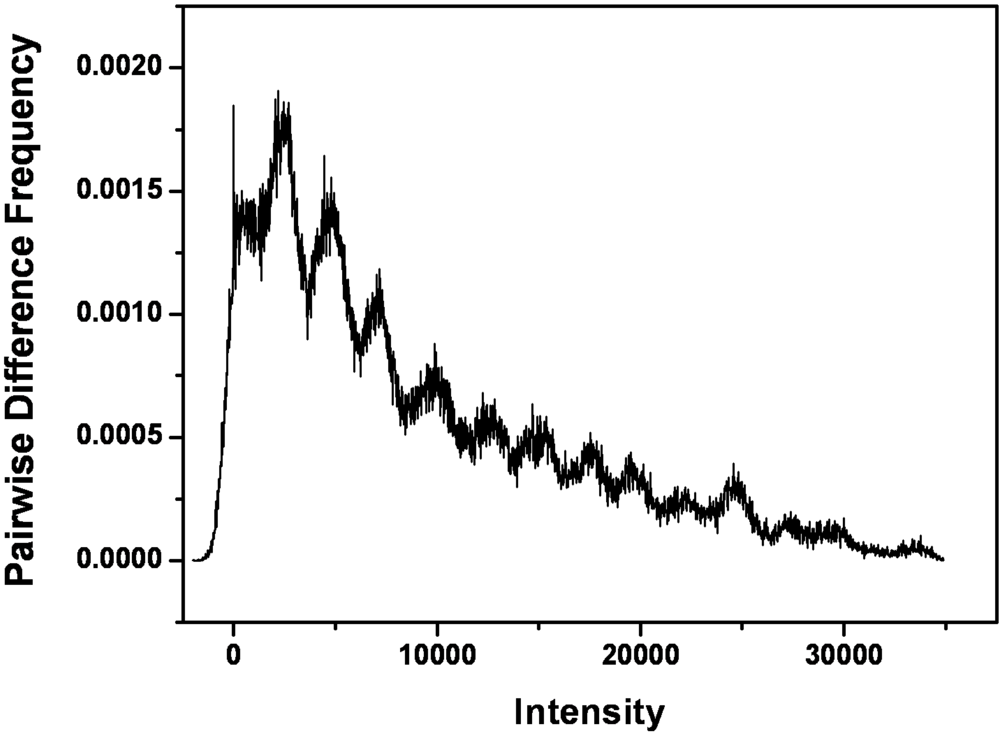

Figure S1 Normalised pairwise difference distribution function (PDDF) of filtered trace in Figure 2A.

References

1. C. Engl, G. Jovanovic, L. J. Lloyd, H. Murray, M. Spitaler, L. M. Ying, J. Errington and M. Buck, *Mol. Microbiol.*, **73**, 382-396 (2009).
2. S. H. Chung and R. A. Kennedy, *J. Neurosci. Meth.*, **40**, 71-86 (1991).
3. M. C. Leake, J. H. Chandler, G. H. Wadhams, B. Fan, R. M. Berry and J. A. Armitage, *Nature*, **433**, 355-358 (2006).
4. S. C. Kuo, J. Gelles, E. Steuer and M. P. Sheetz, *J. Cell Sci.* **14**, 135-138 (1991).
5. T. Lenn, M. C. Leake and C. W. Mullineaux, *Mol. Micobiol.*, **70,** 1397-1407 (2008).
6. P. R. Tadikamalla, *Int. Stat. Rev.*, **48**, 337-344 (1980).