

than one DNA target that has been amplified by PCR is not distinct from a partition that initially contains only one DNA target. Fortunately, the distribution of target molecules across the multiple partitions will be Poissonian in nature (targets distribute between partitions independently and at a fixed rate). By using the Poisson distribution, the initial number of target molecules present can be estimated from the number of positive and negative partitions observed following thermal cycling (Fig. 1). Absolute quantification of the total number of target molecules present in a test sample using dPCR is then relatively straightforward, and can be achieved with application of eqn (1):

$$N1 = -N1 \left(1 - \frac{1}{N}\right) \tag{1}$$

where Nl represents the total number of target copies, N is the

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The current gold standard for measuring specific DNA amounts is quantitative PCR (qPCR). However, qPCR is subject