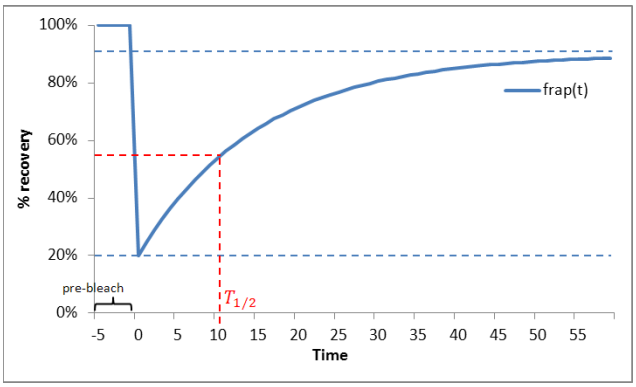
Supplemental Text 1 to FRAP analysis method description.

The GFP fluorescence intensity after photobleaching was modeled using the parametric exponential model (Launholt et al., 2006).

(*) $$frap(t) = \alpha\left(1 - e^{-t/\tau}\right) + \beta;$$



The time to half-recovery of the fluorescence intensity, derived directly from the model equation, is marked below as $T_{1/2}$:

$$\alpha\left(1 - e^{-T_{1/2}/\tau}\right) + \beta = \left\{\lim_{t\to\infty}\left[\alpha\left(1 - e^{-t/\tau}\right) + \beta\right] = \alpha + \beta\right\} = \frac{1}{2}\alpha + \beta$$

$$T_{1/2} = \tau \ln(2)$$

Estimation of model parameters. Model parameters were obtained using the Newton-Raphson optimization algorithm that minimized the sum of squared deviations between the fitted curve and the measurements. To ensure the optimal starting point for the algorithm, an initial search of three-dimensional parameter space (α, β, $T_{1/2}$) was performed. Parameters α, β were tested in the interval (0, 1) at intervals of 0.1, and the $T_{1/2}$ in the interval (0, 100) at intervals of 1. The first one thousand combinations that resulted in the lowest objective function value were used as starting points for the optimization algorithm. The solution that provided the best curve fit to the empirical data indicated the vector of model parameters. For unconstrained estimates, the covariance matrix of model parameters is defined by the following formula:

$$\mathbf{\Sigma} = MSE * (\mathbf{H})^{-1}$$

$$MSE = \mathbf{r}^T\mathbf{r} \big/ (n - p)$$

$$\mathbf{r} = \left(frap(t) - \hat{frap}(t)\right)$$

where $\mathbf{\Sigma}$ is the (3x3) parameter's covariance matrix, $\mathbf{H}$ is a numerical approximation of the Hessian matrix (3x3) of the objective function, n is the number of observations (18), p is the

number of estimable parameters (3), and $\left(frap(t) - \hat{frap}(t)\right)$ represents the difference between the observed measurement and the fitted value. The optimization was performed with SAS 9.2 software using the **IML** procedure (SAS Institute Inc., 2010), and **call nlpnra** was used as the optimization algorithm. The mobile fraction (Mf) for each of the histone variants was calculated according to (Launholt et al., 2006). Each parameter is provided with the standard error of this estimate (these are not 95% confidence intervals). The standard errors of the model parameters and estimates of the mobile fraction were obtained from the covariance matrix $\boldsymbol{\Sigma}$.