Supplementary data for

"Monitoring single-cell bioluminescence of *Arabidopsis* leaves to quantitatively evaluate the efficiency of a transiently introduced CRISPR/Cas9 system targeting the circadian clock gene *ELF3*"

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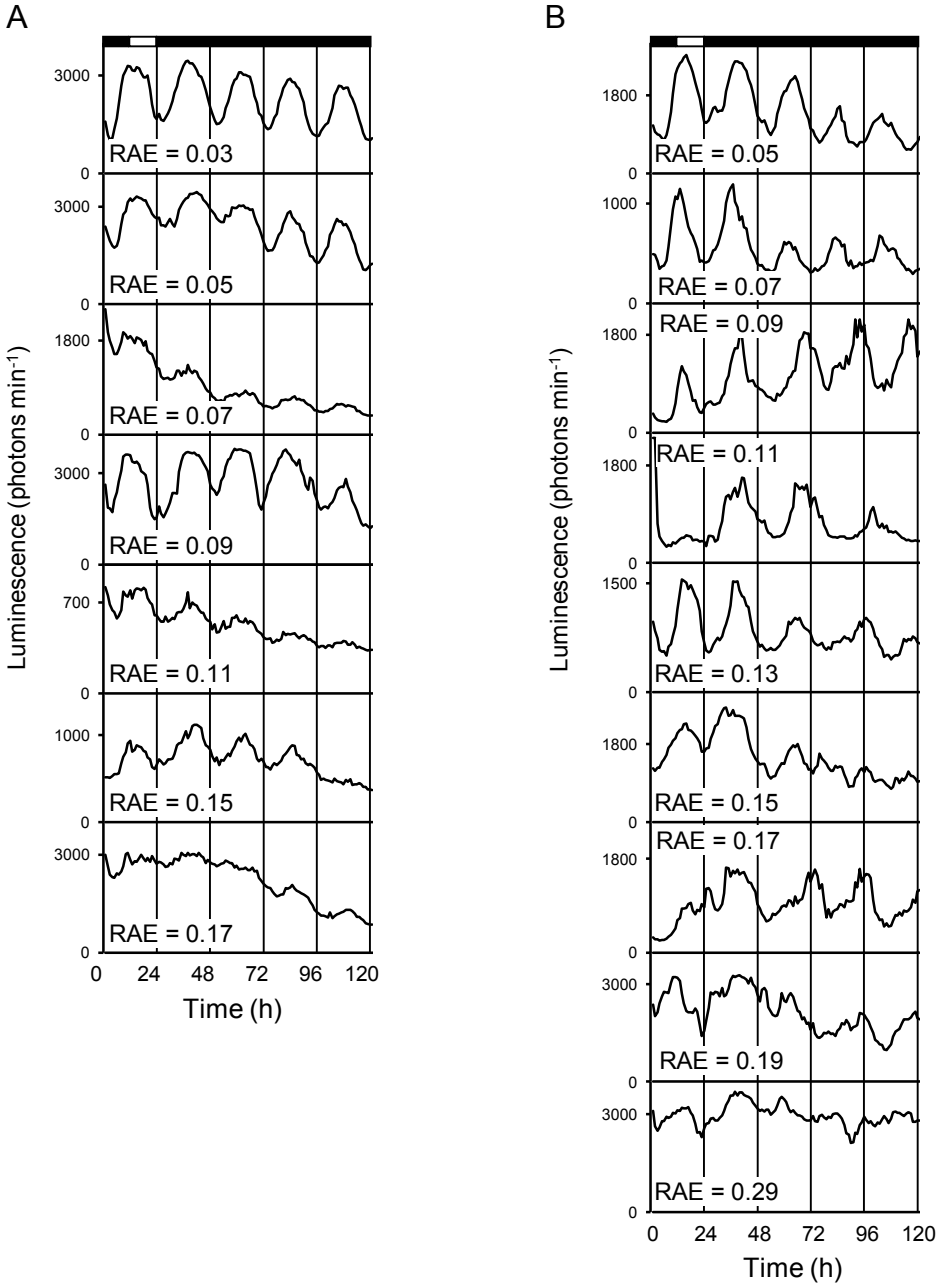
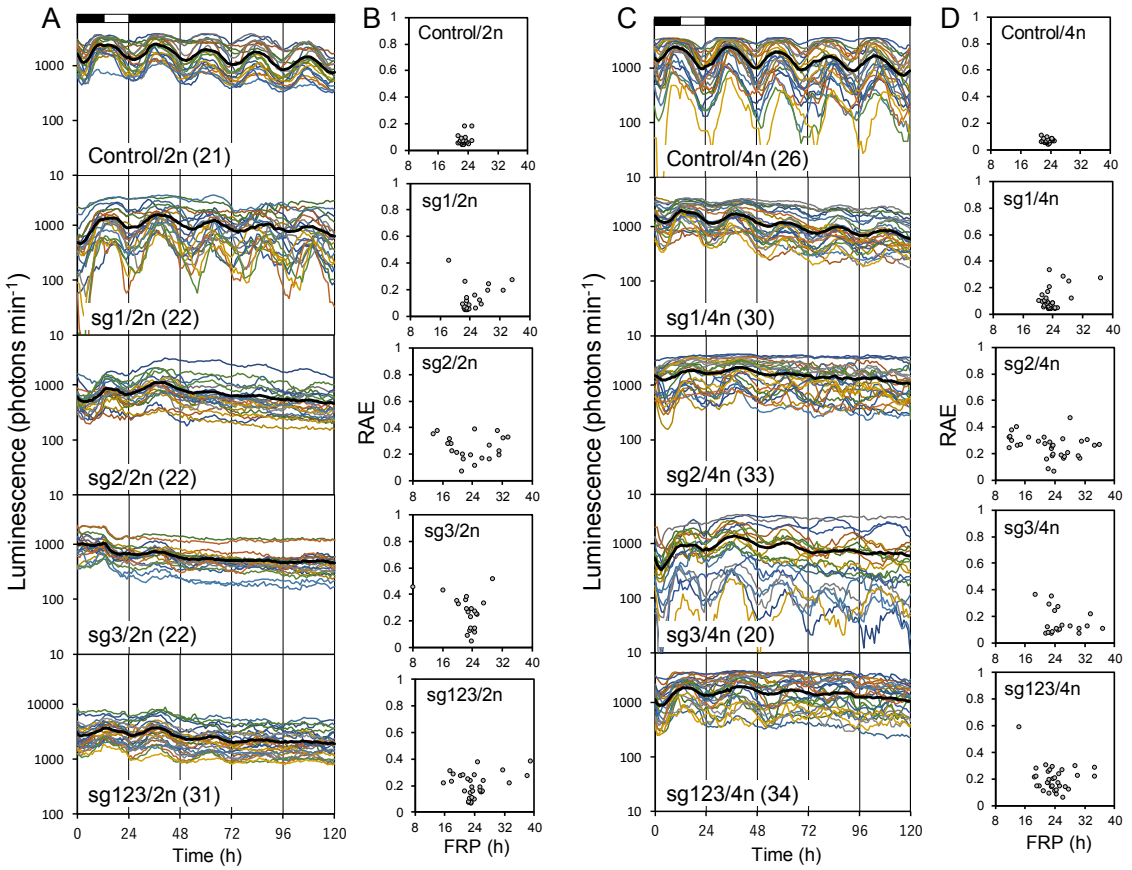
Table S1. Calculated proportions of complete gene-disrupted cells at various ploidy levels by gene-disruption rates on a chromosome.

Cell types	Gene disruption rates in a chromosome (%)							
	99	95	90	85	80	70	50	30
Mesophyll cells in diploid *Arabidopsis*	96	80	64	51	41	26	5	3
Mesophyll cells in tetraploid *Arabidopsis*	91	65	43	29	19	9	2	< 1
Epidermal cells in diploid *Arabidopsis*	97	86	74	63	54	38	17	6
Epidermal cells in tetraploid *Arabidopsis*	94	74	55	41	31	16	4	< 1

The proportions of cells at various ploidy levels were simply assigned as 2n : 4n : 8n (diploid) = 4n : 8n : 16n (tetraploid) = 0.25 : 0.5 : 0.25 for mesophyll cells (del Pozo and Ramirez-Parra 2015; Ferjani et al. 2007), and 2n : 4n : 8n (diploid) = 4n : 8n : 16n (tetraploid) = 0.6 : 0.35 : 0.05 for epidermal cells (Robinson et al. 2018). The proportion of complete gene-disrupted cells by the gene-disruption rate (g) on a chromosome was calculated as follows: $0.25g^2 + 0.5g^4 + 0.25g^8$ (mesophyll cells in diploid), $0.25g^4 + 0.5g^8 + 0.25g^{16}$ (mesophyll cells in tetraploid), $0.6g^2 + 0.35g^4 + 0.05g^8$ (epidermal cells in diploid), $0.6g^4 + 0.35g^8 + 0.05g^{16}$ (epidermal cells in tetraploid). The proportions are indicated as percentages.



Supplementary Figure 1. Examples of bioluminescence traces in individual cells. (A) Cellular bioluminescence traces of control/2n in Experiment 1 with the lowest (0.03), and highest (0.17) relative amplitude error (RAE), and those with the RAE closest to 0.05, 0.07, 0.09, 0.11, and 0.15. (B) Cellular bioluminescence traces of sg123/2n in Experiment 1 with the lowest (0.05), and highest (0.29) RAE, and those with the RAE closest to 0.07, 0.09, 0.11, 0.13, 0.15, 0.17, and 0.19.



Supplementary Figure 2. Bioluminescence traces of individual cells transfected with CRISPR/Cas9 constructs in Experiment 2. (A, C) Mean luminescence (black lines) and luminescence traces of individual cells (lines in other colors) in diploid (A) and tetraploid (C) *Arabidopsis*. The CRISPR/Cas9 target region is indicated in each graph, and the number of measured cells is indicated in parentheses. Note that the y-axis scales differ between panels. (B, D) The free-running periods (FRPs) and the relative amplitude errors (RAEs) of individual cellular rhythms in diploid (B) and tetraploid (D) *Arabidopsis* are plotted. Fourier transform–nonlinear least squares (FFT-NLLS) was performed using the data range 48–120 hours shown in (A) and (C).