

Figure S1. Coefficient of variation (CV) of gene expression variations. Red line indicates CV derived from single-cell RNA-Seq data. Bar graphs show CVs of GL3 expression under the indicated variations (0–100%).

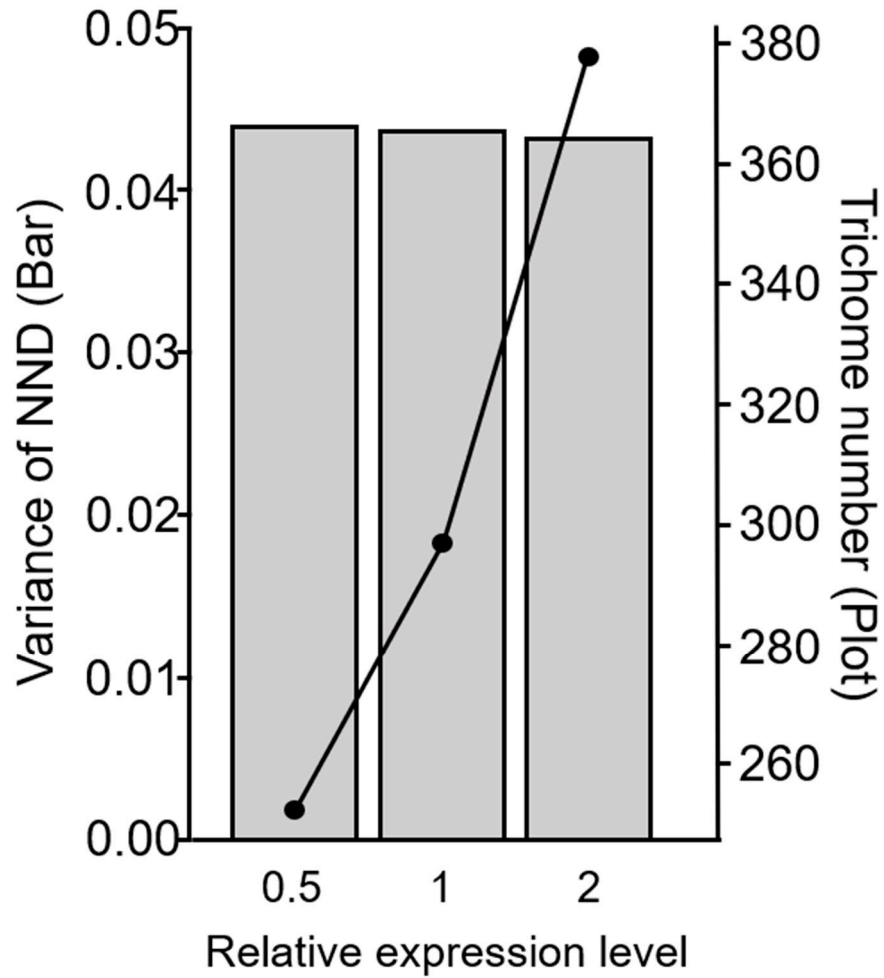
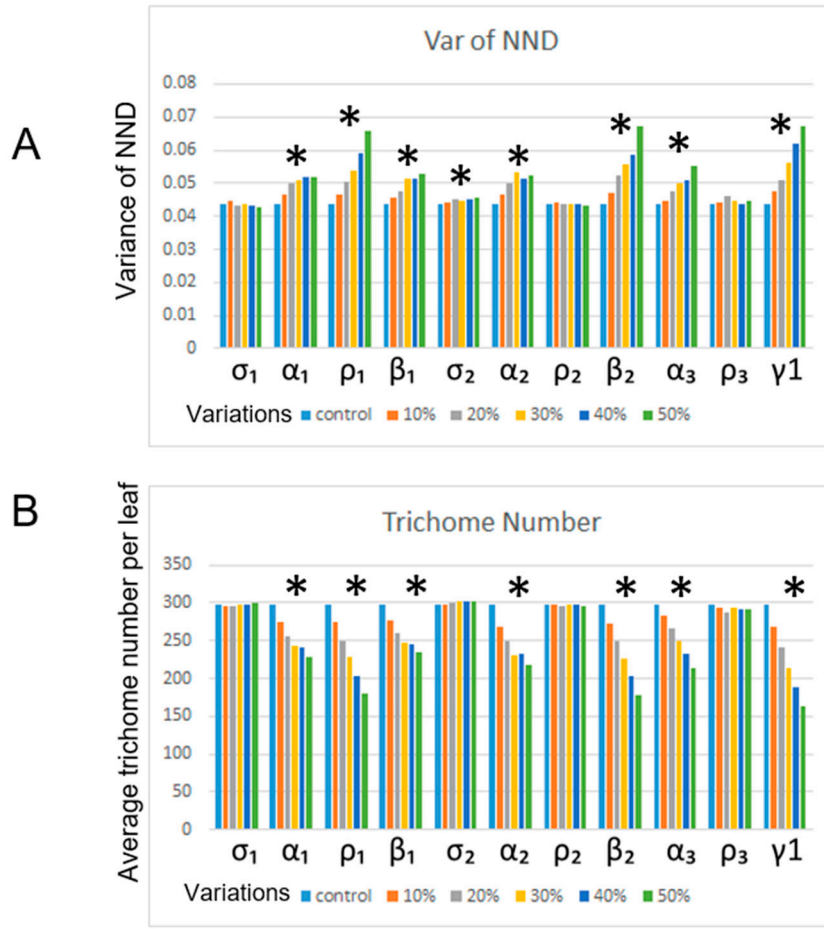


Figure S2. Relationship between the number of trichomes and regularity of the trichome distribution pattern. In our mathematical model, the relative expression level of GL3 was increased up to 2-fold. The numbers of trichomes (solid line) increased significantly, whereas the normalized next-neighbor distance (NND) variances of trichomes remained unchanged (n = 500).



Parameter	Variance of trichome pattern	# of trichome
σ_1	NS	NS
α_1	*	*
ρ_1	*	*
β_1	*	*
σ_2	*	NS
α_2	*	*
ρ_2	NS	NS
β_3	*	*
α_3	*	*
ρ_3	NS	NS
ρ_4	*	*

Figure S3. Variances of the normalized next-neighbor distance (NND) and number of trichomes in mathematical simulations. **(A)** NND variances; **(B)** trichome numbers after 500 trials of calculations. Different colors indicate 0%, 10%, 20%, 30%, 40%, and 50% variations. A summary table is shown at the bottom. NS, not significant; * $p < 0.05$.

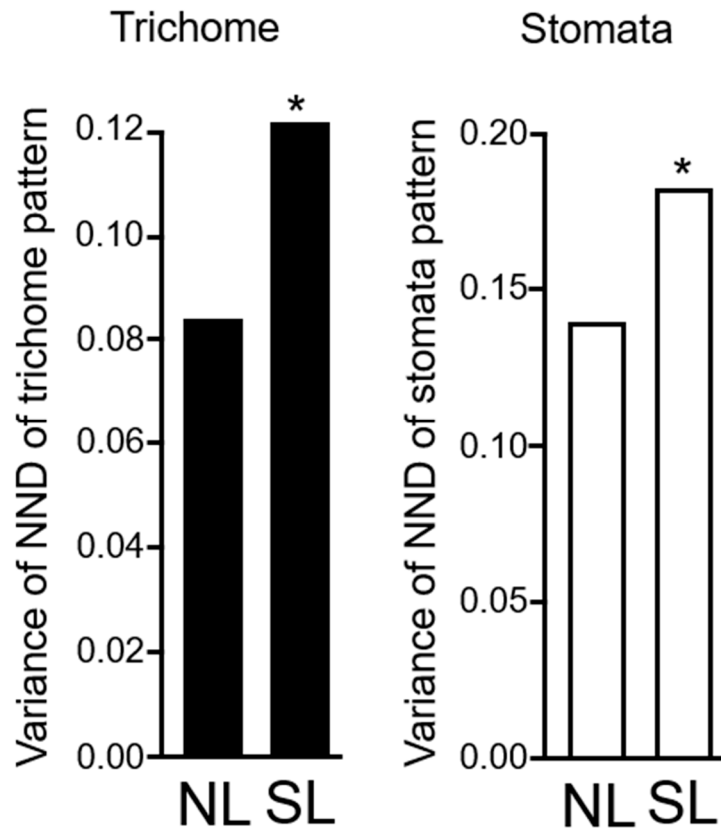
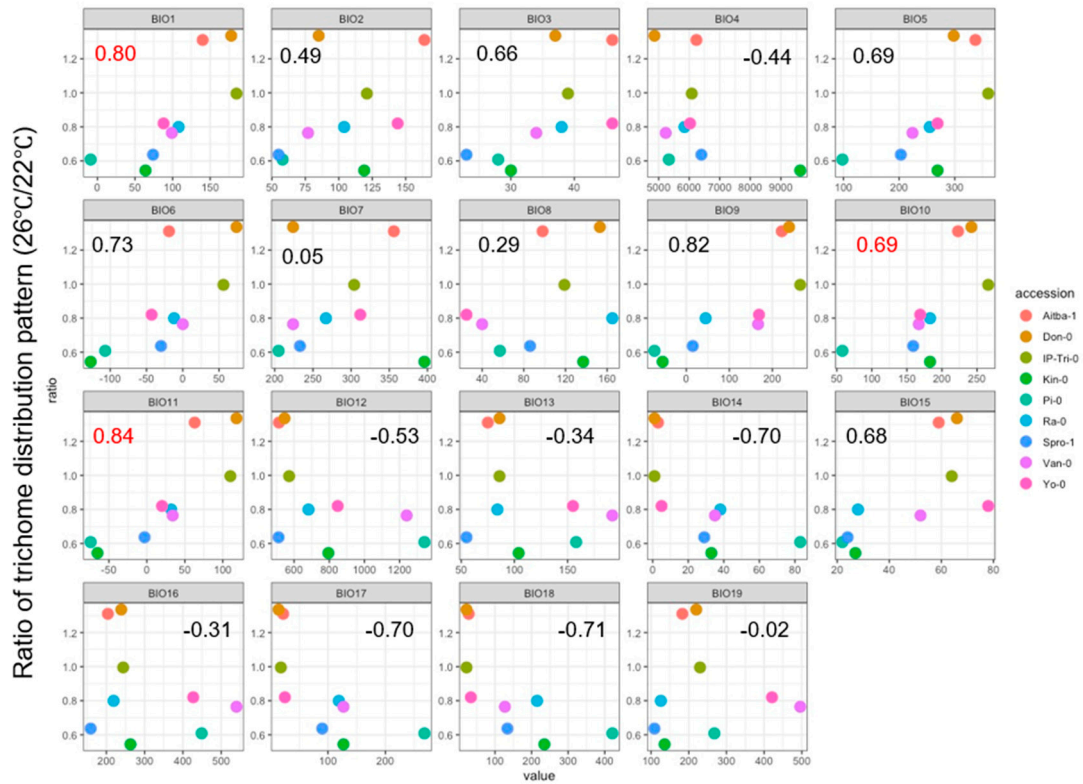


Figure S4. NND variances of trichomes and stomata of *Arabidopsis* plants grown under different light intensities. NL, normal light intensity (1000 lm/m²); SL, strong light intensity (3000 lm/m²). * $p < 0.05$ (F test).



Indices of BIO1~BIO19

Figure S5. Correlation between gene expression variation and BioClim indices. The ratios of the CV of plants (Alba-1, Don-0, IP-Tri-0, Kin-0, Pi-0, Ra-0, Spro-0, Van-0, and Yo-0) at 26 °C relative to that of plants at 22 °C are shown along the y-axis. The 19 indices from the BioClim index are shown along the x-axis. Values in the plots represent Pearson's correlation coefficients (PCCs). The values of PCC with significant correlations ($p < 0.01$) are shown in red.

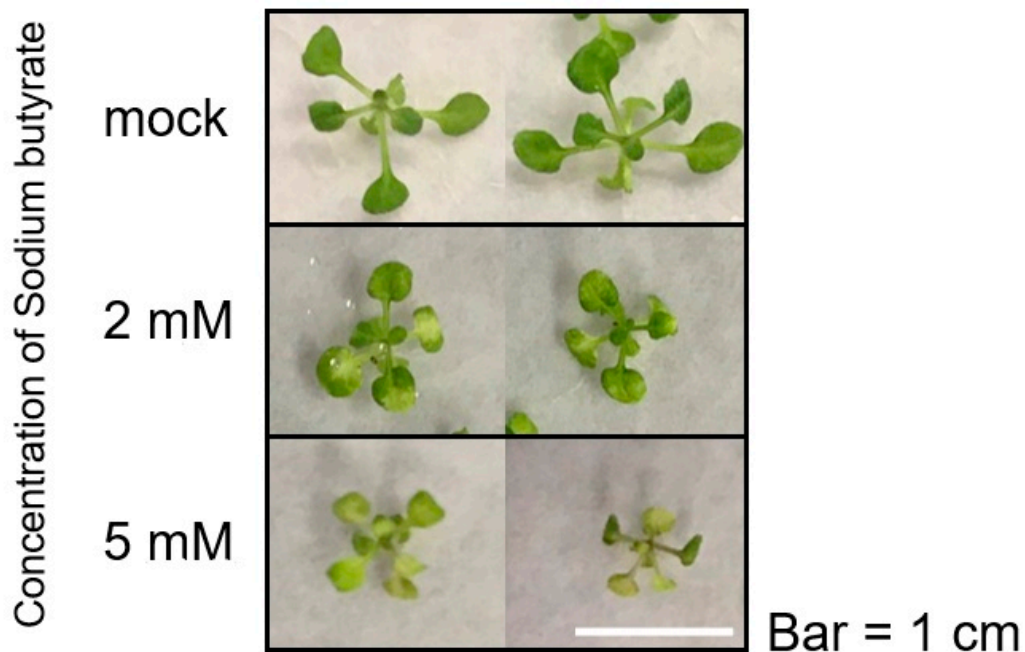
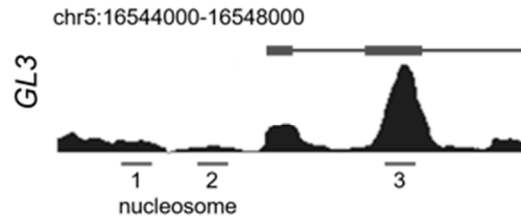


Figure S6. Size of seedlings grown in the presence of various concentrations of sodium butyrate, a histone deacetylase inhibitor.

A



B

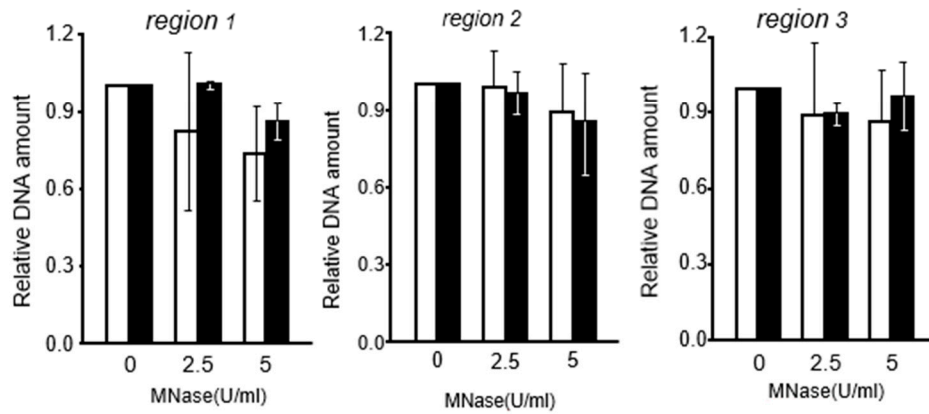


Figure S7. Micrococcal nuclease (MNase) assay. (A) Schematic representation of the upstream region of the GL3 locus. Boxes and lines indicate exons and introns of GL3, respectively. Nucleosome occupancy in the region surrounding the GL3 locus, retrieved from a publicly available website (Relationship between nucleosome positioning and DNA methylation; <http://epigenomics.mcdb.ucla.edu/Nuc-Seq/>), is shown as a density plot. Lines under occupancy are regions used for real-time PCR validation. (B) Relative amount of DNA detected by real-time PCR following treatment with 0, 2.5, and 5 U/ml MNase. White and black bars indicate signals from plants grown at 22 °C and 26 °C, respectively.