

A

PER1_D_cryoxerica

PER1_D_catarinonii

PER1_D_takashimae

PER1_D_hungarica_PT

PER1_D_hungarica_Y22

PER1_D_hungarica_EY

PER1_D_hungarica_PDD24b

0.03

C

Scatter plot C showing the relationship between the p-value (Y-axis, logarithmic scale from 10^{-5} to 10^0) and the K parameter (X-axis, linear scale from 0.6 to 2.2). The plot is divided into two regions by a vertical dashed line at $K = 1.0$: RELAXATION (left, blue background) and INTENSIFICATION (right, orange background). A horizontal dashed red line indicates a significance threshold at $p \approx 0.05$.

Data points are labeled with species names:

- Colletotrichum*
- Tremella*
- Roridomyces*
- Rhodotorula*
- Plant-associated *Dioszegia*
- All *Dioszegia*
- Arabidopsis*-associated *Dioszegia*

D

EY
PT

DhPER2

10kb

0 Identity (%) 100

Unique gene

Differential expression (TPM) $\leq 2x$

EY vs PT Expression differences $2x < \dots < 10x$

EY vs PT Expression differences $\geq 10x$

PT vs EY Expression differences $2x < \dots < 10x$

PT vs EY Expression differences $\geq 10x$

The figure shows a genomic map of the *DhPER2* gene region. The top track shows the EY isoform, and the bottom track shows the PT isoform. A red box highlights the *DhPER2* gene. A scale bar indicates 10kb. A legend explains the symbols: unique genes (grey arrow), differential expression (TPM) (white arrow), and expression differences (colored arrows). The legend also includes a color scale for identity percentage from 0 to 100.