Table S1 Description of 15 cDNA samples used for the validation of reference genes.

cDNA sample	Description
***Oryza sativa* ssp. *japonica* cv. TP309** 1	3 week-old, leaf, watering
2	3 week-old, leaf sheath, watering
3	3 week-old, leaf, 24 h 200 mM NaCl
4	3 week-old, leaf, 24 h 4˚C
O. sativa* ssp. *indica	
cv. KDML105	
5	2 week-old, leaf, without PEG (-0.1 MPa)
6	2 week-old, leaf sheath, without PEG (-0.1 MPa)
7	2 week-old, root, without PEG (-0.1 MPa)
8	45 day-old, mature leaf, watering
9	2 week-old, leaf sheath, 1h 22%PEG (-0.5 MPa)
10	2 week-old, leaf sheath, 3h 22%PEG (-0.5 MPa)
11	2 week-old, leaf sheath, 9h 22%PEG (-0.5 MPa)
cv. NSG19	
12	2 week-old, leaf sheath, without PEG (-0.1 MPa)
13	2 week-old, leaf sheath, 9h 22%PEG (-0.5 MPa)
cv. IR20	
14	2 week-old, leaf sheath, without PEG (-0.1 MPa)
15	2 week-old, leaf sheath, 9h 22%PEG (-0.5 MPa)

Data sets used for the calculation of the average expression stability (M) values:
"All tested samples" included all 15 cDNA samples
"*Indica* and *japonica*" included cDNA samples 2, 6, 12, 14
"Various tissues" included cDNA samples 5, 6, 7, 8
"Various drought" included cDNA samples 6, 9, 10, 11
"*japonica* rice" included cDNA samples 1-4
"*Indica* rice" included cDNA samples 5-15

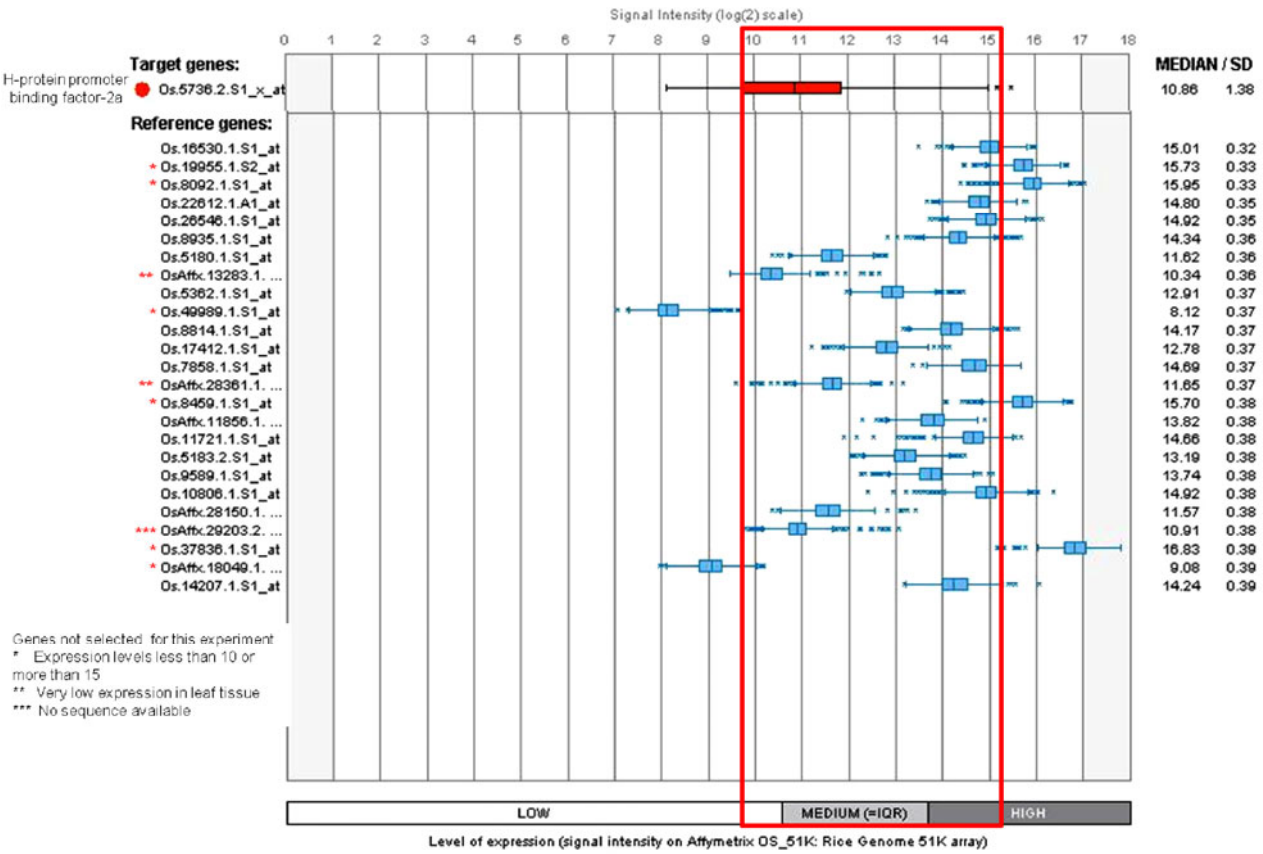

Figure S1 The 25 potential reference genes were obtained from the analysis of 936 microarrays by using the Biomarker Search module in Genevestigator software (https: //www.genevestigator.com/gv/). The microarray data (Array type: OS_51K: Rice Genome 51K array) derived from the Gene Expression Omnibus (765 arrays), ArrayExpress (160 arrays), and PLEXdb (11 arrays) databases is shown. The 15 candidate genes that have the same expression range as the target gene (*Hp2a*) were selected. The expression levels were classified as low (0-10), medium (11-14), and high (>14) according to the signal intensity on an Affymetrix OS_51K: Rice Genome 51K array.

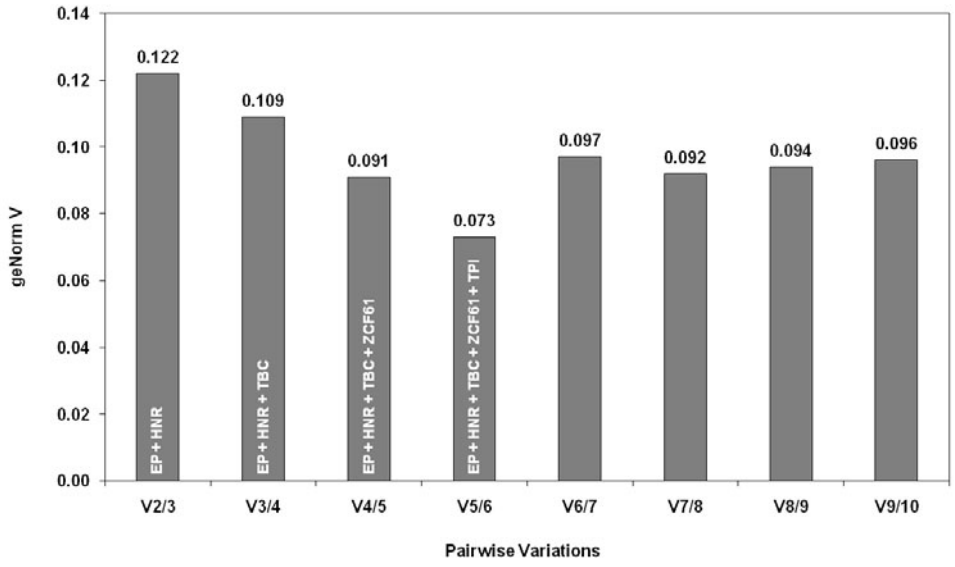

Figure S2 Determination of the optimal number of reference genes for normalization by pairwise variation using geNorm^{PLUS} (Hellemans et al., 2007; Vandesompele et al., 2002). The level of variation (V) in the gene expression is shown. V < 0.15 is recommended (Vandesompele et al., 2002). For example, V2/3 describes the variation of the normalization factor of the two most stable genes (*EP* and *HNR*) and V3/4 describes the variation of the normalization factor of the two most stable genes including the third gene, *TBC*. V6/7 describes the use of *EP*, *HNR*, *TBC*, *ZCF61*, *TPI*, and *GRP*; V7/8 describes the use of six genes including *NBP*, V8/9 describes the use of seven genes including *VPS*, and V9/10 describes the use of eight genes including *ABP*.

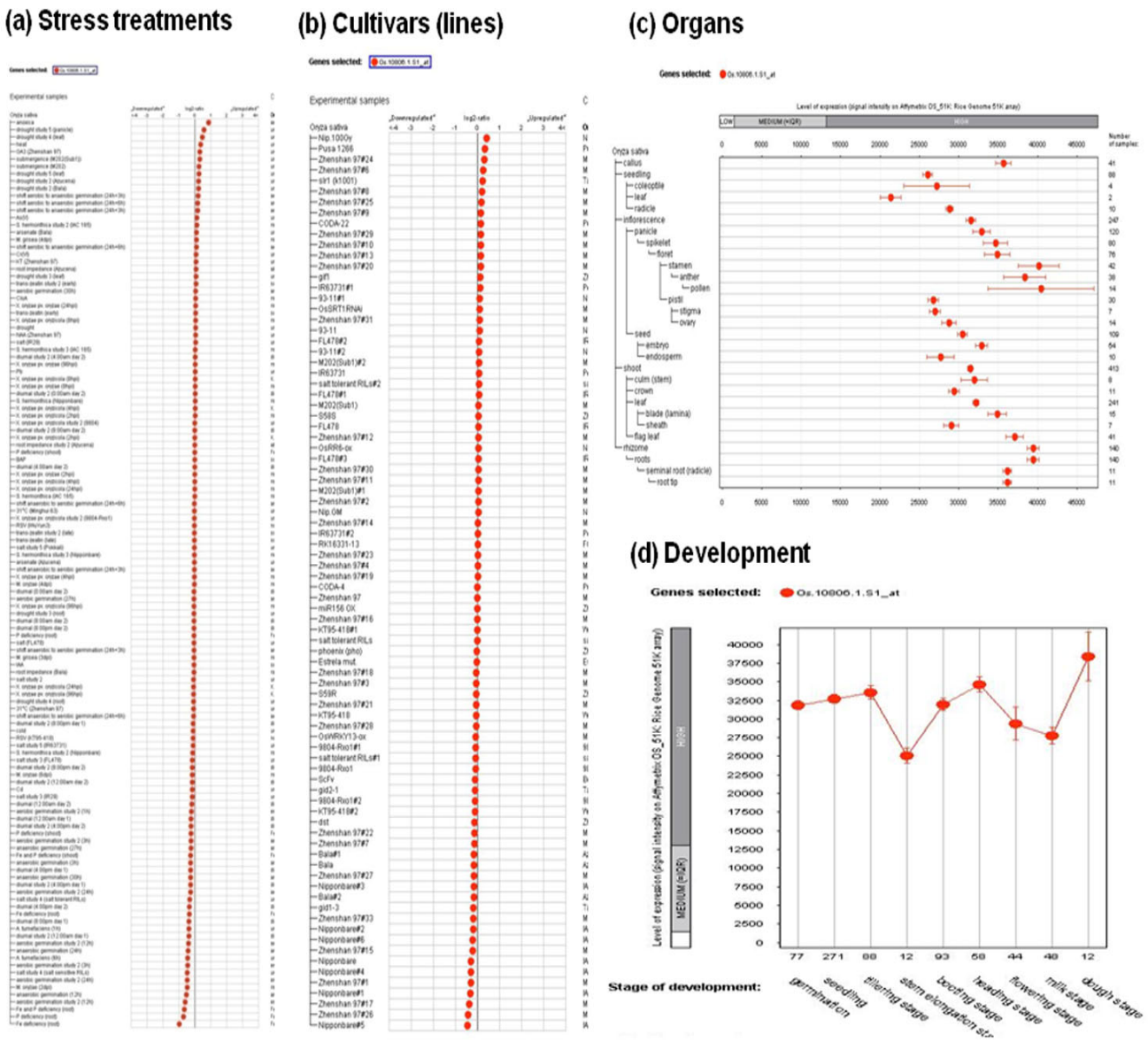

Figure S3 Stable expression of the *EP* (Os.10806.1.S1_at) gene under different stress treatments (a), cultivars (b), organs (c), and development (d) analyzed from the data from the 936 rice microarrays. Data were analyzed using the Meta-Profile Analysis module in the Genevestigator software (https://www.genevestigator.com/gv/). The expression levels of Figure (a) and Figure (b) are presented as log2-ratio where log2-ratio < 0 indicates a down-regulated gene (left) and log2-ratio > 0 indicates an up-regulated gene (right). The expression levels of Figure (c) and Figure (d) are shown as signal intensities on the Affymetrix OS_51K: Rice Genome 51K array.

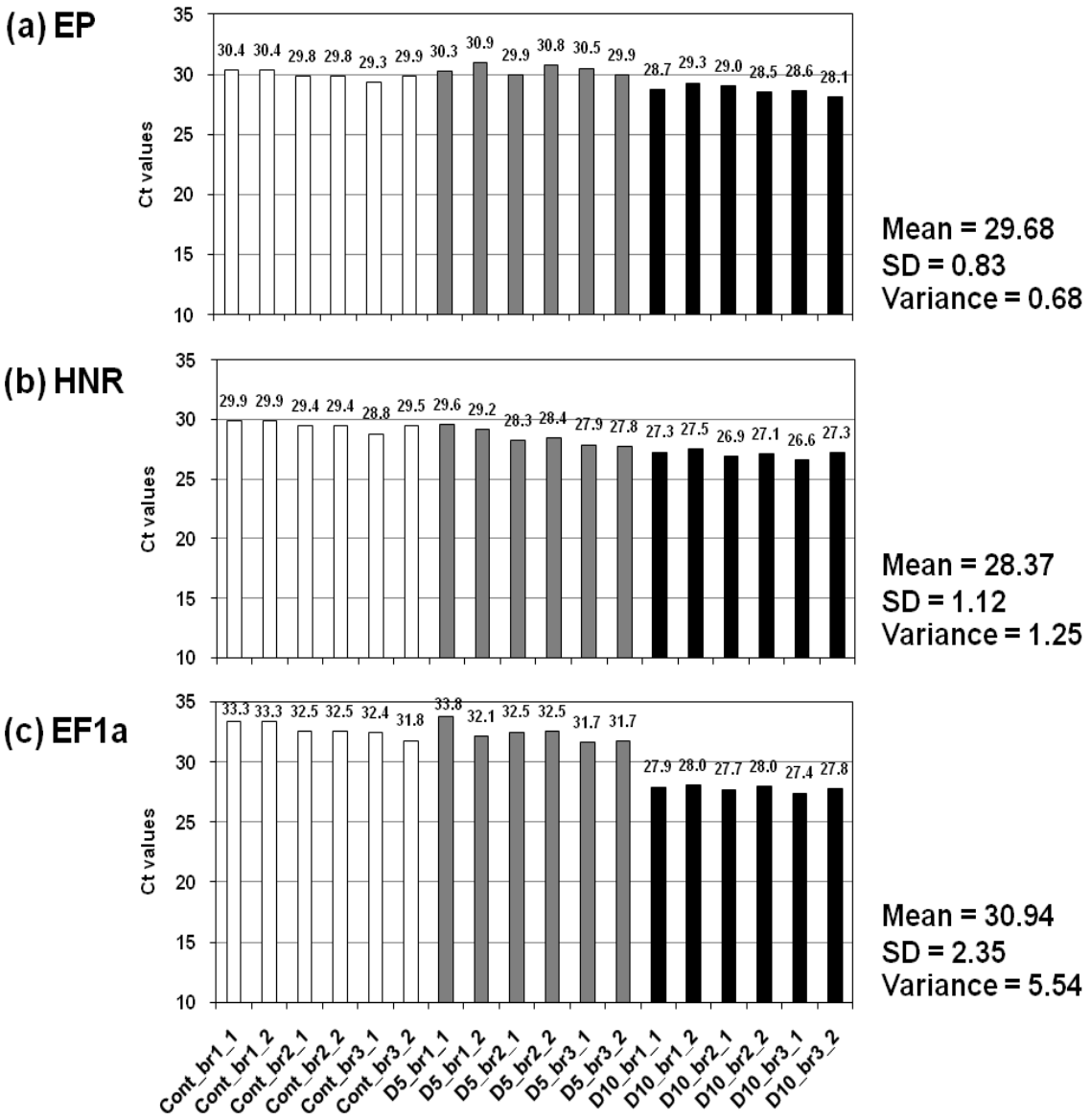

Figure S4 The variability of EP (a), HNR (b), and EF1a (c) expressions were tested in seedlings of TP309 rice exposed to drought stress for 0 (Cont), 5 (D5), and 10h (D10). The Ct values of each replicate were plotted and the descriptive statistics including mean, standard deviation (SD), and variance were analyzed by SPSS software. Data were analyzed from 3 biological replicates (br1, br2, and br3) and 2 technical replicates (1 and 2).