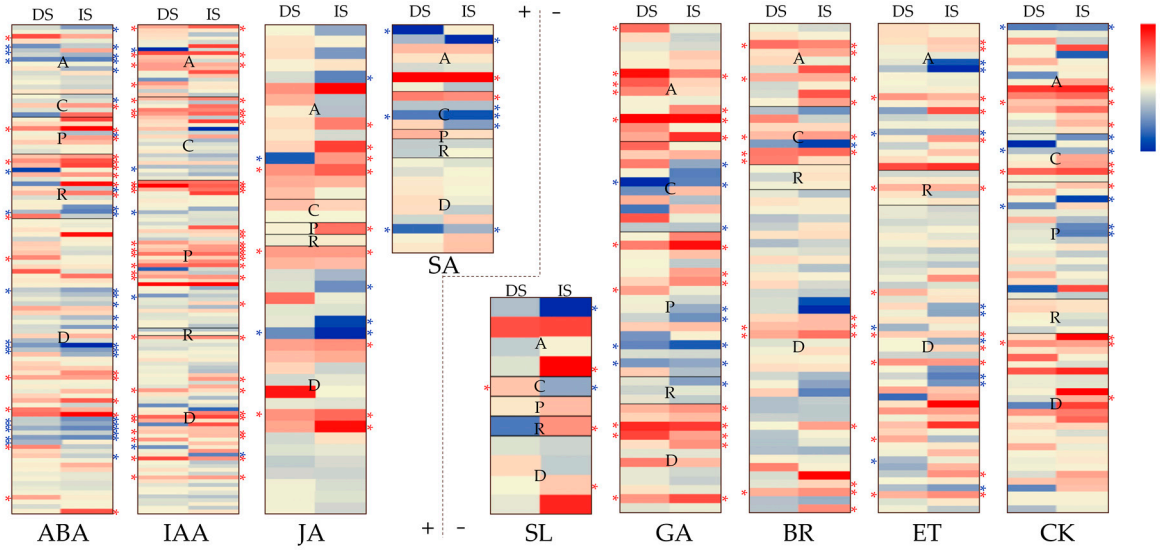

Figure S1. Comprehensive analysis of the influence of DOG1 on the expression of a particular gene in each phytohormone. The heatmap shows the expression alteration of the detectable phytohormone-related genes listed in Table S1. "*" indicates the DEGs. The dashed line divides the phytohormones into two classes: "+" denotes the phytohormones that induce seed dormancy or inhibit seed germination; "-" denotes the phytohormones that release seed dormancy or promote seed germination. DS, dry seeds; IS, imbibed seeds. A, Anabolism; C, Catabolism; P, transPort; R, Receptor; D, transDucer. Red, up-regulation; Blue, down-regulation.

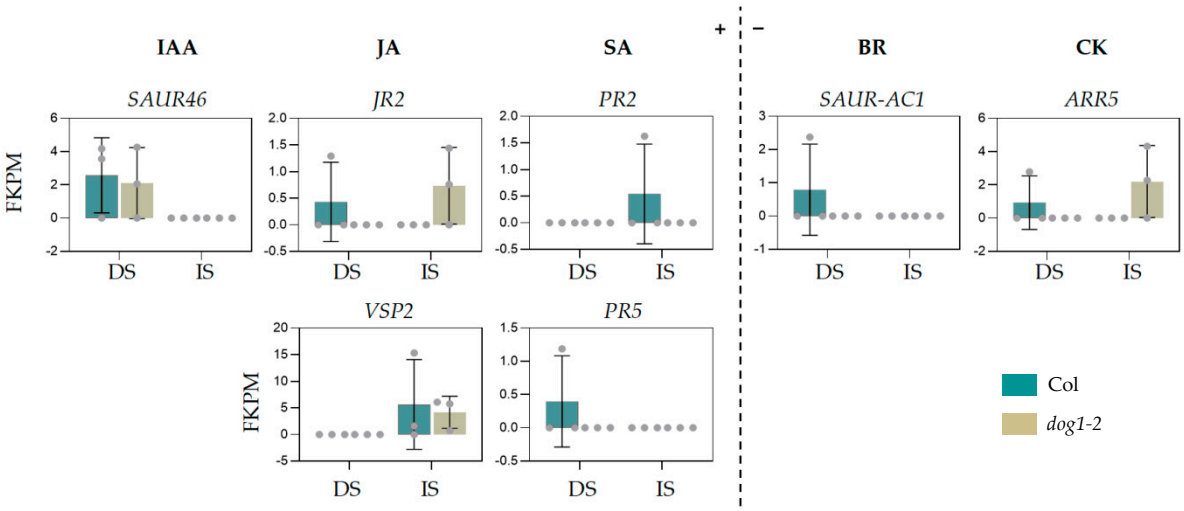

Figure S2. The expression value of marker genes that are not suitable as indicators of hormonal levels within seeds. DS, dry seeds; IS, imbibed seeds. The dashed line divides the phytohormones into two classes: "+" denotes the phytohormones that induce seed dormancy or inhibit seed germination; "-" denotes the phytohormones that release seed dormancy or promote seed germination.

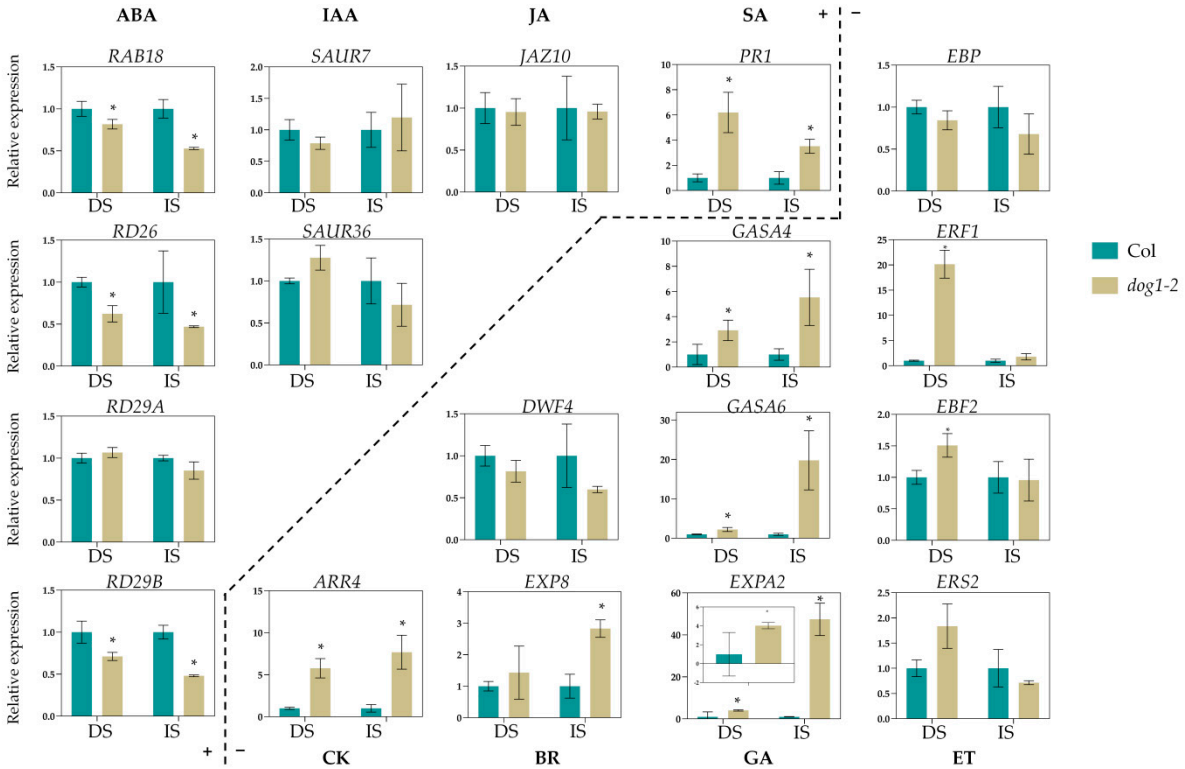

Figure S3: Validation of the Expression of marker genes by RT-qPCR Assays. Relative expression of representative marker genes of the indicated phytohormone pathway in Col and *dog1-2* seeds. DS, dry seeds; IS, imbibed seeds. The dashed line divides the phytohormones into two classes: "+" denotes the phytohormones that induce seed dormancy or inhibit seed germination; " - " denotes the phytohormones that release seed dormancy or promote seed germination. Data represent the average of three replications . *, P<0.05. RT-qPCR primers for each gene is list in Table S3.