A

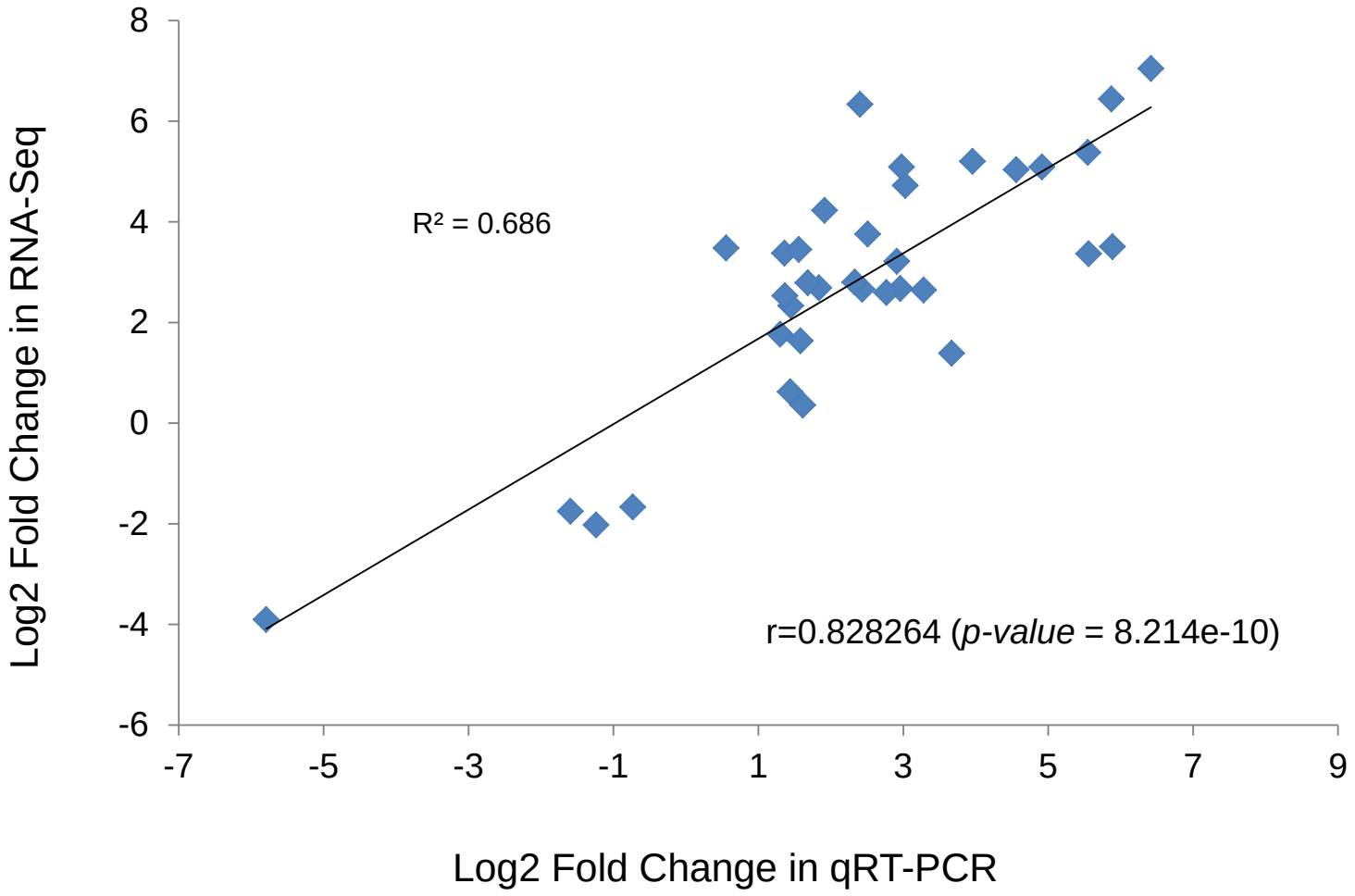

Figure S3. Comparison between qRT-PCR data and RNAseq data of 36 gene transcripts in shoots and roots. (A) Significant correlation between qRT-PCR data and RNAseq data of 36 gene transcripts in *jaz2-1*.

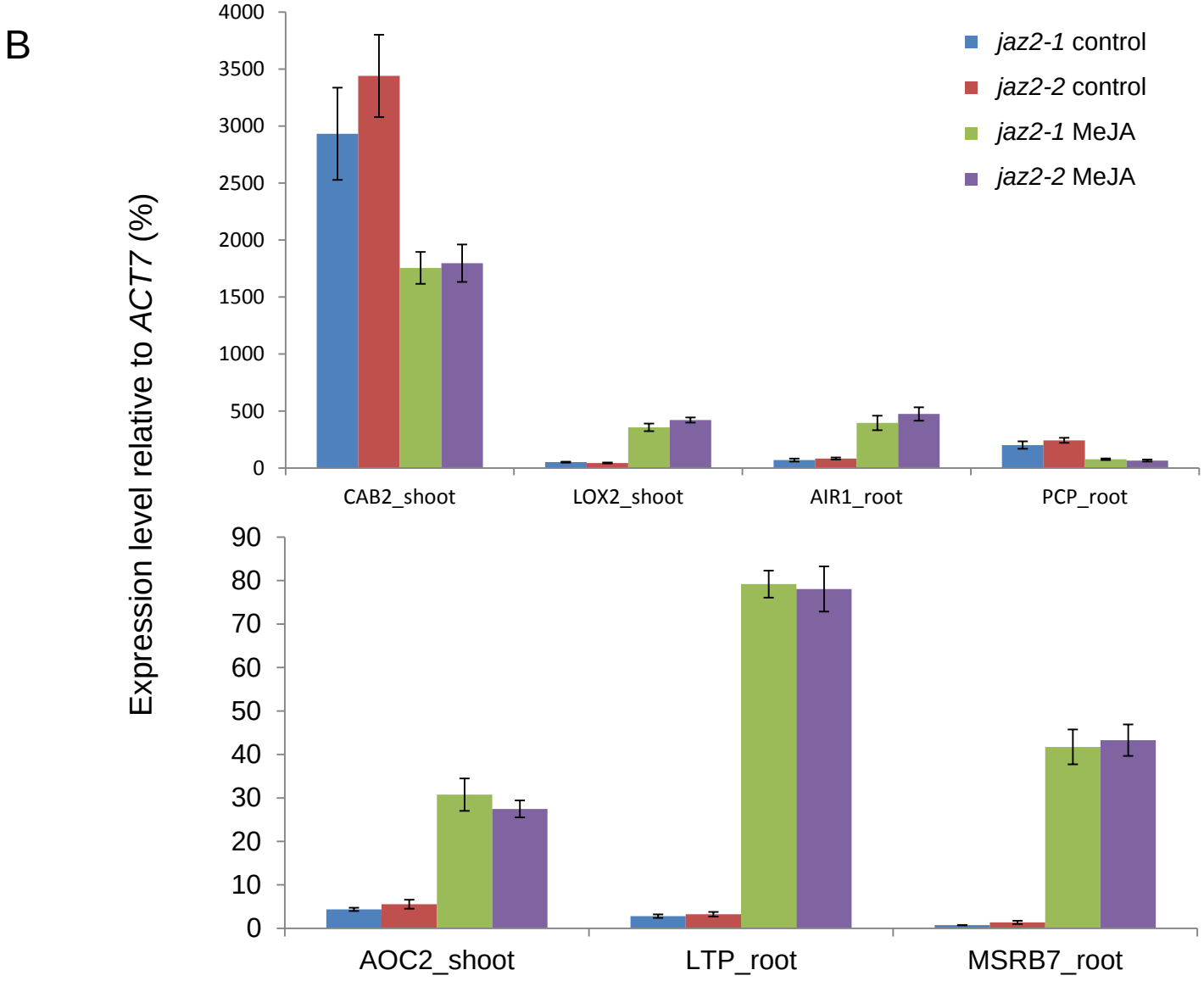

Figure S3. (B) Transcriptomic profiling between *jaz2-1* and *jaz2-2*. CAB2, chlorophyll A/B-binding protein 2 (AT1G29920); LOX2,lipoxygenase 2 (AT3G45140); AIR1, Auxin-Induced in Root cultures 1 (AT4G12550); PCP, Papain family cysteine protease (AT4G11320); AOC2, allene oxide cyclase 2 (AT3G25770); LTP, Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AT4G12545); MSRB7, methionine sulfoxide reductase B7 (AT4G21830).

C

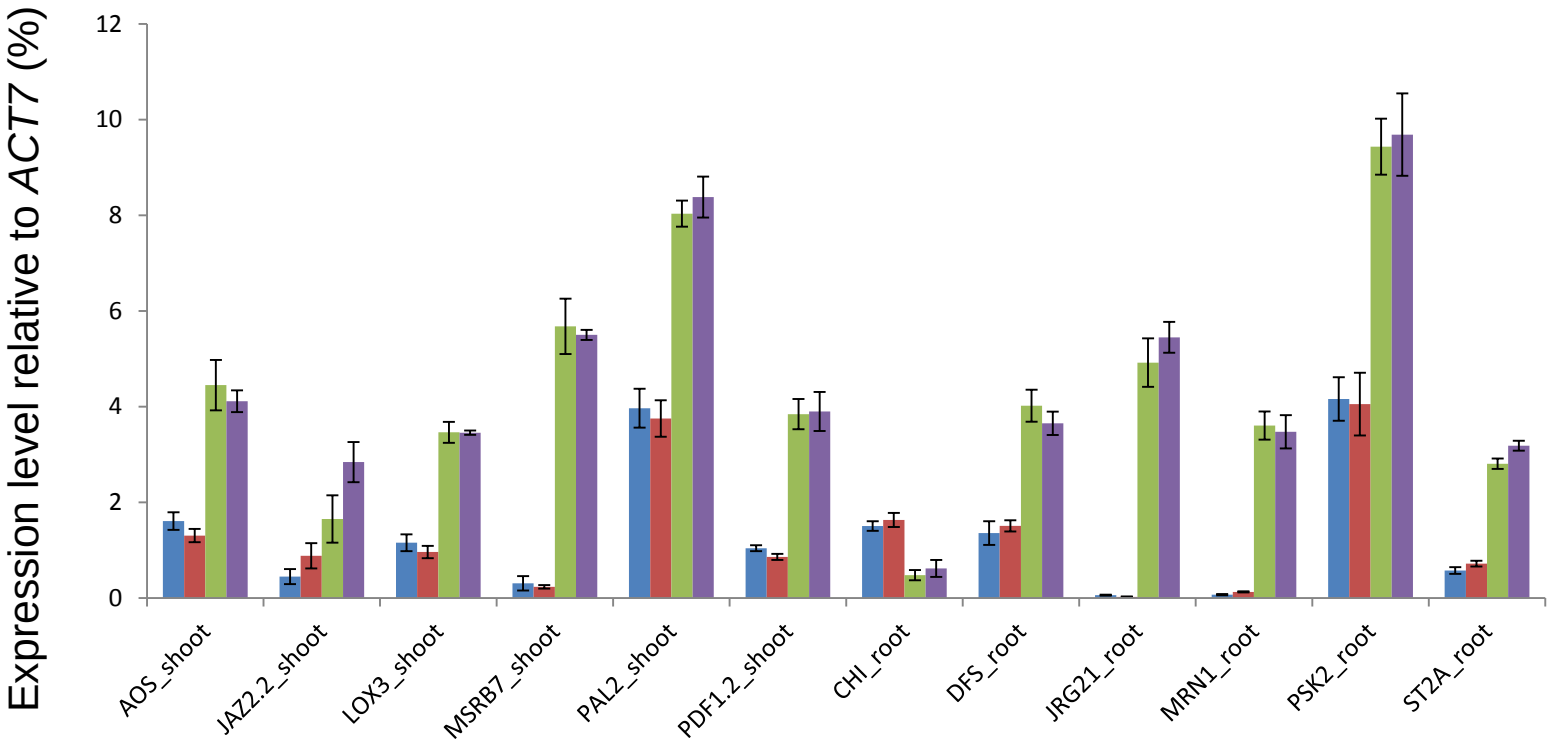

Figure S3. (C) Transcriptomic profiling between *jaz2-1* and *jaz2-2*. AOS, allene oxide synthase (AT5G42650); JAZ2.2, splice variant of jasmonate-zim-domain protein 2 (JAZ2; AT1G74950); LOX3, lipoxygenase 3 (AT1G17420); PAL2, phenylalanine ammonia-lyase 2 (AT3G53260); PDF1.2, plant defensin 1.2 (AT5G44420); CHI, chitinase (AT2G43570); DFS, Arabidopsis defensin-like protein (AT4G22212); JRG21, jasmonate-regulated gene 21 (AT3G55970); MRN1, marneral synthase (AT5G42600); PSK2, phytosulfokine 2 precursor (AT2G22860); ST2A, sulfotransferase 2A (AT5G07010).

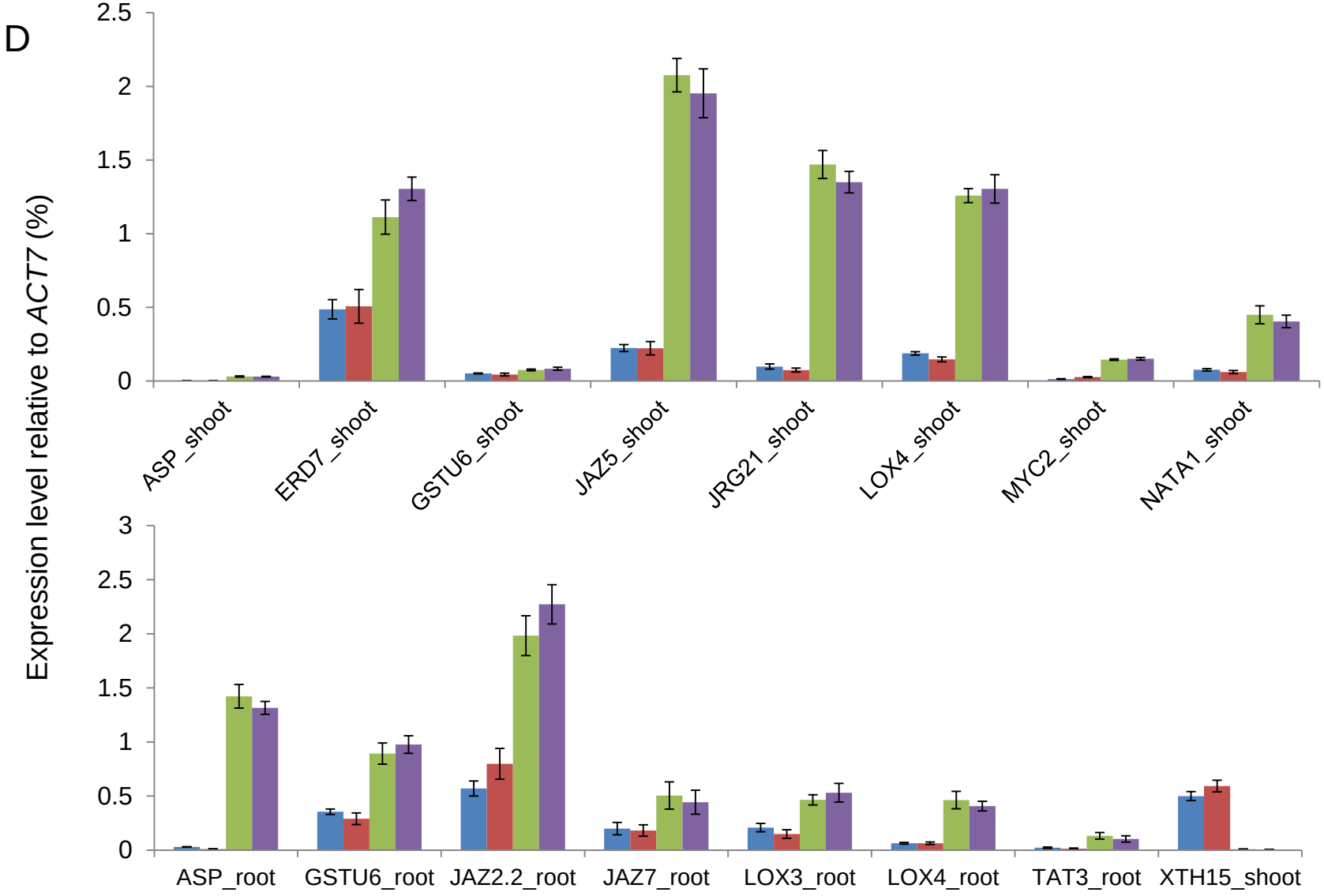

Figure S3. (D) Transcriptomic profiling between *jaz2-1* and *jaz2-2*. ASP, Eukaryotic aspartyl protease family protein (AT5G19110); ERD7, early-responsive to dehydration 7 (AT2G17840); GSTU6, glutathione S-transferase tau 6 (AT2G29440); JAZ5, jasmonate-zim-domain protein 5 (AT1G17380); LOX4 (AT1G72520); MYC2 (AT1G32640); NATA1, Acyl-CoA N-acyltransferases superfamily protein (AT2G39030); JAZ7, jasmonate-zim-domain protein 7 (AT2G34600); TAT3, tyrosine aminotransferase 3 (AT2G24850); XTH15, xyloglucan endotransglucosylase/hydrolase 15 (AT4G14130).

E

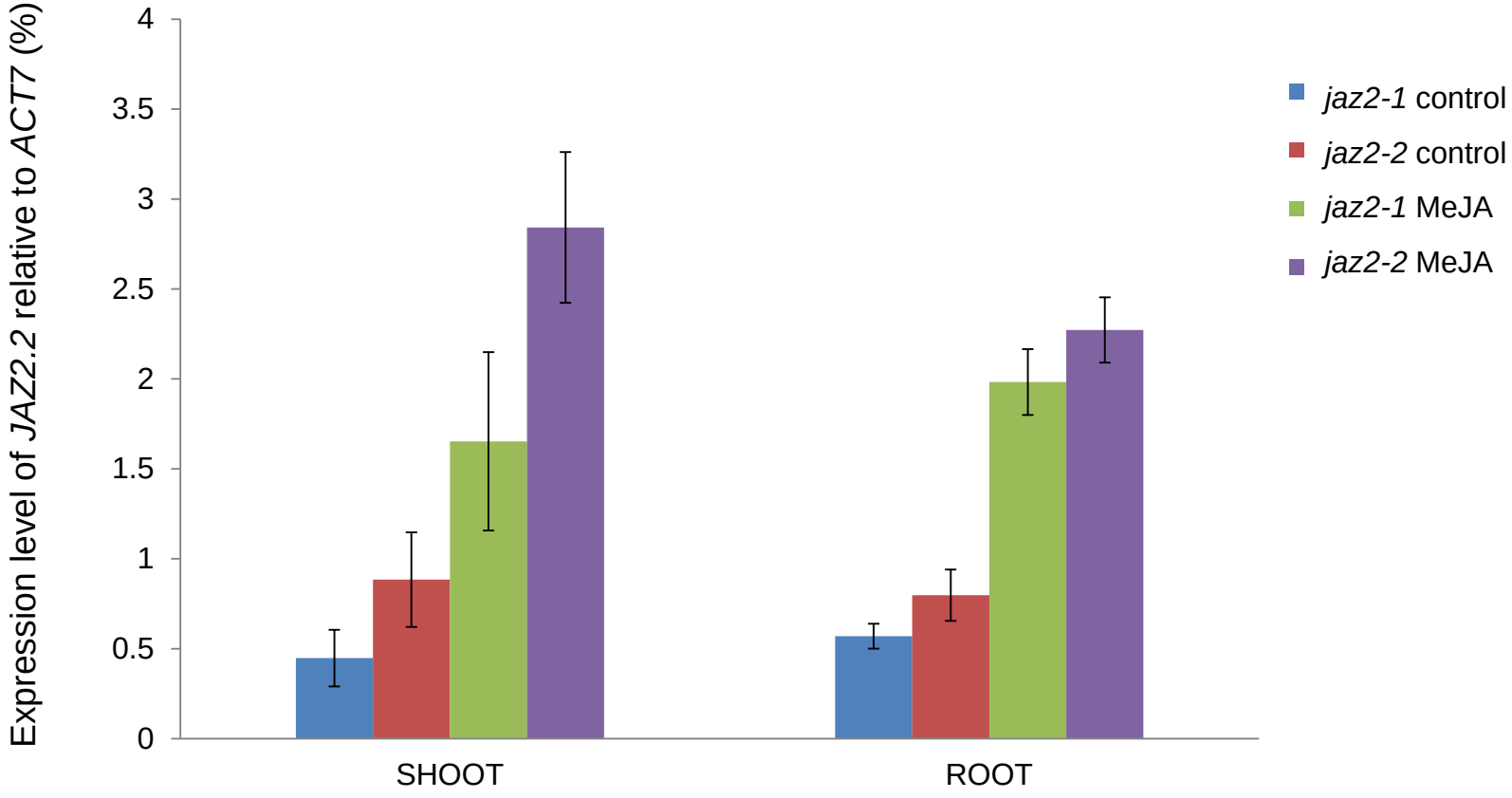

Figure S3. (E) Relative expression patterns of JAZ2.2 in two *jaz2* mutants, *jaz2-1* and *jaz2-2*