Fig. S1

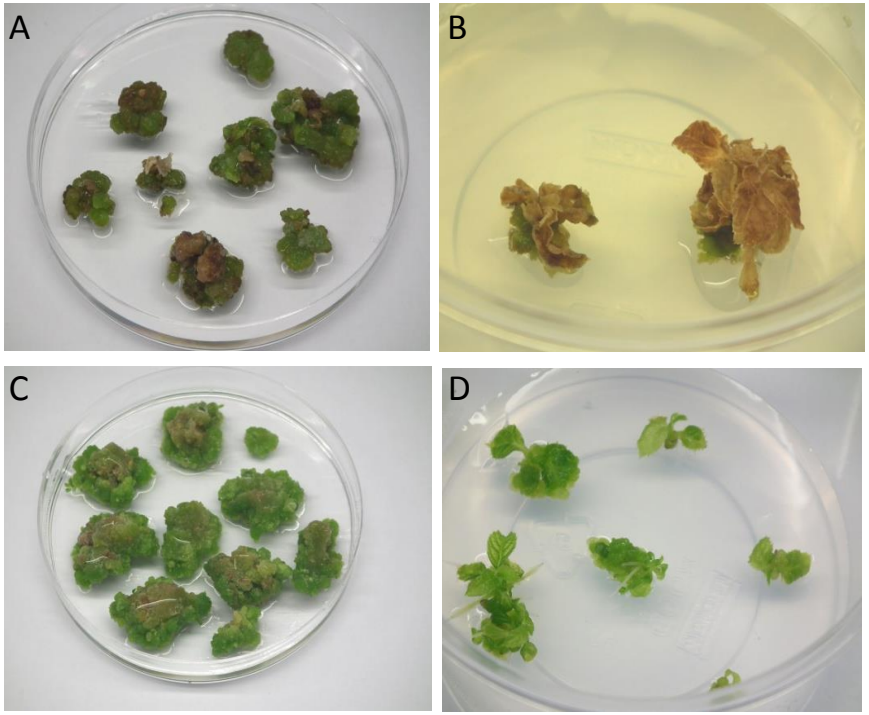
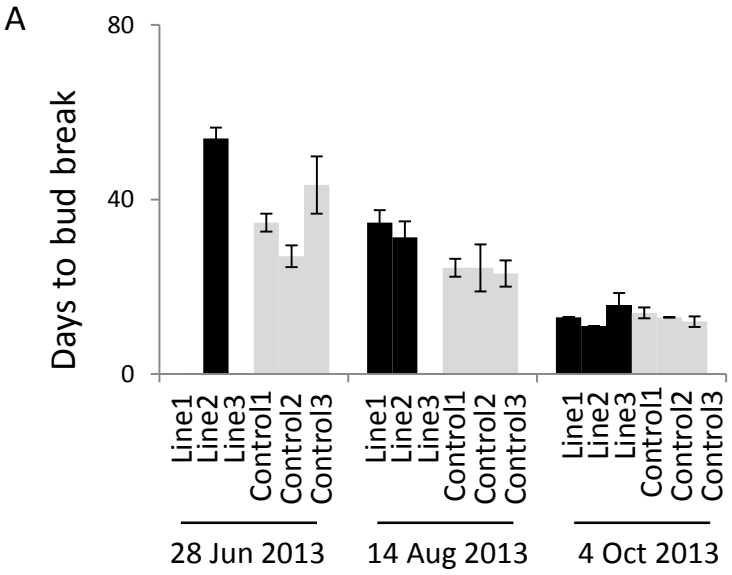


Fig. S1 Transformation of *Actinidia eriantha*. (A) Browning of adventitious *SVP2* shoots on a standard regeneration medium. (B) Shoot tip die-back on a standard elongation medium. (C) Healthy *SVP2* callus with adventitious buds on modified regeneration medium. (D) Healthy transgenic shoots produced on modified elongation medium.

Fig. S2



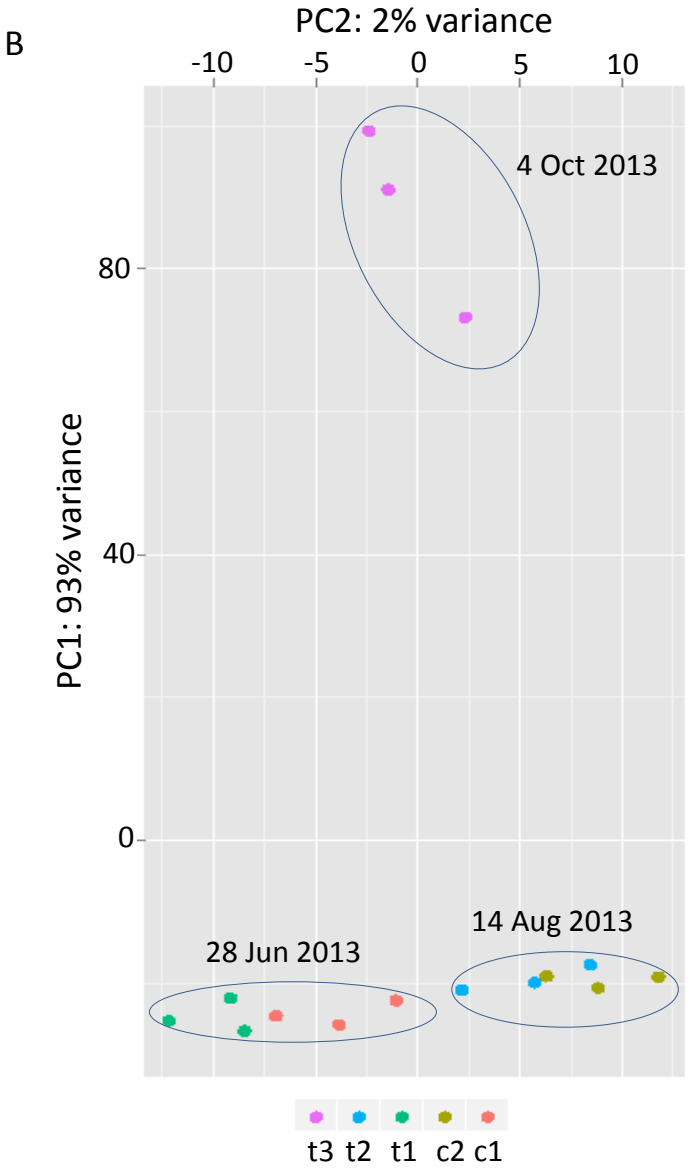


Fig. S2 Evaluation of *A. deliciosa* transgenic and control buds at three stages for RNA-seq experiment. (A) Three single node cuttings with dormant buds were collected from three transgenic (t) and three control (c) lines on 28 Jun, 14 Aug and 4 Oct 2013 and assessed for budbreak under forcing conditions. Error bars represent the standard error of budbreak time of three buds in transgenic and control lines. (B) A principle component analysis (PCA) of three biological replicates collected on 28 Jun (t1, c1), 14 Aug (t2, c2) and 4 Oct of 2013 (t3). The first component (PC1) represents major variance and the second component PC2 represents less variance, which are shown in each axis legend.

Fig. S3

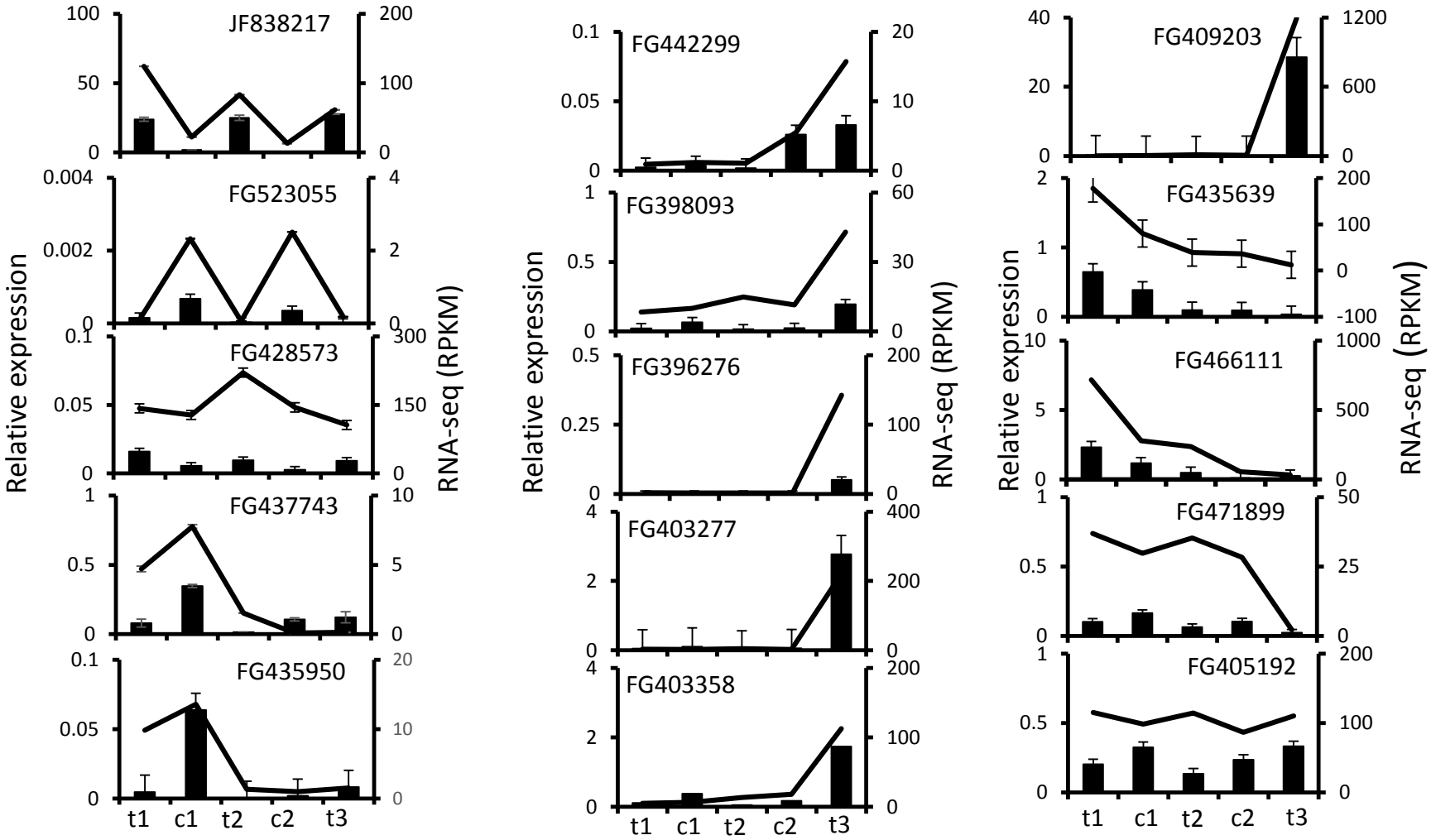
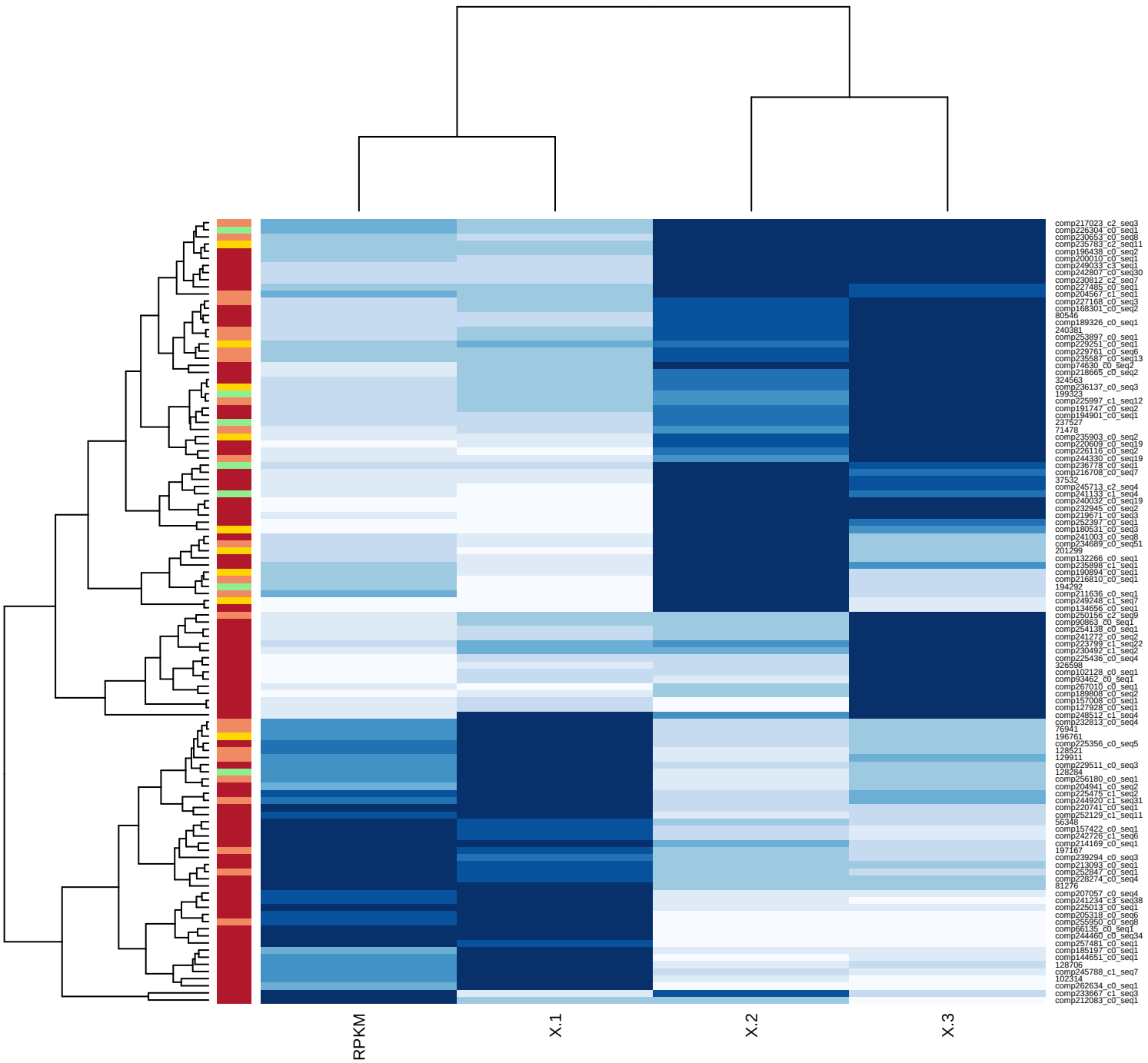


Fig. S3 qPCR validation of RNA-seq expression profiles. 15 genes were randomly selected from differentially expressed genes in c1, c2, t1, t2 and t3. The left y-axis indicates relative gene expression levels determined by qPCR. Error bars represent the standard error for four replicate reactions. The right y-axis indicates gene expression levels calculated by the RPKM method.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comp242807_c0_seq30
comp230812_c2_seq7
comp227485_c0_seq1
comp204567_c1_seq1
comp227168_c0_seq3
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comp189326_c0_seq1
240381
comp253897_c0_seq1
comp229251_c0_seq1
comp229761_c0_seq6
comp235587_c0_seq13
comp74630_c0_seq2
comp218665_c0_seq2
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comp236137_c0_seq3
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comp225997_c1_seq12
comp191747_c0_seq2
comp194901_c0_seq1
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comp226116_c0_seq2
comp244330_c0_seq19
comp236778_c0_seq1
comp216708_c0_seq7
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comp190894_c0_seq1
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comp211636_c0_seq1
comp249248_c1_seq7
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RPKM
X.1
X.2
X.3