



(E D),
e
f f
e (f 2013).
e f e f
C. - (e e 2010; G . 1998).
T f f C. -, e f -
f f C. -, e f -
(T . 2014; G . 1998;
e e 2010).
B f f f

e f i u u u i u i e i u (A260/A230
A260/A280 > 1.8) u u (i u 8) f i eD u -
i i i u i .

cDNA Library Construction and Sequencing

A f 21 eD u i i u u u u u u
uB u , TM

GC content, and the GC content of the sequenced DNA was 48.4%. The sequencing data were analyzed using the Illumina sequencing pipeline (Illumina, 2014). The sequencing data were aligned to the reference genome (Genome Browser, UCSC) using the BWA-MEM algorithm (Li and Durbin, 2009). The aligned reads were then processed using the SAMtools package (Li et al., 2009). The resulting BAM files were converted to BigWig files using the BigWig software (Hindson et al., 2011). The BigWig files were then analyzed using the UCSC Genome Browser (Kent et al., 2002). The resulting tracks were then analyzed using the UCSC Genome Browser (Kent et al., 2002).

Quantitative Real-Time PCR Validation

The relative expression levels of the target genes were determined using quantitative real-time PCR (qPCR). The qPCR reactions were performed using the SYBR Green assay (Applied Biosystems, Foster City, CA, USA). The relative expression levels were calculated using the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen, 2001). The expression levels were normalized to the housekeeping gene *EF1A* (Livak and Schmittgen, 2001). The relative expression levels were then analyzed using the Student's *t*-test (Student, 1908). The relative expression levels were significantly different ($P < 0.05$) between the control and the treated groups.

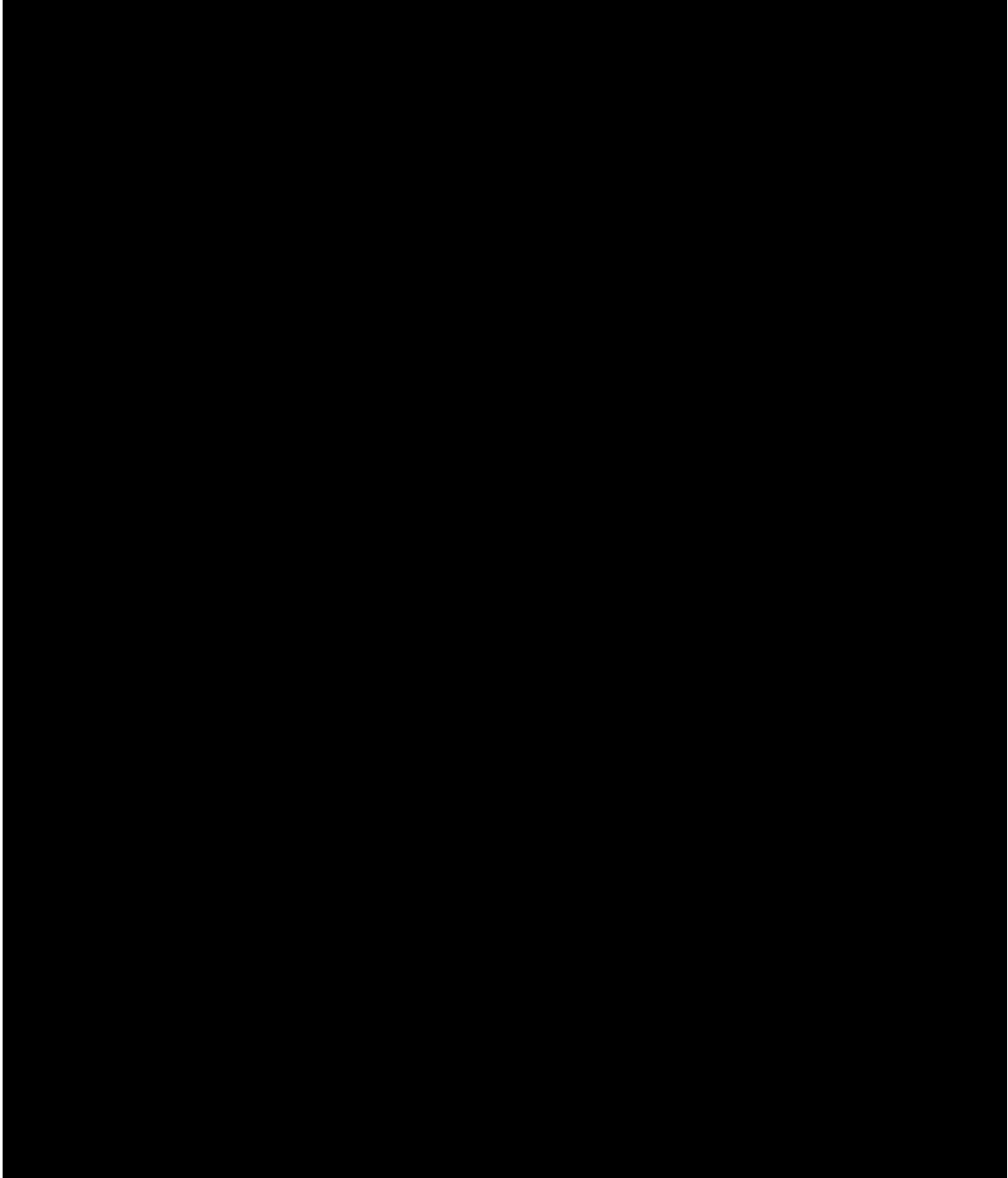
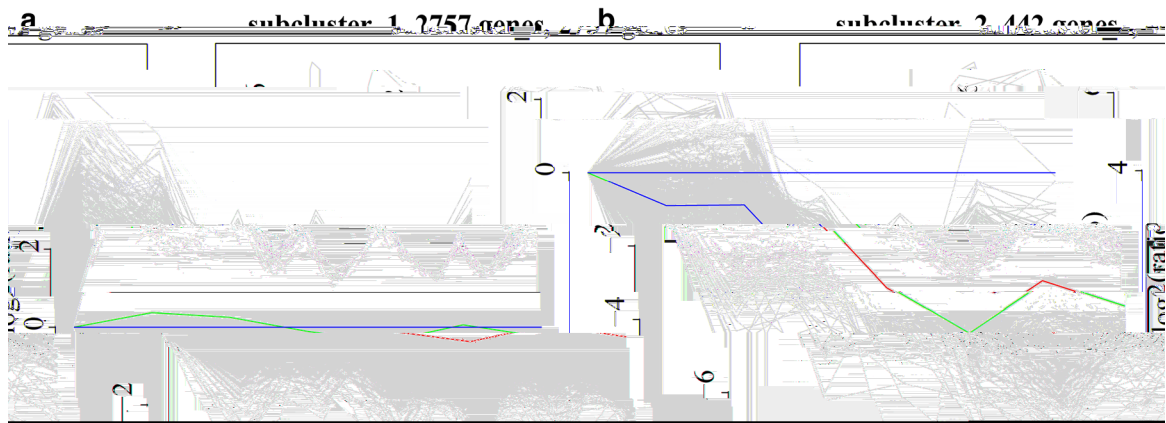
Results

Data Preprocessing and Normalization

The sequencing data were preprocessed and normalized using the DESeq2 package (Love et al., 2014). The raw sequencing data were first filtered for low-quality reads and then normalized using the DESeq2 normalization method (Love et al., 2014). The normalized data were then analyzed using the DESeq2 package (Love et al., 2014). The resulting DESeq2 objects were then analyzed using the DESeq2 package (Love et al., 2014). The resulting DESeq2 objects were then analyzed using the DESeq2 package (Love et al., 2014).

Differential Expression and Cluster Analysis

The differentially expressed genes (DEGs) were identified using the DESeq2 package (Love et al., 2014). The DEGs were then clustered using the hierarchical clustering method (Ward and Jenkinson, 1975). The resulting clusters were then analyzed using the DESeq2 package (Love et al., 2014). The resulting DESeq2 objects were then analyzed using the DESeq2 package (Love et al., 2014). The resulting DESeq2 objects were then analyzed using the DESeq2 package (Love et al., 2014).

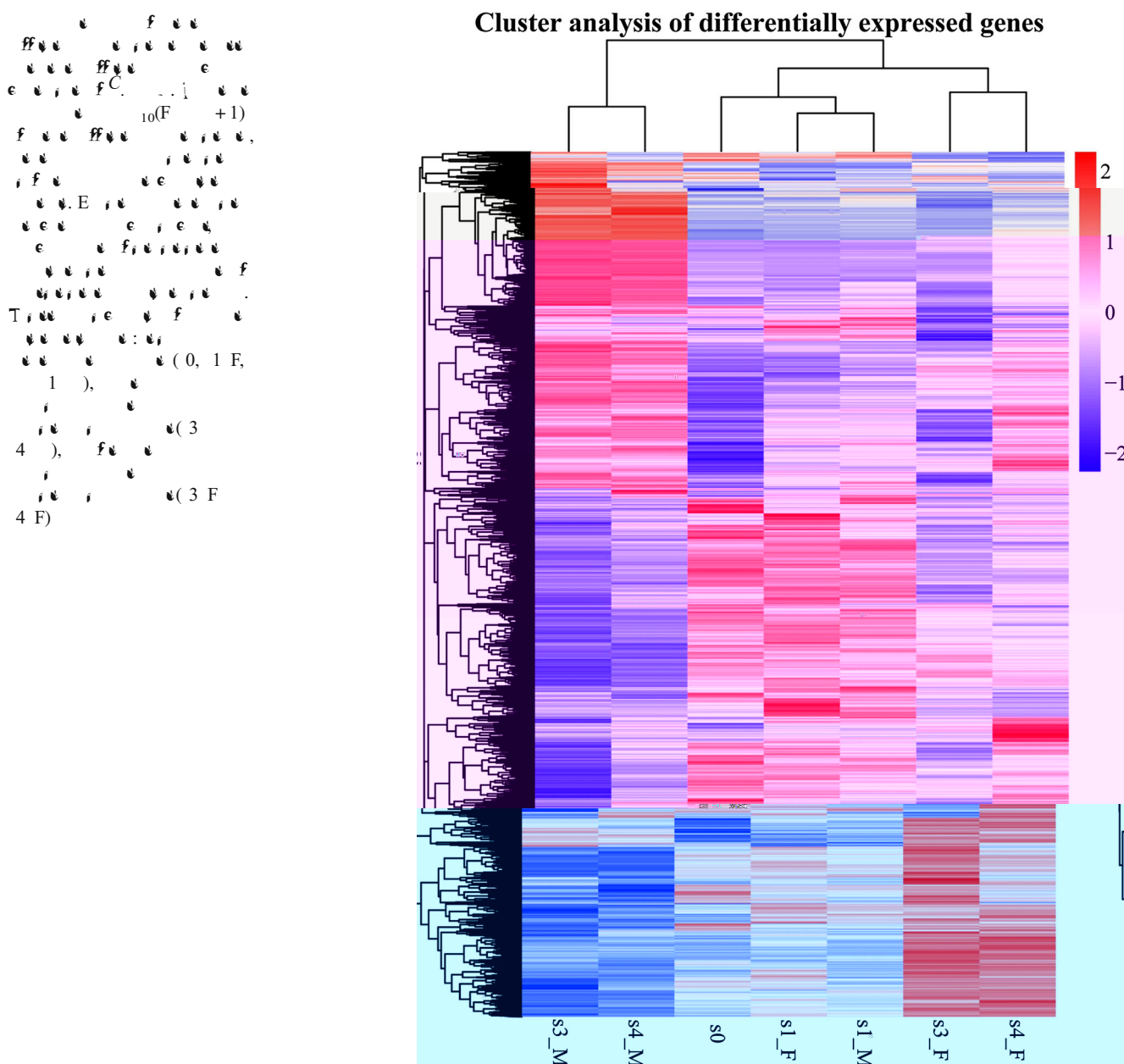


C, ... 1 (F . 1), e 5 fe ... G/ ... EGG ... (F . 1), e 6 (F . 1f), ... 10(F +1) f DEG, ... (0, 1 F, 1), ... (3 4), f ... (3 F 4 F)(F . 2).

Enrichment Analysis of DEGs and Subclusters Generated by Hierarchical Clustering

G/ ... DEG ... 3, 1 Fe ... 3 F, 3 Fe ... 3, "EC ..."

Cluster analysis of differentially expressed genes



T (5'-T), (DA), (N) -
 (F) (2003).
 T C, e -
 (2016). EGG
 5, e
 f, f e f
 A f
 e f
 (2010;
 2016). G/
 e 6
 f e ff
 G/
 EGG
 f, .1
 f C 2 C
 ff C, e 5
 e 6, G e
 e E
 fe e
 T f
 f e - GC
 .

E f e f
 e e e
 C, e f
 C, e
 T f
 GC
 ff
 C 2
 f 1 F 1
 T e f
 f
 Af T- C
 e f e
 e

Long Non-Coding RNA LOC105321313

N- (e) f e
 f e
 (f 2013; .2010; C 2008). e
 e
 G e, e
 e e e -
 e (f 2013; C 2007

C e i i u u e i u e u, i-
e u u , i e u u u u e i Q e e u f
i u u e i i i . i e u u -
.A i i u i u u f e i .

Compliance with Ethical Standards

T u i u i u u u e f e f
u u .

References

- A u , u (2010) D f f u u i u f i u u e u
e . G u u B 11: 106
A u , T, u (2015) T u — f i u i i

W
D, F, B, AD,
F (2002) Ace
T-C
G B 3 0034
W, D, A, Q D N
D, G TD, E, G (2014)
T
f
B, D, T (2007)
3 C
f C- B e
B Ae 1774:35-43

D, G, A (2010) G
f - : ee
11: 14
G, F, G, F,
Q (2012) T
e f f . N 490:49-54
N F, G (2014) G e f e f e
(C -)
e. G3 (B) 4:2207-
2217
(2010) N-e 8 e f6e.