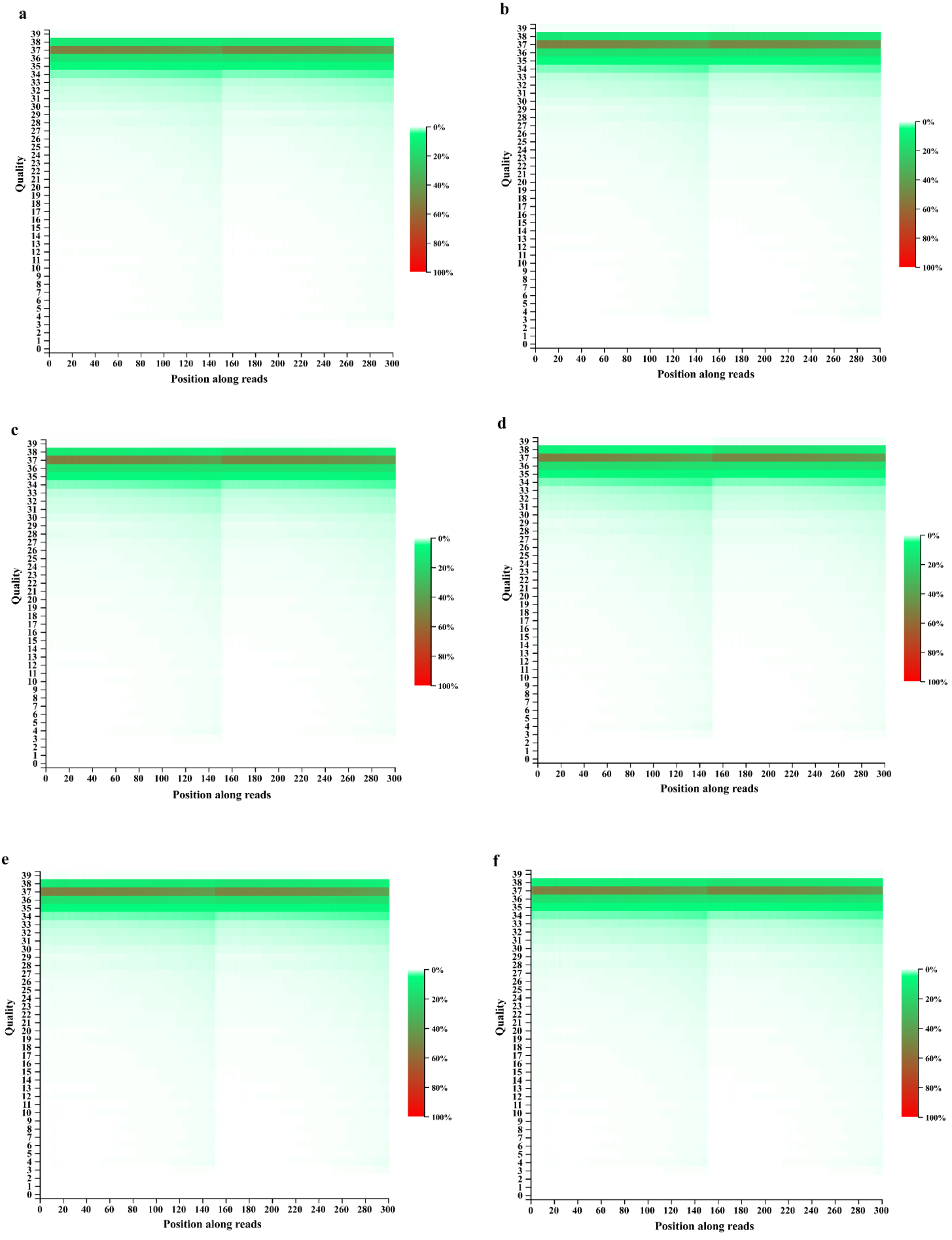
Supplementary Material

The following Supporting Information is available for this article:

Supplementary Figure S1. Base quality analysis of clean reads for sequencing library of LCK_a (a), LCK_b (b), LCK_c (c), LT1_a (d), LT1_b (e), LT1_c (f), LT2_a (g), LT2_b (h) and LT2_c (i). LCK, control; LT1, salinity treatments for 1 d; LT2, salinity treatments for 28 d. a, b, c represent the three repetitions.

Supplementary Figure S2. Pearson correlation analysis between samples based on gene expression profiles. LCK, control; LT1, salinity treatments for 1 d; LT2, salinity treatments for 28 d. a, b, c represent the three repetitions.

Supplementary Table S1. The primer sequences used for quantitative real-time PCR (qRT-PCR) analysis.


a
b
c
d
e
f
Quality
Position along reads
0%
20%
40%
60%
80%
100%

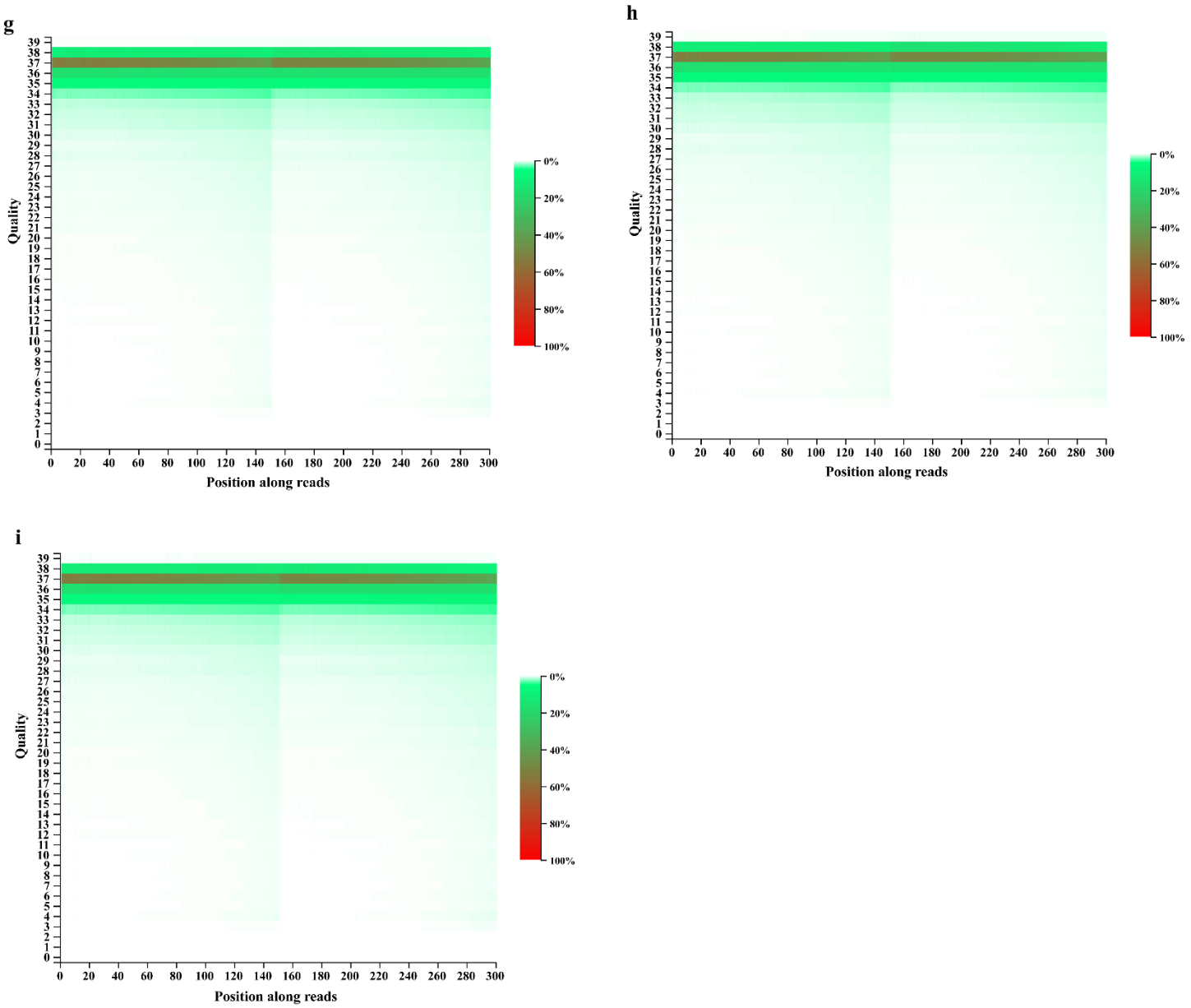


Figure S1. Base quality analysis of clean reads for sequencing library of LCK_a (a), LCK_b (b), LCK_c (c), LT1_a (d), LT1_b (e), LT1_c (f), LT2_a (g), LT2_b (h) and LT2_c (i). LCK, control; LT1, salinity treatments for 1 d; LT2, salinity treatments for 28 d. a, b, c represent the three repetitions.

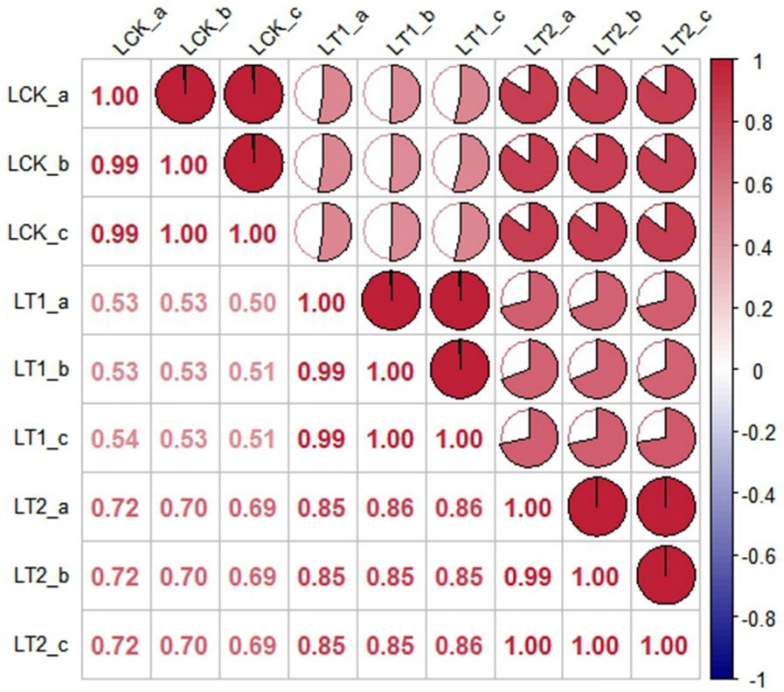


Figure S2. Pearson correlation analysis between samples based on gene expression profiles. LCK, control; LT1, salinity treatments for 1 d; LT2, salinity treatments for 28 d. a, b, c represent the three repetitions.

Table S1. The primer sequences used for quantitative real-time PCR (qRT-PCR) analysis.

Gene ID	Forward primer（5′ →3′ ）	Reverse primer （5′ →3′ ）
isoform_290716	AGCTAGATAACAAGAATGAT	TTATCATTCTTGTTATCTAGC
isoform_82715	CGGTGCTCCTCCTCCTCTTCTG	GAGGCCATCAAAGGCAGAGG
isoform_22449	ACCTATCTATCAGGAGGAATC	CTTCCGAGTCTCTTCCGTCA
isoform_49093	ATTCGCCGAGAAACCGTTCCA	ATTCGCCGAGAAACCGTTCCAC
isoform_158609	TAAGCAGTGGTATCAACGCA	CTCTGCGTTGATACCACTGCTTA
isoform_37195	ATGCTTTCCGTTTGGCACT	AGAGGCGAAGTGCCAAACGGA
18s rRNA	CCGCCTCTGGTGTGCACCGGTC	CCCCCGGAACCCAAGGACT