

Table S1. Primer Sequences Used for qRT-PCR.

Genes	Primer	Sequence
GAPDH	Forward	5'-TGGAGAAAGCGGCCAAATAC-3'
	Reverse	5'-AAAGGTGGAAGAGTGGGTG-3'
STMN1	Forward	5'-GAGAAACTGACCCACAAA-3'
	Reverse	5'-GTTCTTCCGTACTIONTCTTCA-3'
JIP1	Forward	5'-GGTCCAGGTTCCCTATCACA-3'
	Reverse	5'-CCTTGACGCCTATCTTCAGC-3'
JNK3	Forward	5'-GGAGAATCGGCCAAAGTA-3'
	Reverse	5'-AAAGGTGGAAGAGTGGGTG-3'

Table S2. siRNA sequence used for RNA interference

Genes	Primer	Sequence
STMN1-siRNA	Forward	5'-GGAGGAAAUUCAGAAGAAAdTdT-3'
	Reverse	5'-UUUCUUCUGAAUUUCCUCCdTdT-3'
JIP1-siRNA	Forward	5'-GACUCACCGUGCACUUUAAdTdT-3'
	Reverse	5'-UUAAAGUGCACGGUGAGUCdTdT-3'
JNK3-siRNA	Forward	5'-CCAGGAUGUUUACUUAGUAdTdT-3'
	Reverse	5'-UACUAAGUAAACAUCCUGGdTdT-3'

Table S3. Output Statistics of each RNA-seq library

Sample ID	Illumina Pass Filtering Bases (Gb)	Illumina Pass Filtering Reads (M)	\geq Q30 (%)
Control 1	7.0	56.4	90.3
Control 2	6.0	48.0	92.1
1h 1	6.2	49.6	92.1
1h 2	7.5	59.8	90.0
4h 1	5.5	44.2	84.4
4h 2	6.6	52.4	91.8
8h 1	5.6	45.1	93.7
8h 2	6.0	48.4	91.4
12h 1	5.7	45.6	84.7
12h 2	5.5	44.2	91.5

Table S4. Statistics of Matching ratio of Sequencing sequence to Reference sequence

Sample ID	Total Reads	Matching ratio (%)
Control 1	28178090	93.19
Control 2	24019027	94.30
1h 1	24805843	94.34
1h 2	29889832	92.82
4h 1	22092630	92.85
4h 2	26206209	94.07
8h 1	22549573	93.69
8h 2	24176064	93.73
12h 1	22798724	92.70
12h 2	22095325	92.16

Table S5: Differentially expressed genes(1 vs.0h)

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Table S6: DEGs in each cluster

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Table S7: GO terms enriched in cluster1

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Table S8: KEGG pathway enriched in cluster1

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