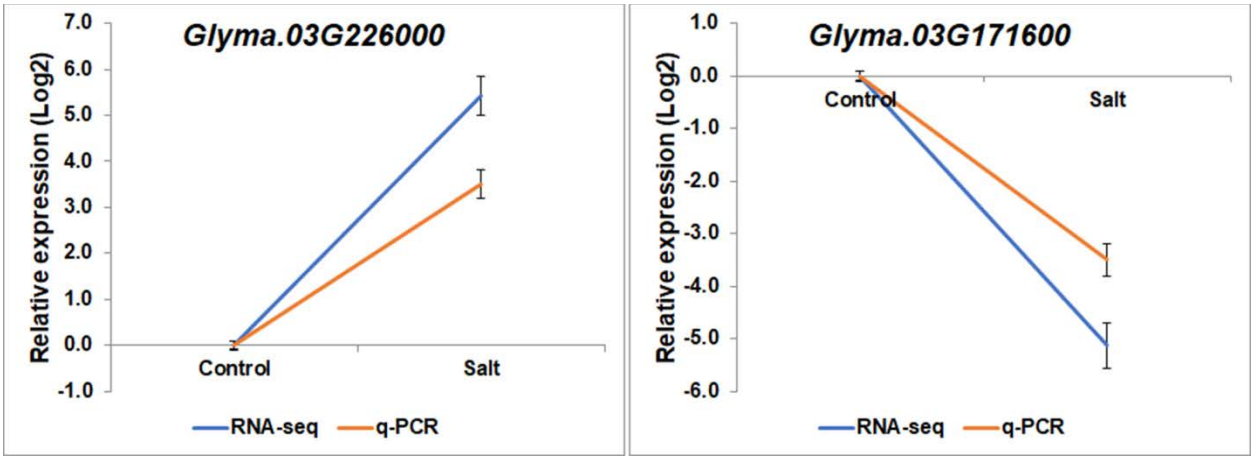
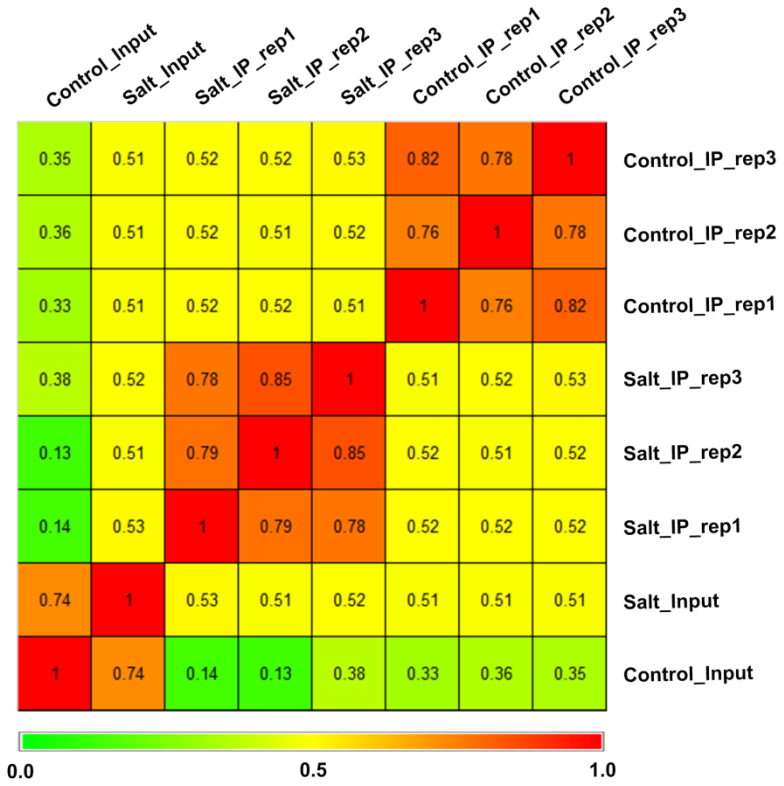
Supplementary data

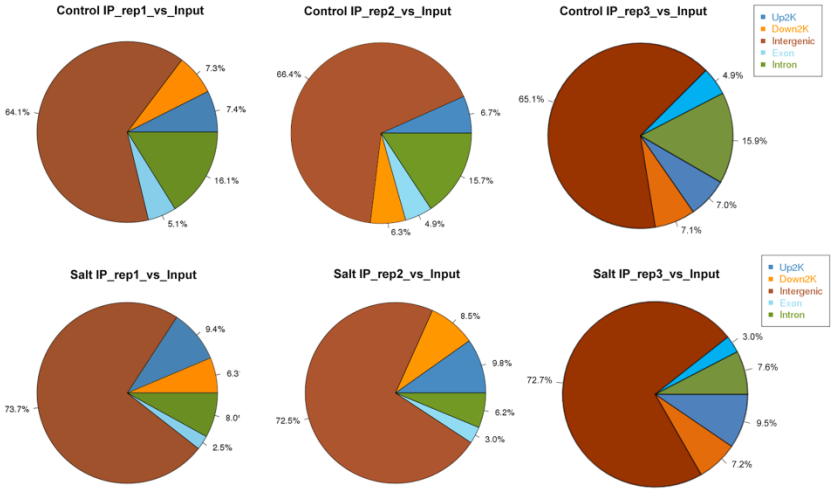


Supplementary Figure 1. The gene expression profile of two known soybean salt stress genes analyzed by RNA-seq and q-PCR. Graphs show the relative expression levels of two known soiybean salt genes, (*Glyma. 03G226000* and *Glyma. 03G171600*), analyzed by RNA-seq and by qPCR which normalized to a *Tubulin* (*Glyma.05G203800*) reference gene. Error bars represent standard deviation (SD).



Supplementary Figure 2. The correlation coefficient of biological replicates of ChIP-seq data. Verification of ChIP-seq results using Pearson correlation analysis showed high correlation coefficients between the biological replicates for each sample in soybean.

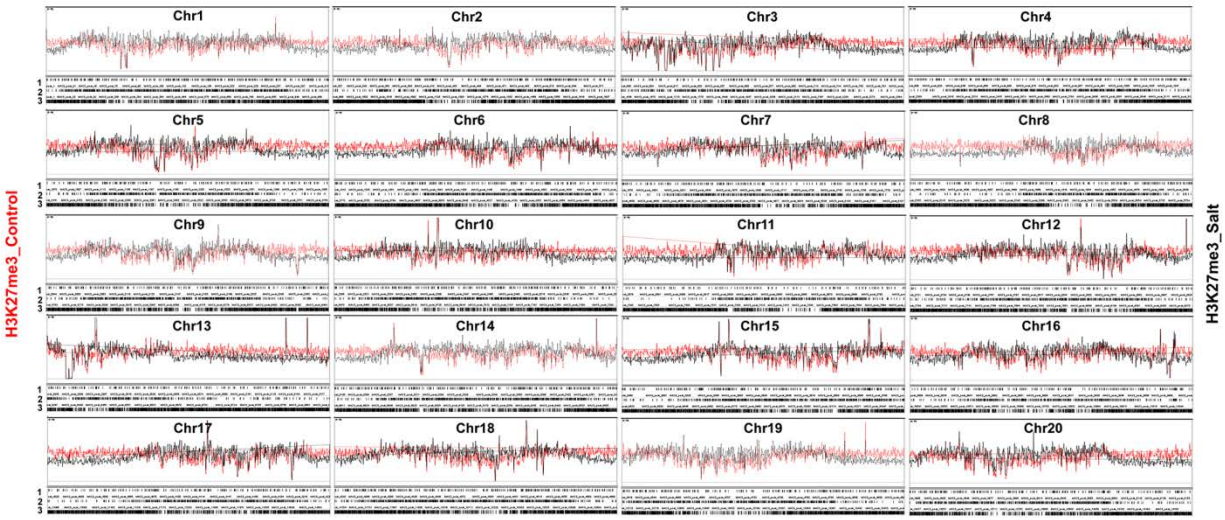
A. Peak distribution



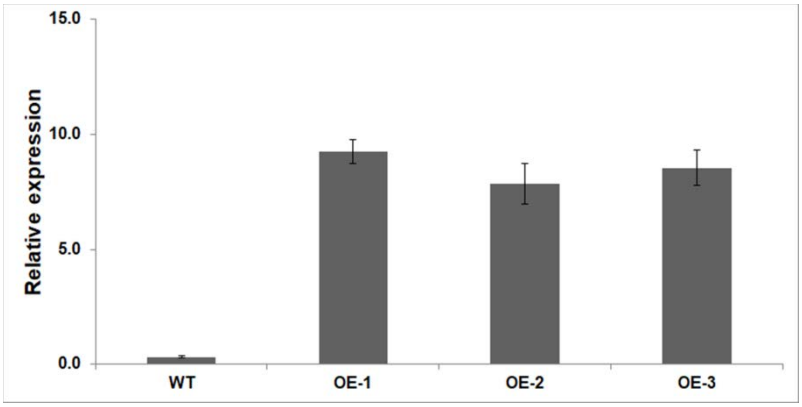
B. Data summary

Samples	Peak #	Average number	Total length	Average length	Total depth	Annotated gene covered with peaks	Overlapped genes
Control	IP_rep1_vs_Input	2574	1807045	702.04	24344548	1707	2357
	IP_rep2_vs_Input	3410	2597346	761.69	49161117		
	IP_rep3_vs_Input	2986	2197367	735.89	37865539		
Salt	IP_rep1_vs_Input	1262	901367	714.24	15439126	746	
	IP_rep2_vs_Input	1635	1148771	702.61	17422797		
	IP_rep3_vs_Input	1458	1036404	710.84	16578646		

Supplementary Figure 3. ChIP-seq data characteristics. **(A)** Peak distribution of ChIP-seq analysis with the following genomic regions: promoter (Up2K, 2 kb upstream of the TSS), downstream (Down2K, 2 kb downstream of the TES)， intergenic, exon and intron regions. **(B)** Summary of ChIP-seq data. The number of total genes with H3K27me3 marks in control and/or salt plants is 2357.



Supplementary Figure 4. Chromosomal distribution of H3K27me3 modification sites on all 20 soybean chromosomes. Y-axis represents the input signals for the immunoprecipitation of H3K27me3 in control on the left side (H3K27me3_Control) and salt-treated soybean on the right side (H3K27me3_Salt). The comparison of H3K27me3 marked in control (red) and salt (black) plants were shown on all chromosomes. Chr and 5mb represent chromosome and 5 megabase, respectively. 1 and 2 indicate MACS peaks identified for control (1) and salt (2) samples using MACS with the default 10^{-5} p-value cutoff with each input as a control for significant peak calling.



Supplementary Figure 5. Expression analysis of *Glyma.17g022500* in transgenic *Arabidopsis*. mRNA expression levels of *Glyma.17g022500* in WT, transgenic *Arabidopsis OE-1*, *OE-2*, *OE-3* plants. Graphs show the relative expression levels measured by qPCR, normalized to a *UBIQUITIN* (*UBQ*) reference gene. Error bars represent standard deviation (SD).

Supplementary Table 1. List of primer sequences used in the experiments.

Gene	Sequence		Purpose
	Forward	Reverse	
Glyma.01G188000	CGCGAATAAAGTGGAGGGTTCA	GCAGTTCCTTCTCTCCGTTGACAT	For qPCR
Glyma.01G204900	GTGGGTTGTGGTTCAACTAATGGT	CCACTGTCAGTTGTTTGACCAAGA	For qPCR
Glyma.04G131800	CCAGAAACCCTACATCTTCGACAT	GGACCTTTTCATCGTATTCGAGG	For qPCR
Glyma.04G187000	TGGCGAGAGGGGAGAGAGC	GCGGTGAGGCTTCATCGG	For qPCR
Glyma.04G192000	CGAGGTTTTGGCATGGCTGAAA	AAGGTGGGAAGGGAGGGATGATTT	For qPCR
Glyma.05G203800	ATGGCTTCGAGCATCCAACA	TGACAGAGGTGCCGCATTTT	For qPCR and ChIP-qPCR
Glyma.07G110300	GAATCAGCGGCAAGAACAACA	GAAGGGTTTGGTGGCAATGTT	For qPCR and ChIP-qPCR
Glyma.08G070700	AGCTTATGATGGCTCACAACAAGG	CACAAATTCTCCCATGTCCCTGT	For qPCR
Glyma.08G127000	GTGAATGAGGAGATAGGGATTGGG	CCACCTCCTTGAACCGAACAAT	For qPCR
Glyma.09G041000	ATTGCTCTTGCTGGTGGCATT	CTGGAAAGCAATGGTGTTGAGTG	For qPCR and ChIP-qPCR
Glyma.10G029800	CCGAAGATATGAAGAGCTTCCAAC	CGGGTGCAGATTGAGATACCATA	For qPCR
Glyma.11G204800	ACCTTGTTGATGTTGTGGTCATGG	GGTCTGCCAAACTTGCGTTTAGAT	For qPCR
Glyma.12G104800	GAGAACCCCATCTTGTGACAAAAG	CCCTCTTTTGACATTTGGCCTT	For qPCR
Glyma.13G043800	CCCTTCTCTCATCTAATTCTGCTGC	CAACTCAAGCACGTACCCTTCTCTT	For qPCR
Glyma.14G176700	TTCTGGAAATTTTGCTGTGGCC	GGGGTGTTTCAATGATCTGTGGTT	For qPCR
Glyma.14G213600	ATGGCGAAAAGGAGCATGTGT	TTATAAGCCGAGTACGTCGCTGA	For qPCR
Glyma.19G124100	TGGAACACCATTTTGGTCAAGG	AGAAACACACACAAAAGGGGCA	For qPCR
Glyma.20G168900	CCAATACAACCAGTTGCTCAGATG	ACATGCATTGTCAGGGTCATCA	For qPCR
Glyma.20G181000	GGTAGTGTTGAAATCCCCAATTGG	GGTTTGGGCAACGGTGGTATAAT	For qPCR
Glyma.20G235300	GGTGCAAAAGGTCCGATGGTAA	ACGACAGTGAATGCGACTTCCTCT	For qPCR
Glyma.04G131800	TTAAGTGCGAGTCCTAACTTCGAGG	AAGCTGCATCAGCCGCATTT	For ChIP-qPCR
Glyma.04G187000	AGTGGTCTTTAAGCTCCAG	GAGTTTGAGGATGGTGAAC	For ChIP-qPCR
Glyma.13G043800	GGTTAATTAGCTCACCTCAGAG	CCAAGCCCTTGAGTCTTAA	For ChIP-qPCR
Glyma.14G213600	ACTATGGTTCGTTGCTTTTGCTTTG	TGCAACACACGAACCACAATTACA	For ChIP-qPCR
Glyma.17g022500	ATGACCTCTGATCATGCTTCCG	AGACCAATGAGAAGGGCAGTGA	For ChIP-qPCR and qPCR
	ATGGCTGTGGAAGCATTGTA	TTAAGTGCAATGCCACTG	For full length cDNA
UBQ	ATGCAGATTTTCGTGAAAACGC	CAAAGTCGACTCTTTCTGGATG	For qPCR

Supplementary Table 2. Summary of RNA-seq data.

Sample	Total reads	Quality filtered reads	Uniquely mapped reads	Mappped rate (%)	Correlation coefficient (R)
Control_rep1	46226862	44201228	42720846	96.65	1&2=0.85 1&3=0.89 2&3=0.86
Control_rep2	51265272	49134852	47431628	96.53	
Control_rep3	50384960	48234122	46590396	96.59	

Salt_rep1	42673942	40656396	36244302	89.15	1&2=0.79 1&3=0.83 2&3=0.85
Salt_rep2	54498130	50711174	48159942	94.97	
Salt_rep3	51367822	48368815	44527591	92.06	

Supplementary Table 3. Expression profile of control and salt-treated soybean analyzed by RNA-seq (See excel file).

Supplementary Table 4. Summary of ChIP-seq data.

Sample Name		Total Reads	Mapped Reads	Mapped Rate (%)	UniqReads
Control	IP_rep1	32309878	24359067	75.39	11323797
	IP_rep2	52498286	39650520	75.53	18464272
	IP_rep3	53376582	41014566	76.84	19082956
Salt	IP_rep1	50123780	39909225	79.62	16346722
	IP_rep2	50123476	39762243	79.33	16478284
	IP_rep3	51702528	41692918	80.64	17177857

Supplementary Table 5. The list of genes with H3K27me3 modification in control soybean plants (See excel file).

Supplementary Table 6. The list of genes with *de novo* H3K27me3 modification in salt-treated soybean plants (See excel file).