

# SlbHLH22-Induced Hypertrophy Development Is Related to the Salt Stress Response of the *GTgamma* Gene in Tomatoes

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## Supplementary Information

**Table S1.** The primers used for qRT-PCR analysis.

Primer Name	Forward Sequences (5'→3')	Reverse Sequences (5'→3')
SICAC	CCTCCGTTGTGATGTAAGTGG	ATTGGTGGAAAGTAACATCATCG
SIEF1a	TACTGGTGGTTTTGAAGCTG	AACTTCCTTCACGATTTCATCATA
SIGT-7	TGGGAGAGGTACGGCATGTA	AATCCTGCGACATGCTTCCA
SIGT-31	GCACAAGAAGTACCCCTCCC	CAAGGAAAGCAATAAGAGCCAA
SIGT-32	TCGTCGCCAGTCCATCCT	TTCTTCGTGTTGCCGTGA
SIGT-34	ACCATCAAGCTTCTAAGCTATCCG	TTTAAACTCCTCTTCCCCTCCTC
SIGT-36	GTCCTGGAGTGGGGTTGAAG	GCACAAGAAGTACCCCTCCC

**Table S2.** Quality control of RNA-seq Reads in different samples.

Samples	Total Reads	Clean Reads	Mapped Reads	Unique Mapped Reads	≥Q30
WT1	48,083,964	24,041,982	45,901,481 (95.46%)	44,645,294 (92.85%)	95.46%
WT2	45,174,334	22,587,167	43,276,087 (95.80%)	42,311,051 (93.66%)	95.55%
WT3	46,112,196	23,056,098	44,245,580 (95.95%)	43,260,602 (93.82%)	95.25%
OE1	55,403,172	27,701,586	53,308,306 (96.22%)	51,967,013 (93.80%)	95.24%
OE2	45,701,750	22,850,875	43,175,875 (94.47%)	42,020,606 (91.95%)	95.15%
OE3	55,210,616	27,605,308	53,059,572 (96.10%)	51,141,744 (92.63%)	95.14%

This metabolic map illustrates the pathways of carbon metabolism, starting from methanol and branching into various products. The map is color-coded to show different metabolic routes: red for glycolysis and gluconeogenesis, green for the citric acid cycle and fatty acid metabolism, blue for amino acid metabolism, and purple for nucleotide metabolism. Key intermediates include methanol, formaldehyde, formate, glycine, alanine, and various fatty acids. The map also shows the conversion of methanol to methanolamine, dimethylamine, and trimethylamine, and the conversion of methanol to methanolamine, dimethylamine, and trimethylamine. The map is a complex network of reactions, with many intermediates and products labeled. The map is a detailed representation of the metabolic pathways of carbon metabolism, showing the flow of carbon from methanol to various products.

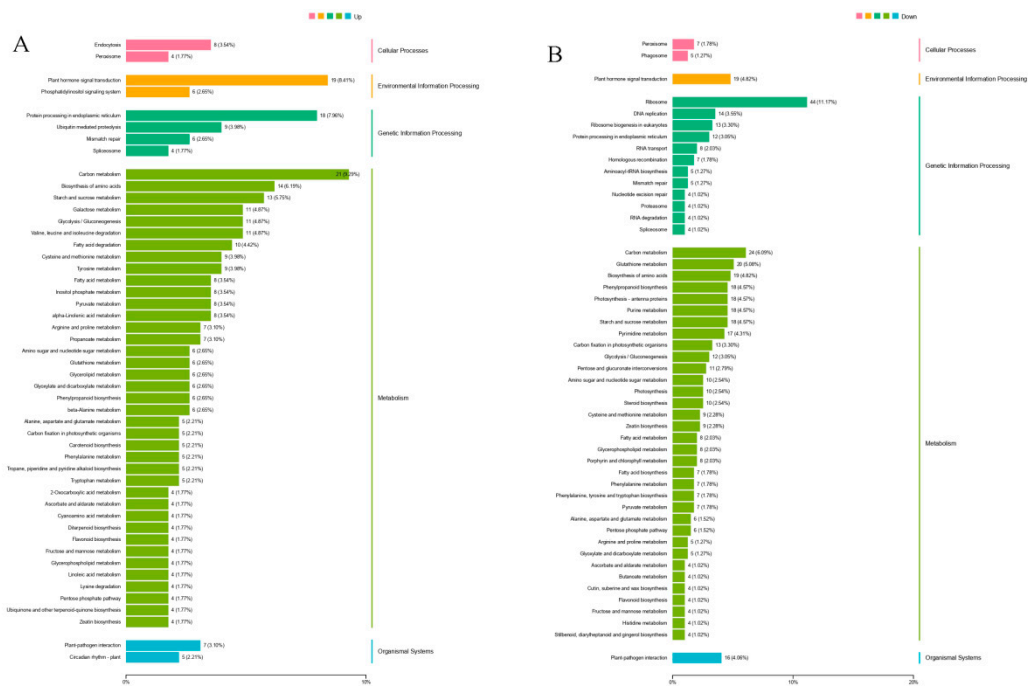
[illegible]

**TAURINE AND HYPOTAURINE METABOLISM**

The diagram illustrates the metabolic pathways of taurine and hypotauroine. Key components include:

- Enzymes (Red Boxes):** 1.3.1.13, 4.1.1.15, 4.1.1.29, 1.8.1.3, 2.3.2.2, 4.1.1.10, 4.1.1.29, 2.3.1.65, 1.4.1.117, 2.3.1.8, 2.3.3.15, 2.7.2.1, 1.1.2.-, 1.1.1.313, 1.2.1.73, 2.7.3.4.
- Metabolites and Intermediates:** Cysteine, Cysteamine, 3-Sulfino-L-alanine, Hypotauroine, L-Cysteine, L-Cystathione, Cysteine and methionine metabolism, Glutathione metabolism, Cysanino acid metabolism, Taurocholate, Aminoacetaldehyde, Sulfite, Sulfur metabolism, Pyruvate, 2-Oxoglutarate, L-Alanine, L-Glutamate, Sulfocetaldehyde, Sulfacetate, Acetyl phosphate, Acetyl-CoA, Acetate, Isethionate, Excretion, Taurocyamine, Taurocyamine phosphate, 5-Glutamyl-taurine.
- Pathway Flow:** Cysteine is converted to Cysteamine and 3-Sulfino-L-alanine. 3-Sulfino-L-alanine is converted to Hypotauroine. Hypotauroine is converted to Taurine. Taurine is converted to various products, including Excretion, Taurocyamine, Pyruvate, 2-Oxoglutarate, L-Alanine, L-Glutamate, Sulfocetaldehyde, Sulfacetate, Acetyl phosphate, Acetyl-CoA, Acetate, and Isethionate. Taurine is also converted to 5-Glutamyl-taurine. Taurine is converted to Taurocholate, which is then converted to Aminoacetaldehyde. Aminoacetaldehyde is converted to Sulfite, which is then converted to Sulfur metabolism. Sulfur metabolism is converted to Pyruvate. Pyruvate is converted to 2-Oxoglutarate. 2-Oxoglutarate is converted to L-Alanine and L-Glutamate. L-Alanine is converted to Sulfocetaldehyde. Sulfocetaldehyde is converted to Sulfacetate. Sulfacetate is converted to Acetyl phosphate. Acetyl phosphate is converted to Acetyl-CoA. Acetyl-CoA is converted to Acetate. Acetate is converted to Isethionate. Isethionate is converted to Excretion. Excretion is converted to Taurocyamine. Taurocyamine is converted to Taurocyamine phosphate. Taurocyamine phosphate is converted to 5-Glutamyl-taurine.

hypotaaurine metabolism; D, zeatin biosynthesis



**Figure S2.** Comprehensive analysis of up- (A) and down- (B) regulated DEGs by KEGG.