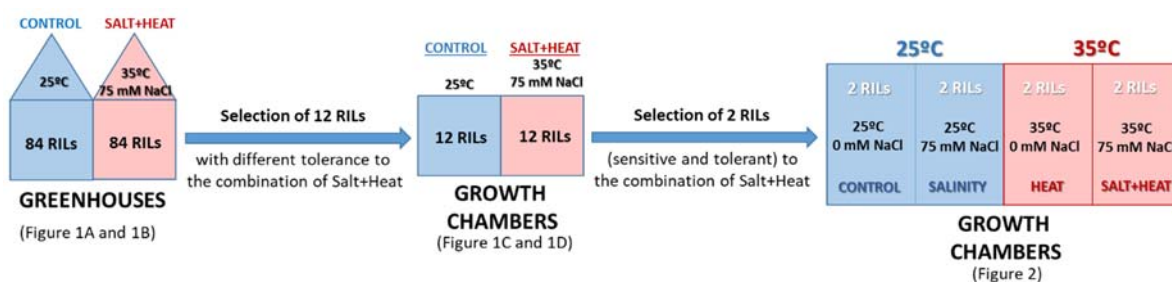


Supplemental Scheme 1. Experimental design for the three experiments carried out for the selection and experimentation with the tomato RILs population



Supplemental Table S1. Absolute values obtained in cations concentration ($\mu\text{mol/g DW}$) in leaves of two tomato recombinant lines (RIL-66 and RIL-76) under control, simple stress (salinity or heat) or the combination of salinity+heat. Values are means ($n=6$)

Treatment	Recomb. Line	Na ⁺	K ⁺	Ca ²⁺	Mg ²⁺
Control	RIL-66	2.47234158	244.607857	113.450981	28.9775737
	RIL-76	2.98536357	308.253496	127.330764	28.4618876
Salinity	RIL-66	110.821929	104.709183	110.388532	11.3756017
	RIL-76	146.06509	158.638543	124.314263	26.8133111
Heat	RIL-66	3.22416865	319.116882	115.430588	28.9804243
	RIL-76	3.10699108	295.30514	117.081159	29.4970716
Sal+Heat	RIL-66	82.6482231	106.63768	90.7005475	12.7424652
	RIL-76	101.407195	291.575017	86.5951295	26.6791909

Supplementary Table S2. Absolute values obtained in amino acids concentration ($\mu\text{mol/g DW}$) in leaves of two tomato recombinant lines (RIL-66 and RIL-76) under control, simple stress (salinity or heat) or the combination of salinity+heat. Values are means ($n=6$)

Treatment	Recomb. Line	$\mu\text{mol/g DW}$												
		GABA	Ala	Val	Pro	Asn	Trp	Tyr	Isoleu	Thr	Arg	Glu	Phe	Gln
CONTROL	RIL-66	0.39	1.26	0.08	0.49	1.99	0.03	0.03	0.11	0.38	8.69	27.49	0.08	7.12
	RIL-76	0.41	1.14	0.07	0.56	1.69	0.03	0.03	0.08	0.43	8.38	27.33	0.07	7.97
SALINITY	RIL-66	0.09	0.62	0.05	3.30	1.05	0.02	0.03	0.09	0.19	7.11	18.15	0.03	3.58
	RIL-76	0.23	0.51	0.05	2.79	1.03	0.01	0.13	0.08	0.18	5.76	40.62	0.02	3.14
HEAT	RIL-66	0.22	0.74	0.10	1.02	3.28	0.02	0.05	0.14	0.28	8.31	17.27	0.06	10.10
	RIL-76	0.43	0.99	0.09	2.36	2.79	0.02	0.04	0.09	0.34	8.18	28.77	0.05	6.38
SAL+HEAT	RIL-66	0.25	0.74	0.08	2.67	1.27	0.02	0.04	0.13	0.24	13.91	23.24	0.04	4.95
	RIL-76	1.54	0.91	0.14	3.48	4.61	0.02	0.05	0.14	0.24	3.45	33.45	0.04	14.93

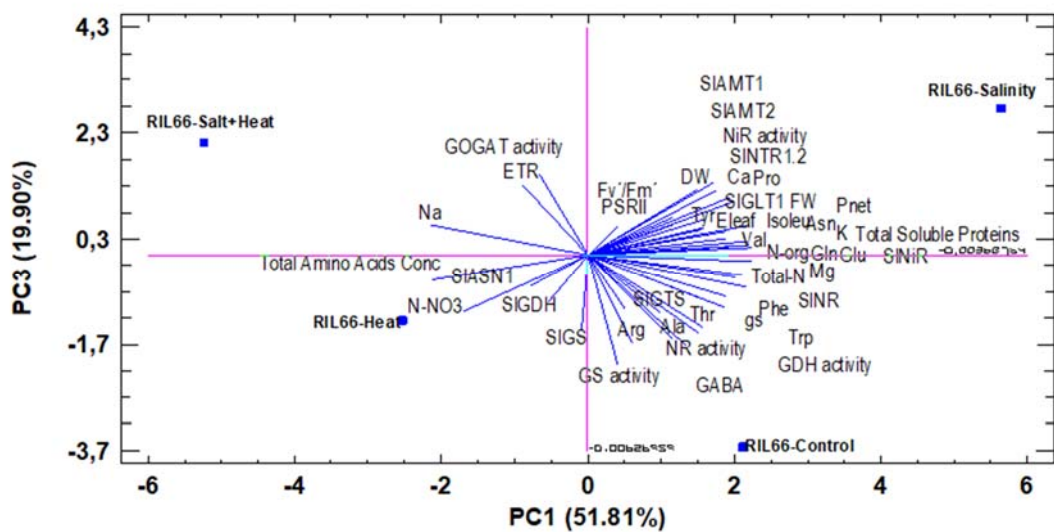
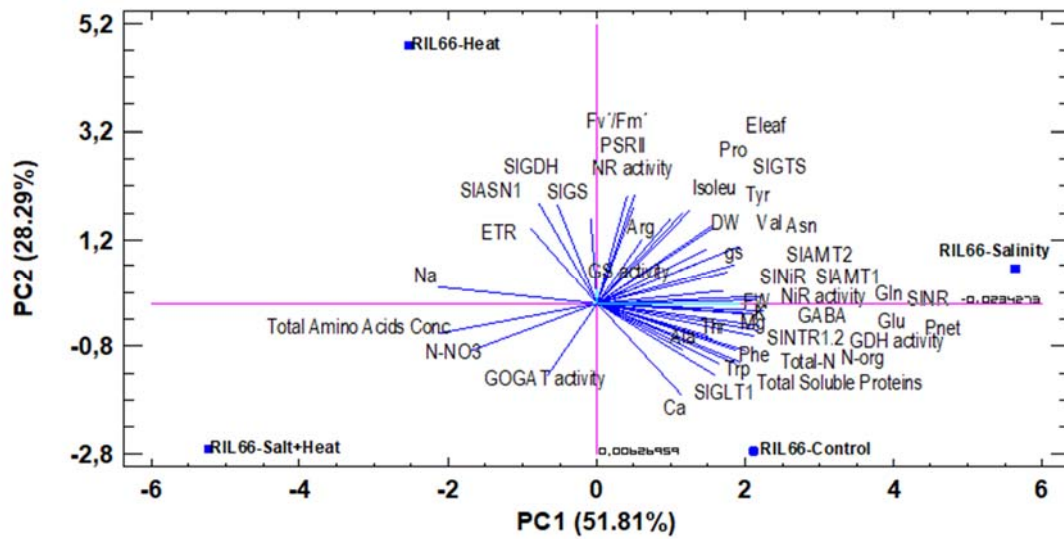
Supplementary Table S3. Primers sequences of the N-metabolism related transcripts tested by qPCR in leaves of two tomato recombinant lines (RIL-66 and RIL-76). *SIEF1* was used as internal control for data normalization.

Gene		Accession	Sense primer sequence	Antisense primer sequence
<i>SINR</i>	Nitrate reductase	Solye11g013810.1.1	GGTTCATCACTCCCGTACCACTT	TCTGCTTCACCATATTCGTCTCT
<i>SINiR</i>	Nitrite reductase	Solye01g108630.2.1	GGATTCATGGGATGCCTGACTAGA	TTCTCGTGGAACTGCACCAAAGT
<i>SIGLT1</i>	Glutamate synthase, NADH/NADPH, small subunit 1	Solye03g083440.2.1	GGGAGAGTTTGGGGTAGGGAATA	CAAGCAAACCTGGCAGCAGACATA
<i>SIGS</i>	Chloroplast Glutamine synthetase	Solye01g080280.2.1	AGCTTGACCTTGTGAGTTCCCT	CACCTCAACTCCAAAGTAGTCTCATCTCT
<i>SIGTS1</i>	Cytosolic Glutamine synthetase	Solye10g083830.1.1	ACACGGAGAAGGAAGGAAAGGGAT	TCCGCGATCATAGAGGTCACAACA
<i>SIGDH1</i>	Glutamate dehydrogenase	Solye10g078550.1.1	GTTTACTGGCTTGGACCTCAGTTT	CACCTTGTCCATGGCAGAACTTACA
<i>SIASNI</i>	Asparagine synthase	Solye04g055200.2.1	AACCTTGATCCTTCTGGTAGGGCT	TCGAGTCATGGACAGCAAGAGACT
<i>SINRT2.1</i>	Nitrate transporter protein 2.1	Solye11g069740.1.1	TCCAGTCAAGGGAACGGAAGAACA	ACCACGCTCTGATCGGCAATTT
<i>SIAMTL1</i>	Ammonium transporter protein 1	Solye09g090730.1.1	ATGTGGGTTCTGTAGCGGCTTGTAGT	TGCTGCTTCAAGTGGATCGTCGTA
<i>SIAMT2</i>	Ammonium transporter protein 2	Solye04g050440.2.1	TTGTACCGCCGCTCTGACAACTTT	CATGGCTCAACAACTGCACAACCT
<i>SIEF1 α</i>	Elongation factor 1α	Solye06g005060.2.1	GAACGTGCCAGTTGGTCTGT	GTCAAACCAGTAGGGCCAAA

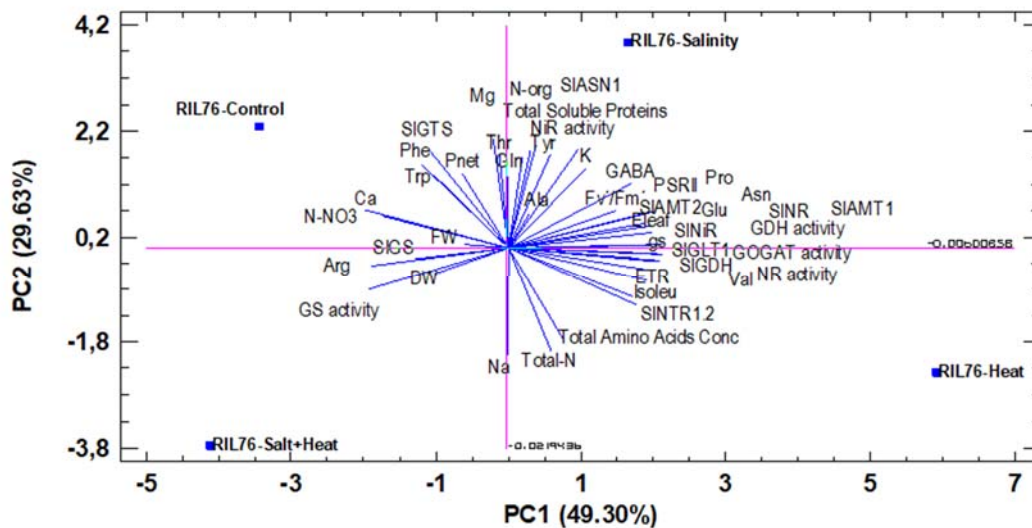
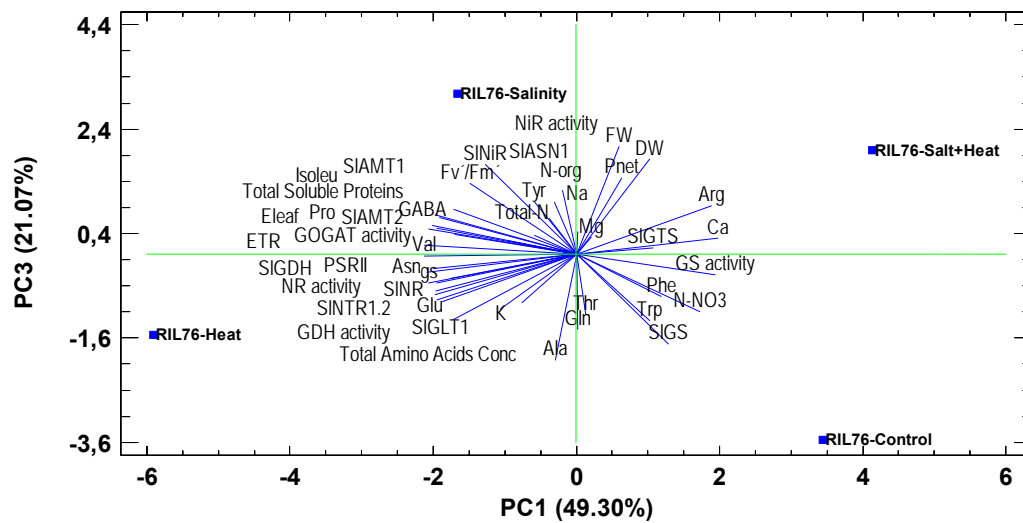
Supplementary Table S4. Log₂ of the expression of a selected set of transcripts related to the N-metabolism. Transcript expression was determined by qPCR (Applied Biosystems, Lincoln, NE) using the primers pair listed in Supplemental Table S3. Normalization of the expression was done using the internal and constitutive control *SIERF1* and samples normalization for log₂ calculation was performed with respect to control plants before stress (n=6).

	SALINITY		HEAT		SALINITY+HEAT	
	RIL-66	RIL-76	RIL-66	RIL-76	RIL-66	RIL-76
<i>SINR</i>	-2.02624257	-1.48715496	0.1003437	0.74896037	-1.0749925	2.04905732
<i>SINiR</i>	-1.01979764	1.34570217	0.42772611	2.1402998	-0.44874573	1.61988386
<i>SIGLT1</i>	-0.21411133	-0.43099817	0.31886355	-0.23856195	-0.93396346	0.89916852
<i>SIGS</i>	-0.67519976	-0.39715735	-0.31491915	-0.802543	0.49639257	-0.57151222
<i>SIGTS</i>	-0.97664611	-0.76421642	-0.19662507	-0.01933543	0.46724923	-1.12042618
<i>SIGDH</i>	-0.2961262	-0.04336866	-0.16730321	0.1210289	1.04047061	0.62991034
<i>SIASNI</i>	-0.3254877	-0.47721831	-0.0112547	1.25095113	0.38	-0.18233999
<i>SINRT 1.2</i>	-0.9604084	0.26059062	3.53222046	0.18383471	-1.34827728	1.27987989
<i>SIATM1</i>	0.24454447	0.64554297	5.78692576	1.9982645	0.06776047	2.99190254
<i>SIATM2</i>	-0.89261818	-0.00200144	6.37705326	2.14450264	0.81360817	2.33149052

Supplementary Figure S1. Principal Component Analysis (PCA) in RIL-66. A PCA analysis was done with the 45 variables studied in this manuscript, with the components PC1, PC2 and PC3 explaining 100% of the variability (PC1 and PC2 explained 80.10% of the variability). **PC1** (51.81%) explained FW, Pnet, gs, Na, K, Mg, Total-N, N-org, Total Soluble Proteins, Total Amino Acids Conc, Val, Asn, Trp, Glu, Phe, Gln, SINR, *SINiR*, *SINTR1.2* and NiR activity. PC1 lets differentiate between the treatments without heat (salinity and control) against those treatments with heat as a factor (heat and salinity+heat). **PC2** (28.29%) explained Pnet, gs, Na, K, Mg, Total-N, N-org, Total Soluble Proteins, Total Amino Acids Conc, Val, Asn, Trp, Glu, Phe, Gln, *SINR*, *SINiR*, *SINTR1.2* and NiR activity. PC2 lets differentiate between the treatments salinity+heat and control against heat and salinity. And **PC3** (19.90%) explained DW, ETR, N-NO₃, GABA, Ala, Thr, Arg, SIGS, *SIAMT1*, *SIAMT2*, GOGAT activity, GS activity, GDH activity. PC3 lets differentiate between the treatments with salinity (salinity and salinity+heat) against those treatments without salinity as a factor (heat and control).



Supplementary Figure S2. Principal Component Analysis (PCA) in RIL-76. A PCA analysis was done with the 45 variables studied in this manuscript, with the components PC1, PC2 and PC3 explaining 100% of the variability (PC1 and PC2 explained 78.93% of the variability). **PC1** (49.30%) Val, Pro, Asn, Isoleu, gs, Eleaf, Ca, N-NO3, Arg, Glu, Gln, SINR, SIAMT1, SIAMT2, SINTR1.2, NR activity, GOGAT activity, GS activity, GDH activity, PSRII, ETR and GABA. This factor lets differentiate between the four treatments applied independently. **PC2** (29.63%) explained Tyr, Thr, Phe, Fv'/Fm', SIGTS, SIASN1, NiR activity, K, Mg, Na, Total-N, N-org, Total Soluble Proteins, Total Amino Acids Conc. PC2 lets differentiate between the treatments with heat (salinity+heat and heat) against those without heat as a factor (control and salinity). And **PC3** (21.07%) explained Ala, Trp, Gln, SINiR, SIGS, DW, Pnet, Fv'/Fm'. PC3 lets differentiate between the treatments with salinity (salinity and salinity+heat) against those treatments without salinity as a factor (heat and control).



Supplementary Figure S3. A. Dendrogram with Ward's method for treatments separation in RIL-66. **B.** Dendrogram with Ward's method for treatments separation in RIL-/6.

