

**Figure S1. Breeding scheme for the production of salt tolerant homozygous mutant plants**

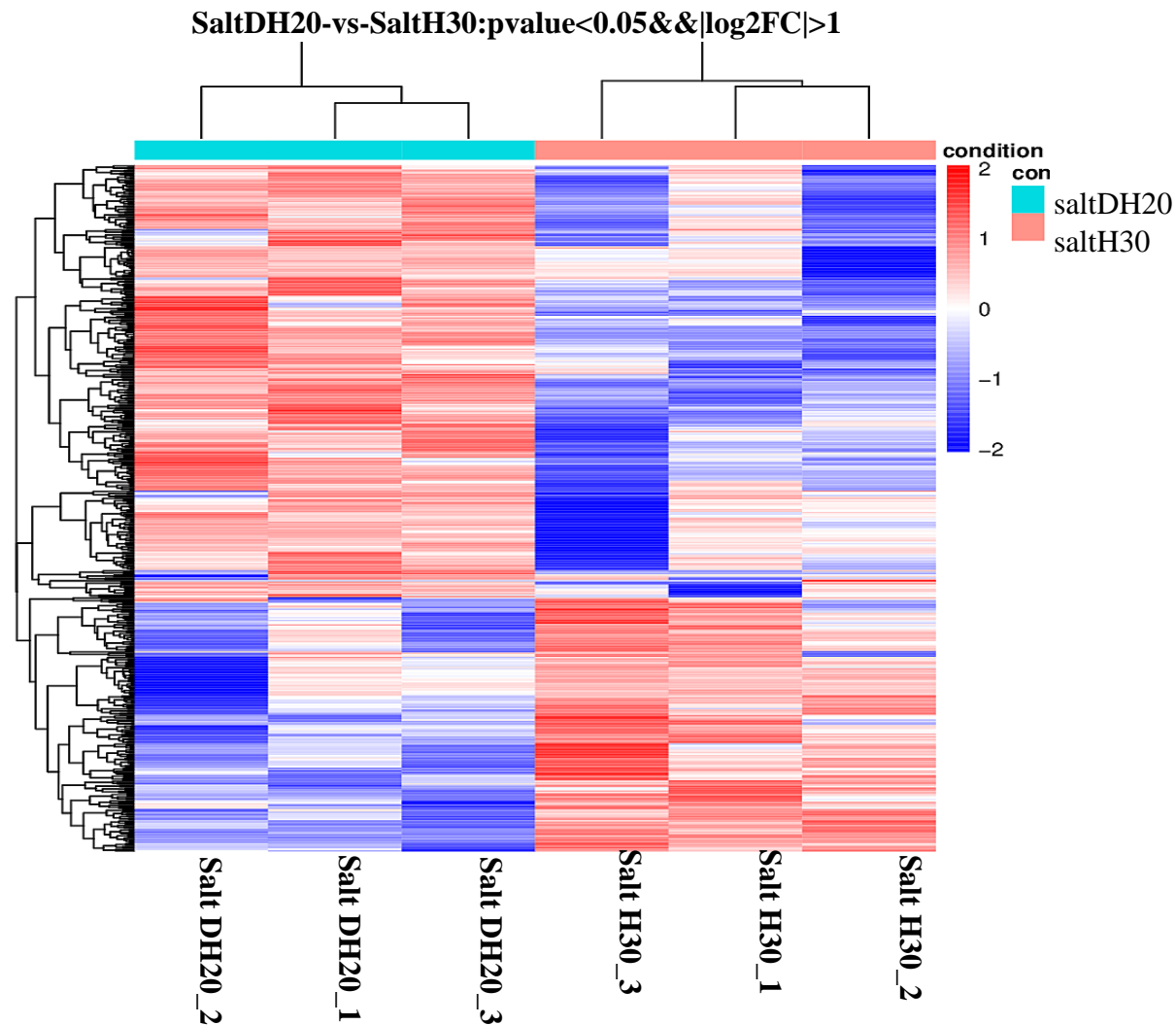


Figure S2. Heatmap analysis of specifically 462 DEGs. Samples and biological replicates of DH20 and H30 are shown. The color gradient (upper right) indicates the pattern of expression from lowly (blue) to highly (red) expressed genes and ranges from  $-2$  to  $+2$  fold changes in expression.

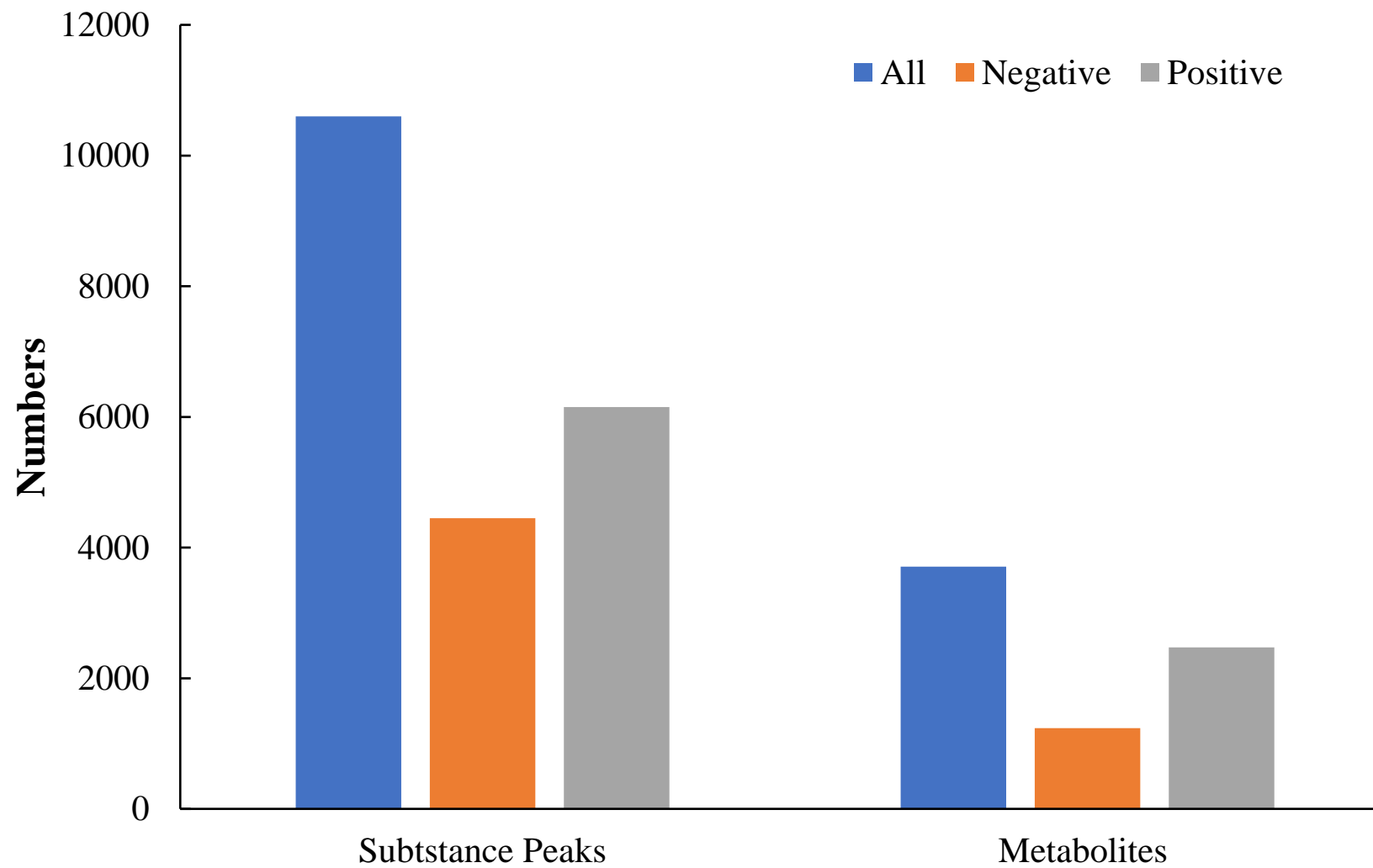


Figure S3. Statistical of substance peaks and metabolites

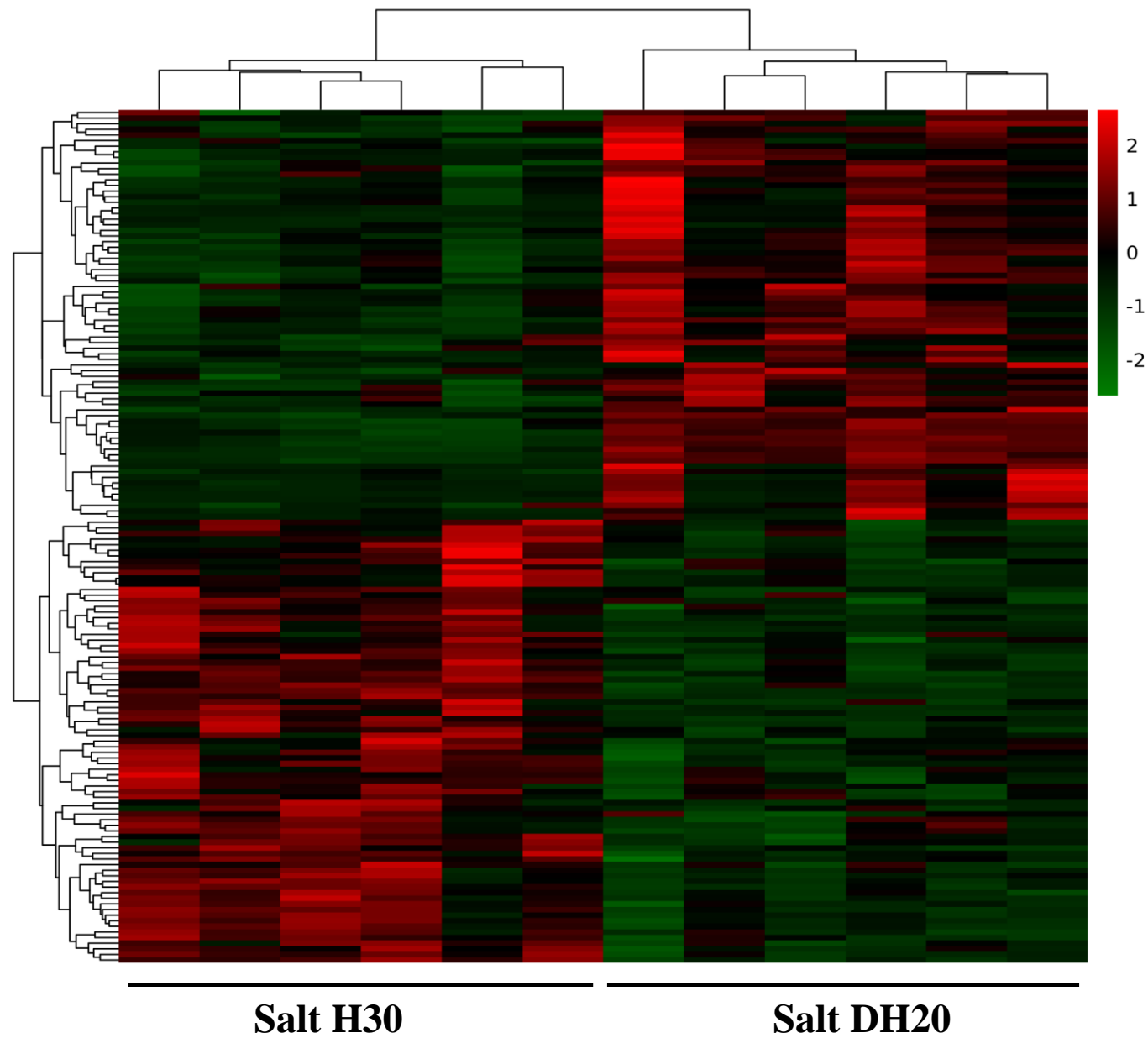


Figure S4. Heatmap analysis of 152 DAMs

**Table S1. Leaf photosynthetic properties in H30 and DH20 under control and salt conditions**

	LSP ( $\mu\text{mol m}^{-2} \text{s}^{-1}$ )	AQE ( $\mu\text{mol m}^{-2} \text{s}^{-1}$ )	Amax ( $\mu\text{mol m}^{-2} \text{s}^{-1}$ )	Vcmax ( $\mu\text{mol m}^{-2} \text{s}^{-1}$ )	Jmax ( $\mu\text{mol m}^{-2} \text{s}^{-1}$ )	Fv'/Fm'
CKH30	648±120.4b	0.03±0.002a	5.98±1.196b	16.83±2.61a	12.06±2.41a	0.52±0.01a
CKDH20	884±185.60a	0.04±0.006a	10.20±2.01a	10.83±2.05b	7.91±1.58b	0.51±0.01a
Salt H30	216±38.88B	0.007±0.0014A	0.95±0.19B	1.32±0.26B	0.74±0.15B	0.34±0.06B
SaltDH20	256±43.52A	0.007±0.00105A	1.25±0.26A	1.55±0.31A	1.32±0.26A	0.46±0.03A

LSP, light saturation point; AQE, apparent quantum efficiency; Amax, maximum net photosynthetic rate; Vcmax, maximum rate of RuBP carboxylation; Jmax, maximum rates of electron transport; Fv'/Fm', the maximal photochemical efficiency of PSII.

**Table S2. Summary of quality control for RNA-seq data**

Sample	Raw_reads	Raw_bases	Clean_reads	Clean_bases	Valid_bases	Q30	GC
CK DH20_1	69.67M	10.45G	61.17M	8.81G	84.26%	90.46%	56.59%
CK DH20_2	64.59M	9.69G	57.34M	8.46G	87.28%	90.87%	56.98%
CK DH20_3	69.37M	10.41G	57.08M	8.10G	77.85%	87.61%	56.29%
CK H30_1	71.97M	10.80G	54.67M	7.74G	71.69%	84.22%	57.41%
CK H30_2	67.21M	10.08G	56.73M	8.36G	82.91%	88.57%	56.32%
CK H30_3	46.54M	6.98G	41.49M	6.09G	87.20%	89.87%	56.48%
Salt DH20_1	65.79M	9.87G	63.78M	9.12G	92.45%	95.04%	55.29%
Salt DH20_2	85.30M	12.79G	49.79M	7.10G	55.48%	74.46%	57.34%
Salt DH20_3	61.69M	9.25G	59.76M	8.61G	93.06%	94.94%	55.84%
Salt H30_1	69.30M	10.39G	61.69M	8.88G	85.45%	91.06%	55.92%
Salt H30_2	68.00M	10.20G	54.43M	7.89G	77.32%	85.13%	56.23%
Salt H30_3	63.82M	9.57G	62.35M	8.86G	92.51%	95.66%	54.94%

Table S3. Primer information for qRT-PCR

Gene	primer sequence (5'-3')	primer sequence (3'-5')
<i>HORVU1Hr1G067480</i>	TGTGCCCCATACTCAAAACA	GTATCGCCTCAAGGATGGAA
<i>HORVU3Hr1G056830</i>	AGGTGTACGACCACCTCTGG	GCCCTACCTCAACCATCTCA
<i>HORVU1Hr1G071890</i>	GAATCTGGCCTTTTGGATGA	TTGGTCAATGCAACACAGGT
<i>HORVU7Hr1G050660</i>	AGTACCTGGGAGGGATGGAG	TGGTTTCATGAGCTGGTACG
<i>HORVU4Hr1G006850</i>	TGCATGGTGACTGGTGATCT	ACTCTTGACGAGGACGCAGT
<i>HORVU1Hr1G093460</i>	CTACACCATCCCCGAAGAGA	ACCAAACCAGCATTACCTC
<i>HORVU2Hr1G115960</i>	GCGTTCTGCATGAATCTTGA	TGCTTGGTATTGTTGGGTGA
<i>HORVU5Hr1G117910</i>	ACCGTCGGCTTATATCAACG	GAACACAAGGGGGTCATGCTT
<i>HORVU4Hr1G011160</i>	CGTTAGCAGGCATCAGTCAA	TTCTTTCCAAAACCCACGAC
<i>HORVU5Hr1G095060</i>	CCTCTTCGTGGACAAGGTGT	CCTGCCATGGTCATCTACCT
<i>HORVU1Hr1G074460</i>	CAATGGTTGACACCGAACTG	CTGGGATTTTCAGCACCAACT
<i>HORVU7Hr1G007220</i>	TGACTGGTCTGGTTGAGCTG	CTGCTCCTCCTTGTCCTTTG