

Supplementary Materials:

Transcriptomics reveals fast changes in salicylate and jasmonate signaling pathways in shoots of carbonate tolerant *Arabidopsis thaliana* under bicarbonate exposure.

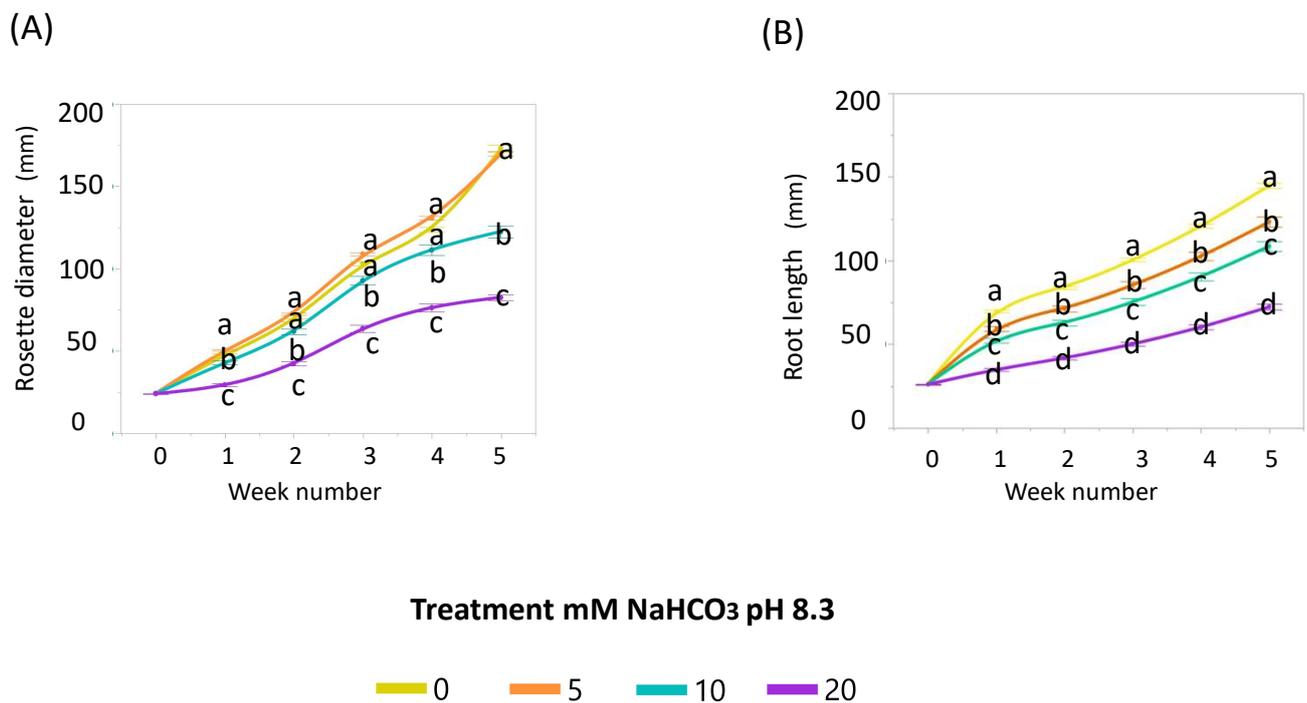


Figure S1: Growth responses of moderately bicarbonate tolerant *A. thaliana* deme to different NaHCO₃ concentrations (A) Rosette diameter (cm) and (B) root length (cm) of Al_(c+) plants grown in hydroponics for 5 weeks. Letters indicate significant differences between treatment (n= 9; p < 0.05 according to Tukey's HSD).

(A)

Gene Name	TAIR id	LFC_3h_A1(+)_bic	LFC_3h_T6(-)_bic	Forward sequence	Reverse sequence
Vacuolar iron transporter (VIT) family protein	AT1G76800	-0.88	-3.13	TTTCCGAGGTGCGATTGTA	CCTAGCCGATGACCTAACCG
MATE efflux family protein	AT2G04050	-2.23	0.40	CTCTCACATGCCGAAACATT	TGCCAACCACTTCCCCTTG
Transmembrane protein	AT2G25510	2.50	-1.10	AGGCACAAACGAACCTGGTC	TTATAGCGCCGTTCCGACAA
NAC domain (NAC044)	AT3G01600	-2.08	0.42	GTGGGATTGGTGGCTCTGAA	ATGCCTGCACTGCTTGTGA
Receptor like protein 39(RLP39)	AT3G24900	1.65	-0.67	TCCTTGGCTTCAAGCTTCTTCT	TATCGCACACACCCCATTC
Peroxidase superfamily protein	AT4G11290	-1.67	1.04	TTGGTGGACCGACATGGAAC	TGGGCACCGGATAACAAGAC
NADP-malic enzyme 3(NADP-ME3)	AT5G25880	-1.86	0.90	TCGTGTCGGTGATGACATGC	GATTGATGCCAGCTCGAGT
Late embryogenesis abundant protein (LEA)	AT5G53820	1.07	-2.52	CAGAGCATGAGCTTCAACGC	ATGGTCTCACTCGCACCTTG

(B)

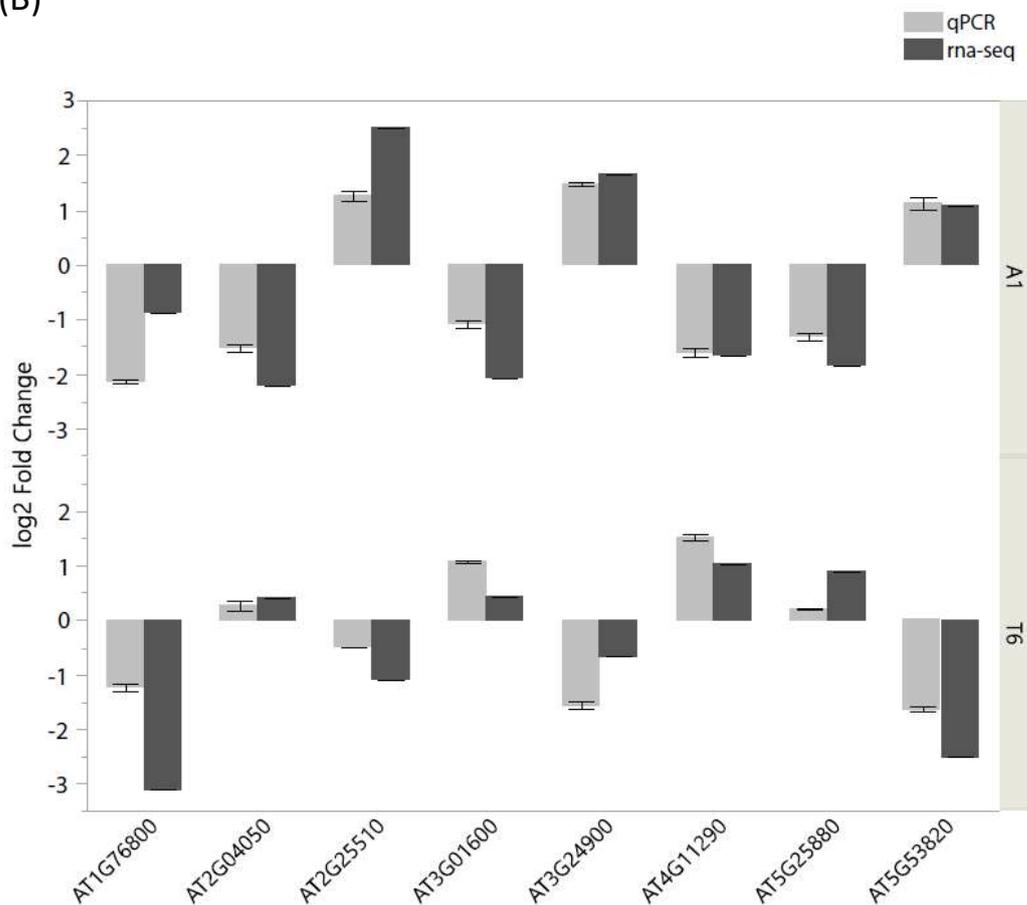


Figure S2: RNA-seq validation. (A) Primer sequence from 8 selected genes used for validation of the RNA-seq expression results. **(B)** Bar plot from RNA-seq (dark grey) and qPCR (light grey) expression results from the selected genes after 3 hours of exposure to bic and pH_{5.9}. Results are expressed in log₂ fold change ; bars indicate standard error.

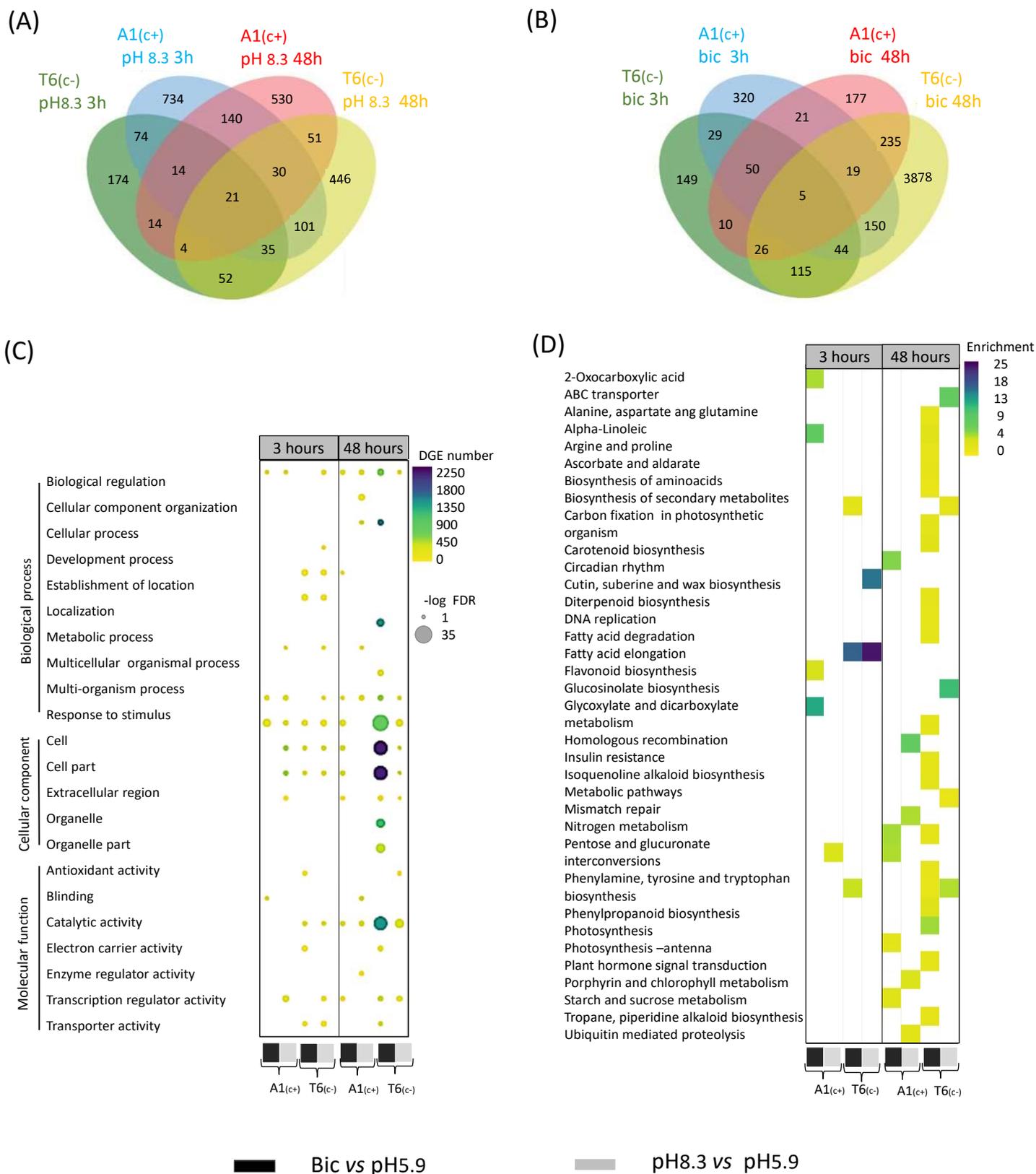


Figure S3: GO and KEEG pathway of demes comparing alkaline treatment at two time points. Venn diagram of up and downregulated DGEs comparing bic vs pH_{5.9} and pH_{8.3} vs pH_{5.9} treatments after 3 h and 48 h between A1_(c+) (A) and T6_(c-) (B) demes. (C) Bubble plot indicating significant GO analysis of DGEs in bic vs pH_{5.9} and pH_{8.3} vs pH_{5.9} treatments after 3 h and 48 h in A1_(c+) and T6_(c-) demes. GO were filtered to adjusted p-value < 0.05. Scale colors indicate number of DGEs, while bubble size indicates -log of adjusted p-value. GO terms were separated into biological function, cellular component, and molecular function. (D) Heatmap plots of KEEG pathway analysis of DGEs in bic vs pH_{5.9} and pH_{8.3} vs pH_{5.9} treatments after 3 h and 48 h between A1_(c+) and T6_(c-) demes. KEEG pathway terms were filtered by p-value < 0.05. Scale colors indicate pathway fold enrichment