Supplementary information for the manuscript:

Artificial Autopolyploidization Modifies the Tricarboxylic Acid Cycle and GABA Shunt in *Arabidopsis thaliana* Col-0

Fredd Vergara[1*], Jun Kikuchi[1,3,4], Christian Breuer[2]

[1]Environmental Metabolic Analysis Research Team, CSRS, RIKEN. 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa-ken, 230-0045, Japan; [2]Cell Function Research Team, CSRS, RIKEN; [3]Graduate School of Medical Life Science, Yokohama City University; [4]Graduate School of Bioagricultural Sciences, Nagoya University

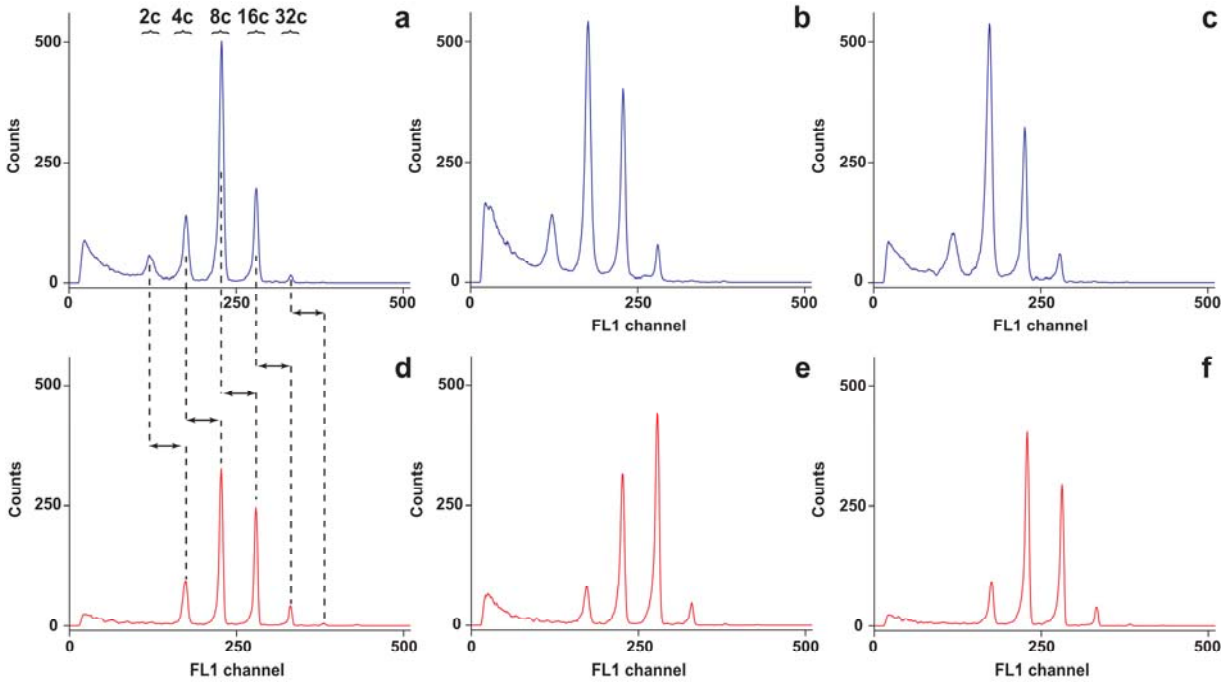

Figure S1. Ploidy level determination. Flow cytometry profiles of three randomly chosen diploid (a-c, blue) and autotetraploid (d-f, red) *Arabidopsis thaliana* col-0. Autotetraploidy is clearly observed as a shift in the location of the peaks between the upper and lower graphs across the FL1-axis (2c to 4c, 4c to 8c and so forth), which represents DNA content as a function of fluorescence.

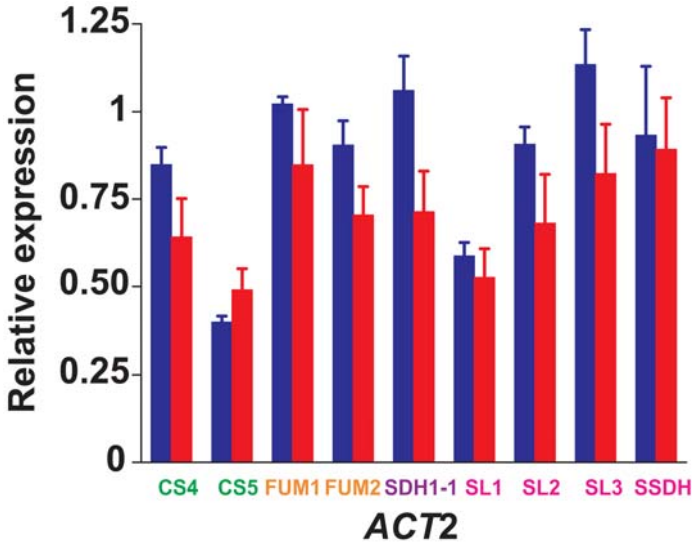

Figure S2. Relative gene expression in *Arabidopsis thaliana* Col-0 above-ground tissue. Graph shows quantitative real-time gene expression of enzymes and participating in the tricarboxylicacid cycle (TCA) and carbon:nitrogen balance. Diploids: blue bars, autotetraploids: red bars. Bars represent means and standard deviations of 8 plants (qRT-PCR) or 30 plants (^{1}H NMR). Actin 2 expression level was used for normalizing qRT-PCR values. Names of genes are colored as their corresponding metabolites (Fig. 5 in main text).

Primer name	Primer sequence (5'–3')	Amplicon region
CS4*F*	AACCTGATTGCTCGTGTTCC	Citrate synthase
CS4*R*	GCCTCATGAGCTCTTTCACC	Citrate synthase
CS5*F*	AACAGTGGCAAGGTTGTTCC	Citrate synthase
CS5*R*	CCACGGGTTCTTGACCTTT	Citrate synthase
FUM1*F*	GGTTTGTGCACAGGTTATGG	Fumarase
FUM1*R*	TTTTTCTCGAACGAAGCTGAA	Fumarase
FUM2*F*	GCAAGCGCTCTCTTACATTC	Fumarase
FUM2*R*	TGAGCTCTTTTGGCTACTGCT	Fumarase
SDH1-1*F*	GGTGTAGGACCGCATAAGGA	Succinate dehydrogenase
SDH1-1*R*	GAACCGTGGGTAAGACAGGA	Succinate dehydrogenase
SDH1-2*F*	TATTCGCTGGTGTCGATGTT	Succinate dehydrogenase
SDH1-2*R*	TCTCCTGCAGCCATTAGTCC	Succinate dehydrogenase
SL1*F*	TCAAACCTGGTGAATGCAAG	Succinate CoA ligase
SL1*R*	ATTAAACGGATCCCCACCA	Succinate CoA ligase
SL2*F*	AACGTGATGAGGCTGAAGAGA	Succinate CoA ligase
SL2*R*	CGGTCCAGAATAATGGAAAAG	Succinate CoA ligase
SL3*F*	GCAGGAGTGACACCGAAGA	Succinate CoA ligase
SL3*R*	CTCAGCCTCAATACCCTCCA	Succinate CoA ligase
SSDH*F*	TAGCTCCCCTTATTCGGTTC	Succinic

		semialdehyde dehydrogenase
SSDH*R*	CGTTCACCCCTACAAGTCCA	Succinic semialdehyde dehydrogenase
ACT2*F*	CTGGATCGGTGGTTCCATTC	Actin 2
ACT2*R*	CCTGGACCTGCCTCATCATAC	Actin 2
UBQ10*F*	GGCCTTGTATAATCCCTGATGAATAAG	Ubiquitin 10
UBQ10*R*	AAAGAGATAACAGGAACGGAAACATAGT	Ubiquitin 10

Table S1. Primers used for qRT-PCR.