Fig A – Blume et al.

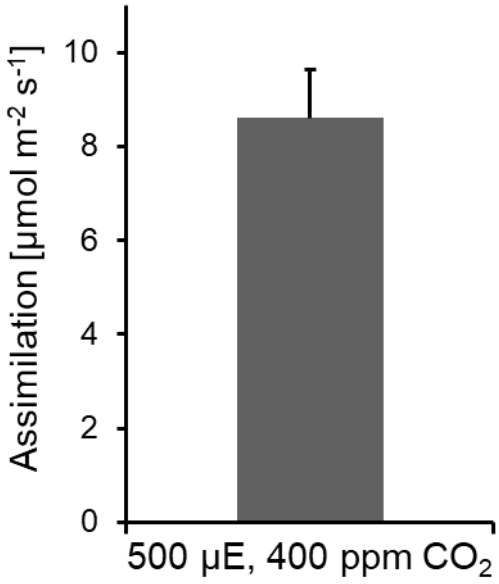

Fig A. CO_2 assimilation of 5-weeks-old *Arabidopsis* plants. Net CO_2 assimilation was recorded under ambient CO_2 conditions (400 ppm) and light saturating conditions (500 µE).

Fig B – Blume et al.

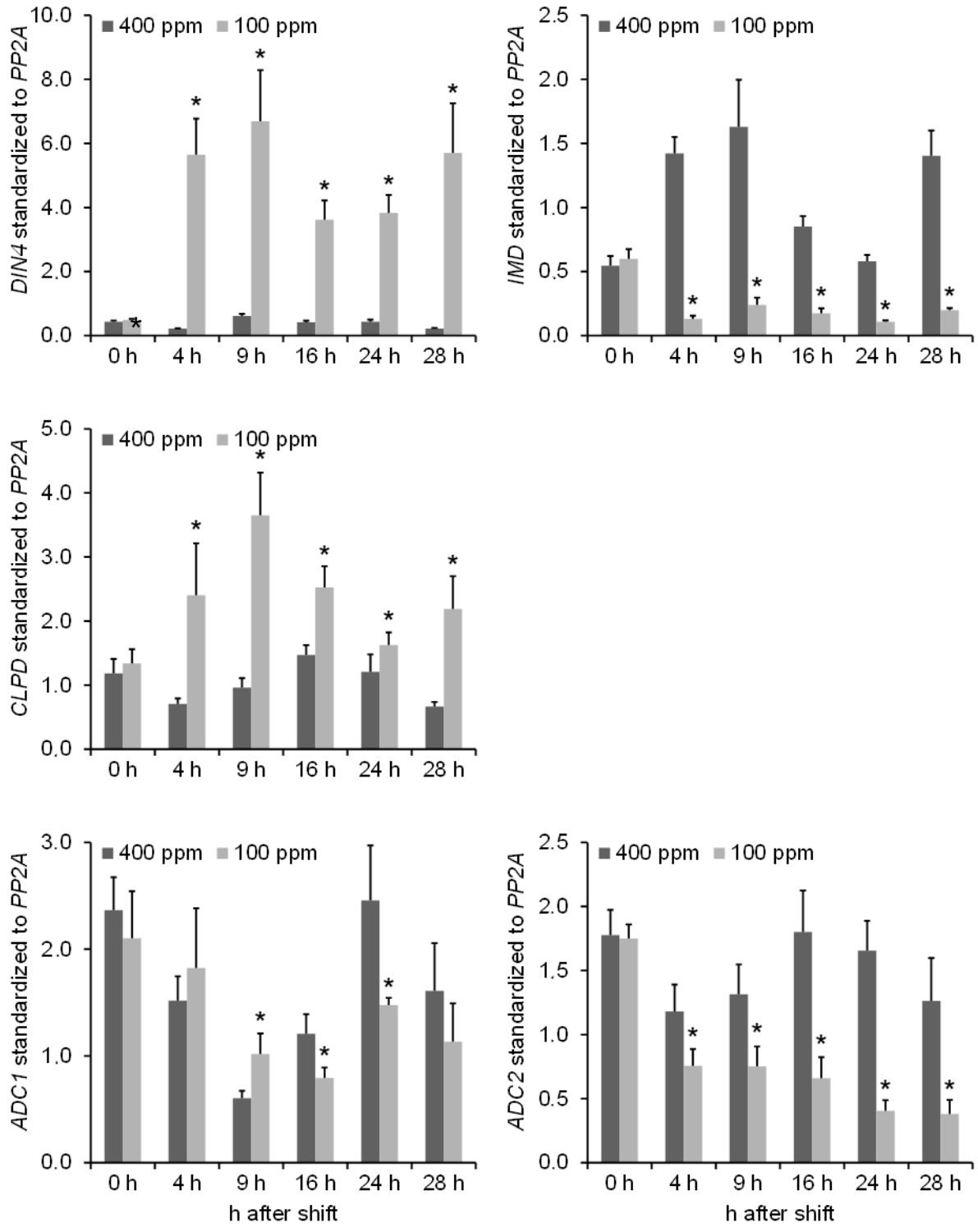

Fig B. Transcript levels of selected genes of leucine synthesis (*IMD*) and degradation (*DIN4*), protein degradation (*CLPD*), and polyamine synthesis (*ADC1, 2*) at 400 ppm and 100 ppm CO_2 standardized to *PP2A*. Data are the mean of five biological replicates ± SD. Significance was tested according to the two-tailed Student's t-test; values were changed to $\log_2$ ratios to allow this test (* $p<0.05$) DIN4, Dark-induced 4; IMD, Isopropylmalate dehydrogenase; CLPD, caseinolytic protease D; ADC, arginine decarboxylase.

Fig C – Blume et al.

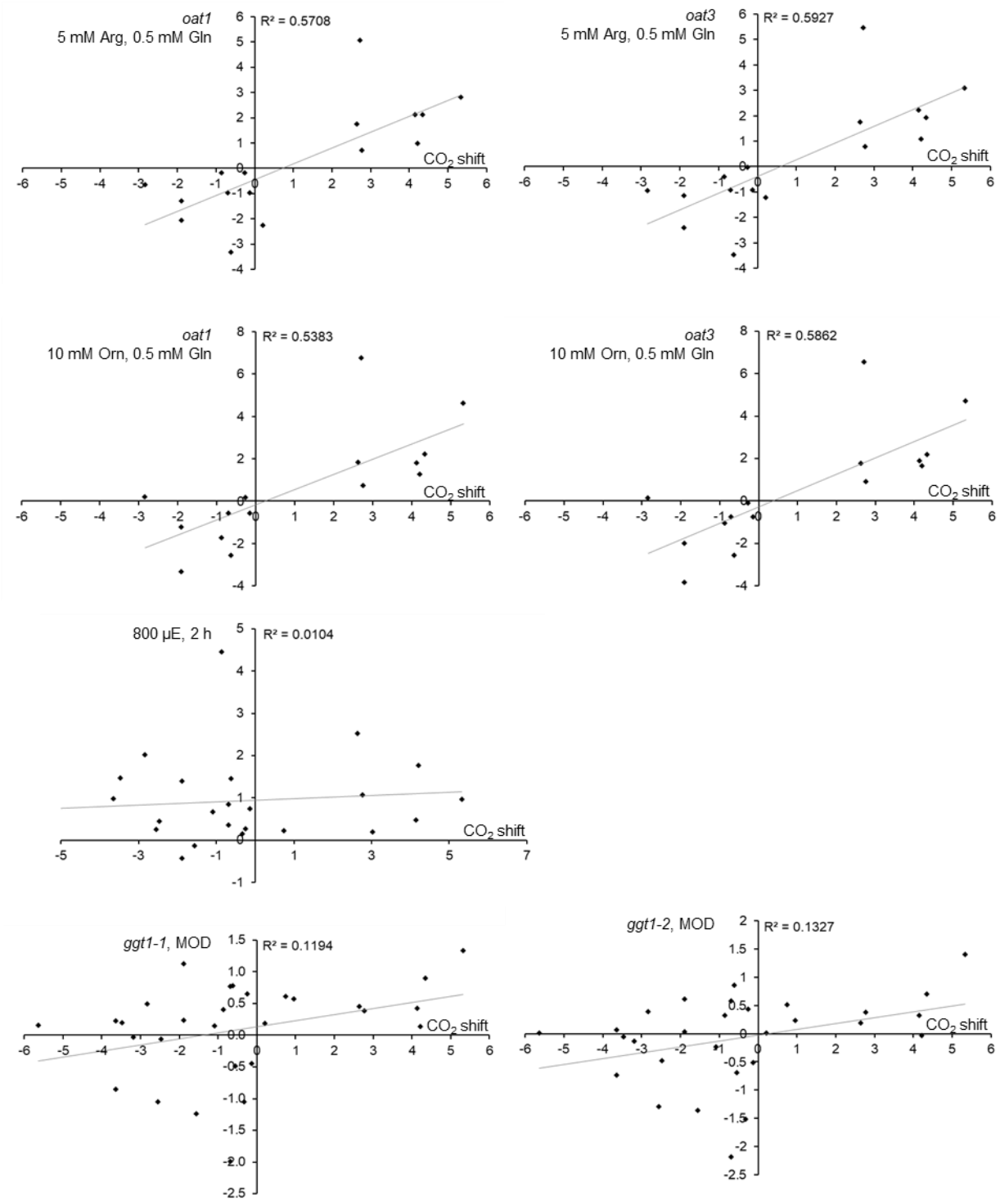

Fig C. Correlation of log2 metabolite changes between the low CO_2 shift and in response to different stresses/different *Arabidopsis* mutants. The fold changes are given in Fig 6.

Fig D – Blume et al.

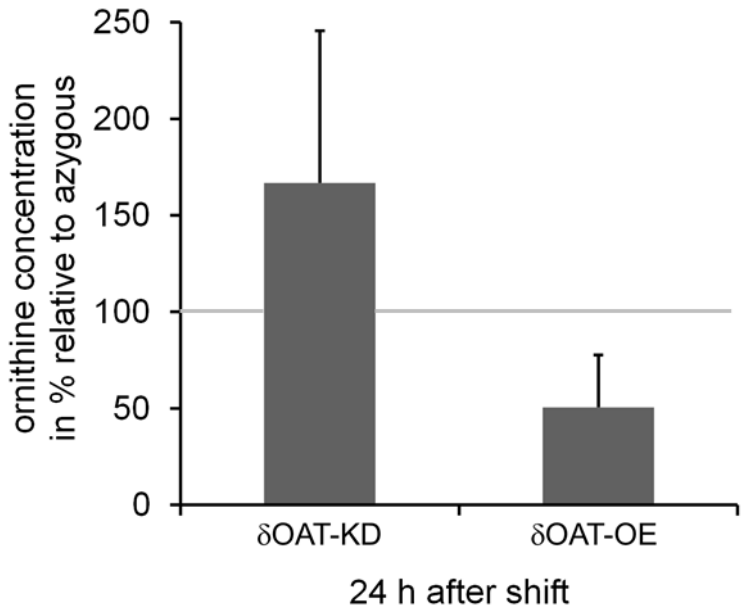

Fig D. Concentration of ornithine in knockdown (KD) and overexpression (OE) lines of *δOAT* after a shift from 400 ppm to 100 ppm CO_2 relative to azygous plants. Plant material was harvested 24 h after shifting the plants to low CO_2 concentrations. Data are the mean of three (KD) or two (OE) biological replicates ± SD. Grey line: wild type *δOAT* level.