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| **Supplementary File 2a. Table of Mixed Effects Model investigating changes in FNR density between different chloroplast sub-compartments in WT Arabidopsis.** Analysis of data presented in Figure 1 Supplement 2. Fixed Effects taking either label density in the stroma as the intercept or label density in the margins/lamellae as the intercept. Linear mixed model fit by REML. Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
| **Deletion test** carried out using using Satterthwaite’s method with the R package lmerTest (Kuznetsova, Brockhoff & Christensen 2017). The model is a mixed effects model with random intercepts. The square root of response is the response variable, tissue is the fixed effect and individual the random effect. |
| Fixed effect deleted | Sum Sq | Mean Sq | Num DF | Den DF | F value | Pr (>F) |  |
| sub-compartment | 284.46 | 94.82 | 3 | 66.825 | 118.88 | 2.20^-16 | \*\*\* |
|  |  |  |  |
| **Model summary:**  |  |  |  |  |  |  |
| Random effects: |  |  |  |  |  |  |  |
| Groups | Name | Variance | Std. Dev. |  |  |  |  |
| individual  | (Intercept) | 0.01648 | 0.1284 |  |  |  |  |
| Residual |  | 0.79758 | 0.8931 |  |  |  |  |
| Number of obs: 91, groups: individual, 25 |  |  |
| Fixed effects when stroma is set as the intercept: |
|  | Estimate | Std. Error | DF | t value | Pr (>|t|) |  |  |
| (Intercept) | 2.3925 | 0.1924 | 86.9198 | 12.438 | <2.00^-16 | \*\*\* |  |
| cytosol | -2.3791 | 0.2612 | 67.8887 | -9.107 | 2.19^-13 | \*\*\* |  |
| grana | -0.2515 | 0.2693 | 65.7707 | -0.934 | 0.354 |  |  |
| margin/lamellae  | 2.5477 | 0.2693 | 65.7707 | 9.462 | 6.86^-14 | \*\*\* |  |
|  |  |  |  |  |  |  |  |
| Fixed effects when margin/lamellae is set as the intercept: |
|  | Estimate  | Std. Error | DF | t value | Pr (>|t|) |  |
| (Intercept) | 4.9402 | 0.1924 | 86.9198 | 25.683 | <2.00^-16 | \*\*\* |
| cytosol | -4.9269 | 0.2612 | 67.8887 | -18.86 | <2.00^-16 | \*\*\* |
| grana | -2.7993 | 0.2693 | 65.7707 | -10.396 | 1.62^-15 | \*\*\* |
| stroma | -2.5477 | 0.2693 | 65.7707 | -9.462 | 6.86^-14 | \*\*\* |

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| **Supplementary File 2b. Mixed Effects Model investigating changes in cytochrome *f* density between different chloroplast sub-compartments in WT Arabidopsis.** Analysis of data presented in Figure 1 Supplement 2. Fixed Effects taking either label density in the stroma as the intercept or label density in the margins/lamellae as the intercept. Linear mixed model fit by REML. Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
| **Deletion test** carried out using using Satterthwaite’s method with the R package lmerTest (Kuznetsova, Brockhoff & Christensen 2017). The model is a mixed effects model with random intercepts. The square root of response is the response variable, tissue is the fixed effect and individual the random effect. |
| Fixed effect deleted | Sum Sq | Mean Sq | Num DF | Den DF | F value | Pr (>F) |  |
| sub-compartment  | 15.211  | 5.0702  | 3 | 39 | 23.586  | 7.135e-09 | \*\*\* |
|  |  |  |  |  |  |  |  |
| **Model summary**: |
| Random effects: |  |  |  |  |  |  |  |
| Groups | Name | Variance | Std. Dev. |  |  |  |  |
| individual  | (Intercept) | 0.007045 | 0.08393 |  |  |  |  |
| Residual |  | 0.214969 | 0.46365 |  |  |  |  |
| Number of obs: 56, groups: individual, 14 |  |  |
|  |  |  |  |  |  |  |  |
| Fixed effects when stroma is set as the intercept: |
|  | Estimate | Std. Error | DF | t value | Pr (>|t|) |  |  |
| (Intercept) | 0.283 | 0.1259 | 51.8434 | 2.247 | 0.0289 | \* |  |
| relevel cytosol | -0.2765 | 0.1752 | 39 | -1.578 | 0.1227 |  |  |
| relevel grana | 0.863 | 0.1752 | 39 | 4.925 | 1.59^-05 | \*\*\* |  |
| relevel margin/lamellae | 0.9072 | 0.1752 | 39 | 5.177 | 7.15^-06 | \*\*\* |  |
|  |  |  |  |  |  |  |  |
| Fixed effects when margin/lamellae is set as the intercept: |
|  | Estimate  | Std. Error | DF | t value | Pr (>|t|) |  |
| (Intercept) | 1.19021  | 0.12593  | 51.84340  | 9.451  | 7.24^-13 | \*\*\* |
| relevel cytosol | 1.18371  | 0.17524  | 39.00000  | -6.755  | 4.66^-08  | \*\*\* |
| relevel grana | -0.04422  | 0.17524  | 39.00000 | -0.252  | 0.802 |  |
| relevel stroma | -0.90724  |  0.17524  | 39.00000 | -5.177  | 7.15^-06 | \*\*\* |

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| **Supplementary File 2c. Fitting parameters and errors in comparison of light dependent NADP+ reduction by different genotypes.**  Analysis performed using the data in Figure 4. Fits were calculated from experiments on individual chloroplast preparations, and then the parameters, and the fitting errors averaged. |
|  | Fitting parametersParameters calculated individually for 3-6 biological replicates and then averaged ± s.d. | Errors (absolute, 95% confidence)Errors in the fit calculated individually for 3-6 biological replicates and then averaged ± s.d. |
|  | $$F\_{\infty }$$ | $$A\_{fast}$$ | $$A\_{slow}$$ | $$k\_{fast}$$ | $$k\_{slow}$$ |  | $$∆F\_{\infty }$$ | $$∆A\_{fast}$$ | $$∆A\_{slow}$$ | $$∆k\_{fast}$$ | $$∆k\_{slow}$$ |
| wt | 0.0134±0.0072 | 0.697±0.048 | 0.303±0.048 | 3.74±1.62 | 0.111±0.052 |  | 0.000677±0.000465 | 0.0674±0.0455 | 0.0272±0.0144 | 1.51±0.45 | 0.0758±0.0576 |
| *fnr1* | 0.0155±0.0075 | 0.865±0.117 | 0.135±0.117 | 10.8±6.62 | 0.235±0.252 |  | 0.000185±6.48E-05 | 0.0371±0.0338 | 0.00949±0.00889 | 4.88±3.40 | 0.100±0.110 |
| *fnr1*-ZmFNR1 | 0.0201±0.0082 | 0.701±0.060 | 0.298±0.06 | 10.2±5.62 | 0.300±0.122 |  | 0.000243±0.000101 | 0.0597±0.0390 | 0.0239±0.0196 | 3.46±1.70 | 0.0842±0.0384 |
| *fnr1-*ZmFNR2 | 0.0158±0.0037 | 0.696±0.084 | 0.304±0.085 | 8.60±3.12 | 0.388±0.225 |  | 0.00021±2.5E-05 | 0.0705±0.0230 | 0.0367±0.0187 | 5.44±3.26 | 0.106±0.076 |
| *fnr1-*ZmFNR3 | 0.0164±0.0067 | 0.833±0.109 | 0.167±0.120 | 9.04±5.18 | 0.209±0.119 |  | 0.000213±1.31E-05 | 0.0552±0.0120 | 0.0159±0.0049 | 4.34±3.34 | 0.106±0.053 |

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| **Supplementary File 2d. Statistical analysis on the contribution of the fast phase to total amplitude of light dependent fluorescence change in the chloroplast assay of NADP+ reduction.** Analysis performed using the data in Figure 4 and Averaged in Supplementary File 2c.One Way Analysis of Variance  |
| Normality Test (Shapiro-Wilk): Passed (P = 0.642)  |
| Equal Variance Test (Brown-Forsythe): Passed (P = 0.629)  |
|   | *n* | *missing* | *mean* | *Std Dev* | *SEM* |
| wt | 3 | 0 | 0.697 | 0.0479 | 0.0276 |
| *fnr1* | 3 | 0 | 0.865  | 0.117 | 0.0675 |
| *fnr1*-ZmFNR1 | 4 | 0 | 0.702  | 0.0600 | 0.0300 |
| *fnr1-*ZmFNR2 | 5 | 0 | 0.696 | 0.0848 | 0.0379 |
| *fnr1-*ZmFNR3 | 5 | 0 | 0.833 | 0.110 | 0.0490 |
|  |
| Source of Variation  | *DF*  | *SS*  | *MS*  | *F* | *P* |
| Between Groups | 5 | 0.114 | 0.0228 | 2.995 | 0.043 |
| Residual | 16 | 0.122 | 0.00761 |  |  |
| Total  | 21 | 0.236 |  |  |  |
|  |
| The differences in the mean values among the treatment groups are greater than would be expected by chance; there is a statistically significant difference (P = 0.043).  |
| Power of performed test with alpha = 0.050: 0.514  |
|  |
| Multiple Comparisons versus Control Group (Holm-Sidak method):  |
|  |
| Comparison | Diff of Means  | t  | P  |
| wt vs. *fnr1* | 0.169 | 2.368 | 0.145 |
| wt vs. *fnr1-*ZmFNR3 | 0.136 | 2.136 | 0.180 |
| wt vs. *fnr1*-ZmFNR1 | 0.00503 | 0.0756 | 0.996 |
| wt vs. *fnr1*-ZmFNR2 | 0.000679 | 0.0107 | 0.992 |

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| **Supplementary File 2e. Fitting parameters and errors in comparison of dark NADPH oxidation by different genotypes.**  Analysis performed using the data in Figure 4. Fits were calculated from experiments on individual chloroplast preparations, and then the parameters, and the fitting errors averaged. |
|  | Fitting parameters (Hill)Parameters calculated individually for 3-6 biological replicates and then averaged ± s.d. |  | Errors (absolute, 95% confidence)Errors in the fit calculated individually for 3-6 biological replicates and then averaged ± s.d. |
|  | $$F\_{\infty }'$$ | $$k\_{rec}$$ | $$n$$ |  | $$∆F\_{\infty }'$$ | $$∆k\_{rec}$$ | $$∆n$$ |
| wt | -0.00344 ±0.00112 | 0.415±0.0980 | 1 |  | 0.000619±7.2E-05 | 0.109±0.038 | - |
| *fnr1* | -0.00341±0.00414 | 0.455±0.410 | 1 |  | 0.000694±0.00013 | 0.141±0.1812 | - |
| *fnr1-* ZmFNR1 | -6.38E-04±0.00147 | 0.202±0.098 | 1 |  | 0.00103±0.00052 | 0.0406±0.0115 | - |
| *fnr1-* ZmFNR2 | -0.00361±0.00196 | 0.373±0.034 | 1 |  | 0.00070±0.00013 | 0.0966±0.0145 | - |
| *fnr1-* ZmFNR3 | -0.00287±0.0029 | 0.185±0.034 | 1 |  | 0.00089±0.00011 | 0.0312±0.0005 | - |

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| **Supplementary File 2f. Pm values and statistical analysis of plants used for PAM analysis of the high light response.** Analysis performed using the data in Figure 5, with example traces given in Figure 5 Supplement 1. Pm determination of dark-adapted leaves in order to calculate PSI parameters in response to high light treatment of Wt, *fnr1*, and *fnr1* plants expressing either ZmFNR1, ZmFNR2 or ZmFNR3 Arabidopsis plants (see Figure 5). n = 5-7 replicates. Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 |
|  | Mean ± sd |
| wt | 1.04 | ±0.07 |  |  |
| *fnr1* | 0.91 | ±0.25 |  |  |
| *fnr1-* ZmFNR1 | 1.11 | ±0.22 |  |  |
| *fnr1-* ZmFNR2 | 1.05 | ±0.23 |  |  |
| *fnr1-* ZmFNR3 | 1.11 | ±0.23 |  |  |
|  |  |  |  |  |
| ANOVA (One - way ) and Post hoc TSD Tukey test of the Pm determination for assessing the PSI responses to high light treatment on leaves from wild type, *fnr1*, and *fnr1* plants expressing either ZmFNR1, ZmFNR2 or ZmFNR3 (n>6 replicates). Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 in .Overall ANOVA |
|  | Df  | Sum Sq | Mean Sq | F value | Pr(>F) |
| genotype | 4 | 0.3142 | 0.07854 | 1.719 | 0.16 |
| Residuals | 52 | 2.3757 | 0.04569 |  |  |
| Post hoc TSD Tukey |  |  |  |
|  | Estimate | Std. Error | t value | Pr(>|t|) |
| ZmFNR1-fnr1 | 0.193861 | 0.094252 | 2.057 | 0.254 |
| ZmFNR2-*fnr1* | 0.135583 | 0.08726 | 1.554 | 0.533 |
| ZmFNR3-*fnr1* | 0.200417 | 0.085565 | 2.342 | 0.148 |
| wt-*fnr1* | 0.096689 | 0.089221 | 1.084 | 0.814 |
| ZmFNR2-ZmFNR1 | -0.058278 | 0.094252 | -0.618 | 0.971 |
| ZmFNR3-ZmFNR1 | 0.006556 | 0.092685 | 0.071 | 1 |
| wt-ZmFNR1 | -0.097172 | 0.09607 | -1.011 | 0.849 |
| ZmFNR3-ZmFNR2 | 0.064833 | 0.085565 | 0.758 | 0.941 |
| wt-ZmFNR2 | -0.038894 | 0.089221 | -0.436 | 0.992 |
| wt-ZmFNR3 | -0.103727 | 0.087565 | -1.185 | 0.76 |