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SUPPLEMENTARY INFORMATION

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Overexpression of Rubisco subunits with RAF1 increases Rubisco content in maize

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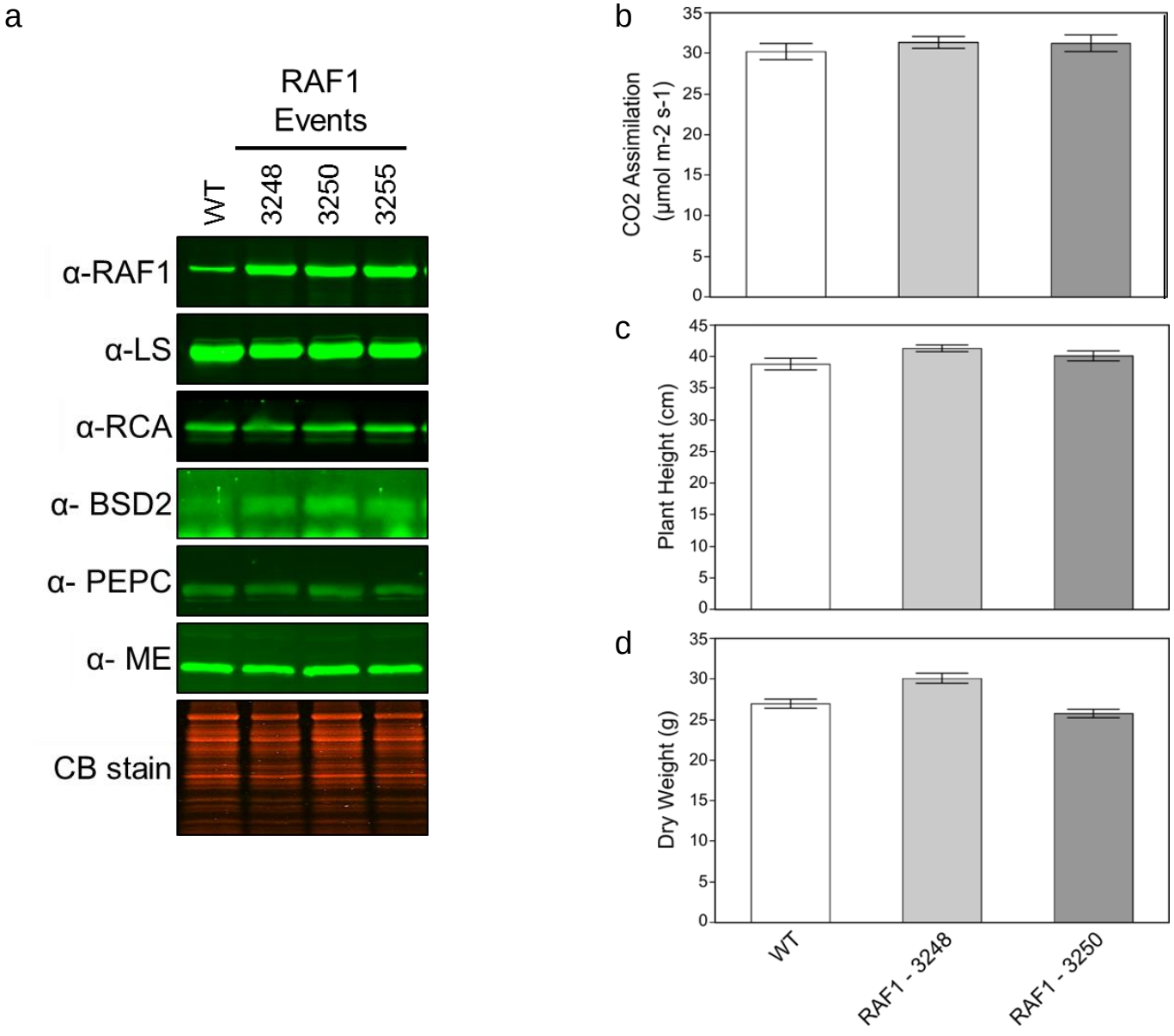

Fig. S1. Comparison of different RAF1 transgenic events. **(a)** Soluble protein was isolated on a leaf area basis from total leaf tissue of three transgenic events and analyzed by immunoblot (n=3 biologically independent experiments). **(b)** Light-saturated photosynthetic rate, **(c)** plant height and **(d)** dry weight were measured for two RAF1 transgenic events. Values are shown as the mean ± SE (n=5 biologically independent samples). No significant differences were observed ($P<0.05$); one-way ANOVA Tukey HSD.

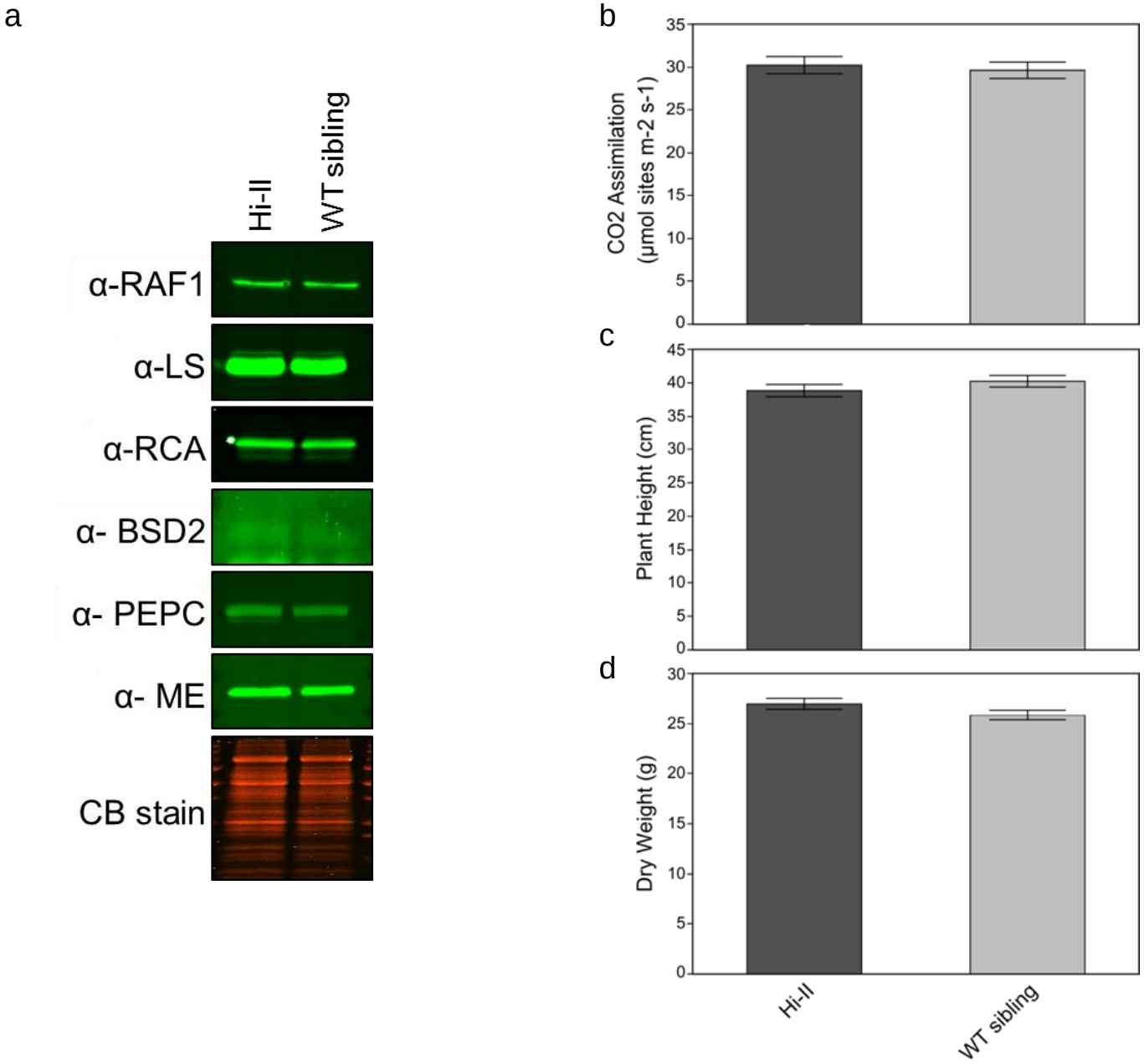

Fig. S2. Comparison of Hi-II WT controls and WT non-transgenic siblings used in this study. **(a)** Soluble protein was isolated on a leaf area basis from total leaf tissue of Hi-II and WT siblings and analyzed by immunoblot (n=3 biologically independent experiments). **(b)** Light-saturated photosynthetic rate, **(c)** plant height and **(d)** dry weight were compared. Values are shown as the mean ±SE (n=5 biologically independent samples). No significant differences were observed ($P<0.05$); one-way ANOVA Tukey HSD.

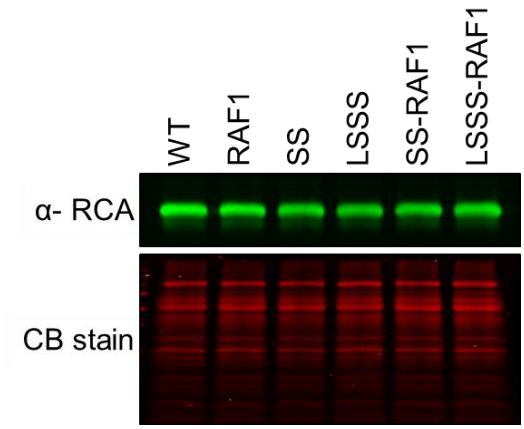

Fig. S3. Comparison of Rubisco activase expression between WT and transgenic lines. Soluble protein was extracted from leaf tissue of 2½ week-old plants on an equal leaf area basis and analyzed by immunoblotting using the Rubisco activase antibody, indicated at left (n=3 biologically independent experiments).

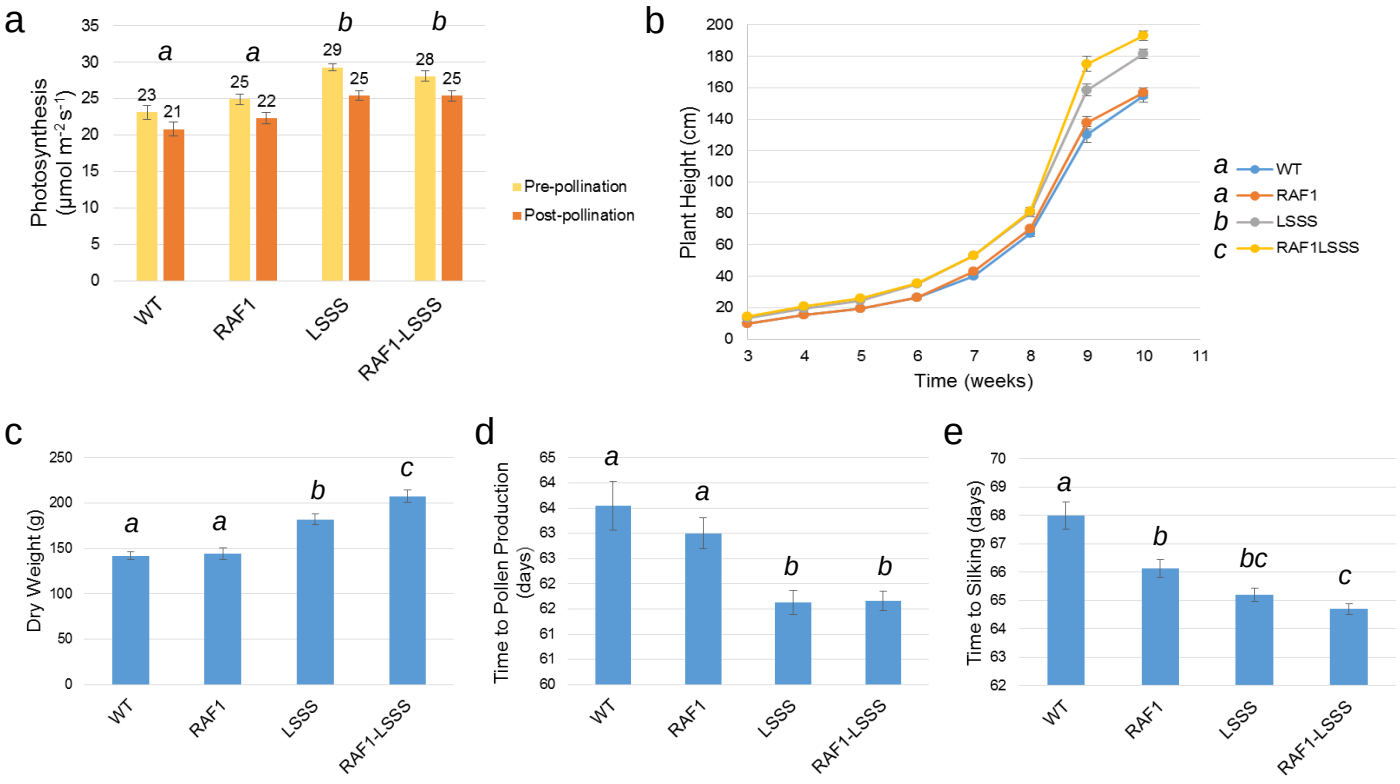

Fig. S4. Growth analysis under greenhouse conditions. **(a)** CO_2 assimilation rate pre-pollination (the day silks emerge, n= the number of individual plants used for measurements; WT=23, RAF1=28, LSSS=30, LSSS-RAF1=29) and post-pollination (2 weeks after silk emergence, n= the number of individual plants used for measurements; WT=20, RAF1=28, LSSS=30, LSSS-RAF1=29), **(b)** plant height over time (n= the number of individual plants used for measurements; WT=29, RAF1=29, LSSS=30 , LSSS-RAF1=30), **(c)** dry weight at maturity (n= the number of individual plants used for measurements; WT=28, RAF1=28, LSSS=30, LSSS-RAF1=29), **(d)** time to pollen production (n= the number of individual plants used for measurements; WT=29, RAF1=28, LSSS=30, LSSS-RAF1=30), and **(e)** time to silking (n= the number of individual plants used for measurements; WT=27, RAF1=29, LSSS=30, LSSS-RAF1=27) were measured for each genotype. Values are shown as the mean ±SE. Different lowercase letters indicate significant differences (P<0.05); one-way ANOVA Tukey HSD. The significance of the height measurement at 10 weeks is noted alongside the genotype legend.