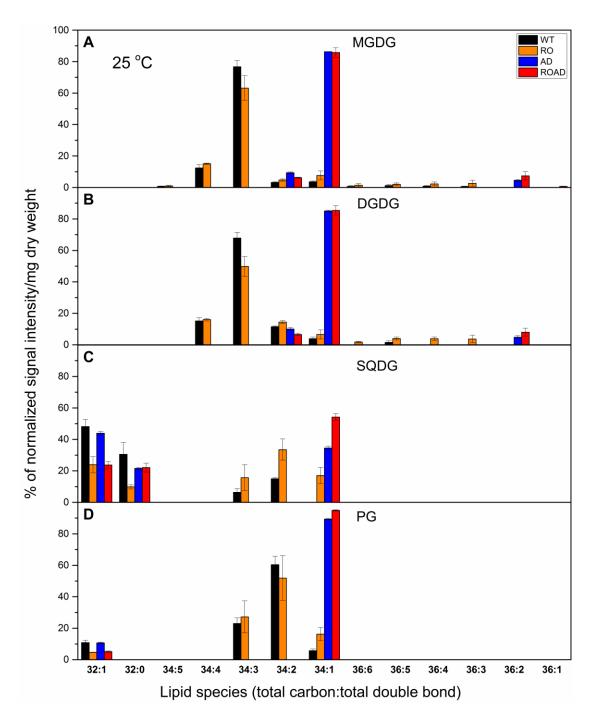
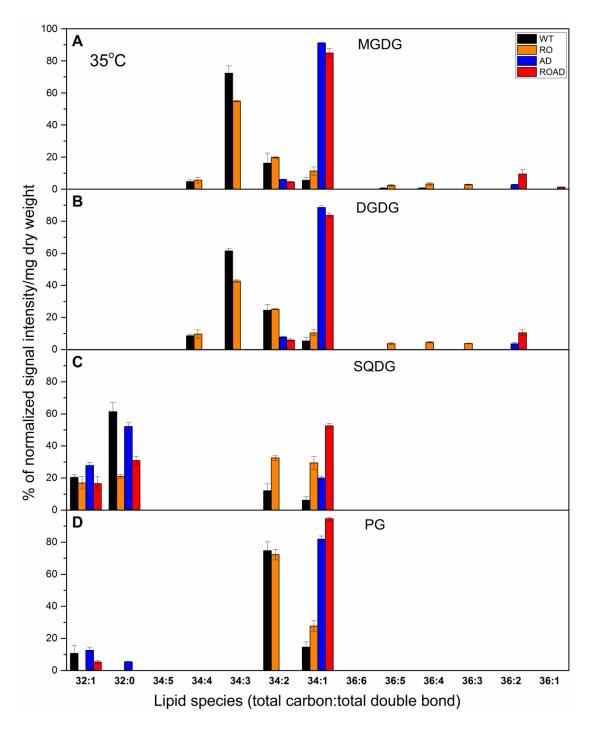
Supplementary Table 1. Prediction of the fatty acid content of the lipid molecular species belonging to different lipid classes, isolated from *Synechocystis* wild-type (WT) and RO, AD and ROAD mutants and determined by MS.

Compound (total carbon: total	MGDG fatty acids	DGDG fatty acids	SQDG fatty acids	PG fatty acids
double bond)	(sn-1/sn-2)	(sn-1/sn-2)	(sn-1/sn-2)	(sn-1/sn-2)
32:1	_	_	16:1/16:0	16:1/16:0
32:0	-	-	16:0/16:0	16:0/16:0
34:5	18:4/16:1	-	-	-
34:4	18:3/16:1	18:3/16:1	-	-
34:3	18:3/16:0	18:3/16:0	18:2/16:1	18:3/16:0
34:2	18:1/16:1	18:1/16:1	18:2/16:0	18:2/16:0
34:1	18:1/16:0	18:1/16:0	18:1/16:0	18:1/16:0
36:6	18:3/18:3	18:3/18:3	-	-
36:5	18:3/18:2	18:3/18:2	-	-
36:4	18:2/18:2	18:3/18:1	-	-
36:3	18:2/18:1	18:2/18:1	-	-
36:2	18:1/18:1	18:1/18:1	-	-
36:1	18:1/18:0	-	-	-

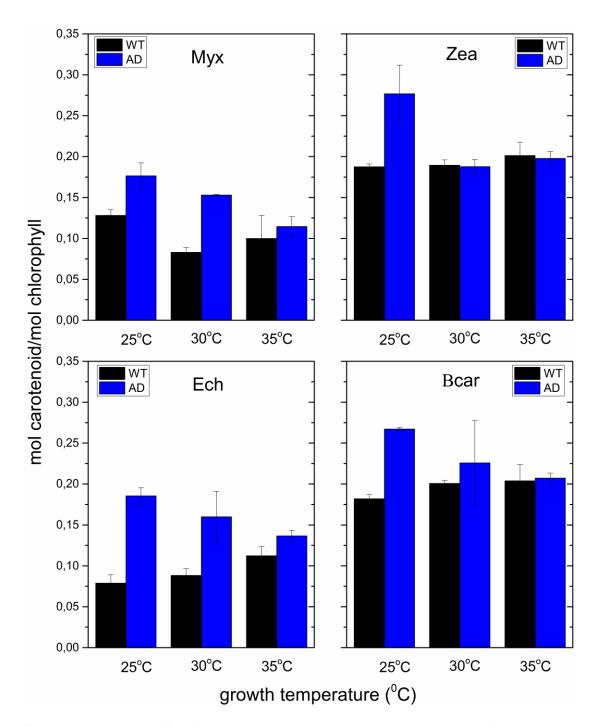
Lipid molecular species are denoted as number of carbon atoms: number of double bond. In prediction of the fatty acid composition of the different molecular species we considered the largest acyl peak combinations obtained from MS/MS. Acyl positions were estimated on the basis of the the known preferences of acyl-transferases (Murata et al. 1992).



Supplementary Fig. S1. Lipid species of *Synechocystis* wild-type (WT) and mutants (RO, AD, ROAD) grown at 25°C. (A) MGDG, (B) DGDG, (C) SQDG and (D) PG lipid species. First numbers denote total carbon number, second numbers the total double bonds. Data shown are means±SD of three independent biological replicates.



Supplementary Fig. S2. Lipid species of *Synechocystis* wild-type (WT) and mutants (RO, AD, ROAD) grown at 35°C. (A) MGDG, (B) DGDG, (C) SQDG and (D) PG lipid species. First numbers denote total carbon number, second numbers the total double bonds. Data shown are means±SD of three independent biological replicates.



Supplementary Fig. S3. Changes in individual carotenoid content of WT an AD cells grown at 25°C, 30°C and 35°C. Abbreviations used: Myx (myxoxanthophyll); Zea (zeaxanthin); Ech (echinenon); β car (β -carotene). The values are averages±SD of three independent biological replicates.