SUPPLEMENTAL DATA

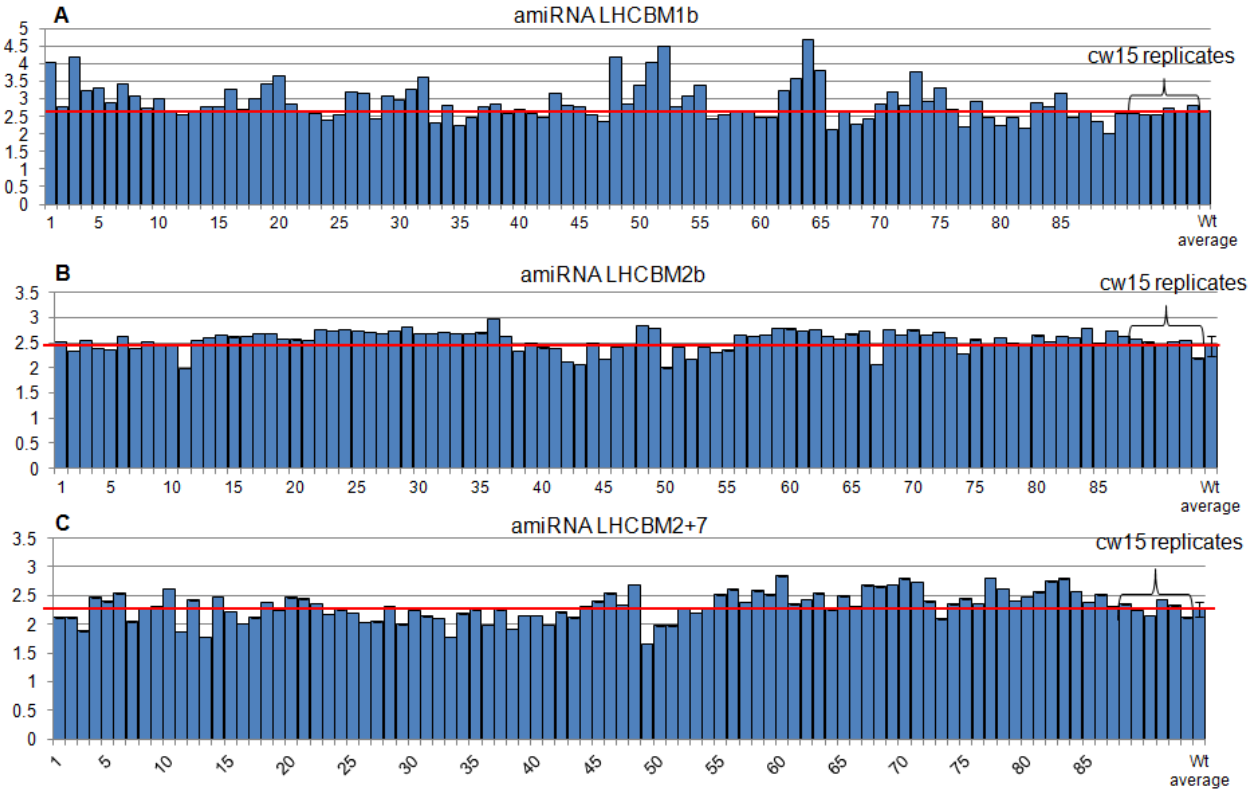
Additional Table 1: *LHCBM* nomenclature and accession numbers. In the first column the new *LHCBM* nomenclature adopted in this paper is reported while in the second and the third column the accession numbers of the sequences (respectively mRNA and protein) are listed. The correspondence with the sequences published in (1) is reported in the fourth column.

Name of *LHCBM* gene	Accession # mRNA	Accession # protein	Nomenclature in (1)
LHCBM1	XM_001700191	XP_001700243.1	*LHCBM1*
LHCBM2	XM_001693935.1	XP_001693987.1	*LHCBM2*
LHCBM3	XM_001703647.1	XP_001703699.1	*LHCBM3*
LHCBM4	XM_001695292.1	XP_001695344.1	*LHCBM11*
LHCBM5	XM_001697474.1	XP_001697526.1	*LHCBM5*
LHCBM6	XM_001695301.1	XP_001695353.1	*LHCBM6*
LHCBM7	XM_001694063.1	XP_001694115.1	*LHCBM8*
LHCBM8	XM_001695415.1	XP_001695467.1	*LHCBM4*
LHCBM9	XM_001695414.1	XP_001695466.1	*LHCBM9*

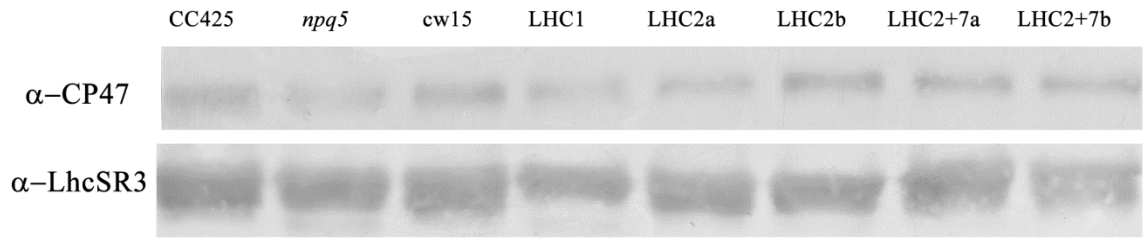
Additional Table 2. Densitometric analysis of the three LHCII bands resolved in Tris-Tricine +Urea SDS-PAGE. The three LHCII bands in Tris-Tricine +Urea SDS-PAGE (Figure 4) were selected according to western blot analysis as detected by the anti-LHCII antibody (Figure 5). Results are the mean of two replicated gels. Each band intensity has been extracted with the GelPro software as described in (2) and normalised to the intensity of the reaction at the slowest migrating band in wild type cw15 or CC425 (which exhibited essentially the same signal amplitude upon normalization to the PSII RC as detected by the reaction with anti-CP47 antibody) set to 100%. Errors are reported in the table. Data significantly different with respect to wild type (CC425 in the case of *npq5* mutant) are in bold. n.d.: not detected.

	cw15	CC425	*npq5*	LHC1	LHC2a	LHC2b	LHC2+7a	LHC2+7b
Slowest migrating-26 kDa	100,0 ± 1,0	100,0 ± 3,0	**132,8** ± 3,1	89,9 ± 1,1	103,9 ± 1,1	98,7 ± 1,6	95,5 ± 5,2	**117,0** ± 0,9
Intermediate migrating-23 kDa	53,2 ± 0,8	62,0 ± 1,3	**n.d.**	**31,6** ± 2,1	53,3 ± 2,1	52,9 ± 4,0	41,0 ± 6,2	64,6 ± 2,0
Fastest migrating-22 kDa	77,6 ± 0,9	85,4 ± 2,1	**109,8** ± 1,1	65,9 ± 3,3	72,0 ± 3,3	66,6 ± 4,6	**36,1** ± 1,1	**38,3** ± 7,1

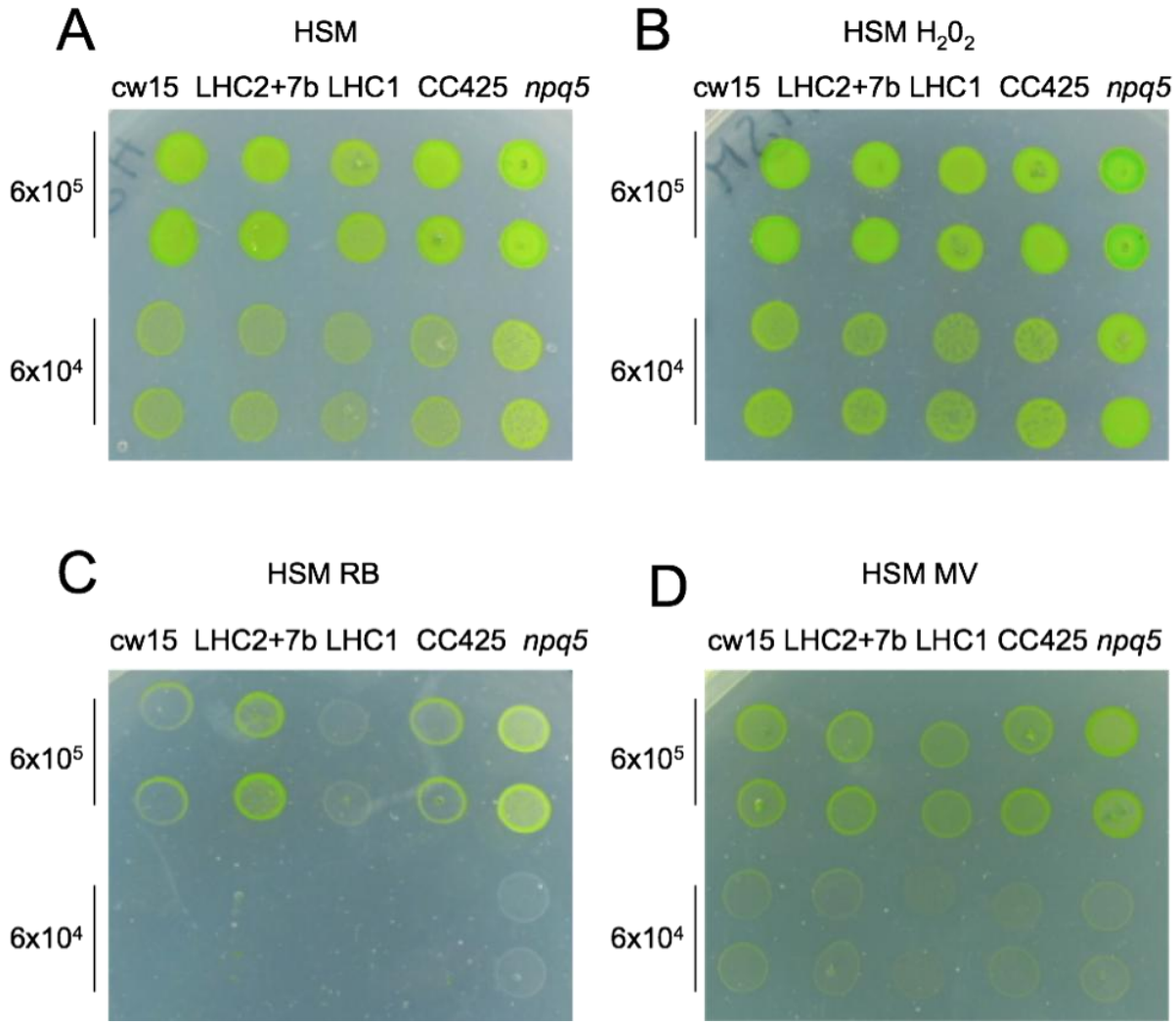
Additional Figure 1. Results of the high-throughput screening of transformants grown in microtiter wells. Results obtained with constructs LHCBM1b, LHCBM2b and LHCBM2+7, are reported respectively in Panel A, B and C. Each bar represents the ratio between absorption in the Chl *a* (660-665 nm) *versus* Chl *b* (644-648 nm) spectral region of pigments extracted with 80% acetone. This value, as explained in the text, is indicative of antenna size reduction. Transformants significantly higher than wild type +/- SD (above the red line) were retained for further analysis. Best lines were selected for full characterisation.



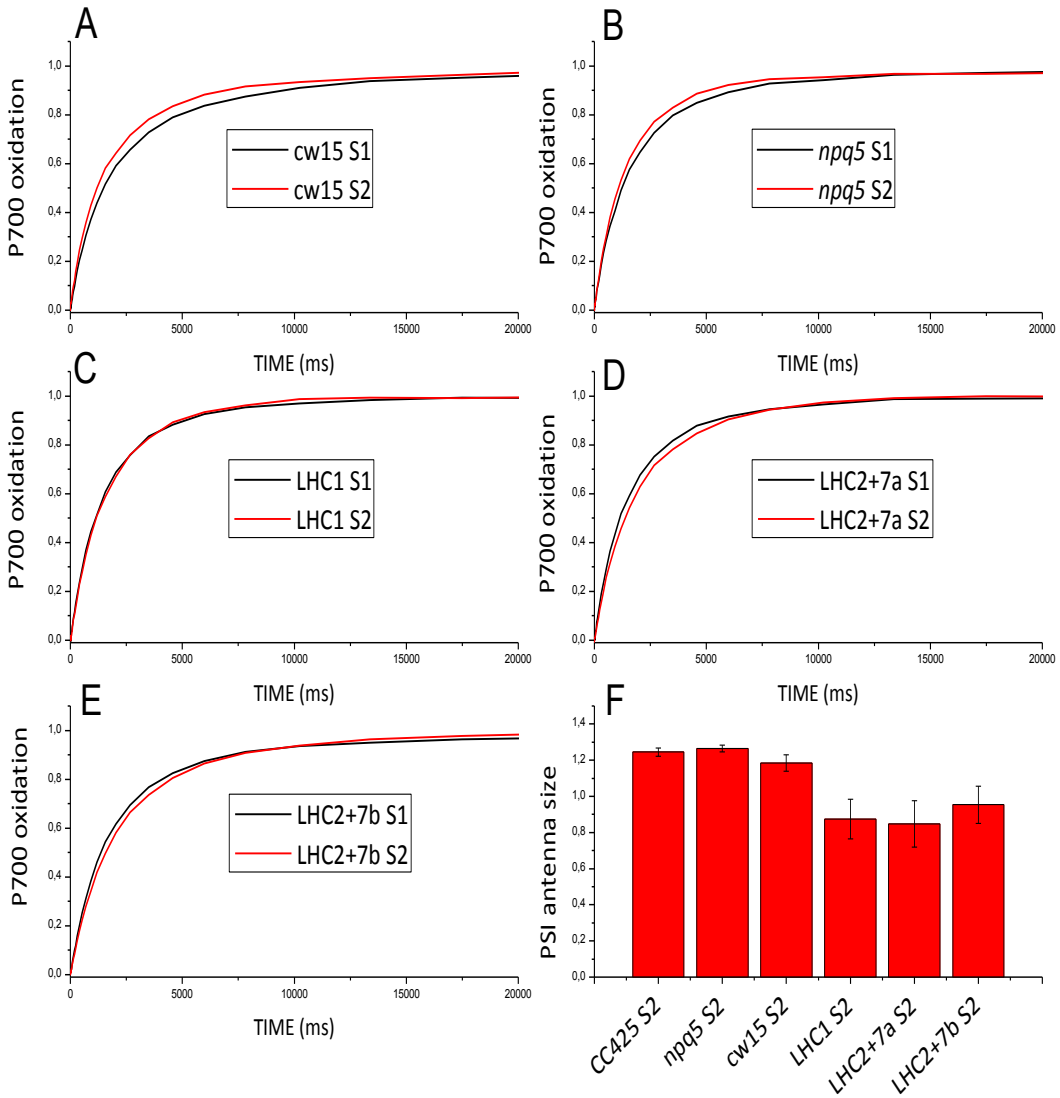
Additional Figure 2. Western blot analysis on LHCSR3 polypeptide. Western blot analysis was performed using a specific antibody against LHCSR3 protein. In the SDS-PAGE gel 3 μg of total protein extract from high light acclimated cells were loaded. The upper panel shows CP47 polypeptide as loading control.



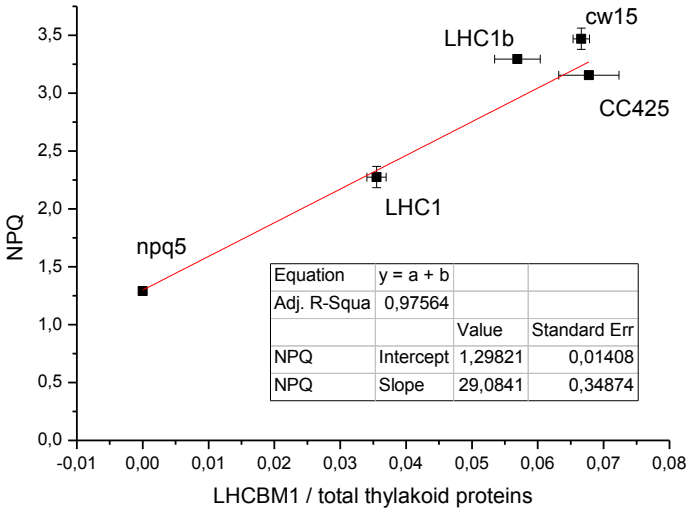
Additional Figure 3. Response of wild type, LHC2+7, LHC1 silenced transformants and *npq5* mutant to different ROS in HS medium. Cells were cultured in TAP medium until mid-log phase. Then $6x10^5$ and $6x10^4$ cells were spotted on HS agar (1%) medium containing 0,5 mM H_2O_2, 7,5 µM rose bengal (RB), 0,17 µM methyl viologen (MV) and on plain HSM as control. HS medium was supplemented with arginine 50 µg/ml since CC425 is an Arg auxotrophic strain. Plates were grown in continuous light at 60 µE m^{-2} s^{-1} at 25°C for eight days and finally growth was scored. No significant differences in the growth rate of the strains were observed. The experiment was repeated three times.



Additional Figure 4. PSI antenna size in State 1 and in State 2. Antenna size of PSI in State 1 and 2 was estimated by measuring the kinetic of P700 oxidationin thylakoid isolated from cells in State 1 and State 2 as described in Experimental Procedure section. In Panel A-E the P700 oxidation kinetic in State 1 (black) and in State 2 (red) of cw15, *npq5*, LHC1, LHC2+7a and LHC2+7b are respectively reported. In the case of CC425 similar results were obtained compare to cw15 (not shown). The kinetics reported in Panel A-E were fitted with a single exponential function: PSI antenna size was thus estimated as inverse function of and the time constants obtained by the fitting procedure. In Panel F are reported the PSI antenna size in State 2 normalized to the respective PSI antenna size in State 1.



Additional Figure 5. Correlation between LHCBM1 content and NPQ induction. The maximum level of NPQ in CC425, *npq5*, cw15, LHC1 and an additional LHC1 trasformant called LHC1b was plotted as a function of the amount of LHCBM1 per total thylakoid protein. In the case of LHC1b the level of LHCBM1 accumulation is 87% compared to the wild type cw15.



REFERENCES

1. Elrad, D., and Grossman, A. R. (2004) A genome's-eye view of the light-harvesting polypeptides of Chlamydomonas reinhardtii *Curr Genet* **45**, 61-75
2. Ballottari, M., Govoni, C., Caffarri, S., and Morosinotto, T. (2004) Stoichiometry of LHCI antenna polypeptides and characterization of gap and linker pigments in higher plants Photosystem I *Eur J Biochem* **271**, 4659-4665