

Supplemental information

Allele 1

Wild type allele 1	1	ATGAAATTATCCTTGGCTATCCTTGCGCTTTGCGCCAGCACTAGTGCCGCTTTCGCTCCT	60
x2KO_b allele 1	1	ATGAAATTATCCTTGGCTATCCTTGCGCTTTGCGCCAGCACTAGTGCCGCTTTCGCTCCT	60
Wild type allele 1	61	TCTGTTTCCCAGAGGACGTCTGTCTCTCTCCGAGAATCATTGGACCCACGGACTCCATG	120
x2KO_b allele 1	61	TCTGTTTCCCAGAGGACGTCTGTCTCTCTCCGAGAATCATTGGACCCACGGACTCCATG	120
Wild type allele 1	121	TCGGAAGTGAAGGCGCCGTGAAAGACGCGGCTCCCAAAGTCTCCGACCCTTTCGACAGC	180
x2KO_b allele 1	121	TCGGAAGTGAAGGCGCCGTGAAAGACGCGGCTCCCAAAGTCTCCGACCCTTTCGACAGC	180
Wild type allele 1	181	CCTCGTGATCTTGCCGGAGTCGTCGCTCCTACCGGCTTTTTCGATCCGGCAGGCTTCGCT	240
x2KO_b allele 1	181	CCTCGTGATCTTGCCGGAGTCGTCGCTCCTACCGGCTTTTTCGATCCGGCAGGCTTCGCT	240
Wild type allele 1	241	GCCCGAGCCGATGCCGGAACCATGAAGCGTTACCGGGAAGCGAAGTTACTCACGGACGT	300
x2KO_b allele 1	241	GCCCGAGCCGATGCCGGAACCATGAAGCGTTACCGGGAAGCGAAGTTACTCACGGACGT	300
Wild type allele 1	301	GTGGGCATGATGGCCGTTGTGCGGCTTTCTTGCGGGCGAAGCCGTCGAGGGATCGTCCTTT	360
x2KO_b allele 1	301	GTGGGCATGATGGCCGTTGTGCGGCTTTCTTGCGGGCGAAGCCGTCGAGGGATCGTCCTTT	360
Wild type allele 1	361	CTCTTTGACTCGCAAGTCAGCGGACCCG CCATTACTCACCTCAACCAG ATTTCCTTCCATC	420
x2KO_b allele 1	361	CTCTTTGACTCGCAAGTCAG-----AACCAGATTTCCTTCCATC	398
Wild type allele 1	421	TTTGGATTCTCCTCACGGTGGGCATTGGTGCTTCCGAAGTCACGCGCGCTCAAATTGGT	480
x2KO_b allele 1	399	TTTGGATTCTCCTCACGGTGGGCATTGGTGCTTCCGAAGTCACGCGCGCTCAAATTGGT	458
Wild type allele 1	481	TGGGTACGTATCGGGAGTTGTTGGTGCCAAACAGTTTCGCTTTGTCCGTCTCTCACGCGTT	540
x2KO_b allele 1	459	TGGGTACGTATCGGGAGTTGTTGGTGCCAAACAGTTTCGCTTTGTCCGTCTCTCACGCGTT	518
Wild type allele 1	541	CTTTTCCTTTCCATTTCGTTTTCCAGGTTGAACCCGAGAACGTCCCACCGGGCAAGCCGGG	600
x2KO_b allele 1	519	CTTTTCCTTTCCATTTCGTTTTCCAGGTTGAACCCGAGAACGTCCCACCGGGCAAGCCGGG	578
Wild type allele 1	601	TCTCCTCCGCGACGATTACGTCCCGGGTGACATTGGCTTTGATCCTCTCGGCTTGAAGCC	660
x2KO_b allele 1	579	TCTCCTCCGCGACGATTACGTCCCGGGTGACATTGGCTTTGATCCTCTCGGCTTGAAGCC	638
Wild type allele 1	661	TTCCGACGCGCAGGCTCTCAAATCGATCCAGACCAAAGAAGTGCAGAGTAAGTCATTTCG	720
x2KO_b allele 1	639	TTCCGACGCGCAGGCTCTCAAATCGATCCAGACCAAAGAAGTGCAGAGTAAGTCATTTCG	698
Wild type allele 1	721	TGTTGTTGCTGTTACTGTGCTCCTTGGTACTATCGTGTTTACAGTTAGTTCACTGCGTCA	780
x2KO_b allele 1	699	TGTTGTTGCTGTTACTGTGCTCCTTGGTACTATCGTGTTTACAGTTAGTTCACTGCGTCA	758
Wild type allele 1	781	GAGTGTAACCGTGTCTACTGTTAATCCCACTAACTAACCATTGAATATAACTCGTTTTT	840
x2KO_b allele 1	759	GAGTGTAACCGTGTCTACTGTTAATCCCACTAACTAACCATTGAATATAACTCGTTTTT	818
Wild type allele 1	841	CTTTGGCTAGACGGACGTCTCGCCATGTTGGCGGCGGCTGGGTGCATGGCTCAGGAATTG	900
x2KO_b allele 1	819	CTTTGGCTAGACGGACGTCTCGCCATGTTGGCGGCGGCTGGGTGCATGGCTCAGGAATTG	878
Wild type allele 1	901	GCCAACGGAAAGGGCATTCTCGAAAACCTTGGTCTCTAA	939
x2KO_b allele 1	879	GCCAACGGAAAGGGCATTCTCGAAAACCTTGGTCTCTAA	917

Allele 2

Wild type allele 2	1	ATGAAATTATCCTTGGCTATCCTTGCGCTTTGCGCCAGCACTAGTGCCGCTTTTCGCTCCT	60
x2KO_b allele 2	1	ATGAAATTATCCTTGGCTATCCTTGCGCTTTGCGCCAGCACTAGTGCCGCTTTTCGCTCCT	60
Wild type allele 2	61	TCTGTTTCCCAGAGGACGTCTGTCTCTCTCCGAGAATCATTGGACCCACGGAATCCATG	120
x2KO_b allele 2	61	TCTGTTTCCCAGAGGACGTCTGTCTCTCTCCGAGAATCATTGGACCCACGGAATCCATG	120
Wild type allele 2	121	TCGGAAGTGAAGGCGCCGTGAAAGACGCGGCTCCCAAAGTCTCCGACCCTTTTCGACAGC	180
x2KO_b allele 2	121	TCGGAAGTGAAGGCGCCGTGAAAGACGCGGCTCCCAAAGTCTCCGACCCTTTTCGACAGC	180
Wild type allele 2	181	CCTCGTGATCTTGCCGGAGTCGTCGCTCCTACCGGCTTTTTCGATCCGGCAGGCTTCGCT	240
x2KO_b allele 2	181	CCTCGTGATCTTGCCGGAGTCGTCGCTCCTACCGGCTTTTTCGATCCGGCAGGCTTCGCT	240
Wild type allele 2	241	GCCCCAGCCGATGCCGGTACCATGAAGCGTTACCGGGAAGCGGAAGTTACTACGGACGT	300
x2KO_b allele 2	241	GCCCCAGCCGATGCCGGTACCATGAAGCGTTACCGGGAAGCGGAAGTTACTACGGACGT	300
Wild type allele 2	301	GTGGGCATGATGGCCGTTGTCGGCTTTCTTGCGGGCGAAGCCGTCGAGGGATCGTCGTTT	360
x2KO_b allele 2	301	GTGGGCATGATGGCCGTTGTCGGCTTTCTTGCGGGCGAAGCCGTCGAGGGATCGTCGTTT	360
Wild type allele 2	361	CTCTTTGACTCGCAAGTCAGCGGACCCG CCATTACTCACCTCAACCAG ATTTCCTTCCATC	420
x2KO_b allele 2	361	CTCTTTGACTCGCAAGTCAGCGGACCCGCCAT- ACTCACCTCAACCAGATTTCCTTCCATC	419
Wild type allele 2	421	TTTTGGATTCTCCTCACGGTGGGCATTGGTGCTTCCGAAGTCACGCGGGCTCAAATTGGT	480
x2KO_b allele 2	420	TTTTGGATTCTCCTCACGGTGGGCATTGGTGCTTCCGAAGTCACGCGGGCTCAAATTGGT	479
Wild type allele 2	481	TGGGTACGTATCGGGAGTTGTTGGTTCCAAACAGTTTCGCTTTGTCCGTCTCTACGCGTT	540
x2KO_b allele 2	480	TGGGTACGTATCGGGAGTTGTTGGTTCCAAACAGTTTCGCTTTGTCCGTCTCTACGCGTT	539
Wild type allele 2	541	CTTTTCCTTTCCATTCTGTTTTCCAGGTTGAACCCGAGAACGTCCCACCGGGCAAGCCGGG	600
x2KO_b allele 2	540	CTTTTCCTTTCCATTCTGTTTTCCAGGTTGAACCCGAGAACGTCCCACCGGGCAAGCCGGG	599
Wild type allele 2	601	TCTCCTCCGCGACGATTACGTCCCGGTTGACATTGGCTTTGATCCTCTCGGCTTGAAGCC	660
x2KO_b allele 2	600	TCTCCTCCGCGACGATTACGTCCCGGTTGACATTGGCTTTGATCCTCTCGGCTTGAAGCC	659
Wild type allele 2	661	TTCGACGCGCAGGCTCTCAAATCGATCCAGACCAAGGAAGTGCAGAGTAAGTCATTTCG	720
x2KO_b allele 2	660	TTCGACGCGCAGGCTCTCAAATCGATCCAGACCAAGGAAGTGCAGAGTAAGTCATTTCG	719
Wild type allele 2	721	TGTTGCTGCTGTTACTGTGCTCCATGGTACTATCGTGTTTACAGTTAGTTCACTGCGTCA	780
x2KO_b allele 2	720	TGTTGCTGCTGTTACTGTGCTCCATGGTACTATCGTGTTTACAGTTAGTTCACTGCGTCA	779
Wild type allele 2	781	GAGTGTAACCGTGTCTACTGTTAATCCACCAAATAACCGATTGAATATAACTCGTTTTT	840
x2KO_b allele 2	780	GAGTGTAACCGTGTCTACTGTTAATCCACCAAATAACCGATTGAATATAACTCGTTTTT	839
Wild type allele 2	841	CTTTGGCTAGACGGACGTCTCGCCATGTTGGCGCGGCTGGGTGCATGGCTCAGGAATTG	900
x2KO_b allele 2	840	CTTTGGCTAGACGGACGTCTCGCCATGTTGGCGCGGCTGGGTGCATGGCTCAGGAATTG	899
Wild type allele 2	901	GCCAACGGAAAGGGCATTCTCGAAAACCTTGGGCTCTAA	939
x2KO_b allele 2	900	GCCAACGGAAAGGGCATTCTCGAAAACCTTGGGCTCTAA	938

Fig S1: Sequences of the two *Lhcx2* alleles in x2KO_b.

Highlighted in blue is the binding site for the CRISPR-Cas construct. In red the deletions are shown. In allele 1 of *Lhcx2*, x2KO_b has a deletion of 22 bp and in allele 2 a deletion of 1 bp. Both deletions lead to a frameshift and knockout of the gene.

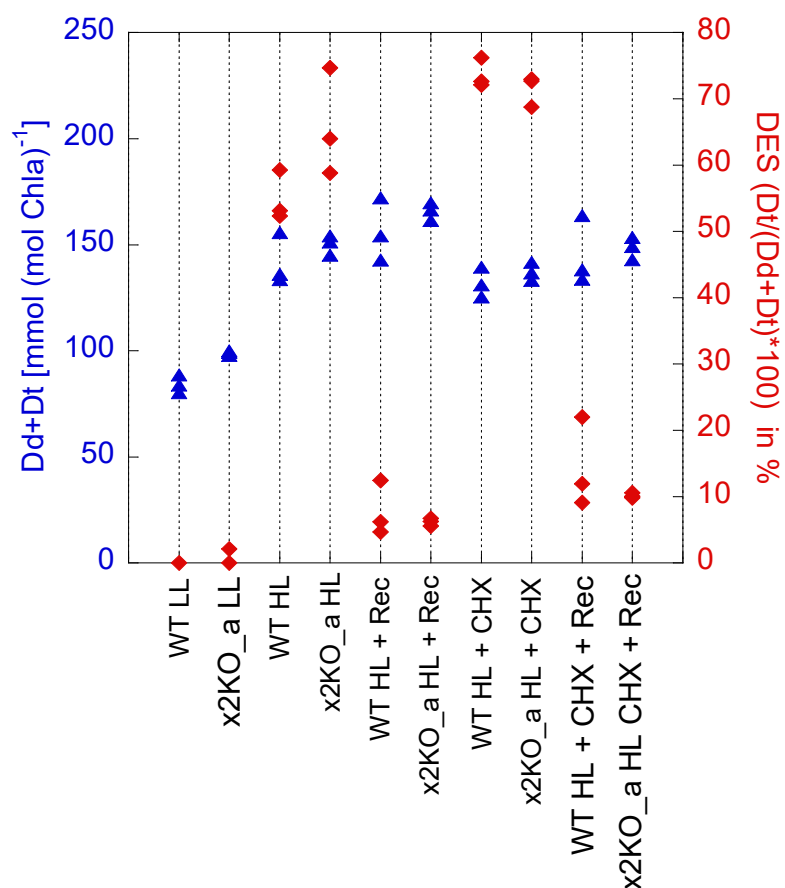


Fig. S2: Xanthophyll-cycle pigment pool size (Dd+Dt) and de-epoxidation state (DES) of wild type and x2KO_a.

Cells were low light acclimated, treated with 2 h of high light (HL; 1700 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$) or 2 h HL treated followed by a 30 min recovery phase with 40 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ (HL + Rec). Additionally, the same experiments were performed with 2 $\mu\text{g mL}^{-1}$ cycloheximide (CHX) which was added before the illumination with the aim to block translation of nuclear encoded genes. Each experiment was performed in three biological replicates.

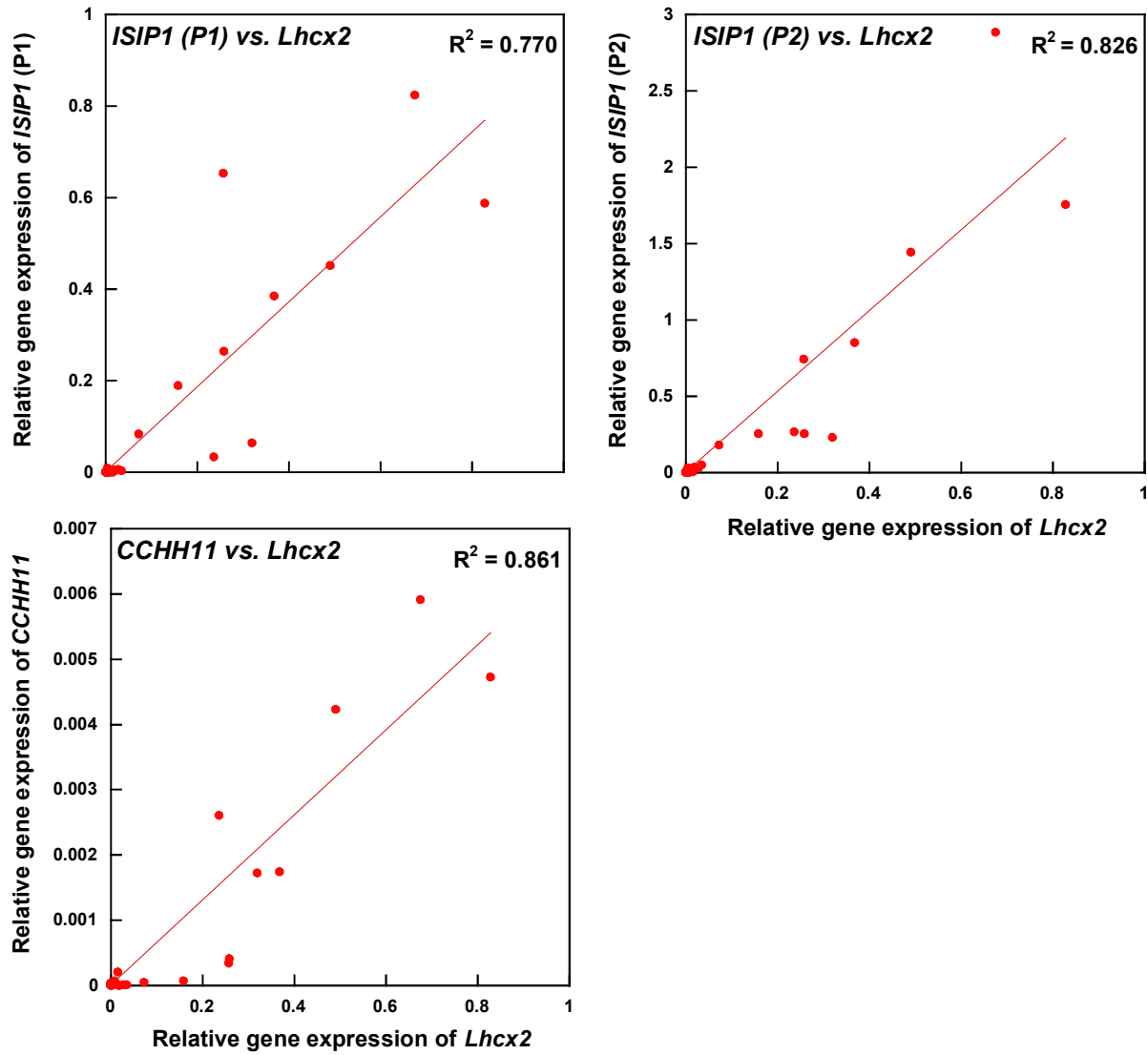


Fig. S3: Linear regression of the expression levels of *LhcX2* and the two marker genes *ISIP1* and *CCHH11* under iron limitation.

The distributions of the expression levels suggest linear correlations of both marker genes with the expression of *LhcX2*. $n = 28$.

Table S1: Correlation coefficients of the Spearman correlation tests between *LhcX2*, *ISIP1* and *CCHH11* expression levels under iron limitation.

All of the three tested genes correlated positively with each other. P values are shown in brackets, indicating the probability of correlation. $n = 28$.

Gene	<i>ISIP1 (P1)</i>	<i>ISIP1 (P2)</i>	<i>CCHH11</i>
<i>LhcX2</i>	0.895 ($p = 2.00 \times 10^{-7}$)	0.913 ($p = 2.00 \times 10^{-7}$)	0.753 ($p = 2.00 \times 10^{-7}$)
<i>ISIP1 (P1)</i>		0.983 ($p = 2.00 \times 10^{-7}$)	0.689 ($p = 2.95 \times 10^{-6}$)
<i>ISIP1 (P2)</i>			0.711 ($p = 2.96 \times 10^{-6}$)