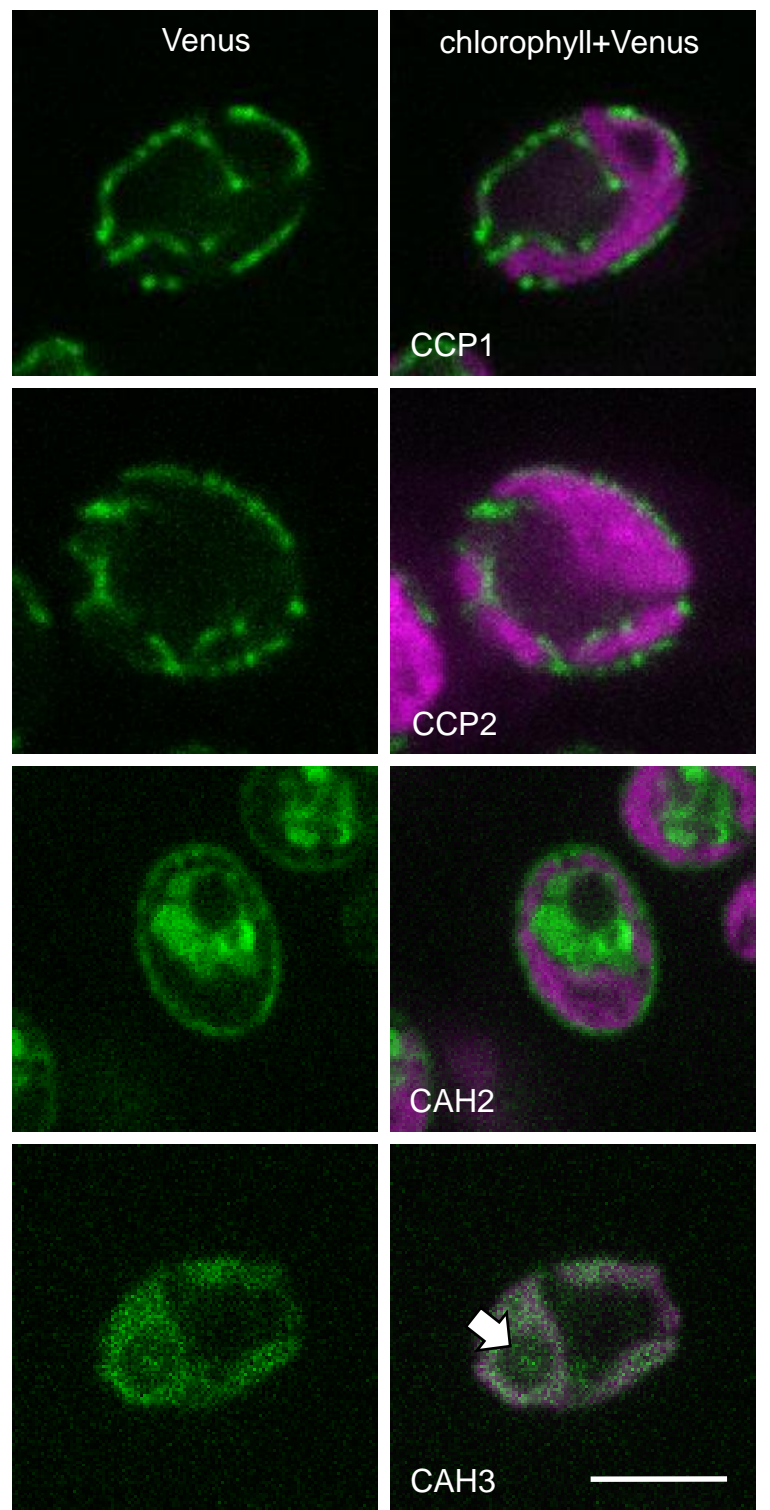
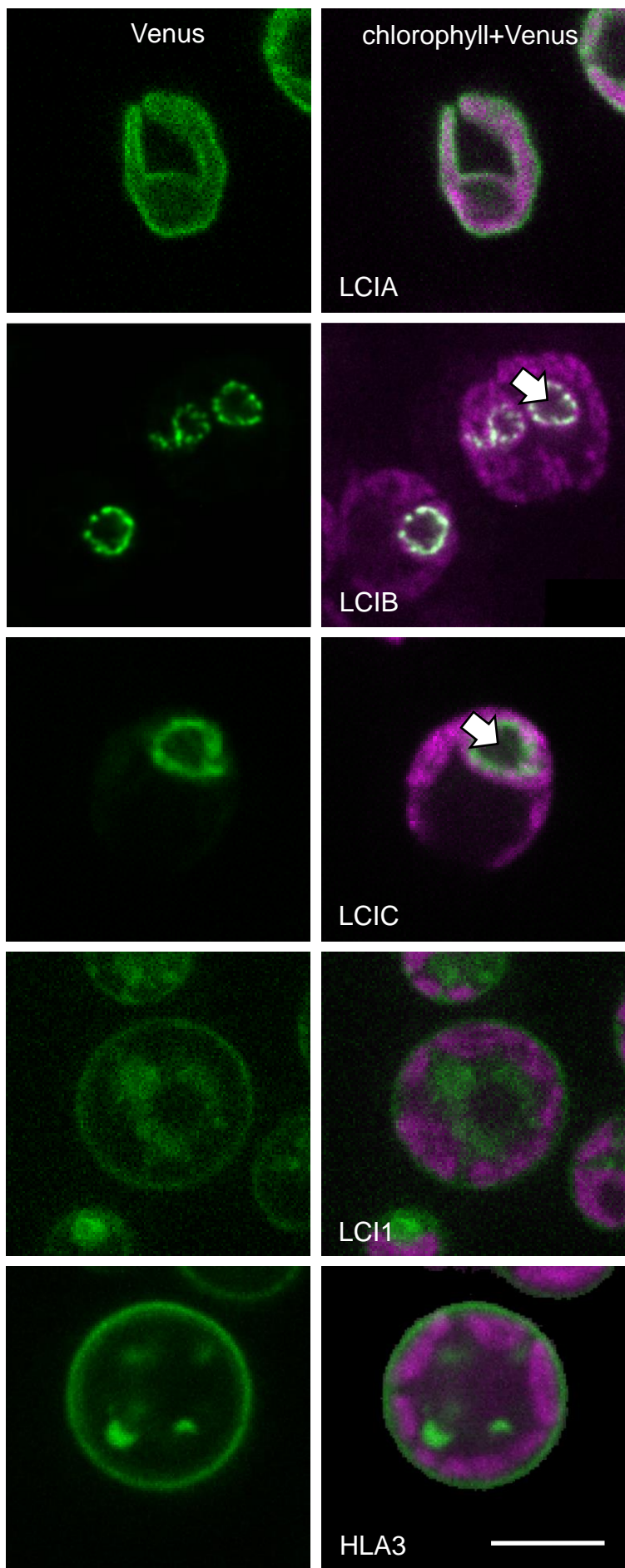


(a)



(b)

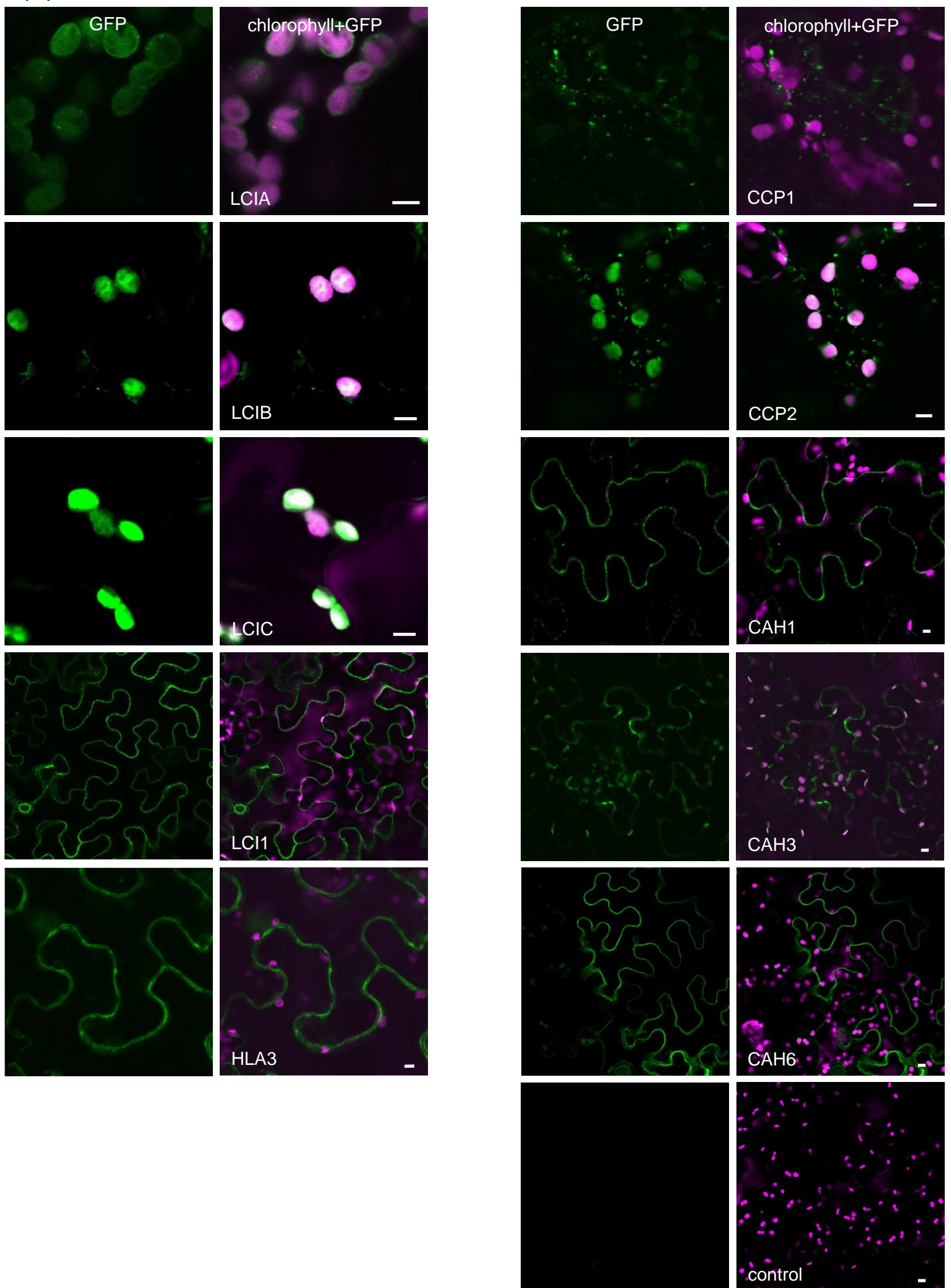


Figure S1. Expression of fluorescent-tagged CCM components in *Chlamydomonas* and tobacco (from Fig. 1). Expression of Venus-fused CCM-components in *Chlamydomonas reinhardtii* (a). Expression in tobacco of GFP-fused CCM components from *Chlamydomonas* (b). Green and purple signals are Venus or GFP fluorescence and chlorophyll autofluorescence, respectively. Overlaid images of these signals are shown: overlaps are white. Arrowhead shows the label-free area is the algal pyrenoid, a micro-compartment composed primarily of RuBisCO. A non-transformed control is included. Scale bar = 5 μm (all 5 μm for *Chlamydomonas* images).

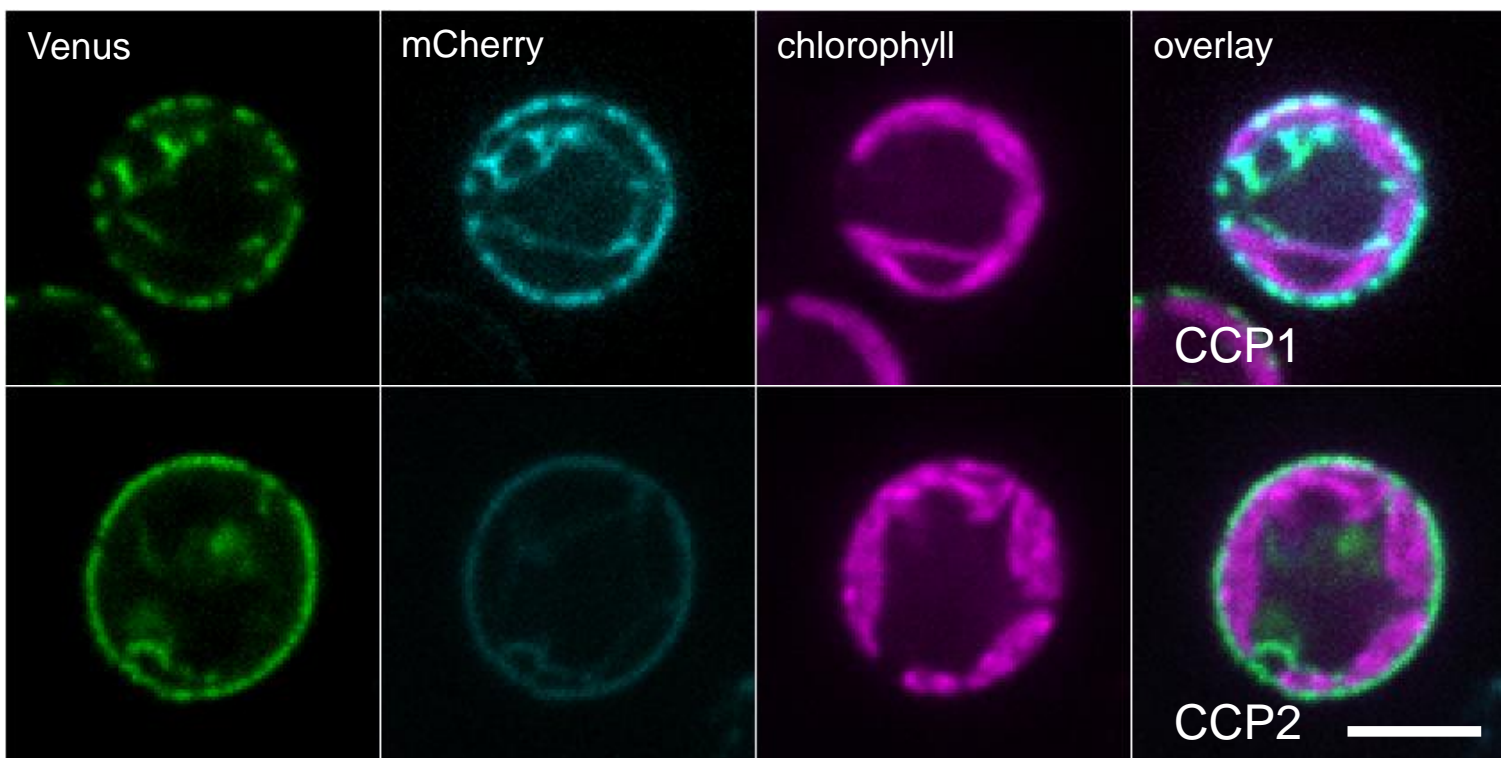


Figure S2. Co-expression of Venus-fused CCM components with Mitotracker® Red CMXRos in Chlamydomonas. Purple, green and cyan signals are chlorophyll autofluorescence, Venus and Mitotracker fluorescence, respectively. Overlaid images of these signals are shown: overlaps of Venus and Mitotracker are pale green. Scale bar = 5 μ m.

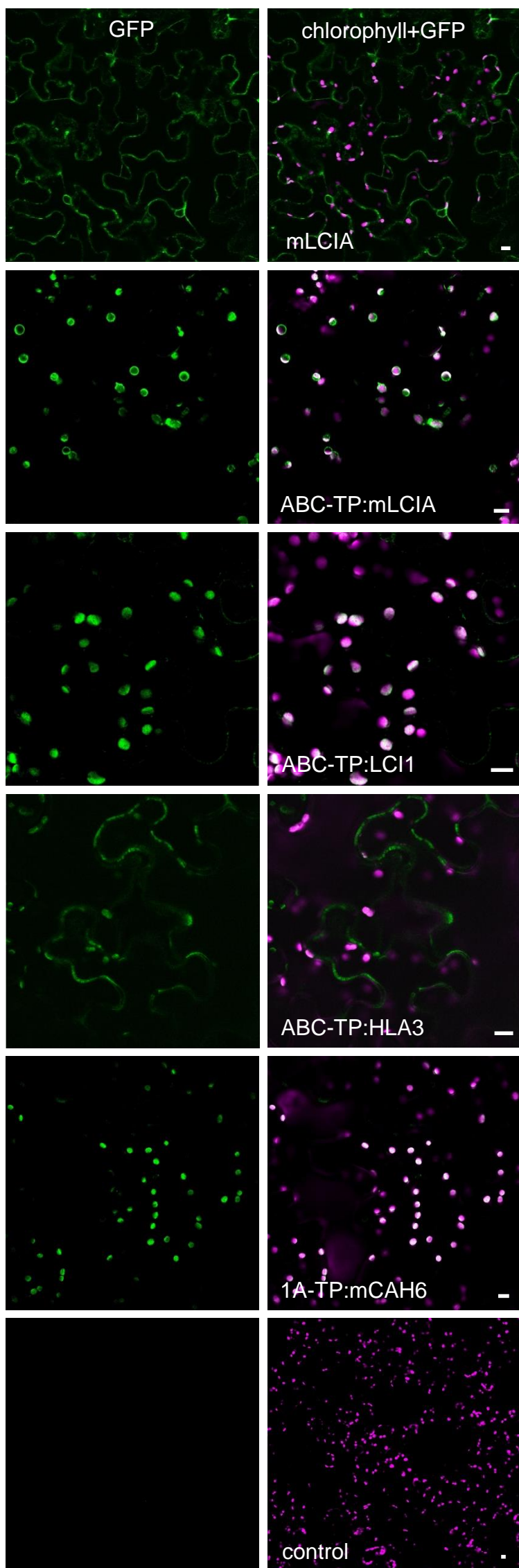


Figure S3. Expression of GFP-fused CCM components carrying native Arabidopsis chloroplast transit peptides in tobacco (from Fig. 3). Green and purple signals are GFP fluorescence and chlorophyll autofluorescence, respectively. Overlaid images of these signals are shown: overlaps are white. A non-transformed control is included. Scale bar = 10 μ m.

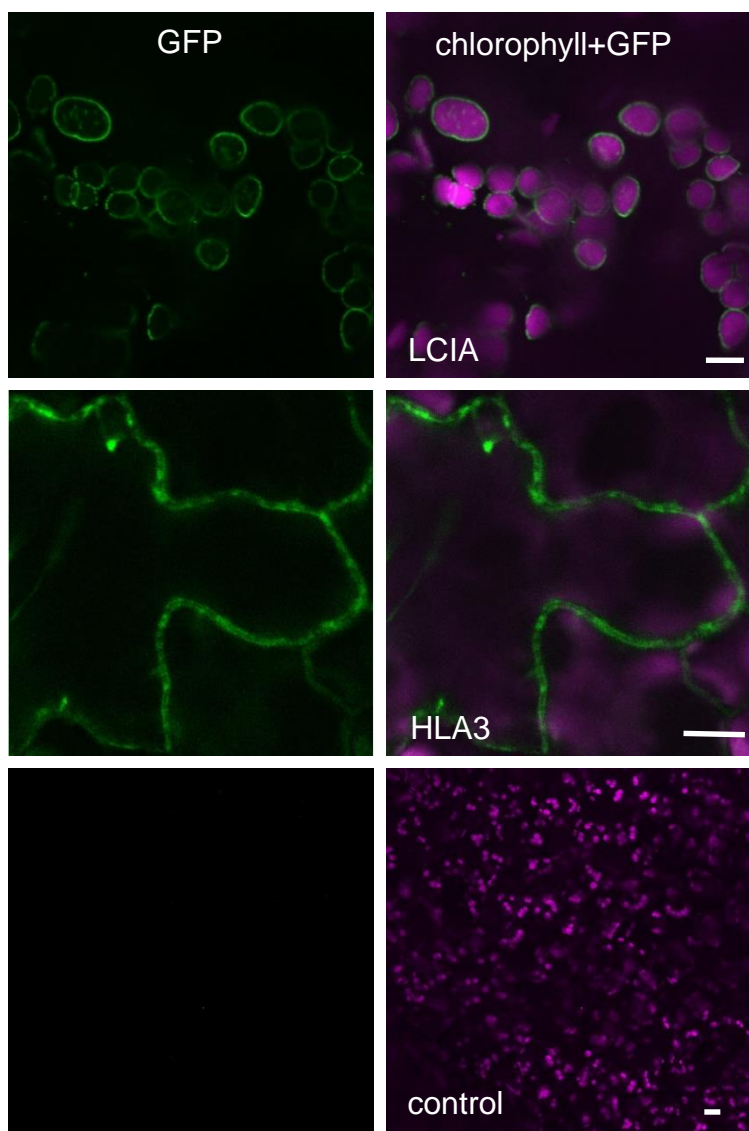


Figure S4. Stable expression of LCIA:GFP and HLA3:GFP in Arabidopsis (from Fig. 5a). Green and purple signals are GFP fluorescence and chlorophyll autofluorescence, respectively. Overlaid images of these signals are shown: overlaps are white. A non-transformed control is included. Scale bar = 10 μ m.

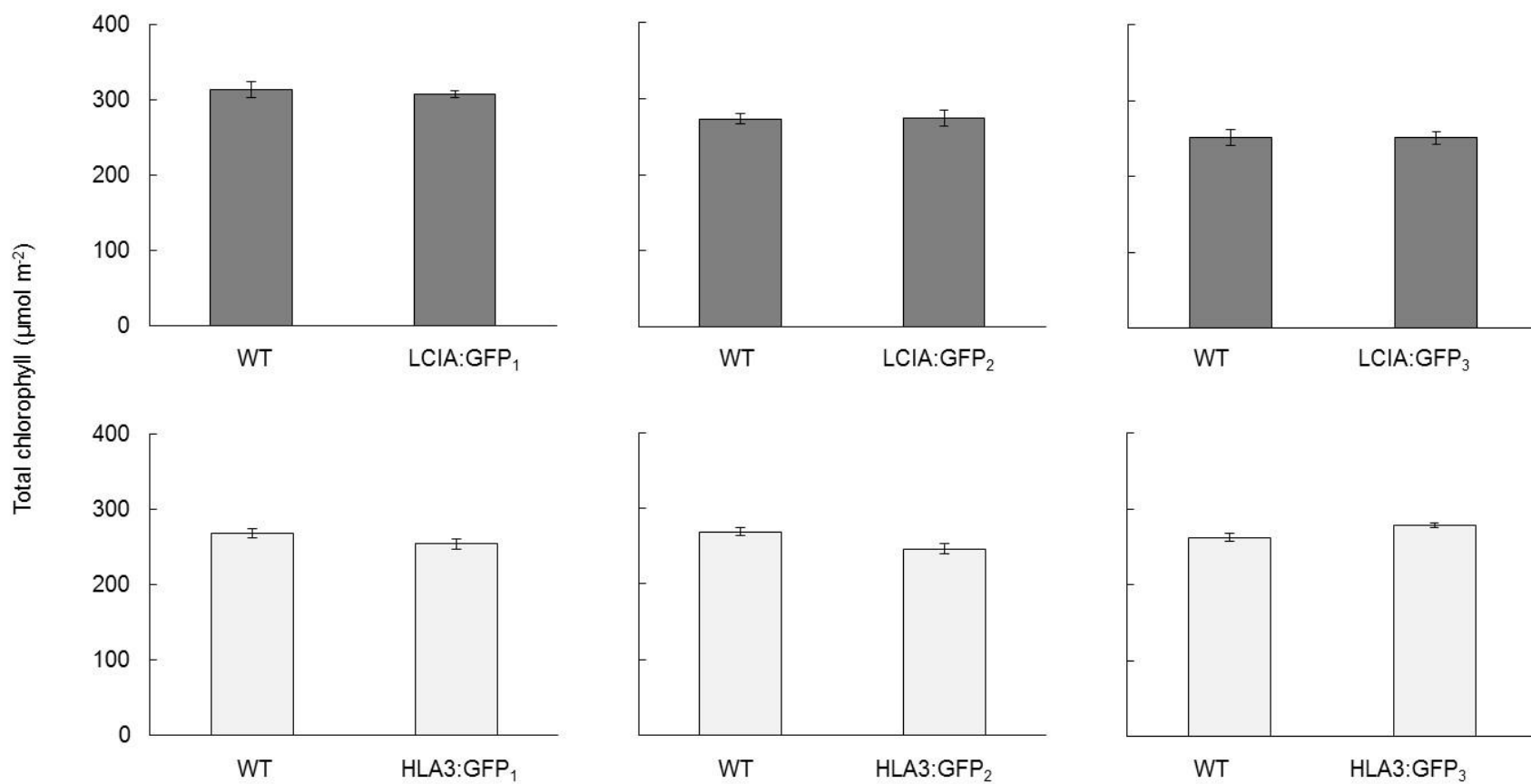


Figure S5. Chlorophyll content of transgenic *Arabidopsis* plants expressing LCIA or HLA3. Chlorophyll content measurements are shown for 8 separate plants, bars are means \pm SE. ANOVA revealed that there were no statistically significant differences between samples ($P < 0.05$).

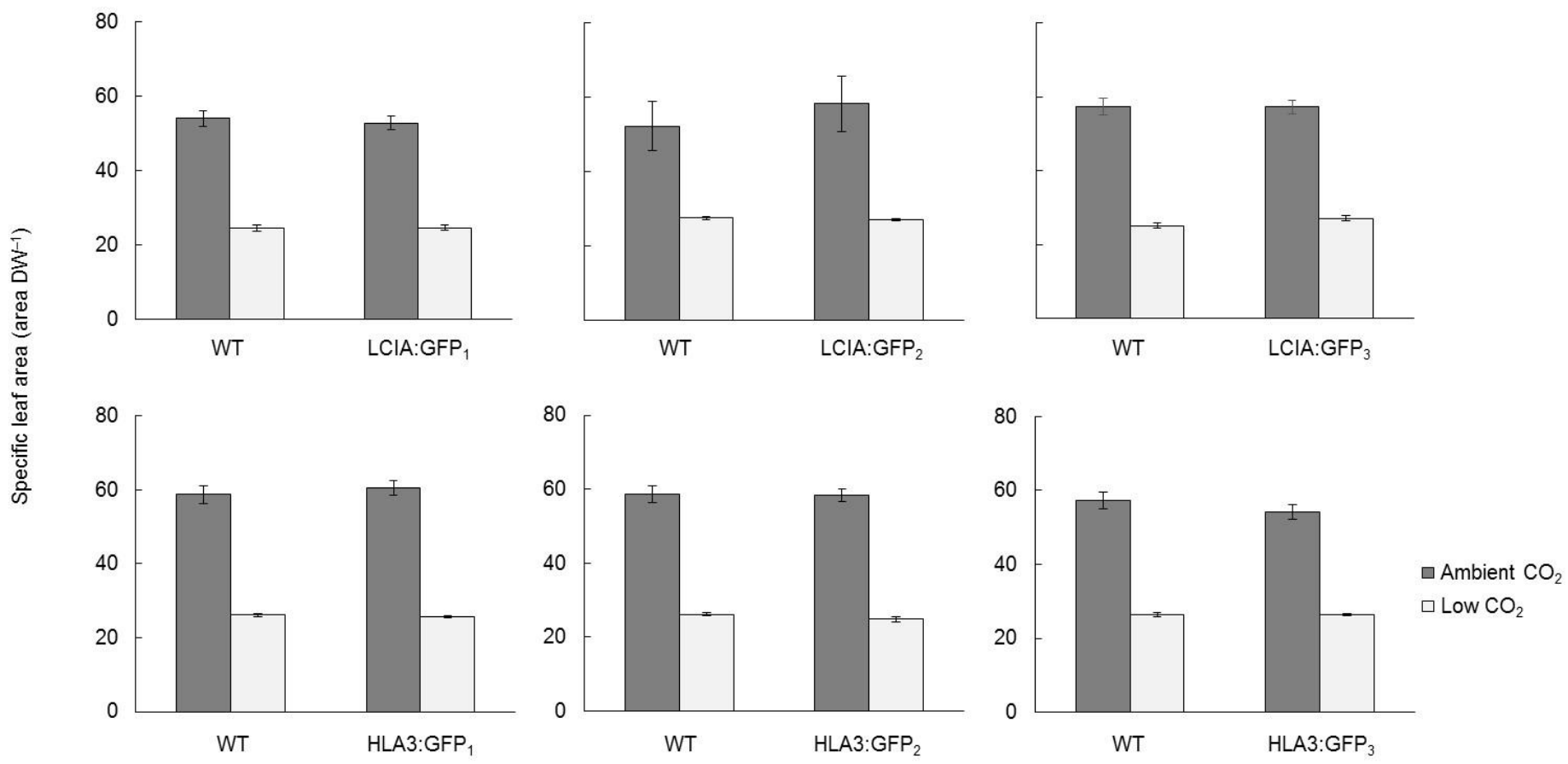


Figure S6. Specific leaf area (area/DW) of transgenic LCIA or HLA3 Arabidopsis plants. Values are the means \pm SE of measurements made on 24 rosettes. Growth conditions refer to those outlined in Fig. 6.

Codon optimised LCIA (1011 bp)

ATGCAGACAACTATGACAAGACCTTGTAGCCAGCCAGTGTACGATCCAGAGTTCTTAGATCGCCAATGC
GGGTTGTGCTGCTAGTGCTCCGACAGCTGTGACAACTGTCGTACCTCAAATGGAAATGGGAACGGGCACTT
TCAGGCGGCTACGACTCCTGTGCCACCAACGCCAGCTCCTGTAGCTGTGTCTGCGCCTGTCAGGGCTGTTAGT
GTTCTGACACCCCTCAAGTTTATGAAAACGCAATTAACGTTGGAGCCTATAAAGCTGGACTTACTCCGCTGGC
AACATTCGTACAAGGTATTCAAGCCGGTGCATACATCGCATTGGCGCTTTCTTAGCTATAAGCGTCGGCGGC
AATATCCCGGAGTTGCTGCTGCAAACCTGGACTAGCAAAGTTGCTATTTGCTCTCGTGTTCCTGTGCGACT
TTCGATGGTGACTAATTGTTGGTGCAGAACTTTCCACGGTAACACCATGATGTTGACATGCGCCTTAATCGAG
AAAAAGGCCACTTGGGGCAACTCCTTAAGAACTGGTCTGTGTCTTACTTTGGTAACTCGTTGGTAGTATCG
CTATGGTAGCGGCAGTTGTTGCCACCGTTGCCTCACCACGAATACTCTACCAGTTCAAATGGCGACACTTAA
GGCGAATTTGGGATCACTGAGGTTTTAAGTCGTTCAATCCTCTGTAATTGTTGGTATGTTGTGCAGTTTGGT
CAGCCTCCGACGACGAGCCTTCCGGGAAGGATTCTGCTCTTTGGCCCTGCATCACTGCCTTCGTGGCAAT
AGGATTGGAACATTCCGTGGCTAATATGTTTGAATTCCACTCGGGATGATGCTAGGAGCGGAGGTGACTTG
GAGCCAGTTTTCTTAAACAACCTGATTCCCGTTACGCTGGGCAATACCATAGCTGGTGTCTTGATGATGGCAA
TAGCATATTCTATTTCAATTCGGTTCTTTGGGTAAATCTGCTAAACCTGCTACAGCATGA

Codon optimised HLA3 (3978 bp)

ATGGGAGAGGGGAAGGTGGCCGAGAGAGGTCATGATCCTACTGCAGGCTTCTTCAACAAGTTTGCTTTCCGG
TGGATGTACAAATGGATTGGTGTGCTAGGCGAGGTGAAGAACTTAATGCCGAAGAAATGGGTATGCCACCA
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GCAAATGCGGATGGTCAACATTGCTGATTCTGGTGTCTTTACTTTGTGCGTTCACTCTTGTGCGATGTCAACT
ATGTAGATGCTCCTACGAAAAAGTGGACAACGGCTGAACTTTGTATGGCCAAACAACCGCTGGATGGCTCTT
AATGATGGGTTTACAATAGATGCTTGGCTTTTGGGACTTTGTCTCAAAGAATGGGTTACATATGCATGACG
GTTGGTATCCGTGCGAGAGCTGCTCTTGTCCAAGCGTTACTCATAAAGCTTTCCGACTTAATACGGTTAGAG
CTGATCAATCAGCCGCGATTGTCAACTTCGTGGCTTCCGATATCCAGAAAATCTACGATGGGGCGTTAGAGTT
TCATTATCTTTGGACCGCCCTTTTGAAGCCGAGCAATCCTTGCCCTCTTGGGATACTTGACACAAGACTCCAT
GCTCCCAGGATTGGGGGTCAATTTGCTAGTGTTCCTATGCAGTATTACTTCGGTTATAAGATTGTACAAATCA
AGCTTCAAACGCTAAGCATGTTGCTCTCCGGTCAGCAATTATGCAGGAAGTGCTTCTGCTATCAAGCTTGTT
AAGTACTACGCATGGGAACAGTCTTTCGAGAACCAAATCTCAAAGTACGTAGGGAGGAAATAAGGTTGAAC
TTCTGGAATTGCGTCATGAAGTCAATTAACGTTGCATGTGTATTTGTGTTCCGCCTATGACAGCCTTTGTGAT
CTTACCCTTATGAGTTTCAACGCGCTAGATTAGTATCTTCTGTGGCGTTTACTACACTCAGCTTATTCAATAT
CCTGCGCTTTCCGTTGGTTGTTTTGCCAAAGGCTCTGAGAGCTGTTTCTGAAGCTAACGCTAGCTTGCAAAGAT
TGGAAGCGTATTTGTTGGAAGAGGTTCCATCTGGAACAGCAGCAGTAAAGACTCCTAAGAATGCGCCACCGG
GAGCGGTCATTGAAAACGGGGTGTTCATCATCCCTCTAACCCAAATTGGCATCTCCACGTACCAAAGTTTGA
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TGGCTCCAAAACCTTTCTTTCGAGACAACGTGCTTTTGGTGAACAATTTGACGAGAATAAGTACACGGATG
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GGAGTGAATTTCTCCGTGGGCAAAGACAAAGGGTCAACCTTGTCTGTTGTGCCTACGCAGACGCCGACCTT
GTCCTGTTGGACAACGCGCTGTCCGCGGTGGATCATCATACGGCGCATCACATTTTTGATAAATGTATCAAAG
GATTATTCAGTGATAAAGCCGTAGTGTCTGTTACTCACCAGATTGAGTTCATGCCTAGGTGTGATAACGTTGCT
ATCATGGATGAGGGCCGATGTCTCTACTTCGTAAGTGAACGAAGAGGCTCAACATCTTCTGGGAAAATTG
CTCCCTATCACACATCTCCTTACGCCGAGGCTCGCAGGAAGCTCCTCCAGCACCGAAGAAAAAGGCAGAAG
ATAAGGCAGGGCCACAAAAGTCACAGAGTTTACAGTTAACACTTGCCTAACCTCTATAGGAAAGCCCACCGA
AAAACCAAAGATGTTCAAAGCTTACGGCCTACCAGGCTGCACTTATCTATACCTGGTATGGAAATTTGTTCT

TGGTGGGAGTTTGTTCCTTCTTCTTCTGCTGCTCAATGTTCCCGCCAGATCTCAGACTTTTGGGTGAGGTGG
TGGGTTAATGATGAATACAAGAAGTTTCTGTCAAGGGAGAACAAGACTCGGCTGCAACTACCTTTACTGCT
TGATATATCTTCTACTAGTTGGTCTGTTTTACATTTTCATGATCTTTAGGGGTGCGACCTTTCTCTGGTGGGTAT
TGAAAAGCTCCGAAACAATTCGTGTAAGGCACTGCATAACGTCCTAAATGCTCCAATGGGGTTCTTCTTGTG
ACACCAGTTGGAGATCTGTTGCTTAACCTTACAAAAGATCAAGACATAATGGATGAAAATCTTCCGGACGCCG
TGCACTTTATGGGAATCTATGGCTTGATATTGTTAGCCACCCTATAACTGTAAGTGTGACTATTAACCTTCTCG
CTGCTTTTACAGGTGCGTTGATAATCATGACGCTCATCATGTTATCAATCTATCTGCCAGCTGCTACAGCACTTA
AGAAAGCAAGAGCAGTGTGAGGTGGGATGCTAGTGGGACTTGTGCTGAAGTCTTGGAGGGGCTCGGTGTG
GTGCAAGCATTCAATAAGCAAGAGTATTTCAATTGAAGAGGCTGCTAGACGTACAAAACATCACTAATAGTGCTG
TTTTCAACGCAGAGGCTTTGAACCTCTGGTTAGCATTTTGGTGTGACTTCATTGGTGTGCTTGGTGGGCGTC
GTTTCTGCGTTTGCAGTTGGGATGGCAAAGGATTTAGGTGGCGCTACTGTTGGTCTGGCATTCTAATATCAT
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GAATGGCTTATTTGGCAGATTATGTGCCACACGATGGAGTGTGTTTATGACCAGCGTCAAAAAGATGGAGTCGC
TAAGCAAATAGTTTACCGGATGGTAATATCGTCCCAGCGGCTCCAAGGTTCAAGTTGTTGTGGATGACGCA
GCGTTGGCTCGATGGCCTGCTACAGGAAAATATCAGATTTGAAGATGTGTGGATGCAATATCGTTTAGATGCC
CTTGGGCGCTTAAAGGCGTAACTTTCAAATCAATGACGGTGAGAAGGTGGGTGCAAGTGGGAAGAACAGGA
TCTGGTAAAAGTACAACGCTTTTAGCTCTGTACAGGATGTTGAACTCGGAAAAGGGAGAATCTTAGTCGACG
GCGTGGATATAGCTACATTGTCTTTGAAGAGACTCCGTACCGGGCTCAGTATTATCCCCAAGAGCCAGTTAT
GTTACAGGAACTGTTCCGGTCTAATCTGGATCCCTTGGAGAGTTCAAGGATGACGCCATACTTTGGGAAGTG
CTCAAGAAAGTTGGATTAGAGGACCAGGCTCAGCACGCCGGTGGATTGGACGGACAAGTCGACGGAAGTGG
TGGCAAAGCTTGGTCGCTCGGACAAATGCAATTGGTATGCCTTGCTAGAGCAGCACTCAGAGCCGTGCCATT
TTGTGTCTTGATGAGGCCACTGCAGCGATGGATCCTCATACTGAAGCAATTGTTCAACAGACGATAAAGAAAG
TATTCGATGACCGGACCACTATCACTATCGCACATCGTTAGATACGATCATAGAAAGCGACAAGATTATCGT
TATGGAGCAAGGCTCTTATGGAATATGAATCGCCTAGTAAGCTGCTGGCTAACCGAGATTCGATGTTCTCC
AAACTCGTTGATAAACTGGACCTGCAGCTGCGGCAGCTCTACGTAAGATGGCTGAAGATTTTTGGAGTACGC
GTTACAGCGCAAGGCCGTAATCAATGA

Figure S7. DNA sequences of codon-optimised LCIA and HLA3.

Table S1. Sequences of synthetic oligonucleotides used in this study.

Gene name	Phytozome 10.2 Cr v5.5 (Augustus u11.6)	Gene length (bp)	Forward primer	Reverse primer	Internal forward primer	Internal reverse primer
Full-length ORFs						
LCIA	Cre06.g309000	2001	GCTACTCACAACAAGCCCAGTTATGCAGACCAC TATGACTCGCCCTTG	GAGCCACCCAGATCTCCGTTGCGGGTGGCG GGCTTGG		
LCIB	Cre10.g452800	2172	GCTACTCACAACAAGCCCAGTTATGTTGCTCTG TCTTCGC	GAGCCACCCAGATCTCCGTTGTTCTTGGGG GCCTCGAAG		
LCIC	Cre06.g307500	2161	GCTACTCACAACAAGCCCAGTTATGGCCCTTGC TCAGAAGATGAACGTG	GAGCCACCCAGATCTCCGTTGTTTATGTTGG CGAGCTCGGGC		
LCI1	Cre03.g162800	1616	GCTACTCACAACAAGCCCAGTTATGTCGGGCTT GAACAAGTTCATC	GAGCCACCCAGATCTCCGTTTACCTTGGTG GCGCCGTC		
HLA3*	Cre02.g097800	6068	GCTACTCACAACAAGCCCAGTTATGGGCGAGGG CAAGGTGGCC	GAGCCACCCAGATCTCCGTTCTGTTGCGG CCCTGCGCG	ACTTCTCCGGTGGC CAGCGC	CAGCACCAGGTCGG CGTCGG
CCP1	Cre04.g223300	1891	GCTACTCACAACAAGCCCAGTTATGTCATCCGA CGCTATGACTATCAACGA	GAGCCACCCAGATCTCCGTTCTGCGCGGCG GTGGGCG		
CCP2	Cre04.g222750	1801	GCTACTCACAACAAGCCCAGTTATGGCATCCGA CGCTATGACTATCAACG	GAGCCACCCAGATCTCCGTTCTGAGCGGTG GCGGGGCC		
CAH2	Cre04.g223050	3309	GCTACTCACAACAAGCCCAGTTATGGCGGTAC TGGCGTCTAC	GAGCCACCCAGATCTCCGTTCTCGTAGCGG GCCAGCTTGATG		
CAH3	Cre09.g415700	1594	GCTACTCACAACAAGCCCAGTTATGCGCTCAGC CGTTCTAC	GAGCCACCCAGATCTCCGTTCTAGCTCGTATT CGACCAGG		
CAH6	Cre12.g485050	1226	GCTACTCACAACAAGCCCAGTTATGGGATGCGG TGCCAGCGTG	GAGCCACCCAGATCTCCGTTCTCGGCGCTG CTGCCGCC		
cDNA						
LCIA	Cre06.g309000	1008	ATGCAGACCACTATGACTCGCC	CGCGGTGGCGGGCTTGGC		
LCIB	Cre10.g452800	1344	ATGTTGCTCTGCTTCGCG	GTTCTTGGGGCCTCGAAG		
LCIC	Cre06.g307500	1329	ATGGCCCTTGCTCAGAAGATG	GTTTATGTTGGCGAGCTCG		
LCI1	Cre03.g162800	576	ATGTCGGGCTTGAACAAGTTCATCTATGTGG	CACCTTGGTGGCGCCGTCAG		
HLA3	Cre02.g097800	3975	ATGGGCGAGGGCAAGGTG	CTGTTGCGGCCCTGCGC		
CCP2	Cre04.g222750	1065	ATGGCATCCGACGCTATGACTATCAACGAGG	CTGAGCGGTGGCGGGCCGAT		
CAH1	Cre04.g223100	1131	ATGGCGCTACTGGCGCTC	GTGATAGCGGGCCAGCTTGATG		
CAH3	Cre09.g415700	930	ATGCGCTCAGCCGTTCTAC	CAGCTCGTATTCGACCAGG		
CAH6	Cre12.g485050	792	ATGGGATGCGGTGCCAGCGTGC	CTCGGCGGTGCTGCCCCCTT		
LCIA	synthetic codon optimised (Fig. S7)	1008	ATGCAGACAACCTATGACAAGACCT	TGCTGTAGCAGGTTTAGCAGAT		
HLA3	synthetic codon optimised (Fig. S7)	3975	ATGGGAGAGGGGAAGGTG	TTGATTACGGCCTTGGC		