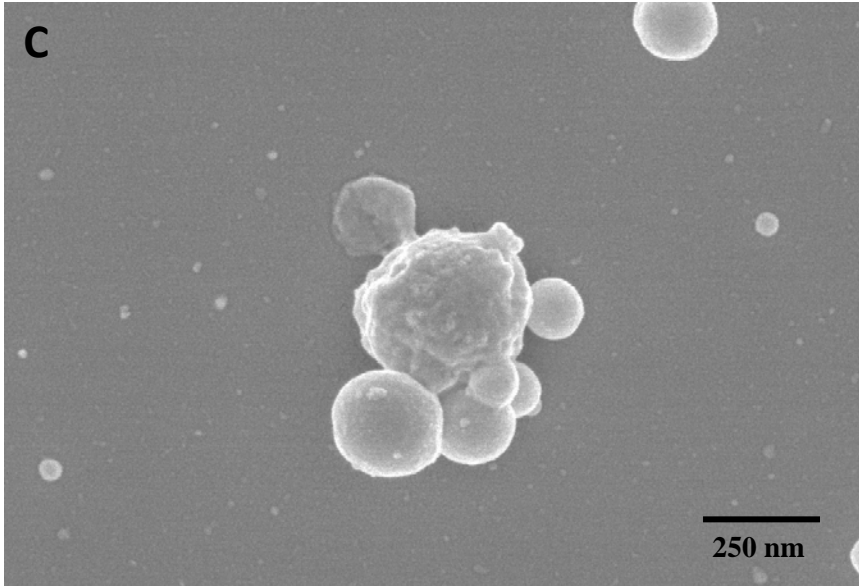
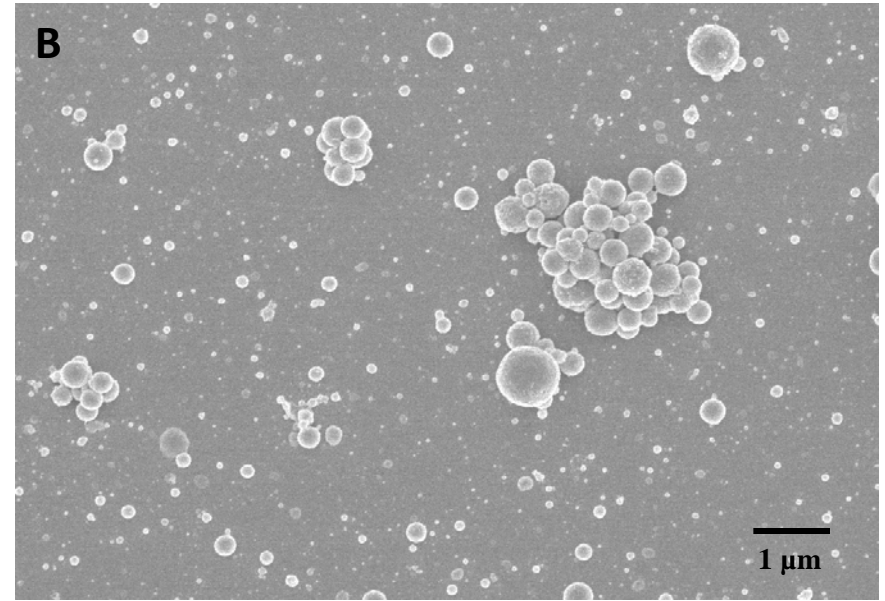
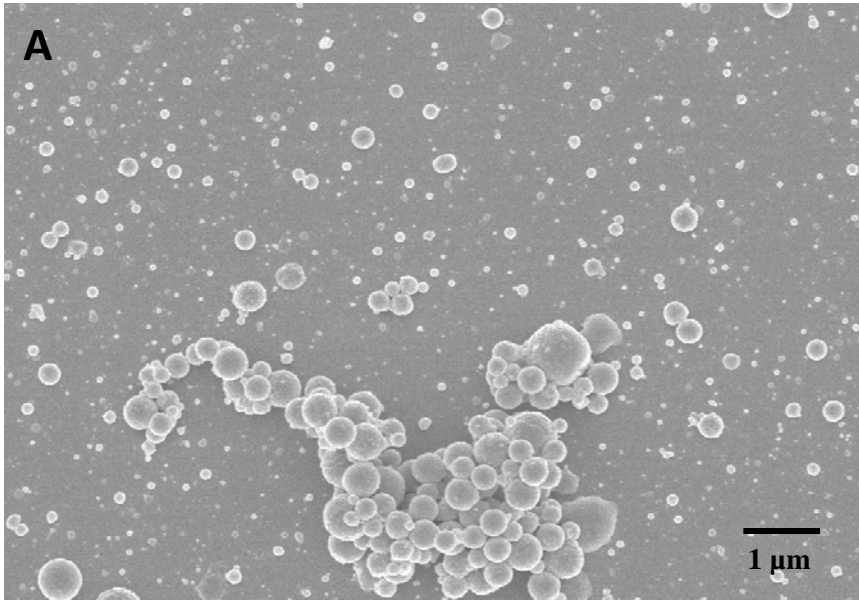




Suppl. Fig. 1 Five-day light-stressed wild-type *A. thaliana* plant, representative of those used in this work.



Suppl. Fig. 2. Scanning electron micrographs of PG preparations. A and B, Representative images demonstrating PG clustering. C, Representative amorphous globule, likely representing stromal lamellae thylakoid attached to PGs.

Chlorophyllide biosynthesis

Consensus

| | CHLI-1 | CHLI-2 | CHLD | GUN5 | CHLM | CHL27 | DVR | PORA | PORB | PORC |
|--------|--------|--------|------|------|------|-------|-----|------|------|------|
| CHLI-1 | | | | | | | | | | |
| CHLI-2 | x | | | | | | | | | |
| CHLD | x | x | | | | | | | | |
| GUN5 | x | x | x | | | | | | | |
| CHLM | x | x | x | x | | | | | | |
| CHL27 | x | x | x | x | x | | | | | |
| DVR | x | x | x | x | x | | | | | |
| PORA | | | | | | | | | | |
| PORB | | | | | | | | | | |
| PORC | x | x | x | x | x | x | x | | x | |

ClpPR complex

Consensus

| | ClpR1 | ClpR2 | ClpR3 | ClpR4 | ClpP3 | ClpP4 | ClpP5 | ClpP6 | ClpP2 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| ClpR1 | | | | | | | | | |
| ClpR2 | | | | | | | | | |
| ClpR3 | x | | | | | | | | |
| ClpR4 | x | x | | | | | | | |
| ClpP3 | x | x | x | x | | | | | |
| ClpP4 | | x | x | x | x | | | | |
| ClpP5 | x | x | x | x | x | x | | | |
| ClpP6 | | x | x | x | x | x | x | | |
| ClpP2 | | | | | | | | | |

Chlorophyllide bioynthesis

MetaOmGraph

| | CHLI-1 | CHLI-2 | CHLD | GUN5 | CHLM | CHL27 | DVR | PORA | PORB | PORC |
|--------|--------|--------|------|------|------|-------|-----|------|------|------|
| CHLI-1 | | | | | | | | | | |
| CHLI-2 | x | | | | | | | | | |
| CHLD | x | x | | | | | | | | |
| GUN5 | x | x | x | | | | | | | |
| CHLM | x | x | x | x | | | | | | |
| CHL27 | x | x | x | x | x | | | | | |
| DVR | x | x | x | x | x | | | | | |
| PORA | | | | | | | | | | |
| PORB | | | | | | | | | | |
| PORC | x | x | x | x | x | x | x | | x | |

ClpPR complex

MetaOmGraph

| | ClpR1 | ClpR2 | ClpR3 | ClpR4 | ClpP3 | ClpP4 | ClpP5 | ClpP6 | ClpP2 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| ClpR1 | | | | | | | | | |
| ClpR2 | | | | | | | | | |
| ClpR3 | x | | | | | | | | |
| ClpR4 | | x | | | | | | | |
| ClpP3 | x | x | x | x | | | | | |
| ClpP4 | | x | x | x | x | | | | |
| ClpP5 | x | x | x | x | x | x | | | |
| ClpP6 | | x | x | x | x | x | x | | |
| ClpP2 | | | | | | | | | |

BAR - Utoronto

| | CHLI-1 | CHLI-2 | CHLD | GUN5 | CHLM | CHL27 | DVR | PORA | PORB | PORC |
|--------|--------|--------|------|------|------|-------|-----|------|------|------|
| CHLI-1 | | | | | | | | | | |
| CHLI-2 | | | | | | | | | | |
| CHLD | x | x | | | | | | | | |
| GUN5 | | x | x | | | | | | | |
| CHLM | x | x | x | x | | | | | | |
| CHL27 | | x | x | x | x | | | | | |
| DVR | x | x | x | x | | | | | | |
| PORA | | | | | | | | | | |
| PORB | | | | | | | | | | |
| PORC | x | | | | | | | | | |

BAR - Utoronto

| | ClpR1 | ClpR2 | ClpR3 | ClpR4 | ClpP3 | ClpP4 | ClpP5 | ClpP6 | ClpP2 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| ClpR1 | | | | | | | | | |
| ClpR2 | | | | | | | | | |
| ClpR3 | | | | | | | | | |
| ClpR4 | x | x | | | | | | | |
| ClpP3 | x | | x | | | | | | |
| ClpP4 | | x | x | x | x | | | | |
| ClpP5 | x | | | x | x | x | | | |
| ClpP6 | | x | | x | | x | x | | |
| ClpP2 | | | | | | | | | |

ACT - Univ Leeds

| | CHLI-1 | CHLI-2 | CHLD | GUN5 | CHLM | CHL27 | DVR | PORA | PORB | PORC |
|--------|--------|--------|------|------|------|-------|-----|------|------|------|
| CHLI-1 | | | | | | | | | | |
| CHLI-2 | x | | | | | | | | | |
| CHLD | x | x | | | | | | | | |
| GUN5 | x | x | x | | | | | | | |
| CHLM | x | x | x | x | | | | | | |
| CHL27 | x | x | x | x | x | | | | | |
| DVR | x | x | x | x | x | | | | | |
| PORA | | | | | | | | | | |
| PORB | | | | | | | | | | |
| PORC | x | x | x | x | x | x | x | | | |

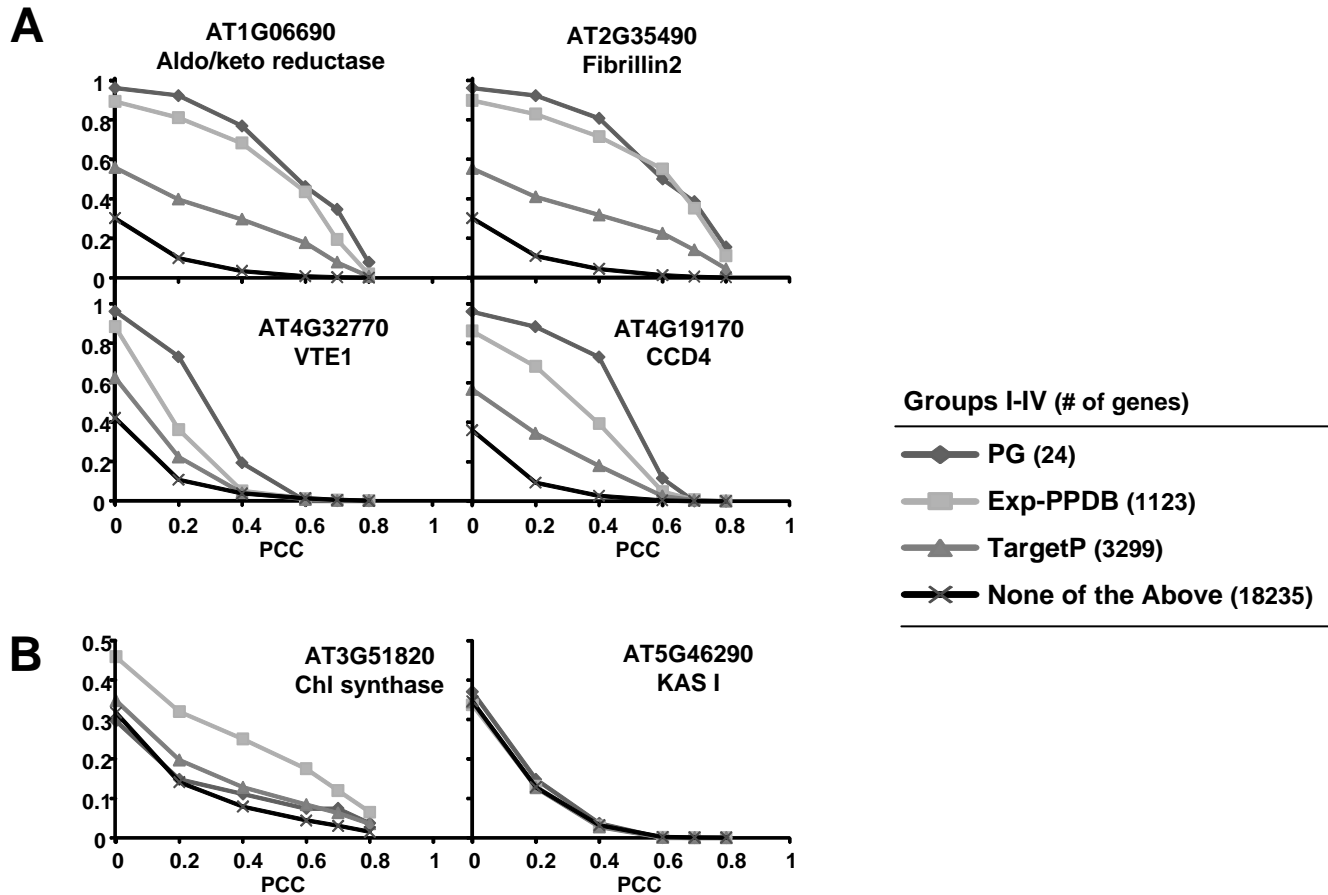
ACT - Univ Leeds

| | ClpR1 | ClpR2 | ClpR3 | ClpR4 | ClpP3 | ClpP4 | ClpP5 | ClpP6 | ClpP2 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| ClpR1 | | | | | | | | | |
| ClpR2 | | | | | | | | | |
| ClpR3 | | | | | | | | | |
| ClpR4 | x | x | | | | | | | |
| ClpP3 | x | | x | | | | | | |
| ClpP4 | | x | | x | x | | | | |
| ClpP5 | x | x | | x | x | x | | | |
| ClpP6 | | x | | x | | x | x | | |
| ClpP2 | | | | | | | | | |

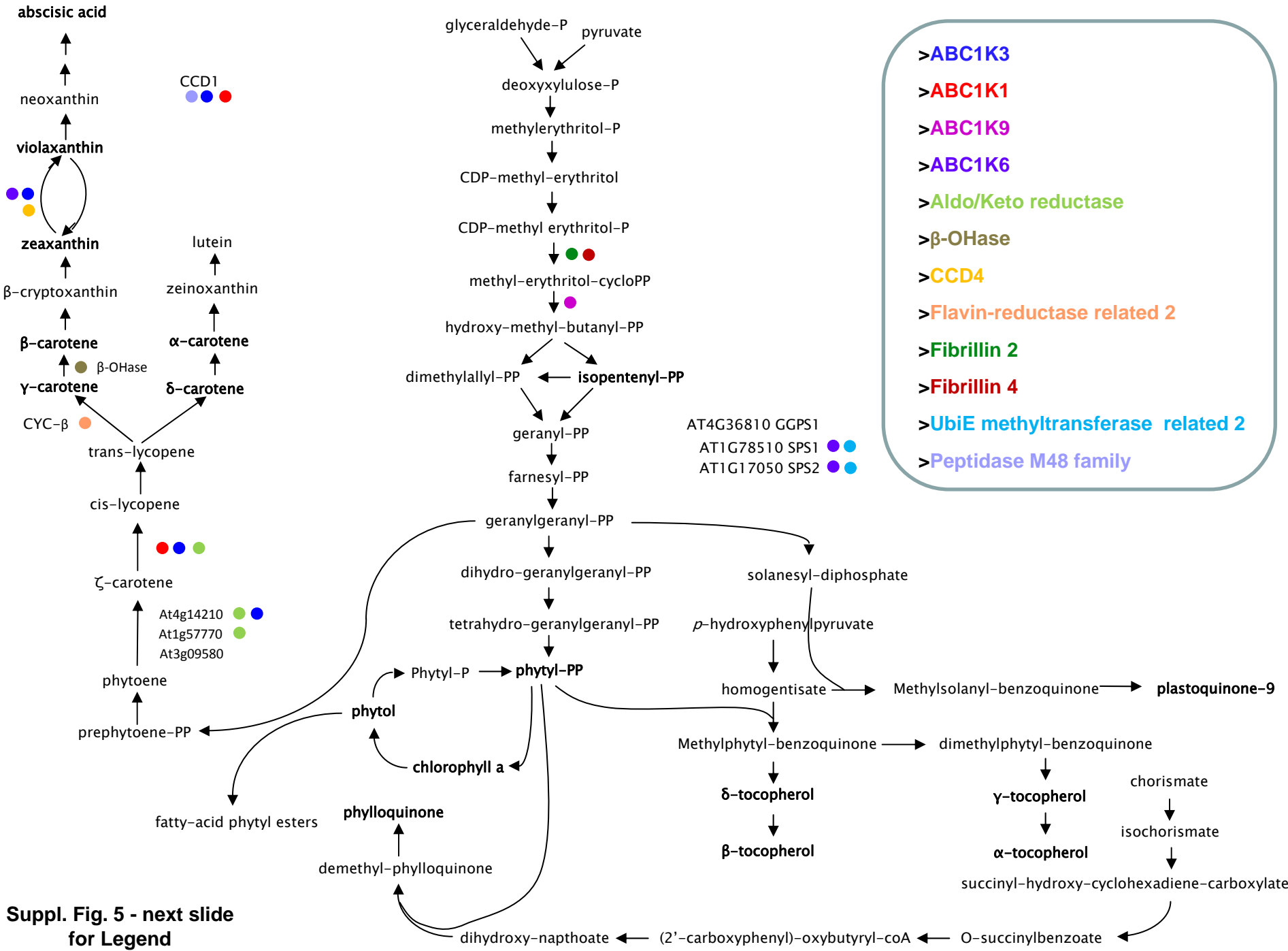
Suppl. Fig. 3

Legend on next page

Suppl. Fig. 3. Co-expression within gene sets of chlorophyllide biosynthesis and the ClpPR protease complex. A, All pairwise combinations of genes in each geneset are illustrated. Gene pairs demonstrating co-expression in all three software programs are indicated with a red “x”. Gene pairs demonstrating co-expression in one or two of the software programs are indicated with a black “x”. Presumed true-positive interactions are indicated with green, presumed true-negatives in red. B, All co-expression pairs from each of the three software programs are shown. Enzymes of the chlorophyllide synthesis pathway are named as follows: CHLI-1, Mg-protoporphyrin IX chelatase I-1; CHLI-2, Mg-protoporphyrin IX chelatase I-2; CHLD, Mg-protoporphyrin IX chelatase D; GUN5, Mg-protoporphyrin IX chelatase H (CHLH); CHLM, Mg-protoporphyrin IX methyltransferase; CHL27, Mg-protoporphyrin IX monomethyl ester cyclase; DVR, 3,8-divinyl protochlorophyllide 8-vinyl reductase; POR, protochlorophyllide oxidoreductase.



Suppl. Fig. 4. PG genes preferentially maintain co-expression with other PG genes at higher PCCs. Genes analyzed for co-expression correlation were annotated for inclusion in 4 groups describing sub-cellular localization: Group I: PG-localized as determined in this paper “PG”, Group II: plastid-localized as curated in the Plant Proteome Database (Sun et al., 2009), based on experimental evidence “PPDB”, Group III: plastid-predicted by TargetP (Emanuelsson et al., 2000), “TargetP”, Group IV: all genes not fitting in any of Group I-III “none of the above”. The fraction of genes above each of the given PCCs were plotted and the size of each group is indicated in the key. See the supplemental text for an explanation of abbreviations. A, Graphs of four representative PG genes are illustrated. The fraction of genes of Group I (PG) co-expressing above each PCC are consistently as high or higher than the fractions of the other 3 groups. B, Two plastidic, non-PG genes (Chl synthase, KAS I) demonstrate that Group I “PG” enrichment at each PCC value is not a general response of plastid genes.



Suppl. Fig. 5 - next slide for Legend

Suppl. Fig. 5. Co-expression relationships between PG genes and isoprenoid metabolism genes found in MetaOmGraph have been projected onto the isoprenoid pathway. The MEP pathway and downstream metabolic pathways of carotenoid, quinone, tocopherol and chlorophyll metabolism have been overlaid with their co-expressing PG genes. Colored circles indicate which PG gene(s) co-express with each gene in the pathway. GGPS: geranylgeranyl diphosphate synthase, SPS1: solanesyl diphosphate synthase isoform 1, SPS2: solanesyl diphosphate synthase isoform 2, CYC- β : lycopene β -cyclase, β -OHase: β -ring carotenoid hydroxylase, CCD1: carotenoid cleavage dioxygenase 1.