Volatile and non-volatile metabolome characterization of tomato San Marzano mutants altered in berry pigmentation

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Metabolites (submitted)

SUPPLEMENTARY FIGURES

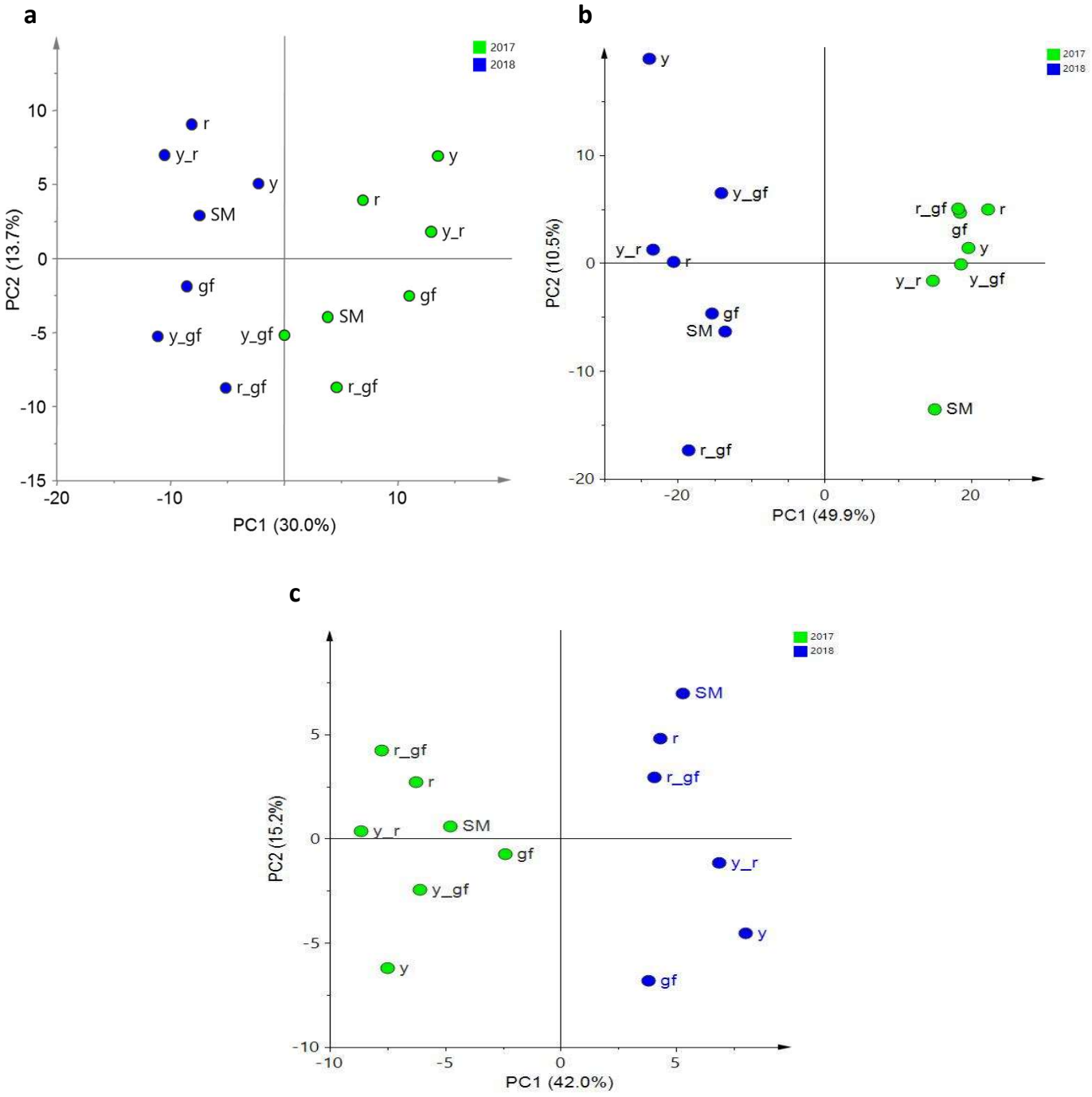


Figure S1: PC1 X PC2 score plots of the six mutated lines plus San Marzano (SM), sampled in two different years, according to relative values of 263 volatile (a), 746 non-polar (b) and 110 polar (c) metabolites measured by a Solid-phase micro-extraction Gas-Cromatography coupled with a mass spectrometry instrument (HS-SPME-GC-MS).

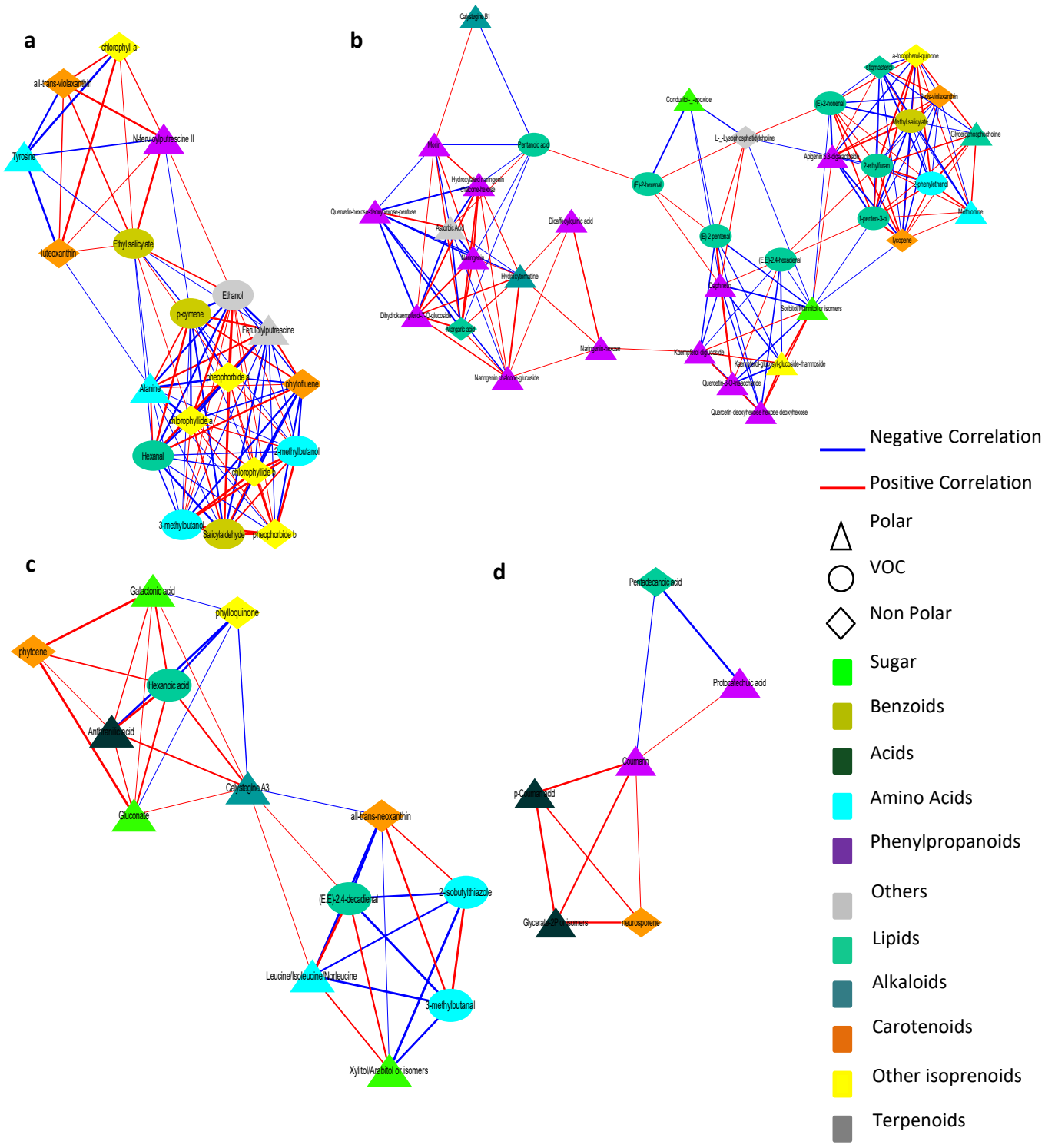


Figure S2: Subnetworks generated from the *y*, *gf* and *y_gf* global network of Fig. 8, using the MCODE Cytoscape plugin. Each subnetwork highlights the highest densely connected regions present in the global network. Each node represents a VOC (turquoise circle), non-polar (diamond) or a polar metabolite (triangle). Lines joining the nodes represent correlations; direct and inverse correlations are shown in red and blue, respectively. Node sizes are proportional to the corresponding node strengths (nss), which are shown in Supplemental Table S7. Node color is depending on the metabolic class of each compound as indicated in the figure. Number of nodes (n) and network strength (NS) are shown on top of each network. Only correlations with $|\rho|>0.95$ are shown (*p-value* 0.05).

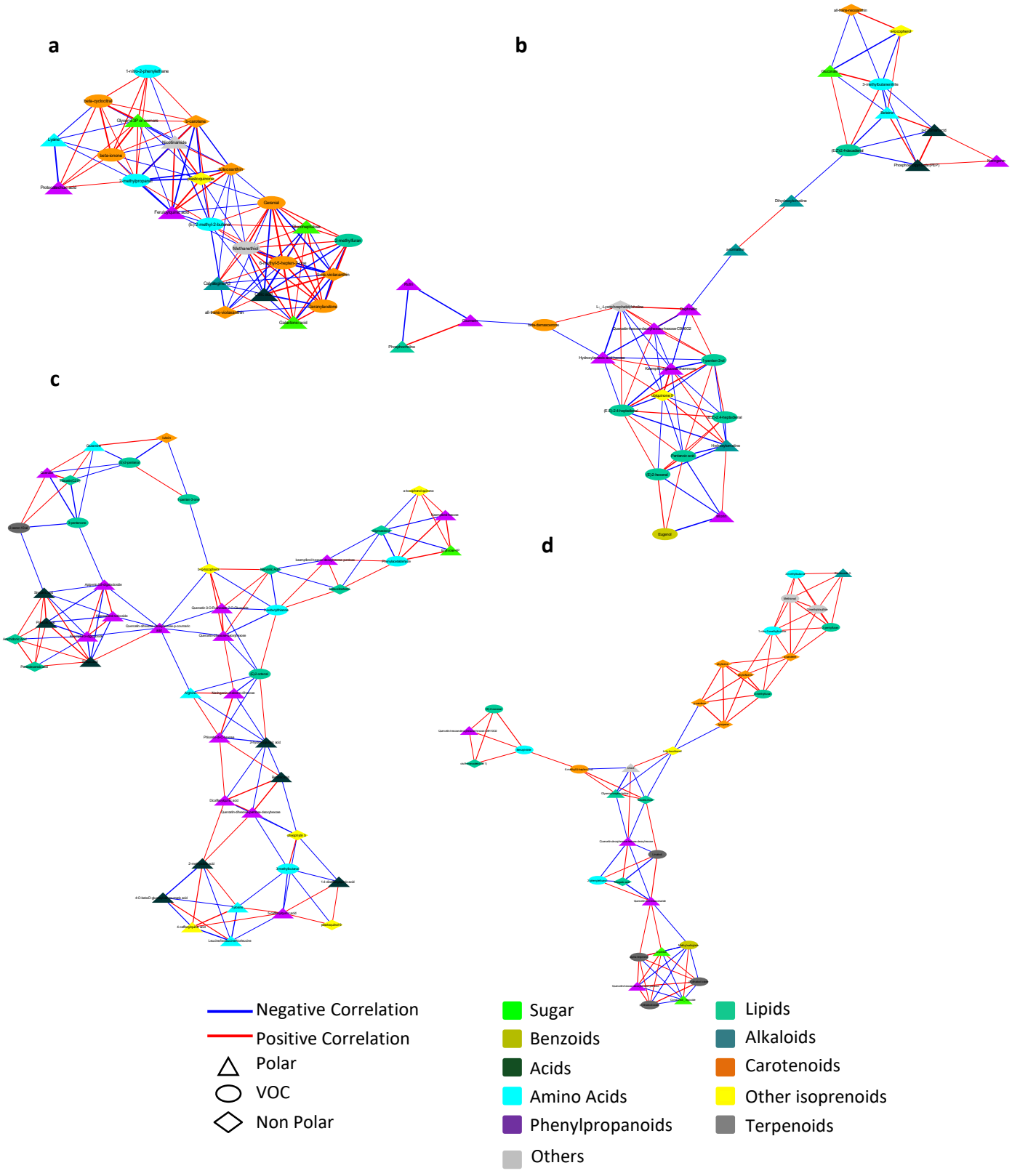


Figure S3: Subnetworks generated from the *y*, *r* and *y_r* global network of Fig. 8 using the MCODE Cytoscape plugin. Each subnetwork highlights the highest densely connected regions present in the global network. Each node represents a VOC (turquoise circle), non-polar (diamond) or a polar metabolite (triangle). Lines joining the nodes represent correlations; direct and inverse correlations are shown in red and blue, respectively. Node sizes are proportional to the corresponding node strengths (nss), which are shown in Supplemental Table S7. Node color is depending on the metabolic class of each compound as indicated in the figure. Number of nodes (n) and network strength (NS) are shown on top of each network. Only correlations with $|\rho|$ >0.95 are shown (*p-value* 0.05).

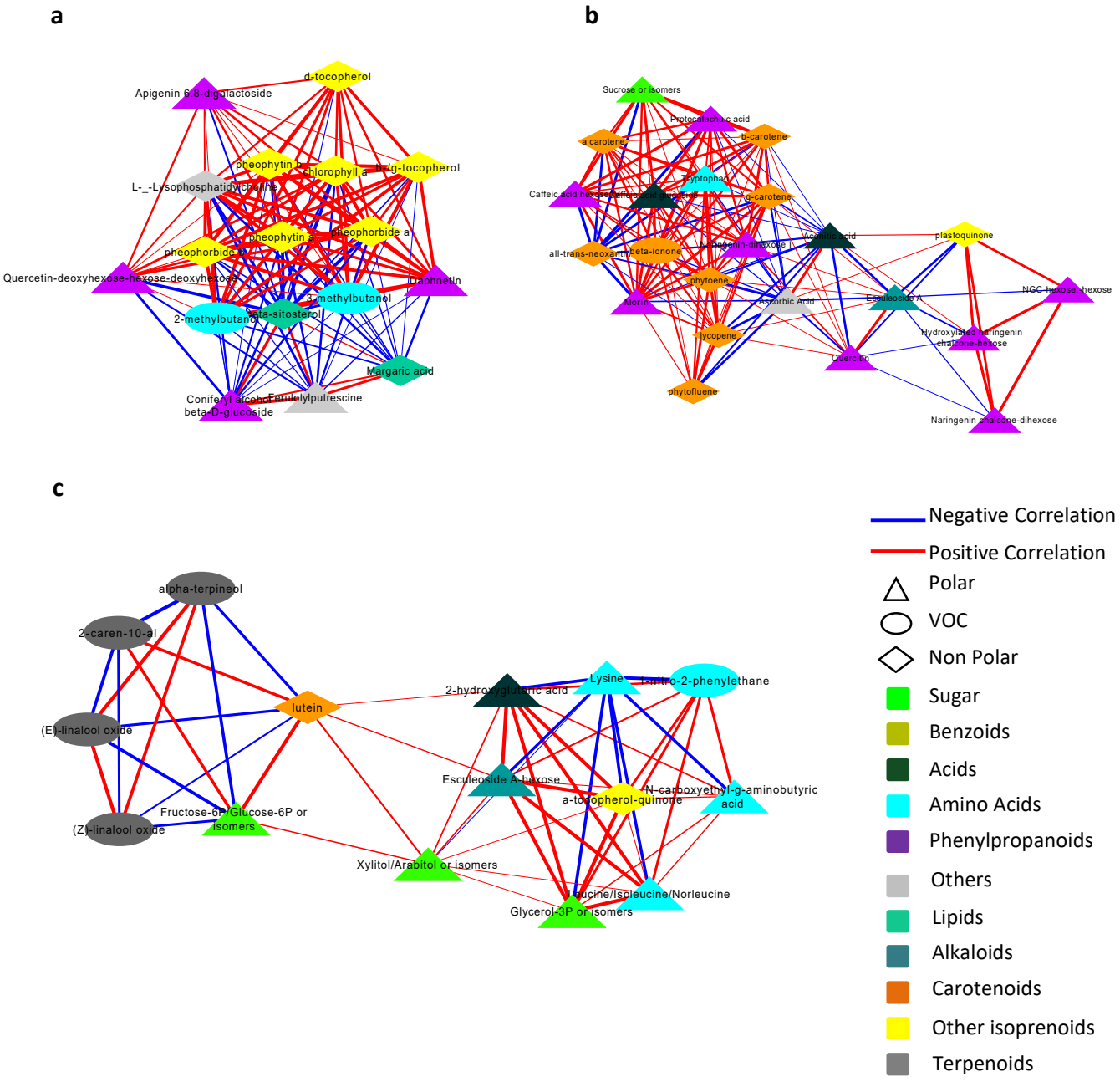


Figure S4: Subnetworks generated from the *r, gf* and *r_gf* global network of Fig. 8 using the MCODE Cytoscape plugin. Each subnetwork highlights the highest densely connected regions present in the global network. Each node represents a VOC (turquoise circle), non-polar (diamond) or a polar metabolite (triangle). Lines joining the nodes represent correlations; direct and inverse correlations are shown in red and blue, respectively. Node sizes are proportional to the corresponding node strengths (nss), which are shown in Supplemental Table S7. Node color is depending on the metabolic class of each compound as indicated in the figure. Number of nodes (n) and network strength (NS) are shown on top of each network. Only correlations with $|\rho|>0.95$ are shown (*p-value* 0.05).