

Figure S1. Comparison of metabolite contents distribution before and after normalization.

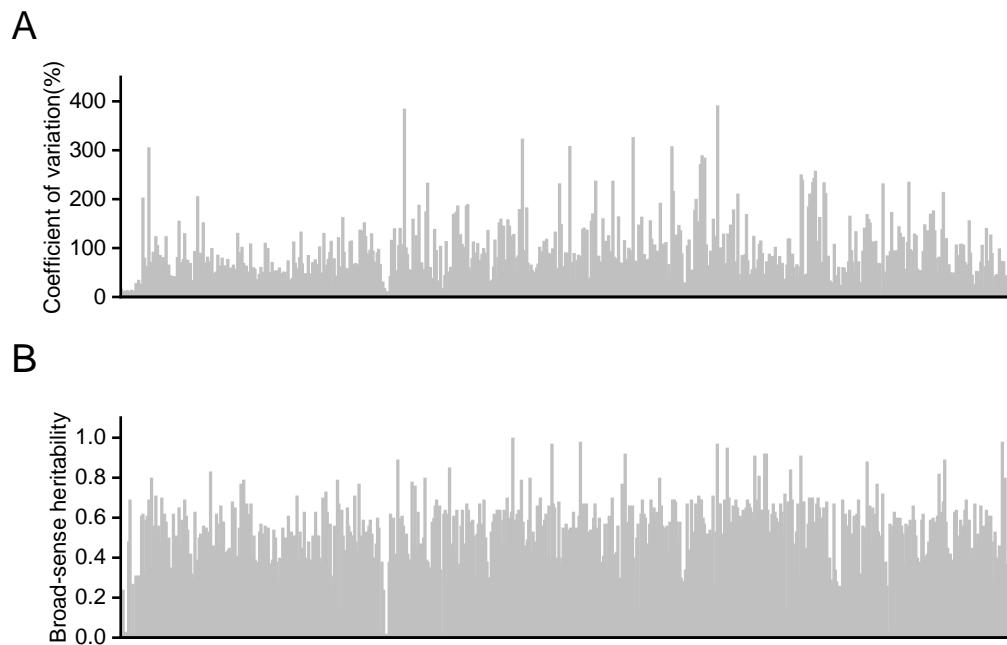
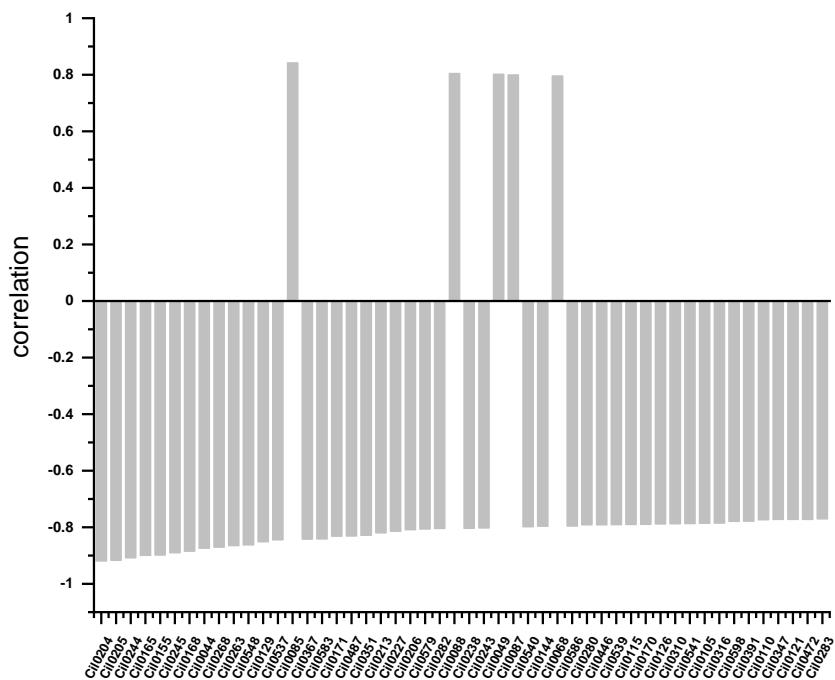


Figure S2. **(A)** Distribution of variation coefficients and **(B)** the broad-sense heritability of metabolites.



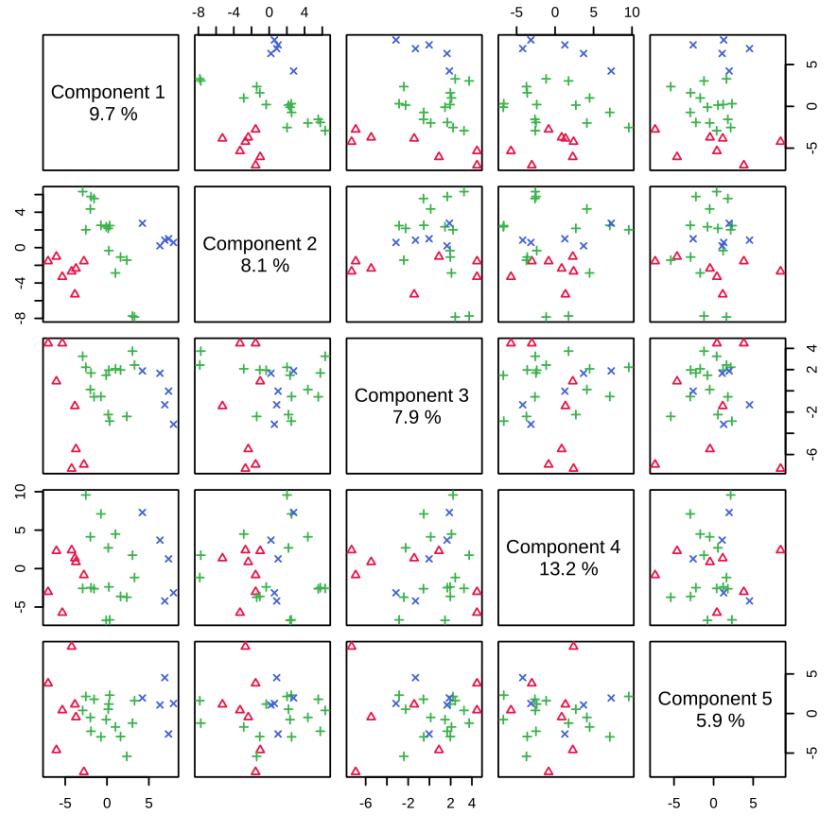


Figure S4. Pairwise scores plots between the top 5 components by PLS-DA analysis.

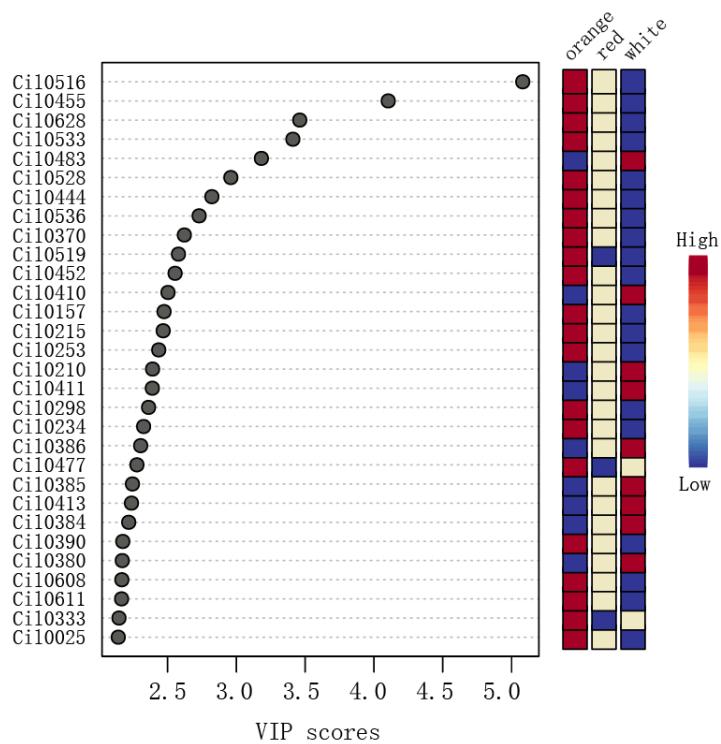


Figure S5. Important metabolic traits identified by PLS-DA analysis. The colored boxes on the right indicate the corresponding metabolite relative contents in each group.

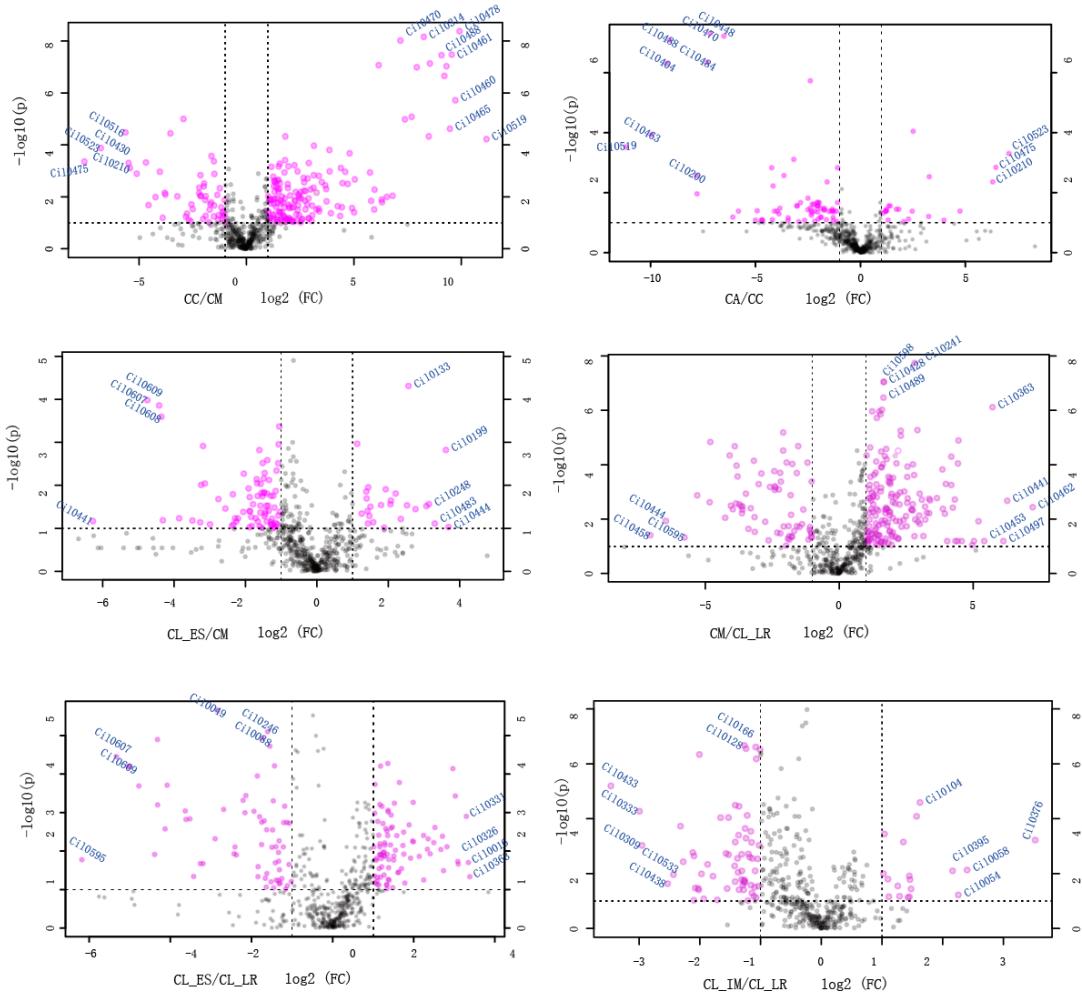


Figure S6. Important features selected by volcano plot with fold change

threshold (x) 2 and t-tests threshold (y) 0.1. The red circles indicate

metabolites above the threshold. CC, *C. colocynthis*; CA, *C. amarus*; CM, *C. mucosospermus* (egusi); CL_ES, *C. lanatus* edible seed watermelon; CL_LR, *C. lanatus* landrace watermelon; CL_IM, *C. lanatus* improved watermelon.