

**Widely targeted metabolome and transcriptome landscapes of *Allium fistulosum*–*A. cepa* chromosome addition lines revealed a flavonoid hot spot on chromosome 5A**

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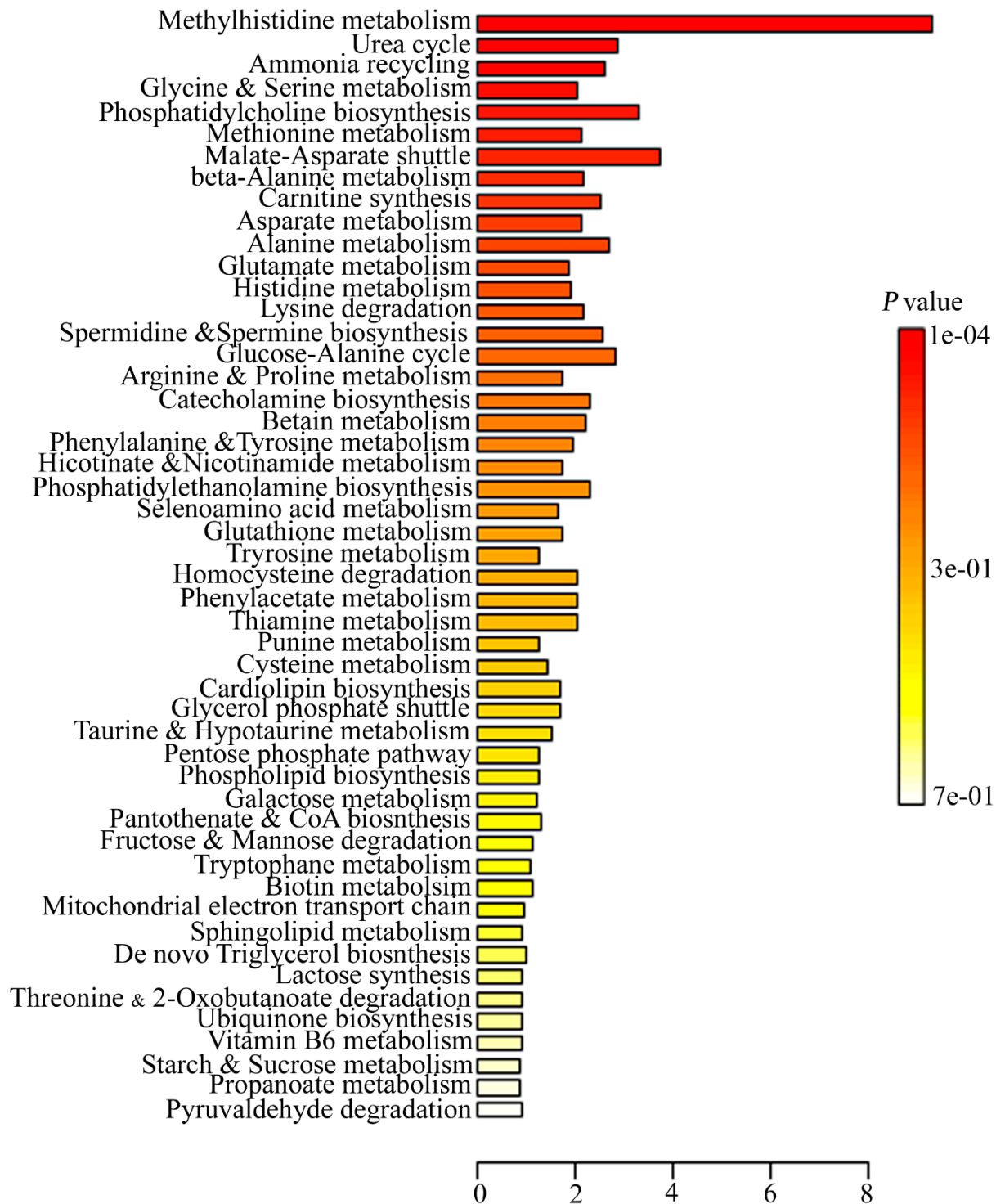
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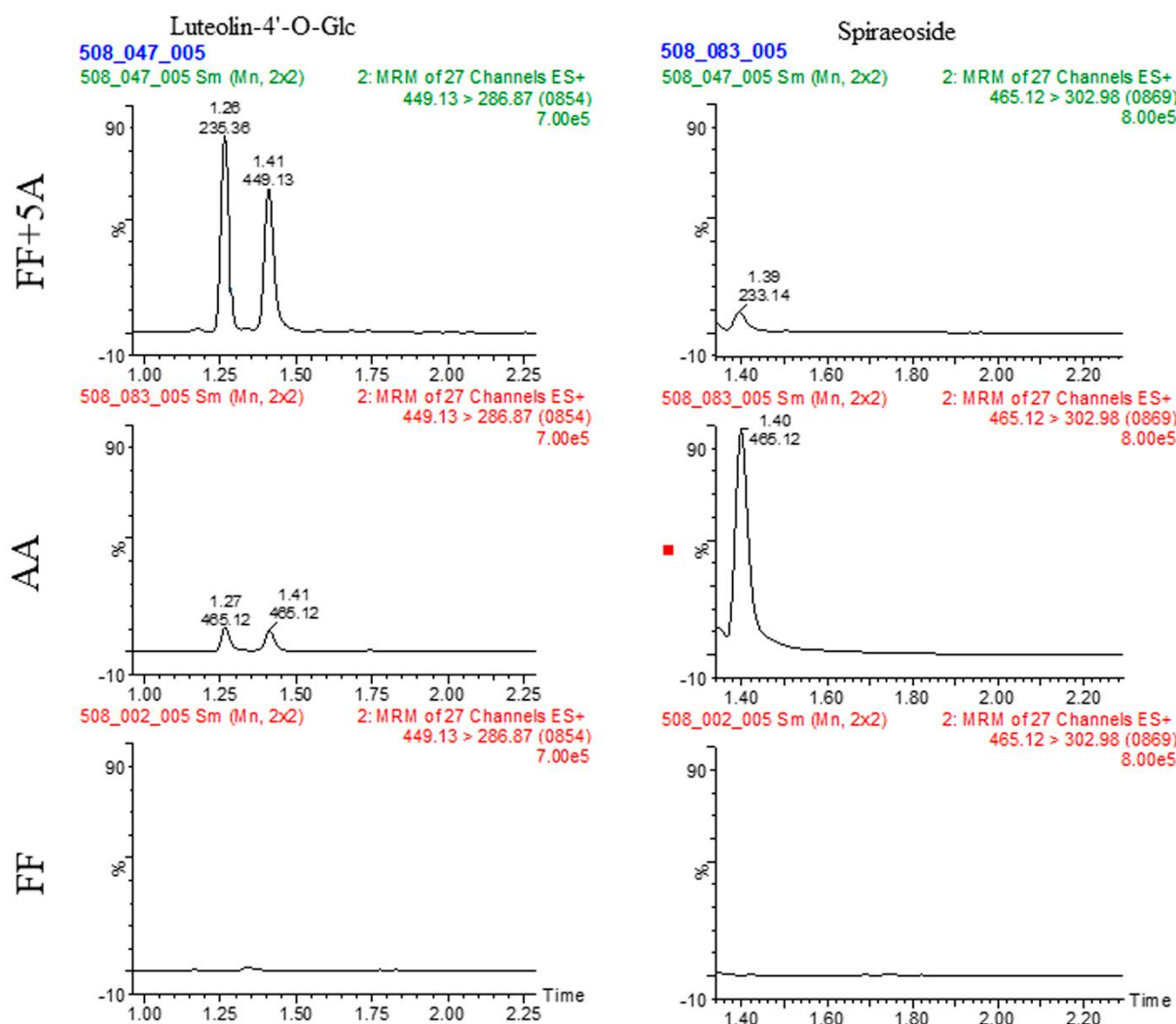
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**Supplementary Figure S1.** Enrichment pathway analysis of all 123 metabolites using MetaboAnalyst 4.0.



**Supplementary Figure S2.** Ultra-high-performance liquid chromatography–photo diode array (UPLC-PDA) chromatograms with assigned mass spectra for luteolin-4'-O-glucoside and spiraeoside/querctetin-3,4'-diglucoside in the *Allium cepa* L. Aggregatum group (AA), *A. fistulosum* (FF), and *A. fistulosum* with extra chromosome 5A from the shallot (FF5A). In the y-axis, ion count intensities were adjusted at  $7 \times 10^5$  for luteolin-4'-O-glc and  $8 \times 10^5$  for spiraeoside/querctetin-3,4'-diglucoside. The x-axis represents the retention time.