

Supplementary Table S4 | Robustness Check of CT-Metabolite Association Asymmetry

Three correlation methods applied to the same 18 CT × 624 metabolite pairs (11,232 pairs per variety).

Method	Metric	W5 (count)	CK (count)	Asymmetry
Pearson correlation	$ r > 0.99$	55	0	✓
Pearson correlation	$ r > 0.95$	147	0	✓
Spearman rank correlation	$ \rho > 0.95$	48	0	✓
First-differencing Pearson	$ r > 0.95$	41	2	✓
Permutation test (10,000×)	Median $ r > 0.99$	0 (observed: 55, $p < 0.0001$)	—	✓

Interpretation: All three correlation methods (parametric Pearson, non-parametric Spearman, and detrended first-differencing Pearson) preserve the inter-variety asymmetry pattern, confirming that the finding is not an artefact of the linearity assumption or shared developmental trends.

Method:

- **Pearson correlation:** Computed on $n = 5$ time-point means ($df = 3$) per variety, FDR-corrected across 11,232 pairs.
- **Spearman rank correlation:** Rank-based non-parametric correlation on the same data.
- **First-differencing (FD) Pearson:** Each time series was first-differenced ($x_{t+1} - x_t$) before Pearson correlation, removing shared temporal trends.

- **Permutation test:** Time-point labels shuffled 10,000 times; under permutations, median $|r| > 0.99$ pairs = 0 (95% CI 0-1).