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Supplementary data

Aspartame promotes tumor growth through stress-induced metabolic reprogramming

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Supplementary figures

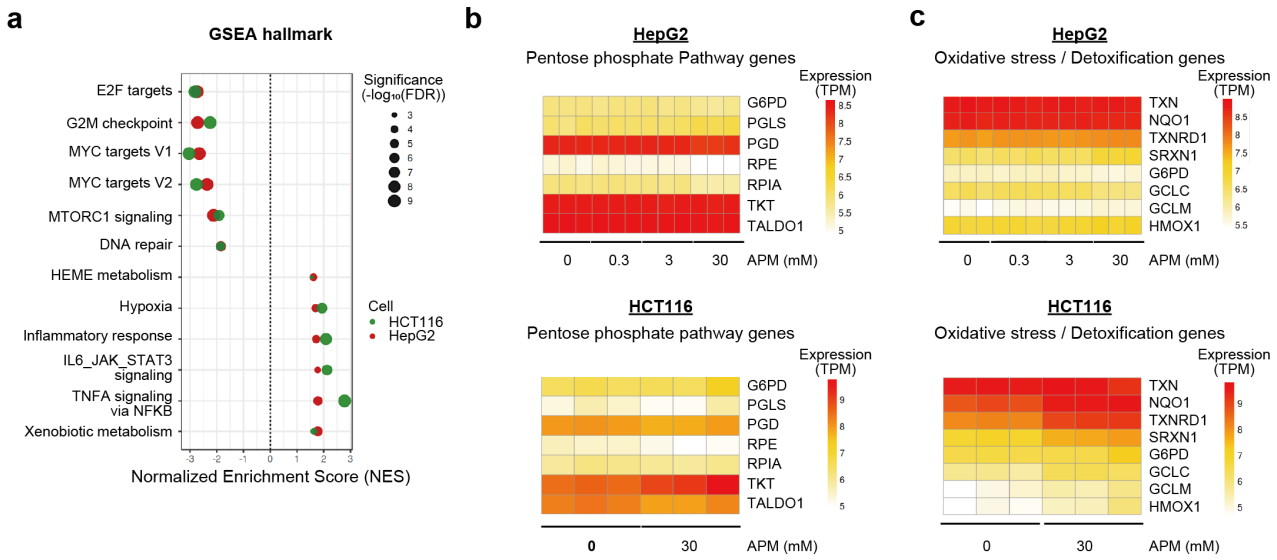

Figure S1. Re-analysis of transcriptomic responses to aspartame in HCT116 and HepG2 cells, related to Figure 2. **(a)** GSEA of Hallmark pathways in HCT116 and HepG2 cells treated with 30 mM aspartame for 24 h. Dot color indicates normalized enrichment score (NES), and dot size represents statistical significance [−log10(FDR)]; **(b, c)** Heatmap showing expression of PPP genes **(b)** or oxidative stress/detoxification genes **(c)** in HCT116 and HepG2 cells following treatment with 30 mM aspartame. Expression levels are shown as TPM values.

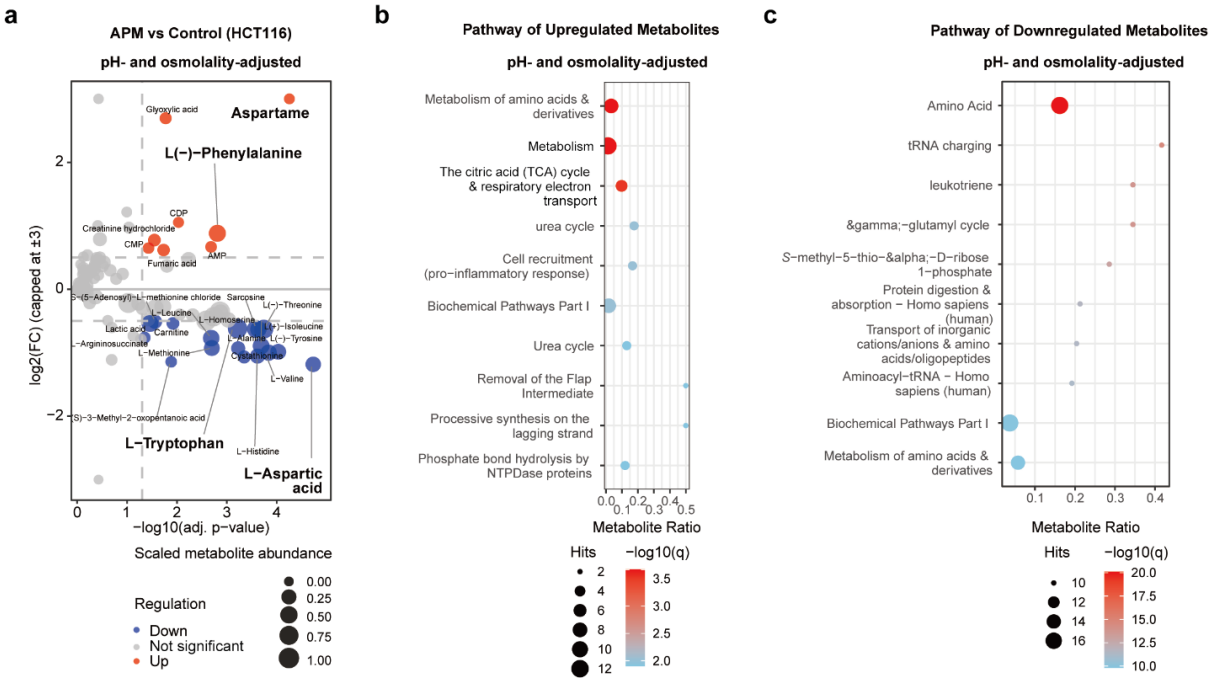

Figure S2. Metabolomic analysis of pH- and osmolality-adjusted aspartame-treated HCT116 cells, related to Figure 3. **(a)** Volcano plot showing metabolite changes in HCT116 cells treated with 30 mM aspartame under pH- and osmolality-adjusted culture conditions; **(b)** Pathway enrichment analysis of significantly upregulated metabolites identified under pH- and osmolality-adjusted conditions; **(c)** Pathway enrichment analysis of significantly downregulated metabolites identified under pH- and osmolality-adjusted conditions.

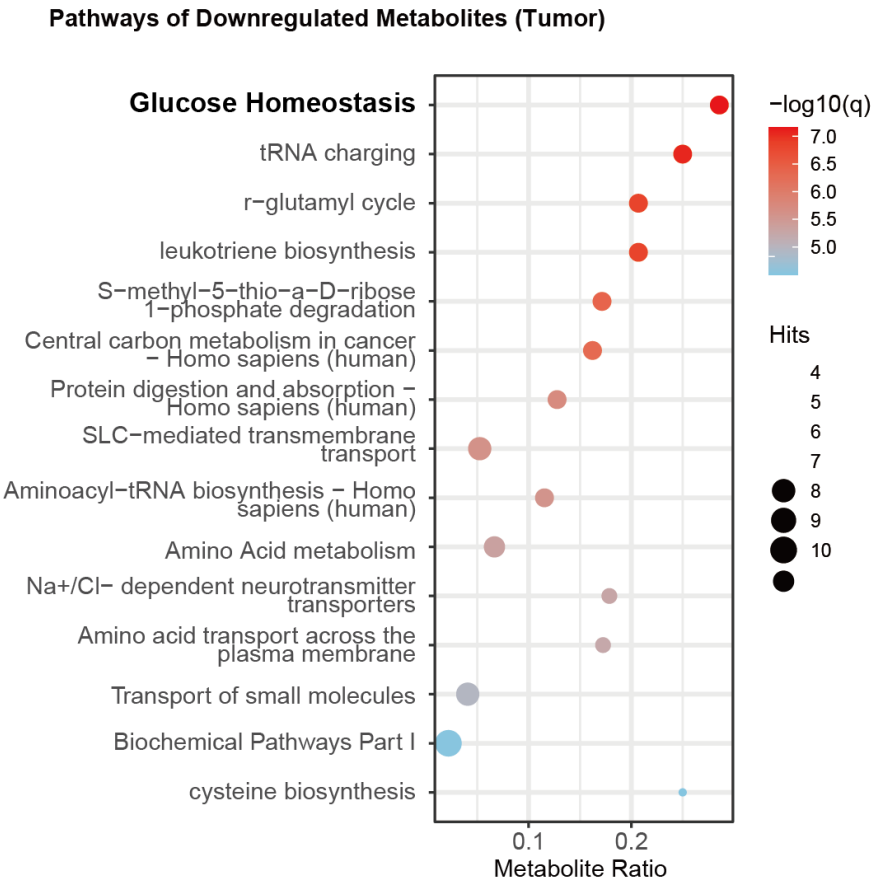

Figure S3. Pathway enrichment analysis of aspartame-downregulated metabolites in tumors, related to Figure 4. Pathway enrichment analysis of metabolites significantly decreased in tumors from aspartame-treated mice compared with control mice. The panel shows pathways enriched among aspartame-downregulated metabolites. Color indicates FDR-adjusted significance (−log10 q value), and circle size represents the number of metabolites contributing to each pathway.

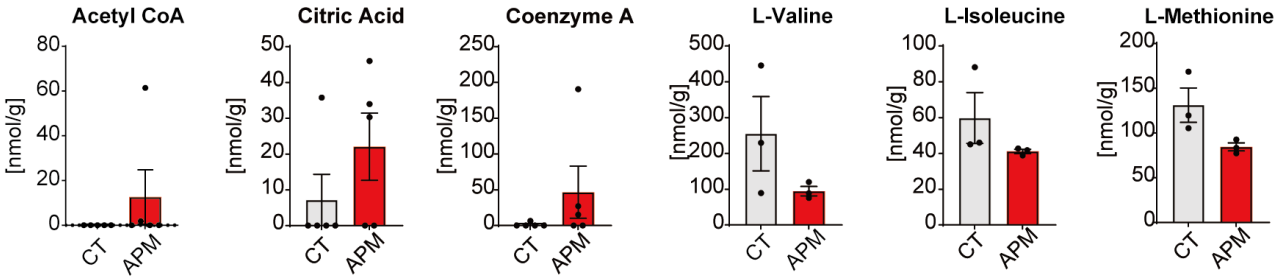

Figure S4. Representative tumor metabolites associated with pathway enrichment analysis, related to Figure 4. Metabolite levels (nmol/g tissue) of representative metabolites associated with the enriched pathways identified in Figure 4f. Data are presented as mean ± SEM.