

Cognitive Impairment Mechanisms in High-Altitude Exposure: Proteomic and Metabolomic Insights

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supporting materials list

materials type	materials name
Supporting Figure	Figure S1
	Figure S2
	Figure S3
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	Figure S6
	Figure S7
	Figure S8

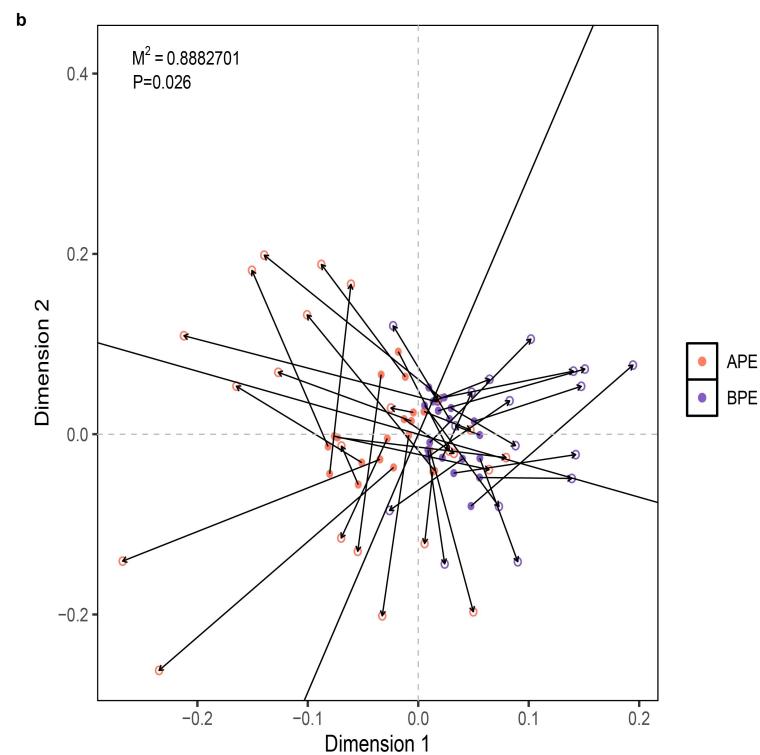
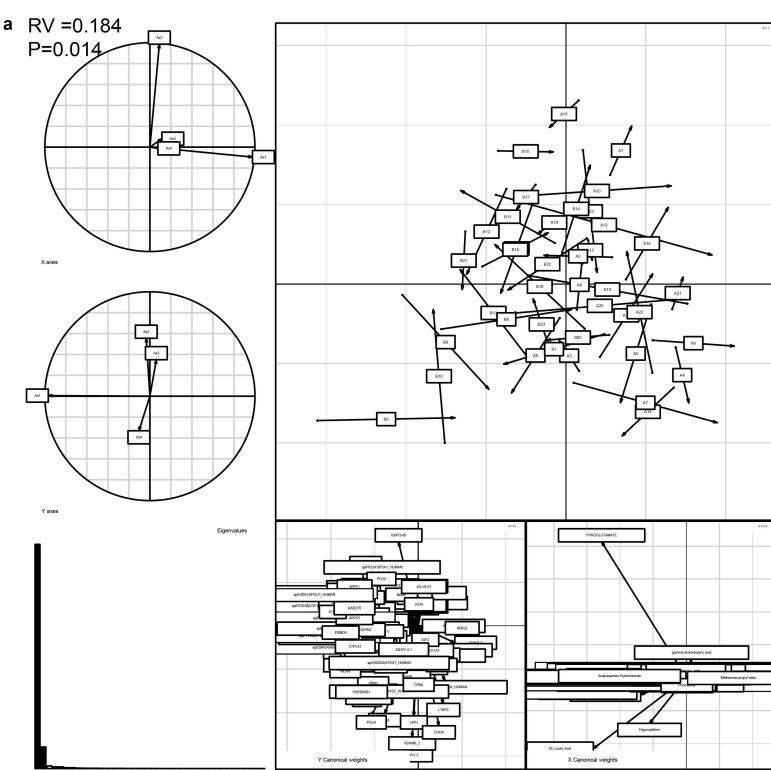
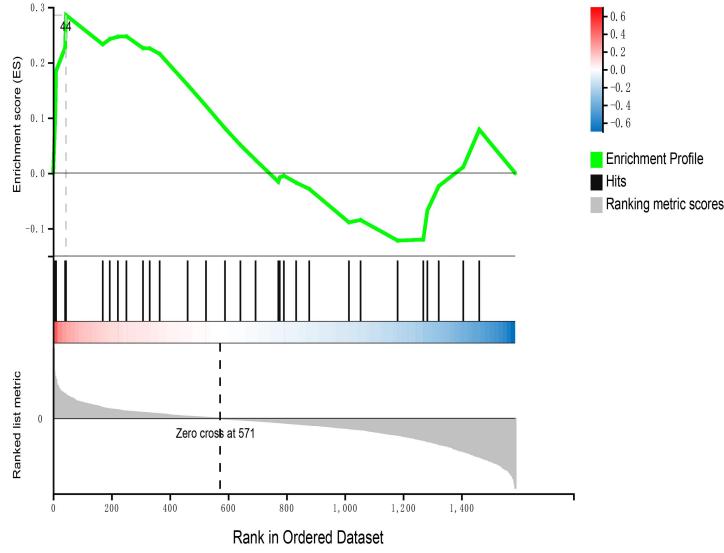
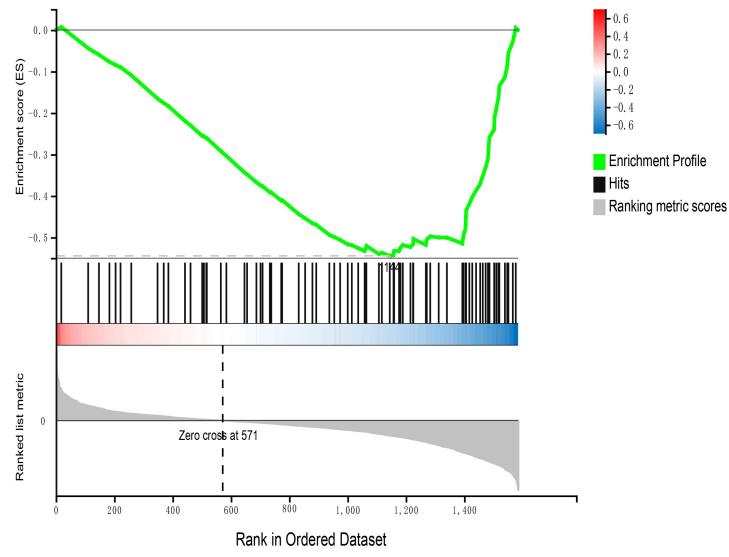


Figure S1.a. Correlation analysis between proteomics and metabolomics for COIA. b. Procrustes Analysis between proteomics and metabolomics.

Enrichment plot: REACTOME_GPCR_DOWNSTREAM_SIGNALING



Enrichment plot: REACTOME_IMMUNE_SYSTEM



Enrichment plot: REACTOME_SIGNALING_BY_RHO_GTPASES

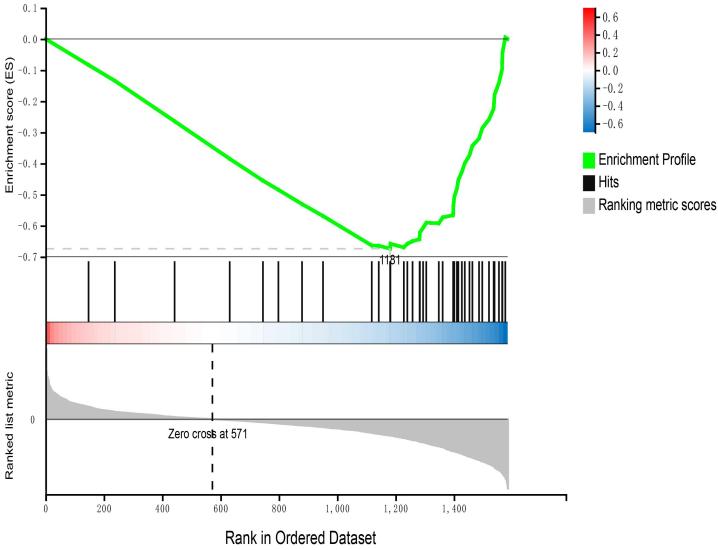
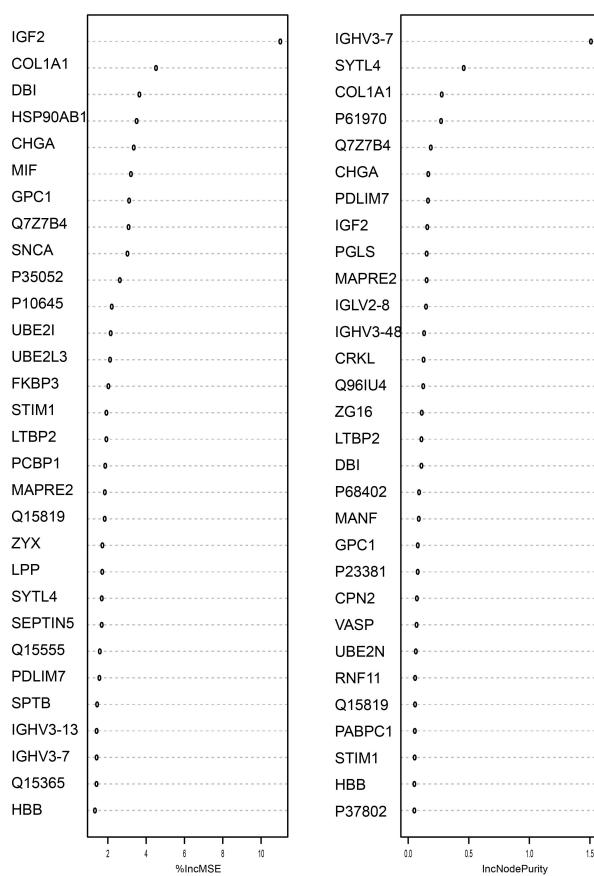


Figure S2.GSEA enrichment analysis of DEP.

a

Top 30 - variable importance



b

Top 30 - variable importance

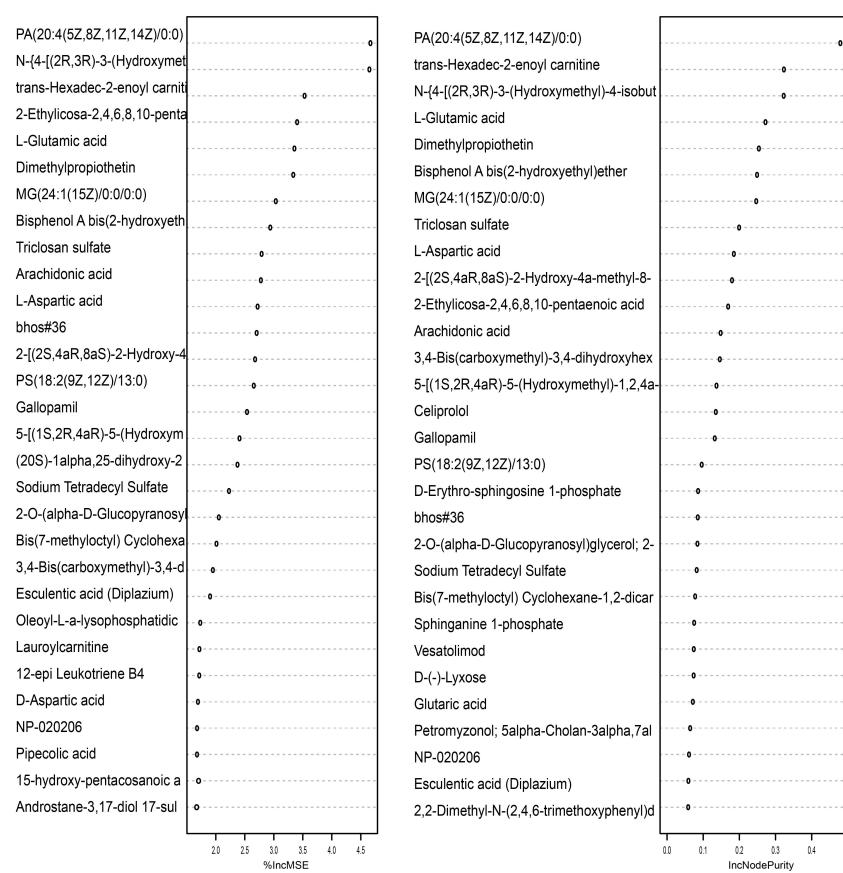


Figure S3.a. Top 30 protein predictors of high-altitude exposure based on random forest variable importance. b. Top 30 metabolic predictors of high-altitude exposure based on random forest variable importance.

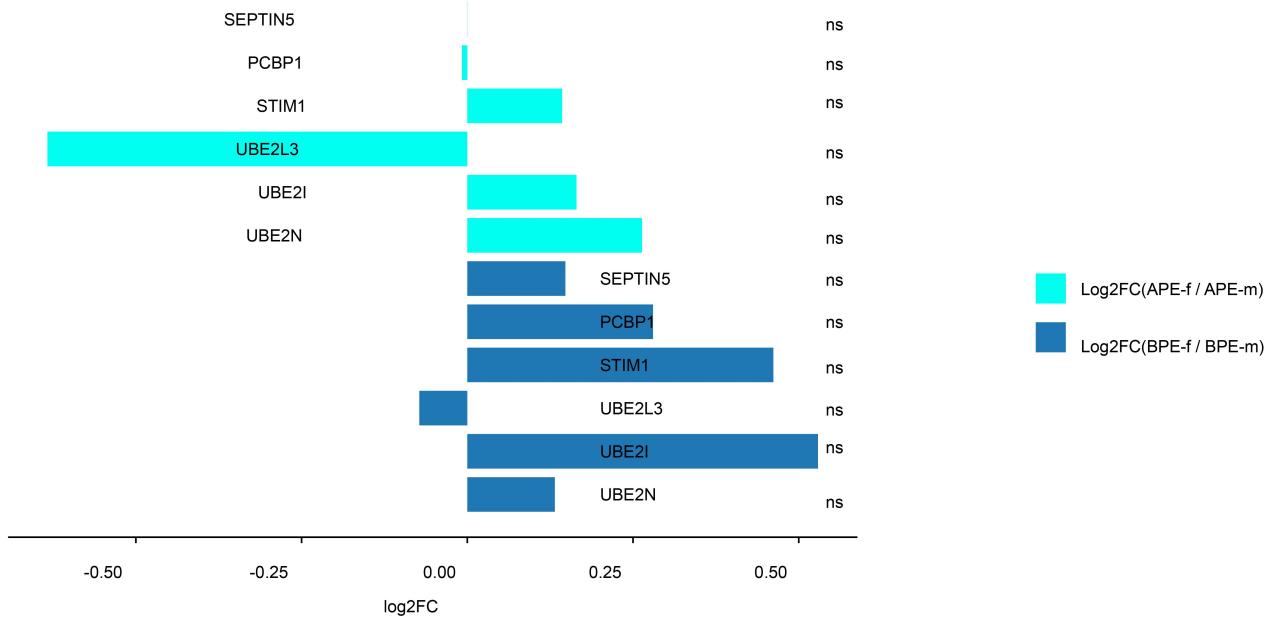
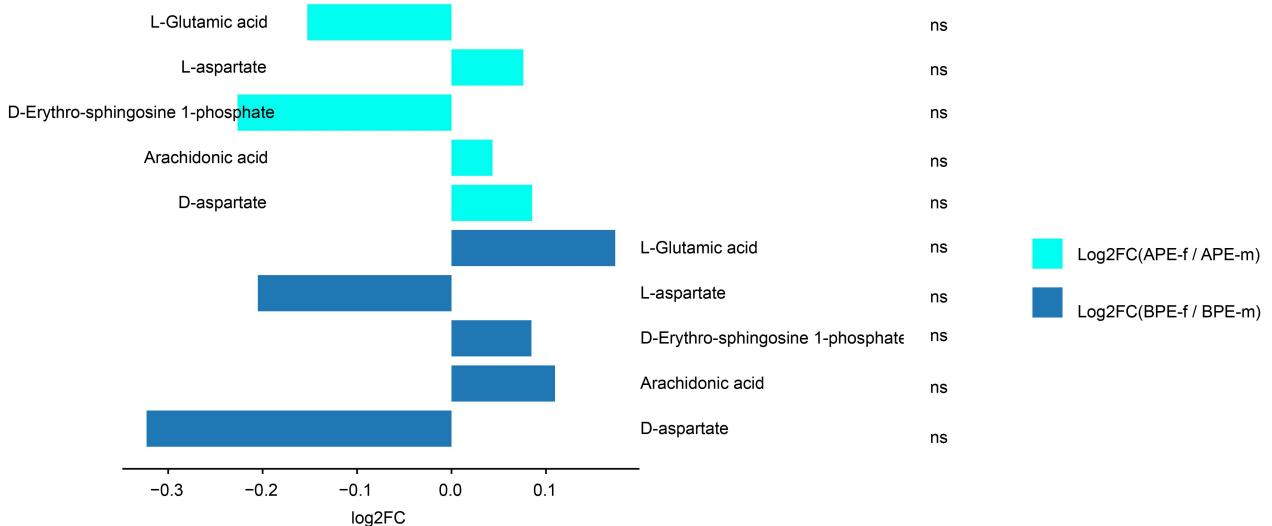
a**b**

Figure S4. a. Log2FC values of proteins (SEPTIN5, PCBP1, STIM1, UBE2L3, UBE2I, UBE2N) in APE-f/APE-m and BPE-f/BPE-m. b. Log2FC values of metabolites (L-glutamic acid, L-aspartic acid, arachidonic acid, D-aspartic acid, and S1P) in APE-f/APE-m and BPE-f/BPE-m. APE-f: Female group after plateau exposure; BPE-f: Female group before plateau exposure; APE-m: Male group after plateau exposure; BPE-m: Male group before plateau exposure. ns, $p > 0.05$.

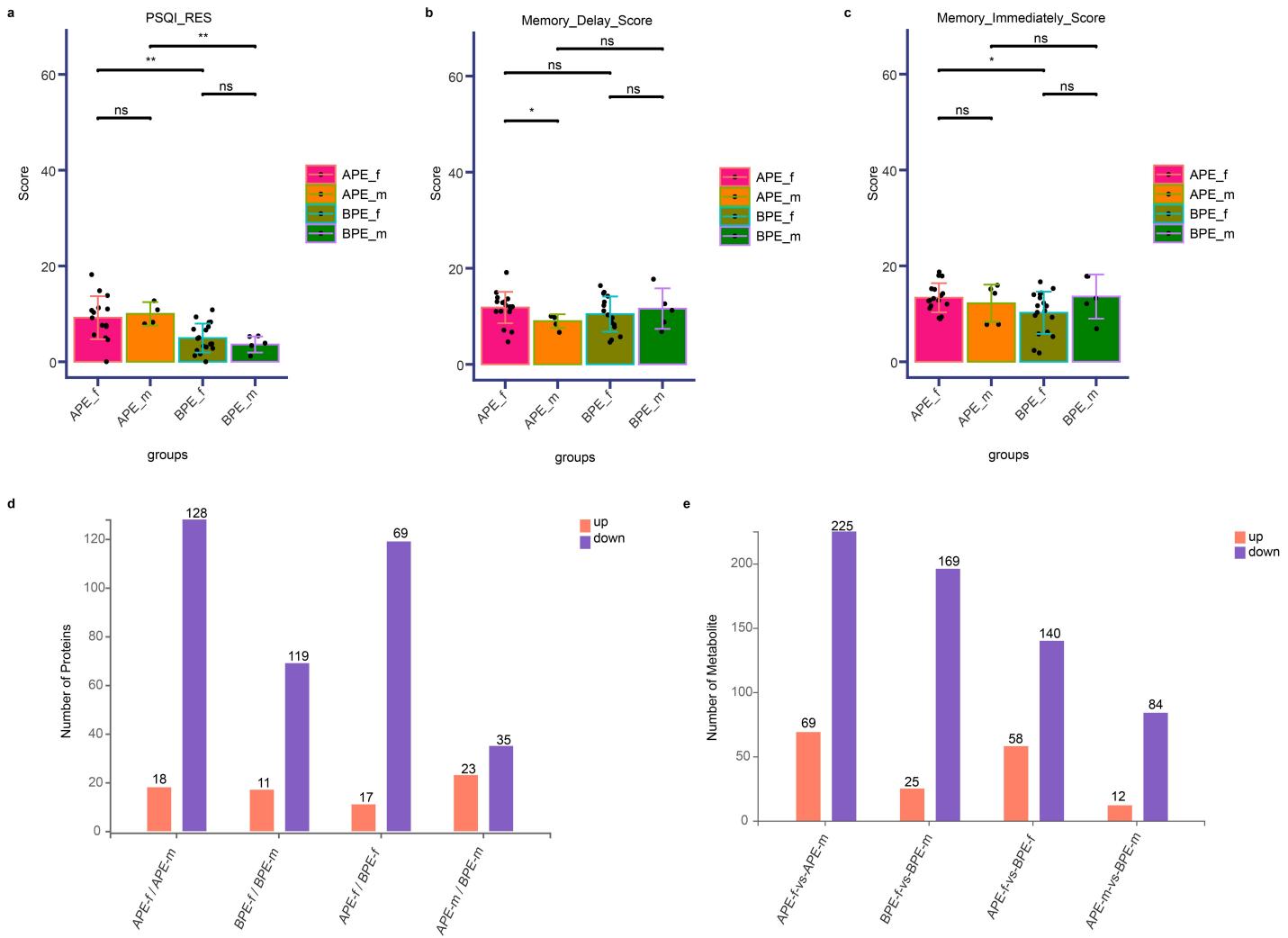


Figure S5.a. Bar chart of t-test analysis of differences between groups after grouping PSQI_RES by gender. b. Bar chart of t-test analysis of differences between groups after grouping Memory_Delay_Score by gender. c. Bar chart of t-test analysis of differences between groups after grouping Memory_Immediately_Score by gender. d. Number of differentially expressed proteins between groups after grouping proteome by gender. e. Number of differentially expressed metabolites between groups after grouping metabolome by gender. APE-f: Female group after plateau exposure; BPE-f: Female group before plateau exposure; APE-m: Male group after plateau exposure.

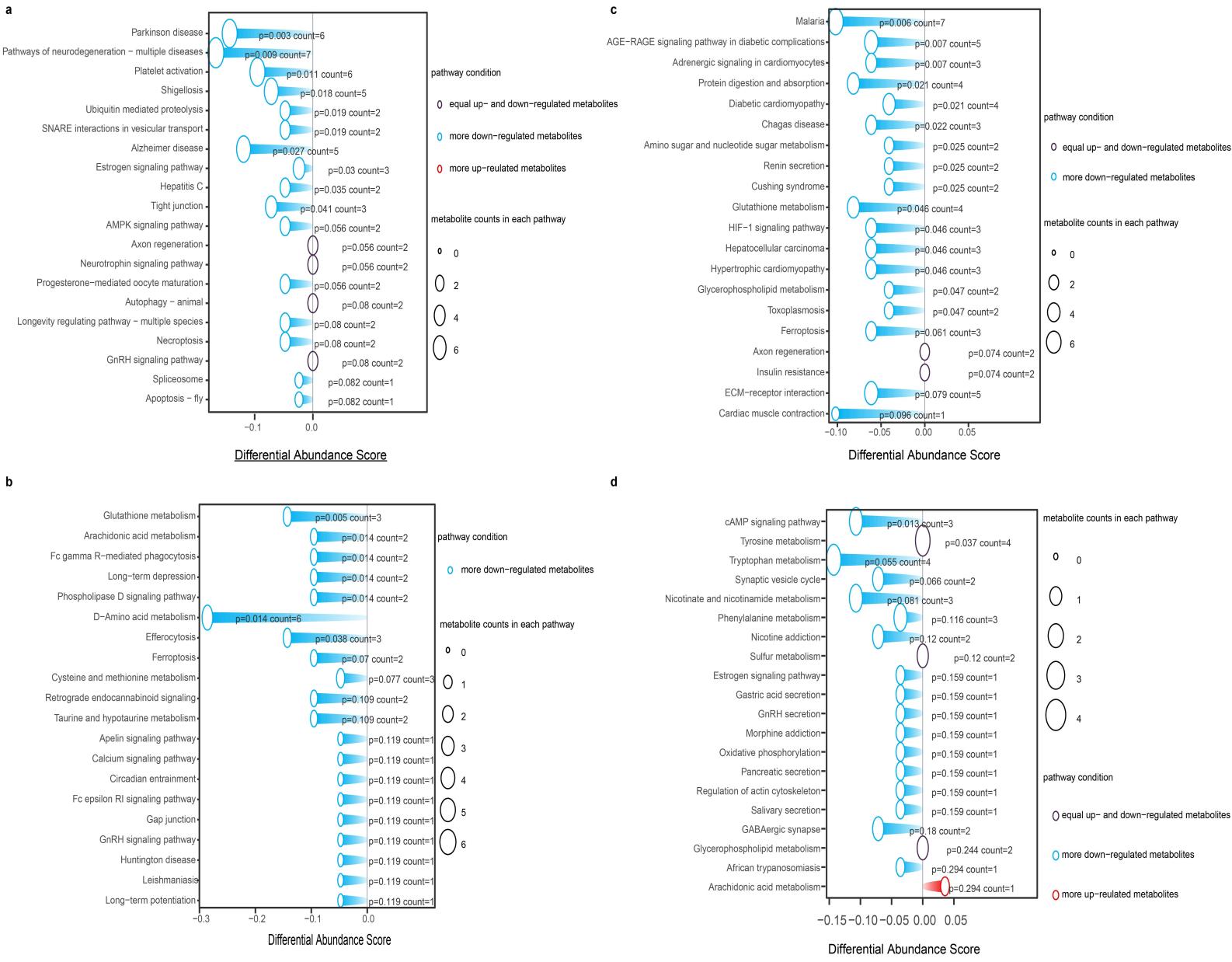
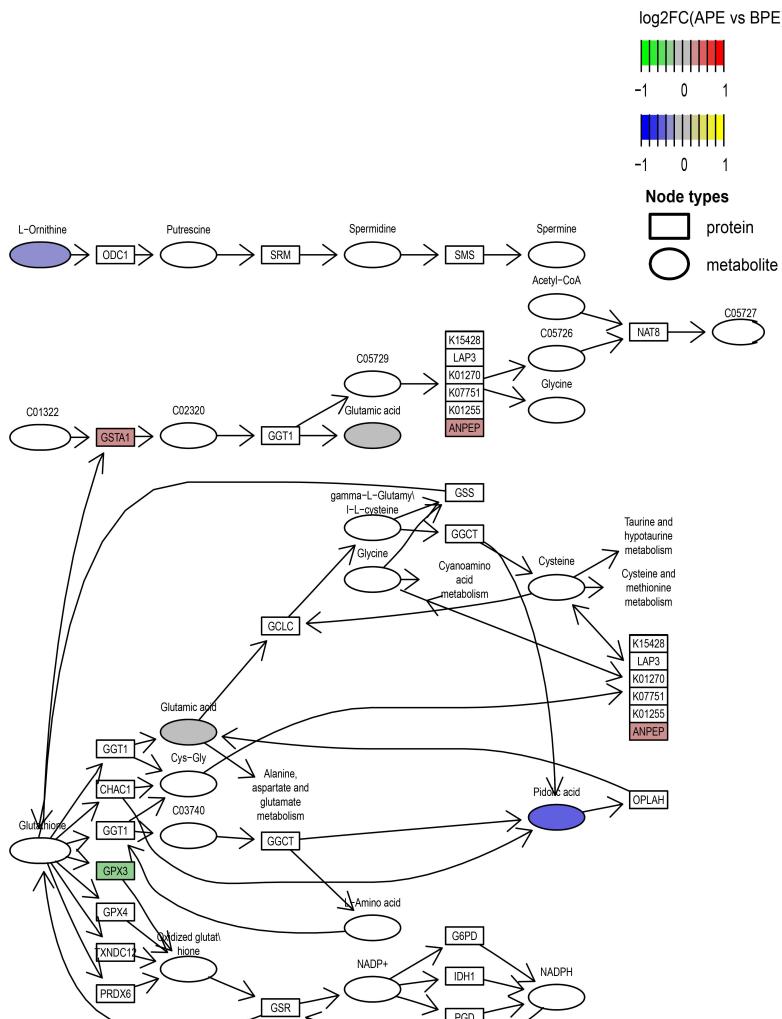
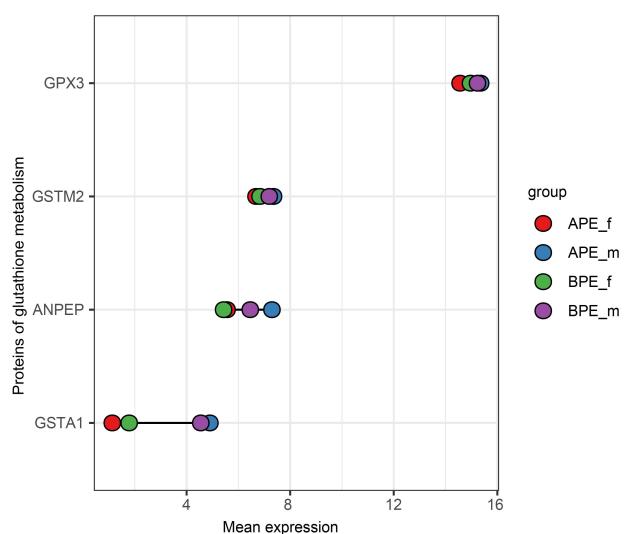


Figure S6. a. Top 20 KEGG enrichments of DEPs in the comparison group between APE-f and BPE-f. b. Top 20 KEGG enrichments of DEMs in the comparison group between APE-f and BPE-f. c. Top 20 KEGG enrichments of DEPs in the comparison group between APE-f and APE-m. d. Top 20 KEGG enrichments of DEMs in the comparison group between APE-f and APE-m. APE-f: Female group after plateau exposure; BPE-f: Female group before plateau exposure; APE-m: Male group after plateau exposure.

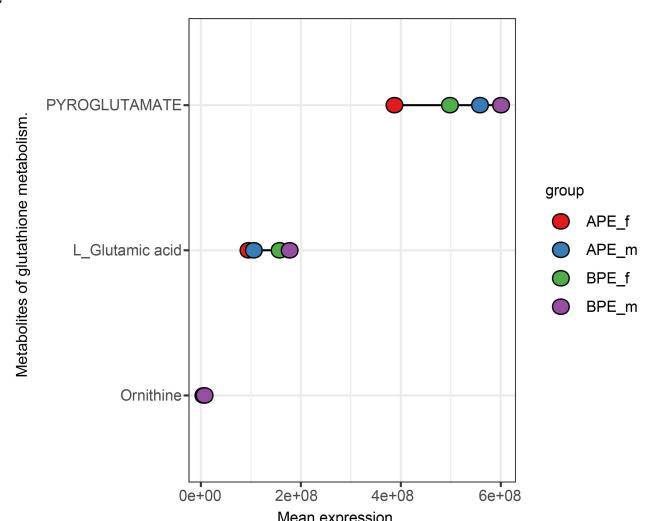
a



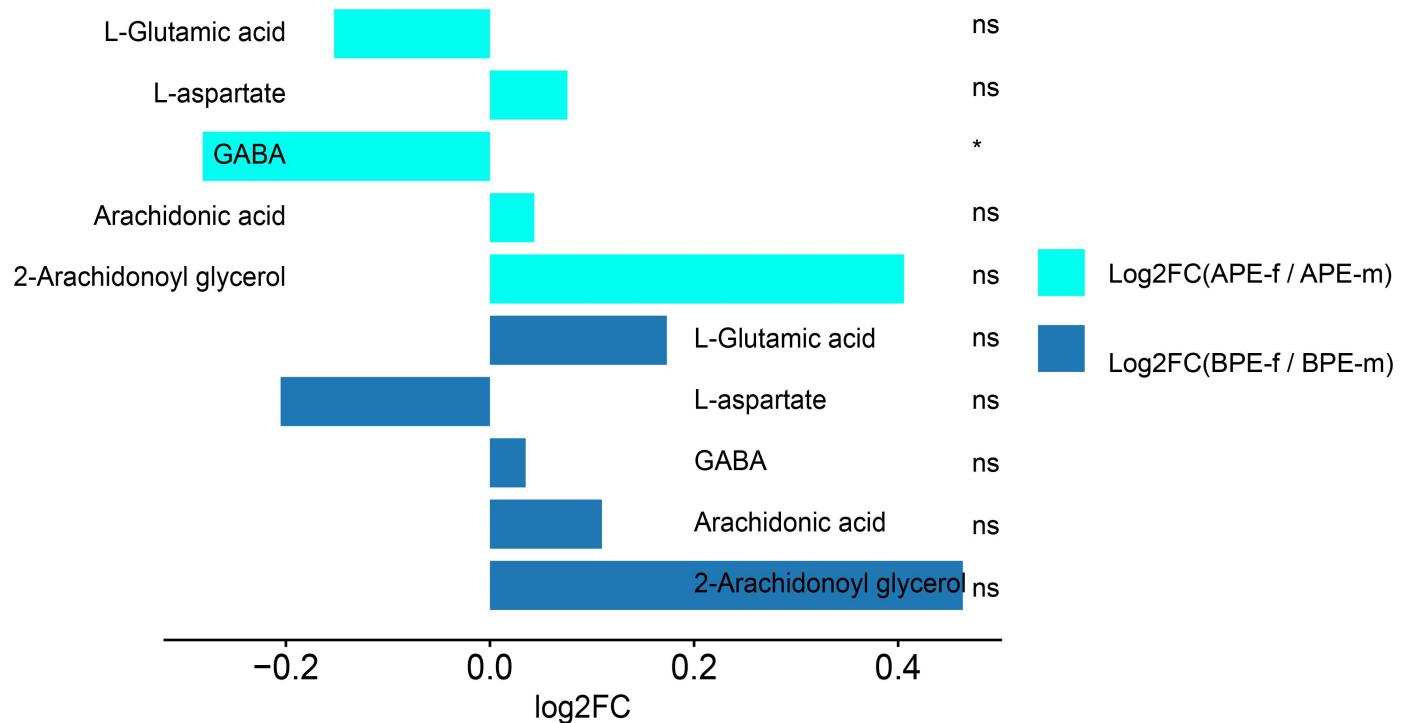
b



c



FigureS7.a.Glutathione metabolism KEGG pathway diagram. b.Comparison of the mean expression values of differentially expressed proteins involved in glutathione metabolism in each group. c.Comparison of the mean expression values of differentially expressed metabolites involved in glutathione metabolism in each group.



FigureS8. Log2FC values of metabolites (GABA, arachidonic acid, L-glutamic acid, 2-arachidonoyl glycerol, and D-aspartic) in APE-f/APE-m and BPE-f/BPE-m. APE-f: Female group after plateau exposure; BPE-f: Female group before plateau exposure; APE-m: Male group after plateau exposure; BPE-m: Male group before plateau exposure. ns, p > 0.05; *, p < 0.05.