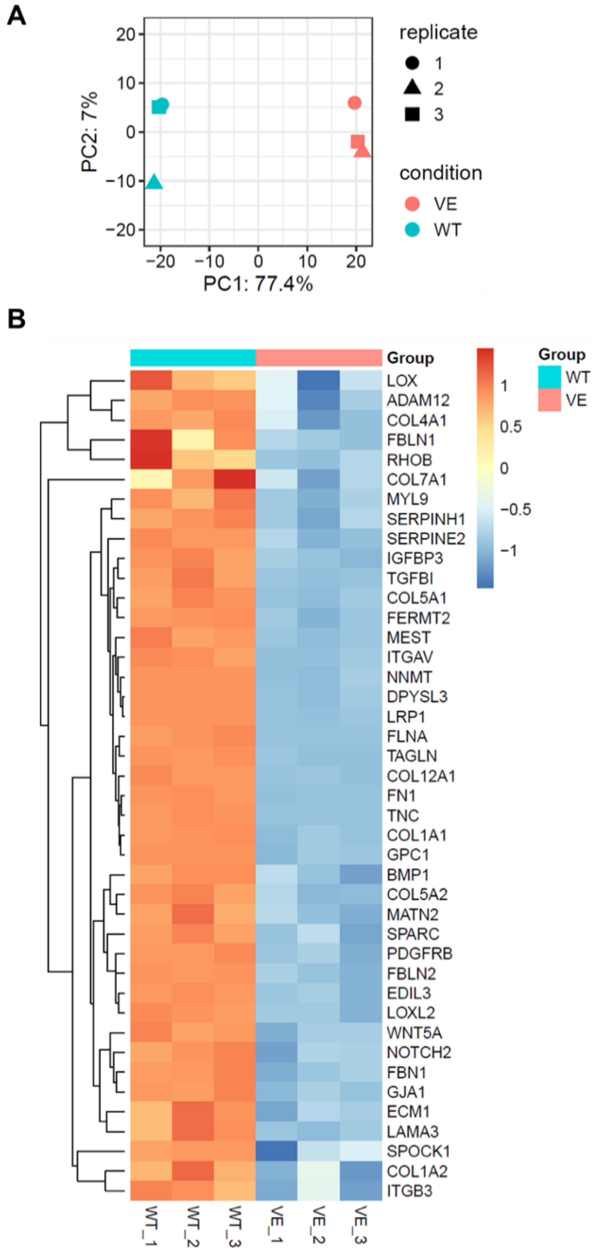
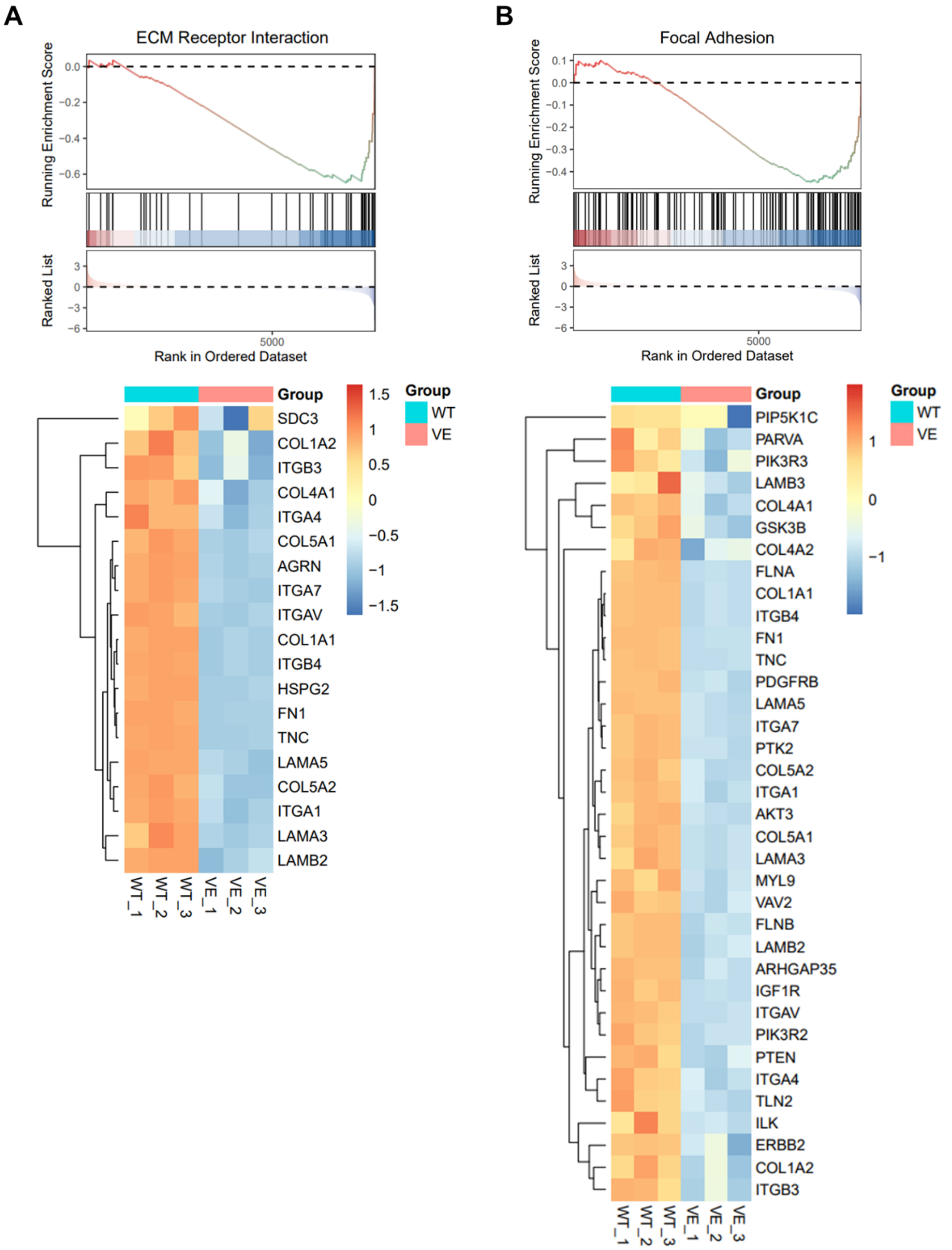
Proteomic and metabolomic dissection of the BRAF V600E mutation-induced cellular state transition in the lung epithelial cells

Fengting Liu, Fan Yang, Hailin Xiong, Jingnan Huang, Zhenhui Huang, Jingying Song, Xinyi Liu, Hongchao Zhou, Jing Xu, Jimin Yuan, Lin Jia, Lingyun Dai

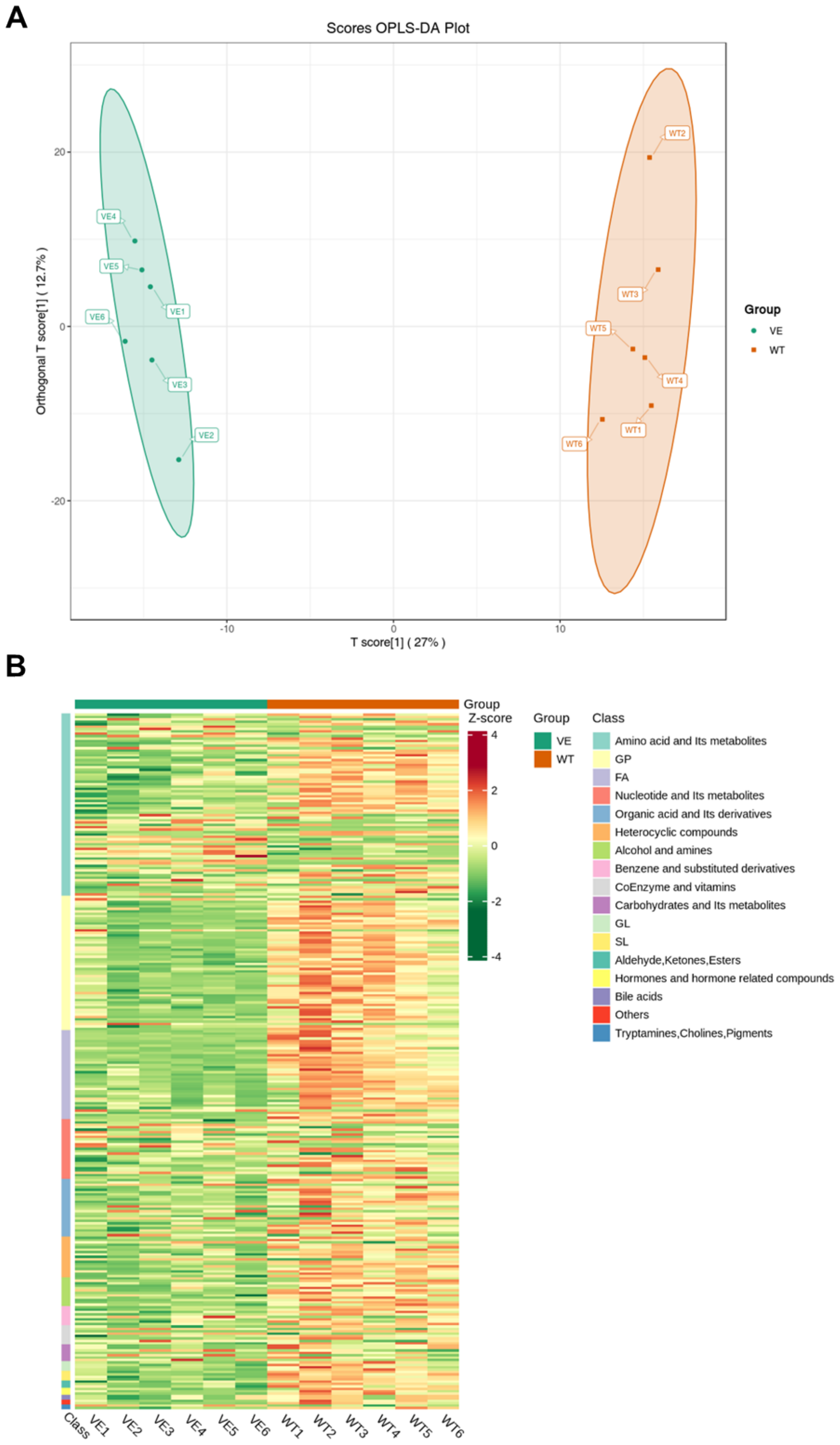
Supplementary Figures



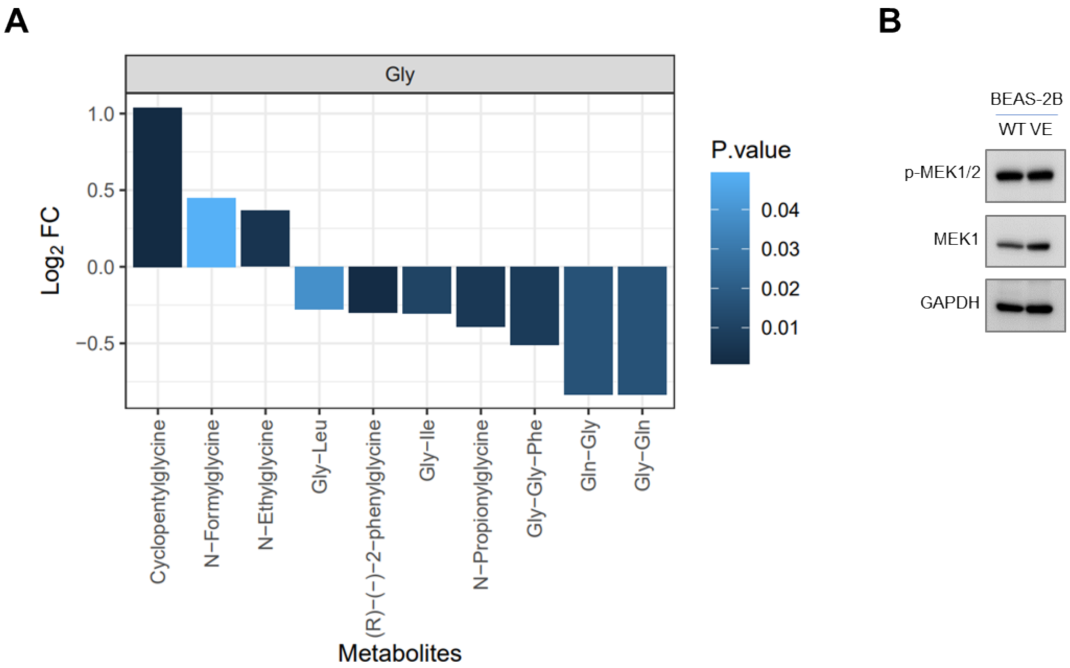
Supplementary Figure 1 Proteomics analysis of BEAS-2B-VE and BEAS-2B-WT cells. (**A**) PCA plot of normalized proteomics data. (**B**) The heatmap of core enrichment proteins of the EMT pathway.



Supplementary Figure 2 Proteomics analysis of BEAS-2B-VE and BEAS-2B-WT cells. (**A**) The GSEA result (top panel) and heatmap (bottom panel) of core enrichment proteins of ECM receptor interaction pathway. (**B**) The GSEA result (top panel) and heatmap (bottom panel) of core enrichment proteins of focal adhesion pathway.



Supplementary Figure 3 Metabolomics analysis of BEAS-2B-VE and BEAS-2B-WT cells. (**A**) OPLS-DA plot of metabolomics data. (**B**) The heatmap of the differential metabolites, grouped by the classes to which the metabolites belong.



Supplementary Figure 4 Metabolomics analysis of BEAS-2B-VE and BEAS-2B-WT cells. (**A**) The fold changes of glycine-related differential metabolites in BEAS-2B-VE cells vs BEAS-2B-WT cells. (**B**) Western blot analysis of phospho-MEK1/2 and MEK1 protein.