

Figure S14

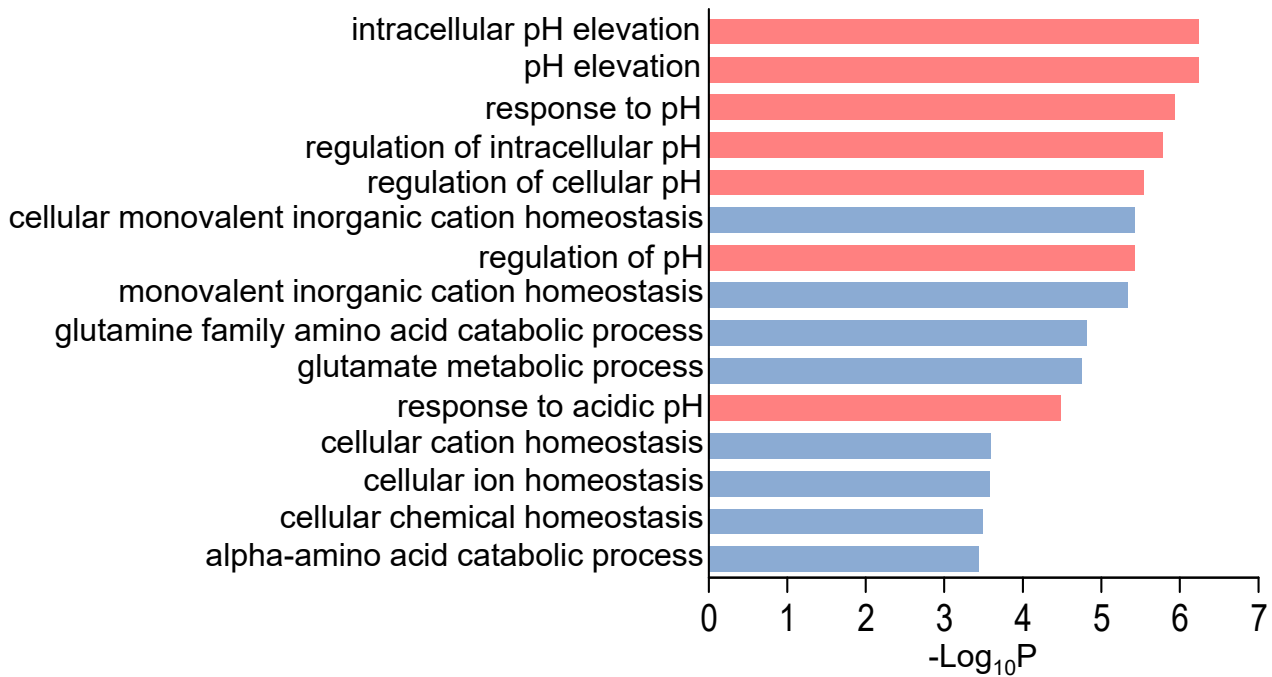


Figure S14. Bioinformatic analysis of the up-regulated genes using KOBAS3.0.

RNA-seq analysis was performed in BW25113 cells under conditions of high and low BacFlash activity. The genes upregulated by ≥ 5 folds were analyzed. Note that pH response pathways (marked in red) were highly enriched.