Abstract

According to a recent report, a low Ki67 level after short-term preoperative hormone therapy (post-Ki67) might suggest a more favorable prognosis compared with a high post-Ki67 level in patients with hormone receptor-positive/human epidermal growth factor 2-negative (HR+/HER2-) breast cancer with high levels of Ki67. This study aimed to evaluate the pre-treatment genetic differences between these two patient groups. Forty-five luminal B-like patients were stratified into two groups, namely, a group with high (H→H) and one with low (H→L) Ki67 levels after short-term preoperative aromatase inhibitor (AI) treatment. We compared pre-treatment gene expression profiles between the two groups. In gene level analysis, there was no significant difference between the two groups by the class comparison test. In pathway analysis, five metabolism-related gene sets were significantly upregulated in the H→L group ($P \leq 0.05$). In the search for novel targets, five genes (*PARP*, *BRCA2*, *FLT4*, *CDK6*, and *PDCD1LG2*) showed significantly higher expression in the H→H group ($P \leq 0.05$). Several metabolism-related pathways were associated with sensitivity to AI. In the future, it will be necessary to seek out new therapeutic strategies for the poor prognostic group with high post-Ki67.