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Erratum to: Integrative analysis of multi-omics data for identifying multi-markers for diagnosing pancreatic cancer

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Erratum
After publication of this article [1] it was brought to the Editors' attention that there were inaccurate descriptions of validation data in its abstract and list of abbreviations. For the validation, we used the three datasets from Gene Expression Omnibus (GEO), not the Cancer Genome Atlas (TCGA).

The corrected description for line 8–10 in abstract is as below:

"For selecting even more reliable and robust markers, we performed validation by independent datasets from the Gene Expression Omnibus (GEO) data depository."

In page 9, the corrected description of list of abbreviations used is as follows:

"AUC, Area under curve; BA, Balanced accuracy; BR, Breast cancer; GEO, Gene Expression Omnibus; GO, Gene ontology; HCC, Hepatocellular carcinoma; LC, Lung cancer; LOOCV, Leave-one-out cross-validation; LP, Lymphoma; mRNA, messenger RNA; miRNA, microRNA; PDAC, Pancreatic ductal adenocarcinoma; SVM, Support vector machine;"

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Reference
1. Kwon M-S, et al. Integrative analysis of multi-omics data for identifying multi-markers for diagnosing pancreatic cancer. BMC Genomics. 2015;16 Suppl 9:S4.

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