RETRACTION

To the Editor:

In the December issue, we reported the results of a study formed to determine whether *WASF2* and *GALE* genes are responsible for pure benign familial infantile convulsion syndrome.¹ One exonic variant (1047A→G) and one intronic variant (IVS10+13G→A), neither causing a modification of the physiological messenger RNA maturation, were found. We regretfully report that our previous results (single nucleotide polymorphisms [SPNs] IVS10 + 13→G in *GALE* and 1047A→G in *WASF2*) are incorrect. The error was discovered when we tried to repeat the analysis to confirm our results. The same batches of samples were used for polymerase chain reaction and DNA sequencing. No SPNs were found in figures 1 to 4.

Also, in the Chinese National Laboratory of Medical Genetics, our colleague, Prof Tang Bei Sha (presided by the China National Nature Science Foundation Committee to fund a major research project, of which, our research is a small part), temporarily failed to confirm our results. We suppose that the errors we listed before were caused

by a systematic dysfunction in the equipment and by Taq DNA polymerase (that already contained MgCl₂) instability. Our original conclusion that “(1047A→G) and (IVS10 + 13G→A)” is inconsistent with this body of knowledge. We have to form a team to conduct further study and provide new conclusions.

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■ REFERENCE

1. Xiaohong Z, Abuhamed M, Ya-Qin W. Mutation analysis of *WASF2* and *GALE* genes in one Chinese family with benign familial infantile convulsions with a novel locus. *J Investig Med*. 2007;55:439–443.