ERRATUM

Identification of a novel recombinant mutation in Korean patients with Gaucher disease using a long-range PCR approach

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During typesetting of the above paper, incorrect text was applied to Figures 1 and 2, and was published as such. The publishers apologize for the same and are now happy to correct this mistake.

In Figure 1a i, *Gene conversion alleles*: GBA-f+ψMTX1-r → GBA-f+GBA-r (~6.5 kb) should have read *Gene conversion alleles*: GBA-f+ψMTX1-r → GBA-f+GBA-r (~6.5 kb).

In Figures 2a i and ii, *MTX1P* should have read *MTX1*.

The correct figures are shown below:

Figure 1 Amplification of β-glucocerebrosidase (*GBA*) recombinant alleles using three sets of long-range PCR primers. (a) Schematic representation of three types of predicted *GBA* recombinant alleles. *GBA* and *MTX1* genes are represented by the closed box above the line and slashed box below the line with their pseudogenes (ψ), respectively. The PCR primer locations and directions used for amplification of the *GBA* recombinant alleles are indicated with their names, and putative lengths of amplicons are indicated. Asterisk (*) indicates a non-recombinant, intact *GBA* locus next to the reciprocal gene duplication allele after the recombination occurs. (b) Agarose gel images of the long-range PCR amplification from genomic DNAs of a normal control (NC) (wt/wt) and patient control (PC) (G46E/L444P), and four patients (P1–P4). The primer pairs used for PCR are indicated below each panel.

Figure 2 Southern blot analysis of genomic DNAs digested with *SspI* restriction enzyme. **(a)** Schematic representation of the *SspI* digestion sites in proximity to β -glucocerebrosidase (*GBA*) and *MTX1* and their pseudogenes on the normal allele of a normal control (NC), point mutation allele (G46E or L444P) of a patient control (PC), gene conversion alleles (Rec 1a and Rec 8a) of P1 and P2 and reciprocal gene fusion allele (Rec 1b) of P3. The expected sizes by *SspI* digestion are indicated. **(b)** Autoradiographic images of the Southern blot analysis from genomic DNAs ($\sim 20 \mu\text{g}$) of a NC (wt/wt), a PC (G46E/L444P), P1 (R496H/Rec 1a), P2 (G46E/Rec 8a) and P3 (F213I/D315E+Rec 1b). In the lane of P3, the 17- and 12-kb bands generated from the normal allele and the 13.6-kb band generated from the reciprocal gene fusion allele are indicated.