PLOS ONE

CORRECTION

Correction: Targeted Next-Generation Sequencing for Clinical Diagnosis of 561 Mendelian Diseases

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S3, S4 and S5 Tables appear incorrectly in the published article. Please see the correct tables below.

Supporting Information

S3 Table. The list of 561 Mendelian diseases.
(XLSX)

S4 Table. Results of normalization analysis of three patients (P88, P89 and P90). We detected a microduplication of chromosome 10 in patient P88, the gender ratio was about 1.42. We detected a microduplication of chromosome 9 in patient P89, the gender ratio was about 1.31. We detected a microdeletion in chromosome 17 (16773072–20222149) in patient P90, the gender ration was about 0.55.
(DOC)

S5 Table. Primer pairs designed for validation of mutations by Sanger sequencing or real-time PCR.
(DOC)

Reference

1. Liu Y, Wei X, Kong X, Guo X, Sun Y, Man J, et al. (2015) Targeted Next-Generation Sequencing for Clinical Diagnosis of 561 Mendelian Diseases. PLoS ONE 10(8): e0133636. doi:10.1371/journal.pone.0133636 PMID: 26274329

Citation: Liu Y, Wei X, Kong X, Guo X, Sun Y, Man J, et al. (2016) Correction: Targeted Next-Generation Sequencing for Clinical Diagnosis of 561 Mendelian Diseases. PLoS ONE 11(1): e0148154. doi:10.1371/journal.pone.0148154

Published: January 28, 2016