Correction

The authors of "Essential and nonredundant roles for Diaphanous formins in cortical microtubule capture and directed cell migration" (Mol. Biol. Cell [2014] 25, 658–668; originally published in *MBoC In Press* as 10.1091/mbc.E13-08-0482) wish to make a correction to the legend of Fig. 4. The original legend corresponds to an early version of the figure and not to the published version of the figure. One sentence of the legend should not be there because it refers to a panel that had been moved to the supplemental materials section. The correct legend is below.

The HTML and PDF versions were corrected on the *Molecular Biology of the Cell* website on June 16, 2015. These corrections may not appear on copies of the article that reside on other websites.

FIGURE 4: Rab6IP2 interacts with FH2 and contributes to microtubule capture. (A) Identification of proteins interacting with the FH2 domain of mDia1. Volcano plot showing the proteins associating with EGFP-FH2 relative to the control bait, identified by mass spectrometry. Fold change vs. significance (ANOVA) are plotted. Right, zoom on the proteins of highest interest. A typical experiment is shown. Proteins that are reproducibly found in biological replicates (see Table 1) are labeled (UniProt nomenclature). DIAP1, DIAP3, and RB6I2 correspond to mDia1, mDia2, and Rab6IP2, respectively. (B) Role of Rab6IP2, HAX1, and IQGAP1 in microtubule capture. Cells were transfected with the indicated siRNAs. The percentage of cells showing peripheral microtubules was evaluated as described in Figure 1. Mean ± SEM; $*p < 0.01$. (C) Rab6IP2 binds to full-length mDia1 and IQGAP1. An immunoprecipitation using GFP-Trap beads was performed on EGFP-Rab6IP2– or EGFP-expressing cell lysates; binding of ectopically expressed mDia1 and IQGAP1 was visualized by Western blotting. (D, E) Recruitment of Rab6IP2 to cell membranes and ruffles is dependent on mDia1. SKBr3 cells were transfected with mDia1 siRNA for 48 h, before addition of HRG for 20 min. EGFP-Rab6IP2 immunofluorescence was visualized by confocal microscopy (D). The percentage of cells showing membrane labeling was evaluated (E). A total of 300 cells were counted for each condition in three independent experiments. Mean ± SEM; $*p < 0.01$.