Correction

The authors of "The alternate AP-1 adaptor subunit Apm2 interacts with the Mil1 regulatory protein and confers differential cargo sorting" (Mol. Biol. Cell [2016] 27, 588–598; originally published in *MBoC In Press* as 10.1091/mbc.E15-09-0621) wish to make a correction to Figure 4G of the article. In the original HTML and PDF versions, the bottom (horizontal) label incorrectly read "*apm2Δ*." This label has been changed to "*mil1Δ*" in the corrected figure below.

The HTML and PDF versions were corrected on the *Molecular Biology of the Cell* website on July 5, 2016. These corrections may not appear on copies of the article that reside on other websites.

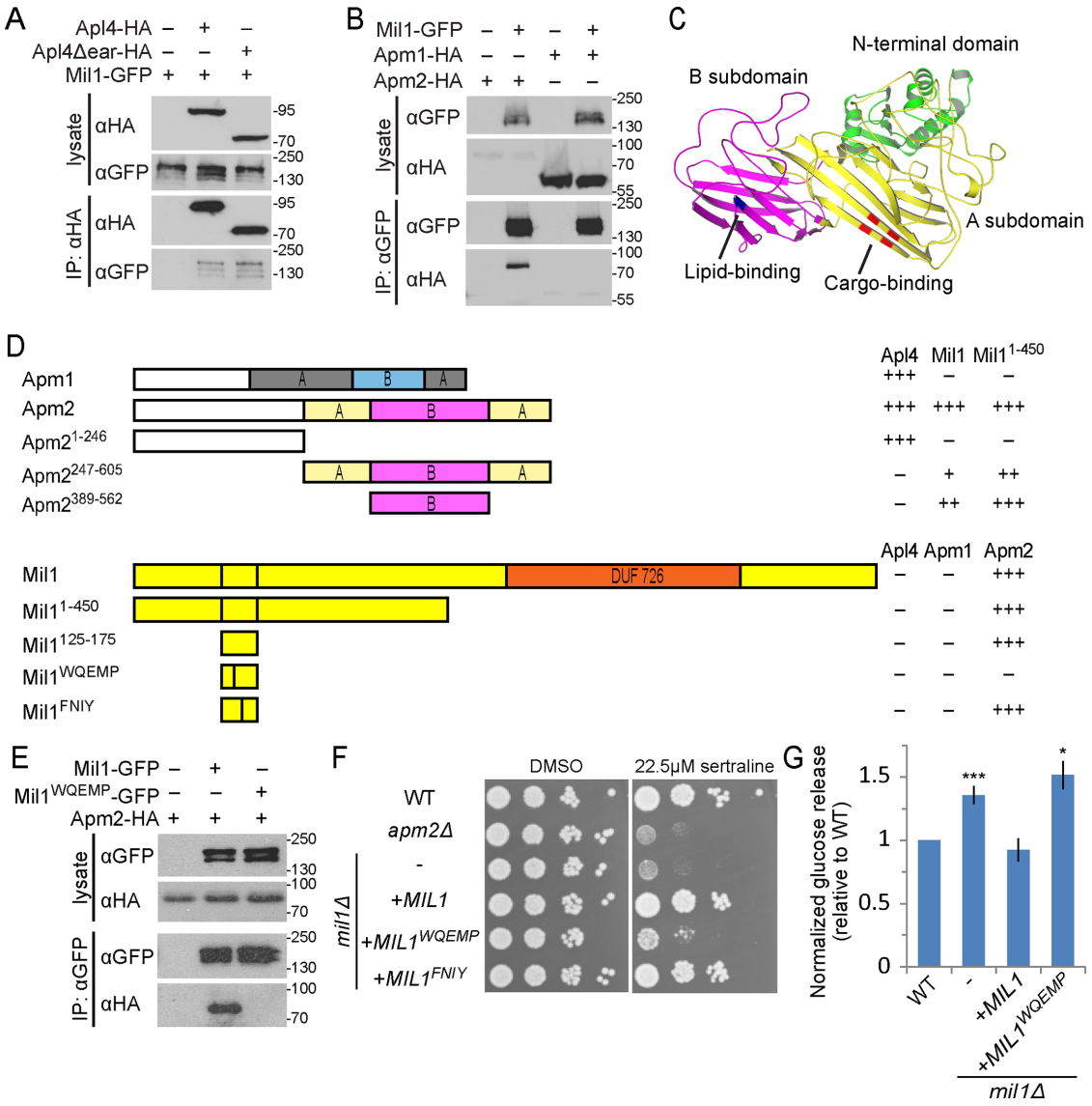

FIGURE 4: Mil1 interacts with Apm2 through its WQEMP motif. (A) Mil1-GFP copurified with immunoprecipitated Apl4-3HA and with a truncated version lacking the γ appendage (Apl4Δear-HA) known to bind several AP-regulatory proteins. Loading of lysate relative to immunoprecipitate was 1:9. All proteins were genomically tagged. (B) Pull down of Mil1-GFP in strains coexpressing either Apm1-3HA or Apm2-3HA shows that Mil1 binds specifically to Apm2. All proteins were genomically tagged. (C) Phyre2 homology model of Apm2, colored to indicate the N-terminal AP-binding domain (green) and a C-terminal region composed of A (yellow) and B (magenta) subdomains. Key residues predicted to be involved in YxxΦ binding (red) or lipid binding (blue) based on alignment with regions of AP-1 and AP-2 μ subunits are indicated. (D) Yeast two-hybrid mapping of Apm2-Mil1–binding domains. Full-length or truncated Apm2 constructs were fused to the GAL4 DNA-binding domain (GBD), and full-length, truncated, or mutated Mil1 constructs were fused to the GAL4-activating domain (GAD). Qualitative interaction strengths are

indicated. Mil1^{WQEMP} represents the W^{143}QEMP>AAEAA mutant, and Mil1^{FNIY} represents the F^{152}NIY>ANAA mutant. (E) Anti-GFP immunoprecipitation of plasmid-expressed wild-type Mil1-GFP or Mil1^{WQEMP}-GFP from strains coexpressing genomically tagged Apm2-3HA. (F) Sertraline sensitivity was assessed by plating strains in a 10× dilution series on YPD containing 22.5 μM sertraline or DMSO as a control. (G) The *mil1^{WQEMP}* mutant is unable to restore sorting of the Snc1 reporter GSS. Cell-surface GSS levels in the indicated strains were determined by quantifying invertase activity and normalizing to levels in wild-type cells. Unpaired *t* test compared with wild type, ***$p <$ 0.0001 and *$p < 0.05$. Error bars represent SEM ($n = 10$).