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CORRECTION

Correction: Spindle checkpoint silencing at kinetochores with submaximal microtubule occupancy (doi:10.1242/jcs.231589)

Banafsheh Etemad, Abel Vertesy, Timo E. F. Kuijt, Carlos Sacristan, Alexander van Oudenaarden and Geert J. P. L. Kops

There were errors in *J. Cell Sci*. (2019) **132**, jcs231589 (doi:10.1242/jcs.231589).

Labels for Spindly, MAD2 and ZW10 were incorrect in Fig. 2C. In Figs S1 and S2, a biological replicate of pMELT that had technical issues was inadvertently used. Replicate e2 has been replaced for pMELT in Fig. S1D,E and analysis of the pMELT samples in Fig. S3C,D,F has been corrected. The corrected main and supplementary figures are shown here, along with the original versions for reference.

The online and PDF versions of the article and the supplementary material have been updated. The authors apologise to readers for these errors, which do not impact the conclusions of the paper.

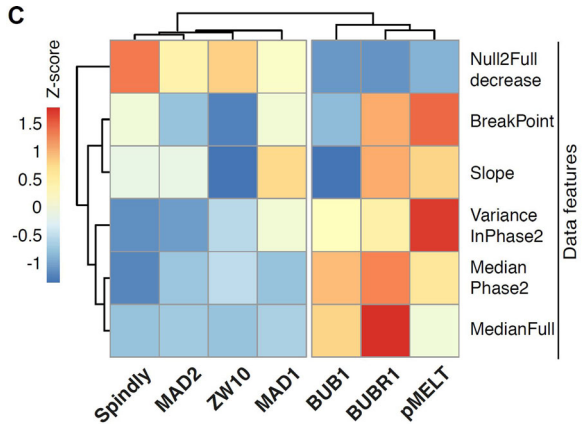

Fig. 2C (corrected panel). Microtubule attachments evoke two distinct SAC protein responses. (C) Hierarchical cluster analysis of Z-score normalized features extracted from data in Fig. 1B-H as depicted in B.

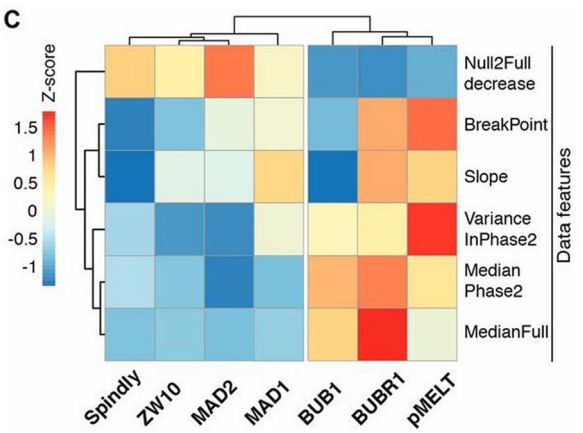

Fig. 2C (original panel). Microtubule attachments evoke two distinct SAC protein responses. (C) Hierarchical cluster analysis of Z-score normalized features extracted from data in Fig. 1B-H as depicted in B.

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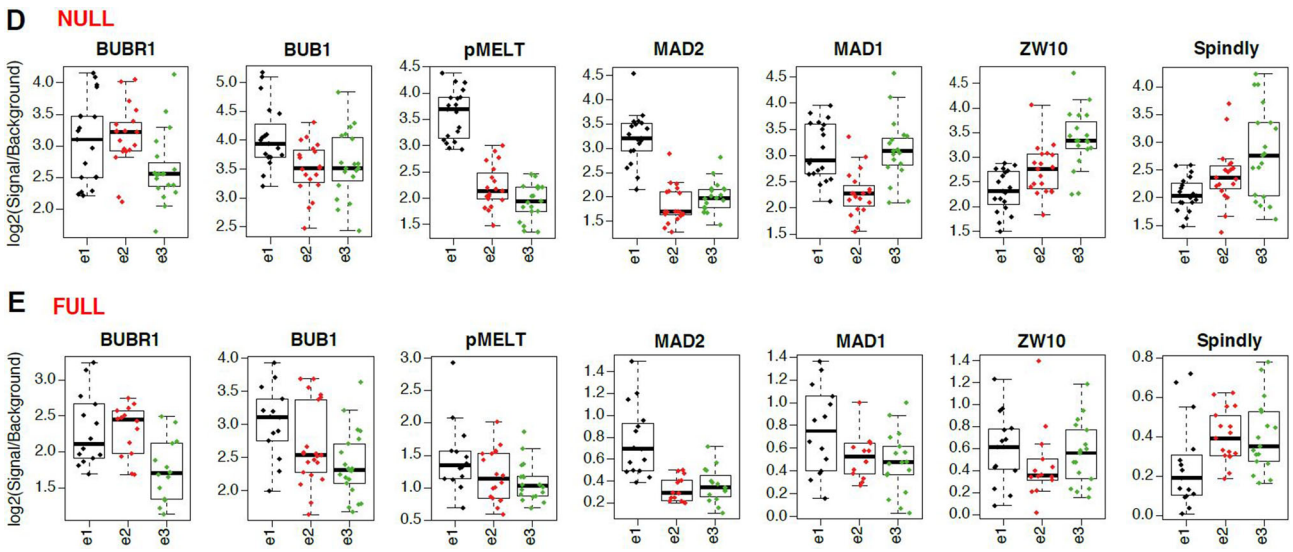
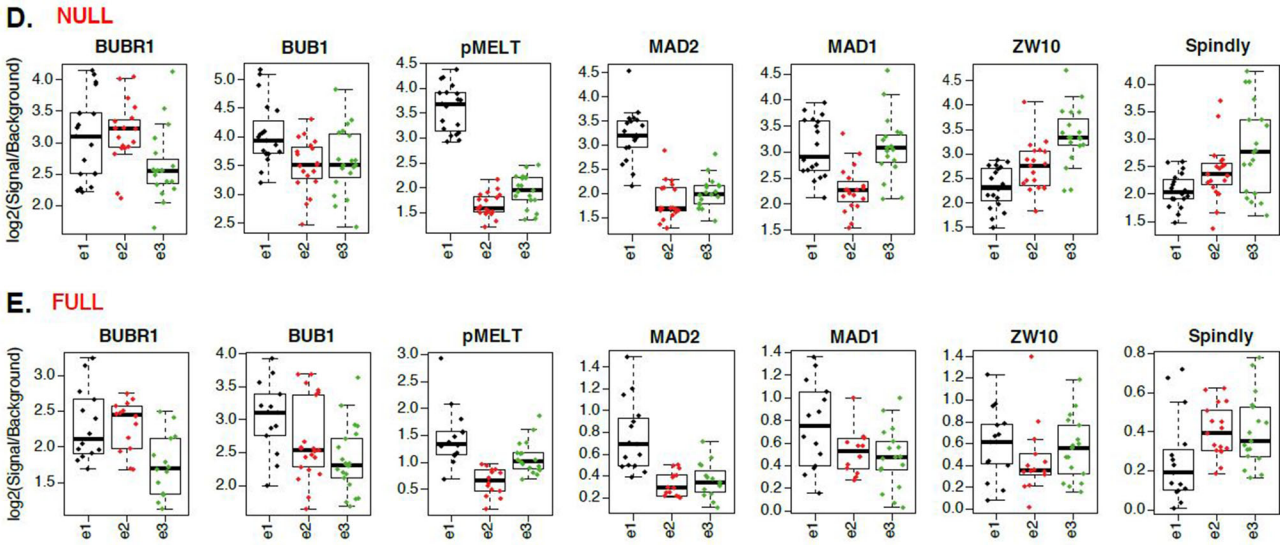


Fig. S1D,E (corrected panels). Single kinetochore measurements reveal differences between SAC protein localization independent of signal-to-noise ratios. (D,E) Signal-to-noise ratios of SAC proteins measured on kinetochores of unattached (D, 'NULL') and fully microtubule-occupied kinetochores (E, 'FULL'). Each biological replicate is plotted separately and represented by 'e1', 'e2', and 'e3'. All proteins and experiments in NULL condition (D) show similar signal-to-noise ratios, suggesting that variability in values measured in this condition is equally affected by noise across all experiments. In the FULL condition (E) signal-to-noise ratio is much better in proteins with kinetochore retention and high variation (BUB1, BUBR1, and pMELT), strongly supporting that the observed behavior (shown in Figure 1B-H) is not due to skewed signal intensities.



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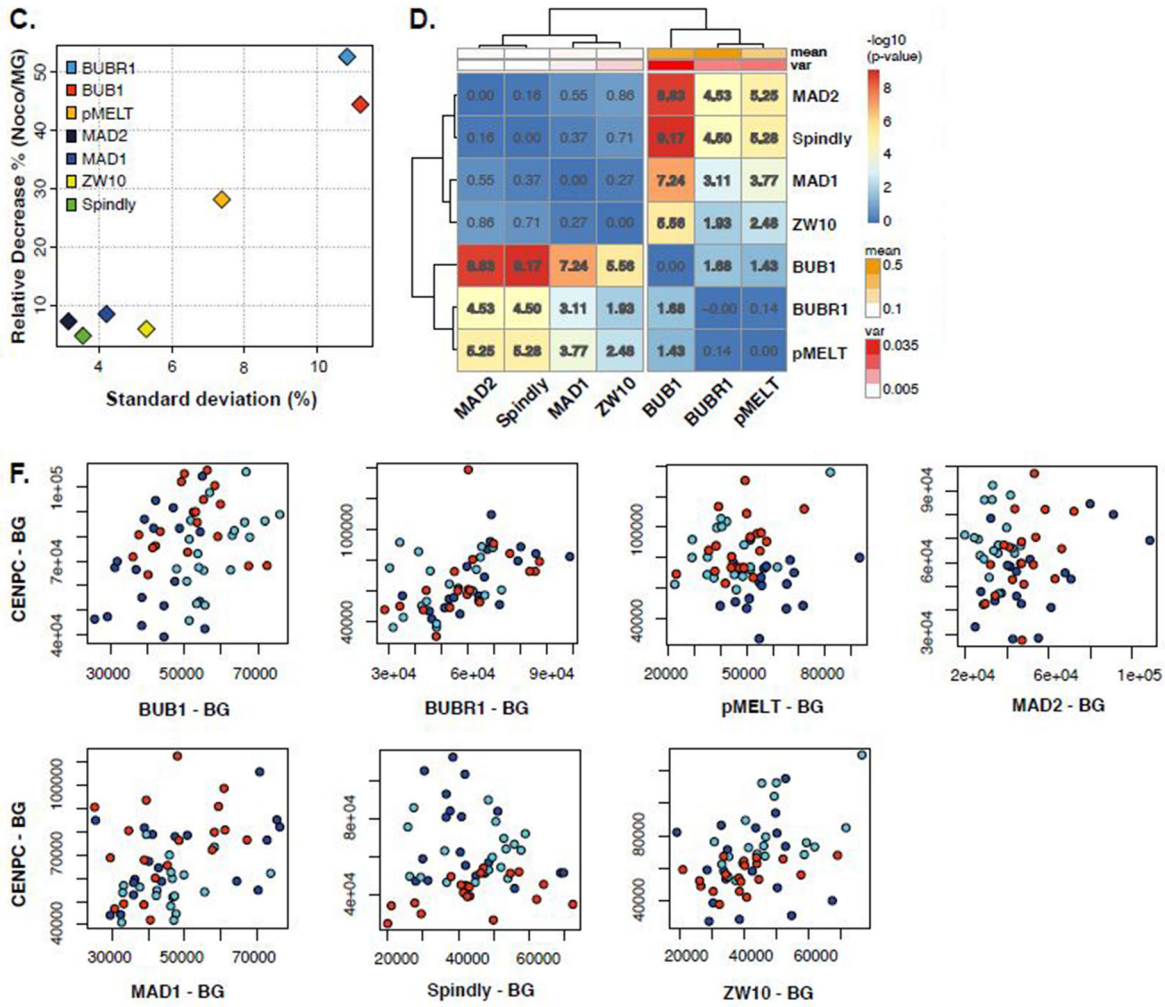

Fig. S3C,D,F (corrected panels). High variability of protein levels on unattached kinetochores is independent of CENP-C levels, the kinetochore size, antibody penetration or differences between replicates. (C) Plot depicting correlation between the relative protein decrease from NULL to FULL conditions and the standard deviation measured at FULL attachment (data shown in insets of Figure 1 B-H). (D) To test how similar the variability of the FULL datasets (insets Figure 1B-H) between different SAC proteins are, we applied pairwise Levene's test. Figure shows clustering heat map of P-values from these tests. –log10(p-values) are displayed. Significant differences are in bold. Top bars represent variance (red) and average levels (orange) of each protein. (F) Staining efficiency is similar in the biological replicates of experiments shown in Figure 1. Graphs show background (BG)-corrected levels of SAC proteins at unattached kinetochores, plotted against corresponding BG-corrected CENP-C levels. Different colors depict individual experiments.

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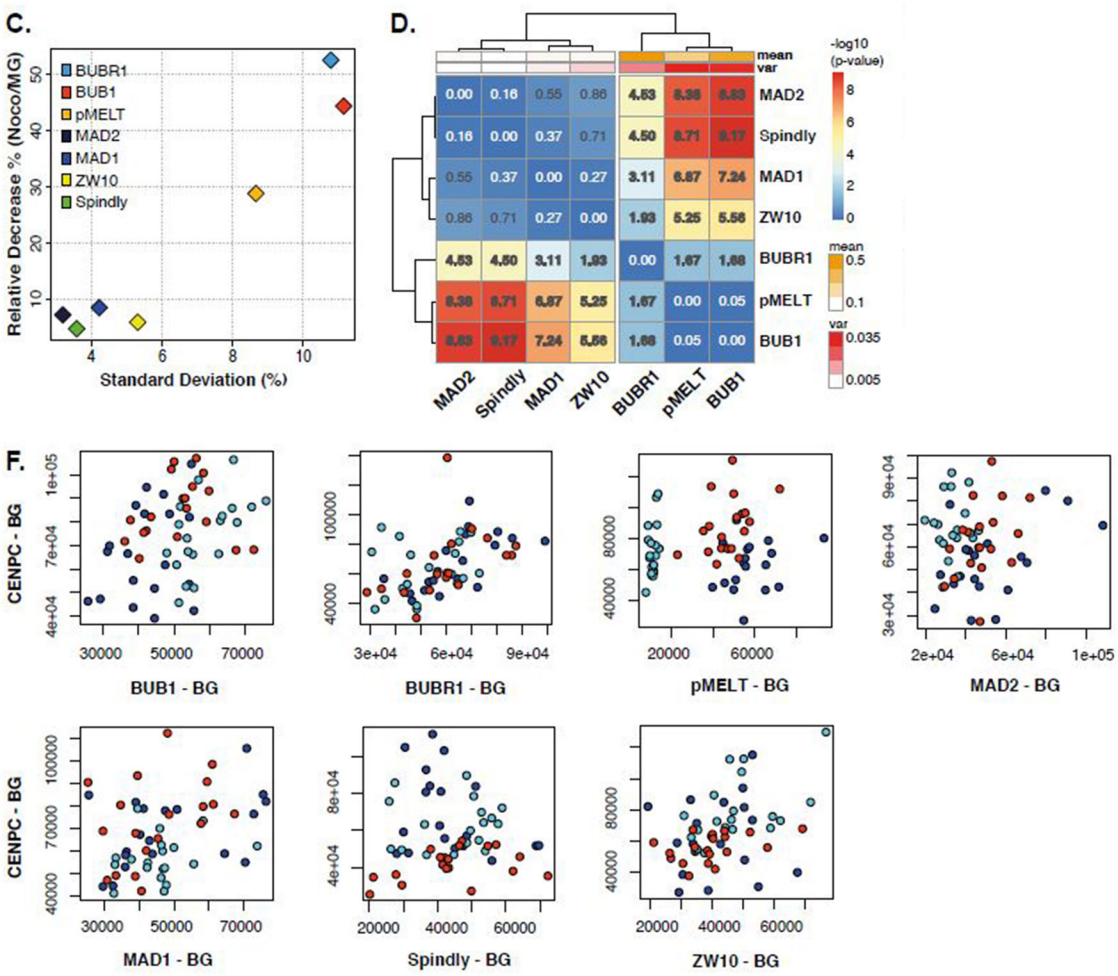

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