





Figure S2. Effect size estimations of changes in p53 fluorescence signals

(A) For the data in Figure 3A, the median difference for nuclear mKate2 comparisons between p53(V272M) and WT p53 are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (B) For the data in Figure 3B, the median difference for nuclear mKate2 comparisons between the indicated p53 mutants and WT p53 are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (C) For the data in Figure 3C, the median difference for nuclear total p53 (mKate2) comparisons, nuclear BiFC (Venus) comparisons, and nuclear BiFC/total p53 comparisons between the indicated co-expressed BiFC alleles are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (D) For the data in Figure S3B, the median difference for nuclear total p53 (mKate2) comparisons, nuclear BiFC (Venus) comparisons, and nuclear BiFC/total p53 comparisons between the indicated co-expressed BiFC alleles are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (E) For the data in Figure 4B, the median difference for BiFC/total p53 comparisons between p53(R273H) or p53(V272) and WT p53 are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (F) For the data in Figure 5C, the median difference for nuclear/cytosolic mKate2 comparisons between chaperone-overexpressing cells and empty vector are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars. (G) For the data in Figure 5D, the median difference for nuclear and cytosolic mKate2 comparisons between Sis1-overexpressing cells and empty vector are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence

interval is indicated by the ends of the vertical error bars. (H) For the data in Figure 6A, the median difference for nuclear/cytosolic mKate2 comparisons between radicicol- and DMSO-treated cells are shown in Cumming estimation plots as bootstrap sampling distributions. Each median difference is depicted as a dot. Each 95% confidence interval is indicated by the ends of the vertical error bars.