Wild-type p53 overexpression in *NPM1*-mutated acute myeloid leukemia: potential implications for disease biology and therapy response

Authors

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Group	Number of cases per group	Minimum # of cells	Maximum # of cells	Median
NPM1-mutated	33	1869	31151	10528
TP53-mutated	5	3379	23273	8598
NPM1/TP53-WT	7	2747	22935	8703
All cases	45	1869	31151	8957

Supplemental Figure 1. Total nucleated cells analyzed by MxIF across all cases/groups.
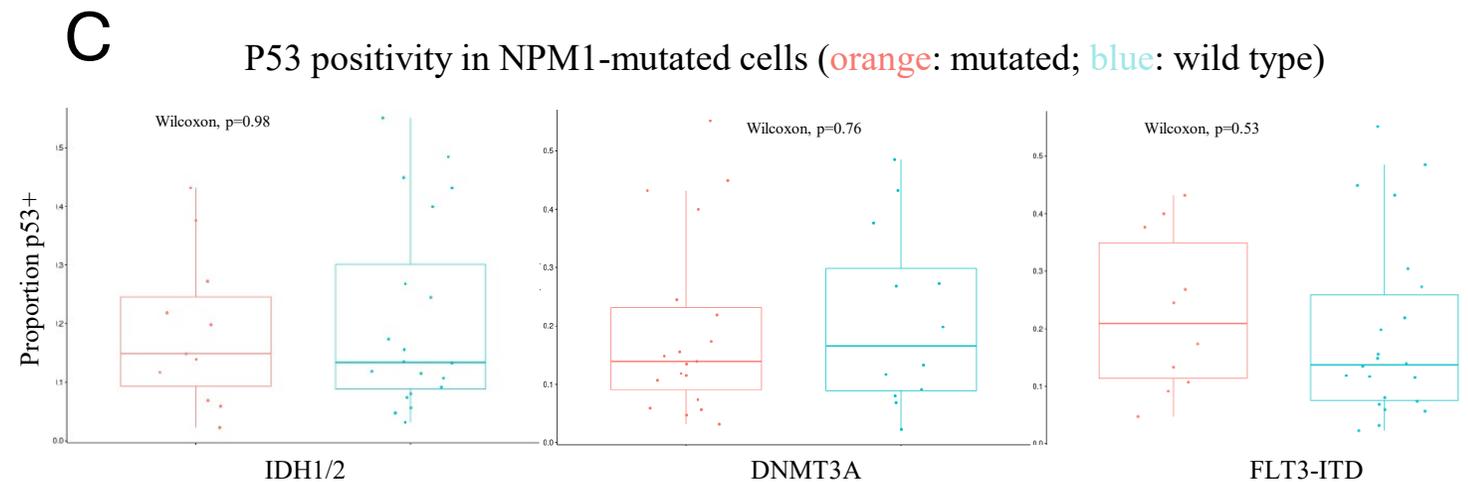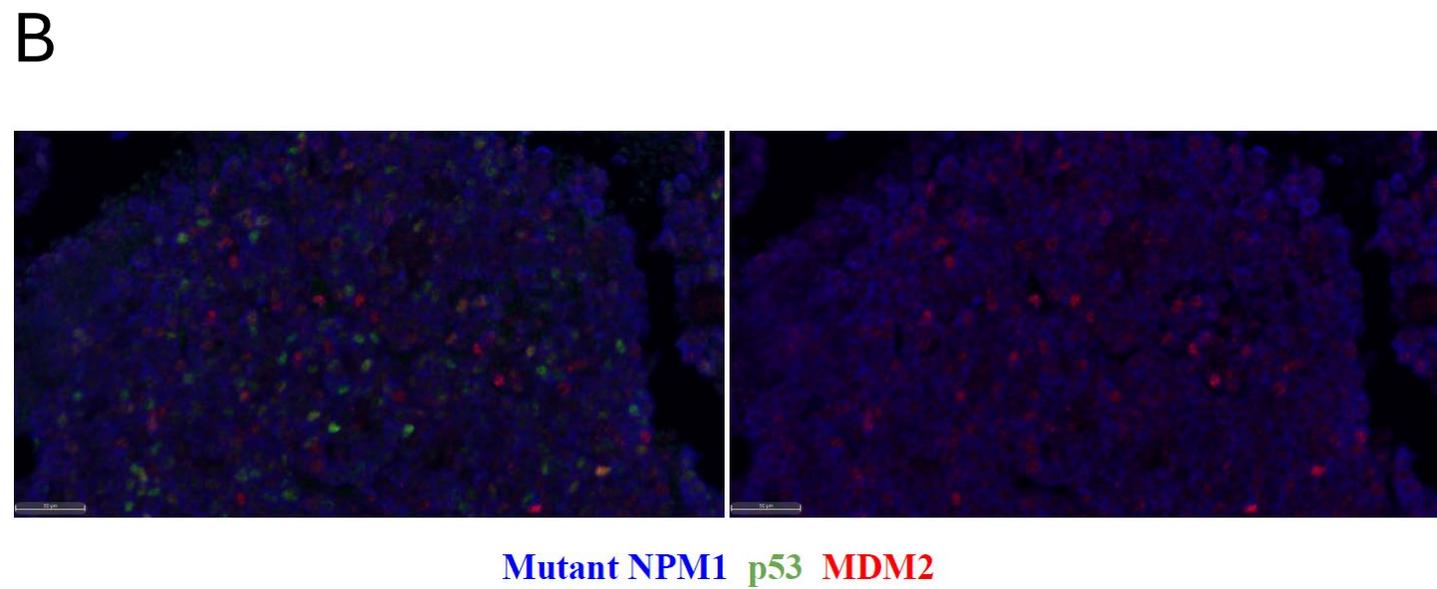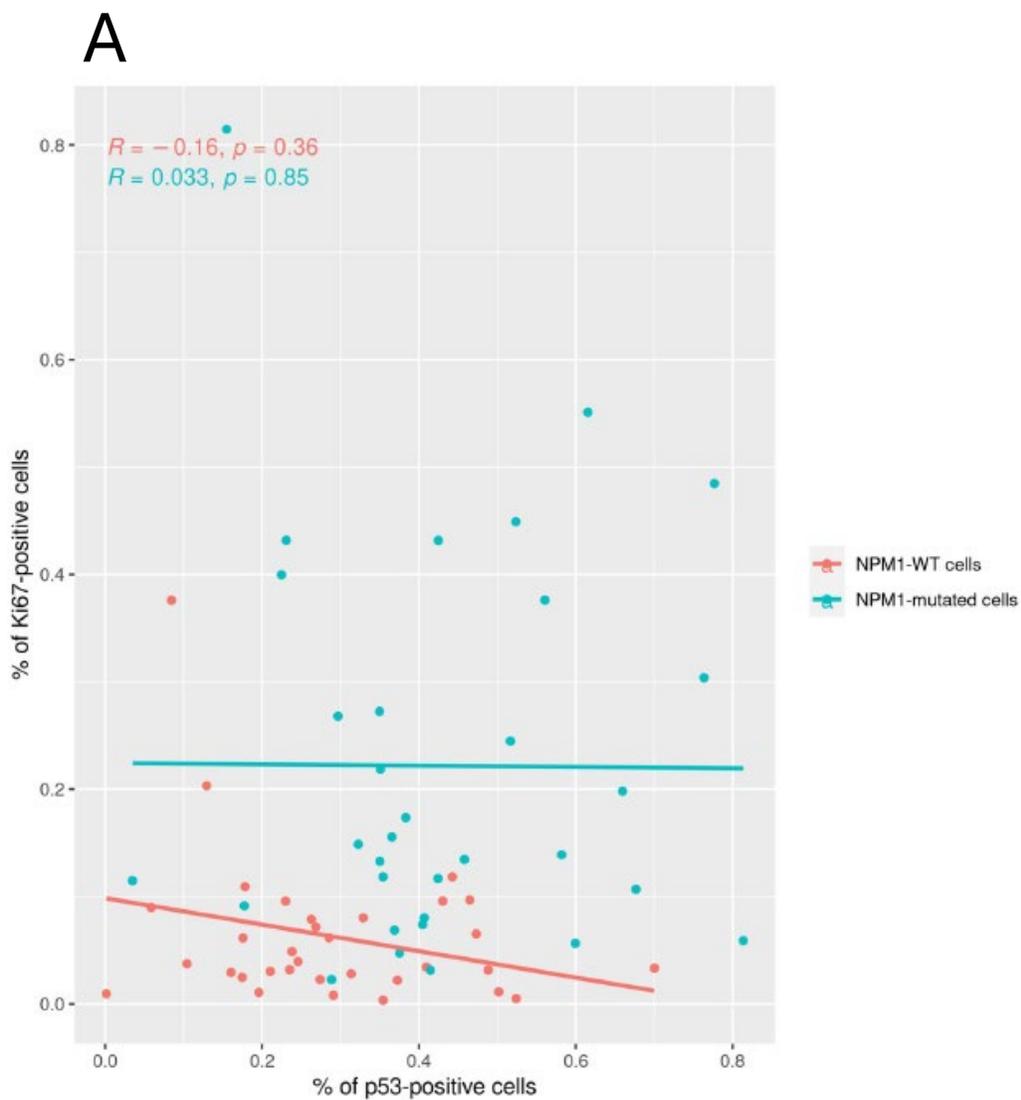
Supplemental Figure 2. A. No correlation between frequency of p53-positive and Ki67-positive cells in cases *NPM1*-AML. B. Representative example of an *NPM1*-AML case stained with antibodies to mutant NPM1 (blue), p53 (green), and MDM2 (red). The MDM2 signal is predominantly nuclear; evidence of cytoplasmic (i.e. blue/green overlap) dislocation of MDM2 is inconspicuous. C. Frequency of p53 expression among *NPM1*-mutated cells does not differ based on presence or absence of co-mutation in *IDH1/2* (left), *DNMT3A* (center), or *FLT3-ITD* (right).
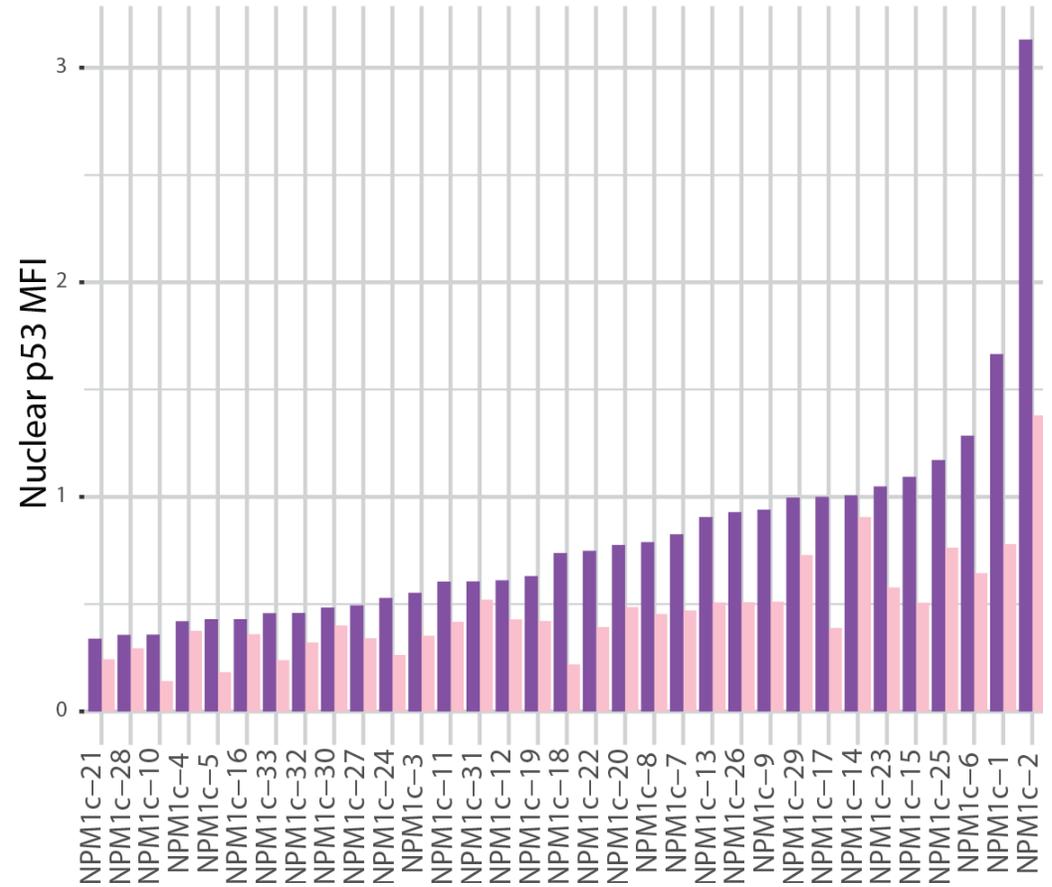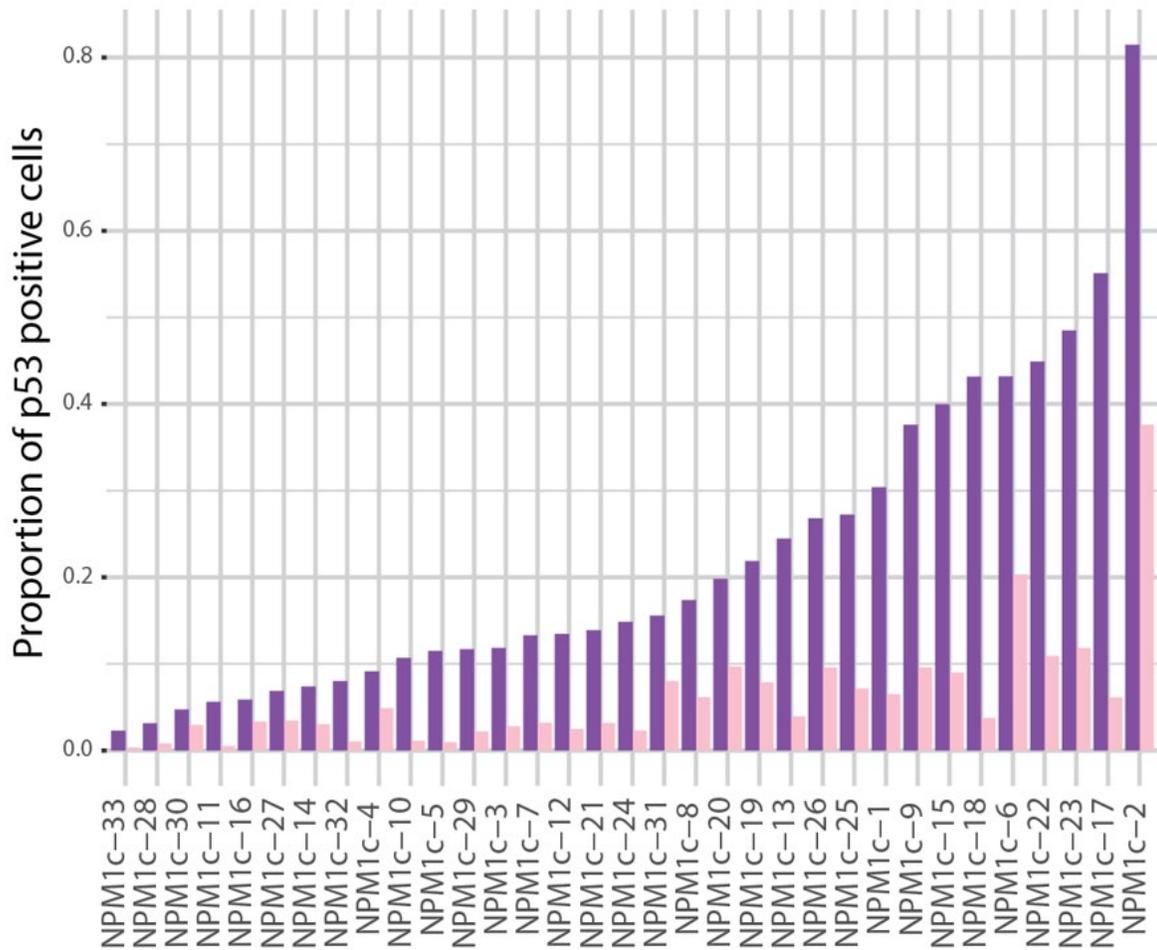
Supplemental Figure 3. Within each case of *NPM1*-AML analyzed by MxIF, a greater proportion of *NPM1*-mutated cells are p53-positive (left) and have higher nuclear p53 MFI (right), compared to *NPM1*-WT cells. Aggregate data demonstrating the statistical significance of the differences between *NPM1*-mutated cells and *NPM1*-WT cells are shown in Figure 2 of the main paper.