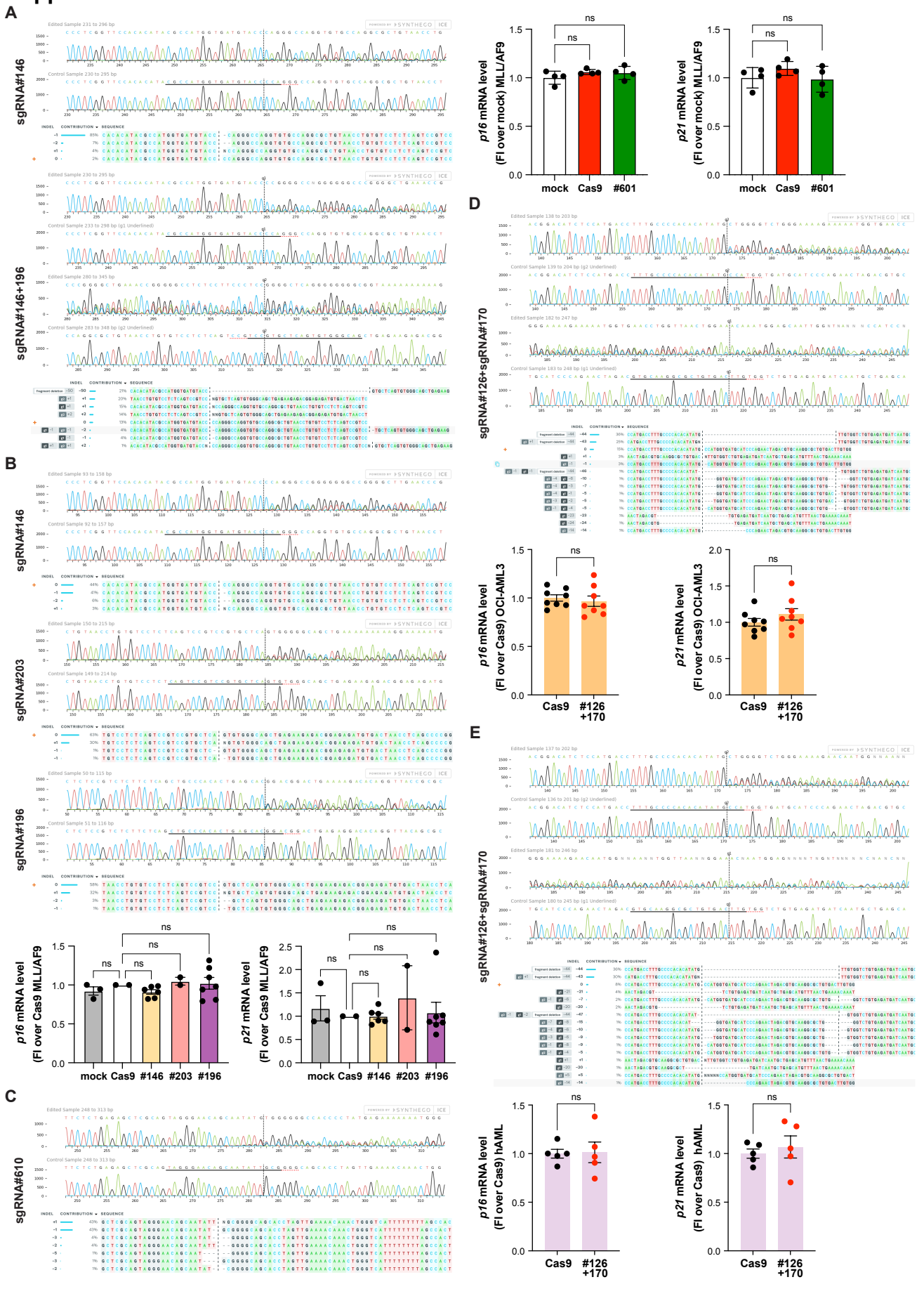
Supplemental Item 1



Supplemental Item 1. Related to Figures 3, 5, S3 and S5. Sanger sequencing files and indel contribution* analysis 72h after nucleofection for (**A**) WEHI-3B cells nucleofected with Cas9 and sgRNA#146 or the combination of sgRNA#146 and sgRNA#196, targeting exon 3 of *Ido1*. (**B**) MLL/AF9 cells nucleofected with Cas9 and the indicated sgRNAs (#146, #203 or #196) targeting exon 3 of *Ido1.* Below *p16* and *p21* mRNA levels in the indicated MLL/AF9 cells. (**C**) MLL/AF9 nucleofected with Cas9 and with sgRNA#610, targeting exon 4 of *Ido1*. Top next column *p16* and *p21* mRNA levels in the indicated MLL/AF9 cells. (**D**) OCI-AML3 cells nucleofected with Cas9 and with the combination of sgRNA#126 and sgRNA#170 targeting exon 3 of *IDO1*. Below *p16* and *p21* mRNA levels in the indicated OCI-AML3 cells. (**E**) Patient-derived AML cells isolated from BM PDX NSGS mice and nucleofected with Cas9 together with the combination of sgRNA#126 and sgRNA#170 targeting exon 3 of *IDO1*. Below *p16* and *p21* mRNA levels in the indicated patient-derived human AML cells.

* Indel contribution and trace file analyses were performed using the *ICE Synthego analysis tool*. Trace files span the expected Cas9 cut site (vertical dotted lines) and the region around the sgRNA sequence comparing the wild-type -WT- (control) and the edited samples. sgRNA sequence is underlined in black, PAM sequence is denoted by a dotted red underline in the control sample. The contributions show the inferred sequences present in the edited population and their relative proportions. Cut sites are represented by black vertical dotted lines, and the WT sequence is marked by a "+" symbol on the far left.