

Supplemental_Fig_S1

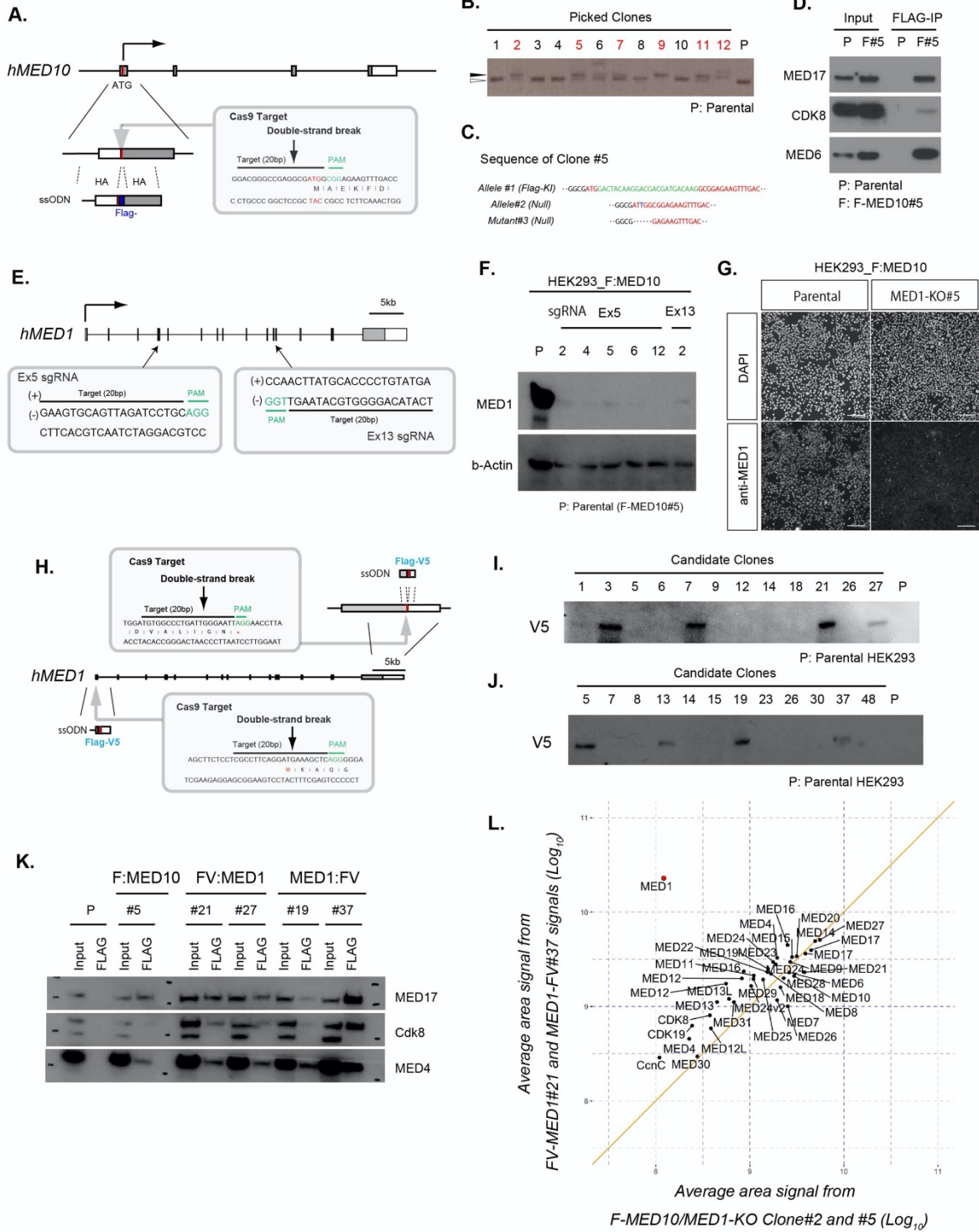


Figure S1: Assessment of Mediator subunits in the MED1-KO Mediator

A) Design of CRISPR/Cas9 mediated Flag-tag knock-in strategy at the *MED10* locus in HEK293 cells. **B)** Genomic PCR of a region flanking the first ATG of *MED10*. Bands with slower migration (marked with black arrowhead) correspond to FLAG-tag inserted alleles. **C)** Sequence of the amplified product of clone #5 shown in (B). Note that this clone carried three copies of *MED10*, and alleles that were untagged resulted in a non-functional allele. **D)** Immunoprecipitation followed by immunoblotting of Mediator subunits (MED17, CDK8, MED6). Parental HEK293 cells were used as a control. Flag-tagged *MED10* efficiently precipitates other Mediator subunits. **E)** Design of *MED1*-knockout by CRISPR/Cas9. sgRNAs were designed to sequences present in either exon 5 or exon 13. **F)** Immunoblot of lysates showing the absence of *MED1* in established *MED1* knockout clones. Parental cells (HEK293_F:MED10#5) were used as a control. **G)** Representative image of immunocytochemical analysis of *MED1* in parental cells and in one of the derived *MED1*-KO clones. Note the absence of a nuclear *MED1* signal in the knockout clone. White bars indicate 100 μ m. **H)** Design of Flag-V5 tandem tag *MED1* knock-ins at the N- and C-termini of *MED1*. **(I and J)** Immunoblot of lysates showing the successful V5-tag knock-in either at the N-terminus (I) or at the C-terminus (J) of *MED1*. **K)** Immunoprecipitation followed by immunoblotting of Mediator subunits (MED17, CDK8, MED4). A parental HEK293 and F-MED10#5 clone was used as a control. FlagV5-tagged *MED1* efficiently precipitates other Mediator subunits. **L)** Comparison of Mediator subunit abundance by mass spectrometry. Two independent Mediator preparations from *MED1* knockout clones (KO#2 and KO#5) and two independent *MED1*-containing Mediator preparations (FV-MED1#21 and MED1-FV#37) were compared. The abundance of each subunit was calculated based on the three most abundantly detected peptides for each subunit. Signals between samples were normalized to the abundance of *MED14* (a structural backbone subunit) and averaged between replicates, and all Mediator subunits were plotted. Despite the loss of *MED1*, other subunits were detected at comparable levels.