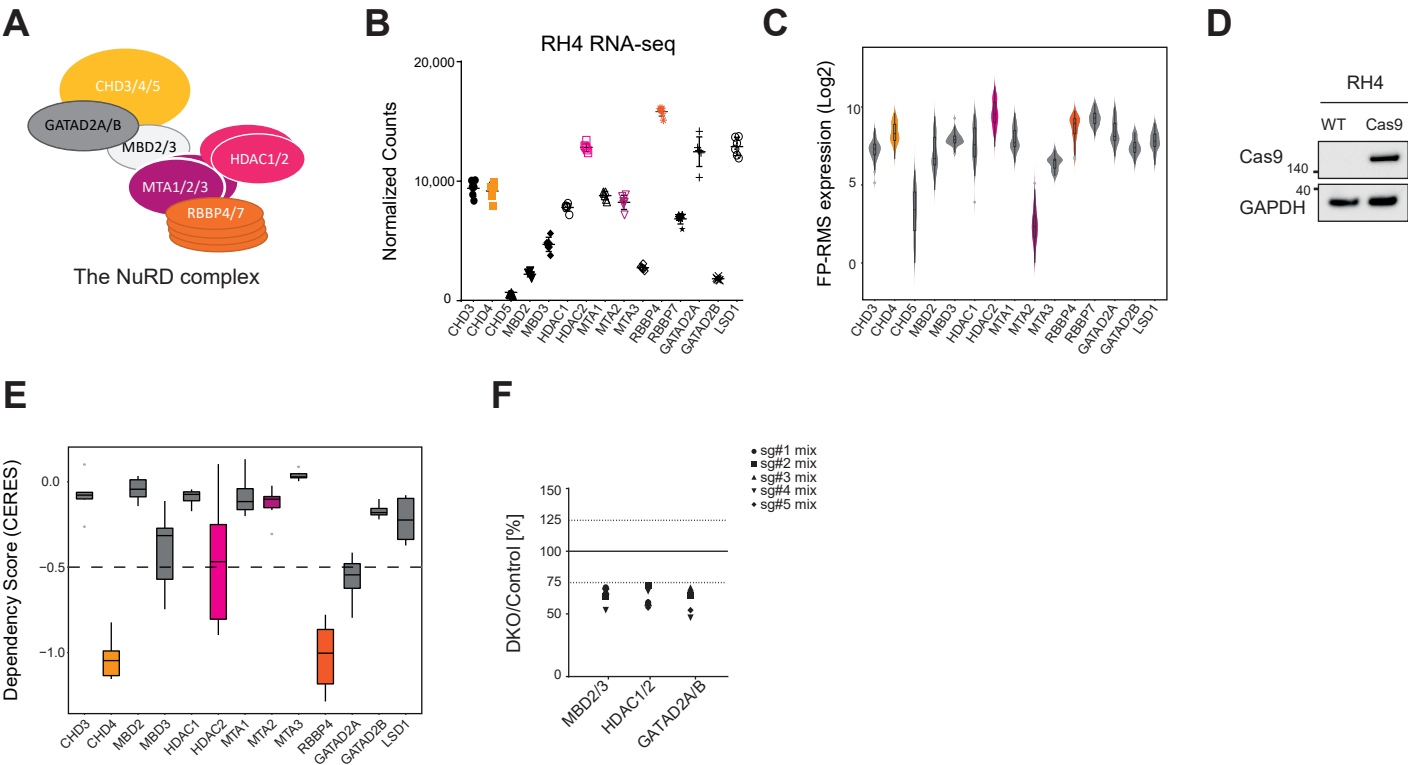


Figure 1 - figure supplement 1



**Figure 1 - figure supplement 1** The NuRD complex expression and function in FP-RMS. **A** Representation of NuRD complex according with Bornelöv et al and Torrado et al. **B** Expression levels, as normalized counts, of the displayed NuRD subunits (CHD4 in orange, HDAC2 in pink, MTA2 in dark pink, and RBBP4 in dark orange) obtained from RNA-seq data of RH4 cells expressing a tetracycline-inducible shRNA scramble construct at 24 and 48hrs of doxycycline treatment (n=3, see Materials and Methods for details). **C** Violin plot depicting the expression levels of NuRD subunits in FP-RMS tumor tissue. Displayed are microarray data from three independent studies (Davicioni et al., 2006; Sun et al., 2015; Wachtel et al., 2004) available on the R2 gene expression database (r2.afl.nl). **D** Immunoblot depicting Cas9 expression in RH4-Cas9 cells. GAPDH was used as a loading control and wildtype RH4 cells (WT) served as negative control. **E** Box plot depicting the tumor dependency scores, calculated as CERES, of the indicated NuRD members in 6 FP-RMS cell lines (CRISPR Avana Public 19Q2, depmap.org). **F** Results of CRISPR/Cas9 double knockout screen displayed as ratio between the indicated NuRD members double knockout (DKO) population and the control population (sgAAVS1) at day 12 normalized to day 2. Each point represents the average of 3 biological replicates.