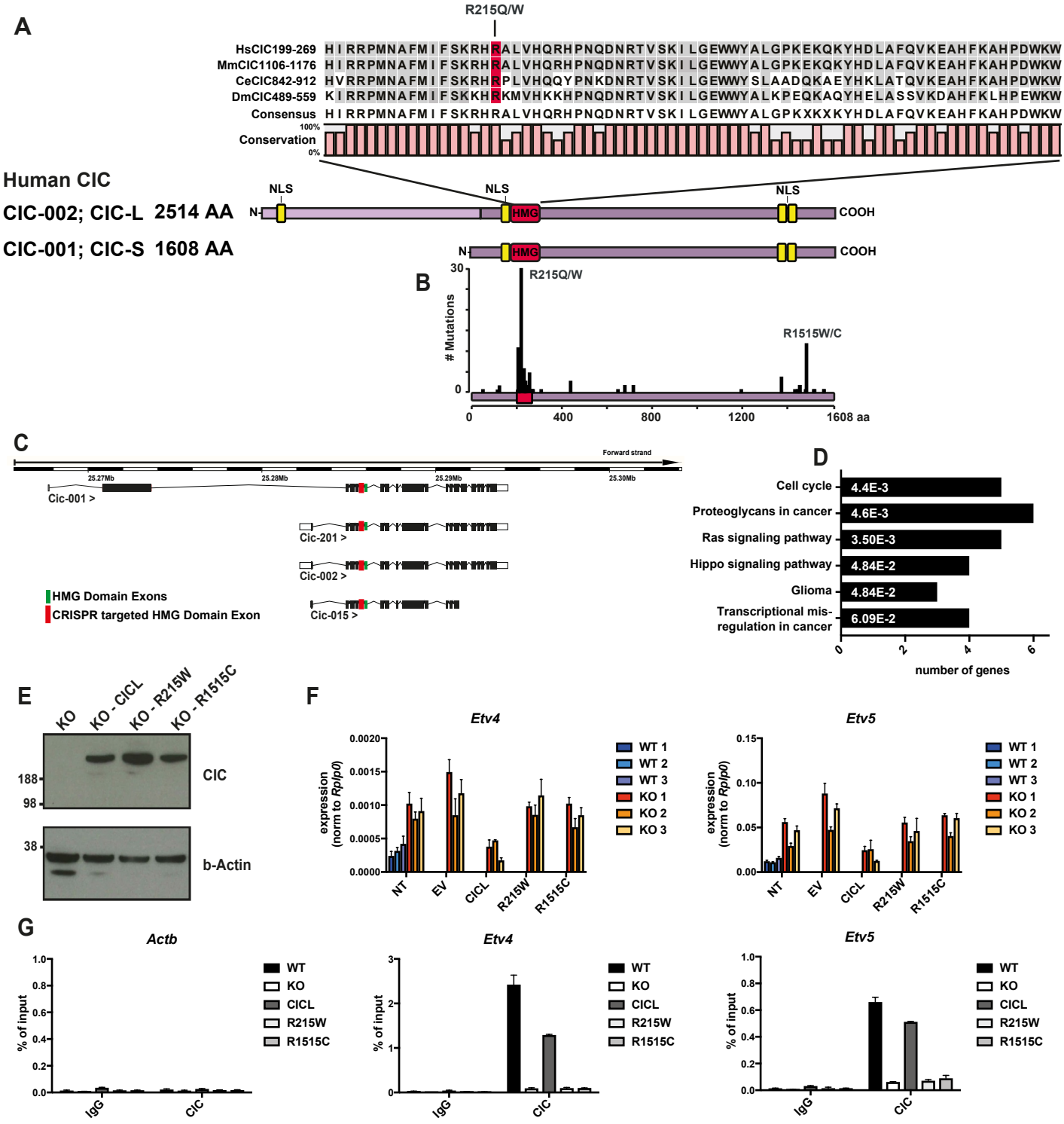
Supplementary Figure S1



Supplementary Figure S1:
A) Schematic representation of human CIC isoforms and distribution of CIC mutations in glioma. The HMG - DNA binding domain (residues 199 to 269) is magnified showing sequence conservation in human (Hs) mouse (Mm) *Caenorhabditis elegans* (Ce) and *Drosophila melanogaster* (Dm). Identical amino acids are shaded in grey, the conserved arginine residue 215 that is frequently mutated in ODG is highlighted in red. NLS – Nuclear Localization Signal, HMG – High Mobility Group. **B)** Distribution and number (#) of CIC missense mutations in glioma reported in the COSMIC database **C)** Intron-exon structure of Cic transcripts in mouse. HMG domain exons and HMG exons targeted by CRISPR in the current study are shown in red and green respectively **D)** DAVID - Gene ontology of the identified CIC target genes. Corresponding p-Values are shown within the bars. **E)** Overexpression of human CIC-L, CIC-L R215W and CIC-L R1515C in one *Cic*-KO clone. **F)** *Etv4* and *Etv5* gene expression levels of cells shown in E. Expression values are normalized to housekeeping gene *Rplp0.* Data are represented as mean ±SD, n=3 **G)** ChIP-qPCR of CIC and nonspecific control (IgG) in WT, Cic-KO and Cic-KO overexpressing CIC-L mESCs at *Etv4* and *Etv5* with *Actb* as control region. Data are represented as mean ±SD, n=3.