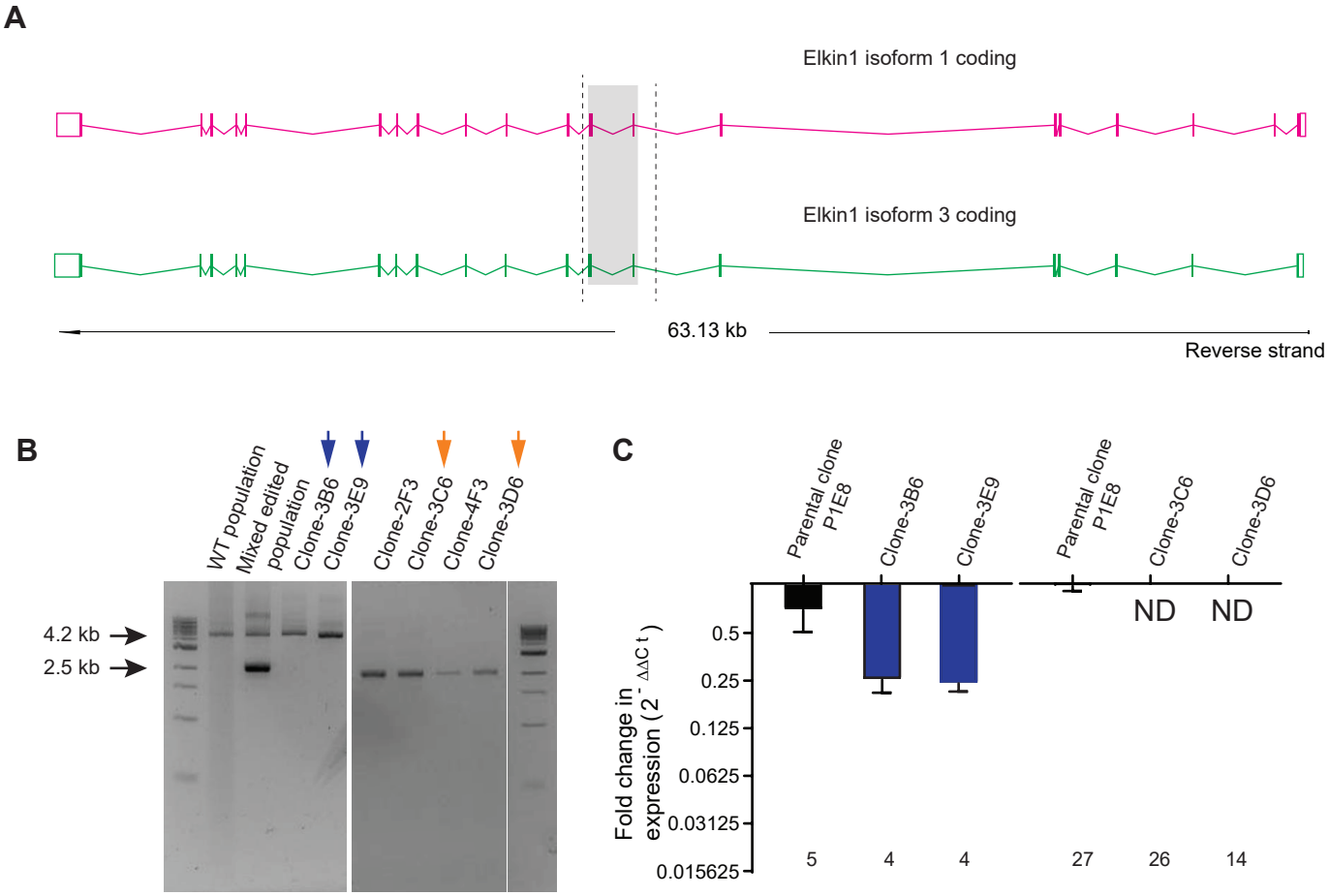

Figure 5- figure supplement 1: CRISPR/Cas9 editing of WM266-4 cells
(**A**) Schematic representation of *Elkin1* gene. *Elkin1* is located on the reverse strand, Chromosome 15: 42,210,452-42,273,663. The CRISPR-Cas9 nickase was used in order to counter off-target effects that can arise from using the nuclease and gRNAs were designed using the web-base CRISPR design tool from the Zhang laboratory MIT (http://crispr.mit.edu/). The editing strategy used two gRNAs targeting intron 7 and two gRNAs targeting exon 9, to create a deletion of 1.7 kb from chromosome 15. Screening primers for gPCR are marked with dashed lines. (**B**) Gel electrophoresis of gPCR products. The WT yields a band 4.2 kb in length. The band corresponding to successful editing is 2.5 kb in length. In the mixed edited population both bands are visible. Isolated clones 3B6 and 3E9 (marked with blue arrows) were selected as WT clones. Clones 3C6 and 3D6 (marked with orange arrows) were selected as Elkin1-KO clones. (**C**) a qPCR analysis of mRNA isolated from individual clones confirms that *Elkin1* transcript is detected in the WT clones, but is not detected in the Elkin1-KO clones.