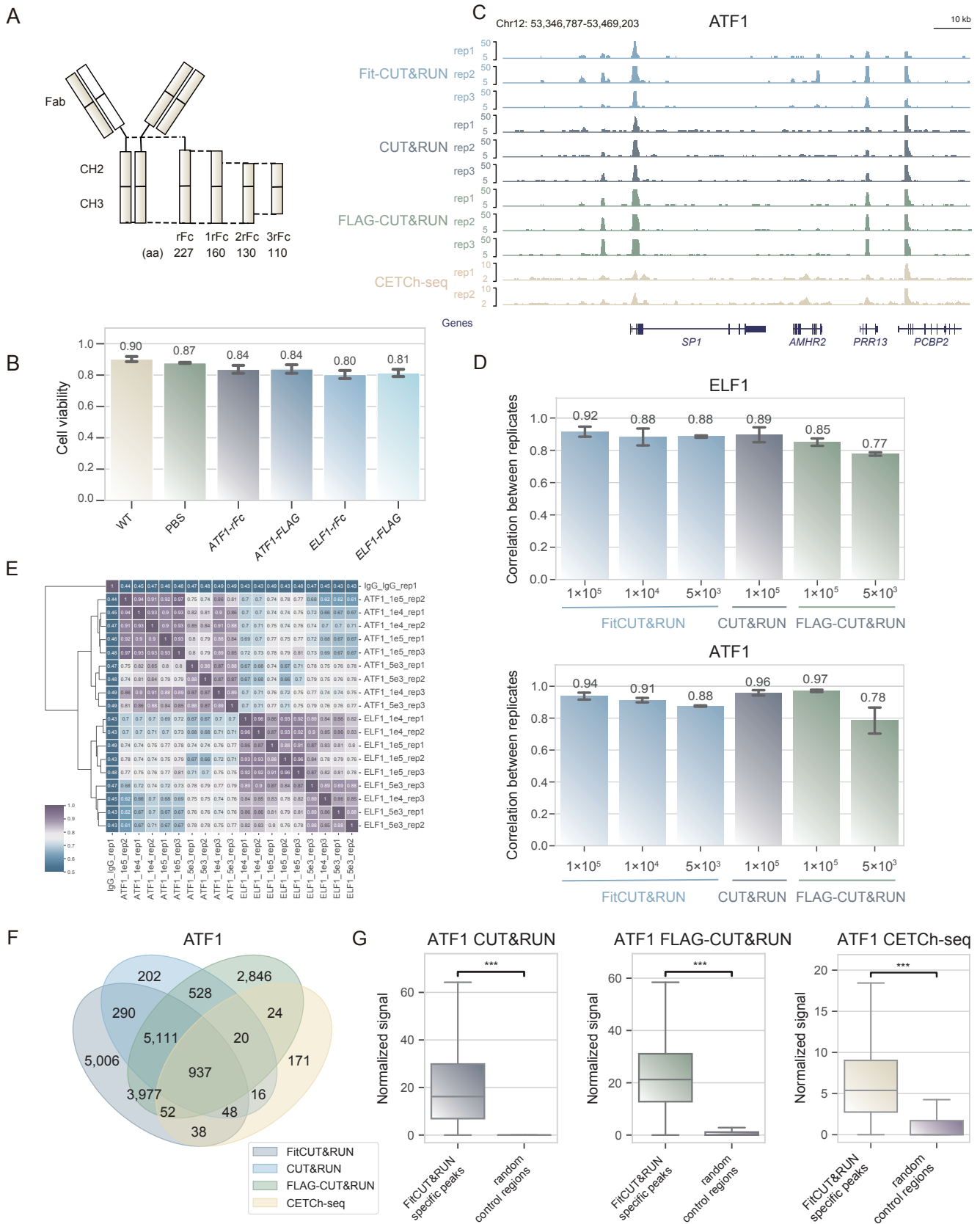




Supplemental Figure 1. Performance of FitCUT&RUN with K562 cells. (A) A diagram of different truncated rFc fragments. (B) Bar plot of cell viability ratio for K562 cells analyzed upon different conditions. The ratios were calculated by FACS analysis. For each condition, three replicates were performed. (C) The genome browser view shows ATF1 FitCUT&RUN, CUT&RUN, FLAG-CUT&RUN (three replicates for each) and CETCh-seq (two replicates) signals around *SP1* loci as a representative example of the consistency among

these methods. *(D)* Bar plots showing the correlation for FitCUT&RUN, CUT&RUN, FLAG-CUT&RUN replicates. The high correlation confirms the reproducibility of the FitCUT&RUN data. *(E)* Heatmap showing the correlation among FitCUT&RUN samples. The correlations between distinct TFs are lower than replicates of the same TF. *(F)* Venn diagram showing the overlap status between ATF1 FitCUT&RUN, CUT&RUN, FLAG-CUT&RUN and CETCh-seq data. The majority of the CETCh-seq, CUT&RUN and FLAG-CUT&RUN peaks can also be detected by FitCUT&RUN. *(G)* Boxplots showing that the normalized ATF1 CETCh-seq, CUT&RUN and FLAG-CUT&RUN signal on FitCUT&RUN-specific peaks is significantly greater than that on random control regions, confirming the reliability of the FitCUT&RUN data.