



SUPPLEMENTARY FIG. S5. Guide-specific modeling predicts cleavage efficiencies in random libraries and in genomes. **(A)** Neural network training scores randomized target DNA across guide models. Box-plot distributions are shown for various guides surveyed. GIMP scores for each guide are listed below the x-axis. **(B)** Neural network training scores putative genomic off-target DNA across guide models. Box-plot distributions are shown for various guides surveyed on targets with up to six mismatches in the human genome. **(C)** Venn diagram of all off-targets with up to six mismatches in the human or mouse genome. **(D)** Venn diagram of only the top 5% of predicted off-targets in human or mouse genomes. **(C)** and **(D)** are not to scale with each other.