

Supplementary information, Figure S6

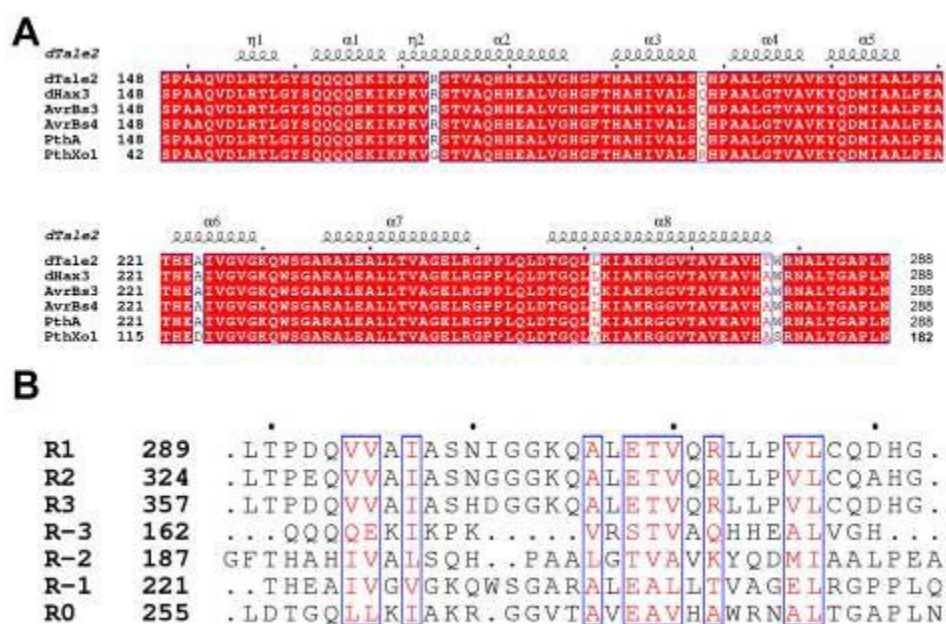


Figure S6 The sequence alignment of the NTR. **(A)** The NTR among different TALE proteins are highly conserved in the structure-based sequence alignment. **(B)** The alignment of the N terminal four atypical repeats to the canonical TAL repeats. Identical amino acids are boxed in dark red; similar amino acids are boxed in light red; different amino acids are shown in dark. The locations of the α -helices are shown above the alignment. The program ClustalW was used for sequence alignment.