

Expansion of target repertoire in coding sequence

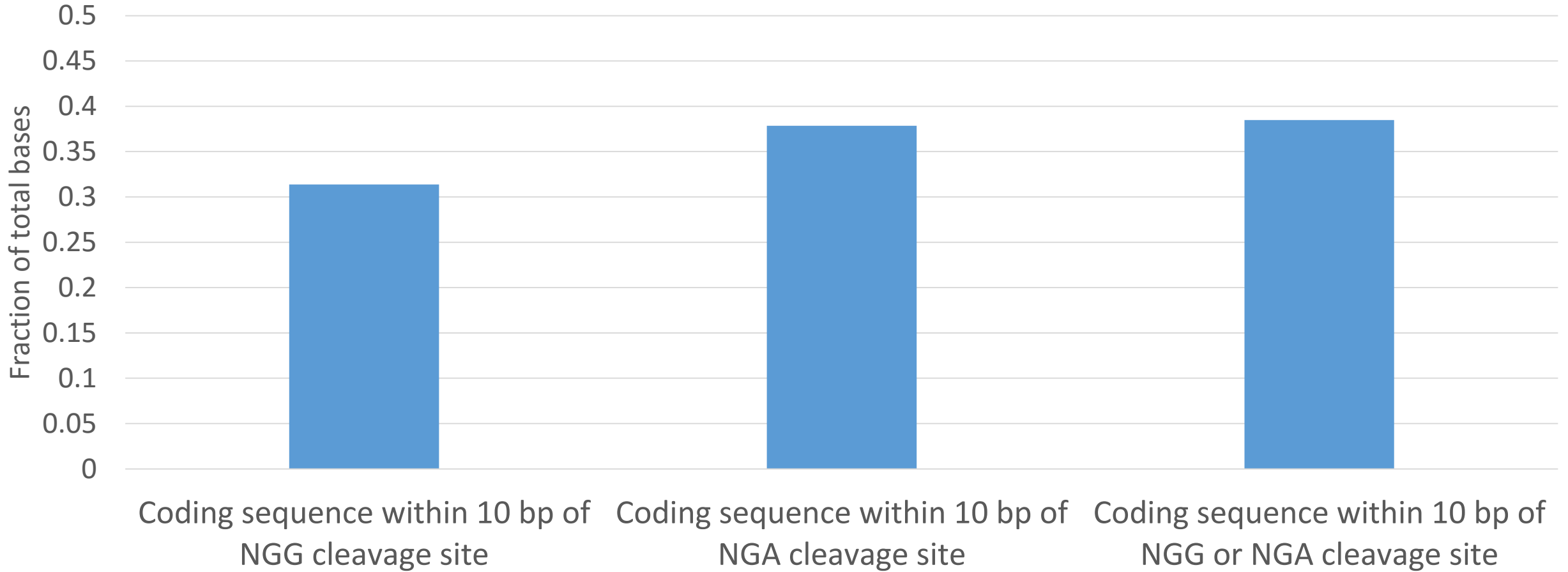


Figure S2a: The fraction of all bases in the annotated *C. elegans* RefSeq genes which have Cas9 cleavage sites within 10 bp induced using NGG, or NGA, or either NGG or NGA PAMs.

The bases depicted meet the following criteria: 1. A distance of ≤ 10 bp from a Cas9 induced cleavage site, and 2. The associated sgRNA sequence would have no runs of more than 4 T bases and a GC content between 20-80%.

Enlargement of target repertoire in coding sequence

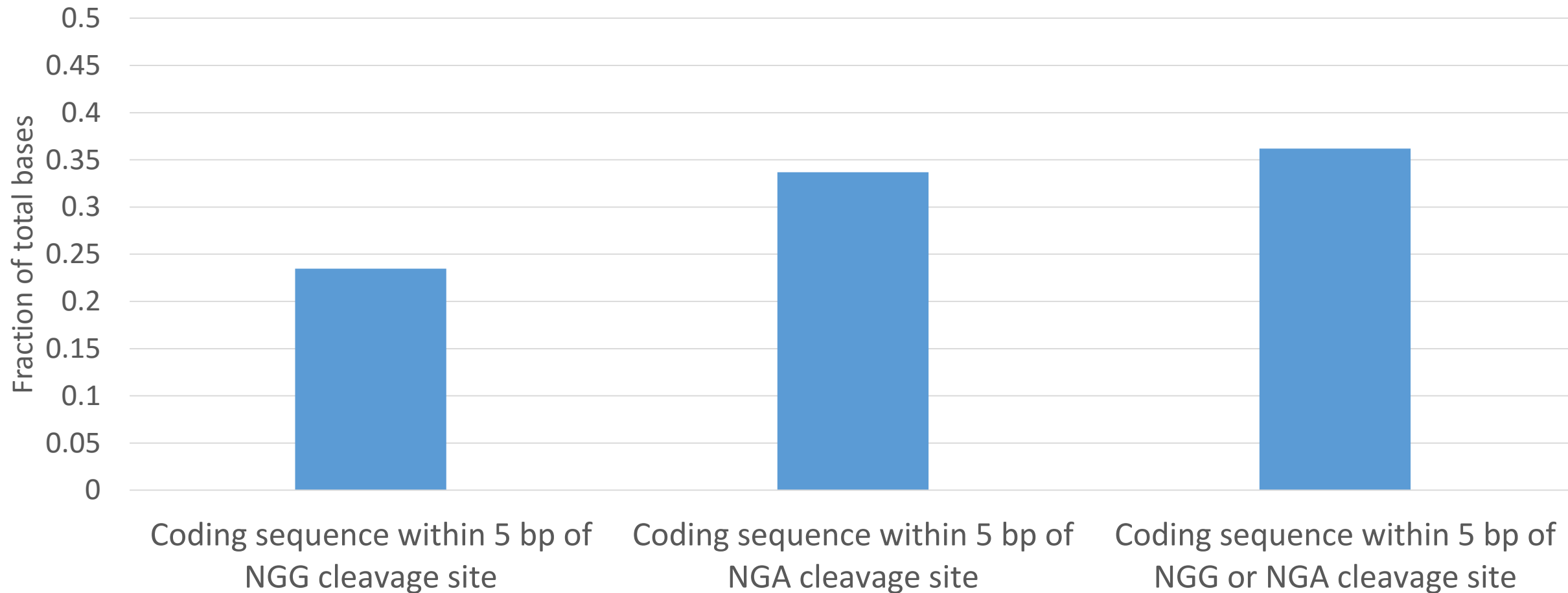


Figure S2b: The fraction of all bases in the annotated *C. elegans* RefSeq genes which have Cas9 cleavage sites within 5 bp induced using NGG, or NGA, or either NGG or NGA PAMs.

The bases depicted meet the following criteria: 1. A distance of ≤ 5 bp from a Cas9 induced cleavage site, and 2. The associated sgRNA sequence would have no runs of more than 4 T bases and a GC content between 20-80%.

Expansion of 3' UTR target repertoire

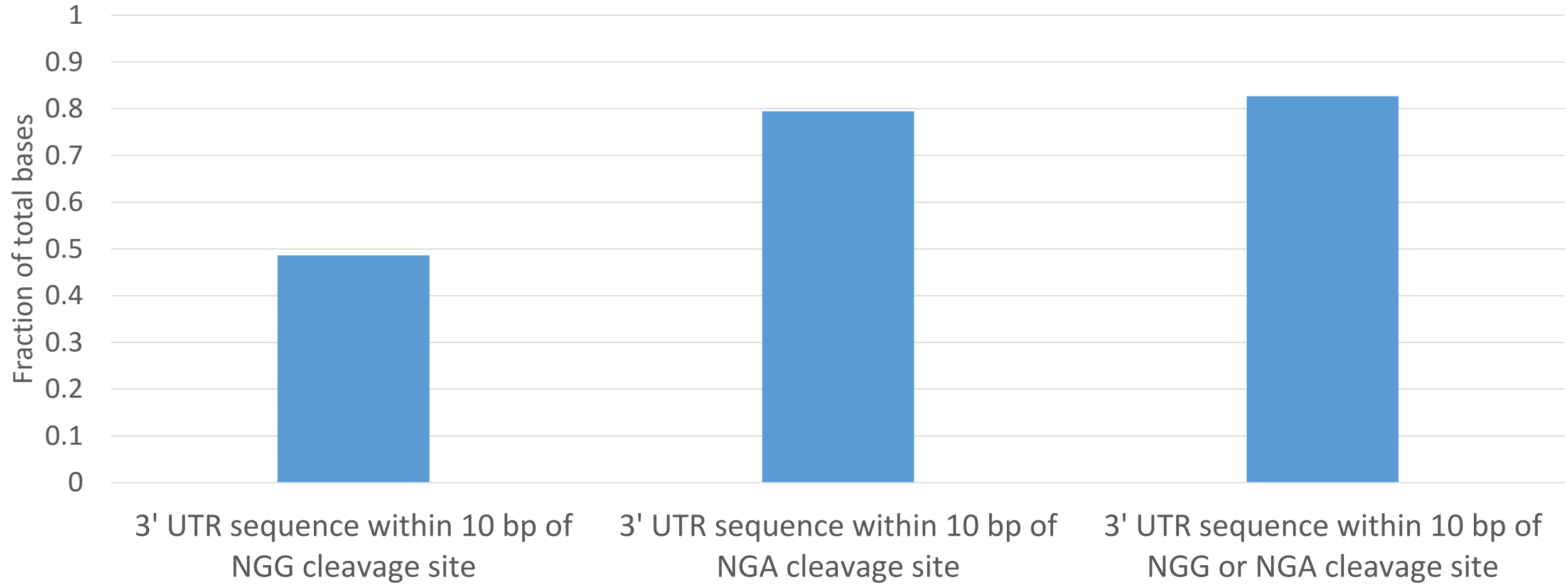


Figure S2c: The fraction of all bases in *C. elegans* 3' UTRs which have Cas9 cleavage sites within 10 bp induced using NGG, or NGA, or either NGG or NGA PAMs.

The bases depicted meet the following criteria: 1. A distance of ≤ 10 bp from a Cas9 induced cleavage site, and 2. The associated sgRNA sequence would have no runs of more than 4 T bases and a GC content between 20-80%.

Expansion of 3' UTR target repertoire

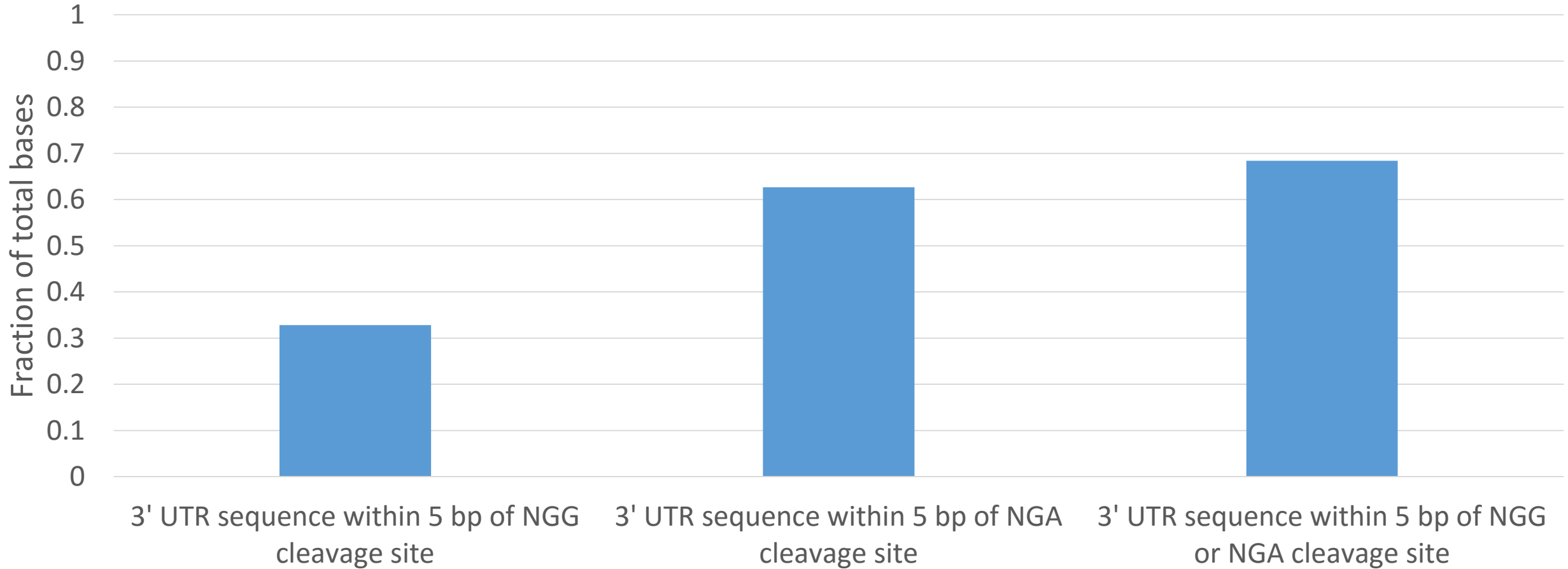


Figure S2d: The fraction of all bases in *C. elegans* 3' UTRs which have Cas9 cleavage sites within 5 bp induced using NGG, or NGA, or either NGG or NGA PAMs.

The bases depicted meet the following criteria: 1. A distance of ≤ 5 bp from a Cas9 induced cleavage site, and 2. The associated sgRNA sequence would have no runs of more than 4 T bases and a GC content between 20-80%.