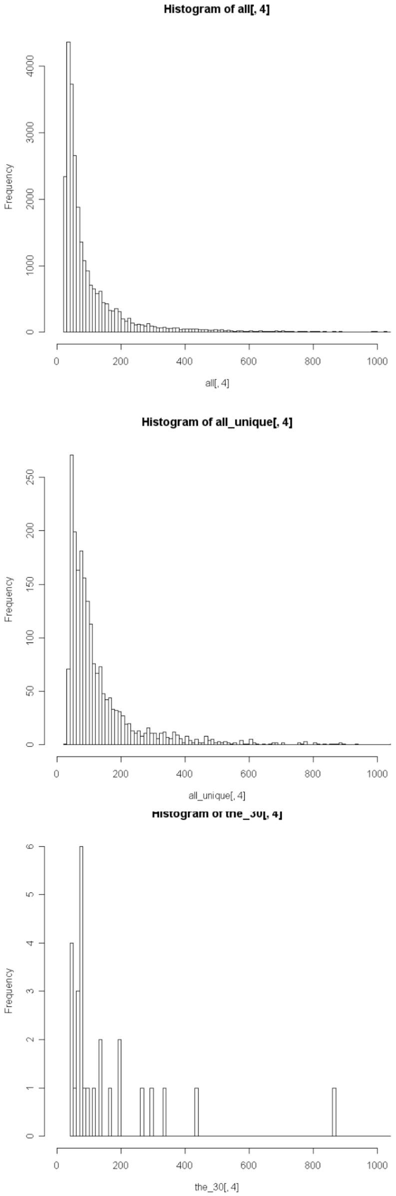
**Supplemental Figure 3.** Comparisons of the repeat characteristics of all TRs, unique TRs and unique TRs associated with siRNAs



all TRs

all unique TRs

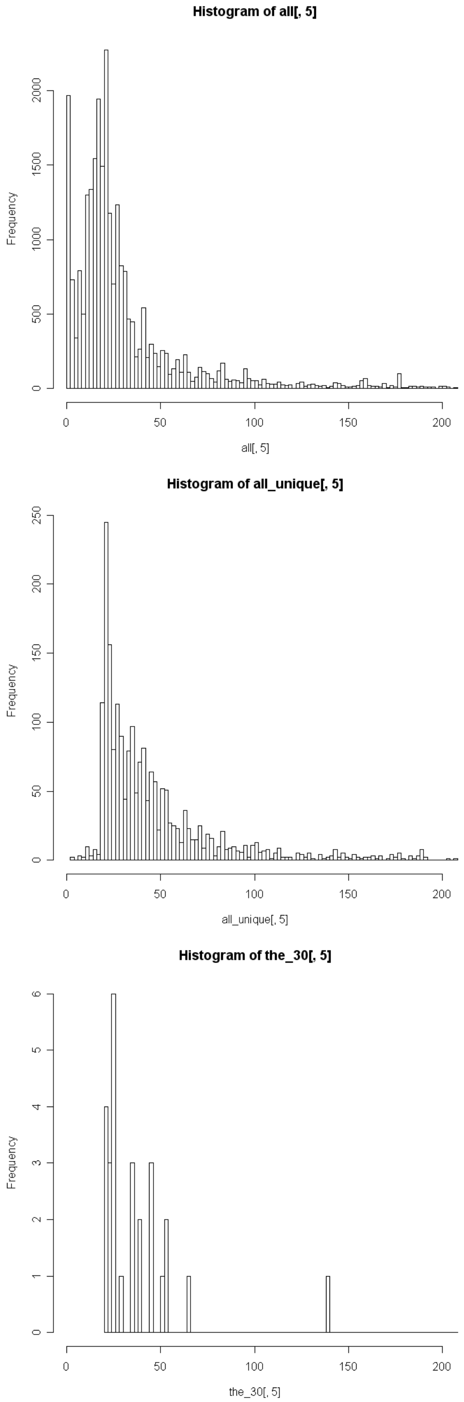
unique TRs

with siRNAs

**Supplemental Figure 3A.** Comparison of the length of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: length of each TR

*y*-axis: frequency



all TRs

all unique TRs

unique TRs

with siRNAs

**Supplemental Figure 3B**. Comparison of the repeat unit length of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: repeat unit length length of each TR

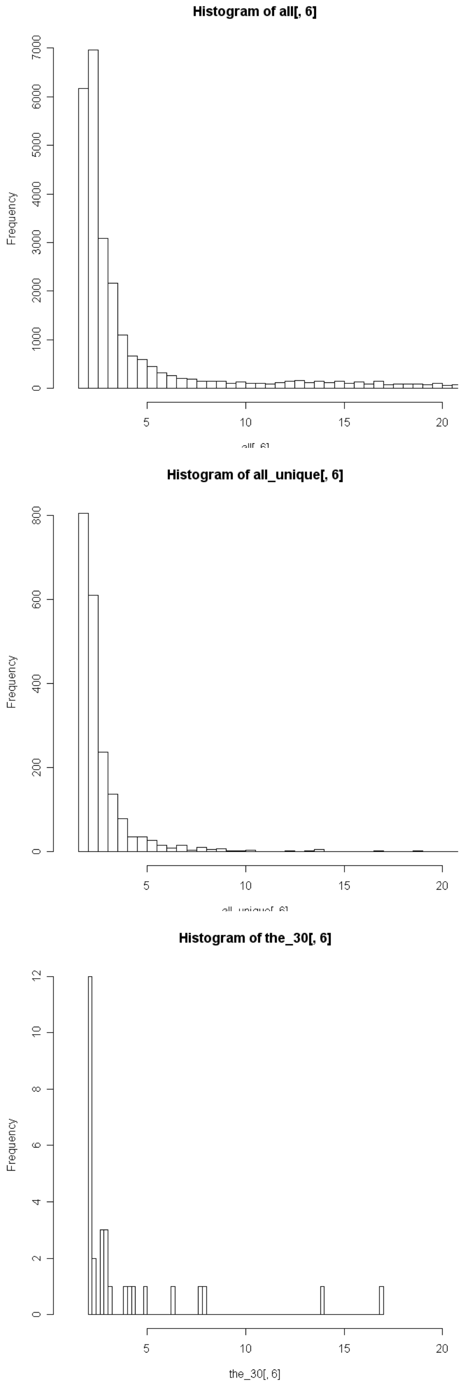
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3C**. Comparison of the number of repeat units within each TR, for all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: number of repeat units within each TR

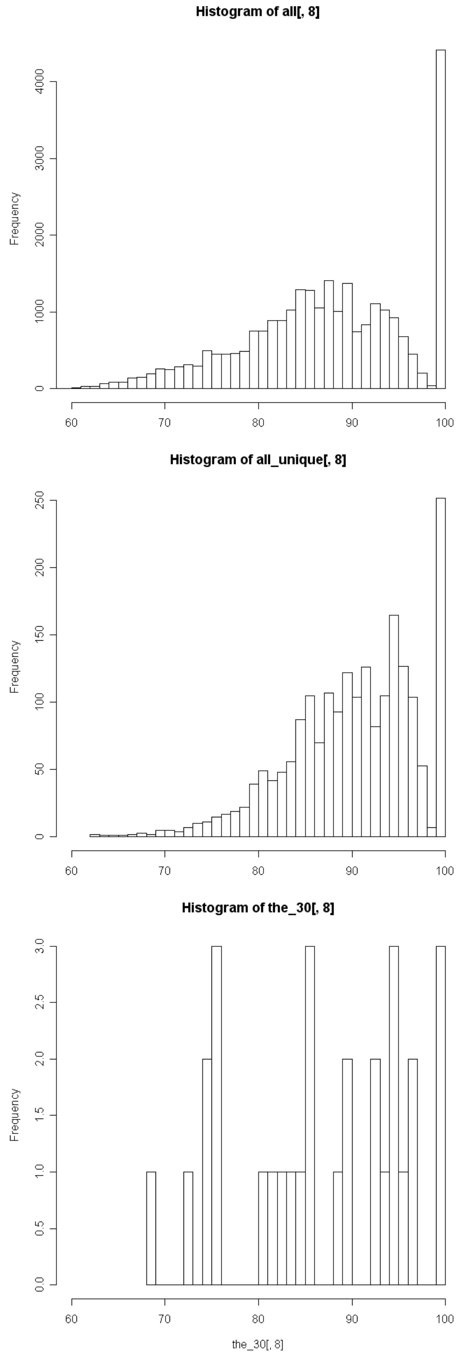
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3D**. Comparison of the average identity among the repeat units within each TR, for all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: average identity among the repeat units within each TR

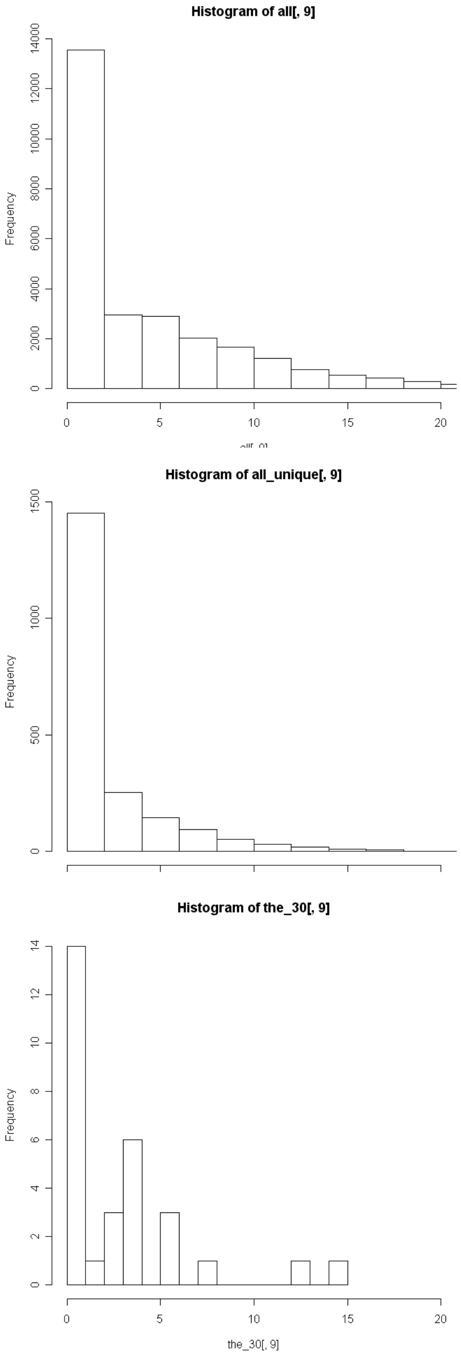
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3E**. Comparison of the percentage of insertions and deletions (indels) among the repeat units within each TR, for all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: percentage of indels among the repeat units within each TR

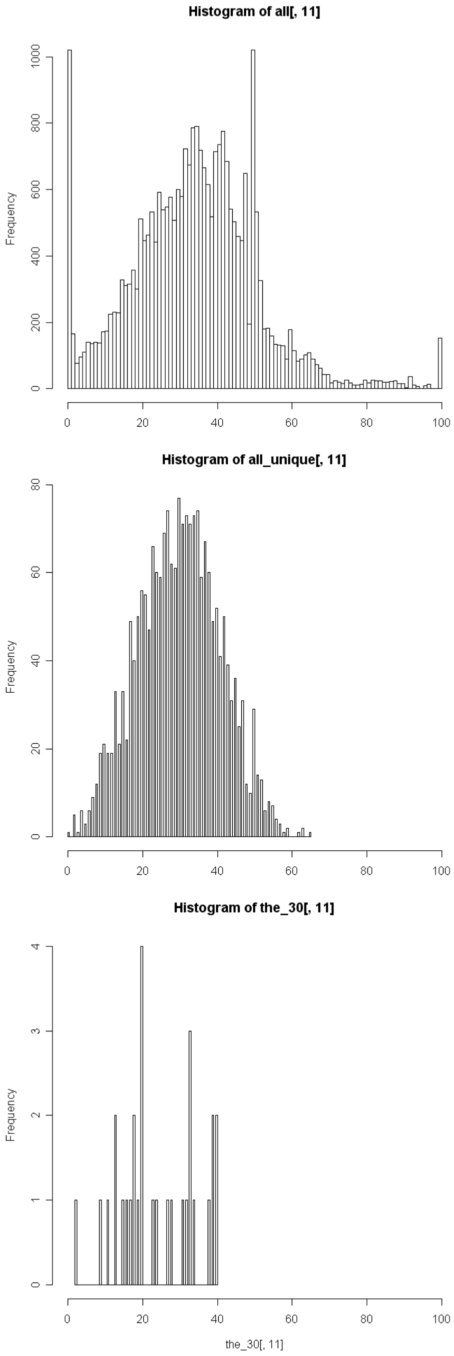
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3F**. Comparison of the sequence content (% of A) of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: percentage of indels among the repeat units within each TR

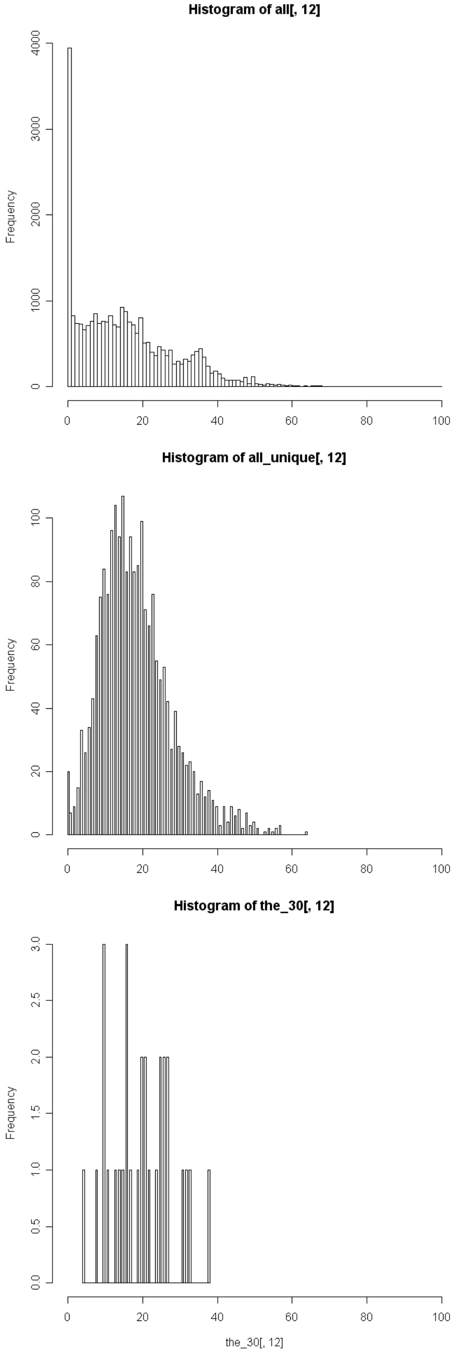
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3G**. Comparison of the sequence content (% of C) of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: percentage of indels among the repeat units within each TR

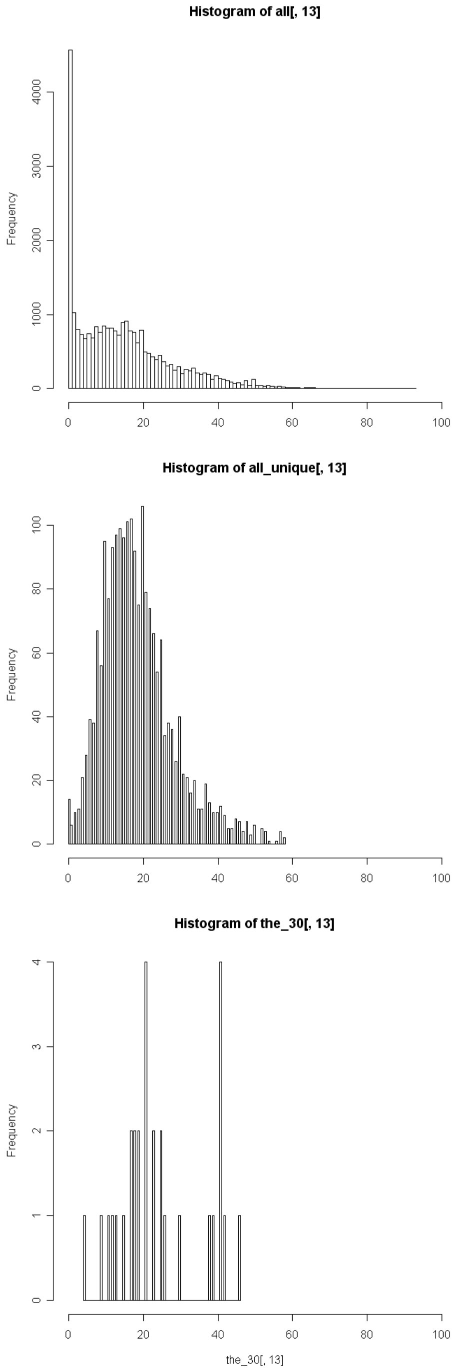
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3H**. Comparison of the sequence content (% of G) of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: percentage of indels among the repeat units within each TR

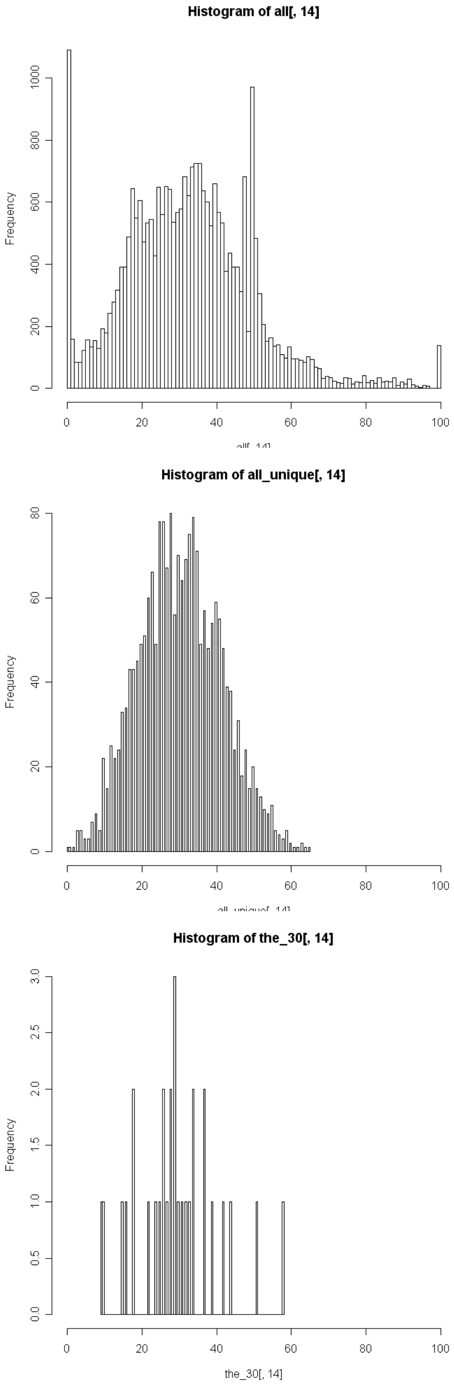
*y*-axis: frequency

all TRs

all unique TRs

unique TRs

with siRNAs



**Supplemental Figure 3I**. Comparison of the sequence content (% of T) of all TRs (top), unique TRs (middle) and unique TRs associated with siRNAs (bottom).

*x*-axis: percentage of indels among the repeat units within each TR

*y*-axis: frequency