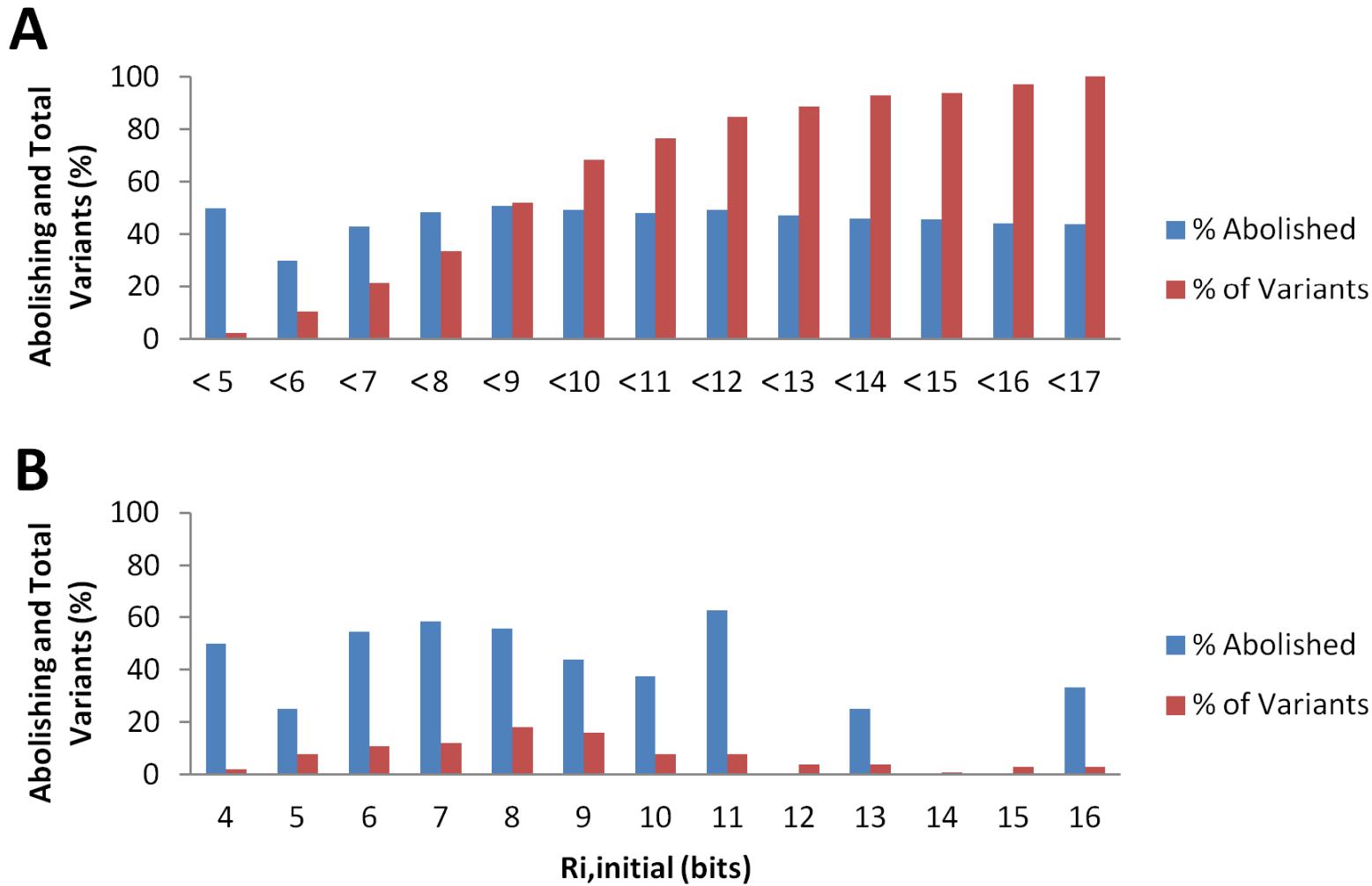


Supplementary Figure 1.



Supplementary Figure 1. Frequency of Abolishing Variants in Relation to Initial Strength. All experimentally verified variants affecting natural sites (where leaky splicing could be assessed) were organized based on the $R_{i,initial}$ of the altered natural site (N = 98). Variants predicted to abolish splicing were filtered according to $R_{i,final} < R_{i,min}$; $\Delta R_i < 7.0$ bits. Histograms display results either cumulatively (A) or are binned (B). In panel (A), the X-axis represents all variants in natural splice sites which are weaker than the indicated R_i values. In panel (B), the X-axis represents $R_{i,initial}$ in 1 bit intervals. The Y-axis shows the percentage of analyzed variants in that interval, as well as the percentage of those variants which were experimentally shown to abolish splicing. Variant ZRANB3: g.136148401A>T is an outlier mutation, with a high $R_{i,initial}$ value (20.4 → 17.6 bits and results in leaky splicing) that was omitted to facilitate the display of the rest of the mutation distribution.

Supplementary Bibliography

This list contains all references that were reviewed for the purpose of this manuscript. Primary research articles, review articles, book chapters, theses, and abstracts that refer to information theory-based sequence analysis and were published up until September 2014 are included. We also reviewed the early literature describing information theory-based analysis. Certain items on this list were not referred to in the main document, because the authors did not perform information theory-based analysis, or because the article did not pertain to human disease and splicing.

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