Complete Data Sets

There were a total of three data sets used in this analysis. The first data set, consisting of sequences for training and testing the models, is included here. The sequence and splice site data for the *Leishmania* genes data set were derived from the GenBank entries for selected genes. The GenBank accession numbers for these genes are reported in Supplemental Data 2. The sequence and annotation data for chromosomes 1 and 3 of *Leishmania major* are publicly available from the Sanger Institute website [44].

EST mapped data

The training data consist of 214 EST-mapped sequences wwith a splice site determined as described in Methods. For each of the sequences here, 400 nucleotides of upstream sequence are reported. In each instance, the splice site is at position 400 (end of sequence) in the reported sequence. As described in Methods, ten data sets of training and testing data were generated from these data by randomly partitioning 90% of the sequences into a training set and reserving 10% for testing.

The sequence identifiers indicate the chromosome from which the sequence derives and list the dbEST identifier for the EST which was used in that mapping. For example, the id

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>lmaj_01_2 with EST W88316 10020, 10420
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indicates that the sequence derives from Chromosome 1 of *L. major*, is the second such EST mapping on Chromosome 1 and that the mapping derives from EST id W88316. The two coordinates 10020 and 10420 indicate the beginning and end of the extracted sequence region with regard to the chromosomal sequence.

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Coding data

As a negative control, we utilized 198 coding regions that had been experimentally verified. These sequences were retrieved from GenBank and are reported below. For each gene, the coordinates for the protein-coding region are listed as well as the GenBank annotation of function.

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