Supplemental Fig S6

A. Relative frequency (%), when compared to sets of control exons, of G, C, A, CA, AC, CT, or TC (di)nucleotides of exons containing ClIP-derived signals corresponding to SRSF1, SRSF3, TRA2, HNRNPK, HNRNPL, or PTBP1. Binding sites of individual splicing factors were recovered and merged from BED files of publicly available ClIP-seq datasets (see Supplemental Table S1). Only ClIP reads included in exons from coding genes were analyzed in terms of nucleotide composition. (*) Randomization test FDR < 0.05.

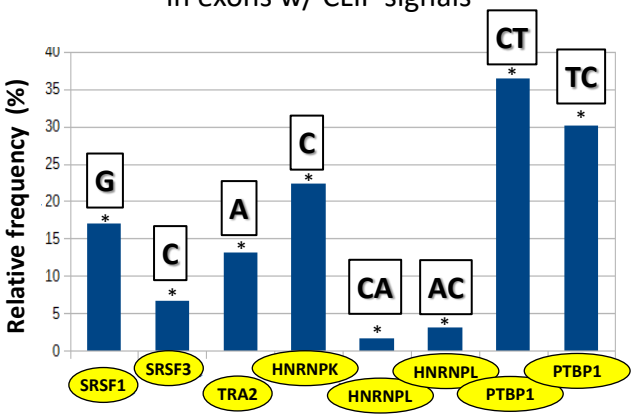
B. Relative frequency (%), when compared to sets of control exons, of Gly, Pro, Lys, His, Gln, Thr, Leu, or Ser of exons having ClIP binding sites for SRSF1, SRSF3, TRA2, HNRNPK, HNRNPL, or PTBP1. (*) Randomization test FDR < 0.05.

C. Relative frequency (%), when compared to sets of control exons, of G, C, A, CA, AC, CT, or TC (di)nucleotides of exons regulated by and having ClIP binding sites for SRSF1, SRSF3, TRA2, HNRNPK, HNRNPL, or PTBP1. (*) Randomization test FDR < 0.02.

D. Relative frequency (%), when compared to sets of control exons, of Gly, Pro, Lys, His, Gln, Thr, Leu, or Ser of exons regulated by and having ClIP binding sites for SRSF1, SRSF3, TRA2, HNRNPK, HNRNPL, or PTBP1. (*) Randomization test FDR < 0.05.

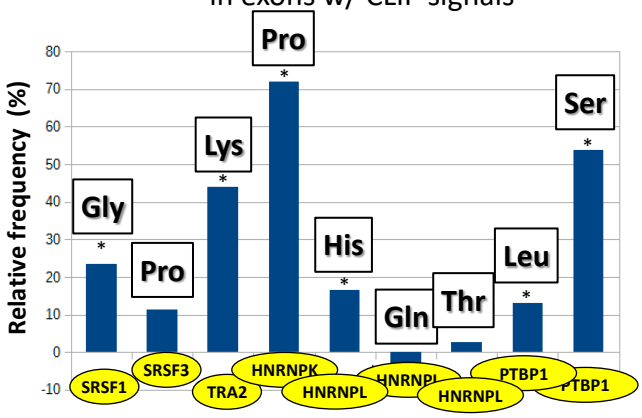
A

(di)nucleotide composition bias in exons w/ CLIP signals



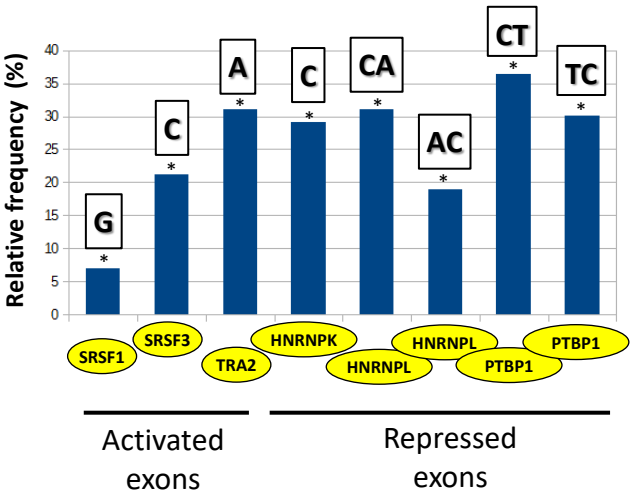
B

Amino acid composition bias in exons w/ CLIP signals



C

(di)nucleotide composition bias in splicing factor regulated-exons & w/ CLIP signals



D

Amino acid composition bias in splicing factor regulated-exons & w/ CLIP signals