

Supplemental Fig S3

A. Color code of the relative frequency, when compared to sets of control exons, of the codons of SRSF1-, SRSF2-, SRSF3-, and TRA2-activated or -repressed exons using datasets generated from different cell lines as indicated. The frequency of each codon was calculated in activated and repressed exons and expressed as the % of the average frequency calculated in 10 000 sets of control exons. Red and green colors indicate when the frequency is higher and lower, respectively, in the set of regulated exons compared to sets of control exons. The “activated vs. repressed” column shows the relative frequency of each codon calculated in activated exons, when compared to the frequency calculated in repressed exons.

B. Same as above using exons regulated by HNRNPH1, HNRNPK, HNRNPL, or PTBP1. The “repressed vs. activated” column shows the relative frequency of each codon calculated in repressed exons compared to the frequency calculated in activated exons.

B

Activated exons



Repressed exons

Repressed
vs. activated

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HNRNPH1*G-rich*

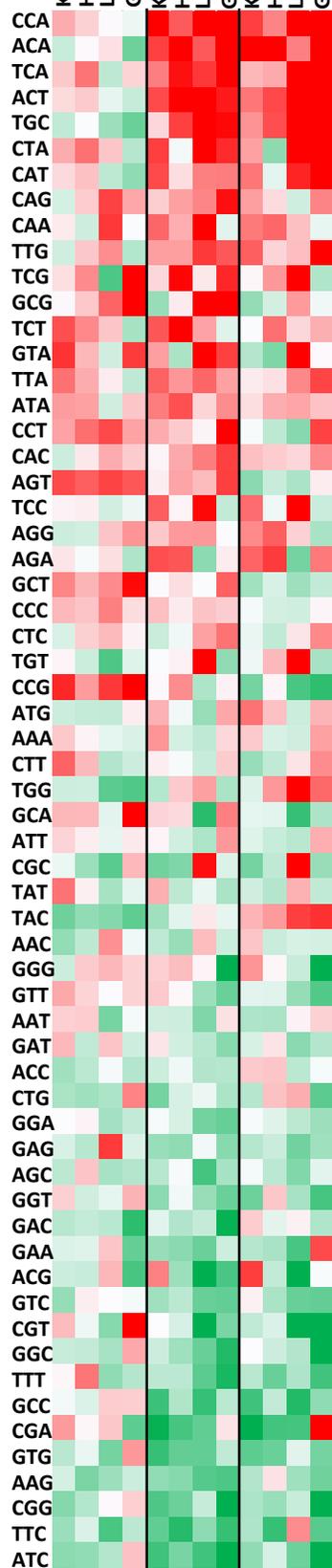
293T 293T 293T

**HNRNPK***CcA_nCC*

K562 GM HepG2 K562 GM HepG2 K562 GM HepG2

**HNRNPL***ACAc_nA*

K562 HepG2 LnCap GM K562 HepG2 LnCap GM K562 HepG2 LnCap GM

**PTBP1***CT-rich*

K562 293T HepG2 HeLa K562 293T HepG2 HeLa K562 293T HepG2 HeLa

