

```

ENST00000395392 RNLQOELETQNKQLQRQFSDKRRLEARLQGMVTETTMKWEKECERRVAAKQLEMQNKLWV
ENST00000352331 RNLQOELETQNKQLQRQFSDKRRLEARLQGMVTETTMKWEKECERRVAAKQLEMQNKLWV

ENST00000395392 KDEKCLKQLKAIVTEPKTEKPERPSRERDREKVTQRSVSPSPVPLSSNYIAQISNGQQLMS
ENST00000352331 KDEKCLKQLKAIVTEPKTEKPERPSRERDREKVTQRSVSPSPVP-----

ENST00000395392 QPQLHRRSNSCSSISVASCISEWEQKIPTYNTPLKVTSIARRRQQEPGQSKTCIVSDRRR
ENST00000352331 -----

ENST00000395392 GMYWTEGREVVPTFRNEIEIEEDHCG-----RNAPP IRLRHRRSRSAGDRWVDHKPAS
ENST00000352331 -----LLFQPDQNAPP IRLRHRRSRSAGDRWVDHKPAS

ENST00000395392 NMQTETVMQPHVPHAITVSVANEKALAKCEKYMLTHQELASDGEIETKLIKDIYKTRGG
ENST00000352331 NMQTETVMQPHVPHAITVSVANEKALAKCEKYMLTHQELASDGEIETKLIKDIYKTRGG

```

Figure S6. *KIF23* Internal substitution.

A section of the pairwise alignment between two *KIF23* isoforms. The internal exon substitution results in a swap 100 residues for just six residues. There is no homology. These substitutions were very rare in the proteomics experiments.