

Table S2. Structural Comparisons of the Selected Four Pairs of Alternative Splice Isoforms in Table 1.

| Exon gene | Skipped exon^a | Longer isoform^b | Shorter isoform^c | C-score^d | RMSD (Å)^e | TM-score^f |
|------------------|---------------------------------|-----------------------------------|------------------------------------|----------------------------|-----------------------------|-----------------------------|
| RNF8 | 7 (69 aa) | ENSP000000362578 | ENSP000000229866 | -1.28/-2.30 | 7.34 | 0.199 |
| SLC25A15 | 3 (46 aa) | ENSP000000342267 | ENSP000000368838 | 1.39/-0.81 | 3.57 | 0.354 |
| PPP5C | 5 (22 aa) | ENSP000000012443 | ENSP000000375786 | 0.22/0.36 | 0.66 | 0.739 |
| NARF | 3 (45 aa) | ENSP000000309899 | ENSP000000283996 | 0.38/1.00 | 2.37 | 0.809 |

^a Position of skipped exon in longer isoform. The length of amino acid encoded by the skipped exon is given in parenthesis.

^b Isoform including the exon which is skipped in shorter isoform.

^c Isoform in which exon is skipped.

^d Confidence score for the quality of predicted models by I-TASSER. C-score of higher value signifies a model with a high confidence and vice-versa. (longer isoform/shorter isoform)

^e Value between residues that are structurally aligned by TM-align.

^f Scale for measuring the structural similarity between two structures. TM-score >0.5 indicates a model of correct topology and a TM-score<0.17 means a random similarity.