The C. elegans ortholog of KIF5B is unc-116

worm fly fish human	1	MEP-RTDGAECGVQVFCRIRPLNKTEEKNADRFLPKFPSEDSISLGGKVYVFDKVFK MSAEREIPAEDSIKVVCRFRPLNDSEEKAGSKFVVKFPNNVEENCISIAGKVYLFDKVFK MVDAAECCVKVMCRFRPLNESEINRGDKYIPKFKGEDTVVIAGKPYIFDRVLP MADLAECNIKVMCRFRPLNESEVNRGDKYIAKFQGEDTVVIASKPYAFDRVFQ
		T <u>hr9</u> 0
worm	57	PNTTQEQVYKGAAYHIVQDVLSGYNGTVFAYGQTSSGKT ITMEGVIGDNGLSGIIPRIVA
fly	61	PNASQEKVYNEAAK <mark>SIVTDVLAGYNGTIFAY</mark> GQTSSGKT <mark>ITMEGVIGD</mark> SVKQGIIPRIVN
fish	54	PNTTQEQVY <mark>DTC</mark> AKQIVKDVLDGYNGTIFAY <mark>GQTSSGKT</mark> TMEGQLHNAQLMGIIPRI <mark>A</mark> Q
human	54	SSTSQEQVYNDCAKKIVKDVLEGYNGTIFAYGQTSSGKT ITMEGKLHDPEGMGIIPRIVQ
		Thr87
worm	117	DIFNHIYSMDENL <mark>QFHIKVSYYEIYN</mark> EKIRDLLD <mark>PE</mark> K <mark>V</mark> NLSIHEDKNRVPYVKG <mark>A</mark> TERFV
fly	121	DIFNHIY <mark>AMEV</mark> NLEFHIKVSYYEIYMDKIRDLLDVSK <mark>V</mark> NLSVHEDKNRVPYVKG <mark>A</mark> TERFV
fish	114	DIF <mark>E</mark> HIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSK <mark>T</mark> NL <mark>A</mark> VHEDKNRVPFVKG <mark>C</mark> TERFV
human	114	DIFN <mark>Y</mark> IYSMDENLEFHIKVSYFEIYLDKIRDLLDVSK <mark>T</mark> NLSVHEDKNRVPYVKG <mark>C</mark> TERFV

## S2 Fig. KIF5B P-loop nucleotide binding domain is highly conserved between species.

Multiple sequence alignment of the N-terminal part of the motor domain of *KIF5B* and orthologs in other organisms. The highly conserved P-loop region of the ATP-binding domain is highlighted with a green box. The KIF5B p.Thr87Ile variant in proband 1 (red arrowhead) and corresponding *C. elegans* (worm) *unc-116* Thr90 residue (blue arrowhead) are shown.