

COLORFY MAJORITY IDENTITY : 61-70 71-80 81-90 91-100  
COLORFY CONSERVED MINORITY : 61-70 71-80 81-90 91-100

*Mm* ..WSDQIKFVDSLNKPEPK...KYNVLTFFDSLGMVLLQVINLVLAIEDPKQ.DVDIREEMPEQTAKRMSLGLGLYKYPGNATDM 83  
*Hs* ..WSDQIKFVDSLNKPEPK...KYNVLTFFDSLGMVLLQVINLVLAIEDPKQ.LVDIREEMPEQTAKRMSLGLGLYKYPGNATDM 83  
*Gg* ..WSDQIKFVDSLNKPEPK...KYNVLTFFDSLGMVLLQVINLVLAIEDPKH.AVDIREEMPEQTAKRMSLGLGLYKYPGNATDM 83  
*Xt* ..WSDQIKFVDSLNKPEPK...KYNVLTFFDSLGMVLLQVINLVLAIEDPKH.SVDIREEMPEQTAKRMSLGLGLYKYPGNATDM 83  
*Dr* ..MSEQLKFIVEQNKPEPK...KNVNLTFDSLGMVLLQVINLVLAIEDPKQ.AIDIREEMPEQTAKRMSLGLGLYKYPGNATDM 83  
*Sp* ..WSTILKVVVEQNKPEPK...RNVNLTFDSLGMVLLQVINLVLAIEDPKH.KLDIREEMPEQTAKRMSLGLGLYKYPGNATDM 80  
*Ci* ..WTEEAKLIVELNKPEPK...KNVNLTFDSLGMVLLQVINLVLAIEDPKQ.SGDIREEMPEQTAKRMSLGLGLYKYPGNATDM 82  
*Cr* ..MGDVSIVDSLNKPEPK...YQMSLLSFTKGGQELLQVLSVDFSTSSKHQKVDVAKVEPEQTAKRMSLGLGLYKYPGNATDM 81  
*Mp* MVLGDDIAIVARKEPFGGARYASLTGPELSEGGDATRELCEAFATVAVAWGDDARDARGHHGGEDPLDFRHAHYAAPP.STIA 89

*Mm* STFRQGLVIISKPIVYVWHLNLTORTNELKKRAYLARFLIKLEVSEFLQDE...TVADINKOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Hs* STFRQGLVIISKPIVYVWHLNLTORTNELKKRAYLARFLIKLEVSEFLQDE...TVADINKOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Gg* STFRQGLVIISKPIVYVWHLNLTORTNELKKRAYLARFLIKLEVSEFLQDD...TVADINKOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Xt* STFRQGLVIISKPIVYVWHLNLTORTNELKKRAYLARFLIKLEVSEFLQDD...TVADINKOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Dr* STFRQGLVSIISKPIVYVWHLNLTORIPELAKRAYLARFLIKLEVSEFLQDD...VIAETVHYOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Sp* STFRQGLVSIISKPIVYVWHLNLTORIPELAKRAYLARFLIKLEVSEFLQDD...VIAETVHYOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Ci* STFRQGLVSIISKPIVYVWHLNLTORIPELAKRAYLARFLIKLEVSEFLQDD...VIAETVHYOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Cr* STFRQGLVSIISKPIVYVWHLNLTORIPELAKRAYLARFLIKLEVSEFLQDD...VIAETVHYOYEELMFAFKTLHKECEOLKTSGLSTAE 170  
*Mp* LLMGAAFAAEHDFVFAAEVFLSDDLRCARAVVGHFLADVPVPEPTRDD...DVQELIHERH...QROFVEIEAVDAARAFKDPVK 176

*Mm* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLIKLARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Hs* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLIKLARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Gg* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Xt* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Dr* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Sp* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Ci* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Cr* IRRDISAMEEEKDOLIKRVERLKRVRITVONHOR...MLELARQLVVEKEREEFLAQKQKPKNQLFHAVORLQVONDKSMRHAAD 256  
*Mp* LKQRATQLRERKAIASAVAVVCKIASRVDRSRVAALTRHATSRAAREEEMELARALRECYEKKSDAKYCAAVRLEHRASTAS 266

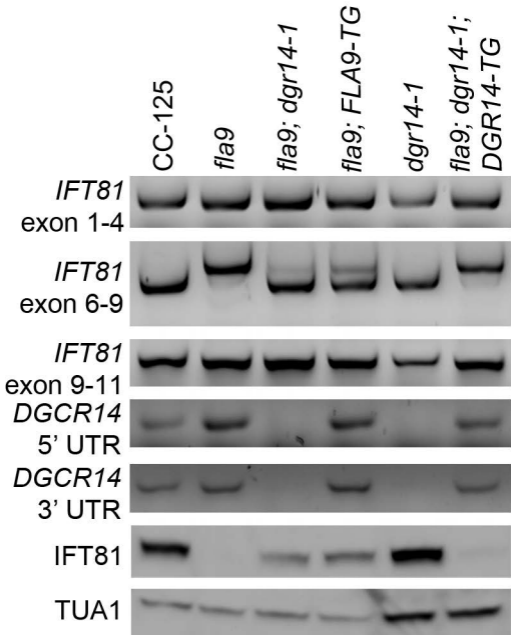
*Mm* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Hs* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Gg* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Xt* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Dr* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Sp* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Ci* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Cr* AKPESIMKLEEEIKFNSMVTTEFFKELSKKELHFLQKVVSEFAMGHSDLLETKVNEVNTENQLEKMMRNEIEEG...L 341  
*Mp* GNNAIAAASDVENARALAREHLEAEKKRARSVAKEIASDARADSRRATEDVNALQAEITREESVAVLTKARDAD...AA 353

*Mm* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Hs* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Gg* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Xt* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Dr* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Sp* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Ci* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 423  
*Cr* SLYRQOASISRAKKEAKAELEQETKEKLASLERVLVLTNQTREF...DTEVLKGDDEFKRYVVKLSKSTVFKKKHQIIEAFKA 424  
*Mp* RQAQVYKVAARKDATRKRDKLRRARDRTSYETGAVVREGDNTGTRERGAAGGGLDEEMRQKFETVKAALARYKQLKRLDVEAA 424

*Mm* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 513  
*Hs* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 513  
*Gg* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 513  
*Xt* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 513  
*Dr* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 512  
*Sp* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 512  
*Ci* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 514  
*Cr* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 514  
*Mp* EFLQRTTEBLKQKHENIQOQAIKXKKSISYSDTOEELRVSALNSVDEMKGRTIDDMSEMVKKINSVSEKKSALAVYKELRQ 513

*Mm* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 603  
*Hs* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 603  
*Gg* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 603  
*Xt* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 603  
*Dr* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 602  
*Sp* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 602  
*Ci* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 601  
*Cr* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 594  
*Mp* LRQKQDELTQPCDEKKAQVDSCAAGLESNRSKLCEVRGLREECLQEEESRYHYTNMKNLVEVLRATDEMAYVNSDQEKRAKAIHQ 613

*Mm* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 676  
*Hs* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 676  
*Gg* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 676  
*Xt* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 676  
*Dr* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 675  
*Sp* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 675  
*Ci* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 679  
*Cr* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 683  
*Mp* YTKNTAEOENLGRHRLTLPLRLCSGTILAHSAFYQRWDFPTLAR...LVNSN...QVIOEGGE...DRL... 686





## A. *ift121-2* intron retention transcript

TTCCAGGT . . . . . AGAGCGTG . . . . . CCAAGTACGCCAACCCACTCCTGGAGAAGGAGAAG **G** TAGGCGGGGC

change to A

GGGGCATTGCCACGGGTTTAGG **TAG** CTTGAGCGGCAGCAGGACTTCCATGCAGTTTGCGGGGCGTGTATGTGAA

PTC generated by inclusion of intron 21

TGGTCTTAATTTGATTGCCATTATCGAGTCGTTGTATTGATCACGTGTGTATCCGGGTGCAGGTC **ATG** GACGCC

putative start codon to resume translation

ATCGAGCTGTACCGCAAGGCCAACCCACTCCATGGAGGCGGCTCGGCTCCTGCAGGTTGGGACGCAAGTGGGCTGG  
ATCATGGGGGGCAGAGAGCCGGACCGCTGTGTTTCAGCCACACCCTAGGAGCCATTGCGCCTCTGACACGCACC  
TGCGGCCCGGGCCCGTGCACCCCCACAGGACCTGGCAAAGAAGTGTGCGGACCAGAAGGTGCACCCGCTACGCG  
TTAAGAAGCTGTACGTGCTGGCGGCGCTGGAGATTGAGAAATCAAGAAGCGCACCGTAGACATGGCAGGGCCG  
GACAAGACCGCCGCCACGCTGCTGGGCACCGGCGGCACCG

## B. *ift121-2* exon truncation transcript

TTCCAGGT . . . . . AGAGCGTG . . . . . CCAAGTACGCCAACCCACTCCTGGAGAAGGAGAAG **S** TAGGCGGGGC

new donor splice site

change to A

GGGGCATTGCCACGGGTTTAGGTAGCTTGAGCGGCAGCAGGACTTCCATGCAGTTTGCGGGGCGTGTATGTGAA  
TGGTCTTAATTTGATTGCCATTATCGAGTCGTTGTATTGATCACGTGTGTATCCGGGTGCAGGTCATGGACGCC  
ATCGAGCTGTACCGCAAGGCCAACCCACTCCATGGAGGCGGCTCGGCTCCTGCAGGTTGGGACGCAAGTGGGCTGG  
ATCATGGGGGGCAGAGAGCCGGACCGCTGTGTTTCAGCCACACCCTAGGAGCCATTGCGCCTCTGACACGCACC  
TGCGGCCCGGGCCCGTGCACCCCCACAGGACCTGGCAAAGAAGTGTGCGGACCAGAAGGTGCACCCGCTACGCG  
TTAAGAAGCTGTACGTGCTGGCGGCGCTGGAGATTGAGAAATCAAGAAGCGCACCGTAGACATGGCAGGGCCG

PTC generated by deletion of 31 nt of exon 21

GACAAGACCGCCGCCACGCTGCTGGGCACCGGCGGCACCG

## C. *ift121-2* rev26

TTCCAGGT . . . . . AGAGCGTG . . . . . CCAAGTACGCCAACCCACTCCTGGAGAAGGAGAAG **S** TAGGCGGGGC

change to A change to A

GGGGCATTGCCACGGGTTTAGGTAGCTTGAGCGGCAGCAGGACTTCCATGCAGTTTGCGGGGCGTGTATGTGAA  
TGGTCTTAATTTGATTGCCATTATCGAGTCGTTGTATTGATCACGTGTGTATCCGGGTGCAGGTCATGGACGCC  
ATCGAGCTGTACCGCAAGGCCAACCCACTCCATGGAGGCGGCTCGGCTCCTGCAGGTTGGGACGCAAGTGGGCTGG  
ATCATGGGGGGCAGAGAGCCGGACCGCTGTGTTTCAGCCACACCCTAGGAGCCATTGCGCCTCTGACACGCACC  
TGCGGCCCGGGCCCGTGCACCCCCACAGGACCTGGCAAAGAAGTGTGCGGACCAGAAGGTGCACCCGCTACGCG  
TTAAGAAGCTGTACGTGCTGGCGGCGCTGGAGATTGAGAAATCAAGAAGCGCACCGTAGACATGGCAGGGCCG  
GACAAGACCGCCGCCACGCTGCTGGGCACCGGCGGCACCG

## D. *ift121-2* rev28

TTCCAGGT . . . . . AGAGCGTG . . . . . CCAAGTACGCCAACCCACTCCTGGAGAAGGAGAAG **S** TAGGCGGGGC

new donor splice site

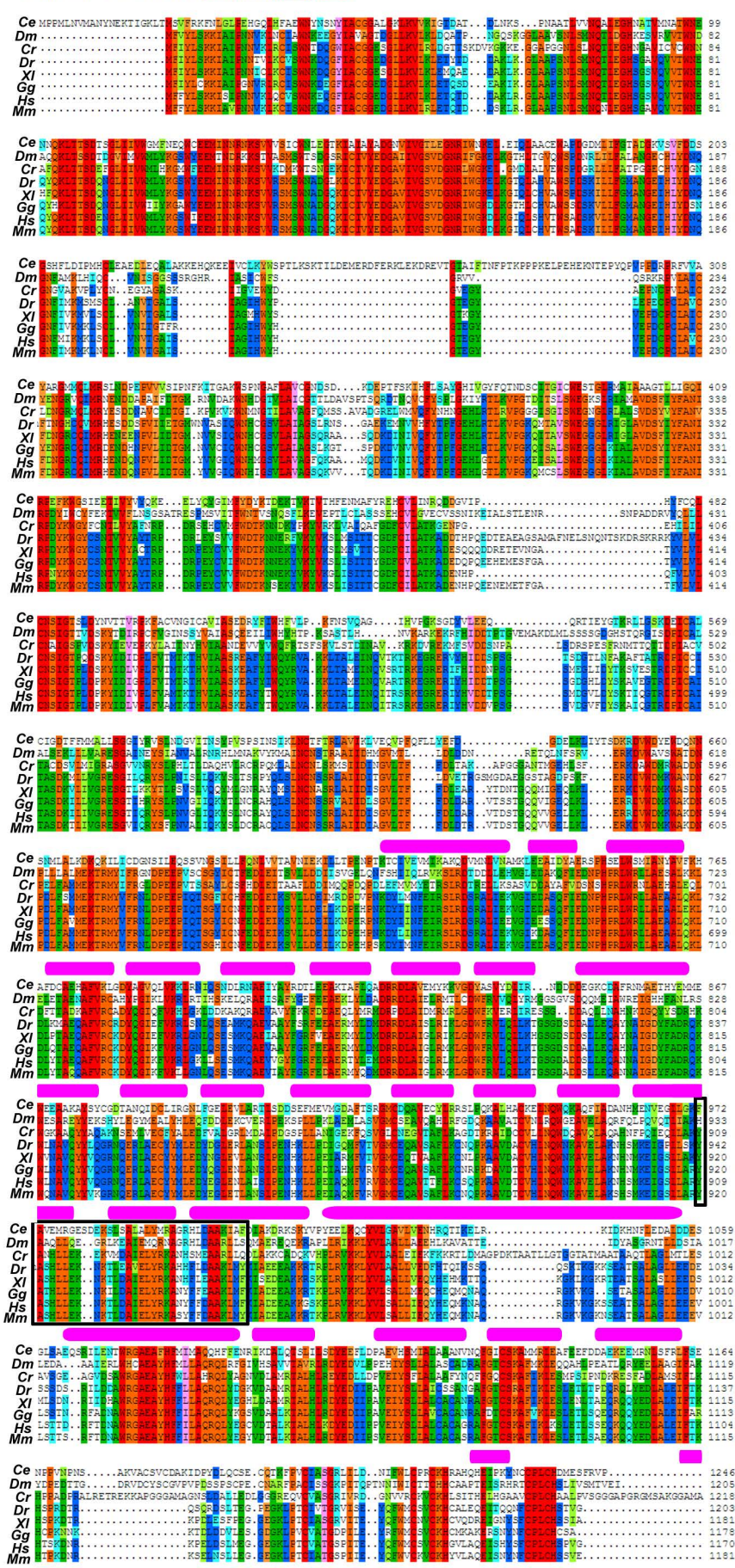
change to A

GGGGCATTGCCACGGGTTTAGGTAGCTTGAGCGGCAGCAGGACTTCCATGCAGTTTGCGGGGCGTGTATGTGAA  
TGGTCTTAATTTGATTGCCATTATCGAGTCGTTGTATTGATCACGTGTGTATCCGGGTGCAGGTCATGGACGCC  
ATCGAGCTGTACCGCAAGGCCAACCCACTCCATGGAGGCGGCTCGGCTCCTGCAGGTTGGGACGCAAGTGGGCTGG

change to A new donor splice site

ATCATGGGGGGCAGAGAGCCGGACCGCTGTGTTTCAGCCACACCCTAGGAGCCATTGCGCCTCTGACACGCACC  
TGCGGCCCGGGCCCGTGCACCCCCACAGGACCTGGCAAAGAAGTGTGCGGACCAGAAGGTGCACCCGCTACGCG  
TTAAGAAGCTGTACGTGCTGGCGGCGCTGGAGATTGAGAAATCAAGAAGCGCACCGTAGACATGGCAGGGCCG  
GACAAGACCGCCGCCACGCTGCTGGGCACCGGCGGCACCG

COLOR BY MAJORITY IDENTITY: ■ 100-70 ■ 71-80 ■ 81-90 ■ 91-100  
 COLOR BY CONSERVED MINORITY: ■ 61-70 ■ 71-80 ■ 81-90 ■ 91-100



Ce ..... 1246  
 Dm ..... 1205  
 Cr QMYGAY 1224  
 Dr ..... 1203  
 Xi ..... 1181  
 Gg ..... 1178  
 Hs ..... 1170  
 Mm ..... 1181

COLORFY MAJORITY IDENTITY :

61-70 71-80 81-90 91-100

COLORFY CONSERVED MINORITY:

61-70 71-80 81-90 91-100

Ce ....MDPKRIRNPFYHGIDDLQSDFGDEPSSSSKPKRKGDFLNKDYSSSEILKKRKTIDGRGGFFEHHGRMHR. ....MAKMMSSNNYDRHKEMNNLYIYYSPG 93  
 Cr .....MANFGETRRSAFGRHAHAAOCHYATITLGLNADRRRLVNDYLYTYAR 47  
 At .....MTSSAAIRSDIYDREERKQQYQAHIRGLNAYERHKKFLKDYVRFYK 47  
 Dm .....NNLSKKEKRNKYLNNVNLNPN 22  
 Dr MMSDMDKSALDLVKVHGGGGYDSDFSDDDGGGHSKIDGENRAGQDEL.LQKPFQKQKHTKVAHKNVAAHWLREEARNR.RCHLISMNAFERHKKFVSDYIYYYG 103  
 Hs .....MHGGGGYDSDFSDDERCGESSKRRKRTVEDDLQKPFQKEKHKQVAHQAVAELLREEARNR.RFHLIAMDAYQRHTFVNDYIYYYG 90  
 Mm .....MHGGGGYDSDFSDDEQGGGSSKRRKRTVEDELLTKPFQKERHGKVAHQVAADLLREEARNR.RFHLIAMDAYQRTFVNDYIYYYG 90

Ce ATKLLNRKIQDE....TITDVLKPKHHRFVSSDEIINASQDPKNSHWETIRMAKYDYDKLFEKYCTVDLSMYTIRIEMRWRTENEWKEKKGQLSGARKCNETA 193  
 Cr GVPGPQGGPPPAGAEKAVRTDADALREHHRIRTEEDGDH....GWEARLAKRYDRIFKENVIVDLSFYFYSRLGMRWRTQKQVSGKGFVCGALGCEASD 146  
 At DKPAEVKLPV.....KIQDITLREGYRIRSEEIDLDPE....SWEQRLVRYDYDKLFEKYCIADLRYMRYTKMGLRWRTQKQVSGKGFVCGALGCEASD 139  
 Dm ETESRRH.....RQDIQVIRENHRRLVDEEDLDS...DTLSWEQRLALRYRKLFEKYCIADLRYMRYTKMGLRWRTQKQVSGKGFVCGALGCEASD 113  
 Dr KIEDLRSTSKD....KITDLVVKENHRRLNNEEDADM....TWEKRLAKRYDYDKLFEKYCIADLRYMRYTKMGLRWRTQKQVSGKGFVCGALGCEASD 197  
 Hs KKEDFKRLGEND....KITDLVIRENHRRLNNEEDADM....TWEKRLAKRYDYDKLFEKYCIADLRYMRYTKMGLRWRTQKQVSGKGFVCGALGCEASD 184  
 Mm KREDFKRLGEND....KITDLVIRENHRRLNNEEDADM....TWEKRLAKRYDYDKLFEKYCIADLRYMRYTKMGLRWRTQKQVSGKGFVCGALGCEASD 184

Ce HRSWEVNFTHKEDNVRKSTLVKARLHPKSEKINIGTRKR.....QVVQKRA.....VQKWEKERKRKKDEEEDDDVELNQHEA 270  
 Cr SACSYEVNFAQEAAGERKQALVYLVVPCAFKLNVRKQVQKADAAAKKRREEREEAALETADPLVREALQYVKRYAAGDKAAGEGAAGEGLGEEDLLR 251  
 At SASYEVNFAQEAAGEDKQALVYLVVPCAFKLNVRKQVQKADAAAKKRREEREEAALETADPLVREALQYVKRYAAGDKAAGEGAAGEGLGEEDLLR 228  
 Dm NRSWEVNFTHKEDNVRKSTLVKARLHPKSEKINIGTRKR.....QVVQKRA.....VQKWEKERKRKKDEEEDDDVELNQHEA 202  
 Dr SACSYEVNFAQEAAGEKRNALVKLRQLPECSYKLNHHKRR.....EVIAKRARRSKENLDVSKSSKSKSRKQKDKRKHKKRKHHSSEESQESDK 294  
 Hs HRSWEVNFTHKEDNVRKSTLVKARLHPKSEKINIGTRKR.....QVVQKRA.....VQKWEKERKRKKDEEEDDDVELNQHEA 275  
 Mm SACSYEVNFAQEAAGEKRNALVKLRQLPECSYKLNHHKRR.....EVIAKRARRSKENLDVSKSSKSKSRKQKDKRKHKKRKHHSSEESQESDK 275

Ce KNQETKVPSTST.....LSASTDIWE.GSPPAEETKTVDDLIDEDFLDDELFL... 316  
 Cr AARDVAPPVAAAAGGSGPAGAGGAAGVGPAPAIITLPADNSVWE..SKPAQETATABE.MDAYFEGLFM.. 319  
 At RSQSHEIDTDEE.....DRKGTTRKSKLESADREGKDDENDEYMEGMFPNG 278  
 Dm ASKEPTDSKDDT.....TAEQINQQQSDISREQASREQLFERYLEDLIF.. 247  
 Dr GSDDDDDDEDADG.....PSESEHKKGPAAVAVEEKSREEEYFEYFQDDELFL... 339  
 Hs RNSDEEES.....ASESELWK.GPLPETFDEKSEQEELFDEYFQDDELFL... 315  
 Mm RNAAEEDS.....ASDSELWK.GPLPETFDEKSEQEELFDDYFQDDELFL... 315



CC-124

CC-125

*ift121-2*

*ift121-2; fra10*

*ift121; fra10;*  
*FRA10-TG*

#3

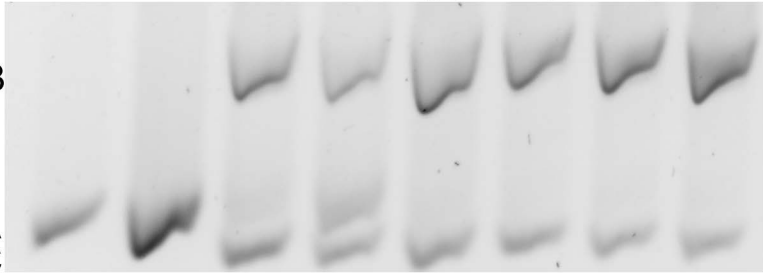
A3

E8

H12

B

A  
C





**Supplemental Figure 1.** Protein sequence alignment of IFT81. Sequence similarity percentage is displayed by colors shown above the alignment. The position of exon 8, which is skipped in some of the *flag* transcripts, is indicated in the dashed black box. The three amino acids (V<sub>275</sub>N<sub>276</sub>E<sub>277</sub>) that are deleted in some of the *flag* transcripts, are indicated by reversed triangles in magenta. Abbreviations of species and NCBI accession numbers of individual proteins used in alignment are the following: *Ci*, *Ciona intestinalis*, XP\_002126367.1; *Cr*, *Chlamydomonas reinhardtii*, XP\_001697224.1; *Dr*, *Danio rerio*, AAI63882.1; *Gg*, *Gallus gallus*, NP\_001239238.2; *Hs*, *Homo sapiens*, NP\_001334876.1; *Mm*, *Mus musculus*, NP\_034009.2; *Mp*, *Micromonas pusilla* CCMP1545, XP\_003061494.1; *Sp*, *Strongylocentrotus purpuratus*, XP\_011667377.1; *Xt*, *Xenopus tropicalis*, XP\_004910569.1.

**Supplemental Figure 2.** The *IFT81* transcripts and the IFT81 protein at 32 °C. The cells were initially incubated at 21 °C for 2 hours. One-half of the cells was transferred to 32 °C and incubated for 4 hours while the other was maintained at 21 °C (Figure 2B and 2C). Isolation of both RNA (top four panels) and proteins (bottom two panels) from samples at both temperatures were performed at the end of 6 hours since first incubation.

**Supplemental Figure 3.** Protein sequence alignment of DGR14. Sequence similarity percentage is displayed by colors shown above the alignment. Two predicted coiled coil domains (CC) are labeled. The second CC domain is predicted in the human protein but not in the *Chlamydomonas* homolog. Abbreviations of species and NCBI accession numbers (unless indicated otherwise) of individual proteins used in alignment are the following: *At*, *Arabidopsis thaliana*, NP\_187436.1; *Ce*, *Caenorhabditis elegans*,

NP\_001022580.1; *Cr*, *Chlamydomonas reinhardtii*, Cre11.g482050 (*Chlamydomonas* Phytozome genome assembly v5.5); *Dm*, *Drosophila melanogaster*, NP\_572480.1; *Dr*, *Danio rerio*, NP\_001082799.2; *Hs*, *Homo sapiens*, NP\_073210.1; *Mm*, *Mus musculus*, AAC40077.1; *Sp*, *Schizosaccharomyces pombe*, NP\_587842.1.

**Supplemental Figure 4.** Nucleotide sequences and splicing details of *IFT121* in various *ift121* mutants. Exon sequences are indicated with bold letters and intron sequences are indicated with plain letters. Mutations and splicing effects are indicated with underlines. (A) The *ift121-2* mutant contains an intron retention transcript. The single nucleotide mutation in *ift121-2* is indicated in magenta. The premature termination codon (PTC) is highlighted in red. The putative start codon to resume translation is highlighted in green. (B) The *ift121-2* mutant also contains a transcript that deletes the last 31 nucleotides of exon 21. Both single nucleotide mutation and the new donor splice site are indicated in magenta. The 31 nucleotides that are removed due to the choice of the new donor site are indicated in the dashed blue box. (C) The *ift121-2 rev26* mutant carries a single nucleotide mutation (highlighted in orange) 7 nucleotides upstream of the original mutation (highlighted in magenta). No deletion of 31 nucleotides is detected in this strain. (D) The *ift121 rev28* mutant contains a single nucleotide mutation (highlighted in blue) in intron 22. A new donor site that is 7 nucleotides downstream of this change is indicated in blue. The skipped 31 nucleotides (same as in (B)) are indicated in the dashed blue box and the newly included 7 nucleotides are indicated in the solid blue box.

**Supplemental Figure 5.** Protein sequence alignment of IFT121. Sequence similarity percentage is displayed by colors shown above the alignment. Alpha helices predicted

by YASPIN are indicated by magenta blocks above the sequences. The amino acids that are replaced in *ift121 rev28* are indicated in the black box. Abbreviations of species and NCBI accession numbers of individual proteins used in alignment are the following: *Ce*, *Caenorhabditis elegans*, NP\_508940.4; *Cr*, *Chlamydomonas reinhardtii*, XP\_001702021.1; *Dm*, *Drosophila melanogaster*, NP\_647653.1; *Dr*, *Danio rerio*, NP\_001139061.1; *Gg*, *Gallus gallus*, XP\_419970.3; *Hs*, *Homo sapiens*, AAH36659.1; *Mm*, *Mus musculus*, AAH56925.1; *Xl*, *Xenopus laevis*, XP\_018121446.1.

**Supplemental Figure 6.** Protein sequence alignment of FRA10. Sequence similarity percentage is displayed by colors shown above the alignment. Abbreviations of species and NCBI accession numbers (unless indicated otherwise) of individual proteins used in alignment are the following: *At*, *Arabidopsis thaliana*, NP\_193239.5; *Ce*, *Caenorhabditis elegans*, NP\_001129806.1; *Cr*, *Chlamydomonas reinhardtii*, Cre07.g336250 (*Chlamydomonas* Phytozome genome assembly v5.5); *Dm*, *Drosophila melanogaster*, AAM48345.1; *Dr*, *Danio rerio*, NP\_001006006.2; *Hs*, *Homo sapiens*, NP\_660289.2; *Mm*, *Mus musculus*, NP\_001074544.1.

**Supplemental Figure 7.** Partial protein sequence alignment of SMG1 around the highly-conserved phosphatidylinositol 3-kinase-related kinase domain. Sequence similarity percentage is displayed by colors shown above the alignment. Abbreviations of species and NCBI accession numbers of individual proteins used in alignment are the following: *Ce*, *Caenorhabditis elegans*, NP\_001021053.1; *Cr*, *Chlamydomonas reinhardtii*, XP\_001693485.1; *Dm*, *Drosophila melanogaster*, CAD89223.1; *Dr*, *Danio rerio*, NP\_001073513.2; *Hs*, *Homo sapiens*, NP\_055907.3; *Mm*, *Mus musculus*, NP\_001026984.1; *Zm*, *Zea mays*, XP\_008665371.1.

**Supplemental Figure 8.** *IFT121* splicing in *ift121-2; fra10; FRA10-TG* transformants.

Four independent *ift121-2; fra10; FRA10-TG* transformants (#3, A3, E8, H12) all replicated the alternative splicing pattern of *IFT121* between exons 20 to 23 as found in *ift121-2*. Transformant #3 was used for further study. The A, B, C bands are identical to those described in Figure 4B.

**Supplemental Table 1: Primers used in this study.**

Strain	Forward primer sequence	Reversed primer sequence	Annealing temperature	Enzyme	Fragments (bp, wild-type; mutant)
<i>fla9/ift81-2</i>	CCGGTATTGTCTTAGGGAGCTT	ACTTTGCGCTCCTGGATCT	53 °C	<i>FspI</i>	168+135; 303
<i>ift121-2</i>	GCACAACCTCCCGCAGAT	CAC TTCTTTGCCAGGTCCTG	53 °C	<i>MboII</i>	419; 343+76
<i>4c/dgr14-1</i>	CTTCCAAGGGTACCCGTAAT	GCTGGAGAGAAGATGCAGAG	53 °C	n/a	115; no amp
<i>dgr14-2</i>	TGGCAGAGGGAATGATGGAA	GCCACCGCCAGTTTGTG	53 °C	n/a	202; no amp
<i>sup15/fra10-1</i>	CATCCCAGCCTGCCGTCTC	GCCGCCTCCTCACGCTCGCGCTTA	61 °C	n/a	132; no amp
<i>smg1-1</i>	ACGAGGTGGCTTGGATGG	CTGCCACTGTTGCTGT	53 °C	<i>AcuI</i>	89+61; 150
<i>smg1-2</i>	CTTGCCTACAACGCCTTCC	GCAGGCGCGCAATTCATAAT	53 °C	<i>BsrBI</i>	159+83; 242
<i>smg1-3</i>	CTGCTGCCACACCTTCAG	CCTGCTGTTGCTGCCTATG	53 °C	<i>AluI</i>	169; 113+56
<i>smg1-4</i>	AAGAGCACGAACAGGCACAG	CGGTGGTGCTGCACATGTT	53 °C	<i>MseI</i>	145; 125+20
<i>smg1-5</i>	CGCTATCCCATCTACTGCCA	CTCACGGCCCTCCAGCTT	53 °C	<i>MnII</i>	100+57+18; 157+18

Primer	Sequence
IFT81 ex1-ex4 F	TGAGCTACATCGTGGACAGC
IFT81 ex1-ex4 R	ATCGGGGAAGCTCAGGTAGT
IFT81 ex6-ex9 F	GAGGAGGTCAACCTGTCCAC
IFT81 ex6-ex9 R	GCTTGCTCTTCATGCTCTCA
IFT81 ex9-ex11 F	TGAGAGCATGAAGAGCAAGC
IFT81 ex9-ex11 R	GATGGCGTTGTTGATCTCCT
IFT121 rt-1F	ACATCGGCGAGAAGTTCCAG

IFT121 rt-1R	CACTTCTTTGCCAGGTCCTG
FRA10-1F	GGCACTGCGTCTAGTTGGGG
FRA10-1R	CCTCAGCTGCAGGGACGAAG
DGR14 5'F	CTTCCAAGGGTACCCGTAAT
DGR14 5'R	GCTGGAGAGAAGATGCAGAG
DGR14 3'F	CTTACGTTCGCAGTTGGCTAT
DGR14 3'R	CAGGCACGGAGCAGTACTAT
SMG1 ex5 F	ACGAGGTGGCTTGGATGG
SMG1 ex5 R	CTGCCACTGTTGCTGT
SMG1 ex13 F	CTGCTGCCACACCTTCAG
SMG1 ex13 R	CCTGCTGTTGCTGCCTATG
SMG1 ex30 F	CGCTATCCCATCTACTGCCA
SMG1 ex30 R	CTCACGGCCCTCCAGCTT

**Supplemental Table 2. Summary of whole genome sequencing results**

Strain	Total reads	Aligned reads	Coverage	% Aligned	# of Total changes	# of Unique changes	# of Putative changes	Gene
4c	193037602	186941282	17	96.8	81824	1193	0	<i>DGR14</i>
db35	43153902	37130207	34	86.0	42347	4873	23	<i>IFT121, RPG1</i>
<i>ift121-2;</i> <i>fra10</i>	57912006	54666636	50	94.4	66592	3449	5	<i>FRA10</i>
<i>smg1-1</i>	44901754	37928187	51	84.5	41270	5667	66	<i>SMG1</i>
<i>smg1-2</i>	46883800	40780679	55	87.0	43036	6431	49	<i>SMG1</i>
<i>smg1-3</i>	64887908	58420470	79	90.0	46260	6524	68	<i>SMG1</i>
<i>smg1-4</i>	42498864	36026593	49	84.8	42988	6145	52	<i>SMG1</i>
<i>smg1-5</i>	68079544	61463903	83	90.3	62894	7727	64	<i>SMG1</i>