| co<br>co   | DORFY MAJORITY IDENTITY : 61-70 71-80 81-90 91-100<br>DORFY CONSERVED MINORITY: 61-70 71-80 81-90 91-100   |  |
|--|--|--|
| Mm<br>Gg<br>Xt<br>Dr<br>Sp<br>Ci<br>Cr<br>Mp       | MSDQIKFIVDSINKEPFKKNYNLITFDSIGPMQLLQVINDVIAEID KQ.DVDIREEMPEQTAKRMINL GILKYK PGNATIM<br>MSDQIKFIMDSINKEPFKKNYNLITFDSIEPMQLLQVISDVIAEID KQ.LVDIREEMPEQTAKRMISL GILKYK PGNATIM<br>MSDQIFIVEKINQEPFKKNYNLITFDSIEPMQLLQVISDVIAEID KH.AVDIREELPENTAKRMITL GILKYK PGNATIM<br>MSDQIKFIVEKINGEPFKKNYNLITFDSIEPMQLLQVISDVIAEID KH.SVDIREEMPEQTAKRMITL GILKYK PGNYTDI<br>MSDQIKFIVEKINKEPFKKNYNLITFDSIEPMQLLQTISDVIAEID KH.SVDIREEMPEQTAKRMITL GILKYK PGNYTDI<br>MSDQIKFIVEKINKEPFKKNYNLITFDSIEPMQLLQTISDVIAEID KH.SVDIREEMPEQTAKRMITL GILKYK PGNYTDI<br>MSEQIKFIVEQINKEPFKKNYNLISTEALEPMQLLQTISDVIAEID KH.SVDIREEMPEQTAKRMISU GILKYK PGNYTDI<br>MSEQIKFIVEQINKEPFKKNYNLISTALEPLQIQUIDVISUIAEID KH.SVDIREEMPEQTAKRMISU GILKYK SGGMGEV<br>MSTILKYVEQINKEPFKKNYNLISTALEPLQILQVINDVISEVN QH.KLDIREETEDATAMRMISE RVLKYK SGGMGEV<br>MGTILKYVEQINKEPFKKNYNLISTALEPLQILQVINDVISEVN QH.KLDIREETEDATAMRMISE RVLKYKTVEP<br>MTEBAKLIVELINKEFKKNYNLISTA GEVGEQULQLINDVIATID SQ.SGJIRDASDARTORT GGIKNIKYT P.PNAV<br>MGDVSYIVDSIGIPPSYQMSLISTEKGFQELLQLISDVFSTISKHQKVDVAKEVFDQTADRIGFIKIIKYR NVQDP<br>MVLGDDIAFIVARIKEPFGGGARYASLTGPSISE GEDATRELCFIAFAIV AWGDDARDARGHHGGEDPL  | 83<br>83<br>83<br>83<br>83<br>80<br>82<br>81<br>89                 |
| Mm<br>Gg<br>Xt<br>Dr<br>Sp<br>Ci<br>Cr<br>Mp       | STFROGLVISSKPVIYEVIHWLLORSNELKKRAYLARFLIKLEVESSFLODETVADTNKOVEELMEA KTLHKECEOLKTSGFSTAE<br>STFROGLVISSKPVIYEVIHWLLORTNELKKRAYLARFLIKLEVESSFLODETVADTNKOVEELMEA KTLHKEYEOLKISGFSTAE<br>SAFROGLVASSKPVIHEVIHWLLORTNELKKRAYLARFLIKLEVESSFLODETVADTNKOVEELMEA KTLHKEYEOLKISGFSTAE<br>SVFROGLVASSKPVIHEVIHWLLORTNELKKRAYLARFLIKLEVEEFLODDTVADINKOVEELMEA KKILHKECEOLKSSGFSTAE<br>SSFROGLVSSSRPVHEITHWLLORTNELKKRAYLARFLIKLEVEEFLODDTVADTNKOVEELMEA KKILHKECEOLKSSGFSTAE<br>SSFROGLVSSSRPVHEITHWLLORTPELKKRAYLARFLIKLEVEEFLODDTVADTNKOVEELMEA KKILHKECEOLKSSGFSTAE<br>SSFROGLVASSRPVHEITHWLLORTPELKKRAYLARFLIKLEVEEFLODDTVADTNKOVEELMEN KMIHKECEOLKSSGFSTAE<br>SSFROGLVASSRPVHEITHULORTPELKKRAYLARFLIKTEVESTODDVIAETYHOVEELVEG KNIHKECEOLKSSGFSTAE<br>SSFROGLVASSRPVHEITHULORTPELKKRAYLARFLIKTEVESTIGDDDINSTYHOVEELVEG KNIHKECEOLKSSGFSTAE<br>SSFROGLVAADRETYDOITTOLKKRAYLARFLIKKIEVEG HAASSDFAMOESWIKKOLOEH HOMRELTDLKKOSHGS<br>LLFROLVAADRETYDOIT WUPQAOLLEKAEVGYTSSFPMEEENFDPDIMBLKEEIKAMOOE IELHSSDAIKTSLORD   | 170<br>170<br>170<br>170<br>170<br>167<br>172<br>168<br>176        |
| Mm<br>Hs<br>Gg<br>Dr<br>Sp<br>Cr<br>Mp             | IRRDISAMESEKDOLMKRVERLKRVETVCNHORMIKIAROLAVEKEREEFLAODKOECKNOLFHAVORLORVONDIKSMRHAAAD<br>IRKDISAMESEKDOLIKRVEHLKRVETAONHOWMIKIAROLAVEKEREEYLAODKOECKNOLFHAVORLORVONDIKSMRHAAAD<br>IRRDISAMESEKDOLIKRVERLKRVETVONHORMILEIAROLAVEKEREESLAODKOECKNOLFHAVORLORVONDIKSMRHAAAD<br>IRRDISAMESEKDOLIKRVERLKRVETVONHORMILEIAROLAVEKEREESLAODKOECKNOLFHADORLORAOLHLKEMOHAVVD<br>IRRDISAMESEKDOLIKRVERLKRVETVONHORMILEIAROLAVEKEREESLAODKOECKNOLFHADORLORAOLHLKEMOHAVVD<br>IRRDISAMESEKDOLIKRVERLKRVETVONHORMILEIAROLAVEKERESLAODKOECKNOLFHADORLORAOLHLKEMOHAVVD<br>IRRDISAMESEKDOLIKRVERLKRVETVONHORMILEIAROLAVEKERESLAODKOECKNOLFHADORLORAOLOLKMENAAAD<br>IRRDIVAMESEKDOLIKRVERLKRVETVONHORMILIAROLAVEKERESLAODKOECKNOLFHADORLORAOLOLKMENAAAD<br>IKKDISOMEDEKDOLIKRVERLKKVETVPNYEHMISIAROLAVERERESLAHOKOECKNOLFHADORLORAOLOLKMENOT<br>IKKDISOMEDEKDOLAKRIERLKKVETVPNYEHMISIAROLAVEKEREEDIOKKIOORRIMOSADOTLOKKOOLKMEKOECKNO<br>IKKDIKTMESEKENIMEKVERVEKKASGTPDFADSIOLAORMIKEKEREDIOKKIOODERLMOSADOTLOKKOOVYEMKOECKN<br>LKNKIKSLEEDERENGEKVERAGANDKLPDRSSYMEVCINLKOODEEVNISTAIOTRALDEKABASYH AAARIREDISYOE<br>LKORTOLERIKEATASVANVEKEREDIDESYOE   | 256<br>256<br>256<br>256<br>256<br>253<br>258<br>258<br>254<br>266 |
| Mm<br>Hs<br>Gg<br>Xt<br>Dr<br>Sp<br>Ci<br>Cr<br>Mp | AK PESIMKRLEEEIKENS MYT KEEKELESKKKELHELOKVYSEPANGHSDILELETKVNEVN TEINOLIEKKMARNEFIEGK<br>AKPESIMKRLEEEIKENLMYT KEEKELINKKKELHELOKVYSEPANGHSDILELESKINEINTEINOLIEKKMARNEFIEGK<br>SKPESEMKKLEEEINENSTIATEKIPELESKINSVYELOKATAEPANGOSDINVLESKINEVNAOINOLIEKKMARNEFIEGK<br>AKPEGIMKRLEEEINENSTIATEKIPELESKINSVYELOKATAEPANGOSDINVLESKINEVNAOINOLIEKKMARNEFIEGK<br>EKPESIMKRLEEDINENSTIATEKIPELENMRKVVOYLOKASEPANGOADITELEEKIHEVNIOINOLIEKKMARNEFIEGK<br>SSPESIMKRLEEDINENSTIATEKIPELENMRKVVOYLOKVSEPANSOADITELEEKIHEVNIOINOLIENKIMANDEMDDK<br>SSPESIISEMOEDNRLAEVINEKLEKLEKUSTIKKAVOILERVYNEFANSOADITELEEKIHEVNIOINOLIEKKMANDEMDDK<br>GSAGKILETINEDVKNIAAMEEKIKKINSVOOLOHERVYNEFANSOADITELEEKIHEVNIOINELEKKMANDEMDDK<br>GSAGKILETINEDVKNIAAMINEKIKEVEKIKAVAALSEALASGISTEMDIORIDAINENTEINETINEINKIKKMANDEMDK<br>GNINAIIAALSDEVENARALARKIPEALEKKRARSVAVKEVIASISTEMDIORIORIOINELEESSINKIPESSI<br>SVADDAVKKIDEENKINAAMINEKIPEEVIKROKROAALSEALASGISTEMDIORIORIOINELEESSINKIKIESSINAADINEMDKAROODKA | 341<br>341<br>340<br>341<br>338<br>343<br>343<br>344<br>353        |
| Mm<br>Gg<br>Dr<br>Sp<br>Ci<br>Cr<br>Mp             | SLYROOA SIIS RKKEAKAE ELO ETKEKLASLER VLVKTNOTREFDCTEVLKGDEFKRYVSKLESKSTVFKKKHOIIAEFKA<br>SLYROOA SIIS RKKEAKAE ELO EAKEKLASLER ASVKRNOTREFDCTEVLKGDEFKRYVSKLESKSTVFKKKHOIIAEFKA<br>MYROOA SIIS RKKEAKAE ELO EAKEELO EAKEETANLER ASVKRNOTREFDCSEVLKGDE KRYVNKLESKSTVFKKKHOIIAEIKA<br>SLFROOA AIIARKKETKAE ELO EAKEETANLER I  | 423<br>423<br>402<br>422<br>420<br>420<br>424<br>424<br>424        |
| Mm<br>Gg<br>Xt<br>Dr<br>Sp<br>Cr<br>Mp             | EFGL ORTEEL KOROETIOHOURTIEEKKOISUVSYTOEELERVÄÄLÄSEV EMKGRIT DDMEEMVKKINSLVSEKASALAEVIKEIPO<br>EFGL ORTEEL KORHENIOOO OTMEEKKOISUVSYTOEELERVÄÄLÄSEV EMKGRIT DDMEEMVKKINSLVSEKASALASVIKEIPO<br>EYGI ORTEELIKORHENIOOO OTMEEKKOISUVSYTOEELERVÄÄLÄSEV EMKORITDDMEEMVKKINSLVSEKASALASVIKEIPO<br>ENGVIORTEELIKORHENIOOO OSLEACROILVSDTOEELERVÄÄLÄSEV EMKORITDDI EDVKKINSVAAVAKKISSLAPVIKEIP<br>EYGVIORTEELIKORHENIOOO OSLEACROISUVSTOEELERVÄÄLÄSELEMKARISELEMKORITDDI EDVKKINSVIAEKKSISLAPVIKEIP<br>EYGVIORTEELIKORHENIOOO OSLEACROISUVSTOEELERVÄÄLÄSELEMKORITDDI EDVKKINSVIAEKKSISLAPVIKEIP<br>EYGVIORTEELIKORHENIOOO OSLEACROISUVSTOEELERVÄÄLÄSELEMKORITDDI EDVKKINSVIAEKKSISAPVIKEIP<br>EYGVIORTEELIKORHENIOOO OSLEACROISUVSTORELERVÄÄLÄSELEMKORITDDI EDVKKINSVIAEKKAN SPIIKELEP<br>EYGVIORTEELIKORHENISVIA SKIRAKKSVARYHDIOELERVÄÄNSELERVÄÄLÄSELEMKORITIDDI EDVKKINSVIAEKKAN SPIIKELEP<br>EYGVIORITETI OKINDOSORKINVIENKRYSIPROTODELEKVÄÄNNSDE EAKHRITDDMEDVHOINSVIODKINLAPVIKELEP<br>EYGVIORITETI OKINDOSORKINVIENKRYSIPROTODELEKVÄÄNSDE EAKKSITIEN PARASVIODEN HORVHOINSVIODEN LAPVIKELER<br>EVEVIAHTEELASOEGELEKVKRIIKOO ISITETIAOHLEKVEAKSOVERKOPIEKKINSI IEI RIVEEINNAINORKOOLAPOIKKINS<br>ATTIASTEELIRERISVSGUVAEERRAVITERAAVTERKORITEVERKSANSVERKORA EELISAFIOEINKKINER OKLAPOIKKINS   | 513<br>513<br>513<br>492<br>512<br>510<br>514<br>514<br>533        |
| Mm<br>Gg<br>Xt<br>Dr<br>Sp<br>Ci<br>Cr<br>Mp       | LROKCO S LTO S CDEKKAQ YDSCAR GLESNRSKLEQ EV RGLRBECLO EESKYHYTNOMIKNLEVEL RRATDEMKAYVS S DQOEKRKAIREQ<br>LROKYO E LTO S CDEKKAQ YDSCAR GLESNRSKLEQ EV RGLRBECLO SESRYHYTNOMIKNLEVQL RRATDEMKAYVS S DQOEKRKAIREQ<br>LROKCO E LTO S CDEKKIQ YDSCAR GLESNRSTLEQ EV KGLEBECTO EESNYHYTNOMIKNLEVQL ORVKEEMKTYVS P DPQERRKAIREQ<br>LRORCO E LTO S HDDKKAQ YD S CAR GLESNRSTLEQ EV KGLEBECTO EESNYHYTNOMIKNLEVQL ORVKEEMKTYVS P DPQERRKAIREQ<br>LRORCO E LTO S HDDKKAQ YD S CAR GLESNRSTLEQ EV KGLEBECTO EESNYHYTNOMIKNLEVQL ORVKEEMKTYVS P DPQERRKAIREQ<br>LRORCO E LTO S HDDKKAQ YD S CAR GLESNRSKIS O EV RGIRESCO LESO YHLINLMKKS VEVQI ORAADSMKAYVS P DPQDRRKAI. S<br>LROEHA LAP SY E KRAQ YET CAA GLESNRSTL O EV RTIRESTAD EESNYHYLH MOEREI I ESO I ORAAD OS KISO S MOVQVRRTAL S L<br>ROCO E SYNYHYN S KRAQ Y S CAR GLESNRSKIS O EV RGIRESCO S DE S RYYHLINDEREI I ESO I ORAAD OS KISO S MOVQVRRTAL S<br>LROCA S MOVYYD D KNTAN D TKAA GLESNRSKIS O EV RAYREE CSO S S RYYHLINDEREN I ESO I ORAAD OS KISO S MOVQVRRTAL S<br>NORCO E IMTE YN EKKISH YD S VAA GLESNRSKIS O EV RAYREE CSO S S S RYYHLINDEREN I LOG KID S MKAYT S AD MEKKAFR D<br>MORCO E IMTE YN EKKISH YD S VAA GLESNRSOLE HAVAAL REE OMNHD SRFHYI O SMNKILOG S D S S MKAYT S AD MEKKAFR D<br>N ROCO E IMTE YN EKKISH YD S VAA GLESNRSOLE HAVAAL REE CMNHD SRFHYI O SMNKILOG S D S S MKAYT S G D KKKSFREI<br>VRODFAFFEAXYLEK FTA D D NY TFEART S AL G S S G KAE V S S TKY HYLH D OLH IT D ONIKKVTSGP   | 603<br>603<br>580<br>602<br>600<br>601<br>594<br>613               |
| Mm Hs<br>Gg Xt<br>Dr<br>Sp<br>Cr<br>Mp             | ITKNITEOENLGEKLEEKONAVRESHGPNMKOAKMARDLEOIMECKKOOFLKOOSPASIGOVIOEGGE.DRLVI.6<br>ITKNTAEOENLGERRNLTLLPRLEOSGTILAHSAFOYRWDFTMLARLVSNS  | 76<br>54<br>76<br>52<br>75<br>75<br>83<br>86                       |



| COLORFY MAJORITY IDENITY :<br>COLORFY CONSERVED MINORITY:  | 61-70 71-80 81-90 91-100   | CC   |  |
|--|--|--|--|
| SpMSLARKI DDLEKQ<br>AtMFS.Br HSPQ SSPBSS.<br>CeMSSFUNDERQ)<br>CrMALVS BARBASREDELRRI<br>Dm MSATTRIFATE IFGTPSSLAREV<br>DrMASSREAVC RSUTT<br>HSMETERASSLIFAASI<br>MmMSTERSAL  | LVKPVNEQTYKKPIP<br>SYSDDILSTPRSSSSIIPRNPRKBM<br>LMPFSNIEGKWKISGKLIVKNIG<br>LMPPPPRAPAVPLS.RPV<br>RRVGNSALAFFKKFIA.MVRHKNFKI<br>RRVGNSALAFFKKFIA.MVRHKNFKI<br>RPFRKEAGEAGATS.RCF<br>APSRKEAGEAGEAGV.ARSEC   |  | EVESTEA  |
| Sp   | DERLEY IARN. S<br>DTEGETC HES<br>SFRT I I RS. T<br>SML FEL FAGA POTGANGAAT POTGVL<br>R. RINNAMPA<br>R. RINNAMPA<br>S. RINNAMPA<br>P. F<br>EPPP YW RA<br>EPPP YW RA<br>EPPP YW RA<br>F  | DELRKRLPSLÄIHEI.<br>TINPTPLDETORT RATPOVGREFRVEVD.<br>ALDVSPADDT GESSATSSAHDWOSPHE<br>REAHTPLVGGDAARGGGAGGAGGAGGA<br>TFVSQARCSNELENSRATDTPFSTD<br>FTDGRSASPSSQSKSRAREDK.<br>THD.RSPSSSSSKSRAREDK.<br>THD.RSPSSSSSSSA   | .TKAQIDGENKP114<br>ABDORDIDIN165<br>FANEGONDAN165<br>FANEGONDAN167<br>DEGAADAGSAAAASAA 189<br>FEXSDAGADDI164<br>DECKSKRDP164<br>.ACEPEKEP166<br>ACEPEKEP160                        |
| SpISVASUONEF SED<br>At   | SE DE DESRURADOMERSE OVISOO<br>ES SE LE KVINR VEREVER DE REGER<br>SE DAVINE REDRARFIVE LE REGER<br>OVILLE EDNARKRAVINELE REDRA<br>OVILLE EDNARKRAVINELE REDRA<br>SE DE LE TABAT BOUNDE DE NEU<br>SE DE DE LE DE NEURAMENT DA LE F<br>SE DE LE TABAT BOUNDE DE NEURAMENT<br>SE DE LE VARE SERREMENT DA LE F | PSNSIQTIGYSNSDAIKSIAWKEKD<br>SKSIEDVKRDIITDGVGTSDQPFST.<br>VKNLVTRDIIAEADVQLALKHAVDADDN<br>DATRQLLIEGPKEFSGVGTSGQAFWTILFAFE<br>AFQLQAALMISSIETQFFEFDEL<br>KEHEQNLALFSSEKQAFECTKA<br>KENQKENLELFSAEHQATESSQA<br>KEQKENLELFSAEHQATESSQA  | KS. IKE NIQENAL 197<br>EGRUTELL 246<br>RELIVDNA KWUTZ 246<br>RELIVDNA KWUTZ 246<br>ETON SQRA. 291<br>ETON TIMESIE 220<br>ETON TIMESIE 220<br>VETRORKINS 22<br>VETRORKINS 22<br>    |
| Spitetnussis   | TE QADA OLSQSFLEA.<br>RET VEN TH HEKINDS. RE<br>DINKE REPOSHEK. RE<br>SINSA ELFOSHEK. RE<br>SINSA ELFOSHEK. ALK<br>REVENTE DE PEC. ALK<br>REVENTE LED FFC. ALK<br>REVENTE LED FFC. ALK<br>REVENTE LED FFC. ALK<br>REVENTE LED FFC. ALS   | ANQPSIDEIVE PSVETDASV.<br>DSSVELIVT FIASS PHI SERDANSKA VDLDD<br>CANTRAVSHELANA KYDFI NEVTPANS.<br>ANDA MAAA LANA KYDFI NEVTPANS.<br>ANDA MAAA LAAL PRAEVITAAVAAAAAAAAA<br>REMETKLINDEVEQNIAGAITATPKV.<br>SIIQQLAALM QKKQ MYGEDIXELIPCESPKV.<br>SIIQQLAALM QKKQ MYGEDIXELIPCESPKV. | 253<br>LRKT PNPFYVESDKRAD 342<br>34AAGLPVSAPAPAAMG 389<br>289<br>289<br>295<br>CCC   |
| Spis. Velue. Vii<br>Arise. Vor Ritera. Filosereri<br>Ce. Filosi Inn. South Star<br>Grativas Strategian Star<br>Dima. Folksberger. Fearbeit<br>Dr. S. Vorgen and Star<br>Brade. Soffatter. Starbeit<br>Minde. Soffatter. Starbeit | AVGSSS<br>CONCERNMENT OF THE OBSADE HAVE<br>DOESNEL AGAD WY VEDDON<br>DESNEL AGAD WY VEDDONY HAS<br>NEEDONF FLOGGT L. REFO. HAS<br>DESNEL AGAST L. REFO.<br>HENDER VESSET Y. VORTP. HAR<br>WY VEL WESSET Y. VORTP. HAR<br>WY VEL WESSET Y. VORTP. HAR<br>WY VEL WESSET Y. VORTP. HAR                       | NIFERFERIHAMR. VRDIRSKSTN<br>IFSAFFDURAHSL. SRDISRIFS<br>IFVENSKIASSM. MDSIAAFYD<br>VOMIIHTARHAANSSGIPA RATTAARS<br>INTMOSEDNIAIAL RSSIFA RATTAARS<br>INTMOSEDNIAIAL RSSIFA RATTAARS<br>INTPPCREATCHM. ANDAANDRA<br>IL PGRERLOLM. ANDRAADDRA<br>IL PGRERLOLM. ANDRAADDRA           | TTITSUDAATAAN Y. 316<br>RANAYERKPF.PP. 432<br>KRAVEMRAAEGAHRIPG 415<br>ATTPL SALRKATGG. 492<br>QAQMA DIARANIGP. 398<br>RAQEARAVIENIA 384<br>RAQEARRVIENIA 384<br>RAQEARRVIENIA 385 |
| Sp strukt RKLING TE ARKIVA.<br>At HRSGSA ENVELLGE AGKER.<br>Ce FOSKAN DELAGLERAKARAT.<br>Cr. AGGGST. VVPL SE AGGAAAI<br>DMLIKTINGE. LANG ALLAT.<br>DFLIFKGLE. AAL GELKIVN.<br>HS LIFKGLE. AAL GELKIVN.                           | KAIAASS<br>KHIGIZM<br>KAGGAATEAGANAAGARGLAASSTVAGG<br>CKLGIRG<br>RSSRVI<br>RIASKVI<br>RIASKVI<br>RIASKVI   | regegefraggetgehenkvddhilwrgskrilig  | 338<br>461<br>464<br>VGGGAARGEAAAAVAKG 595<br>266<br>400<br>410<br>414   |
| Sp   | HOSS BASH. TA<br>RGAR RGAS.<br>AS KIMSINGSRES. SS<br>LLOGAN IT FILL RGGGGGCQKVGGGGA<br>TS BAS. GR<br>T SGAR A. S.<br>T SGAR. SS<br>T SGAR. S<br>T SGAR. S  | LTSI KFSMPI WWSTAF HKRV.<br>FGAVT KSVRISRFGKDGTSSIRF<br>KASTI GSAWSRGSITFG.SSWSGAQ POIPGIE<br>GGART VYSV VAVYGG.KRSASGAGAGAGA<br>GGART VYSV THIFILGERK XQAALIS RAAVU<br>LGART SGGITTIFVR RASS.<br>FLART SGGITTIFVR RASS.<br>FLART SGGITTIST APGSA R FILTO.                         | SHIRRAGINVOFSTSAG 508<br>SMIRRAGINVOFSTSAG 518<br>GAGKVIGSSVEDDIKI 699<br>TID.IGSTENDICI 499<br>D.DPASITINII (2 459<br>DPASITINII (2 456<br>DPASITINII (2 470                      |
| Sp   |  |  |  |

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change to A new donor splice site

| COLOR  | RFY MAJORITY IDENTITY :<br>RFY CONSERVED MINORITY:  | 61-70 71-80 81-90<br>61-70 71-80 81-90  | 91-100<br>91-100  |  |   |   |
|--|---|---|---|--|---|---|
| Ce MI<br>Dm<br>Cr<br>Dr<br>XI<br>Gg<br>Hs<br>Mm                      | PPMLNVMANYNEKTIGKLT GVEF<br>EVI<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>II<br>I  | KENLGLIERGCHFAA<br>SKRIAT RINNENDIAN<br>SKRIATRINNER DÜISM<br>SKRIATRINNER DÜISM<br>SKRIATRINIC KOISM<br>SKRIATRINIC KOISM<br>SKRIATRINIC KOISM<br>SKRIATRINK ZUISM<br>SKRIATRINK KOISM   | YNSNY DOC AL 2 H<br>DECYDROC AL 2 H<br>DECYDROC ESCLW<br>TDCYDROC ESCLW<br>YDC FIACCESCLW<br>YDC FIACCESCLW<br>TEC FIACCESCLW<br>CEC FIACCESCLW   | VERGEDAT BLINKS<br>LEIDQAIPNGQSKG<br>IRDGTISKDVKGKE.<br>LEIDGTISKDVKGKE.<br>LEILENQAEQAILK.<br>LEILENQAEQAILK.<br>LEILENQAEQAILK.<br>LEILENGEDQAILK.<br>REELGTDQSLR.   | . PNAAT IVIN 2. EENA<br>AAVENUS NGT DOORE<br>AFGENUS INGT DOORE<br>AABENUS NGT EENS<br>LABENUS NGT EENS<br>LABENUS NGT EENS<br>LABENUS NGT EENS<br>AABENUS NUT EENS<br>AABENUS NUT EENS   | I MNAINNE 99<br>S REVIEW D 82<br>A ICIC N 84<br>A OVIEW 81<br>S OVIEW 81<br>S OVIEW 81<br>S OVIEW 81<br>A OVIEW 81  |
| Ce<br>Dm A<br>Cr A<br>Dr Q<br>XI H<br>Gg Q<br>Hs Q<br>Mm Q           |   | ELE INNENSY VEICA<br>REFILLER <u>E</u> SI<br>ELE INNENSY KEAS<br>ELE INNENSY KEAS<br>ELE INNENSY RISSA<br>ELE INNENSY RISSA<br>ELE INNENSY RISSA<br>ELE INNENSY RISSA<br>ELE INNENSY RISSA<br>ELE INNENSY RISSA   | LE TK A A A ANU<br>SDERICTVIEDANT<br>ANEKICTVIEDANT<br>ADIKICTVIEDANT<br>ADIKICTVIEDANT<br>ADIXICTVIEDANT<br>ADIXICTVIEDANT<br>ADIXICTVIEDANT<br>ADIXICTVIEDANT                             | VOTLE SARIWANGEIG<br>VOSVDORR IFGRE INGT<br>VOSVDORR INGTE INGT<br>VOSVDORR INGTE INGT<br>VOSVDORR INGT INGT<br>VOSVDORR INGT DIGGT<br>VOSVDORR INGT DIGGT   | AACE AB GOMINETATI<br>TCTO SE NRITIFAIN<br>Alte SE GRITEAIN<br>Alte SE GRITEAIN<br>CHA SE GRITEGAR<br>CHA SE STILLEAN<br>CHA SE STILLEAN<br>CHA SE STILLEAN<br>CHA SE STILLEAN<br>CHA SE STILLEAN   | KUSVEDS 203<br>DECHIYONG 187<br>DECHYDIG 187<br>DECHYDIG 186<br>DETHIYONG 186<br>DETHIYONG 186<br>DETHIYONG 186<br>DETHIYONG 186  |
| Ce<br>Dm<br>Cr<br>Dr<br>XI<br>Gg<br>Hs<br>Mm                         | HELDIEME CARDING LAKE<br>JAMERIC MESSISSING<br>JAMERIC SCHOOL STATE<br>JAMERIC SCHOOL STATE<br>JAMERIC SCHOOL SCHOOL<br>SCHOOL SCHOOL SCHOOL<br>SCHOOL SCHOOL STATE<br>IN THE SCHOOL SCHOOL SCHOOL<br>SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL<br>SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL<br>SCHOOL SCHOOL SCHOOL<br>SCHOOL SCHOOL SCH   | HQKEE VCLKYMSPTLKS<br>HR. JSCNSS.<br>JSVEWDD.<br>AGIHWYP<br>AGYNYS.<br>AGIHWYH<br>AGIHWYH<br>AGIHWYH<br>AGIHWYH   | KTILDEMERDFERKLE  | KDREVT TAIFTKPP<br>RVV<br>TEG<br>TEG<br>TEG<br>TEG<br>TEG<br>TEG<br>TEG<br>TEG<br>TEG  | PKELPEHEKNTE PYQP P<br>QS<br>AB<br>LE<br>VE<br>VE<br>VE<br>VE   | E REVVA 308<br>RKR VIAIO 234<br>NEEVIAIO 232<br>E COLAVO 230<br>EDCECIAIO 230<br>EDCECIAIO 230<br>EDCECIAIO 230<br>EDCECIAIO 230<br>EDCECIAIO 230                       |
| Ce<br>Dm<br>Cr<br>Dr<br>Tr<br>Ki<br>Gg<br>Hs<br>Mm<br>Mm             |   | NITGAN SPN AF LAVC<br>RNTDAY NED TILL VA<br>RNTDAY NED TILL VA<br>RNTSCHORMENTIE VA<br>NUTSCHORMECSVEITA<br>NUTSCHORMECSVEITA<br>NUTSCHORMECSVEITA  | NDSDKDEPTFSK<br>TILDAVSFTSORETIN<br>FØMSS.AVADCREIMM<br>SIRNSGAEREY<br>SORAASODKUINI<br>SIRSISEDKUINI<br>FØRAAMODKUVNI<br>FØRAAMODKUVNI<br>SORVVTODKUINI                                    | IA LSAX HIVOYEQINDS<br>CYSHII XXYALIYYEI<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC<br>QANHAYAKII SIXYAC | CITETCHEST GLEMAIAA<br>DITESSINGES BRAMAN<br>CISEISNIGESBUCH<br>VITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITAVSHEGESBUCH<br>QITASSINGESBUCH<br>QITASSINGESTING   | AGTILIGQI 409<br>DSFIYFANI 338<br>DSYYYFANI 335<br>DSYYYFANI 331<br>DSFIYFANI 331<br>DSFIYFANI 331<br>DSFIYFANI 331<br>DSFIYFANI 331                                    |
| Ce at<br>Dm at<br>Cr at<br>Dr At<br>Gg at<br>Hs at<br>Mm             | ERKIGSTER I NY GOREEL<br>D'E GYEREN Y ENGREATER<br>D'E GYEREN Y AN ENGRATER<br>D'YE GYEREN Y AN ENGRA<br>D'YE GYEREN Y AN ENGRA<br>D'YE GYEREN Y AN ENGRA<br>D'YE GYEREN Y AN ENGRA<br>D'YE GYEREN Y YA YER<br>D'YE GYEREN YA YER<br>D'YE GYEREN YER<br>D'YE GYEREN YE GYEREN YER<br>D'YE GYEREN YE GYEREN YER  | YOLGIN YOYITDU TU<br>ISSUETUNITUSI (SEL<br>SUBTINITUSI (SEL<br>USSUETUNITUSI (SEL<br>USSUETUNITUSI<br>EXCITISTICISE<br>EXCITISTICISE<br>EXCITISTICISE<br>EXCITISTICISE<br>EXCITISTICISE<br>EXCITISTICISE<br>EXCITISTICISE   | T THFENMAFYRER V<br>E EPTICLASSSER V<br>Y RELVA QAFGE V<br>Y RSMITCODE I<br>Y RSMITCODE I<br>Y RSMITCODE I<br>Y RSMITCODE I<br>Y RSMITCODE I<br>Y RSMITCODE I                               | INECESCUTE.<br>GVECVSNIKEIALSTLE<br>ATVSNICEIALSTLE<br>ATVSNICE<br>ATVADEQCODORTEVU<br>ATVADEQCODORTEVU<br>ATVADEQCODORTEVU<br>ATVADENTE<br>ATVADENTE<br>ATVADENTE<br>ATVADENTE                                  | NR.SNFA<br>Samafnelsnontskors<br>Gr<br>Gr   | HYFCQ 482<br>DDRVHQIL 431<br>EHIIL 406<br>KRRKYVV 434<br>TYVVI 414<br>TYVVI 414<br>CFVIV 414<br>TYVIV 414<br>TYVIV 414  |
| Ce<br>Dm<br>Cr<br>Dr<br>XI<br>Gg<br>Hs<br>Mm                         | SI I SI YIVI IYA KA CONGI<br>SI I YA SKUTIKA CONGINS<br>SI I YA SKUTIKA CONGINS<br>SI I SI   | CAVIA SEDRYETI HEVILP<br>MTALI SÇELLI HEHTE<br>HVIA NDEVVE <mark>N ÇERIS<br/>HVIA SEARTI QUEVA<br/>HVIA SEARTI QUEVA<br/>HVIA SEARTI QUEVA<br/>HVIA SEARTI QUEVA<br/>HVIA SEARTI QUEVA</mark>   | . SINSVQAGIH<br>ISASILHNV<br>FSVLSTLINAVKR<br>KRITALSINQVKRIR<br>.KRLTALSINQVKRIR<br>.KRLTALSINQVARIR<br>.KRLTALSINQIIRSR<br>.KRLTALSINQIIRSR   | VFEXSEL VLEEQ.<br>ARKEXEFIDITETEVEM<br>OVERMENDESSE<br>CORERTITETESS<br>CORERTITETESS<br>CORERTYTETESS<br>CORERTYTETESS<br>CORERTYTETESS   | QRTIEYGTARII<br>AKDIMLSSSSCIGHSTOR<br>LDRSPESTRINNTT<br>TSDTINRALAFT<br>MEDIIDYTKSVE<br>SCHELDYSTAVE<br>SCHELDYSTATIO   | SKEPICAL 569<br>ISPEICAL 529<br>CTIFIACV 502<br>AFRIECCI 530<br>SCREPICCI 510<br>STREPICAL 510<br>STREPICAL 499<br>STREPICAL 510  |
| Ce CI<br>Dm Al<br>Cr M<br>Dr M<br>XI<br>Gg M<br>Hs M<br>Mm           | G TERMALLING YEVEL NDOV<br>BELLING ARBOR AND YEVEL<br>SVY MIR RAVING YEVEL<br>DAVING MARKAN TICK YEVEL<br>DAVING MARKAN TICK YEVEL<br>DAVING TO AND TICK YEVEL<br>SVM TIL YEVEL<br>SVM TIL YEVEL<br>SVM TIL YEVEL<br>SVM TIL YEVEL<br>TICK YEVEL<br>SVM TIL YEVEL<br>TICK YEVEL<br>SVM TIL YEVEL<br>SVM | ITNS FYSENDER<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT<br>IRNEHLMARVYRMAT  | TETRLAVIZUVEQVPE<br>NETRAIIDHCVTI<br>NERVEIDICVCTF<br>NERVIIDICVCTF<br>NERVIIDSCUTF<br>NERVIIDSCUTF<br>NERVIIDSCUTF   | 2FLLXEFD<br>DTDDN<br>DTTAKAPGGA<br>DVETGSMGDADG<br>FDIEARVIDATQ<br>FDIEARVIDATQ<br>DIEARVIDATQ<br>DIEARVIDATQ  |   | DYE DON 660<br>AVS ATD: 618<br>DMRADD: 596<br>DMRADD: 596<br>DMRADD: 627<br>DMRAD: 605<br>DMRAD: 605<br>DMRAD: 605<br>DMRAD: 605  |
| Ce SN<br>Dm 11<br>Cr 12<br>Dr 10<br>XI<br>Gg 10<br>Hs 10<br>Mm 10    | MLELYD OR TLEODANSIL OSS<br>E a Lwe orwy er gwyrei arys<br>arwer frwy fraewir yn gwyr<br>gwyr arwy fraewir yn gwyr<br>argwre trwy fraewir yn gwyr<br>argwre trwy fraewir yn gwyr<br>E gwyr trwy fraewir yn gwyr   | VISSIL ON VIA NI<br>CSGITTED FITEVIL<br>SANDS HD FITEVIL<br>SAFICED FITEVIL<br>TSGITCED FIREVIL<br>TSGITCE D FIREVIL<br>TSGITCE D FIREVIL<br>TSGITCE D FIREVIL  | EKILLTENTTTOV<br>DDISVGROQISHI<br>DDINQEDQEHERV<br>DRINETRYKOVI<br>DEINDENKOVI<br>DEINDEHENKOVI<br>DRINETRYKOVI<br>DRINETRYKOVI<br>DRINETRYKOVI<br>DRINETRYKOVI<br>DRINE                    | EVALUARO EVAN VNAASU<br>ISRVISER TIDI LEHVEL<br>VETRSIRGER ISRVI<br>VETRSIRGER ISVO<br>VETRSIRGER ISVO<br>VETRSIRGER ISVO<br>VETRSIRGER ISRVI<br>VETRSIRGER ISVO<br>VETRSIRGER ISVO                              | ERIDAR ESE SU SM<br>BRACTEDNE FRIER<br>DATE FURSTS<br>ERIF<br>ERIF<br>ERIF<br>ERIF<br>ERIF<br>ERIF<br>ERIF<br>ERIF  | IRNYAVERH 765<br>LESTIKEI 723<br>LESTIKEI 723<br>LETIEQI 701<br>LETIQEI 732<br>LETIQEI 710<br>LETIQEI 710<br>LETIQEI 710  |
| Ce AF<br>Dm E<br>Cr D<br>Dr D<br>XI D<br>Gg D<br>Hs D<br>Mm D        |   | I I S NUCLEN I I Y M R DT<br>THE KELOR I I S TYRE<br>M DOKANCRA NAV FE<br>NIC S AND C I I A Y I S<br>NIC S SNOC I TA Y I S<br>NIC S SNOC I VA Y I S   | LECIKTA FUQA DER DL<br>FERHETI YURA DER DL<br>FORMOUT VARIADER<br>FURA EXVIDIMENT<br>FURA EXVIDIMENT<br>FURA EXVIDIMENT<br>FURA EXVIDIMENT<br>FURA EXVIDIMENT                               | VENYKEVE MAS ME IR<br>TERTIC WERVE YR<br>IDERMELGWER FEIR<br>ISRIKSWEREDIR<br>IGRIKSWEREDIR<br>IGRIKSWEREDIR<br>IGRIKSCWERTICIS<br>IGRIKSCOWERTICISK   | NEDE EGKCE FRAM<br>MEGSEVS QOM I WREI<br>ESEL. DIACEN HIPT<br>INSERTAL EC YMAT<br>HIST STALLEC YMAT<br>I SOIS STALLEC YMAT<br>I SOIS STALLEC HIMAT<br>I SOIA I SLECHMAT   | AE THYEMME 867<br>THEANLRS 828<br>CONSORNA 804<br>SONFADROK 815<br>SONFADROK 815<br>SONFADROK 815<br>SONFADROK 815<br>SONFADROK 815<br>SONFADROK 815                    |
| Ce<br>Dm<br>Cr<br>Dr<br>Dr<br>XI<br>K<br>Gg<br>Hs<br>Mm              | E AKA SYCODTANCI DULIACH<br>S REW PERSIYI BOWLAI PHLE<br>2 AU 20 ARAY S MUYADI PHLE<br>2 AU 20 ARAY S MUYADI PHLE<br>2 AU 20 ARAY S MUYADI PHLE<br>2 AU 20 AND SHARACU MLE<br>2 AU 20 AND SHARACU MLE<br>2 AU 20 AV 20 AND SHARACU MLE<br>2 AU 20 AV 20 AND SHARACU MLE   | LECE EVILERI SDOSE<br>OFDI E KOVER PEKSE<br>EVA GRIMDA BOSSE<br>DID E RIANS PERKE<br>DID E RIANS PERKE<br>DID E RIANS PERKE<br>DIG E RIANS PERKE<br>DIG E RIANS PERKE   | MEVNGDA TISH M DO<br>LE KIA DI LAS VENCSE<br>LANGERE DO MI NEL<br>LE DI GOLATI VENCE<br>LE DI ANTI VENCE    | E ECY RESI CAR HAAR<br>A CHE RECOCEANATON<br>STRE CACOLER DECOM<br>SAFEKONG AND CO<br>CAR CONCEANTON<br>SAFEKONE CANDEN<br>SAFEKONE CANDEN<br>SAFEKONE CANDEN<br>SAFEKONE CANDEN<br>SAFEKONE CANDEN              | ENOR CELOSINE AL DANNE EL<br>NEORE AVELA GREGLES<br>LINCOLO CULLA GREGLES<br>LINCOLO VELA CHENTRE<br>LINCOLO VELA CHENTRE<br>LINCOLO VELA CHENTRE<br>LINCOLO VELA LENTES KE<br>LINCOLO VELA LENTES KE   | YYCHIGHE 972<br>YYTIIAH 933<br>EQTIAH 993<br>EQTIAH 999<br>EQTIAH 942<br>ECSIAH 920<br>ECSIAH 920<br>ECSIAH 909<br>ECSIAH 909   |
| Ce<br>Dm<br>Cr<br>Dr<br>Dr<br>XI<br>Gg<br>Hs<br>Mm                   | EMROPENEN SI SI ENDINE ORH<br>CIDO: . GRIXE IEMORI ORH<br>DIE: . E VALUE IEMORI ORH<br>DIE: . TO CIDO: CONTRACT<br>DIE: . TO CIDO: CONTRACT<br>DIE: . NOTE OFENEN MY<br>HIER NOTE IELVRO MY<br>HIER NOTE IELVRO MY<br>HIER NOTE IELVRO MY   | I DARMIAE DE AVDRAS M<br>I DARMIE LS MARR OF S<br>ME AR LO LA AKO DOM<br>LEASING LA RECOMME<br>LEASING LA COMMENSION<br>FLANING LA COMMENSION<br>FLANI | VPYEEL QOTNIG VE<br>AFIERE KIVIAIL<br>VHERVIKLVIAIE<br>IRERVIKLVIAIE<br>SKERVIKLVIAII<br>SKERVIKLVISII<br>IKERVIKLVISII<br>IKERVIKLVISII  | THROITELR.<br>ERIKAVAITE.<br>FREKKTIDMAOPOKTAA<br>TOFTIQISS.<br>COTECMONAQ.<br>COTECMONAQ.<br>TQVEEQMONAQ  | KIDKHNE<br>DYANG<br>TLLGT GTATMAAT MAQT<br>QST KKKEAT FA<br>KGT KKKEAT FA<br>REVYKE SST TAA<br>REVYKE SST TAA<br>REVYKE SST TAA   | EDALDES 1059<br>RNTIDSIA 1017<br>LAGINTES 1012<br>LAGITEEDE 1034<br>LAGITEEDS 1012<br>LAGITEEDV 1010<br>LAGITEEV 1001<br>LAGITEEV 1012                                  |
| Ce GL<br>Dm LE<br>Cr AV<br>Dr SS<br>XI ML<br>Gg LS<br>Hs LS<br>Mm LS | ERCE IIENT ROBE HIMM<br>DA. AATERI HO Z YHME<br>DE. ACVISH ROBEYHNE<br>DS. HILDAR ROBEYHNE<br>DN. HILMAR ROBEYHNE<br>DN. FRANK ROBEYHNE<br>TT. FRANK ROBEYHNE<br>TT. FRANK ROBEYHNE<br>TT. FRANK ROBEYHNE<br>TT. FRANK ROBEYHNE<br>TT. FRANK ROBEYHNE<br>TT. FRANK  | CONFERNICICO S<br>CROIRFEIN HENVIN<br>HROLLARITI HENVIN<br>CROILERIN ANNA<br>CROILERIN ANNA<br>CROILERIN ANNA<br>CROILERIN AN ANA<br>CROILERIN TILKIAL<br>CROILERIN TILKIAL   | I SDYEFT DPAEVE<br>R BUYDDY PFT YN<br>R BYDDIT PFT YN<br>R BYDDIT PFT<br>R BYDDIT RAFLYS<br>R BYDDIT RAFLYS<br>R BYDDIT RAFLYS<br>R BYDDIT RFFYRYS<br>R BUYDDIT RFYFLYS<br>R BUYDDIT SYFLYS | III CALANING GI CARA<br>III AS HIDRA GI CARA<br>III AS HIDRA GI CARA<br>III CASHIGA GI CARA<br>III CACANA CALANA<br>III CACANA CALANA<br>III CACASA<br>III CACASA<br>III CACASA                                  | KRIBAF EFDAEKEEMA<br>Mole Coart Frant Brit<br>Internet for the former for<br>the set of the former for<br>the set of the former for<br>the set of the former former<br>the set of the former former<br>former former former former former<br>former former former former former<br>former former former former former former<br>former former former former former former<br>former former former former former former former former<br>former former former former former former former former<br>former former former former former former former former former former former<br>former former | N SFRI BE 1164<br>A AGTIAN 1119<br>D AMS II 1115<br>D ALBINT 1137<br>D ALBINT 1137<br>D ALBINT 1137<br>D ALBINT 1137<br>D ALBINT 1134<br>D ALBINT 1134<br>D ALBINT 1135 |
| Cent<br>Dm YD<br>Cr F<br>Dr S<br>XI<br>Gg C<br>Hs T<br>Mm T          | VNPNSAKVACSVCDAKI<br>EFITGDRVDCVSCGVPA<br>ALEALETREKKAPGGAMAG<br>RDTQ<br>KUTRQ<br>KUTR  | DPYILQCSE.COT FFV<br>PDSSPSCPE.CNARF2A.<br>NSEDALLIDDIGGREQUY<br>SCRUSLIDDIGGREQUY<br>PDISFPG.BEALLY<br>TLIDVLIS.EDOKLEY<br>PDISFUG.GEAKLEY<br>SCRUSLIG.EDOKLEY   | ISRLILDNIMI<br>SSRLFIQPINNII<br>VISRLVRDGNVVR<br>VIRVISKOMV<br>VIRVISKOMV<br>VIRVISKOMV<br>VIRVISKOMV<br>VIRVISKOMV<br>VIRVISKOMV   | PR HE RAHOH JPHING<br>TI HE CAAPT IS RHRT<br>MWKLLSTH HEGAAV<br>SWIKE CALECO I COM<br>NUCK CVDA I COM<br>SWIKE CHARKE RSWING<br>SWIKE GVLAC IS HEST<br>WIKE YVLAC IS HEST  | ELC DMESFRVP.<br>PLC BLIVSMIVEI.<br>PLC ALFVSGGAPGRG<br>PLC BIVG.<br>PLC SIA.<br>PLC SIA.<br>PLC BVG.<br>PLC SVE.   | 1246<br>  |
| Ce<br>Dm<br>Cr <sup>QM</sup><br>Dr<br>XI<br>Gg<br>Hs<br>Mm           | 1246<br>1205<br>VGAY 1224<br>1203<br>1181<br>1178<br>1170<br>1181   |   |   |  |   |   |

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

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

| CeMDPRKIRNPYHGIDDLQSDFGDEPSSSSKPKRKGDFLNKDYSSEILKKRKTDGRGGFEEHGRMHF                       | NEYDR   | KEMINLY  | YSYPG  | 93  |
|---|---------|----------|--------|-----|
| CrMANFGETRRSAFGEAHAAQHYATTLLGI  | NAADR   | HRKLVNDY | LTYYAR | 47  |
| AtMISSAAIRSDIYDREERKQQYQAHIRGI  | NAYER   | HKKFLKDY | VRFYGK | 47  |
| DmDm  | SAKER   | HNYILSNY | VINLPN | 22  |
| Dr MMSDMDKSALDLVKVHGGGGYDSDFSDDDGGGHSKDGENRAGQDEL.LQKPFQKGKHTKVAHKNVAAHEWDREEARNR.RQHLISI | MAFER   | HKKFVSDY | ILYYGG | 103 |
| <b>Hs</b>   | 1DA YQR | HTKFVNDY | ILYYGG | 90  |
| Mm  | DAYOR   | HTKFVNDY | ILYYGG | 90  |

| Ce ATKLLNRKIQDE . | TTOLOVLK                | KHHREVNSEI                | INASQPDKNS | SWETRMAKEYY | DKLEKEYCIVDLS                   | MYRTNKIGMRW                               | RTENEVKE  | KGQLSC | GARKCNETA | 193 |
|-------------------|-------------------------|---------------------------|------------|-------------|---------------------------------|---|-----------|--------|-----------|-----|
| Cr GVPGQPGGPPAGE  | CAKAVRTDADALRI          | EHHRFIRT EF               | DGDH       | WEARLAKRYY  | DRIFKEY <mark>A I</mark> VDIS   | FYNESRLGMRW                               | RTOKEVVS  | KGQEVC | GAKGCEASD | 146 |
| At DKPAEVKLPV     | KIDQUILRI               | EGYRFIRSE                 | DLDP       | SWECRLVKRYY | DKL FKEYC I <mark>A</mark> DMS  | RYNTGRMGLRW                               | RTEREVMTO | KGQFMC | GSKHODEKE | 139 |
| Dm ETESRRH        | KRDIDVIR                | ENHRFI <mark>M</mark> .EI | LDSDTL     | SWECRLALRYY | RKIFKEYC <mark>IA</mark> DIS    | R <mark>YKEN</mark> KIAL <mark>RW</mark>  | RTECEVVIC | TGOFCC | GSRHCGERD | 113 |
| Dr KIEDLRRSTSKD.  | <mark>KTOLOV</mark> VKI | ENHRFL <mark>W</mark> KEE | EEDM       | WE KELAKKYY | DKLFKEYC <mark>IA</mark> DLS    | RYKENKFGFRM                               | RIENEVISC | KGQFLC | GNKRCESKE | 197 |
| HS KKEDFKRLGEND.  | <mark>KTDLDV</mark> IRI | ENHRFI <mark>W</mark> NEE | DEMDM      | WERRLAKEYY  | dki fke yc <mark>ia</mark> di s | K <mark>YKEN</mark> KF <mark>G</mark> FRW | RVEREVIS  | KGQFFC | GNKYCDKKE | 184 |
| Mm KREDFKRLGEND.  |                         | ENHREIMNEE                | TEADM      | WERRLARRY   | DKLEKEYCI <mark>A</mark> DLE    | RYKENKEGERW                               | RIEVEVISO | REOFFC | GNRCCNERE | 184 |

| Ce | HSS   | EVNE | TK  | DN  | RVKST | IVRA | RIC | PKCSE                | KLN        | GTR | KR. |     |     | NQ.   | QKK  | RA. |      |      |      |       | v                    | RKWE | KER | KRTK  | DEE  | EDDI | VEL | QHEA | 270 |
|----|-------|------|-----|-----|-------|------|-----|----------------------|------------|-----|-----|-----|-----|-------|------|-----|------|------|------|-------|----------------------|------|-----|-------|------|------|-----|------|-----|
| Cr | GICSI | EVNE | AVQ | AG  | ERKQA | IVKL | RVC | PACAF                | KIN        | RKE | KQ/ | QKA | ADA | AAA   | KRK  | RER | EEAA | ALE  | TADE | LVRE  | ALQYV                | KRY7 | AGD | KAAGI | GAA  | GEGG | LGE | DLLR | 251 |
| At | GLASI | EVNE | SYH | EAG | EDKQA | IVEL | VAC | ER <mark>C</mark> AE | KL Y       | KKR | KE. |     |     | . GE  | SES  | KE. |      |      | KKKÇ | KRKR  | SKSHS                | EDDI | DEE | EKRKE | GER  | SESN | EKK | QKRN | 228 |
| Dm | NERSU | EVNE | RII | EKG | EPLNA | IVRV | RIC | PTHTD                | QEN        | RTK | KR. |     |     | . ECP | KKQR | RR. |      |      | EKEE | RRAE  | K <mark>K</mark> RKR | RKLI | VGH | ESSGE | EEE  | EPVE | PAS | SHPE | 202 |
| Dr | GIKSU | EVNE | AVV | EQG | EKRNA | IVK  | RIC | PE <mark>CS</mark> Y | <b>KIN</b> | HHK | RK. |     |     | . EVI | TAK  | RRR | SKEN | LDV  | SKKS | KSSK. | SRKNK                | RKD  | RKH | KKRR  | EHS  | SSSS | EES | ESDK | 294 |
| Hs | GIKSV | EVNE | GII | EHG | EKRNA | IVEL | RIC | QE <mark>CS</mark> I | KIN        | HHR | RK. |     |     | EIP.  | SKK  | RK. |      | . DK | TKKE | CEES  | S <mark>H</mark> KKS | RLSS | AEE | ASKKR | (DKG | HSSS | KKS | DSLL | 275 |
| Mm | GIRSU | EVNE | GIT | EHG | EKRNA | IVKL | RLC | QE <mark>CS</mark> F | KIN        | HHR | RK. |     |     | EIP.  | STK  | ĸĸ. |      | .SK  | TTPE | CDES  | PRKKS                | RSPE | SEE | ASKG  | DEG  | HSSS | KKS | DSRN | 275 |

| Ce KNQETKVQPSTST                       | LSASTDINE.GEPRAETEKTVDDE.IDEFLDDEFL   | 316 |
|--|---------------------------------------|-----|
| Cr AARDVAPPPAAAAGGGSGPAGAGGAAGVGQAPAII | ILPADNSVWESKRAQETATAREE.MDAYFEGLEM :  | 319 |
| At RSQSHSEYDTDEE                       | DRRKGKTRKSKLESADREGKDDENEDEYMEGMEPGNG | 278 |
| Dm ASKEPTDSKDDT                        | TADEQINQQQHDISREQASREQE.FERVLEDIIF    | 247 |
| Dr GSDDDDDDDDDADG                      | PSESEHWK.GRAPAVEEKSREEF.FDEYFEDMFL :  | 339 |
| Hs RNSDEEES                            | ASESELWK.GELFETDEKSQEEF.FDEYFQDLFL :  | 315 |
| Mm RNAEEEDS                            | ASDSELWK.GPLPETDEKSQEEE.FDDYFQDLFL :  | 315 |

| CO   | DLORFY MAJORITY IDENTITY : <b>61-70 11-80 81-90 11-10</b><br>DLORFY CONSERVED MINORITY: <b>61-70 71-80 81-90 91-100</b>   |  |
|--|---|--|
| Cr<br>Zm<br>Ce<br>Dr<br>Dr<br>Hs<br>Mr       | ALAASVTIRALQLSPECSRAWRAWCICLERATKEQRAFVAAATAAAAATAGRESSOGGAAAADAAGMAAAGGAAAAGCAAAACCRYALSYSTEF.<br>VTCARSSIGTAAGAPETSREDDFAAULAS. ELUVLCKCOSKNDTAFLIGKITEINSERKENVIGAAAAACCYYSSS.STELSSYN.<br>VRARSDO   | 2468<br>1649<br>1444<br>1599<br>1750<br>1773<br>1771 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Hs<br>Mm       | C. GOGGARA DET PVL CL HINGE GAA ESL AAC AAN FE AA SA LAC. POR GAA RLEAAL RAY AAA SUVLEY VEVRADAAAAAAA.<br>HEALMENTASTINER YL HEMINIGYE MET SE STY DLE PETER FA SSEGKIT ELISST LEMEKUS CSINET TO DISACE.<br>   | 2568<br>1745<br>1538<br>1695<br>1854<br>1877<br>1875 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Dr<br>Hs<br>Mm | GIDOGDVQEEGISASPSFAASMVPELRALLAD GRSR OLLAG OILVG NVALVINER AALLADVEVIS A.<br>GEPSELQBISDRYNKLY MLIKI KLALP GUNTY HE G. QST DELKONKA<br>DGEELEEQQNDONRVRA CERLETIN QSI NLIKT KLALP GUNTY HE G. QST DELKONKA<br>DGEELEEQQNDONRVRA CERLETIN QSI NLIKT ROFALDE ILL NE K SVNOTMEHENER E<br>AFTIEDAC VYSLIGE KAS SVNOTMEHENS<br>LFSLFFLLGNIQGEELLGGES FGGSFSGESSREENVNYSSBDJANDOT YSKIVDE SAN THE C. QHIALGRAVIN HE GAT DONNEY KAN DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAN DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAN DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAN DONNEY KAS NEDANDOT YSKIVDEN SAN THE C. QHIALGRAVIN HE GAT DONNEY KAN                                | 2645<br>1803<br>1609<br>1765<br>1959<br>1981<br>1979 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Hs<br>Mm       | VS OARAA WAEBSSISPARHONELASHYOTU AFA VUL ROLAA AAAAA TEH RE AATVLERIRA AAA ROBEGAAAAAAVUGAGTAAPSAPVVADM<br>NI KOEAN MAANSTISSA DWE MAAHYSAN TID WA HABLYSIS REPRING MI HEEMAAKIKSATTI KOG POSP.<br>SU REINARTESALETIASY NOL IVKRIVLI TAQIFOV HEEMOOVI TEPKYKNI EE VIA AEVITTI OOSATISTISTI<br>SA ARI. FROMENE KOMEYVMEDELLAH AAVVI SISPATITI KOS REPONDA KANNIN<br>COLEDIVKNIQHNIT KREEN HAMEKHIAAN VIA HEMATIA. AAAATME EN QETIGOAHHINLEEN SEINE<br>OO EEDIVKNIQHNIT KREENTA MEEMATAKITIFA HHYRITA. AAATME EN QETIGOAHHINLEEN KITISTISTI<br>OO EEDIVKNIQHNIT KREENTA MEEMATAKITIFA HHYRITA. AAATME EN QONNGOABLISTERISTISTISTISTI<br>OO EEDIVKNIQHNIT KREENTA MEEMATAKITIFA HHYRITA. AAATME EN QONNGOABLINGEN KITISTISTISTI  | 2750<br>1885<br>1690<br>1835<br>2040<br>2062<br>2060 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Hs<br>Mm       | PEVAL AL LAAAAA SE HDPLPE ALES A RINDRETEN LADODOADOOSGYGVEATNALSAASGAALPHOGAAFSAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  | 2852<br>1950<br>1750<br>1893<br>2098<br>2120<br>2118 |
| Cr<br>Zm<br>Ce<br>Dr<br>Dr<br>Hs<br>Mr       | VACISSEVEL REMEVALES COSTOFIL REDERVE LE LA CONTRARSLET. DADCAR SLACVE SUBJOR DE LE PUIS E AVERS<br>19 E CONTRARS IN REMEVALES COSTOFIL REDERVE E LA TELLY, SOUTHER LA CONTRARS IN LONG AND THE SAVERS<br>29 EN ARCHINE SUB REMEVALES COSTOFIL REDERLES VOI SECONDOPENDENDES AND HE SI LONG AND THE SAVERS<br>20 EN ARCHINE SUB REMEVALES CONTRARS IN A CONTRAL DE CONTRARS INTERNATIONAL SECONDOPENDENDES<br>20 EN ARCHINE SUBJOR DE LA CONTRAR SUBJOR DE LA CONTRARS INTERNATIONAL SECONDOPENDENDES<br>20 EN ARCHINE SUBJOR DE LA CONTRAR SUBJOR DE LA CONTRARS INTERNATIONAL SECONDOPENDENDES<br>20 EN ARCHINE SUBJOR DE LA CONTRAR SUBJOR DE LA CONTRAR SUBJOR DE LA CONTRARS INTERNATIONE<br>20 EN ARCHINE SUBJOR DE LA CONTRAR SUBJOR DE LA C | 2956<br>2052<br>1855<br>1996<br>2200<br>2222<br>2220 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Hs<br>Mm       | AALLE MAANA AROEGAAKAAAGA GA PPPELE PEAARS EMDITISMEVEATIRE SATERO PELEA FAR AAAS ROLLGRVE AGGSAAG<br>KSOLAH HAROVSIVSTONIH PUAPE   | 3059<br>2144<br>1940<br>2078<br>2287<br>2309<br>2307 |
| Cr<br>Zm<br>Ce<br>Dm<br>Dr<br>Hs<br>Mm       | A RECERTION METERICAL DURING LEGGE COMMUNICIES DURING SERVICE DE SERVICE DE SERVICE DURING VERUNAL DURING DURING VERUNAL DURING VERUNA DURING VERUNAL DURING VERUNAL DURING VERUNA DURING VERUNAL DURING VERUNA DURING VE                      | 3164<br>2249<br>2045<br>2158<br>2392<br>2414<br>2412 |
| Cr<br>Zm<br>Dm<br>Dr<br>Hs                   | TAVECTOR AVE  | 3253<br>2323<br>2084<br>2158<br>2476<br>2498         |



**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 *fla9* 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 *fla9* 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 indicate 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 helixes 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,* Creo7.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<br>temperature | Enzyme        | Fragments<br>(bp, wild- |
|--------------|-------------------------|--------------------------|--------------------------|---------------|-------------------------|
|              |                         |                          | -                        |               | type;<br>mutant)        |
| fla9/ift81-2 | CCGGTATTGTCTTAGGGAGCTT  | ACTTTGCGCTCCTGGATCT      | 53°C                     | FspI          | 168+135;<br>303         |
| ift121-2     | GCACAACTTCCCGCAGAT      | CACTTCTTTGCCAGGTCCTG     | 53°C                     | MboII         | 419;<br>343+76          |
| 4c/dgr14-1   | CTTCCAAGGGTACCCGTAAT    | GCTGGAGAGAAGATGCAGAG     | 53°C                     | n/a           | 115; no amp             |
| dgr14-2      | TGGCAGAGGGAATGATGGAA    | GCCACCGCCAGTTTGTG        | 53°C                     | n/a           | 202; no                 |
|              |                         |                          |                          |               | amp                     |
| sup15/fra10- | CATCCCAGCCTGCCGTCTC     | GCCGCCTCCTCACGCTCGCGCTTA | 61°C                     | n/a           | 132; no                 |
| 1            |                         |                          |                          |               | amp                     |
| smg1-1       | ACGAGGTGGCTTGGATGG      | CTGCCACTGTTGCTGT         | 53°C                     | AcuI          | 89+61; 150              |
| smg1-2       | CTTGCCTACAACGCCTTCC     | GCAGGCGCGCAATTCATAAT     | 53°C                     | <i>Bsr</i> BI | 159+83;                 |
|              |                         |                          |                          |               | 242                     |
| smg1-3       | CTGCTGCCACACCTTCAG      | CCTGCTGTTGCTGCCTATG      | 53°C                     | AluI          | 169; 113+56             |
| smg1-4       | AAGAGCACGAACAGGCACAG    | CGGTGGTGCTGCACATGTT      | 53°C                     | MseI          | 145;                    |
|              |                         |                          |                          |               | 125+20                  |
| smg1-5       | CGCTATCCCATCTACTGCCA    | CTCACGGCCCTCCAGCTT       | 53°C                     | MnlI          | 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    | CTTACGTCGCAGTTGGCTAT |
| 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   |

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

Supplemental Table 2. Summary of whole genome sequencing results