Article

https://doi.org/10.1038/s41467-024-49002-9

An axonemal intron splicing program sustains *Plasmodium* male development

Received: 14 December 2023

Accepted: 15 May 2024

Published online: 01 June 2024

Check for updates

Jiepeng Guan^{1,4}, Peijia Wu^{1,4}, Xiaoli Mo^{1,4}, Xiaolong Zhang^{2,4}, Wenqi Liang¹, Xiaoming Zhang¹, Lubin Jiang², Jian Li $\mathbb{O}^1 \otimes$, Huiting Cui¹ \otimes & Jing Yuan $\mathbb{O}^{1,3} \otimes$

Differentiation of male gametocytes into flagellated fertile male gametes relies on the assembly of axoneme, a major component of male development for mosquito transmission of the malaria parasite. RNA-binding protein (RBP)mediated post-transcriptional regulation of mRNA plays important roles in eukaryotic sexual development, including the development of female Plasmodium. However, the role of RBP in defining the Plasmodium male transcriptome and its function in male gametogenesis remains incompletely understood. Here, we performed genome-wide screening for gender-specific RBPs and identified an undescribed male-specific RBP gene Rbpm1 in the Plasmodium. RBPm1 is localized in the nucleus of male gametocytes. RBPm1deficient parasites fail to assemble the axoneme for male gametogenesis and thus mosquito transmission. RBPm1 interacts with the spliceosome E complex and regulates the splicing initiation of certain introns in a group of 26 axonemal genes. RBPm1 deficiency results in intron retention and protein loss of these axonemal genes. Intron deletion restores axonemal protein expression and partially rectifies axonemal defects in RBPm1-null gametocytes. Further splicing assays in both reporter and endogenous genes exhibit stringent recognition of the axonemal introns by RBPm1. The splicing activator RBPm1 and its target introns constitute an axonemal intron splicing program in the post-transcriptional regulation essential for *Plasmodium* male development.

Malaria is a worldwide infectious disease caused by the protozoan parasite *Plasmodium*¹. The spread of *Plasmodium* depends on the transition between the mammal host and the *Anopheles* mosquito. In mammal hosts, a small proportion of intraerythrocytic asexual parasites undergo sexual development, irreversibly differentiating into the sexual precursor gametocytes, which are transmission-competent for the mosquito vector². Within 10 min after being ingested into the mosquito midgut, the gametocytes escape from host erythrocytes and develop into fertile gametes, a process known as gametogenesis³. A flagellated motile male gamete fertilizes with a female gamete to form a zygote. After the zygote-ookinete-oocyst-sporozoite development in

mosquitoes, the parasites are finally injected from the salivary gland into a mammal host, completing the transmission of the malaria parasite⁴.

Sexual development plays a central role in malaria transmission^{5,6}. When activated by two joint environmental stimuli (a temperature drop⁷ and a metabolite xanthurenic acid⁸) in the mosquito midgut, a female gametocyte produces a haploid gamete, while a male gametocyte gives rise to 8 haploid gametes³. Female gametogenesis undergoes minor morphological changes, while male gametogenesis involves fast and spectacular changes^{9,10}. During the male gametogenesis, two spatially distinct components are coordinated. One is the

¹State Key Laboratory of Cellular Stress Biology, School of Life Sciences, Faculty of Medicine and Life Sciences, Xiamen University, Xiamen, China. ²Shanghai Institute of Immunity and Infection, Chinese Academy of Sciences, Shanghai, China. ³Department of Infectious Disease, Xiang'an Hospital of Xiamen University, School of Medicine, Faculty of Medicine and Life Sciences, Xiamen University, Xiamen, China. ⁴These authors contributed equally: Jiepeng Guan, Peijia Wu, Xiaoli Mo, Xiaolong Zhang. e-mail: lbjiang@siii.cas.cn; jianli_204@xmu.edu.cn; cuihuiting@xmu.edu.cn; yuanjing@xmu.edu.cn cytoplasmic assembly of 8 basal bodies and axonemes, and the other is the 3 successive rounds of genome replication without nuclear division, resulting in an octoploid nucleus. Subsequently, 8 axonemes with chromosomes attached are released from the cell body of male gametocytes, resulting in 8 flagellated daughter gametes, which is the process termed "exflagellation".

Parasite stage transition during the *Plasmodium* life cycle requires a fine-tuned multilayer regulation of gene expression¹¹⁻¹³. Previous studies have identified transcriptional and epigenetic programs critical for the sexual commitment and development of the gametocytes¹⁴⁻²³. However, how the Plasmodium establishes distinct repertoires of transcripts between male and female gametocytes remains incompletely illustrated. RNA-binding proteins (RBPs) can interact with transcripts in all manner of RNA-driven processes²⁴. RBPs regulate all aspects of the life cycle of mRNA, including mRNA transcription, splicing, modification, trafficking, translation, and decay^{25,26}. RBPcontaining ribonucleoprotein complexes, such as the DOZI (development of zygote inhibited) complex and CITH (CARI/Trailer Hitch homolog) complex, had been shown to repress the translation of multiple mRNAs in female gametocytes²⁷⁻²⁹. So far, our understanding of post-transcription control is still limited in the male gametogenesis. Recent transcriptome studies in both human malaria parasite P. falciparum and mouse malaria parasite P. berghei revealed that certain RBPs are specifically or preferentially expressed in male gametocytes^{30,31}, implying gender-specific roles of RBPs in the posttranscriptional regulation for male development. However, systematic identification of male RBPs for male gametogenesis and their precise roles in defining the gender distinct transcriptome via the posttranscription regulation have not been reported.

In this work, we perform comparative transcriptome analysis on male and female gametocytes and obtain a list of gender-specific RBPs in the rodent malaria parasite *P. yoelii*. From this list, we identify a functionally unknown gene (PY17X_0716700, named as *Rbpm1* in this study), which is specifically transcribed in male gametocytes. We demonstrate that RBPm1 is a nuclear RBP essential for male gametogenesis and mosquito transmission of parasite. RBPm1 interacts with the spliceosome E complex and initiates the splicing of certain introns in a group of axonemal genes. RBPm1-deficient parasites cannot express these axonemal proteins and fail to assemble the axoneme. These findings reveal an RBPm1-mediated intron splicing program of the axonemal genes essential for *Plasmodium* male development.

Results

RNA-binding protein RBPm1 is expressed in the nucleus of male gametocytes

Approximately 180 putative Plasmodium RBPs had been predicted in silico³². To identify the key RBPs for male gametogenesis, we searched the male gametocyte-specific RBPs in the rodent malaria parasite P. yoelii. Using the fluorescence-activated cell sorting, highly purified male and female gametocytes were collected from a P. yoelii reporter line DFsc7 (Fig. 1A and Supplementary Fig. 1A), in which fluorescent proteins GFP and mCherry are expressed in male and female gametocytes, respectively³³. We performed RNA-seq and obtained genderspecific gametocyte transcriptome (Supplementary Fig. 1B and Supplementary Data 1). Among the 179 P. yoelii RBPs, an unstudied gene (PY17X_0716700) was identified with the greatest enrichment in male compared to female gametocytes (Fig. 1B, left panel). This gene was named as Rbpm1 for RBP in male gametocyte. Notably, the Rbpm1 orthologs PBANKA 0716500 and PF3D7 0414500 are also among the top male RBP genes of P. berghei and P. falciparum, respectively, (Fig. 1B, middle and right panels) based on the gender gametocyte transcriptomes^{30,31}.

To investigate RBPm1 expression during the parasite life cycle, we tagged endogenous RBPm1 with a sextuple HA (6HA) at the carboxyl (C)-terminus in the *P. yoelii* 17XNL strain (wild type or WT) using CRISPR-

Cas9^{34,35}. The tagged parasite *Rbpm1::6HA* developed normally in mice and mosquitoes, indicating no detectable detrimental effect of tagging on protein function. Immunofluorescent assav (IFA) showed that RBPm1 was expressed only in gametocytes, but not in asexual blood stages. ookinetes, oocysts, or sporozoites (Fig. 1C, upper panel). Immunoblot also confirmed the gametocyte-restricted expression of RBPm1 (Fig. 1D). Gametocyte-specific expression of RBPm1 was observed in another parasite line *Rbpm1::gfp*, in which RBPm1 was tagged with GFP from the 17XNL (Fig. 1C, lower panel). To dissect whether RBPm1 expression is male-specific, the Rbpm1::6HA gametocytes were co-stained with antibodies against HA and α -Tubulin II (a highly expressed protein in male gametocytes³⁶. RBPm1 was only detectable in the male gametocytes (Fig. 1E). Additionally, we tagged RBPm1 with 6HA in the reporter line DFsc7 and observed the male-specific expression of RBPm1 (Fig. 1F). We noticed the nuclear localization of RBPm1 in all the male gametocytes tested (Fig. 1C, E, F), which was further confirmed by immunoblot of nuclear and cytoplasmic fractions from the Rbpm1::6HA gametocytes (Fig. 1G). Last, we analyzed the localization dynamics of RBPm1 throughout the process of gametogenesis (0, 2, 8, and 15 min post activation. mpa) in the *Rbpm1::6HA* parasites. Both IFA and immunoblot revealed consistent protein expression profile and nuclear localization of RBPm1 during gametogenesis (Fig. 1H, I). Together, these results demonstrated that RBPm1 was a nuclear protein specifically expressed in the male gametocytes.

RBPm1 is essential for male gametogenesis and mosquito transmission of parasite

P. yoelii Rbpm1 gene encodes a protein of 361 amino acid (aa) residues, with two RNA recognition motifs (RRM1 and RRM2). To investigate its function, we generated a mutant line, $\Delta Rbpm1$, by deleting the entire genomic sequence (1904 bp) of Rbpm1 gene in P. yoelii 17XNL strain using CRISPR-Cas9 (Fig. 2A). *ARbpm1* produced normal level of male and female gametocytes in mice (Fig. 2B), indicating that RBPm1 is not essential for asexual blood stage proliferation and gametocyte formation. We next measured the male gametogenesis by counting exflagellation centers (ECs) in vitro after stimulation with 50 µM xanthurenic acid (XA) at 22 °C. *ARbpm1* showed a striking deficiency in the EC formation (Fig. 2C, D) and male gamete release (Fig. 2E). In contrast, RBPm1 disruption had no impact on female gamete formation in vitro (Fig. 2F), which corresponded with no RBPm1 expression in female. △Rbpm1 produced no ookinetes in vitro (Fig. 2G) or midgut oocysts and salivary gland sporozoites in the infected mosquitoes (Fig. 2H, I), indicating transmission failure in mosquito. Additionally, we deleted each of the RNA recognition motifs RRM1 (119-190 aa) and RRM2 (203-274 aa) of endogenous RBPm1 in the 17XNL (Fig. 2A). Both mutants, $\Delta rrm1$ and $\Delta rrm2$, displayed similar defects as those observed in △Rbpm1 (Fig. 2B, D), suggesting essential role of both two RNA recognition motifs in RBPm1 function.

To further confirm that the $\Delta Rbpm1$ phenotype was caused by *Rbpm1* deficiency, we introduced a sequence consisting of the coding region of *Rbpm1* and a N-terminal quadruple Myc epitope (4Myc) back to the *Rbpm1* locus in the $\Delta Rbpm1$ line, generating the complemented line, referred to as *rescue* (Fig. 2A). The 4Myc-tagged RBPm1 was detected in the *rescue* gametocytes (Fig. 2J) and localized in the nucleus of male gametocytes (Fig. 2K). The *rescue* parasites restored the formation of ECs (Fig. 2C, D), male gametes (Fig. 2E), ookinetes (Fig. 2G), midgut oocysts (Fig. 2H), and salivary gland sporozoites (Fig. 2I).

Lastly, we performed genetic crosses between $\Delta Rbpm1$ mutant and the male-deficient line $\Delta map2$ or the female-deficient line $\Delta nek4$. As expected, the cross between $\Delta map2$ and $\Delta nek4$ produced the ookinetes in vitro (Fig. 2L). The ookinete formation was restored in the $\Delta Rbpm1$ parasites that were crossed with $\Delta nek4$ but not $\Delta map2$, further confirming the defective male gamete formation in the $\Delta Rbpm1$. Together, these results demonstrated that RBPm1 is essential for male gametogenesis and mosquito transmission of parasites.



Fig. 1 | **RNA-binding protein RBPm1 is expressed in the nucleus of male gametocytes. A** Flowchart showing the purification and transcriptome analysis of male (green, GFP+) and female (red, mCherry+) gametocytes from a *P. yoelii* parasite reporter line *DFsc7.* **B** Gender analysis of gene transcription for the *Plasmodium* genome-wide putative RBPs between male and female gametocytes. The top male gene PY17X_0716700, *RBPm1*, is marked in red. CITH (orange dot) is a known female RBP. The results of *P. berghei* (middle panel) and *P. falciparum* (right panel) were based on the published gametocyte transcriptomes contributed by Yeoh, L.M. 2017 and Lasonder, E. 2016. The *p*-values were calculated by quasilikelihood F-test and adjusted by false discovery rate (FDR). **C** Stage expression of RBPm1 during the *P. yoelii* life cycle. Immunofluorescence assay (IFA) of RBPm1 expression in the *Rbpm1::GFP* protein in the *Rbpm1::gfp* parasites (bottom panel). Nuclei were stained with Hoechst 33342. Three independent experiments

with similar results. Scale bars: 5 µm. D Immunoblot of RBPm1 in the asexual blood

stage (ABS) and gametocyte of the *Rbpm1::6HA* parasites. BiP as a loading control. Three independent experiments with similar results. **E** IFA of HA-tagged RBPm1 and α -Tubulin (male gametocyte marker protein) in *Rbpm1::6HA* gametocytes. Three independent experiments with similar results. Scale bars: 5 μ m. **F** IFA of HA-tagged RBPm1 and mCherry (expressed in female gametocytes) in the *DFsc7;Rbpm1::6HA* gametocytes. Three independent experiments with similar results. Scale bars: 5 μ m. **G** Immunoblot of RBPm1 in cytosolic and nuclear fractions of *Rbpm1::6HA* gametocytes. Enolase (cytoplasmic/Cyto) and histone H3 (nuclear/Nuc) proteins used as controls respectively. Two independent experiments with similar results. **H** IFA of HA-tagged RBPm1 and histone H3 during male gametogenesis of the *Rbpm1::6HA* parasites. mpa: minute post activation. Three independent experiments with similar results. Scale bars: 5 μ m. **I** Immunoblot of RBPm1 expression in the *Rbpm1::6HA* parasites during male gametogenesis. Two independent experiments with similar results.



Fig. 2 | RBPm1 is essential for male gametogenesis and mosquito transmission of parasite. A A schematic showing genetic modification at the Rbpm1 locus in the P. yoelii parasite. The top panel depicts the protein structure of RBPm1 with two RNA recognition motifs RRM1 (residues 119-190, yellow) and RRM2 (residues 203-274, purple). Δ*Rbpm1*, deletion of the whole coding sequence from the 17XNL (wild type) strain; *rescue*, the $\Delta Rbpm1$ line complemented with *Rbpm1* fused with a 4Myc tag; Δrrm1 and Δrrm2, deletion each of RRM1 and RRM2 from the 17XNL. B Female and male gametocyte formation in mice for the modified parasite. Data are means ± SEM of three independent experiments. C Exflagellation center (EC) formation of activated male gametocytes at 10 mpa. Cell clusters representing the EC are marked with white arrows. Four independent experiments with similar results. Scale bars: 20 um, D Quantification of EC formation. The ECs were counted within a 1×1-mm square area in the hemocytometer under a light microscope. n represents the number of fields counted. Means ± SEM, one-way ANOVA with Tukey multiple pairwise-comparisons. Three independent experiments. E Light microscope images of the exflagellated male gametes (black arrow) after Giemsa staining. Four independent experiments with similar results. Scale bars: 5 µm. F Female gamete formation assayed by P28 staining. P28 is a female gamete plasma membrane protein. n = 32 and 35 female gametocytes in 17XNL and $\Delta Rbpm1$ respectively. Scale bars: 5 µm. G Ookinete formation in vitro. Data are means ± SEM from three

Defective axoneme assembly in RBPm1-deficient male gametogenesis

Next, we delineated more detailed defects of $\Delta Rbpm1$. During male gametogenesis, the parasites undergo axoneme assembly, genome replication, rupture of the parasitophorous vacuole membrane (PVM) and erythrocyte membrane (EM), and finally releasing eight uniflagellated male gametes. We first assessed the axoneme assembly. At 0 mpa, both α - and β -Tubulin were evenly distributed in the cytosol of male gametocytes of WT and $\Delta Rbpm1$ (Fig. 3A, upper panel). Immunoblot also detected comparable level for both Tubulins in gametocytes between WT and $\Delta Rbpm1$ (Fig. 3B). At 8 mpa, the axonemal

independent experiments, one-way ANOVA with Tukey multiple pairwisecomparisons. H Midgut oocyst formation in mosquitoes at 7 days after blood feeding. x/y at the top represents the number of mosquitoes containing oocysts/ the number of dissected mosquitoes, and the percentage represents the infection prevalence of mosquitoes. Red lines show the mean value of oocyst numbers, oneway ANOVA with Tukey multiple pairwise-comparisons. Three independent experiments with similar results. I Salivary gland sporozoite formation in mosquitoes at 14 days after blood feeding. At least 20 infected mosquitoes were counted in each group. Data are means ± SEM of three independent experiments, one-way ANOVA with Tukey multiple pairwise-comparisons. J Immunoblot analysis of RBPm1 expression in gametocytes of the complemented line rescue. BiP as a loading control. Two independent experiments with similar results. K IFA of Myc-tagged RBPm1 and α -Tubulin in gametocytes of the *rescue* parasite. Three independent experiments with similar results. Scale bars: 5 µm. L Gender gamete fertility assay of the $\Delta Rbpm1$ by parasite genetic cross. Fertility was determined by ookinete development of $\Delta Rbpm1$ gametes after cross-fertilization with mutant lines that are defective in either female ($\Delta nek4$) or male ($\Delta map2$) gametes. Data are means ± SEM of three independent experiments, one-way ANOVA with Tukey multiple pairwisecomparisons.

microtubules (MTs) were observed to be coiled around the enlarged nucleus in the WT gametocytes. However, aberrant axonemes were formed in $\Delta Rbpm1$ (Fig. 3A, middle panel). At 15 mpa, $\Delta Rbpm1$ failed to produce flagellated male gametes (Fig. 3A, lower panel). Under ultra-structure expansion microscopy (U-ExM)³⁷, the axonemes lost bundled structures at 8 mpa in $\Delta Rbpm1$ compared to the organized axonemes in WT (Fig. 3C). We used electron microscope to dissect the ultra-structural defects of axoneme in $\Delta Rbpm1$ male gametocytes at 8 mpa. The majority of axonemes (93%, 150 axonemes from 43 section images) displayed 9 + 2 arrangement of MTs in WT (Figs. 3D). In contrast, no intact axonemes (from 69 section images) were detected in either



Fig. 3 | Defective axonemal assembly in RBPm1-null male gametogenesis. A Detection of formation and exflagellation of axonemes during male gametogenesis (0, 8, and 15 mpa) by staining α -Tubulin (left panels) and β -Tubulin (right panels). Nuclei were stained with Hoechst 33342. Four independent experiments with similar results. Scale bars: 5 μ m. **B** Immunoblot of α - and β -Tubulins in gametocytes. The numbers indicate the relative intensities of the bands in the immunoblots. BiP as a loading control. Two independent experiments with similar results. **C** Ultrastructure expansion microscopy (U-ExM) of the axonemes in male

longitudinal or cross sections of $\Delta Rbpm1$ (Figs. 3D). All the axonemes in $\Delta Rbpm1$ showed severe defects with loss of either central singlet MTs or peripheral doublet MTs (Fig. 3D), consistent with the observation of Tubulin staining in Fig. 3C. In the complemented line *rescue*, the axoneme assembly restored to normal as in WT (Figs. 3D). These results demonstrated that RBPm1 is required for axoneme assembly during male gametogenesis.

We additionally analyzed genome replication and erythrocyte rupture during male gametogenesis. Flow cytometry analysis of male gametocytes at 8 mpa detected a comparable increase in DNA content in both parental *DFsc7* and its derivative mutant *DFsc7;* $\Delta Rbpm1$ parasites (Supplementary Fig. 2A). These results indicated normal genome replication in the absence of RBPm1, consistent with the enlarged nucleus observed in the activated $\Delta Rbpm1$ male gametocytes from both the fluorescence and electron microscope images (see Fig. 3A, D). gametocytes stained with α -Tubulin antibody at 8 mpa. Three independent experiments with similar results. Scale bars: 5 μ m. **D** Transmission electron microscopy of axoneme architecture in male gametocytes at 8 mpa. Inset panels show longitudinal sections (top panels) and cross sections (bottom panels) of axonemes. The enclosed area (black box) was zoomed in. Pie charts show the quantification of axoneme ("9 + 2" microtubules) in the mutant parasites. n is the total number of intact and defective axoneme structures observed in each group. Three independent experiments with similar results. Scale bars: 1 μ m.

In addition, immunostaining of SEP1 (parasite PVM protein) and TER119 (mouse EM protein) showed that RBPm1 deficiency had no notable effect on parasite rupture from the gametocyte-residing ery-throcytes (Supplementary Fig. 2B, C).

RBPm1 deficiency causes defective intron splicing of axonemal genes

To investigate the mechanism of RBPm1 in regulating the axoneme assembly, we performed RNA-seq to examine the changes in male transcriptome due to the loss of RBPm1 (Fig. 4A). To purify the RBPm1-null male gametocytes for comparison, we deleted *Rbpm1* in the *DFsc7* line. The mutant line *DFsc7*; $\Delta Rbpm1$ displayed the same phenotypes as $\Delta Rbpm1$ (Supplementary Fig. 3A–D). Purified male gametocytes of the *DFsc7*; $\Delta Rbpm1$ were collected by fluorescence-activated cell sorting for RNA-seq (Supplementary Fig. 3E, F). We analyzed the differentially



Fig. 4 | RBPm1 deficiency causes intron retention and protein loss of axonemal genes. A A schematic showing the transcriptome analysis of RBPm1-null male gametocytes. *DFsc7*; $\Delta Rbpm1$ is a *DFsc7*-derived RBPm1 mutant line. *DFsc7* (parental) and *DFsc7*; $\Delta Rbpm1$ (mutant) male gametocytes were sorted by FACS for RNA-seq. **B** Global analysis of differential intron retention identified 30 retained introns (blue dots) in the mutant versus the parental line. Retained introns with log₂FC ≥ 1 and *p* ≤ 0.05 were further verified manually by visualization in IGV. The *p*-values were calculated by quasi-likelihood F-test and adjusted by FDR. These introns were originated from 26 genes. Detailed information of these genes and introns is provided in Supplementary Fig. 4A. **C** List of the 26 genes with intron retention from (**B**), categorized by protein function. **D–I.** RT-PCR confirmation of intron retention in 6 selected genes *kinesin8b*, *PF16*, *dhc6*, *dlc1*, *dlc2*, and *PY17X_1109100*. Genomic DNA (gDNA) from 17XNL parasite, complementary DNA

expressed genes between *DFsc7* and *DFsc7*; $\Delta Rbpm1$ (Supplementary Data 2). As expected, the *Rbpm1* transcripts were undetectable in the *DFsc7*; $\Delta Rbpm1$ (Supplementary Fig. 3G, H). RBPm1 deficiency led to changed expression of several genes (Supplementary Fig. 3G), but none of the differentially expressed genes was known to be implicated in axoneme assembly during male gametogenesis.

(cDNA) from male gametocytes of parental and mutant parasites were analyzed. Exons are indicated by boxes and introns by lines. Three independent experiments with similar results. RT-PCR analysis for all 26 genes is presented in Supplementary Fig. 5A. **J**–**O**. Protein expression analysis of the 6 genes shown in (**D**–**I**) in male gametocytes after loss of RBPm1. Each endogenous gene was tagged with a 6HA at the C-terminus in both 17XNL and $\Delta Rbpm1$ parasites (the schematic in the top left panel), generating two tagged lines. Immunoblot of the 6HA-tagged protein in gametocytes with and without RBPm1 (bottom left panel). IFA of the 6HA-tagged protein in male gametocytes with and without RBPm1 (right panel). x/y at bottomleft represents the number of HA-positive male gametocytes/the total number of male gametocytes tested. Three independent experiments with similar results. Scale bars: 5 µm.

We found 30 intron retention (IR) events in transcripts of 26 genes after loss of RBPm1 (Fig. 4B, C) by bioinformatic analysis of global intron retention and manual examination on Integrative Genomics Viewer³⁸. These genes were specifically or preferentially transcribed in the male gametocytes (Supplementary Fig. 4A). Among them (Fig. 4C), the orthologs of *kinesin8b* and *PF16* had been reported essential for axoneme assembly of male gametogenesis in P. berghei³⁹⁻⁴¹. Six putative dynein motor-associated genes. dhc6 (dynein heavy chain. PY17X 0603800). dhc7 (dvnein heavy chain. PY17X 0510800). dlc1 (dvnein light chain, PY17X 1241500), dlc2 (dynein light chain, PY17X 0302800), drc1 (dynein regulatory complex protein, PY17X 0721100), and *dbc* (dynein beta chain, PY17X 1333900), were included. The md2 (male development protein 2, PY17X 1450400), a male gene recently identified⁴², was also included. The rest 17 IR genes had not been previously described in the Plasmodium. Gene Ontology (GO) enrichment analysis of these IR genes found significant GO terms that are associated with MT or cytoskeleton (Supplementary Fig. 4B). RT-PCR using the primers anchored in the flank exons of each of 26 introns further confirmed that these introns were retained in the transcripts in the absence of RBPm1, while their neighboring introns were correctly removed (Fig. 4D-I and Supplementary Fig. 5A). Using RT-qPCR, we further confirmed the IR of kinesin8b intron1 and PF16 intron1 in the RBPm1-null male gametocytes (Supplementary Fig. 5B). Interestingly, the whole part of intron was retained in the transcripts for most IR genes, while only a N-terminal part of intron was retained for three IR genes, including PF16 intron1, dlc1 intron4, and PY17X 1311800 intron5 (Fig. 4D-I and Supplementary Fig. 5A). Therefore, RBPm1 is required for the splicing of selective introns in certain male genes, especially MT or cytoskeleton-related genes.

We speculated that the RBPm1-regulated IR genes are axonemal given the following facts: (1) RBPm1 depletion causes defective axoneme assembly; (2) All IR genes are male-specific; (3) 8 IR genes are axoneme-related. To test it, we selected 12 out of the 26 genes, including 6 annotated (*kinesin8b*, *PF16*, *dhc6*, *dhc7*, *dlc1*, *dlc2*) and 6 unannotated (PY17X_1109100, PY17X_0521800, PY17X_1311800, PY17X_1323900, PY17X_1357300, PY17X_1335600). Each gene was endogenously tagged at the N- or C-terminus with a 6HA in the 17XNL. All 12 proteins were specifically expressed in male gametocytes during parasite life cycle (Supplementary Fig. 6A), in agreement with their transcript profile. In the inactivated gametocytes, these proteins were distributed in the cytoplasm, while after activation, 11 of 12 proteins displayed axoneme localization in the flagellating male gametes (Supplementary Fig. 6B–M). These results suggested that RBPm1 controls intron splicing for a group of the axonemal genes.

Intron retention leads to loss of axonemal protein in RBPm1-null male gametocytes

Nucleotide sequence analysis revealed that IR would result in premature translation and thus cause loss of protein expression for the axonemal genes (Supplementary Fig. 7). To analyze the effect of IR on the axonemal proteins after RBPm1 loss, we deleted *Rbpm1* gene in each of two tagged lines *kinesin8B::6HA* and *PF16::6HA* (Fig. 4J, K). In the absence of RBPm1, 6HA-tagged Kinesin8B, and PF16 were not detected or under detectable thresholds in male gametocytes compared to the parental counterparts in both IFA and immunoblot (Fig. 4J, K). To further confirm the protein loss, we analyzed 4 other IR genes *dhc6, dlc1, dlc2,* and PY17X_109100. Endogenous *Rbpm1* gene was deleted in all the 4 tagged lines (*dhc6::6HA, dlc1::6HA, dlc2::6HA,* and *1109100::6HA*) (Fig. 4L–O). These 6HA-tagged proteins lost expression in the RBPm1-null male gametocytes (Fig. 4L–O), similarly as Kinesin8B and PF16 did. These results demonstrated that RBPm1 deficiency causes expression loss of target axonemal proteins.

To confirm the essential roles of *P. yoelii* Kinesin8B and PF16 in axoneme assembly as reported in *P. berghet*³⁹⁻⁴¹, we disrupted *kinesin8b* and *PF16* genes in the 17XNL, obtaining mutant lines $\Delta kinesin8b$ and $\Delta PF16$ (Supplementary Fig. 8A). As expected, depletion of *kinesin8b* or *PF16* either blocked or severely impaired male gamete formation, respectively (Supplementary Fig. 8B). Neither mutant produced any midgut oocysts in the infected mosquitoes (Supplementary Fig. 8C). Ultrastructure analysis of male gametocytes at 8 mpa revealed that the $\Delta kinesin8b$ mutant failed to develop "9 + 2" axoneme,

with loss of both central and peripheral MTs, while most of the axonemes lost central MTs (shown as "9+0" or "9+1") in the $\Delta PF16$ (Supplementary Fig. 8D, E), in line with gene disruption phenotypes in *P. berghei*³⁹⁻⁴¹. Therefore, depletion of Kinesin8B or PF16 phenocopies RBPm1 deficiency in axoneme assembly.

Intron deletion restores axonemal proteins and partially rectifies axoneme assembly defects in RBPm1-null gametocytes

Since IR disrupted the axonemal proteins expression, we tested whether enforced genomic deletion of the retained intron could restore protein expression by bypassing intron splicing at the transcripts in RBPm1-null male gametocytes. The endogenous kinesin8b intron1 (239 bp) was removed in the *kinesin8b::6HA*; $\Delta Rbpm1$ parasite by CRISPR-Cas9 (Fig. 5A), generating the intron-null mutant kine $sin8b\Delta intron1$ (kinesin8b $\Delta I1$). Both IFA and immunoblot revealed that the deletion of intron1 restored Kinesin8B::6HA expression to WT level in the RBPm1-null gametocytes (Fig. 5B, C). To further confirm the restoration effect, we tested 3 other retained introns (PF16 intron1, dlc1 intron4, and PY17X 1109100 intron1). Compared to the parental RBPm1-null parasites, the expression of PF16::6HA and 1109100::6HA in male gametocytes were fully restored (Fig. 5D-F, J-L), while the Dlc1::6HA was partially restored after removal of the corresponding intron (Fig. 5G-I). Expression restoration of these axonemal proteins (Kinesin8b, PF16, Dlc1, and PY17X 1109100) via intron deletion strongly confirmed the causative effect of IR on axonemal protein loss in the absence of RBPm1.

We next tested whether genomic deletion of the retained introns could rescue or rectify the defective axoneme assembly in the $\Delta Rbpm1$ mutant. We deleted the *kinesin8b* intron1 in the $\Delta Rbpm1$ line, but this deletion of single intron failed to restore any EC formation in the ∆*Rbpm1;kinesin8b*∆*intron1* parasites. However, compared to complete lack of axonemes showing "9 + 2", "9 + 1", or "9 + 0" MTs in the parental $\Delta Rbpm1$, some axoneme-like structures ("9 + 2": 1%, "9 + 1": 3%, and "9 + 0": 15%) were detected in the $\Delta Rbpm1$:kinesin8b Δ intron1 (Fig. 5M, N), indicating that deletion of *kinesin8b* intron1 could partially rescue the defective axoneme assembly caused by RBPm1 deficiency. Notably, additional deletion of the *PF16* intron1 in the $\Delta Rbpm1$;kinesin8b\intron1 parasite further mitigated axoneme defects in the resulted $\Delta Rbpm1$;kinesin8b Δ intron1;PF16 Δ intron1 parasite line ("9 + 2": 1%, "9 + 1": 11%, and "9 + 0": 32%) (Fig. 5M, N). These results demonstrated that RBPm1 regulates axoneme assembly by controlling intron splicing of a group of axonemal genes. Without RBPm1, deletion of 2 introns (kinesin8b intron1 and PF16 intron1) was insufficient to restore axoneme assembly to the WT level ("9 + 2": 93%) (Fig. 5M, N). Therefore, in addition to kinesin8b and PF16, other axonemal genes targeted by RBPm1 may also play important roles in axoneme assembly during male gametogenesis.

RBPm1 interacts with spliceosome E complex and introns of axonemal genes

To investigate whether RBPm1 associates with the spliceosome responsible for intron splicing, we used the biotin ligase TurbolDbased proximity labeling to identify RBPm1-interacting proteins in the gametocytes. The endogenous RBPm1 was tagged with a HA::TurbolD motif in the 17XNL, generating the line *Rbpm1::TurbolD* (Fig. 6A). A control parasite *Rbpm1::T2A::TurbolD* was generated by fusing endogenous RBPm1 with a "ribosome skip" T2A peptide, a NLS (nuclear localization signal), and a HA::TurbolD (Fig. 6A), permitting separated expression of RBPm1 and biotin ligase. Gametocytes expressing the ligase were incubated with 50 μ M biotin for 20 min at 37 °C. Staining with fluorescent-conjugated streptavidin and anti-HA antibody detected a nuclear distribution of biotinylated proteins in both TurbolD-modified gametocytes (Supplementary Fig. 9A), indicating biotinylation of the potential RBPm1-interacting proteins in the nucleus. Mass spectrometry of the streptavidin affinity purified proteins from the



Fig. 5 | Intron deletion restores axonemal protein expression and partially rectifies axoneme assembly defects in RBPm1-null male gametocytes. A A schematic showing the genomic deletion of retained intron (*kinesin8b* intron1, orange) in the *kinesin8b::*6HA; Δ Rbpm1 parasite (abbreviated as Δ Rbpm1), generating the mutant *kinesin8b::*6HA; Δ Rbpm1;*kinesin8b*\Delta*intron1* (abbreviated as *kine-sin8b*\Delta*l1*). B Immunoblot of 6HA-tagged Kinesin8b protein in gametocytes. Three independent experiments with similar results. C IFA of 6HA-tagged Kinesin8B in male gametocytes. x/y represents the number of HA-positive male gametocytes/the total number of male gametocytes tested. Three independent experiments with similar results. Scale bars: 5 µm. D, E, F Effect of intron deletion (*PF16* intron1) on the restoration of PF16 protein in RBPm1-null male gametocytes. Similar analysis as in

protein in RBPm1-null male gametocytes. **J**, **K**, **L** Effect of intron deletion (*PY17X_1109100* intron1) on the restoration of PY17X_1109100 protein in RBPm1null male gametocytes. **M** Transmission electron microscopy of axoneme architecture in male gametocytes at 8 mpa. $\Delta Rbpm1$;kinesin8b Δ II is a $\Delta Rbpm1$ -derived modified line with deletion of kinesin8b intron1. $\Delta Rbpm1$;kinesin8b Δ II;*PF1*6\DeltaII is a $\Delta Rbpm1$ derived modified line with deletion of both kinesin8b intron1 and *PF16* intron1. Scale bars: 100 nm. **N** Quantification of axoneme formation from parasites in (**M**). n is the total number of the intact and defective axoneme structures observed in each group. Three independent experiments with similar results.

(A, B, C). G, H, I Effect of intron deletion (dlc1 intron4) on the restoration of Dlc1

Rbpm1::TurbolD resulted in a list of 113 proteins enriched with high confidence compared to the control (Fig. 6B and Supplementary Data 3). RBPm1 was the top hit, confirming cis-biotinylation of RBPm1 (Fig. 6B). Among the significantly enriched proteins, we found the components of the spliceosome earliest assembling E complex⁴³⁻⁴⁵, including the U1 small nuclear ribonucleoproteins (snRNP) U1-70K, U1-A, U1-C, Sm-B, Sm-D1, Sm-D2, Sm-D3, Sm-E, Sm-F and Sm-G (Fig. 6B, C), and three E complex key factors SF1, U2AF1, and U2AF2 (Fig. 6B, C). Tagging the endogenous U1-70K, U1-A, and U1-C proteins with 4Myc in the *Rbpm1::6HA* parasite showed that these three U1 snRNPs colocalized with RBPm1 in the nucleus (Fig. 6D). Co-immunoprecipitation also confirmed the interaction between RBPm1 and these U1 snRNPs (Fig. 6E–G). Spliceosome A, B, and C complex are formed after the

assembly of splicing initiating E complex^{46,47}. However, the components of A, B, and C complex were not detected (Supplementary Fig. 9B, C). Therefore, RBPm1 interacted only with spliceosome E complex, possibly helping to initiate splicing for certain introns in the axonemal genes (Fig. 6H).

Nuclear localization and interaction with spliceosome E complex imply that RBPm1 may bind to the target introns in the pre-mRNA of axonemal genes. We performed UV crosslinking RNA immunoprecipitation (UV-RIP) followed by RT-qPCR with primers recognizing the target pre-mRNAs. In the *Rbpm1::6HA* gametocytes, RBPm1 bound to the intron1 of the *kinesin8b* transcripts using anti-HA nanobody (Fig. 6I). As a control, RIP using anti-GFP nanobody detected no binding (Fig. 6I). Additionally, we analyzed the interaction between



RBPm1 and five other target introns (*PF16* intron1, *dhc6* intron20, *dlc1* intron4, *dlc2* intron1, and *PY17X_1109100* intron1). As expected, RBPm1 bound these target introns. As expected, RBPm1 bound these target introns but not the neighboring introns or exons since each intron is individually excised as a lariat RNA during the splicing (Fig. 6J–N).

Furthermore, we used RNA pull-down to validate the interaction of RBPm1 with the *kinesin8b* intron1 and *PF16* intron1. A biotinylated 500nt RNA probe *kinesin8b* I1 and a control probe *kinesin8b* I4 were synthesized (Fig. 6O, upper panel) and incubated with the *Rbpm1::6HA* gametocyte lysate. The potential RNA-interacted proteins were precipitated using the streptavidin beads and detected by immunoblot. The *kinesin8b* I1 probe retrieved more RBPm1 protein than the *kinesin8b* I4 probe (Fig. 6O). Similarly, the *PF16* I1 probe captured more RBPm1 protein than the probe *PF16* E1 (Fig. 6P). Both RIP and RNA pulldown experiments supported that RBPm1 binds the *kinesin8b* intron1 and *PF16* intron1.

RBPm1 directs splicing of axonemal introns inserted in a reporter gene

To further investigate the interaction between RBPm1 and the axonemal introns, we test whether RBPm1 could direct splicing of target introns when inserted into a reporter gene. We developed a blue fluorescence protein (BFP) reporter assay that allows an easy splicing readout in male and female gametocytes of the *DFsc7* parasite. The intact *bfp* transcript driven by the *hsp70* 5'-UTR and the *dhfr* 3'-UTR was integrated into the *p230p* locus of *DFsc7* using CRISPR-Cas9, generating the control line *BFP* (Fig. 7A). The *kinesin8b* intron1 (*Kin8b*I1, 239 bp) was inserted to the *bfp* gene at the nucleotides Fig. 6 | RBPm1 interacts with spliceosome E complex and introns of axonemal genes. A A schematic showing two modified parasite lines generated for searching RBPm1-interacting proteins by TurboID-based proximity labeling and mass spectrometry. The motif of HA::TurboID and T2A::3NLS::HA::TurboID, respectively, was inserted at the C-terminus of the endogenous RBPm1, generating the line Rbpm1::TurboID and the control line Rbpm1::T2A::TurboID. B Volcano plot displaying 113 significantly enriched proteins (pink dot, cutoffs $\log_2 FC \ge 1$ and $p \le 0.05$) in the *Rbpm1::TurbolD* versus *Rbpm1::T2A::TurbolD*. Among them, 13 subunits (red dot) of the early spliceosome E complex were included. The p-values were calculated by two-sided t-test and adjusted by FDR. C Protein interaction analysis between RBPm1 and six spliceosome E complex subunit proteins (U1-70K, U1-A, U1-C, SF1, U2AF1, and U2AF2) from (B). D IFA of 6HA-tagged RBPm1 and 4Myctagged U1 snRNP proteins (U1-70K, U1-A, and U1-C) in male gametocytes of three double-tagged parasites. Three independent experiments with similar results. Scale bars: 5 µm. E Co-immunoprecipitation of RBPm1 and U1-70K in gametocytes of the double-tagged parasite U1-70K::4Myc;Rbpm1::6HA. Anti-Myc nanobody was used. Bip as a loading control. Three independent experiments with similar results. F Coimmunoprecipitation of RBPm1 and U1-A in gametocytes of the double-tagged parasite U1-A::4Myc;Rbpm1::6HA. Three independent experiments with similar results. G Co-immunoprecipitation of RBPm1 and U1-C in gametocytes of the double-tagged parasite U1-C::4Myc;Rbpm1::6HA. Three independent experiments

with similar results. H Proposed model showing the interaction between RBPm1 and early spliceosome E complex for intron splicing of axonemal genes. I-N. UV-RIP detection of RBPm1 interaction with the retained introns of 6 axonemal genes (kinesin8b, PF16, dhc6, dlc1, dlc2, and PY17X 1109100). A top schematic shows the exon-intron structure of the RBPm1 target axonemal genes. The retained introns are indicated with orange lines, and the genomic regions for qPCR amplicon are shown. UV-RIP was performed in Rbpm1::6HA lines using anti-HA nanobody. Anti-GFP nanobody was used as a control. Bound RNA was analyzed by RT-qPCR. Means ± SEM from three independent experiments, two-sided t-test. O RNA pulldown assay detecting RBPm1 interaction with kinesin8b intron1. A top schematic shows the exon-intron structure of the kinesin8b gene. The retained introns are indicated in orange lines. A biotinylated 500 nt RNA probe I1 (comprising intron1 and its flanking sequences) and a control probe I4 (comprising intron4 and its flanking sequences) were used. Proteins via RNA pull-down were immunoblot with anti-HA antibody. The numbers are the relative intensities of bands in the blot. Histone H3 and Bip were used as negative controls. Two independent experiments with similar results. P RNA pull-down assay detecting RBPm1 interaction with PF16 intron1. A top schematic shows the exon-intron structure of the PF16 gene. The retained introns are indicated in orange lines. A biotinylated 500 nt RNA probe I1 (comprising intron1 and its flanking sequences) and a control probe E1 in exon1 were used. Two independent experiments with similar results.

396-397, generating the line BFP-Kin8bl1 (Fig. 7B). The inserted kinesin8b intron1 would result in premature translation of the bfp transcript if it is not spliced. In the control BFP line, BFP was expectedly detected in both male (GFP+) and female (mCherry+) gametocytes (Fig. 7A). However, in the BFP-Kin8bl1 line, BFP was detected only in male gametocytes (Fig. 7B), indicating that splicing of kinesin8b intron1 in the *bfp* transcripts occurred only in male gametocytes. To prove that splicing of kinesin8b intron1 in male was RBPm1-dependent, we deleted Rbpm1 in the BFP-Kin8bl1 line and obtained the mutant line BFP-Kin8bI1;∆Rbpm1 (Fig. 7C). RBPm1 deletion disrupted BFP expression in the *BFP-Kin8b*I1;Δ*Rbpm1* male gametocytes (Fig. 7C). We parallelly analyzed the kinesin8b intron2 (Kin8bl2, 148 bp), whose splicing from the native gene transcript required no RBPm1 (Supplementary Fig. 5A). In both transgenic line BFP-Kin8bI2 (Fig. 7D) and its derivative mutant line BFP-Kin8bI2;ΔRbpm1 (Fig. 7E), BFP was detected in both male and female gametocytes, confirming RBPm1-independent splicing of kinesin8b intron2 from the bfp transcript.

Using the reporter assay, we tested 3 other target introns, including PF16 intron1 (Fig. 7F, G), dlc1 intron4 (Supplementary Fig. 10A, B), and PY17X_1109100 intron1 (Supplementary Fig. 10C, D). The *PF16* intron1 (276 bp) was inserted to the *bfp* at the nucleotides 500-501 (Fig. 7F), the *dlc1* intron4 (193 bp) at the nucleotides 455–456 (Supplementary Fig. 10A), while the PY17X_1109100 intron1 (353 bp) at the nucleotides 390-391 (Supplementary Fig. 10C). As expected, these introns were spliced from the *bfp* transcript only in male gametocytes (Fig. 7F, Supplementary Fig. 10A, C). Similarly, these introns were not spliced at male gametocytes in the RBPm1-null parasites compared to their parental parasites (Fig. 7G, Supplementary Fig. 10B, D). Additionally, we analyzed the PY17X 1109100 intron2 (272 bp), which could be spliced in the RBPm1-null parasites (Supplementary Fig. 5A), and found that RBPm1 was not required for splicing of this intron from bfp transcript in both male and female gametocytes (Supplementary Fig. 10E, F).

Furthermore, we analyzed the RBPm1 interaction with the *kinesin8b* intron1 and *PF16* intron1 in the *bfp* transcript by RNA pull-down. A biotinylated RNA probe *bfp-Kin8b*11, corresponding to the *kinesin8b* intron1-inserted *bfp* transcript (Fig. 7H, upper panel), retrieved significantly more RBPm1 from the *Rbpm1::6HA* gametocyte lysate compared to the control probe *bfp* (Fig. 7H, middle panel). Similarly, the probe *bfp-PF16*11, corresponding to the *PF16* intron1-inserted *bfp* transcript, captured more RBPm1 than the control probe *bfp* (Fig. 7H, lower panel). Therefore, RBPm1 could recognize the axonemal introns in the reporter transcript for splicing (Fig. 7I).

RBPm1 directs splicing of axonemal introns inserted in an endogenous gene

In addition to the reporter gene, we also tested whether RBPm1 could direct splicing of target introns when inserted into an endogenous gene which does not require RBPm1 for intron splicing. We chose the gep1, a 4-exon gene expressed in both gender gametocytes and essential for initiating both genders' gametogenesis⁴⁸. We analyzed male and female gametogenesis by measuring EM rupture (TER119 staining), genome replication (DNA staining), and axoneme assembly (α -Tubulin staining). Compared to 17XNL, the *gep1*-deleted parasite line $\Delta gep1$ expectedly lost ability in EM rupture, genome replication, and axoneme assembly in activated male gametocytes, as well as EM rupture in activated female gametocytes (Fig. 8A, B, E, F, G, and H). Using CRISPR-Cas9, the kinesin8h intron1 was inserted into the exon3 of gep1 locus at the nucleotides 273-274 in the 17XNL (Fig. 8C), while the PF16 intron1 inserted into the exon1 at the nucleotides 885-886 (Fig. 8D). In both intron-inserted lines gep1-Kin8bl1 and gep1-PF16l1, normal male gametogenesis and defective female gametogenesis was speculated because GEP1 is not expressed in female due to no RBPm1mediated intron splicing from the gep1 transcript. Notably, both the gep1-Kin8b I1 and gep1-PF16 I1 parasites underwent EM rupture only in male (Fig. 8C-F). These results supported that both kinesin8b intron1 and PF16 intron1 were spliced from the gep1 transcript only in male gametocytes with RBPm1 expression. Consistent with GEP1 expression in male gametocytes, normal genome replication and axoneme assembly were detected during male gametogenesis in both gep1-Kin8b I1 and gep1-PF16 I1 parasites (Fig. 8C, D, G, H). Collectively, the results from the reporter and the endogenous gene assays (Fig. 81) indicated that the tested axonemal introns themselves could be specifically recognized by RBPm1 for splicing.

Intron retention prevents expression of axonemal proteins in female gametocytes

Despite the male-biased transcription, the axonemal genes still displayed low-level transcripts in female gametocytes (Supplementary Fig. 11A, C, E). However, no axonemal proteins are expressed in female gametocytes (Supplementary Fig. 11B, D, F). The facts of no protein product of low-level transcripts for the axonemal genes observed in this study are consistent with results from previous transcriptomic and proteomic studies^{30,31,49,50}, suggesting a post-transcription regulation for the axonemal genes in female gameto-cytes. Enforced genomic deletion of the retained intron could restore expression of the axonemal proteins Kinesin8b, PF16, Dlc1,



and PY17X_1109100 in the RBPm1-null male gametocytes (Fig. 5A–L). Strikingly, we found that deletion of these introns (*PF16* intron1, *dlc1* intron4, and *PY17X_1109100* intron1) unexpectedly resulted in low-level expression of PF16, Dlc1, and PY17X_1109100 in the counterpart female gametocytes (Supplementary Fig. 11B, D, F). Kinesin8B was not detected in female gametocytes after deletion of *kinesin8b intron1* (Supplementary Fig. 11H), fitting with the extremely low

transcription of *kinesin8b* in female gametocytes (Supplementary Fig. 11G). Furthermore, RT-PCR not only detected the transcripts of these axonemal genes (*PF16, dlc1,* and *PY17X_1109100*), but also IR in these transcripts from the purified female gametocytes (Supplementary Fig. 11I–L). These results indicated a role of the RBPm1-target introns in preventing the expression of axonemal proteins in female gametocytes.

Fig. 7 | RBPm1 directs splicing of axonemal introns inserted in a reporter gene. A A top schematic shows a transgenic line BFP with a bfp reporter expression cassette integrated at the p230p locus of the DFsc7 reporter line. The intact bfp is driven by the 5'UTR of *hsp70* and the 3'UTR of *dhfr*, allowing expression of BFP in both male (GFP+) and female (mCherry+) gametocytes. Live cell imaging was shown. Three independent experiments with similar results. Scale bars: 5 µm. B. A transgenic line BFP-Kin8bl1 with a kinesin8b intron 1 (Kin8b II, purple line)-inserted bfp cassette integrated at the p230p locus of the DFsc7 line. Kin8b II (purple) was inserted into the bfp gene at the nucleotides 396-397 to mimic the splice site (vertical lines) of in situ Kin8b II. BFP expression was detected specifically in male gametocytes of the BFP-Kin8bl1 parasites. Three independent experiments with similar results. Scale bars: 5 µm. C A BFP-Kin8bl1 derived RBPm1 mutant line BFP-*Kin8b*11:Δ*Rbpm1*. No BFP expression was detected in male gametocytes of the *BFP*-Kin8bl1;ΔRbpm1 parasites. Three independent experiments. Scale bars: 5 μm. D Effect of the kinesin8b intron 2 (Kin8b l2) insertion on the gametocyte expression of BFP. Similar analysis as in (B). BFP expression was detected in both male and female gametocytes of the BFP-Kin8bl2 parasites. E A BFP-Kin8bl2 derived RBPm1

mutant line *BFP-Kin8b*I2;∆*Rbpm1*. Similar analysis as in (**C**). BFP expression was detected in both male and female gametocytes of the BFP-Kin8bl2; ARbpm1 parasites. F Effect of the PF16 intron1 (PF16 II) insertion on the gametocyte expression of BFP. Similar analysis as in (B). BFP expression was detected specifically in male gametocytes of the BFP-PF16l1 parasites. G A BFP-PF16l1 derived RBPm1 mutant line *BFP-PF16*11;Δ*Rbpm1*. Similar analysis as in (**C**). No BFP expression was detected in male gametocytes of the BFP-PF1611; \Delta Rbpm1 parasites. H RNA pull-down assay detecting RBPm1 interaction with the Kin8b I1 and PF16 I1 -inserted bfp transcripts from BFP-Kin8bl1 and BFP-PF16l1 gametocytes, respectively. Three biotinylated RNA probes bfp, bfp-Kin8bl1 (corresponding to the Kin8b I1-inserted bfp transcript), bfp-PF1611 (corresponding to the PF16 I1-inserted bfp transcript) were used. Proteins via RNA pull-down were immunoblotted with anti-HA antibody. The numbers are the relative intensities of bands in the blot. Histone H3 and Bip were used as negative controls. Two independent experiments with similar results. I A schematic of RBPm1-dependent splicing of axonemal introns inserted in the reporter transcript.

Discussion

For efficient transmission, the malaria parasites in the vertebrate host differentiate into sexual precursor gametocytes that are poised to rapidly activate to fertile gametes upon entering into the mosquito midgut for fertilization and further development. So far, a limited number of transcription and epigenetic factors have been identified during gametocyte and gamete development^{51,52}. Among ~180 putative *Plasmodium* RBPs, about one-third of RBP genes exhibit stage specific or elevated expression in the gametocyte³². From this list of RBPs, we identified a previously undescribed male-specific nuclear RBP, RBPm1, which is essential for male gametogenesis and mosquito transmission of the *Plasmodium*. RBPm1 operates as a stage- and gender-specific splicing factor for spliceosome assembly initiation and regulates the protein expression of a group of 26 male genes, most of which are axoneme-related.

Recent studies had discovered several RBPs playing roles in the developmental programs of gametocyte and gametes. During gametocytes development, UIS12 contributes to the development of gametocytes of both genders⁵³. Disrupting *Puf1* led to a reduction in gametocytes, especially female gametocytes⁵⁴, while *ccr4-1* gene deletion obstructs male gametocyte development⁵⁵. Puf2 knockout, on the other hand, promotes male gametocyte development⁵⁶. The CCCH zinc finger protein MD3 regulates the gametocyte maturation and male gametocytogenesis⁵⁷. In female gametocytes, the DOZI/ CITH/ALBA translation repressor complex and PUF2 hold the stored mRNAs for translation repression until their proteins were needed during the development of post fertilization^{28,58}. Additionally, the CAF1/CCR4/NOT complex also plays a role in safeguarding the stored mRNAs from degradation. In male gametocytes, two functional RBPs have been identified. The alternative splicing factor SR-MG promotes the establishment of sex-specific splicing patterns and knocking it out reduces the formation of male gamete⁵⁹; the ZNF4's knockout results in deregulation of 473 genes, including axonemal dynein-related genes⁶⁰. These documented RBPs and RBPm1 identified in this study may function together at the posttranscriptional regulation to shape the male transcriptome for gametocyte and gamete development.

During the manuscript preparation of this study, another work by ref. 42 demonstrated that deletion of the *Rbpm1* ortholog of *P. berghei* (PBANKA_0716500, named as *md5*) had no effect on female and male gametocyte formation, but resulted in male-specific infertility. These findings are consistent with the defective male gamete formation phenotype of the $\Delta Rbpm1$ in *P. yoelii* in this study, indicating conserved function of RBPm1 in the rodent malaria parasites. As *P. falciparum* is the most lethal human malaria parasite, future studies are worthy to investigate whether the RBPm1 ortholog in the *P. falciparum* functions similarly in male gametogenesis.

The RBPm1-deficient parasites showed specific defects in axoneme assembly during male gametogenesis (Fig. 3). Axoneme is a MT cytoskeleton essential for the eukaryotic flagellar motility, consisting of a central pair of singlet MTs encircled by 9 outer doublet MTs. This 9+2 organization of axonemes is highly conserved in the eukaryotes, including *Plasmodium*⁶¹. However, the axoneme in *Plasmodium* differs from that in other model organisms in several aspects^{10,62,63}. First, the biogenesis of axoneme in Plasmodium male gametogenesis is extremely fast, taking only 6-8 min to assemble 8 axonemes^{9,10}. Second, location of basal body. In the canonical cilium, the basal body is localized under the plasma membrane. In Plasmodium male gametocytes, the basal bodies are residing at the nuclear membrane⁶³. Third, location for axoneme assembly. The canonical axoneme protrudes distally from the cell simultaneously when growing from the basal body. The *Plasmodium* assemblies the axoneme within the cytoplasm, independent of intraflagellar transport required for cilium formation^{10,62}. Last, each assembled axoneme associates with a haploid nuclei to progressively protrude from the parasite plasma membrane, resulting in a free motile flagellum¹⁰. Mechanisms underlying the cytoplasmic assembly and exflagellation of axonemes in Plasmodium remain largely unknown, although the involvement of some conserved basal body and axonemal proteins has been described, including armadillo repeat protein PF16⁴¹, motor protein Kinesin8B^{39,40,64}, basal body proteins SAS4 and SAS6^{63,65-67}, and radial spoke protein RSP9⁶⁸. It is possible that the Plasmodium had evolved novel mechanisms to fulfill the requirement for the axoneme. In this study, we identified a group of 26 male genes targeted by RBPm1. Several known or putative axoneme-associated genes were included. Importantly, analysis of endogenous protein localization showed that most of the tested proteins encoded by RBPm1-target genes co-localizing with axoneme (Supplementary Fig. 6B-M), suggesting their roles in biogenesis, structure, regulation, or function of axoneme. For future studies, it will be intriguing to understand the roles of these 26 RBPm1-regulated genes, especially 17 previously undescribed ones, during male gametogenesis in the Plasmodium.

In the RBPm1 deficient male gametocytes, 30 IR events were detected in 26 male genes. One intron was retained in each of 22 genes while two introns were retained in each of 4 other genes, respectively (Fig. 4B and Supplementary Fig. 4A). Mechanistically, RBPm1 not only bound to the intron-retained transcripts, but also interacted with spliceosome E complex. U1 snRNPs recognize and pair with the 5' splice site of intron. SF1, U2AF1 and U2AF2 form a complex and bind to branch point, 3' splice site, and polypyrimidine tract respectively^{69,70}. These above factors assemble the E complex as a spliceosome earliest stage. After that, the spliceosome dynamically releases and recruits different snRNPs to establish the assembly for further stages, including spliceosome A, B, and C complex. RBPm1 was detected to interact



Proof Constitution Constitutio

exclusively with the components of spliceosome E complex, but not those of the A, B, and C complex (Supplementary Fig. 9C). Therefore, RBPm1 likely function as a splicing activator, linking spliceosome E complex with the selective introns of axonemal genes for splice site recognition. In mammals and plants, a RBP of Dek played a similar role and promoted the splicing of certain introns by bridging the intron with the U1/U2 snRNPs^{71,72}. At this stage, the data support an association of RBPm1 and spliceosome E complex, but it is not yet clear if it is a direct association.

Both RIP and RNA pull-down assays demonstrated that RBPm1 interacts with the target introns in transcripts of the axonemal genes, suggesting the presence of signals recognized by RBPm1 in these introns. To investigate if the signals for RBPm1 recognition are imparted by the introns themselves but not the adjoining exons, we analyzed the splicing capability of these introns when they were inserted in either a reporter gene (*bfp*) or an irrelevant endogenous



gene (gep1). The results from both intron splicing assays establish stringent dependencies of splicing on RBPm1 for these axonemal introns, suggesting intrinsic signals within the introns for RBPm1 recognition. In addition, the adjoining exons may play less modulatory role in the RBPm1 recognition of the axonemal introns. We attempted to search for the common features, such as length, GC content, splice sites, and motif enrichment, but unfortunately observed seemingly no shared features among these 30 RBPm1 target introns. The molecular basis for the axonemal intron recognition by RBPm1 is still unknown. One possibility is that RBPm1 target introns may possess the sequenceindependent features, such as RNA structures or epigenetic modifications, for RBPm1 recognition. The structure of RBPm1 is not available yet. To understand the recognition or interaction between RBPm1 and its target introns, future studies into an atomic resolution structure of the protein (RBPm1)-RNA (intron) complex will be required.

Axoneme is an essential cellular structure specifically required for male gametogenesis during the life cycle of *Plasmodium*. Consistent with this physiological requirement of male gametocytes, the axonemal genes display significant male-biased transcription^{30,31,49}. Interestingly, these axonemal genes also showed low-level transcripts in female gametocytes in many others and our studies^{30,31,49}, likely due to the transcription leaking. However, no axonemal proteins are detected in female gametocytes⁵⁰, suggesting a post-transcription regulation for the expression turn off of axonemal genes in female gametocytes. We found that genomic deletion of the retained intron (kinesin8b intron1, PF16 intron1, dlc1 intron4, and PY17X 1109100 intron1) could bypass the intron splicing and thus restore expression of the axonemal proteins (Kinesin8b, PF16, Dlc1, and PY17X_1109100) in the RBPm1-null male gametocytes. Notably, these introns deletion unexpectedly resulted in low-level expression of PF16, Dlc1, and PY17X_1109100 in female gametocytes (Supplementary Fig. 11B, D, F). The level of proteins restored was correlated with the level of transcripts for these axonemal genes in female gametocytes. These results confirmed the low-level transcripts of these axonemal genes in female gametocytes. In addition, no protein products of these low-level transcripts could be explained by IR and translation failure in female gametocytes. Based on these results, we proposed a dual role of RBPm1-target introns in axonemal gene expression in male and female gametocytes respectively (Supplementary Fig. 11M). In male gametocytes, RBPm1 (as a key)-directed splicing of axonemal intron (as a lock) allows protein expression of axonemal genes for axoneme assembly. In female gametocytes, dual blockage via weak transcription and IR shuts the protein expression of the axonemal genes. The splicing activator RBPm1 and its target introns constitute an intron splicing program, safeguarding the expression of axonemal proteins in male gametocytes while preventing the expression of these proteins in female gametocytes, to fulfill the sexually dimorphic protein profiles during sexual development of the Plasmodium.

Methods

Animals and ethics statement

The animal experiments conducted in this study were approved by the Committee for Care and Use of Laboratory Animals of Xiamen University (XMULAC20190001). Female ICR mice aged 5–6 weeks were acquired from the Animal Care Center of Xiamen University. The mice were housed in a controlled environment at 22-24 °C, relative humidity of 45–65%, and a 12-h light/dark cycle. They were used for parasite propagation, drug selection, parasite cloning, and mosquito feeding. The larvae of *Anopheles stephensi* mosquitoes (Hor strain) were maintained in an insect facility under controlled conditions of 28 °C, 80% relative humidity, and a 12-h light/12-h dark cycle. Adult mosquitoes were fed with a 10% (w/v) sucrose solution containing 0.05% 4-aminobenzoic acid and kept at 23 °C.

Plasmid construction

All genetically modified parasites in this study are listed in Supplementary Table 1. The CRISPR/Cas9 plasmid pYCm was used for gene editing^{34,73}. To construct plasmids for gene tagging, the 5'- and 3'flanking sequences (300–700 bp) at the designed insertion site of target genes were amplified as homologous templates. DNA fragments encoding 6HA, GFP, or 4Myc were placed between them and in-frame with the target gene. To construct the plasmids for gene knockout, the left and right homologous arms consisted of 400–700 bp sequences upstream and downstream of the coding sequences of the target gene. To construct the plasmids for domain or intron deletion, the left and right homologous arms consisted of 200–700 bp sequences upstream and downstream of the domain or intron were PCR-amplified and inserted into specific restriction sites in pYCm. To construct the plasmids for intron insertion, the left and right homologous arms were composed of gene genomic sequences ranging from 300–600 bp upstream and downstream of the insertion site, respectively. The left homologous arm, intron, and right homologous arm were connected by overlap PCR, and the fused fragment was inserted into specific restriction sites in pYCm. In each modification, at least two small guide RNAs (sgRNAs) were designed. To construct the plasmids for the *bfp* reporter assay, the intact *bfp* reporter (717 bp) driven by the 5'-UTR (1755 bp) of the *hsp70* gene and the 3'-UTR (561 bp) of the *dhfr* gene were inserted into specific restriction sites between the left and right homologous arms for transgenic integration in the *p230p* locus of *P*. *yoelii*⁷⁴. The *kinesin8b* intron1 (239 bp), *kinesin8b* intron2 (148 bp), *PF16* intron1 (276 bp), *dlc1* intron4 (193 bp), PY17X_1109100 intron1 (353 bp), and PY17X_1109100 intron2 (272 bp) were inserted into the *bfp* reporter by overlap PCR. All primers and oligonucleotides used in the plasmid construction are listed in Supplementary Table 2.

Parasite transfection and genotyping

The procedures for parasite transfection and genotyping were carried out as previously described^{34,73}. Briefly, the schizonts were isolated from infected mice using a 60% Nycodenz density gradient centrifugation. The parasites were then electroporated with 5 µg plasmid using a Nucleofector 2b Device (Lonza, Germany). The transfected schizonts were immediately intravenously injected into a naïve mouse, and pyrimethamine (Pyr) selection (6 mg/ml in drinking water) was applied the day following transfection. Pyr-resistant parasites were typically observed about 7 days after drug selection. Single clone of parasite was obtained by limiting dilution in mice, and genomic DNA was extracted from infected mouse blood for PCR genotyping using specific primers listed in Supplementary Table 2. PCR confirmation of correct 5' and 3' homologous recombination in each gene modification are presented in Supplementary Fig. 12.

Negative selection with 5-fluorocytosine

To remove the pYCm plasmids, we employed negative selection using 5-fluorocytosine. A mouse infected with the modified parasite clone was given drinking water containing 2 mg/ml of 5-fluorocytosine (Sigma-Aldrich, cat#F6627) in a dark bottle. After -3 days, most of the surviving parasites no longer carried pYCm plasmids and underwent limiting dilution cloning by injecting into mice via the tail vein. Seven days later, blood smears were used to identify the mice that were infected with parasites, and these parasites were genotyped again and used as the single cloned parasite.

Gametocyte induction in mice

The ICR mice were treated with phenylhydrazine ($80 \mu g/g$ body weight; Sangon Biotech, China, cat#A600705-0025) to induce hyperreticulocytosis. Three days post-treatment, the mice were infected with 4×10^6 asexual stage parasites via tail vein injection. The peak of gametocytaemia usually occurred on day three post-infection. Male and female gametocytes were counted using Giemsa-stained thin blood films, and gametocytaemia was calculated as a percentage of the number of male or female gametocytes over the number of parasitized erythrocytes.

Gametocyte purification

The procedures for gametocyte purification were carried out according to previously described methods⁴⁸. Briefly, ICR mice were intraperitoneally treated with phenylhydrazine 3 days prior to parasite infection. Starting from 2 days post-infection, the mice were orally administered 0.12 mg/d of sulfadiazine (Sigma, cat#S8626) for 2 days to eliminate asexual stage parasites. Approximately 1 ml of mouse blood containing gametocytes was collected from the orbital sinus and then suspended in 6 ml of gametocyte maintenance buffer (GMB). GMB comprises 137 mM NaCl, 4 mM KCl, 1 mM CaCl₂, 20 mM glucose, 20 mM HEPES, 4 mM NaHCO₃, 0.1% BSA, and has a pH of 7.2. The 7 ml parasite sample was layered on top of a 2 ml 48% Nycodenz/GMB cushion in a 15 ml centrifugation tube. The cushion consisted of 27.6% w/v Nycodenz in 5 mM Tris-HCl (pH 7.2), 3 mM KCl, and 0.3 mM EDTA. After centrifugation at 1900g for 20 min, the gametocytes were collected from the interphase and washed twice with GMB for further use.

Exflagellation assay of male gametocytes

2.5 μ l of mouse tail blood with gametocytes was mixed with 100 μ l of exflagellation medium. The exflagellation medium was composed of RPMI 1640 supplemented with 100 μ M xanthurenic acid (XA, Sigma, cat#D120804), 2 unit/ml heparin, and pH 7.4. The mixture was incubated at 22 °C for 10 min. The number of parasite exflagellation centers (ECs) and total red blood cells were counted within a 1 × 1-mm square area of a hemocytometer under a light microscope. The exflagellation rate was calculated as the number of ECs per 100 male gametocytes.

In vitro ookinete culture

Mouse blood with the gametocytes was collected in the heparincontaining tubes and immediately mixed with the ookinete culture medium. This medium consisted of RPMI 1640 supplemented with 25 mM HEPES, 10% fetal calf serum, 100 μ M XA, and had a pH of 8.0. The blood/medium volume ratio was 1:10. The parasite samples were incubated at 22 °C for 16 h and analyzed using Giemsa-stained thin blood films. The number of ookinetes (including normal and abnormal ookinete in morphology) per 100 female gametocytes was calculated as the ookinete conversion rate.

Parasite genetic cross

ICR mice were treated intraperitoneally with phenylhydrazine for gametocyte induction. Three days post-treatment, an equal number (3×10^6) of asexual stage parasites from two different gene knockout lines were mixed and injected via the tail vein into the phenylhydrazine pre-treated mice. After 3 days, mouse blood with mixed gametocytes from two different parasite lines was collected from the mice and subjected for the in vitro gametocyte-gamete-zygote-ookinete development analysis using the in vitro ookinete culture described above.

Mosquito transmission of the parasite

Approximately 100 female *Anopheles stephensi* mosquitoes were allowed to feed on an anesthetized mouse with 4–6% gametocytaemia for 30 min. To evaluate midgut infection of parasite, mosquito guts (n - 30) were dissected and stained with 0.1% mercurochrome 7 days post-feeding, and oocysts were tallied under a microscope. For quantifying salivary gland sporozoites, mosquito salivary glands (n - 30) were dissected 14 days after feeding, with the sporozoites counted using a hemocytometer. Transmission efficacy was assessed by allowing -30 infected mosquitoes to feed on a naïve mouse for 30 min at day 14 post-feeding. Parasite transmission from mosquito to mouse was monitored 5 days later via Giemsa-stained thin blood films. These procedures were performed in triplicate.

Flow cytometry analysis and sorting of male and female gametocytes

To analyze DNA content of male gametocytes, parasites containing gametocytes from the *DFsc7* or *DFsc7*; Δ *Rbpm1* lines were divided into two equal parts. One part was promptly fixed with 4% paraformalde-hyde in PBS, while the other was exposed to exflagellation medium at 22 °C for 8 min to initiate gametogenesis before fixation. After staining with 4 μ M Hoechst 33342 (Thermo Fisher Scientific, cat# 62249) for 10 min at room temperature and subsequent PBS washes, the samples were analyzed via flow cytometry on a BD LSRFortessa device (BD Biosciences, San Jose, CA, USA). Based on cell size and granularity, forward and side scatter signals were used to distinguish red blood cells from debris, doublets and white blood cells. Male gametocytes were identified by GFP fluorescence and analyzed for Hoechst 33342

fluorescence. For sorting gametocytes, parasites containing gametocytes were kept in GMB at 4 °C and sorted on a BD FACS AriallI based on GFP and mCherry fluorescence for male and female gametocytes, respectively. Sorted gametocyte purity was verified by re-analysis of a sample fraction.

Bulk RNA sequencing (RNA-seq)

Total RNA from 2×10^7 purified gametocytes was isolated using TRIzol (Thermo Fisher Scientific, cat#15596026) according to the manufacturer's instructions. RNA integrity was confirmed with an Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). mRNA was isolated with Oligo (dT) beads, fragmented, and reverse-transcribed to cDNA using random primers. Using DNA polymerase I, RNase H, dNTPs, and buffer, a second cDNA strand was synthesized. The resulting cDNA fragments were purified with the QIAQuick PCR Purification Kit (Qiagen, cat#28104), end-repaired, A-tailed, and ligated to Illumina sequencing adapters. The ligation products were size-selected using the Illumina NovaSeq 6000 by Genedenovo Biotechnology Co., Ltd (Guangzhou, China).

Differential expression analysis of RNA-seq data

Illumina-generated paired-end FASTQ files were trimmed using Trim Galore (v0.6.10)75 (trim_galore --illumina -q 20 --paired --stringency 3 --length 25 -e 0.1 --fastqc --gzip) to remove the sequencing adapters and low quality reads. To refine the dataset, rRNA and tRNA were removed via a genome alignment program HISAT2 (v2.2.1)76 (hisat2 -p 12 -q --unconc-gz). The cleaned reads, around 40 million per sample, were aligned to the Plasmodium yoelii 17X reference genome (PlasmoDB-62 release) using HISAT2 (hisat2 -p 12 -q). The resulting BAM files were sorted by position and indexed with SAMtools (v1.16.1)⁷⁷ (samtools -sort | samtools index). Mapped reads were summarized using featureCounts (v2.0.3)⁷⁸. Gene expression analysis were performed in R (v4.2.1). Gene expression levels were normalized using transcripts per million (TPM) with the R package t-arae/ngscmdr (v0.1.0.181203)⁷⁹. Differential expressed genes (DEGs, fold change > 2, and false discovery rate < 0.05) were assessed by the R package edgeR (v3.40.2)⁸⁰. The volcano plot of DEGs were generated by the ggplot2 (v3.4.2)⁸¹.

Bioinformatic analysis of global intron retention

A GFF file containing genomic intron information was crafted using a perl script from agat package⁸² and an in-house bash script, then converted into a BED file with BEDOPS convert2bed (v2.4.41)⁸³. Deep-Tools bamCoverage (v3.5.1)⁸⁴ was used to generate the bigWig files for peak visualization in Integrative Genomics Viewer (IGV, v2.16.1)³⁸, and calculate the peak score of each exon and intron regions. Low expressed genes (TPM below 30) were excluded. To exclude potential false hits, introns with peak scores exceeding 50% of adjacent exons were discarded in parental parasites. In mutant parasites, introns with peak scores under 50% of neighboring exons were also omitted. Before differential intron retention analysis, the introns were normalized based on the gene expression level:

Normalized intron counts =
$$\frac{\text{Intron region counts} \times 1000}{\text{Corresponding gene counts}}$$

Differentially retained introns (fold change > 2 and false discovery rate <0.05) were assessed with the R package edgeR (v3.40.2)⁸⁰. These introns were further validated by IGV visualization and RT-PCR.

Bioinformatic analysis of RBP in the *P. falciparum* and *P. berghei* 189 putative RBPs had been predicted in silico in the *P. falciparum*³². Among them, 179 RBPs have homologous proteins in *P. yoelii* and *P. berghei*. Differential expression analysis of the 179 RBPs between male and female gametocytes of *P. berghei* was based on the public dataset by Yeoh, L.M., 2017³¹. The RNA-seq FASTQ files from NCBI SRA database (Accession: PRINA374918) were processed using Trim Galore (v0.6.10) and HISAT2 (v2.2.1) for quality trimming and rRNA/tRNA removal, respectively. The cleaned reads were mapped to the P. berghei ANKA strain genome (PlasmoDB-62 release) using HISAT2 (v2.2.1), and the resulting BAM files were sorted and indexed with SAMtools (v1.16.1). Mapped reads were summarized using featureCounts (v2.0.3), and the differential expression analysis of RBPs was performed by the R package edgeR (v3.40.2). Differential expression analysis of the 189 RBPs between male and female gametocytes of *P. falciparum* is based on the public dataset from Lasonder E. 2016³⁰. The RNA-seq FASTQ files from NCBI SRA (Accession: PRINA305391) were processed similarly as above. The cleaned reads were mapped to the Plasmodium falciparum 3D7 reference genome. Given the absence of biological replicates in this dataset, differential expression analysis was performed by Cufflinks (v2.2.1)⁸⁵ (cuffdiff -p 8 --dispersion-method blind --library-norm-method geometric --library-type ff-firststrand). RBPs with fold change > 2 and false discovery rate <0.05 were considered differentially expressed. The volcano plot of differentially expressed RBPs were generated by the ggplot2 (v3.4.2).

Antibodies and antiserum

The following primary antibodies were utilized: rabbit anti-HA (Cell Signaling Technology, cat#3724 S; IFA, 1:1000 dilution; IB, 1:1000 dilution), rabbit anti-mCherry (Abcam, cat# ab167453; IFA, 1:1000 dilution), rabbit anti-histone H3 antibody (Abcam, cat#ab1791; IFA, 1:1000 dilution), rabbit anti-Myc (Cell Signaling Technology, cat#2272 S; IFA, 1:1000 dilution; IB, 1:1000 dilution), mouse anti-α-Tubulin (Sigma-Aldrich, cat#T6199; IFA, 1:1000 dilution; IB, 1:1000 dilution; U-ExM, 1:500 dilution), mouse anti-β-Tubulin (Sigma-Aldrich, cat#T5201; IB, 1:1000 dilution) and mouse anti-HA (Santa Cruz Biotechnology, cat#sc-57592; IFA, 1:200 dilution). The secondary antibodies included: Alexa Fluor 555 goat anti-rabbit IgG (Thermo Fisher Scientific, cat#A-21428; IFA, 1:1000 dilution), Alexa Fluor 488 goat antirabbit IgG (Thermo Fisher Scientific, cat#A-31566; IFA, 1:1000 dilution), Alexa Fluor 555 goat anti-mouse IgG (Thermo Fisher Scientific, cat# A-21422; IFA, 1:1000 dilution; U-ExM, 1:500 dilution), Alexa Fluor 488 goat anti-mouse IgG (Thermo Fisher Scientific, cat#A-11001: IFA. 1:1000 dilution), Alexa Fluor 488 goat anti-mouse TER-119 (BioLegend, cat#116215; IFA, 1:500 dilution), Alexa Fluor 488 conjugated streptavidin (Invitrogen, cat# S32354; IFA, 1:1000 dilution), HRP-conjugated goat anti-rabbit IgG (Abcam, cat#ab6721; IB, 1:5000 dilution) and HRPconjugated goat anti-mouse IgG (Abcam, cat#ab6789; IB, 1:5000 dilution). The antiserum, including rabbit anti-BiP (IB, 1:1000 dilution) and rabbit anti-P28 (IFA, 1:1000), were previously in-house prepared in the laboratory⁸⁶.

Immunofluorescence assay

Parasites fixed in 4% paraformaldehyde in PBS were placed on poly-Llysine-coated coverslips in a 24-well plate and centrifuged at 550 *g* for 5 min. They were then permeabilized with 0.1% Triton X-100 in PBS for 10 min at room temperature, blocked with 5% BSA/PBS at 4 °C overnight, and incubated with primary antibodies in 5% BSA/PBS for 1 h at room temperature. After three PBS washes, the samples were incubated with fluorescently labeled secondary antibodies in 5% BSA/PBS for 1 h at room temperature. Hoechst 33342 at a 1:5000 dilution in PBS was applied for 15 min at room temperature. Finally, the coverslips were washed, mounted in 90% glycerol, and sealed with nail varnish. Imaging was performed with a Zeiss LSM 780 confocal microscope at 100 × magnification.

Ultrastructure expansion microscopy (U-ExM)

According to the method described in⁸⁷, gametocytes were fixed in 4% paraformaldehyde in PBS, then transferred to poly-D-lysine-coated coverslips in a 24-well plate and centrifuged. They were incubated in a

1.4% formaldehyde (Sigma-Aldrich, cat#F8775) and 2% acrylamide (Sigma-Aldrich, cat# A4058) mixture in PBS overnight at 37 °C. Afterward, the coverslips were gelled in a monomer solution containing 23% sodium acrylate (Sigma-Aldrich, cat#408220), 10% acrylamide, and 0.1% N,N'-methylenbisacrylamide (Sigma-Aldrich, cat#M1533) in PBS with tetramethylethylenediamine (TEMED) and ammonium persulfate (APS) at 37 °C for 1h of polymerization. After polymerization, the coverslips were moved to a 6-well plate with denaturation buffer (200 mM SDS, 200 mM NaCl, 50 mM Tris-HCl, and pH 8.8) for 15 min at room temperature to detach the gels. The gels were denatured in 1.5 ml Eppendorf tubes with denaturation buffer at 95 °C for 30 min, incubated with ddH₂O at room temperature overnight in a 10 cm dish for the first round of expansion. The expanded gels were incubated with mouse anti-α-Tubulin antibody diluted in 2% BSA/PBS at room temperature for 3 h, washed 3 times with PBS, and incubated with antimouse Alexa 555 diluted in 2% BSA/PBS at room temperature for 3 h. After 3 washes in PBS, the gels were transferred into 10 cm dishes and incubated with ddH₂O at room temperature for the second round of expansion. Subsequently, gel blocks of ~5 mm × 5 mm were excised from the expanded gels and placed in the cavity well of cavity well microscope slides, covered with a coverslip, and imaged using a Zeiss LSM 980 confocal microscope.

Protein extraction and immunoblot

Asexual blood parasites, gametocytes or ookinetes were lysed in RIPA buffer (Solaribio, cat#R0010) containing a protease inhibitor cocktail (MedChemExpress, cat#HY-K0010). After ultrasonication, the lysate was centrifuged at 14,000 g at 4 °C for 10 min. The resulting supernatant was mixed with SDS-PAGE loading buffer and heated at 95 °C for 5 min. Following SDS-PAGE separation, samples were transferred to a PVDF membrane (Millipore, cat#IPVH00010) and blocked with 5% milk in 1×TBST (20 mM Tris-HCl pH 7.5, 150 mM NaCl, 0.1% Tween20) at 4 °C overnight. PVDF membranes were then incubated with primary antibodies at room temperature for 1h. After washing with 1×TBST, the membranes were incubated with an HRP-conjugated secondary antibody and then washed again with 1 × TBST. Finally, the membranes were visualized using a high-sensitivity ECL chemiluminescence detection kit (Vazvme, cat#E412-01), and the light emission was recorded either by X-ray film or by Azure Biosystems C280 (Azure Biosystems, USA).

Isolation of nuclear and cytoplasmic fractions

The procedures were performed with modifications according to the previous study⁸⁸. Nycodenz-purified gametocytes were first released from red blood cells by incubating them with 0.15% saponin/PBS on ice for 5 min and then washed twice with ice-cold PBS. The parasite pellet was resuspended in ice-cold lysis buffer (20 mM HEPES pH 7.9, 10 mM KCl, 1.5 mM MgCl₂, 1 mM EDTA, 1 mM EGTA, 1 mM DTT, and 0.65% Nonidet P-40) supplemented with protease inhibitor cocktail. The lysate was transferred to a 1ml Dounce tissue grinder and homogenized gently for 80 strokes on ice. Nuclei were pelleted at 9000 g at 4 °C for 10 min, and the resulting supernatant represented cytoplasmic fractions. The nuclear pellet was washed twice with ice-cold lysis buffer before resuspension in one pellet volume of high salt buffer (20 Mm HEPES pH 7.8, 1 M KCl, 1 mM EDTA, 1 mM EGTA, and 1 mM DTT) supplemented with a protease inhibitor cocktail. After vigorous shaking at 4 °C for 30 min, the extract was centrifuged at 14,000 g at 4 °C for 10 min, and the resulting supernatant represented nuclear fractions. Immunoblotting was performed to analyze the proteins in each fraction.

Protein immunoprecipitation

Nycodenz-purified gametocytes containing 3×10^7 male gametocytes were lysed in 1 ml lysis buffer (0.01% SDS, 20 mM Tris-HCl pH 8.0, 50 mM NaCl, 1 mM DTT) supplemented with protease inhibitor

cocktail. The lysate was transferred to a 1 ml Dounce tissue grinder and homogenized gently for 100 strokes on ice. The homogenate was transferred to an Eppendorf tube and incubated on ice for 10 min before centrifugation at 14,000 g at 4 °C for 10 min. The resulting supernatant was divided into two equal portions, with one portion mixed with 20 µl pre-balanced anti-GFP nanobody agarose beads (KT HEALTH, cat#KTSM1301) and the other portion mixed with anti-Myc nanobody agarose beads (KT HEALTH, cat#KTSM1306). Both portions were incubated at 4 °C for 2 h with rotation. The beads were then washed three times with lysis buffer before elution with SDS-PAGE loading buffer, followed by incubation at 95 °C for 5 min. Immunoblotting was performed on equal volumes of the supernatant samples.

Transmission electron microscopy

Nycodenz-purified gametocytes were fixed at 8 mpa and 15 mpa in 2.5% glutaraldehyde in 0.1M phosphate buffer at 4 °C overnight, as previously described⁸⁹. Then, the samples were post-fixed in 1% osmium tetroxide at 4 °C for 2 h, treated *en bloc* with uranyl acetate, dehydrated, and embedded in Spurr's resin. Thin sections were sliced, stained with uranyl acetate and lead citrate, and examined in an HT-7800 electron microscope (Hitachi, Japan).

TurboID-based proximity-labeling and biotinylated protein pull-down

Nycodenz-purified gametocytes containing 1×10^8 male gametocytes from either the Rbpm1::TurboID or Rbpm1::T2A::TurboID line were incubated with 50 µM biotin (Sigma-Aldrich, cat#B4639) at 37 °C for 20 min. After biotinylation, the parasites were pelleted, washed thrice with 1 ml ice-cold PBS to remove excess biotin, and then lysed with RIPA buffer containing a protease inhibitor cocktail via ultrasonication. The lysate was incubated on ice for 10 min before centrifugation at 14,000 g at 4 °C for 10 min. The supernatant was then mixed with 50 µl pre-balanced streptavidin sepharose (Thermal Scientific. cat#SA10004) at 4 °C overnight. The beads were washed five times with 1 ml ice-cold RIPA buffer and then washed five times with 1 ml icecold PBS. The washed beads were resuspended in 200 µl 100 mM Tris-HCl pH 8.5 followed by digestion with 1 µg trypsin at 37 °C overnight.

Peptide desalting and mass spectrometry

Trifluoroacetic acid (TFA; Sigma-Aldrich, cat#T6508) was added to the trypsin-digested sample to a final concentration of 1%, and the precipitation of sodium deoxycholate was removed by centrifugation. The resulting supernatant was desalted using in-house-made StageTips that were packed with SDB-RPS (3 M EMPORE, cat#2241) and conditioned with 50 µl of 100% acetonitrile (ACN; Sigma-Aldrich, cat# 34851). After loading the supernatant onto the StageTips, centrifugation was performed at 3000 g for 5 min. The StageTips were then washed twice with 50 µl of 1% TFA/isopropyl alcohol (Sigma-Aldrich, cat# I9030) followed by a wash with 50 µl of 0.2% TFA. The peptides were eluted in glass vials (CNW Technologies, cat# A3511040) using 80% ACN/5% NH₄OH and dried at 45 °C using a vacuum centrifuge (Eppendorf, Hamburg, Germany, cat#5305). The peptide samples were resolved in 2% ACN/0.1FA for LC-MS analysis. Liquid chromatography was performed on a high-pressure nano-flow chromatography system (Elute UHPLC, Bruker Daltonics). Peptides were separated on a reversed-phase column (40 cm $\times\,75\,\mu m$ i.d.) at 50 °C packed with 1.8 µm 120 Å C18 material (Welch, Shanghai, China) with a pulled emitter tip. A solution is 0.1% FA in H₂O, and B solution is 0.1% FA in ACN. The gradient time is 60 min and the total run time is 75 min including washes and equilibration. Peptides were separated with a linear gradient from 0 to 5% B within 5 min, followed by an increase to 30% B within 55 min and further to 35% B within 5 min, followed by a washing step at 95% B and re-equilibration. LC was coupled online to a hybrid TIMS quadrupole time-of-flight mass spectrometer (Bruker timsTOF Pro) via a CaptiveSpray nano-electrospray ion source. We

performed data-dependent data acquisition in PASEF mode with 10 PASEF scans per topN acquisition cycle. Singly charged precursors were excluded by their position in the m/z-ion mobility plane and precursors that reached a 'target value' of 20.000 a.u. were dynamically excluded for 0.4 min. We used 100 ms to accumulate and elute ions in the TIMS tunnel. The MS1 m/z-range was acquired from 100 to 1700, and the ion mobility range from 1.5 to 0.7 V cm⁻². For dataindependent acquisition, we adopted the isolation scheme of 25 Da × 32 windows to cover 400-1200 mz. DIA files (raw) files were input to DIA-NN (v1.8.1)⁹⁰ FASTA files downloaded from https://www.uniprot. org (UP000072874) were added. "FASTA digest for library-free search" and "Deep learning-based spectra, RTs, and IMs prediction" were enabled. "Generate spectral library" was also enabled. "Protein inference" was set to "gene". Other parameters were kept at their default settings. The protein groups and precursor lists were filtered at 1% FDR, using global q-values for protein groups and both global and runspecific q-values for precursors.

RNA isolation, RT-PCR and RT-qPCR

Total RNA was extracted from parasites using TRIzol reagent. cDNA was synthesized with the HiScript II 1st Strand cDNA Synthesis Kit (Vazyme, cat#R212-02), using provided random hexamers, and utilized for PCR or qPCR analysis. qPCR was performed using 2×RealStar Green Fast Mixture (GenStar, cat#A301-101) with the following cycling program: a single incubation at 95 °C for 30 s, followed by 40 cycles (95 °C for 5 s, 60 °C for 40 s) on a CFX96 Real-Time PCR System (Bio-Rad, Hercules, CA, USA). The housekeeping gene *gapdh* (PY17X_1330200) was used as a reference gene in the RT-qPCR. The relative expression was calculated using the $2^{\Delta\Delta Ct}$ method. The primers used for RT-PCRs and RT-qPCRs are listed in Supplementary Table 2.

UV crosslinking RNA immunoprecipitation (UV-RIP)

The Nycodenz-purified gametocytes, containing 6×10^7 male gametocytes in 6 ml ice-cold PBS, were placed in 10 cm dishes. Subsequently, they were irradiated using an HL-2000 HybriLinker (UVP. Upland. CA, USA) with 254 nm UV light at intensities of 400 mJ/cm^2 and 200 mJ/cm². The gametocytes were then collected, centrifuged, and resuspended in 1 ml lysis buffer (1% TritonX-100, 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1 mM EDTA, 1 mM EGTA) supplemented with 400 U/ml RNaseOUT (Thermo Fisher Scientific, cat#10777019) and a protease inhibitor cocktail. The lysate was transferred to a 1 ml Dounce tissue grinder and gently homogenized for 100 strokes on ice. The homogenate was then transferred to a tube and incubated at 4 °C for 25 min with rotation, followed by treatment with 30 U TURBO DNase (Thermo Fisher Scientific, cat#AM2238) at 37 °C for 15 min. The lysates were centrifuged at 14,000 g and 4 °C for 10 min. The supernatant was divided into two equal parts. One part was mixed with 20 μ l of anti-GFP nanobody agarose beads (KT HEALTH, cat#KTSM1301), and the other part was mixed with 20 µl of anti-HA nanobody agarose beads (KT HEALTH, cat#KTSM1305). The mixtures were incubated with rotation at 4 °C for 2 h. The beads were washed six times with 500 µl RIP wash buffer (Millipore, cat#CS203177) at 4 °C and then incubated with 117 µl RIP wash buffer, 15 µl 10% SDS and 18 µl 10 mg/ml proteinase K (Millipore, cat#CS203218) at 55 °C for 30 min. RNA was isolated using phenol-chloroform extraction, and the purified RNA was reverse transcribed with random hexamer primers and determined by RT-qPCR.

In vitro RNA transcription (IVT)

To prepare biotinylated probes for Fig. 6O, P, IVT templates with T7 RNA polymerase promoter were obtained by PCR using the *P. yoelii* genome as a template. For Fig. 7H, IVT templates with T7 RNA polymerase promoter were obtained by PCR using the plasmid used in the *bfp* reporter assay as a template. Supplementary Table 2 provides a list of primers used to obtain the IVT templates. Subsequently,

Biotinylated RNA was produced using a MEGAscript kit (Thermo Fisher Scientific, cat#AM1334) and a biotin RNA labeling mix (Roche, cat#11685597910). To create a 20 µl reaction volume, 1 µg of PCR-amplified IVT templates were incubated at 37 °C for 2 h with 2 µl of 10× reaction buffer, 2 µl of T7 RNA polymerase enzyme mix, 2 µl of biotin RNA labeling mix, and RNase-free water. The DNA templates were then removed from the RNA using TURBO DNase, and the biotinylated RNA was purified using the RNAclean Kit (TIANGEN, cat#4992728). In this process, the *kinesin8b* 14 probe, *kinesin8b* 11 probe, *PF16* E1 probe, and *PF16* 11 probe all have a length of 500 nt. Additionally, the *kinesin8b* 14 probe, *kinesin8b* 11 probe span the corresponding intron sequences.

RNA pull-down

Biotinylated RNA pull-down was performed using an RNA pull-down Kit (BersinBio, cat# Bes5102) following the manufacturer's protocol. Briefly, 1 µg of biotinylated RNA was denatured at 90 °C for 2 min and immediately cooled on ice for 2 min. The denatured RNA was then incubated with RNA structure buffer and RNase-free water at room temperature for 20 mi to facilitate RNA secondary structure formation. For cell lysate preparation, Nycodenz-purified gametocytes containing 3×10^7 male gametocytes were lysed by RIP buffer, and the resulting lysate was centrifuged at 14,000 g at 4 °C for 10 min. The supernatant was then incubated with DNase I and agarose beads to remove the chromosomes, followed by incubation with folded RNAs, streptavidincoupled beads, and RNase inhibitor at room temperature for 2 h. The beads were subsequently washed five times with NT2 buffer at 4 °C, and proteins were retrieved from the beads by rinsing them with protein elution buffer. The retrieved proteins were then subjected to immunoblot assay.

bfp reporter assay

The Nycodenz-purified gametocytes from either *DFsc7* or *DFsc7;* $\Delta Rbpm1$ lines, which contain a *bfp* expression cassette in the *p230p* locus, were suspended in 200 µl of GMB. The samples were then transferred to a 15 mm glass bottom cell culture dish and imaged using a Zeiss LSM 780 confocal microscope at room temperature with 100× magnification. The laser illumination was set at 561 nm (mCherry), 491 nm (GFP), and 405 nm (BFP). BFP-positive parasites indicated that the intron in the *bfp* expression cassette had been spliced.

Other bioinformatic analysis and tools

The genomic sequences of target genes were downloaded from the PlasmoDB database (http://plasmodb.org/plasmo/). The sgRNAs of target gene were designed using EuPaGDT (http://grna.ctegd.uga.edu/). The analysis of flow cytometry data was performed using the FlowJo software (Tree Star, Ashland, OR, USA). The Gene Ontology (GO) enrichment analysis was performed using PlasmoDB. Statistical analysis was performed using GraphPad Prism (GraphPad Software Inc., San Diego, CA, USA) with either a two-tailed Student's *t*-test or Mann-Whitney test as appropriate. Error bars represent the standard error of the mean (SEM) for triplicate experiments. *p* values were indicated in the figures above the two groups being compared, with a value <0.05 considered significant. The protein signal on the blotting membrane was quantified using ImageJ software (NIH, Bethesda, MD, USA), and the background was subtracted from each signal.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

All relevant data in this study are submitted as supplementary source files. Source data are provided with this paper. The RNA-seq data for

Code availability

All code and supporting files for transcriptome and intron retention analysis in this study were available in Zenodo (https://doi.org/10.5281/zenodo.10979262).

the P. yoelii male- and female gametocyte transcriptome have been

References

- 1. WHO. World Malaria Report 2019. (WHO, 2019).
- Baker, D. A. Malaria gametocytogenesis. Mol. Biochem. Parasitol. 172, 57–65 (2010).
- 3. Guttery, D. S. et al. Commit and transmit: molecular players in plasmodium sexual development and zygote differentiation. *Trends Parasitol.* **31**, 676–685 (2015).
- 4. Bennink, S., Kiesow, M. & Pradel, G. Malaria parasite development in the mosquito midgut. *Cell. Microbiol.* **18**, 905–918 (2016).
- 5. Guttery, D. S. et al. Division and transmission: malaria parasite development in the mosquito. *Annu Rev. Microbiol* **76**, 113–134 (2022).
- Sinden, R. E. Sexual development of malarial parasites. Adv. Parasitol. 22, 153–216 (1983).
- Sinden, R. E. & Croll, N. A. Cytology and kinetics of microgametogenesis and fertilization in Plasmodium yoelii nigeriensis. *Parasitology* **70**, 53–65 (1975).
- 8. Billker, O. et al. Identification of xanthurenic acid as the putative inducer of malaria development in the mosquito. *Nature* **392**, 289–292 (1998).
- 9. Sinden, R. E. The biology of Plasmodium in the mosquito. *Experientia* **40**, 1330–1343 (1984).
- Sinden, R. E., Canning, E. U. & Spain, B. Gametogenesis and fertilization in Plasmodium yoelii nigeriensis: a transmission electron microscope study. *Proc. R. Soc. Lond. B Biol. Sci.* **193**, 55–1976 (1110).
- Briquet, S. et al. Preparing for transmission: gene regulation in Plasmodium sporozoites. Front. Cell. Infect. Microbiol 10, 618430 (2020).
- 12. Hollin, T. & Le Roch, K. G. From genes to transcripts, a tightly regulated journey in Plasmodium. *Front Cell Infect. Microbiol* **10**, 618454 (2020).
- Hollin, T., Chahine, Z. & Le Roch, K. G. Epigenetic regulation and chromatin remodeling in malaria parasites. *Annu. Rev. Microbiol.* 77, 255–276 (2023).
- 14. Kafsack, B. F. et al. A transcriptional switch underlies commitment to sexual development in malaria parasites. *Nature* **507**, 248–252 (2014).
- Sinha, A. et al. A cascade of DNA-binding proteins for sexual commitment and development in Plasmodium. *Nature* 507, 253–257 (2014).
- 16. Josling, G. A. et al. Dissecting the role of PfAP2-G in malaria gametocytogenesis. *Nat. Commun.* **11**, 1503 (2020).
- Yuda, M. et al. Female-specific gene regulation in malaria parasites by an AP2-family transcription factor. *Mol. Microbiol* **113**, 40–51 (2020).
- Shang, X. et al. A cascade of transcriptional repression determines sexual commitment and development in Plasmodium falciparum. *Nucleic Acids Res* 49, 9264–9279 (2021).
- Li, Z. et al. Plasmodium transcription repressor AP2-O3 regulates sex-specific identity of gene expression in female gametocytes. *EMBO Rep.* 22, e51660 (2021).

- Kaneko, I. et al. Differentiation of Plasmodium male gametocytes is initiated by the recruitment of a chromatin remodeler to a malespecific cis-element. *Proc. Natl Acad. Sci. USA* **120**, e2303432120 (2023).
- Filarsky, M. et al. GDV1 induces sexual commitment of malaria parasites by antagonizing HP1-dependent gene silencing. *Science* 359, 1259–1263 (2018).
- Usui, M. et al. Plasmodium falciparum sexual differentiation in malaria patients is associated with host factors and GDV1dependent genes. *Nat. Commun.* **10**, 2140 (2019).
- Brancucci, N. M. B. et al. Lysophosphatidylcholine regulates sexual stage differentiation in the human malaria parasite Plasmodium falciparum. *Cell* **171**, 1532–1544.e15 (2017).
- Corley, M., Burns, M. C. & Yeo, G. W. How RNA-binding proteins interact with RNA: molecules and mechanisms. *Mol. Cell* 78, 9–29 (2020).
- Hentze, M. W. et al. A brave new world of RNA-binding proteins. Nat. Rev. Mol. Cell Biol. 19, 327–341 (2018).
- Gebauer, F. et al. RNA-binding proteins in human genetic disease. Nat. Rev. Genet. 22, 185–198 (2021).
- 27. Mair, G. R. et al. Regulation of sexual development of Plasmodium by translational repression. *Science* **313**, 667–669 (2006).
- Mair, G. R. et al. Universal features of post-transcriptional gene regulation are critical for Plasmodium zygote development. *PLoS Pathog.* 6, e1000767 (2010).
- 29. Guerreiro, A. et al. Genome-wide RIP-Chip analysis of translational repressor-bound mRNAs in the Plasmodium gametocyte. *Genome Biol.* **15**, 493 (2014).
- Lasonder, E. et al. Integrated transcriptomic and proteomic analyses of P. falciparum gametocytes: molecular insight into sexspecific processes and translational repression. *Nucleic Acids Res.* 44, 6087–6101 (2016).
- Yeoh, L., et al. Comparative transcriptomics of female and male gametocytes in Plasmodium berghei and the evolution of sex in alveolates. *BMC Genom.* 18, 1–16 (2017).
- 32. Reddy, B. P. et al. A bioinformatic survey of RNA-binding proteins in Plasmodium. *BMC Genom.* **16**, 890 (2015).
- Liu, C. et al. Generation of Plasmodium yoelii malaria parasite carrying double fluorescence reporters in gametocytes. *Mol. Biochem. Parasitol.* 224, 37–43 (2018).
- Zhang, C. et al. Efficient editing of malaria parasite genome using the CRISPR/Cas9 system. *MBio* 5, e01414-14 (2014).
- Zhang, C. et al. Systematic CRISPR-Cas9-mediated modifications of Plasmodium yoelii ApiAP2 genes reveal functional insights into parasite development. *MBio* 8, e01986–17 (2017).
- Rawlings, D. J. et al. Alpha-tubulin II is a male-specific protein in Plasmodium falciparum. *Mol. Biochem Parasitol.* 56, 239–250 (1992).
- Bertiaux, E. et al. Expansion microscopy provides new insights into the cytoskeleton of malaria parasites including the conservation of a conoid. *PLoS Biol.* **19**, e3001020 (2021).
- Thorvaldsdóttir, H., Robinson, J. T. & Mesirov, J. P. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Brief. Bioinform.* 14, 178–192 (2013).
- Depoix, D. et al. Vital role for Plasmodium berghei Kinesin8B in axoneme assembly during male gamete formation and mosquito transmission. *Cell. Microbiol.* 22, e13121 (2020).
- Zeeshan, M. et al. Kinesin-8B controls basal body function and flagellum formation and is key to malaria transmission. *Life Sci. Alli*ance 2, e201900488 (2019).
- Straschil, U. et al. The Armadillo repeat protein PF16 is essential for flagellar structure and function in Plasmodium male gametes. *PLoS* One 5, e12901 (2010).

- 42. Russell, A. J. C. et al. Regulators of male and female sexual development are critical for the transmission of a malaria parasite. *Cell Host Microbe* **31**, 305–319.e10 (2023).
- 43. Li, X. et al. A unified mechanism for intron and exon definition and back-splicing. *Nature* **573**, 375–380 (2019).
- Kondo, Y. et al. Crystal structure of human U1 snRNP, a small nuclear ribonucleoprotein particle, reveals the mechanism of 5' splice site recognition. *Elife* 4, e04986 (2015).
- 45. Wan, R. et al. How is precursor messenger RNA spliced by the spliceosome? *Annu. Rev. Biochem.* **89**, 333–358 (2020).
- 46. Sorber, K., Dimon, M. T. & DeRisi, J. L. RNA-Seq analysis of splicing in Plasmodium falciparum uncovers new splice junctions, alternative splicing and splicing of antisense transcripts. *Nucleic Acids Res* **39**, 3820–3835 (2011).
- 47. Wilkinson, M. E., Charenton, C. & Nagai, K. RNA splicing by the spliceosome. *Annu Rev. Biochem* **89**, 359–388 (2020).
- Jiang, Y. et al. An intracellular membrane protein GEP1 regulates xanthurenic acid induced gametogenesis of malaria parasites. *Nat. Commun.* 11, 1764 (2020).
- Howick, V. M. et al. The Malaria Cell Atlas: Single parasite transcriptomes across the complete Plasmodium life cycle. *Science* 365, eaaw2619 (2019).
- Khan, S. M. et al. Proteome analysis of separated male and female gametocytes reveals novel sex-specific Plasmodium biology. *Cell* 121, 675–687 (2005).
- Bunnik, E. M. et al. The mRNA-bound proteome of the human malaria parasite Plasmodium falciparum. *Genome Biol.* 17, 147 (2016).
- 52. Rios, K. T. & Lindner, S. E. Protein-RNA interactions important for Plasmodium transmission. *PLoS Pathog.* **15**, e1008095 (2019).
- 53. Müller, K. et al. Pleiotropic roles for the Plasmodium berghei RNA Binding Protein UIS12 in transmission and oocyst maturation. *Front Cell Infect. Microbiol* **11**, 624945 (2021).
- Shrestha, S. et al. The RNA-binding protein Puf1 functions in the maintenance of gametocytes in Plasmodium falciparum. J. Cell Sci. 129, 3144–3152 (2016).
- 55. Hart, K. J. et al. Plasmodium male gametocyte development and transmission are critically regulated by the two putative deadenylases of the CAF1/CCR4/NOT complex. *PLoS Pathog.* **15**, e1007164 (2019).
- Miao, J. et al. The Puf-family RNA-binding protein PfPuf2 regulates sexual development and sex differentiation in the malaria parasite Plasmodium falciparum. J. Cell Sci. 123, 1039–1049 (2010).
- 57. Farrukh, A. et al. The Plasmodium falciparum CCCH zinc finger protein MD3 regulates male gametocytogenesis through its interaction with RNA-binding proteins. *Mol Microbiol*, **121**, 543–564 (2023).
- Miao, J. et al. Puf mediates translation repression of transmissionblocking vaccine candidates in malaria parasites. *PLoS Pathog.* 9, e1003268 (2013).
- Yeoh, L. M. et al. Alternative splicing is required for stage differentiation in malaria parasites. *Genome biology* 20, 1–13 (2019).
- 60. Hanhsen, B. et al. The Plasmodium falciparum CCCH zinc finger protein ZNF4 plays an important role in gametocyte exflagellation through the regulation of male enriched transcripts. *Cells* **11**, 1666 (2022).
- 61. Sinden, R. E. et al. The flagellum in malarial parasites. *Curr. Opin. Microbiol* **13**, 491–500 (2010).
- 62. Briggs, L. J. et al. More than one way to build a flagellum: comparative genomics of parasitic protozoa. *Curr. Biol.* **14**, R611–R612 (2004).
- 63. Rashpa, R. & Brochet, M. Expansion microscopy of Plasmodium gametocytes reveals the molecular architecture of a bipartite

microtubule organisation centre coordinating mitosis with axoneme assembly. *PLoS Pathog.* **18**, e1010223 (2022).

- Liu, T. et al. Mechanochemical tuning of a kinesin motor essential for malaria parasite transmission. *Nat. Commun.* 13, 6988 (2022).
- Zeeshan, M. et al. Plasmodium SAS4: basal body component of male cell which is dispensable for parasite transmission. *Life Sci. Alliance* 5, e202101329 (2022).
- 66. Francia, M. E., Dubremetz, J. F. & Morrissette, N. S. Basal body structure and composition in the apicomplexans Toxoplasma and Plasmodium. *Cilia* **5**, 3 (2015).
- Marques, S. R. et al. An essential role of the basal body protein SAS-6 in Plasmodium male gamete development and malaria transmission. *Cell Microbiol* 17, 191–206 (2015).
- Ramakrishnan, C. et al. Radial spoke protein 9 is necessary for axoneme assembly in Plasmodium but not in trypanosomatid parasites. J. Cell Sci. 136, jcs260655 (2023).
- 69. Will, C. L. & Lührmann, R. Spliceosome structure and function. *Cold* Spring Harb. Perspect. Biol. **3**, a003707 (2011).
- Rino, J. et al. Splicing factors SF1 and U2AF associate in extraspliceosomal complexes. *Mol. Cell Biol.* 28, 3045–3057 (2008).
- 71. Yue, L. et al. Dek modulates global intron retention during muscle stem cells quiescence exit. *Dev. cell* **53**, 661–676.e6 (2020).
- 72. Zuo, Y. et al. Dek42 encodes an RNA-binding protein that affects alternative pre-mRNA splicing and maize kernel development. *J. Integr. Plant Biol.* **61**, 728–748 (2019).
- Zhang, C. et al. CRISPR/Cas9 mediated sequential editing of genes critical for ookinete motility in Plasmodium yoelii. *Mol. Biochem. Parasitol.* 212, 1–8 (2017).
- Liu, C. et al. Generation of Plasmodium yoelii malaria parasite for conditional degradation of proteins. *Mol. Biochem. Parasitol.* 241, 111346 (2021).
- Krueger, F. TrimGalore: A wrapper around Cutadapt and FastQC to consistently apply adapter and quality trimming to FastQ files, with extra functionality for RRBS data.[(accessed on 27 August 2019)].
- Kim, D. et al. Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. *Nat. Biotechnol.* 37, 907–915 (2019).
- 77. Danecek, P. et al. Twelve years of SAMtools and BCFtools. *Gigascience* **10**, giab008 (2021).
- Liao, Y., Smyth, G. K. & Shi, W. featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. *Bioinformatics* **30**, 923–930 (2014).
- 79. R Core Team, R. R: A language and environment for statistical computing. 2013.
- Robinson, M. D., McCarthy, D. J. & Smyth, G. K. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *bioinformatics* 26, 139–140 (2010).
- Wickham, H. ggplot2. Wiley Interdiscip. Rev. Comput. Stat. 3, 180–185 (2011).
- Dainat, J. AGAT: Another Gff Analysis Toolkit to handle annotations in any GTF/GFF format. (Version v0.7.0). Zenodo. https://doi.org/ 10.5281/zenodo.3552717 2020.
- Neph, S. et al. BEDOPS: high-performance genomic feature operations. *Bioinformatics* 28, 1919–1920 (2012).
- Ramírez, F. et al. deepTools2: a next generation web server for deep-sequencing data analysis. *Nucleic Acids Res.* 44, W160–W165 (2016).
- Trapnell, C. et al. Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nat. Protoc.* 7, 562–578 (2012).
- Gao, H. et al. ISP1-anchored polarization of GCbeta/CDC50A complex initiates malaria ookinete gliding motility. *Curr. Biol.* 28, 2763–2776.e6 (2018).
- Gambarotto, D., Hamel, V. & Guichard, P. Ultrastructure expansion microscopy (U-ExM), in *Methods in Cell Biology*. 57–81. (Elsevier, 2021)

- 88. Voss, T. S. et al. Plasmodium falciparum possesses a cell cycleregulated short type replication protein A large subunit encoded by an unusual transcript. *J. Biol. Chem.* **277**, 17493–17501 (2002).
- Ferguson, D. J. et al. Maternal inheritance and stage-specific variation of the apicoplast in Toxoplasma gondii during development in the intermediate and definitive host. *Eukaryot. Cell* 4, 814–826 (2005).
- Demichev, V. et al. DIA-NN: neural networks and interference correction enable deep proteome coverage in high throughput. *Nat. Methods* 17, 41–44 (2020).

Acknowledgements

This work was supported by the National Natural Science Foundation of China (32170427 by J.Y., 32270503 by H.C.), the Natural Science Foundation of Fujian Province (2021J01028 by J.Y.), and the 111 Project sponsored by the State Bureau of Foreign Experts and Ministry of Education of China (BP2018017 by J.Y.).

Author contributions

J.G. and J.Y. designed the study. J.G., P.W., X.Z.(Xiaoming Zhang), W.L., and X.Z. (Xiaolong Zhang) generated the modified parasites. J.G. performed phenotype analysis, protein analysis, electron microscopy, RNA analysis, and reporter assays. P.W. conducted mass spectrometry and protein analysis. X.M. performed the bioinformatics analysis. L.J., J.L., H.C., and J.Y. supervised the work. J.G., X.M., and J.Y. wrote the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary information The online version contains supplementary material available at https://doi.org/10.1038/s41467-024-49002-9.

Correspondence and requests for materials should be addressed to Lubin Jiang, Jian Li, Huiting Cui or Jing Yuan.

Peer review information *Nature Communications* thanks the anonymous, reviewer(s) for their contribution to the peer review of this work. A peer review file is available.

Reprints and permissions information is available at http://www.nature.com/reprints

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/ licenses/by/4.0/.

© The Author(s) 2024

Supplemental Information

An axonemal intron splicing program sustains *Plasmodium* male development

Jiepeng Guan^{1,#}, Peijia Wu^{1,#}, Xiaoli Mo^{1,#}, Xiaolong Zhang^{3,#}, Wenqi Liang¹, Xiaoming Zhang¹, Lubin Jiang^{3,*}, Jian Li^{1,*}, Huiting Cui^{1,*} and Jing Yuan^{1,2,*}

- 1. Supplementary Figures 1-13 and figure legends
- 2. Supplementary Table 1. List of genetically modified parasite strains used in this study
- 3. Supplementary Table 2. Oligonucleotides and primers used in this study



Male					Female			
		1	2	3	1	2	3	
Male	1	1.000	0.993	0.996	0.030	0.025	0.027	
	2	0.993	1.000	0.995	0.029	0.025	0.027	
	3	0.996	0.995	1.000	0.032	0.028	0.030	1 .0
Female	1	0.030	0.029	0.032	1.000	0.998	0.998	0.8
	2	0.025	0.025	0.028	0.998	1.000	0.998	0.6
	3	0.027	0.027	0.030	0.998	0.998	1.000	- 0.2

в

Supplementary Figure 1. Purification of male and female gametocytes of the *P. yoelii* parasite for transcriptome analysis

A. Purification of male (GFP+) and female (mCherry+) gametocytes from a *P. yoelii* parasite reporter line *DFsc7* using flow cytometry sorting. The purity of gametocytes was shown. Representative from three independent experiments.

B. Pearson's correlation coefficient analysis of global gene expression between male and female gametocytes based on RNA-seq data with three biological replicates.







Supplementary Figure 2. Normal ability of genome replication and erythrocyte rupture for the RBPm1-null parasite during male gametogenesis

A. Flow cytometry analysis of genomic DNA content in male gametocytes during gametogenesis. The DFsc7; $\Delta Rbpm1$ is a DFsc7-derived RBPm1-null parasite line. Male gametocytes (GFP+) were gated, and genomic DNA content was measured based on the Hoechst 33342 fluorescence intensity. Representative for three independent experiments.

B. IFA detection of the parasitophorous vacuole membrane (PVM) rupture. SEP1 protein is a marker for PVM. Male gametocytes from the *sep1::4Myc* parasite and the derived RBPm1-null parasite *sep1::4Myc*; $\Delta Rbpm1$ were analyzed. Representative for three independent experiments. Scale bars: 5 µm.

C. IFA detection of the erythrocyte plasma membrane (EM) rupture. TER-119 protein is a marker of mouse EM. Male gametocytes from the 17XNL and $\Delta Rbpm1$ parasites were stained with anti-TER-119 antibody. Representative for three independent experiments. Scale bars: 5 µm.



Е

Parental: DFsc7 (ccp2::mCherry;dhc1::gfp)

Mutant: DFsc7;∆Rbpm1







F



Supplementary Figure 3. Generation, purification and transcriptome analysis of male gametocytes with RBPm1 deficiency

A-D. Phenotype analysis of *DFsc7* (parental) and *DFsc7*; $\Delta Rbpm1$ (mutant) parasite lines, including gametocyte formation (**A**), male gamete formation (**B**), ookinete formation *in vitro* (**C**), and salivary gland sporozoite in mosquitoes (**D**). Data are means \pm SEM of three independent experiments, two-sided *t*-test.

E. Flowchart showing the purification of male gametocytes (green, GFP+) from both DFsc7 and $DFsc7;\Delta Rbpm1$ parasites for transcriptome analysis via RNA-seq.

F. Flow cytometry detection of male gametocytes (GFP+) before and after sorting, with indicated purity. Representative results from three independent experiments.

G. A heatmap showing the Pearson correlation coefficient between *DFsc7* (parental) and *DFsc7*; $\Delta Rbpm1$ (mutant) male gametocyte RNA-seq data.

H. A volcano plot showing the differentially expressed genes in male gametocytes between the *DFsc7* (parental) and *DFsc7*; $\Delta Rbpm1$ (mutant) lines. The threshold for the log₂ fold change (log₂FC) and false discovery rate (FDR) are ±2 and 0.05, respectively. There are 481 genes up-regulated and 295 genes down-regulated in male gametocytes after loss of RBPm1. Three down-regulated genes (PY17X_1109100, PY17X_0833600, and PY17X_1216400), which exhibited intron retention in further study, are highlighted.

Α

26 genes with intron retention

Molecular function	Gene ID	Total number of introns in gene	# of the retained intron	Length of the retained intron (bp)	Male transcription (normalized counts)	Female transcription (normalized counts)	Ratio (Male/Female)
Basal body &	kinesin8b (PY17X_0204100)	4	1	239	5148	2	3217
axoneme assembly	<i>PF16</i> (PY17X_0919000)	1	1	276	580	38	15
	dhc6 (PY17X_0603800)	33	20	241	842	5	160
	dhc7 (PY17X_0510800)	10	7	235	1070	3	318
Axoneme motility	dlc1 (PY17X_1241500)	5	4	193	296	68	4
Axoneme mounty	dlc2 (PY17X_0302800)	3	1	195	503	19	27
	drc1 (PY17X_0721100)	9	2, 3	179, 150	597	93	6
	dbc (PY17X_1333900)	5	1	772	2059	40	51
	md2 (PY17X_1450400)	1	1	505	1534	53	29
	PY17X_1109100	3	1	353	1662	55	30
	PY17X_0521800	16	1	278	777	38	20
	PY17X_1311800	13	5	248	1342	3	446
	PY17X_1323900	1	1	322	710	103	7
	PY17X_1357300	7	5, 7	212, 143	2644	4	630
	PY17X_1335600	1	1	338	1320	3	417
	PY17X_1452900	13	1	367	1686	6	295
Function unknown	PY17X_1122300	2	1	240	161	10	15
	PY17X_0523500	5	2, 3	192, 318	348	1	533
	PY17X_0508900	7	5	380	485	10	49
	PY17X_1320300	3	2	183	195	24	8
	PY17X_0833600	2	2	302	526	12	46
	PY17X_1341200	5	1	208	731	1	803
	PY17X_1305400	15	11, 12	261, 330	1583	14	116
	PY17X_0415900	13	13	171	431	2	201
	PY17X_0105800	1	1	193	107	3	33
	PY17X_1216400	10	5	134	712	1	596





Supplementary Figure 4. Expression and function information of 26 intronretained genes identified in the RBPm1-null male gametocytes

A. List of 26 genes with intron retention detected in the RBPm1-null male gametocytes. Among them, 22 genes had one retained intron while 4 genes (*drc1*, PY17X_1357300, PY17X_0523500, and PY17X_1305400) possessed two retained introns after loss of RBPm1. Information including the protein function, gene ID, exon-intron structure, retained intron, and gender transcription, is provided. Gender transcription (TMM normalized counts) were from the gametocyte transcriptome data in this study.

B. Gene ontology enrichment analysis of the 26 genes indicates male-specific or preferential biological processes. Hypergeometric test was applied.



Supplementary Figure 5. Verification of intron retention for 30 introns at 26 genes in the RBPm1-null male gametocytes

A. RT-PCR confirmation of intron retention in the 26 genes after loss of RBPm1. For each gene, the mapped views of the RNA-seq results (*DFsc7* in green and *DFsc7*; $\Delta Rbpm1$ in blue, representative for three biological replicates) and the exonintron structure (black) are shown in the upper panels. Intron retention is highlighted with red boxes. The primers (F or R) designed for detecting the intron via RT-PCR and the expected PCR products are shown. RT-PCR analysis using the genomic DNA (gDNA) from 17XNL parasite, complementary DNA (cDNA) from male gametocytes of parental and mutant parasites showed the intron retention (red) and intron splicing (black).

B. RT-qPCR confirmation of intron retention in the *kinesin8b* and *PF16* genes after loss of RBPm1. The top schematic of gene exon-intron structure shows the positions of the retained intron (orange line) and the RT-qPCR amplicon. RT-qPCR analysis using cDNA from male gametocytes of parental and mutant parasites showed the retention of *kinesin8b* intron1 and *PF16* intron1. Data are means \pm SEM from three independent experiments, two-sided *t*-test.



Supplementary Figure 6. RBPm1-regulating genes encode axoneme-associated proteins

A. Summary of protein stage expression and localization of 12 selected intron-retained genes in the *P. yoelii*. These genes include 6 annotated genes (*kinesin8b*, *PF16*, *dhc6*, *dhc7*, *dlc1*, *dlc2*) and 6 unannotated genes (PY17X_1109100, PY17X_0521800, PY17X_1311800, PY17X_1323900, PY17X_1357300, PY17X_1335600). Each gene was endogenously tagged at the N- or C-terminus with a 6HA in the 17XNL, generating the HA-tagged lines for protein expression and localization analysis. Due to the space limit, only the results of protein expression at the gametocytes were shown in **B-M**.

B-M. Protein expression and localization analysis of the 12 intron-retaining genes in gametocytes. IFA of the HA-tagged target protein and α -Tubulin in female gametocytes (0 mpa) and male gametocytes (0 and 15 mpa). Representative results from two independent experiments. Scale bars: 5 μ m.



Supplementary Figure 7. Intron retention causes premature stop codons in RBPm1 target transcripts

Amino acid and nucleotide sequence analysis of the retained introns in the 26 genes. For each gene, intron retention (highlighted in orange lowercase letter) creates at least one premature stop codon (red asterisk) at the transcripts in the RBPm1-null parasites.



g

'000° 00 Ø Å B "9+0"

"9+1"

1%

1%

0%

0%

1/33

3.0%

p=5.36×10⁻⁸

10%

52%

Supplementary Figure 8. Depletion of *kinesin8b* or *PF16* phenocopies RBPm1 deficiency

A. Female and male gametocyte formation in mice. Data are means \pm SEM from three independent experiments.

B. Exflagellation center (EC) formation of male gametocytes at 10 mpa. Data are means \pm SEM from three independent experiments, two-sided *t*-test.

C. Midgut oocyst formation in mosquitoes at 7 days after blood feeding. x/y at the top represents the number of mosquitoes containing oocysts/the number of dissected mosquitoes, and the percentage represents the infection prevalence of mosquitoes. Red lines show the mean value of oocyst numbers, two-sided Mann–Whitney U test. Representative results from two independent experiments.

D. Transmission electron microscopy of axoneme architecture in male gametocytes at 8 mpa. Scale bars: 100 nm.

E. Quantification of axoneme formation in the mutant parasites in **D**. n is the total number of the intact and defective axoneme structures observed in each group. Representative for three independent experiments.



Supplementary Figure 9. RBPm1 interacts with spliceosome E complex

A. A schematic of two modified parasite lines generated for detecting the RBPm1interacting proteins in gametocytes by TurboID ligase-based proximity labeling. Endogenous RBPm1 was C-terminally tagged with an HA::TurboID motif by CRISPR-Cas9 in 17XNL, generating the *Rbpm1::TurboID* line. A control line *Rbpm1::T2A::TurboID* was generated, in which a "ribosome skip" T2A was inserted between RBPm1 and 3NLS::HA::TurboID for separated nuclear expression of RBPm1 and TurboID.

B. Co-staining of HA-tagged TurboID ligase (red) and biotinylated proteins (SA-488, green) in male gametocytes of the *Rbpm1::TurboID* and *Rbpm1::T2A::TurboID* lines. Gametocytes incubated with 50 μ M biotin at 37°C for 20 minutes were co-stained with the fluorescent-conjugated streptavidin (SA-488) and anti-HA antibody. Scale bars: 5 μ m. Representative for three independent experiments.

C. Protein interaction analysis between RBPm1 and spliceosome at different stages of assembly based on the data from TurboID-based proximity labeling and mass spectrometry. The upper panels show the spliceosome complexes from early to later stages during assembly, including E, A, B, and C complexes. The lower panels show the enrichment level (log₂FC value) of protein components in different spliceosome complexes.

D. Proposed model showing RBPm1 interaction with the early spliceosome E complex for intron splicing of axonemal genes.



Supplementary Figure 10. RBPm1-dependent splicing of axonemal introns inserted in the reporter gene. Related to Figure 7

A. A transgenic line *BFP-dlc1*I4 with a *dlc1* intron4 (*dlc1*I4, purple line)-inserted *bfp* cassette integrated at the *p230p* locus of the *DFsc7* line. Similar analysis as in **Figure 5B**. *dlc1* intron4 was inserted into the *bfp* gene at the nucleotides 455-456 to mimic the splice site (vertical lines) of *in situ dlc1*I4. BFP expression was detected specifically in male gametocytes of the *BFP-dlc1*I4 parasites. Representative for three independent experiments. Scale bars: 5 μ m.

B. A *BFP-dlc1*I4 derived RBPm1 mutant line, *BFP-dlc1*I4; $\Delta Rbpm1$, showed no BFP expression in male gametocytes. Representative for three independent experiments. Scale bars: 5 µm.

C. Effect of the *PY17X_1109100* intron1 (*BFP-1109100*I1) insertion on the gametocyte expression of BFP. Similar analysis as in **A**. *PY17X_1109100* intron1 was inserted into the *bfp* gene at the nucleotides 390-391 to mimic the splice site (vertical lines) of *in situ PY17X_1109100* intron1. BFP expression was detected specifically in male gametocytes of the *BFP-1109100*I1 parasites.

D. A *BFP-1109100*I1 derived RBPm1 mutant line, *BFP-1109100*I1; $\Delta Rbpm1$, showed no BFP expression in male gametocytes. Similar analysis as in **B**.

E. Effect of the *PY17X_1109100* intron2 (*BFP-1109100*I2) insertion on the gametocyte expression of BFP. Similar analysis as in **A**. *PY17X_1109100* intron2 was inserted into the *bfp* gene at the nucleotides 384-385. BFP expression was detected in both male and female gametocytes of the *BFP-1109100*I2 parasites.

F. A *BFP-1109100*I2 derived RBPm1 mutant line *BFP-1109100*I2; $\Delta Rbpm1$, showed BFP expression in both male and female gametocytes. Similar analysis as in **B**.



P



s <i>in8b</i> ed counts	н	kinesin8b::6HA	kinesin8t ΔRbpi kinesin8	0∷6HA; m1; 3b∆l1
this stud	, ₩	8		
2		¥`´	``´´0/43	0
<i>hei</i> [31]	ą			140
Female	Ę			
34	Ŭ			A STATE
arum [30]	t Tub		Es.	1200
Female	Hs.		C. C.	6
146	ЧH		and the second s	
	sin8b ed counts this study Female 2 thei [31] Female 34 arum [30] Female 146	H sin8b ed counts This study Female 2 thei [31] Female 34 arum [30] Female 146	H sin8b ed counts h this study Female 2 the i [31] Female 34 arum [30] Female 146	H kinesin8b kinesin8b::6HA kinesin8b htis study Female 2 thei [31] Female 34 arum [30] Female 146



1 2

1 2

ð Q

bp Μ

500-

200-



dlc1

δ Q

cDNA

4 5

4 5

4 5



Supplementary Figure 11. Intron retention prevents expression of axonemal proteins in female gametocytes

A. Transcription level of the *PF16* gene in male and female gametocytes. TMM normalized counts are from the gametocyte transcriptomes in this study and the published dataset contributed by Yeoh, L.M. and Lasonder, E.

B. IFA of 6HA-tagged PF16 in female and male gametocytes of the *PF16::6HA* and *PF16::6HA*; $\Delta Rbpm1$;*PF16\Delta I1* (*PF16* intron1-deleted line described in the **Figure 5D**) parasites. In each image, one male and one female gametocytes were shown. The HA-positive female gametocyte was highlighted with an asterisk. x/y represents the number of HA-positive female gametocytes/the total number of female gametocytes tested. Representative for three independent experiments. Scale bars: 5 µm.

C and D. Low-level expression of the Dlc1 protein detected in female gametocytes after deletion of the *dlc1* intron4. Similar illustration as in A and B. The *dlc1* intron4-deleted line was described in the Figure 5G.

E and **F**. Low-level expression of the PY17X_1109100 protein detected in female gametocytes after deletion of the *PY17X_1109100* intron1. Similar illustration as in **A** and **B**. The *PY17X_1109100* intron1-deleted line was described in the **Figure 5J**.

G and H. Undetectable expression of the Kinesin8B protein in female gametocytes after deletion of the *kinesin8b* $\Delta intron1$. Similar illustration as in **A** and **B**. Note that the *kinesin8b* transcripts are almost undetectable in female gametocytes of *P. yoelii*.

I, J, K, and L. RT-PCR confirmation of intron retention at the transcripts of 4 genes (*PF16, dlc1, PY17X_1109100,* and *kinesin8b*) in female gametocytes. Genomic DNA (gDNA) from 17XNL parasite, complementary DNA (cDNA) from the purified male and female gametocytes of *DFsc7* were analyzed. Exons are indicated by boxes and introns by lines. Representative for three independent experiments.

M. Proposed different roles of RBPm1-target introns in axonemal gene expression at male and female gametocytes respectively. In male gametocytes, RBPm1 (as a key)-directed splicing of axonemal intron (as a lock) allows protein expression of the axonemal genes. In female gametocytes, dual blockage via weak transcription and IR prevents protein expression of the axonemal genes.



K PCR genotyping of parasite clones with modification at the *p230p* locus.

p1/p2

p3/p4

L PCR genotyping of parasite clones with axonemal intron inserted at the gep1 locus.

Supplementary Figure 12. Genotyping of genetically modified parasite lines

A-C. Schematic diagrams showing CRISPR/Cas9-mediated gene tagging at C-terminus (A), gene tagging at N-terminus (B), and gene deletion (C) via double cross-over homologous recombination. 'p' represents the primers for PCR, and the red lightning bolt represents the sites for sgRNA recognition.

D-L. Genotyping PCR results showing correct 5' and 3' homologous recombination in the modified parasite lines in this study. For each modification, usually 1-3 parasite single clones (sc) were obtained via limiting dilution. The red-colored sc was selected for further analysis. Oligo sequences used for plasmid construction and primers used for genotyping PCR are listed in Supplementary Table 2.

Supplementary Figure 13. Flow cytometry gating strategies

A. Gating strategy for sorting male and female gametocytes from a *P. yoelii* parasite reporter line *DFsc7* presented in Supplementary Fig. 1A. Forward and side scatter signals were used to distinguish red blood cells from debris, doublets, and white blood cells. Male and female gametocytes were sorted based on GFP fluorescence and mCherry fluorescence. After sorting, gametocyte purity was assessed by re-analysis of a sample fraction.

B. Gating strategy for analyzing DNA content of male gametocytes presented in Supplementary Fig. 2A. Forward and side scatter signals were used to distinguish red blood cells from debris, doublets, and white blood cells. Male gametocytes were identified by GFP fluorescence and analyzed for Hoechst 33342 fluorescence.

C. Gating strategy for sorting male gametocytes from the *DFsc7* and *DFsc7*; $\Delta Rbpm1$ lines presented in Supplementary Fig. 3F. Forward and side scatter signals were used to distinguish red blood cells from debris, doublets, and white blood cells. Male gametocytes were sorted based on GFP fluorescence. After sorting, male gametocyte purity was assessed by re-analysis of a sample fraction.

Table S1. List of genetically modified parasite strains in this study

Strain	Parental strain	Description	Resource						
17XNL	/	Plasmodium yoelii 17XNL strain	NIH						
Parasites with gene tagging									
DFsc7	17XNL	DFsc7 expresses mCherry and GFP reporters mutual-exclusively in the female and male armetocytes	Liu et al. 2018						
sep1::4Myc	17XNL	sep1 C-terminally tagged with 4Myc	Jiang et al. 2020						
Rbpm1::6HA	17XNL	Rbpm1 C-terminally tagged with 6HA	Fig S12						
Rbpm1::gfp	17XNL	Rbpm1 C-terminally tagged with GFP	Fig S12						
DFsc7;Rbpm1::6HA	DFsc7	Rbpm1 C-terminally tagged with 6HA	Fig S12						
Rbpm1::HA::TurbolD	17XNL	Rbpm1 C-terminally tagged with HA-TurboID	Fig S12						
Rbpm1::T2A::TurboID	17XNL	Rbpm1 C-terminally tagged with 3NLS-HA-TurboID	Fig S12						
kinesin8b::6HA	17XNL	kinesin8b C-terminally tagged with 6HA	Fig S12						
PF16::6HA	17XNL	PF16 C-terminally tagged with 6HA	Fig S12						
dhc6::6HA	17XNL	dhc6 C-terminally tagged with 6HA	Fig S12						
dhc7::6HA	17XNL	0510800 C-terminally tagged with 6HA	Fig S12						
dlc1::6HA	17XNL	dlc1 C-terminally tagged with 6HA	Fig S12						
dlc2::6HA	17XNL	d/c2 C-terminally tagged with 6HA	Fig S12						
1109100::6HA	17XNL	1109100 C-terminally tagged with 6HA	Fig S12						
0521800::6HA	17XNL	0521800 C-terminally tagged with 6HA	Fig S12						
1311800::6HA	17XNL	1311800 C-terminally tagged with 6HA	Fig S12						
HA::1323900	17XNL	1323900 N-terminally tagged with HA	Fig S12						
1357300::6HA	17XNL	1357300 C-terminally tagged with 6HA	Fig S12						
1335600::6HA	17XNL	1335600 C-terminally tagged with 6HA	Fig S12						
Rbpm1::6HA ;U1-70K::4Myc	Rbpm1::6HA	U1-70K C-terminally tagged with 4Myc	Fig S12						
Rbpm1::6HA ;U1-A::4Myc	Rbpm1::6HA	U1-A C-terminally tagged with 4Myc	Fig S12						
Rbpm1::6HA ;U1-C::4Myc	Rbpm1::6HA	U1-C C-terminally tagged with 4Myc	Fig S12						
	[
∆Rbpm1	17XNL	Deletion of the whole coding sequences of <i>Rbpm1</i>	Fig S12						
∆nke4	17XNL	Deletion of the partial coding sequences of <i>nek4</i>	Jiang et al. 2020						
∆map2	1/XNL	Deletion of the partial coding sequences of map2	Jiang et al. 2020						
sep1::4Myc;DRbpm1	sep1::4Myc	Deletion of the whole coding sequences of Rbpm1	Fig S12						
	DFSC7	Deletion of the whole coding sequences of Rbpm1	Fig S12						
ARTIE	17XNL	Deletion of the N-terminal 1184 bp coding sequence of <i>kinesin8b</i>	Fig S12						
	1/XNL	Deletion of the whole coding sequences of PF16	Fig S12						
	Linosin [®] h::6UA	Deletion of the whole coding sequences of Phrm1	Fig S12						
RINESINSDOFA, DRDpm1	RITESITIODOFTA	Deletion of the whole coding sequences of Rbpm1	Fig S12						
	dbc6::6HA	Deletion of the whole coding sequences of Rbpm1	Fig S12						
dict::6HA:\ARbom1	dic1::6HA	Deletion of the whole coding sequences of Rhpm1	Fig S12						
dic2::6HA:\ARbom1	dic?::6HA	Deletion of the whole coding sequences of Rbpm1	Fig S12						
1109100::6HA:\\Rbpm1	1109100::6HA	Deletion of the whole coding sequences of Rbpm1	Fig S12						
Δαep1	17XNL	Deletion of the whole coding sequences of <i>rep1</i>	Jiang et al. 2020						
Parasites with RRM deletion at the Rbpm1	locus		g						
Arrm1	17XNL	Deletion of the 565-981 bp coding sequence of <i>Rbpm1</i>	Fig S12						
Δrrm2	17XNL	Deletion of the 1018-1519 bp coding sequence of <i>Rbpm1</i>	Fig S12						
Parasites with gene compelementation									
rescue	∆Rbpm1	In situ complementation of Rbpm1 N-terminally tagged with 4Myc	Fig S12						
Parasites with intron deletion	1 ·								
kinesin8b∷6HA ;∆Rbpm1 ;kinesin8b ∆I1	kinesin8b∷6HA ;∆Rbpm1	Deletion of Kinesin8b intron 1	Fig S12						
PF16::6HA ;ΔRbpm1 ;PF16 ΔI1	PF16::6HA ;∆Rbpm1	Deletion of <i>PF16</i> intron 1	Fig S12						
dlc1::6HA ;ΔRbpm1 ;dlc1 Δl4	dlc1::6HA ;∆Rbpm1	Deletion of <i>dlc1</i> intron4	Fig S12						
1109100::6HA ;ΔRbpm1 ;1109100 ΔI1	1109100::6HA ;∆Rbpm1	Deletion of 1109100 intron 1	Fig S12						
$\Delta Rbpm1$;kinesin8b $\Delta I1$	∆Rbpm1	Deletion of kinesin8b intron 1	Fig S12						
$\Delta Rbpm1$;kinesin8b $\Delta I1$;PF16 $\Delta I1$	$\Delta Rbpm1$;kinesin8b $\Delta I1$	Deletion of <i>PF16</i> intron 1	Fig S12						
Parasites with modification at the p230p lo	cus								
BFP	DFsc7	Coding region of p230p gene was replaced with the BFP expression cassette	Fig S12						
BFP-Kin8b11	DFsc7	Coding region of p230p gene was replaced with the BFP-Kin8b11 expression cassette	Fig S12						
BFP-Kin8b11;∆Rbpm1	DFsc7 ;∆Rbpm1	Coding region of p230p gene was replaced with the BFP-Kin8b11 expression cassette	Fig S12						
BFP-Kin8b12	DFsc7	Coding region of p230p gene was replaced with the BFP-Kin8b I2 expression cassette	Fig S12						
BFP-Kin8b12;ΔRbpm1	DFsc7 ;∆Rbpm1	Coding region of p230p gene was replaced with the BFP-Kin8b12 expression cassette	Fig S12						
BFP-PF1611	DFsc7	Coding region of p230p gene was replaced with the BFP-PF1611 expression cassette	Fig S12						
BFP-PF1611;ΔRbpm1	DFsc7;∆Rbpm1	Coding region of p230p gene was replaced with the BFP-PF1611 expression cassette	Fig S12						
BFP-dic1 14	DFsc7	Coding region of p230p gene was replaced with the BFP-dlc1 l4 expression cassette	Fig S12						
BFP-dlc1 l4;∆Rbpm1	DFsc7;∆Rbpm1	Coding region of p230p gene was replaced with the BFP-dlc1 l4 expression cassette	Fig S12						
BFP-110910011	DFsc7	Coding region of p230p gene was replaced with the BFP-110910011 expression cassette	Fig S12						
BFP-110910011;∆Rbpm1	DFsc7;∆Rbpm1	Coding region of p230p gene was replaced with the BFP-110910011 expression cassette	Fig S12						
BFP-110910012	DFsc7	Coding region of p230p gene was replaced with the BFP-110910012 expression cassette	Fig S12						
Brr-110910012;&Rbpm1	U⊢sc7;∆Rbpm1	Coung region of p230p gene was replaced with the BFP-110910012 expression cassette	Fig S12						
rarasites with axonemal intron inserted at f		Insertion of VinceinOb integer 4 into 0	Fig. 640						
		Insertion of <i>Nitestinov</i> Intron 1 into exon 3 of gep1	Fig S12						
nt not tested	TANL		1 19 0 12						

Table S2. Oligonucleotides and primers used in this study

Digo sequences for constructing gene tagging plasmids

			Left here		Diskt have		Towned alt	
Gene name	Gene ID	Tag	Left homo	logous arm	Right homo	Beveree arimer	l arget site	of sgRNA
Bhom 1	DV17V 0716700	C terminal RHA	CCCAAGCTTGCCGAACCTA	CATGCCATGGATTGTTATAA	CCGCTCGAGTTTATGTCATT	CCGGAATTCGTTCCAATGAA	TATTGTAAGGGAAAGGACC	AAACTTTATGGGTCCTTTCC
Nopini	1111X_0110100		AGAAGCCAAA	TCCGGTTGTTGC	TTTTGAGGT	GACAAACAA	CATAAA	CTTAC
Rbpm1	PY17X_0716700	C-terminal GFP	AGAAGCCAAA	TCCGGTTGTTGC	TTTTGAGGT	GACAAACAA	CATAAA	CTTAC
Rbpm1	PY17X_0716700	C-terminal HA-TurboID	CCCAAGCTTGCCGAACCTA	CATGCCATGGATTGTTATAA	CCGCTCGAGTTTATGTCATT	CCGGAATTCGTTCCAATGAA	TATTGTAAGGGAAAGGACC	AAACTTTATGGGTCCTTTCC
Rhom1	PY17X 0716700	C-terminal 3NI S-HA-TurbolD	CCCAAGCTTGCCGAACCTA	CATGCCATGGATTGTTATAA	CCGCTCGAGTTTATGTCATT	CCGGAATTCGTTCCAATGAA	TATTGTAAGGGAAAGGACC	AAACTTTATGGGTCCTTTCC
			AGAAGCCAAA CCCAAGCTTGATGACCAAAT	TCCGGTTGTTGC CATGCCATGGAGTTTTATTT	TTTTGAGGT CCGCTCGAGAAATGTTTGA	GACAAACAA GGGCTTAAGGAAAAAGGCA	CATAAA	CTTAC AAACTCATAAATTAACTGAC
kinésinöb	PY17X_0204100	C-terminal 6HA	GAAGAGCTT	TTTGTGATGCTAG	ACTITACCATTC	ATGATGCCAT	ATGA	GCAC
PF16	PY17X_0919000	C-terminal 6HA	TTCTAAAATC	TTTTCAACTTC	TAATAACAAGT	CTCCTTTTGC	TGTG	ACACCACATGAAGTATGTAC
dhc6	PY17X_0603800	C-terminal 6HA	CCCAAGCTTGTGTGTGCAA	CATGCCATGGATTATATATA	CCGCTCGAGAAAAAATACG	CCGGAATTCACGATTATATT	TATTGGAAGTAGAAATGCC	AAACACAACGGCATTTCTAC
dbc7	DV17V 0E10900	C terminal GHA	CGGGGTACCTGATGATAAT	CATGCCATGGTAGTAGCAT	CCGCTCGAGTTTTTCGTTTA	CCCCTTAAGCATCACATTCT	TATTGTGGAGACTAGGATCT	AAACCCTTCAGATCCTAGTC
0.107	1111X_0310000		GAATTTATTT	ATGAACTTTAA	ATTITITAA	TTCATTTTA	GAAGG	TCCAC
dlc1	PY17X_1241500	C-terminal 6HA	CTTCCTCTCAA	TACGGATCCATC	CAACATGCTCA	GAAATTGCAA	TTATA	GTAAC
dlc2	PY17X_0302800	C-terminal 6HA	CGGGGTACCCCTTATCATA	CATGCCATGGACACTTATAT	CCGCTCGAGAATATGATAAT	GGGCTTAAGGGGGGTGAAAA	TATTGCTATATGATGTATGC	AAACTATAGCATACATCATA
1109100	PY17X 1109100	C-terminal 6HA	CCCAAGCTTGTACCACAAA	CGGGGTACCGGATTGTCGT	CCGCTCGAGGGGGGTCCATA	CCGGAATTCTGGGTTTAAC	TATTGTTGCTGCTTGGCTTG	AAACAGCAACAAGCCAAGC
			CAATGGTGGA CGGGGTACCCAATAAATAG	CATTATTGTAAGTG CATGCCATGGCAGTTTATCC	TAAGATGGAA CCGCTCGAGATATTGATAAT	CTTGTACACC	TTGCT TATTGTGAAGTCTATATGAC	AGCAAC AAACACTTGGTCATATAGAC
0521800	PY17X_0521800	C-terminal 6HA	TGGAAACAAA	CCTAATAAAT	AATAATCTC	ATATACGAAT	CAAGT	TTCAC
1311800	PY17X_1311800	C-terminal 6HA	CGGGGTACCCCCCGAGGA	AAATAATACA	AAATAAAGAA	AAGTATGTTC	TATTAATCAGAGGATGAAGT TGCA	GATT
1323900	PY17X_1323900	N-terminal HA	CCCAAGCTTGGCATTACTGT	CATGCCATGGATTAATTACA	CCGCTCGAGATGGAACAAA	CCCCTTAAGACCTGTTTATC	TATTGTAAATATGAAGGGAG	AAACTCCTCCTCCCTTCATA
1257200	DV17V 1357300	C terminal 6HA	CGGGGTACCACCCCCGATC	CATGCCATGGATCTATTTCA	CCGCTCGAGCATACAAATA	CCCCTTAAGTATGCCAGCTT	TATTGCATATGCACATTATC	AAACCTTTTGATAATGTGCA
1337300	1111X_1337300		TTAATACAAC	AAATAATTTT	AATTAAAAAG	GTATGCCAG	AAAAG	TATGC
1335600	PY17X_1335600	C-terminal 6HA	GAGATAAA	TATTTGTCTTTAAAAG	TGAACTTAGC	TTAATTGC	TATTA	AGGGC
U1-70K	PY17X_1144300	C-terminal 4Myc	CCCAAGCTTGGAAAAGGTC	CATGCCATGGTTCATACCCT	CCGCTCGAGAAGTTTTTCGT	CCGGAATTCGTAACTTGCTT	TATTGACAGAGATAGAGGC	AAACTCTCTGCCTCTATCTC
U1-A	PY17X 1407100	C-terminal 4Mvc	CCCAAGCTTCAGGATTTGTT	CATGCCATGGTCGTTTCGC	CCGCTCGAGCCTTTTTTTT	GGGCTTAAGGCATATCTGT	TATTGTATGTCCATATTCCC	AAACAAATAGGGAATATGGA
		o tarminar enirjo	GAAGCCAGA CCCAAGCTTCACATAGTTCA	ATATGATATTTTTAAC	TTTTTGGAATTATT	GTGCTTTGTA GGGCTTAAGGAGTATATAC	TATTT TATTAGAGCAGGCTATGTTC	CATAC AAACGGGGGGGAACATAGCCT
U1-C	PY17X_1426800	C-terminal 4Myc	CCAGTAGGT	TTATTTACAAAATTTGC	GGAAGTATAT	ACGTTCGAAA	CCCC	GCTCT
Diagnositc PCR primers for 0	C-terminal tagging							
Gene name	Gene ID	Tag	P1	P2	P3	P4		
Rham1	DV47V 0740700		GGATAAAATGGTTGAAGTTA	GGTTAAAAGCTAAAAAGGC	TGAAAATATGCAACAACCG			
Rupini	PY17X_0/16/00	C-terminal 6HA	G	C	G	IGATICIACCIGIACACCAG		
Rbpm1	PY17X_0716700	C-terminal GFP	GGATAAAATGGTTGAAGTTA	C	G	TGATTCTACCTGTACACCAG		
Rbpm1	PY17X_0716700	C-terminal HA-TurboID	GGATAAAATGGTTGAAGTTA	GGTTAAAAGCTAAAAAGGC	TGAAAATATGCAACAACCG	TGATTCTACCTGTACACCAG		
Rhpm1	PV17X 0716700	C-terminal 3NI S HA Turketo	GGATAAAATGGTTGAAGTTA	GGTTAAAAGCTAAAAAGGC	TGAAAATATGCAACAACCG	TGATTCTACCTGTACACCAC		
Rupini	PY17X_0/16/00	C-terminal 3NLS-HA-TurbolD	G	C	G	IGATICIACCIGIACACCAG		
Rbpm1	PY17X_0716700	C-terminal 6HA	GGATAAAATGGTTGAAGTTA	C	G	TGATTCTACCTGTACACCAG		
kinesin8b	PY17X_0204100	C-terminal 6HA	TTAATAAACAAACTAGTTGC	GAATGGTAAAGTTCAAACAT	CGCACCAAAGATCTCAAAC	CCCACTTAGATATTTCGAAA		
PE16	PV17V 0010000	C terminal 6HA	CTAATGAGTCATCTGATGAT	TATAGTAAGAAATAGCAGAC	CACACCTGGATATTCTGAAA	COTTGAAGTAATCTTATCAC		
						001101010110110101		
dhc6	PY17X_0603800	C-terminal 6HA	CGTTAAGATATGCAACTGTC	TACAAAAATAGCAAACGGTT	CC	GTCTCGAACAAATTTAAATG		
dhc7	PY17X_0510800	C-terminal 6HA	GACGATGAATCAAATTCGAA	ACAGGTTAAAAAATTAAACG	GCCATGCATCCATAGCAAA	GTTTTGAATTTCTTCTAACTC		
dlc1	PY17X 1241500	C-terminal 6HA	GGTCCAACATAATTTGTGAA	GAAAATTTAGAAAACATATG	AGATGGATCCGTAGCTCAT	GACCTCTTACTATGTGTAAC		
			G GGCATAAGTTGAATAAGCAT	T	C GCATTATTTTGTAGGAGGAG	ATCATTCCCTATATTTCCTG		
dic2	PY17X_0302800	C-terminal 6HA	TCA	CATATGAGTGTTTTCATCCC	Т	AATT		
1109100	PY17X_1109100	C-terminal 6HA	TCTACAAAAGAGGAAGCTTC	TTCCATCTTATATGGACCCC	GACACTTACAATAATGACGA	CCGAAGCACAATTAGCAAT C		
0521800	PY17X 0521800	C-terminal 6HA	CAAGGTAATAATATGTACAT	AACTTCCATGATATTTTGAG	ATTTATTAGGGGATAAACTG	TGTGTATATTGACAACATCC		
4044000		O toronale al QUIA	G		CAGAGGATGAAGTTGCATG	GGCGTAAGCCAAAGAATGA		
1311800	PY17X_1311800	C-terminal 6HA	ATAGGAAAAACTGGATTTCC	ICCCITIGITITITICGTIG	G	AC		
1357300	PY17X_1357300	C-terminal 6HA	C	G	G	ACAATATGCCACGTGCACA		
1335600	PY17X_1335600	C-terminal 6HA	CTGATGATATTTTTGAAACC	TAGGAAATATGAATTAGGAG	AAAATCGAGAGATGCAAAA	ATGATTATGGGGATATAGTC		
111-70K	PY17X 1144300	C-terminal 4Mvc	TACCTAGAAGATTAGGAGG	TATCATTTGGAATATCAAAG	GCCAGGAAAATGGAGAATA	CCCTATATATGTGGTTATAT		
		o tarminar miljo	G	G	Т	С		
U1-A	PY17X_1407100	C-terminal 4Myc	GAAAATGTTAATACTGAAGC	CTACATATATTGTGCGTTTT	AGTTAAAAATATCATATGCG	TAACGGATGGTTAGATAAGA		
U1-C	PY17X_1426800	C-terminal 4Myc	GTGAATATTGCGATATATAT	ATAACTTAAACATTTCATGT	CAAATGAATAAAGAAAATGC	CGGAATAACTGCTCATTTAT		
Diagnositc PCR primers for M	-terminal tagging		0	0				
				1	1	1		
Gene name	Gene ID	Tag	P5	P6	P7	P8		
1323900	PY17X_1323900	N-terminal HA	GGGGGGAATGATGGAAAAA	ACTAAATGAAGGCGACTCA	GTTCTTTTACCTTTCCTTGT	GGAAAGGTTTTGTGTAGCTA		
kinesin8b	PY17X 0204100	N-terminal 6HA	GTTTACTCTCTTGTCCACAT	GATCCTGCACATTTTTAAGA	GTGGATCTACTTGATATACT	CATCATAATATTGAGTTTTA		
			GCAAAAATGTAGACAATAAT					
0540	PY1/X_0919000	N-terminal 6HA	CC	CGACCTATTATAATCGTCAA	AAAAAATTTCACAAAAAAGG	GGTATGATACCTITATCAAC		
PF16								
PF16 Oligo sequences for constru-	cting gene knockout plasmids							
PF16 Oligo sequences for constru- Gene name	cting gene knockout plasmids Gene ID	Gene size (bp) / deleted	Left homo	logous arm	Right homo	plogous arm	Target site	of sgRNA
PF16 Oligo sequences for construct Gene name	cting gene knockout plasmids Gene ID	Gene size (bp) / deleted gene size (bp)	Left homo	logous arm Reverse primer	Right home Forward primer	Reverse primer	Target site	of sgRNA Reverse oligo
PF16 Oligo sequences for construct Gene name Rbpm1	Cting gene knockout plasmids Gene ID PY17X_0716700	Gene size (bp) / deleted gene size (bp) 1904/1904	Left homo Forward primer CGGGGTACCGCATACACGA GGAAATACTA	logous arm Reverse primer CATGCCATGGTTTGTGTATT TTATTTTTCGTCG	Right home Forward primer CCGCTCGAGTTTATGTCATT TTTTGAGGT	logous arm Reverse primer CCGGAATTCGTTCCAATGAA GACAAACAA	Target site Forward oligo TATTGTAGGGGGGGTTAAGC TACTAT	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC CCTAC
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin8b	Cting gene knockout plasmids Gene ID PY17X_0716700 PY17X_0204100	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184	Left homo Forward primer CGGGGTACCGCATACACGA GGAAATACTA CGGGGTACCCGGTTGTGC ATTACTACT	logous arm Reverse primer CATGCCATGGTTTGTGTATT TTATTTTCGTCG CATGCCATGGATTTGATCT TTACTATATT	Right home Forward primer CCGCTCGAGTTTATGTCATT TTTTGAGGT CCGCTCGAGACAGAACAAC	Reverse primer CCGGAATTCGTTCCAATGAA GACAACAA CCGGAATTCCTTTCTCTTCA TCATTCCTTC	Target site Forward oligo TATTGTAGGGGGGGTTAAGC TACTAT TATTGTTACCCTCAGTATAC	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC CCTAC AAACATTTTGTATACTGAGG
PF16 Oligo sequences for construct Gene name Rbpm1 kinesin8b PF16	ting gene knockout plasmids Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204000	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809	Left homo Forward primer CGGGGTACCGCATACACGA GGAAATACTA CGGGGTACCCGGTTGTGC ATTTATTATT CCCAAGCTTACGGTTTCTAA	logous arm Reverse primer CATGCCATGGTITGTGTATT TTATTITCGTCG CATGCCATGGATTITGATCT TTACTATATT CATGCCATGGTTTTTTTTT	Right homo Forward primer CCGCTCGAGTTATGTCATT TTTTGAGGT CCGCTCGAGACAGAACAAC TTAATGGACAG CCGCTCGAGAACAAGGAAA	Reverse primer CCGGAATTCGTTCCAATGAA GACAAACAA CCGGAATTCCTTTCTCTTCA TTCATTTCTTG GGGCTTAAGCTCGCAATTC	Target site Forward oligo TATTGTAGGGGGGTTAAGC TACTAT TATTGTTACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC CCTAC AAACATATTTGTATACTGAGG GTAAC AAACACAGTCCAAACACATG
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin8b PF16	Gene ID PY17X_0716700 PY17X_0204100 PY17X_020919000	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809	Left homo Forward primer CGGGGTACCGCATACACGA GGAATACCTA CGGGGTACCCCGGTTGTGC ATTTATTATT CCCAAGCTTACGGTTTCTAA AGTAATAATATCAC	logous arm Reverse primer CATGCCATGGTTTGTGTATT TTATTITTCGTCG CATGCCATGCATGCATTTTGATCT TTACTATATT CATGCCATGGTTTTTTTTTT	Right home Forward primer CCGCTCGAGTTATGTCATT TITITGAGGT CCGCTCGAGACAGAACAAC TTAATGGACAG CCGCTCGGAACAAGGAAA TAATAACAAGT	Reverse primer CCGGAATTCGTTCCAATGAA GACAAACAA CCGGAATTCCTTCCTTCA TTCATTTCTTG GGGCTTAAGCTCGCAATTC CTCCTTTTGC	Target site Forward oligo TATTGTAGGGGGGTAAGC TACTAT TATTGTTACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC CCTAC AAACATTITGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g	Gene ID 9217X_0716700 PY17X_0204100 PY17X_0919000 ene knockout	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809	Left homo GGGGTACCGATACACGA GGGGTACCCGATACACGA GGAATACTA CGGGGTACCCCGGTTGTGC ATTATTATT CCCAAGCTTACGGTTTCTAA AGTAATAATATCAC	logous arm Reverse primer CATGCCATGCTTTGTGTATT TTATTTTTCGTCG CATGCCATGC	Right home Forward primer CCGCTCGAGACHTATGTCATT TITTGAGGT CCGCTCGAGACAGAACAAC TTAATGGACAG CCGCTCGAGAACAAGGAAA TAATAACAAGGT	Reverse primer CCGGAATTCGTTCCAATGAA GACAAACAA CCGGAATTCCTTTCCT	Target site Forward oligo TATIGTAGGGGGGTAAGC TACITAT TATIGTACCTCAGTATAC AAAAT TATIGTGCATGTGTTTGGA CTGT	of sgRNA Reverse oligo AAACATHGTAGCTTAACCCC CCTAC AAACATHTTGTATACTGAGG GTAAC AAACACAGGTCAAACACATG CACT
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin80 PF16 Diagnostic PCR primers for g Gene name	Cene ID PY17X_0716700 PY17X_0204100 PY17X_0919000 pene knockout Gene ID	Gene size (bp) / deleded gene size (bp) 1904/1904 5137/1184 1809/1809 P9	Left homo Forward primer CGGGTACCCCATACACGA GGAAATACTA CGGGGTACCCCGGTTGTGC ATTTATTATT CCCAAGCTTACGGTTTCTAA AGTAATAATATCAC P10	logous arm Reverse primer CATGCCATGCTITGTGTATT TTATITITGTCG CATGCCATGCATTTGATCT TTACTACAGTCA TTATTACAGTCA P11	Right home Forward primer CCGCTCGAGACTITATGTCATT TITTGAGGT CCGCTCGAGACAGAACAAG CCGCTCGAGAACAAGAGAA TAATAACAAGT P12	Nogous arm Reverse primer CCGGAATICGATCGATGAA GACAAACAA CCGGAATICCTITCCTTCA TICATTICTIC GGCCTTAACCTCGCAATIC CTCCTTTICC P13	Target site Forward oligo TATGTAGGGGGGTAAGC TACTAT TATTGTTACCCTCAGTATAC AAAAT TATTGGTACGCATGTGTTTGGA CTGT P14	of sgRNA Reverse oligo AAACATAGTAGCTFAACCCC CCTAC AAACATTITIGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru- Ropm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm1	Citing gene knockout plasmids Gene ID PY17X_0716700 PY17X_0204100 PY17X_0019000 gene knockout Gene ID PY17X_0716700	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG	Left homo Forward primer CGGGGTACCCGATACACGA GGAATACTA CGGGGTACCCCGGTTGTGC ATTTATTATT CCCCAAGCTTACGGTTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGGC	Iogous arm Reverse primer CATGCCATGCTTGTGTATT ITATITTGGTCG CATGCCATGCATTTGATCT ITACTATATT CATGCCATGCATTTTGATCT P11 CGACGAAAAATAAAATAAA	Right home Forward primer CCGC/CGA/GA/GA/GA/GA/GA/ CCGC/CGA/GA/GA/GA/GA/ TAATGA/CA/GT P12 CGT/AATTTCAAAAATGAAGA	Nogous arm Reverse primer CCGGMATICCTTGCAATGAA GACAAACAA CCGGMATICCTTICTCTTCA CGGGATTAACGCTGCCAATTC CTCCTTTTGC P13 CCGGGACACTCTAAGTACTG	Target site Forward oligo TATTGTAGGGGGGTTAAGC TATTGTTACCCTCAGTATAC AAAAT TATTAGTGCATGGATGGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATTATTACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b	Cene ID PY17X_0716700 PY17X_0204100 PY17X_0919000 ene Knockout Gene ID PY17X_0716700 PY17X_0716700 PY17X_0716700 PY17X_0716700	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GUTLACIC CETTER COACE	Left homo Forward primer CGGGGTOACCCGATACACGA GGAATACTA CGGGGTOACCCGGGTGTGGC ATTTATTATT CCCCAAGCTIACGGTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGGC CGTGCCCATTAAGTTGTTCTG	logous am Reverse primer CATGCCATGCATTGTGTATT TIATTTTCGTCG CATGCCATGCATGCATTGTGGC CATGCCATGCATGTTGATCT TIACTATATT CATGCCATGCATGTTTTTTTTTTTTTTTTATTAACAGTCA P11 CGACGAAAAATAAAATACACC AAA CGACGAAAAATAAAAATACACC CAACCATGTGGATCTACTT	Right home Forward primer CCCCTCGARGACAGACTATT TTTTGAGGT CCCCTCGAGACAGAACAAGACAAC TTAATGACAAG CCCCTCGAGACAAGAACAAGAA TAATAACAAGT P12 CGTAATTTCAAAAATGAAGA TATGATATTTTCAAAAATGAAGA	Reverse primer CoGAAATCATGACATGAA GACAAACAA COGGAATCCTTCCATGAA COGGATTCCTTTCCTTCA GGCCTTAACCTCCGCAATTC CTCCTTTTGC P13 GCGGAACCATCTAACATCT G CGAGCGAAACTATAACATCT	Target site Forward oligo TATTGTAGGGGGGTAAGC TACTAT TATTGTACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT C GATTCTGTATGTTGAGGGG	of sgRNA Reverse oligo AAACATAGTAGCTAACCCC CCTAC AAACATUTTGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b	Gene ID PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0716700 PY17X_0716700 PY17X_0204100	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTITACTCTCTTGTCCACAT	Left homo Forward primer CGGGGTACCCCB GGAGATACTA GGAGATACTA CGGGCTACCCCGGTTGTGC ATTTATTATT CGCCARGCTTACGGTTTCTAA AGTAAAAGCTAAAAAGGC CGTCCATTAAGTTGTTCTG T	Iogous arm Reverse primer CATGCCATGCHTIGTGATT TIATTITIGATC CATGCCATGCATCATTIGATCT TTACTATATT CATGCCATGCATGCATTITITITT TTACTATATT CATGCCATGCATGCATT CATGCCATGCATGCATCACTC P11 CGACGAAAAATAAAATACAC AAA CTATATATGTGGATCTACTT G	Відін Номо Гогмат дірімог Сосстісокара дірімог Сосстісокаралара Сосстісокаралара Сосстісокаралара Сосстісокаралара Сосстісокаралара Сосстісокаралара Рі2 Соталітісокаралара Гаталагітітарасара Гаталагітітарасара	Nogous arm Reverse primer CGGAATCOTTICAATGAA GACAAACAA CGGAAACAA CGGGATTAACCTCGCTATTCCTTCA ITCATTTCTTG GGCCTTAACCTCGCAATTC CTGCTTTTGC P13 CCGACACTCTAAGTACTG G CGATGCCAAACTATAACATCT	Target site Forward ligg TATTETAGGGGGTTAAGC TATTATAGCCCCAGTATAGC AMAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT GATTCTGTATGTTGAGGGG T	of sgRNA Reverse oligo AAACATAGTAGCTHAACCCC CCTAC AAACATHTIGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo equences for constru Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 ene knockout Gene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0919000	Gene size (bp) / deleded gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTITACTCTTGTCCACAT CAGATTATTGTCATATCATC	Left homo Forward primer CGGGGTACCCGATACACGA GGAATACTA CGGGGTACCCGGTTGCGG ATTTATATT CCCCAAGCTTACGGTTTCTA AGTAATAATATATCAC P10 GGTTAAAAGCTAAAAAGGC C CTGTCCCATTAAAGTGTTCTG T AAAGCACAATAATGTATTGG	Iogous arm Reverse primar CATGCCATGCTTIGTGTATT ITATTITTCGTCC CATGCCATGCATTIGTATT ITACTANICSATTIGTATT ITACTANICSATTIGTATT CATGCCATGCTTTTTTTTT ITTATTAGCAGTCA P11 CGACGAAAAATAAAATACAC AA CTATTATTGTGGATCTACTT G CCTCCCCCACTTTTAGTACTG	Right home Forward primer CCGCICGACAGACAGAACAAC CCGCICGACACAGAACAACAAC TIAATGACAG CCGCICGACAACAAGAACAAC TAATAACAAGT P12 CGTAATTTCAAAAATGAAGA TATGATATTTCGACAGGT G	Nogous arm Reverse primer CGGAAT/CGTTCCATGAA GACAAACAA CGGAATACCAT CGGATTACCTTGCTTCAT CGGCTTAACGTCGCAATC CTGCTTTGC P13 CGGAGACACTCTAAGTACTG G CGATGCAAACTATAACATCT GCAACAGTAATACTAGCGA A	Target site Forward oligo TATTGTAGGGGGGTTAAGC TACTAT TATTGTACCCTCAGTATAC AMAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACCAAAGGCAAACCCT C GATTCTGTATGTTGAGGGG T AAGCTTCAAGATCCGTAACT	of sgRNA Reverse oligo AAACATAGTAGCCCC CCTAC AAACATATTACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru- Nopm1 kinesin8b PF16 Oligo sequences for constru-	Cene iD Gene iD PY17X_0716700 PY17X_0204100 PY17X_0019000 ene Knockout Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 Cting RRM deletion plasmids	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCCTTGTCCACAT CAGATTATTGTCATATCATC	Left homo Forward primer CGGGGTACCCGATIACACGA GGAATACTA CGGGGTACCCCGGTTGTGC ATTTATTATT CCCCAGGTTACGGTTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGGC C CGTCCATTAAGTTGTTCTG T AAAGCACAATAATGTATTGG	Iogous am Reverse primer CATGCCATGCATTGTGTGT TTATTTTGCTG CATGCCATGCATTGTGG CATGCCATGCATTGTGATCT TTACTATATT CATGCCATGCTTTTTTTTTT TTACTAACAGTCA P11 CGACGAAAAATAAAATACAC AAA CGACGAAAAATAAAAATACAC CAAC CTATATATGTGGATCTACTT G CCTCCCCACTTTTAGTACTG	Right home Forward primer CCGCTCGACAGATTATGTCATT TTTTGAGGT CCGCTCGACACAGACAAGACAAC TTAATGACAAG CCGCTCGACAAGAACAAGAA TAATAACAAGT P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGACAAGGT CGACATGACTTGTACAGGT G	Nogous arm Reverse primer CCGGAATCCATTGAATGAA GACAAACAA CCGGAATTCCTTTCCTTCA TCGATTTCTTG GGGCTTAACGCTGCCAATTC CTCCTTTTGC P13 GCGGACACTCTAAGTACTG G GCGACCAGCAAACTATAACATCT GCAACAGTAATACTAGCGAA A	Target site Forward oligo TATTGTAGGGGGGTTAACC TACTAT TATTGTTACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT GATTCTGTATGTTGAGGGGG T AAGCTTCAAGATCCGTAACT	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATTGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru	Gene ID PY17X_0716700 PY17X_0016700 PY17X_0019000 gene ID PY17X_0019000 PY17X_0716700 PY17X_0204100 PY17X_00190000 cting RRM deletion plasmids Homolog	Gene size (bp) deleted gene size (bp) 1904/1904 5137/1184 1809/1809 RAGCGAAATAAATGAAACG G GTITACTCTCTTGTCCACAT CAGATATATTGTCATATCATC GOUSS arm 1900	Left homo Forward primer CGGGGTACCCCG GGGGTACCCCG GGGGTACCCCG GGGGTACCCCGGTTGTGC ATTTATTATT CCCCANCOLLAGGTTTCTAA AGTAAAATATATCAC P10 GGTTAAAAAGCTAAAAAGGC CGTTCCATTAAGTTGTTCTG AAAGCACAATAATGTATTGG	logous arm Reverse primer CATGCCATIGGTTI CATGCCATIGGTGT CATGCCATIGCATTITIGATCT TITACTATATT CATGCCATGCATGTTIGATCT TITACTATATT CATGCCATGCATGTTIGATCT CATGCCATGCATGTACACAC P11 CGACGAAAAATAAAATACAC AAAA CTATATATGTGGATCTACTT CCTCCCCCACTITTIAGTACTG Mutation	Right home Forward primer CCGCTCGARTITATGTCATT TITTGAGGT CCGCTCACAGAGAGAACAAC TAGATACAAGT P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGGCGTCTC CGACATGACTTGTACAGGT G primers	Nogous arm Reverse primer CGGAATCOTTICCATGAA GACAAACAA CGGAAACAA CGGGATAACCTCGCTACTTCA ITCATTICTTC GGGCTTAACCTCGCAATTC CTCCTTTTGC P13 CGGGACACTCTAAGTACTG G CGAACAGTAATACTAGCAA A	Target site Forward oligo TATTETRGGGGGGTTAAGE TACTAT TATTGTACCCTCAGTATAGE TACTAT TATTAGTGACCTCAGTATAGE ANAAT P14 GGTTACAAAAGGCAAACCCT GATTCTGTATGTTGAGGGG TGTTGTAGTGTGAGGGGG Target site Target site	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATTHTGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru- Strain	Gene ID PY17X_0716700 PY17X_0204100 PY17X_0019000 gene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0319000 cting RRM deletion plasmids Homolog Forward primer	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AGGGAAATAAATGAAAGG GITTACTCTCTTGTCCACAT CAGATTATTGTCATATCATC CAGATTATTGTCATATCATC	Left homo Forward primer CGGGGTACCCGATACACGA GGAATACTA CGGGGTACCCCGATTGCTCA AGTAATAATATATCAC P10 GGTTAAAAGCTACAAAAGGC C CGCCACCTACGGTTGTCGT T AAAGCACAATAATGTGTTCG T AAAGCACAATAATGTATTGG	logous arm Reverse primer CATGCCATCGTTGTGTATT TIATTITGGTCG CATGCCATCGATTGTGATCT TIACTATATT CATGCCATCGATTGTTTTTTTT TATGTCATT CATGCCATGGATCACAT CTATGTCATGCATCGATCT G CCTCCCCCACTTTTAGTACTG Mutation d primer	Right home Forward primer CGCCICGARGACAGAACAAC GCCCICGACAGAACAGAACAAC CGCCICGACAGAACAAGAACAAC TTAATGGACAG P12 CGTAATTTCAAAAATGAAGA TATGAAATTAACAAGA TATGAAATTAACAAGA TATGAAATTAACAAGA TATGAAATTAACAAGA TATGAAATTAACAAGA TATGAAATTAACAAGA TATGAAATTACAAGA TATGAATTATTAGAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAATTATACAAGA TATGAAATTACAAGA TATGAAATTACAAGA TATGAAATTACAAGA	Nogous arm Reverse primer CGGAATCOTTICAATGAA CGGAATCCTTTCTTCATGAA CGGGATTACGTTGCTTCA TCATTICTTG GGGCTTAAGCTGGCAATTC CTGCTTTTGC P13 GCGGACACTCTAAGTACTG GCGACACGTAATACTAGCGA A e primer	Target site Forward site TATTGTAGGGGGTTAAGC TACTAT TATTGTAGGGGGTTAAGC TACTAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT C GATTCTGTATGTTGAGGGG T AAGCTTCAAGATCCGTAACT Target site Forward oligo	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATHTIGTATACTGAGG GTAAC AAACACAGTCCAAACACATG CACT
PF16 Oligo sequences for constru- Ropm1 kinesin8b PF16 Oligo sequences for constru- kinesin8b PF16 Oligo sequences for constru- Strain Δrm1	Concent plasmids Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0019000 gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 Cting RRM deletion plasmids Hormolog Forward primer COGCICCAGCCAGAGACGAA GTTTATCTAA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 Pg AAGCGAAATAAATGAAACG G GTTTACTCTTGTCACAT CAGATTATTGTCATATCATC Gous arm Reverse primer GGCCTTAACGGACATATAC ATATTCTCCT	Left homo Forward primer CGGGTACCCGATIACCAG GGAATACTA GGAATACTA CGGGGTACCCGGTTGCGGTTGCGC ATTTATTATT CCCCAAGCTTACGGTTCGCA P10 GGTTAAAAGCTAAAAAGCC CTGTCCATTAAGTTGTTCG AAAGCACAATAATGTATTGG Forwar GTAACTCCAAAAAATATAAATG	Iogous am Reverse primer CATGCCATGCATTGTGTATT TTATTTTGCTG CATGCCATGCATTGTGG CATGCCATGCATTGTGATCT TTACTAACAGTCA P11 CATGCCATGCATTGTTTTTTTTT TTACTAACAGTCA P11 CGCCCACGATAAAATAACACC AAA CGCCCACTTTGTGAACTCACTT G CCTCCCCACTTTTAGTAACTG Mutation d primer AACCATTTGAGGAACACAAT	Right home Forward primer CCGCTCGACAGATTATGTCATT TITTGAGGT CCGCTCGACACAGAACAAC TAATGACAG P12 CGTAATTICAAAAATGAAGA TATGATATTITTGGCGTCTC CGACATGACTTGTACAGGT G primers Revers ATCTGAAGGTGTCGTATTGT TAT	Nogous arm Reverse primer CCGGAATCCGTTCCAATGAA GACAAACAA CCGGAATCCTTCCTTCCTTCA CGGCTTAACCTGCCAATCC CTCCTTTTGC P13 GCGGACACCTCTAAGTACTG G GCAGCCAAACTATAACATCT GCAACAGTAATACTAGCGA A e primer GTTCCTCAAATGGTTCATTTA	Target site Forward oligo TATTGTAGGGGGGTTAAGC TATTGTACCCTCAGTATAC AMAT TATTGTACCCTCAGTATAC AMAT P14 GGTTACAAAGGCAAACCCT C GATTCTGTATGTTGAGGGGG T AAGCTTCAAGATCCGTAACT Target site Forward oligo TATTATTAGAAAAATAAAAAT TGT	of sgRNA Reverse oligo AAACATAGTAGCGTTAACCCC CCTAC CCTAC AAACATAGTAACTAGTAACCCC GTAAC GTAAC AAACACAGTCAAACAACACAG rof sgRNA Reverse oligo AAACACAATTITTATTITCT AAT
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2	Cene ID PY17X_0716700 PY17X_0204100 PY17X_00190000 gene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_00191000 PY17X_00919000 Ctting RRM deletion plasmids Homolog Forward primer COGCICOACGAGAGAGAAA GOGCICAACGAGAGAAGAAA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCCAAATAAATGAAACG G GTTTACTCTCTTGTCCACAT CAGATTATTGTATATCATCC GGGCTTAAGGGACATATAC ATATCTCCT GGCTTAAGGGACATATAC GGCTTAAGTGTTATAATCC	Left homo Forward primer CGGGTACACCBA GGAATACTA GGAGATACTA GGGGTAACCCGGTTGTGC ATTLATAT CGGGTGAACCCGGTTGTGC AGTAAAAAGCTAAAAAGGC CGT GTTAAAAAGCTAAAAAGGC CT GTCAATAAAGCTAAAAAGGC CT GTCAATAAAGCACAATAATGTATTGG Forwar GTAACTCAAAAAATATAAAGT	logous arm Reverse primer CATGCCATGCATTIGTGATTI TIATTITTGCG CATGCCATGCATTIGTGATCT TIACTATAT TTACTATAT CATGCCATGCATTITTGATCA TTACTATAT CATGCCATGCATTITTTTTTTTTTTTTTTTTTTTTTTTTT	Right home Forward primer CGCCTCCAGTTTATGTCATT TTTTGAGGT CCGCTCCAGAGACAAGGAACAAC CCGCTCCAGAACAAGGAAC CCGCTCCAGAACAAGGAAC P12 CGTAATTTCAAAAATGAAGA P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGGCGTCTC CGACATGACTTGTACAGGT G nprimers Revers ATCTGAGGGTGCCTTATGT TAT TATGCTTCTAGGTTCGTGCTGCT	Nogous arm Reverse primer CCGGAATCGTTCCAATGAA GACAAACAA CCGGAATTCCTTTCCTTCA TTCATTTCTTG GGCCTTAACCTGCCAATTC CTCCTTTTGC P13 GCGGACACTCTAAGTACTG G CGATCCCAACTCTAAGTACTG G CGATCCCAACTATAACCATCT GCAACAGTAATACTAGCGA A e primer GTTCCTCAAATGGTTCATTTA TTTCTTTGAATATCTGAG	Target site Forward oligo TATTETAGGGGGGTTAAGC TACTAT TATTGTTACCCTCAGTATACC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAAGGCAAACCCT GATTCTGTATGTTGAGGGG T AAGCTTCAAGATCCGTAACT Target site Forward oligo TATTATTGAAAAAATAAAAAT TATTATTGAAAAAATAAAAAT	of sgRNA Reverse oligo AAACATAGTAGGTAACCCC CCTAC AAACATATTAGTAACTGAGG GTAAC AAACACATAGTACAACACATG CACT of sgRNA Reverse oligo AAACACATTITTATGGGTCCTTTCC AAAC
PF16 Oligo sequences for constru- Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru- Strain Arrm1 Arrm1	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0019000 gene ID PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0019000 cting RM deletion plasmids Gene ID PY17X_0019000 cting RM deletion plasmids GOC11C6ACGAGGACGAGGAGAGGAGA ATTC7AACGAGAGA COCC1C6ACGACTTGGAGGAGA ATTC2ACAAA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTITACTCCTTIGTCACAAT CAGATTATTGTCATATCATCC GGCTTAACGGACATATAC ATATTCTCCT GGCCTTAACGGACATATACATCC GGGCTTAACTGTTATAATCC GGGCTTAACTGTTATAATCC GGGTTGTTGC	Left homo Forward primer CGGGCTACCCCGATACACGA GGAAATACTA CGGGCTACCCCGATTGCTGC AGTTAATACCCCGATTGTCG AGTTAAAAGCTAAAAAGGC CGGTCAAAAAGCTAAAAAGGC CGGTCAATAAAAGCTAAAAAGGC CG CGTCCATTAAGTTGTTCTG T AAAGCACAATAATAATATGATTGG Forwar GTAACTCAAAAAAATATAAATG ACG CGACACCCTCAGAATATCAA	logous arm Reverse primer CATGCCATGCATGCATGTIGTGATT TIATTITOGTCG CATGCCATGCATGCATTTGATCT TTACTATAT CATGCCATGC	Right home Forward primer CCGCTCGAGACAGAACAAC CCGCTCGAGACAGAACAAC CCGCTCGAGACAGAACAAC TAATAACAAGAT P12 CGTAATTTCAAAAATGAAGA TAATAACAAGT P12 CGTAATTTCGACAAG P12 CGTAATTTCGACAAGGAC CGACATGACTTGTACAGGT G Revers ACTGAAGGGTGTCCTATTGT TAT TGGCTTCTTAGGTCGGCT	Nogous arm Reverse primer CGGAATICCTTCAATGAA GACAAACAA CGGAATACCTTCCTTCAT CGGATTACTTCTTCC P13 GCGGACAATCTAAGTACTG GCGACAACTATAACATCT GCAAGCAAACTATAACATCT GCAAGCAAACTATAACATCT GCAAGCAAGTAATACTAGCGA A primer gTTCCTCAAATGGTTCATTTA TTTCTTTGGATATCTGAG	Target site Forward oligo TATTETAGGAGAAAGGAACC TATTATAGGAAAAGGAAAGGAACCTG TATTATAGGCATGTGTTTGGA CTGT P14 GC	of sgRNA Reverse oligo AAACATAGTAGGTAACCCC CCTAC AAACATAGTAGGTTAACCGACG GTAAC AAACACAGTCCAAACACATG CACT of sgRNA Reverse oligo AAACCACATITIATITIATITICT AAACTICACATITITIATITICT AAACTICACATITITIATITICT
PF16 Oligo sequences for constru Rbpm 1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm 1 kinesin8b PF16 Oligo sequences for constru Strain Δrm1 Δrm2 Diagnostic PCR primers for for	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0716700 PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_020400 Forward primer CGGCTCGACGCAGAACGAA CTTCATCAGCATTGGAGGA ATTCCCAAGAATGAGGA RTM deletion	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCACACT CAGATTATTGTCATATCATAC Gott TAACGGACATATACA TATTCTCCT GGGCTTAACGGACATATACA TATTCTCCT GGGCTTAACGGACATATACA GGGCTTAACGGACATATACA ATATCTCCT GGGCTTAACGGACATGTATATACA	Left homo Forward primer CGGGGTACCCGATACACGA GGAAATACTA GGAGATACTA GGAGATACTA CGCCAAGCTIACGGTTGTGC CCCAAGCTIACGGTTGTGA AGTAATAATATACAC P10 GGTTAAAAGCTAAAAAGGC CG GGCCACCATAAAGTGTGTTCTG T AAAGCACAATAATGTATTGG Forwar GTAACTCAAAAAATATAAATCA CG CGACCCCCAAGATATTCAA	Iogous arm Reverse primer CATGCCATGCATGCATGTITGTGTATT TTATTTTOTOCCC TATTTTOTOCCC TTATTTTOTOCCC TTATTTATTTTAT	Right home Forward primer CCGCICGACRAGACAGAACAAC CCGCICGACAGACAGAACAAC CCGCICGACACAAGAACAAC TIAATGACAAG P12 CGTAATTICAAAAATGAAGA TATAACAAGGT CGCACATGACTIGTACAGGT a primers Revers ATCTGAGAGGTGTCCTATGT TAT TIGGCTTCTTAGGTTCGGCT	Nogous arm Reverse primer CGGAAT/CGTTCCATGAA GACAAACAA CGGAAT/CCTTCCTTCATGA GGGCTTAACGCTGGCAATIC CTGCTTTIGC P13 GCGGACACCTCTAAGTACTG G GGGCGAACTATAACAATCT GCAAGACAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA	Target site Forward Starget site Forward Starget Starg	of sgRNA Reverse oligo AAACATAGTAGCCCC CCTAC CCTAC AAACATATTACTGAGG GTAAC AAACACAGTCCAAACACAGTG CACT of sgRNA Reverse oligo AAACACAATITITATITICT AAACTITATGGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Ropm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm1 kinesin8b PF16 Oligo sequences for constru Strain Δrm1 Δrm2 Diagnostic PCR primers for for Strain	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0019000 Cting RRM deletion plasmids Homolog COCCITCASCGAGAACGAA COCCITCASCGAGAACGAA ATTCOTAS OCCCITCASCAGAACGAA RRM deletion RM deletion P1	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCCTTGTCCAAT CAGATTATTGTCATATCAATC GGGCTTAACGGACATATAC ATATTCFCCT GGGCTTAACGGACATATAC ATATTCFCCT GGGCTTAACGGACATATAC GGGCTTAACGGACATATACC GGCTTGTCC	Left homo Forward primer CGGGTACCCGATIACCAGA GGAAATACTA CGGGGTACCCCGATIACCAGA GGAAATACTA CCCAAGCTTACCGATTGTGC ATTTATTATT CCCCAAGCTTACGGTTTCGA P10 GGTTAAAAGCTAAAAAGCC CTGTCCATTAAGTTGTTCTG T AAAGCAACAATAATGTATTGG Forwar GTAACTCAAAAAATATAAATG ACG CGACACCCTCAAGATATTCAA	Iogous am Reverse primer CATGCCATGCATTGTGTGT TIATTTTGCTG CATGCCATGCATTGTGGC CATGCCATGCATTGTGATCT TIACTATAT CATGCCATGCATTTTGATCT TIACTATAT CATGCCATGCATGTTTGATCA P11 CATGCCATGCATGATCTACTT G CCTCCCCACTTTTAGTACATCT G CCTCCCCACTTTTAGTACTG Mutation d primer AGCATTTGAGGAACACAAT AGAAAAGCCGAACCTAAG P4	Right home CGC:TOCAGTTITATGTCATT TTTTGAGGT CGC:TOCAGAGA CGC:TOCAGAGA CGC:TOCAGAACAAGGAA CGC:TOCAGAACAAGGAA P12 CGTAATTTCAAAAATGAAGA P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGGCGTCTC CGACATGACTTGTACAGGT G n primers ACCTGAGGGTGTCATTGT TAT TAGGTTCTTAGGTTCGGCT	Nogous arm Reverse primer CCGGAATICCTTTCAATGAA GACAAACAA CCGGAATICCTTTCTTTCTTG GCGCTTAACGCTGCCAATIC CTTCTTTGC P13 GCGGACTAACCTGCAACTATAACTACTG G CCGATCCAAACTATAACAACTC GCAACAACTAATAACTAGCGA a primer GTTCCTCAAATGGTTCATTTA TTTCTTTGGAATATCTGAG P6	Target site Forward oligo TATTCTAAGGGGGGTTAAGC TACTATGTAAGCGGGGGTTAAGC TACTATGTAAGCCTCAGTATAGC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGGCAAACCCT GATTCTGATGTTGAGGGG TATTGTAAGGAAAGCCCT Target site Forward oligo TATTGTAAGGAAAGAACCCC CATAAA	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC CCTAC AAACATAGTACGTTAACCGAGG GTAAC AAACACAGTCAAAACACATG AAACACAGTCAAAACACAGT Reverse oligo AAACACAGTITITATTITCT AAACTITATGGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Ropm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm1 kinesin8b PF16 Oligo sequences for constru Strain Arrm1 Arrm1 Diagnostic PCR primers for f Strain Arrm1	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_00190000 cting RRM deletion plasmids Gene CCAGCAGAGAGAA CCGC1CGACGAGAGAGAA CCGC1CGACGAGAGAGAA CCGC1CGACGAGAGAGAA RRM deletion PI CAACAATTGTGAAAAACAGAGA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTIACTCTCTTGTCACAAT CAGATTATTGTCATATCATC GGCTTAACGGACATATAC GGCTTAACGGACATATAC GGGCTTAAGGACATATAC GGGCTTAAGGACATATAC GGGCTTAAGGACATATAC GGGCTTAAGGACATATAC GGGCTTAATGTTATAATC GGGCTTAAGTGTTATAATC GGGCTTAATGTTATCATCC P2 AGGGGTCGTATTGTGTTCC	Left homo Forward primer CGGGCTACCCCGCATACCCAG GGAAATACTA GGAGATACTA GGGGCTACCCCGGTTGTGC ATITATATT CGCCAAGCTTACGGTTTCTAA AGTAAAAGCTAAAAAGGC P10 GGTTAAAAAGCTAAAAAGGC CTGTCCAATAAGTGTTCTG AAAGCACAATAATATATAATG CGACACCCTCAAGAATATAAATG ACG P3 CTTCCAACAGGAATTATGAA	logous arm Reverse primer CATGCCATGCATTGTGTGT TIATTTTGTCG CATGCCATGCATGCATTGTGGTCT TTACTATATT CATGCCATGCATGCATTTTGATCT TTACTATATT CATGCCATGCATGCATTTTTTTTTTTTTTTTTTTTTTTT	Right home Forward primer CGCTICGARGACAGAACAAC TTATTGTTTTTTTGGAGAG CGCTICGAGACAGAACAAC TTATGGACAG CACTICGACAGACAAGAACAAC TTATGCAGG P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGGCGTCC CGACATGACAT	Nogous arm Reverse primer CGGAATICCTTCAATGAA GACAAACAA CGGAATACCTTCCTTCAT CGGACTTAAGTCCTTTCTTCA GGGCTTAAGCTCGCAATTC CTCCTTTTCC P13 GCGGACAACTCTAAGTACTG GCACAACTAATAACATCT GCAACAACTAATAACATCT GCAACAACTAATAACATCT GCAACAACTAATAACATCT GCAACAACTAATAACATCT GCACCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGATGACATGG	Target site Forward oligo TATTCTAGGCGGGTTAAGC TACTAT TAGTAT TACTAT TACTAT TATTAGTGACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTCCAAAAGGCAAACCCT GGATTCTGTATGTTAGGAGAAGCCCT GATCTGTATGTTAGAAAAATAAAT TGT TGTTATAGAAAAATAAAAAAT TGT TG	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CATAC AAACATAGTAGGTTAACCCC GTAAC GTAAC AAACATAGGTCCAAACACATG CACT of sgRNA Reverse oligo AAACATATTGTTATTGTTCT AAT AAACATTATTGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Ropm 1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm 1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm1 Arm2	Cene ID Gene ID PY17X_0716700 PY17X_0204100 PY17X_0019000 gene knockout Gene ID PY17X_0716700 PY17X_0706700 PY17X_0204100 PY17X_0204100 PY17X_0019000 cting RM deletion plasmids CCCCTCCASCCGAGAACGAA CCCCTCCASCCGAGAACGAA CCCCTCCASCCGAGAACGAA CCCCTCCASCCGAGAACGAA ATTCCAGAAACAAGGAA RM deletion P1 CCAACAATTGTGAAAACAGAGA CATGCGAGAACACAGAGA CATGCGACACTATCTGAACGAGA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAATGAAACG G GTTTACTCTCTIGTCACAT CAGATTATTGTCATATCATAC GGGCTTAAGGGACATATACATATAC GGGCTTAAGGGACATATACATATAC GGGCTTAAGGGACATATACATATAC AGGGTGTCGTATGTGTTATAATCC GTTAACTGTCTTATTGTGTTC AGGGTGTCGATATGTGTTATATACC AGGGTGTCGATATGTGTTC AGGGTGTCGATATGATATACATGTGTC CAGGTGTGCGATATATACATGTGTTC	Left homo Forward primer CGGGGTACCCGATIACCGA GGAGATACTA GGAGATACTA GGGGGTACCCGGTTGCGCA CGCCATGCTTACGGTTTGTA AGTAATATATCAC P10 GGTTAAAAGCTAAAAAGGC CGCCCCCCATTAAGTTGTTGTG T AAAGCACAATAATATATAGTATTGG Forwar GTAACTCAAAAAATATATAATG AGG CGAACCCCTCAGATATTCAA P3 CTTCAACAGGAATTATTGAA	Iogous arm Reverse primer CATGCCATGCATGCATTGTIGTATT TIATTTTGGTCG CATGCCATGCATGCATTGTGCG CATGCCATGC	Right home Forward primer CGCCICGAGACAGAACAAC CGCCICGAGACAGAACAAC CGCCICGAGACAGAACAAC TTAATGGACAG P12 CGCACICGAGACAAGAACAAC TAATAACAAGT P12 CGTAATTTCAAAAATGAAGA TATGAAGATTTTCAGAGACTTGTACAGGT G n primers Revers ATCTGAAGGGTGTCGTATTGT TT TGGCTTCTTAGGTTCGAC P5 TTTCATTGGAGGAATTCACAC	Nogous arm Reverse primer CGGAATCOTTCCATGAA GACAAACAA CGGGAATTCCTTTCTTCATGAA GACGAACAA CGGGATTACGTTGCTTCATTCA TTCATTTCTTG P13 GCGGACACTCTAAGTACTG G GCGACACTCTAAGTACTG GCACACAGTAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGATGACAATGG	Target site Forward Starget site Forward Starget Starg	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATTATTGTATACTGAGG GTAAC AAACACAGTCCAAACACAGG CACT of sgRNA Reverse oligo AAACACAGATITITATTTTCT AAACTITATGGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Ropm1 kinesin8b PF16 Oligo sequences for constru Ropm1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm1 Arm2	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0716700 PY17X_0716700 PY17X_0019000 gene ID PY17X_0019000 Edge ID PY17X_00191000 Ctrigg RRM deletion plasmids Forward primer CCCCCTASCGAGAACGAA ATTCCACACAT ATTCCACACAA RRM deletion P1 CAACAATTGTGAAAACAGAGA GTTGGCACATATGGAAAACAGAGA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG GITTACTCTTGTCCACAT CAGATTATTGTCATATCATCC GOUS arm Reverse primer GGCCTTAACGACCATATAC ATATTCTCCT GGGCTTAAC GGTTAATAATC GGGCTTAAC GGTTATAACAC P2 AGGGCTGTATTGTATCACAC ATGAGCCAATACACACACAC	Left homo Forward primer CGGGTACCGATACACGA GGAAATACTA GGAGATACTA CGGGGTACCGGATACACGA GGAGATACTA AGTAATAATATCAC P10 GGTTAAAGCTAAAAAGCC CGCCACGCTTACGGTTCTGA T AAAGCACAATAATGTATTGG GTAACTCCAATAAAGTTGTATTGG GTAACTCCAAAAAATATAAATCAC Forwar GTAACTCCAAAAAATATAAAATCAC P3 CTCCAACAGGAATATGTATTGA AATGAACGGGAAACGGGAACGGGAACGGGAACGGGAACGGGAACGGGAACGGGGGG	Iogous am Reverse primer CATGCCATGCATTGTGTGATT TTATTTTGCAG CATGCCATGCATTGTGG CATGCCATGCATGTTGATCT TTACTATATT CATGCCATGCATGTTTTTTTTTTTTACTACAG P11 CATGCCATGCATGAAAAATAAAACAC CACGAAAAAATAAAAATACAC AAA CTATATATGTGGATCTACTT G CCTCCCCACTTTTAGTACTG Mutation d primer AGAAAAGCCGAACCTAAG P4 CTCCTCATTCCACTATTATT GTTCCAATGAAGACAAACAA	Right home Forward primer CCGCTCGACAGACAGACAAGACAAC CCGCTCGACAGACAAGACA	Negous arm Reverse primer CCGGAATCCGTTCCAATGAA CCGGAATCCTTTCCATGA CCGGAATCCTTTCTTCC CCGCTTACCTGCA CCGGATTCCTTTCCT	Target site Forward oligo TATIC TAGGGGGGTTAAGC TACTAT TAGGGGGGGTTAAGC TACTATGTTACCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAGGGCAAACCCT C GATCTGTATGTTGAGGGG TATATAGAAAAAT TGTTATGTAAGGGGAAAGGACC CATAAA	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATAGTAGGTTAACCCCG GTAAC AAACATAGTAGTAACACAGG GTAAC AAACACAGGTCAAACACAGG CACT of sgRNA Reverse oligo AAACACAGATITTATTTTCT AAACTITTAGGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Ropm1 kinesin80 PF16 Diagnostic PCR primers for g Gene name Ropm1 kinesin80 PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm2 Oligo sequences for constru	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0019000 pene knockout Gene ID PY17X_0019000 pene knockout Gene ID PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 Citing RRM deletion plasmids Forward primer CCGC1CGACGAGAGAAA CCGC1CGACGATGGAGGA ATTCCAACAAA CCGC1CGACACATTGGAGGA RM deletion P1 CAACAATTGTGAAAAACAGAG GTTGGCAACATATCTGAAACAGAGA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCCAAATAAATGAAACG G GTTTACTCTTTGTCACACAT CAGATTATTGTATATCCT GGCTTAACGGACATATAC ATATTCTCCT GGGCTTAACGGACATATAC GGGCTTAACGGACATATAC GGGCTTAACGGACATATAC GGGTTGTAGC P2 AGGGCTAACGTATACATACACAC C AGGGTGTCGTATTACTATCGTC C Cadattatatatatatatatatatatatatatatatatat	Left homo Forward primer CGGGGTACCCOGATIACCAG GGAAATACTA GGAGATACTA GGGGTAACCCCGGTTGTGCA ATTATATT CGGGGTAACCCGGTTGTGCA AGTAAAAGCTAAAAAGCC P10 GGTTAAAAGCCCAATAATGTGTTCTG T AAAGCACCAATAATGTGTTCTG T AAAGCACCAATAATGTATTGG GTAACTCCAAAAAATATAAATCAA Forwar GTAACTCCAAAAAATATAAATCAA FOrwar GTAACTCCAAAAAATATAAATCAA FORWAR GTAACAGGAATATCAA	logous arm Reverse primer CATGCCATGCATIGTGTGT TTATTTTGCAGCATTGGTGG CATGCCATGCATTGTGG CATGCCATGC	Right home Forward primer CGCTICAGAGAAGAACAAC TTATTTTTTTTGAGGT CGCTICAGAGAAGAACAAC TTAATTATCAGAG P12 CGTAATTTCGAGAGAACAACGAC ACTAGACATATTTTGGCGTCC CGACATGACAT	Nogous arm Reverse primer CGGAATCOTTICAATGAA GACAAACAA CGGAATACCTTICCTTTAA GGGCTTAAGCTGGCAATTC CTGCTTTTTCC P13 GCGGACAACTATAACATCG GGCCTAAGCAACTATAACATCT GCAACAGTAATAACATCT GCAACAGTAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA ITTCTTTGAATATCTGAG P6 ATTTATATGAGATGACATGG CTAACTTCAACCATTTATC	Target site Forward oligo TATTCTAGGGGGGTTAAGC TACTAT TATTGTAGGGCGGGTTAAGC TACTAT TATTGTAGGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT GATTCTGTAGGTTGAGGGG T Target site Forward oligo TATTATGAAAGGAAAATAAAT TGT TGT TGT TGT T	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC CCTAC AAACATAGTAACTAGTAGGTCACCC GTAAC GTAAC AAACATAGTAGTACACATG AAACATAGTAGTACACATG Reverse oligo AAACATAGTAGTACTTCC CTTAC CTTAC
PF16 Oligo sequences for constru Rbpm1 kinesin8b PF16 Oligo sequences for constru kinesin8b PF16 Oligo sequences for constru Strain Arrm1 Arrm2 Diagnostic PCR primers for F Strain Arrm1 Arrm2 Oligo sequences for constru Oligo sequences for constru Cene name	Gene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0016000 Cting RRM deletion plasmids Homolog Forward primer COCCTCGACGACATGGAGGA ATTCCAACAA RRM deletion P1 CAACAATTGTGAAAACAGAG GTTGGCAACATATGTGAAGAG GTTGGCAACATATCTGAAGAG GTTGGCAACATATCTGAAGAG GTTGGCAACATATCTGAAGAG GTTGGCAACATATCTGAAGGA GTTGGCAACATATCTGAAGAGGA GTTGGCAACATATCTGAAGAGAGAGGA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTIGTCCACAT CAGATTATTGTCATATCATACC GOUS arm Reverse primer GGGCTTAACGGACATATAATCC GGGCTTAACGGACATATACATACC GGGCTTAACGGACATATACATATCC AGGGGTGTCGTATGTGTTATAATCC AGGGGTGTCGTATGTGTTC ATGAGCCAATACATACACACACA atton plasmids Tag	Left homo Forward primer CGGGGTACCCGCATACCACG GGGGATACCCC GGGGTACCCCGGTTGCCG ATTTATTATT CGCCAACCLTACGGTTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGGC CG GGTCAACTACAGTATTATTGG Forwar GTAACTCAAAAAAATATATATGA GG CGACCCCTCAGAATATCAAA GG P3 CTTCAACAGGAATTATTGA ATTGAATGGGAAACGAGTG G Left homo Executed	logous arm Reverse primer CATGCCATGCATGCATTGTGTGT TTTTTTTGTCATGTCG CATGCCATGC	Right home Forward primer CGCCTCGARGACAGAACAA GGCCTCGARGACAGAACAAC GGCCTCGARGACAGAACAAC TTAATGGACAG P12 CGTAATTTGGACAG P12 CGTAATTTGGACAG CGACATGACAAGGAAA TAATAACAAGGA TATGAAAGTAATTTGGCGTCTC CGACATGACTTGTACAGGT G primers Revers ATCTGAAGGGTGTCGTATTGT TAT TTGGCTTCTTAGGTTCCAC GGGGGTTAAGCTACTATTG G Right home Escentration	Nogous arm Reverse primer CGGAATCOTTCCATTGAA GGCAAACAA CGGGATTCCTTTCTTCTCTCATGAA GGCGTAAGTCCTTTCTTTCTC P13 GGGGCTAAGCTGGCAATTC CTCCTTTTEC P13 GCGGACACTCTAAGTACTG GGGCTAAGCACTATAACATCT GGCACACGTAATACTAGCGA a p pimer GTTCCTCCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGATGACATGG CTAACTTCAACCATTTTATC Nogous arm Nogous arm	Target site Forward oligo TarTertAGGAGAAAGGACC CATATA FACTATA FATAGGCATAGCATAGCAAAGGAAAGGACC FI FI4 FI4 FI4 FI4 FI4 FI4 FI4 FI4 FI4	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATATTIGTATACTGAGG GTAAC CACT of sgRNA Reverse oligo AAACACATITITATITITCT AAACATACACATITITATITITCT AAACTACACATITITATITITCT AAACTACACATITITATITITCT AAACTACACATITITATITITCT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT AAACTACACATITITATICT Reverse oligo Reverse oligo Rever
PF16 Oligo sequences for constru Ropm 1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm 1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm1 Arm2 Oligo sequences for constru Gene name	Cene iD PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0016700 PY17X_0016700 PY17X_0019000 gene ID PY17X_0019000 Edge ID PY17X_0019000 CC60:CCAACGAGAACGAG HOmolog Forward printeGrad ATTECACAAA CAACAATTGTGAAAACAGAG GTIGGCAACATATGTGAAACAGAG GTIGGCAACATATCTGAAAC Citing gene in situ complement Gene ID	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTACTCTTGTCACAT CAGATTATTGTCATATCATACC GGCTTACGCACATATACATATACA ATATTCTCCT GGGCTTAACTGTTATAATCC GGGCTTAACGCACATATACA ATATTCTCCT GGGCTGTATGTGTTATAATCC GGGCTGTTGC P2 AGGGTGTCGTATTGTATACATACACC atlon plasmids Tag	Left homo Forward primer CGGGTACCCGATACACGA GGAATACTA GGAGATACTA GGAGATACTA CGGGCTACCGGTTGCGGTTGCG ATTTATTTC CCCCAAGCTTACGGTTGCTA AAGTAAAAATATACAC P10 GGTTAAAAGCTAAAAAGGC CGCCATCCCATAAAAAGC TGTACCCCATTAAAGTTGTGTGT GTACCTCAAAAAATATATAATCA CGGCCAACCACAAAAAATATAAAATCA CGACAACAGAAAAATATAAAATCA CGACAACAGAAAAATATAAAATCA CGACAACAGAAAAATATAAAATCA CGACAACAGAAAAATATAAAATCA CGACAACAGAAAAATATAAAATCA CGACAACAGGAAAACATATTGAA ATTGAATGGGAAACAGGAACACACACACACACACACACAC	Iogous arm Reverse primer CATGCCATGCATTGTATT TTATTTTCGCATGCATGCATTGTGG CATGCCATGC	Right home Forward primer CCGCICGACRAGAAGAACAAC CCGCICGACAGAAGAACAAC CCGCICGACAAGAACAACAAC TIAATGACAAG P12 CGTAATTICAAAAATGAAGA TAATAACAAGT P12 CGTAATTICAAAAAATGAAGA TAATAACAAGT ATAGATATTITIGGCGTCTC CGACAATGAATGAAGA TAGATATTITIGGCGTCTC G Right nome Forward primer Forward prime Forward Forward Prime Forward F	Negous arm Reverse primer CGGAATCCGTTCCATGAA GACAAACAA CGGGATTCCTTTCTTCG CGGATTCCTTTGCTTCA GGGCTTAACGTCGCTGCAATGC GGGCTTAACGTCGCAATGCTGA CGATGCAAACTATAACAATCT GCACACAGTAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGAATGACATGG CTAACTCAACCATTTAATC Nogous arm Reverse primer GREverse primer GREverse primer CGGGAATCCGTTCAATGACA	Target site Forward oligo TATIC TAGGGGGGTTAAGC TACTAT TATTGTTAGCGCTCAGTATAGC TACTAT TATTGTTAGCCTCAGTATAGC AAAAT TATTAGTGCATGTGTTIGGA CTGT P14 GGTTACAAAGGGCAAACCCT G GATCTGTATGTTGAGGGG TATGTGAGGAGACCCGTAGTGTAGGGGGAAGGGACC CATAAA Target site Forward oligo Target site Forward oligo TatTGCGGGACCCTAATGTAAG	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATAGTAGGTTAACCCC CCTAC AAACATAGTAGTAACCACAGG GTAAC AAACACAGGTCAAACACAGG CACT of sgRNA Reverse oligo AAACACAGTTTATGGGTCCTTTCC CTTAC of sgRNA Reverse oligo Reverse oligo AAACACAGGTCAGGTTAACCGGTTAGCGT
PF16 Oligo sequences for constru Repm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm2 Oligo sequences for constru Gene name Rbpm1	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_09190000 ctting RRM deletion plasmids Forward primer CC6C1C6ACGAGAGAGAA ATTCCAACAAA CC4C1CAGACAATTGGAGAAACAGAG GTTGGCAACATATCTGAACA CTGGGCAACATATCTGAACA Ctting gene <i>in situ</i> complement Gene ID PY17X_0716700	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCCAAATAAATGAAACG G GTTTACTCCTTGTCCACAT CAGATTATTGTCATATCCT GGCTTAACGGACATATAC ATATTCCCT GGCTTATAGGGACATATAC ATATTCCCT GGCTTATAGGGACATATACC GGCTTATAGGGACATATACC GGCTTATAGGGACATATACC GGCTTATGC P2 AGGGTGTCGTATTGTGTC ATGAGCCAATACATACACAC ation plasmids Tag N-lerminal 4Myc	Left homo Forward primer CGGGGTACCCGGTTACCGGA GGAGATACTA GGGGTAACCGGGTTACGGGTTACGGA GGGGTAACCGGGTTACGGTTTCTAA AGTAATAATATCAG P10 GGTTAAAAGCTAAAAAGGC CTGTCCATTAAGTTGTTCTG AAAGCACAATAATGTATTGG Forwar GTAACTGCAATAAATATAAATG ACG P3 CTTCAACAGGAATATTGAA ATTGAATGGGAAACCAGTG G Forward primer CGGGGTACCGCATACACAG	logous arm Reverse primer CATGCCATGCATGGATTIGTGG CATGCCATGCATGGATTIGTGG CATGCCATGCATGGATTITGATCT TITATTAACAGTG P11 CATGCCATGGTTITTTTT TITATTAACAGTGA P11 CAGCGAAGAATAAAATACAC AAA CAACATTGGGATCTACTT G CCTCCCACTTITAGTGACCAAGA AGACAACTAAG P4 CTCCCTCATTCAGGAACCAAAG P4 CTCCCACTGCACTATTAGT CATGCCATGCATGTGTGTATT TATTTAGTGAG	Right home Forward primer CGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Nogous arm Reverse primer CGGAAATCGTTCAATGAA GGCAAACA CGGAATTCCTTTCATGAA GGCATAAGCTGGCAATTC CITCCTTTCA P13 GCGGCACACTCTAAGTACTG G CGAACAGTAATACCTGGCAATTC GCAACAGTAATACCAGGA a primer GTTCCTCAAATGGTTCATTTA TCTTTGAATATCTGGG P6 ATTTATATGAGATGACATGG CTAACTGTCAATGATCATGAC Nogous arm Reverse primer CGGGAATTCGTTCCATGAA	Target site Forward oligo TATTCTAAGGGAAAGGACC GTTACTATTGTAAGGTAAG	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC CCTAC AAACATAGTAGCTTAACCCC CATAC AAACATAGTAGCTAACCCC GTAAC AAACATAGCAGTCCAAACACATG CACT of sgRNA Reverse oligo AAACTAGCTAATGAGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTAACCTTGCGGC
PF16 Oligo sequences for constru Ropm 1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm 1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm1 Arm2 Oligo sequences for constru Gene name Ropm 1 Diagnostic PCR primers for J	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0019000 cting RRM deletion plasmids GOTCGACCAGAGACGAG CCGCCTCGACGACATGAGGGA CCGCCTCGACGACATGAGGGA CTTGGCACAATATGTGAAGAA CGGTGGCACATATCTGAACT Cting gene <i>in situ</i> complement Gene ID PY17X_0716700 n situ complementation gene	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCACAAT CAGATTATTGTCATATCATA	Left homo Forward primer CGGGGTACCCGATIACACA GGAGATACTA CGGGGTACCCGGTTGCGC ATTLATTATT CGCCARGETTACGGTTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGGC C CTGTCCCATTAAGTTGTTCTG T AAAGCACAATAATATATTGA GGACACAATAATATAAATGAATGA GGACATCAA P3 CTTCCAACAGGAATTATTGA ATTGAATGGGAAACGAGTG G Left homo Forward primer CGGCGTACCGCATACACGA GGAAATACTA	logous arm Reverse primer CATGCCATGCATGGATT TIATTITIGATCT TATGTCATG CATGCCATGCATGCATTIGATCT TTACTATAT CATGCCATGCATGCATTIGATCT TTACTATAT CATGCCATGCATGCATTITITTT TTATTAACAGTCA P11 CCACCGACGAAAAATAAAATACACA AAA CTATATGTGGATCTACTT G CCTCCCCCACTTTTAGGATCTACTG P4 CTCCTCATTGAGGAACACAAT AGAAAAGCCGAACCTAAG P4 CTCCCACTGCAATGAACAACAA COgous arm Reverse primer CATGCCATGCTTGTGTATT TTATTTTTCGTCG	Right home Forward primer CCGCTCGAGTTTATGTCATT TTTTGAGGT CCGCTCGAGTTAGGCATT CCGCTCGAGACAAGAACAAC CCGCTCGAGACAAGAACAAC CACCAGACAAGAACAAGAACAAC CACCAGACAAGAACAAGAACAAGAACAAC CACACAGACAAGAAATGAAAGA TAATAACAAGAAGT P12 CGGACATGACAAGAACAAGAACAACGAAA CAACAAGAAATGAAAGA TAATAATTTTGGCGCTCCGAGTTGGCATT TGGCTTCTAAGGTCGCATT CGGCTCGAGTTTATGTCATT G Right home Forward primer CCGCTCGAGTTTATGTCATT TTTTGAGGT	Nogous arm Reverse primer CGGAATCOTTACATGAA GGCAAACAA CGCGAATCCTTTCCTTCA GGCATAACGTCGTTCCTTCA GGCATAACGTCGCAATTC CTTCTTTGC	Target site Forward oligo TATTCTAGGGGGGTTAAGC AAAAT TATTAGTGCACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GGTTACAAAAGGCAAACCCT GGTTCCGTATGTTAGGAGGGCAAGCCCTACT Target site Forward oligo TATTGTCAAGGGAAAGGACC CATAAA TGT TGT TGT TGT TGT TGT TGT TGT TG	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATAGTAGGTTAACCCC CACT of sgRNA Reverse oligo AAACACATITITATITITCT AAACACAATITITATITITCT AAACACAATITITATITITCT AAACTAGGTCCTTCC CTTAC of sgRNA Reverse oligo AAACTAGGTACGATTAGCGGT CCGC
PF16 Oligo sequences for constru Rbpm 1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm 1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm1 Arm1 Coligo sequences for constru Gene name Rbpm 1 Diagnostic PCR primers for <i>I</i> Diagnostic PCR primers for <i>I</i> Strain	Construction Construction PY17X_0716700 PY17X_0716700 PY17X_0016700 COGC170CACGAGAACGAA COGC170CACGATAGGAAACGAA COGC170CACATTGGAGAAACGAA RRM deletion P1 CAACAATTGGAAAACAGAG GTTGGCACATATCGAACTAACGAAG GTTGGCACATATCGAACTAACGAAG GTTG GCACATATCGAACTAACGAAG P1 CAACAATTGTGAACATACGAACGAAGAG P1 CAACAATTGTGAAAACGAAGAGAGAGAAGAAGAAGAAGAAGAAGAAGAGAGAGAAG	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCCACAT CAGATCATTGTCATATCATC CAGATCATTGTCATATCATA	Left homo Forward primer CGGGGTACCCGATACACGA GGAGATACTA GGAGATACTA GGAGATACTA CGGGGTACCGGTTGCGC ATTTATTATT CGCCAACGTTACGGTTTCTAA AGTAATAATATACAC P10 GGTTAAAAGCTAAAAAGGC CGCCACCCATAAAGGC CGCCACCCATAATAGTATTGA Forwar GTAACTCAAAAAATATATAATCA GGGGTACCAGGAATATTGAA ATTGAATGGGGAAACCAGTG G Left homo Forward primer CGGGGTACCGATACTCA	Iogous arm Reverse primer CATGCCATGCTTIGTGTATT TTATTTTCGCATGCATGCTTGTGG CATGCCATGC	Right home Forward primer CGCCICGAGACAGAACAAC CGCCICGAGACAGAACAAC CGCCICGAGACAGAACAAC TIAATGGACAG P12 CGCACICGAGACAAGAACAAC TAATAACAAGA TAATAACAAGT P12 CGTAATTITCAAAAATGAAGA TATGATATTITTGGCGTCIC CGACACTGATGACAGGT TATGAGGGTGTCGTATCAT TTGGGCTCCTTAGGTGGGGGTTAAGCTACTATIG G P5 TITCATTGGAGGAATTCCAC GGGGGTTAAGCTACTATIG G Right home Forward primer CGCCICGACTTATCCACT GG	Nogous arm Reverse primer CGGAATCOTTCAATGAA GGCAAACAA CGGAATCCTTTCTTCA GGGCTTAACGTCGCATGAT GGCTTAACGTCGCAATTC CTTCTTTGC P13 GCGGACACTCTAAGTACTG G GGGCTAACGTCAATGGTCATTTA GGAGACACTATAACATCT GCAACAGTAATACTAGCGA a primer GCCCAACTGAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGAATGGACATGG CTAACTCAACAATGGTCATTTA C Nogous arm Reverse primer CGCAAATCCATCCATGAA GACAAACAA	Target site Forward oligo TATTC TAGGGGGGTTAAGC TACTAT TATTGTTAGGCATGTGTTAGC TACTAT TATTGTTAGGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT C GTTCCTATGTTGAGGGG T AAGCTTCAAGATCCGTAAGC TGT TATTGTAAGAGAACGACC TG TGT TATTGTAAGGGAAAGGACC CATAAA TGT TATTGTAAGGCAAACGTACT	of sgRNA Reverse oligo AAACATAGTAGCCCC CCTAC CCTAC AAACATAGTAGCTAACCCC GTAAC GTAAC GTAAC AAACACAGTCAAACACAGG AAACACAGTCAAACACAGG AAACACAGTCAAACACAGG AAACACACAGTCAAACACAGG AAACACACAGTCAGGTCAAACACAGG CTAC AAACACAGTCAGGGTCCTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTACGGATCAGGT CCGC
PF16 Oligo sequences for constru- Repm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru- Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm2 Oligo sequences for constru- Gene name Rbpm1 Diagnostic PCR primers for J Diagnostic PCR primers for J Strain	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0019000 sene ID PY17X_0019000 sene ID PY17X_0019000 sene ID PY17X_0019000 cting RRM deletion plasmids Homolog Forward primer COGCICGACGAGAGAGAA CACCACTATGGAAACAGAG GTTGGCAACATATGGAACAGAG GTTGGCAACATATCTGAACA Citing gene <i>in situ</i> complement Gene ID PY17X_0716700 n situ complementation gene PACCAACATATGAAACAGAG GHTGGCAACATATAGAAACAGAAG	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCACACT CAGATTATTGTCATATCATC GGGCTTAAGGGACATATAC ATATTCTCCT GGGCTTAAGGGACATATAC ATATTCTCCT GGGCTTAAAGGGACATATAC ATATTCTCCT GGGCTTAAAGGGACATATAC ATATTCTCCT GGGCTTAAAGGGACATATAC ATATTCCCT GGGCTTAAAGGGACATATAC ATATTCCCT GGGCTTAAAGGGACATATACATACACAC atton plasmids Tag N-terminal 4Myc P2 GGTTAAAGGCTAAAAAGGC	Left homo Forward primer CGGGGTACCCGGATACCCAG GGAGTACCCAG GGAGTACCCCGGATGCCGA GGAGTACCCGGTTGTGC ATTLATATT CGGCGTACCCGGTTGTGCA AGTAAAAGCACAATAAGTGTTCTG T AAAGCACCATTAAGTTGTTCTG T AAAGCACAATAATATAAT	logous arm Reverse primer CATGCCATGCATGGATTIGTGG CATGCCATGCATGGATTIGTGG CATGCCATGCATGGATTIGATCT TIATTIACTAATA CATGCCATGGATTATGATCT TIATTAACASTCA P11 CATGCCATGGATCTACTT G CCTCCCACTTITAGTAACATCAC AAA AAACAATTAGTGGATCTACTT G CCTCCCACTTITAGTAACATCAC AAACCATTGAGGAACACAAT AGAAAAGCCGAACCTAAG P4 CTCCTCATTCACTGCATTATT GTTCCAATGAAGAACAAACAA logous arm Reverse primer CATGCCATGCATGTGGAT CATGCCATGCATGTGGAT CATGCCATGC	Right home Forward primer CGCCTCGAGTTTATGTCATT TTTTGAGGT CGCCTCAGAGAAGAACAAC CGCCTCAGAGAAGAACAACAC CGCCTCAGAGAAGAACAACAC CGCCTCGAGTCGAG	Nogous arm Reverse primer CGGAATCCTTCAATGAA GACAAACAA CGGAATACCTTCCATTGAA GACAAACAA CGGACTAACCTCGCAATTC CITCCTTTCC P13 CGGGCTAACCTCGAAGTACTC GGCCTAAGCACTCAAGTACTCG CGACACGTCAATGACTATCACACTC CCCACAAGTAATACTAGCCA A a primer GTTCCTCAAATGGTTCATTTA CCGGACACTCAACGATTCGG P6 ATTTATATGAGATGACATGG CTAACTCTCAACCATTTATC Nogous arm Reverse primer CCGGAAATCCTTCAATGAA	Target site Forward oligo TATTCTAAGGGGGGTTAAGC TACTAAGGGAAAGGCACCT AGAAAT P14 GGTTACCACAGGAAAGGCAAACCCT GGTTACAAAAGGCAAACCCT GGTTACAAAAGGCAAACCCT GGTTACCAAAGATCGTAGGGGG T AAGCTTCAAGATCGTAGGGGAA GGTA Target site Forward oligo TATTGTGAAGGAAAGGACC CATAAA TATTATGAAAGGGAAAGGACC CATAAA TATGTAAGGGAAAGGACC CATAAA TATGTAAGGGAAAGGACC CATAAA GCTA GCT	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC CCTAC AAACATAGTAGGTTAACCACC GTAAC AAACACACHTIGTATACTGAGG CACT of sgRNA Reverse oligo AAACTAGGTACCTITCC CTAC of sgRNA Reverse oligo AAACTAGGTACCTITCC CTAC
PF16 Oligo sequences for constru Gene name Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm2 Oligo sequences for constru Gene name Rbpm1 Diagnostic PCR primers for for Strain Commandation Diagnostic PCR primers for for Strain Diagnostic PCR primers for for Diag	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_00190000 cting RRM deletion plasmids Gene ID PY17X_01919000 cting RRM deletion plasmids CCGC1C0ACCAGAGACGAGAGAGA CCGC1C0ACCAGAGAGAGA CCGC1C0ACCAGAGAAGAA CGGC1C0ACCAGAGAAGAA RRM deletion P1 CAACAATTIGTGAAAAACAGAG GTTGGCAACATATCTGAACT cting gene <i>in situ</i> complement Gene ID PY17X_0716700 n situ complementation gene P1 AAGCGAAATAAATGAAACG G	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCACAT CAGATTATTGTCATATCATC GGCTTAACGGACATATACATACACAT GGCTTAACGGACATATACATACC GGCTTAACGGACATATACATACACAC AGGGTGTCGTATGTGTTC ATGAGCCAATACATACACACC atton plasmids Tag N-derminal 4Myc P2 AGGTTAAAGCTAAAAAGGC	Left homo Forward primer CGGGCTACCCGCATACACGA GGAATACTA GGAGATACTA CGGCGTACCCGGTTGCGCA GGAGATACCCCGGTTGCGCA TTATATTCCC P10 GGTTAAAAGCTAAAAAGCCAAAAAGGC CGCCCATCACGATGTTCTG T AAAGCACAATAATATATATAGC Forwar GTACCTCAACAAGAATATAAATTCAA FGAACGGAATAATATAAATGAATGA CGACAACAAGAATAATAAAATACAC P3 CTTCCAACAGGAATAATAAAATACACC AAA	Iogous arm Reverse primer CATGCCATGCTTIGTGGATT TITATTITGCG CATGCCATGCATGCATTGTGGTCT TTATTTTCGTCG CATGCCATGC	Right home Forward primer CCGCTCGAGTTTATGTCATT TTTTGAGGT CCGCTCGAGTTATGTCATT TTTTGGAGAG CCGCTCGAGAGAAGAACAAGGAAA TAATAAGAAGT P12 CGTAATTTCAAAAATGAAAGA TAATAATTTTGGCGTCC CGACATGACAT	Nogous arm Reverse primer CGGAATCOTTCAATGAA GACAAACAA CGGAATACTTCTTCA GGGATTAAGTACGTTCATTGAT GGGCTTAAGTACGTGCAATTC CTGCTTTTGC P13 GCGGACAATCATAAGTACTAG GGGCTAAGTACTAAGTACTG GGACAACAATAACATCT GGCAACAGTAATACTAGCGA a primer GTGCTCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGATGACATGG CTAACTGATCAATGAT S SOgous arm Reverse primer CGGGAATTCGTTCCAATGAA GACAAACAA	Target site Forward oligo TATTCTAGGCGGGTTAAC AAAAT TATTAGTGACCCTCAGTATAC AAAAT TATTAGTGCATGTGTTTGGA CTGT P14 GC GATTCTGTATGTTAGGCAAACCCT CGATCTGTATGTTAGGAGGGGA AGCCTCAGGATCGTGATGTGAGGGGG TATGTGAGGAAAGTCGTAACT TGT TGT TGT TGT TGT TGTGAGAAAAATAAAAAAAA	of sgRNA Reverse oligo AAACATLATIAGGTTAACCCC CCTAC AAACATLATIAGGTTAACCCC CACAC GTAAC AAACACAGTCAAACACAGG GTAAC AAACACAGGTCAAACACAGG CACT of sgRNA Reverse oligo AAACTTAGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGGTACGGTCCTTTCC CTTAC
PF16 Oligo sequences for constru Rbpm1 kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm1 Arm2 Oligo sequences for constru Gene name Rbpm1 Diagnostic PCR primers for <i>i</i> Strain PF10 Oligo sequences for constru	Cene ID PY17X_0716700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0019000 CCGC17CACCAGAGACGAA GENE ID PY17X_0019000 Cting RRM deletion plasmids FOrward primer CCGC17CGACCAGAGACGAA GTTGACCAGAGAACGAA GTTGACCAGAGAACGAA RRM deletion P1 CAACAATTGTAGAAAACAGAGA GTTGGCCACATATCGAACGAA GTTGGCCACATATCGAACAGAG GTTGGCCACATATCGAACAGAGA P17X_0016700 n situ complementation gene P1 AAGCGAAATAATGAAACGA G Cting intron deletion plasmids	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCCACAT CAGATCATTGTCATATCAT CAGATCATTGTCATATCAT GGGCTTAACGGACATATACA ATATTCTCCT GGGCTTAACGGACATATACA ATATTCTCC C ATGAGCCAATACATACACAC C ATGAGCCAATACATACACAC C ATGAGCCAATACATACACAC C TSg N-terminal 4Myc P2 GGTTAAAGCTAAAAAGGC	Left homo Forward primer CGGGGTACCCGATIACACA GGAGATACTA GGAGATACTA CGGGGTACCCGGTTGCGC ATTTATTATT CGCCAACCTTACGGTTTCTAA AGTAATAATATCAC P10 GGTTAAAAGCTAAAAAGCC CGCCCCTCACGATGTTCG T AAAGCACAATAATATATATGA Forward Forward P3 CTTCAACAGGAATTATTGAA ATTGAATGGGAAACCAGTG G Left homo Forward primer CGGCGTACCGCATCACCA GGAAATACTA	Iogous arm Reverse primer CATGCCATGCATTGGTGATT TTATTTTGCATGCCATGC	Right home Forward primer CCCCICGACAGACAGACAAGACAAG CCCCICGACAGACAGACAAGACA	Nogous arm Reverse primer CGGAATCOTTCCATGAA GACAAACAA CGGGATTCCTTTGCTTCATGAT GGGCTTAACGTCGCTGCATGAT GGGCTTAACGTCGCAATTC CTTCTTTGC P13 GCGGACACTCTAAGTACTG GCGACACTCTAAGTACTG GCGACACTCTAAGTACTG GCACACGATAATACTAGCGA a primer GTCCTCAAATGGTTCATTTA TTTCTTTGAATATCTGAG P6 ATTTATATGAGATGACATGG CTAACTTCAACCATTTATC Nogous arm Reverse primer GGGAATCGTTCCATTGACA GACAAACAA	Target site Forward oligo TATTC TAGGGGGGTTAAGC TAGTAT TATTGTTAGGCATGTGTTAGG TATTAGTAAGGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT C GTTACAAAGGCAAACCCT GTTCAAAGGCAAACCCTGATGTTAAGGAAAGGA	of sgRNA Reverse oligo AAACATAGTAGCTAACCCC CCTAC CCTAC AAACATAGTAGCTAACCCC GTAAC GTAAC AAACACAGTCAAACACAGG CACT of sgRNA Reverse oligo AAACACAGTITITATITITCT AAACTITATGGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTACGATTAGCGT CCGC
PF16 Oligo sequences for constru Ropm 1 kinesin8b PF16 Oligo sequences for constru Gene name Ropm 1 kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for for Strain Arm1 Construction Strain Construction Gene name Ropm 1 Diagnostic PCR primers for <i>i</i> Strain Pispostic PCR primers for <i>i</i> Strain Pispostic PCR primers for <i>i</i> Strain Pispostic PCR primers for <i>i</i> Strain Pispostic PCR primers for <i>i</i> Strain	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0016700 PY17X_016700 PY17X_0204100 PY17X_016700 PY17X_016700 PY17X_01919000 Cting RRM deletion plasmids Homolog COCCTCACCACCAAGAGAAAACAGAGA QRM deletion RRM deletion CAACAATTGTGAAAACAGAGA GTTGGCAACATATCTGAAACAGAGA GTTGGCAACATATCTGAAACAGAGA GTTGGCAACATATCTGAAACAGAGA Gene ID PY1X_0716700 n situ complementation gene P1 AAGCGAAATAATGAAAACG Cing intron deletion plasmids	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTTTGTCCACAT CAGATTATTGTCATATCATAC GOTTACCGCACATATAC ATATTCCCGCACATATAC ATATTCCC GGCTTAACGCACATATACA ATATTCCCGCACATATACCA GGCTTAACGCACATATACACAC ATAGCCCAATACATACACACAC AGGGGTGTCGTATTGTGTTC C P2 AGCCAATACATACACACAC attom plasmids Tag N-terminal 4Myc P2 GGTTAAAAGCTAAAAAGGC C GGTTAAAAAGGTAAAAAGGC	Left homo Forward primer CGGGGTACCCGGATACCCAG GGAGTACCCGGATACCCAG GGAGTACCCCGGATGACCAG GGAGTACCCCGGATGACCAG P10 GGTTAAAAGCTACAGATGATCG P10 GGTTAAAAGCTACAAAAGGC CTGTCCATTAAGTTGTTGTA AAGCACCATAATGTGTTGG AAGCACCAGTGATATTCAA FOrward FOrward primer CGGGCTACCAGGATACCAGATG CGACACCGGATACCAGGG CAGCAGCAACAAAAATAAAAT	logous arm Reverse primer CATGCCATGCTTIGTGG CATGCCATGCATTGGTGG CATGCCATGCATTGTGG CATGCCATGC	Right home Forward primer CGCTCGAGAGA CGCTCGAGAGAGAAGAACAAC CGCTCGAGAGAGAAGAACAAC CGCTCGAGAGAGAAGAACAAC P12 CGTAATTTCAAAAATGAAGA TATGATATTTTGGCGTCT CGACATGACTTGTACAGGT G a primers Revers ACTGAAGGGTGTCGTATGT TATGATTGGAGGGTGACGTTGTGT TATGATTGGAGGGTGAGTTCGCC GGGGGTTAAGCTCCAC GGGGGTTAAGCTCCAC GGGGGTTAAGCTACTATTG CCGCTCGAGTTAGGTCCACT GGGGGTTAAGCTACTATTG CCGCTCGAGTTAGGTCCACT Right home Forward primer CCGCTCGAGTTAGGTCCATTTG CCGCTCGAGTTAGGTCCACT CGGGGTTAAGCTACTATTG NTTGAGGGT NTTGAGGGT NTTGAGGGT NTTGAGGGT NTTGAGG NTTGAGGT NTTGAGG NTTGAGG NTTGAGGT NTTGAGGT NTTGAGG NTTGAGGT NTTGAGG	Nogous arm Reverse primer CGGGAATCCTTCAATGAA GGCAAACAA CGGGAATACCTTCCATGAA GGCGTAACCTCGCTATTCTCA GGGCTTAACCTCGCAATTC CTTCCTTCA P13 GCGGACACTCTAAGTACTG GGCGGACACTCTAAGTAACTATG GGCGGACACTCTAAGTAACTATG GGCGGACAGTGAATACTAGGGA a primer GTTCCTCAAATGGTTCATTTA TTCTTTGAATACTGAG P6 ATTTATATGAGAATGACATGG CTAACTGCAATCGATCGATCGACATGGA CTAACTTCAACTGACATTCACGTCCAATTGAC CGGGACAATCGTCCAATGAA CGCGAACACA	Target site Forward oligo TATTCTAAGGGGGGTTAAGC TACTAAGGGAAACCTCAGTATAGC AAAAT TATTGTAAGGCATGTGTTTGGA CTGT P14 GGTTACAAAGGGCAAACCCT GATTCTGATGTTGAGGGG T AAGCTTCAAGATCGTAAGTTGAGGGG TATTGTAAGGTGAAGGACC CATAAA TGT TATTGTAAGGGAAAGGACC CATAAA TGT Target site Forward oligo TATTGCGACGCTAATCGTA GCTA Target site Ta	of sgRNA Reverse oligo AAACATAGTAGCTTAACCCC AAACATAGTAGCTTAACCCC GTAAC GTAAC AAACATAGTAACAGTAACACATG CACT of sgRNA Reverse oligo AAACTAGCTATTAGTGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTACGATTAGCGT CCGC
PF16 Oligo sequences for constru Repm1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Repm1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm2 Oligo sequences for constru Gene name Repm1 Diagnostic PCR primers for i Strain Arm2 Oligo sequences for constru Gene name Repm1 Diagnostic PCR primers for i Strain rescue Oligo sequences for constru	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0019000 per knockout Gene ID PY17X_0019000 pere knockout Gene ID PY17X_0716700 PY17X_0019000 citing RRM deletion plasmids CGCCTC6ACGACGAGAGAA CGCCTC6ACCACGAGAGAGA ATTCCAACAAA CCGCCTC6ACACTTGGAGAGA CACAATTGTGAAAAACAGAG GTTGGCAACATATCTGAAACC GTTGGCAACATATGATGAACG Gare ID PY17X_0716700 nsitu complementation gene P1 AACCGAAAATAAATGAAACG Gitig intron deletion plasmids Citig intron deletion plasmids	Gene size (bp) deleted gene size (bp) 1904/1904 1904/1904 5137/1184 1809/1809 1 AGCCAAATAAATGAAACG 1 GTTACTCCTTGTCACAAT CAGATTATCGTCACAAT CAGATTATTGTCATATCATC 1 GGGCTTAACGGACATATAC 1 GGGCTTAACGGACATATAC 1 AGGGTGTCGTATTGTGTTC 1 AGGGTGTCGTATTCGTGTTC 1 AGGGTGCGATATACATACACAC 1 ATGAGCCAATACATACATACACAC 1 AGGGTCGTATTGTGTTC 1 P2 GGGTTAAAAGCTAAAAGGC C 2 P2 GGGTAAAAAGCTAAAAAGCC C 1 SGTAAAAAGCTAAAAAGCAAAAAGCCAAAAAAGCCAAAAAGCTAAAAAGCAAAAAGCAAAAAGCAAAAAAAA	Left homo Forward primer CGGGGTACCCGGATACCCAG GGAATACTA GGAGATACTA GGAGATACCCCGGATGCCCA GGGGTACCCGGATGCCAG HITATATT CCCCCAGGTTACCGGTTGCA AAGCACCATAAATATAATCAC P10 GGTTAAAAGCCTAAAAAGGCC CCCCCCAGATATTGA GTAACTACAAATATAAATGAATG Forward FOrward FOrward P3 CTTCAACAGGAATAATAAAATACAC AAA FGAAAGAACAAAAATAAAATACACC AAA Forward Forwar	logous arm Reverse primer CATGCCATGCTTIGTGG CATGCCATGCATGGATTITGATCT TTATTTACTATAT CATGCCATGCATGGATTITGATCT TTATTAACAGTGCA P11 CATGCCATGCATGGATCTACTT G CCTCCCCACTTTTAGTAAAATACAC AAA CCTTTGAGGAACACAAT AGAAAAGCCGAACCTAAG P4 CTCCCTCATTCGAGGAACACAAT AGGAAAAGCCGAACCTAAG P4 CTCCCTCATTCGAGGAACAAAAAAA IGGOUS arm Reverse primer CATGCCATGCATGGATTTACT GTTCCAATGAAGACAAAAAAA GGOUS arm Reverse primer CATGCCATGCATGGTTTTTTTTTTTTTTTTTTTTTTTTGGGGA CATGCATGCATGGATCTACTG P4 CGTAATTCAAAAATGAAGA Mutatiod d primer	Right home Forward primer CCCCTCGAGTTTATGTCATT TTTTGAGGT CCCCTCAGAGAAGAACAAC TTAATGAAGA CCCCTCAGAGAAGAACAAC CTTTAATGAGAGA P12 CGTAATTTCAAAAATGAAGA TAATAACAAGT P12 CGTAATTTGCACGCTCCCGAGTAACTGAAAATGAAAATGAAGA primers Revers CGACATGACATGTACAGGT FS TTTCATTGGAGGTGTCGTACTGGCT P5 TTTCATTGAGGGTGTCGTACTATTG G Right home Forward primers Revers CCCCTCGAGTTATGTCATT TTTTCAGGGT Right home Revers Re	Nogous arm Reverse primer CGGAATCCTTCAATGAA GGCAAACAA CGGAATACTTCTCA GGCTTAAGTAAGTCCTTTCTTCA GGCCTTAAGTACTCCTTCCTTCA GGCCTTAAGCTCGCAATTC CTGCTTTTGC P13 GCGGACAACTATAACATCT GGCACTAAGCACTAAGAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA TTTCTTTGGATATCTGAG P6 ATTTATATGAAATGGTTCATTTATC Nogous arm Reverse primer CCGGAATTCCTTCCAATGAA	Target site Forward oligo TATTCTAGGGAGGGGTTAAGC TAGTAT TATTGTAGGGAGGGGGTTAAGC TAGTAT TATTAGTGACCTCAGTATAGC AAAAT TATTAGTGCATGTGTTGGA CTGT P14 GGTTACAAAGGGCAAAGCCTC GATTCTGTATGTTGAGGGG ATTCTGTATGTTGAGGGGAAGGGCC ATTCTGTAGGTGAGGGGAAAGGACC CATAAA TATTAGTAAAGGAAAAGGACC CATAAA TATTGTAAGGGAAAGGACC CATAAA TATTGTAAGGGAAAGGACC CATAAA TATGTGAGGGAAAGGACC CATAAA TATGTGAGGGAAGGACC CATAAA TATGTGAGGGAAGGACC CATAAA TATGTGAGGGAAGGACC CATAAA TATGTGAGGGAAGGACC CATAAA TATGTGAGGGAAGGGA	of sgRNA Reverse oligo AAACATAGTAGGTTAACCCC CCTAC AAACATAGTAGGTTAACCCC CATAC AAACATAGTAGGTCAACACATG CACT of sgRNA Reverse oligo AAACATAGGGTCCATTAGGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTAGGTAGGTAGGGT CCGC of sgRNA Reverse oligo AAACTAGCTAGGTAGGATAGCGG CGC
PF16 Oligo sequences for constru Ropm 1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Ropm 1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm1 Arm2 Oligo sequences for constru Gene name Ropm1 Diagnostic PCR primers for <i>i</i> Strain Ingen ame Ropm1 Diagnostic PCR primers for <i>i</i> Strain Ingen ame Ropm1 Diagnostic PCR primers for <i>i</i> Strain	Cene ID PY17X_0716700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0016700 PY17X_0019000 ctime ID PY17X_0016700 PY17X_0019000 ctime RRM deletion plasmids Gene ID Forward primer CG6C10CACCATGAGAGGAA GTTGACCAAGAGAGGAA GTTGACCAAGAGAGGAA ATTCCACAAA GACAAATTGTGAAAACAGAGGA ATTCCACAAA GACGACATATGGAAACAGAGGA P1 CAGCACATTGTGAACATGAAACAGAGGA GTTGGCCACATATGGAACGAGGA P1 CAGCACATTGTGAAAACAGAGGA P1 CAGCGAACTATCTGAACAAGAAACAGAGG P1 AGCGAAATAGAAACAGAACGA Gitt complementation gene P1 AAGCGAAATAATGAAACG Gitting intron deletion plasmids Homolog Forward primer CATGCCATGGTGATAAAGG AAAAACACACG	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCCACAT CAGATTATTGTCATATCAT CAGGTGTTAGGGACATATACA TATTCTCCT GGGCTTAAGGGACATATACA ATATTCTCCT AGGGTGTCGTAATGTATACA CagGGTGTGCGAATACATACACAC ation plasmids Tag N-lerminal 4Myc P2 AGGGTGTGGTAAACATACACACACACACACACACACACAC	Left homo Forward primer CGGGGTACCCGGATACACGA GGAGATACTA GGGGGTACCCGGATACACGA GGGGTACCCGGGTTGTCG T GGTGAAAAAGCACATAATGTATTGG GGTGAACAGAGAAAAATAAAAGCACAGG P10 GGTGAACTCAAAAAGCACATAATGTATTGG GGTAACTCAAAAAAAAATAAAAT	Iogous arm Reverse primer CATGCCATGCATTGTTGG CATGCCATGCATGGTTTGTGGTCG CATGCCATGC	Right home Forward primer CCGCTCGAGATTATGTCATT TTTTGAGGT P12 CGTATTTGACAGA CCGCTCGAGACAGAACAAGGAAA TAATAACAAGGA TAATAACAAGGA TAATAACAAGGA TAATAACAAGGAAATGAAAGAA TAATAACAAGGA P12 CGTAATTTCAAAAATGAAAGA TAATAACAAGGA TAATAACAAGGAAATGAAGA TAATAACAAGGAA TAAGAAGGT P12 CGGACATGACTTGTACAGGT G Right home Forward primer CCGCTCGAGTTAAGCTACTATTG G Right home Forward Strate Right Home Forward	Nogous arm Reverse primer CGGAATCOTTCCATGAA GACAAACAA CGGAATTCCTTTCTTCTCTCATGAA GGGCTTAAGCTGGCAATTC CTTCTTTTGC	Target site Forward oligo TATTC TAGGGGGGTTAAGC TAGTAT TATTGTTAGGGAGGGGTTAAGC TAGTAT TATTGTTAGGCATCTGTTTGGA CTGT P14 GGTTACAAAGGCAAACCCT C GTTACTAAAGGCAAACCCT GGTTCATGTTAAGGGAAAGGACC GTTCTGAAGGTCCAAGATCAGAAAGGACC CATAAA Target site Forward oligo TATTGTAAGGGAAAGGACC GTA Target site Forward oligo TATTGTGACGGCTGACTAAC GGTA	of sgRNA Reverse oligo AAACATAGTAGCCC CCTAC CCTAC AAACATAGTAGCTAACCCC CCTAC AAACATAGTAGCTAACCCCG GTAAC GTAAC AAACACAGTCAAACACAGG GTAAC AAACACAGTCAAACACAGG CACT of sgRNA Reverse oligo AAACACATTGTTAGGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACACATCGTAGCAGCGT CGGC of sgRNA Reverse oligo AAACCATCGTAGCAGCGT CGGC GTCAC CTACC
PF16 Oligo sequences for constru Repm1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Rbpm1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for f Strain Arm1 Arm2 Oligo sequences for constru Gene name Rbpm1 Diagnostic PCR primers for f Strain Construit Gene name Rbpm1 Diagnostic PCR primers for f Strain Oligo sequences for constru Gene name Rbpm1 Diagnostic PCR primers for f Strain Construit Strain Construit Strain Coligo sequences for constru Strain Coligo sequences for constru Strain Coligo sequences for constru Strain Kinesin8b Al1	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0204100 PY17X_0919000 gene ID PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 PY17X_0204100 CGCTC62CCGAGACGAA CGCTC62CCGAGACGAAA CGCTC62CCGAGACGAAA CGCTC62CCGAGACGAAA CGCTC62CCGAGACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCGAAATAAATGAAACG G GTTTACTCTCTTGTCCACAT CAGGATATATGTGTCATATCAT CAGGATATATGTGTCATATCATA	Left homo Forward primer CGGGGTACCCGGATACCCAG GGAATACTA GGAGATACTA GGGGTACCCGGATGACGAG GGGTAACCGGATGATGATA GTTAAAAGCTACAGATTATATATCAC P10 GGTTAAAAGCTACAAAAAGTGTTCTG AAAGCACCATAAAGTGTGTTCG TGTCCAATAAAGTGTGTTCG Forward GTAACTCCAGATATTCAA TTGAACTGGAAAACTATATAATCAC P3 CTTCAACAGGAATTATTGAA TTGAACTGGAAAACTATCAC P3 CGCGCAAAAAATAAAAATACACCAAGTG P3 CGCGCGAAAAATATAAAATACAC AAA Forward CGCGCGAAAAAATAAAAATACACCAAA	logous arm Reverse primer CATGCCATGCTTIGTGGATT TIATTITTGCTG CATGCCATGCATTGCTGG CATGCCATGCATGCATTTTGATCT TTACTAATAT CATGCCATGC	Right home Forward primer CGCTCACAGAGA FORMATICACTATILATICATI FITTIGAGGT CGCTCACAGAGAACAACAAC CGCTCACAGAGAACAACAACGACA P12 CGTAATTICAAAAATGAAGA TATAAACAAATGAAAATGAAGA P12 CGTAATTICAAAAATGAAGAATGAAGAA TAGATATTITGGCGTCCCGAGTGACCAGGT G CGGACATGACATGACGACACACGGT ACTGAGGGTGACGTGTCCTTAGGTGCGTATGT TAT TGGCTCTTAGGTGCGTATGG FORWARD primer CGCCTCGAGTTAGGTGCACTATTG CGGCGGTAAGCACACTATG Right home Forward primer CCCCTCGAGTTAGGTGCACTATTG CGGTGAGGTAAGCACTACTATTG CGGTGCGTTAGGTTCCACT GGGGGTAAGCACTACTATTG CGCTGCGAGTTAAGCACTATG AAATACAATGGGGATAAAATG	Nogous arm Reverse primer CGGAATACTATCATTGA GGCTTAACGTGAATGG P13 GGGCTTAACGTGAATGG GGCCTAAGTACTGGCAATTC GTGCTTAAGTAACTATGGG CGAACAGTAATACTAGGCAA a primer GTGCTCAAATGGTTCATTTA TTTCTTGAATGCTGAGAATGG P6 ATTTATATGAGATGACATGG CTAACTGTCAATGATGACTGG Reverse primer GCGGCAATCGTTCAATGACTGA a primer agtimer agti	Target site Forward oligo TATTCTA/GGGGGGTTAAGC TACTA/CAAAGC TACTA/CAAAGC P14 GGTTACAAAGGCAAACCCT GGTTACAAAGGCAAACCCT GGTTACAAAGGCAAACCCT GGTTACTAAAGTCGATGGGGG T AAGCTTCAAGATCGTAAGTTGAGGGG TATTGCAAGATCGTAAGTAGGAAAGGACC CATAAA TGT Target site Forward oligo TATTGCGACGGCTAATCGTA GCTA Target site Forward oligo TATTGCGCGCGCCAATCGTA GCTA Target site Forward oligo TATTGCGCGCGCCAATCGTA GCTA Target site Forward oligo TATTGCGCGCGCCAATCGTA GCTA	of sgRNA Reverse oligo AAACATAGTAGCCCACAGC CCTAC CACACAACAACATGACACACAGG CACT of sgRNA Reverse oligo AAACTAGGGGCCATAGCGGTCACCCTTAC CTTAC of sgRNA Reverse oligo AAACTAGCTAGCAGTAGGGTCCTTACCGTTAGCGGC of sgRNA Reverse oligo AAACTAGCTACGTTAGCGGTCGTTAGCGG CGCC
PF16 Oligo sequences for constru Repm1 Kinesin8b PF16 Diagnostic PCR primers for g Gene name Repm1 Kinesin8b PF16 Oligo sequences for constru Strain Arm1 Arm2 Diagnostic PCR primers for F Strain Arm2 Oligo sequences for constru Gene name Repm1 Diagnostic PCR primers for f Strain Arm2 Oligo sequences for constru Gene name Repm1 Diagnostic PCR primers for f Strain Prescue Oligo sequences for constru Gene name Repm1 Diagnostic PCR primers for f Strain rescue Oligo sequences for constru Strain Rescue Oligo sequences for constru Strain Kinesin8b Δ/1 PF16 J/1 det f J/4	Cene ID PY17X_0716700 PY17X_0716700 PY17X_0019000 per knockout Gene ID PY17X_0019000 per knockout Gene ID PY17X_0716700 PY17X_0019000 citing RRM deletion plasmids Homolog CGCCTC6ACCATGAGAGA ATTCCAACACACACACACACACACACACACACACACACA	Gene size (bp) / deleted gene size (bp) 1904/1904 5137/1184 1809/1809 P9 AAGCCAAATAAATGAAACG G GTTTACTCCTTGTCCACAT CAGATTATTGTCATATCATC GGCTTAACGGACATATAC ATATTGTCAT GGCTTAACGGACATATAC ATATTCCCT GGCTTAACGGACATATAC ATATCTCCT GGCTTAACGGACATATAC ATATCTCCT GGCTTAACGGACATATAC ATATGGCCAATACATACACAC ation plasmids Tag N-lerminal 4Myc P2 GGTTAAAAGCTAAAAGGC CCCCCCAGCTCATTAGG CAGATAATGT CCCCCCCCAGCTCTTCGGT AGGCTCAATGCTCTACA	Left homo Forward primer CGGGGTACCCGGATACCCAG GGAATACTA GGGGTACCCGGATACCCAG GGGGTACCCGGATACCCAG GGGTAACCGGATATCAG P10 GGTTAAAAGCTAAAAAGCTAAAAGGC CGCCCTCATTATAGTTGTTCG AAAGCACCAATAATGATAGTATTGG GTAACTCAACAGGAATATTAAATGACGAGC CGACCACCCTCAGATATTCAA TGAACGGAAAACGAGTG G Left homo Forward primer CGGGGTACCGCATACACGA P3 CTTCCAACAGGAAAATAAAATACACCAA P3 CGACGAAAAATAAAATACACCA P3 CGACGAAAAATAAAATACACCAA Forwar ACTCAACTAAAGGAAAACATTTC	logous arm Reverse primer CATGCCATGCTTIGTGG ATGCCATGCATGGATTITGATCT TTATTTACTATAT CATGCCATGCATGGATTTTGATCT TTATTAACAGTCA P11 CATGCCATGGATTATCACAC AAA CAACATTTAGTAAAATACACACAAT G CCTCCCCACTTTTAGTAACATCACACAAT AGAAAAGCCATAGAACAACAAT AGAAAAGCCATTGAGAACACAAT AGAAAAGCCATTGAGAACAAAT CATGCCATGC	Right home Forward primer CCCCTCGAGTTTATGTCATT TTTTGAGGT CCCCTCAGTTTATGTCATT TTTTGAGGT CCCCTCAGTTAGGCATT CAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	Nogous arm Reverse primer CGGAATCCTTTAGTGAA GGCAAACAA CGGAATACTTTGCTTCATTGAA GGCATAAGTCCTTTCTTCA GGCATTAAGTCCTTTCTTCA P13 GCGGACTAAGTCTTAAGTACTG G CGACTCAAGTAATACTAGCGGA G CGACACCAATACTATACCACTG GCACACAGTAATACTAGCGA a primer GTTCCTCAAATGGTTCATTTA CGGGAATACTCAGAGA P6 ATTTATATGAAGATGACATGG CTAACTCGATCCATGAG CTAACTCGTTCCAATGAG CTAACTCGTTCCAATGAA GACAAACAA a primer aGTGATTGCGTTT TTACTGGCAATATTT TGACTGGCAAATATTT TGACTGGCAAATATTT TGACTGGCAAATATTT	Target site Forward oligo TATTCTAGGGAGGGGTTAAGC TAGTAT TATTGTAGGGGGGGTTAAGC TAGTAT TATTGTAGGCATGTGTTTGGA CTGT P14 GGTTACAAAGGCAAAGCCT GGTTACAAAGGGCAAAGCCT GGTTACAAAGGCAAAGCCT GATCTGTATGTTGAGGGG A AGCTTCAAGATCGTAGGGGC ATTGTGAGGAAAAGTAAAT TATTGTAAAGGGAAAAGGACC CATAAA TATTGTAAGGGAAAGGACC CATAAA TATTGTAAGGGAAAGGACC CATAAA TATGTAAGGGAAAGGACC CATAAA TGT GT Target site Forward oligo TATTGCGGACGCTAATCGTA GCTA Target site Forward oligo TATGCGGACGCTAATCGTA GCTA TaTGTAAGGGAAAGGACC GATG TATGCGACGCTGACTAACT TATGTATGTAGAGGAAAGGACC GATG TATGCGCACGCTGACTAACT TATGTAGTAGTGACGACTCGACAATTA TGT TATGCACTTCACAAATATCTAACTCACAACTCACTA GCTA	of sgRNA Reverse oligo AAACATATTAGGTTAACCCC CCTAC AAACATAGTAGCTTAACCCC CCTAC AAACATATTGGTATACTGAGG GTAAC of sgRNA Reverse oligo AAACATAGTGAGTAGTACGAC of sgRNA Reverse oligo AAACTAGCTATTAGGGTCCTTTCC CTTAC of sgRNA Reverse oligo AAACTAGCTAGTAGGAC CCGC of sgRNA Reverse oligo AAACTAGCTAGGTAGGAC CCGC of sgRNA Reverse oligo AAACCTAGCTAGGTAGGAC CCGC

	CGGGGTACCGTACGTACAT GTAGGACAAA	CCGGAATTCGTGGGAAAAA ATAAGTATTAC	GTTGAGCGCGGGTTCTAAGC	CCTTAGAAATATGGAA	AAGGGCTTAGAACCCGCGC	FCAACAAGAGTGACAAT	TATTGGAAAATGAGAACAAA AAAA	AAACTTTTTTTGTTCTCATTT TCC
Diagnostic PCR primers for in	ntron deletion							
Strain	P1	P2	P3	P4	P5	P6		
kinesin8b∆l1	GAAC	GCATTGTCTTTATCTGTTAT	AATTTGGGTTCTATAACCCC	AC	GGGGCTAGTTAGATCGTAC C	CGGATAATGAACCATCGATT		
PF16∆/1	GTACGTGCAGGTGCTTTAC C	CCTCACATGAAGTATGTACA	CATTTATTAAATCAGGGTGC	GCACAATAATGTATTGGAAA	CCTAGTTGTAATTTCTCAAA	ACGATTTGGTTATATATAAT		
dic1∆l4	GCACACGTAATCAAATTTAA	TCTTTAAAATGTAGCAACTT A	GCTTCCTCTCAAATACATTA	CCATCTGATACTTTCAATGC	TTCAAAAAGTAGAAGTATGC	CTGAAAAGTACGTTATAAGG		
1109100∆/1	CATATGCAAATAATATTTGC AC	TATTTCTAAGGGCTTAGAAC	ATTGTCACTCTTGTTGAGCG	TATTCATCTAAGCAGAAAAA T	CGGTAGCAGTATATGTAGTT	CTGATTATAAAAGGAAAGAC		
Oligo sequences for construc	cting bfp reproter assay plasm	nids			r	r	P	
Expression element	Forward primer	Reverse primer	Reporter gene	Forward primer	Reverse primer	Expression element	Forward primer	Reverse primer
The 5'-UTR of hsp70	CGGGGTACCGTAAAGAGGA TGATGTATGT	CATGCCATGGCTTTTTTTT TTTTAATTGCAA	bfp	CATGCCATGGGGGATGGTGA GCAAGGGCGAGGAGCT	CCGCTCGAGTTACTTGTACA GCTCGTCCATGC	The 3'-UTR of dhfr	CCGCTCGAGTGTTCATTTTT CTTATTTAT	CCGGAATTCCCTGAAGAAG AACAGTCCGA
Reporter gene	Upstream b Forward primer	fp sequence Reverse primer	Int Forward primer	ron Reverse primer	Downstream Forward primer	bfp sequence Reverse primer	Overla Forward primer	PCR Reverse primer
bfp-Kin8b11	CATGCCATGGGGATGGTGA	TAGCCCCAACCTTGAAGTC	CGACTTCAAGGTTGGGGCT	TGCCGTCCTCCTACAAATAA	TTATTTGTAGGAGGACGGC	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
bfp-Kin8b12	CATGCCATGGGGATGGTGA	CTGAATATACTTGTGGCCGT	ACGGCCACAAGTATATTCA	CACGCTGAACCTGTTTACAT	ATGTAAACAGGTTCAGCGT	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
bfp-PF1611	CATGCCATGGGGATGGTGA	TTTATTTTACTTGAAGTTCAC	TGAACTTCAAGTAAAATAAA	GTGGCGGATCCTAAATAAA	TTTTATTTAGGATCCGCCAC	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
bfp-dic1 14	CATGCCATGGGGATGGTGA	AATATGTTACTAGATGTTGT	ACAACATCTAGTAACATATT	GGCCATGATACTGAAAAGT	TACTITICAGTATCATGGCC	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
bfp-110910011	CATGCCATGGGGATGGTGA	ATTAAATTACGTCGACGCCC	GGGCGTCGACGTAATTTAA	CCTCCTTGAACTGATTATAA	TTATAATCAGTTCAAGGAGG	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
bfp-110910012	CATGCCATGGGGATGGTGA	TAAGTATTACGTCGACGCC	GGGCGTCGACGTAATACTT	CCTCCTTGAACTAAGCAGAA	TTCTGCTTAGTTCAAGGAGG	CCGCTCGAGTTACTTGTACA	CATGCCATGGGGAGGA CATGCCATGGGGATGGTGA	CCGCTCGAGTTACTTGTACA
Diagnostic PCR primers for e	expression cassette integrated	d into the p230p locus	ATTTTTCCCA	AAATTTTAAA	ACGGCAACAT	GETEGTECATGE	GCAAGGGCGAGGA	GUICGICCAIGC
P1	P2	P3	P4	P5	P6			
GGAAAAGTATGATAACGAT	GACGGACACATACATCATC	TCGGACTGTTCTTCTTCAGG	AGATGATATCGCTATATATC	GATGCATCTATAACTCCAGA	TGCTGAGTCAGTGGTGTTC			
G Oligo sequences for construc	C cting plasmids with axonemal	intron insertion into gep1			C			
Strain	Upstream ge	p1 sequence	Int	ron	Downstream g	ep1 sequence	Overla	ap PCR
	Forward primer	Reverse primer	Forward primer	Reverse primer	Forward primer	Reverse primer	Forward primer	Reverse primer
gep1-Kin8b11	GAAGTITIGGA	CTGATATAAG			TTATTTTGT	GAGAGTGTGGG	GAAGTTTGGA	GAGAGTGTGGG
gep1-PF1611	ATAAAAGATG	ATGGAGCCG e of sgRNA	ACAAAACAAA	GAGAAAAGCC	GAGGAAGATT	CAACTTCATT	ATAAAAGATG	CAACTTCATT
Strain	Forward oligo	Reverse oligo						
gep1-Kin8b11	TATTGTATTGATTCCGAGTC TGAAA	AAACTTTCAGACTCGGAATC AATAC						
gep1-PF1611	TATTGTTATTGCAAGAGATT AATGG	AAACCCATTAATCTCTTGCA ATAAC						
Diagnostic PCR primers for a	xonemal intron inserted into	gep1						
Strain	P1	P2	P3	P4				
gep1-Kin811	TATTGAGCTACTGTCAGCAG	ACAAAAATAATACATCTATC	GCTTATATCAGCATCAAAAA G	CTCATTTTTCGGCTTATCAC				
gep1-PF1611	GTGATGTACGAAAAATTCGA	GGCAAGTGTTTATAGAATTG	CGGCTCCATTTTTATTGCAA	GAAAGCAATGATGTCTCATC C				
Primers for RT-PCR				-				
Primer name	Primer sequence	Primer name	Primer sequence		Primer name	Primer sequence	Primer name	Primer sequence
kinesin8b F1	CAAAGTTAATCTTCAAGAGT	kinesin8b R1	AGTTCATCTTGCAATCCTTC		PY17X_1357300 F6	GGAATTTGCAGAAAGTACC C	PY17X_1357300 R6	CGATTTTTTTTCCGATTTTT
kinesin8b F2	GAAAACATAACAGATAAAGA	kinesin8b R2	CTCCTCAAGCATCTTAATAT		PY17X_1357300 F7	GGAGAAGCCACTCAACTTA	PY17X_1357300 R7	GTATCATTAAACATGGAATC
PF16 F1	CATTTATTAAATCAGGGTGC	PF16 R1	TCGGTATTTTCAACTTCATC		PY17X_1335600 F1	CAATGAAGAAGGAAATTCC	PY17X_1335600 R1	GAACTATCCGAGCAACTCT
dhc6 F19	CAAGAAAATGATGCATTAAA	dhc6 R19	GTAGCGTTGATTTTCCACTA		PY17X_1452900 F1	CAGCCTGAATATAAACCTAA	PY17X_1452900 R1	ATATGCTGTTTAAACTCCAC
dhc6 F20	TTTCTACAACAAGAGAGAAT	dhc6 R20	GGAGTCATATAATTGATCTT		PY17X_1452900 F2	GTGGAGTTTAAACAGCATAT	PY17X_1452900 R2	ATCAGCAAAACTTATGTGGG
dhc7 F6	GAGGCAATTATGATGACGT	dhc7 R6	CTTCAAAACATGATTTAACA		PY17X_1122300 F1	GCCTTTTTAGCTATTTTTGT	PY17X_1122300 R1	GTAGAATCCGAAGTAATTCG
dhc7 F7	CCTACTAATCTTATAACATT	dhc7 R7	TTTGTATCTCAATAAGCTTC		PY17X_1122300 F2	CGAATTACTTCGGATTCTAC	PY17X_1122300 R2	TTCCATTTATGATAATCGTC
dhc7 F8	ATCTGATCCAAGAATACAAC	dhc7 R8	GCTCACGAATATTAGTTCCC		PY17X 0523500 F1	TAACACCATATAACAATAAC	PY17X 0523500 R1	ATAATGTGAAAAGATCTTCC
dic1 E3						0100101T0T1T0TT10010	DV47V 0500500 D0	CCCATCCACAATTCCAACC
uiu i l U	ACGTTTTAAAGAACAAAATG	dlc1 R3	TAATGTATTTGAGAGGAAGC		PY17X 0523500 F2	CACCACATCTATCTTACCAG	PY17X 0523500 R2	GOGATCCAGAATTGCAAGG
dlc1 F4	ACGTTTTAAAGAACAAAATG TGGTCCAACATAATTTGTGA	dic1 R3 dic1 R4	TAATGTATTTGAGAGGAAGC TGAATAGAAGTCTCTGCATT		PY17X_0523500 F2 PY17X_0523500 F3	GACAATATTCCAGACACTAA	PY17X_0523500 R2	AATTTGTGGAAATGTCCAGA
dic1 F4 dic1 F5	ACGTTTTAAAGAACAAAATG TGGTCCAACATAATTTGTGA AG GCTACATTTTAAAGAATTCG	dic1 R3 dic1 R4 dic1 R5	TAATGTATTTGAGAGGAAGC TGAATAGAAGTCTCTGCATT CG GCACAATATATATGAGCATG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4	GACAATATTCCAGACACTAA CAAATTCCCAGACACTAA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X 0508900 R4	AATTTGTGGAAATGTCCAGA
dic1 F4 dic1 F5 dic2 F1	ACGTITTAAAGAACAAAATG TGGTCCAACATAATTTGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTTTTC	dic1 R3 dic1 R4 dic1 R5 dic2 R1	TAATGTATTTGAGAGGAGGA TGAATAGAAGTCTCTGCATT CG GCACAATATATATATGAGCATG TTCAACTTGTATAGCATTTG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5	GACAATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGAGGACTTAATTCA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5	AATTTGTGGAAATGTCCAGA CCTTCTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT
dic1 F4 dic1 F5 dic2 F1 dic2 F2	ACGTITTAAAGAACAAAATG TGGTCCAACATAATTTGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTTTTC AAATCTAATATTCCTTATCA	dic1 R3 dic1 R4 dic1 R5 dic2 R1 dic2 R2	TAATGTATTTGAGAGGAAGC TGAATAGAAGTCTCTGCATT CG GCACAATATATATGAGCATG TTCAACTTGTATAGCATTTG CTTTGCTGAGATGTTAAACG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6	GACAATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGGACTTAATTCA G GCTTTCTTATGATGTTAACA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6	AATTTGTGGAAATGTCCAGA CCTTCTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTIGCTTTCTTCGCTC
dic1 F4 dic1 F5 dic2 F1 dic2 F2 dic2 F1	ACGTITTAAAGAACAAAATG TGGTCCAACATAATTTGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTTTTC AAATCTAATATTCCTTATCA ATGCTACAAAACAATCTTAA	dic1 R3 dic1 R4 dic1 R5 dic2 R1 dic2 R2 dic2 R2 dic1 R1	TAATGTATTTGAGAGGAAGC TGAATAGAAGTCTCTGCATT CG GCACAATATATATGAGCATG TTCAACTTGTATAGCATTTG CTTTGCTGAGATGTTAACCG TTTCCAAATTTCTTAACAGAC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1	GACAACATCHATCHACLAG GACAATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGAGGACTTAATTCA G GCTTTCTTATGATGTTAACA GGGAAGATAACATTGAGGA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1	AATTIGIGGAAATGICAGA CCTICTTTTACTCATTAAT GTGTGICATCAATTAGTIGT CGCATTIGCTTICTICGCTC TATGIACTAGTTTTTICTGC
dc1 F4 dc1 F5 dc2 F1 dc2 F2 dc2 F2 dc1 F1 dc2 F2	ACGTITITAAAGAACAAAATG TGGTCCAACATAATTIGTGA AG GCTACATTITAAAGAATTCG ATGAGTTCCGAAAATTITTC AAATCTAATATTCCTTATCA ATGCTACAAAAACAATCTTAA GTCCAACCACTTTAAGATGG	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R1 dict R2	TAATGTATTTGAGAGGAAGC TGAATAGAAGTCTCTGCATT CG GCACAATATATATGAGCATG TTCAACTTGTATAGCATTTG CTTTGCTGAGATGTTAAACG TTTGCAAATTTCTTAACAGAC CTATTAACACATTTACACTG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508500 F4 PY17X_0508500 F5 PY17X_0508500 F6 PY17X_0508500 F6 PY17X_1320300 F1 PY17X_1320300 F2	GACAATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGGACTTAATTCA G GCTTTCTTATGATGTTAACA GGGAAGATAACATTGAGGA G CTCATGAAAATTTGGAAGAG	PY17X_0823500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R2	ATTIGTGGAAATGCCAGA CCTTCTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTTCTCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGTGATTGCTTAA
de: F 5 de: F 5 de: 2 F 1 de: 2 F 2 de: 1 F 1 de: 1 F 3	АСЭТТТТАААСААААТЭ ТСЭСТССААСАТААТТТЭТСА АС СТАСАТТТТАААСААТТЭ АТСАСТТССБАААТТТС ААТСТААТАТТССТТАТСА АТССТААСААТСТТАА СТССААССАСТТТААСАТЭС ЭПТССААССАСТТААСТАСТСААТСЭ	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R1 dict R2 dict R3	TAATGTATTGACAGGAGC TGAATAGAAGTCTCTGCATT GG GCAATATATATGAGCATG TTCAACTTGTATAGCATTG CTTGCTGAGAGTGTTAACGG TTTGCAGATTTCTTAACAGAC CTATTAACACATTTAACAGG CGTTTTATCACCATTTACCTGC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_132000 F3 PY17X_132000 F3 PY17X_132000 F3 PY17X_13200 F3 PY17X_132000 F3 PY17X_13200 F3 PY17X_1200	GACAGACIATOTATOTIATOTIATOTIATO GACAGAGAGACACTAA GACAGAGGAGTTAATICA GCTITICITATGAGGATTAATICA GGGAAGATAACATIGAAGGA GCTCATGAAAATITIGGAAGAGG AAAATATTAAAATITGGAAGGG	PY17X_0523500 R3 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3	AATTIGTGGAAATGTCAGA CCTICTITTIACTCATAAT GTGTGTCATCAATAGTTGT CGCATTIGCTTCTCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGGATTGCTTAA CATTCATGGATTGCTTAA
dc1 F 4 dc1 F 5 dc2 F 1 dc2 F 2 dc1 F 1 dc1 F 2 dc1 F 3 dcc F 1	АССТІТТАЛАСААСАЛАТС ТОСТССАЛСАТАЛТІТСТСА АС ССТАСАТТІТАЛАСАЛТІСТ АТСАСТТССАЛЛАТТІС АЛТСАСТАСТАЛТАТТСТ АЛТСТАЛТАТТССТТАТСА ТОССЛАССАСТТТАЛАСТСА СССАЛССАСТТАЛАСТСАЛС АПТІТСАЛАСАТСАЛСАСАС СССАЛСССАСТАЛСАСАСА	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 drc1 R1 drc1 R2 drc1 R3 drc1 R3	ТААТБАТТТАСААGGAAGC ТСААТАGAAGTCTCTGCATT GC GC GCACATATATATGAGCATG TTCAACTTGTATAGCATTG CTTGCTGAGAGTGTTAACG TTTCAACATTTCTTAACAGAC C CGTTTTACACATTTACATCG C CGTTTTACACTTTCTTCCT		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_033600 F1	GACAGATATTCCAGACACTAA GACATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGGACTTAATTCA G GCTTTCTTATGATGTTAACA GGGAAGATAACATTGGAAGGG CTCATGAAAATTTGGAAGGG AAAATATTAAAATTGGAAGG	PY17X_0523500 R3 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_033600 R1	ATTIGTGGAAATGCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTGCTTCTTCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGAGTTTTCTTTGC CATTCATGAGTTGCTTAA CATTCATGAGTTGCTTTGA TTTTAAAGGGTCGGGGTTCT
de: F4 de: F5 de: F1 de: F1 de: F2 de: F3 de: F1 de: F2	АССТІТТАЛАСААСАЛАТС ТОСТССАЛСАТАЛТІТСТСА АС ССТАСАТТІТАЛАСАЛТІСТ АЛТАСТІТССАЛЛАТТІСТ АЛТСТАЛТАТТССТТАТСА АТССТАЛСАЛТАСТТАЛ СССАЛССАЛТТАЛАСТСА АПТІТСАЛАСАТСТАЛАСТСАЛ С СССАЛСССАЛТАЛТАСАЛА С	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 drcf R1 drcf R2 drcf R3 dbc R1 dbc R2	ТААТБАТТТАСААGGAAGC ТСААТАGAAGTCTCTGCATT GG GCACAATATATATGAGCATG TTCAACTTGTATAGCATTG CTTTGCTGAGATGTTAACCG TTTCAAATTTCTTAACAGAC CCTATTAACACATTTACTACCG C CGTTTTATCATTTACTTCCTCC CGTACTTTAATTTACCTCCT CGTACTTAATTTACCTCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_033600 F2 PY17X_0833600 F2 PY17X_083600 F2 PY17X_08407	GACAGATATTCCAGACACTAA GACAGAGAGGACTTTATCCGA AGACAGAGGACTTAATTCA G GCTTTCTTATGATGTTAACA GGGAAGATAACATTGGAAGGG CTCATGAAAATTTGGAAGGG AAAATATTAAAATTGGAAGC CAGATGCGGAGTATTAATGGC CAGGAACCCCGACCCTTTAA	PY17X_0523500 R3 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_0833600 R1	ATTIGTGGAAATGCCCAGA
dict F4 dict F4 dict F5 dic2 F1 dic2 F2 dict F1 dict F2 dict F3 dict F3 dict F1 dict F2 dict F3 dict F1 dict F2 dict F4 dict F	АСБТІТТАЛАВААСАЛАТБ ТБЕТССАЛСАТАЛТІТБГА АБ ВСТАСАТТІТАЛАВАЛТІСБ АТБАБТІССБАЛААТТІСТ АЛАТСТАЛТАТТССТТАТСА АТБСТАСАЛАСАЛТСТТАЛ БТССАЛССАСТТТАЛАВАТБ АПТІТБАЛАВАТБАТСАЛАБ С GCGACGGASTATATCCA C GGACGGASTATATCCA TCTACCTAGAGCTATGCGT	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 drcf R1 drcf R2 drcf R3 dbc R1 dbc R2 mrd B1	ТААТБАТТТАСААGGAAGC ТСААТАGAAGTCTCTGCATT GC GC GCACAATATATATGAGCATG TTCAACTTGTATAGCATTG CTTTGCTGAGAGTGTTAACGG CTATTAACAGATTTACTGCG CGTTTTATCATTACTTCCT TTCAAAATTTACTTCCTCC CGTACTTAATTTACTTCCTCC C		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_141200 F1	CACACATOTATOTATOTATOTATOTATO GACAATATOCAGACACTAA CAAATTOCAGACTATTACAG GCITICOTATGATGATAACA GGGAAGATAACATTGAGGA GCITAGAAAATTGAGGA GCAGATGAGAGATATAATGGAAAGC CACATGAGAGTATTAATGGC AAAATATTAAAATTGAAAGC CACAGATGGACATTGACAT CACAGTAGGCAATGGACATTGAAT CACAGTATGGACATTGGACATGGACT	PY17X_0523500 R2 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_0833600 R1 PY17X_0833600 R2 PY17X_141200 R1	ATTIGTGGAAATGCCAGA ATTIGTGGAAATGCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTTCTTGCCTC TATGTACTAGTTTTTTCTGC CTCGTCATGAGTTTTTTTCTGC CTCGTCATGAGGTTCTTTTGA TTTAAAGGGTCGGGGGTTCT G TATTTAATGCCTCAATTTTC GGAGTGCCGGGTTTTTTCG
dc1 F4 dc2 F5 dc2 F1 dc2 F2 dc1 F1 dc1 F1 dc1 F1 dc1 F3 dc F1 dc F1 dc F1 dc2 F2 md2 F1	АСБІТІТАААGААСАААТС ТСБСТССААСАТААТТІСТБА АС АГАСАТТІТАААGАЛТСС АЛАГСТААТАТСССТААТСА АТСААТТАТТССТТАТСА АЛТСТААТАТТССТТАТСА АЛТСТААСААСААТСТТАА GCCAACCGGATAATCCAA CGCAGCGGATAATATCCAA CGCAGCGGATAATATCCAA CAGCTTATCAAAAACAATCGGA J TIGTGACTAGAAGCTATGCCGA	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 drcf R1 drcf R2 drcf R3 dbc R1 dbc R2 md2 R1 PYTX 1100100 R4	ТАЛТБАТТТАСААGAAGC ТСААТАGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TCAACTIGATAGCATTG TTCAACTIGATAGCATTG CTITTGCTGAGATGTTAAACGAC TTTTCAAATTTCTTAACAGAC CTATTAACACATTTACACTGC C GGTACTTTAACTACATTTACCTCC GGTACTTTAATTACCTCCC GGTACTTAATTACCTCCTGTGAATC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1	CACACATOTATOTATOTATOTATOTATO GACAATATOCAGACACTAA CAAATTOCAGACACTAA GCITICTIATGATGTTAACA GCITICTIATGATGTTAACA GGGAAAAATACATTGAGGA G CICATGAAAATTTGGAAGAG AAAATATTAAAATTGGAAGGA CAGATGGACATTAAATGGC CAGATGACAATAGAAGT A GCAGTAAAACTOCACTOCACTOCA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R1 PY17X_0833600 R1 PY17X_0833600 R2 PY17X_1341200 R1 PY17X_1341200 R1	AATTIGTGGAAATGCCAGA CCTICTITTACTGGAAATGCCAGA CCTICTITTACTCATTAAT GGGGTCACAATAGTTGT CGGATTGCTTCGCTC TATGTACTAGTTTTTCTGGC CTCGTCATGTGATTGCTTAA CATTCATGAGGGTCGGGGGTTCT G TATTTAAGGGCTCGAGGTTTTTTC GGATGTCGAGTTTTTTTCCCT
dc1 F4 dc2 F2 dc2 F2 dc1 F5 dc2 F2 dc1 F1 dc1 F2 dc1 F3 dc6 F1 dc6 F1 dc7 F2 md2 F1 PY17X_1100100 F1 PY17X_100100 F2	АСЭТТТТАААВААСАААТЭ ТӨӨТССААСАТААТТТӨТА АЭ ССТАСАТТТТААВААЛТТӨТС АЛАТСТААТАТТССТТАТСА АТВСТАССААЛТСТТАС АТВСТАССААЛТСТТАА СССАСССАСТТТААВАТЭЭ СССАСССАСТТТААВАТЭЭ СССАСССАСТТТААВАТЭЭ СССАСССАСТАТААСАТССА САЭТТАСТААВАСТАТССАТА САЭТТАСТАВАЭСТАТСССАТА ЛТВССАСССТТЭТСАССАСССС ОДСТБСТАСААЛССТТЭ	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R2 dict R2 dict R3 dick R1 dick R2 md2 R1 PY17X_1109100 R1 PY17X_1109100 R2	ТАЛТБАТТТАСАСАДОАСС ТСАЛТАДАЛАГСТСТССАТТ СС СС ССАСАЛАТАТАТАТАСАСАТС ПСААСТТБАТАВСАТТС СТИТССТСАДАТТТАСАСАСС СТИТТАССАСАТТТАСАСТС ССТИТТАСАСАТТТАСАССС СССТИТААСАСТТТАСССС СССТИТААТТТАСТССС СССТИТААТТТАСТССС СССТИТААТТТАСТССС СССТИТААТТАСТССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССС СССТИТААТТАСТСССССССССС		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1341200 F2 PY17X_134120	CACCACITICTATCTATCTATCA GACAATATTCCAGACACTAA CAAATTCCAGACACTAA GCTTTCTTATGATGTTAACA GCTTTCTTATGATGTTAACA GCTTCTTATGATGATAACA GGAAAGATAACATTGAAGAG CTCATGAAAATTTGAAAGAC CAGATGGAGTATTAATGGC AGAATTGCAATAGAAG GAGAATGCACATAGAAGT GAGATACCCGAACTCCGACATCC GAGATTGCAATAGCAATGCAAT	PY17X_0523500 R2 PY17X_0523500 R4 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_0833600 R2 PY17X_0833600 R2 PY17X_1341200 R1 PY17X_1341200 R1 PY17X_1341200 R2 PY17X_1341200 R2	ATTIGTGGAAATIGCAAAG AATTIGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGGTCATCAATTAGTTGT CGCATTTGGCTTCTTGCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGAGTTTCTTTGA TTTAAAGGGTCCGGGGTTCT G TATTTAAGGCTCCAGTTTTACCT TACAAATGATACTTTTGCG CGCGGCTCCAGTTTTACCG
dict F4 dict F5 dict F5 dict F5 dict F1 dict F2 dict F3 dict F3 dict F3 dict F1 dict F3 dict F1 dict F3 dict F1 PY17X_1109100 F1 PY17X_021800 F1	АСЭТІТТАААGААСАААТЭ ТӨĞТССААСАТААТІТӨТА АĞ GCTACATITTAAAGAATTCG ATBAĞTICCGAAAATITITC AATGCTATATICCTITATC AATGCTATATICCTITATC ATGCTACAAAACAATCTTAA GTCCAACCACTITAAGATGG CGCAGCGGATAATATCCAA GAĞTTATCAAAAACAATGGA CTAGCTAGAGCTATGCGTA CTAGCTAGAGCTATGCGTA TIGTCACTCTTGTTGAGCC GGGTGTTGAAAAAGTTT	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R2 dict R2 dict R3 dic R1 dick R2 md2 R1 PY17X_1109100 R1 PY17X_0109100 R2 PY17X_021800 R1	ТАЛТБАТТАGAAGAAGC ТGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGTATAGCATTG CTTTGCTGAGATGTTAAACG TTTTCAAATTTGTAACAGAC CTATTAACACATTTACACTG C CGTTTATCATTTTCTTCCT TTCAAAATTTACTTCCTC TCAATAGGAACTTGTGAATC GCTGTGTATATGTACGAGTC TTCGGAAAGTTCTTCGACAC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0333600 F1 PY17X_0333600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_13415400 F10 PY17X_1305400 F10 PU17X_1305400 F10 PU17X	САССАСАТСТАТСТАТСТАТСТАТСА GACAATTCCAGACACTAA CAAATTCCAGACACTAA CAAATTCCAGAGAGACTTAATTCA G GCTTTCTTATGATGTTAACA GGGAAGATAACATTGAGAGA CACATGAAAATTTGAAAGC CAGAATCCCCGACCCTTTAA GCAGTAATGACTAGAAATT GCAGTAATGACAATGGAAATT GAGATTTGTACCAATGCAATCGCA CACAAAGAAAGGCAATCATCG	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_0833600 R1 PY17X_0833600 R2 PY17X_1341200 R1 PY17X_1305400 R12 PY17X_1305400 R12	ATTIGTGGAAATIGCAAGA AATTIGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTGGTGTCTTCGCCC TATGTACTAGTTTTTCTGC CTCGTCATGAGTTTCTTTGA TTTAAAGGGTCCGGGGTTCT G TATTTAATGCCCCAATTTTC GGATGGAGTTTTTATCCT TACAAATGATACTTTTGCC CCTGACTCCATATTATATCT
dc1 F4 dc2 F4 dc2 F5 dc2 F1 dc2 F2 dc1 F1 dc1 F2 dc1 F3 dc6 F1 dc6 F2 md2 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F2	АСЭТІТТАААGААСАААТЭ ТӨĞТССААСАТААТІТӨТА АĞ GCTACATITTAAAGAATICG ATGAGTICCGAAAATITICG AATGCTAACAAACAATCTTAA ATGCTACAAAACAATCTTAA GTCCAACCACTITAAGATGG ATTTGAAGATGATCAAGAG CGCAGCGGATAATATCCAA GCTAGCTAGAGCTATGCGTA TIGTCACTCTTGTTGAGACTGA TIGTCACTCTTGTTGAGACATT CGAAACGAATATAACAGTTA	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R2 dict R2 dict R2 dict R3 dic R2 md2 R1 PV17X_1109100 R1 PV17X_0521800 R1 PV17X_0521800 R2	ТАЛТБАТТАСААGAAGC ТGATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGATAGCATTG TTTCAACTTGATAGCATTG TTTCAATTTGTAAGCATT CATTAACACATTTACACGG CGTTTTATCATTTCTTCCT TTTCAAAATTTACTTCCTC CGTACTTTAATTACTTCCTC GCTGTGTATATGTACGAGTC TCGAAAAGTTCTTCCACAC CTCGTCAGAATTAAAGTATT		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F2 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PU17X_1305400 F13 PU17X_	CACCARACTATCICAGE GACAATATCCAGACACTAA CAAATTACCAGACACTAA CAAATTACCAGACACTAA CGCAAGAGGAGACTTAATTCA G GCTTICTTATGATGATTAACA GGGAAGGATAACATTGGGAG CTCATGAAAATTTGGAAGAG AAATATTAAAATTGGAAGAG CAGATGGAGTATTAATGGC CAGATGGAGTATTAATGGC AGGATAAAAACTCGACATCCA GAGATTGTACGAATTGCGA CACAAAGAAAGGCAATTCATG T	PY17X_0523500 R2 PY17X_0523500 R4 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R1 PY17X_1320300 R1 PY17X_0833600 R1 PY17X_0833600 R2 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R12	AATTIGAGAAATGCCAGA CCTICTITTIGGGAAATGTCCAGA CCTICTITTIGGGAAATGTCCAGA CCTICTITTIGCATCAATAGTTGT CGCGATTIGCTICTCTCGCC TAGTACAGGATTGCTTAA CATTCATGAGTTGCTTGA TITTAAAGGGTCGGGGGTTCT G GATGTCGAGGTTGTTTGCG CCTGACTCGATAGTATATCT GTCATTGATAAGTGTTCGTCG GATGTCGATGATGTTCGTCG
dic 1 F3 dic 2 F4 dic 2 F5 dic 2 F1 dic 2 F2 dic 1 F3 dic F1 dic F1 dic F2 dic 1 F3 dic F1 PV17X_1109100 F1 PV17X_1109100 F1 PV17X_0621800 F1 PV17X_0621800 F2 PV17X_0621800 F2 PV17X_0621800 F2	АСЭТТТТАААGААСАААТЭ ТGGTCCAACATAATTIGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTTTCA ATGCTACAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCCAACCACTTTAAGATGA ATTTTGAAGATGATCAAGAG CGCAGCGGATAATATCCAA C GAGTTATCAAAACAGTGAT A TTGTCACTGATGAGAGTATT CGAAACTGATGTTAAAAATA CGCAGTAAATATAGAGTTAG	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R2 dict R2 dict R3 dick R2 dict R3 dick R2 md2 R1 PY17X_1109100 R1 PY17X_1109100 R2 PY17X_0521800 R1 PY17X_0521800 R2	ТАЛТБАТТАСААGAAGC ТСААТАGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGATAGCATTG TTCAACTTGATAGCATTG TTTCAATTTGTTAACGATC CTTTTCAATTTCTTAACGAC CATTTAACACATTTACACTG C CGTTTTATCATTTACTTCCT TTCAAAATTTACTTCCTC TCAAAAGTTACTTCCTCC GCTGTGTATATGTACGACT TCGAAAAGTTCTTCGACAC CTCGTCAGAATTAACGTCTT TATAAAAACTTCTTCGCAG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F2 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_1	CACCACATCHATCHATCHATCAG GACAATATTCCAGACACTAA CAAATTCCAGACACTAA GGCAGAGGACTTAATTCA GCTTTCTTATGATGTTAACA GGGAAGGATAACATTGGAGAG CTCATGAAAATTTGGAAGAG AAATATTAAAATTGGAAGAG CAGATGGAGTATTAATGGC A GGGATAACCCCGACCCTTTAA GCAGTAATGACCATCGACATCC GAGATTGTACGAGAATGTCCACATCG GACAAAGAAGGCAATCATG GATTCTGAGGAATTTGACA	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_0833600 R1 PY17X_0833600 R1 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R13 PY17X_1305400 R13	AATTIGAGAAATGCCAGA CCTICTITTIGGGAAATGCCAGA CCTICTITTIGGGAAATGTCCAGA CCTICTITTIGGTGTCATCAATTAGTTGT GGGGTTGGCATCAATTAGTTGT CGCATTIGGTTGCTTGCGCC CTCGTCATGGGATTGCTTAA CATTCATGAGGGTGGGGGGTTCT G GATGTCGAGGTTTTTGCG CCTGACTCGAGTGTTTGCG TAGTGATGATGATGATGATCTG GATCATTGATTAGTTGCAT
de 1 F3 de 1 F4 de 2 F5 de 2 F1 de 2 F2 de 1 F3 de F1 de F2 de 1 F3 de F1 PY17X_1109100 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F2 PY17X_0521800 F4 PY17X_1311800 F4	АСБТІТТАЛАВААСАЛАТБ ТБĞТССАЛСАТАЛТІТБТА АĞ GCTACATTITAAAGAATTCG ATGAGTICCGANAATTITC AAATCTAATATTCCITATCA ATGCTACAAAACAATCTTA GTGCCAACCACTTIAAGATGG ATTITGAAGATGATCAAGAG CGCAGCGGGATAATATCCAA C GGGTGTGAGAGCTATGGGTA A TIGTCACTGTTGTGAGACGTTG GGGTGTTGTAGAAAAGTTTT CGAAGTGATTTACCAAAAC	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dic7 R1 dic7 R2 dic7 R3 dic R3 dic8 R1 dic8 R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_051800 R5	TAATGTATTTAGAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGTATAGCATG TTTGCTGAGATGTAAACG TTTGCTGAGATGTAAACG TTTGCAATTTCTTAACAGAC CGTTTTATCATTTTCTTCCT CGTACTTAACTTTACCTCC CGTACTTAACTTCCTCCC CGTACTTAACTTCTCCTCC CGTGTGTATATGTACGAGTC TTCGAAAAGCTTCTCGACAC CTCGTCGAAATTAAAGTATT TATAAAAACTTCTCCCCCG GGTCTCTATTTCCCCCCTC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_015500 F12 PY1	САССАСАТСТАТСТАТСТАТСА GACAATATTCCAGACACTAA CAAATTCCGATTTTACGAT AGACAGAGGACTTAATTCA GCTTTCTTATGATGTTAACA GGGAAGATAACATTGGAGAG AAAATATTGAAAATTTGAAAGC CAGATGGAGTATTAATGGC A AGGATAAAAACTCGACATCG GAGATATGACAATAGGAAGT AGGATAAAAACTCGACATCG GAGTATGAGAAGGCAATCATG CACAAAGGAGGCAATCATG CACAAAGGAAGGCAATCATG CACGAAGAATTTGCCAAACT	PY17X_0523500 R2 PY17X_0503500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R6 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_0833600 R1 PY17X_0833600 R1 PY17X_0833600 R1 PY17X_1341200 R1 PY17X_1305400 R12 PY17X_0415900 R12 PY17X_0415900 R12 PY17X_015900 R12	AATTIGAGAAATGCCAGA CCTICTITTIGGGAAATGCCAGA CCTICTITTIGGGAAATGTCCAGA CCTICTITTIGGTATCAATTAGTIGT GGGGTTGCATCAATTAGTIGT CGCATTIGCTTICTICGCC CTCGTCATGGGTTGTTTGA THTAAAGGGTCGGGGGTTCT G CATGATGAGGATGATGATCGT AATTGAAAGGGTCGGGGTTCT GCCGACTCCATATTATCT GTCATGATAAGGTGATCTGCAA CATCATTGGCATTTATCTCG CATCATTGGCATTTATCTCG CATCATTGGCATTTATCTCCA TCTTATGCATTTATCTCCCA
de 1 F4 de 1 F4 de 2 F2 de 2 F1 de 2 F2 de 1 F3 de F1 de F2 de 1 F3 de F1 de F2 md 2 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F4 PY17X_1311800 F5 PY17X_1311800 F5	АСБТІТТАЛАGААСАЛАТБ ТGGTCCAACATAATTIGTGA AG GCTACATTITIAAAGAATTCG ATGAGTTCCGAAAATTITG AAATCTAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTGCAACCACTTTAAGATGG CGCAGCCACCTTAAGATGG GGGTGGGGGATAATATCCAA C GGGTGGGGGGATAATATCGGA T TGTCACTCATGTTGAGACGG GGGTGGTTGGAGAGCTATGCGTA A TGTCACTCATGTTGAGACGGT GGAGTGATAATATAGAGTTGG GATATTACCCATAAGGTGG GATATTACCCATAAGGTGG	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dic7 R1 dic7 R1 dic7 R2 dic7 R3 dic8 R2 dic8 R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_051800 R2 PY17X_1311800 R4	TAATGTATTGAGAGGAGC TGAATAGAAGTCTCTGCATT GG GGACAATATATATGAGCATG CTTGCTGAGATGTAAGCATTG CTTGCTGAGATGTAAACG TTTGACTGAGATGTAAACG TTTGACACATTTACACTG C CTTTTATCATTTACTCCTC CGTACTTTAACTACCT CCGTGTGATATGTACGAGTC TCGAAAAGGTCTTCGACAC CTCGTCAGAATTAAGTATT TATAAAACTTCTTCGCCG GTCTCTATTTCCCACCT CGTAGCTAAATTCATGTGGAG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F13 PY17X_0415900 F12 PY17X_0415900 F13 PY17X_041590 PY17X_04150 PY17X_0415 PY17X_04150 PY17X_04150 PY17X_0415 PY17X_0415 PY17X_04	САССАСАТСТАТСТАТСТАТСА GACAATATTCCAGACACTAA CAAATTCCAGACACTAA GCTTTCTTATGATGTTAACA GCTTATGAGACATTGAGGA GCTCATGAAAATTTGAAAGGA CAGATGGAGTATTAATGGCA AAAATATTAAAATTGAAAGC CAGATGGAGTATTAATGGCA A GCAGTAATGACCACGACCCTTTAA A GCAGTAATGACACTGACATCG GATATTGACGAATATGTCCA CACAAAGAAGGCCACTCTGA GATTCGAAGAAGTGTCCACTCG GATTCGAAGAAGTTTGATCACACAATG GCCACATTTTTACGAAAATG	PY17X_0523500 R3 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_05083060 R1 PY17X_0633600 R1 PY17X_0383600 R2 PY17X_1320300 R1 PY17X_0833600 R1 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_0415900 R12 PY17X_0415900 R12 PY17X_0415900 R13 PY17X_0415900 R13 PY17X_0415900 R13 PY17X_0415900 R13 PY17X_0415900 R13	AATTIGTGGAAATGCCAGA CCTICTITTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTCTICTCGCCC TATGTACTAGTTTTTCTCGCCCC TATGTACTAGGTTTTTTCTGC CCTCGTCATGGAGTTCTTTGA TITTAAAGGGTCGGGGGTTCT GGATGTCGAGGTTTTTTCC GGATGTCGAGGTTTTTTCCG CCTGACTCGAGTCTTTGCA TCTTATGCATTTTTCCC AGTATGCTCTGGCCCTTAT
dic1 F4 dic1 F4 dic1 F5 dic2 F1 dic2 F2 dic1 F1 dic1 F2 dic1 F2 dic1 F3 dic1 F3 dic	АСЭТТТТАААGААСАААТЭ ТGGTCCAACATAATTIGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTGT AAATCTAATATTCCTTATCA ATGCTACAAAACAATCCTTAA GTGCCAACCACTTTAAGATGG GTGCAACCACCTTAAGATGG ATTTTGAAGATGATCAAGAG GGGGGGGGATAATATCCAA CTAGCTAGAGCTATGCGTA A TTGTCACTCTTGTTGAGCGC GGGTGTGTTAGAAAAGTTTT CGAAACTGATGTTAAAATA CGCAGTAAATATAGAGTTAG ATATGCTTTACCAAAAC	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dic1 R1 dic2 R2 dict R1 dict R2 dict R3 dick R3 dick R4 dick R3 dick R4 dick R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R5 PY17X_1311800 R6	TAATGTATTGAAGAGAAGC TGAATAGAAGTCTCTGCATT GG GGACAATATATATGAGCATG TTCAACTTGTATAGCATTG CTTTGCTGAGATGTTAAGCATTG CTTTGCTGAGATGTTAACGAC CTATTAACACATTTACACTG C CGTTTTATCATTTACTTCTC TTCAAAATTACTTCCTCC CGTACTTTAATTACTTCCTCC CGTGTGTATATGTACGAGTC TTCGAAAAGTACTGTGGAATC GCTGTGTATATGTACGAGTC TTCGAAAAGTTCTTCGACAG CTCGTCAGAATTAAAGTATT TATAAAAACTTCTTCGCACG GTCTTCATTTCCACCTC CGTACTAATTCCATGGCAG ATATCTATATCCATGGCAG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_0833600 F2 PY17X_1305400 F10 PY17X_1305400 F10 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_0105800 F1 PY17X_0105800 F1 PY17X_0105800 F1	САСАСАТСТАТСТАТСТАТСТАТСА GACAATTCCAGACACTAA CAAATTCCAGACTTTACGA GCTTCTTATGATGTTAACA GGCTTCTTATGATGTTAACA GGCTAGAAAATTGAGAGA CTCATGAAAATTGGAAGAGA AAAATATTAAAATTGAAAGC CAGATGGAGTATTAATGGC AGGATAAAACTCGACATCG GACATGGACAATAGAAGT GCTGACAAGGAATTGATCA CGCTGACATTTTACGAAATG CCACATTTTTACGAAATG CCACATTTTTACGAAATG CCACATCTTTCCTCAA GCTACCTGTCTTATTTTAC GAGAGGAAACATAAATTGTTCC	P117X_0523500 R2 P117X_0508900 R4 P117X_0508900 R4 P117X_0508900 R5 P117X_0508900 R5 P117X_0508900 R6 P117X_1320300 R1 P117X_1320300 R2 P117X_1320300 R1 P117X_0833600 R1 P117X_0833600 R1 P117X_1341200 R2 P117X_1305400 R10 P117X_1305400 R10 P117X_1305400 R13 P117X_0415900 R13 P117X_045900 R13 P1	AATTIGTGGAAATGCCAGA CCTICTITTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTCTTGCCCTC TATGTACTAGTTTTTTCTGCCCC CTCGTCATGTGATTGTTTTGA CATCCATGGAGTTCTTTTGA TATTAAAGGGTCGGGGGTTCT GAATGCCGAGGTTCTTTTGCG CCTGACTCGAGTTCTTTTGCG CCTGACTCCATAGTGATCGC CATCATGATAAGTTGATCTG GCATGTCCTGGCCTTAT ACGTCCTCAAACTTGAGCCT CATTCCATGCACTGAGCCTC
dc1 F4 dc1 F4 dc1 F5 dc2 F1 dc2 F2 dc1 F1 dc1 F2 dc1 F3 dc F1 dc1 F3 dc F1 dc1 F3 dc F1 pv17X_1109100 F1 pv17X_1109100 F1 pv17X_0521800 F1 pv17X_0521800 F2 pv17X_0521800 F5 pv17X_1311800 F6 pv17X_1323900 F1 pv17X_1323900 F1	АСЭТІТТАААСААААТС ТСӨСТССААСАТААТТІСТСА АС АТАСАТТІССВАААТТІТС АЛАГСТААТАТІССТІТАГСА АТАСТАТАТАТІССТІТАГСА АТАСТАТАТАТІССТІТАГСА АТТІСААСАСАТТТААДАТСЯ СССАССССАТТТААДАТСЯ СССАССССАТТААДАТСАА СССАСССАТТААСАТССАА СССАСССАТАТАТАССАА ТІСТАССТАСАТТАССАА СССАСТАСАТТАСААСАСТСА СОСАСТАСАТТАСАСАТ СССАСТАДАТСТААДАТТА СССАСТАЛАТТАСААТТАС АТАТТАСССАТААСТТАС АТАТТАСССАТАЛСТІС АТАТТАСССАТАЛСТІС АТТАТАСССАТАЛСТІСС	dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dicf R2 dicf R3 dic R2 dicf R3 dic R1 dic R2 md2 R1 PY17X_1109100 R1 PY17X_109100 R2 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1323900 R1	TAATGTATTGAGAGGAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGGAGCATG TTGACTGGAGATGTAAACG TTTGACAGACTGTAAACG CTATTAGCAGATTTACACTG C CGTTTTATCACACATTTACACTG C CGTTTTATACACATTTACTTCCTC TTCAAAATTTACTTCCTCC GGTACTTTACTT		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0105800 F1 PY17X_1216400 F1 PY17X_005800 F1 PY17X_005800 F1 PY17X_005800 F1 PY17X_005800 F1 PY17X_1216400 F1 PY17X_005800 F1 PY17X_005800 F1 PY17X_1216400 F1 PY17X_005800 F1 PY17X_00580 F1	CACACATOCIATO INICINAL INICAS GACAATATTCCAGACACTAA CAAATTCCAGATTITACGA GCITICTIAIGATGITAACA GGAAGAGAAGATAACATTGAGGA GCITICTIAIGATGITAACA GGGAAAGATAACATTGAGGA AAAATATTAAAAATTGAAAGC CAGATGGAGTATTAATGGC AAGATGGAGTATTAATGGC AAGATGCCCGACACTTAA A GCAGTAATGACAATAGAAG CACAAAGAAGGCAATCGACATCG GACATCGAGGAAATTGATCA CGCAGACATTTAACAGAATG GCCACCTGICTIAITTTATC GAGAGGAAACATTAAAAGAGG CGCAGACATTAAAAGAGG	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_0833600 R1 PY17X_0833600 R1 PY17X_0833600 R1 PY17X_1341200 R1 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R13 PY17X_0415900 R13 PY17X_0415900 R13 PY17X_10415900 R13 PY17X_1216400 R4 PY17X_1216400 R4	AATTIGGAAATIGCAAAA AATTIGGAAAATGTCCAGA CCTICTTTTACTCATTAAT GTGGTCATCAATTAGTTGT CGCATTIGGTTGCTTCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGAGTTTGTTTGA CATTCATGAGTGGTTTTTG GATGTCGAGGTTTTTG GGATGTCGAGTTTTTTG GCATCGTCATGATTATATCT GCATCGTCATGATTATATCT GCATCGTCATGATTTTTGCA TCTTATGCATTTTTGCCA TCTTATGCTCTGGCCCTTAT ACGTCCTCCAAACTTGGCCC CTTTCTCAACTCATAAGTTTG
dc1 F4 dc1 F5 dc2 F2 dc1 F5 dc2 F2 dc1 F1 dc1 F2 dc1 F2 dc1 F3 dc F1 dc F2 dc F1 dc F1 dc F1 dc F2 dc F1 dc F1 dc F2 dc F1 dc F1 dc F2 dc F1 dc F1 dc F2 dc F1 dc F1 dc F1 dc F2 dc F1 dc F1 dc F2 dc F1 dc F1 dc F1 dc F2 dc F1 dc F1 dc F1 dc F2 dc F1 dc F2 dc F1 dc F1 dc F2 dc F1 dc F1 dc F1 dc F2 dc F1 dc F1 dc F1 dc F1 dc F2 dc F1 dc F1	АСЭТІТТАААВААСАААТЭ ТЕĞƏTCCAACATAATTIGTĞA AĞ GCTACATTITAABĞAATTGĞ ATISAĞITCCGAAAATTITC AATGCTATCATATTCCTTATCA ATGCTACCAACATCTTAA GTCCAACCACTTTAAĞATGĞ GTCCAACCACTTTAAĞATGĞ ATTITGAAĞATĞATCAAĞĞ GĞGTGTGTAGAAGACTATĞĞA TIĞTCCACCCTTIĞTTĞAĞĞA AĞGTGTTGTAĞAAAĞTTT GĞAACTĞATĞTTAAAATA CGCAĞTAATATAĞAĞTTĞĞ ATTATACCATAAĞĞTGTĞ ATTTAAĞATIĞTATCCTACAĞ	dict R3 dict R4 dict R4 dic2 R1 dic2 R1 dic2 R1 dic2 R2 dict R3 dic R2 dic1 R3 dic R2 dic1 R3 dic R2 md2 R1 PY17X_1109100 R1 PY17X_021800 R1 PY17X_021800 R2 PY17X_021800 R2 PY17X_1311800 R4 PY17X_1311800 R6 PY17X_1300 R5	TAATGTATTGAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTGATAGAAGTGTAGAGCATG TTTGCTGAGATGTTAAACG TTTTGCTGAGATGTTAAACG CTATTAACACATTTACACTG C CGTTTTATCATTTTCTTCCT TTCAAATTGCTCCC CGTCTTTAATTACCTGCC GCTGTCAGAATTACGTACG GCTGTCAGAATTACGACG GTCTCTATTTCCTCCACTCT CGTAGCTAAATTCCTCCCCCG GTCTTCTATTTCCTCCACTCT CGTAGCTAAATTCCTCGTCAG GTCTCTATTTCCTCCACTCT CGTAGCTAAATTCCTCGTCAG GTCTTCTATTTCCTCCACTGT GTAGCTAAATTCCTCGTCAG GTCTTCTATTTCCTCCACCG GTCTTCCAGTTTTATCCACA		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_13203000 F2 PY17X_1341200 F1 PY17X_0833600 F1 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0105800 F1 PY17X_0105800 F1 PY17X_1216400 F4 PY17X_1216400 F5	САССАСАТСТАТСТАТСТАТСТАТСА GACAATTCCAGACACTAA CAAATTCCAGACACTAA GCTTTCTTATGATGTTAACA GCTTTCTTATGATGTTAACA GCTTCTTATGATGATTGAAGA CTCATGAAAATTTGGAAGAG AAAATATTAAAATTGGAAAGAC CAGATGGAGTATTAATGGC AGGATATGACAATAGAAGT GCAGTAATGACCCGACCCTTTAA AGGATAAAAACTCGACATGCCA CACAAAGAAGGCAATCACAG CACAAAGAAGGCAATCACTG CTCCGACAATTGTACCAATGTCCA GCTCCTGACGAAATGTTCCTCAA GCCACAATTTTACGAAAATG GCTACCTGTCTTATTTATC GAGAGGAAACATAAATTTGT CGCCAGACATTAAAAAGGGG	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_13203000 R2 PY17X_0833600 R2 PY17X_0833600 R2 PY17X_0833600 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R13 PY17X_0105800 R1 PY17X_0105800 R1 PY17X_0125400 R4 PY17X_1216400 R5	AATTIGTGGAAATGTCAGAA AATTIGTGGAAATGTCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGGTTCTTCGCTC TATGTACTAGTTTTTTCTGC CTCGTCATGTGATTGGTTTGC CTCGTCATGTGATTGGTTTGA TTTAAAGGGTCCGGGGTTCT G TATTTAATGCCCCAATTTTC GGATGTGGAGTTTTTTGCG CCTGACTCCATATTATATCT CATCATGATAGTTGGACTG CATCGTTCTGCACTGGCCTTAT ACGTCTCTAACTGACCTC CTTGTCACTCAAGTTGGACTC CTTGTCTCTCGTTCCGTTC
def F4 def F5 def F5 def F5 def F1 def F2 def F1 def F2 def F3 def F1 def F2 def F3 def F1 def F2 md2 F1 PY17X_1108100 F1 PY17X_1108100 F1 PY17X_0521800 F1 PY17X_0521800 F2 PY17X_0521800 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_137300 F5 PY17X_137300 F5 PY18X_157300 F5	АСЭТІТТАААВААСАААТЭ ТЕĞƏTCCAACATAATTIGTĞA AĞ GCTACATTITAAABGATITGĞ ATBAĞITCCGAAAATITITC AATGCTACTATATTCCTITATCA ATGCTACCAACAACATCTTAA GTCCAACCACTTTAAGATGG ATTITGAAGATGATCAAGAG GCGAGCGGATAATATCCAA GAĞTTATCAAAAACAACTGGA CIAGCTAAGAGCTATGGCGTA CIAGCTAGAGCTATGGCGTA GAĞTGTGTGAGAAAGTTTT CGAAACTGATGTTAAAAATA GCGCAGTAATATAGAGTGG ATTATACCCATAAGGTGTG ATTATAAGATTGTATCCTACAG GATATTACCCAAAAAGTGTG AATATAAGCATCATACAGAGT	dict R3 dict R4 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R2 dict R3 dic R1 dict R3 dic R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_1311800 R4 PY17X_1311800 R6 PY17X_13123300 R1 PY17X_13157300 R5			PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0333600 F1 PY17X_0333600 F2 PY17X_1321200 F1 PY17X_1341200 F2 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_0415900 F13 PY17X_0105800 F1 PY17X_1216400 F4 PY17X_1216400 F5	CACCACATOTATOTATOTATOTATO GACAATATOCAGACACTAA CAAATTACCAGACACTAA GCTITCITATGATGTTAACA GCTITCITATGATGTTAACA GCCACAGAGAGATAACATTGAGGA GCACAGAGATAACATTGAGGA GCACATGGAGATATAAATGGC CAGATGGAGATATAAATGGC AGGATACCACGAATGCGAA CACAAGAGGCAATCAGACT CACAAAGAGGCAATCAGT CACAAGAGGCAATCAGT GCTICGAAGAATGTTTCCTCAA GCCACATTITTACGAAAATG GCTACCTGTCTTATTTTATC GCGCAGGCAACATAAAATTGT CCCACAACATTAAAAAGGGG	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R3 PY17X_13203000 R1 PY17X_0833600 R1 PY17X_0833600 R2 PY17X_1305400 R1 PY17X_1305400 R12 PY17X_1305400 R12 PY17X_1305400 R13 PY17X_0105800 R1 PY17X_0105800 R1 PY17X_1216400 R5	
def F4 def F5 def F5 def F1 dez F2 def F5 def F6 der F1 dec F1 dec F2 md2 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_1357300 F5 Pterst or RT-qPCR Location	ACGITITIAAAGAACAAATG TGGTCCAAACATAATTIGTGA AG GCTACATTITIAAAGAATTCG ATGAGTICCGAAAATTITIC AAATCTAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTITGAAGATGATCAAGAG CGCAGCGGATAATATCCAA CTAGCTAGAGCATATGCGTA ATGTGTTATCAAAAACATGGA TTGTCACTCTTGTTGAGCGC GGGTGTTAGAAAATATGGGTT GAAACTGATGTTAAAAATA CGCAGTAAATATAGAGTTGG ATTAAGATTGTATCCTACA GTATTTACCAAAAGTGTGTG ATTAAGATTGTATCCTCCG GTATTAGCACCAAAAATG AATATAAGCATCTATCCAAGG GGGGD	dict R3 dict R4 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R2 dict R2 dict R2 dict R3 dice R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_1300 R5 PY17X_131300 R5 PY17X_13100 R5 PY17X_13100 R5 PY17X_13100 R5 PY17X_13100 R5 PY17X_1300 R5 PY1	TAATGTATTGAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGATAGCATTG CTTTGCTGAGATGTTAAGCATG TTTCAAATTTGTAACGACT CTTTCAATTTCTTAACAGAC CTTTTAACACATTTACACTG CGTTTTATCATTTCTTCCT TTCAAAATTTACTTCCTC GCTGTGTATATGTACGAGTC CCGTCGTCAGAATTAAGTACT GCTGTGTATATGTACGAGTC TTCGAAAAGTTCTTCGACAC CTCGTCAGAATTAAGTACTT CGTAGCTAAAATTCATGTGGA ATATCTATTCTCAGTTTATACAC GGACGTTTTATGTACCAA GGATCGTTTTATGTACCAA Reverse primer Reverse primer		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0333600 F1 PY17X_0333600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_0115900 F12 PY17X_0115900 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location	CACCACATOCIATO TRACATA GACAATATTCCAGACACTAA CAAATTACCAGACACTAA CAAATTACCAGACACTAA GCTITCITATGATGTTAACA GCTITCITATGATGATTGAAGGA GCTITCITATGATGAAATTGGAAGGA AAAATATTAAAATTGGAAGGG CAGAATGGAGTATTAATGGC CAGAACCCCGACCCTTTAA GCAGTAATGACATGGAGATGTTGGA CAGAAAGACATAGAATG GGGATAAGAAGCAATGTTGGA CACAAAGAAAGGCAATCATG GCTTCGAAGGAATTTGATCG GCACATTITTACGAAAATG GCTCCTGTCTTATTTTATC GGGGGAAACATAAAATG GCACCCGGCTTATTTTATC GGGGGAACATTAAAAAGGG G Gene ID	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_0333600 R1 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R13 PY17X_0105600 R1 PY17X_1216400 R4 PY17X_1216400 R5 Forward primer	AATTIGAGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTTCTCGCTC TATGTACTAGGTTTCTTCGC CTCGTCATGTGATTGCTTTAA CATTCATGAGTTTCTTTGA TTTAAAGGGTCGGGGGTTCT G GATGTCGAGTGCATGTTTATCCT TACAAATGATACTTTTTGCG CCTGACTCCATATTATATCT GTCATTGATAAGTGTGATCTG CATCATTAGTTCTTTGCA ACGTTCCTCAGCTCAAGTTC GTCATTGACTCTGGCCCTTAT ACGTCCTCAACTGAAGTTC GTCGTTACTCTGGTCAGGTC CTTGCTCACCTCAAGTTC GTCGTTCCTCTGGTTCAG
def F4 def F5 def F1 de2 F2 de1 F5 de2 F1 de2 F2 de1 F3 de2 F1 de6 F1 de7 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_1357300 F5 Ptimers for RT-qPCR Location GAPDH attribute 2	ACGITITIAAAGAACAAATG TGGTCCAAACATAAATTG AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTITGA ATGCTACAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTTTGAAGATGATCAAGAG CGCAGCGGATAATATCCAA CTAGCTAGAGCATGACGTA TTGTCACTCTTGTTGAGCGC GGGTGTTAGAAAAGTTTT CGAAACTGATGTTAAAAATA CGCAGTAAATATAGAGTTGG ATTAGTGTTTATCCTAAGTG ATATGTGTTTATCCTAAGTG GTATTTGCCCACAAGAGTGG ATTAAGAATTGTATTCCTTCC GTATTTGCCCCACAAAATG AATATAAGCATCTATCCAAG CTAGCTAGAGTCTATCCAAG GTATTACCCATAGGTGTG ATTAAGAATGTATCCTTCC GTATTGCCCCACAAAATG AATATAAGCATCTATCCAAG CGCAGTAAATATAGAGTTGC ATTAAGAATGTATCCTTCC GTATTGCCCCACAAAATG AATATAAGCATCTATCCACAG	dict R3 dict R4 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R2 dict R2 dict R2 dict R3 dice R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_1317300 R5 PY17X_1317300 R5 PY17X_1300 R5 PY17	TAATGTATTGAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG TTCAACTTGATAGCATTG CTTTGCTGAGATGTAAGCATG TTCAACTTGATAGCATTG CTTTGCTGAGATGTAACG CTTTTAACACATTTACACGG CGTTTTATCATTTCTTCCT TTCAAAATTTACTTCCTC GCTGTGTATATGCTCCC CGTAGTTAATTACTTCCTG TCGTGTATATGTACGAGTC TCGTCAGAATTAAGTACTTCGCACG CTCGTCAGAATTAAGTACTT CGTAGCTAAATTCCATGTGG ATATCTATTCCAGTTTATACACG GGACGTGTTTATGTACCAG Reverse primer ACTCTAAAGCAACCACG CAACTTGATCACGGGGCAT		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_132141200 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location 1216400 bf	CACCACATOCIATO TRACATA GACAATATTCCAGACACTAA CAAATTACCAGACACTAA CAAATTACCAGAGAGACATTAATTCA G GCTITCITTATGATGTITAACA GGGAAGATAACATTGAGGA G CTCATGAAAATTTGAAAGG CAGAATGGAGTATTAATGGC AGAATCCCCGACCCTTTAA GCAGTAATGACATGGAGATGTTGGA CAGAAAGCACATGTAG GAGATTTGTACGAATGTCGA CACAAAGAAAGCCACACTCC GAGATTTGTACGAATGTTCGCA CACAAAGAAAGGCAATCATG GCTCCTGGAGAATTTGATCG GATTCTGAGGAAATTGTCCCAA GCCACATTTTTACGAAAATG GCTACCTGTCTTATTTTATC GAGAGGAAACATAAAATG GCACCAGGAACATAAAATG GCACCAGGAACATAAAATG GCACCAGGAACATAAAATG GCACCAGGAACATAAAATG GCACGAGAACATAAAATG GCACCAGGAACATAAATTGTC CGCAGGAACATTAAAAAGAGG G Gene ID PY17X_1216400	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R13 PY17X_0105600 R1 PY17X_1216400 R4 PY17X_1216400 R5 CAACCTCAAGAGATACCT GGCTAGTTAGATCGTACGTA	AATTIGTGGAAATGTCCAGA CCTICTTTTGGGAAATGTCCAGA CCTICTTTTTGCGAATGTCCAGA CCTICTTTTGCTGCATTAAT GTGGTCATCATTAGTTGT CGCGATTIGCTTGCTGCCCT TATGTACTAGGTTTGCTTGA CATCATGAGGTCCGGGGGTCT G GATGTCGAGGTCCGAGGTTCTTGA TTTAAAGGGTCCGAGGTTCTG GATGTCGATCAGTTTATCCT TACAAATGATACTTTTGCG CCTGACTCCATATTATATCT GTCATTGATAAGTTGATTTATCTCC AGTACTGCTCAGCAGTTCTGCAA CCTGCCCCAAACTTGAGCTCC CTTATGCCTCAGCCCTTAT ACGTCCCCAAACTTGAGCTC CTTGCTCACCCAAACTTGAGCTC CTTGCTCCCCCAACTTGAGCTC CTTGCTCCCCCAACTTGAGCTC CTTGCTCCCCCAACTTGAGCTC CTTGCTCCCCCCAACTTGAGCTC CTGCTCCCCCCCCTCCTGCAGCCC ACGCCCCCCCCCC
def F4 def F4 def F5 def F1 dez F2 def F1 def F3 def F1 def F2 md2 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F1 PY17X_0521800 F3 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_1323900 F1 PY17X_1357300 F5 Primers for RT-qPCR Location GAPDH a-tubula 2	ACGITITIAAAGAACAAAATG TGGTCCAAACATAATTIGTGA AG GCTACATTITIAAAGAATTGA ATGCTACAATATTACA ATGCTACAAAACAATCTTAA ATGCTACAAAACAATCTTAA GTCCCAACCACTTTAAGATGG ATTTTGAAGATGATCAAAGA CGCAGCGGATAATATCCAA CC GGGTGTTAGAGATGATCAAGAG TTGTCACTGATGATGACATGA TTGTCACTGATGTTGAAAAACTGA A TTGTCACTGATGTTGAAAAAGTTG CGAGACAAATATAGAGTTG ATATAAGATTGTATTCCTAACC GATATTACCCATAAGGTGTG ATTTAGGATGTATTACCTAAATC GATATTACCCATAAGGTGTG ATTTAAGATTGTATTCCTACAC GATATTACCAAAACAACTGAA TATAAGACTCATCCAAAATG AATATAAGCATCTATCCAAACC GTATTTGCCCACAAAAATG AATATAAGCATCTATCCAAGA PY17X_1330200 PY17X_0524100	dict R3 dict R4 dict R4 dict R5 dic2 R1 dic2 R2 dict R1 dict R2 dict R2 dict R2 dict R3 dick R1 dick R2 dict R3 dick R1 PY17X_1109100 R1 PY17X_1109100 R2 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_131300 R5 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_131800 R5 PY17X_131800 R5 PY17	TAATGTATTGAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG CTTTGCTGAGATGTTAAGCATG TTCAACTTGATAGCATTG TTTGCAGATTGTTAAGGATTG CTTTGCTGAGATGTTAACGG CTTTTACATTTCTTACCTC CGTACTTTAATTACTCCTCC GCTGTGTATATCATTCTCCTCC GCTGTGTATATCATCTGTGAATC GCTGTGTATATGTACGAGTC TTCGAAAAGTTCTTCGACAC CTCGTGCAGAATTAAGTATT TATAAAAACTTCTTCGCACG GTCTTCTCAGAATTAAGTACTT TATAAAAACTTCTTCGCACG GTCTTCCAGATTAATCATGTGG GTCTTCCAGATTTATGTACCAG GGACTGTTTATGTACCAG Reverse primer ACTCTAAGGCAACACCAG TTA GCACTGATAAGGCAACCACGGCTTT GTCACAGAGTGGCAATCTG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F2 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_015800 F1 PY17X_015800 F1 PY17X_1216400 F4 PY17X	CACCACATOCIATOCIATOCIATOCIATOCIATOCIATOC	PY17X_0523500 R2 PY17X_0523500 R3 PY17X_0508900 R4 PY17X_0508900 R5 PY17X_0508900 R5 PY17X_1320300 R1 PY17X_1320300 R2 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R3 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_1320300 R2 PY17X_1341200 R1 PY17X_1305400 R10 PY17X_1305400 R12 PY17X_1305400 R12 PY17X_0105800 R1 PY17X_1216400 R4 PY17X_1216400 R5 CAACCTGAAGAGATACCT CAACCTGAAGAGATACCTGGAACA AAGCAAGGAAAATGCAACA	AATTIGAGAAATGCAGAA AATTIGGAAAATGCAGAA CCTICTTTTIGGAAATGTCCAGA CCTICTTTTIGGATAGTTGT GGGATTIGGCTTCATGATTGT CGCATTIGGTTGCTTGCGCC CCGGCATGTGGATTGCTTAA CATTCATGAGGTTGCTTTAG TTTAAAGGGTCGGGGGTTCT GGATGTCGAGGTTTTTTCG GGATGTCGAGGTTTTTTCG CCTGACCAAGTTGATCAG GCCGTCCATAGTGTCTCC AGTACTGATAAGTGGATCTG CATCATTAGTTCTGCGAC CTGCCCAAACTTGGCAC CTTGCCCCAAACTTGGCCC CTGCCCCCAACTTGAGCTC CTTGCCCCAACTTGAGCTC CTGCCCCCAACTTGAGCTC CTGCCCCCAACTTGGCCCCTAC CGCCCTTGCCTCACCGATATGGCCC CTGCCCCCAACTTGGCCCCTACACGATG
dc1 F4 dc1 F5 dc2 F1 dc2 F1 dc2 F2 dc1 F5 dc2 F1 dc2 F1 dc1 F5 dc1 F1 dc1 F2 dc1 F1 dc2 F1 dc1 F2 dc1 F3 dc2 F1 PY17X_1109100 F1 PY17X_1109100 F2 PY17X_0521800 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_132300 F1 PY17X_132300 F5 Pimers for RT-qPCR Location GAPDH a-tubulin 2 b-tubulin	ACGITITIAAAGAACAAAATG TGGTCCAACATAATTIGTGA AG GCTACATTITAAAGAATTCG ATGAGTTCCGAAAATTITTC AATGCTACAATATTACA ATGCTACAAAACAATCTTAA GTCCCAACCACTTTAAGATGG ATTTTGAAGATGATCAAGAG CGCAGCGGATAATATCCAA C GGGTGTTAGAGATGATCAAGAG GGCAGCAAATATGGATTAG CGAAACTGATGTTAGAGAGTTAG ATATGGTTTTACCAAAGGTGTG ATATGCCTGAGAGCTATGCGTA ATAGTGTTTTACCAAAGGTGTG ATATGACTGATGTATACCAAAGTG ATATGACTGATGTATCCTAACC GTATTTGCCCGACAAAATG AATATAAGCATCCTAACGG PV17X_1330200 PV17X_052100	dict R3 dict R4 dict R3 dict R4 dict R5 dic2 R1 dic2 R2 dict R1 dict R2 dict R3 dick R2 dict R3 dick R2 md2 R1 PY17X_1109100 R1 PY17X_1109100 R2 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1357300 R5 Forward primer GAGCAGGTAGGTAGCAGGTAT GGGGAGAGGTATGGACGAGTAT GGGGAGAGGTATGGACGAGTAT	TAATGTATTTAGAGGAGAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATGGAGCATTG TTGAATAGAAGTCTGGAGATGGTAAAGC TTTGCTGAGATGTTAAGCATTG TTTGCAGATTGTTAAGGATC CTTTTGCAGAATTTGCTACCTCC CGTTTTATCATTTACTTCCTCC GCTGTGTATATGCTACCTCC CGTAGTTTAATTTACTTCCTCC GCTGTGTATATGCTACGAGTC TTGGAAAAGTTCTTCGGACC CTCGTGGTATATGTACGAGTC GTCTTCTATTTCCCACTCT CGTACGTAAATGTCTCCACCC GTCTTCTATTTCCCACTCT CGTACGTTTATTCTCCCCC GGTCGTTTATTCTCCCCC GGTCGTTTATTCCCACTCT CGTACGTCTATTCCCCCC GGTCGTTTATTCCCCCC GGTCGTTTATTCCCCCC GTCTTCCACCGTTTTATGTACCA GGTCGTTTATTCTCCCCCC GGTCGTTTATGTACCCA CTCTTCCACCGGTTTTATGTACCCA CACTTGATCAGGCGCCCCG TTTCCCGCCGCTTCGCCCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0503500 F3 PY17X_0508500 F4 PY17X_0508500 F5 PY17X_0508500 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_0333600 F1 PY17X_0333600 F1 PY17X_0333600 F1 PY17X_0335600 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_1216400 F4 PY17X_1216400 F5 Location 1276400 Kinesin8b 11 kinesin8b 14	CACATATCCARCITATC TATCA GACATATTCCAGACACTAA CAAATTCCCAGATTTTACGAT GCTTTCTTATGATGTTAACA GCTTTCTTATGATGTTAACA GGAGAGATAACATTGAAGA CTCATGAAAATTTGGAAGAG AAAATATTAAAATTGAAAGC CAGATATGGAGTATTAATGGC AGAGATGACATAGAAGC GAGATATGACAATAGAAG GCAGTAATGACAATAGGAATTGCAC GAGATGAAAGAAGGCAATCATG T GATTCTGAGGAATTTGCCAA GCTGCAATTTTACGAAATG GCTACCTGTCTTATTTATC GAGAGGAAACATAAATTGTTCCCAA GCGCAGACATTAAAAGAGG G GCGCAGCATTAAAAAGAGGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAAGAGG G CGCAGACATTAAAAGAGGCAATCATG C CGCAGACATTAAAAAGAGGG C CGCAGACATTAAAAGAGGGAATCATAATTGT C CGCAGACATTAAAAGAGAGGCAATCATAATTGC C CGCAGACATTAAAAAGAGGG C CGCAGACATTAAAAGAGAGGCAATCATAATTGC C CGCAGACATTAAAAAGAGGCAATCATAATTGC C CGCAGACATTAAAAGAGAGGCAATCATAATTGC C CGCAGACATTAAAAGAGGCAATCATAAATGC C C CCCAGACATTAAAAAGAGGCAATCATAAATGC C C C C C C C C C C C C C C C C C C	PHTA_0523500 R2 PHTA_0523500 R3 PHTA_0523500 R4 PYTA_0508900 R4 PYTA_0508900 R5 PYTA_0508900 R5 PYTA_0508900 R6 PYTA_0508900 R1 PYTA_050800 R1 PYTA_050800 R1 PYTA_050800 R1 PYTA_0833600 R1 PYTA_0833600 R1 PYTA_0833600 R1 PYTA_0833600 R1 PYTA_0141200 R1 PYTA_1305400 R10 PYTA_015800 R12 PYTA_015800 R12 PYTA_015800 R13 PYTA_015800 R1 PYTA_1216400 R4 PYTA_1216400 R5 CAACCCTCAAGGAAATGCAACG AGGCAAGGAAAATGCAACG AGGCAAGGAAAATGCAACG	AATTIGTGAAAATGACAATGACGAA AATTIGTGGAAATGTCCAGA CCTICTTTTGGGAAATGTCCAGA CCTICTTTTGGGTATCATTAGTTGT GGGATTIGCTTTCTGGCTC TATGTACTAGGTTTGTTTGG CTCGTCATGGGATTGCTTAA CATTCATGAGGTGGGGGGTTCT G GATGTCGAGGTTTTTTCG GGATGTCGAGGTTTTTTCG CCTGACATGATGATTATCT GTCATTGATAAGGTGCATTTTATCTG GATATTGTCTGGCCCTTAT ACGTTCTGTCGACGCTTGGCCC CTTTCTAACTCGAACTTGAGCTC CTTTCTACCCAACTTGAGCTC GACGCTTCACTCACGATAT GCCGCTTGACTACGCATGGCCC CACATTGTTCTTCTCCACGATAT GCCGCTTGACTCACGCATGGCCC
dict F4 dict F4 dict F5 dict F1 dict F2 dict F1 dict F2 dict F1 dict F2 dict F1 dict F2 dict F2 dict F1 dict F2 dict F1 dict F2 dict F2 dict F2 dict F2 PY17X_1109100 F1 PY17X_109100 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_1307300 F1 PY17X_1307300 F5 PV17Res for RT-qPCR Location GAPDH actubulin 2 β-tubulin Rbpm1	ACGITITIAAAGAACAAAATG TGGTCCAACATAAATTGTGA AG GCTACATTTTAAAGAATTCG ATGAGTTCCGAAAATTTTCA AATGAGTTCCGAAAATTTTCA AATGCTATCCGAAAATTTTCA AATGCTAATATTCCTTATCA ATGCTACCAACTATTAAGATGG ATTTTGAAGATGATCAACAACTGGA TTTTGAAGATGATCAAAGACTGGA CGGCGGCGGCAGAAATATCCAA GGGTGTGTTAGAAAACACTGGA TTGTCACTCTTGTTGGAGCGC GGGTGTGTTAGAAAATA CGCAGTAAATATAGAGTTAG ATATACCCATAAGGTTG ATTATCCCAATAGGTGTG ATTAAGATTGTATCCTCC GTATTTACCCAATAGGTGTG ATTAAGATTGTATCCTCC GTATTAGCAACTAATGCAAAATG AATATAAGGATCTATCGAAAATG AATATAAGGATCTATCCGACAAAAATG AATATAAGCATCTATCGGACAAAAATG AATATAAGCATCTATCGGACAAAAATG AATATAAGCATCTATCGGC GGene D PY17X_1330200 PY17X_016700	dict R3 dict R4 dict R4 dict R5 dic2 R1 dic2 R2 dict R1 dict R2 dict R2 dict R3 dick R1 dict R2 dict R3 dick R1 dict R2 dict R3 dick R4 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_13157300 R5 Forward primer GAGCAGGTAGGAGCAGGTATC GGGCACAGGTAGGAGCAGGTATC CGGCACAGGTATGGACCAGGATAC CGGCACAGGTATGGACCAGGATAC	TAATGTATTTAGAGGAGAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATGGAGAGCATT G TICAACTTGATAGCATTTG TTTGCTGAGATGTAAACGATTTG TTTGCAGATTGTTAACGACT C CTTTTACAATTTCTTAACGAC C CTTTTACAATTTACTTCCTCC CGTACTTTAATTTACTCCTC CGTGTGTATATGCTGTGAATC GCTGTGTATATGTACGACG CTCGTGGTATATGTACGACG CTCGTGGTAATGCAGCAC GTCTTCTATTTCCACTCT CGTAGCTAAATCCAGTTTATACCAC GGTCTTCTATTTCCACTCT CGTGGTAAATCCAGTTGA GGTCTTCTATTCCACCCG GGTCGTTTATTCCACCCG GGTCGTCTATTCCACCCG GGTCGTTTATGTCCACCCG GGTCGTCTATTCCACCCG GGTCGTCTATTCCACCCG CTCTCCAGAGTTTATGTACCAG GGTCTTCCAGGTTTTATGCACCG GGTCGTCTAAAGGCACCACCAG CAACTGACCACCGGTTCG CAACTGGCCGCTCTCG CAACTGGCCGCTCTCG CAACCCCGGTTCCCCCTCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F6 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF16 11 PF16 11 PF16 11 PF16 11 PF17	CACACATICTATCITATCITATCA GACATATTCCAGACACTAA CAAATTCCCAGATTTTACGAT GCTTTCTTATGATGTTAACA GGCAGAGAGATAACATTGAGGA GCTTCCTTATGATGATGAGGA CTCATGAAAATTGGAAGGA CTCATGAAAATTGGAAGGAG CTCATGAAAATTGGAGAGGA CTCATGAAAATTGGAGAGG CAGATGGAGTATTAATGGC CAGATGGAGTATTAATGGC CAGATGGAGATATGACAACTCG GAGATGGACATGACAATGGCG CAGAAGGGAATTGATCAC CGCAGAACATGAAGGGAATTGGTCG GCTACCTGTCTTATTTATC GAGAGGAAACTTAAAAGGGG CGCAGACATTAAAAAGGG G CGCAGACATTAAAAAGGG G CGCAGACATTAAAAAGGG G CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGGG CGCAGACATTAAAAAGAGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAAGGG CGCAGACATTAAAAAGAAGGG CGCAGACATTAAAAAGAAGGG CGCAGACATTAAAAAGAAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAAGAGGG CGCAGACATTAAAAGAGGGG CGCAGACATTAAAAGAAGGG CGCAGACATTAAAAAGAAGGG CGCAGACATTAAAAAGAGGGG CGCAGACATTAAAAAGAGGGG CGCAGACATTAAAAAGAGGGG CGCAGACATTAAAAAGAGGGG CGCAGACATTAAAAAGGCAATGG CGCAGACATTAAAAAGAGGCAGGG CGCAGACATTAAAAAGAGGCAGGG CGCAGACATTAAAAAGAGGGCAGGGG CGCAGACATTAAAAAGAGGCAGGGG CGCAGACATTAAAAGAGGCAGGGGGGGGGG	PHTA_0022300 R2 PYT7X_0523500 R3 PYT7X_0508900 R4 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R6 PYT7X_0508900 R5 PYT7X_0508900 R6 PYT7X_0508900 R1 PYT7X_0833600 R1 PYT7X_0833600 R2 PYT7X_0833600 R2 PYT7X_0833600 R2 PYT7X_0833600 R1 PYT7X_1305400 R10 PYT7X_1305400 R12 PYT7X_0415900 R13 PYT7X_0105800 R1 PYT7X_0105800 R1 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_0105800 R1 PYT7X_0	AATTIGTGAAAATGTCCAGA CCTICTTTTGGGAAATGTCCAGA CCTICTTTTGGGAAATGTCCAGA CCTICTTTTGGGTATCATTAGTTGT CGCATTTGCTTCTTCGCCTC TATGTACTAGGTTTTTTCTGC CTCGTCATGGGTGGGGGGTTCT G TATTTAAAGGGTCGGGGGTTCT G GATGTCGAGGTTTTTTCG CCTGACTGCAGTTTTTTCG CCTGACTGCAGTTTTTTTCG CATCATTAGTTGTATCAGCCT CATCATTAGTTCTTGCA TCTTATGCATTTTTTTCCC AGTATGTCTTGGCCCTTAT CCTGACTCCAAACTTGGACTCC CTTGTCTACTCAAACTTGGACTTC G CCCGTTATCTTCTCTCATCAGGAC CCCGTTACCTTCATCAGGACTCC CACATTGGTTAAATGAGCAGCA CCAATGTGGTAAACTAGGCATCT
dci F4 dci F5 dci F5 dci F5 dci F1 dci F5 dci F1 pit17x_101000 Gappen1 1109100	ACGITITIAAAGAACAAAATG TGGTCCAAACATAAATTG TGGTCCAAACATAATTTGTGA AG ATGAGTTCCGAAAATTTTCC AAATCTAATATTCCTTATCA ATGCTACCAACTATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG AATTTGAAGATGATCAAAGA GGCAGCGGATAATCCAA GGCAGCGGATAATACCAA GGCTGTTTGAAAACACTGGA TTGTCACTCTTGTTGAGCGCG GGGTGTGTTTGAAAACATTG CGAAACTGATGTTAGAATTA CGCAGTAAATATAGAGTTAG ATTATACCATAAGGTTAG ATTATACCATAAGGTTACCTAAC GATATTACCCATAAGGTGTG ATTATAGCATCTATCCTAACG GTATTTACCCAAAAAATG AATATAAGCATCTATCCTAACG GTATTGCCCGACAAAAATG AATATAAGCATCTATCCTACAG GGCGGTGTTTAAAAATG ATTAAGATTGTATTCCTCAAG GGCGTGTTTACCTCAACAGGTGTG ATTATAGCATCTATCCACAG QGCCGCGACGACAAAAATG AATATAGCATCTATCCACAG QCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	dict R3 dict R3 dict R3 dict R3 dic2 R1 dic2 R2 dicf R3 dic4 R2 dicf R3 dic6 R1 dic7 R3 dic6 R1 dic7 R3 dic6 R1 dic7 R3 dic6 R1 dic7 R3 dic7 R3 dic	TAATGTATTGAGAGGAGAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATGGAGACTG TTCAACTGGAATGTAAACGAC TTTGACTGGAGATGTTAAACGAC CTATTAGCAATTTGCTTAACAGAC CTATTAACACATTTACACTGC C GGTTTTATACACATTTACCTCC GGTACTTTAATTACTTCCTCC TCAATAGGAACTTGTGAATC GCTGTGAGAATTAACGTATC GCTGTGAGAATTACGTGTGAGAC GCTGTCGTAATGTACGAGC GTCTTCATTTCCACTCT CGTACGTAAAGTTCTTCGACG GTCTTCATTTCCACTCT GGTACGTAAATATCATGTAG ATATCTATATGTATCACGG GTCTCTATTTCCACTCT GGTACGTAAATATCATGTAG GTCTCTAATGCCACCC GTCTTGATGGCAACCCCG TCATCAGCGAGCACACCCG TCACTGAGCGAACACCCG CTCCTCAAGGCAACACCCG CTCCTGAAGGCAACACCCG CTCCTGAAGGCAACACCCG CTCCTGAAGGCAACACCCG CTCCTGAAGGCAACACCCG CTCCTGAAGGCAACACCCG CTCCCAGCGCTTCGACGCACTCTG ATA CACCCTGTGCAGCGCCCTCTG CTCCCACGCGTTCCCCCTCG CTCCCCCACGCGTTCCCCCCTCG CTCCCCCCCGCGCGCCCTCTG CTCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF17 PT17 PT17 PT17 PT17 PT17 PT17 PT17 PT	CACCACATOCIATO INTO INICIAIO GACAATATTCCAGACACTAA CAAATTCCAGATTITACGAT GCITICTTAIGATGITAACA GCITICTTAIGATGITAACA GCITICTTAIGATGATGAGA CTCATGAAAATTIGAAGAG CACATGAGAGATAACATTGAGAGA AAAATATTAAAATTGAAAGC CACATGAGAGTATTAATGGC AGGATAATGACAATAGAAGT GCAGACCCCGACCCTTAA A GCAGTAATGACAATAGAAGC GAGATGICACAATAGAAG CACAATGACAATGACAATG GCAGACACTGICTTAITTIATC GACTGCGAGAACATAGAATG GCACACTTITACGAAATG GCACACATTTAACGAATTGC GCAGACACTTAAAAAGGG G GCACCTGICTTAITTIATC GACAGGAAACATAAAATTG CGCAGACATTAAAAAGGG G GCACACTTICACGAAATAGAATG CGCAGACATTAAAAAGGG G GCACACTGICTIATTTATC GACAGGAAACATAAAATTGT C CGCAGACATTAAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAACAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAACAACGAGG G QCACCTGICTTAATTAAAAGGG G QCACCTGICTTAATTAACAACTAAATTGI C CGCAGACACTTAAAAAAAAAGGG G QCACCTGICTTAATTAAAAGGAGG QCACCTGICTTAATTAACAAAAAAGGG QCACACTGICTTAATTAAAAAGGG QCACCTGICTTAATTAAAAAAAAAAAAAAAAAAAAAAAAAA	PHTA_0022300 R2 PYT7X_0523500 R3 PYT7X_0508900 R4 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R6 PYT7X_050800 R1 PYT7X_0833600 R1 PYT7X_0833600 R2 PYT7X_0833600 R1 PYT7X_0833600 R1 PYT7X_1305400 R10 PYT7X_1305400 R12 PYT7X_1305400 R12 PYT7X_0105800 R1 PYT7X_0105800 R1 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 PYT7X_1216400 R4 CAACCCTGAAGAGAAATGCAACGT CAA GGCTAGTTAGATTGCAACG CTCAA GTGTGTACATACTTCATGTG	AATTIGTGGAAATGTCCAGA CCTICTITTACTCATTAAT GTGGTCATCAATAGTTGT CGCATTTGGCAATAGTTGT CGCATTGGCTTCTTGCGTC TATGTACTAGTTTTTTCTGC CTCGTCATGAGATTGCTTAA CATTCATGACTGGGTTTTTG CATCATGAGGTGCGGGGTTCT G GATGTCGAGGTTTTTTC GGATGTCGAGGTTTTTTG CATCATAGGTGCTTTGCCA AGTAGTCCTCAGCGCTTAT ACGTCCTCAACGTCAGCTC CTTTCCTAACTCAGCGCTC CATCATTAGTTCTTCAGC Reverse primer CCCGTTACTTCATCAGCGA TGGCGCTTACTTCATCAGCA G GACGTTCCTTCATCAGCATAT GGCAGTTGACTAACGATGAGCA G CCAATTGGTGGAATAGCGCA
abs 1 b dict F4 dict F5 dict F1 dict F2 dict F3 dict F1 dict F2 dict F1 dict F2 dict F1 dict F2 dict F1 dict F2 md2 F1 PV17X_100100 F1 PV17X_0521800 F1 PV17X_0521800 F2 PV17X_1311800 F4 PV17X_1311800 F6 PV17X_13123000 F1 PV17X_131300 F6 PV17X_1305700 F5 Primers for RT-qPCR Location GAPDH a-tubulin 2 β-tubulin Rbpm1 1109100 0838600	ACGITITIAAAGAACAAATG TGGTCCAAACATAAATG TGGTCCAACATAATTIGTGA AG ATGAGTTCCGAAAATTITC AAATCTAATATTCCTTATCA ATGCTACCAACTATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG AATTTGAACATGATCAAAGA CGCAGCGGATAATATCCAA GCCAGCGGATAATATCCAA CGCAGCGGATAATATCCAA ATTTGAAGATGATAGAGTTG GAGGTAGTTGAGAACACTGGA ATATTAGGATGTTAGAGATTG GATATTACCCATAGGGTGG ATTATACCCATAGGTGTG ATTATAGGATGTATCCTTCC GATATTACCCATAGGTGTG ATTATAGGATGTATCCTACAG CGCGG QGCGGGTGTTTATCCTAAATG GATATTACCCATAGGTGTG ATTATAGGATGTATCCTTCC GATATTACCCATAGGTGTG ATTAAGATTGTATCCTACAG CGCG QCCCGACCTGACAAAATG AATTAAGGATCTATCCAAG QCCC QCCCGACCACTAGGTG QCCCCCACAAGATGTAGACTG QCCCCACAAGAGTGTACAAGGTGG ATTAAGATGTATCCTACAGG QCCCCACAAGAGTGTACAAGGTGG QCCCCCACAAGAGTGTAGACTCACCAG QCCCCCACAAGAGTGTACAAGGTGG QCCCCACACAAGAGTGTACAAGGTGTG ATTAAGATGTATCCTACACAG QCCCCACAAGAGTGTACCAAGGTGTG QCCCCCACACAAGAGTGTACAAGGTGTG ATTAAGATGTATCCTACACAG QCCCCCACAAGAGTGTACAAGAGTGTAGAGTGTACAAGGTGTACCAAGGTGTGTACAAGGTGT QCCCCCCACAAGAGTGTACAAGGTGTG QCCCCCCCCCCACAAGAGTGTG QCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	dict R3 dict R4 dict R3 dict R4 dic2 R1 dic2 R1 dic2 R1 dic1 R2 dic1 R3 dic2 R1 dic1 R2 dic1 R3 dic R1 dic R2 md2 R1 PY17X_1109100 R1 PY17X_1109100 R1 PY17X_109100 R2 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1313000 R5 PY17X_1313000 R5 PY17X_131000 R5 PY17X_131000 R5 PY17X_131000 R5 PY17X_13000 R5 PY17X_1300	TAATGTATTGAGAGAAGC TGAATAGAAGTCTGCGATT GG GCACAATATATATAGGAGCATG GTTGCTGAGATGTAAACG CTTTGCTGAGATGTAAACG CTTTGCTGAGATGTAAACG CTATTAACACATTTACACTG C CGTTTTATACACATTTACACTGC C GGTGTTTAATTACTTCCTCC GTACTTTAATTACTGCTCC CGTACTTTAATTACTGCAGTC GCTGTGTATATGTACGGAC GCTGTGTATATGTACGGAC GCTGTGAGAATTACATGTAG GTCTCTATTTCCACTCT CGGAGCTAAATATCATGTAG GTCTCTATTCCACCTC GGAGCTTAATGCACCACG GTCTCTGATGACGCACCCACG GTCTCTGATGACGCACCCCAG GTCTCTGATGCCACGGCATTTG C CACCTGAGCAGGCAACACCAG CTCCACGGCGGGCACTTG CATA CACCGCGGGGGGCACTTG CATACCACGGGGGCACTCG CATCCACGGGGGGCACTCG CATCCACGCGGTGGGCACTCG CACCTGGTGATATGCACGGCACCCG CTCCACGCGGTGGGCACTCG CACCTGGTGGTATATGCACGGGCACTCG CACCTGGTGGTATATGCACGGCACCCG CTCCCGCGGGGGCACTCG CACCTGGTGGTATATGCACGGCACCCG CTCCCGCGGGGGCACCTCG CACCTGGTGGTATATGCACGGGCACCTCG CACCTGGTGGTATATGCACGGCACCTCG CACCTGGTGGTATATGCACGGCCACCTCG CACCTGGTGGTATATGCACGGCCACCTCG CACCTGGTGGTATATGCACGGCCACCCCG CTCCCGCGGGGGCACCTCG CACCTGGTGGGTATCCCGCCCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11	CACCACATOCIATO INTO INICIAIO GACAATATTCCAGACACTAA CAAATTCCAGATTITACGAT GCITICTTAITGATGITTAACA GCITICTTAITGATGITAACA GGAAAGATAACATTGAGGA CTCATGAAAATTTGAAAGAC CAGATGGAGTAITAATGGC AGAGATGGAGTAITAATGGC AGAGATGGAGTAITAATGGC AGAGATGACAATAGAAG GAGATATGACAATAGAAG GACATATGACAATAGAAG GACATATGACAATAGAAG GCAGAAGGAAATGITTCCTCAA GCITCGAGGAAACATGGACATCG GCAGACGTTAATTTAATGGC GCAGACGAACATTAAAAGGG GCAGACGAACATAAAATG CGCAGACACTTAAAAGAGG GCAGACGACATTAAAAGGG GCAGACGACATTAAAAGGG GCAGACGACATTAAAAGAGG GCAGACGACATTAAAAGAGG GCAGACGACATTAAAAGAGG GCAGACGAACATAAAATG GCGAGACACATAAAATGG GCAGAGGAAACATAAATTGT C GCGCAGACATTAAAAAGAGG G GCAGAGGAAACATAAATTGATCA CGCAGACACATTAAAAAGAGG G CGCAGACACATTAAAAAGAGG G CGCAGACACATAAATGAGG G CGCAGACACATAAATGAGG G CGCAGACACATAAATGAGGG G CGCAGACACATAAAATGAGGG G CGCAGACACATAAAAGAGGG G CGCAGACACATAAAAGAGGG G CCACACATTAAAAAGAGGGAACATAAATG CGCAGACACATAAAAGAGG G CCACACATTAAAAAGAGG G CCACACACTTAAAAAGAGGGAACATAAATG CGCAGACACATAAAAAGAGG G CCACACACTGACACATAAAAAGAGG G CCACACACTGACATAAAAGAGGG G CCACACACTGACATAAAAGAGGG G CCACACACTGACATAAAAAGAGGG G CCACACACTGACACACACATAAAAGAGG G CCACACACTGACACATAAAAAGAGG G CCACACACTGACACTAAAAGAGAGGAACATAAATG C CGCAGACACACATAAAACACACACACACACACACACACAC	PHTA_0022300 R2 PYT7X_0523500 R3 PYT7X_0508900 R4 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R5 PYT7X_0508900 R2 PYT7X_0833600 R1 PYT7X_0833600 R2 PYT7X_0833600 R1 PYT7X_0305400 R10 PYT7X_1305400 R12 PYT7X_1305400 R13 PYT7X_0415900 R13 PYT7X_0105800 R1 PYT7X_1216400 R4 PYT7X_1216400 R5 Forward primer CAACCCTGAAGAGATACCT AGGCAAGGAAATGCAACGT AGGCAAGGAAATGCAACGT CAACCTGATAGATGAAATGCAACG	AATTIGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGGTCATCAATTAGTTGT CGCGATTTGGTACTAATTAGTTGT CGCGATTGGTTGCTTCGCCTC TATGTACTAGTGTTTTTGGGTC CTCGTCATGTGATTGGTTTGA TTTAAAGGGTCCGGGTTCT G GATGTCCGAGTTTTAATGCC GGATGTCCGAGTTTTATCCT TACAAATGATACTTGGCG CTCGATCGCATATTATCT GCGTCTCATAGTTGTTTGCA TCTTATGCATTTTGCCA ACGTCCCTCAAACTGAGCTC GTTCTTAGCTCTTCTGTCAG Reverse primer CCCGTTATCTTCTTCAACGATT GGCCTTGACTAACATGAGCA G ACGATGTCAACAATGAGCA CAATGTGCAACAATGAGCA CCAATGTGCAACAATGAGCA CCAATGTGCAACAATGAGCA
det F4 det F5 det F5 det F1 det F2 det F3 det F1 det F5 det F1 det F2 md2 F1 PY17X_1109100 F1 PY17X_0521800 F2 PY17X_1311800 F4 PY17X_1311800 F5 PY17X_131300 F5 PY17X_131300 F5 PY17X_131300 F3 Primers for RT-qPCR Location GAPDH a-tubulin 2 β-tubulin Rbpm1 100100 0833600 Primers for RP-qPCR	ACGITITIAAAGAACAAAATG TGGTCCAAACATAAATTG AG ATGAGTICCGAAAATTITGA ATGAGTICCGAAAATTITIC AAATCTAATATTCCTITATC AATCTAATATTCCTITATC ATGCTACCAACTATATCCTITATG ATTTTGAAGATGATCAAGAG GCCAGCGGATAATATCCAA GAGTTATCAAAAACAATGGA AAGTTATCAAAAACACTGGA CTAGCTAGAGGCTATGCGTA ATTTGCACTGTGTGAGACGC GGGTGTGTTAGAAAACACTGGA CGCAGTAAATATAGAGTTG ATTATACCCATAAGGTGTG ATTATACCCATAAGGTGTG ATTATAGCATCTACCAAAATG GAACTGAACT	dict R3 dict R4 dict R3 dict R4 dict R5 dic2 R1 dic2 R1 dict R2 dict R3 dict R3 dick R3 dick R3 dick R1 dick R2 md2 R1 PY17X_1109100 R1 PY17X_1109100 R2 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_1311800 R4 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_131800 R6 PY17X_132900 R1 PY17X_131800 R6 PY17X_132900 R1 PY17X_131800 R6 PY17X_132900 R1 PY17X_131800 R6 PY17X_132900 R1 PY17X_131800 R6 PY17X_132900 R1 PY17X_132900 R1 PY17X_131800 R6 PY17X_132900 R1 PY17X_132900 R1 PY17X_132900 R1 PY17X_132900 R1 PY17X_132900 R1 PY17X_1300 R5 PY17X_1300 R5 PY17X_1			PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_1305400 F13 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location 1276400 kinesin8b 11 kinesin8b 14 PF16 11 PF16 PF16 PF1 PF1 PF16 PF1 PF16 PF1 PF1 PF1 PF16 PF1	CACCACATOCIATO INTO INCOME GACAATATTCCAGACACTAA CAAATTCCAGACACTAA GCAATTCCCAGATTITACCA GCITTCTTATGATGTTAACA GGAAAGATAACATTGAGGA GCACTAGAAAATTTGGAAGGA AAAATATTAAAAATTGAAAGC CAGATGGAGTATTAATGGC CAGATGGAGTATTAATGGC CAGATGGAGTATTAATGGC CAGATATGACAATGACAC GAGATCTGACGACATTGACA CACAAAGAAGGCAATCGACATG CACAAAGAAGGCAATCGACATG CACAAAGAAGGCAATCGACATG CACAAAGAAGGCAATCGACATG CACAAAGAAGGCAATCGACATG CGCAGACATTTAACAAGG GCTCCCTGACGTAAAATG GCCACAATGTTCCAA GCCCCGACACTTAAAAAGG GCCAGACATTAAAAAGG GCCAGACATTAAAAAGG GCCAGACATTAAAAAGG GCCAGACATTAAAAAGGG G GCCAGACATTAAAAAGGC GCCAGACATTAAAAAGGG G CGCAGACATTAAAAAGGC GCCAGACATTAAAAAGGG G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CGCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCCAGACACTTAAAAAGGC G CCAGACACTTAAAAACTTAAAAGAGGC G CCCAGACACTTAAAAACTTAAAAAGAGC G CCCAGACACTTAAAAAGACGC G CCCAGACACTTAAAAAGGC G CCAGACACTTAAAAAGGCACTTAAAAAGAGG G CCCAGACACTTAAAAACCTACACTACA	P117x_0523500 R2 P17x_0523500 R4 P17x_0508900 R4 P117x_0508900 R5 P117x_0508900 R5 P117x_0508900 R5 P117x_0508900 R2 P117x_1320300 R2 P117x_1320300 R2 P117x_033600 R2 P117x_033600 R2 P117x_033600 R2 P117x_1341200 R1 P117x_03400 R10 P117x_1305400 R12 P117x_1305400 R13 P117x_0415900 R13 P117x_0415900 R13 P117x_0415900 R13 P117x_0105800 R1 P117x_1216400 R4 P117x_1216400 R5 Forward primer CAACCCTGAAGAGATACCT CACCACGTGAAGAGATACCT CACCACGTGAAGAGATACCTCATGTG ATTCCTAGTTGTAATTTCTC	
def F4 def F5 del2 F1 del2 F1 del7 F5 del7 F3 del7 F1 del7 F2 del7 F3 del7 F1 del7 F1 del7 F2 del7 F3 del7 F1 PY17X_100100 F1 PY17X_100100 F2 PY17X_0521800 F1 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_1317300 F5 PY17X_1300 F5 PY17X_1300 F3 PY17X_1300 F3 PY17X_131300 F4 PY17X_1300 F5 PY17X_1300 F3 PY17X_1300 F3 PY17X_1300 F3 PY17X_1300 F3 PY17X_1300 F3 PY17X_1000 F3 P1000 F3 0835600 P1000 0835600 P1000	ACGITITIAAAGAACAAAATG TGGTCCAAACATAAATTG AG ATGAGTICCGAAAATTTGA ATGAGTICCGAAAATTTGA ATGAGTICCGAAAATTTTC AAATCTAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTTTGAAGATGATCAAGAG GGGTGTGAAGAGCTATGCGTA ATAGCTAAGAGCTATGCGTA ATAGCTAGAGCTATGCGTA ATAGCTAGAGCTATGCGTA CGGAGTGTTGAAAAGTTT CGGAATGTTAACAATG GATATTACCCATAAGGTGTG ATTATACCCATAAGGTGTG ATTATAAGATGTATCCTACAG GTGTTGTCGACACAAAAGTG ATTTAAGCTAGCGTCTTCC GTATTTACCCATAAGGTGTG ATTTAAGCTGATGTTCCTACAG CGCAGTAATTAGCGACAAAAGTG ATTTAAGCTGTCGTACCAAAATG AATATTAAGCATCTACCAG CGCAGTAATTGCTCCC GTATTGCCGACAAAAGTG CGCAGTACTTCCC GTATTGCCGCCCC GTATTGCCGCCCCC GTATTGCCGCCCCCC GTATTGCCGCCCCCC GTATTGCCGCCCCCC GTATTGCCGCCCCCCC GTATTGCCGCCCCCCCCCC	dict R3 dict R4 dict R3 dict R4 dic2 R1 dic2 R1 dic2 R1 dic4 R2 dic1 R3 dic4 R2 dic1 R3 dic6 R1 dic7 R2 dic1 R3 dic8 R1 PY17X_0109100 R1 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R4 PY17X_1311800 R4 PY17X_1311800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY1	TAATGTATTGAAGGAAGC TGAATAGAAGTCTCTGCATT GG CGACAATATATATGAGAGCATG CG CTTTGCTGAGATGTTAAGCATG TTCAACTTGATAGCATTG CTTTGCTGAGATGTTAAACG TTTTCAAATTTCTTAACAGAC CTATTAACACATTTACACTG C CGTTTTATCATTTCTTCCTC TTCAAAATTTACTCTCCC CGTATTTAACACATTTACACTG CC CGTGTGTATATGTACGAGTC TTCGAAAAGTCTTTCGTCAG GCTGTGTATATGTACGAGTC CTCGTCAGAATTACATGTAG GCTGTCTATTTCCTCCACTG CGTGTCCAGTTTTCTCCACCG GCTGTCTATTTCTCACAGC GGACGTTTTATGTACCAC GGACGTGTTCATGTACCAC GGCTGTGATATGCACGGCACTTTG ATACCACTGGCAGCACCCCAG TC CAACTGACACTGGTCCCACTCT ATACAAAGCGCACCCCG GCTGTGTATATGTACCACG GGCGTGTGATATGCACGGCACTTTG ATACCACTGGTCCCATTCC ATCCACTGGTACAGCGCACCTTG CTCACGCAGTGGCACTTGC CTCACGCAGTGGCACTTGC CGCGTGTGTATATGTACCAGTC GGCGTGTGTATATGTACCAGTC GGCGTGTGTATATGTACCAGTC GGCGTGTGTATATGTACCAGTC GGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCGCTCCATTCCACTCC CGCGTGTGTATATGTACCAGTC CGCGTGTGTATATGTACCGCTCCCATTCCACTCCCCCTCCCCTTCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_13203000 F2 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1015800 F1 PY17X_1216400 F4 PY17X_1216400 F5 Location 1276400 kinesin8b 11 kinesin8b 14 PF16 11 PF16 11/E2 Location	CACCACATOCIATOCIATOCIATOCIATOCIATOCIATOC	PHTA_0022300 R2 PYTZ_0523500 R3 PYTZ_0523500 R4 PYTZ_0508900 R4 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R2 PYTZ_050800 R2 PYTZ_0333600 R1 PYTZ_033600 R2 PYTZ_033600 R2 PYTZ_1341200 R1 PYTZ_1341200 R1 PYTZ_1305400 R12 PYTZ_1305400 R12 PYTZ_1305400 R13 PYTZ_1305400 R13 PYTZ_1216400 R4 PYTZ_1216400 R5 CAACCTGAAGAGATACCT CAAA AGCAAGGAAAATGCAACG C ATTCCTAGTTGAATTCATCATCATGTG GTGTGTACATACTTCATGTG Forward primer	AATTGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGGTTACTTGCGTC TATGTACTAGGTTTGTTGCGTC TATGTACTAGGTTTGTTGGGT CCTCGTCATGTGATTGGTTGCT ACTTCATGAGTTGTTTTGA TTTAAAGGGTCCGGGGTTCT G TATTTAATGCCCCAATTTTGCG GCATGTGCAGTGTGATAGTGGTCG CCTGACTCCATGAGTGGTCG GTCATGTGTCCTCGGCCCTTAT ACGACTTCATCGGCACTTGAGA CGTCGTCCCCAACTGAGCTC CTTTCTCACTCGTCTCGT
def F4 def F5 del2 F1 de2 F2 de1 F5 de2 F1 de2 F2 de1 F5 de1 F5 de2 F1 de2 F1 de1 F5 de1 F5 de1 F2 de1 F2 de1 F1 dbc F1 dbc F2 md2 F1 PY17X_1109100 F1 PY17X_0521800 F1 PY17X_0521800 F2 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_131300 F5 Primers for RT-qPCR Location GAPDH -ubulin 2 β-tubulin Rbpm1 1109100 0838600 Primers for RIP-qPCR Location kinesin8b 11	ACGITITIAAAGAACAAATG TGGTCCAAACATAAATG GGTCAATTTGAA AG GTACATTTCAAAGAATTGA ATGAGTICCGAAAATTITC AAATCTAATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTTGAAGATGATCAAGAG GGCGCGGATAATATCCAA GAGTTATCAAAAACAATGGA CGCAGCGGATAATATCCAA GAGTTATCAAAAACAATGGA CTAGCTAGAGGCTATGGCGT CGGCGTGTGAGAAAGTTT CGAAACTGATGTTAAAAATA CGCAGTAAATATAAGAGTTAG ATTAAGATTGTATACCTAACG GTATTACCCATAAGGTGTG ATTAAGATTGTATCCTACAG GTATTACCAAAAGACTCAG CGCAGTAAATATACGAGTAG ATATTAAGGATCTATCCTACG GTATTGCCGCACAAAAATG AATATAAGCATCTATCCAAG CGCAGTAAATGTCTTCC GTATTGCCGACAAAAGTGTG PY17X_1109100 PY17X_0204100 PY17X_0204100	dict R3 dict R4 dict R3 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R2 dicf R1 dict R2 dicf R3 dic R1 dic R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_13100 R5 PY17X_13100 R5 PY17X_13100 R5 PY17X_13100	TAATGTATTGAAGAGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATGAGAGCATG GCACAATATATATGAGCATG TTCAACTTGATAAGCATTG CTTTGCTGAGATGTTAAACG TTTCAAATTTGTAACAGAC CTATTAACACATTTACACTG CGTTTTATATACACATTTACACTG CGTTTTATTATCTTCTCCT TTCAAAATTTACTTCCTC GCGTGTATATGTACGAGT CGTGTGATATGTACGAGC GCGTGTGATATGTACGAGC GCTGTGATATGTACGAGC GCTGTCATATTCCTCCACGT CGTAGCTAAAATTTCTCCACG GGTGTCTATTTCCTCCACGT CGTAGCTAAATTCCTGCACG GGTGTCTATTTCCTCCACGT CGTCGCAGGCAACCCCG GCTCTTCAGGCAACCCCG GCTGTGATATGCACGGCATT G CACCTGAAGGCAACCCCGG CTTCCACGTGGCACCCCG GCTGTGATATGCACGGCATTTG ATACAACTGTTCCCCCTTCC ATCCCACTGGTGCCACTTCG ATCCCACTGGTGCCCCTTCC ATCCCCCCTGCCCCCTTCCCCTTCC ATCCCCCCCTGCCCCCCTTCCCCCTTCC CGCCGTGGTATATGTACCACGCCTTCCCCCTTCCCCCTTCCCCCTTCCCCCCTTCCCCCTTCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0333600 F1 PY17X_13203600 F2 PY17X_1341200 F2 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F13 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1216400 F2 UCCation 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF16 11/E2 Location dc1 14	CACCACATOCIACITACITACIAC GACAATATTCCAGACACTAA CAAATTACCAGACACTAA GCITTCTTATGATGTTAACA GCITTCTTATGATGTTAACA GGCAAGATAACATTGAGGA GCACGAGAGATAACATTGAGGA CACATGGAGTATTAACATGGCA GAGAACCCCGACCCTTTAA AGGAACACCCGACCCTTTAA AGGATAACACCGACACTCGACATG CACGAAGAGGAACATCGACATG CACGAAGAGGAACATCGACATG CACGAAGAGGAACATCGACATG CACGAAGAGGAACATCAAG GCTTCGAGGAAACATGTTCCTCAA GCCACATTTTTACGAAAATG GCCAGACATTGAACATGGCAACTGC GCCAGACATTGACAATGGAACT GCCAGACATTGACGAATGCGAC GCCAGACATTGACAACGAATTGACA CGCAGACATTGACAAATG CCCCGACCTGTCTTATTTTATC CGCAGACATTGAAAATGTTCCTCAA GCCAGACATTGAACATGAACTG GCCAGACATTAAAAAGAGGG GCCAGACATTAAAAAGAGGG GCCAGACATTAAAAAGAGGG GCCAGACATTAAAAAGAGGG CCCCGCAGACATCAGC CCCAGACATTGACGACATGACTG CCCAGACATTGACGAACTGACG CCCAGACATTGACGAACTGACG CCCAGACATTGACGACATGACTG CCCAGACATTGACGACATGACTG CCCAGACATTGACGACATGACTG CCCAGACATTGACGACATGACGG CCCAGACATTGACGACATGACTG CCCAGACATTGACGACATGACGACG CCCAGACATTGACGACATGACGACG CCCAGACATTGACGACATGACGACGACGACGACGACATGACGACATGACGACATGACGAGGACATGACGACGACATGACGGGA CCCAGACATTGACGACATGACGG CCCAGACACTTAAAAAAGGGGG CCCCGCAGACATGACCGCGACGACGACGACGACGACGACGACGACGACATGACGAGGACATGACGAGGACGAGGGA CCCCGCAGACATTGACGACGACGACGACGAGGGGAGCCGGGGAGACCTGACGGAGGCAGGGACGACGAGGGGAGGGGAGGGGGGGG	PHTA_0022500 R2 PYTX_0523500 R3 PYTX_0523500 R4 PYTX_0508900 R4 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R2 PYTX_050800 R2 PYTX_033600 R2 PYTX_033600 R2 PYTX_033600 R2 PYTX_1341200 R1 PYTX_1305400 R12 PYTX_1305400 R12 PYTX_1305400 R12 PYTX_1045900 R13 PYTX_1216400 R4 PYTX_1216400 R5 CAACCTGAAGAATAGCAACGTACCT CAAC AGCAAGGAAAAGTGCAACGT C ATTCCTAGTTGTAATTCATGTG GTGTGTACATACTTCATGTG TTCAAAAAGTGCAACGTACCT CACCTAGTTGTACTTCATGTG	AATTIGAGAAATGTCCAGA CCTICTITTIGGGAAATGTCCAGA CCTICTITTIGGGAAATGTCCAGA CCGCITTIGGTGTCATTAAT GTGTGTCATCAGTTGTTCGCC TAGTGACAGGTTGTTTGCGC CCGCATGTGGATGTGTTTAA CATTCATGAGTGGTCGGGGGTTCT G GATGTGGAGGTGGGGGGGGTCT G GATGTGGAGTGGA
def F4 def F5 def F5 def F1 dez F1 dez F2 def F5 def F5 def F1 dec F2 md2 F1 PY17X_05100 F1 PY17X_0521800 F1 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_131300 F5 PHerror For RT-qPCR Location GAPDH -4ubulin 2 >4ubulin Rbpm1 1109100 0833600 Primers for RIP-qPCR Location kinesin8b 11 kinesin8b 14	ACGITITIAAAGAACAAATG TGGTCCAAACATAAATG GGTACATTITAAAGAATTGA AG GCTACATTITAAAGAATTGA ATGAGTICCGAAAATTITGA ATGCTACAATATTACTTATA GTCCAACCACTTTAAGATGG ATTTGAAGATGATCAAGAG CGCAGCGGATAATATCCAA CGCAGCGGATAATATCCAA CTAGCTAGAGGCTATGCGTA ATTATCACAAAACAATGTTA GAGTATCAAAAACAATGTAAAAAGTTT CGAACTAGAGTGTAGAAAAGTTT CGAAACTGATGTTAAAAATA CGCAGTAAAATATAGAGTTAG ATTATACCATAATGTATTACCAAAAG CGCAGTAAAATATAGAGTTAG ATTATACCATAAGGTGTG ATTAAGATTGTATCCTACAG CGCAGTAAAATATACCAAAG CGCAGTAAAATATACCAAAAGTGG ATTTACCATAAGGATTGCAAAAG CGCAGTAAAATATACCAAAAGTG ATTAAGATTGTATCCTACAG CGCAGTAAAATATACGACTCACAG CGCAGTAACTGACTCAAAAGTG ATTAAGATTGTATCCTACAG CGCAGTAAAGCATCTATCCAAAAG CGCAGTAAATAAGCATCTATCCAAG CGCAGTAACTGACTCAAAAGTG ATTAAGATTGTTTCCTCC CTATTGCCGACAAAAATG AATATAAGCATCTATCCAAG CGCAGTAACTGACTCAAAATG AATATAAGCATCTATCCAAG CGCAGTAACTGACTCAAAAATG AATTAAGCATCTATCCAAG CGCAGTAACTGACTCAACAG CGCAGTAACAAGCACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAGTGG ATTAAGATTGTATCCTCCC CTATTGCCCACAAAAATG AATTAAGCATCTATCCAAAAGCACTCACAG CGCAGTAACTGACTCAACAG CGCAGTAACTGACTCAACAGTGG ATTAAGAATTGTCCTCCC CTATTGCCCACAAAAATG AATTAAGCATCTATCCCAACAG CGCAGTAACTGACGACTCAACAGG CGCAGTAACTGCCCCACAAAATG AATTAAGCATCTATCCCACAAAATG AATTAAGGATTGTATCCTCCC CTATTGCCCACAAAAATG AATTAAGGATTGTATCCTCCC CTATTGCCCACAAAAATG AATTAAGCATCCACAAAAGCACTCACAGG CGCGCGAGTAATTAGCACTCACACAGG CGCAGTAACTGCCCCCACAAAATG AATTAACCACTCACCACAAAATG AATTAAGAATGCACCCACAAAATG AATTAAGAATGCACCACAAAATG AATTAAGATTGTACCCACAAAATG AATTAAGAATGCACCACAAAAGCACCACAAAATG AATTAAGAATGCACCACAAAATG AATTAAGAATGCACCACAAAATG AATTAAGAATGCACCACAAAATG AATTAAGAATGCACCACAAAATG AATTAAGAATGCACCACAAAAATG AATTAAGAATGCACCACAAAATGCACAAAATG AATTAAGAATGCACCACAAAATGCACACACAGAGAAAGCACACAAAATGCACACAAAATGCACACAAAAAGCACACACA	dict R3 dict R3 dict R4 dict R3 dic2 R1 dic2 R1 dic2 R1 dic2 R2 dic1 R3 dic2 R2 dic1 R3 dic2 R1 dic4 R2 dic1 R3 dic8 R1 PY17X_1109100 R1 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_0521800 R4 PY17X_1311800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 PY17X_13100 R5 PY17X_1300 R5 PY17X_1300 R5 PY17X_1300 R5 PY17X	TAATGTATTGAGAGAAGC TGAATAGAAGTCTCTGCATT GG CGACAATATATATAGGAGCATG GCACAATATATATAGGACATG TTCAACTTGATAGCATG CTTTGCTGAGATGTTAAAGC TTTCAAATTTGTAAGCATG CTATTAACACATTTACACTG CGTTTTATCATTTCTTCTCT TTCAAAATTTACTTCCTC CGTACTTTAATTACTTCCTC CGTACTTTAATTACGTATC GCTGTGTATATGTACGAGTC TCGTCAAAATTACGACAC CTCGTCAGAATTAAGCAACTGCGG CTCTTCAGTATATGTACGAGTC CTCGTCAGAATTACATGTGG ATATCTATATTCATGTCCACC GCTCTTCAGTTTTATGATCCAG GCTCTTCAGTTTTATGATCCAG GCTCTTCAGTTTCAGACCC GCTCTTCAGTTTCAGACCC GCTCTTCAGTTTCAGCCCG GCTCTTCAGTTTCAGCCCG CTCTCAGCAGTCGCCCG CTCCAGCCGTTTCCCATCG ACCCTAAGCACACCCGG CACCTGATCACCGGCACTCTG ATCCCACTGGTTTCCCATCG ACTCTAAGCCAACCCCG CTCCAGCCGTTCCCATCC ACTCCAGCGTTCCCATCG CACCTGACTGCCTGCCCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0503500 F4 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F3 PY17X_0333600 F1 PY17X_13203600 F2 PY17X_1341200 F2 PY17X_1341200 F2 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_0105800 F1 PY17X_0105800 F1 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF16 11 PF16 11 EVENT	CACCACATOCIACITACITACIAC GACAATATTCCAGACACTAA CAAATTACCAGACACTAA GCTITCITAIGAIGITAACA GCTITCITAIGAIGITAACA GGAAGAGAAGATAACATTGAGGA GCTITCITAIGAAAATTIGAAAGG GCAGAGACACCCCGACCCTITAA AAATATTAAAATTGAAAGC CAGAACCCCGACCCTITAA AGGATAATAACTCGACATTGACA CAGAACCCCGACCCTITAA GCAGAACACAATAGAAAT GCAGAACACAATAGCAATGCGA CACAAAGAAAGCCAATCACA CGTICAAAAATGTITCCTCAA GCCACATITTACGAAAATG GCTACCIGTCITAITTATC GGAGGAAACATAAAATG GCTACCIGTCITAITTATC GGAGGAAACATAAAATG GCACCACGACATTAAAAGGG G CTACCIGTCITAITTATC GGAGGAAACATAAAATG CGCACACTITAAAAAGGG G CCCCCIGTCITAITTATC GGAGGAAACATAAATG CTCCCIGTCITAITTATC GGAGGAAACATAAATG CGCACATITTACGAAAATG CTACCIGTCITAITTATC GGAGGAAACATAAATG CGCACATTITACGAAAATG CGCACATTITACGAAAATG CGCACATTAAAAAGGG G CGCCCIGTCITAITTATC GGAGGAAACATAAATG CGCACATTAAAAAGGG C CGCACATTITACGAAAATG CGCACATTAAAAAGGG C CGCACATTAAAAAGACATAAATTG CGCACACTITAAAAAGGG C CGCACATTAAAAACCIGACATCACA CGCACACTITAAAAAGGG C CGCACATTITACGAAAATG CCCCIGTCITAITTATC CGCAGACATTAAAAAGGG C CCCCCIGTCITAITTACCAAAAGGG C C CGCACACTITAAAAACCIGACACTCAAATG C CGCACACATTAAAAACATG C CCCCCIGTCITAITTACCAAAAGGG C C CCCCCCIGTCITAITTACCAAAAGGG C C C C C C C C C C C C C C C	PHTA_0022300 R2 PYTX_0523500 R3 PYTX_0523500 R4 PYTX_0508900 R4 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R2 PYTX_0333600 R1 PYTX_0333600 R2 PYTX_0333600 R2 PYTX_1341200 R1 PYTX_1341200 R1 PYTX_1305400 R12 PYTX_1305400 R12 PYTX_104500 R12 PYTX_104500 R13 PYTX_1216400 R4 PYTX_1216400 R5 CACCCTAAGAGATACCT CACCTAAGAGATACCT CACCTAAGAGATACCTGACCA CTCAAAAGTAGAAATGCAACG C CTCAAAAAGTAGAAAATGCAACG C CTCAAAAAGTAGAAAATGCAACG C CTCAAAAAGTAGAAAATGCAACG C PTCAAAAAGTAGAAAATGCAACG C POWARD primer TTCAAAAAAGTAGAAATGCAACG C CTGCATATCTACATCCTACAGGTATCC CTGCATATACTACACACACGT CAACCA	AATTIGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGGTTTCTTGCGTC TATGTACTAGGTTTCTTTGCG CTCGTCATGTGATTGTTTTGA CATTCATGAGTTTCTTTTGA TTTAAAGGGTCGGGGGTTCT G GATGTCGATGGTCAGTTTTTTCTG CCTGACCATGAGTTGTTTGCG CCTGACTCCATGTTTATCCT TACAAATGATACTTTTGCG CCTGACTCCATGTTTATCTC GTCATTGGTAGTGATGTTGCA CATCATTGTTCTTGCGACTTAT ACGTTCCTCAGCTGACTTAGTTC CTTATGCCTCAACTGAGCAC CTTGCTCCAGCGCCTTAT ACGTTCCTCAGCTGACAACTGAGCA C CCGGTTACTCTGTGCAACTGATG CACATTGTGTGAAATATTGCAT CGGGTACACGACATTACT
abs 13 dict F4 dict F5 dict F1 dict F2 dict F1 dict F2 dict F3 dict F2 dict F3 dict F2 dict F3 dict F1 dict F2 mdz F1 PY17X_1109100 F1 PY17X_1109100 F2 PY17X_10521800 F2 PY17X_1311800 F4 PY17X_1311800 F4 PY17X_1323900 F1 PY17X_1323900 F1 PY17X_1323900 F1 PU100 G033560 Primers for RIP-qPCR Location Kinesin8b 11 Kinesin8b 14 PF16 E1	ACGITITIAAAGAACAAATG TGGTCCAAACATAAATG GGTACATTITAAAGAATTGA AG GCTACATTITAAAGAATTGA ATGGATCCGAAAATTITGA ATGGTACAAAACAATCTTAA GTGCCAACCACTTTAAGATGG ATTTGAAGATGATCAAGAG GGCAGCAAAACAATCTTAA GTGCCAACCACTTTAAGATGG ATTTTGAAGATGATCAAGAG CGCAGGATAATATCCAA GGGTGTTAGAGAAGCTATGGGTA A TTGTCACTCTTGTTGAGAGCC GGGGTGTTAGAAAACATGT GGCAGTAAATATGGGTTA GGCAGTAAATATGGGTTG GGAAACTGATGTTAAAAATA CGCAGTAAATATGGAGTTGG ATTAGTGTTTATCCTAAGC GTATTTGCCCACAAAAGTGG ATTATAAGCATCTATCCTACG GTATTTGCCCACAAAAATG ATATAAGCATCTATCCTACG GTATTGCCCCACAAAAATG ATATAAGGATCTATCCTACG GTATTGCCCACAAAAATG ATATAAGCATCTATCCACAG PY17X_0100 PY17X_0100 PY17X_00100 PY17X_00100 PY17X_00100	dict R3 dict R4 dict R3 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R1 dic4 R2 dict R2 dict R3 dick R1 dick R2 dict R3 dick R1 dick R2 md2 R1 PY17X_1109100 R1 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R3 PY17X_0521800 R4 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_1311800 R5 PY17X_131300 R5 Forward primer GGACAAGGTAGATCAGCAGGTAT CC CGACAAGGTAGATCAGCAGGTAT CGCACAAGGTAGATCAGCAGCACA ATGTCGGTCAAGCAGGACAA ATGTCGGTCAAGCAGGTAT CGCACAAGGTATGAACACACG CGACAAGGTATGAATCGTACACA ATGTCGCTAAGTCAGACCACG CTTAGCTAGTTAGATCGACACAG GCTAAGTTAGATCGACACG GCTAAGTATAGTCGTCGCACACG CTTAGCTAGTTAGATCGACACG CTTAGCTAGTTAGATCGACACG GCTAAGTATAGTCGTCGC AGCTAAGTTAGATCGACACG CTTAGCTAGTTAGATCGACACG CTTAGCTAGTTAGATCGACACG GCTAAGTATAGTCGTCGC CABATAGTTAGACCACCACG CTTAGCTAGTTAGATCGACACG CTTAGCTAGTTAGTCGTACCA	TAATGTATTICAGAGGAAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGACTG CTTTGCTGAGATGTAAGCATTG CTTTGCTGAGATGTTAAGCATG CTTTGCTGAGATGTTAAGCATG CTTTGCAATTTCTTACAGAGC CTTTTAAAATTTACTTCCTC CGTACTTTAATTACTTCCTC CGTACTTTAATTACTTCCTC CGTGTGTATATGCAGCAG CCTGTGTATATGCAGCAG CTCGTCAGAATTAGTACAGG CTCGTCAGAATTAGTACGAG CTCTCTAGAAAGTTCTTCGCACC CTCGTCCAGATTACTAGTGCAG CGTCTCTATTTCCCACTCT CGTACCTAAATATCATGTAGA CGTCTCTAATATCATGCAG CGTCTCTCAGGTTTATACACCAG CACCTGATCAGTGCACCACCAG CACCTGATCAGTGCACCACCAG CACCTGATCAGTGCACCACCAG CACCTGACCAGTGCACCACCAG CACCTGACCAGTGCACCACCAG CACCTGACCAGTGCACCACCAG CACCTGATTACGTCACGACTACT CACCCACTGGTTTCACGACTGC CGTCGCGTGACTAACGCATAT GGCGGTGTATAACAATGCGTTA		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 Pf16 Pf16 Pf1 Pf16 Pf16 Pf16 Pf1 Pf16 Pf1 Pf16 Pf16 Pf1 Pf16 Pf16 Pf1 Pf16 Pf16 Pf1 Pf16 Pf16 Pf1	CACATATTCCAGACACTAA CAAATTCCAGACACTAA CAAATTCCCAGACACTAA GCAAATTCCCAGATTTTACGAT GCTTTCTTATGATGTTAACA GGAGAGAGATAACATTGAGGA GCTTCCTTATGAAAATTGGAAGAG AAAATATTGAAAATTGGAAGAG CTCATGAAAATTTGGAAGAGG CAGATATGACATTAAAGC CAGATATGACAATGACCCCTTTAA GCAGTATGACAATGGCAATGC GAGATATGACAATGGCAATGCG GCAGTATGACAATGGCAATGCG GCAGTATGACAATGGCAATGCG GCAGTATGACAATGGCAATGCG GCTGCATGTGTAGAAATGTTCCCCAA GCTGCAAGGAAATTTACGGAATGCC GGCAGACATTAAAAGGGCAATCATG CCGCAAGACGTAAAATGTTCCCCAA GCTGCAATGGCAATGTTCCCCA GCGCAGACATTAAAAGGGGAATTCATG CCGCAGACATTAAAAGGGG GCGCAGCATTAAAAAGAGGG GCGCAGCATTAAAAAGAGGG GCGCAGCATTAAAAAGAGGG GCGCAGCATTAAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCGCAGCATTAAAAGAGGG GCCGCAGCATTAAAAGAGGG GCCGCGCGCGCCGCGC	PHTA_0523500 R2 PHTA_0523500 R3 PHTA_0523500 R4 PHTA_0508900 R4 PHTA_0508900 R5 PHTA_0508900 R5 PHTA_0508900 R5 PHTA_0508900 R5 PHTA_1320300 R1 PHTA_050800 R4 PHTA_0508900 R5 PHTA_0508900 R5 PHTA_0508900 R5 PHTA_0500 R1 PHTA_1305400 R10 PHTA_1305400 R12 PHTA_1305400 R13 PHTA_015900 R13 PHTA_015900 R13 PHTA_1216400 R4	AATTIGTGAAAATGTCCAGA CCTICTTTTACTCATTAAT GTGTGTCATCAATTAGTTGT CGCATTTGCTTTTCTGC CGCATTTGCTTGTTTCTGC CTCGTCATGGATTGTTTGT CGCATGTGGTGTGTTAA CATTCATGAGGTTTCTTTGA TATGTACTGGAGGTTCTTTGA GGATGTCGAGGTTTTTTTTTT
abs 1 bit dict F4 dict F5 dict F1 dict F2 dict F2 dict F1 Det F2 md2 F1 PY17X_1109100 F1 PY17X_109100 F2 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_1311800 F6 PY17X_1307300 F1 PY17X_1307300 F1 PY17X_1307300 F3 Primers for RT-qPCR Location GAPDH atubulin 2 β-tubulin Ba33600 Primers for RIP-qPCR Location kinesin8b I1 kinesin8b I4 PF16 E1 PF16 I1	ACGITITIAAAGAACAAATG TGGTCCAACATAAATG GGTCAACATTITGAA AG GCTACATTITCAAAGAATTCG ATGAGTTCCGAAAATTITTC AAATCTAATATTCCTTATCA ATGCATCCGAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTTGAAGATCATCAAGA GGCAGCGGATAATATCAAGA GGCAGCGGATAATATCAAGACTAT GGCAGCGGATGATGACAAAAATA CGCAGTAGAGCTATGCGTA A TIGTCACTCTTGTTGAGCGCC GGGTGTGTTAGAAAACACTGGA TIGTCACTGTTGGAGCAAGGTTA CGAAACTGATGTTAGAAAATA CGCAGTAAATATAGAGTTAG ATATAAGATGTTATACTCTC GTATTTAGCAAAAATG ATATAAGGATCTATCCAAAAATG AATATAAGGATCTATCCAAAAATG AATATAAGGATCTATCCAAAAATG AATATAAGGATCTACTCC GTATTACCCATAAGGTGTG ATTAAGATTGTATCCTCC GTATTGCTCGACAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATATAAGCATCTACCAAAAATG AATTAAGCATCTACCAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACCAAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACTACCAAAAATG AATTAAGAATGTACCAAAAAATG AATTAAGAATGTACCAAAAAATG AATTAAAGAATGTACCAAAAAATG AATTAAGAATGTACCAAAAAATG AATTAAAGAATGAAAGAAGGACGAAAAATG AATTAAGAATGTACCAAAAAATG AATTAAAGAATGTACAAAAGAAGAAGGACGAAAAAATG AATTAAAGAATGTACCAAAAAAATGAAGAGGAAGAAGAAGAAGAAGAAGAAGAAGA	dict R3 dict R4 dict R3 dict R4 dict R5 dic2 R1 dic2 R1 dic2 R2 dict R3 dict R2 dict R2 dict R3 dict R2 dict R3 dict R2 dict R3 dick R1 PY17X_1109100 R1 PY17X_1109100 R2 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R4 PY17X_1311800 R8 PY17X_1311800 R8 PY17X_1311800 R8 PY17X_1311800 R8 PY17X_131300 R5 PY17X_131300 R5 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1317300 R5 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_1323900 R1 PY17X_132300 R5 CGCACAAGGTAGGAGGAGTAT GGCAGAAGGTAGGAGGAGTAT GGCAGAAGGTAGGAGGAGTAT GGCAGAAGGTAGGAGGAGGAGCAGGAA ATOTCGGTCAAGGTAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA	TAATGTATTICAGAGGAGAGC TGAATAGAAGTCTCTGCATT GG GCACAATATATATAGAGCATG CTTTGCTGAGATGTAAGCATG TTGAATAGAAGTTGTAAAGCATTG CTTTGCTGAGATGTAAAGCATTTG CTTTGCAAATTTGCTACCTG CGTTTTATCATTTACTTCCTC TTTCAAAATTTACTTCCTCC GCTGTGTATATCATTCCTCC GCGTGTGTATATGTGTGAATC GCGTGTGTATATGTGTGAGATC GCGTGTGTATATGTGTGAGAC CTCGTGGTATATGTGTGAGAC GTCTTCAGAAATTCATGTGGG GTCTTCCGGTTTTATGTACCAG GGACTGTTTATGTACCAGT Reverse primer ACTCTAAGGCAGTGGGCATTG GACGTGTATATGTGTGCGAG GCGCTTGCGTTGCG		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F2 PY17X_1320300 F1 PY17X_0033600 F1 PY17X_0033600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_1305400 F1 PY17X_1305400 F1 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 Pf1	CACCACATOCIATOCIATOCIATOCIATOCIATOCIATOC	PTTX_0523500 R2 PYTX_0523500 R3 PYTX_0508900 R4 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R6 PYTX_0508900 R2 PYTX_050800 R1 PYTX_0833600 R1 PYTX_0833600 R1 PYTX_1305400 R10 PYTX_1305400 R10 PYTX_1305400 R12 PYTX_0415900 R13 PYTX_0105800 R1 PYTX_0105800 R1 PYTX_01216400 R4 PYTX_1216400 R5 CAACCCTCAAGAGATACCT CAACCATAATGCAACAG CTC AGGGTACATAGTAGAAGAGATACCT CGTGGTACATACTTCATGTG TTCCAAAAGTAGAAGAGATAGCAACG CTTC GTTACATACTACAACGGATACCT GTTACAAAGTAGAAGAGTAGCAACG GTTACAAAGTAGAAGTAGCAACGGATACCT GTTACAAGCAATAATAAGCGAAACGGATACCT GTTACAAGCAATAATAAGCGAAACGGATACCT GTTACAAGCAATAATAAGCGAAATGCAACGGATACCT GTACAGGATATACTACACACGGATACCT	AATTIGTGAAAATGTCAGAA CCTICTTTTAGGAAATGTCCAGA CCTICTTTTGGGAAATGTCCAGA CGTGTTGCATCAATTAGTTGT CGCATTTGCTTGCTTGCGTC TATGTACTAGGTTTGTTGCG CTCGTCATGGGTTGCTTAA CATTCATGAGGTGGGGGGTTCT G GATGTCGAGGTTTTTTGCG CCTGACTGGAGGTTTTTTCG GATGTCGAGGTGGGGGTTCT G GATGTGGATAGGTGGAGGTTTTTGCA TCTTATGCATCATGTGGCAC CTTTCTCTCGGGAGTCTG GATGTCTCTGCGCCTTAT ACGTTCCTCGGCCCTTA CGTGCTCAACTTGATCAGGCC CTTTTCTTCTCTCGTGGAGTTC G GACAGTGTAACAATGAGCA CCCGGTTAACTGTGGCAATGAGCA G CCCGGTTAACTGTGGGAATCCTC CGGGTTAACGATGGCAC CCGGTTAAGTGGTAACCAATGAGCA G CCCGGTTAAGTGGGAATCCTCA C CCGGTTAAGTGGGAATCCTCC CCGGTTAAGTGGGAATCCTCC CCGGTTAAGTGGGAATCCTCC CCGGTTAAGTGGGAATCCTCC CCGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCA CCAATGGTGAACAATGAGCACCC CGGGATACACACACTTACTAT CCCGAATTGGGGAATCCTCCA C CGGGATACACACACATTACTAT
abc 1 F4 dic1 F4 dic1 F5 dic2 F1 dic2 F2 dic1 F3 dic2 F1 dic1 F3 dic1 F1 dic2 F2 dic1 F3 dic2 F1 dic1 F3 dic1 F3 dic2 F1 PV17X_1100100 F1 PY17X_10100 F2 PY17X_10521800 F1 PY17X_1311800 F4 PY17X_1311800 F6 PY17X_131300 F1 PY17X_131300 F1 PY17X_131300 F3 PY17X_131300 F4 PY17X_131300 F5 PY17X_1335300 F1 PY17X_13357300 F5 Primers for RT-qPCR Location GAPDH c4ubulin 2 β-ubulin B33600 Primers for RIP-qPCR Location kinesin8b 11 kinesin8b 14 PF16 E1 PF16 I1 dic6 I20	ACGITITIAAAGAACAAATG TGGTCCAACATAAATG GGTCACATTITAAAGAATTGA AG GCTACATTITAAAGAATTGA ATGAGTTCCGAAAATTTTC AAATCTAATATTCCTTATCA ATGCTACCAACTATATTCCTTATCA ATGCTACCAACTATATTCCTTATCA ATGCTACCACCACTTTAAGATGG ATTTGAACATCATAACAATGGA ATTTTGAACATCATAACACTGGA T GGCAGCGGATAATATACAGAACACTGGA T GGCAGTGAGAGCTATGCGTA A TGTCACTCTTGTTGAGCGCG GGGGTGTGTTAGAAAACACTGGA T GGCAGTAAATATAGAGTTAG ATATACCATGATGTTAGAAATT CGCAGTAAATATAGAGTTAG ATATACCATGATGTTAAAAATG GGAGTGTTTAGAAAAGACTGGA ATTATGACTGATGTTAGAAAAGT GTATTACCCATAAGGTGTG ATTAAGATTGTATTCCTTCC GTATTGCCGACAAAAATG AATATAGCATCTATCGACAAAAATG AATATAGCATCTATCCAACAG Gene ID PY17X_018700 PY17X_018700 PY17X_0204100 PY17X_0019000 PY17X_0019000 PY17X_0019000 PY17X_0019000 PY17X_003800	dict R3 dict R3 dict R3 dict R3 dic2 R1 dic2 R2 dic4 R2 dic4 R2 dic4 R2 dic4 R2 dic4 R2 dic4 R3 dic6 R1 dic8 R2 md2 R1 PY17X_1109100 R1 PY17X_109100 R2 PY17X_0521800 R1 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1317300 R5 Forward primer CGCAGGGTAGGAAGCAGGTAT CC CGCAGGGAAGGATAGCAGGTAT CGCAAGGAAGGATAGCAGCGAA ATG CGCAAGGAAGGATAGCAAGCAGC GCTAGCTAGTAGATCGTACCA GCAAGGTAAGTAAGCACCCC CACGGCTAGTAAGTAGCACCCCCC CACGCCTAATATTCATCCTACCA	TAATGTATTIGAAGGAAGC TAATGATTIGAAGGAAGC TGAATAGAAGTCTCTGCATT G GCACAATATATATAGGAGCTG TTCAACTIGATAGCATTG TCAACTIGATAGCATTG CTTTGCTGAGATGTTAAACG CTTTTACCAGATTTACACGG C CGTTTTATACACATTTACCTCC CGTACTTAACACATTTACCTCC CGTCGTAAATTTACTTCCTCC CGTCGTAAAGTTCTTCGACGG CCTCTGTATATGTACGGAG CCTCTGTAGAACTTGTGAAC GCTGTGGAGAATTAAGTATT TATAAAAACTTCTTCGCACG GTCTTCTATTTCCACTCT CGTACGTAAATATCATGTAG GCTTCCAGTTTATGTACCACG CTCTCAAAGGCACCCCG GTCTTCATTTCCAGTTTTATGTACCA GGATTCCCAGTGGCAACACCCG GTCTCTGATGGCAACACCCG CTTCCAGTTGATCACGGCATTCG ATA CACCTCAAGGCAGCGCACTCTG CTCCGCCAGCGCATCTG CTCCGCCAGCGCACCCCG CTTCGTATATGTACCGCGCATCT GGGCTTCGCTGCTAACGAGCA CTCCTCACGTCGTCCCACGCC CTCCGCCGCGCGCCCCCCCCCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F2 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1341200 F1 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0105800 F1 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF16	CACCACATOCIACITACIACIA GACATATTCCAGACACTAA CAAATTCCCAGACACTAA GCAAATTCCCAGATTTTACGA GCITTCTTATGATGTTAACA GGCAGAGATAACATTGAGGA CTCATGAAAATTGAGAAG CTCATGAAAATTGAGAGA CTCATGAAAATTGAAAGC CAGATGGAGTATTAATGGC AGAGTACGCCGGACCCTTAA A GCAGTAATGACAATAGAAG GAGATAGCACATAGAAAG GAGATAGCACATGTCGACATCG GAGAGGAAAGAAGGCAATCGTCG GCAGCACATTTTACCGACATCG GCTACCTGTCTTATTTAC GACTACCTGTCTTATTTAC GCGCAGACATTAAAAGG GCAGACATTAAAAGGG GCAGCACATTAAAAGGG GCAGCACATTAAAAGGG GCAGGAAACATAAAATG CGCAGACATTAAAAGGG GCAGGAAACATAAAATG C GCAGAGGAAACATAAAATTGT C GCGCAGACATTAAAAAGGG G GCAGGGAAACATAAAATG C GCCAGACATTAAAAAGGG G CGCAGACATTAAAAAGGG C CGCAGACATTAAAAAGGG C C CGCAGACATTAAAAAGAGG C C C C C C C C C C C C C C C	PHTA_0022300 R2 PYTX_0503900 R3 PYTX_0503900 R4 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R5 PYTX_0508900 R2 PYTX_050800 R1 PYTX_0303600 R1 PYTX_0303600 R1 PYTX_0303600 R1 PYTX_0341200 R2 PYTX_1305400 R10 PYTX_1305400 R12 PYTX_1305400 R12 PYTX_0105800 R1 PYTX_0105800 R1 PYTX_0105800 R1 PYTX_1216400 R5 CAACCCTGAAGAGATAGCT AGCAAGGAAAATGCAACG C AGCCAAGGAAAATGCAACG GTGTGTACATACTTCATGTG GTGTGTACATACTTCATGTG GTGTGTACATACTTCATGTG GTGGTAGCATACTCAACGGTTG GCTAGCATATACTACACGGTTG GCTAGCAGTATACTACACGGTT GCTAGCAGTATACTGCTACACGGTT GCTGGTAGCATATATAGCGAAAT GCTAGCAGTATACTGCTACACGGTT	AATTIGGAAATGTCCAGA CCTICTITTACTCATTAAT GGGGTGTCATCAATAGTGTCCAGA CCTICTITTTACTCATTAAT GGGGTGTGCATCAATAGTGTT CGCATTGGTGTTGCGTGC CTCGTCATGTGATTGCTTAA CATTCATGAGTTGCTTAA CATTCATGAGTGGGGTTCT GGATGTCGAGGTTTTAATGCCCAATTTATGCG CCTGACTCCATATTTATCTC GGATGTCCCAATTTATCTC GCATCGTCATGATGTGCTCAG CATCATTAGGTCTTGGCACTAT GCATGGTTCCTCGGCCCTTAT ACGTCCCTCAATGTGTCCA AGTAGTCCTCAACGTATT GGCGCTTGACTCAACGATAT GGCGCTTGCTTCGTGCAACGATAT GGGGATACCACACATTACTG CCCATTGGTGCACGGCACTTA CGGTGTCCCCAATTGCGCACTTA GGGGATGCTCGGGAATCTCAG CCCATTGGTGCACGCACTTACTGC CCCATTGGTGGCACTCACGCACTTA CGGGGTGCCCCAATTGCGCACTTA CGGGGATACCACCACATTACTAT CCCAATGTGTGACAACAATGGCCAC CCCAGTTCCTTCGTGCCACTTCA CGGGGTACCCCACATTACTAT CCCAATGTGTGCACGCACTTCCACGCACTTATCCACGCACTTCCTCCACCACTTACTCACTC
abs 1 50 dicl 1 F3 dicl 7 F1 dicl 7 F2 dicl 7 F3 dicl 7 F3 dicl 7 F3 dicl 7 F3 dicl 7 F1 dicl 7 F3 PV17X_1100100 F1 PV17X_1311800 F4 PV17X_13123000 F1 PV17X_101010 GAPDH a-tubulin 2 F-tubulin Cocat	ACGITITIAAAGAACAAATG TGGTCCAACATAAATG TGGTCAACATAATTIGTGA AG AG ATGAGTTCCGAAAATTITC AAATCTAATATTCCTTATCA ATGCTACCAACTATATTCCTTATCA ATGCTACAAAACAATCTTAA GTCCAACCACTTTAAGATGG ATTTGAACATCATAACAATGG ATTTGAACATCATAACAATGGA ATTTTGAACATCATAACAATGGA ATTTTGAACATCATAGAGTATCCAA CGCAGCGGATAATATCCAA AGGTATTGAAGACTATGGCAT ACGCTAGCAGCATGTGAAAAAT CGCAGTAAATATAGAGTTGG ATAATAACACTGAGTTAGACTTAG GATATTACCCATAAGGTGTG ATTATACCATAGGTGTG ATTATAGCATCATCCTACCAG CGCAGTGAAATATAGAGTTGG ATTATACCCATAAGGTGTG ATTAAGATTGTATTCCTACACG CGCAG CGCAGTGAAATATAGAGTTGG ATTATAGCATCATCCAACAG CGCAGTGAAATATAGAGTTGG ATTAAGATTGTATTCCTACACG CGCAGTGAAATATAGAGTTGG ATTAAGATTGTATTCCTACACG CGCAGTGAAATATAGAGTTGG CGCAGTGAAATATAGGAGTGG CGCAGTGAAATATAGAGTTGG CGCAGTGAAATATAGAGTTGG CGCAGTGAAAAGAGTGG CGCAGTGAAAATATAGAGTTGG CGCAGTGAAAAGAGTGG CGCAGTGAAAAGAGTGG CGCAGTGAAAAGAGTGG CGCAGTGAAAAGAGG CGCAGTGAAAAGAGTGG CGCAGTGAGAGAGAG CGCAGTGAAAGAGTGG CGCAGTGAGAGAGAG CGCAGTGAGAGAGAGAG CGCAGTGAGAGAGAG CGCAGTGAGAGAGAGAG CGCAGTGAGAGAGAGAGAGAGAGAG CGCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	dict R3 dict R4 dict R3 dict R4 dic2 R1 dic2 R2 dic4 R4 dic2 R2 dic4 R4 dic4 R2 dic4 R2 dic4 R3 dic6 R1 dic6 R2 md2 R1 PY17X_1109100 R1 PY17X_109100 R2 PY17X_0521800 R1 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_0521800 R2 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_1311800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_131800 R6 PY17X_1367300 R5 Forward primer GGCGAGGTAGGAAGGTATGGACGAA CGACAGGATAGGTAGGACAGGTAT CC CGGGGGTGGGAAAAATCACAGCATAT CGCTAGTAATATGTGCTGACAA CAACCACTATATGTGCTGACAAGGAAAATCAACG CAACACTATATGTGCTGACAAGGAAAATCAACG CAACACTATATGTGCTGACAAGGAAACTCACACTATATGTGCTGACAAGGAAAATTTAACCAACTATATGTGCTGACAAGGAAAATTTAACCAACTATATGTGCTGACAACTACTAGGCAACCCC CCTCCTATAGGCGAACTCAAATTTAACCAACTCAACTAAGGCAACCCCC CCTCCTATAGGCCAACTACTAAGCCAACTCAACTAAGGCAACCCCCC CCTCCTATAGGCCAACTCAAATTTAACCAACTCAACTAA	TAATGTATTIGAAGGAAGC TGAATAGAAGTCTTGCAATT GG CGACAATATATATAGGAAGC TG CGACAATATATATAGGACTG TTGCAGGACTGTGAAGC TTTGCTGGGACTTTAACAGC TTTGCTGGGACTTTAACAGC CTTTTACACATTTACACTGC C CGTTTTATCATTTCTTCCTC TTCAAATTGCTCCC CGTCGTATATGCACGAC CGTGTGTATATGCACGAC GCTGTGTATATGCACGAC GCTGTGTATATGCACGAC GCTGTCGACAGACTTGCAG GCTTCTATTTCCACCTC CGGGCGACTTAAGTCTC CGGGCGACTTAAGTCCC GTGTCGTAAAGTCTTCGCACG GTCTCTATTTCCACCTC GGACTTTAATTCCACCTC CGGGCGACTAAGACTCTGCAG GTCTCTATTTCCACCTC GGACGTTAATTCCACCCG GTCTCTATTTCCACCTC GGACGTTAAGGCAACACCCA GTCTCACGCAGTGGCACTTG ATACCACGCGTGGGCACCTG GTCCGCGGGGGGCACCTG GTCCGGCGGTGGCACCCG CTCCGCGCGTGGCACCCG CTCCGCGGCGGGGCACCTG GCGCGTGGCACACCCAG CTCCGCGCGTGGCCACCCG CTCCGCGCGGGGCACCTG GGCGCTTGACTAACGACGC GGACTTCCCTTCC		PY17X_0523500 F2 PY17X_0523500 F3 PY17X_0508900 F4 PY17X_0508900 F5 PY17X_0508900 F5 PY17X_1320300 F1 PY17X_1320300 F3 PY17X_1320300 F3 PY17X_1320300 F2 PY17X_1320300 F1 PY17X_0833600 F1 PY17X_0833600 F1 PY17X_1305400 F10 PY17X_1305400 F12 PY17X_1305400 F12 PY17X_1305400 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_0415900 F13 PY17X_1216400 F5 Location 1216400 kinesin8b 11 kinesin8b 14 PF16 11 PF17X_1109100 11 PY17X_109100 12	CACCACATOCTATC TATCA GACAGAGAGACACTAA AGACAGAGAGACATAATTCA GCTTTCTTATGATGTTAACA GCTTTCTTATGATGTTAACA GCTTCTTATGATGTTAACA GCTTCATGAAAATTTGAGAGAG AAAATATTAAAAATTGAAAGC CACGAGAGGAGATATTAATGGC AGAGAGCCCCGACCCTTTAA GCAGTATGACAATAGAAGC GACAGACCCCGACCCTTAA A GCAGTATGACAATAGAACT GACATACCCGGACACTCATG GACAGCCGGAGAACATGGCA CACAAAGAAGGGAATCGACATG GCTACCTGTCTTATTTAC GACAGAGAAAATGTTCCCAA GCCACAATTGACAATGTCAC GCAGACGAAACATAAATG GCCACACTTTATCGACAATG GCCACACTTTACGAAATG GCCACACTTTAAAAAGGG GCCACACTTTTACGAAAATG GCCACACTTTAAAAAGGG GCCACACTTTAAAAAGGG GCCACACTTAAAAAGAGG GCCACACTTAAAAAAGAGG GCCACACTTAAAAAAGAGG GCCACACTTAAAAAGAGG GCCACACTTAAAAAGAGG GCCACACTTAAAAAGAGG GCCACACTTAAAAAGAGG GCCACACTTAAAAAAAAAA	PHTA_0022300 R2 PYTZ_0503900 R4 PYTZ_0508900 R4 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R5 PYTZ_0508900 R2 PYTZ_050800 R1 PYTZ_050800 R1 PYTZ_0303600 R1 PYTZ_030500 R1 PYTZ_030500 R1 PYTZ_1305400 R10 PYTZ_1305400 R12 PYTZ_1305400 R13 PYTZ_0105800 R1 PYTZ_1305400 R13 PYTZ_1216400 R4 PYTZ_1216400 R5 Forward primer CAACCCTGAAGAGAAATGCAACG CC GGTAGATAACATCATCATCATCATGTG GTTAGAGAGAAAAGTAGAAGTACCT AGGCAATAATAAGCGAAAT GTTAGAGCAATACTCAACGGTT GGTAGCAATACTCAACGTACATCATCATCATCATCATCATCATCATCATCATCATCA	ATTIGTGAAAATGTCAAGA AATTGTGGAAATGTCCAGA CCTICTTTTACTCATTAAT GTGGTCATCAATTAGTTGT CGCATTTGTGGTCTTTGGCTC TATGTACTAGTTGTTTGGCTC CTCGTCATGTGATTGGTTTGA TTTAAAGGGTCCGGGTTCT G GATGTCCGAGTTTTATGC CCTGACTGCGAGTTTTTGA TTTAAAGGGTCCGGGTTCT G GATGTCGAGGTTTTTGCG CCTGACTGCAGATTTATCT GCATGATAGTTGTTCGCA TCTTATGCATTTTGCC AGTATGTCTTGGCCCTTAT ACGTCCCTCAAACTTGGCCC CTTGTCAACTCAAC

Probe	Gene ID	Forward primer	Reverse primer		Probe	Gene ID	Forward primer	Reverse primer
kinesin8b 14 probe	PY17X_0204100	TAATACGACTCACTATAGGG AGACTAAAATGGAAAACCA GTTAC	TAAGGTGAATGGTAAAGTTC		bfp	/	TAATACGACTCACTATAGGG AGAATGGTGAGCAAGGGCG AGGA	CTTGTACAGCTCGTCCATG C
kinesin8b 11 probe	PY17X_0204100	TAATACGACTCACTATAGGG AGAATGAAAAATTATTTATA GAC	TAAGTTCATCTTGCAATCCT		bfp-Kin8b 11	/	TAATACGACTCACTATAGGG AGAATGGTGAGCAAGGGCG AGGA	CTTGTACAGCTCGTCCATG C
PF16 E1 probe	PY17X_0919000	TAATACGACTCACTATAGGG AGAAGATAAAGTTCCTATAG TTC	AAAATTTGATTAAATTTGGT		bfp-PF16 I1	/	TAATACGACTCACTATAGGG AGAATGGTGAGCAAGGGCG AGGA	CTTGTACAGCTCGTCCATG C
PF16 I1 probe	PY17X_0919000	TAATACGACTCACTATAGGG AGACTAAAATCACCTTTAAA ACT	TCAGAATATCCAGGTGTGTA					
Note: The blue sequ	ences are designed f	or the restriction enzy	me digestion. The rec	l sequences are T7 p	romoter sequence.			