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RNA-binding protein Rbm24 as a multifaceted post-transcriptional regulator of embryonic lineage differentiation and cellular homeostasis

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Short title: Dynamic Rbm24 function in cell differentiation

Abstract

RNA-binding proteins control the metabolism of RNAs at all stages of their lifetime. They are critically required for the post-transcriptional regulation of gene expression in a wide variety of physiological and pathological processes. Rbm24 is a highly conserved RNA-binding protein that displays strongly regionalized expression patterns and exhibits dynamic changes in subcellular localization during early development. There is increasing evidence that it acts as a multifunctional regulator to switch cell fate determination and to maintain tissue homeostasis. Dysfunction of Rbm24 disrupts cell differentiation in nearly every tissue where it is expressed, such as skeletal and cardiac muscles, and different head sensory organs, but the molecular events that are affected may vary in a tissue-specific, or even a stage-specific manner. Recent works using different animal models have uncovered multiple post-transcriptional regulatory mechanisms by which Rbm24 functions in key developmental processes. In particular, it represents a major splicing factor in muscle cell development, and plays an essential role in cytoplasmic polyadenylation during lens fiber cell terminal differentiation. Here we review the advances in understanding the implication of Rbm24 during development and disease, by focusing on its regulatory roles in physiological and pathological conditions.

Key words: RNA-binding protein; Rbm24; cell differentiation; alternative splicing; cytoplasmic polyadenylation; muscle; head sensory organs; lens; inner ear.

1. Introduction

RNA-binding proteins (RBPs) play key roles in the post-transcriptional regulation of gene expression in a variety of biological processes. Vertebrate cells express hundreds to thousands of RBPs that display unique binding activity to their RNA targets and specific interaction with other protein partners. They control RNA metabolism at multiple levels, from alternative splicing, to transport, subcellular localization, stability, polyadenylation, and translation [1]. Thus, protein-RNA interactions are critical for maintaining the homeostasis of protein synthesis during early development and in adult life. Large-scale analyses of protein expression regulation have made the unprecedented finding that protein abundances within the proteome and mRNA levels within the transcriptome are entirely uncoupled in many conditions [2,3]. This highlights the importance of additional regulations by the ribonome, which embodies mRNAs and associated RBPs within a rich ribonucleoprotein (RNP) infrastructure in the cell [4]. Due to the crucial roles exerted by the processes downstream of transcription in the spatiotemporal control of gene expression, it is not surprising that a growing number of human diseases, such as neurodegenerative disorders and various types of cancers, are associated with RNAs and RBPs [5-9]. Therefore, RBPs may have the potential to be used as therapeutic targets in many diseased conditions [10,11,12].

Rbm24 (RNA-binding motif protein 24) is an evolutionarily conserved RBP that contains a single RNA recognition motif (RRM) in its N-terminal region [13,14,15]. It exhibits strongly restricted tissue-specific expression patterns during vertebrate development [16], and emerges as an important regulator of cellular differentiation and a potential factor implicated in human disease. Although no mutation of human *RBM24* gene has been associated to any disease up today, deficiency in its expression level could be the cause of congenital disorders, such as cardiomyopathy, myopathy or blindness, which affect the normal function of related tissues where crucial roles of this gene have been demonstrated in different animal models. It seems that vertebrate Rbm24 could be involved in nearly all aspects of post-transcriptional regulation. Most importantly, it functions as a key factor that regulates alternative splicing to establish the contractile function in developing cardiac and skeletal muscles [17,18,19], and plays an important role in cytoplasmic polyadenylation (CPA) to ensure the accumulation of crystallin

proteins during lens fiber cell terminal differentiation [20]. There is thus accumulating evidence that Rbm24 acts as a multifaceted regulator to initiate cell differentiation through distinct mechanisms, which may vary in a tissue-specific and even a stage-specific manner. Moreover, Rbm24 presents almost the same characteristics in RNA and protein interactions, and often performs similar functions, as the closely related ancient paralog Rbm38 (RNPC1) in regulating cell cycle progression and apoptosis [21,22], adding more complexity of its functional implication in various cellular processes. Mechanistic insights on how Rbm24 controls gene expression are beginning to be elucidated using *in vivo* and *in vitro* approaches. However, a number of important questions remain unanswered and await further investigation, such as its dynamic subcellular localization and tissue-specific function, the modulation of its activity through interaction with other partners, and its potential implication in human pathologies. In this review, we present recent advances in understanding the regulatory roles of Rbm24 in development and disease.

2. Rbm24 functional domains

Rbm24 proteins display deep evolutionary conservation. The RRM is located in the N-terminal half and contains two characteristic consensus RNP sequences, RNP1 and RNP2 [23]. This domain shows extremely high levels of sequence identity among different species, ranging from nematode to human (Fig. 1). In addition, it is almost identical to the RRM of Rbm38, such that both Rbm24 and Rbm38 prefers similar GU-rich sequences in target mRNAs [21,24]. Although the sequence outside the RRM is relatively divergent, at least two conserved domains can be identified in the C-terminal half of vertebrate Rbm24 and Rbm38 [25]. In particular, a motif close to the extreme C-terminus, which contains a serine residue (serine 181 in Rbm24 and serine 195 in Rbm38), interacts with eukaryote initiation factor 4E (eIF4E) and disrupts the assembly of translation initiation complex [26,27]. However, at least in several cancer cell lines, phosphorylation of the serine residue by glycogen synthase kinase 3 (GSK3) prevents the interaction with eIF4E and converts Rbm24 or Rbm38 into an activator of mRNA translation [28]. A second conserved motif is the extreme C-terminus, whose implication in Rbm24 function

is not clear. The C-terminal half of Rbm24 also interacts with a number of other partners, but the exact motif implicated has not been determined and the interaction is often assisted by the RRM. For example, both the N-terminal and C-terminal regions of Rbm24 are required for interaction with the Stk38 kinase [29]. Although the N-terminal region of zebrafish Rbm24a do not directly interacts with cytoplasmic polyadenylation element-binding protein 1b (Cpeb1b) and cytoplasmic poly(A)-binding protein 1l (Pabpc1l), its absence decreases the capacity of the C-terminal region to interact with these partners [20]. Thus, Rbm24 displays biochemical and functional conservation with respect to Rbm38, and its functionality in different cellular processes may be regulated through interaction with specific protein partners.

3. Rbm24 displays restricted expression patterns in developing vertebrate embryos

Another strikingly conserved aspect of vertebrate Rbm24 is the highly restricted developmental expression patterns (Fig. 2). During gastrulation, *Xenopus rbm24*, also called *XSeb4* or *MTG1*, is mainly expressed in the dorso-lateral mesoderm regions flanking the axial midline, which mostly overlap with the expression domains of *MyoD* [13,30]. During organogenesis, analyses by in situ hybridization and immunofluorescence staining indicate that Rbm24 is expressed in the somites, heart, and head sensory organs in different vertebrate embryos, including zebrafish, *Xenopus*, chick and mouse [13,14,16,31-36]. Zebrafish genome contains two *rbm24* paralogs, *rbm24a* and *rbm24b*. The sites of *rbm24a* expression are identical as those of other vertebrate *Rbm24*, whereas *rbm24b* is mainly expressed in the somites and heart, but not in head sensory organs [33,34]. Within each tissue, Rbm24 is generally expressed in a subset of cells undergoing differentiation. The cellular localization of Rbm24 protein in different tissues has been analyzed in more detail during mouse embryonic development [16,36]. Interestingly, Rbm24 displays dynamic subcellular localization during muscle cell development. In the myotome and in C2C12 cells it is first accumulated in the cytoplasm of MyoD-positive myoblasts entering into the differentiation program, but not in Pax3-positive muscle progenitor cells, while in mature myotubes it is mainly present in the nucleus (Fig. 3). A cytoplasmic localization of Rbm24 protein is also detected in different head sensory organs [36]. In the developing lens, it

is restricted to differentiating fiber cells in the posterior and equatorial regions; in the otic vesicle, it co-localizes with Myo7A in inner ear hair cells; in the olfactory epithelium, it is expressed in fate-committed neuronal precursors and terminally differentiated olfactory receptor neurons. Thus, the predominant localization of Rbm24 in the cytoplasmic compartment of different cell types closely correlates with their entry into the process of differentiation. Detailed Rbm24 expression and subcellular localization will be further described in sections addressing its tissue-specific function.

4. Rbm24 regulates muscle cell development through distinct mechanisms

4.1. Rbm24 in skeletal myogenesis

The conserved expression of Rbm24 in the paraxial mesoderm and in the somites of vertebrate embryos suggests that it may play a role in skeletal muscle development. Indeed, *Xenopus rbm24* (*XSeb4*) gene has been shown to be a transcriptional target of MyoD and early B cell factor (EBF) family members of transcription factors, and relays the function of these factors during myogenesis [30,37]. In zebrafish, single knockdown of *rbm24a* and *rbm24b* indicates that they are required for somitogenesis, but *rbm24a* seems to display a predominant activity [34]. It is unclear whether *rbm24a* and *rbm24b* cooperate in skeletal muscle development, and this question needs to be addressed by inhibiting the function of both genes. In chick embryos, knockdown of *Rbm24* in the somites severely alters the expression of muscle-specific myosin, indicating that it is required for myogenic differentiation [16]. In *Rbm24* mutant mice, although no myofiber degeneration can be observed in skeletal muscles, there is a loss of M-bands in sarcomeres, which is accompanied by a reduced inclusion of muscle-specific exons in muscle cells [17]. This finding suggests that Rbm24 may be involved in skeletal muscle development through regulation of muscle-specific alternative splicing. It is consistent with the function of SUP-12, a *Caenorhabditis elegans* homolog of vertebrate Rbm24 that regulates alternative splicing of fibroblast growth factor (EGL-15) pre-mRNA in sex myoblast migration [38,39,40]. Thus, Rbm24 may represent an important conserved regulator of muscle-specific alternative splicing events in skeletal muscles. At present, the transcriptional control of muscle cell

specification and differentiation has been relatively well documented [41,42], but the contribution of post-transcriptional regulation to muscle development remains largely unclear [43]. However, mis-regulation of several RBPs, including CELF, MBNL and FOX families of proteins, disrupts muscle-specific alternative splicing and has been linked to skeletal muscle disease such as myotonic dystrophy [7,43]. Because skeletal muscle is one of the first tissues in which alternative splicing generates abundant contractile proteins from widely expressed genes has been identified [44], these observations provide mechanistic insights into muscle cell differentiation and function.

There are several lines of evidence suggesting that Rbm24 may not only function as a splicing factor, it also regulates skeletal myogenesis through other mechanisms. In vitro studies indicate that Rbm24 promotes myogenic differentiation of C2C12 cells by inducing cell cycle arrest upon binding to target mRNAs encoding cell cycle regulators [45], and by stabilizing *myogenin* mRNA through binding to its 3'-untranslated region [46]. These functionalities are entirely distinct from the regulation of alternative splicing. Thus, Rbm24 may display multiple or dynamic roles during the process of muscle cell development, which is consistent with its differential subcellular localization in myoblasts and multinucleated myotubes. Further in vivo analyses will be necessary to identify Rbm24-mediated stage-specific post-transcriptional mechanisms that trigger muscle lineage specification and differentiation.

4.2. Rbm24 is required for heart development

Loss of Rbm24 severely impairs heart development in zebrafish and mouse embryos [14,17,20,33,47]. Knockdown or knockout of *rbm24a* in zebrafish is sufficient to cause severe cardiogenic defects [14,20,33]. Although *rbm24a* morphants or mutants have a beating heart, blood is only transported back and forth between the ventricle and atrium. This is due to the defective atrioventricular separation, which impairs blood circulation in the whole body [20]. In *Rbm24* homozygous mutant mice, heart malformations, including defective ventricular septum, reduced myocardial compaction, dilated atria and abnormal atrioventricular endocardial cushions, become evident at E10.5, these are followed by growth retardation at subsequent stages and embryonic lethality at E13.5 [17,47]. In addition to regulating early heart

development, Rbm24 also plays a pivotal role in later cardiac sarcomerogenesis. Both in zebrafish and mice, loss of Rbm24 function causes disrupted Z-discs and sarcomere organization due to a decreased expression of sarcomeric proteins, a phenotype reminiscent of cardiomyopathy [14,17,19]. Although no defective alternative splicing is present in *Rbm24* heterozygous mutant mice, which are normal and viable, there is an increased sarcomere slack length and a lower myofilament passive stiffness in cardiomyocytes [48]. This raises a possibility that Rbm24 haploinsufficiency may influence disease penetrance in congenital heart disorders.

RNA-seq analyses have provided important insights on Rbm24-mediated post-transcriptional control of cardiac differentiation. Altered splicing of a large number of differentiation-related muscle genes has been identified in mouse embryos lacking Rbm24 function [17]. A majority of these altered splicing events is also present in zebrafish *rbm24a* mutants [20], suggesting a functional conservation of Rbm24-regulated alternative splicing in heart development. Further study on the consequences of Rbm24 deficiency in post-natal heart development using conditional knockout mice indicates a global disruption of alternative splicing events, which mostly affects those genes coding for sarcomere structure proteins involved in muscle contraction, including in particular *Ttn* [19]. It has been shown that the isoform switch of *Ttn* in cardiomyocytes is dependent on the function of Rbm20 [49], which possesses a single central RRM and regulates a large number of heart genes [50]. Moreover, mutations of both RBM20 and *TTN* genes in humans cause dilated cardiomyopathy [51,52,53]. This raises a possibility that human RBM24 may cooperate with RBM20 to regulate cardiac muscular functionality and may represent a new but rare gene associated with heart diseases [54]. Supporting the cooperation between Rbm24 and Rbm20 in heart development, it has been reported that the two proteins interact biochemically and bind to the same intronic region to promote the splicing of short *Enigma homolog (Enh)* splice variants, which encode LIM-less PDZ-LIM proteins that can prevent the hypertrophic growth of cardiomyocytes [55]. Similarly, in *Caenorhabditis elegans*, SUP-12 and its cofactors regulate muscle-specific alternative splicing through recognition of juxtaposed *cis*-elements on the target RNA to form a ternary complex [39,40,56].

Although defective alternative splicing represents an important event caused by loss of Rbm24 during heart development, other post-transcriptional regulatory processes are also affected. In particular, deficiency of Rbm24 in mice leads to aberrant activation of p53-dependent apoptosis in heart tissues, whereas overexpression of Rbm24 can inhibit p53 protein expression [47]. Mechanistically, *in vitro* studies suggest that Rbm24 prevents eIF4E from binding to p53 mRNA through the eIF4E-binding motif in the absence of phosphorylation at serine 181, thereby interfering with the cap-binding function of eIF4E and repressing p53 expression. In contrast, phosphorylation of this serine residue converts Rbm24 into an activator of p53 expression [47]. These observations suggest that Rbm24 may be involved in regulating p53 activity during heart development in a phosphorylation-dependent manner. Since p53 induces apoptosis in disease- or aging-related failing heart [57], Rbm24 may exert a protective role to reduce the incidence of heart failure. Thus, it would be interesting to examine this possibility and to analyze the regulation of Rbm24 activity by phosphorylation during heart development. Consistent with its implication in regulating post-transcriptional processes downstream of alternative splicing, immunofluorescence staining indicates that Rbm24 protein is abundantly accumulated in the cytoplasm of mouse cardiomyocytes at E11.5 [16]. The distinct roles of Rbm24 during cardiac muscle development imply that it could be involved in various aspects of post-transcriptional regulation. Indeed, RNA immunoprecipitation assay followed by microarray analysis in cardiac myoblast cell lines suggests that Rbm24 binds to, and regulates numerous targets through distinct mechanisms, including mRNA stability, alternative splicing and transcriptional initiation, and mRNA translation [58]. This highlights the importance of Rbm24-organized RNA regulon in coordinating and stabilizing the expression of structural and functional genes in cardiac muscle [59].

4.3. Dynamic subcellular localization and function of Rbm24

Analysis of Rbm24 subcellular localization provides further support on the possibility of its multiple and dynamic functions during muscle cell development. Within the myotome of mouse embryos at E11.5, Rbm24 protein only accumulates in the cytoplasm of MyoD-positive myoblasts engaged in the differentiation program, but not in Pax3-expressing premyogenic

progenitors [16], which represent a proliferating population of muscle stem cells [60]. This implies that Rbm24 functions in the cytoplasmic compartment during the differentiation step of muscle development, but its post-transcriptional regulatory roles remain to be explored. Interestingly, and consistent with its function in regulating alternative splicing of those mRNAs encoding muscle-specific contractile proteins, the localization of Rbm24 protein in myofibers of adult muscles is only restricted to the nucleus. This translocation as a function of cell differentiation state can be also observed in C2C12 cell line expressing Rbm24-GFP. The fusion protein is first expressed in the cytoplasm of mononucleated myoblast cells, and then accumulates in the nucleus of multinucleated myotubes (Fig. 3). These in vivo and in vitro observations suggest that Rbm24 may exert distinct post-transcriptional activities in differentiating myoblasts and terminally differentiated myofibers. Thus, there is a possibility that its regulatory roles on muscle cell differentiation and muscular functionality may be cell-type specific and may depend on its subcellular localization and the presence or absence of its co-factors.

It is likely that the cytoplasmic localization of Rbm24 in myoblasts functions to regulate the stability and/or translation of mRNAs encoding muscle differentiation-promoting factors required for early differentiation steps, such as myogenin [46], thereby switching them into the differentiation program. As cells become further differentiated during later steps of myofibrillogenesis, Rbm24 accumulates in the nucleus to promote the expression of muscle structural and contractile proteins through alternative splicing. Consistent with its role in regulating the transition from embryonic cell pluripotency to differentiation, overexpression of Rbm24 is able to induce the specification and trigger the differentiation of mouse embryonic stem cells into cardiomyocytes [61]. Thus, the dynamic subcellular localization of Rbm24 argues that it may regulate multiple steps of myogenic differentiation through distinct post-transcriptional mechanisms. However, the shift of Rbm24 protein from cytoplasm to nucleus during muscle differentiation raises an important question as to how it is shuttling between these subcellular compartments. Whether this depends on the presence or absence of a signal/co-factor that also displays dynamic changes during muscle cell maturation? Interestingly, a similar

cytoplasm to nucleus translocation has been observed for MBNL in post-natal skeletal muscle [62], but its cytoplasmic function during early development is not clear [7]. Therefore, the significance of the dynamic characteristic of RBP subcellular localization during muscle development is intriguing and merits further investigation.

5. Rbm24 in head sensory organ development

5.1. Rbm24 regulates lens fiber cell differentiation

Although much attention has been focused on Rbm24 function in cardiac and skeletal muscle cell differentiation, several recent works have revealed an interesting expression profile and an important role of this protein during the development of vertebrate head sensory organs [20,35,36,63,64]. In particular, it has been shown that Rbm24 is required for lens fiber cell terminal differentiation in zebrafish and in mice, providing evidence for an important regulatory role mediated by RBPs in vertebrate lens development. Indeed, several RBPs have been shown to be required for eye development in humans or animal models [65]. For example, mutations of the Tudor domain RBP TDRD7 in humans cause cataract formation [66], illustrating a critical implication of post-transcriptional events in lens morphogenesis.

Lens transparency is established by abundant accumulation of crystallin proteins and denucleation in lens fiber cells [67]. Loss of Rbm24a function in zebrafish directly prevents the efficient translation of *crystallin* mRNAs into functional proteins, and indirectly affects lens fiber cell denucleation due to impaired blood circulation [20]. As a consequence, *rbm24a* mutant embryos develop a severe cataract phenotype (Fig. 4A, B). Detailed examination of Rbm24 protein expression in mouse embryos indicates that it not only shows specific expression in differentiating lens fiber cells, but it is also accumulated in the cytoplasm of these cells [36]. During zebrafish development, the expression of *rbm24a* in the lens placode can be detected around 17 hpf (hours post-fertilization), several hours before the initiation of primary fiber cell differentiation. At early stages of lens development, Rbm24a may participate in the post-transcriptional regulation of several genes involved in the specification of the lens placode, such as *Pax6* and *Sox2*. Consistently, Rbm24a deficiency results in decreased stability of *Sox2*

mRNA [64]. As lens fiber cell differentiation proceeds, *rbm24a* exhibits highly localized expression patterns [20]. After 24 hpf, it is progressively restricted to the posterior and equatorial regions of the lens mass, where differentiation of primary fiber cells and initial formation of secondary fiber cells take place [68]. This dynamic characteristic of *rbm24a* expression in lens fiber cells makes it a strong candidate in regulating lens fiber cell terminal differentiation. Indeed, the localization of Rbm24a protein in the cytoplasm of differentiating lens fiber cells before and after nuclear degradation suggests that it should regulate post-transcriptional events other than alternative splicing.

Importantly, The RRM of Rbm24a binds to a wide spectrum of lens-specific mRNAs that encode either small heat shock proteins or lens structural proteins, and the C-terminal region interacts with members of the cytoplasmic polyadenylation element-binding protein (CPEB) and cytoplasmic poly(A)-binding protein (PABPC) families [20]. CPEB and PABPC are key components of the CPA complex that regulates poly(A) tail elongation of nuclear exported mRNAs [69,70,71]. They are required for translational activation in a variety of processes, including oogenesis and early embryonic development [72,73]. Loss of Rbm24a specifically reduces the poly(A) tail length of many *crystallin* mRNAs, which severely prevents the accumulation of lens transparent proteins and causes cataract formation [20]. The demonstration that Rbm24a may function in the CPA complex is significant in understanding the regulatory mechanism underlying mRNA translational activation to switch and maintain lens fiber cell differentiation. Indeed, when transcriptional contribution declines during denucleation of differentiating lens fiber cells, a post-transcriptional mechanism that promotes the efficient translation of lens-specific mRNAs will be necessary for the production of high amounts of transparent proteins. Zebrafish and mouse Rbm24 is expressed at the right time and place to play a critical role in this process, suggesting that similar post-transcriptional mechanisms control lens development in vertebrates. The importance of post-transcriptional regulation after lens fiber cell denucleation has been also demonstrated for other aspects of lens morphogenesis. Analysis of Tdrd7 function in mice indicates that it is required for maintaining cytoskeletal organization and lens fiber cell morphology by regulating the expression of heat

shock protein HSPB1 [74]. Moreover, members of the PABPC family are ancient paralogs of Rbm24, and they are coexpressed in different tissues. For example, zebrafish *Pabpc4* also displays strongly localized expression in the somites and lens primordium during early development [75]. This correlative evidence further supports a potential interaction between these RBPs in regulating CPA during lens differentiation. Nevertheless, it remains to be determined how Rbm24 functions precisely within the CPA complex to control mRNA translation in lens fiber cells, and whether it regulates cell differentiation in other tissues through the same mechanism.

5.2. Rbm24 and Rbm38 in retinal differentiation

Immunofluorescence staining indicates that mouse Rbm24 protein is expressed in the optic vesicle at E9.5 to E11.5 [64], but not at more late stages [36,64]. Although both zebrafish and mouse *Rbm24* mutants display microphthalmia phenotype [20,63,64], this seems to be indirectly caused by the absence of blood supply because rescue of blood circulation in the mutants prevents microphthalmia but not cataract formation [20]. Thus, it is at present still unclear whether Rbm24 plays a role in retinal development. Nevertheless, XSeb4R (Rbm38) has been shown to regulate retinal neuronal differentiation during *Xenopus* development. It is expressed in retinoblasts and undifferentiated post-mitotic neurons. Gain-of-function of XSeb4R promotes neural differentiation, whereas loss of function causes an increased number of glial cells [25]. The post-transcriptional mechanism in retinogenesis mediated by XSeb4R is not clear. However, given the biochemical and functional conservation between Rbm24 and Rbm38, there is a possibility that it may bind to, and stabilize *Sox2* mRNA in the gene regulatory network of the optic vesicle [64].

5.3. Rbm24 is required for inner ear hair cell development

The strongly restricted expression of vertebrate Rbm24 in the inner ear also makes it a potential post-transcriptional regulator of hair cell differentiation and regeneration. In the cristae of the neonatal mouse vestibular system, *in situ* hybridization analysis shows that the expression of *Rbm24* gene in a subset of hair cells is directly regulated by the transcription factor *Atoh1* [35]. In the embryos at E14.5, Rbm24 protein co-localizes with *Myo7A* in mechanosensory cells of

the auditory and vestibular systems [36]. These expression patterns suggest that Rbm24 may function downstream of hair cell fate specification, and may participate in hair cell differentiation or function. Nevertheless, it is at present still unclear whether and how Rbm24 regulates hair cell development in mammalian embryos, and generally, post-transcriptional regulatory mechanisms underlying hair cell development and homeostasis remain largely elusive, mostly due to the lack of functional studies on related gene regulatory networks.

Zebrafish has become particularly attractive for understanding otic development and human diseases affecting hearing function [76,77]. Although the precise localization of zebrafish *rbm24a* expression in inner ear hair cells has not been analyzed in detail, single cell RNA-seq analysis indicates that it dynamically changes from non-cycling progenitors to differentiated hair cells, suggesting that Rbm24a may participate in the differentiation program [78]. A recent study has established a functional requirement of Rbm24a for hair cell development [79]. Rbm24a deficiency does not affect the specification of the otic vesicle, however, it prevents the differentiation of hair cells in the anterior, lateral and posterior cristae corresponding to the sensory patches for each of the three semicircular canals. This is associated with a disorganization of hair cells and a reduced height of their kinocilia that are involved in the morphogenesis of the hair bundle and in mechanotransduction (Fig. 4C, D). Loss of Rbm24a also impairs the formation of hair cells in the neuromasts of the posterior lateral line system. RNA-seq and qRT-PCR analyses reveal a reduced expression level of several zebrafish orthologs of human deafness genes, such as *smpx*, *gsdmeb* and *otofa* in *rbm24a* mutants [79]. Mutations of these genes in humans have been associated with X-linked deafness-4, autosomal dominant nonsyndromic deafness 5 and sensorineural hearing loss, and autosomal recessive nonsyndromic deafness 9, respectively. Inhibiting their function in zebrafish produces similar defects in the developing ear as observed in *rbm24a* mutants [80,81]. Consistently, loss of Rbm24a causes hearing and balancing deficits, demonstrating its functional requirement for hair cell differentiation and/or function [79]. Since no defective alternative splicing of these genes has been detected by RNA-seq analysis in *rbm24a* mutants [20], how Rbm24 regulates their expression remains unclear. Further study on the regulatory hierarchy implicating Rbm24 in the

development of inner ear sensory receptors will help to understand the post-transcriptional mechanism operating in this lineage.

5.4. Rbm24 and differentiation of olfactory sensory neurons

The functional implication of Rbm24 in the differentiation of sensory neurons within the olfactory epithelium has not been investigated to date. Immunofluorescence staining of mouse embryonic sections indicates that Rbm24 expression is restricted to differentiating neurons [36]. At E10.5 and E11.5, it mainly accumulates in the cytoplasm of fate-committed immediate neuronal precursors (INPs) and terminally differentiated olfactory receptor neurons (ORNs) within the nasal pit, suggesting that it may promote neurogenic differentiation by regulating the translation of target mRNAs. At more late stage (E14.5), Rbm24 protein is strongly expressed in basal neural stem cells and weakly expressed in differentiating olfactory neurons. These observations raise the possibility for a role of Rbm24 in maintaining the progenitor population and/or switching their progression toward more committed olfactory neuronal cells. During olfactory epithelium development, it is well established that transcriptional and epigenetic controls of spatiotemporal gene expression determine the formation of olfactory sensory neurons and non-neuronal cell types [82]. However, there is also evidence that mRNAs encoding olfactory receptors in neural lineages are protected from degradation, suggesting a requirement of RBPs-mediated post-transcriptional regulatory mechanisms in their stabilization [83]. Thus, it is worth to analyze whether and how neuronal differentiation in the olfactory epithelium is affected following loss of Rbm24 function, in order to elucidate the molecular and cellular mechanisms underlying neurogenesis of the olfactory system.

6. Rbm24 in embryonic germ layer formation

In *Xenopus* and zebrafish, *XSeb4* and *rbm24a* are expressed as maternal transcripts [13,14]. However, their spatial localizations within the cleavage stage embryos and their maternal functions are not clear and await further investigation. Knockdown of *XSeb4* by injecting translation-blocking morpholino oligonucleotide into fertilized *Xenopus* eggs has been shown to inhibit the expression of mesoderm genes at the early gastrula stage, such as the pan-

mesoderm marker *brachyury* [30]. Nevertheless, it is unclear whether this represents a direct effect or an indirect consequence due to disruption of more upstream events, such as maternal regulators of *brachyury* gene. Interestingly, several studies have focused on the maternal function of XSeb4R (Rbm38). It has been shown that XSeb4R regulates germ layer formation by binding to the vegetally-localized maternal *VegT* mRNA and positively regulating its stability and translation [84]. Since *VegT* is a key T-box transcription factor required for inductive interaction and germ layer specification [85], the regulation of its expression by Rbm24-related proteins may be important for the initial formation of endoderm and mesoderm tissues. Maternal *XSeb4R* transcripts are also enriched in the ectoderm, where the translated protein binds to, and promotes the translation of maternal *Sox3* mRNA [86]. The importance of maternal XSeb4R functions in promoting germ layer-specific translational activation of maternally stored mRNAs demonstrates a major contribution of post-transcriptional regulation in setting up maternal inputs to trigger zygotic developmental program. On the other hand, the spatiotemporal activation and function of zygotic genes also depends on RBPs-mediated clearance of maternal mRNAs [87]. Therefore, whether Rbm24-related proteins may be also implicated in this process merits an investigation.

It is well established that maternal RBPs are critical mediators of translational regulation in the early embryos [88]. Before meiotic maturation, the translation of many maternal mRNAs is repressed partly due to the lack of an appropriate length of poly(A) tails [88,89]. Upon fertilization and during cell-cycle progression, CPA mediated by members of the CPEB and PABPC families plays a critical role in the stabilization and translational activation of oocyte-stored mRNAs by elongating their poly(A) tails [88,89,90]. Inhibition of CPA prevents transcription of zygotic genes and results in failure of maternal to zygotic transition and delay of developmental progression [91]. Since Rbm24 interacts with *Cpeb1b*, *Pabpc1l* and eIF4E [20,47], which are conserved mRNA interactors required for the translational activation of maternal mRNAs [88], it is potentially involved in the regulation of CPA. Thus, it would be of interest to examine whether maternal Rbm24 regulates the dynamics of CPA for differentially activating or repressing the translation of germ layer-specific maternal mRNAs coding for

important mediators of inductive interaction. It is equally important to understand how the spatiotemporal activity of Rbm24 is regulated by other factors in this process.

7. Potential implication of Rbm24 in disease

7.1. A possible tumor suppressor activity of Rbm24 and Rbm38

RBPs regulate gene expression at multiple levels, and they are implicated in a large variety of biological processes through versatile interactions with RNAs. Alterations in protein-RNA interactions have been causally related to the occurrence of various cancers in humans [9]. Since Rbm24 protein contains a canonical RRM that binds to GU-rich ligand present in a wide spectrum of target mRNAs [21,24], it would be not surprising that inappropriate regulation of its expression or function in humans perturbs the homeostasis of protein synthesis and leads to cancer development. There are several lines of evidence that Rbm24 displays a tumor repressive activity. In several cancer cell lines, such as MCF7 and HaCaT cells, both Rbm24 and Rbm38 are transcriptional targets of the tumor suppressor p53, and their overexpression increases the stability of p21 mRNA [92,93]. Thus, they can function to induce cell cycle arrest and to prevent tumor cell proliferation. However, this p53-induced anti-tumor activity of Rbm24 and Rbm38 needs to be reconciled with their oncogenic potential, which is related to their repressive function on p53 mRNA translation and p53-dependent apoptosis [26,47]. Since serine phosphorylation in the eIF4E-binding motif of Rbm24 and Rbm38 converts them into an activator of p53 expression [28], it will be intriguing to compare their phosphorylation status between normal and tumor cells, in order to understand how they regulate mRNA translation in pathological processes. Another enigma is the significance of Rbm24 and Rbm38 in preventing p63-mediated tumor suppression because they have been shown to destabilize p63 mRNA in overexpression experiments [94,95]. Again, this may be modulated by serine phosphorylation. An increase in the level of phosphorylated Rbm38 by GSK3 β enhances p63 expression, but this seems to be dependent on its dissociation with the Ago2-miR203 mRNA decay complex, instead of eIF4E [96]. Thus, the functionality of Rbm24 and Rbm38 in tumorigenesis seems to be regulated by the activity of their associated kinases.

In other situations, the tumor suppressor activity of Rbm24 does not seem to be dependent on its phosphorylation. A recent study indicates that in prostate cancer, the microRNA miR-106a-5p promotes cell proliferation by inhibiting Rbm24 expression, and overexpression of wild-type Rbm24 is able to inhibit tumorigenesis [97]. It has been also shown that in nasopharyngeal carcinoma, the expression of Rbm24 is reduced, which leads to the down-regulation of miR-25 that has the ability to suppress cell proliferation by targeting the pro-oncogenic lncRNA MALAT1. Increasing the expression of Rbm24 can suppress cellular proliferation, migration and invasion [98]. These observations thus demonstrate an inhibitory effect of Rbm24 in tumorigenesis. A further understanding of the functional consequences of Rbm24 and Rbm38 in regulating cancer-related gene expression should help to define novel therapeutic strategies for modulation of their activity. Moreover, deciphering the detailed mode of RNA-binding by the conserved RRM of Rbm24 and Rbm38 could provide a basis to generate engineered mutants to modulate their interactions with RNA targets [99,100]. It is also important to understand how the expression and activity of Rbm24 or Rbm38 are dysregulated in cancer cells. In this regard, it has been shown that in hepatocellular carcinoma, the expression of *Rbm24* and several cancer-related genes is reactivated due to increased demethylation of their enhancers [101], suggesting that epigenetic modulation of Rbm24 expression in tumor cells may have the potential to prevent aberrant cell proliferation.

7.2. Interaction between Rbm24 and microRNAs to maintain cellular homeostasis

It has become increasingly evident that the interplay between RBPs and microRNAs represents a new level of complexity in the regulation of gene expression in various cellular processes, which either promotes or represses cancer development [102]. As in prostate cancer and nasopharyngeal carcinoma, Rbm24 also interacts with microRNAs in other tissues to maintain cellular homeostasis. The MIR143 host gene (MIR143HG) is a precursor of miR-143 and miR-145, and is overexpressed in colon tissues of patients with Hirschsprung disease (HSCR). Rbm24 forms a negative feedback loop with MIR143HG, and regulates its expression and stability. Thus, an alteration of this balance could lead to defective proliferation or migration of enteric neural crest cells and gangliogenesis in the gut of HSCR patients [103]. Interestingly, the

expression of miR-125b-5p is enriched in heart valves. It binds to, and inhibits the expression of, *Rbm24* mRNA [104]. Since loss of *Rbm24* leads to heart valve defects, this raises a possibility that an imbalance between miR-125b-5p and *Rbm24* may disrupt heart development and function. Similarly, miR-222 prevents myogenic differentiation and myoblast fusion. It exerts these effects partially by inhibiting *Rbm24* expression [105]. These observations suggest that *Rbm24* may function downstream of microRNAs in post-transcriptional regulatory interactions with potential contributions to muscle physiopathology.

7.3. *Rbm24* in congenital disorders and infection diseases

A more plausible implication of *Rbm24* in human disease is its ability to promote U1 snRNP recognition of the mutated, but not the wild-type 5' splicing site in *IKBKAP* gene (*inhibitor of κ light polypeptide gene enhancer in B cells, kinase complex-associated protein*) in familial dysautonomia (FD), an autosomal recessive disease [106]. The intronic 5' splicing site mutation of *IKBKAP* gene in FD disrupts the splicing of exon 20, but this produces altered spliced mRNA product only in a tissue-specific manner, affecting essentially sensory and autonomic nervous system [107]. *Rbm24* binds to an element downstream of the mutated splicing site and functions as splicing enhancer [106]. Thus, its tissue-specific expression may help to correct the abnormal splicing and to reduce the penetrance of genetic disorders, making it a potential therapeutic target for FD. This observation highlights the importance of regulated *Rbm24* activity in maintaining cellular function and homeostasis. Indeed, as presented above, loss of *Rbm24* in mice causes cardiomyopathy [14,17,19], but overexpression of *Rbm24* has been shown to induce cardiac fibrosis in mouse model by promoting collagen synthesis [108]. Moreover, *Rbm24* not only regulates the expression of organism's own genes, several in vitro analyses suggest that it can also function as a host factor to participate in the translation, replication and pregenomic RNA packaging of types B and C of hepatitis viruses [109,110,111]. Thus, we are just beginning to perceive the involvement of *Rbm24*-mediated post-transcriptional events in the etiology of various cellular dysfunctions. It is clear that the increasing association of *Rbm24* with various human diseases requires a more comprehensive mechanistic understanding of its post-transcriptional regulatory functions.

8. Conclusions and perspectives

Rbm24 emerges as a major post-transcriptional regulator in the switch of cell differentiation during vertebrate development. It represents a multifunctional RBP that orchestrates different gene expression circuits in a tissue-specific and stage-specific manner. There is also accumulating evidence that it maintains the homeostasis of protein synthesis in adult tissues. Thus, it is not surprising that dysfunction of Rbm24-mediated post-transcriptional regulation of gene expression affects early development and leads to the occurrence of various diseases. Many intriguing questions regarding Rbm24 function during development and disease remain unanswered, such as its maternal activity in translational regulation, the mechanism underlying its dynamic subcellular localization and function during muscle cell differentiation, the biochemical mechanism underlying its implication in CPA, and its association with human diseases. At present, no human congenital disorders have been directly linked to Rbm24 mutations, probably due to the lethality resulted from impaired heart development and blood circulation. In this regard, it would be also of interest to identify and understand the function of those *cis*- and *trans*-regulatory elements that control the spatiotemporal expression of Rbm24, which may be disrupted in human diseases. In addition, due to the importance of RBP auto-regulation to maintain protein homeostasis or to switch cell fate changes [112], it would be important to understand how Rbm24 self-regulates to maintain cellular homeostasis or to initiate cell differentiation during development. Furthermore, vertebrate Rbm24 also interacts and cooperates with other closely related RBPs, such as Rbm20 and Rbm38, in the regulation of cell differentiation and function [45,55]. Mutations of RBM20 have been clearly associated with human congenital disorders, such as cardiomyopathy [51,53], while inappropriate expression of RBM38 is associated with tumorigenesis [26]. Thus, understanding the mechanisms by which Rbm24 cooperates with other factors in gene expression regulation should help to develop approaches for therapeutic manipulation.

Author contributions

R.G., M.S., and D.L.S. designed research and analyzed data; R.G., M.S., and A.S. performed research; R.G. and D.L.S. wrote the paper.

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Conflicts of interest

The authors declare no conflict of interest.

References

1. Glisovic, T., Bachorik, J.L., Yong, J., and Dreyfuss, G. RNA-binding proteins and post-transcriptional gene regulation. *FEBS Lett.* **2008**, *582*, 1977-1986. doi: 10.1016/j.febslet.2008.03.004.
2. Vogel, C., and Marcotte, E.M. Insights into the regulation of protein abundance from proteomic and transcriptomic analyses. *Nat. Rev. Genet.* **2012**, *13*, 227-232. doi: 10.1038/nrg3185.
3. Liu, Y., Beyer, A., and Aebersold, R. On the dependency of cellular protein levels on mRNA abundance. *Cell* **2016**, *165*, 535-550. doi: 10.1016/j.cell.2016.03.014.
4. Morris, A.R., Mukherjee, N., and Keene, J.D. Systematic analysis of posttranscriptional gene expression. *Wiley Interdiscip. Rev. Syst. Biol. Med.* **2010**, *2*, 162-180. doi: 10.1002/wsbm.54.
5. Lukong, K.E., Chang, K.W., Khandjian, E.W., and Richard, S. RNA-binding proteins in human genetic disease. *Trends Genet.* **2008**, *24*, 416-425. doi: 10.1016/j.tig.2008.05.004.
6. Castello, A., Fischer, B., Hentze, M.W., and Preiss, T. RNA-binding proteins in Mendelian disease. *Trends Genet.* **2013**, *29*, 318-327. doi: 10.1016/j.tig.2013.01.004.
7. Brinegar, A.E., and Cooper, T.A. Roles for RNA-binding proteins in development and disease. *Brain Res.* **2016**, *1647*, 1-8. doi: 10.1016/j.brainres.2016.02.050.
8. Conlon, E.G., and Manley, J.L. RNA-binding proteins in neurodegeneration: mechanisms in aggregate. *Genes Dev.* **2017**, *31*, 1509-1528. doi: 10.1101/gad.304055.117.
9. Pereira, B., Billaud, M., and Almeida, R. RNA-binding proteins in cancer: old players and new actors. *Trends Cancer* **2017**, *3*, 506-528. doi: 10.1016/j.trecan.2017.05.003.
10. Hong, S. RNA binding protein as an emerging therapeutic target for cancer prevention and treatment. *J. Cancer Prev.* **2017**, *22*, 203-210. <https://doi.org/10.15430/JCP.2017.22.4.203>.
11. Shotwell, C.R., Cleary, J.D., and Berglund, J.A. The potential of engineered eukaryotic RNA-binding proteins as molecular tools and therapeutics. *Wiley Interdiscip. Rev. RNA* **2020**, *11*, 1573. doi: 10.1002/wrna.1573.
12. Schultz, C.W., Preet, R., Dhir, T., Dixon, D.A., and Brody, J.R. Understanding and targeting the disease-related RNA binding protein human antigen R (HuR). *Wiley Interdiscip. Rev. RNA* **2020**, *23*, e1581. doi: 10.1002/wrna.1581.
13. Fetka, I., Radeghieri, A., and Bouwmeester, T. Expression of the RNA recognition motif-containing protein SEB-4 during *Xenopus* embryonic development. *Mech. Dev.* **2000**, *94*, 283-286. doi: 10.1016/S0925-4773(00)00284-7.
14. Poon, K.L., Tan, K.T., Wei, Y.Y., Ng, C.P., Colman, A., Korzh, V., and Xu, X.Q. RNA-binding protein RBM24 is required for sarcomere assembly and heart contractility. *Cardiovasc. Res.* **2012**, *94*, 418-427. doi: 10.1093/cvr/cvs095.
15. Sun, W., Hu, Y., Xu, H., He, H., Han, C., Liu, H., Wang, J., and Li, L. Characterization of the duck (*Anas platyrhynchos*) Rbm24 and Rbm38 genes and their expression profiles in myoblast and skeletal muscle tissues. *Comp. Biochem. Physiol. B Biochem. Mol. Biol.* **2016**, *198*, 27-36. doi: 10.1016/j.cbpb.2016.03.008.
16. Grifone, R., Xie, X., Bourgeois, A., Saquet, A., Duprez, D., and Shi, D.L. The RNA-binding protein Rbm24 is transiently expressed in myoblasts and is required for myogenic differentiation during vertebrate development. *Mech. Dev.* **2014**, *134*, 1-15. doi: 10.1016/j.mod.2014.08.003.

17. Yang, J., Hung, L.H., Licht, T., Kostin, S., Looso, M., Khrameeva, E., Bindereif, A., Schneider, A., and Braun, T. (2014) RBM24 is a major regulator of muscle-specific alternative splicing. *Dev. Cell* **2014**, *31*, 87-99. doi: 10.1016/j.devcel.2014.08.025.
18. Weeland, C.J., van den Hoogenhof, M.M., Beqqali, A., and Creemers, E.E. Insights into alternative splicing of sarcomeric genes in the heart. *J. Mol. Cell. Cardiol.* **2015**, *81*, 107-113. doi: 10.1016/j.yjmcc.2015.02.008.
19. Liu, J., Kong, X., Zhang, M., Yang, X., and Xu, X. RNA binding protein 24 deletion disrupts global alternative splicing and causes dilated cardiomyopathy. *Protein Cell* **2019**, *10*, 405-416. doi: 10.1007/s13238-018-0578-8.
20. Shao, M., Lu, T., Zhang, C., Zhang, Y.Z., Kong, S.H., and Shi, D.L. Rbm24 controls poly(A) tail length and translation efficiency of *crystallin* mRNAs in the lens via cytoplasmic polyadenylation. *Proc. Natl. Acad. Sci. U. S. A.* **2020**, *117*, 7245-7254. doi: 10.1073/pnas.1917922117.
21. Ray, D., Kazan, H., Cook, K.B., Weirauch, M.T., Najafabadi, H.S., Li, X., Gueroussov, S., Albu, M., Zheng, H., Yang, A., et al. Rapid and systematic analysis of the RNA recognition specificities of RNA-binding proteins. *Nat. Biotechnol.* **2009**, *27*, 667-670. doi: 10.1038/nbt.1550.
22. Lucchesi, C., Zhang, J., and Chen, X. (2016) Modulation of the p53 family network by RNA-binding proteins. *Transl. Cancer Res.* **2016**, *5*, 676-684. doi: 10.21037/tcr.2016.08.30.
23. Afroz, T., Cienikova, Z., Cléry, A., and Allain, F.H.T. One, two, three, four! How multiple RRM s read the genome sequence. *Methods Enzymol.* **2015**, *558*, 235-278. doi: 10.1016/bs.mie.2015.01.015.
24. Qian, K., Li, M., Wang, J., Zhang, M., and Wang, M. Structural basis for mRNA recognition by human RBM38. *Biochem. J.* **2020**, *477*, 161-172. doi: 10.1042/BCJ20190652.
25. Boy, S., Souopgui, J., Amato, M.A., Wegnez, M., Pieler, T., and Perron, M. XSEB4R, a novel RNA-binding protein involved in retinal cell differentiation downstream of bHLH proneural genes. *Development* **2004**, *131*, 851-862. doi: 10.1242/dev.00983.
26. Zhang, J., Cho, S.J., Shu, L., Yan, W., Guerrero, T., Kent, M., Skorupski, K., Chen, H., and Chen, X. Translational repression of p53 by RNPC1, a p53 target overexpressed in lymphomas. *Genes Dev.* **2011**, *25*, 1528-1543. doi: 10.1101/gad.2069311.
27. Lucchesi, C.A., Zhang, J., Ma, B., Chen, M., and Chen, X. Disruption of the Rbm38-eIF4E complex with a synthetic peptide Pep8 increases p53 expression. *Cancer Res.* **2019**, *79*, 807-818. doi: 10.1158/0008-5472.CAN-18-2209.
28. Zhang, M., Zhang, J., Chen, X., Cho, S.J., and Chen, X. Glycogen synthase kinase 3 promotes p53 mRNA translation via phosphorylation of RNPC1. *Genes Dev.* **2013**, *27*, 2246-2258. doi: 10.1101/gad.221739.113.
29. Liu, J., Kong, X., Lee, Y.M., Zhang, M.K., Guo, L.Y., Lin, Y., Lim, T.K., Lin, Q., and Xu, X.Q. Stk38 modulates Rbm24 protein stability to regulate sarcomere assembly in cardiomyocytes. *Sci. Rep.* **2017**, *7*, 44870. doi: 10.1038/srep44870.
30. Li, H.Y., Bourdelas, A., Carron, C., and Shi, D.L. The RNA-binding protein Seb4/RBM24 is a direct target of MyoD and is required for myogenesis during *Xenopus* early development. *Mech. Dev.* **2010**, *127*, 281-291. doi: 10.1016/j.mod.2010.03.002.
31. Miller, R.A., Christoforou, N., Pevsner, J., McCallion, A.S., and Gearhart, J.D. Efficient array-based

- identification of novel cardiac genes through differentiation of mouse ESCs. *PLoS One* **2008**, *3*, e2176. doi: 10.1371/journal.pone.0002176.
32. Xu, X.Q., Soo, S.Y., Sun, W., and Zweigerdt, R. (2009) Global expression profile of highly enriched cardiomyocytes derived from human embryonic stem cells. *Stem Cells* **2009**, *27*, 2163-2174. doi: 10.1002/stem.166.
 33. Maragh, S., Miller, R.A., Bessling, S.L., McGaughey, D.M., Wessels, M.W., de Graaf, B., Stone, E.A., Bertoli-Avella, A.M., Gearhart, J.D., Fisher, S., et al. Identification of RNA binding motif proteins essential for cardiovascular development. *BMC Dev. Biol.* **2011**, *11*, 62. doi: 10.1186/1471-213X-11-62.
 34. Maragh, S., Miller, R.A., Bessling, S.L., Wang, G., Hook, P.W., and McCallion, A.S. Rbm24a and Rbm24b are required for normal somitogenesis. *PloS One* **2014**, *9*, e105640. doi: 10.1371/journal.pone.0105460.
 35. Cai, T., Jen, H.I., Kang, H., Klisch, T.J., Zoghbi, H.Y., and Groves, A.K. Characterization of the transcriptome of nascent hair cells and identification of direct targets of the Atoh1 transcription factor. *J. Neurosci.* **2015**, *35*, 5870-5883. doi: 10.1523/JNEUROSCI.5083-14.2015.
 36. Grifone, R., Saquet, A., Xu, Z.G., and Shi, D.L. Expression patterns of Rbm24 in lens, nasal epithelium, and inner ear during mouse embryonic development. *Dev. Dyn.* **2018**, *247*, 1160-1169. doi: 10.1002/dvdy.24666.
 37. Green, Y.S., and Vetter, M.L. EBF proteins participate in transcriptional regulation of *Xenopus* muscle development. *Dev. Biol.* **2011**, *358*, 240-250. doi: 10.1016/j.ydbio.2011.07.034.
 38. Anyanful, A., Ono, K., Johnsen, R.C., Ly, H., Jensen, V., Baillie, D.L., and Ono, S. The RNA-binding protein SUP-12 controls muscle-specific splicing of the ADF/cofilin pre-mRNA in *C. elegans*. *J. Cell Biol.* **2004**, *167*, 639-647. doi: 10.1083/jcb.200407085.
 39. Kuroyanagi, H., Ohno, G., Mitani, S., and Hagiwara, M. The Fox-1 family and SUP-12 coordinately regulate tissue-specific alternative splicing in vivo. *Mol. Cell. Biol.* **2007**, *27*, 8612-8621. doi: 10.1128/MCB.01508-07.
 40. Ohno, G., Ono, K., Togo, M., Watanabe, Y., Ono, S., Hagiwara, M., and Kuroyanagi, H. Muscle-specific splicing factors ASD-2 and SUP-12 cooperatively switch alternative pre-mRNA processing patterns of the ADF/cofilin gene in *Caenorhabditis elegans*. *PLoS Genet.* **2012**, *8*, e1002991. doi: 10.1371/journal.pgen.1002991.
 41. Buckingham, M. Myogenic progenitor cells and skeletal myogenesis in vertebrates. *Curr. Opin. Genet. Dev.* **2006**, *16*, 525-532. doi: 10.1016/j.gde.2006.08.008.
 42. Zammit, P.S. Function of the myogenic regulatory factors Myf5, MyoD, Myogenin and MRF4 in skeletal muscle, satellite cells and regenerative myogenesis. *Semin. Cell Dev. Biol.* **2017**, *72*, 19-32. doi: 10.1016/j.semcd.2017.11.011.
 43. Nikonova, E., Kao, S.Y., Ravichandran, K., Wittner, A., and Spletter, M.L. Conserved functions of RNA-binding proteins in muscle. *Int. J. Biochem. Cell Biol.* **2019**, *110*, 29-49. doi: 10.1016/j.biocel.2019.02.008.
 44. Llorian, M., and Smith, C.W. Decoding muscle alternative splicing. *Curr. Opin. Genet. Dev.* **2011**, *21*, 380-387. doi: 10.1016/j.gde.2011.03.006.

45. Miyamoto, S., Hidaka, K., Jin, D., and Morisaki, T. RNA-binding proteins Rbm38 and Rbm24 regulate myogenic differentiation via p21-dependent and -independent regulatory pathways. *Genes Cells* **2009**, *14*, 1241-1252. doi: 10.1016/j.biocel.2017.11.002.
46. Jin, D., Hidaka, K., Shirai, M., and Morisaki, T. RNA-binding motif protein 24 regulates myogenin expression and promotes myogenic differentiation. *Genes Cells* **2010**, *15*, 1158-1167. doi: 10.1111/j.1365-2443.2010.01446.x.
47. Zhang, M., Zhang, Y., Xu, E., Mohibi, S., de Anda, D.M., Jiang, Y., Zhang, J., and Chen, X. Rbm24, a target of p53, is necessary for proper expression of p53 and heart development. *Cell Death Differ.* **2018**, *25*, 1118-1130. doi: 10.1038/s41418-017-0029-8.
48. de Groot, N.E., van den Hoogenhof, M.M.G., Najafi, A., van der Made, I., van der Velden, J., Beqqali, A., Pinto, Y.M., and Creemers, E.E. Heterozygous loss of Rbm24 in the adult mouse heart increases sarcomere slack length but does not affect function. *Sci. Rep.* 2020, *10*, 7687. doi: 10.1038/s41598-020-64667-0.
49. Guo, W., Schafer, S., Greaser, M.L., Radke, M.H., Liss, M., Govindarajan, T., Maatz, H., Schulz, H., Li, S., Parrish, A.M., et al. RBM20, a gene for hereditary cardiomyopathy, regulates titin splicing. *Nat. Med.* **2012**, *18*, 766-773. doi: 10.1038/nm.2693.
50. Fochi, S., Lorenzi, P., Galasso, M., Stefani, C., Trabetti, E., Zipeto, D., and Romanelli, M.G. The emerging role of the RBM20 and PTBP1 ribonucleoproteins in heart development and cardiovascular diseases. *Genes (Basel)* **2020**, *11*, 402. doi: 10.3390/genes11040402.
51. Brauch, K.M., Karst, M.L., Herron, K.J., de Andrade, M., Pellikka, P.A., Rodeheffer, R.J., Michels, V.V., and Olson, T.M. Mutations in ribonucleic acid binding protein gene cause familial dilated cardiomyopathy. *J. Am. Coll. Cardiol.* **2009**, *54*, 930-941. doi: 10.1016/j.jacc.2009.05.038.
52. Ware, J.S., and Cook, S.A. Role of titin in cardiomyopathy: from DNA variants to patient stratification. *Nat. Rev. Cardiol.* **2018**, *15*, 241-252. doi: 10.1038/nrcardio.2017.190.
53. Hey, T.M., Rasmussen, T.B., Madsen, T., Aagaard, M.M., Harb, M., Molgaard, H., Moller, J.E., Eiskaer, H., and Mogensen, J. Pathogenic RBM20-variants are associated with a severe disease expression in male patients with dilated cardiomyopathy. *Circ. Heart Fail.* **2019**, *12*, e005700. doi: 10.1161/CIRCHEARTFAILURE.118.005700.
54. Gaertner, A., Brodehl, A., and Milting, H. Screening for mutations in human cardiomyopathy- is RBM24 a new but rare disease gene? *Protein Cell* **2019**, *10*, 393-394. doi: 10.1007/s13238-018-0590-z.
55. Ito, J., Iijima, M., Yoshimoto, N., Niimi, T., Kuroda, S., and Maturana, A.D. RBM20 and RBM24 cooperatively promote the expression of short enh splice variants. *FEBS Lett.* **2016**, *590*, 2262-2274. doi: 10.1002/1873-3468.12251.
56. Kuwasako, K., Takahashi, M., Unzai, S., Tsuda, K., Yoshikawa, S., He, F., Kobayashi, N., Güntert, P., Shirouzu, M., Ito, T., et al. RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. *Nat. Struct. Mol. Biol.* **2014**, *21*, 778-786. doi: 10.1038/nsmb.2870.
57. Morita, H., and Komuro, I. Heart failure as an aging-related phenotype. *Int. Heart J.* **2018**, *59*, 6-13. doi: 10.1536/ihj.17-519.
58. Lin, Y., Tan, K.T., Liu, J., Kong, X., Huang, Z., and Xu, X.Q. Global profiling of Rbm24 bound RNAs

- uncovers a multi-tasking RNA binding protein. *Int. J. Biochem. Cell Biol.* **2018**, *94*, 10-21. doi: 10.1016/j.biocel.2017.11.002.
59. Ehler, E. RBM24: a 'regional business manager' in charge of the maintenance of sarcomeric protein expression 24 h a day? *Cardiovasc. Res.* **2012**, *94*, 393-394. doi: 10.1093/cvr/cvs151.
 60. Relaix, F., Rocancourt, D., Mansouri, A., and Buckingham, M. A Pax3/Pax7-dependent population of skeletal muscle progenitor cells. *Nature* **2005**, *435*, 948-953. doi: 10.1038/nature03594.
 61. Zhang, T., Lin, Y., Liu, J., Zhang, Z.G., Fu, W., Guo, L.Y., Pan, L., Kong, X., Zhang, M.K., Lu, Y.H., et al. Rbm24 regulates alternative splicing switch in embryonic stem cell cardiac lineage differentiation. *Stem Cells* **2016**, *34*, 1776-1789. doi: 10.1002/stem.2366.
 62. Lin, X., Miller, J.W., Mankodi, A., Kanadia, R.N., Yuan, Y., Moxley, R.T., Swanson, M.S., and Thornton, C.A. Failure of MBNL1-dependent post-natal splicing transitions in myotonic dystrophy. *Hum. Mol. Genet.* **2006**, *15*, 2087-2097. doi: 10.1093/hmg/ddl132.
 63. Brastrom, L.K., Scott, C.A., Dawson, D.V., and Slusarski, D.C. A high-throughput assay for congenital and age-related eye diseases in zebrafish. *Biomedicines* **2019**, *7*, E28. doi: 10.3390/biomedicines7020028.
 64. Dash, S., Brastrom, L.K., Patel, S.D., Scott, C.A., Slusarski, D.C., and Lachke, S.A. The master transcription factor SOX2, mutated in anophthalmia/microphthalmia, is post-transcriptionally regulated by the conserved RNA-binding protein RBM24 in vertebrate eye development. *Hum. Mol. Genet.* **2020**, *29*, 591-604. doi: 10.1093/hmg/ddz278.
 65. Dash, S., Siddam, A.D., Barnum, C.E., Janga, S.C., and Lachke, S.A. RNA-binding proteins in eye development and disease: implication of conserved RNA granule components. *Wiley Interdiscip. Rev. RNA* **2016**, *7*, 527-757. doi: 10.1002/wrna.1355.
 66. Lachke, S.A., Alkuraya, F.S., Kneeland, S.C., Ohn, T., Aboukhalil, A., Howell, G.R., Saadi, I., Cavallero, R., Yue, Y., Tsai, A.C., et al. Mutations in the RNA granule component TDRD7 cause cataract and glaucoma. *Science* **2011**, *331*, 1571-1576. doi: 10.1126/science.1195970.
 67. Cvekl, A., Ashery-Padan, R. The cellular and molecular mechanisms of vertebrate lens development. *Development* **2014**, *141*, 4432-4447. doi: 10.1242/dev.107953.
 68. Greiling, T.M., Aose, M., and Clark, J.I. Cell fate and differentiation of the developing ocular lens. *Invest. Ophthalmol. Vis. Sci.* **2010**, *51*, 1540-1546. doi: 10.1167/iovs.09-4388.
 69. Eckmann, C.R., Rammelt, C., and Wahle, E. Control of poly(A) tail length. *Wiley Interdiscip. Rev. RNA* **2011**, *2*, 348-361. doi: 10.1002/wrna.56.
 70. Goss, D.J., and Kleiman, F.E. Poly(A) binding proteins: are they created equal? *Wiley Interdiscip. Rev. RNA* **2013**, *4*, 167-179. doi: 10.1002/wrna.1151.
 71. Nicholson, A.L., and Pasquinelli, A.E. Tales of detailed tails. *Trends Cell Biol.* **2019**, *29*, 191-200. doi: 10.1016/j.tcb.2018.11.002.
 72. Charlesworth, A., Meijer, H.A., and de Moor, C.H. Specificity factors in cytoplasmic polyadenylation. *Wiley Interdiscip. Rev. RNA* **2013**, *4*, 437-461. doi: 10.1002/wrna.1171.
 73. Reyes, J.M., and Ross P.J. Cytoplasmic polyadenylation in mammalian oocyte maturation. *Wiley Interdiscip. Rev. RNA* **2016**, *7*, 71-89. doi: 10.1002/wrna.1316.
 74. Barnum, C.E., Al Saai, S., Patel, S.D., Cheng, C., Anand, D., Xu, X., Dash, S., Siddam, A.D.,

- Glazewski, L., Paglione, E., et al. The Tudor-domain protein TDRD7, mutated in congenital cataract, controls the heat shock protein HSPB1 (HSP27) and lens fiber cell morphology. *Hum. Mol. Genet.* **2020**, *18*, ddaa096. doi: 10.1093/hmg/ddaa096.
75. Mishima, Y., Fukao, A., Kishimoto, T., Sakamoto, H., Fujiwara, T., Inoue, K. Translational inhibition by deadenylation-independent mechanisms is central to microRNA-mediated silencing in zebrafish. *Proc. Natl. Acad. Sci. U. S. A.* **2012**, *109*, 1104-1109. doi: 10.1073/pnas.1113350109.
 76. Blanco-Sánchez, B., Clément, A., Phillips, J.B., and Westerfield, M. Zebrafish models of human eye and inner ear diseases. *Methods Cell Biol.* **2017**, *138*, 415-467. doi: 10.1016/bs.mcb.2016.10.006.
 77. Nicolson, T. The genetics of hair-cell function in zebrafish. *J. Neurogenet.* **2017**, *31*, 102-112. doi: 10.1080/01677063.2017.1342246.
 78. Lush, M.E., Diaz, D.C., Koenecke, N., Baek, S., Boldt, H., St Peter, M.K., Gaitan-Escudero, T., Romero-Carvajal, A., Busch-Nentwich, E.M., Perera, A.G., etv al. scRNA-Seq reveals distinct stem cell populations that drive hair cell regeneration after loss of Fgf and Notch signaling. *Elife* **2019**, *8*, e44431. doi: 10.7554/eLife.44431.
 79. Cheng, X.N., Zhang, J.J., and Shi, D.L. Loss of Rbm24a causes defective hair cell development in the zebrafish inner ear and neuromasts. *J. Genetics & Genomics* **2020**, in press.
 80. Chatterjee, P., Padmanarayana, M., Abdullah, N., Holman, C.L., LaDu, J., Tanguay, R.L., and Johnson, C.P. Otoferlin deficiency in zebrafish results in defects in balance and hearing: rescue of the balance and hearing phenotype with full-length and truncated forms of mouse otoferlin. *Mol. Cell Biol.* **2015**, *35*, 1043-1054. doi: 10.1128/MCB.01439-14.
 81. DeSmidt, A.A., Zou, B., Grati, M., Yan, D., Mittal, R., Yao, Q., Richmond, M.T., Denyer, S., Liu, X.Z., and Lu, Z. Zebrafish model for nonsyndromic X-linked sensorineural deafness, DFNX1. *Anat. Rec.* **2020**, *303*, 544-555. doi: 10.1002/ar.24115.
 82. Sokpor, G., Abbas, E., Rosenbusch, J., Staiger, J.F., and Tuoc, T. Transcriptional and epigenetic control of mammalian olfactory epithelium development. *Mol. Neurobiol.* **2018**, *55*, 8306-8327. doi: 10.1007/s12035-018-0987-y.
 83. Shum, E.Y., Espinoza, J.L., Ramaiah, M., and Wilkinson, M.F. Identification of novel post-transcriptional features in olfactory receptor family mRNAs. *Nucleic Acids Res.* **2015**, *43*, 9314-9326. doi: 10.1093/nar/gkv324.
 84. Souopgui, J., Rust, B., Vanhomwegen, J., Heasman, J., Henningfeld, K.A., Bellefroid, E., and Pieler, T. The RNA-binding protein XSeb4R: a positive regulator of VegT mRNA stability and translation that is required for germ layer formation in *Xenopus*. *Genes Dev.* **2008**, *22*, 2347-2352. doi: 10.1101/gad.479808.
 85. Carron, C., and Shi, D.L. Specification of anteroposterior axis by combinatorial signaling during *Xenopus* development. *Wiley Interdiscip. Rev. Dev. Biol.* **2016**, *5*, 150-168. doi: 10.1002/wdev.217.
 86. Bentaya, S., Ghogomu, S.M., Vanhomwegen, J., Van Campenhout, C., Thelie, A., Dhainaut, M., Bellefroid, E.J., and Souopgui, J. The RNA-binding protein XSeb4R regulates maternal Sox3 at the posttranscriptional level during maternal-zygotic transition in *Xenopus*. *Dev. Biol.* **2012**, *363*, 362-372. doi: 10.1016/j.ydbio.2011.12.040.
 87. Despici, V., and Neugebauer, K.M. RNA tales - how embryos read and discard messages from mom.

- J. Cell Sci.* **2018**, *131*, jcs201996. doi: 10.1242/jcs.201996.
88. Christou-Kent, M., Dhellemmes, M., Lambert, E., Ray, P.F., and Arnoult, C. Diversity of RNA-binding proteins modulating post-transcriptional regulation of protein expression in the maturing mammalian oocyte. *Cells* **2020**, *9*, 662. doi: 10.3390/cells9030662.
 89. Mendez, R., and Richter, J.D. Translational control by CPEB: a means to the end. *Nat. Rev. Mol. Cell Biol.* **2001**, *2*, 521-529. doi: 10.1038/35080081.
 90. Villalba, A., Coll, O., and Gebauer, F. Cytoplasmic polyadenylation and translational control. *Curr. Opin. Genet. Dev.* **2011**, *21*, 452-457. doi: 10.1016/j.gde.2011.04.006.
 91. Winata, C.L., Łapiński, M., Prysycz, L., Vaz, C., Bin Ismail, M.H., Nama, S., Hajan, H.S., Lee, S.G.P., Korzh, V., Sampath, P., et al. Cytoplasmic polyadenylation-mediated translational control of maternal mRNAs directs maternal-to-zygotic transition. *Development* **2018**, *145*, dev159566. doi: 10.1242/dev.159566.
 92. Jiang, Y., Zhang, M., Qian, Y., Xu, E., Zhang, J., and Chen, X. Rbm24, an RNA-binding protein and a target of p53, regulates p21 expression via mRNA stability. *J. Biol. Chem.* **2014**, *289*, 3164-3175. doi: 10.1074/jbc.M113.524413.
 93. Shu, L., Yan, W., and Chen, X. RNPC1, an RNA-binding protein and a target of the p53 family, is required for maintaining the stability of the basal and stress-induced p21 transcript. *Genes Dev.* **2006**, *20*, 2961-2972. doi: 10.1101/gad.1463306.
 94. Zhang, J., Cho, S.J., and Chen, X. RNPC1, an RNA-binding protein and a target of the p53 family, regulates p63 expression through mRNA stability. *Proc. Natl. Acad. Sci. U. S. A.* **2010**, *107*, 9614-9619. doi: 10.1073/pnas.0912594107.
 95. Xu, E., Zhang, J., Zhang, M., Jiang, Y., Cho, S.J., and Chen, X. RNA-binding protein RBM24 regulates p63 expression via mRNA stability. *Mol. Cancer Res.* **2014**, *12*, 359-369. doi: 10.1158/1541-7786.MCR-13-0526.
 96. Zhang, Y., Feng, X., Sun, W., Zhang, J., and Chen, X. Serine 195 phosphorylation in the RNA-binding protein Rbm38 increases p63 expression by modulating Rbm38's interaction with the Ago2-miR203 complex. *J. Biol. Chem.* **2019**, *294*, 2449-2459. doi: 10.1074/jbc.RA118.005779.
 97. Wei, P., Yang, J., Zhang, D., Cui, M., and Li, L. lncRNA HAND2-AS1 Regulates Prostate Cancer Cell Growth Through Targeting the miR-106a-5p/RBM24 Axis. *Oncotargets Ther.* **2020**, *13*, 4523-4531. doi: 10.2147/OTT.S246274.
 98. Hua, W.F., Zhong, Q., Xia, T.L., Chen, Q., Zhang, M.Y., Zhou, A.J., Tu, Z.W., Qu, C., Li, M.Z., Xia, Y.F., et al. RBM24 suppresses cancer progression by upregulating miR-25 to target MALAT1 in nasopharyngeal carcinoma. *Cell Death Dis.* **2016**, *7*, e2352. doi: 10.1038/cddis.2016.252.
 99. Amrane, S., Rebora, K., Zniber, I., Dupuy, D., and Mackereth, C.D. Backbone-independent nucleic acid binding by splicing factor SUP-12 reveals key aspects of molecular recognition. *Nat. Commun.* **2014**, *5*, 4595. doi: 10.1038/ncomms5595.
 100. Upadhyay, S.K., and Mackereth, C.D. (1)H, (15)N and (13)C backbone and side chain resonance assignments of the RRM domain from human RBM24. *Biomol. NMR Assign.* **2016**, *10*, 237-240. doi: 10.1007/s12104-016-9674-y.
 101. Cao, Q., Anyansi, C., Hu, X., Xu, L., Xiong, L., Tang, W., Mok, M.T.S., Cheng, C., Fan, X., Gerstein,

- M., et al. Reconstruction of enhancer-target networks in 935 samples of human primary cells, tissues and cell lines. *Nat. Genet.* **2017**, *49*, 1428-1436. doi: 10.1038/ng.3950.
102. Ciafrè, S.A., and Galardi, S. microRNAs and RNA-binding proteins: a complex network of interactions and reciprocal regulations in cancer. *RNA Biol.* **2013**, *10*, 935-942. doi: 10.4161/rna.24641.
103. Du, C., Shen, Z., Zang, R., Xie, H., Li, H., Chen, P., Hang, B., Xu, X., Tang, W., and Xia, Y. Negative feedback circuitry between MIR143HG and RBM24 in Hirschsprung disease. *Biochim. Biophys. Acta* **2016**, *1862*, 2127-2136. doi: 10.1016/j.bbadis.2016.08.017.
104. Vacchi-Suzzi, C., Hahne, F., Scheubel, P., Marcellin, M., Dubost, V., Westphal, M., Boeglen, C., Büchmann-Møller, S., Cheung, M.S., Cordier, A., et al. Heart structure-specific transcriptomic atlas reveals conserved microRNA-mRNA interactions. *PLoS One* **2013**, *8*, e52442. doi: 10.1371/journal.pone.0052442.
105. Cardinali, B., Cappella, M., Provenzano, C., Garcia-Manteiga, J.M., Lazarevic, D., Cittaro, D., Martelli, F., and Falcone, G. MicroRNA-222 regulates muscle alternative splicing through Rbm24 during differentiation of skeletal muscle cells. *Cell Death Dis.* **2016**, *7*, e2086. doi: 10.1038/cddis.2016.10.
106. Ohe, K., Yoshida, M., Nakano-Kobayashi, A., Hosokawa, M., Sako, Y., Sakuma, M., Okuno, Y., Usui, T., Ninomiya, K., Nojima, T., et al. RBM24 promotes U1 snRNP recognition of the mutated 5' splice site in the *IKBKAP* gene of familial dysautonomia. *RNA* **2017**, *23*, 1393-1403. doi: 10.1261/rna.059428.116.
107. Slaugenhaupt, S.A., and Gusella, J.F. Familial dysautonomia. *Curr. Opin. Genet. Dev.* **2002**, *12*, 307-311. doi: 10.1016/s0959-437x(02)00303-9.
108. van den Hoogenhof, M.M.G., van der Made, I., de Groot, N.E., Damanafshan, A., van Amersfoort, S.C.M., Zentilin, L., Giacca, M., Pinto, Y.M., and Creemers, E.E. AAV9-mediated Rbm24 overexpression induces fibrosis in the mouse heart. *Sci. Rep.* **2018**, *8*, 11696. doi: 10.1038/s41598-018-29552-x.
109. Cao, H., Zhao, K., Yao, Y., Guo, J., Gao, X., Yang, Q., Guo, M., Zhu, W., Wang, Y., Wu, C., et al. RNA binding protein 24 regulates the translation and replication of hepatitis C virus. *Protein Cell* **2018**, *9*, 930-944. doi: 10.1007/s13238-018-0507-x.
110. Yao, Y., Yang, B., Cao, H., Zhao, K., Yuan, Y., Chen, Y., Zhang, Z., Wang, Y., Pei, R., Chen, J., et al. RBM24 stabilizes hepatitis B virus pregenomic RNA but inhibits core protein translation by targeting the terminal redundancy sequence. *Emerg. Microbes Infect.* **2018**, *7*, 86. RNA binding protein 24 regulates the translation and replication of hepatitis C virus. doi: 10.1038/s41426-018-0091-4.
111. Yao, Y., Yang, B., Chen, Y., Wang, H., Hu, X., Zhou, Y., Gao, X., Lu, M., Niu, J., Wen, Z., et al. (2019) RNA-binding motif protein 24 (RBM24) is involved in pregenomic RNA packaging by mediating interaction between hepatitis B virus polymerase and the epsilon element. *J. Virol.* **2019**, *93*, e02161-18. doi: 10.1128/JVI.02161-18.
112. Müller-McNicoll, M., Rossbach, O., Hui, J., and Medenbach, J. Auto-regulatory feedback by RNA-binding proteins. *J. Mol. Cell Biol.* **2019**, *11*, 930-939. doi: 10.1093/jmcb/mjz043.

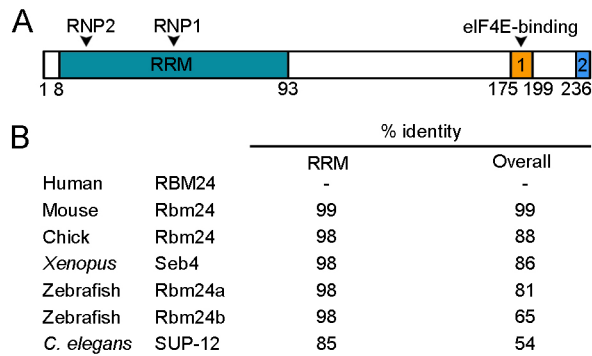


Figure 1. Rbm24 is a highly conserved RBP. (A) Schematic representation of human RBM24 protein domains. The amino-terminal half contains a canonical RRM with two consensus RNP sequences (RNP1 and RNP2), and the C-terminal region contains two conserved domains (1 and 2) including an eIF4E-binding motif. Amino acid positions are indicated below. (B) Identity in the overall sequence and in the RRM between human RBM24 and Rbm24 proteins from other species. Human RBM24, NM_001143942.2; mouse Rbm24, NM_001081425.1; chick Rbm24, NM_001012863.3; *Xenopus laevis* Seb4, NM_001087526.1; zebrafish Rbm24a, NM_212865.1; zebrafish Rbm24b, NM_001328141.1; *C. elegans* SUP-12, NM_076273.5.

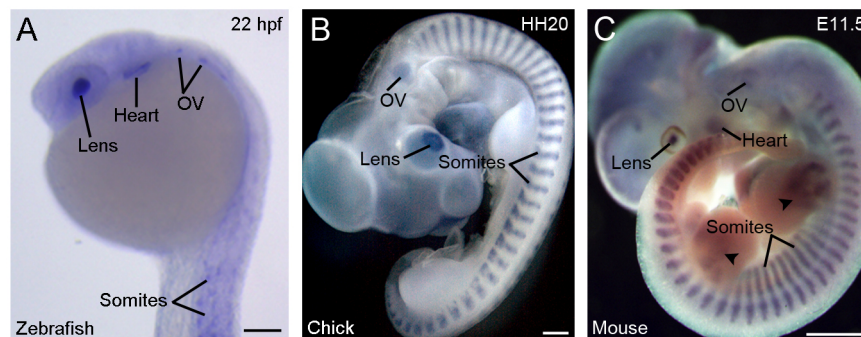


Figure 2. Conserved and restricted expression patterns of Rbm24 in vertebrate embryos. (A) The expression of *rbm24a* in a zebrafish embryo at 22 hpf. (B) A chick embryo at HH20 (3 days). (C) A mouse embryo at E11.5. Arrowheads indicate Rbm24 expression in limb muscles. In all vertebrates, Rbm24 is expressed in the somites, heart, lens, and otic vesicle (OV). Scale bars: (A) 100 μ m; (B) 1 mm; (C) 1 mm.

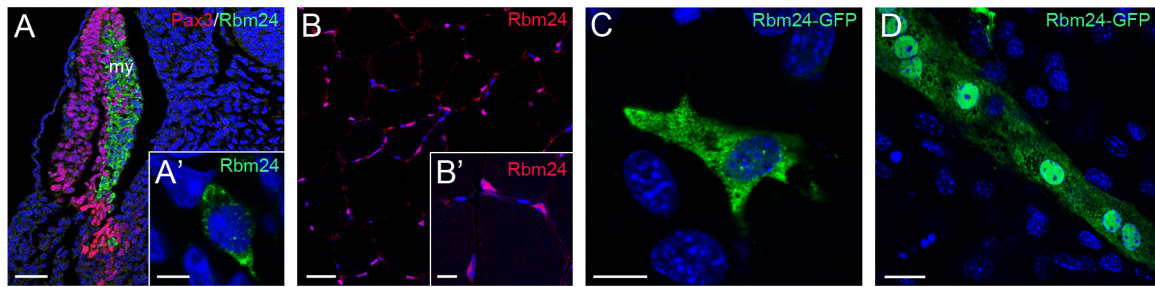


Figure 3. Dynamic subcellular localization of Rbm24 protein during muscle cell differentiation. (A) Immunofluorescence staining of a mouse embryonic section at E11.5 shows Rbm24 expression in differentiating myoblasts within the myotome (my), but not in Pax3-positive premyogenic progenitors. Some Pax3-expressing cells are intermingled with Rbm24-positive cells, but they do not yet express Rbm24. (A') Higher magnification shows the punctate cytoplasmic staining of Rbm24 in a myoblast. (B) Immunofluorescence staining of Rbm24 in adult muscles. (B') Higher magnification shows nuclear localization of Rbm24. (C) Localization of Rbm24-GFP in the cytoplasm of myoblasts from C2C12 cells. (D) Strong nuclear and weak cytoplasmic localization of Rbm24-GFP in differentiated myotubes. Nuclei are stained with DAPI. Scale bars: (A) 50 μ m; (A') 10 μ m; (B) 20 μ m; (B') 10 μ m; (C) 10 μ m; (D) 10 μ m.

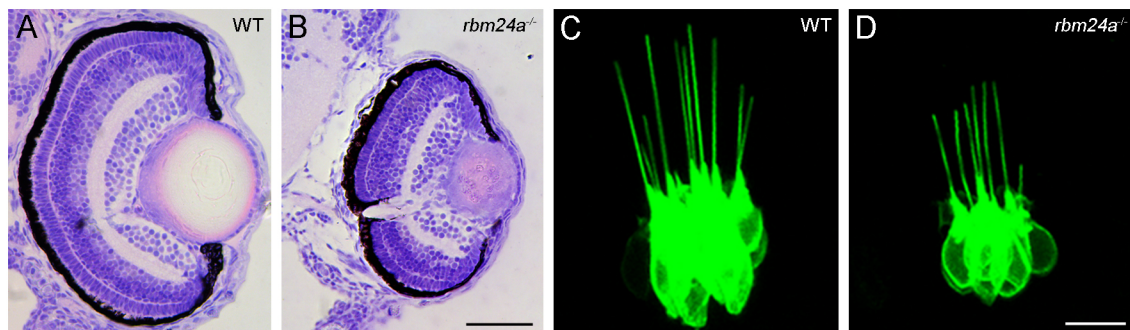


Figure 4. Loss of Rbm24a function impairs lens transparency and affects inner ear hair cell development in zebrafish. (A, B) Histological sections of ocular tissues at the level of optic nerve compares lens differentiation between a wild-type sibling (A) and an *rbm24a* mutant (B) at 3 dpf (days post-fertilization). The sections were stained by hematoxylin and eosin. Loss of Rbm24a disrupts lens differentiation and causes cataract formation, but has no effect on retina differentiation. The microphthalmia phenotype and defective lens fiber cell denucleation are secondary consequences due to impaired blood circulation. (C, D) Confocal microscopic analyses compare hair cell development and organization of the lateral crista in the zebrafish inner ear from a wild-type sibling (C) and an *rbm24a* mutant (D) at 3 dpf, under the *Tg(pou4f3:GAP-GFP)* transgenic background. Scale bars: (A, B), 50 μ m; (C, D), 10 μ m.