

# KBP interacts with SCG10, linking Goldberg–Shprintzen syndrome to microtubule dynamics and neuronal differentiation

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**Goldberg–Shprintzen syndrome (GOSHS) is a rare clinical disorder characterized by central and enteric nervous system defects. This syndrome is caused by inactivating mutations in the *Kinesin Binding Protein (KBP)* gene, which encodes a protein of which the precise function is largely unclear. We show that *KBP* expression is up-regulated during neuronal development in mouse cortical neurons. Moreover, *KBP*-depleted PC12 cells were defective in nerve growth factor-induced differentiation and neurite outgrowth, suggesting that *KBP* is required for cell differentiation and neurite development. To identify *KBP* interacting proteins, we performed a yeast two-hybrid screen and found that *KBP* binds almost exclusively to microtubule associated or related proteins, specifically *SCG10* and several kinesins. We confirmed these results by validating *KBP* interaction with one of these proteins: *SCG10*, a microtubule destabilizing protein. Zebrafish studies further demonstrated an epistatic interaction between *KBP* and *SCG10* *in vivo*. To investigate the possibility of direct interaction between *KBP* and microtubules, we undertook co-localization and *in vitro* binding assays, but found no evidence of direct binding. Thus, our data indicate that *KBP* is involved in neuronal differentiation and that the central and enteric nervous system defects seen in GOSHS are likely caused by microtubule-related defects.**

## INTRODUCTION

Goldberg–Shprintzen syndrome (GOSHS) is an autosomal recessive disorder characterized by polymicrogyria, mental retardation, microcephaly, facial dysmorphisms and, in most

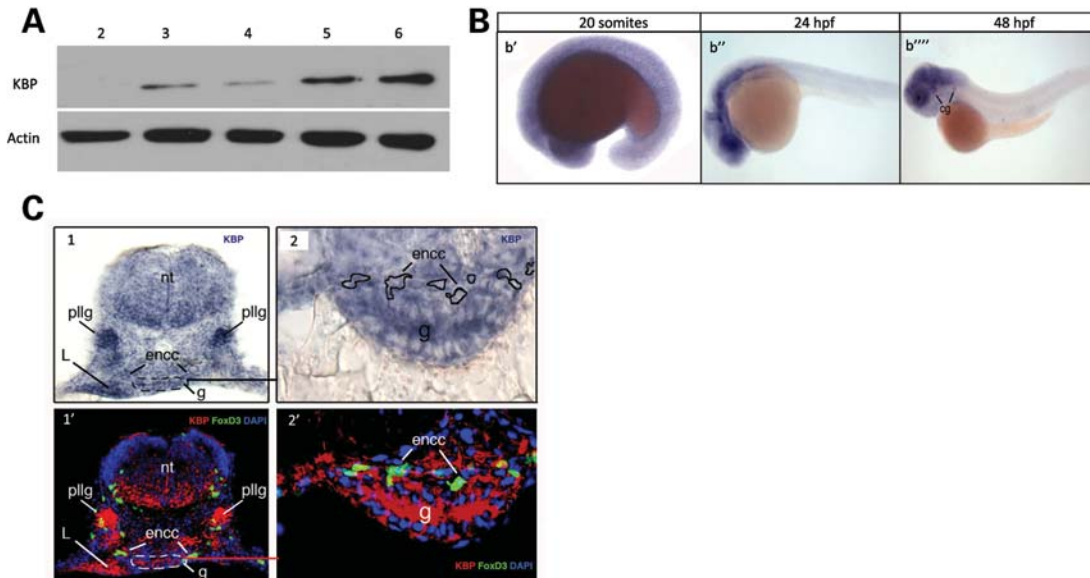
cases, by Hirschsprung disease (1,2). Homozygosity mapping studies showed linkage to chromosome 10 and subsequent sequence analysis of all 35 genes in this region led to the identification of truncating mutations in the *KIAA1279* gene (2). *KIAA1279* encodes a protein with two tetratric

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**Figure 1.** KBP expression during neuronal development and neuronal maturation. (A) Western blot analysis of mouse primary cortical neurons cultured for 6 days showed that KBP expression levels increase during neuronal development. (B) Whole-mount *in situ* hybridization of KBP in zebrafish. At 20-somite stage KBP is expressed ubiquitously (B'). At 24 hpf KBP expression is restricted to the anterior CNS and to the anterior gut (B''). This pattern of expression is maintained at 48 hpf with cranial ganglia (cg) also expressing KBP (B'''). (C) KBP expression in the hindbrain, cranial ganglia and the gut. Transverse sections of whole-mount KBP *in situ* hybridization/GFP immunohistochemistry performed in *Tg(foxd3:gfp)* zebrafish at 48 hpf showed a strong KBP expression in the ventral neural tube (nt), the posterior lateral line ganglia (pll), the developing liver (L) and gut (g) (C1 and C1'). A magnified view of the gut shows that GFP/Foxd3 positive enteric neural crest cells (encc) express only low levels of KBP (C2 and C2').

peptide repeats whose function is still uncertain. Based on the GOSHS clinical phenotype, it is clear that mutations in *KIAA1279* are associated with both central and enteric nervous system defects. Subsequent studies by Wozniak *et al.* (3) led to *KIAA1279* being named kinesin binding protein (KBP) due to its interaction with the motor domain of two related kinesin-like proteins, KIF1C and KIF1B $\alpha$ . The interaction with KIF1B $\alpha$  suggested that KBP plays a role in mitochondria localization and distribution (3). More recently, KBP has been implicated in the regulation of neuronal microtubules organization, and in axonal growth and maintenance (4). This finding stemmed from the characterization of a *kbp* mutant zebrafish, the first animal model to be described for GOSHS (4). However, the mechanism by which KBP exerts its effect on microtubules is still unknown.

Microtubules are dynamic structures that provide mechanical support for the shape of cells, and a track along which molecular motors, kinesins and dyneins move organelles from one part of the cell to another (5). To perform these functions, a cell must carefully control the assembly and orientation of its microtubule cytoskeleton. Several proteins have been described that modulate microtubule dynamics and they can be divided into two groups: microtubule stabilizing proteins (MAPs) and microtubule destabilizing proteins (6). Although much is known about the role of MAPs, relatively little is known about the molecular machinery that controls the microtubule destabilizing family of proteins, especially with respect to neuronal development and regulation (7).

Here we describe the identification of several KBP interacting proteins, all of which are implicated in microtubule transport and microtubule dynamics, and show that KBP is necessary for proper neuronal differentiation and neuronal development.

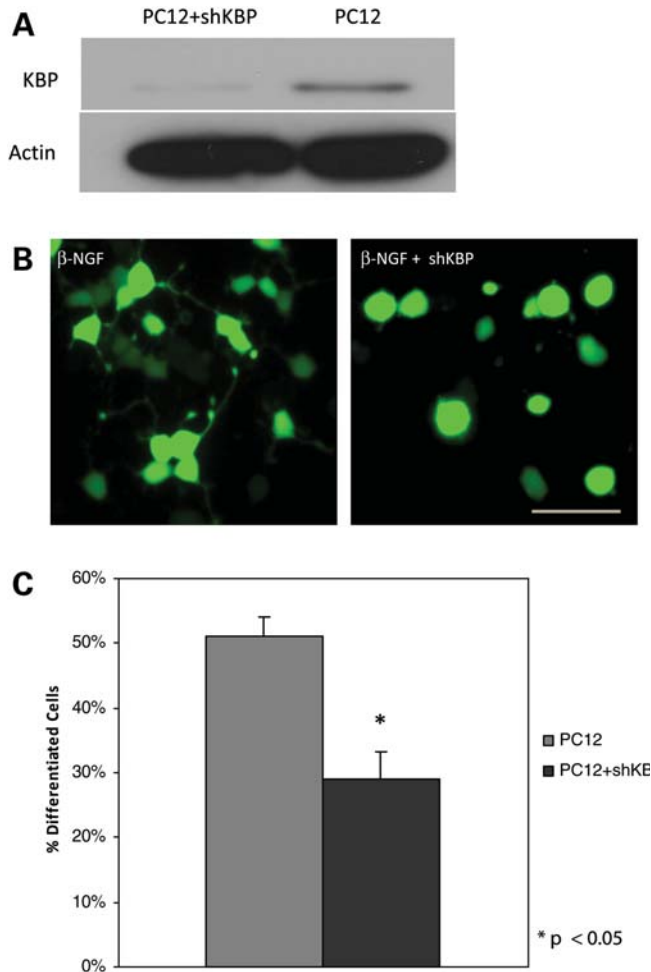
## RESULTS

### KBP plays a role in neuronal development and neuronal differentiation

GOSHS is a developmental disorder in which both the central and enteric nervous systems are affected. To determine KBP expression levels in neuronal cells, we isolated E15 mouse cortical neurons and cultured them for 6 days. Cells were lysed each day from the second day of the experiment onwards, and protein levels were analyzed by western blotting (Fig. 1A). Our data show that there is an up-regulation of KBP expression levels in primary cortical neurons that seem to go hand-in-hand with neuronal differentiation.

*In situ* hybridization performed in zebrafish confirmed the expression of KBP both in the central and enteric nervous systems (Fig. 1B). A detailed examination of the expression pattern in the developing gut revealed that KBP is only expressed at low levels in migrating enteric neural crest stem cells during the initial period of gut colonization (Fig. 1C). Taken together, these mouse and zebrafish results suggest that KBP plays a role during the development of the central and enteric nervous systems.

To determine whether KBP is required for neuronal maturation, we reduced KBP expression in PC12 cells using a shRNA expressing vector (Fig. 2A). We used PC12 cells because they have the ability to differentiate into neuronal-like cells in the presence of nerve growth factor ( $\beta$ -NGF) (8). After co-transfection of PC12 cells with shRNA expressing vector targeting KBP mRNA and a GFP expressing plasmid to monitor the transfected cells, GFP expressing cells were counted (approx. 4000 cells/condition) and morphologically analyzed for the presence of neurites (Fig. 2B). We considered



**Figure 2.** KBP is required for PC12 differentiation. (A) Western blot analysis of KBP expression in PC12 cells transfected with GFP alone or in combination with a shRNA expression vector targeting KBP mRNA. (B) Morphology of  $\beta$ -NGF-treated PC12 cells expressing a GFP vector alone or in combination with the shKBP vector was analysed using a fluorescence microscope. (C) The number of green differentiated cells was counted in the absence and in the presence of the shKBP and showed to be significantly lower when KBP expression was reduced ( $P < 0.05$ ). Scale bars, 15  $\mu$ m.

any extension that could be seen from the cellular body, a neurite, and the presence of one small extension was enough to consider the cell as differentiated. Our results show that the number of PC12 cells that differentiate and produce neurites when KBP expression was impaired was significantly lower ( $P < 0.05$ ) than for the control (Fig. 2C). These data indicate that KBP strongly contributes to the NGF-induced neuronal differentiation of PC12 cells.

### Yeast two-hybrid interactions of KBP

KBP contains two tetratricopeptide repeats which mediate protein–protein interactions (9), suggesting that KBP likely binds to other proteins. To identify KBP interacting partners, a pre-transformed E11 mouse cDNA library was screened using a yeast two-hybrid screen. The E11 mouse library was used, as this is a critical stage in brain development and

**Table 1.** Yeast two-hybrid results for KBP

7 clones	KIF5B
1 clone	KIF5C
1 clone	KIF7
2 clones	KIF2C
1 clone	KIF3A
6 clones	KIFC1
3 clones	Tubulin $\alpha$ 7
19 clones	Superior cervical ganglia, neural specific 10—SCG10

coincides with the stage at which the colon is being colonized by neural crest cells.

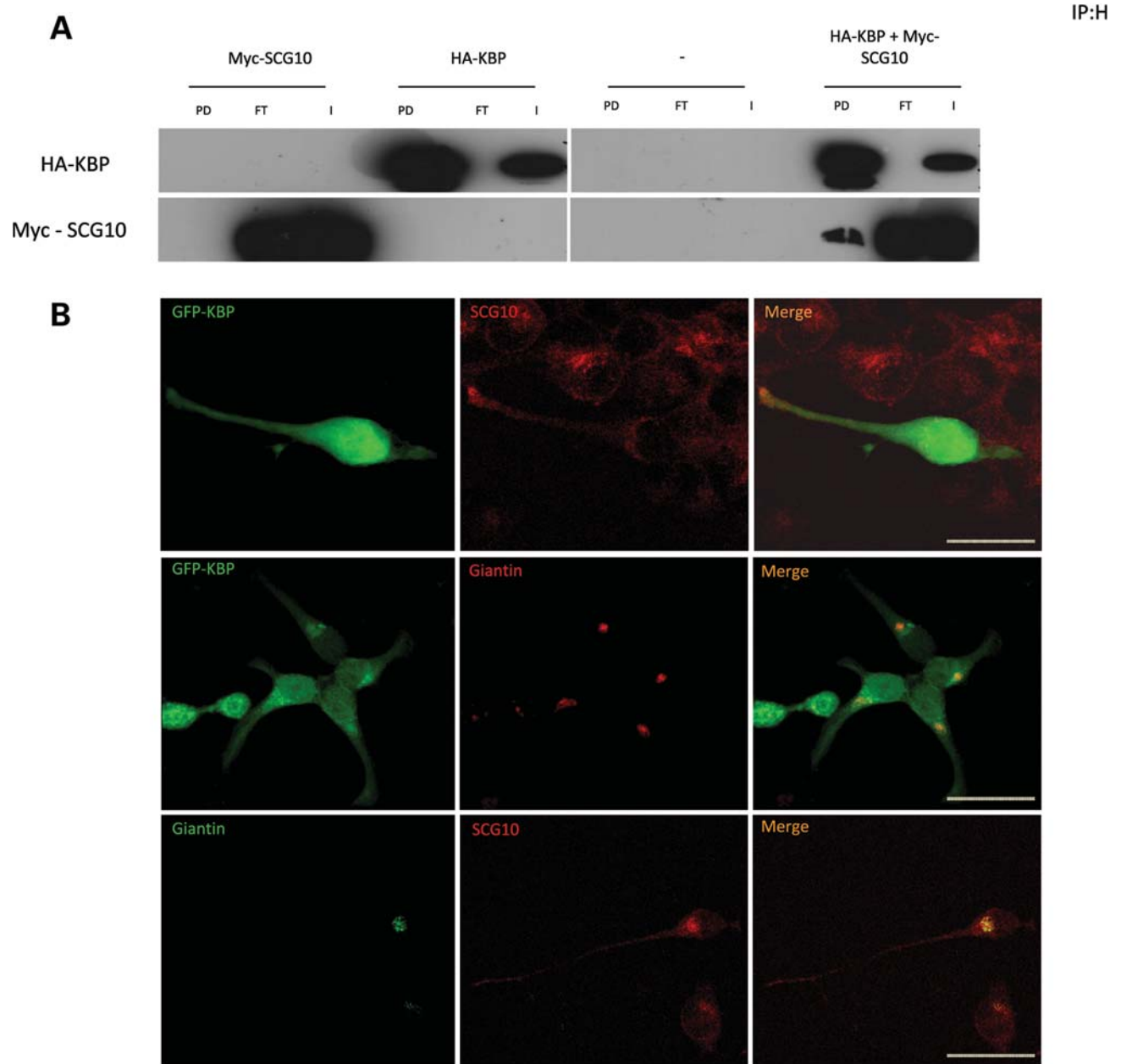
From our yeast two-hybrid screen, we selected 69 positive clones which we isolated and sequenced. Nineteen of these 69 clones encoded for the same protein, SCG10, a stathmin-like protein. In addition, six kinesins were found among these inserts, namely KIF5B, KIF5C, KIF7, KIF2C, KIF3A and, also, KIFC1. A blast search using the cDNA of the kinesins found revealed that they all interact with KBP via their motor domain. None of the kinesins previously described to interact with KBP (3), KIF1C and KIF1B $\alpha$ , were found in our screen. Additionally, three of these 69 clones encoded for tubulin, the main constituent of microtubules (Table 1). Taken together, these results strongly suggest a role for KBP in microtubule organization and stability. Moreover, the fact that all these kinesins were obtained in this screen reinforced the idea that KBP is involved in kinesin-mediated microtubular transport and is indeed a kinesin binding protein.

Since the majority of clones obtained encoded for microtubule associated or microtubule interacting proteins, we conclude that KBP might be involved in microtubule-related events. In order to confirm the validity of this result, we decided to further study KBP interaction with the most frequently found clone, SCG10.

### KBP interacts with SCG10

SCG10 is a member of the stathmin family of proteins, all of which bind to tubulin to act as a sequestering agent and promote microtubule disassembly (10). SCG10 is a membrane-associated neuronal protein that is largely expressed during development and whose expression correlates with neurite outgrowth (10). It possesses a unique N-terminal domain that is critical for membrane binding, is responsible for SCG10 localization to the Golgi complex and is important in the targeting of SCG10 to the growth cones (11,12).

To confirm the specificity of the KBP interaction with SCG10, we performed a co-immunoprecipitation assay. HA-KBP was expressed in Human Embryonic Kidney cells (HEK293) alone or in combination with Myc-tagged SCG10. Expression of exogenous Myc-SCG10 was necessary, as HEK293 cells do not endogenously express SCG10. Precipitation of Myc-SCG10 was only observed in the presence of HA-KBP (Fig. 3A), confirming an interaction between KBP and SCG10. This interaction was further supported by co-localization studies in a mouse neuroblastoma cell line, N1E-115. This cell line was chosen due to its ability to differentiate in neuronal-like



**Figure 3.** KBP interacts with SCG10. (A) HA pull-down performed in HEK293 cells co-expressing HA-KBP alone or in combination with Myc-SCG10 showed that Myc-SCG10 precipitates only in the presence of HA-KBP (I, input, FT, flow through, PD, pull down). (B) Confocal images of N1E/115 cells showed that GFP-KBP co-localizes with SCG10 in the Golgi complex and in the neurites. Giantin staining was performed to confirm KBP and SCG10 co-localization in the Golgi complex. Scale bars 20  $\mu$ m.

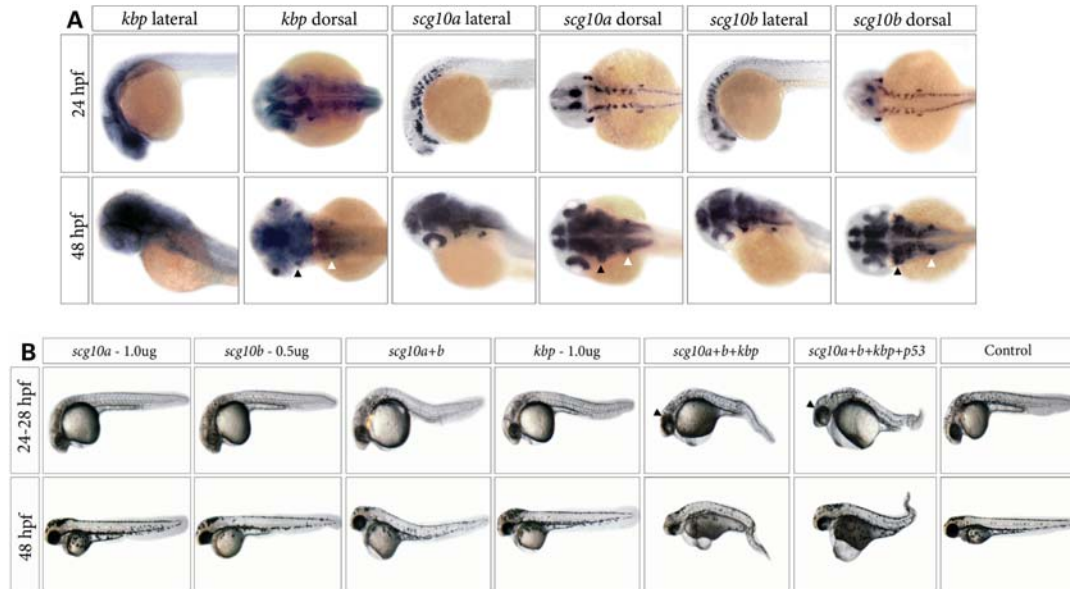
cells when incubated in the presence of low serum concentrations. Using this cell line, we evaluated GFP-KBP and SCG10 cellular distribution in the cell. SCG10 is enriched in the Golgi complex and in the growth cones as expected (12), while KBP shows a cytoplasmic distribution in the cell that overlaps with SCG10 specifically in the Golgi complex (Fig. 3B). To confirm KBP and SCG10 co-localization in the Golgi complex, we used a specific antibody against a Golgi protein, giantin (13), as a Golgi marker (Fig. 3B).

These results support our yeast two-hybrid data and confirm the cellular interaction between KBP and SCG10.

### Epistatic interaction between KBP and SCG10 in zebrafish

To further validate the KBP-SCG10 interaction, the distribution of the mRNA transcripts for both these proteins was evaluated and epistasis was determined using a zebrafish model.

The zebrafish genome contains one *KBP* gene and two *SCG10* orthologs (4,14). To determine the spatial expression pattern of the zebrafish *scg10a* and *scg10b* and to compare it with *kbp* orthologs during embryogenesis, matched whole-mount *in situ* hybridizations were performed using riboprobes



**Figure 4.** Epistatic interaction of KBP with SCG10. (A) Whole-mount *in situ* hybridizations performed in zebrafish at 24 and 48 hpf show expression patterns of *scg10a*, *scg10b* and *kbp* orthologues. (B) SBMO targeted against *scg10a*, *scg10b* and *kbp* transcripts were injected in zebrafish embryos at 1–2 cell stage. When injected individually hardly any phenotype was seen. *scg10a* and *scg10b* double injections lead to a general delay in development. However, when *kbp* SBMO was injected in combination with *scg10a* and *scg10b*, morphants showed a severe phenotype with malformed body axis, very small head and eyes, necrotic areas in the brain and heart edema. A *p53* morpholino was combined to exclude potential cytotoxic side effects of the morpholinos used.

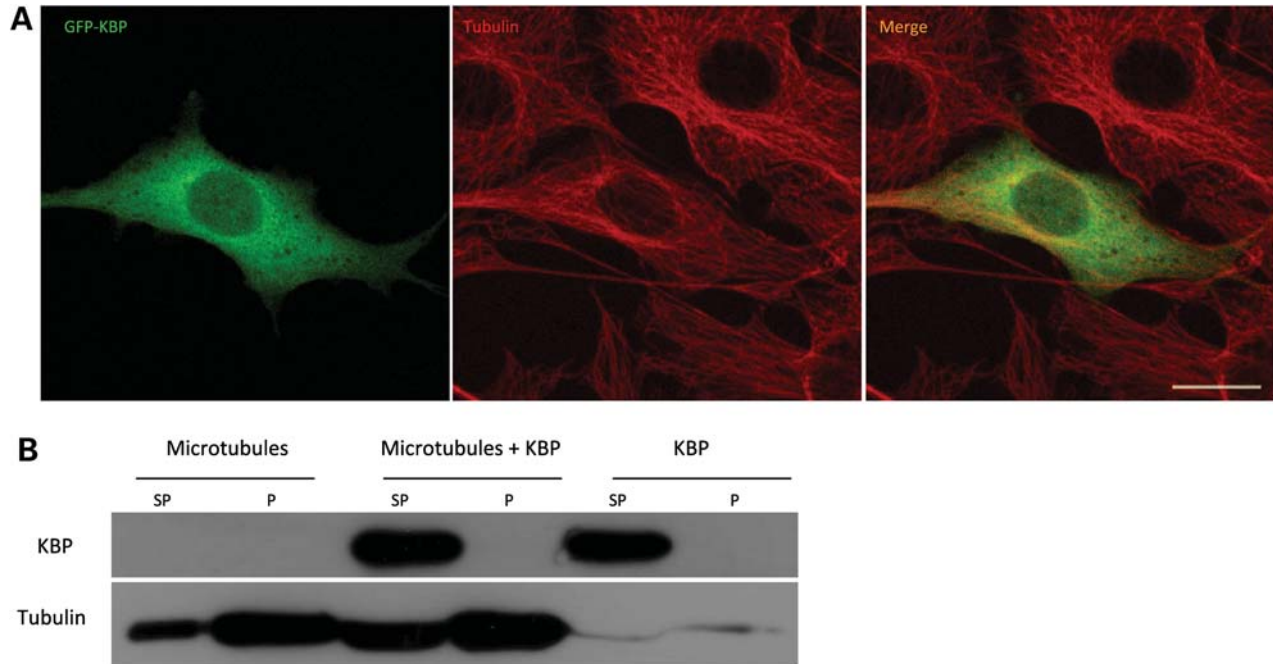
for all three genes. Discrete patterns of expression were detectable as early as 16 h post-fertilization (hpf). At this stage, expression of both *scg10a* and *scg10b* genes is restricted to the posterior lateral line (PLL) ganglia and Rohon-Beard sensory neurons in the spinal cord (Fig. 4A). In contrast, expression of *kbp* is initially rather diffused and ubiquitous in the whole embryo (Fig. 1B'). From 24 hpf, *kbp*'s expression becomes predominantly restricted to the anterior central nervous system (CNS) and this pattern of expression persists throughout all the stages examined in the present study. *kbp* transcript is present in all brain regions, as well as in the anterior lateral line (ALL) and PLL ganglia (Figs 1C and 4A). SCG10 expression at 24 hpf can be detected within the anterior CNS regions including ventral telencephalon and diencephalon, all hindbrain rhombomeres, the ALL and PLL and primary sensory neurons of the spinal cord (Fig. 4A). At 48 hpf, expression of the *SCG10* genes becomes more abundant but like the pattern of *kbp* expression, they are primarily restricted to the anterior CNS and cranial ganglia. Further in development (72 and 96 hpf), SCG10 transcripts remain expressed in the same CNS regions and are also expressed in the enteric neurons (14). The pattern of expression of both *SCG10* orthologues in zebrafish is very similar, although *scg10a* transcript is much more abundant (14). At 48 hpf expression of *scg10a*, *scg10b* and *kbp* overlap in the forebrain region, retina, optic tectum, trigeminal, vagal ganglia, ALL and PLL ganglia, and in the hindbrain (Fig. 4A).

To determine whether there is an epistatic interaction between KBP and SCG10, 1–2-cell stage zebrafish embryos were injected with splice blocking morpholinos (SBMO) targeted against *scg10a*, *scg10b* and *kbp* transcripts (15). Injections were carried out either separately or in combination.

In addition, combined injections were performed with a *p53* morpholino (MO) to exclude potential cytotoxic side effects of MOs used (16). The concentration of *scg10* and *kbp* MOs was titrated to the sub-threshold doses so that when injected separately they resulted in no apparent phenotype (Fig. 4B). In contrast, when the MOs were injected in combination, perturbation in development became apparent. In the case of *scg10a* and *scg10b* double injections, morphants displayed a general delay in development, smaller heads and eyes and axial defects (Fig. 4B). This result suggests that the *scg10* genes are functionally redundant and this is consistent with their almost identical patterns of expression. Injections of *scg10a*, *scg10b* and *kbp* MOs together resulted in a much more severe phenotype. Triple morphants were significantly smaller with severely malformed body axis, very small head and eyes, necrotic areas in the brain and heart edema. Injections with *p53* MO reduced the cell death in the retina and optic tectum areas but did not change the general morphology of the morphants, confirming that the observed morphant phenotype is not the result of offsite effects of the MOs (Fig. 4B) (16). These results strongly suggest an epistatic interaction between *kbp* and *scg10* genes and support the results of the yeast two-hybrid screen and co-immunoprecipitation assays.

#### KBP interaction with microtubules

Based on the yeast two-hybrid results and on the direct interaction between KBP and SCG10, a microtubule destabilizing protein, we hypothesize that KBP plays a role in microtubule organization or microtubule stability and dynamics. Furthermore, the recent study characterizing a *kbp* mutant zebrafish showed that the loss of KBP function leads to a disorganization



**Figure 5.** KBP association with microtubules. (A) Confocal images of NIH-3T3 cells expressing GFP-KBP and stained with an anti-tubulin antibody showed that KBP does not co-localize with microtubules. (B) Microtubule *in vitro* binding assay showed that KBP does not precipitate with Taxol-stabilized microtubules when subjected to high-speed centrifugation (P, pellet; SP, supernatant). Scale bars 20  $\mu$ m.

of axonal microtubules and to an improper orientation of microtubules along the axonal axis (4). In an attempt to further explain this microtubule effect, we investigated whether there is a direct interaction between KBP and microtubules by determining the co-localization of GFP-KBP with tubulin in mouse fibroblast cells (NIH-3T3). We detected no co-localization between KBP and tubulin (Fig. 5A). To rule out the possibility that the interaction of KBP with microtubules is very transient and thus difficult to detect in co-localization studies, *in vitro* microtubule binding assays were performed. Taxol-stabilized microtubules were purified and mixed with cytosolic cell extracts of NIH-3T3 cells expressing KBP. Microtubules were pelleted by high-speed centrifugation and the binding of KBP to the microtubules was determined by co-sedimentation. We found that KBP remains in the supernatant both in the absence and presence of microtubules, suggesting that KBP does not directly associate with microtubules (Fig. 5B).

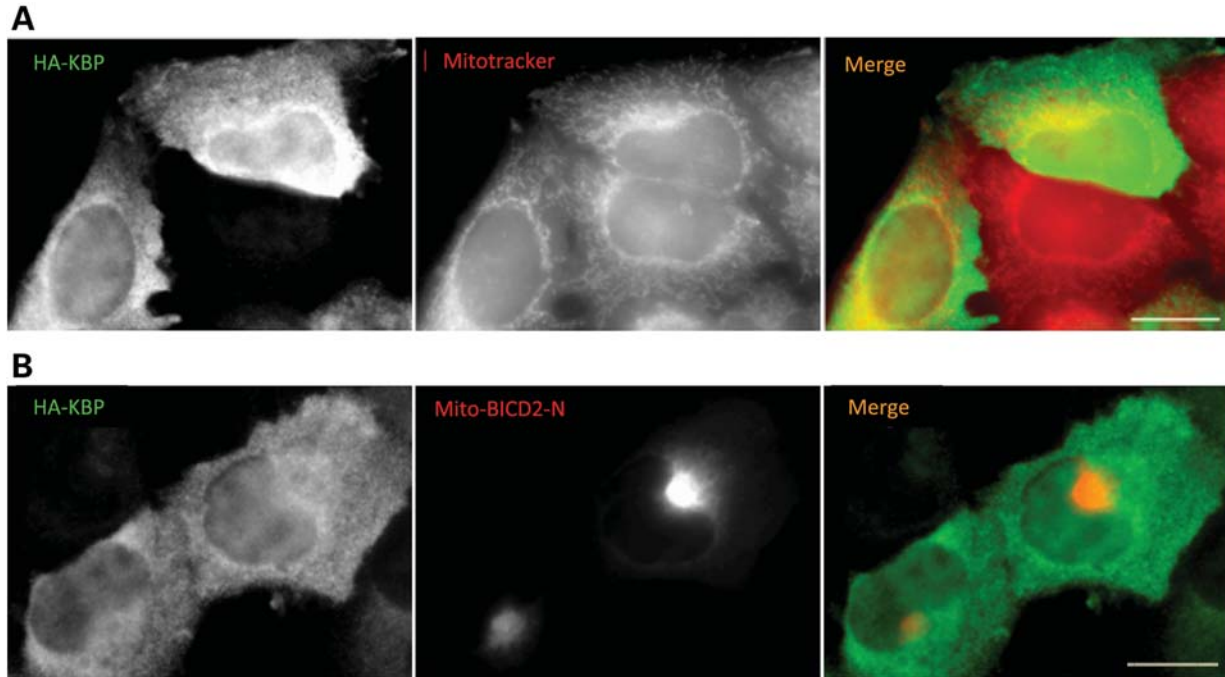
### KBP has a cytoplasmic localization

During the co-localization studies performed, we noticed that KBP was distributed throughout the cytoplasm. Previous studies performed in NIH-3T3 cells reported that KBP co-localizes with mitochondria and that it plays a role in mitochondria distribution by interaction with KIF1B $\alpha$  (3). To reassure ourselves that the GFP tag was not influencing KBP localization in the cell, we expressed HA-human KBP in HeLa cells. Using an anti-HA antibody and a specific marker for mitochondria (MitoTracker), we repeatedly observed that KBP is distributed throughout the cytoplasm and is not specifically localized to mitochondria (Fig. 6A).

To further support this observation, we co-expressed a modified Bicaudal D2 (BICD2-N) construct in HeLa cells with the HA-human KBP construct (Fig. 6B). BICD2 is a motor-adaptor protein involved in the transport of various cargoes by dynein-mediated transport in *Drosophila* and mammals. Previous studies have shown that in the absence of its C-terminal, BICD2-N-terminal strongly binds to dynein and impairs its normal function leading to disruption of the retrograde distribution of membranous organelles (17). When we over-expressed BICD2-N in HeLa cells, mitochondria became aggregated; however, we saw no change in KBP localization (Fig. 6B). Since NIH-3T3 cells were also used by us with no change in the diffuse localization of KBP in the cell (Fig. 5A), maybe a difference in the experimental procedure used could explain the differences in co-localization seen by us and by the previous study (3). However, based on our results, we conclude that KBP has a cytoplasmic localization and does not co-localize with mitochondria.

### DISCUSSION

Homozygous nonsense mutations in the *KIAA1279/KBP* gene encoding KBP lead to GOSHS. Affected patients have undetectable levels of KBP and show both central and enteric nervous system defects (2). Based on the clinical phenotype, KBP is required for normal neuronal development, but its precise function is largely unclear. Subsequent to our initial identification of *KBP* mutations underlying the GOSHS phenotype, two independent studies have investigated the function of the KBP protein. The first study showed that KBP has a mitochondrial localization and that it interacts with the  $\alpha$  isoform of KIF1B, increasing its motility. The



**Figure 6.** KBP has a cytoplasmic localization. **(A)** Confocal images of HeLa cells expressing HA-hKBP and stained with a mitochondrial marker (Mitotracker) showed that KBP has a cytoplasmic distribution and does not co-localize with mitochondria. **(B)** Co-expression of HA-hKBP and BicD2-N constructs in HeLa cells confirms KBP cytoplasmic localization. Scale bars 20  $\mu\text{m}$ .

same study showed that a reduction in the expression levels of KBP led to mitochondrial aggregation, suggesting that KBP regulates mitochondria distribution in the cell by controlling KIF1B $\alpha$  activity (3). The second study characterized a zebrafish *kbp* mutant, which had reduced axonal growth and disruption of axonal microtubules (4). Axonal degeneration and mislocalization of mitochondria were also observed in the neurons at later stages of development, suggesting that KBP is a regulator of the neuronal cytoskeleton (4). Although both studies shed some light on KBP function, they only partially explain the role of KBP in GOSHS.

Our results show that KBP plays a role in neuronal development and is necessary for neuronal differentiation. Using zebrafish as a vertebrate model, we clearly show that KBP is strongly expressed in the CNS during embryonic development. KBP is also expressed in some peripheral nervous system structures, such as the cranial ganglia, although its expression is low in the migrating enteric precursors. Our study also shows that KBP interacts with several microtubule-related proteins, including the stathmin SCG10, a microtubule destabilizing protein. Based on this interaction, we suggest that KBP potentially modulates the proper organization of microtubules. We also show that KBP interacts with several kinesins, as previously described (3), further confirming that KBP is indeed a kinesin binding protein and suggesting that KBP may regulate multiple aspects of intracellular transport along microtubules. Furthermore, we cannot exclude the possibility that KBP may be involved in signaling pathways mediated by primary cilium especially because one of the kinesins that we found in our yeast two-hybrid screen, KIF7, was shown to be a cilia-associated protein (18).

Taken together, these results provide further insights into the cellular mechanisms that are perturbed in GOSHS patients and that underlie the clinical phenotype.

### KBP, SCG10 and microtubules

Microtubules are dynamic structures composed of  $\alpha$  and  $\beta$  tubulin dimers. These structures are necessary for many processes in the cell, including transport and maintenance of neuritic processes (19–22). Microtubule dynamics are characterized by stages of catastrophe alternated with stages of polymerization; this process is called dynamic instability. Although dynamic instability occurs both at the plus and minus ends of purified microtubules *in vitro*, it is more pronounced at the plus ends (22).

Several proteins are known to regulate microtubule dynamics, including KBP (4). Our results show that KBP interacts with SCG10, a stathmin-like protein previously reported to be involved in microtubule dynamics (23,24). Moreover, during differentiation, SCG10 enhances neurite outgrowth, a phenomenon that is believed to depend on microtubule dynamics (24,25).

Our results strongly suggest that KBP's role in microtubule organization/dynamics is not a result of its direct interaction/association with microtubules but is instead due to its interaction with SCG10. As KBP interacts with several kinesins, a possible function for KBP would be as an adaptor molecule for the transport of SCG10 to the growth cones via kinesin-related transport. However, our yeast two-hybrid screen showed that KBP's interaction with the kinesins is via the kinesin motor domain. Knowing that the motor domain is

responsible for the docking of kinesins to the microtubules, it is very unlikely that KBP is directly involved in the transport of SCG10 to the growth cones. However, KBP might be involved in the process that precedes the transport of SCG10 to the growth cones. Additionally, KBP might regulate SCG10 activity, leading to a change in its microtubule destabilizing properties and may thus be involved in the maintenance of microtubule dynamics. Another possibility is that KBP might mediate SCG10 interaction with tubulin. Consistent with this, we observed an interaction between KBP and tubulin in our yeast two-hybrid study. Potentially, KBP could control the levels of free tubulin available for microtubule polymerization. If either of these mechanisms are correct, KBP will affect neurite extension and axonal growth, and this is in line with our data and the analysis of the zebrafish *kbp* mutant (4). Furthermore, as the expression pattern of SCG10 is restricted to neuronal tissue, any perturbation of the KBP–SCG10–tubulin interaction will potentially result in neuronal development defects consistent with the GOSHS clinical phenotype.

Finally, our observation that KBP is required for neuronal maturation of PC12 cells is consistent with our biochemical studies that showed an interaction between KBP and SCG10.

### **KBP implications in GOSHS and HSCR**

GOSHS is a rare but severe genetic disorder characterized by central and enteric nervous system defects. Based on our results, we propose that the GOSHS phenotype is caused by a reduction in neuronal differentiation and perturbed microtubule dynamics due to a deregulation of SCG10 activity. The data we now present supports previous findings (4).

Since GOSHS patients frequently have Hirschsprung disease (HSCR), KBP interacting proteins could bring some new insights about HSCR development. Currently, the genetic basis of this condition can only be explained in ~20% of all the cases, with *RET* being the major gene involved (26). SCG10 has been previously identified as a down-regulated gene in a *RET* mouse model for HSCR (27) and we have shown that SCG10 interacts with KBP *in vitro* and *in vivo*. Both these facts suggest that SCG10 might also play a role in HSCR development, but it is still not clear what mechanism is involved. SCG10 activity is known to be controlled by two post-translational modifications: palmitoylation and phosphorylation (28,29). The former is responsible for growth cones targeting of SCG10 and the latter is responsible for controlling SCG10 activity. As *RET* modulates several signaling pathways, it is possible that *RET*, via one of its downstream pathways, controls SCG10 activity, linking this gene directly to HSCR. Further studies are required to determine if there is any association between *RET* and SCG10 and a possible involvement of SCG10 in HSCR.

### **Conclusions**

Our study shows that KBP is necessary for neuronal development and neuronal maturation. Furthermore, we show that KBP interacts with several microtubule-associated and microtubule-related proteins *in vitro* and *in vivo*, being likely

involved in microtubule organization/stability. Our results provide new insights into perturbed cellular mechanisms that lead to GOSHS and suggest that KBP has an important role in modulating SCG10 function during neuronal development.

## **MATERIALS AND METHODS**

### **Constructs**

Design of vectors and oligonucleotides used are described in Supplementary Material, Table S1.

### **Cell culture and transfections**

HEK293, NIH-3T3, HeLa and N1E/115 cells were cultured in DMEM high medium containing 4.5 g/l of glucose, L-glutamine and pyruvate (Gibco), supplemented with 10% fetal calf serum (BioWhittaker) or with 10% newborn calf serum (Gibco) (for NIH-3T3) and 1% penicillin/streptomycin (Gibco), at 37°C and 5% CO<sub>2</sub>.

For transient transfections, 300 000 cells of HEK293, HeLa, 3T3 and N1E/115 were seeded in 6-well plates. Transfections were performed 24 h after seeding using jetPei (Promega).

### **Culture of primary cortical neurons**

Primary cortical neurons were prepared from embryonic brains (E15–16) of C57Bl/6J mice. After mechanical dissociation, neurons were plated on 6-well plates previously coated with poly-D-lysine (2 µg/ml). Neurobasal medium (GIBCO) supplemented with B27-supplement (GIBCO), 0.5 mM glutamine (BioWhittaker), 1% penicillin/streptomycin (Gibco) and 2.5 µg/ml amphotericin B (Sigma-Aldrich) was used as culture medium. After 48 h, cells were treated with 10 µM cytosine arabinoside (Sigma-Aldrich) and incubated for another 48 h to inhibit non-neuronal cell growth.

### **Yeast two-hybrid screen**

The yeast two-hybrid screen was performed using the Matchmaker 3 System (ClonTech) according to the manufacturer's instructions. A detailed description can be found in Supplementary Material.

### **Cell lysates, co-immunoprecipitation assays and western blot analysis**

Cell lysates were prepared as follows: cells were washed with ice-cold PBS and incubated with lysis buffer (200 mM NaCl, 20 mM Tris–HCl pH 7.8, 1% Triton X-100 and protease inhibitors) for 30 min on ice. Cell lysates were collected by scraping and cleared by centrifugation at 14000 rpm for 10 min in a pre-cooled (4°C) centrifuge. Supernatants were stored at –80°C before they were processed further for SDS–PAGE followed by western blot analysis. For immunoprecipitation, lysates were incubated with HA-coupled sepharose beads (Roche) ON at 4°C. Precipitates were washed with lysis buffer and protein was eluted in loading buffer. Antibodies used for western blot detection can be found in Supplementary Material.

### Microscopy and image analysis

For immunofluorescence analysis, N1E/115, 3T3 and HeLa cells were cultured on poly-D-lysine coated cover slips. Two percent PFA was used as fixative agent for N1E/115 and HeLa cells and 3T3 cells were fixed in ice-cold methanol for 3 min at  $-20^{\circ}\text{C}$ . Cells were made permeable with 1% BSA and 0.1% Triton X-100 in PBS. Antibodies used for immunofluorescence can be found in Supplementary Material. Fluorescent images were made using a Leica TCS SP2 (AOBS) microscope.

### *In vitro* polymerization of microtubules and high-speed fractionation

NIH-3T3 cells were lysed in tubulin buffer (Cytoskeleton) containing 0.1% Triton X-100. Lysates were centrifuged at 100 000g for 1 h in an Optima<sup>TM</sup> MAX-E- Beckman Coulter ultracentrifuge. Supernatant fractions were incubated for 30 min at  $37^{\circ}\text{C}$  with purified, taxol-stabilized microtubules, which were generated according to the manufacturer's indications (Cytoskeleton<sup>TM</sup>). Microtubules were pelleted down by centrifugation (100 000g for 1 h) and both supernatant and pellet fractions were checked by western blotting.

### PC12 culture, differentiation and transfection

PC12 cells were cultured in RPMI 1640 (Gibco) supplemented with 10% horse serum (Gibco), 5% fetal calf serum (Gibco) and 1% penicillin/streptomycin (Gibco), at  $37^{\circ}\text{C}$  and 5%  $\text{CO}_2$ .

For transient transfections, 50 000 PC12 cells were seeded in 12-well culture plates coated with laminin (Millipore). Twenty-four hours after, cells were transfected with pEGFP-N1 vector alone or in combination with pSuper-shKBP vector using lipofectamine 2000 (Invitrogen). Twenty-four hours after transfection, cells were cultured in low serum concentration for 12 h at  $37^{\circ}\text{C}$  and 5%  $\text{CO}_2$ .  $\beta$ -NGF (R&D systems) was then added to the culture medium and 48 h after green cells were counted and analyzed for the presence of neurites.

### Fish and embryos

Zebrafish were kept and bred under standard conditions at  $28.5^{\circ}\text{C}$  (30). Embryos were staged and fixed at specific hours post-fertilization (hpf) as described elsewhere (31). To better visualize *in situ* hybridization results, embryos were grown in 0.2 mM 1-phenyl-2-thiourea (Sigma) to inhibit pigment formation (30).

### Antisense oligonucleotide (Morpholinos) injections

Splice blocking *scg10a*, *scg10b* and *kbp* morpholinos (SBMO) were designed to complement the sequences corresponding to the splice donor site at the predicted exon2/exon3 junction for *scg10a*, exon1/exon2 for *scg10b* and exon3/exon4 for *kbp* (Supplementary Material, Table S1).

The MOs (Supplementary Material, Table S1) were diluted in sterile filtered water over a concentrations range of 1–5  $\mu\text{g}/\mu\text{l}$ . Approximately 1 nl of diluted MO was injected at the 1–2-cell stage using a gas-driven microinjection apparatus to determine

the effects of knocking down single genes or combinations of them. The standard control MO from Gene Tools was injected as a negative control for the MO experiments. A p53 MO (Supplementary Material, Table S1) was injected in combination with other MOs to eliminate potential apoptotic side effects of MO injections (32).

### Whole mount *in situ* hybridization and double-labeling immunohistochemistry in zebrafish

Digoxigenin-labeled riboprobes that complement *scg10a*, *scg10b* and *kbp* mRNAs were generated by linearization of pCR TOPO II vectors that contained partial ORFs of the genes. SCG10a and SCG10b plasmids were linearized with *EcoRV* (New England Biolabs) and subsequently transcribed with SP6 polymerase (Promega). KBP plasmid was linearized with *SalI* (New England Biolabs) and transcribed with T7 polymerase (Promega). Embryos were collected and processed for whole-mount *in situ* hybridization as previously described (33). Digoxigenin-labeled probes were detected using a standard NBT/BCIP staining reaction.

For immunohistochemistry, FoxD3-GFP transgenic embryos (34,35) were fixed in 4% PFA. To obtain frozen sections, tissues were cryoprotected overnight in a 20% sucrose/PBS solution and placed for 1 h at  $37^{\circ}\text{C}$  in a 20% sucrose/5% gelatin solution. Afterwards, tissues were rapidly frozen in isopentane pre-cooled in liquid nitrogen to  $-60^{\circ}\text{C}$ . Frozen sections were cut at  $14\ \mu\text{m}$ , collected on Superfrost Plus microscope slides (BDH Laboratories), air dried and stored at  $-20^{\circ}\text{C}$ . Prior to labeling, sections were placed in warmed PBS ( $37^{\circ}\text{C}$ ) for 15 min in order to remove the sucrose/gelatin, and then rinsed in PBS ( $2 \times 5\ \text{min}$ ). Histochemical staining was done using a polyclonal rabbit anti-GFP antibody (Molecular Probes) as previously described (36). Sections were then stained with DAPI (5 min). In order to observe any co-localization of KBP RNA and FoxD3-GFP, bright field *in situ* images were converted into grayscale, inverted and then inserted into the red channel before being overlaid with FITC images using Adobe Photoshop software.

### SUPPLEMENTARY MATERIAL

Supplementary Material is available at *HMG* online.

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