Long non-coding (lnc) RNAs are defined as non-protein coding RNAs distinct from housekeeping RNAs such as tRNAs, rRNAs, and snRNAs, and independent from small RNAs with specific molecular processing machinery such as micro- or piwi-RNAs. Recent studies of IncRNAs across different species have revealed a diverse population of RNA molecules of differing size and function. RNA sequencing studies suggest transcription throughout the genome, so there is a need to understand how sequence relates to functional and structural relationships amongst RNA molecules. Our synthesis of recent studies suggests that neither size, presence of a poly-A tail, splicing, direction of transcription, nor strand specificity are of importance to IncRNA function. Rather, relative genomic position in relation to a target is fundamentally important. In this review, we describe issues of key importance in functional assessment of IncRNA and how this might apply to IncRNAs important in neurodevelopment.

Keywords: non-coding RNA, epigenetics, gene regulation, neurodevelopment
CHARACTERIZATION OF IncRNAs
Several recent reviews have delineated ncRNA species into sub-categories based on size (less or greater than 200 bases – often used as the definition of long versus short ncRNA), position (e.g., RNA species generated from the 3′UTRs or 5′UTRs), molecular interactions (e.g., Drosha- or Dicer-dependent), and molecular function, a good example of which is competitive antisense (AS) RNA that binds to microRNA and acts as a sponge to inhibit competitively microRNA from binding to a sense mRNA transcript (Cossart et al., 2011). It is unclear whether these categories are empirically determined, or whether they will prove relevant to categorization as future ncRNAs are discovered; indeed, the identification of such a wide diversity of RNA is consistent with what might be expected from an ancient, flexible molecule, capable of forming 3D structures and interacting with DNA, protein, or other RNAs.

What makes a IncRNA a IncRNA rather than some other RNA species? Are they a functionally distinct RNA product or are they a small part of the transcriptome that has been suggested to occur from large portions of the genome, mostly from recent ENCODE data (Carninci et al., 2005; Birney et al., 2007)? Certainly, a recent report (Guttman et al., 2013) suggests that intergenic IncRNAs are indeed non-coding, an issue that has been previously determined using algorithms (Lin et al., 2011) to assess whether different combinations of potential codons are similar to any other previously identified amino acid molecule. Most studies of IncRNA also attempt to determine whether an RNA species is localized to the nucleus, usually using RNA fluorescence in situ hybridization (FISH). Because translation occurs in the cytoplasm this might be evidence for the lack of coding potential. This analysis is somewhat arbitrary though, because ncRNA might be identified in the nuclear, chromatin, or cytoplasmic fraction of cells. Compartimentalization of IncRNAs in one of these fractions may be a defining feature of different IncRNA and may help to guide future classification schemes. Functional studies of IncRNA have also led to a proliferation of potential future categories for IncRNA, some of which are listed in Table 1, but this categorization creates its own problems in that many IncRNAs have overlapping features. This is a major issue at the moment and one likely to increase in complexity given the number of RNAs that can be detected from so many regions of the genome.

The current classification system will likely evolve as more RNA species are discovered, and classification of each ncRNA might follow a similar trajectory to that of protein coding gene classification. Genes that lead to an mRNA product are not divided up by length, genomic position, whether they are spliced or not for example, and numerous coding genes fit into different classification categories. Instead they are classified by function or conserved domains. Likely it is the novelty of the RNA field, facilitated by the detection of so many transcripts by massively parallel sequencing that is leading to the classification conundrum, but this may diminish as individual RNAs are functionally analyzed.

Several recent reports have carefully documented IncRNAs over a very unique range of function. To understand how IncRNAs are similar or different in both structure and function, we synthesize this information from recent papers to determine if there are any patterns or consistencies across RNA species. We focus on currently defined long RNA (>200 bp) and omit discussion of small RNAs such as microRNA, piwiRNA, or imprinting-related RNAs.

FUNCTIONAL STUDIES OF IncRNAs
The recognition of HOTAIR (Birns et al., 2007) as a IncRNA that regulates gene expression in cis and trans (it is transcribed on chromosome 12 from the HoxC cluster and can regulate the chromosomes 2 HoxD gene cluster) opened a new chapter for RNA molecules. HOTAIR defined a class of molecules distinct from housekeeping RNAs, microRNAs, and others, and which were not involved in fundamental imprinting processes. It hinted at the existence of RNA in the genome with regulatory functions directly related to their particular sequence and position.

Table 1 | Some examples of categorization of non-coding RNA.

<table>
<thead>
<tr>
<th>Category</th>
<th>Description</th>
<th>Example</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intronic</td>
<td>Expressed from the intron of target</td>
<td>DMD IncRNA</td>
<td>Boosteleta et al. (2012)</td>
</tr>
<tr>
<td>H3K4me3</td>
<td>Has a methylated H3K4 promoter</td>
<td>IncRNA-p21</td>
<td>Huarte et al. (2011)</td>
</tr>
<tr>
<td>Antisense</td>
<td>Expressed from the non-coding strand and acts on the complementary target</td>
<td>BACE1-AS</td>
<td>Fagotto et al. (2009)</td>
</tr>
<tr>
<td>Enhancer</td>
<td>Expressed to enhance expression at a locus at some distance from target</td>
<td>p53 eRNAs</td>
<td>Melo et al. (2013)</td>
</tr>
<tr>
<td>Promoter</td>
<td>Acting on and expressed from the promoter of target</td>
<td>DBE-T</td>
<td>Cabianca et al. (2012)</td>
</tr>
<tr>
<td>Intergenic</td>
<td>Expressed at some distance from coding genes</td>
<td>IncRNA00299</td>
<td>Talukder et al. (2012)</td>
</tr>
<tr>
<td>Trans-acting</td>
<td>Acting at some distance from target</td>
<td>Ev2</td>
<td>Bond et al. (2009)</td>
</tr>
<tr>
<td>cis-acting</td>
<td>Acting on an adjacent target</td>
<td>ARN</td>
<td>Santoro et al. (2013)</td>
</tr>
<tr>
<td>Small</td>
<td>Less than 200 bp in size</td>
<td>microRNA 137</td>
<td>Ripea et al. (2011)</td>
</tr>
<tr>
<td>Long</td>
<td>Greater than 200 bp in size</td>
<td>Fendr</td>
<td>Grote et al. (2013)</td>
</tr>
<tr>
<td>5′UTR</td>
<td>Expressed near the 5′UTR of target</td>
<td>5′UTR ELK-1</td>
<td>Rahim et al. (2012)</td>
</tr>
</tbody>
</table>
provided an explanation for the targeting specificity required by ubiquitous binding molecules such as large chromatin modifying complexes. Since *HOTTIP*'s description, the function of many other lncRNAs has been revealed. Shown below is the large diversity of these molecules, from their genomic position in relation to the genes they regulate, their size, processing, and mechanism of action. While this diversity is large, there are also similarities, especially in reference to function. To demonstrate differences and similarities, we have selected all reports from the last 2 years (2011–2013) that have characterized positional, processing, and functional information of specific lncRNAs. Table 2 lists structural information from lncRNAs that have been characterized functionally and this information is synthesized with the functional characteristics in the concluding remarks.

The lncRNA COLDAIR presents a series of themes for lncRNAs with respect to function. COLDAIR recruits polycomb repressive complex 2 (PRC2), a complex of proteins that can alter histone chemical groups to decrease gene expression, through an intermediate protein (homolog of Enhancer of zeste, *Drosophila*) and the binding of COLDAIR occurs through a CNC domain of this intermediate protein (see Table 3 for a discussion of RNA:protein interaction domains). COLDAIR is expressed at equal ratios over time, despite an increasing repression of the target, suggesting increased affinity for the PRC2 interaction. COLDAIR reveals several potential areas of diversity/similarity amongst lncRNAs. What determines expression of the lncRNA itself? Is the lncRNA regulated in conjunction with the target or independently from it? Is the lncRNA action direct on the target or indirect? Is the lncRNA repressive or activating? Does it act on a single target or a cluster of targets at a locus?

The lncRNA *IRT1* differs significantly from the mechanistic action of COLDAIR, but also functions in a repressive manner to block expression of the target gene *IME1*. *IRT1* can respond within hours to a cell stressor to aid in the inhibition of gametogenesis, which means the repressive mechanism used by *IRT1* may be specific to fast-acting effects. *IRT1* completely covers the 2 kb promoter of the target gene and functions to block transcription factors from binding and promoting transcription and acts in cis, similar to COLDAIR. Because *IRT1* is transcribed over the promoter of the target gene in the sense direction, it has an identical specificity to the DNA of the *IME1* promoter. The blocking of transcription factors in combination with aiding in the establishment of a repressive chromatin state through histone methyltransferases

**Table 2** | Processing and positional diversity of lncRNA (in order described in text).

<table>
<thead>
<tr>
<th>LncRNA [Ref]</th>
<th>Species</th>
<th>Description of all structural properties reported</th>
</tr>
</thead>
<tbody>
<tr>
<td>COLDAIR (Heo and Sung, 2011)</td>
<td><em>A. thaliana</em></td>
<td>110 base RNA expressed from the sense strand relative to target, has no poly-A tail, expressed from an intron of the target gene</td>
</tr>
<tr>
<td><em>IRT1</em> (van Werven et al., 2012)</td>
<td><em>S. cerevisiae</em></td>
<td>Expressed from promoter of target, 1.4 kb in length, not spliced and is transcribed from the same strand as the gene it regulates</td>
</tr>
<tr>
<td>NaST (Gomez et al., 2013)</td>
<td><em>M. musculus</em></td>
<td>Encoded on the antisense strand, contains six exons spread over a 45 kb region, transcript is 914 bases</td>
</tr>
<tr>
<td>Braveheart (Klattenhoff et al., 2013)</td>
<td><em>M. musculus</em></td>
<td>590 base RNA with three exons, 33% confined to the nucleus</td>
</tr>
<tr>
<td>NaST (Gomez et al., 2013)</td>
<td><em>M. musculus</em></td>
<td>Encoded on antisense strand, contains six exons spread over a 45 kb region, primary transcript is 914 bases</td>
</tr>
<tr>
<td>D BE-T (Cabianca et al., 2012)</td>
<td><em>H. sapiens</em></td>
<td>9.5 kb is one major product, transcribed from same strand as target genes, transcript contains one of many targets, nuclear and chromatin associated</td>
</tr>
<tr>
<td>HOTTIP (Wang et al., 2013)</td>
<td><em>H. sapiens</em></td>
<td>3,764-nucleotide, spliced and polyadenylated intergenic RNA, ~330 base product, regulates gene cluster</td>
</tr>
<tr>
<td>ANRIL (Lin et al., 2011)</td>
<td><em>H. sapiens</em></td>
<td>~126 kb transcript, spliced, 19 exons with an ~11 kb transcript, 13 isoforms transcribed in the antisense orientation of gene cluster, overlaps one target gene</td>
</tr>
<tr>
<td>IncMD1 (Cai et al., 2013)</td>
<td><em>M. musculus</em></td>
<td>Three exons and two introns in 14 kb of genomic space, spliced product of 521 bases, accumulates as cytoplasmic poly-A RNA, transcribed on same strand in same orientation as microRNAs for which it acts as a decoy</td>
</tr>
<tr>
<td>TINCR (Kretz et al., 2013)</td>
<td><em>H. sapiens</em></td>
<td>Three exons, 3.7 kb transcript predominantly cytoplasmically expressed, over 100 different targets dispersed through genome</td>
</tr>
<tr>
<td>UCHL1-AS (Carrieri et al., 2012)</td>
<td><em>M. musculus</em></td>
<td>Four exons spanning 70 kb, overlaps the first 73 bases of UCHL1, including the AUS start codon, transcribed in reverse orientation in a head-to-head fashion, second intron of UCHL1 contains the TSS for UCHL1-AS, enriched in the nucleus</td>
</tr>
<tr>
<td>12/15dR1 (Gong and Maquat, 2011)</td>
<td><em>H. sapiens</em></td>
<td>Present in cytoplasm, poly-A+, two alternative transcripts consist of 688 nucleotides, multiple targets throughout genome</td>
</tr>
</tbody>
</table>
and deacetylases suggests that IRT1 can physically hinder TFs but also guide repressive chromatin complexes. Here the repressive effects are different than COLDAIR in that repression is due to the deposition of H3K4me2 and H3K36me. The effects of COLDAIR are due to the recruitment of PRC2 at the repeat region, thus the basal state in adult cells is the repression of genes at this chromosomal locus. Loss of PRC2 at the repeat region corresponds with the binding of ASH1L, a histone lysine N-methyltransferase that is part of the Triplet group, which recruits DBE-T to chromatin. Thus, this IncRNA is at the crossroads of crosstalk between conflicting histone modifying complexes. While little is known about the regulation of IncRNAs, DBE-T may be an example of a post-transcription feedback loop which may be a common theme for other IncRNAs – in other words, IncRNA expression may be regulated by targets of the target that the IncRNA itself regulates.

Similar to the positive feedback observed between DBE-T and ASH1L, HOTTIP IncRNA and WDR5 operate analogously. Similar to NeST, HOTTIP physically interacts with WDR5, and WDR5 forms a complex with ML1L1, which is a H3K4 methyltransferase, triggering gene expression. HOTTIP maintains an appropriate level of the WDR5/ML1L1 at a gene cluster, and its influence over the gene cluster dissipates as a function of distance from its site of transcription. Thus, this IncRNA interacts indirectly with a histone modifying complex, is involved in a feedback loop with its interacting partner, and activates expression of a cluster of genes as a function of distance from its site of expression.

ANRIL is a IncRNA transcribed immediately upstream of a cluster of genes important in human cell proliferation and is probably the most studied IncRNA to date because of its important role in cancer. ANRIL is transcribed on the AS strand of three intimately linked genes. It can bind to the transcript of the nearest gene at the locus, INK4, through complementary base pairing and can act at the promoter to recruit both PRC1 and PRC2 to repress transcription. ANRIL, while seemingly with a wider diversity of function than other polycomb recruitment IncRNAs, may actually foreshadow the function of other PRC-rerecruiting IncRNAs. Specifically, that they may have a wide variety of functions at a particular locus, and the only reason this has not yet been identified is because of experimental design strategies. We suspect many PRC-interacting IncRNAs will have many other functions that complement their effects. The multi-mechanistic function of ANRIL also showcases the idea that not all IncRNAs operate by recruiting large histone modifying complexes. Instead, recently identified IncRNA often operate by binding to the primary target or acting as a decoy of repressive effectors of the target.

IncMD1 and TINCR are two examples of non-PRC-recruiting IncRNAs with novel function to refine expression of a target. In contrast to IncRNAs COLDAIR, IRT1, NeST, BVHT, DBE-T, HOTTIP, and ANRIL, IncMD1, is an IncRNA that appears to be a by-product or remnant of microRNA processing (Ailha et al., 2013). Specifically, this IncRNA can act as a decoy for the targets of microRNA produced from the same locus as IncMD1 (Cesana et al., 2011). TINCR also differs from all reported IncRNAs to date as it appears to bind to a 25 bp "TINCR-box" present in the RNA of different coding transcripts and influence levels of those transcripts in a STAU-dependent manner. STAU is an RNA guidance protein initially identified for its
involvement in oocytes of Drosophila. All lncRNA described to date provide locus specificity for activating or repressive complexes to neighboring target genes, or interact directly with a target through sequence complementarity. TINCR on the other hand, appears to target specific RNA transcripts actively through an RNA sequence motif. lincMD1 also diverges drastically in that it is a by-product of pri-microRNA processing and acts to sponge the microRNAs from which it was initially processed. There may be many other pri-microRNA by-products that function similarly.

Another lncRNA that reportedly does not use large histone modifying complexes to alter a target, but instead operates through binding of a primary target, is AS-UCHL1. AS-UCHL1 has been shown recently to be important for proper targeting of sense transcript to polysomes, suggesting a stabilizing function for this lncRNA, demonstrated by a strong increase in UCHL1 protein with no difference in UCHL1 transcript on over-expression of AS-UCHL1. This principle of RNA stabilization to affect protein levels of targets may be a continuing theme for lncRNAs (e.g., Yoon et al., 2012). This lncRNA has a single target, binds directly, and functions to increase protein of the primary target by stabilizing the mRNA. Besides this novel functional effect for a lncRNA, AS-UCHL1 action is driven by repeat elements within the AS transcript. Specifically, an orientation-specific SINEB2 repeat is required for the stabilizing function and protein synthesis activation of the sense strand. The overlapping portion of the AS gene with the sense gene thereby provides targeting information, while the SINEB2 region, which is not overlapped by the sense strand, confers protein synthesis activation (see Figure 1A).

The idea of repeat elements in the genome, acting through lncRNAs, has also been described with respect to Alu repeats, one of the most common repeats in the human genome. The description of overlapping Alu repeats, one in an AS strand and one in the 3′UTR of the sense strand, can lead to formation of a STAU1 binding site, which allows for STAU1 to stabilize base pairing and target the RNA duplex for degradation. Similar to all lncRNAs described here, these Alu-containing lncRNAs can regulate the levels of a transcript through an mRNA decay pathway. This was specifically demonstrated for SERPINE1 and FLJ21870 mRNAs between their 3′ UTR Alu element and the Alu element in a single lncRNA (see Figure 1B).

**SYNTHESIS OF lncRNA FEATURES FROM DIFFERENT SPECIES**

These examples support an important role for lncRNAs in the genome, and highlight the diverse function of lncRNAs, but also some similarities. First, there appears to be no relationship between the particular function of a lncRNA, its size, or how it is processed. This suggests that lncRNAs will represent a diverse range of characteristics. Second, neither transcriptional direction nor strand specificity appears to have an effect on function. The key element is that lncRNAs are produced either within their target gene or in the vicinity of target genes. Those lncRNAs produced from overlapping regions of their target gene are more likely to bind to the target, however, due to direct complementarity with the target. Whether these lncRNAs come from the same or the AS strand as a target appears not to have functional impact. Future experiments should document this for all newly described
IncrRNAs to determine whether this remains the case. These ideas may help guide issues of categorization of IncrRNAs, and we propose a system that anchors IncrRNAs in the target molecule. This may not prove useful for those IncrRNAs, like the intergenic IncrRNAs, that do not appear to have nearby targets. Their function may prove to be completely different and independent from those IncrRNAs expressed in relationship to mRNA.

Most IncrRNAs are modulators of a primary transcript suggesting that, evolutionarily, they arose after the primary transcript. For example, HOXTIIE2 either evolved with or after the HOX gene cluster that it regulates. There is little evidence for IncrRNAs that operate in isolation (although the IncrRNAs may be an exception, reflected by their distinct locations and conservation across species (Managadze et al., 2011), but rather form part of a transcriptional regulation complex of a specific target or a cluster of targets. This suggests that characterizing IncrRNA might best be done grounded in the primary target rather than through effector status.

Many IncrRNAs act though histone modifying complexes and appear to affect either a single target gene or a cluster of genes in a local region. They may require an intermediate binding partner for recruitment of the histone complex or interact directly with one of the proteins in these complexes. Determining whether IncrRNAs bind directly to the target, interact directly with a histone modifying complex, or require a partner to bind histone modifying complex, will be important information as new IncrRNAs are uncovered. Most IncrRNAs do not share any sequence similarity (i.e., no indication yet of any conserved domain within IncrRNAs) and it seems the position of IncrRNAs in relation to the target(s) are of fundamental importance to their function. While there are many remarkable functions attributed to IncrRNAs, we strongly suspect that the function of even these IncrRNAs will prove more diverse as they undergo further investigation.

IncrRNAs IN CNS DEVELOPMENT

Functional and mechanistic data generated by studying IncrRNAs in different molecular systems and species suggests IncrRNAs likely play an important role in all cellular systems. As evidenced in the previous sections, IncrRNAs most likely act as modifiers of a complementary RNA, interact with large histone complexes, interact with complementary DNA sequences, or act completely independently in the nucleus with no obvious partners required. Given this diverse potential, the complexity of the nervous system in any species might be partially due to the additional level of control over the cellular machinery by IncrRNAs. IncrRNAs may provide a means to tweak a cellular system at many levels and to operate rapidly in response to external signals whether axon guidance cues or environmental exposure. In line with these ideas, we synthesize recent reports of IncrRNAs in the developing nervous system.

IncrRNA IN NEURAL STEM CELLS

Some of the first experiments to underscore the importance of IncrRNAs were done in mouse or human stem cells from. Stem cells used for research are either derived from the inner cell mass of a fertilized embryo (Thomson et al., 1998) or induced pluripotent stem cells (Takahashi and Yamanaka, 2006) in terminally differentiated cells. These stem cells can be differentiated to a neural stem cell (NSC) fate and these NSCs can then give rise to glia and neurons (Hu et al., 2010). In a wide ranging, exploratory analysis, Ng and colleagues (Ng et al., 2012) examined neuronal differentiation from human embryonic stem cells (hESCs). They used a two-step differentiation protocol from radial glial-like cells to largely dopaminergic cells, and then assessed global gene expression levels of pre-selected IncrRNAs in radial-glial cells compared to dopaminergic-like cells. They identified 35 IncrRNAs that were differentially expressed between progenitor and mature states, and then tested some of these for functionality. Following similar designs of non-neuronal studies of IncrRNA, they assessed the association of differentially expressed IncrRNA with SUZ12 and the neurogenesis repressor complex REST/NRFSF (neural restrictive silencer factor; Naruse et al., 1999). In a study using just three IncrRNAs, their data supported interaction of one IncrRNA with REST and another IncrRNA with SUZ12. While the SUZ12 interaction is consistent with previous IncrRNA studies, the interaction with REST/NRFSF is novel for IncrRNAs in neurons, although it does associate with HOTAIR in non-neuronal cell types to repress expression of neuronal genes. This suggests that the IncrRNA in the Ng et al. (2012) study may interact with REST to regulate neuronal gene expression.

While ES (embryonic stem cells)- and iPSC (induced pluripotent stem cell)-derived NSCs may not perfectly capture the developmental progression of the human brain, they provide an excellent model with which to screen for important factors as the cells develop from stem cells to electrically active neurons. A study monitoring iPSC-NSC differentiation accompanied by RNA sampling at different timepoints, contrasted with brain temporal lobe tissue RNA levels from the same donor has revealed a gradual increase in the expression of different IncrRNAs as NSCs differentiate (Hjelm et al., 2013). This is supported by our own study, where we observed an increase in the neurodevelopmentally important intergenic IncrRNA0299 as iPSC-NAs differentiated (Takahowski et al., 2012). A recent report using adult NSCs in mice has further confirmed that IncrRNAs increase as cells differentiate. Ramos et al. (2013) sorted stem cells of the sub-ventricular zone of mice and screened these cells for expression levels of different IncrRNAs creating publicly accessible expression maps for IncrRNAs that may be relevant to glial-neuron specification in adult brain.

IncrRNA IN DEVELOPING BRAIN

In the mammalian brain, IncrRNAs have long been recognized as important in neurodevelopment, although they were traditionally referred to as AS transcripts. An example of this is the AS transcripts near the Sod and Sodl1 loci produced during development of the mouse cerebral cortex (Ling et al., 2009). Son transcripts contain a high mobility group, and this refers to the ability of these proteins to bind and bend DNA. Using global gene expression analysis tools, Ling et al. (2011) showed that AS Sod and Sodl1 transcripts are produced during proliferating and differentiating states, suggesting that the regulation of these important genes is by complementary IncrRNAs. Recently, this same group documented a similar effect with respect to Ngenes and Camk2n1 gene product in mouse cerebral corticogenesis. A recent study in adult brain also suggests that electrical activity in neurons stimulates IncrRNA
Aid, T., Kazantseva, A., Piirsoo, M., Ala, U., Karreth, F. A., Bosia, C., et al. (2012). Some, meaning that paternally expressed genes likely provide the intellectual disability, sleep disorders, and psychosis, and can be caused by deletion of 15q11-13 on the paternal chromosome. Genes in this region are suppressed on the maternal chromosome, meaning that paternally expressed genes likely provide the optimal dosage of expression. The minimal required locus within this ~10 Mb region implicates 116HG, a lncRNA retained in the nucleus, as well as the small nuclear RNA SNORD126 (Sahoo et al., 2008). Both lncRNAs are the control of the imprinting control region, involving multiple overlap of genes – suggesting that transcription and splicing in this region are complex. Recently, Powell et al. (2013) reported the first experiments to determine the function of lncRNA 116HG. They found that 116HG forms RNA “clouds” specific to nuclei in mouse brain, and that these 116HG RNA clouds change size and shape in a predictable way as the brain develops. Using RNA and DNA FISH mapping, they show that 116HG likely interacts with the paternal UBE3A locus, a gene found immediately upstream of the 116HG locus and known to be important in neurodevelopment. Their data further suggest that 116HG interacts with RBBP5, a subunit of the MLL complex, which acts as a transcriptional activator by methylation of H3K4. This model conforms nicely to what is known of lincRNA functions in other species; 116HG might associate with MLL complex and interact with histones at the UBE3A locus. How 116HG itself is regulated is unknown, but this will be clearly important to understand better the neurobiology of PWS.

lncRNAs likely have a role in many aspects of the cell, and brain development might be an area where their structure and function is particularly suited. This may suggest that many more lncRNAs await discovery in novel systems as well as in added layers of control for well known processes of neurodevelopment.

ACKNOWLEDGMENTS

Carl Ernst is supported by a Canada Research Chair and holds funding from the Banting Foundation of Toronto and the Natural Science and Engineering Research Council of Canada. Cynthia C. Morton acknowledges support from the NIH (GM061354).

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Ernst and Morten Identification of long non-coding lncRNA
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