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Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression

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We recently showed that the mammalian genome encodes >1,000 large intergenic noncoding (linc)RNAs that are clearly conserved across mammals and, thus, functional. Gene expression patterns have implicated these lincRNAs in diverse biological processes, including cell-cycle regulation, immune surveillance, and embryonic stem cell pluripotency. However, the mechanism by which these lincRNAs function is unknown. Here, we expand the catalog of human lincRNAs to ~3,300 by analyzing chromatin-state maps of various human cell types. Inspired by the observation that the well-characterized lincRNA HOTAIR binds the polycomb repressive complex (PRC2), we tested whether many lincRNAs are physically associated with PRC2. Remarkably, we observe that ~20% of lincRNAs expressed in various cell types are bound by PRC2, and that additional lincRNAs are bound by other chromatin-modifying complexes. Also, we show that siRNA-mediated depletion of certain lincRNAs associated with PRC2 leads to changes in gene expression, and that the up-regulated genes are enriched for those normally silenced by PRC2. We propose a model in which some lincRNAs guide chromatin-modifying complexes to specific genomic loci to regulate gene expression.

We therefore conclude that lincRNAs are a new class of functional noncoding RNAs that function through association with chromatin-modifying complexes.
hybridized poly(A) transcripts. In these 3 cell types, RNA hybridization revealed 1,703 loci (Fig. S1A). We further focused on the 535 K4-K36 domains that were lower is represented on the x axis as a log-odd enrichment score (compared with random genomic regions of equivalent size). The cumulative number of exons with a given score or lower is represented on the y axis.

Results

Identification of Human lincRNAs. We recently identified lincRNAs in the mouse genome by analyzing chromatin-state maps of 4 mouse cell types: mES, lung fibroblasts (mLFs), neural precursor cells (NPCs), and mouse embryonic fibroblasts (MEFs) (1). Specifically, we used a computational algorithm to identify K4-K36 domains that do not overlap known protein-coding genes, and then eliminated the small proportion (>5%) that showed any significant protein-coding capacity. We were left with 1,586 previously uncharacterized K4-K36 domains. We demonstrated that the vast majority of these regions encode lincRNAs, with 95% showing significant conservation to the human genome within their transcripts. To further extend the catalog of lincRNAs, we sought to analyze chromatin-state maps of 6 human cell types: hESC (10), 2 hematopoietic stem cells (CD133+ and CD36+) (15), T-cells (6), hLFs (1), and normal embryonic kidney (hEK). Using our previous computational approach, we identified K4-K36 domains that are well-separated from (i) the regions containing known protein-coding genes and all known classes of small noncoding RNAs in human and (ii) the orthologous regions of known protein-coding genes in mouse, rat, and dog. We also eliminated the orthologous regions of our previously identified mouse lincRNAs. We previously showed that, for similar cell types in mouse and human, lincRNA loci show cross-species conservation not only at the level of nucleotide sequence, but also with respect to the presence of K4-K36 domains (1). We found a total of 1,833 previously uncharacterized intergenic K4-K36 domains in these 6 human cell types (Fig. 1A; Table 1 in Dataset S1). We analyzed the coding potential of each such K4-K36 domain using the codon substitution frequency score (SI Methods), and found that <8% showed any evidence of protein-coding capacity (Fig. S1C) (16). After eliminating these cases, we were left with 1,703 loci encoding putative lincRNA genes.

To test whether these loci actually encode lincRNAs, we designed genomic tiling microarrays (at 10-base resolution) across 1,147 of the 1,703 loci (SI Methods) to determine their exonic structure. We hybridized poly(A)-amplified RNA from hES, brain, breast, hEK, hFF, hLF, K62, ovary, skin, spleen, testis, and thymus tissues. We analyzed the hybridization data using our previously reported peak-calling algorithm. This analysis revealed multieXonic RNA transcripts in 74% of the K4-K36 domains examined (Fig. 1A). There was an average of 4 exons per K4-K36 domain (total of 4,860 exons). We further focused on the 535 K4-K36 domains that were discovered in cell types in which RNA from the same cell type was hybridized. In these 3 cell types, RNA hybridization revealed multieXonic RNA transcripts in 85% of the tested loci; this detection rate is similar to that previously seen for K4-K36 domains corresponding to known protein-coding genes and lincRNA loci in mouse (1). Given that such a high proportion of the human K4-K36 domains tested were validated as encoding lincRNAs, we conclude that the vast majority of the full set of 1,703 loci encode bona fide lincRNAs. We then studied the evolutionary conservation of the lincRNA loci. For each exon, we calculated the extent of sequence conservation across 21 mammalian species as previously described (SI Methods) (1). Human lincRNAs showed evolutionary conservation at levels similar to those seen for the lincRNAs in our previous study (Fig. 1B; Table 2 in Dataset S1) (1).

Combining the 1,586 human orthologs of the lincRNA genes reported in our previous study with the 1,703 recently discovered human lincRNA genes identified in this study, our catalog of human lincRNA genes now includes 3,289 distinct loci. This catalog is certainly to be incomplete, because it is based on chromatin-state maps of only 10 cell types (4 mouse and 6 human). Nonetheless, it is possible to make a rudimentary estimate of the total number of human lincRNAs based on the observation that 73% of all protein-coding genes are expressed in at least 1 of the 10 cell types analyzed here. If a similar proportion applies to lincRNAs, the total number of human lincRNAs would be estimated to be ~4,500. If lincRNAs
To demonstrate the presence of HOTAIR, to test whether other coprecipitated RNA was then subjected to locus-specific RT-PCR, the total (non-cross-linked) nuclear extract was incubated with an antibody against the SUZ12 protein, a component of PRC2. This physical association was shown by RIP-PCR assay: lincRNA HOTAIR has been shown to physically associate with EZH2, components of PRC2 (8). As noted above, the mechanism by which lincRNAs function. As noted above, the many more tissues. A complete catalog will require generating chromatin-state maps across the total number could be considerably higher. Obtaining a complete catalog will require generating chromatin-state maps across many more tissues.

Many lincRNAs Are Associated with PRC2. We next explored the mechanism by which lincRNAs function. As noted above, the lincRNA HOTAIR has been shown to physically associate with PRC2 (8). This physical association was shown by RIP-PCR assay: total (non-cross-linked) nuclear extract was incubated with an antibody against the SUZ12 protein, a component of PRC2; the extract was precipitated with Protein-A-coupled beads; and the coprecipitated RNA was then subjected to locus-specific RT-PCR to demonstrate the presence of HOTAIR. To test whether other lincRNAs are also associated with PRC2, we designed a “RIP-Chip” assay (SI Methods) to assay many lincRNAs simultaneously (Fig. 2). Briefly, we used antibodies against the proteins SUZ12 and EZH2, components of PRC2 (9, 10). The antibodies were incubated with non-cross-linked nuclear extracts from 3 human cell types: HeLa cells, h lung (L), and h foot (F); these cell types were chosen because they have previously been shown to have distinctive epigenetic landscapes and diverse gene expression patterns (8). We analyzed the coprecipitated RNAs by hybridization to a custom “exon-tiling” array (at 10-base resolution), containing exons from ~900 human lincRNA loci and ~1,000 human protein-coding genes; the protein-coding genes were previously known to be expressed in at least 1 of the 3 cell types. In parallel, we carried out a mock control with a nonimmune rabbit IgG polyclonal antibody to assess nonspecific interactions that may occur in RIP.

To identify lincRNAs and protein-coding genes that are coprecipitated with each of the PRC2 components, we analyzed the hybridization data with a peak-calling algorithm that finds regions in which the signal from the RIP assay is significantly enriched over the signal from the mock controls (SI Methods). Regions were defined based on a maximum familywise error rate (FWER) < 0.05 (SI Methods and table 3 in Dataset S1) (1). Given that RIP assays are known to show considerable variability (with typical reproducibility of ~60%) (8), we performed several biological replicates for each cell type. We observed that ~76% of the genes detected in one replicate are also detected in a second replicate (hLF, 70%; hFF, 75%; HeLa, 83%; see table 3 in Dataset S1). As a positive control, we checked whether HOTAIR and XIST were detectably coprecipitated in our RIP-Chip data. Consistent with previous reports, HOTAIR coprecipitated with PRC2 in both HeLa and hFFs, but not in hLFs. Similarly, XIST, which is expressed only in female cells, was detectably coprecipitated in the hLF cells (which came from a female source), but not the hFF cells (which came from a male source) (Fig. 2). These results were consistent across all replicates.

In addition to the RIP assay, we also assayed expression patterns of lincRNAs and protein-coding genes on the custom exon-tiling array. We extracted total RNA from the same 3 human cell types (HeLa, hLF, and hFF), prepared poly(A+)-amplified cDNA, and hybridized the product to the exon-tiling array. Of the lincRNA genes on the array, we found that 47% were detectably expressed in at least 1 of the 3 cell types (HeLa, 25%; hLF, 37%; and hFF, 33%; see table 4 in Dataset S1). Consistent with the design of the tiling array, essentially all of the protein-coding genes were detectably expressed in the relevant cell type. Analysis of the RIP-Chip results, in conjunction with the expression analysis, suggests that a significant proportion of all lincRNAs expressed in 1 of these 3 cell types are physically associated with PRC2. Specifically, we find that ~30% of expressed lincRNAs are detected in at least 1 of the replicates. As a conservative estimate, we only considered lincRNAs detected in at least 2 replicates. Using this criterion, we observe that 24% of lincRNAs (114 of 469) expressed in 1 of the 3 cell types is detected as physically associated with PRC2 (Fig. 2; Fig. S2).

As an independent validation of the association with PRC2, we selected 5 lincRNAs that were detected in our RIP-Chip data as associated with PRC2 in both HeLa and hFF, and performed RIP-quantitative (q)PCR assays for these transcripts, using qRT-PCR. In all 10 tests (5 lincRNAs in 2 cell types), the results were confirmed (Fig. S3 and table 5 in Dataset S1). Notably, the RIP-qPCR assays showed a higher degree of enrichment than the RIP-Chip assays, consistent with the fact that arrays have a narrower dynamic range. As a validation that the associations of lincRNAs with PRC2 are specific, we tested whether the enrichment in the RIP-Chip experiment was simply a reflection of transcript abundance, which would suggest nonspecific interactions. We found no significant correlation between transcripts levels of the lincRNAs and their level of PRC2 enrichment ($r = -0.109, P > 0.99$; Fig. S4).

As a second approach to assess the specificity of PRC2 binding to lincRNAs, we examined the proportion of mRNAs bound to PRC2. In sharp contrast to the lincRNAs, very few of the mRNAs assayed in the RIP-Chip experiments showed physical association with PRC2. Of the 1,000 mRNAs represented on the array, only 16 (<2%) were detected in 2 replicates (Fig. 3A). We suspect that...
many of these 16 cases are artifacts, because only a small proportion (<1% of expressed mRNAs) are detected in 3 replicates. Thus, the proportion of transcripts associated with PRC2 is much higher for lincRNAs than for mRNAs. To demonstrate that this result is not simply due to a low concentration of mRNAs in the nucleus, we compared the concentration of lincRNAs and mRNAs in the nucleus (SI Methods). Although lincRNAs tend to have greater abundance in the nucleus than mRNAs, we find that the distributions of nuclear abundance of lincRNAs and mRNAs show substantial overlap, with at least 25% of mRNAs being expressed at levels comparable with the 50th percentile level for lincRNAs (Fig. S5). We also reasoned that lincRNAs associated with PRC2 should have significant representation in the nucleus. Therefore, we examined the abundance of lincRNAs in the nucleus, and we found that PRC2-bound lincRNAs show a significantly higher abundance in the nucleus than non-PRC2-bound lincRNAs (SI Methods and Fig. S5). We also performed RNA-FISH on HOTAIR, XIST, and additional lincRNAs detected as associated with PRC2. For all cases, the lincRNAs showed either exclusively nuclear or nuclear and cytoplasmic localization (Fig. 3F). Last, we explored whether a lincRNA that is expressed in 2 cell types (A and B), and associated with PRC2 in one cell type (A), is also associated with PRC2 in the second cell type (B). Considering all pairs of cell types, we found that the case for ~85% of lincRNAs (table 3 in Dataset S1). Collectively, these results provide strong evidence that a substantial portion (20–30%) of lincRNAs is specifically bound by PRC2 (Figs. 2 and 3A).

**Association of lincRNAs with Other Chromatin-Modifying Complexes.** Having found that many lincRNAs are associated with PRC2, we then explored whether they might be associated with other repressive chromatin-modifying complexes. We examined CoREST, a repressor of neuronal genes (17). We performed RIP-Chip using an antibody against CoREST in the same 3 cell types (HeLa, hLF, and hFF). Applying the analysis above, we found that 63 of the 469 lincRNAs expressed in HeLa cells were reproducibly detected as bound to CoREST (Fig. 3A; Fig. S6 and table 6 in Dataset S1). As with PRC2, <2% of mRNAs coprecipitated with CoREST. We note that ~60% of the lincRNAs associated with CoREST are not associated with PRC2 in HeLa cells, indicating that each complex has specific lincRNAs associated with it. The observation that 40% of the lincRNAs associated with CoREST are also associated with PRC2 suggests that the 2 complexes share some regulatory targets. Considering PRC2 and CoREST together, we find that ~38% of lincRNAs expressed in at least 1 of the cell types examined were reproducibly bound to at least 1 of the 2 complexes (180 of 469 expressed). This proportion is likely to be an underestimate, because we only count lincRNAs that were detected in at least 2 replicates; the proportion could be as high as 52%. These results raise the possibility that lincRNAs may be associated with additional chromatin-modifying proteins. Intriguingly, preliminary results involving RIP-Chip with SMCX, a histone H3K4me3 demethylase, suggest that this enzyme also binds a significant number of lincRNAs. We also tested whether chromatin proteins themselves (rather than chromatin-modifying proteins) are associated with lincRNAs. Specifically, we performed RIP-Chip with antibodies against the modified histones H3K27me3 and H3K4me2. We found no significant enrichment of lincRNAs (Fig. 2). These findings are consistent with other studies that identified XIST to coprecipitate with PRC2, but not H3K27me3, despite their immediate nuclear proximity (11).

**Functional Evidence That lincRNAs Act Through the PRC2 Pathway.** Having found that a substantial fraction of lincRNAs is physically associated with PRC2, we sought evidence that they have a functional role in polycomb-mediated repression. Previously, we have shown that depletion of HOTAIR causes up-regulation of genes normally repressed by PRC2 (8). To test whether other lincRNAs have a similar effect, we studied HOTAIR and 5 additional lincRNAs found to be associated with PRC2. For each of these 6 lincRNAs, we designed pools consisting of 4 siRNAs targeting each lincRNA (SI Methods). We also used standard control siRNA pools that do not correspond to any human sequence. We transfected the siRNA pools into hLF (3 pools), hFF (3 pools), or both (1 pool), with each experiment performed in duplicate. We measured the level of lincRNA knock-down by qRT-PCR, and compared the results to the control siRNA pool; we only used experiments in which we achieved >2-fold depletion (Fig. S7).

We hybridized the total RNA from these experiments to standard gene-expression arrays to measure the resulting changes in gene expression. Specifically, for each of the 6 lincRNAs, we determined the gene sets (S1, S2, …, S6) that were up-regulated relative to the control siRNA pools [at a false discovery rate (FDR) < 0.1]. These sets contained between 103 and 352 genes (Fig. 4A, Fig. S8A). The sets of genes affected by each lincRNA did not show significant overlap, suggesting that each lincRNA has distinct target sets. We searched for, but found no common motifs enriched among the up-regulated genes for each lincRNA. However, given the small number of target genes and the inability to...
A dashed line denotes FDR. Results are shown from knockdown experiments in hLFs (gray) and in hFFs (black). An enrichment score in red and down-regulation in blue. Of a gene in the lincRNA gene set is indicated by tick marks (below each enrichment score plot). We selected TUG1 as 1 of the 6 lincRNAs above that we depleted with siRNA pools. Depletion of TUG1 led to significant up-regulation of 120 genes, which were strongly enriched for those involved in cell-cycle regulation (regulation of mitosis, spindle formation, and cell-cycle phasing) (Fig. 4B; table 7 in Dataset S1). Thus, TUG1 is induced by p53, binds to PRC2, and has a role in repressing specific genes involved in cell-cycle regulation. Interestingly, p53 is well known to cause both activation and repression of many genes. Although p53 has been shown to be a direct activator of many genes, the mechanism of p53-induced repression remains unknown. Our results suggest the intriguing hypothesis that TUG1, and perhaps other lincRNAs, may function as downstream repressors in transcriptional pathways.

**Discussion**

It is becoming clear that the mammalian genome encodes thousands of lincRNAs that are highly conserved and, thus, biologically functional (1, 27). The results of our previous article (1) and this study together identify 3,289 lincRNAs, and suggest that the total may be in the range of \( \sim 4,500 \). Expression patterns suggest that these lincRNAs are involved in diverse biological processes, including cell-cycle regulation, innate immunity, and ES pluripotency, but the mechanisms by which they have their roles were completely unknown. Inspired by studies of the lincRNAs HOTAIR (8) and XIST (11), we investigated the idea that many lincRNAs are involved in the establishment of chromatin states. In this study, we report that a substantial proportion (24%) of lincRNAs expressed in a cell type are physically associated with the repressive chromatin-modifying complex PRC2, and the proportion is even larger (38%) when additional chromatin-modifying proteins (CoREST and SCMX) are included. Thus, it seems likely that a significant fraction of lincRNAs will be associated with chromatin-modifying proteins. Beyond the physical association, our functional analysis demonstrates that siRNA-mediated depletion of these lincRNAs results in preferential derepression of PRC2 regulated genes at distant loci, consistent with a trans-acting mechanism. Collectively, these results suggest that many lincRNAs collaborate with chromatin-modifying proteins to repress gene expression at specific loci.

There is a growing body of literature from yeast to mammals suggesting the noncoding RNAs have an important role in chromatin-state formation (4, 21). In *Schizosaccharomyces pombe*, a
have been shown to have an important role in the establishment of heterochromatin formation over centromeric repeats (22). Similarly, short RNAs has been shown to have an important role in heterochromatin process known as RNA induced transcriptional silencing (RITS).

HOTAIR serves as a downstream repressor in the HOXA13 transcriptional network. This model raises many mechanistic questions, including (i) whether most lincRNAs associated with chromatin-modifying complexes directly guide the complexes to specific loci, and (ii) if so, how the guidance is accomplished (e.g., by direct base pairing at specific sequence motifs).

Our experiments have focused on chromatin-modifying complexes that add repressive chromatin marks. It is possible that many additional lincRNAs are associated with chromatin-modifying complexes that confer activating modifications, as has been recently reported in a few cases (14). These questions can be addressed by performing RIP experiments with a wide range of antibodies across a wide range of cell types, to create a catalog of lincRNA-protein interactions. Last, although we have found that a substantial proportion of lincRNAs are associated with repressive chromatin-modifying complexes, we do not mean to suggest that all lincRNAs necessarily function in this manner. There may be classes of lincRNAs that function in entirely different ways. For example, the lincRNAs NEAT1 and NEAT2 have been recently shown to be important in the formation of paraspeckles (25), and the lincRNA NRON has a role in repression nuclear import (26). It is possible that additional lincRNAs have roles in these and numerous other cellular pathways. The full range of biological diversity of lincRNAs and their mechanisms clearly remains to be explored.

Materials and Methods

Identification of K4-K36 domains was performed as previously described (1). RIP was performed as previously described (8) with some modifications. Hybridization to tiling arrays was performed as previously described (1). For detailed methods, see SI Methods. The data concerning the lincRNAs and the experiments here are available in Dataset S1 and public databases. All microarray data including RNA hybridization to tiling arrays, RIP-Chip experiments, and gene expression profiling of lincRNA knockdowns is deposited at the Gene Expression Omnibus (GEO) under accession no. GSE16226.

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