

Post-transcriptional splicing can occur in a slow-moving zone around the gene

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Abstract

Splicing is the stepwise molecular process by which introns are removed from pre-mRNA and exons are joined together to form mature mRNA sequences. The ordering and spatial distribution of these steps remain controversial, with opposing models suggesting splicing occurs either during or after transcription. We used single-molecule RNA FISH, expansion microscopy, and live-cell imaging to reveal the spatiotemporal distribution of nascent transcripts in mammalian cells. At super-resolution levels, we found that pre-mRNA formed clouds around the transcription site. These clouds indicate the existence of a transcription site proximal zone through which RNA move more slowly than in the nucleoplasm. Full-length pre-mRNA undergo continuous splicing as they move through this zone following transcription, suggesting a model in which splicing can occur post-transcriptionally but still within the proximity of the transcription site, thus seeming co-transcriptional by most assays. These results may unify conflicting reports of co-transcriptional versus post-transcriptional splicing.

eLife assessment

This **fundamental** study addresses a long-standing mystery in splicing regulation: does splicing occur co- or post-transcriptionally? The authors provide **compelling** evidence demonstrating that splicing can occur post-transcriptionally at a transcription site proximal zone, changing the way we think about splicing.

Introduction

The mRNA transcribed by many eukaryotic genes are spliced, a process in which the intronic RNA are removed and the exonic RNA are joined together to form the ultimate mature mRNA. A major question in the field is how tightly associated the processes of transcription and splicing are. Some work suggests that splicing occurs very shortly after the RNA polymerase transcribes a particular splice junction (1–4), while other work suggests that many pre-mRNAs are fully transcribed before splicing occurs (5–9). The relative spatial locations of nascent pre-mRNA, fully transcribed pre-mRNA, and mature mRNA species have the potential to directly reveal where—and consequently in what order—the processes of transcription and splicing occur. However, to date, the use of molecular imaging to systematically measure the locations of these partially-processed RNA intermediates has been limited in scope, interrogating either single-intron reporter genes or single introns within endogenous genes (7, 10–11).

In lieu of direct visualization, many studies have used biochemical fractionation to infer the location of various intermediates (6, 12–17). Fractionation methods separate cellular RNA into different compartments, such as the putatively chromatin associated RNA, nucleoplasmic RNA, and cytoplasmic RNA (13, 18). The implicit assumption made by such fractionation-based methods is that the RNA species in the “chromatin fraction” represent nascent pre-mRNA that are tethered to the gene body by the RNA polymerase II itself, and that once the pre-mRNA disengages with RNA polymerase II, it immediately moves directly into the nucleoplasm. Under these assumptions, any splicing observed in the chromatin fraction would be assumed to be co-transcriptional. However, this assumption may not hold; it is possible that pre-mRNA remains in a chromatin associated compartment for some time after transcription completes, and thus splicing observed in the chromatin compartment may in fact still be post-transcriptional (19). Some groups have further purified nascent RNA via metabolic labeling or by using RNA Polymerase II antibodies, but these methods still have the potential to co-purify mature RNA (20). Ultimately, such alternative explanations are difficult to eliminate without an independent and explicit verification of which RNA intermediates reside in particular compartments.

Advances in RNA imaging have enabled researchers to image RNA intermediates with single-molecule resolution, both in fixed and living cells (7, 10–11, 21–23). Imaging using probes targeting both exonic and intronic regions of RNA has revealed bright nuclear foci that represent nascently transcribing RNA (11, 23). The general lack of intronic signal away from these transcription sites has been taken as evidence for co-transcriptional splicing, with notable examples of post-transcriptional splicing at speckles being observed in special cases (11). However, owing to the diffraction limit for optical microscopy, it has been difficult to visualize RNA intermediates in the immediate vicinity of the gene undergoing transcription, thus making it difficult to observe whether RNA are still actively being transcribed during splicing or remain at the site of transcription for some time after transcription is complete. Since splicing would appear to occur in the “chromatin fraction” in both of these scenarios, it is possible that much of splicing actually occurs in this transcription-proximal region after transcription is complete (“proximal post-transcriptional splicing”). Indeed, recent live-cell imaging methods showed that the splicing of a reporter gene is 85% post-transcriptional (7), suggesting the latter possibility, but as RNA from endogenous genes may be processed differently, the use of reporter genes leaves open the question of when endogenous genes undergo splicing relative to their transcription.

Here, we designed probes to comprehensively interrogate the spatial localization of several RNA intermediates using a combination of RNA FISH and expansion microscopy (24–25), allowing for visualization of newly-transcribed RNA at high resolution. We found that the proportion of splicing that occurs post-transcriptionally varies from intron to intron within a single gene, but that all endogenous genes we tested displayed at least some degree of post-transcriptional splicing. We also employed expansion microscopy and live cell imaging to demonstrate that newly synthesized RNA dwell and undergo continuous splicing near the site of transcription after

transcription is complete within a proximal slow-moving zone. These RNA are untethered to the site of transcription and eventually diffuse into either the nucleoplasm or near nuclear speckles. These results suggest a model for splicing dynamics that unifies existing data.

Results

At least one intron of each observed endogenous gene is spliced post-transcriptionally

The extent to which splicing is coupled to transcription, both in space (distance from transcription site) and time (time since transcription has begun) has been difficult to measure. To address this question, we directly visualized the locations of spliced and unspliced RNA relative to the site of transcription in situ using single molecule RNA FISH (26–27), to simultaneously fluorescently label the exons and several individual introns for a number of genes of interest: *CPS1*, *EEF2*, *TM4SF1*, and *FKBP5*. *CPS1* was chosen because it is a long and highly expressed gene. *EEF2* was chosen because it is a highly expressed housekeeping gene. *TM4SF1* was chosen because it is highly expressed and sequencing data suggested it was highly post-transcriptionally spliced (see Methods for details). Finally, *FKBP5* was chosen because it is inducible in A549 cells by application of dexamethasone.

By distinguishing the separate fluorescent signals from probes bound to exons and introns, we could visualize splicing intermediates (represented by colocalized intron and exon spots) relative to the site of transcription (represented by bright colocalized intron and exon spots) and fully spliced products (represented by exon spots alone). We were particularly interested in visualizing the location of splicing intermediates in order to distinguish between two possibilities: 1) an intron from a pre-mRNA being spliced out at the site of transcription and 2) an intron from a pre-mRNA being spliced out away from the site of transcription (**Figure 1A**; right; i and ii versus iii). Observing spliced RNA at the site of transcription could represent RNA that is spliced either co-transcriptionally (tracking along with or shortly behind the polymerase; **Figure 1Ai**) or proximally post-transcriptionally (near the site of transcription but after the process of transcription has been completed) (**Figure 1Aii**). However, observing pre-mRNA with unspliced introns that were sufficiently far away from the site of transcription such that they could no longer be attached to the location of the gene itself would suggest that that intron must be spliced out post-transcriptionally (distal post-transcriptional splicing, **Figure 1Aiii**).

To determine what fraction of splicing occurred far from the site of transcription, we first needed to classify each colocalized exon and intron spot as either a transcription site or a dispersed pre-mRNA. We computationally identified spots for both introns and exons of a particular gene, then each intron spot that was within 0.65µm of an exon spot was designated a colocalized exon and intron spot (0.65µm is the 75th percentile of mRNA lengths determined by measuring the distance from 5' to 3' signal; **Figure 1B**, see Supplementary Figure 1E for mRNA lengths), which we assumed represents at least one nascent pre-mRNA (potentially several nascent pre-mRNA when found at the site of transcription). We chose this colocalization threshold such that at least 78% of exons (depending on the gene, *CPS1* = 78%, *EEF2* = 85%, *TM4SF1* = 87%) colocalized with other exons of the same gene in the cytoplasm; however, varying this threshold from 0.13µm (one pixel) to 2.6µm (20 pixels) did not significantly change dispersal patterns (Supplementary Figure 1C). Intron spots that did not colocalize with an exon spot were presumed to be degradation products or non-specific background and were discarded (these were generally <25% of intron spots; **Table 1**). We used an intensity threshold to categorize each colocalized exon and intron spot as either a transcription site or a dispersed pre-mRNA (**Figure 1B-C**, see Supplementary Figure 1A-B for the scheme for the classification of transcription sites). We also tried several other methods for choosing transcription sites, all of which showed qualitatively similar results (Supplementary Figure 1A), showing that the detection of dispersal is not dependent on the choice of method. Our

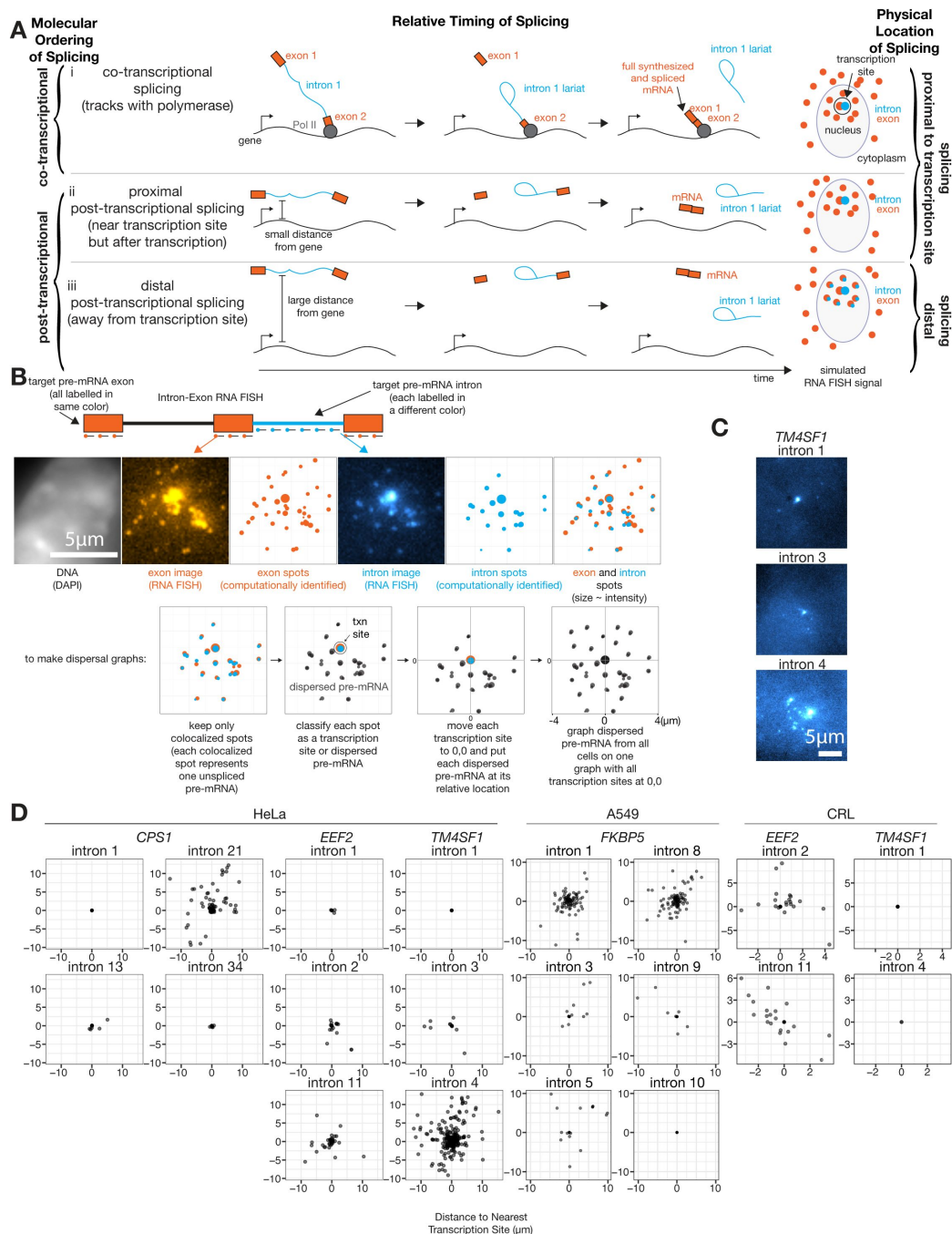


Figure 1

At least one intron from every tested endogenous gene is post-transcriptionally spliced.

A. Schematic depicting three categories of splicing.

B. Schematic depicting RNA FISH method and translation of RNA FISH images into dispersal graphs. Computed spots are calculated by fitting a gaussian to the distribution of intensity signals and pinpointing the center of that gaussian at sub-pixel resolution. Gene depicted is *FKBP5*.

C. Example images of dispersed (intron 4) and not dispersed (introns 1 and 3) transcription sites, via RNA FISH. Each image is a max merge of 30 optical Z sections, 0.3μm step distance.

D. Graphs indicating dispersal distance or the distance of each detected pre-mRNA to its nearest transcription site. Leftmost graphs of *CPS1*, *EEF2*, and *TM4SF1* data are from HeLa cells, *FKBP5* data is from A549 cells after 8 hours in dexamethasone, rightmost graphs of *EEF2* and *TM4SF1* data are from CRL-2097. All scale bars represent 5μm unless otherwise noted.

chosen strategy likely grouped together the signal from multiple pre-mRNA (introns and exons) at the transcription site, rendering them indistinguishable at this level of spatial resolution; we separately analyzed these transcription sites further later (see [Figure 2](#)).

We then calculated the distance of each dispersed pre-mRNA from the nearest transcription site for all cells, yielding population-wide measurements of dispersal per intron ([Figure 1D](#)). We found that for the genes *CPS1*, *EEF2*, *TM4SF1*, and *FKBP5*, at least one intron was present in dispersed pre-mRNA in both transformed cell lines (HeLa and A549) and non-transformed cells (CRL-2097) (3-5 introns tested per gene, [Figure 1D](#)), suggesting that pre-mRNA dispersal is a generic feature of transcription and splicing that is not dependent on the particular cell line used. However, we found that the dispersal patterns for any one particular intron were not necessarily consistent between HeLa and CRL-2097 cells, suggesting splicing patterns may be influenced by cellular context. The presence of intermediates away from the site of transcription showed that for all the genes we tested, some introns were spliced post-transcriptionally and away from the gene body itself. We never observed introns in cytoplasmic mRNA, suggesting that all of these introns are eventually spliced out (i.e., transcripts with retained introns cannot be exported from the nucleus). We observed a large range in the number of pre-mRNA observed per cell (from 0 to ~20), which also varied from intron to intron (Supplementary Figure 1B).

As a corroboration of RNA FISH dispersal as a metric to quantify distal post-transcriptional splicing, we turned to nascent RNA sequencing, using a combination of metabolic labeling and cellular fractionation to capture RNAs that are both newly synthesized and co-sediment with the chromatin fractions of cells ([6](#)) (Supplementary Figure 2). We found a modest association between splicing index and both mean dispersal and transcription site size, suggesting that sequencing of nascent RNA was at least consistent with RNA FISH assessments of distal post-transcriptional splicing; however, more work is required to fully establish a quantitative correspondence between the metrics.

It is possible that pre-mRNA away from the transcription site are ultimately degraded without ever being spliced and thus represent an alternative “dead end” fate for the pre-mRNA rather than an intermediate on the path to a mature mRNA. This alternative possibility is difficult to eliminate with data relying on a snapshot in time, and hence studies using sequencing or fixed cell imaging (such as ours) suffer from this limitation. The further development of live cell imaging capable of tracking individual mRNA throughout their lifetime may help resolve these issues. However, we do note that pre-mRNA contain fewer introns as they increase in distance from the transcription site (Supplementary Figure 1G), which is at least consistent with our assumption that these introns are spliced as they travel away from the transcription site. Furthermore, pulse-chase experiments have shown that the “yield” of splicing events is high for mRNA, suggesting that most pre-mRNA do not go down a dead-end pathway ([28](#)–[29](#)). Given this assumption, the dispersion we observe suggests that at least one intron of each observed gene is spliced partly post-transcriptionally.

Different introns within the same gene are spliced largely independently of each other

In these experiments, we observed individual pre-mRNA with some but not all introns retained, and wondered whether these introns could be spliced in any order. Thus, we quantified the number of transcript intermediates that contained different introns in the same RNA molecule. For each RNA containing a pair of introns A and B, there are two alternative routes to generate a fully spliced mature mRNA: either intron A is spliced before intron B, or intron B is spliced before intron A. Were the splicing of these introns ordered, for instance if B always gets spliced after A, then we would expect the vast majority of partially spliced transcripts to contain intron B only, and that very few transcripts would contain intron A without intron B. We thus identified and counted partially spliced transcripts which contain only one intron without the other ([Table 2](#)).

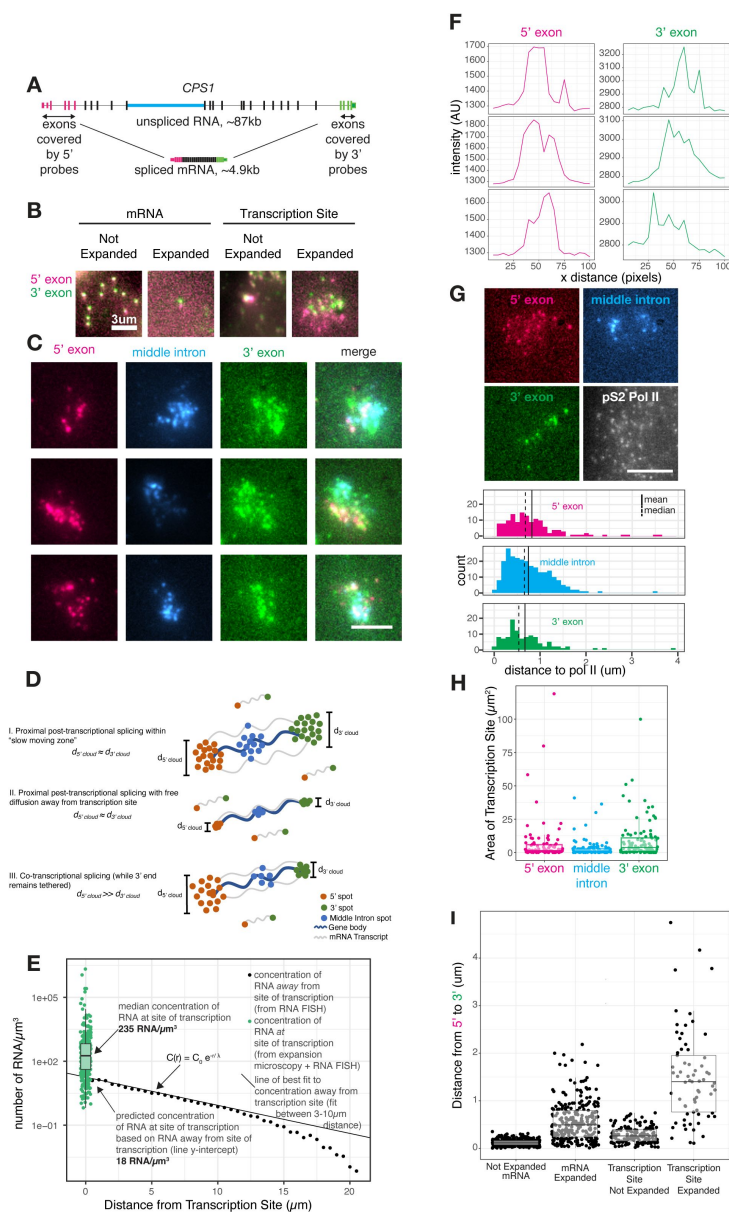


Figure 2

Transcripts dwell at the site of transcription after transcription is completed.

A. Gene and probe position diagram for CPS1 pre-mRNA and mRNA.

B. Example images of RNA FISH for CPS1 before and after expansion microscopy for individual mRNA and transcription sites (in HeLa cells, different representative cells shown in each image).

C. Example images of 5', 3', and middle intron CPS1 RNA FISH after expansion.

D. Schematic depicting simulated RNA FISH signal for three potential scenarios: a slow moving zone around the site of transcription (I), free diffusion away from the transcription site (II), or co-transcriptional splicing of tethered transcripts (III).

E. Schematic depicting RNA FISH signal for diffusion or a slow moving proximal zone for completed (but not necessarily spliced) transcripts

F. Line scans of fluorescence intensity (arbitrary units) from transcription sites like in C.

G. Example images of co-IF (polymerase II) and RNA FISH for CPS1 after expansion. Quantification of images like that in G, and others, representing distance from each RNA spot to the nearest polymerase II IF spot.

H. Graph depicting area (in pixels) of polygons drawn around individual transcription sites after expansion.

I. Distance from 5' to 3' of expanded and unexpanded mRNA and transcription sites, as detected by CPS1 RNA FISH. This distance was calculated using nearest neighbors with replacement. All scale bars represent 5 μm unless otherwise noted. All expanded images and calculations are shown in expanded space scale (reduce by 4.65X to yield original space scale).

Gene	Intron #	# of Probes	% coloc with exon	mean dispersal (um)	% of intensity that is not local to txn site
CPS1	1/37	10	75.5814	0	0
CPS1	13/37	12	88.2716	0.067485645	1.337543
CPS1	21/37	24	74.71264	2.0966995	27.7981585
CPS1	34/37	16	88.88889	0.03229656	1.952689
EEF2	1/14	21	91.66667	0.93700431	15.69285
EEF2	2/14	21	91.73554	0.41633783	6.482196
EEF2	11/14	13	94.08867	1.67628235	24.386486
TM4SF1	1/4	17	98.59155	0	0
TM4SF1	3/4	24	94.78261	0.34731502	2.422979
TM4SF1	4/4	24	87.84648	3.00480873	47.094267
FKBP5**	1/10	32	77.52809	1.2286272	22.451107
FKBP5**	3/10	32	94.64286	0.4514456	3.692255
FKBP5**	5/10	32	73.4375	2.852407	6.836791
FKBP5**	8/10	32	81.41593	1.4870159	33.077603
FKBP5**	9/10	14	93.89671	0.5677152	3.679758
FKBP5**	10/10	11	71.60494	0	0

** reflects values after 8 hours in dexamethasone

Table 1

Per probe set dispersal and percent of splicing that occurs distally post-transcriptional

To estimate the confidence in our measurements, we labeled the fourth intron of *TM4SF1* with two colors; in this case, any transcripts detected as containing one color without the other must be due to technical reasons, thereby setting a “noise floor” (see methods for details). The dye used to label each intron also did not affect these measurements (*FKBP5* introns 8 and 9 dye-swap, rows 13 and 14 of **Table 2**). It was also difficult for us to discriminate between models if both introns are spliced so rapidly that intermediates are not observed.

We observed a variety of patterns of splicing intermediates, some showing strong ordering (94% of intermediate transcripts of *FKBP5* contain intron 8 without intron 5) and some showing a lack of ordering (50.3% of intermediate transcripts of *EEF2* contain intron 2 without intron 1). Lack of ordering between introns did not depend on distance between them, with no ordering observed for the neighboring *EEF2* introns 1 and 2 as well as the distant *CSP1* introns 1 and 34.

Overall, our data support a model in which splicing of different introns within the same primary transcript can occur in any order.

Transcripts are untethered to the transcription site and move through a slow-moving transcription site proximal zone where splicing occurs after transcription is completed

While conventional single molecule RNA FISH allowed us to determine what portion of splicing is happening post-transcriptionally and far from the site of transcription (**Table 1**, Supplementary Figure 1D), the resolution limits of conventional light microscopy made it impossible to distinguish whether transcripts are being spliced during the process of transcription (co-transcriptional) or after the completion of transcription but before the pre-mRNA moves away from the site of transcription (proximal post transcriptional). Conventional light microscopy cannot easily distinguish these possibilities because all the RNA at or near the site of transcription are sufficiently close together that they are typically only visible as one large transcription site spot (see **Figure 1B** for example). It is therefore possible that lower mobility of transcripts near the transcription site may lead to the classification of proximal post transcriptional splicing as co-transcriptional when using low-resolution imaging methods.

We thus used expansion microscopy to physically expand the transcription site (by around 4.6x, Supplementary Figure 3) followed by staining by RNA FISH (**Figure 2A**) and imaging, thereby separating the single bright transcription site blob into visually distinct individual RNA intermediates at the site of transcription (**Figure 2B**) (24–25). We labeled the 5' and 3' regions, as well as one interior intron, of the gene *CPS1*, for which the unspliced transcript would be quite long (~87kb) but the spliced transcript is comparatively short (~5kb) (**Figure 2A**). This labeling scheme allowed us to measure the locations of 5' exons, a middle intron, and 3' exons of pre-mRNA or processed mRNA in the vicinity of the expanded transcription site. Based on previous work (24), we expected expansion of transcription sites to be isotropic. To confirm isotropic expansion in our system, we imaged the same cell before and after expansion with and without a perturbation that changed the localization of introns (pladeinolide B treatment, which inhibits splicing and causes the introns of *EEF2* to form a well-defined blob, see **Figure 4**) and indeed observed that both the transcription site and the blob of *EEF2* introns expanded isotropically (Supplementary Figure 3B, displaying the same cells before and after expansion). To further ensure that expansion microscopy did not alter the morphology of the transcription site, we confirmed that the transcription sites in expanded samples were the same size as those imaged using stochastic optical reconstruction microscopy (STORM) (30), a superresolution imaging technique that does not rely on expansion (Supplementary Figure 4A-B).

Lower mobility of transcripts near the site of transcription may lead to a buildup of multiple transcripts in the vicinity of the transcription site. Upon expanding, labeling, and imaging, we indeed observed that the 5', 3', and middle intron probe signals formed small clouds where we had

Gene	Intron A (5')	Intron B (3')	Total Captured Transcripts	Total Intermediate Products	% that splice Intron A first	% that splice Intron B first
EEF2	Intron 1	Intron 11	66272	427	42.85714286	57.14285714
EEF2	Intron 2	Intron 1	55769	270	50.37037037	49.62962963
EEF2	Intron 2	Intron 11	42077	190	63.68421053	36.31578947
TM4SF1	Intron 1	Intron 4	20412	406	88.42364532	11.57635468
TM4SF1	Intron 1	Intron 3	30345	129	58.91472868	41.08527132
TM4SF1	Intron 3	Intron 4	26041	725	87.44827586	12.55172414
TM4SF1	Intron 4evens**	Intron 4odds**	25726	122	60.6557377	39.3442623
FKBP5	Intron 3	Intron 10	4534	213	19.24882629	80.75117371
FKBP5	Intron 3	Intron 5	4260	164	65.24390244	34.75609756
FKBP5	Intron 1	Intron 8	155	69	73.91304348	26.08695652
FKBP5	Intron 5	Intron 8	2745	284	94.01408451	5.985915493
FKBP5	Intron 8	Intron 9	3045	367	5.449591281	94.55040872
FKBP5	Intron 8\$	Intron 9\$	2648	273	11.72161172	88.27838828
FKBP5	Intron 9	Intron 10	2025	33	72.72727273	27.27272727
FKBP5	Intron 1.2	Intron 1.1	4049	262	47.32824427	52.67175573
CSP1	Intron 1**	Intron 13**	22960	31	48.38709677	51.61290323
CSP1	Intron 13	Intron 21	17032	62	77.41935484	22.58064516
CSP1	Intron 13**	Intron 34**	21977	47	53.19148936	46.80851064
CSP1	Intron 1	Intron 21	20879	95	70.52631579	29.47368421
CSP1	Intron 21	Intron 34	19775	76	25	75
CSP1	Intron 1	Intron 34	13640	35	57.14285714	42.85714286

\$ = dye swap experiment

** = measurements below noise threshold (see methods)

Table 2

Percent of intermediate products that splice in one order versus the other

previously observed the tight transcriptional focus (**Figure 2C** [↗](#), quantified in Supplementary Figure 4C). Of note, the expanded transcription site contains multiple 3' and 5' spots, while expanded cytoplasmic mRNA contain one 3' and 5' spot, indicating the presence of multiple transcripts at the transcription site as opposed to a single transcript broken into multiple parts as a result of expansion (**Figure 2B** [↗](#)). The variable brightness between spots in expanded versus unexpanded samples may have been due to variable lengths of transcribing RNA or RNA fragmentation during expansion, as each RNA is likely linked to the gel in multiple locations.

The presence of these clouds precluded any model of immediate, free movement of the transcript away from the RNA polymerase upon completion of transcription. If transcripts freely diffused away right after their transcription, then a mathematical model would predict an exponential decrease in pre-mRNA concentration with increasing distance away from the transcription site ([31](#) [↗](#)) (see methods for details, **Figure 2D** [↗](#) scenario II). We fit such a model to pre-mRNA that were between 3 and 10 microns away from the site of transcription, in which range the diffusion model fit well. From these data, we were able to estimate what the concentration should be at or near the transcription site given the free diffusion model (essentially, the y-intercept of the concentration curve). We found that the predicted concentration (18 molecules per cubic micron) was far lower than the actual concentration (235 molecules per cubic micron) in the vicinity of the transcription site measured by expansion microscopy (**Figure 2E** [↗](#)). This high concentration in the “cloud” is not consistent with free diffusion subsequent to the completion of transcription (**Figure 2D** [↗](#) scenario II), but is compatible with the existence of a distinct “proximal zone” surrounding the transcription site through which pre-mRNA move more slowly than in the more distant nucleoplasm (**Figure 2D** [↗](#) scenario I).

We wondered whether the pre-mRNA present in this zone were partially spliced intermediates or full pre-mRNA, the former signifying co-transcriptional splicing and the latter signifying predominantly post-transcriptional splicing. If splicing occurred concurrently or shortly after transcription, then we would expect to see a potential cloud of 5' ends but a tight spot of 3' ends corresponding to the point of transcriptional termination (**Figure 2D** [↗](#) scenario III). However, if splicing occurred some time after the entire full length pre-mRNA was transcribed, one would expect to see separate clouds for both the 5' and 3' ends, representing pre-mRNAs that have completed transcription and are slowly diffusing through the proximal zone (**Figure 2D** [↗](#) scenario I). We observed similarly-sized clouds for both the 5' and 3' ends of the pre-mRNA in the proximal zone. Since RNA polymerase II can transcribe beyond the poly-A site ([32](#) [↗](#)–[33](#) [↗](#)), it may be possible that observed clouds are a result of transcripts tethered beyond the 3' poly-A site of the gene body. To eliminate this possibility, we performed RNA FISH for a sequence 2kb beyond the 3' poly-A site of *CSP1*. We found that the 3' and post 3' transcription sites were also approximately the same size, suggesting these transcripts are not tethered to chromatin as splicing is occurring (Supplementary Figure 4D-F).

Based on the size of these clouds, we estimated the diameter of this cylindrical slow-moving zone around the gene body to be around 0.3 microns (**Figure 2F** [↗](#), see methods for calculations). This width does not depend on the length of an individual transcript or gene body, but rather extends radially outward from the gene body.

We concluded that pre-mRNA are not spliced immediately upon transcription, but rather that a large proportion of the splicing occurs post-transcriptionally while the pre-mRNA were moving through the proximal zone. (Splicing that occurred while in this zone would appear to be co-transcriptional by conventional single molecule RNA FISH.) To further test for the occurrence of splicing while pre-mRNA were in this zone, we simultaneously labeled an intron while labeling the 5' and 3' ends of the pre-mRNA. Similar to the signals from the 5' and 3' ends, the intronic signal also formed a cloud, showing that splicing has not yet been completed as the pre-mRNA move through this proximal zone (**Figure 2G** [↗](#), H). Furthermore, the clouds of the 5' and 3' ends

of the pre-mRNA are typically non-overlapping and are further apart than the mature mRNA we found in the cytoplasm, suggesting that these clouds do not represent fully mature, spliced mRNA (**Figure 2I** [↗](#)).

We next wanted to confirm the presence of this slow-moving zone in a live cell as transcription is actively taking place, as this method does not require manipulation through fixation or expansion. We obtained data from cells in which the 3' UTR of the gene *TFF1* was labeled with MS2-GFP (**34** [↗](#)), allowing us to observe the geometry of transcription sites in living cells. If transcripts immediately and rapidly diffused away from the transcription site after synthesis at the same diffusion rate as in the nucleoplasm, then the 3' end of the transcripts would form a tight, diffraction limited spot at the site of transcription, much like the 3' ends of individual transcripts we detected by mRNA FISH (**Figure 2B** [↗](#)). (Note that the limit of detection of MS2-GFP was such that only transcription sites, presumably with multiple transcripts on them, would be detectable; hence, individual mRNA were not detectable.) If, on the other hand, there were a gene-proximal zone in which diffusion was slower, one would expect to see primary transcripts at a higher concentration within the zone (see **Figure 2E** [↗](#)). This higher concentration would translate into a cloud of primary transcripts visible as a blob that was larger than the diffraction limit, reflecting the size of the putative slow moving zone. Thus, the presence of transcription site spots larger than the diffraction limit would be an indicator of the presence of a cloud of primary transcripts and hence a slow-moving zone around the site of transcription.

It is challenging to rigorously discriminate between a diffraction limited spot and a blob with larger spatial extent based solely on the area of the fluorescent region because the thresholds chosen in determining area can be somewhat arbitrary, and the underlying data is often noisy. Hence, we instead used eccentricity (a measure of deviation from a perfect circle, ranging from 0 to 1) as a means to distinguish diffraction limited spots from blobs, reasoning that blobs larger than the diffraction limit could potentially be asymmetric, thus exhibiting increased eccentricity as compared to pure diffraction limited spots. Visually, several images showed evidence for such asymmetry (**Figure 3A-C** [↗](#)). We quantified the asymmetry by measuring the eccentricity for 205 transcription site images from 36 total temporal transcription site tracks (**Figure 3D** [↗](#)). We found that the majority of images (141 of 205) showed evidence of substantial eccentricity (defined as eccentricity > 0.6) (**Figure 3C** [↗](#)). As these sites are unambiguously larger than a diffraction limited spot, we concluded that RNA were likely retained at the site for some time following transcription, corroborating the existence of the slow-moving zone.

It should be noted that not all transcription site images appeared eccentric. Possible reasons are that the transcription burst duration was short enough that there was not time for a buildup of pre-mRNA in the slow moving zone, or that the blob happened to grow in a symmetric fashion, or that the three-dimensional orientation of the asymmetry was such that it was not detectable in the single x-y plane of the microscope.

Similarly, in our expansion microscopy data, the relative positions of the 5', 3', and middle intron clouds adopted a wide variety of conformations, suggesting that the linear genomic order of the pre-mRNA may not be strictly maintained during transit through the proximal zone (**Figure 2C** [↗](#)). The length of each intron, as well as the strength of its 3' and 5' splice site, did not affect its dispersal from the transcription site, suggesting that transcript size and splice site sequence are not major contributors to the dynamics of the slow moving zone (Supplemental Figure 5, Supplementary Table 2). Also, neither the 5' exon nor 3' exon signals overlapped with actively elongating RNA Polymerase II immunofluorescence signals (see methods), potentially suggesting the relatively few mRNA spots that are quite close to RNA polymerase II signal are undergoing active transcription, while the majority of pre-mRNA in the slow moving proximal zone are not being actively transcribed (**Figure 2G** [↗](#)). It is important to note, however, that we do not label the entirety of the pre-mRNA molecule, nor can we be sure that we can detect single molecules of RNA

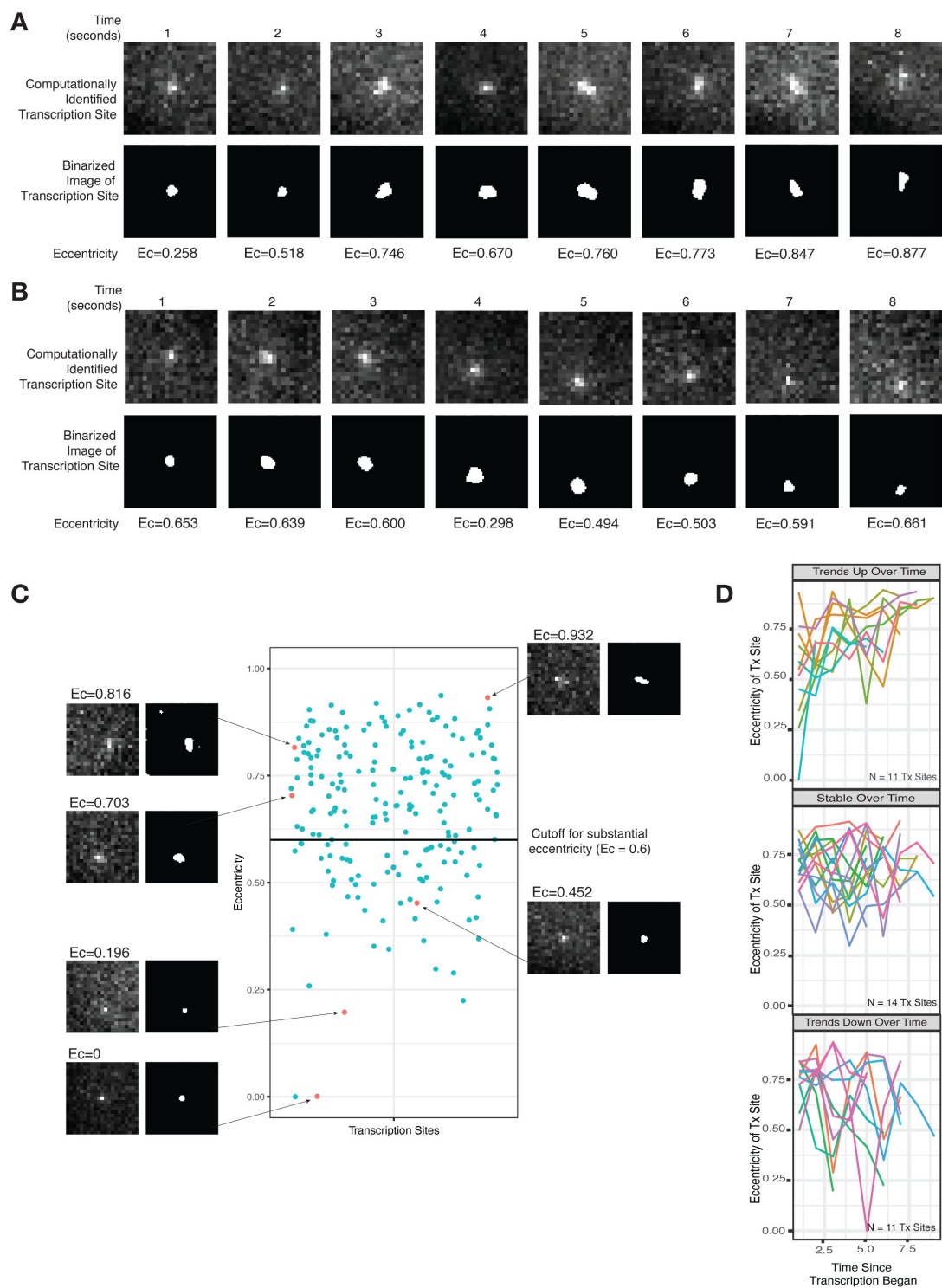


Figure 3

Live cell imaging corroborates a slow moving zone around the site of transcription

A-B. Representative images from two cells of a transcriptional burst of TFF1 labeled with MS2-GFP. Each image is taken one second apart. Shown are the raw, computationally identified transcription site images, as well as the binarized image used to calculate eccentricity.

C. Plot of eccentricity for each transcription site image, alongside representative images that show both eccentric and non-eccentric sites.

D. Graphs of eccentricity measured in individual transcription sites tracked over time

polymerase II, thus it is difficult to eliminate the possibility that some other part of the pre-mRNA is close to RNA polymerase II or that a pre-mRNA is localized to an undetected single RNA polymerase II molecule.

Another interesting observation was that the size of 5', intron, and 3' clouds, the number of spots in each cloud, and the area of live cell transcription sites varied considerably from cell to cell (**Figure 2C**, **2H**, **3A-B**). In some cases, we observed more 5' spots than 3' spots, which may be due to the interception of an ongoing transcriptional burst (where RNA polymerase II has already synthesized the 5' ends of the RNA but has not yet synthesized the 3' ends). We also observed some cases where there were more 3' spots than 5' spots and indeed many cases where the 3' clouds are more dispersed than the 5' clouds, which may suggest that the spots of 5' probe may represent a pileup of transcripts at the 5' end, such that we only see one bright spot where we should see several. When the dyes of the two probes are swapped, the 3' clouds are still consistently larger than the 5' clouds, suggesting that it's unlikely to be a dye-bias effect (Supplementary Figure 3C).

Thus, expansion microscopy revealed that after the completion of transcription, pre-mRNA move slowly through a slow-moving proximal zone, during which splicing may be ongoing. This finding potentially unites existing conflicting reports of co-transcriptional versus post-transcriptional splicing, as splicing within the slow moving zone would appear co-transcriptional when evaluated by conventional light microscopy but in reality occurs after transcription has been completed.

Localization of unspliced pre-mRNA to speckle-proximal compartments is gene specific

We wondered where transcripts went after they were released from the slow-moving transcription-site-proximal zone that was revealed by expansion microscopy (see **Figure 2C**). We hypothesized that the transcripts could do one of three things: (**Figure 4A**)

- 1) freely diffuse away from the transcription-site-proximal zone through the nucleoplasm (nuclear dispersal)
- 2) be tethered to the transcription site proximal zone in some manner (tethering)
- 3) fill a compartment, potentially around or adjacent to the transcription-site-proximal zone or other nuclear bodies (compartmentalization).

Owing to the lack of dispersal of some introns, relatively few unspliced RNA were detectable outside of the transcription-proximal zone, making it difficult to discriminate between these hypotheses. Thus, we inhibited splicing to generate more pre-mRNAs, making it easier to track their localization after leaving the transcription-site-proximal zone. Upon splicing inhibition, we observed three distinct trafficking behaviors for pre-mRNA species: one in which there are increased numbers of dispersed pre-mRNA throughout the nucleus (nuclear dispersal; consistent with scenario 1), one in which the pre-mRNA are located in a large blob, likely around the transcription-site-proximal zone or another nuclear body (blobs; scenario 2 or 3), and one in which the pre-mRNA dispersal pattern looked identical with or without splicing inhibition (non-splicing inhibited) (**Figure 4B,C**).

The compartmentalization pattern only appeared for three out of the 16 genes we tested (*EEF2*, *GAPDH*, and *RPL13A*), whereas we observed a nuclear dispersal phenotype for 7 genes and no change in dispersal for 6 genes. To test for potential tethering of transcripts to some location in the nucleus, we labeled the 5' and 3' ends of the pre-mRNA in different colors, reasoning that if either end of the pre-mRNA was tethered to a particular location, then the signal from that particular end would form a tighter spot in the nucleus while the other end would fill the compartment

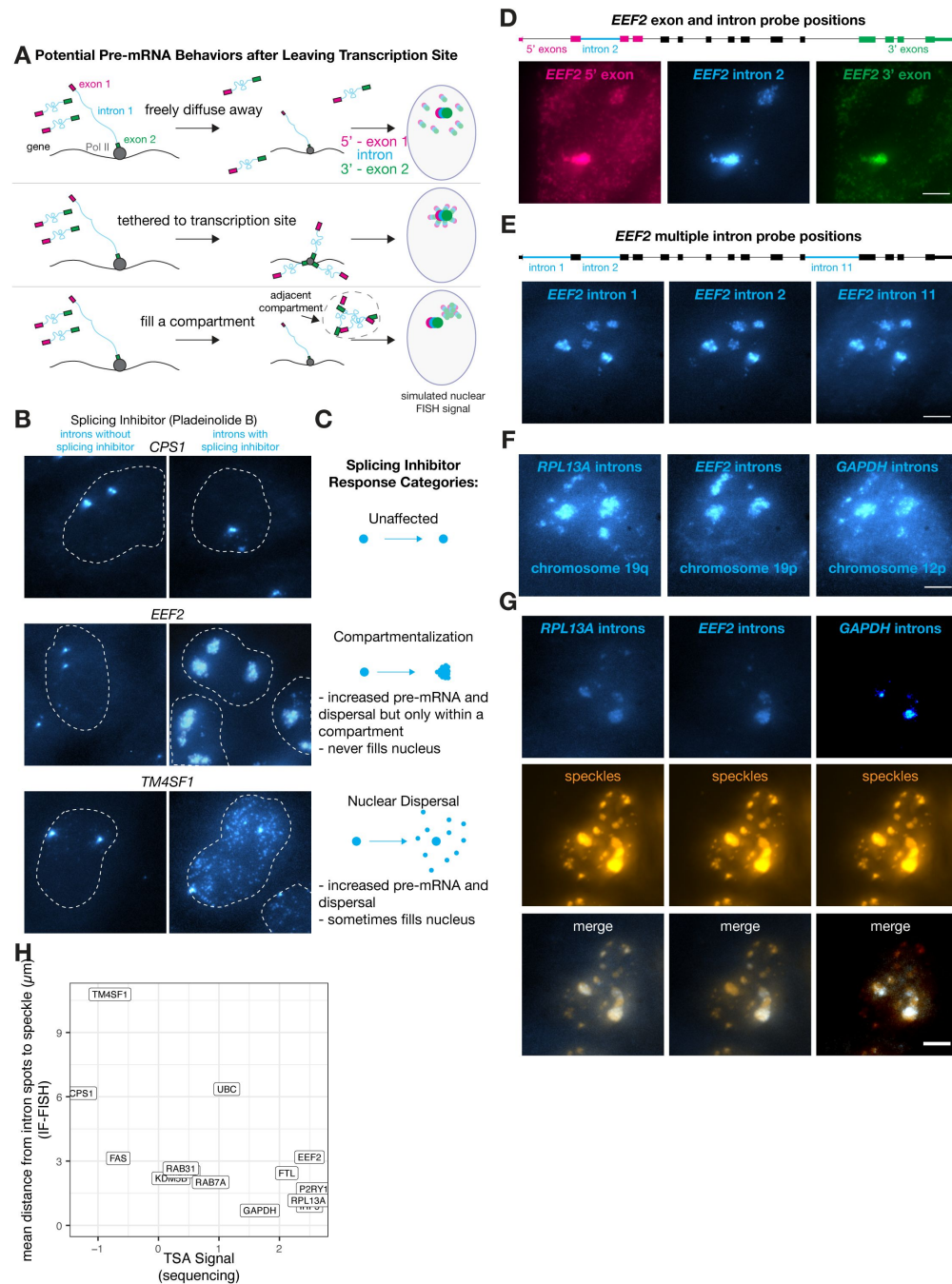


Figure 4

Some transcripts localize to a speckle proximal compartment after splicing inhibition.

A. Schematic of possibilities for RNA movement post-transcription.

B. Example images of introns of specified genes before and after pladeinolide B treatment (treatment status as indicated on figure). Outline represents nucleus.

C. Description of 3 response types to pladeinolide B.

D. *EEF2* RNA FISH exon and intron images with pladeinolide B treatment. Scale bar = 5μm.

E. *EEF2* RNA FISH intron only images with pladeinolide B treatment. Scale bar = 5μm.

F. *RPL13A*, *GAPDH*, and *EEF2* RNA FISH intron images with pladeinolide B treatment. Scale bar = 5μm.

G. Costaining of RNA FISH for specified intron and SC35 IF in the same cell treated with pladeinolide B. Scale bar = 5μm.

H. Quantification of speckle decile from previously published data (TSA Seq 2.0), compared with distance from nearest speckle calculated based on RNA FISH of specified genes without pladeinolide B treatment.

(**Figure 4D** [↗](#), Supplementary Figure 6A). We found, however, that the 5' and 3' ends of the pre-mRNA both filled the entire blob, suggesting that the pre-mRNA spread to fill the entire putative compartment (as in scenario 3 described above, compartmentalization) (**Figure 4A** [↗](#), **4D** [↗](#)).

We wondered if these compartmentalized pre-mRNA were located near nuclear speckles, which are compartments in the nucleus that contain concentrated splicing and transcription factors (**21** [↗](#)). To test this hypothesis, we performed RNA FISH simultaneously with immunofluorescence for SC35, a component of speckles, and saw that these compartmentalized pre-mRNA did indeed appear near nuclear speckles both before (Supplementary Figure 6C) and after (**Figure 4G** [↗](#)) splicing inhibition.

We corroborated the spatial association we observed between speckles and compartmentalized pre-mRNA by analyzing previously published high throughput sequencing data (TSA Seq 2.0) that quantified the distance of genes from speckles and other nuclear compartments (**35** [↗](#)–**36** [↗](#)). We found that even in the absence of pladeinolide B, the genes that localized to compartments post-splicing inhibitor treatment were indeed the closest to speckles. Furthermore the distance from speckles (without splicing inhibitor treatment) was anticorrelated with the signal from TSA (Tyramide Signal Amplification)-Seq 2.0, which measures the distance from all genes to various physical anchors in the nucleus (in this case, speckles). Those data showed that 3 compartmentalized genes were all within the most speckle associated transcripts, while all other tested genes (both nuclear dispersal and non-responsive; 11 genes) exhibited a much broader range of distances to speckles (**Figure 4H** [↗](#)). This anticorrelation is to be expected, because the genes closest to speckles will receive the most reads in TSA-Seq and should have the smallest distance to speckles as measured by IF-FISH.

Speckles form a set of subcompartments within the nucleus. We thus wondered whether pre-mRNA from the genes exhibiting “compartmentalization” in their post-transcriptional trafficking would go to all of these speckle compartments, or rather just a gene-specific subset. To test these possibilities, we performed RNA FISH on multiple introns within the same “compartmentalization” gene (*EEF2*) as well as introns from several different “compartmentalization” genes simultaneously (*EEF2*, *GAPDH*, and *RPL13A*). We observed that multiple introns retained in pre-mRNA from the same gene colocalized to the same subset of speckles (**Figure 4E** [↗](#)), suggesting that all unspliced pre-mRNA from a particular gene localize to the same subset of speckles. We also observed that pre-mRNA from multiple “compartmentalization” genes (*EEF2*, *GAPDH*, and *RPL13A*) localize to a similar set of speckles after splicing inhibition (**Figure 4F** [↗](#)), although there are some differences. However, when observing the intron distributions of pre-mRNA from *EEF2*, *GAPDH*, and *RPL13A* before splicing inhibition, they do not appear to colocalize with one another or with the same speckles (Supplementary Figure 6C), suggesting perhaps that splicing inhibition impacts these responses. Overall, our results suggest that mRNA trafficking upon leaving the slow-moving zone is gene specific.

Dispersal is not an inherent trait of individual introns and can vary with transcription level

We wondered whether the degree of dispersal (and thus, the degree of post-transcriptional splicing) was an inherent property of each intron or whether dispersal could vary due to other factors such as the level of transcription. To test whether the level of transcription affected the degree of dispersal, we treated A549 cells with dexamethasone to induce transcription of the gene *FKBP5*, and then performed RNA FISH against introns 1, 8, and 9 at various time points in dexamethasone to measure the degree of dispersion (**Figure 5A** [↗](#), B). We saw an increase in both exon and intron spot counts (**Figure 5B** [↗](#)) over time and a corresponding increase in the dispersal of some, but not all, introns (**Figure 5C** [↗](#)).

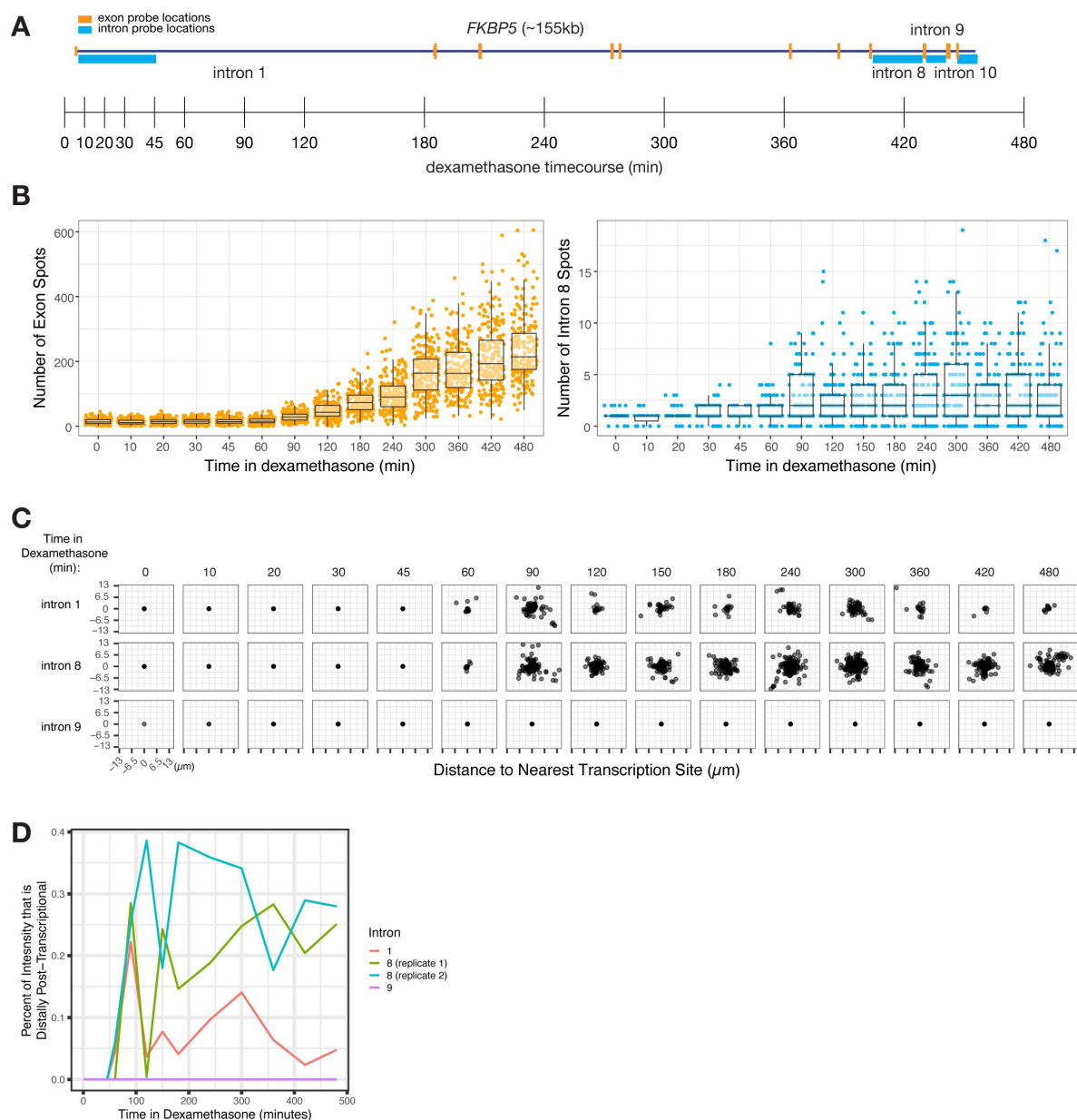


Figure 5

Intron dispersal varies with transcription level and is therefore not an inherent property of each intron.

A. Gene and probe diagram for *FKBP5* and schematic of dexamethasone treatment schedule.

B. Quantification of *FKBP5* RNA FISH exon and intron spots over time of treatment in dexamethasone (in A549 cells).

C. Dispersal graphs (as quantified from RNA FISH) of *FKBP5* introns 1, 8, and 9 over time in dexamethasone (in A549 cells).

D. Graph showing the percentage of intron intensity that is distally post-transcriptional for 3 *FKBP5* introns over time in dexamethasone

The fact that intron dispersal increased with transcription level for at least some introns shows that dispersal is not an inherent property of each intron but can depend on other variables like the level of transcription (**Figure 5C** [↗](#)). Intron 9 did not exhibit an increase in dispersal even with long exposure to dexamethasone (8 hours) (**Figure 5C** [↗](#)).

We believe that the increased dispersal represents an escape of unprocessed pre-mRNA from the site of transcription. This increase would only happen in cases where splicing was slow enough that splicing of all introns was not completed before termination of transcription, therefore allowing time for these pre-mRNA to disperse away from the site of transcription. The lack of dispersal of some introns, even with increased transcription, suggests that these introns are spliced so quickly that pre-mRNA containing those introns have no time to disperse away from the site of transcription even in case of increased transcription.

We hypothesized that the increased dispersal of some introns during periods of increased transcription may be due to a local depletion of splicing factors. A local depletion of splicing factors could occur as more pre-mRNA fill the local area and absorb the local pool of splicing factors (or particular splicing cofactors), resulting in more pre-mRNA escaping from the transcription proximal region before undergoing splicing. If the concentration of splicing factors remained constant (i.e., no local depletion), we would expect the rate of splicing to remain constant, and the percentage of unspliced pre-mRNA far from the transcription site to be unchanged, regardless of transcription rate. Instead, we observed a significant increase in the proportion of intron signal for two introns over time (from 0 to 22% for intron 1 and from 0 to 29% for intron 8; **Figure 5D** [↗](#)), suggesting a possible local depletion of splicing factors at the transcription site. (Of note, we may potentially miss post-transcriptional splicing occurring after a burst has concluded.) These increases in the percent of distal post-transcriptional splicing show that even the same intron can exhibit a range of spatiotemporal patterns of splicing depending on expression levels and potentially on limiting splicing factors in the vicinity of the gene itself.

Discussion

By using expansion microscopy combined with single molecule RNA FISH, we were able to obtain direct measurements of the spatial distribution of splicing intermediates in the vicinity of the transcription site. We found evidence for extensive post-transcriptional splicing that occurs throughout that zone. Our results support a model that unifies many of the observations made of both co-transcriptional and post-transcriptional splicing. We argue that splicing can occur continuously and post-transcriptionally while pre-mRNA move through this slow moving zone. Fractionation approaches may have interpreted such splicing intermediates as arising co-transcriptionally owing to proximity to the transcription site. We also found introns that seemed to be spliced out so close to the site of transcription that we were unable to distinguish whether they were spliced co- or post-transcriptionally. As methods are developed with ever increasing spatio-temporal resolution, it may soon be possible to discriminate splicing dynamics for these introns as well.

Our results suggest that pre-mRNA are not tethered to the site of transcription while they move through this transcription-site-proximal compartment, in contrast to what is suggested by Dye et al., where the authors suggest that exons are tethered to polymerase II as splicing is occurring ([37](#) [↗](#)). The lack of colocalization of introns with polymerase II also suggests that splicing is not happening close to polymerase II. This conclusion stands in contrast to the data of Alexander et al., which suggested that almost all splicing occurs while polymerase II is still paused proximal to the intron that was recently transcribed ([50](#) [↗](#)). This discrepancy may be due to species-specific differences. In yeast, polymerase II has been found to pause at several sites involved in splicing,

including the terminal exon, the 3' SS, and internal exons (for a review, see (39)). It is also possible that increased resolution made possible by expansion microscopy has allowed us to detect previously indistinguishable distances between introns and polymerase II.

Our model stands in contrast to some number of prior studies of the timing of splicing, which suggest that splicing happens immediately (within 15-20 seconds or 45-100 nucleotides of transcription) after transcription of each intron is completed (2, 4, 22, 28, 40–43). This discrepancy may arise from a variety of reasons, including but not limited to species-specific differences and the use of different assays to measure the timing of splicing (a thorough review is available in reference (41)). Of note, we see that increased transcription level correlates with intron dispersal, suggesting that the percentage of splicing occurring away from the transcription site is regulated by transcription level for at least some introns. This may explain why we observe post-transcriptional splicing of all genes we measured, as all were highly expressed. Our model is in agreement with fractionation work by Pandaya-Jones et al. and by Drexler et al. that suggest that specific transcripts are retained in the chromatin and that splicing is not completed until transcription has finished (6, 15). Our model is also in agreement with several other studies which suggest that there can be significant delays between RNA transcription and splicing (29, 44–49).

What might the slow moving zone represent, physically? A natural candidate is the chromatin in the vicinity of the gene itself. Live imaging studies have shown that mRNA exhibit slow diffusion in chromatin-dense regions (50). Furthermore, recent work tracking cells over time by sequencing shows that mRNA spends relatively more time on chromatin than in the nucleoplasm (51), further lending credence to this hypothesis.

Our expansion microscopy results suggest that the distance between the 5' end and the 3' end of RNA at the site of transcription is greater than the distance between the 5' end and 3' end of mRNA. This increased 5'-3' distance suggests that the transcripts at the site of transcription are either unpackaged (perhaps due to decreased RNA binding proteins occupancy) or are simply longer because there are likely more introns incorporated into the transcripts close to the site of transcription than away from it due to progressive splicing over time. If this 5' to 3' distance increase were due to increased retention of introns, that would also support the post-transcriptional splicing model. We note that it is difficult to know which particular 5' and 3' spots correspond to the same pre-mRNA molecule near the site of transcription; further expansion or live tracking of individual mRNA might help make those connections and refine our measurement of distances between 5' and 3' ends of transcripts.

One of the original models for splicing is the “first come, first serve” model in which each intron is immediately spliced upon the completion of transcription, in a 5' to 3' order (52). Our results suggest that first come, first serve is not the case, based on seeing low splicing rates (or high dispersion) for even the 5' most introns of some genes. This lack of first come, first serve splicing is confirmed by others in several different situations (53–55). Our results also suggest that introns are spliced independently of one another, whether they are genomically proximal or distal to each other. This conclusion is in contrast to other work which suggests splicing of particular introns is controlled or gated by the splicing of other introns or exons within the same gene (6, 9, 56).

Our splicing inhibition results show that the trafficking of transcripts after they escape the slow moving transcription proximal zone varies by gene. Our results were consistent with sequencing-based metrics, and those metrics are in turn largely consistent across multiple cell types, suggesting that the speckle-associative property is not subject to cell-type specific regulation (35). The association between specific genes and speckles has been observed before in several studies by Jeanne Lawrence (57–59). Our observations are also consistent with those of Girard et al. in which certain genes are retained post-transcriptionally at speckles as splicing

occurs and then are released and immediately exported from the nucleus (60 [↗](#)). Wang et al. also observed speckle localization of RNA upon microinjection into nuclei (61 [↗](#)). Our data further support the conclusion that speckle association can be gene specific and can help retain pre-mRNA in the gene's vicinity until post-transcriptional splicing is completed.

Study Limitations

With the notable exception of our live cell data in **Figure 3** [↗](#), the experiments in this study utilize fixed cells and capture transcription at a single moment in time. As a result, many of the conclusions we draw can be strengthened by future work that evaluates active transcription through live cell imaging or other methods that do not involve fixation. Our investigation of intron localization in **Figure 4** [↗](#) relies upon the inhibition of splicing, which may impact several aspects of cellular physiology. This paper also does not address potential relationships between splicing and other co-transcriptional events, such as 5' capping or 3' end formation. Future work may unravel dependencies between these events and the splicing of introns, and a potential role for the transcription-site-proximal slow moving zone in other aspects of mRNA processing. Lastly, a major outstanding question is what sequence-based features determine the distinct behaviors of different introns. Large-scale imaging and synthetic libraries of introns may be required to make such conclusions.

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Author Contributions

AJC and AR conceived of the research with preliminary input and method development by SB. AJC and CC designed and performed experiments with guidance from AR. AJC, AO, and CC analyzed the data with guidance from AR. HLD designed and performed nascent RNA sequencing experiments with guidance from LSC and analyzed the data in conjunction with AJC. AJC and KAA contributed to the design of speckle experiments with guidance from SB. AJC and AO wrote the paper with guidance from AR. FC, AW, and AJC conducted initial optimization of expansion microscopy experiments with guidance from EB. YW conducted the live cell imaging experiments. ID, MD, RP, KP, and JPC conducted STORM imaging.

Figure Captions

Supplementary Figure 1: Transcription site choice and defining post-transcriptionality.

A. Histograms of intron intensities for TM4SF1 intron 1 and intron 4, before, after, and during defining a global thresholding cutoff and other transcription site selection methods, as well as dispersal graphs generated based on those transcription site selections.

- B. Number of dispersed pre-mRNA per cell.
- C. Parameter sweep of colocalization threshold and associated dispersal graphs.
- D. Example classification of pre-mRNA as either transcription sites or dispersed pre-mRNA.
- E. Distances between 5' and 3' ends of RNA as detected by RNA FISH for either the 3' or 5' end of the RNA of interest.
- F. Example classification of RNA as “distal” or “proximal” to the transcription site
- G. Histogram showing type of pre-mRNA as defined by RNA FISH for stated introns in FKBP5, as a function of distance to the nearest transcription site.

Supplementary Figure 2: Sequencing corroborates RNA FISH dispersal results.

- A. Schematic of sequencing experiment design (in HeLa cells).
- B. Comparison of mean dispersal (as assessed by RNA FISH, see [Figure 1](#)) and mean splicing index (as assessed by sequencing). FKBP5 is not present on this graph due to low read counts in HeLa cells (FISH was performed for FKBP5 in A549 cells).
- C. Splicing index of each intron for which we obtained RNA FISH measurements. Error bars represent mean $\pm$ sd. n = 2
- D. Comparison of transcription site size (as assessed by RNA FISH) and splicing index, as assessed by sequencing.

Supplementary Figure 3: Expansion microscopy yields a 4.65 fold linear expansion and expands isotropically.

- A. Comparison of radii of nuclei (based on DAPI staining, and assuming spherical nuclei) before and after expansion.
- B. Images of the same cell before and after expansion, with or without pladeinolide B treatment (as noted). Scale bars = 5 μ m.
- C. Transcription site area (microns squared) for 5' and 3' probes, with and without dye swap.

Supplementary Figure 4: Storm Validation and Post 3' RNA FISH

- A. Sample STORM image to demonstrate identification of transcription sites
- B. Comparison of *CSP1* transcription site size in cells imaged through expansion microscopy and STORM. Distances are in unexpanded space
- C. Quantification of spots within transcription site clouds exemplified in [Figure 2C](#)
- D. Gene and probe position diagram for *CPS1* pre-mRNA to test for a potential tether beyond the 3' end of the gene
- E. Representative images of 3' and post-3' RNA FISH signal at transcription sites (in unexpanded cells)

F. Comparison of 3' and post-3' RNA FISH signal at transcription sites

Supplementary Figure 5: Intron characteristics do not influence dispersal

A. Comparison of intron size versus mean dispersal by RNA FISH

B-C. Comparison of 3' splice site (X3SS, B) and 5' splice site (X5SS, C) scores versus mean dispersal by RNA FISH.

Supplementary Figure 6: Compartmentalization genes before splicing inhibition.

A. Schematic of compartmentalization phenotype with and without tether.

B. RNA FISH of RPL13A, EEF2, and GAPDH introns before pladienolide B treatment. Scale bar = 5 μm .

C. Combined RNA FISH for the stated introns and IF for SC35, before pladienolide B treatment. Scale bar = 5 μm .

STAR Methods

Key Resources Table:

Reagent or Resource	Source	Identifier
<i>Antibodies</i>		
SC35	Abcam	ab11826
Phospho S2 polymerase II	Active Motif	61083
<i>Cell Lines and Cell Culture</i>		
HeLa	Lab of Dr. Phillip Sharp (MIT)	N/A
HeLa-S3	ATCC	CCL-2.2
A549	ATCC	CCL-185
CRL-2097	ATCC	CCD-1079Sk
DMEM	Gibco	11995040
Penicillin / Streptomycin	Invitrogen	15140122
Fetal Bovine Serum (FBS)	Fisher	16000044
Pladienolide B	Tocris Biosciences	6070500U
Dexamethasone	Sigma	D2915
4sU (4-thiouridine)	Sigma	T4509
<i>Oligonucleotides</i>		
Single molecule RNA FISH probes targeting CSP1, FKBP5, TM4SF1, and EEF2	See Table S1	N/A
<i>Software and Algorithms</i>		
rajlabimagetools	Raj et al, 2008	https://github.com/arjunrailaboratory/rajlabimagetools
STAR (v2.5.1a)	Dobin et al, 2013	N/A
All data and code used to produce figures in this paper	This paper	https://www.dropbox.com/sh/el816d3aqdgrh70/AAD0_uTOqjSpZTi1md0cKRKta?dl=0

Resource Availability

Lead Contact

Further information and requests should be directed to and will be fulfilled by the lead contact, Arjun Raj (arjunrajlab@gmail.com)

Materials Availability

This study did not generate new materials.

Method Details

Cell culture, splicing inhibition, and FKBP5 induction

HeLa (kind gift of the lab of Dr. Phillip Sharp, MIT) and A549 (human lung carcinoma, A549, ATCC CCL-185) cells were cultured in DMEM (Gibco) supplemented with 50 U/mL penicillin, 50 µg/mL streptomycin, and 10% fetal bovine serum (FBS, Fisher). Splicing inhibition was accomplished by

treating HeLa cells with 1μM Pladienolide B (Tocris Biosciences, 6070500U) for 4 hours, as described by (16). HeLa cells were then fixed and used for RNA FISH as described below. FKBP5 was induced by treating A549 cells with 25nM dexamethasone (Sigma, D2915) for the specified lengths of time. A549 cells were then fixed and used for RNA FISH as described below.

RNA fluorescence in situ hybridization, STORM, and expansion microscopy

Single-molecule RNA FISH was performed on samples as described previously(58). Cells were fixed in 4% formaldehyde and permeabilized with 70% ethanol before in situ hybridization was performed using the probes described in Supplementary Table 1. Samples were simultaneously co-stained with probes for the exon of gene of interest (labelled in cy3), two introns of the gene of interest (labelled in alexa594 or atto647N), and cyclin mRNA (labelled in either atto700 or atto647N) (Stellaris oligonucleotides, Biosearch Technologies). Samples were then washed twice with 2 X saline sodium citrate buffer (SSC) containing 10% formamide (Ambion), and then 2XSSC supplemented with DAPI (Molecular Probes D3571) to stain the cell nuclei. Cells were submerged in 2XSSC with DAPI for imaging. Chromatic aberration was evaluated using multi-color fluorescent beads and was far smaller than any biologically relevant distances we measured (see Supplementary Figure 1E).

Stochastic optical reconstruction microscopy (STORM) was performed on the 5' exons and middle intron of CSP1 in HeLa cells. Cells were imaged in Vutara d-STORM imaging buffer (20mM cysteamine (MEA) + 1% 2-mercaptoethanol + 1x Gloxy (glucose oxidase + catalase dissolved in 50mM Tris-HCl + 10mM NaCl) in buffer B (50mM Tris-HCl + 10mM HCL + 10% glucose). Samples were imaged on a Vutara VXL microscope and exported points were reconstructed in Matlab. Transcription sites were identified by alignment with widefield images, and area was calculated using the polyarea() function in R.

For combined expansion microscopy and RNA FISH, expansion microscopy was performed as described by Chen et al. (20). Briefly, Acryloyl-X, SE (6-((acryloyl)amino)hexanoic acid, succinimidyl ester, here abbreviated AcX; Thermo-Fisher) was resuspended in anhydrous DMSO at a concentration of 10 mg/mL, aliquoted and stored frozen in a desiccated environment. Label-IT® Amine Modifying Reagent (Mirus Bio, LLC) was resuspended in the provided Mirus Reconstitution Solution at 1mg/ml and stored frozen in a desiccated environment. To prepare LabelX, 10 μL of AcX (10 mg/mL) was reacted with 100 μL of Label-IT® Amine Modifying Reagent (1 mg/mL) overnight at room temperature with shaking. LabelX was subsequently stored frozen (−20 °C) in a desiccated environment until use.

Fixed cells were washed twice with 1× PBS and incubated with LabelX diluted to 0.002 mg/mL in MOPS buffer (20 mM MOPS pH 7.7) at 37 °C for 6 hours followed by two washes with 1× PBS.

Monomer solution (1x PBS, 2 M NaCl, 8.625% (w/w) sodium acrylate, 2.5% (w/w) acrylamide, 0.15% (w/w) N,N'-methylenebisacrylamide) was mixed, frozen in aliquots, and thawed before use. Prior to embedding, monomer solution was cooled to 4°C to prevent premature gelation. Concentrated stocks (10% w/w) of ammonium persulfate (APS) initiator and tetramethylethylenediamine (TEMED) accelerator were added to the monomer solution up to 0.2% (w/w) each. 100μL of gel solution specimens were added to each well of a Lab Tek 8 chambered coverslip and transferred to a humidified 37° C incubator for two hours.

Proteinase K (New England Biolabs) was diluted 1:100 to 8 units/mL in digestion buffer (50 mM Tris (pH 8), 1 mM EDTA, 0.5% Triton X-100, 0.8 M guanidine HCl) and applied directly to gels in at least ten times volume excess. The gels were then incubated in digestion buffer for at least 12 hours. Gels were then incubated with wash buffer (10% formamide, 2× SSC) for 2 hours at room temperature and hybridized with RNA FISH probes in hybridization buffer (10% formamide, 10%

dextran sulfate, 2× SSC) overnight at 37 °C. Following hybridization, samples were washed twice with wash buffer, 30 minutes per wash, and washed 4 times with water, 1 hr per wash, for expansion. Samples were imaged in water with 0.1µg/mL DAPI.

Imaging Cells were imaged using a Leica DMI600B automated widefield fluorescence microscope equipped with a X100 Plan Apo objective, a Pixis 1024BR cooled CCD (charge-coupled device) camera, a Prior Lumen 220 light source, and filter sets specific for each fluorophore. Images in each fluorescence channel were taken as a series of optical z-sections (0.3 microns per section).

Intron splice site strength (Supplementary Figure 5, Supplementary Table 2) was calculated using MaxEnt (62 [DOI](#)).

Immunofluorescence

Staining for SC35 and polymerase II were performed with antibodies against SC35 (abcam ab11826, 1:200, NOTE: it has recently been described that this antibody may instead target SRRM2) and phospho S2 polymerase II (Active Motif, 61083, 1:200), respectively. Briefly, staining was performed on cells fixed and permeabilized as described above for RNA FISH. Primary antibody hybridization was carried out in 1XPBS overnight at 4°C. Samples were then washed with 1XPBS and incubated with secondary antibody (1:200) for 1 hour in 1XPBS at room temperature. Samples were then fixed for an additional 10 minutes in formaldehyde, washed with 1XPBS, and RNA FISH was performed as described above. RNA FISH quantification RNA FISH was quantified as described previously (58 [DOI](#)). Briefly, cells were manually segmented, a gaussian filter was applied to all spots, signal was distinguished from noise through semi-automated thresholding, each called spot was further fit to a gaussian to get sub pixel resolution, and transcription sites were chosen based on a global brightness threshold (Supplementary Figure 1A,B). Data was processed to assess distances and graphed in R. Calculation of mRNA length was based on the 75th percentile of 5'-3' distances of labelled mRNA seen in Supplementary Figure 1C.

Live Cell Imaging

The live cell imaging was conducted using human bronchial epithelial cells (single cell clones containing 24 X MS2 stem-loops in RAB7A first intron). To capture the diffusing RNA with MS2 labeling, live cell imaging was performed on a Zeiss LSM780 laser scanning confocal microscope using 37°C incubation and 5% CO₂. Imaging was performed using 488 nm excitation, pinhole size of 2 airy units. The pixel size was 0.066 microns. One z plane was imaged every 1 sec for 60 frames. Transcription site intensity tracks were analyzed using KNIME pipeline https://github.com/CBIIT/Larson-Lab-CCR-NCI/tree/master/Wan_GeneTrap_2019/KNIME_Workflows [DOI](#). MSD analysis was performed using MATLAB.

Transcription site intensity tracks were then analyzed in Matlab. Briefly, we identified the brightest pixel in each track, and called its location as the transcription site. We then cropped a 30×30 pixel region around this site, and used `imresize()` to increase resolution without interpolation. We then set a threshold of $((\text{max pixel intensity} - \text{median pixel intensity}) / 2) + \text{median pixel intensity}$ to create a binarized, Gaussian filtered image of the transcription site, for which we calculated the eccentricity using `regionprops()`. Images without clear, identifiable transcription sites were discarded.

4sU labeled chromatin-associated RNA sequencing and splicing index analysis

HeLa S3 cells (ATCC, CCL-2.2) were maintained in DMEM media containing 10% FBS, 100 U/ml penicillin, and 100 µg/ml streptomycin to 75% confluency. Cells were labeled in media containing 500 µM 4-thiouridine (4sU, Sigma, T4509) for 7.5 minutes. Plates were washed twice with 1X PBS and cells were lifted by scraping. Labeled cells were collected by centrifugation at 500 g for 2

minutes. To purify chromatin associated RNA, steps 8-21 were followed exactly as described in (59). In brief, nuclei were collected by lysing samples of 10M cells in 200 µl cytoplasmic lysis buffer (0.15% (vol/vol) NP-40 (Thermo Fisher Scientific, 28324), 10 mM Tris-HCl (pH 7.0), and 150 mM NaCl) for 2 min, layering over a 500 µl sucrose cushion (10 mM Tris-HCl (pH 7.0), 150 mM NaCl, 25% (wt/vol) sucrose), and centrifuging at 16,000 g for 10 minutes. The nuclei pellet was washed in 800 µl wash buffer (0.1% (vol/vol) Triton X-100, 1 mM EDTA, in 1X PBS) and collected by centrifuging at 1,150 g for 1 minute. Nuclei were resuspended in 200 µl glycerol buffer (20 mM Tris-HCl (pH 8.0), 75 mM NaCl, 0.5 mM EDTA, 50% (vol/vol) glycerol, 0.85 mM DTT), and mixed with 200 µl nuclei lysis buffer (1% (vol/vol) NP-40, 20 mM HEPES (pH 7.5), 300 mM NaCl, 1 M urea, 0.2 mM EDTA, 1 mM DTT) by pulse vortex and incubated on ice for 2 minutes. The chromatin pellet was collected by centrifugation at 18,500 g for 2 minutes and resuspended in 1X PBS. All steps were performed at 4°C and buffers were prepared with 25 µM α-amanitin (Sigma, A2263), 0.05U/µl SUPERase.In (ThermoFisher Scientific, AM2694), and protease inhibitor mix (Roche, 11873580001). Chromatin-associated RNA was extracted using Qiazol lysis reagent (Qiagen, 79306) following the manufacturer's instructions.

50 µg RNA per reaction was subjected to 4sU purification as described in (60, 61). In brief, labeled RNA (1 µg / 10 µl) was incubated with 10% biotinylation buffer (100mM Tris pH 7.5, 10mM EDTA) and 20% EZ-Link Biotin-HPDP (1 mg/mL resuspended in DMF, Thermo Fisher Scientific, 21341) for 1.5 hours 24°C in the dark and 800 rpm to mix. RNA was purified by shaking the sample with a 1:1 volume of chloroform/isoamylalcohol (24:1), separating using a phase-lock tube at 16,000 g for 5 min, and performing isopropanol precipitation. Biotinylated RNA was separated using the µMACS streptavidin kit (Miltenyi Biotec, 130-074-101) by mixing with µMACS streptavidin beads at a 2:1 ratio by volume at 800 rpm and 24°C for 15 min. RNA-streptavidin beads mix was transferred to the µMACS column and washed with wash buffer (100 mM Tris pH 7.5, 10 mM EDTA, 1 M NaCl, 0.1% Tween 20) at 65°C and room temperature 3 times each. Selected RNA was eluted off the magnet using the reducing agent, DTT (0.1M), and purified using the miRNeasy micro kit (Qiagen, 217084) with on-column DNase I treatment (Qiagen, 79254). For the poly(A) depleted sample, the RNA was first concentrated using the RNA Clean and Concentrator kit (ZymoResearch, R1015). 10 µL Oligo(dT) Dynabeads (ThermoFisher, 61002) were washed in 10 µL Binding Buffer (20mM Tris.HCl pH 7.5, 1M LiCl, and 2mM EDTA). The sample was mixed with 10 µl binding buffer, heated to 65°C for 2 min, moved to ice, and mixed with 1 µl SUPERase.In (ThermoFisher Scientific, AM2694). The sample and beads were mixed thoroughly and annealed by rotating continuously on a mixer for 5 minutes at room temperature. Poly(A) RNAs were collected on a magnet while depleted supernatant was removed and purified using the RNA Clean and Concentrator kit (ZymoResearch, R1015). Illumina sequencing libraries were prepared using the Ovation Universal RNA-seq System (NUGEN, 0343-32) with Universal Human rRNA strand selection reagent (NUGEN, S01859) following the manufacturer's instructions.

All samples were sequenced 2×80 on a NEXTseq 500 sequencer (Illumina, San Diego, CA, USA) in the Biopolymers Facility at Harvard Medical School. Paired-end reads were aligned to the ENSEMBLE GRCh38 (release-86) reference genome using STAR (v2.5.1a)(62) with default parameters (except for readFilesCommand=cat, limitIObufferSize=200000000, limitBAMsortRAM=6400000000, outReadsUnmapped=Fastx, outSAMtype=BAM SortedByCoordinate, outSAMattributes=All, outFilterMultimapNmax=101, outSJfilterOverhangMin=3 1 1 1, outSJfilterDistToOtherSJmin=0 0 0 0, alignIntronMin=11, alignEndsType=EndToEnd). Splicing index calculations were determined by summing the number of spliced and unspliced read pairs that span exon junctions by at least 3 nucleotides and calculating the total spliced read pairs divided by the total unspliced read pairs for each gene; $\text{splicing index} = 2 \times \text{spliced read pairs} / (5'SS \text{ unspliced} + 3'SS \text{ unspliced read pairs})$.

Calculation of Intron Splicing Order

For all independence calculations, it was first determined what proportion of RNA fell into each of the following categories:

1. Fully unspliced (exon spot with both introns)
2. Partially spliced with intron A removed
3. Partially spliced with intron B removed
4. Fully spliced (exon spot without either intron)

Spots within 0.65 microns of each other were considered to be colocalized spots (as described in [Figure 1](#)). Colocalized spots that contained exon, intron A, and intron B were designated as a “3 color spot” (category 1). Spots that contained only exon signal were designated as fully spliced (category 4). Colocalized spots with only one intron signal were designated by the intron that was removed (for example, if intron B is present, then intron A was removed, and the transcript is in category 2). Categories 2 and 3 represent mutually exclusive pathways to generate the final product of a mature transcript.

Once each transcript was categorized, we focused our attention on partially spliced transcripts, and determined the proportion of these transcripts in either category 2 or category 3. Should the splicing rate of different introns be remarkably different from each other, or should intron splicing be dependent on the splicing of other introns, we would expect an overrepresentation of one splicing pathway.

We labeled the 4th intron of TM4SF1 with two colored probes, and determined the number of intermediate transcripts identified using this method, allowing us to measure the noise inherent in this analysis method. With 100% detection efficiency, we would expect this set of two probes labelling the same intron to be spliced out of pre-mRNA simultaneously. To calculate a “noise floor” of intermediate transcripts, we took the number of intermediate transcripts divided by two (as both category 2 and category 3 in this case measure the same type of error), and divided by the total number of transcripts captured in this experiment. Values below this noise floor are likely below our ability to faithfully detect differences in intron splicing behavior. Rows marked with ** in [Table 2](#) show intron pairs that fall below this threshold, potentially due to the low number of intermediate transcripts captured for fast-splicing introns.

Calculation of slow-moving zone dimension

To find the diameter of each (roughly circular) cloud, we used the equation $d = 2 \cdot \sqrt{(\text{median area}) / \pi}$, then converted these values from expanded space into unexpanded space by dividing by 4.65. Because the 5' end, 3' end, and intron clouds were of a similar size, we averaged the values from each cloud to give an approximate slow moving zone diameter of 0.36 microns. Given the uncertainties inherent to these calculations, these estimates are meant to provide an order of magnitude for the size of the zone, rather than precise measurements.

Below are the full calculations:

3' cloud:

Median cloud area = 3.596 microns²

Cloud Diameter = $2 \cdot \sqrt{(3.596) / \pi} = 2.14$ microns

In unexpanded space, cloud diameter = **0.46** microns

5' cloud:

Median cloud area = 1.862 microns²

Cloud Diameter = $2 \cdot \sqrt{(1.862) / \pi} = 1.54$ microns

In unexpanded space, cloud diameter = **0.33** microns

Intron cloud:

Median cloud area = 1.474 microns²

Cloud Diameter = $2 \cdot \sqrt{(1.474) / \pi} = 1.37$ microns

In unexpanded space, cloud diameter = **0.29** microns

Approximate size of the slow moving zone: **0.36** microns

Comparison to point source diffusion with degradation model

In order to evaluate whether diffusion of pre-mRNA from the site of transcription was compatible with our observations of clouds at the site of transcription revealed by expansion microscopy, we used a model of pre-mRNA diffusion that assumed a source at the site of transcription and a constant rate of degradation. The equation describing this model is given by (27):

$$\partial C / \partial t = D \Delta C - \gamma C + R_0 \delta(r),$$

where C is the concentration as a function of the radial distance and time, D is the diffusion constant, gamma is the degradation rate, R₀ is the rate of production, and $\delta(r)$ is the delta function. The steady state solution in 3D is given by:

$$C(r) = C_0 \exp(-r/\lambda),$$

where C₀ is the concentration at the site of transcription, and lambda is $\sqrt{D/\gamma}$.

We fit this formula to the radial distribution of pre-mRNA density from the region from 3 to 10 microns away from the transcription site, in which region we assume that the pre-mRNA are freely diffusing in the nucleoplasm. Note that our estimate for lambda in this region was roughly 3.34 microns. As a check for numerical consistency, we used an estimate of nucleoplasmic diffusion of 0.034 microns²/sec (7) to obtain a degradation rate gamma of approximately 0.183 per minute, which yields an average lifetime of around 5.46 minutes for the pre-mRNA. This value is in line with what is generally accepted in the field and thus provided validation for the accuracy of our model and fit procedure. In order to see what concentration the diffusion and degradation model would predict at the transcription site itself, we extrapolated to the y-axis (radial distance = 0), yielding an estimated concentration of 18 molecules per cubic micron. We then measured the actual transcription site density at the site of transcription by counting the number of molecules in the vicinity using expansion microscopy and dividing by an estimated transcription site volume,

yielding 235 molecules per cubic micron. (The volume was estimated by taking the area of the transcription site spots in 2D, estimating the radius of a putatively circular transcription site, and then using that radius to compute the volume of a 3D sphere.)

Data and Code Availability

All data and code to generate figures can be found at https://www.dropbox.com/sh/sqr9zk2icptemfa/AABHRHroWbcowgPr_4VS2x9ba?dl=0 .

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Reviewer #1 (Public Review):

The manuscript has helped address a long-standing mystery in splicing regulation: whether splicing occurs co- or post-transcriptionally. Specifically, the authors (1) uniquely combined smFISH, expansion microscopy, and live cell imaging; (2) revealed the ordering and spatial distribution of splicing steps; and (3) discovered that nascent, not-yet-spliced transcripts move more slowly around the transcription site and undergo splicing as they move through the clouds. Based on the experimental results, the authors suggest that the observation of co-transcriptional splicing in previous literature could be due to the limitation of imaging resolution, meaning that the observed co-transcriptional splicing might actually be post-transcriptional splicing occurring in proximity to the transcription site. Overall, the work presented here clearly provides a comprehensive picture of splicing regulation.

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Reviewer #2 (Public Review):

Allison Coté et al. investigated the ordering and spatial distribution of nascent transcripts in several cells using smFISH, expansion microscopy, and live-cell imaging. They find that pre-mRNA splicing occurs post-transcriptionally at the clouds around the transcription start site, termed the transcription site proximal zone. They show that pre-mRNA may undergo

continuous splicing when they pass through the zone after transcription. These data suggest a unifying model for explaining previously reported co-transcriptional splicing events and provide a direction for further study of the nature of the slow-moving zone around the transcription start site.

This paper is well-written. The findings are very important, and the data supports the conclusions well. However, some aspects of the image and description need to be clarified and revised.

1. The sentence "By distinguishing the separate fluorescent signals from probes bound to exons and introns, we could visualize splicing intermediates (represented by colocalized intron and exon spots) relative to the site of transcription (represented by bright colocalized intron and exon spots) and fully spliced products (represented by exon spots alone)." is accidentally repeated twice, one of them should be deleted.
2. The authors describe Figure 4E and 4F results in the main text as that "we performed RNA FISH simultaneously with immunofluorescence for SC35, a component of speckles, and saw that these compartmentalized pre-mRNA did indeed appear near nuclear speckles both before (Supplementary Figure 6C) and after (Figure 4E) splicing inhibition." However, no SC35 staining is shown in the Figure 4E. A similar situation happened in describing Figure 4F.

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Author Response

The following is the authors' response to the original reviews.

Reviewer #1 (Public Review):

The manuscript has helped address a long-standing mystery in splicing regulation: whether splicing occurs co- or post-transcriptionally. Specifically, the authors (1) uniquely combined smFISH, expansion microscopy, and live cell imaging; (2) revealed the ordering and spatial distribution of splicing steps; and (3) discovered that nascent, not-yet-spliced transcripts move more slowly around the transcription site and undergo splicing as they move through the clouds. Based on the experimental results, the authors suggest that the observation of co-transcriptional splicing in previous literature could be due to the limitation of imaging resolution, meaning that the observed co-transcriptional splicing might actually be post-transcriptional splicing occurring in proximity to the transcription site. Overall, the work presented here clearly provides a comprehensive picture of splicing regulation.

Major points:

1. *Linearity of expansion microscopy. For Figure 2B, it would be helpful to display the same sample before and after expansion, just like Supplementary Figure 3, but with a transcription site and "cloud". In the current version, the transcription site looks quite different in the not-expanded (more green dots on the left) and expanded image (more green dots on the top).*

We thank the reviewer for this comment on linearity of expansion. Based on our prior manuscript (Chen et al 2015 Nature Methods. PMID: 27376770), we expect expansion microscopy to yield isotropic expansion. Indeed, as shown in Supplemental Figure 3, we confirmed that expansion of nuclei (3B, top) and transcripts (3B, bottom) is isotropic. Additionally, before splicing inhibition, we demonstrated the linearity of expansion for a

transcription site (3B, left), shown at standard resolution with intron stain. The images shown in Figure 2B are meant solely to illustrate the change in resolution upon expansion, and are not meant to imply spatial matching between the expanded and unexpanded image. We apologize for the confusion and have clarified this in the figure legend for Figure 2.

We also point the reader towards Supplemental Figure 4, in which we validate the use of expansion microscopy in these findings. We show that transcription sites in expanded samples were the same size as those imaged using stochastic optical reconstruction microscopy (STORM), demonstrating that expansion did not significantly alter the morphology of the site.

1. *FISH dot colocalization. What is the colocalization rate of FISH dots in general under experimental conditions? In addition, in Figures 2C and 2G, why do some 3'exon dots not have co-localized 5'exon dots?*

We thank the reviewer for asking for these important clarifications. Under standard (non-expanded) conditions, our colocalization of 3' and 5' spots varies by gene, but more than 75% of intron spots colocalize with exon spots for the vast majority of transcripts we evaluated. The percentage of colocalization for each gene and intron can be found in column 4 of Table 1.

Regarding the second point—these individual images may not reflect the actual quantitative number of spot counts at the site, as these transcription sites have a sizable Z dimension that is difficult to capture in one image, and certain dyes are more easily visually distinguished in contrasted images than others. These factors may cause some 3' spots to appear without a corresponding co-localized 5' spot in these images. We refer the reviewer to Supplemental Figure 4C for quantitative spot counting of an expanded transcription site, for which there are a similar number of 3' end and 5' end spots within the entire Z-stacked image. Importantly, these transcription site clouds contain longer, unspliced transcripts, potentially leading to further separation between the 5' and 3' ends of a single transcript when compared to a cytoplasmic, spliced transcript (quantified in Figure 2I).

1. *It would be helpful if the authors uploaded a few examples of live cell imaging movies.*

Certainly! Please refer to the new Supplementary Movies 1-3 for representative examples of live cell imaging data.

1. *It is recommended to double-check the text for errors.*

We apologize for errors in the original manuscript, and have made the appropriate corrections.

Reviewer #2 (Public Review):

Allison Coté et al. investigated the ordering and spatial distribution of nascent transcripts in several cells using smFISH, expansion microscopy, and live-cell imaging. They find that pre-mRNA splicing occurs post-transcriptionally at the clouds around the transcription start site, termed the transcription site proximal zone. They show that pre-mRNA may undergo continuous splicing when they pass through the zone after transcription. These data suggest a unifying model for explaining previously reported co-transcriptional splicing events and provide a direction for further study of the nature of the slow-moving zone around the transcription start site.

This paper is well-written. The findings are very important, and the data supports the conclusions well. However, some aspects of the image and description need to be clarified and revised.

The authors describe Figure 4E and 4F results in the main text as that "we performed RNA FISH simultaneously with immunofluorescence for SC35, a component of speckles, and saw that this compartmentalized pre-mRNA did indeed appear near nuclear speckles both before (Supplementary Figure 6C) and after (Figure 4E) splicing inhibition." However, no SC35 staining is shown in the Figure 4E. A similar situation happened in describing Figure 4F.

We thank the reviewer for noting this error. We mistakenly called in text for Figure 4E, when we meant to refer to Figure 4G, which shows combined RNA FISH and SC35 immunofluorescence show compartmentalization within nuclear speckles. Figures 4E and 4F do not show SC35 immunofluorescence. We have altered the text and figure captions accordingly. Recommendations for the authors: please note that you control which revisions to undertake from the public reviews and recommendations for the authors Reviewer #1 (Recommendations For The Authors):

Minor points:

- 1. For Figures, it would be better to mark co-transcriptional and proximal post-transcriptional splicing in a clearer way. Like in Figure 1A, the simulated RNA FISH signals are almost identical across two conditions, which is a bit confusing. Overlapping and close proximity shall be better illustrated in related figures.*

We thank the reviewer for these suggestions. We have iterated these figures through multiple revisions and have found that these diagrams tend to resonate the most, so we have elected to keep them as is, but we do appreciate the suggestion.

- 1. May include some details of expansion microscopy in the last paragraph of the Introduction. For example, why introduce expansion microscopy? To what level it can help overcome the diffraction limit?*

We thank the reviewer for this comment, and have added additional text to this paragraph to further set up the use of expansion microscopy.

- 1. Double-check the formatting. Some sub-titles are in Bold, some in Italic.*

We apologize for any formatting errors, and have made the appropriate corrections.

1. Please double-check the writing. I find many incompatible parts across the manuscript. For example, as described in the Figure 1D caption, there aren't "first" and "second" graphs in the figure. Moreover, some writings require additional refinement. For instance, in the Introduction part, the paragraph discussing RNA imaging, various techniques (such as FISH and live imaging), and concerns (such as microscopy resolution, chromatin fraction, and limitations related to reporter genes) are intertwined without clear indexing or logical structuring. Similar cases in other paragraphs too. Last but not least, I can even find repetitive sentences across the manuscript. For instance, I believe that the authors forgot to delete "By distinguishing the separate fluorescent signals from probes bound to exons and introns, we could visualize splicing intermediates (represented by colocalized intron and exon spots) relative to the site of transcription (represented by bright colocalized intron and exon spots) and fully spliced products (represented by exon spots alone)." in the first paragraph of the Results part, as the exact same sentence re-occurs right after. I've only listed a few examples here. Please refine the manuscript.

We apologize for any errors in the original manuscript, and have made the appropriate corrections.

Reviewer #2 (Recommendations For The Authors):

1. The sentence "By distinguishing the separate fluorescent signals from probes bound to exons and introns, we could visualize splicing intermediates (represented by colocalized intron and exon spots) relative to the site of transcription (represented by bright colocalized intron and exon spots) and fully spliced products (represented by exon spots alone)." is accidentally repeated twice, one of them should be deleted.

We apologize for this duplication, and have made the appropriate correction.