Full-length mRNA sequencing uncovers a widespread coupling between transcription and mRNA processing

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ABSTRACT

The multifaceted control of gene expression requires tight coordination of regulatory mechanisms at transcriptional and post-transcriptional level. Here, we studied the interdependence of transcription, splicing and polyadenylation events on single mRNA molecules by full-length mRNA sequencing. In MCF-7 breast cancer cells, we found 2,700 genes with interdependent alternative transcription, splicing and polyadenylation events, both in proximal and distant parts of mRNA molecules. The analysis of three human primary tissues revealed similar patterns of interdependency between transcription and mRNA processing events. We predict thousands of novel Open Reading Frames from the sequence of full-length mRNAs and obtained evidence for their translation by shotgun proteomics. The mapping database rescued 358 previously unassigned peptides and improved the assignment of others. By recognizing sample-specific amino-acid changes and novel splicing patterns, full-length mRNA sequencing improved proteogenomics analysis of MCF-7 cells. Our findings demonstrate that our understanding of transcriptome complexity is far from complete and provides a basis to reveal largely unresolved mechanisms that coordinate transcription and mRNA processing.
INTRODUCTION

The formation of a mature messenger RNA (mRNA) is a multi-step process. In higher eukaryotes, variations in each of these steps, including alternative transcription initiation, differential splicing of exons, and alternative polyadenylation site usage, change the content of the mature transcript. The multitude of transcripts arising from these events offers an enormous diversity of protein isoforms that can be produced from a single gene locus. Tight regulation and coordination of these processes ensures the production of a (limited) set of cell-, tissue- and condition-specific transcript variants to meet variable cellular protein requirements1-4. Whether or not these processes are co-transcriptionally linked is currently largely unknown, as are the mechanisms that couple transcription with 5’ end capping, splicing, and 3’ end formation (reviewed in 5). Thus, resolving full transcript structures and accurate quantification of the abundance of alternative transcripts are important steps towards the detection and understanding of these mechanisms.

RNA sequencing (RNA-Seq) has become a central technology for deciphering the global RNA expression patterns. However, reconstruction and expression level estimation of alternative transcripts using standard RNA-Seq experiments is limited and prone to error due to relatively short read length (typically up to 150 nucleotides) and required amplification steps of second-generation sequencing technologies6-7. It is apparent that single-molecule long reads that capture the entire RNA molecule can offer a better understanding of the rich patterns of alternative transcription and mRNA processing events and, hence, the underlying biology.

Despite a number of studies that have pursued long read sequencing to connect different exons or even capture entire transcripts with a rather limited sequencing depth8-14, the coupling between transcription and mRNA processing has not been extensively studied. Here, we investigate the global pattern of coupling between transcription, splicing and polyadenylation in MCF-7 human breast cancer cell line and three human tissues, which are deeply sequenced using the single-molecule real-time Pacific Biosciences RSII sequencing platform. We show that transcription and mRNA processing are tightly coupled and that such interdependencies can be found across the entire RNA molecule and across large intra-molecular distances. We demonstrate that transcript identification and understanding of coupling between processes that are involved in the formation of these transcripts is far from complete, even in well-characterized human cell lines such as MCF-7. This study provides an in-depth view of the true complexity of the transcriptome and, for the first time, shows the tight and global interdependency between alternative transcription, splicing and polyadenylation. We also show the value of this resource in relation to translation and sample-specific survey of the proteome.

RESULTS

Detection of transcript variants and the associated interdependencies between alternative exons

To investigate the genome-wide coupling of transcription and mRNA processing events, full-length mRNAs from MCF-7 human breast cancer cells were sequenced on 147 SMRT cells using Pacific Biosciences RSII platform (Supplementary Table 1). Prior to sequencing, parts of the sequencing library were size selected to allow for a good representation of longer transcripts.

Transcript structures were defined by applying the isoform-level clustering algorithm (ICE) on full-length reads, capturing the entire mRNA molecule (containing both 5’ and 3’ primer sequences). Transcript sequences were further polished using both full-length and partial reads (Fig. 1A). The analysis pipeline precisely determined the position of polyadenylation sites (presence of poly(A) tail in the sequence) and intron-exon boundaries, as evident from the presence of the canonical GU motif in 93% of donor splice sites and the canonical AG motif in 95% of acceptor splice sites. In fact, 90% of introns are defined by canonical splice-site motifs (GU-AG). In addition to 7,364 single-exon transcripts, the MCF-7 transcriptome consists of 11,350 multi-exon genes of which 69% produced multiple transcript structures (Supplementary Fig. 1). Transcripts range from 54bp to 10,792bp in length with an average of 82 supporting reads (Supplementary Fig. 1). Interestingly, 49% of identified transcripts in MCF-7 are identified as potentially novel in comparison with the GENCODE annotation (Supplementary Table 2).

The gene expression levels measured in full-length mRNA sequencing data showed significant Spearman correlations (correlation coefficient greater than 0.74) with 5 publicly available RNA-Seq datasets that were generated on Illumina HiSeq2000 or HiSeq2500 platforms (Supplementary Fig. 2A). Differences in library preparation protocols, presence of fewer duplicates and uniformity of coverage in the PacBio data as well as contrast in sequencing dynamics contribute to minor differences observed in estimated gene expression levels15. Although we observed some inter-dataset differences in detected genes, for most genes, the results from all datasets were in concordance (Supplementary Fig. 2B). Transcript lengths and loading bias did not significantly contribute to inter-platform differences for gene detection as similar results were also found for intra-platform comparisons (Supplementary Fig. 2C). Thus, the full-length mRNA sequencing data can be reliably used for locus-specific quantification of transcript abundance in MCF-7 cells.

To detect and characterize the dependency between transcription and mRNA processing events, we designed the following analysis strategy (Fig. 1F): For each gene, the union of all exonic sequences was considered as the available sequence and the union of all unique transcription start sites (TSSs), exons (defined as having distinct donor and acceptor splice sites), and polyadenylation sites (PASs) was used as a set of available features (Fig. 1B). Mutual inclusivity or exclusivity of all possible combinations of features was assessed based on the number of reads that support the inclusion or exclusion of each pair of features. Subsequently, we applied a Fisher's exact test to evaluate statistical significance of the interdependency between a pair of features (Fig. 1C; also see Methods). It is important to note that as features may be coupled to a few other features, the actual coupling events can be summarized into a series of network components within a gene-specific interaction network to capture the independent coupling events (Fig. 1D). These components can be summarized based on the level of connectivity or mutual inclusivity or exclusivity within each network to construct subnetworks. We subsequently searched the sequences containing the coupled alternative exons or poly(A) sites for enriched sequence motifs and tested whether they contain motifs of known RNA-binding proteins (Fig. 1E).
The MCF-7 transcriptome data consist of 11,350 multi-exon genes that present 3,532,796 combinations of features (TSSs, exons, and PASs). Most combinations represent exon-exon pairs as many loci contain only a single TSS or PAS whereas all loci are multi-exonic (Supplementary Fig. 3). Since the test is only valid for genes with multiple transcripts, only 7,708 genes and 3,055,099 pairs of features (TSSs, exons, and PASs) were included in the statistical analysis. Importantly, pairs of features that are naturally interdependent (such as overlapping features or PASs and the terminal exons) have been removed from the analysis.

Almost ten percent of all feature pairs were significantly coupled (p-value < 1.4e-08, after Bonferroni correction for multiple testing). Generally, we observed large effect sizes for coupled features with almost equal distribution over mutually inclusive (52%) and mutual exclusive pairwise interdependencies (Supplementary Fig. 4A). Remarkably, we observed coupling between mRNA features in over 60% of all multi-exon genes (6,825 out of 11,350; Fig. 2A), represented by 18,078 mutually inclusive and 10,092 mutually exclusive subnetwork components (Fig. 2B). Particularly, alternative TSSs appear to have a significant impact on mRNA processing as over 80% of multi-transcript genes exhibit interdependency between the choice of TSS and alternative splicing. We found a substantial amount of interdependencies between all types of features (Fig. 2B; Supplementary Fig. 4A). Of the 6,825 genes with at least one coupling event, 2,700 (37%) showed interdependencies between all classes of features: alternative TSS linked to alternative exons, alternative exon to alternative exon linkage, alternative PAS linked to alternative exons, and alternative TSSs to alternative PASs. Thus, the deep sequencing of full-length mRNAs provided a first image of the large degree of coordination in the usage of alternative TSSs, exons and PASs, restricting the number of produced transcripts given the substantial amount of combinatorial possibilities.

**General properties of coupling in human MCF-7 transcriptome**

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The length of individual transcripts was not associated with the likelihood of a significant coupling event in that transcript (Supplementary Fig. 4B). However, after examining the length of the union of exonic sequences per gene and the likelihood of observing coupling, we found that significant coupling events were enriched in genes with larger available exonic sequences (Supplementary Fig. 4B). Expectedly, larger exonic regions in each locus gives rise to a larger repertoire of possible transcripts, requiring more extensive regulation of the synthesis for transcripts containing different subset of features.

We also examined the effect of the relative position in the gene and the distance between features on the observed degree of coupling. As expected, most TSSs were located at the most 5'-end of genes. However, interdependency of alternative TSSs was observed across the entire gene (Fig. 2C, left panel). Alternative TSSs were preferentially coupled to alternative splicing events in relatively close proximity to the TSSs, near the 5'-end, as well as distal exons at the 3'-end (Fig. 2C, right panel). Nevertheless, examples of the coupling of alternative TSS and alternative exon usage across large distances, and spanning multiple exons were also frequently observed (Supplementary Fig. 5,6; ALDOA and C1QTNF6). More evidence for interactions across the entire length of genes comes from the significant coupling between TSS and PAS, the two most distant features in an mRNA molecule (Supplementary Fig. 7; NCAPD2).

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The fraction of alternative exons was higher at the 5’-end; however, dependencies between multiple alternative splicing events were uniformly observed across the entire gene (Fig. 2D; Supplementary Fig. 8, LMNA). Despite the uniform distribution of exon-exon coupling events and the presence of distant coupling events (Supplementary Fig. 9, RELA), most interdependent alternative splicing events were between nearby or neighboring exons (Supplementary Fig. 10, CALU).

Like alternative transcription start sites, coupling events linked to alternative PAS usage were found across the entire gene (Fig. 2E). In concordance with published literature16-18, alternative PAS usage was preferentially coupled to nearby alternative exons (Fig. 2E). Nevertheless, a substantial proportion of PASs was coupled to alternative exons in more 5’-regions of genes.

We performed Sanger sequencing to independently verify identified coupling events for a set of gene loci. Due to limited range of alternative technologies such as Sanger sequencing, only relatively close coupling events could be assessed. In most cases, the Sanger sequencing results were in full concordance with the coupling events identified using full-length mRNA sequencing (Supplementary Fig. 5, 6, 8, 9). Next, we carried out a single-molecule RNA in situ fluorescence (smRNA FISH) co-localization approach19, 20 to examine the alternative splicing events that were identified by full-length RNA sequencing and confirmed by Sanger sequencing. Four probe sets were designed to detect different segments of the CALU mRNAs at single-molecule level. The full CALU_E probe set covers the common exons on the full-length variants, whereas the 9-oligo CALU_E4 and CALU_E5 sets were designed to specifically hybridize to either exon 4 or 5. The signal from the common exon probes was easily detected (Supplementary Fig. 10), and could be used for co-localized signals from the exon 4, exon 5 and intron 1 sets. The average numbers and distribution of signals revealed that cytoplasmic mRNAs predominantly either include exon 4 (~50 copies per cell) or exon 5 (~10 copies per cell), followed by mRNAs that do not include exon 4 and 5 (~9 copies per cell). The co-localized signals from all three exon-sets and all four sets were exclusively located in the nuclear domain with much lower abundance (Supplementary Fig. 10). This is consistent with active CALU gene transcription bursts that contain pre-mRNAs in various states of post-transcriptional processing, and thus expected to contain common exons, alternative exons, and introns. In short, by applying RNA FISH, we could reveal the identity and distribution of single mRNA molecules of CALU as well as independently confirm the mutual exclusivity of exon 4 and 5 in MCF-7 cells. Together, the results of Sanger sequencing and RNA FISH experiments are in concordance with full-length RNA sequencing and support the coupling events identified.

Poly(A) signal usage for coupled polyadenylation sites

Most alternative PASs in MCF-7 cells were found in tandem (in the same terminal exon, generating a longer or shorter 3’-UTR). From 5,498 genes with multiple PASs, we identified 10,927 tandem PASs in the same exon across 3,983 genes (72%). From these, 3,465 loci (87%) included PASs that were significantly coupled with alternative TSSs or alternative exons. The high number of tandem 3’ UTRs, in both coupled and uncoupled PAS-exon pairs, partly disagrees with previously reported general shortening of 3’ UTRs in MCF-7 cell line21. Nevertheless, many coupling events between alternative PASs and inclusion or exclusion of alternative exons are due to the use of exonic and intronic PASs (8,171 non-tandem PASs), leading to the formation of new 3’ UTRs.

To assess whether certain poly(A) signals are preferentially associated with alternative transcription and splicing, we searched for canonical (AATAAA and ATTAAA) and eleven known non-canonical poly(A) signals in the 35bp sequences upstream of the identified PASs. Canonical poly(A) signals could be found in the 35bp sequences upstream of 54% of all PASs (Fig. 3A). The
that can be recognized by the splicing modulators RBM24 26 and SAMD4A27 proteins. In addition, the R2 sequences were enriched
(Supplementary Fig. 11A). In total, we identified 7% of 789,054 possible combinations to be significantly interdependent.

To ensure that we could assess for coupling between transcription and mRNA processing, 30.7% were found to have at least one coupling

primary tissues was lower than that of MCF-7, we could only examine the relatively abundant genes. In human brain, of 5,381 genes
also be found in the full-length transcriptomes of three primary human tissues: brain, heart and liver. As the sequencing depth in the
We investigated whether the interdependent transcription, splicing and polyadenylation events identified in MCF-7 cancer cells could
Conservation of interdependencies across human tissues

Our approach involved analyzing the potential involvement of RNA-binding proteins (RBPs) in the coordination of alternative transcription and mRNA processing events by enrichment analysis. The results indicate that RBPs play a significant role in regulating alternative splicing and mRNA stability. For instance, the AKCCTGG motif was found to be enriched in sequences upstream of PASs that were coupled with alternative TSSs. This suggests the importance of MBNL proteins in mediating alternative splicing and alternative polyadenylation.

Identification of binding motifs for RNA-binding proteins potentially involved in coupling

We identified several motifs associated with alternative splicing modulators, such as FUS32-34, SRSF235, RBM536-38, PCBPI1 and PCBPI239, 40

For coupled nonterminal exons, the sequences from the R1 domain (upstream of the acceptor) were enriched for motifs (Table 2) that can be recognized by the splicing modulators RBM2434 and SADMA427 proteins. In addition, the R2 sequences were enriched for binding sites of RBM4824, NOVA229, 30, and RBM2821 proteins, known to play a role in regulating alternative splicing. However, these motifs were not found to be preferentially associated with exons that were coupled with alternative TSSs or alternative exons. Together, these results suggest an important role of MBNL proteins in mediating alternative splicing and alternative polyadenylation.

Conservation of interdependencies across human tissues

We assessed the conservation of individual coupling events in different samples. From the total number of feature pairs that were found to be interdependent in at least one sample, by far the majority were found to be specific to a given tissue or MCF-7 cells since only 6 – 14% were found to be coupled in two examined datasets (Supplementary Fig. 11C). Interestingly, feature pairs that were

Table 1 – Enrichment of MBNL binding site motifs in sequences upstream of alternative PAS with unknown poly(A) signal that are coupled with alternative TSS or alternative exons.

<table>
<thead>
<tr>
<th>Motifs</th>
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<th>P-value a</th>
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<tr>
<td>AKCCTGG</td>
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<td>CTSCYB</td>
<td>Masuda, 2012 24</td>
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<td>YGCV</td>
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<td>RSCWTGSK</td>
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</tr>
<tr>
<td>TGCTYSSY</td>
<td>Batra, 2014 27 – MBLN2</td>
<td>95</td>
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<tr>
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Table 1: The enrichment of binding motifs in sequences upstream of PASs without a known poly(A) signal were calculated by Fisher’s exact test (two-sided). A randomly generated set was used as a background for enrichment analysis.

b Coupled PAS Not Coupled PAS P-value 
6,979 6,979 – 3,614 3,338 –

* The enrichment of binding motifs in sequences upstream of PASs without a known poly(A) signal were calculated by Fisher’s exact test (one-sided). A randomly generated set was used as a background for enrichment analysis.

§ PASs without significant coupling were used as the background set to identify a binding site that is enriched in the coupled PASs without a known poly(A) signal.

Table 2 – Enrichment of MBNL binding site motifs in sequences upstream of alternative PAS with unknown poly(A) signal that are coupled with alternative TSS or alternative exons.

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found to be interdependent in two samples were generally (~77%) mutually inclusive or exclusive in both tissues (Supplementary Fig. 11C). This observation suggests that although most coupling events are tissue- or condition-specific, there seems to be a set of interdependencies that are conserved across multiple human tissues.

Characterization of the proteome of MCF-7 cells in light of full-length transcripts

The MCF-7 transcriptome consists of 11,350 multi-exon genes and 7,364 polyadenylated single-exon transcripts, from which we could identify open-reading frames (ORFs) for 10,385 and 3,591, respectively, based on full-length mRNA sequences associated with each gene locus (Supplementary Fig. 12). While almost every one of the 7,814 multi-transcript genes were found to have coding capacity (97.4%), we could identify ORF for a smaller proportion of 3,536 single-transcript genes (78.4%). In addition, 48.8% of single-exon transcripts were found to have a predicted ORF.

To assess the translational characteristics of MCF-7 cells especially in relation to alternatively spliced isoforms and identified interdependencies between transcription and mRNA processing, we analyzed a publicly available coverage, bottom-up mass-spectrometry (MS) dataset. For MS searching, a customized proteomics search database was constructed, consisting of protein sequences derived from Gencode v19 (95,309 entries), ORFs predicted from MCF-7 PacBio sequences (47,325 entries), and a database of frequently observed contaminant proteins (115 entries). The inclusion of the Gencode database allows for identification of any peptides derived from transcripts that were missed by the PacBio data. The MS searching was done using the Morpheus algorithm, wherein all theoretical peptides resulting from an in silico tryptic digestion of protein entries (from Gencode, PacBio, or contaminants database) were matched against the raw mass spectra to identify peptides. We detected 38,628 unique peptides, passing the FDR of 1%, that could be unambiguously associated with the Gencode (version 19) and/or PacBio-based predicted protein-coding sequences in MCF-7 cells. In 2,872 cases, the identified peptide was only present in the Gencode database, whereas in 358 cases, the peptide was only found in the PacBio database. In addition, we found 2,150 peptides associated with 481 single-exon transcripts.

Identified peptides range from 7 to 56 amino acids (aa) with an average of over 15aa in size (Fig. 4A). We observed a strong correlation ($r = 0.96; p < 2.2e-16$) for the number of peptides per gene based on full-length PacBio or Gencode transcripts (Fig. 4B), suggesting that full-length RNA sequencing data can capture a comparable repertoire of protein coding sequences in MCF-7 cells. Still, it is evident that for a few select ultra-long transcripts, such as AHNAK, DYNC1H1 and PLEC, peptides were underrepresented in PacBio database compared to Gencode. This is likely because it is quite challenging to synthesize ultra-long transcripts using current full-length cDNA synthesis protocols. The central domain of AHNAK consists of 128aa repeat that is mostly absent in PacBio transcripts.

Comparison between Gencode- and PacBio-based classification of peptides revealed that PacBio-based analysis of protein peptides provides a more specific peptide assignment, most likely due to use of a sample-specific set of predicted ORFs from the MCF-7 full-length transcriptome as compared with Gencode annotation (Fig. 4C,D; Supplementary Table 3). Indeed, Gencode represents protein annotations for the entire human proteome, whereas the MCF-7 derived proteome is specific to breast cancer cells. As shown...
in the empirical cumulative distribution of relative peptide counts per gene (Fig. 4C), there is a clear enrichment of peptides that discriminate between different ORFs derived from the same gene locus in PacBio data compared to Gencode annotation whereas the overall peptide counts per gene remain the same between the two annotations. In fact, 50% of peptides that are classified as single-gene hits (matching all transcripts of the associated gene) were classified as sub-gene hit based on PacBio transcripts due to alternative splicing events that are absent in Gencode version 19 annotation (Supplementary Table 3). Likewise, most peptides that were classified as single-transcript hits were either categorized as sub-gene (46%) or single-gene (18%) hits in PacBio.
We identified 358 novel peptide hits that were missed in Gencode (Fig. 4D; Supplementary Fig. 18) and were mainly represented by sub-genie class of peptides (73%). The quality of these novel peptides was adequate as we observed no difference in the quality of peptide hits between those found only in PacBio (‘novel’ peptides) versus peptides found in Gencode (‘known’ peptides), as well as peptides with discordant classification based on Gencode or PacBio (Supplementary Fig. 19). Essentially, the distribution of peptide MS search scores (i.e., Q value or Morpheus score) was undistinguishable between each group. However, we found different gene assignments for a set of peptides mainly due to single amino acid substitutions (SAS) in MCF-7 compared to the reference sequence (Supplementary Fig. 20). Presence of SAS events without knowledge of their existence through sample-specific protein database can either lead to mismatch or failure to detect peptides using general annotations such as Gencode41. This is more prominent for sample-specific differential expression of paralogous genes (Supplementary Fig. 21,22). These observations are partly reflected by 41% multi-genie peptides that can be specifically assigned to a single gene using PacBio data.

Although most peptide hits were found within a single exon boundary, 30% were associated with exon-exon junctions covering up to 5 consecutive exons (Fig. 4E). From 49,263 peptides derived from parts of the transcripts that span exon-exon junctions, 10,364 peptides were associated with exons that were found to be mutually inclusive as we rarely (<2%) observed peptides that matched mutually exclusive exons (Fig. 4E). As shown for ITGB4 gene (Fig. 4F), differential splicing pattern in MCF-7 transcriptome can significantly influence the characterization of matching peptides as well as the impact of coupling in coding protein.

DISCUSSION
Short-read RNA sequencing has become central in assessing the global RNA expression patterns. However, as a result of the complexity of human transcriptome and limited size of the sequenced RNA fragment, this approach disappoints in precise reconstruction and reliable expression estimation of transcript variants6, 7, 44. In contrast, single-molecule long-read sequencing provides a unique opportunity to reveal the true complexity of the transcriptome6, 10, 45, 46 as it can determine the full structure of individual transcripts by full-length sequencing.

Here, we have analyzed the deepest and longest transcriptome data so far to better understand the extent of interdependencies between transcription and mRNA processing. Notably, full-length mRNA sequencing and de novo identification of high-quality sequence of transcript variants uncovered an unprecedented amount of potentially novel transcripts in MCF-7 cells and three human tissues. Our findings not only unravel a higher level of alternative transcription, splicing and polyadenylation in MCF-7 transcriptome than previously appreciated, but also provide valuable information on the preferential selection and interdependency between these processes.

We showed that transcription initiation, splicing and 3’ end formation are tightly coupled in over 60% of genes with multiple transcripts and such interdependencies can be found across the entire length of the mRNA molecule. Notably, we report an unforeseen and unprecedented number of genes that undergo a vigorous preferential selection during transcription and mRNA processing as the choice of transcription initiation subsequently influences both alternative splicing of exons and the usage of alternative poly(A) site. Ample evidence points at the critical role for RNA Pol II in the coordination between transcription and mRNA processing (reviewed in 5, 47-49). It has been shown that RNA Pol II initiation, pausing, and elongation rate can influence alternative splicing and polyadenylation of transcripts50-53. Moreover, the C-terminal domain of RNA Pol II likely acts as a scaffold for regulatory factors that are involved in splicing and polyadenylation (reviewed in 49). Concordantly, we found an enrichment of coupling events in larger genes that seem to undergo a more extensive regulation during mRNA synthesis. However, the exact mechanisms by which the coordination is achieved remain largely unclear.

From previous studies, it became clear that polyadenylation couples with splicing machinery to influence the removal or inclusion of the last intron16, 54, 55. We now show that (i) the interdependencies between splicing and polyadenylation are not necessarily restricted to the final introns, (ii) that they can also involve introns that are far from the poly(A) site and (iii) that the coupling between splicing and alternative polyadenylation is not restricted to tandem 3’ UTRs. The exact mechanisms by which these coupling events are achieved fall beyond the scope of this study. Previously, it has been shown that spliceosome components are also part of the human pre-mRNA 3’-end processing complex40. Moreover, it is likely that there are RNA-binding proteins with a dual role in alternative splicing and polyadenylation to coordinate mRNA processing events. hnRNP H18, CstF6455, MBNL1 and ELAV1 (HuR)22, 57-59 are components of the pre-mRNA 3'-end processing complex56. Moreover, it is likely that there are RNA-binding proteins with a dual role in alternative splicing and polyadenylation of transcripts50-53. From 49,263 peptides derived from parts of the transcripts that span exon-exon junctions, 10,364 peptides were associated with exons that were found to be mutually inclusive as we rarely (<2%) observed peptides that matched mutually exclusive exons (Fig. 4E). As shown for ITGB4 gene (Fig. 4F), differential splicing pattern in MCF-7 transcriptome can significantly influence the characterization of matching peptides as well as the impact of coupling in coding protein.

Based on the reported sequence preference of MBNL proteins23, MBNL3 is the most likely candidate of the MBNL family responsible for the coordination between alternative splicing and polyadenylation in transcripts of MCF-7 cells. However, it is not clear to what extent these findings can be extrapolated to other cell lines and cell types. In MCF-7 cells, although we generally do not find very long transcripts, we do not see any evidence for a shift to more proximal poly(A) sites that were previously reported21, 40 as many genes have tandem poly(A) sites. Nevertheless, we observe many cases in which the use of alternative poly(A) site is utilized through different 3’ UTRs and not tandem poly(A) sites in the same 3’ UTR region. In such cases, the absence of binding sites for regulatory proteins and miRNAs can enhance the tumorigenic activity of MCF-7 cells by allowing transcripts to escape from inhibition21. It is not clear whether MBNL-mediated polyadenylation, coupled with transcription initiation and splicing, is achieved through direct recruitment of RNA processing machinery or via alteration of secondary structure and formation of RNA molecules that, in turn, affect the choice...
for poly(A) site usage. Our analysis also identified a few more candidates with dual roles in mRNA processing, notably multiple RBM proteins SAMD4A, NOVA2, FUS and SRSF2, which warrant further investigations by performing additional functional assays.

In MCF-7 cells, the multitude of protein isoforms arising from alternative transcription and mRNA processing is not fully reflected in Gencode protein annotation as sample-specific set of predicted open-reading frames seem to provide a better specificity in discriminating peptides based on differences in open-reading frames derived from the same gene locus. Furthermore, as shown in this study, the presence of sample-specific single amino acid substitutions can lead to loss or mismatch of peptides when using a generic reference peptide database. Thus, sample-specific set of potentially coding sequences serves as a valuable resource to capture the true complexity of the proteome and to study the global functional divergence between protein isoforms. However, it is important to note that the comprehensiveness of such database vastly depends on the sequencing depth and library preparation strategy and, therefore, it is currently indispensable that such analyses need to be performed using the combination of Gencode and sample-specific protein sequences.

This study demonstrates that our understanding of transcript structures and coordinating mechanisms that regulate transcription and mRNA processing is far from complete, even in well-characterized human cell lines such as MCF-7. Single-molecule full-length RNA sequencing of other human tissues also provide an additional evidence for the true complexity of the human transcriptome. Moreover, although it has been shown that single-nucleotide variants can alter the inclusion of exons in transcripts, it is of interest to identify variants that can affect allele-specific coupling between transcription and mRNA processing. Together, these can offer a better understanding of the mechanisms that control transcription and mRNA processing. As alternative splicing is a key mechanism in functional divergence of human genes, access to full-length sequence of potential protein isoforms allows us to better understand biological function through examining interactions and cross-tissue dynamics of protein isoforms. In turn, this unique set of protein isoform interactions serves as a global view of protein functional repertoire and thereby provide valuable insights into underlying mechanisms of diverging physiological, developmental or pathological conditions.
METHODS

RNA sample preparation, library preparation, and sequencing
The methodologies and experimental settings for RNA preparation, cDNA synthesis, library preparation, and sequencing are described at: https://github.com/PacificBiosciences/DevNet/wiki/Seq-Data-Release-whole-human-transcriptome. We downloaded the 2015 dataset, which is an updated version of the original 2013 release. In addition, we used publicly available data from three human tissues (brain, heart and liver) for comparative analysis. These datasets are described at: http://www.pacb.com/blog/data-release-whole-human-transcriptome/.

Annotation of transcripts using isoform-level clustering algorithm (ICE)
The identification, polishing, and annotation of transcripts were previously carried out using the ICE algorithm and made public by Pacific Biosciences. To find transcript clusters, ICE performs a pairwise alignment and reiterative assignment of full-length reads to clusters based on likelihood. This process is followed by consensus calling and further polishing of the sequence to reduce the redundancy and increase the overall accuracy of sequences for identified transcript variants. For further information on the methodology and experimental settings visit: https://github.com/PacificBiosciences/cDNA_primer/wiki.

Comparison to the GENCODE annotation
We used GENCODE annotated transcripts (version 19) as reference to compare with the identified transcripts in the human MCF-7 transcriptome data. The comparison was carried out using cuffcompare from the Cufflinks suite.

Comparison to standard RNA-Seq datasets
We used five publicly available RNA-Seq datasets (SRR1035698, SRR1107833, SRR1107834, SRR1107835 and SRR1313067; generated on Illumina HiSeq2000 or Illumina HiSeq2500 platforms) to evaluate the reliability of gene expression quantification based on full-length mRNA sequencing data used in this study. As accurate transcription reconstruction is not feasible for short-read RNA-Seq data, the comparison is made at the gene level using GENCODE annotation (version 19). Median gene coverage (fragment counts adjusted for gene length) was used as a measure for gene expression quantifications using the GENTRAP pipeline (http://biopet-docs.readthedocs.io/en/latest/pipelines/gentrap/).

Definition of transcription start site, polyadenylation site, and donor and acceptor splice sites
In this study, by processing the GFF file that contains the annotation of all identified transcripts and exon/intron boundaries (defined by the genomic position and strand on the hg19 reference sequence), a list of all transcription and mRNA processing events is produced. Transcription start sites (TSSs) are defined as the first genomic position of each transcript structure. Polyadenylation sites (PASs) are defined as the last genomic position of each transcript. The most upstream and downstream genomic positions of exons were used to define donor and acceptor splice-sites, respectively. However, for the first exon only the donor site is described as the first position is defined as transcription start site. Likewise, the last exon does not contain a donor splice site as the position is defined as polyadenylation site. If multiple transcripts share the same feature, then only one copy is kept in the unique set of features at each locus. Furthermore, the union of all unique exons is defined as the available sequence at each locus. This is also illustrated in Fig. 1B. Terminal positions of transcripts were curated based on 10bp window to remove stochastic noise and minimize the number of false TSS and PAS for each locus.

Alignment and quantification of supporting reads for each transcript
The number of reads aligned to each transcript was used as the supporting evidence for each transcript structure. To identify the number of supporting reads, the polished sequences of all unique transcripts were used as a reference for the unique alignment of raw reads using BLASR. Other parameters were set default and according to the PacBio guidelines.

Statistical analysis
After defining unique features (transcription start sites, exons, and polyadenylation sites) and identifying the number of supporting reads for transcripts at each locus, all possible pairwise comparisons between features were made. To do this, the sum of all reads that support the presence of the two selected features in all observed transcripts is reported in a two-by-two contingency table. The table describes the number of times two features are observed in the same transcript or exclusively, as well as the sum of reads that are mapped to transcripts that do not support the presence of either features (Fig. 1C). A significant linkage between two features is assessed using the Fisher's exact test. The mutual inclusivity or exclusivity of coupled features are defined using their log-transformed odds-ratio. All p-values are adjusted using Bonferroni multiple testing correction.

Coping network is constructed based on detected interdependencies between pairs of features for each gene. Nodes represent features and mutual inclusivity or exclusivity is represented by black or red edges, respectively, in the network. Mutual inclusivity or exclusivity sub-networks are constructed after removing all the other edges. No further filtration is performed on gene coupling networks. All statistical analyses were performed in R and Python.

Sanger sequencing validation
The PCR for Sanger sequence validation was performed using the 2x Phusion High-Fidelity PCR master mix with HF buffer (NEB). Briefly, the PCR was run for 30 cycles with 1 min elongation at 72°C. The PCR products were purified using Ampure XP beads following the guidelines of the manufacturer. The sizing of the amplicons was checked using Agilent's Labochip system. The Sanger sequencing of the products was performed by the LGTC and the sequences were analyzed using Sequence Scanner Software 2 (Applied Biosystems, CA USA).

Single-molecule RNA fluorescence in situ hybridization
Single-molecule RNA FISH relies on the combined fluorescence from 25-48 singly fluorophore labeled oligonucleotides bound to the same RNA. By using the fluorescence from a guide probe set in one dye, the fluorescence from one or more exon-specific probe sets with <25 oligonucleotides, and each labeled with a separate dye, can be accurately registered as belong to the same RNA. The optimal
number of oligonucleotides per specific set must be experimentally determined.

Probe sets
Four probe sets were designed at www.biosearchtech.com/stellarisdesigner to detect: 1) the common exons of the human CALU (Calumenin; NCBI Gene ID: 813; 7q32.1) mRNAs (CALU_E), 2) the alternatively spliced exon 4 (CALU_E4), 3) the alternatively spliced exon 5 (CALU_E5), and the common first intron (CALU_I1). The probe set target sequences were as follows: CALU_E: NM_001199671.1, nts 1-141, 957-1188, 1383-1610, 1811-2875, CALU_E4: NM_001199671.1, nts 1177-1394, CALU_E5: NM_001199672.1, nts 1177-1394, and CALU_I1: NC_000007.14, nts 128739433-128747432. CALU_E is an inclusive probe set designed to detect the following variants: NM_001219.4, NM_001130674.2, NM_001199671.1, NM_001199672.1, NM_001199673.1, and NR_074086.1. Both CALU_E and CALU_I1 are full sets with >32 oligonucleotides each, whereas the sets targeting the short exons 4 and 5 have 9 oligonucleotides each. The four sets were synthesized at LGC Biosearch Technologies as custom Stellaris’ probe sets with unique fluorophores: CALU_E: Quasar* 670, CALU_E4: Quasar 570, CALU_E5: Cal Fluor* Red 610, and CALU_I1: FAM. The CALU_E4 and CALU_E5 probes were further purified by reverse phase HPLC, to ensure full labeling.

Reagents and smRNA FISH
Human breast adenocarcinoma MCF-7 cells (ATCC-HTB-22) were obtained from ATCC (Manassas, VA) and cultured as recommended by the provider. The hypotriphloid karyotype is available at the provider's web site, and shows three chromosomal loci for 7q32.1. 2-(4-Aminophenyl)-6-indolecarbamidine dihydrochloride, 4’-6-Diamidino-2-phenylindole dihydrochloride (DAPI), molecular biology grade ethanol, acetic acid, and methanol were from Sigma Aldrich (St. Louis, MO). Vectashield was from Vector Laboratories (Burlingame, CA). Stellaris RNA FISH hybridization and wash buffers were from LGC Biosearch Technologies. Stellaris RNA FISH was performed as previously described for methanol/acetic acid-fixed cultured cells65, 66.

Image acquisition and analysis
DAPI-stained nuclei, fluorescein (FAM), Quasar 570 (Q570), CalFluor 610 (CF610) and Quasar 670 (Q670) dyes were imaged through a 60X 1.4NA oil-immersion lens on a Nikon Ti widefield microscope using the appropriate filters: 49000-ET-DAPI, 49011-ET-FITC, SP102v1, SP103v2, 49022-ET-Cy5.5 respectively. The exposure and sequence of channels to acquire were determined based on the brightness and photostability of the dye with which each probe set was labeled. The sequence of exposure was Q670, followed by FAM, and then either or both Q570, CF610. Each Z-slice was exposed for 1 s, except for Q670 which required 2 s exposures. For each field of view, a range spanning the vertical dimension of the cell (typically 10 µm) is defined and for each channel, a series of images were acquired through this span at 0.3 µm increments by using Nikon Elements’ Advanced Research software.

Each Z-series was collapsed and rendered as a single, max-intensity projected image. Translational registration to align images shifted relative to another was accomplished by ImageJ macros after identification of a region containing overlapping signals in each channel. Peak positions of these signals were determined relative to each other to inform the shift of each channel. Next, spots and their centroid positions were identified in each channel using the ImageJ Find Maxima utility. These positions were then compared against one another and co-localized spots were grouped if within 3 pixels (330 nm). Based on these groupings, spots were categorized into separate transcript variants and displayed on the image for review. Finally, cell borders were defined and spots associated with distinct cells for per-cell and per-transcript variant copy number determination. RNA FISH features were counted in at least ten cells.

Sequence motif analysis relative to polyadenylation sites
For each detected locus, we reported the last nucleotide as polyadenylation site. Each genomic location was converted into a BED format. Strand specific genomic sequences located up to 35 nucleotides upstream each unique polyadenylation site were extracted, in a FASTA format, using UCSC Table Browser (GRCh37/hg19). FASTA files were parsed using a custom bash script to count the number of sequences containing specific 6-mer motifs: one of the two canonical polyadenylation signals AATAAA and ATTAAA, or one of the eleven non-canonical polyadenylation signals (AAGAAA, AATACA, AATAGA, AATATA, AATGAA, ACTAAA, AGTAAA, CATAAA, GATAAA, TATAAA, TTTAAA). Subsequently, the same 6-mer motifs were counted for each unique PAS significantly coupled to TSSs or exons and for each unique PAS that did not show a significant coupling.

For PASs that could not be attributed to known poly(A) signals, we ran DREME67 (v. 4.11.4) to identify enriched motifs. Randomly shuffled set of sequences was generated from the original sequences of the examined PASs and used as a background set. In addition, the sequences of known recognition motifs for MBNL proteins23-25 were counted for each set using a custom script. Subsequently, the enrichment of each motif was assessed by Fisher's exact test.

Tandem 3’ UTR analysis
This analysis was performed to identify loci that contain tandem 3’ UTRs (loci that contain more multiple PASs located in the same last exon). Custom scripts were used to identify loci that contain at least two PASs that share the same coordinates of the last exon start. The number of loci with tandem 3’ UTRs was calculated for those in which PAS was significantly coupled to alternative exons and for those that did not show any significant interdependencies between alternative exons and the PAS usage.

Sequence motif analysis relative to acceptor and donor sites
For each detected locus, we reported the first and last nucleotide of each exon as acceptor splice site and donor splice site, respectively. Each unique genomic position was converted into a BED format and the strand specific sequences of 2 nucleotides length were extracted using UCSC Table Browser (GRCh37/hg19) for both acceptor and donor splice sites. A custom bash script was used to count the number of dinucleotide sequences containing ‘GT’ and/or ‘AG’.

RNA binding motif analysis
We used MEME suite tools to identify enriched sequence motifs present in exons significantly coupled with TSSs, PASs or other alternative exons. For each unique exon, three regions were considered: R1 (containing up to 35 nucleotides upstream the acceptor splice site), R2 (containing 32 nucleotides downstream the acceptor splice site and 32 nucleotides upstream the donor splice site),
and R3 (containing up to 40 nucleotides downstream the donor splice site). R1, R2 and R3 regions were obtained by extracting strand specific FASTA sequences using UCSC Table Browser (GRCh37/hg19).

We locally ran DREME67 (v. 4.11.4) for each region separately, and performed a motif search using a negative background (R1, R2 and R3 regions from exons that were not significantly coupled). In each case, a maximum of 10 motifs with E-values < 0.05 was reported. The remaining parameters were kept as default. We then compared each motif found by DREME against the human RNA-binding motifs database CISBP-RNA using TOMTOM Motif Comparison tool68. We ran the analysis by setting the Pearson correlation coefficient as comparison function and considered only matches with a minimum false discovery rate (q-values) < 0.05.

Open reading frame prediction and proteomics data analysis

ORF prediction was done on the PacBio MCF-7 sequences using ANGEL (http://www.github.com/Magdoll/ANGEL). Prediction was done on both the PacBio consensus reads and a genome-corrected version of the transcript, and whichever produced the longer ORF was chosen to represent the transcript CDS. The predicted MCF-7 ORF sequences were concatenated with Gencode version 19 and protein sequences representing common mass spectrometry (MS) contaminants, creating a customized FASTA file (i.e., proteomics search database). The Morpheus software (version 131) was employed for MS searching of the custom database against the MCF-7 Thermo Raw files obtained from Geiger et al.41 study. Unknown precursor charge state range was set to +2 to +4. Absolute and relative MS/MS intensity thresholds were disabled. Maximum number of MS/MS peaks were set to 400. Absolute and relative MS/MS intensity thresholds were disabled. Maximum number of MS/MS peaks were set to 400. Assign charge state was set to true. De-isotoping was disabled. The protease specificity was set to trypsin with no proline rule enabled. Up to 1 missed cleavage was allowed and N-terminal methionine truncations was variable. Fixed modifications used were carbamidomethylation of cysteines. Variable modification used was oxidation of methionines. Precursor mass tolerance used was 2.1 Daltons (monoisotopic) and product mass tolerance was 0.025 Daltons (monoisotopic). Modified forms of the same peptide were collapsed and treated as one peptide identification for calculation of false discovery rate (FDR). An FDR of 1% was used to filter for final peptide identifications. All identified peptides were categorized as: single-transcript if the peptide matches to only one gene with one transcript; sub-gene if the peptide matches to a subset of transcripts of only one gene; single-gene if the peptide matches to all transcripts of only one gene; and multi-gene if the peptide matches to multiple transcripts from multiple genes.

Data availability

Detailed description of the methodologies along with all open-source Python scripts and generated results are made publicly available at: https://git.lumc.nl/s.y.anvar/mRNA-Coupling/wikis/home.

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AUTHOR CONTRIBUTIONS

SYA, SWT and PAC’tH designed the study. SYA, WGA, EdK, MV performed the computational and statistical analyses. ET carried out the identification of unique transcripts, alignment to the genome and open-reading frame predictions. GS performed the proteomics analysis. SYA, ET and GS performed the integration of transcriptomic and proteomic findings. RHY and HEJ carried out the smRNA-FISH experiments. YA performed the Sanger sequencing validation. JTdD and SWT contributed to the experimental design and the interpretation of the findings. SYA and PAC’tH oversaw the project. SYA wrote the manuscript that was subsequently read and approved by all co-authors.
REFERENCES


24. Masuda, A. et al. CUGBP1 and MBNL1 preferentially bind to 3’ UTRs and facilitate mRNA decay. Scientific reports 2, 209 (2012).


34. Yamaguchi, A. & Takanashi, K. FUS interacts with nuclear matrix-associated protein SAFB1 as well as Matrin3 to regulate splicing and ligand-mediated transcription. Scientific reports 6, 35195 (2016).


43. Sheynkman, G.M., Shortreed, M.R., Frey, B.L., Scaf, M. & Smith, L.M. Large-scale mass spectrometric detection of variant peptides resulting


55. Movassat, M., Crabb, T., Busch, A., Shi, Y. & Hertel, K. Coupling between alternative polyadenylation and alternative splicing is limited to terminal introns (560.2). The FASEB Journal 28 (2014).


