A systematic survey of PRMT interactomes reveals the key roles of arginine methylation in the global control of RNA splicing and translation

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Abstract

Arginine methylation, catalyzed by various protein arginine methyltransferases (PRMTs), is increasingly recognized as a widespread post-translational modification in eukaryotes. Thousands of proteins undergo arginine methylation, however, a full picture of the catalytic network for each PRMT is lacking, limiting the global understanding of their biological roles. In this study, we reported a systematic identification of interacting proteins for all human PRMTs, and the resulting interactomes are significantly overlapped with the known proteins containing methylarginine. The conserved motifs for arginine methylation by each PRMT were further determined, with several novel motifs being validated. Among different PRMTs, we found a high degree of overlap in their substrates and high similarities between their putative methylation motifs, suggesting possible functional complementation. We demonstrated that arginine methylation is significantly enriched in RNA binding proteins involved in regulating RNA splicing and translation. Consistently, inhibition of PRMTs leads to global alteration of alternative splicing and suppression of translation. In particular, the ribosomal proteins are pervasively modified with methylarginine, and the mutations on methylation sites inhibit ribosome assembly and translation. Collectively, this study provides a global network of different PRMTs and putative substrates, revealing critical functions of arginine methylation in the regulation of mRNA splicing and translation.

Keywords

Protein arginine methyltransferase (PRMT), Arginine methylation, Post-translational modification (PTM), RNA-binding protein (RBP), alternative splicing, mRNA translation

Introduction

Arginine N-methylation was first discovered in the early 1970s (Paik and Kim 1970; Baldwin and Carnegie 1971; Kakimoto 1971) and later was recognized as a widespread post-translational modification (PTM) in many proteins (Gary and Clarke 1998; Ong et al. 2004; Bedford and Richard 2005; Pahlich et al. 2006; Bedford 2007; Blanc and Richard 2017). It is catalyzed by a class of enzymes known as protein arginine methyltransferases (PRMTs), which covalently link methyl groups to the arginine side chains. Although arginine methylation does not alter the electric charge of arginine, it increases amino acid bulkiness and protein hydrophobicity, thus can affect how proteins interact with their partners. This type of PTM has been found to play key roles in various cellular processes, including DNA damage repair, transcriptional regulation, RNA metabolism, etc. (Bedford and Richard 2005; Pahlich et al. 2006; Bedford 2007; Sylvestersen et al. 2014; Blanc and Richard 2017; Peng and Wong 2017). As a result, arginine methylation has a profound effect on human diseases such as cancer (Yang and Bedford 2013; Poulard et al. 2016; Blanc and Richard 2017) and cardiovascular diseases (Stuhlinger et al. 2001).

Nine PRMTs, PRMT1 to PRMT9, have been identified in the human genome (Fig. 1A), which were classified into three types according to the final methylarginine products. Type I PRMTs, including PRMT1, 2, 3, 4, 6, and 8, catalyze the formation of ω-N^G, N^G-asymmetric dimethylarginine (aDMA). Type II PRMTs, including PRMT5 and PRMT9, catalyze the formation of ω-N^G,

N^G-symmetric dimethylarginine (sDMA). PRMT7 is the only type III PRMT and catalyzes ω-N^G-monomethylarginine (MMA). Methylation of arginine by PRMTs consumes a great deal of cellular energy (12 ATPs for each methyl group added) (Gary and Clarke 1998) and is found in >10% of all human proteins (Larsen et al. 2016), implying an essentail role of arginine methylation in cell growth and preliferation.

The biological functions of PRMTs are largely determined by its substrates and regulating partners, and therefore identifying the full scope of the interactors for each PRMT will greatly improve our understanding of the function of arginine methylation. The substrates of several individual PRMTs (e.g., PRMT4 and PRMT5) have been determined using various approaches, however, the substrates or interactors of other PRMTs remain largely unknown. On the other hand, thousands of human proteins have been identified to undergo arginine methylation using mass spectrometry combined with specific methylarginine antibodies (Guo et al. 2014; Larsen et al. 2016), and thus it will be highly valuable to connect these proteins with the PRMTs that catalyze their methylation.

In this study, we systematically identified interactome of each PRMT using BioID that allows identification of transient protein-protein interactions (Roux et al. 2012; Roux et al. 2013; Roux et al. 2018), and further determined the substrate specificity and consensus arginine methylation motifs of each PRMT. Our results showed a high degree of overlap in substrate specificity of different

PRMTs, suggesting a possible functional complementation. Remarkably, PRMT interactors are significantly enriched for RNA binding proteins involved in mRNA splicing and translation, and inhibition of PRMTs leads to global alteration of alternative splicing and reduction of mRNA translation. We also found that the mutations on methylation site of ribosomal proteins inhibited ribosome assembly. Collectively, this study provides new insight into biological functions of PRMTs and links each PRMT and arginine methylation events in a systematic manner, revealing critical functions of arginine methylation in regulation of RNA metabolism.

Results

Identification of the interacting proteins of each PRMT

As catalytic enzymes, the interaction between PRMTs and their substrates are usually dynamic, making it difficult to identify the interacting partners. To systematically characterize interactome of different PRMTs *in vivo*, we applied the highly sensitive BioID technology to label interacting proteins with biotin. Based on previous reports that N-terminus of PRMT is responsible for substrate recognition (Tang et al. 1998; Frankel and Clarke 2000; Goulet et al. 2007; Shishkova et al. 2017), we fused a promiscuous biotin ligase BirA* ($BirA^{R118G}$) to the C-terminus of each PRMT and expressed the fusion proteins in HEK293T cells. Biotinylated proteins were subsequently purified with streptavidin beads followed by mass spectrometry analysis (Fig. 1B, and experimental procedures). As expected, many purified proteins are indeed biotinylated as judged by western blot (Fig. 1C, left), with the PRMTs themselves being the most heavily biotinylated proteins (Fig. 1C, right).

In total, we have identified 1657 candidate proteins bound by at least one of the nine PRMTs (Table S1 and Fig. S1A), a lot of which overlapped with the proteins identified in the earlier proteomic studies using immunoprecipitation with antibodies against methylarginine-containing oligopeptides (Guo et al. 2014; Larsen et al. 2016) (Fig. 1D), indicating the BioID technology is reliable and sensitive in identifying PRMT interactors.

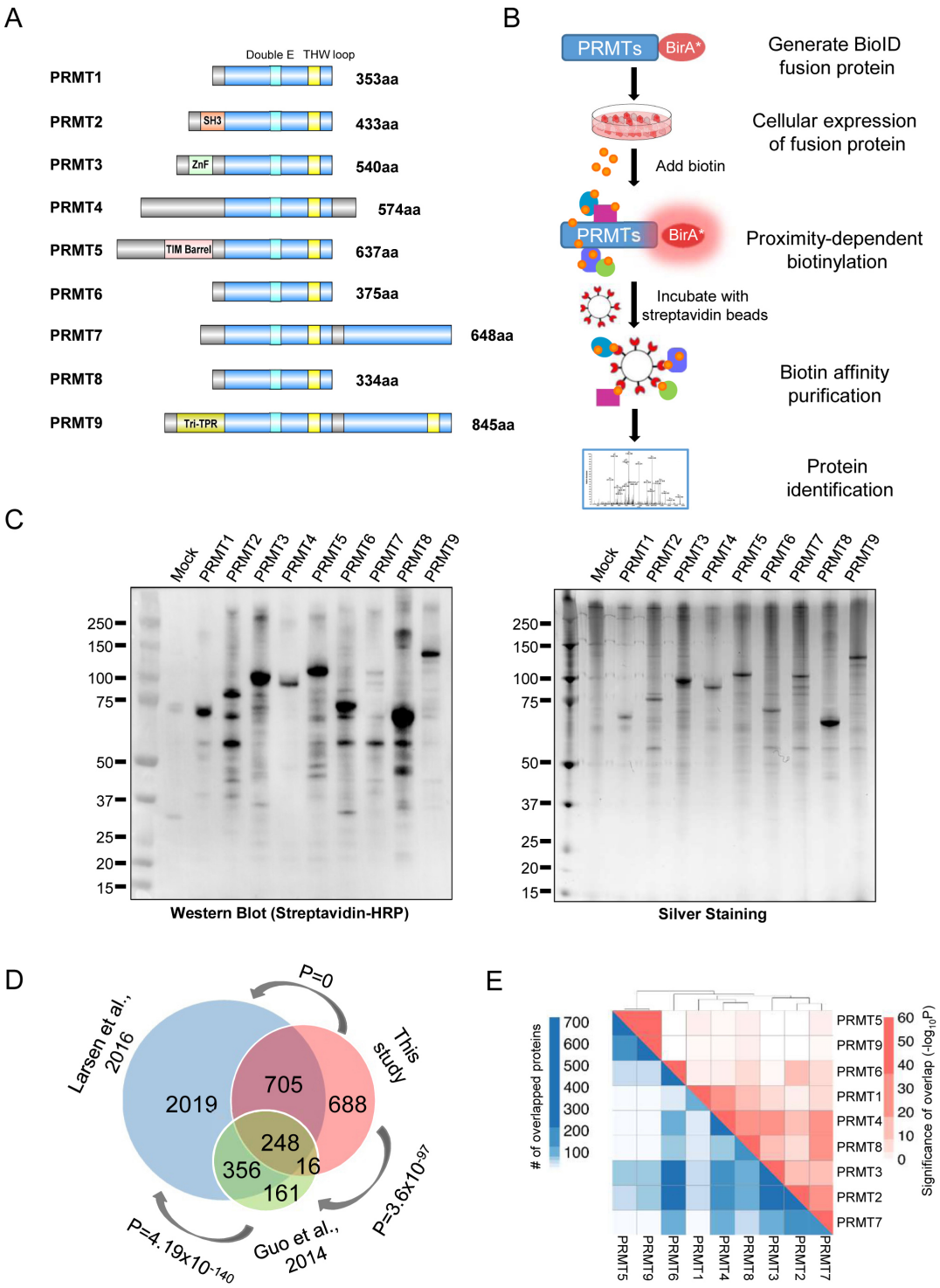

Figure 1. Systematic identification of PRMT interactome.

(A) Schematic diagram of PRMT1 to PRMT9. The light blue boxes represent the catalytic domains, the cyan and yellow boxes represent Double E Motifs and THW loop Motifs that are specific to PRMTs, respectively. (B) The workflow for identification of PRMT interacting proteins via BioID. (C) The biotinylated PRMT interacting proteins as detected by western blot using streptavidin-HRP (left) and by silver staining (right). (D) The Venn diagram illustrating the PRMT interactome from this study compared to methylarginine-containing proteins identified in Larsen et al., 2016 and Guo et al., 2014. The

correlation is calculated by Fisher's exact test, with the whole genome as the background. (E) The overlap of the interactome among different PRMTs. Fishers' exact test is used to calculate the *p*-value of the overlap. The PRMT interactomes are clustered by overlap significance (shown in red) and the numbers of overlapped protein are indicated in blue.

In addition to the methylation substrates, the interactome of PRMTs may also include proteins that regulate PRMT functions, which could not be identified by immunoprecipitation with methylarginine antibodies. For example, PRMT5 exerts arginine methyltransferase function in the form of a complex with MEP50 (WDR77) (Saha et al. 2016), a co-factor that was also identified in the PRMT5 interactome by our experiments. Importantly, only 4% of newly identified PRMT interacting proteins (70 out of 1657 proteins) have been collected in the IntAct online PPI database (https://www.ebi.ac.uk/intact/), suggesting that our results significantly expanded the interactome of each PRMT (Fig. S1B).

Substrate preference of individual PRMTs

To further determine the substrate preference of the putative substrates for different PRMTs, we compared the newly identified putative substrates for each PRMT. Our results indicated that many proteins are recognized by multiple PRMTs, suggesting a great deal of substrate redundancy for each PRMT (Fig. S1C). For example, RPS3 can be recognized by all 9 PRMTs as judged by our results, and 372 proteins can be recognized by at least 3 out of 9 PRMTs tested (Fig. S1D). We further examined the overlaps of the interacting

proteins between each PRMT (Fig. 1E), and found that the PRMTs can be roughly clustered into two groups based on the similarity of their interactomes. Interestingly, such classification reflects the differences in the dimethylation step of PRMT-catalyzed reactions, with the type II PRMTs (PRMT5 and PRMT9) that catalyze symmetric arginine dimethylation being separated from the other PRMTs that either catalyze asymmetric arginine dimethylation (type I) or does not catalyze dimethylation (PRMT7, type III).

Identification and validation of consensus motifs for arginine methylation

Previous studies have reported that the glycine and arginine rich (GR-rich) motifs are preferably targeted for methylation by many PRMTs (including PRMT1, PRMT3, PRMT5, PRMT6, and PRMT8) (Bedford and Clarke 2009; Thandapani et al. 2013; Blanc and Richard 2017). However, additional consensus motifs such as proline/glycine/methionine rich (PGM-rich) or RxR motifs were also found to be enriched near the methylarginine sites by mass spectrometry (Cheng et al. 2007; Feng et al. 2013), suggesting that other sequences beside GR-rich motifs may also be recognized as arginine methylation sites and that individual PRMTs may have different preferences of their substrate.

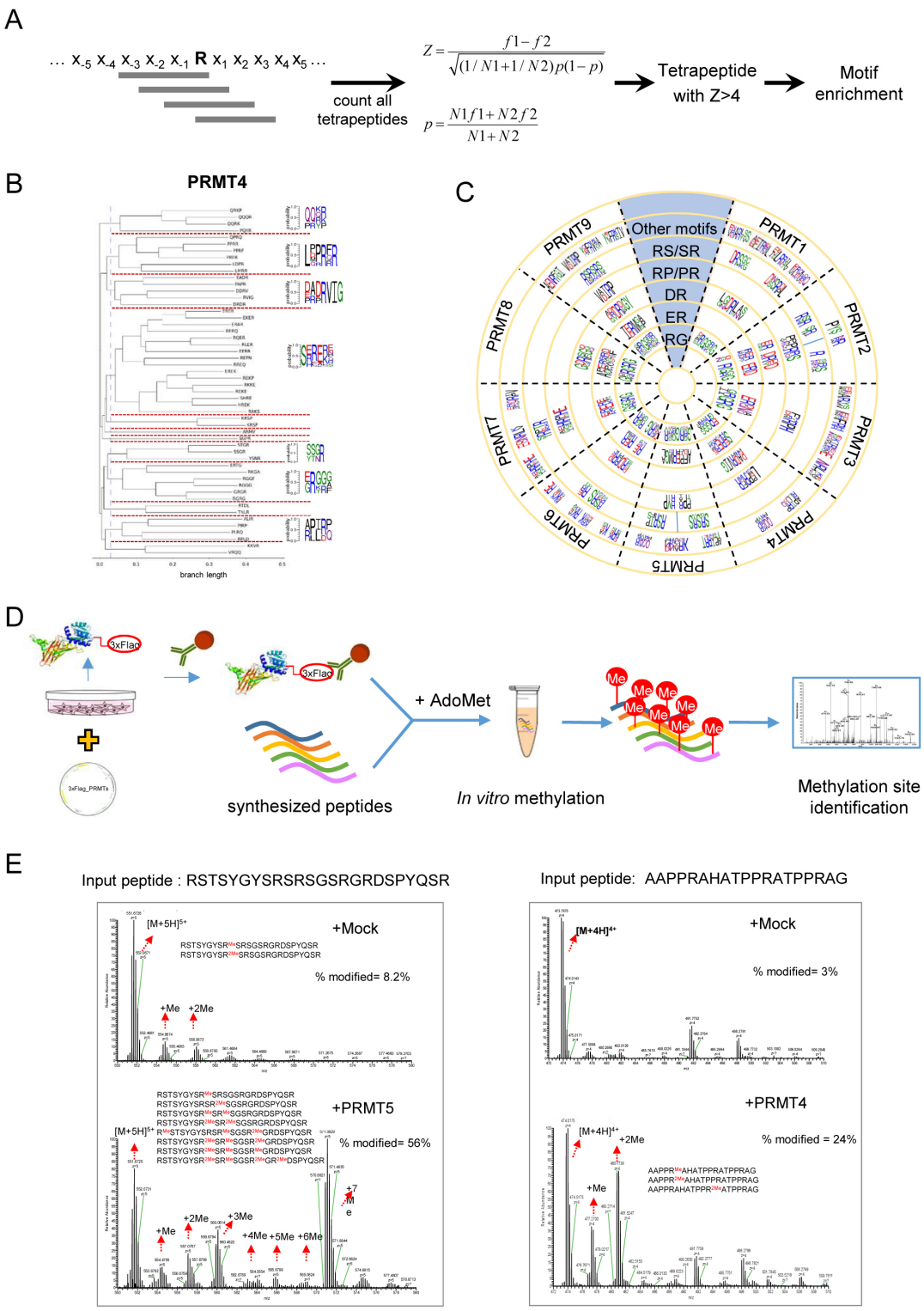

Figure 2. Identification and validation of consensus motifs for arginine methylation.

(A) The schematic diagram for identification of the enriched motif in PRMT interactome. All tetrapeptides around arginine are counted, and the frequencies of each tetrapeptide in PRMT interactomes were compared to the background of all human proteins to identify enriched tetrapeptides (see methods). (B) The clustering of enriched tetrapeptides in PRMT4 interactome is shown as an example. The enriched tetrapeptides are collected as input in clustalw2 (v2.0.9) to generate the phylogenetic tree, and the

consensus motifs were listed besides each group. (C) A summary of all enriched motifs found in each PRMT interactome. Similar motifs are placed in the same concentric circle. (D) The experimental workflow of *in vitro* methylation and identification of methylarginine-containing peptides. R^{Me} and R^{2Me} are set as dynamic modifications with a mass shift of 14.01565 and 28.0313. (E) The arginine methylation pattern of two representative peptides in SR-rich and PR-rich motifs as detected by mass spectrum. In each case, the upper spectrum indicates the negative control without adding enzymes, and the lower spectrum shows the methylarginine signals after *in vitro* methylation. For each peptide, the ratio of methylation was calculated as the sum of the peak areas from the TIC values of the modified peptides divided by the peak area of the total peptides. The methylarginines were labeled in red font.

To further determine the substrate preference for different enzymes, we analyzed the newly identified putative PRMT substrates by measuring the statistic enrichment of the sequences around the potential methylarginine (Fig. 2A, see methods for details). For each PRMT, the tetrapeptides around the potential methylarginine sites were compared with the arginine-containing tetrapeptides in all proteins from UniProt database to calculate the enrichment Z-scores (Fig. 2A). The enriched tetrapeptides were further clustered into different groups to obtain consensus motifs for arginine methylation by each PRMT. As an example, the clusters and the consensus motifs for PRMT4 substrates were shown in Fig. 2B and the clusters of all PRMTs were shown in supplementary figure S2. We further compared the consensus motifs of all tested PRMTs (Fig. 2C), and found that in addition to the known RGG motifs from the substrates of many PRMTs, several other new consensus motifs like SR-rich, PR-rich, DR-rich, and ER-rich motifs were also be identified in PRMT substrates. These results provided a comprehensive profile for the substrate preference of different PRMTs, suggesting that a diverse range of proteins could be potentially modified by PRMTs at different consensus motifs.

In order to validate these newly identified arginine methylation motifs, we selectively synthesized several peptides containing newly identified consensus motifs to measure methylation of arginine by the cognate PRMTs using *in vitro* methylation reaction (Fig. 2D). The peptides were incubated with purified PRMTs (Fig. S3A and S3B) in the presence of methyl donor S-adenosylmethionine, and resulting samples were analyzed with mass spectrometry. As a positive control, the GR-rich motifs known to be heavily methylated were confirmed in our *in vitro* methylation assay (not shown). In addition, we found that the arginine residues within the SR-rich, PR-rich, and DR-rich motifs can be robustly methylated by different PRMTs, with both methylation and dimethylation being detected (Fig. 2E, Fig. S3C), indicating that these newly identified consensus motifs can indeed be methylated at the arginine sites.

Potential functions of PRMT substrates

To examine the functional consequence of arginine methylation, we inferred the potential functions of the newly identified substrates using gene ontology (GO) analyses (https://david.ncifcrf.gov/) (Huang da et al. 2009a; Huang da et al. 2009b). In order to increase the specificity of our analysis and reduce the statistic noises from the large number of potential substrates, we first focused on the proteins that were identified in both our dataset and from earlier reports of methylarginine-containing proteins (Guo et al. 2014;

Larsen et al. 2016). We found that these proteins were significantly enriched for biological processes involving RNA metabolisms, such as mRNA splicing, translation initiation and nonsense mediated decay. Consistently, these proteins are also enriched for RNA binding domains such as RNA recognition motif (RRM), RNA binding domain (RBD), ATPase dependent RNA helicase (Helicase_C) (Fig. 3A, left). The significant involvement of PRMT substrates in RNA metabolism supported the previous reports that many proteins with methylarginine modification participate in RNA processing (Guo et al. 2014; Larsen et al. 2016). In addition, the PRMT-interacting proteins that do not overlap with previously reported methylarginine-containing proteins are likely to be the regulator of PRMTs rather than their substrates (e.g. WDR77), and these proteins are enriched for RNA-unrelated functions, such as cell division and cell-cell adhesion (Fig. 3A, right).

We further examined protein-protein interactions among the potential substrates of each PRMT using STRING database, and found that the two largest and most densely connected clusters primarily consisted of proteins involved in RNA splicing and translation, including a large number of ribosomal proteins and splicing factors (Fig. 3B). Although the potential substrates of different PRMTs showed distinct clustering pattern, such dramatic functional clustering in splicing and translation are universal across different PRMTs (Fig. S4). In addition, we found that the core ribosomal proteins and the splicing factors identified in our study generally have a significantly higher frequency of

arginine in their amino acid composition as compared to all human proteins (Fig. 3C), further supporting the prevalent methylarginine modification observed in these proteins.

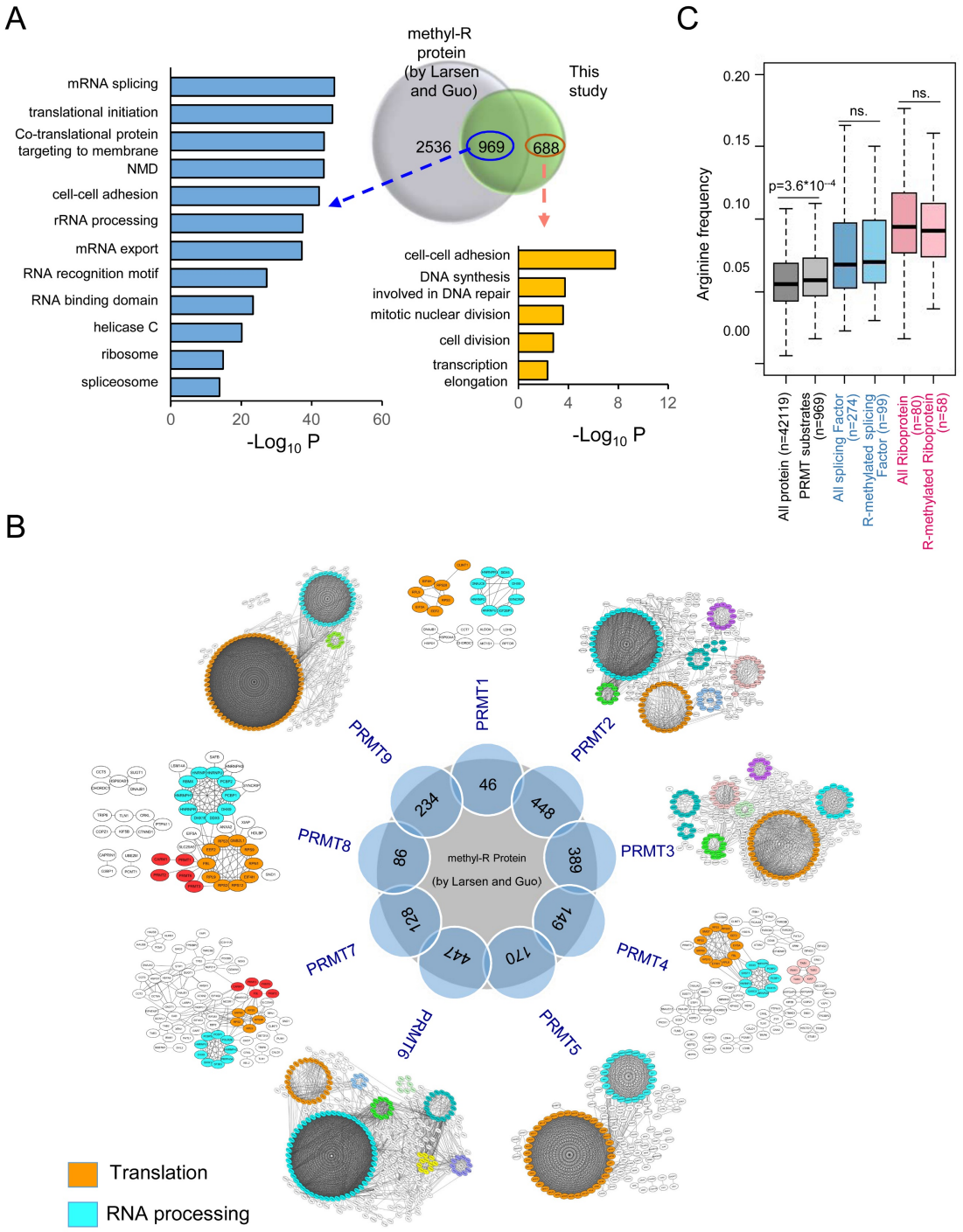

Figure 3. Arginine methylation is highly involved in RNA splicing and translation.

(A) Gene Ontology analysis (by DAVID) of the 969 putative PRMT substrates detected in both this study and previously identified methylarginine-containing proteins (blue bar), as well as the 688 PRMT interacting proteins identified in only this study (orange bar). (B) The putative PRMT substrates were subjected to protein-protein interaction analysis from the STRING database (v10.5, the minimum required interaction score was set to high confidence at 0.7), the resulting networks were clustered by MCODE in Cytoscape software. The orange nodes indicate functions related to translation and the cyan nodes indicate functional enrichment in RNA processing. (C) Arginine frequency of splicing factors/splicing factors containing methylarginine (blue) as well as core ribosomal proteins/ribosomal protein containing methylarginine (red) in their amino acid composition compared to all human proteins, Wilcoxon test was used to calculate the *p*-value.

PRMT inhibitions generally altered alternative splicing of RNA

The majority of human genes undergo alternative splicing (AS) that is generally regulated by various RNA-binding proteins (i.e., splicing factors) that recognize regulatory *cis*-elements to promote or suppress the use of adjacent splice sites (Matera and Wang 2014). It was previously reported that some PRMTs (e.g., PRMT4 and PRMT5) can affect splicing by modifying selected splicing factors or proteins involved in spliceosome maturation (Cheng et al. 2007; Kuhn et al. 2011; Bezzi et al. 2013). Since many proteins involved in splicing regulation were identified as PRMT substrates (Fig. 3B and Fig. S4), we further examined the effect of PRMT inhibition on alternative RNA splicing. We achieved effective gene silence with shRNAs in six different PRMTs (Fig. S5A) and examined their effect on splicing using RNA-seq (Fig. 4A). For each PRMT we identified the alternative splicing events that are significantly altered in cells with PRMT knockdown compared to the control cells with scramble RNAi (Fig. 4A).

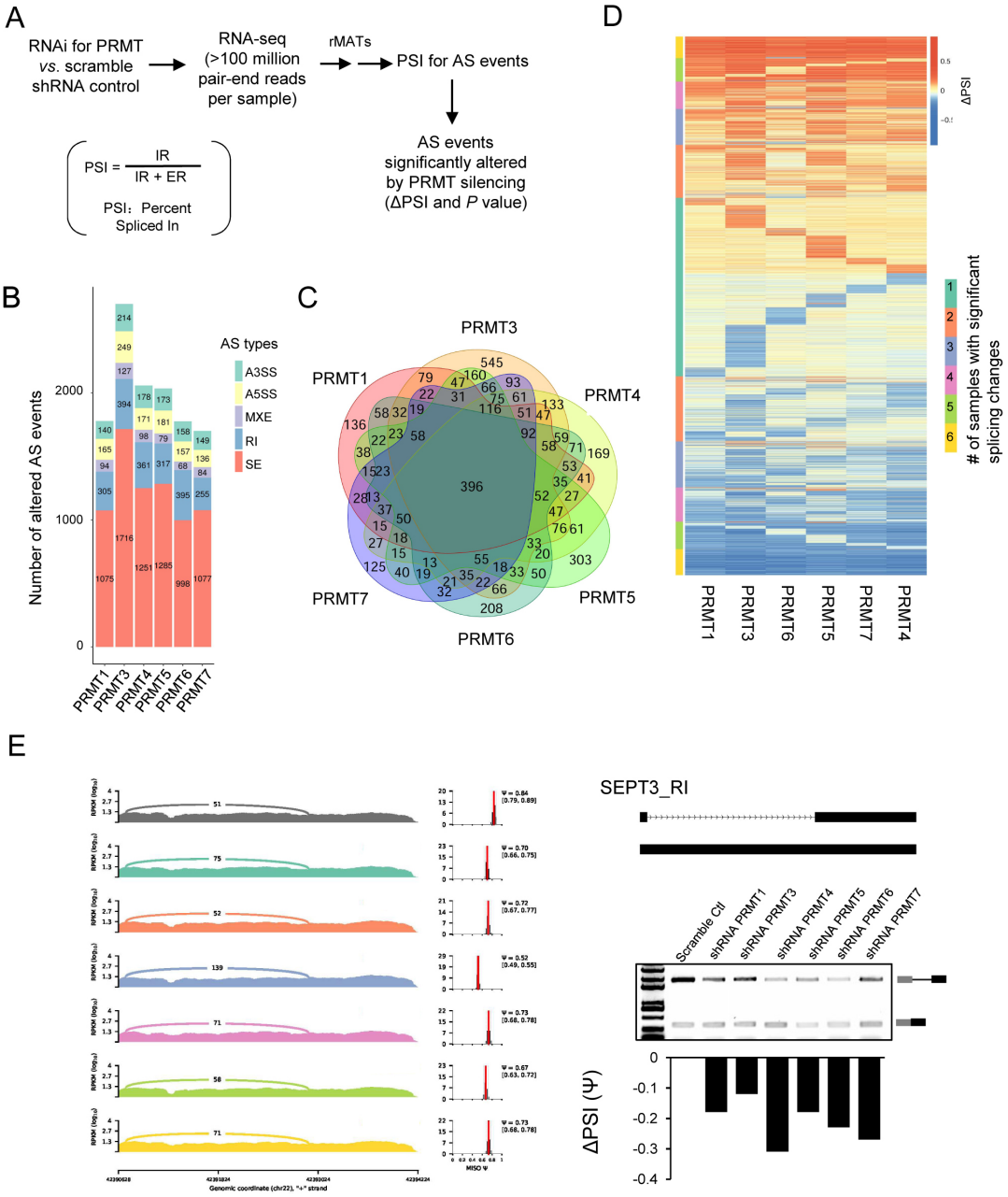

Figure 4. PRMT inhibition leads to global alteration of alternative splicing.

(A) The workflow of RNA splicing analysis for PRMT knockdown samples using RNA-seq and analyzed by MISO pipeline to calculate PSI (percent spliced in) values. We used |ΔPSI| >0.1 and read counts>50 as the cutoff to identified significantly altered splicing events. (B) The count of different types of altered splicing events after PRMT knockdown. A3SS, alternative 3′ splice site; A5SS, alternative 5′ splice site; MXE, mutually exclusive exon; RI, retained intron; SE, skipped exon. (C) The intersection of altered AS events upon silencing of different PRMTs. (D) All AS events altered upon silencing of each PRMT were colored according to ΔPSI. The AS events were also clustered by the numbers of PRMT RNAi samples with the significant splicing changes (e.g., the clusters labeled in yellow include AS events affected by RNAi of all the six PRMTs tested). (E) Experimental validation of spicing alteration. Sashimi plot of splicing change in SEPT3 was presented in the left, including the counts of junction read, the PSI value and its confidence interval. Semi-quantitative PCR was shown in the right. Additional examples of altered AS events can be found in fig. S5B

We found that inhibition of different PRMTs caused significant changes of splicing in hundreds of genes harboring various AS types (Fig. 4B). Many of AS events are affected by the inhibition of more than one PRMT (i.e., large overlaps between splicing targets of different PRMTs), suggesting that the arginine methylation of proteins by PRMTs play a general role to regulate alternative splicing (Fig. 4C). Interestingly, the inhibition of different PRMTs generally had similar effects on splicing of specific genes (i.e., the ΔPSI are either positive or negative in most affected genes, Fig. 4D), implying that the arginine methylation of same RNA-binding proteins by different PRMTs produces similar effects on their activities. The splicing changes of selected AS events were further validated using semi-quantitative RT-PCR. For example, the splicing of a retained intron in SEPT3 (neuronal-specific septin-3) gene is promoted by inhibition of all six PRMTs tested (Fig. 4E), and many other genes have undergone alteration of splicing in the same direction (Fig. S5B), supporting the consistent regulation of splicing by different PRMTs.

Ribosomal proteins are pervasively arginine methylated

According to the gene ontology and protein-protein interaction analyses, proteins involved in mRNA translation are significantly enriched in the newly identified PRMT substrates, including >72% core components of ribosomes (58 out of 80 ribosome proteins) and many canonical translation factors (such as EIF4G1, EIF4B, EIF2A, etc,). In table S2, we listed all the 80 ribosome

proteins with newly identified interacting PRMTs and the putative methylarginine sites. Our finding is consistent with earlier reports in the late 1970s that both subunits of the ribosome contain methyl arginine as judged by chromatography of short peptides or amino acid residues originated from ribosomal proteins (Chang et al. 1976; Goldenberg and Eliceiri 1977; Kruiswijk et al. 1978). More recently, several ribosomal proteins were also reported to contain methylarginine, including yeast RPL12 and RPS2 (Polevoda and Sherman 2007) and human RPS3 and RPS10 (Shin et al. 2009; Ren et al. 2010). Our finding revealed a prevalent arginine methylation in core ribosomal proteins, suggesting that this type of PTM plays critical roles in protein translation.

To directly test this hypothesis, we performed polysome profiling to isolate different ribosome fractions (the 40S, 60S, 80S, and polysome, Fig. 5A) and detect their methylation status by pan-arginine methylation antibodies (Fig. 5B). Our data demonstrated that ribosomal proteins (most having a MW range of 10-50 kD) are pervasively R-methylated in different ribosome profiling fractions (Fig. 5B). We also found that PRMTs were not co-purified with ribosomes (Fig 5A), suggesting that the methylation of ribosomal proteins occurs before ribosome assembly, which is consistent with the absence of PRMTs from the known ribo-interactome (Simsek et al. 2017). In addition, we used different types of methylarginine antibodies (MMA, aDMA and sDMA antibodies) to precipitate proteins containing methylarginine and detected many ribosomal

proteins in the immunoprecipitated samples (Fig. 5C), further supporting our conclusion that ribosome proteins are pervasively methylated at arginine residues.

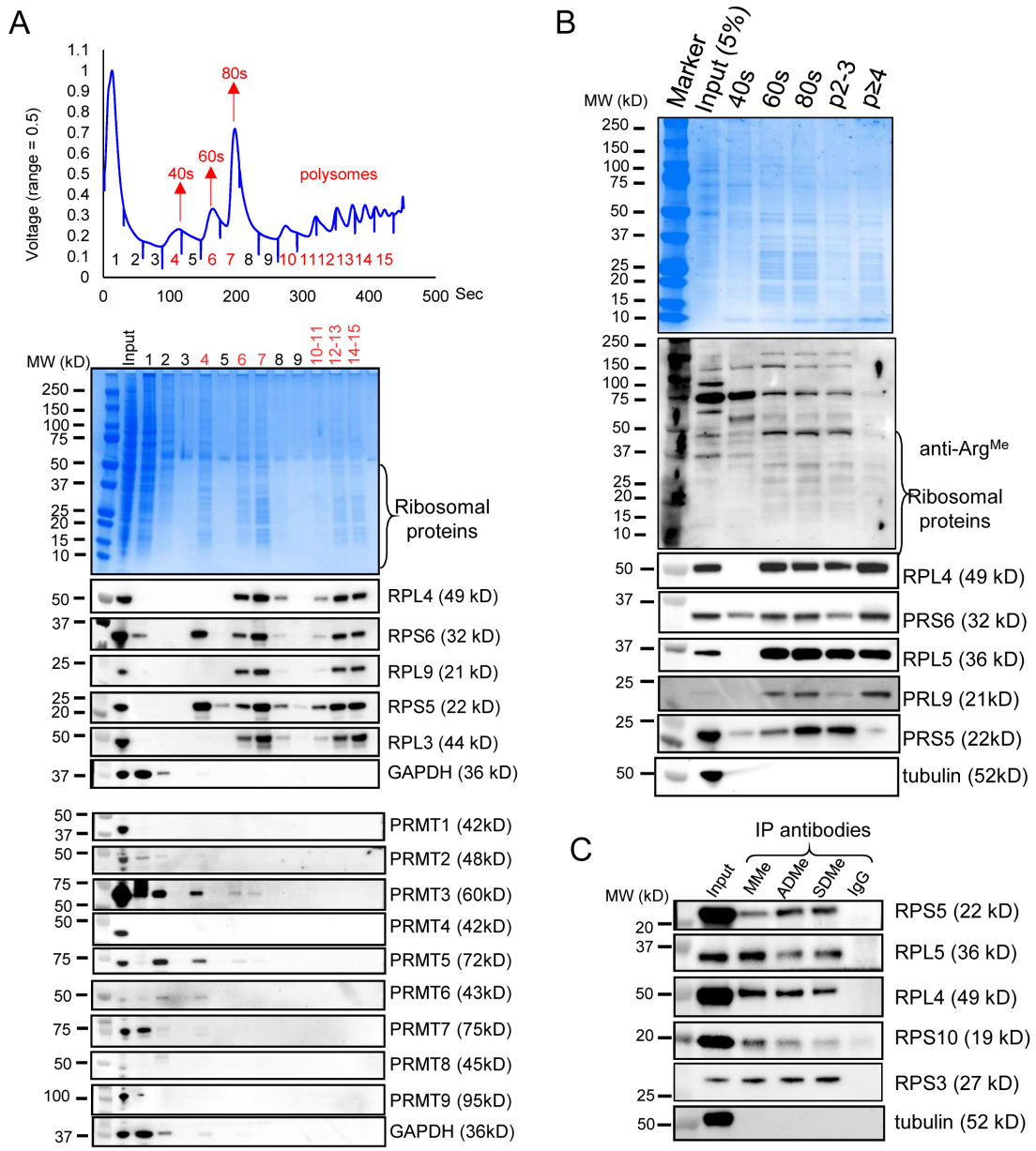

Figure 5. Ribosomal proteins are pervasively methylated.

(A) Fractionation of polysomes using HEK293T cell lysis. Each fraction was collected, and proteins in each fraction were precipitated for SDS-PAGE assay. Both coomassie blue staining (top) and western blots (bottom) were used to detect the proteins in each fraction. Accumulation of ribosomal proteins can be observed on the gel (MW between 15-50 kD, Middle). (B) The arginine methylation of ribosomal proteins as detected by combination of pan-methylarginine antibodies that can recognize MMA, aDMA and sDMA. (C) The HEK293T cell lysate were subjected to immunoprecipitation with different methylarginine antibodies, and the selected ribosomal proteins were detected with western blot.

Arginine methylation is critical for assembly and function of ribosomes

Based on the pervasive arginine methylation of ribosomal proteins and translation factors, we hypothesize that PRMT inhibition may affect translation on a global scale. Consistent with this idea, PRMT3 was reported to directly contact with RPS2 and responsible for the homeostasis of the ribosome in a methyltransferase-independent manner (Perreault et al. 2009). To test this hypothesis, we used puromycin incorporation assay to test global protein synthesis in three different types of cells after treatment by the PRMT specific inhibitors (Fig. 6A, Fig. S6A and S6B for cell lines HEK 293, HCT116 and U2OS, respectively). We used chemical inhibitors of PRMTs because they could provide a more rapid suppression of ribosomal activity that might otherwise be compensated in cells with stable knockdown of PRMTs.

We found that the inhibitors of PRMT1 and PRMT4/CARM1 effectively reduced arginine methylation and global protein synthesis across multiple cell lines (Fig. 6A and Fig. S6), and the inhibition of these two PRMTs produced the most obvious reduction in arginine methylation. Therefore, we selected PRMT1 and PRMT4 for further analyses of how PRMT activities affect translation. Using polysome profiling, we found that the inhibition of PRMT1 or PRMT4 effectively reduced the abundances of polysomes *vs.* monosomes (Fig. 6B), suggesting a global reduction of mRNAs undergoing active translation.

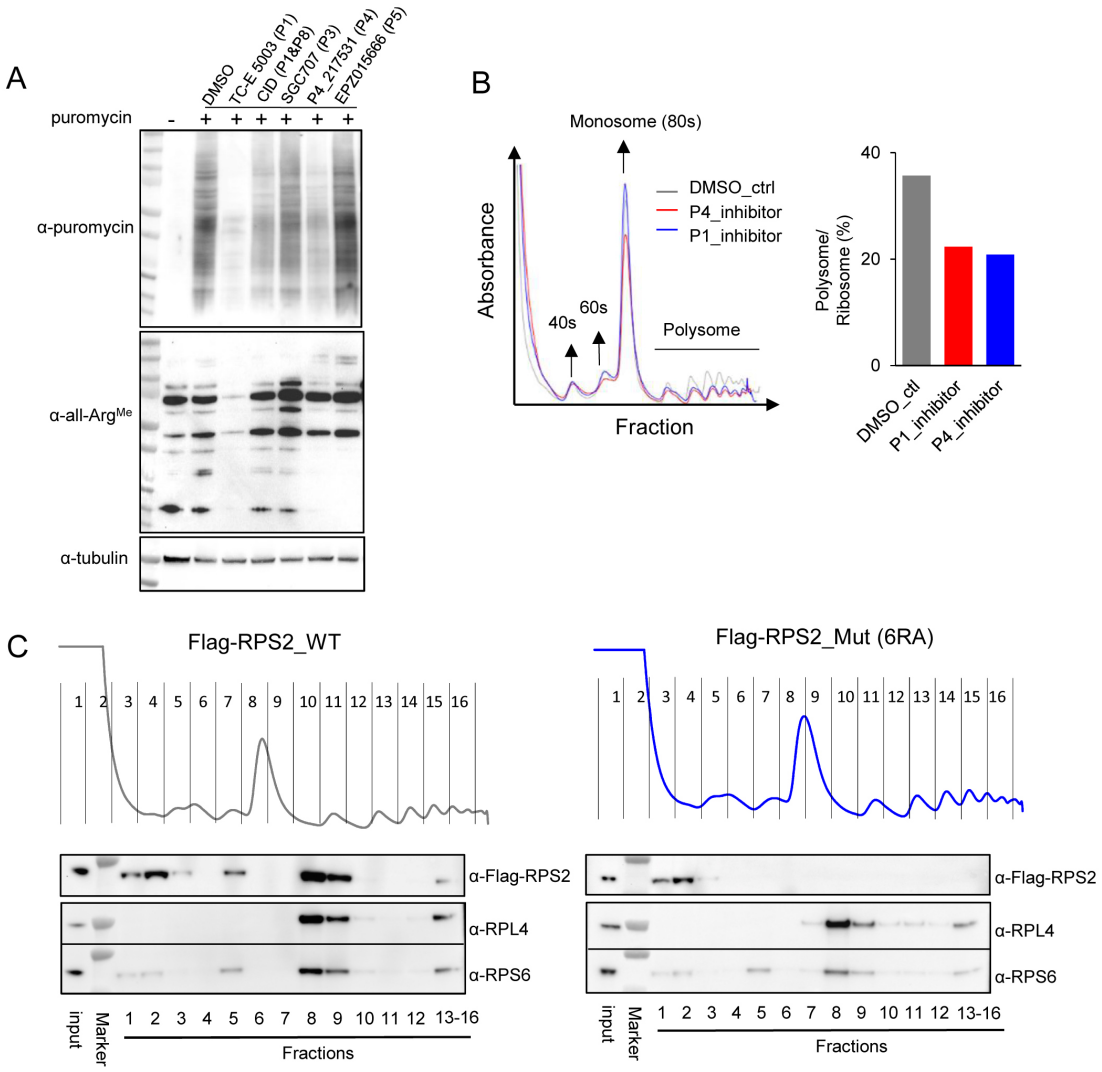

Figure 6. Arginine methylation affects translation efficiency and assembly of ribosomal proteins. (A) Puromycin incorporation assay of translation efficiency upon inhibition of specific PRTMs. HEK293T cells were treated with different PRMT inhibitors for 24h, and puromycin was added 30 min before cell harvest. The incorporations of puromycin were detected by western blot using anti-puromycin antibody. The pan-methylarginine antibody was used to measure changes in arginine methylation status. (B) The effect of PRMT inhibition on ribosome fractions. The cells treated with PRMT1 and PRMT4 inhibitors were analyzed using polysome profiling, with the percent of monosome and polysomes calculated by the peak areas. (C) Arginine methylation of RPS2 affects ribosome assembly. Flag-RPS2 (WT) or Flag-RPS2 (6RA) was transfected into HEK293T cells for 24hr, followed by polysome profiling. Fractions were collected and used for western blotting with anti-Flag, anti-RPS6 and anti-RPL4 antibodies as indicated.

To further examine the potential mechanisms of how arginine methylation affects mRNA translation, we selected the ribosomal protein RPS2, a newly

identified PRMT1 and PRMT4 substrate in our dataset, for more detailed study. RPS2 has an N-terminal GR-rich motif that is the consensus motif for efficient arginine methylation. We made mutations on the potential methylarginine sites (6RA, with 6 Arg to Ala substitution, see table S2) to examine if such mutations can affect the assembly of RPS2 into ribosome. Using polysome profiling followed by western blotting, we found that the cells transfected with Flag-tagged wide-type PRS2 can efficiently assemble Flag-RPS2 into ribosomes (in fractions of small subunit, monosome and polysomes), however the RPS2 with mutated methylarginine sites are completely depleted from all ribosomal fractions (Fig. 6C). Consistently, the deletion of the N-terminal GR-rich motif in RPS2 also cause depletion of PRS2 from the assembled ribosomes, suggest the arginine methylation in this region is critical for the assembly of this protein into ribosomes (Fig. S7).

Inhibition of PRMT activity cause global translation deficiency

To further examine how PRMT inhibitions affect the translation of different mRNAs, we sequenced the mRNA population associated with different ribosomal fractions after treatment of PRMT1 and PRMT4 inhibitors (Fig. 7A). Compared to the control samples treated with DSMO, the inhibition of PRMTs can significantly reduce the level of mRNAs bound by single ribosomes or polysomes (Fig. 7B). More specifically, among the 6783 protein-coding genes detected with reliable numbers of RNA-seq reads, 4392 mRNAs in the

PRMT1-inhibited sample (~65%) and 3830 mRNAs in the PRMT4-inhibited sample (~56%) showed a consistent decrease in the association with different ribosomal fractions (i.e.,both monosome and polysomes), suggesting a general reduction of translation efficiency on most mRNAs (Fig. 7C). Interestingly, the GO analysis of these mRNAs failed to produce any functional enrichment (not shown), again suggesting a global reduction of mRNA translation rather than translation inhibition on a specific subgroup of mRNAs.

We next determined how PRMT inhibition affects translation of different mRNAs using Ribo-seq to measure the distribution of ribosome protected RNA fragments in control and PRMT inhibition samples (Fig. 7D). This analysis can generate a “snapshot” of all mRNAs that are occupied by active ribosomes (i.e., undergoing active translation) in a cell at a particular condition (Ingolia 2016). As expected, the ribosome occupancy is higher in the coding region compared to the 5’ and 3’ UTRs upon normalized against average coverage (Fig. 7E). In addition, the binding of ribosomes on mRNA was slightly enriched in the region around the start codon and before the stop codon, suggesting a ribosome pausing after the initiation and the delayed ribosome release (Fig. 7E), which is also consistent with the ribosomal profiling results from other groups (reviewed in (Ingolia 2016)). Interestingly, we found that the inhibition of PRMT activity did not change the distribution of ribosome occupancy on different regions of mRNAs (Fig. 7E). Given the observation of translation reduction by PRMT inhibitions (Fig. 6A and 6B), this result again

suggested that PRMTs may affect the maturation of ribosomes before they are assembled onto the mRNAs, consistent with our finding that arginine methylation of ribosomal proteins is essential for ribosome assembly.

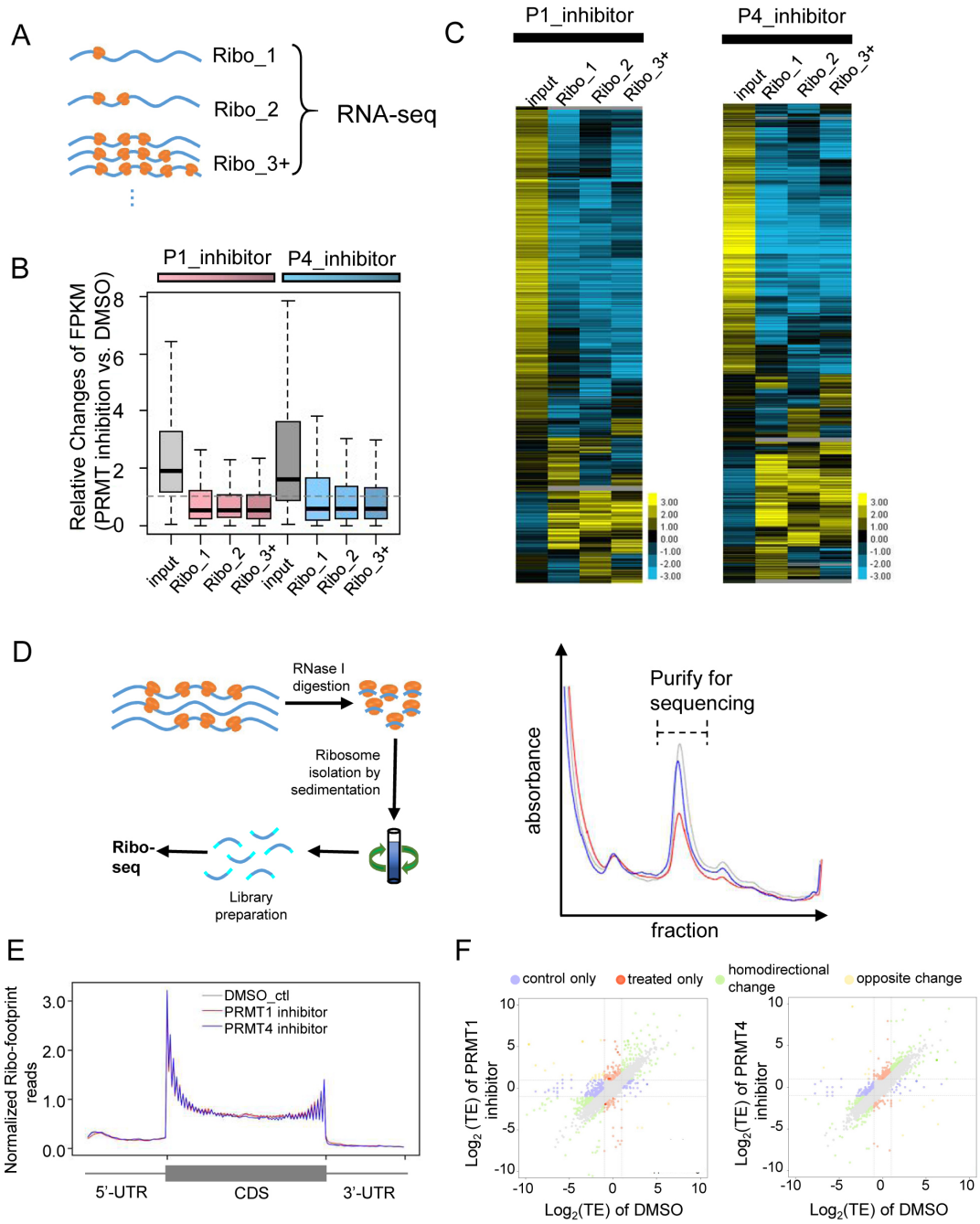

Figure 7. The inhibition of PRMT activity leads to global translation deficiency in thousands of genes.

(A) Schematic diagram of experiments. Polysome profiling was performed to fractionate different

ribosome fractions upon treatment of PRMT inhibitors in HEK293T cells. The mRNAs bound to one ribosome (ribo_1), two ribosome (ribo_2) and more than three ribosomes (ribo_3+) were collected and subjected to RNA-seq, respectively. (B) The relative FPKM changes of input mRNAs and ribosome-bound mRNAs (with PRMT1 and PRMT4 inhibition compared to DMSO control) were represented as box plot. (C) Hierarchical clustering of different mRNAs in the input and ribosome-bound fractions after treatment with PRMT1 and PRMT4 inhibitors. The log2 fold change of each mRNA was calculated and hierarchically clustered. (D) The samples with PRMT1 and PRMT4 inhibition were treated with RNase I to collect ribosome protected RNAs for high-throughput sequencing (Ribo-seq assay). The schematic diagram of experiments (left) and the isolated ribosome fractions for sequencing (right) were shown. (E) Ribosome protected RNA reads were mapped to the human genome, with the number of ribosome footprint reads in the different region of transcripts being normalized by average coverage of each transcript. All transcripts were combined to plot the distribution of normalized reads along the transcript regions. (F) Changes of translation efficiency (TE) upon PRMT inhibition. The changes of each transcript were plotted as scatter plot (more significant p-values presented with darker color). Blue: genes with large TE changes only in control sample; Red: genes with large TE changes in PRMT1 or PRMT4 inhibition sample; Green: genes with TE changes homodirectionally in two conditions; Yellow: genes with TE changes oppositely in two conditions.

We further determined the specific genes whose translation efficiency (TE) was preferably affected by PRMT inhibition by using Xtail pipeline (Xiao et al. 2016) to measure the genes with significant TE change after PRMT inhibition (Fig. 7F). We found that the inhibition of PRMT1 significantly changed the TE of only eight coding genes, whereas the TE of 46 protein-coding genes was significantly altered upon inhibition of PRMT4 (Fig. 7F). Interestingly, among the 46 genes affected by PRMT4 inhibition, 25 ribosomal protein genes have significantly increased TE, suggesting a potential functional complementation after the translation suppression.

Discussion

As a common but relatively underappreciated PTM, the methylation of arginine has been found in many proteins with global identifications of

methylation sites (Boisvert et al. 2003; Ong et al. 2004; Pahlich et al. 2006). Many PRMTs were found to catalyze this type of PTM, however the relationship between PRMTs and their substrates were not established on a global scale. In this study, we have for the first time identified the putative substrates for each of the human PRMTs and further characterized the novel consensus methylation motifs for individual human PRMT. We found a high degree of overlap in substrate specificity of different PRMTs, as well as a significant enrichment for RNA binding proteins in the substrates of all PRMTs. In particular, the splicing factors and ribosomal proteins are heavily methylated and overrepresented in PRMT substrates, and consistently the inhibition of PRMTs leads to global deficiency of RNA translation. Collectively, the identification and characterization of substrates for all human PRMTs provide a foundation for further studies on their biological functions.

One interesting observation is that the majority of the consensus motifs for arginine methylation are short fragments with low sequence complexity, including the well known GR-rich motifs and newly identified SR- and PR- rich motifs (Fig. 2 and Fig. S2). Since low complexity domains (e.g., GR and SR-rich domain in RNA binding proteins) usually form a non-structural region, the recognition by PRMTs likely happens in the unstructured regions of proteins, suggesting a structure independent recognition, which is supportive to the promiscuous binding between PRMTs and many of their targets. This promiscuous binding may help to explain the high overlaps between the

binding partners of different PRMTs, suggesting a certain degree of functional complementation among PRMTs. Consistently, the knockout mice of most PRMTs have only mild phenotypes (Yang and Bedford 2013; Jeong et al. 2016; Penney et al. 2017), with the exception of PRMT1 and PRMT5 that cause lethal phenotype after knockout (Pawlak et al. 2000; Nicholson et al. 2009; Tee et al. 2010). Therefore we speculate that the additional specificity is provided by the spatial/temporal control of expression for PRMTs and their potential targets.

Arginine methylation usually increases protein hydrophobicity, thus may affect how proteins interact with their partners and assemble into a functional complex. Here we found that the core ribosomal proteins are among the largest protein groups recognized and methylated by PRMTs, raising the possibility that the methylarginine modification of ribosomal proteins can affect the assembly and function of ribosomes. It is well known that ribosome heterogeneity contributes to the regulation of mRNA translation (Genuth and Barna 2018; Emmott et al. 2019), and thus we expect that the methylarginine modification status of ribosomal proteins is a major source for ribosome heterogeneity. Here we proved that mutations on methylation sites of RPS2 can inhibit its assembly into ribosomes, and found that inhibitions of certain PRMTs impose a global suppression on translation. Rather than affecting a specific step of translation, our data implied that the translation reduction may be caused by the defects of ribosome biogenesis before they are assembled

onto mRNA.

Although the ribosomal proteins are significantly enriched with arginine residue and are the most overrepresented targets of PRMTs, we speculate that they are differentially modified by different PRMTs. As a result, inhibition of different PRMTs affected the translation efficiency of distinct sets of mRNAs. More detailed analyses on how each PRMT differentially affects the assembly and functions of ribosomes will be an important subject for future studies.

Like many PTM, methylation of arginine also has the specific “readers”, “erasers” and “readers”. Although nine PRMTs were identified as methylarginine writer, so far there is only one “eraser protein”, JMJD6, was reported for methylarginine (Chang et al. 2007) and several proteins containing “Tudor” domains were proposed function as putative “reader” (Vagin et al. 2009; Kirino et al. 2010; Chen et al. 2011). We expect that the biological functions of methylarginine modification are probably determined by the networks consisting of different “writers”, “erasers”, “readers” and their substrates. Therefore, mapping such interacting network will provide useful information on the function of arginine methylation in various proteins. This study represents a start point for a comprehensive mapping of a network containing methylarginine “writers”, “erasers”, “readers” and their substrates, and thus may serve as a foundation and reference for future research on this topic.

Materials and Methods (see supplemental methods for more detailed information)

Resources

Antibodies: Detailed information for antibodies applied in this study is listed in Table S3.

Cell lines: HEK293T, HCT116 and U2OS cells were cultured according to instructions of American Type Culture Collection (ATCC). The cell lines have been authenticated in GENEWIZ and has been tested to have no mycoplasma contamination by mycoplasma contamination test kit (C0296, Beyotime).

Tools: software, databases and services were available in supplemental methods.

Plasmids

For identification of interacting proteins of each PRMT, Human PRMT1-PRMT9 were amplified by PCR and inserted into the pcDNA3.1-BirA-HA plasmid (#36047, Addgene). For *in vitro* methylation, 3×Flag-tagged PRMTs (PRMT1 to PRMT9) were inserted into pcDNA3.1-3×Flag plasmids. For ribosome assembly, Flag-tagged hRPS2 were generated by PCR from human cDNA and inserted in frame with pcDNA3.1-Flag. The RPS2 mutants with arginine to alanine substitution (R22/26/34/36/227/279A, 6RA) and with deletion of GR-rich motif (amino acids 34-53) were generated by site directed mutagenesis.

Identification of interacting proteins for each PRMT

Human PRMT1-PRMT9 were amplified by PCR and inserted into the pcDNA3.1-BirA plasmid. The BioID experiments were performed as described in Roux et al. (Roux et al. 2012) with minor modifications. Briefly, the HEK293T cells transiently expressing PRMT-BirA fusion proteins were collected and lysed, and the protein complexes were purified using streptavidin beads. The resulting protein mixture was further separated through HPLC using a homemade 15 cm-long pulled-tip analytical column, and analyzed using mass spectrometry. The acquired MS/MS data were compared to the UniProt database using Integrated Proteomics Pipeline. A decoy database containing the reversed sequences of all the proteins was appended to the target database to accurately estimate peptide probabilities and false discovery rate (FDR), and FDR was set at 0.01.

Motif enrichment analysis

We retrieved the full sequences of all identified interactors of each PRMT from the UniProt database. We counted all tetrapeptide with arginine amino acid at each position (candidate PRMT's binding sites) and calculated the frequency of each tetrapeptide in each PRMT interactome and compared with the background tetrapeptide frequency of all human proteins from UniProt database. The enrichment score of each tetrapeptide was calculated as Z score based on published methods (Fairbrother et al. 2002). We collected all

motifs with enrichment score larger than 4 and motif number larger than 6 as an input of clustalw2 (v2.0.9) to generate a phylogenetic tree, then clustered these motifs based on branch length and modified manually to ensure the similar motifs in one class. Finally, we used Weblogo3 (WebLogo: A sequence logo generator) to draw the consensus sequence of each cluster.

In vitro methylation and MS detection of arginine methylated peptides

The HEK293T cells transiently overexpressing 3×Flag-tagged PRMT were lysed, and the overexpressed proteins were purified using Anti-FLAG M2 Magnetic Beads. *In vitro* methylation assay was carried out according to Cheng et al (Cheng et al. 2012) with minor modifications. Peptide substrates containing predicted motifs and recombinant enzyme (on beads) were incubated in the presence of S-Adenosyl-L-methionine (AdoMet). The reaction mixture was further separated through HPLC using a homemade analytical column and analyzed using mass spectrometry. The acquired MS/MS data were analyzed on a homemade database including all target peptides with Integrated Proteomics Pipeline (IP2, http://integratedproteomics.com/) and pFind (version 3.1.3 (Chi et al. 2018)). Methylation and dimethylation were set as a dynamic modification with mass shift at 14.01565 and 28.0313, respectively. For each peptide, the sum of the peak areas from the TIC values of the modified peptides was divided by the peak area of the reference unmodified peptide and this value was used as a relative index of the

methylation and dimethylation.

Generation of stable cell lines

Production of lentivirus was carried out according to Addgene pLKO.1 protocol. Scramble shRNA and PRMT shRNA sequences were listed in Table S3. Lentiviruses were packaged by transfection of three plasmids (pLKO.1, psPAX2, and pMD2.G.) into HEK293T cells, and the stably transfected cells were selected with puromycin for at least two weeks. The knockdown efficiency was determined by PRMT antibodies.

RNA-seq

HEK293T cells stably transfected with scramble shRNA or shRNAs against PRMT were harvested in Trizol reagent and RNAs were extracted according to the manufacturer's protocol. Poly(A)+ RNA-seq libraries were prepared by using Illumina TruSeq Stranded mRNA LT Sample Prep Kit (Illumina) and subjected to deep sequencing with Illumina Hiseq X10 under PE150 sequencing model.

Immunoprecipitation and substrate validation

The lysate of HEK293T cells was separated into trisection and incubated with ADme-, SDme- and Mme- arginine antibody, respectively. The A/G PLUS-Agarose beads (Santa Cruz) were used for immunoprecipitation of

methylarginine-containing substrates. The candidate substrates (ribosomal proteins) were detected via western blot.

Polysome profiling

Polysome profiling was carried out according to Lin et al. and Vyas et al. (Vyas et al. 2009; Lin et al. 2010). DMSO or Inhibitor-treated HEK293T cells were lysed in polysome lysis buffer. The lysates were loaded onto 10-50% sucrose gradients and ultracentrifuged. Fractions were collected using a Brandel Density Gradient Fractionation System. Samples were precipitated with Methanol/chloroform method according to Sucrose Gradient Separation Protocol (http://www.mitosciences.com/PDF/sg.pdf). The protein precipitate was assayed by western blot to detect arginine methylation status using combined anti-methylarginine antibody. Meanwhile, ribosomal proteins and PRMTs were also detected via western blot (antibodies listed in Table S3).

RNA-seq of polysome profiling fractions

mRNAs from indicated fractions of polysome profiling samples were extracted with TriZol reagent. RNA-seq libraries were prepared by NEBNext®EUltra™ II Directional RNA Library Prep Kit for Illumina (NEB) and subjected to deep sequencing with Illumina Hiseq X10 under PE150 sequencing model.

Measurement of global protein synthesis by puromycin incorporation

HEK293T, HCT116 and U2OS cells were incubated with specific inhibitors (see Table S3) against several PRMTs. Subsequently, puromycin incorporation assay was performed according to Kelleher et al. (Kelleher et al. 2013). Puromycin was added to the medium of inhibitor-treated cells 30 min before harvest. An equal quantity of protein lysates was separated on SDS/PAGE and probed with anti-puromycin antibody (Millipore).

Ribosome footprint

Cleared cell lysates from polysome profiling procedure were treated with RNase I to obtain ribosome-protected mRNA fragments (RPF). Subsequently, lysates were loaded onto 10-50% sucrose gradients, ultracentrifuged and fractionated as described above. Fractions containing monoribosome particles were combined and undergone RNA clean-up by TriZol reagent. The RNA sequencing library was prepared according to Ingolia et al. (Ingolia et al. 2012) with some modifications. The RPF library was prepared as described in Illumina Small RNA Library Prep Reference Guide. RNA samples were reverse-transcribed and cDNA libraries were gel purified and amplified by limited-cycle PCR with index primers. Libraries were cleaned up and subjected to next-generation sequencing on Illumina Hiseq X10.

Bioinformatics analyses

The R package GeneOverlap was used to test the significance of substrates overlap between different PRMTs, with total number of interacting proteins identified in this study as the background. Gene Ontology (GO) analysis of putative PRMT substrates was performed using Database for Annotation, Visualization and Integrated Discovery (DAVID, v6.8), with total proteins in human genome as background. Protein-protein interactions were obtained from STRING database (Szklarczyk et al. 2015) with interaction score set to high confidence, then clustered by MCODE in Cytoscape software.

For analysis of alternative splicing, the RNA-seq reads were mapped onto the human genome reference (Ensembl GRCh37), and the PSI (Percent Spliced In) values were estimated using MISO and rMATs for each annotated splicing event. For significant change of spicing were filtered using FDR cutoff of 0.01, we also required the ΔPSI cutoff at 0.1 with minimal read count at 50.

To analyze RNA-seq data after the polysome profiling, we trimmed the adaptors and low-quality bases of paired-end 150bp reads using Cutadapt (v1.18). The trimmed reads with length < 20 nt were excluded, and the remaining reads were mapped to the human genome (GRCh37 with annotation of GENCODE v27lift37) using STAR (v2.5.3a). Genes expression levels (FPKM) were estimated by RSEM, and the relative fold changes were calculated. The Hierarchical clustering of log2 fold changes was carried out using Cluster 3.0 with centered correlation and average linkage parameter, the

heatmap was visualized by TreeView.

Ribo-seq data were analyzed according to Calviello et al. (Calviello et al. 2016). The translation efficiency of each gene was estimated by dividing the TPM of ribosome-protected mRNA with the relative transcript abundance. For coverage plot, we scaled each transcript and divided 5'-UTR, CDS, and 3'-UTR regions to 20, 100, and 50 windows, respectively. The average coverage in each window was normalized to mean coverage of the entire transcript. To assess the statistical changes of translation efficiency, Ribo-seq signals and RNA-seq signals were analyzed using Xtail pipeline (Xiao et al. 2016), and the genes with adjusted *p*-values (less than 0.05) were used as differential translation efficiency genes.

Acknowledgements

We thank Han Yan at Omics Core of Bio-Med Big Data Center, CAS-MPG Partner Institute for Computational Biology (PICB), for assistance with next-generation sequencing. We also thank Yu-Jie Chen at Uli Schwarz Quantitative Biology Core Facility, PICB, for experimental support with this study. We thank Dr. YanZhong Yang and Prof. Mark T. Bedford at the University of Texas MD Anderson Cancer Center for their generous gift of several PRMT plasmids.

Declarations

Ethics approval and consent to participate

There is no human participants or animal models used in this work. All the experiments using biological samples are conducted according to the regulation of biosafety laws in China.

Consent for publication

Not applicable

Availability of data and material

All sequencing data during the current study are available in The National Omics Data Encyclopedia (NODE) data depository (http://www.biosino.org/node/project/detail/OEP000307), with open access after publication.

Antibodies and other resources used in this study were listed in Table S3.

Competing interests

The authors declare that they have no competing interests.

Funding

This work was supported by National Natural Science Foundation of China (NSFC grant #31570823, #31661143031, and #31730110) and a grant from Science and Technology Commission of Shanghai Municipality (STCSM grant # 17JC1404900) to Z.W. It was also supported by an NSFC grant #91753135 to Y.Y.. H.H.W. is supported by a scholarship from the Science and

Technology Commission of Shanghai Municipality (STCSM grant # 18XD1404400)

Authors' contributions

H.H.W. and Z.W. conceived the project. H.H.W. and M.G. carried out the molecular and biochemical experiments. X.J.F., Y.H., and Z.Y.F analyzed the RNA-seq and Ribo-seq data as well as did other bioinformatic analyses. P.W., S.X.G., X.X.T, and C.P. conducted mass spectrometry experiments. X.J.F., Y. H., Y.Y., H.H.W, and Z.W. were responsible for study design and interpretation of data. All authors were involved in drafting the manuscript and revising it critically for important intellectual content.

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