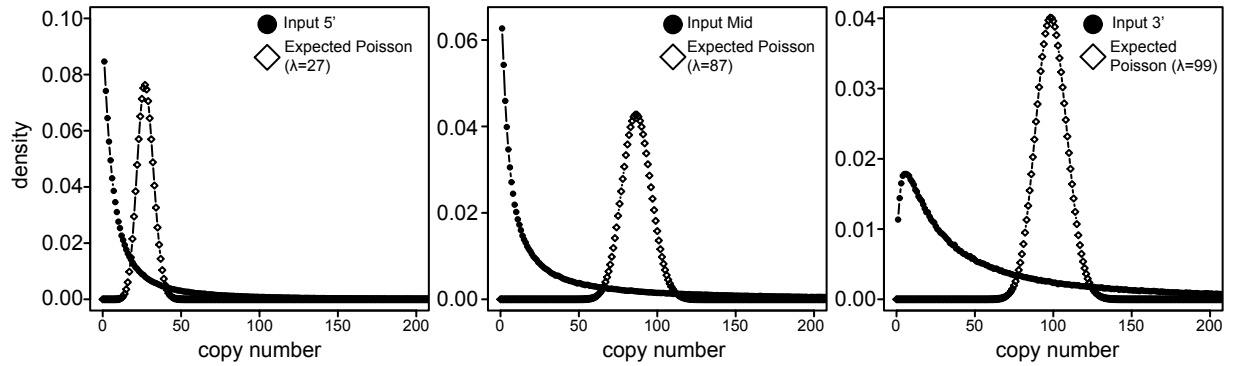
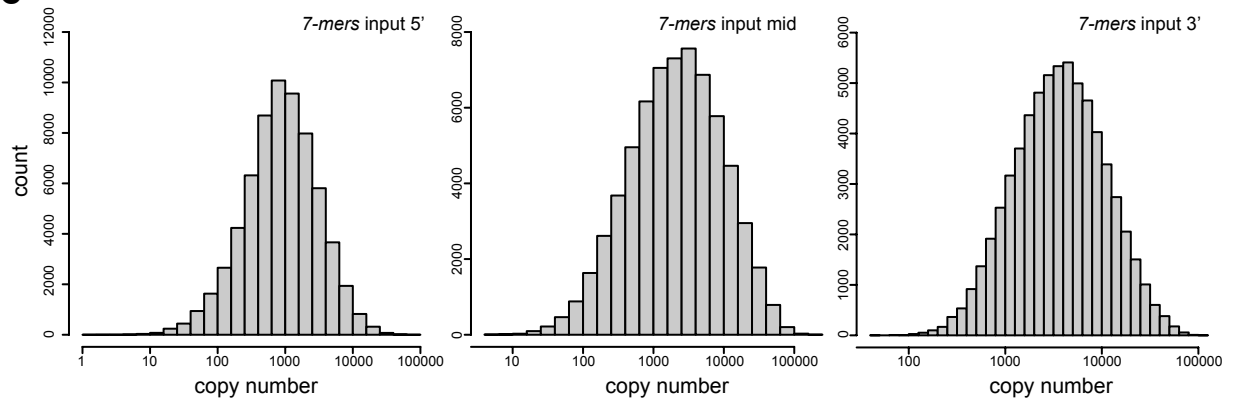


A

Sample	Read Counts				Number of Distinct Sequences			
	5' Randomized	Mid Randomized	3' Randomized	Total	5' Randomized	Mid Randomized	3' Randomized	Total
Input	28,687,463	91,174,453	103,691,491	255,326,507	964,513	983,624	1,042,185	2,990,322
PPR10 WT	272,260	697,915	2,291,180	3,261,355	162,495	256,469	546,262	965,226
PPR10 Rpt15(TD)	186,282	676,097	1,941,153	2,803,532	128,225	248,198	514,407	890,830
PPR10 Rpt6.7(TD)	328,444	1,045,231	1,766,564	3,140,239	167,926	286,778	512,054	966,758
PPR10 Rpt6.7(TN)	292,532	932,667	2,047,142	3,272,431	176,260	291,341	540,286	1,007,887
PPR10 Rpt7(ND)	201,295	473,212	1,315,960	1,990,467	107,159	198,429	382,511	688,099

B**C**

SUPPLEMENTAL FIGURE S1. Overview of bind-n-seq read counts. (A) Number of reads and distinct sequences from each pool in each bind-n-seq assay. (B) Frequency distribution of sequences with various copy numbers in the input RNA pool. The distributions for the 5', middle and 3' randomized RNA pools are shown to the left, middle, and right, respectively, and are overlaid with the expectation based on a Poisson distribution. Lambda was calculated as the number of input reads divided by 410, the theoretical number of sequences represented by each partially randomized oligonucleotide. (C) Frequency distribution of 7-mers found in various copy number in the input RNA pool. 99% of the 196,608 possible 7-mers were represented at least 50 times in the sequenced aliquot of input RNA.