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**Titles:**

Target features that determine binding thermodynamics to the 3′-end of the miRNA

Thermodynamics of miRNA 3′-pairing relies on an interplay of miRNA-independent and dependent factors.

**Abstract:**

The current understanding of animal microRNAs (miRNAs) largely pertains to the nucleotides at positions 2–8 of the miRNA guide sequence, referred to as the “seed” region. The function of ~14 positions 3′ of the seed, which are highly conserved for many miRNAs, remains enigmatic, with discordant findings across a handful of studies. We therefore performed RNA bind-n-seq (RBNS) with purified AGO2–miRNA complexes and libraries with partially randomized RNA sequence to measure the relative binding affinity of over ~12,000 distinct 5′- and 3′-bipartite pairing configurations for each of three naturally occurring miRNAs and five synthetic derivatives. These data demonstrate upwards of 100-fold increase in binding affinity contributed by extensive pairing to the miRNA 3′ region in comparson to seed pairing alone. In addition, we find that the extent of this increase is highly variable, and is primarily influenced by 1.) the predicted stability of the pairing between the miRNA 3′ region and the target RNA sequence, 2.) the length and sequence content of the unpaired segment of the target RNA between the miRNA seed– and 3′–paired regions, and 3) the specific miRNA–target pairing configuration within the seed region. These affinity measurements are used to train a predictive linear model and quantifies importance of different features to a general model for 3′ pairing energetics.

Depending on the end:

We find that a model utilizing these additional features enhances miRNA-target prediction and unearths additional potential target sites.

These data are used to train a predictive linear model that enhances miRNA-target prediction.

A high-throughput reporter assay of mRNAs containing these types of sites demonstrates that these *in vitro* affinities (or this linear mode)l is predictive of *in vivo* repression.

**Introduction:**

miRNAs are ~22-nt regulatory RNAs that are processed from hairpin precursors and, upon association with an Argonaute (AGO) protein, pairing to sites within mRNAs to direct their destabilization and translational repression (Guo et al, 2010, Eichhorn et al, 2014, Bartel, 2019). For most sites that confer repression in mammalian cells, pairing to miRNA nucleotides 2–7, referred to as the miRNA seed, is critical for target recognition, with an additional pair to miRNA position 8 or an A at target position 1 often enhancing targeting efficacy (Lewis, 2005, Bartel, 2009, Schirle et al., 2015). Such sites with a perfect 6–8-nt matches to the miRNA seed region (Fig 1A) are heuristically predictive of repression, with longer sites being more effective than shorter ones and more sites being more effective than fewer sites (Grimson et al., 2007, Agarwal et al., 2015). Features of site context can also influence targeting efficacy. For example, sites are more effective if they reside near to other sites that can act cooperatively, within a region that does not form occlusive secondary structure, and in the 3′-untranslated region (UTR), i.e., out of the path of the scanning initiation complex and the ribosome (Grimson et al., 2007, Wan et al., 2014).

Pairing to the miRNA 3′ region, particularly nucleotides 13–16, can supplement perfect seed pairing to enhance targeting efficacy, and more extensive pairing to this region can compensate for imperfect seed pairing to enable targeting (Grimson, et al., 2007). These two bipartite site types are referred to as 3′-supplementary and 3′-compensatory sites, respectively (Fig 1A). Although much less common than sites with only a seed match, thousands of sites with preferentially conserved 3′-supplementary pairing are present in human 3′-UTRs have (Friedman 2009). Indeed, while conserved 3′-compensatory sites are even less common, such sites can have crucial biological functions. For example, let-7-mediated repression of *lin-41* is required for viability in *C. elegans* through two 3′-compensatory (Reinhart *et al*., 2000). Moreover, the use of 3′-compensatory sites rather than canonical sites provides a mechanism by which to confer differential target specificity between miRNAs that share common seed sequences but differ at their 3′ regions, which is proposed to prevent precocious repression of *lin-41* by earlier-expressed let-7 paralogs (REFs).

Although analyses of site conservation can detect the preferential conservation of 3′-supplementary and 3′-compensatory pairing (Grimson et al., 2007), and a global contribution to targeting efficacy can be detected for 3′-supplementary pairing after introducing a miRNA to cells (REF), the biochemical contribution of pairing to the miRNA 3′ region is poorly understood. Studies of a few target sites of a few miRNAs indicate that pairing to the 3′ region of the miRNA confers either negligible-to-small (2–7-fold) (REF Wee Saloman) or moderate (>20-fold, REF MacRae) increases in binding stability. With this paucity of biochemical information, many fundamental questions regarding pairing to the miRNA 3′ region (hereafter referred to as “3′ pairing”) have at best only begun to be answered. For example, what is the influence of 1) the extent of pairing, 2) the register of pairing within the miRNA, 3) the length of the loop linking the two parts of the bipartite site, or 4) the identity of imperfections in seed pairing (Fig 1B); and how might the identity of the miRNA modify the influence of each of these features? A fuller understanding of the contribution of paring to the miRNA 3′ region requires the acquisition of many more measurements. Without a more general model of how pairing to the miRNA 3′ end occurs and the magnitude of its effects for different miRNAs, it is difficult to predict the occurrence and efficacy of these types of sites *in vivo*.

RNA bind-n-seq (RBNS) allows for unbiased, high-throughput assessment the relative binding activities of RNA *k*-mers of variable length embedded within a larger random-sequence context (REF). We recently adapted RBNS for the study of miRNA targeting, and we built a computational analysis pipeline enabling calculation of relative equilibrium dissociation constants (*K*D,Rel values) of many thousands of different RNA sequences, which allowed for quantitative comparisons of putative site types and sequence features that is not possible through the analysis of *k*-mer enrichment alone (McGeary et al.). Applying this AGO-RBNS platform to miRNA–AGO complexes with six different miRNAs revealed unanticipated site preferences for these miRNAs and enabled a principled biochemical model of miRNA-targeting efficacy (McGeary et al.,).

When considering how little is known about the features of 3′ pairing that contribute to affinity, AGO-RBNS would an ideal technique to characterize these features, as it reveals the binding affinities between a miRNA–AGO complex and its target sites without *a priori* knowledge of what these sites might be. However, as previously implemented, AGO-RBNS does not provide information on sites with more than ~5 supplementary/compensatory pairs because such sites, which involve >12 nt of total pairing (Fig 1A), are too rare in the initial random-sequence library to allow accurate calculation of enrichment values. Here, we construct RNA libraries more suitable for characterizing 3′-compensatory sites and use these libraries to generate AGO-RBNS data that enable the systematic analysis of pairing to the miRNA 3′ region.

**Results**

**Binding-affinity profiles for let-7a 3′-compensatory sites**

As previously implemented, AGO-RBNS begins with the incubation of purified AGO–miRNA complex with an RNA library that contains a central region of 37 random-sequence nucleotides flanked by primer-binding sites (Fig 2A, top). Five binding reactions are performed, each with a constant library concentration of 100 nM and a different miRNA-AGO concentration spanning a 100-fold range. After reaching binding equilibrium, each reaction is applied to a nitrocellulose filter membrane under vacuum, which retains the AGO–miRNA complex and any bound RNA library molecules. The bound library molecules are isolated and subjected to high-throughput sequencing, along with the input RNA library. This allows for the fractional abundance of *k*-mers of various lengths in the bound libraries to be compared to the corresponding fractional abundance in the input library (Fig 2B). For any *k*-mers of interest that are ≤12 nt, relative *K*D values can be fit to its observed abundance profile constructed from multiple samples spanning a range of AGO–miRNA concentrations, using a biochemical model of the binding equilibrium between the *k*-mers within library sequences and the AGO–miRNA complex. This procedure simultaneously determines *K*D,Rel values for tens of thousands of *k*-mers, which allows the binding affinity of the same 5–8 nt site of a particular miRNA to be evaluated in the context of many longer *k*-mers, thereby report on the effects of different flanking nucleotide possibilities (McGeary et al., 2019).

3′-compensatory sites typically require >12 nt of pairing (Fig. 1A), and so would be expected to be sequences less than twice for every million reads from a 37-nt random library. Such extreme rarity of relevant sites renders these libraries fundamentally unsuited for comprehensive identification and dissection of the complex features within the seed and 3′ region that together modulate overall binding affinity. We therefore constructed an RNA library to investigate the 3′-compensatory sites of let-7a; this library included a programed region of imperfect seed pairing with 25- and 4-nt of random-sequence RNA (Fig 2A, bottom) separating the programed region from the 5′ and 3′ constant sequences, respectively. The programed region contained imperfect seed pairing with a match to let-7a at position 8, an A nucleotide across from position 1, and a match at all but one position to the seed nucleotides 2–7, such that each library molecule contained one of 18 possible single-nucleotide seed mismatches (including wobbles) with approximately equal probability. With this programed region of imperfect seed pairing, each library contained 3′-compensatory sites at a ~16,000-fold greater frequency than expected with a fully randomized RNA library.

AGO-RBNS performed with let-7a and this programmed RNA library yielded binding-affinity profiles for a massive number of bipartite site architectures combinatorially varying in pairing to both the seed region and the miRNA 3′ region— two regions of each bipartite site hereafter termed the “seed site” and “3′ site,” respectively. Within the randomized region 5′ of the programed seed site (Fig 2A), most library molecules varied with respect to 1) the length of the 3′ site, 2) the register of the 3′ site, as defined by the 5′-most miRNA position paired to the 3′ site, 3) the position and nucleotide identity of the seed mismatch, and 4) the length and sequence composition of the loop in the target that bridges the seed site and 3′ site (Fig 1B).

AGO-RBNS was performed using this programed library and purified AGO2–let-7a–silencing complex. Anticipating that 3′ sites would have preferred registers and preferred loop lengths, we searched for the top enriched *k*-mer, considering each position of the bound library molecules. Among *k*-mers ≤8 nt, the most enriched one was AUACAACC—the perfect Watson–Crick match to positions 11–18 of the let-7a miRNA, which was enriched up to 16-fold in the sample with 840 pM AGO2–let-7a (Fig. 2C). This 8-nt 3′ site was most strongly enriched when occurring at positions 14–21 of the library, thereby creating an asymmetric internal loop between seed pairing and 3′ pairing, which included miRNA positions 8–9 and library positions 13–9 (Fig. 2C, right). This 8-mer 3′ site was also ≥5-fold enriched at eight other positions of the library, indicating that other lengths of the loop in the target were functional, albeit to a lower degree (Fig. 2C).

The second-most enriched *k*-mer was UACAACCU—the perfect Watson–Crick match to let-7a positions 10–17 (Fig 2C). Although this 3′ site also had an optimal length of 5 nt separating the seed site and the 3′ site, its distribution of suboptimal loop lengths was shifted to be about 1 nt shorter than that of the AUACAACC site, consistent with the single-nucleotide shift in its pairing register. The next 18 most enriched *k*-mers revealed additional 3′-site possibilities, together with their preferred and tolerated pairing registers and loop lengths (Fig 2C). Each had a contiguous stretch of 6–8 perfect Watson–Crick pairs to the let-7a 3′ region, with no bulges, wobbles, or mismatches, and usually including the ACAACC 6-mer, which matched miRNA positions 11–16.

**3′ pairing can substantially increase affinity and compensate for a seed mismatch**

For more comprehensive examination of 3′ sites of varied lengths and within different contexts (Fig. 1B), we enumerated, for each of the 18 seed-mismatch possibilities, 3′ sites of lengths 5–9 nt that perfectly paired to the miRNA starting at or 3′ of miRNA nucleotide 11, allowing loops of 0–17 nt to separate the seed site from the 3′ sites. Of these 12,960 site possibilities, 12,638 has sufficient read coverage for analysis, and for each of these, the enrichment profile across AGO2–let-7a concentrations was used to calculate its relative *K*D value, using a previously described computational pipeline (McGeary, Lin, et al., 2019). These relative *K*D values spanned a >100-fold range, with strong agreement observed between the results of replicate experiments performed independently with different preparations of both the AGO2–let-7a complex and the let-7a 3′-compensatory RNA library (*r*2 = 0.86, Fig 3A). Furthermore, for 3′-compensatory sites that had 5-nt 3′ sites, which by virtue of their small number of specified residues could be evaluated using results from a conventional random-sequence library, the *K*D values determined from the programmed library correlated well with those determined from a random-sequence library (Fig S3A), indicating that the fitting procedure was robust to library composition.

Indeed, the majority of the 12,638 potential 3′-compensatory sites examined had *K*D values resembling those of their seed-mismatched sites alone, as might be expected when performing an unbiased analysis of putative sites. However, the detection of \_\_\_\_\_\_ 3′‑compensatory sites with affinities as highas that of canonical 7mer sites (Fig 3A) motivated us to perform a systematic investigation of which features of the seed- and 3′-portion of a 3′-compensatory site can together impart such affinity.

We first examined the relative *K*D values of 3′-compensatory sites as stratified by both 3′-site pairing length and target-RNA loop length (Fig 3B). Although all possibilities examined were at least 1.5-fold better than the seed-mismatched site alone, only 3′ sites ≥6 nt in length and with loop lengths ranging from ~3–8 nt conferred affinities exceeding those of the canonical 6-nt site. As also indicated in our analysis of enriched 8-nt k-mers across from the miRNA 3′ end (Fig 2C), the optimal loop length for 3′ sites beginning at register 11 was 5 nt (Fig 3B). At this loop length, an 8-nt 3′ site conferred a ~60-fold increase in affinity over the seed-mismatched site alone, enabling the affinity of the 3′-compensatory site to surpass those of the canonical 7-nt seed sites and approach that of the canonical 8-nt seed site (Fig 3B).

This 60-fold increase in affinity conferred by optimally positioned 3′ pairing was substantially greater than the 2-fold increase observed for 3′ pairing in the context of a perfectly paired target (Wee et al., 2012), perhaps because of the shorter suboptimal loop length of the perfectly paired target. It was also somewhat greater than the 20-fold increase measured for miR-122 pairing to the GCGG site at register 13 and loop-length of 4 nt (MacRae REF). Nonetheless, it was substantially less than expected based on the predicted free energy of RNA pairing in solution. For example, the predicted free energy (∆*G*) of a 7-nt segment paring to let-7a positions 11–17 is 7.1 kcal/mol, which corresponds to a 164,000-fold difference in binding affinity (from ∆*K*eq = *e*–∆∆*G*/*RT*). This large discrepancy is presumably due to the energetic costs of 1) displacing favorable contacts between the miRNA 3′ region and AGO2, and 2) undergoing any conformational changes needed to accommodate 3′ pairing (REF haley). Indeed, the benefit of extending the 3′ site plateaued at about 7 or 8 nt (Fig 3B), implying that these costs were even more severe when pairing to the last five nucleotides of let-7a.

**The type of seed-mismatch affects the affinity of 3′ pairing**

To examine the influence of position and nucleotide identity of seed mismatches, we examined another slice through the multidimensional feature space of 3′ pairing, holding 3′-site length, register, and loop length at a near-optimal values (pairing to let-7a positions 11–17 with a loop length of 4 nt) and examined the overall binding affinity of the 18 different seed mismatch types (Fig 3C). We observed a >100-fold range in relative *K*D for this seed- and 3′-site architecture depending on position and identity of the seed mismatch; by comparison, we observed only a XX-fold range in relative *K*D for these 18 seed mismatch sites in the absence of any 3′ pairing. This demonstrates that the energetics of the seed- and 3′-sites are not independent, such that the potential benefit of 3′ pairing is differentially available when paired with different seed mismatch types. To directly analyze the dependence of 3′-pairing on seed mismatch type, we divided the relative *K*D value of each 3′-compensatory site by that of its seed site to generate a *K*D fold-change value representing the contribution of the 3′ site to overall affinity (Fig 3C). Even after this normalization for the differential effects of the 18 mismatches on seed-site affinity, a 11.7-fold range in affinities was observed at the optimal loop lengths (Fig 3D). This variation was reproducible, with only 1.X-fold attributable to experimental variability (Fig. S3), and it did not correlate noticeably with either the type of seed mismatch or the measured affinity of the seed site (Fig 3D). Notably, a let-7a compensatory site that occurs naturally within the 3′ UTR of *C. elegans* *lin-41* mRNA contains a seed mismatch, register, and loop length with one of the higher 3′-pairing affinity contributions (Fig 3D, bottom).

The strong effect of the seed-mismatch identity suggested a long-range conformational coupling allowing the pairing state at the seed region to communicate with the pairing potential at the 3′ region. This inferred coupling is reminiscent of mismatches between the CRISPR-Cas13a guide RNA and RNA target having differential effects on HEPN nuclease activation compared to their effects on binding affinity (Tambe et al., 2018). Structures of loaded human AGO2 with targets that pair to the miRNA seed (g2-g7, g2-g8, and g2-g9) display a change in the 3′ residues of the miRNA to be more available for pairing than without a seed-matched target (REF), suggesting there exists coordination to relay the seed-pairing state to protein residues that contact the 3′ end of the miRNA. Moreover, in the recent structure of loaded AGO2 bound to a fully complementary target, the seed conformation is slightly different, in particular at guide nucleotides 7 and 8 (REF). It is possible that the criteria for the conformational change is simply having a target bound such that any seed-match or mismatch will have an equal likelihood of promoting the conformational change of the 3′ end. In this scenario, the contribution of the 3′ pairing to overall binding affinity would be the same regardless of different amounts of seed pairing, or mismatches. On the other hand, various mismatches in the seed region may promote or inhibit this conformational change, and thus change the fraction of time the complex is competent to make 3′ base pairs. There is precedent for analogous behavior; it has been shown previously that a G-G mismatch at position 6 in the miRNA guide promote zebrafish’s Argonaute2 target cleavage reaction (Chen et al., 2017). This second model predicts that the contribution of 3′ pairing to overall binding affinity would be different for different seed-mismatches.

**The preferred pairing register differs for different miRNAs**

Repeating the analysis of Fig 3D for each of the seven possible pairing registers for a 7-nt 3′ site for let-7a revealed that the register of pairing had a dramatic effect on the affinity of compensatory pairing. This affinity sharply diminished at register 12 and did not exceed background levels at registers 13–16 (Fig 4A, top row). At registers 9 and 10, affinity of compensatory pairing was retained, although somewhat diminished. At register 9, two loop-length optima were observed, one of which was at a loop length of 0 nt, consistent with pairing of seed and 3′ sites forming a single contiguous helix. However, in the context of most seed mismatches, the optimum that occurred at a loop length of 2 nt was somewhat more favorable, implying preference for non-contiguous pairing. Indeed, even at a loop length of 0 nt the potential pairing at positions 9 and 10 might not form, as indicated by the similar affinities observed at this loop length when substituting a U for the A at target position 9 (Fig SX). This apparent lack of pairing to miRNA position 9 indicates that, as with the miRNA 3′ terminal nucleotides, the energetic costs of displacing favorable contacts and undergoing conformational changes prevent stable pairing to miRNA nucleotide 9.

The optimal register for 3′ pairing to let-7a, occurring at miRNA nucleotides 11–17 (Fig 4B), was somewhat offset from the optimal register previously determined from the repression and conservation data, which centered on miRNA nucleotides 13–18 (Fig. 1A) (REF Grimson). Because the previous analyses pooled data from multiple miRNAs, and because different miRNAs can have diverse site-type preferences (McGearyREF), we acquired the 3′-pairing profiles of two other miRNAs, miR-1 and miR-155, for comparison to the let-7a profiles. As with let-7a, we synthesized programed libraries enriched for all possible single-nucleotide seed mismatches at positions 2–7, performed AGO-RBNS, and calculated *K*D, Rel values for 7-nt 3′ sites in all possible registers, over a 0–16-nt range of loop lengths, in the context of each of the 18 seed mismatches. Normalizing for the contribution of the mismatched seed sites yielded 3′-pairing profiles at each register (Fig 4A).

Clear evidence for stabilizing 3′ pairing was observed for miR-1 at registers 11–13 and for miR-155 at registers 10–13 and 15–17 (Fig 4C). As observed for let-7a, 3′-site affinity for miR-1 and miR-155 varied with the position and identity of the seed mismatch. The optimal register for 3′ pairing to miR-1 occurred at miRNA nucleotides 12–18, whereas the optimal register of 3′ pairing to miR-155 occurred at miRNA nucleotides 15–21 (Fig 4C and D). Thus, on the whole, the different optimal pairing registers observed for the three miRNAs (11–17, 12–18 and 15–21) concurred with the conclusion derived from pooling repression and conservation data from multiple miRNAs, which stated that optimal 3′ pairing centers on miRNA nucleotides 13–18 (Grimson). However, the current results revealed unanticipated differences between miRNAs in optimal register of pairing. We also observed differences between miRNAs in the strength of 3′ pairing; compared to 3′-site affinities observed for let-7a, affinities were somewhat lower for miR-1 and miR-155 (maximal *K*D fold-change values for 7nt of 3′ pairing, 43, 15, and 14 for let-7a, miR-1 and miR-155, respectively) (Fig 4D). Thus, our results indicate that the sequence of the miRNA, not common interactions with the protein, influence the contribution and the preferred register for 3′ pairing.

These trends were recapitulated using AGO-RBNS data from random-sequence libraries (McGeary et al., 2018), albeit with more error due to lower counts of site occurrences, even when confining our analysis to shorter, 5-nt 3′ sites (Fig S4 ). Of the six miRNAs examined, lsy-6 had the highest-affinity 3′ pairing—up to 100-fold for a 5-nt 3′ site pairing to miRNA nucleotides 13–17. In contrast, miR-7 had the lowest-affinity 3′ pairing, with little signal for a contribution of 5-nt 3′ sites detected above background (Fig S4).

Our finding that the identity and position of the seed mismatch can exert such a striking influence on the added affinity conferred by 3′ pairing raised the question of how this added affinity might differ for canonical sites, which have no seed mismatches. To answer this question, we analyzed the AGO-RBNS results from random-sequence libraries, focusing on 5-nt 3′ site sites in the optimal register and aggregating results for the 5 most optimal loop lengths (Fig S5). Overall, the additional affinities conferred by 3′ pairing associated with canonical sites fell within the range of affinities conferred by 3′ pairing associated with seed-mismatched sites (Fig S5). Thus for most miRNAs, even the highest-affinity seed-matched sites can be improved with optimally positioned 3′-supplementary pairing. The exception was miR-7, for which a contribution of 3′ pairing was difficult to detect for both seed-mismtached and seed-matched sites.

**The optimal 3′-pairing register depends on the identity of the 3′ sequence.**

To begin to examine the determinants of the optimal 3′-pairing register, we repeated the AGO-RBNS procedure with let-7a variants that had single-nucleotide insertions and deletions that shifted the let-7a 3′ sequence by a single nucleotide in either direction while maintaining the length of the miRNA (Fig 5A, let7a(–1) and let7a(+1)). Analysis of these new datasets revealed that the optimal 7-nt 3′ site (UACAACC) remained the same, regardless of the shift in the register of the corresponding segment within the let-7a variant. Thus, the preferred register of 7-nt 3′ sites, which was 11–17 for let-7a, shifted to 10–16 for let-7a(–1) and to 12–18 for let-7a(+1) (Fig 5B and 5C). These results showed that particularly favorable 3′ pairing, such as that involving nucleotides 11–17 of let-7a, can dictate the preferred register of pairing and that this phenomenon can help to confer different optimal registers to different miRNAs.

This observation can be further quantified by comparing the correlation between 3′ pairing matrices of the register shifted let-7a variants to the wildtype let-7a matrices (Fig S4); specifically, register 10 and 11 are most correlated between the minus1/WT 3′ pairing matrices, and 12 and 11 for the plus1/WT 3′ pairing matrices (R2 = 0.9x and 0.9y, respectively). The high correspondence of 3′ pairing contribution for offset registers to offset guide miRNAs strongly suggests that the sequence of the 3′ end of the miRNA dictates its preferred register for pairing.

**AGO2 inhibits pairing to the end of most miRNAs but can be overcome by basepairing energetics**

Structures of human AGO2 show that the PAZ domain holds the last 3-4 3′-nucleotides of the miRNA in a conformation that might preclude pairing. Moreover, in structures that contain the a guide-target pairing that forms supplemental pairing, the 3′ end is still bound by the PAZ domain (Sheu-G). Since the contribution of 3′ pairing to overall affinity is much smaller than expected for RNA-RNA interactions, this, along with previous biochemical and aforementioned structural data suggests that the protein inhibits access to the 3′-most residues of the miRNA (Model 1 Fig S5A; Haley, Wee,Soloman). On the other hand, there is evidence for miRNA target sites that include extensive and exclusive (REF McGeary) pairing to the end of the miRNA and machinery that recognizes the 3′ of the guide to tail and trim the guide, indicating there are cases where the 3′ of the guide is free from the protein. It could be that a certain amount of pairing energy to a target may be sufficient to favor a state where the 3′ end of the miRNA is dislodged from the protein and bound to a target (Model 2 Fig S5A).

Fig 4B show that for let-7a and miR-1, the 3′ pairing contribution matrices do not have signal for registers that correspond to pairing to the end of the miRNA, while miR-155 shows a relatively stronger signal for pairing at the end of the miRNA compared to registers around guide nucleotides 11-13. To determine which guide nucleotide to which pairing iis inhibited, we compared the 3′ pairing contributions of a 7nt target to the contribution 6nt region that spans the 7nt target except for the final (5′) residue. This comparison will determine whether the addition of that extra nucleotide confers and increase in affinity. For let-7a, comparing the 3′ pairing contribution matrices to g11-g17 to g11-g16 showed an increase in contribution due to the addition of g17 (Fig S5B). A similar comparison for g18 shows a slight increase, while g19 showed no increase in affinity. miR-1 shows an increase in affinity due to the addition of g18 and g19, but not g20 (Fig S5C). These data quantitatively support the model that let-7a and miR-1 don’t use pairing past g18 and g19 respectively, which encompasses the last 3-4 nt of the guide. Similar comparisons for miR-155 show that guide nucleotides 21-23 all contribute to a 7nt site of 3′ pairing affinity (Fig S5D), strongly suggesting that miR-155 pairs through the end of the miRNA. An alternative model is that the binding signal for miR-155 at these 3′-most registers is due to previously described “3′-only” sites, whereby the 3′ end of the miRNA pairs to the target without seed-sites pairing (McGeary et al., ). While we are unable to deconvolute the enrichments due to binding through these two modes, there are variations in the binding energy across different seed-mismatches for miR-155 at these 3′-most registers, supporting the model that these energetics are, in some part, due to bipartite binding at both the seed and 3′ sites (Fig 4B).

These data suggest that the miR-155 pairing stability at these registers is sufficient to stabilize the target bound state compared to being held in the protein, unlike let-7a and miR-1. Notably, miR-155 includes four consecutive guanosine residues in its far 3′ end (g19-g22), which represents as significant amount of potential binding energy. Furthermore, miR-155 is 23 nucleotides long, which others (Sheu-G) have shown slight increases in the dissociation rate of target sequences compared to shorter guides (22 and 21 nt). These data suggest that strong “enough” pairing to the 3′ end likely can dislodge the miRNA 3′ end, and expose it. We speculate that these types of miRNAs, specifically longer miRNAs with strong pairing at their 3′end, may be more prone to target-mediated degradation (REF).

**The seed-mismatched and 3′-sequence effects act independently**

The large range of 3′ pairing stabilities observed across different seed mismatches and positions (Fig 2C) raised the question of whether these differences depended on the seed-mismatch type and position alone, or whether this variability also depended on the sequence of the 3′ region. To answer this question, we generated two chimeric miRNAs, one fusing the seed of miR-155 to the 3′ region of let-7a and the other fusing seed of let-7a to the 3′ region of miR-155 (Fig 6A), and then we performed RBNS using the respective seed-mismatched libraries. Natural and chimeric miRNAs containing the same seed sequences had remarkably similar relative affinities of mismatched seed sites (Fig S6A). Moreover, miRNAs containing the same 3′ ends had very similar preferences for 3′-pairing registers, with similar rise and fall across the registers and similar overall magnitude of *K*D fold-change (Fig 6B–D), which further supported the conclusion that the identity of the miRNA 3′ region dictates the preferred pairing register and the potential contribution of 3′ pairing. Indeed, the largest deviation in the average profile, which was the one observed at register 14 when comparing results for let-7a and the let-7a–miR-155 chimera (Fig 6B), could be explained by potential partial pairing of the let-7a seed to that 3′ site in the let-7a 3′ region, which would augment its enrichment (Fig S6B).

Importantly, when comparing miRNAs that contained the same seed sequence but different 3′ sequences, the effects of the 18 seed mismatches on the efficacy of 3′ pairing were strikingly recapitulated (Fig 6D). Thus, within each matrix of 3′-pairing fold-change values, the magnitude differences between rows were similar for let-7a and the let-7a–miR-155 chimera, and the same was true for miR-155 and the miR-155–let-7a chimera, as shown for matrices depicting results for 7-nt 3′ sites at the optimal register of each miRNA (Fig 6D). For example, the pyrimidine–pyrimidine mismatches at position 6 of let-7a inhibit 3′ pairing contributions for both let-7a and the let-7a–miR-155 chimera (cells outlined in red). Similarly, a A-G mismatch a position 4 and AA mismatch in position 3 in miR-155 confer a large decrease in 3′ pairing contribution and a U-G mismatch at position 5 has a larger increase, both of which are also seen in the miR-155-let-7a chimera (see blue outlines). Indeed, the matrix of 3′-pairing fold-change values observed for the let-7a–miR-155 chimera could be accurately predicted by multiplying the magnitudes across the rows of the let-7a matrix (which predicted the effects of the seed mismatch on 3′-pairing affinity) by the magnitudes across the columns of the miR-155 matrix (which predicted the effects of the 3′ sequence on 3′-pairing affinity), and an analogous procedure predicted the fold-change values observed for the miR-155–let-7a chimera (Fig 6E). These results showed that the influence of the seed mismatch on the magnitude of 3′-pairing affinity depended primarily on the seed-mismatch type and position, with relatively little dependence on the sequence of the 3′ region.

To quantify this result, we compared the correlation values of the 3′ pairing contributions across seed mismatches across a single maximal loop value (Fig 6E), which shows that the miRNAs harboring the same seeds sequences have similar effects of mismatches on their 3′ pairing contributions (R2 = 0.53 and 0.62) (Fig 6E). As a positive control we compared the effects of mismatches on the 3′ pairing contribution of the let-7a replicates, which had an R2 value of 0.96 respectively. To rule out the effects of seed position on the mismatch effects, the average effect across position was compared for miRNAs containing the same seed (Fig 6F; R2 = 0.54 and 0.74) versus the same 3′ regions but different seed sequences, which showed significantly lower correlations (Fig 6G; R2 = 0.02 and 0.41), except in the case of let-7a versus the let-7a/miR-155 chimera, which had an R2 of 0.68 .

**3′ pairing contributions can largely be predicted by nearest neighbor rules**

The results from the previous sections suggest that the RNA sequence of the guide in the major determinant of the preferred pairing register. We wondered if the thermodynamic preferences, such as register preferences, or even over 3′ pairing contribution, could be predicted by nearest neighbor (NN) rules for RNA duplex hybridization in solution (i.e. the RNAfold algorithm). If so, pairing to the 3′ end may be more generally predicted by NN rules than previous work had concluded (Ref Grimson). We first compared the predicted NN energetics for a sequence that corresponds to the sequence of different registers across miRNAs to the mean of each 3′ pairing matrix, as a proxy for the average increase in affinity due to that particular sequence pairing to the miRNA (Fig 7A, left). The values of the mean observed 3′ pairing energy correlated well with predicted NN affinity (R2 = 0.57-0.80 for each miRNA, slope ~0.1). We also find this relationship is not just due increasing the length of pairing, as there exists strong correlation among all 6,7, and 8mer sequences of 3′ pairing across miRNAs (Fig 7A, right).

**An linear model of 3′ site features predicts affinities and improves target site prediction**

While we are able to identify features that contribute to the affinity of 3′ paired sites, we wanted to determine the relative contributions of each feature to aid in design of future high affinity target sites and to improve prediction of potential endogenous targets. We built a linear model for the contribution of 3′ target sites parameterized by previously denoted features: register (reg), loop length (loop len), seed-mismatch type (seedMMtype), seed-mismatch position (seedMMpos), affinity of the seed (dGseed), length of the 3′-paired region (len3p), and the NN predicted affinity for the sequence of the 3′ paired region (dG\_3pred). After normalization of the continuous variables to range between 0 and 1 (as in Agarwal et al, ), the model was trained on 70% of all the affinity data for each natural miRNA (let-7a, miR-1, and miR-155) and then predicted the affinity for the 30% of the data that was left out of the training.

A linear model including just the NN predicted affinity can predict 47% of the variation in the affinity data (R2 = 0.47, Fig 7B). A linear model including all previously denoted features above (Fig 1B) resulted in an increase in predictive power of the combined affinity data (R2 = 0.55 +/-, Fig 7C). Moreover, the affinity data was reparameterized to include two additional features that we postulated might be important to target pairing: 1) the offset of target site, defined as the difference in the size of the internal loop in the miRNA versus target between seed and 3′ paired sites 2) the center of target pairing with respect to the guide (Fig 7D). These two additional features lead to a modest increase in prediction power of the linear model (R2 = 0.61; Fig S7A) .

We found that this model trained on each miRNA separately did better than all the miRNAs combined (Fig. S8B-D, R2 = 0.50-0.79). There were notable similarities in parameter coefficients between each miRNA, such as the loop length dependencies. Moreover, data trained on let-7a and miR-155 and can predict the both chimeric miRNA affinities with an R2 of 0.55, suggesting that training on miR-155 and let-7a together has enough information to predict a chimera of the two miRNAs, and that there is not new behavior along these parameters that arises from a chimeric sequence (Fig S7D).

We observe differences between miRNAs, such as in the register coefficients; these differences were exemplified by the observation that training on two miRNAs was unable to predict another as well as itself (Fig S7E-G, R2 = 0.35-0.44). A correlation of each parameter’s coefficients of the natural miRNAs to the that of the chimeric miRNAs resolves two classes of parameters (Fig 7F)--ones that relate to the seed region (seed mismatch position and type) and ones that report on the miRNA 3′ region (register, and register center). For example, there is a high correlation of the let-7a-miR-155 chimera seed mismatch position and seed mismatch type coefficients with let-7a, let-7a +1, and let-7a -1’s, while a low correlation with their register coefficients. On the other hand, let-7a-miR-155 and miR-155 have a highly correlated register coefficients. Furthermore, there are features that seem similar across miRNAs regardless of sequence composition, such as offset, length, and loop length, as seen as high correlations across all miRNAs.

Since there exists miRNA-specific differences, we included interaction terms between the miRNA and various other parameters to determine whether they increased the prediction power of the linear model, and found that an interaction between miRNA and register had the largest increase in prediction power for left-out data (R2=0.61; Fig 7D). The observation that there are miRNA-specific differences in model for predicting the effects of 3′-pairing is not surprising, given that models for seed-pairing required miRNA-specific terms as well. While this makes a general model for 3′-pairing for the effects on *in vivo* repression more distant, we find that this model does significantly better than the current 3′ pairing score (Fig 7E) in predicting affinity, and as shown below, for repression of 3′ paired sites for the miRNAs assayed herein.

**Displaced scraps worth considering:**

, and it seems that certain seed-mismatch positions have higher 3′ pairing contributions; however, with data for only a single miRNA that cannot span all possible seed mismatch locations and types it is difficult to draw generalizable conclusions.

In the simplest model, AGO2 is interpreting different seed-mismatches through interactions with the major and minor groove of the seed-target duplex (REF), and these interactions could change the likelihood of undergoing a conformational change to promote formation of the 3′ paired sequences. Alternatively, the sequence of the 3′ end of the miRNA could affect the conformation of AGO, such that it is more or less likely poised to allow formation of 3′ pairing interactions--i.e. some synergistic interaction between the seed and 3′ pairing regions of the guide RNA.