A

Mono-adenylated miRNAs

Percentage of nucleotides (y-axis: 0–60)

Legend: ☐A ☐U ■G ▨C

x-axis: nt -3, nt -2, nt -1, last 3' nt

Unmodified miRNAs

Percentage of nucleotides (y-axis: 0–60)

Legend: ☐A ☐U ■G ▨C
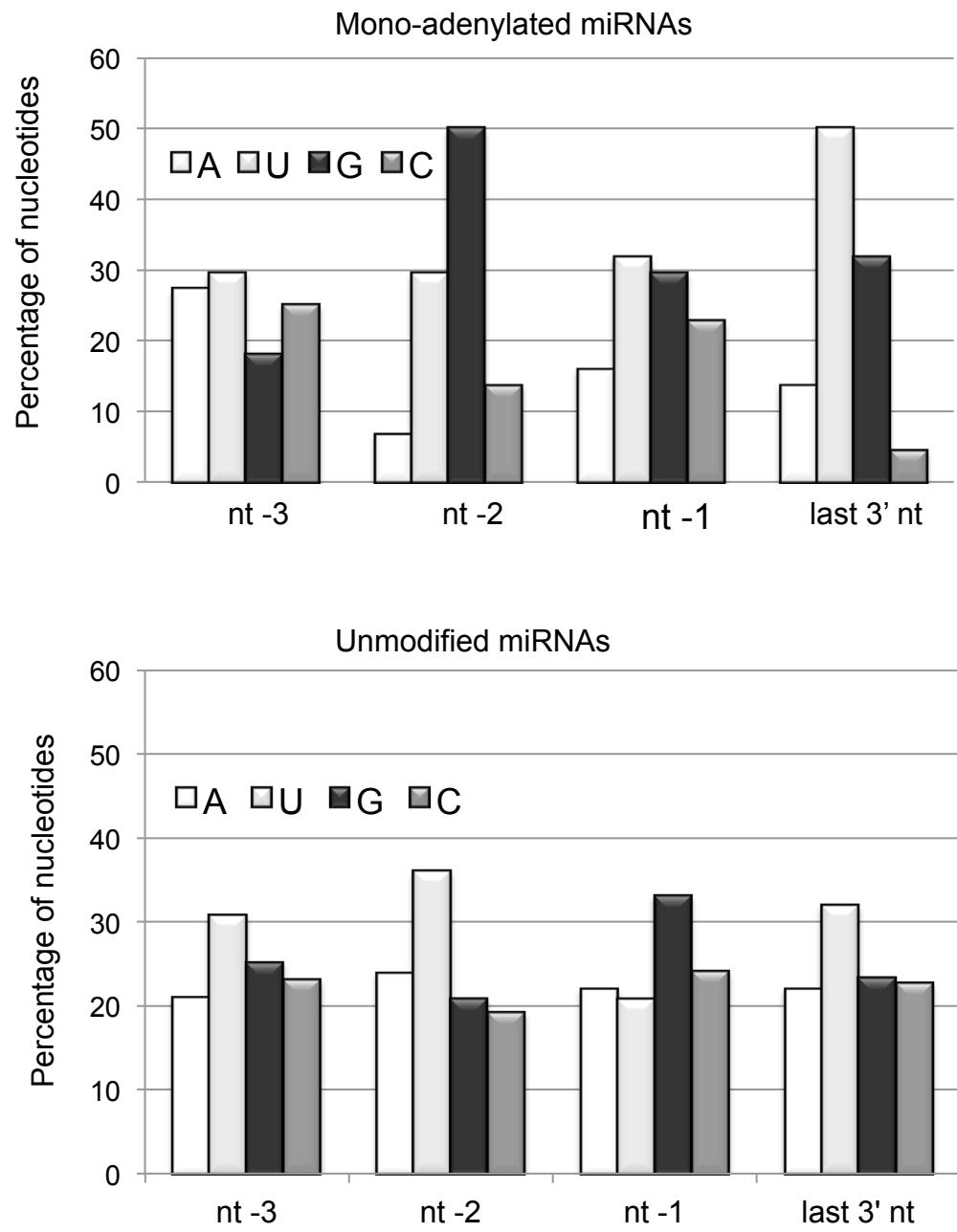
x-axis: nt -3, nt -2, nt -1, last 3' nt

B

Alignment of mono-adenylated miRNAs

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Reference sequence (1): let-7i-5p
Identities normalised by aligned length.
Colored by: consensus/70% and group property

                           1 [      .       . ] 24
 1  let-7i-5p      100.0%   -UGAGGUAGUAGUUUGU-GCUGUU
 2  let-7g-5p       90.9%   -UGAGGUAGUAGUUUGU-ACAGUU
 3  miR-99b-5p      13.6%   -CACCCGUAGAACCGAC-CUUGCG
 4  miR-127-3p      30.4%   UCGGAUCCGUC-UGAGC-UUGGCU
 5  miR-128-3p      26.1%   UCA-CAGUGAA-CCGGU-CUCUUU
 6  miR-137-3p      30.4%   UUAUUGCUUAAGGAAUAC-GCGUAG
 7  miR-138-2-3p    13.6%   -GCUAUUUCAC-GACAC-CAGGGU
 8  miR-142a-3p     30.4%   UGUAGUGUUUCCUACUU-UAUGGA
 9  miR-154-5p      21.7%   UAGGUUAUCCG-UGUUG-CCUUGA
10  miR-129-5p      34.8%   CUU-UUUGCGG-UCUGG-GCUUGC
11  miR-185-5p      36.4%   -UGGAGAGAAAGGCAGU-UCCUGA
12  miR-24-3p       27.3%   -UGGCUCAGUUCAGCAG-GAACAG
13  miR-190a-5p     26.1%   UGA-UAUGUUUGAUAUA-UUAGGU
14  miR-30d-5p       8.7%   UGUAAACAUCC-CCGAC-UGGAAG
15  let-7a-5p       81.8%   -UGAGGUAGUAGGUUGU-AUAGUU
16  let-7b-5p       86.4%   -UGAGGUAGUAGGUUGU-GUGGUU
17  let-7c-5p       81.8%   -UGAGGUAGUAGGUUGU-AUGGUU
18  let-7e-5p       77.3%   -UGAGGUAGGAGGUUGU-AUAGUU
19  let-7f-5p       81.8%   -UGAGGUAGUAGAUUGU-AUAGUU
20  miR-15a-5p      26.1%   UA-GCAGCACAUAAUGG-UUUGUG
21  miR-16-5p        4.3%   UA-GCAGCACGUAAAUA-UUGGCG
22  miR-22-5p       27.3%   -AGUUCUUCAGUGGCAA-GCUUUA
23  miR-26a-5p      39.1%   UUCAAGUAAUC-CAGGA-UAGGCU
24  miR-26b-5p      39.1%   UUCAAGUAAUU-CAGGA-U-AGGU
25  miR-98-5p       81.8%   -UGAGGUAGUAAGUUGU-AUUGUU
26  miR-326-3p      26.1%   CCUCUGG-GCC-CUUCC-UCCAGU
27  miR-328-3p      21.7%   CUGGCCCUCUC-UGCCC-UUCCGU
28  miR-139-5p      26.1%   UCUACAGUGCA-CGUGU-CUCCAG
29  miR-218-5p      31.8%   -UUGUGCU-UGAUCUAA-CCAUGU
30  miR-138-1-3p    18.2%   -CGGCUACUUCACAACA-CCAGGG
31  miR-219a-2-3p   17.4%   AGAAUUGUGG-CUGGAC-AUCUGU
32  miR-376a-3p     38.1%   --AUCGUAGAGGAAAAU-CCACGU
33  miR-382-5p      50.0%   --GAAGUUGUUCGUGGUGGAUUCG
34  miR-384-3p      21.7%   AUUCCUAGAA-AUUGUU-CACAAU
35  miR-487b-3p     40.9%   -AAUCGUACAGGGUCAU-CCACUU
36  miR-1249-3p     21.7%   ACGCCCUUCCC-CCCU-UCUUCA
37  miR-667-3p       8.7%   UGACACCUGCCACCCAG-CCAAG
38  miR-3099-3p     36.4%   -UAGGCUAGAGAGAGGU-UGGGGA
39  miR-497a-5p     30.4%   CA-GCAGCACACUGUGG-UUUGUA
40  miR-676-3p      36.4%   -CCGUCCUGA-GGUUGU-UGAGCU
41  miR-92b-3p      30.4%   UA-UUGCACUCGUCCCG-GCCUCC
42  miR-1839-5p     27.3%   -AAGGUAGAUAGAACAG-GUCUUG
43  miR-486b-5p     26.1%   UCCUGUACUGA-GCUGC-CCGAG
    consensus/100%          ........................
    consensus/90%           ........................
    consensus/80%           ........................
    consensus/70%           ..............r. .y....
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Supplementary Fig.3