Table S7.
The top 10 most enriched GO terms of biological processes, molecular functions and cellular components in predicted targets of 5 abundant novel miRNAs.

| Description of GO term                                                                 | Human testis | Genome | E-ratio | p-value |
|---------------------------------------------------------------------------------------------------------------------------------------------|--------------|--------|---------|---------|
| **The top 10 most enriched biological processes**                                                                                                                                                     |              |        |         |         |
| Proximal/distal pattern formation (GO:0009954)                                                                                                                                                    | 6            | 23     | 5.82    | 4.32E-04 |
| B cell activation (GO:0042113)                                                                                                                                                                        | 6            | 29     | 4.62    | 1.61E-03 |
| Vasculature development (GO:0001944)                                                                                                                                                                   | 6            | 30     | 4.46    | 1.94E-03 |
| Activation of pro-apoptotic gene products (GO:0008633)                                                                                                                                             | 6            | 31     | 4.32    | 2.31E-03 |
| Induction of apoptosis by intracellular signals (GO:0008629)                                                                                                                                           | 7            | 44     | 3.55    | 3.31E-03 |
| Neuromuscular process controlling balance (GO:00050885)                                                                                                                                              | 6            | 40     | 3.35    | 8.53E-03 |
| Odontogenesis of dentine-containing tooth (GO:0042475)                                                                                                                                             | 8            | 55     | 3.25    | 3.10E-03 |
| T cell activation (GO:0042110)                                                                                                                                                                        | 6            | 44     | 3.04    | 1.35E-02 |
| Embryonic digit morphogenesis (GO:0042733)                                                                                                                                                              | 6            | 44     | 3.04    | 1.35E-02 |
| JNK cascade (GO:0007254)                                                                                                                                                                             | 7            | 56     | 2.79    | 1.25E-02 |
| **The top 10 most enriched cellular components**                                                                                                                                                      |              |        |         |         |
| Synaptobrevin 2-SNAP-25-syntaxin-1a-complexin I complex (GO:0070032)                                                                                                                               | 2            | 3      | 14.98   | 5.79E-03 |
| Mre11 complex (GO:0030870)                                                                                                                                                                            | 2            | 5      | 8.99    | 1.82E-02 |
| Pre-autophagosomal structure (GO:0000407)                                                                                                                                                               | 2            | 6      | 7.49    | 2.65E-02 |
| U7 snRNP (GO:0005683)                                                                                                                                                                                 | 2            | 7      | 6.42    | 3.60E-02 |
| Platelet dense tubular network membrane (GO:0031095)                                                                                                                                                  | 2            | 7      | 6.42    | 3.60E-02 |
| PTW/PP1 phosphatase complex (GO:0072357)                                                                                                                                                                | 2            | 7      | 6.42    | 3.60E-02 |
| Melanosome membrane (GO:0033162)                                                                                                                                                                       | 2            | 8      | 5.62    | 4.65E-02 |
| Nuclear chromatin (GO:0000790)                                                                                                                                                                         | 11           | 64     | 3.86    | 1.20E-04 |
| Chromatin (GO:0000785)                                                                                                                                                                                | 12           | 78     | 3.46    | 1.80E-04 |
| Nuclear body (GO:0016604)                                                                                                                                                                             | 4            | 28     | 3.21    | 3.45E-02 |
| **The top 10 most enriched molecular functions**                                                                                                                                                      |              |        |         |         |
| Nucleoside kinase activity (GO:0019206)                                                                                                                                                                 | 3            | 6      | 11.18   | 1.63E-03 |
| 3'-phosphoadenosine 5'-phosphosulfate binding (GO:0050656)                                                                                                                                           | 3            | 6      | 11.18   | 1.63E-03 |
| SNARE binding (GO:000149)                                                                                                                                                                             | 4            | 18     | 4.97    | 7.48E-03 |
| Galactosyltransferase activity (GO:0008378)                                                                                                                                                              | 5            | 25     | 4.47    | 4.56E-03 |
| Peptide antigen binding (GO:0042605)                                                                                                                                                                   | 3            | 15     | 4.47    | 2.74E-02 |
| Syntaxin binding (GO:0019905)                                                                                                                                                                          | 4            | 21     | 4.26    | 1.31E-02 |
| Oxygen binding (GO:0019825)                                                                                                                                                                            | 6            | 33     | 4.06    | 3.19E-03 |
| Epidermal growth factor receptor binding (GO:0005154)                                                                                                                                                 | 3            | 18     | 3.73    | 4.44E-02 |
| Extracellular matrix binding (GO:0050840)                                                                                                                                                               | 3            | 18     | 3.73    | 4.44E-02 |
| Beta-amyloid binding (GO:0001540)                                                                                                                                                                       | 4            | 26     | 3.44    | 2.75E-02 |