

**Table S4. lists the predicted targets among a large number of target genes according to miRTar**

| p-value   | Fold-change | UniqueID      | Target genes   |
|-----------|-------------|---------------|--|
| 0.0497246 | 2.59        | hsa-miR-411   |  |
| 0.0104239 | 2.17        | hsa-miR-663   | CALB2 CTF KIAA0140 ARID3B LYPLA2 IQSEC2 HRG22 KIAA1196 SAT2                          |
| 0.0061796 | 2.1         | hsa-miR-622   | ACVR2B OAS2 NUDT5  |
| 0.0100798 | 1.83        | hsa-miR-647   | FLOT2 CTF D8 KIAA0140 ARID3B IQSEC2 KIAA1196   |
| 0.0261367 | 1.81        | hsa-miR-376a* | ACVR2B   |
| 0.0145554 | 1.77        | HS_188        |  |
| 0.0478704 | 1.45        | HS_254        |  |
| 0.0462693 | 0.69        | hsa-miR-589   | OAS2 DLL1 VEZATIN LIN28B   |
| 0.0297875 | 0.66        | hsa-miR-517*  |  |
| 0.0198896 | 0.63        | hsa-miR-107   | ACVR2B OAS2 KIAA0140 LYPLA2 DLL1 VEZATIN KIAA1196                                    |
| 0.0122158 | 0.57        | HS_279_a      |  |
| 0.0359646 | 0.57        | HS_160        |  |
| 0.0373665 | 0.57        | hsa-miR-195   | ACVR2B PAPSS2 KIAA0140 LYPLA2 HRG22 VEZATIN KIAA1196                                 |
| 0.0101263 | 0.56        | hsa-miR-187   | ACVR2B PAPSS2 IQSEC2   |
| 0.0432036 | 0.49        | HS_303_b      |  |
| 0.0319011 | 0.31        | hsa-miR-363   |  |
| 0.0108576 | 0.27        | hsa-miR-497   | ACVR2B FLOT2 PAPSS2 KIAA0140 ARID3B LYPLA2 IQSEC2 HRG22 DLL1 VEZATIN KIAA1196 LIN28B |