**Supplementary Table 1. miRNAs significantly correlated with FST Escape Time in Males**

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| **Supplementary Table 1.**  miRNAs significantly correlated with FST Escape Time in Males | | |
| **miRNA** | **Significance** | **R** |
| Amyg-let-7e-3p | 0.044 | -.823\* |
| Amyg-miR-1298 | 0.043 | .826\* |
| Amyg-miR-148b-5p | 0.035 | -.844\* |
| Amyg-miR-184 | 0.020 | .882\* |
| Amyg-miR-191a-5p | 0.013 | -.905\* |
| Amyg-miR-204-5p | 0.011 | .913\* |
| Amyg-miR-25-5p | 0.006 | -.937\*\* |
| Amyg-miR-26b-3p | 0.047 | -.818\* |
| Amyg-miR-28-5p | 0.013 | -.904\* |
| Amyg-miR-411-3p | 0.042 | -.829\* |
| Amyg-miR-490-3p | 0.016 | -.894\* |
| Amyg-miR-495 | 0.035 | .843\* |
| Amyg-miR-532-5p | 0.027 | .862\* |
| Amyg-miR-6315 | 0.023 | -.874\* |
| Amyg-miR-879-3p | 0.004 | -.948\*\* |
| Hipp-miR-216b-5p | 0.016 | -.895\* |
| Hipp-miR-224-5p | 0.007 | -.930\*\* |
| Hipp-miR-26a-5p | 0.036 | .841\* |
| Hipp-miR-3084a-1-5p | 0.014 | .900\* |
| Hipp-miR-653-5p | 0.031 | -.852\* |
| PFC-miR-106b-5p | 0.006 | .938\*\* |
| PFC-miR-124-3p | 0.015 | .899\* |
| PFC-miR-125b-2-3p | 0.001 | -.975\*\* |
| PFC-miR-126a-5p | 0.024 | .872\* |
| PFC-miR-1306-5p | 0.012 | .910\* |
| PFC-miR-130a-3p | 0.038 | .836\* |
| PFC-miR-135a-5p | 0.002 | .961\*\* |
| PFC-miR-135b-5p | 0.018 | .888\* |
| PFC-miR-139-3p | 0.006 | -.934\*\* |
| PFC-miR-143-5p | 0.025 | .869\* |
| PFC-miR-148a-3p | 0.046 | -.820\* |
| PFC-miR-148b-3p | 0.014 | -.902\* |
| PFC-miR-150-3p | 0.002 | -.967\*\* |
| PFC-miR-151-3p | 0.009 | -.922\*\* |
| PFC-miR-154-3p | 0.047 | .818\* |
| PFC-miR-15a-5p | 0.044 | .823\* |
| PFC-miR-16-5p | 0.002 | .963\*\* |
| PFC-miR-17-5p | 0.010 | .916\* |
| PFC-miR-181c-5p | 0.008 | .924\*\* |
| PFC-miR-186-5p | 0.010 | .919\*\* |
| PFC-miR-187-3p | 0.016 | .895\* |
| PFC-miR-190a-5p | 0.023 | .874\* |
| PFC-miR-195-5p | 0.020 | .883\* |
| PFC-miR-19b-3p | 0.026 | .865\* |
| PFC-miR-212-5p | 0.010 | -.918\*\* |
| PFC-miR-221-5p | 0.027 | -.861\* |
| PFC-miR-222-3p | 0.003 | -.954\*\* |
| PFC-miR-28-5p | 0.000 | .982\*\* |
| PFC-miR-29a-3p | 0.010 | .916\* |
| PFC-miR-29b-5p | 0.040 | .832\* |
| PFC-miR-3068-5p | 0.031 | .853\* |
| PFC-miR-30a-3p | 0.009 | -.923\*\* |
| PFC-miR-30b-3p | 0.036 | -.842\* |
| PFC-miR-30e-3p | 0.030 | -.855\* |
| PFC-miR-3102 | 0.014 | .903\* |
| PFC-miR-335 | 0.001 | .975\*\* |
| PFC-miR-337-5p | 0.011 | -.912\* |
| PFC-miR-344b-5p | 0.024 | -.870\* |
| PFC-miR-345-3p | 0.011 | .912\* |
| PFC-miR-369-5p | 0.011 | -.914\* |
| PFC-miR-370-3p | 0.002 | -.961\*\* |
| PFC-miR-370-5p | 0.013 | -.906\* |
| PFC-miR-376b-3p | 0.033 | .849\* |
| PFC-miR-379-3p | 0.049 | -.813\* |
| PFC-miR-382-5p | 0.006 | -.934\*\* |
| PFC-miR-384-3p | 0.012 | .909\* |
| PFC-miR-384-5p | 0.007 | .929\*\* |
| PFC-miR-409a-3p | 0.012 | -.910\* |
| PFC-miR-409a-5p | 0.040 | -.831\* |
| PFC-miR-411-3p | 0.008 | -.925\*\* |
| PFC-miR-412-5p | 0.003 | -.955\*\* |
| PFC-miR-433-3p | 0.024 | -.870\* |
| PFC-miR-449a-5p | 0.001 | .976\*\* |
| PFC-miR-485-3p | 0.017 | -.892\* |
| PFC-miR-493-5p | 0.040 | -.832\* |
| PFC-miR-497-5p | 0.005 | .941\*\* |
| PFC-miR-541-5p | 0.005 | -.941\*\* |
| PFC-miR-598-3p | 0.003 | -.958\*\* |
| PFC-miR-6319 | 0.046 | -.820\* |
| PFC-miR-6331 | 0.018 | -.890\* |
| PFC-miR-671 | 0.016 | -.896\* |
| PFC-miR-674-3p | 0.007 | -.930\*\* |
| PFC-miR-708-5p | 0.036 | .841\* |
| PFC-miR-760-3p | 0.010 | -.915\* |
| PFC-miR-770-3p | 0.017 | -.892\* |
| PFC-miR-7a-1-3p | 0.031 | .852\* |
| PFC-miR-93-3p | 0.011 | .912\* |
| PFC-miR-93-5p | 0.033 | .848\* |

Expression of 88 miRNAs was correlated (fdr<0.05) with forced swim test escape time in male animals; n=6. abbreviations: PFC-prefrontal cortex.

**Supplementary Table *2*. Validated gene targets of significant MS**

**miRNAs**



Using miRWalk 2.0, we found 13 validated targets of miRNAs which

were significantly altered in MS animals.

**Supplementary Table 3. Top 20 miRWalk predicted MS miRNA gene targets**



miRWalk 2.0 was used to predict targets for miRNAs significantly affected by MS. 1,848 miRNAs were predicted targets based on agreement between at least 6 prediction software in miRWalk. The top 20 significantly predicted (fdr<0.05) targets with the most targeting miRNAs are listed.

**Supplementary Table *4*. Validated gene targets of significant**

**sex-mediated MS miRNAs**



miRWalk identified 31 validated gene targets of miRNAs which

were significantly altered by MS and Sex.

**Supplementary Table 5.** **Top 20 miRWalk predicted MS x sex miRNA gene targets.**



1,988 gene targets of miRNAs significantly affected by the interaction between MS

and sex were predicted by at least 6 software within miRWalk 2.0. The top 20

significantly predicted (fdr<0.05) targets with the most targeting miRNAs are listed.