

## ABBREVIATIONS

*ACVR1C*: activin A receptor, type IC; *ADCY1*: adenylylate cyclase 1; *ADCY2*: adenylylate cyclase 2; *ADRA1B*: adrenergic, alpha-1B-, receptor; *AKT3*: v-akt murine thymoma viral oncogene homolog 3; *BMP6*: bone morphogenetic protein 6; *BMP2*: bone morphogenetic protein receptor, type II; *CACNB2*: calcium channel, voltage-dependent, beta 2 subunit; *CALM1*: calmodulin 1; *CBL*: Cbl proto-oncogene, E3 ubiquitin protein ligase; *CD86*: CD86 molecule; *CDKN1B*: cyclin-dependent kinase inhibitor 1B; *DGKB*: diacylglycerol kinase, beta 90kDa; *DUSP8*: dual specificity phosphatase 8; *E2F5*: E2F transcription factor 5, p130-binding; *EIF4E*: eukaryotic translation initiation factor 4E family member 2; *EIF4E2*: eukaryotic translation initiation factor 4E family member 2; *ERBB2IP*: erbb2 interacting protein; *F2R*: coagulation factor II (thrombin) receptor; *FBXW11*: F-box and WD repeat domain containing 11; *FZD3*: frizzled family receptor 3; *FZD6*: frizzled family receptor 6; *GAB1*: GRB2-associated binding protein 1; *IFNAR1*: interferon (alpha, beta and omega) receptor 1; *IL13RA1*: interleukin 13 receptor, alpha 1; *IL15RA*: interleukin 15 receptor, alpha; *IL9R*: interleukin 9 receptor; *ITGA4*: integrin, alpha 4; *KAT2B*: K(lysine) acetyltransferase 2B; *MAML1*: mastermind-like 1; *MAP3K14*: mitogen-activated protein kinase kinase kinase 14; *MAP3K2*: mitogen-activated protein kinase kinase kinase 2; *MAP3K3*: mitogen-activated protein kinase kinase kinase 3; *MAP3K5*: mitogen-activated protein kinase kinase kinase 5; *MAP4K3*: mitogen-activated protein kinase kinase kinase kinase 3; *MAP4K4*: mitogen-activated protein kinase kinase kinase kinase 4; *MEF2C*: myocyte enhancer factor 2C; *MKNK2*: MAP kinase interacting serine/threonine kinase 2; *MTMR2*: myotubularin related protein 2; *NBL1*: neuroblastoma, suppression of tumorigenicity 1; *NFATC2*: nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2; *NGF*: nerve growth factor; *NKDI*: naked cuticle homolog 1; *NRAS*: neuroblastoma RAS viral (v-ras) oncogene homolog; *P2RX5*: purinergic receptor P2X, ligand-gated ion channel, 5; *PIAS4*: protein inhibitor of activated STAT, 4; *PIKFYVE*: phosphoinositide kinase, FYVE finger containing; *PIP4K2A*: phosphatidylinositol-5-phosphate 4-kinase, type II, alpha; *POLR3G*: polymerase (RNA) III (DNA directed) polypeptide G; *PIP5K2*: diphosphoinositol pentakisphosphate kinase 2; *PPP3R1*: protein phosphatase 3, regulatory subunit B, alpha; *PRKAA2*: protein kinase, AMP-activated, alpha 2 catalytic subunit; *PTEN*: phosphatase and tensin homolog; *RAPGEF2*: Rap guanine nucleotide exchange factor (GEF) 2; *RASA1*: RAS p21 protein activator 1; *RASA2*: RAS p21 protein activator 2; *RASGRF2*: Ras protein-specific guanine nucleotide-releasing

factor 2; *RICTOR*: RPTOR independent companion of MTOR, complex 2; *RPS6KA2*: ribosomal protein S6 kinase, 90kDa, polypeptide 2; *RPS6KA5*: ribosomal protein S6 kinase, 90kDa, polypeptide 5; *RYR2*: ryanodine receptor 2; *SFRP4*: secreted frizzled-related protein 4; *SHC4*: SHC (Src homology 2 domain containing) family, member 4; *SIKE1*: suppressor of IKBKE 1; *SMURF2*: SMAD specific E3 ubiquitin protein ligase 2; *SOCS6*: suppressor of cytokine signaling 6; *SOS1*: son of sevenless homolog 1; *STAM*: signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; *SYNJI*: synaptojanin 1; *TBLIX*: transducin (beta)-like 1X-linked; *TGFBRI*: transforming growth factor, beta receptor I; *TOLLIP*: toll interacting protein; *TRADD*: TNFRSF1A-associated via death domain; *ULK1*: unc-51-like kinase 1; *ULK2*: unc-51-like kinase 2; *VANGL1*: vang-like 1; *ZAK*: sterile alpha motif and leucine zipper containing kinase AZK; *ZFYVE9*: zinc finger, FYVE domain containing 9.

**Table S1.** miRNAs that are differentially expressed in the intestinal mucosal layer of the NE-induced Fayoumi chicken line M5.1

| miRNA  | Sequence                   | Fold change | Target genes | Top ranked target gene |
|--|----------------------------|-------------|--------------|------------------------|
| miRNAs upregulated in the NE line M5.1 compared to control |                            |             |              |                        |
| gga-miR-9-5p   | UCUUUGGUUAUCUAGCUGUAUGA    | 37.6000     | 260          | MAP3K3                 |
| gga-miR-133c-3p  | UUGGUCCCCUUCAACCAGCUGC     | 37.0150     | 131          | PRRX1                  |
| gga-let-7a-2-3p  | CUGUACAACCUCCUAGCUUUC      | 34.4301     | 558          | COQ10B                 |
| gga-let-7j-3p  | CUAUACAGUCUAUUGCCUUCU      | 34.4301     | 366          | GABRA1                 |
| gga-miR-146a-3p  | ACCCAUGGGGCUCAGUUCUUCAG    | 34.4301     | 120          | ARHGAP27               |
| gga-miR-1576   | CUCGGGCGGGCGGAGCGGCAC      | 34.4301     | 127          | GIPC3                  |
| gga-miR-1585   | AGUGCCCAGGUGUGGUUAAUCCUG   | 34.4301     | 140          | CLOCK                  |
| gga-miR-1681   | UUCACAUGAUGUCUUGCUGAUG     | 34.4301     | 185          | DENND5A                |
| gga-miR-1703-5p  | AGAGGCUGUAGGUCCCGUGCUIU    | 34.4301     | 277          | RAB8A                  |
| gga-miR-1715-5p  | AGGAUCAGUAGAAGUCAGCUGUGC   | 34.4301     | 97           | NUP153                 |
| gga-miR-1729-5p  | AUCCCUUACUCACAUGAGUAGUC    | 34.4301     | 129          | PHF3                   |
| gga-miR-1735   | AGGGGCUUUGGGCAGCAUCUG      | 34.4301     | 95           | MARVELD3               |
| gga-miR-1742   | AAUCGUCGUUCGGGAUCCGC       | 34.4301     | 1            | LOC100859371           |
| gga-miR-18b-3p   | UACUGCCCUAAAUGCUCCUUCUGGC  | 34.4301     | 132          | ULK2                   |
| gga-miR-18b-5p   | UAAGGUGCAUCUAGUGCAGUUA     | 34.4301     | 188          | ERI1                   |
| gga-miR-19a-5p   | AGUUUUGCAUAGUUGCACUAC      | 34.4301     | 213          | CREB1                  |
| gga-miR-205b   | CCCUUCAUUCACCGGAAUCUG      | 34.4301     | 182          | RAB9B                  |
| gga-miR-2130   | UCCAGUGGAGCUCUGCAAGGAC     | 34.4301     | 205          | KIAA0182               |
| gga-miR-2131-3p  | CUGUUACUGUUCUUCUGAUGG      | 34.4301     | 110          | AUTS2                  |
| gga-miR-301a-3p  | CAGUGCAAUAAUUGUCAAAAGCAU   | 34.4301     | 501          | ST18                   |
| gga-miR-31-5p  | AGGCAAGAUGUUGGCAUAGCUG     | 34.4301     | 222          | HOMER1                 |
| gga-miR-3535   | GGAUUAUGAUGACUGAUUAUCUGAAA | 34.4301     | 105          | ZNF652                 |
| gga-miR-3537   | GUGAGUGCUGUAGGAUGGGGCUC    | 34.4301     | 104          | TAF5                   |
| gga-miR-383-5p   | AGAUCAGAAGGUGAUUGUGGCU     | 34.4301     | 153          | STRN3                  |
| gga-miR-460a-5p  | CCUGCAUUGUACACACUGUGUG     | 34.4301     | 307          | FBN2                   |
| gga-miR-490-3p   | CAACCUGGAGGACUCCAUGCUG     | 34.4301     | 128          | MBLAC2                 |
| gga-miR-6546-3p  | GGAGUUCAGCUGUGCUGCUGC      | 34.4301     | 131          | WDR26                  |
| gga-miR-6596-3p  | CGGAGCUCGGACGGCGUCCCGA     | 34.4301     | 132          | IFFO2                  |
| gga-miR-6609-3p  | ACAGCCCCUGUGCUCUGACCGCA    | 34.4301     | 471          | CYP26B1                |
| gga-miR-7452-5p  | ACAGGGCUGGCUGAUCCGUGC      | 34.4301     | 251          | TNFAIP8L1              |
| gga-miR-99a-3p   | CAAGCUCGCUUCUAUGGGUCU      | 34.4301     | 9            | UTRN                   |
| gga-miR-1720-3p  | AAGCAACGAGAGGUCGGUCUGA     | 3.7442      | 25           | EPB41L5                |
| gga-miR-133a-3p  | UUGGUCCCCUUCAACCAGCUGU     | 3.4812      | 131          | PRRX1                  |
| gga-miR-92-5p  | AGGUUGGGAUCAGUUGCAAUGCU    | 3.4812      | 106          | LOC100858227           |
| gga-miR-204  | UUCCCUUUGUCAUCCUAUGCCU     | 3.1592      | 350          | MGAT3                  |

|  |                            |          |     |              |
|--|----------------------------|----------|-----|--------------|
| gga-miR-211  | UUCCCUUUGUCAUCCUAUGCCU     | 3.1592   | 350 | MGAT3        |
| gga-miR-1416-5p  | UCCUUAACUCAUGCCGCUGUG      | 3.1592   | 62  | PHIP         |
| gga-miR-125b-3p  | ACAAGUCAGGCUCUUGGGACCU     | 2.8962   | 178 | TNKS2        |
| gga-miR-10b-5p   | UACCCUGUAGAACCGAAUUUGU     | 2.8904   | 117 | DAZAP1       |
| gga-miR-222b-5p  | UGCUCAGUAGUCAGUGUAGGAUCUGU | 2.7442   | 203 | MFSD9        |
| gga-miR-6542-3p  | ACGGGACAGUGCUGAAGACUA      | 2.7442   | 22  | ARID1A       |
| gga-miR-155  | UUA AUGCUAAUCGUGAUAGGGG    | 2.3292   | 192 | ZNF652       |
| gga-miR-200b-5p  | UCUUACUGGGCAGCAUUGGA       | 2.2848   | 108 | CDH9         |
| gga-miR-130b-5p  | CCUCUUUCCUGUUGCACUACU      | 2.1592   | 219 | FBXO11       |
| gga-miR-99a-5p   | AACCCGUAGAUCCGAUCUUGUG     | 2.1592   | 18  | KBTBD8       |
| gga-miR-1674   | GGGCUAUGAUGCUGGAUUUCUGAG   | 2.1592   | 54  | LOC100859627 |
| gga-miR-3607-3p  | CUGUAAACGCUUUCUGAUGUGCC    | 2.1592   | 524 | TNRC6A       |
| gga-miR-6648-3p  | UCCGGCAUUCUGAACGCUCUCCU    | 2.1592   | 13  | IGF2BP2      |
| gga-miR-222a   | AGCUACAUCUGGCUCUGGGUCUC    | 2.0682   | 190 | TCF12        |
| gga-miR-146a-5p  | UGAGAACUGAAUCCAUGGGUU      | 2.0117   | 128 | RFXDC2       |
| <hr/>  |                            |          |     |              |
| miRNAs downregulated in the NE line M5.1 compared to control |                            |          |     |              |
| gga-miR-20b-5p   | CAAAGUGCUCUAGUAGCAGGUAG    | -35.2708 | 581 | MAP3K2       |
| gga-miR-126-3p   | UCGUACCGUGAGUAAUAAUGCGC    | -35.2708 | 6   | LRRN4        |
| gga-miR-1306-3p  | UGGACGUUGGCUCUGGUGGUGAU    | -34.2708 | 24  | BAI1         |
| gga-miR-142-3p   | UGUAGUGUUCCUACUUUAUGG      | -34.2708 | 129 | HECTD1       |
| gga-miR-1451-5p  | UCGCACAGGAGCAAGUUACCGC     | -34.2708 | 33  | LOC408180    |
| gga-miR-146b-3p  | CCCUAUGGAUUCAGUUCUGC       | -34.2708 | 78  | NAA15        |
| gga-miR-1556   | UGCAGGCUGGAAGUAGGAGUGU     | -34.2708 | 187 | PLEKHM3      |
| gga-miR-1560-3p  | GCAUCUCUGGACGCGCUCGUUC     | -34.2708 | 189 | FAM126B      |
| gga-miR-183  | UAUGGCACUGGUAGAAUUCACUG    | -34.2708 | 250 | PTPN4        |
| gga-miR-1306-5p  | ACCACCUCUCCUGCAAACGUCCAGU  | -33.2708 | 185 | NAA50        |
| gga-miR-1329-5p  | UACAGUGAUCACGUUACGAUGG     | -33.2708 | 462 | SHROOM2      |
| gga-miR-138-5p   | AGCUGGUGUUGUGAAUC          | -33.2708 | 721 | KCTD10       |
| gga-miR-1465   | UUUCAGAGGUGCUGGGUGCUU      | -33.2708 | 384 | GABPB1       |
| gga-miR-1584   | CCGGGUGGGGCUGGGCUGGG       | -33.2708 | 18  | LOC101748021 |
| gga-miR-1666   | UAACGCCACGGGGCUGAGGCUG     | -33.2708 | 24  | CBFB         |
| gga-miR-16c-5p   | UAGCAGCACGUAAAUCUGGAG      | -33.2708 | 982 | MOB4         |
| gga-miR-1769-5p  | CUUCAGGCUUUCUCACACCUUG     | -33.2708 | 244 | PTPRB        |
| gga-miR-1782   | ACAUUCAUUGGAGCAGGGACA      | -33.2708 | 266 | AHCYL1       |
| gga-miR-18a-3p   | ACUGCCCUAAGUGCUCUUCUG      | -33.2708 | 214 | ITK          |
| gga-miR-190-5p   | UGAU AUGUUUGAUUAUUAGGU     | -33.2708 | 82  | DIRC2        |
| gga-miR-193a-3p  | AACUGGCCUACAAAGUCCAGU      | -33.2708 | 128 | TMEM30A      |
| gga-miR-34a-3p   | CAAUCAGCAAGUAUACUGCCUA     | -33.2708 | 167 | DNAH5        |
| gga-miR-3529   | AGGCAGACUGUGACUUGUUGU      | -33.2708 | 152 | ETV1         |
| gga-miR-6569-5p  | GCCUGUUGGACUAACGGCGUUG     | -33.2708 | 105 | KLHL29       |

|                 |                        |          |     |       |
|-----------------|------------------------|----------|-----|-------|
| gga-miR-6626-5p | AGGAGAGAGAAGGGUUGCU    | -33.2708 | 377 | NTRK2 |
| gga-miR-7       | UGGAAGACUAGUGAUUUUGUUG | -33.2708 | 277 | CNO   |

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**Table S2.** miRNAs that are differentially expressed in the intestinal mucosal layer of the NE-induced Fayoumi chicken line M15.2

| miRNA   | Sequence                  | Fold change | Target genes | Top ranked target gene |
|---|---------------------------|-------------|--------------|------------------------|
| miRNAs upregulated in the NE line M15.2 compared to control   |                           |             |              |                        |
| gga-miR-196-5p  | UAGGUAGUUUCAUGUUGUUGG     | 36.0345     | 92           | AQP4                   |
| gga-miR-130b-3p   | CAGUGCAAUAAUGAAAGGGCGU    | 35.2975     | 510          | MPHOSPH9               |
| gga-miR-146b-3p   | CCCUAUGGAUUCAGUUCUGC      | 34.7125     | 78           | NAA15                  |
| gga-miR-1699  | CCAGAGGGACAUGGCAGGGCAA    | 34.7125     | 358          | TSHZ3                  |
| gga-miR-1703-5p   | AGAGGCUGUAGGUCCCGUGCUUU   | 34.7125     | 277          | RAB8A                  |
| gga-miR-2131-3p   | CUGUUACUGUUCUUCUGAUGG     | 34.7125     | 110          | AUTS2                  |
| gga-miR-29a-3p  | UAGCACCAUUUGAAAUCGGUU     | 34.7125     | 410          | TET1                   |
| gga-miR-29c-3p  | UAGCACCAUUUGAAAUCGGU      | 34.7125     | 410          | TET1                   |
| gga-miR-1306-3p   | UGGACGUUGGCUCUGGUGGUGAU   | 33.7125     | 24           | BAI1                   |
| gga-miR-1306-5p   | ACCACCUCUUUCGCAAACGUCCAGU | 33.7125     | 185          | NAA50                  |
| gga-miR-133c-3p   | UUUGUCCCCUUCAACCAGCUGC    | 33.7125     | 131          | PRRX1                  |
| gga-miR-1559-5p   | UUCGAUGCUUGUAUGCUACUCC    | 33.7125     | 12           | ADCY7                  |
| gga-miR-1786  | AUUCUUUCUGUCUGUGUUACU     | 33.7125     | 1265         | CLCN4                  |
| gga-miR-18a-5p  | UAAGGUGCAUCUAGUCGAGAU     | 33.7125     | 188          | ERII                   |
| gga-miR-203   | GUGAAAUGUUUAGGACCACUUG    | 33.7125     | 376          | NECAP1                 |
| gga-miR-223   | UGUCAGUUUGUCAAAUACCCC     | 33.7125     | 168          | HSP90B1                |
| gga-miR-30b-5p  | UGUAAACAUCCUACACUCAGCU    | 33.7125     | 526          | LHX8                   |
| gga-miR-33-5p   | GUGCAUUGUAGUUGCAUUGC      | 33.7125     | 184          | CROT                   |
| gga-miR-451   | AAACCGUUACCAUUACUGAGUUU   | 33.7125     | 12           | CEP55                  |
| gga-miR-455-5p  | UAUGUGCCCUUGGACUACAUCG    | 33.7125     | 118          | IRF2                   |
| gga-miR-460a-5p   | CCUGCAUUGUACACACUGUGUG    | 33.7125     | 307          | FBN2                   |
| gga-miR-489-3p  | AGUGACAUCAUAUGUACGGCUGC   | 33.7125     | 130          | ASXL2                  |
| gga-miR-490-3p  | CAACCUGGAGGACUCCAUGCUG    | 33.7125     | 128          | MBLAC2                 |
| gga-miR-6557-3p   | CGCGCCGAUUGUCUCCUCCGGGCAC | 33.7125     | 132          | ZNF226                 |
| gga-miR-6568-3p   | ACAACCAAGAUGGCGCCCGGGC    | 33.7125     | 173          | USP9X                  |
| gga-miR-6602-5p   | ACAGGGAUUGCAGAGGUUGGAG    | 33.7125     | 123          | PRICKLE1               |
| gga-miR-6604-5p   | UGGCACGGUGCUAGGGAUUUCUGU  | 33.7125     | 57           | CNBP                   |
| gga-miR-6631-5p   | GAAGAGAAUGCUGUGGUUCUGC    | 33.7125     | 687          | ZBTB10                 |
| gga-miR-6643-5p   | CCAGGGCUGGCAGGGGAGGGU     | 33.7125     | 284          | TNFAIP8L1              |
| gga-miR-6658-3p   | CAUGGACGGGGGAAGGAGAUAGC   | 33.7125     | 12           | PAPD7                  |
| gga-miR-6664-3p   | CAGGAAUGGUGCUGGAGGCUGA    | 33.7125     | 256          | TPPP                   |
| gga-miR-99a-5p  | AACCCGUAGAUCCGAUCUUGUG    | 33.7125     | 18           | KBTBD8                 |
| miRNAs downregulated in the NE line M15.2 compared to control |                           |             |              |                        |
| gga-let-7d  | AGAGGUAGUGGGUUGCAUAGU     | -36.8009    | 207          | IGF2BP3                |
| gga-miR-1552-5p   | UUAGUGCGCGGUAAGCUAGGGUG   | -35.8009    | 4            | ZEB2                   |

|                  |                            |          |     |          |
|------------------|----------------------------|----------|-----|----------|
| gga-miR-130b-5p  | CCUCUUUCCCCUGUUGCACUACU    | -34.8009 | 219 | FBXO11   |
| gga-miR-1769-5p  | CUUCAGGCUUUUCUCACACCUG     | -34.8009 | 244 | PTPRB    |
| gga-miR-3528     | CAUGCCCCAGUCGUGUUGCAGA     | -34.8009 | 79  | SOCS5    |
| gga-miR-3535     | GGAUUAUGAUGACUGAUUAUCUGAAA | -34.8009 | 105 | ZNF652   |
| gga-miR-6609-3p  | ACAGCCCCUGUGCUCUGACCGCA    | -34.8009 | 471 | CYP26B1  |
| gga-miR-1563     | GCACAUGAUGAGGAAGCACUGAAA   | -4.2582  | 232 | TOX3     |
| gga-miR-1454     | GUACAAUGAUGAGACUUUGGCUCC   | -3.9952  | 263 | LGALS1   |
| gga-miR-30a-3p   | CUUUCAGUCGGAUGUUUGCAGC     | -2.3362  | 563 | SH3GLB1  |
| gga-miR-30c-2-3p | UGGGAGAAGGCUGUUUACUCU      | -2.0883  | 382 | ADAMTS14 |

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**Table S3.** miRNAs that are differentially expressed in the intestinal mucosal layer between NE-induced Fayoumi chicken lines M5.1 and M15.2

| miRNA  | Sequence                  | Fold change | Target genes | Top ranked target gene |
|--|---------------------------|-------------|--------------|------------------------|
| miRNAs upregulated in the NE-induced line M15.2 compared to M5.1   |                           |             |              |                        |
| gga-miR-1451-5p  | UCGCACAGGAGCAAGUUACCGC    | 36.2975     | 33           | LOC408180              |
| gga-miR-1788-5p  | GGCUUGUUUCCGUUGCCUGCG     | 35.2975     | 125          | TAF4                   |
| gga-miR-146b-3p  | CCCUAUGGAUUCAGUUCUGC      | 34.7125     | 78           | NAA15                  |
| gga-miR-1699   | CCAGAGGGACAUGGCAGGGCAA    | 34.7125     | 358          | TSHZ3                  |
| gga-miR-20b-5p   | CAAAGUGCUCAUAGUGCAGGUAG   | 34.7125     | 581          | MAP3K2                 |
| gga-miR-222b-3p  | AGCUACAUCUGAUUACUGGGUCAC  | 34.7125     | 190          | TCF12                  |
| gga-miR-29a-3p   | UAGCACCAUUUGAAAUCGGUU     | 34.7125     | 410          | TET1                   |
| gga-miR-29c-3p   | UAGCACCAUUUGAAAUCGGU      | 34.7125     | 410          | TET1                   |
| gga-miR-1306-3p  | UGGACGUUGGCUCUGGUGGUGAU   | 33.7125     | 24           | BAI1                   |
| gga-miR-1306-5p  | ACCACCUCUCCUGCAAACGUCCAGU | 33.7125     | 185          | NAA50                  |
| gga-miR-140-5p   | AGUGGUUUUACCCUAUGGUAG     | 33.7125     | 151          | MEF2C                  |
| gga-miR-1560-3p  | GCAUCUCUGGACGCGCUCGUUC    | 33.7125     | 189          | FAM126B                |
| gga-miR-16c-5p   | UAGCAGCAGUAAAACUGGAG      | 33.7125     | 982          | MOB4                   |
| gga-miR-193b-3p  | AACUGGCCACAAAAGUCCCGCUUU  | 33.7125     | 128          | TMEM30A                |
| gga-miR-203  | GUGAAAUGUUUAGGACCACUUG    | 33.7125     | 376          | NECAP1                 |
| gga-miR-223  | UGUCAGUUUGUCAAAUACCCC     | 33.7125     | 168          | HSP90B1                |
| gga-miR-33-5p  | GUGCAUUGUAGUUGCAUUGC      | 33.7125     | 184          | CROT                   |
| gga-miR-451  | AAACCGUUACCAUUACUGAGUUU   | 33.7125     | 12           | CEP55                  |
| gga-miR-489-3p   | AGUGACAUCAUAUGUACGGCUGC   | 33.7125     | 130          | ASXL2                  |
| gga-miR-6557-3p  | CGCGCCGAUUGUCUCCUCCGGGCAC | 33.7125     | 132          | ZNF226                 |
| gga-miR-6568-3p  | ACAACCAAGAUGGCGCCCGGGC    | 33.7125     | 173          | USP9X                  |
| gga-miR-6602-5p  | ACAGGGAUUGCAGAGGUUGGAG    | 33.7125     | 123          | PRICKLE1               |
| gga-miR-6604-5p  | UGGCACGGUGCUAGGGAUUUCUGU  | 33.7125     | 57           | CNBP                   |
| gga-miR-6631-5p  | GAAGAGAAUGCUGUGGUUCUGC    | 33.7125     | 687          | ZBTB10                 |
| gga-miR-6643-5p  | CCAGGGCUGGCAGGGGAGGGU     | 33.7125     | 284          | TNFAIP8L1              |
| gga-miR-6656-5p  | UGCAGGGCGAGUAGAGAAAGGCAU  | 33.7125     | 382          | N4BP3                  |
| gga-miR-6658-3p  | CAUGGACGGGGGAAGGAGAUAGC   | 33.7125     | 12           | PAPD7                  |
| gga-miR-6664-3p  | CAGGAAUGGUGCUGGAGGCUGA    | 33.7125     | 256          | TPPP                   |
| gga-miR-34a-5p   | CAAUCAGCAAGUAUACUGCCCUA   | 2.2085      | 358          | ERC1                   |
| miRNAs downregulated in the NE-induced line M15.2 compared to M5.1 |                           |             |              |                        |
| gga-miR-130b-5p  | CCUCUUUCCCGUUGCACUACU     | -36.4301    | 219          | FBXO11                 |
| gga-miR-6615-5p  | UUGGGGACACCAUCAGAACAGCCA  | -36.0150    | 193          | LOC100858703           |
| gga-miR-128-2-5p   | GGGGGCCGUUACACUGUAAGAGA   | -35.4301    | 33           | MPRIIP                 |
| gga-miR-1674   | GGGCUAUGAUGCUGGAUUUUCUGAG | -35.4301    | 54           | LOC100859627           |
| gga-miR-199-5p   | CCCAGUGUUCAGACUACCUGUUC   | -35.4301    | 213          | PODXL                  |

|                  |                            |          |     |              |
|------------------|----------------------------|----------|-----|--------------|
| gga-miR-3607-3p  | CUGUAAACGCUUUCUGAUGUGCC    | -35.4301 | 524 | TNRC6A       |
| gga-let-7a-2-3p  | CUGUACAACCUCCUAGCUUUC      | -34.4301 | 558 | COQ10B       |
| gga-let-7d       | AGAGGUAGUGGGUUGCAUAGU      | -34.4301 | 207 | IGF2BP3      |
| gga-let-7j-3p    | CUAUACAGUCUAUUGCCUUCU      | -34.4301 | 366 | GABRA1       |
| gga-miR-106-3p   | ACUGCAGUAUAAGCACUUCUGG     | -34.4301 | 420 | FAM8A1       |
| gga-miR-146a-3p  | ACCCAUGGGGCUCAGUUCUUCAG    | -34.4301 | 120 | ARHGAP27     |
| gga-miR-1552-5p  | UUAGUGCGCGGUAAGCUAGGGUG    | -34.4301 | 4   | ZEB2         |
| gga-miR-1576     | CUCGGGCGGGCGGAGCGGCAC      | -34.4301 | 127 | GIPC3        |
| gga-miR-1585     | AGUGCCCAGGUGUGGUUAAUCCUG   | -34.4301 | 140 | CLOCK        |
| gga-miR-1681     | UUCACAUGAUGUCUUGCUGAUG     | -34.4301 | 185 | DENND5A      |
| gga-miR-1715-5p  | AGGAUCAGUAGAAGUCAGCUGUGC   | -34.4301 | 97  | NUP153       |
| gga-miR-1729-5p  | AUCCCUUACUCACAUGAGUAGUC    | -34.4301 | 129 | PHF3         |
| gga-miR-1735     | AGGGGCUUUGGGCAGCAUCUG      | -34.4301 | 95  | MARVELD3     |
| gga-miR-1742     | AAUCGUCGUUCGGGAUCCGC       | -34.4301 | 1   | LOC100859371 |
| gga-miR-1769-3p  | CUUCAGGCUUUUCACACACCUG     | -34.4301 | 141 | COL4A1       |
| gga-miR-18b-3p   | UACUGCCCUAAAUGCUCCUUCUGGC  | -34.4301 | 132 | ULK2         |
| gga-miR-18b-5p   | UAAGGUGCAUCUAGUGCAGUUA     | -34.4301 | 188 | ERI1         |
| gga-miR-19a-5p   | AGUUUUGCAUAGUUGCACUAC      | -34.4301 | 213 | CREB1        |
| gga-miR-205b     | CCCUUCAUUCACC GGAAUCUG     | -34.4301 | 182 | RAB9B        |
| gga-miR-2130     | UCCCAGUGGAGCUCUGCAAGGAC    | -34.4301 | 205 | KIAA0182     |
| gga-miR-218-5p   | UUGUGCUUGAUCUAACCAUGU      | -34.4301 | 367 | ANKRD40      |
| gga-miR-27b-5p   | AGAGCUUAGCUGAUUGGUGAACA    | -34.4301 | 79  | RBM39        |
| gga-miR-301a-3p  | CAGUGCAAUAAUUAUGUCAAAAGCAU | -34.4301 | 501 | ST18         |
| gga-miR-3528     | AGGCAGACUGUGACUUGUUGU      | -34.4301 | 79  | SOCS5        |
| gga-miR-3535     | GGAUUGAUGACUGAUUAUCUGAAA   | -34.4301 | 105 | ZNF652       |
| gga-miR-3537     | GUGAGUGCUGUAGGAUGGGGCUC    | -34.4301 | 104 | TAF5         |
| gga-miR-3538     | GUUCGGUGAUGAAACCAUGGA      | -34.4301 | 12  | PABPC1       |
| gga-miR-383-5p   | AGAUCAGAAGGUGAUUGUGGCU     | -34.4301 | 153 | STRN3        |
| gga-miR-6516-3p  | CAUGUAUGAUACUGCACACAACG    | -34.4301 | 120 | SLC12A2      |
| gga-miR-6546-3p  | GGAGUUCAGCUGUGCUGCUGC      | -34.4301 | 131 | WDR26        |
| gga-miR-6564-3p  | UGGACGGAGGAAGCGCGGGCAG     | -34.4301 | 19  | LOC424998    |
| gga-miR-6596-3p  | CGGAGCUCGGACGGCGUCCCGA     | -34.4301 | 132 | IFFO2        |
| gga-miR-6609-3p  | ACAGCCCCUGUGCUCUGACCGCA    | -34.4301 | 471 | CYP26B1      |
| gga-miR-7452-5p  | ACAGGGCUGGCUGAUCCGUGC      | -34.4301 | 251 | TNFAIP8L1    |
| gga-miR-99a-3p   | CAAGCUCGCUUCUAUGGGUCU      | -34.4301 | 9   | UTRN         |
| gga-miR-1563     | GCACAUGAUGAGGAAGCACUGAAA   | -4.5755  | 232 | TOX3         |
| gga-miR-30c-2-3p | UGGGAGAAGGCUGUUUACUCU      | -4.1770  | 382 | ADAMTS14     |
| gga-miR-133a-3p  | UUGGUCCCCUUAACCAGCUGU      | -3.6244  | 131 | PRRX1        |
| gga-miR-30a-3p   | CUUUCAGUCGGAUGUUUGCAGC     | -3.5755  | 563 | SH3GLB1      |
| gga-miR-10a-5p   | UACCCUGUAGAUCCGAAUUUGU     | -3.4658  | 117 | DAZAP1       |

|                 |                            |         |     |              |
|-----------------|----------------------------|---------|-----|--------------|
| gga-miR-133c-3p | UUGGUCCCCUUCAACCAGCUGC     | -3.3025 | 131 | PRRX1        |
| gga-miR-126-5p  | CAUUUUUUACUUUUUGGUACGCG    | -3.1770 | 299 | FGFRL1       |
| gga-miR-92-5p   | AGGUUGGGAUCAGUUGCAAUGCU    | -3.0395 | 106 | LOC100858227 |
| gga-miR-10b-5p  | UACCCUGUAGAACCGAAUUUGU     | -2.9496 | 117 | DAZAP1       |
| gga-miR-146a-5p | UGAGAACUGAAUCCAUGGGUU      | -2.9325 | 128 | RFXDC2       |
| gga-miR-27b-3p  | UUCACAGUGGCUAAGUUCUGC      | -2.8199 | 537 | GAB1         |
| gga-miR-125b-5p | UCGUACCGUGAGUAAUAAUGCGC    | -2.7473 | 190 | OSBPL9       |
| gga-miR-99a-5p  | AACCCGUAGAUCCGAUCUUGUG     | -2.7175 | 18  | KBTBD8       |
| gga-miR-1454    | GUACAAUGAUGAGACUUUGGCUC    | -2.5249 | 263 | LGALS1       |
| gga-miR-125b-3p | ACAAGUCAGGCUCUUGGGACCU     | -2.4545 | 178 | TNKS2        |
| gga-miR-100-5p  | AACCCGUAGAUCCGAACUUGUG     | -2.3696 | 19  | KBTBD8       |
| gga-miR-204     | UUCCCUUUGUCAUCCUAUGCCU     | -2.3025 | 350 | MGAT3        |
| gga-miR-211     | UUCCCUUUGUCAUCCUAUGCCU     | -2.3025 | 350 | MGAT3        |
| gga-miR-222b-5p | UGCUCAGUAGUCAGUGUAGGAUCUGU | -2.3025 | 203 | MFSD9        |
| gga-miR-30a-5p  | UGUAAACAUCCUCGACUGGAAG     | -2.1789 | 521 | PPARGC1B     |
| gga-miR-1720-3p | AAGCAACGAGAGGUCGGUCUGA     | -2.1326 | 25  | EPB41L5      |
| gga-miR-214     | ACAGCAGGCACAGACAGGCAG      | -2.1326 | 652 | NAA15, EZH1  |
| gga-miR-184-3p  | UGGACGGAGAACUGAUAAAGGGU    | -2.0395 | 19  | LOC424998    |

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**Table S4.** List of gga-miR-9-5p target genes involved in signal transduction and immune system-related pathways

| Major categories             | Minor categories                             | Gene counts | Genes                       |
|------------------------------|--|-------------|-----------------------------|
| Signal transduction pathways | MAPK signaling pathway                       | 3           | MAP3K3, MEF2C, CACNB2       |
|                              | ErbB signaling pathway                       | 0           | -                           |
|                              | Wnt signaling pathway                        | 1           | NFATC2                      |
|                              | Notch signaling pathway                      | 0           | -                           |
|                              | Hedgehog signaling pathway                   | 0           | -                           |
|                              | TGF-beta signaling pathway                   | 1           | SMURF2                      |
|                              | VEGF signaling pathway                       | 1           | NFATC2                      |
|                              | Jak-STAT signaling pathway                   | 3           | STAM, PIAS4, IL15RA         |
|                              | FoxO signaling pathway                       | 0           | -                           |
|                              | Calcium signaling pathway                    | 1           | ADCY1                       |
|                              | Phosphatidylinositol signaling system        | 4           | SYNJ1, DGKB, MTMR2, PPIP5K2 |
|                              | mTOR signaling pathway                       | 2           | ULK2, EIF4E                 |
| Immune system pathways       | Toll-like receptor signaling pathway         | 0           | -                           |
|                              | NOD-like receptor signaling pathway          | 1           | ERBB2IP                     |
|                              | RIG-I-like receptor signaling pathway        | 1           | TRADD                       |
|                              | Cytosolic DNA-sensing pathway                | 0           | -                           |
|                              | Intestinal immune network for IgA production | 1           | IL15RA                      |

**Table S5.** List of gga-miR-20b-5p target genes involved in signal transduction and immune system related pathways

| Major categories             | Minor categories                             | Gene counts                               | Genes  |
|------------------------------|--|---|--|
| Signal transduction pathways | MAPK signaling pathway                       | 16  | MAP3K2, RPS6KA5, MKNK2, MAP3K14, SOS1, RASA2, RASGRF2, PPP3R1, RAPGEF2, MAP4K4, AKT3, MAP3K5, ZAK, DUSP8, RASA1, RPS6KA2 |
|                              | ErbB signaling pathway                       | 4   | GAB1, SOS1, SHC4, AKT3   |
|                              | Wnt signaling pathway                        | 6   | VANGL1, FZD3, FBXW11, PPP3R1, TBL1X, SFRP4   |
|                              | Notch signaling pathway                      | 2   | KAT2B, MAML1   |
|                              | Hedgehog signaling pathway                   | 1   | FBXW11   |
|                              | TGF-beta signaling pathway                   | 5   | ZFYVE9, BMPR2, E2F5, NBL1, BMP6  |
|                              | VEGF signaling pathway                       | 2   | PPP3R1, AKT3   |
|                              | Jak-STAT signaling pathway                   | 4   | SOS1, SOCS6, AKT3, IFNAR1  |
|                              | FoxO signaling pathway                       | 4   | SOS1, AKT3, PTEN, PRKAA2   |
|                              | Calcium signaling pathway                    | 4   | ADRA1B, PPP3R1, RYR2, ADCY2  |
|                              | Phosphatidylinositol signaling system        | 3   | PIP4K2A, PIKFYVE, PTEN   |
| mTOR signaling pathway       | 6  | ULK1, AKT3, PTEN, EIF4E2, RPS6KA2, PRKAA2 |  |
| Immune system pathways       | Toll-like receptor signaling pathway         | 3   | TOLLIP, AKT3, IFNAR1   |
|                              | NOD-like receptor signaling pathway          | 0   | -  |
|                              | RIG-I-like receptor signaling pathway        | 1   | SIKE1  |
|                              | Cytosolic DNA-sensing pathway                | 1   | POLR3G   |
|                              | Intestinal immune network for IgA production | 2   | ITGA4, MAP3K14   |

**Table S6.** List of gga-miR-196-5p target genes involved in signal transduction and immune system related pathways

| Major categories             | Minor categories                             | Gene counts | Genes      |
|------------------------------|--|-------------|------------|
| Signal transduction pathways | MAPK signaling pathway                       | 1           | MAP4K3     |
|                              | ErbB signaling pathway                       | 1           | CDKN1B     |
|                              | Wnt signaling pathway                        | 1           | FZD6       |
|                              | Notch signaling pathway                      | 0           | -          |
|                              | Hedgehog signaling pathway                   | 0           | -          |
|                              | TGF-beta signaling pathway                   | 0           | -          |
|                              | VEGF signaling pathway                       | 0           | -          |
|                              | Jak-STAT signaling pathway                   | 1           | IL13RA1    |
|                              | FoxO signaling pathway                       | 1           | CDKN1B     |
|                              | Calcium signaling pathway                    | 2           | CALM1, F2R |
|                              | Phosphatidylinositol signaling system        | 1           | CALM1      |
| mTOR signaling pathway       | 1  | RICTOR      |            |
| Immune system pathways       | Toll-like receptor signaling pathway         | 1           | CD86       |
|                              | NOD-like receptor signaling pathway          | 0           | -          |
|                              | RIG-I-like receptor signaling pathway        | 0           | -          |
|                              | Cytosolic DNA-sensing pathway                | 0           | -          |
|                              | Intestinal immune network for IgA production | 1           | CD86       |

**Table S7.** List of gga-let-7d target genes involved in signal transduction and immune system related pathways

| Major categories             | Minor categories                             | Gene counts | Genes                             |
|------------------------------|--|-------------|-----------------------------------|
| Signal transduction pathways | MAPK signaling pathway                       | 5           | TGFBR1, MAP4K3, NGF, NRAS, MAP4K4 |
|                              | ErbB signaling pathway                       | 2           | NRAS, CBL                         |
|                              | Wnt signaling pathway                        | 2           | NKD1, FZD3                        |
|                              | Notch signaling pathway                      | 0           | -                                 |
|                              | Hedgehog signaling pathway                   | 0           | -                                 |
|                              | TGF-beta signaling pathway                   | 3           | E2F5, TGFBR1, ACVR1C              |
|                              | VEGF signaling pathway                       | 1           | NRAS                              |
|                              | Jak-STAT signaling pathway                   | 2           | IL13RA1, IL9R                     |
|                              | FoxO signaling pathway                       | 2           | TGFBR1, NRAS                      |
|                              | Calcium signaling pathway                    | 1           | P2RX5                             |
|                              | Phosphatidylinositol signaling system        | 0           | -                                 |
|                              | mTOR signaling pathway                       | 2           | ULK2, RICTOR                      |
| Immune system pathways       | Toll-like receptor signaling pathway         | 0           | -                                 |
|                              | NOD-like receptor signaling pathway          | 0           | -                                 |
|                              | RIG-I-like receptor signaling pathway        | 0           | -                                 |
|                              | Cytosolic DNA-sensing pathway                | 0           | -                                 |
|                              | Intestinal immune network for IgA production | 0           | -                                 |