

Supplemental Figures

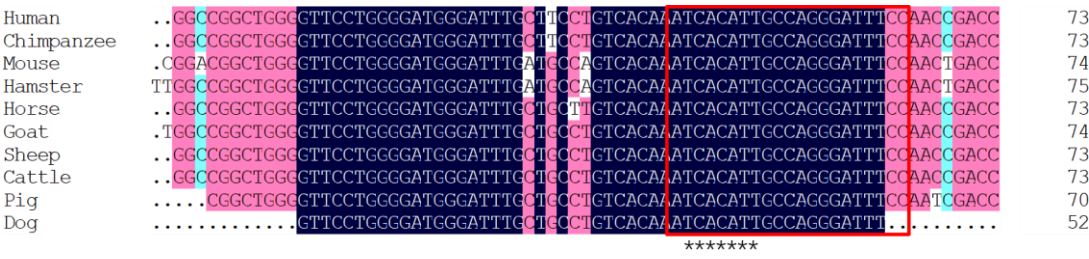


Figure S1. Multi-sequence alignment of pre-miR-23a in mammal. The mature sequence is boxed and the asterisk marks the seed sequence. Black parts represent all species with identical sequences, cyan and magenta represent the same sequence in multiple species.

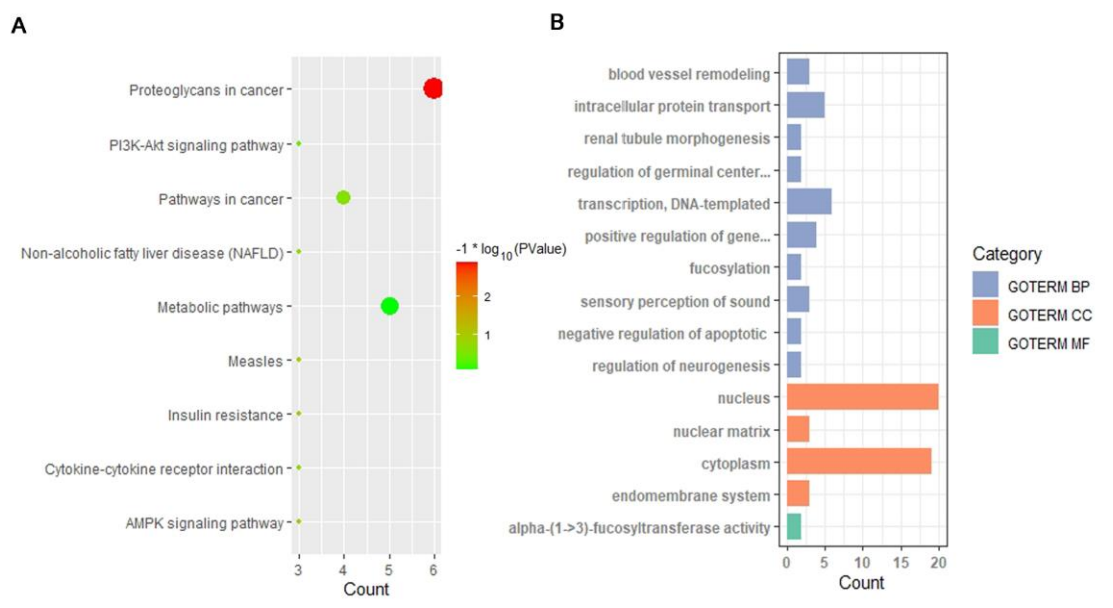


Figure S2. Functional analysis of miR-23a target genes. (A) Analysis of KEGG pathway. PValue, Enrichment significance, was calculated by hypergeometric test. $-1 * \log_{10}(\text{PValue})$ is the ordinate, and the number of enriched genes in each pathway, count, is coordinate. **(B)** GO term analysis. Count is the number of enriched genes in each term. BP means biological process, MF means molecular function, and CC means cellular component.

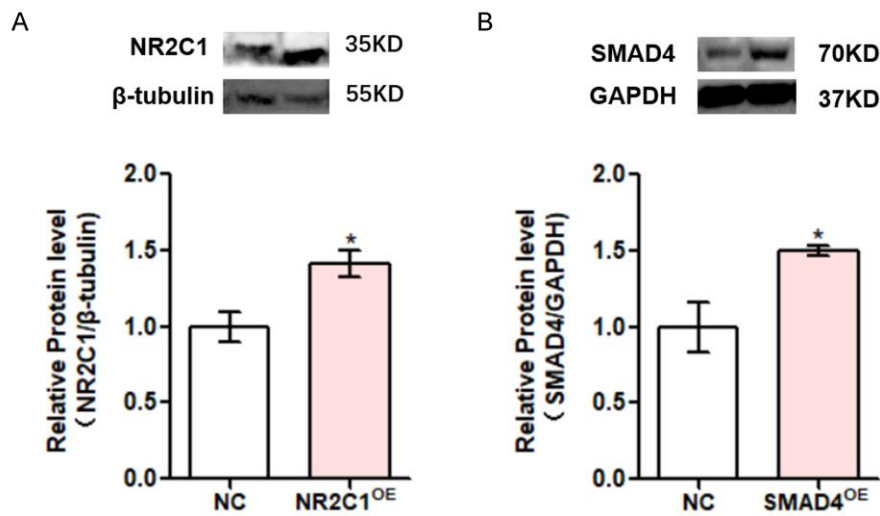


Figure S3. pGCs were treated with pcDNA3.1-SMAD4 and pcDNA3.1-NR2C1, western blotting was performed to detect protein levels of SMAD4 and NR2C1. (A-B) β-tubulin and GAPDH are internal reference of NR2C1 (A) and SMAD4 (B), respectively. Data are expressed as mean ± S.E.M., and significance was tested using a t-test. (*P < 0.05).

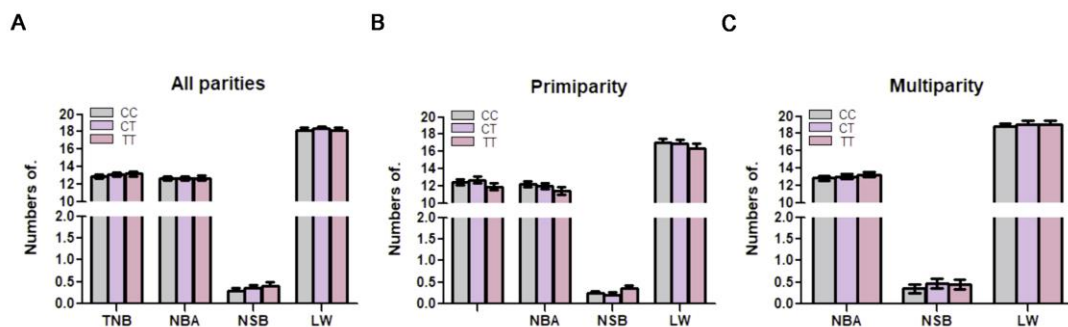


Figure S4. Association analysis of SNV g.-398C>T with reproductive traits in Yorkshire sows. (A) All parities. (B) Primiparity. (C) Multiparity.

Supplemental Tables

Table S1. Information of oligonucleotides.

| Oligonucleotides | Accession number | Oligonucleotide sequence (5' to 3') |
|-------------------|------------------|-------------------------------------|
| mimics NC | (NR_038489) | UUGUACUACACAAAAGUACUG |
| miR-23a mimics | | AUCACAUUGCCAGGGAUUUCC |
| inhibitor NC | (NR_038489) | CAGUACUUUUGUGUAGUACAA |
| miR-23a inhibitor | | GGAAAUCCCUGGCAAUGGAU |

Table S2. Information of primers for qRT-PCR.

| Name | Accession number | Sequence(5' to 3') | Product size | Annealing temp |
|-----------|------------------|-------------------------------------------------------------------|--------------|----------------|
| miR-23a | NR_038489 | F: CGGGCATCACATTGCCAGG R: CAGCCACAAAAGAGCACAAAT | 56 | 60 |
| U6 | EU520423.1 | F: GCTTCGGCAGCACATATACT R: TTCACGAATTTGCGTGTCAT | 86 | 60 |
| NORHA | XR_304632.3 | F: GCTGAACCTGGGGAGTGTCTA R: TCTCTGTCCTTGTTGTTCTGC | 176 | 60 |
| GAPDH | NM_001206359.1 | F: GGACTCATGACCACGGTCCAT R: TCAGATCCACAACCGACACGT | 163 | 60 |
| FoxO1 | NM_214014.3 | F: GCAAATCGAGTTACGGAGGC R: AATGTCATTATGGGGAGGAGAGT | 170 | 60 |
| stem loop | NR_038489 | CCTGTTGTCTCCAGCCACAAAAGAGC ACAATATTTTCAGGAGACAACAGGGG AAATC | | |

Table S3. Information of primers for plasmid construction.

| Name | Accession number | Primer sequence (5' to 3') | Product size (bp) | Annealing temp (°C) |
|----------|------------------|--------------------------------------------------------------------------------------|-------------------|---------------------|
| P189 | NC_010444 | F: <u>CGGGGTACCCCTGGCTTTGGGAGTTCCT</u> R: <u>CCGCTCGAGCTGCCATCCTTTGAGGTCTTG</u> | 189 | 56 |
| P558 | NC_010444 | F: <u>CGGGGTACCGGGAAACTGAGGCTTAAAGGG</u> R: <u>CCGCTCGAGCTGCCATCCTTTGAGGTCTTG</u> | 558 | 58 |
| p1018 | NC_010444 | F: <u>CGGGGTACCCCGTCCTAAATCCTTACCAG</u> R: <u>CCGCTCGAGCTGCCATCCTTTGAGGTCTTG</u> | 1018 | 58 |
| p1346 | NC_010444 | F: <u>CGGGGTACCCCTTCCCGTTCTCGTCCC</u> R: <u>CCGCTCGAGCTGCCATCCTTTGAGGTCTTG</u> | 1376 | 58 |
| pGL3-C/T | NC_010444 | F: <u>CGGGGTACCGCCCTGGTGGTTTCTCCTG</u> R: <u>CCGCTCGAGCTCCCTTCCCCACCACT</u> | 155 | 60 |

Table S4. Information of primer for ChIP.

| Name | Accession number | Sequence(5' to 3') | Product size (bp) | Annealing temp (°C) |
|------|------------------|----------------------------------------------------|-------------------|---------------------|
| MRE | NC_010449.5 | F: TGCTTCGAGGAGCCAGTCTC R: CAGCAGGAGCAGGAAGAAGC | 170 | 55 |
| X | NC_010449.5 | F: CCTTCCTAATCCACCGACTT R: GAGGCACGCTCTGAGATTC | 144 | 62 |
| SBE | NC_010444 | F: GCCCTGGTGGTTTCCTCCT R: TCCCTTCCCCACCACCACT | 154 | 63 |

Table S5. Information of primers for Genotyping.

| Gene | Accession number | Primer sequences | Product size (bp) | Annealing temp (°C) |
|---------|------------------|--------------------------------------------------------|-------------------|---------------------|
| miR-23a | NC_010444 | F: AGGGCACCGAGTTTTTCATT R: ATCAACTGTGTTTCAGCTCAGTAG | 1173 | 58 |

Table S6. The potential targets of miR-23a.

| Targets | Full name |
|----------------|--------------------------------------------------------|
| ALAS1 | 5'-aminolevulinate synthase 1 |
| ANKRD50 | ankyrin repeat domain 50 |
| ANXA2 | annexin A2 |
| ATP11B | ATPase phospholipid transporting 11B (putative) |
| ATXN1 | ataxin 1 |
| ATXN7L3B | ataxin 7 like 3B |
| BICD2 | BICD cargo adaptor 2 |
| BLCAP | BLCAP, apoptosis inducing factor |
| BTAf1 | B-TFIID TATA-box binding protein associated factor 1 |
| BTBD7 | BTB domain containing 7 |
| C2orf69 | chromosome 2 open reading frame 69 |
| C6orf62 | chromosome 6 open reading frame 62 |
| CADM3 | cell adhesion molecule 3 |
| CCDC6 | coiled-coil domain containing 6 |
| CDK17 | cyclin dependent kinase 17 |
| CELF1 | CUGBP Elav-like family member 1 |
| CHD7 | chromodomain helicase DNA binding protein 7 |
| CLCN3 | chloride voltage-gated channel 3 |
| COL4A1 | collagen type IV alpha 1 chain |
| CREBZF | CREB/ATF bZIP transcription factor |
| CUL3 | cullin 3 |
| CXCL12 | C-X-C motif chemokine ligand 12 |
| DCP2 | decapping mRNA 2 |
| DHX15 | DEAH-box helicase 15 |
| DUSP5 | dual specificity phosphatase 5 |
| EGLN2 | egl-9 family hypoxia inducible factor 2 |
| EPAS1 | endothelial PAS domain protein 1 |
| EPS15 | epidermal growth factor receptor pathway substrate 15 |
| ERBB4 | erb-b2 receptor tyrosine kinase 4 |
| ETNK1 | ethanolamine kinase 1 |
| FAM126B | family with sequence similarity 126 member B |
| FUT4 | fucosyltransferase 4 |
| FUT9 | fucosyltransferase 9 |
| HDAC7 | histone deacetylase 7 |
| HMGB2 | high mobility group box 2 |
| HS6ST3 | heparan sulfate 6-O-sulfotransferase 3 |
| IPO5 | importin 5 |
| JARID2 | jumonji and AT-rich interaction domain containing 2 |
| KIAA1109 | KIAA1109 |
| LBR | lamin B receptor |
| LMNB1 | lamin B1 |
| LPAR1 | lysophosphatidic acid receptor 1 |
| LRIG1 | leucine rich repeats and immunoglobulin like domains 1 |
| MAP3K9 | mitogen-activated protein kinase kinase kinase 9 |
| MAPRE1 | microtubule associated protein RP/EB family member 1 |
| MARCKS | myristoylated alanine rich protein kinase C substrate |
| MARCKSL1 | MARCKS like 1 |
| MCFD2 | multiple coagulation factor deficiency 2 |
| MED13L | mediator complex subunit 13 like |
| MEF2C | myocyte enhancer factor 2C |

| | |
|----------|--------------------------------------------------------------------------|
| MSMO1 | methylsterol monooxygenase 1 |
| NAA50 | N(alpha)-acetyltransferase 50, NatE catalytic subunit |
| NAP1L5 | nucleosome assembly protein 1 like 5 |
| NCOA6 | nuclear receptor coactivator 6 |
| NUAK1 | NUAK family kinase 1 |
| ORMDL1 | ORMDL sphingolipid biosynthesis regulator 1 |
| OSBPL8 | oxysterol binding protein like 8 |
| PARD6B | par-6 family cell polarity regulator beta |
| PBRM1 | polybromo 1 |
| PDE7A | phosphodiesterase 7A |
| PDPK1 | 3-phosphoinositide dependent protein kinase 1 |
| PGRMC2 | progesterone receptor membrane component 2 |
| PHYHIPL | phytanoyl-CoA 2-hydroxylase interacting protein like |
| PIK3C2A | phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha |
| PIK3R3 | phosphoinositide-3-kinase regulatory subunit 3 |
| PIP4K2B | phosphatidylinositol-5-phosphate 4-kinase type 2 beta |
| PKIA | cAMP-dependent protein kinase inhibitor alpha |
| PKP4 | plakophilin 4 |
| PNMA2 | PNMA family member 2 |
| PNRC1 | proline rich nuclear receptor coactivator 1 |
| POM121C | POM121 transmembrane nucleoporin C |
| PPP1R12A | protein phosphatase 1 regulatory subunit 12A |
| PSD3 | pleckstrin and Sec7 domain containing 3 |
| PTP4A2 | protein tyrosine phosphatase type IVA, member 2 |
| QKI | QKI, KH domain containing RNA binding |
| QSER1 | glutamine and serine rich 1 |
| RAI14 | retinoic acid induced 14 |
| RCHY1 | ring finger and CHY zinc finger domain containing 1 |
| REPS2 | RALBP1 associated Eps domain containing 2 |
| RNF38 | ring finger protein 38 |
| RPRD2 | regulation of nuclear pre-mRNA domain containing 2 |
| SATB1 | SATB homeobox 1 |
| SEMA6D | semaphorin 6D |
| SETD2 | SET domain containing 2, histone lysine methyltransferase |
| SLC1A1 | solute carrier family 1 member 1 |
| SLC25A36 | solute carrier family 25 member 36 |
| SMS | spermine synthase |
| SNX27 | sorting nexin family member 27 |
| SPRY2 | sprouty RTK signaling antagonist 2 |
| STK35 | serine/threonine kinase 35 |
| STRN | striatin |
| STX12 | syntaxin 12 |
| SYT4 | synaptotagmin 4 |
| TADA1 | transcriptional adaptor 1 |
| TAOK1 | TAO kinase 1 |
| TARDBP | TAR DNA binding protein |
| TBC1D15 | TBC1 domain family member 15 |
| TBC1D9 | TBC1 domain family member 9 |
| TBR1 | T-box, brain 1 |
| TCF24 | transcription factor 24 |
| TGFBR2 | transforming growth factor beta receptor 2 |
| TGFBR3 | transforming growth factor beta receptor 3 |
| TLK1 | tousled like kinase 1 |
| TNFAIP3 | TNF alpha induced protein 3 |

| | |
|--------|--------------------------------------------------|
| TNRC6B | trinucleotide repeat containing 6B |
| USP46 | ubiquitin specific peptidase 46 |
| VCAN | versican |
| VCPIP1 | valosin containing protein interacting protein 1 |
| WNK1 | WNK lysine deficient protein kinase 1 |
| ZCCHC2 | zinc finger CCHC-type containing 2 |
| ZNF292 | zinc finger protein 292 |
