**Table S1.** The methylation of CpG locus at *Agtr1a* and *Prkcb* gene promoter. The data was expressed as mean ± SEM. CON control group, MHF maternal high fat diet group. *P < 0.05

| Gene | Number | Position | CON | MHF | P value | |
|---|---|---|---|---|---|---|
| *Agtr1a* | 1 | 29 | 0.01757±0.004964 | 0.01505±0.000562 | 0.628 | |
| | 2 | 38 | 0.01870±0.005351 | 0.02121±0.003137 | 0.697 | |
| | 3 | 54 | 0.01628±0.003589 | 0.01626±0.001662 | 0.996 | |
| | 4 | 60 | 0.02066±0.003756 | 0.01671±0.001150 | 0.343 | |
| | 5 | 65 | 0.01731±0.002828 | 0.01206±0.003130 | 0.249 | |
| | 6 | 111 | 0.02203±0.003391 | 0.02201±0.002948 | 0.996 | |
| | 7 | 116 | 0.02266±0.003799 | 0.01092±0.001415 | 0.02 | * |
| | 8 | 125 | 0.02198±0.005382 | 0.02146±0.002313 | 0.933 | |
| | 9 | 131 | 0.01915±0.003312 | 0.01468±0.002536 | 0.315 | |
| | 10 | 140 | 0.02392±0.004576 | 0.02647±0.002769 | 0.646 | |
| | 11 | 147 | 0.02458±0.002385 | 0.02019±0.002291 | 0.221 | |
| | 12 | 154 | 0.01925±0.004154 | 0.01587±0.002898 | 0.523 | |
| | 13 | 177 | 0.01708±0.003677 | 0.01632±0.001561 | 0.853 | |
| | 14 | 191 | 0.01304±0.002708 | 0.01054±0.002460 | 0.514 | |
| | 15 | 64 | 0.02459±0.003512 | 0.02628±0.002273 | 0.698 | |
| | 16 | 91 | 0.04522±0.003752 | 0.02966±0.003492 | 0.016 | * |
| | 17 | 117 | 0.02462±0.004641 | 0.01795±0.001863 | 0.219 | |
| | 18 | 139 | 0.04431±0.005855 | 0.02939±0.002574 | 0.048 | * |
| | 19 | 154 | 0.04213±0.005353 | 0.03052±0.003737 | 0.113 | |
| | 20 | 177 | 0.02374±0.006598 | 0.01405±0.002175 | 0.201 | |
| | 21 | 189 | 0.02102±0.004500 | 0.01462±0.002494 | 0.249 | |
| | 22 | 197 | 0.01701±0.004826 | 0.00958±0.001597 | 0.182 | |
| | 23 | 215 | 0.02282±0.005352 | 0.01723±0.002801 | 0.381 | |
| *Prkcb* | 1 | 22 | 0.01242±0.001198 | 0.01212±0.002027 | 0.904 | |
| | 2 | 24 | 0.00932±0.001923 | 0.01051±0.000661 | 0.575 | |
| | 3 | 34 | 0.01066±0.001180 | 0.01348±0.001502 | 0.178 | |
| | 4 | 38 | 0.01783±0.001208 | 0.02107±0.002518 | 0.279 | |
| | 5 | 47 | 0.02055±0.002825 | 0.02091±0.000519 | 0.902 | |
| | 6 | 51 | 0.01312±0.001125 | 0.01304±0.002213 | 0.973 | |
| | 7 | 58 | 0.02307±0.002166 | 0.02453±0.001291 | 0.579 | |
| | 8 | 66 | 0.01601±0.001887 | 0.01639±0.002747 | 0.912 | |
| | 9 | 68 | 0.01231±0.001534 | 0.00836±0.001349 | 0.089 | |
| | 10 | 79 | 0.01418±0.001670 | 0.01819±0.001187 | 0.086 | |
| | 11 | 81 | 0.01325±0.001827 | 0.01218±0.001750 | 0.684 | |
| | 12 | 84 | 0.01851±0.000918 | 0.01849±0.001177 | 0.987 | |
| | 13 | 93 | 0.01736±0.001560 | 0.01652±0.002033 | 0.751 | |
| | 14 | 96 | 0.01158±0.002350 | 0.01393±0.001043 | 0.387 | |
| | 15 | 100 | 0.01655±0.001848 | 0.01780±0.002106 | 0.666 | |

| | 16 | 102 | 0.01461±0.001213 | 0.01178±0.002323 | 0.312 | |
|---|---|---|---|---|---|---|
| | 17 | 104 | 0.01364±0.001297 | 0.01349±0.001349 | 0.936 | |
| | 18 | 106 | 0.01573±0.000968 | 0.01595±0.001740 | 0.915 | |
| | 19 | 108 | 0.01260±0.002167 | 0.01144±0.001698 | 0.686 | |
| | 20 | 126 | 0.01367±0.001241 | 0.01254±0.001675 | 0.602 | |
| | 21 | 140 | 0.01523±0.002214 | 0.01506±0.000559 | 0.944 | |
| | 22 | 164 | 0.01466±0.000567 | 0.01598±0.001129 | 0.328 | |
| | 23 | 31 | 0.01545±0.000696 | 0.01581±0.002281 | 0.885 | |
| | 24 | 48 | 0.01521±0.002201 | 0.01553±0.001059 | 0.9 | |
| | 25 | 56 | 0.01075±0.000992 | 0.01255±0.002184 | 0.475 | |
| | 26 | 65 | 0.01160±0.001405 | 0.01404±0.000809 | 0.171 | |
| | 27 | 78 | 0.01022±0.001917 | 0.00975±0.000761 | 0.825 | |
| | 28 | 82 | 0.01120±0.001812 | 0.01390±0.000944 | 0.223 | |
| | 29 | 86 | 0.01343±0.001924 | 0.00999±0.002311 | 0.286 | |
| | 30 | 111 | 0.01969±0.001905 | 0.01331±0.001140 | 0.021 | * |
| | 31 | 118 | 0.01129±0.000649 | 0.01294±0.001656 | 0.381 | |
| | 32 | 136 | 0.02156±0.002697 | 0.02143±0.001057 | 0.964 | |

CON: Control group; MHF: maternal high fat diet group

**Table S2.** Methylated CpG sites at *Agtr1a* and *Prkcb* gene promoter

| Target | Number | Position | Chromosome | Genome Position | Distance to TSS |
|---|---|---|---|---|---|
| *Agtr1a* | 1 | 29 | chr17 | 35957894 | 183 |
| *Agtr1a* | 2 | 38 | chr17 | 35957903 | 174 |
| *Agtr1a* | 3 | 54 | chr17 | 35957919 | 158 |
| *Agtr1a* | 4 | 60 | chr17 | 35957925 | 152 |
| *Agtr1a* | 5 | 65 | chr17 | 35957930 | 147 |
| *Agtr1a* | 6 | 111 | chr17 | 35957976 | 101 |
| *Agtr1a* | 7 | 116 | chr17 | 35957981 | 96 |
| *Agtr1a* | 8 | 125 | chr17 | 35957990 | 87 |
| *Agtr1a* | 9 | 131 | chr17 | 35957996 | 81 |
| *Agtr1a* | 10 | 140 | chr17 | 35958005 | 72 |
| *Agtr1a* | 11 | 147 | chr17 | 35958012 | 65 |
| *Agtr1a* | 12 | 154 | chr17 | 35958019 | 58 |
| *Agtr1a* | 13 | 177 | chr17 | 35958042 | 35 |
| *Agtr1a* | 14 | 191 | chr17 | 35958056 | 21 |
| *Agtr1a* | 15 | 64 | chr17 | 35957703 | 374 |
| *Agtr1a* | 16 | 91 | chr17 | 35957730 | 347 |
| *Agtr1a* | 17 | 117 | chr17 | 35957756 | 321 |
| *Agtr1a* | 18 | 139 | chr17 | 35957778 | 299 |
| Agtr1a | 19 | 154 | chr17 | 35957793 | 284 |
| *Agtr1a* | 20 | 177 | chr17 | 35957816 | 261 |

| | | | | | |
|---|---|---|---|---|---|
| *Agtr1a* | 21 | 189 | chr17 | 35957828 | 249 |
| *Agtr1a* | 22 | 197 | chr17 | 35957836 | 241 |
| *Agtr1a* | 23 | 215 | chr17 | 35957854 | 223 |
| | | | | | |
| *Prkcb* | 1 | 22 | chr1 | 192233826 | 47 |
| *Prkcb* | 2 | 24 | chr1 | 192233824 | 45 |
| *Prkcb* | 3 | 34 | chr1 | 192233814 | 35 |
| *Prkcb* | 4 | 38 | chr1 | 192233810 | 31 |
| *Prkcb* | 5 | 47 | chr1 | 192233801 | 22 |
| *Prkcb* | 6 | 51 | chr1 | 192233797 | 18 |
| *Prkcb* | 7 | 58 | chr1 | 192233790 | 11 |
| *Prkcb* | 8 | 66 | chr1 | 192233782 | 3 |
| *Prkcb* | 9 | 68 | chr1 | 192233780 | 1 |
| *Prkcb* | 10 | 79 | chr1 | 192233769 | -10 |
| *Prkcb* | 11 | 81 | chr1 | 192233767 | -12 |
| *Prkcb* | 12 | 84 | chr1 | 192233764 | -15 |
| *Prkcb* | 13 | 93 | chr1 | 192233755 | -24 |
| *Prkcb* | 14 | 96 | chr1 | 192233752 | -27 |
| *Prkcb* | 15 | 100 | chr1 | 192233748 | -31 |
| *Prkcb* | 16 | 102 | chr1 | 192233746 | -33 |
| *Prkcb* | 17 | 104 | chr1 | 192233744 | -35 |
| *Prkcb* | 18 | 106 | chr1 | 192233742 | -37 |
| *Prkcb* | 19 | 108 | chr1 | 192233740 | -39 |
| *Prkcb* | 20 | 126 | chr1 | 192233722 | -57 |
| *Prkcb* | 21 | 140 | chr1 | 192233708 | -71 |
| *Prkcb* | 22 | 164 | chr1 | 192233684 | -95 |
| *Prkcb* | 23 | 31 | chr1 | 192234357 | 578 |
| *Prkcb* | 24 | 48 | chr1 | 192234340 | 561 |
| *Prkcb* | 25 | 56 | chr1 | 192234332 | 553 |
| *Prkcb* | 26 | 65 | chr1 | 192234323 | 544 |
| *Prkcb* | 27 | 78 | chr1 | 192234310 | 531 |
| *Prkcb* | 28 | 82 | chr1 | 192234306 | 527 |
| *Prkcb* | 29 | 86 | chr1 | 192234302 | 523 |
| *Prkcb* | 30 | 111 | chr1 | 192234277 | 498 |
| *Prkcb* | 31 | 118 | chr1 | 192234270 | 491 |
| *Prkcb* | 32 | 136 | chr1 | 192234252 | 473 |
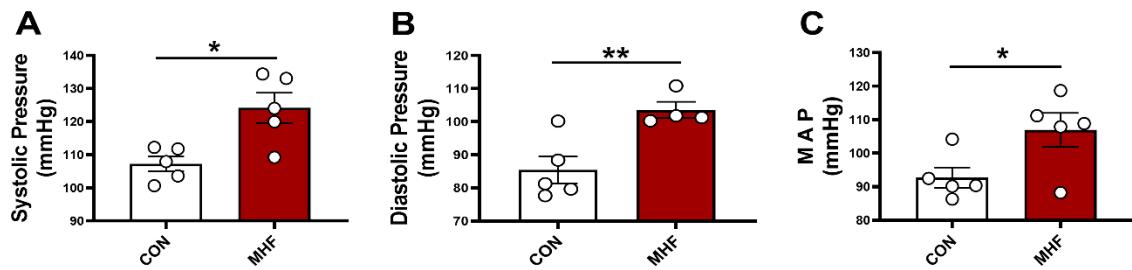
**Table S3.** The primers used in this study.

| qRT-PCR primers | Nucleotide Sequence (5'to 3') |
|---|---|
| | |

| | |
|---|---|
| Gapdh-Forward | AACGACCCCTTCATTGACCT |
| Gapdh-Reverse | CCCCATTTGATGTTAGCGGG |
| Agtr1a-Forward | CTTCTCAATCTCGCCTTGGC |
| Agtr1a-Reverse | AAGGAACACACTGGCGTAGA |
| Agtr1b-Forward | GGTTCAAAGCCTGCAAGTGA |
| Agtr1b-Reverse | CGGTTAACAGTGGCTTTGCT |
| Agtr2-Forward | TGGCTTCCCTTCCATGTTCT |
| Agtr2-Reverse | TCTCTCTCTTGCCTTGGAGC |
| Prkca-Forward | AATTCATCGCCCGCTTCTTC |
| Prkca-Reverse | CACAGAAGGTAGGGCTTCCA |
| Prkcb-Forward | GGGCATCATTTACCGTGACC |

| | |
|---|---|
| Prkcb-Reverse | GGGGCAATGTAGTCTGGAGT |
| Prkcd-Forward | CCACCTTCTGTTCTGTGTGC |
| Prkcd-Reverse | CCTTGAATCGGTGAGGCATG |
| Prkce-Forward | AGCCTCGTCGTCTACTGATG |
| Prkce-Reverse | ATCCTTACCCTTGAGCTCGG |
| **Bisulfite sequencing PCR** | **Nucleotide Sequence (5'to 3')** |
| *Agtr1a*-1-Forward | TTTGGATTTAGATGTGGTGATAAGG |
| *Agtr1a*-1-Reverse | AAAATACCTAACTACTAACCTCCAAACAA |
| *Agtr1a*-2-Forward | TAAAAGTAYGGAGGAAAATTGGTTTGT |

| | |
|---|---|
| *Agtr1a*-2-Reverse | CACCACATCTAAATCCAAAATACTAAAC |
| *Prkcb*-1-Forward | GGGGTTGTAAGTTYGGAGAGG |
| *Prkcb*-1-Reverse | TCCCTCCCCCRCAACTAAA |
| *Prkcb*-2-Forward | TTGTTTTGTYGAGGAGGGATAGTT |
| *Prkcb*-2-Reverse | CCAAATAACCAATCCCTCAAATAC |
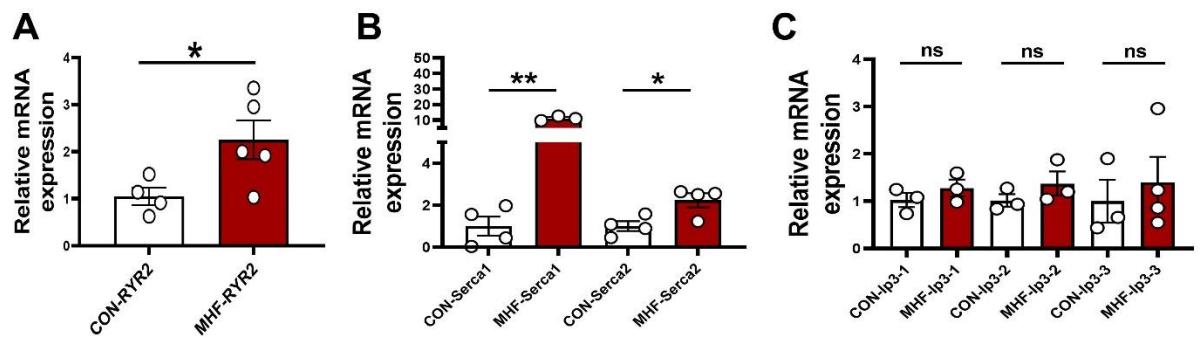


**Figure S1. Systolic pressure, diastolic pressure, and mean arterial pressure**
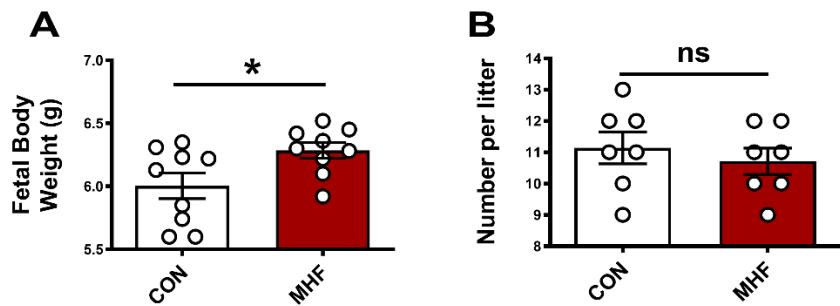
A-C, Systolic pressure, diastolic pressure, and mean arterial pressure (MAP) at

baseline level in the control (CON) and maternal high fat diets (MHF) groups (N=4-5).

N, number of adult male offspring from different litters of each group. Data were presented as mean±SEM and analyzed by Students-t test. * P < 0.05, ** P < 0.01
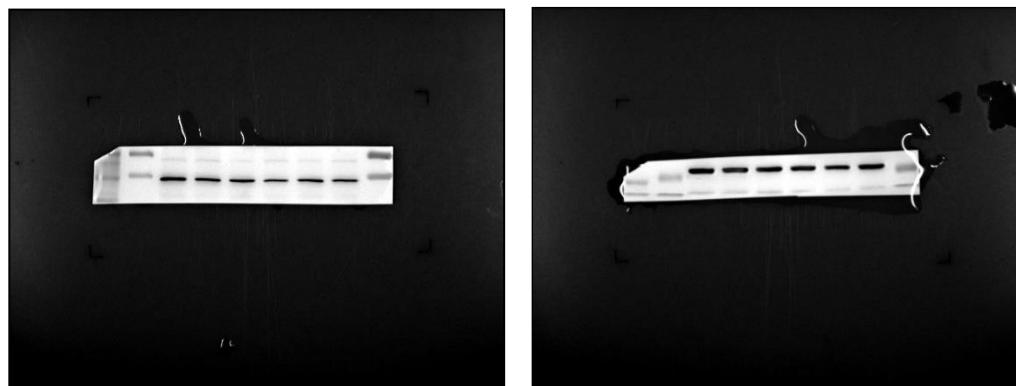


**Figure S2. mRNA analysis between the two groups**

A-C, Expressions of mRNA in RYR2 (a subtype of Ryanodine receptors), Serca1, Serca2, and IP3 subtype1-3 in adult offspring MA determined by qRT-PCR (N=3, n=3-5). N, number of adult male offspring from different litters of each group; n, number of MA rings. Data were presented as mean±SEM and analyzed by Students- t test. * P < 0.05, ** P < 0.01
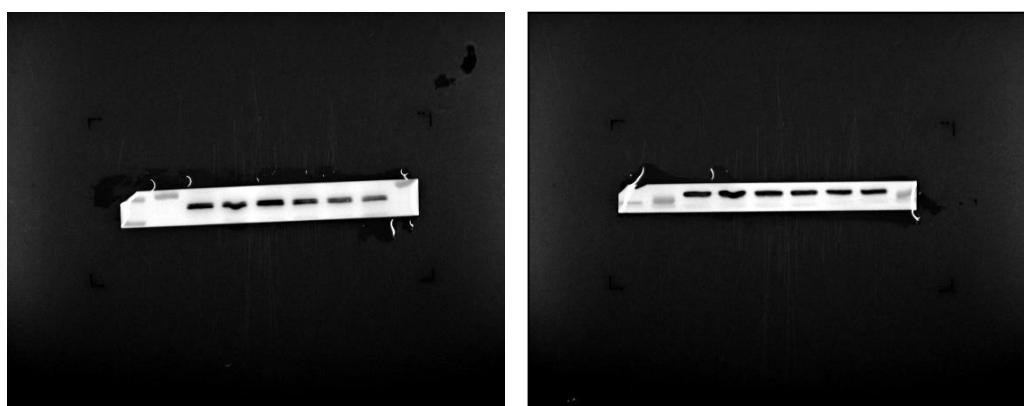
**Figure S3. Fetal weights and number per litter**

A, The effect of maternal normal diet and high fat diet on offspring fetal body weight (N=9 each group). B, Fetal number per litter (N=7 each group). N, number of adult male offspring from different litters of each group. Data were presented as mean ± SEM and analyzed by Student-t test. *P<0.05
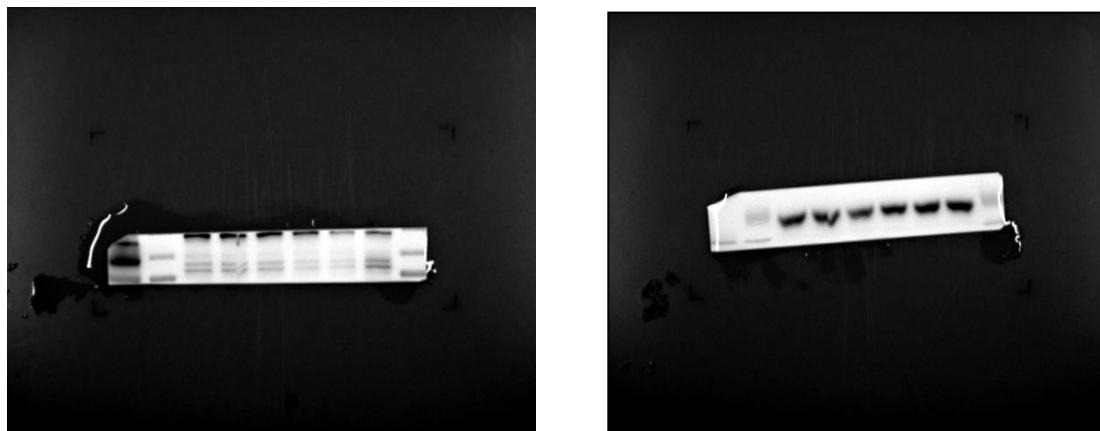


**Figure S4**

The representative protein images of AT1R (left) and Gapdh (right). The three bands on the left were the MHF group, three bands on the right were the CON group.



**Figure S5**

The representative protein images of AT2R (left) and Gapdh (right). The three bands on the left were the MHF group, three bands on the right were the CON group.
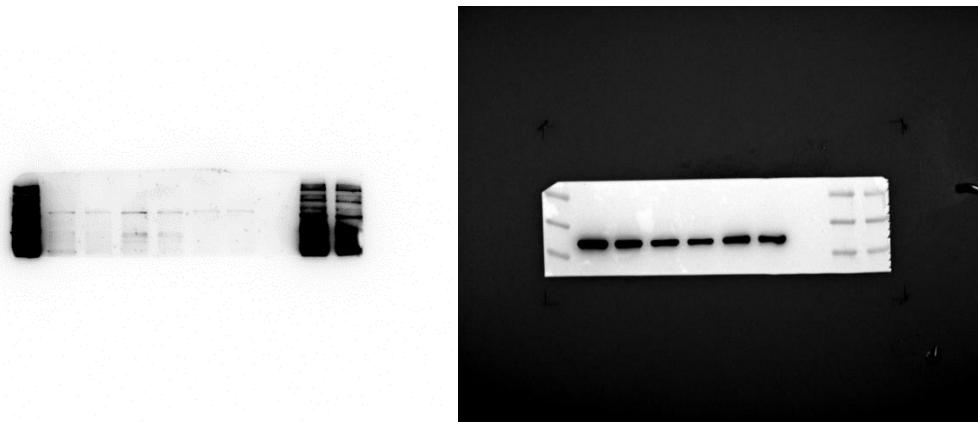






**Figure S6**

The representative protein images of PKCβ (upper left) and Gapdh (upper right and below). The three bands on the left were the MHF group, three bands on the right were the CON group.







**Figure S7**

The representative protein images of Cacna1c (left figure) and Gapdh (middle and right figures). The three bands on the left were the CON group, three bands on the right were the MHF group.



**Figure S8**
The representative protein images of PKCβ (cells of CON group) (right four bands) and Gapdh (right four bands). The two bands on the left were the vehicle group and the two bands on the right are the protein bands with losartan.



**Figure S9**
The representative protein images of PKCβ (cells of MHF group) (right four bands) and Gapdh (right four bands). The two bands on the left were the vehicle group and the two bands on the right are the protein bands with losartan.