Supplementary Figure 1

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                    *        20         *        40         *        60         *        80
PPARg1 :  ATGG--------------------------------------------------------------------------------- :    4
PPARg2 :  ATGGGTGAAACTCTGGGAGATTCTCCTGTTGACCCAGAGCATGGTGCCTTCGCTGATGCACTGCCTATGAGCACTTCACAAGAAA :   85
          ATGG

             *       100         *       120         *       140         *       160         *
PPARg1 :  --------TTGACACAGAGATGCCATTCTGGCCCACCAACTTCGGAATCAGCTCTGTGGACCTCTCCGTGATGGAAGACCACTC :   80
PPARg2 :  TTACCATGGTTGACACAGAGATGCCATTCTGGCCCACCAACTTCGGAATCAGCTCTGTGGACCTCTCCGTGATGGAAGACCACTC :  170
                  TTGACACAGAGATGCCATTCTGGCCCACCAACTTCGGAATCAGCTCTGTGGACCTCTCCGTGATGGAAGACCACTC

             180         *       200         *       220         *       240
PPARg1 :  GCATTCCTTTGACATCAAGCCCTTTACCACAGTTGATTTCTCCAGCATTTCTGCTCCACACTATGAAGACATTCCATTCACAAGA :  165
PPARg2 :  GCATTCCTTTGACATCAAGCCCTTTACCACAGTTGATTTCTCCAGCATTTCTGCTCCACACTATGAAGACATTCCATTCACAAGA :  255
          GCATTCCTTTGACATCAAGCCCTTTACCACAGTTGATTTCTCCAGCATTTCTGCTCCACACTATGAAGACATTCCATTCACAAGA

             260         *       280         *       300         *       320         *       340
PPARg1 :  GCTGACCCAATGGTTGCTGATTACAAATATGACCTGAAGCTCCAAGAATACCAAAGTGCGATCAAAGTAGAACCTGCATCTCCAC :  250
PPARg2 :  GCTGACCCAATGGTTGCTGATTACAAATATGACCTGAAGCTCCAAGAATACCAAAGTGCGATCAAAGTAGAACCTGCATCTCCAC :  340
          GCTGACCCAATGGTTGCTGATTACAAATATGACCTGAAGCTCCAAGAATACCAAAGTGCGATCAAAGTAGAACCTGCATCTCCAC

                   *       360         *       380         *       400         *       420
PPARg1 :  CTTATTATTCTGAAAAGACCCAGCTCTACAACAGGCCTCATGAAGAACCTTCTAACTCCCTCATGGCCATTGAGTGCCGAGTCTG :  335
PPARg2 :  CTTATTATTCTGAAAAGACCCAGCTCTACAACAGGCCTCATGAAGAACCTTCTAACTCCCTCATGGCCATTGAGTGCCGAGTCTG :  425
          CTTATTATTCTGAAAAGACCCAGCTCTACAACAGGCCTCATGAAGAACCTTCTAACTCCCTCATGGCCATTGAGTGCCGAGTCTG

                  *       440         *       460         *       480         *       500         *
PPARg1 :  TGGGGATAAAGCATCAGGCTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTTTTCCGAAGAACCATCCGATTGAAG :  420
PPARg2 :  TGGGGATAAAGCATCAGGCTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTTTTCCGAAGAACCATCCGATTGAAG :  510
          TGGGGATAAAGCATCAGGCTTCCACTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTTTTCCGAAGAACCATCCGATTGAAG

             520         *       540         *       560         *       580         *
PPARg1 :  CTTATTTATGATAGGTGTGATCTTAACTGCCGGATCCACAAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAGTGCC :  505
PPARg2 :  CTTATTTATGATAGGTGTGATCTTAACTGCCGGATCCACAAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAGTGCC :  595
          CTTATTTATGATAGGTGTGATCTTAACTGCCGGATCCACAAAAAAAGTAGAAATAAATGTCAGTACTGTCGGTTTCAGAAGTGCC

             600         *       620         *       640         *       660         *       680
PPARg1 :  TTGCTGTGGGGATGTCTCACAATGCCATCAGGTTTGGGCGGATGCCACAGGCCGAGAAGGAGAAGCTGTTGGCGGAGATCTCCAG :  590
PPARg2 :  TTGCTGTGGGGATGTCTCACAATGCCATCAGGTTTGGGCGGATGCCACAGGCCGAGAAGGAGAAGCTGTTGGCGGAGATCTCCAG :  680
          TTGCTGTGGGGATGTCTCACAATGCCATCAGGTTTGGGCGGATGCCACAGGCCGAGAAGGAGAAGCTGTTGGCGGAGATCTCCAG

                  *       700         *       720         *       740         *       760
PPARg1 :  TGATATCGACCAGCTGAACCCAGAGTCTGCTGATCTGCGAGCCCTGGCAAAGCATTTGTATGACTCATACATAAAGTCCTTCCCG :  675
PPARg2 :  TGATATCGACCAGCTGAACCCAGAGTCTGCTGATCTGCGAGCCCTGGCAAAGCATTTGTATGACTCATACATAAAGTCCTTCCCG :  765
          TGATATCGACCAGCTGAACCCAGAGTCTGCTGATCTGCGAGCCCTGGCAAAGCATTTGTATGACTCATACATAAAGTCCTTCCCG

                   *       780         *       800         *       820         *       840         *
PPARg1 :  CTGACCAAAGCCAAGGCGAGGGCGATCTTGACAGGAAAGACAACGGACAAATCACCATTTGTCATCTACGACATGAATTCCTTAA :  760
PPARg2 :  CTGACCAAAGCCAAGGCGAGGGCGATCTTGACAGGAAAGACAACGGACAAATCACCATTTGTCATCTACGACATGAATTCCTTAA :  850
          CTGACCAAAGCCAAGGCGAGGGCGATCTTGACAGGAAAGACAACGGACAAATCACCATTTGTCATCTACGACATGAATTCCTTAA

             860         *       880         *       900         *       920
PPARg1 :  TGATGGGAGAAGATAAAATCAAGTTCAAACATATCACCCCCCTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGAATTTTTCAAGG :  845
PPARg2 :  TGATGGGAGAAGATAAAATCAAGTTCAAACATATCACCCCCCTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGAATTTTTCAAGG :  935
          TGATGGGAGAAGATAAAATCAAGTTCAAACATATCACCCCCCTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGAATTTTTCAAGG

          940         *       960         *       980         *      1000         *      1020
PPARg1 :  GTGCCAGTTTCGATCCGTAGAAGCCGTGCAAGAGATCACAGAGTATGCCAAAAATATCCCTGGTTTCATTAACCTTGATTTGAAT :  930
PPARg2 :  GTGCCAGTTTCGATCCGTAGAAGCCGTGCAAGAGATCACAGAGTATGCCAAAAATATCCCTGGTTTCATTAACCTTGATTTGAAT : 1020
          GTGCCAGTTTCGATCCGTAGAAGCCGTGCAAGAGATCACAGAGTATGCCAAAAATATCCCTGGTTTCATTAACCTTGATTTGAAT

                  *      1040         *      1060         *      1080         *      1100
PPARg1 :  GACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGAATAAAGATGGAGTCCTCA : 1015
PPARg2 :  GACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGAATAAAGATGGAGTCCTCA : 1105
          GACCAAGTGACTCTGCTCAAGTATGGTGTCCATGAGATCATCTACACGATGCTGGCCTCCCTGATGAATAAAGATGGAGTCCTCA

                   *      1120         *      1140         *      1160         *      1180         *
PPARg1 :  TCTCAGAGGGCCAAGGATTCATGACCAGGGGAGTTCCTCAAAAGCCTGCGGAAGCCCTTTGGTGACTTTATGGAGCCTAAGTTTGA : 1100
PPARg2 :  TCTCAGAGGGCCAAGGATTCATGACCAGGGGAGTTCCTCAAAAGCCTGCGGAAGCCCTTTGGTGACTTTATGGAGCCTAAGTTTGA : 1190
          TCTCAGAGGGCCAAGGATTCATGACCAGGGGAGTTCCTCAAAAGCCTGCGGAAGCCCTTTGGTGACTTTATGGAGCCTAAGTTTGA

             1200         *      1220         *      1240         *      1260         *
PPARg1 :  GTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAGTGACTTGGCTATATTTATAGCTGTCATTATTCTCAGTGGAGACCGC : 1185
PPARg2 :  GTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAGTGACTTGGCTATATTTATAGCTGTCATTATTCTCAGTGGAGACCGC : 1275
          GTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAGTGACTTGGCTATATTTATAGCTGTCATTATTCTCAGTGGAGACCGC

          1280         *      1300         *      1320         *      1340         *      1360
PPARg1 :  CCAGGCTTGCTGAACGTGAAGCCCATCGAGGACATCCAAGACAACCTGCTGCAGGCCCTGGAACTGCAGCTCAAGCTGAATCACC : 1270
PPARg2 :  CCAGGCTTGCTGAACGTGAAGCCCATCGAGGACATCCAAGACAACCTGCTGCAGGCCCTGGAACTGCAGCTCAAGCTGAATCACC : 1360
          CCAGGCTTGCTGAACGTGAAGCCCATCGAGGACATCCAAGACAACCTGCTGCAGGCCCTGGAACTGCAGCTCAAGCTGAATCACC

                  *      1380         *      1400         *      1420         *      1440
PPARg1 :  CAGAGTCCTCTCAGCTGTTCGCCAAGGTGCTCCAGAAGATGACAGACCTCAGGCAGATCGTCACAGAGCACGTGCAGCTACTGCA : 1355
PPARg2 :  CAGAGTCCTCTCAGCTGTTCGCCAAGGTGCTCCAGAAGATGACAGACCTCAGGCAGATCGTCACAGAGCACGTGCAGCTACTGCA : 1445
          CAGAGTCCTCTCAGCTGTTCGCCAAGGTGCTCCAGAAGATGACAGACCTCAGGCAGATCGTCACAGAGCACGTGCAGCTACTGCA

                  *      1460         *      1480         *      1500         *
PPARg1 :  TGTGATCAAGAAGACAGAGACAGACATGAGCCTTCACCCCCTGCTCCAGGAGATCTACAAGGACTTGTATTAG : 1428
PPARg2 :  TGTGATCAAGAAGACAGAGACAGACATGAGCCTTCACCCCCTGCTCCAGGAGATCTACAAGGACTTGTATTAG : 1518
          TGTGATCAAGAAGACAGAGACAGACATGAGCCTTCACCCCCTGCTCCAGGAGATCTACAAGGACTTGTATTAG
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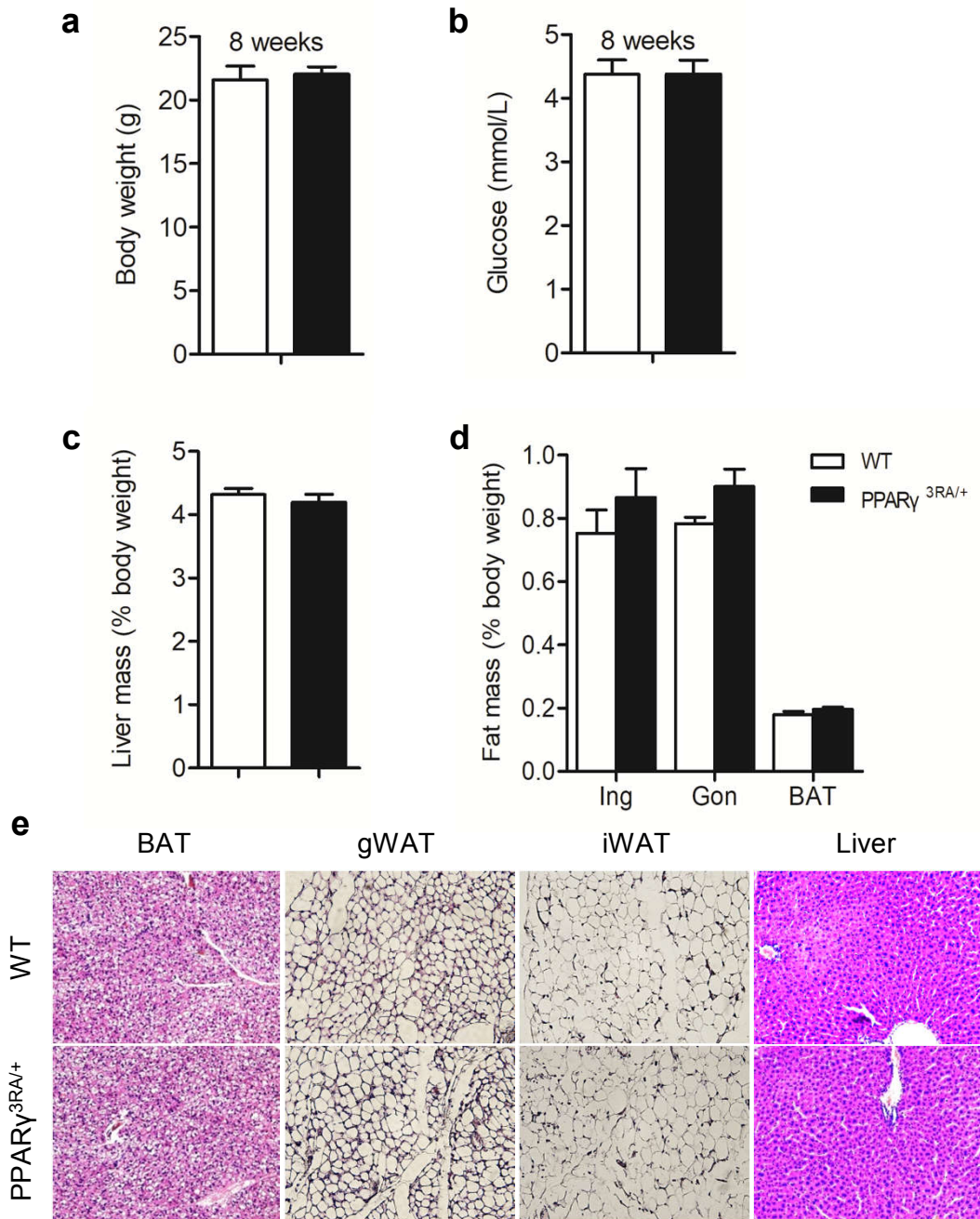
Supplementary Figure 1. The alignment of the CDS sequences of PPARγ1 (Genbank# NM_001127330.2) and PPARγ2 (Genbank# NM_011146.3).
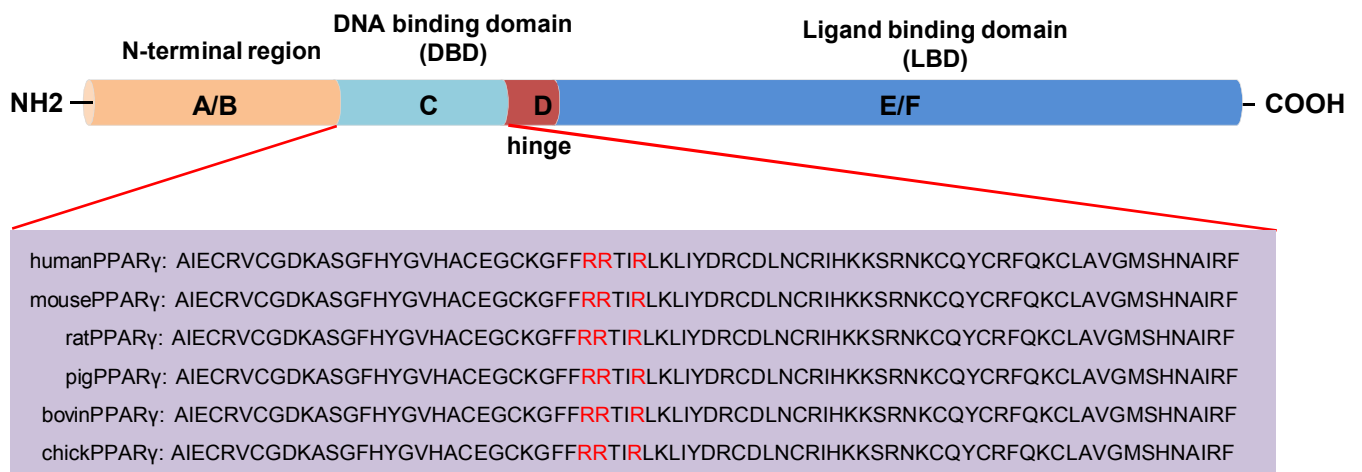
Supplementary Figure 2

Supplementary Figure 2. Phenotype of PPARγ3RA/+ and wild type (WT) littermates under chow diet. Male mice were fed with normal chow diet to 8 weeks old. (a) Body weight. (b) Fasting blood glucose level. (c) Liver/body weight ratio. (d) Fat/body weight ratio. (e) Representative H&E staining of the brown adipose tissue (BAT), gonadal white fat (gWAT), inguinal white fat (iWAT) and liver sections. n=12 per group. Students t-test. A P-value less than or equal to 0.05 is considered statistically significant.

Supplementary Figure 3
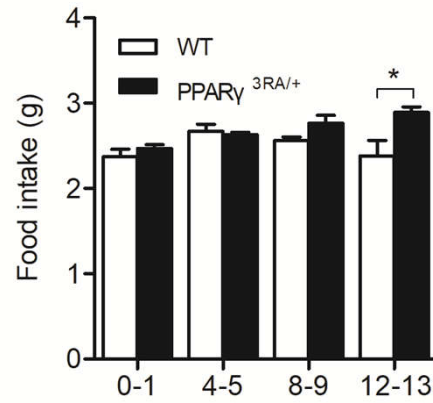
Supplementary Figure 3. Food intake of mice. After fed with chow diet to 8-week old, PPARγ[3RA/+] and wild type (WT) littermates were put to HFD for 15 weeks. The figure showed the HFD food intake of mice at different time course. n=12 per group. Students t-test. *P<0.05.

Supplementary Figure 4

Supplementary Figure 4. Alignment of PPARγ DBD sequence in different species. Domains of nuclear receptors were shown. The mutated three arginine (R) residues were highlighted in red.

Supplementary Table 1. Sequences of the primers for qPCR.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')
β-actin	TACAGCTTCACCACCACAGC	TCTCCAGGGAGGAAGAGGAT
PEPCK	CTCACTGACTCGGCTTACG	CCACTGAATGCAGACACTT
AQP7	TCGGTGTCAACTTGGGTTTTG	CCAGGTCATTCGGCCTAGTG
AP2	AAGGTGAAGAGCATCATAACCCT	TCACGCCTTTCATAACACATTCC
SCD1	ACCTGCCTCTTCGGGATTTT	GTCGGCGTGTGTTTCTGAGA
LPL	TGAAAGTGGGTTTTCCTGAGTAT	GGTTAGCCACCGTTTAATATTTG
GLUT4	CCTTCTATTTGCCGTCCTCC	TGGCCCTAAGTATTCAAGTTCTG
CPT1b	TCTTCTTCCGACAAACCCTGA	GAGACGGACACAGATAGCCC
CD36	CCTCTTCCCGTCAGACTTGTG	TCGGAGGTGTTGGCTAGTATTT